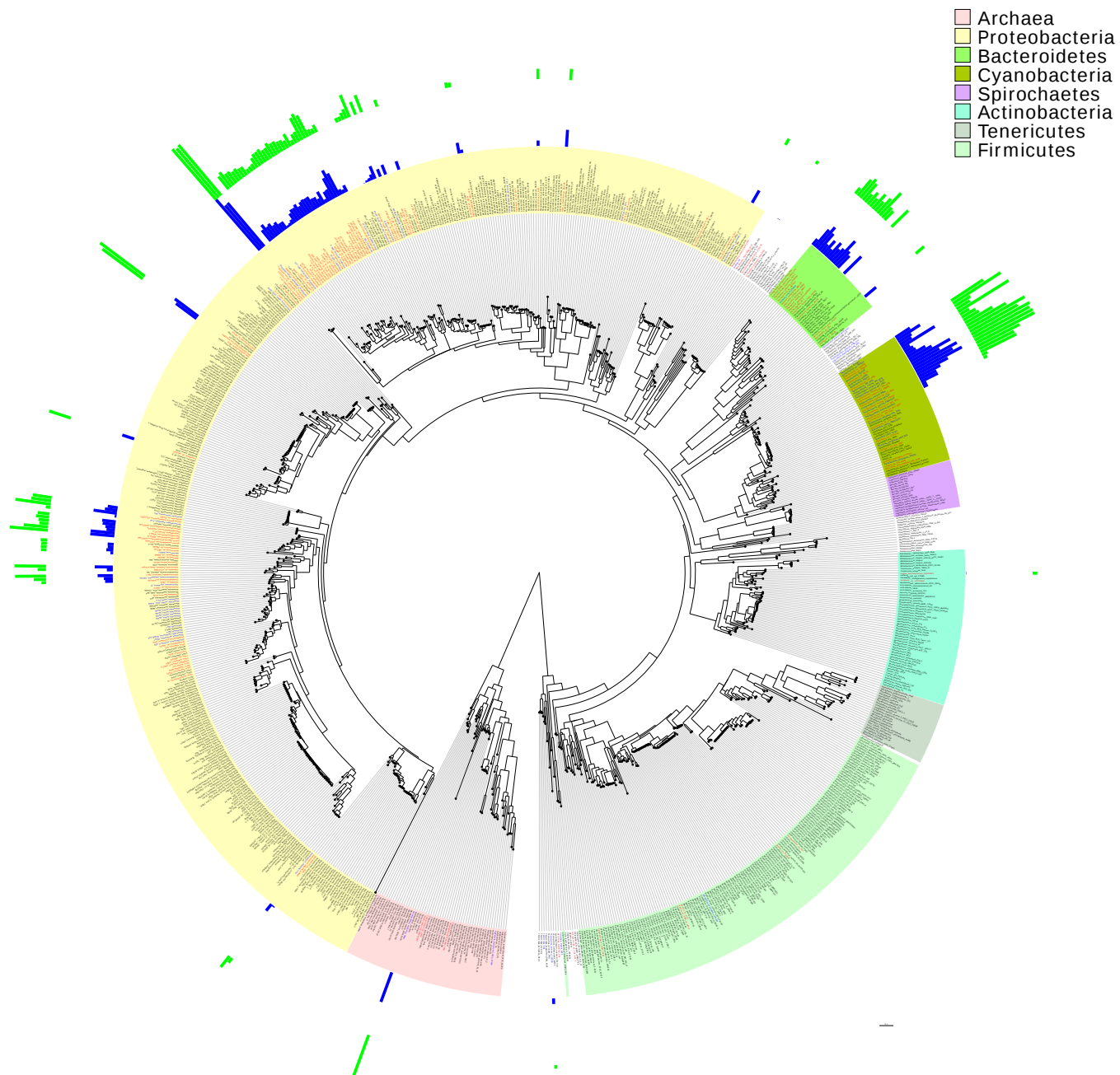


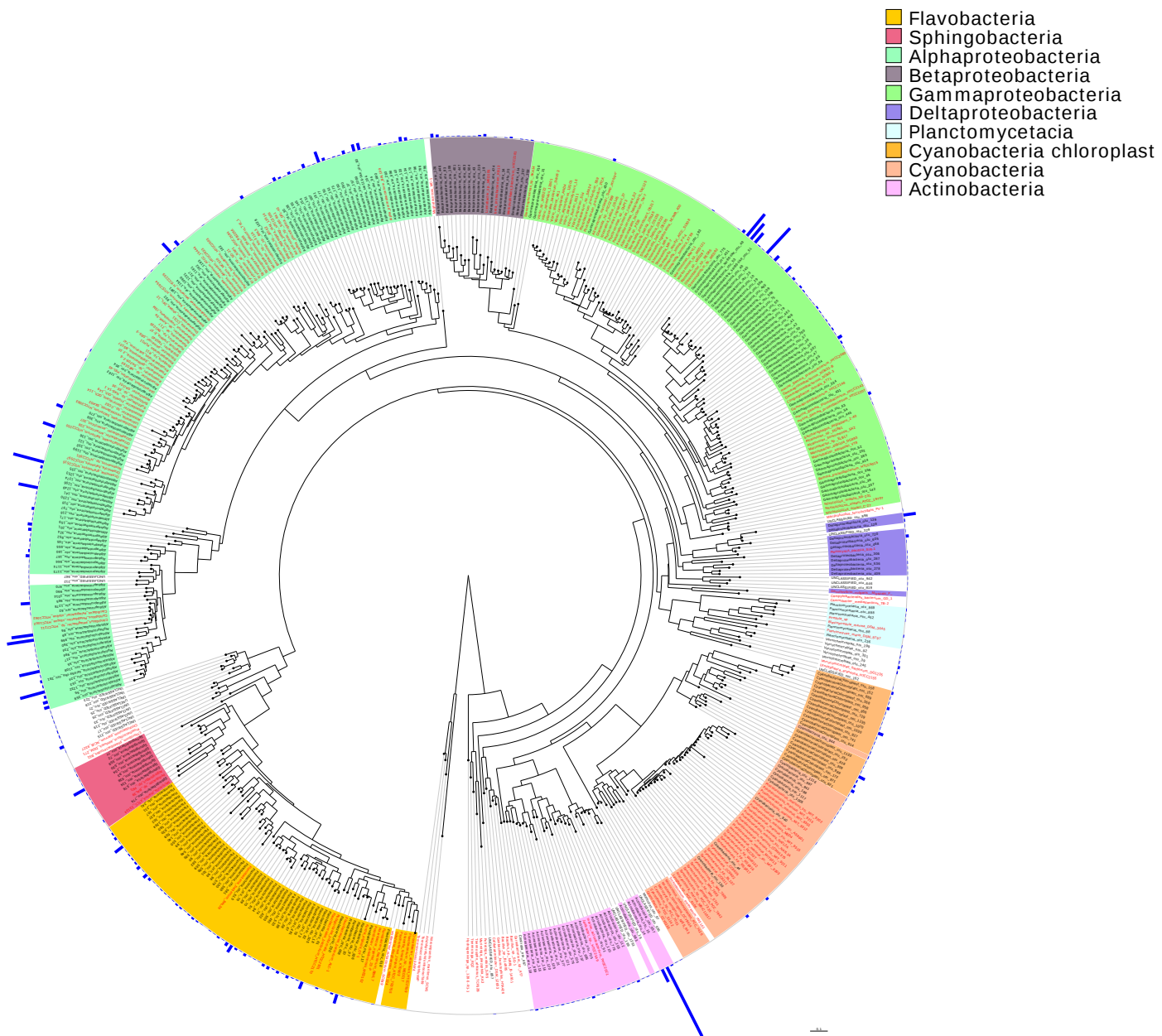
(SF1)

Taxonomic representation of sequenced marine genomes and their abundance in the GOS data. A maximum likelihood phylogeny was constructed using 16S sequences from all sequenced bacterial and archaeal genomes. Archaea and major groups of bacteria are highlighted. The 137 MMGSP genomes are highlighted in red text and the other 60 marine genomes are highlighted in blue text. Blue histograms denote depth of coverage (log scale) and green histograms denote the fraction of genome covered at the 50% match identity threshold. Histograms are shown only for those genomes that have depth of coverage ≥ 0.1 and have $\geq 5\%$ of their length covered.



(SF2)

Maximum likelihood phylogeny of 16S sequences from sequenced genomes and representative 16S sequences of uncultured OTUs. The 197 sequenced marine genomes are denoted in red text. Abundant bacterial classes seen in this analysis are also highlighted. An OTU was assigned to a taxonomic class if all, or a subset, of its sequences were consistently assigned to that class using RDP classifier. Otherwise, it was left as unclassified. In every case, an unclassified OTU had no sequence that had a class level assignment using RDP. However, the classifications of such OTUs can be inferred from the phylogeny. The histograms show the number of RDP and GOS sequences in each OTU. Archaeal 16S sequences were used to root the phylogeny.



(SF3)

The figures shown here relate to the analysis presented in the section *Genomic and functional characterization*.

Page 7 (of this document):

Top left and top right plots - Genome size (as measured by number of proteins in the genome) versus depth of coverage (based on GOS fragment recruitment). The trend lines are shown in blue. **Top left** - Distribution of the (logarithm of) genome size (Y-axis) of the genomes that have been ranked based on their depth of coverage (X-axis). **Top right** - Wilcoxon rank sum based p-values as a function of (logarithm of) the depth of coverage. Negative logarithms of the p-values are shown. Thus, the optimal (smallest) p-value appears as the largest value in the negative logarithm plot.

Bottom left and bottom right plots - %GC of genomes versus depth of coverage; same format as figures at the top.

Pages 8-577 (of this document) show results for protein functional categories. Only those functional categories that are identified as being differentially distributed in the HG and LG sets in both original and normalized data are shown here. Recall that the HG and LG sets were defined using depth of coverage ≥ 1 and < 1 , respectively; this coverage value was selected on the basis that a large number of the functional categories had an optimal Wilcoxon rank sum based p-value at coverage = 1 (Bottom right figures on these pages). The pages 3-572 are organized in groups, respectively, as COGs, HMMs, proteases, KEGG modules, KEGG pathways, and CRISPR systems (#genes and #arrays). Each page (denoting a functional category) has four figures. The legend for each of these pages is as follows:

Top left - Distribution of the number of proteins in this category (Y-axis) in the genomes that have been ranked based on their depth of coverage (X-axis).

Top right - Distribution of normalized (using genome size) number of proteins in the genomes that have been ranked based on their depth of coverage.

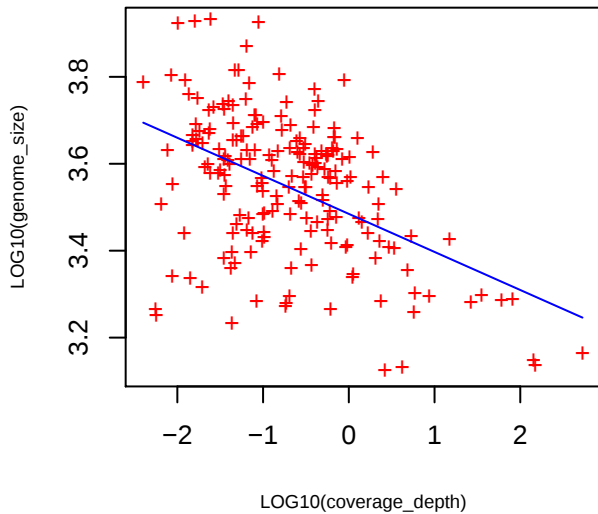
Bottom left - Log-Log plot of genome size versus number of proteins in this category.

Trend lines are shown in blue for the top left, top right, and bottom left figures; the statistics (slope, intercept, and p-values) associated with each trend line are shown above the corresponding figure.

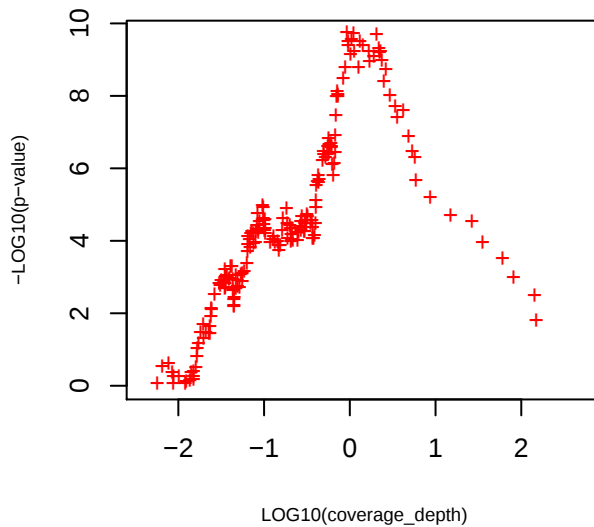
Bottom right - Wilcoxon rank sum based p-values as a function of (logarithm of) the depth of coverage. Negative logarithms of the p-values are shown; thus, the optimal (smallest) p-value appears as the largest value in the negative logarithm plot. Red denotes p-values for original data and green denotes p-values for normalized data.

Coverage vs Genome size

slope= -0.088 p_value= 9.1e-13 intercept= 3.48 p_value= 9e-253

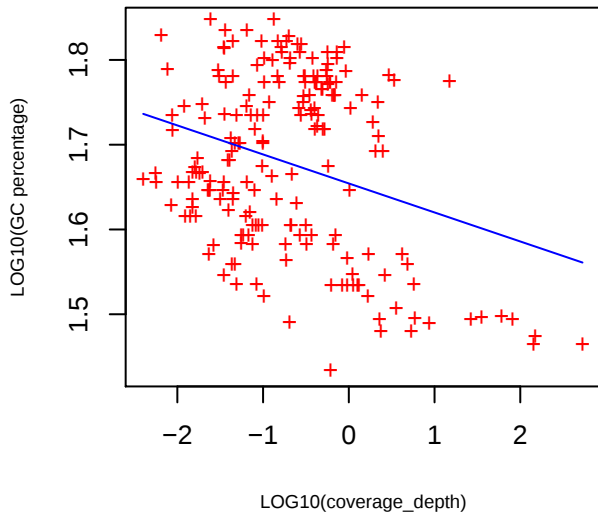


P-value curve

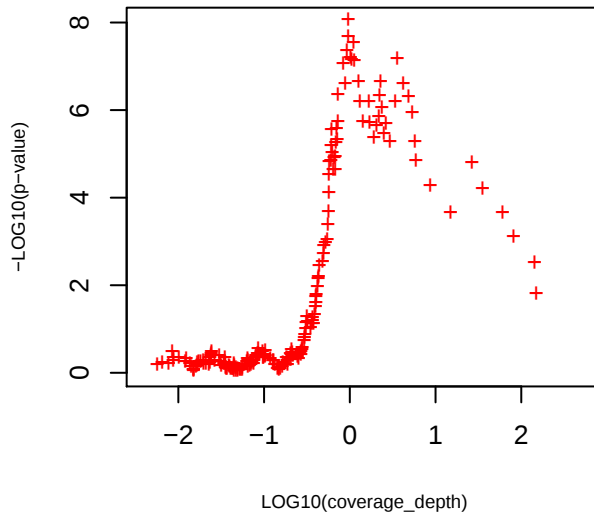


Coverage vs GC

slope= -0.034 p_value= 2.5e-05 intercept= 1.65 p_value= 5.8e-221

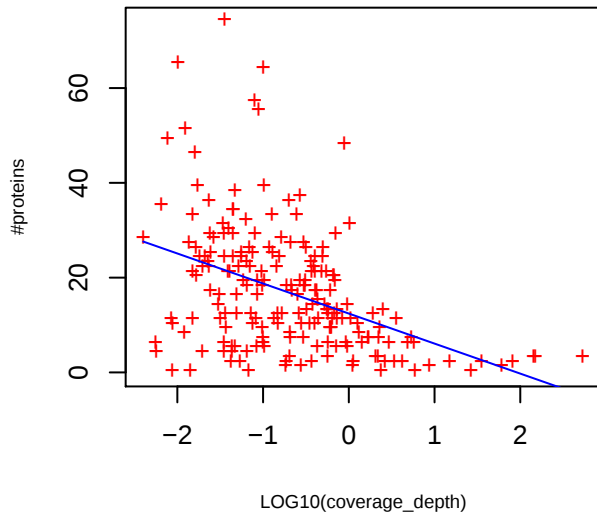


P-value curve



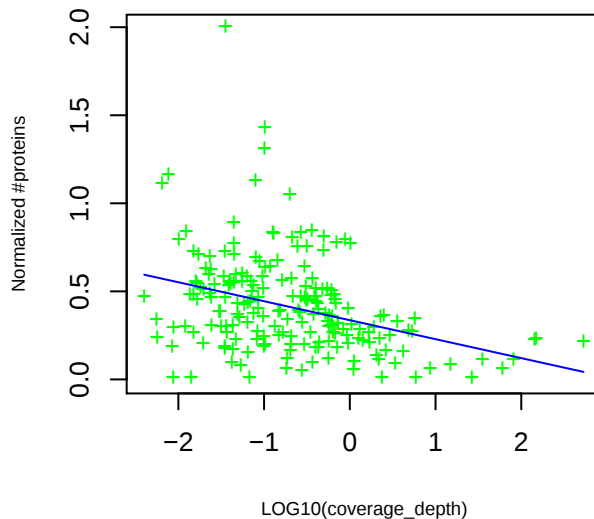
[T] COG0642 Signal transduction histidine kinase

slope= -6.34 p_value= 4.9e-10 intercept= 12.42 p_value= 2.5e-23



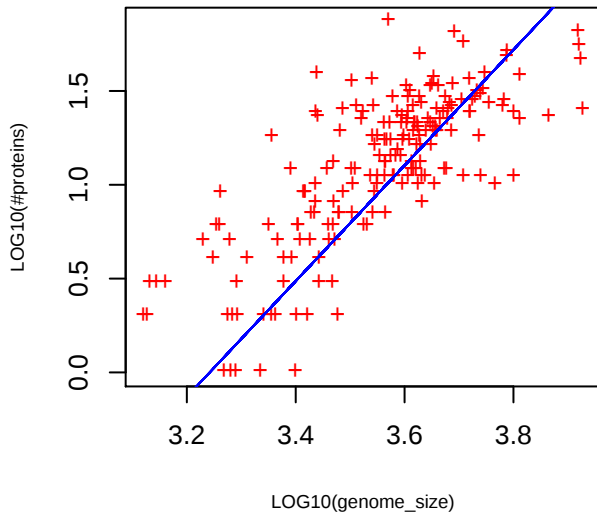
[T] COG0642 Signal transduction histidine kinase

slope= -0.11 p_value= 5.3e-07 intercept= 0.34 p_value= 2.4e-32

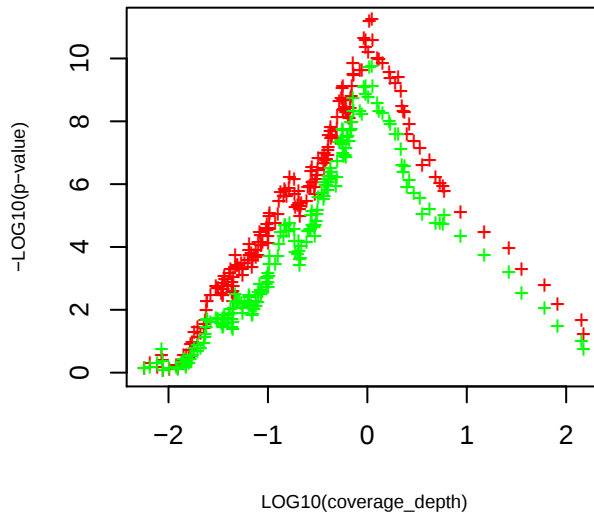


[T] COG0642 Signal transduction histidine kinase

slope= 3.08 p_value= 3.8e-15 intercept= -9.99 p_value= 3.7e-13

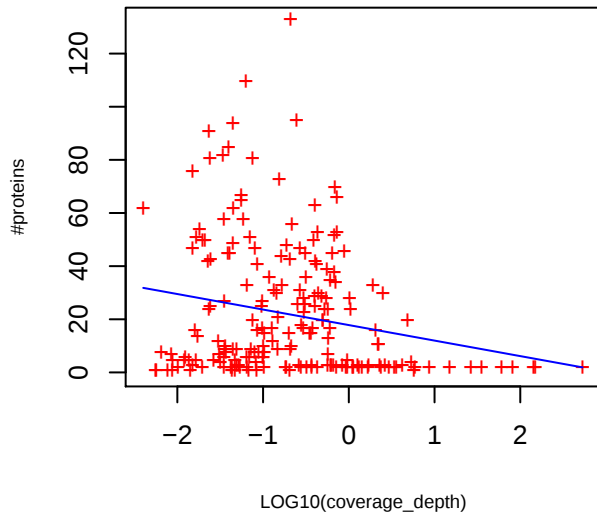


P-value curve ; red (unnorm), green (norm)



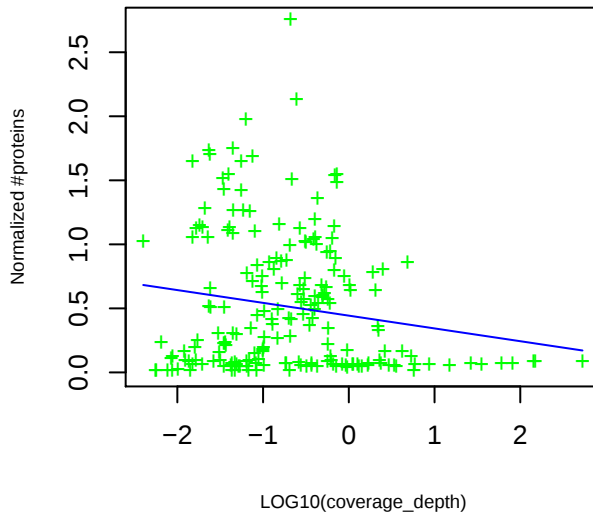
[K] COG0583 Transcriptional regulator

slope= -5.84 p_value= 0.0035 intercept= 17.82 p_value= 1.1e-13



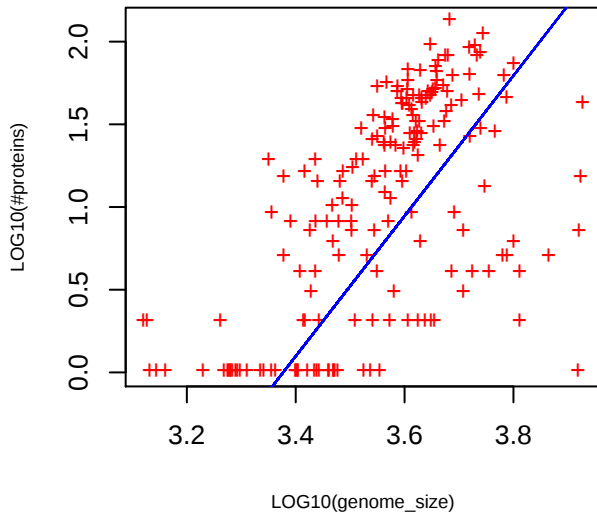
[K] COG0583 Transcriptional regulator

slope= -0.10 p_value= 0.018 intercept= 0.44 p_value= 1.8e-17

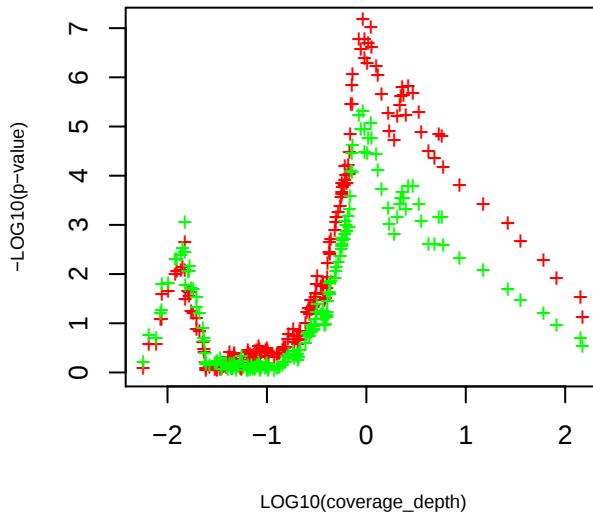


[K] COG0583 Transcriptional regulator

slope= 4.24 p_value= 2.3e-15 intercept= -14.32 p_value= 3.2e-14

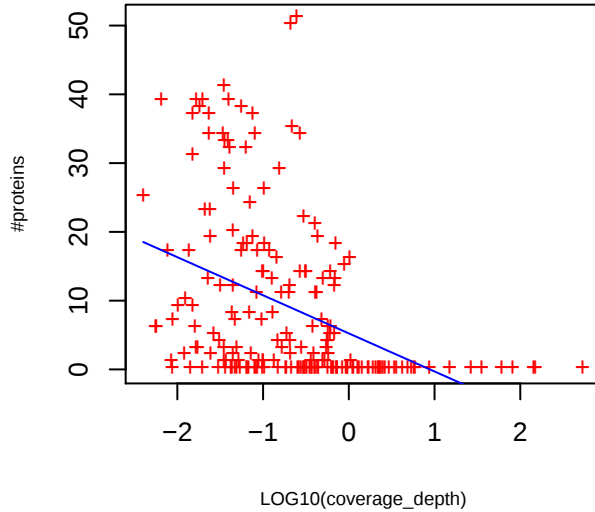


P-value curve ; red (unnorm), green (norm)



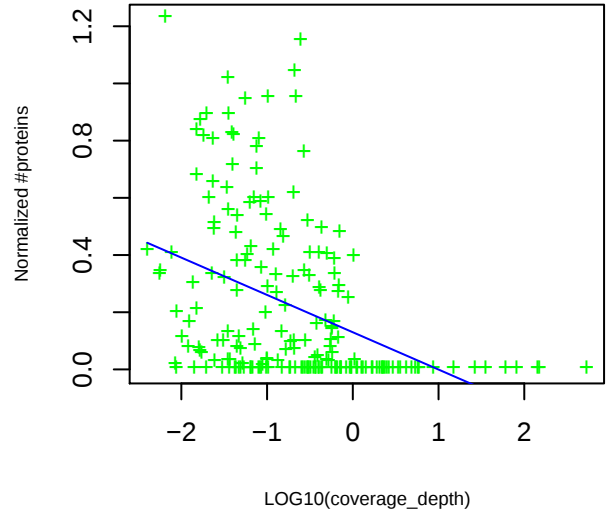
[NT] COG0840 Methyl-accepting chemotaxis protein

slope= -5.54 p_value= 5.5e-09 intercept= 5.24 p_value= 7.7e-07



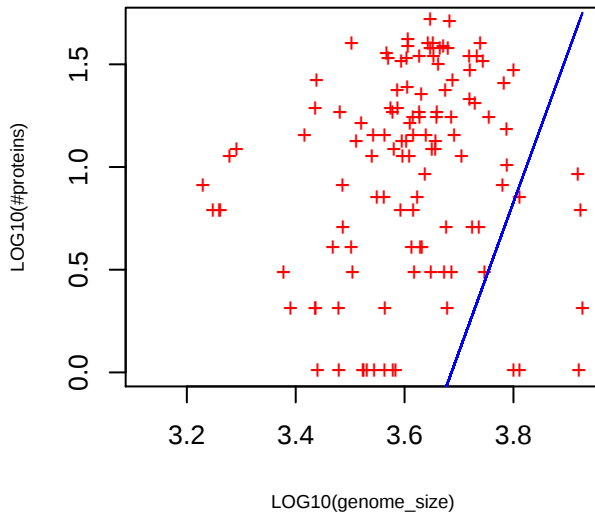
[NT] COG0840 Methyl-accepting chemotaxis protein

slope= -0.13 p_value= 6.9e-09 intercept= 0.13 p_value= 2.5e-07

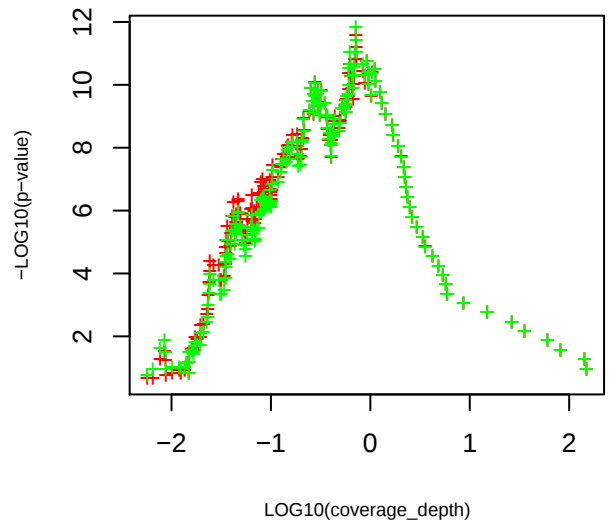


[NT] COG0840 Methyl-accepting chemotaxis protein

slope= 7.28 p_value= 9.2e-13 intercept= -26.82 p_value= 1.5e-13

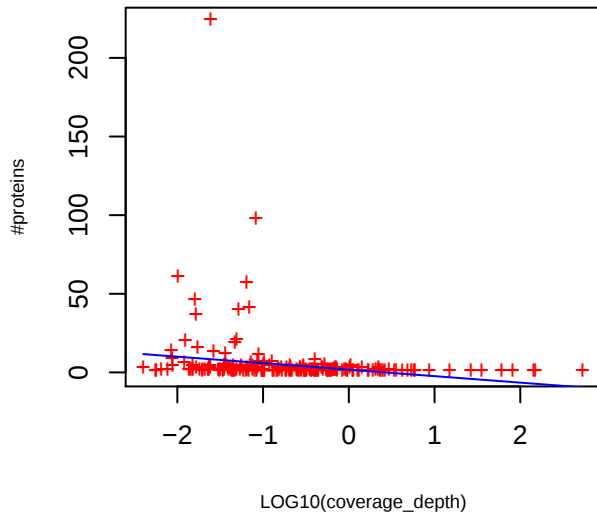


P-value curve ; red (unnorm), green (norm)



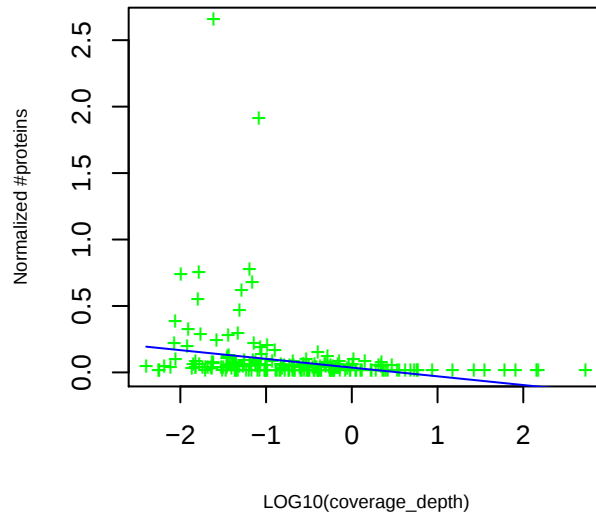
[RTKL] COG0515 Serine/threonine protein kinase

slope= -4.12 p_value= 0.0062 intercept= 1.76 p_value= 0.30



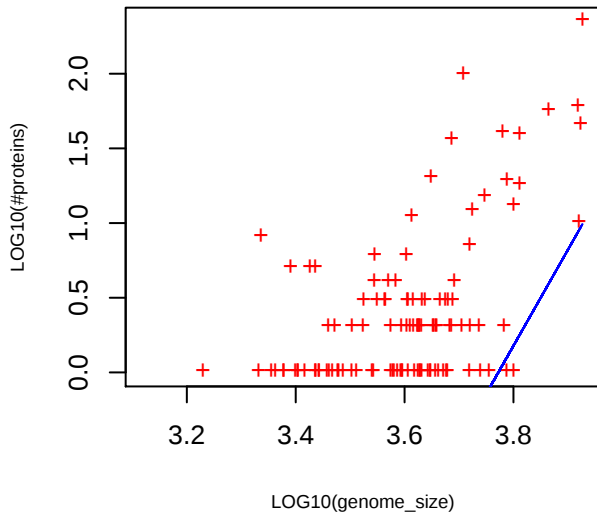
[RTKL] COG0515 Serine/threonine protein kinase

slope= -0.066 p_value= 0.0014 intercept= 0.036 p_value= 0.11

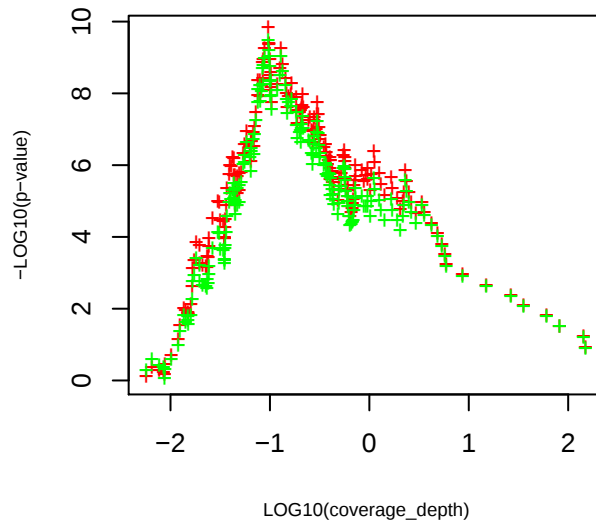


[RTKL] COG0515 Serine/threonine protein kinase

slope= 6.42 p_value= 2.0e-12 intercept= -24.24 p_value= 1.1e-13

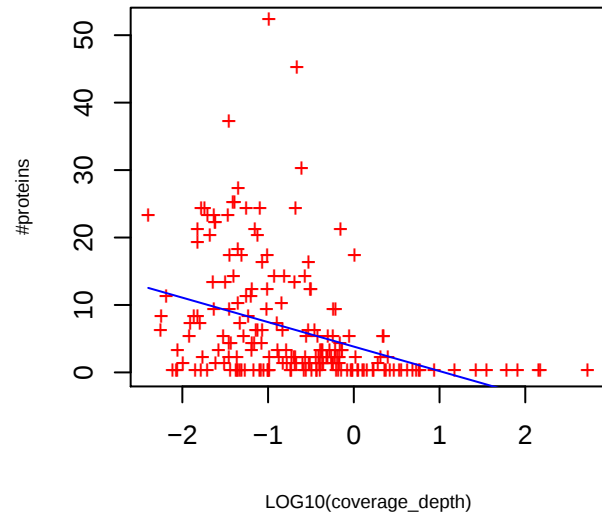


P-value curve ; red (unnorm), green (norm)



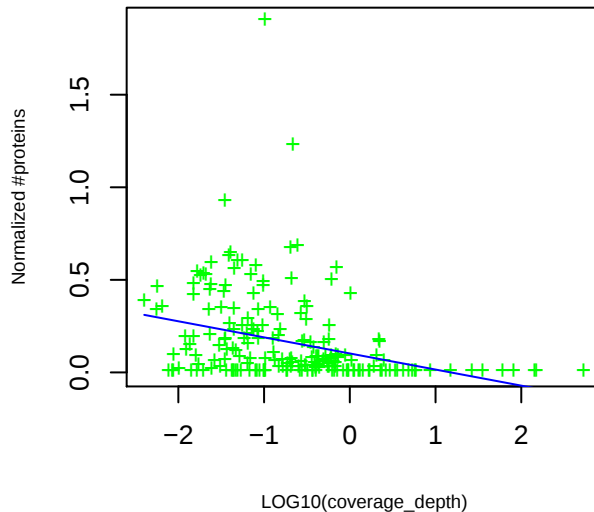
[T] COG2199 FOG: GGDEF domain

slope= -3.63 p_value= 1.5e-07 intercept= 3.83 p_value= 8.2e-07



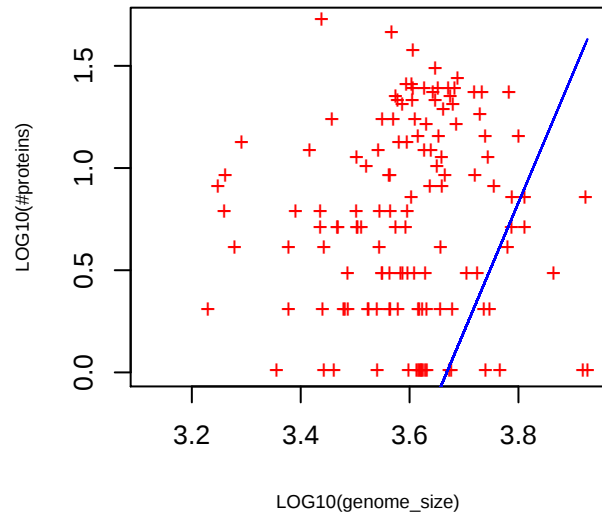
[T] COG2199 FOG: GGDEF domain

slope= -0.087 p_value= 3.3e-06 intercept= 0.10 p_value= 1.3e-06

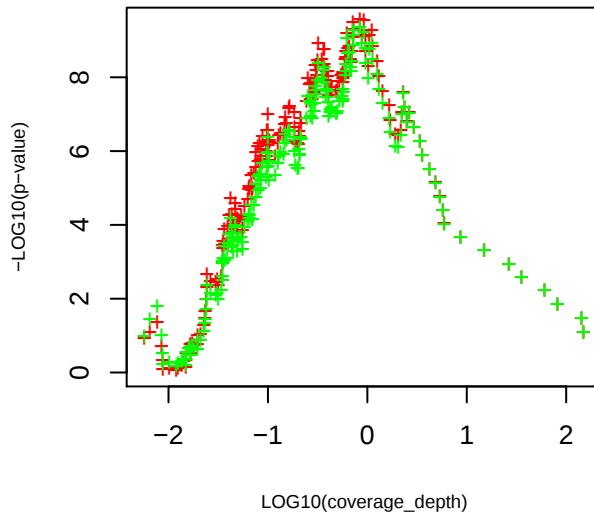


[T] COG2199 FOG: GGDEF domain

slope= 6.31 p_value= 1.4e-11 intercept= -23.15 p_value= 3.5e-12

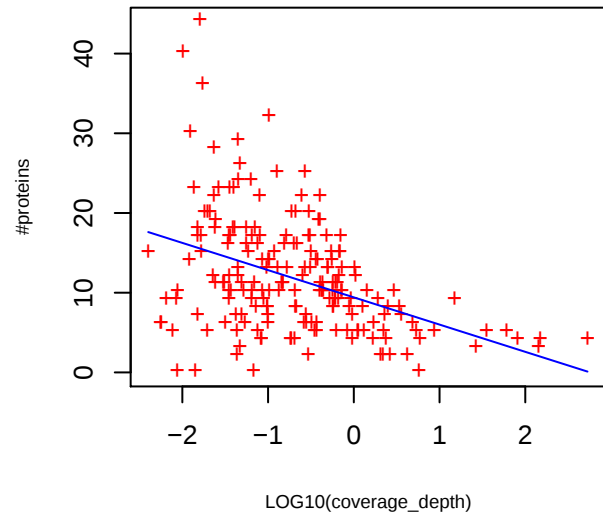


P-value curve ; red (unnorm), green (norm)

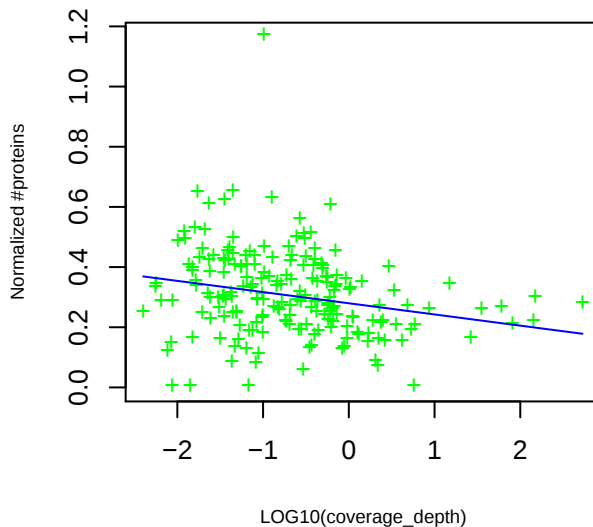


KJ COG0745 Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-bin

slope= -3.42 p_value= 1.1e-09 intercept= 9.42 p_value= 2.8e-36

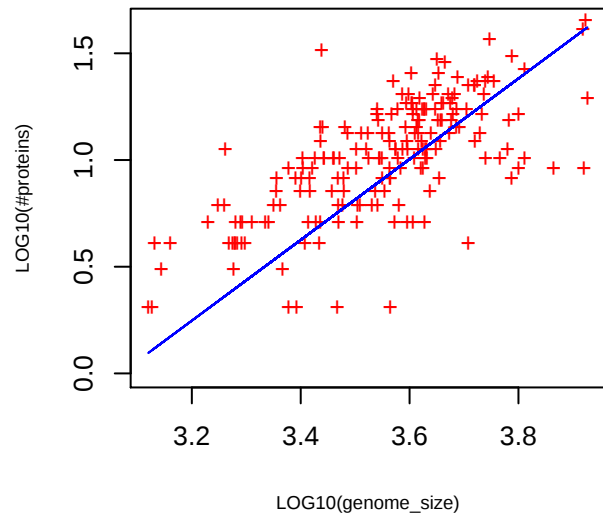


slope= -0.037 p_value= 0.00092 intercept= 0.28 p_value= 7.3e-56

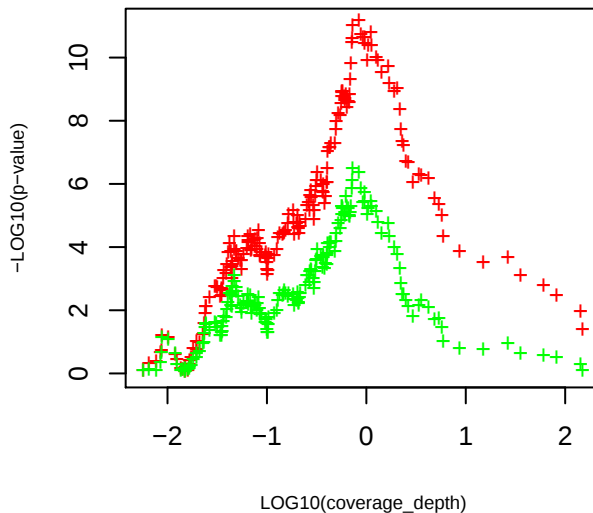


KJ COG0745 Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-bin

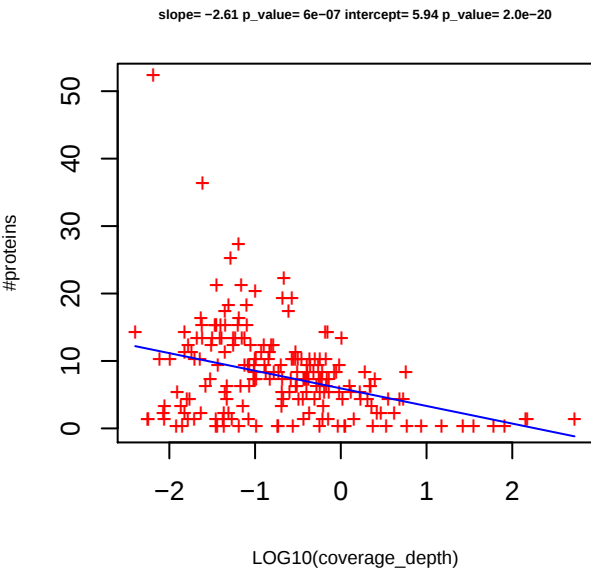
slope= 1.89 p_value= 2.9e-09 intercept= -5.80 p_value= 2.1e-07



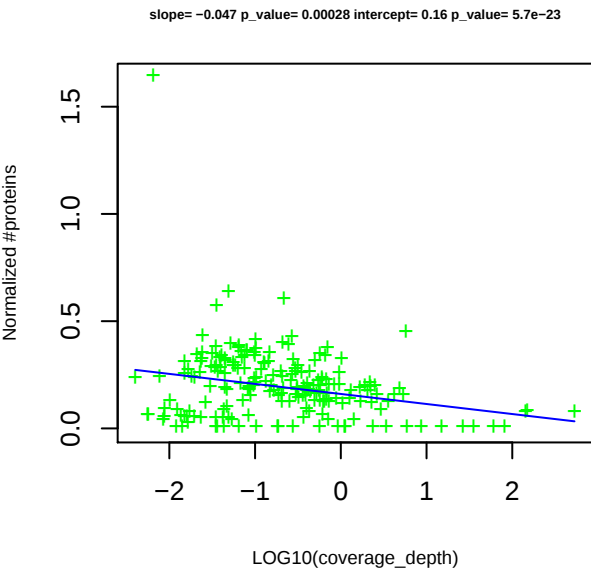
P-value curve ; red (unnorm), green (norm)



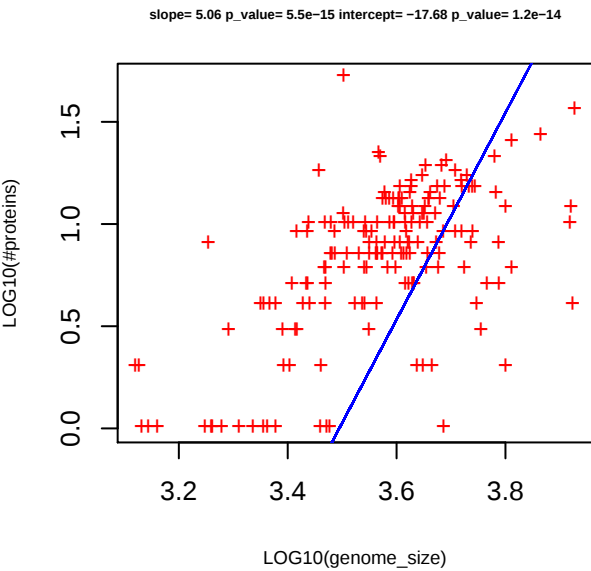
[T] COG2204 Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding c



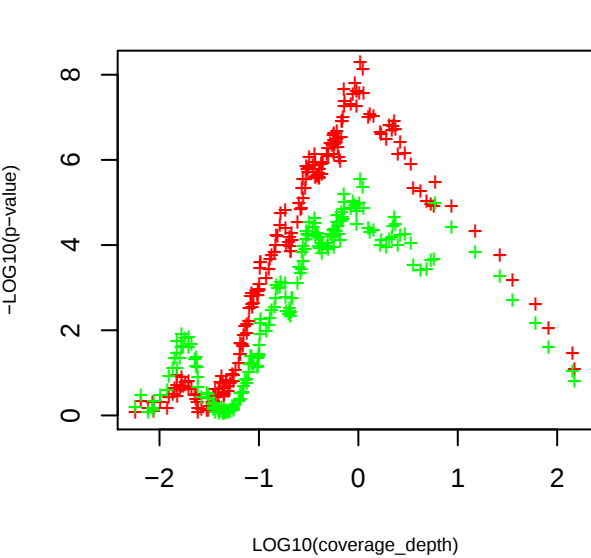
[T] COG2204 Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding c



[T] COG2204 Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding c

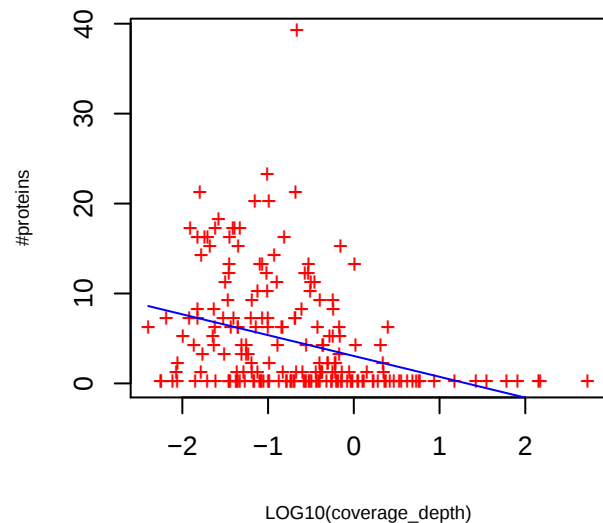


P-value curve ; red (unnorm), green (norm)

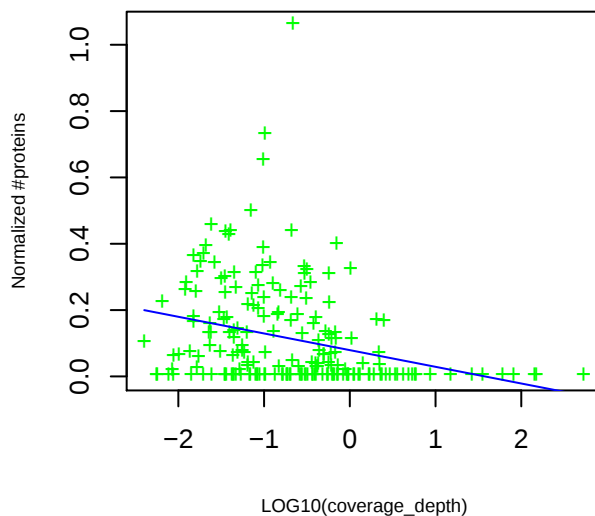


[T] COG5001 Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF [T] COG5001 Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF

slope= -2.32 p_value= 2.0e-06 intercept= 3.05 p_value= 4.1e-08

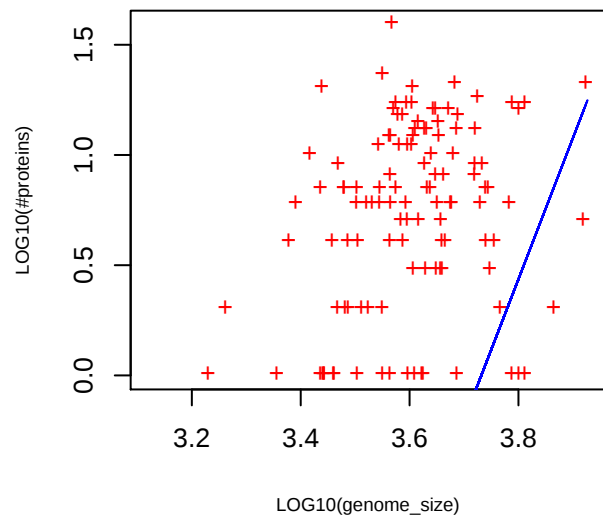


slope= -0.05 p_value= 3.9e-05 intercept= 0.08 p_value= 1.8e-08

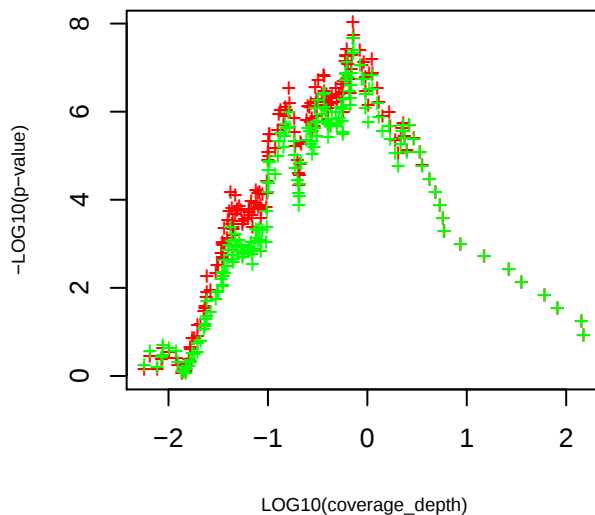


[T] COG5001 Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF

slope= 6.40 p_value= 6.2e-11 intercept= -23.89 p_value= 8e-12

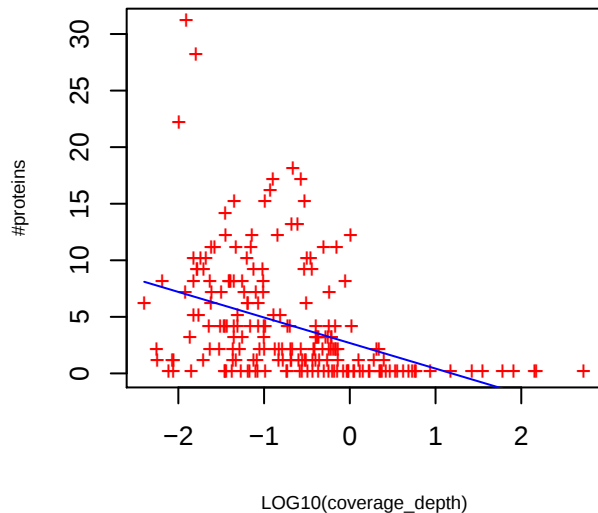


P-value curve ; red (unnorm), green (norm)



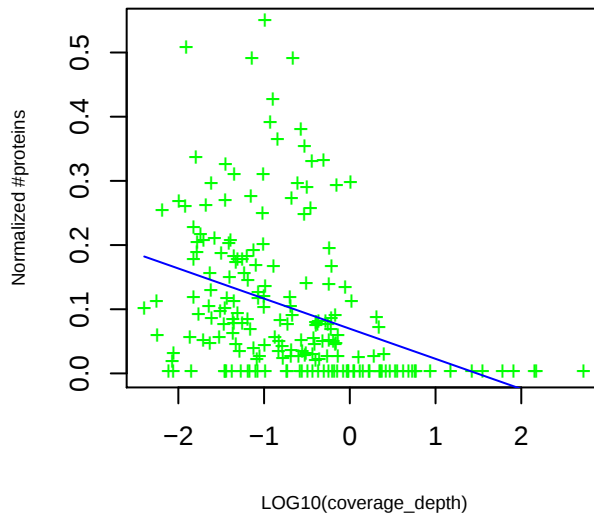
[T] COG3706 Response regulator containing a CheY-like receiver domain and a GGDEF domain

slope= -2.26 p_value= 1.9e-08 intercept= 2.69 p_value= 3.8e-09



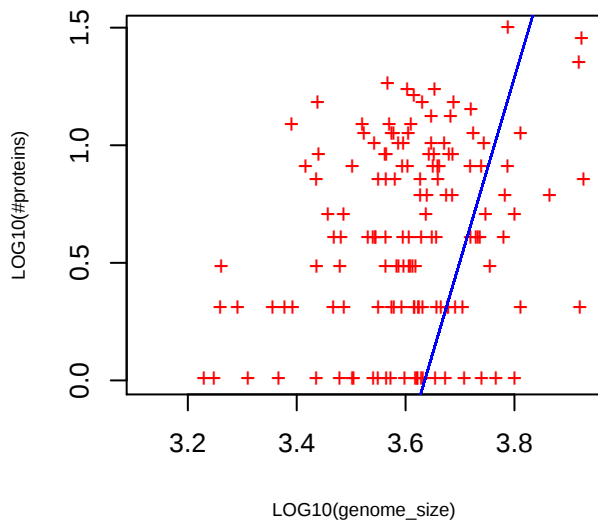
[T] COG3706 Response regulator containing a CheY-like receiver domain and a GGDEF domain

slope= -0.047 p_value= 2.9e-07 intercept= 0.07 p_value= 4.3e-11

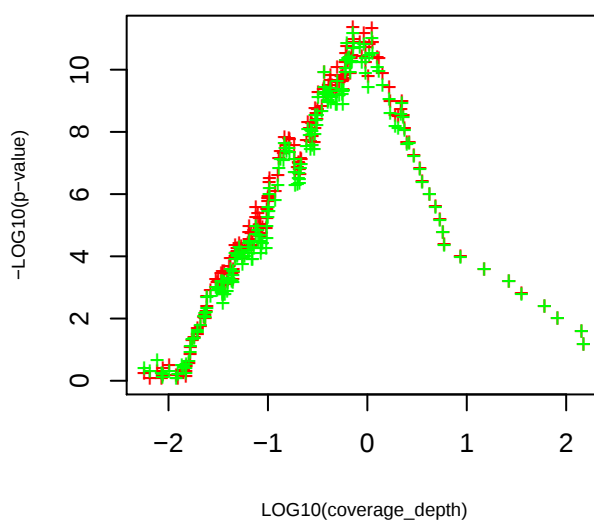


[T] COG3706 Response regulator containing a CheY-like receiver domain and a GGDEF domain

slope= 7.81 p_value= 6e-21 intercept= -28.41 p_value= 1.0e-21

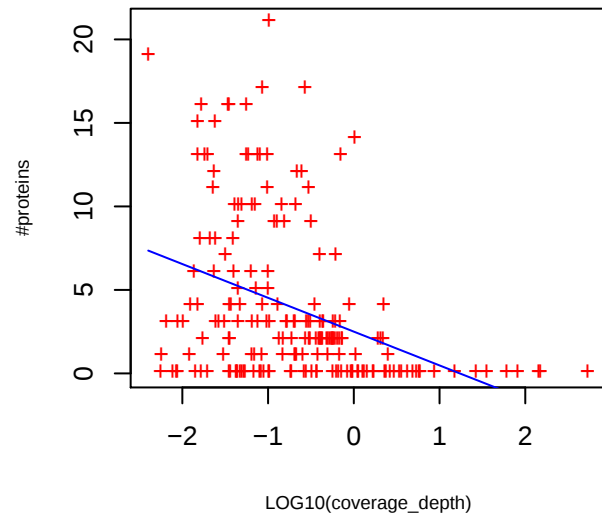


P-value curve ; red (unnorm), green (norm)



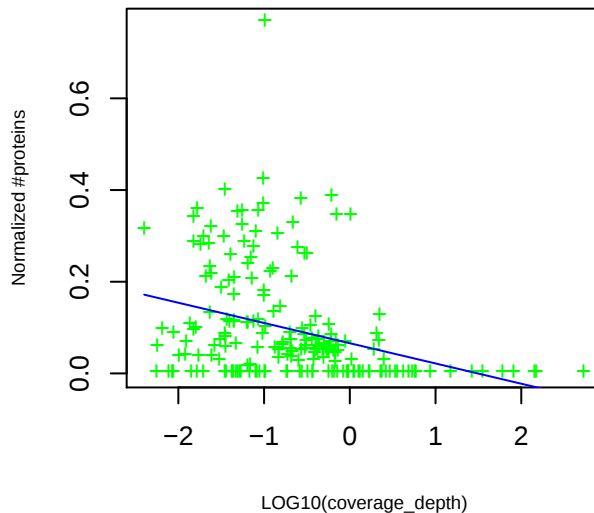
[T] COG2200 FOG: EAL domain

slope= -2.02 p_value= 7.3e-08 intercept= 2.50 p_value= 4.8e-09



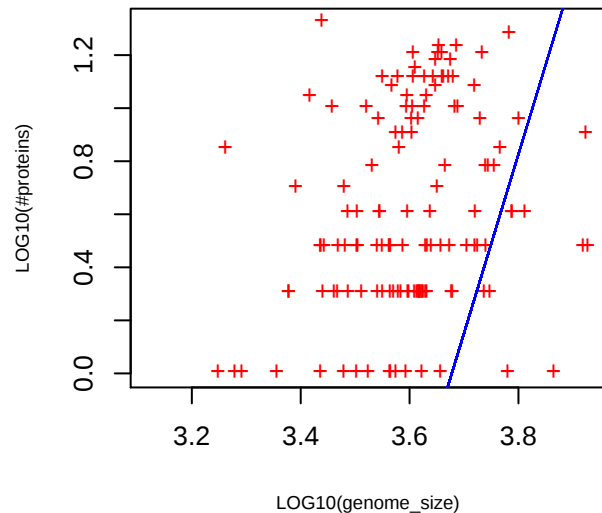
[T] COG2200 FOG: EAL domain

slope= -0.044 p_value= 3.2e-06 intercept= 0.066 p_value= 1.6e-09

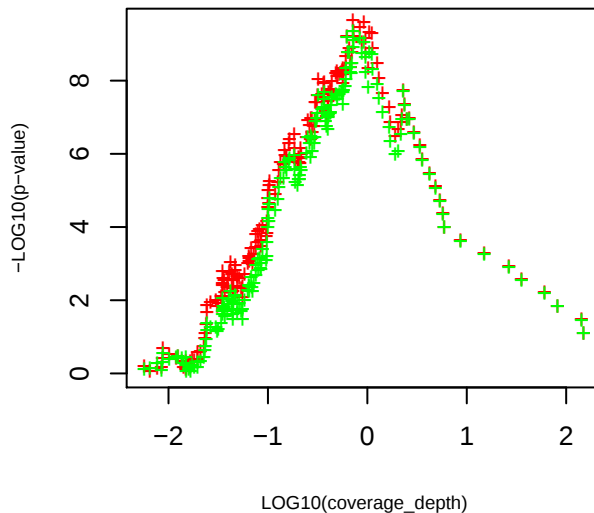


[T] COG2200 FOG: EAL domain

slope= 6.75 p_value= 4.5e-14 intercept= -24.82 p_value= 7.1e-15

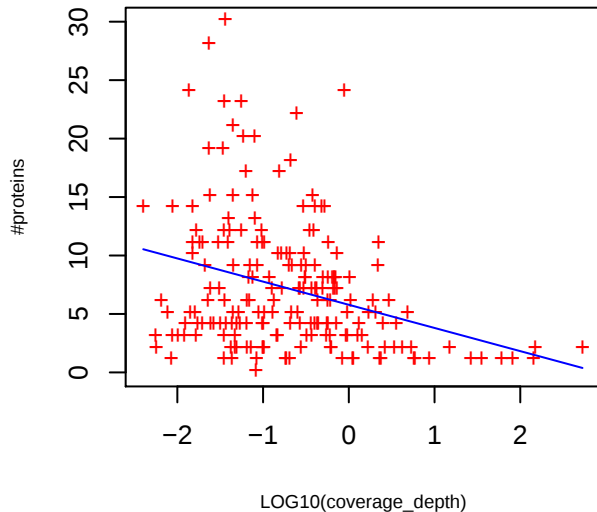


P-value curve : red (unnorm), green (norm)



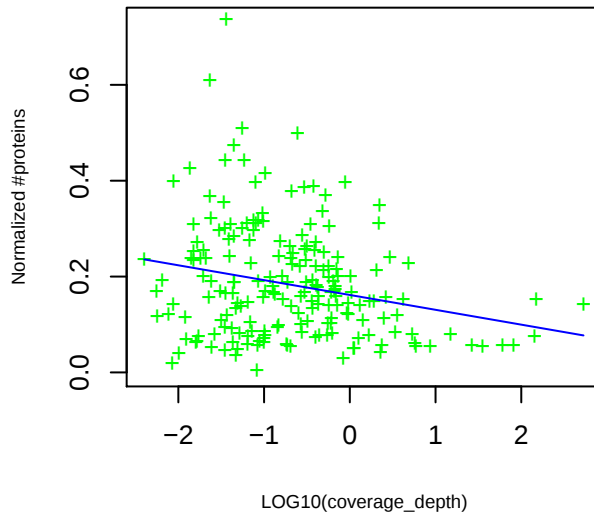
[G] COG2814 Arabinose efflux permease

slope= -1.98 p_value= 8.8e-06 intercept= 5.79 p_value= 1.3e-24



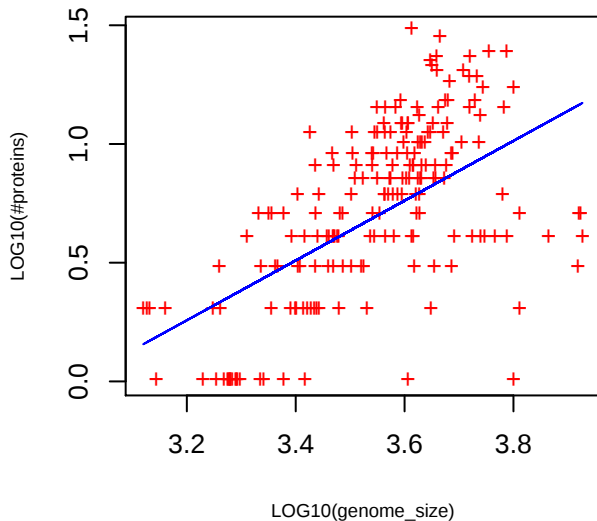
[G] COG2814 Arabinose efflux permease

slope= -0.031 p_value= 9e-04 intercept= 0.16 p_value= 4.6e-36

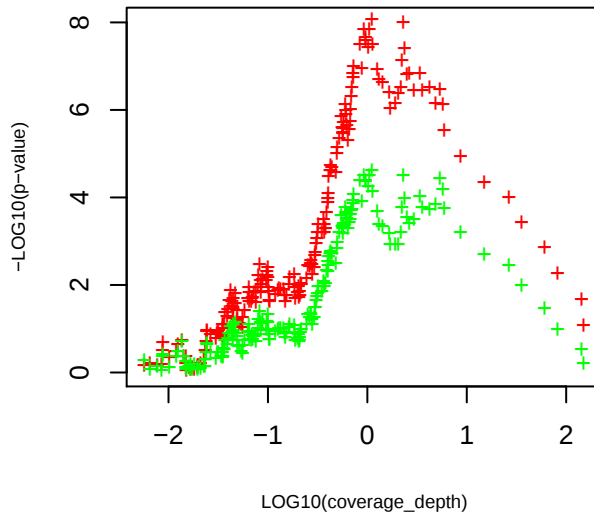


[G] COG2814 Arabinose efflux permease

slope= 1.26 p_value= 2.2e-09 intercept= -3.77 p_value= 3.1e-07

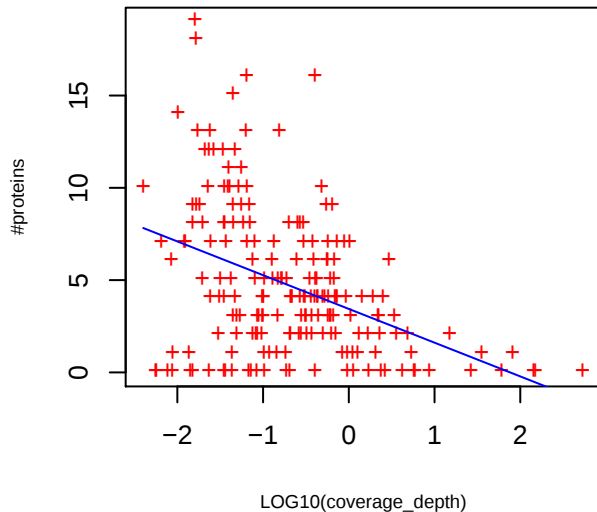


P-value curve ; red (unnorm), green (norm)



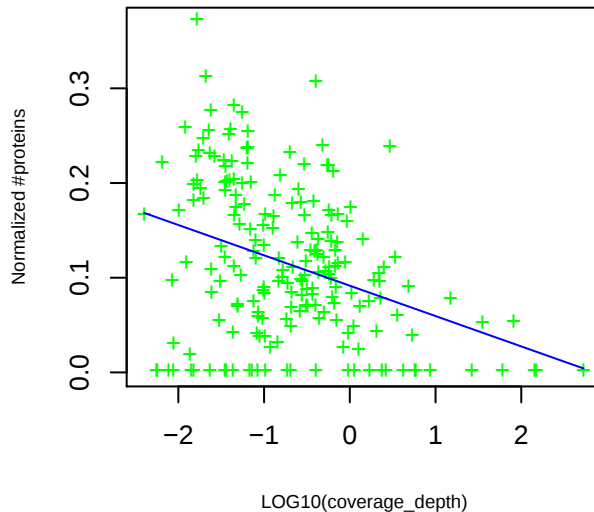
[V] COG1566 Multidrug resistance efflux pump

slope= -1.83 p_value= 2.7e-09 intercept= 3.44 p_value= 2.1e-20



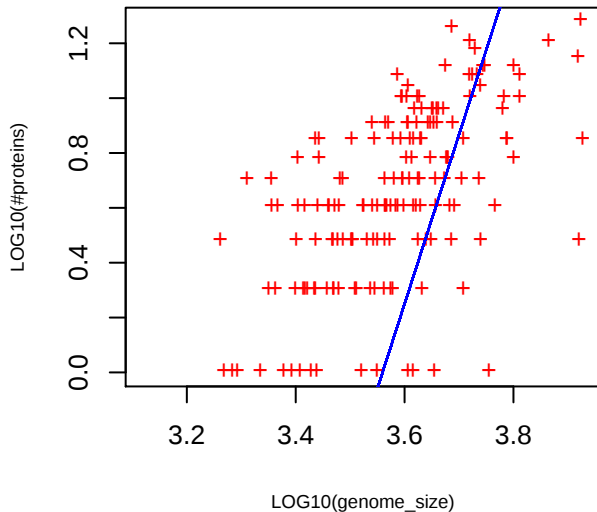
[V] COG1566 Multidrug resistance efflux pump

slope= -0.032 p_value= 3.9e-07 intercept= 0.092 p_value= 4.3e-29

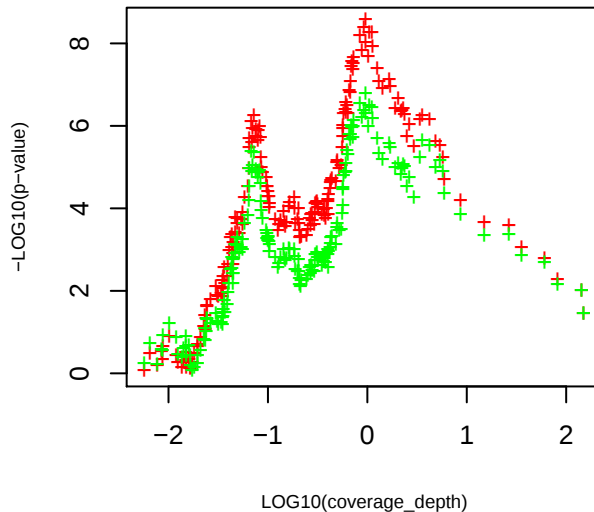


[V] COG1566 Multidrug resistance efflux pump

slope= 6.17 p_value= 1.8e-19 intercept= -21.96 p_value= 1.5e-19

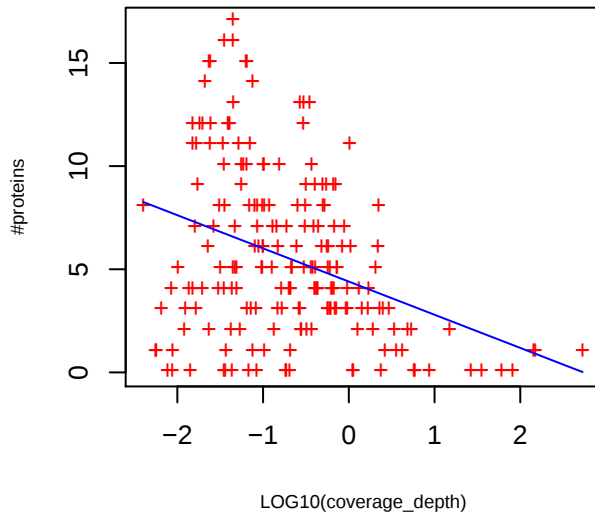


P-value curve ; red (unnorm), green (norm)



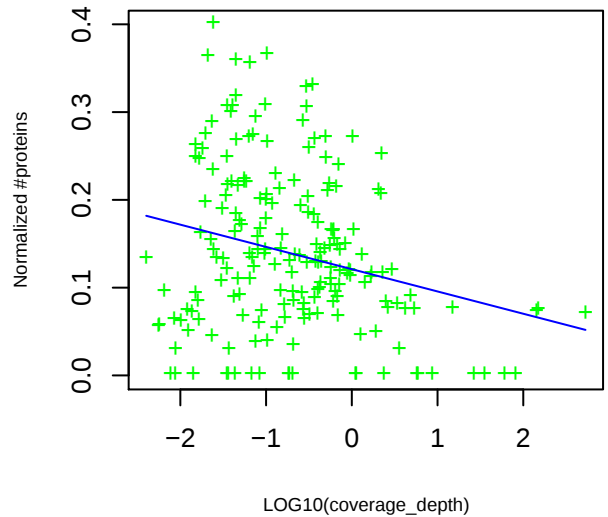
[V] COG0841 Cation/multidrug efflux pump

slope= -1.61 p_value= 4.3e-07 intercept= 4.40 p_value= 2.7e-27



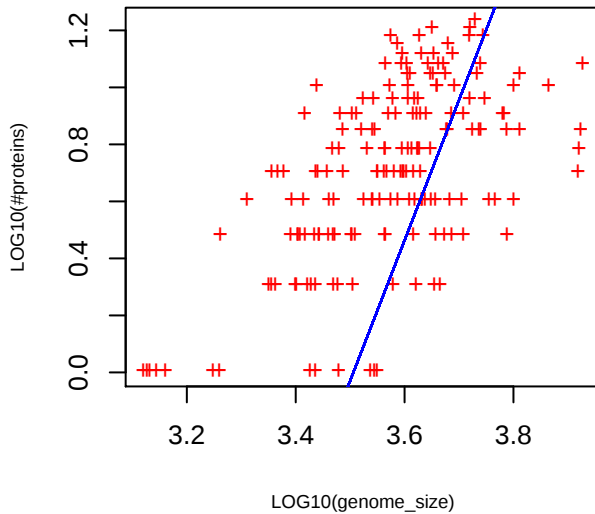
[V] COG0841 Cation/multidrug efflux pump

slope= -0.025 p_value= 0.00048 intercept= 0.12 p_value= 2.4e-34

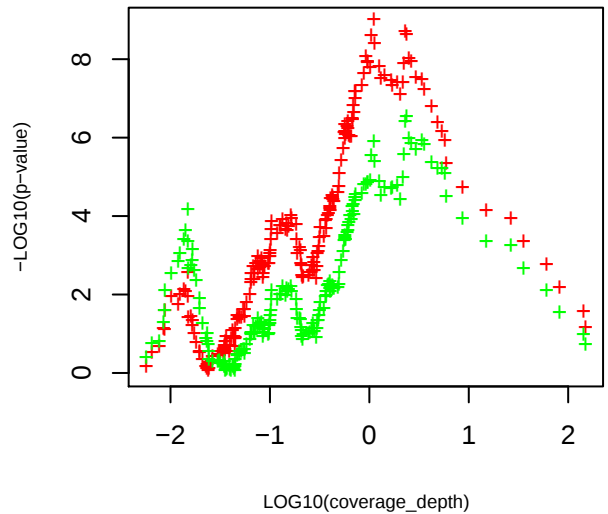


[V] COG0841 Cation/multidrug efflux pump

slope= 4.93 p_value= 2e-16 intercept= -17.27 p_value= 4e-16

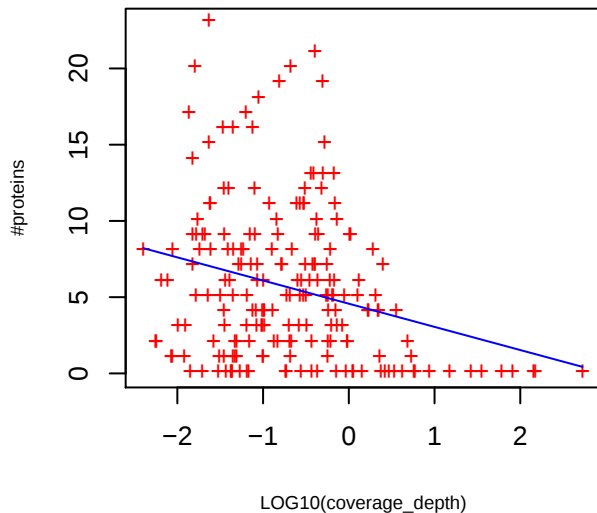


P-value curve ; red (unnorm), green (norm)



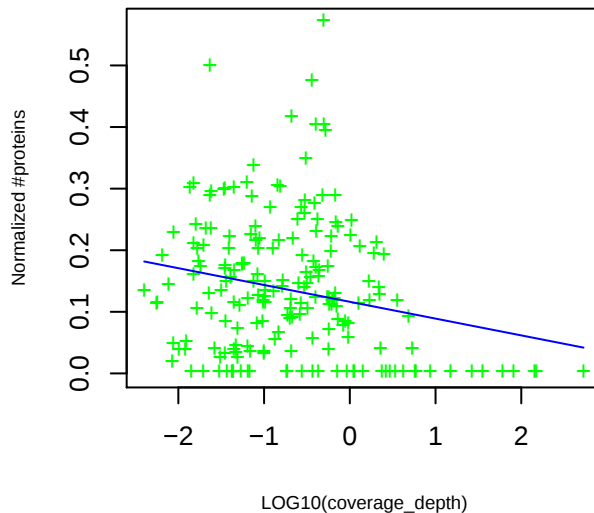
[K] COG1309 Transcriptional regulator

slope= -1.52 p_value= 0.00014 intercept= 4.57 p_value= 2.7e-20



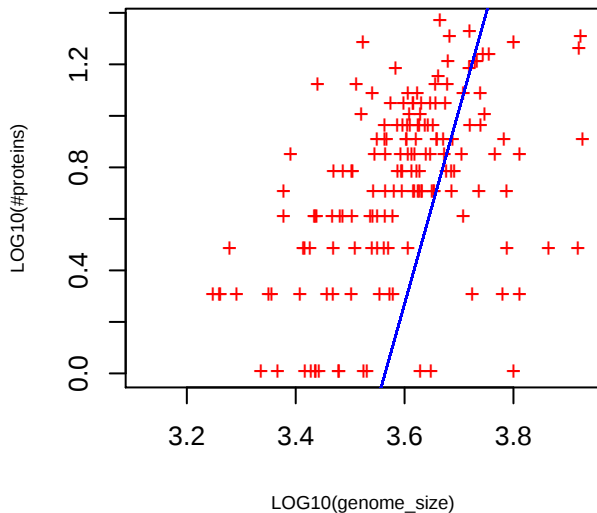
[K] COG1309 Transcriptional regulator

slope= -0.027 p_value= 0.0019 intercept= 0.12 p_value= 7.2e-25

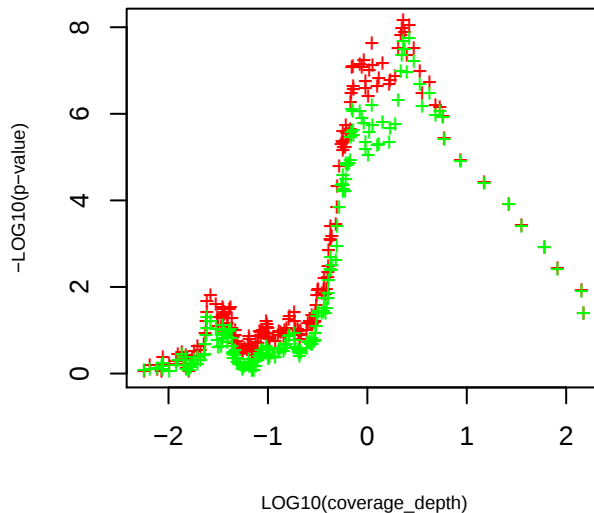


[K] COG1309 Transcriptional regulator

slope= 7.53 p_value= 3.7e-26 intercept= -26.83 p_value= 2.6e-26

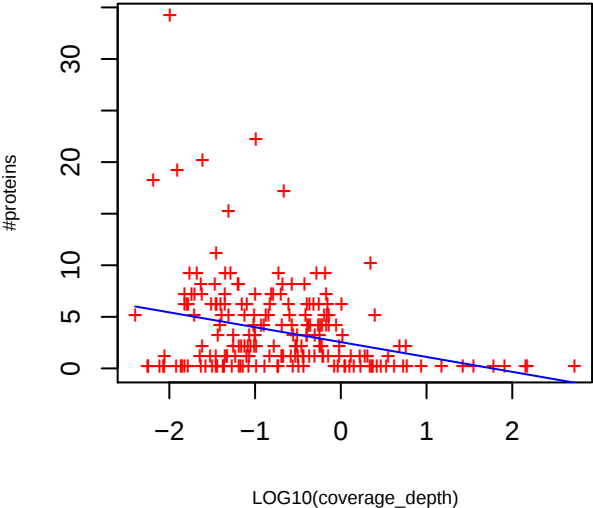


P-value curve ; red (unnorm), green (norm)



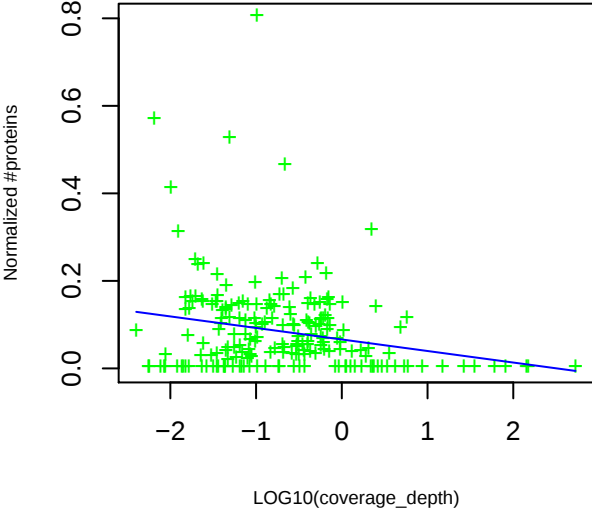
[T] COG4191 Signal transduction histidine kinase regulating C4-dicarboxylate transport system

slope= -1.44 p_value= 4.2e-05 intercept= 2.55 p_value= 4.5e-10



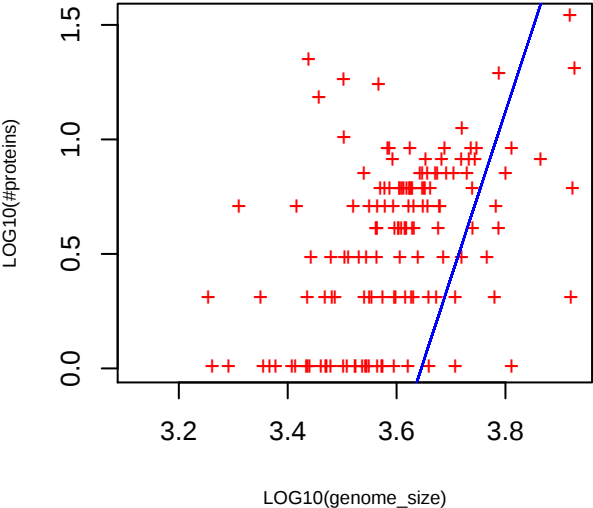
[T] COG4191 Signal transduction histidine kinase regulating C4-dicarboxylate transport system

slope= -0.026 p_value= 0.0014 intercept= 0.066 p_value= 1.2e-11

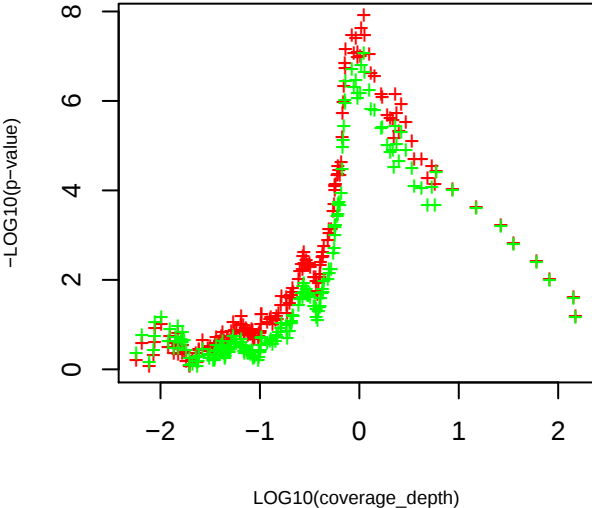


[T] COG4191 Signal transduction histidine kinase regulating C4-dicarboxylate transport system

slope= 7.25 p_value= 1.7e-18 intercept= -26.42 p_value= 3e-19

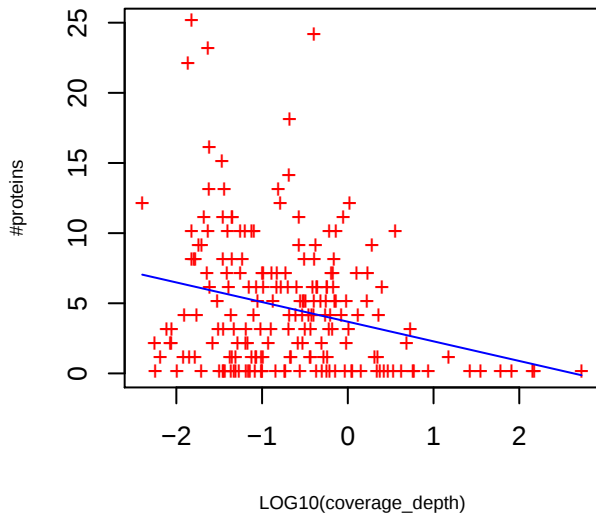


P-value curve ; red (unnorm), green (norm)



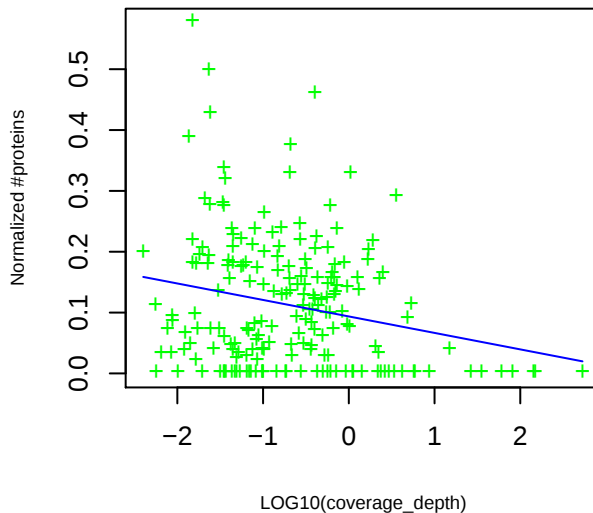
[J] COG1670 Acetyltransferases, including N-acetylases of ribosomal proteins

slope= -1.40 p_value= 0.00023 intercept= 3.69 p_value= 9.6e-16



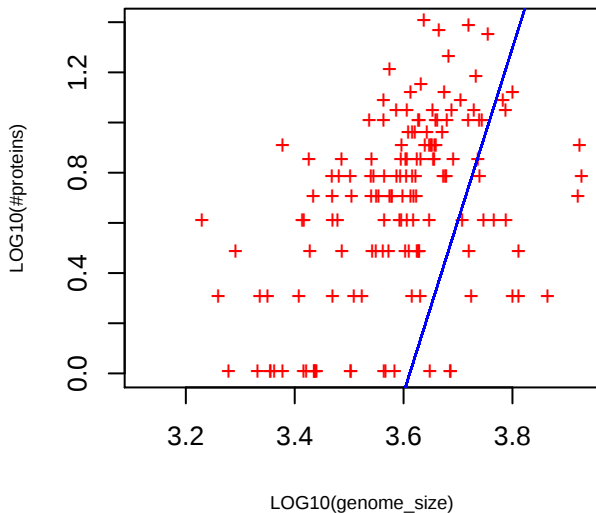
[J] COG1670 Acetyltransferases, including N-acetylases of ribosomal proteins

slope= -0.027 p_value= 0.0014 intercept= 0.094 p_value= 4.7e-19

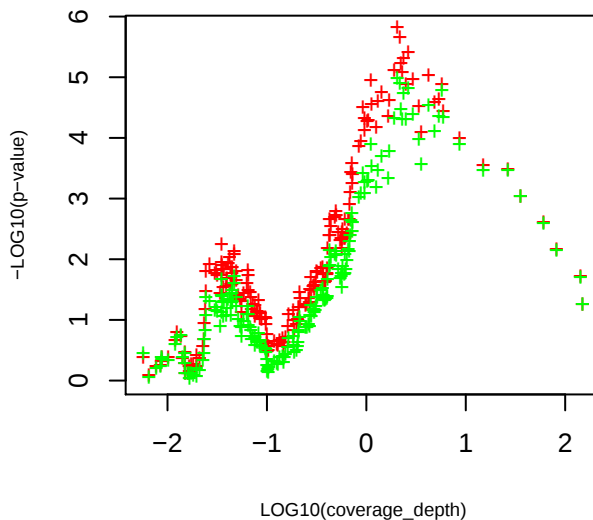


[J] COG1670 Acetyltransferases, including N-acetylases of ribosomal proteins

slope= 6.88 p_value= 2e-17 intercept= -24.84 p_value= 6.9e-18

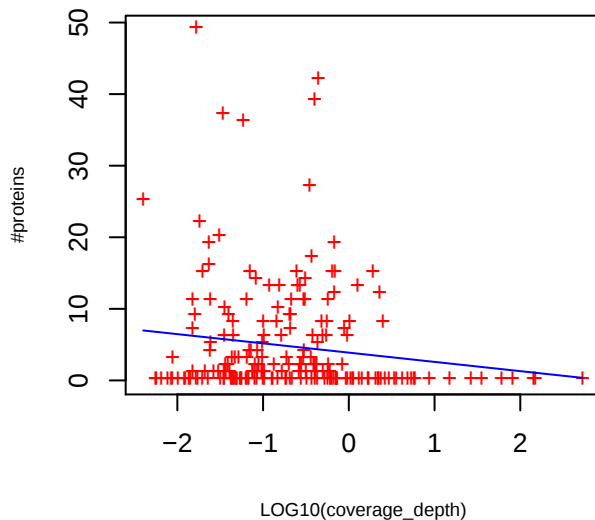


P-value curve : red (unnorm), green (norm)



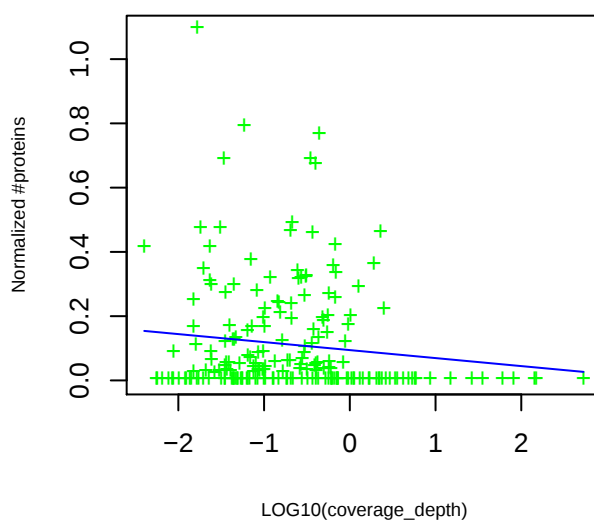
[L] COG2801 Transposase and inactivated derivatives

slope= -1.29 p_value= 0.045 intercept= 3.88 p_value= 2.2e-07



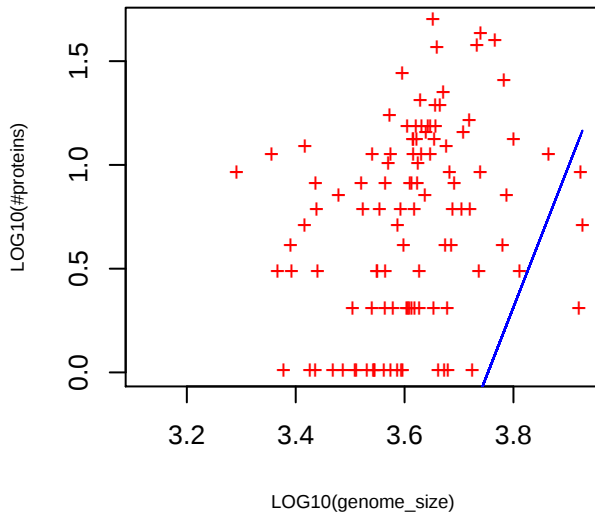
[L] COG2801 Transposase and inactivated derivatives

slope= -0.025 p_value= 0.077 intercept= 0.094 p_value= 1.1e-08

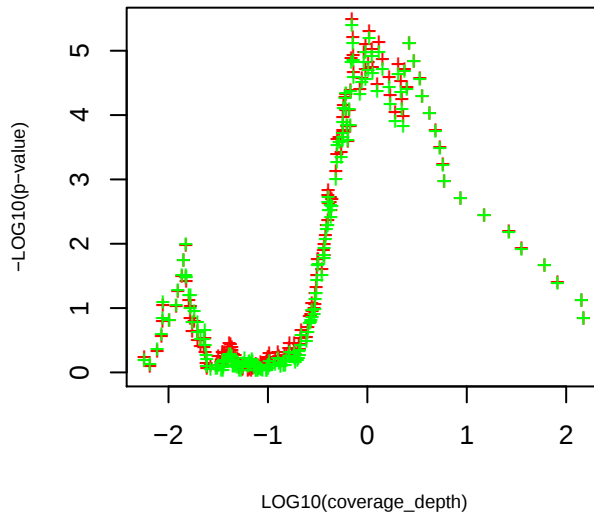


[L] COG2801 Transposase and inactivated derivatives

slope= 6.71 p_value= 9e-12 intercept= -25.19 p_value= 7.6e-13

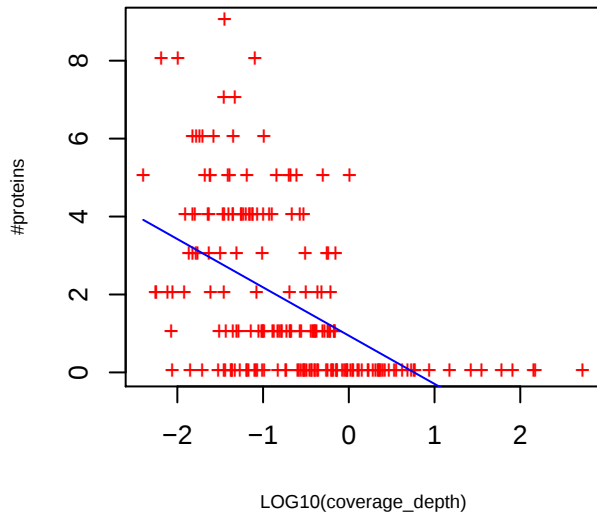


P-value curve ; red (unnorm), green (norm)



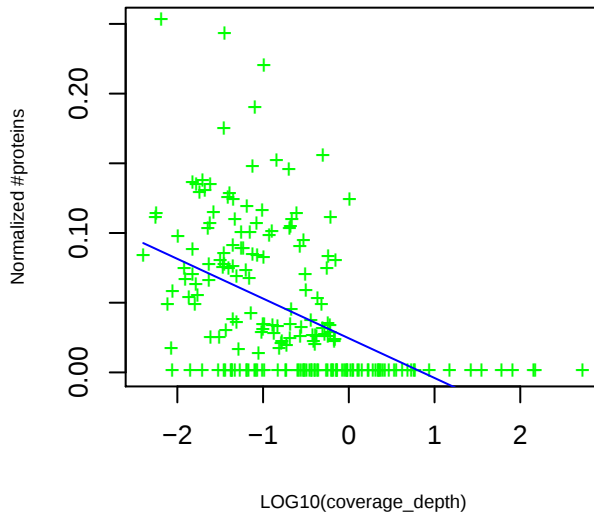
[NT] COG0835 Chemotaxis signal transduction protein

slope= -1.24 p_value= 9.5e-15 intercept= 0.94 p_value= 5.3e-08



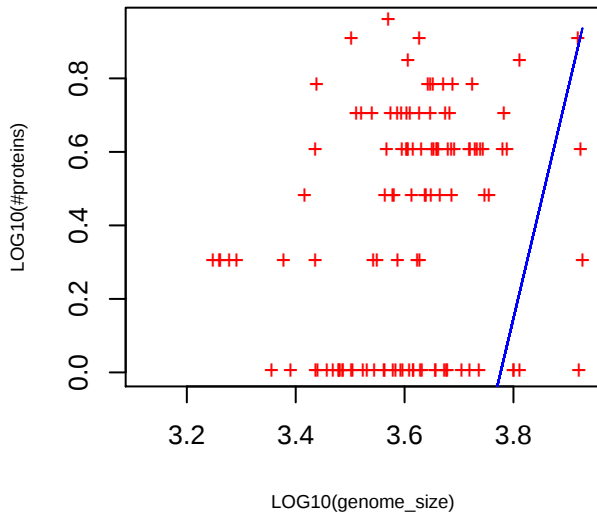
[NT] COG0835 Chemotaxis signal transduction protein

slope= -0.028 p_value= 8.4e-13 intercept= 0.024 p_value= 2.2e-08

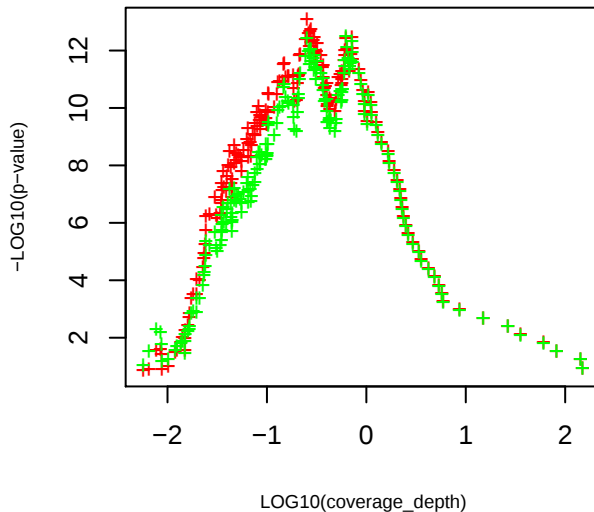


[NT] COG0835 Chemotaxis signal transduction protein

slope= 6.23 p_value= 5.6e-12 intercept= -23.51 p_value= 3.4e-13

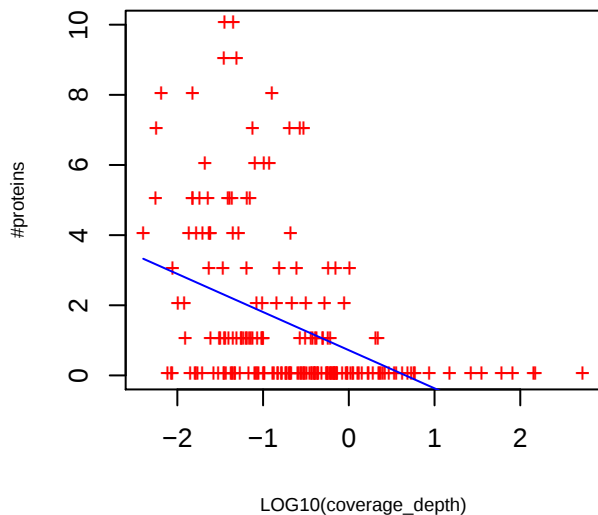


P-value curve ; red (unnorm), green (norm)



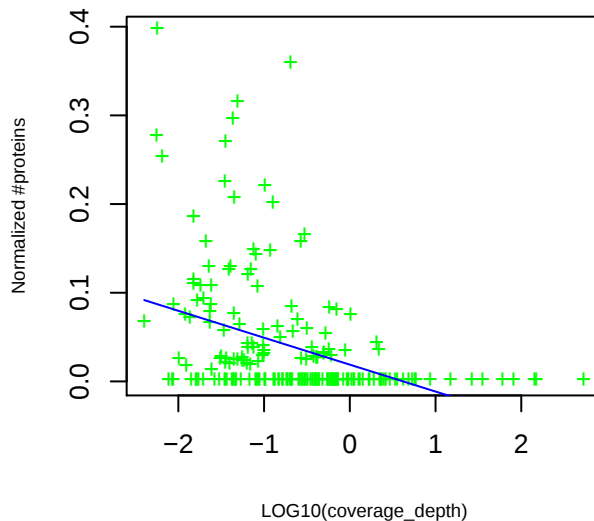
[T] COG2206 HD-GYP domain

slope= -1.09 p_value= 1.3e-09 intercept= 0.72 p_value= 0.00025



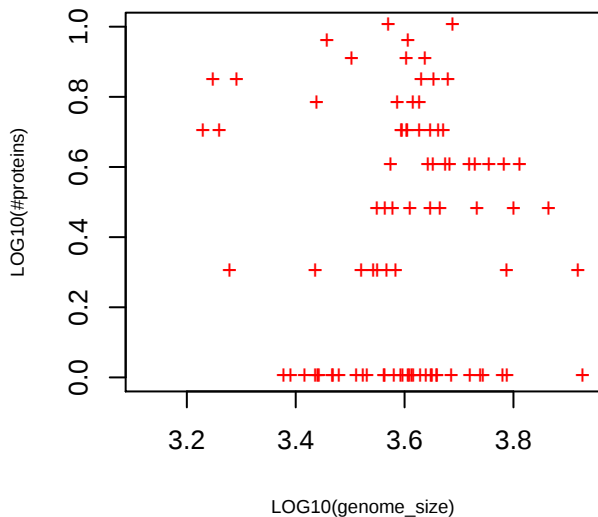
[T] COG2206 HD-GYP domain

slope= -0.030 p_value= 3.5e-08 intercept= 0.019 p_value= 0.0018

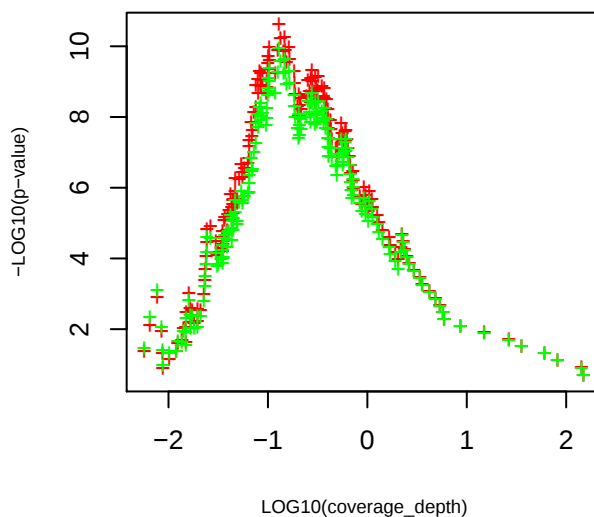


[T] COG2206 HD-GYP domain

slope= 3.90 p_value= 3.8e-05 intercept= -15.87 p_value= 2.7e-06

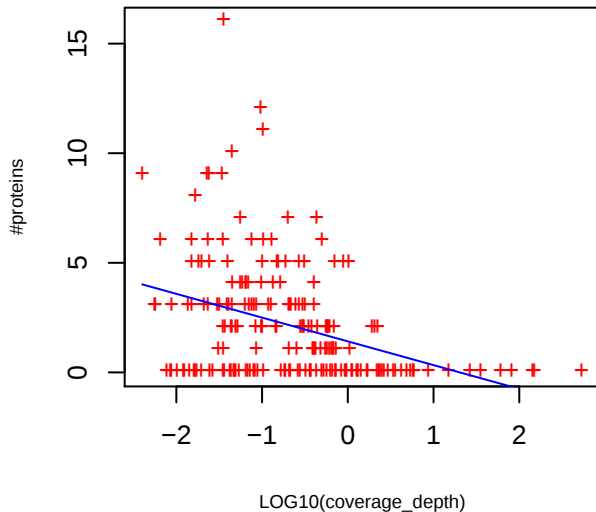


P-value curve ; red (unnorm), green (norm)



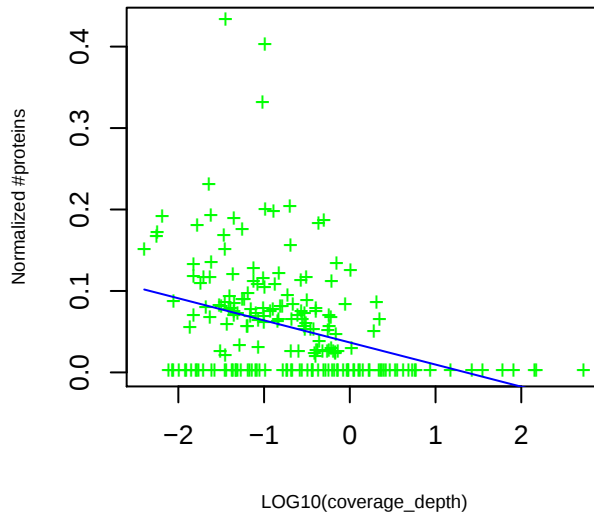
[N] COG1344 Flagellin and related hook-associated proteins

slope= -1.08 p_value= 1.7e-07 intercept= 1.42 p_value= 2.1e-09



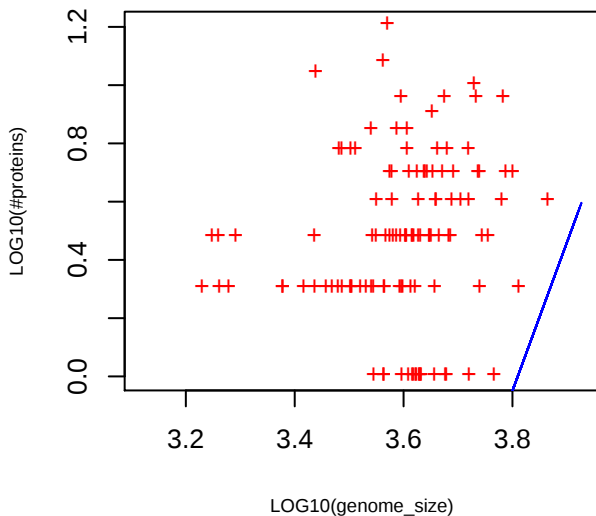
[N] COG1344 Flagellin and related hook-associated proteins

slope= -0.027 p_value= 6.1e-07 intercept= 0.037 p_value= 3.6e-09

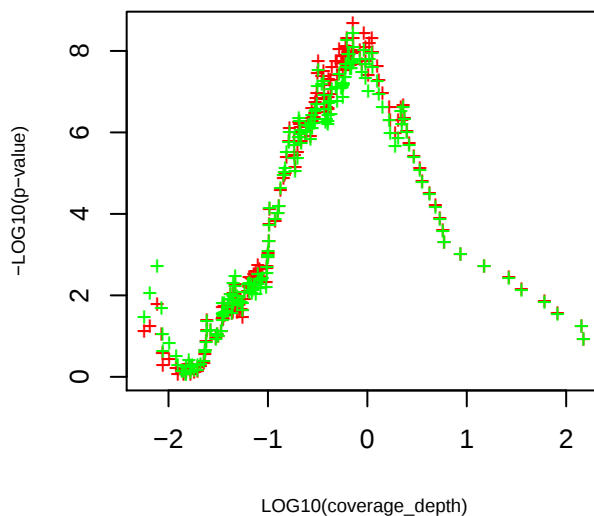


[N] COG1344 Flagellin and related hook-associated proteins

slope= 5.09 p_value= 5.6e-08 intercept= -19.39 p_value= 6.7e-09

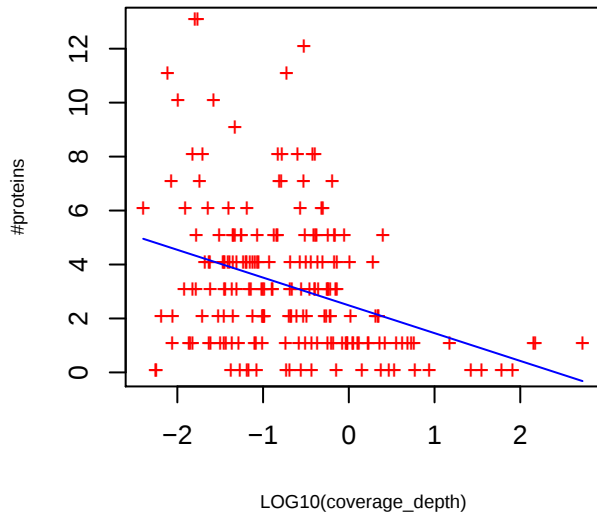


P-value curve ; red (unnorm), green (norm)



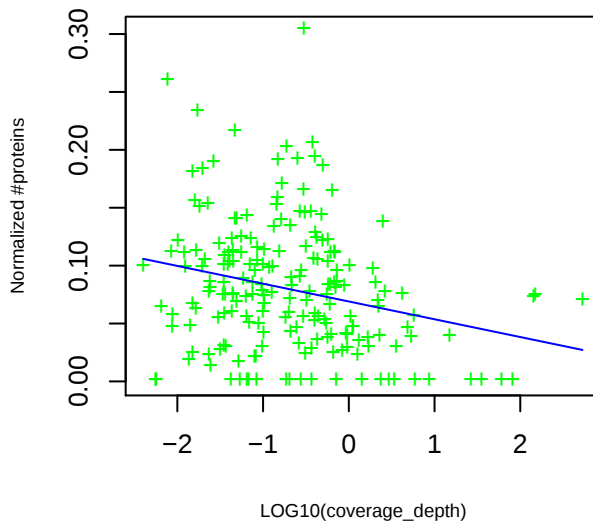
[D] COG1192 ATPases involved in chromosome partitioning

slope= -1.03 p_value= 6e-07 intercept= 2.49 p_value= 2.7e-22



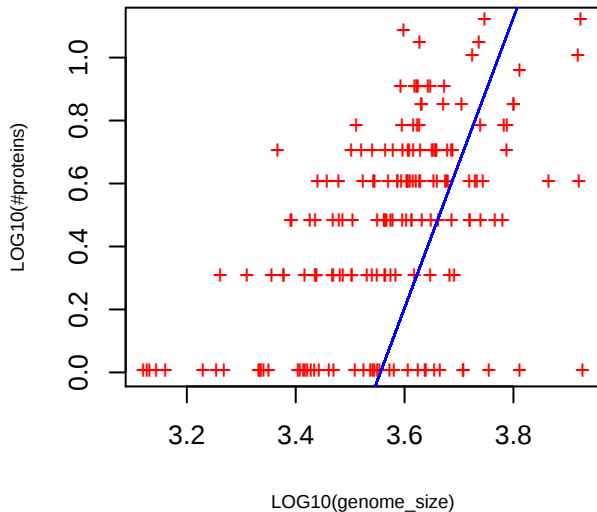
[D] COG1192 ATPases involved in chromosome partitioning

slope= -0.015 p_value= 0.00047 intercept= 0.069 p_value= 9.4e-32

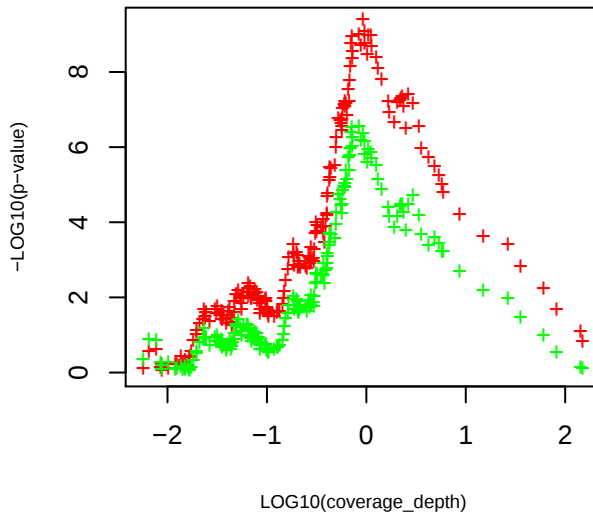


[D] COG1192 ATPases involved in chromosome partitioning

slope= 4.61 p_value= 3e-15 intercept= -16.39 p_value= 2.7e-15

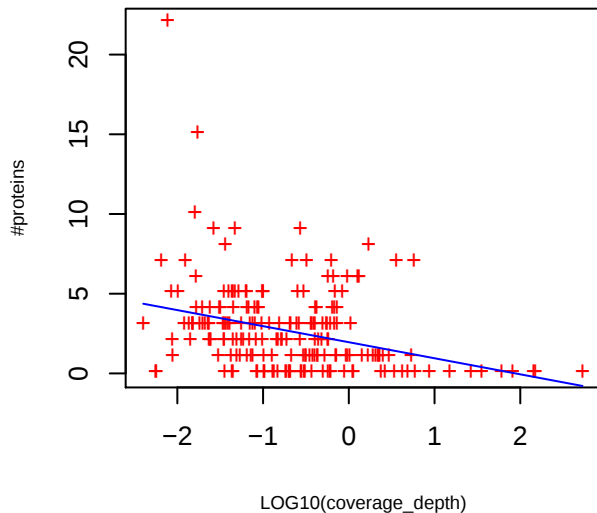


P-value curve ; red (unnorm), green (norm)



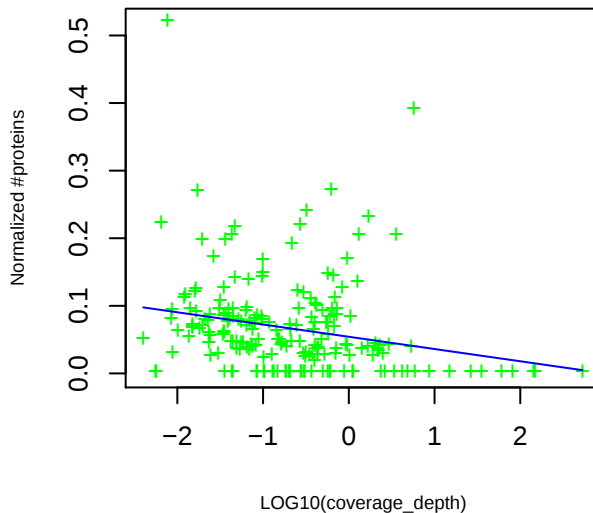
[T] COG0589 Universal stress protein UspA and related nucleotide-binding proteins

slope= -1.01 p_value= 3.2e-06 intercept= 1.96 p_value= 2.3e-14



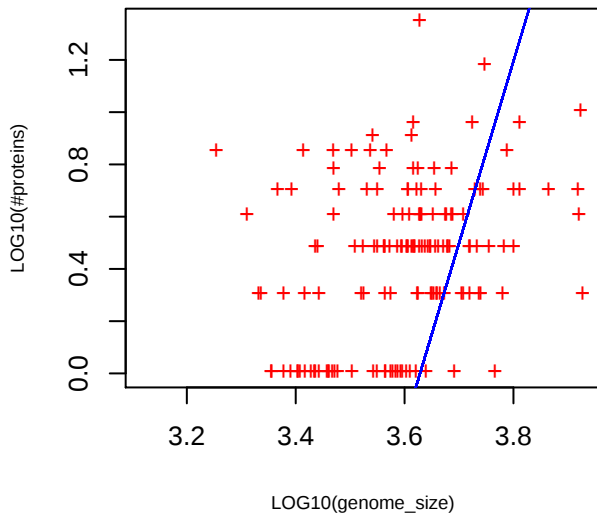
[T] COG0589 Universal stress protein UspA and related nucleotide-binding proteins

slope= -0.018 p_value= 0.0013 intercept= 0.054 p_value= 1.6e-15

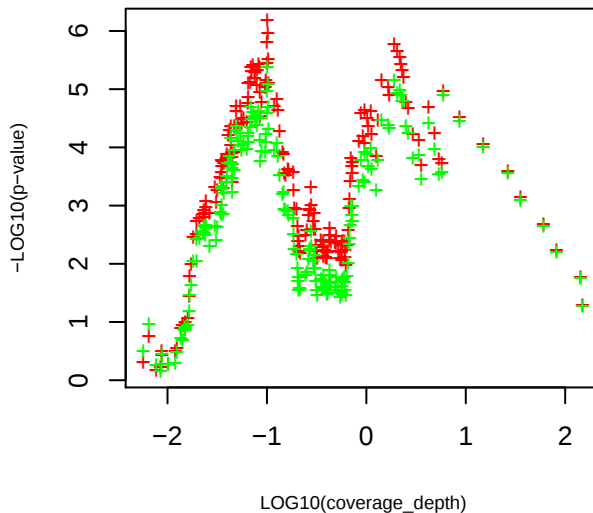


[T] COG0589 Universal stress protein UspA and related nucleotide-binding proteins

slope= 6.96 p_value= 7.6e-21 intercept= -25.27 p_value= 1.5e-21

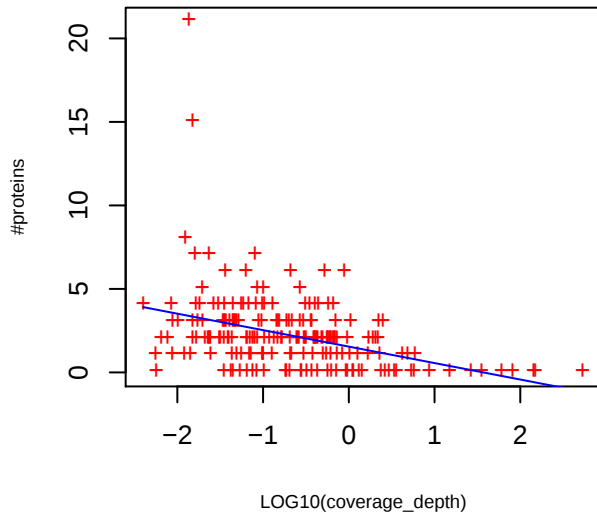


P-value curve : red (unnorm), green (norm)



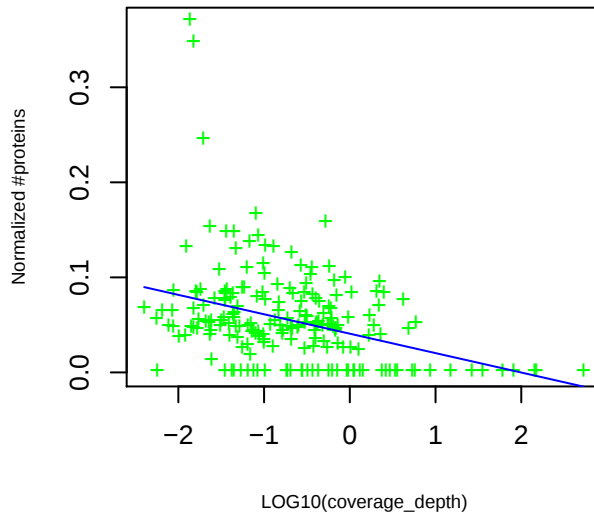
[F] COG1051 ADP-ribose pyrophosphatase

slope= -0.99 p_value= 4.0e-08 intercept= 1.55 p_value= 1.5e-13



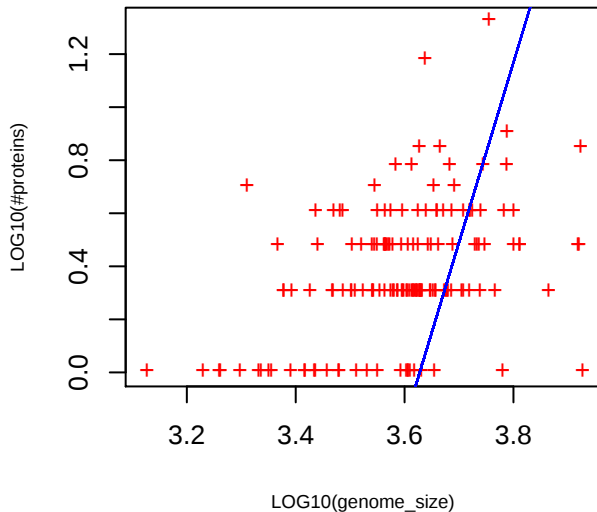
[F] COG1051 ADP-ribose pyrophosphatase

slope= -0.020 p_value= 2.3e-07 intercept= 0.041 p_value= 9.2e-18

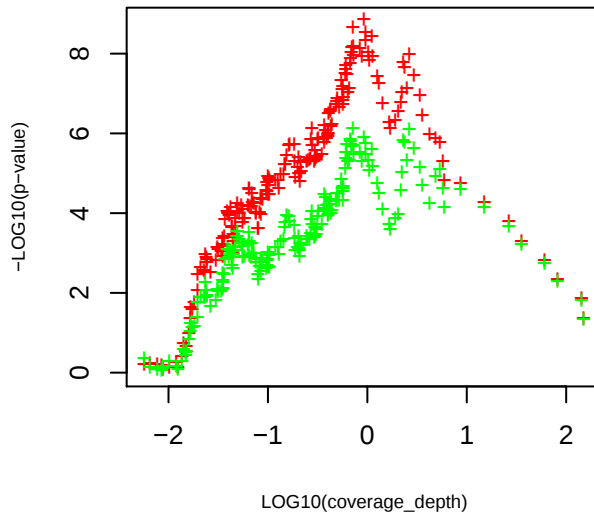


[F] COG1051 ADP-ribose pyrophosphatase

slope= 6.78 p_value= 1.4e-21 intercept= -24.61 p_value= 2.7e-22

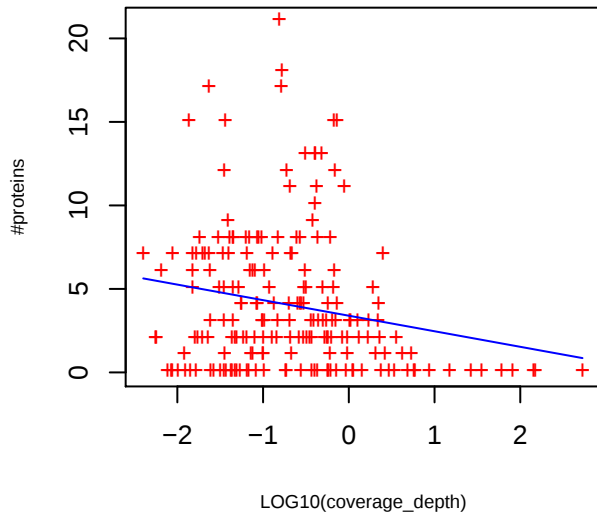


P-value curve ; red (unnorm), green (norm)



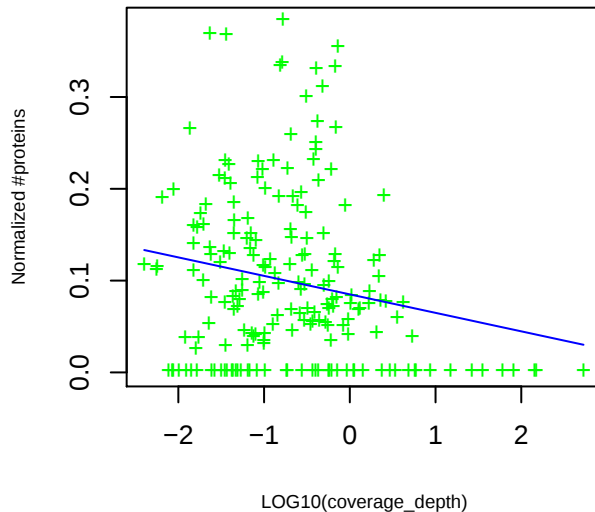
[K] COG1846 Transcriptional regulators

slope= -0.93 p_value= 0.0057 intercept= 3.40 p_value= 1.7e-16



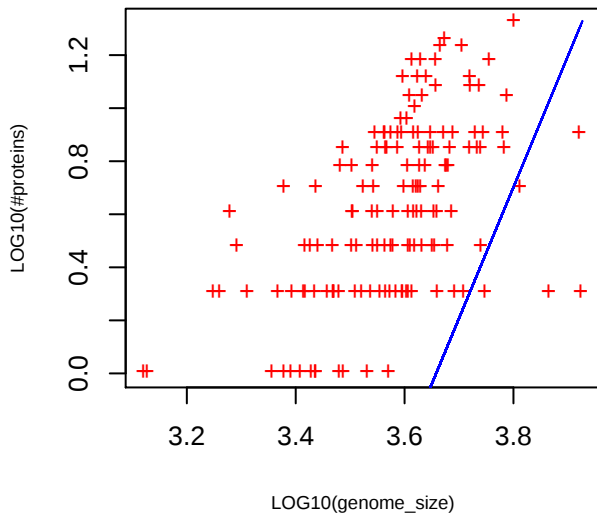
[K] COG1846 Transcriptional regulators

slope= -0.02 p_value= 0.0061 intercept= 0.085 p_value= 2.6e-20

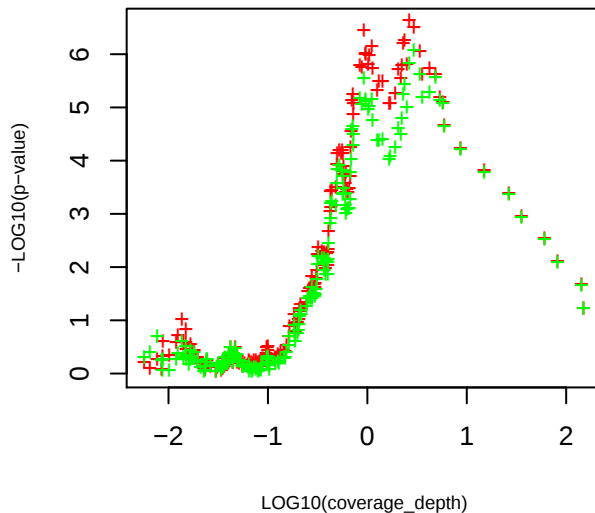


[K] COG1846 Transcriptional regulators

slope= 4.94 p_value= 8.2e-09 intercept= -18.08 p_value= 3.1e-09

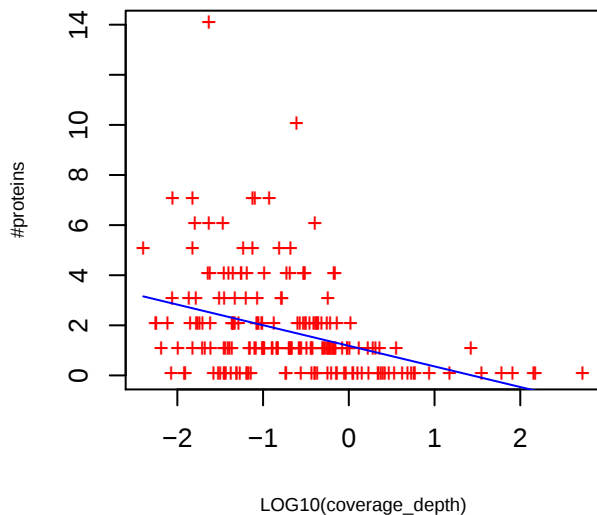


P-value curve : red (unnorm), green (norm)



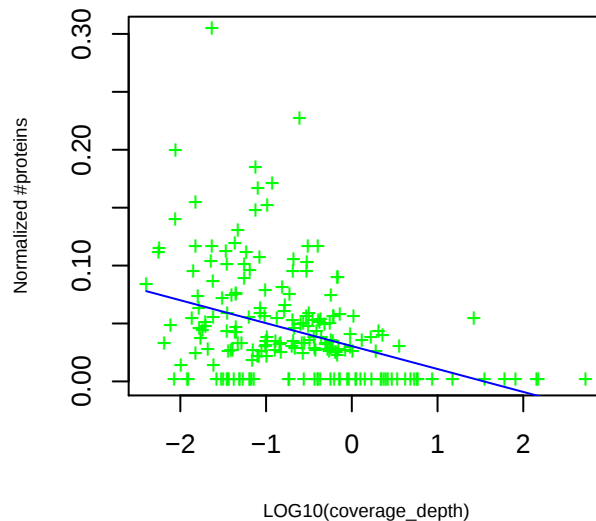
[P] COG0609 ABC-type Fe3+-siderophore transport system, permease component

slope= -0.82 p_value= 1.3e-07 intercept= 1.18 p_value= 4.7e-11



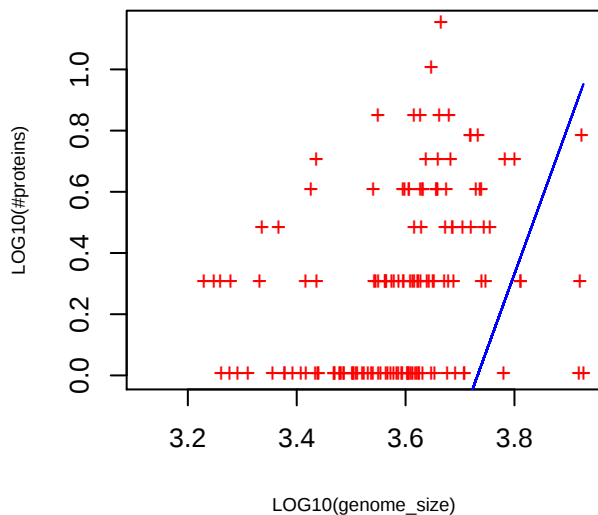
[P] COG0609 ABC-type Fe3+-siderophore transport system, permease component

slope= -0.020 p_value= 6.5e-08 intercept= 0.030 p_value= 7.9e-13

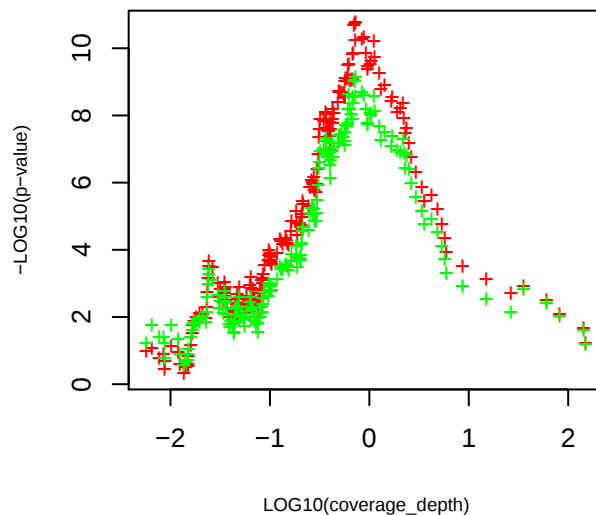


[P] COG0609 ABC-type Fe3+-siderophore transport system, permease component

slope= 4.89 p_value= 1.9e-09 intercept= -18.27 p_value= 3.3e-10

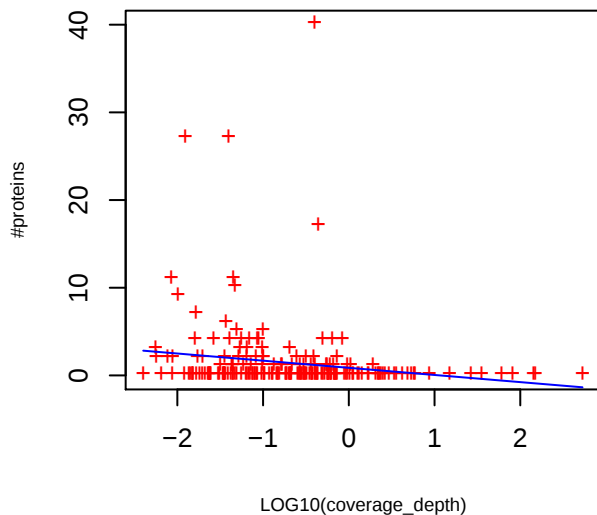


P-value curve ; red (unnorm), green (norm)



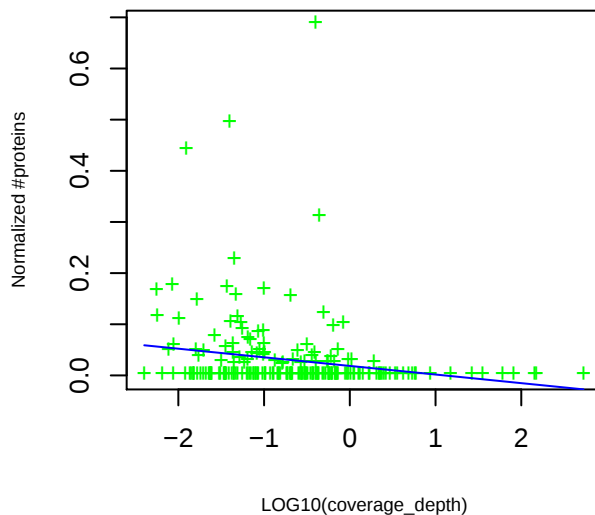
[L] COG1943 Transposase and inactivated derivatives

slope= -0.82 p_value= 0.020 intercept= 0.87 p_value= 0.028



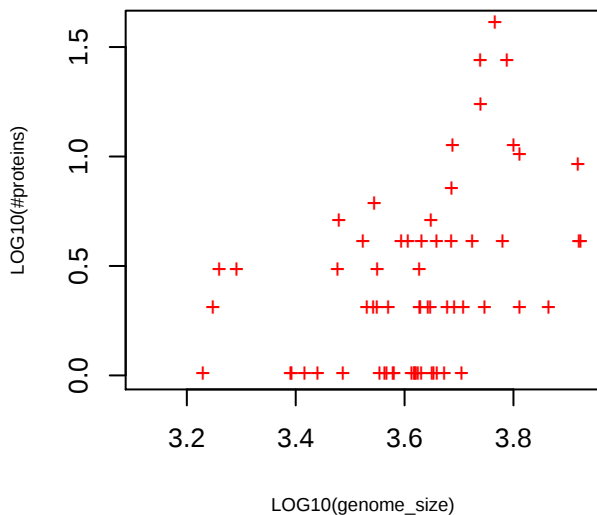
[L] COG1943 Transposase and inactivated derivatives

slope= -0.017 p_value= 0.0076 intercept= 0.019 p_value= 0.0091

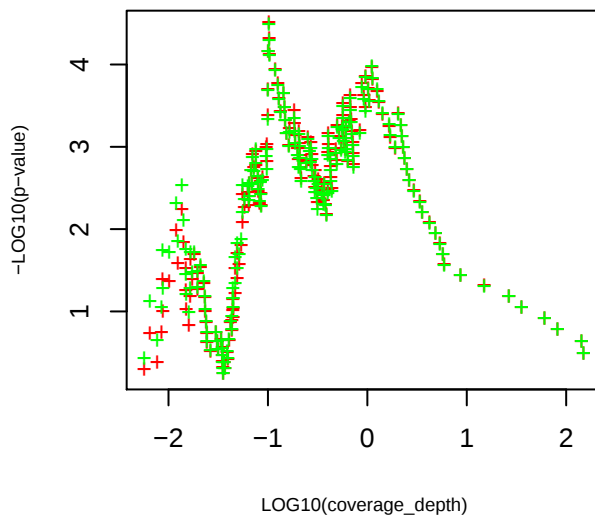


[L] COG1943 Transposase and inactivated derivatives

slope= 4.29 p_value= 1.3e-06 intercept= -17.80 p_value= 2.3e-08

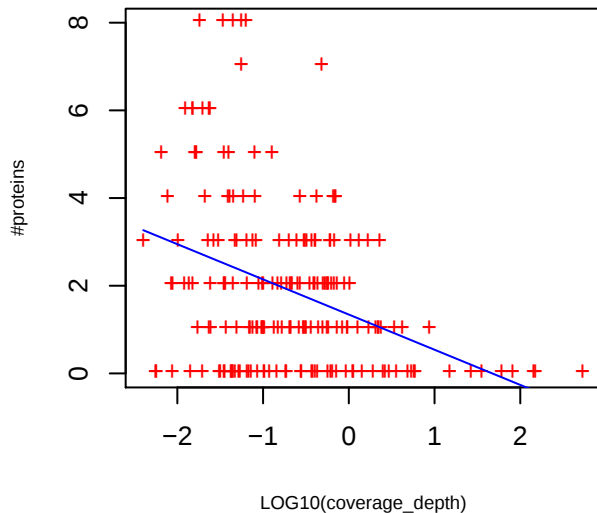


P-value curve ; red (unnorm), green (norm)



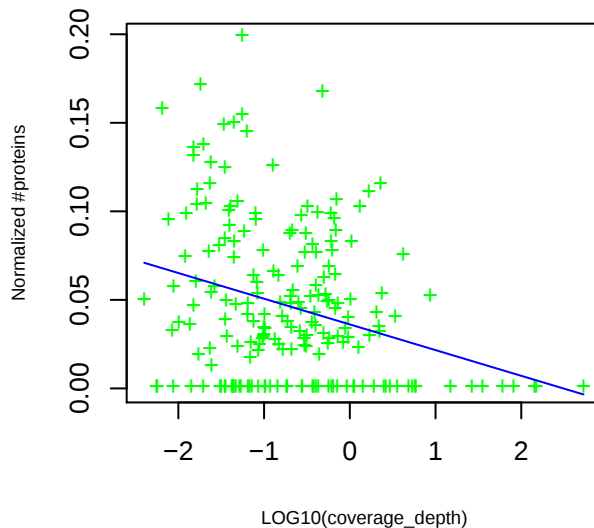
[R] COG0110 Acetyltransferase (isoleucine patch superfamily)

slope= -0.80 p_value= 9.6e-08 intercept= 1.34 p_value= 2.9e-14



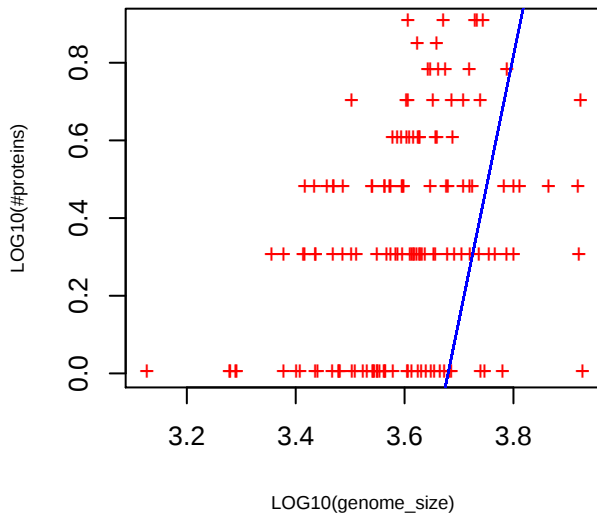
[R] COG0110 Acetyltransferase (isoleucine patch superfamily)

slope= -0.015 p_value= 2.6e-05 intercept= 0.036 p_value= 8e-18

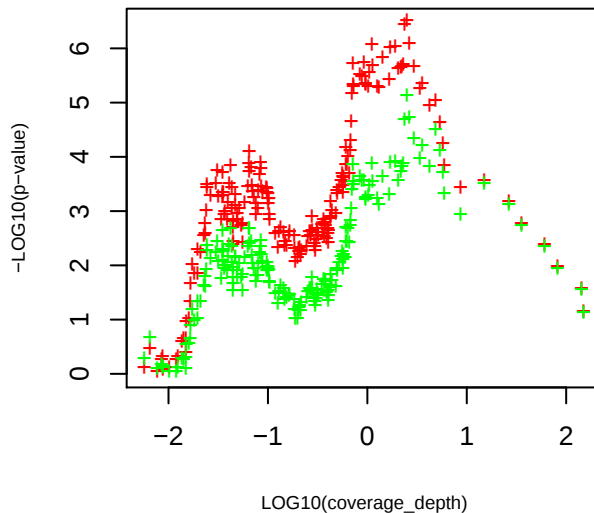


[R] COG0110 Acetyltransferase (isoleucine patch superfamily)

slope= 6.81 p_value= 1.3e-17 intercept= -25.08 p_value= 1.3e-18

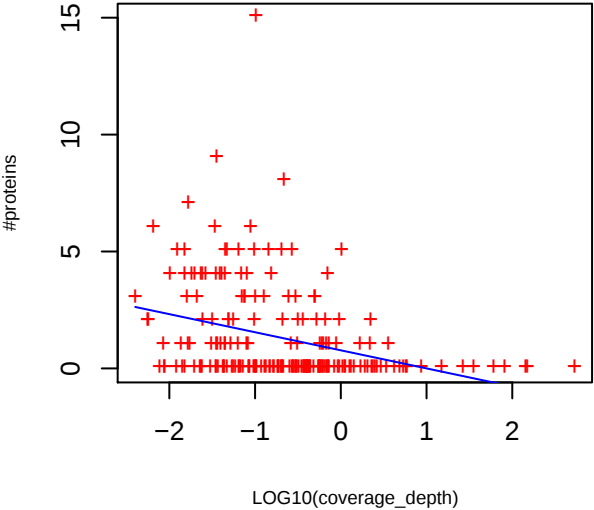


P-value curve ; red (unnorm), green (norm)



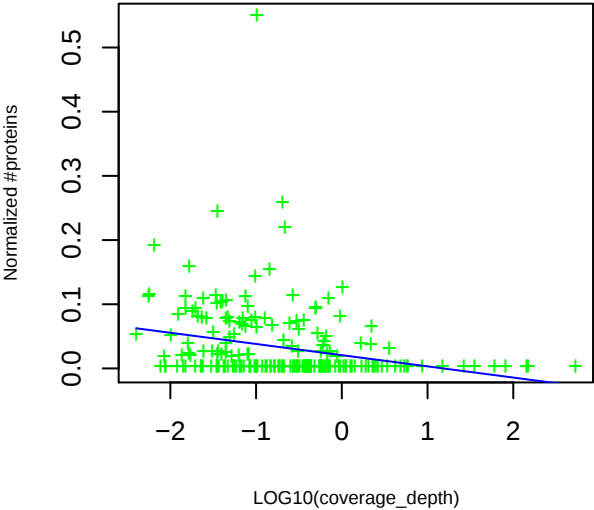
[KT] COG3437 Response regulator containing a CheY-like receiver domain and an HD-GYP domain

slope= -0.77 p_value= 2.5e-06 intercept= 0.77 p_value= 2.7e-05



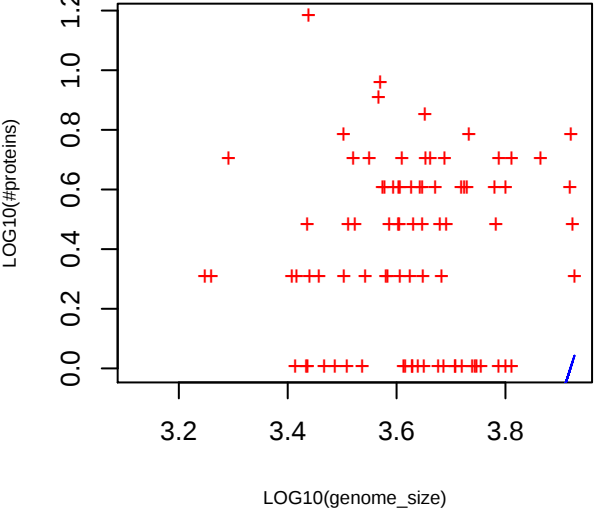
[KT] COG3437 Response regulator containing a CheY-like receiver domain and an HD-GYP domain

slope= -0.017 p_value= 0.00023 intercept= 0.021 p_value= 0.00012

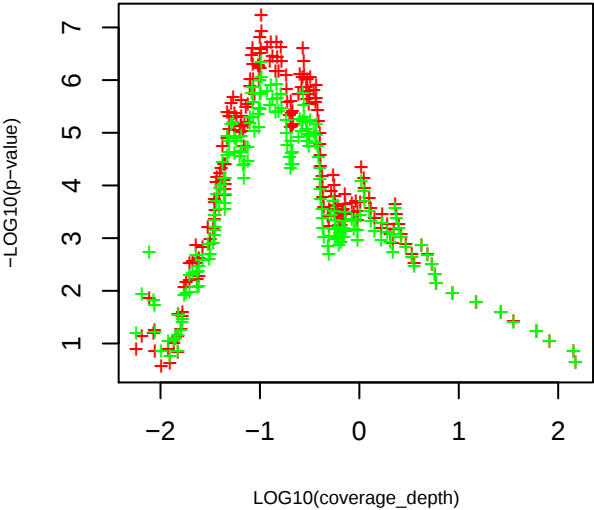


[KT] COG3437 Response regulator containing a CheY-like receiver domain and an HD-GYP domain

slope= 5.69 p_value= 4.8e-10 intercept= -22.31 p_value= 1e-11

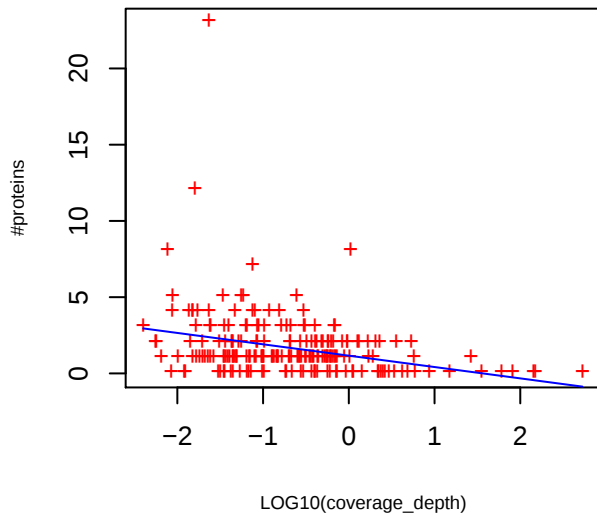


P-value curve ; red (unnorm), green (norm)



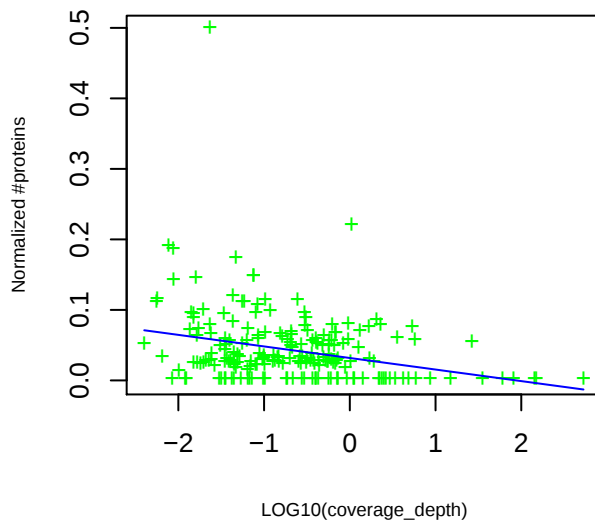
[P] COG0614 ABC-type Fe3+-hydroxamate transport system, periplasmic component

slope= -0.74 p_value= 2.6e-05 intercept= 1.16 p_value= 1.1e-08



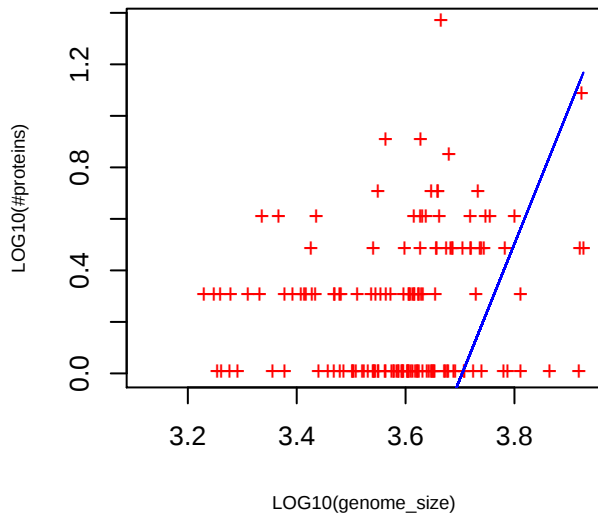
[P] COG0614 ABC-type Fe3+-hydroxamate transport system, periplasmic component

slope= -0.016 p_value= 6.2e-05 intercept= 0.032 p_value= 3.3e-11

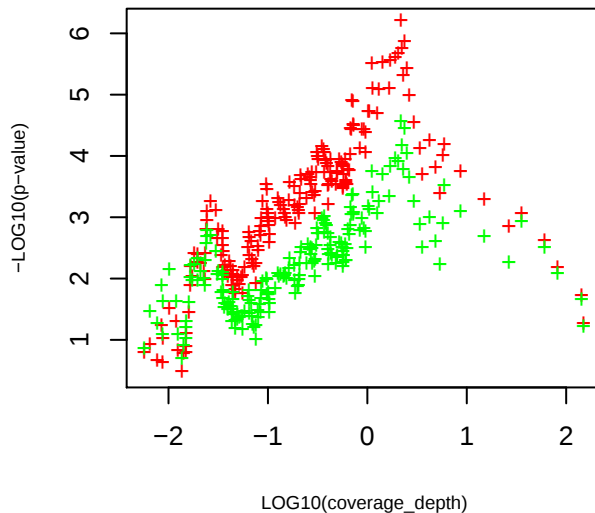


[P] COG0614 ABC-type Fe3+-hydroxamate transport system, periplasmic component

slope= 5.24 p_value= 1.3e-11 intercept= -19.42 p_value= 2.1e-12

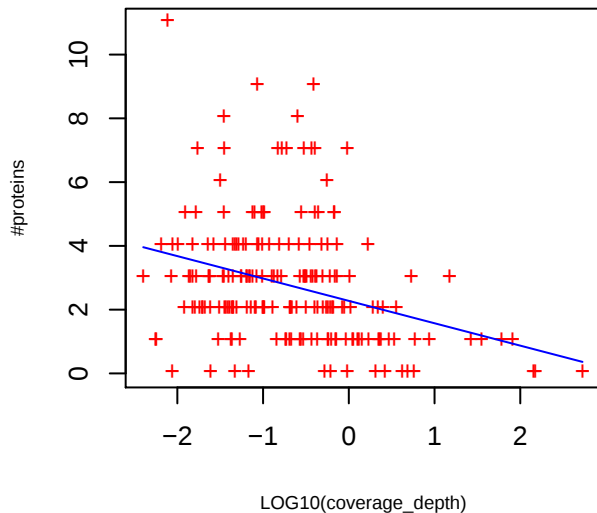


P-value curve ; red (unnorm), green (norm)



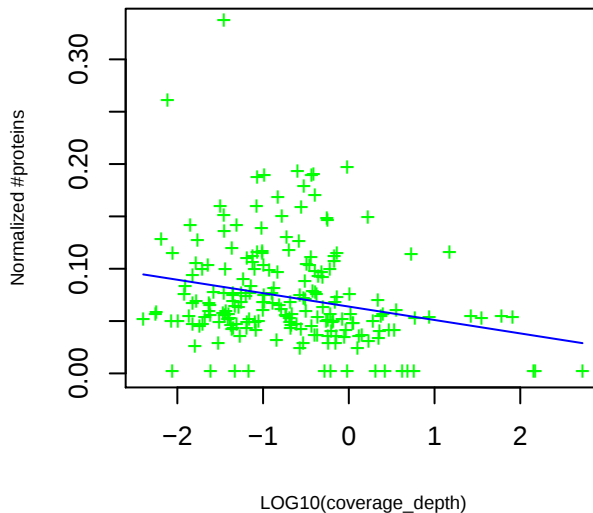
[P] COG2217 Cation transport ATPase

slope= -0.70 p_value= 4.4e-06 intercept= 2.28 p_value= 5.9e-30



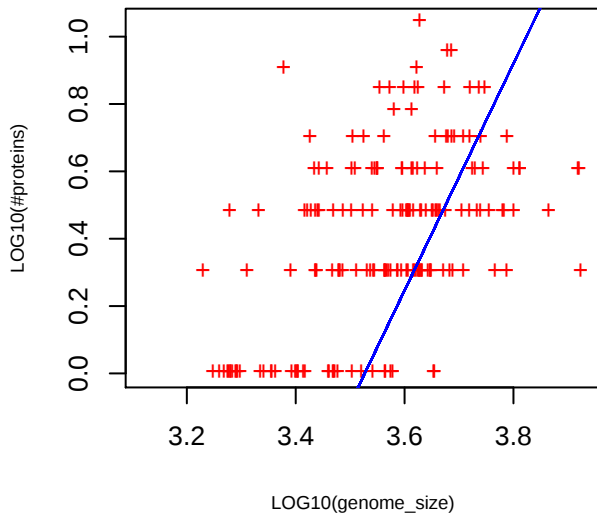
[P] COG2217 Cation transport ATPase

slope= -0.013 p_value= 0.0010 intercept= 0.064 p_value= 2.2e-33

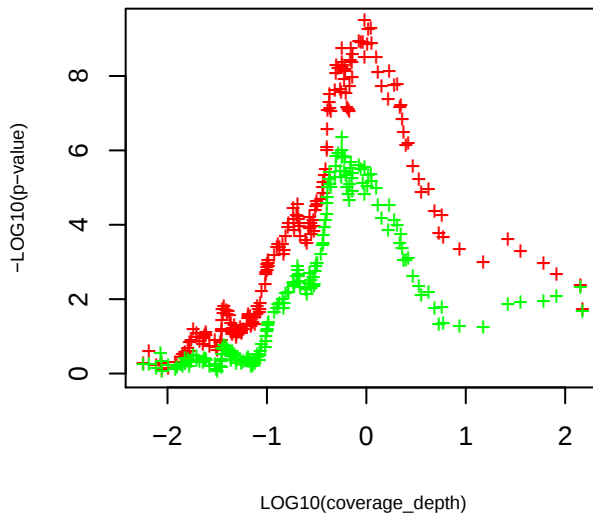


[P] COG2217 Cation transport ATPase

slope= 3.37 p_value= 1.2e-11 intercept= -11.88 p_value= 1.6e-11

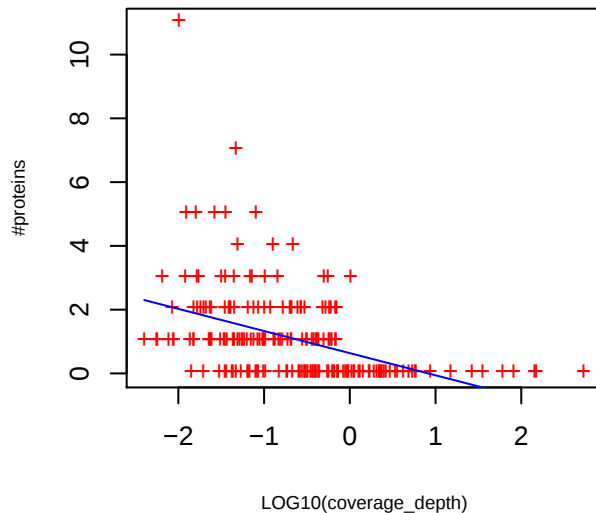


P-value curve ; red (unnorm), green (norm)



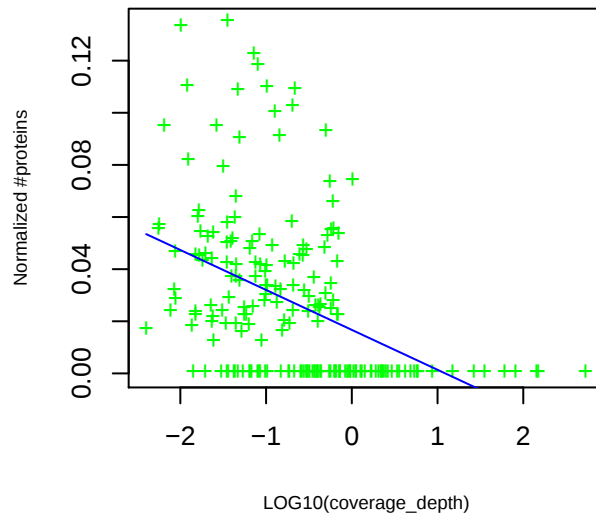
[NT] COG0643 Chemotaxis protein histidine kinase and related kinases

slope= -0.69 p_value= 3.0e-10 intercept= 0.64 p_value= 2.1e-07



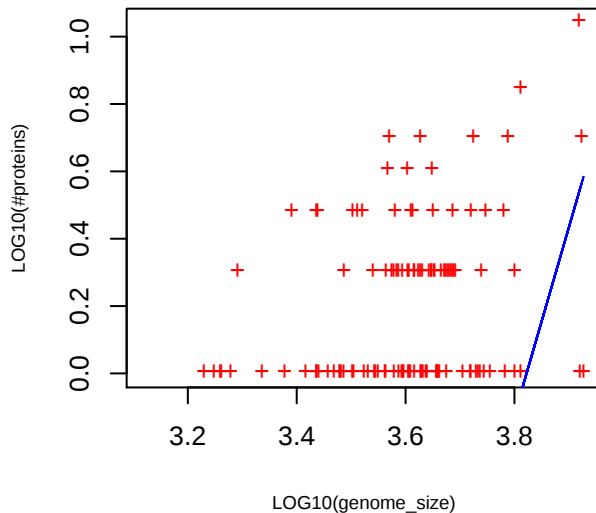
[NT] COG0643 Chemotaxis protein histidine kinase and related kinases

slope= -0.015 p_value= 1.8e-10 intercept= 0.017 p_value= 6.6e-10

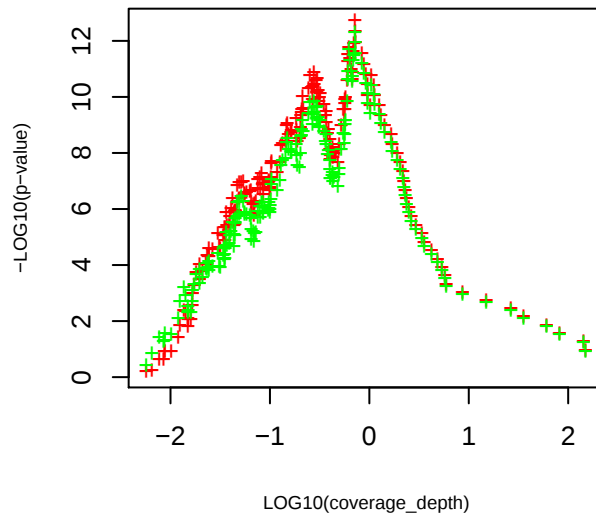


[NT] COG0643 Chemotaxis protein histidine kinase and related kinases

slope= 5.58 p_value= 1.5e-10 intercept= -21.33 p_value= 7.6e-12

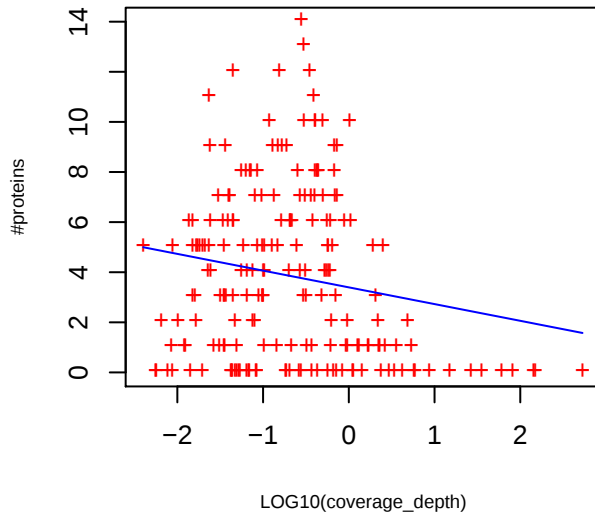


P-value curve ; red (unnorm), green (norm)



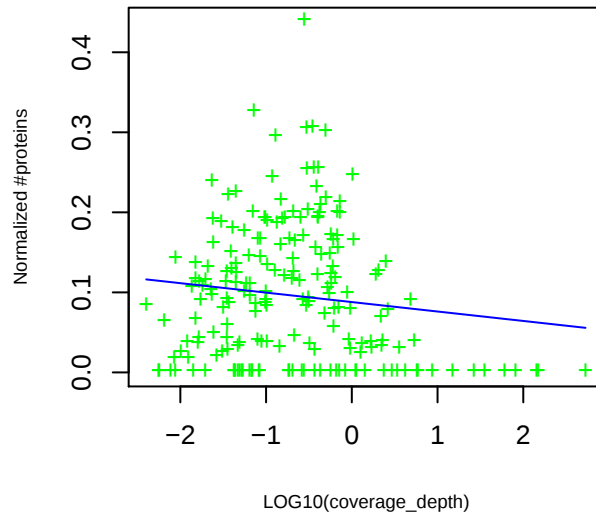
[K] COG0789 Predicted transcriptional regulators

slope= -0.67 p_value= 0.014 intercept= 3.40 p_value= 1.3e-22



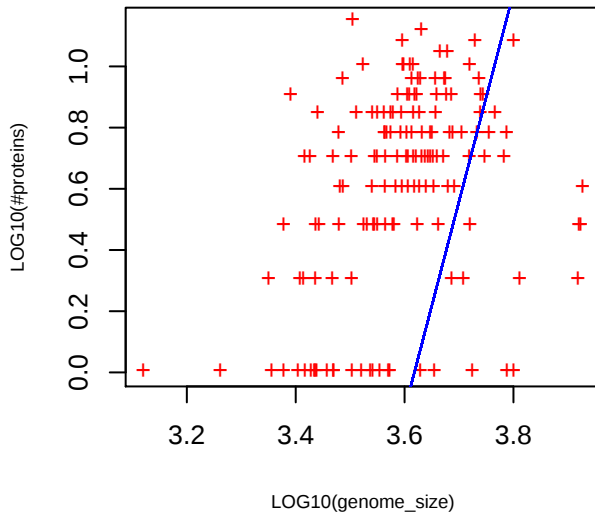
[K] COG0789 Predicted transcriptional regulators

slope= -0.012 p_value= 0.082 intercept= 0.088 p_value= 8.1e-24

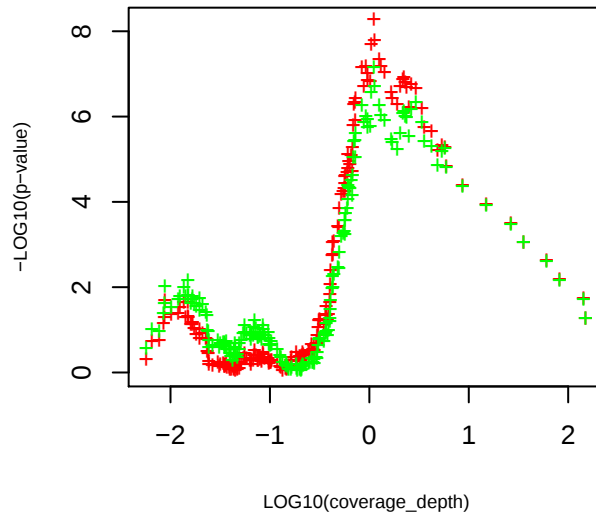


[K] COG0789 Predicted transcriptional regulators

slope= 6.82 p_value= 1.4e-17 intercept= -24.66 p_value= 4.1e-18

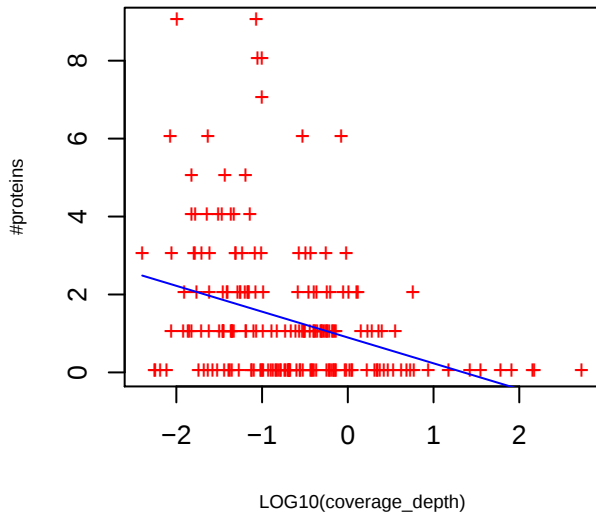


P-value curve ; red (unnorm), green (norm)



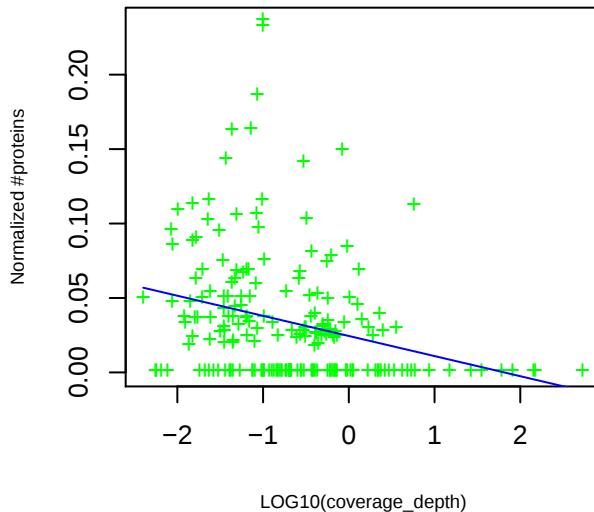
[V] COG0286 Type I restriction-modification system methyltransferase subunit

slope= -0.66 p_value= 2.0e-06 intercept= 0.90 p_value= 1.8e-08



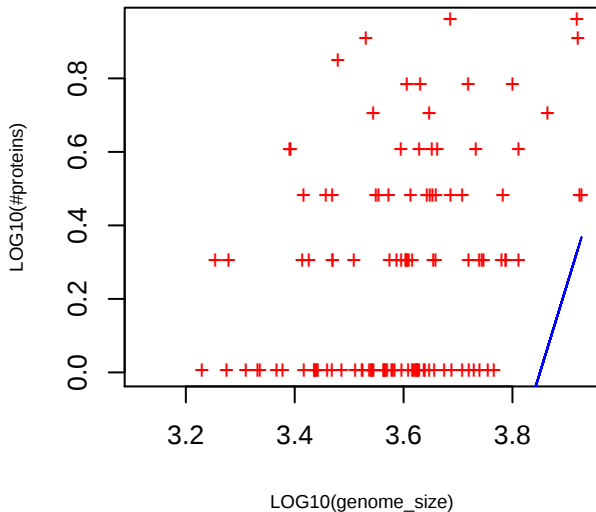
[V] COG0286 Type I restriction-modification system methyltransferase subunit

slope= -0.014 p_value= 6.7e-05 intercept= 0.024 p_value= 5.3e-10

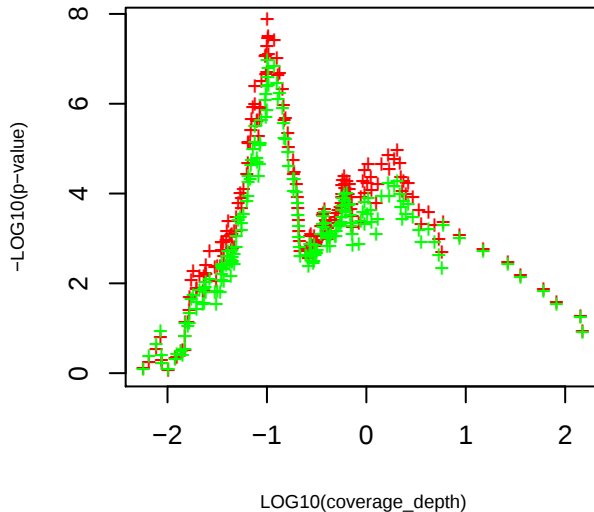


[V] COG0286 Type I restriction-modification system methyltransferase subunit

slope= 4.82 p_value= 6.8e-08 intercept= -18.56 p_value= 5.9e-09

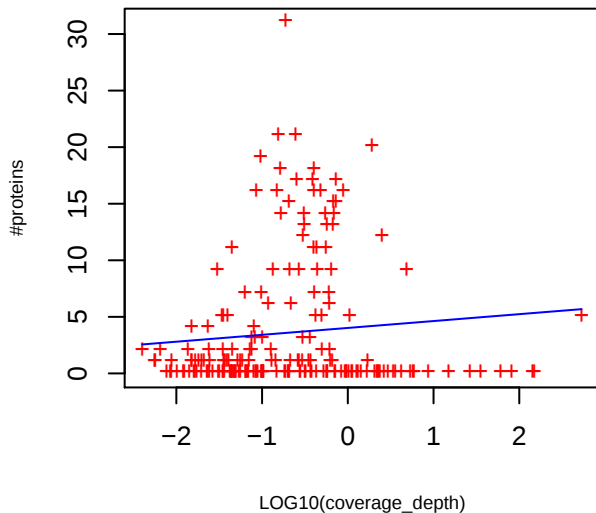


P-value curve ; red (unnorm), green (norm)



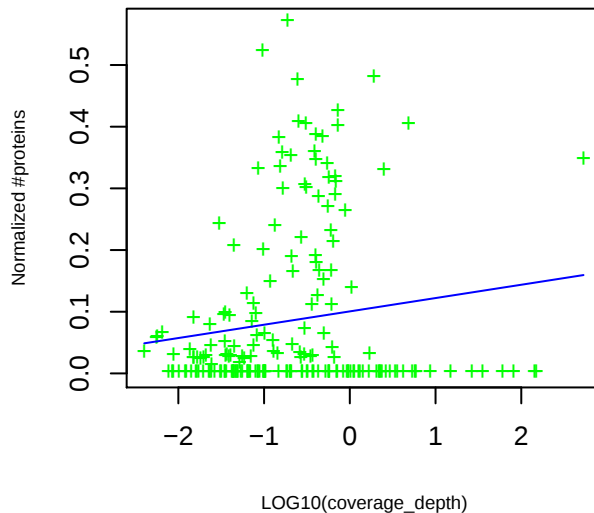
[G] COG1593 TRAP-type C4-dicarboxylate transport system, large permease component

slope= 0.61 p_value= 0.20 intercept= 4.02 p_value= 1.3e-12



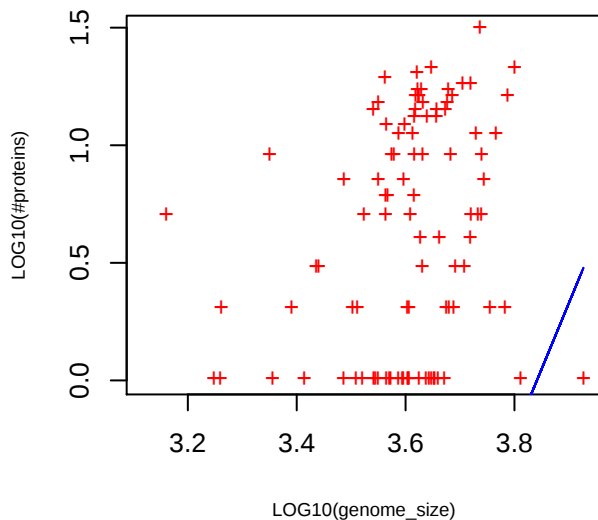
[G] COG1593 TRAP-type C4-dicarboxylate transport system, large permease component

slope= 0.022 p_value= 0.044 intercept= 0.10 p_value= 1.3e-14

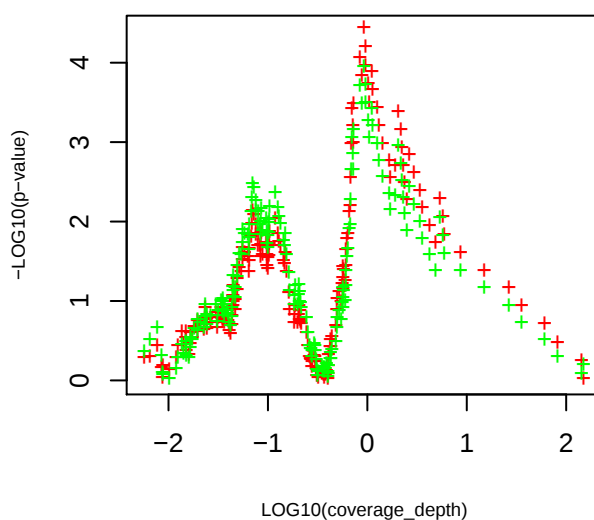


[G] COG1593 TRAP-type C4-dicarboxylate transport system, large permease component

slope= 5.60 p_value= 1.4e-08 intercept= -21.51 p_value= 1.1e-09

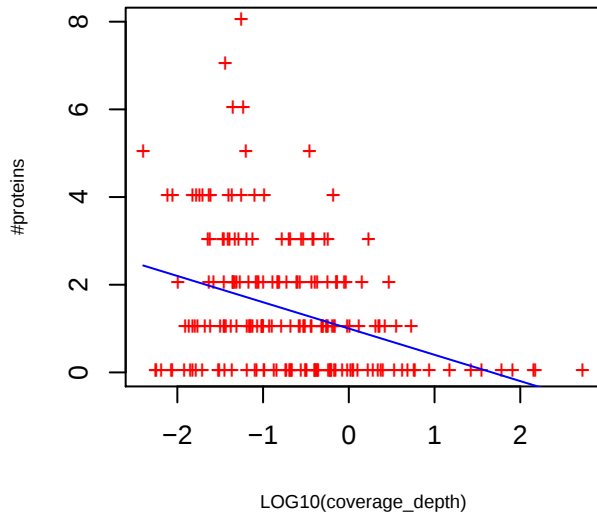


P-value curve ; red (unnorm), green (norm)



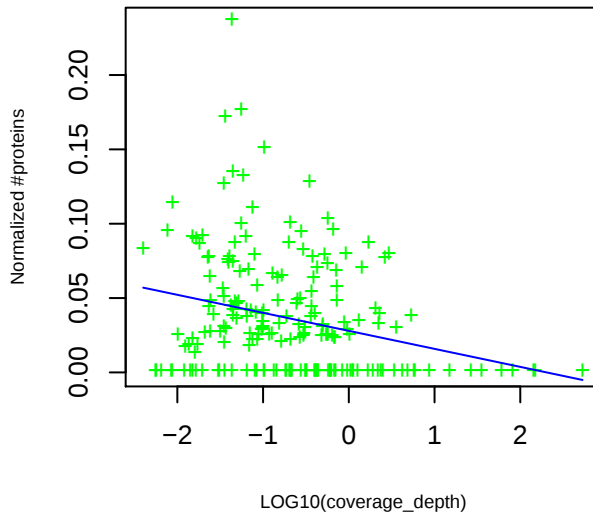
[E] COG0531 Amino acid transporters

slope= -0.60 p_value= 4.3e-07 intercept= 1.00 p_value= 5.4e-13



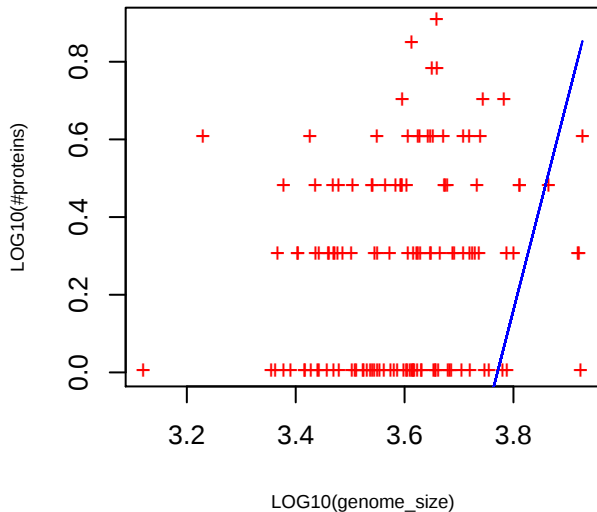
[E] COG0531 Amino acid transporters

slope= -0.012 p_value= 0.00012 intercept= 0.028 p_value= 1e-13

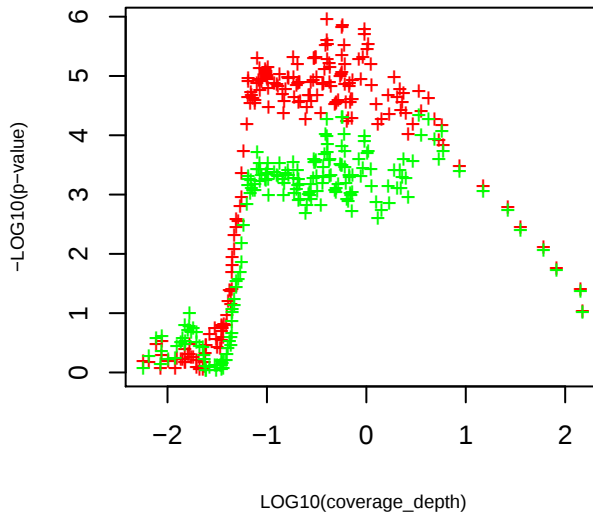


[E] COG0531 Amino acid transporters

slope= 5.46 p_value= 1.8e-10 intercept= -20.59 p_value= 1.6e-11

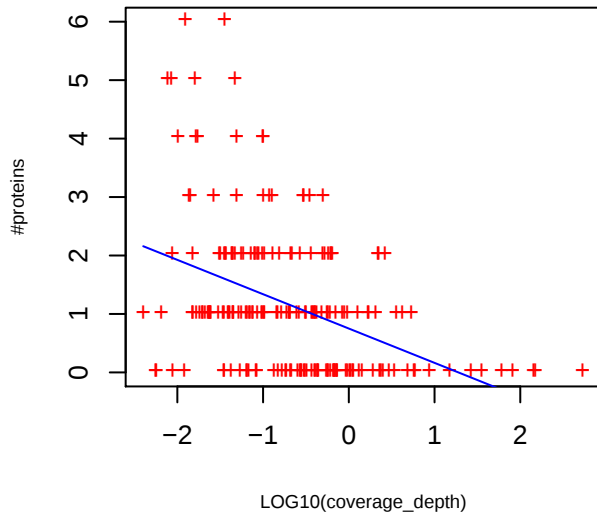


P-value curve ; red (unnorm), green (norm)



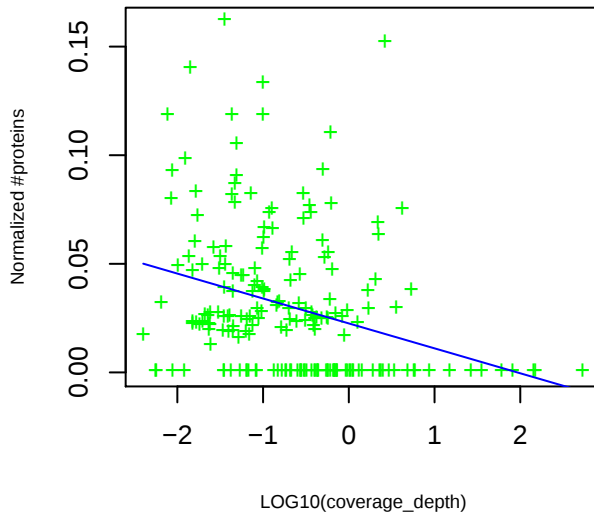
[O] COG0501 Zn-dependent protease with chaperone function

slope= -0.59 p_value= 1.2e-09 intercept= 0.75 p_value= 1.0e-11



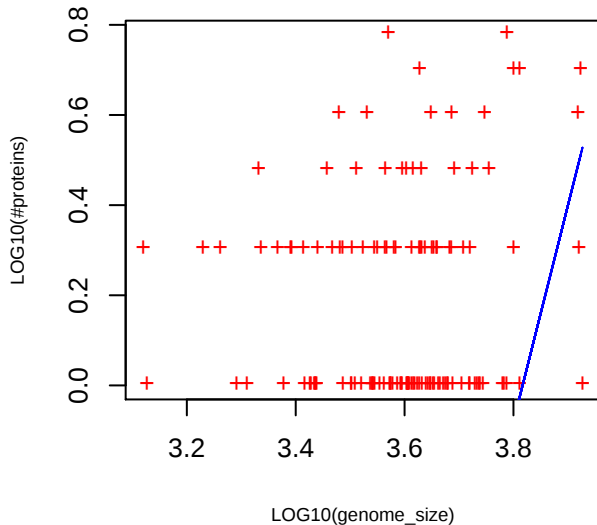
[O] COG0501 Zn-dependent protease with chaperone function

slope= -0.011 p_value= 1.4e-05 intercept= 0.023 p_value= 4.6e-13

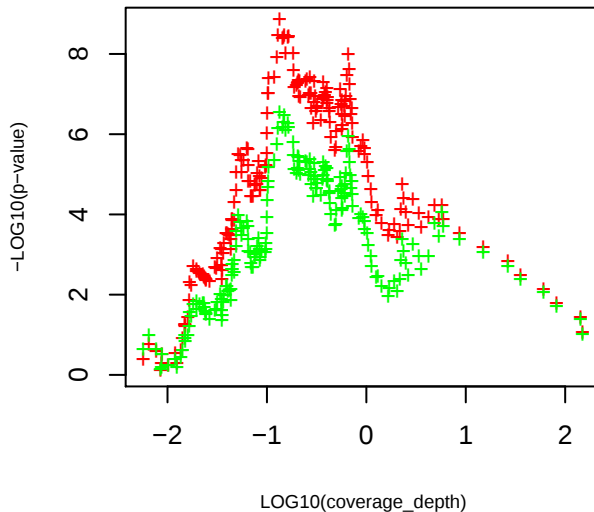


[O] COG0501 Zn-dependent protease with chaperone function

slope= 4.79 p_value= 1.9e-08 intercept= -18.29 p_value= 1.9e-09

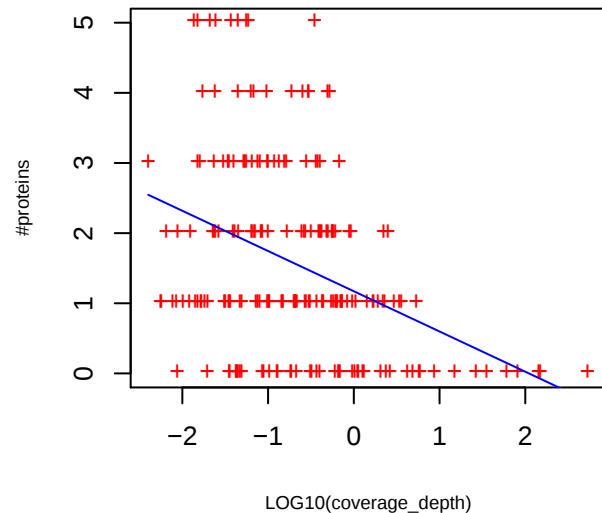


P-value curve ; red (unnorm), green (norm)



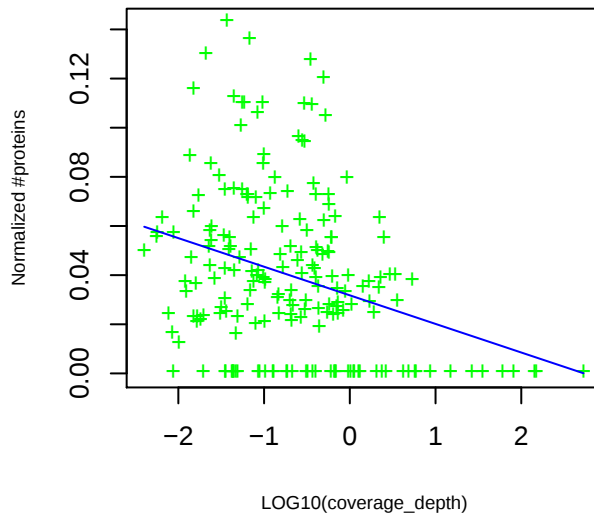
[I] COG1502 Phosphatidylserine/phosphatidylglycerophosphate/cardioliipin synthases and related enz

slope= -0.57 p_value= 7.9e-08 intercept= 1.17 p_value= 1.5e-19



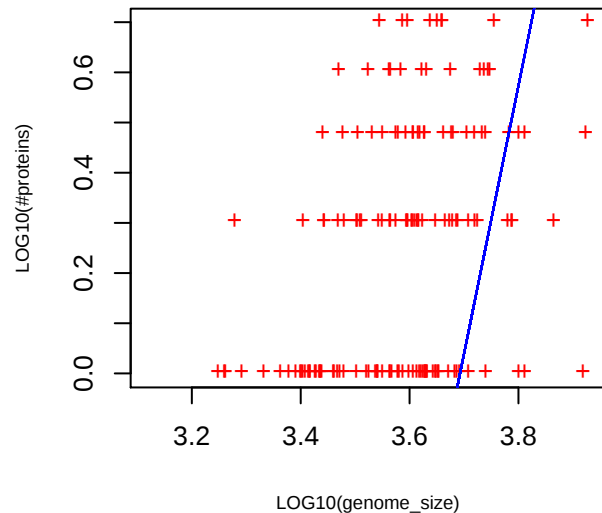
[I] COG1502 Phosphatidylserine/phosphatidylglycerophosphate/cardioliipin synthases and related enz

slope= -0.012 p_value= 1.0e-05 intercept= 0.032 p_value= 4.2e-22

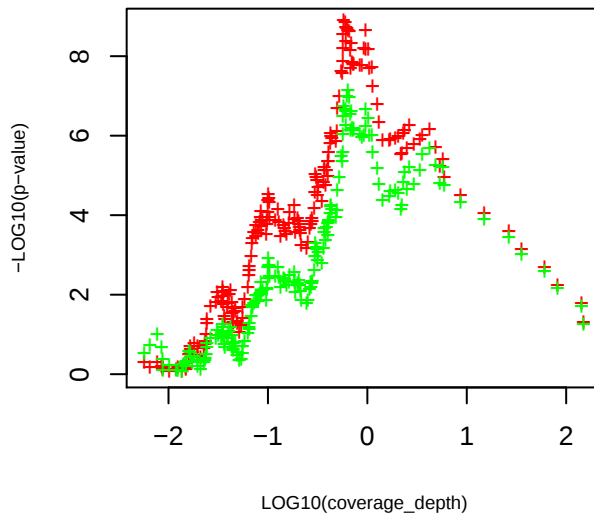


[I] COG1502 Phosphatidylserine/phosphatidylglycerophosphate/cardioliipin synthases and related enz

slope= 5.34 p_value= 2.2e-12 intercept= -19.72 p_value= 3.5e-13

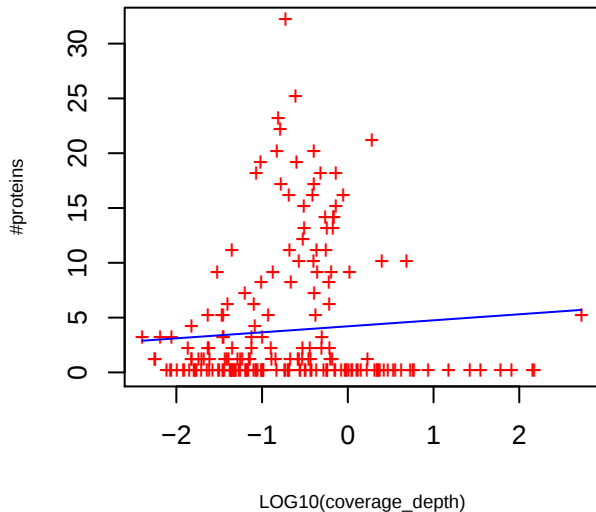


P-value curve ; red (unnorm), green (norm)



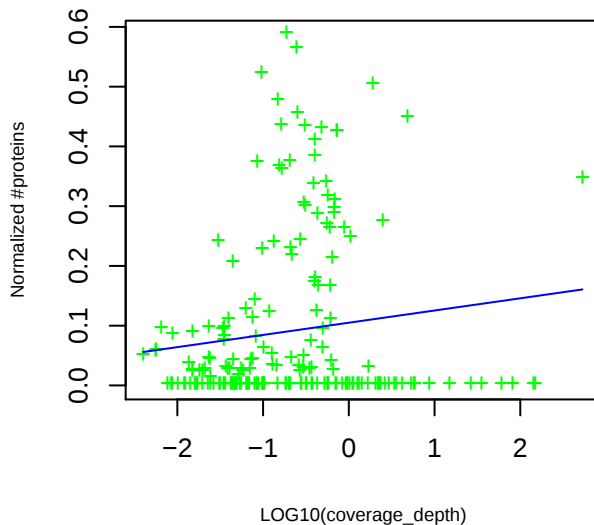
[G] COG1638 TRAP-type C4-dicarboxylate transport system, periplasmic component

slope= 0.55 p_value= 0.28 intercept= 4.21 p_value= 3.5e-12



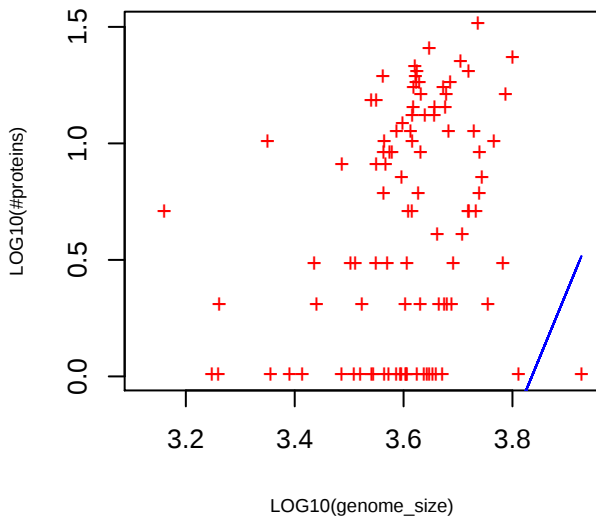
[G] COG1638 TRAP-type C4-dicarboxylate transport system, periplasmic component

slope= 0.020 p_value= 0.074 intercept= 0.10 p_value= 4.1e-14

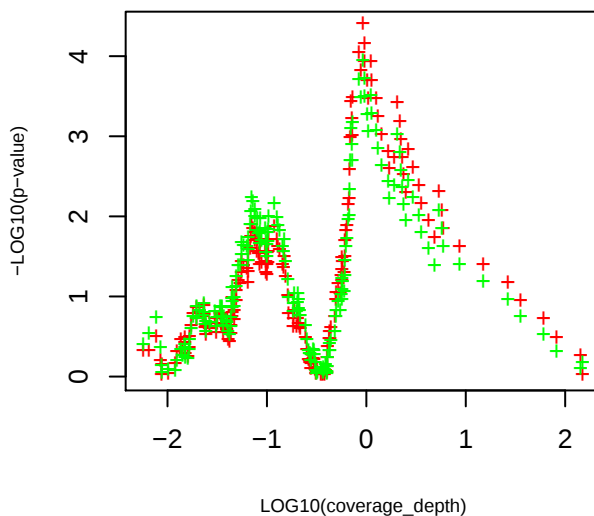


[G] COG1638 TRAP-type C4-dicarboxylate transport system, periplasmic component

slope= 5.66 p_value= 1.2e-08 intercept= -21.72 p_value= 9e-10

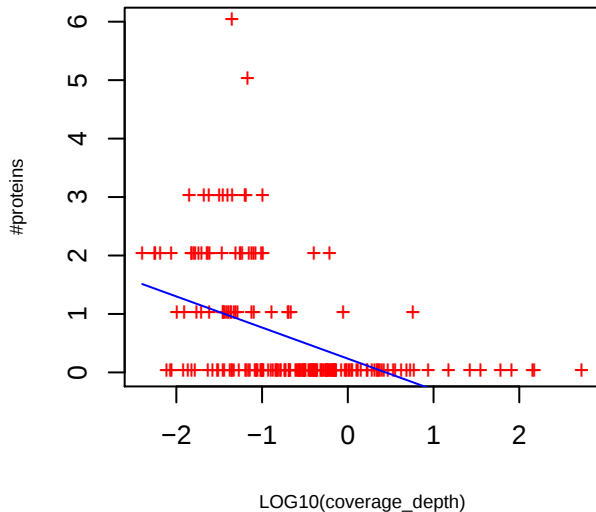


P-value curve ; red (unnorm), green (norm)



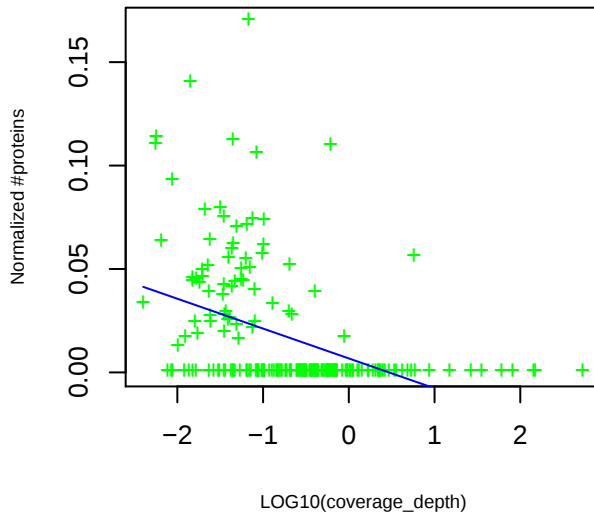
[O] COG1180 Pyruvate-formate lyase-activating enzyme

slope= -0.53 p_value= 1.2e-11 intercept= 0.24 p_value= 0.0052



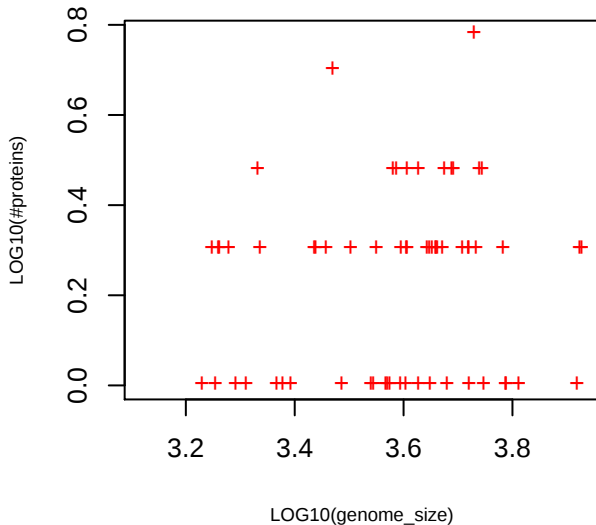
[O] COG1180 Pyruvate-formate lyase-activating enzyme

slope= -0.014 p_value= 4.5e-10 intercept= 0.0068 p_value= 0.007

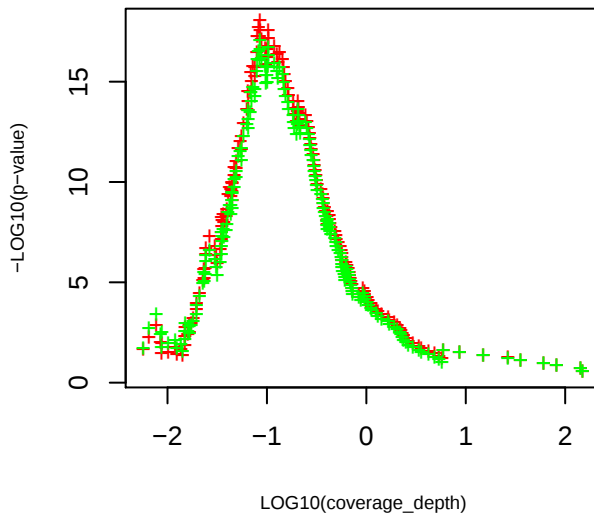


[O] COG1180 Pyruvate-formate lyase-activating enzyme

slope= 1.85 p_value= 0.032 intercept= -9.22 p_value= 0.0028

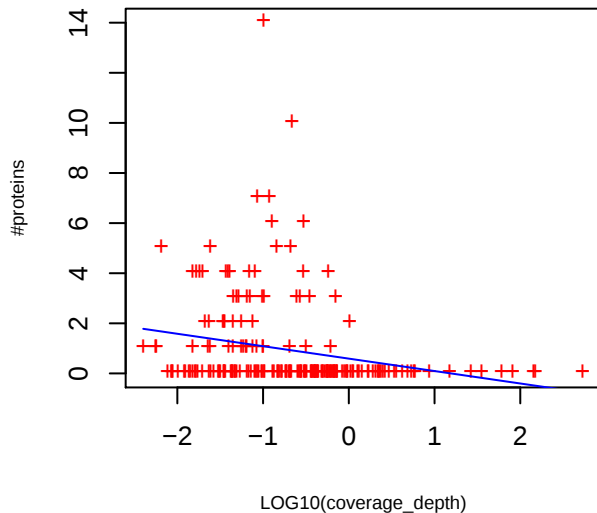


P-value curve ; red (unnorm), green (norm)



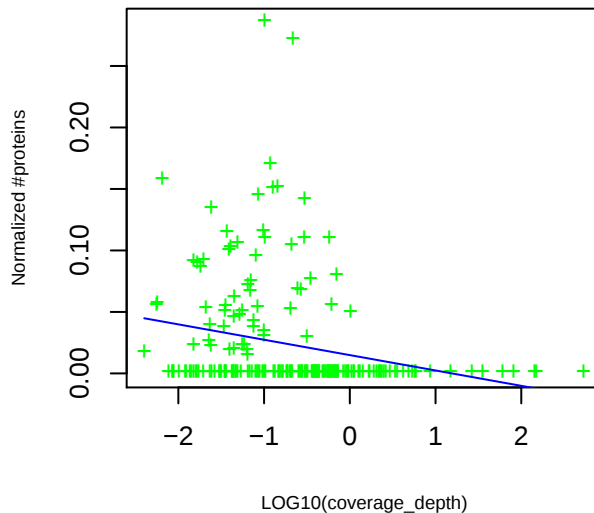
[T] COG1639 Predicted signal transduction protein

slope= -0.50 p_value= 0.0011 intercept= 0.59 p_value= 0.00059



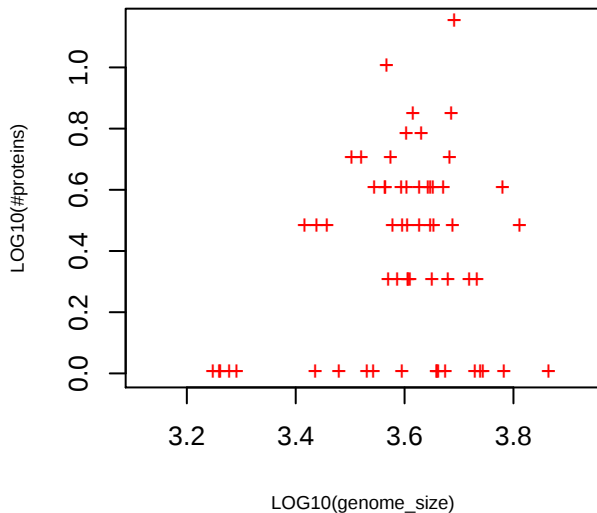
[T] COG1639 Predicted signal transduction protein

slope= -0.012 p_value= 0.00075 intercept= 0.015 p_value= 0.00038

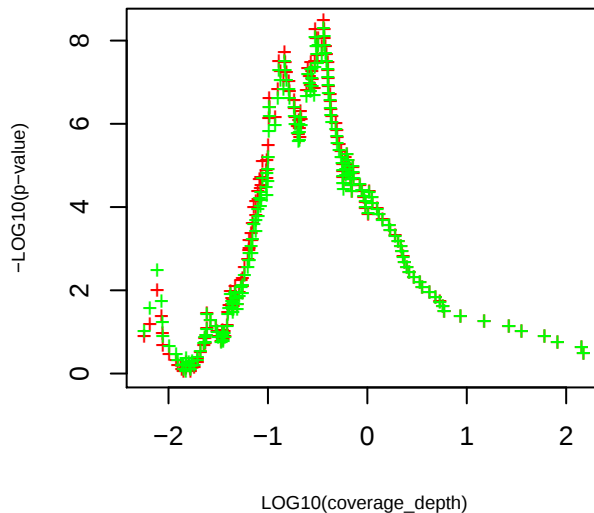


[T] COG1639 Predicted signal transduction protein

slope= 2.58 p_value= 0.0035 intercept= -11.81 p_value= 0.00018

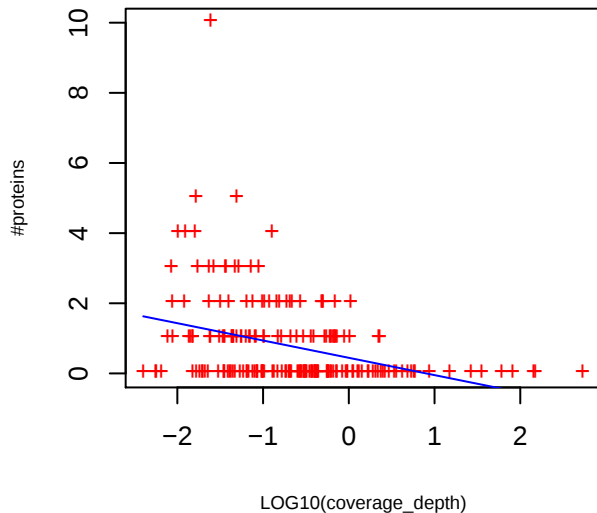


P-value curve ; red (unnorm), green (norm)



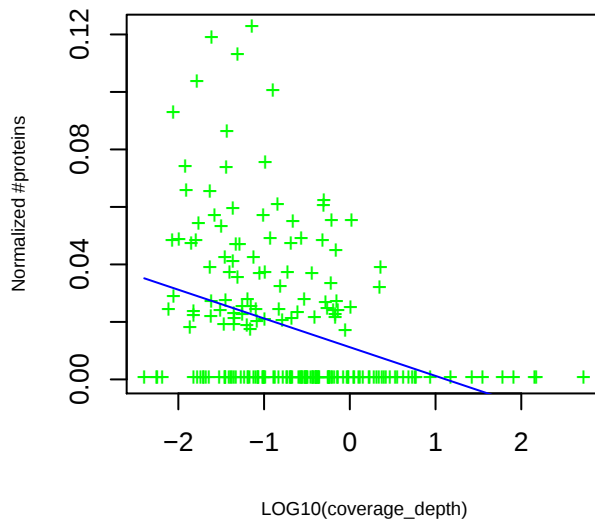
[T] COG0631 Serine/threonine protein phosphatase

slope= -0.49 p_value= 4.9e-07 intercept= 0.45 p_value= 4.8e-05



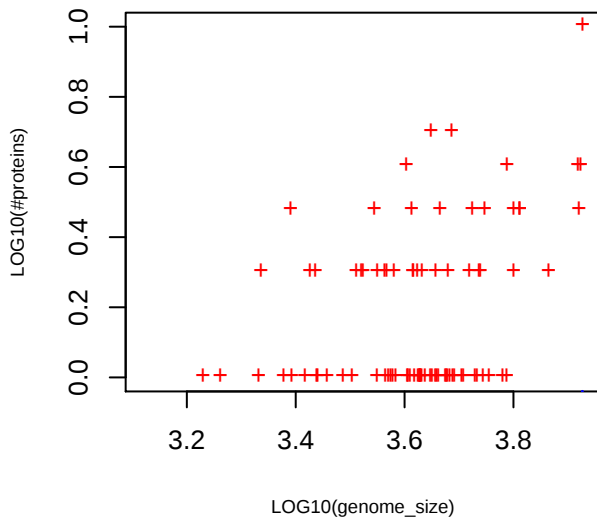
[T] COG0631 Serine/threonine protein phosphatase

slope= -0.01 p_value= 1.1e-06 intercept= 0.011 p_value= 1.2e-06

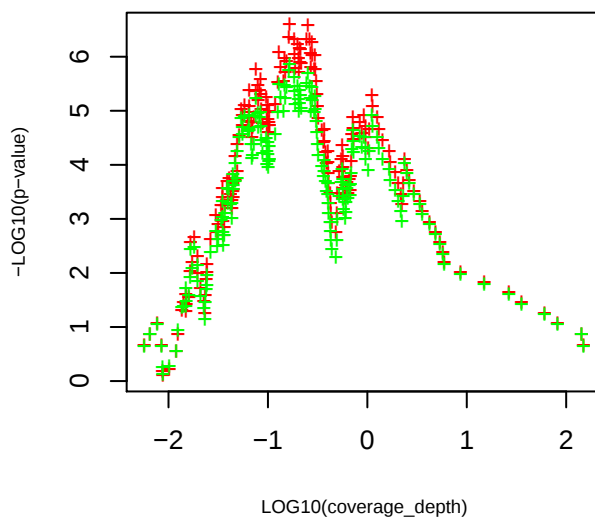


[T] COG0631 Serine/threonine protein phosphatase

slope= 5.65 p_value= 8.2e-11 intercept= -22.22 p_value= 1.1e-12

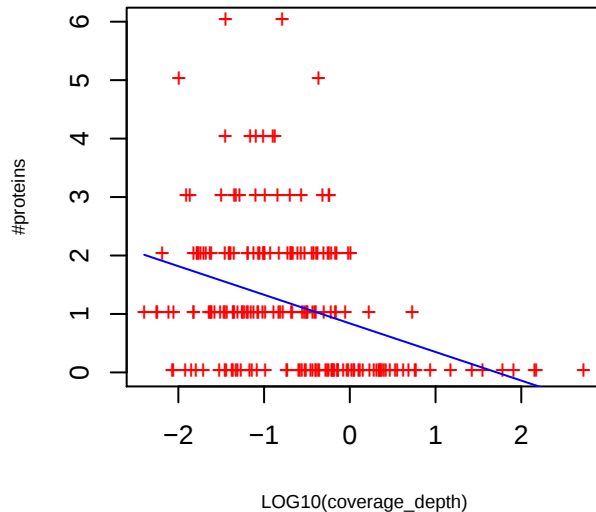


P-value curve ; red (unnorm), green (norm)



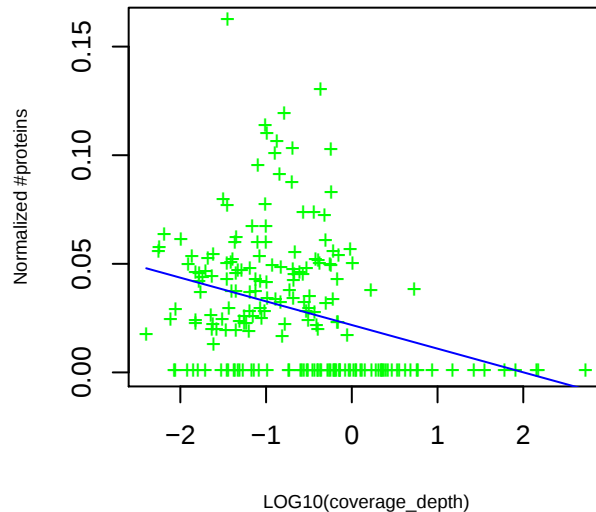
[NT] COG1352 Methylase of chemotaxis methyl-accepting proteins

slope= -0.49 p_value= 4.7e-07 intercept= 0.84 p_value= 1.8e-13



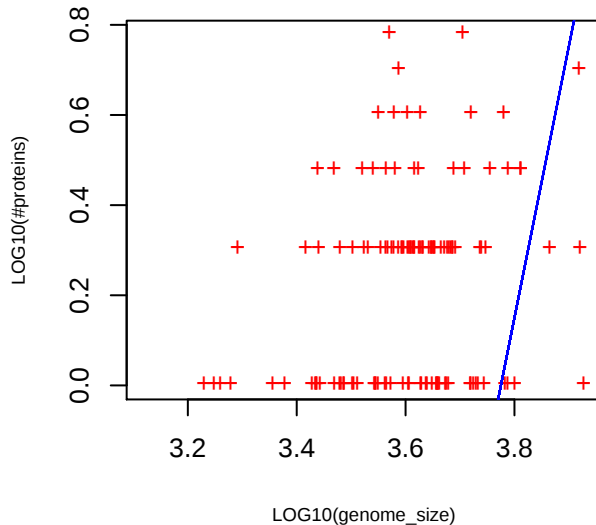
[NT] COG1352 Methylase of chemotaxis methyl-accepting proteins

slope= -0.011 p_value= 7e-06 intercept= 0.022 p_value= 3.3e-14

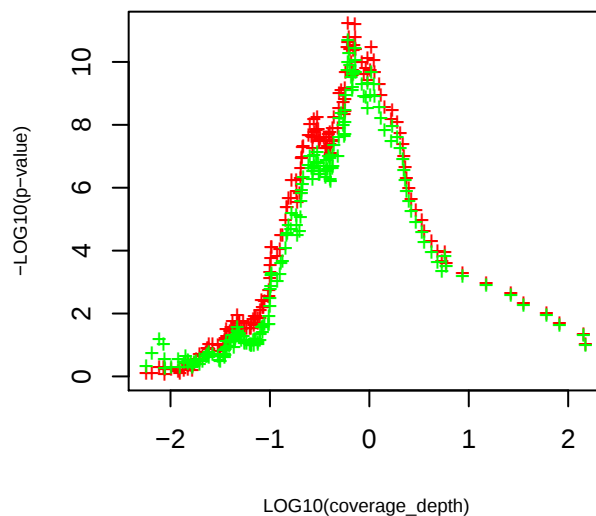


[NT] COG1352 Methylase of chemotaxis methyl-accepting proteins

slope= 6.03 p_value= 1.5e-12 intercept= -22.75 p_value= 8e-14

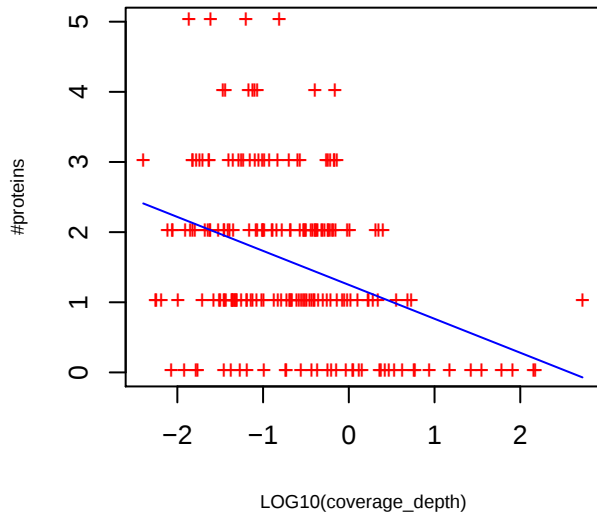


P-value curve ; red (unnorm), green (norm)



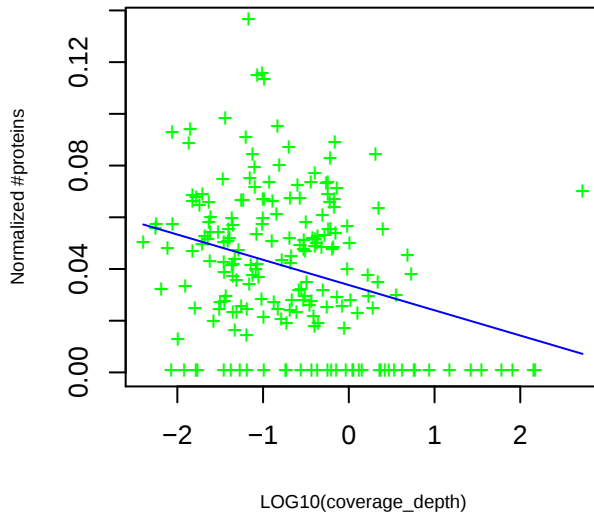
[C] COG0584 Glycerophosphoryl diester phosphodiesterase

slope= -0.48 p_value= 1.5e-07 intercept= 1.25 p_value= 1.5e-26



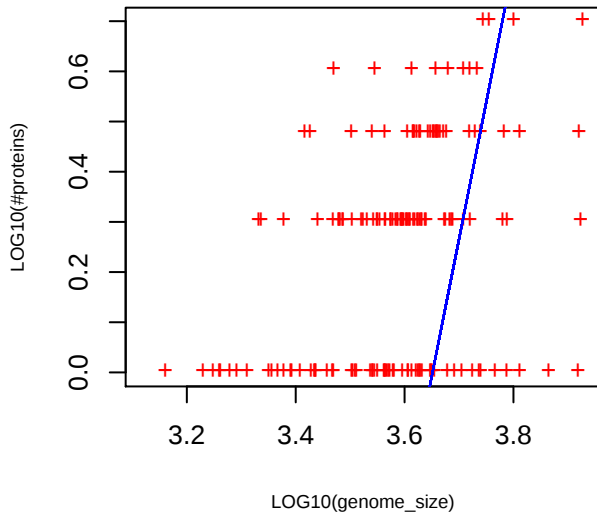
[C] COG0584 Glycerophosphoryl diester phosphodiesterase

slope= -0.0098 p_value= 1.2e-05 intercept= 0.034 p_value= 1.5e-30

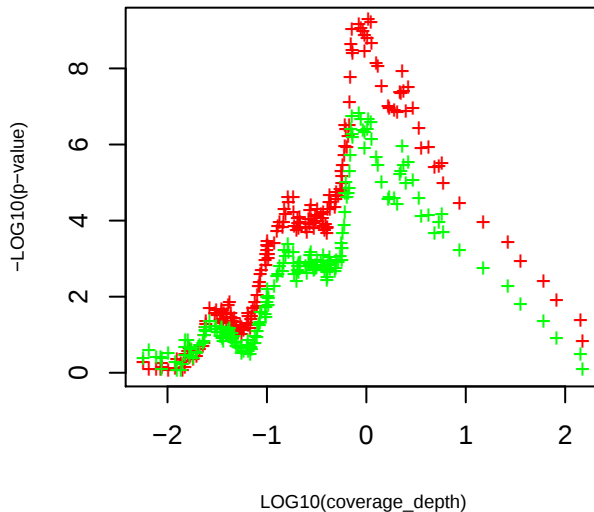


[C] COG0584 Glycerophosphoryl diester phosphodiesterase

slope= 5.46 p_value= 1.8e-15 intercept= -19.92 p_value= 3.7e-16

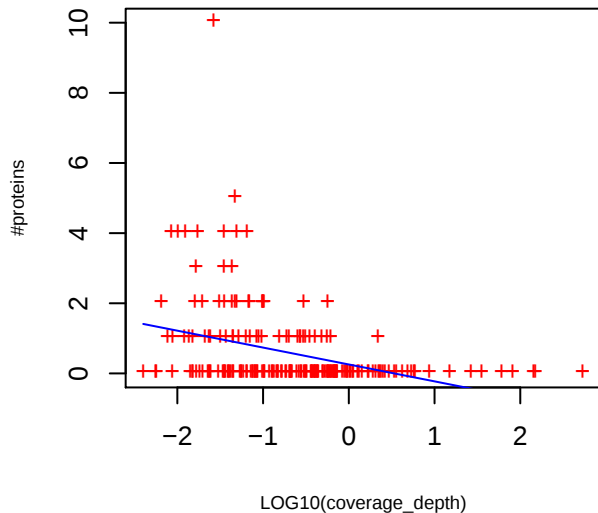


P-value curve ; red (unnorm), green (norm)



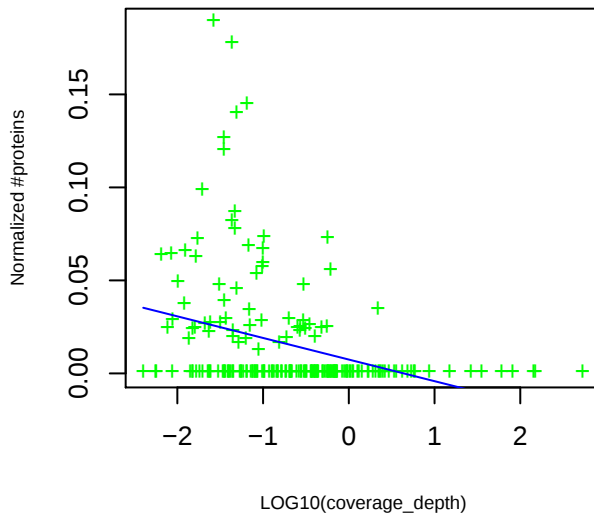
[P] COG0474 Cation transport ATPase

slope= -0.48 p_value= 3.5e-07 intercept= 0.26 p_value= 0.014



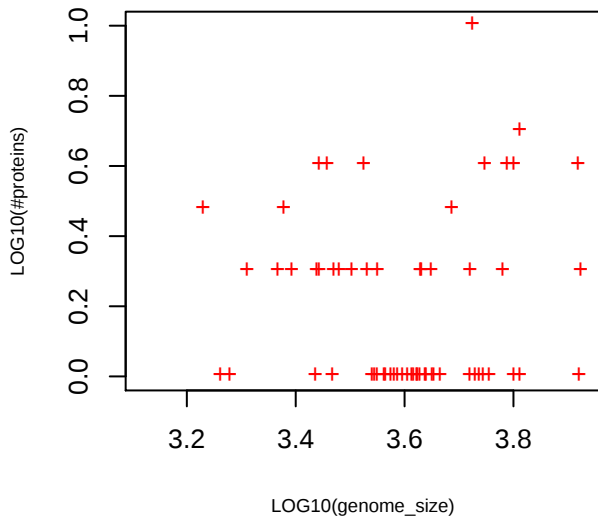
[P] COG0474 Cation transport ATPase

slope= -0.012 p_value= 3.5e-06 intercept= 0.0075 p_value= 0.0072

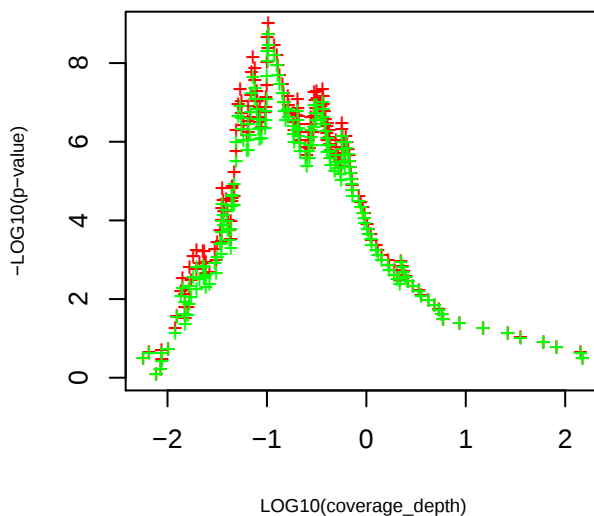


[P] COG0474 Cation transport ATPase

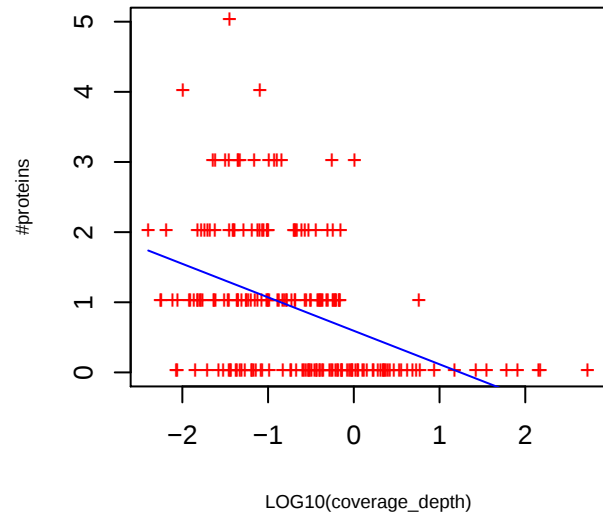
slope= 2.69 p_value= 0.0014 intercept= -12.25 p_value= 5e-05



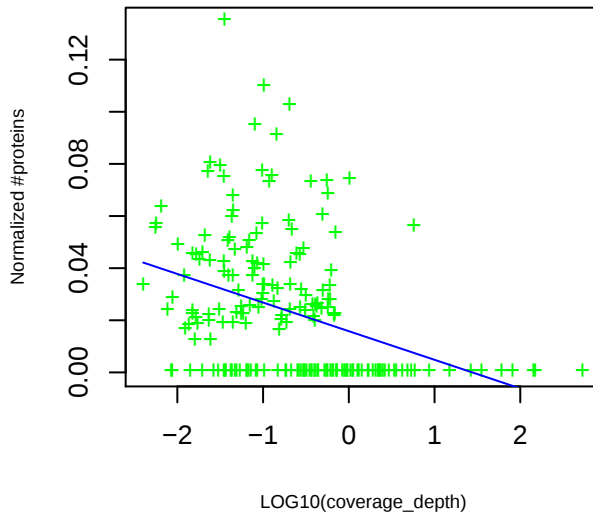
P-value curve ; red (unnorm), green (norm)



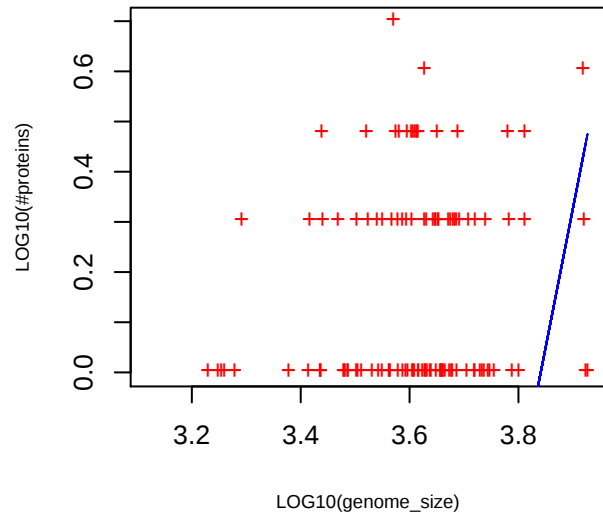
slope= -0.48 p_value= 1.1e-09 intercept= 0.59 p_value= 3.1e-11



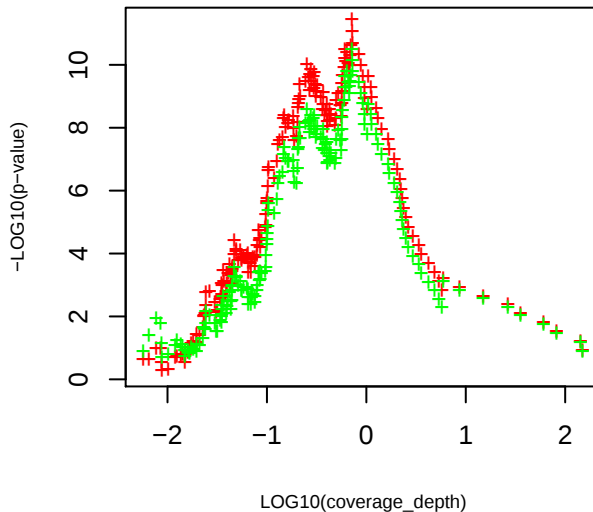
slope= -0.011 p_value= 1.0e-07 intercept= 0.016 p_value= 2.9e-11



slope= 5.53 p_value= 1.7e-10 intercept= -21.22 p_value= 7.4e-12

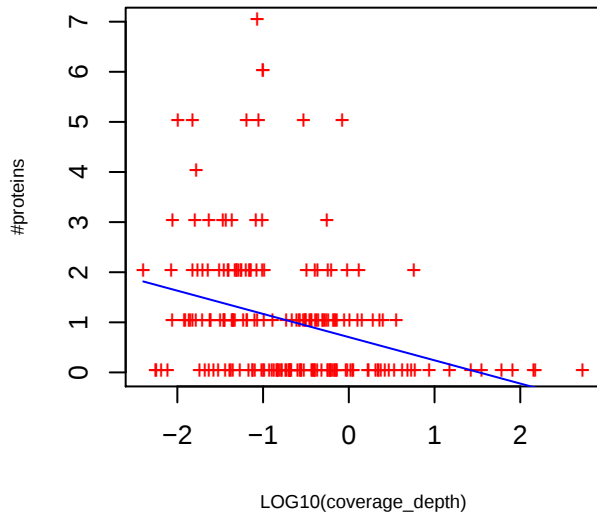


P-value curve ; red (unnorm), green (norm)



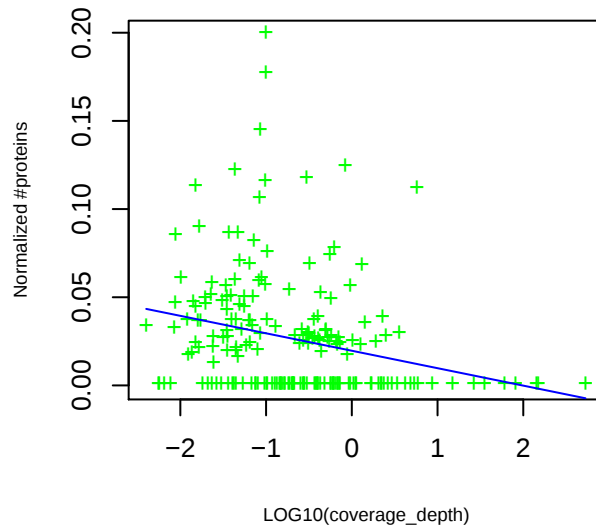
[V] COG0732 Restriction endonuclease S subunits

slope= -0.46 p_value= 7.8e-06 intercept= 0.70 p_value= 3.6e-09



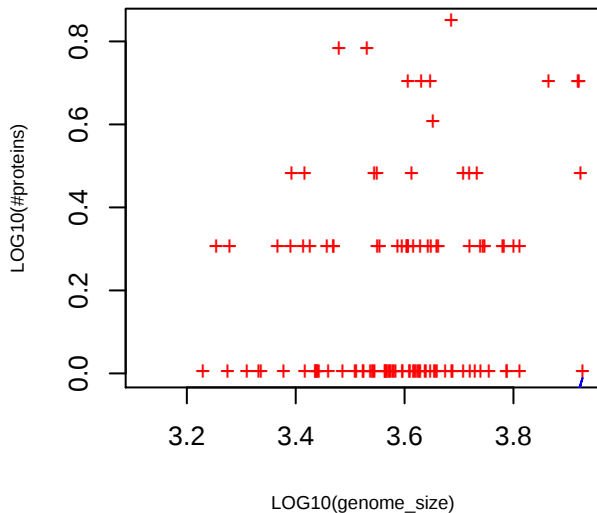
[V] COG0732 Restriction endonuclease S subunits

slope= -0.0099 p_value= 0.00027 intercept= 0.020 p_value= 5.4e-10

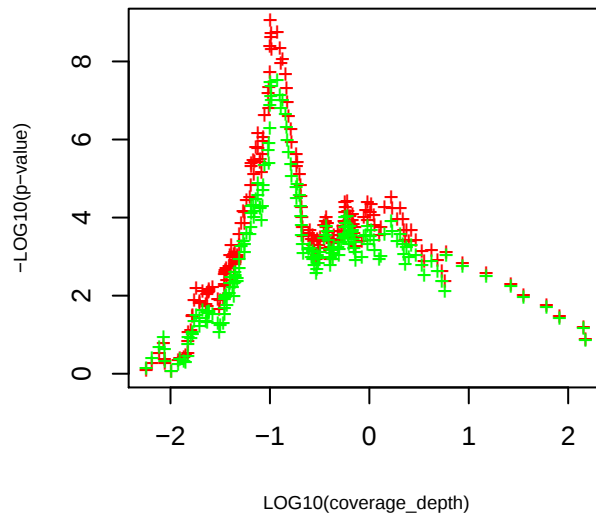


[V] COG0732 Restriction endonuclease S subunits

slope= 4.32 p_value= 1.3e-06 intercept= -16.99 p_value= 1.0e-07

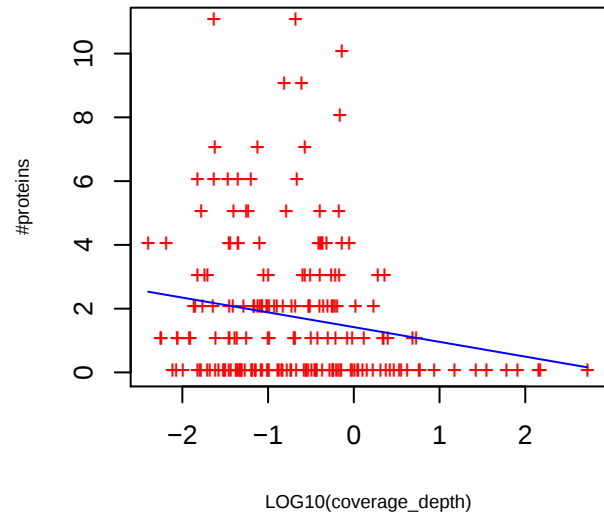


P-value curve ; red (unnorm), green (norm)

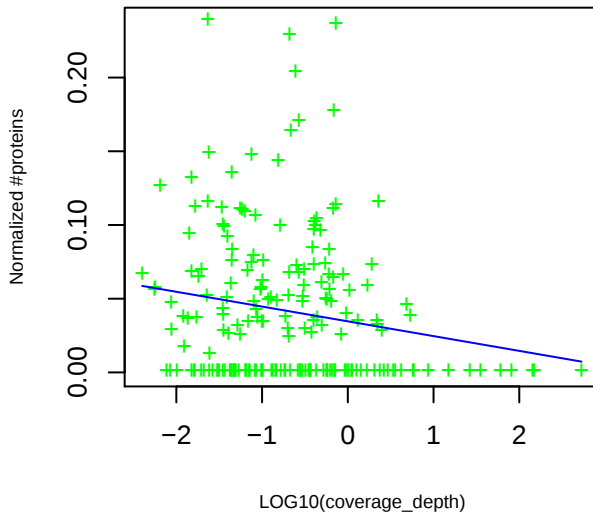


riptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family)

slope= -0.46 p_value= 0.011 intercept= 1.42 p_value= 3.9e-11

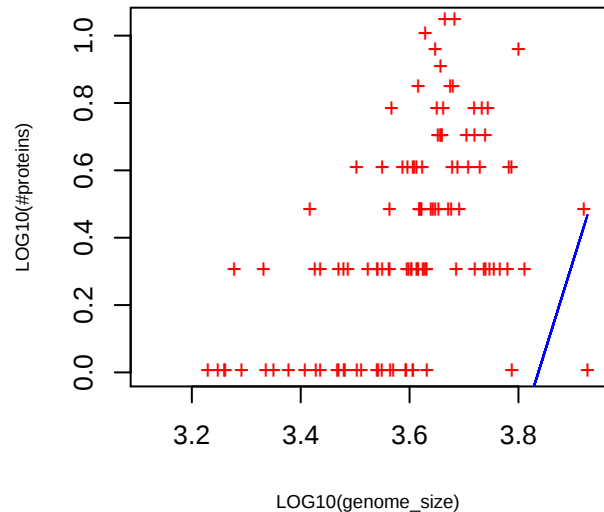


slope= -0.01 p_value= 0.012 intercept= 0.035 p_value= 5.3e-13

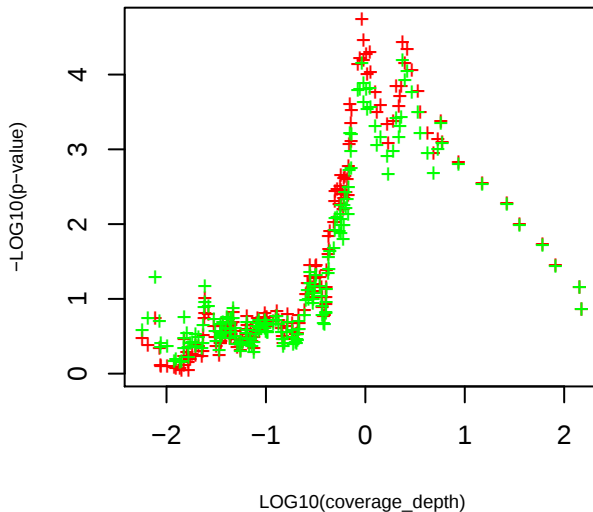


riptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family)

slope= 5.18 p_value= 2.2e-08 intercept= -19.86 p_value= 1.8e-09

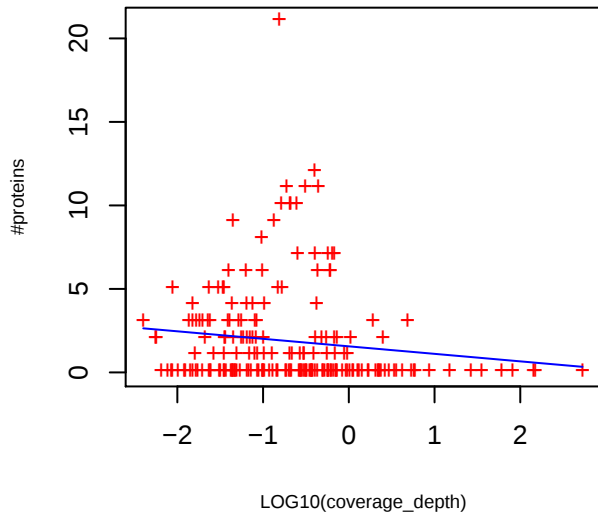


P-value curve ; red (unnorm), green (norm)



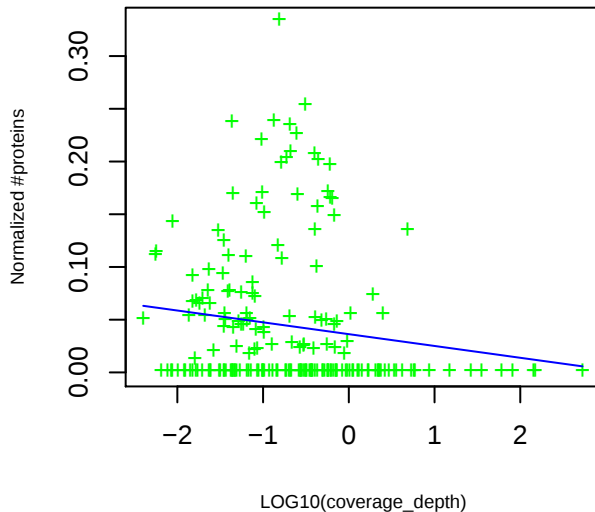
[G] COG1879 ABC-type sugar transport system, periplasmic component

slope= -0.45 p_value= 0.067 intercept= 1.56 p_value= 5.4e-08



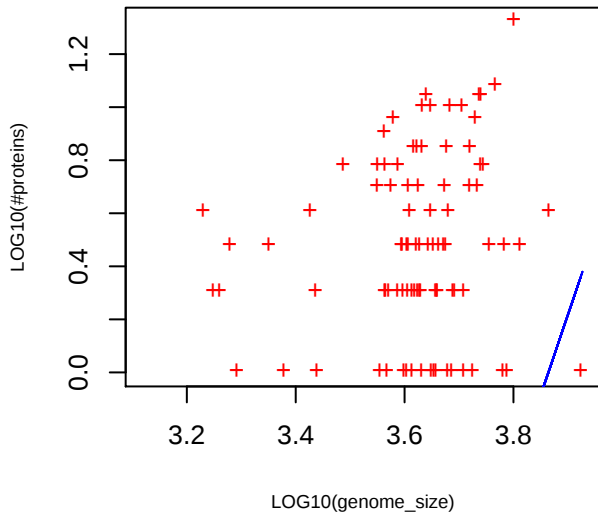
[G] COG1879 ABC-type sugar transport system, periplasmic component

slope= -0.011 p_value= 0.037 intercept= 0.036 p_value= 8.2e-09

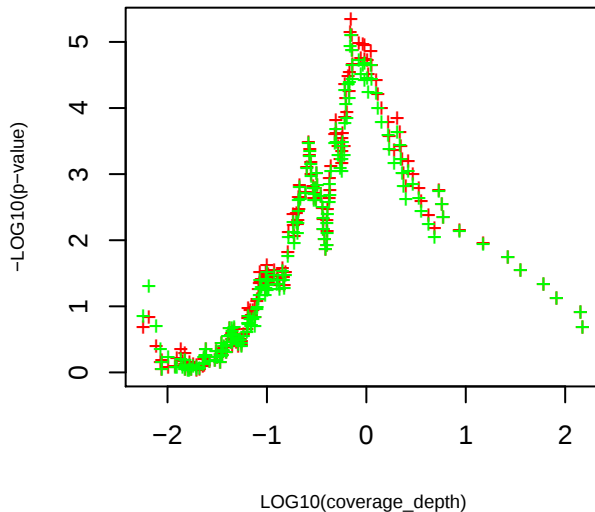


[G] COG1879 ABC-type sugar transport system, periplasmic component

slope= 6.06 p_value= 1.1e-10 intercept= -23.41 p_value= 3.3e-12

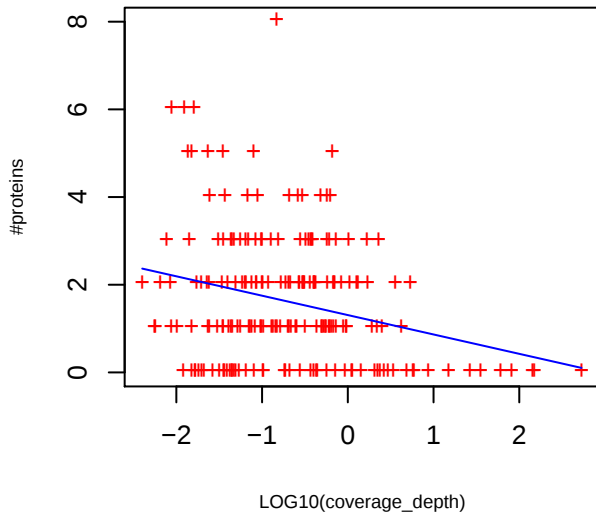


P-value curve ; red (unnorm), green (norm)



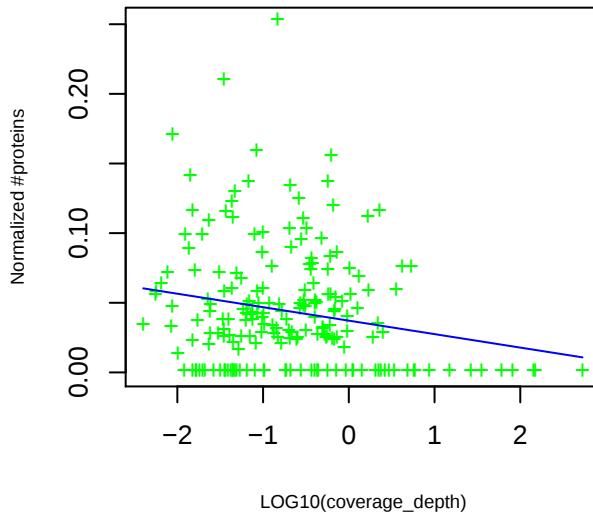
[R] COG2244 Membrane protein involved in the export of O-antigen and teichoic acid

slope= -0.44 p_value= 0.00019 intercept= 1.31 p_value= 3.3e-19



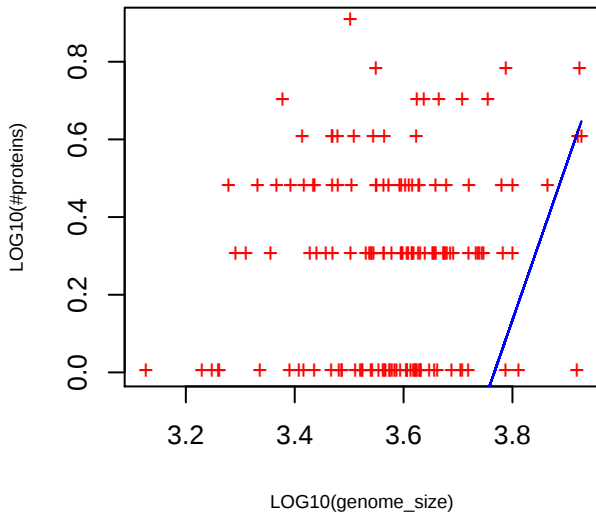
[R] COG2244 Membrane protein involved in the export of O-antigen and teichoic acid

slope= -0.0097 p_value= 0.0051 intercept= 0.037 p_value= 3.2e-18

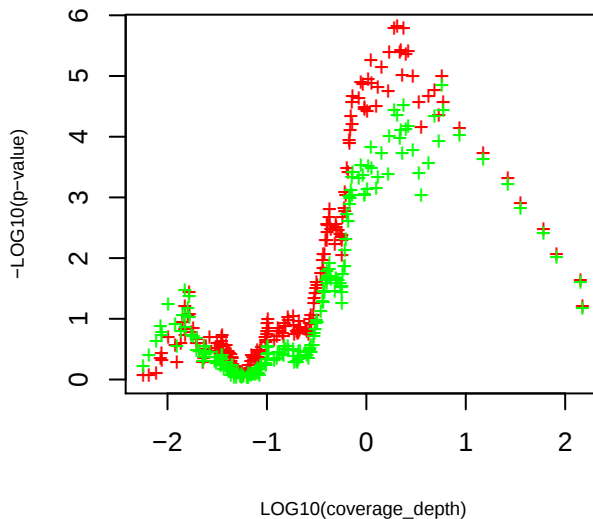


[R] COG2244 Membrane protein involved in the export of O-antigen and teichoic acid

slope= 4.04 p_value= 8.6e-07 intercept= -15.21 p_value= 2.0e-07

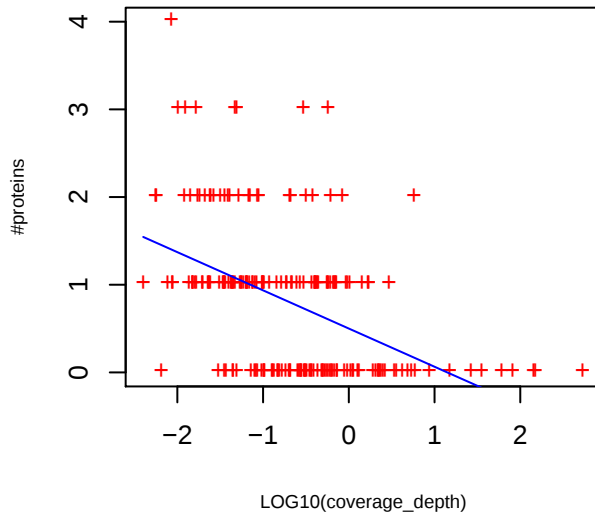


P-value curve ; red (unnorm), green (norm)



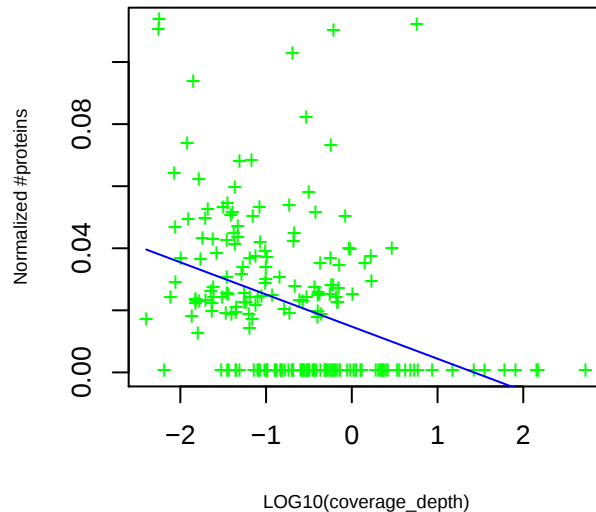
[L] COG0419 ATPase involved in DNA repair

slope= -0.44 p_value= 5.4e-12 intercept= 0.50 p_value= 2.6e-12



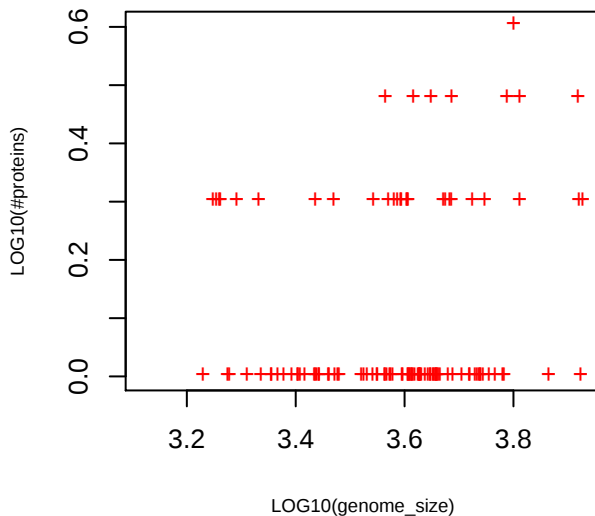
[L] COG0419 ATPase involved in DNA repair

slope= -0.010 p_value= 7.2e-08 intercept= 0.015 p_value= 2.7e-11

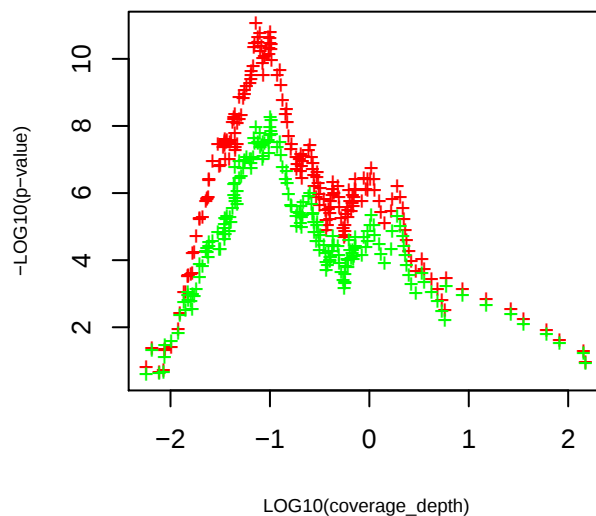


[L] COG0419 ATPase involved in DNA repair

slope= 3.53 p_value= 5.4e-05 intercept= -14.13 p_value= 6e-06

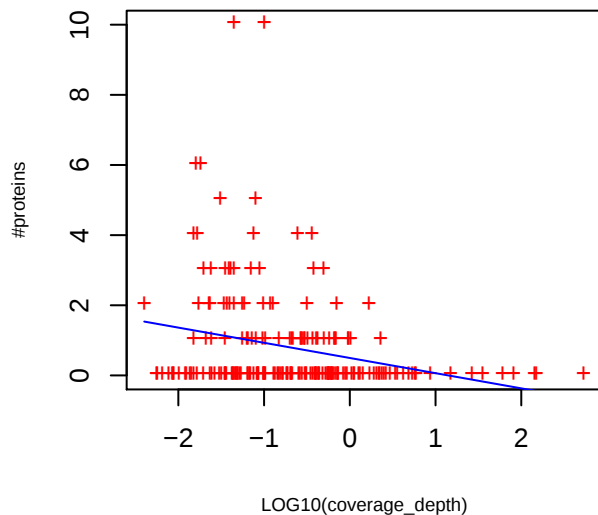


P-value curve ; red (unnorm), green (norm)



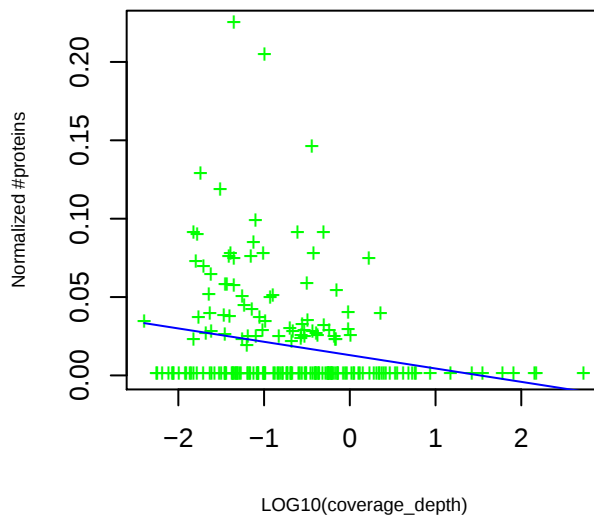
[P] COG4773 Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid

slope= -0.43 p_value= 0.00036 intercept= 0.50 p_value= 0.00029



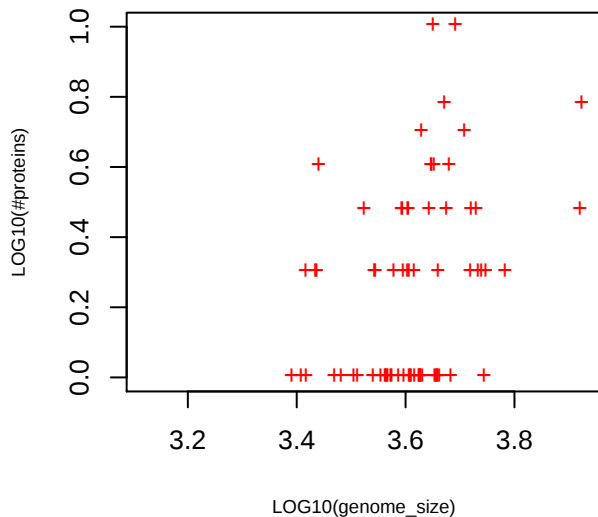
[P] COG4773 Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid

slope= -0.0085 p_value= 0.0019 intercept= 0.013 p_value= 3.5e-05

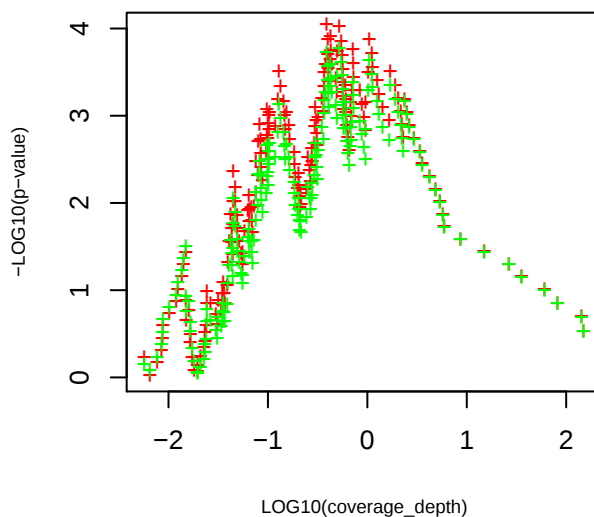


[P] COG4773 Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid

slope= 3.95 p_value= 6.6e-06 intercept= -16.50 p_value= 1.5e-07

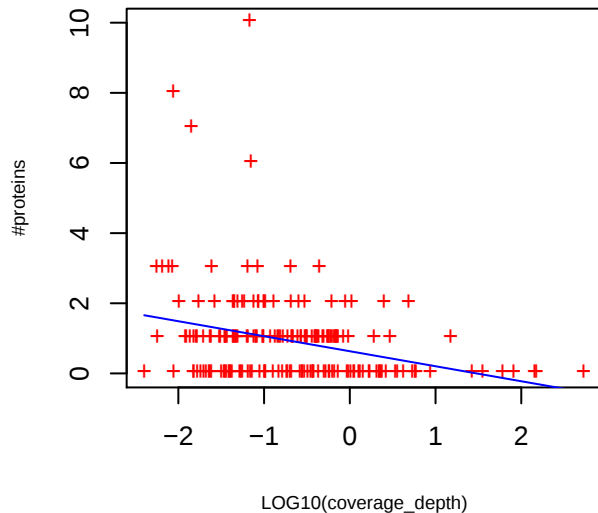


P-value curve ; red (unnorm), green (norm)



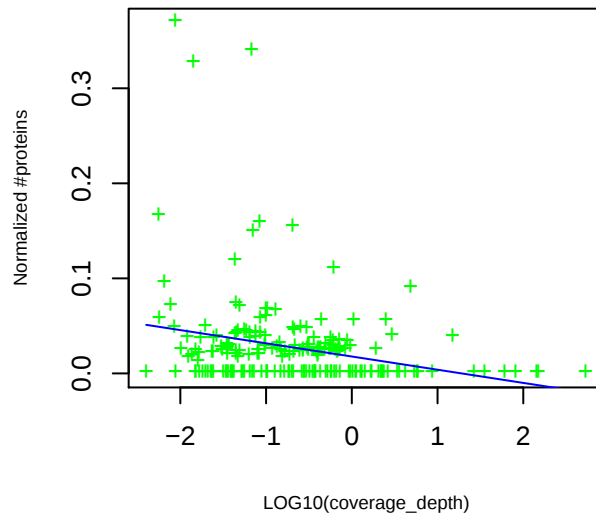
[CP] COG0651 Formate hydrogenlyase subunit 3/Multisubunit Na⁺/H⁺ antiporter, MnhD subunit

slope= -0.43 p_value= 2.8e-05 intercept= 0.63 p_value= 6.7e-08



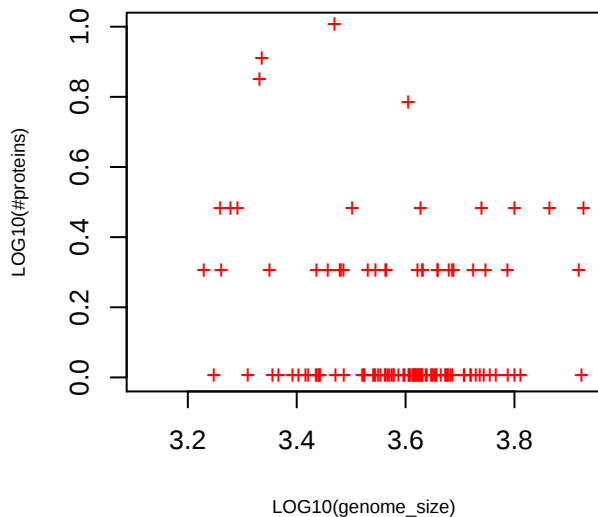
[CP] COG0651 Formate hydrogenlyase subunit 3/Multisubunit Na⁺/H⁺ antiporter, MnhD subunit

slope= -0.014 p_value= 0.00036 intercept= 0.018 p_value= 5.6e-05

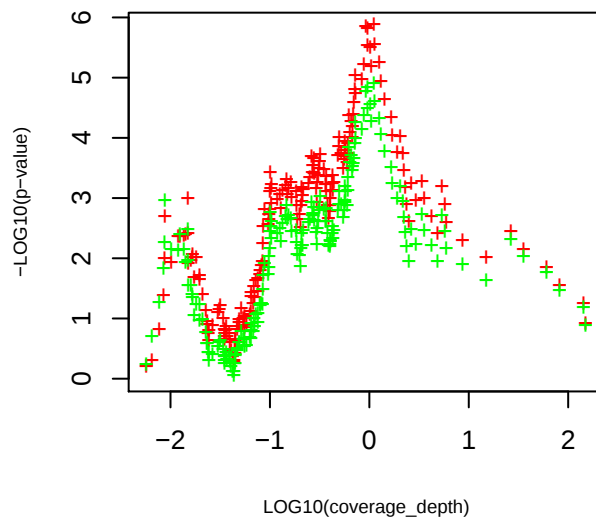


[CP] COG0651 Formate hydrogenlyase subunit 3/Multisubunit Na⁺/H⁺ antiporter, MnhD subunit

slope= 3.51 p_value= 7.2e-05 intercept= -14.06 p_value= 8.4e-06

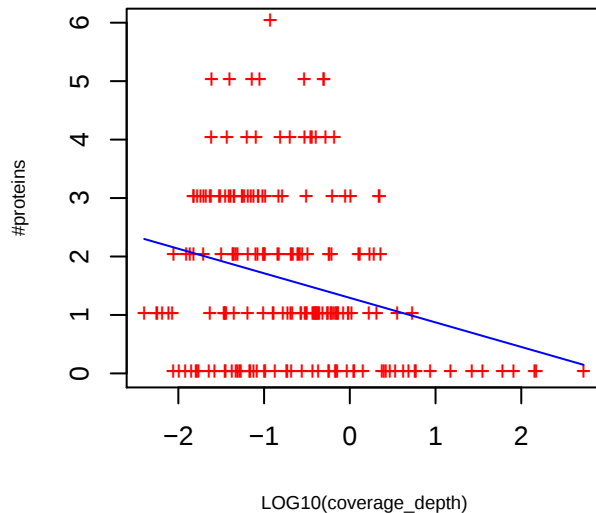


P-value curve ; red (unnorm), green (norm)



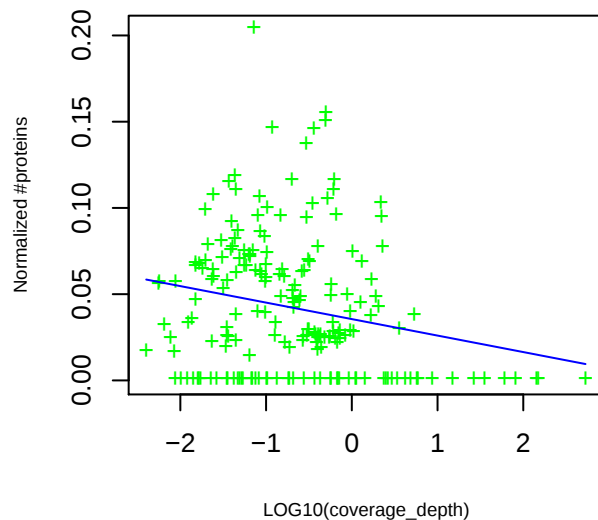
[R] COG1752 Predicted esterase of the alpha-beta hydrolase superfamily

slope= -0.42 p_value= 0.00020 intercept= 1.29 p_value= 2.8e-20



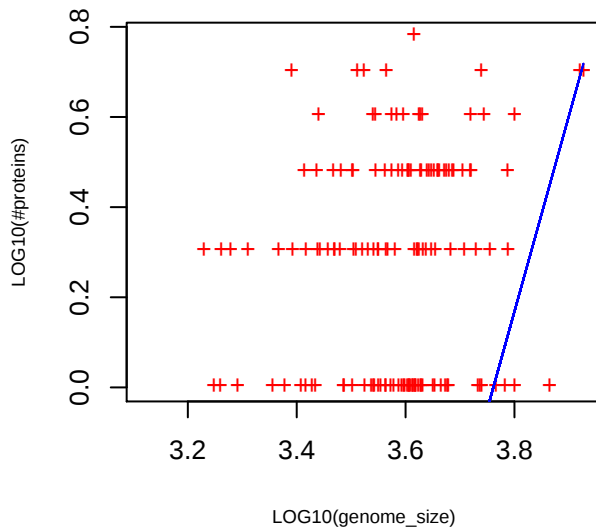
[R] COG1752 Predicted esterase of the alpha-beta hydrolase superfamily

slope= -0.0096 p_value= 0.0021 intercept= 0.036 p_value= 5.2e-20

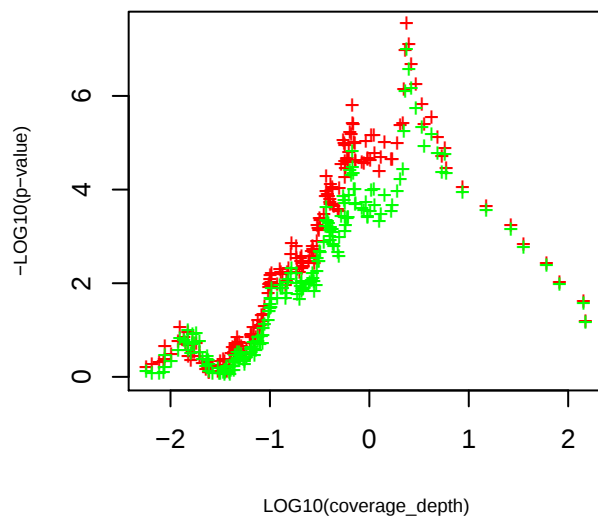


[R] COG1752 Predicted esterase of the alpha-beta hydrolase superfamily

slope= 4.34 p_value= 1.5e-07 intercept= -16.32 p_value= 3e-08

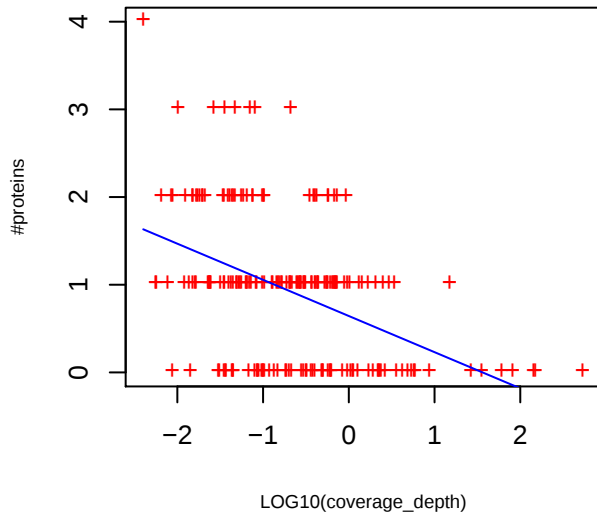


P-value curve ; red (unnorm), green (norm)



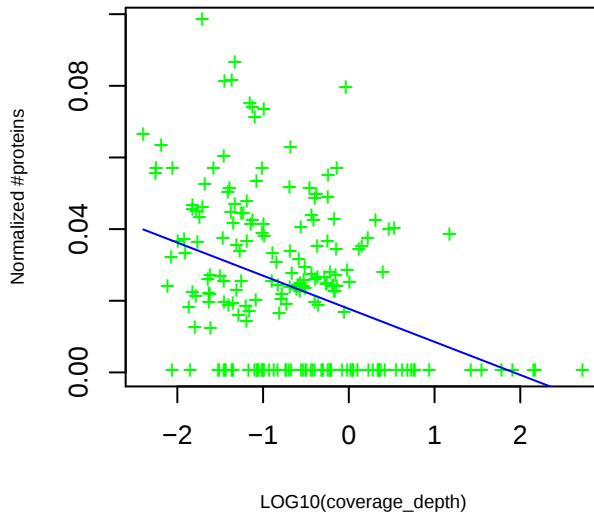
[R] COG0701 Predicted permeases

slope= -0.41 p_value= 1.2e-10 intercept= 0.64 p_value= 1.5e-17



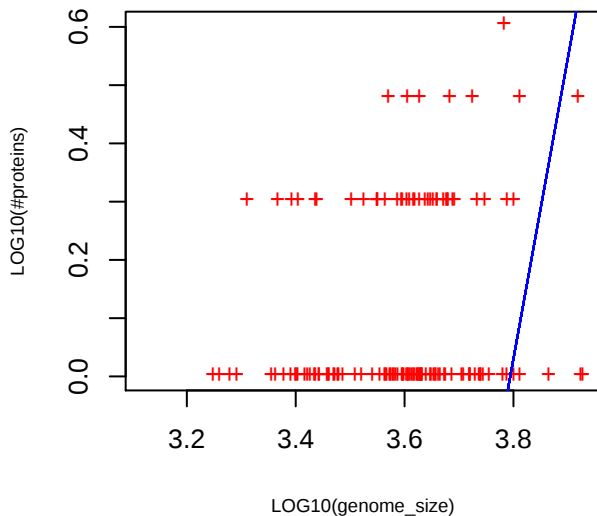
[R] COG0701 Predicted permeases

slope= -0.0092 p_value= 9e-08 intercept= 0.018 p_value= 9.8e-18

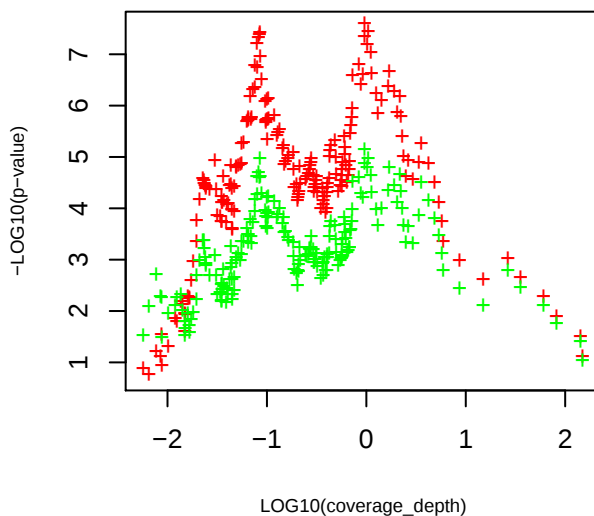


[R] COG0701 Predicted permeases

slope= 5.16 p_value= 2.9e-10 intercept= -19.60 p_value= 2.1e-11

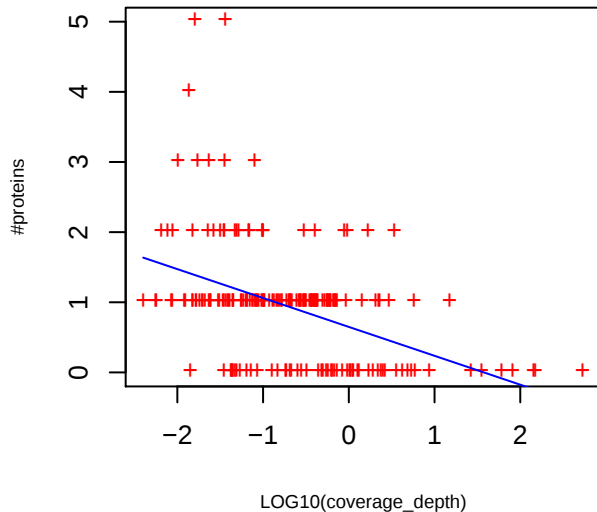


P-value curve ; red (unnorm), green (norm)



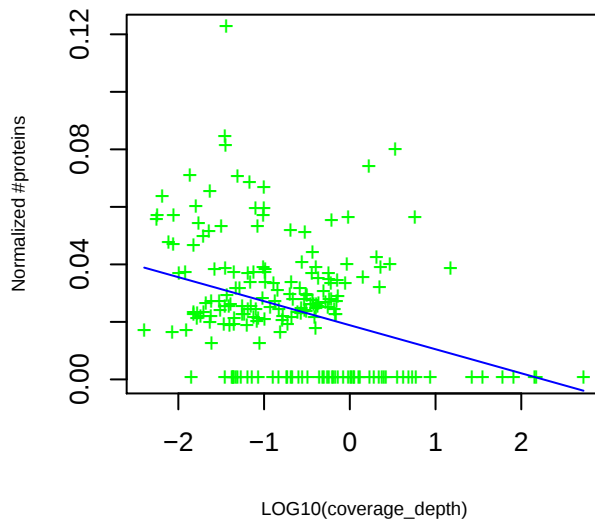
[P] COG0053 Predicted Co/Zn/Cd cation transporters

slope= -0.41 p_value= 1.6e-10 intercept= 0.65 p_value= 1.3e-17



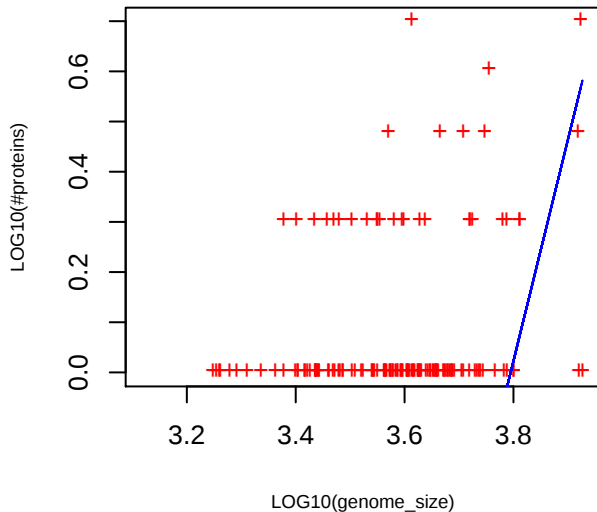
[P] COG0053 Predicted Co/Zn/Cd cation transporters

slope= -0.0084 p_value= 4.9e-07 intercept= 0.019 p_value= 2.0e-20

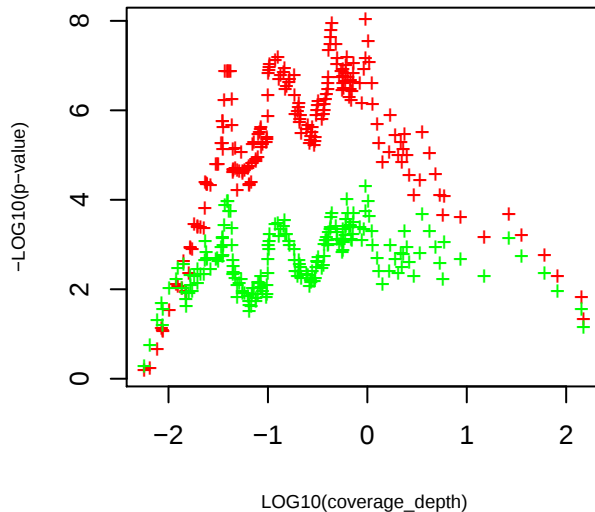


[P] COG0053 Predicted Co/Zn/Cd cation transporters

slope= 4.41 p_value= 2.1e-08 intercept= -16.73 p_value= 2.5e-09

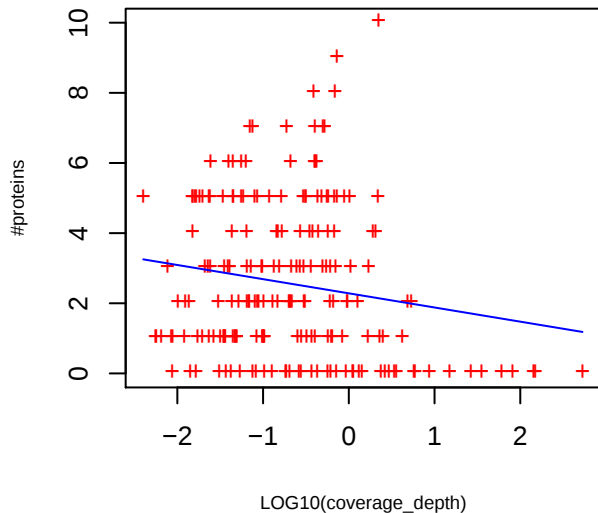


P-value curve ; red (unnorm), green (norm)



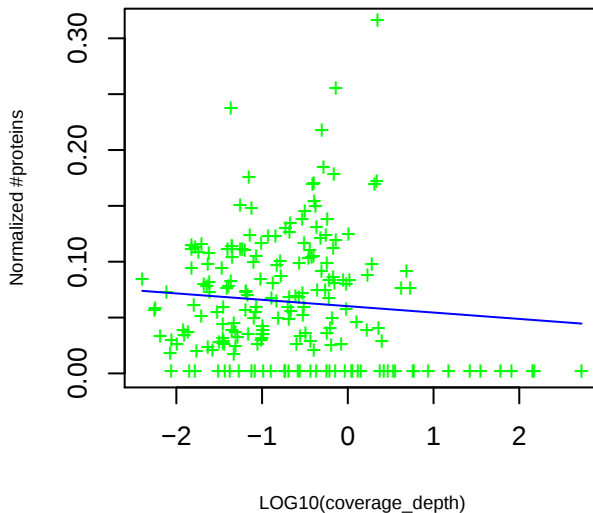
[C] COG1902 NADH:flavin oxidoreductases, Old Yellow Enzyme family

slope= -0.40 p_value= 0.023 intercept= 2.28 p_value= 1.2e-23



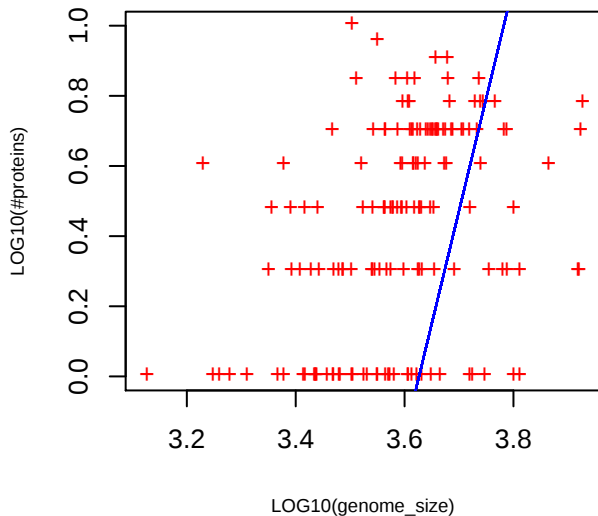
[C] COG1902 NADH:flavin oxidoreductases, Old Yellow Enzyme family

slope= -0.0057 p_value= 0.20 intercept= 0.06 p_value= 2.3e-25

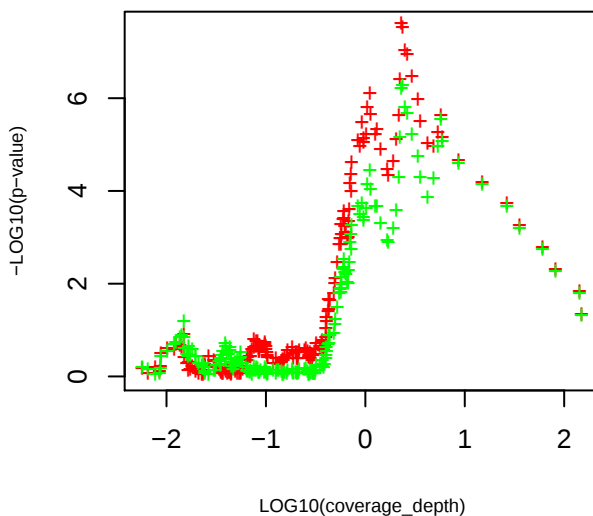


[C] COG1902 NADH:flavin oxidoreductases, Old Yellow Enzyme family

slope= 6.43 p_value= 1.9e-18 intercept= -23.30 p_value= 4.6e-19

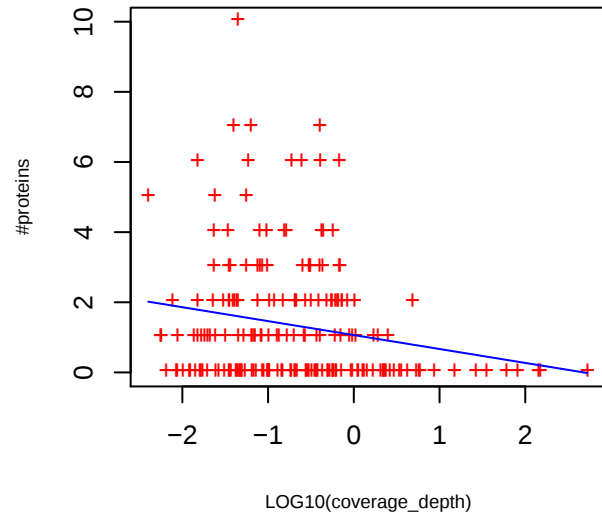


P-value curve ; red (unnorm), green (norm)



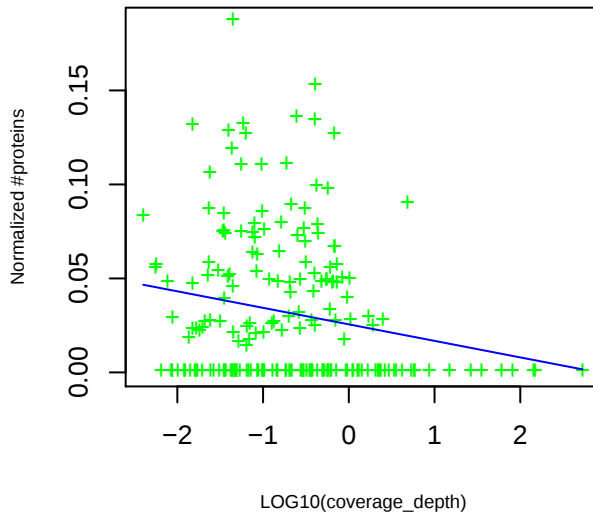
[KG] COG1349 Transcriptional regulators of sugar metabolism

slope= -0.40 p_value= 0.0053 intercept= 1.07 p_value= 2.3e-10



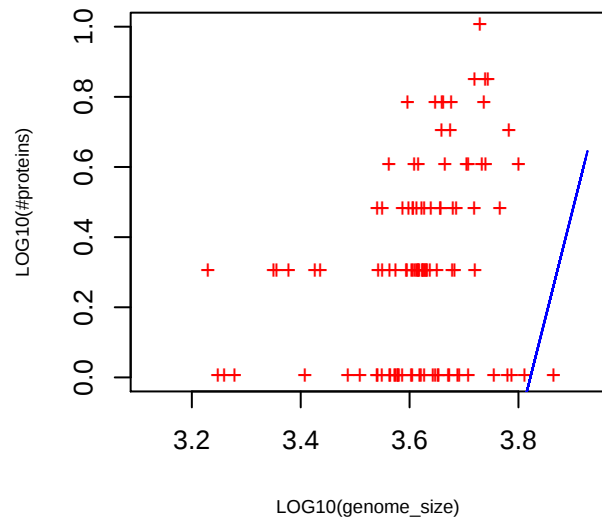
[KG] COG1349 Transcriptional regulators of sugar metabolism

slope= -0.0088 p_value= 0.0048 intercept= 0.026 p_value= 5.6e-12

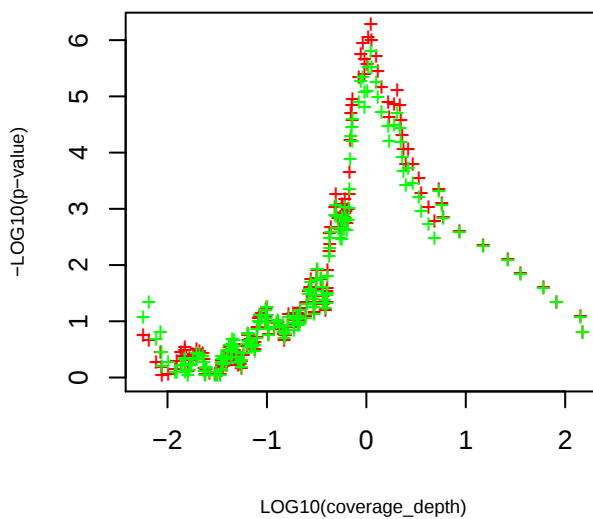


[KG] COG1349 Transcriptional regulators of sugar metabolism

slope= 6.15 p_value= 7.3e-12 intercept= -23.51 p_value= 2.6e-13

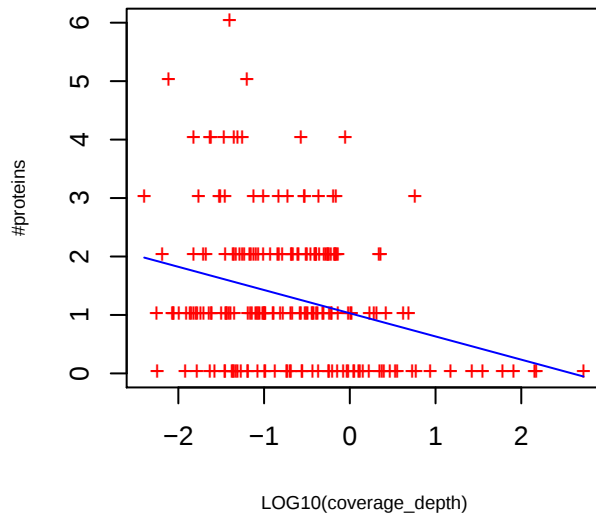


P-value curve ; red (unnorm), green (norm)



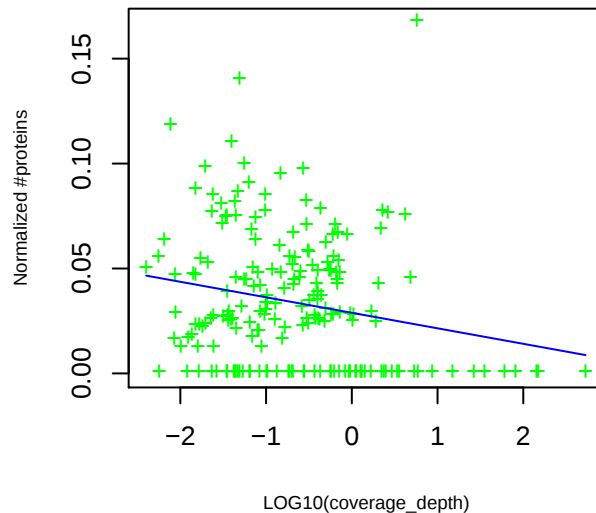
[T] COG2905 Predicted signal-transduction protein containing cAMP-binding and CBS domains

slope= -0.40 p_value= 2.5e-05 intercept= 1.03 p_value= 5.4e-19



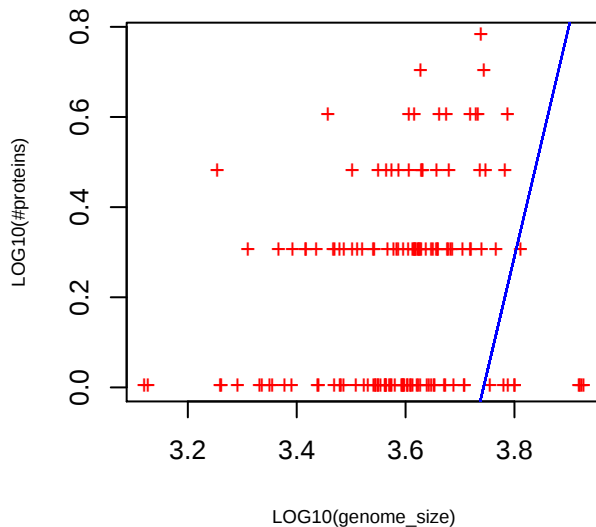
[T] COG2905 Predicted signal-transduction protein containing cAMP-binding and CBS domains

slope= -0.0074 p_value= 0.0028 intercept= 0.029 p_value= 1e-20

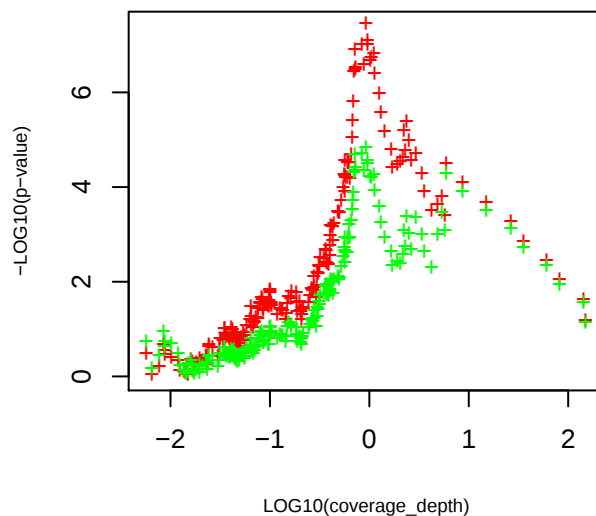


[T] COG2905 Predicted signal-transduction protein containing cAMP-binding and CBS domains

slope= 5.11 p_value= 2e-10 intercept= -19.12 p_value= 2.5e-11

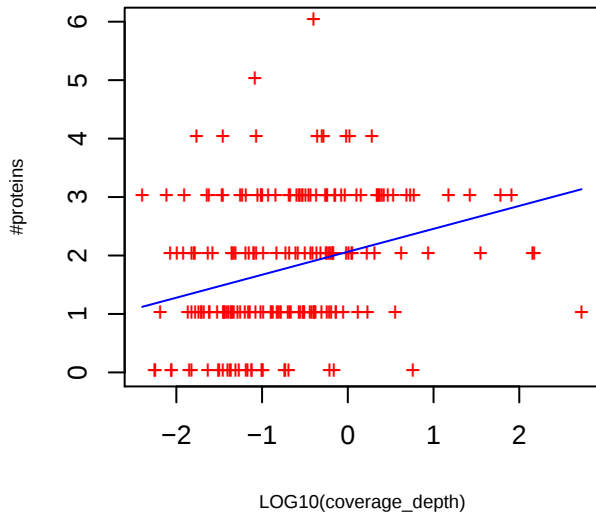


P-value curve ; red (unnorm), green (norm)



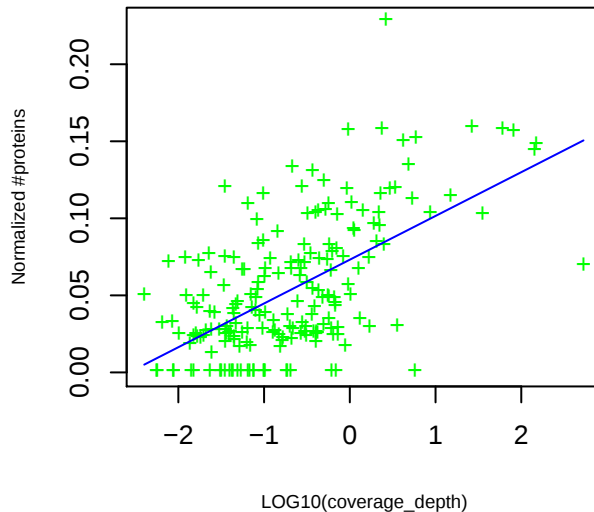
[L] COG0415 Deoxyribodipyrimidine photolyase

slope= 0.39 p_value= 2.5e-05 intercept= 2.06 p_value= 1.9e-49



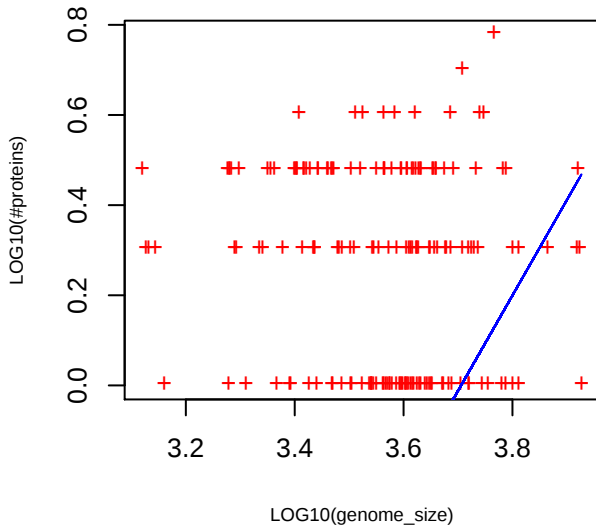
[L] COG0415 Deoxyribodipyrimidine photolyase

slope= 0.028 p_value= 1.3e-19 intercept= 0.073 p_value= 1.1e-57

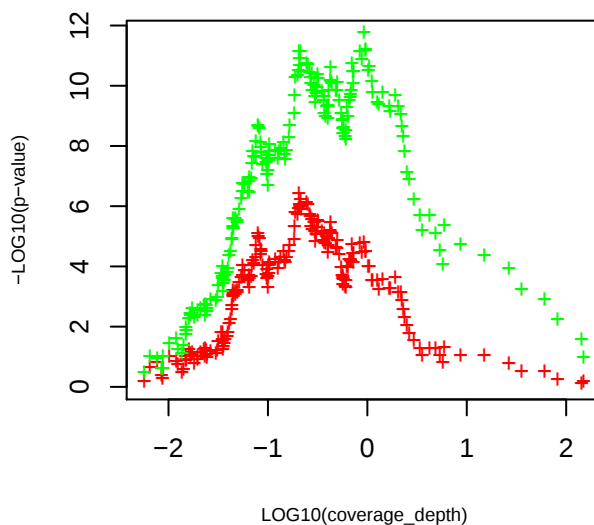


[L] COG0415 Deoxyribodipyrimidine photolyase

slope= 2.12 p_value= 0.0012 intercept= -7.85 p_value= 0.00074

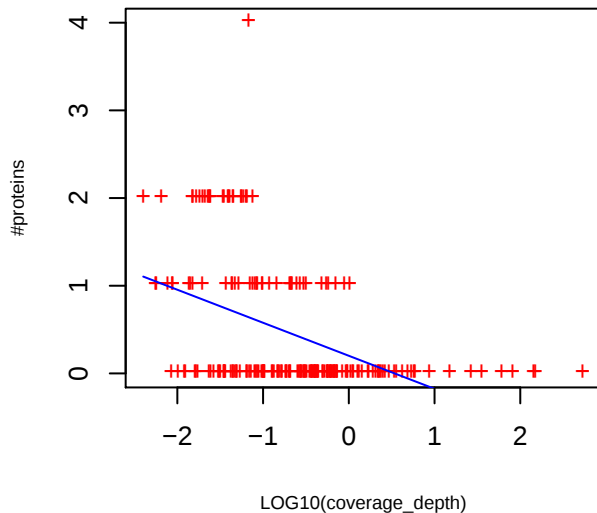


P-value curve ; red (unnorm), green (norm)



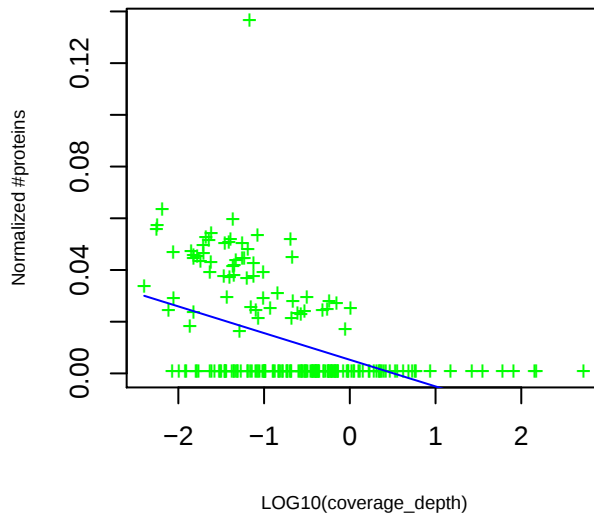
[O] COG1067 Predicted ATP-dependent protease

slope= -0.38 p_value= 4.2e-11 intercept= 0.20 p_value= 0.0011



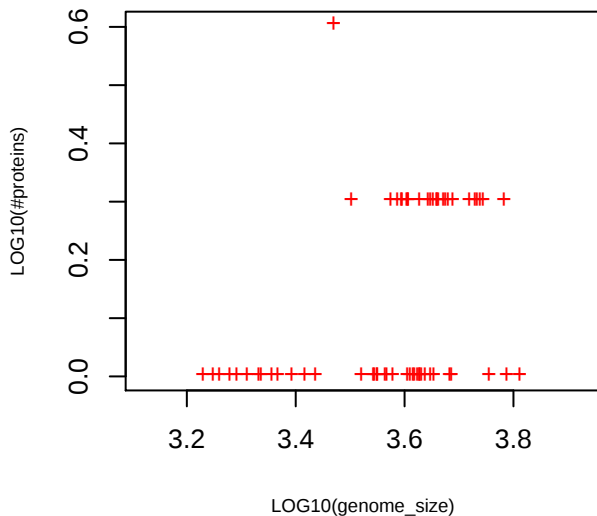
[O] COG1067 Predicted ATP-dependent protease

slope= -0.010 p_value= 4.2e-11 intercept= 0.0053 p_value= 0.0018

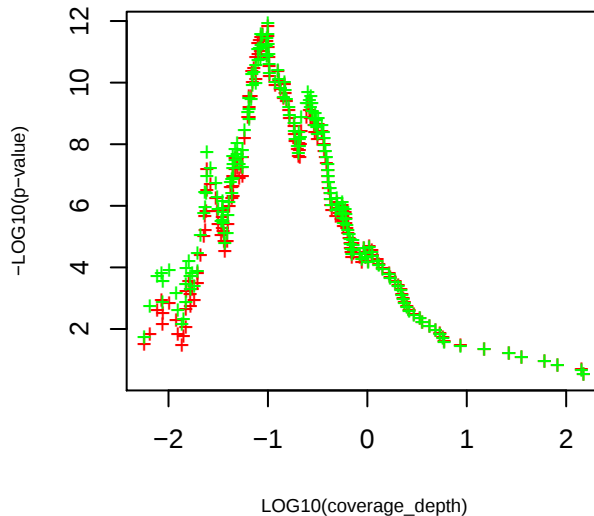


[O] COG1067 Predicted ATP-dependent protease

slope= 1.51 p_value= 0.074 intercept= -8.05 p_value= 0.0077

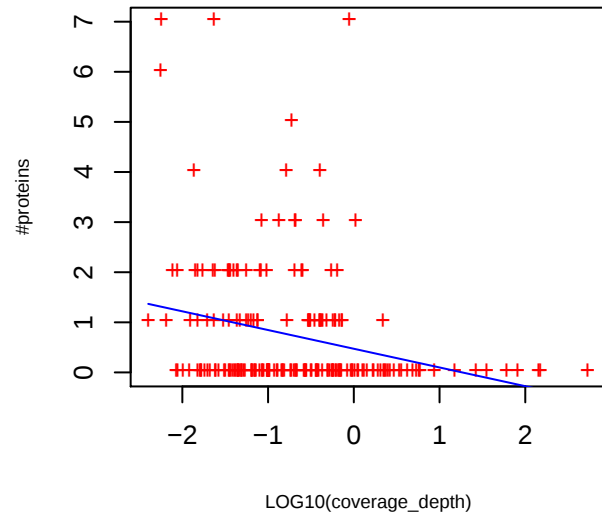


P-value curve ; red (unnorm), green (norm)



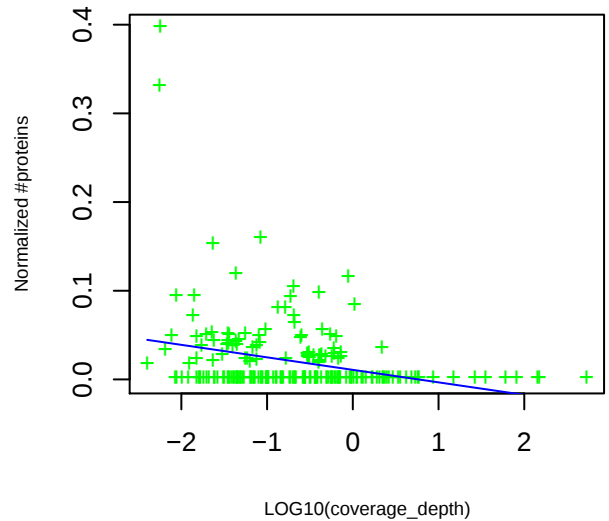
[E] COG4608 ABC-type oligopeptide transport system, ATPase component

slope= -0.37 p_value= 0.00028 intercept= 0.47 p_value= 5e-05



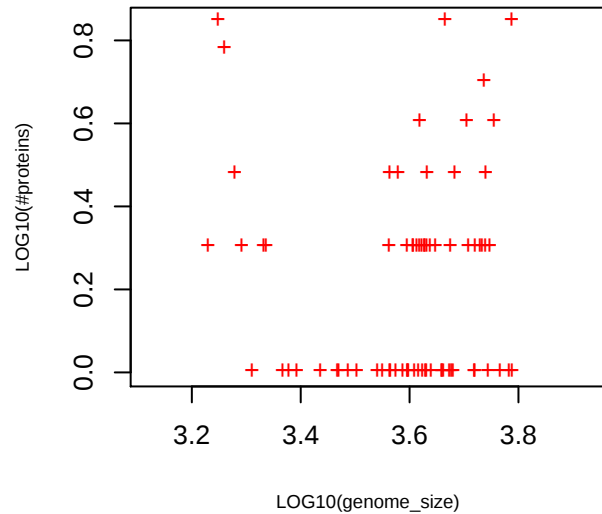
[E] COG4608 ABC-type oligopeptide transport system, ATPase component

slope= -0.014 p_value= 7.7e-05 intercept= 0.011 p_value= 0.0068

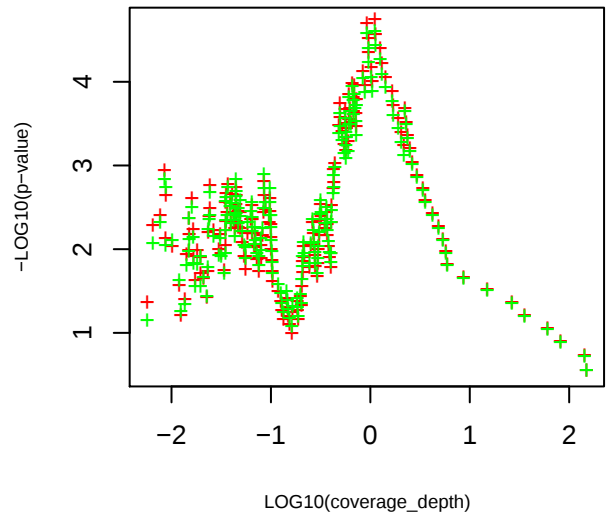


[E] COG4608 ABC-type oligopeptide transport system, ATPase component

slope= 2.68 p_value= 0.0026 intercept= -11.95 p_value= 0.00017

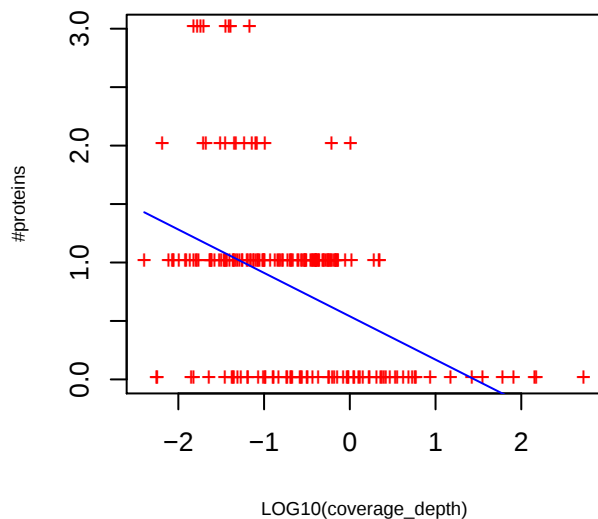


P-value curve ; red (unnorm), green (norm)



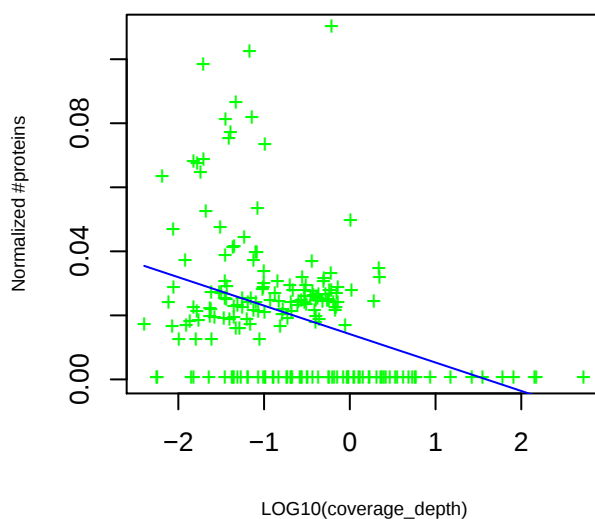
[P] COG0725 ABC-type molybdate transport system, periplasmic component

slope= -0.37 p_value= 4.4e-11 intercept= 0.54 p_value= 2e-16



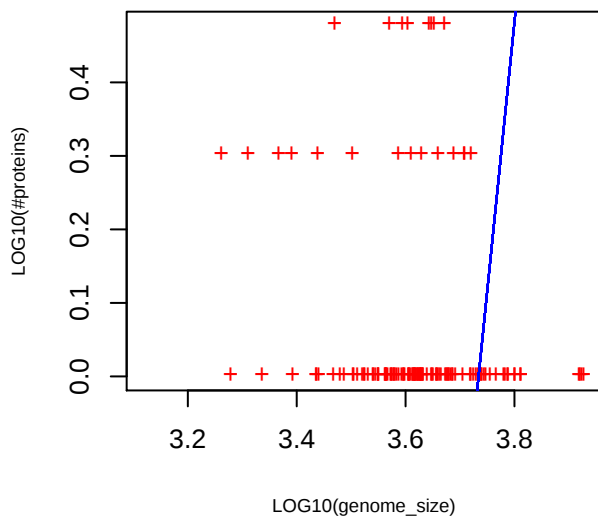
[P] COG0725 ABC-type molybdate transport system, periplasmic component

slope= -0.0089 p_value= 9.8e-08 intercept= 0.014 p_value= 3.4e-13

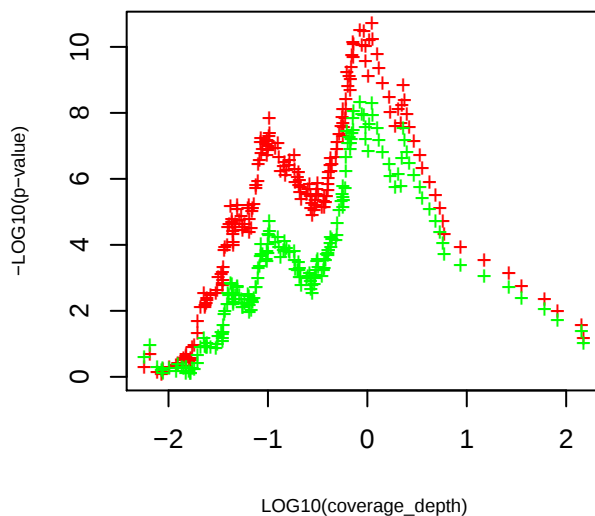


[P] COG0725 ABC-type molybdate transport system, periplasmic component

slope= 7.31 p_value= 1.7e-21 intercept= -27.30 p_value= 3.7e-23

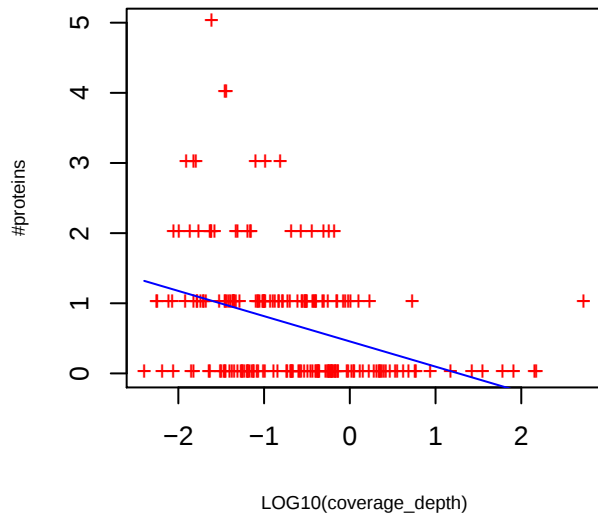


P-value curve : red (unnorm), green (norm)



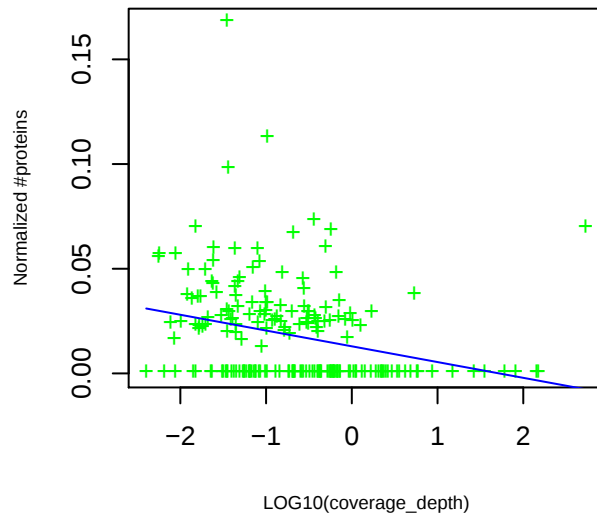
[IR] COG1597 Sphingosine kinase and enzymes related to eukaryotic diacylglycerol kinase

slope= -0.36 p_value= 2.5e-07 intercept= 0.46 p_value= 9.3e-09



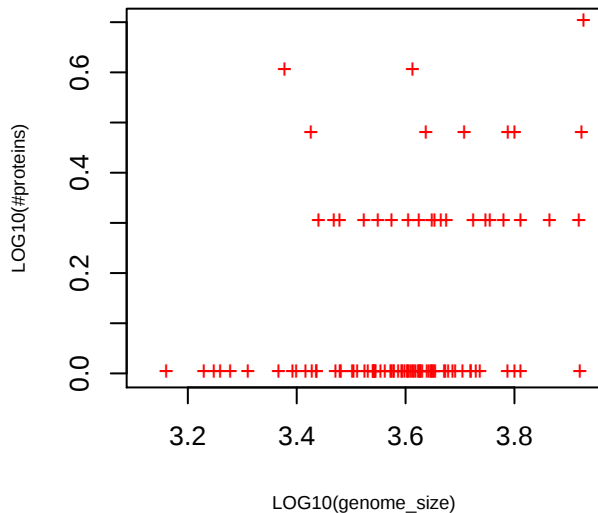
[IR] COG1597 Sphingosine kinase and enzymes related to eukaryotic diacylglycerol kinase

slope= -0.0075 p_value= 6.1e-05 intercept= 0.013 p_value= 2.7e-09

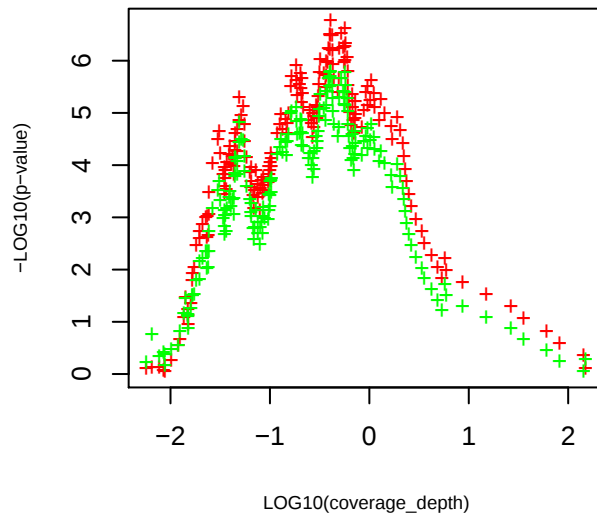


[IR] COG1597 Sphingosine kinase and enzymes related to eukaryotic diacylglycerol kinase

slope= 4.05 p_value= 4.4e-06 intercept= -16.33 p_value= 2.3e-07

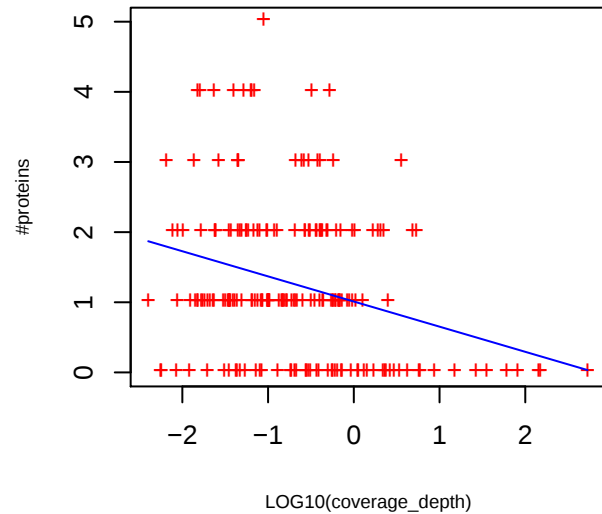


P-value curve ; red (unnorm), green (norm)



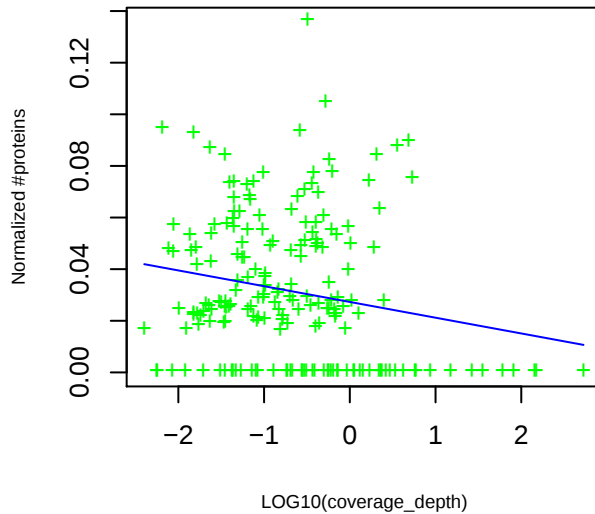
[R] COG0693 Putative intracellular protease/amidase

slope= -0.36 p_value= 5.2e-05 intercept= 1.01 p_value= 3.2e-20



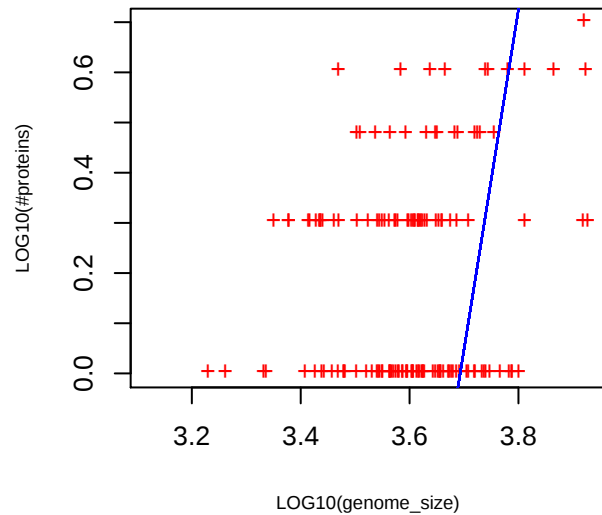
[R] COG0693 Putative intracellular protease/amidase

slope= -0.0061 p_value= 0.0057 intercept= 0.027 p_value= 2.0e-22

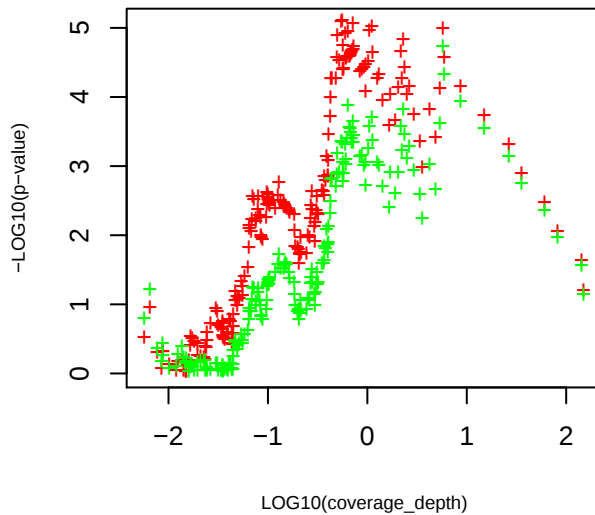


[R] COG0693 Putative intracellular protease/amidase

slope= 6.77 p_value= 4.2e-19 intercept= -25.01 p_value= 2.8e-20

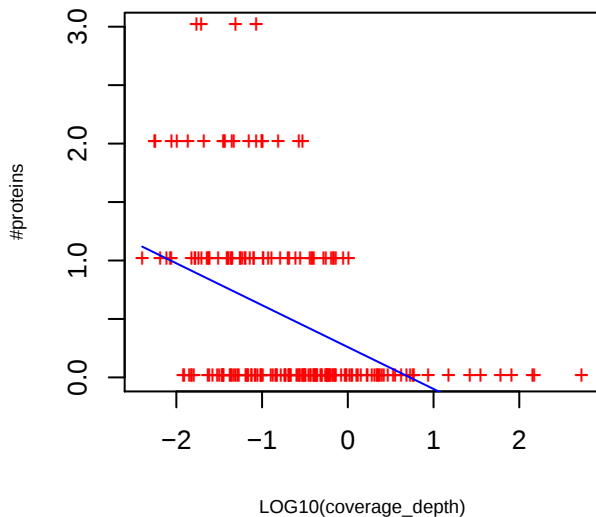


P-value curve ; red (unnorm), green (norm)



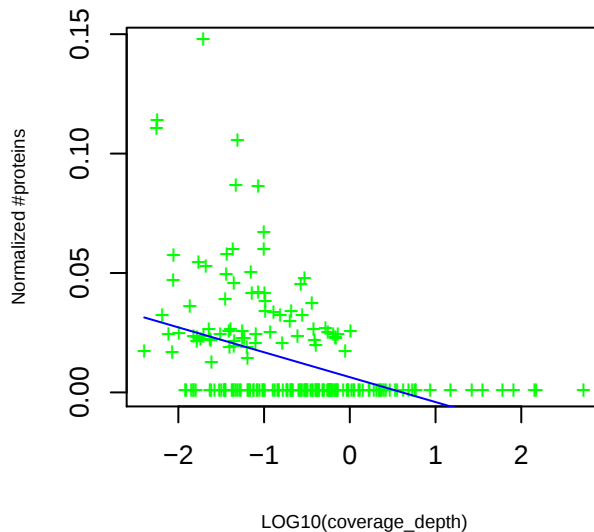
[V] COG0842 ABC-type multidrug transport system, permease component

slope= -0.36 p_value= 4.6e-10 intercept= 0.26 p_value= 3.9e-05



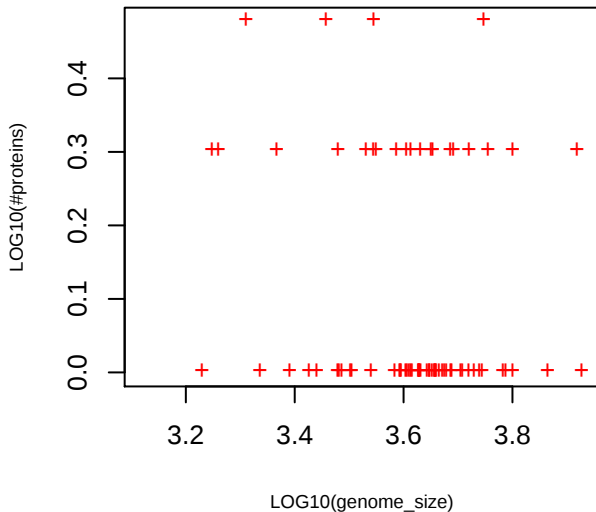
[V] COG0842 ABC-type multidrug transport system, permease component

slope= -0.010 p_value= 8.1e-09 intercept= 0.0064 p_value= 0.0013

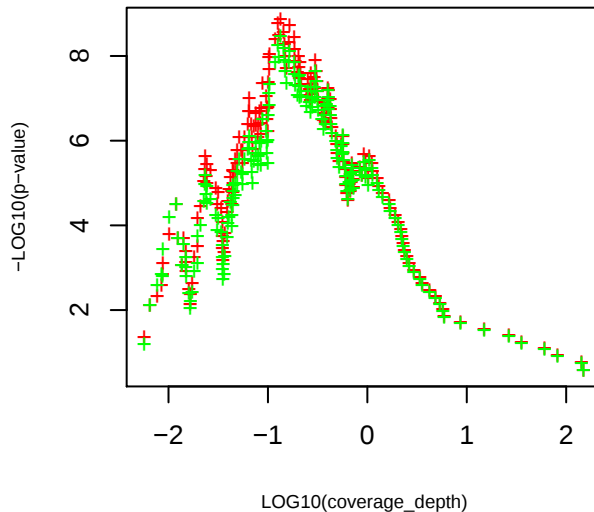


[V] COG0842 ABC-type multidrug transport system, permease component

slope= 3.66 p_value= 1.9e-05 intercept= -15.44 p_value= 4.6e-07

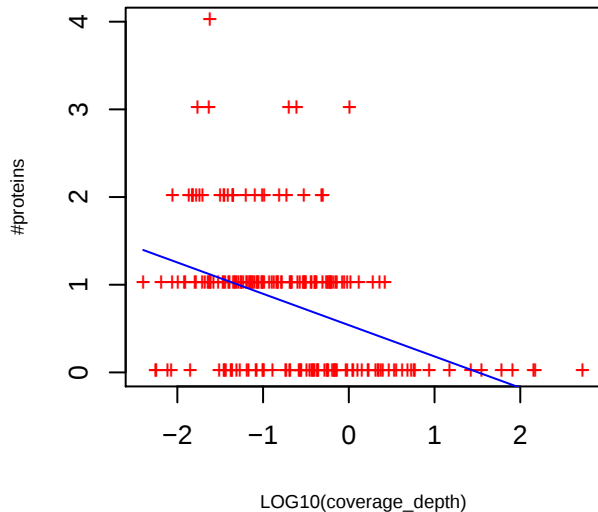


P-value curve ; red (unnorm), green (norm)



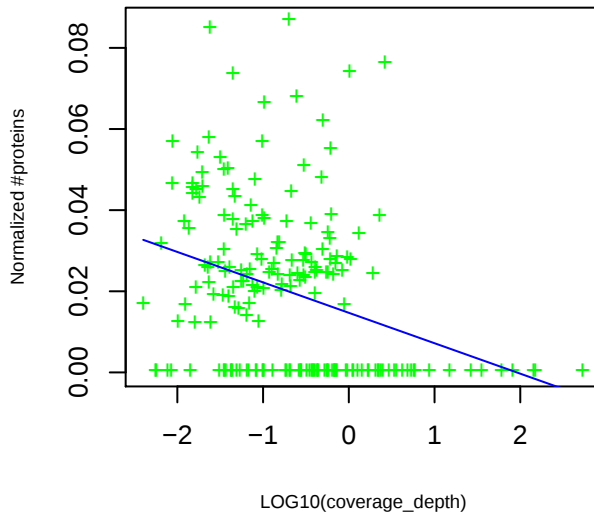
[C] COG1271 Cytochrome bd-type quinol oxidase, subunit 1

slope= -0.36 p_value= 4.2e-09 intercept= 0.54 p_value= 2.7e-14



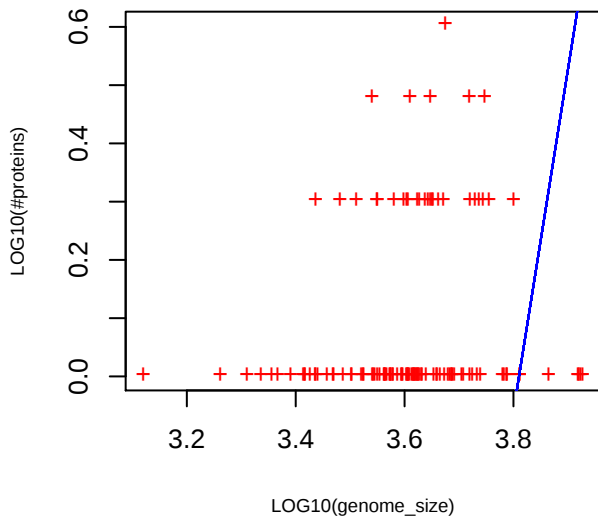
[C] COG1271 Cytochrome bd-type quinol oxidase, subunit 1

slope= -0.0075 p_value= 2.1e-06 intercept= 0.015 p_value= 5.5e-15

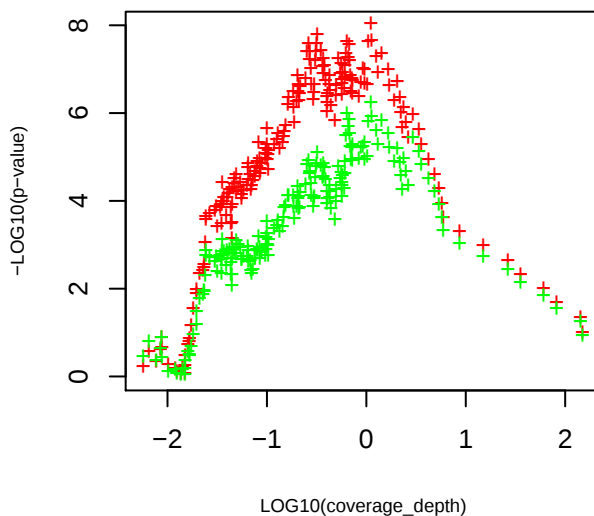


[C] COG1271 Cytochrome bd-type quinol oxidase, subunit 1

slope= 5.86 p_value= 1.8e-12 intercept= -22.33 p_value= 6.2e-14

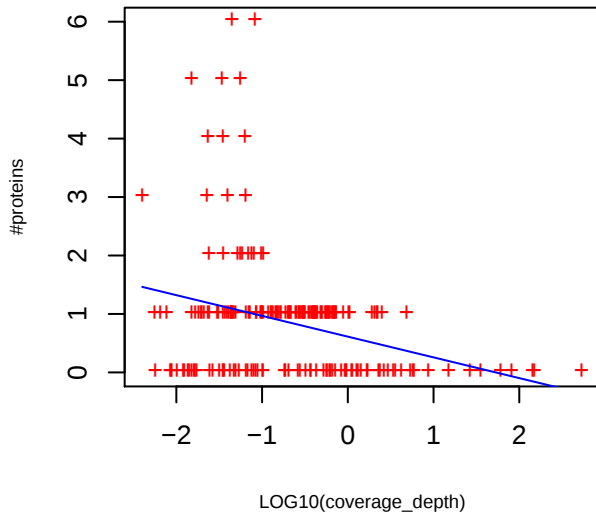


P-value curve ; red (unnorm), green (norm)



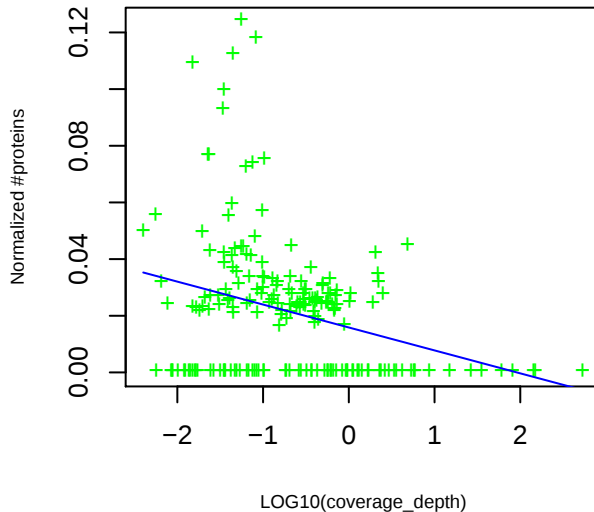
[GT] COG1762 Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)

slope= -0.35 p_value= 2.3e-05 intercept= 0.61 p_value= 3.2e-10



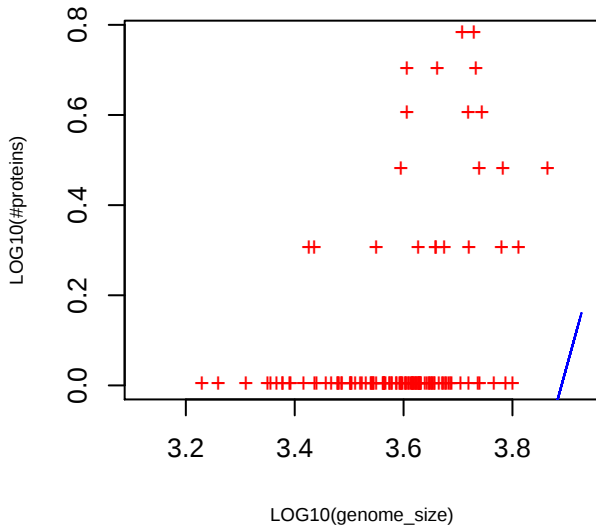
[GT] COG1762 Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)

slope= -0.0081 p_value= 1.5e-05 intercept= 0.016 p_value= 6.9e-13

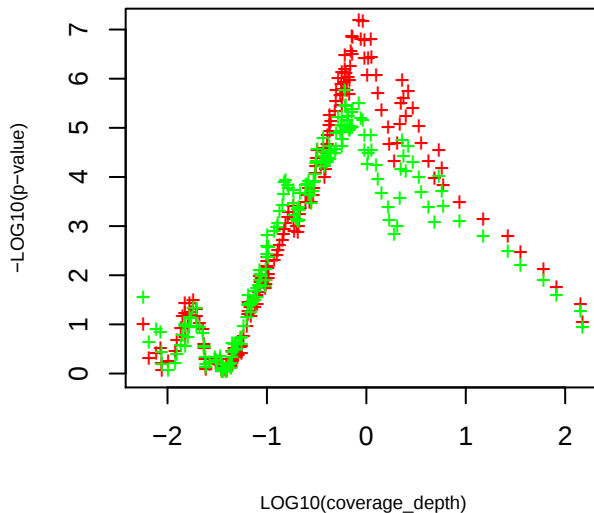


[GT] COG1762 Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)

slope= 4.38 p_value= 2.8e-07 intercept= -17.04 p_value= 2.2e-08

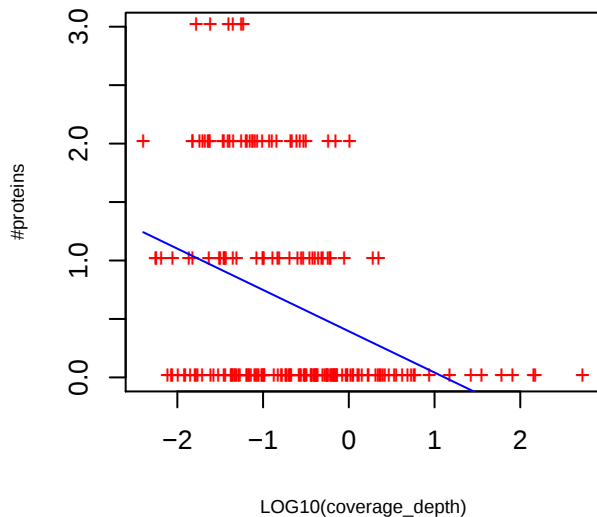


P-value curve ; red (unnorm), green (norm)



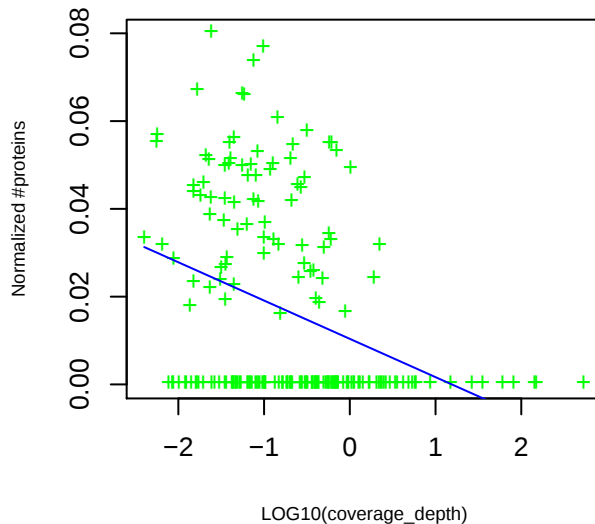
[N] COG1580 Flagellar basal body-associated protein

slope= -0.35 p_value= 2.1e-07 intercept= 0.39 p_value= 2.7e-07



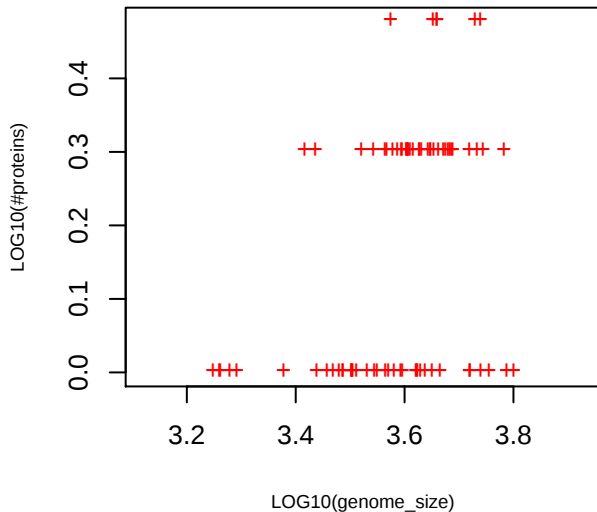
[N] COG1580 Flagellar basal body-associated protein

slope= -0.0087 p_value= 4e-07 intercept= 0.010 p_value= 1.0e-07

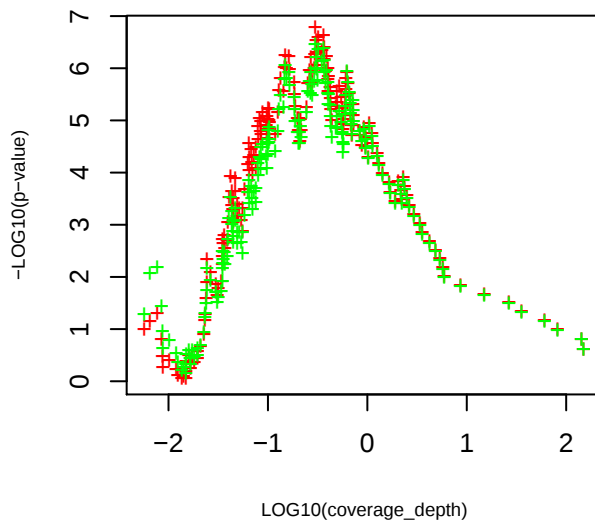


[N] COG1580 Flagellar basal body-associated protein

slope= 2.79 p_value= 0.0017 intercept= -12.22 p_value= 0.00012

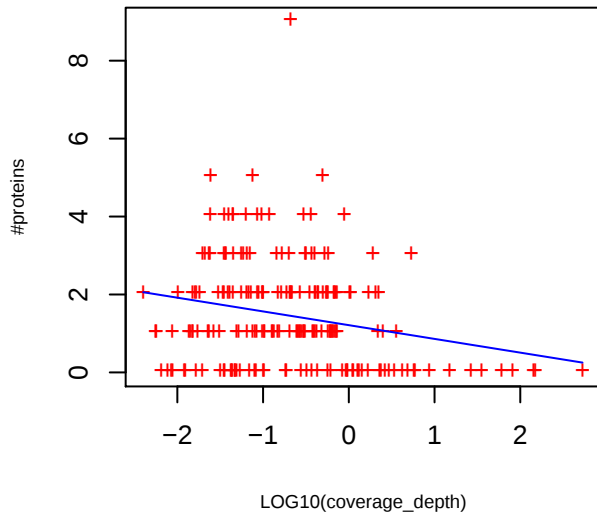


P-value curve ; red (unnorm), green (norm)



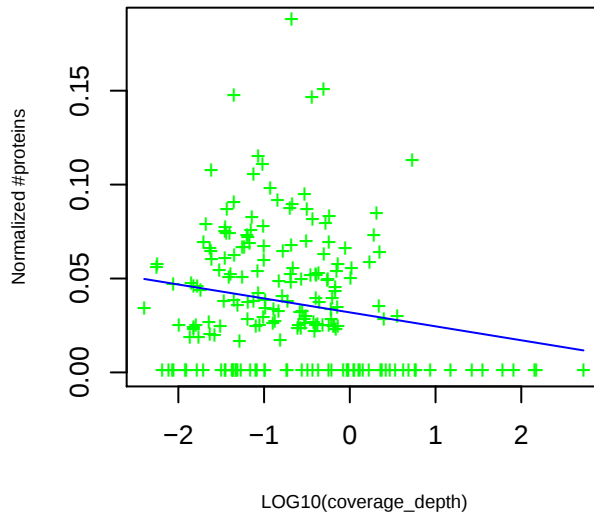
[I] COG2267 Lysophospholipase

slope= -0.35 p_value= 0.0013 intercept= 1.21 p_value= 4.5e-19



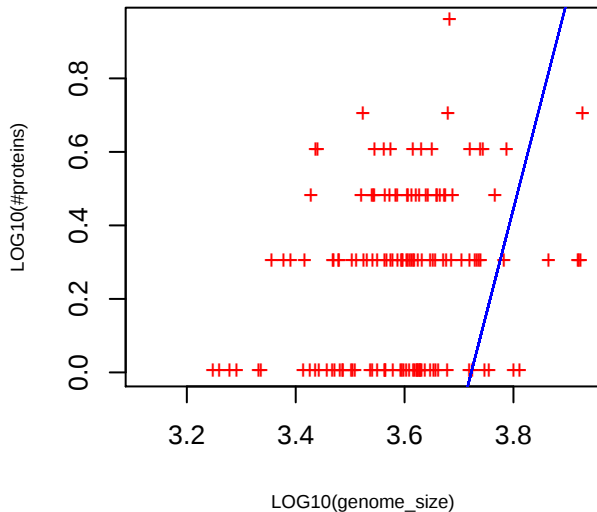
[I] COG2267 Lysophospholipase

slope= -0.0074 p_value= 0.0073 intercept= 0.032 p_value= 3.1e-20

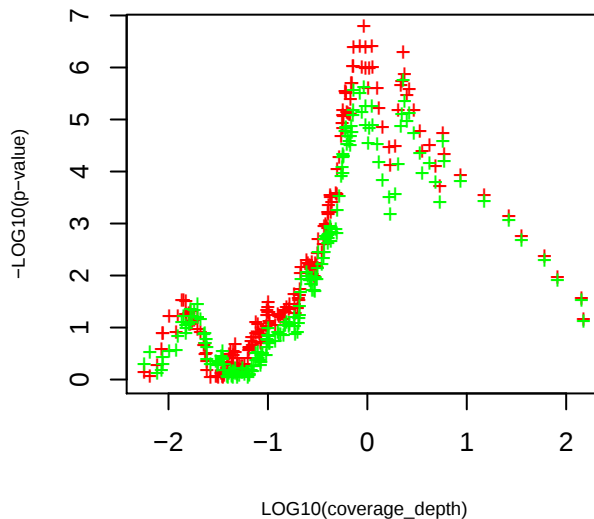


[I] COG2267 Lysophospholipase

slope= 5.75 p_value= 1.4e-12 intercept= -21.39 p_value= 1.5e-13

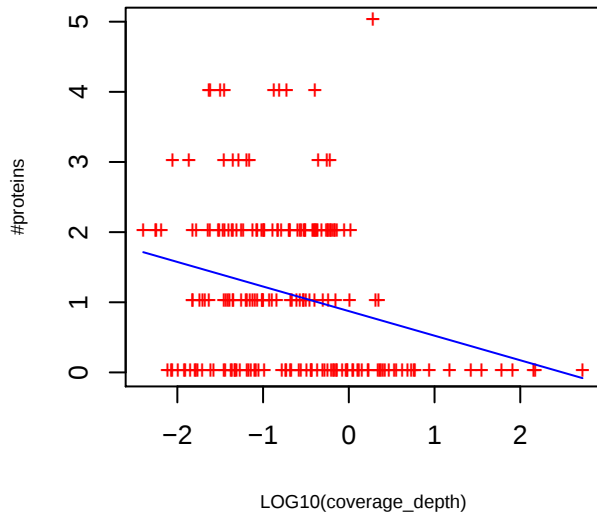


P-value curve ; red (unnorm), green (norm)



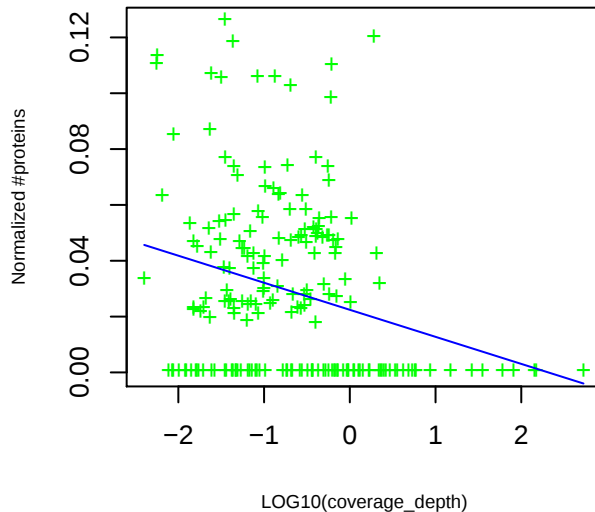
[N] COG4786 Flagellar basal body rod protein

slope= -0.35 p_value= 0.00012 intercept= 0.87 p_value= 1.6e-15



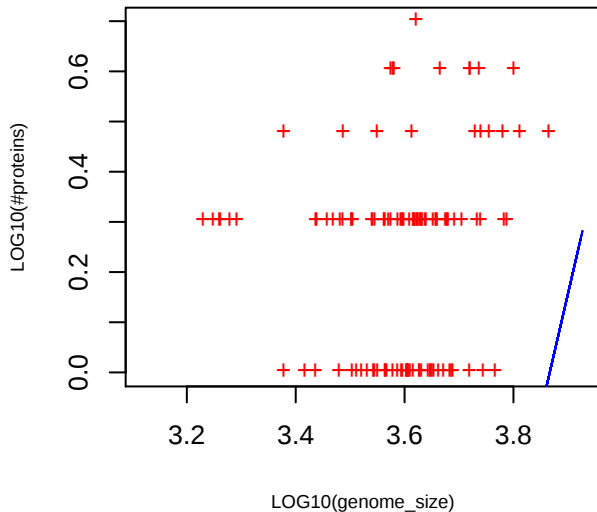
[N] COG4786 Flagellar basal body rod protein

slope= -0.0097 p_value= 9.6e-05 intercept= 0.022 p_value= 3.9e-14

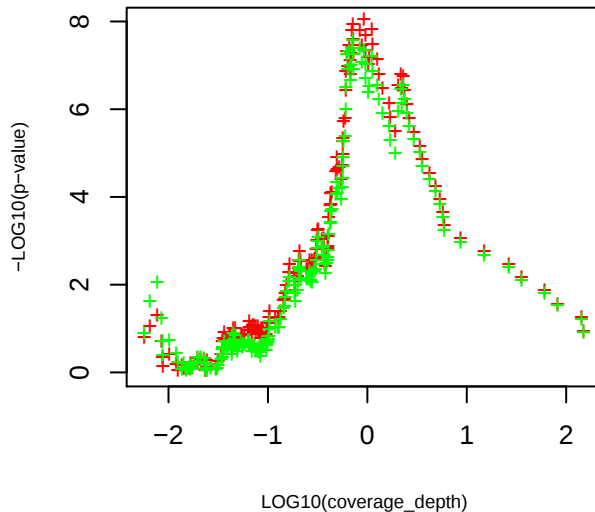


[N] COG4786 Flagellar basal body rod protein

slope= 4.69 p_value= 1.3e-07 intercept= -18.13 p_value= 1.1e-08

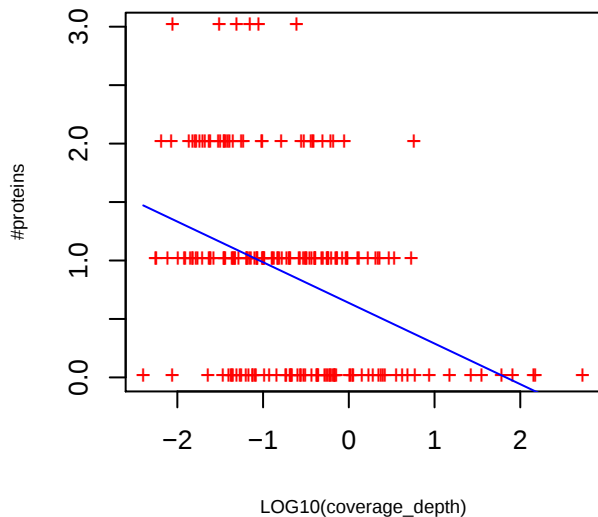


P-value curve ; red (unnorm), green (norm)



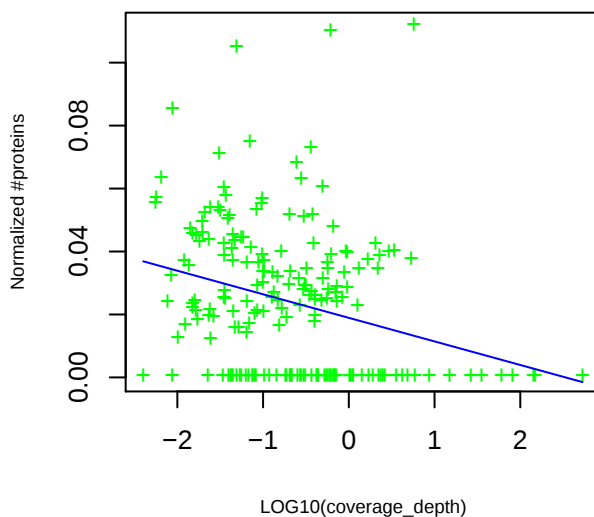
[P] COG0598 Mg²⁺ and Co²⁺ transporters

slope= -0.35 p_value= 1.6e-08 intercept= 0.64 p_value= 4.6e-18



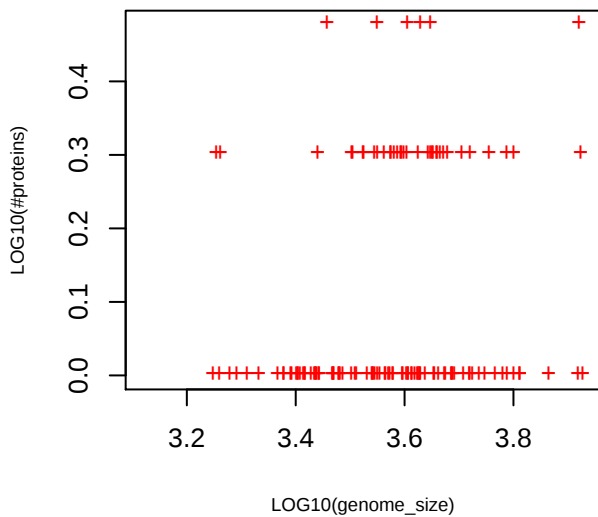
[P] COG0598 Mg²⁺ and Co²⁺ transporters

slope= -0.0075 p_value= 3.8e-05 intercept= 0.019 p_value= 1.2e-17

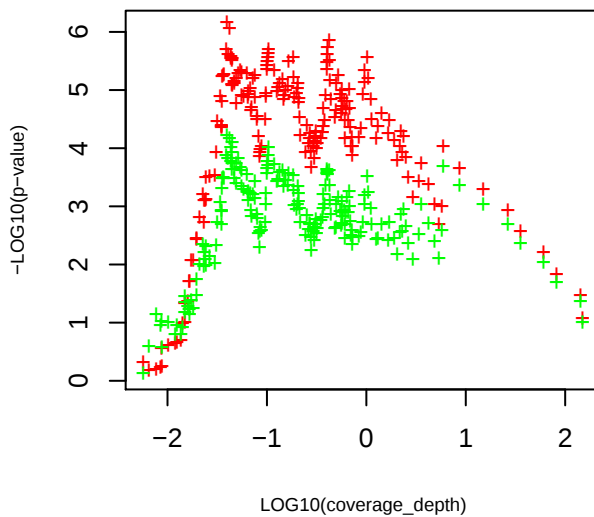


[P] COG0598 Mg²⁺ and Co²⁺ transporters

slope= 3.07 p_value= 0.00032 intercept= -12.24 p_value= 5.7e-05

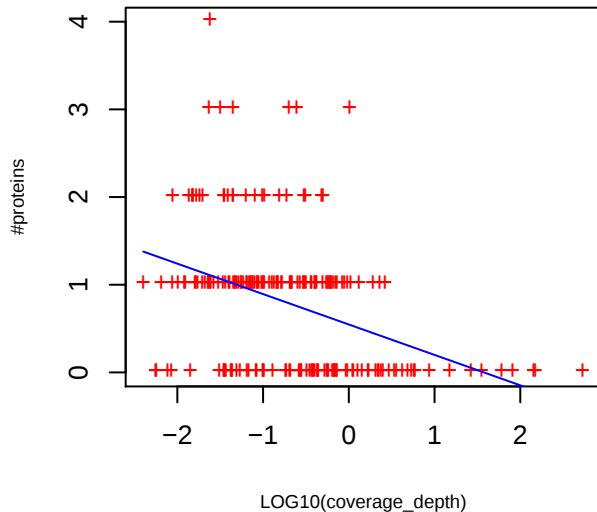


P-value curve ; red (unnorm), green (norm)



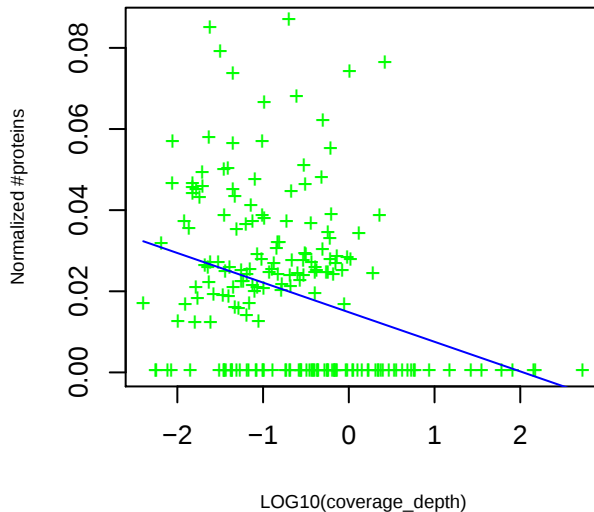
[C] COG1294 Cytochrome bd-type quinol oxidase, subunit 2

slope= -0.35 p_value= 2.2e-08 intercept= 0.55 p_value= 4.7e-14



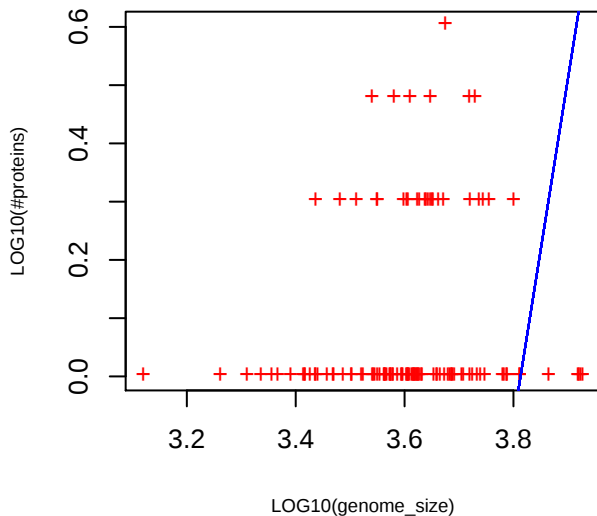
[C] COG1294 Cytochrome bd-type quinol oxidase, subunit 2

slope= -0.0073 p_value= 6.4e-06 intercept= 0.015 p_value= 1.2e-14

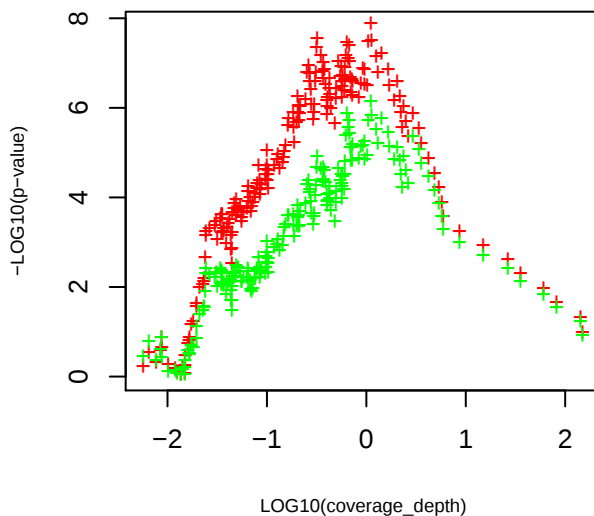


[C] COG1294 Cytochrome bd-type quinol oxidase, subunit 2

slope= 5.87 p_value= 1.9e-12 intercept= -22.38 p_value= 6.3e-14

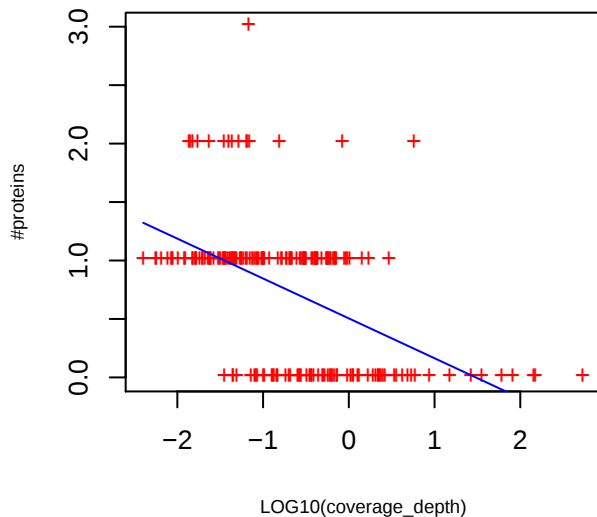


P-value curve ; red (unnorm), green (norm)



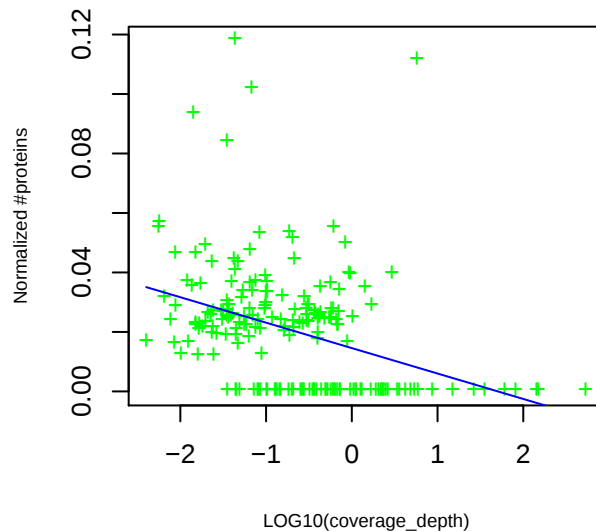
[L] COG0420 DNA repair exonuclease

slope= -0.34 p_value= 1.1e-13 intercept= 0.50 p_value= 1.1e-20



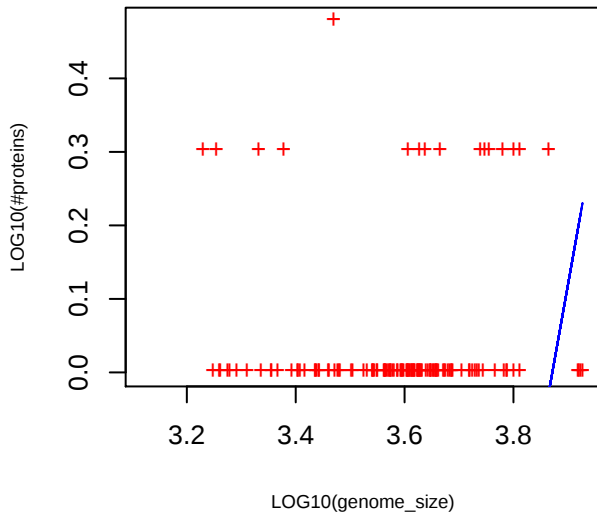
[L] COG0420 DNA repair exonuclease

slope= -0.0086 p_value= 6.4e-08 intercept= 0.015 p_value= 5.4e-15

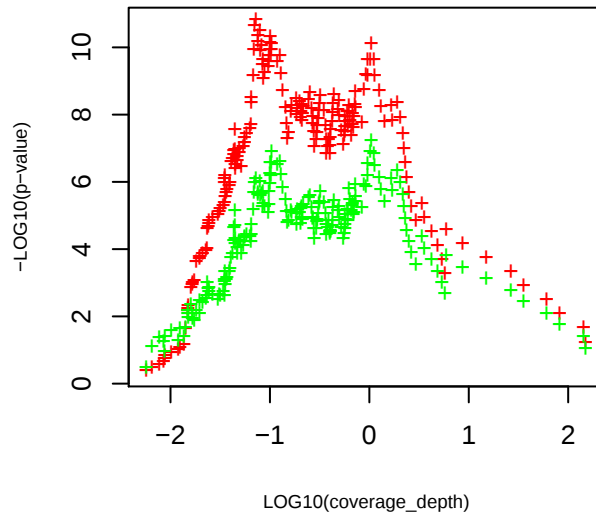


[L] COG0420 DNA repair exonuclease

slope= 4.16 p_value= 4.1e-07 intercept= -16.09 p_value= 3.9e-08

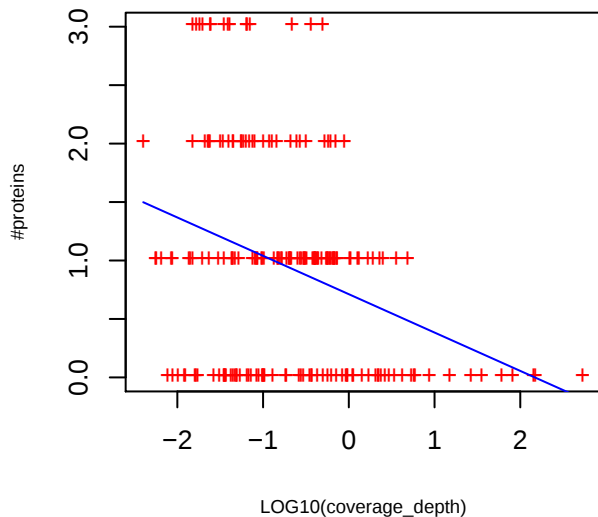


P-value curve ; red (unnorm), green (norm)



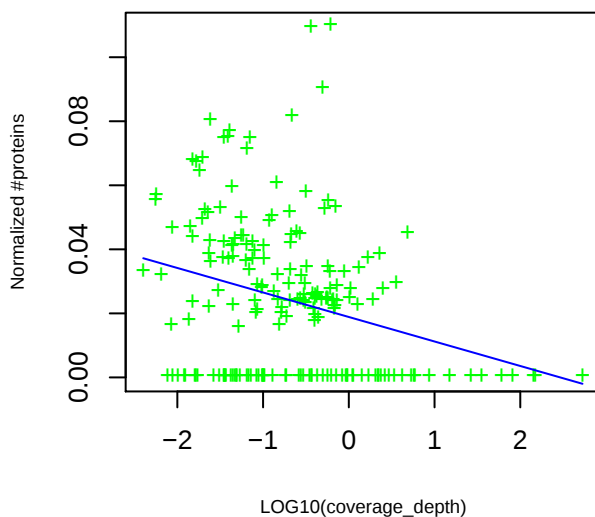
[R] COG1092 Predicted SAM-dependent methyltransferases

slope= -0.33 p_value= 4.1e-06 intercept= 0.71 p_value= 1e-16



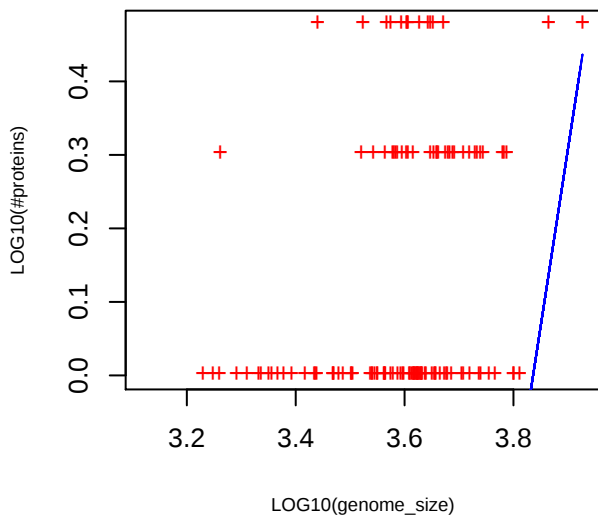
[R] COG1092 Predicted SAM-dependent methyltransferases

slope= -0.0077 p_value= 4.2e-05 intercept= 0.019 p_value= 7.5e-17

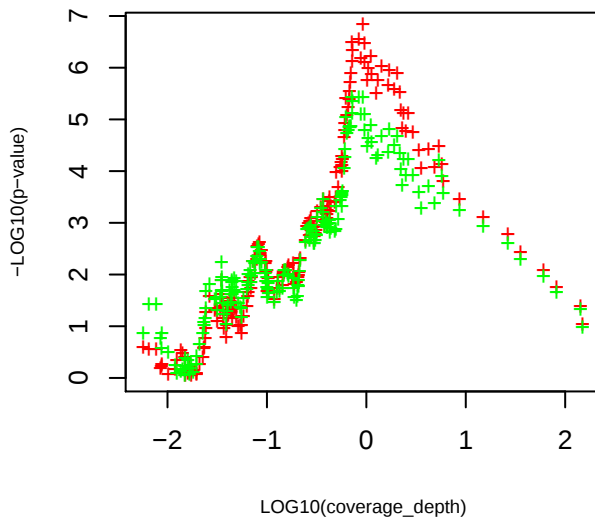


[R] COG1092 Predicted SAM-dependent methyltransferases

slope= 4.81 p_value= 1.4e-08 intercept= -18.45 p_value= 1.1e-09

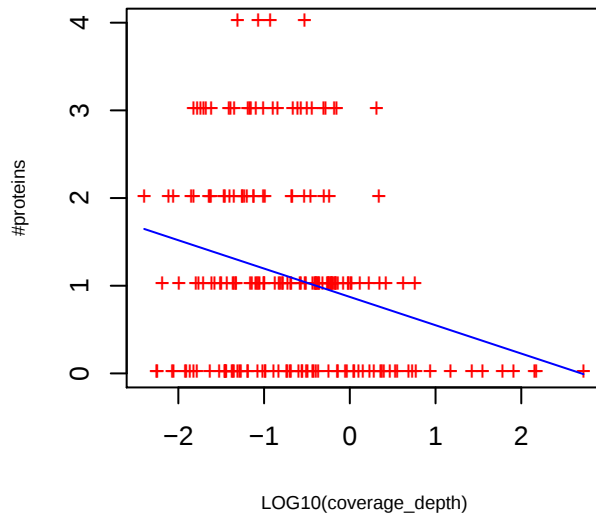


P-value curve ; red (unnorm), green (norm)



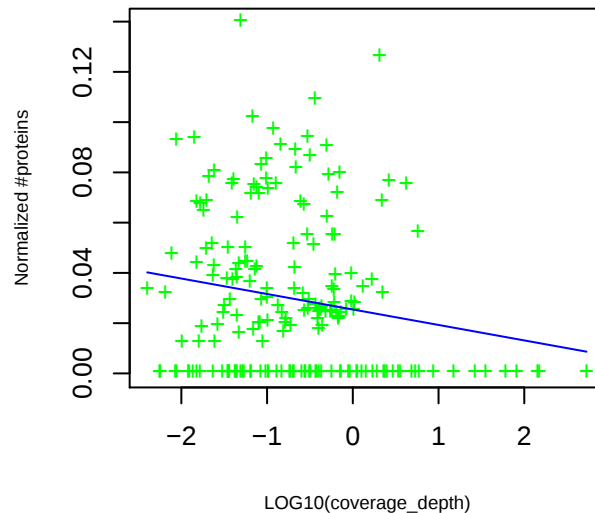
[O] COG1047 FKBP-type peptidyl-prolyl cis-trans isomerases 2

slope= -0.32 p_value= 0.00019 intercept= 0.87 p_value= 1.1e-16



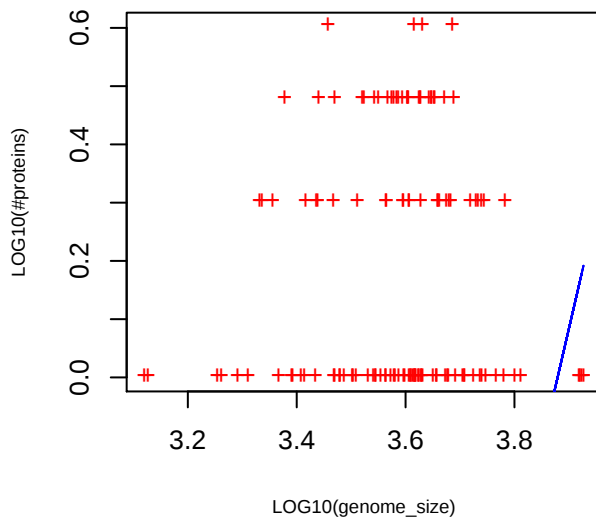
[O] COG1047 FKBP-type peptidyl-prolyl cis-trans isomerases 2

slope= -0.0062 p_value= 0.013 intercept= 0.025 p_value= 7.6e-17

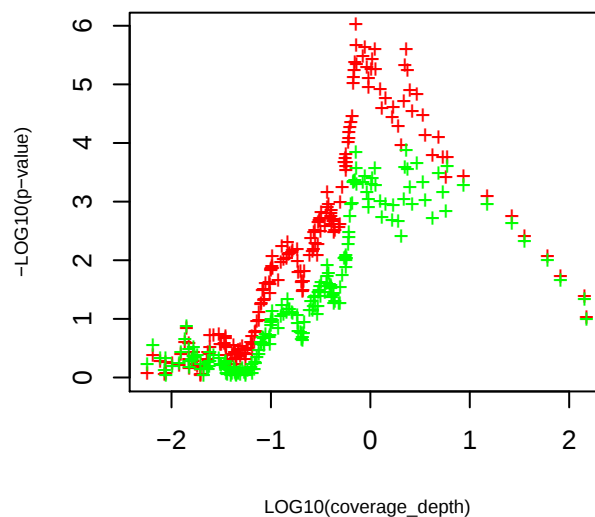


[O] COG1047 FKBP-type peptidyl-prolyl cis-trans isomerases 2

slope= 4.03 p_value= 3.4e-06 intercept= -15.63 p_value= 4.4e-07

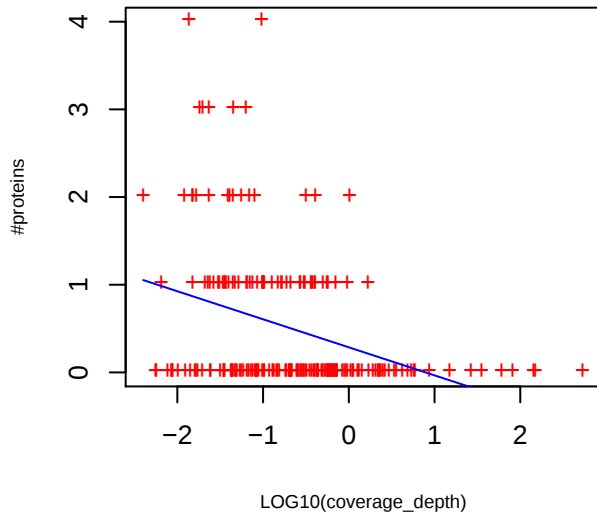


P-value curve ; red (unnorm), green (norm)



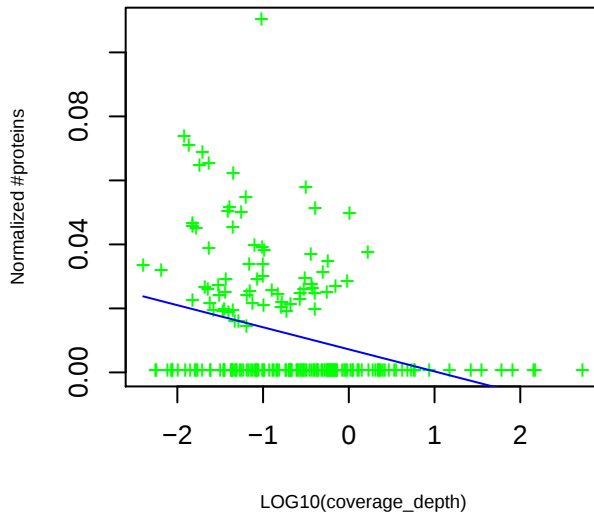
[P] COG0753 Catalase

slope= -0.32 p_value= 5.9e-07 intercept= 0.29 p_value= 6.2e-05



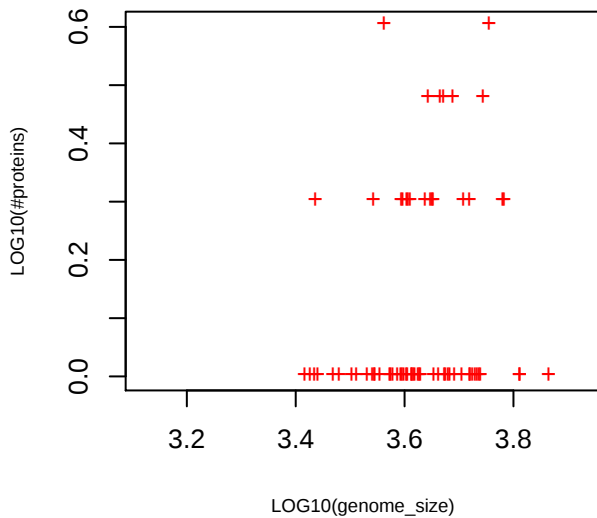
[P] COG0753 Catalase

slope= -0.0069 p_value= 4.8e-06 intercept= 0.0072 p_value= 2.2e-05

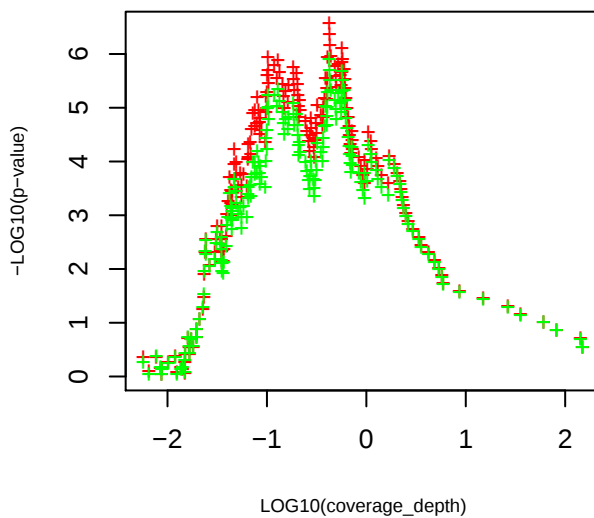


[P] COG0753 Catalase

slope= 4.56 p_value= 4.8e-08 intercept= -18.72 p_value= 4.4e-10

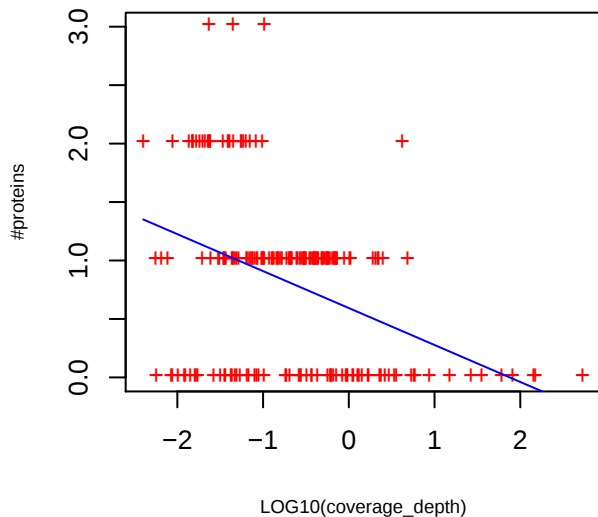


P-value curve ; red (unnorm), green (norm)



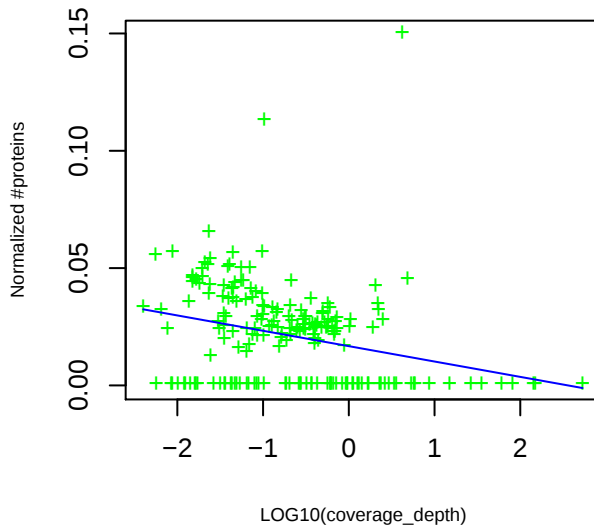
[G] COG1925 Phosphotransferase system, HPr-related proteins

slope= -0.32 p_value= 1.3e-08 intercept= 0.59 p_value= 6.2e-19



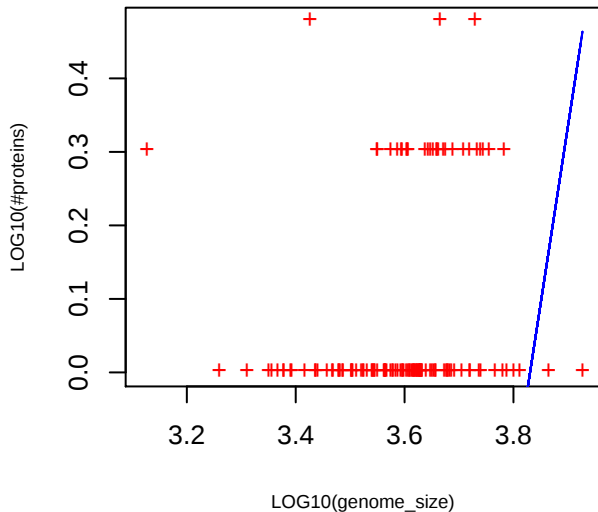
[G] COG1925 Phosphotransferase system, HPr-related proteins

slope= -0.0065 p_value= 5.7e-05 intercept= 0.017 p_value= 2.6e-17

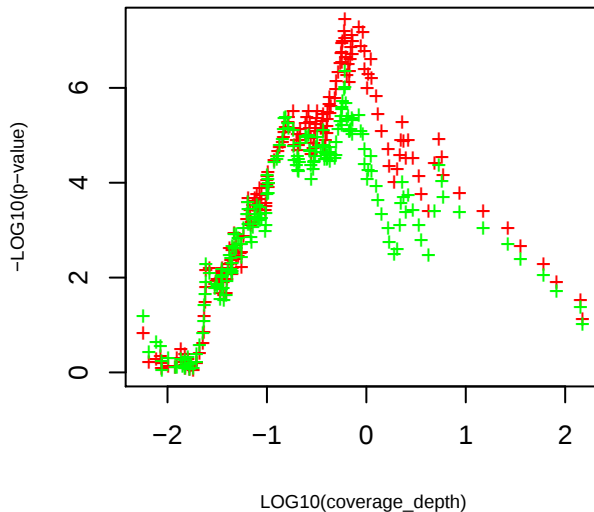


[G] COG1925 Phosphotransferase system, HPr-related proteins

slope= 4.81 p_value= 5.4e-09 intercept= -18.44 p_value= 4e-10

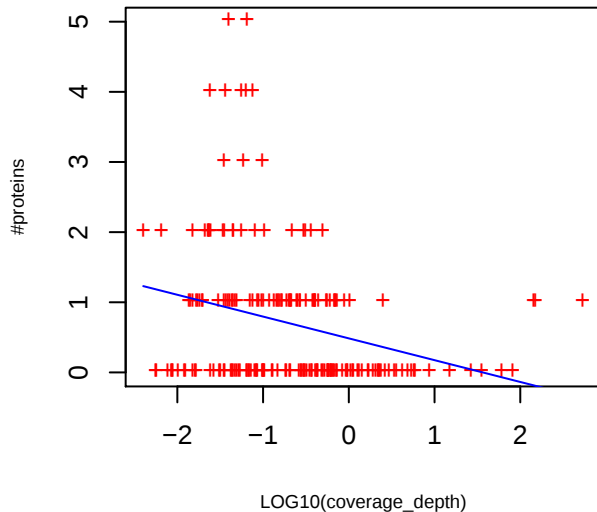


P-value curve ; red (unnorm), green (norm)



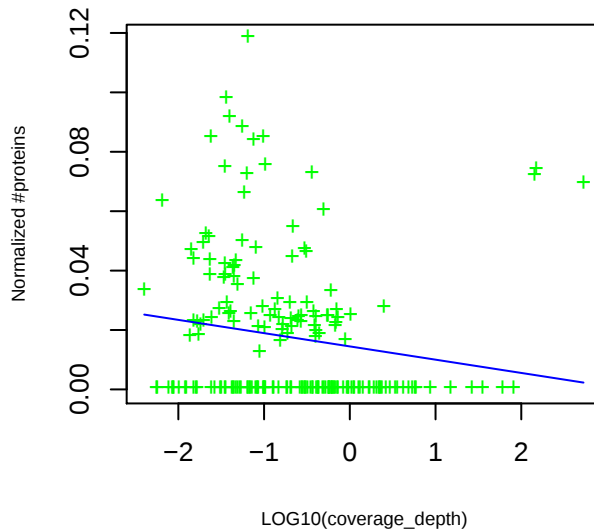
[S] COG2606 Uncharacterized conserved protein

slope= -0.31 p_value= 8.9e-05 intercept= 0.49 p_value= 9.8e-08



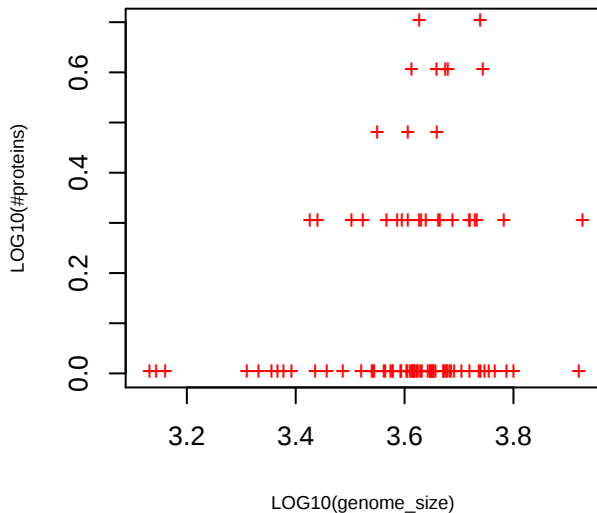
[S] COG2606 Uncharacterized conserved protein

slope= -0.0045 p_value= 0.023 intercept= 0.014 p_value= 4.1e-10

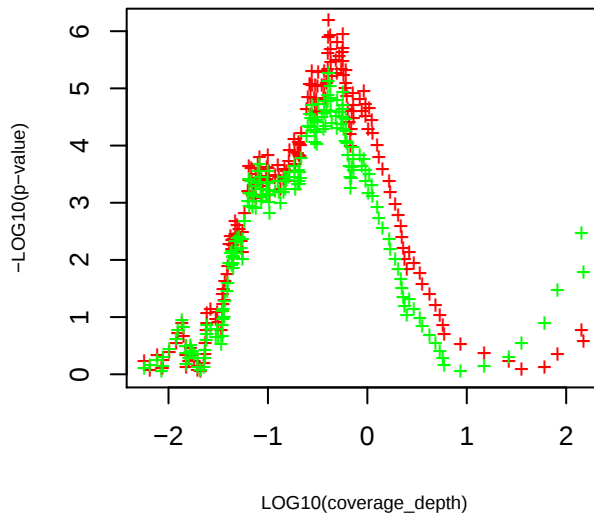


[S] COG2606 Uncharacterized conserved protein

slope= 4.32 p_value= 9.4e-07 intercept= -17.46 p_value= 3.2e-08

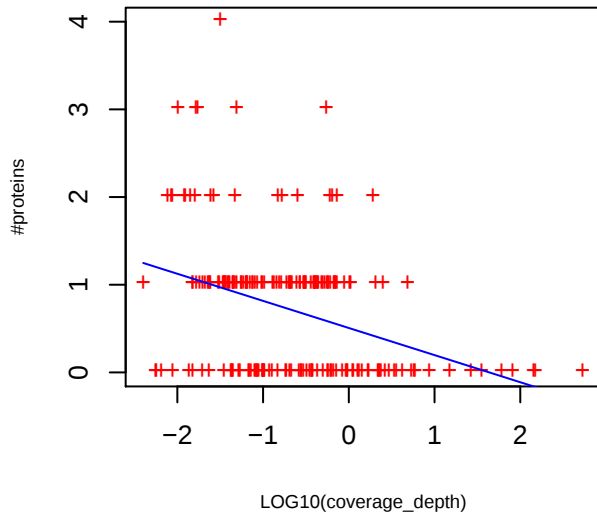


P-value curve ; red (unnorm), green (norm)



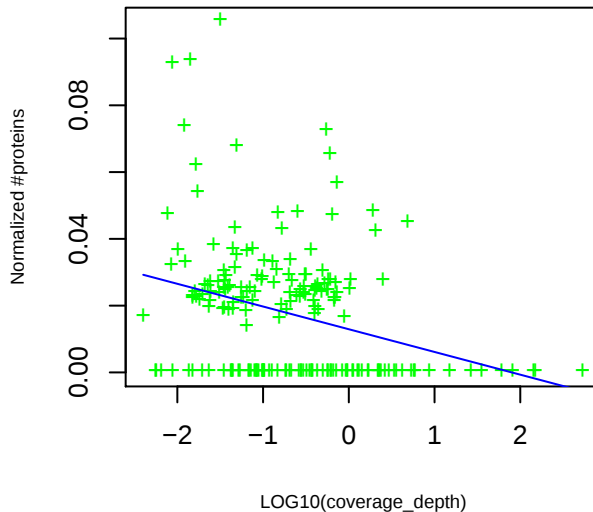
[S] COG1432 Uncharacterized conserved protein

slope= -0.31 p_value= 2.0e-07 intercept= 0.51 p_value= 3.2e-13



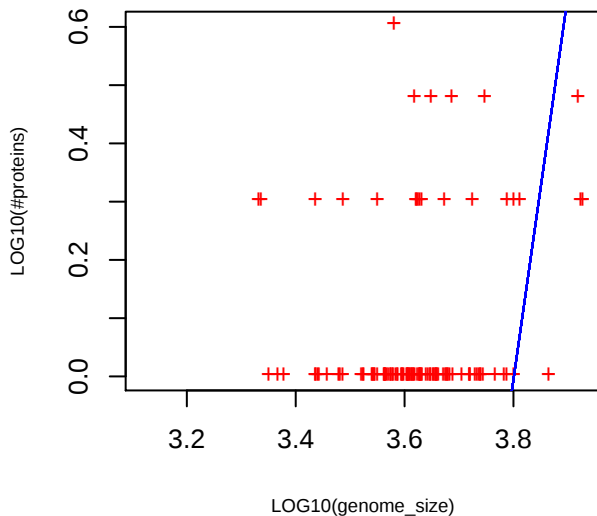
[S] COG1432 Uncharacterized conserved protein

slope= -0.0068 p_value= 9.2e-06 intercept= 0.013 p_value= 8.1e-13

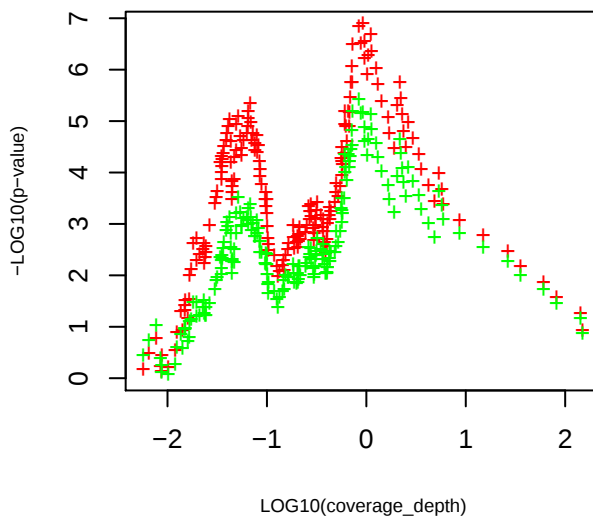


[S] COG1432 Uncharacterized conserved protein

slope= 6.59 p_value= 1.1e-15 intercept= -25.06 p_value= 1.9e-17

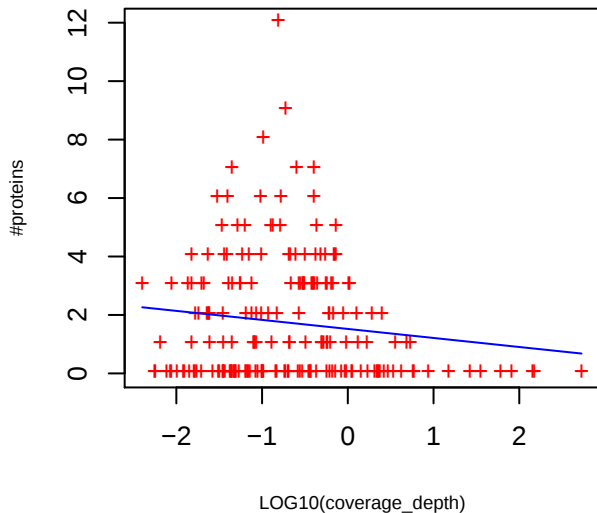


P-value curve ; red (unnorm), green (norm)



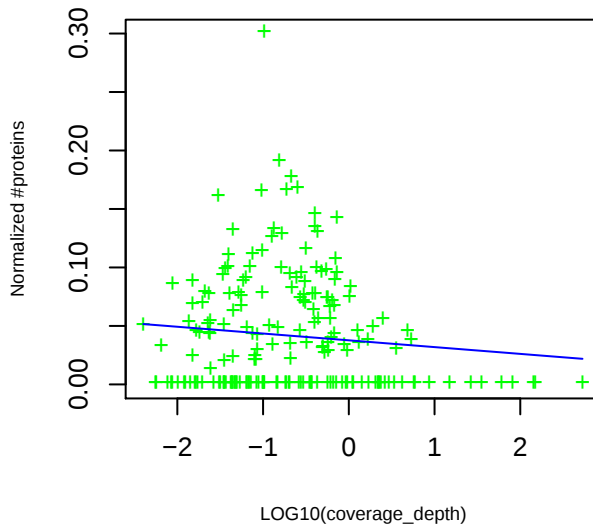
[K] COG2186 Transcriptional regulators

slope= -0.31 p_value= 0.065 intercept= 1.52 p_value= 6.4e-14



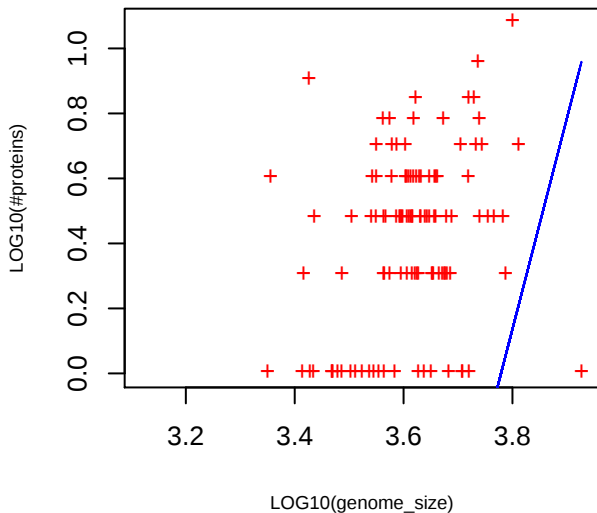
[K] COG2186 Transcriptional regulators

slope= -0.0058 p_value= 0.15 intercept= 0.038 p_value= 8e-15

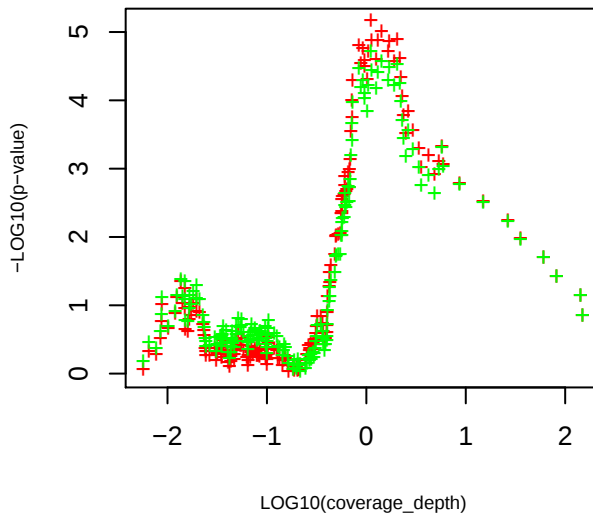


[K] COG2186 Transcriptional regulators

slope= 6.49 p_value= 9.1e-13 intercept= -24.51 p_value= 4.5e-14

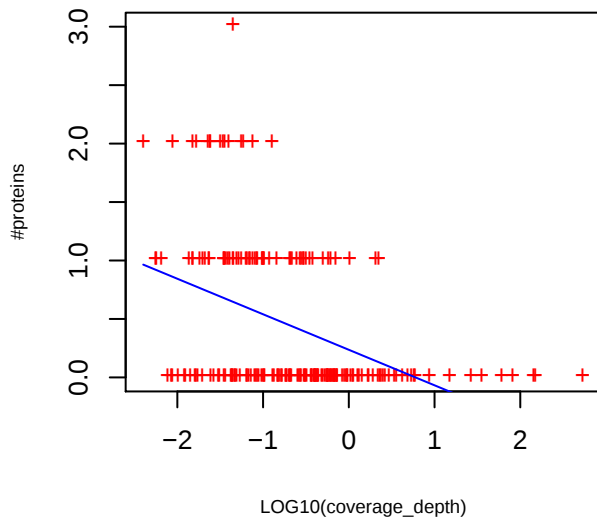


P-value curve ; red (unnorm), green (norm)



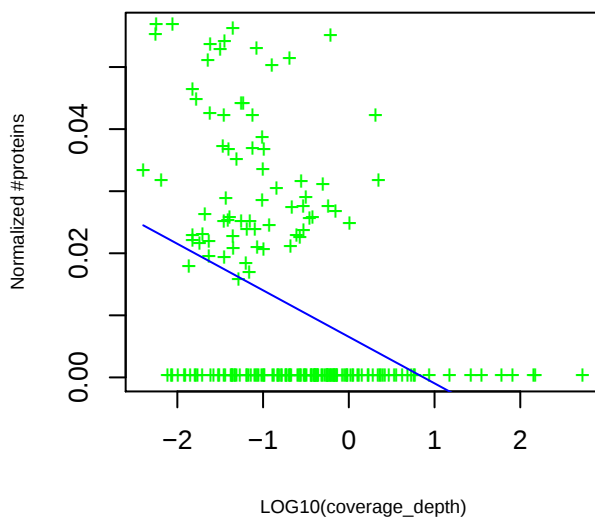
[NUO] COG1516 Flagellin-specific chaperone FliS

slope= -0.30 p_value= 1.6e-09 intercept= 0.24 p_value= 2.0e-05



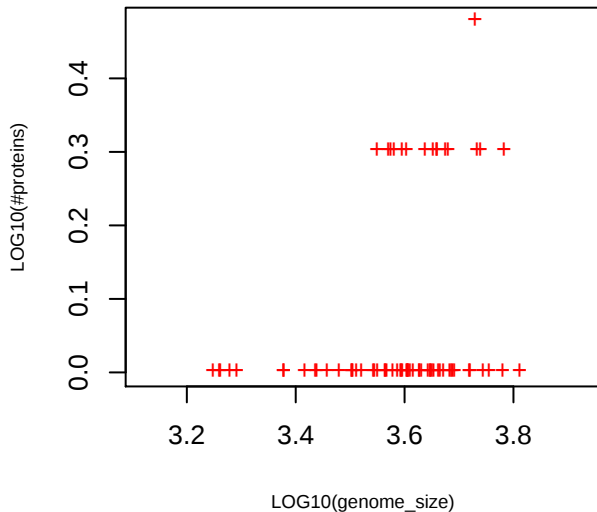
[NUO] COG1516 Flagellin-specific chaperone FliS

slope= -0.0075 p_value= 1.6e-08 intercept= 0.0065 p_value= 9.3e-06

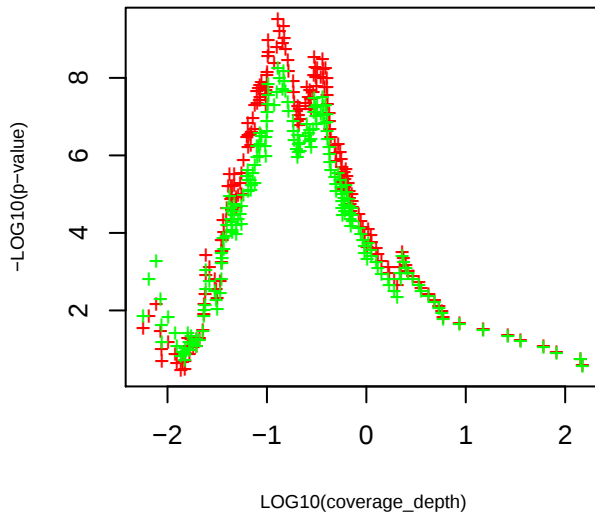


[NUO] COG1516 Flagellin-specific chaperone FliS

slope= 2.32 p_value= 0.0065 intercept= -10.77 p_value= 0.00041

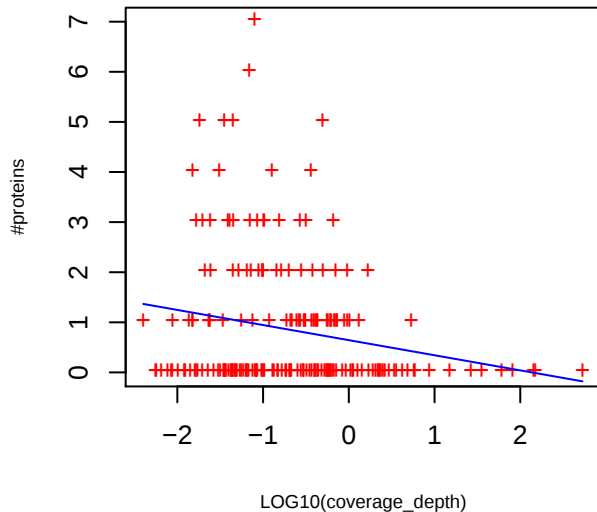


P-value curve ; red (unnorm), green (norm)



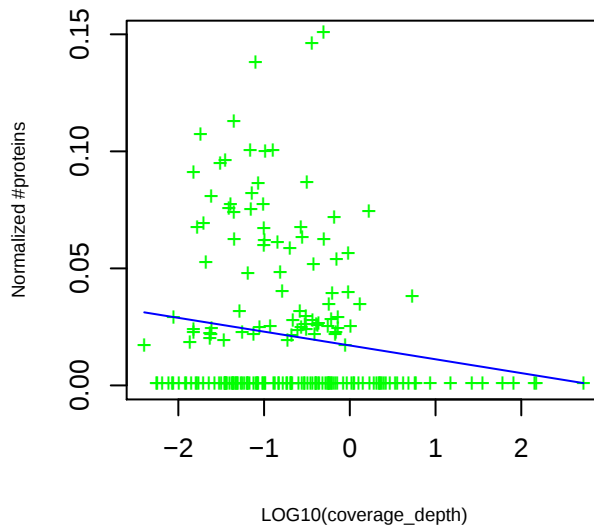
[S] COG3182 Uncharacterized iron-regulated membrane protein

slope= -0.30 p_value= 0.0043 intercept= 0.64 p_value= 1.4e-07



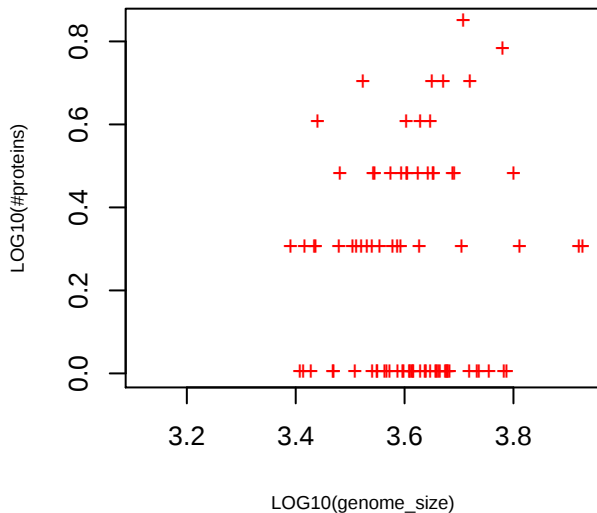
[S] COG3182 Uncharacterized iron-regulated membrane protein

slope= -0.0059 p_value= 0.023 intercept= 0.017 p_value= 1.9e-08

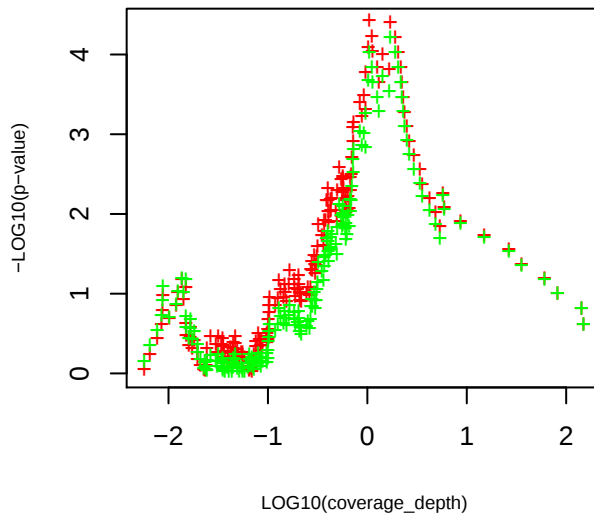


[S] COG3182 Uncharacterized iron-regulated membrane protein

slope= 4.42 p_value= 8e-07 intercept= -17.90 p_value= 2.3e-08

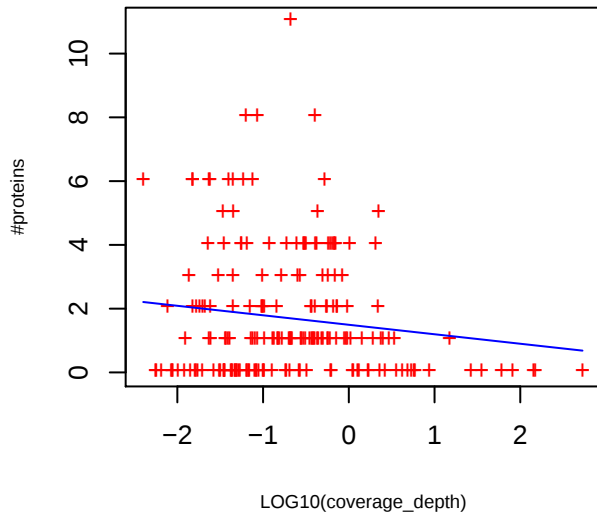


P-value curve ; red (unnorm), green (norm)



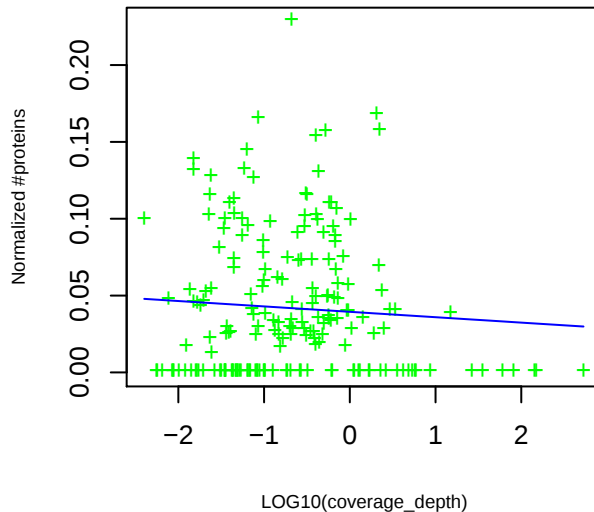
[M] COG1292 Choline-glycine betaine transporter

slope= -0.30 p_value= 0.065 intercept= 1.49 p_value= 2.4e-14



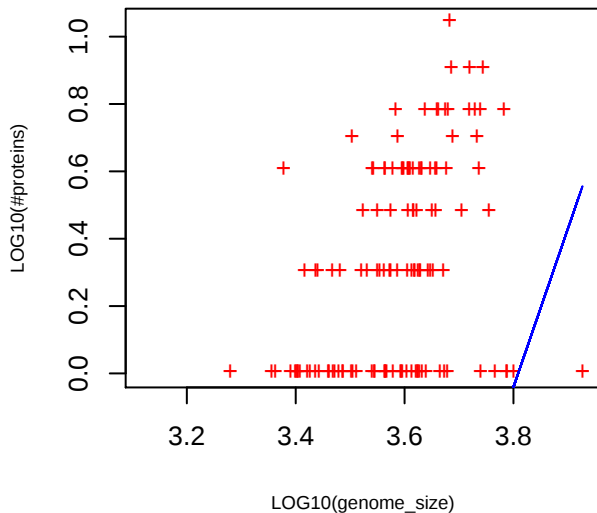
[M] COG1292 Choline-glycine betaine transporter

slope= -0.0035 p_value= 0.34 intercept= 0.039 p_value= 4.3e-18

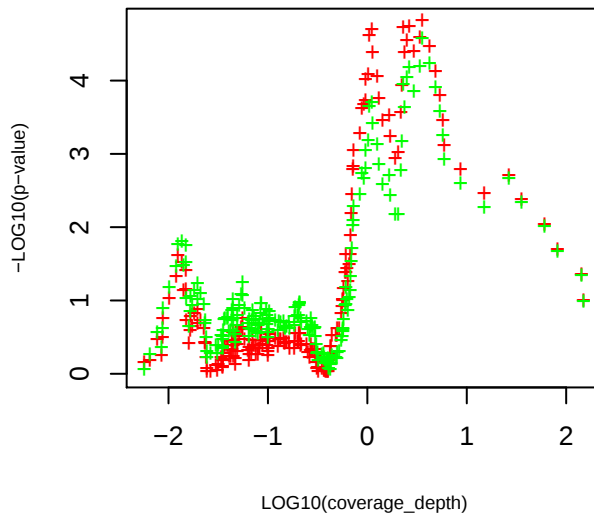


[M] COG1292 Choline-glycine betaine transporter

slope= 4.70 p_value= 1.2e-07 intercept= -17.91 p_value= 1.6e-08

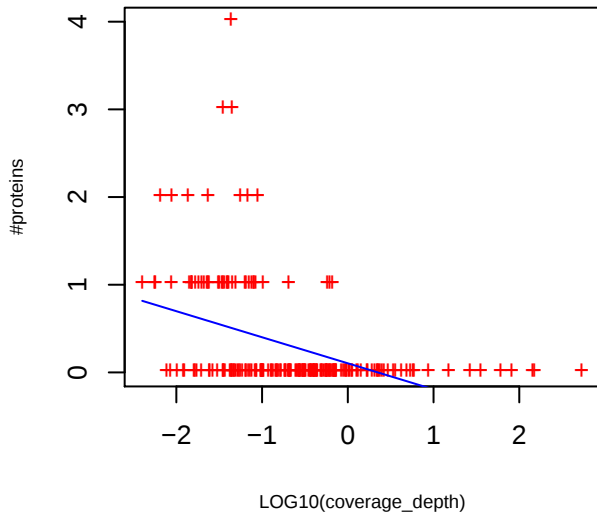


P-value curve ; red (unnorm), green (norm)



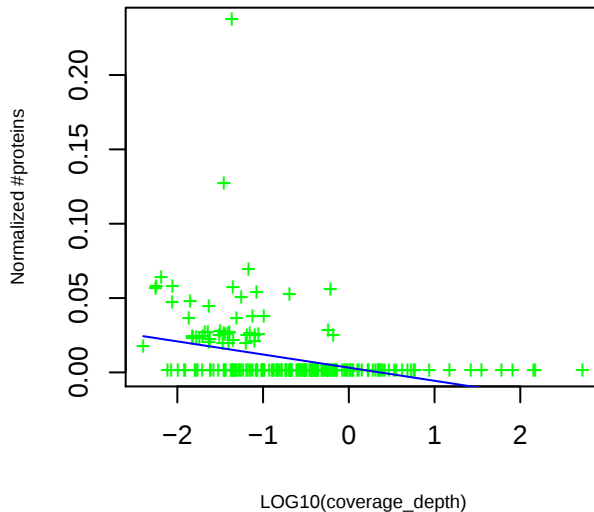
[ER] COG1387 Histidinol phosphatase and related hydrolases of the PHP family

slope= -0.30 p_value= 1.2e-09 intercept= 0.10 p_value= 0.05



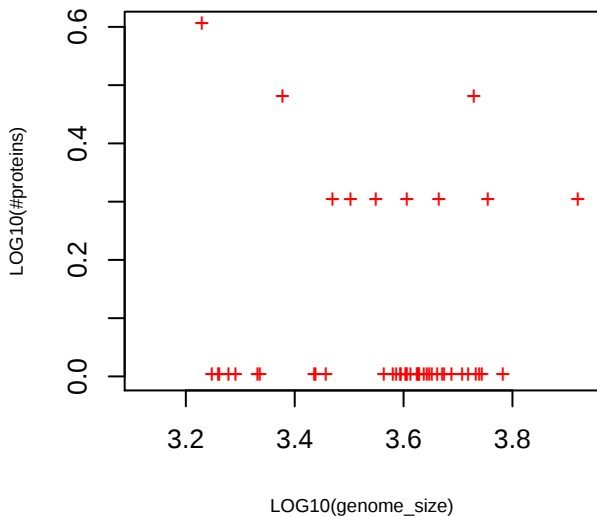
[ER] COG1387 Histidinol phosphatase and related hydrolases of the PHP family

slope= -0.0088 p_value= 2.1e-06 intercept= 0.0032 p_value= 0.12

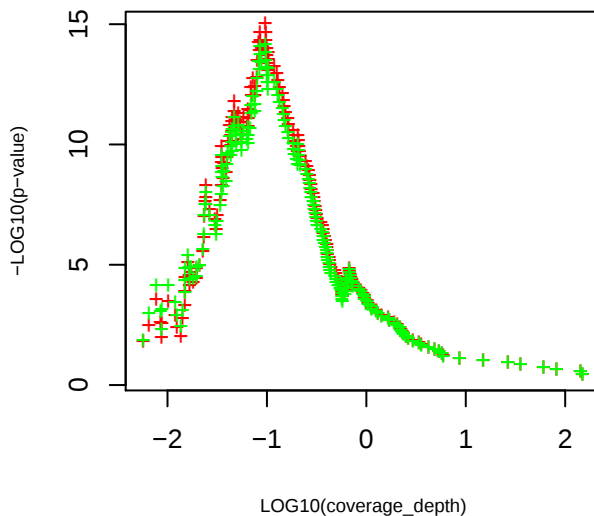


[ER] COG1387 Histidinol phosphatase and related hydrolases of the PHP family

slope= 0.82 p_value= 0.28 intercept= -5.95 p_value= 0.029

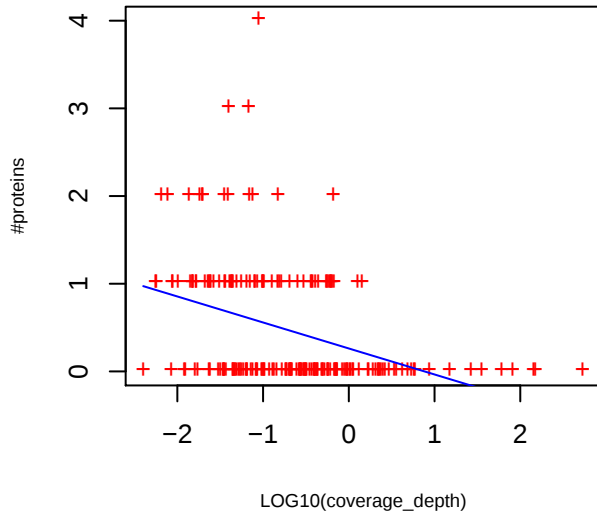


P-value curve ; red (unnorm), green (norm)



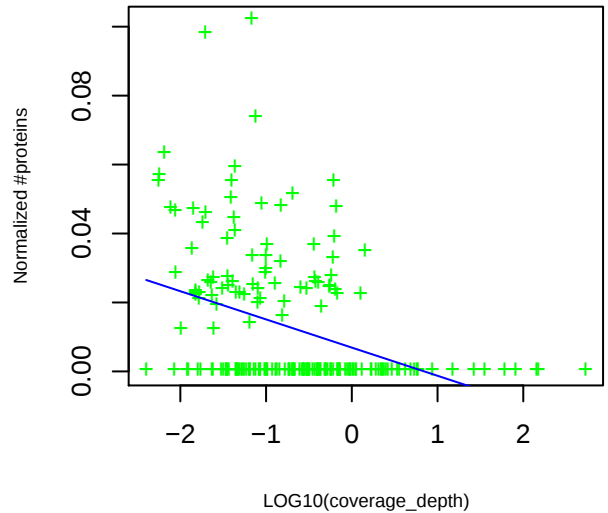
[L] COG1112 Superfamily I DNA and RNA helicases and helicase subunits

slope= -0.30 p_value= 4.8e-08 intercept= 0.26 p_value= 1.5e-05



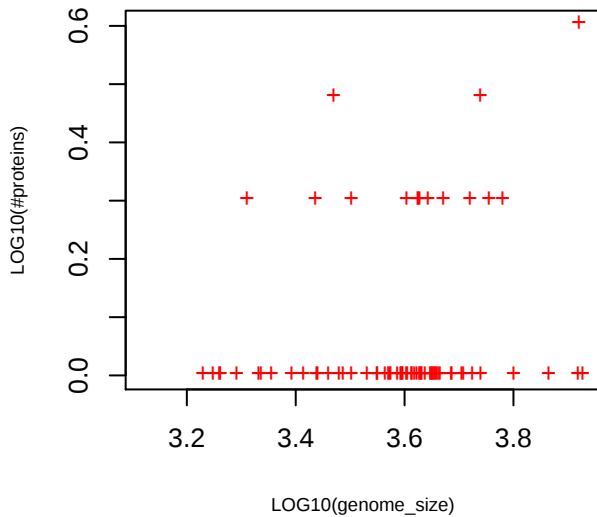
[L] COG1112 Superfamily I DNA and RNA helicases and helicase subunits

slope= -0.0082 p_value= 5.4e-08 intercept= 0.0069 p_value= 3.5e-05

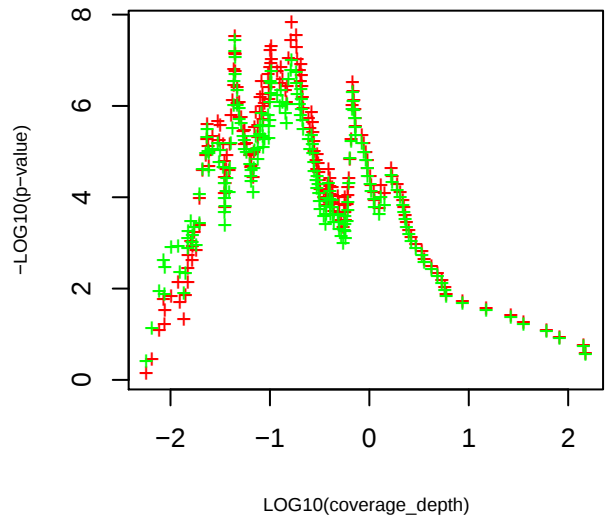


[L] COG1112 Superfamily I DNA and RNA helicases and helicase subunits

slope= 2.33 p_value= 0.0068 intercept= -10.74 p_value= 0.00047

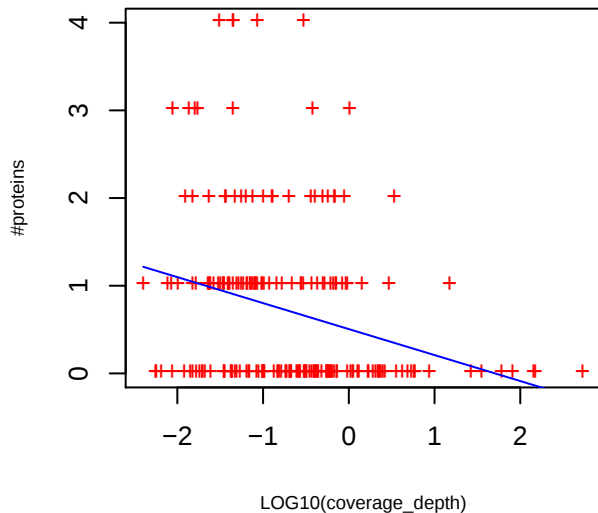


P-value curve ; red (unnorm), green (norm)



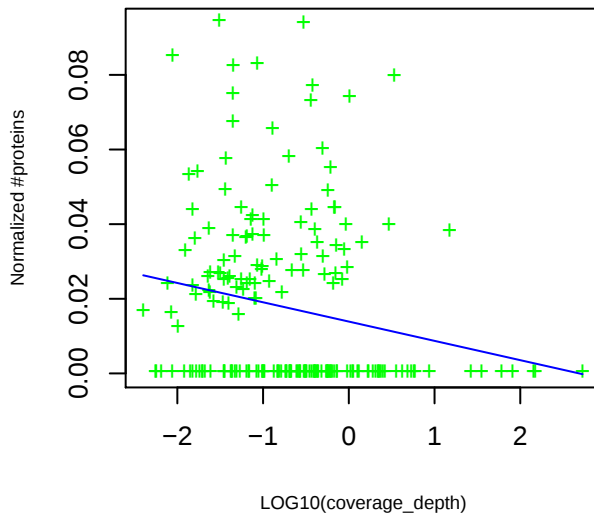
[P] COG2223 Nitrate/nitrite transporter

slope= -0.30 p_value= 0.00010 intercept= 0.51 p_value= 1e-08



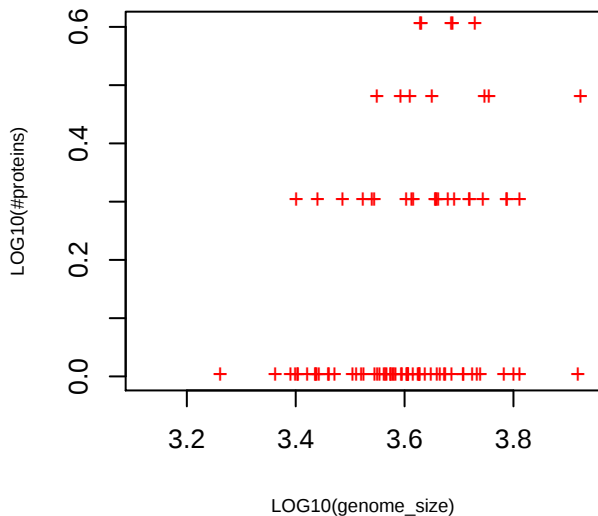
[P] COG2223 Nitrate/nitrite transporter

slope= -0.0052 p_value= 0.0048 intercept= 0.014 p_value= 1.4e-10

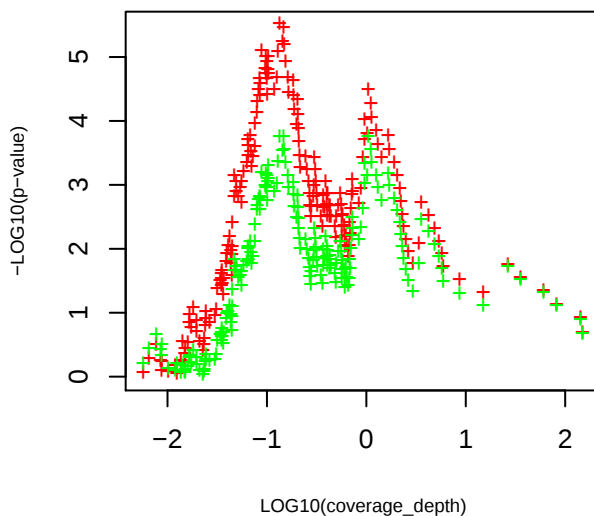


[P] COG2223 Nitrate/nitrite transporter

slope= 4.46 p_value= 4.4e-07 intercept= -17.91 p_value= 1.4e-08

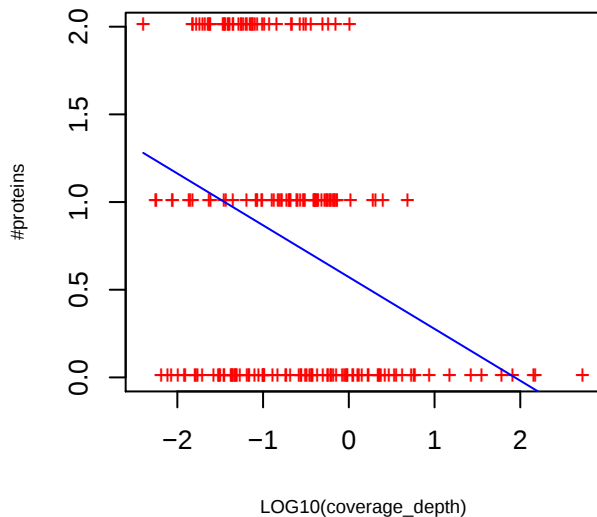


P-value curve ; red (unnorm), green (norm)



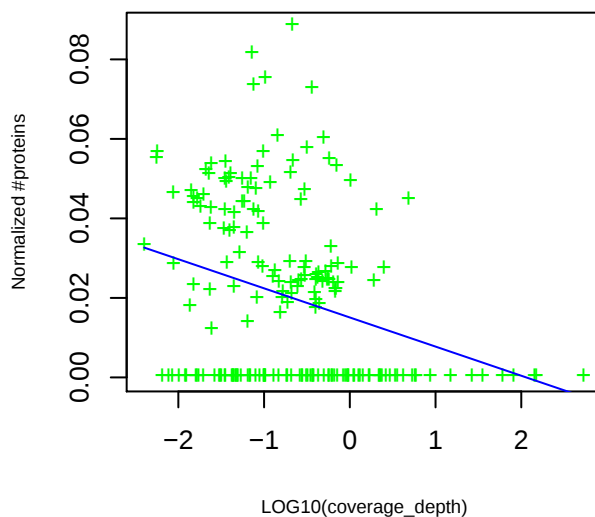
[J] COG2813 16S RNA G1207 methylase RsmC

slope= -0.30 p_value= 2.3e-06 intercept= 0.57 p_value= 1.2e-14



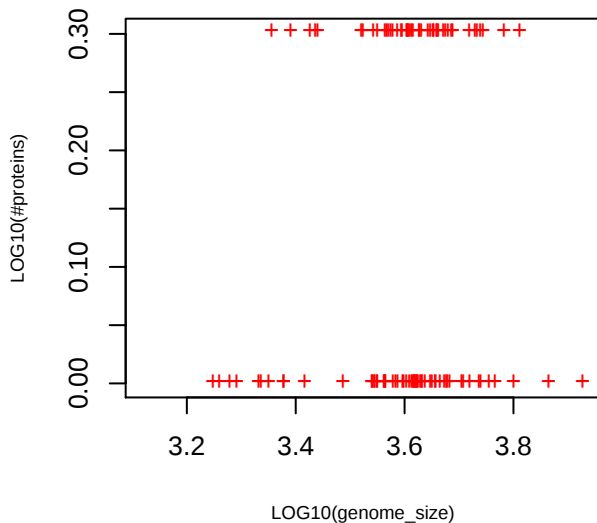
[J] COG2813 16S RNA G1207 methylase RsmC

slope= -0.0073 p_value= 1.8e-05 intercept= 0.015 p_value= 1.0e-13

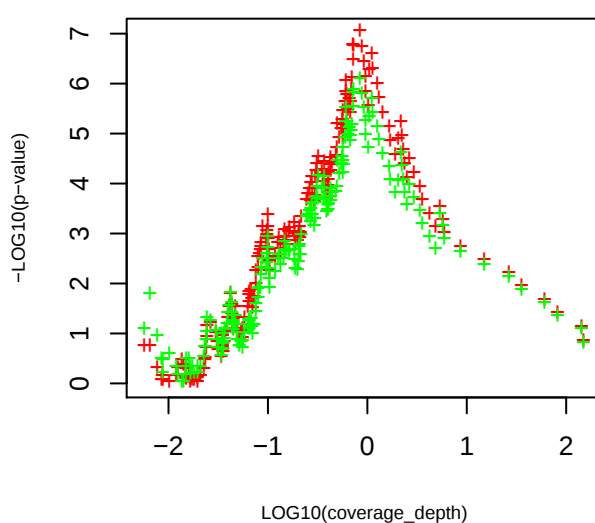


[J] COG2813 16S RNA G1207 methylase RsmC

slope= 4.52 p_value= 2.7e-07 intercept= -17.77 p_value= 1.5e-08

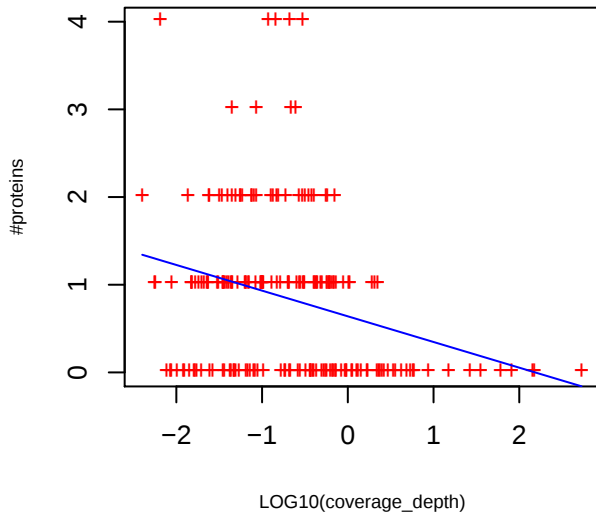


P-value curve : red (unnorm), green (norm)



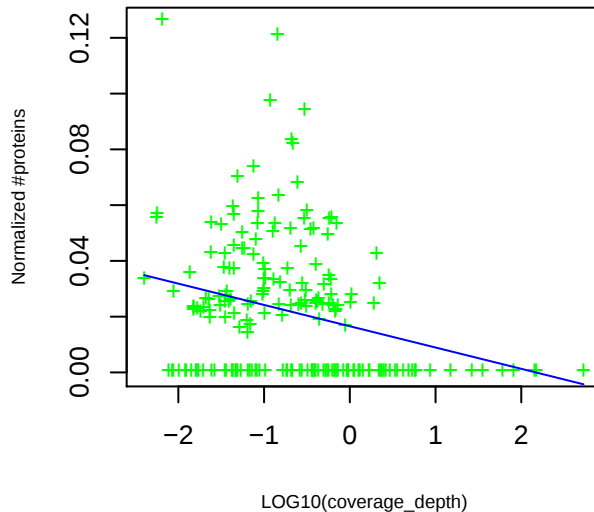
[N] COG1291 Flagellar motor component

slope= -0.29 p_value= 6.3e-05 intercept= 0.64 p_value= 1.8e-13



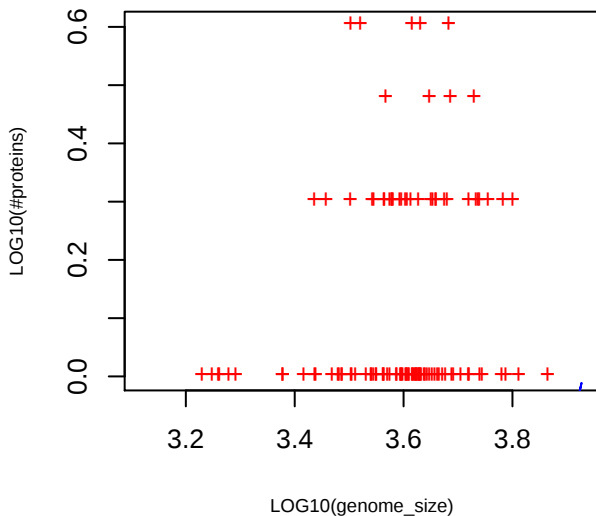
[N] COG1291 Flagellar motor component

slope= -0.0076 p_value= 7e-05 intercept= 0.017 p_value= 3.6e-13

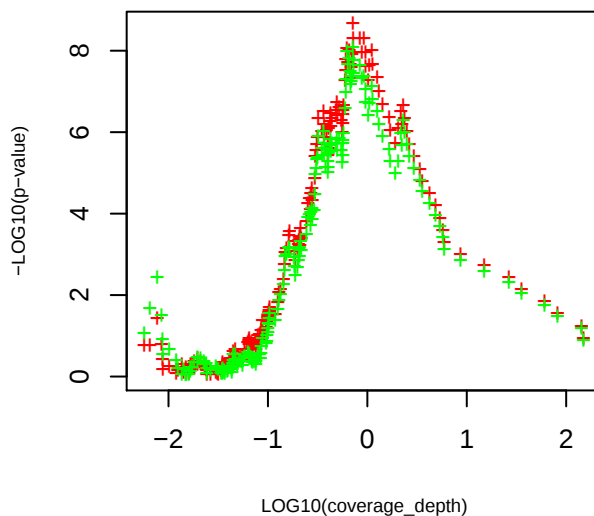


[N] COG1291 Flagellar motor component

slope= 4.25 p_value= 1.1e-06 intercept= -16.72 p_value= 8.7e-08

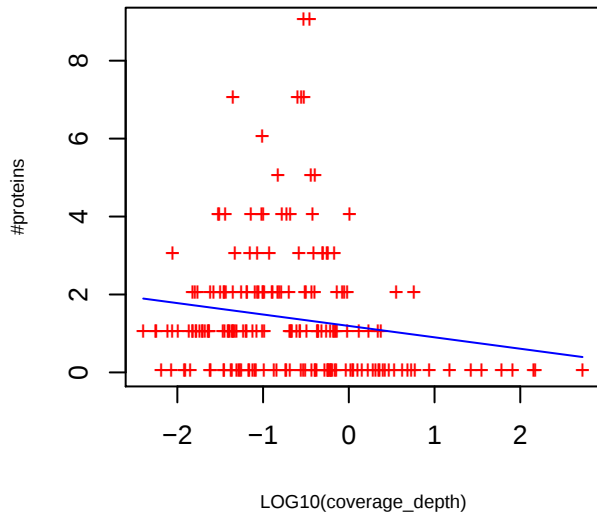


P-value curve ; red (unnorm), green (norm)



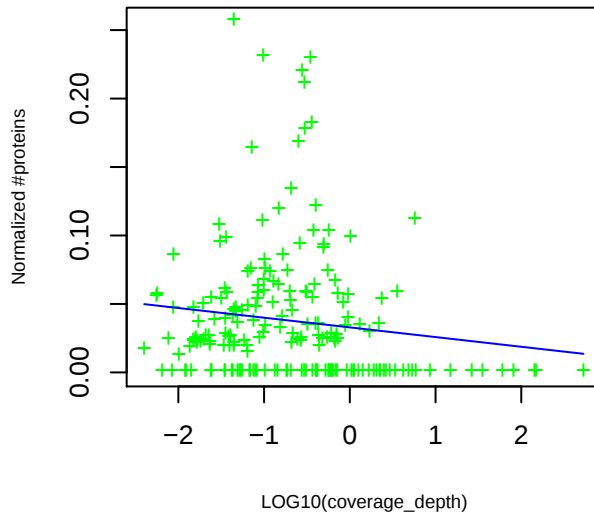
[P] COG1230 Co/Zn/Cd efflux system component

slope= -0.29 p_value= 0.031 intercept= 1.19 p_value= 2.7e-13



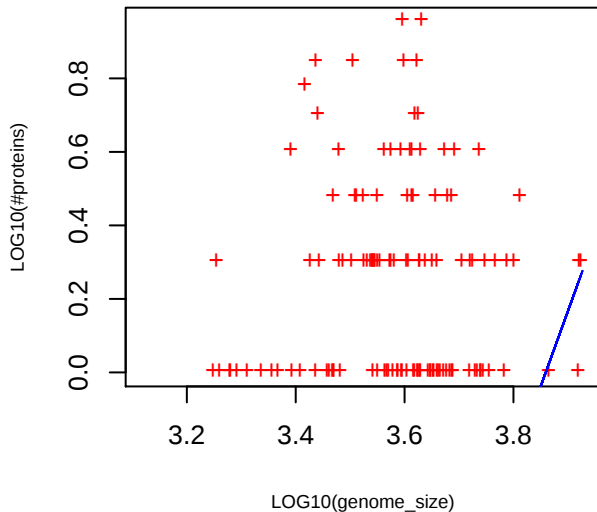
[P] COG1230 Co/Zn/Cd efflux system component

slope= -0.0071 p_value= 0.067 intercept= 0.033 p_value= 1.3e-12

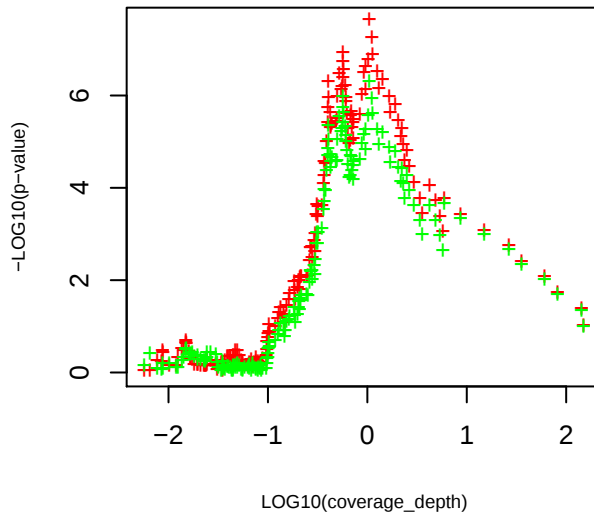


[P] COG1230 Co/Zn/Cd efflux system component

slope= 4.09 p_value= 3.3e-06 intercept= -15.78 p_value= 4.8e-07

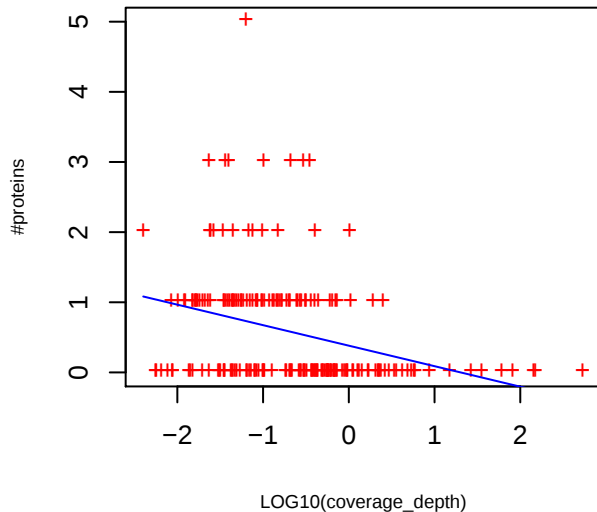


P-value curve ; red (unnorm), green (norm)



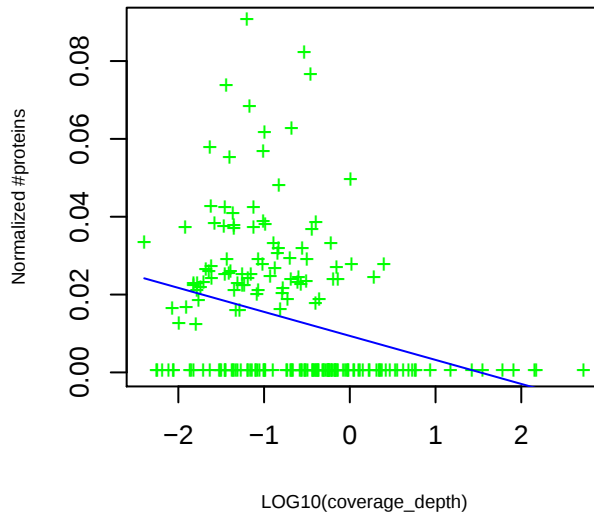
[F] COG1816 Adenosine deaminase

slope= -0.29 p_value= 5.9e-06 intercept= 0.38 p_value= 2.1e-07



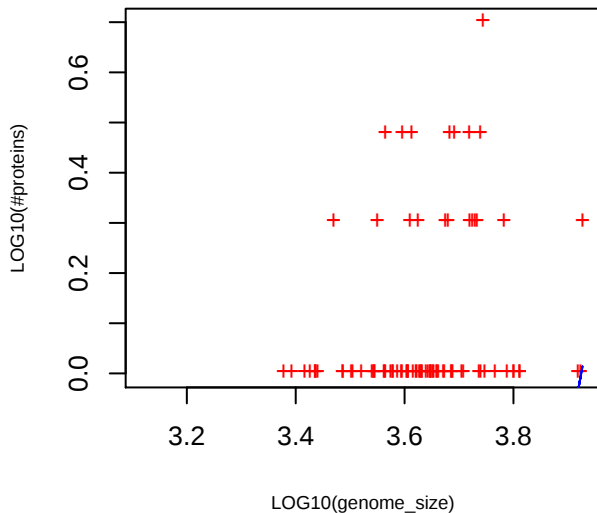
[F] COG1816 Adenosine deaminase

slope= -0.0062 p_value= 3e-05 intercept= 0.0094 p_value= 3.3e-08

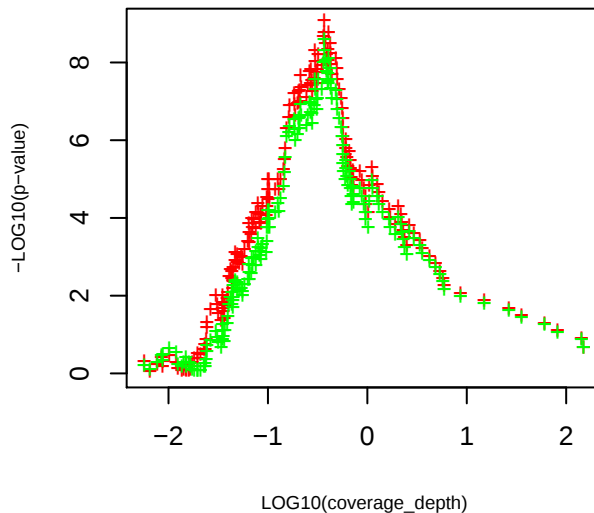


[F] COG1816 Adenosine deaminase

slope= 5.89 p_value= 2.4e-12 intercept= -23.13 p_value= 2.0e-14

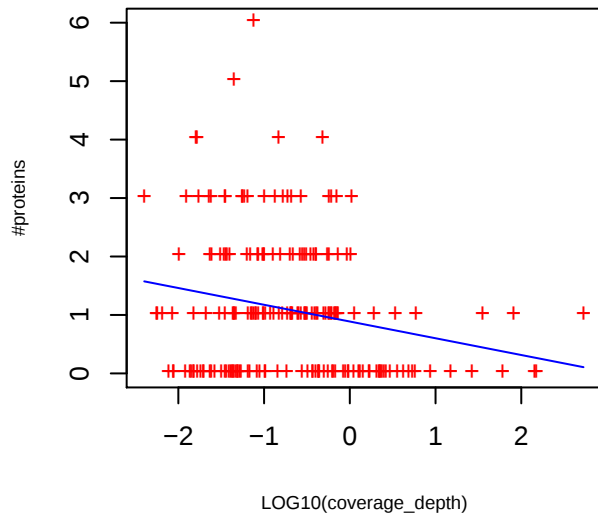


P-value curve ; red (unnorm), green (norm)



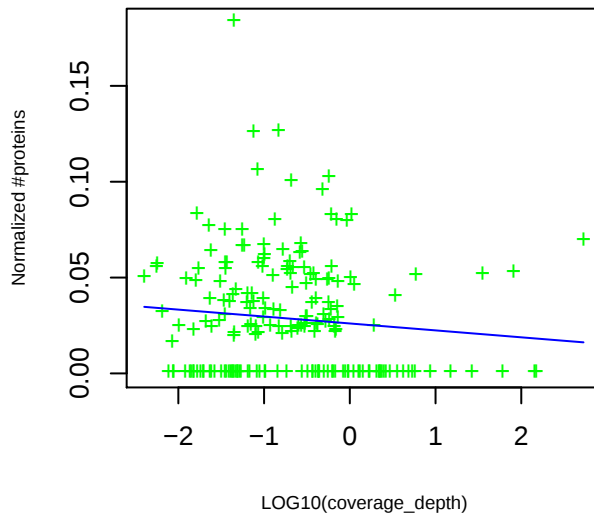
[M] COG3206 Uncharacterized protein involved in exopolysaccharide biosynthesis

slope= -0.29 p_value= 0.0020 intercept= 0.89 p_value= 2.9e-15



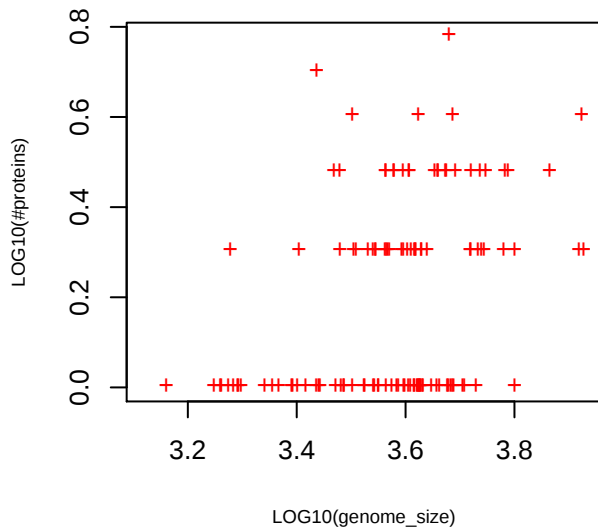
[M] COG3206 Uncharacterized protein involved in exopolysaccharide biosynthesis

slope= -0.0036 p_value= 0.14 intercept= 0.026 p_value= 1.1e-17

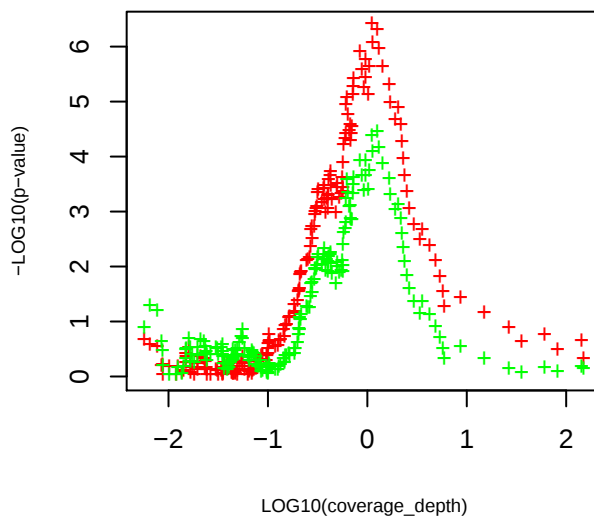


[M] COG3206 Uncharacterized protein involved in exopolysaccharide biosynthesis

slope= 3.30 p_value= 0.00022 intercept= -13.17 p_value= 3.5e-05

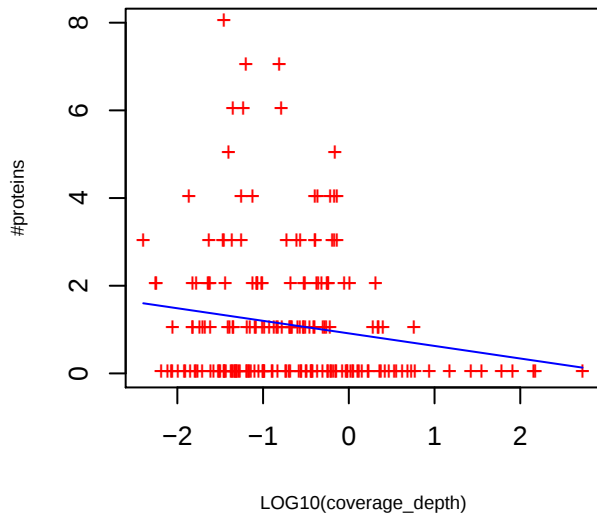


P-value curve ; red (unnorm), green (norm)



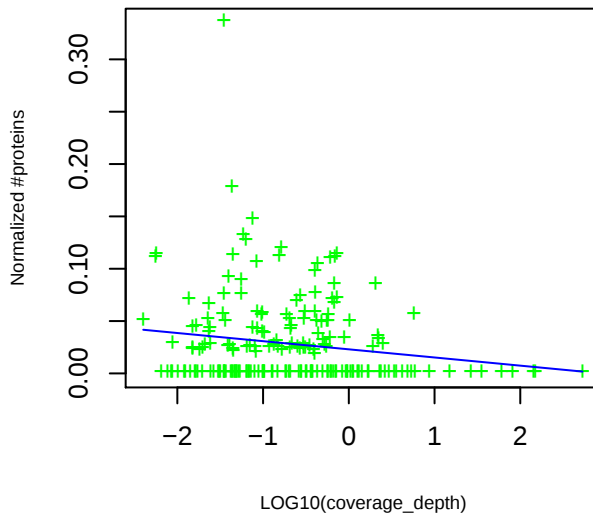
[K] COG1737 Transcriptional regulators

slope= -0.29 p_value= 0.021 intercept= 0.91 p_value= 4.7e-10



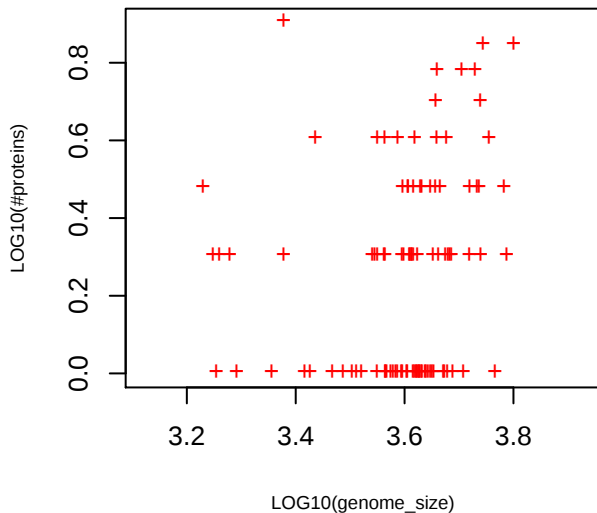
[K] COG1737 Transcriptional regulators

slope= -0.0078 p_value= 0.02 intercept= 0.023 p_value= 4.7e-09

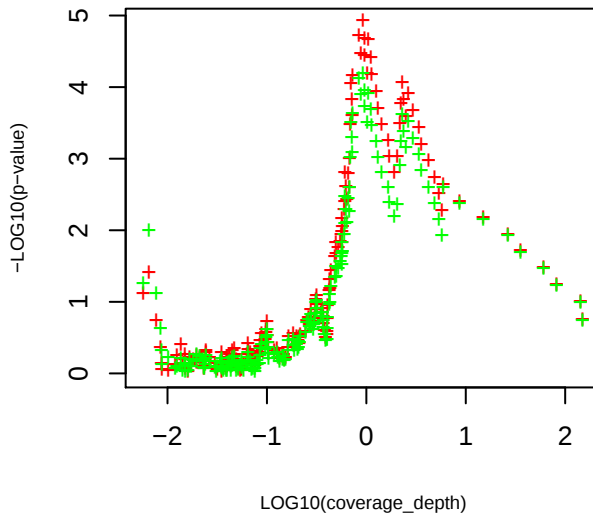


[K] COG1737 Transcriptional regulators

slope= 4.28 p_value= 3.1e-06 intercept= -17.02 p_value= 2.1e-07

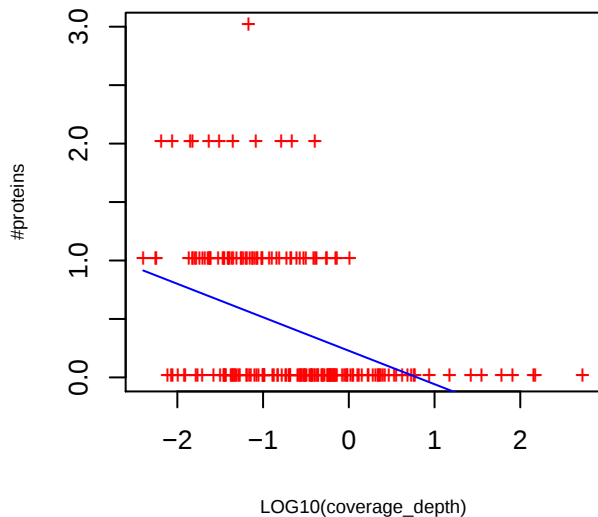


P-value curve ; red (unnorm), green (norm)



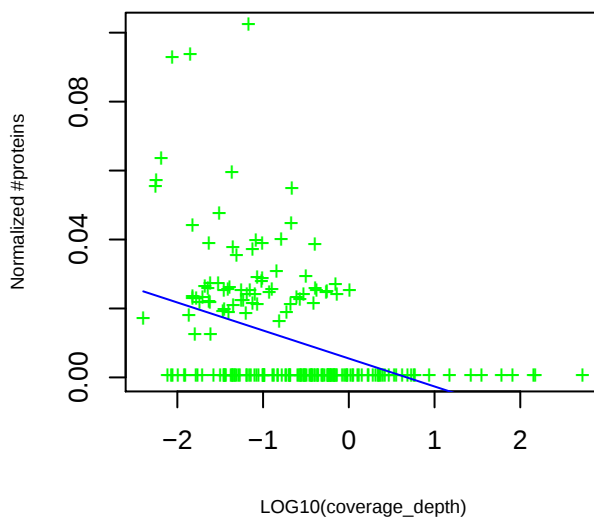
[S] COG1720 Uncharacterized conserved protein

slope= -0.29 p_value= 2.0e-09 intercept= 0.23 p_value= 1.5e-05



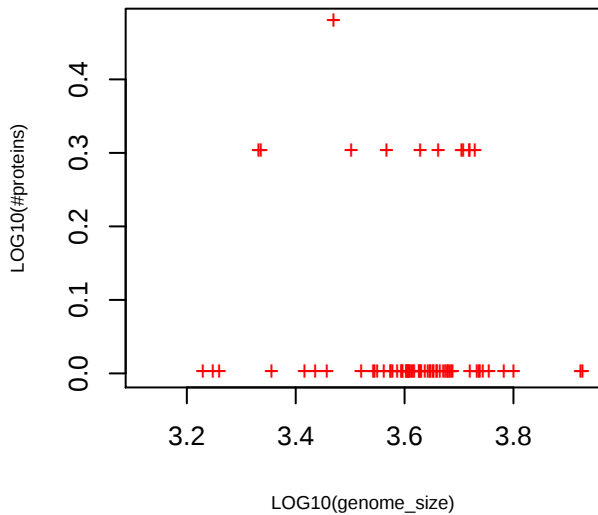
[S] COG1720 Uncharacterized conserved protein

slope= -0.0081 p_value= 5.9e-09 intercept= 0.0055 p_value= 0.00034

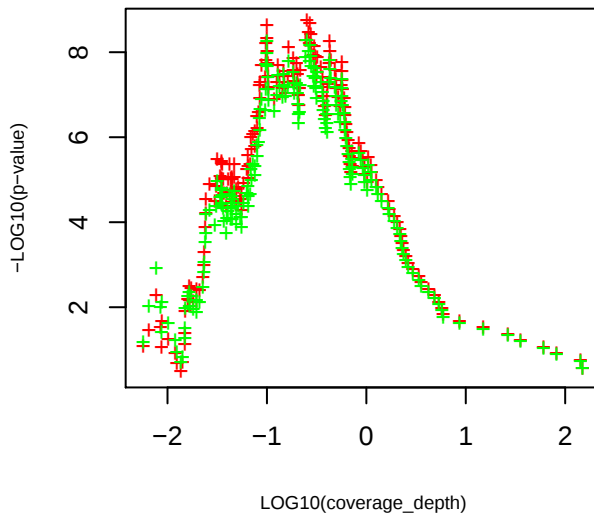


[S] COG1720 Uncharacterized conserved protein

slope= 3.61 p_value= 1.6e-05 intercept= -15.35 p_value= 3.3e-07

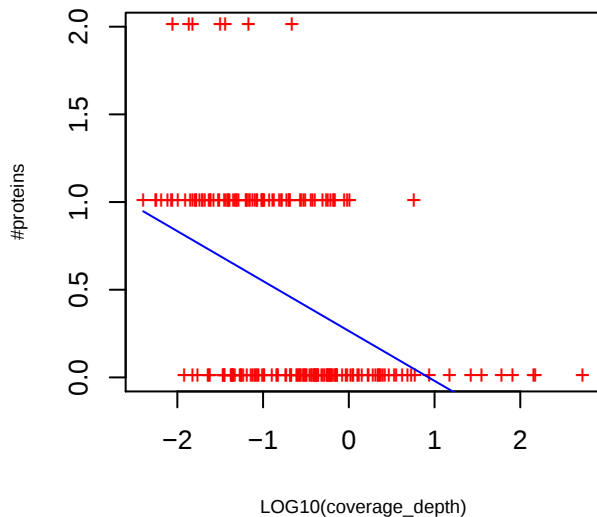


P-value curve ; red (unnorm), green (norm)



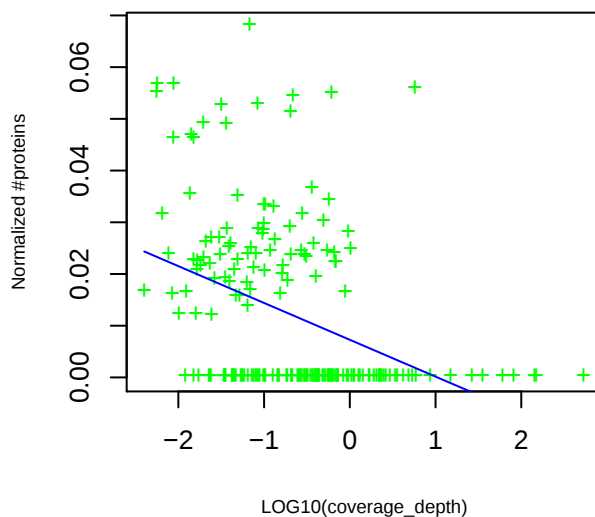
[J] COG1514 2'-5' RNA ligase

slope= -0.28 p_value= 3.6e-11 intercept= 0.26 p_value= 2.9e-08



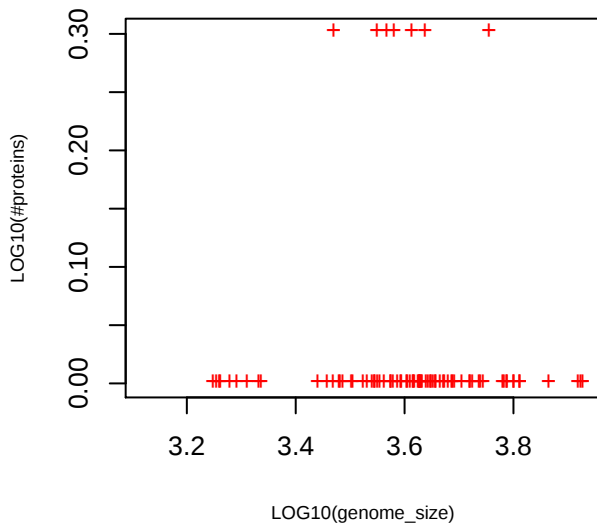
[J] COG1514 2'-5' RNA ligase

slope= -0.0071 p_value= 1.9e-08 intercept= 0.0073 p_value= 3e-07

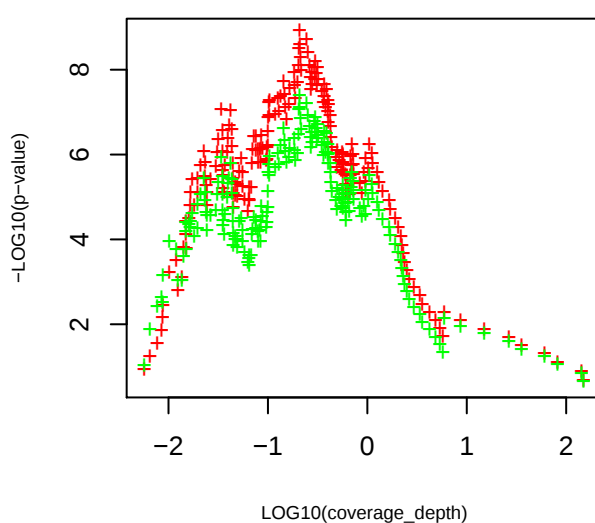


[J] COG1514 2'-5' RNA ligase

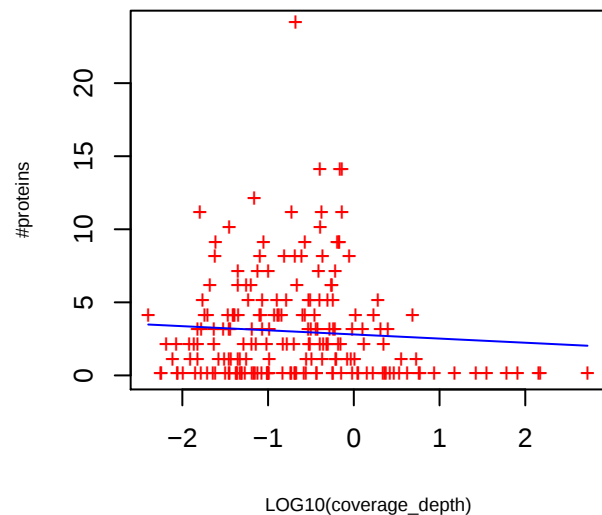
slope= 3.90 p_value= 5e-06 intercept= -16.12 p_value= 1.4e-07



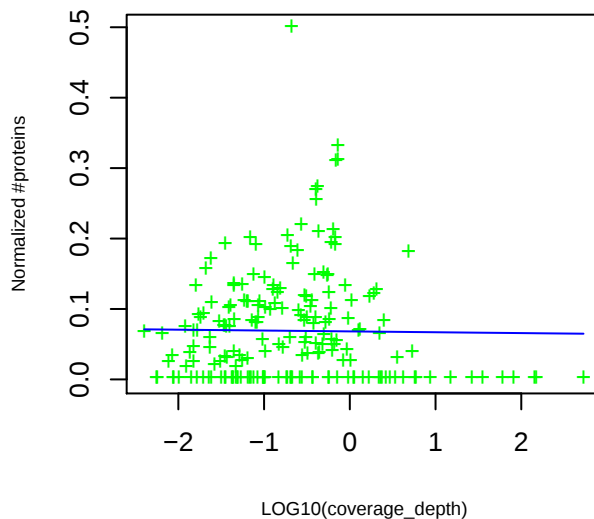
P-value curve ; red (unnorm), green (norm)



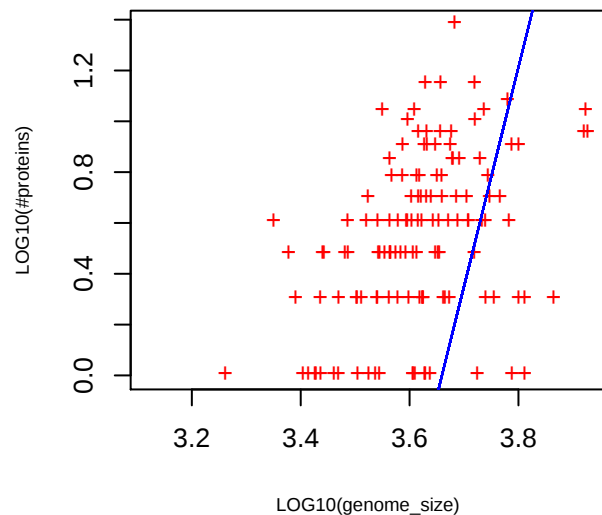
slope= -0.28 p_value= 0.33 intercept= 2.80 p_value= 2.0e-15



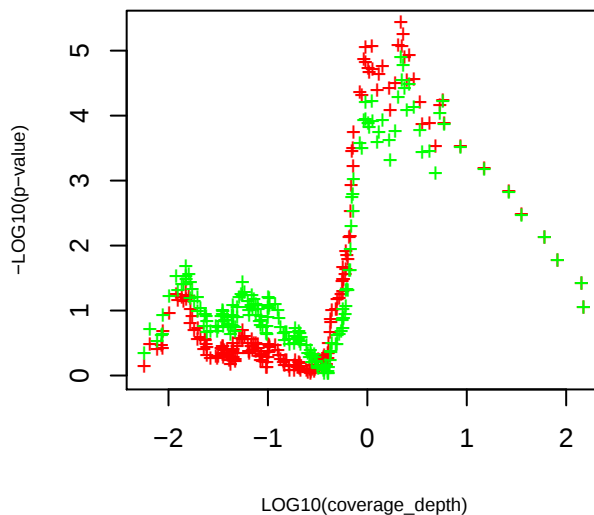
slope= -0.0012 p_value= 0.85 intercept= 0.068 p_value= 2.1e-18



slope= 8.63 p_value= 4.4e-25 intercept= -31.57 p_value= 3.3e-26

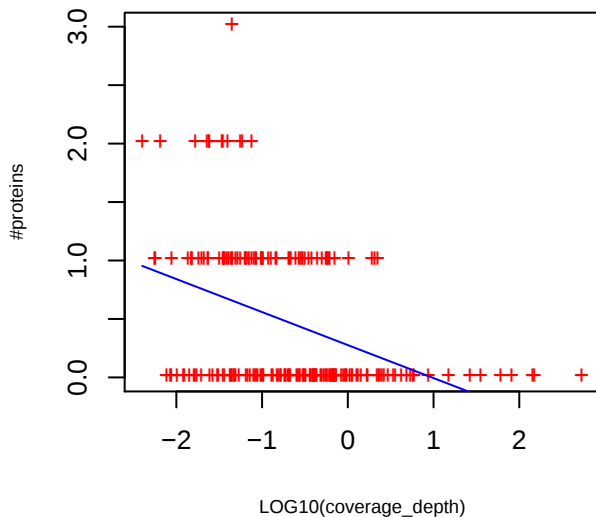


P-value curve ; red (unnorm), green (norm)



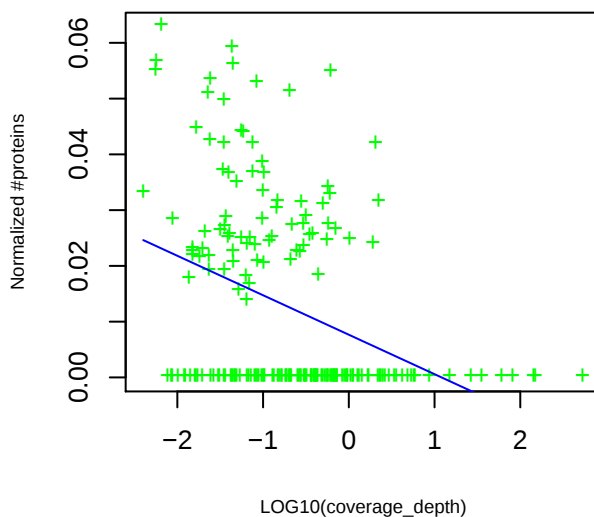
[N] COG1345 Flagellar capping protein

slope= -0.28 p_value= 7.2e-09 intercept= 0.28 p_value= 4e-07



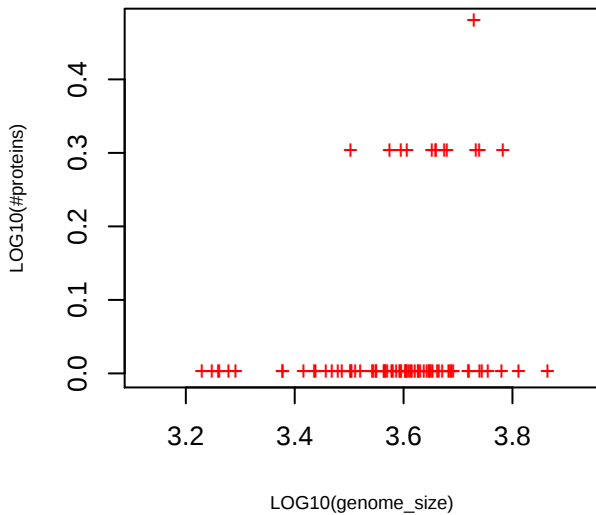
[N] COG1345 Flagellar capping protein

slope= -0.0071 p_value= 8.7e-08 intercept= 0.0077 p_value= 2.7e-07

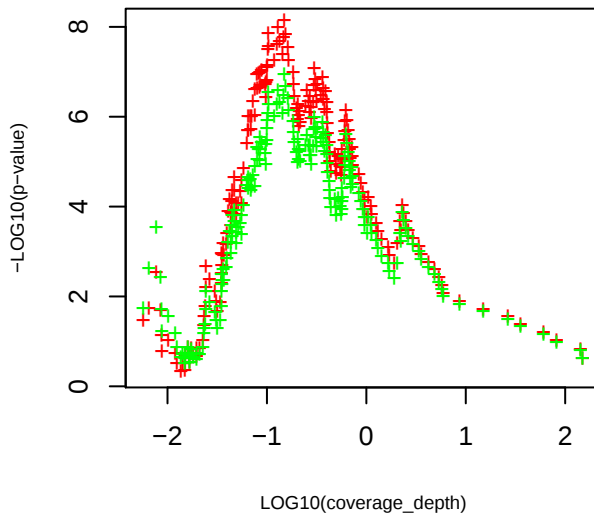


[N] COG1345 Flagellar capping protein

slope= 2.44 p_value= 0.0049 intercept= -11.02 p_value= 0.00037

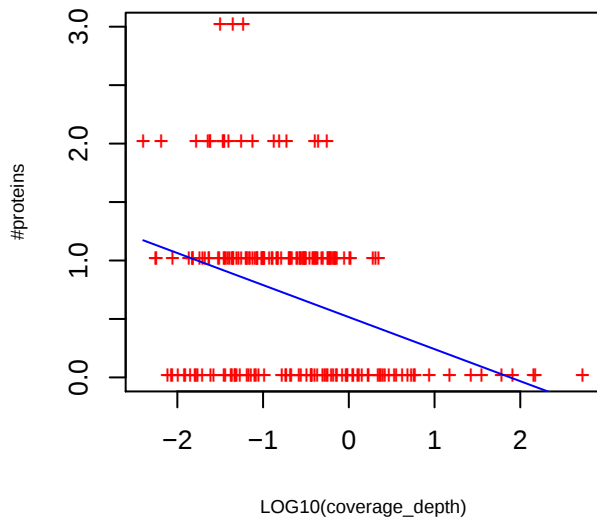


P-value curve ; red (unnorm), green (norm)



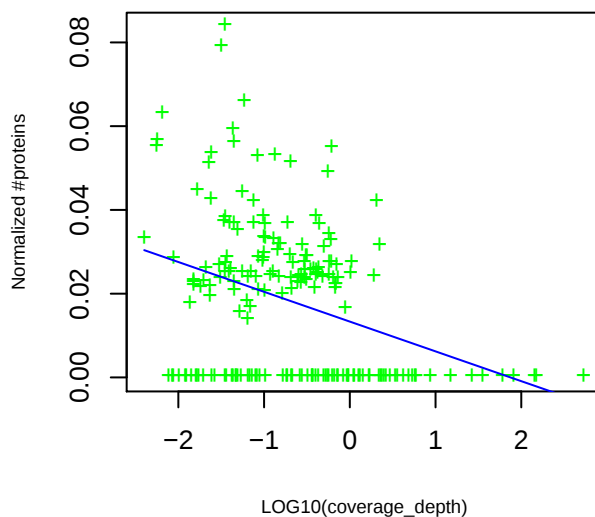
[N] COG1256 Flagellar hook-associated protein

slope= -0.27 p_value= 3.9e-07 intercept= 0.52 p_value= 9.5e-16



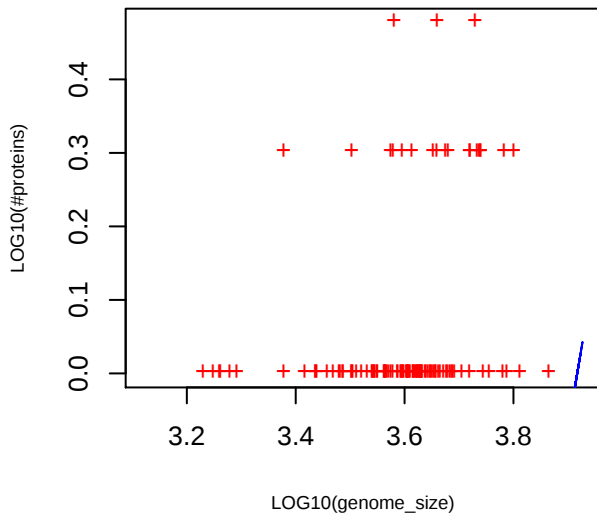
[N] COG1256 Flagellar hook-associated protein

slope= -0.0071 p_value= 5.5e-07 intercept= 0.013 p_value= 2.6e-15

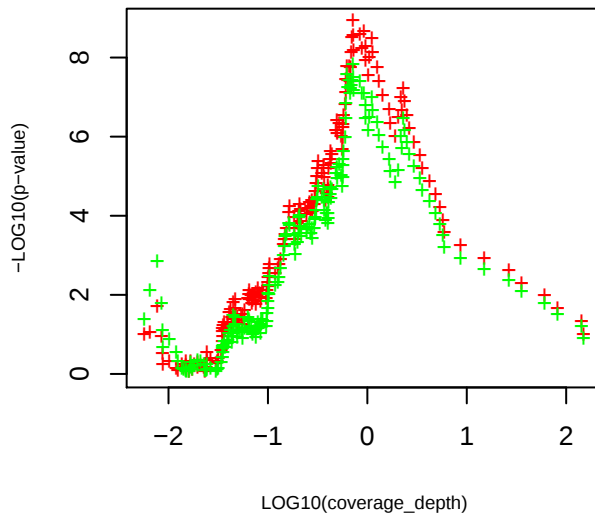


[N] COG1256 Flagellar hook-associated protein

slope= 4.38 p_value= 2.9e-07 intercept= -17.17 p_value= 1.9e-08

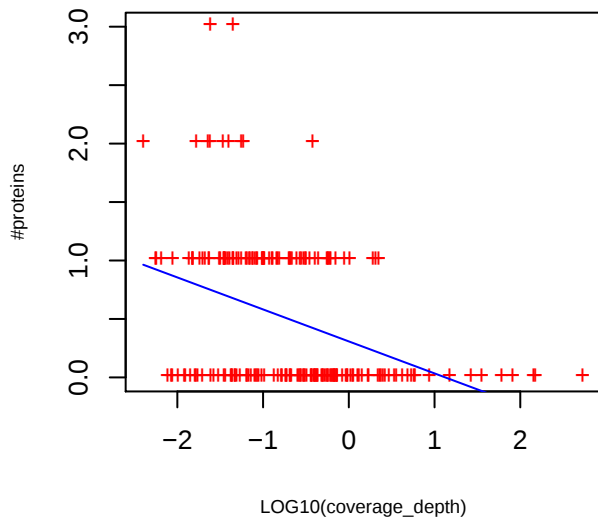


P-value curve ; red (unnorm), green (norm)



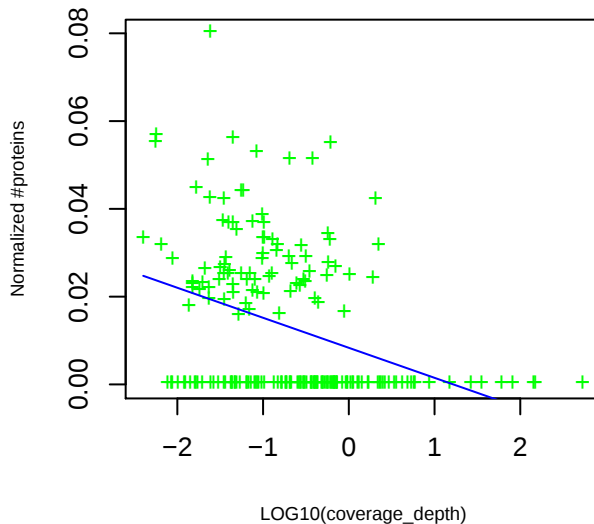
[NU] COG1677 Flagellar hook-basal body protein

slope= -0.27 p_value= 2.3e-08 intercept= 0.31 p_value= 2.6e-08



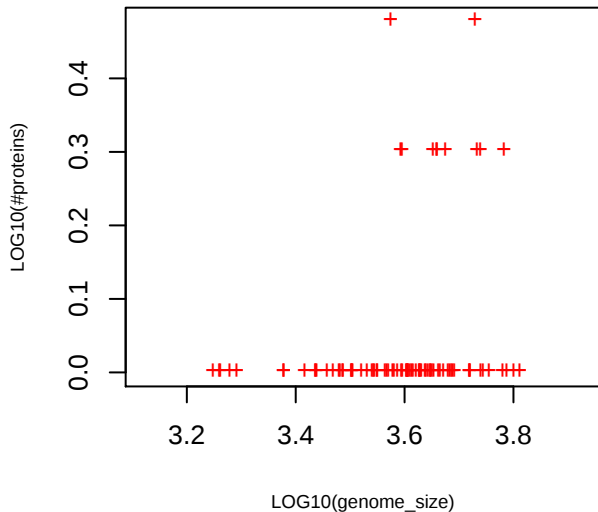
[NU] COG1677 Flagellar hook-basal body protein

slope= -0.0068 p_value= 1.7e-07 intercept= 0.0083 p_value= 1.9e-08

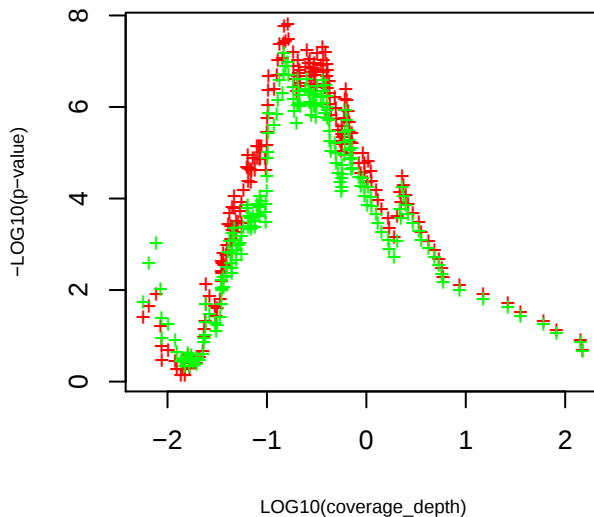


[NU] COG1677 Flagellar hook-basal body protein

slope= 2.90 p_value= 0.00087 intercept= -12.54 p_value= 5.6e-05

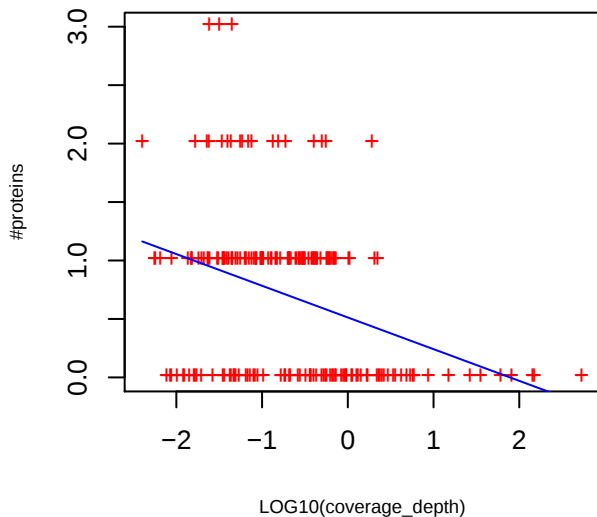


P-value curve ; red (unnorm), green (norm)



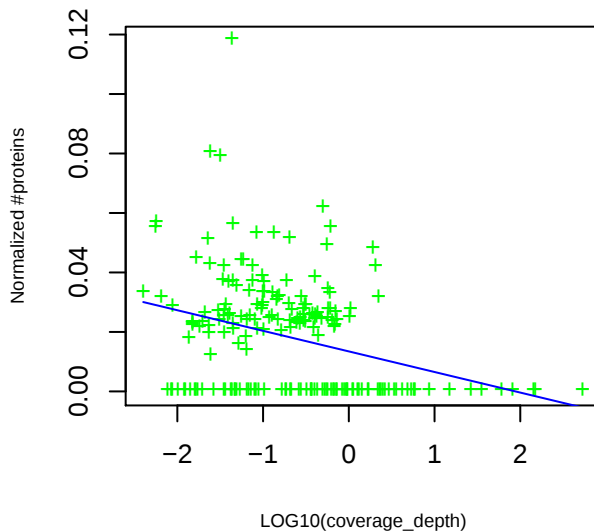
[NU] COG1298 Flagellar biosynthesis pathway, component FlhA

slope= -0.27 p_value= 5.5e-07 intercept= 0.51 p_value= 1.6e-15



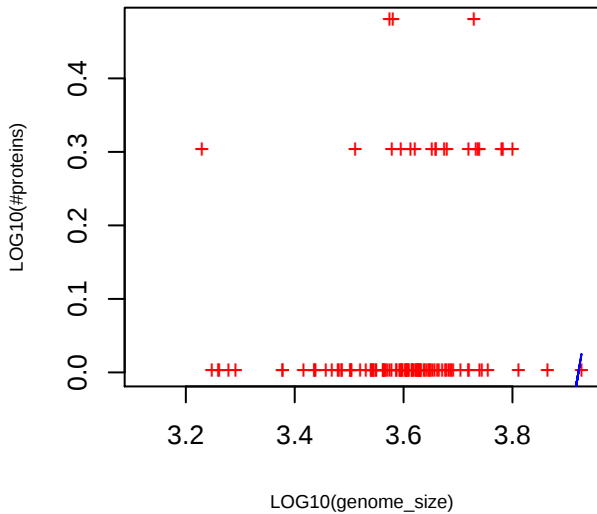
[NU] COG1298 Flagellar biosynthesis pathway, component FlhA

slope= -0.0069 p_value= 3.5e-06 intercept= 0.013 p_value= 2.8e-14

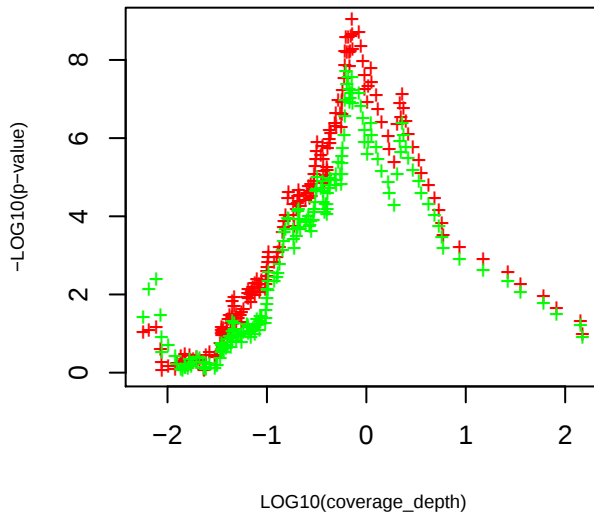


[NU] COG1298 Flagellar biosynthesis pathway, component FlhA

slope= 4.39 p_value= 2.9e-07 intercept= -17.22 p_value= 1.8e-08

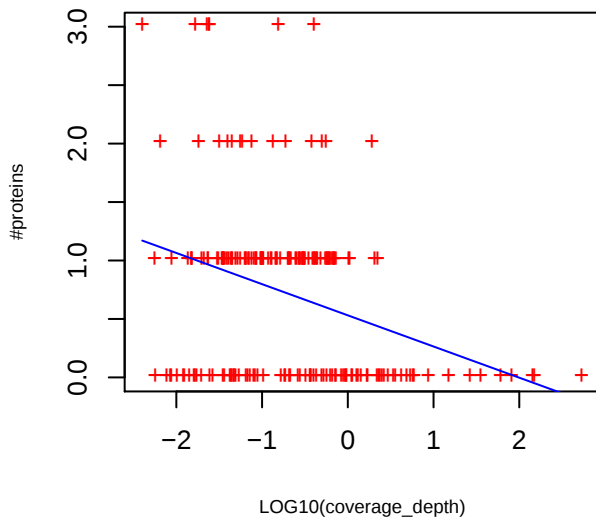


P-value curve ; red (unnorm), green (norm)



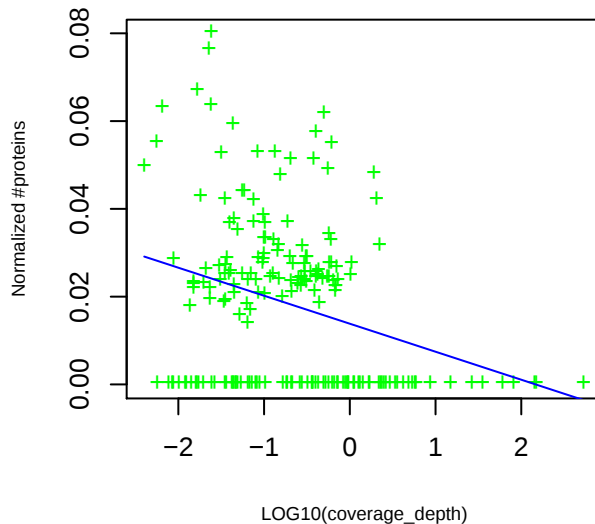
[NU] COG1157 Flagellar biosynthesis/type III secretory pathway ATPase

slope= -0.27 p_value= 5.2e-06 intercept= 0.53 p_value= 2.1e-14



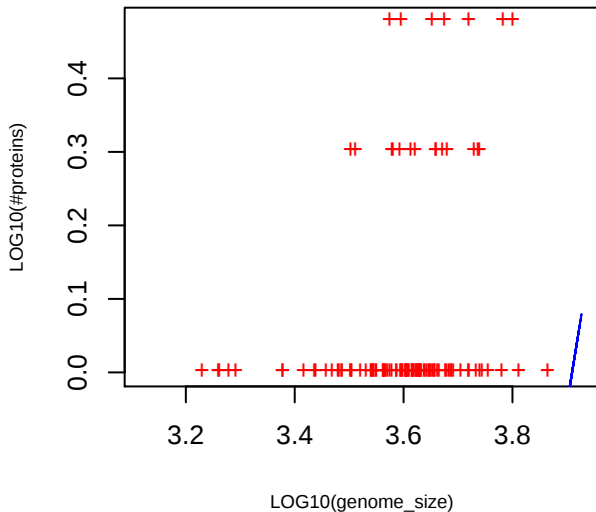
[NU] COG1157 Flagellar biosynthesis/type III secretory pathway ATPase

slope= -0.0064 p_value= 1.4e-05 intercept= 0.014 p_value= 3.8e-15

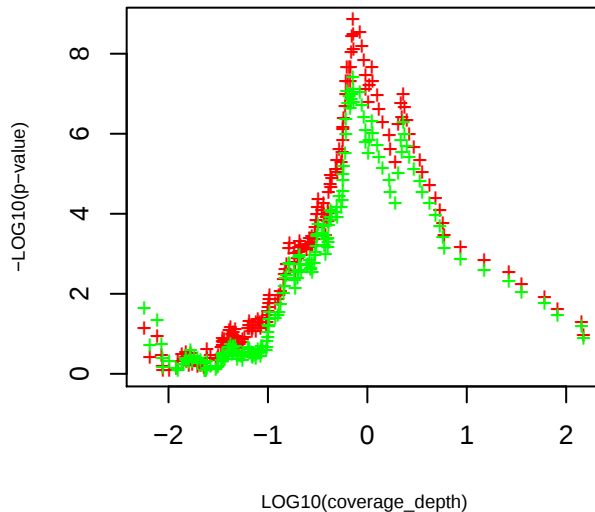


[NU] COG1157 Flagellar biosynthesis/type III secretory pathway ATPase

slope= 4.58 p_value= 9.1e-08 intercept= -17.89 p_value= 5.1e-09

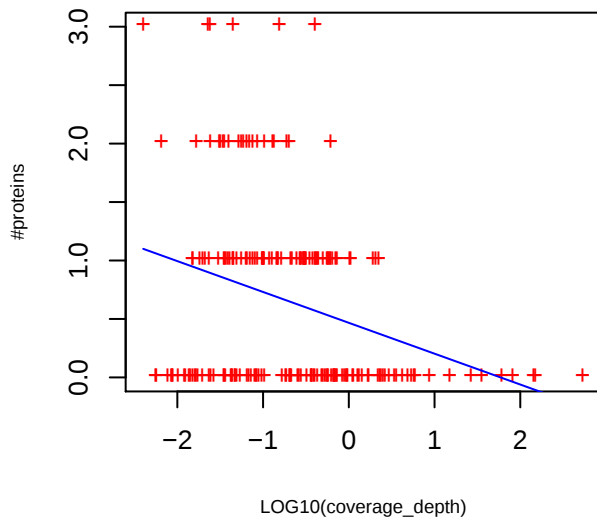


P-value curve ; red (unnorm), green (norm)



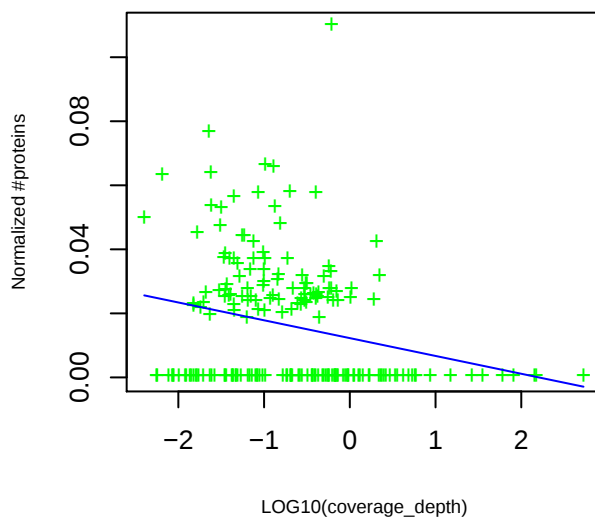
[NU] COG1886 Flagellar motor switch/type III secretory pathway protein

slope= -0.26 p_value= 2.1e-05 intercept= 0.47 p_value= 1.0e-10



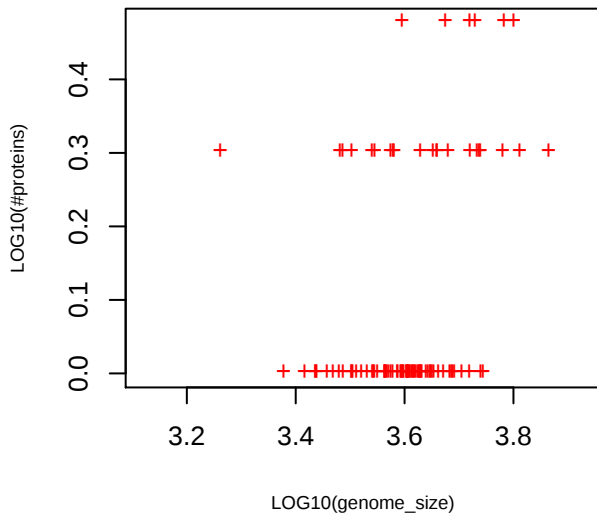
[NU] COG1886 Flagellar motor switch/type III secretory pathway protein

slope= -0.0056 p_value= 0.00034 intercept= 0.012 p_value= 2e-11

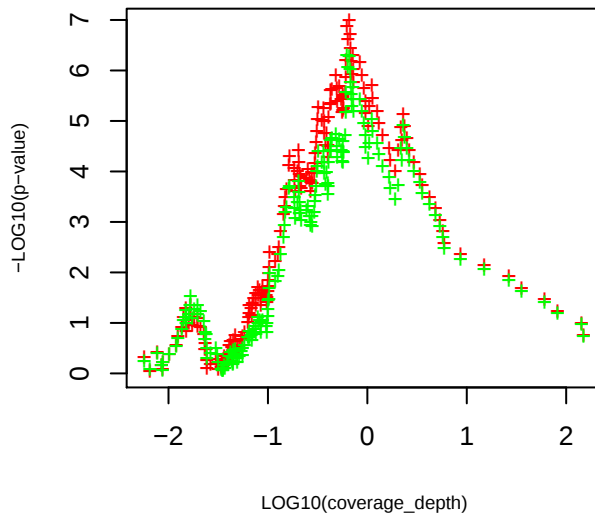


[NU] COG1886 Flagellar motor switch/type III secretory pathway protein

slope= 4.51 p_value= 2.5e-07 intercept= -18.01 p_value= 8.5e-09

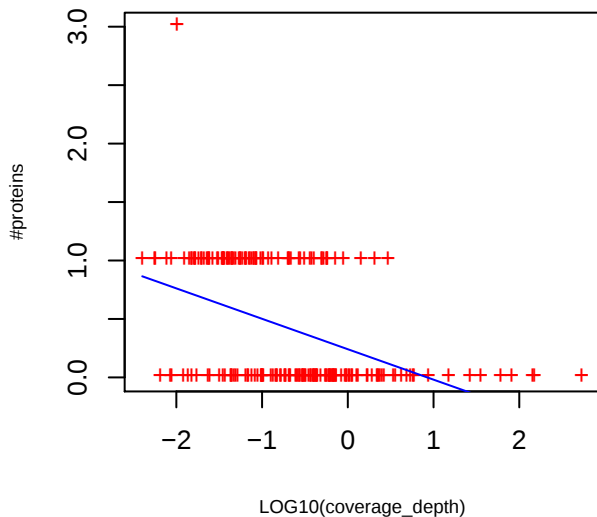


P-value curve ; red (unnorm), green (norm)



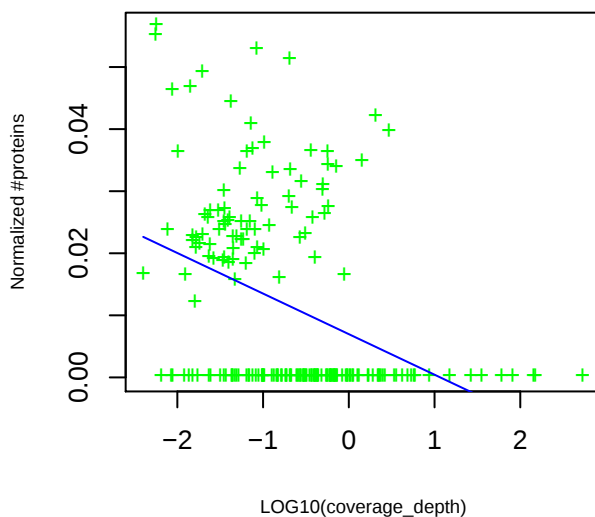
[OU] COG1585 Membrane protein implicated in regulation of membrane protease activity

slope= -0.26 p_value= 6.9e-11 intercept= 0.24 p_value= 5.2e-08



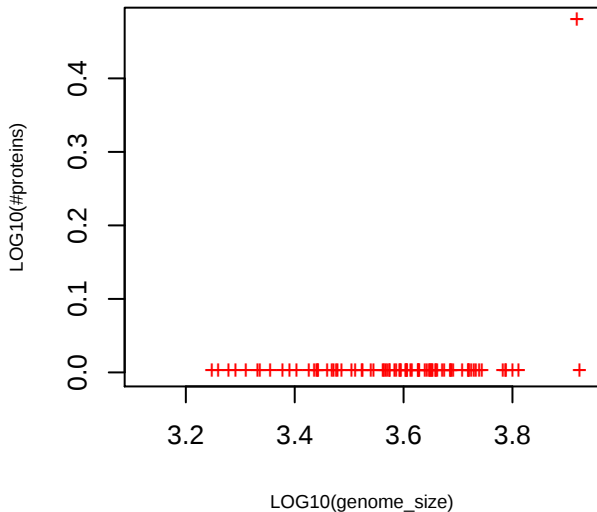
[OU] COG1585 Membrane protein implicated in regulation of membrane protease activity

slope= -0.0065 p_value= 2.2e-08 intercept= 0.007 p_value= 1.1e-07

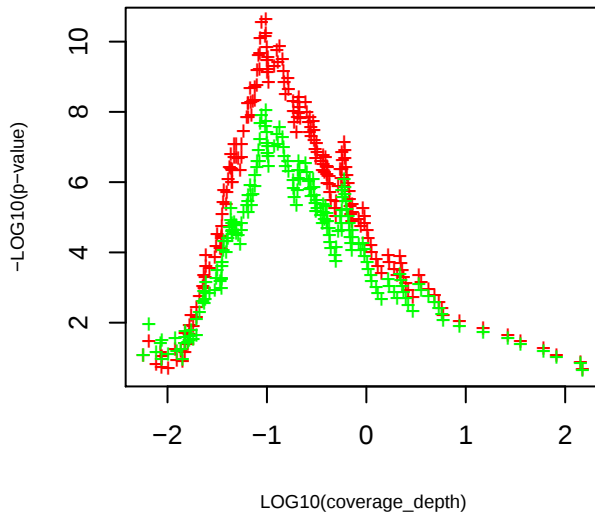


[OU] COG1585 Membrane protein implicated in regulation of membrane protease activity

slope= 2.39 p_value= 0.0054 intercept= -10.84 p_value= 0.00042

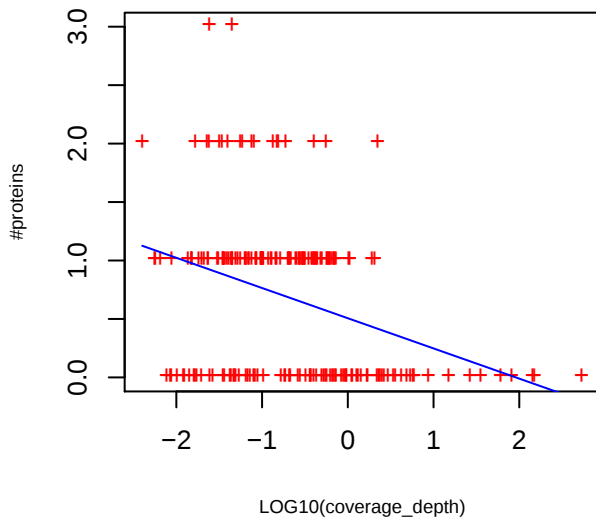


P-value curve ; red (unnorm), green (norm)



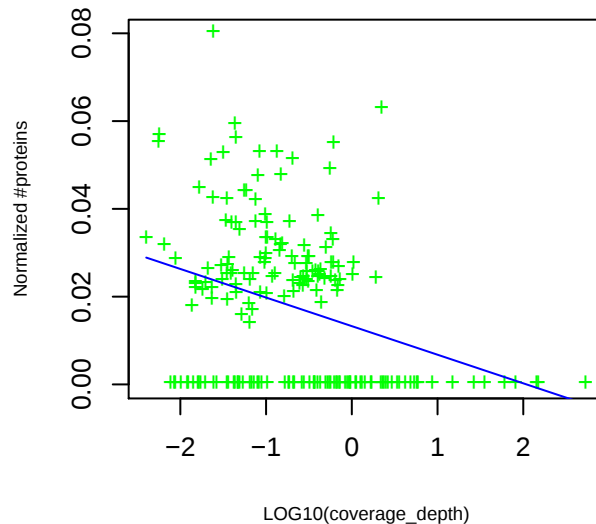
[NU] COG1766 Flagellar biosynthesis/type III secretory pathway lipoprotein

slope= -0.26 p_value= 1e-06 intercept= 0.51 p_value= 9.1e-16



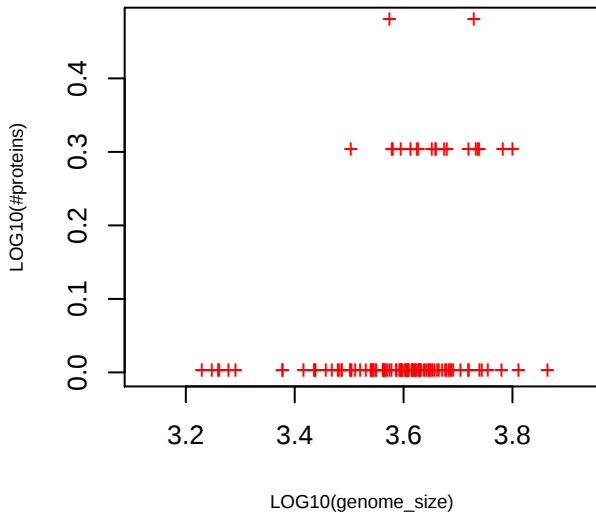
[NU] COG1766 Flagellar biosynthesis/type III secretory pathway lipoprotein

slope= -0.0065 p_value= 2.5e-06 intercept= 0.013 p_value= 9.8e-16

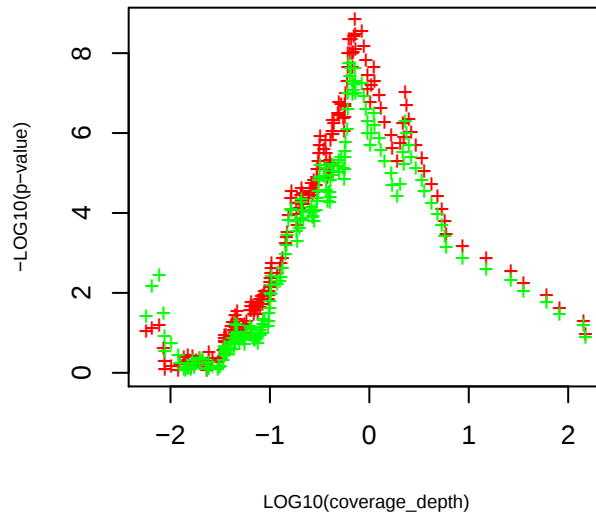


[NU] COG1766 Flagellar biosynthesis/type III secretory pathway lipoprotein

slope= 4.11 p_value= 1.8e-06 intercept= -16.23 p_value= 1.3e-07

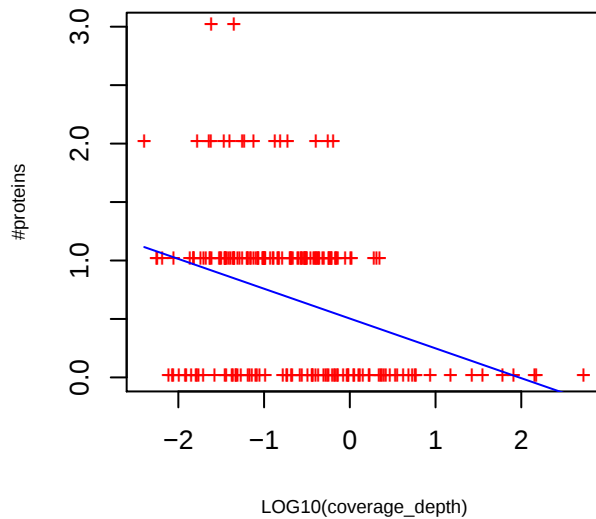


P-value curve ; red (unnorm), green (norm)



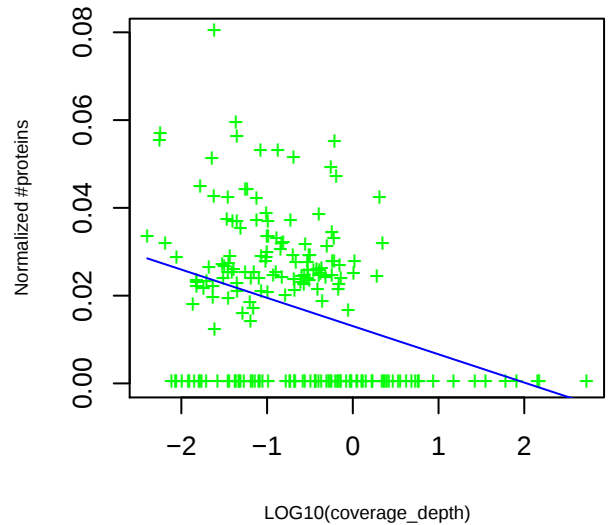
[NU] COG1338 Flagellar biosynthesis pathway, component FlIP

slope= -0.26 p_value= 6e-07 intercept= 0.50 p_value= 1.7e-16



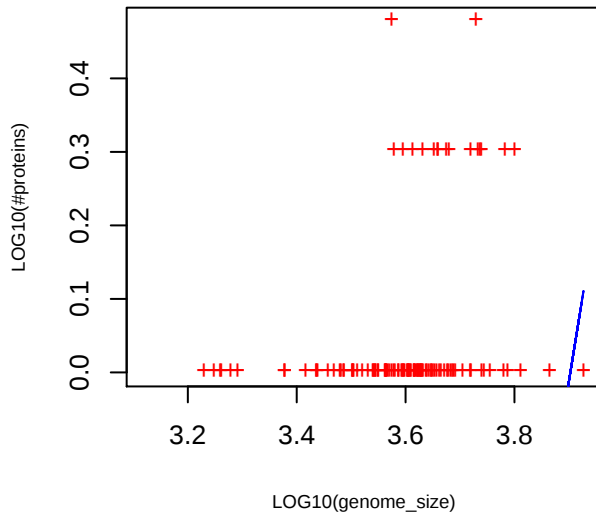
[NU] COG1338 Flagellar biosynthesis pathway, component FlIP

slope= -0.0064 p_value= 1.3e-06 intercept= 0.013 p_value= 2.5e-16

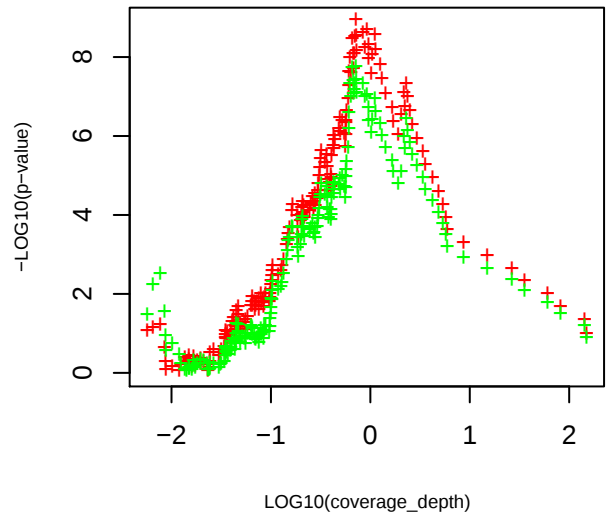


[NU] COG1338 Flagellar biosynthesis pathway, component FlIP

slope= 4.58 p_value= 6.7e-08 intercept= -17.88 p_value= 3.8e-09

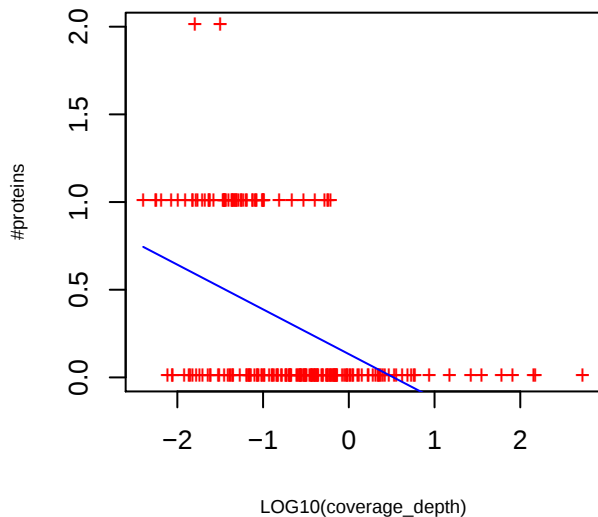


P-value curve ; red (unnorm), green (norm)



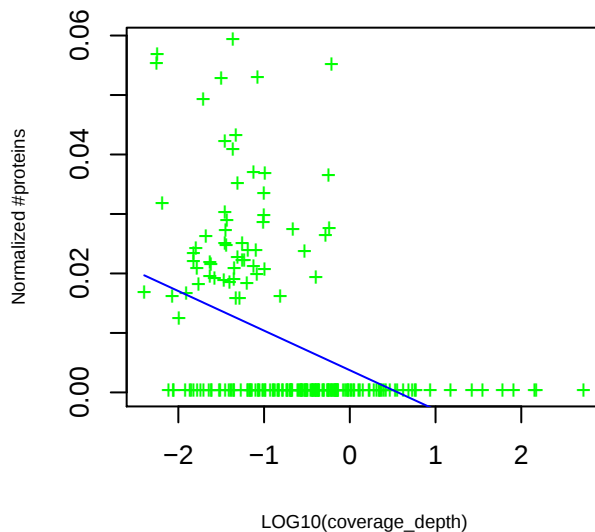
[R] COG0390 ABC-type uncharacterized transport system, permease component

slope= -0.25 p_value= 3.2e-12 intercept= 0.13 p_value= 0.00071



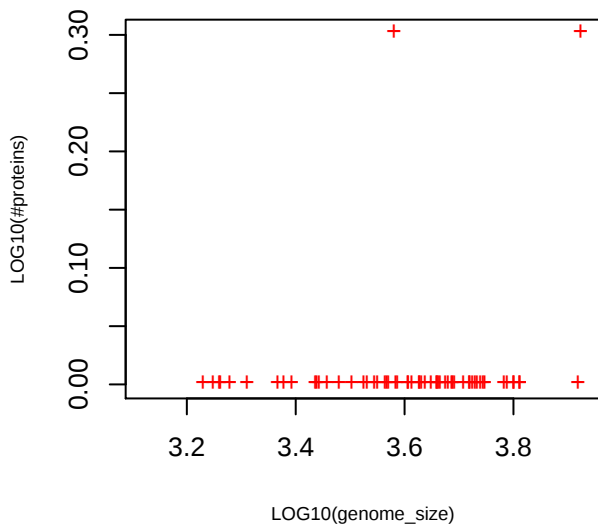
[R] COG0390 ABC-type uncharacterized transport system, permease component

slope= -0.0067 p_value= 1.3e-09 intercept= 0.0037 p_value= 0.0018

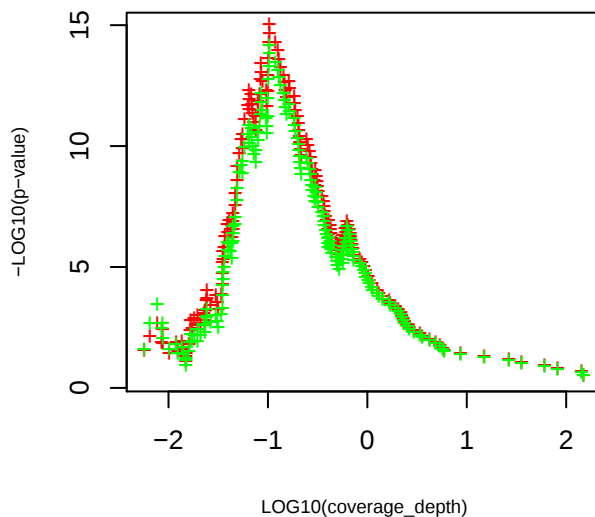


[R] COG0390 ABC-type uncharacterized transport system, permease component

slope= 2.46 p_value= 0.0021 intercept= -11.51 p_value= 5.9e-05

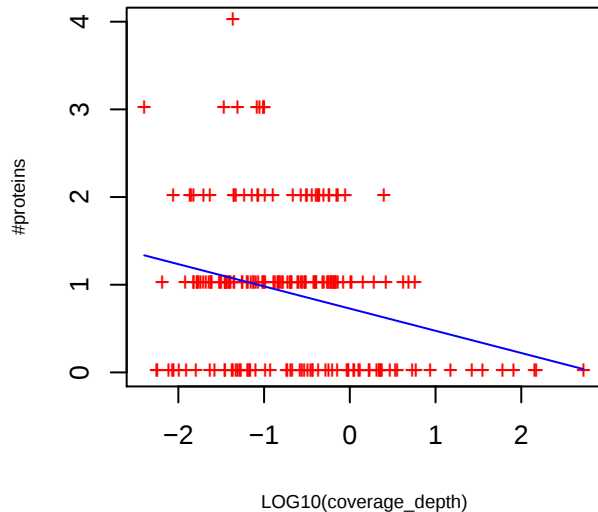


P-value curve ; red (unnorm), green (norm)



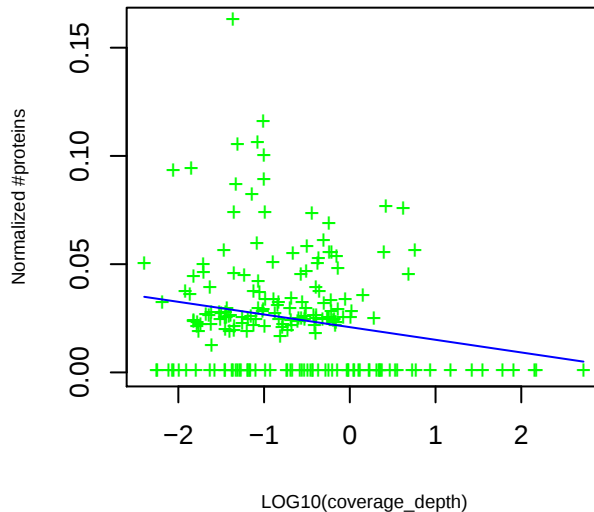
[R] COG1451 Predicted metal-dependent hydrolase

slope= -0.25 p_value= 0.00013 intercept= 0.73 p_value= 4.8e-19



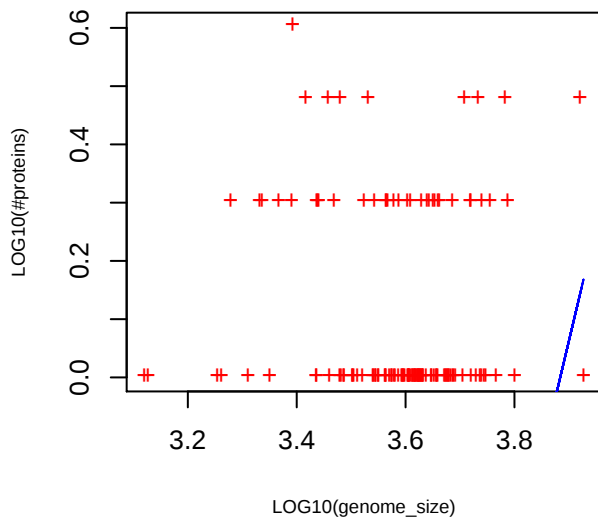
[R] COG1451 Predicted metal-dependent hydrolase

slope= -0.0058 p_value= 0.006 intercept= 0.021 p_value= 7.4e-16

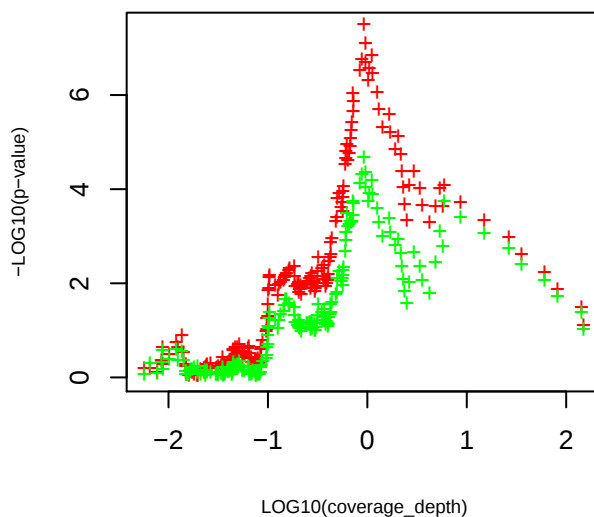


[R] COG1451 Predicted metal-dependent hydrolase

slope= 3.93 p_value= 3.1e-06 intercept= -15.26 p_value= 3.8e-07

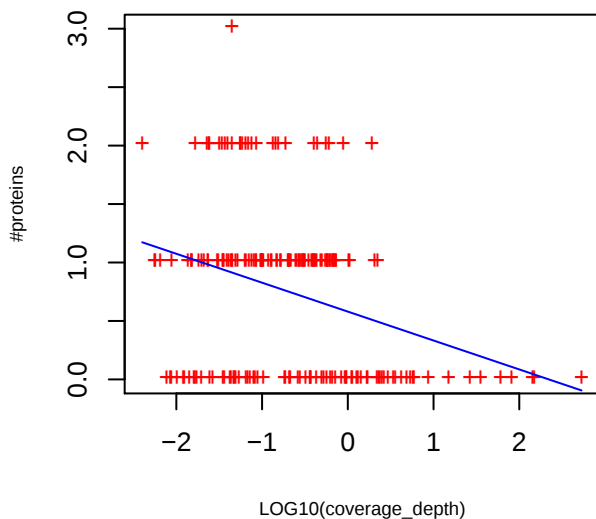


P-value curve ; red (unnorm), green (norm)



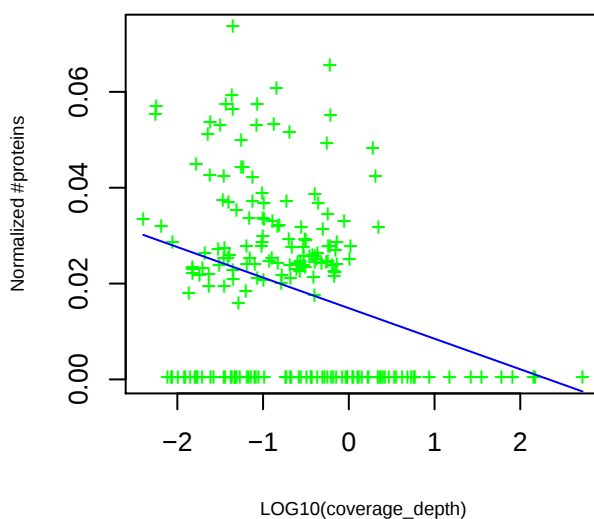
[N] COG1536 Flagellar motor switch protein

slope= -0.25 p_value= 6.6e-06 intercept= 0.58 p_value= 3.7e-18



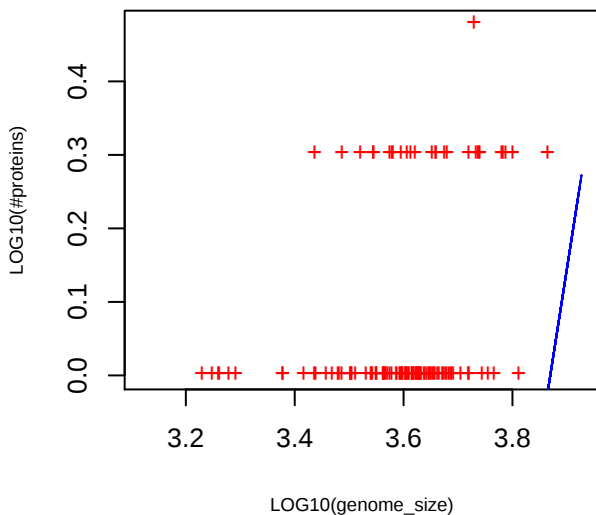
[N] COG1536 Flagellar motor switch protein

slope= -0.0064 p_value= 8.1e-06 intercept= 0.015 p_value= 9.8e-18

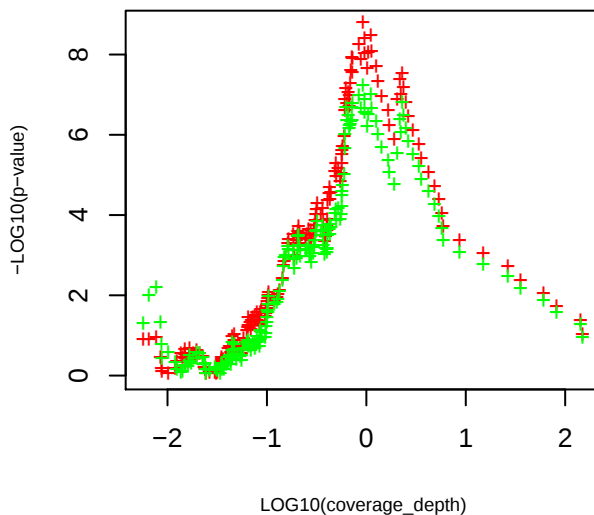


[N] COG1536 Flagellar motor switch protein

slope= 4.75 p_value= 1.9e-08 intercept= -18.38 p_value= 1.2e-09

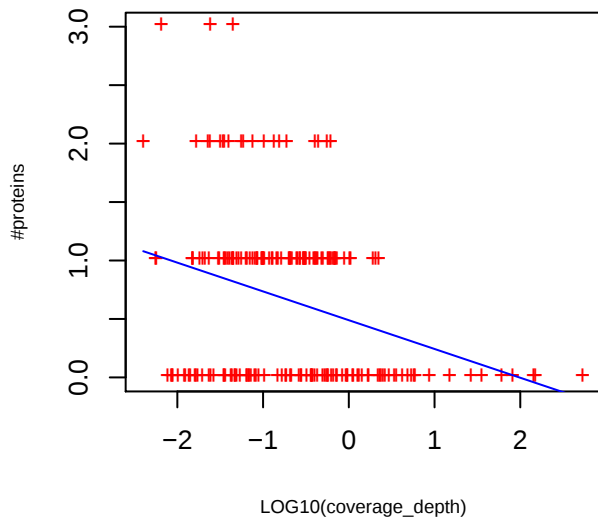


P-value curve ; red (unnorm), green (norm)



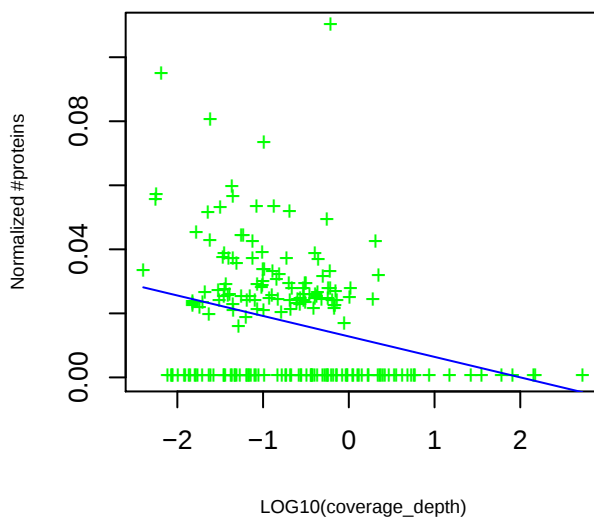
[N] COG1749 Flagellar hook protein FigE

slope= -0.25 p_value= 1.1e-05 intercept= 0.49 p_value= 1.4e-13



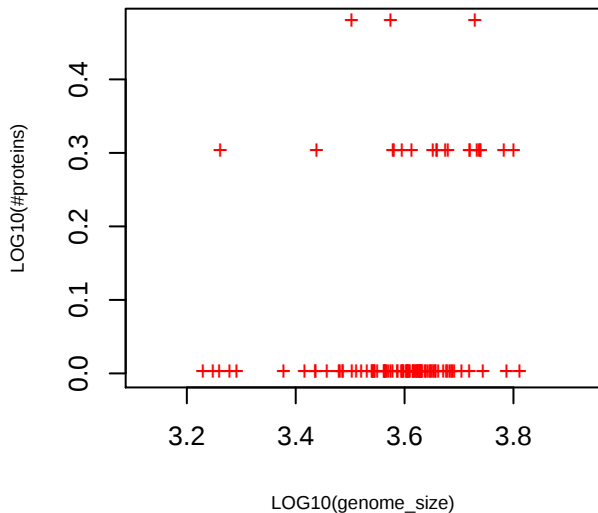
[N] COG1749 Flagellar hook protein FigE

slope= -0.0064 p_value= 3.3e-05 intercept= 0.013 p_value= 1.8e-12

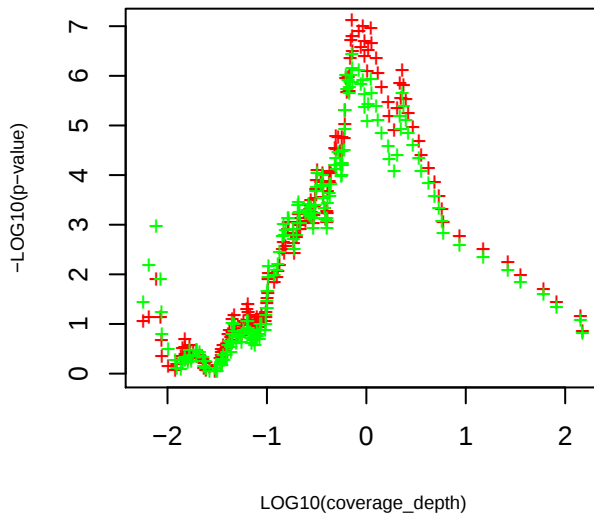


[N] COG1749 Flagellar hook protein FigE

slope= 3.90 p_value= 8e-06 intercept= -15.66 p_value= 5.3e-07

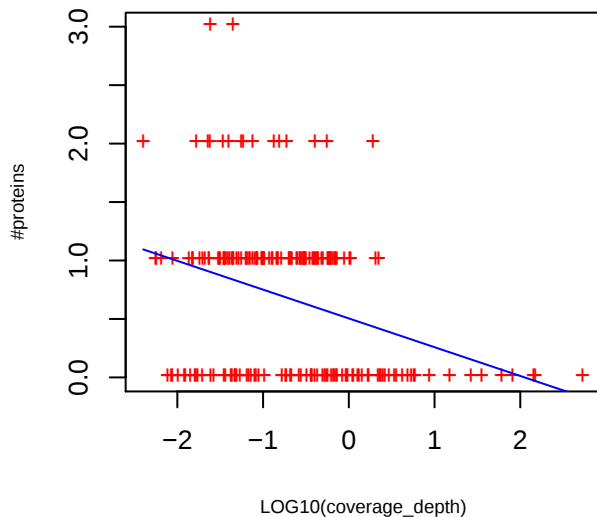


P-value curve ; red (unnorm), green (norm)



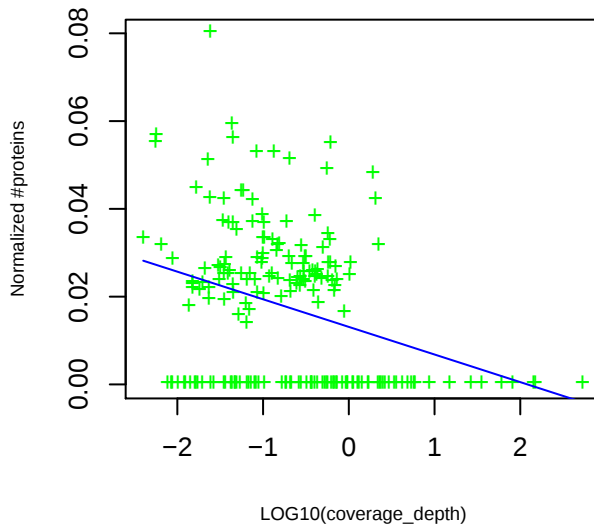
[NU] COG1684 Flagellar biosynthesis pathway, component FlIR

slope= -0.25 p_value= 1.6e-06 intercept= 0.50 p_value= 2.3e-16



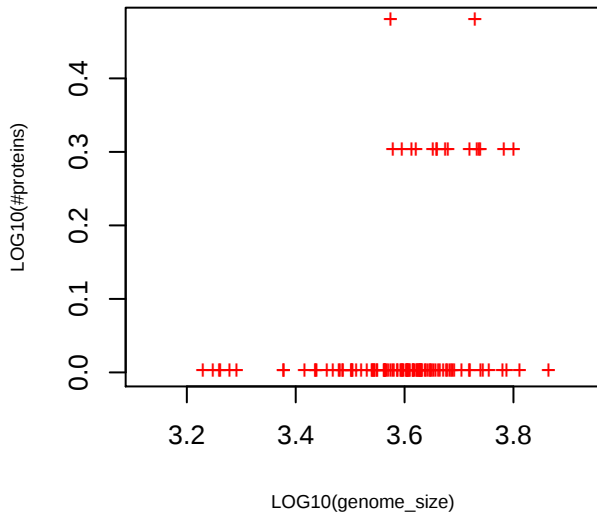
[NU] COG1684 Flagellar biosynthesis pathway, component FlIR

slope= -0.0063 p_value= 2.5e-06 intercept= 0.013 p_value= 2.9e-16

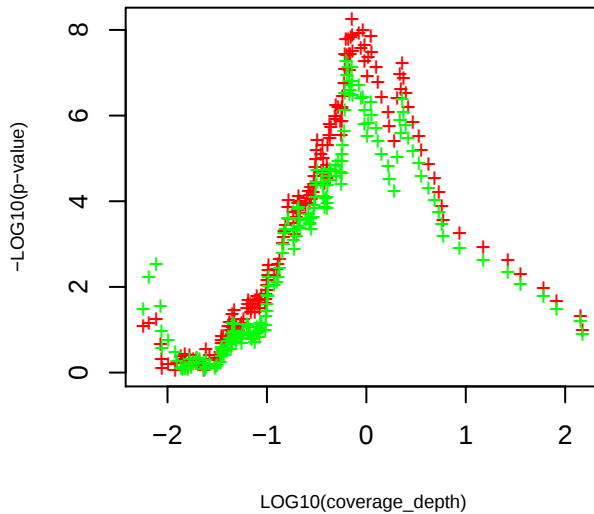


[NU] COG1684 Flagellar biosynthesis pathway, component FlIR

slope= 4.29 p_value= 5.2e-07 intercept= -16.86 p_value= 3.4e-08

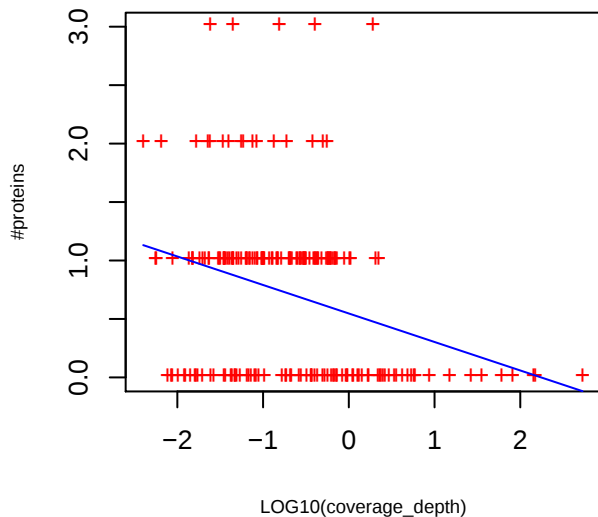


P-value curve ; red (unnorm), green (norm)



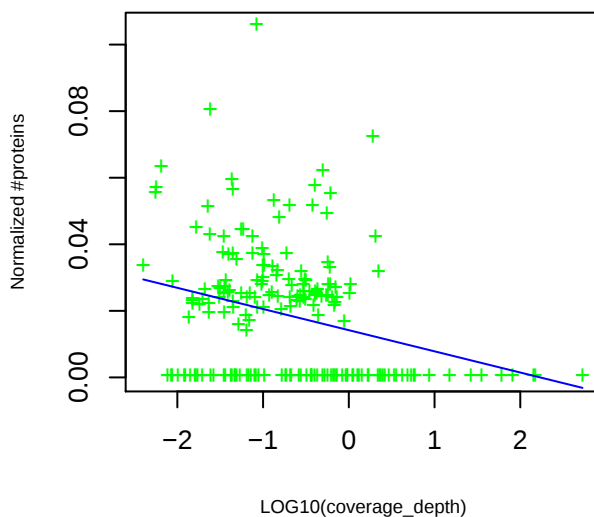
[NU] COG1377 Flagellar biosynthesis pathway, component FlhB

slope= -0.24 p_value= 1.6e-05 intercept= 0.55 p_value= 7.6e-16



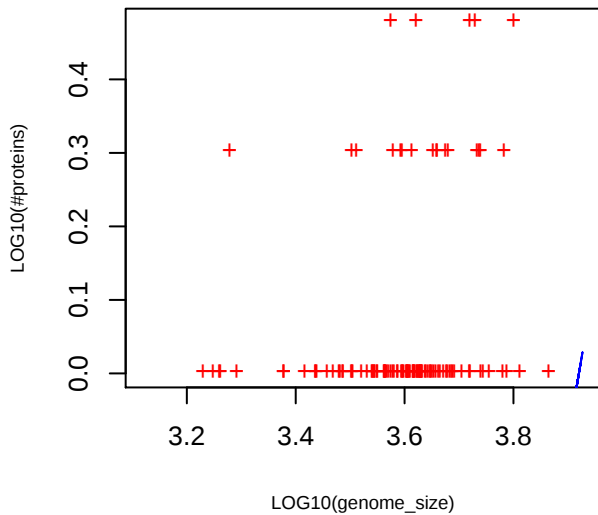
[NU] COG1377 Flagellar biosynthesis pathway, component FlhB

slope= -0.0064 p_value= 2.4e-05 intercept= 0.014 p_value= 3.4e-15

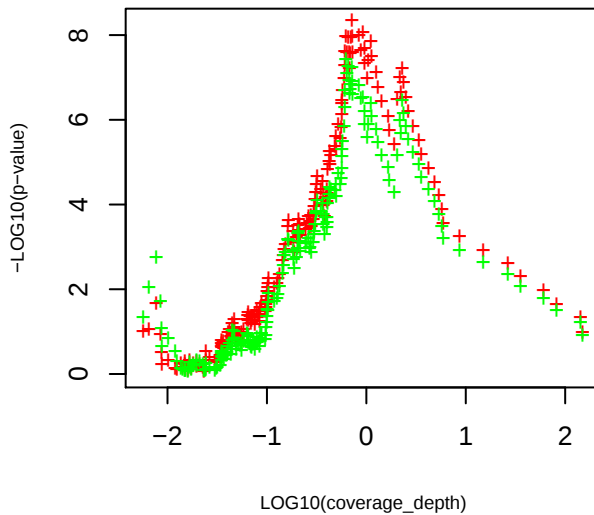


[NU] COG1377 Flagellar biosynthesis pathway, component FlhB

slope= 4.34 p_value= 3.9e-07 intercept= -17.02 p_value= 2.6e-08

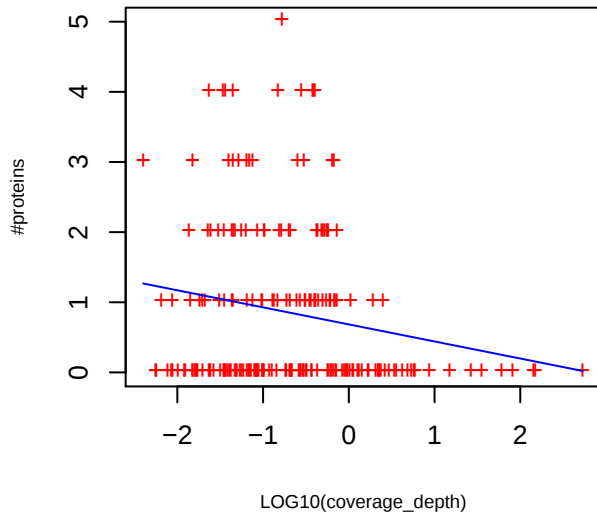


P-value curve ; red (unnorm), green (norm)



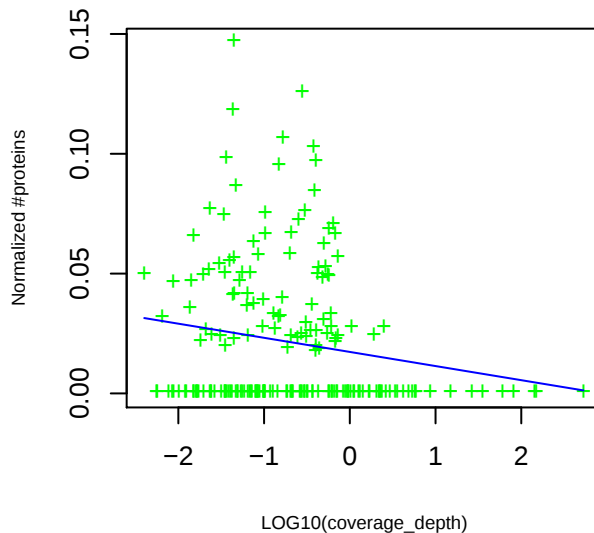
[U] COG4962 Flp pilus assembly protein, ATPase CpaF

slope= -0.24 p_value= 0.01 intercept= 0.68 p_value= 7.3e-10



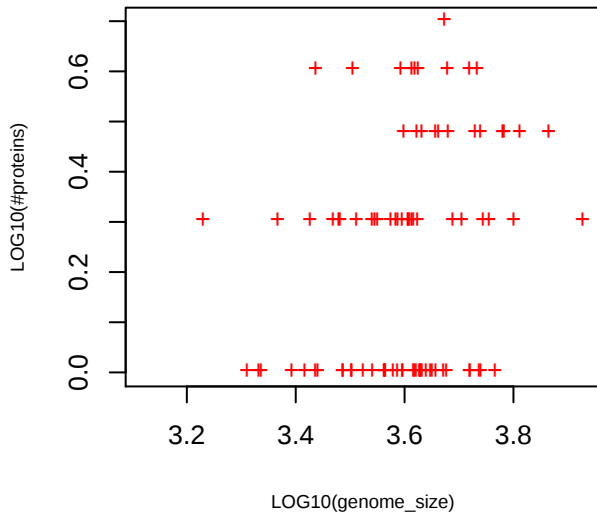
[U] COG4962 Flp pilus assembly protein, ATPase CpaF

slope= -0.0059 p_value= 0.014 intercept= 0.017 p_value= 7.5e-10

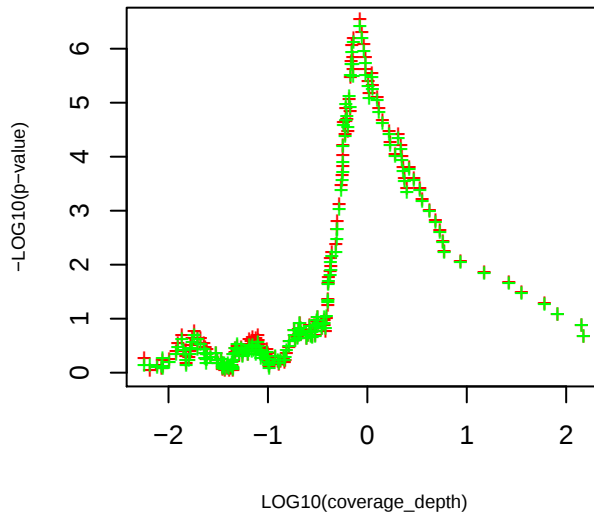


[U] COG4962 Flp pilus assembly protein, ATPase CpaF

slope= 4.05 p_value= 7.4e-06 intercept= -16.51 p_value= 3.3e-07

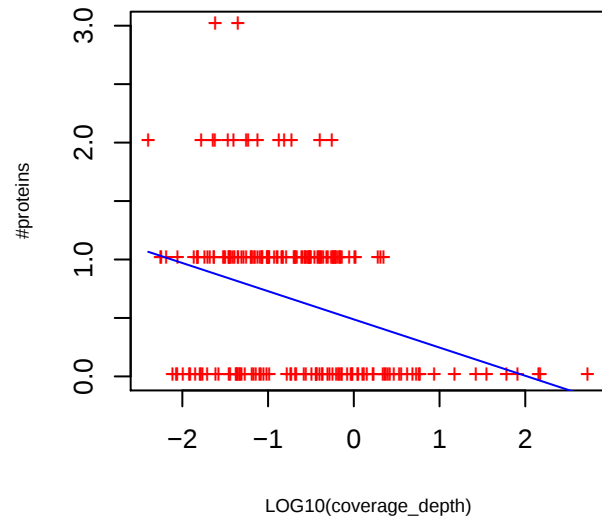


P-value curve ; red (unnorm), green (norm)



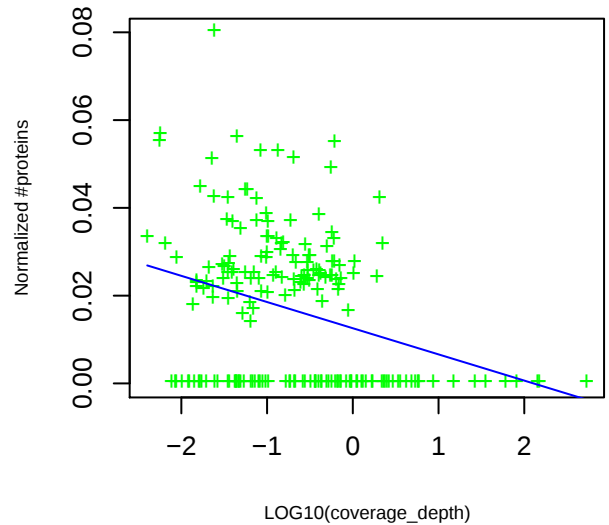
[NU] COG1987 Flagellar biosynthesis pathway, component FliQ

slope= -0.24 p_value= 2.4e-06 intercept= 0.49 p_value= 1.4e-15



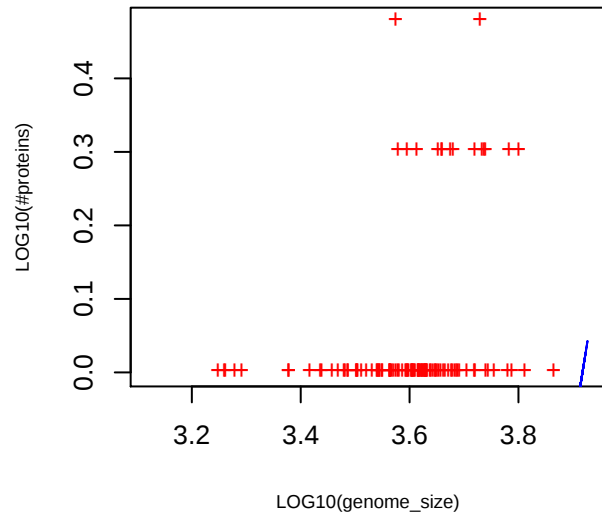
[NU] COG1987 Flagellar biosynthesis pathway, component FliQ

slope= -0.006 p_value= 5.5e-06 intercept= 0.013 p_value= 1.2e-15

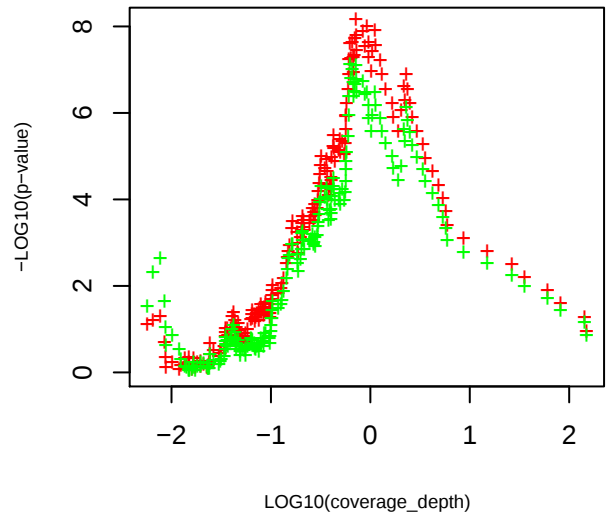


[NU] COG1987 Flagellar biosynthesis pathway, component FliQ

slope= 4.62 p_value= 6.2e-08 intercept= -18.10 p_value= 3.1e-09

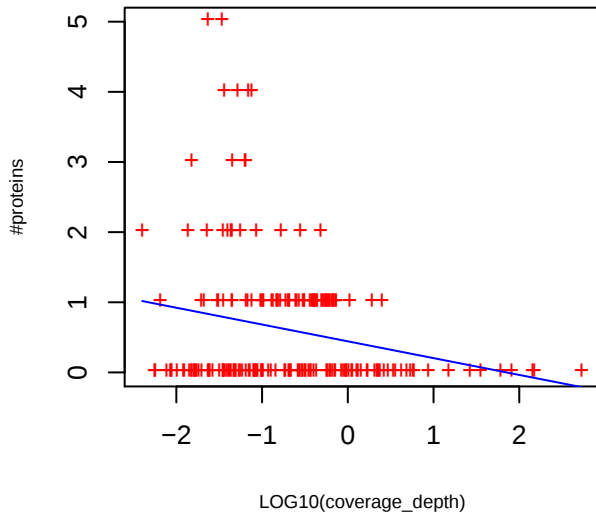


P-value curve ; red (unnorm), green (norm)



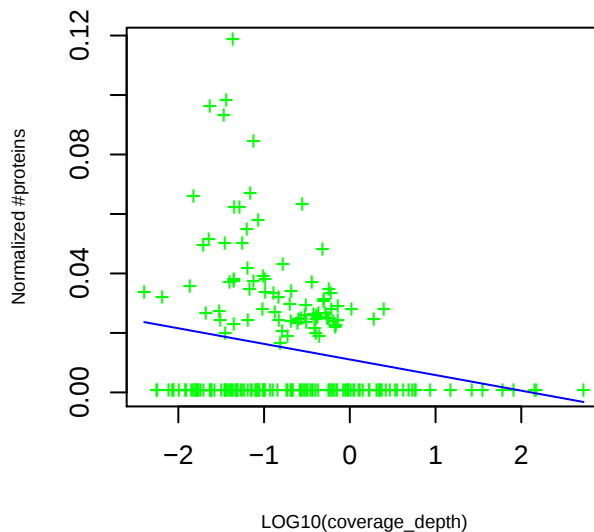
[U] COG4965 Flp pilus assembly protein TadB

slope= -0.24 p_value= 0.0017 intercept= 0.44 p_value= 4.9e-07



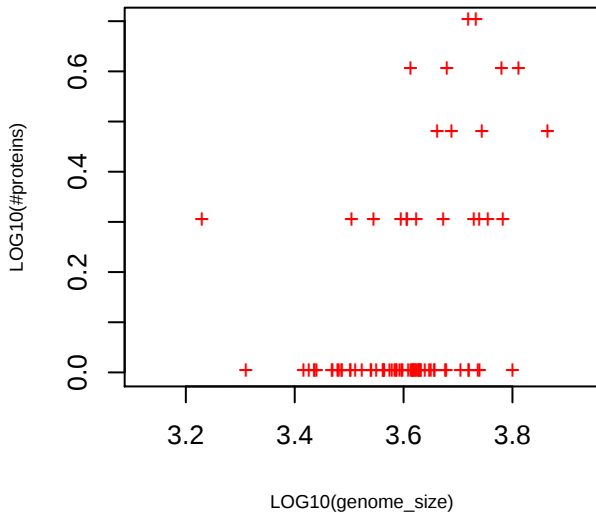
[U] COG4965 Flp pilus assembly protein TadB

slope= -0.0052 p_value= 0.0025 intercept= 0.011 p_value= 3.9e-08

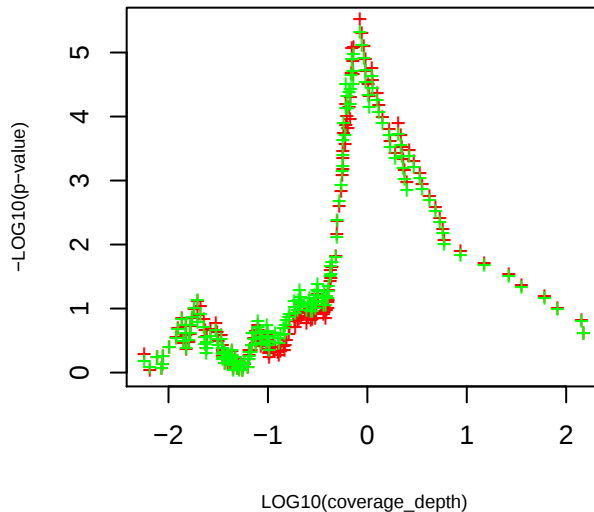


[U] COG4965 Flp pilus assembly protein TadB

slope= 3.89 p_value= 7.8e-06 intercept= -16.13 p_value= 2.3e-07

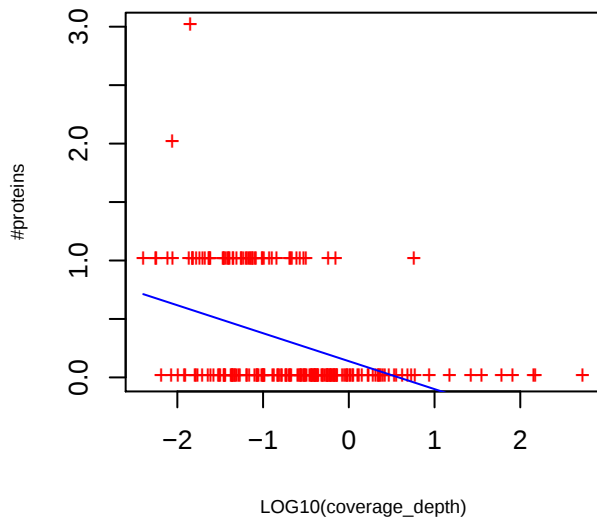


P-value curve ; red (unnorm), green (norm)



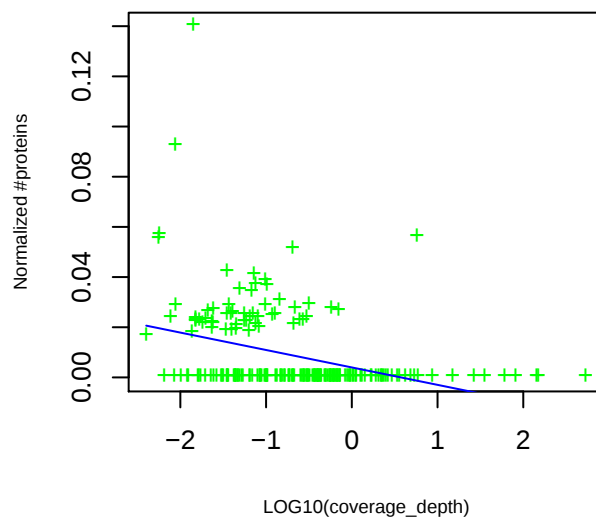
[H] COG0301 Thiamine biosynthesis ATP pyrophosphatase

slope= -0.24 p_value= 5e-10 intercept= 0.14 p_value= 9e-04



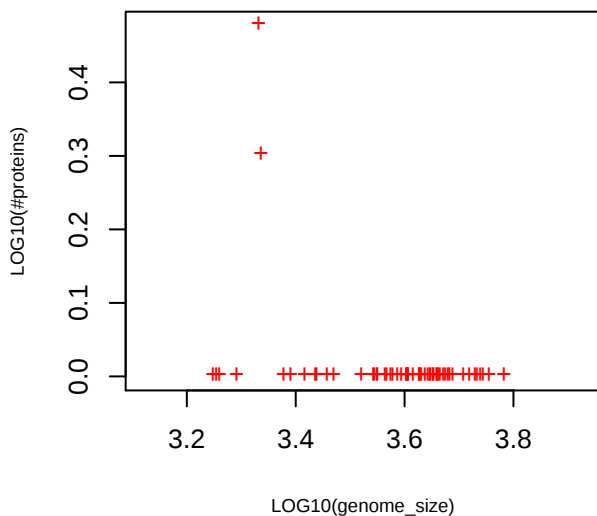
[H] COG0301 Thiamine biosynthesis ATP pyrophosphatase

slope= -0.007 p_value= 2.2e-07 intercept= 0.004 p_value= 0.007

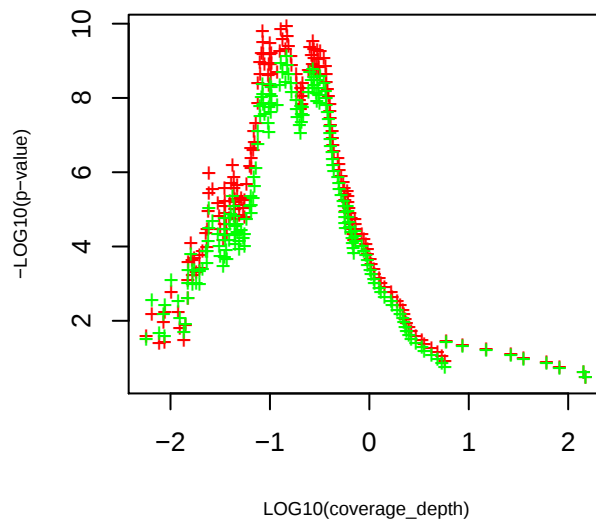


[H] COG0301 Thiamine biosynthesis ATP pyrophosphatase

slope= 1.33 p_value= 0.095 intercept= -7.57 p_value= 0.008

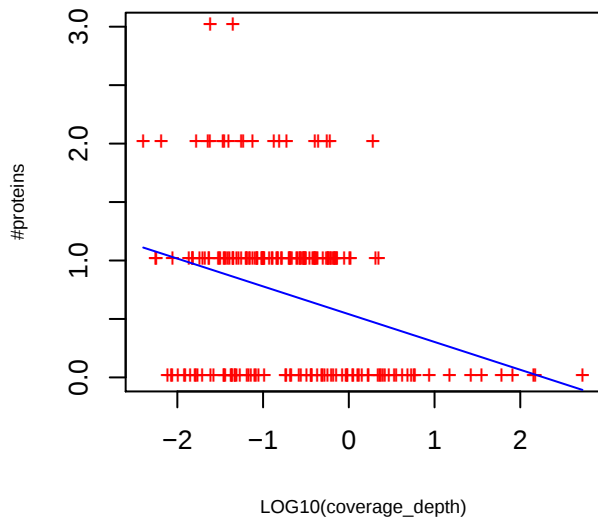


P-value curve ; red (unnorm), green (norm)



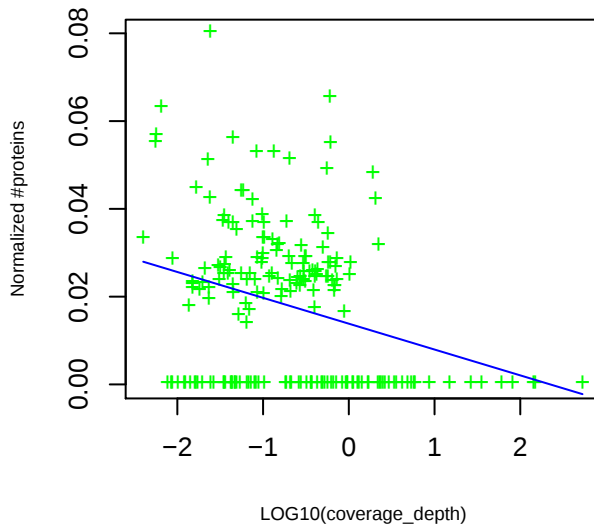
[N] COG1843 Flagellar hook capping protein

slope= -0.24 p_value= 8e-06 intercept= 0.54 p_value= 4.1e-17



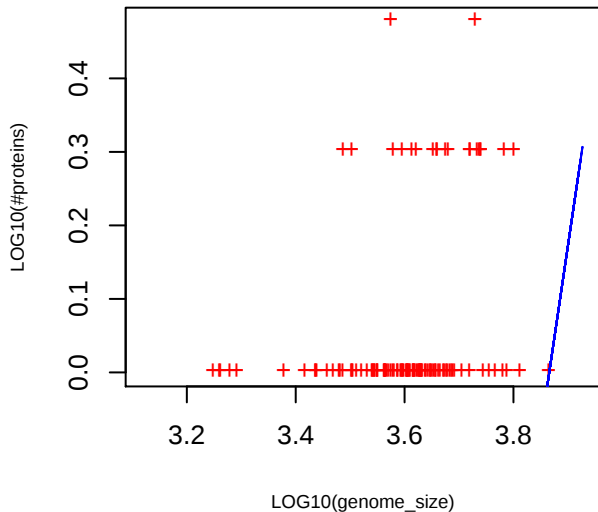
[N] COG1843 Flagellar hook capping protein

slope= -0.0059 p_value= 1.6e-05 intercept= 0.014 p_value= 5.3e-17

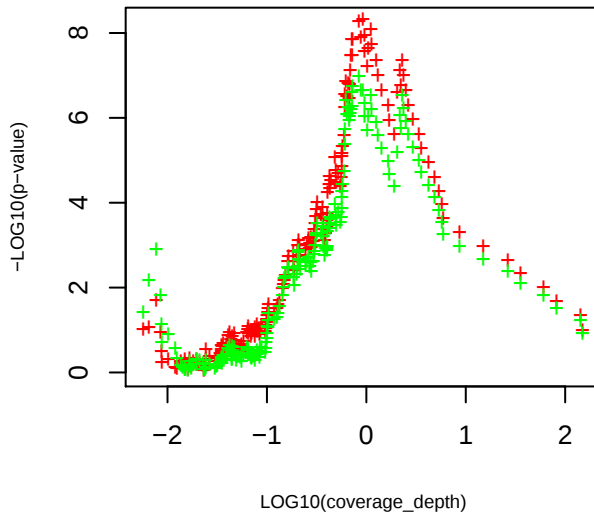


[N] COG1843 Flagellar hook capping protein

slope= 5.03 p_value= 2.4e-09 intercept= -19.43 p_value= 1.1e-10

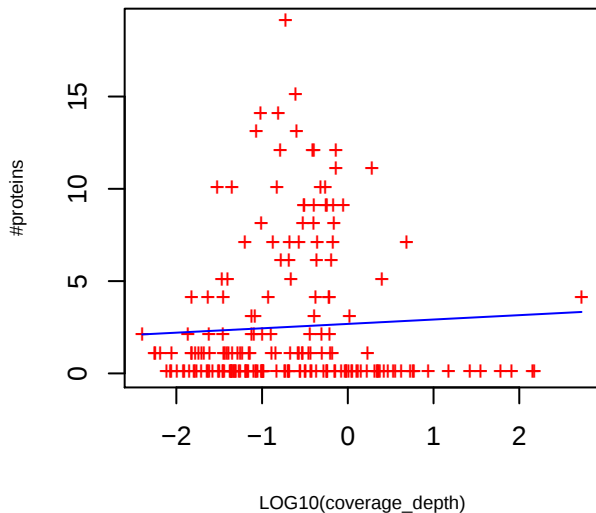


P-value curve ; red (unnorm), green (norm)



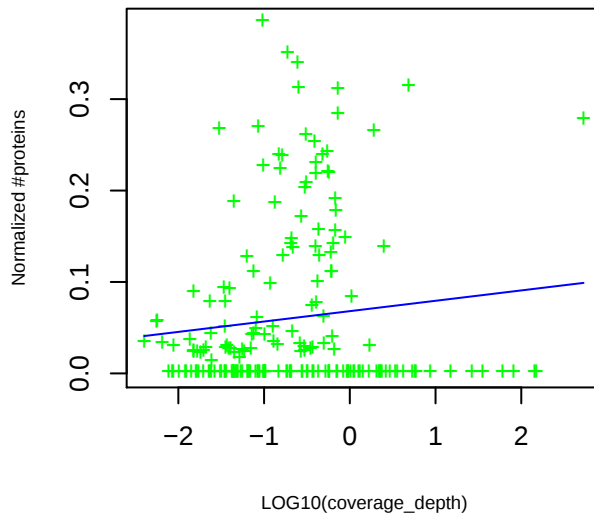
[G] COG3090 TRAP-type C4-dicarboxylate transport system, small permease component

slope= 0.24 p_value= 0.45 intercept= 2.68 p_value= 1.7e-12



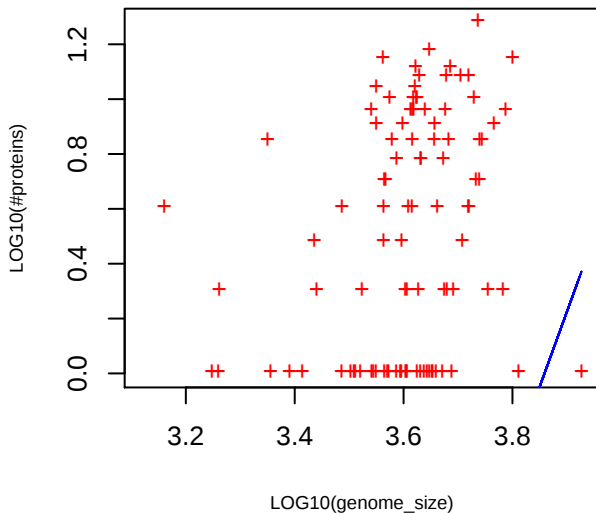
[G] COG3090 TRAP-type C4-dicarboxylate transport system, small permease component

slope= 0.011 p_value= 0.12 intercept= 0.068 p_value= 1.9e-14

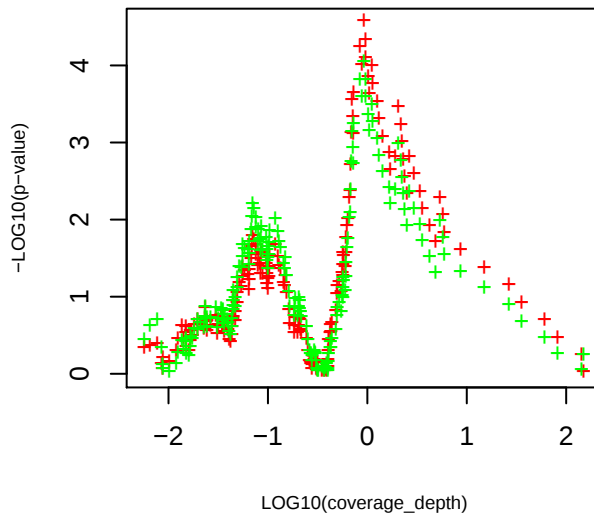


[G] COG3090 TRAP-type C4-dicarboxylate transport system, small permease component

slope= 5.46 p_value= 1.4e-08 intercept= -21.08 p_value= 8.7e-10

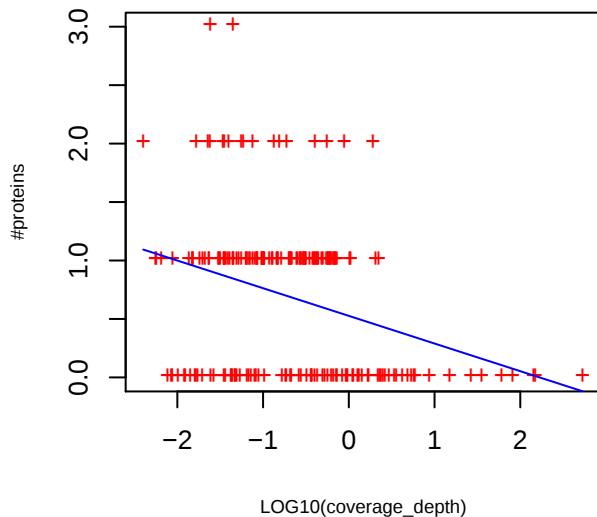


P-value curve ; red (unnorm), green (norm)



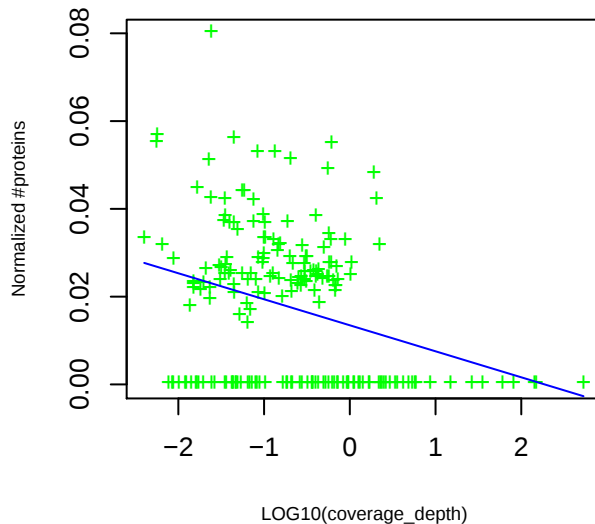
[N] COG1558 Flagellar basal body rod protein

slope= -0.24 p_value= 6.3e-06 intercept= 0.53 p_value= 7.5e-17



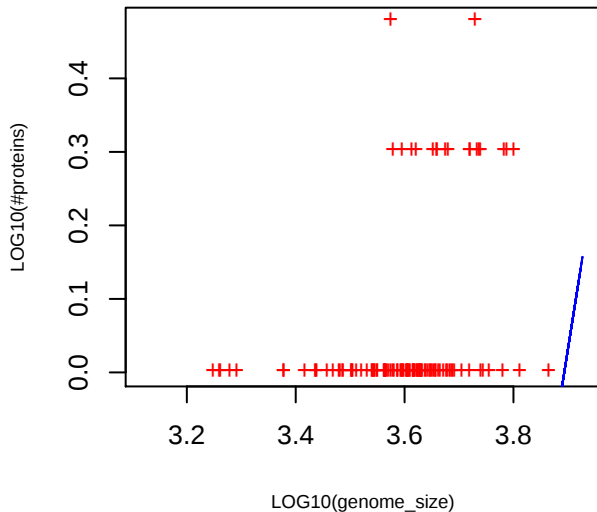
[N] COG1558 Flagellar basal body rod protein

slope= -0.0059 p_value= 7.8e-06 intercept= 0.013 p_value= 4.1e-17

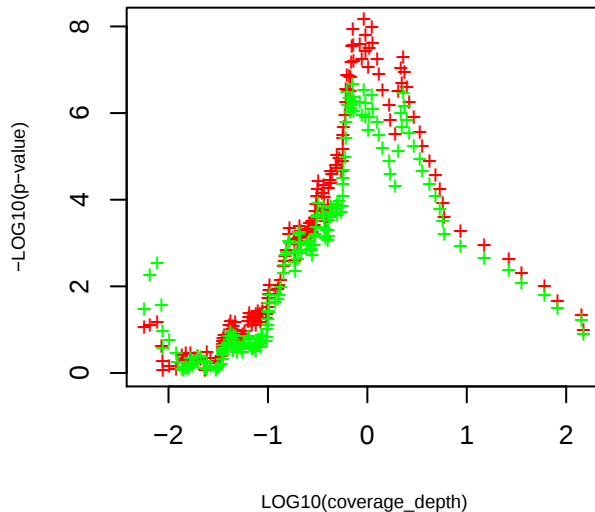


[N] COG1558 Flagellar basal body rod protein

slope= 4.69 p_value= 3.1e-08 intercept= -18.28 p_value= 1.7e-09

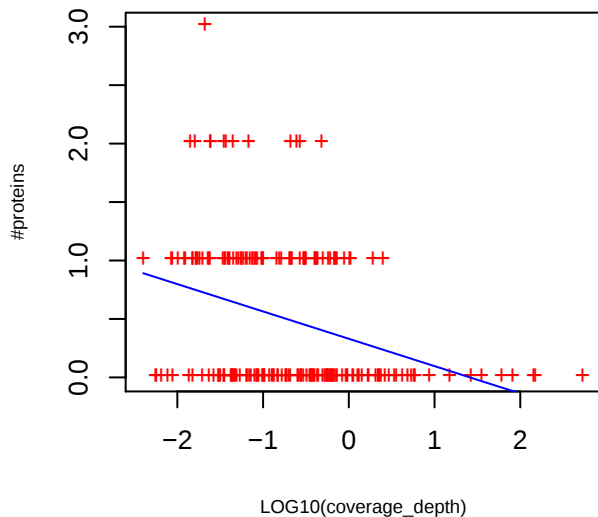


P-value curve ; red (unnorm), green (norm)



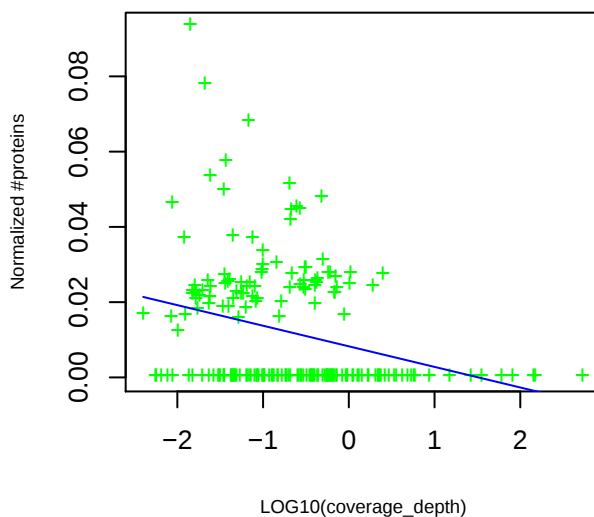
[R] COG0121 Predicted glutamine amidotransferase

slope= -0.23 p_value= 2.4e-06 intercept= 0.33 p_value= 6e-09



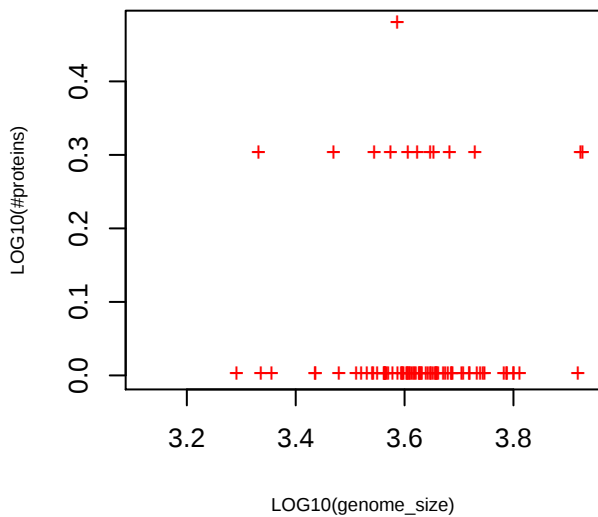
[R] COG0121 Predicted glutamine amidotransferase

slope= -0.0055 p_value= 3e-05 intercept= 0.0083 p_value= 4e-08

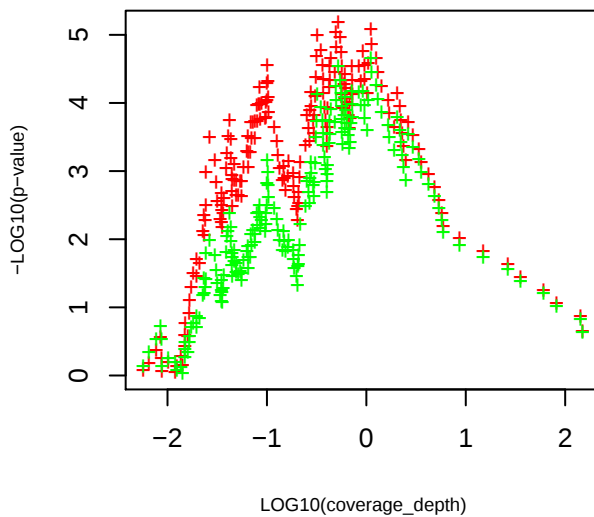


[R] COG0121 Predicted glutamine amidotransferase

slope= 5.32 p_value= 2.3e-10 intercept= -21.14 p_value= 2.2e-12

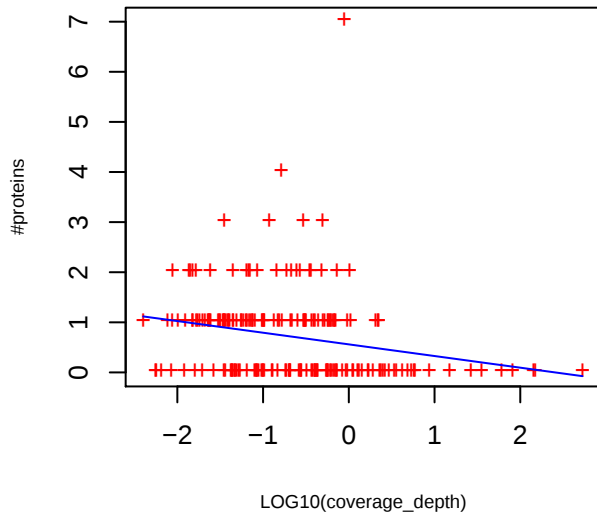


P-value curve ; red (unnorm), green (norm)



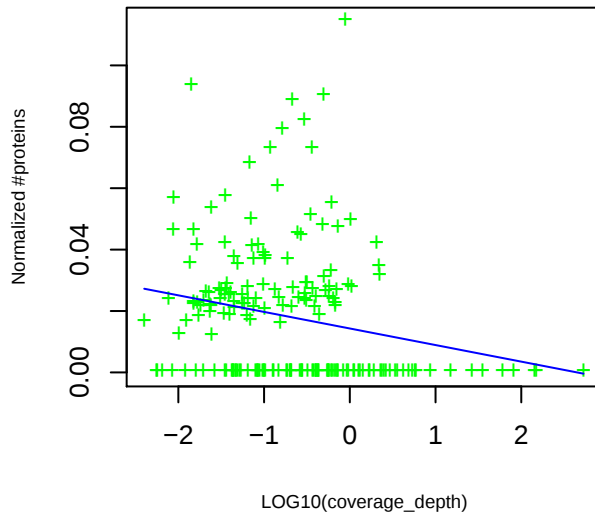
[H] COG1893 Ketopantoate reductase

slope= -0.23 p_value= 0.0011 intercept= 0.56 p_value= 3.0e-11



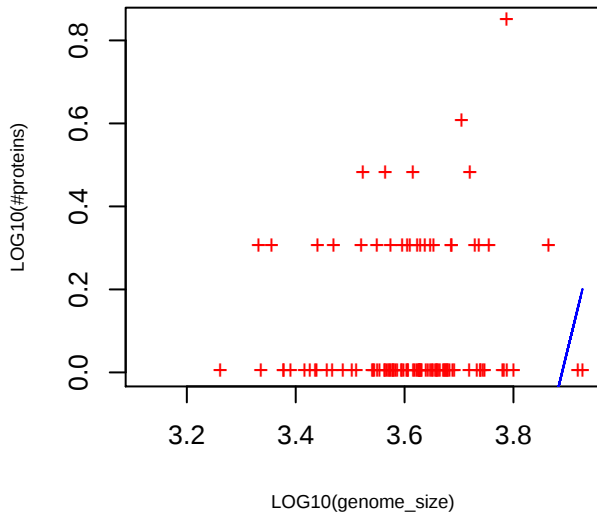
[H] COG1893 Ketopantoate reductase

slope= -0.0054 p_value= 0.002 intercept= 0.014 p_value= 5.1e-12

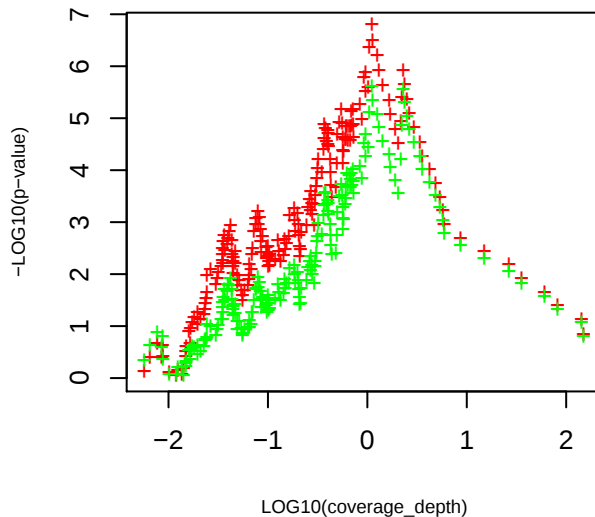


[H] COG1893 Ketopantoate reductase

slope= 5.35 p_value= 5e-10 intercept= -20.79 p_value= 1.4e-11

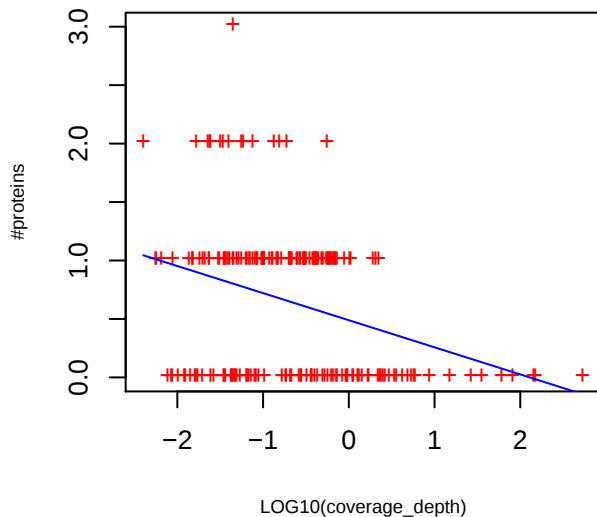


P-value curve ; red (unnorm), green (norm)



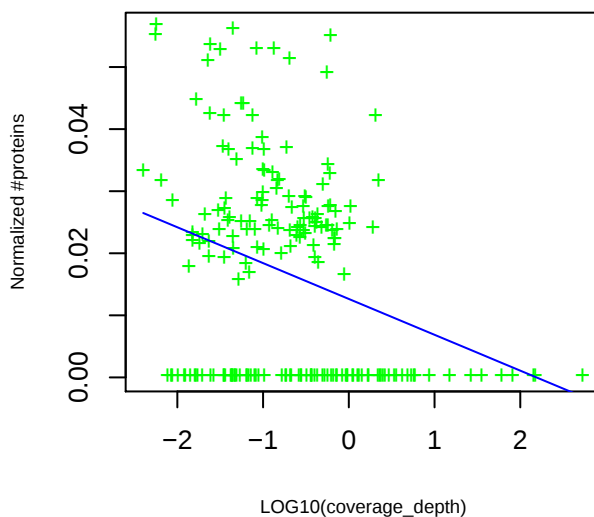
[N] COG1815 Flagellar basal body protein

slope= -0.23 p_value= 3.7e-06 intercept= 0.49 p_value= 3.8e-16



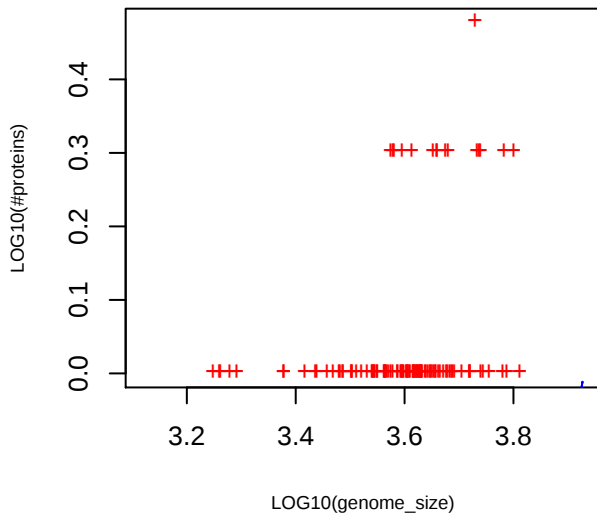
[N] COG1815 Flagellar basal body protein

slope= -0.0058 p_value= 7.6e-06 intercept= 0.013 p_value= 3.5e-16

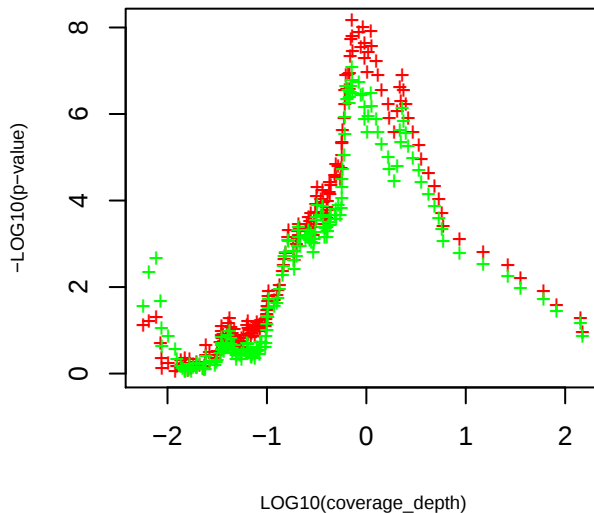


[N] COG1815 Flagellar basal body protein

slope= 4.48 p_value= 1.6e-07 intercept= -17.60 p_value= 8.5e-09

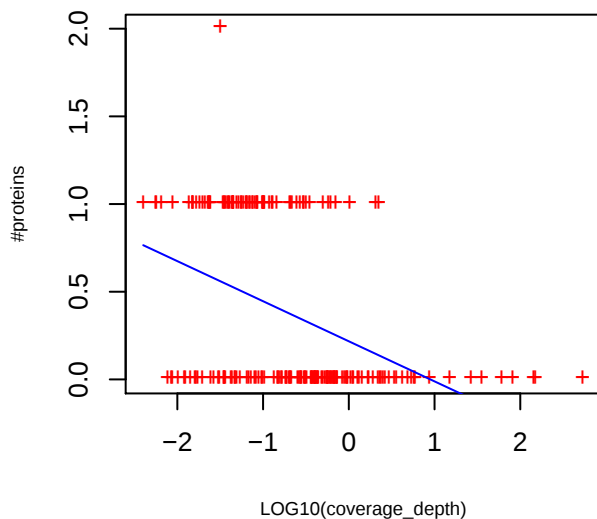


P-value curve ; red (unnorm), green (norm)



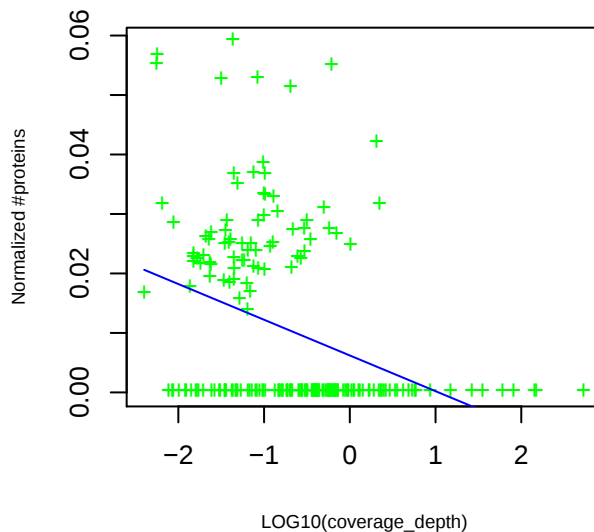
[N] COG1419 Flagellar GTP-binding protein

slope= -0.23 p_value= 1.8e-09 intercept= 0.22 p_value= 2.8e-07



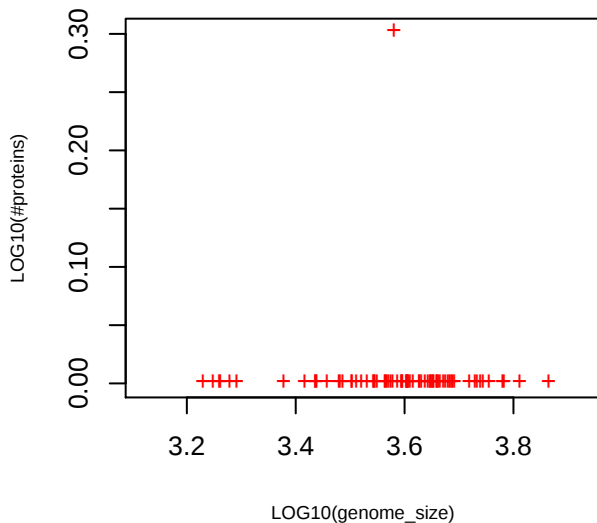
[N] COG1419 Flagellar GTP-binding protein

slope= -0.006 p_value= 2.1e-07 intercept= 0.0062 p_value= 1.7e-06

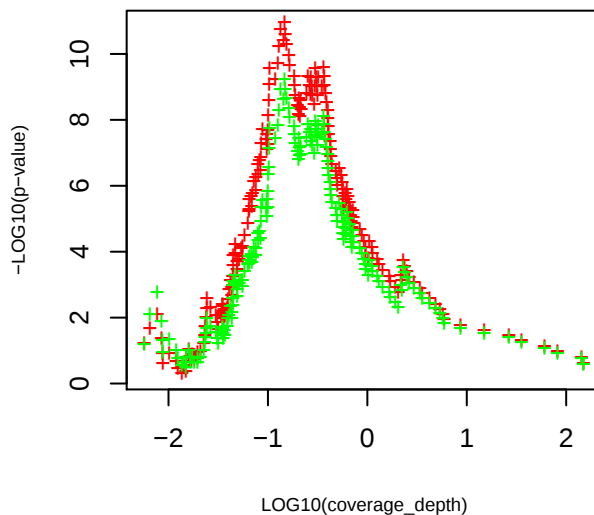


[N] COG1419 Flagellar GTP-binding protein

slope= 2.02 p_value= 0.017 intercept= -9.68 p_value= 0.0014

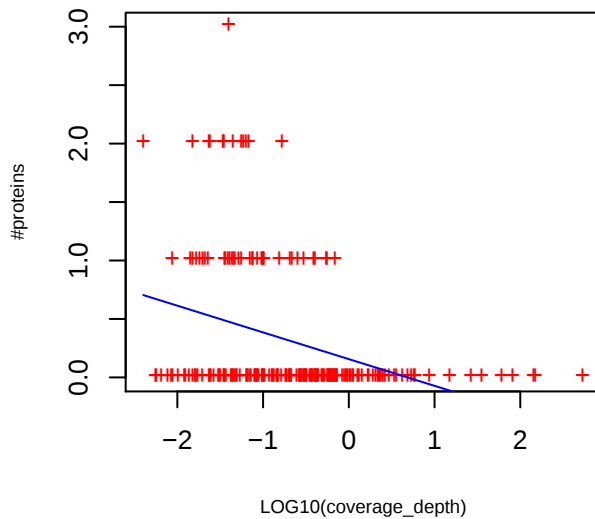


P-value curve ; red (unnorm), green (norm)



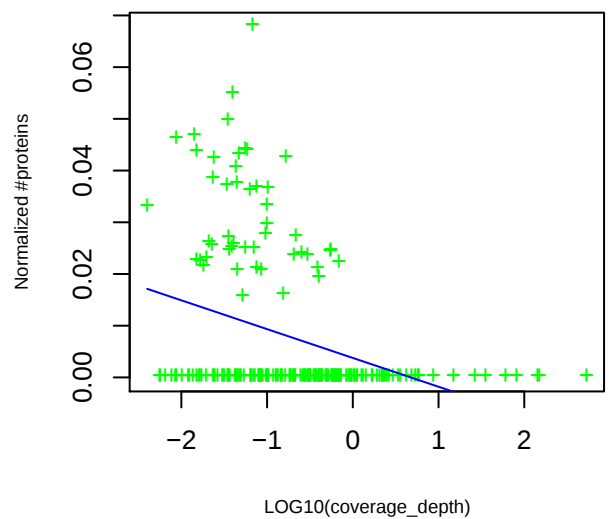
[P] COG1275 Tellurite resistance protein and related permeases

slope= -0.23 p_value= 1.4e-06 intercept= 0.16 p_value= 0.0028



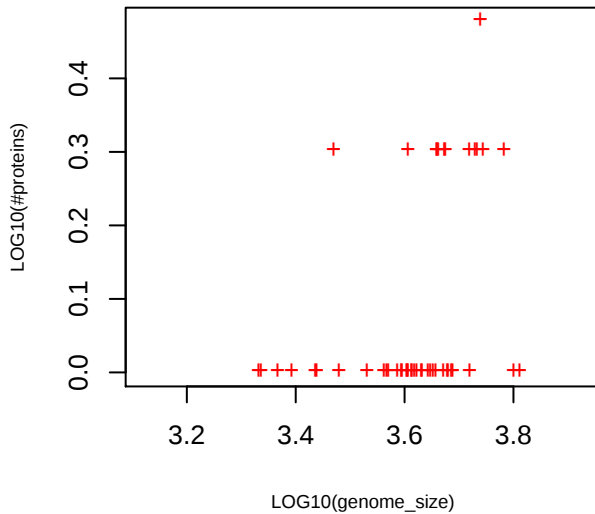
[P] COG1275 Tellurite resistance protein and related permeases

slope= -0.0056 p_value= 8.3e-07 intercept= 0.0038 p_value= 0.0026

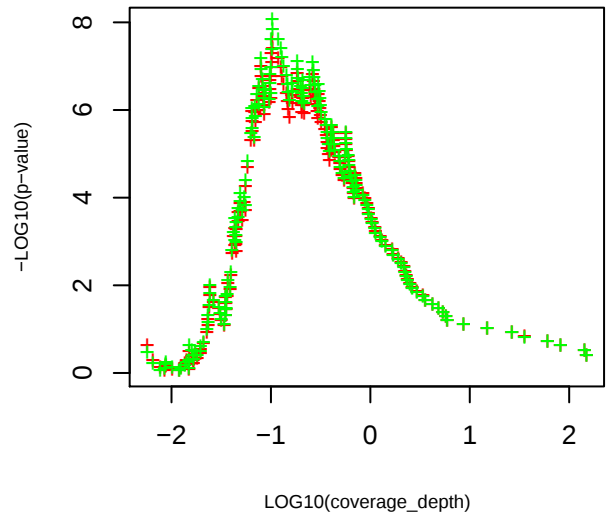


[P] COG1275 Tellurite resistance protein and related permeases

slope= 2.67 p_value= 0.00045 intercept= -12.48 p_value= 5e-06

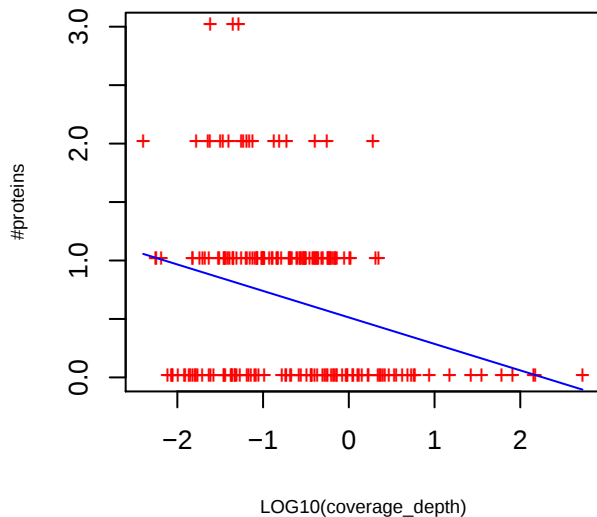


P-value curve ; red (unnorm), green (norm)



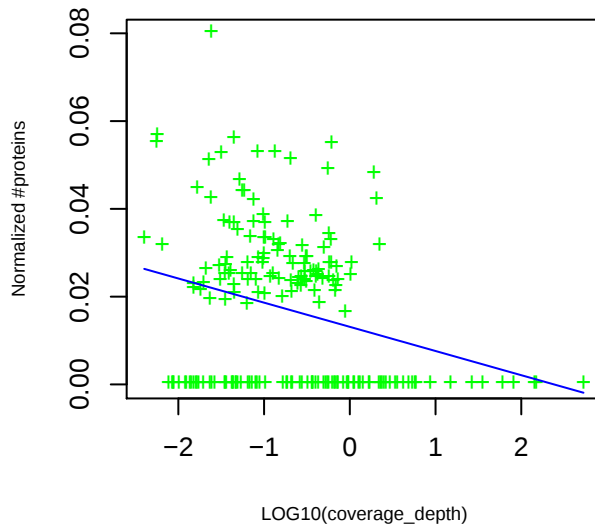
[N] COG1706 Flagellar basal-body P-ring protein

slope= -0.23 p_value= 4.3e-05 intercept= 0.51 p_value= 9.2e-15



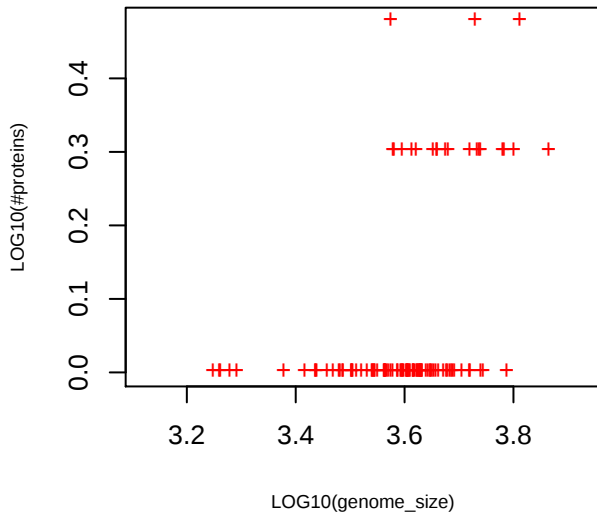
[N] COG1706 Flagellar basal-body P-ring protein

slope= -0.0055 p_value= 5.5e-05 intercept= 0.013 p_value= 1.4e-15

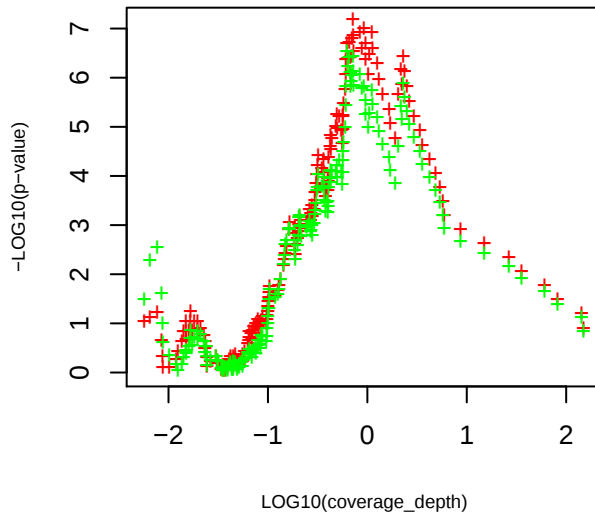


[N] COG1706 Flagellar basal-body P-ring protein

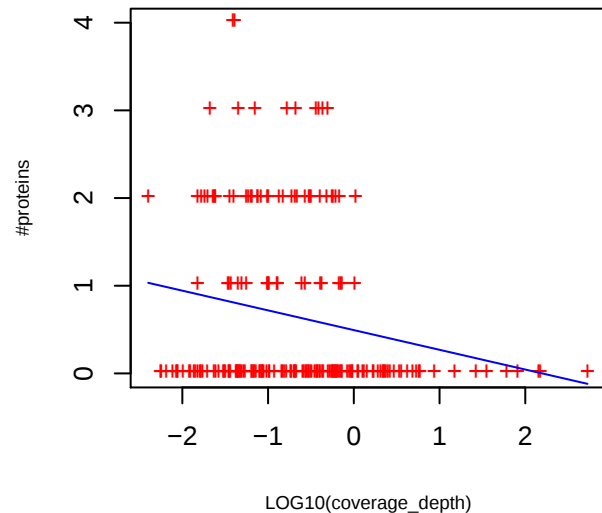
slope= 4.39 p_value= 3.7e-07 intercept= -17.34 p_value= 2e-08



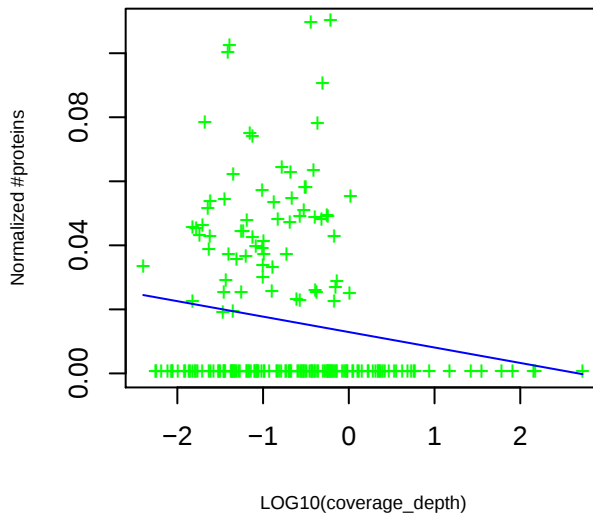
P-value curve ; red (unnorm), green (norm)



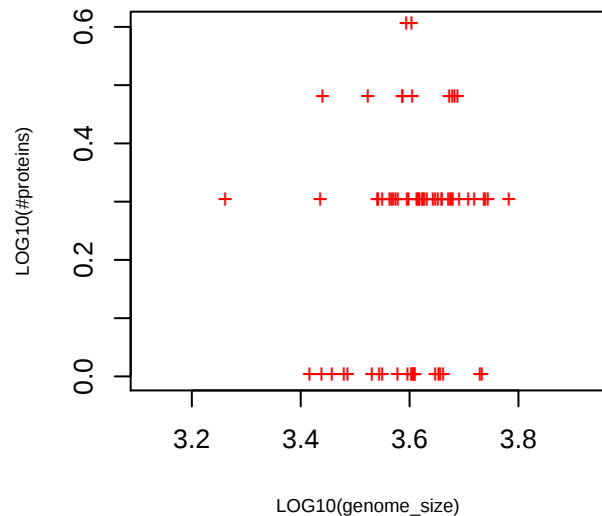
[S] COG2995 Uncharacterized paraquat-inducible protein A
 slope= -0.22 p_value= 0.0045 intercept= 0.49 p_value= 7.4e-08



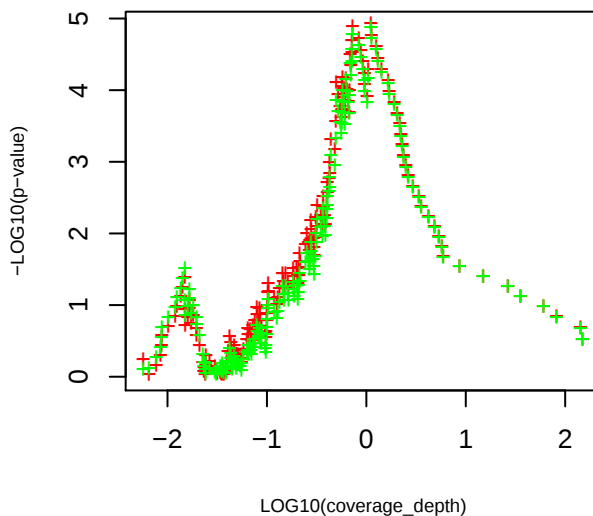
[S] COG2995 Uncharacterized paraquat-inducible protein A
 slope= -0.0048 p_value= 0.018 intercept= 0.013 p_value= 5.7e-08



[S] COG2995 Uncharacterized paraquat-inducible protein A
 slope= 3.45 p_value= 7.6e-05 intercept= -14.78 p_value= 2.2e-06

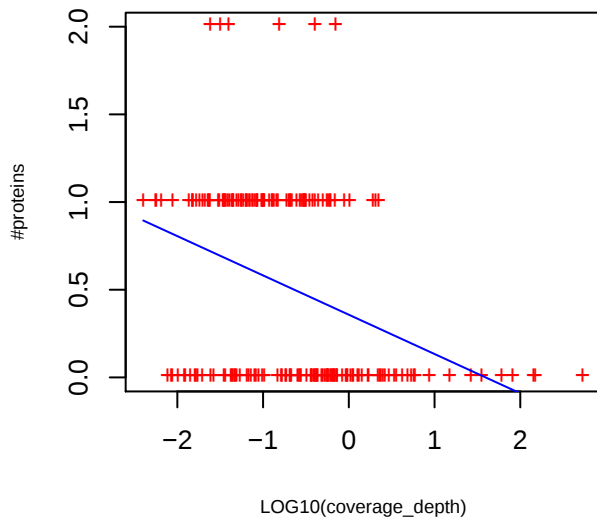


P-value curve ; red (unnorm), green (norm)



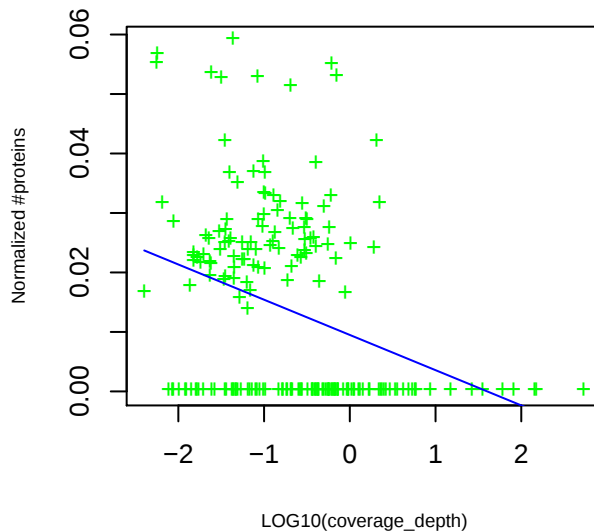
[N] COG1868 Flagellar motor switch protein

slope= -0.22 p_value= 2.3e-07 intercept= 0.36 p_value= 1.4e-12



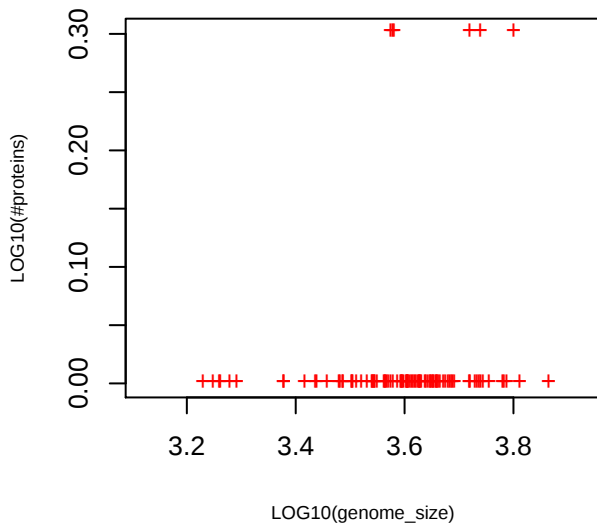
[N] COG1868 Flagellar motor switch protein

slope= -0.0059 p_value= 1.4e-06 intercept= 0.0095 p_value= 2.9e-11

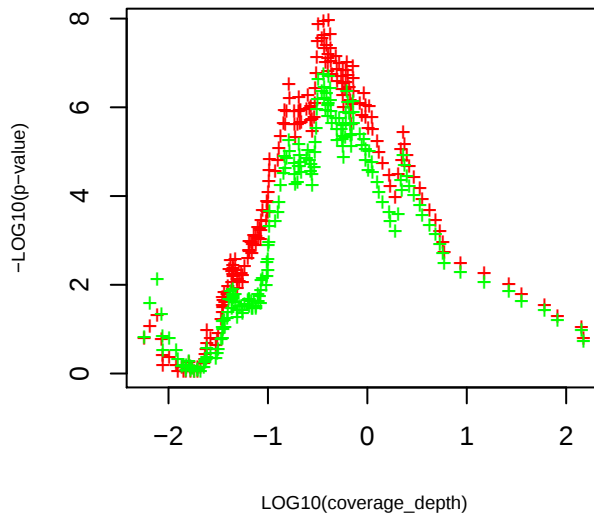


[N] COG1868 Flagellar motor switch protein

slope= 3.47 p_value= 6.5e-05 intercept= -14.35 p_value= 3.7e-06

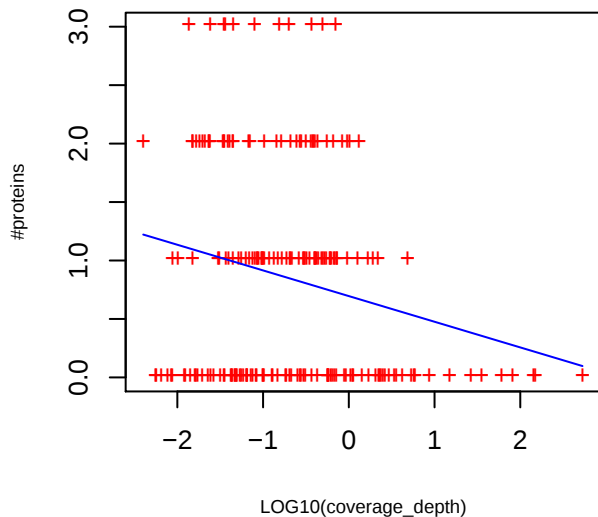


P-value curve ; red (unnorm), green (norm)



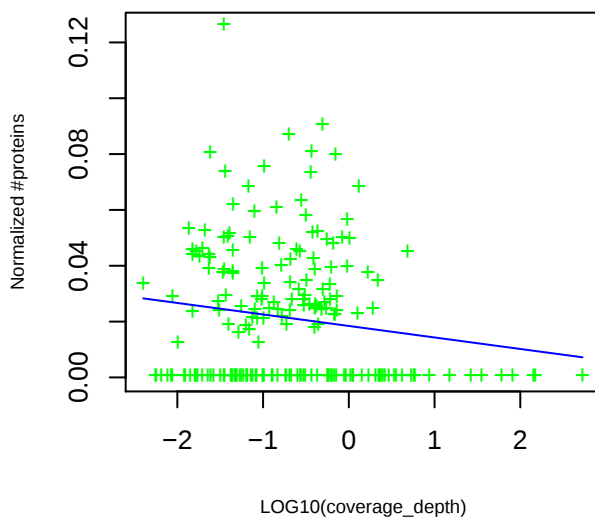
[O] COG1764 Predicted redox protein, regulator of disulfide bond formation

slope= -0.22 p_value= 0.0027 intercept= 0.70 p_value= 4.3e-15



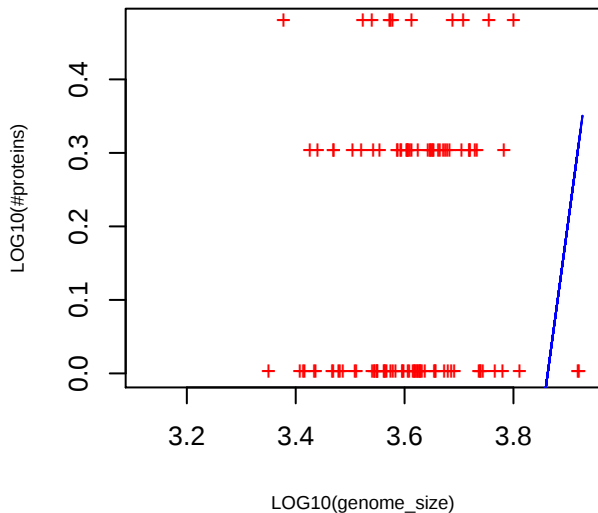
[O] COG1764 Predicted redox protein, regulator of disulfide bond formation

slope= -0.0041 p_value= 0.033 intercept= 0.018 p_value= 4.0e-15

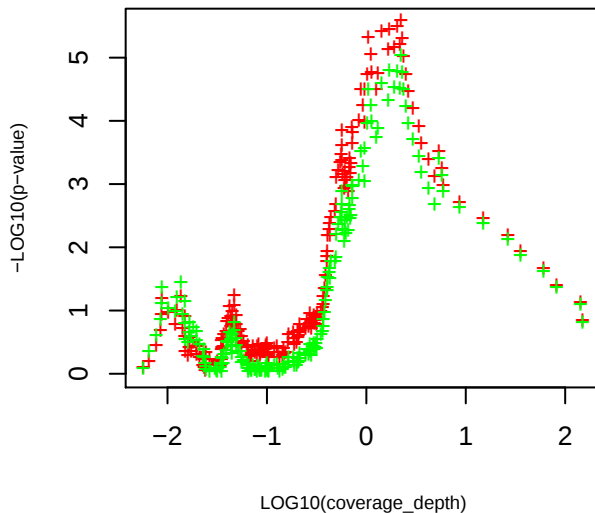


[O] COG1764 Predicted redox protein, regulator of disulfide bond formation

slope= 5.49 p_value= 2.8e-10 intercept= -21.19 p_value= 1e-11

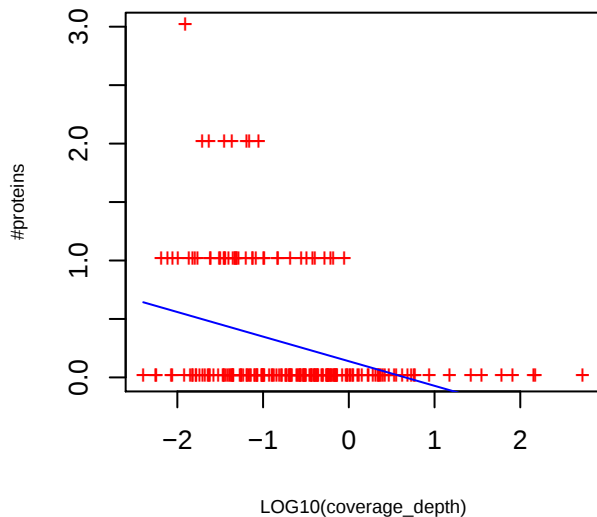


P-value curve ; red (unnorm), green (norm)



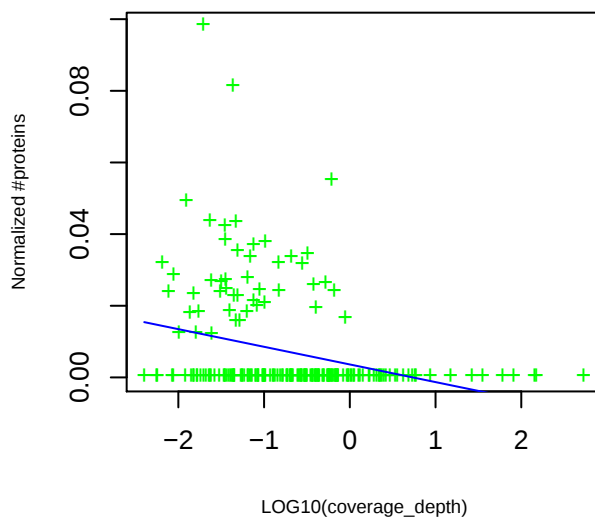
[H] COG1232 Protoporphyrinogen oxidase

slope= -0.21 p_value= 1.0e-06 intercept= 0.14 p_value= 0.0036



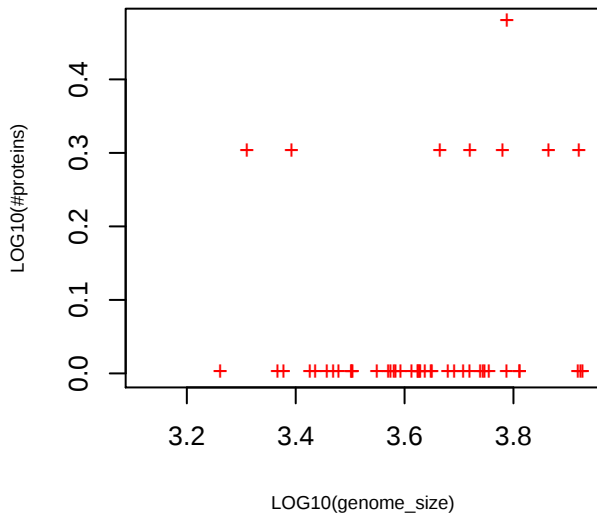
[H] COG1232 Protoporphyrinogen oxidase

slope= -0.0049 p_value= 2.2e-05 intercept= 0.0036 p_value= 0.0051

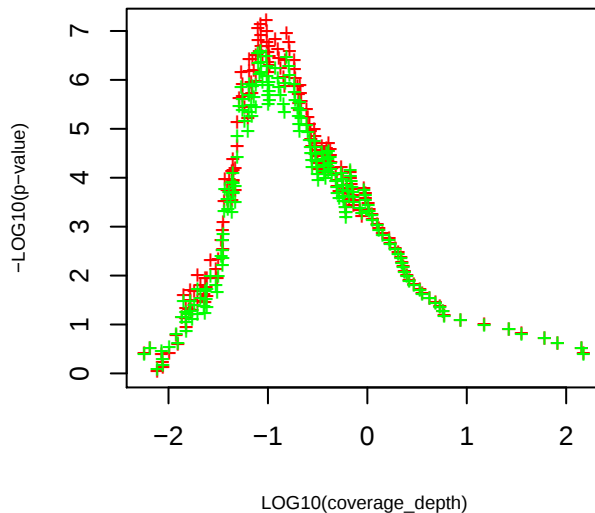


[H] COG1232 Protoporphyrinogen oxidase

slope= 3.19 p_value= 1.9e-05 intercept= -14.34 p_value= 8.8e-08

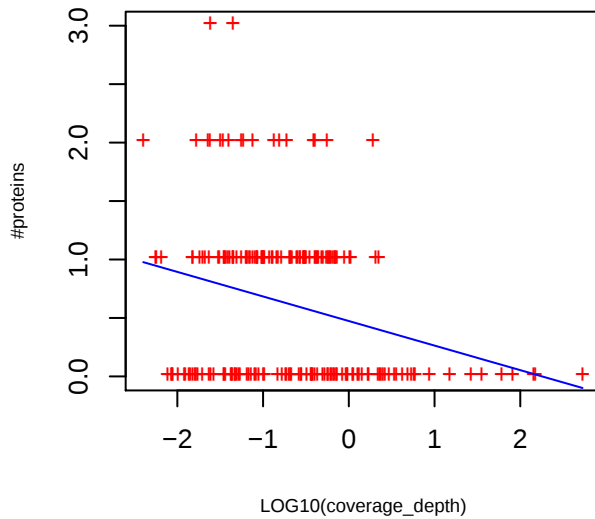


P-value curve ; red (unnorm), green (norm)



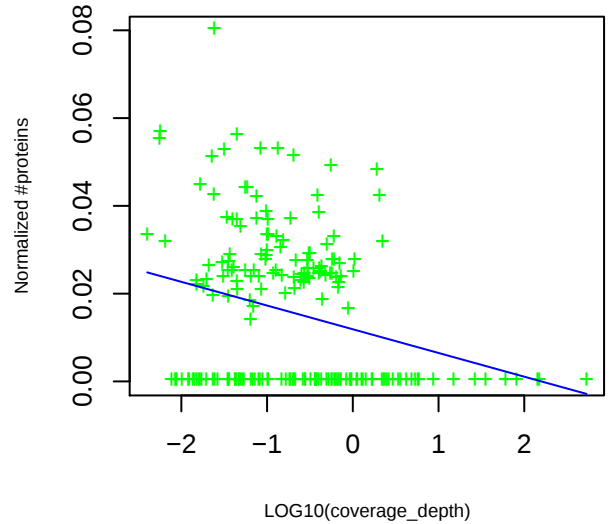
[NO] COG1261 Flagellar basal body P-ring biosynthesis protein

slope= -0.21 p_value= 1e-04 intercept= 0.47 p_value= 1.6e-13



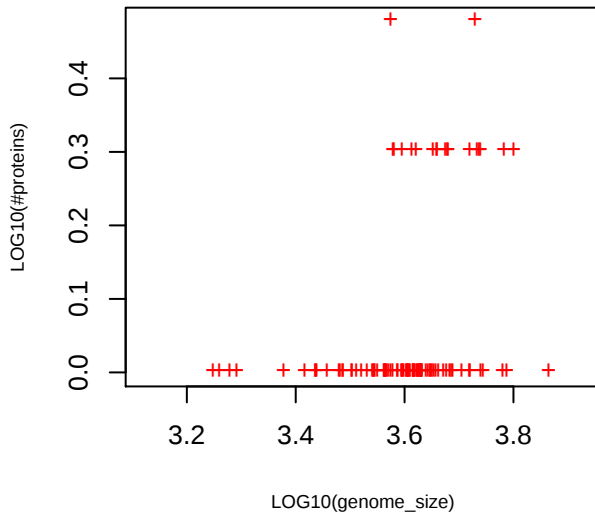
[NO] COG1261 Flagellar basal body P-ring biosynthesis protein

slope= -0.0054 p_value= 6.4e-05 intercept= 0.012 p_value= 1.4e-13

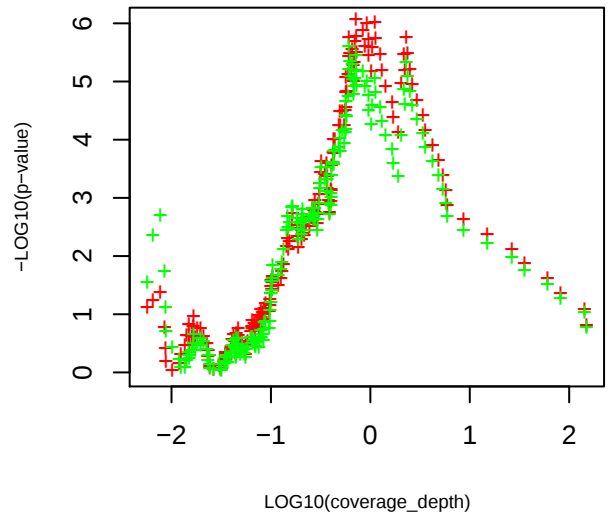


[NO] COG1261 Flagellar basal body P-ring biosynthesis protein

slope= 4.39 p_value= 4.1e-07 intercept= -17.48 p_value= 1.7e-08

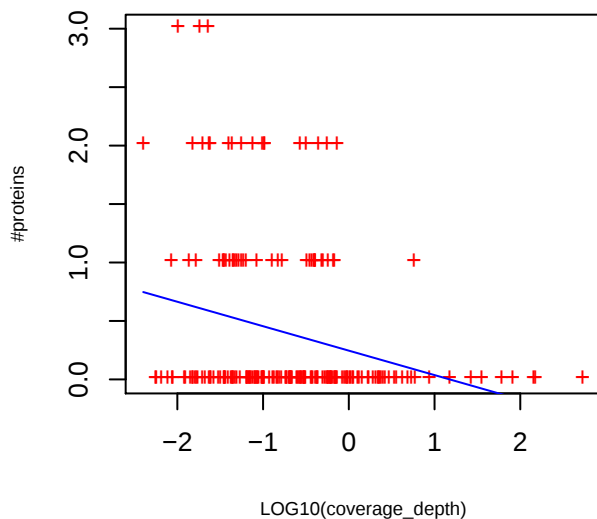


P-value curve ; red (unnorm), green (norm)



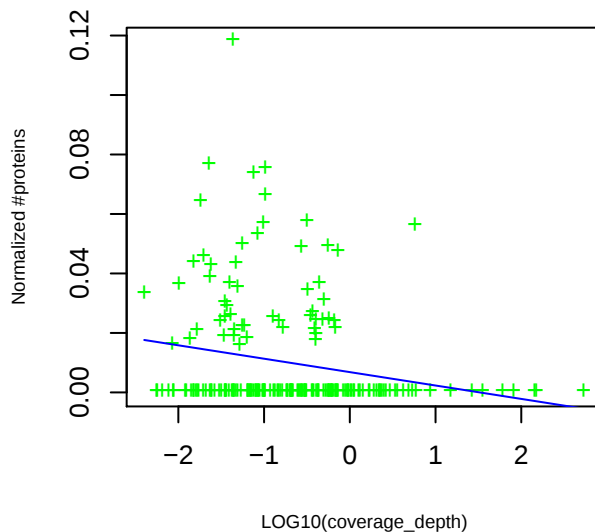
[L] COG3593 Predicted ATP-dependent endonuclease of the OLD family

slope= -0.21 p_value= 0.00019 intercept= 0.25 p_value= 1e-04



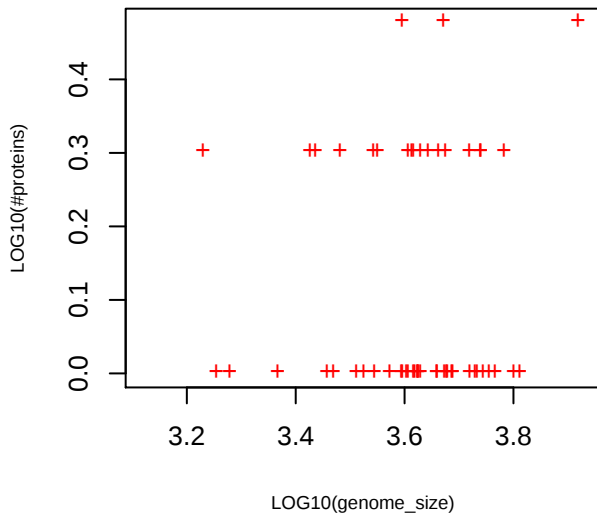
[L] COG3593 Predicted ATP-dependent endonuclease of the OLD family

slope= -0.0045 p_value= 0.0032 intercept= 0.0068 p_value= 8.8e-05

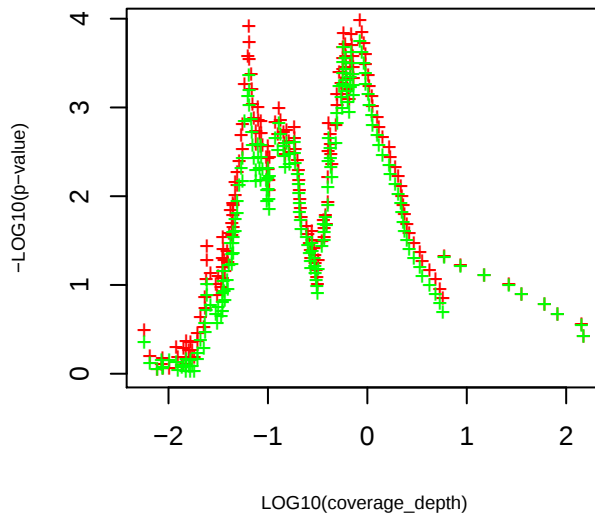


[L] COG3593 Predicted ATP-dependent endonuclease of the OLD family

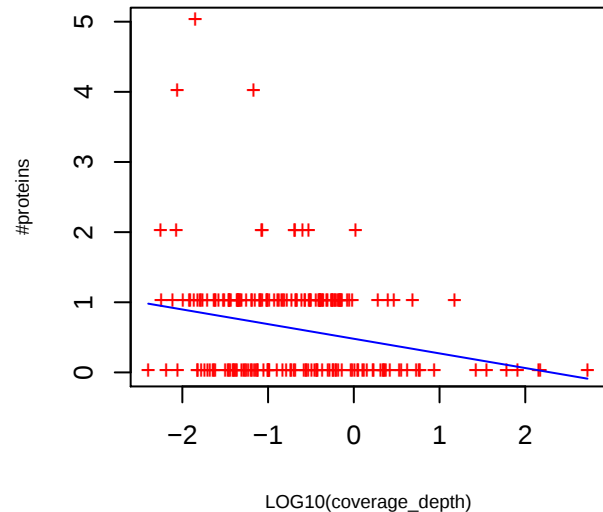
slope= 2.95 p_value= 0.00021 intercept= -13.34 p_value= 3.1e-06



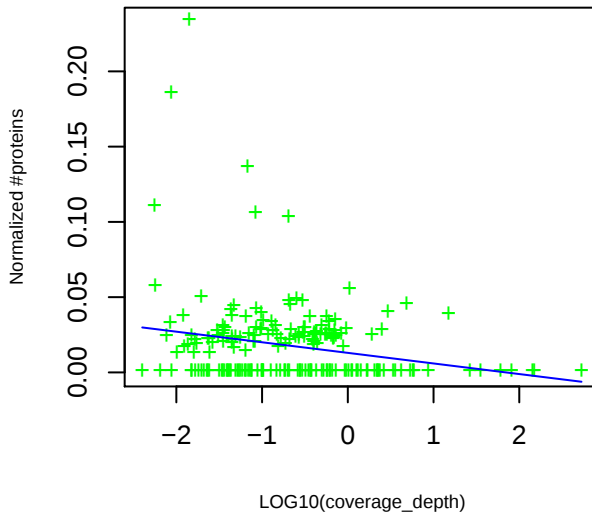
P-value curve ; red (unnorm), green (norm)



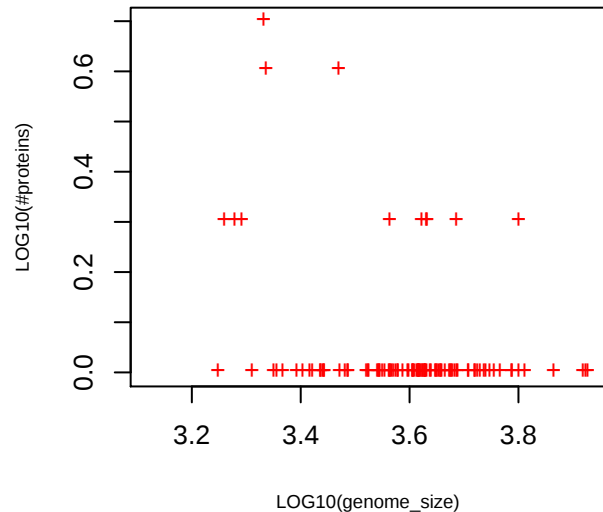
[P] COG1006 Multisubunit Na⁺/H⁺ antiporter, MnhC subunit
 slope= -0.21 p_value= 0.00037 intercept= 0.48 p_value= 4.5e-12



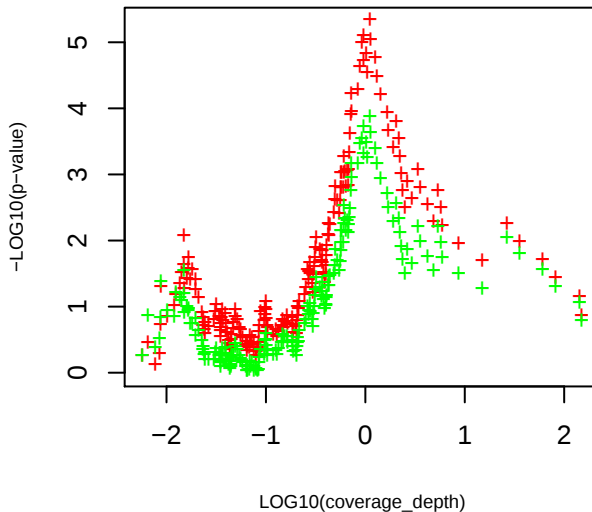
[P] COG1006 Multisubunit Na⁺/H⁺ antiporter, MnhC subunit
 slope= -0.007 p_value= 0.0017 intercept= 0.013 p_value= 5.1e-07



[P] COG1006 Multisubunit Na⁺/H⁺ antiporter, MnhC subunit
 slope= 3.80 p_value= 1.2e-05 intercept= -15.35 p_value= 7.9e-07

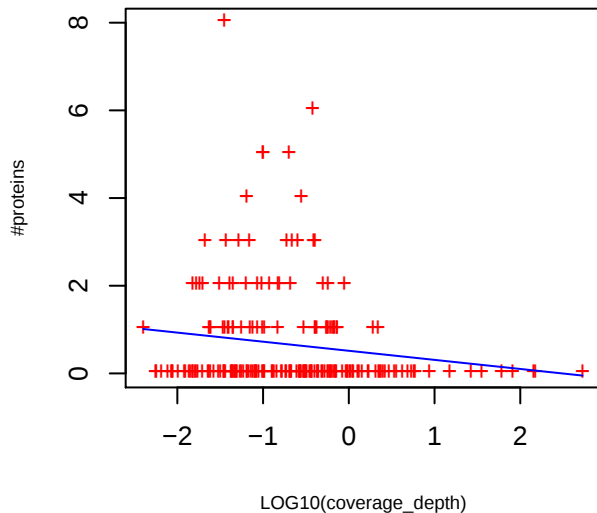


P-value curve ; red (unnorm), green (norm)



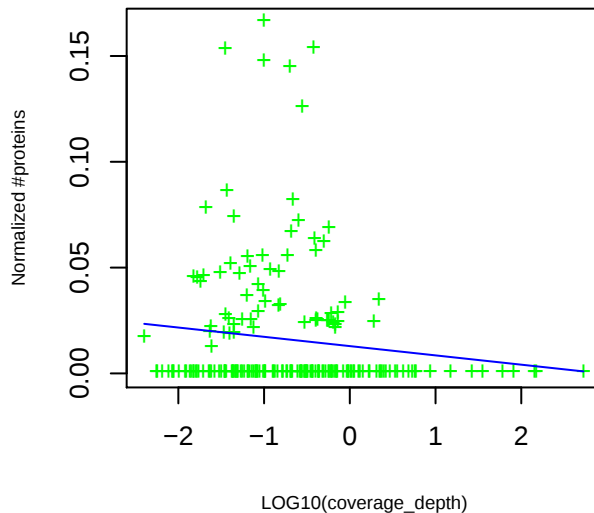
[T] COG4566 Response regulator

slope= -0.21 p_value= 0.036 intercept= 0.52 p_value= 6.1e-06



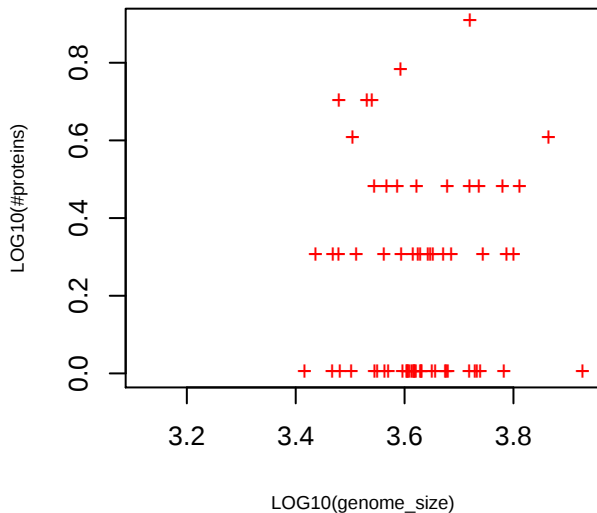
[T] COG4566 Response regulator

slope= -0.0044 p_value= 0.076 intercept= 0.013 p_value= 6.3e-06

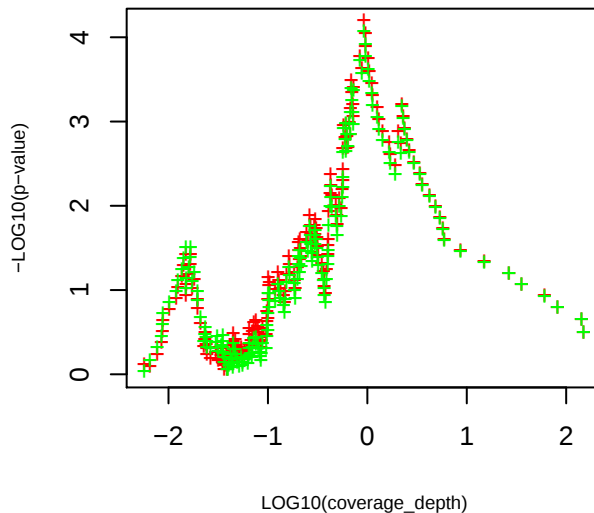


[T] COG4566 Response regulator

slope= 4.42 p_value= 1.9e-07 intercept= -18.26 p_value= 2e-09

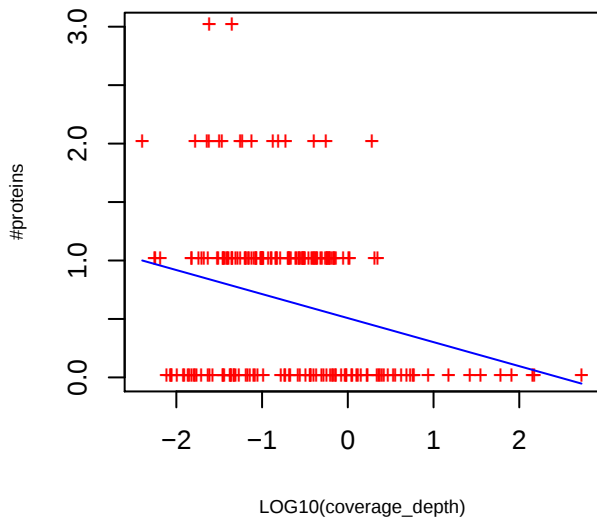


P-value curve ; red (unnorm), green (norm)



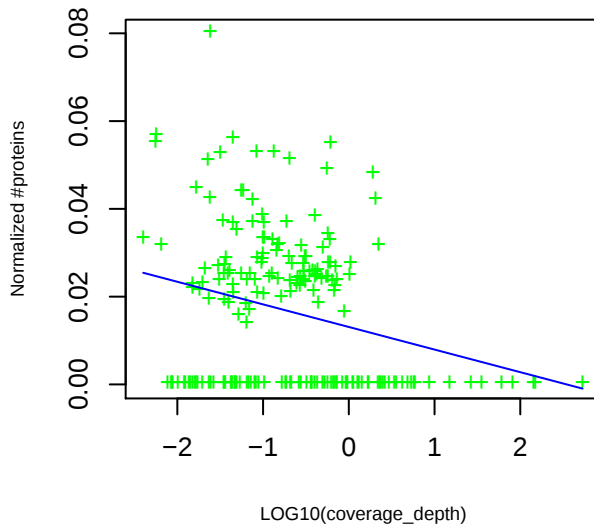
[N] COG2063 Flagellar basal body L-ring protein

slope= -0.21 p_value= 8.5e-05 intercept= 0.51 p_value= 8.7e-16



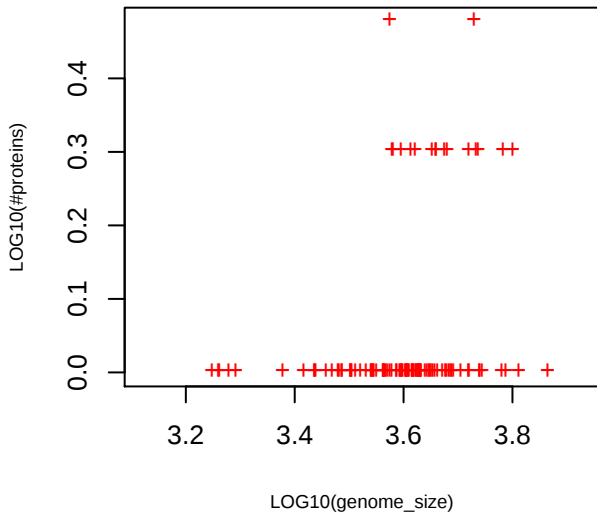
[N] COG2063 Flagellar basal body L-ring protein

slope= -0.0051 p_value= 0.00013 intercept= 0.013 p_value= 8.4e-16

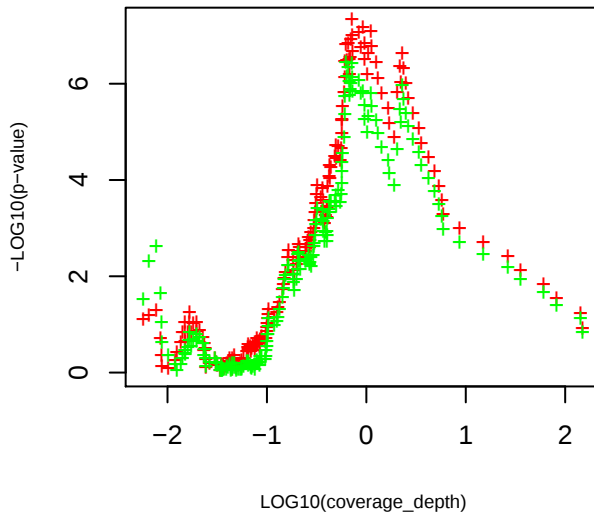


[N] COG2063 Flagellar basal body L-ring protein

slope= 4.38 p_value= 3.6e-07 intercept= -17.28 p_value= 1.9e-08

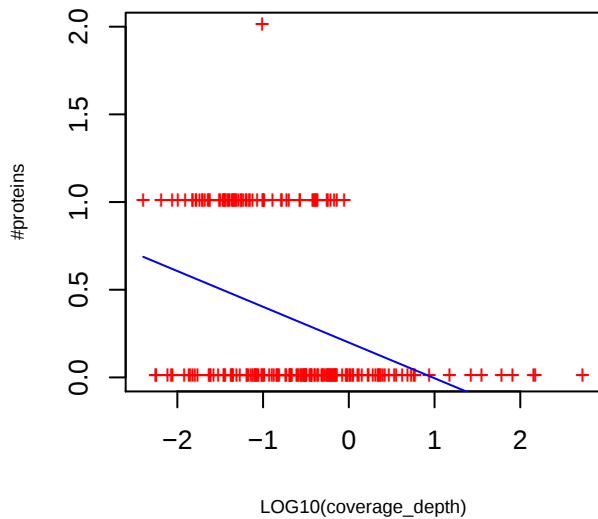


P-value curve ; red (unnorm), green (norm)



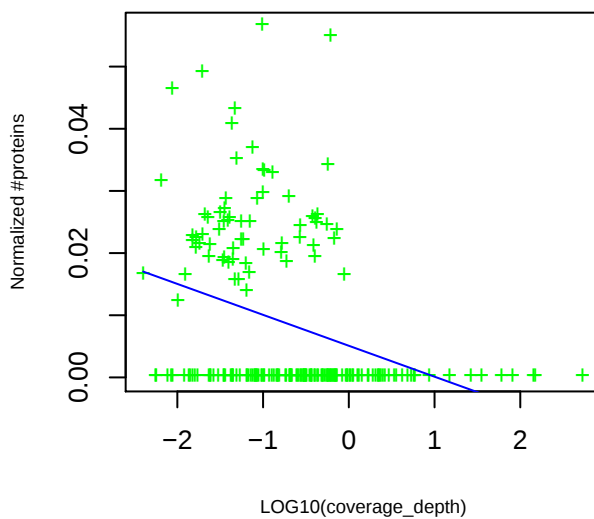
[S] COG1872 Uncharacterized conserved protein

slope= -0.20 p_value= 5.5e-08 intercept= 0.20 p_value= 2.1e-06



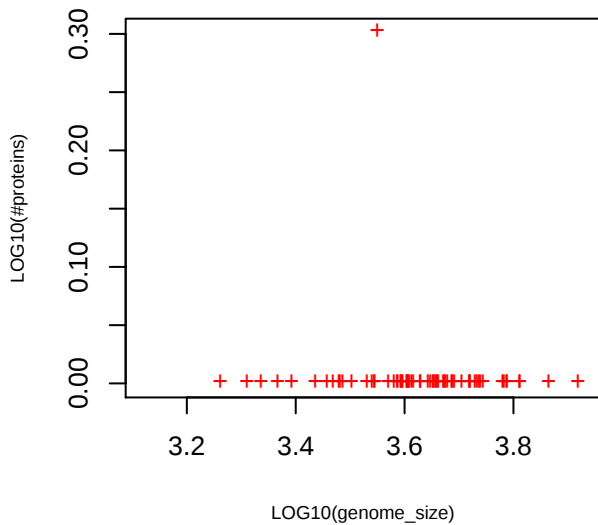
[S] COG1872 Uncharacterized conserved protein

slope= -0.005 p_value= 1.1e-06 intercept= 0.0051 p_value= 9.3e-06

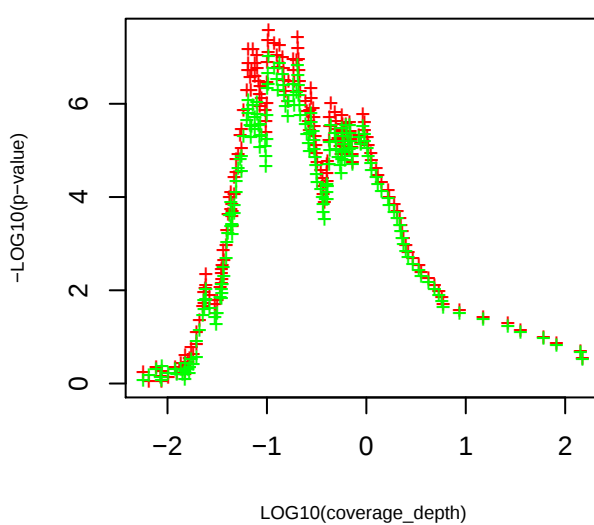


[S] COG1872 Uncharacterized conserved protein

slope= 3.84 p_value= 2.1e-06 intercept= -16.28 p_value= 2.2e-08

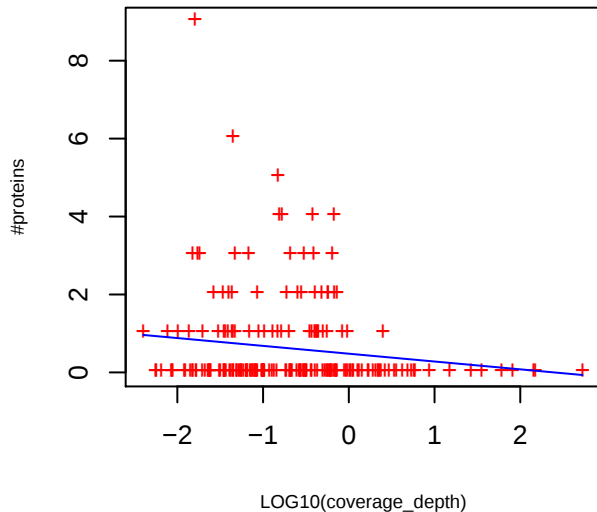


P-value curve ; red (unnorm), green (norm)



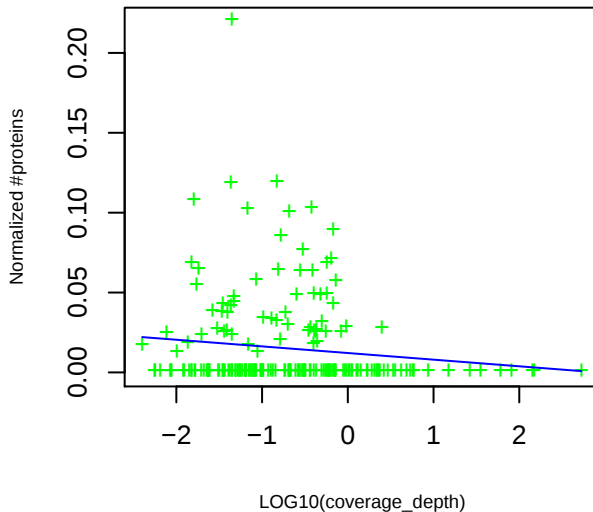
[U] COG3505 Type IV secretory pathway, VirD4 components

slope= -0.20 p_value= 0.041 intercept= 0.48 p_value= 2.2e-05



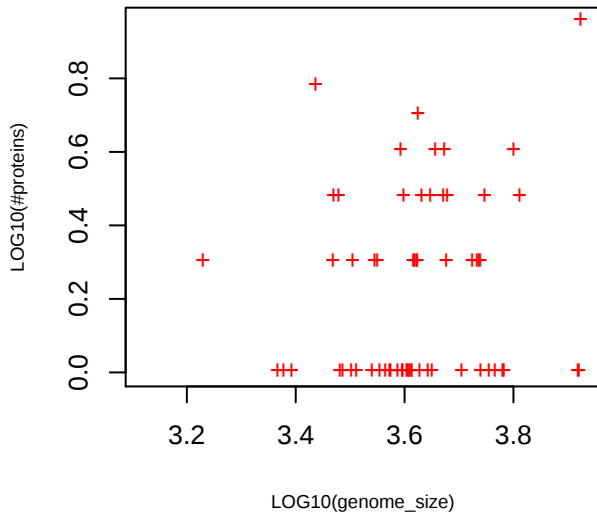
[U] COG3505 Type IV secretory pathway, VirD4 components

slope= -0.0042 p_value= 0.081 intercept= 0.012 p_value= 1e-05

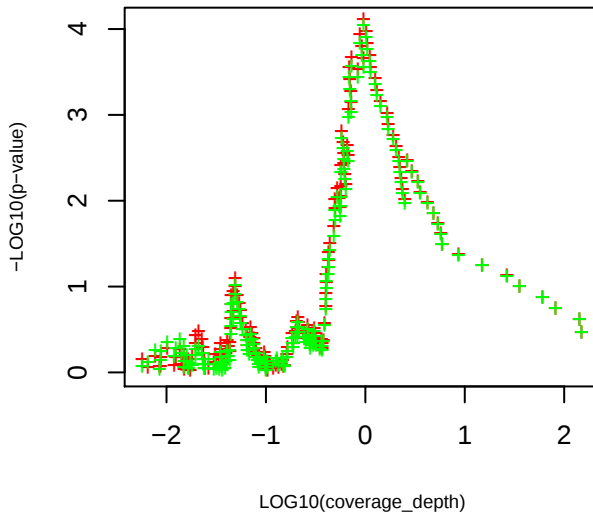


[U] COG3505 Type IV secretory pathway, VirD4 components

slope= 3.78 p_value= 7e-06 intercept= -16.08 p_value= 9.7e-08

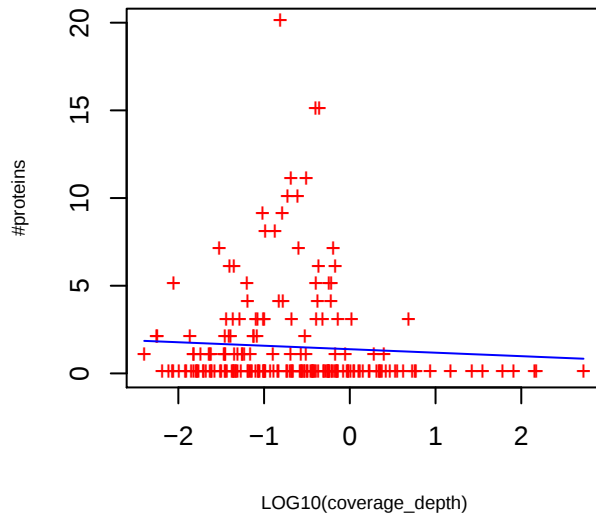


P-value curve ; red (unnorm), green (norm)



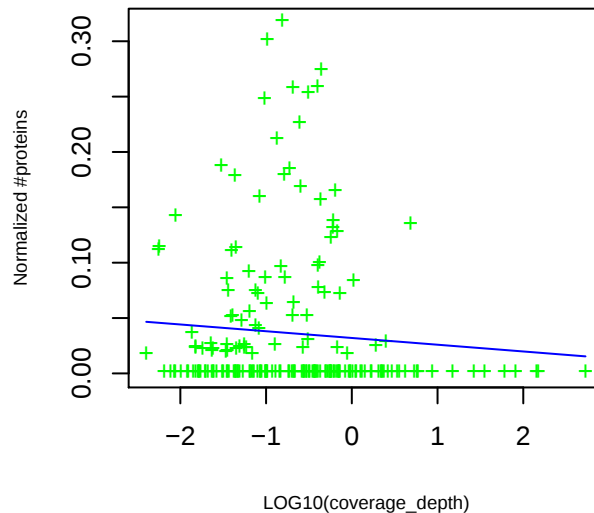
[G] COG1129 ABC-type sugar transport system, ATPase component

slope= -0.20 p_value= 0.41 intercept= 1.38 p_value= 1.1e-06



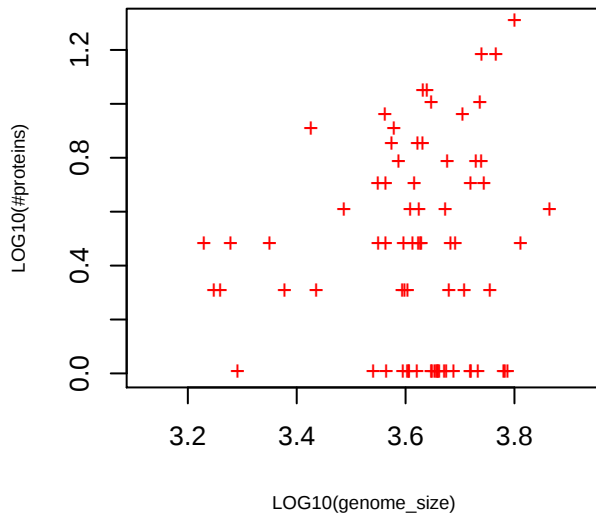
[G] COG1129 ABC-type sugar transport system, ATPase component

slope= -0.0061 p_value= 0.26 intercept= 0.032 p_value= 3.1e-07

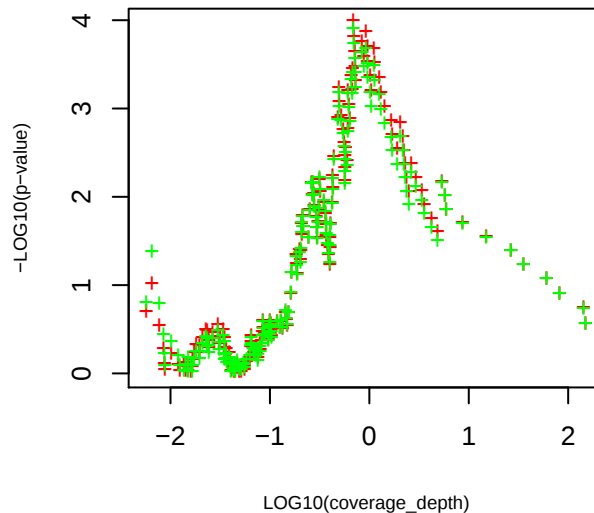


[G] COG1129 ABC-type sugar transport system, ATPase component

slope= 4.67 p_value= 4.5e-07 intercept= -18.86 p_value= 1.3e-08

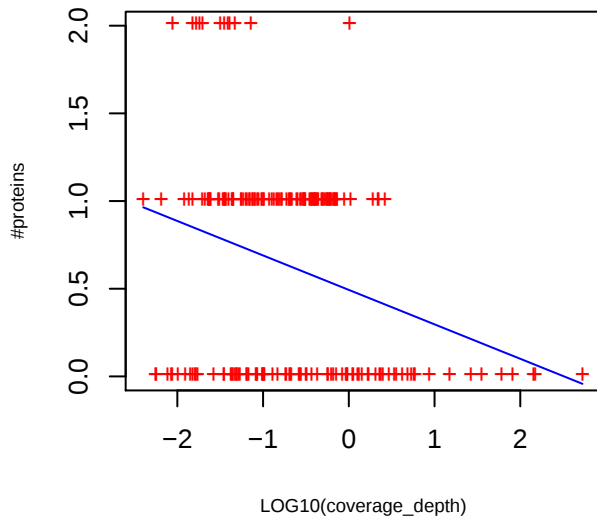


P-value curve ; red (unnorm), green (norm)



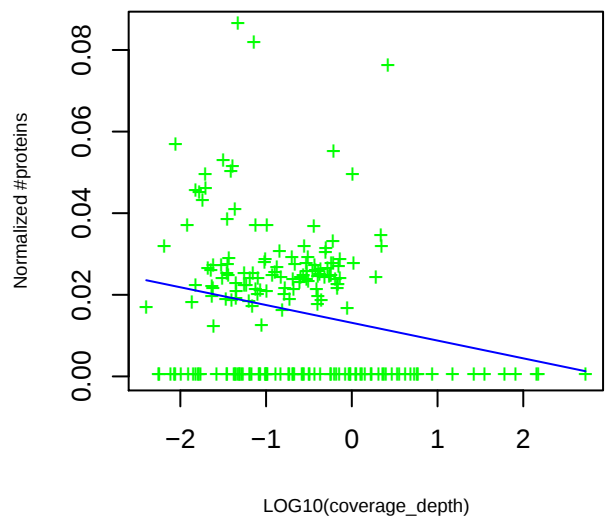
[P] COG4149 ABC-type molybdate transport system, permease component

slope= -0.20 p_value= 2.7e-05 intercept= 0.49 p_value= 5.4e-18



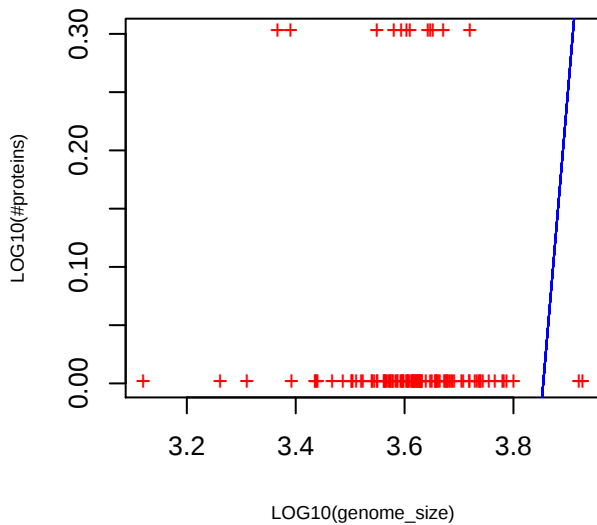
[P] COG4149 ABC-type molybdate transport system, permease component

slope= -0.0044 p_value= 0.0012 intercept= 0.013 p_value= 8e-16

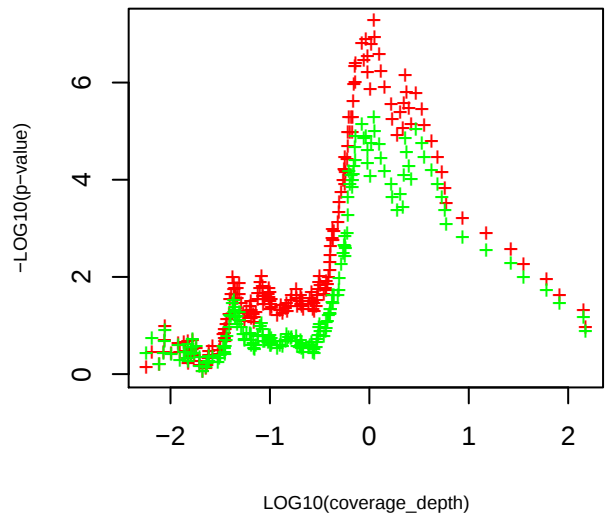


[P] COG4149 ABC-type molybdate transport system, permease component

slope= 5.52 p_value= 3.6e-11 intercept= -21.27 p_value= 1.1e-12

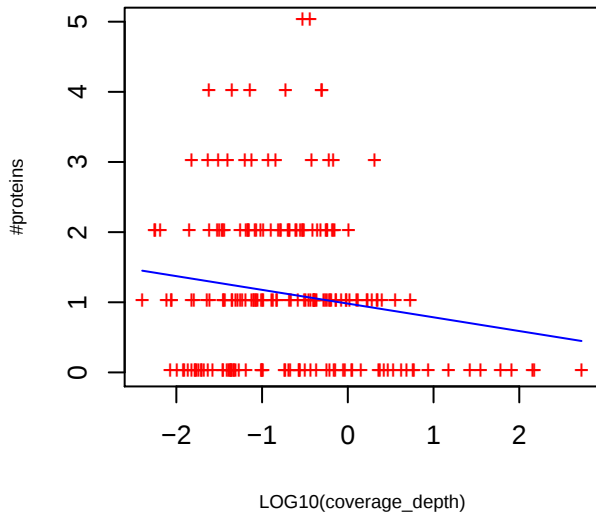


P-value curve ; red (unnorm), green (norm)



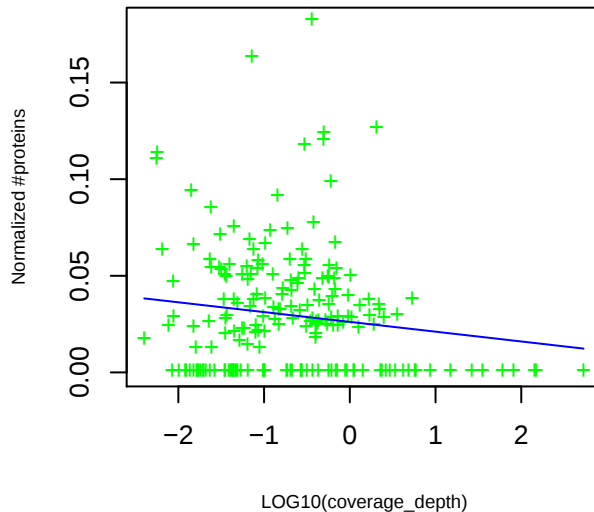
[C] COG1251 NAD(P)H-nitrite reductase

slope= -0.20 p_value= 0.027 intercept= 0.98 p_value= 6.2e-19



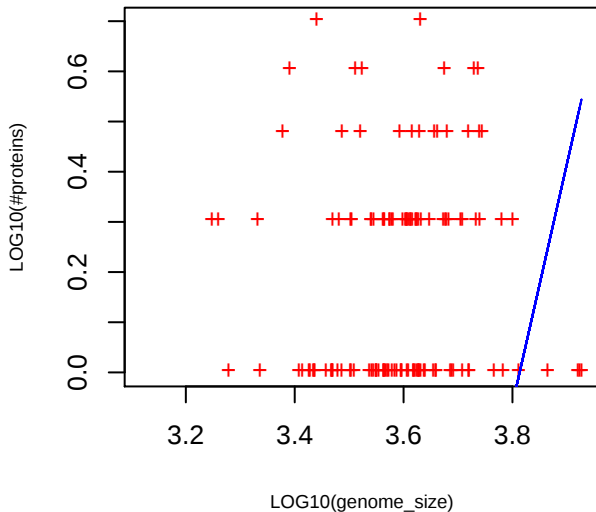
[C] COG1251 NAD(P)H-nitrite reductase

slope= -0.0051 p_value= 0.047 intercept= 0.026 p_value= 9.6e-17

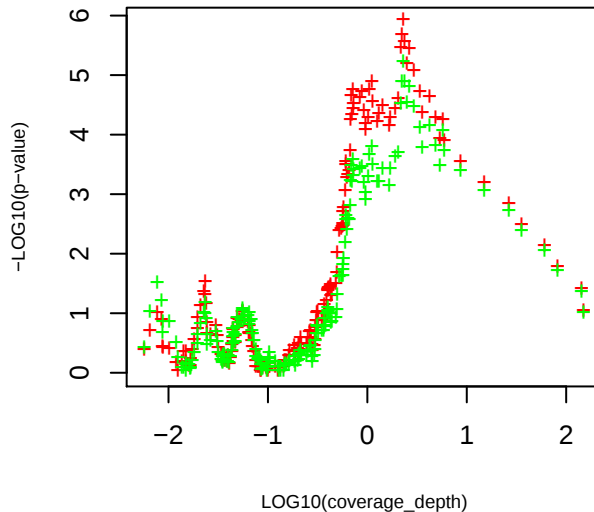


[C] COG1251 NAD(P)H-nitrite reductase

slope= 4.79 p_value= 1.7e-08 intercept= -18.25 p_value= 1.7e-09

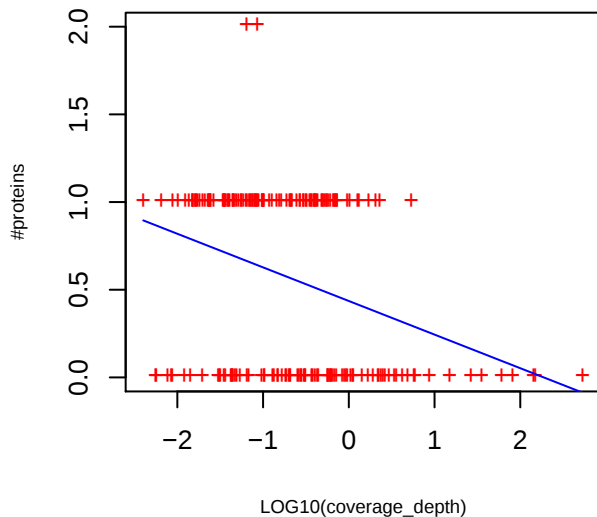


P-value curve ; red (unnorm), green (norm)



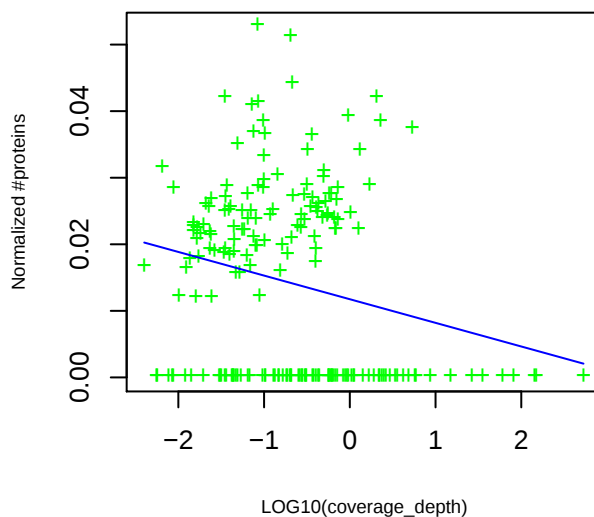
[K] COG2183 Transcriptional accessory protein

slope= -0.19 p_value= 1.9e-06 intercept= 0.44 p_value= 6e-19



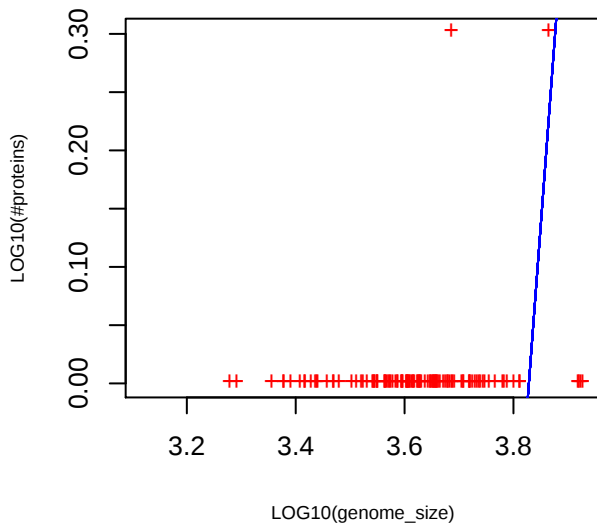
[K] COG2183 Transcriptional accessory protein

slope= -0.0036 p_value= 0.0013 intercept= 0.012 p_value= 4.8×10^{-18}

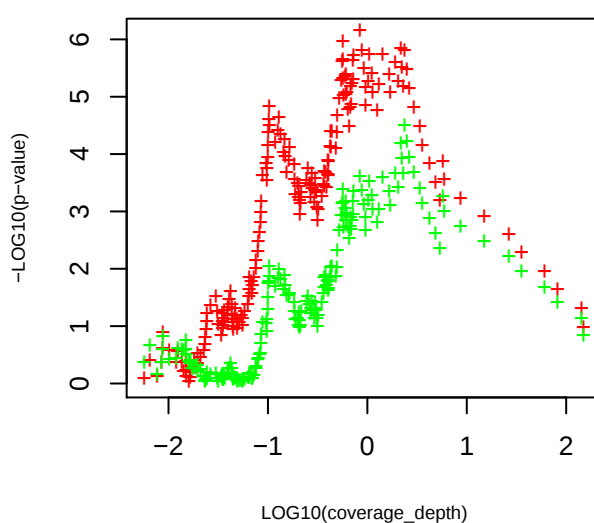


[K] COG2183 Transcriptional accessory protein

slope= 6.23 p_value= 2.2×10^{-14} intercept= -23.85 p_value= 3.6×10^{-16}

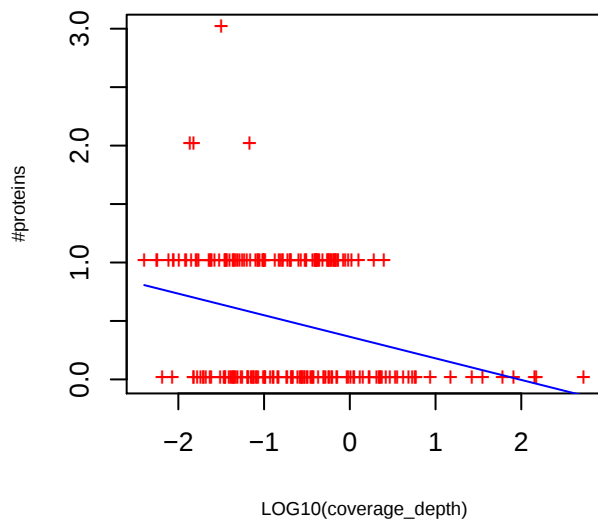


P-value curve ; red (unnorm), green (norm)



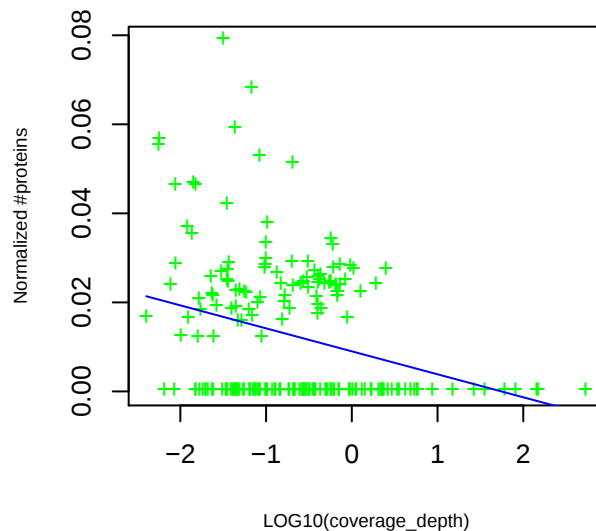
[H] COG1488 Nicotinic acid phosphoribosyltransferase

slope= -0.18 p_value= 2.5e-05 intercept= 0.36 p_value= 1.6e-12



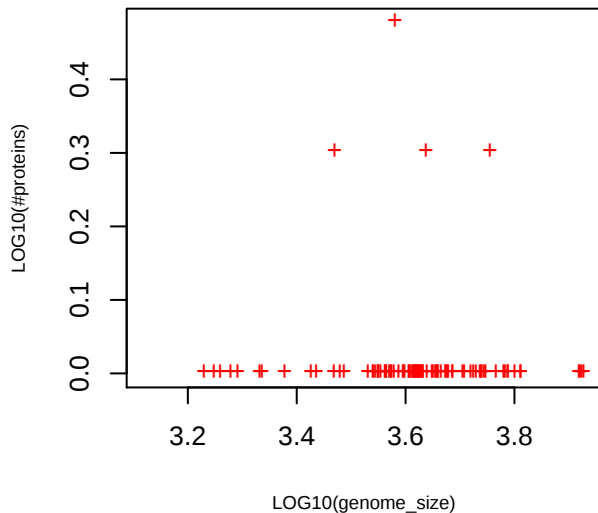
[H] COG1488 Nicotinic acid phosphoribosyltransferase

slope= -0.0052 p_value= 3e-05 intercept= 0.009 p_value= 3.7e-10

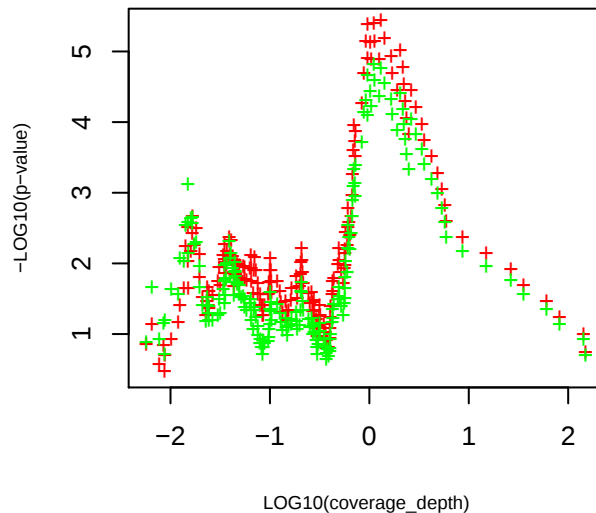


[H] COG1488 Nicotinic acid phosphoribosyltransferase

slope= 5.11 p_value= 1.4e-09 intercept= -20.24 p_value= 2.3e-11

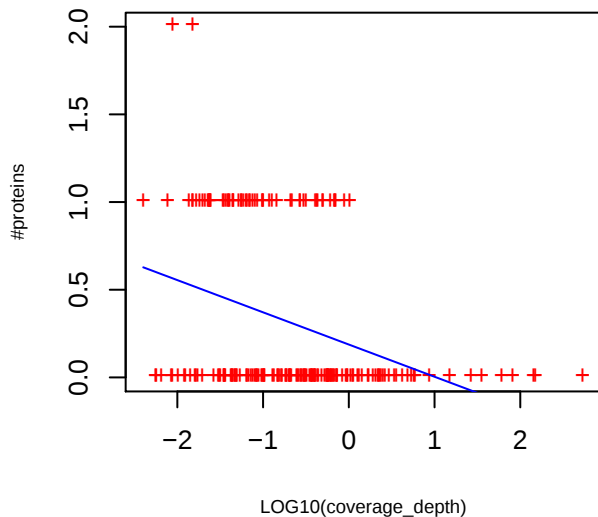


P-value curve : red (unnorm), green (norm)



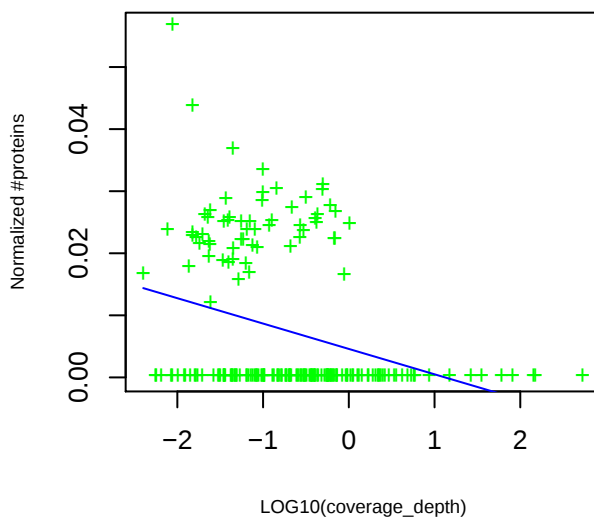
[S] COG2719 Uncharacterized conserved protein

slope= -0.18 p_value= 1.3e-06 intercept= 0.19 p_value= 1.1e-05



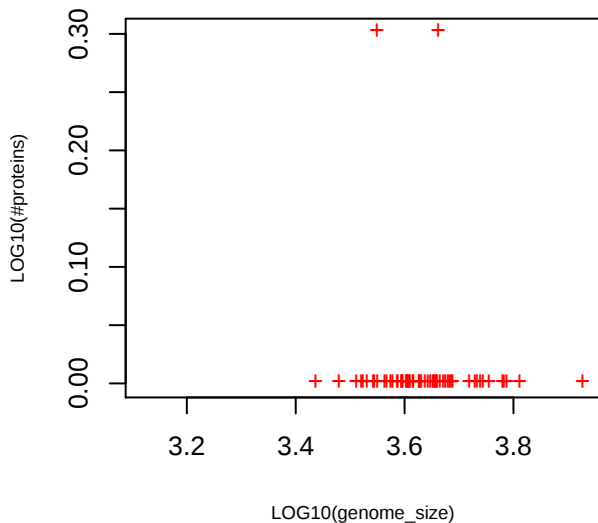
[S] COG2719 Uncharacterized conserved protein

slope= -0.0041 p_value= 9.8e-06 intercept= 0.0046 p_value= 1.1e-05

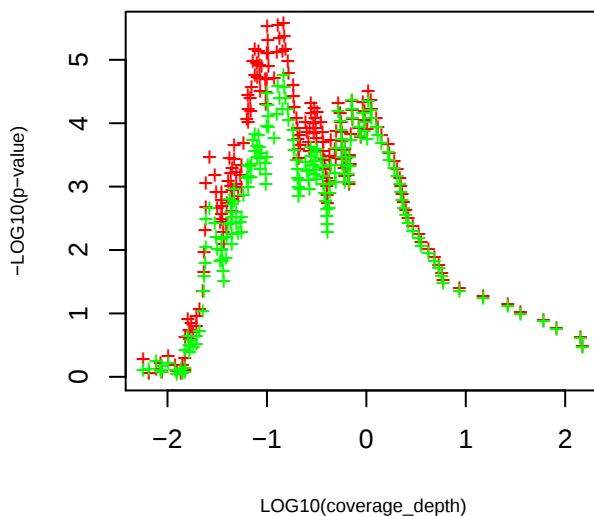


[S] COG2719 Uncharacterized conserved protein

slope= 4.21 p_value= 7.9e-08 intercept= -17.72 p_value= 3.5e-10

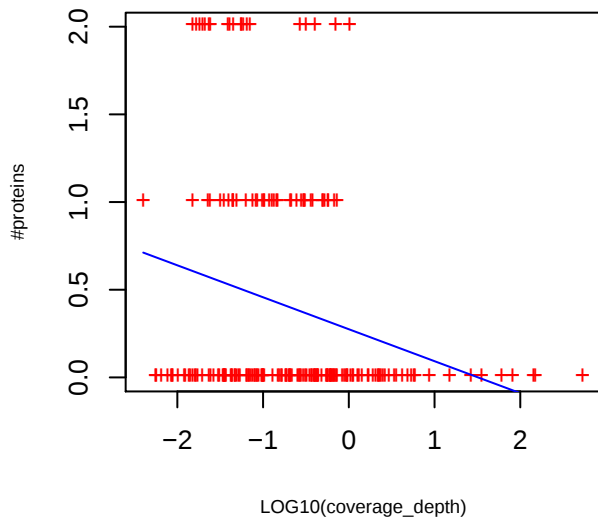


P-value curve ; red (unnorm), green (norm)



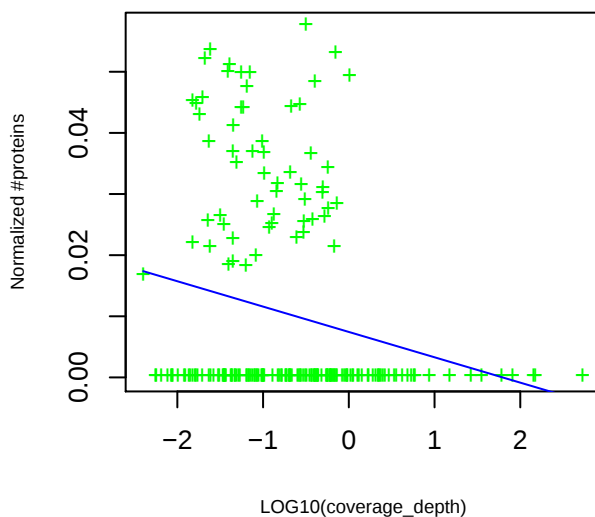
[M] COG3137 Putative salt-induced outer membrane protein

slope= -0.18 p_value= 0.00054 intercept= 0.27 p_value= 5e-06



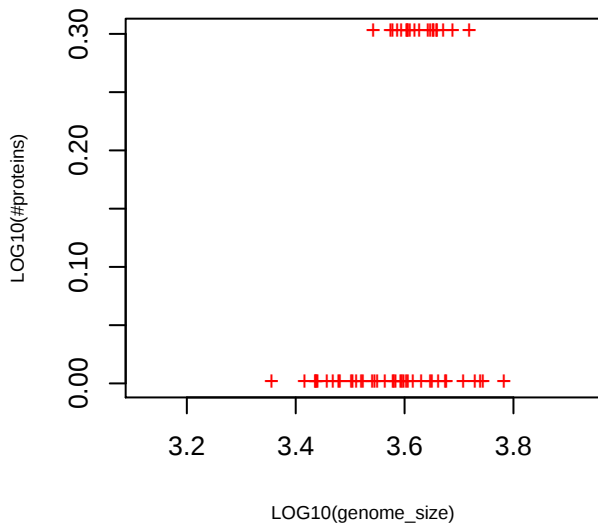
[M] COG3137 Putative salt-induced outer membrane protein

slope= -0.0041 p_value= 0.0020 intercept= 0.0074 p_value= 1.4e-06

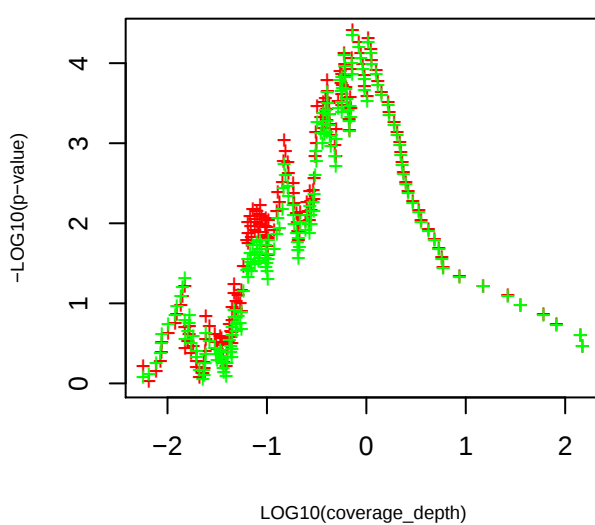


[M] COG3137 Putative salt-induced outer membrane protein

slope= 2.04 p_value= 0.013 intercept= -10.00 p_value= 0.00067

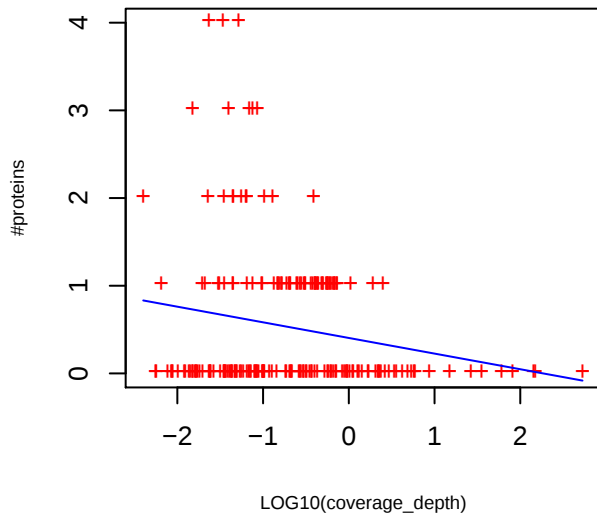


P-value curve ; red (unnorm), green (norm)



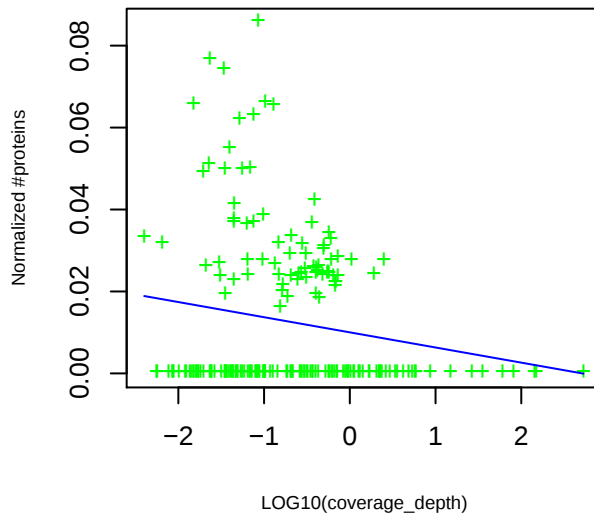
[U] COG4964 Flp pilus assembly protein, secretin CpaC

slope= -0.18 p_value= 0.0073 intercept= 0.40 p_value= 1.5e-07



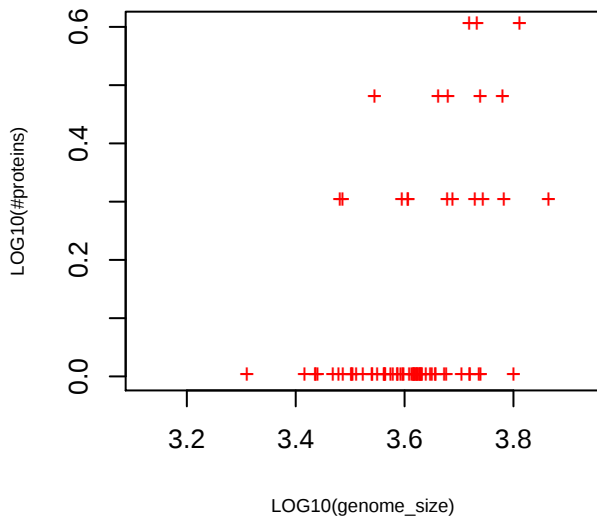
[U] COG4964 Flp pilus assembly protein, secretin CpaC

slope= -0.0037 p_value= 0.013 intercept= 0.01 p_value= 9.6e-09

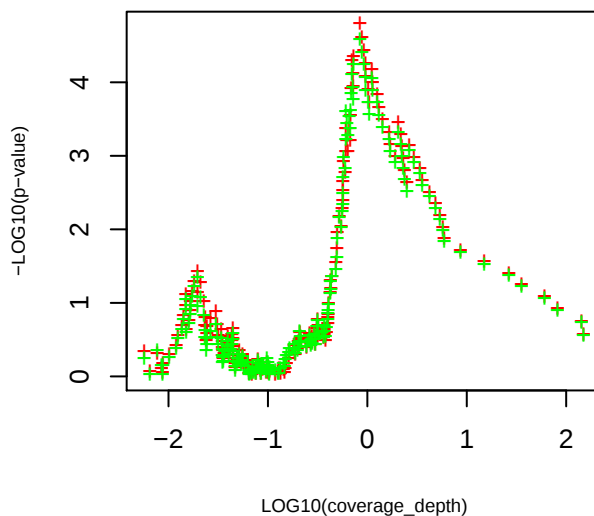


[U] COG4964 Flp pilus assembly protein, secretin CpaC

slope= 4.00 p_value= 2.7e-06 intercept= -16.65 p_value= 5.2e-08

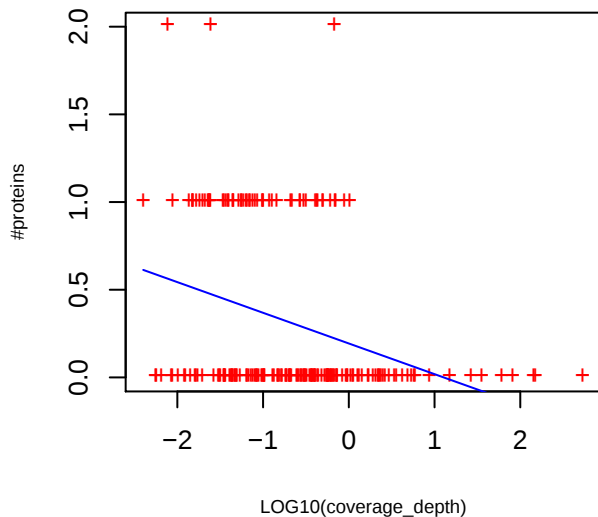


P-value curve ; red (unnorm), green (norm)



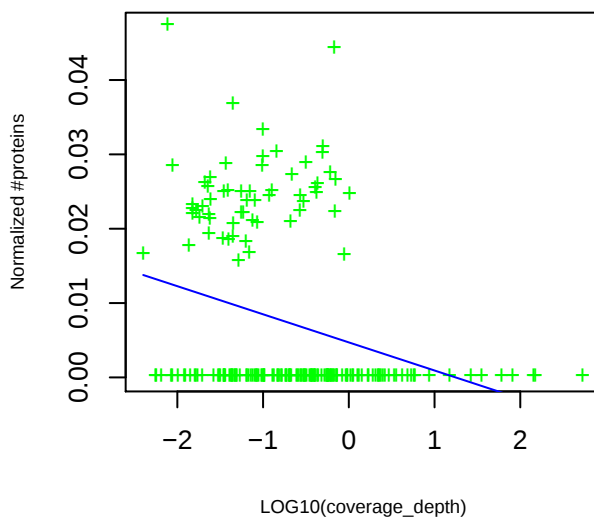
[T] COG2766 Putative Ser protein kinase

slope= -0.17 p_value= 6.7e-06 intercept= 0.19 p_value= 1e-05



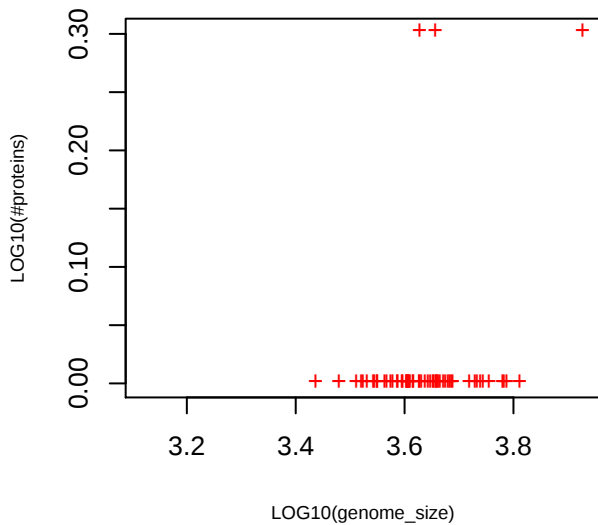
[T] COG2766 Putative Ser protein kinase

slope= -0.0038 p_value= 3.7e-05 intercept= 0.0047 p_value= 5.8e-06

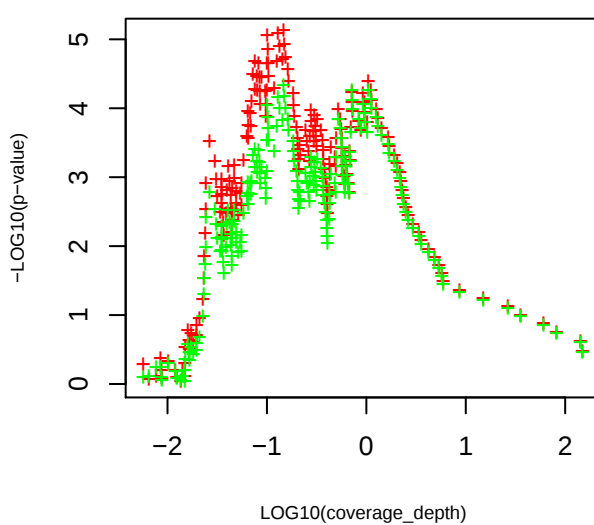


[T] COG2766 Putative Ser protein kinase

slope= 4.20 p_value= 7.7e-08 intercept= -17.70 p_value= 3.2e-10

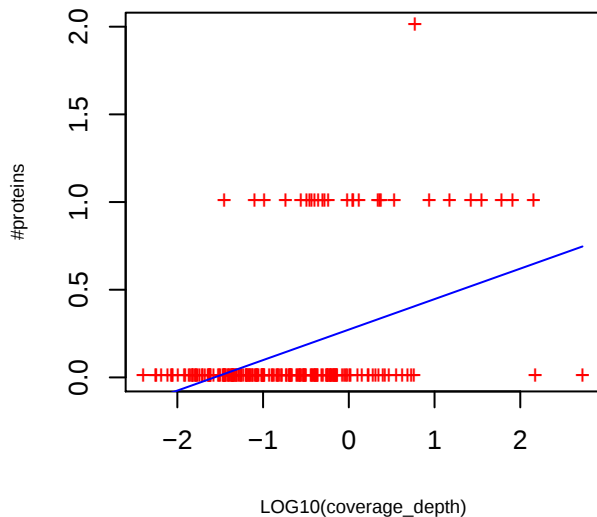


P-value curve ; red (unnorm), green (norm)



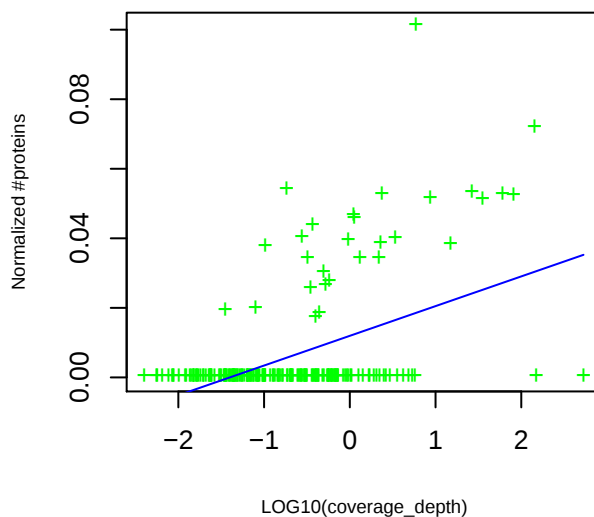
[S] COG4487 Uncharacterized protein conserved in bacteria

slope= 0.17 p_value= 1.2e-09 intercept= 0.27 p_value= 4.9e-16



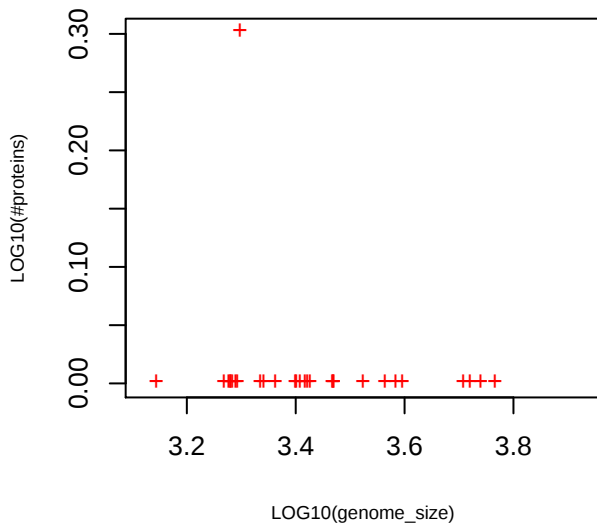
[S] COG4487 Uncharacterized protein conserved in bacteria

slope= 0.0085 p_value= 1.3e-12 intercept= 0.012 p_value= 1.4e-17

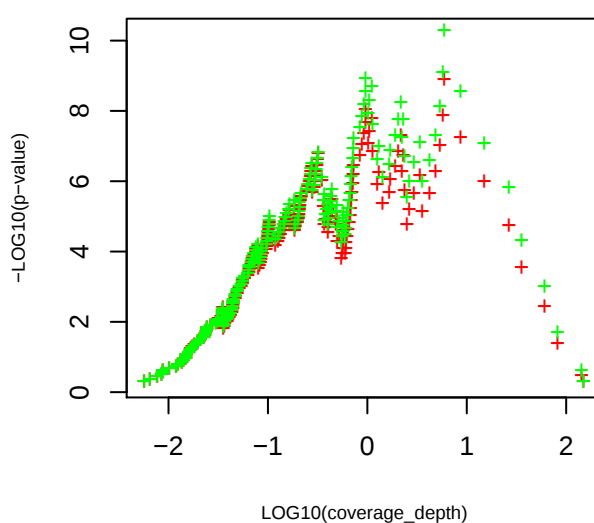


[S] COG4487 Uncharacterized protein conserved in bacteria

slope= -2.54 p_value= 3.5e-05 intercept= 5.58 p_value= 0.0093

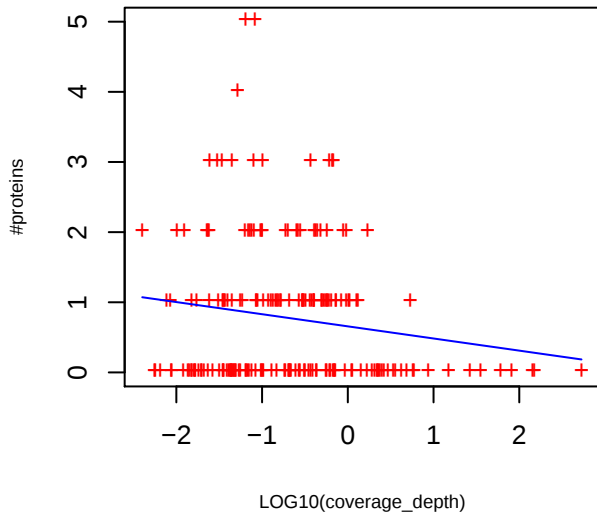


P-value curve ; red (unnorm), green (norm)



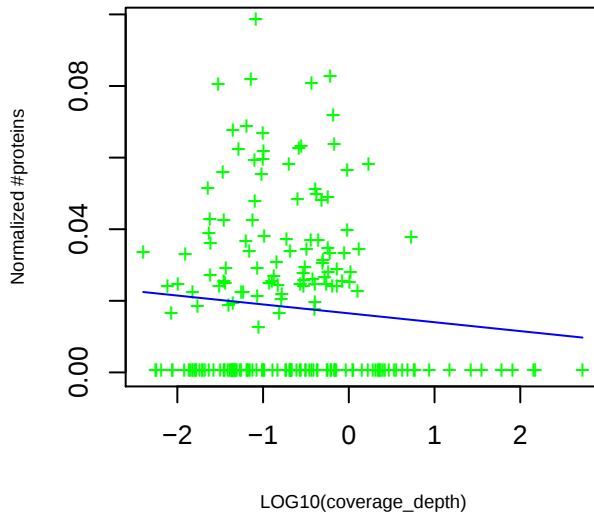
[R] COG3568 Metal-dependent hydrolase

slope= -0.17 p_value= 0.032 intercept= 0.66 p_value= 8.3e-12



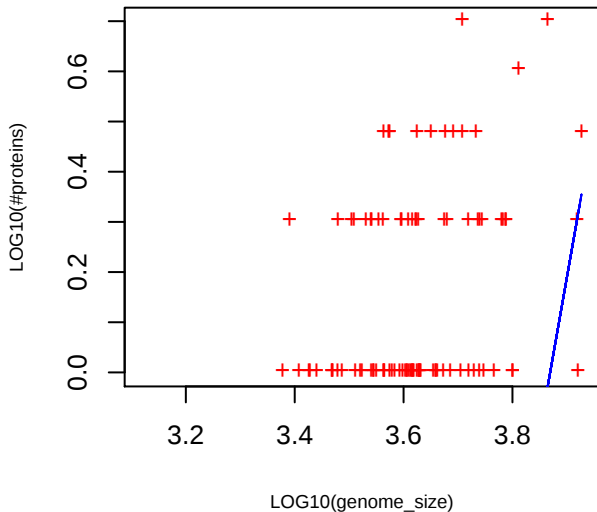
[R] COG3568 Metal-dependent hydrolase

slope= -0.0025 p_value= 0.17 intercept= 0.017 p_value= 7.9e-14

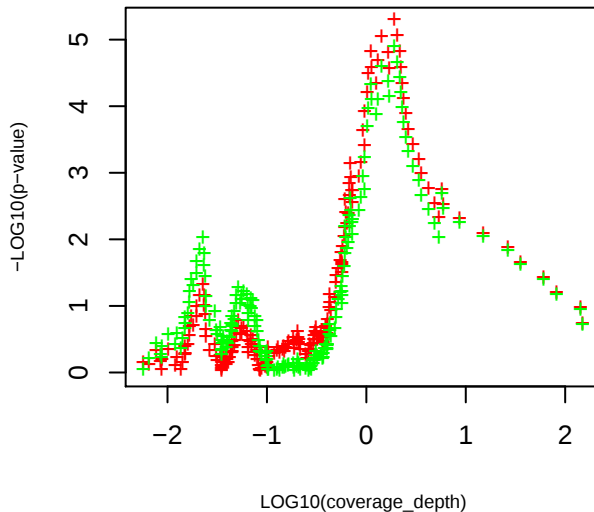


[R] COG3568 Metal-dependent hydrolase

slope= 6.16 p_value= 8.3e-13 intercept= -23.83 p_value= 1.2e-14

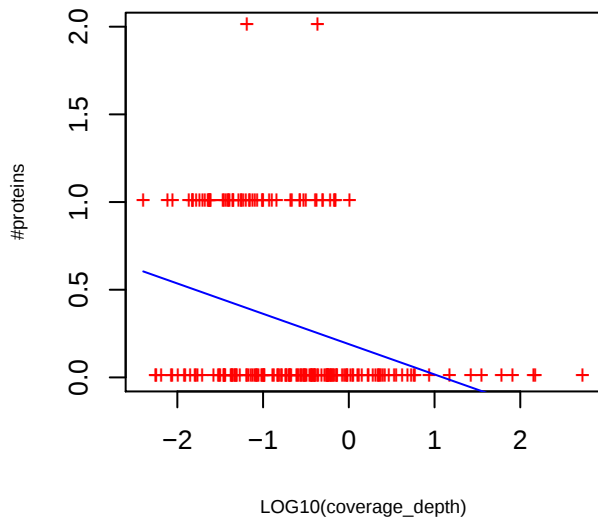


P-value curve ; red (unnorm), green (norm)



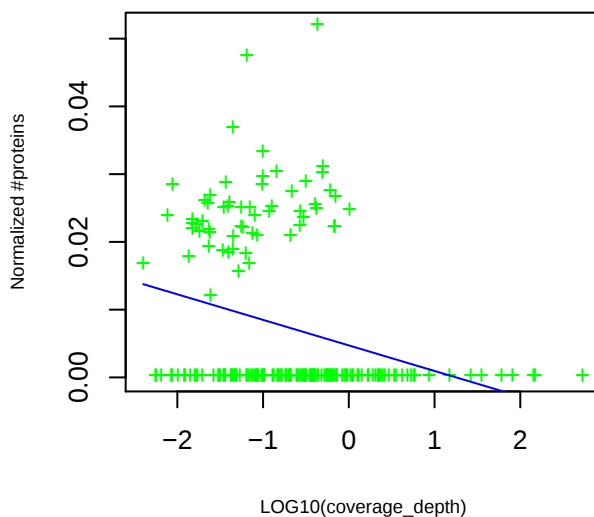
[S] COG2718 Uncharacterized conserved protein

slope= -0.17 p_value= 5e-06 intercept= 0.19 p_value= 8.7e-06



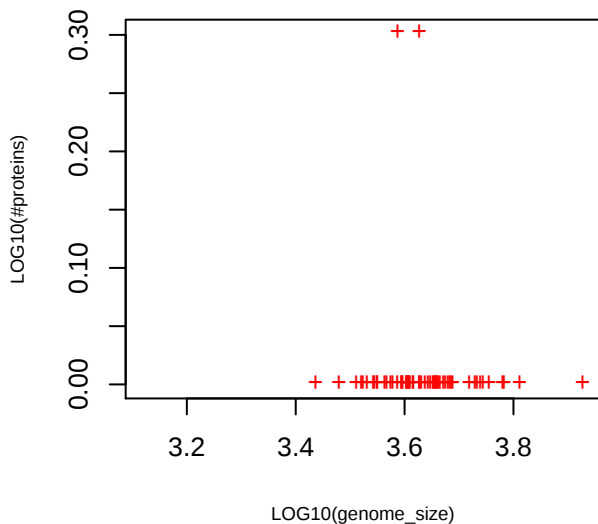
[S] COG2718 Uncharacterized conserved protein

slope= -0.0038 p_value= 4.6e-05 intercept= 0.0047 p_value= 6.8e-06

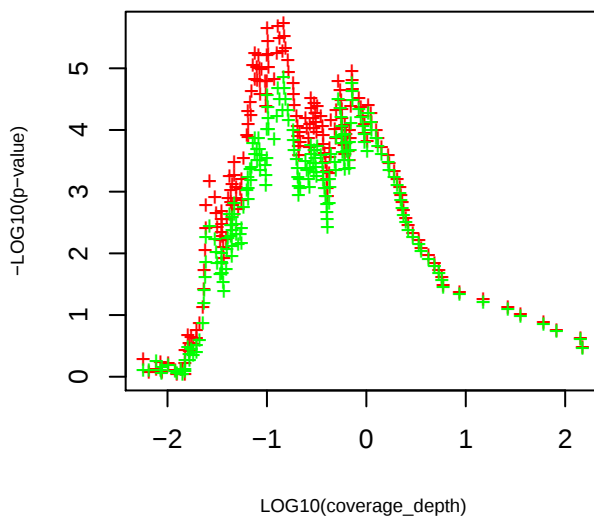


[S] COG2718 Uncharacterized conserved protein

slope= 4.03 p_value= 2.7e-07 intercept= -17.08 p_value= 1.4e-09

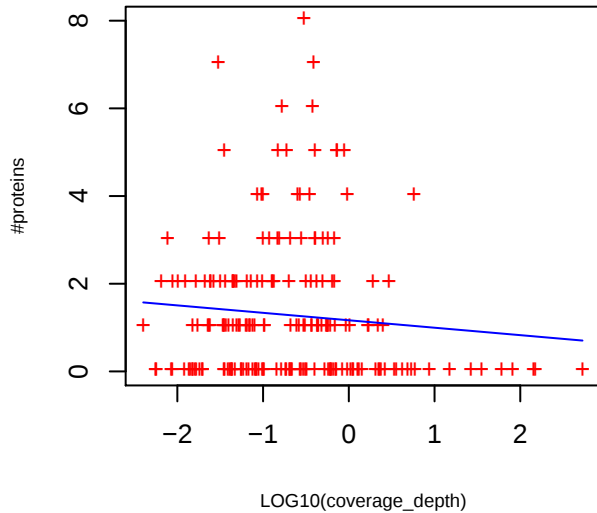


P-value curve ; red (unnorm), green (norm)



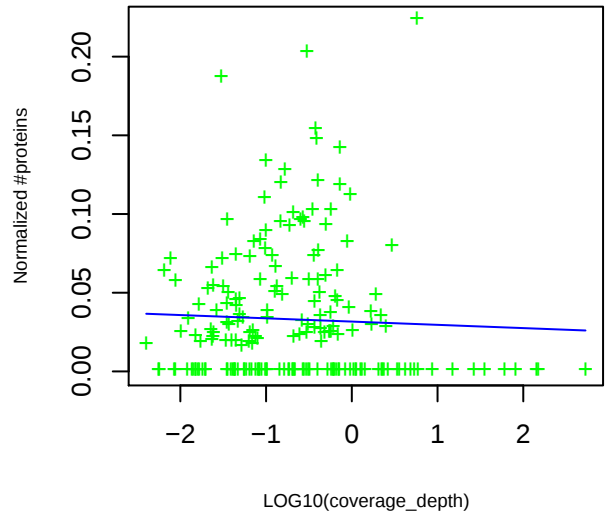
[Q] COG2132 Putative multicopper oxidases

slope= -0.17 p_value= 0.19 intercept= 1.17 p_value= 9.7e-14



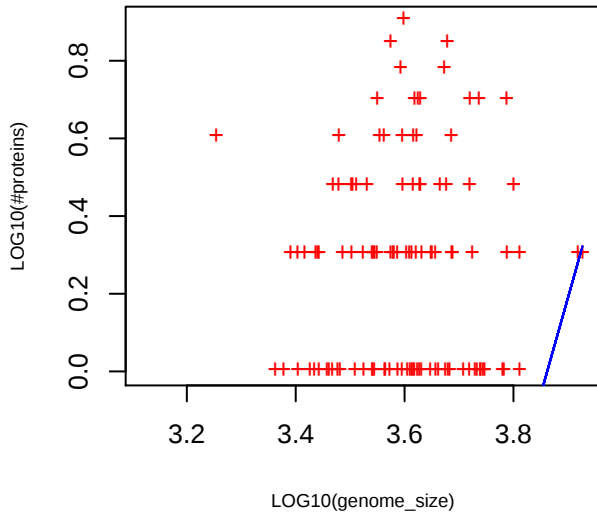
[Q] COG2132 Putative multicopper oxidases

slope= -0.0021 p_value= 0.54 intercept= 0.032 p_value= 2.3e-14

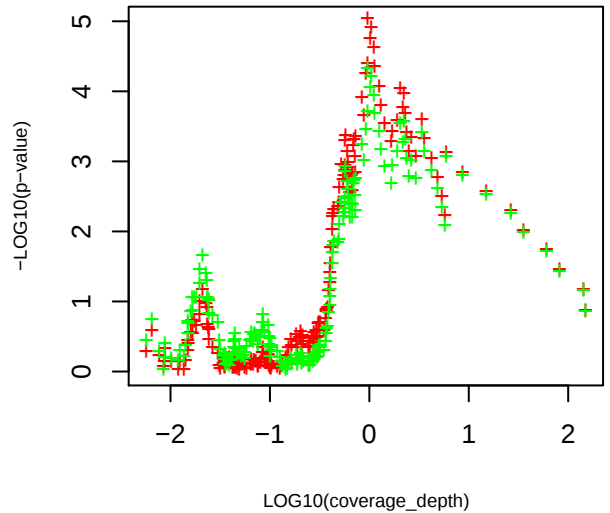


[Q] COG2132 Putative multicopper oxidases

slope= 4.97 p_value= 3.6e-08 intercept= -19.18 p_value= 2.6e-09

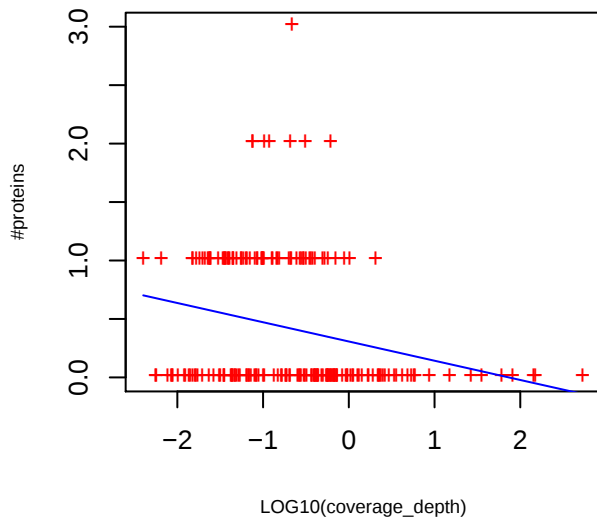


P-value curve ; red (unnorm), green (norm)



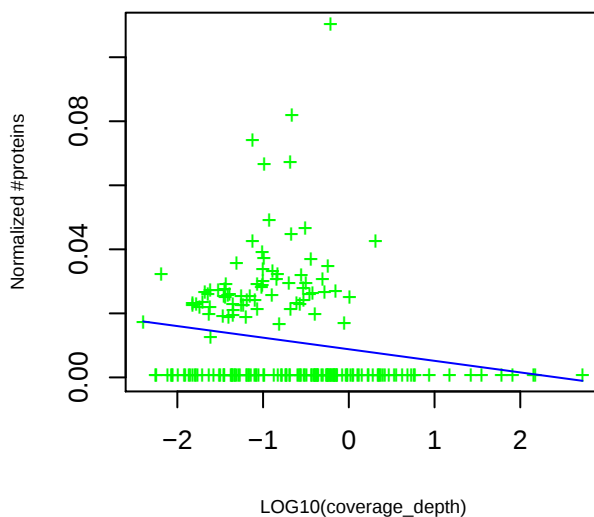
[E] COG2902 NAD-specific glutamate dehydrogenase

slope= -0.16 p_value= 4e-04 intercept= 0.31 p_value= 1.2e-08



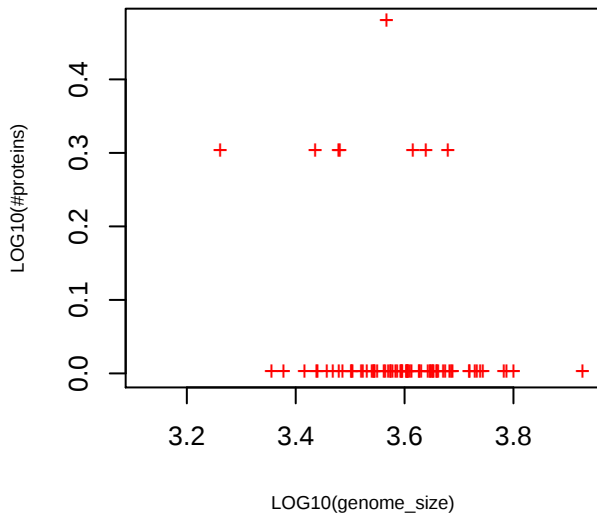
[E] COG2902 NAD-specific glutamate dehydrogenase

slope= -0.0036 p_value= 0.0091 intercept= 0.0088 p_value= 5e-08

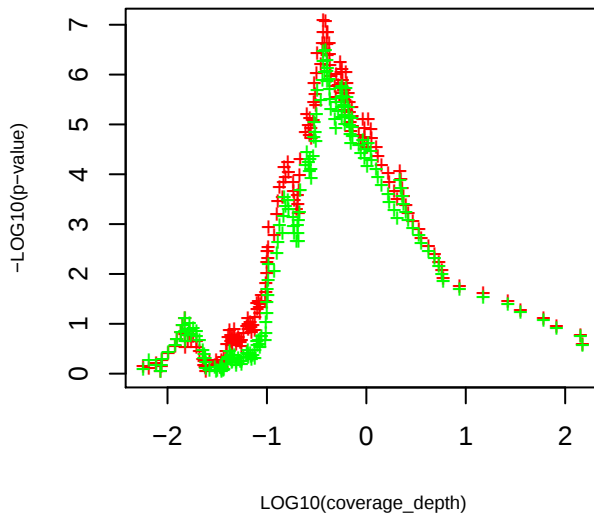


[E] COG2902 NAD-specific glutamate dehydrogenase

slope= 2.75 p_value= 0.0012 intercept= -12.22 p_value= 5.9e-05

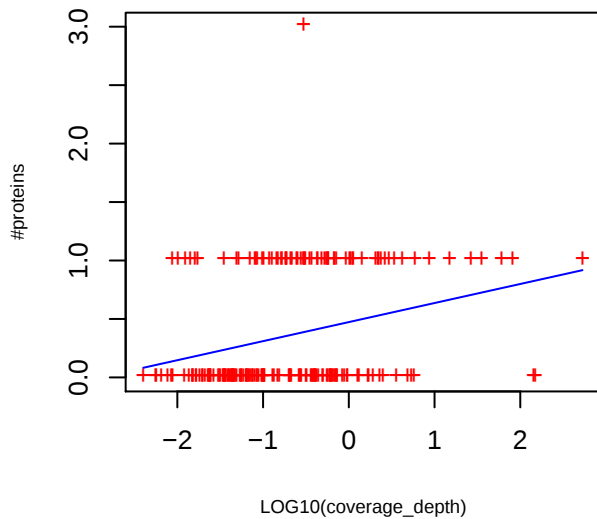


P-value curve ; red (unnorm), green (norm)



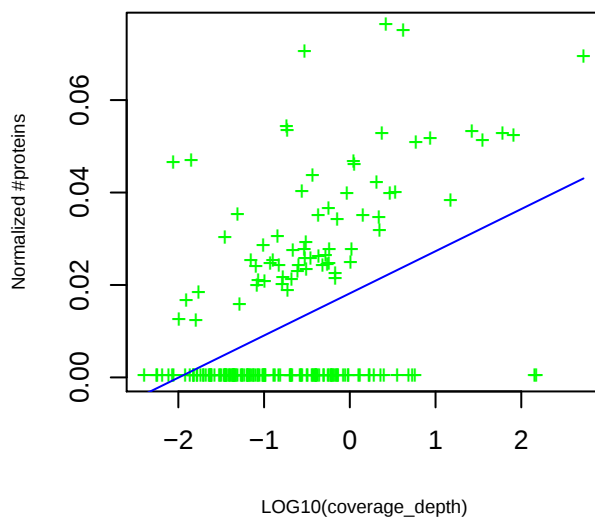
[R] COG3769 Predicted hydrolase (HAD superfamily)

slope= 0.16 p_value= 5e-05 intercept= 0.47 p_value= 3.3e-21



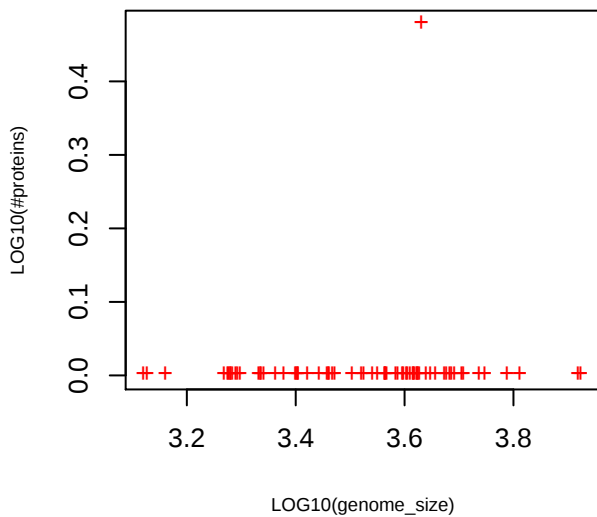
[R] COG3769 Predicted hydrolase (HAD superfamily)

slope= 0.0091 p_value= 7.7e-11 intercept= 0.018 p_value= 1.1e-25

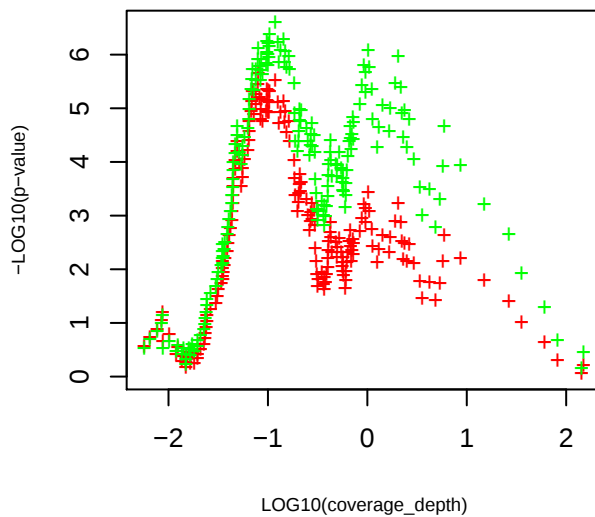


[R] COG3769 Predicted hydrolase (HAD superfamily)

slope= -1.57 p_value= 0.061 intercept= 2.97 p_value= 0.32

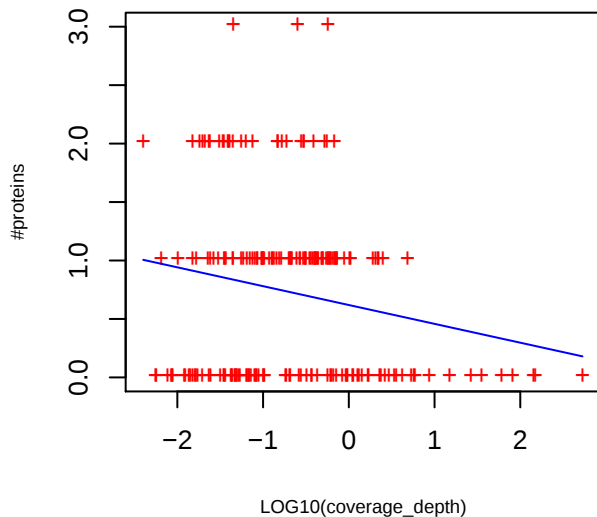


P-value curve ; red (unnorm), green (norm)



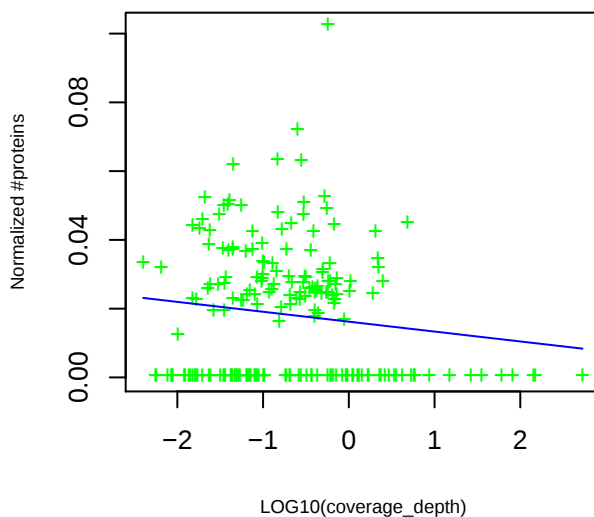
[O] COG4235 Cytochrome c biogenesis factor

slope= -0.16 p_value= 0.0075 intercept= 0.62 p_value= 5.6e-17



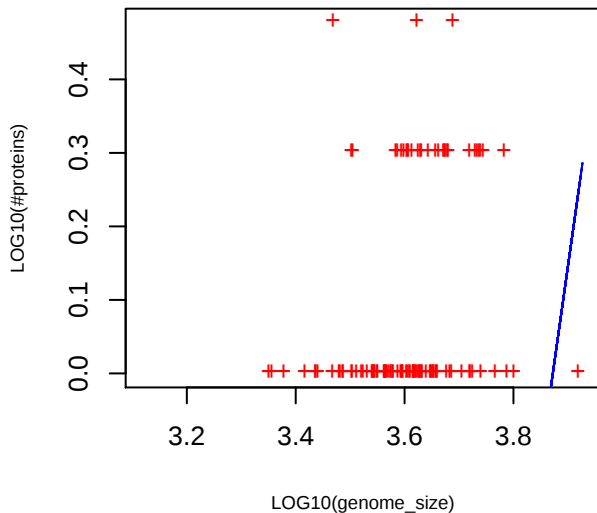
[O] COG4235 Cytochrome c biogenesis factor

slope= -0.0029 p_value= 0.058 intercept= 0.016 p_value= 6.5e-18

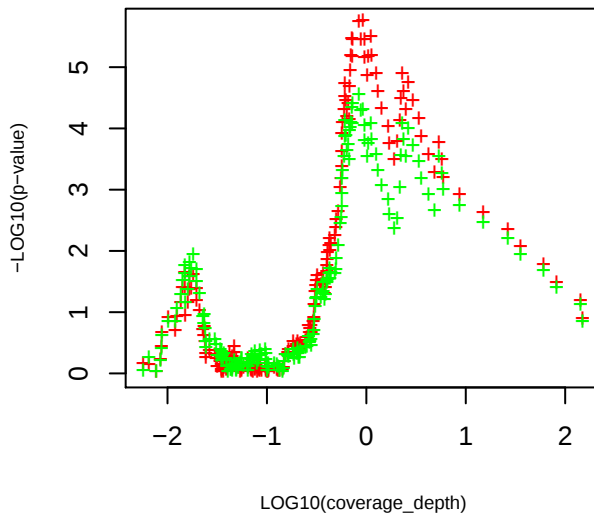


[O] COG4235 Cytochrome c biogenesis factor

slope= 5.25 p_value= 8.3e-10 intercept= -20.32 p_value= 3.1e-11

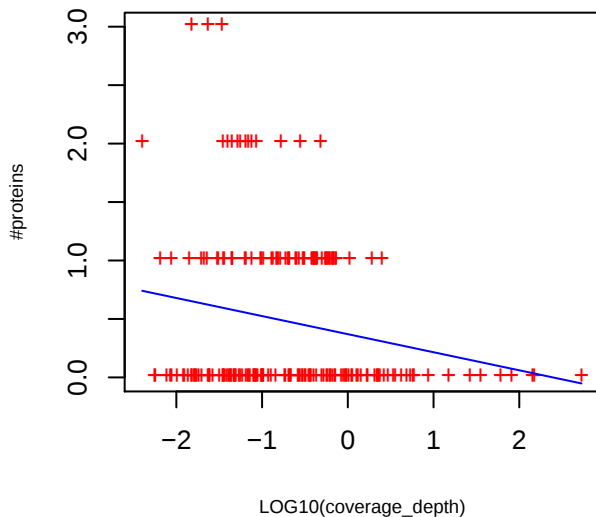


P-value curve ; red (unnorm), green (norm)



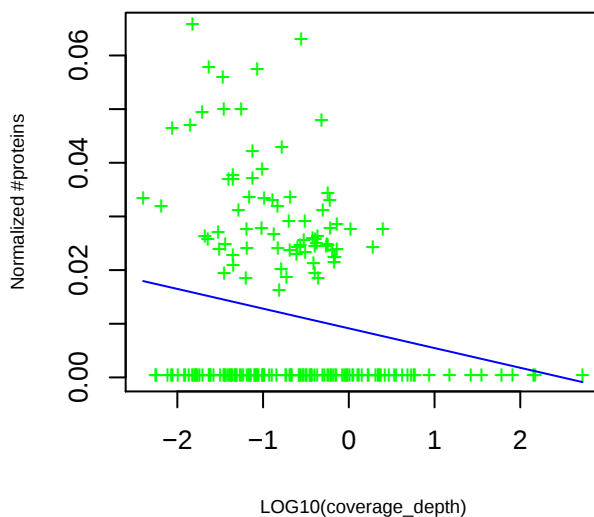
[NU] COG2064 Flp pilus assembly protein TadC

slope= -0.15 p_value= 0.0047 intercept= 0.37 p_value= 6.9e-09



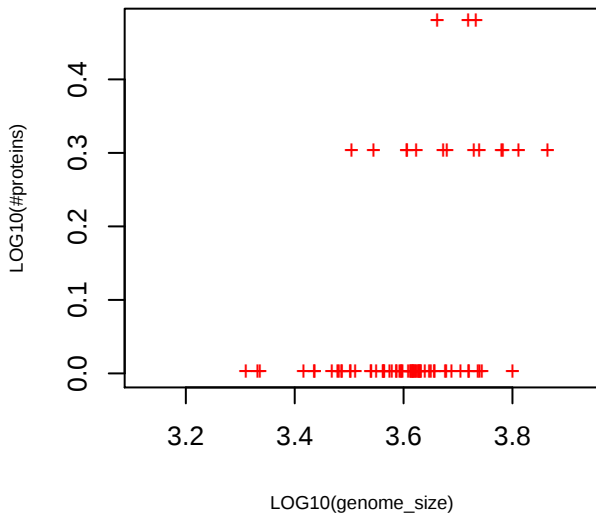
[NU] COG2064 Flp pilus assembly protein TadC

slope= -0.0037 p_value= 0.0049 intercept= 0.0091 p_value= 2.2e-09

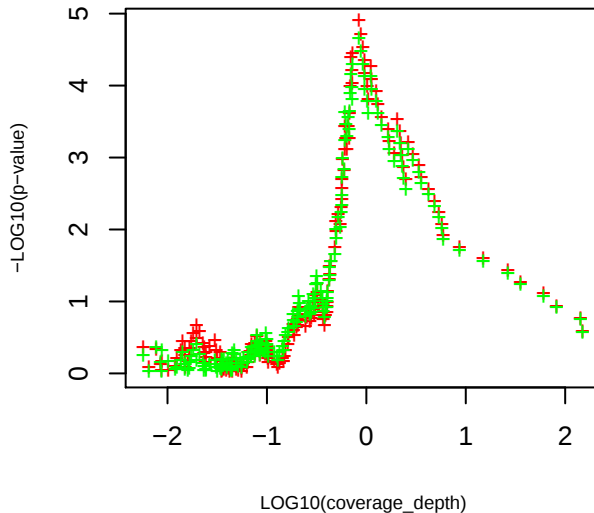


[NU] COG2064 Flp pilus assembly protein TadC

slope= 3.77 p_value= 9.4e-06 intercept= -15.81 p_value= 2.1e-07

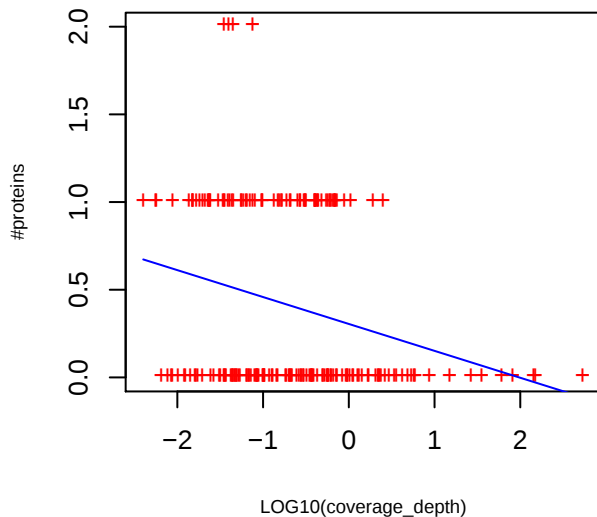


P-value curve ; red (unnorm), green (norm)



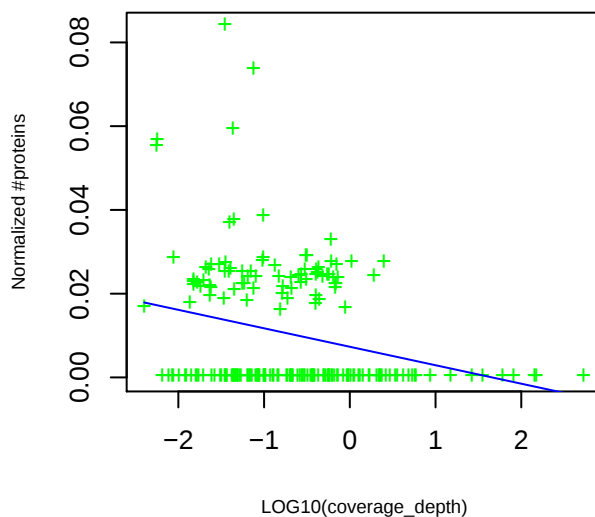
[G] COG1015 Phosphopentomutase

slope= -0.15 p_value= 0.00026 intercept= 0.30 p_value= 5.1e-10



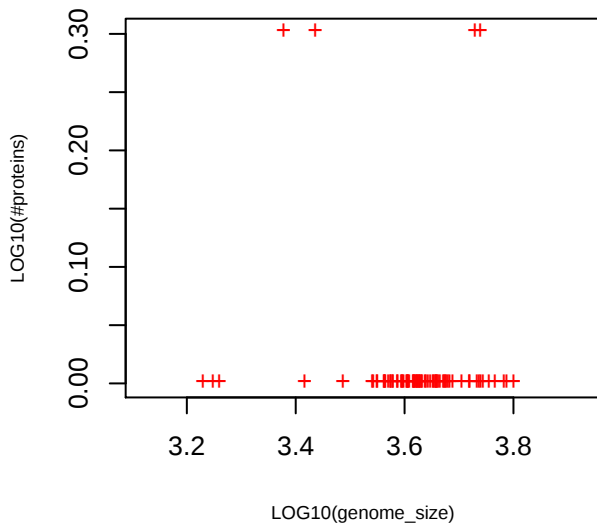
[G] COG1015 Phosphopentomutase

slope= -0.0044 p_value= 0.00016 intercept= 0.0073 p_value= 5.3e-08

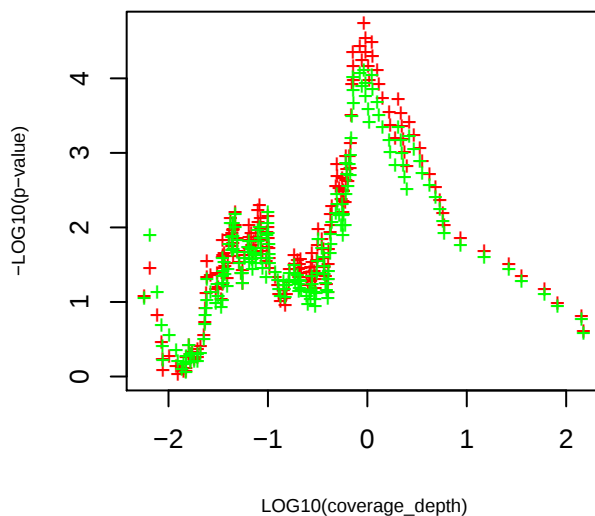


[G] COG1015 Phosphopentomutase

slope= 4.23 p_value= 4.3e-07 intercept= -17.43 p_value= 6.4e-09

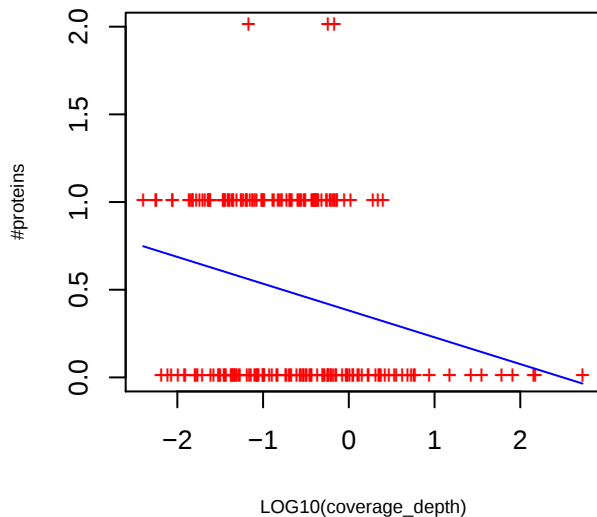


P-value curve ; red (unnorm), green (norm)



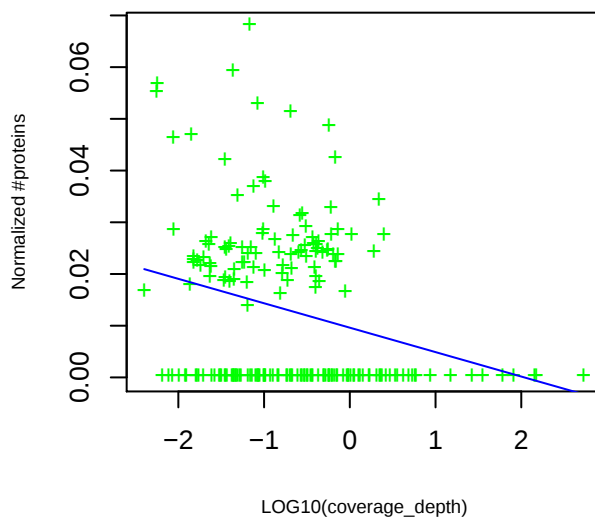
[F] COG0213 Thymidine phosphorylase

slope= -0.15 p_value= 0.00026 intercept= 0.38 p_value= 2.7e-14



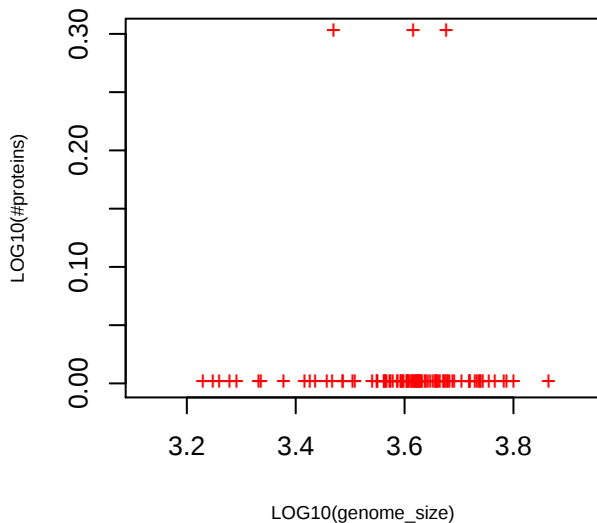
[F] COG0213 Thymidine phosphorylase

slope= -0.0047 p_value= 9.6e-05 intercept= 0.0096 p_value= 1.4e-11

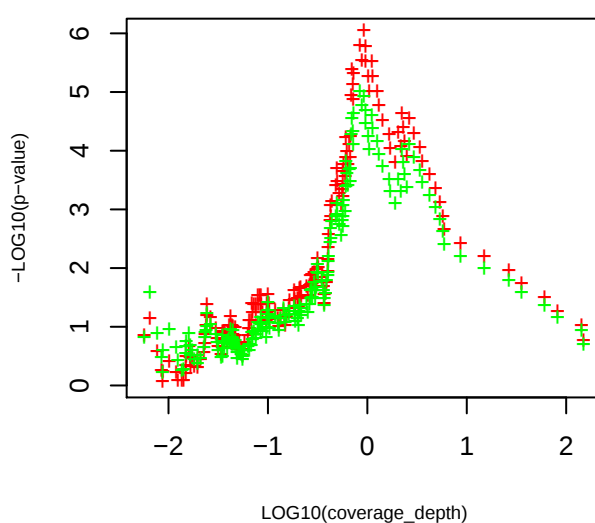


[F] COG0213 Thymidine phosphorylase

slope= 3.75 p_value= 1.3e-05 intercept= -15.41 p_value= 5.8e-07

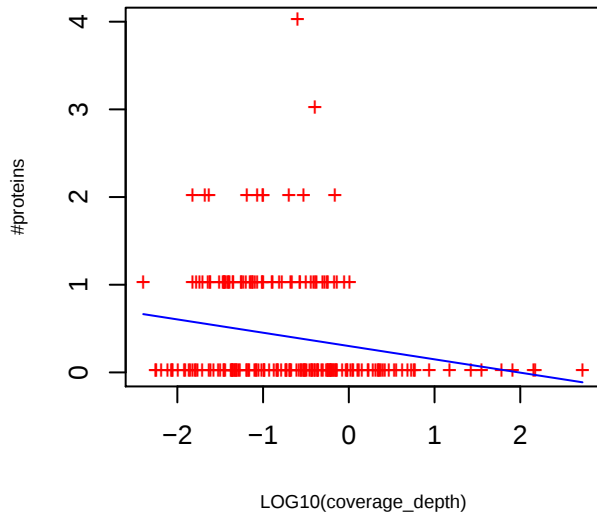


P-value curve ; red (unnorm), green (norm)



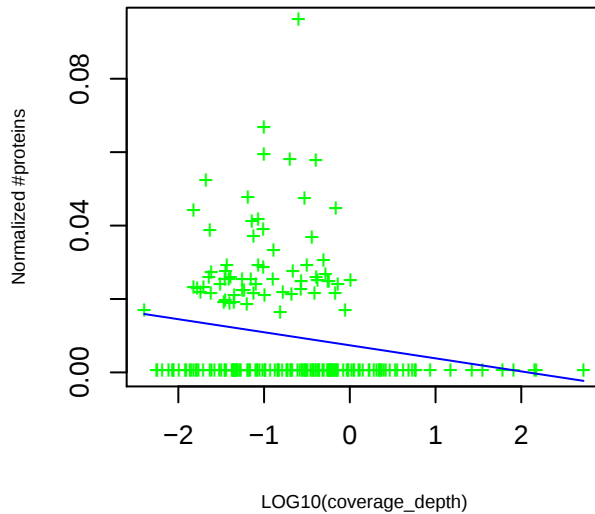
[P] COG3213 Uncharacterized protein involved in response to NO

slope= -0.15 p_value= 0.0038 intercept= 0.30 p_value= 6.3e-07



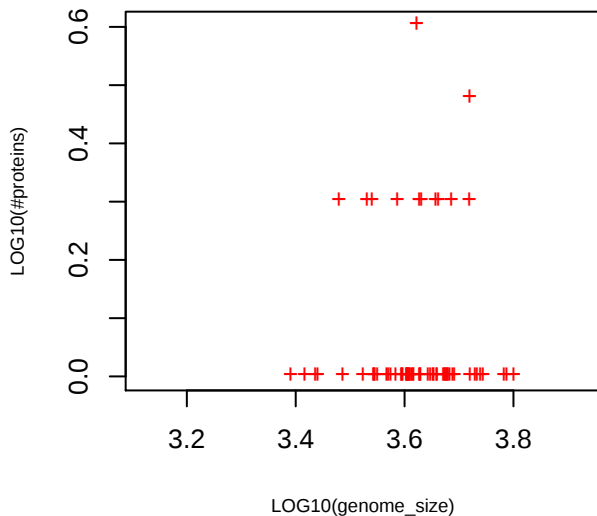
[P] COG3213 Uncharacterized protein involved in response to NO

slope= -0.0036 p_value= 0.0058 intercept= 0.0074 p_value= 6.7e-07

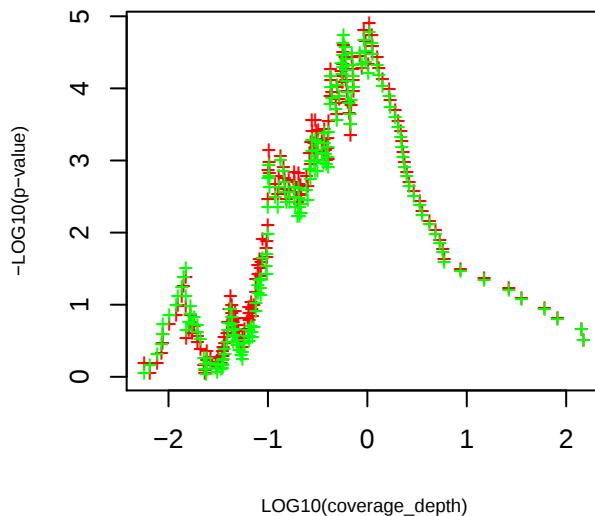


[P] COG3213 Uncharacterized protein involved in response to NO

slope= 3.91 p_value= 1.8e-06 intercept= -16.51 p_value= 2.0e-08

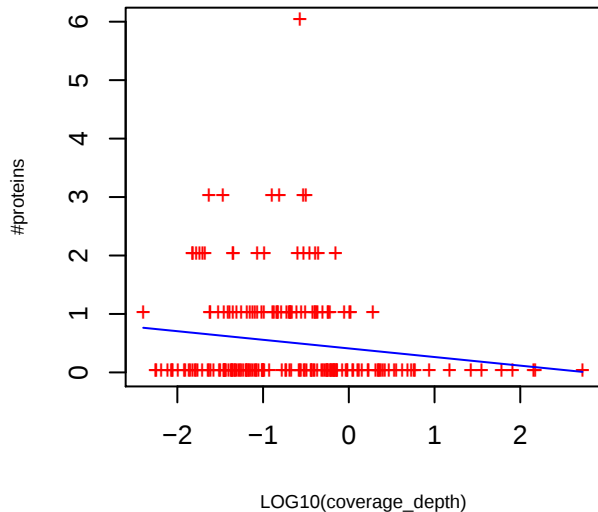


P-value curve ; red (unnorm), green (norm)



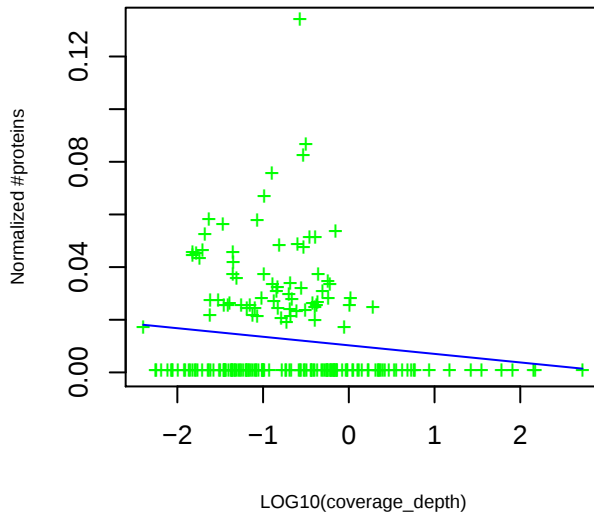
[M] COG3713 Outer membrane protein V

slope= -0.15 p_value= 0.033 intercept= 0.41 p_value= 3.1e-07



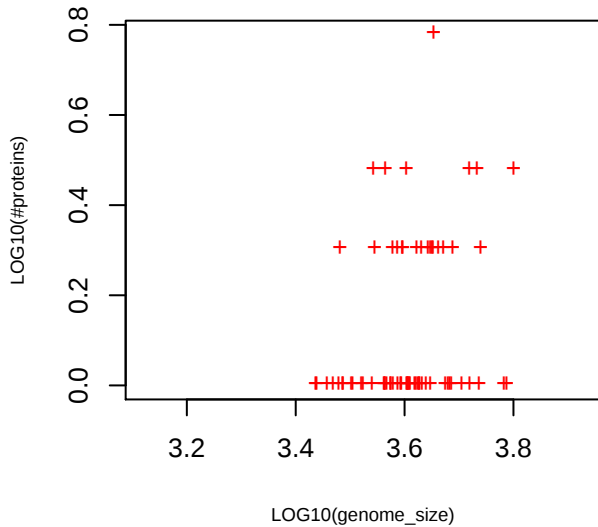
[M] COG3713 Outer membrane protein V

slope= -0.0033 p_value= 0.049 intercept= 0.010 p_value= 9e-08

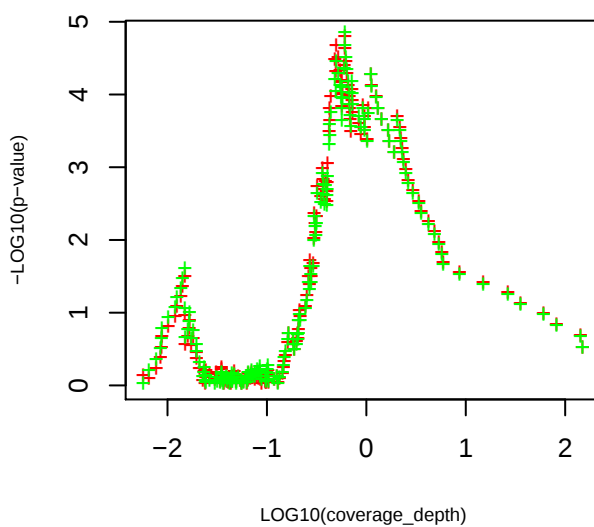


[M] COG3713 Outer membrane protein V

slope= 3.42 p_value= 5.6e-05 intercept= -14.70 p_value= 1.3e-06

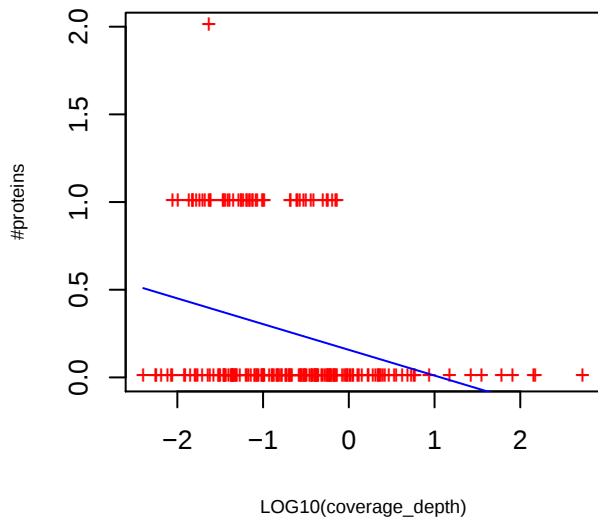


P-value curve ; red (unnorm), green (norm)



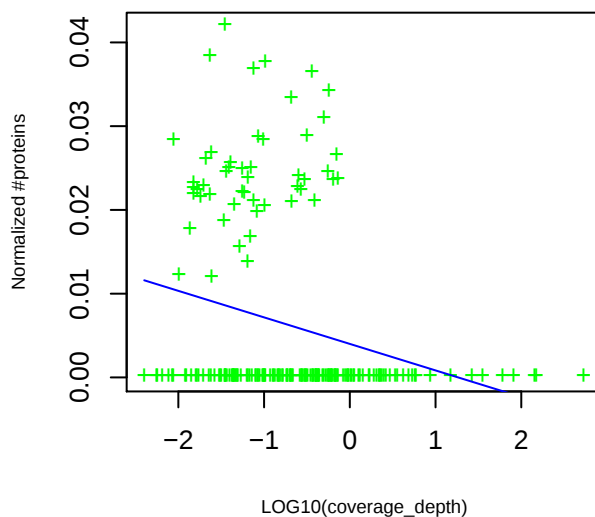
[S] COG3326 Predicted membrane protein

slope= -0.15 p_value= 3.3e-05 intercept= 0.16 p_value= 7.8e-05



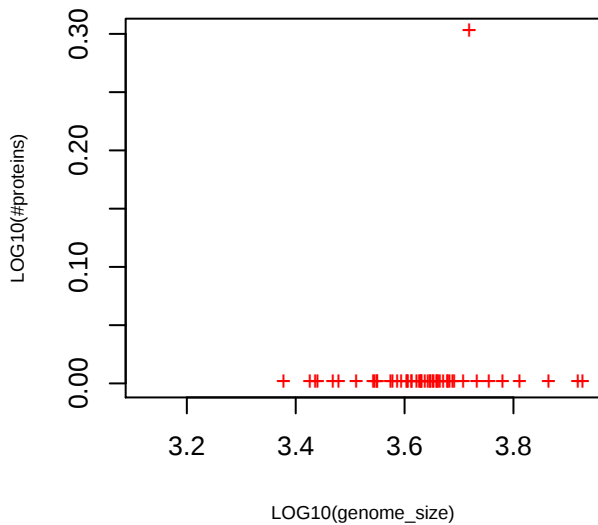
[S] COG3326 Predicted membrane protein

slope= -0.0032 p_value= 0.00031 intercept= 0.004 p_value= 5.8e-05

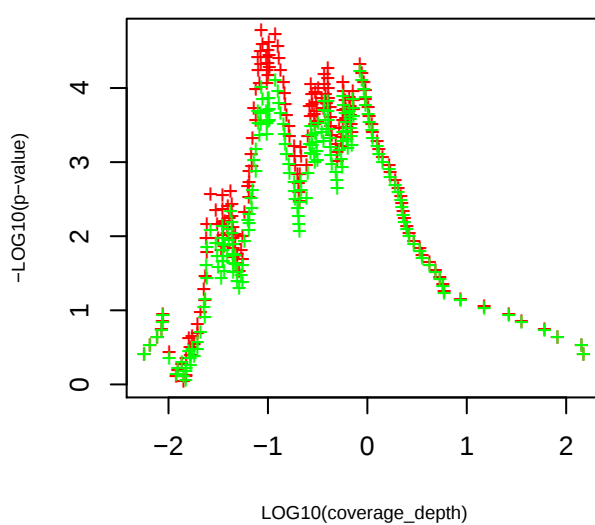


[S] COG3326 Predicted membrane protein

slope= 3.39 p_value= 5.9e-06 intercept= -15.01 p_value= 2.5e-08

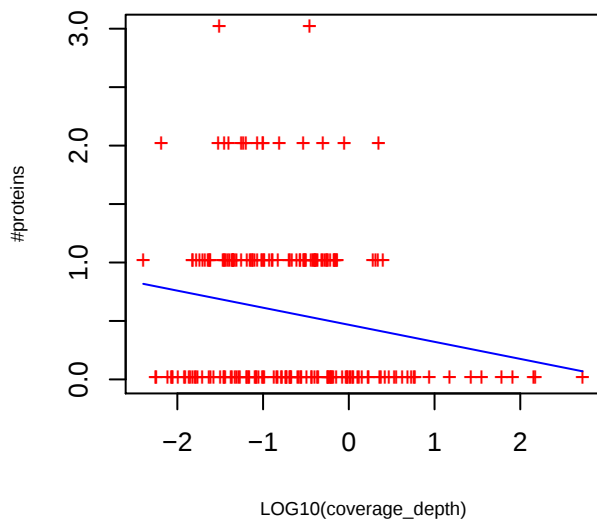


P-value curve ; red (unnorm), green (norm)



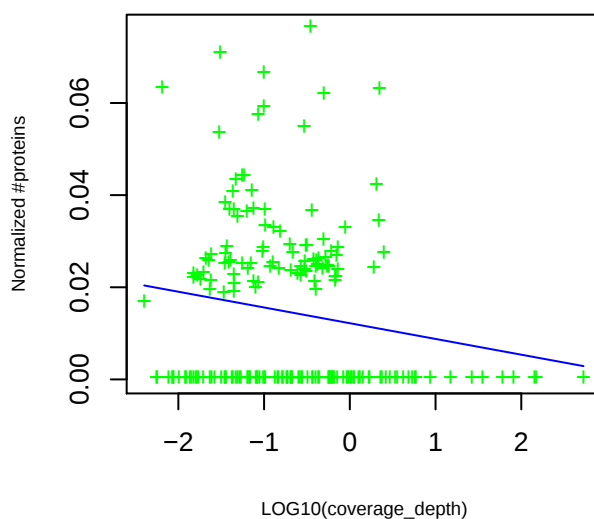
[M] COG2982 Uncharacterized protein involved in outer membrane biogenesis

slope= -0.15 p_value= 0.0068 intercept= 0.47 p_value= 4.6e-13



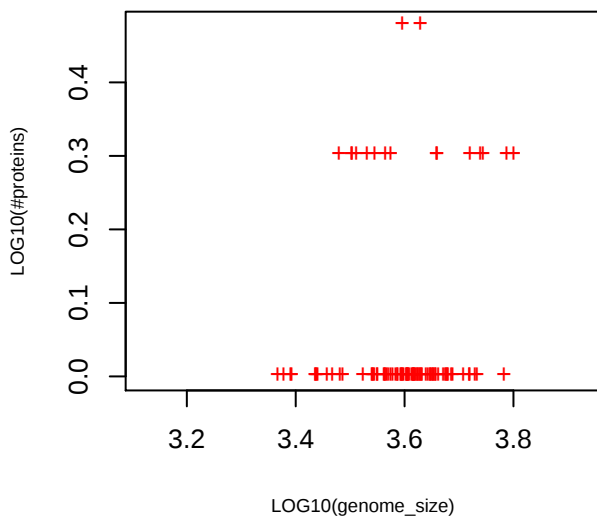
[M] COG2982 Uncharacterized protein involved in outer membrane biogenesis

slope= -0.0034 p_value= 0.016 intercept= 0.012 p_value= 6e-13

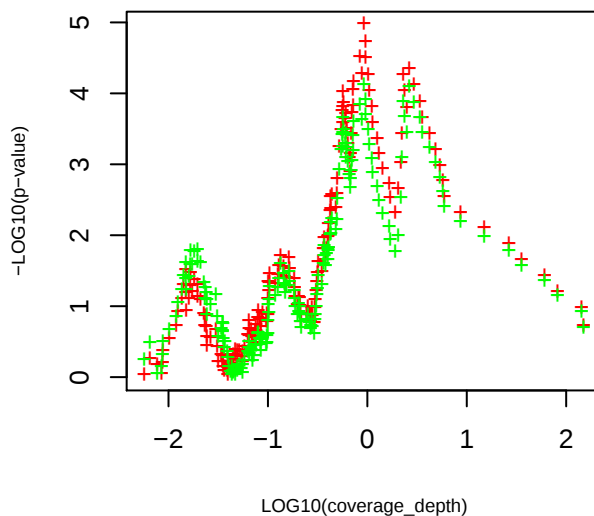


[M] COG2982 Uncharacterized protein involved in outer membrane biogenesis

slope= 3.82 p_value= 1.2e-05 intercept= -15.63 p_value= 5.5e-07

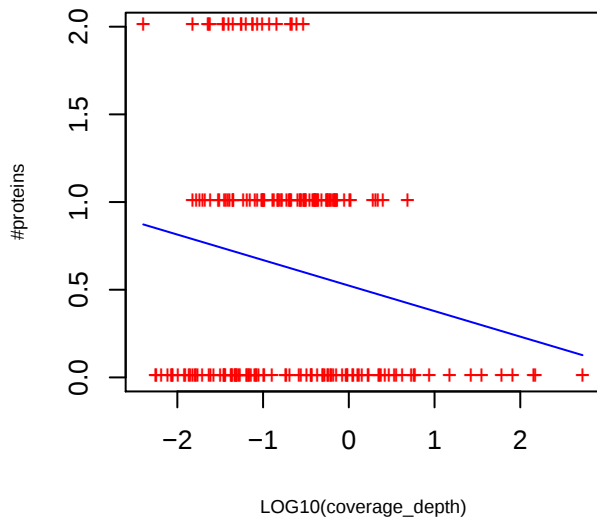


P-value curve ; red (unnorm), green (norm)



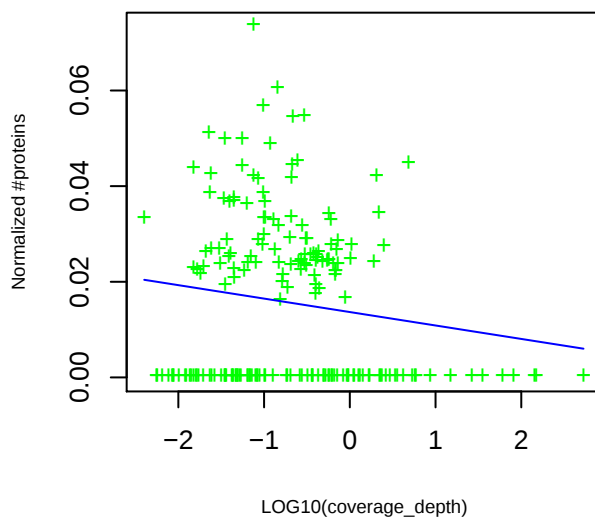
[C] COG4230 Delta 1-pyrroline-5-carboxylate dehydrogenase

slope= -0.15 p_value= 0.0069 intercept= 0.52 p_value= 1.4e-15



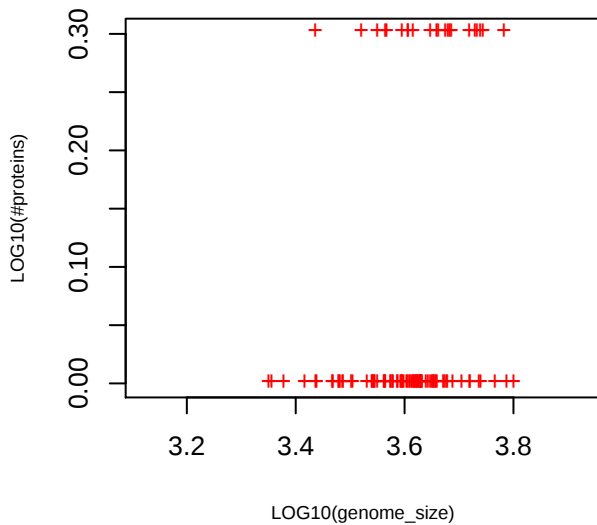
[C] COG4230 Delta 1-pyrroline-5-carboxylate dehydrogenase

slope= -0.0028 p_value= 0.039 intercept= 0.014 p_value= 2.7e-16

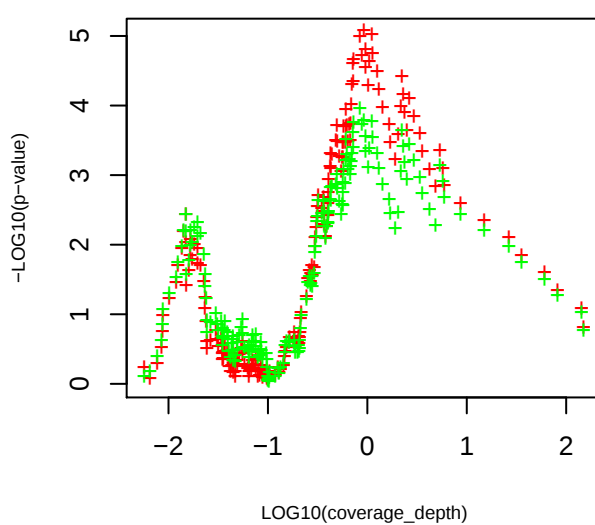


[C] COG4230 Delta 1-pyrroline-5-carboxylate dehydrogenase

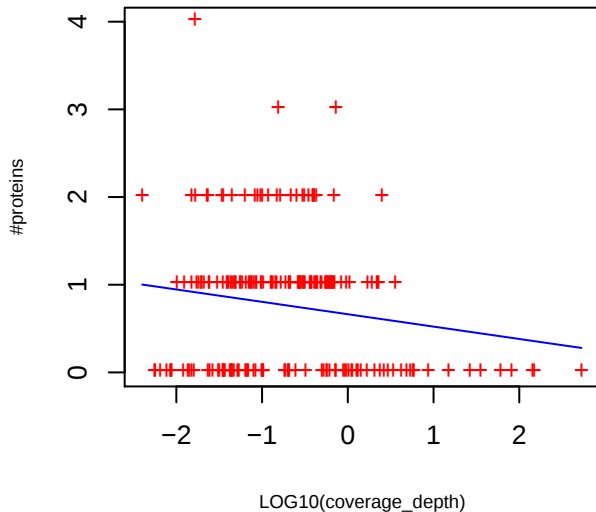
slope= 4.72 p_value= 4.7e-08 intercept= -18.64 p_value= 1.6e-09



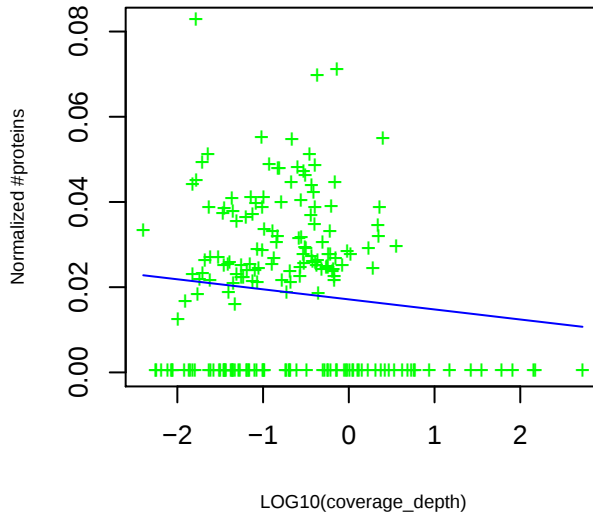
P-value curve ; red (unnorm), green (norm)



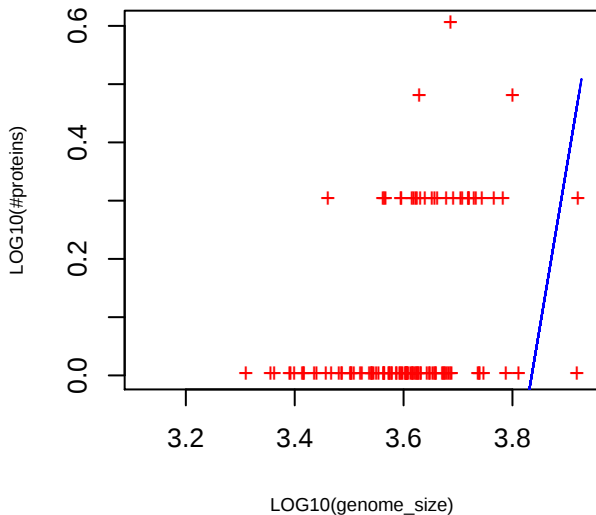
[C] COG2010 Cytochrome c, mono- and diheme variants
 slope= -0.14 p_value= 0.021 intercept= 0.66 p_value= 2.4e-18



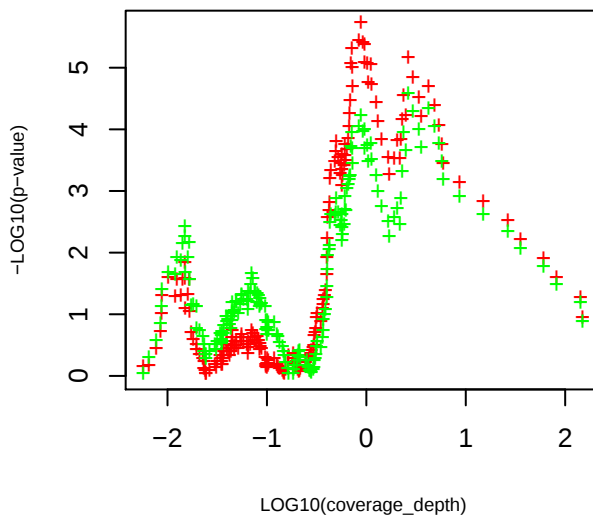
[C] COG2010 Cytochrome c, mono- and diheme variants
 slope= -0.0024 p_value= 0.11 intercept= 0.017 p_value= 1.7e-20



[C] COG2010 Cytochrome c, mono- and diheme variants
 slope= 5.56 p_value= 3.9e-11 intercept= -21.34 p_value= 1.4e-12

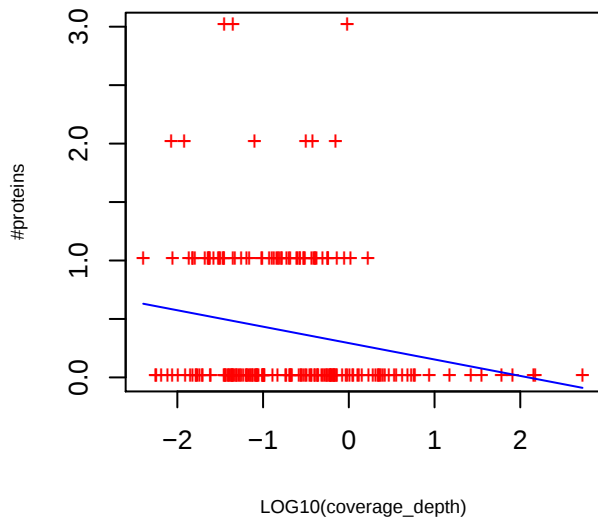


P-value curve ; red (unnorm), green (norm)



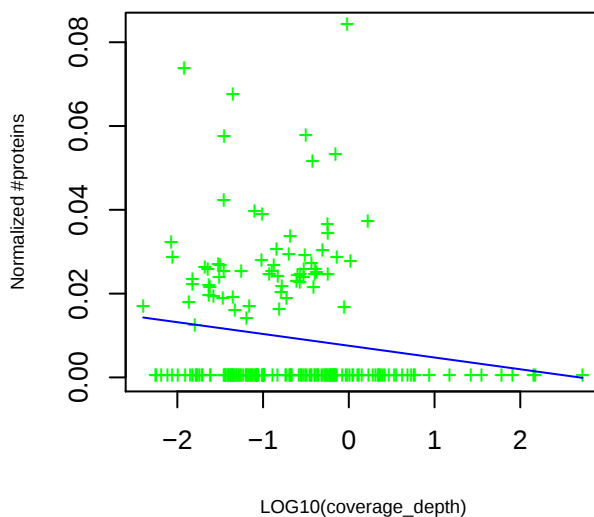
[S] COG1285 Uncharacterized membrane protein

slope= -0.14 p_value= 0.0047 intercept= 0.29 p_value= 3.2e-07



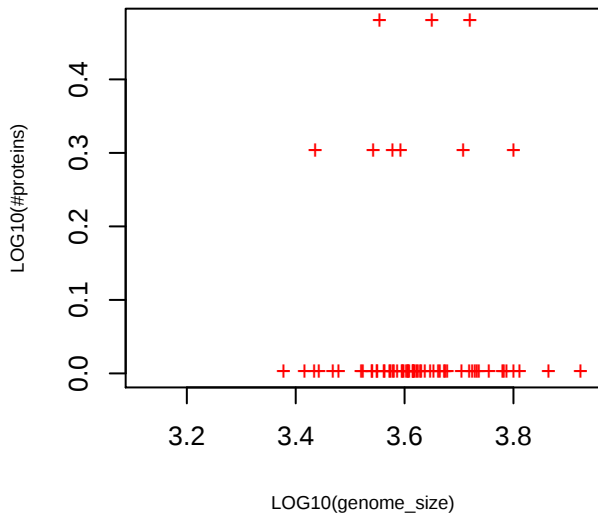
[S] COG1285 Uncharacterized membrane protein

slope= -0.0028 p_value= 0.025 intercept= 0.0076 p_value= 2.1e-07

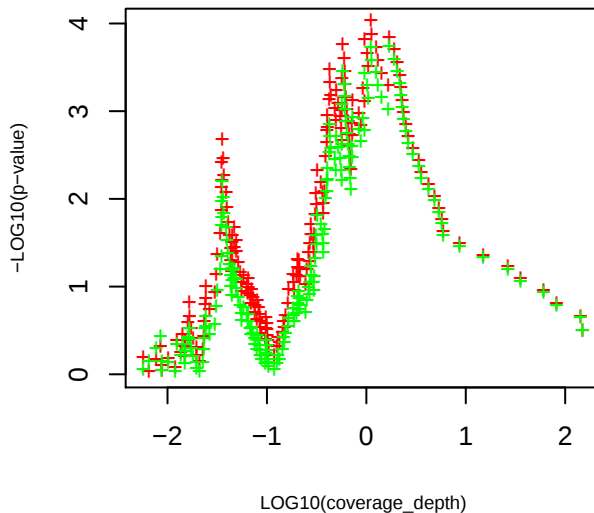


[S] COG1285 Uncharacterized membrane protein

slope= 4.14 p_value= 3.6e-07 intercept= -17.33 p_value= 3.0e-09

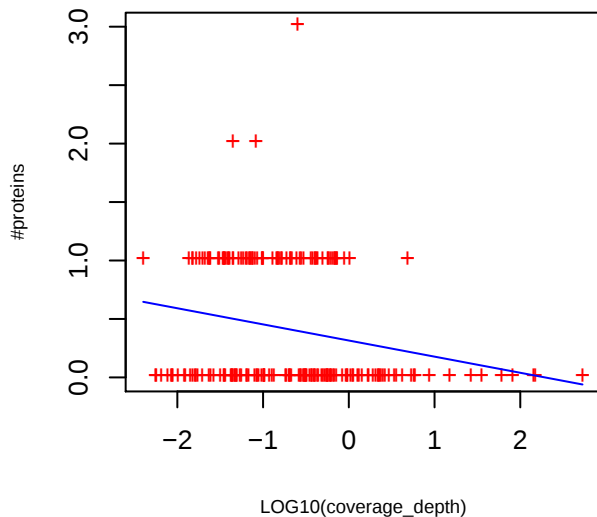


P-value curve ; red (unnorm), green (norm)



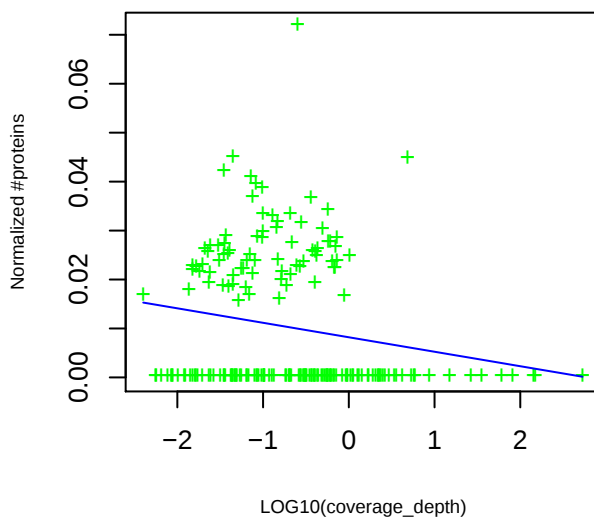
[S] COG2832 Uncharacterized protein conserved in bacteria

slope= -0.14 p_value= 0.0013 intercept= 0.32 p_value= 3.6e-10



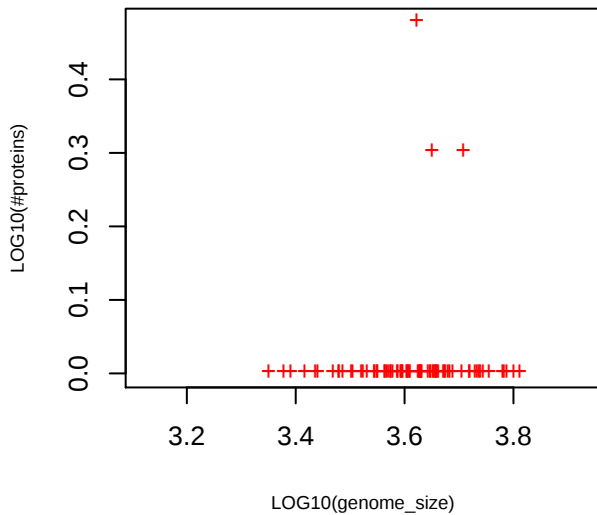
[S] COG2832 Uncharacterized protein conserved in bacteria

slope= -0.0030 p_value= 0.0073 intercept= 0.0082 p_value= 2.7e-10

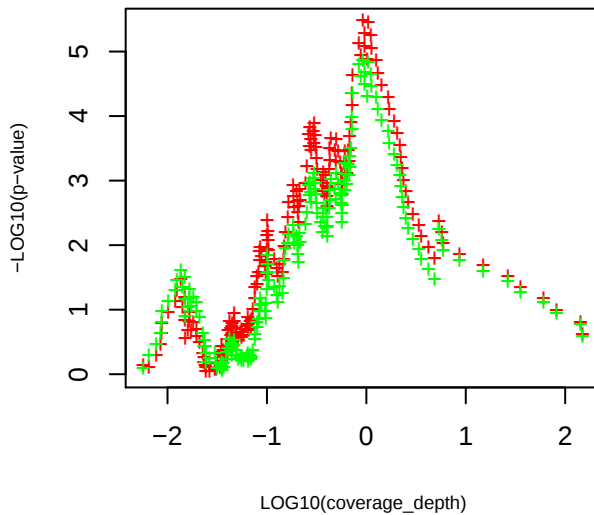


[S] COG2832 Uncharacterized protein conserved in bacteria

slope= 4.02 p_value= 1.6e-06 intercept= -16.69 p_value= 2.9e-08

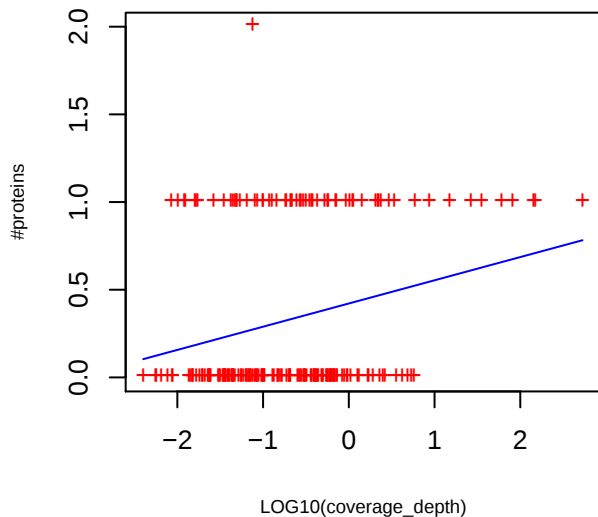


P-value curve ; red (unnorm), green (norm)



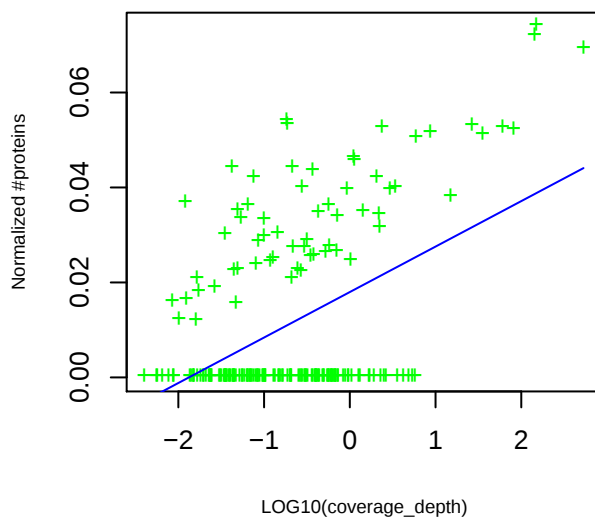
[R] COG4240 Predicted kinase

slope= 0.13 p_value= 5e-04 intercept= 0.42 p_value= 3.3e-19



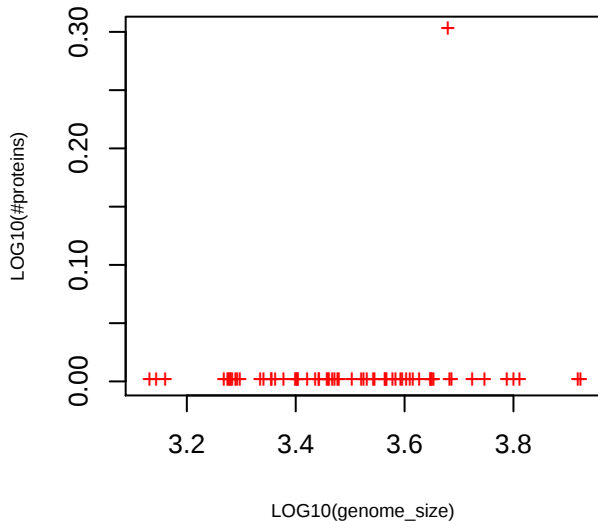
[R] COG4240 Predicted kinase

slope= 0.0096 p_value= 3.1e-12 intercept= 0.018 p_value= 2.5e-26

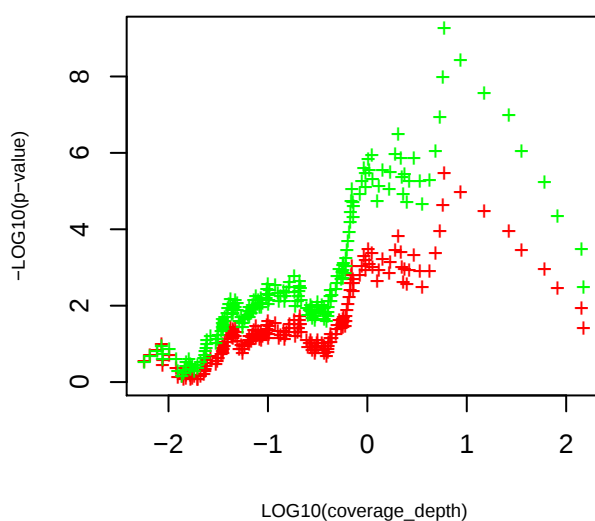


[R] COG4240 Predicted kinase

slope= -2.40 p_value= 0.0033 intercept= 5.82 p_value= 0.044

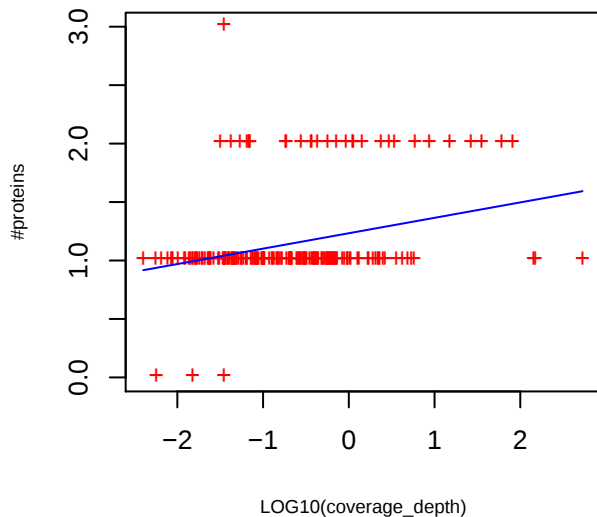


P-value curve ; red (unnorm), green (norm)



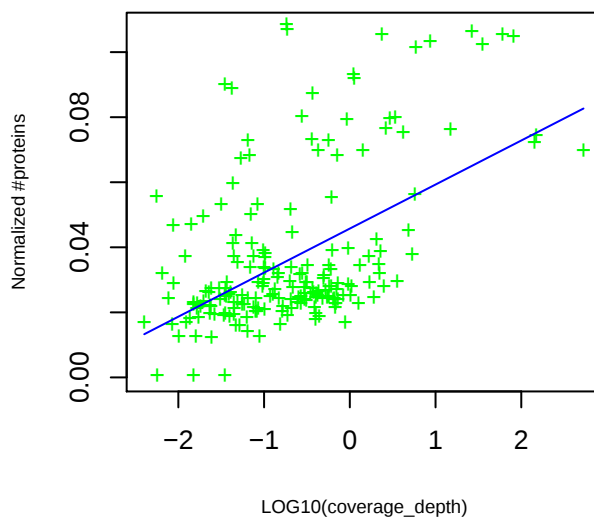
[F] COG0127 Xanthosine triphosphate pyrophosphatase

slope= 0.13 p_value= 3.2e-05 intercept= 1.23 p_value= 1.3e-86



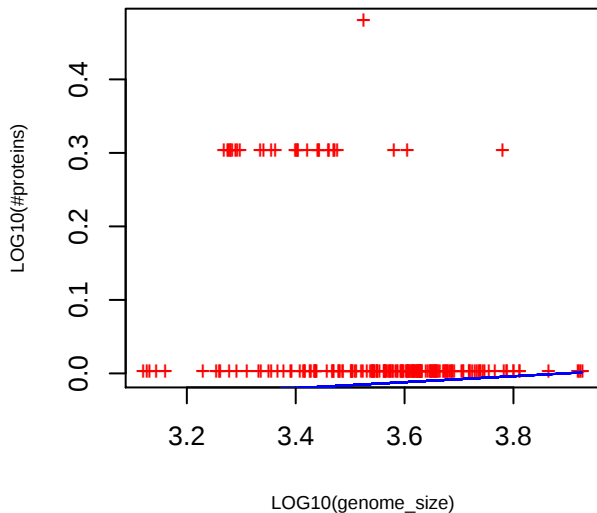
[F] COG0127 Xanthosine triphosphate pyrophosphatase

slope= 0.014 p_value= 2.6e-14 intercept= 0.046 p_value= 8.6e-62

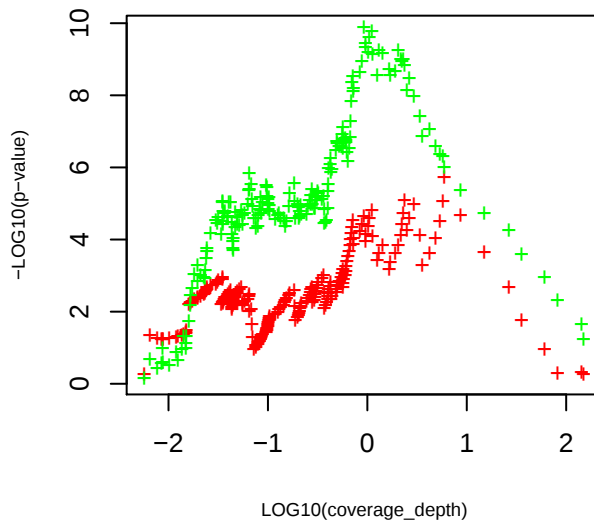


[F] COG0127 Xanthosine triphosphate pyrophosphatase

slope= 0.041 p_value= 0.86 intercept= -0.16 p_value= 0.84

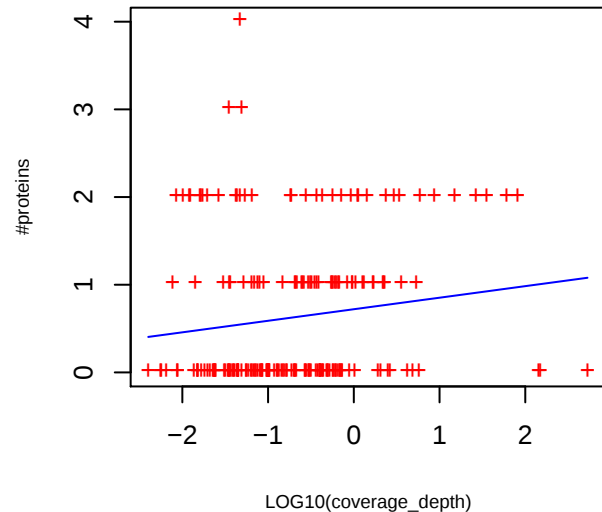


P-value curve ; red (unnorm), green (norm)



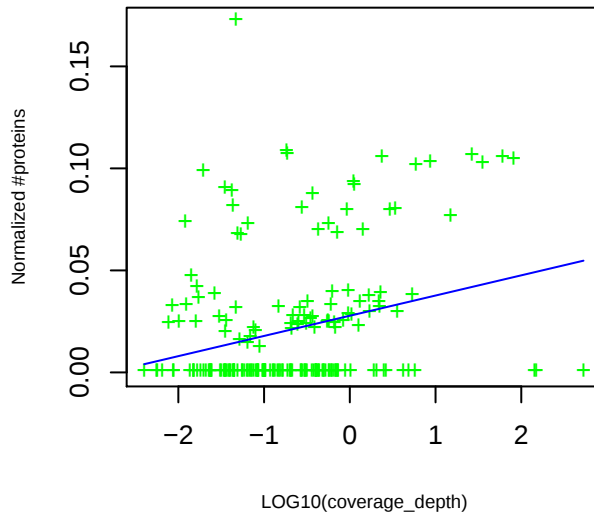
[H] COG1239 Mg-chelatase subunit ChII

slope= 0.13 p_value= 0.051 intercept= 0.72 p_value= 6.7e-18



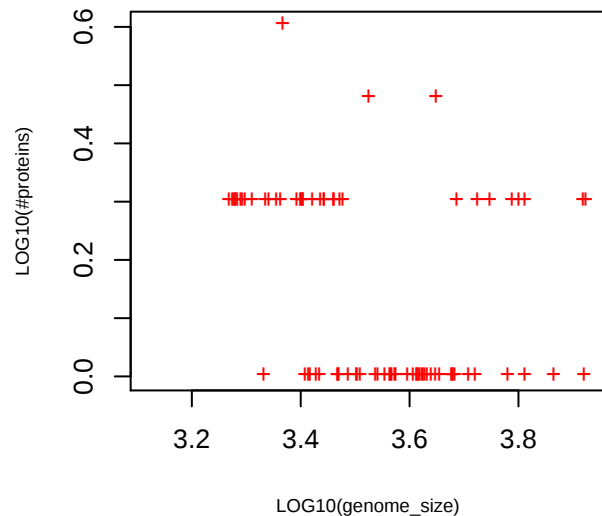
[H] COG1239 Mg-chelatase subunit ChII

slope= 0.01 p_value= 0.00012 intercept= 0.028 p_value= 1.5e-18

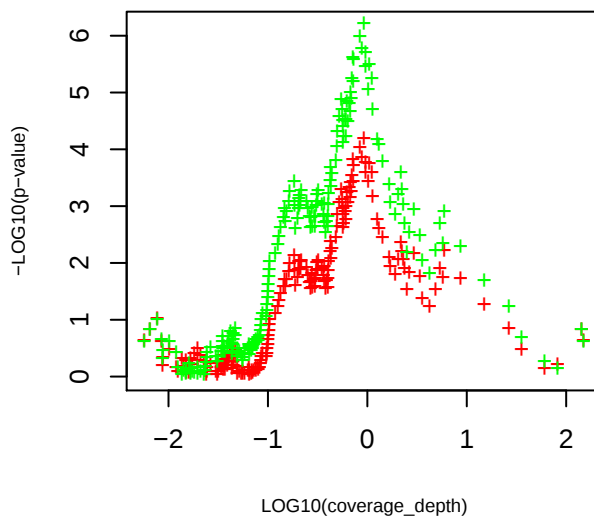


[H] COG1239 Mg-chelatase subunit ChII

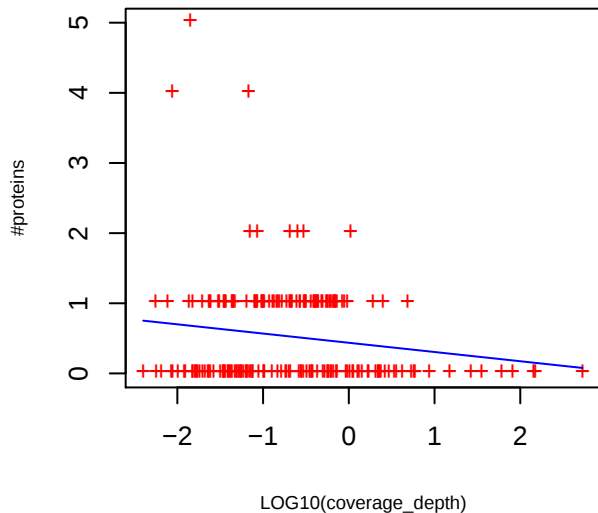
slope= -0.92 p_value= 0.31 intercept= 1.00 p_value= 0.75



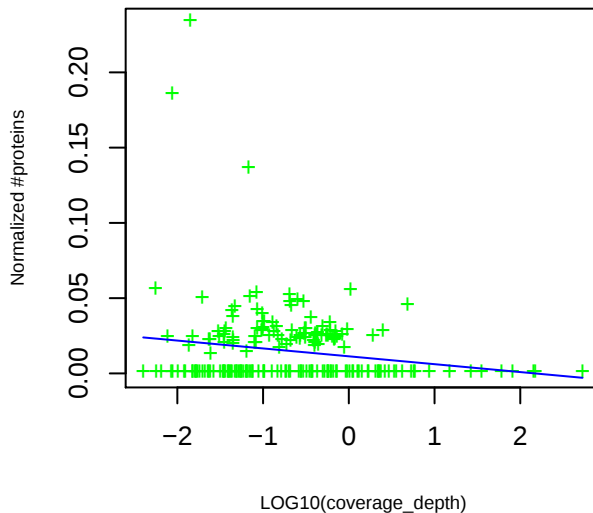
P-value curve ; red (unnorm), green (norm)



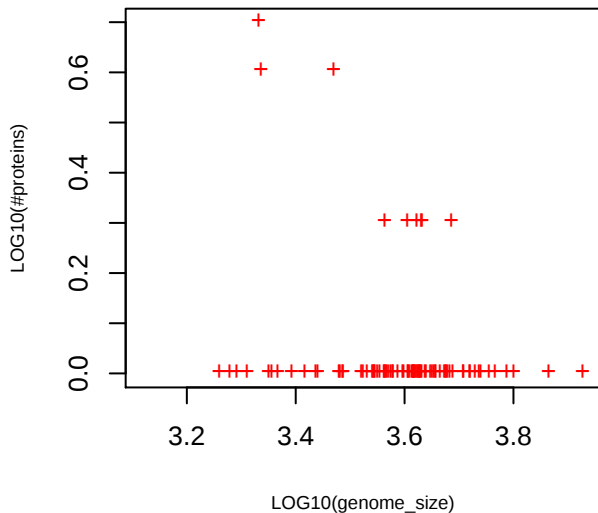
[P] COG1863 Multisubunit Na⁺/H⁺ antiporter, MnhE subunit
slope= -0.13 p_value= 0.024 intercept= 0.44 p_value= 2.4e-10



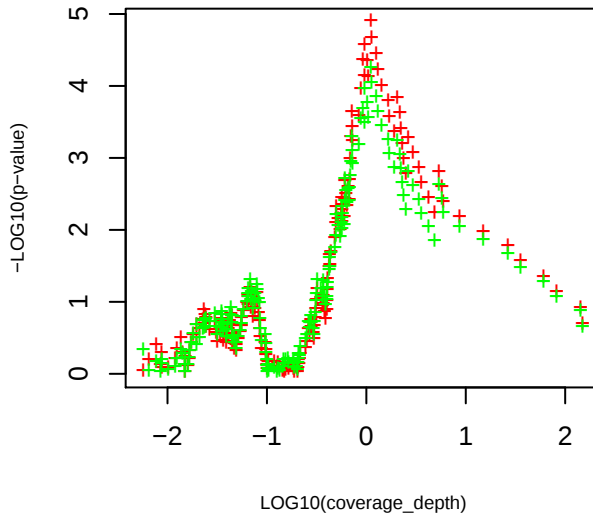
[P] COG1863 Multisubunit Na⁺/H⁺ antiporter, MnhE subunit
slope= -0.0052 p_value= 0.013 intercept= 0.011 p_value= 3.1e-06



[P] COG1863 Multisubunit Na⁺/H⁺ antiporter, MnhE subunit
slope= 2.79 p_value= 0.0014 intercept= -12.10 p_value= 0.00011

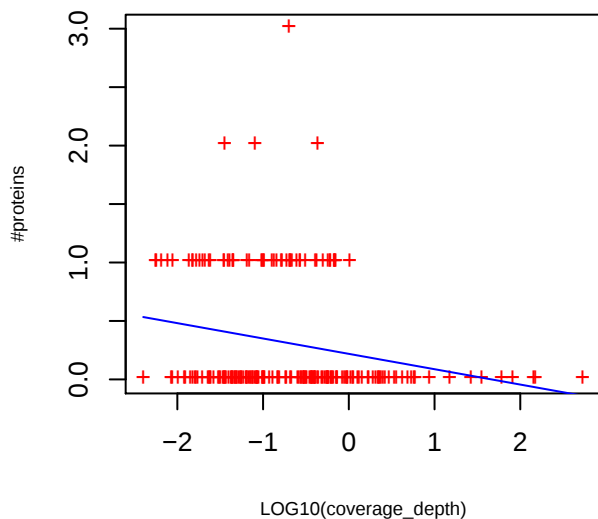


P-value curve ; red (unnorm), green (norm)



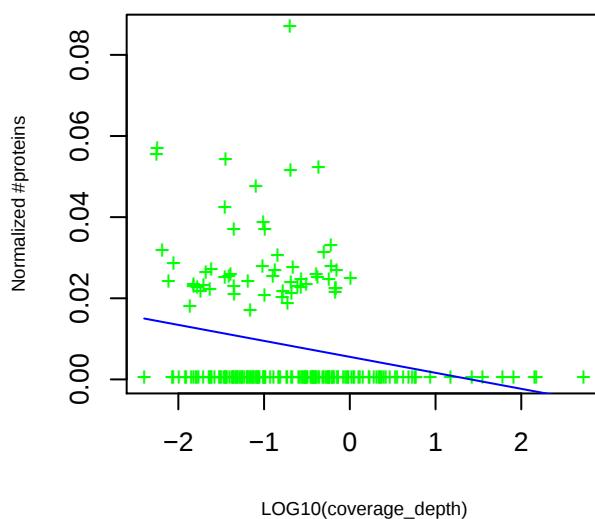
[NT] COG1871 Chemotaxis protein; stimulates methylation of MCP proteins

slope= -0.13 p_value= 0.0016 intercept= 0.22 p_value= 4.4e-06



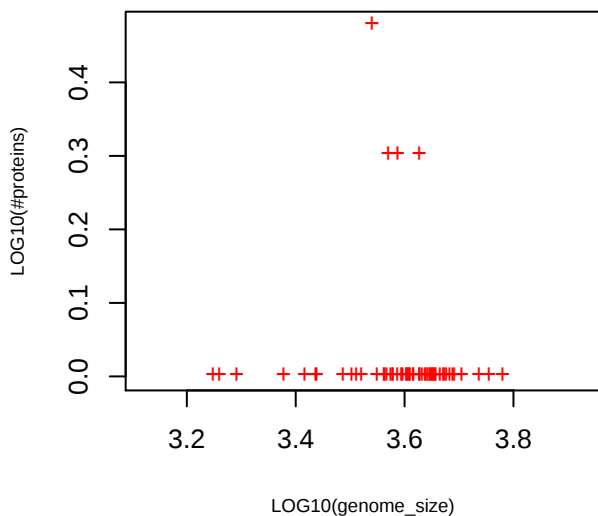
[NT] COG1871 Chemotaxis protein; stimulates methylation of MCP proteins

slope= -0.0039 p_value= 0.00074 intercept= 0.0056 p_value= 2.9e-05

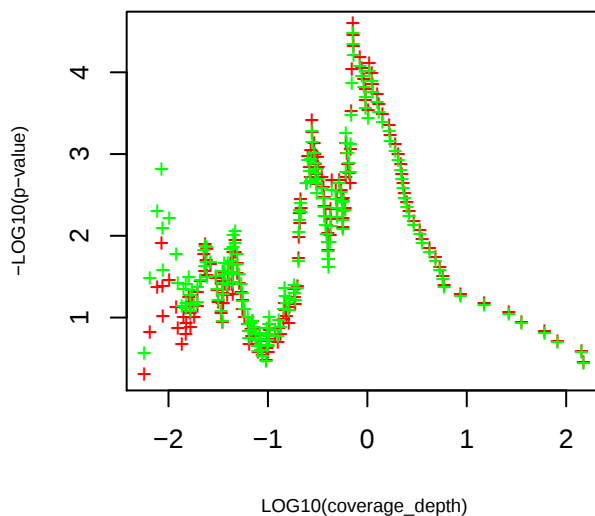


[NT] COG1871 Chemotaxis protein; stimulates methylation of MCP proteins

slope= 1.84 p_value= 0.021 intercept= -9.37 p_value= 0.00098

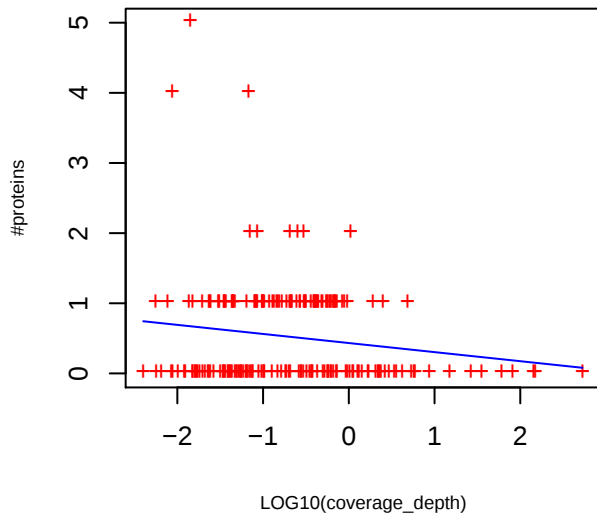


P-value curve ; red (unnorm), green (norm)



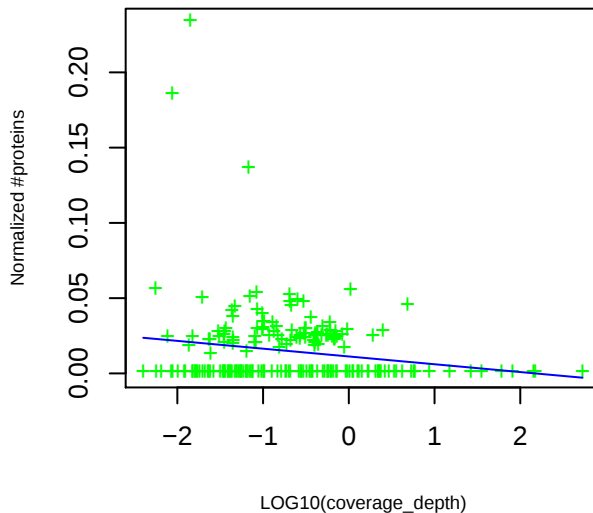
[P] COG1320 Multisubunit Na⁺/H⁺ antiporter, MnhG subunit

slope= -0.13 p_value= 0.026 intercept= 0.43 p_value= 3.3e-10



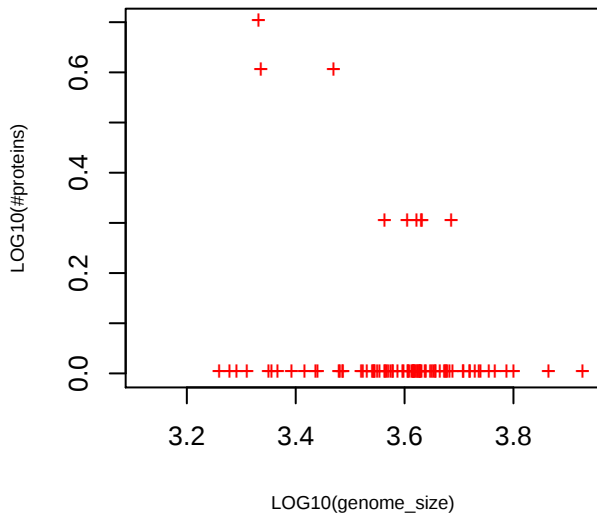
[P] COG1320 Multisubunit Na⁺/H⁺ antiporter, MnhG subunit

slope= -0.0052 p_value= 0.014 intercept= 0.011 p_value= 3.8e-06

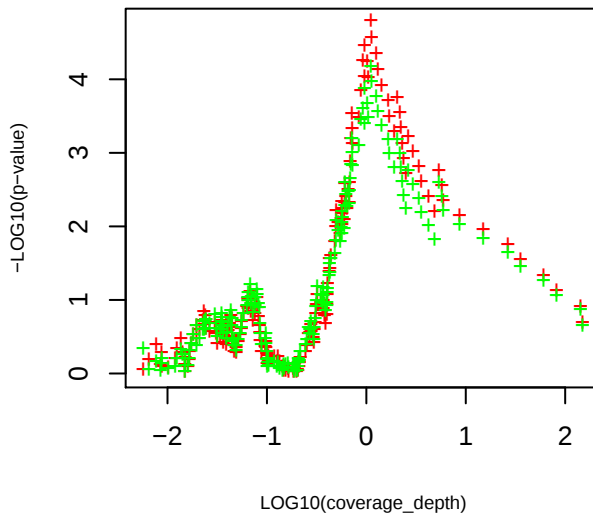


[P] COG1320 Multisubunit Na⁺/H⁺ antiporter, MnhG subunit

slope= 2.78 p_value= 0.0015 intercept= -12.07 p_value= 0.00011

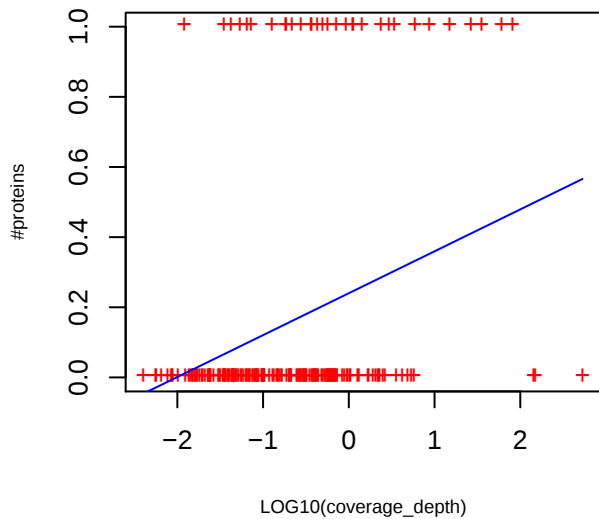


P-value curve ; red (unnorm), green (norm)



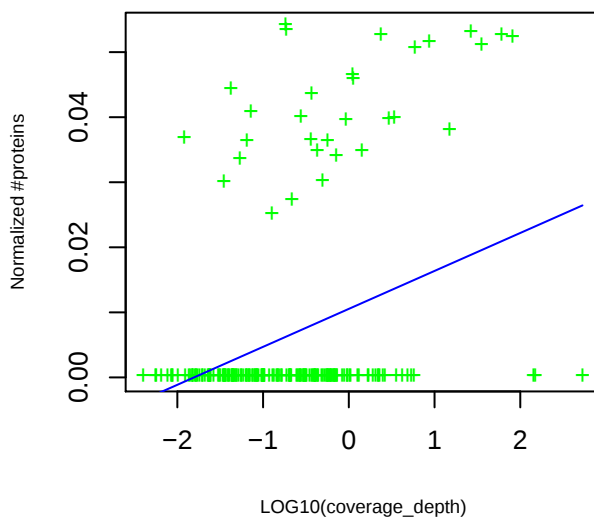
[S] COG3556 Predicted membrane protein

slope= 0.12 p_value= 3e-05 intercept= 0.24 p_value= 1.2e-12



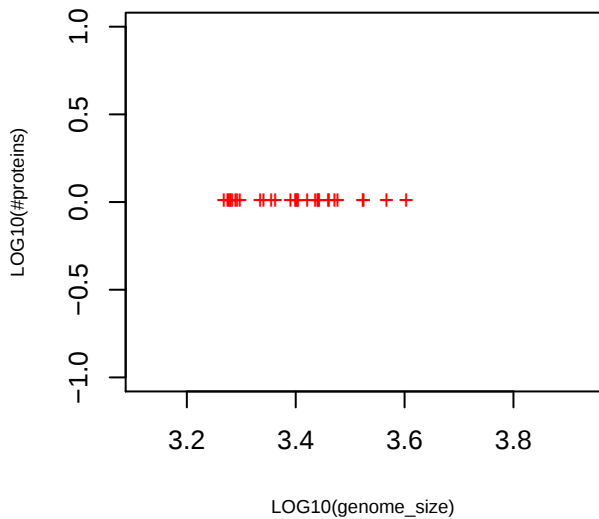
[S] COG3556 Predicted membrane protein

slope= 0.0058 p_value= 1.2e-06 intercept= 0.011 p_value= 9.5e-14

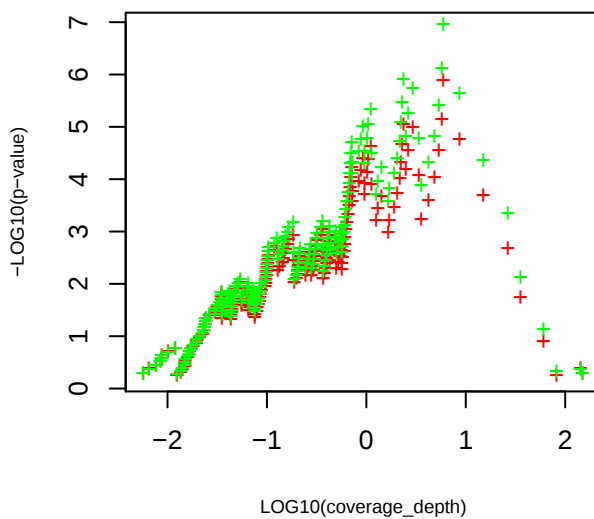


[S] COG3556 Predicted membrane protein

slope= -3.61 p_value= 4.4e-09 intercept= 9.42 p_value= 1.1e-05

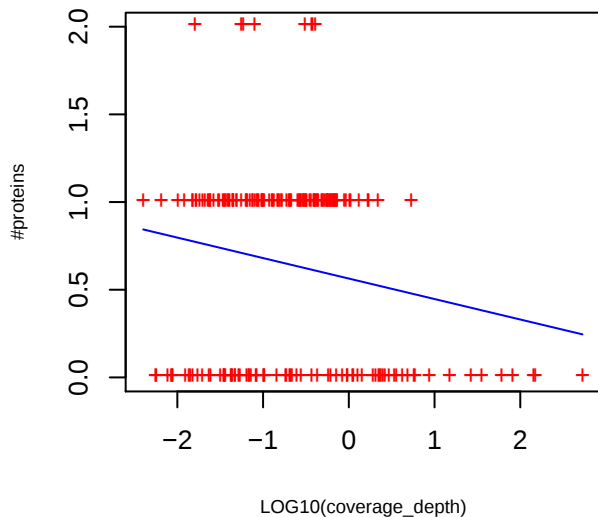


P-value curve ; red (unnorm), green (norm)



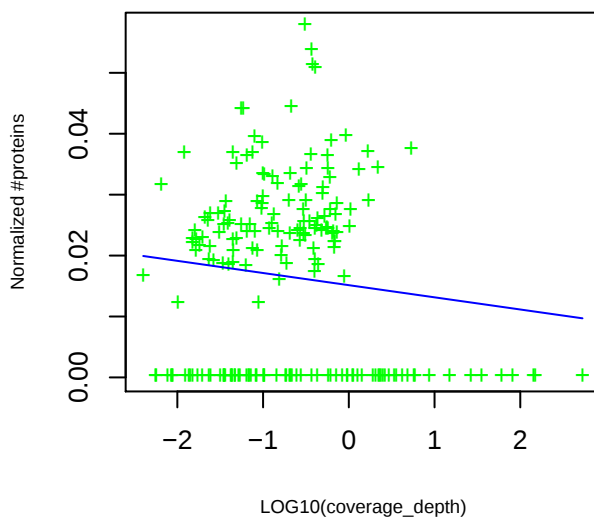
[S] COG2911 Uncharacterized protein conserved in bacteria

slope= -0.12 p_value= 0.0085 intercept= 0.56 p_value= 2.7e-23



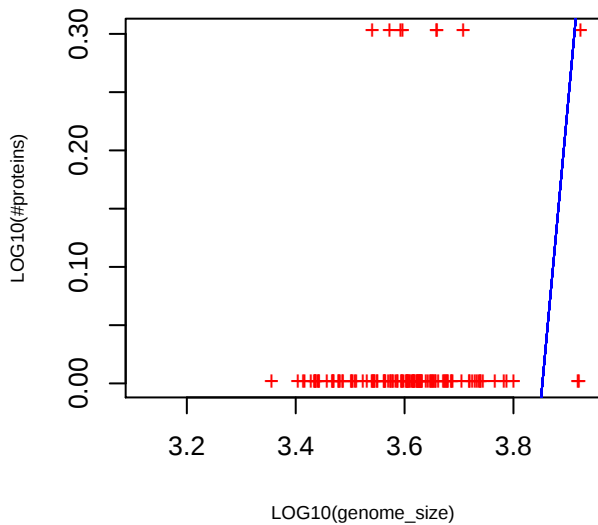
[S] COG2911 Uncharacterized protein conserved in bacteria

slope= -0.002 p_value= 0.092 intercept= 0.015 p_value= 2.5e-23

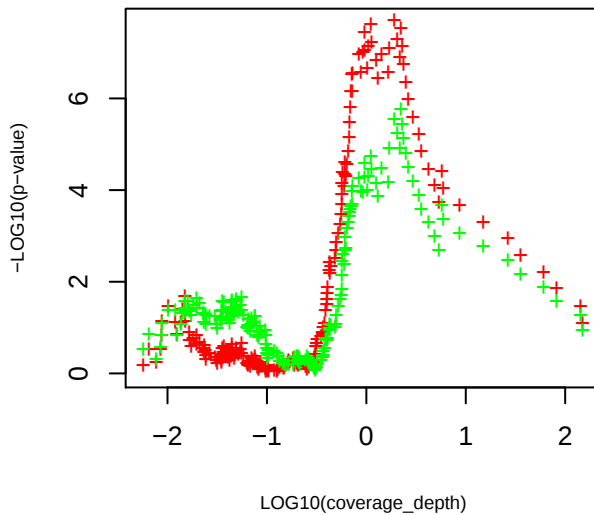


[S] COG2911 Uncharacterized protein conserved in bacteria

slope= 5.10 p_value= 6.5e-10 intercept= -19.67 p_value= 2.9e-11

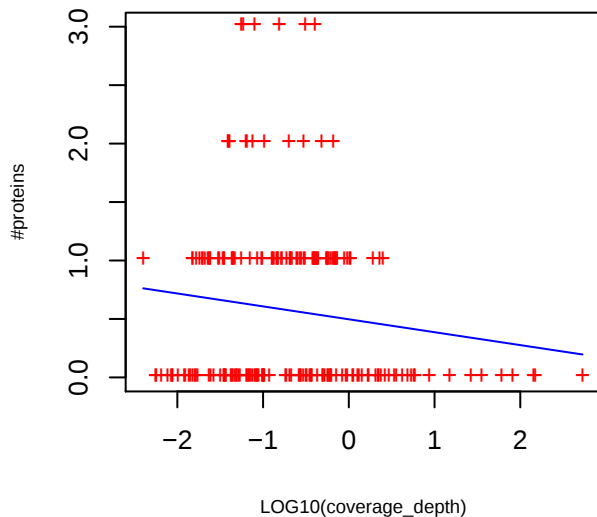


P-value curve ; red (unnorm), green (norm)



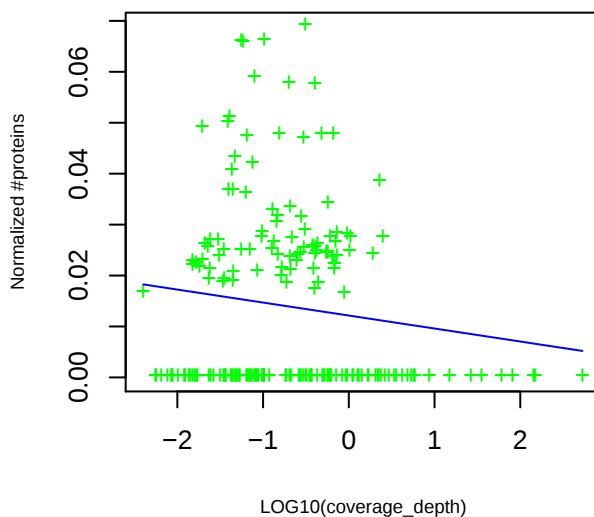
[S] COG2989 Uncharacterized protein conserved in bacteria

slope= -0.11 p_value= 0.06 intercept= 0.50 p_value= 1.7e-12



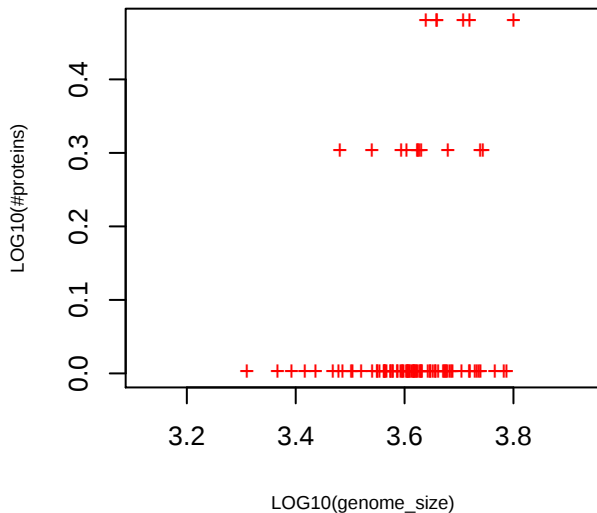
[S] COG2989 Uncharacterized protein conserved in bacteria

slope= -0.0025 p_value= 0.067 intercept= 0.012 p_value= 4.5e-13

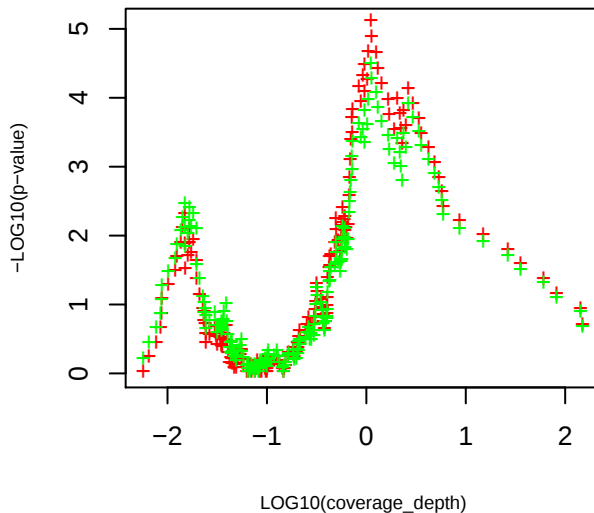


[S] COG2989 Uncharacterized protein conserved in bacteria

slope= 4.95 p_value= 7.6e-09 intercept= -19.71 p_value= 1.5e-10

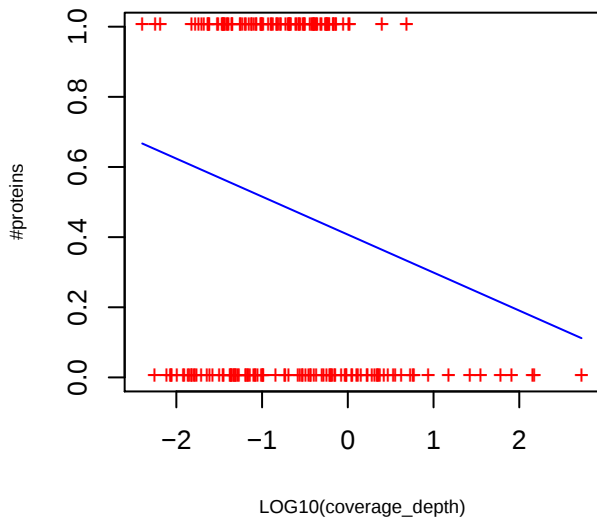


P-value curve ; red (unnorm), green (norm)



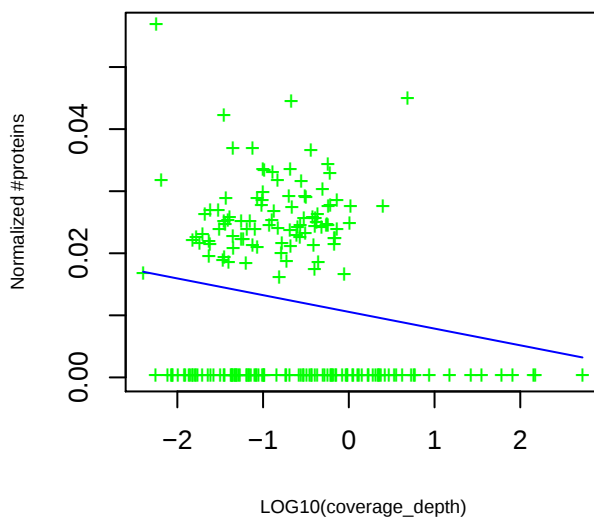
[L] COG1722 Exonuclease VII small subunit

slope= -0.11 p_value= 0.0065 intercept= 0.41 p_value= 7e-17



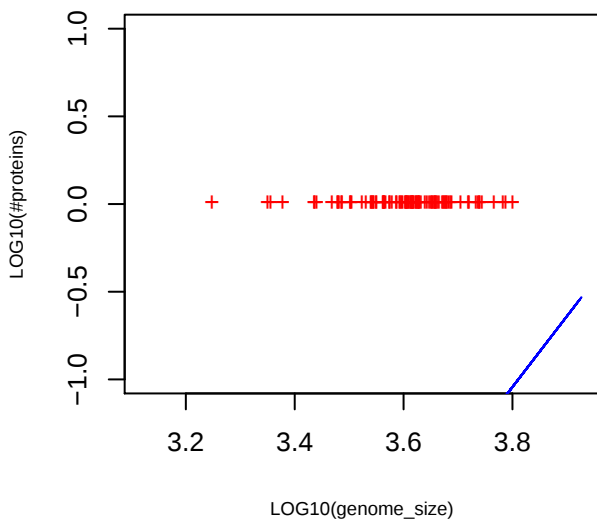
[L] COG1722 Exonuclease VII small subunit

slope= -0.0027 p_value= 0.013 intercept= 0.011 p_value= 1.5e-15

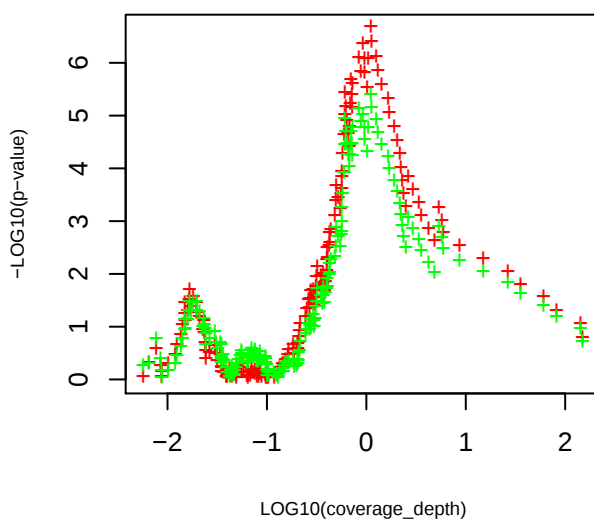


[L] COG1722 Exonuclease VII small subunit

slope= 4.03 p_value= 2.5e-06 intercept= -16.38 p_value= 9.2e-08

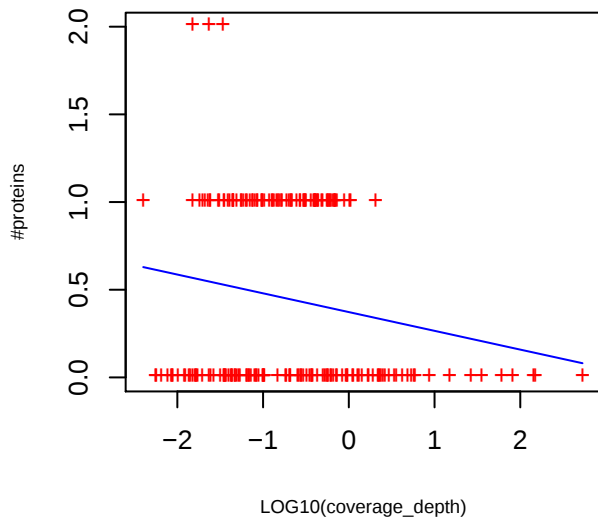


P-value curve ; red (unnorm), green (norm)



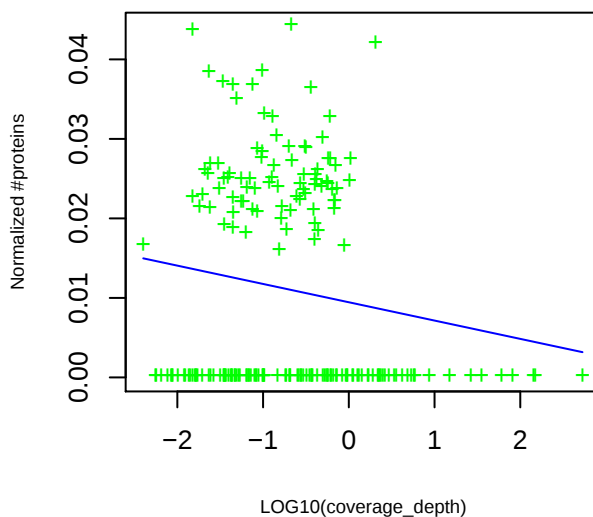
[R] COG2961 Protein involved in catabolism of external DNA

slope= -0.11 p_value= 0.011 intercept= 0.37 p_value= 1.6e-13



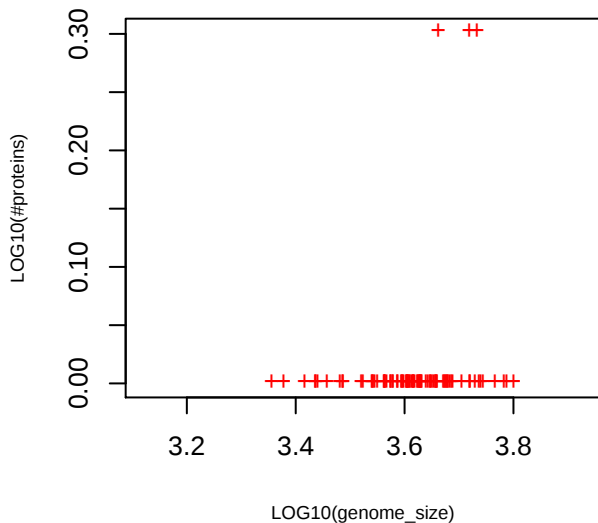
[R] COG2961 Protein involved in catabolism of external DNA

slope= -0.0023 p_value= 0.03 intercept= 0.0095 p_value= 1.5e-13

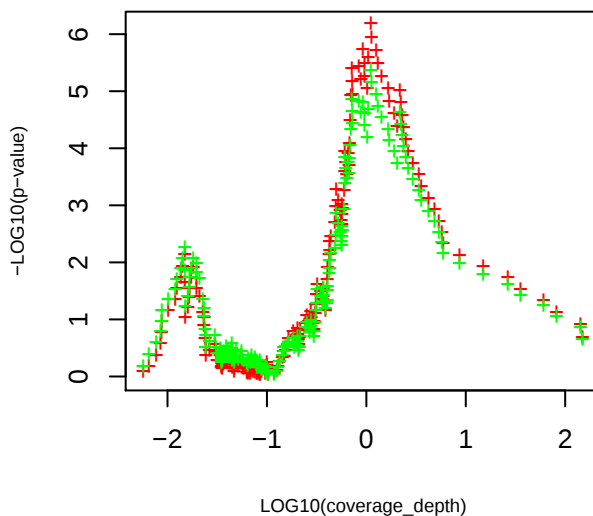


[R] COG2961 Protein involved in catabolism of external DNA

slope= 4.46 p_value= 1.3e-07 intercept= -18.09 p_value= 2.4e-09

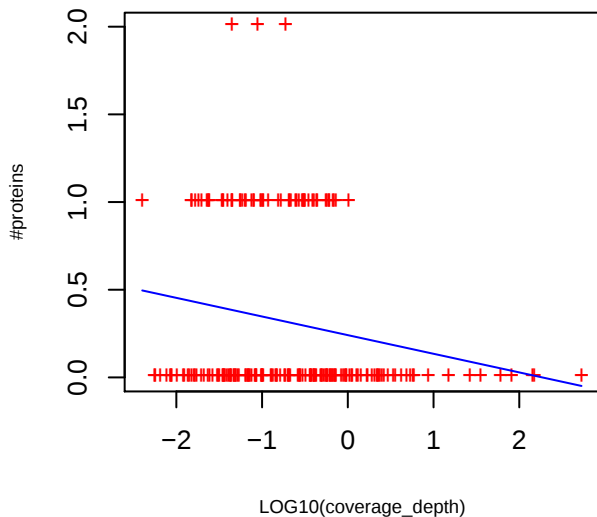


P-value curve ; red (unnorm), green (norm)



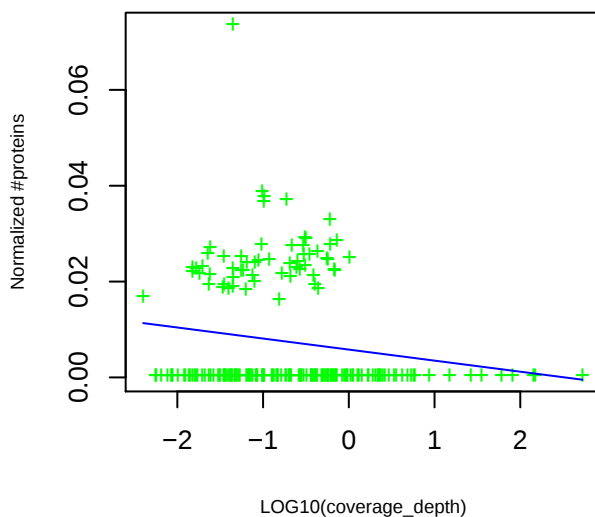
[P] COG4558 ABC-type hemin transport system, periplasmic component

slope= -0.11 p_value= 0.0071 intercept= 0.24 p_value= 1.4e-07



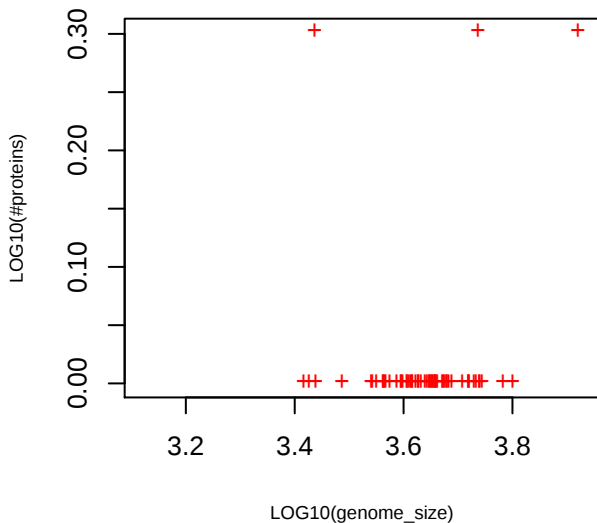
[P] COG4558 ABC-type hemin transport system, periplasmic component

slope= -0.0023 p_value= 0.017 intercept= 0.0058 p_value= 2.4e-07

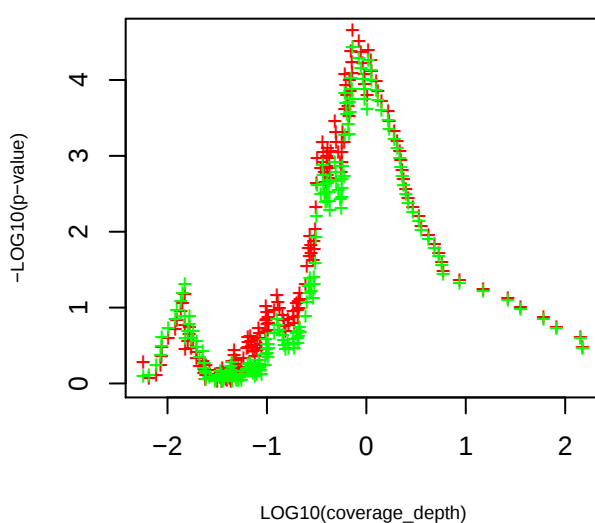


[P] COG4558 ABC-type hemin transport system, periplasmic component

slope= 4.18 p_value= 9e-08 intercept= -17.62 p_value= 3.9e-10

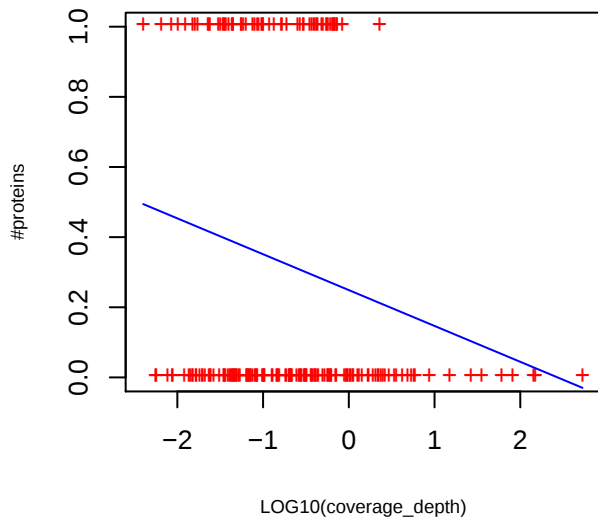


P-value curve ; red (unnorm), green (norm)



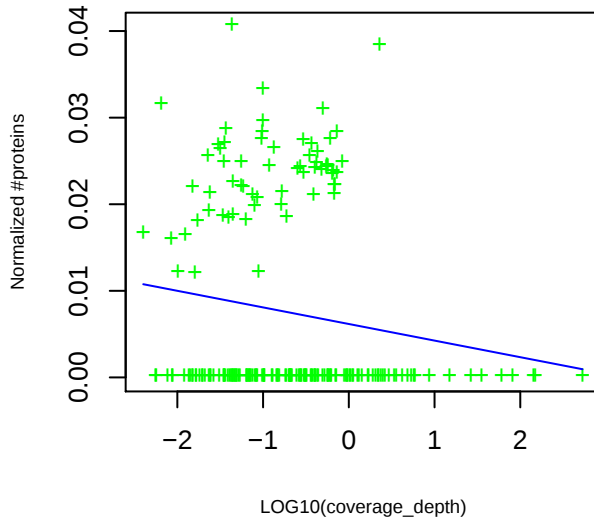
[S] COG3016 Uncharacterized iron-regulated protein

slope= -0.10 p_value= 0.0059 intercept= 0.25 p_value= 9.2e-09



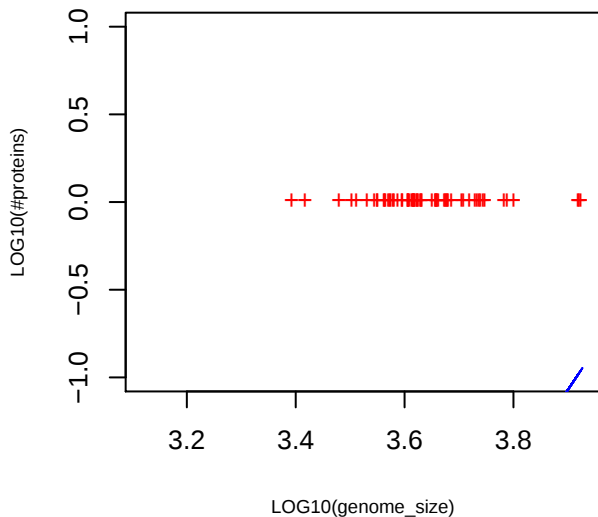
[S] COG3016 Uncharacterized iron-regulated protein

slope= -0.0019 p_value= 0.034 intercept= 0.0062 p_value= 6.4e-09

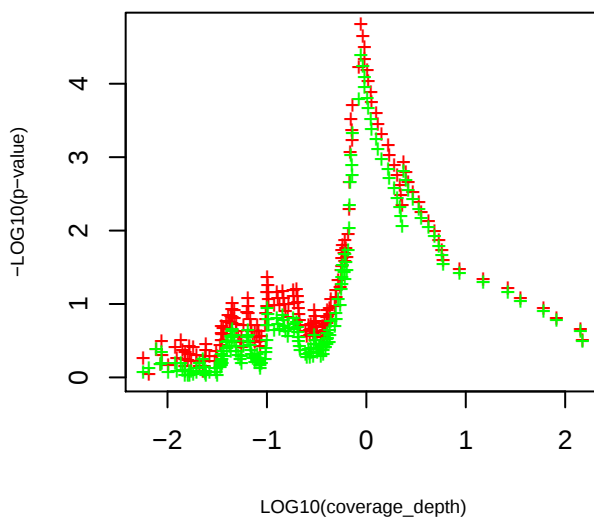


[S] COG3016 Uncharacterized iron-regulated protein

slope= 4.65 p_value= 3.4e-09 intercept= -19.21 p_value= 1.2e-11

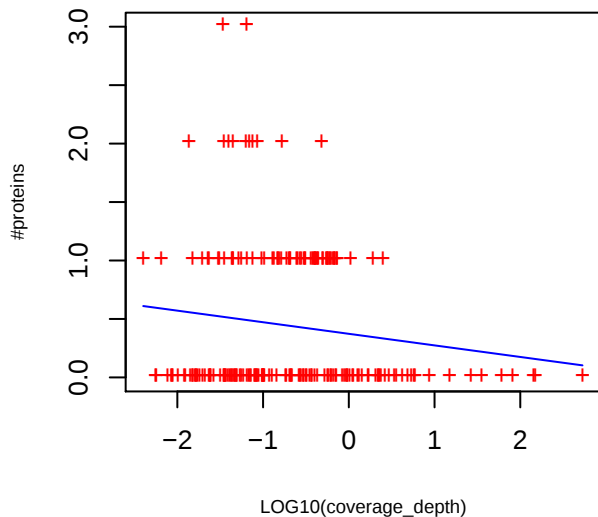


P-value curve ; red (unnorm), green (norm)



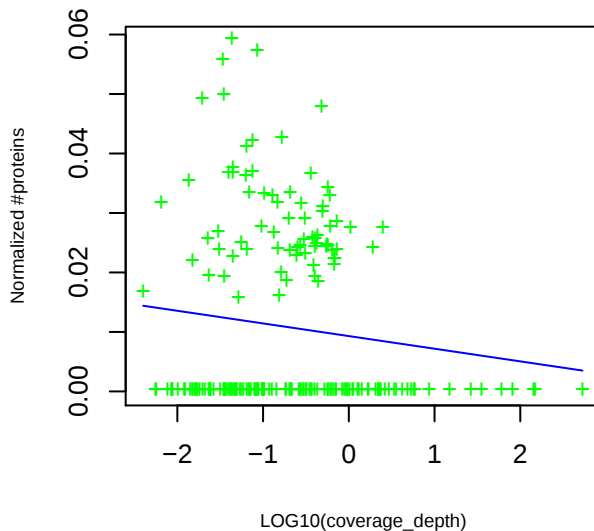
[U] COG4963 Flp pilus assembly protein, ATPase CpaE

slope= -0.10 p_value= 0.053 intercept= 0.37 p_value= 6.7e-10



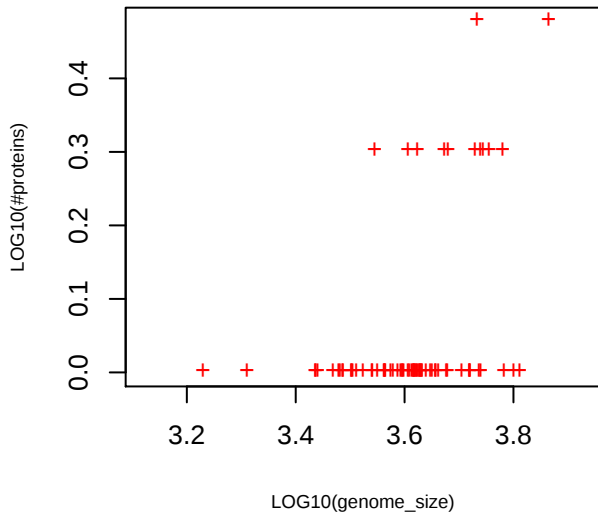
[U] COG4963 Flp pilus assembly protein, ATPase CpaE

slope= -0.0021 p_value= 0.08 intercept= 0.0093 p_value= 1.1e-10

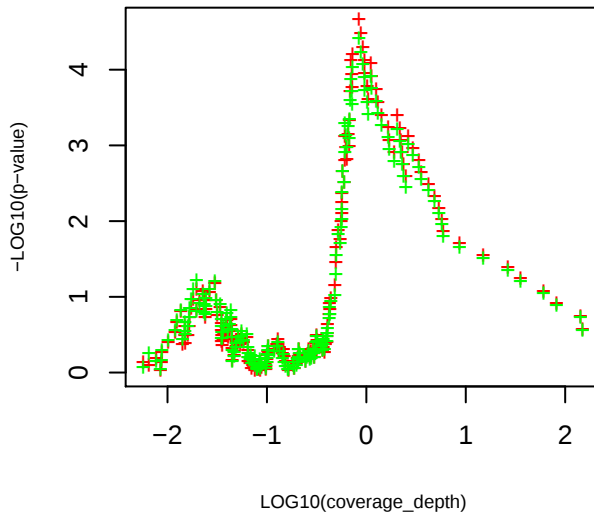


[U] COG4963 Flp pilus assembly protein, ATPase CpaE

slope= 3.80 p_value= 6.4e-06 intercept= -15.97 p_value= 1.2e-07

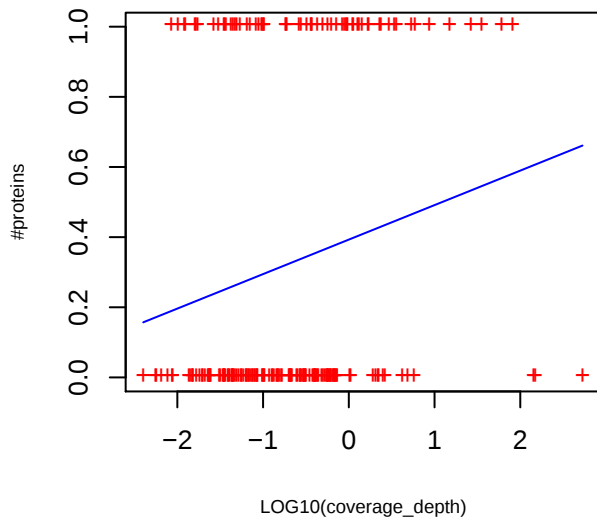


P-value curve ; red (unnorm), green (norm)



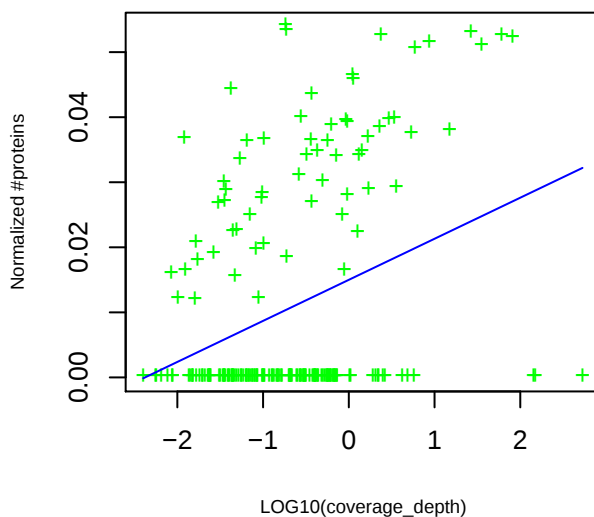
[S] COG2954 Uncharacterized protein conserved in bacteria

slope= 0.098 p_value= 0.0084 intercept= 0.39 p_value= 1.3e-17



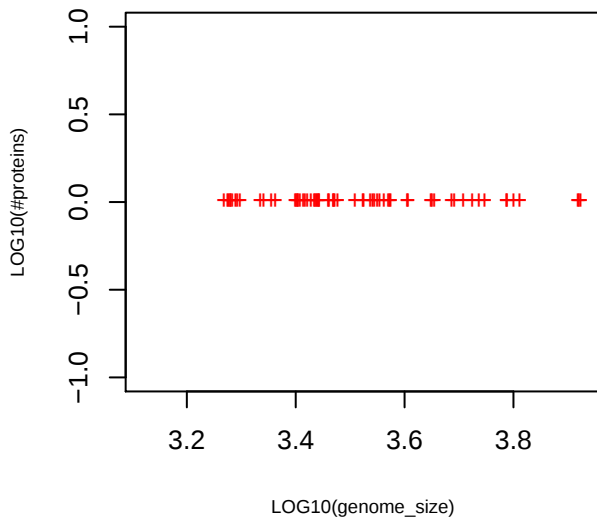
[S] COG2954 Uncharacterized protein conserved in bacteria

slope= 0.0063 p_value= 1.3e-06 intercept= 0.015 p_value= 8.2e-21

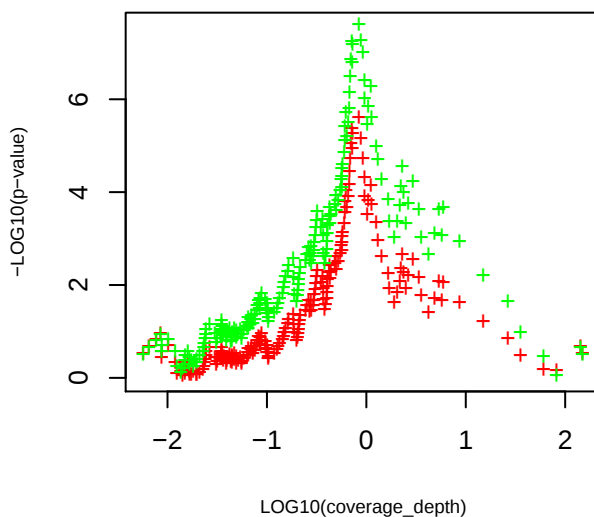


[S] COG2954 Uncharacterized protein conserved in bacteria

slope= -1.42 p_value= 0.084 intercept= 2.35 p_value= 0.42

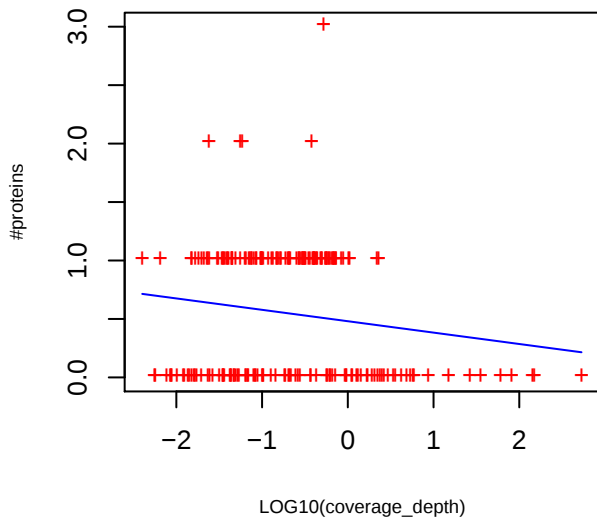


P-value curve : red (unnorm), green (norm)



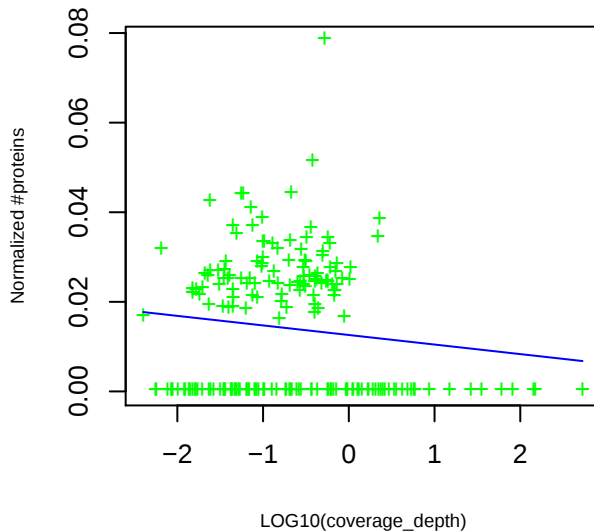
[M] COG0729 Outer membrane protein

slope= -0.097 p_value= 0.031 intercept= 0.48 p_value= 7.5e-18



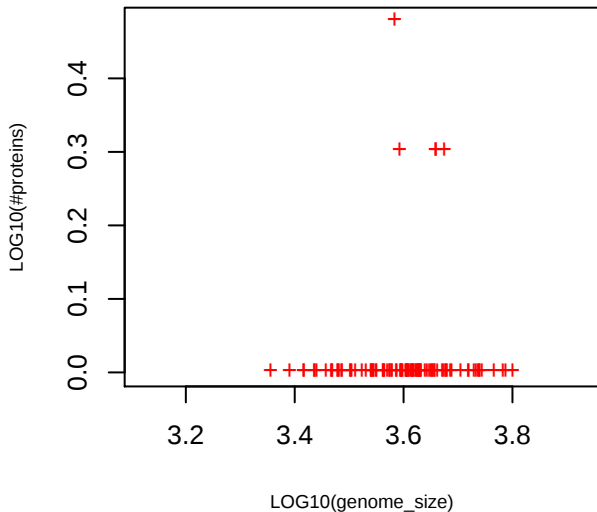
[M] COG0729 Outer membrane protein

slope= -0.0021 p_value= 0.073 intercept= 0.013 p_value= 1.3e-17

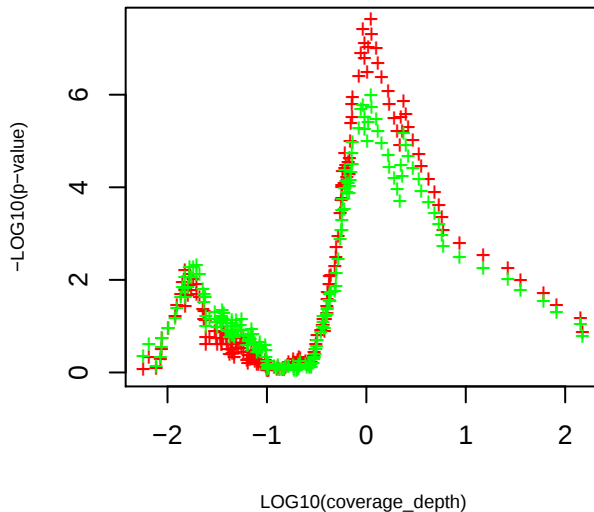


[M] COG0729 Outer membrane protein

slope= 4.18 p_value= 1.1e-06 intercept= -16.76 p_value= 4.9e-08

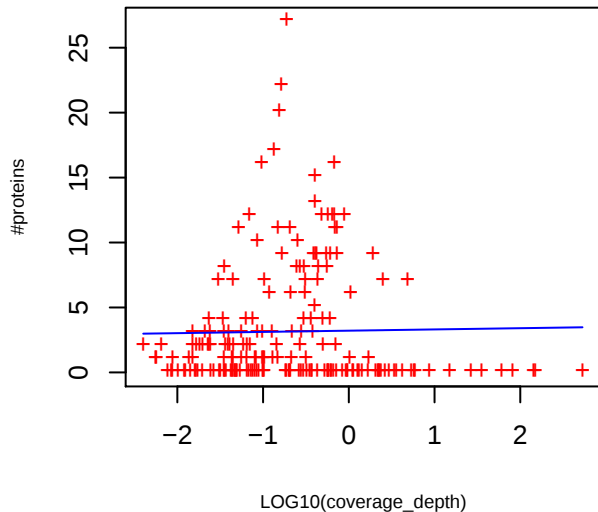


P-value curve ; red (unnorm), green (norm)



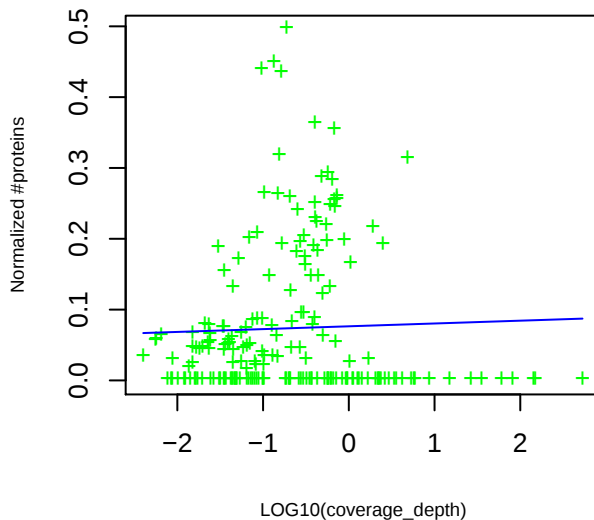
[K] COG1802 Transcriptional regulators

slope= 0.096 p_value= 0.80 intercept= 3.21 p_value= 2.2e-12



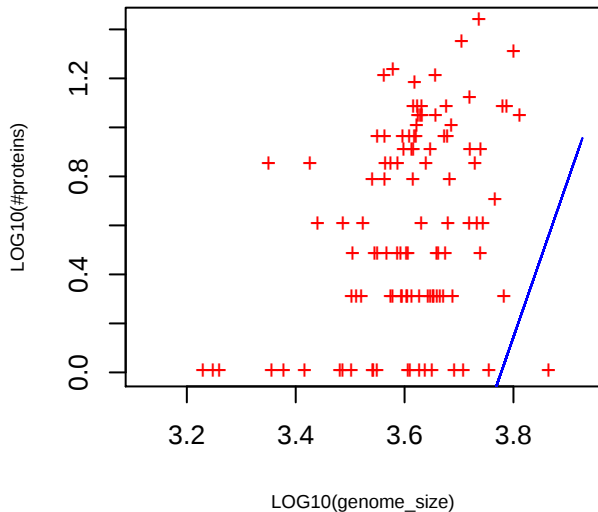
[K] COG1802 Transcriptional regulators

slope= 0.004 p_value= 0.64 intercept= 0.076 p_value= 9e-14

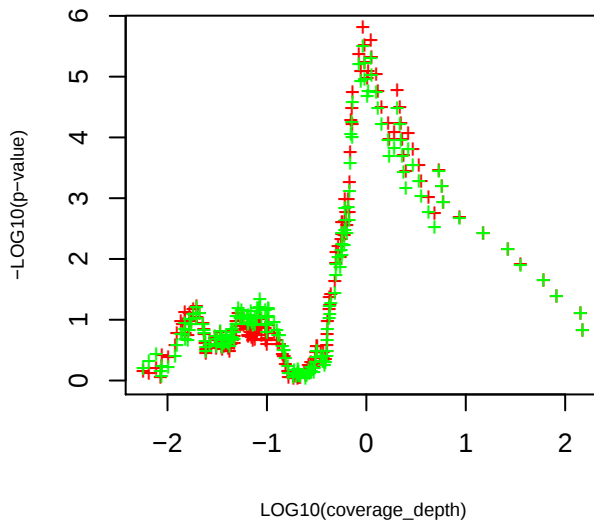


[K] COG1802 Transcriptional regulators

slope= 6.41 p_value= 2.4e-11 intercept= -24.20 p_value= 1.7e-12

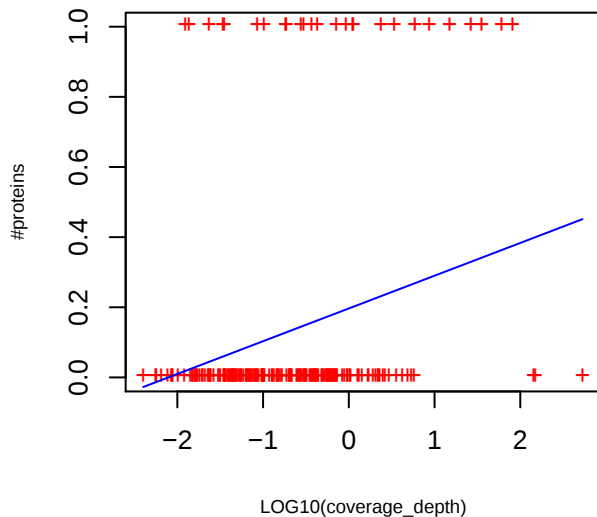


P-value curve : red (unnorm), green (norm)



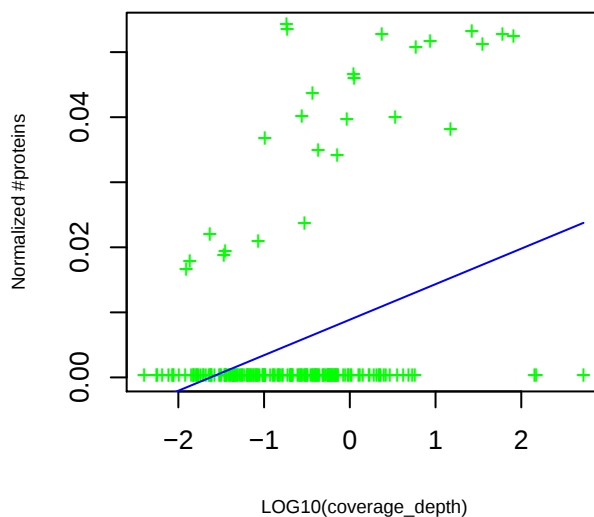
[F] COG3613 Nucleoside 2-deoxyribosyltransferase

slope= 0.093 p_value= 0.00049 intercept= 0.20 p_value= 3.5e-10



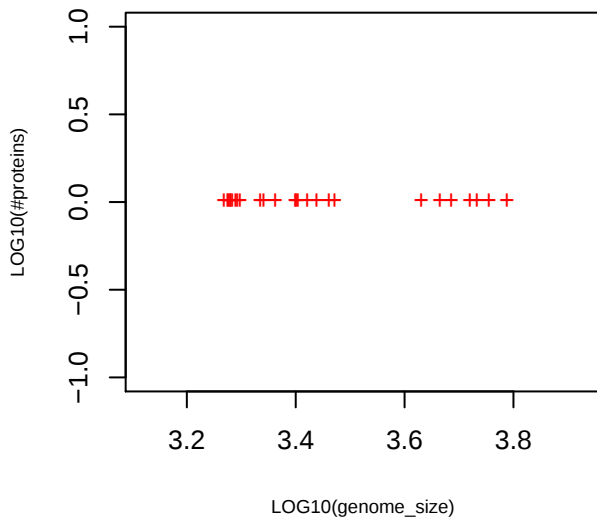
[F] COG3613 Nucleoside 2-deoxyribosyltransferase

slope= 0.0055 p_value= 4.4e-07 intercept= 0.0089 p_value= 1.9e-12

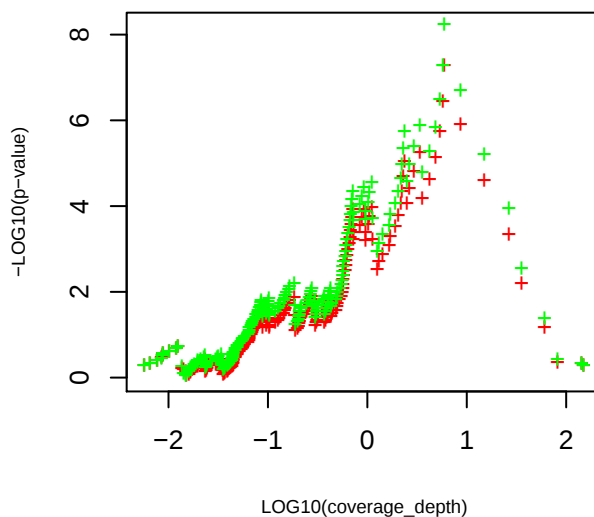


[F] COG3613 Nucleoside 2-deoxyribosyltransferase

slope= -2.01 p_value= 0.00062 intercept= 3.66 p_value= 0.076

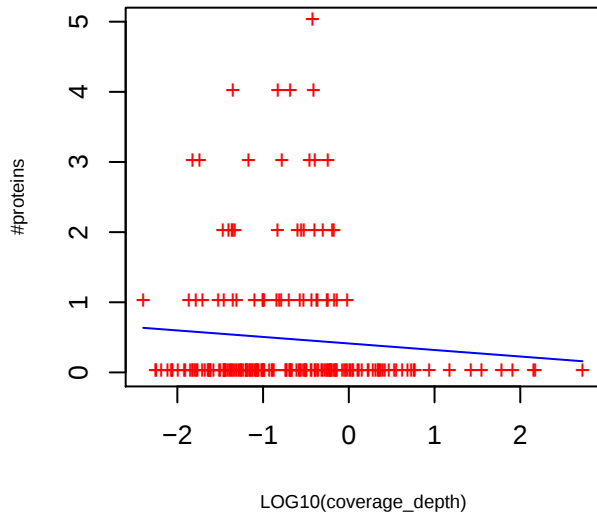


P-value curve ; red (unnorm), green (norm)



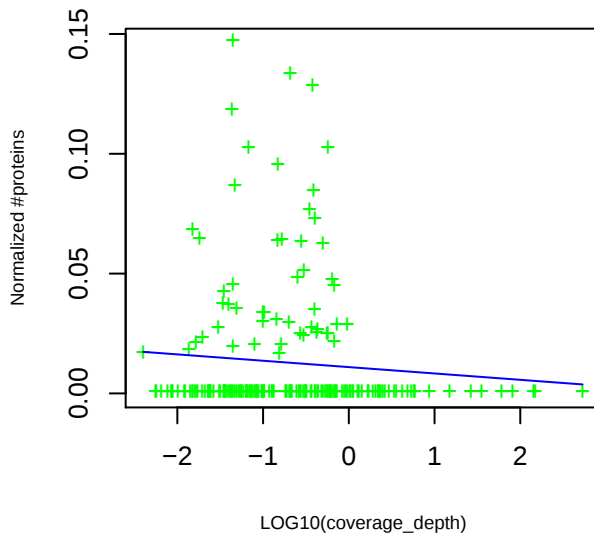
[U] COG3451 Type IV secretory pathway, VirB4 components

slope= -0.093 p_value= 0.23 intercept= 0.41 p_value= 4.6e-06



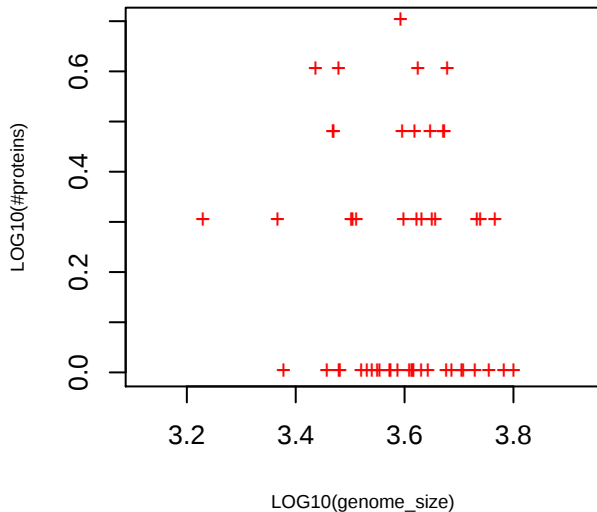
[U] COG3451 Type IV secretory pathway, VirB4 components

slope= -0.0027 p_value= 0.23 intercept= 0.011 p_value= 1.6e-05

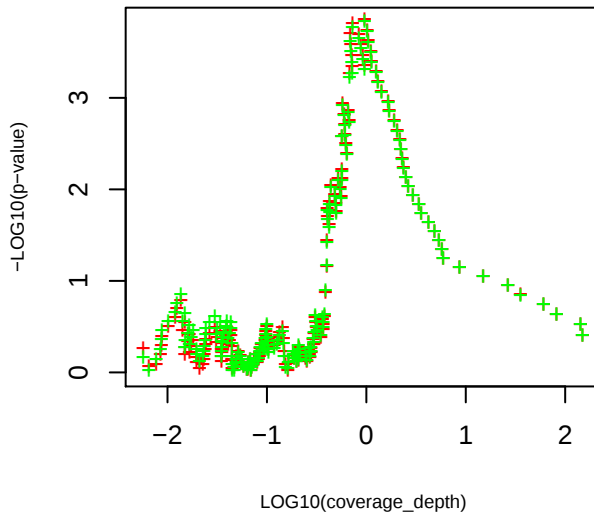


[U] COG3451 Type IV secretory pathway, VirB4 components

slope= 1.95 p_value= 0.016 intercept= -9.81 p_value= 0.00068

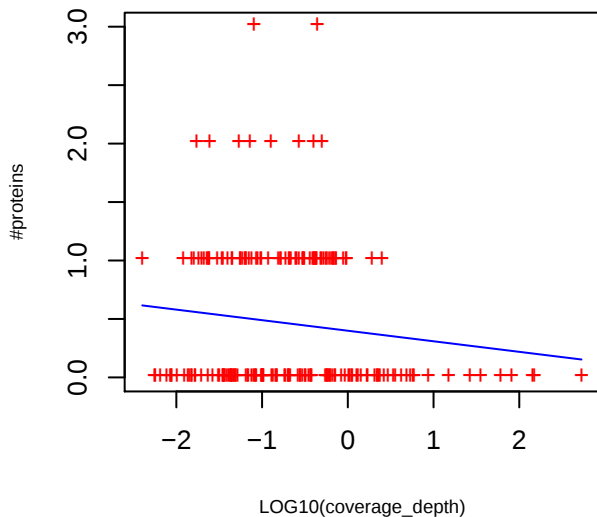


P-value curve ; red (unnorm), green (norm)



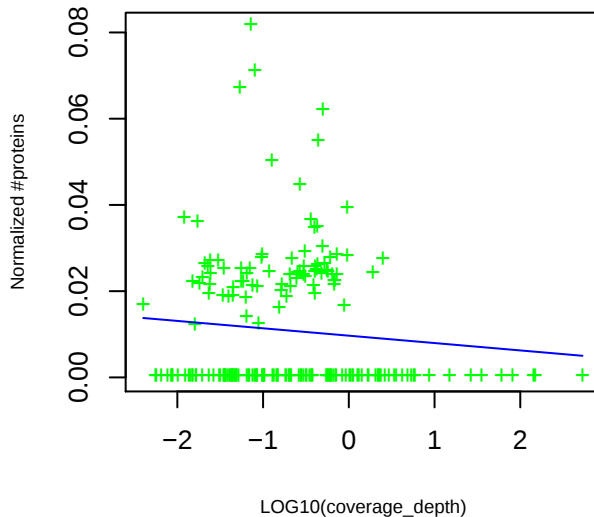
[C] COG3488 Predicted thiol oxidoreductase

slope= -0.09 p_value= 0.071 intercept= 0.40 p_value= 2.2e-11



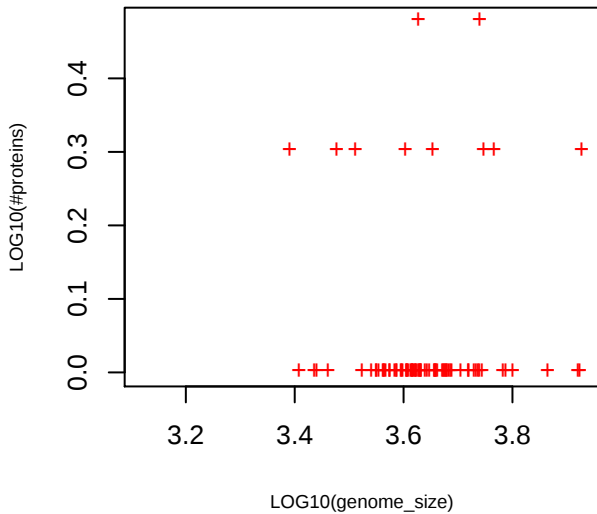
[C] COG3488 Predicted thiol oxidoreductase

slope= -0.0017 p_value= 0.17 intercept= 0.0097 p_value= 4.8e-11

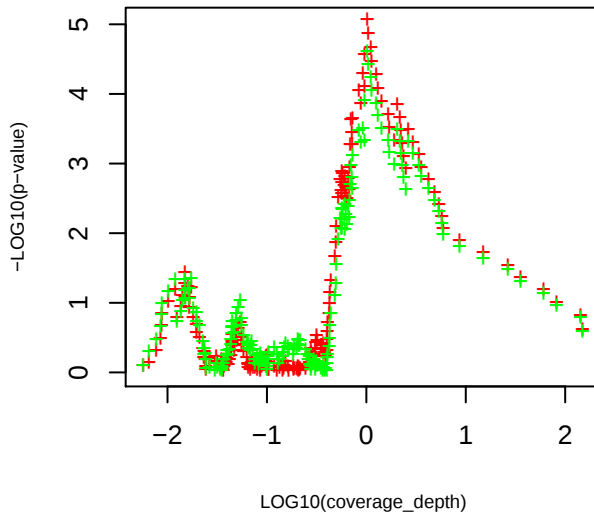


[C] COG3488 Predicted thiol oxidoreductase

slope= 5.85 p_value= 9.5e-13 intercept= -23.13 p_value= 4.6e-15

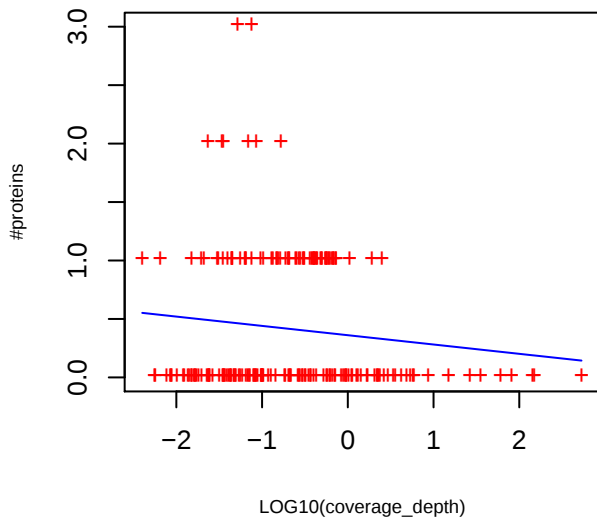


P-value curve ; red (unnorm), green (norm)



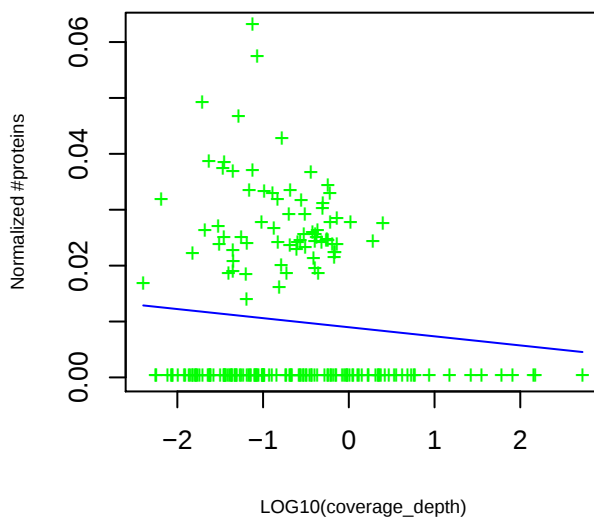
[U] COG3745 Flp pilus assembly protein CpaB

slope= -0.08 p_value= 0.10 intercept= 0.36 p_value= 3e-10



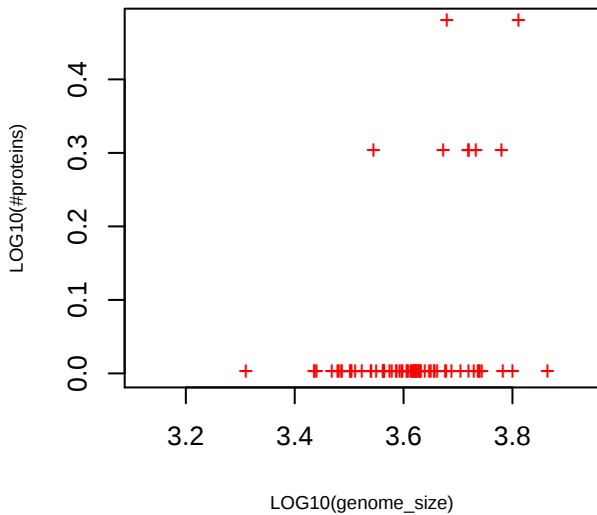
[U] COG3745 Flp pilus assembly protein CpaB

slope= -0.0016 p_value= 0.16 intercept= 0.009 p_value= 5.3e-11

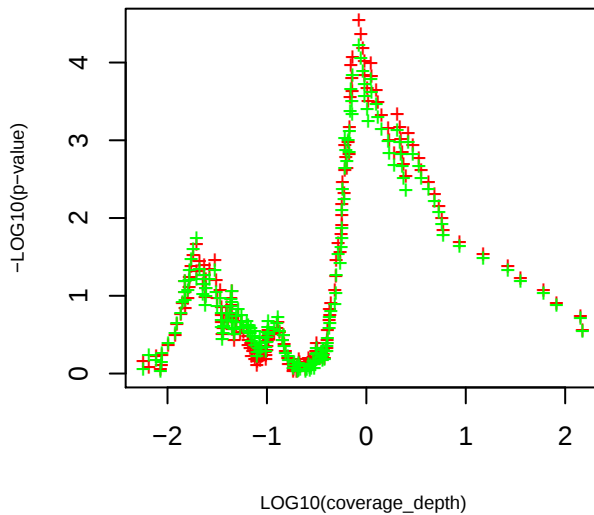


[U] COG3745 Flp pilus assembly protein CpaB

slope= 3.94 p_value= 2.3e-06 intercept= -16.51 p_value= 3.4e-08

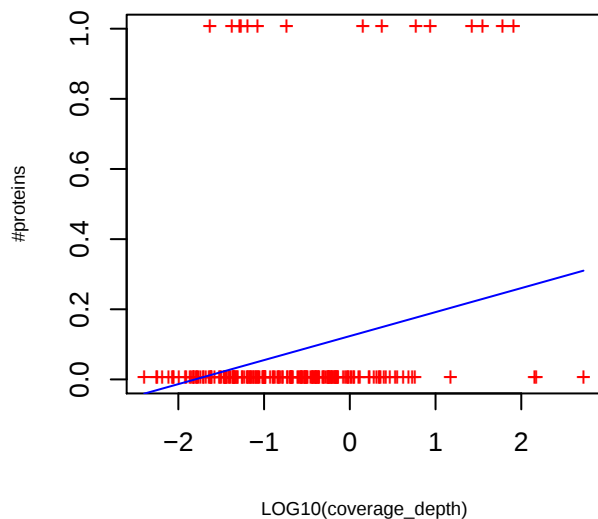


P-value curve ; red (unnorm), green (norm)



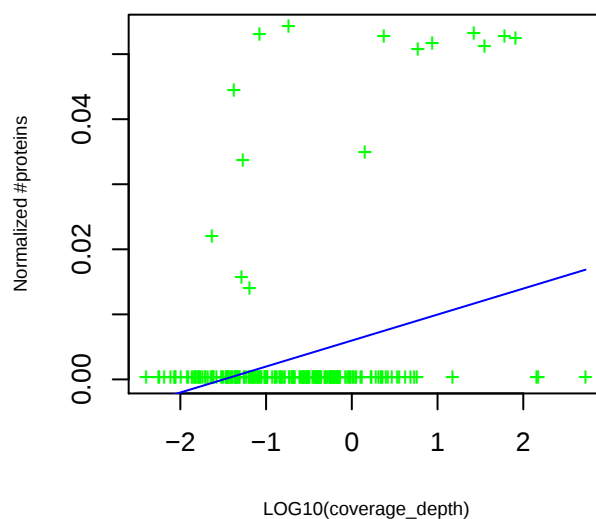
[C] COG0636 F0F1-type ATP synthase, subunit c/Archaeal/vacuolar-type H⁺-ATPase, subunit K

slope= 0.068 p_value= 0.0011 intercept= 0.12 p_value= 3.4e-07



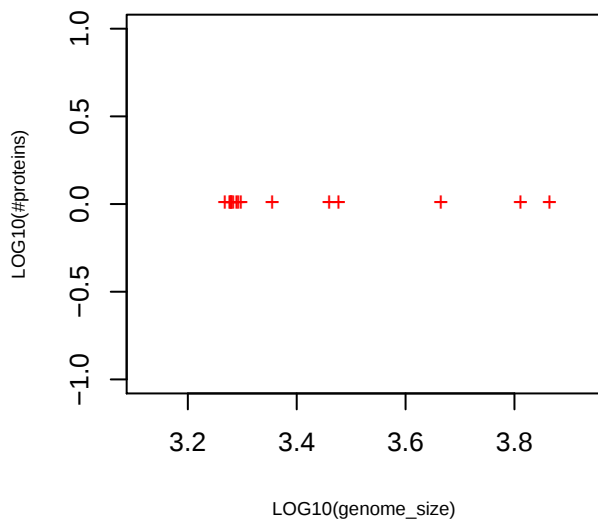
[C] COG0636 F0F1-type ATP synthase, subunit c/Archaeal/vacuolar-type H⁺-ATPase, subunit K

slope= 0.004 p_value= 1.7e-05 intercept= 0.006 p_value= 2.2e-08

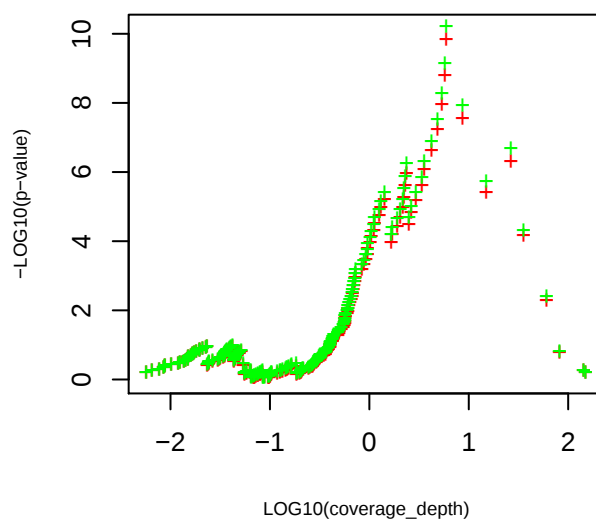


[C] COG0636 F0F1-type ATP synthase, subunit c/Archaeal/vacuolar-type H⁺-ATPase, subunit K

slope= -1.54 p_value= 0.00087 intercept= 1.75 p_value= 0.28

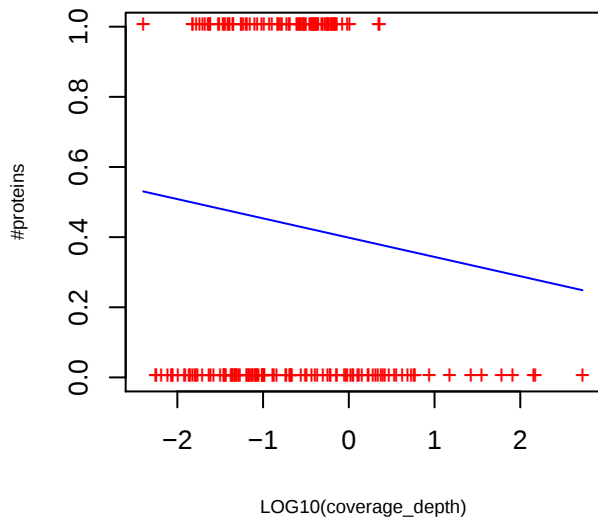


P-value curve : red (unnorm), green (norm)



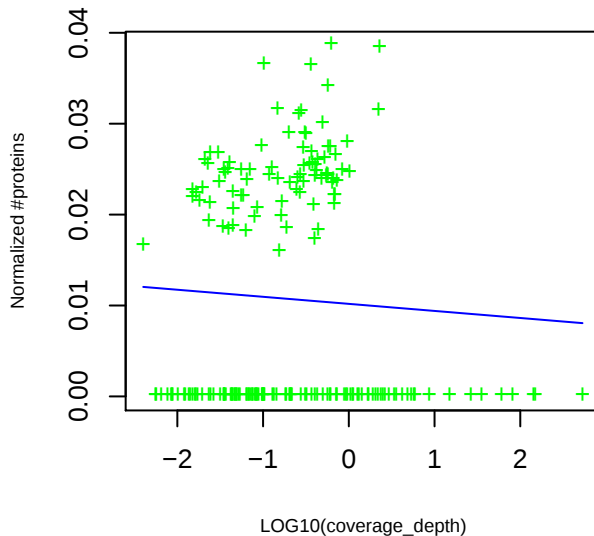
[S] COG2354 Uncharacterized protein conserved in bacteria

slope= -0.055 p_value= 0.17 intercept= 0.40 p_value= 3.7e-16



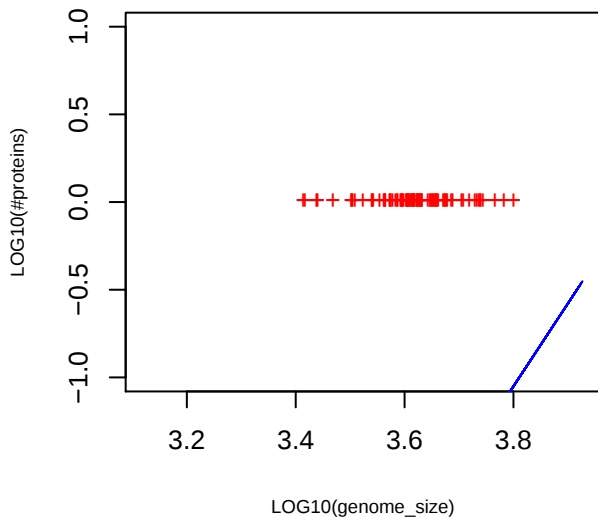
[S] COG2354 Uncharacterized protein conserved in bacteria

slope= -0.00078 p_value= 0.44 intercept= 0.010 p_value= 2.4e-16

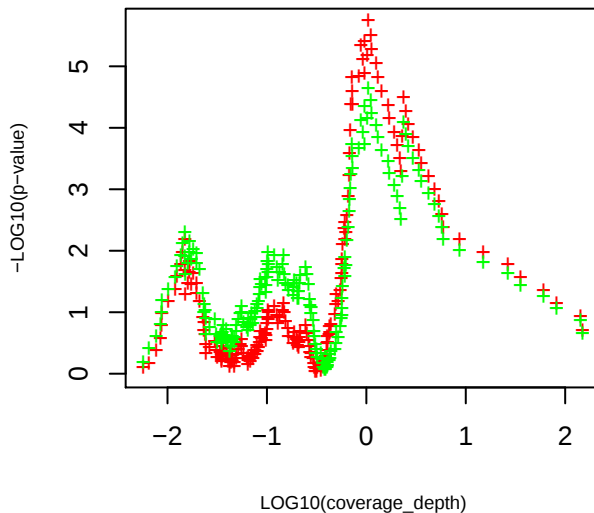


[S] COG2354 Uncharacterized protein conserved in bacteria

slope= 4.72 p_value= 1.9e-08 intercept= -19.00 p_value= 2.9e-10

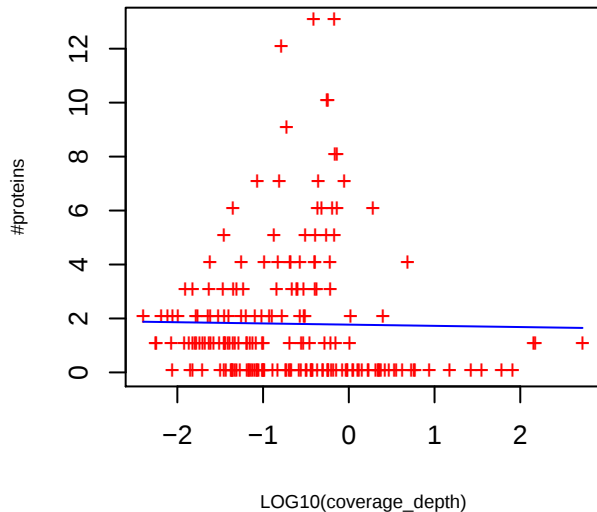


P-value curve ; red (unnorm), green (norm)



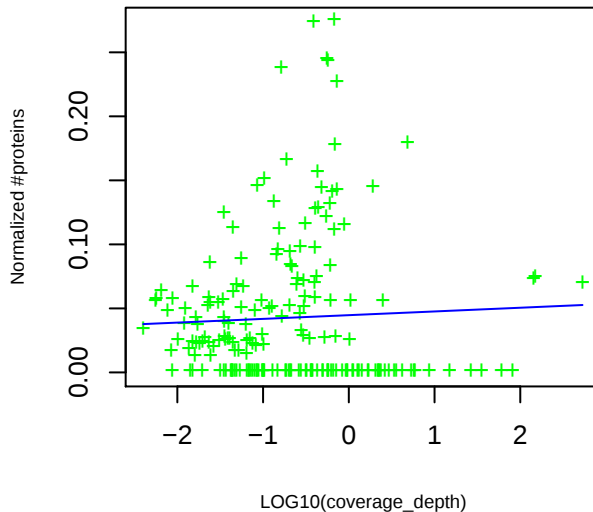
[E] COG0687 Spermidine/putrescine-binding periplasmic protein

slope= -0.045 p_value= 0.83 intercept= 1.77 p_value= 5.8e-13



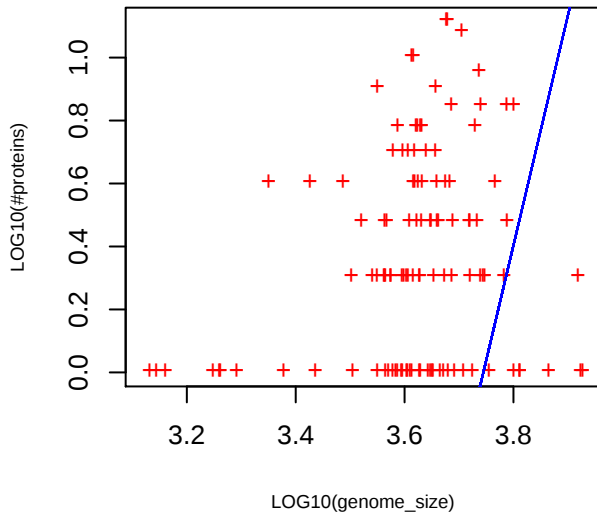
[E] COG0687 Spermidine/putrescine-binding periplasmic protein

slope= 0.0029 p_value= 0.53 intercept= 0.045 p_value= 2.4e-15

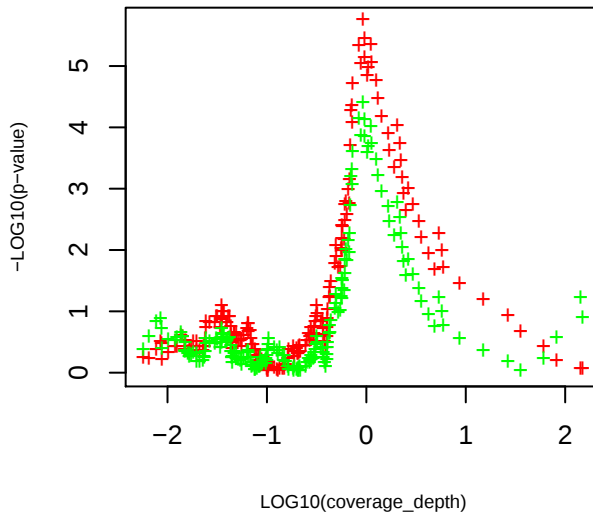


[E] COG0687 Spermidine/putrescine-binding periplasmic protein

slope= 7.30 p_value= 7.2e-17 intercept= -27.33 p_value= 2.6e-18

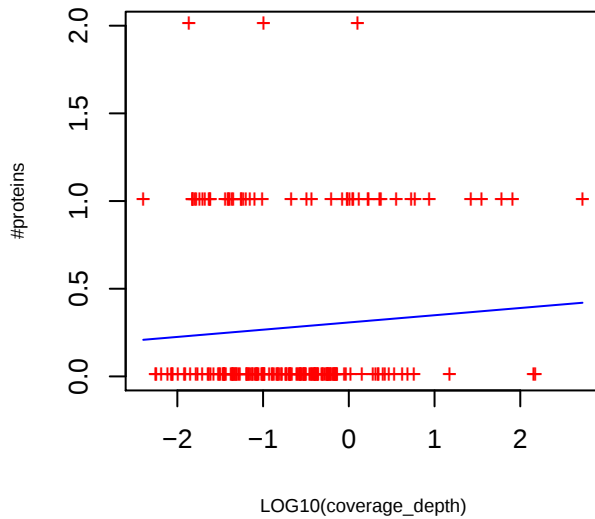


P-value curve ; red (unnorm), green (norm)



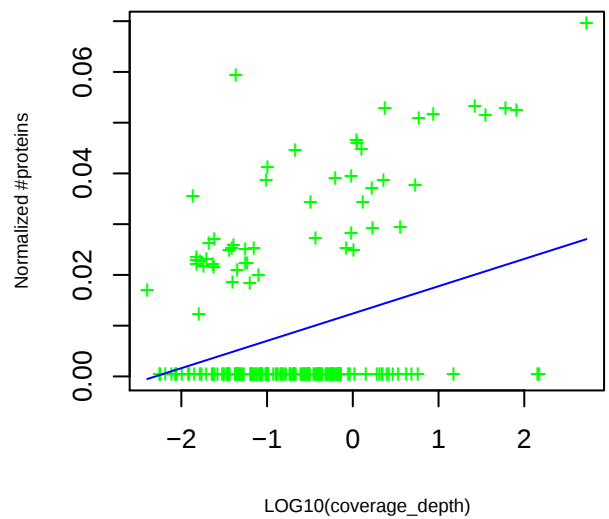
[E] COG3340 Peptidase E

slope= 0.041 p_value= 0.29 intercept= 0.31 p_value= 2.6e-11



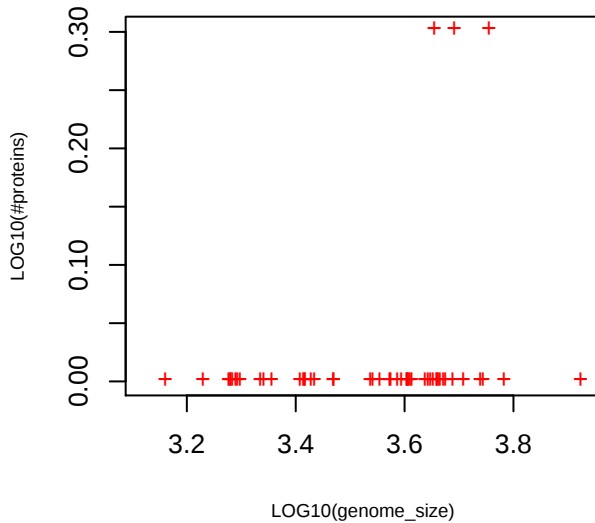
[E] COG3340 Peptidase E

slope= 0.0054 p_value= 1.6e-05 intercept= 0.012 p_value= 1.9e-16

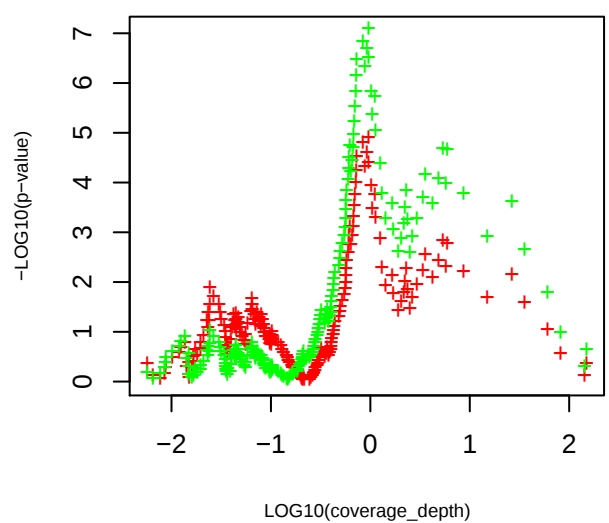


[E] COG3340 Peptidase E

slope= -0.45 p_value= 0.57 intercept= -1.35 p_value= 0.63

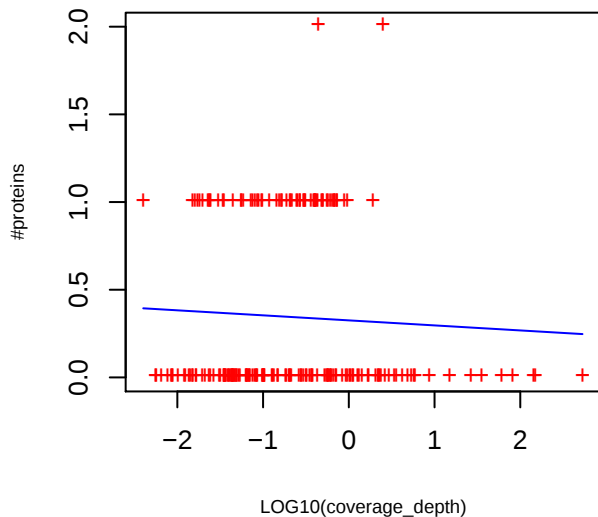


P-value curve ; red (unnorm), green (norm)



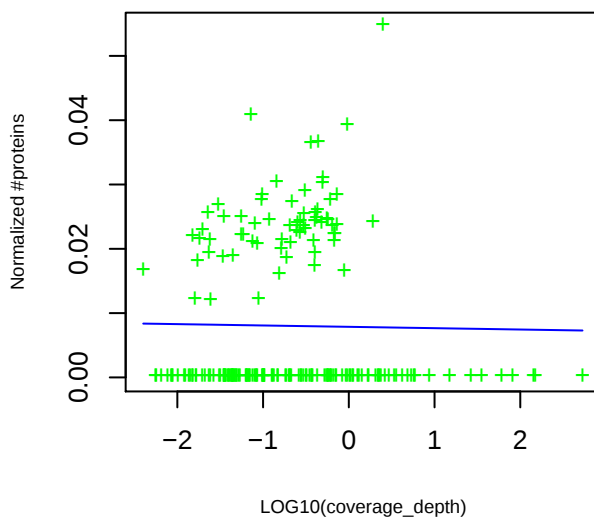
[P] COG3487 Uncharacterized iron-regulated protein

slope= -0.029 p_value= 0.47 intercept= 0.33 p_value= 1e-11



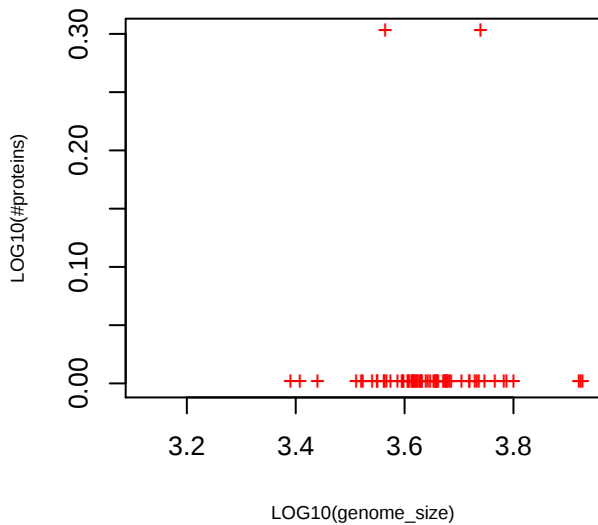
[P] COG3487 Uncharacterized iron-regulated protein

slope= -0.00021 p_value= 0.83 intercept= 0.0079 p_value= 8.2e-12

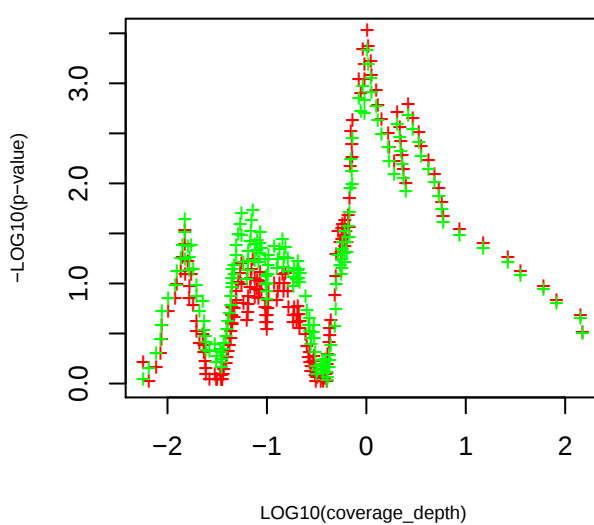


[P] COG3487 Uncharacterized iron-regulated protein

slope= 5.08 p_value= 1.4e-10 intercept= -20.67 p_value= 4.4e-13

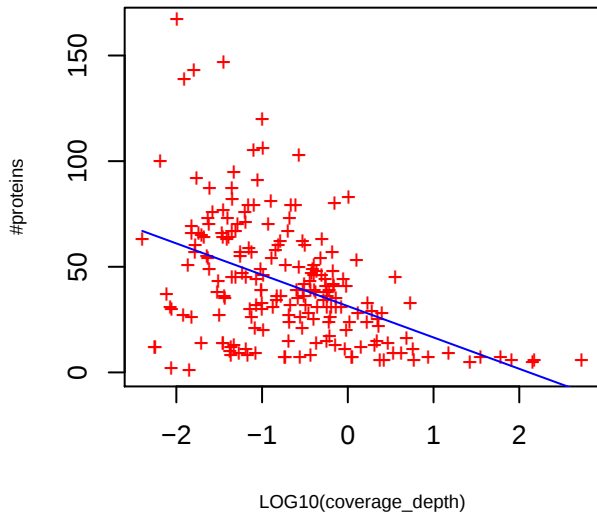


P-value curve ; red (unnorm), green (norm)



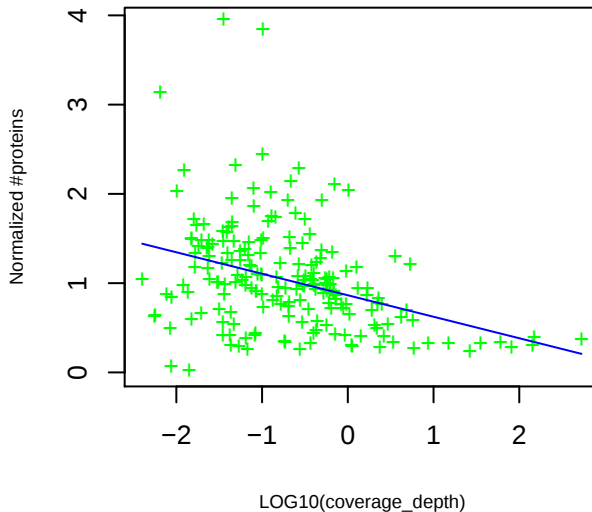
PF00072 Response_reg: response regulator receiver domain

slope= -14.84 p_value= 4e-11 intercept= 31.38 p_value= 1.4e-28



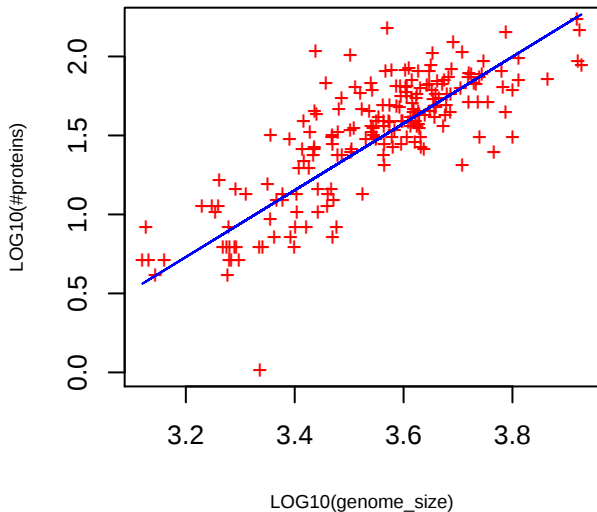
PF00072 Response_reg: response regulator receiver domain

slope= -0.24 p_value= 1.9e-07 intercept= 0.86 p_value= 7.1e-41

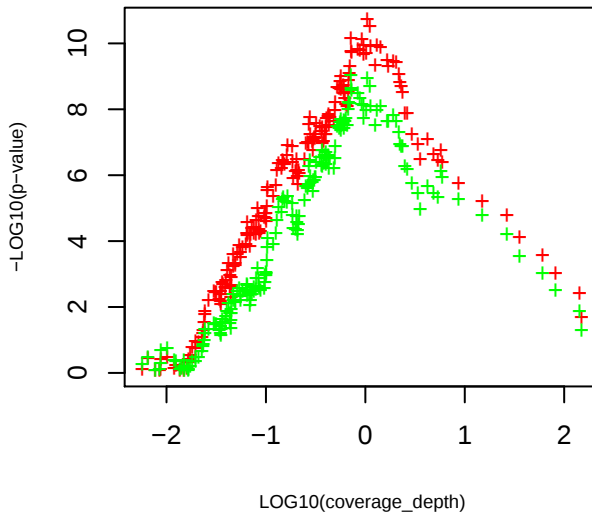


PF00072 Response_reg: response regulator receiver domain

slope= 2.11 p_value= 4.6e-23 intercept= -6.03 p_value= 1.2e-16

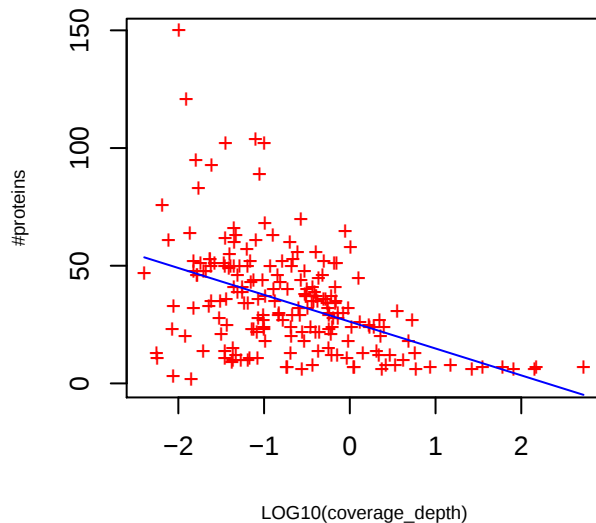


P-value curve : red (unnorm), green (norm)



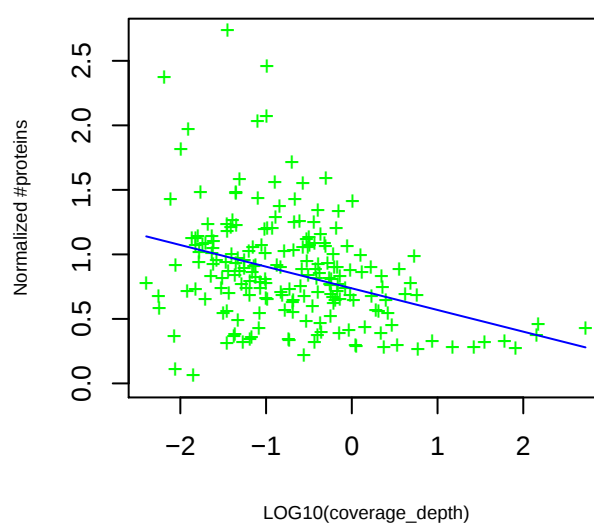
PF02518 HATPase_c: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein

slope= -11.40 p_value= 7.5e-11 intercept= 26.23 p_value= 2.2e-31



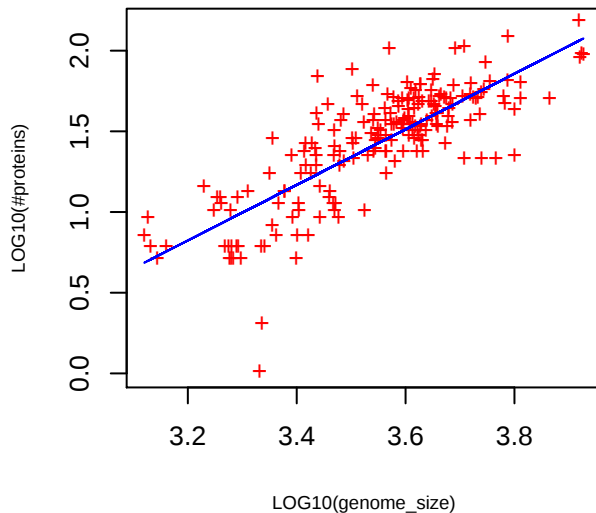
PF02518 HATPase_c: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein

slope= -0.17 p_value= 3.2e-07 intercept= 0.74 p_value= 9.8e-51

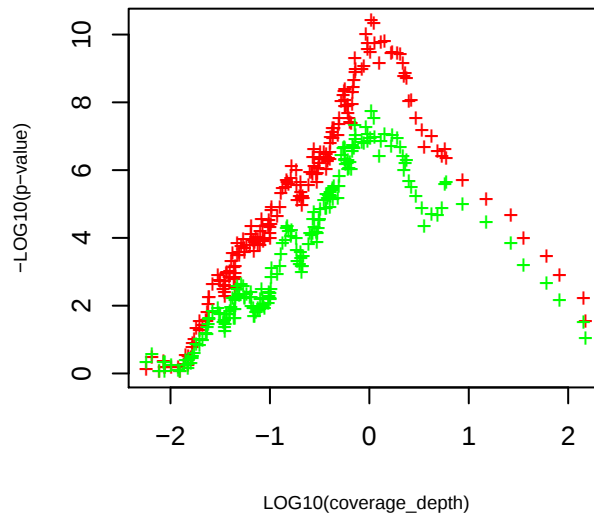


PF02518 HATPase_c: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein

slope= 1.72 p_value= 9.5e-45 intercept= -4.69 p_value= 8e-32

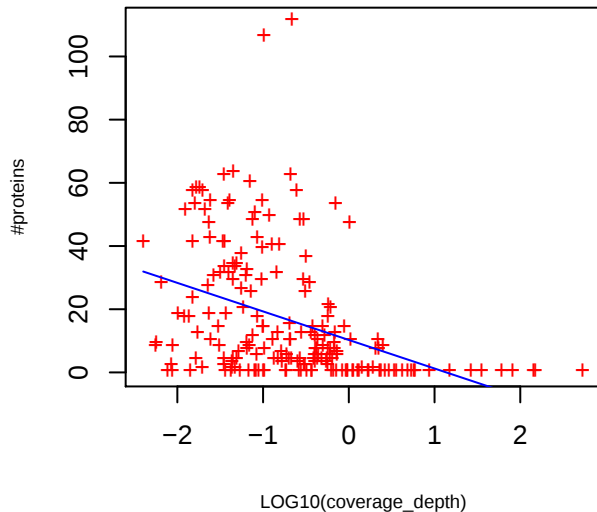


P-value curve ; red (unnorm), green (norm)



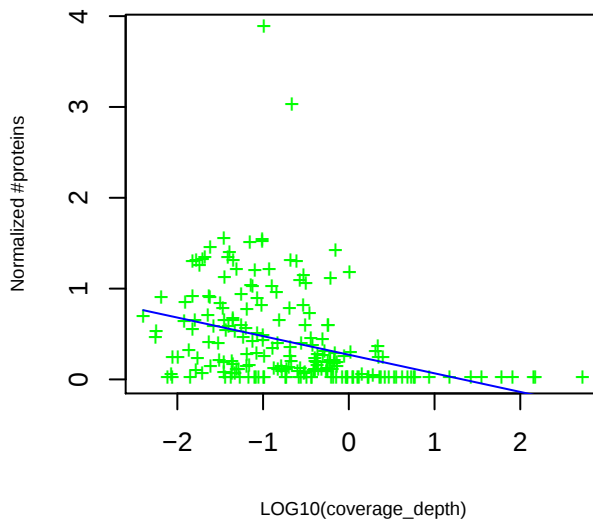
PF00990 GGDEF: GGDEF domain

slope= -9.03 p_value= 1.2e-08 intercept= 10.27 p_value= 1e-08



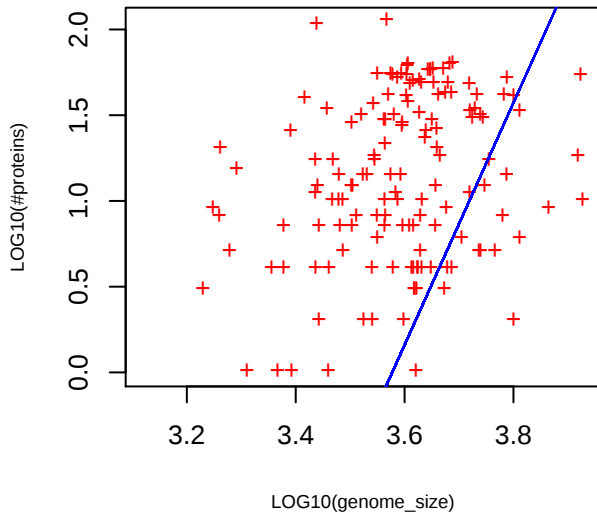
PF00990 GGDEF: GGDEF domain

slope= -0.20 p_value= 9e-07 intercept= 0.27 p_value= 1.1e-08

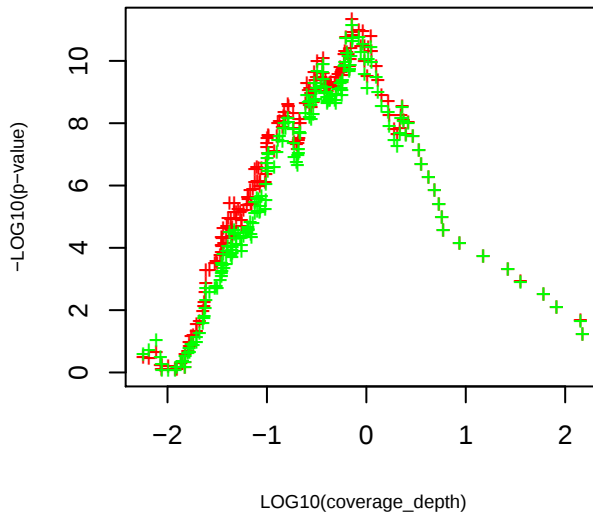


PF00990 GGDEF: GGDEF domain

slope= 7.06 p_value= 7.7e-14 intercept= -25.26 p_value= 5.2e-14

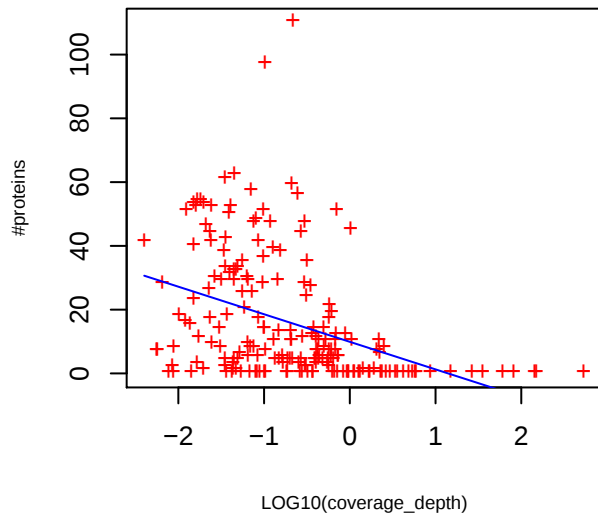


P-value curve : red (unnorm), green (norm)



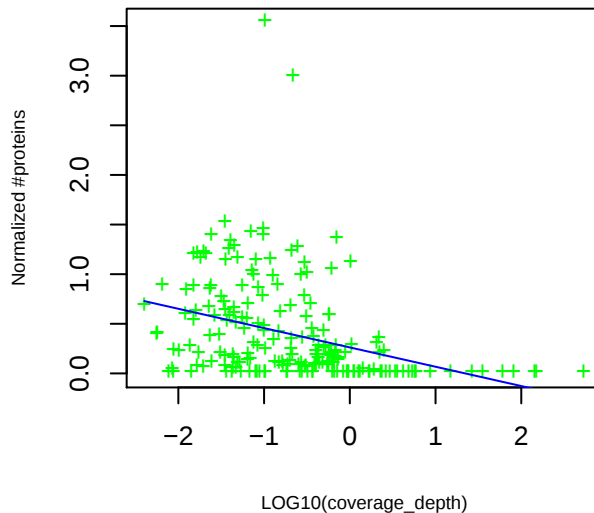
TIGR00254 GGDEF: diguanylate cyclase (GGDEF) domain

slope= -8.65 p_value= 1.3e-08 intercept= 9.91 p_value= 8.4e-09



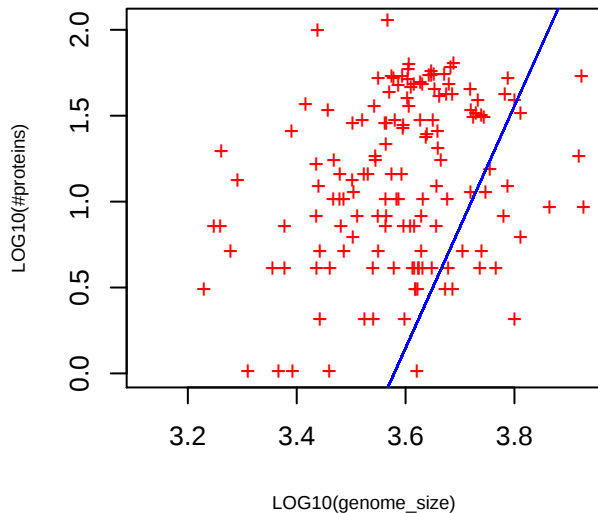
TIGR00254 GGDEF: diguanylate cyclase (GGDEF) domain

slope= -0.19 p_value= 9.2e-07 intercept= 0.26 p_value= 7.5e-09

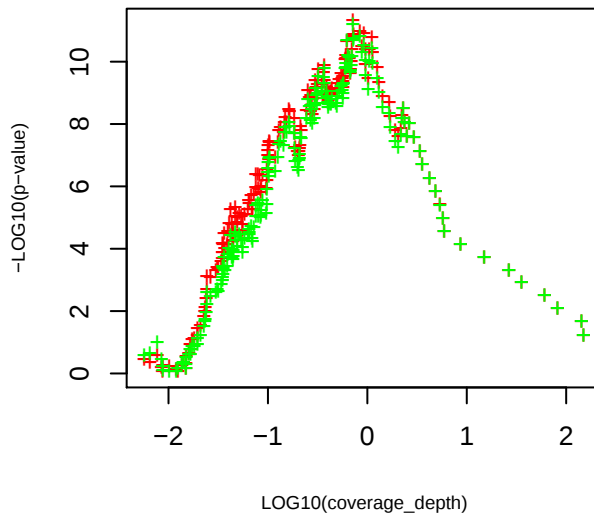


TIGR00254 GGDEF: diguanylate cyclase (GGDEF) domain

slope= 7.04 p_value= 7.3e-14 intercept= -25.21 p_value= 4.8e-14

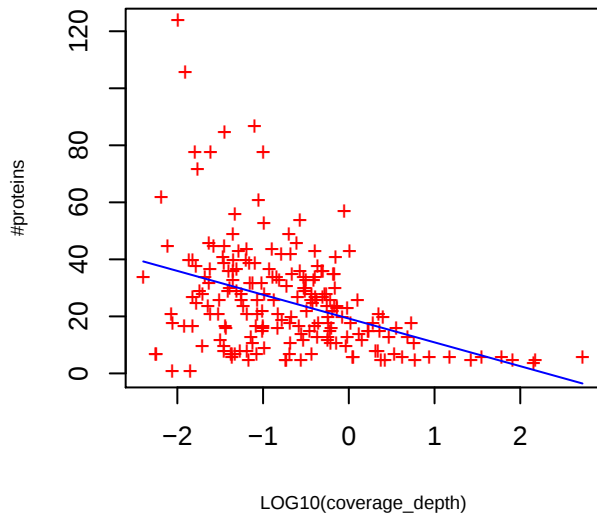


P-value curve : red (unnorm), green (norm)



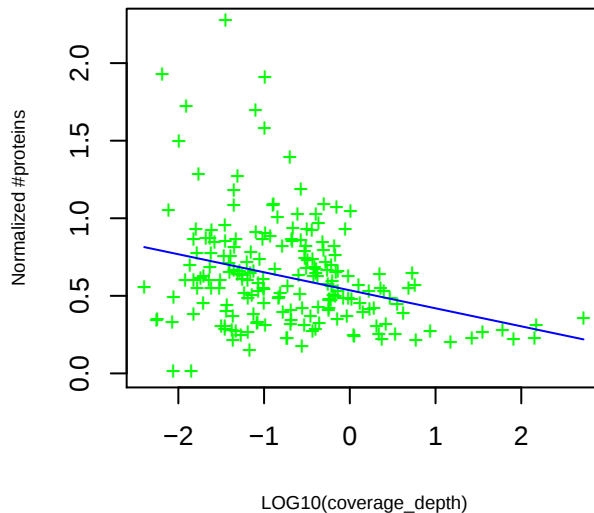
PF00512 HisKA: His Kinase A (phosphoacceptor) domain

slope= -8.35 p_value= 8.7e-09 intercept= 19.24 p_value= 5.1e-26



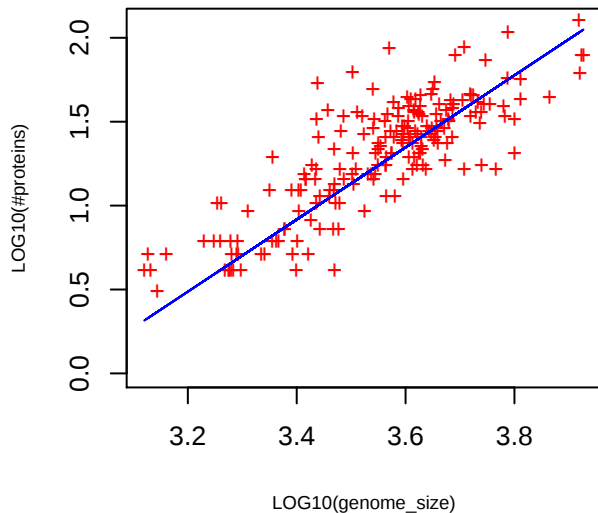
PF00512 HisKA: His Kinase A (phosphoacceptor) domain

slope= -0.12 p_value= 1.8e-05 intercept= 0.54 p_value= 3.8e-43

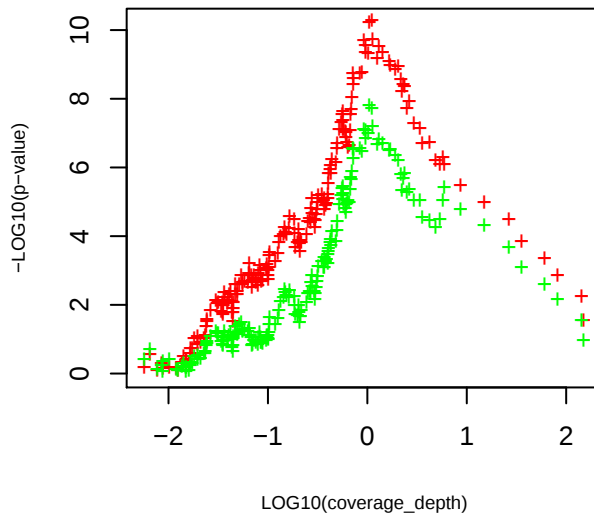


PF00512 HisKA: His Kinase A (phosphoacceptor) domain

slope= 2.15 p_value= 2.7e-17 intercept= -6.39 p_value= 3.6e-13

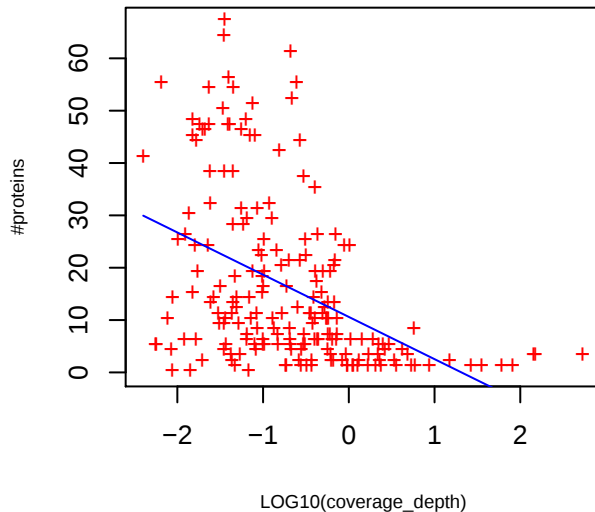


P-value curve ; red (unnorm), green (norm)



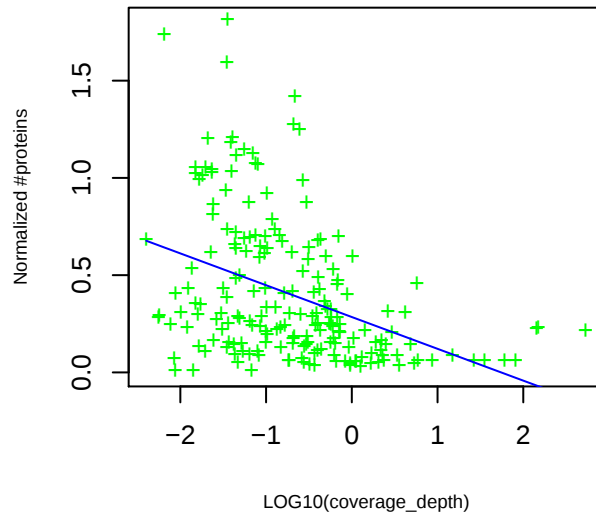
PF00672 HAMP: HAMP domain

slope= -8.07 p_value= 8.6e-11 intercept= 10.60 p_value= 1.2e-13



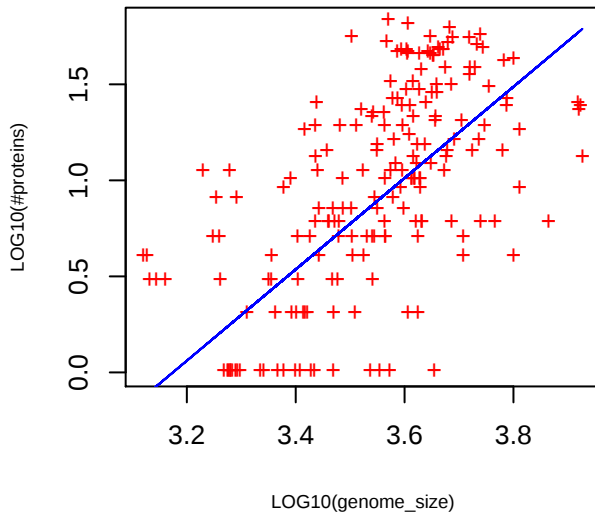
PF00672 HAMP: HAMP domain

slope= -0.16 p_value= 7.7e-09 intercept= 0.28 p_value= 2.6e-17

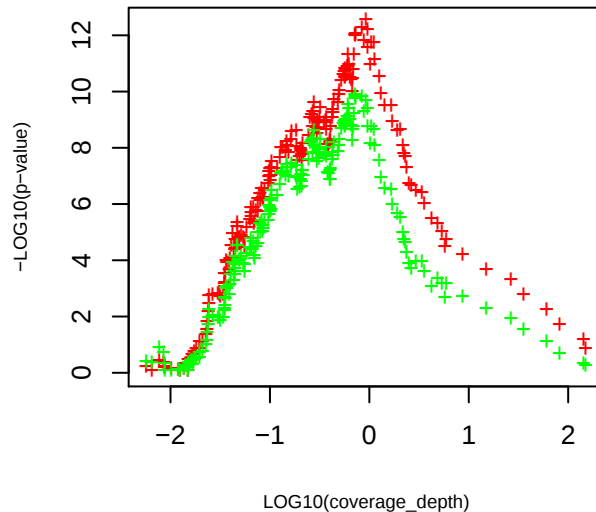


PF00672 HAMP: HAMP domain

slope= 2.38 p_value= 6.3e-13 intercept= -7.55 p_value= 7.3e-11

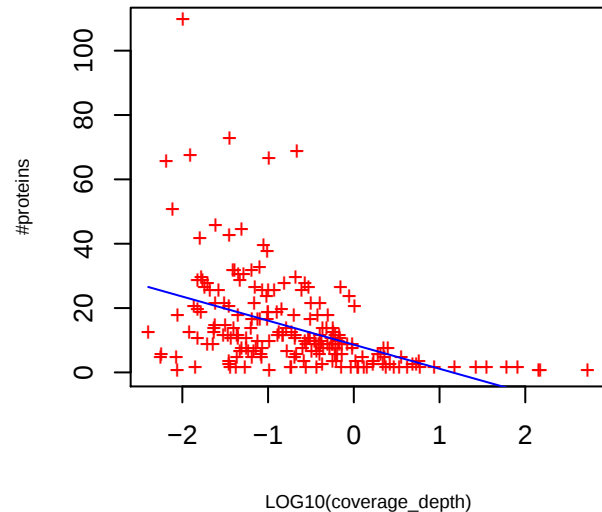


P-value curve ; red (unnorm), green (norm)



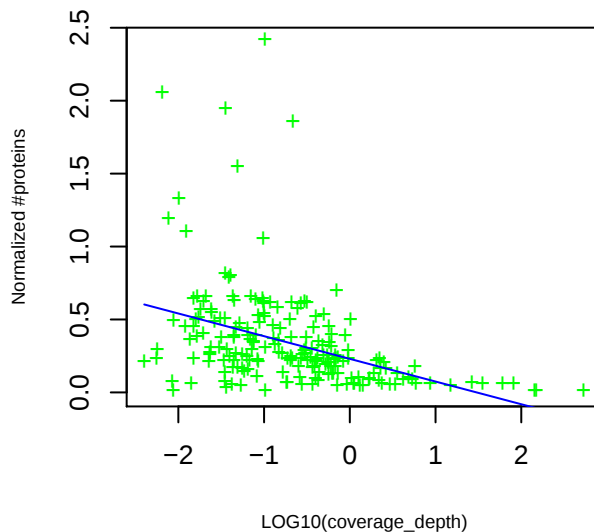
TIGR00229 sensory_box: PAS domain S-box

slope= -7.48 p_value= 8.2e-11 intercept= 8.61 p_value= 3.9e-11



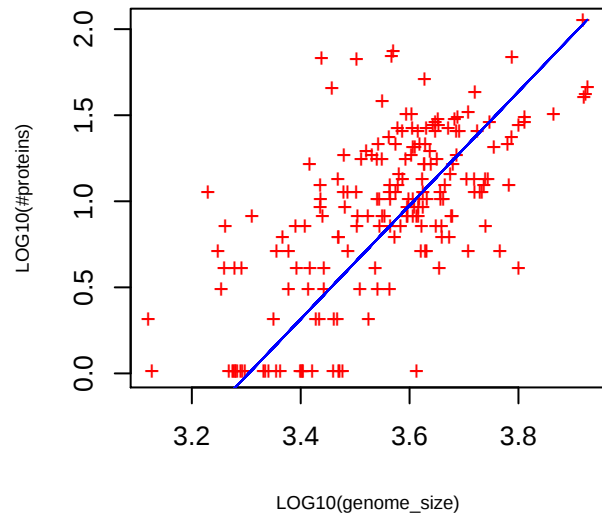
TIGR00229 sensory_box: PAS domain S-box

slope= -0.16 p_value= 7.1e-09 intercept= 0.23 p_value= 1.7e-13

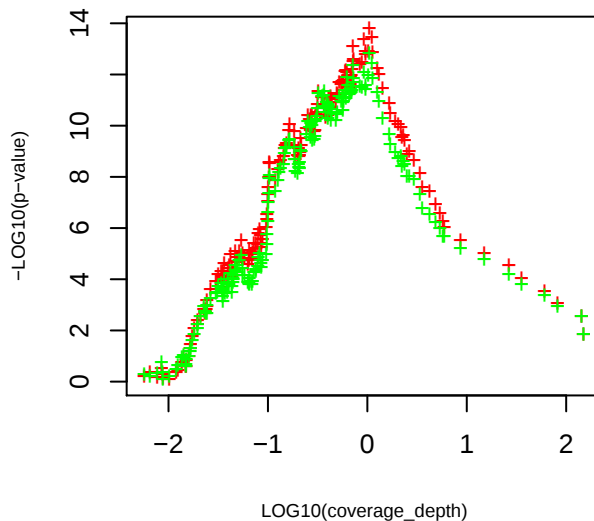


TIGR00229 sensory_box: PAS domain S-box

slope= 3.30 p_value= 9.6e-20 intercept= -10.91 p_value= 1e-17

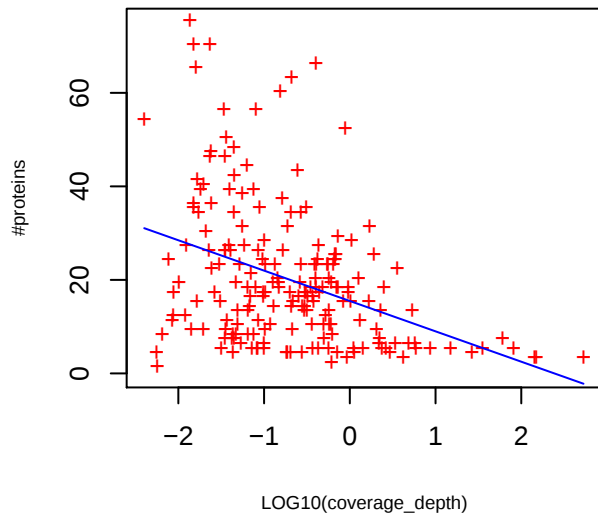


P-value curve : red (unnorm), green (norm)



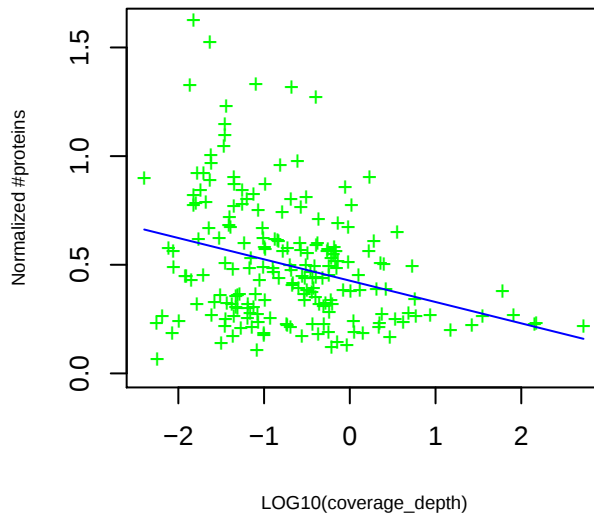
PF00583 Acetyltransf_1: acetyltransferase, GNAT family

slope= -6.49 p_value= 3.8e-08 intercept= 15.49 p_value= 1.7e-25



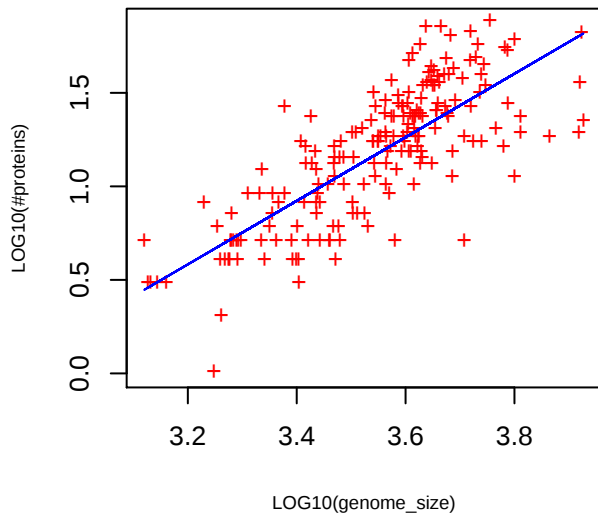
PF00583 Acetyltransf_1: acetyltransferase, GNAT family

slope= -0.098 p_value= 1.1e-05 intercept= 0.43 p_value= 1.6e-41

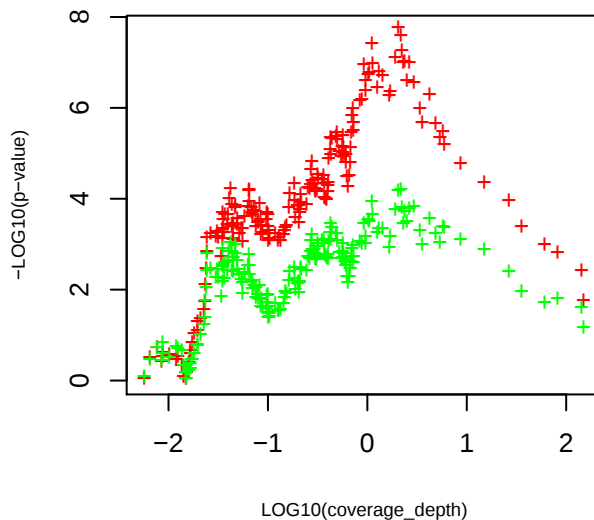


PF00583 Acetyltransf_1: acetyltransferase, GNAT family

slope= 1.70 p_value= 1.7e-40 intercept= -4.85 p_value= 1.9e-30

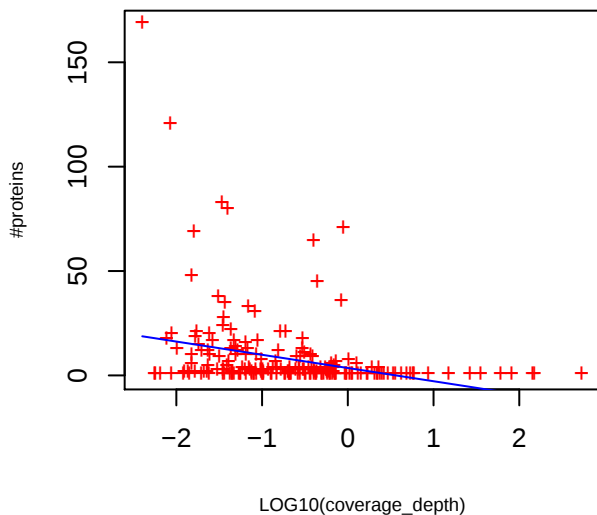


P-value curve ; red (unnorm), green (norm)



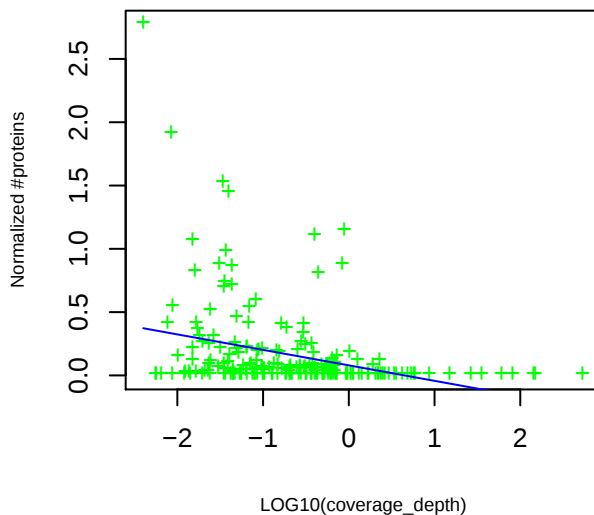
PF01609 Transposase_11: transposase, IS4 family

slope= -6.34 p_value= 3.6e-05 intercept= 3.55 p_value= 0.037



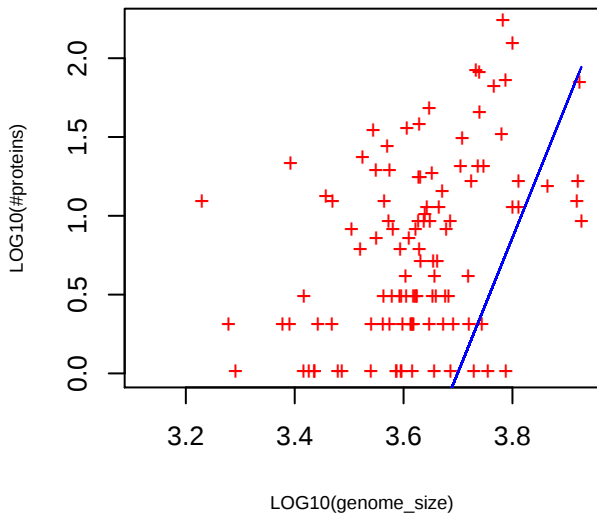
PF01609 Transposase_11: transposase, IS4 family

slope= -0.12 p_value= 7.2e-06 intercept= 0.08 p_value= 0.0086

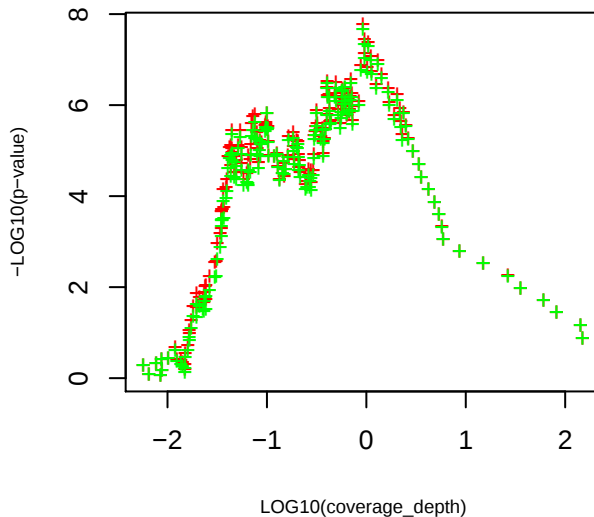


PF01609 Transposase_11: transposase, IS4 family

slope= 8.55 p_value= 4.9e-19 intercept= -31.62 p_value= 2.9e-20

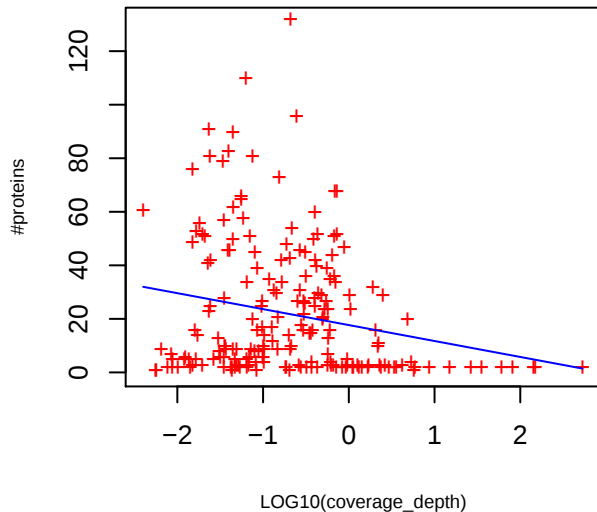


P-value curve : red (unnorm), green (norm)



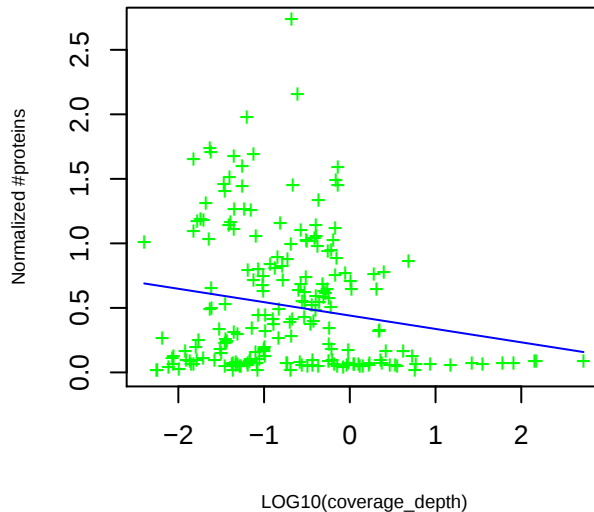
PF00126 HTH_1: transcriptional regulator, LysR family

slope= -5.96 p_value= 0.0026 intercept= 17.69 p_value= 9.2e-14



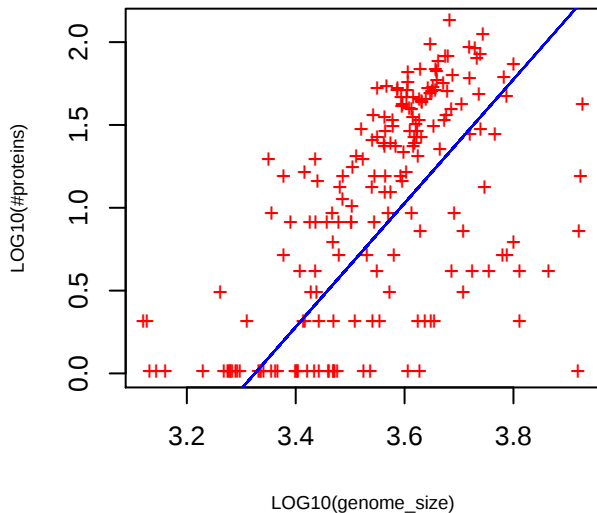
PF00126 HTH_1: transcriptional regulator, LysR family

slope= -0.10 p_value= 0.013 intercept= 0.44 p_value= 1.2e-17

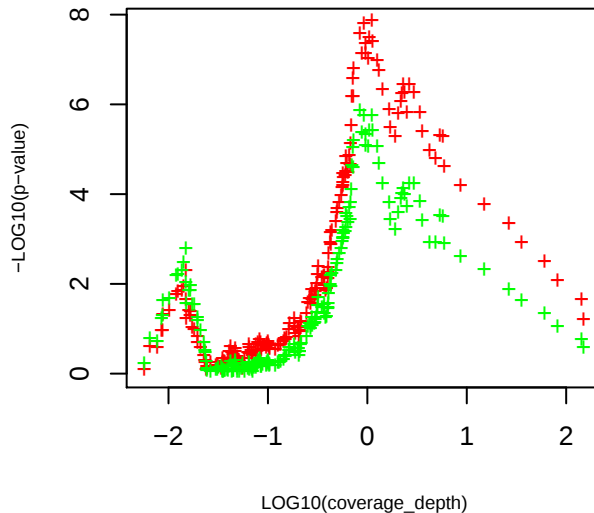


PF00126 HTH_1: transcriptional regulator, LysR family

slope= 3.74 p_value= 4.6e-18 intercept= -12.42 p_value= 2.3e-16

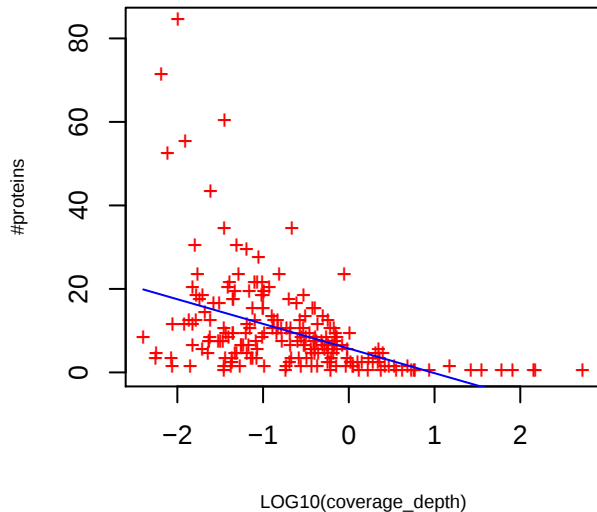


P-value curve ; red (unnorm), green (norm)



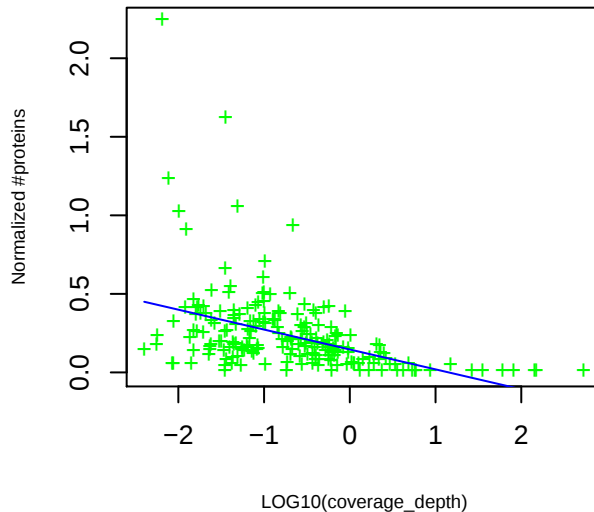
PF08448 PAS_4: PAS fold

slope= -5.90 p_value= 4.9e-11 intercept= 5.73 p_value= 1.0e-08



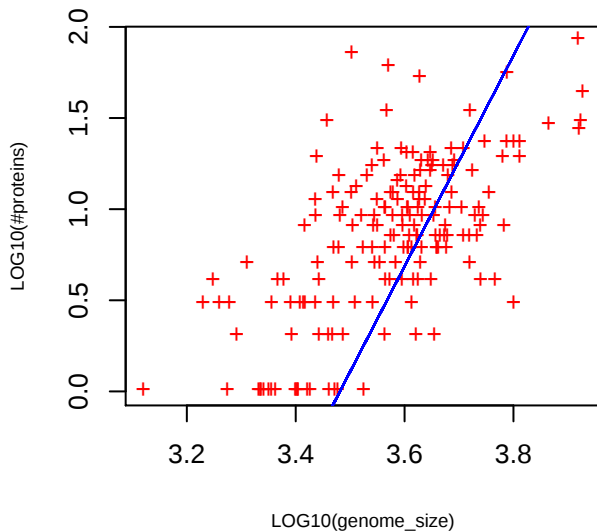
PF08448 PAS_4: PAS fold

slope= -0.13 p_value= 2.4e-10 intercept= 0.15 p_value= 1.1e-10

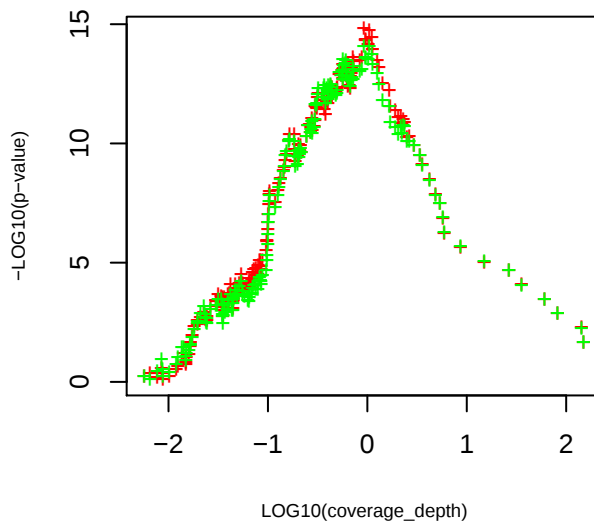


PF08448 PAS_4: PAS fold

slope= 5.78 p_value= 2e-23 intercept= -20.13 p_value= 9e-23

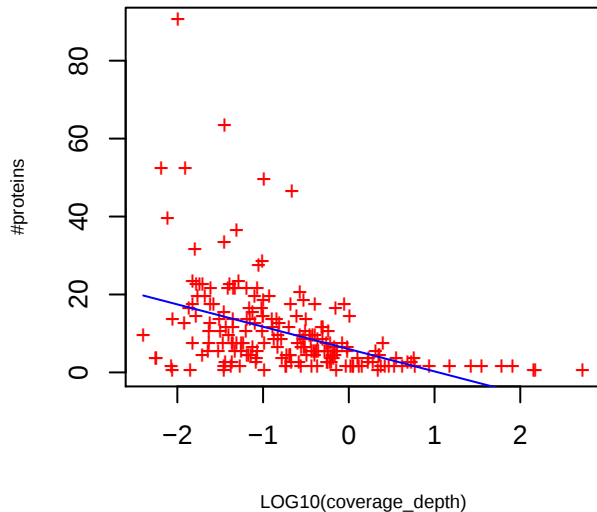


P-value curve ; red (unnorm), green (norm)



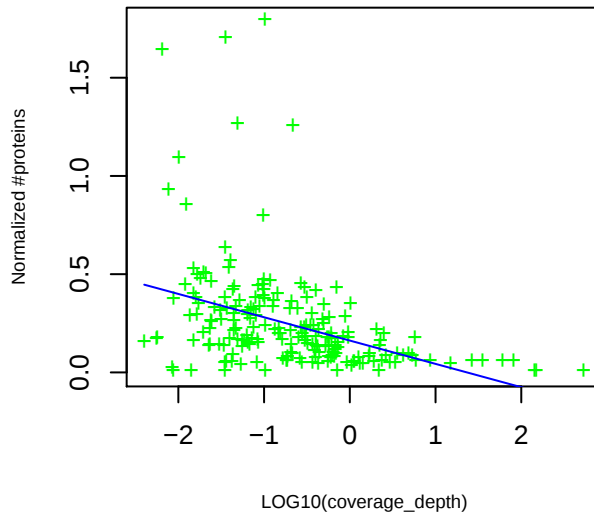
PF00989 PAS: PAS fold

slope= -5.73 p_value= 1.6e-10 intercept= 5.99 p_value= 2.5e-09



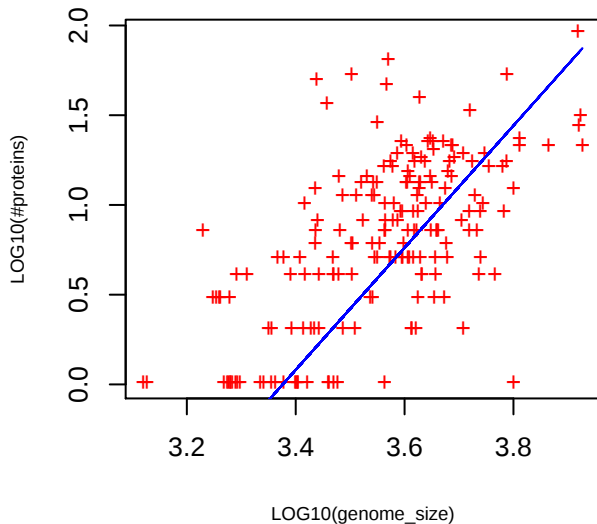
PF00989 PAS: PAS fold

slope= -0.12 p_value= 1.4e-08 intercept= 0.16 p_value= 1.5e-11

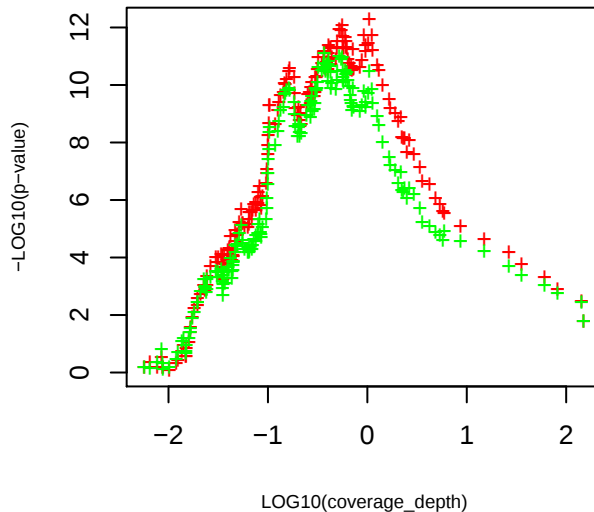


PF00989 PAS: PAS fold

slope= 3.40 p_value= 4.7e-14 intercept= -11.49 p_value= 5.3e-13

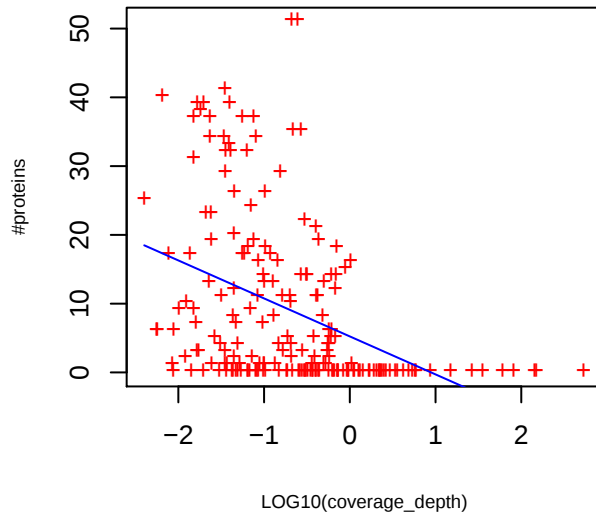


P-value curve ; red (unnorm), green (norm)



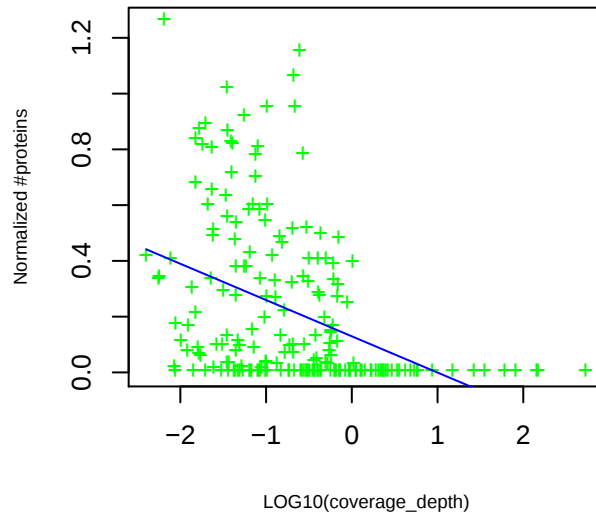
PF00015 MCPsignal: Methyl-accepting chemotaxis protein (MCP) signaling domain

slope= -5.52 p_value= 6.5e-09 intercept= 5.24 p_value= 8.1e-07



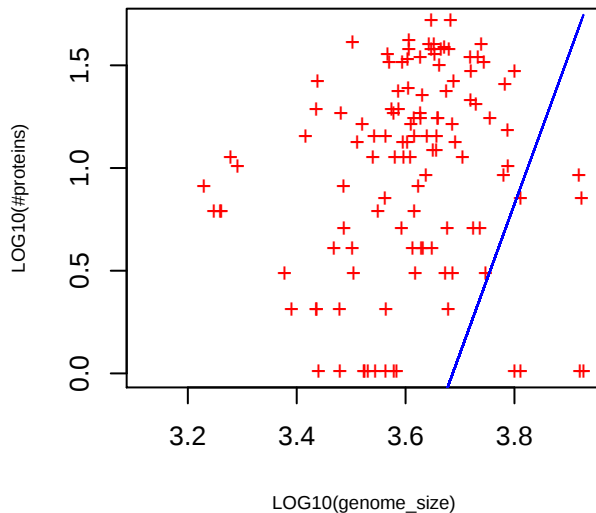
PF00015 MCPsignal: Methyl-accepting chemotaxis protein (MCP) signaling domain

slope= -0.13 p_value= 7.4e-09 intercept= 0.13 p_value= 2.7e-07

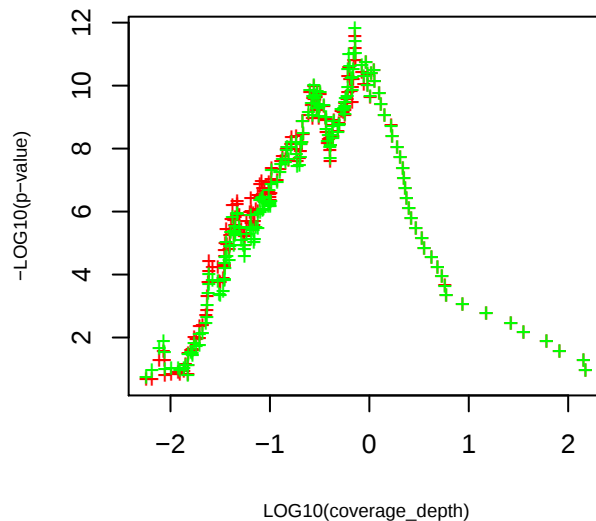


PF00015 MCPsignal: Methyl-accepting chemotaxis protein (MCP) signaling domain

slope= 7.27 p_value= 9.8e-13 intercept= -26.79 p_value= 1.6e-13

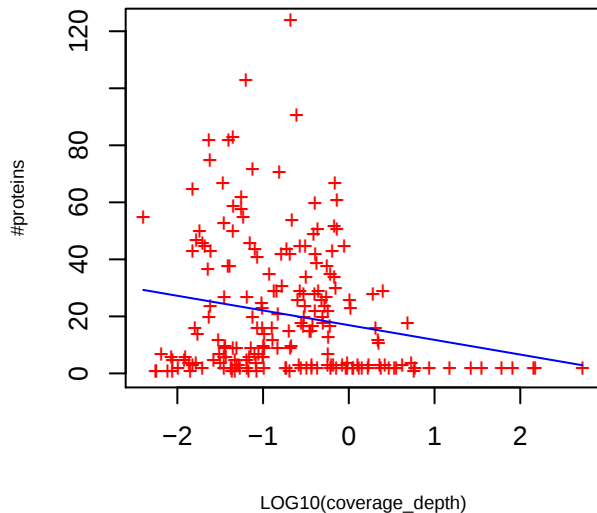


P-value curve ; red (unnorm), green (norm)



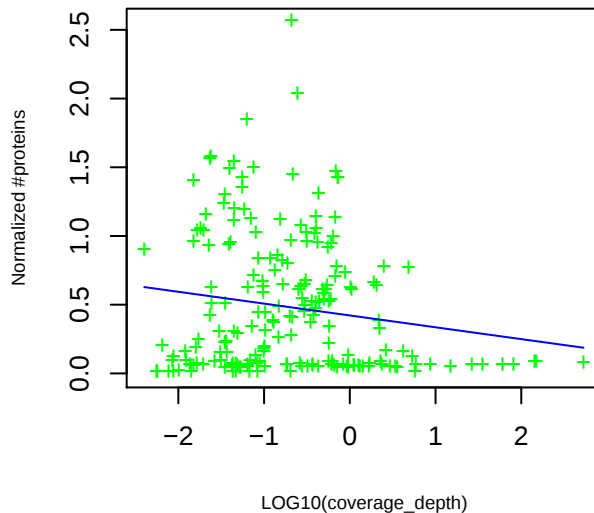
PF03466 LysR_substrate: LysR substrate binding domain

slope= -5.16 p_value= 0.0053 intercept= 16.92 p_value= 3.4e-14



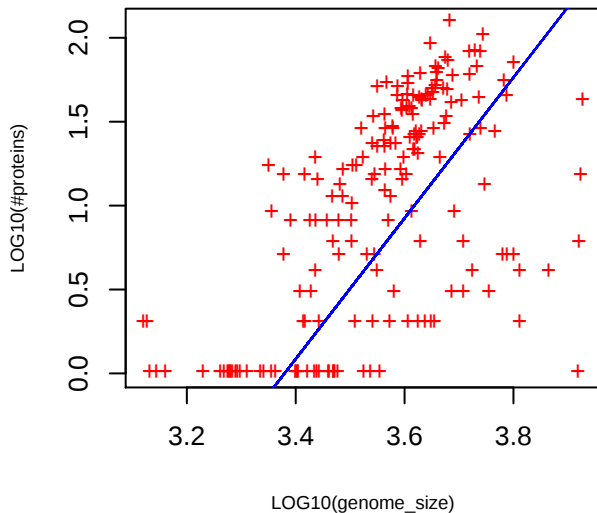
PF03466 LysR_substrate: LysR substrate binding domain

slope= -0.086 p_value= 0.028 intercept= 0.42 p_value= 3.6e-18

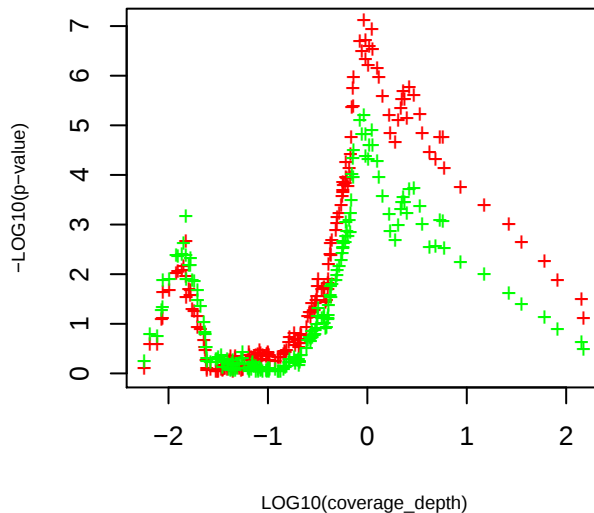


PF03466 LysR_substrate: LysR substrate binding domain

slope= 4.19 p_value= 3.5e-15 intercept= -14.17 p_value= 4.4e-14

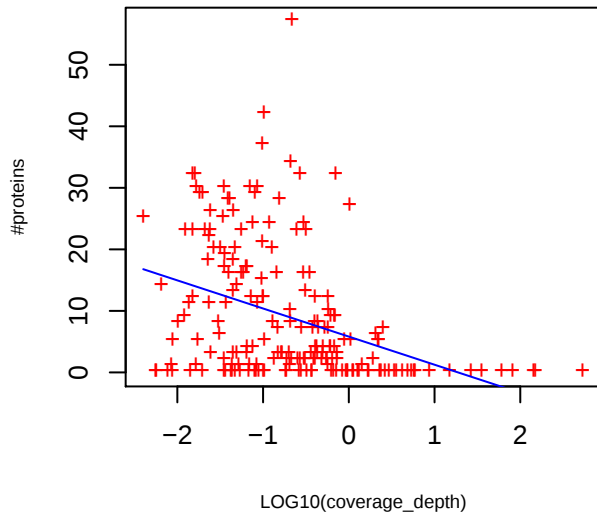


P-value curve ; red (unnorm), green (norm)



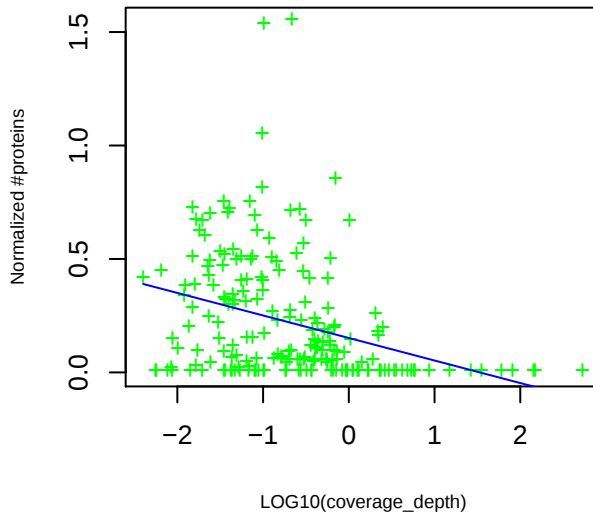
PF00563 EAL: cyclic diguanylate phosphodiesterase (EAL) domain

slope= -4.57 p_value= 4.7e-08 intercept= 5.82 p_value= 1.0e-09



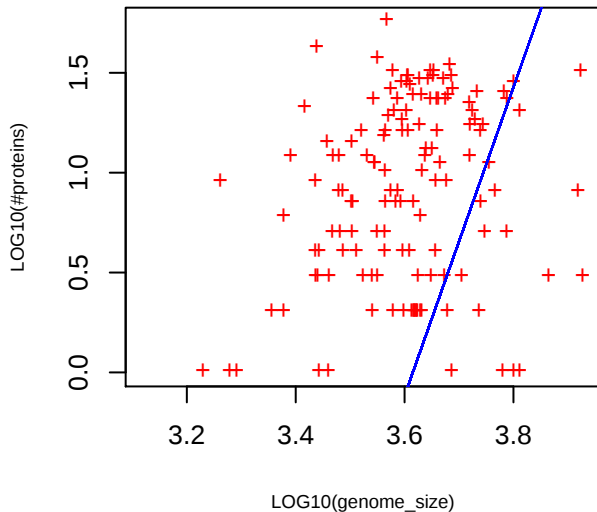
PF00563 EAL: cyclic diguanylate phosphodiesterase (EAL) domain

slope= -0.10 p_value= 2.5e-06 intercept= 0.15 p_value= 4.7e-10

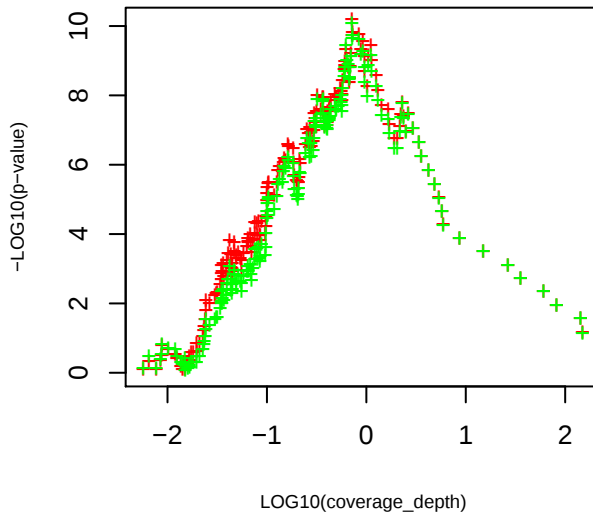


PF00563 EAL: cyclic diguanylate phosphodiesterase (EAL) domain

slope= 7.72 p_value= 3.2e-17 intercept= -27.92 p_value= 1.0e-17

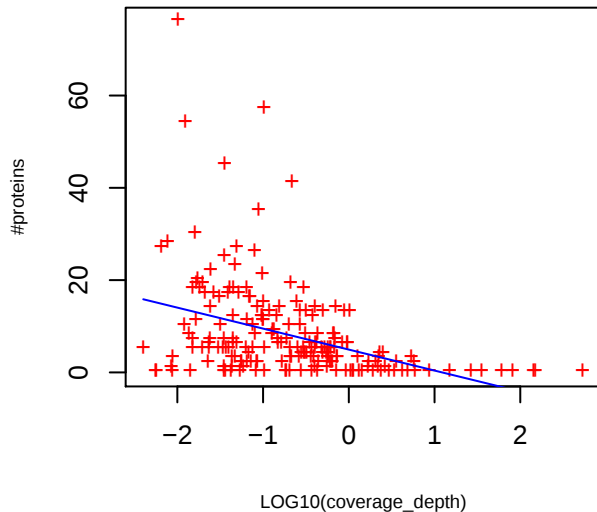


P-value curve ; red (unnorm), green (norm)



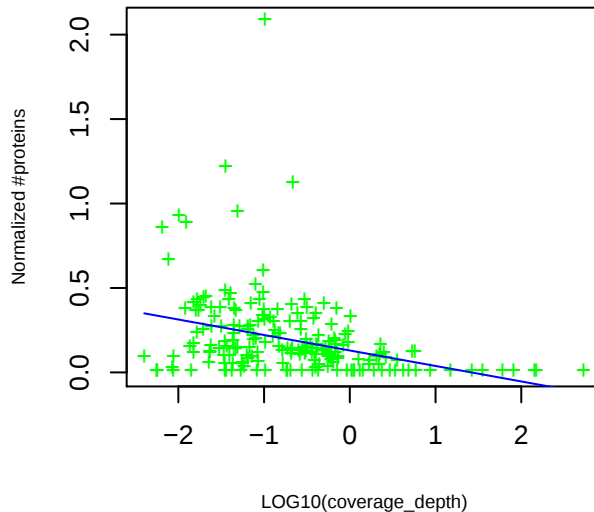
PF08447 PAS_3: PAS fold

slope= -4.55 p_value= 1.9e-08 intercept= 4.95 p_value= 5.6e-08



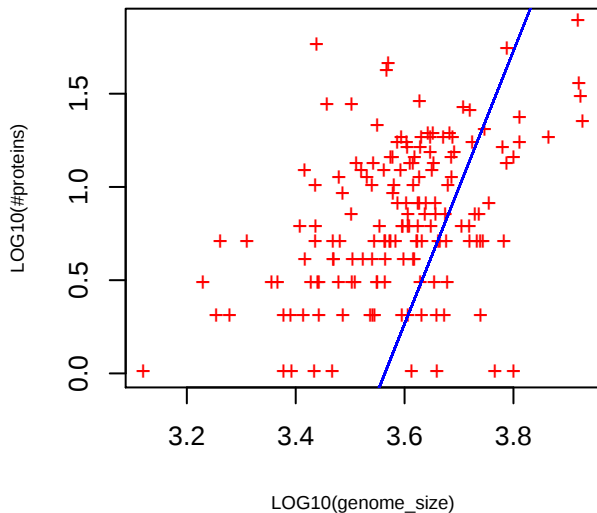
PF08447 PAS_3: PAS fold

slope= -0.092 p_value= 1.2e-06 intercept= 0.13 p_value= 2e-09

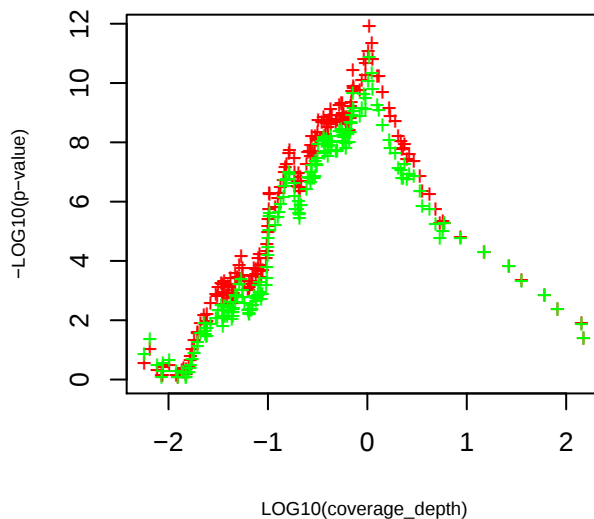


PF08447 PAS_3: PAS fold

slope= 7.32 p_value= 2.2e-21 intercept= -26.08 p_value= 1.6e-21

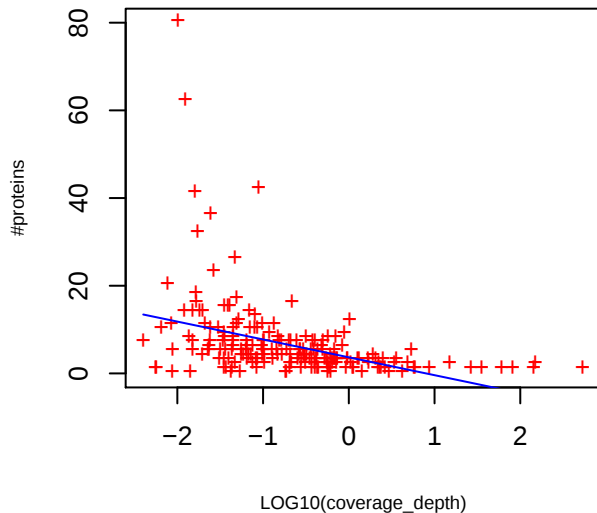


P-value curve ; red (unnorm), green (norm)



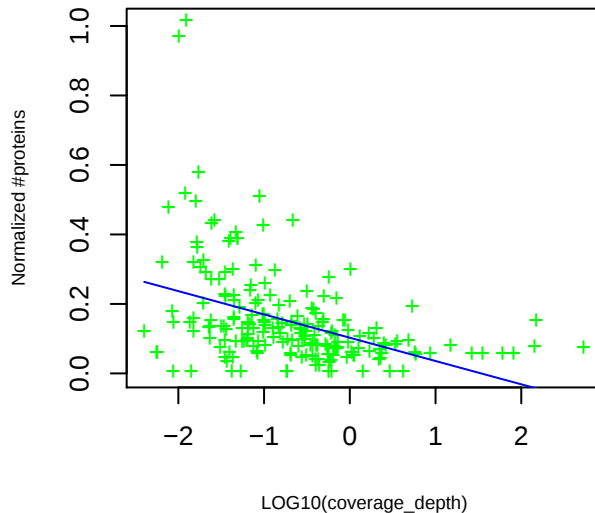
PF01590 GAF: GAF domain

slope= -4.07 p_value= 1.0e-08 intercept= 3.67 p_value= 3.6e-06



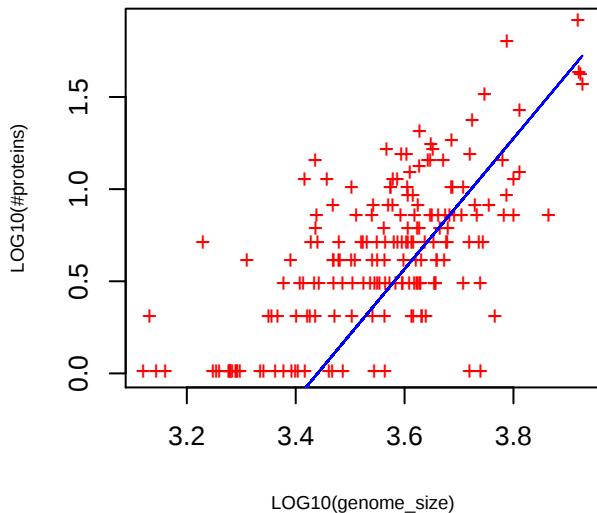
PF01590 GAF: GAF domain

slope= -0.067 p_value= 7.7e-10 intercept= 0.10 p_value= 8.3e-16

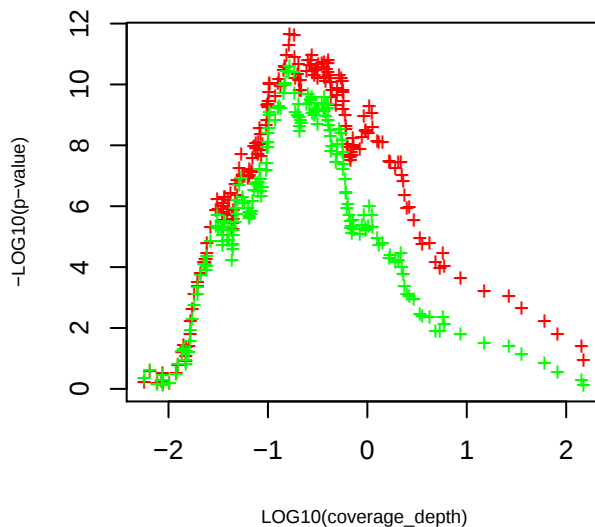


PF01590 GAF: GAF domain

slope= 3.54 p_value= 2.5e-14 intercept= -12.19 p_value= 1.2e-13

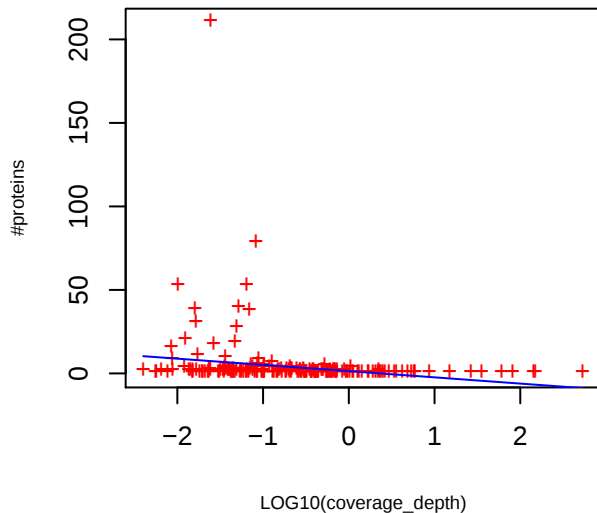


P-value curve ; red (unnorm), green (norm)



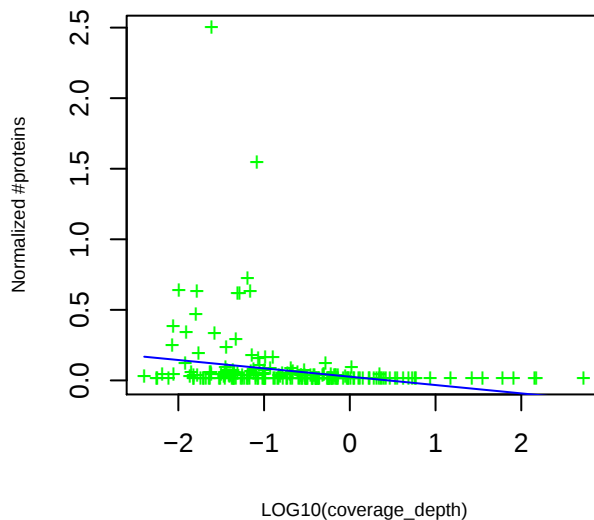
PF00069 Pkinase: protein kinase domain

slope= -3.73 p_value= 0.0074 intercept= 1.38 p_value= 0.38



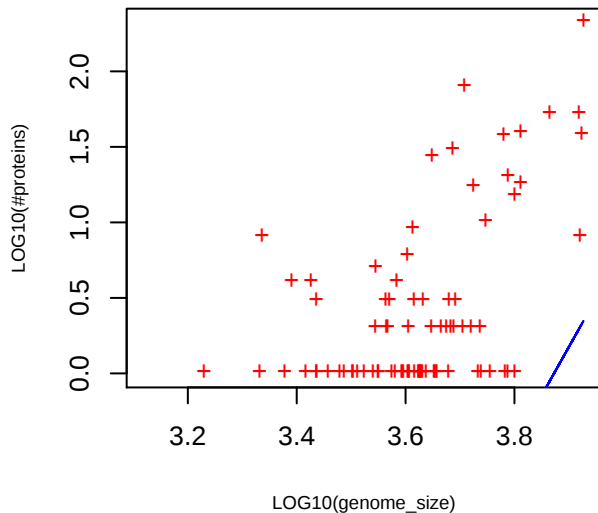
PF00069 Pkinase: protein kinase domain

slope= -0.059 p_value= 0.0016 intercept= 0.026 p_value= 0.21

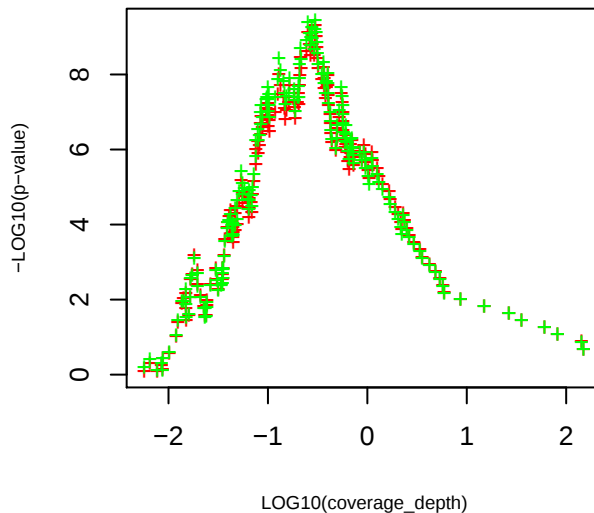


PF00069 Pkinase: protein kinase domain

slope= 6.42 p_value= 2.7e-12 intercept= -24.84 p_value= 4.4e-14

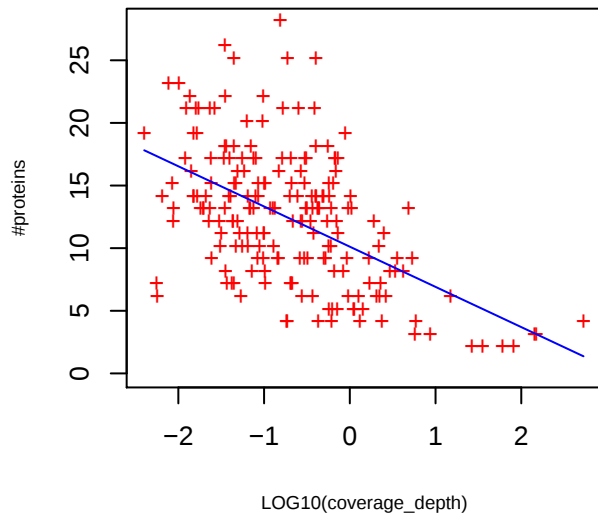


P-value curve ; red (unnorm), green (norm)



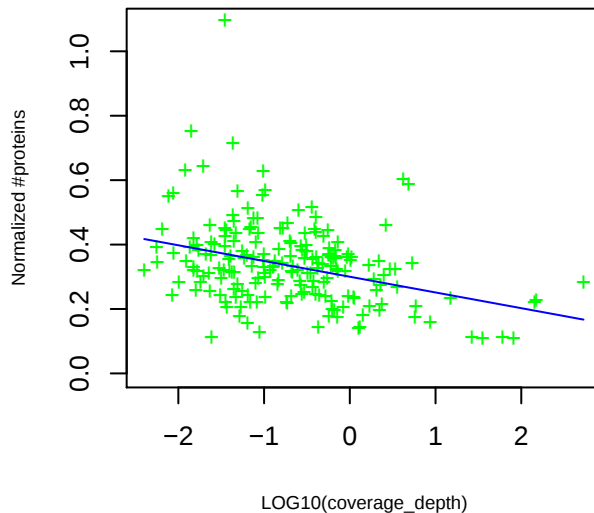
PF00702 Hydrolase: haloacid dehalogenase-like hydrolase

slope= -3.21 p_value= 1.1e-15 intercept= 10.12 p_value= 4.3e-61



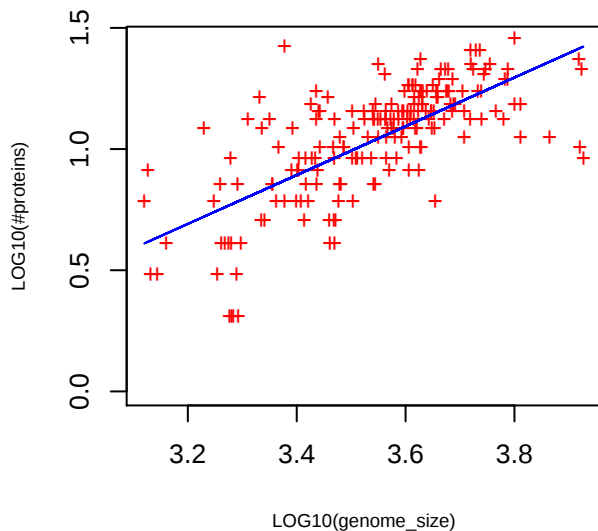
PF00702 Hydrolase: haloacid dehalogenase-like hydrolase

slope= -0.049 p_value= 7e-07 intercept= 0.30 p_value= 4.5e-70

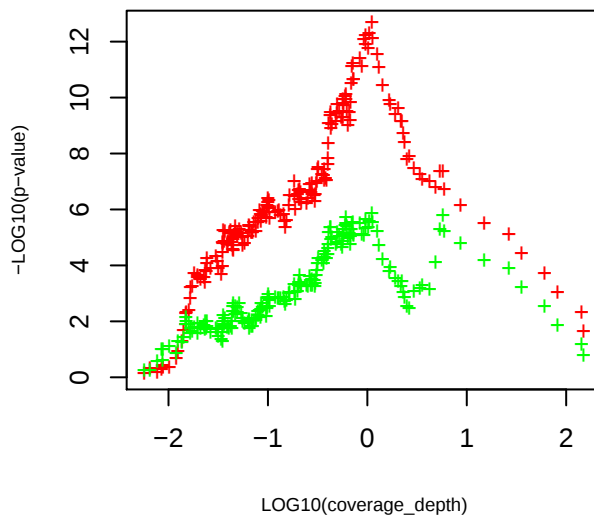


PF00702 Hydrolase: haloacid dehalogenase-like hydrolase

slope= 1.01 p_value= 1.3e-30 intercept= -2.53 p_value= 1.4e-18

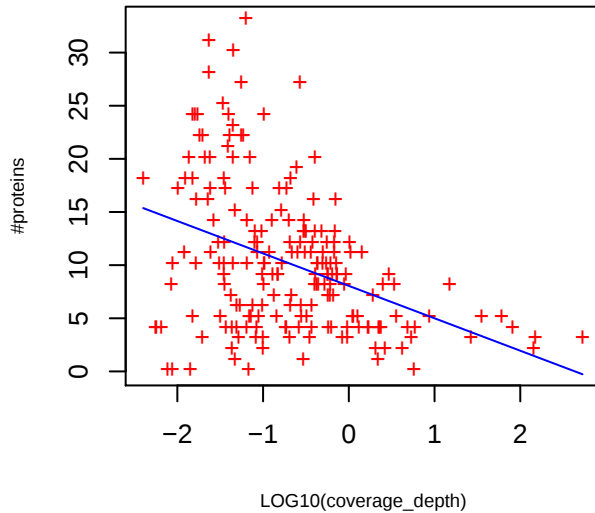


P-value curve ; red (unnorm), green (norm)



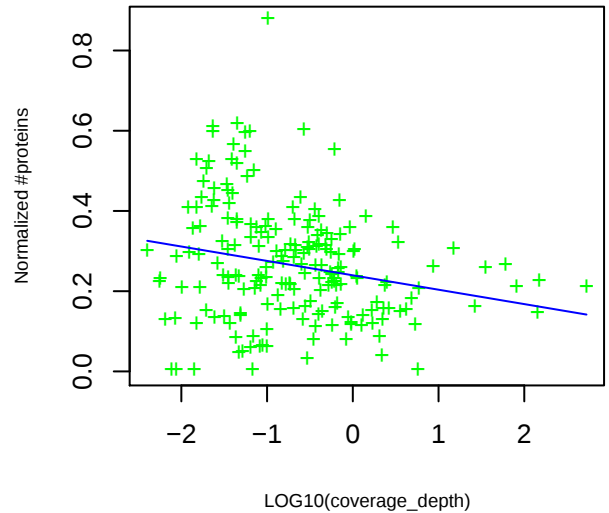
PF00486 Trans_reg_C: transcriptional regulatory protein, C-terminal

slope= -3.05 p_value= 9.4e-09 intercept= 8.05 p_value= 2.4e-31



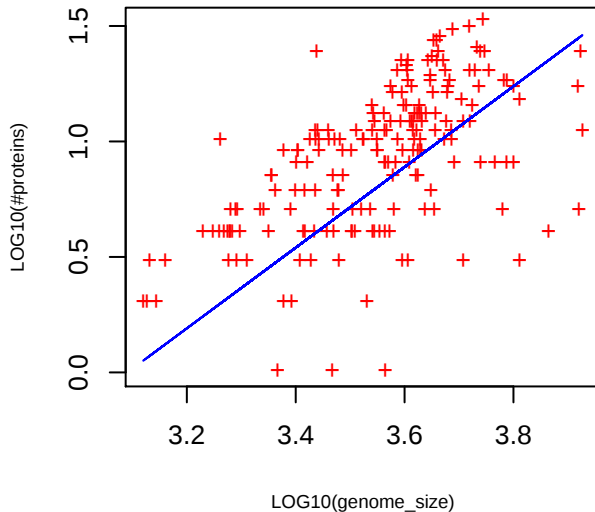
PF00486 Trans_reg_C: transcriptional regulatory protein, C-terminal

slope= -0.036 p_value= 0.0015 intercept= 0.24 p_value= 2.7e-46

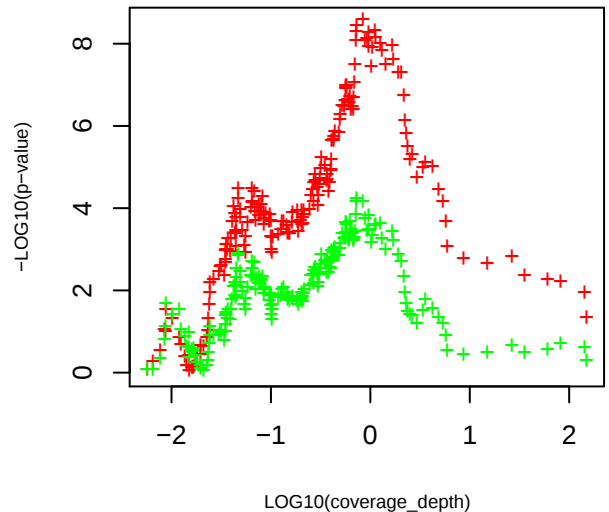


PF00486 Trans_reg_C: transcriptional regulatory protein, C-terminal

slope= 1.75 p_value= 9.2e-07 intercept= -5.40 p_value= 1.7e-05

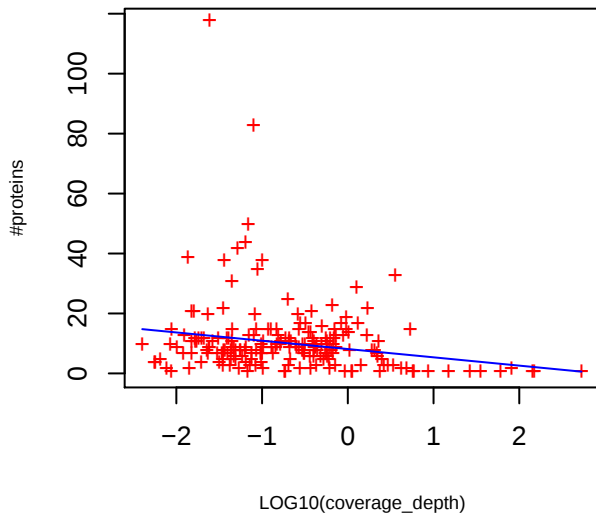


P-value curve ; red (unnorm), green (norm)



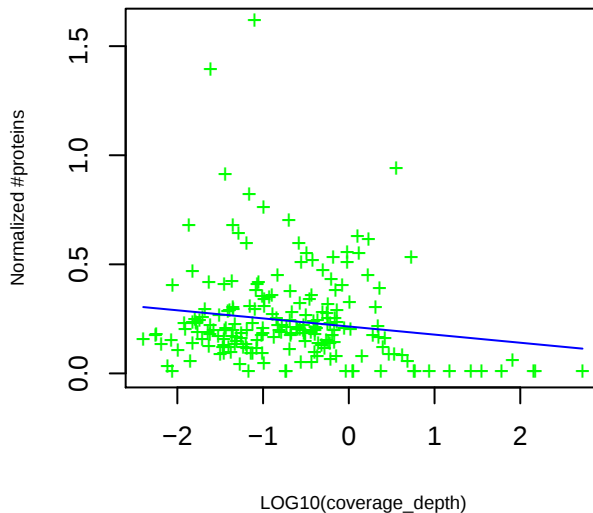
PF08281 Sigma70_r4_2: Sigma-70, region 4

slope= -2.77 p_value= 0.0051 intercept= 8.13 p_value= 4.8e-12



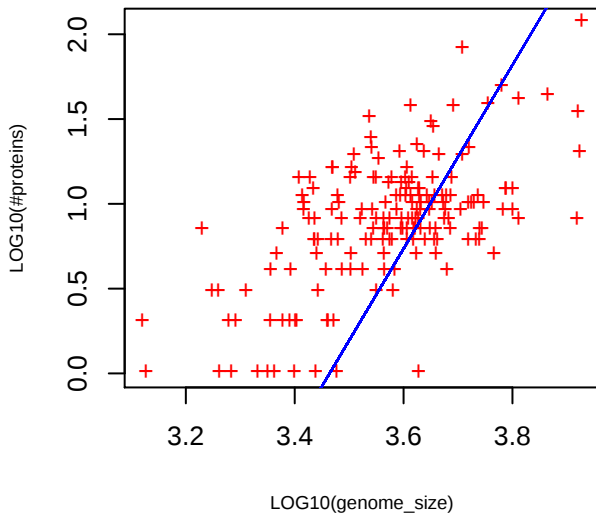
PF08281 Sigma70_r4_2: Sigma-70, region 4

slope= -0.037 p_value= 0.034 intercept= 0.21 p_value= 4.3e-22

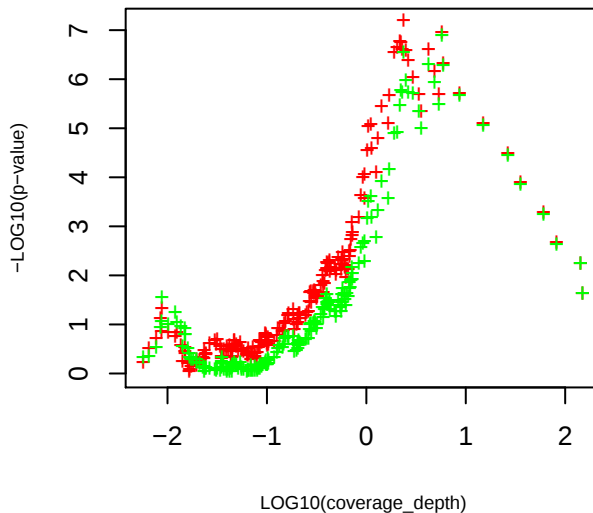


PF08281 Sigma70_r4_2: Sigma-70, region 4

slope= 5.41 p_value= 3.8e-21 intercept= -18.75 p_value= 2.1e-20

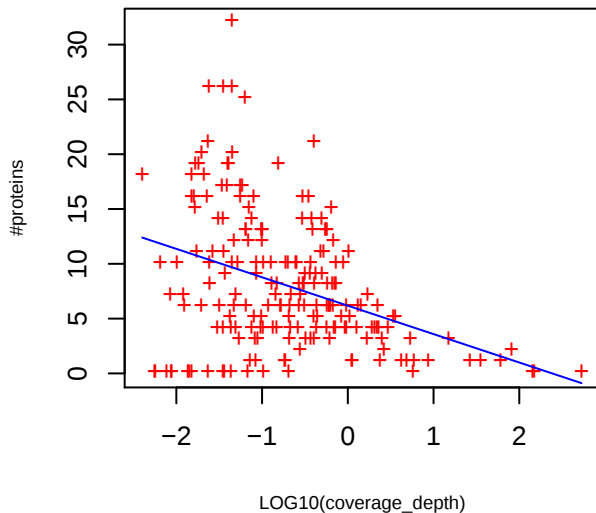


P-value curve ; red (unnorm), green (norm)



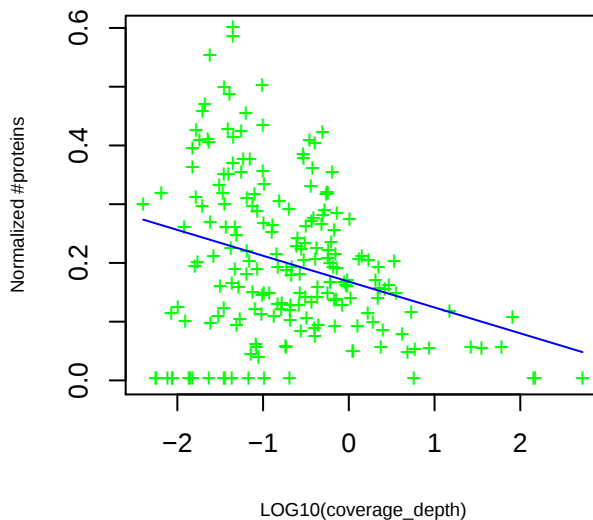
PF00529 HlyD: auxiliary transport protein, membrane fusion protein (MFP) family

slope= -2.59 p_value= 1.0e-07 intercept= 6.18 p_value= 3.2e-24



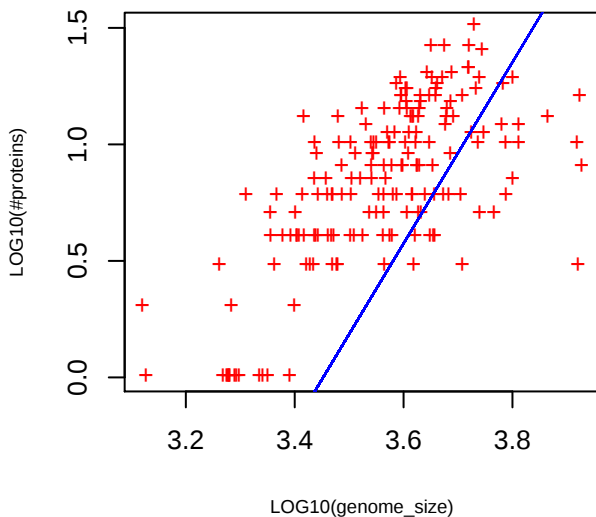
PF00529 HlyD: auxiliary transport protein, membrane fusion protein (MFP) family

slope= -0.044 p_value= 2.8e-05 intercept= 0.17 p_value= 6.5e-33

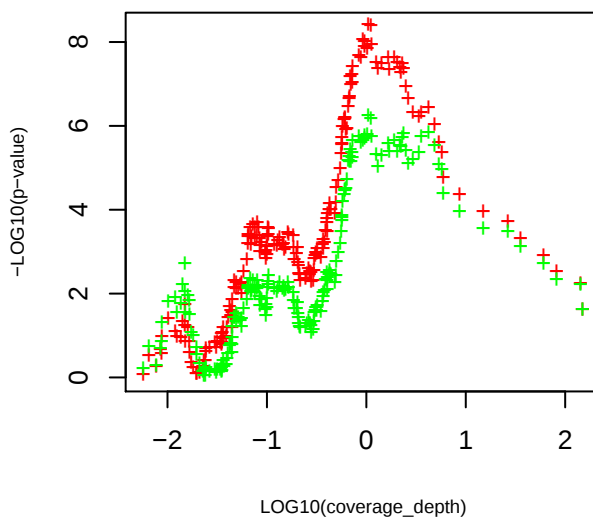


PF00529 HlyD: auxiliary transport protein, membrane fusion protein (MFP) family

slope= 3.89 p_value= 2.3e-10 intercept= -13.43 p_value= 6.3e-10

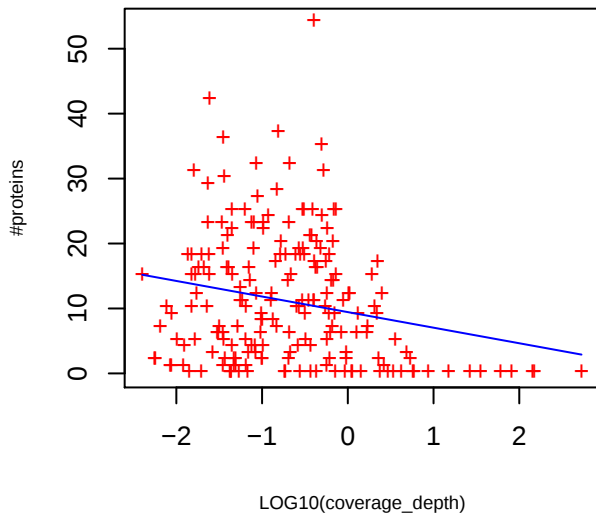


P-value curve : red (unnorm), green (norm)



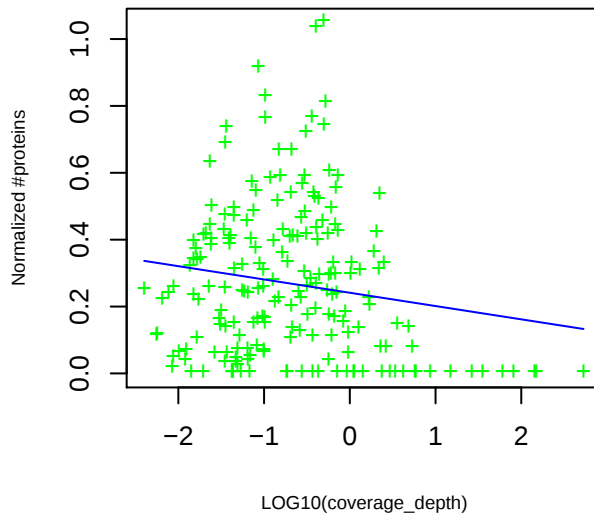
PF00440 TetR_N: transcriptional regulator, TetR family

slope= -2.40 p_value= 0.0024 intercept= 9.44 p_value= 2.2e-21



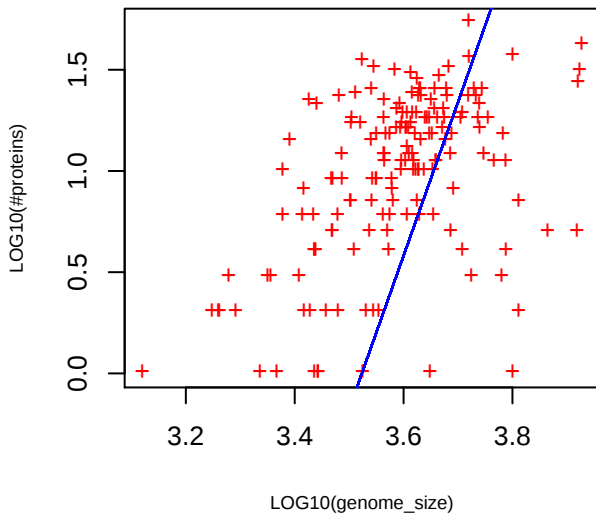
PF00440 TetR_N: transcriptional regulator, TetR family

slope= -0.04 p_value= 0.028 intercept= 0.24 p_value= 6e-25

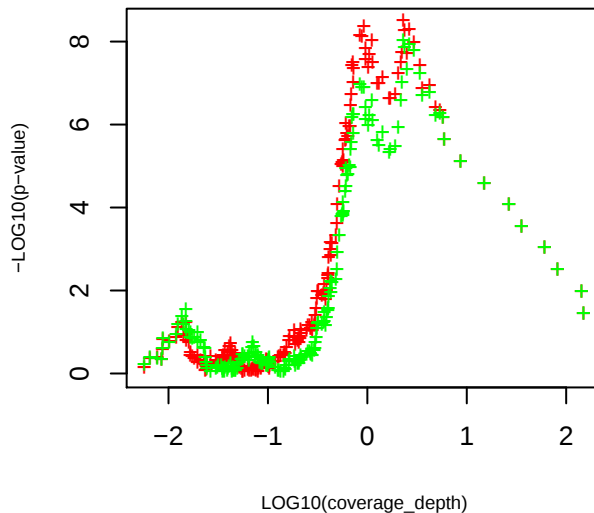


PF00440 TetR_N: transcriptional regulator, TetR family

slope= 7.59 p_value= 6.8e-26 intercept= -26.73 p_value= 1.3e-25

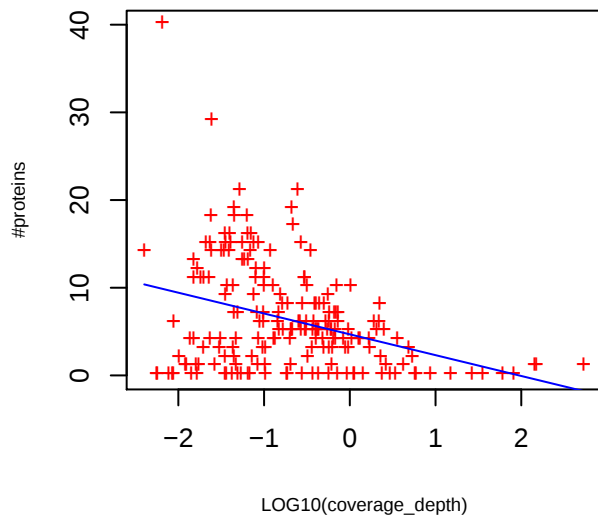


P-value curve ; red (unnorm), green (norm)



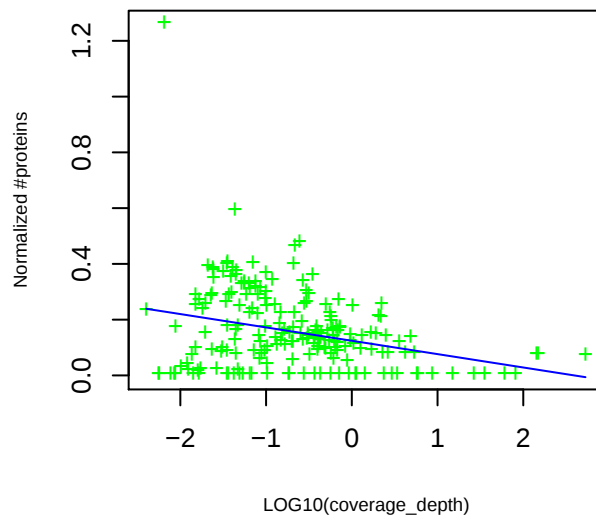
PF00158 Sigma54_activat: Sigma-54 interaction domain

slope= -2.37 p_value= 5.3e-07 intercept= 4.69 p_value= 1.3e-16



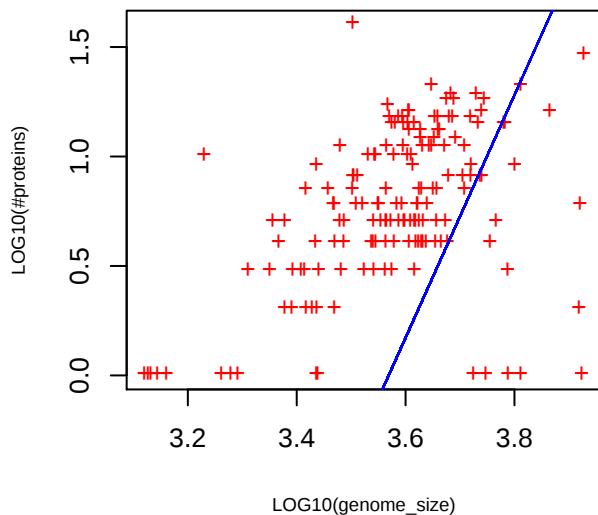
PF00158 Sigma54_activat: Sigma-54 interaction domain

slope= -0.048 p_value= 3.3e-05 intercept= 0.12 p_value= 1.3e-18

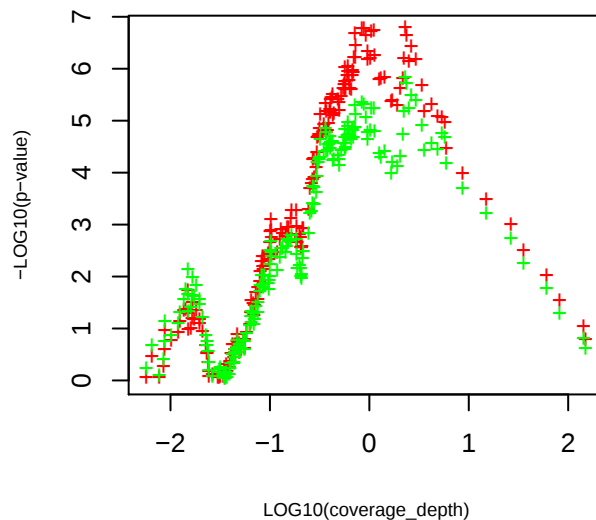


PF00158 Sigma54_activat: Sigma-54 interaction domain

slope= 5.54 p_value= 1.3e-12 intercept= -19.78 p_value= 1.0e-12

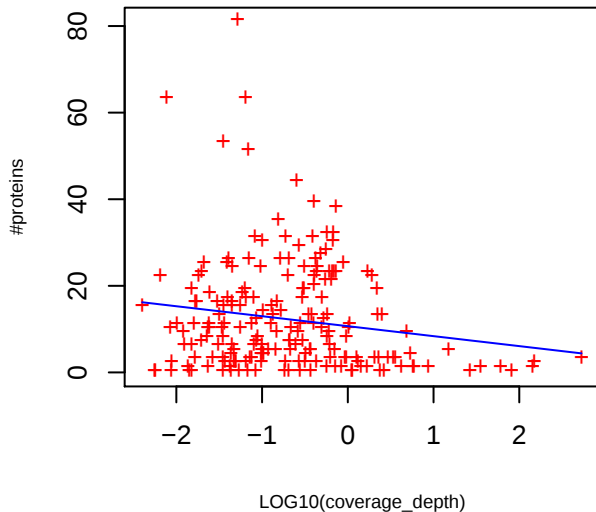


P-value curve ; red (unnorm), green (norm)



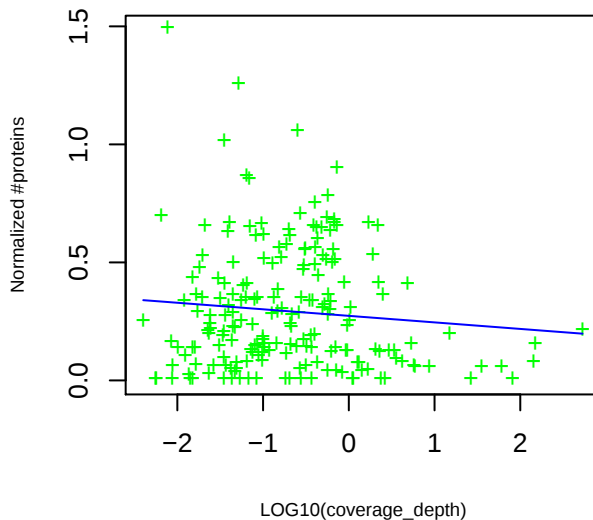
TIGR01409 TAT_signal_seq: Tat (twin-arginine translocation) pathway signal sequence

slope= -2.30 p_value= 0.024 intercept= 10.68 p_value= 2.4e-17



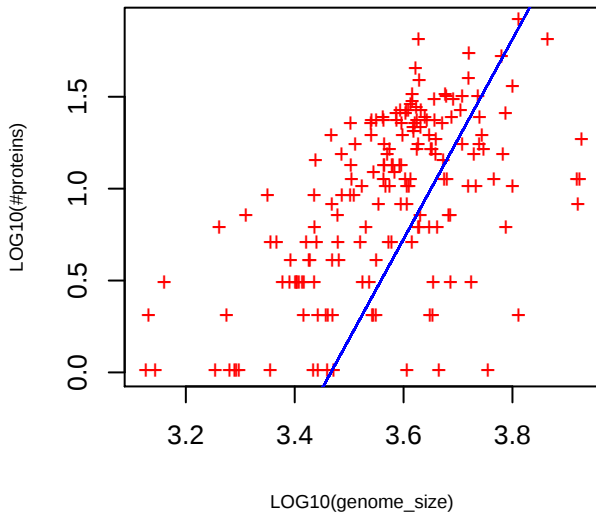
TIGR01409 TAT_signal_seq: Tat (twin-arginine translocation) pathway signal sequence

slope= -0.028 p_value= 0.18 intercept= 0.27 p_value= 3.7e-24

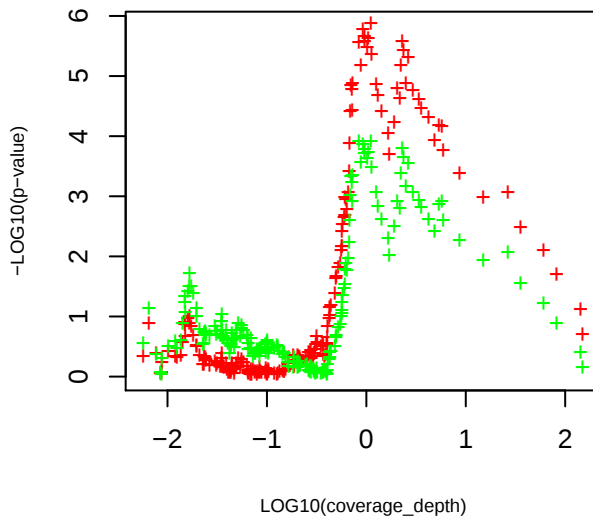


TIGR01409 TAT_signal_seq: Tat (twin-arginine translocation) pathway signal sequence

slope= 5.44 p_value= 2.6e-18 intercept= -18.85 p_value= 1.1e-17

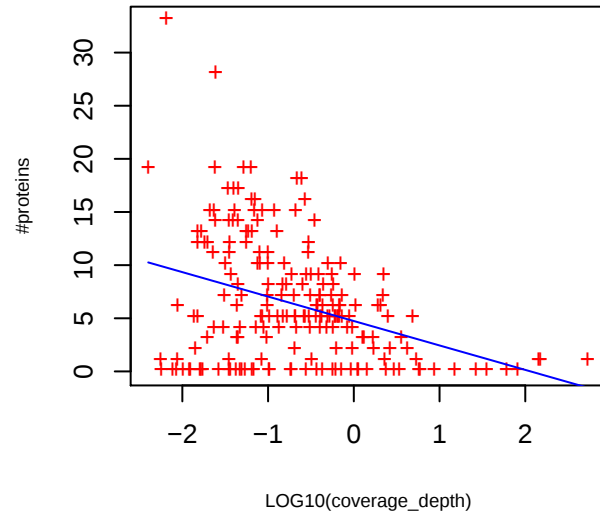


P-value curve ; red (unnorm), green (norm)



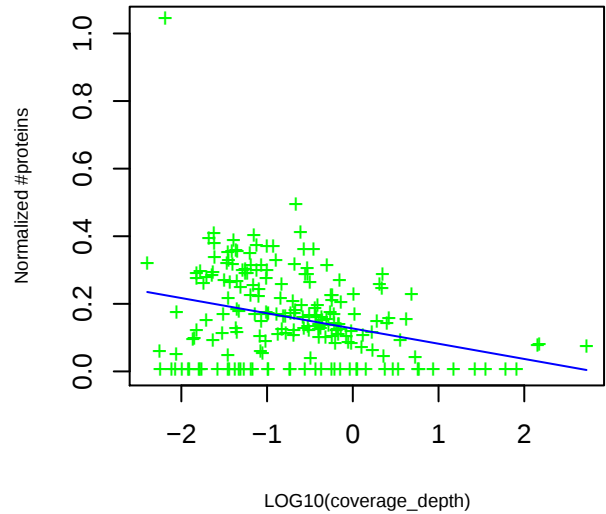
PF02954 HTH_8: transcriptional regulator, Fis family

slope= -2.30 p_value= 3.9e-07 intercept= 4.74 p_value= 4.2e-18



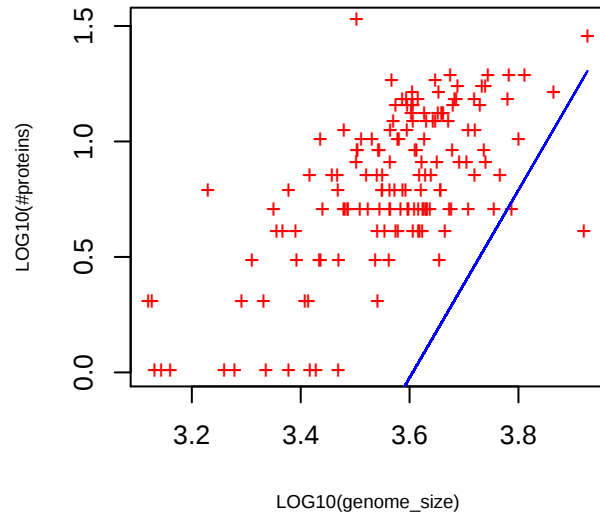
PF02954 HTH_8: transcriptional regulator, Fis family

slope= -0.045 p_value= 2.2e-05 intercept= 0.13 p_value= 8.5e-22

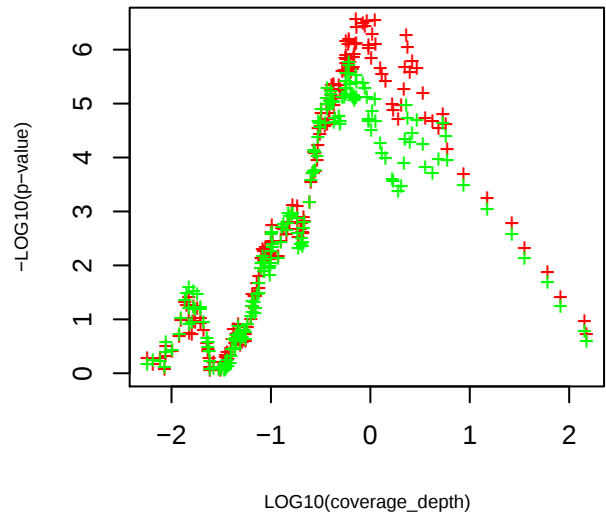


PF02954 HTH_8: transcriptional regulator, Fis family

slope= 4.06 p_value= 2.2e-06 intercept= -14.66 p_value= 1.6e-06

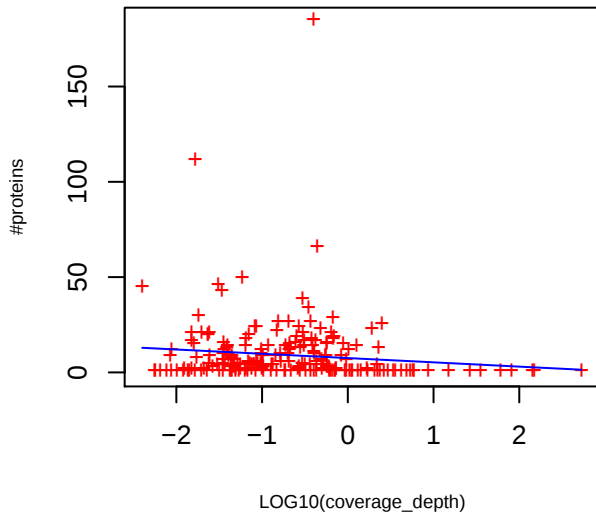


P-value curve : red (unnorm), green (norm)



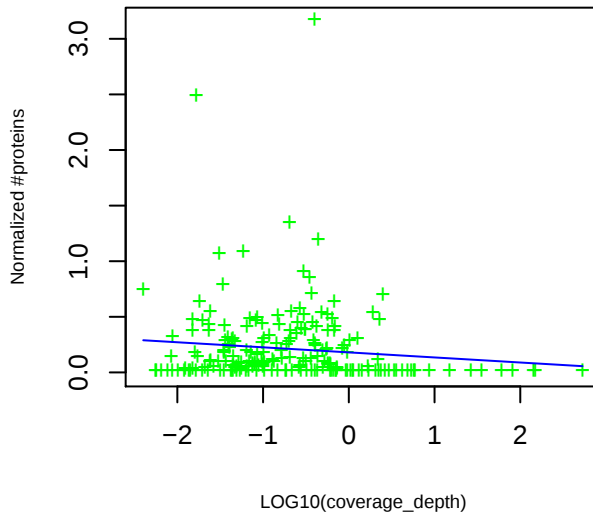
PF00665 rve: integrase core domain

slope= -2.25 p_value= 0.12 intercept= 7.54 p_value= 5.4e-06



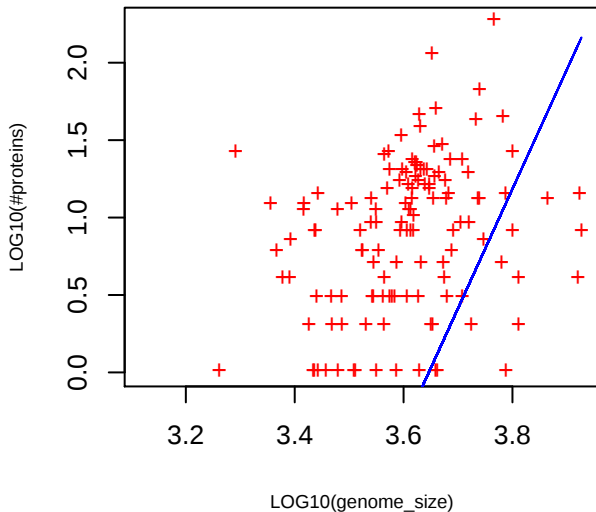
PF00665 rve: integrase core domain

slope= -0.045 p_value= 0.12 intercept= 0.18 p_value= 9.2e-08

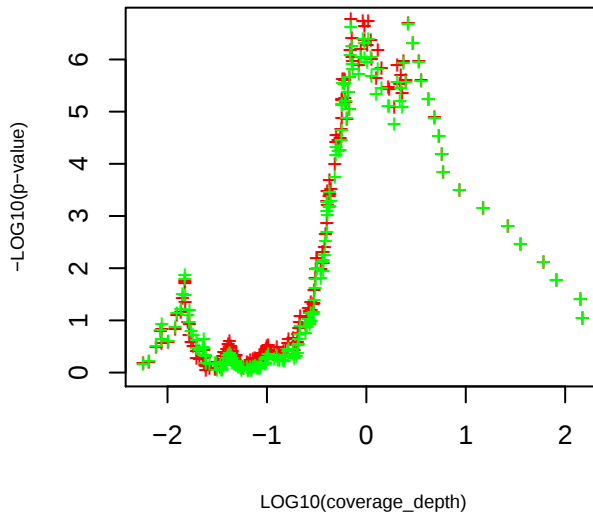


PF00665 rve: integrase core domain

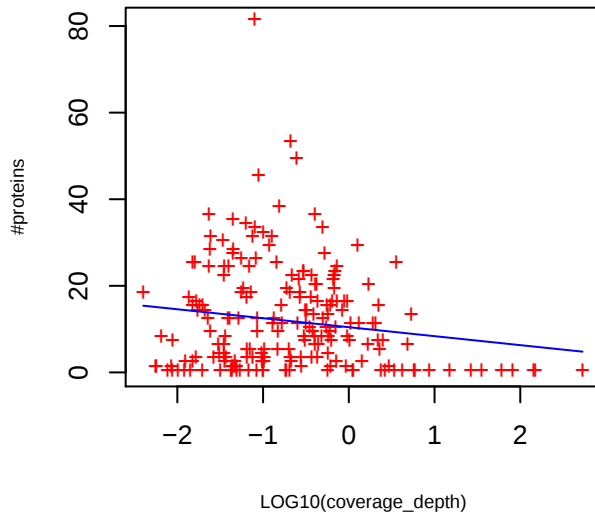
slope= 7.71 p_value= 5.9e-16 intercept= -28.12 p_value= 1.2e-16



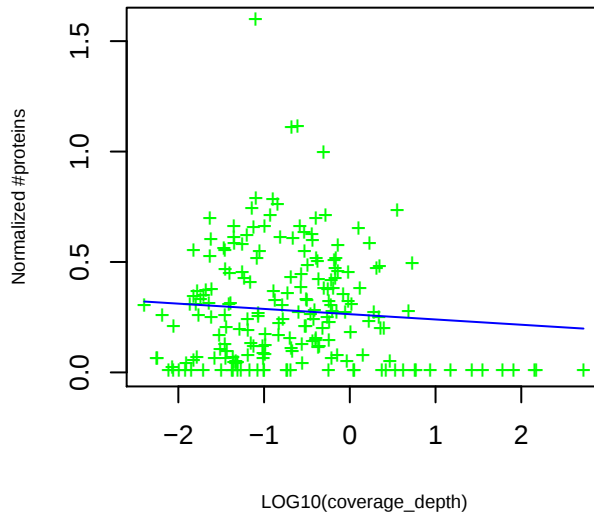
P-value curve ; red (unnorm), green (norm)



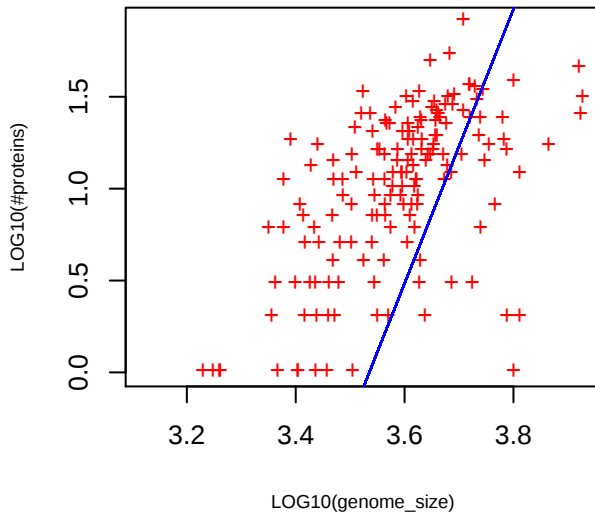
PF00165 HTH_AraC: transcriptional regulator, AraC family
 slope= -2.07 p_value= 0.032 intercept= 10.44 p_value= 3.4e-18



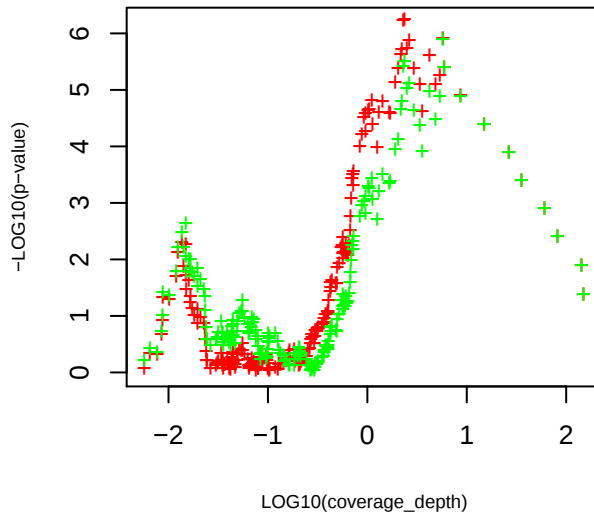
PF00165 HTH_AraC: transcriptional regulator, AraC family
 slope= -0.024 p_value= 0.25 intercept= 0.26 p_value= 3.8e-23



PF00165 HTH_AraC: transcriptional regulator, AraC family
 slope= 7.46 p_value= 5.1e-22 intercept= -26.38 p_value= 6.9e-22

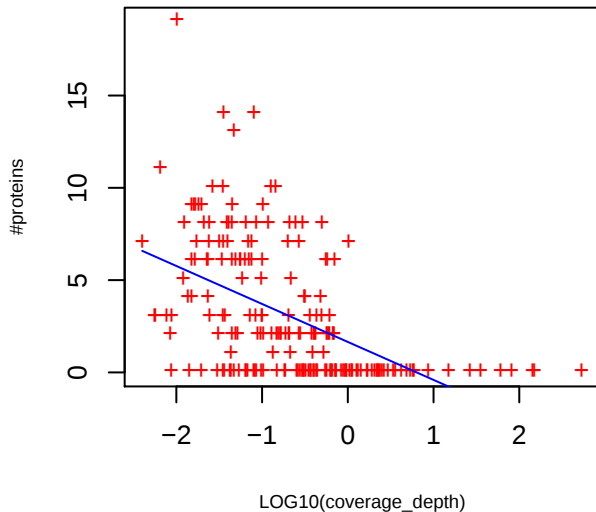


P-value curve : red (unnorm), green (norm)



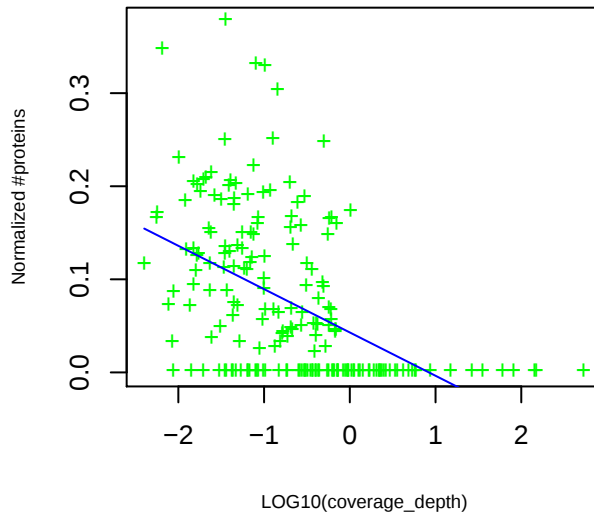
PF01584 CheW: CheW-like domain

slope= -2.06 p_value= 2.0e-14 intercept= 1.65 p_value= 1.7e-08



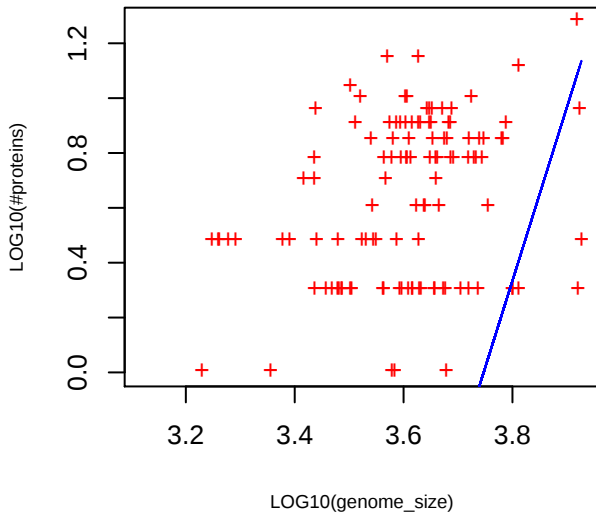
PF01584 CheW: CheW-like domain

slope= -0.047 p_value= 3.3e-13 intercept= 0.043 p_value= 1.2e-09

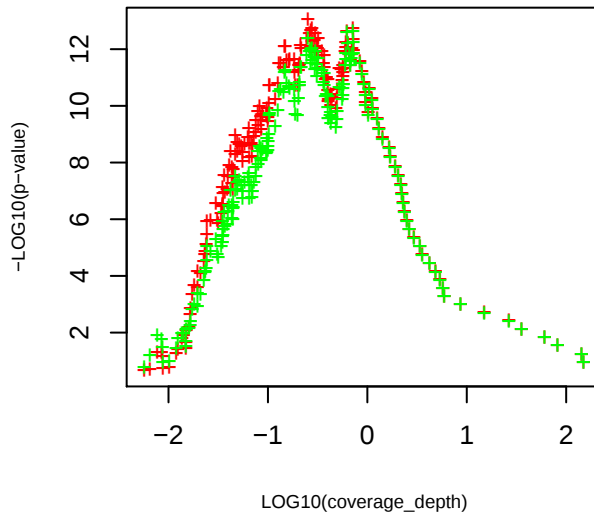


PF01584 CheW: CheW-like domain

slope= 6.32 p_value= 3.5e-11 intercept= -23.69 p_value= 3.6e-12

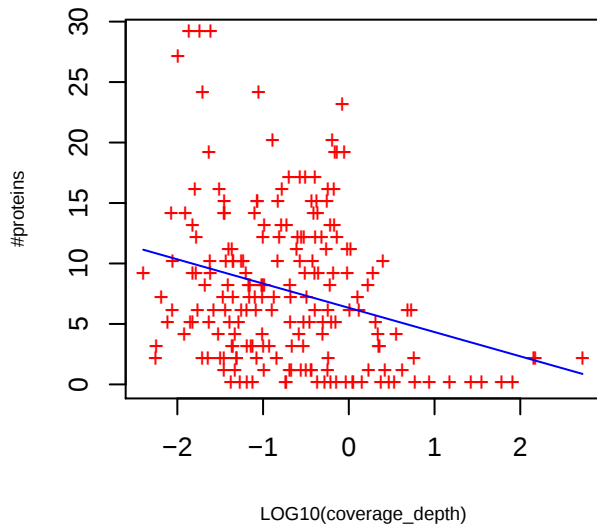


P-value curve : red (unnorm), green (norm)



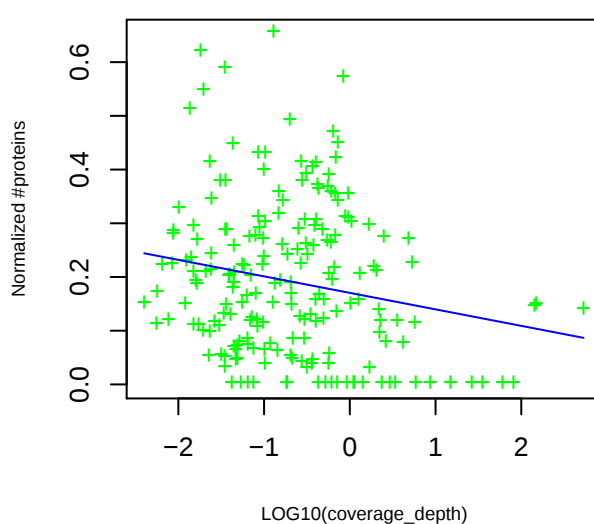
PF01381 HTH_3: Helix-turn-helix

slope= -2.00 p_value= 7.3e-05 intercept= 6.33 p_value= 3.2e-23



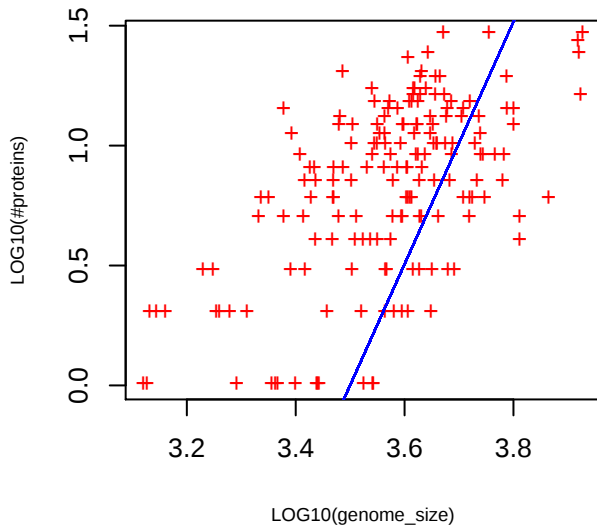
PF01381 HTH_3: Helix-turn-helix

slope= -0.031 p_value= 0.0067 intercept= 0.17 p_value= 1.2e-29

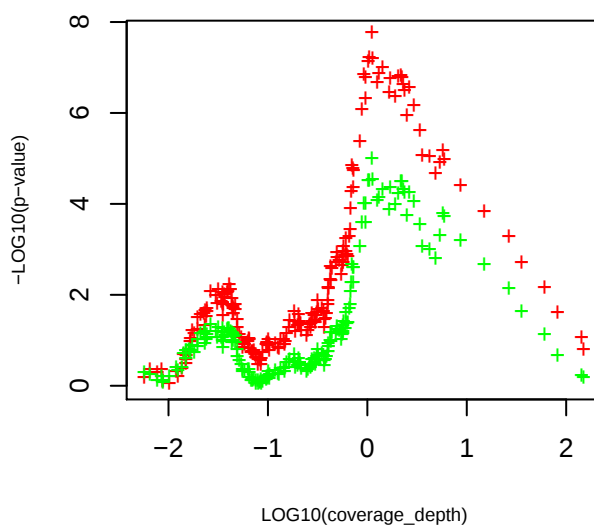


PF01381 HTH_3: Helix-turn-helix

slope= 5.05 p_value= 2.1e-14 intercept= -17.68 p_value= 4.4e-14

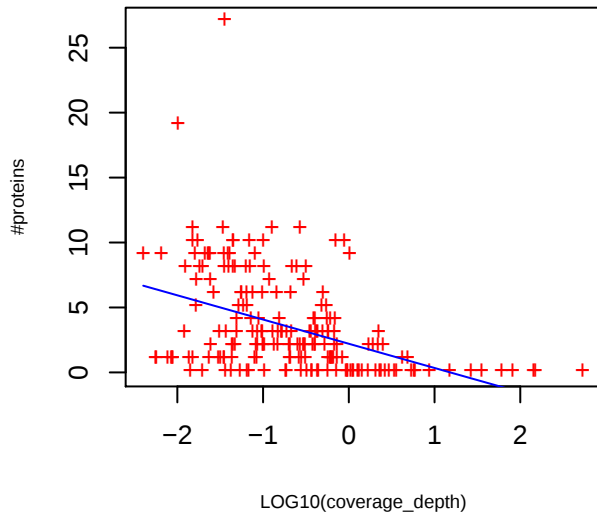


P-value curve ; red (unnorm), green (norm)



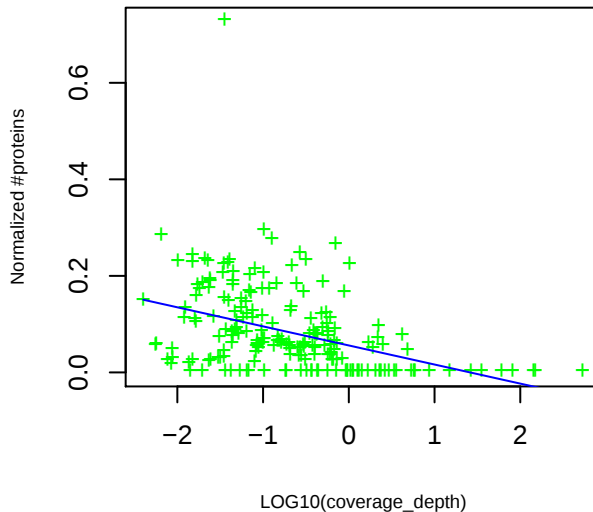
PF01627 Hpt: Hpt domain

slope= -1.86 p_value= 2.7e-10 intercept= 2.21 p_value= 4.5e-11



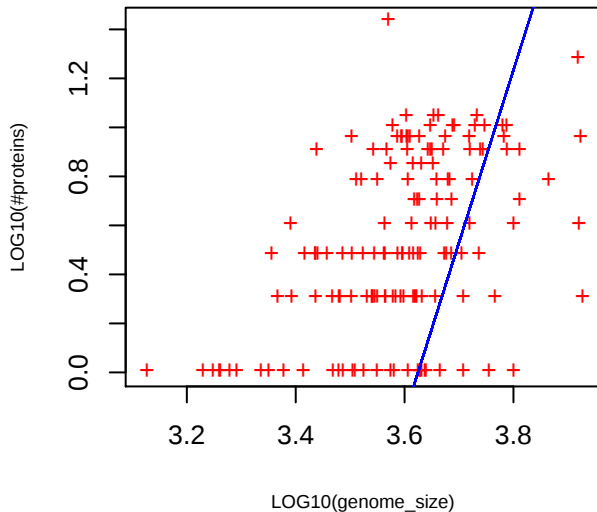
PF01627 Hpt: Hpt domain

slope= -0.040 p_value= 5.5e-09 intercept= 0.056 p_value= 9.5e-13

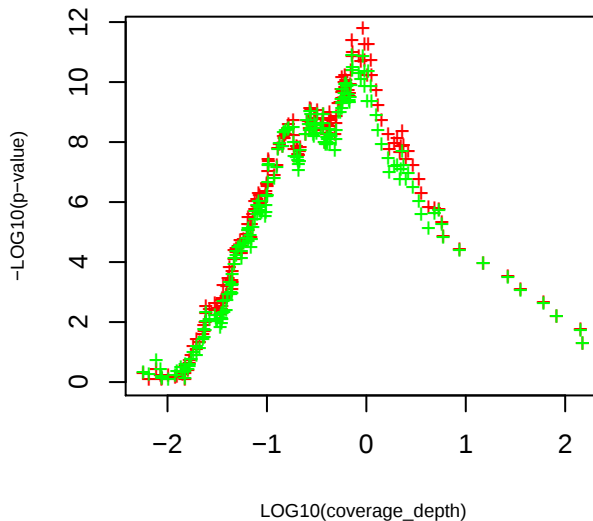


PF01627 Hpt: Hpt domain

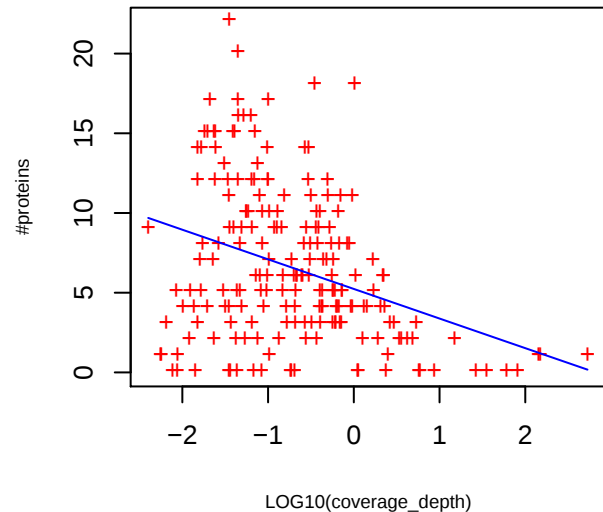
slope= 7.04 p_value= 1.4e-19 intercept= -25.51 p_value= 3.4e-20



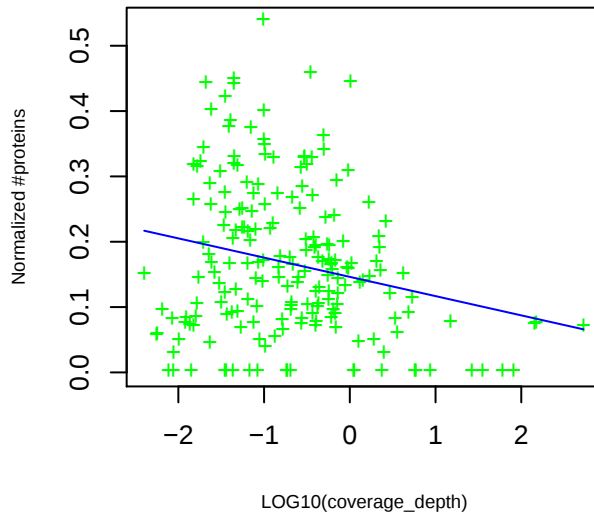
P-value curve : red (unnorm), green (norm)



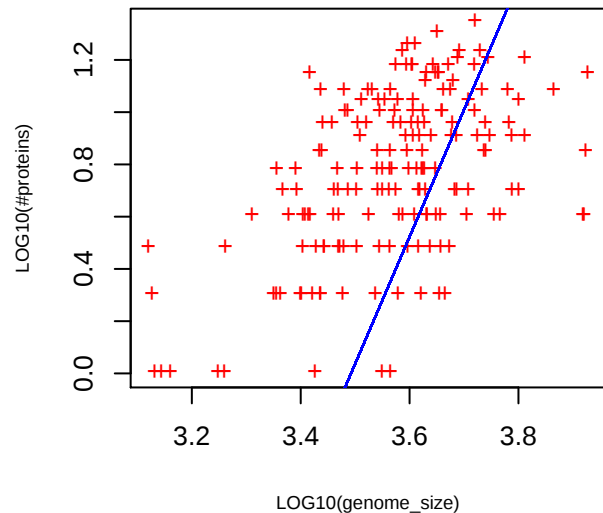
slope= -1.86 p_value= 1.0e-06 intercept= 5.24 p_value= 5.5e-27



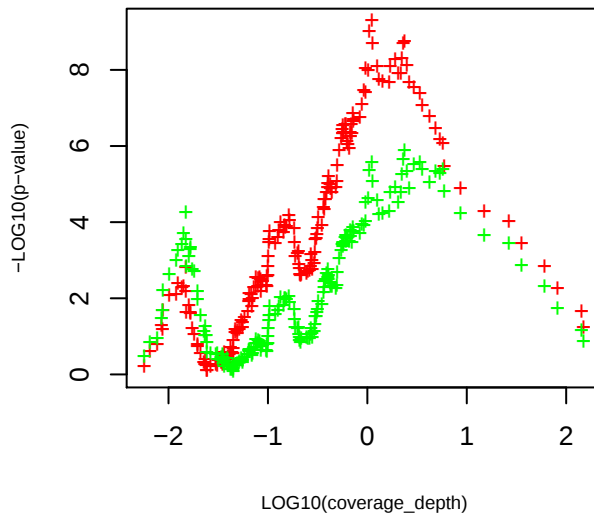
slope= -0.029 p_value= 0.0014 intercept= 0.15 p_value= 3.6e-32



slope= 4.86 p_value= 1.8e-15 intercept= -16.98 p_value= 4.2e-15

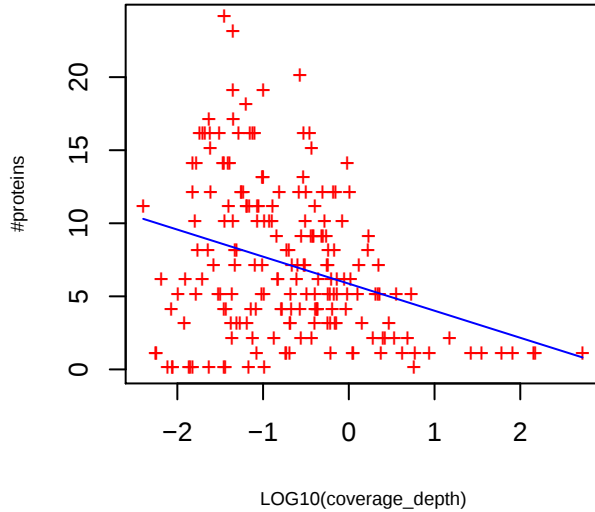


P-value curve ; red (unnorm), green (norm)



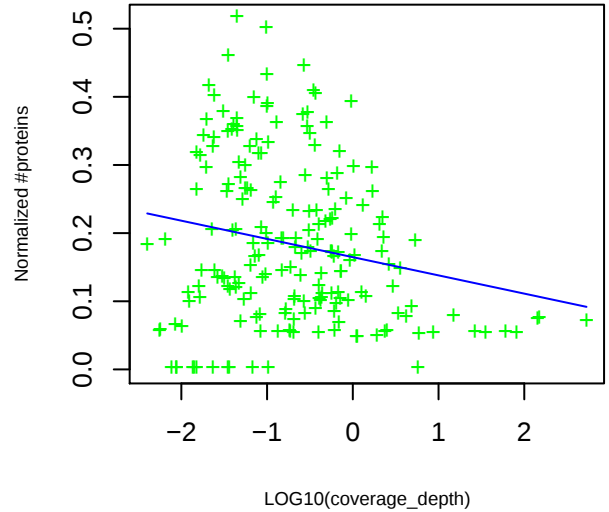
TIGR01730 RND_mfp: efflux transporter, RND family, MFP subunit

slope= -1.85 p_value= 7e-06 intercept= 5.87 p_value= 3.8e-28



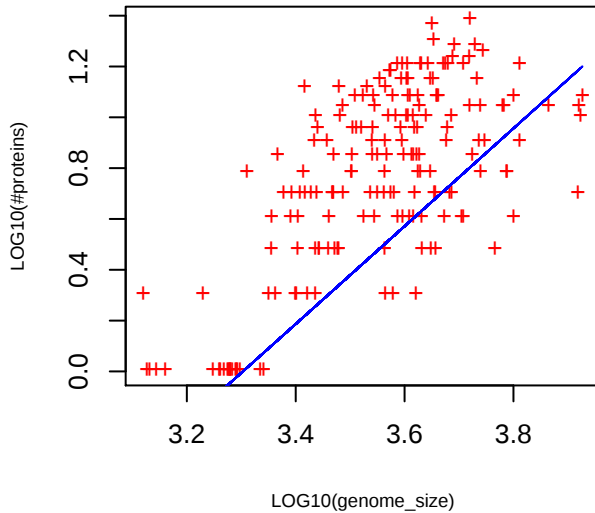
TIGR01730 RND_mfp: efflux transporter, RND family, MFP subunit

slope= -0.027 p_value= 0.0049 intercept= 0.16 p_value= 6.2e-36

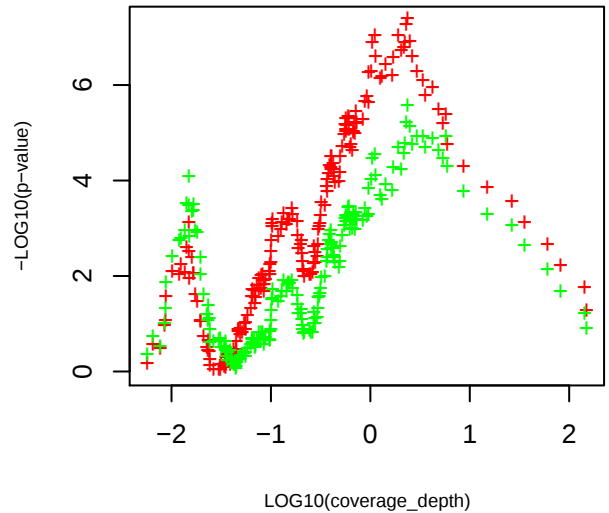


TIGR01730 RND_mfp: efflux transporter, RND family, MFP subunit

slope= 1.92 p_value= 0.00019 intercept= -6.36 p_value= 0.00051

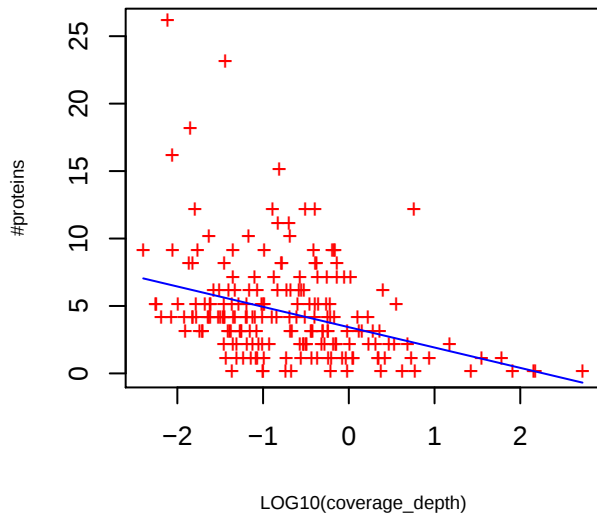


P-value curve : red (unnorm), green (norm)



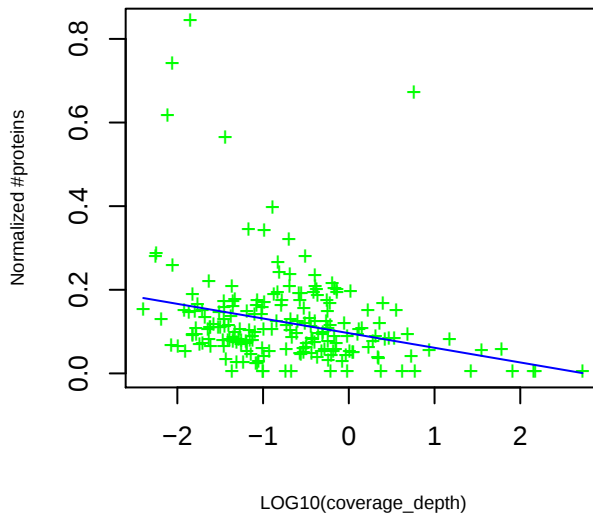
PF01022 HTH_5: transcriptional regulator, ArsR family

slope= -1.51 p_value= 3.9e-07 intercept= 3.43 p_value= 6.1e-21



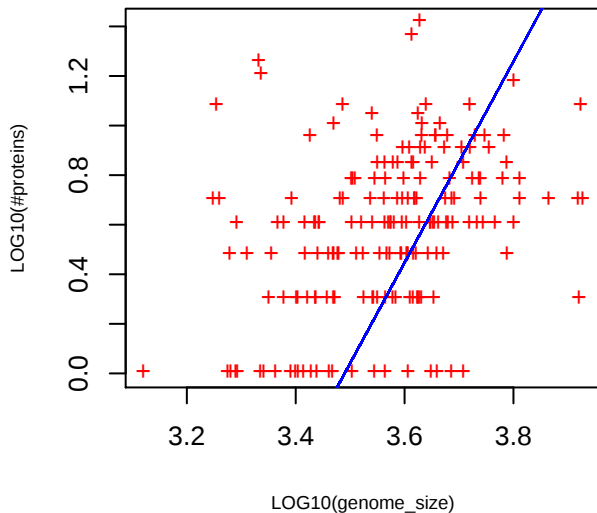
PF01022 HTH_5: transcriptional regulator, ArsR family

slope= -0.035 p_value= 0.00014 intercept= 0.096 p_value= 1.2e-17

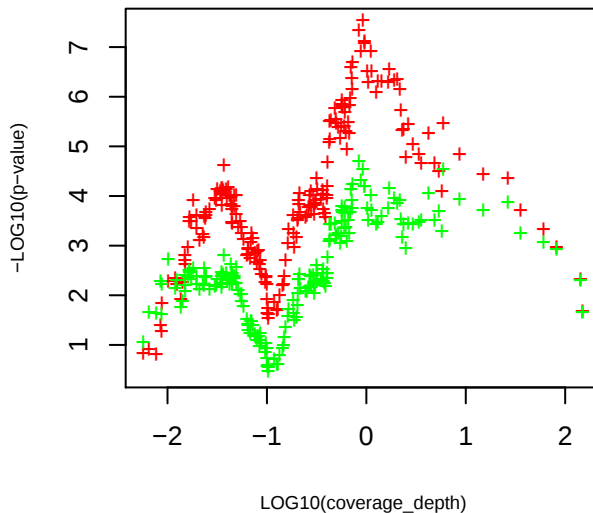


PF01022 HTH_5: transcriptional regulator, ArsR family

slope= 4.06 p_value= 1.7e-15 intercept= -14.16 p_value= 4.2e-15

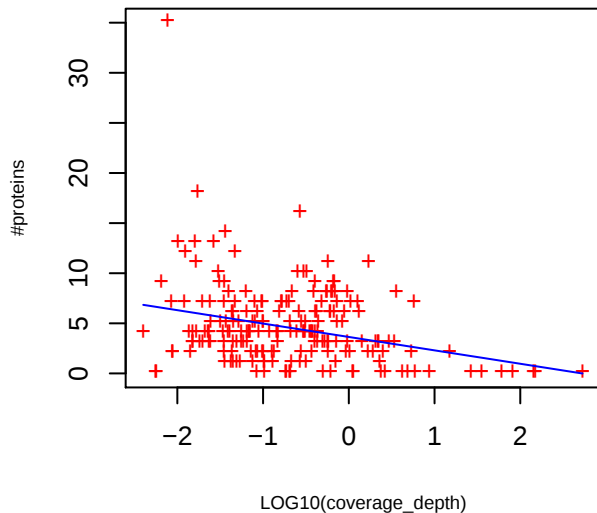


P-value curve ; red (unnorm), green (norm)



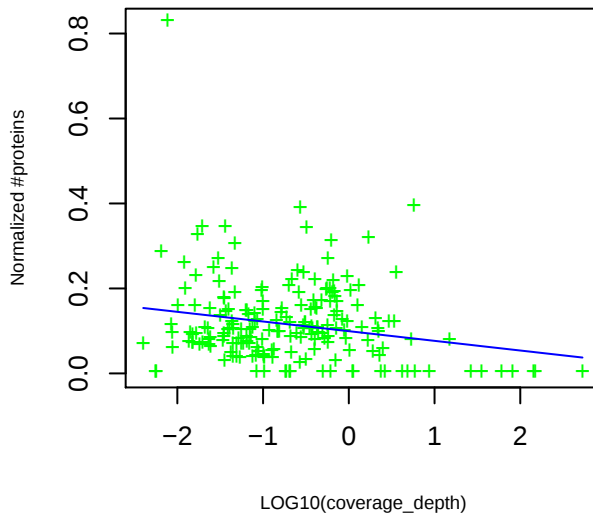
PF00582 Usp: universal stress protein family

slope= -1.34 p_value= 2.4e-05 intercept= 3.64 p_value= 1.6e-20



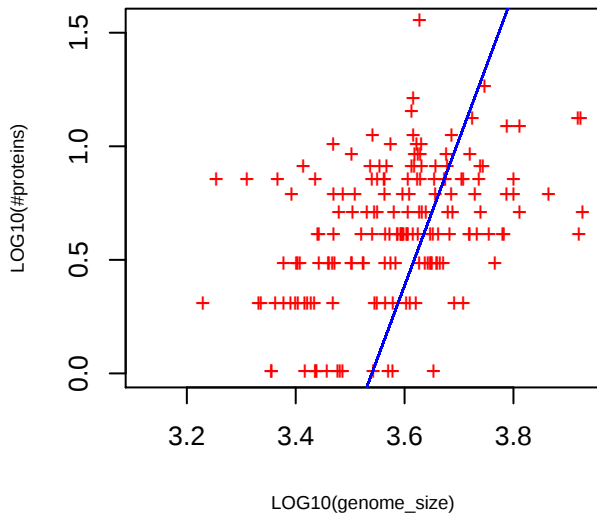
PF00582 Usp: universal stress protein family

slope= -0.023 p_value= 0.0032 intercept= 0.10 p_value= 8e-24

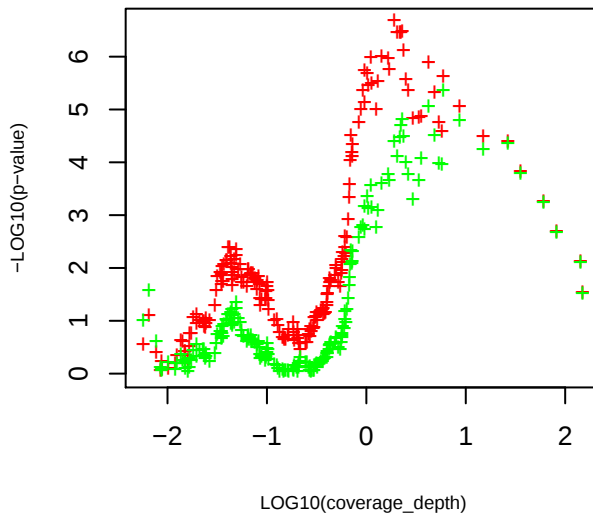


PF00582 Usp: universal stress protein family

slope= 6.43 p_value= 6.3e-27 intercept= -22.76 p_value= 7.8e-27

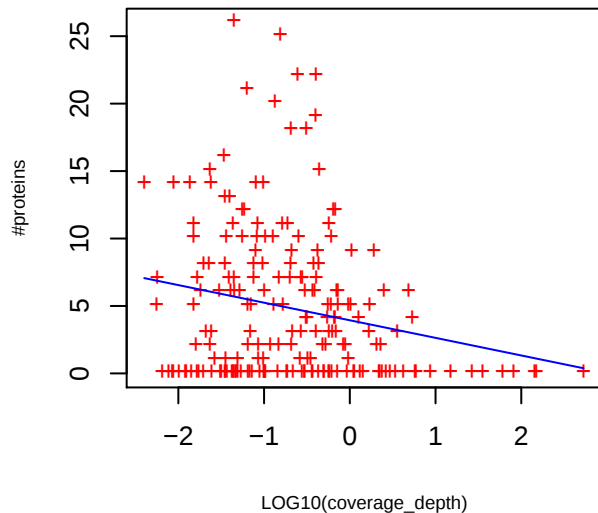


P-value curve ; red (unnorm), green (norm)



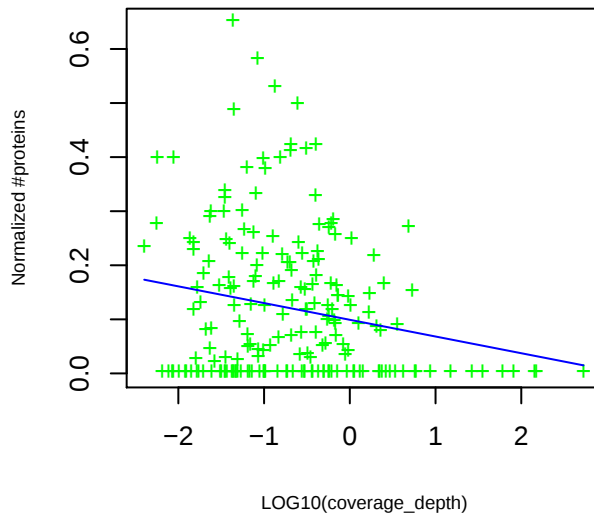
PF00532 Peripla_BP_1: Periplasmic binding proteins and sugar binding domain of the LacI family

slope= -1.30 p_value= 0.0036 intercept= 3.94 p_value= 2.3e-13



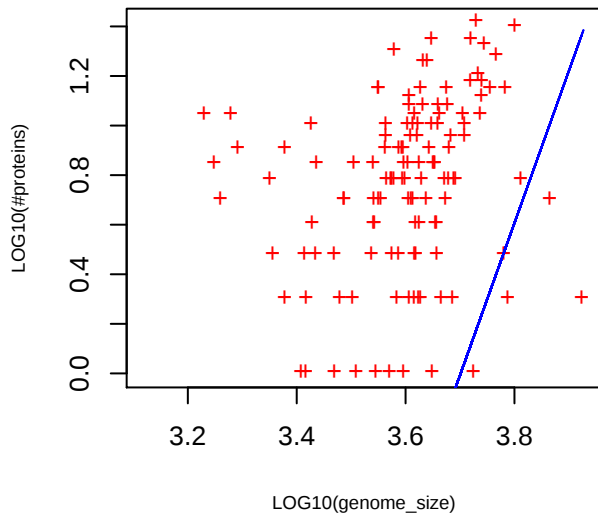
PF00532 Peripla_BP_1: Periplasmic binding proteins and sugar binding domain of the LacI family

slope= -0.031 p_value= 0.0044 intercept= 0.10 p_value= 3.3e-14

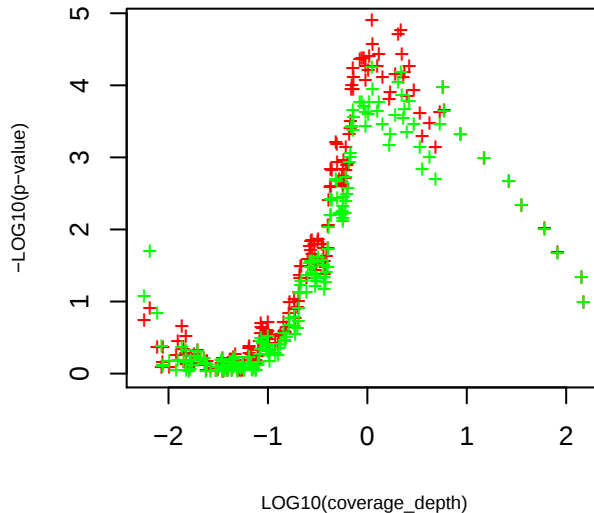


PF00532 Peripla_BP_1: Periplasmic binding proteins and sugar binding domain of the LacI family

slope= 6.14 p_value= 1.9e-10 intercept= -22.72 p_value= 3.8e-11

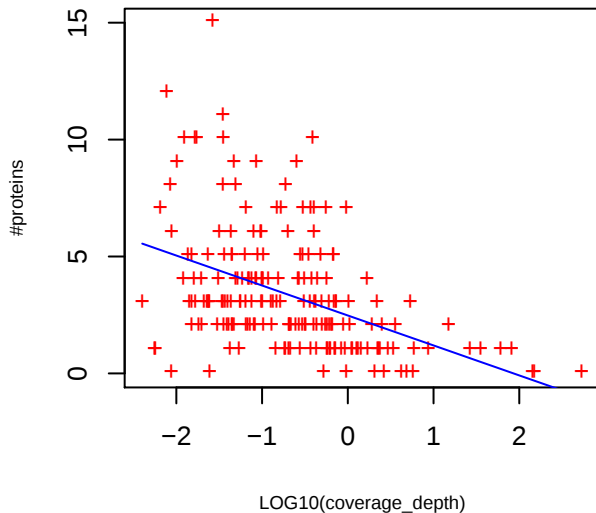


P-value curve ; red (unnorm), green (norm)



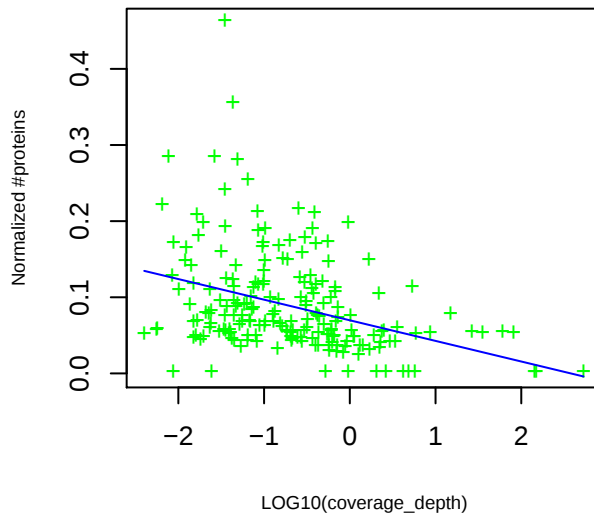
TIGR01494 ATPase_P-type: ATPase, P-type (transporting), HAD superfamily, subfamily IC

slope= -1.28 p_value= 1.3e-10 intercept= 2.48 p_value= 4.6e-24



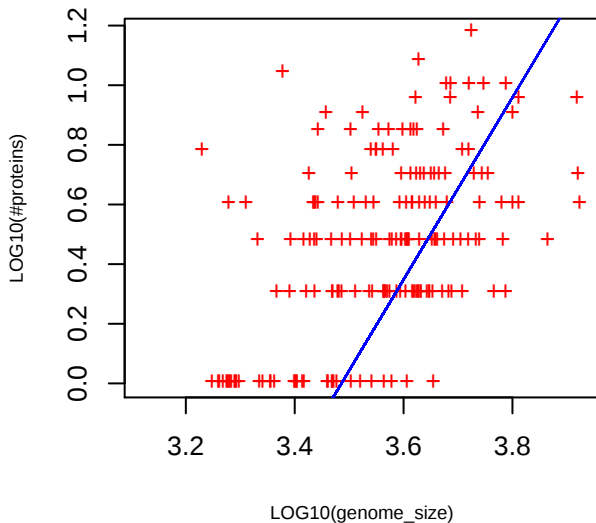
TIGR01494 ATPase_P-type: ATPase, P-type (transporting), HAD superfamily, subfamily IC

slope= -0.027 p_value= 1.8e-07 intercept= 0.07 p_value= 2.9e-26

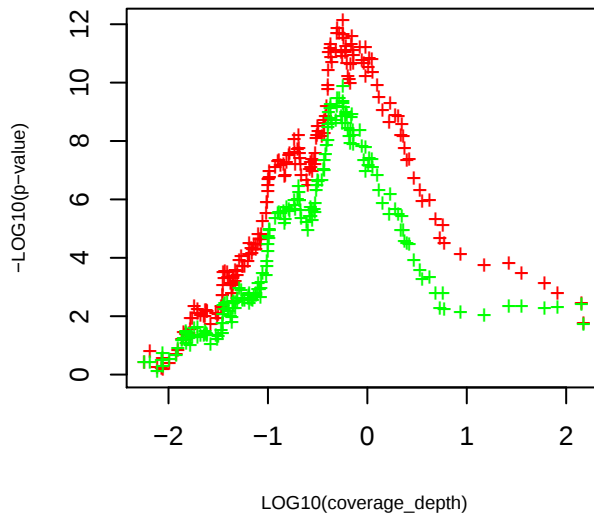


TIGR01494 ATPase_P-type: ATPase, P-type (transporting), HAD superfamily, subfamily IC

slope= 3.05 p_value= 3.4e-11 intercept= -10.64 p_value= 6.9e-11

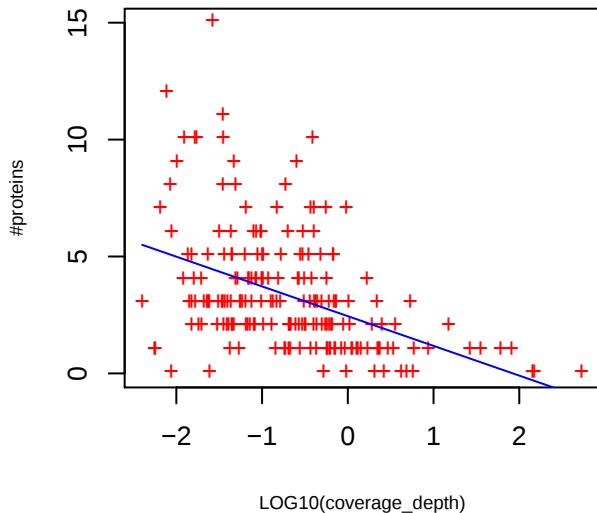


P-value curve ; red (unnorm), green (norm)



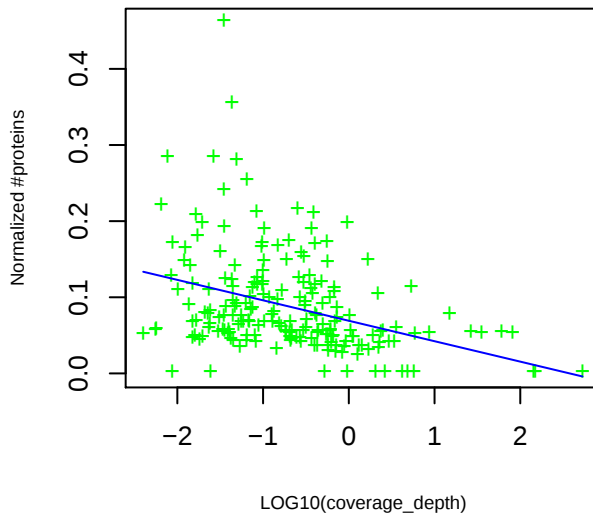
PF00122 E1-E2_ATPase: E1-E2 ATPase

slope= -1.27 p_value= 9.4e-11 intercept= 2.45 p_value= 3e-24



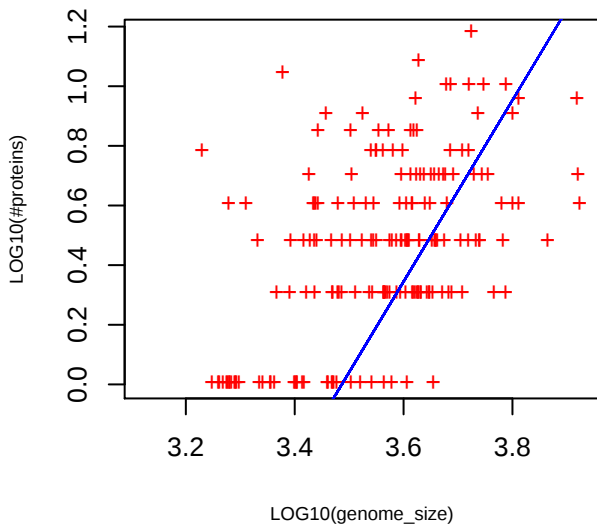
PF00122 E1-E2_ATPase: E1-E2 ATPase

slope= -0.027 p_value= 1.8e-07 intercept= 0.069 p_value= 3.1e-26

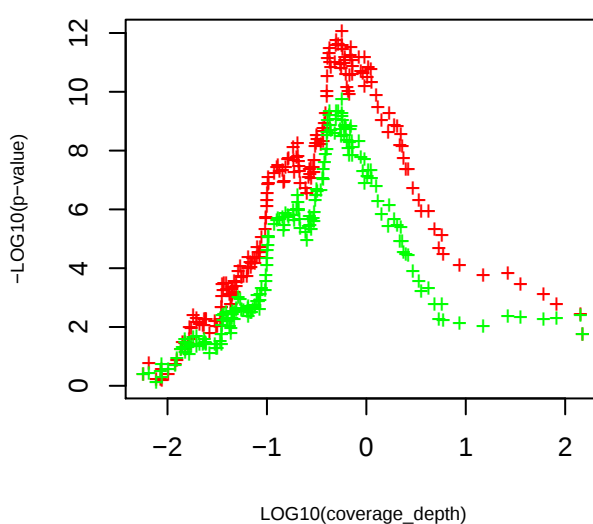


PF00122 E1-E2_ATPase: E1-E2 ATPase

slope= 3.04 p_value= 3.9e-11 intercept= -10.60 p_value= 7.9e-11

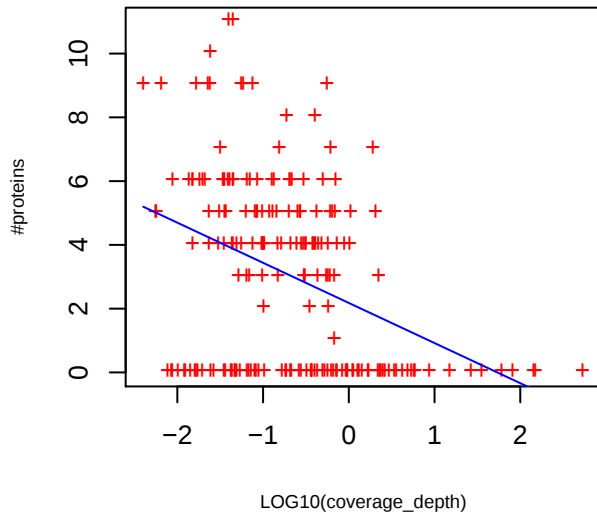


P-value curve ; red (unnorm), green (norm)



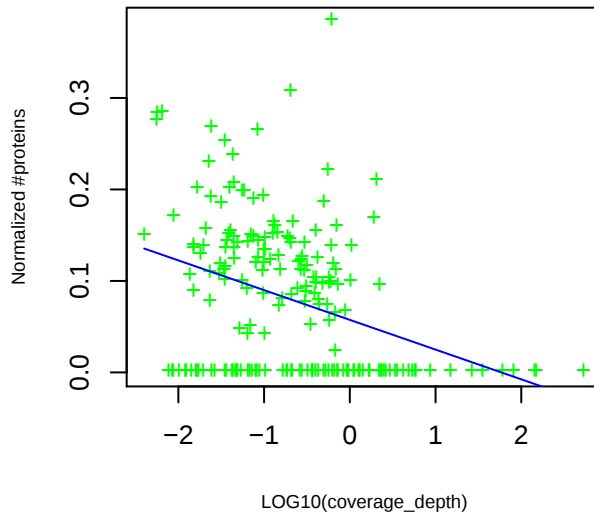
PF00460 Flg_bb_rod: Flagella basal body rod protein

slope= -1.26 p_value= 3.1e-08 intercept= 2.18 p_value= 5.4e-16



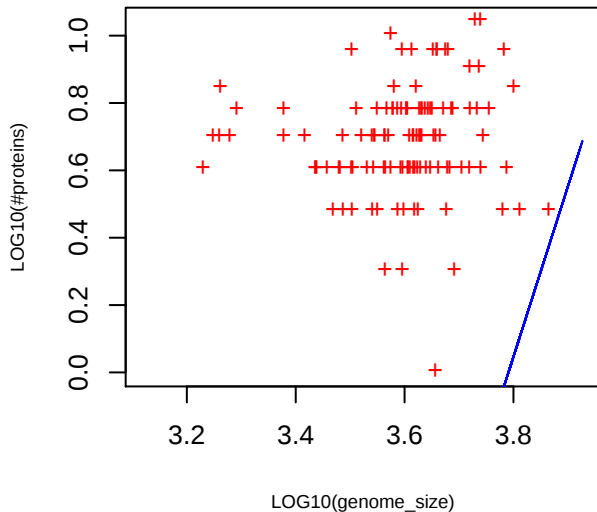
PF00460 Flg_bb_rod: Flagella basal body rod protein

slope= -0.033 p_value= 2.5e-07 intercept= 0.057 p_value= 1.1e-14

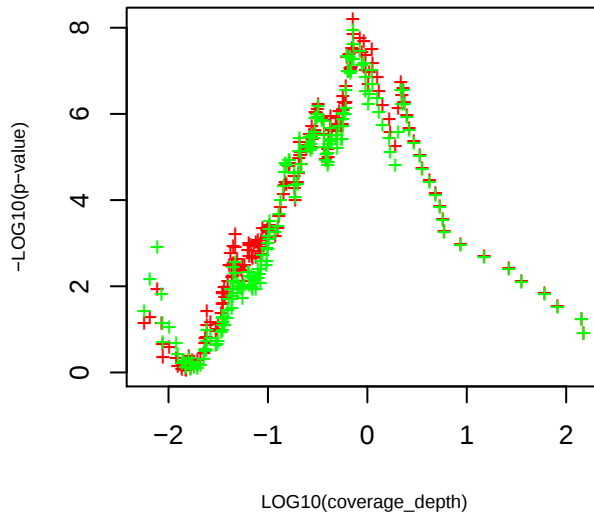


PF00460 Flg_bb_rod: Flagella basal body rod protein

slope= 5.06 p_value= 2.8e-07 intercept= -19.17 p_value= 4.7e-08

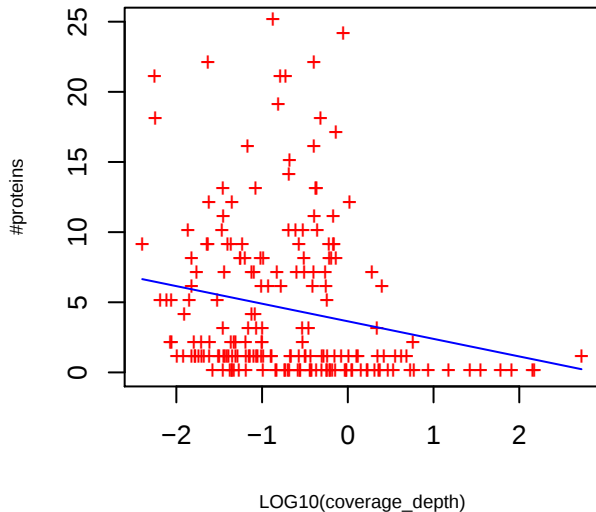


P-value curve ; red (unnorm), green (norm)



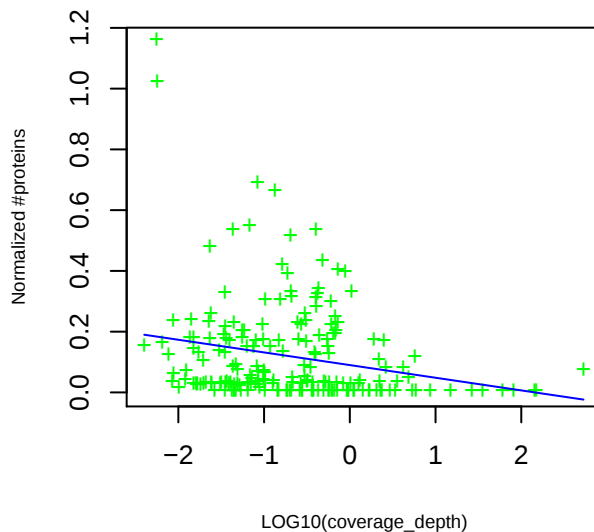
PF08352 oligo_HPYP: Oligopeptide/dipeptide transporter, C-terminal region

slope= -1.25 p_value= 0.0055 intercept= 3.64 p_value= 1.1e-11



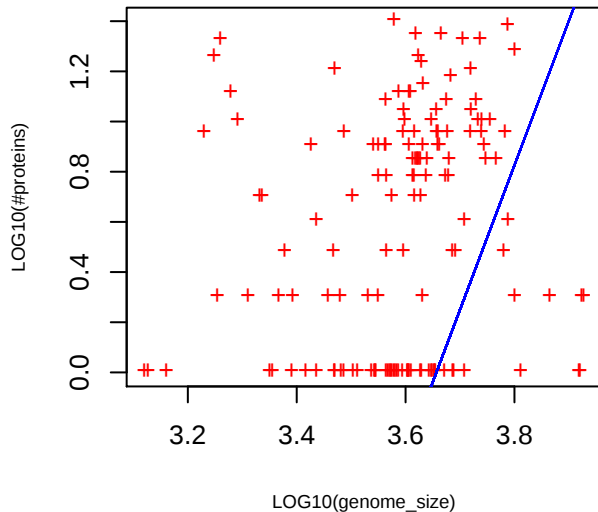
PF08352 oligo_HPYP: Oligopeptide/dipeptide transporter, C-terminal region

slope= -0.042 p_value= 0.0018 intercept= 0.09 p_value= 6.9e-09

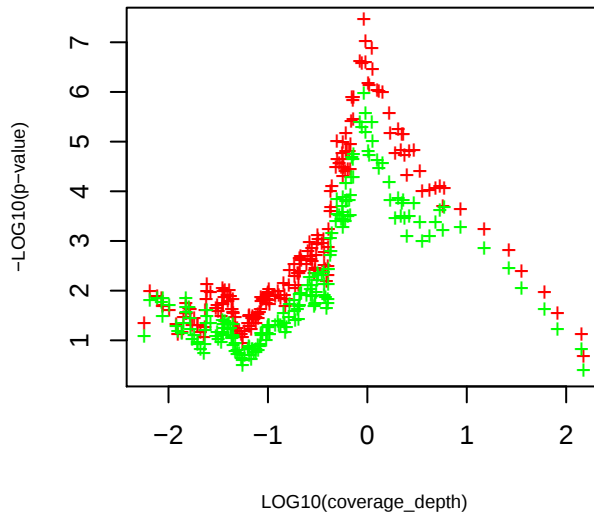


PF08352 oligo_HPYP: Oligopeptide/dipeptide transporter, C-terminal region

slope= 5.76 p_value= 1.6e-11 intercept= -21.06 p_value= 4.4e-12

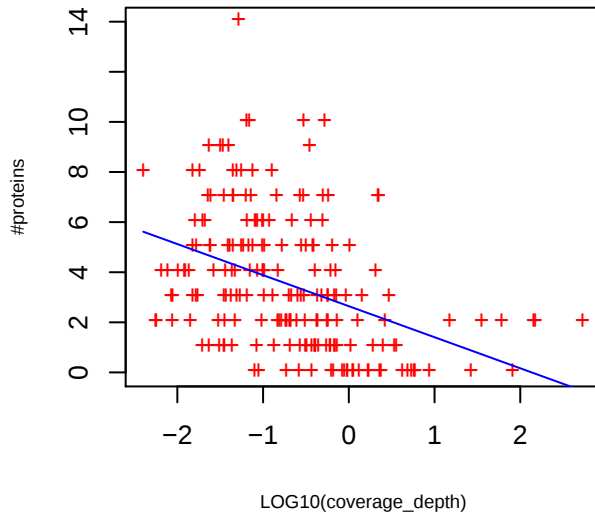


P-value curve : red (unnorm), green (norm)



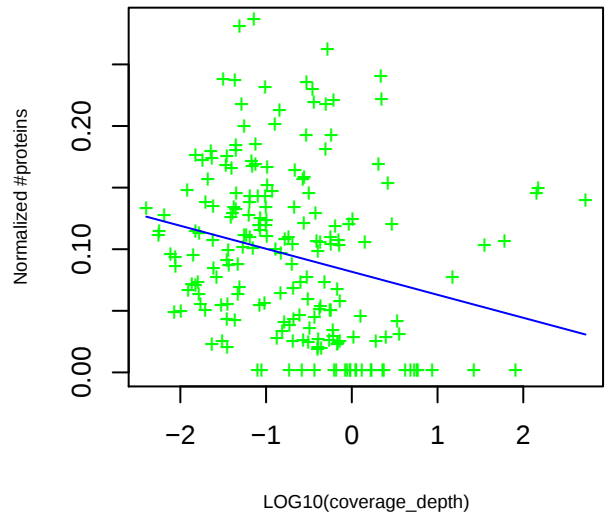
PF00437 GSPII_E: Type II/IV secretion system protein

slope= -1.24 p_value= 3.4e-09 intercept= 2.64 p_value= 2.7e-24



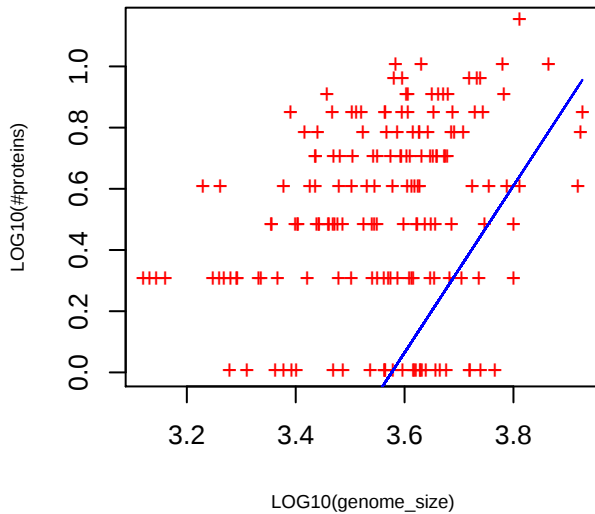
PF00437 GSPII_E: Type II/IV secretion system protein

slope= -0.019 p_value= 0.00057 intercept= 0.082 p_value= 5.4e-30

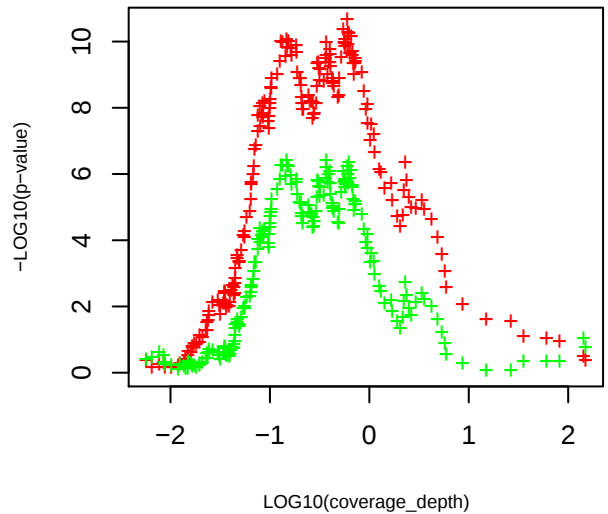


PF00437 GSPII_E: Type II/IV secretion system protein

slope= 2.73 p_value= 4.7e-05 intercept= -9.76 p_value= 4.1e-05

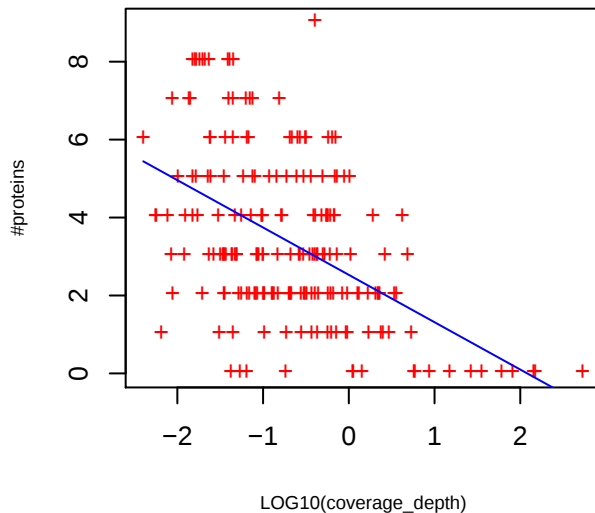


P-value curve ; red (unnorm), green (norm)



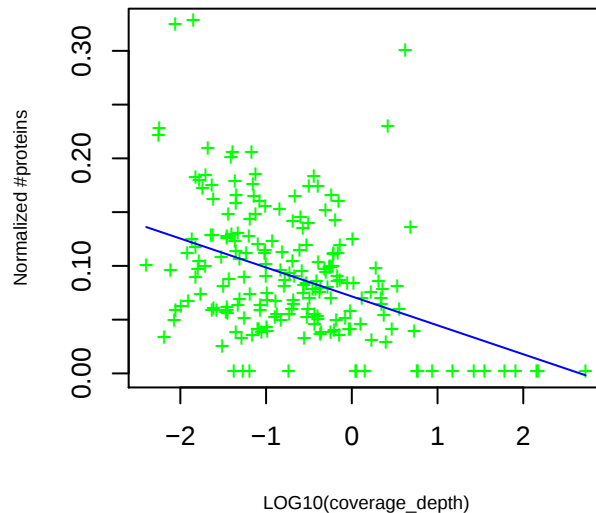
TIGR01549 HAD-SF-IA-v1: HAD-superfamily hydrolase, subfamily IA, variant 1

slope= -1.22 p_value= 8.4e-14 intercept= 2.53 p_value= 9e-34



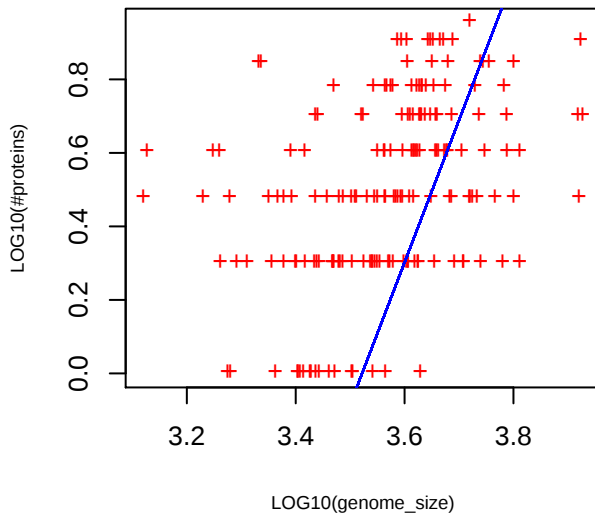
TIGR01549 HAD-SF-IA-v1: HAD-superfamily hydrolase, subfamily IA, variant 1

slope= -0.027 p_value= 4.9e-09 intercept= 0.072 p_value= 1.2e-32

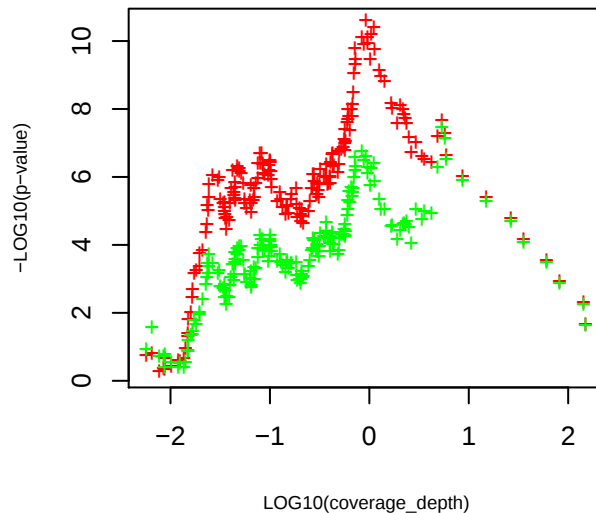


TIGR01549 HAD-SF-IA-v1: HAD-superfamily hydrolase, subfamily IA, variant 1

slope= 3.87 p_value= 1.4e-12 intercept= -13.63 p_value= 2.0e-12

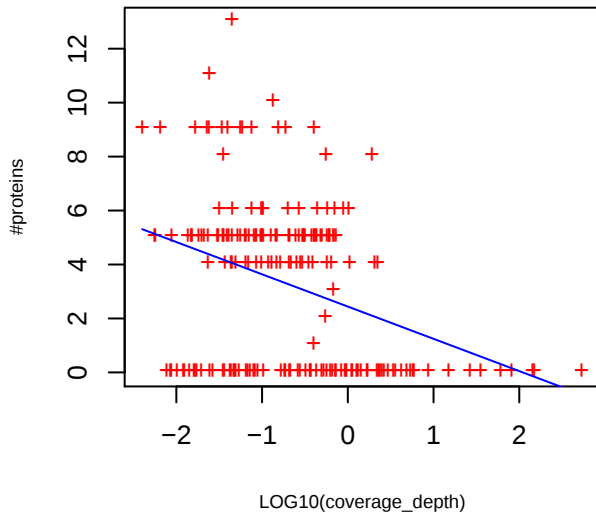


P-value curve ; red (unnorm), green (norm)



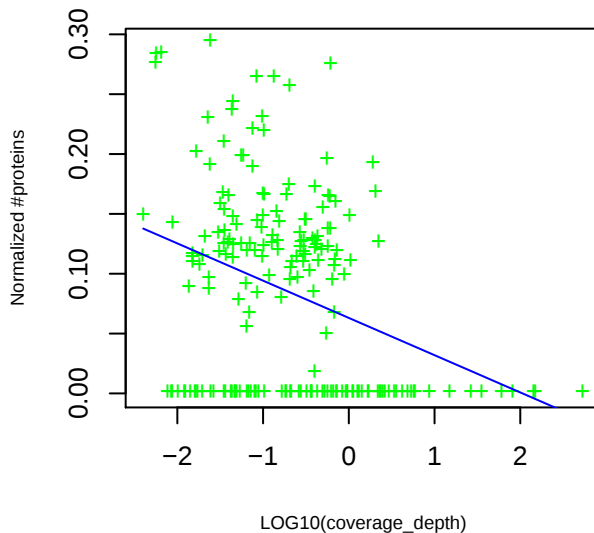
PF06429 DUF1078: Domain of unknown function (DUF1078)

slope= -1.20 p_value= 4.8e-07 intercept= 2.44 p_value= 1.4e-17



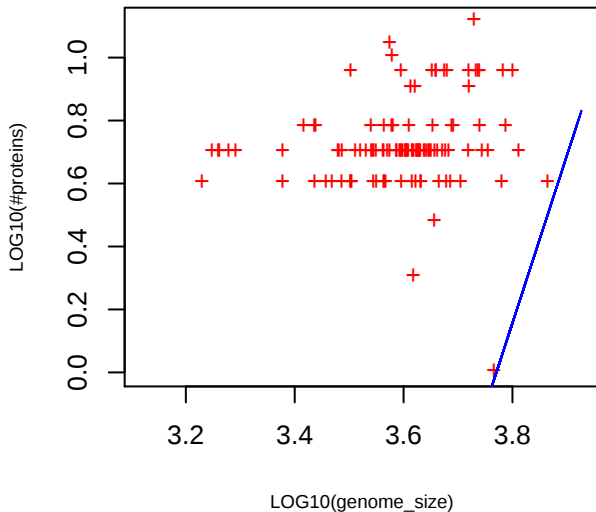
PF06429 DUF1078: Domain of unknown function (DUF1078)

slope= -0.031 p_value= 8e-07 intercept= 0.063 p_value= 7.7e-17

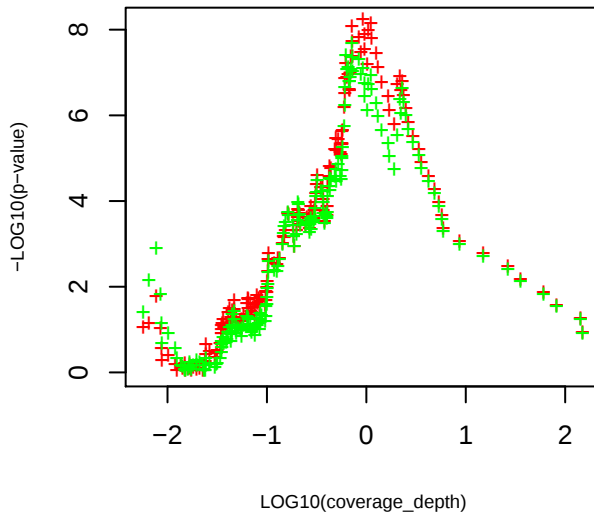


PF06429 DUF1078: Domain of unknown function (DUF1078)

slope= 5.32 p_value= 6.9e-08 intercept= -20.05 p_value= 1.2e-08

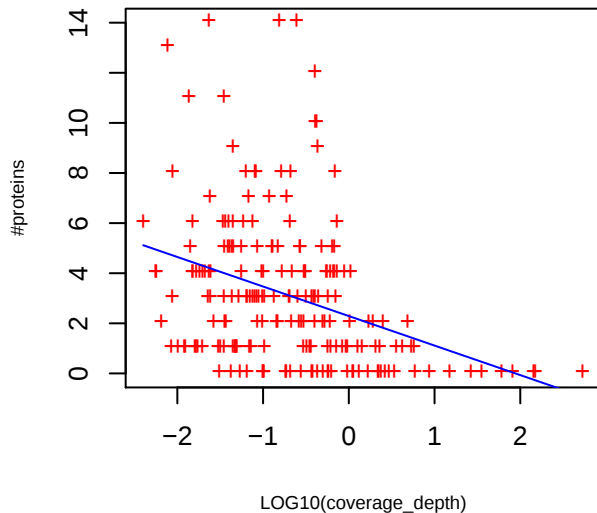


P-value curve ; red (unnorm), green (norm)



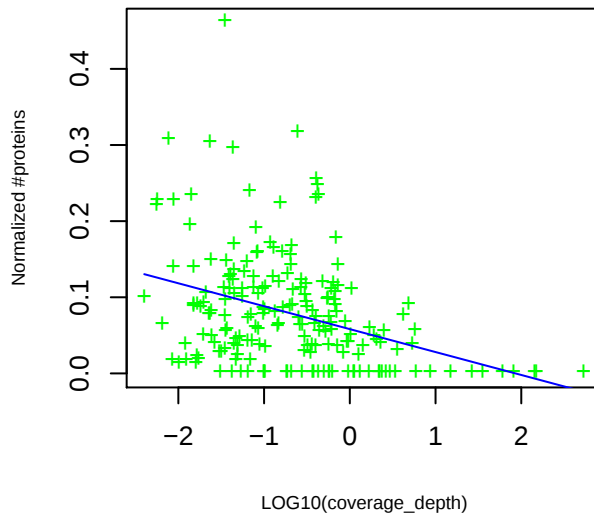
PF08279 HTH_11: HTH domain

slope= -1.18 p_value= 4.6e-07 intercept= 2.29 p_value= 2.4e-16



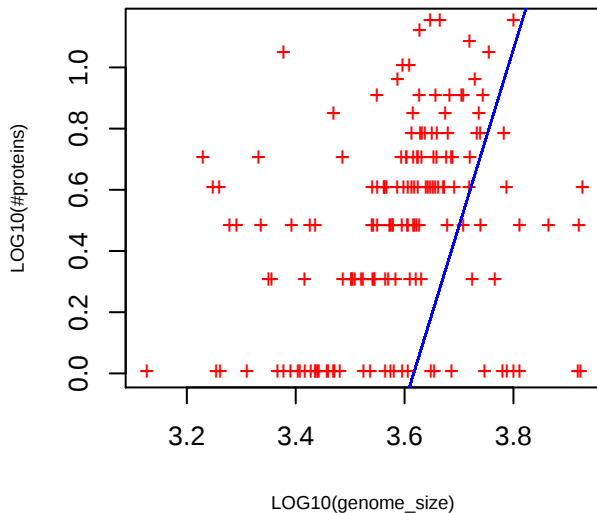
PF08279 HTH_11: HTH domain

slope= -0.03 p_value= 2.1e-07 intercept= 0.058 p_value= 5e-17

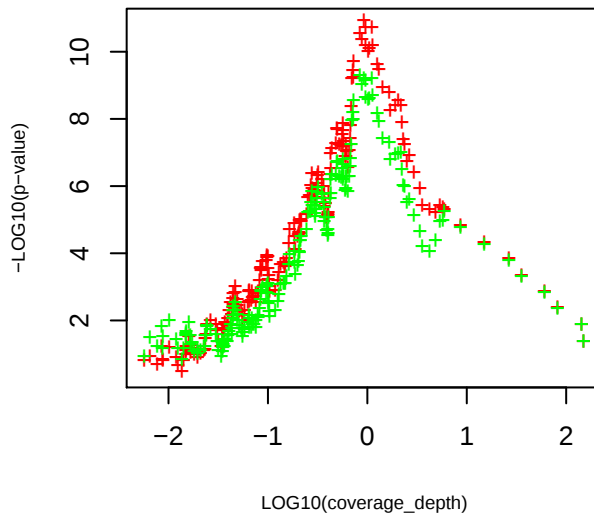


PF08279 HTH_11: HTH domain

slope= 5.78 p_value= 4.5e-15 intercept= -20.91 p_value= 1.6e-15

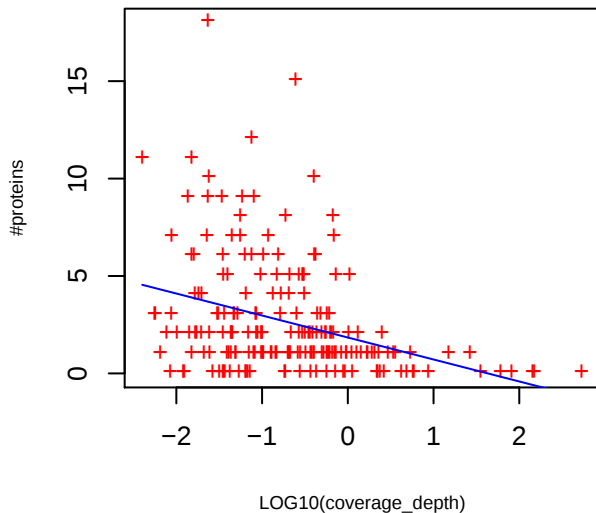


P-value curve ; red (unnorm), green (norm)



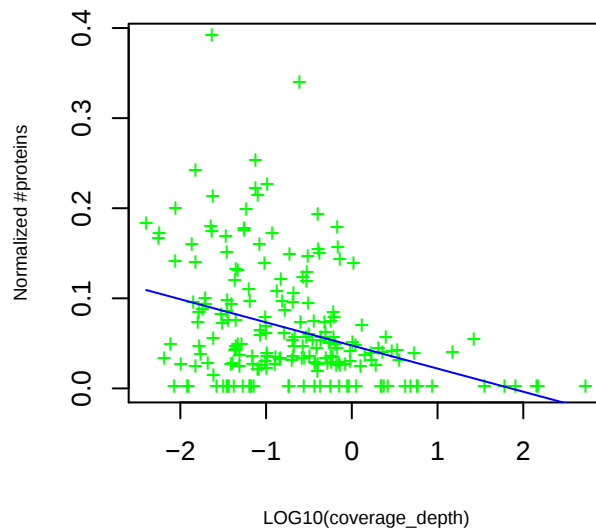
PF01032 FecCD: ABC transporter, iron chelate uptake transporter (FeCT) family, permease protei

slope= -1.13 p_value= 1.2e-06 intercept= 1.84 p_value= 9.2e-12



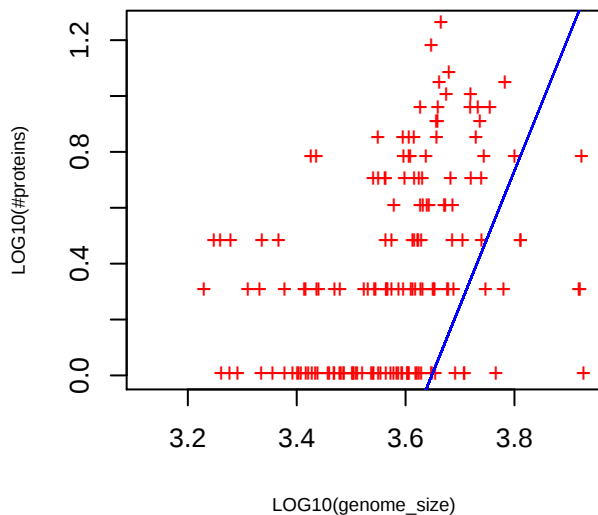
PF01032 FecCD: ABC transporter, iron chelate uptake transporter (FeCT) family, permease protei

slope= -0.026 p_value= 7.9e-07 intercept= 0.048 p_value= 9.5e-15

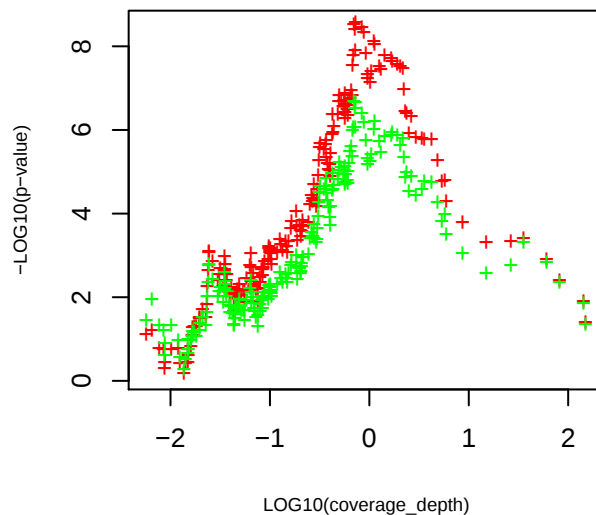


PF01032 FecCD: ABC transporter, iron chelate uptake transporter (FeCT) family, permease protei

slope= 4.82 p_value= 6.7e-11 intercept= -17.59 p_value= 2.2e-11

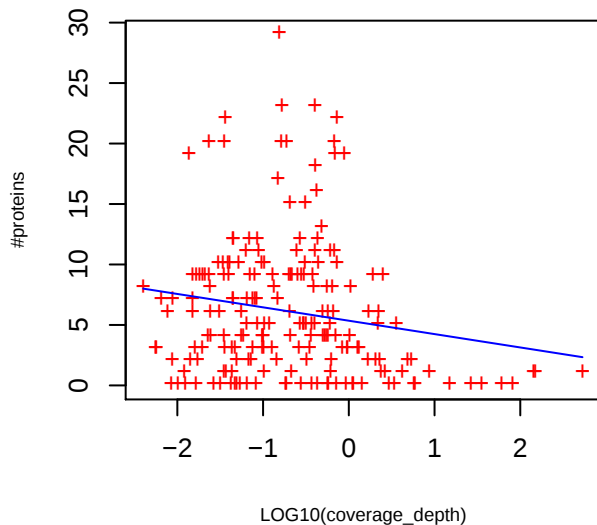


P-value curve ; red (unnorm), green (norm)



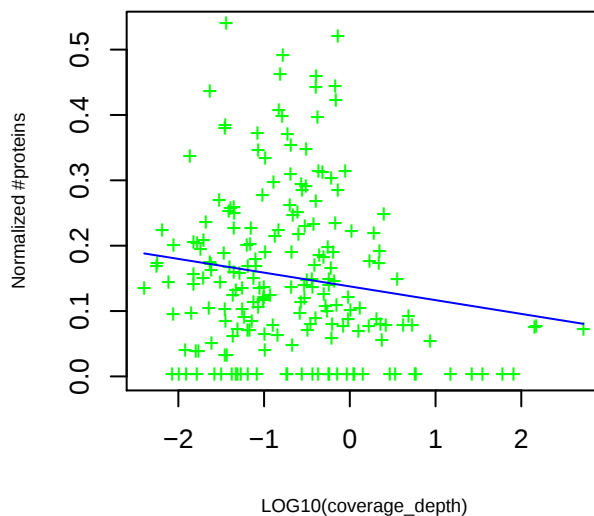
PF01047 MarR: transcriptional regulator, MarR family

slope= -1.11 p_value= 0.015 intercept= 5.35 p_value= 1.0e-20



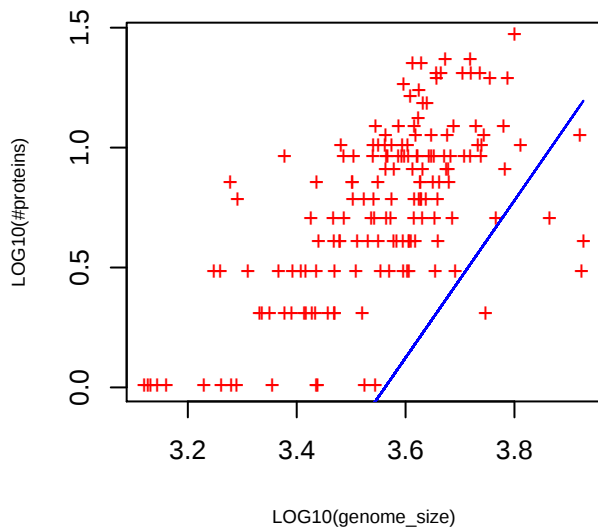
PF01047 MarR: transcriptional regulator, MarR family

slope= -0.021 p_value= 0.033 intercept= 0.14 p_value= 1.1e-26

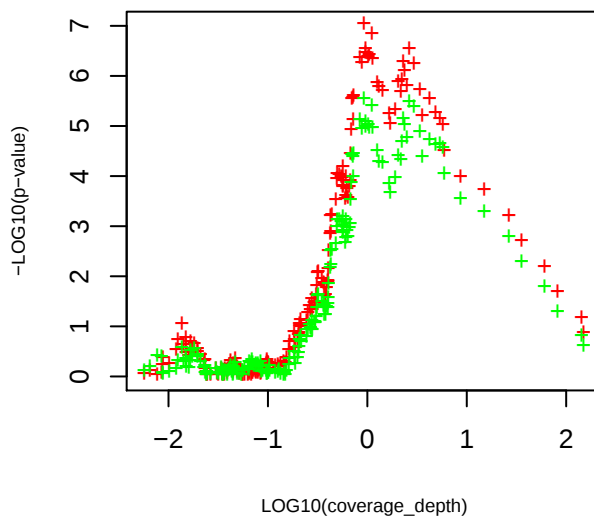


PF01047 MarR: transcriptional regulator, MarR family

slope= 3.28 p_value= 2.3e-05 intercept= -11.68 p_value= 2.2e-05

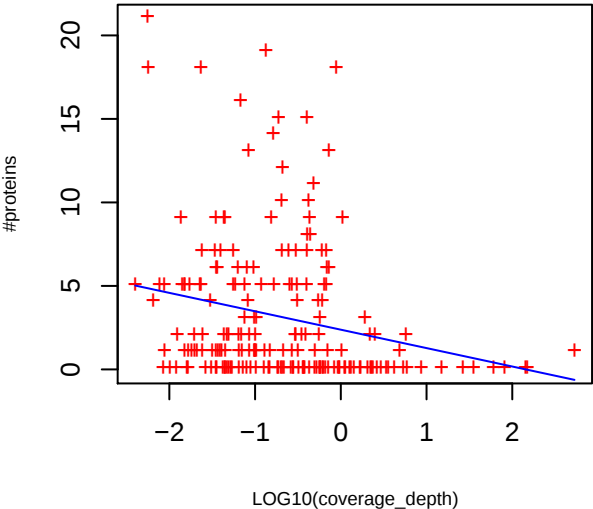


P-value curve ; red (unnorm), green (norm)



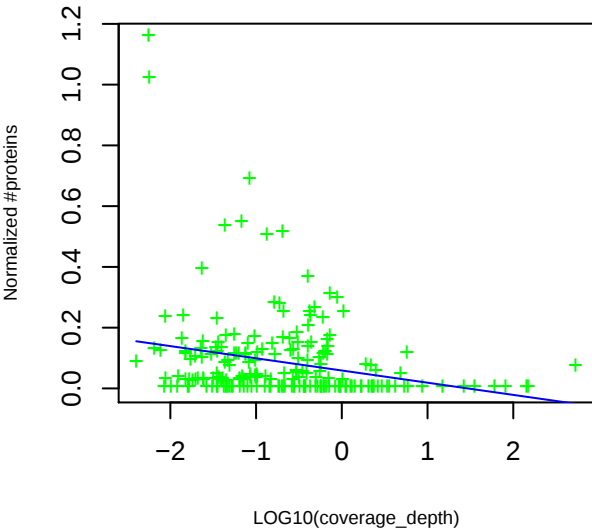
TIGR01727 oligo_HPY: oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-terminal doi

slope= -1.10 p_value= 0.0014 intercept= 2.38 p_value= 3.2e-09



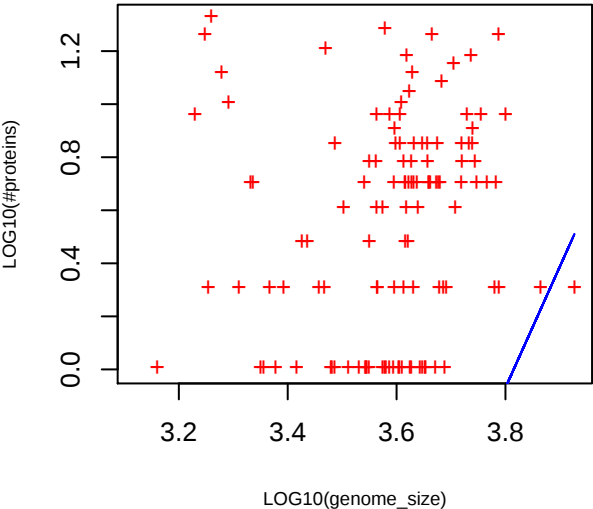
TIGR01727 oligo_HPY: oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-terminal doi

slope= -0.04 p_value= 0.00078 intercept= 0.059 p_value= 1.5e-05

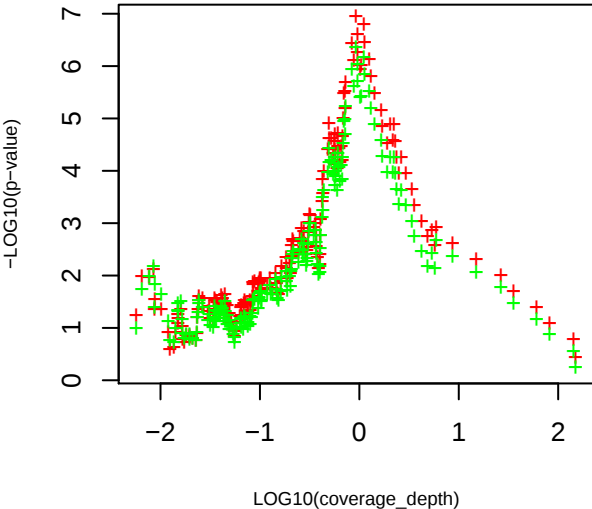


TIGR01727 oligo_HPY: oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-terminal doi

slope= 4.57 p_value= 1.9e-06 intercept= -17.43 p_value= 3.4e-07

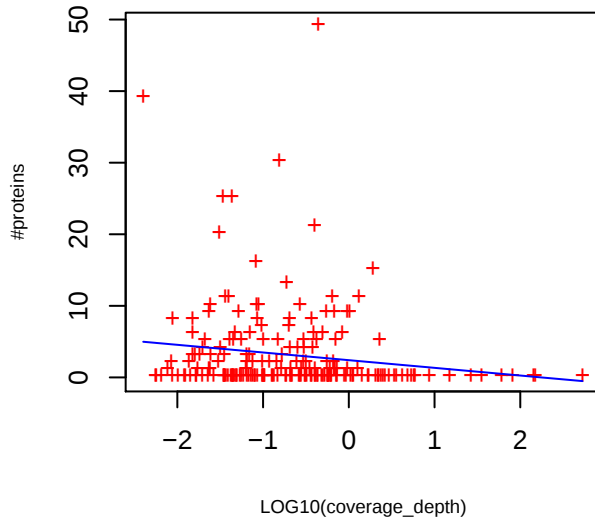


P-value curve : red (unnorm), green (norm)



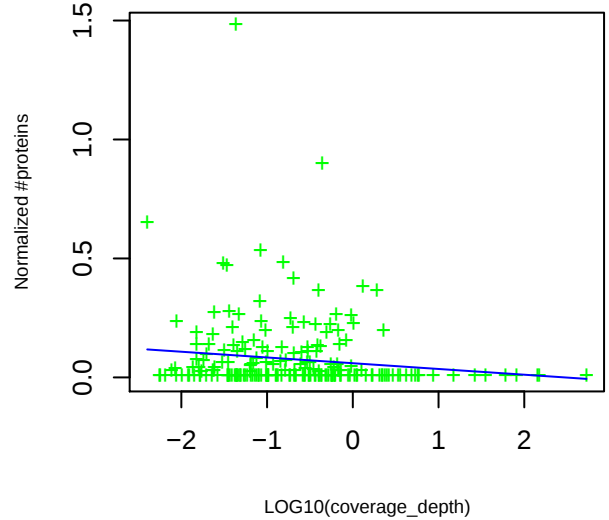
PF02371 Transposase_20: transposase, IS116/IS110/IS902 family

slope= -1.07 p_value= 0.036 intercept= 2.41 p_value= 4.2e-05



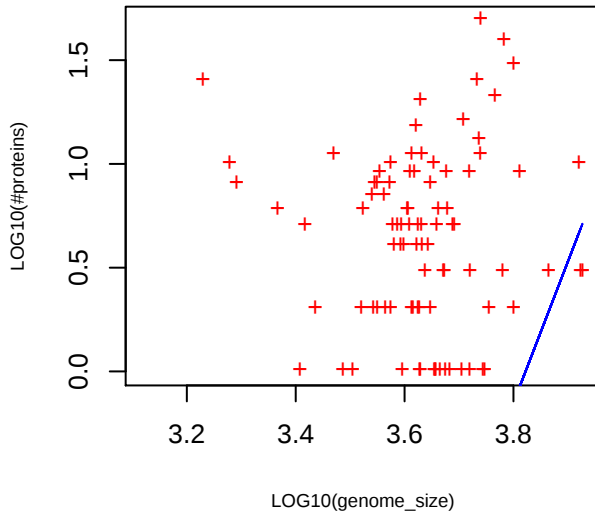
PF02371 Transposase_20: transposase, IS116/IS110/IS902 family

slope= -0.024 p_value= 0.062 intercept= 0.06 p_value= 6e-05

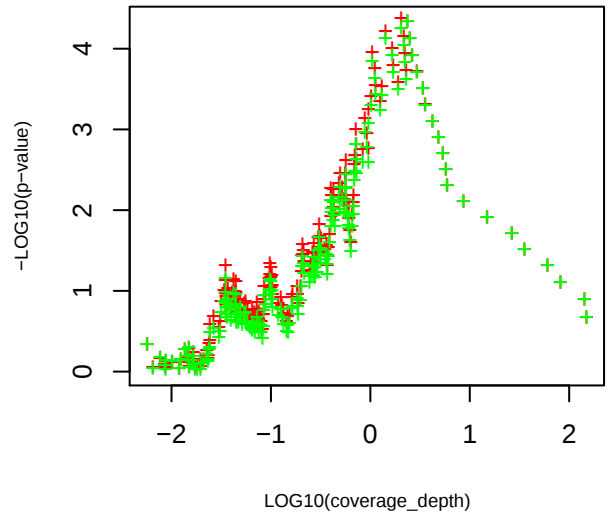


PF02371 Transposase_20: transposase, IS116/IS110/IS902 family

slope= 6.80 p_value= 1.6e-12 intercept= -26.01 p_value= 4.6e-14

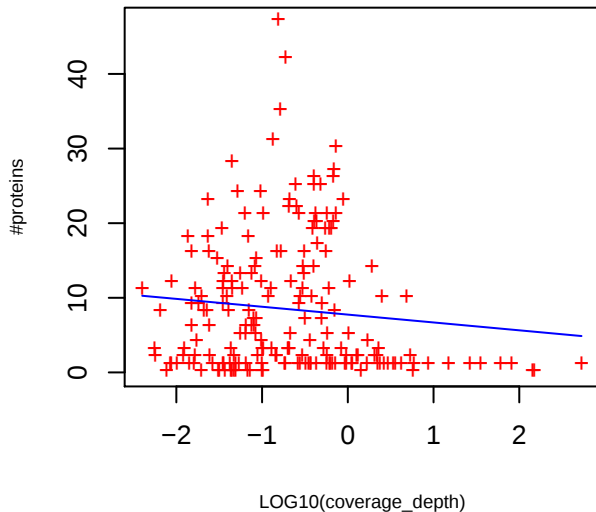


P-value curve ; red (unnorm), green (norm)



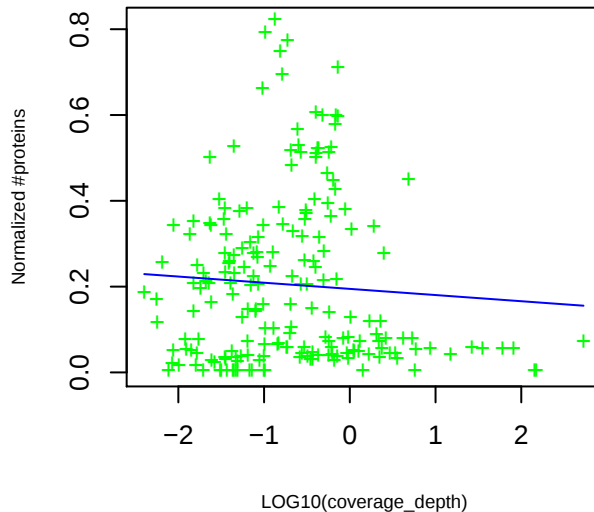
PF00392 GntR: transcriptional regulator, GntR family

slope= -1.05 p_value= 0.15 intercept= 7.75 p_value= 6.6e-18



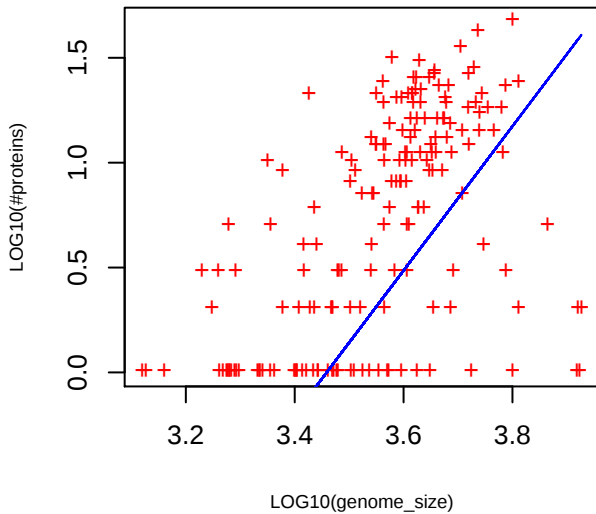
PF00392 GntR: transcriptional regulator, GntR family

slope= -0.014 p_value= 0.36 intercept= 0.19 p_value= 2.3e-22

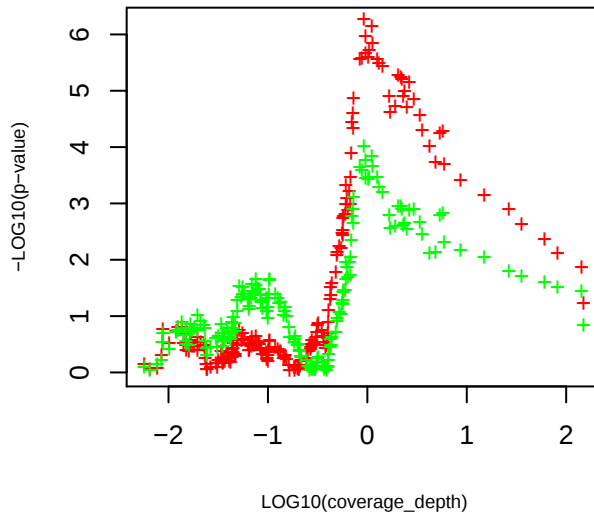


PF00392 GntR: transcriptional regulator, GntR family

slope= 3.44 p_value= 8.6e-09 intercept= -11.89 p_value= 1.9e-08

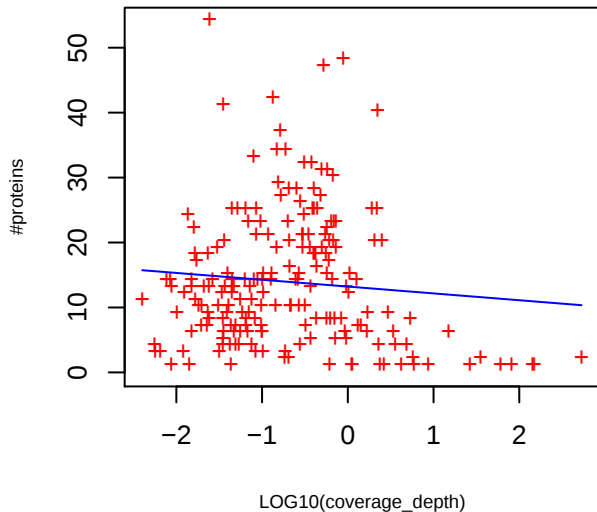


P-value curve : red (unnorm), green (norm)



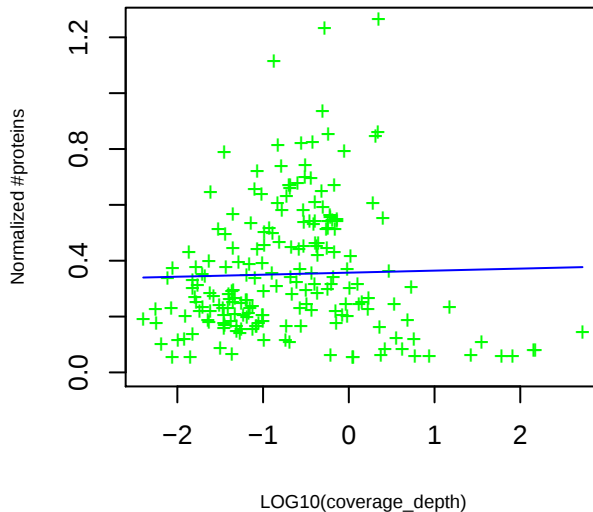
PF08659 KR: KR domain

slope= -1.05 p_value= 0.20 intercept= 13.22 p_value= 3.7e-32



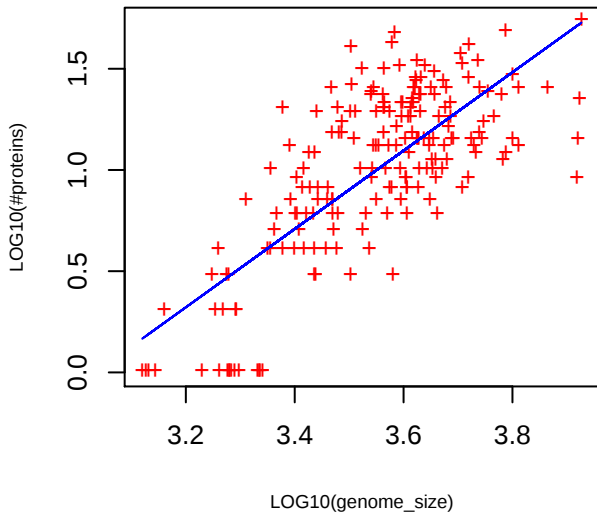
PF08659 KR: KR domain

slope= 0.0073 p_value= 0.69 intercept= 0.36 p_value= 1.3e-40

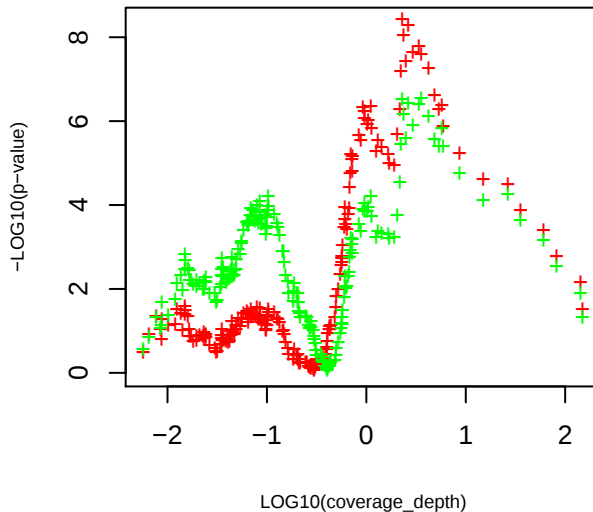


PF08659 KR: KR domain

slope= 1.93 p_value= 3.0e-36 intercept= -5.87 p_value= 2.4e-29

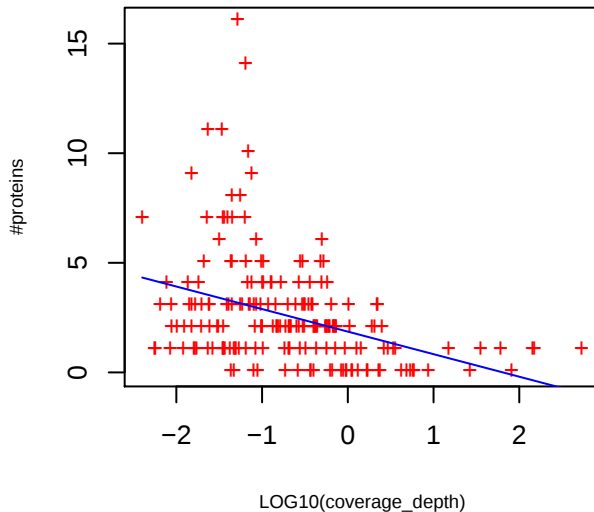


P-value curve ; red (unnorm), green (norm)



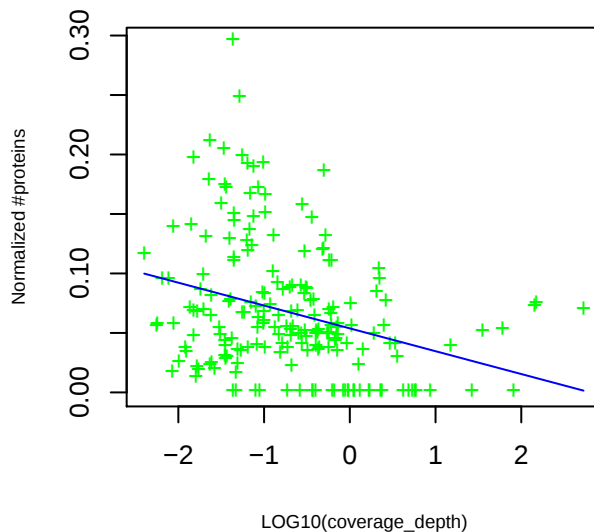
PF00482 GSP11_F: Bacterial type II secretion system protein F domain

slope= -1.03 p_value= 1.2e-07 intercept= 1.86 p_value= 6.5e-16



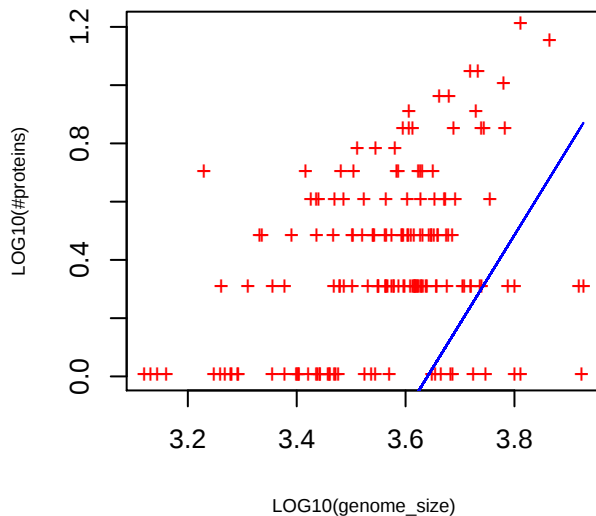
PF00482 GSP11_F: Bacterial type II secretion system protein F domain

slope= -0.019 p_value= 8.9e-06 intercept= 0.054 p_value= 3.4e-23

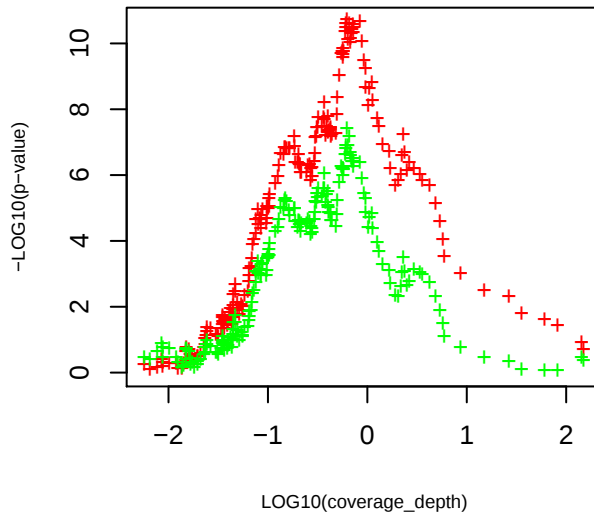


PF00482 GSP11_F: Bacterial type II secretion system protein F domain

slope= 3.04 p_value= 9.5e-06 intercept= -11.06 p_value= 5.7e-06

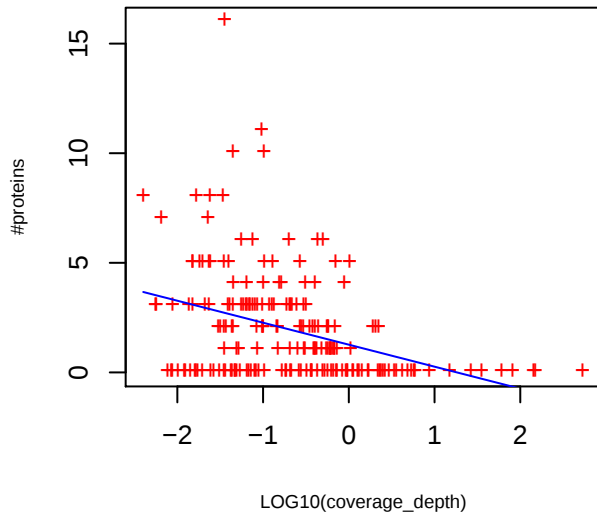


P-value curve : red (unnorm), green (norm)



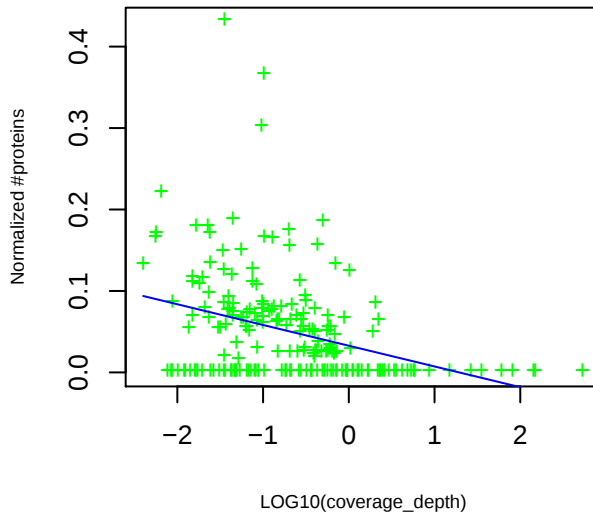
PF00669 Flagellin_N: Bacterial flagellin N-terminus

slope= -1.00 p_value= 1.8e-07 intercept= 1.27 p_value= 7.2e-09



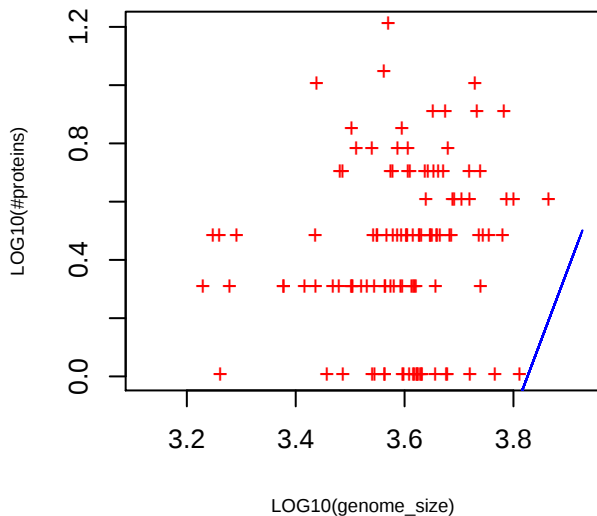
PF00669 Flagellin_N: Bacterial flagellin N-terminus

slope= -0.025 p_value= 5.6e-07 intercept= 0.033 p_value= 1.6e-08

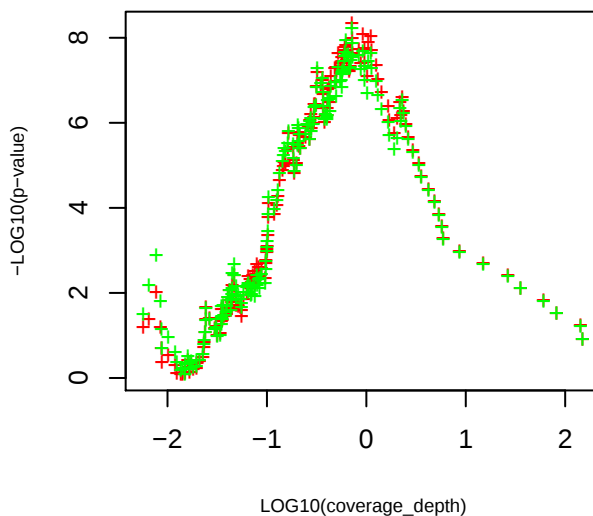


PF00669 Flagellin_N: Bacterial flagellin N-terminus

slope= 4.97 p_value= 9.6e-08 intercept= -19.00 p_value= 1.1e-08

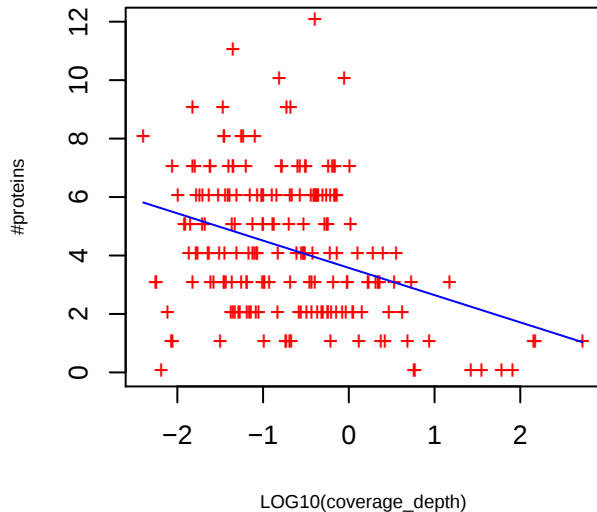


P-value curve ; red (unnorm), green (norm)



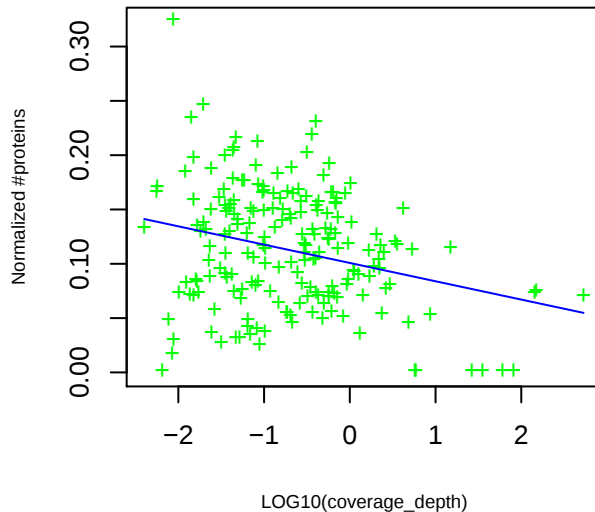
TIGR01509 HAD-SF-IA-v3: HAD-superfamily hydrolase, subfamily IA, variant 3

slope= -0.93 p_value= 4.9e-07 intercept= 3.58 p_value= 2.3e-42



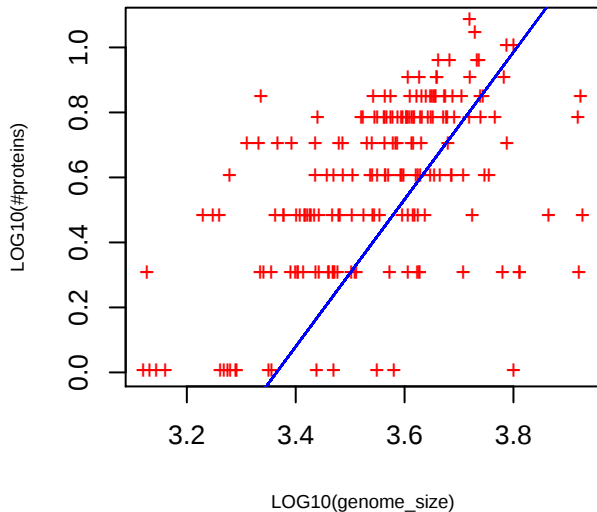
TIGR01509 HAD-SF-IA-v3: HAD-superfamily hydrolase, subfamily IA, variant 3

slope= -0.017 p_value= 9e-05 intercept= 0.10 p_value= 2.0e-52

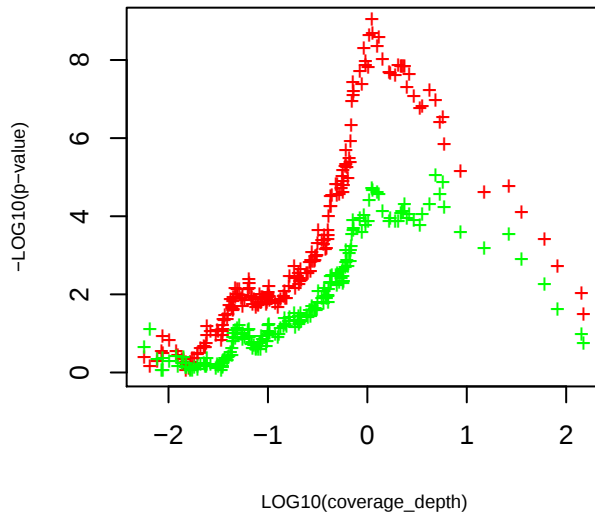


TIGR01509 HAD-SF-IA-v3: HAD-superfamily hydrolase, subfamily IA, variant 3

slope= 2.26 p_value= 1.2e-09 intercept= -7.62 p_value= 7e-09

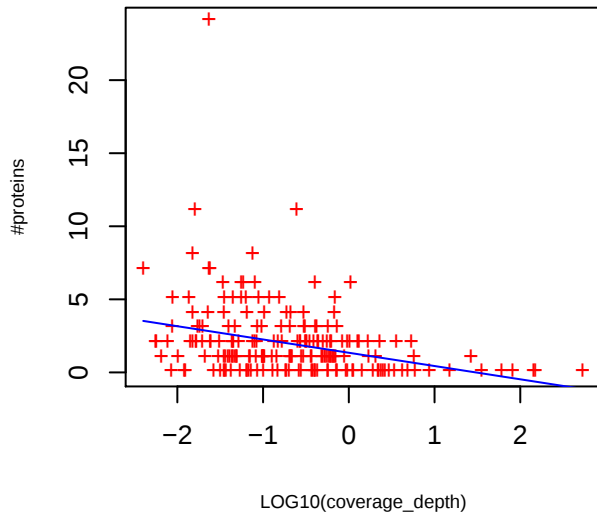


P-value curve ; red (unnorm), green (norm)



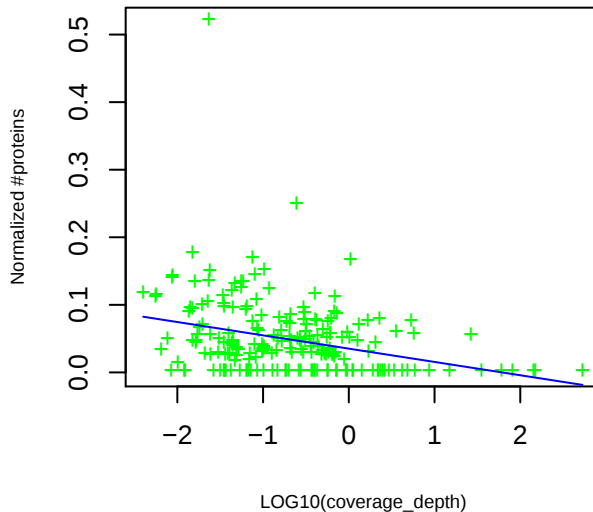
PF01497 Peripla_BP_2: Periplasmic binding protein

slope= -0.91 p_value= 6.5e-06 intercept= 1.35 p_value= 6.1e-09



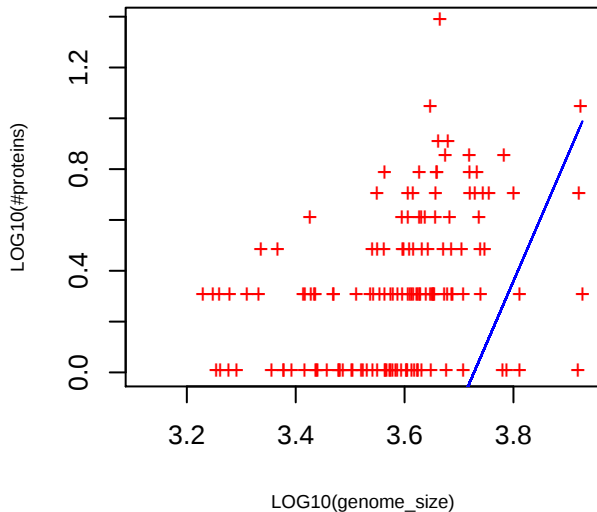
PF01497 Peripla_BP_2: Periplasmic binding protein

slope= -0.020 p_value= 7.7e-06 intercept= 0.035 p_value= 8.3e-12

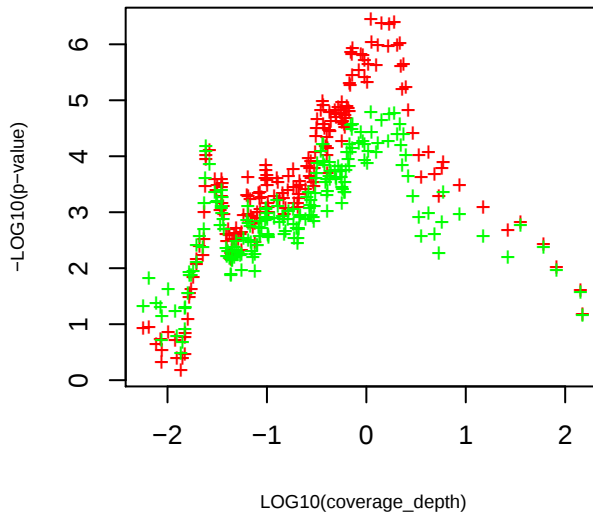


PF01497 Peripla_BP_2: Periplasmic binding protein

slope= 4.96 p_value= 2.1e-09 intercept= -18.50 p_value= 3.8e-10

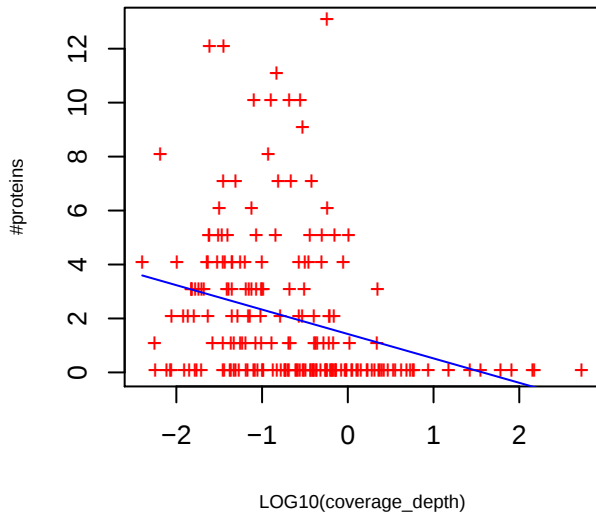


P-value curve ; red (unnorm), green (norm)



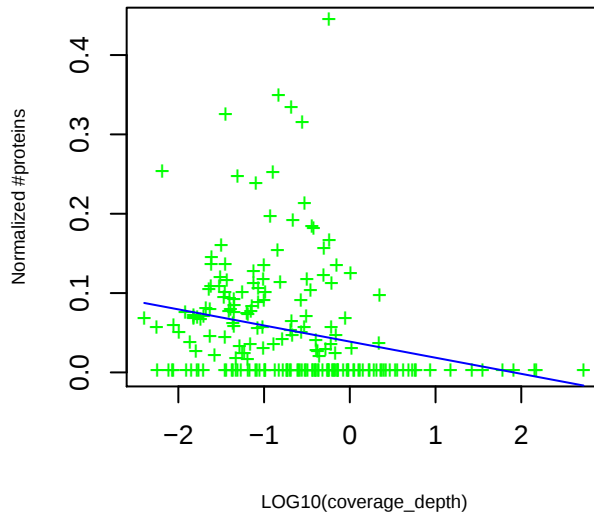
PF07238 PilZ: Type IV pilus assembly protein PilZ

slope= -0.90 p_value= 3.6e-05 intercept= 1.42 p_value= 1.6e-08



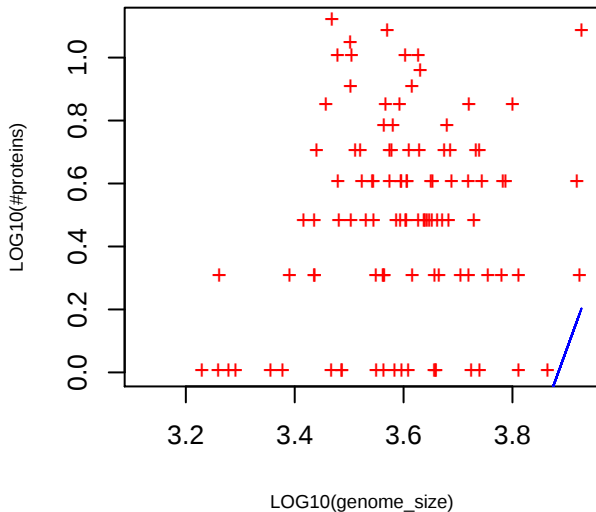
PF07238 PilZ: Type IV pilus assembly protein PilZ

slope= -0.020 p_value= 7e-04 intercept= 0.039 p_value= 2.2e-08

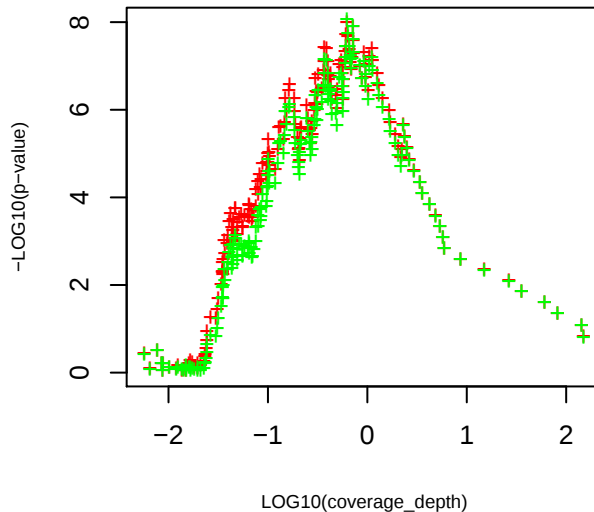


PF07238 PilZ: Type IV pilus assembly protein PilZ

slope= 4.76 p_value= 7.1e-07 intercept= -18.49 p_value= 6.8e-08

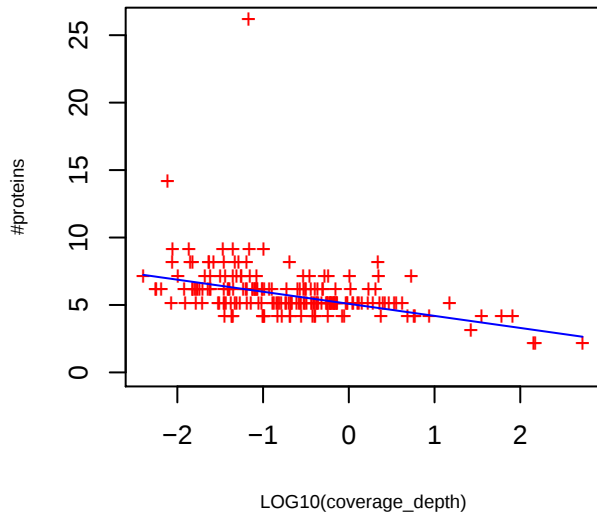


P-value curve ; red (unnorm), green (norm)



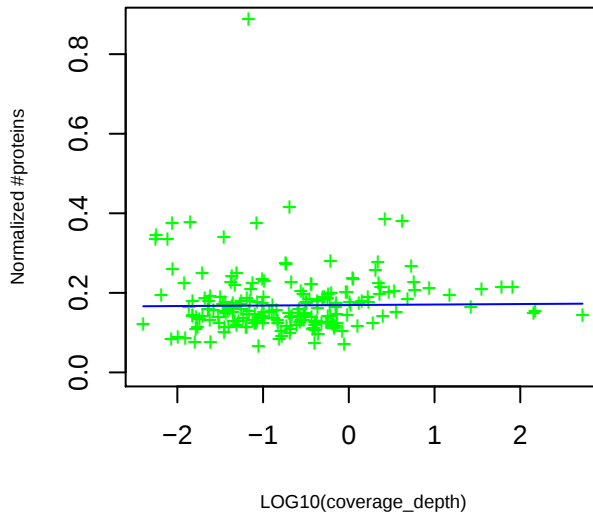
PF01336 tRNA_anti: OB-fold nucleic acid binding domain

slope= -0.89 p_value= 1.1e-08 intercept= 5.09 p_value= 3.5e-75



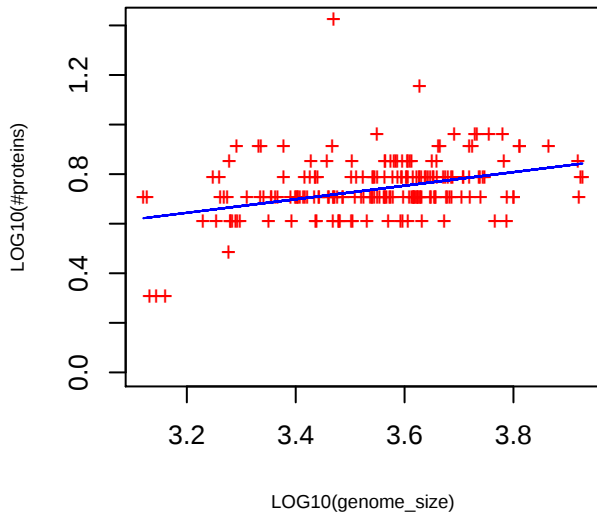
PF01336 tRNA_anti: OB-fold nucleic acid binding domain

slope= 0.0013 p_value= 0.85 intercept= 0.17 p_value= 1.8e-57

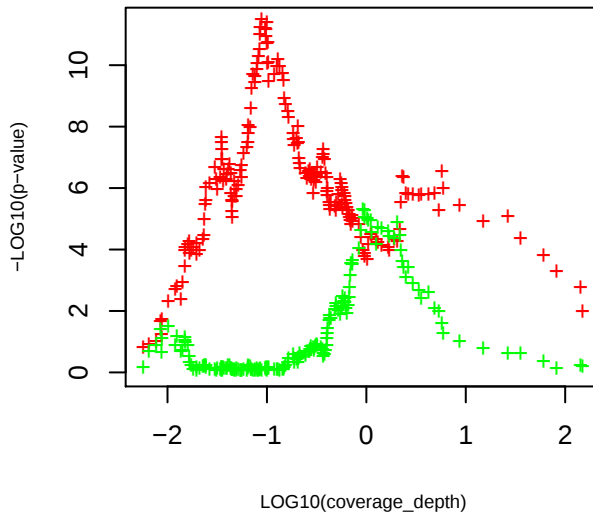


PF01336 tRNA_anti: OB-fold nucleic acid binding domain

slope= 0.27 p_value= 6.3e-08 intercept= -0.23 p_value= 0.18

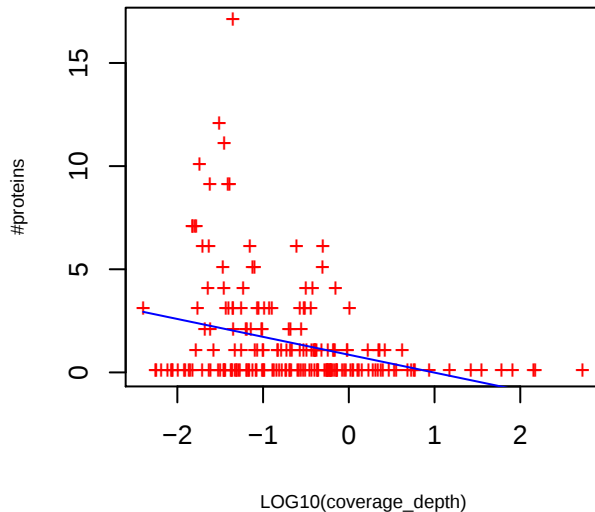


P-value curve ; red (unnorm), green (norm)



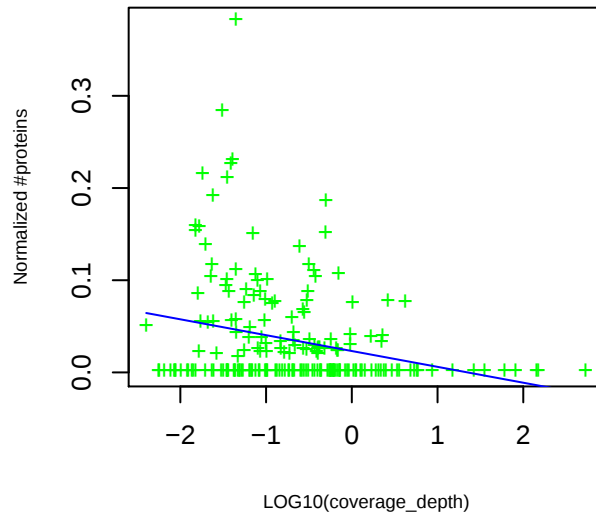
TIGR01783 TonB-siderophor: TonB-dependent siderophore receptor

slope= -0.87 p_value= 1.5e-05 intercept= 0.86 p_value= 0.00014



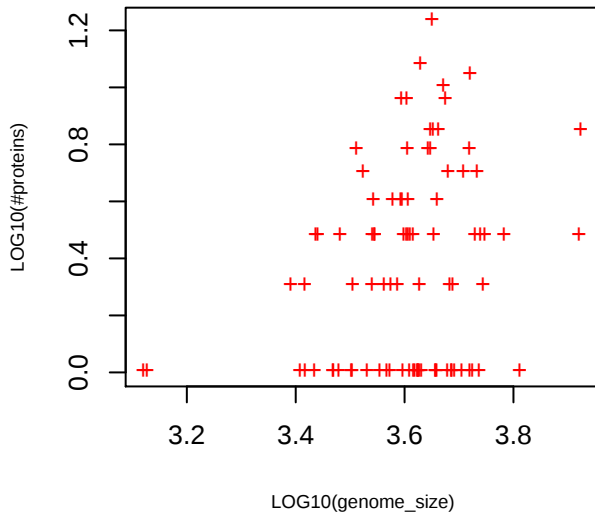
TIGR01783 TonB-siderophor: TonB-dependent siderophore receptor

slope= -0.017 p_value= 0.00021 intercept= 0.023 p_value= 1.1e-05

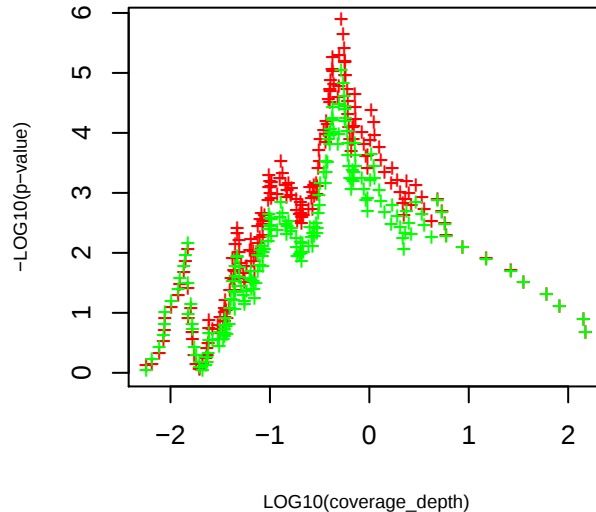


TIGR01783 TonB-siderophor: TonB-dependent siderophore receptor

slope= 4.61 p_value= 8e-07 intercept= -18.37 p_value= 3.8e-08

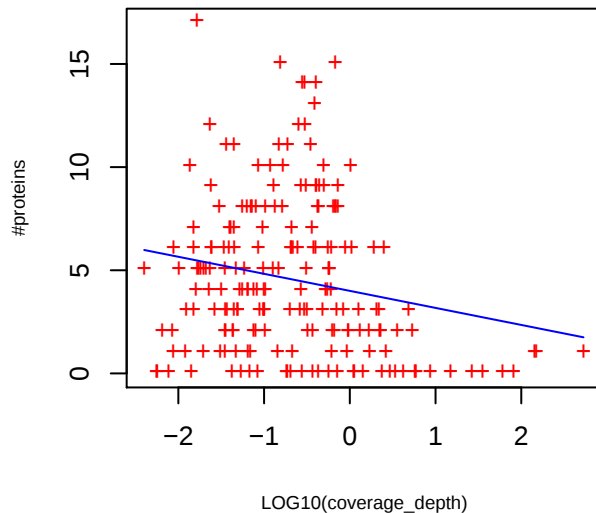


P-value curve ; red (unnorm), green (norm)



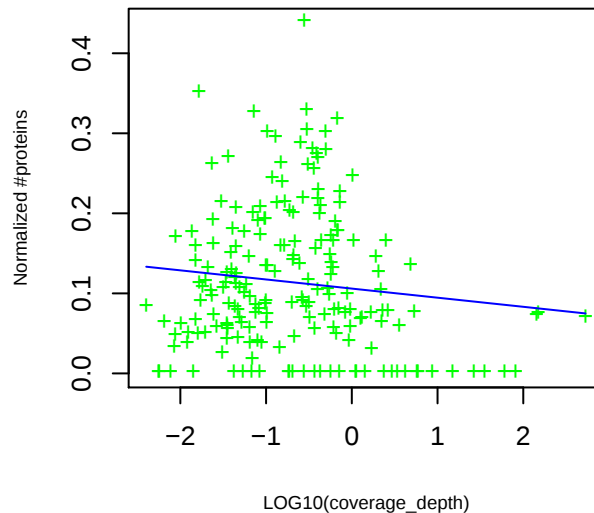
PF00376 MerR: transcriptional regulator, MerR family

slope= -0.83 p_value= 0.0056 intercept= 4.00 p_value= 2.8e-25



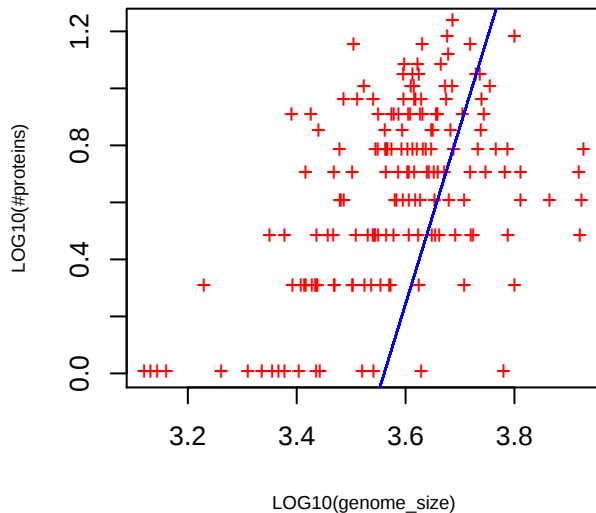
PF00376 MerR: transcriptional regulator, MerR family

slope= -0.011 p_value= 0.11 intercept= 0.11 p_value= 4.6e-29

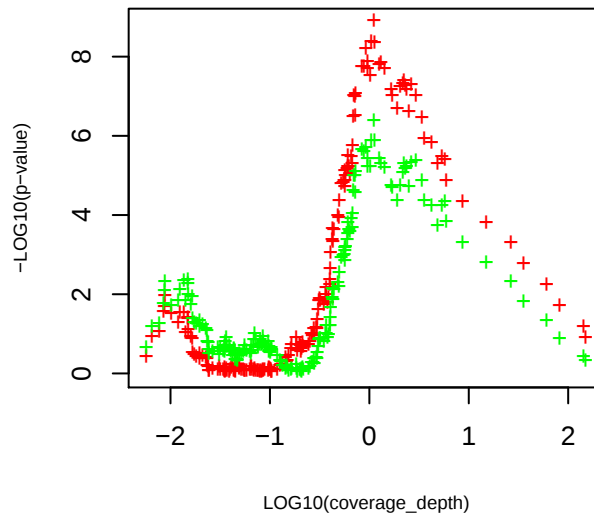


PF00376 MerR: transcriptional regulator, MerR family

slope= 6.21 p_value= 7e-20 intercept= -22.13 p_value= 5.6e-20

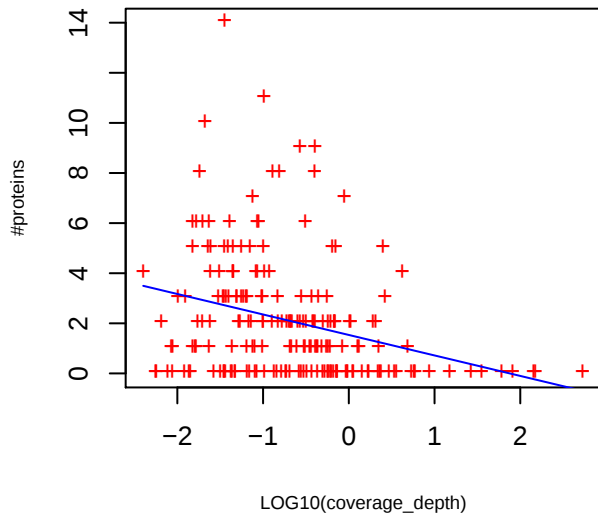


P-value curve ; red (unnorm), green (norm)



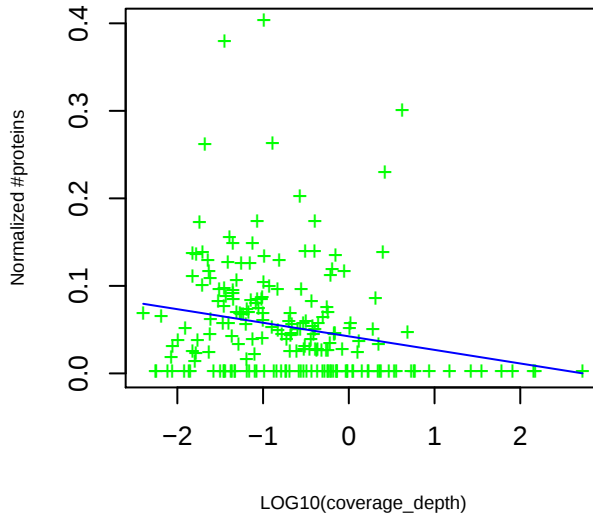
PF08238 Sel1: Sel1 repeat

slope= -0.82 p_value= 2.2e-05 intercept= 1.54 p_value= 1.1e-11



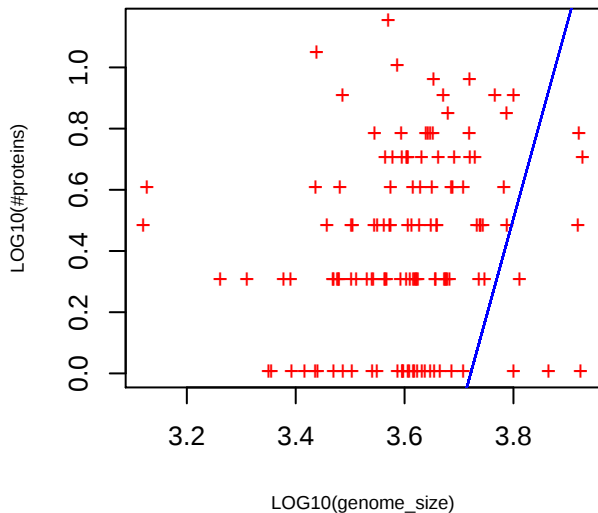
PF08238 Sel1: Sel1 repeat

slope= -0.016 p_value= 0.0029 intercept= 0.042 p_value= 6.7e-12

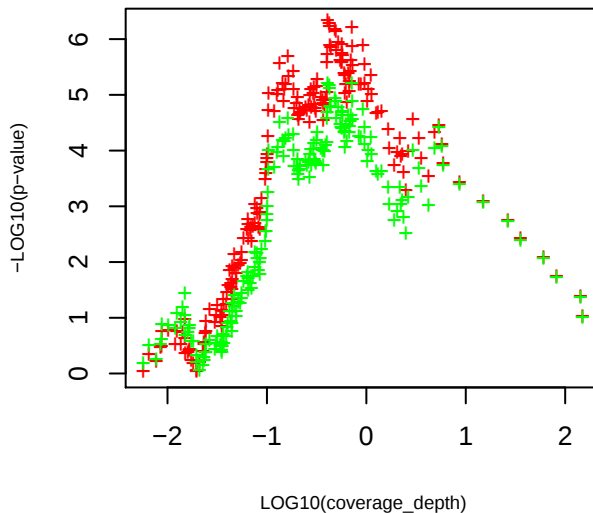


PF08238 Sel1: Sel1 repeat

slope= 6.45 p_value= 1.3e-13 intercept= -24.00 p_value= 1.2e-14

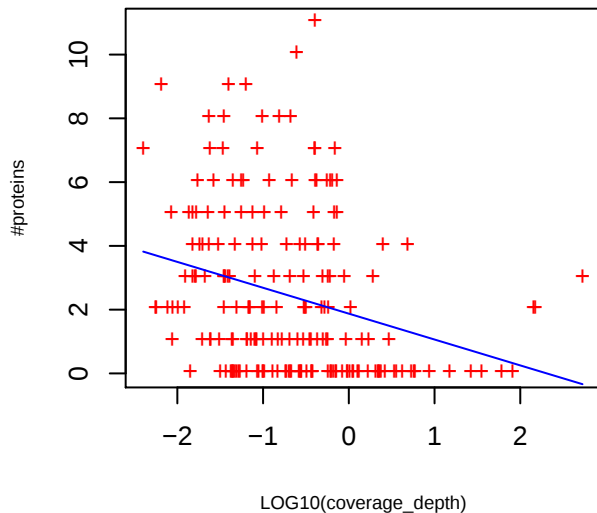


P-value curve : red (unnorm), green (norm)



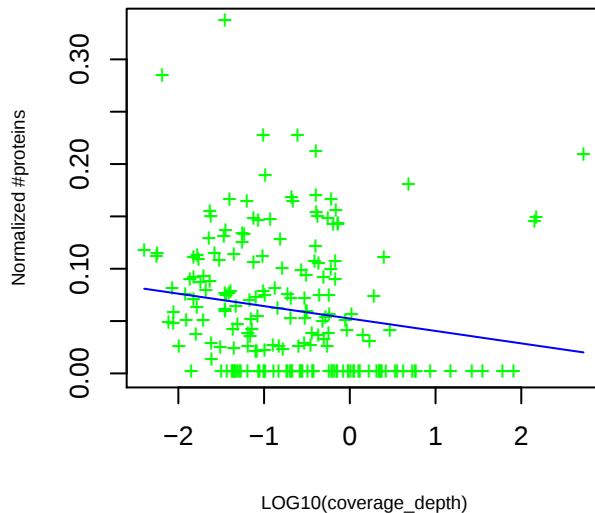
PF00497 SBP_bac_3: bacterial extracellular solute-binding protein, family 3

slope= -0.81 p_value= 6.4e-05 intercept= 1.87 p_value= 1.2e-14



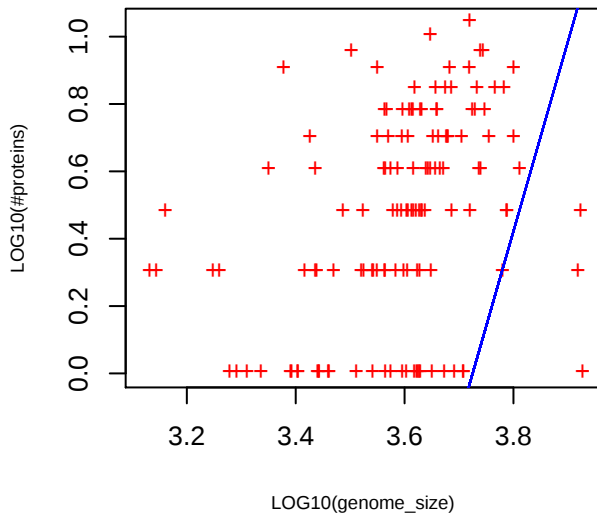
PF00497 SBP_bac_3: bacterial extracellular solute-binding protein, family 3

slope= -0.012 p_value= 0.018 intercept= 0.052 p_value= 2.4e-17

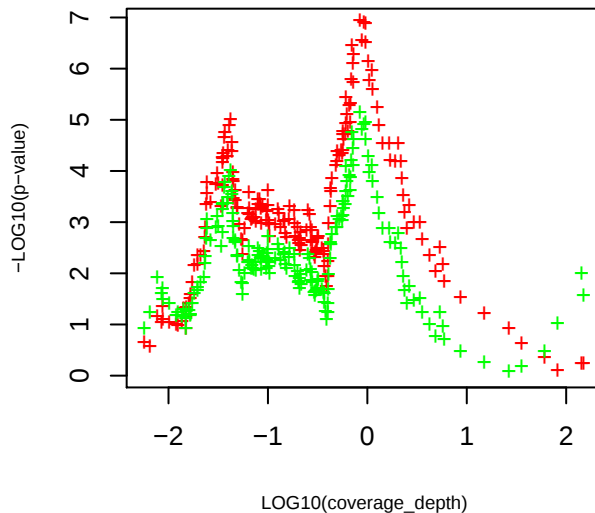


PF00497 SBP_bac_3: bacterial extracellular solute-binding protein, family 3

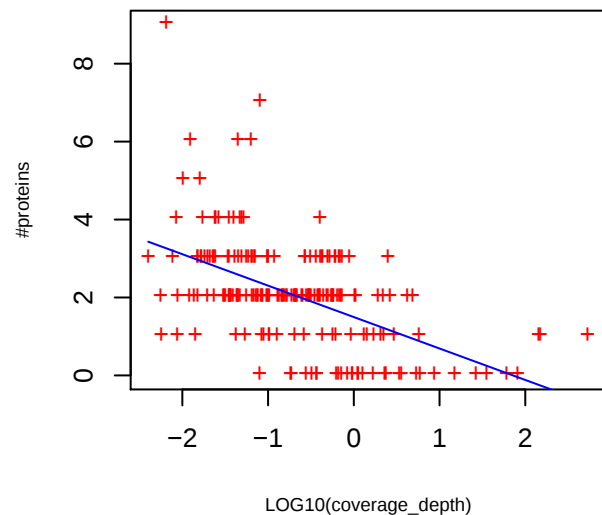
slope= 5.63 p_value= 2e-10 intercept= -20.97 p_value= 3e-11



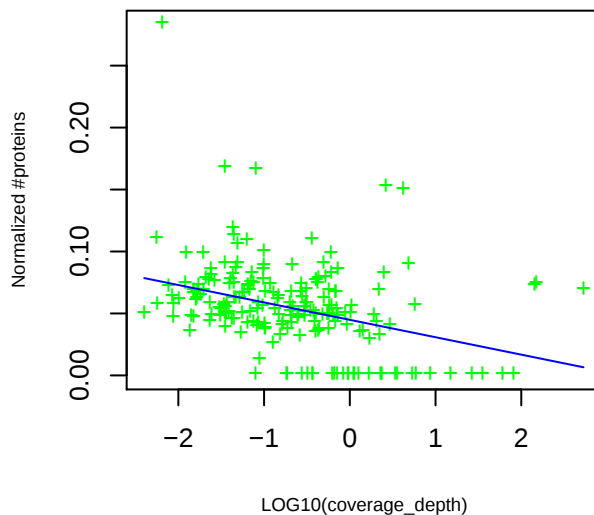
P-value curve ; red (unnorm), green (norm)



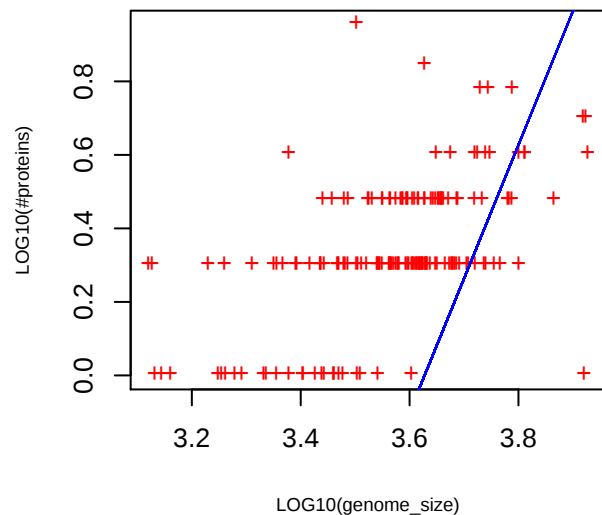
PF00391 PEP-utilizers: PEP-utilizing enzyme, mobile domain
 slope= -0.81 p_value= 2.0e-15 intercept= 1.50 p_value= 6.6e-32



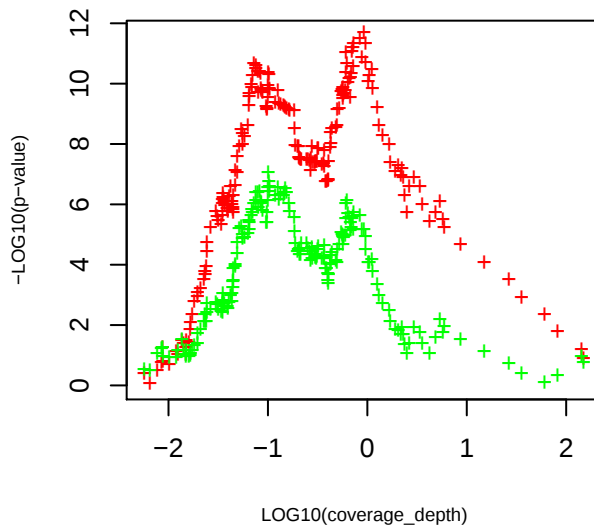
PF00391 PEP-utilizers: PEP-utilizing enzyme, mobile domain
 slope= -0.014 p_value= 3.7e-07 intercept= 0.045 p_value= 5.3e-34



PF00391 PEP-utilizers: PEP-utilizing enzyme, mobile domain
 slope= 3.64 p_value= 3e-08 intercept= -13.19 p_value= 1.6e-08

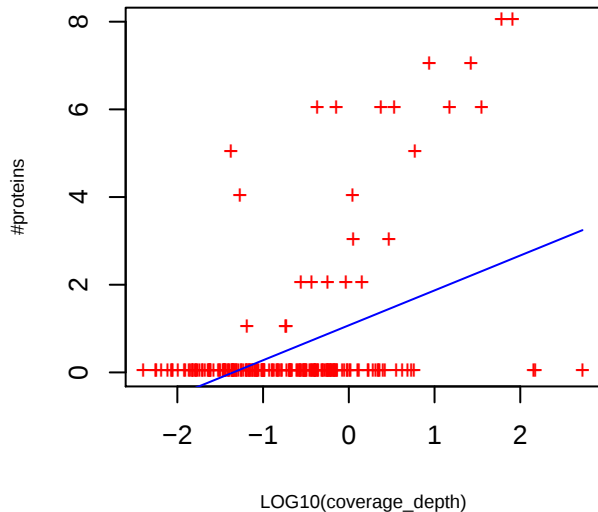


P-value curve ; red (unnorm), green (norm)



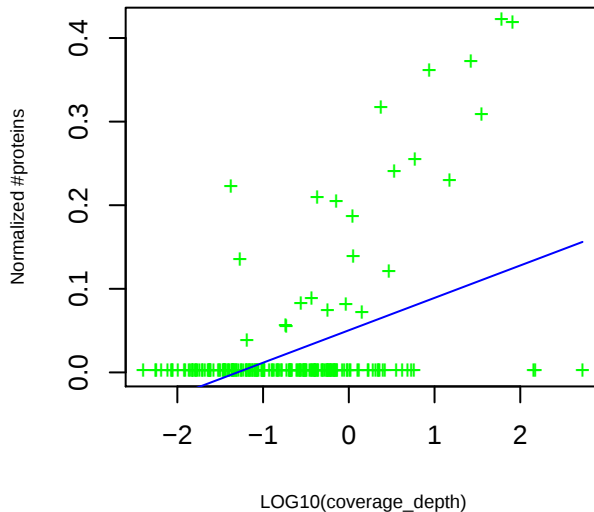
PF07864 DUF1651: Protein of unknown function (DUF1651)

slope= 0.80 p_value= 8.7e-11 intercept= 1.07 p_value= 3.2e-14



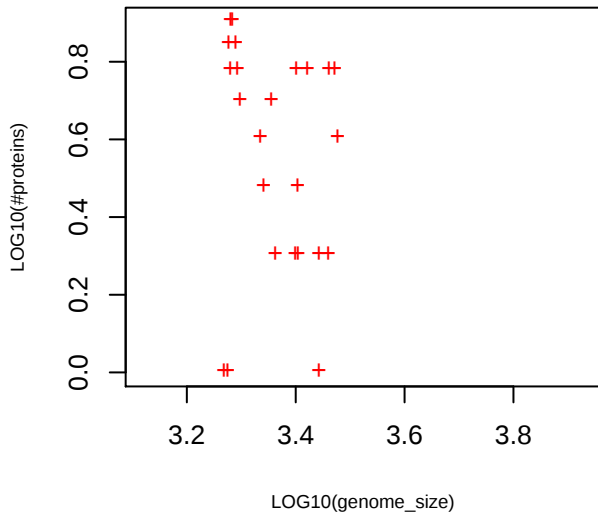
PF07864 DUF1651: Protein of unknown function (DUF1651)

slope= 0.039 p_value= 1.4e-11 intercept= 0.05 p_value= 2.0e-14

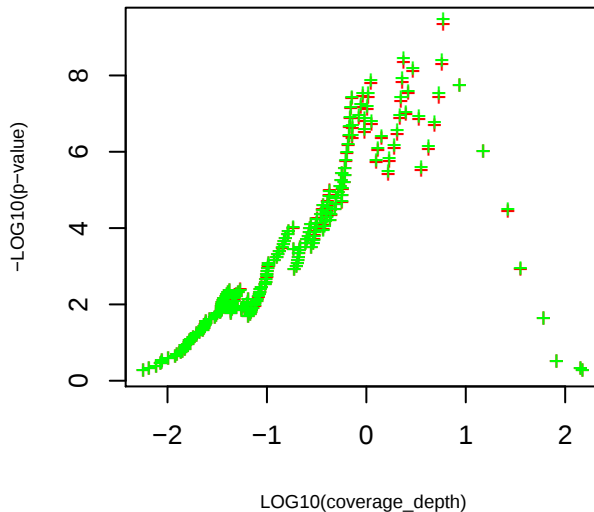


PF07864 DUF1651: Protein of unknown function (DUF1651)

slope= -3.83 p_value= 1.0e-09 intercept= 10.14 p_value= 3.4e-06

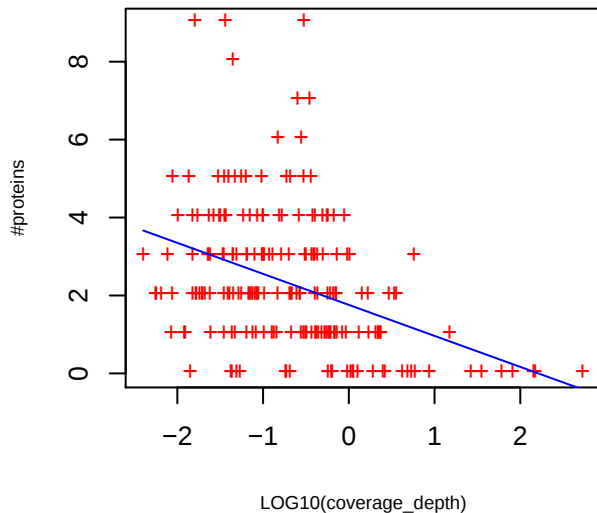


P-value curve ; red (unnorm), green (norm)



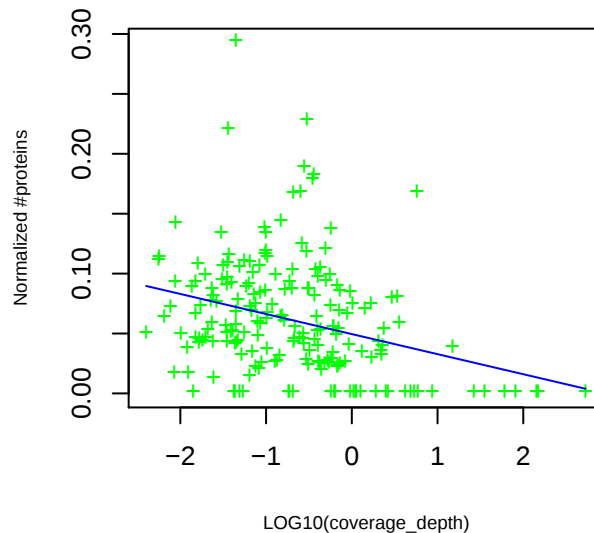
PF01545 Cation_efflux: cation efflux family protein

slope= -0.80 p_value= 1.7e-08 intercept= 1.76 p_value= 9.3e-24



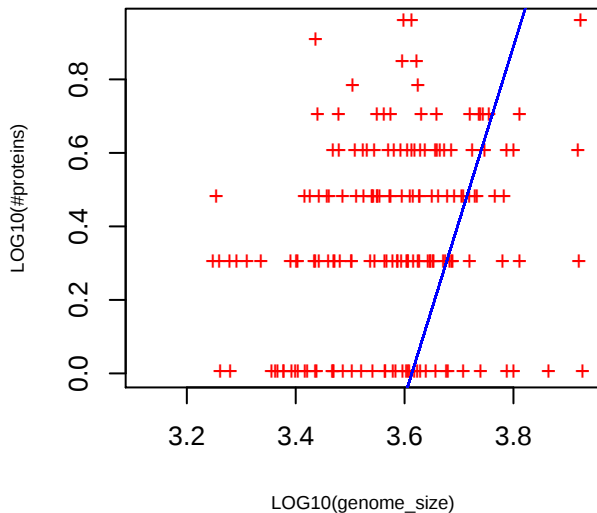
PF01545 Cation_efflux: cation efflux family protein

slope= -0.017 p_value= 1e-05 intercept= 0.05 p_value= 7.7e-25

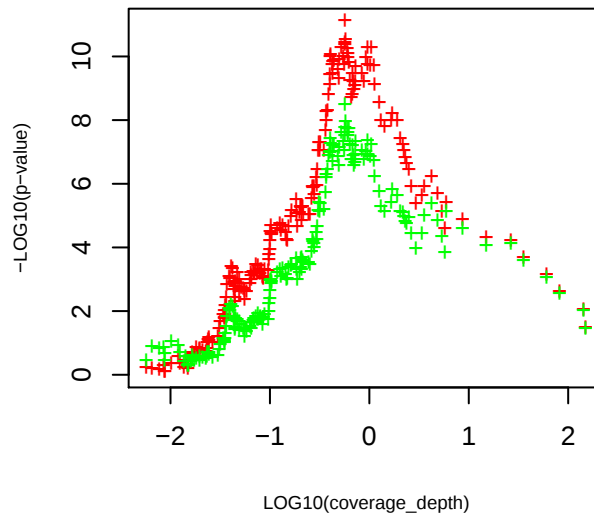


PF01545 Cation_efflux: cation efflux family protein

slope= 4.76 p_value= 7e-13 intercept= -17.22 p_value= 3.0e-13

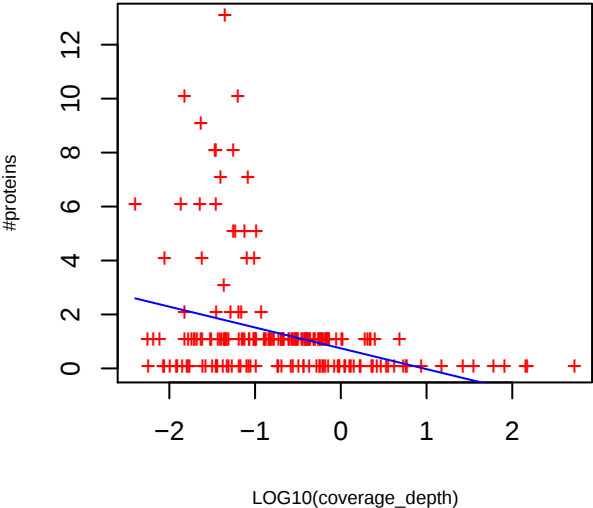


P-value curve ; red (unnorm), green (norm)



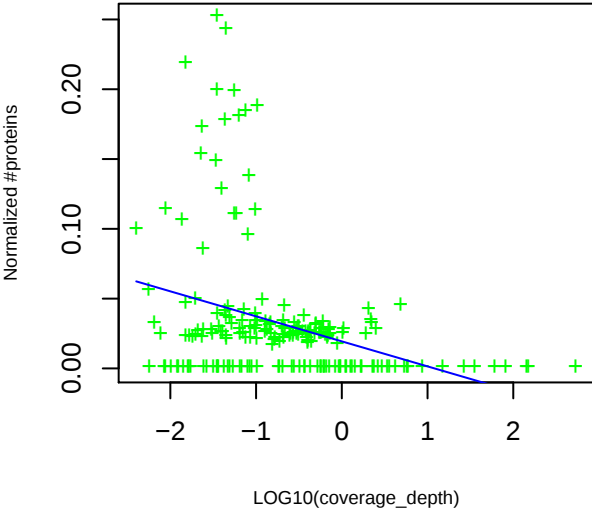
PF00359 PTS_EIIA_2: phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA

slope= -0.77 p_value= 2.1e-06 intercept= 0.74 p_value= 4.5e-05



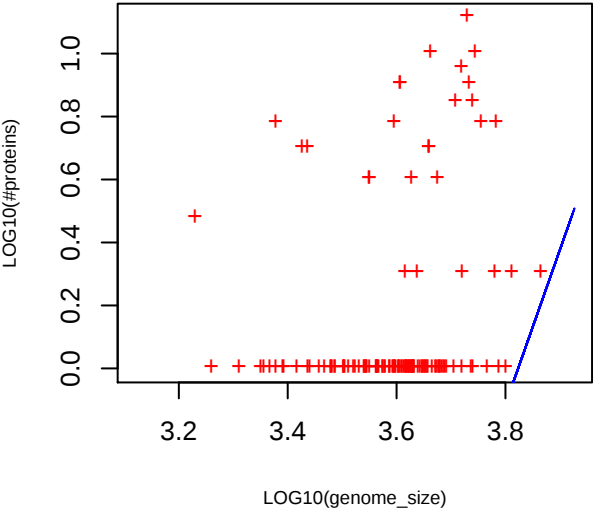
PF00359 PTS_EIIA_2: phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA

slope= -0.018 p_value= 2.2e-06 intercept= 0.019 p_value= 5.6e-06

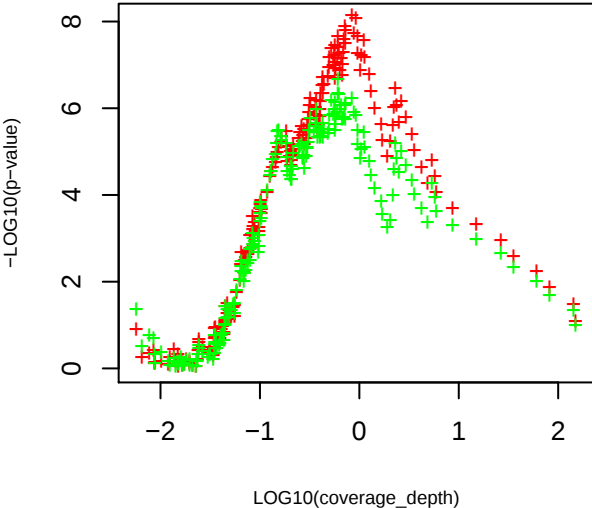


PF00359 PTS_EIIA_2: phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA

slope= 4.91 p_value= 8.1e-09 intercept= -18.77 p_value= 6.8e-10

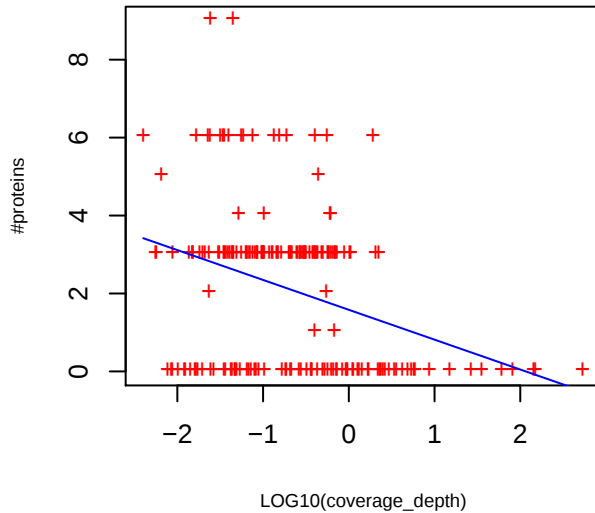


P-value curve : red (unnorm), green (norm)



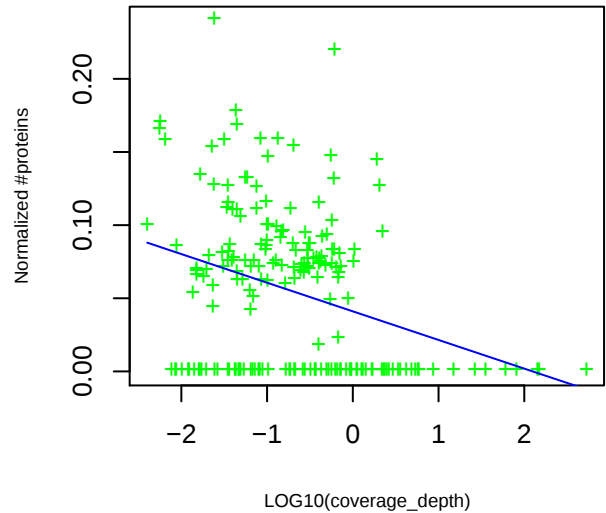
TIGR03506 FigEFG_subfam: flagellar hook-basal body proteins

slope= -0.77 p_value= 1.3e-06 intercept= 1.58 p_value= 9e-17



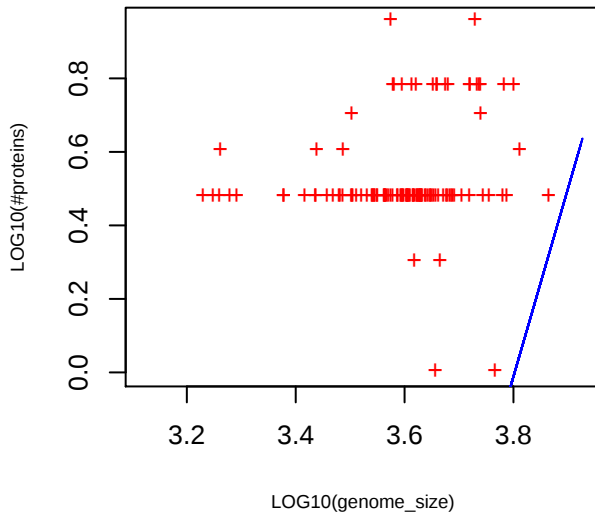
TIGR03506 FigEFG_subfam: flagellar hook-basal body proteins

slope= -0.020 p_value= 2.7e-06 intercept= 0.041 p_value= 2.4e-16

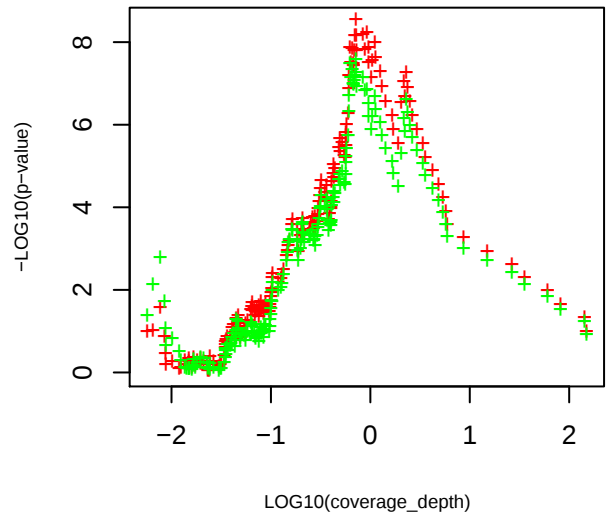


TIGR03506 FigEFG_subfam: flagellar hook-basal body proteins

slope= 5.11 p_value= 6.6e-08 intercept= -19.42 p_value= 8.6e-09

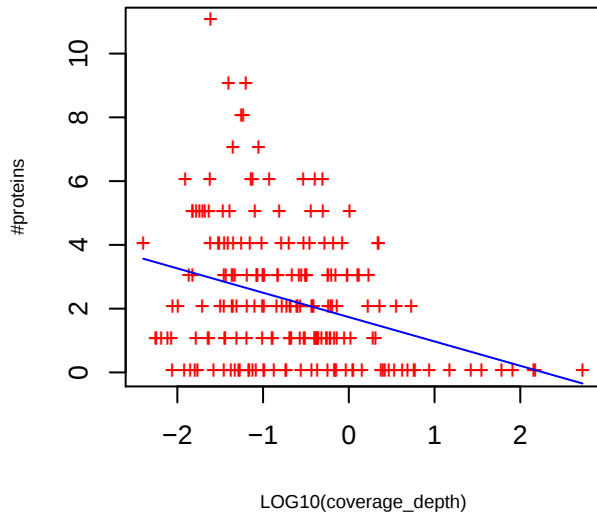


P-value curve ; red (unnorm), green (norm)



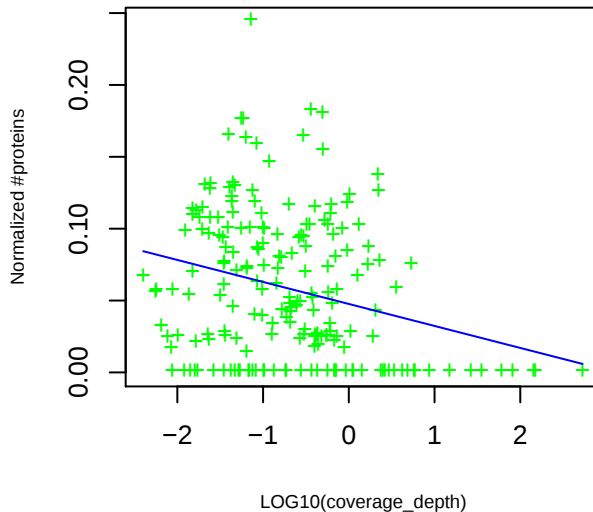
PF01734 Patatin: phospholipase, patatin family

slope= -0.76 p_value= 3.9e-06 intercept= 1.74 p_value= 5.5e-18



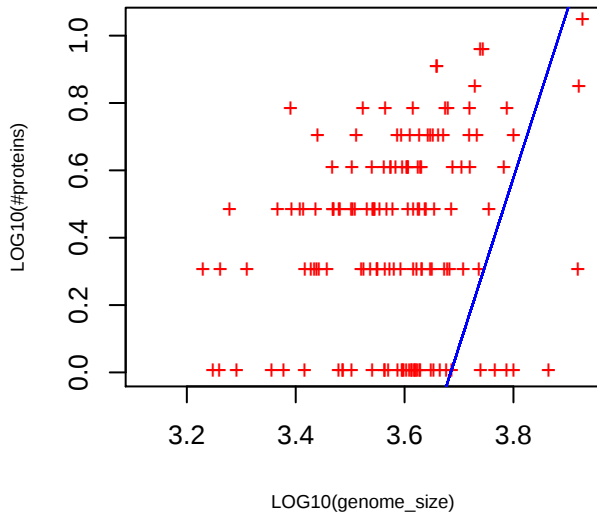
PF01734 Patatin: phospholipase, patatin family

slope= -0.015 p_value= 0.00013 intercept= 0.048 p_value= 1.4e-21

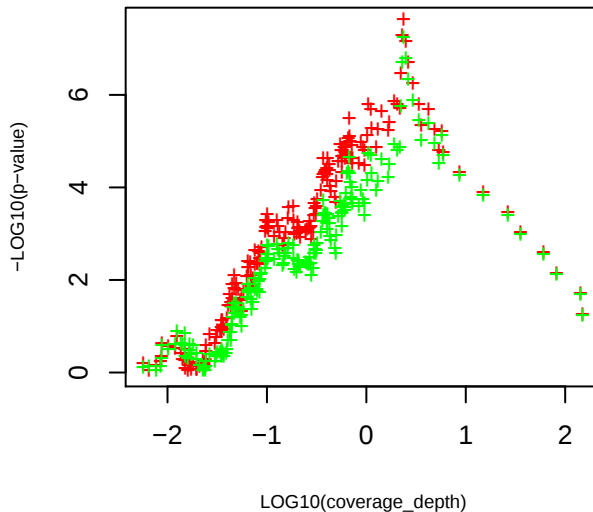


PF01734 Patatin: phospholipase, patatin family

slope= 5.02 p_value= 4.2e-10 intercept= -18.49 p_value= 1.0e-10

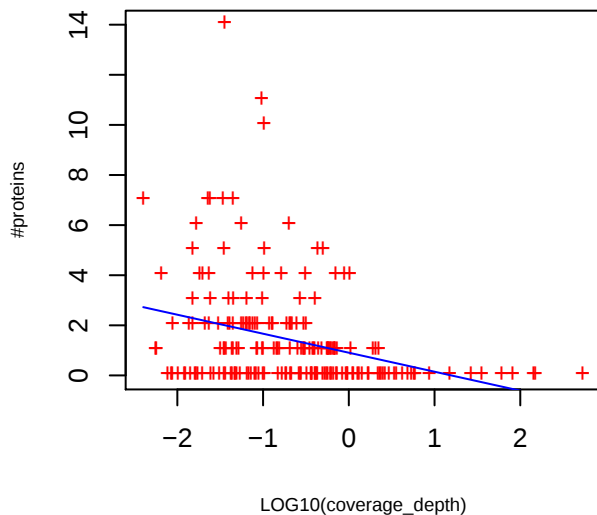


P-value curve ; red (unnorm), green (norm)



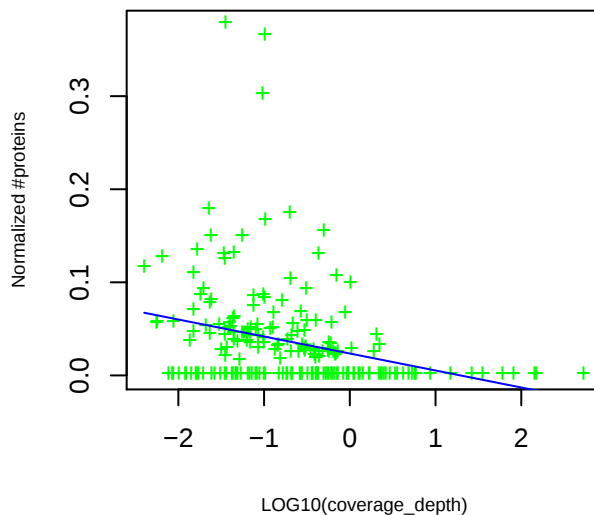
PF00700 Flagellin_C: Bacterial flagellin C-terminus

slope= -0.76 p_value= 5.6e-06 intercept= 0.91 p_value= 1.7e-06



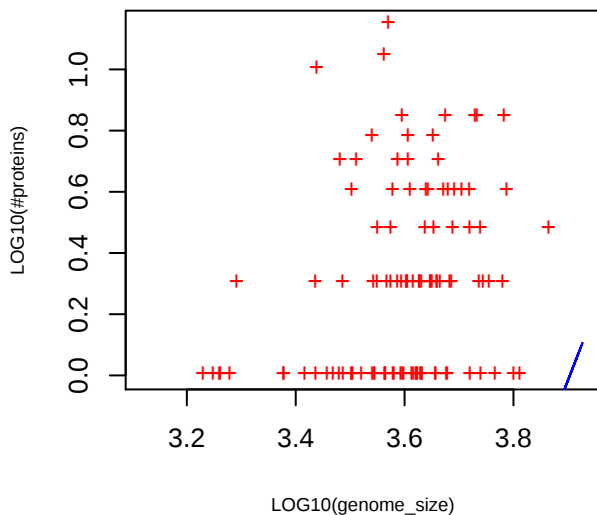
PF00700 Flagellin_C: Bacterial flagellin C-terminus

slope= -0.018 p_value= 3.4e-05 intercept= 0.024 p_value= 2.6e-06

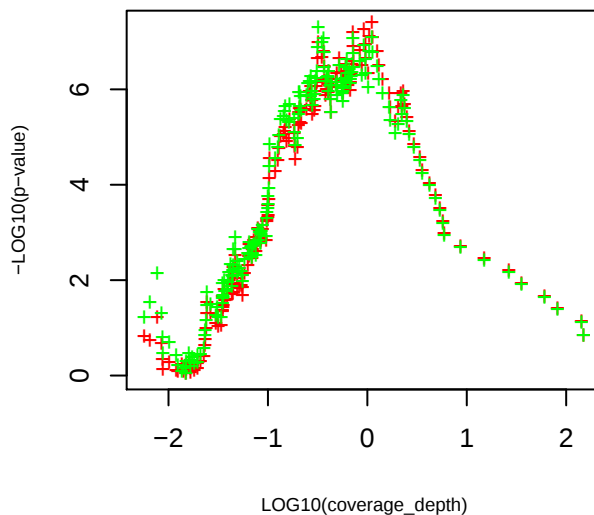


PF00700 Flagellin_C: Bacterial flagellin C-terminus

slope= 4.59 p_value= 5.9e-07 intercept= -17.91 p_value= 4.8e-08

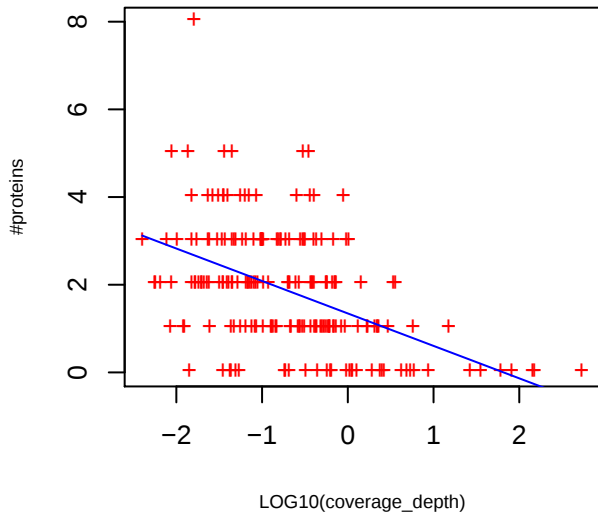


P-value curve ; red (unnorm), green (norm)



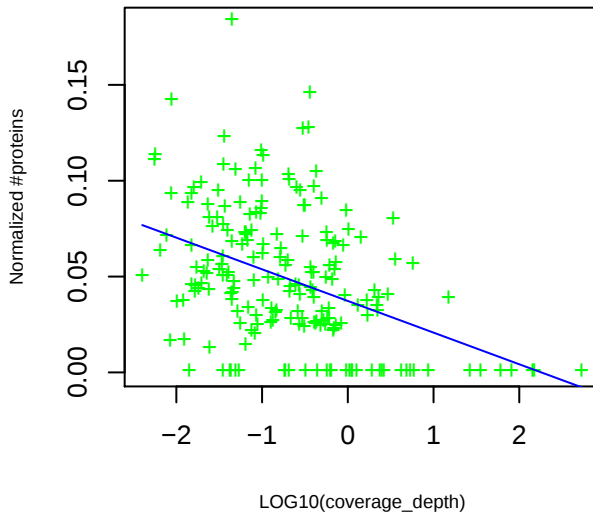
TIGR01297 CDF: cation diffusion facilitator family transporter

slope= -0.74 p_value= 1.2e-12 intercept= 1.35 p_value= 6.7e-26



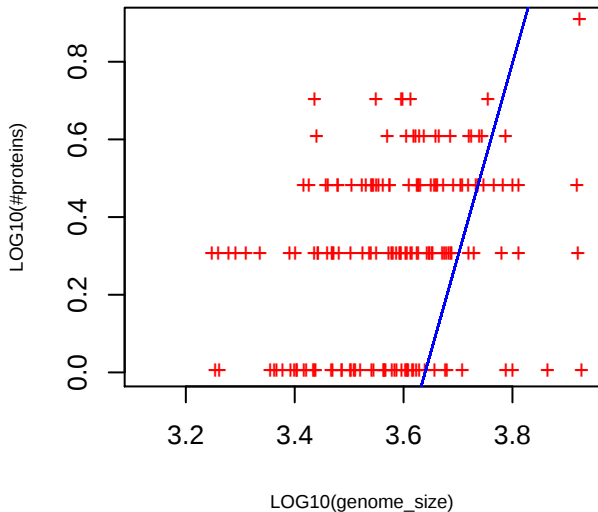
TIGR01297 CDF: cation diffusion facilitator family transporter

slope= -0.017 p_value= 1.4e-09 intercept= 0.037 p_value= 2.4e-27

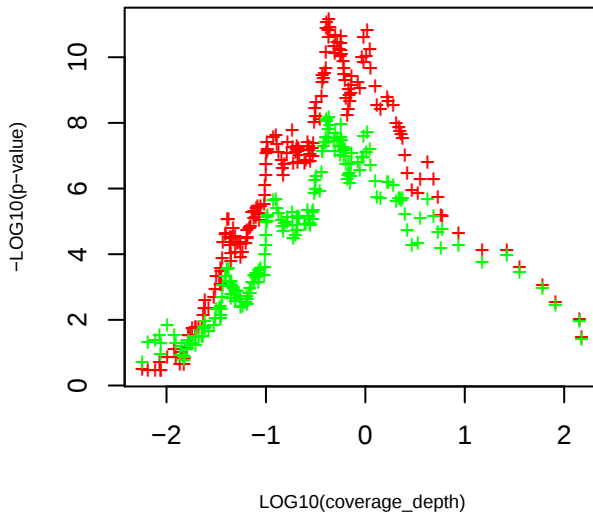


TIGR01297 CDF: cation diffusion facilitator family transporter

slope= 4.96 p_value= 3.6e-13 intercept= -18.06 p_value= 1.1e-13

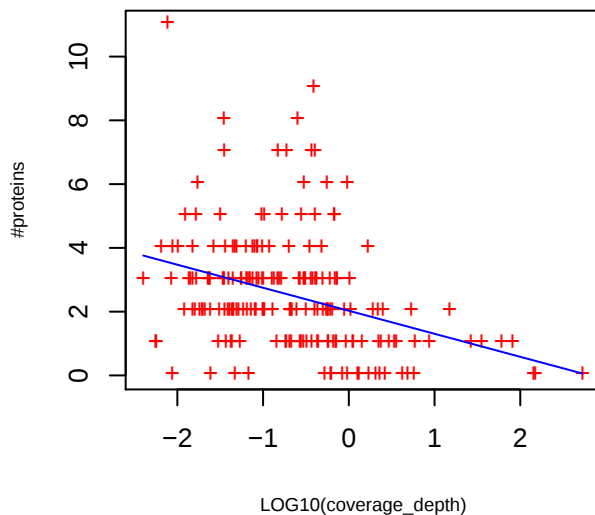


P-value curve : red (unnorm), green (norm)



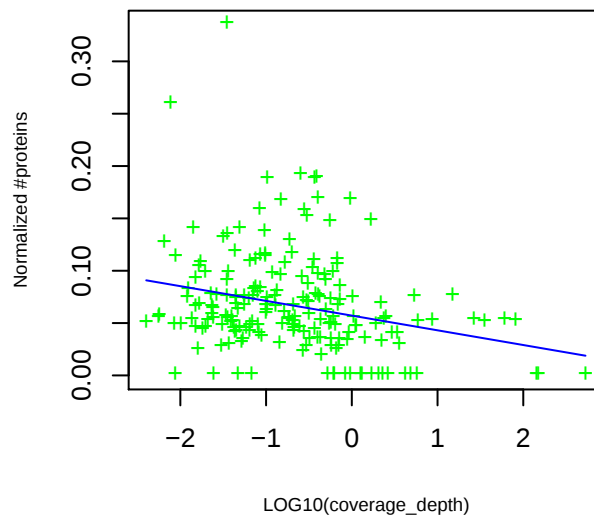
TIGR01525 ATPase-IB_hvy: heavy metal translocating P-type ATPase

slope= -0.72 p_value= 5.4e-07 intercept= 2.03 p_value= 6.7e-28



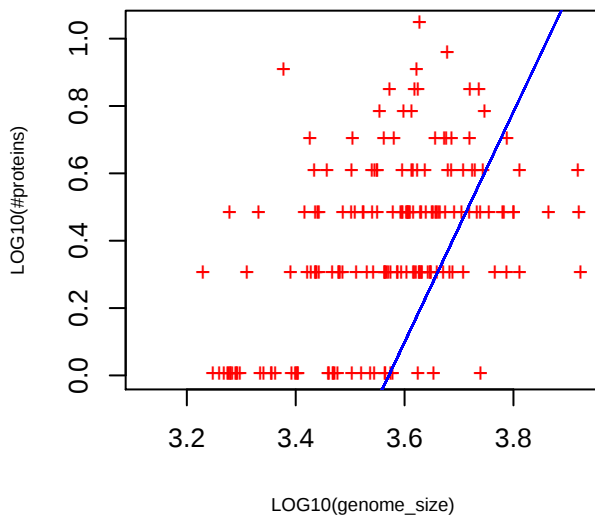
TIGR01525 ATPase-IB_hvy: heavy metal translocating P-type ATPase

slope= -0.014 p_value= 0.00020 intercept= 0.057 p_value= 3.9e-30

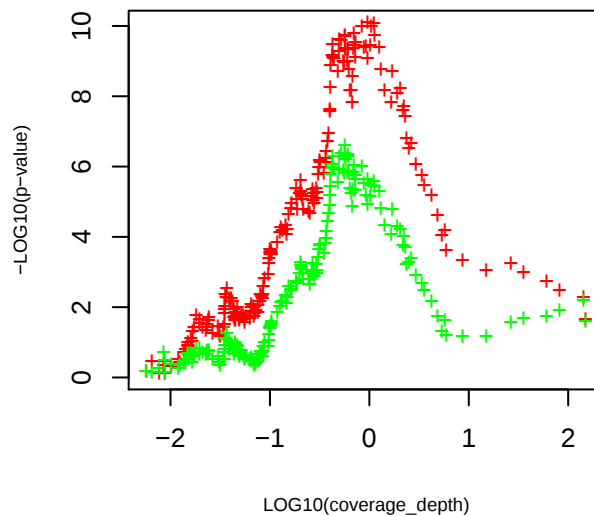


TIGR01525 ATPase-IB_hvy: heavy metal translocating P-type ATPase

slope= 3.42 p_value= 3.5e-09 intercept= -12.21 p_value= 2.8e-09

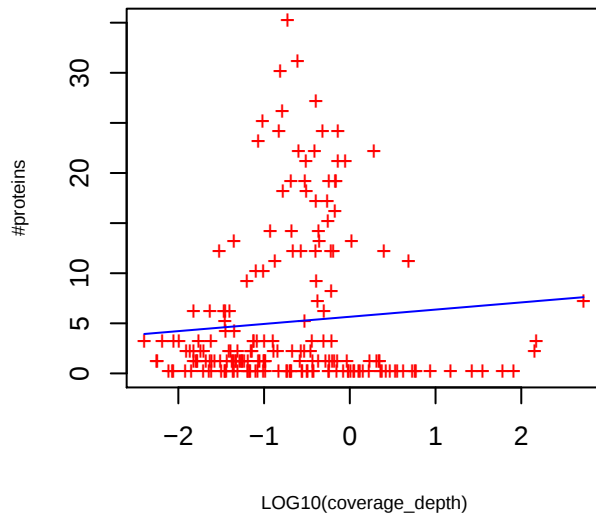


P-value curve ; red (unnorm), green (norm)



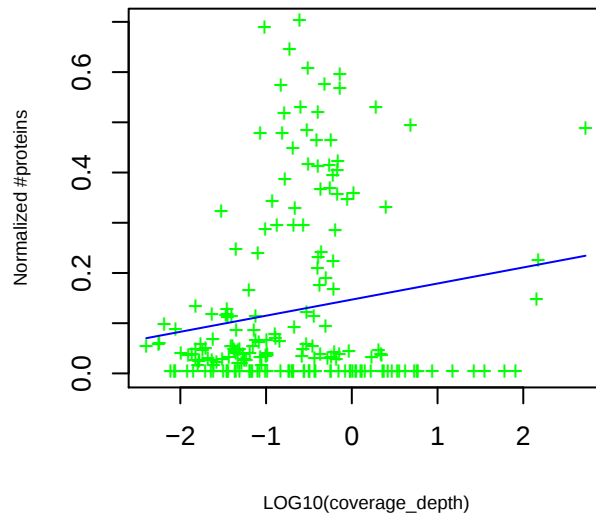
PF03480 SBP_bac_7: Bacterial extracellular solute-binding protein, family 7

slope= 0.72 p_value= 0.25 intercept= 5.65 p_value= 6.8e-14



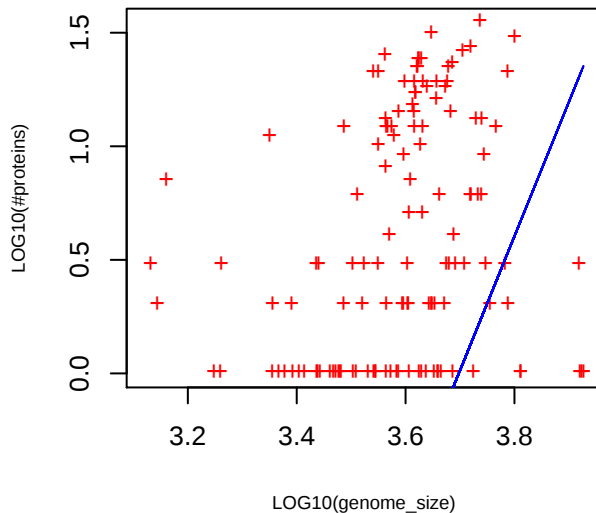
PF03480 SBP_bac_7: Bacterial extracellular solute-binding protein, family 7

slope= 0.032 p_value= 0.024 intercept= 0.15 p_value= 4.6e-17

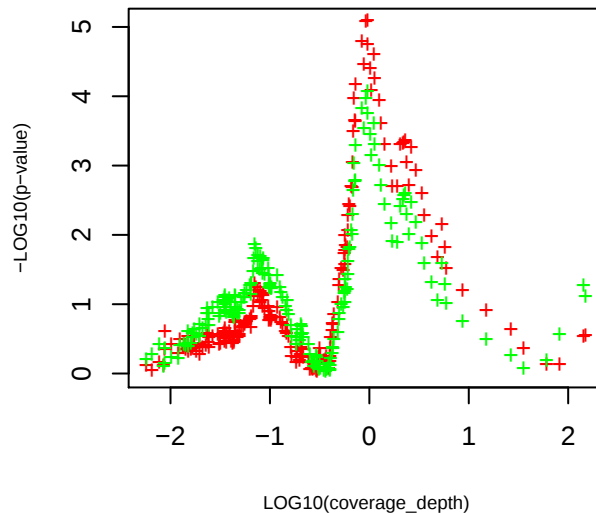


PF03480 SBP_bac_7: Bacterial extracellular solute-binding protein, family 7

slope= 5.91 p_value= 1.2e-10 intercept= -21.85 p_value= 2.3e-11

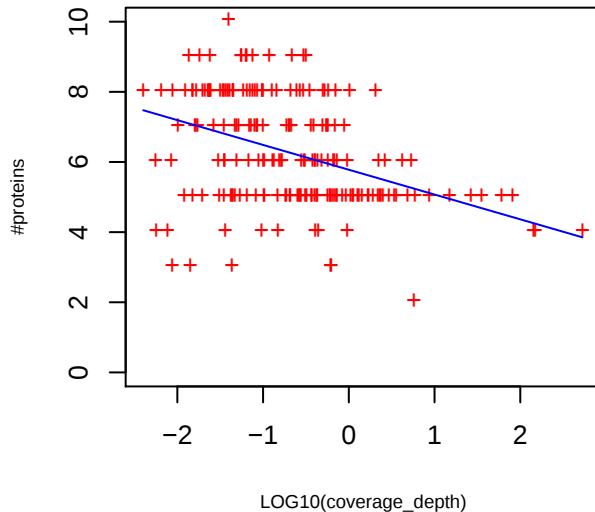


P-value curve : red (unnorm), green (norm)



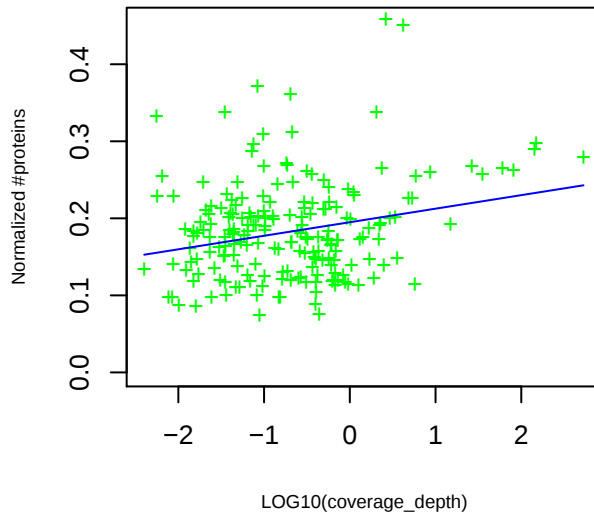
PF00575 S1: S1 RNA binding domain

slope= -0.71 p_value= 4.7e-09 intercept= 5.78 p_value= 6.8e-104



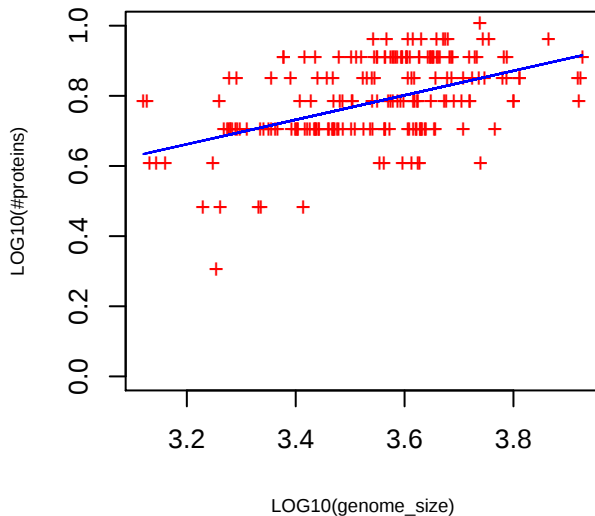
PF00575 S1: S1 RNA binding domain

slope= 0.018 p_value= 0.00048 intercept= 0.19 p_value= 9.2e-86

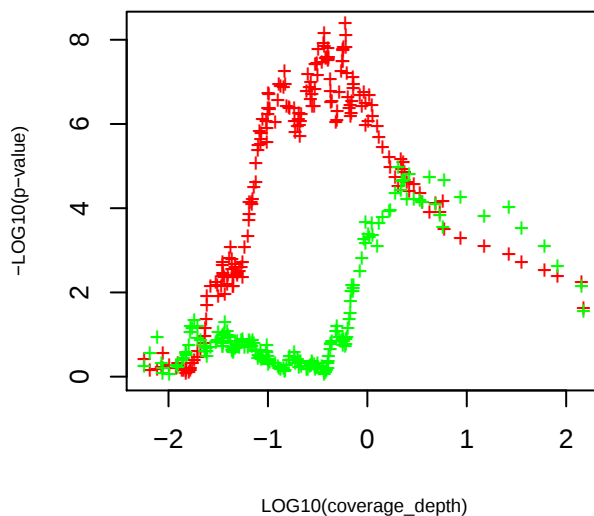


PF00575 S1: S1 RNA binding domain

slope= 0.35 p_value= 3.2e-13 intercept= -0.46 p_value= 0.0045

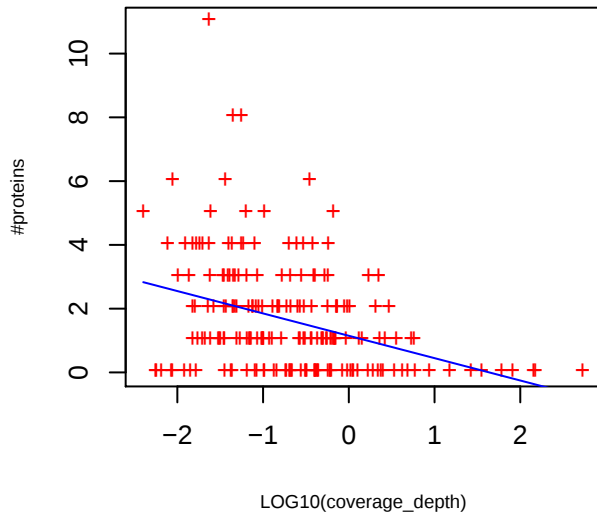


P-value curve ; red (unnorm), green (norm)



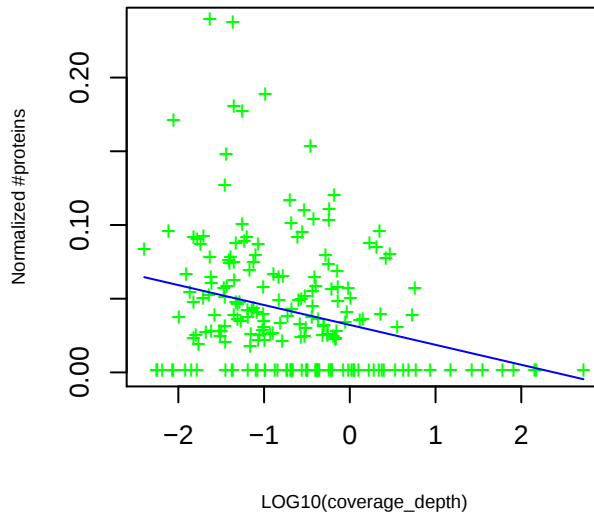
PF00324 AA_permease: Amino acid permease

slope= -0.70 p_value= 2.8e-07 intercept= 1.15 p_value= 5.8e-13



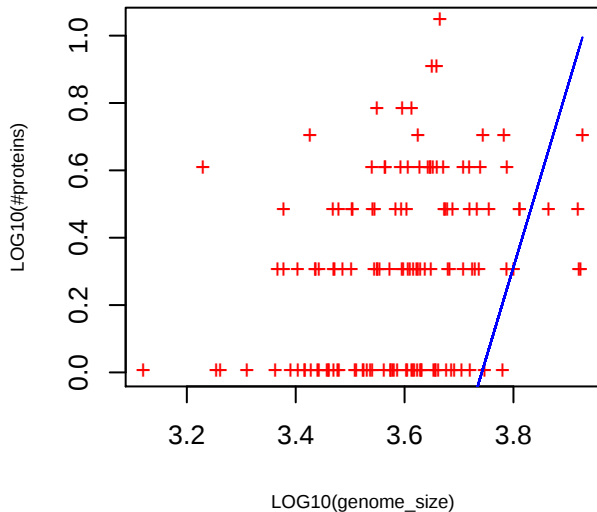
PF00324 AA_permease: Amino acid permease

slope= -0.014 p_value= 0.00011 intercept= 0.032 p_value= 1.5e-14

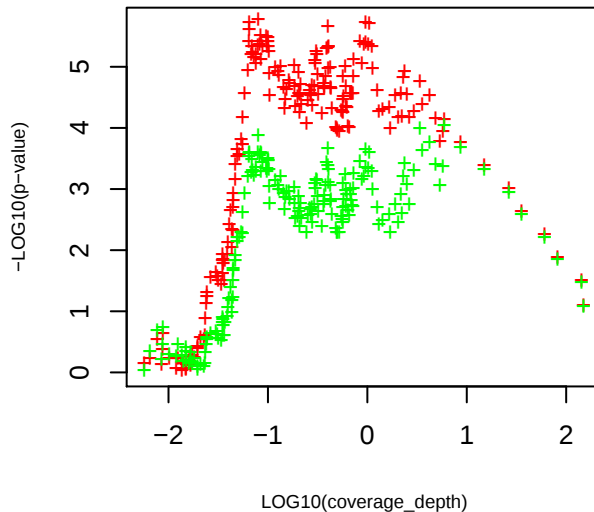


PF00324 AA_permease: Amino acid permease

slope= 5.38 p_value= 1.4e-10 intercept= -20.14 p_value= 1.8e-11

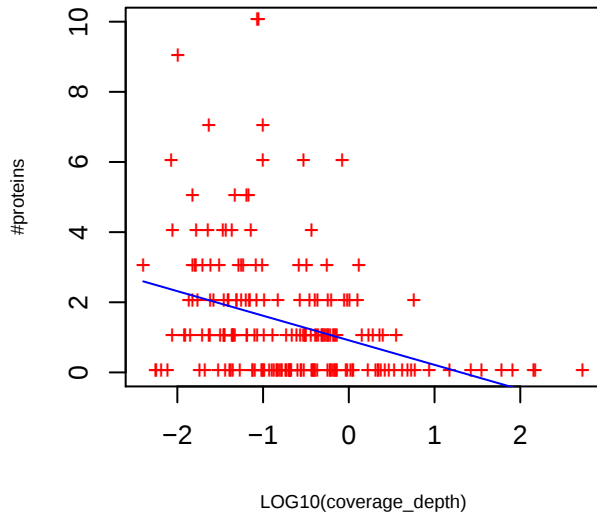


P-value curve ; red (unnorm), green (norm)



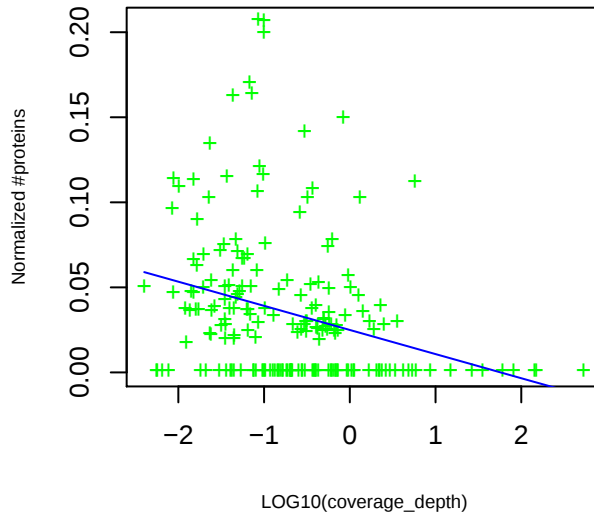
PF02384 N6_Mtase: N-6 DNA Methylase

slope= -0.70 p_value= 1.2e-06 intercept= 0.92 p_value= 2.5e-08



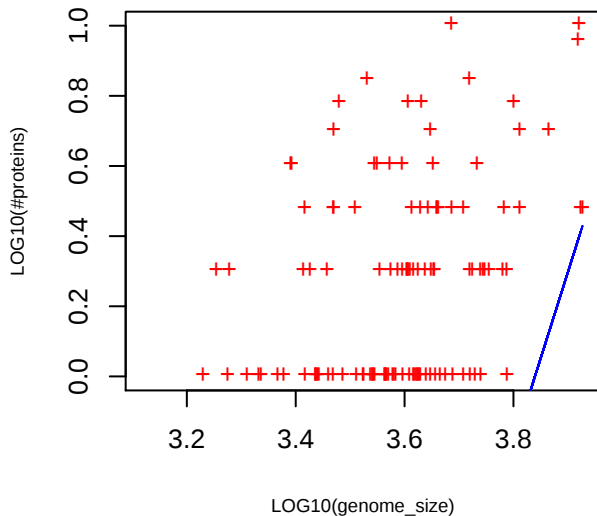
PF02384 N6_Mtase: N-6 DNA Methylase

slope= -0.014 p_value= 3.1e-05 intercept= 0.025 p_value= 2.9e-10

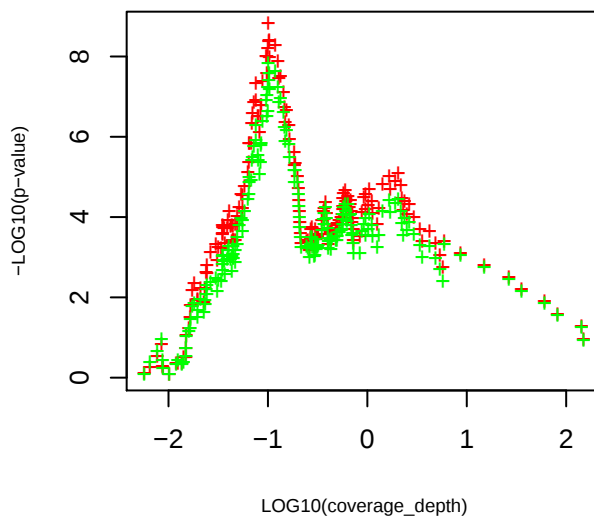


PF02384 N6_Mtase: N-6 DNA Methylase

slope= 4.91 p_value= 3.7e-08 intercept= -18.85 p_value= 3.3e-09

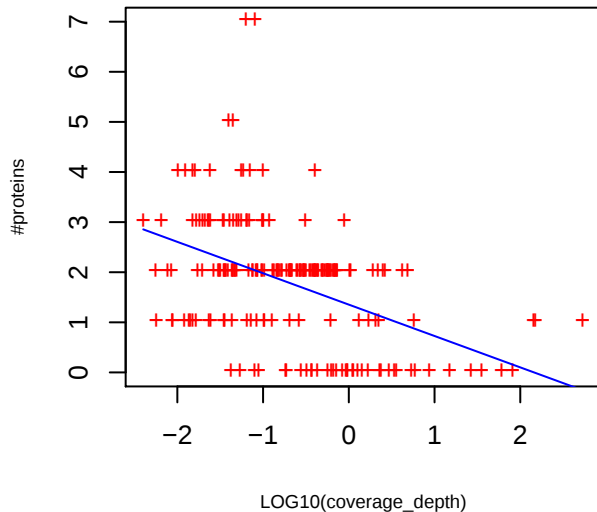


P-value curve ; red (unnorm), green (norm)



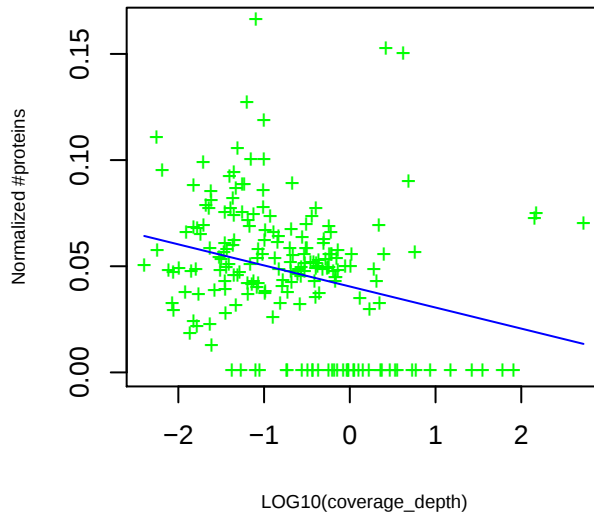
PF02896 PEP-utilizers_C: PEP-utilizing enzyme, TIM barrel domain

slope= -0.63 p_value= 3.1e-11 intercept= 1.35 p_value= 1.1e-29



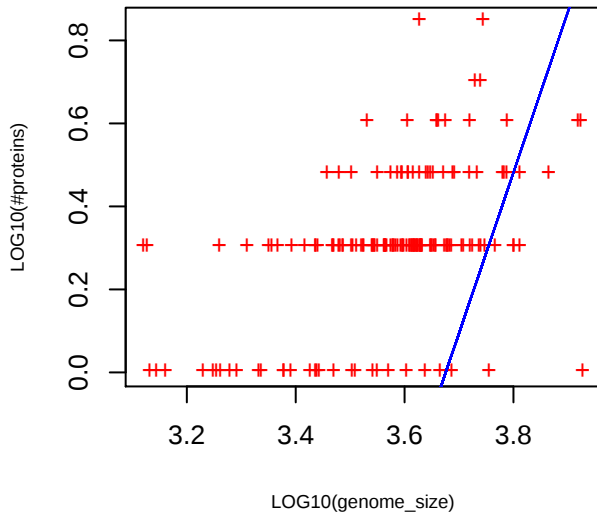
PF02896 PEP-utilizers_C: PEP-utilizing enzyme, TIM barrel domain

slope= -0.01 p_value= 5.8e-05 intercept= 0.040 p_value= 6.8e-34

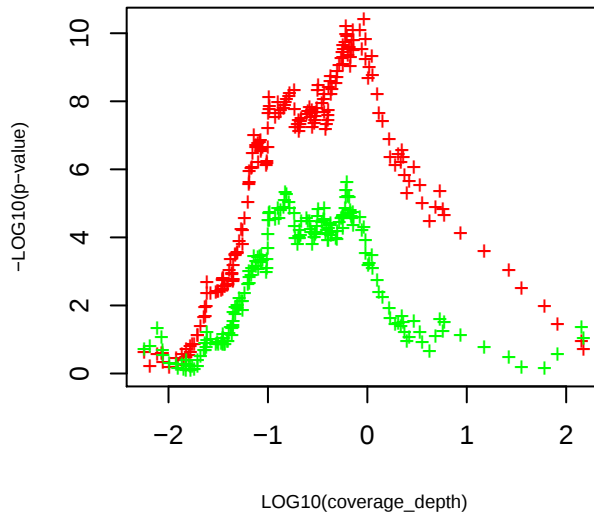


PF02896 PEP-utilizers_C: PEP-utilizing enzyme, TIM barrel domain

slope= 3.87 p_value= 6.9e-08 intercept= -14.23 p_value= 2.5e-08

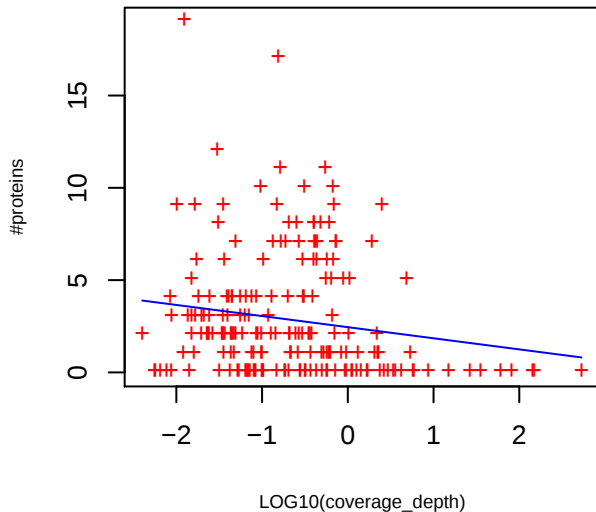


P-value curve ; red (unnorm), green (norm)



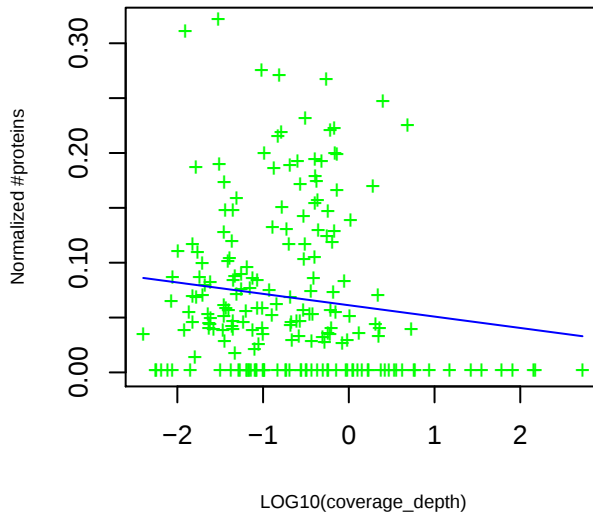
PF01471 PG_binding_1: Putative peptidoglycan binding domain

slope= -0.60 p_value= 0.023 intercept= 2.45 p_value= 2.2e-14



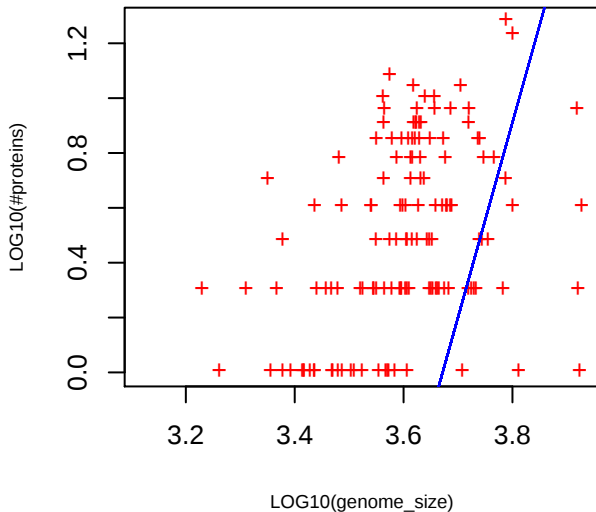
PF01471 PG_binding_1: Putative peptidoglycan binding domain

slope= -0.010 p_value= 0.078 intercept= 0.061 p_value= 3.6e-17

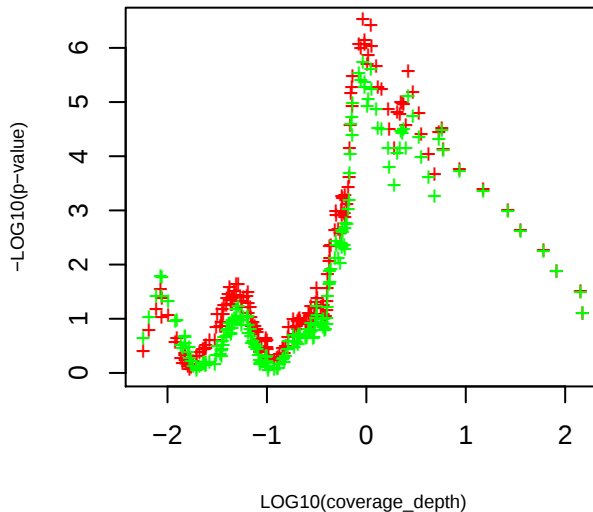


PF01471 PG_binding_1: Putative peptidoglycan binding domain

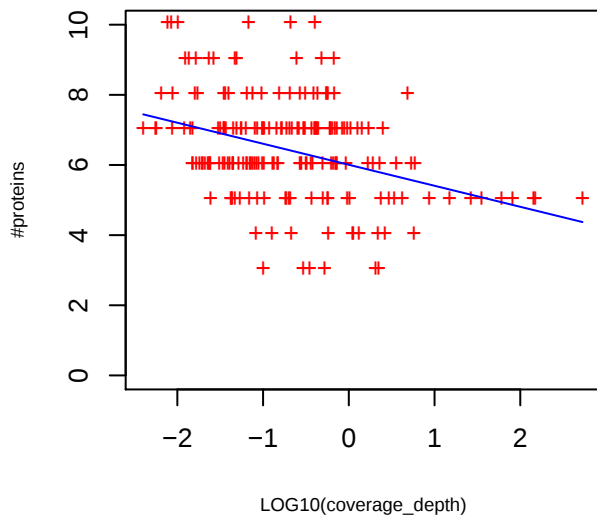
slope= 7.11 p_value= 4.6e-17 intercept= -26.09 p_value= 5.8e-18



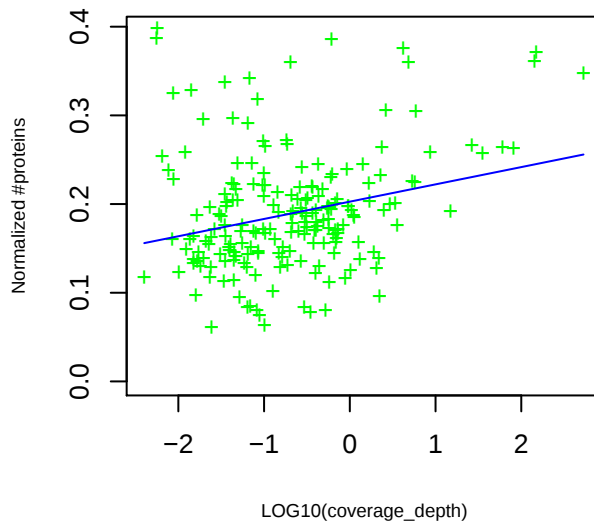
P-value curve : red (unnorm), green (norm)



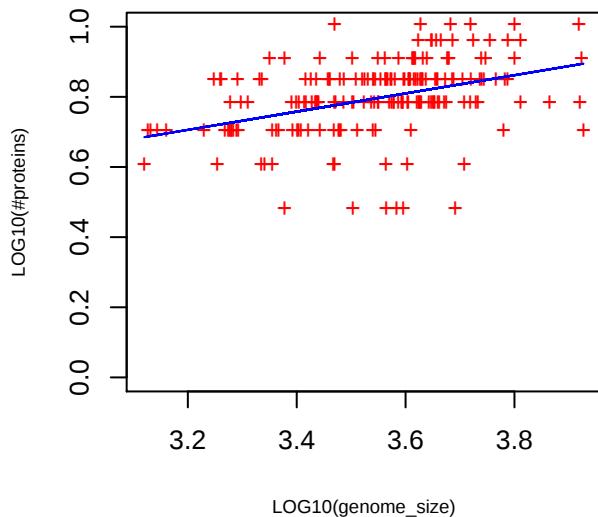
PF00156 Pribosyltran: Phosphoribosyl transferase domain
 slope= -0.60 p_value= 1.1e-07 intercept= 6.01 p_value= 2.1e-111



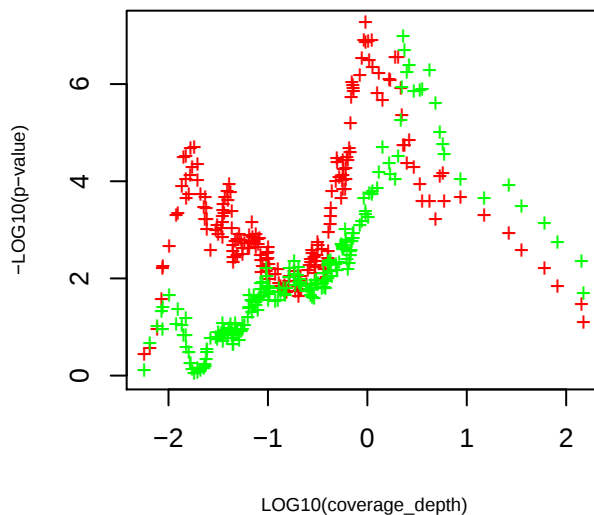
PF00156 Pribosyltran: Phosphoribosyl transferase domain
 slope= 0.019 p_value= 0.00022 intercept= 0.20 p_value= 3.3e-85



PF00156 Pribosyltran: Phosphoribosyl transferase domain
 slope= 0.26 p_value= 5.2e-09 intercept= -0.13 p_value= 0.41

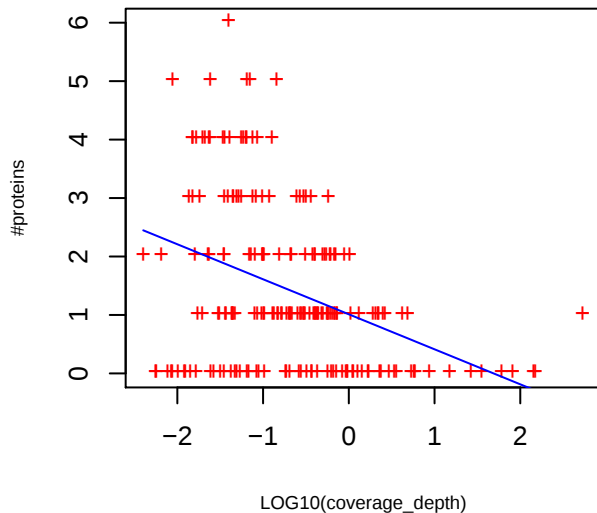


P-value curve ; red (unnorm), green (norm)



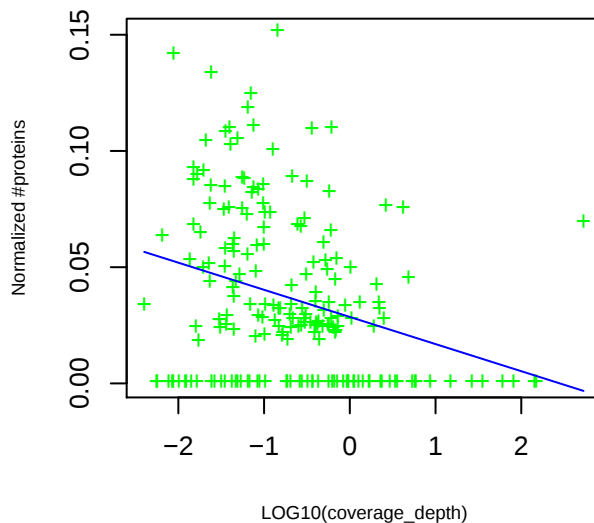
PF02810 SEC-C: SEC-C motif

slope= -0.60 p_value= 4.4e-08 intercept= 1.01 p_value= 4.3e-15



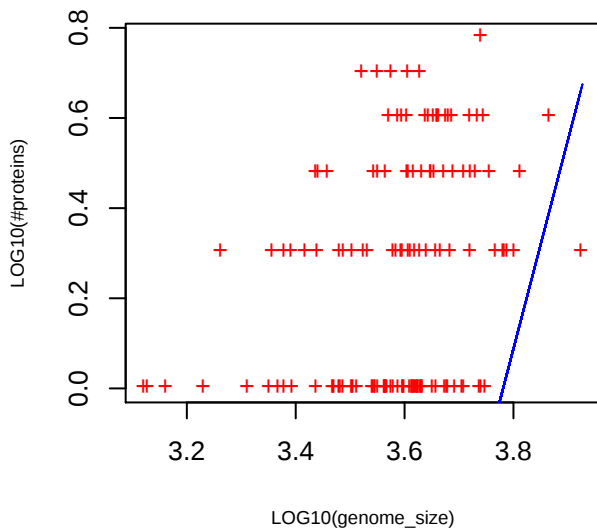
PF02810 SEC-C: SEC-C motif

slope= -0.012 p_value= 2.7e-05 intercept= 0.029 p_value= 2.6e-17

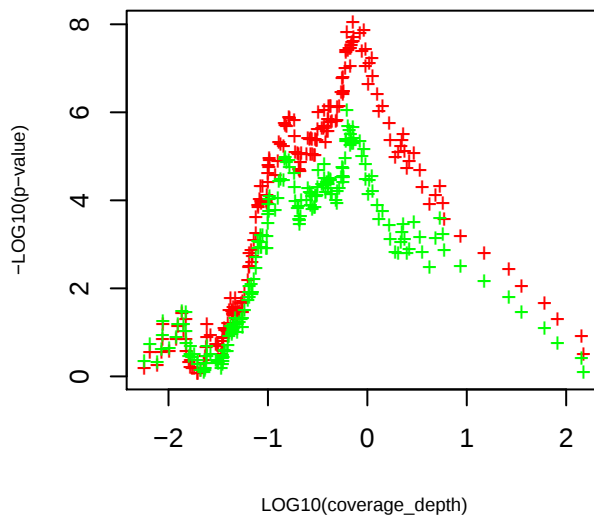


PF02810 SEC-C: SEC-C motif

slope= 4.63 p_value= 3.7e-08 intercept= -17.50 p_value= 5.4e-09

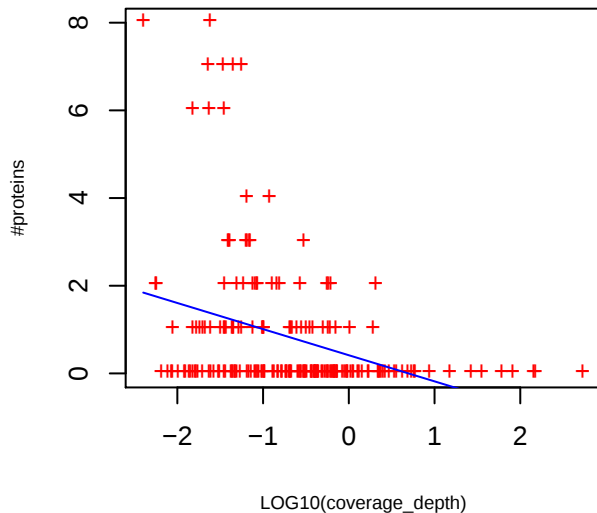


P-value curve ; red (unnorm), green (norm)



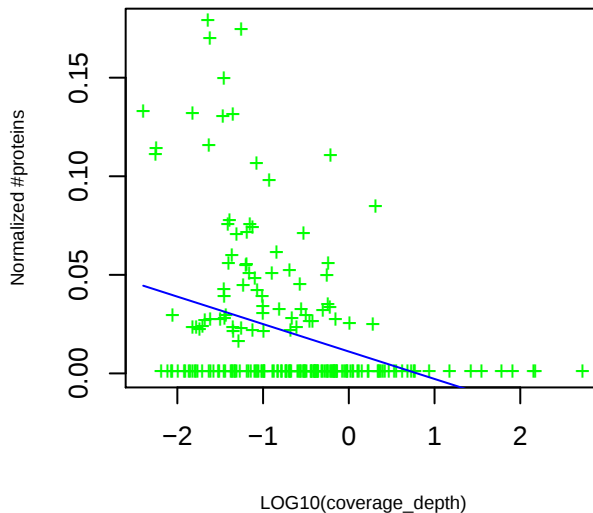
PF07196 Flagellin_IN: Flagellin hook IN motif

slope= -0.60 p_value= 1.8e-06 intercept= 0.41 p_value= 0.0028



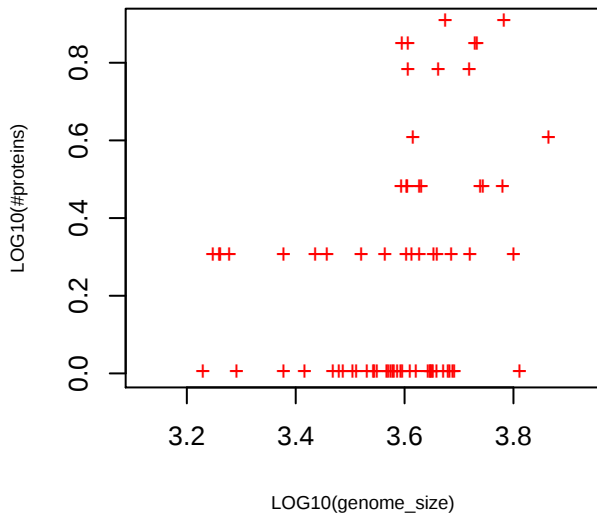
PF07196 Flagellin_IN: Flagellin hook IN motif

slope= -0.014 p_value= 1.7e-06 intercept= 0.011 p_value= 6e-04

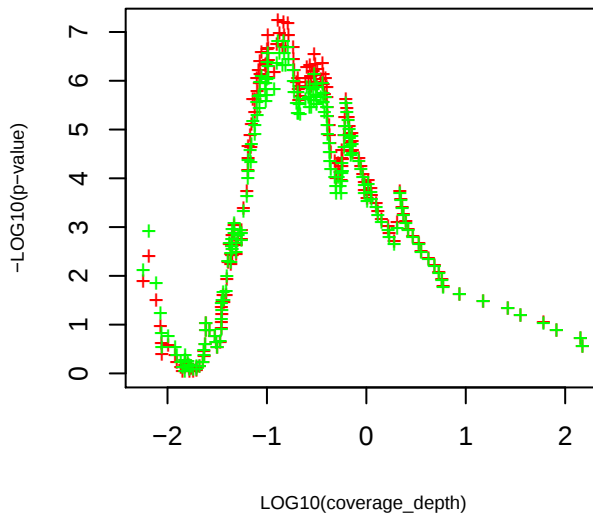


PF07196 Flagellin_IN: Flagellin hook IN motif

slope= 2.52 p_value= 0.0048 intercept= -11.40 p_value= 0.00036

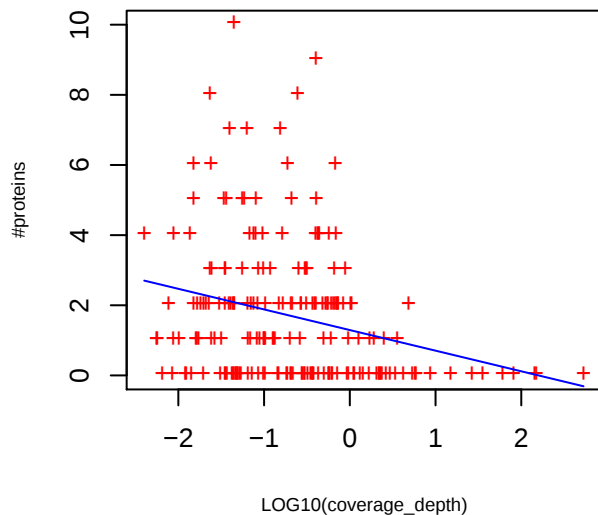


P-value curve ; red (unnorm), green (norm)



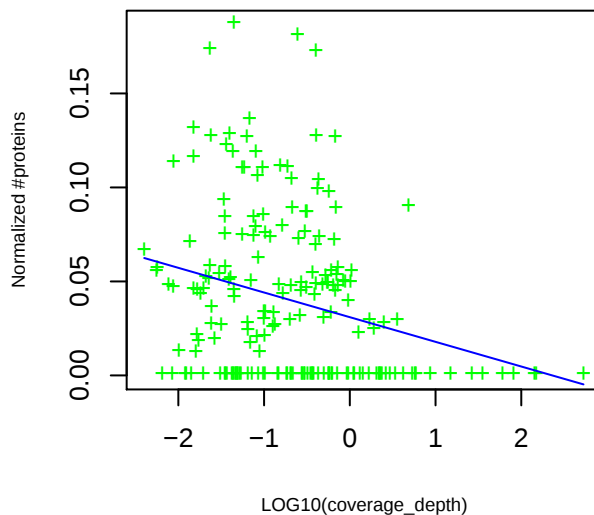
PF08220 HTH_DeoR: DeoR-like helix-turn-helix domain

slope= -0.59 p_value= 0.00019 intercept= 1.29 p_value= 3.6e-12



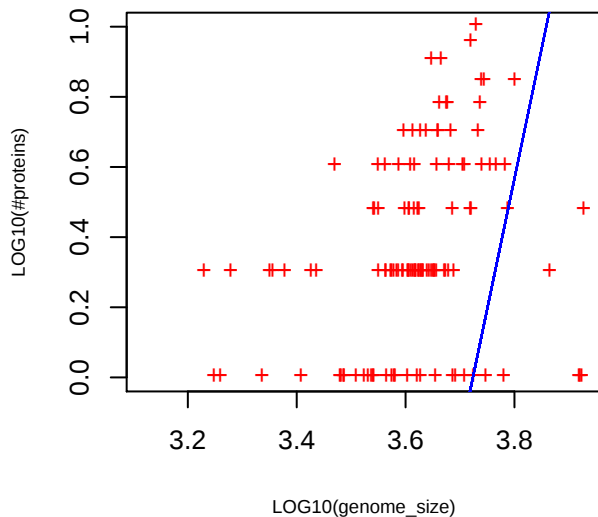
PF08220 HTH_DeoR: DeoR-like helix-turn-helix domain

slope= -0.013 p_value= 0.00013 intercept= 0.031 p_value= 4.5e-14

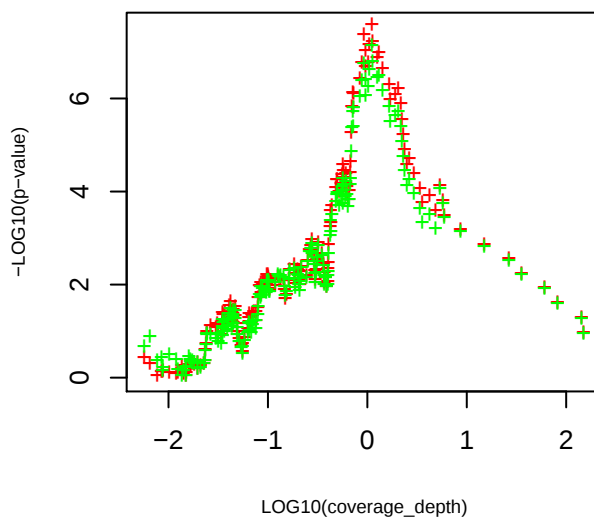


PF08220 HTH_DeoR: DeoR-like helix-turn-helix domain

slope= 7.42 p_value= 4e-18 intercept= -27.65 p_value= 1.7e-19

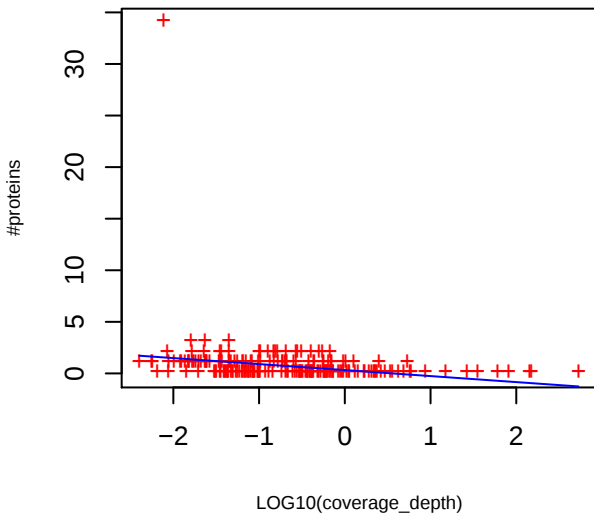


P-value curve ; red (unnorm), green (norm)



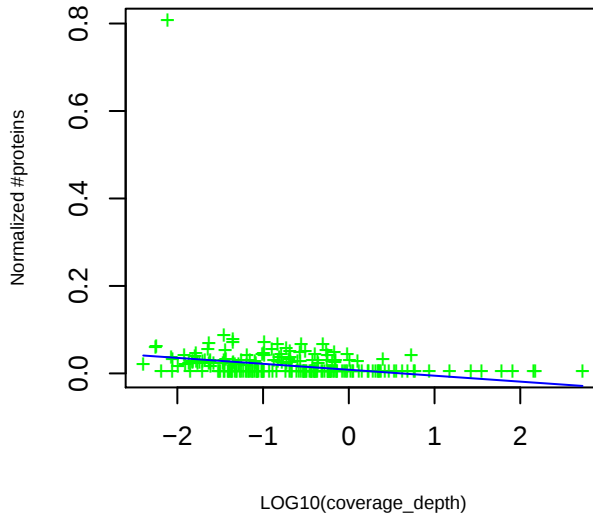
PF04967 HTH_10: HTH DNA binding domain

slope= -0.58 p_value= 0.0033 intercept= 0.32 p_value= 0.14



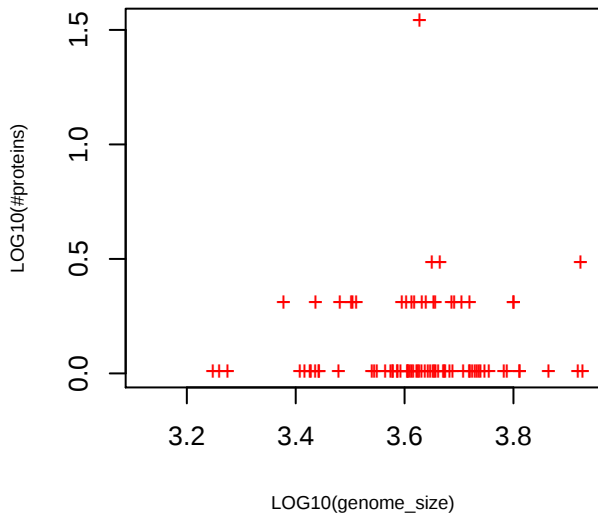
PF04967 HTH_10: HTH DNA binding domain

slope= -0.014 p_value= 0.0039 intercept= 0.0084 p_value= 0.11

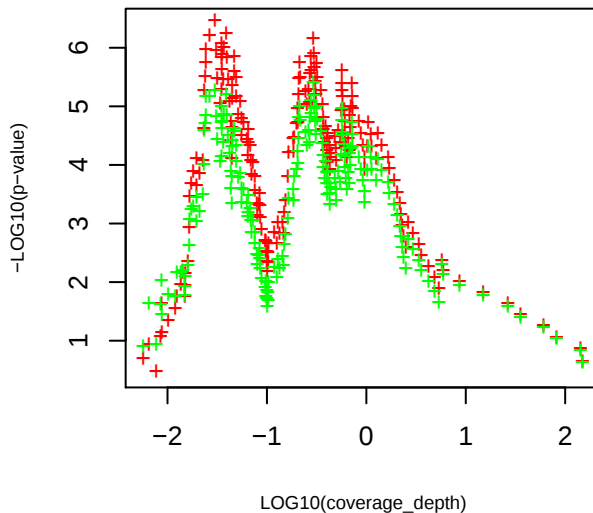


PF04967 HTH_10: HTH DNA binding domain

slope= 5.19 p_value= 1.3e-09 intercept= -20.67 p_value= 1.8e-11

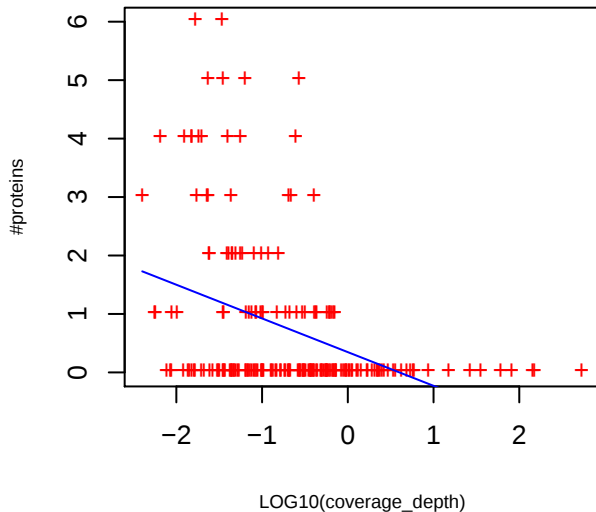


P-value curve ; red (unnorm), green (norm)



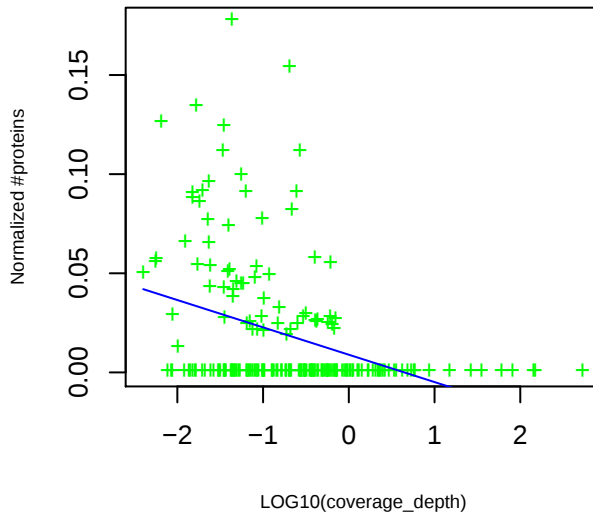
PF02743 Cache_1: Cache domain

slope= -0.58 p_value= 3.4e-08 intercept= 0.35 p_value= 0.0025



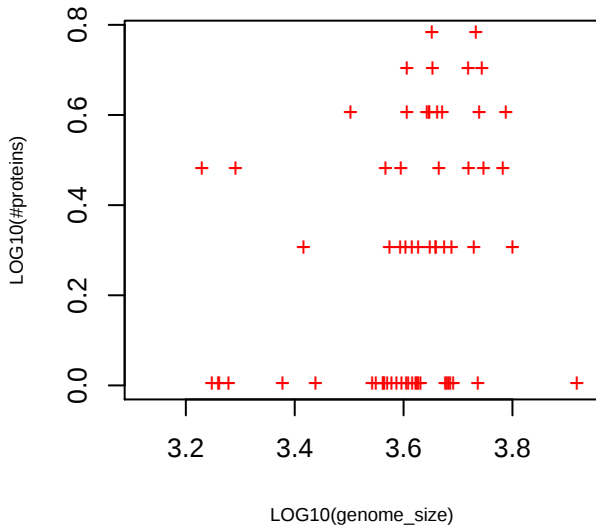
PF02743 Cache_1: Cache domain

slope= -0.014 p_value= 1.1e-07 intercept= 0.009 p_value= 0.0018

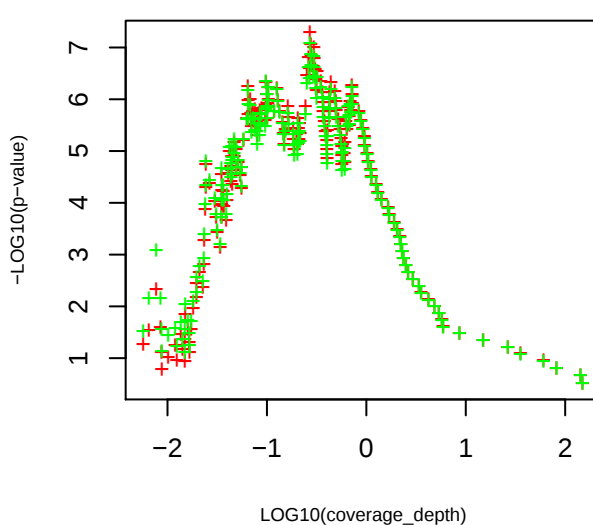


PF02743 Cache_1: Cache domain

slope= 3.27 p_value= 0.00018 intercept= -14.19 p_value= 5.5e-06

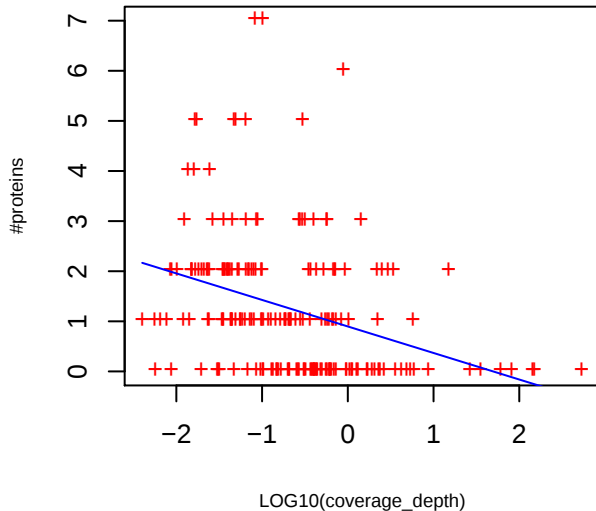


P-value curve ; red (unnorm), green (norm)



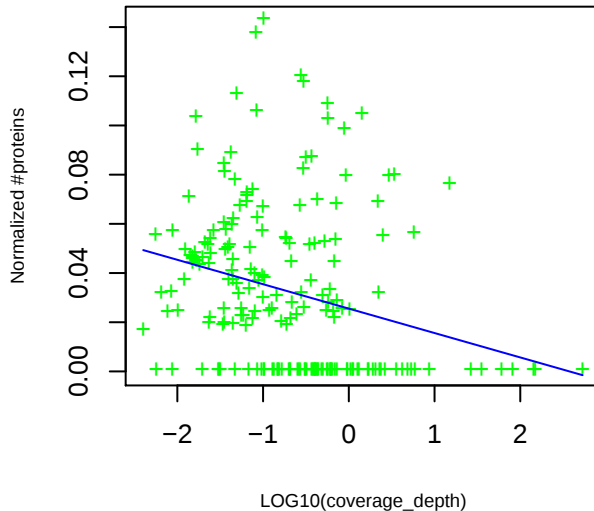
PF00176 SNF2_N: SNF2 family N-terminal domain

slope= -0.53 p_value= 1.2e-06 intercept= 0.90 p_value= 1.8e-12



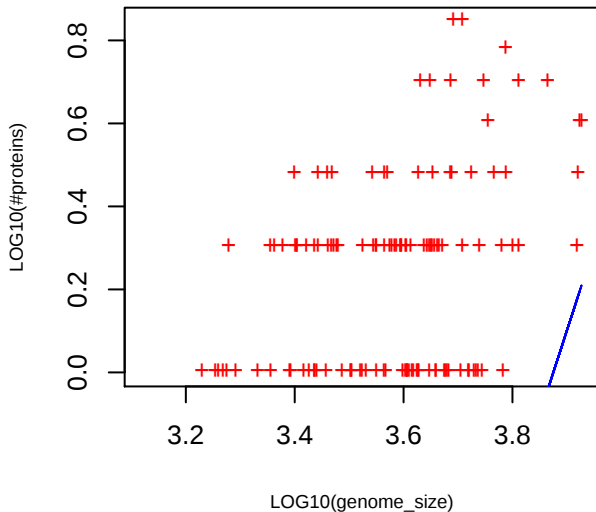
PF00176 SNF2_N: SNF2 family N-terminal domain

slope= -0.01 p_value= 0.00014 intercept= 0.026 p_value= 4.8e-16

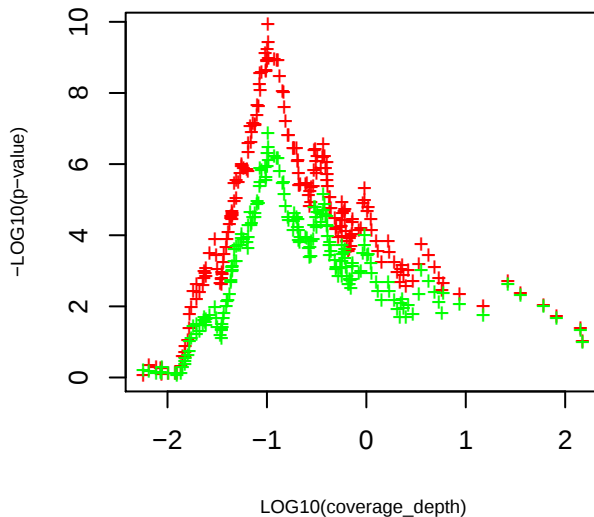


PF00176 SNF2_N: SNF2 family N-terminal domain

slope= 4.05 p_value= 4.5e-06 intercept= -15.68 p_value= 6.2e-07

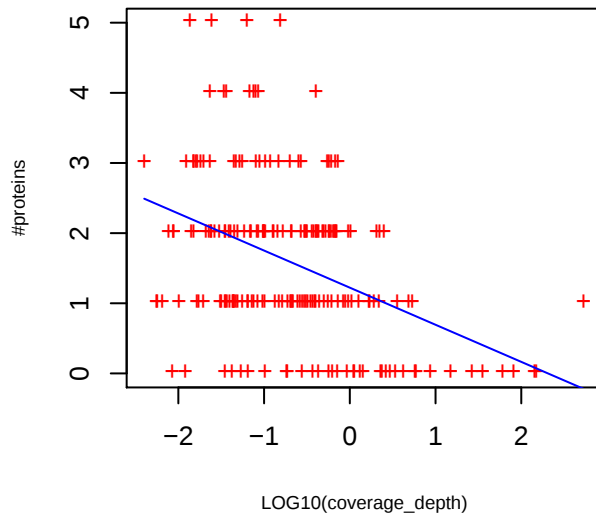


P-value curve ; red (unnorm), green (norm)



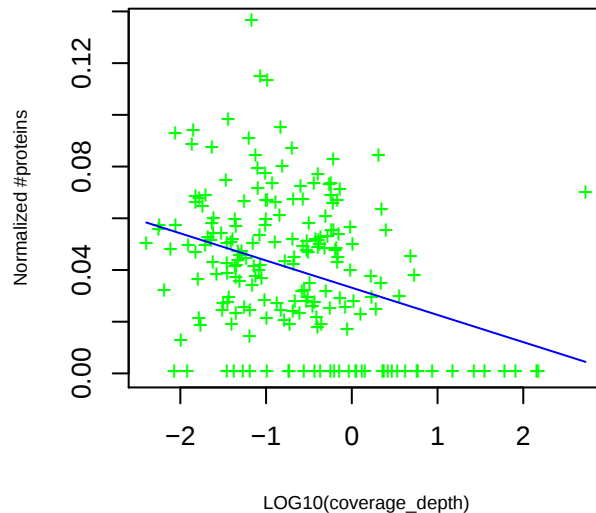
PF03009 GPD: glycerophosphodiester phosphodiesterase family

slope= -0.53 p_value= 3.6e-09 intercept= 1.22 p_value= 3.5e-27



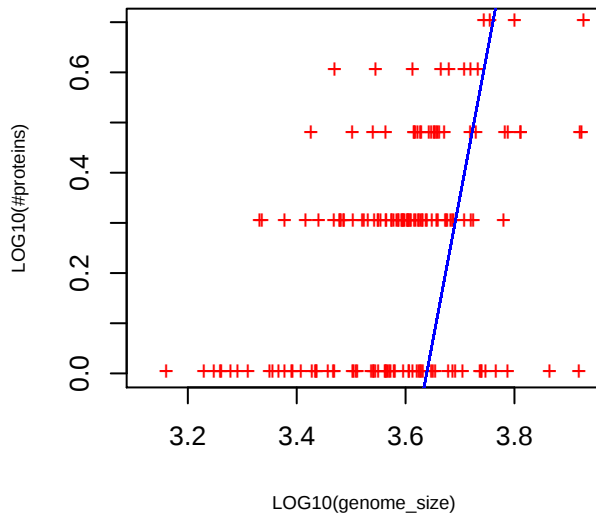
PF03009 GPD: glycerophosphodiester phosphodiesterase family

slope= -0.011 p_value= 9e-07 intercept= 0.033 p_value= 9.3e-32

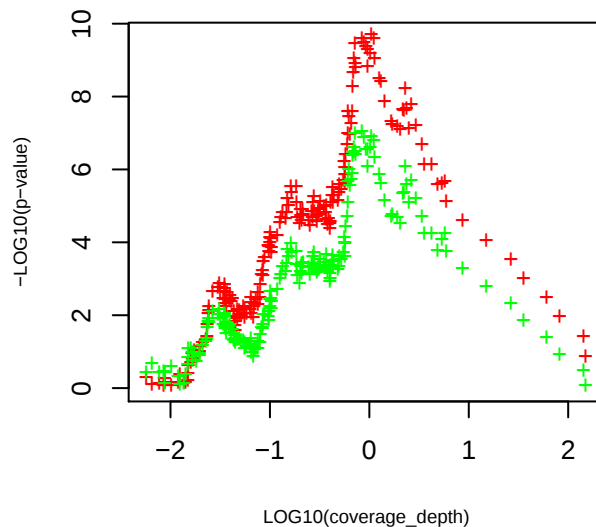


PF03009 GPD: glycerophosphodiester phosphodiesterase family

slope= 5.75 p_value= 3.4e-18 intercept= -20.94 p_value= 6.8e-19

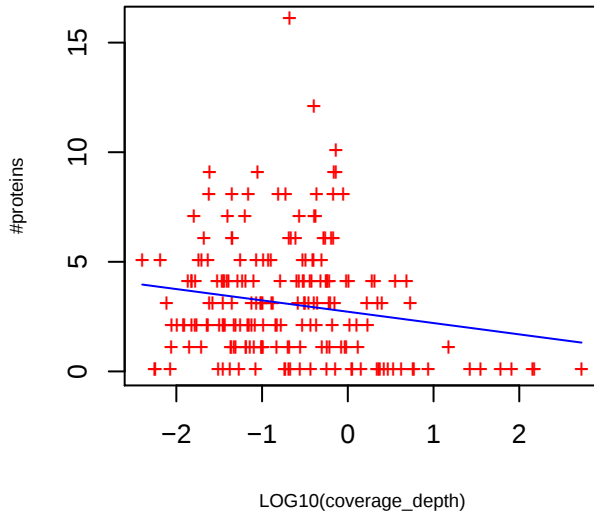


P-value curve : red (unnorm), green (norm)



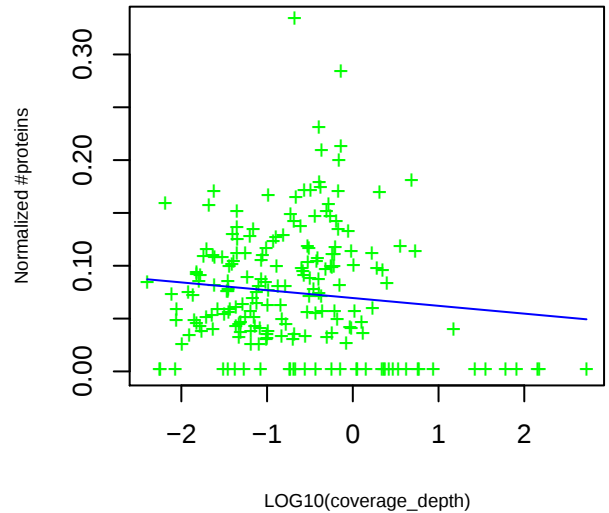
PF01965 DJ-1_Pfpl: DJ-1/Pfpl family

slope= -0.52 p_value= 0.014 intercept= 2.72 p_value= 9.5e-24



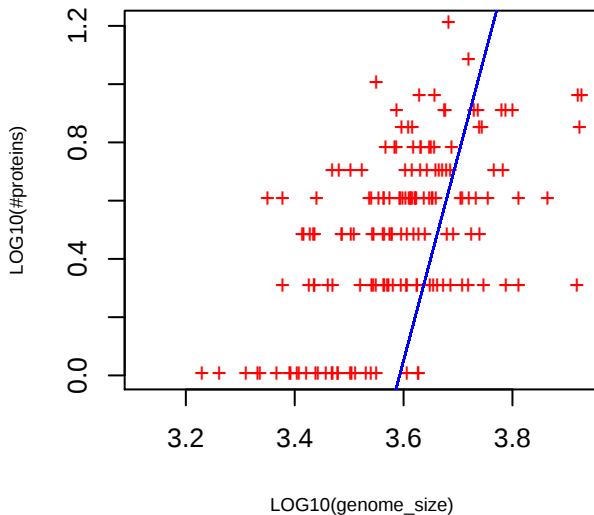
PF01965 DJ-1_Pfpl: DJ-1/Pfpl family

slope= -0.0074 p_value= 0.11 intercept= 0.07 p_value= 4.2e-29

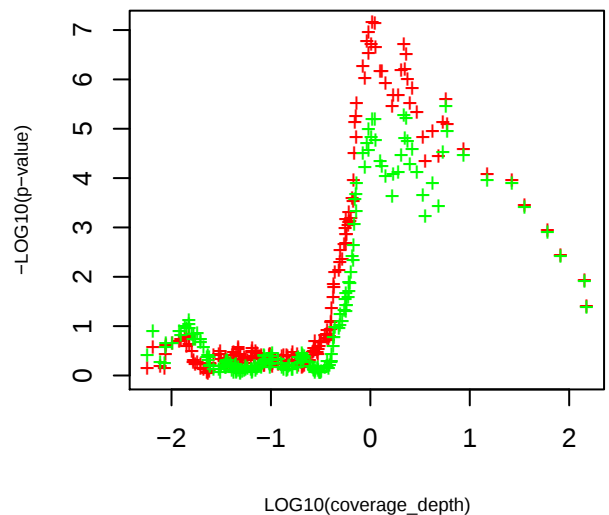


PF01965 DJ-1_Pfpl: DJ-1/Pfpl family

slope= 7.03 p_value= 3.0e-25 intercept= -25.26 p_value= 1.1e-25

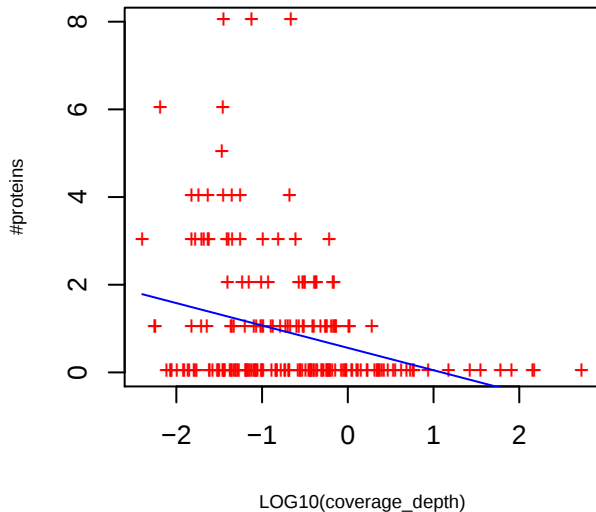


P-value curve : red (unnorm), green (norm)



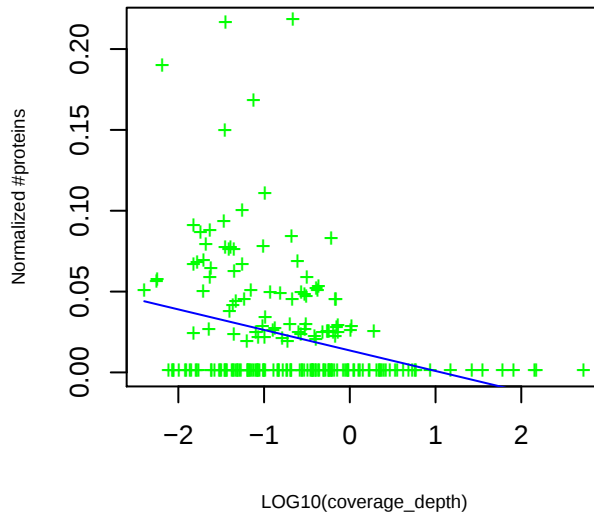
PF08269 Cache_2: Cache domain

slope= -0.51 p_value= 2.4e-05 intercept= 0.56 p_value= 3.9e-05



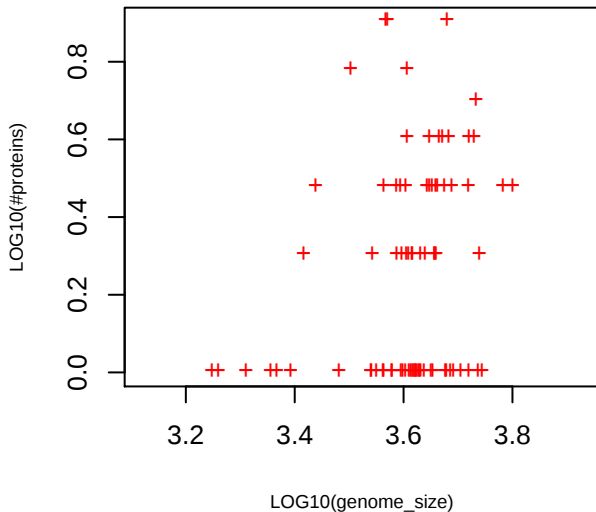
PF08269 Cache_2: Cache domain

slope= -0.013 p_value= 2.0e-05 intercept= 0.014 p_value= 5.1e-05

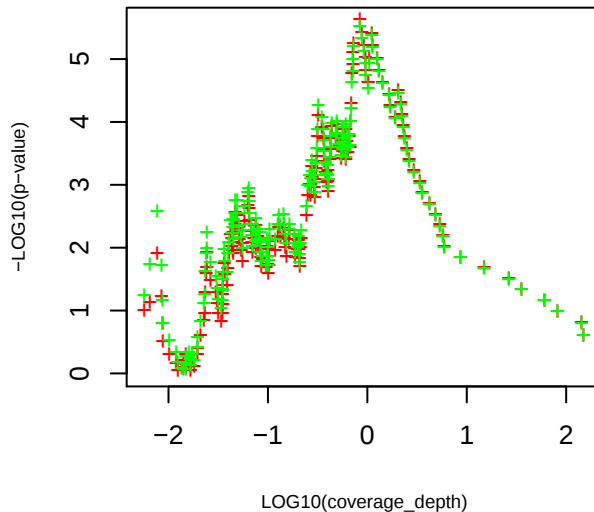


PF08269 Cache_2: Cache domain

slope= 4.16 p_value= 3.9e-06 intercept= -17.01 p_value= 1.3e-07

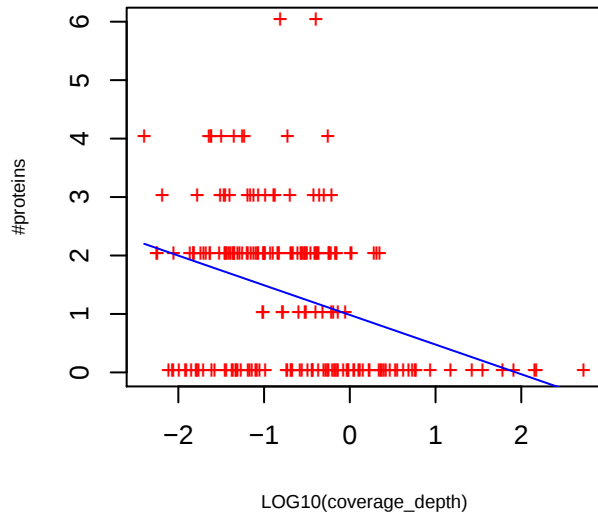


P-value curve ; red (unnorm), green (norm)



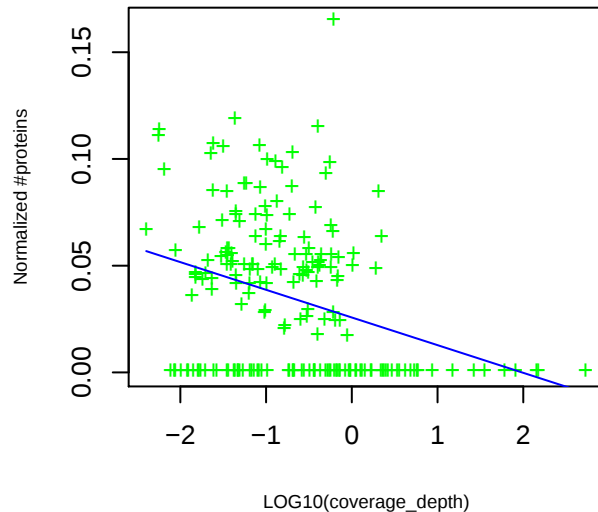
PF01052 SpoA: Surface presentation of antigens (SPOA) protein

slope= -0.51 p_value= 8.3e-07 intercept= 0.98 p_value= 1.1e-15



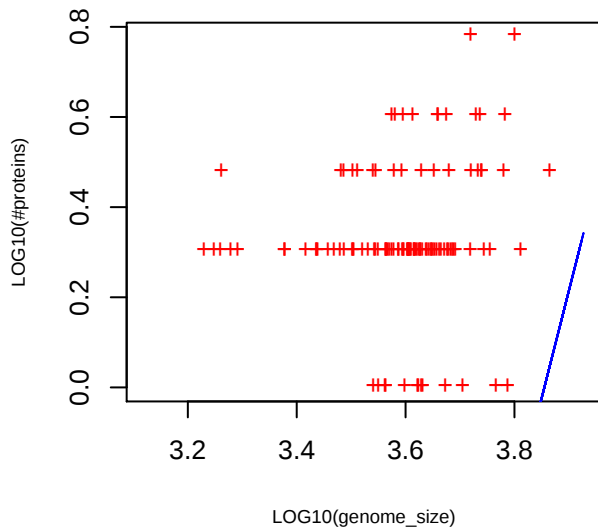
PF01052 SpoA: Surface presentation of antigens (SPOA) protein

slope= -0.013 p_value= 2.4e-06 intercept= 0.026 p_value= 3.9e-15

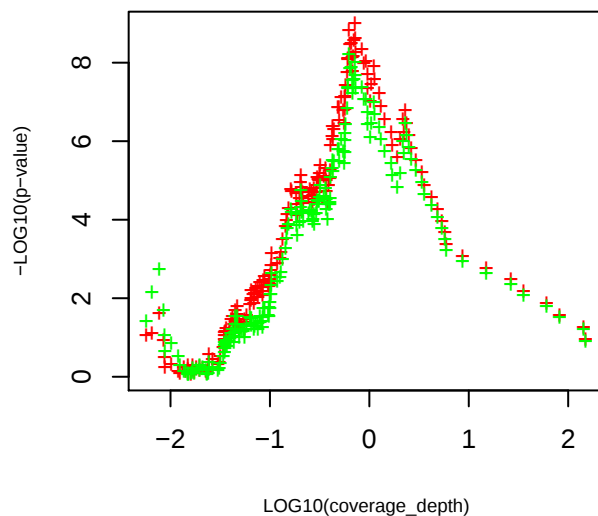


PF01052 SpoA: Surface presentation of antigens (SPOA) protein

slope= 4.76 p_value= 1.7e-07 intercept= -18.34 p_value= 1.7e-08

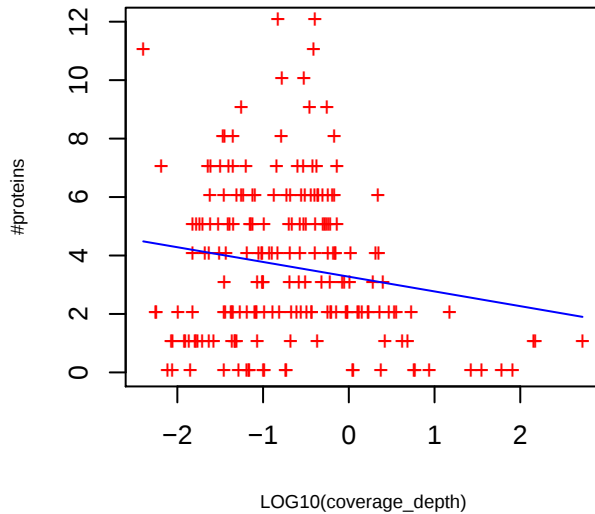


P-value curve ; red (unnorm), green (norm)



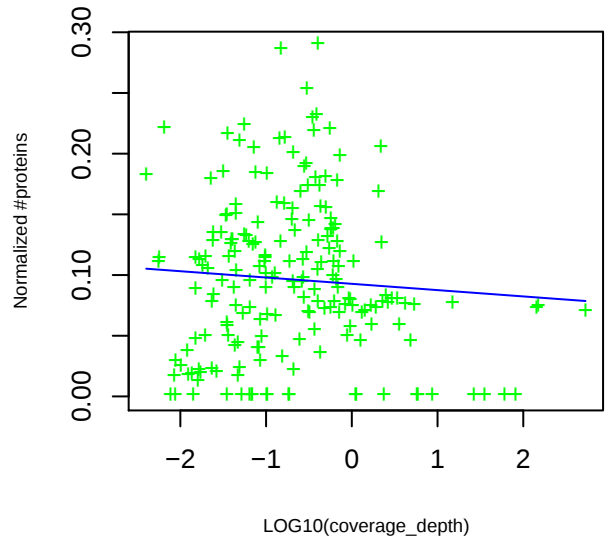
PF01464 SLT: Transglycosylase SLT domain

slope= -0.50 p_value= 0.018 intercept= 3.28 p_value= 1.5e-30



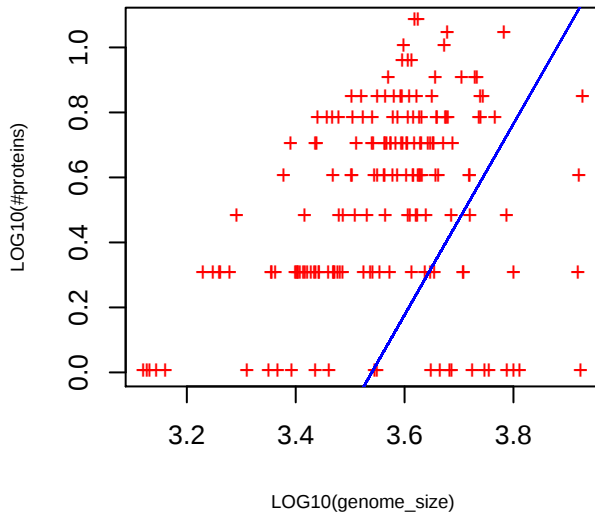
PF01464 SLT: Transglycosylase SLT domain

slope= -0.0052 p_value= 0.31 intercept= 0.093 p_value= 3.1e-37

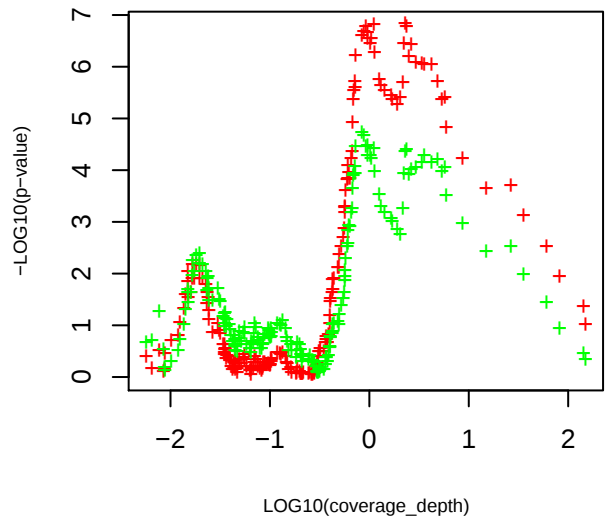


PF01464 SLT: Transglycosylase SLT domain

slope= 2.94 p_value= 2.3e-06 intercept= -10.41 p_value= 2.4e-06

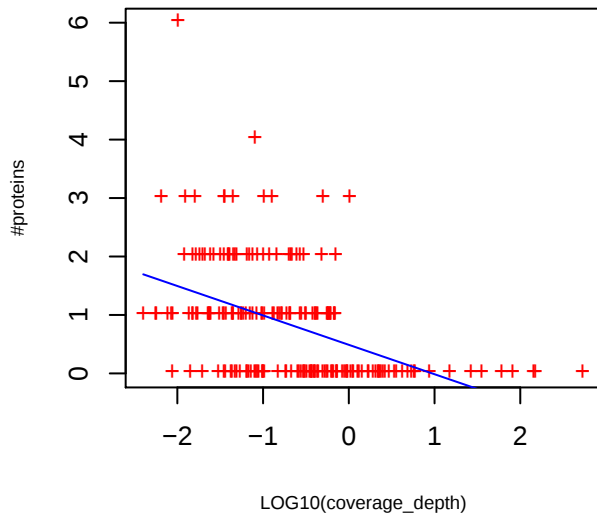


P-value curve ; red (unnorm), green (norm)



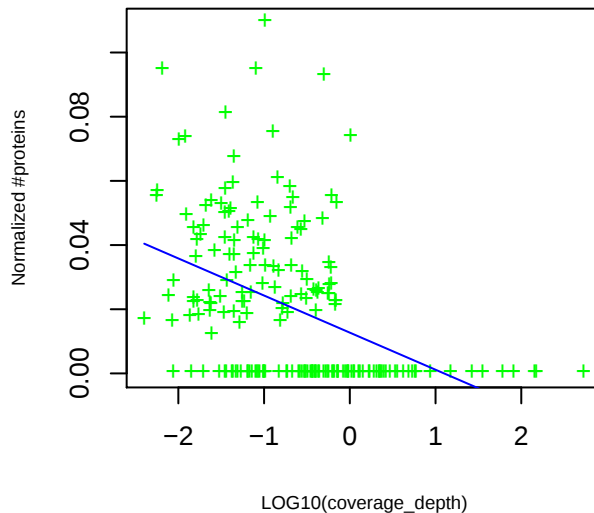
PF02895 H-kinase_dim: Signal transducing histidine kinase, homodimeric domain

slope= -0.50 p_value= 1.6e-11 intercept= 0.49 p_value= 4e-09



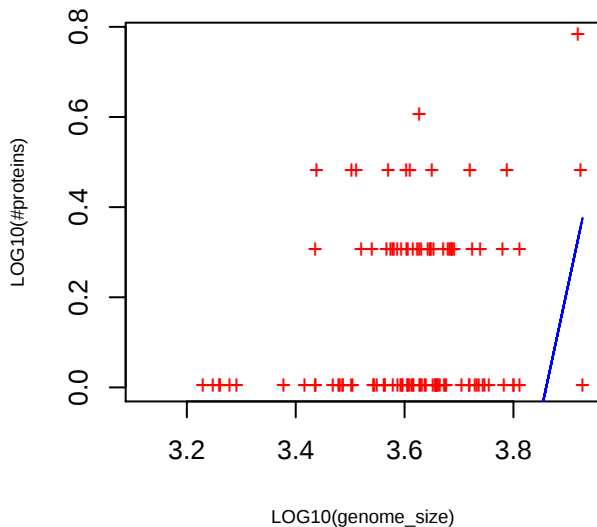
PF02895 H-kinase_dim: Signal transducing histidine kinase, homodimeric domain

slope= -0.012 p_value= 2.5e-10 intercept= 0.013 p_value= 6.5e-10

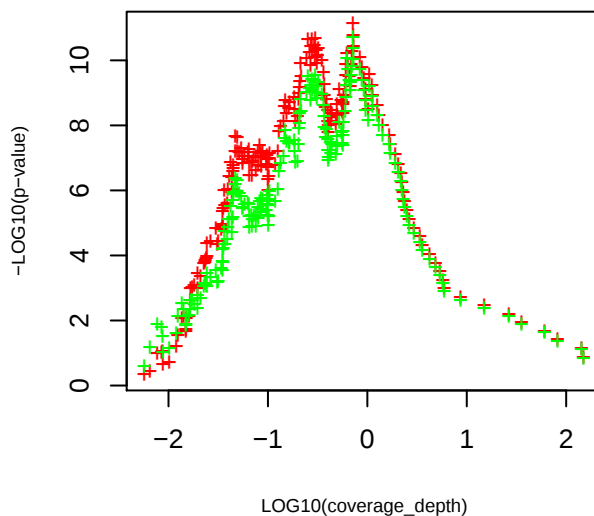


PF02895 H-kinase_dim: Signal transducing histidine kinase, homodimeric domain

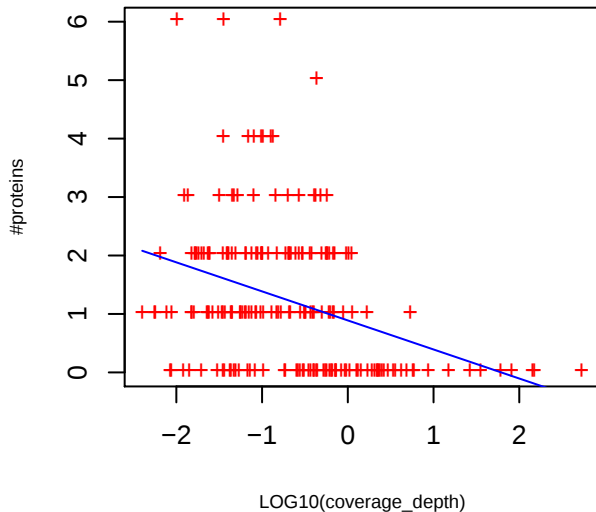
slope= 5.62 p_value= 8.7e-11 intercept= -21.69 p_value= 2.7e-12



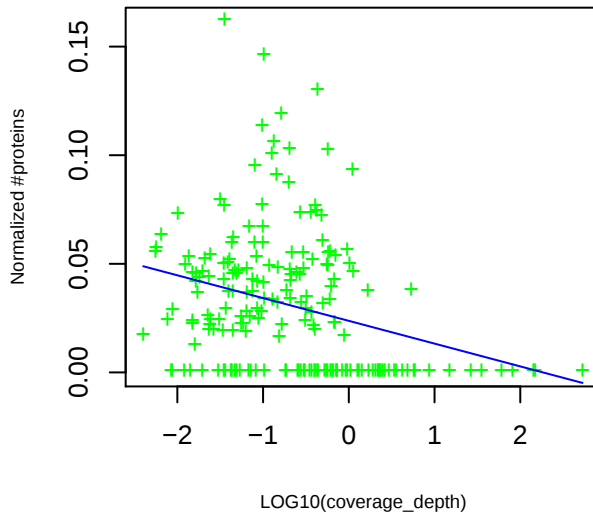
P-value curve ; red (unnorm), green (norm)



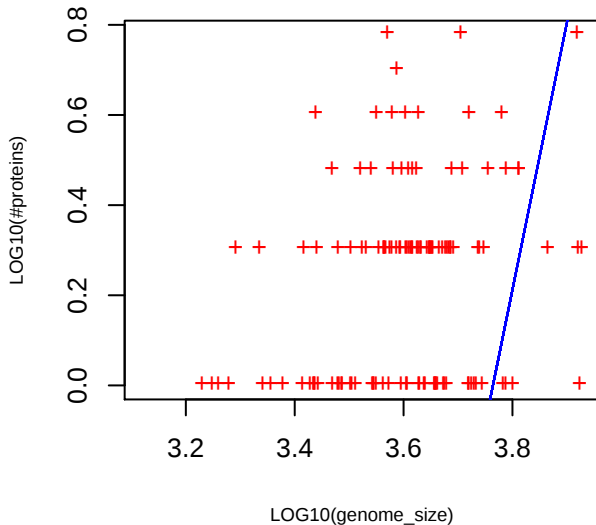
PF01739 CheR: CheR methyltransferase, SAM binding domain
 slope= -0.50 p_value= 5.3e-07 intercept= 0.89 p_value= 2.8e-14



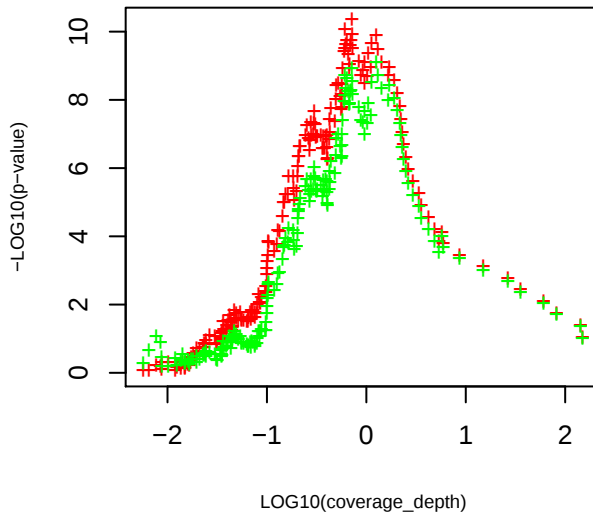
PF01739 CheR: CheR methyltransferase, SAM binding domain
 slope= -0.010 p_value= 2.7e-05 intercept= 0.024 p_value= 2.3e-15



PF01739 CheR: CheR methyltransferase, SAM binding domain
 slope= 5.92 p_value= 2.3e-12 intercept= -22.29 p_value= 1.5e-13

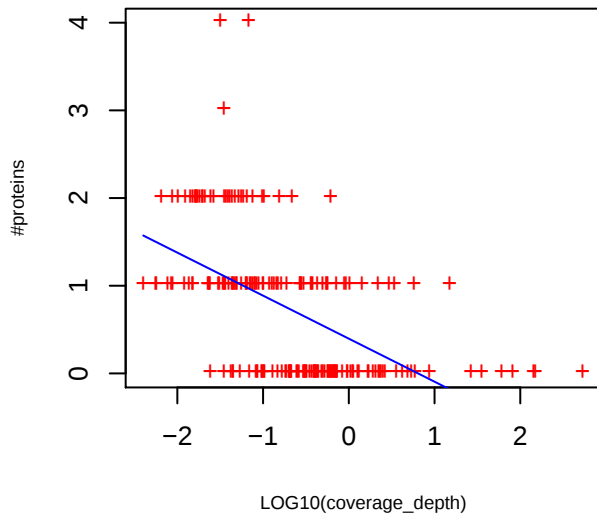


P-value curve ; red (unnorm), green (norm)



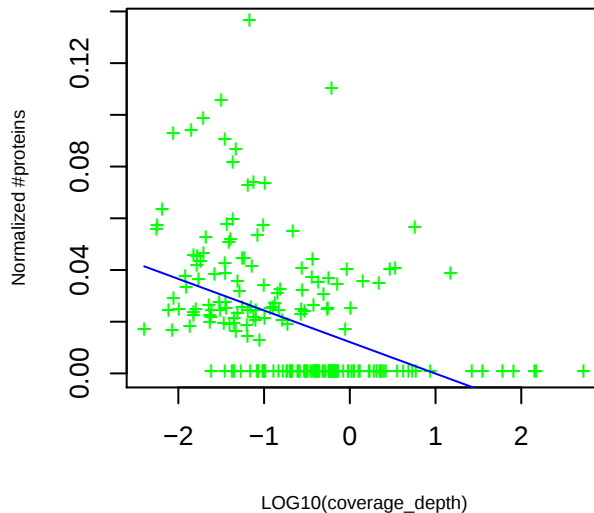
PF00708 Acylphosphatase: acylphosphatase

slope= -0.49 p_value= 6.2e-16 intercept= 0.40 p_value= 1.8e-09



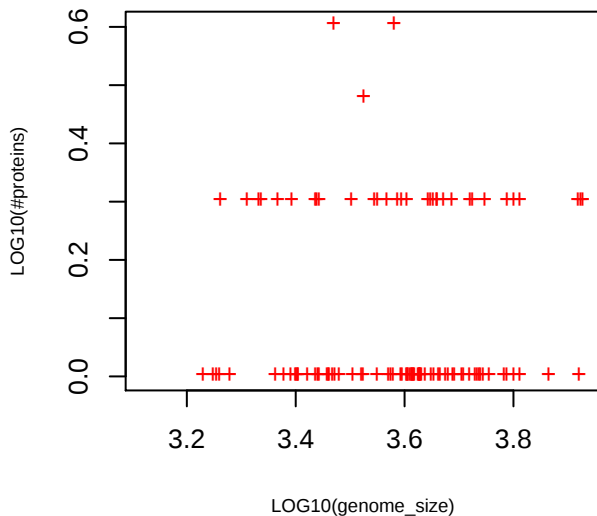
PF00708 Acylphosphatase: acylphosphatase

slope= -0.012 p_value= 5.3e-10 intercept= 0.012 p_value= 3.3e-08

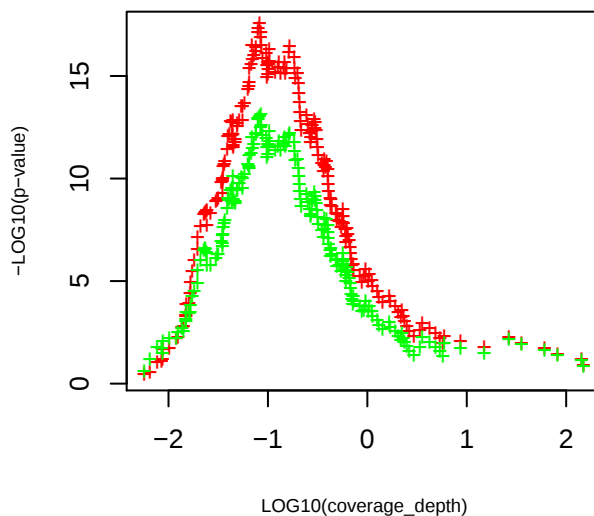


PF00708 Acylphosphatase: acylphosphatase

slope= 3.10 p_value= 5e-04 intercept= -12.81 p_value= 5.6e-05

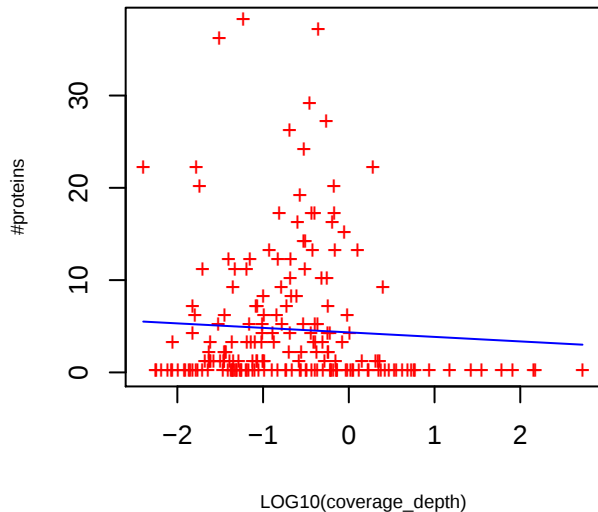


P-value curve ; red (unnorm), green (norm)



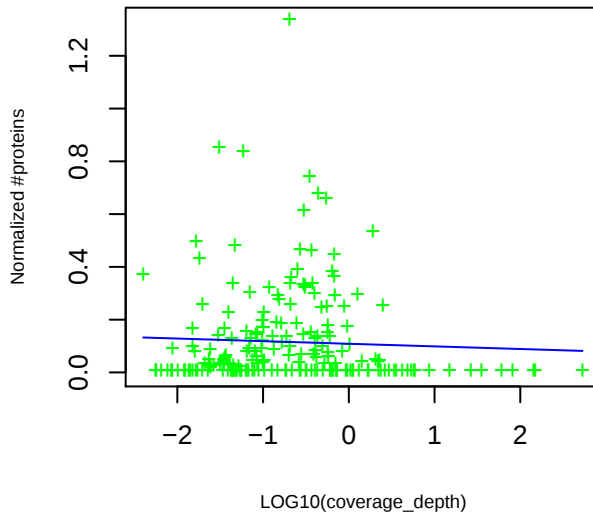
PF01527 Transposase_8: transposase

slope= -0.49 p_value= 0.41 intercept= 4.34 p_value= 8.8e-10



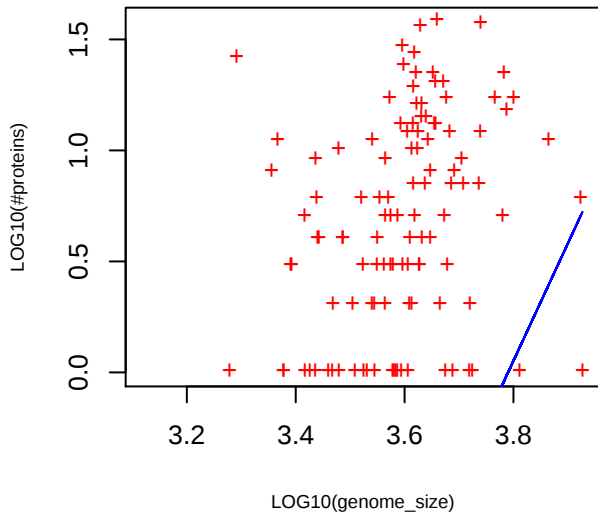
PF01527 Transposase_8: transposase

slope= -0.01 p_value= 0.51 intercept= 0.11 p_value= 1.2e-09

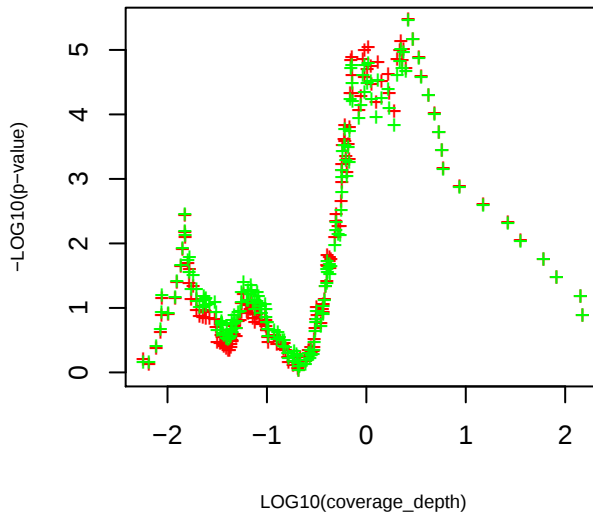


PF01527 Transposase_8: transposase

slope= 5.29 p_value= 1.0e-07 intercept= -20.05 p_value= 1.5e-08

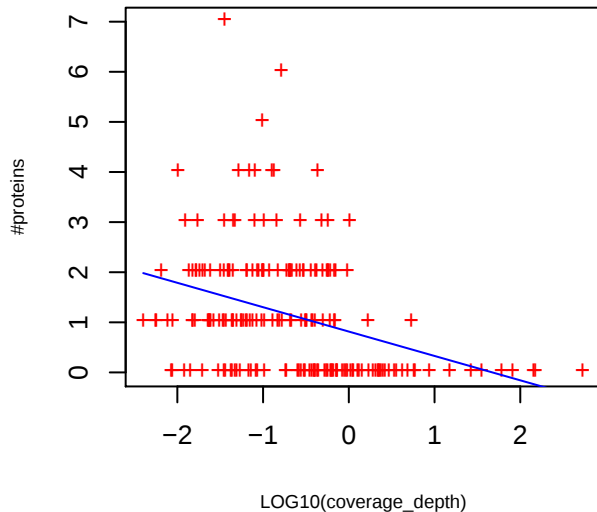


P-value curve ; red (unnorm), green (norm)



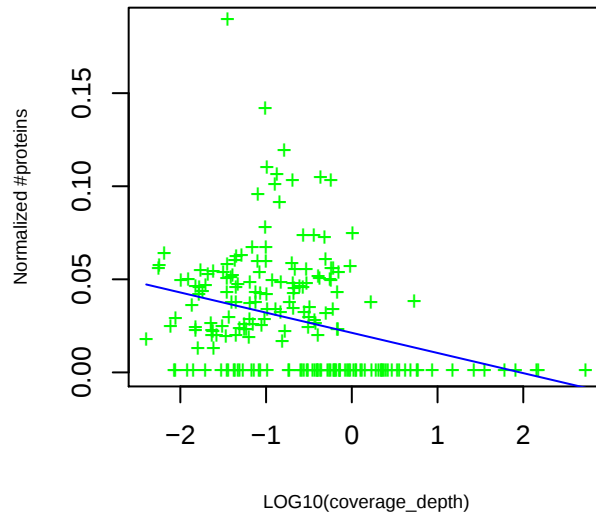
PF01339 CheB_methyl: protein-glutamate methyltransferase CheB

slope= -0.49 p_value= 5.6e-07 intercept= 0.82 p_value= 7.6e-13



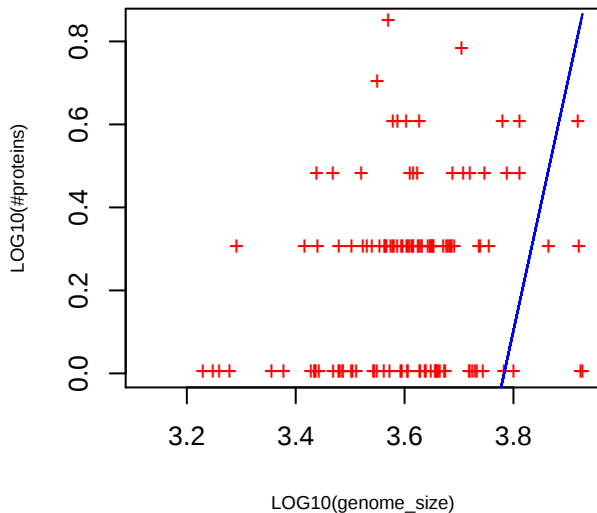
PF01339 CheB_methyl: protein-glutamate methyltransferase CheB

slope= -0.011 p_value= 1.0e-05 intercept= 0.021 p_value= 2.3e-13

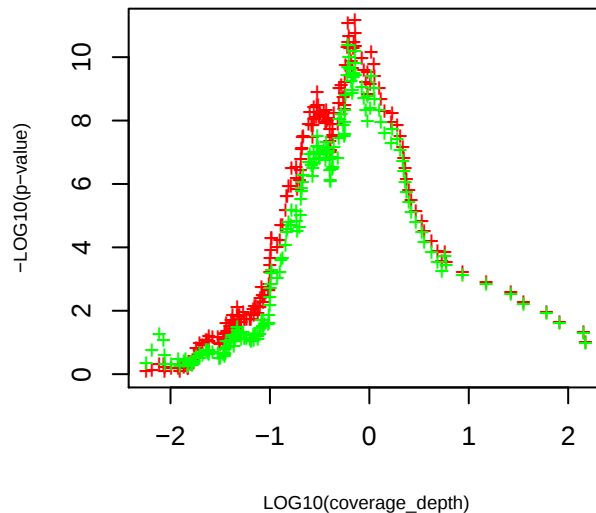


PF01339 CheB_methyl: protein-glutamate methyltransferase CheB

slope= 6.02 p_value= 2.1e-12 intercept= -22.76 p_value= 1.1e-13

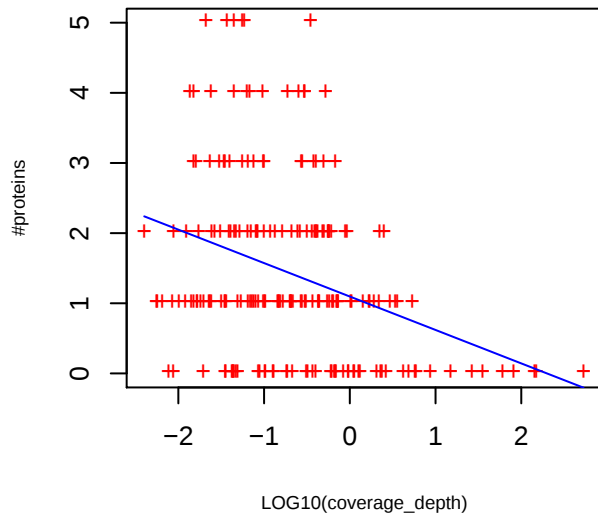


P-value curve : red (unnorm), green (norm)



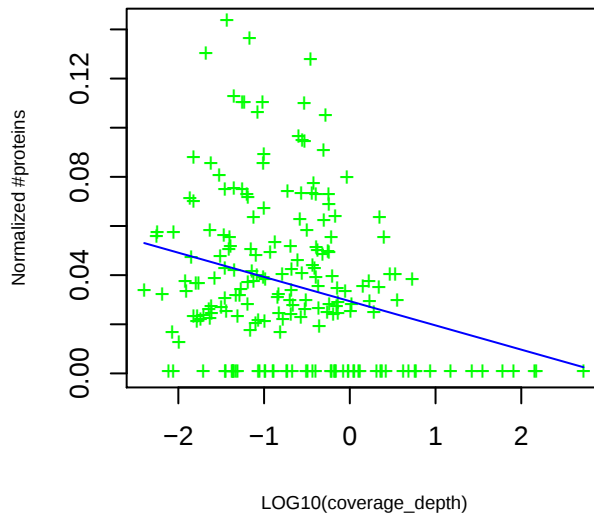
PF00614 PLDc: phospholipase D active site domain protein

slope= -0.48 p_value= 2.8e-06 intercept= 1.10 p_value= 9.2e-19



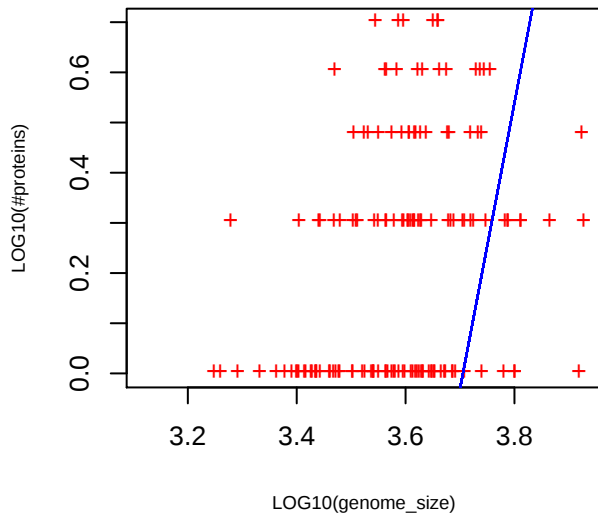
PF00614 PLDc: phospholipase D active site domain protein

slope= -0.0099 p_value= 0.00012 intercept= 0.029 p_value= 2.2e-20

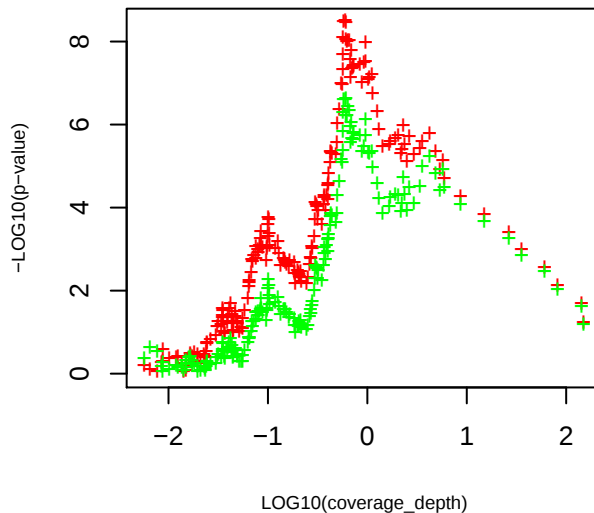


PF00614 PLDc: phospholipase D active site domain protein

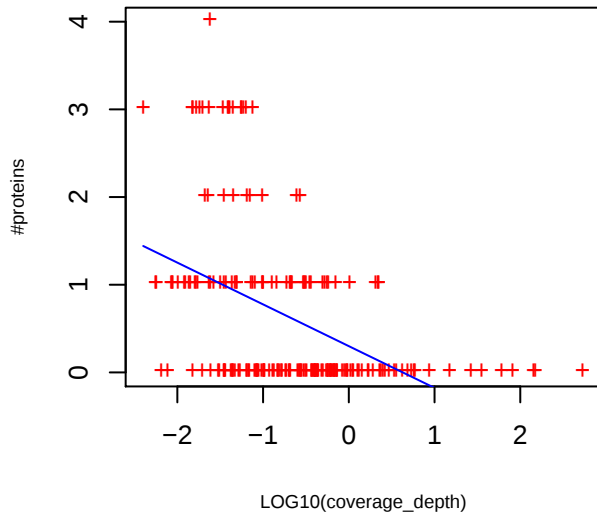
slope= 5.70 p_value= 2.2e-13 intercept= -21.11 p_value= 2.6e-14



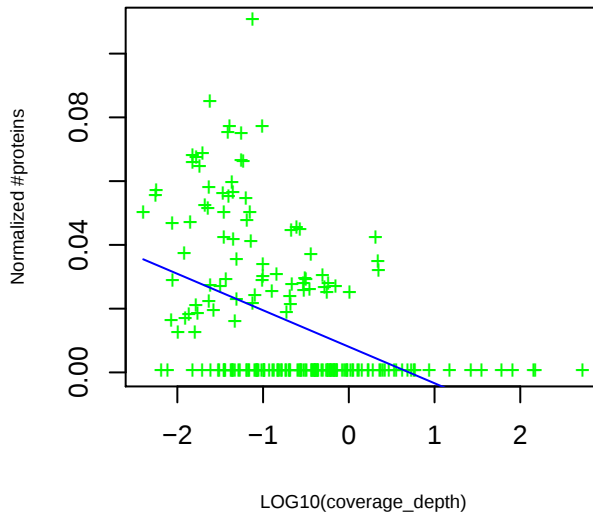
P-value curve ; red (unnorm), green (norm)



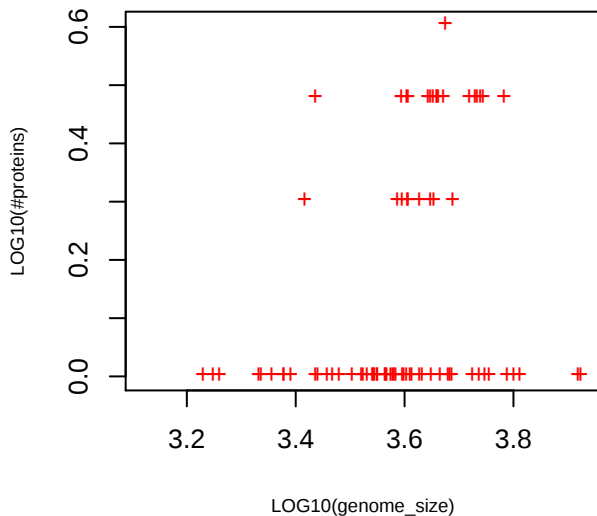
TIGR00933 2a38: potassium uptake protein, TrkH family
 slope= -0.48 p_value= 4.5e-11 intercept= 0.30 p_value= 0.00014



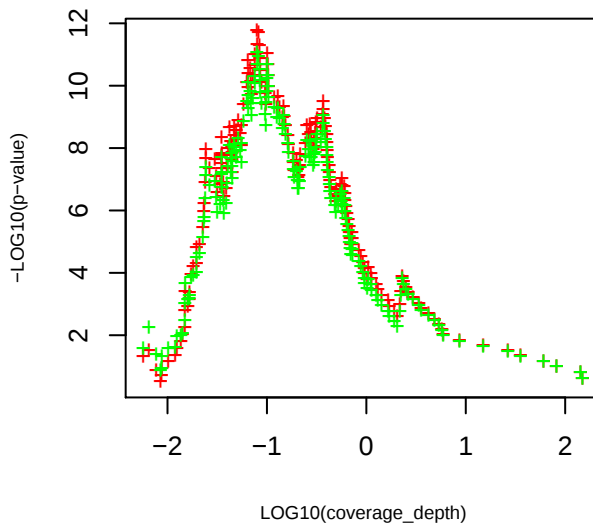
TIGR00933 2a38: potassium uptake protein, TrkH family
 slope= -0.011 p_value= 1.3e-10 intercept= 0.008 p_value= 3.6e-05



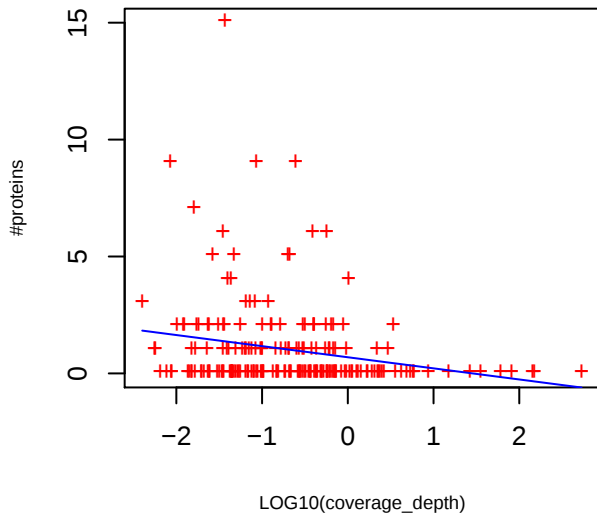
TIGR00933 2a38: potassium uptake protein, TrkH family
 slope= 3.07 p_value= 0.00051 intercept= -13.23 p_value= 2.7e-05



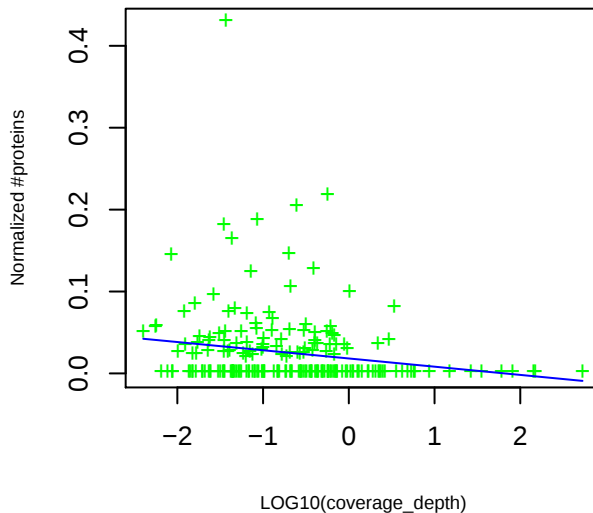
P-value curve : red (unnorm), green (norm)



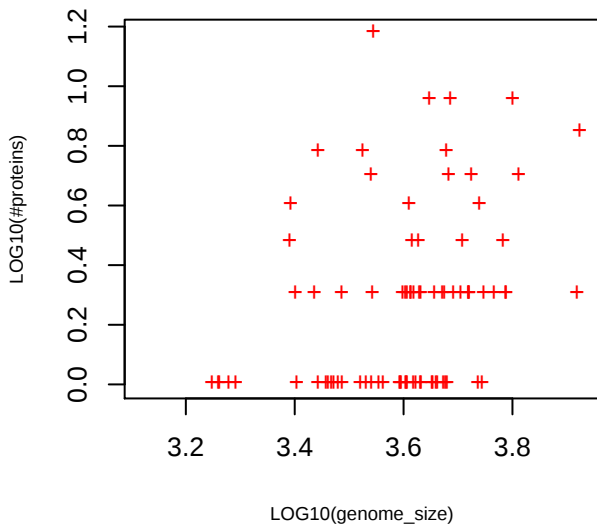
TIGR01552 phd_fam: prevent-host-death family protein
 slope= -0.48 p_value= 0.0022 intercept= 0.69 p_value= 8.8e-05



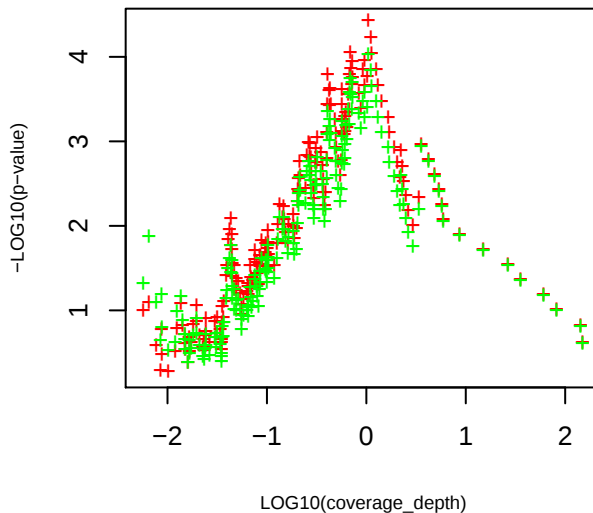
TIGR01552 phd_fam: prevent-host-death family protein
 slope= -0.01 p_value= 0.01 intercept= 0.018 p_value= 4.1e-05



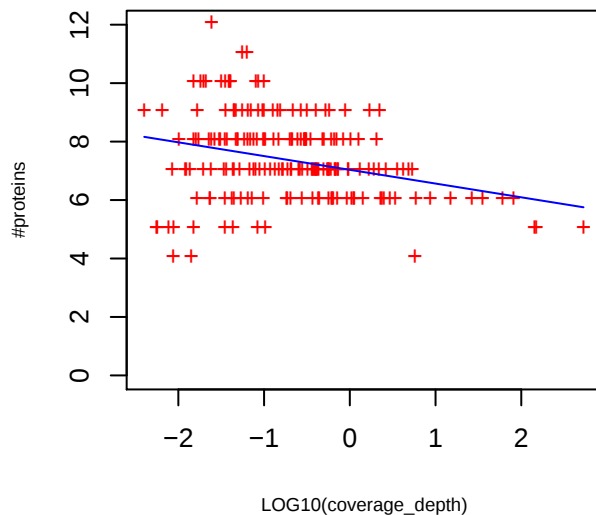
TIGR01552 phd_fam: prevent-host-death family protein
 slope= 3.85 p_value= 2.3e-05 intercept= -15.88 p_value= 1.1e-06



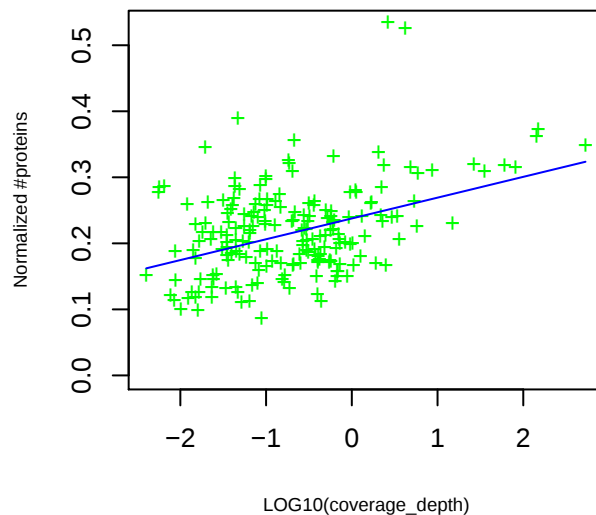
P-value curve ; red (unnorm), green (norm)



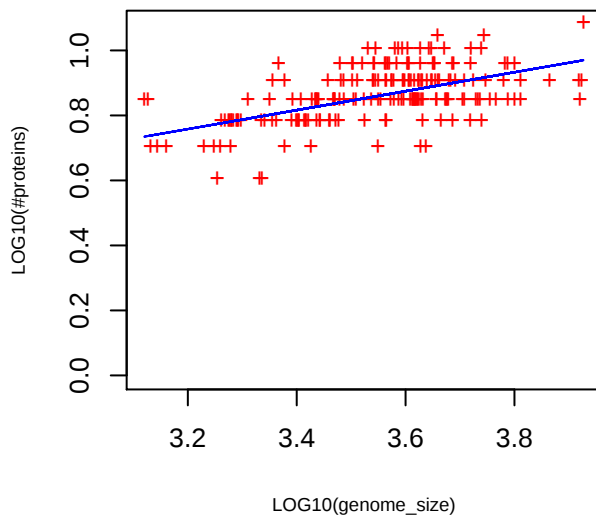
PF00009 GTP_EFTU: Elongation factor Tu GTP binding domain
 slope= -0.47 p_value= 2.5e-05 intercept= 7.03 p_value= 8.2e-124



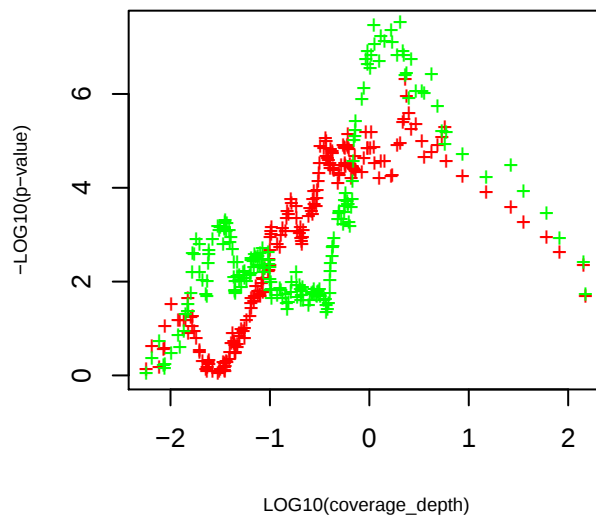
PF00009 GTP_EFTU: Elongation factor Tu GTP binding domain
 slope= 0.032 p_value= 1.7e-09 intercept= 0.24 p_value= 4.9e-100



PF00009 GTP_EFTU: Elongation factor Tu GTP binding domain
 slope= 0.29 p_value= 2.7e-17 intercept= -0.17 p_value= 0.12

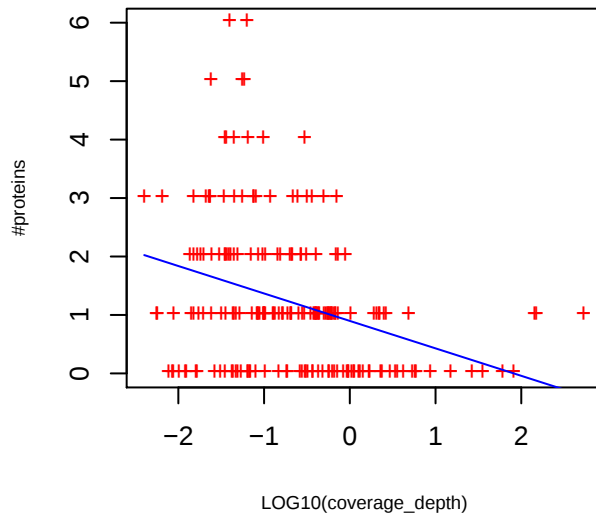


P-value curve ; red (unnorm), green (norm)



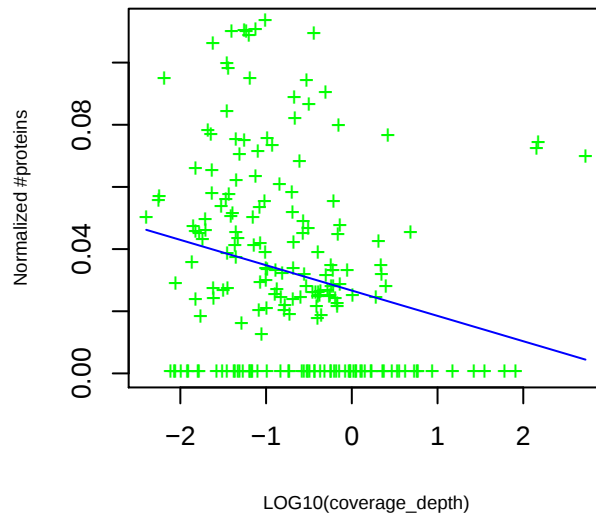
PF04073 YbaK: YbaK / prolyl-tRNA synthetases associated domain

slope= -0.47 p_value= 2.2e-06 intercept= 0.90 p_value= 2.2e-14



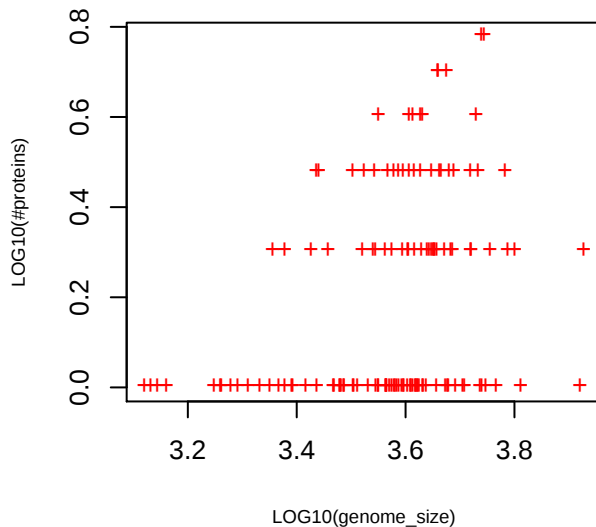
PF04073 YbaK: YbaK / prolyl-tRNA synthetases associated domain

slope= -0.0082 p_value= 0.0010 intercept= 0.027 p_value= 2.9e-18

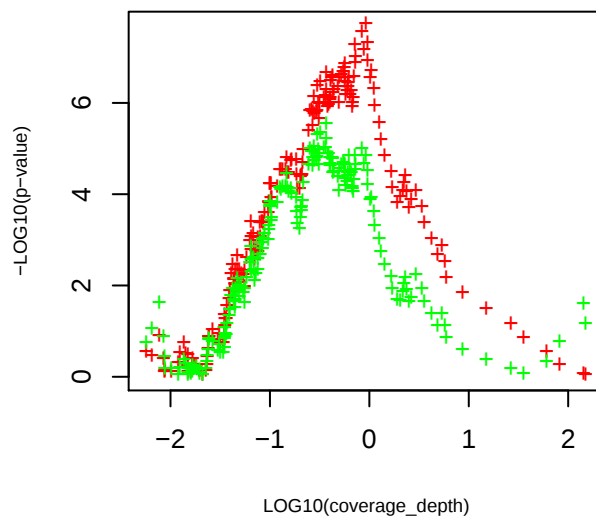


PF04073 YbaK: YbaK / prolyl-tRNA synthetases associated domain

slope= 3.07 p_value= 0.00037 intercept= -12.11 p_value= 8.3e-05

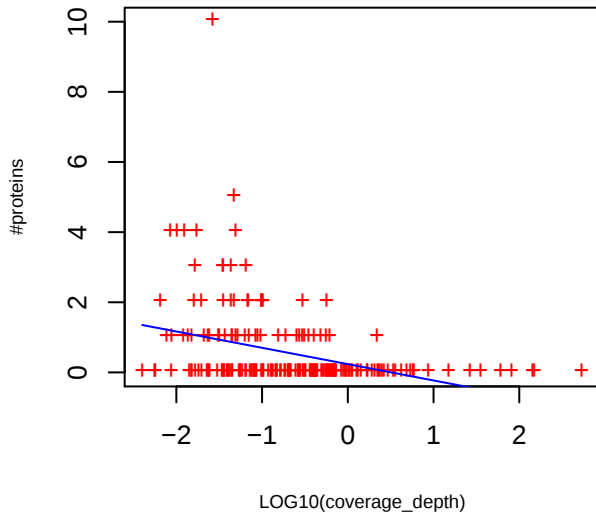


P-value curve ; red (unnorm), green (norm)



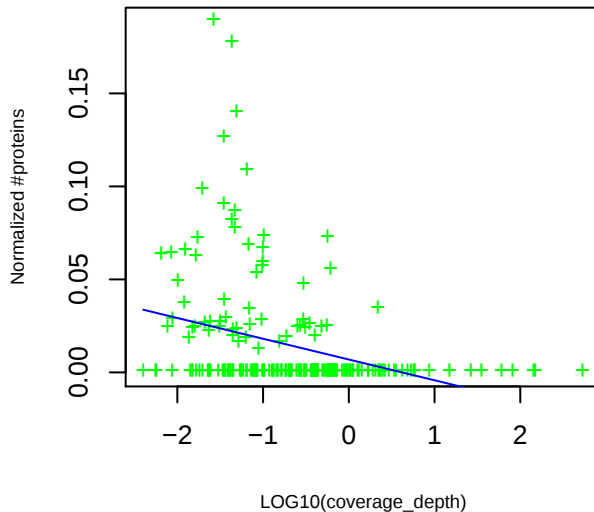
PF00690 Cation_ATPase_N: Cation transporter/ATPase, N-terminus

slope= -0.47 p_value= 4.5e-07 intercept= 0.24 p_value= 0.02



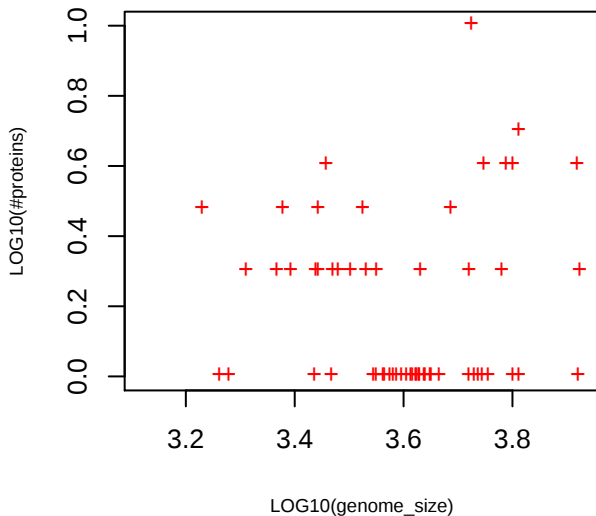
PF00690 Cation_ATPase_N: Cation transporter/ATPase, N-terminus

slope= -0.011 p_value= 3.6e-06 intercept= 0.007 p_value= 0.0093

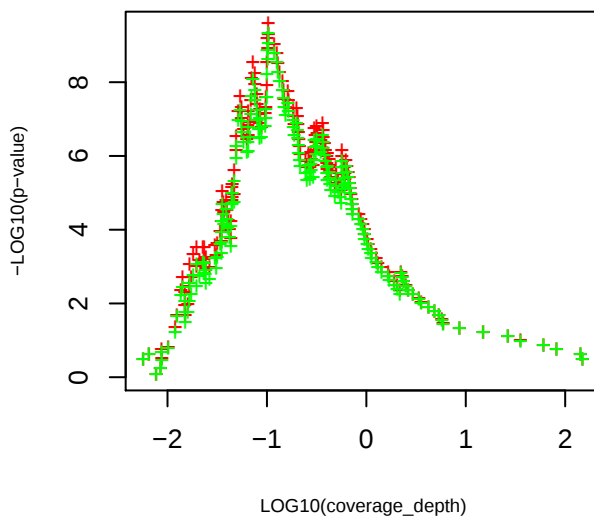


PF00690 Cation_ATPase_N: Cation transporter/ATPase, N-terminus

slope= 2.60 p_value= 0.0018 intercept= -11.99 p_value= 6e-05

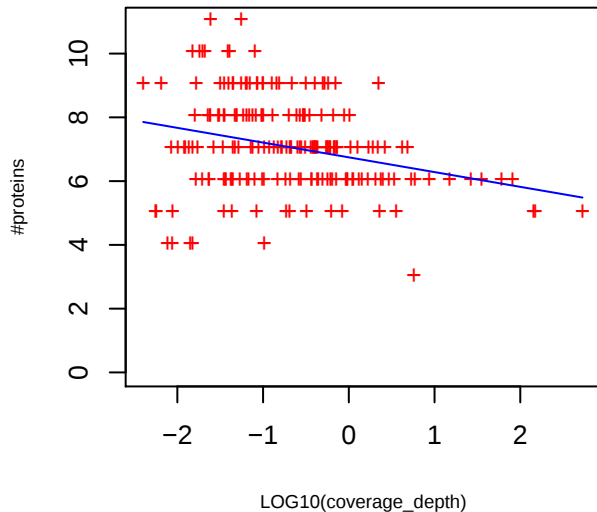


P-value curve ; red (unnorm), green (norm)



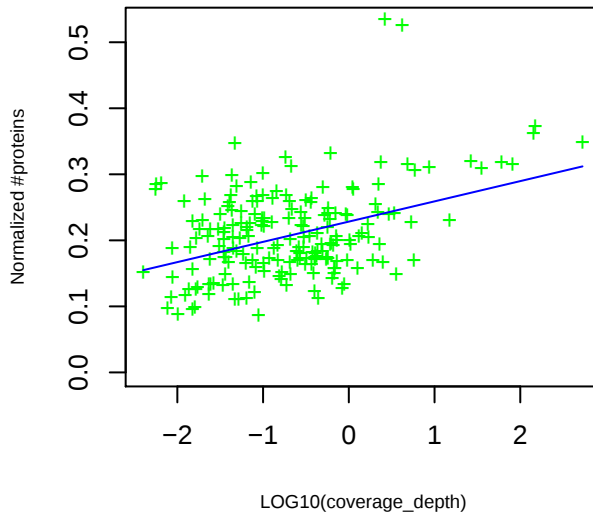
PF03144 GTP_EFTU_D2: Elongation factor Tu domain 2

slope= -0.46 p_value= 4.6e-05 intercept= 6.75 p_value= 5.6e-119



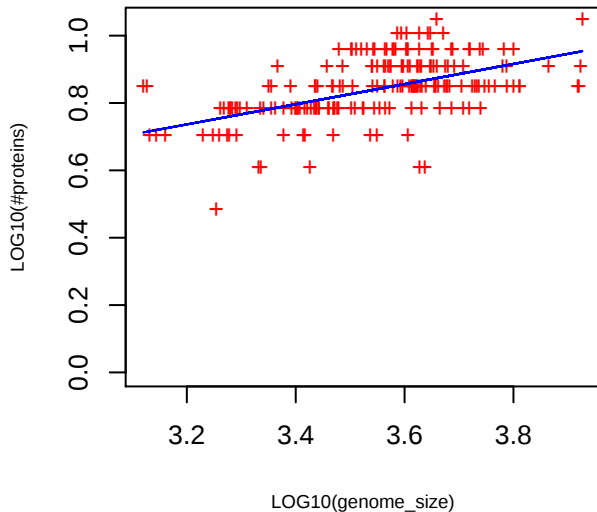
PF03144 GTP_EFTU_D2: Elongation factor Tu domain 2

slope= 0.031 p_value= 3.3e-09 intercept= 0.23 p_value= 1.4e-97

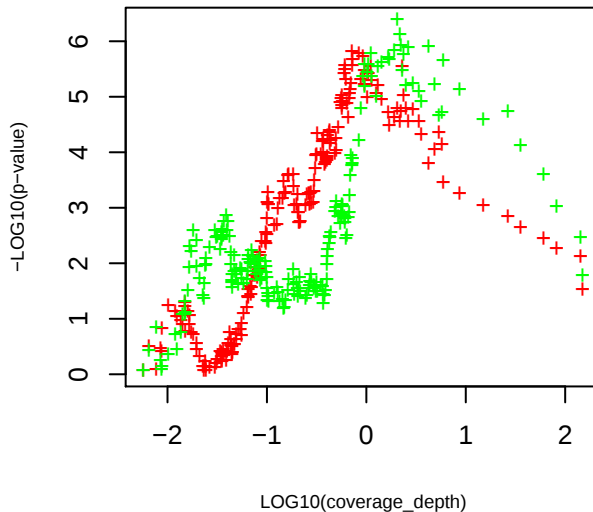


PF03144 GTP_EFTU_D2: Elongation factor Tu domain 2

slope= 0.30 p_value= 1.5e-15 intercept= -0.22 p_value= 0.072

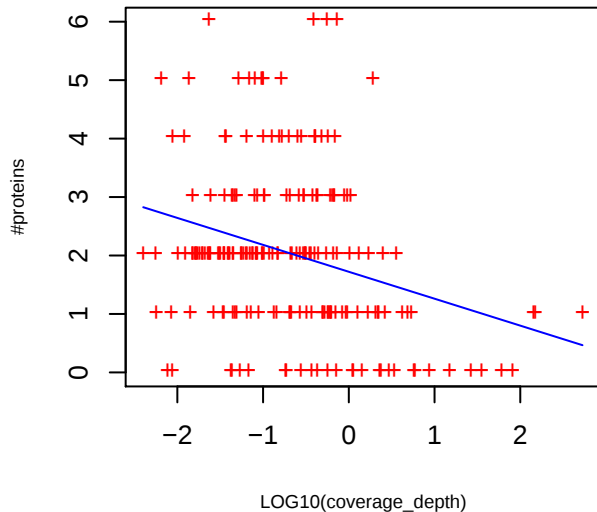


P-value curve ; red (unnorm), green (norm)



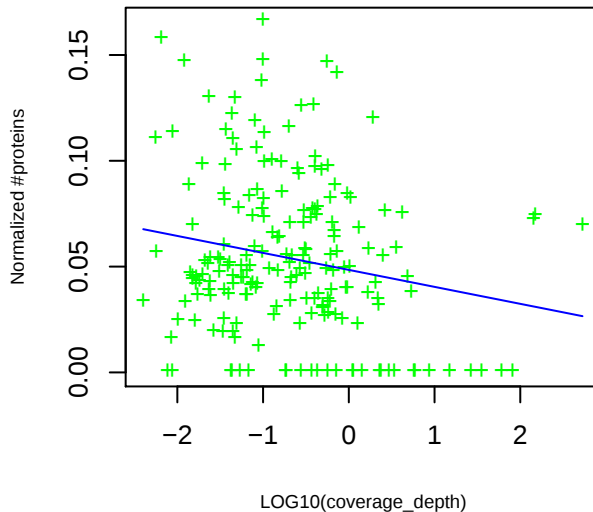
PF02082 Rrf2: Transcriptional regulator

slope= -0.46 p_value= 4.7e-05 intercept= 1.72 p_value= 1.3e-30



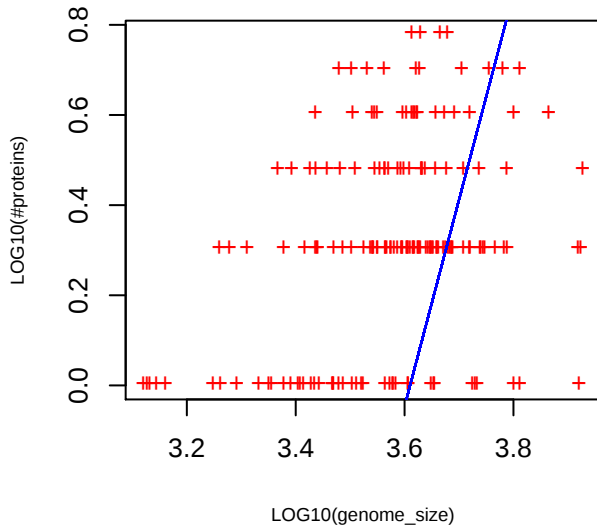
PF02082 Rrf2: Transcriptional regulator

slope= -0.008 p_value= 0.007 intercept= 0.048 p_value= 5.2e-33

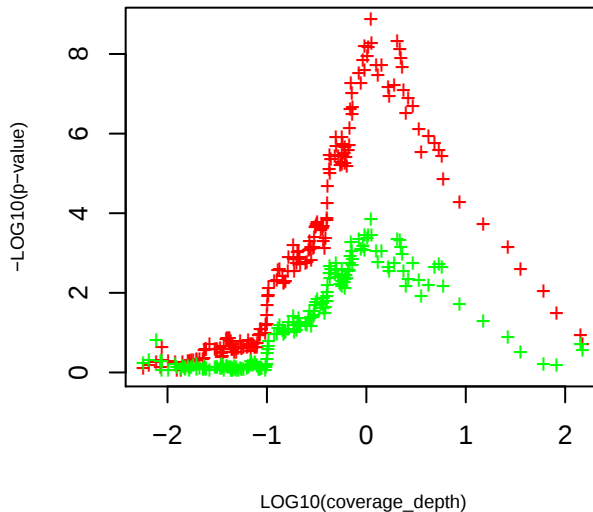


PF02082 Rrf2: Transcriptional regulator

slope= 4.58 p_value= 3e-13 intercept= -16.53 p_value= 1.3e-13

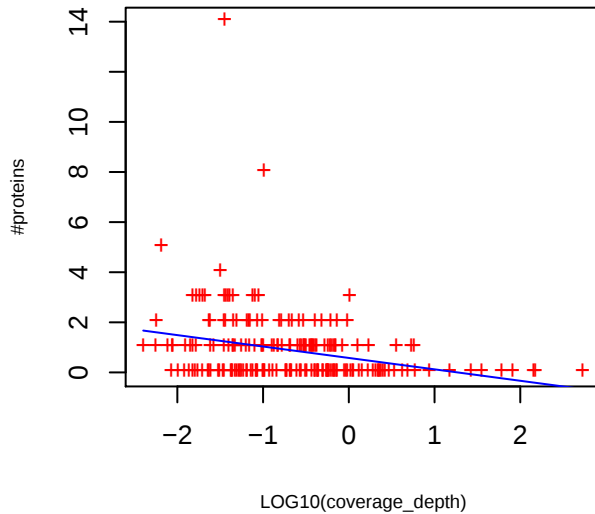


P-value curve ; red (unnorm), green (norm)



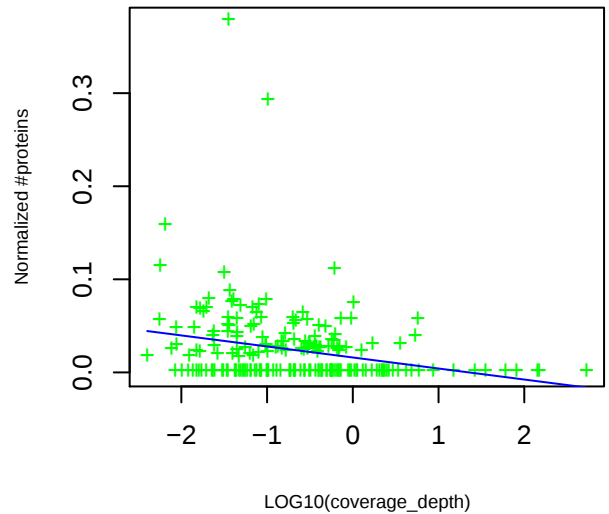
PF01814 Hemerythrin: Hemerythrin HHE cation binding domain

slope= -0.46 p_value= 7.3e-05 intercept= 0.58 p_value= 9.3e-06



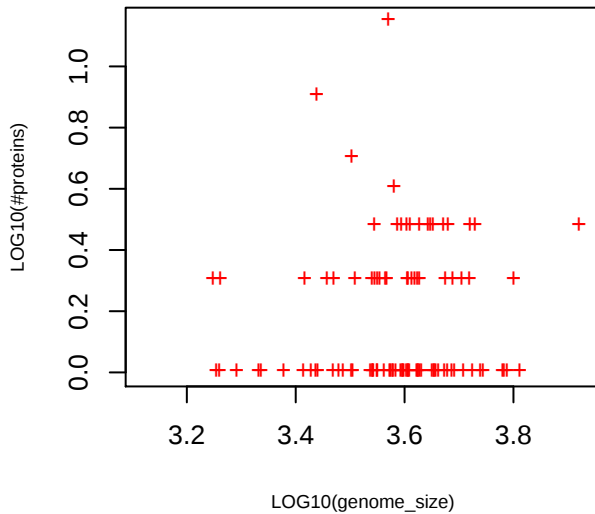
PF01814 Hemerythrin: Hemerythrin HHE cation binding domain

slope= -0.012 p_value= 0.00034 intercept= 0.016 p_value= 2e-05

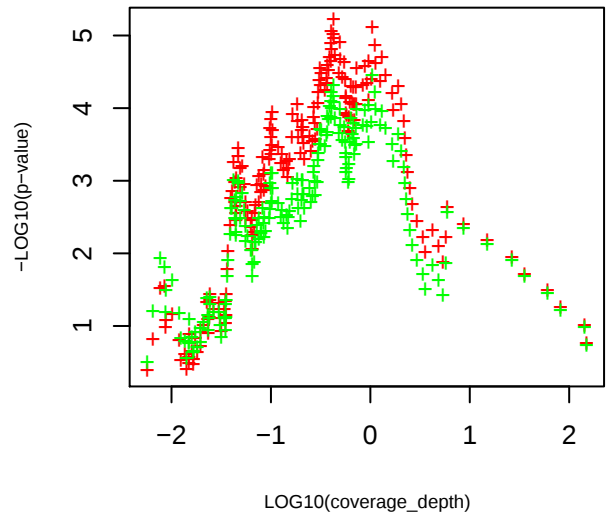


PF01814 Hemerythrin: Hemerythrin HHE cation binding domain

slope= 2.91 p_value= 0.0014 intercept= -12.22 p_value= 0.00017

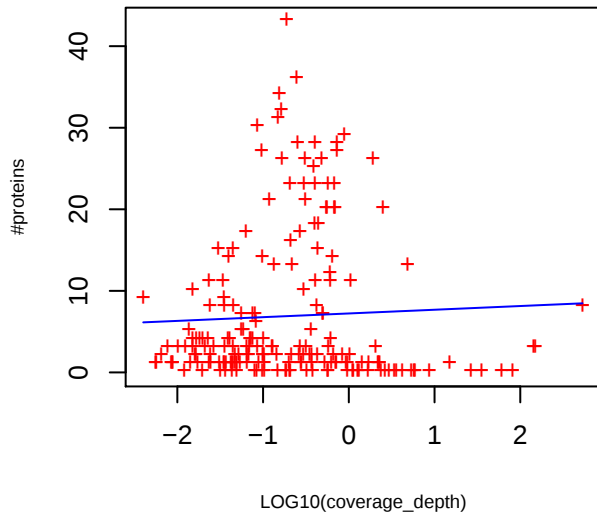


P-value curve ; red (unnorm), green (norm)



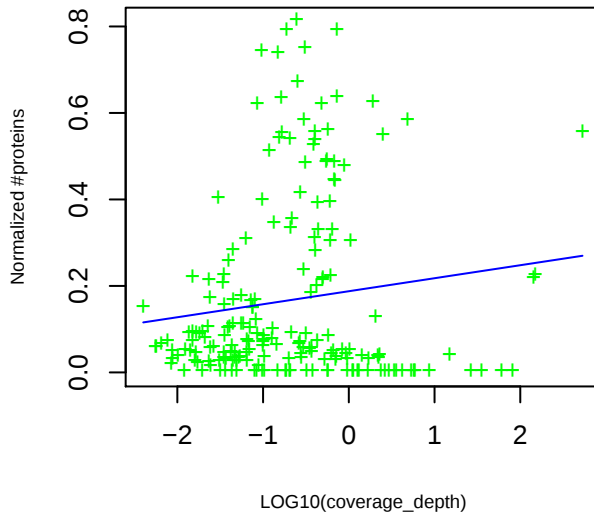
PF06808 DctM: TRAP transporter, DctM-like membrane protein

slope= 0.46 p_value= 0.54 intercept= 7.23 p_value= 2.0e-15



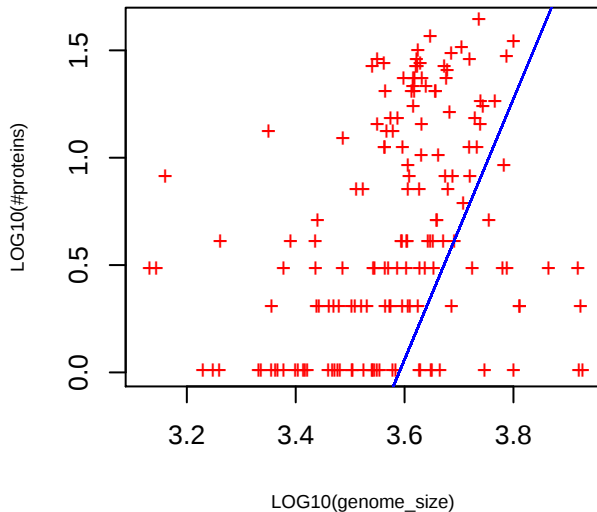
PF06808 DctM: TRAP transporter, DctM-like membrane protein

slope= 0.03 p_value= 0.073 intercept= 0.19 p_value= 3.9e-19

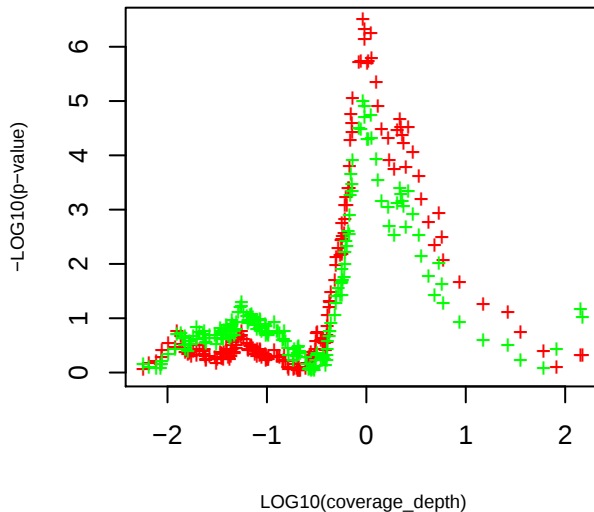


PF06808 DctM: TRAP transporter, DctM-like membrane protein

slope= 6.07 p_value= 7.4e-15 intercept= -21.79 p_value= 4e-15

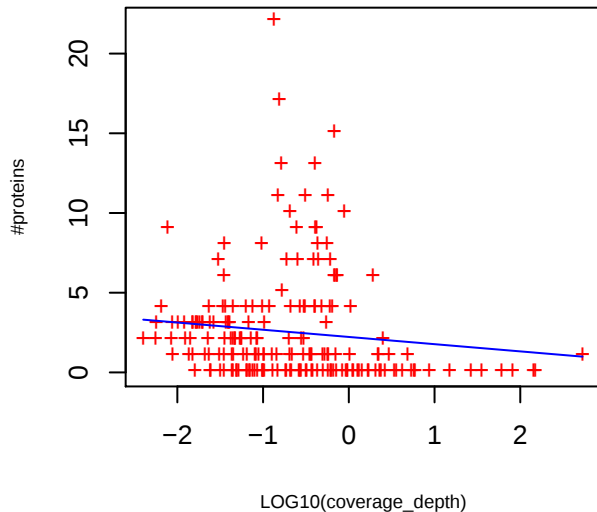


P-value curve : red (unnorm), green (norm)



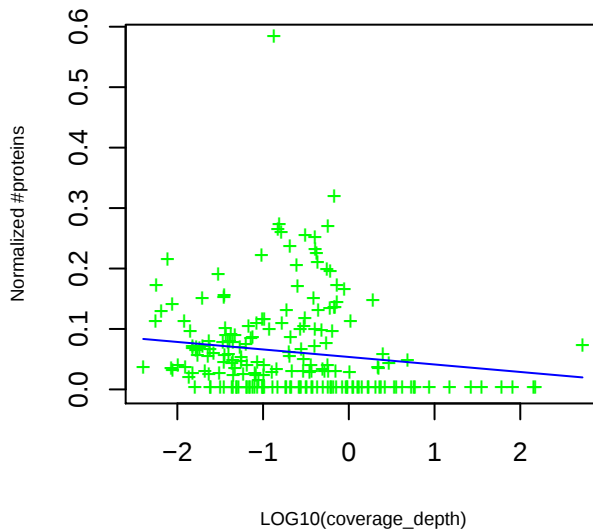
PF03459 TOBE: TOBE domain

slope= -0.45 p_value= 0.10 intercept= 2.22 p_value= 1.8e-11



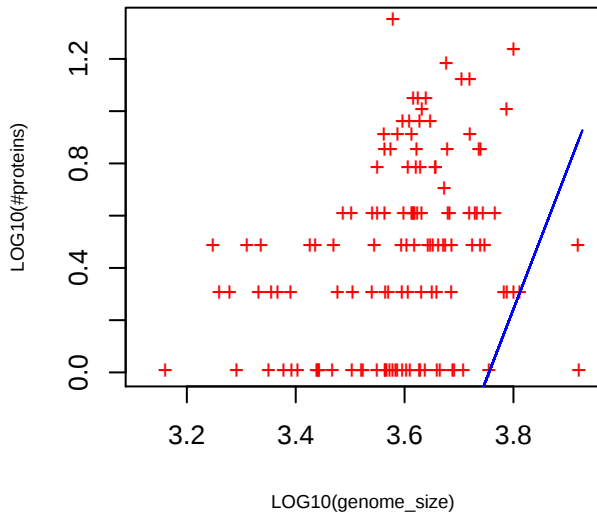
PF03459 TOBE: TOBE domain

slope= -0.012 p_value= 0.052 intercept= 0.054 p_value= 2.3e-12

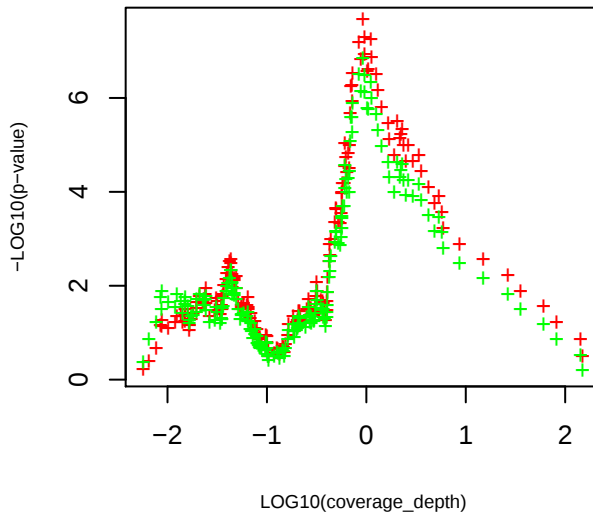


PF03459 TOBE: TOBE domain

slope= 5.40 p_value= 2.4e-09 intercept= -20.28 p_value= 3.4e-10

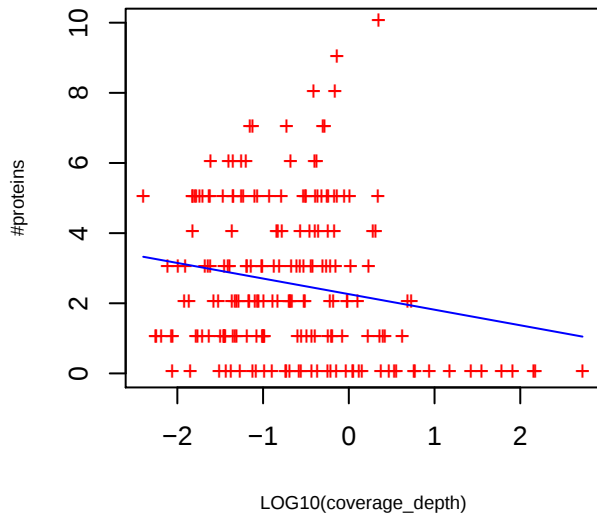


P-value curve ; red (unnorm), green (norm)



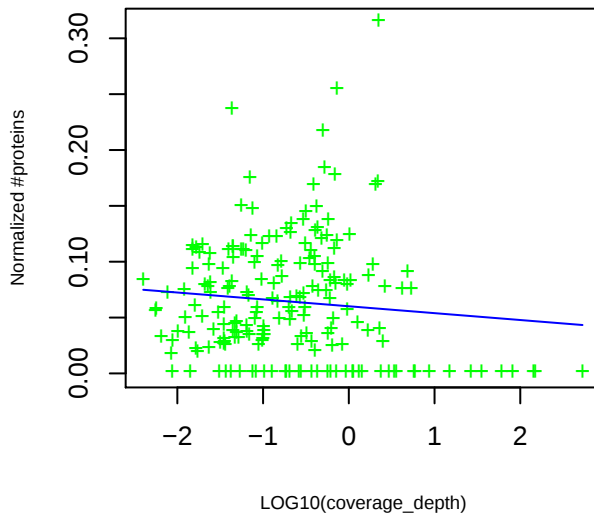
PF00724 Oxidored_FMN: oxidoreductase, FAD/FMN-binding

slope= -0.44 p_value= 0.010 intercept= 2.26 p_value= 3.5e-24



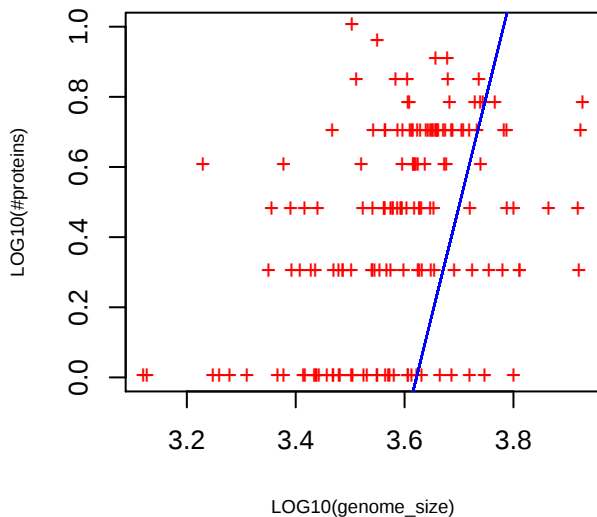
PF00724 Oxidored_FMN: oxidoreductase, FAD/FMN-binding

slope= -0.0062 p_value= 0.16 intercept= 0.06 p_value= 3.7e-26

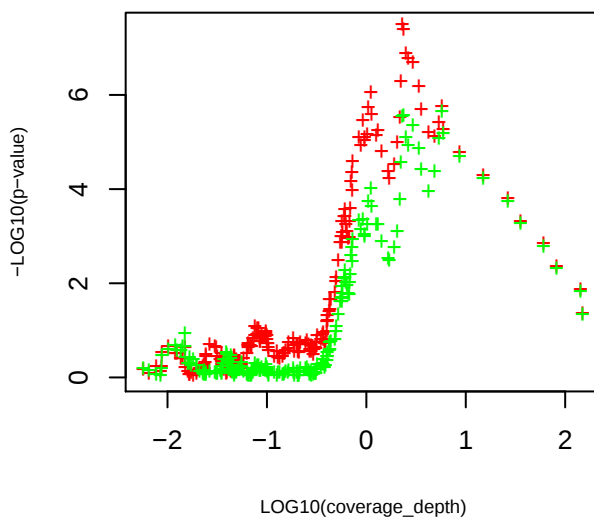


PF00724 Oxidored_FMN: oxidoreductase, FAD/FMN-binding

slope= 6.25 p_value= 4.8e-18 intercept= -22.63 p_value= 1.3e-18

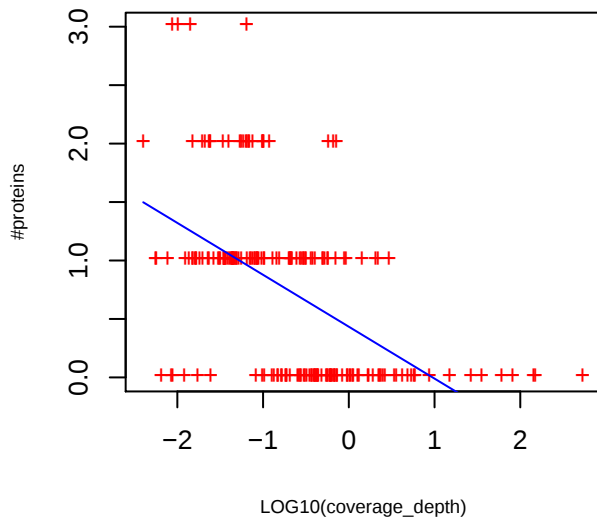


P-value curve : red (unnorm), green (norm)



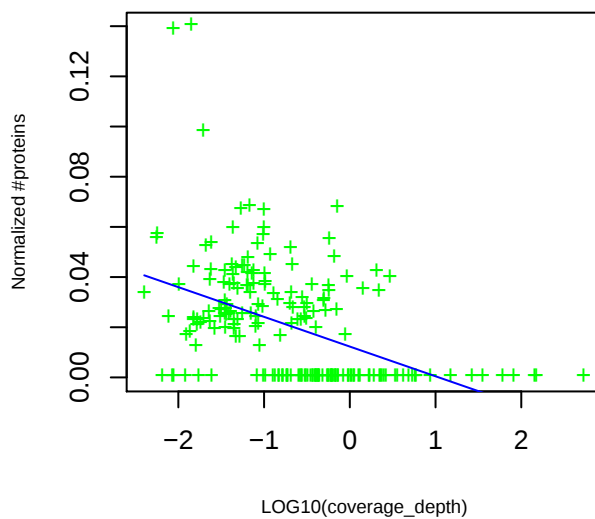
PF01957 NfeD: Nodulation efficiency protein D (NfeD)

slope= -0.44 p_value= 2.2e-15 intercept= 0.43 p_value= 2.7e-12



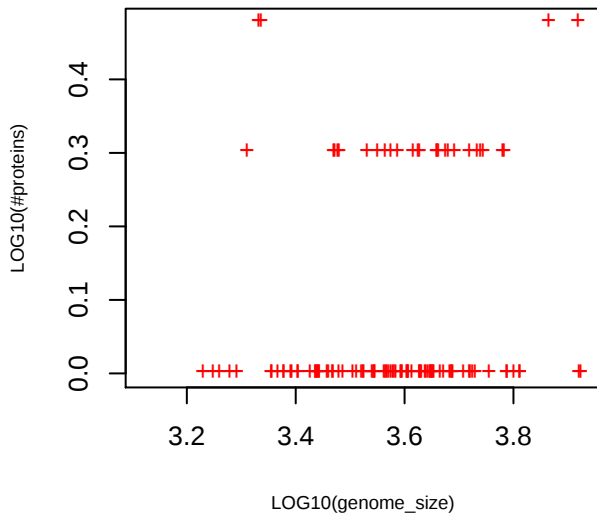
PF01957 NfeD: Nodulation efficiency protein D (NfeD)

slope= -0.012 p_value= 1.7e-11 intercept= 0.012 p_value= 4.3e-10

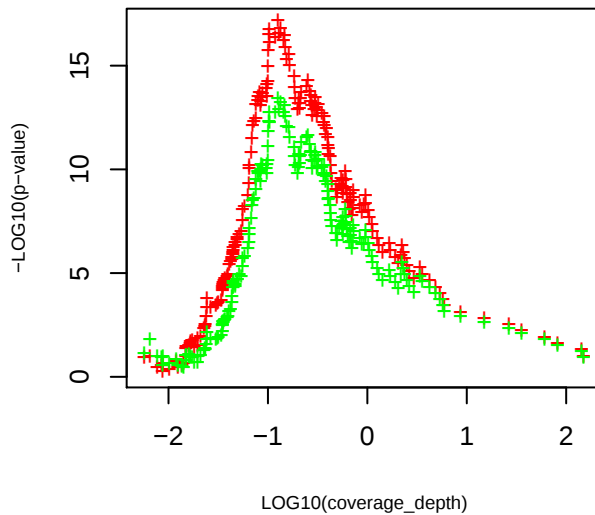


PF01957 NfeD: Nodulation efficiency protein D (NfeD)

slope= 2.90 p_value= 0.00098 intercept= -11.93 p_value= 0.00014

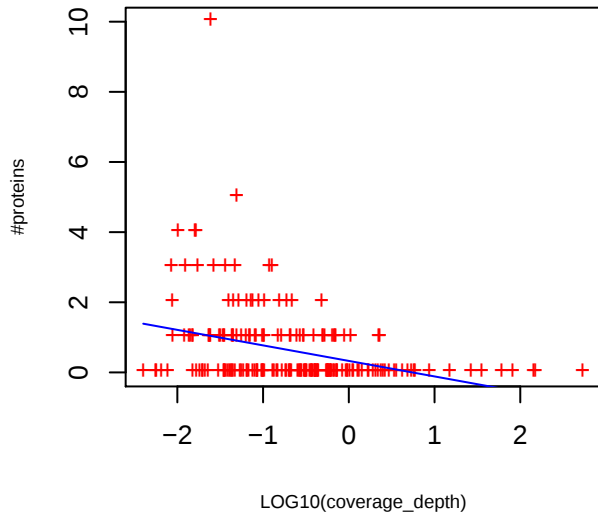


P-value curve ; red (unnorm), green (norm)



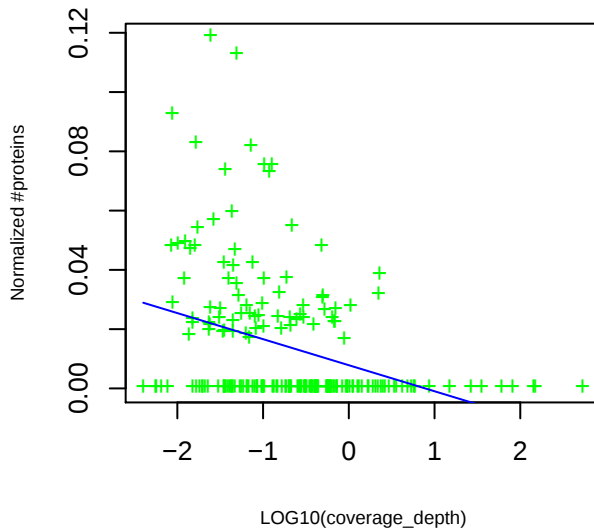
PF00481 PP2C: protein phosphatase 2C

slope= -0.44 p_value= 1.0e-06 intercept= 0.33 p_value= 0.0011



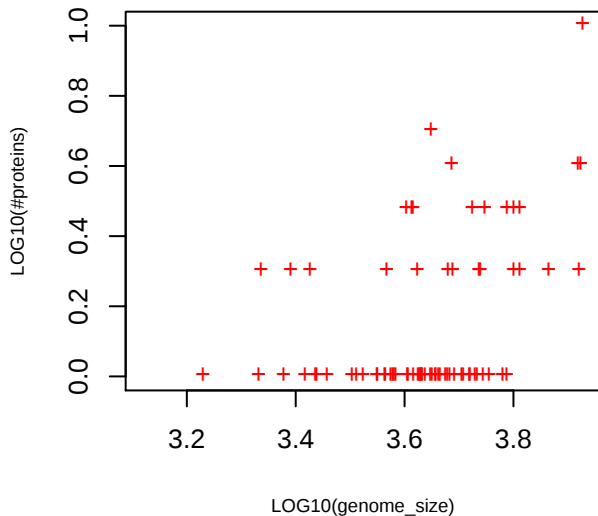
PF00481 PP2C: protein phosphatase 2C

slope= -0.0088 p_value= 4.9e-07 intercept= 0.0078 p_value= 6e-05

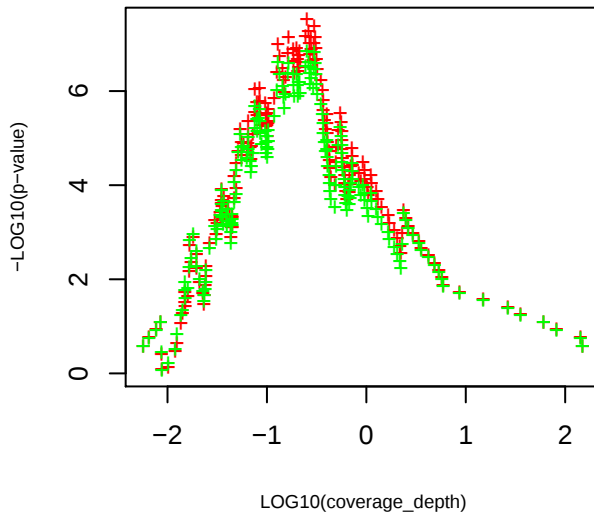


PF00481 PP2C: protein phosphatase 2C

slope= 5.84 p_value= 2.7e-12 intercept= -23.16 p_value= 1.3e-14

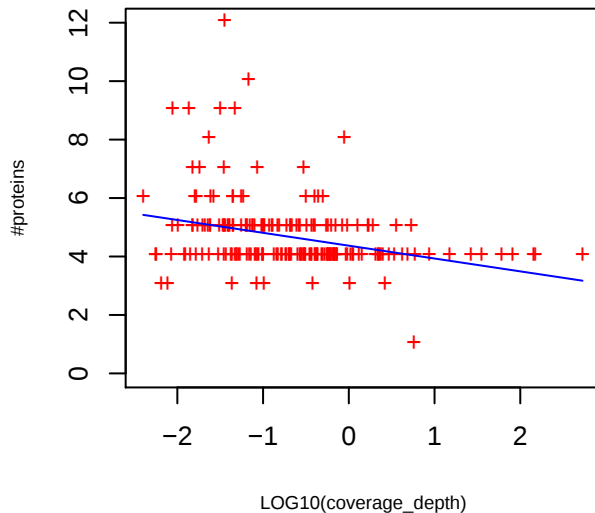


P-value curve ; red (unnorm), green (norm)



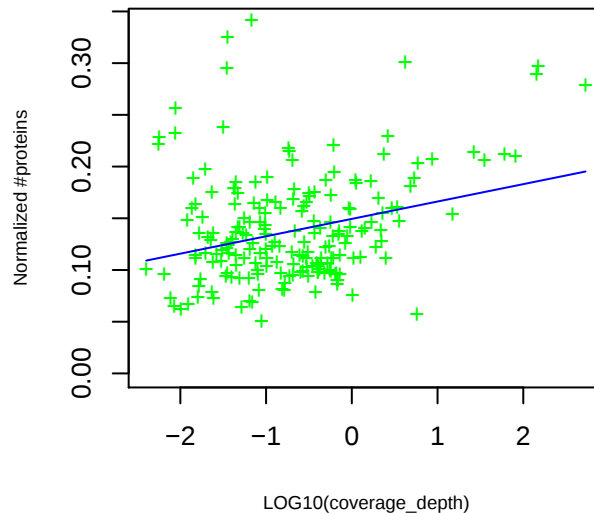
PF01751 Toprim: Toprim domain

slope= -0.44 p_value= 1e-05 intercept= 4.37 p_value= 7.5e-96



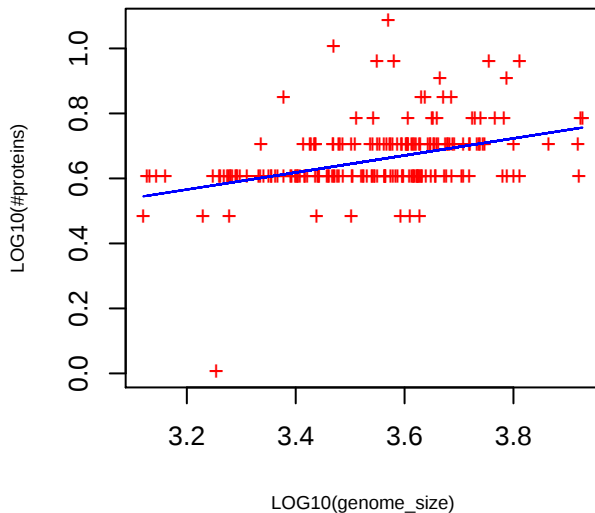
PF01751 Toprim: Toprim domain

slope= 0.017 p_value= 3.9e-05 intercept= 0.15 p_value= 5.1e-82

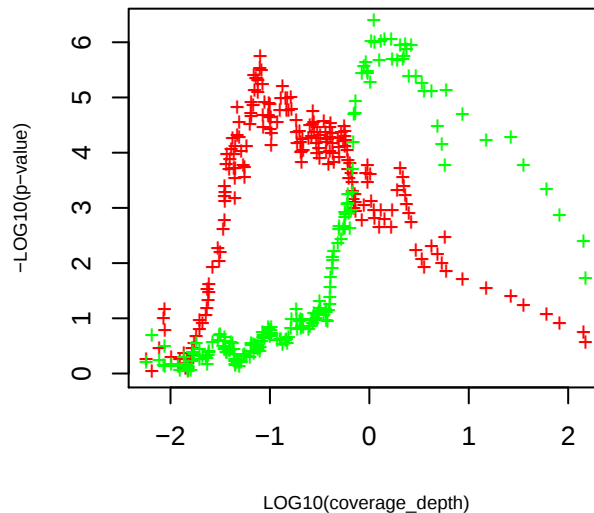


PF01751 Toprim: Toprim domain

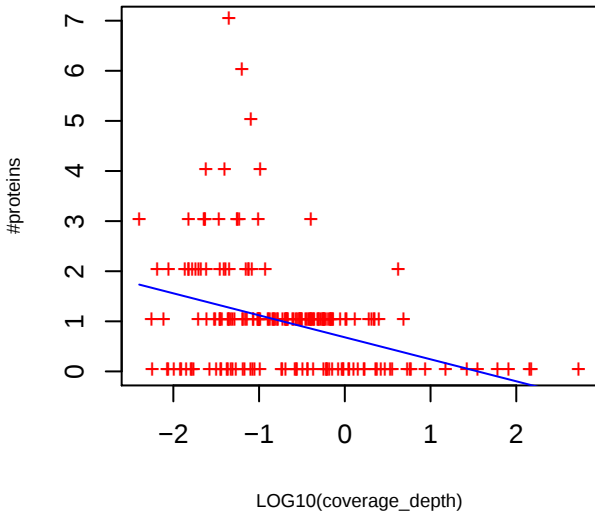
slope= 0.26 p_value= 5.7e-09 intercept= -0.27 p_value= 0.075



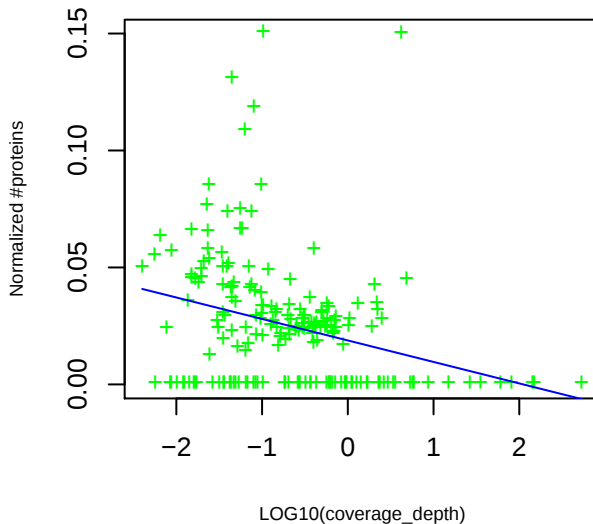
P-value curve ; red (unnorm), green (norm)



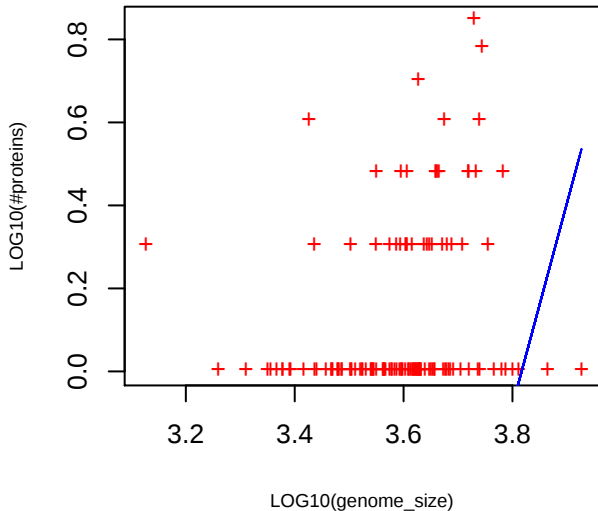
PF00381 PTS-HPr: PTS HPr component phosphorylation site
 slope= -0.44 p_value= 2.6e-07 intercept= 0.68 p_value= 5.9e-12



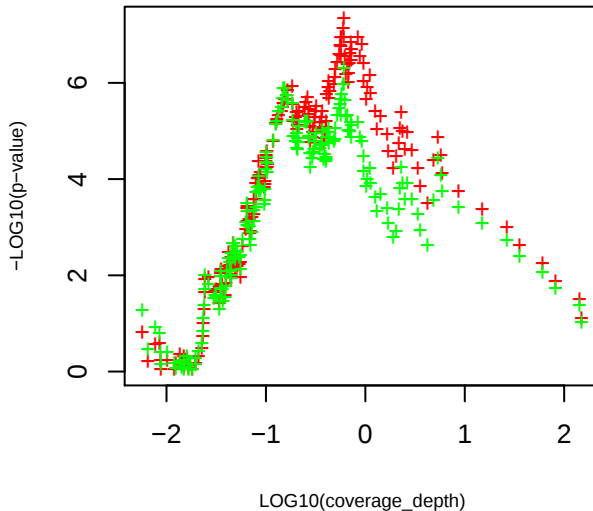
PF00381 PTS-HPr: PTS HPr component phosphorylation site
 slope= -0.0092 p_value= 1.5e-05 intercept= 0.019 p_value= 7.8e-14



PF00381 PTS-HPr: PTS HPr component phosphorylation site
 slope= 4.87 p_value= 5e-09 intercept= -18.59 p_value= 4.1e-10

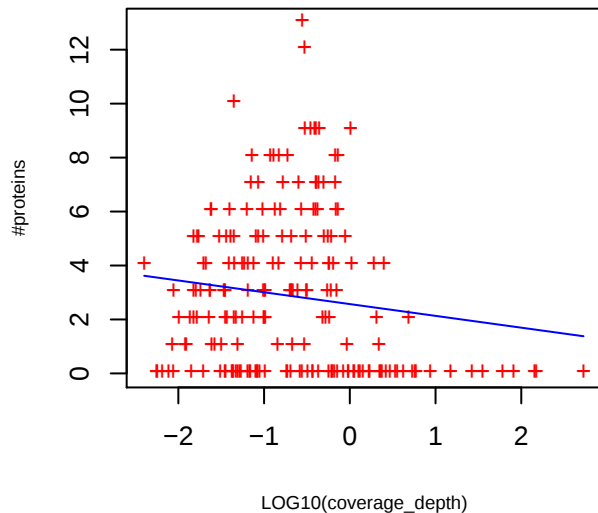


P-value curve ; red (unnorm), green (norm)



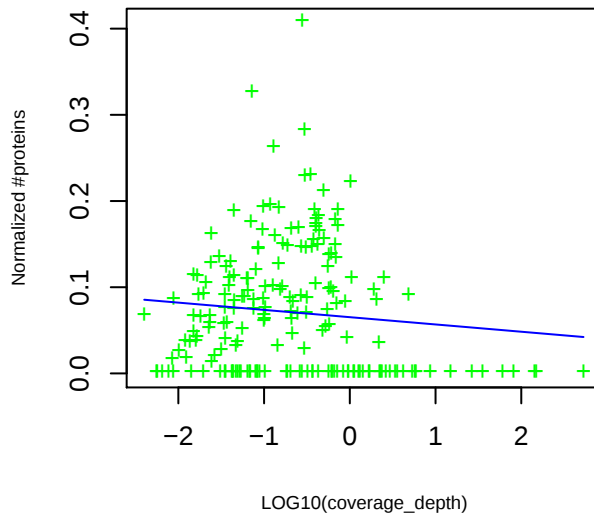
PF09278 MerR-DNA-bind: MerR, DNA binding

slope= -0.44 p_value= 0.059 intercept= 2.57 p_value= 6.5e-19



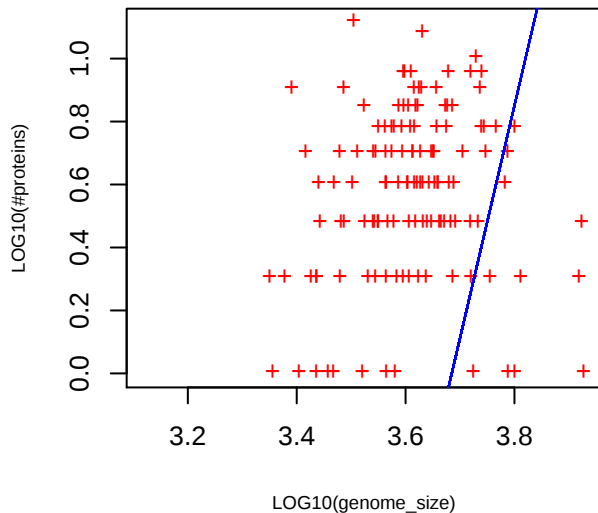
PF09278 MerR-DNA-bind: MerR, DNA binding

slope= -0.0084 p_value= 0.15 intercept= 0.065 p_value= 8e-19

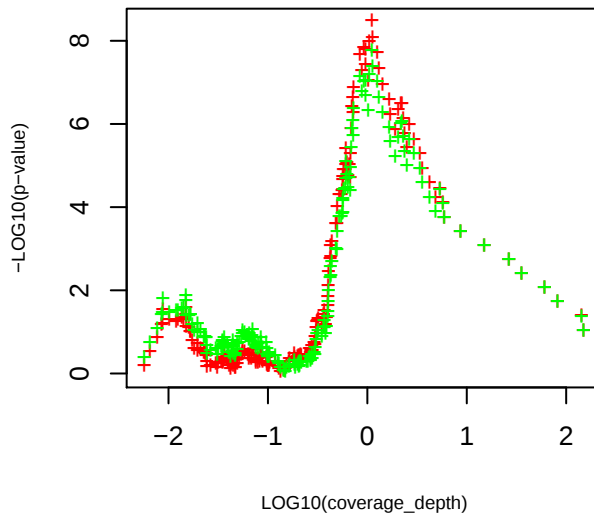


PF09278 MerR-DNA-bind: MerR, DNA binding

slope= 7.39 p_value= 7.6e-17 intercept= -27.21 p_value= 7.8e-18

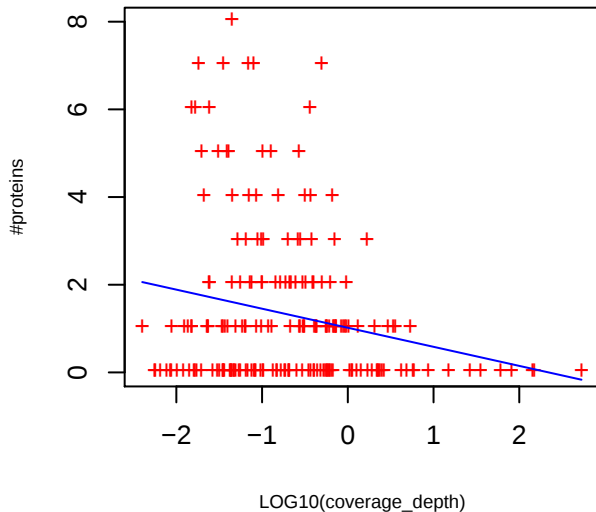


P-value curve ; red (unnorm), green (norm)



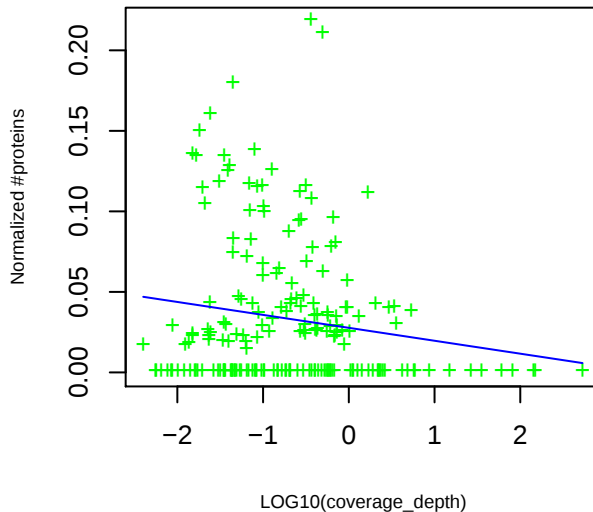
PF03929 PepSY_TM: PepSY-associated TM helix

slope= -0.43 p_value= 0.0025 intercept= 1.02 p_value= 1.5e-09



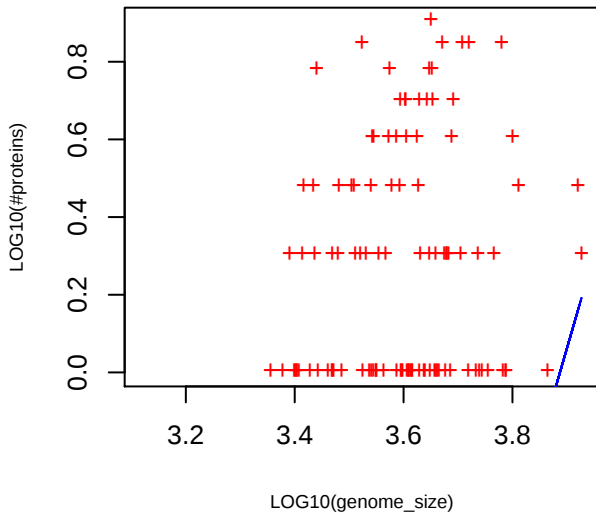
PF03929 PepSY_TM: PepSY-associated TM helix

slope= -0.008 p_value= 0.025 intercept= 0.028 p_value= 7.4e-11

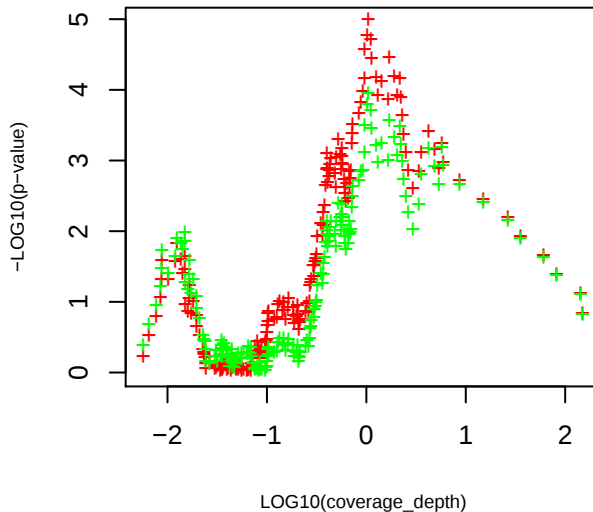


PF03929 PepSY_TM: PepSY-associated TM helix

slope= 4.85 p_value= 9.9e-08 intercept= -18.84 p_value= 6.8e-09

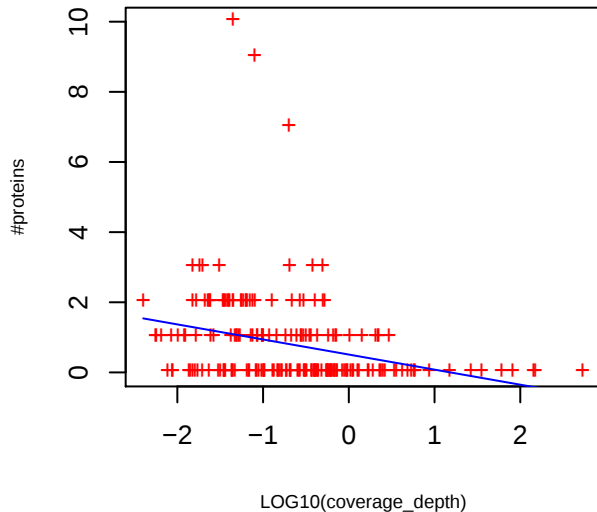


P-value curve ; red (unnorm), green (norm)



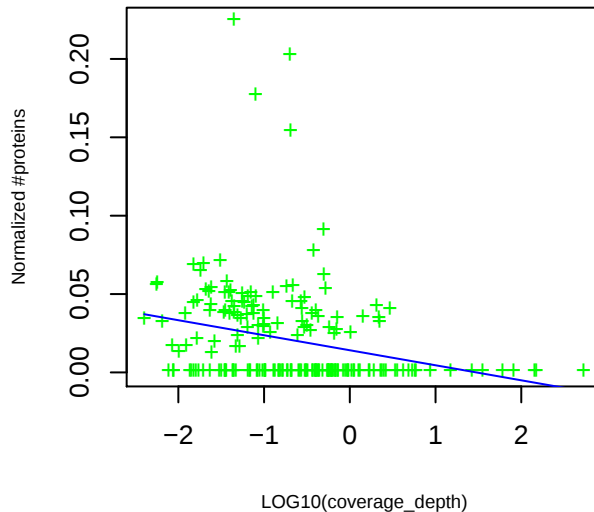
PF07660 STN: Secretin and TonB N terminus short domain

slope= -0.43 p_value= 3.4e-05 intercept= 0.51 p_value= 1.4e-05



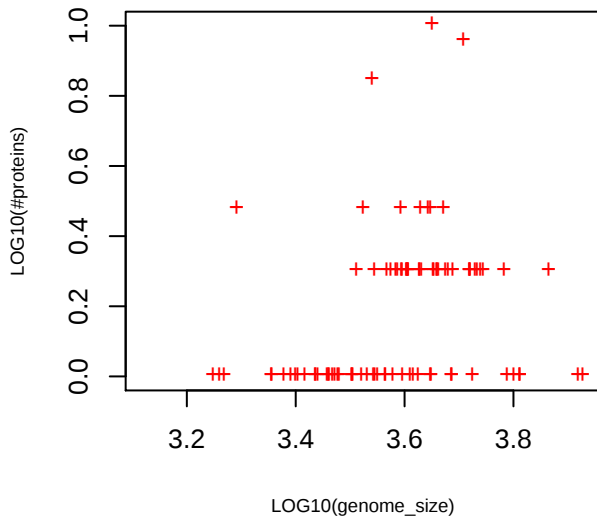
PF07660 STN: Secretin and TonB N terminus short domain

slope= -0.0096 p_value= 2e-04 intercept= 0.014 p_value= 1.6e-06

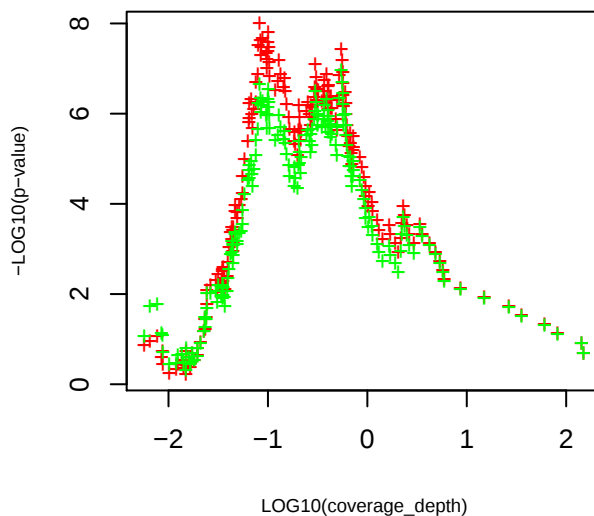


PF07660 STN: Secretin and TonB N terminus short domain

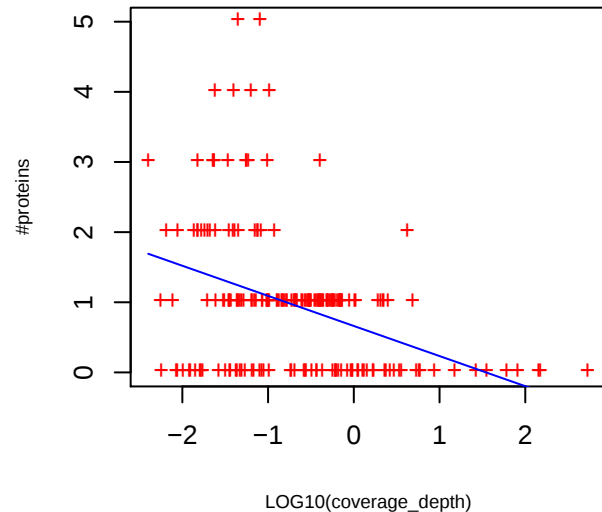
slope= 3.16 p_value= 0.00048 intercept= -13.32 p_value= 3.8e-05



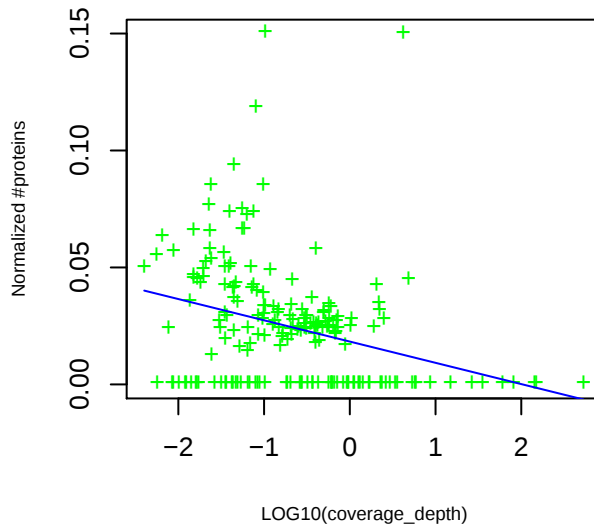
P-value curve ; red (unnorm), green (norm)



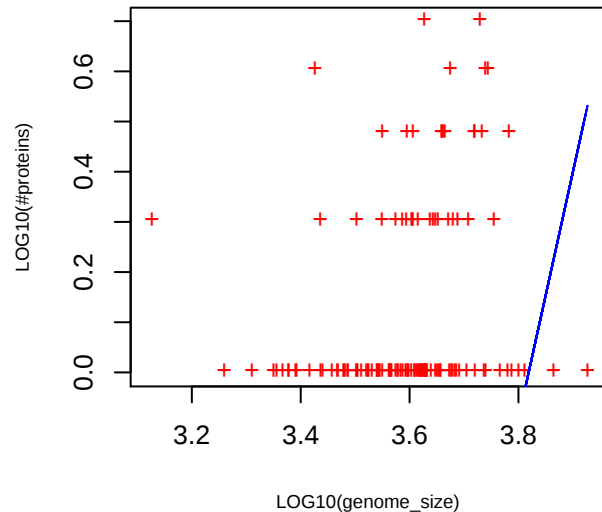
TIGR01003 PTS_HPr_family: phosphocarrier, HPr family
 slope= -0.43 p_value= 4.2e-08 intercept= 0.66 p_value= 3.7e-13



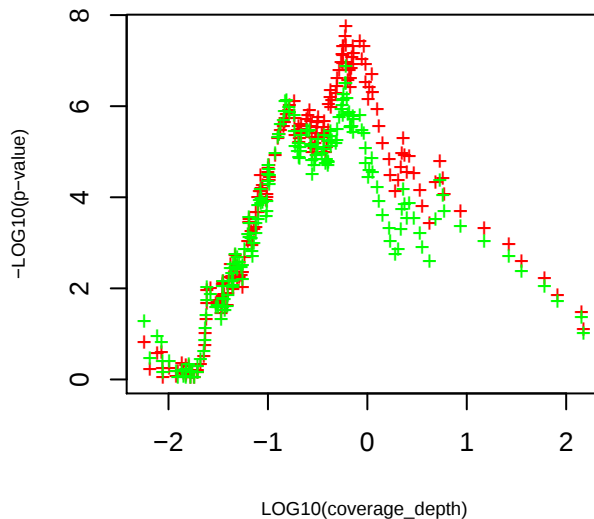
TIGR01003 PTS_HPr_family: phosphocarrier, HPr family
 slope= -0.009 p_value= 8.2e-06 intercept= 0.018 p_value= 3.5e-14



TIGR01003 PTS_HPr_family: phosphocarrier, HPr family
 slope= 4.92 p_value= 3.8e-09 intercept= -18.78 p_value= 3e-10

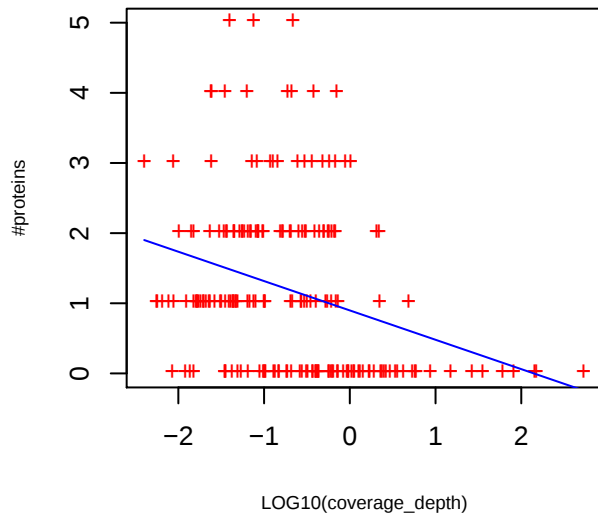


P-value curve ; red (unnorm), green (norm)



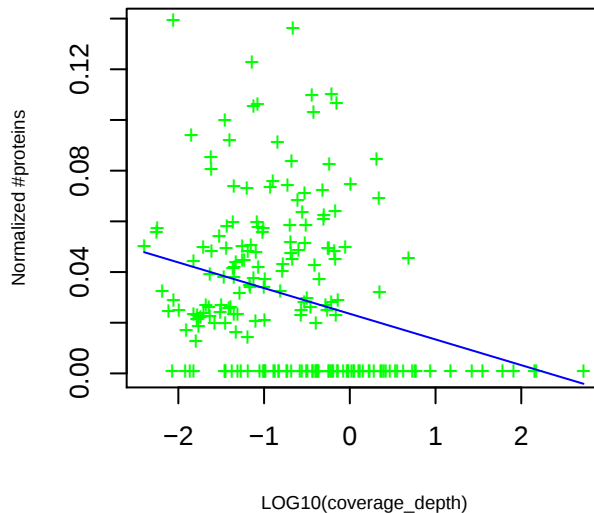
PF04324 Fer2_BFD: BFD-like [2Fe-2S] binding domain

slope= -0.42 p_value= 1.4e-05 intercept= 0.90 p_value= 5.4e-15



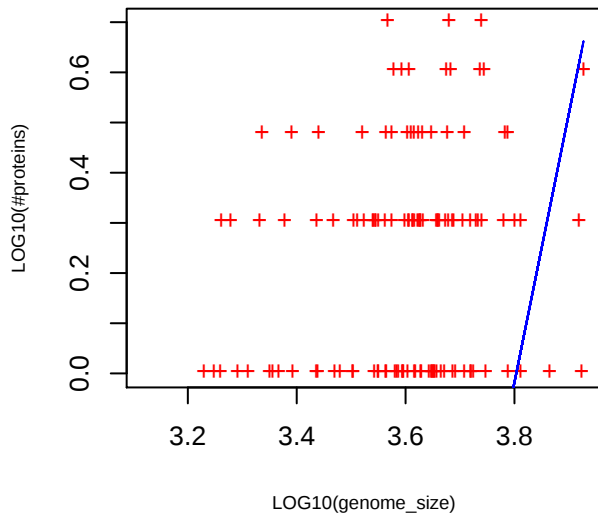
PF04324 Fer2_BFD: BFD-like [2Fe-2S] binding domain

slope= -0.010 p_value= 6.3e-05 intercept= 0.024 p_value= 8.4e-15

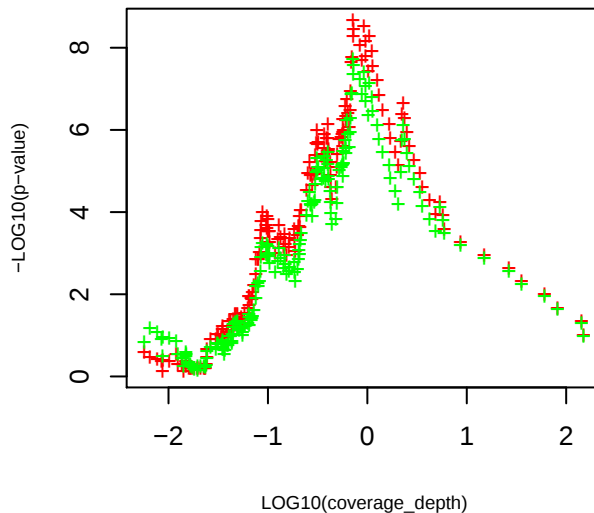


PF04324 Fer2_BFD: BFD-like [2Fe-2S] binding domain

slope= 5.36 p_value= 6e-10 intercept= -20.37 p_value= 4.5e-11

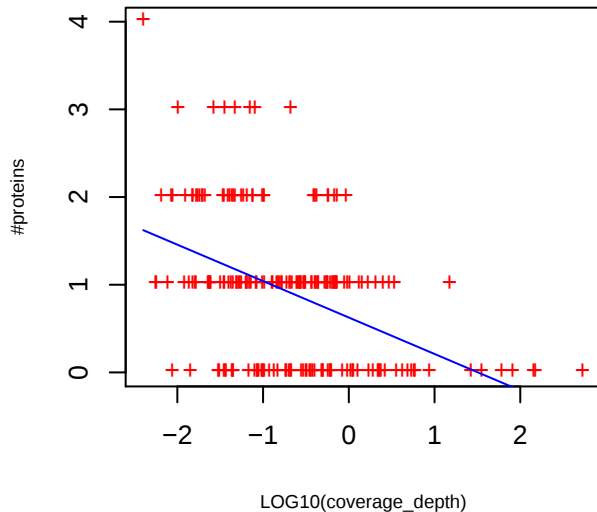


P-value curve ; red (unnorm), green (norm)



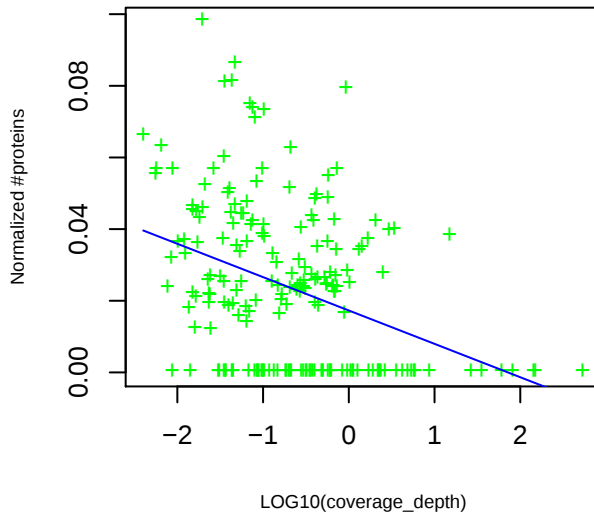
PF03773 DUF318: Predicted permease

slope= -0.42 p_value= 9.4e-11 intercept= 0.63 p_value= 8.2e-17



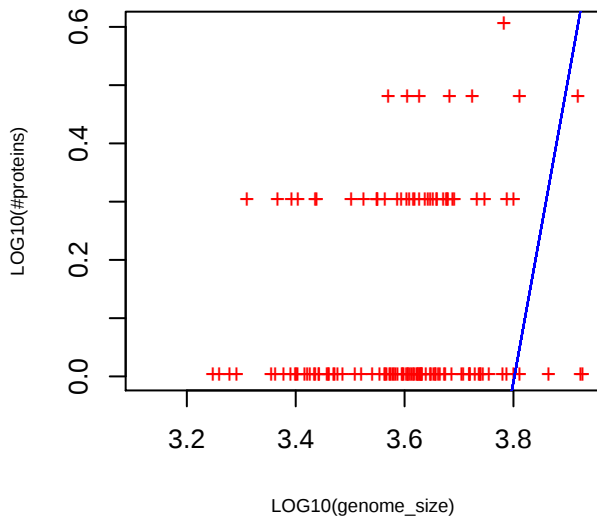
PF03773 DUF318: Predicted permease

slope= -0.0093 p_value= 7.2e-08 intercept= 0.017 p_value= 5.5e-17

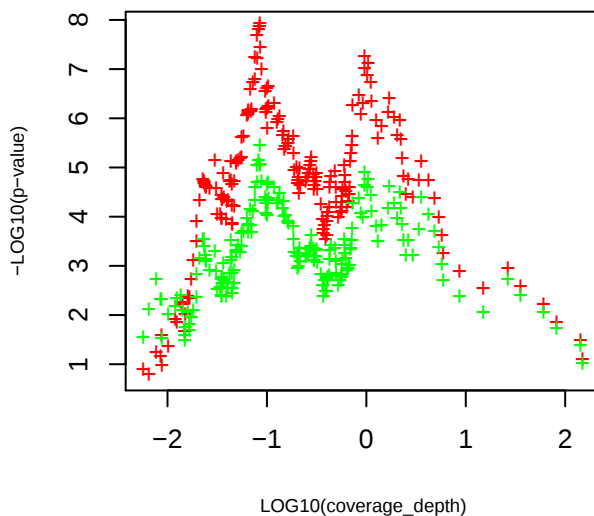


PF03773 DUF318: Predicted permease

slope= 5.17 p_value= 3.6e-10 intercept= -19.67 p_value= 2.5e-11

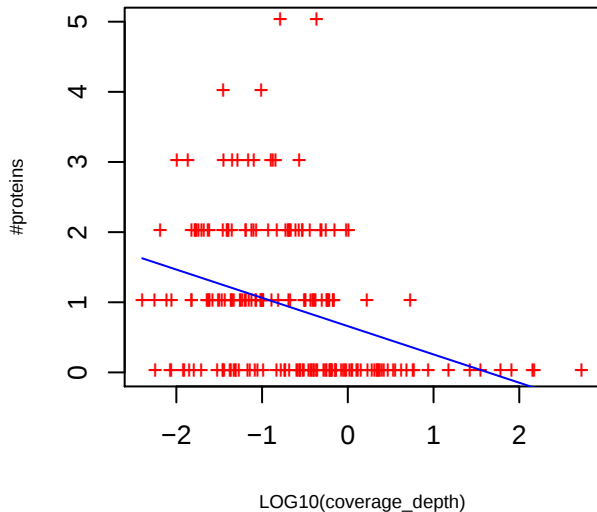


P-value curve ; red (unnorm), green (norm)



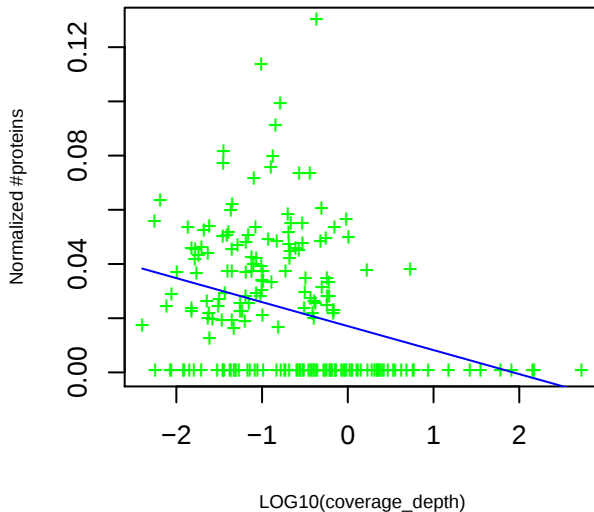
PF03705 CheR_N: CheR methyltransferase, all-alpha domain

slope= -0.40 p_value= 8.3e-07 intercept= 0.66 p_value= 4.5e-12



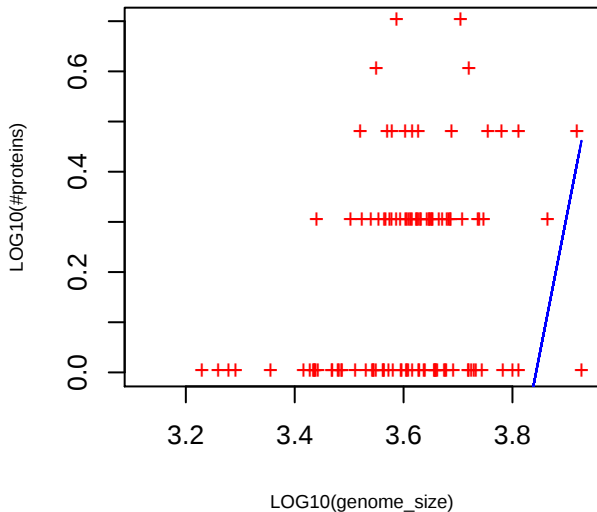
PF03705 CheR_N: CheR methyltransferase, all-alpha domain

slope= -0.0089 p_value= 9.5e-06 intercept= 0.017 p_value= 4.3e-13

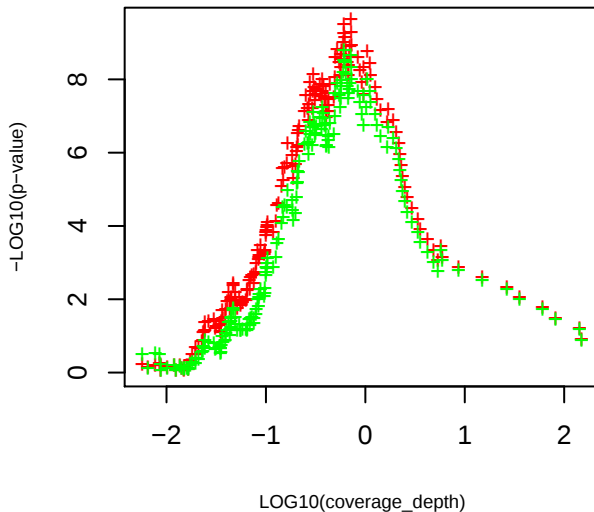


PF03705 CheR_N: CheR methyltransferase, all-alpha domain

slope= 5.53 p_value= 2.0e-10 intercept= -21.25 p_value= 8.5e-12

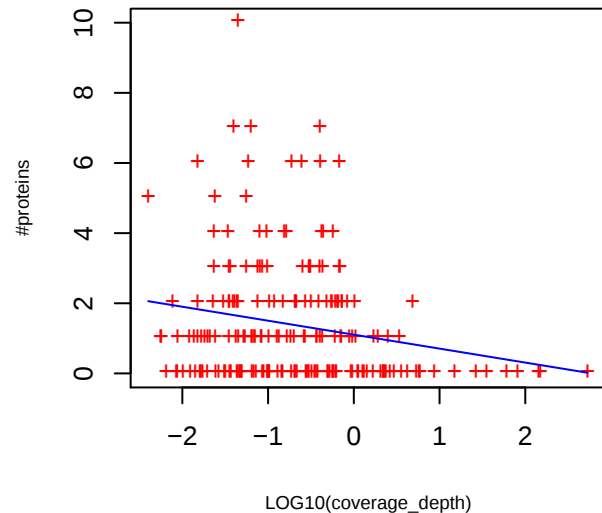


P-value curve : red (unnorm), green (norm)



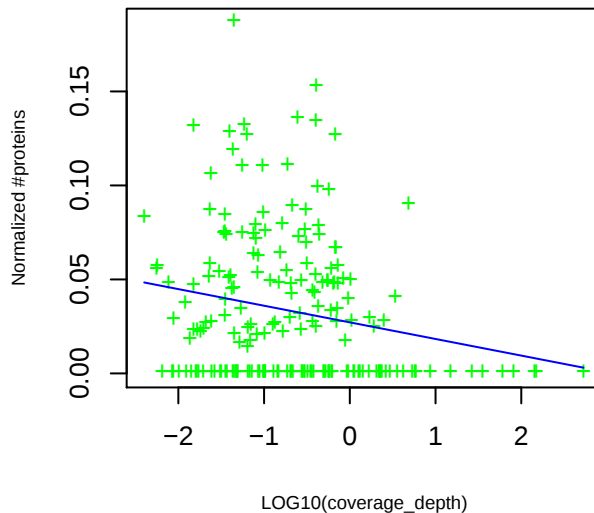
PF00455 DeoR: transcriptional regulator, DeoR family

slope= -0.40 p_value= 0.0047 intercept= 1.11 p_value= 3.5e-11



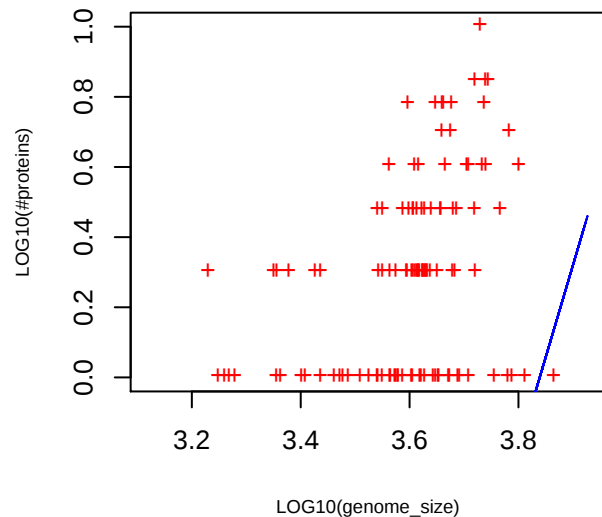
PF00455 DeoR: transcriptional regulator, DeoR family

slope= -0.0088 p_value= 0.0041 intercept= 0.027 p_value= 1.9e-13

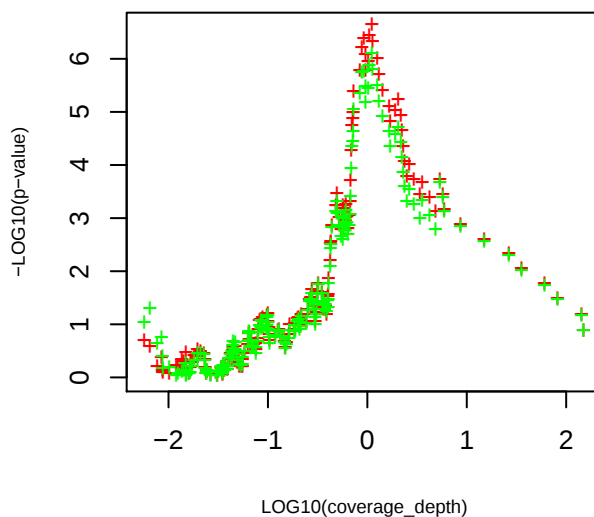


PF00455 DeoR: transcriptional regulator, DeoR family

slope= 5.24 p_value= 5.8e-09 intercept= -20.12 p_value= 4e-10

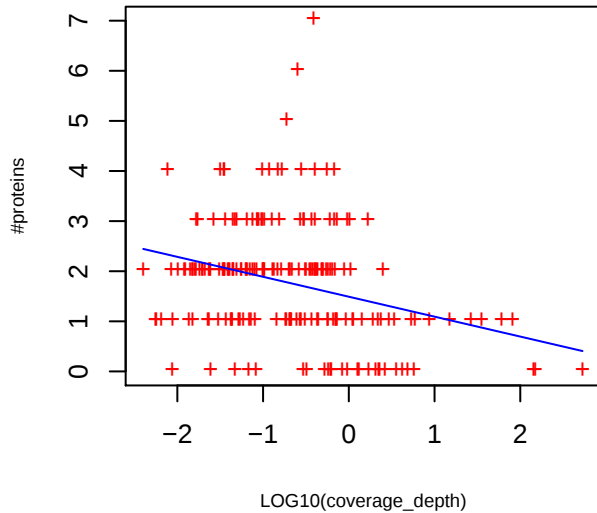


P-value curve ; red (unnorm), green (norm)



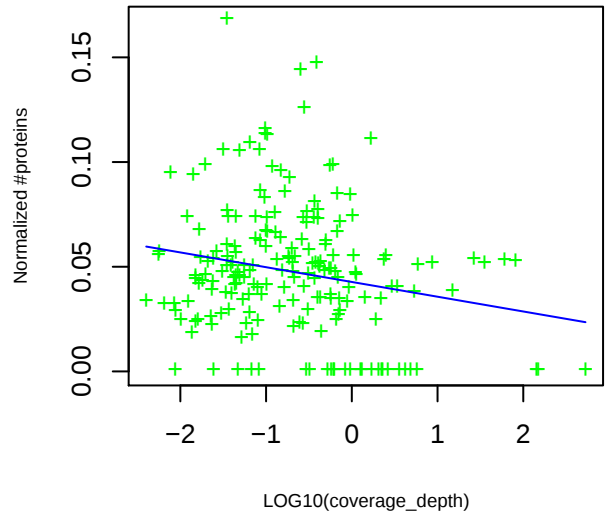
TIGR01511 ATPase-IB1_Cu: copper-translocating P-type ATPase

slope= -0.40 p_value= 2.1e-05 intercept= 1.49 p_value= 1e-32



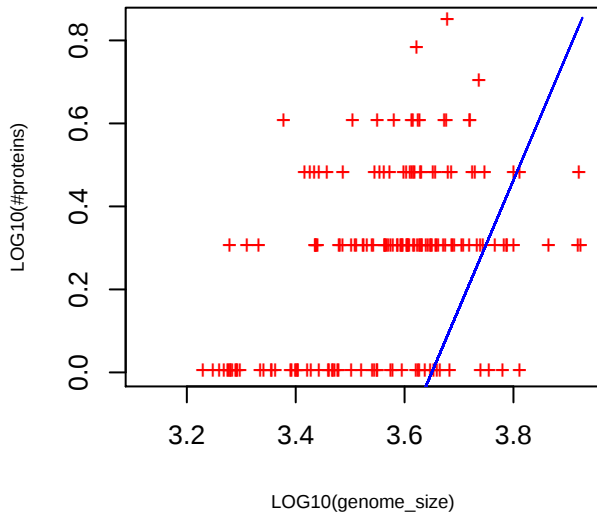
TIGR01511 ATPase-IB1_Cu: copper-translocating P-type ATPase

slope= -0.007 p_value= 0.0043 intercept= 0.043 p_value= 8.2e-36

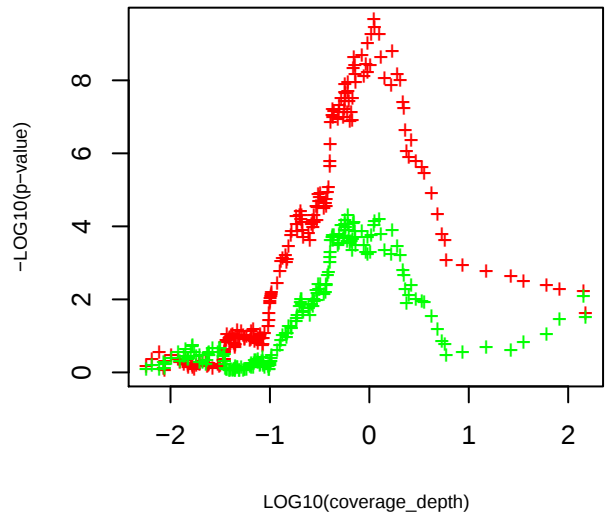


TIGR01511 ATPase-IB1_Cu: copper-translocating P-type ATPase

slope= 3.09 p_value= 1.0e-06 intercept= -11.27 p_value= 5.3e-07

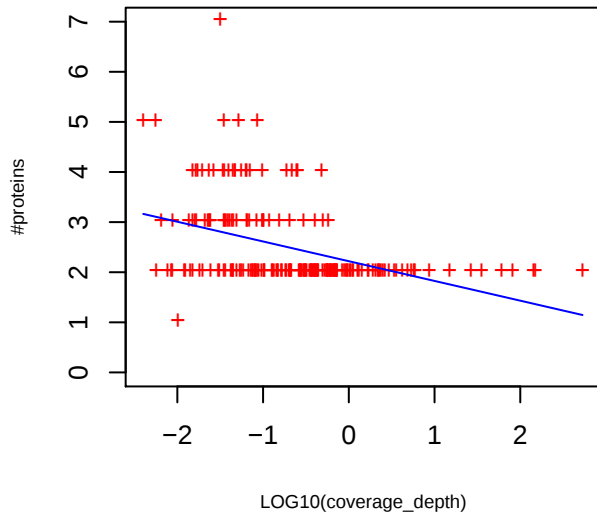


P-value curve ; red (unnorm), green (norm)



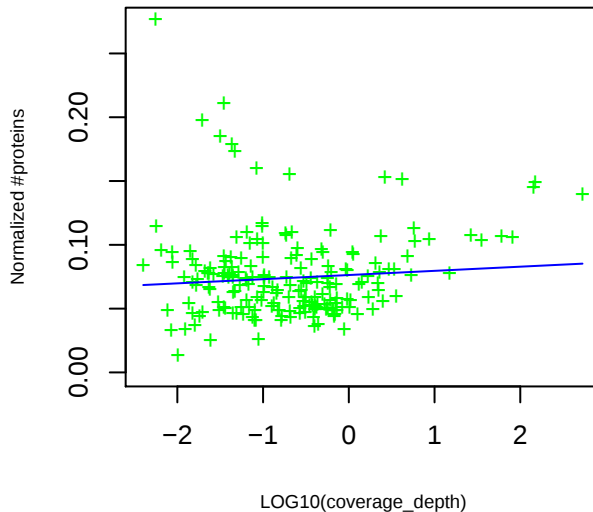
PF02874 ATP-synt_ab_N: ATP synthase alpha/beta family, beta-barrel domain

slope= -0.39 p_value= 2.4e-09 intercept= 2.22 p_value= 7.2e-78



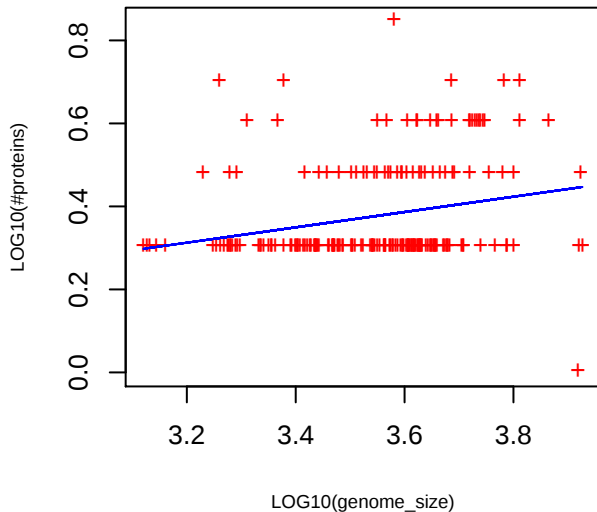
PF02874 ATP-synt_ab_N: ATP synthase alpha/beta family, beta-barrel domain

slope= 0.0033 p_value= 0.24 intercept= 0.076 p_value= 4.1e-61

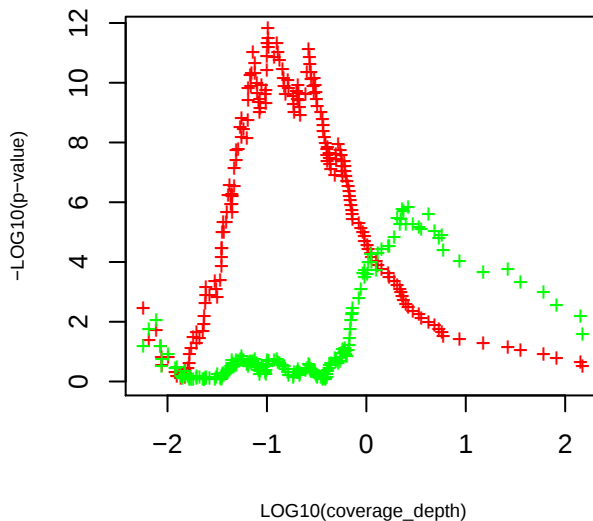


PF02874 ATP-synt_ab_N: ATP synthase alpha/beta family, beta-barrel domain

slope= 0.18 p_value= 0.00072 intercept= -0.28 p_value= 0.15

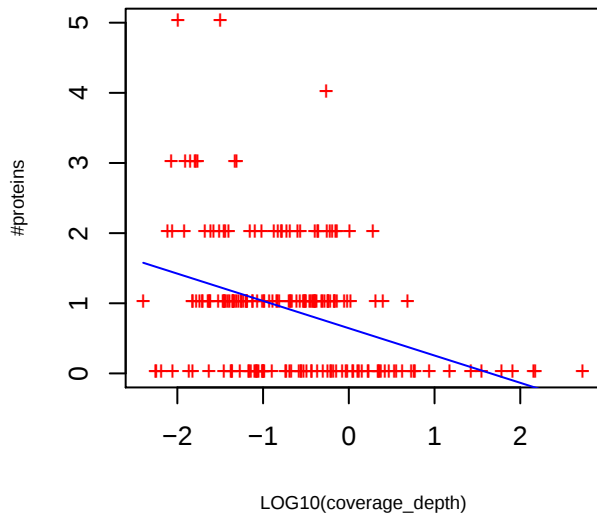


P-value curve ; red (unnorm), green (norm)



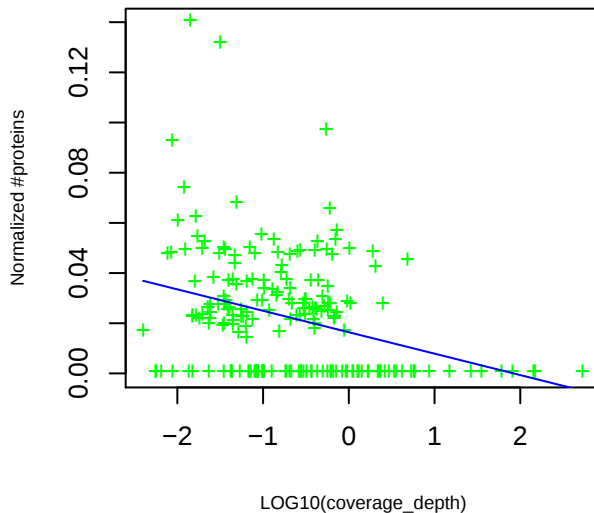
PF01936 DUF88: Protein of unknown function

slope= -0.39 p_value= 1.3e-07 intercept= 0.64 p_value= 8.3e-14



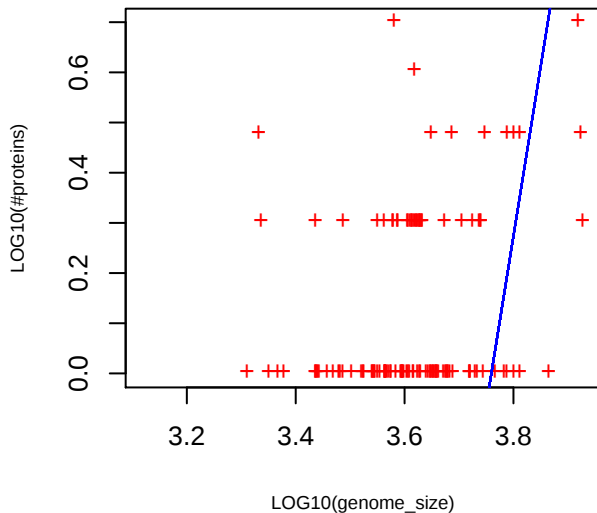
PF01936 DUF88: Protein of unknown function

slope= -0.0085 p_value= 3.1e-06 intercept= 0.016 p_value= 3.6e-14

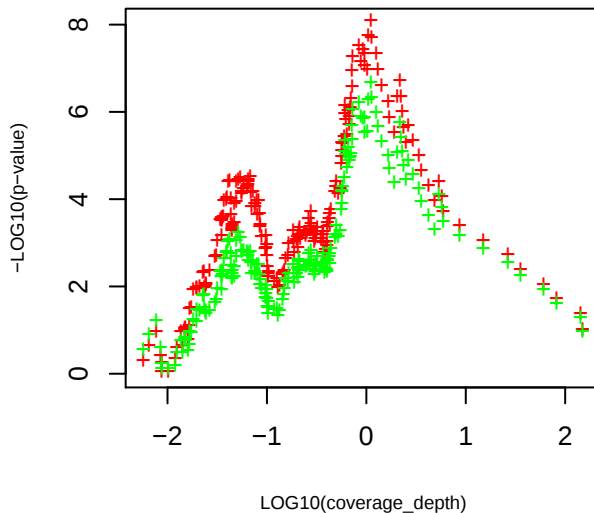


PF01936 DUF88: Protein of unknown function

slope= 6.75 p_value= 9.3e-17 intercept= -25.38 p_value= 2.7e-18

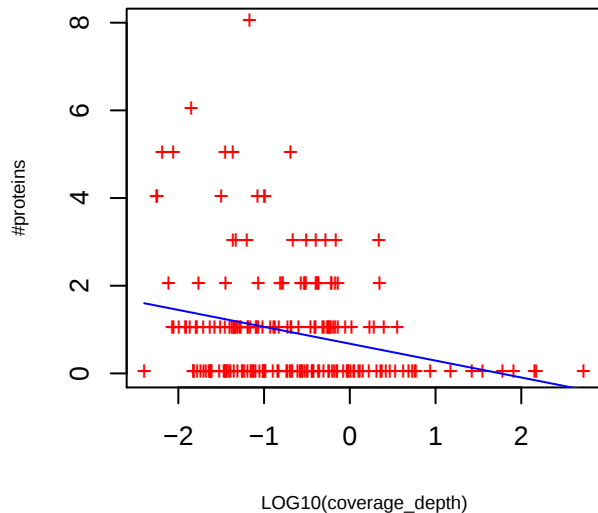


P-value curve ; red (unnorm), green (norm)



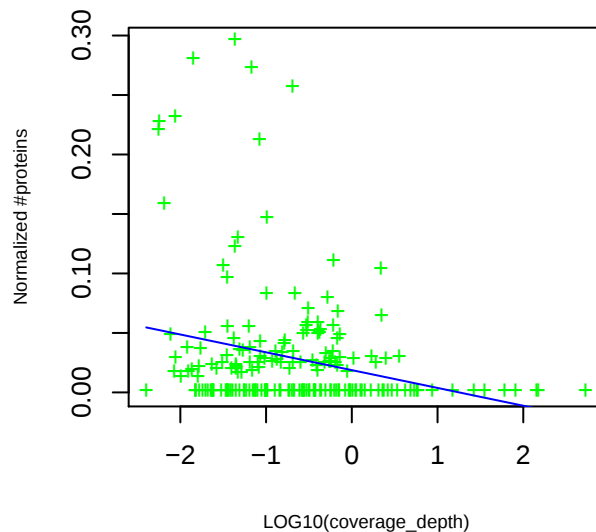
PF01558 POR: 2-oxoacid:ferredoxin/flavodoxin oxidoreductases, gamma subunit

slope= -0.39 p_value= 0.00033 intercept= 0.68 p_value= 4.5e-08



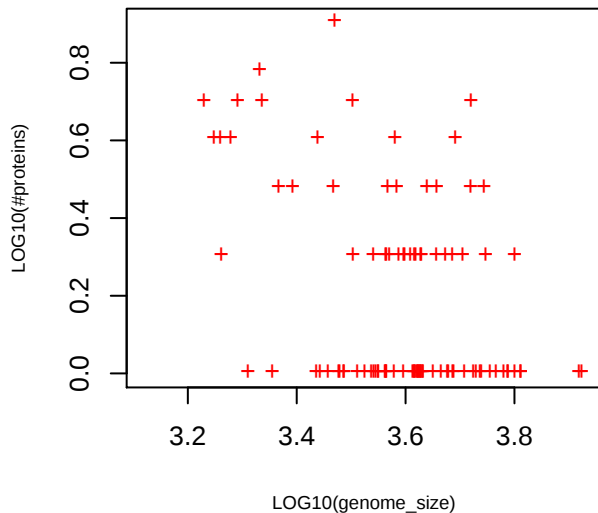
PF01558 POR: 2-oxoacid:ferredoxin/flavodoxin oxidoreductases, gamma subunit

slope= -0.015 p_value= 0.00044 intercept= 0.019 p_value= 0.00010

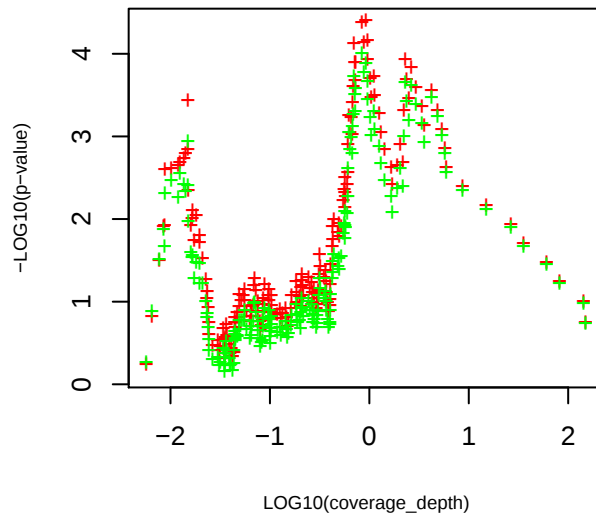


PF01558 POR: 2-oxoacid:ferredoxin/flavodoxin oxidoreductases, gamma subunit

slope= 3.15 p_value= 0.00058 intercept= -13.06 p_value= 6.2e-05

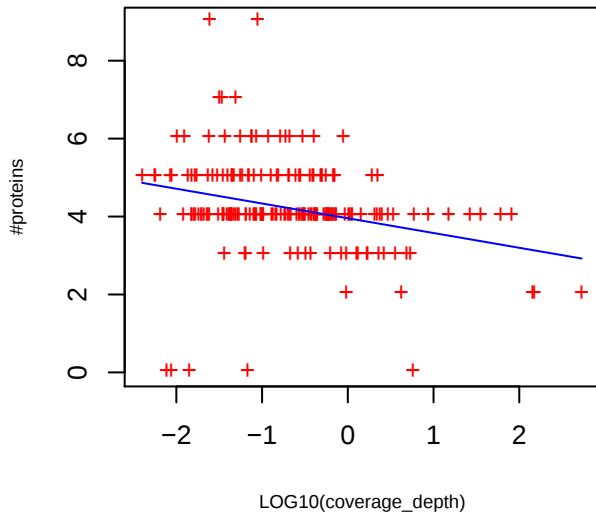


P-value curve : red (unnorm), green (norm)



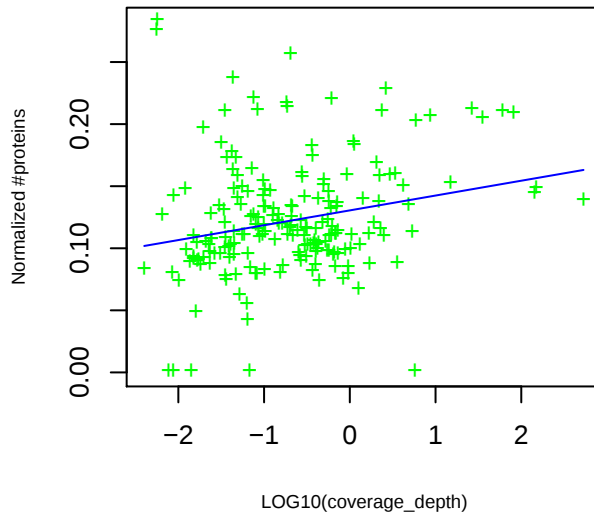
PF07724 AAA_2: ATPase family associated with various cellular activities (AAA)

slope= -0.38 p_value= 7.8e-05 intercept= 3.96 p_value= 8.9e-91



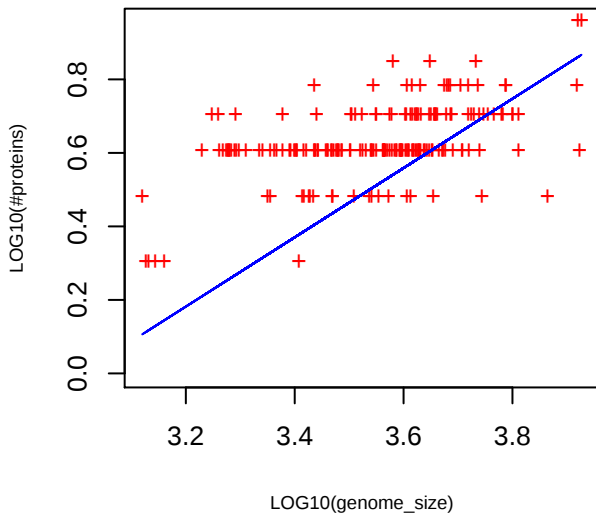
PF07724 AAA_2: ATPase family associated with various cellular activities (AAA)

slope= 0.012 p_value= 0.0011 intercept= 0.13 p_value= 1.8e-79

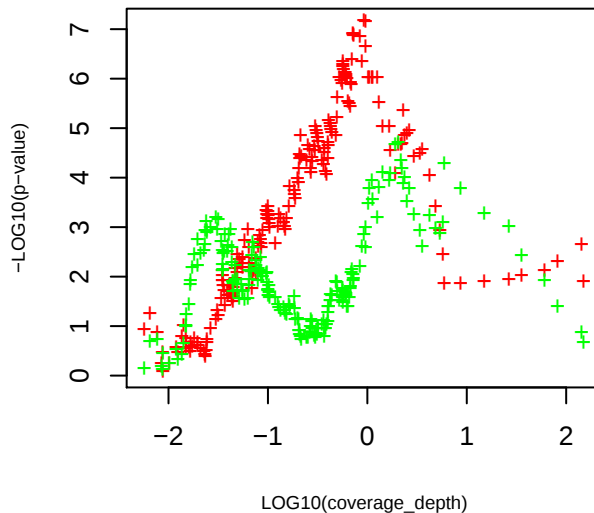


PF07724 AAA_2: ATPase family associated with various cellular activities (AAA)

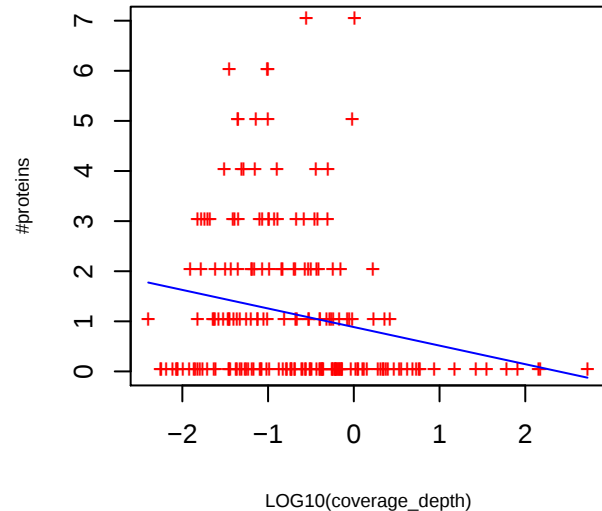
slope= 0.94 p_value= 0.0032 intercept= -2.83 p_value= 0.012



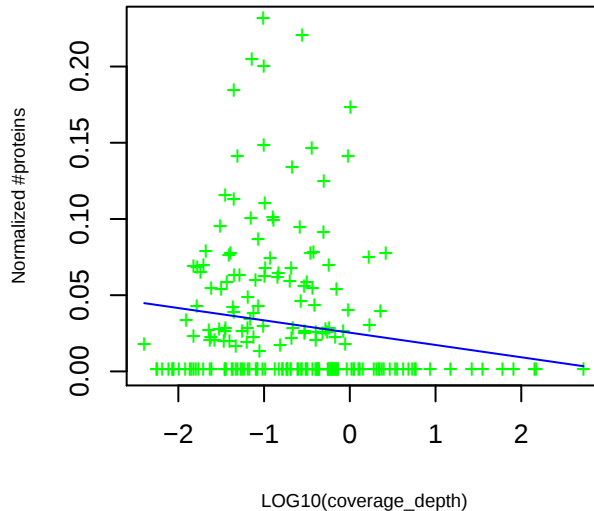
P-value curve ; red (unnorm), green (norm)



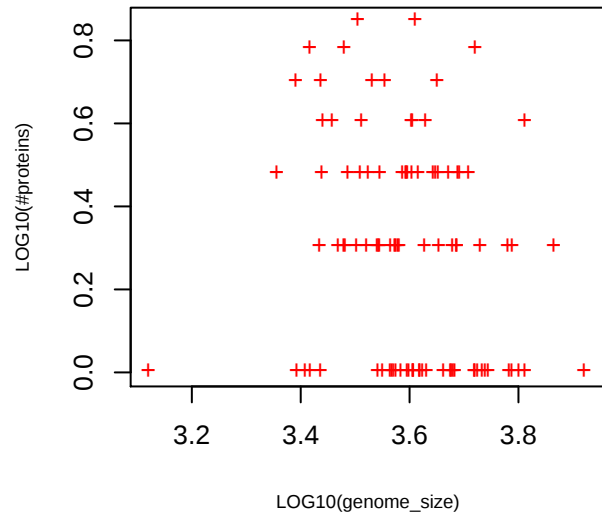
TIGR00914 2A0601: heavy metal efflux pump, CzcA family
 slope= -0.37 p_value= 0.003 intercept= 0.89 p_value= 1.4e-09



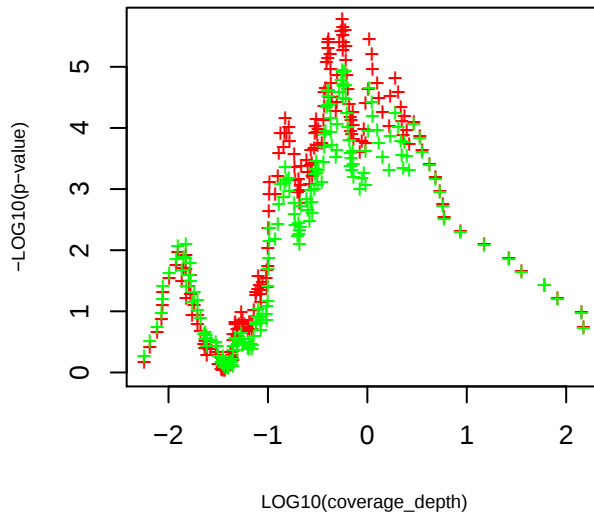
TIGR00914 2A0601: heavy metal efflux pump, CzcA family
 slope= -0.008 p_value= 0.03 intercept= 0.025 p_value= 6e-09



TIGR00914 2A0601: heavy metal efflux pump, CzcA family
 slope= 4.07 p_value= 1.1e-05 intercept= -16.35 p_value= 7.6e-07

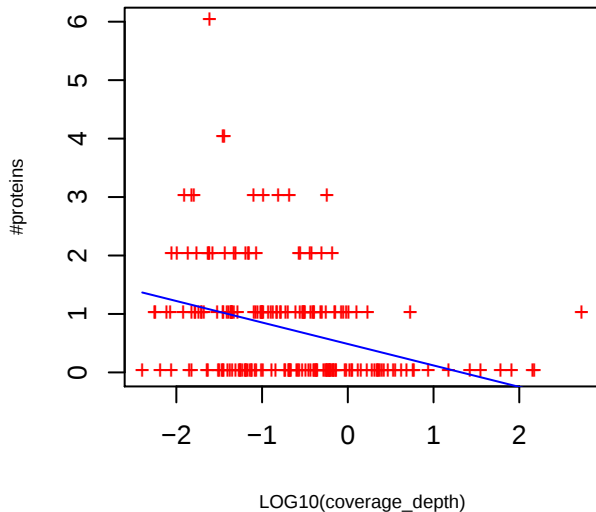


P-value curve ; red (unnorm), green (norm)



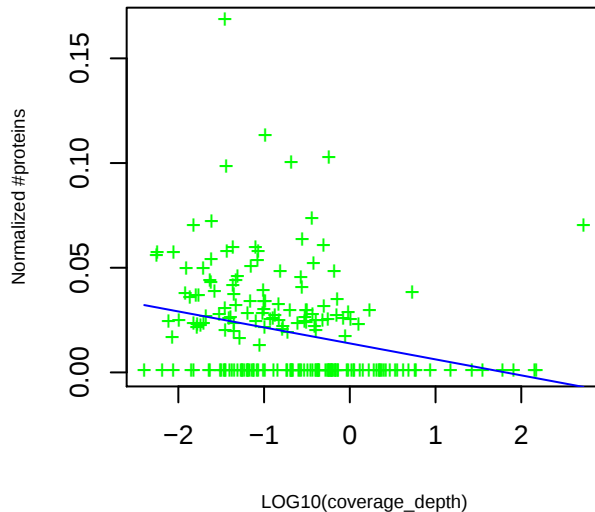
PF00781 DAGK_cat: Diacylglycerol kinase catalytic domain (presumed)

slope= -0.37 p_value= 9.3e-07 intercept= 0.49 p_value= 1.2e-08



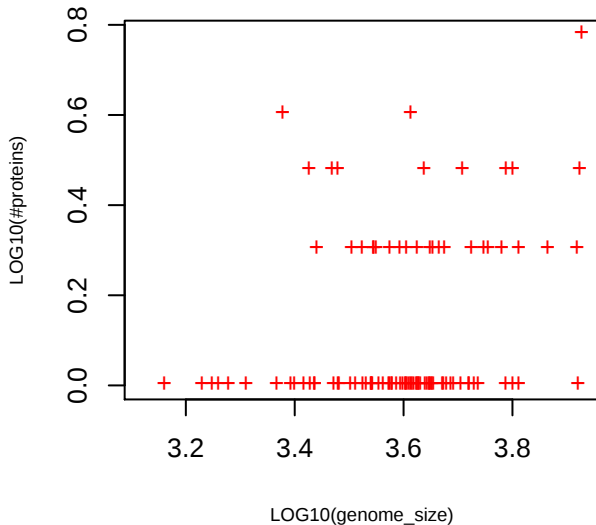
PF00781 DAGK_cat: Diacylglycerol kinase catalytic domain (presumed)

slope= -0.0076 p_value= 0.00014 intercept= 0.014 p_value= 2.7e-09

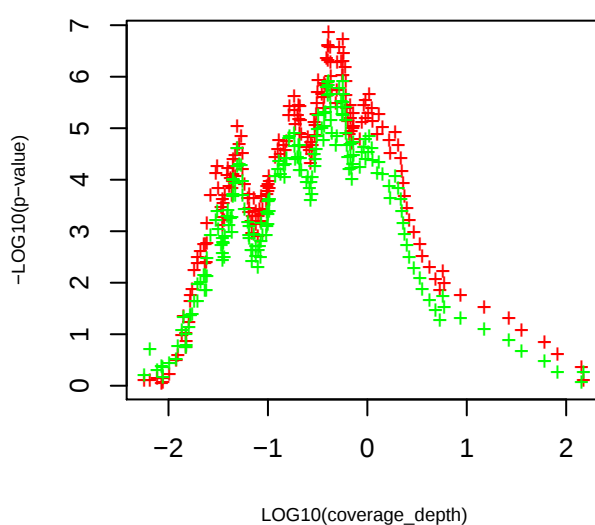


PF00781 DAGK_cat: Diacylglycerol kinase catalytic domain (presumed)

slope= 4.06 p_value= 4.8e-06 intercept= -16.33 p_value= 2.6e-07

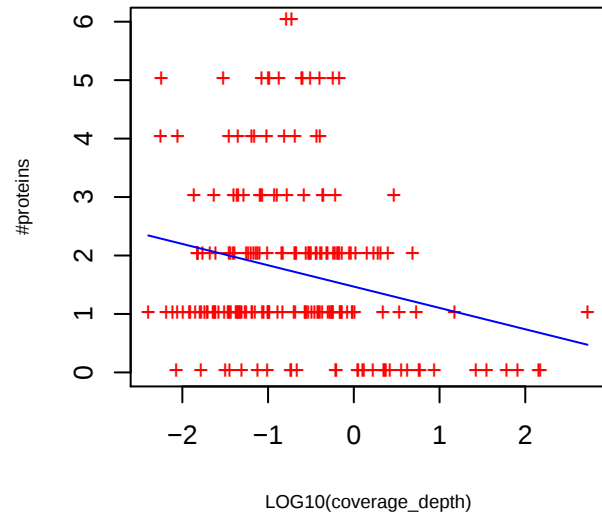


P-value curve ; red (unnorm), green (norm)



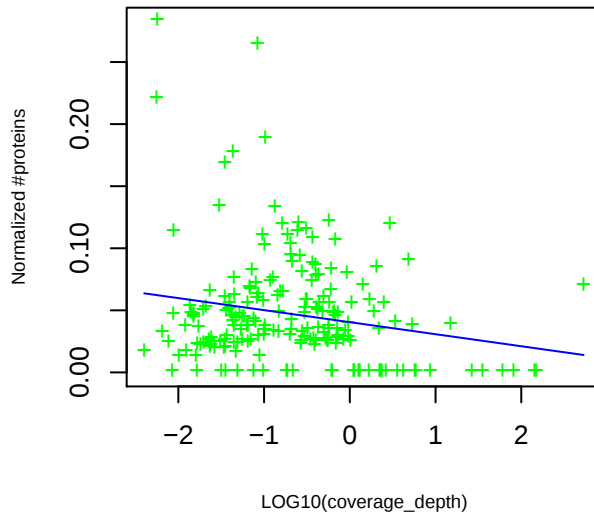
PF02782 FGGY_C: FGGY family of carbohydrate kinases, C-terminal domain

slope= -0.36 p_value= 0.0010 intercept= 1.47 p_value= 8.2e-25



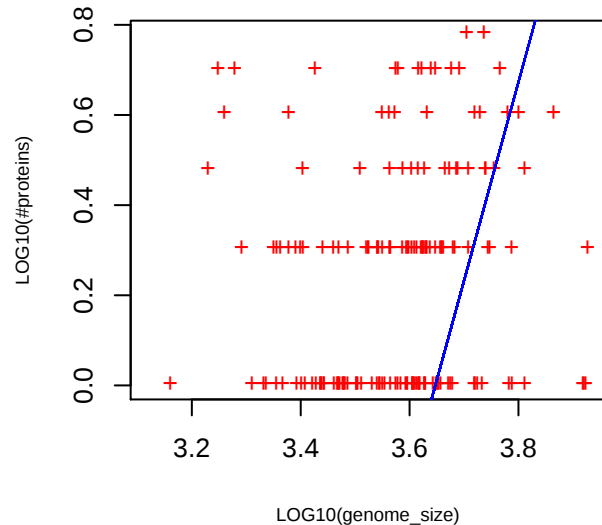
PF02782 FGGY_C: FGGY family of carbohydrate kinases, C-terminal domain

slope= -0.0097 p_value= 0.0057 intercept= 0.040 p_value= 3e-20

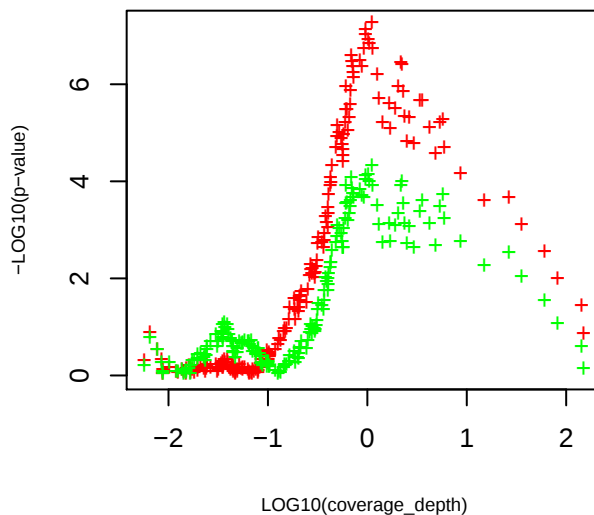


PF02782 FGGY_C: FGGY family of carbohydrate kinases, C-terminal domain

slope= 4.41 p_value= 2.2e-11 intercept= -16.07 p_value= 6.9e-12

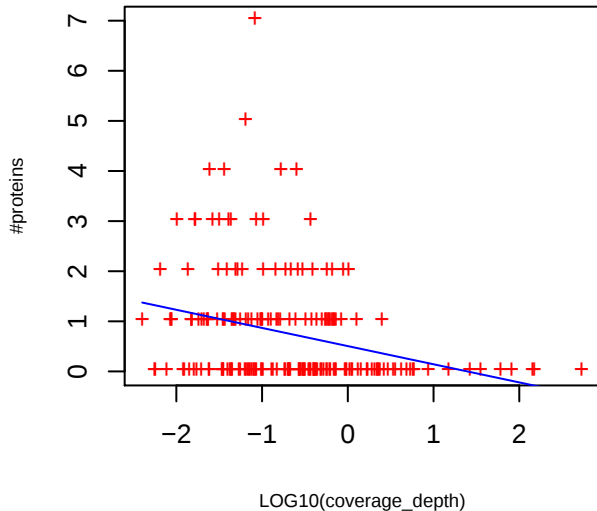


P-value curve ; red (unnorm), green (norm)



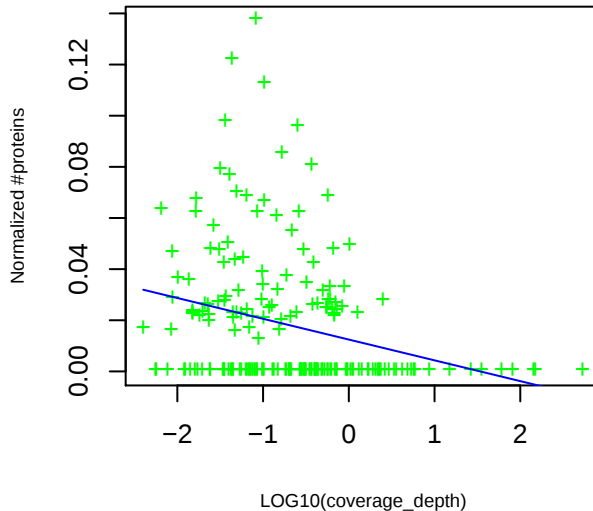
TIGR01764 excise: DNA binding domain, excisionase family

slope= -0.36 p_value= 3.2e-05 intercept= 0.51 p_value= 3.9e-07



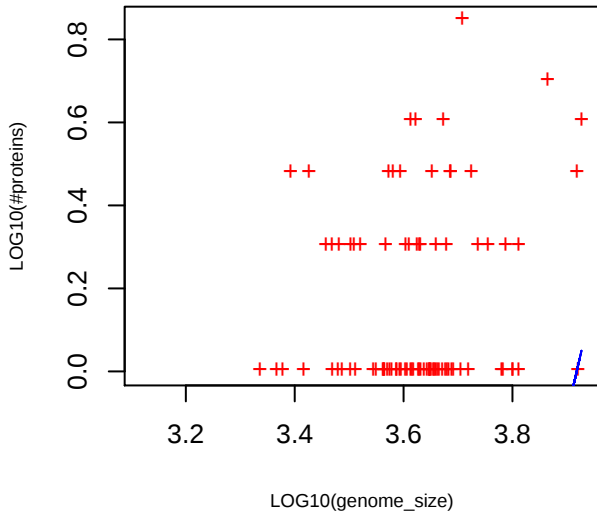
TIGR01764 excise: DNA binding domain, excisionase family

slope= -0.0081 p_value= 7.9e-05 intercept= 0.012 p_value= 1.3e-07

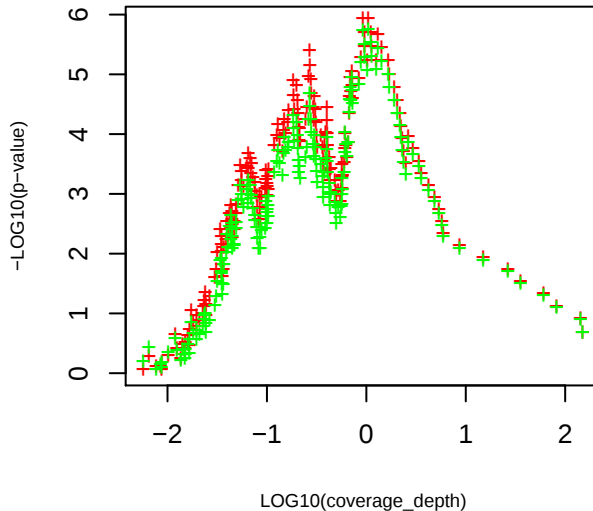


TIGR01764 excise: DNA binding domain, excisionase family

slope= 5.69 p_value= 5.2e-11 intercept= -22.29 p_value= 7.5e-13

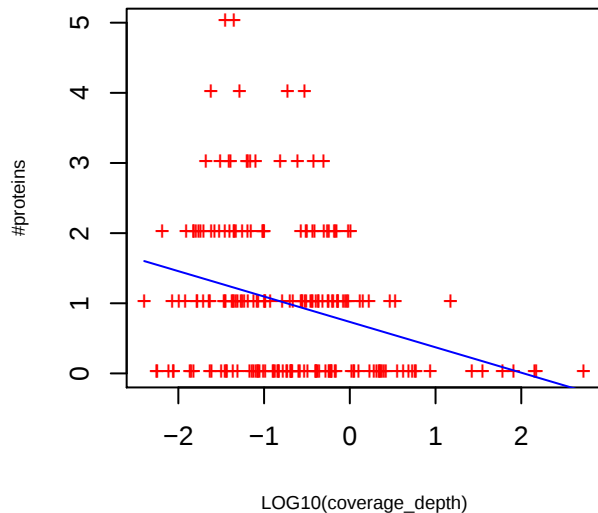


P-value curve : red (unnorm), green (norm)



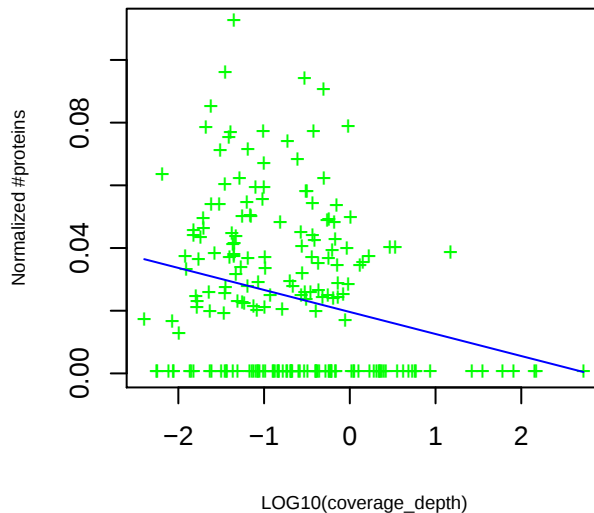
TIGR00915 2A0602: RND transporter, hydrophobe/amphiphile efflux-1 (HAE1) family

slope= -0.36 p_value= 2.5e-05 intercept= 0.73 p_value= 4.6e-13



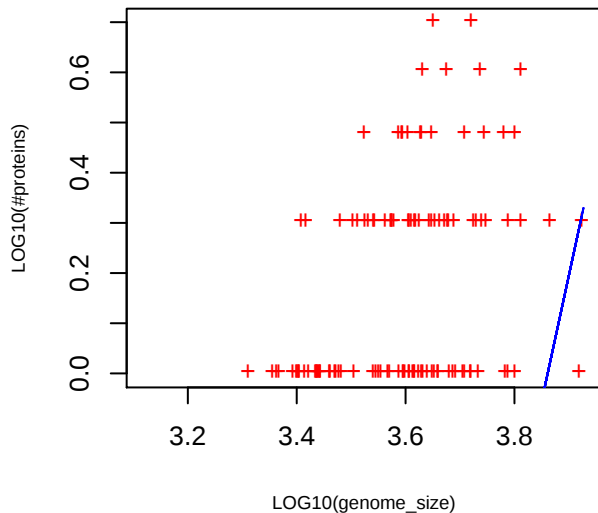
TIGR00915 2A0602: RND transporter, hydrophobe/amphiphile efflux-1 (HAE1) family

slope= -0.007 p_value= 0.00057 intercept= 0.020 p_value= 1.8e-15

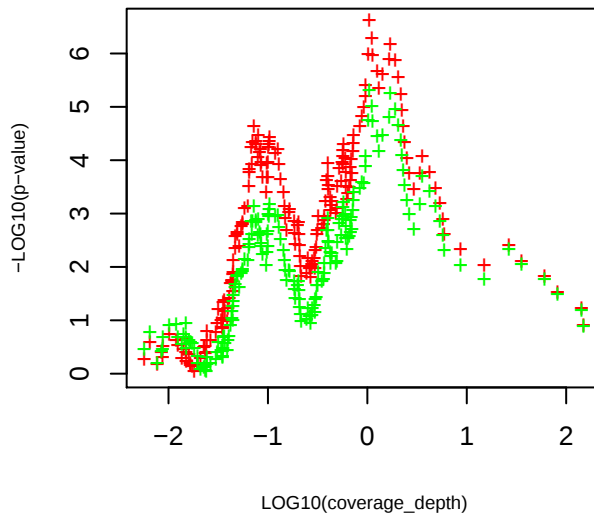


TIGR00915 2A0602: RND transporter, hydrophobe/amphiphile efflux-1 (HAE1) family

slope= 5.01 p_value= 1.0e-08 intercept= -19.34 p_value= 6.3e-10

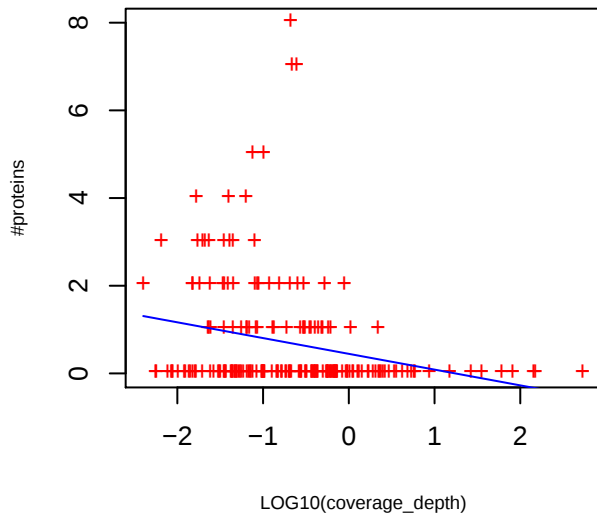


P-value curve ; red (unnorm), green (norm)



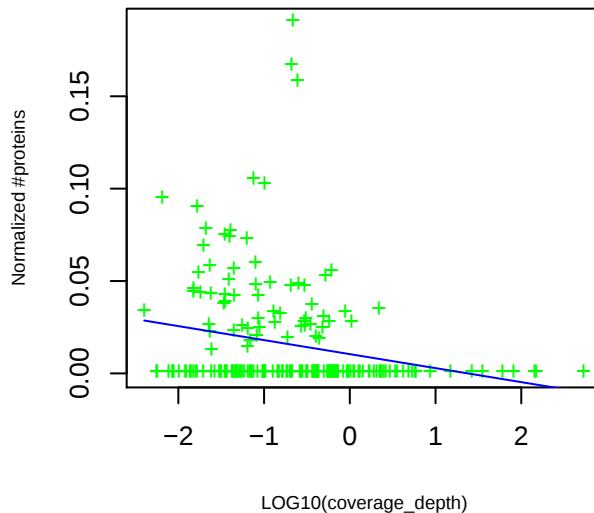
PF02311 AraC_binding: AraC-like ligand binding domain

slope= -0.36 p_value= 0.00065 intercept= 0.45 p_value= 0.00019



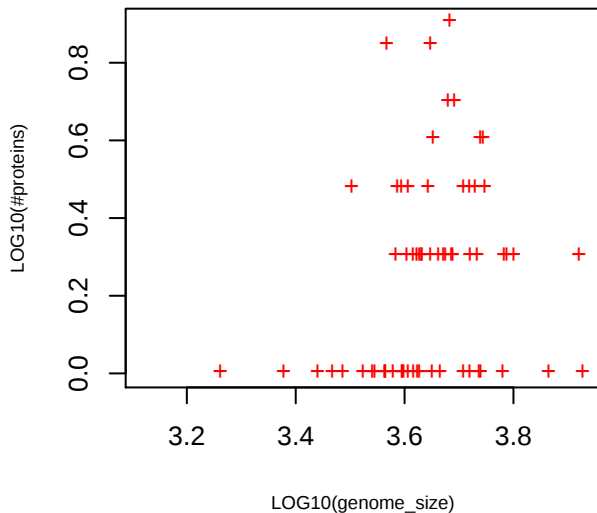
PF02311 AraC_binding: AraC-like ligand binding domain

slope= -0.0076 p_value= 0.0015 intercept= 0.010 p_value= 0.00012

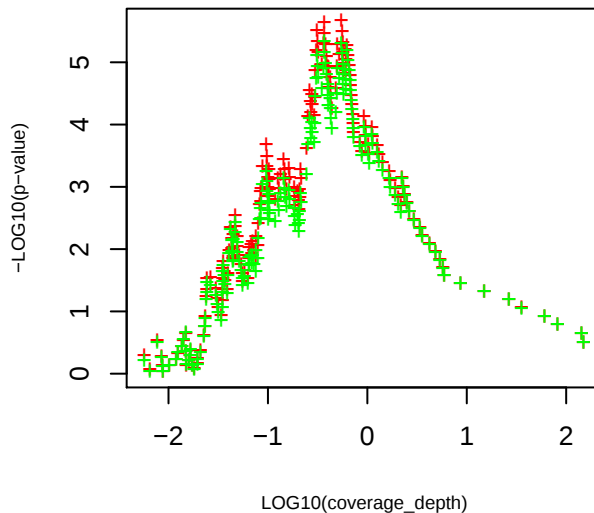


PF02311 AraC_binding: AraC-like ligand binding domain

slope= 5.29 p_value= 2.5e-10 intercept= -21.37 p_value= 1.2e-12

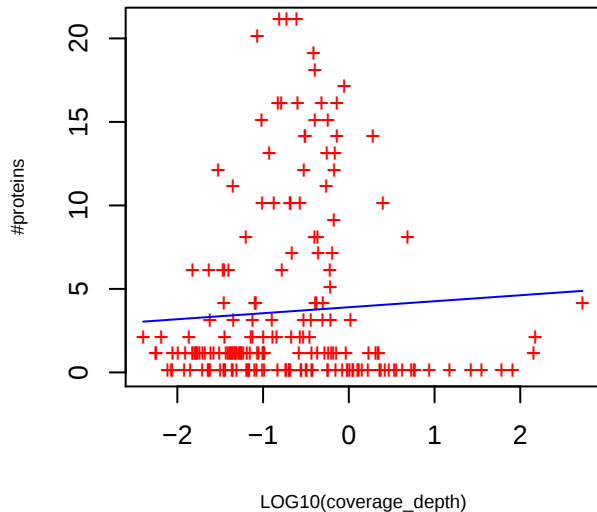


P-value curve ; red (unnorm), green (norm)



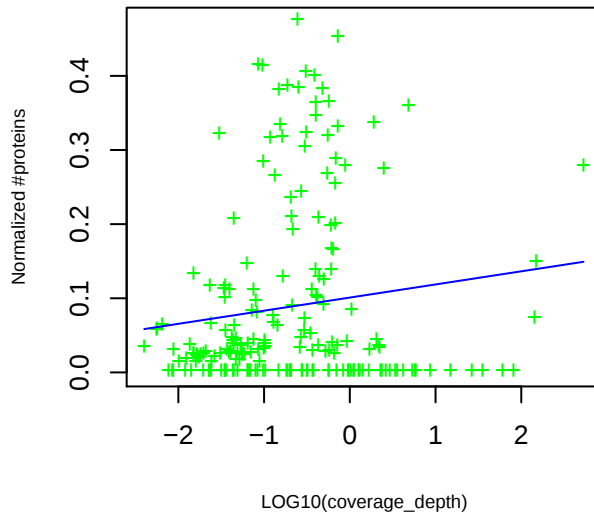
PF04290 DctQ: TRAP transporter, DctQ-like membrane protein

slope= 0.36 p_value= 0.40 intercept= 3.90 p_value= 7.7e-14



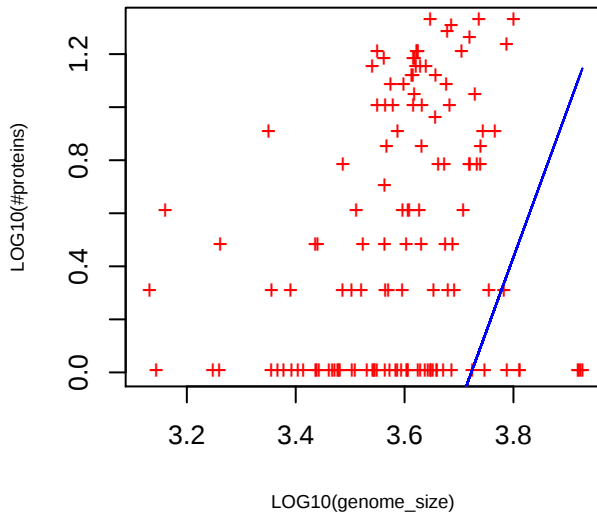
PF04290 DctQ: TRAP transporter, DctQ-like membrane protein

slope= 0.018 p_value= 0.07 intercept= 0.10 p_value= 6.4e-17

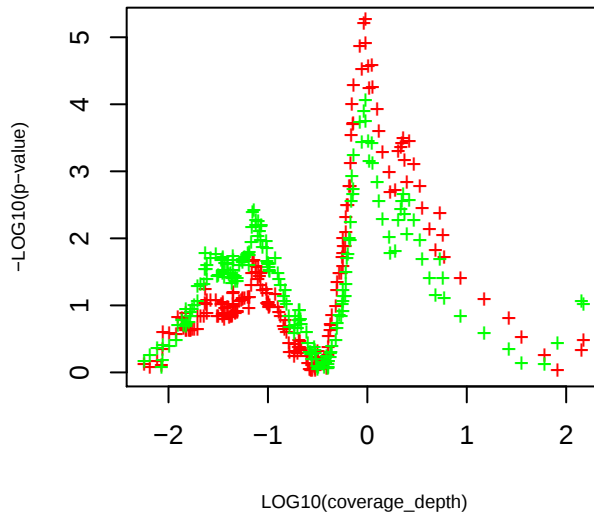


PF04290 DctQ: TRAP transporter, DctQ-like membrane protein

slope= 5.62 p_value= 4.3e-10 intercept= -20.90 p_value= 7.2e-11

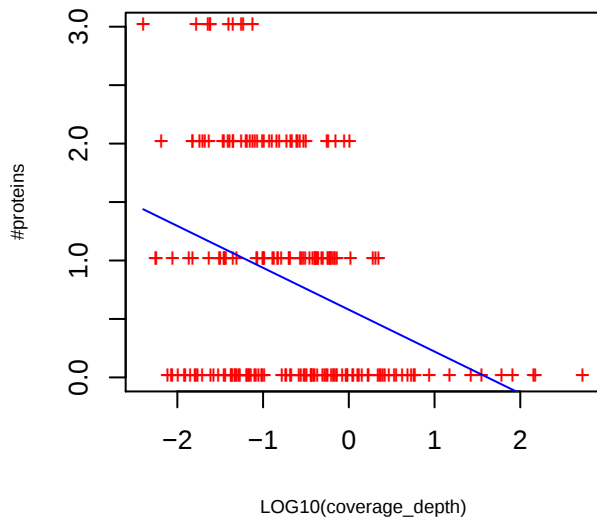


P-value curve ; red (unnorm), green (norm)



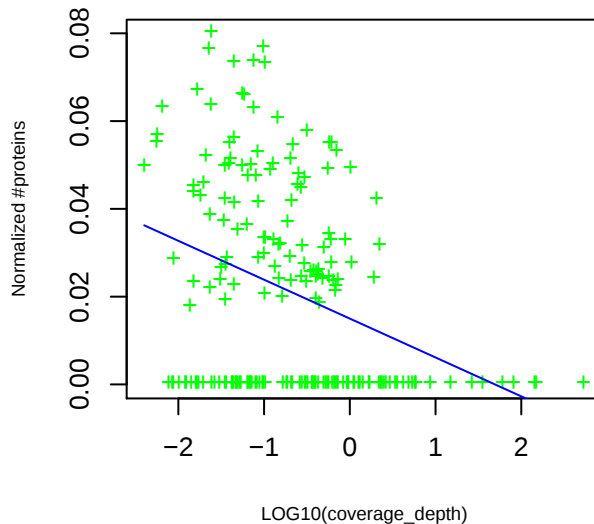
PF03748 FliL: flagellar basal body-associated protein FliL

slope= -0.36 p_value= 5.4e-07 intercept= 0.58 p_value= 3.4e-12



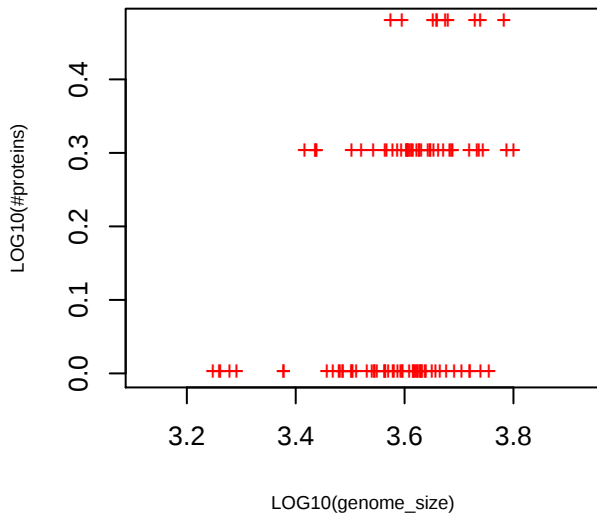
PF03748 FliL: flagellar basal body-associated protein FliL

slope= -0.0089 p_value= 8.1e-07 intercept= 0.015 p_value= 9.5e-13

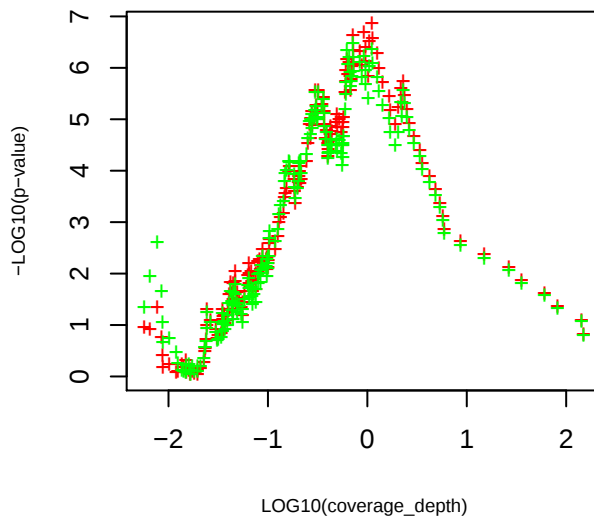


PF03748 FliL: flagellar basal body-associated protein FliL

slope= 3.86 p_value= 1.6e-05 intercept= -15.50 p_value= 1.3e-06

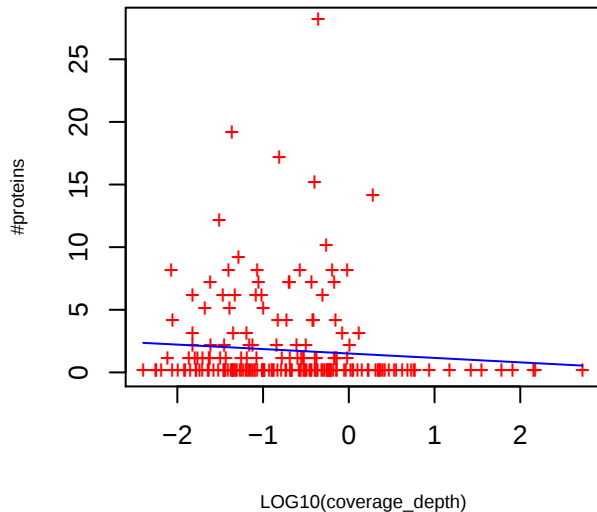


P-value curve ; red (unnorm), green (norm)



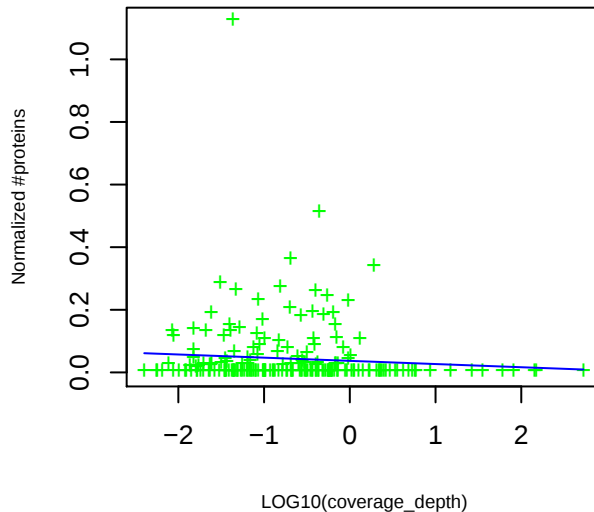
PF01548 Transposase_9: transposase

slope= -0.35 p_value= 0.24 intercept= 1.51 p_value= 1.2e-05



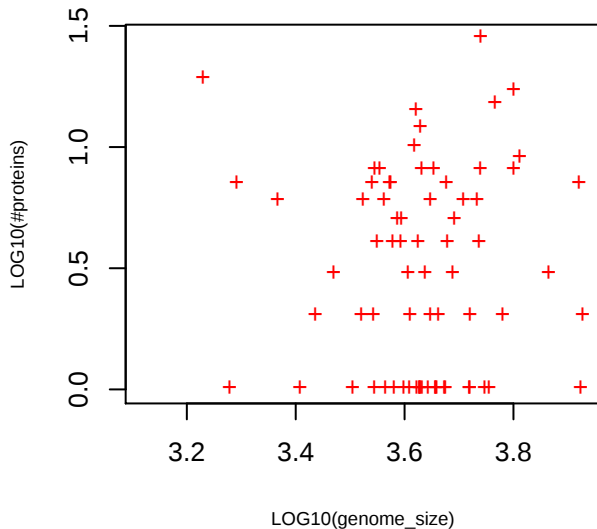
PF01548 Transposase_9: transposase

slope= -0.010 p_value= 0.25 intercept= 0.037 p_value= 0.00024

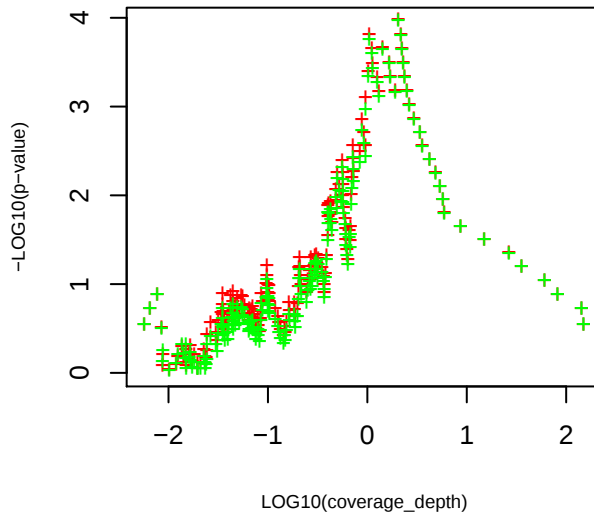


PF01548 Transposase_9: transposase

slope= 5.37 p_value= 5.6e-09 intercept= -21.36 p_value= 9.8e-11

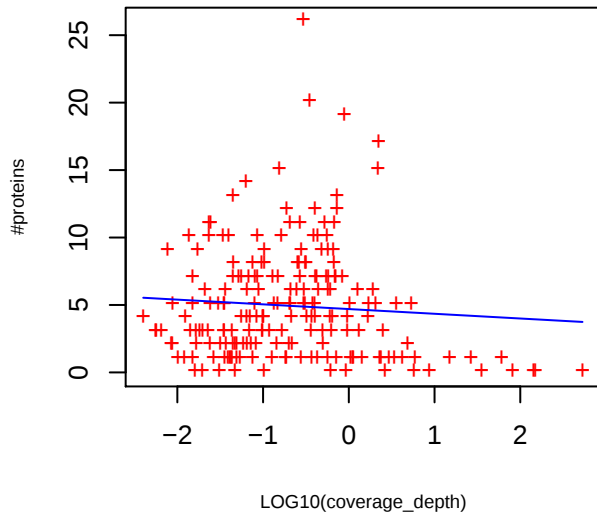


P-value curve ; red (unnorm), green (norm)



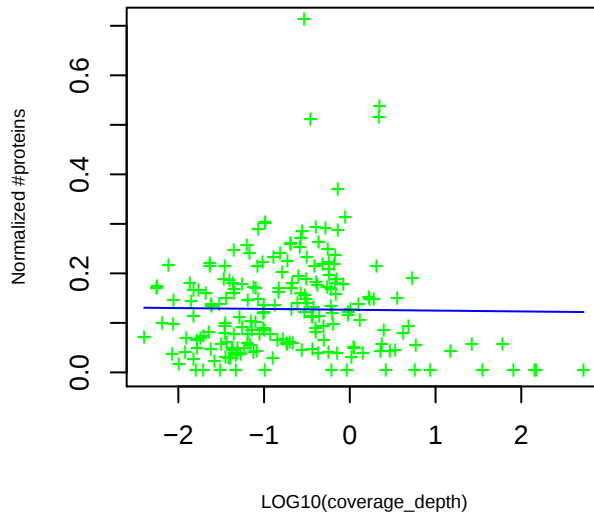
PF07969 Amidohydro. 3: Amidohydrolase family

slope= -0.35 p_value= 0.30 intercept= 4.70 p_value= 1.7e-26



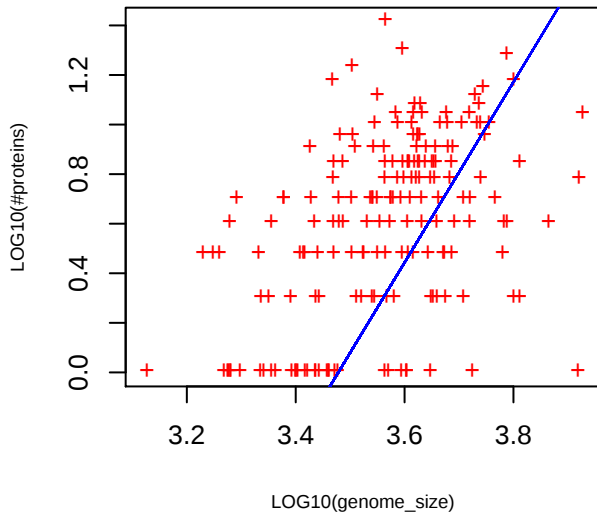
PF07969 Amidohydro. 3: Amidohydrolase family

slope= -0.0017 p_value= 0.84 intercept= 0.13 p_value= 6.4e-30

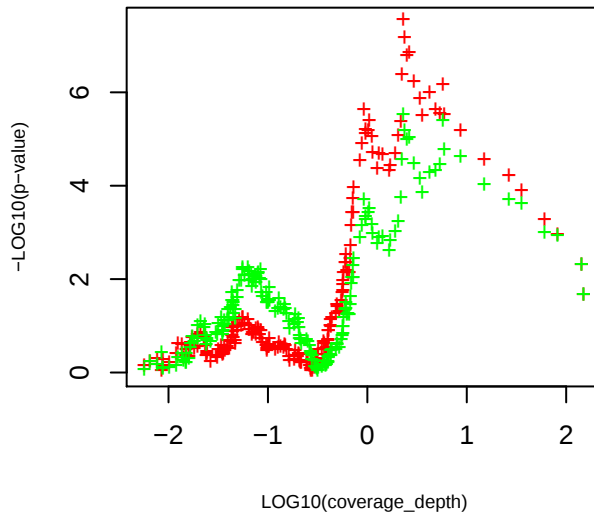


PF07969 Amidohydro. 3: Amidohydrolase family

slope= 3.64 p_value= 4.5e-12 intercept= -12.66 p_value= 1.1e-11

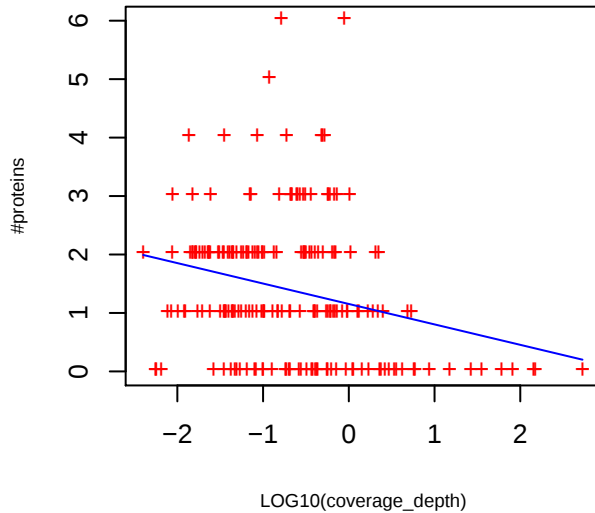


P-value curve ; red (unnorm), green (norm)



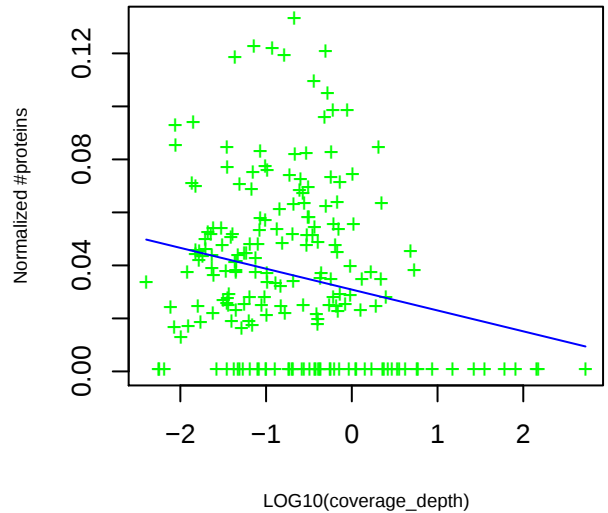
PF02558 ApbA: Ketopantoate reductase PanE/ApbA

slope= -0.35 p_value= 0.00027 intercept= 1.15 p_value= 1.0e-21



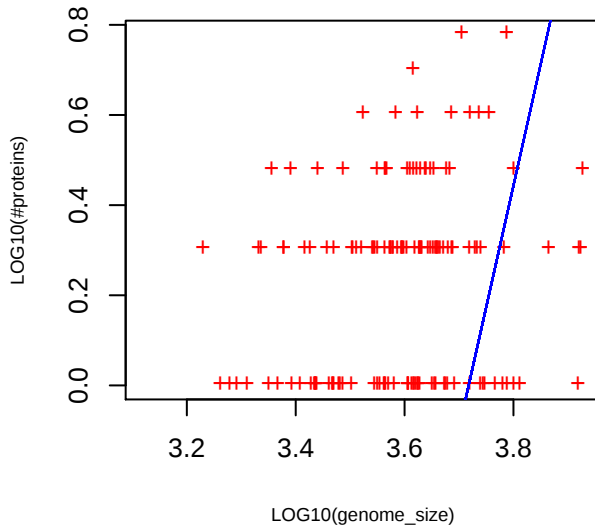
PF02558 ApbA: Ketopantoate reductase PanE/ApbA

slope= -0.0079 p_value= 0.0017 intercept= 0.031 p_value= 2.5e-22

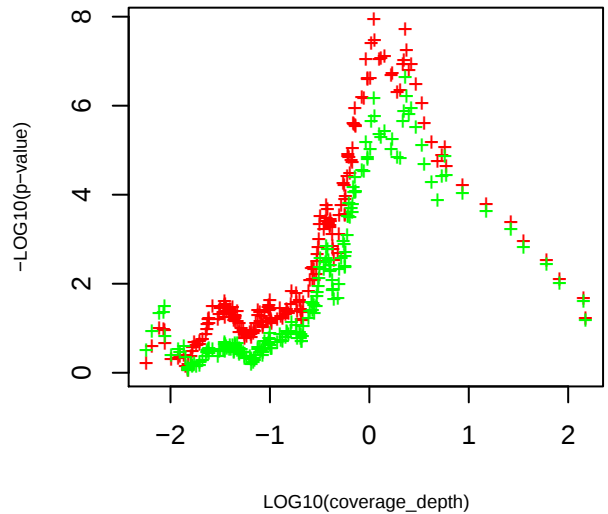


PF02558 ApbA: Ketopantoate reductase PanE/ApbA

slope= 5.39 p_value= 8.3e-12 intercept= -20.02 p_value= 1.1e-12

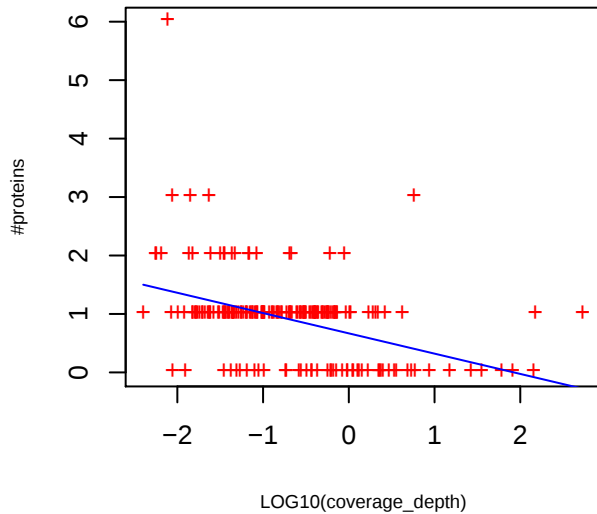


P-value curve : red (unnorm), green (norm)



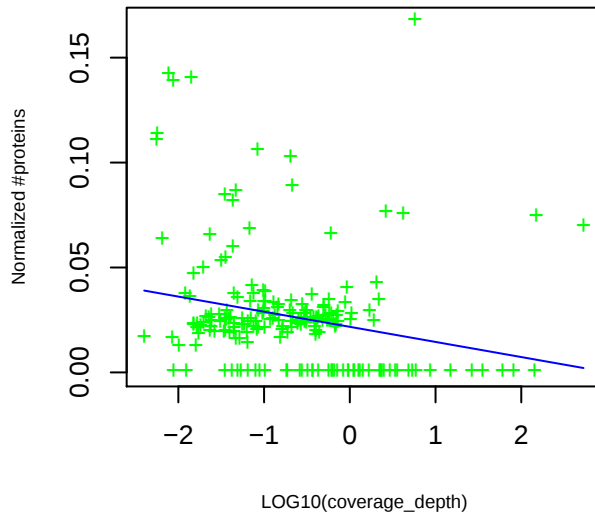
PF01895 PhoU: PhoU family

slope= -0.35 p_value= 7e-10 intercept= 0.67 p_value= 2.1e-22



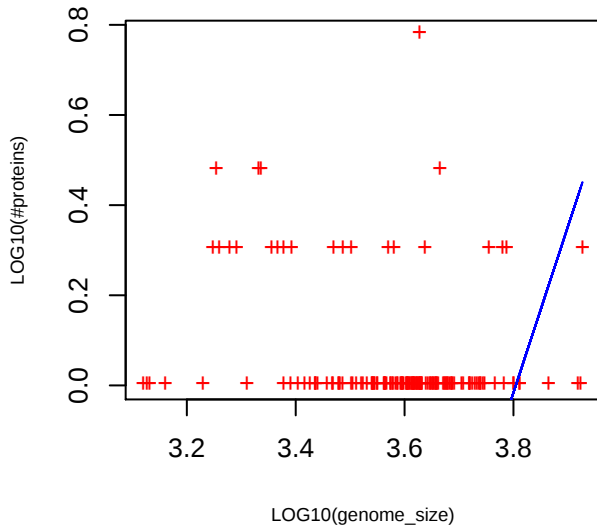
PF01895 PhoU: PhoU family

slope= -0.0072 p_value= 0.0012 intercept= 0.022 p_value= 9.4e-16

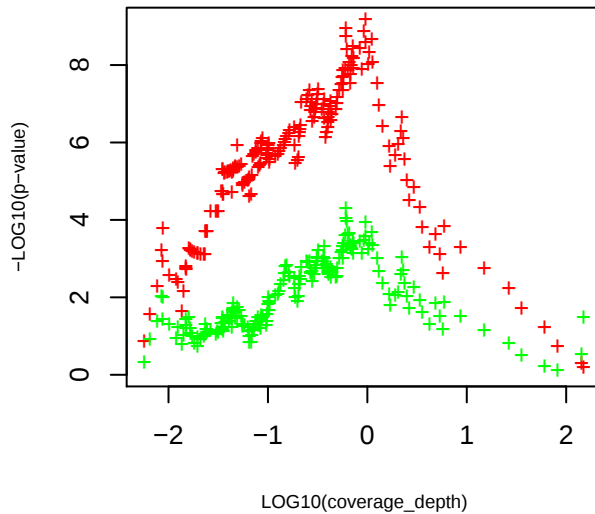


PF01895 PhoU: PhoU family

slope= 3.68 p_value= 9.6e-07 intercept= -14.01 p_value= 1.7e-07

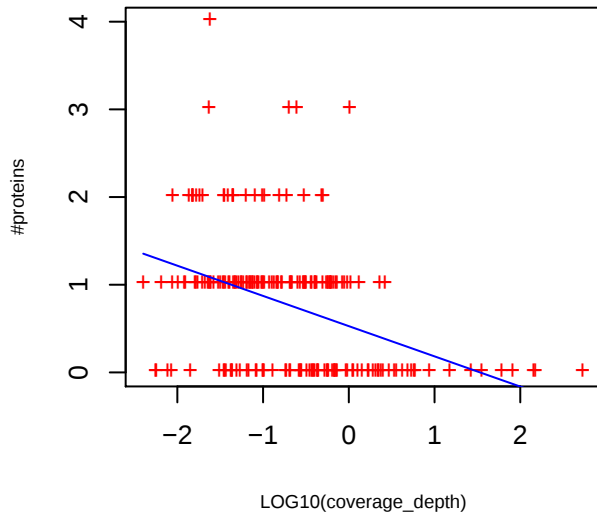


P-value curve ; red (unnorm), green (norm)



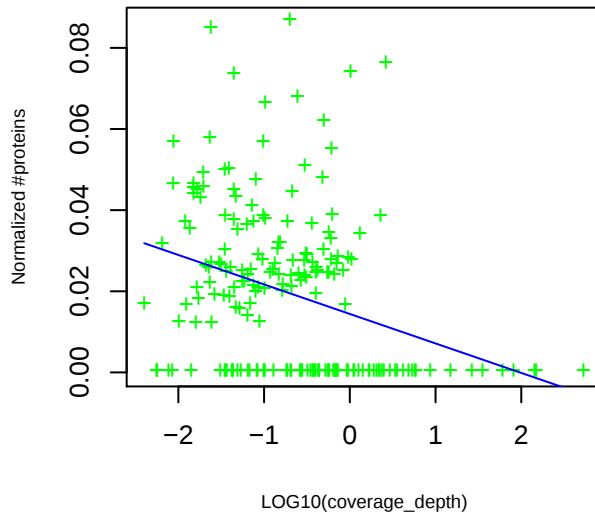
PF01654 Bac_Ubq_Cox: Bacterial Cytochrome Ubiquinol Oxidase

slope= -0.34 p_value= 6.6e-09 intercept= 0.53 p_value= 2.6e-14



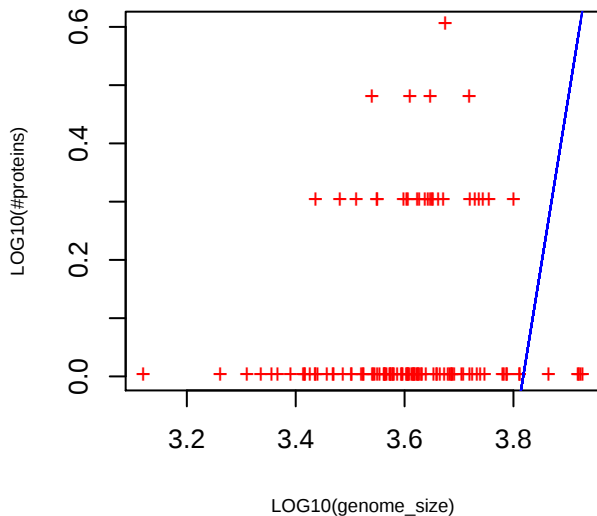
PF01654 Bac_Ubq_Cox: Bacterial Cytochrome Ubiquinol Oxidase

slope= -0.0073 p_value= 3.4e-06 intercept= 0.014 p_value= 9.3e-15

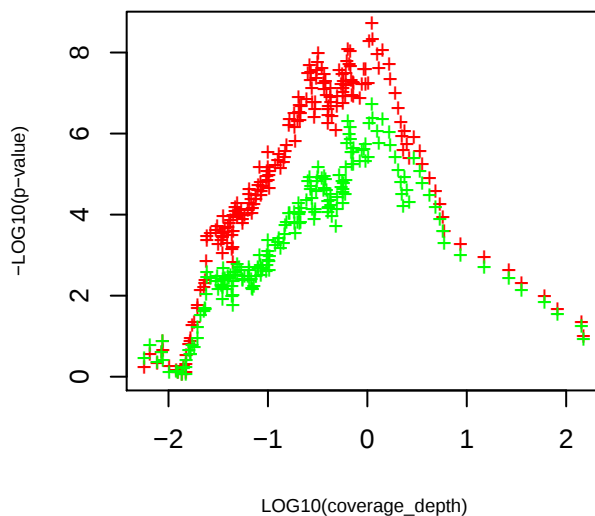


PF01654 Bac_Ubq_Cox: Bacterial Cytochrome Ubiquinol Oxidase

slope= 5.78 p_value= 3.9e-12 intercept= -22.07 p_value= 1.4e-13

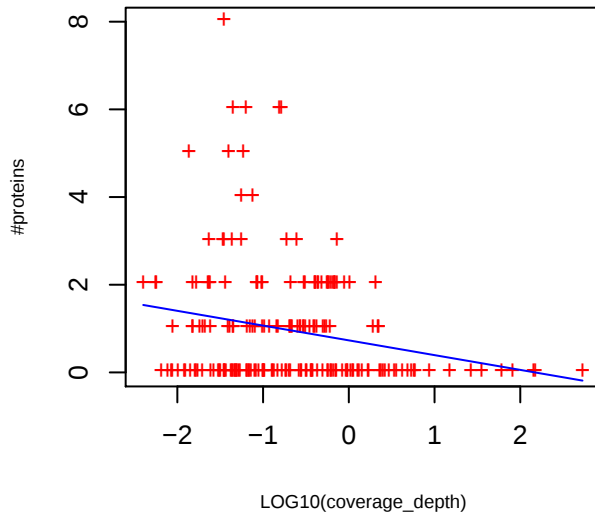


P-value curve ; red (unnorm), green (norm)



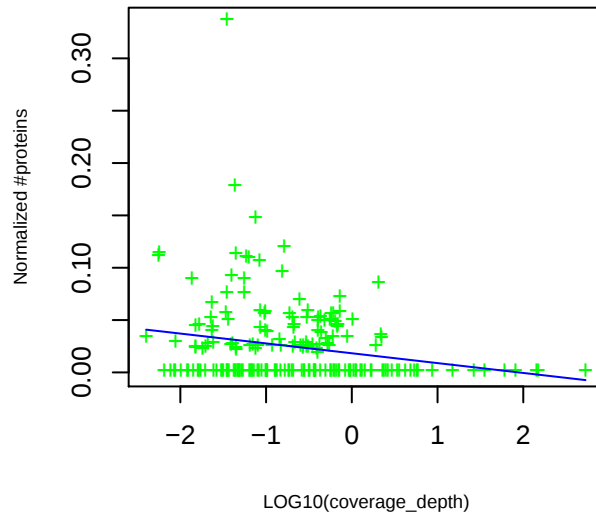
PF01418 HTH_6: transcriptional regulator, RpiR family

slope= -0.34 p_value= 0.0024 intercept= 0.73 p_value= 1.5e-08



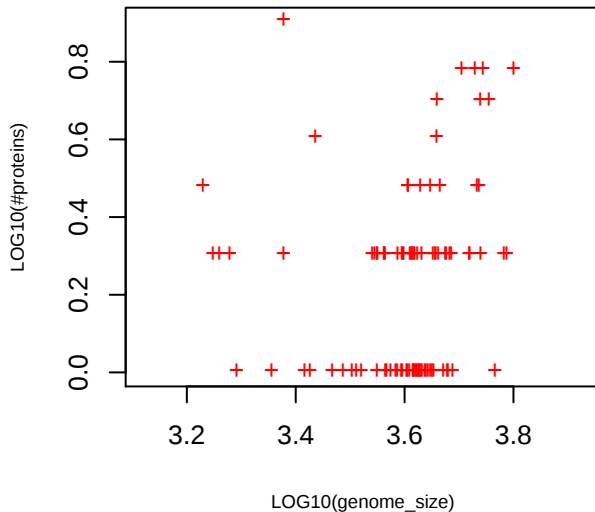
PF01418 HTH_6: transcriptional regulator, RpiR family

slope= -0.0094 p_value= 0.0025 intercept= 0.018 p_value= 3.3e-07

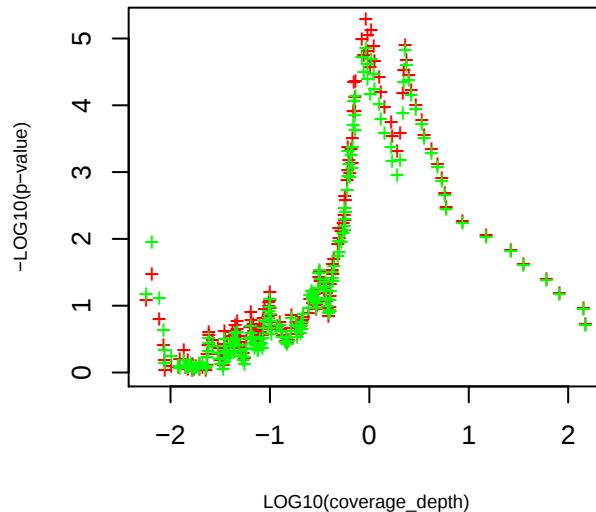


PF01418 HTH_6: transcriptional regulator, RpiR family

slope= 4.17 p_value= 4.6e-06 intercept= -16.76 p_value= 2.6e-07

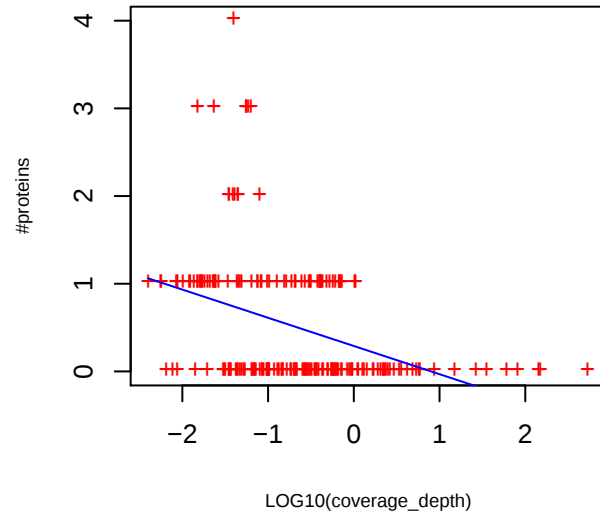


P-value curve ; red (unnorm), green (norm)



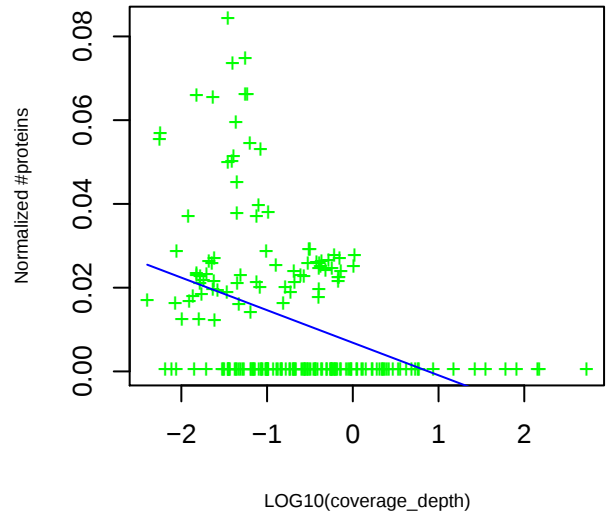
TIGR00221 nagA: N-acetylglucosamine-6-phosphate deacetylase

slope= -0.32 p_value= 3.0e-08 intercept= 0.29 p_value= 7.4e-06



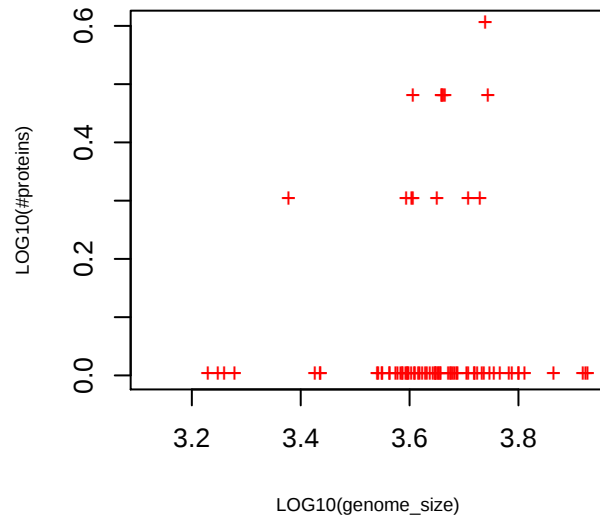
TIGR00221 nagA: N-acetylglucosamine-6-phosphate deacetylase

slope= -0.0078 p_value= 3.8e-08 intercept= 0.0069 p_value= 1.3e-05

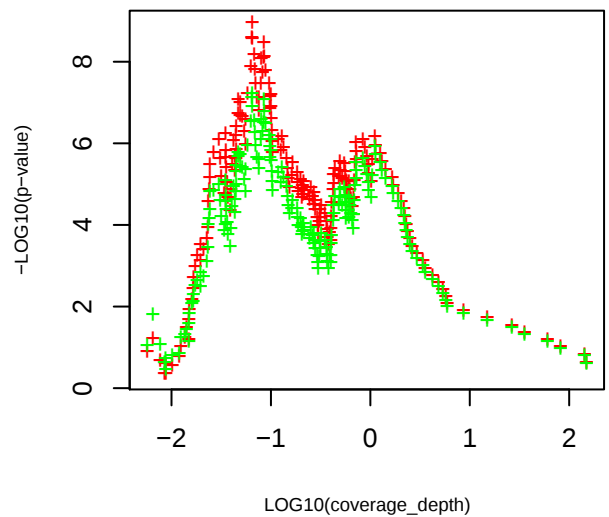


TIGR00221 nagA: N-acetylglucosamine-6-phosphate deacetylase

slope= 5.73 p_value= 5.1e-12 intercept= -22.67 p_value= 3e-14

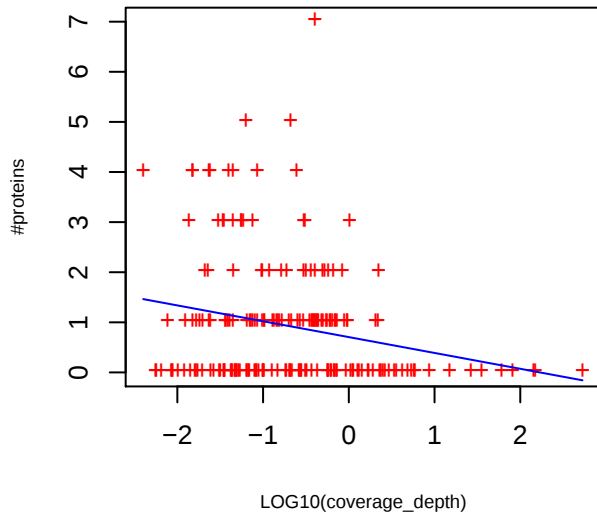


P-value curve ; red (unnorm), green (norm)



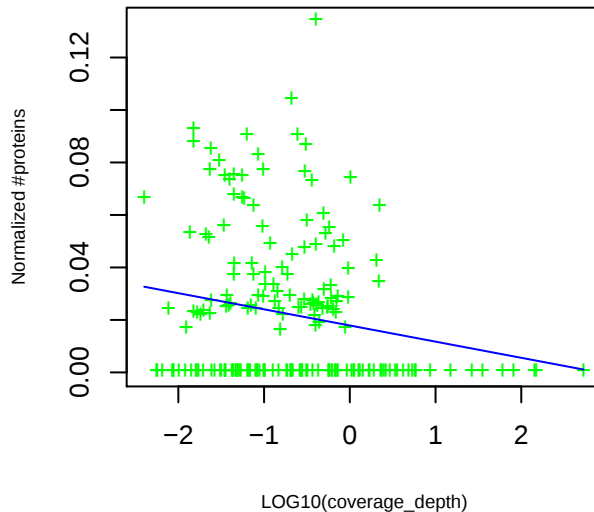
TIGR00842 bcct: transporter, betaine/carnitine/choline transporter (BCCT) family

slope= -0.32 p_value= 0.0015 intercept= 0.70 p_value= 1.5e-09



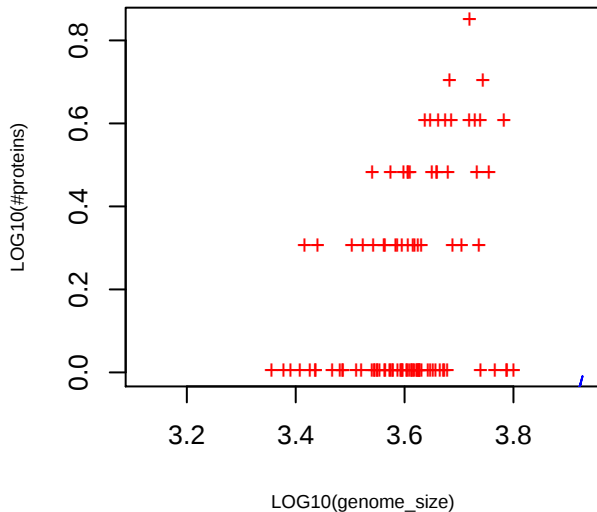
TIGR00842 bcct: transporter, betaine/carnitine/choline transporter (BCCT) family

slope= -0.0062 p_value= 0.0056 intercept= 0.018 p_value= 1.2e-11

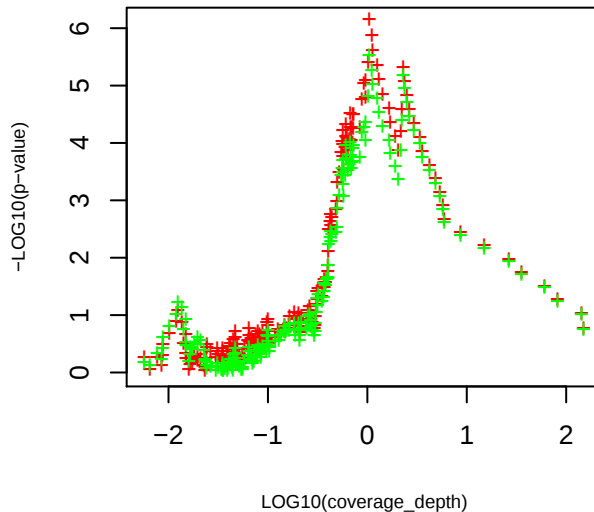


TIGR00842 bcct: transporter, betaine/carnitine/choline transporter (BCCT) family

slope= 4.94 p_value= 3e-08 intercept= -19.41 p_value= 1.2e-09

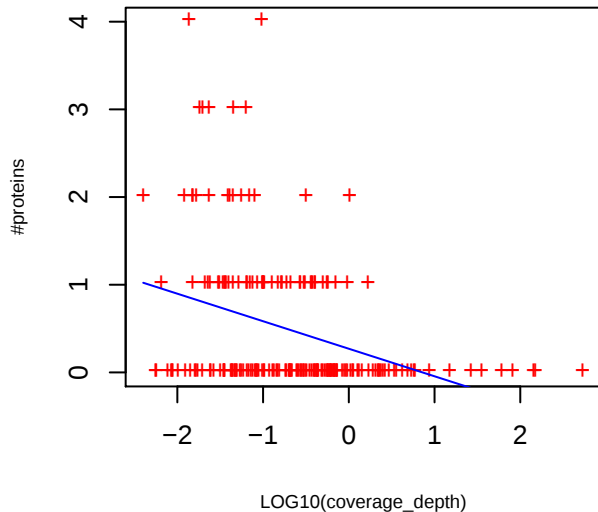


P-value curve ; red (unnorm), green (norm)



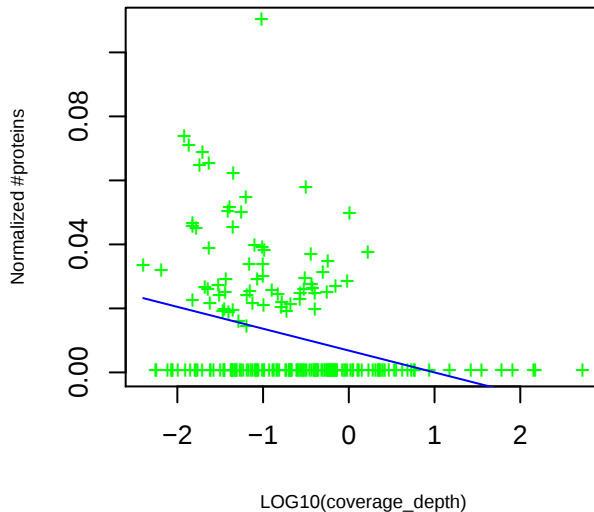
PF00199 Catalase: catalase

slope= -0.31 p_value= 8e-07 intercept= 0.27 p_value= 0.00014



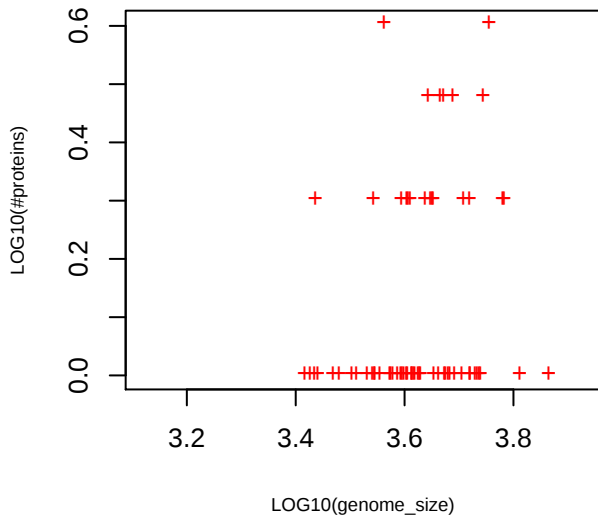
PF00199 Catalase: catalase

slope= -0.0068 p_value= 5.1e-06 intercept= 0.0068 p_value= 4.9e-05

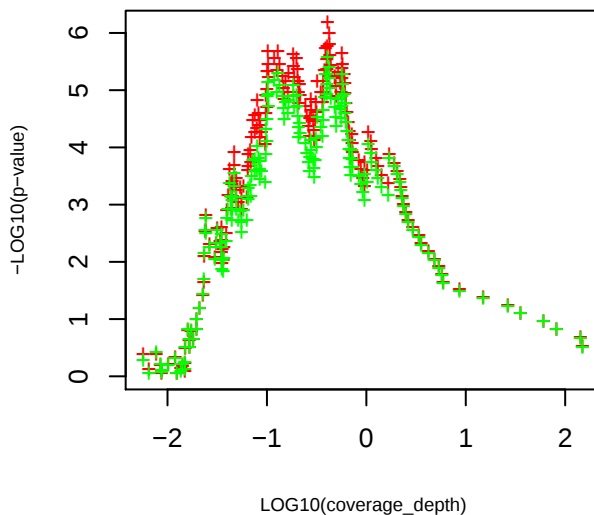


PF00199 Catalase: catalase

slope= 4.18 p_value= 5.1e-07 intercept= -17.42 p_value= 5.3e-09

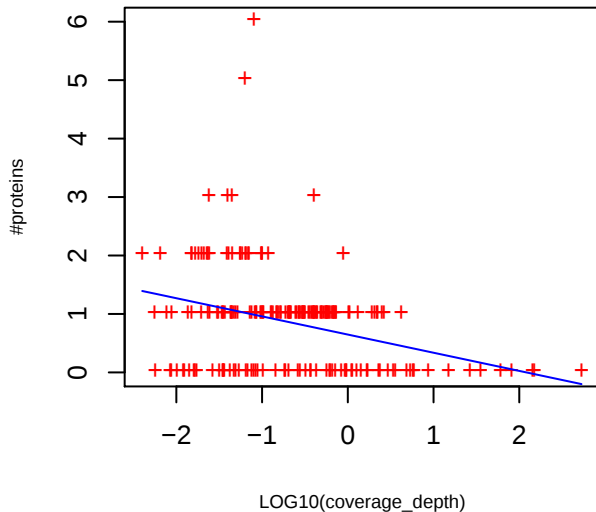


P-value curve ; red (unnorm), green (norm)



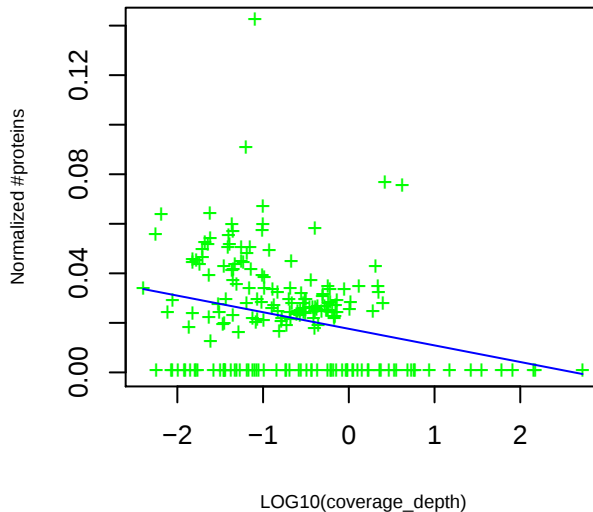
TIGR01417 PTS_1_fam: phosphoenolpyruvate-protein phosphotransferase

slope= -0.31 p_value= 5e-06 intercept= 0.65 p_value= 1.8e-15



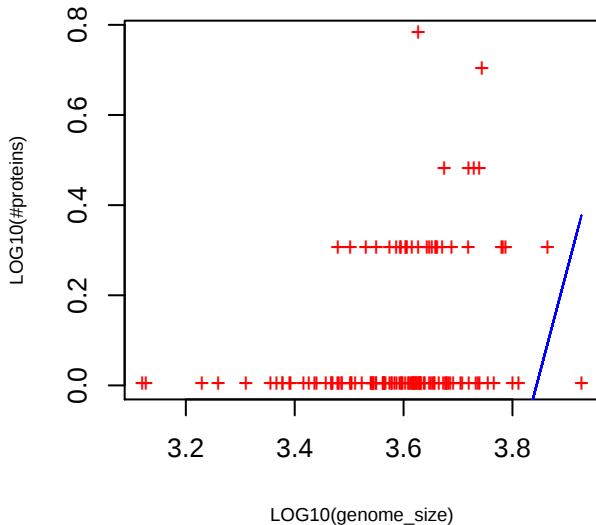
TIGR01417 PTS_1_fam: phosphoenolpyruvate-protein phosphotransferase

slope= -0.0067 p_value= 7.2e-05 intercept= 0.018 p_value= 1.2e-17

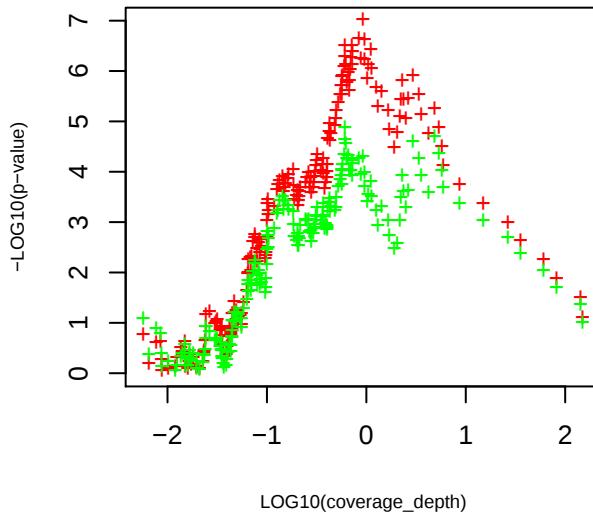


TIGR01417 PTS_1_fam: phosphoenolpyruvate-protein phosphotransferase

slope= 4.56 p_value= 4.2e-08 intercept= -17.55 p_value= 3.6e-09

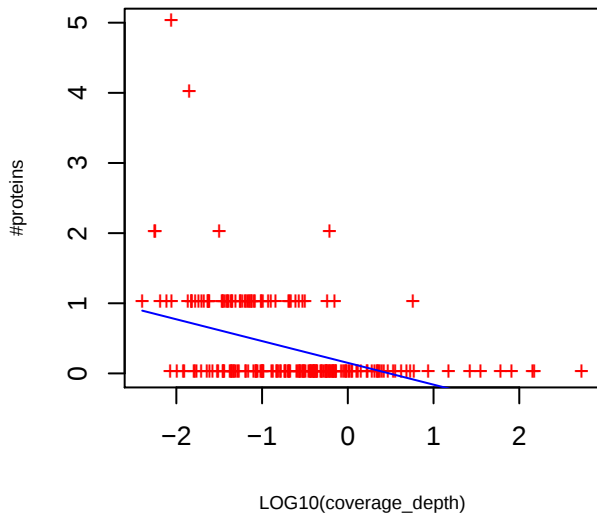


P-value curve ; red (unnorm), green (norm)



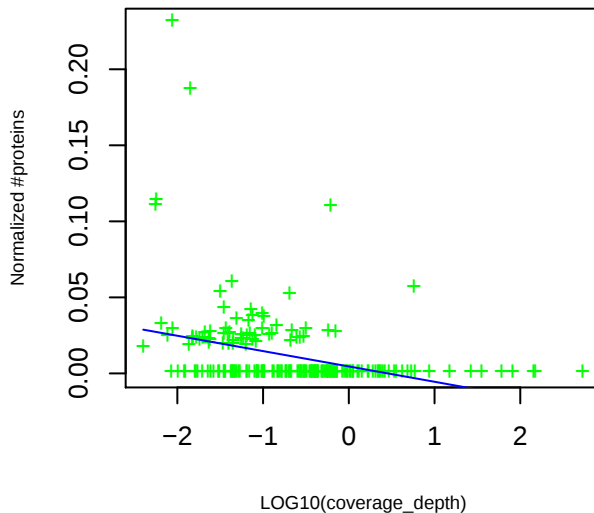
PF02568 ThiI: Thiamine biosynthesis protein (ThiI)

slope= -0.31 p_value= 8e-10 intercept= 0.15 p_value= 0.0061



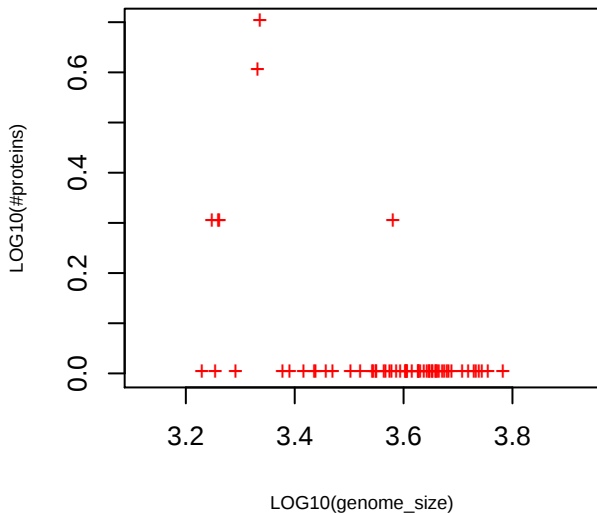
PF02568 ThiI: Thiamine biosynthesis protein (ThiI)

slope= -0.01 p_value= 2.0e-06 intercept= 0.0046 p_value= 0.049

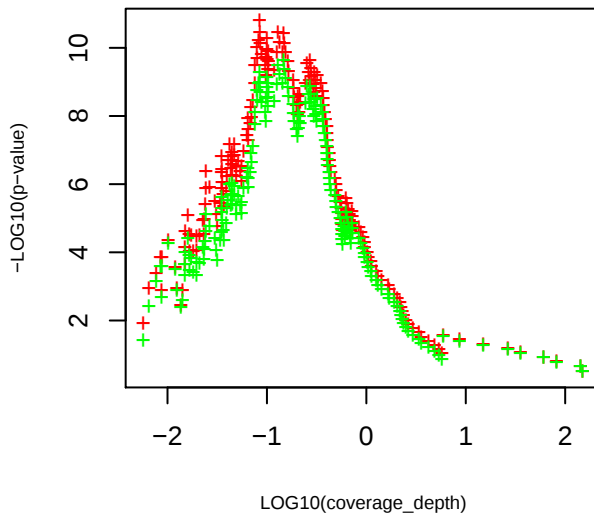


PF02568 ThiI: Thiamine biosynthesis protein (ThiI)

slope= 0.80 p_value= 0.33 intercept= -5.58 p_value= 0.057

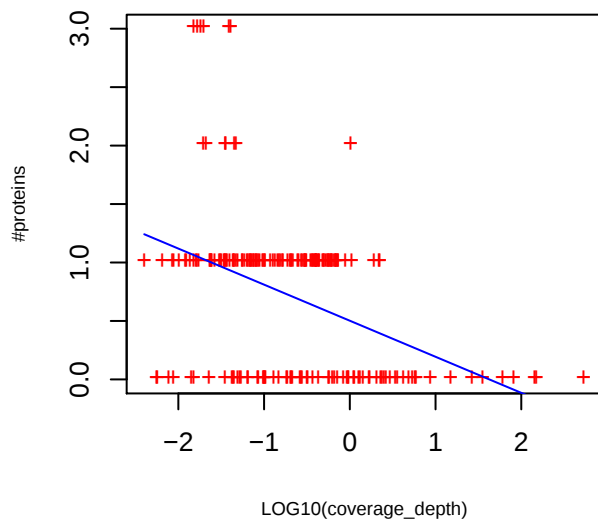


P-value curve ; red (unnorm), green (norm)



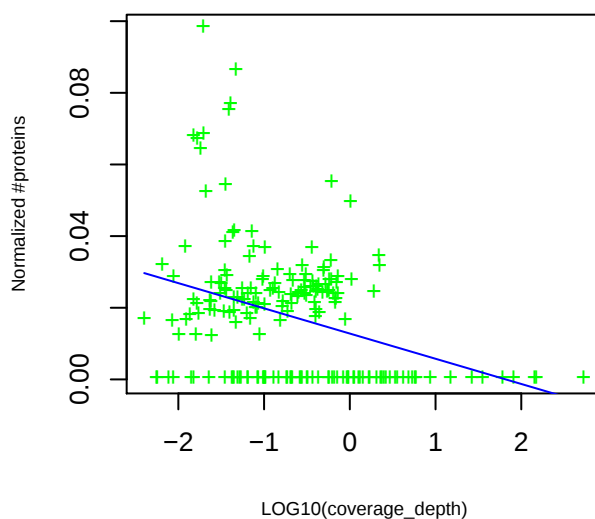
TIGR01256 modA: molybdate ABC transporter, periplasmic molybdate-binding protein

slope= -0.31 p_value= 2.9e-09 intercept= 0.50 p_value= 2.5e-16



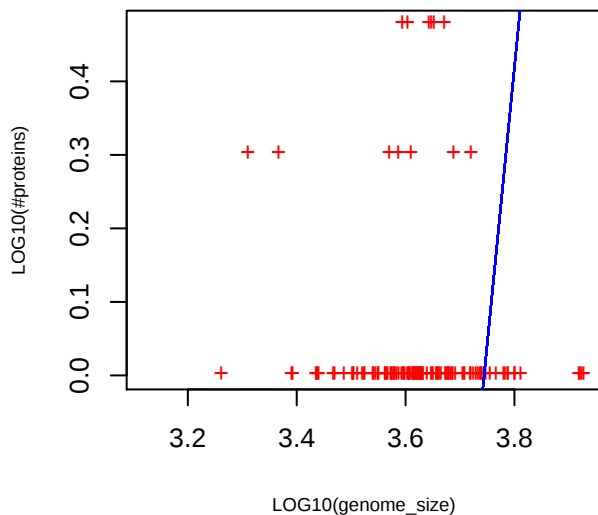
TIGR01256 modA: molybdate ABC transporter, periplasmic molybdate-binding protein

slope= -0.007 p_value= 6e-07 intercept= 0.013 p_value= 1.5e-14

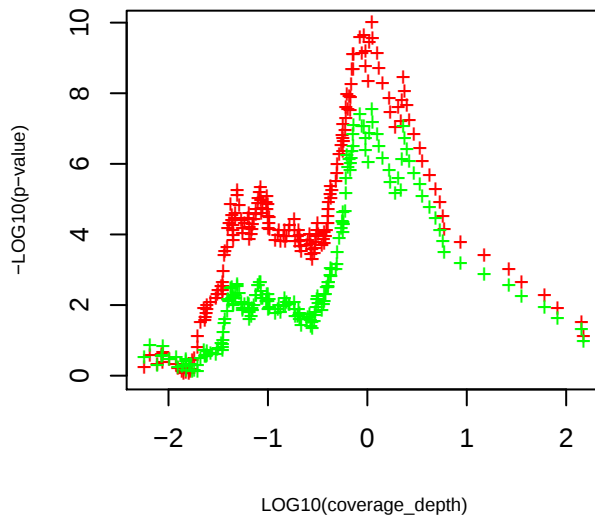


TIGR01256 modA: molybdate ABC transporter, periplasmic molybdate-binding protein

slope= 7.52 p_value= 1.5e-22 intercept= -28.18 p_value= 2.1e-24

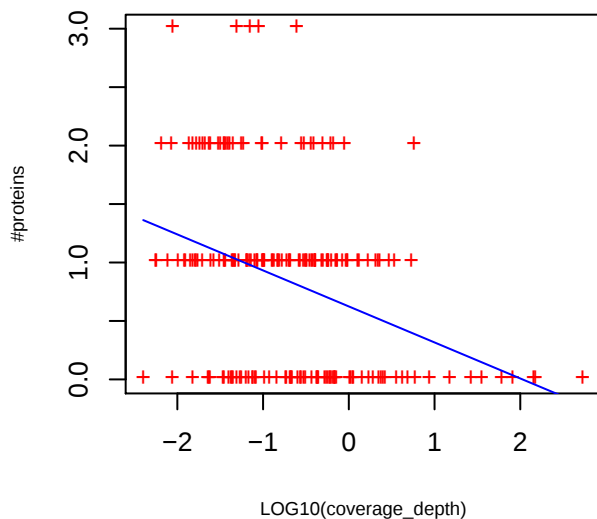


P-value curve ; red (unnorm), green (norm)



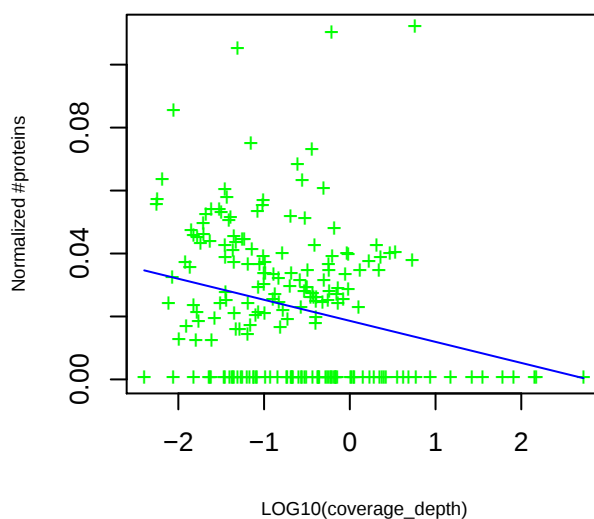
PF01544 CorA: CorA-like Mg2+ transporter protein

slope= -0.31 p_value= 4.3e-07 intercept= 0.62 p_value= 1.6e-17



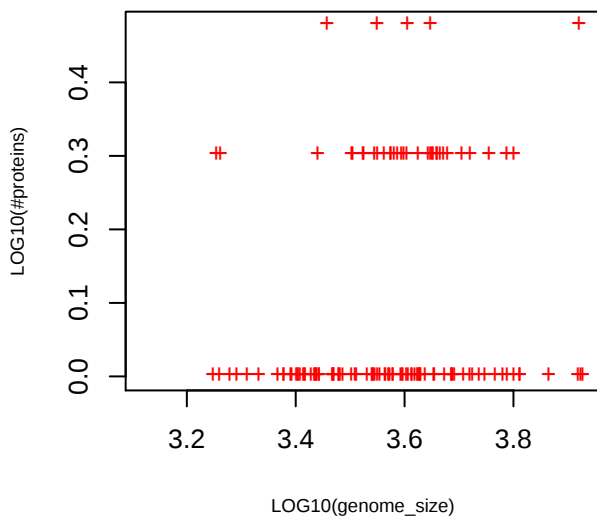
PF01544 CorA: CorA-like Mg2+ transporter protein

slope= -0.0067 p_value= 0.00024 intercept= 0.019 p_value= 4.8e-17

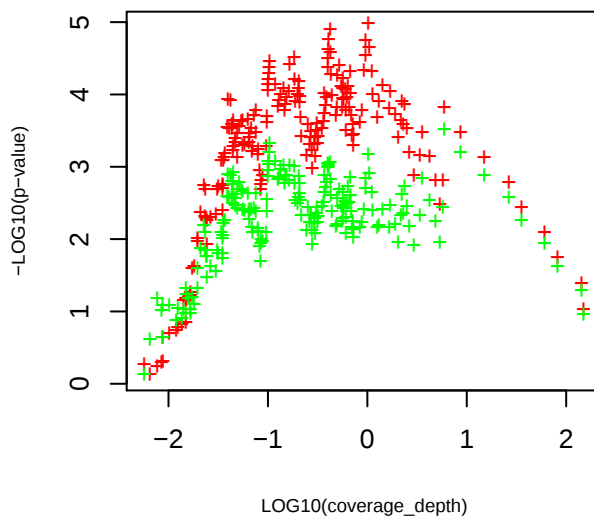


PF01544 CorA: CorA-like Mg2+ transporter protein

slope= 2.67 p_value= 0.0021 intercept= -10.90 p_value= 0.00041

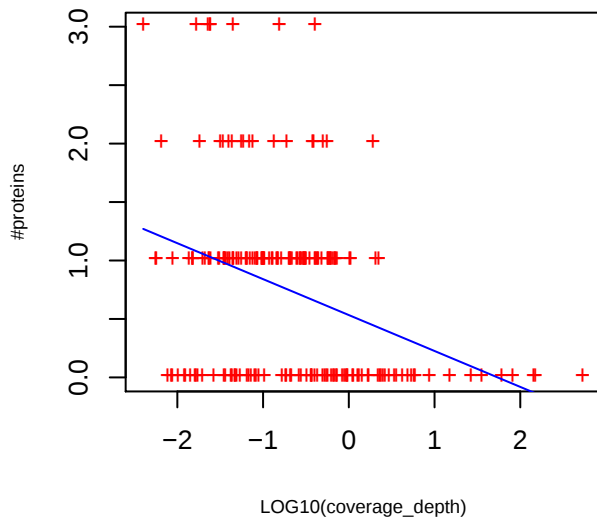


P-value curve ; red (unnorm), green (norm)



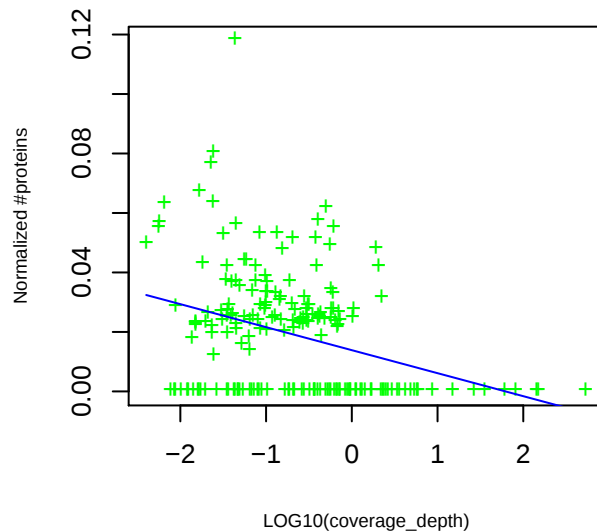
PF00771 FHIPEP: FHIPEP family

slope= -0.31 p_value= 3.8e-07 intercept= 0.53 p_value= 6.7e-14



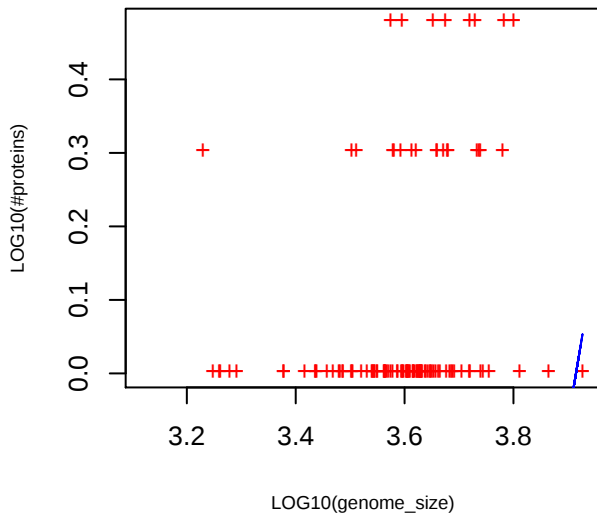
PF00771 FHIPEP: FHIPEP family

slope= -0.0077 p_value= 9.9e-07 intercept= 0.014 p_value= 9.2e-14

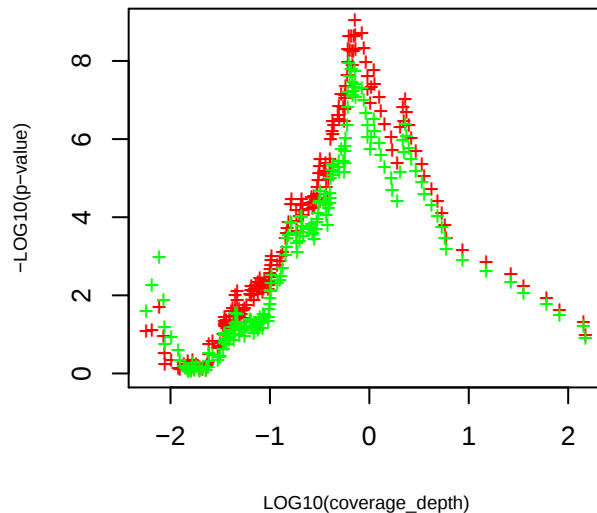


PF00771 FHIPEP: FHIPEP family

slope= 4.44 p_value= 2.5e-07 intercept= -17.37 p_value= 1.6e-08

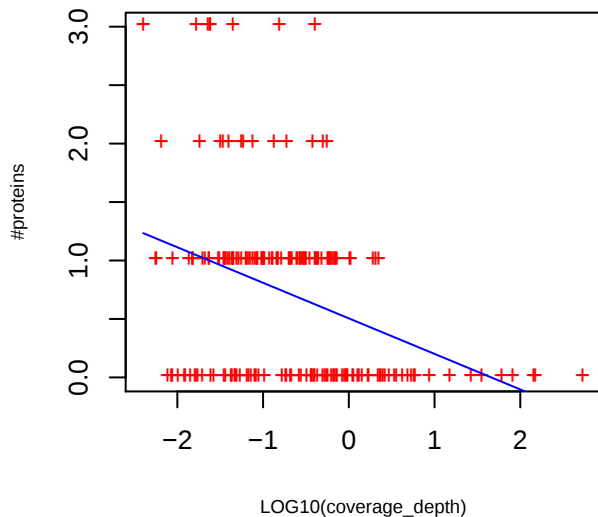


P-value curve ; red (unnorm), green (norm)



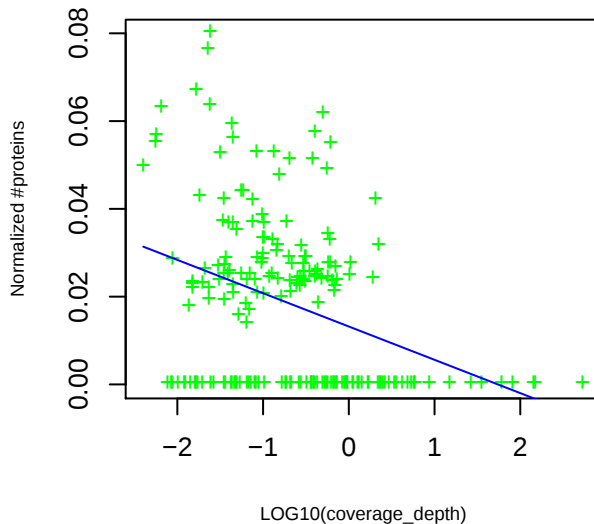
PF01514 YscJ_FliF: Secretory protein of YscJ/FliF family

slope= -0.30 p_value= 2.7e-07 intercept= 0.51 p_value= 2.9e-13



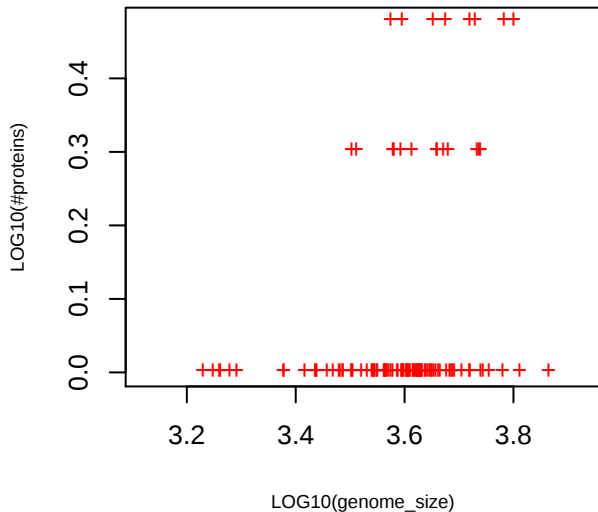
PF01514 YscJ_FliF: Secretory protein of YscJ/FliF family

slope= -0.0076 p_value= 3.2e-07 intercept= 0.013 p_value= 4.4e-14

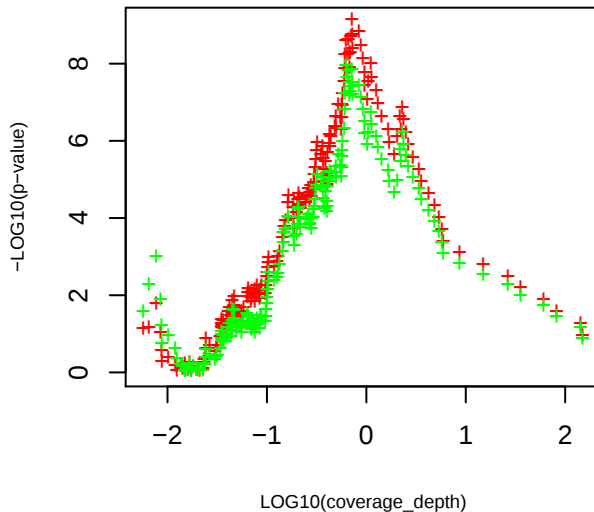


PF01514 YscJ_FliF: Secretory protein of YscJ/FliF family

slope= 4.03 p_value= 3.2e-06 intercept= -15.99 p_value= 2.3e-07

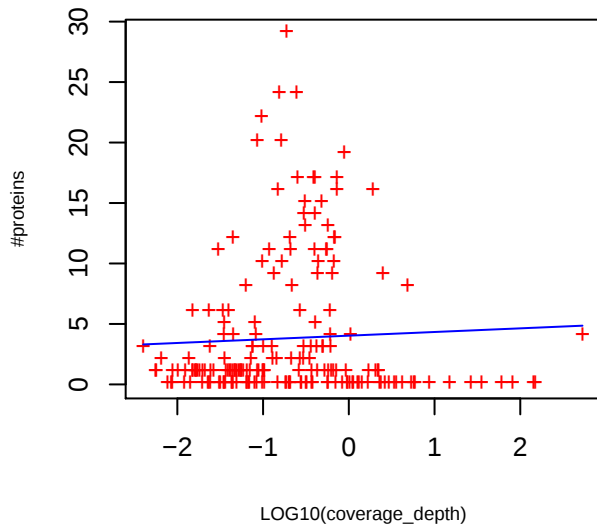


P-value curve ; red (unnorm), green (norm)



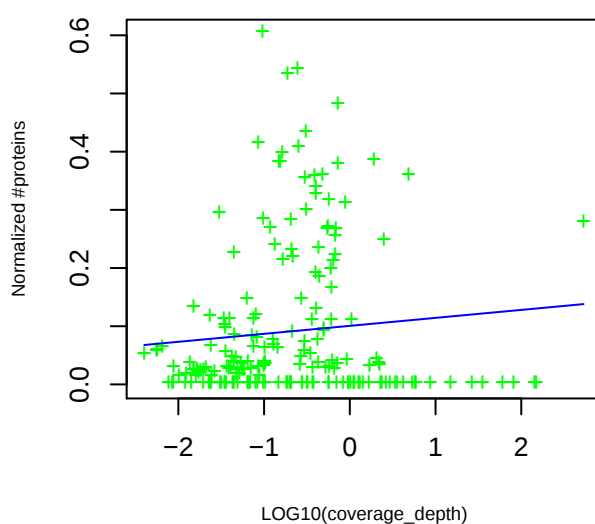
TIGR00786 dctM: TRAP transporter, DctM subunit

slope= 0.30 p_value= 0.52 intercept= 4.03 p_value= 8.8e-13



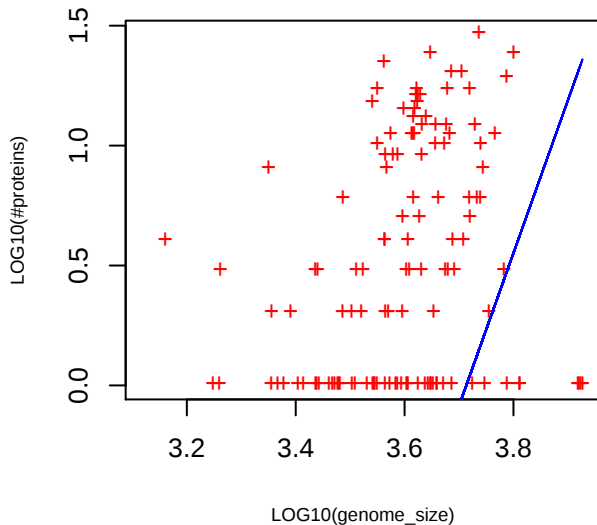
TIGR00786 dctM: TRAP transporter, DctM subunit

slope= 0.014 p_value= 0.19 intercept= 0.10 p_value= 4.8e-15

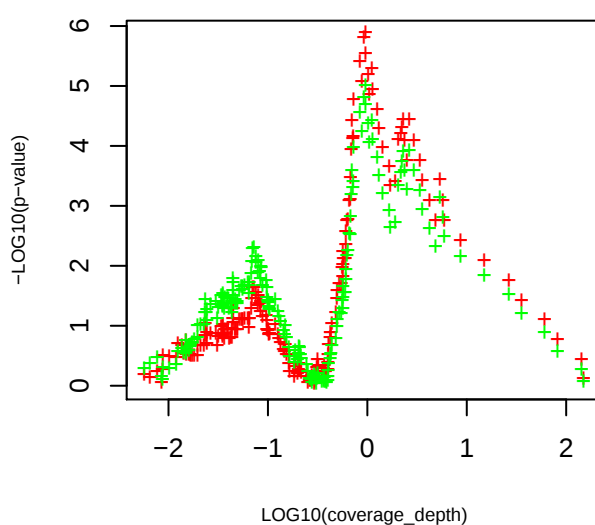


TIGR00786 dctM: TRAP transporter, DctM subunit

slope= 6.37 p_value= 2.0e-12 intercept= -23.65 p_value= 2.5e-13

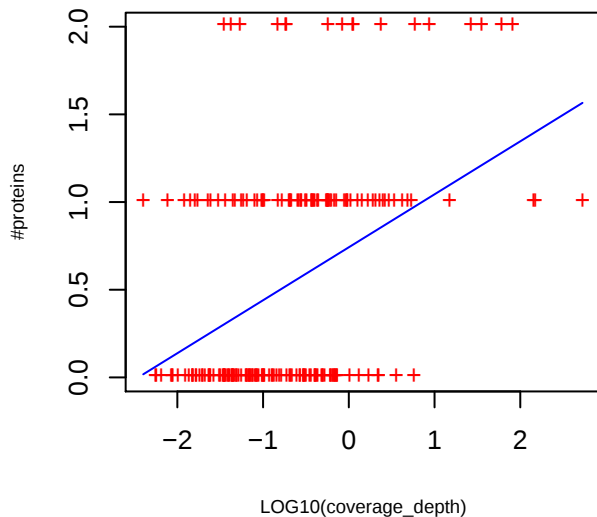


P-value curve ; red (unnorm), green (norm)



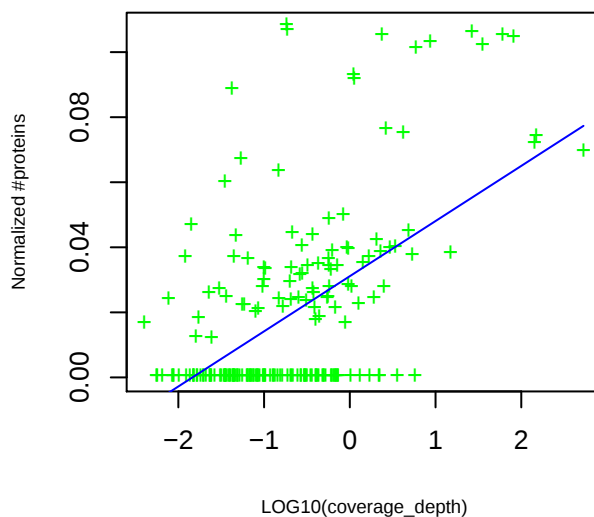
PF05834 Lycopene_cycl: Lycopene cyclase protein

slope= 0.30 p_value= 1.3e-09 intercept= 0.74 p_value= 7.4e-31



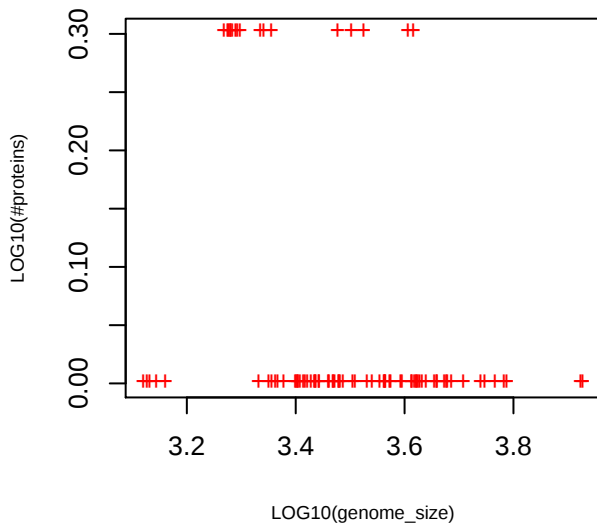
PF05834 Lycopene_cycl: Lycopene cyclase protein

slope= 0.017 p_value= 2.9e-16 intercept= 0.031 p_value= 6.2e-33

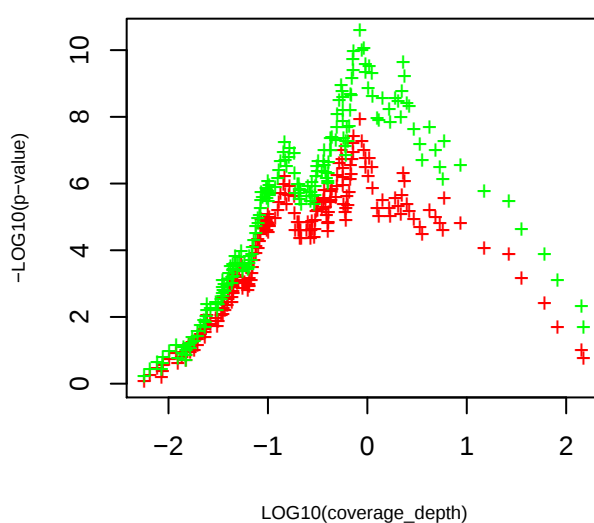


PF05834 Lycopene_cycl: Lycopene cyclase protein

slope= -3.87 p_value= 8.4e-06 intercept= 11.52 p_value= 0.00017

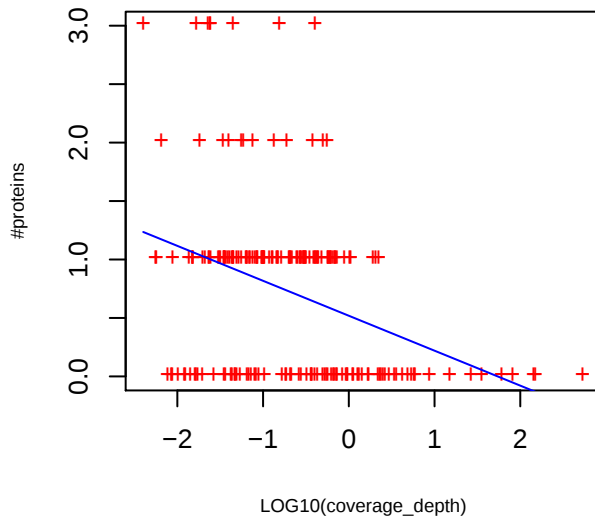


P-value curve ; red (unnorm), green (norm)



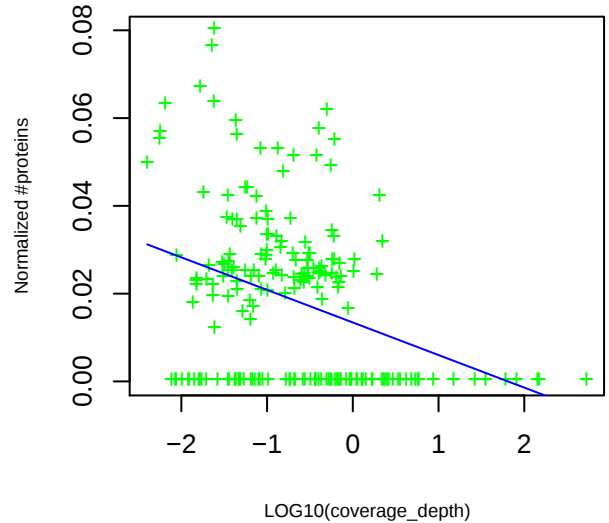
PF00813 FliP: FliP family

slope= -0.30 p_value= 3.1e-07 intercept= 0.52 p_value= 4.3e-14



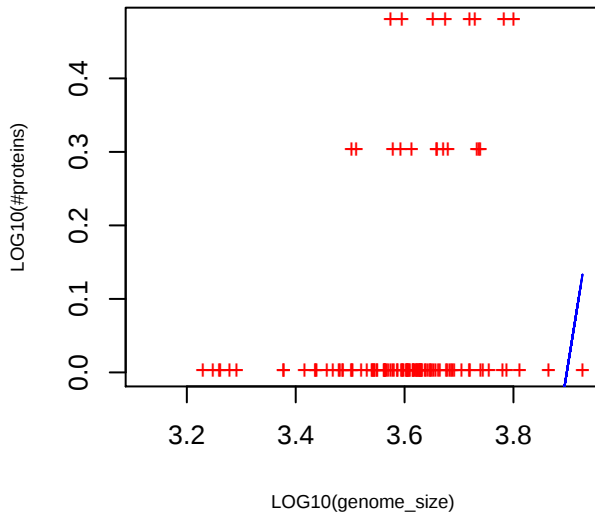
PF00813 FliP: FliP family

slope= -0.0074 p_value= 4.1e-07 intercept= 0.013 p_value= 8.8e-15

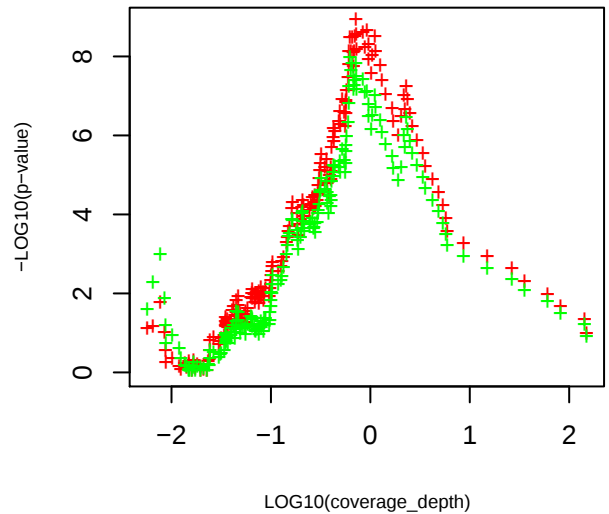


PF00813 FliP: FliP family

slope= 4.61 p_value= 6.2e-08 intercept= -17.98 p_value= 3.6e-09

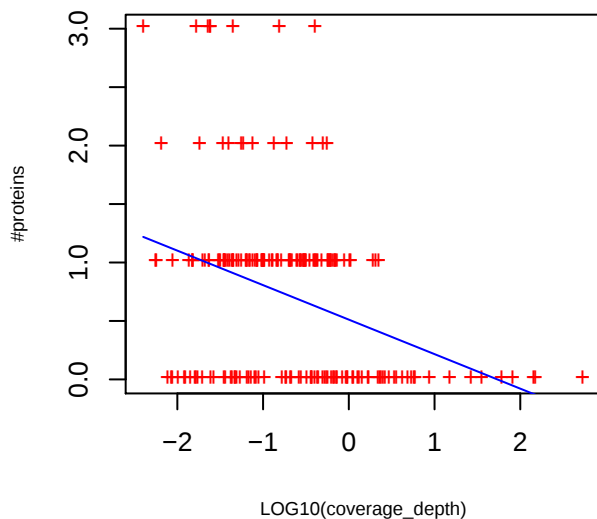


P-value curve ; red (unnorm), green (norm)



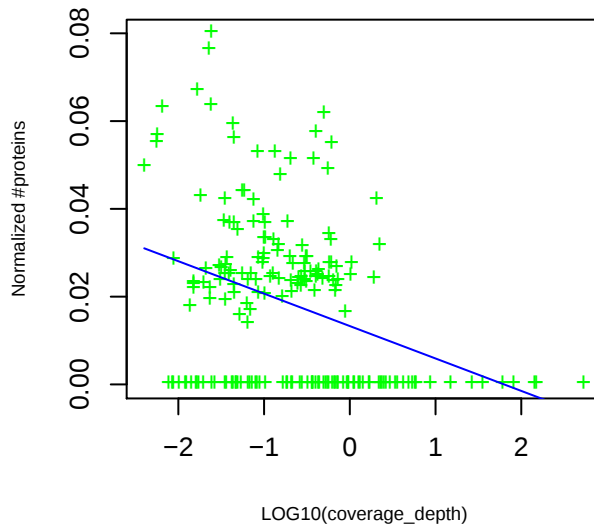
PF01312 Bac_export_2: FlhB/HrpN/YscU/SpaS family

slope= -0.30 p_value= 5e-07 intercept= 0.51 p_value= 1.2e-13



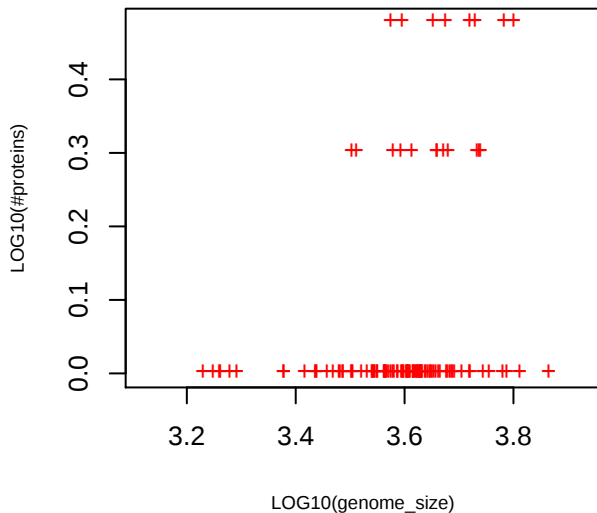
PF01312 Bac_export_2: FlhB/HrpN/YscU/SpaS family

slope= -0.0074 p_value= 5.2e-07 intercept= 0.013 p_value= 2e-14

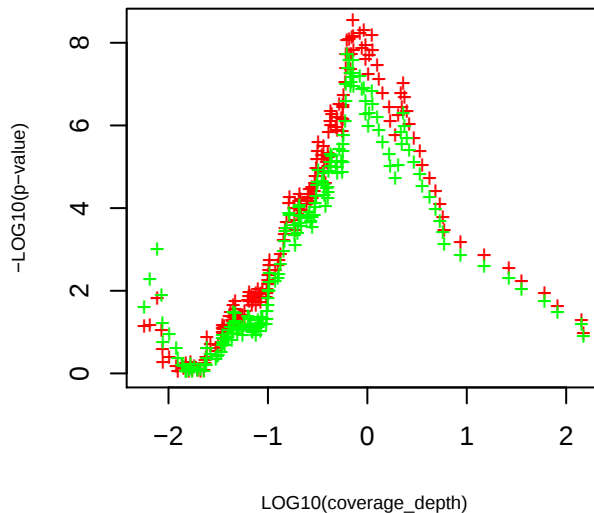


PF01312 Bac_export_2: FlhB/HrpN/YscU/SpaS family

slope= 4.17 p_value= 1.3e-06 intercept= -16.46 p_value= 9.1e-08

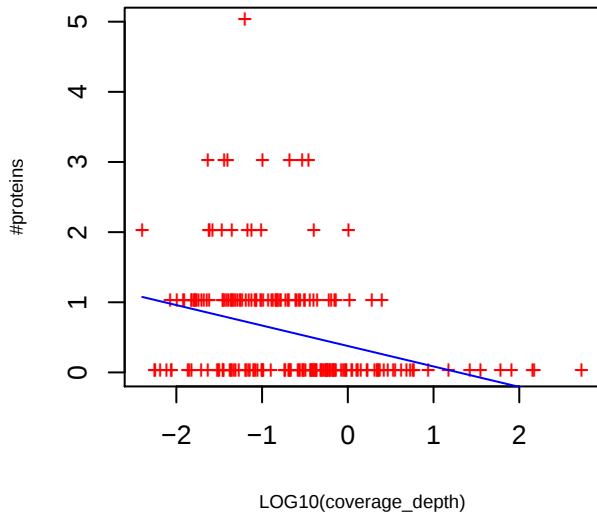


P-value curve ; red (unnorm), green (norm)



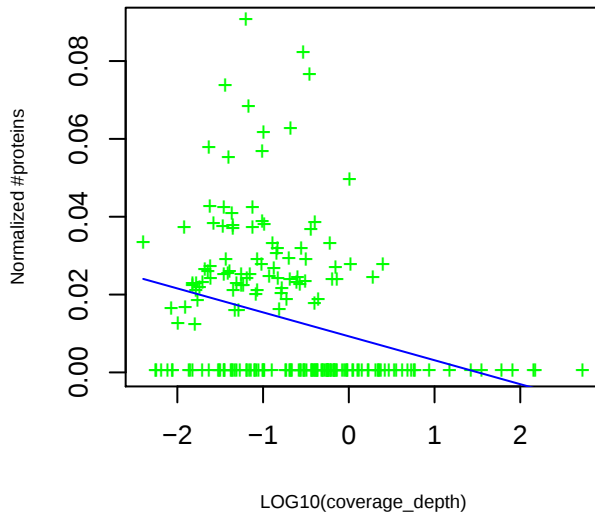
PF00962 A_deaminase: Adenosine/AMP deaminase

slope= -0.29 p_value= 5.4e-06 intercept= 0.38 p_value= 2.4e-07



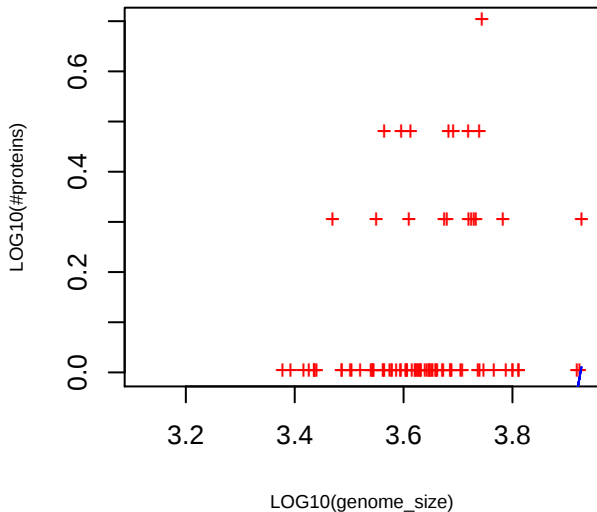
PF00962 A_deaminase: Adenosine/AMP deaminase

slope= -0.0061 p_value= 2.8e-05 intercept= 0.0093 p_value= 3.7e-08

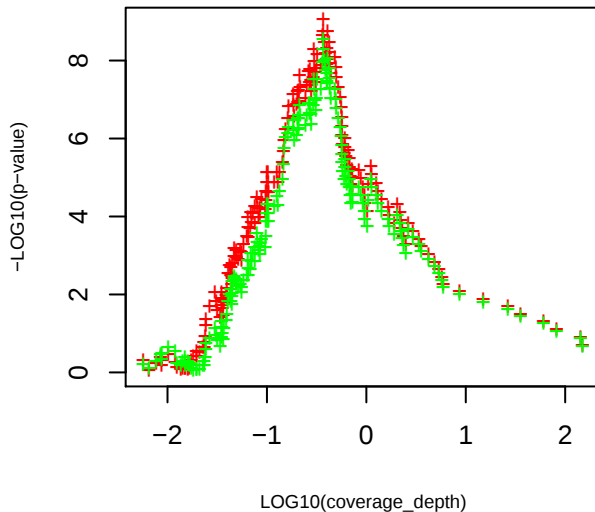


PF00962 A_deaminase: Adenosine/AMP deaminase

slope= 5.89 p_value= 2.4e-12 intercept= -23.12 p_value= 1.9e-14

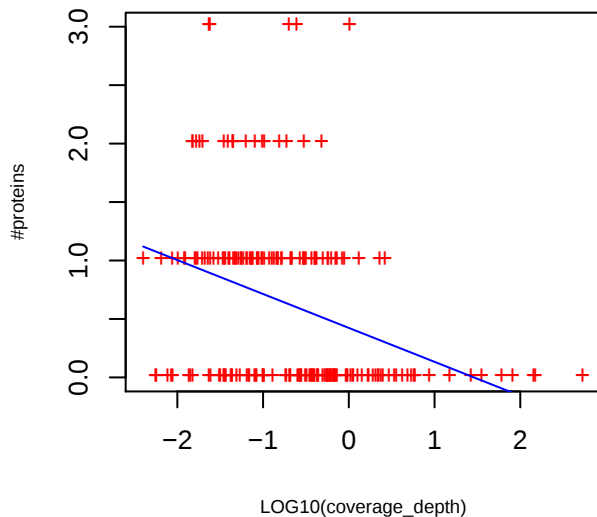


P-value curve ; red (unnorm), green (norm)



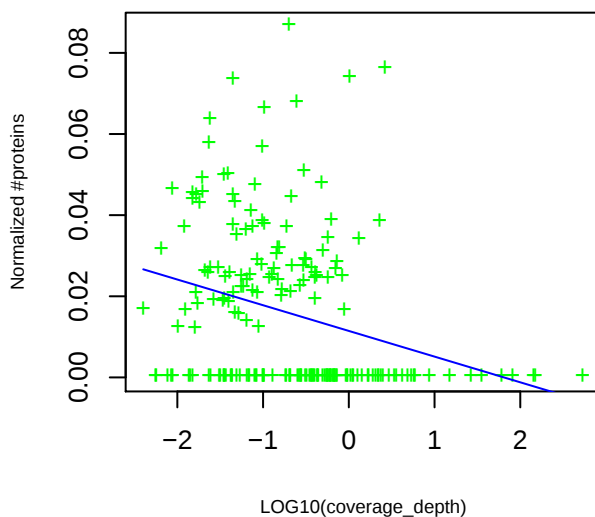
TIGR00203 cydB: cytochrome d ubiquinol oxidase, subunit II

slope= -0.29 p_value= 8e-07 intercept= 0.42 p_value= 4e-10



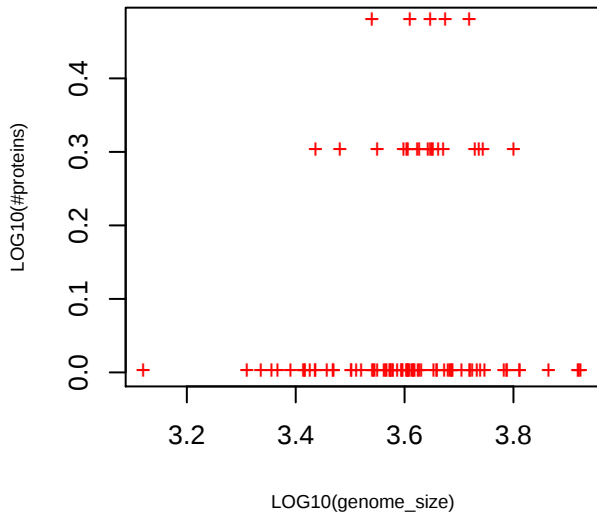
TIGR00203 cydB: cytochrome d ubiquinol oxidase, subunit II

slope= -0.0063 p_value= 4e-05 intercept= 0.011 p_value= 1.8e-10

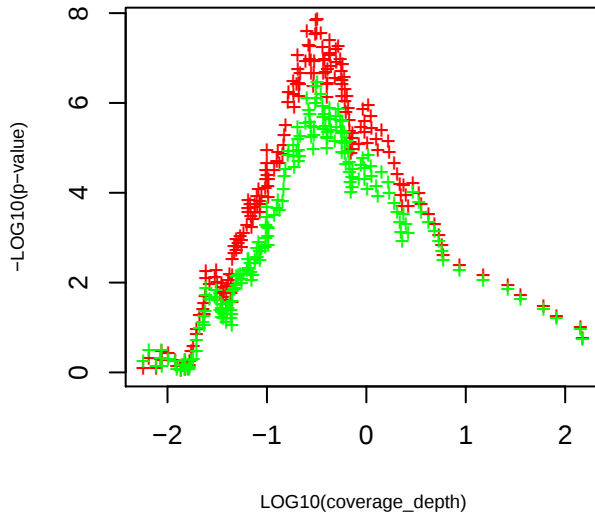


TIGR00203 cydB: cytochrome d ubiquinol oxidase, subunit II

slope= 4.72 p_value= 5.4e-08 intercept= -18.75 p_value= 1.6e-09

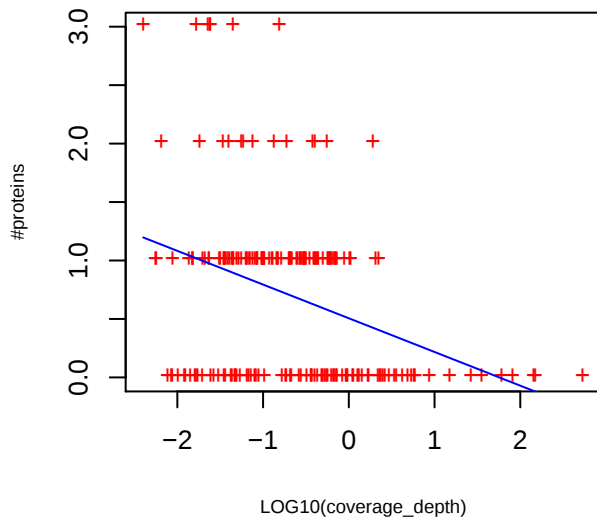


P-value curve : red (unnorm), green (norm)



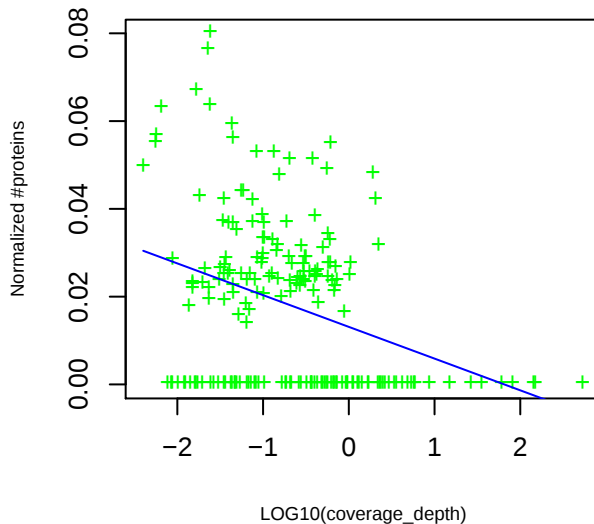
PF01311 Bac_export_1: Bacterial export proteins, family 1

slope= -0.29 p_value= 6.4e-07 intercept= 0.51 p_value= 1.1e-13



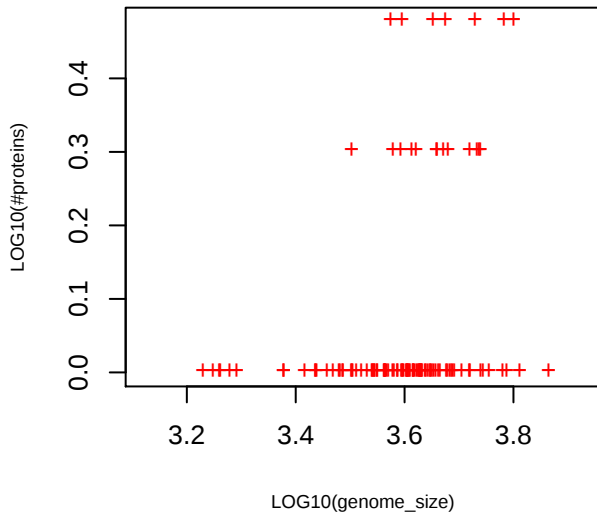
PF01311 Bac_export_1: Bacterial export proteins, family 1

slope= -0.0072 p_value= 6.6e-07 intercept= 0.013 p_value= 2.3e-14

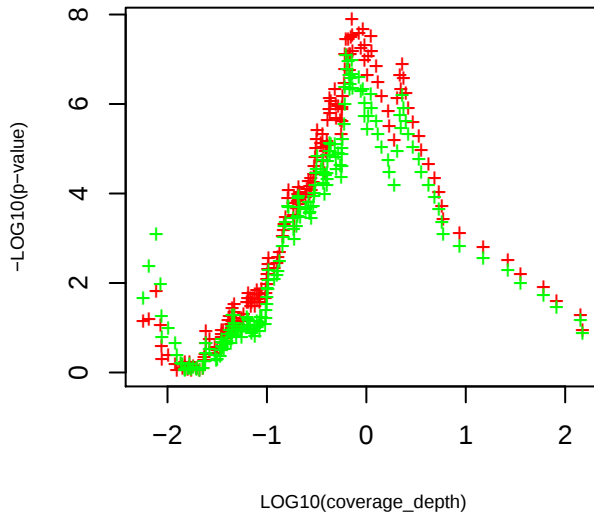


PF01311 Bac_export_1: Bacterial export proteins, family 1

slope= 4.24 p_value= 8.8e-07 intercept= -16.72 p_value= 5.8e-08

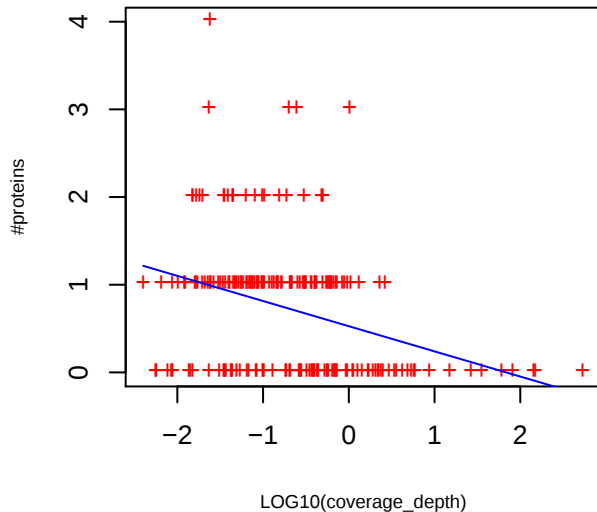


P-value curve ; red (unnorm), green (norm)



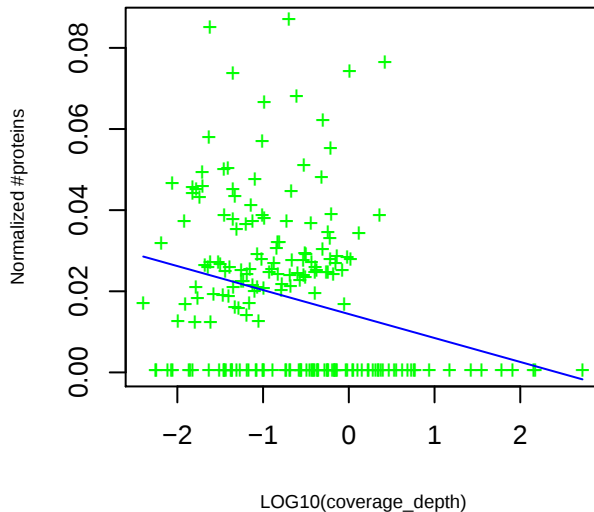
PF02322 Cyto_ox_2: cytochrome oxidase subunit II

slope= -0.29 p_value= 1.5e-06 intercept= 0.53 p_value= 7e-14



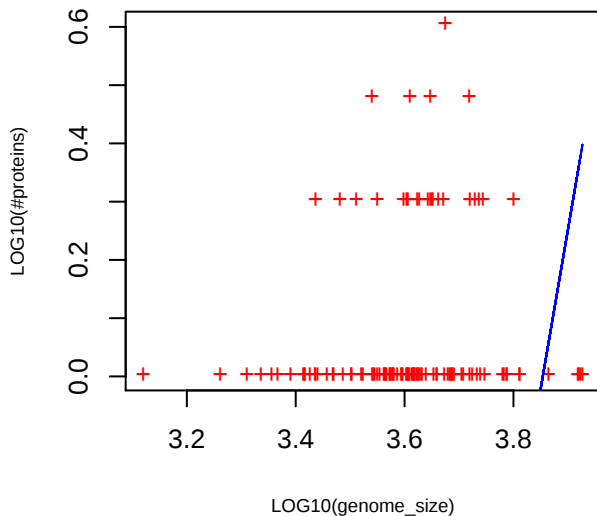
PF02322 Cyto_ox_2: cytochrome oxidase subunit II

slope= -0.0059 p_value= 0.00017 intercept= 0.014 p_value= 2.1e-14

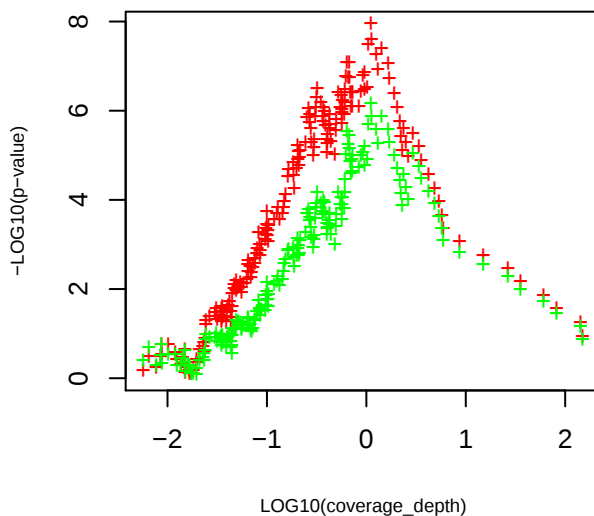


PF02322 Cyto_ox_2: cytochrome oxidase subunit II

slope= 5.45 p_value= 1.2e-10 intercept= -21.01 p_value= 4e-12

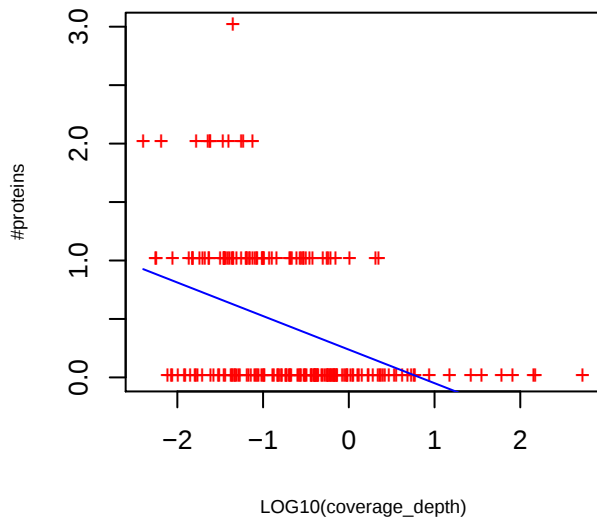


P-value curve ; red (unnorm), green (norm)



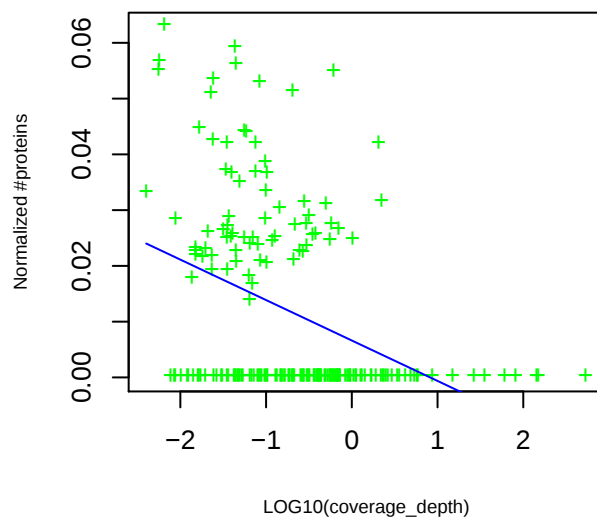
PF02465 FliD_N: flagellar hook-associated protein 2

slope= -0.29 p_value= 2.0e-09 intercept= 0.24 p_value= 7e-06



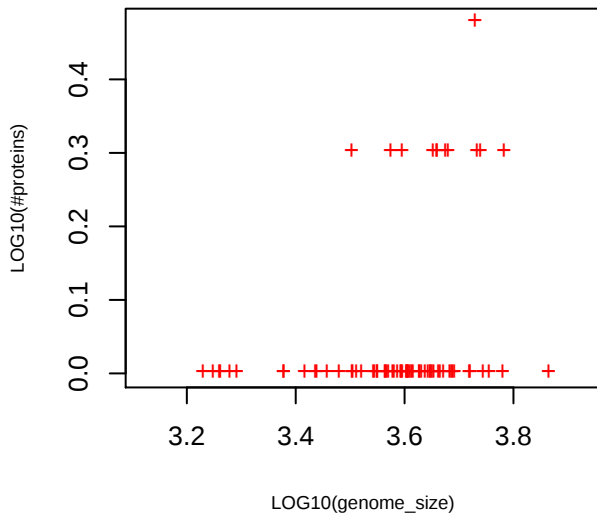
PF02465 FliD_N: flagellar hook-associated protein 2

slope= -0.0073 p_value= 2.2e-08 intercept= 0.0066 p_value= 4.6e-06

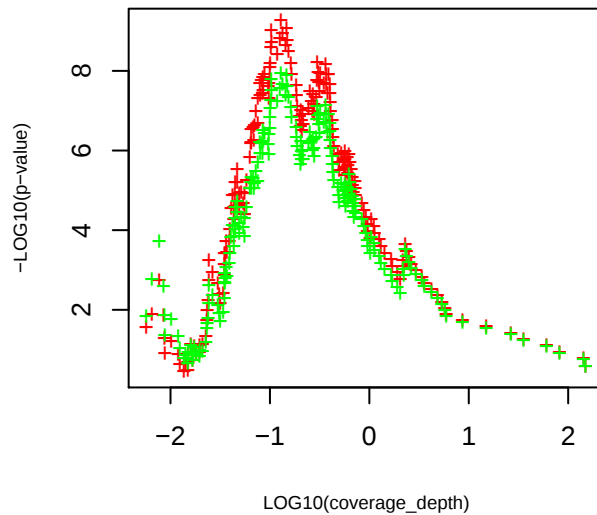


PF02465 FliD_N: flagellar hook-associated protein 2

slope= 2.16 p_value= 0.012 intercept= -10.16 p_value= 9e-04

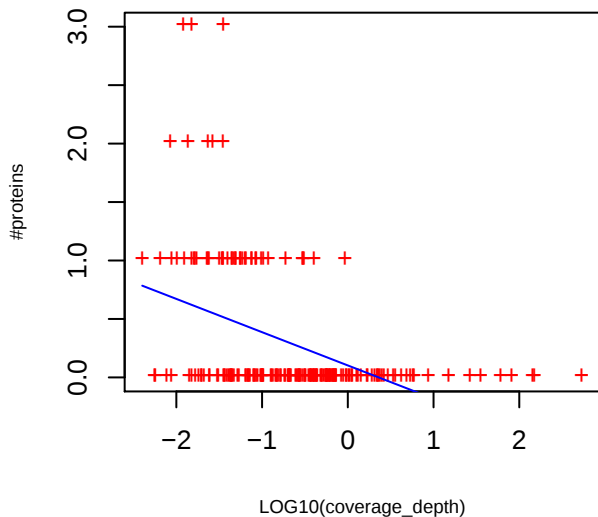


P-value curve ; red (unnorm), green (norm)



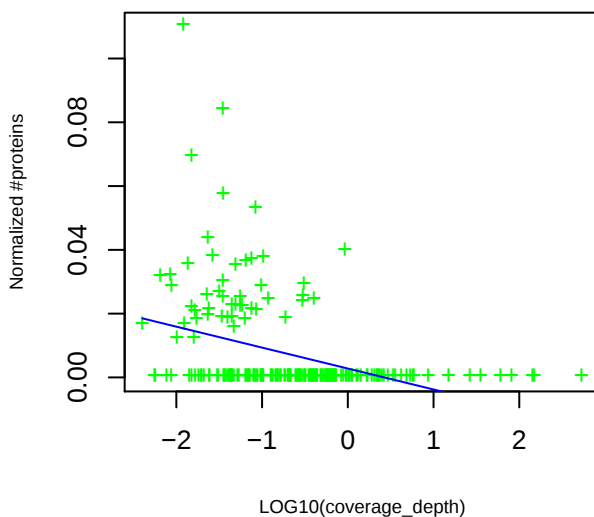
PF09383 NIL: NIL domain

slope= -0.28 p_value= 3.6e-10 intercept= 0.10 p_value= 0.036



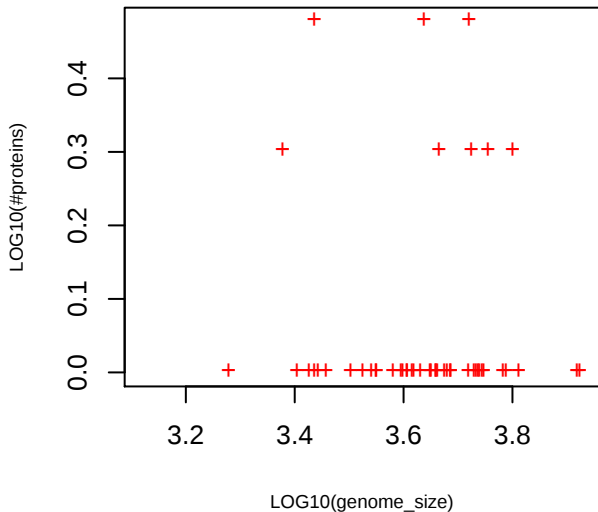
PF09383 NIL: NIL domain

slope= -0.0066 p_value= 6.6e-08 intercept= 0.0028 p_value= 0.036

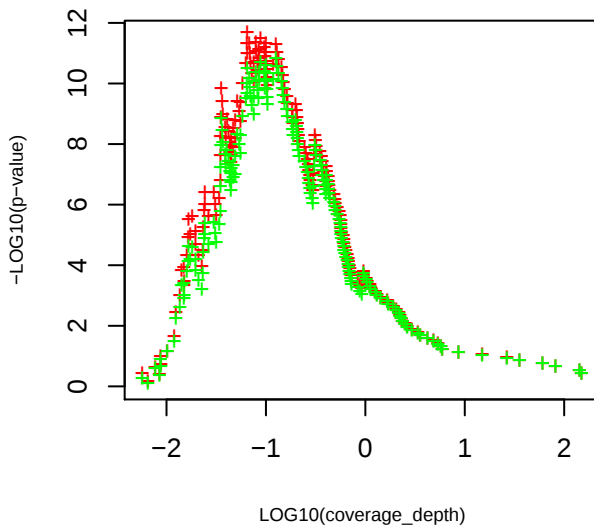


PF09383 NIL: NIL domain

slope= 3.34 p_value= 8.8e-06 intercept= -14.84 p_value= 3.9e-08

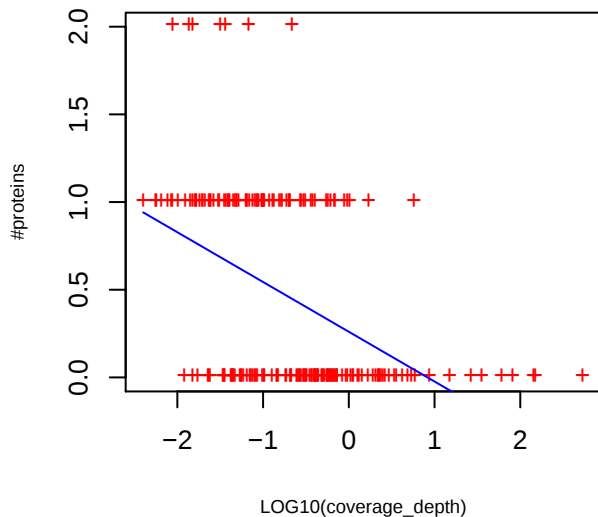


P-value curve ; red (unnorm), green (norm)



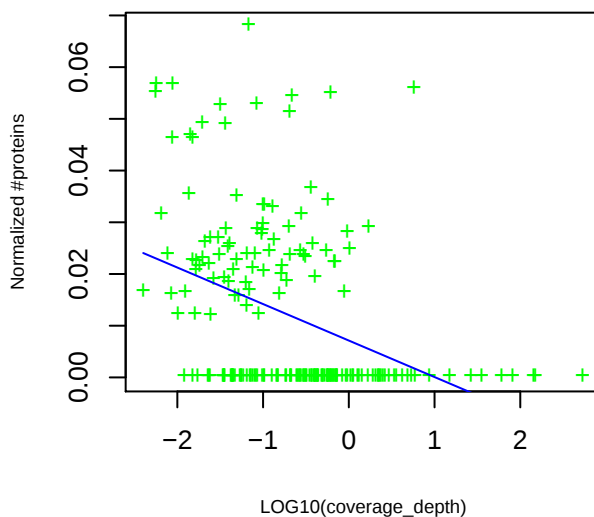
PF02834 2_5_RNA_ligase: 2',5' RNA ligase family

slope= -0.28 p_value= 4e-11 intercept= 0.26 p_value= 4.7e-08



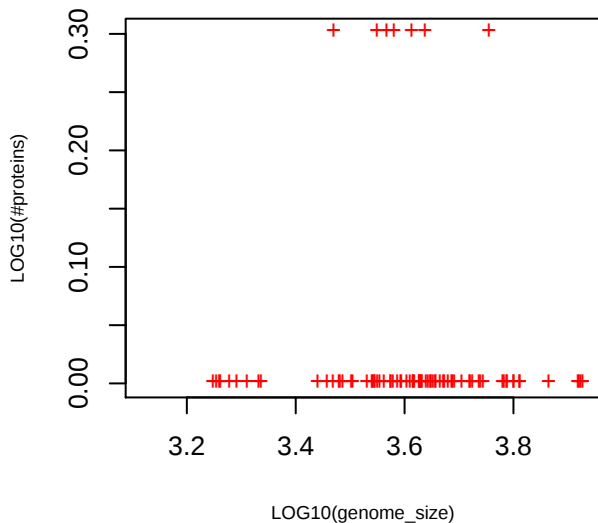
PF02834 2_5_RNA_ligase: 2',5' RNA ligase family

slope= -0.007 p_value= 2.4e-08 intercept= 0.0071 p_value= 5e-07

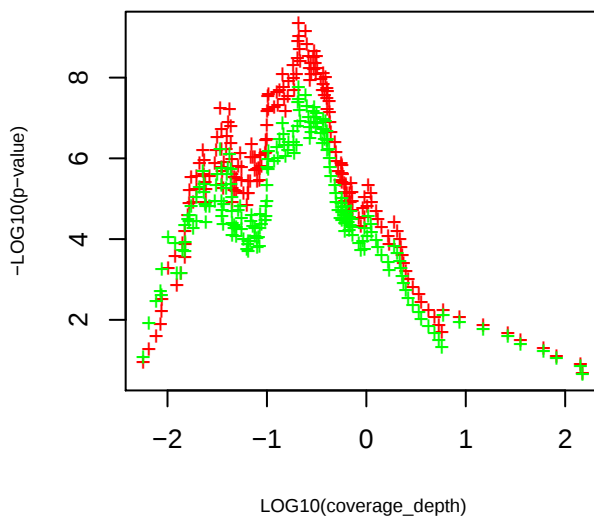


PF02834 2_5_RNA_ligase: 2',5' RNA ligase family

slope= 4.10 p_value= 1.5e-06 intercept= -16.83 p_value= 3.5e-08

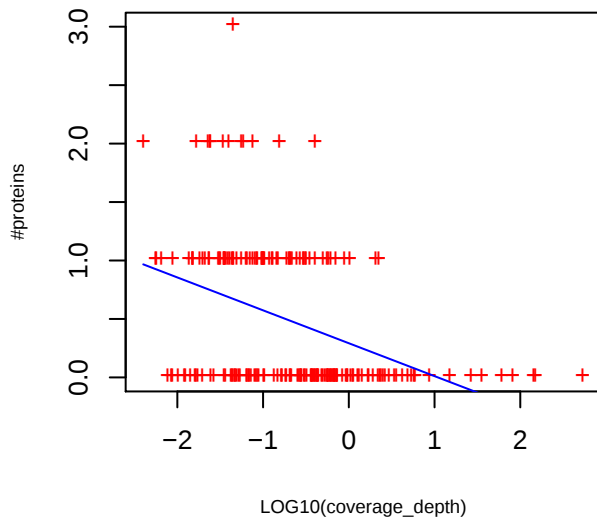


P-value curve ; red (unnorm), green (norm)



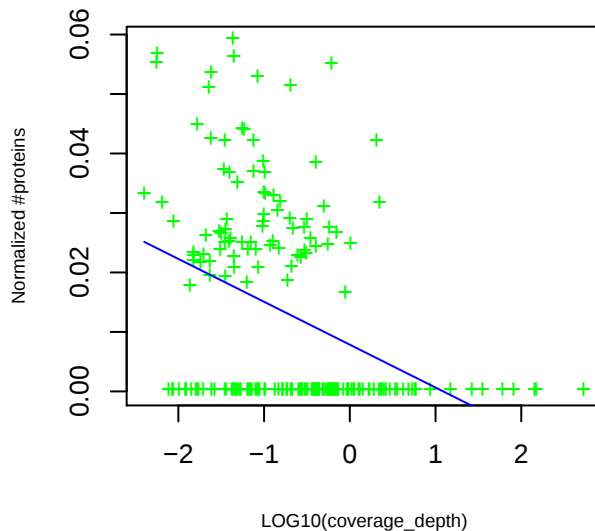
TIGR00328 flhB: flagellar biosynthetic protein FlhB

slope= -0.28 p_value= 8.5e-09 intercept= 0.29 p_value= 9.7e-08



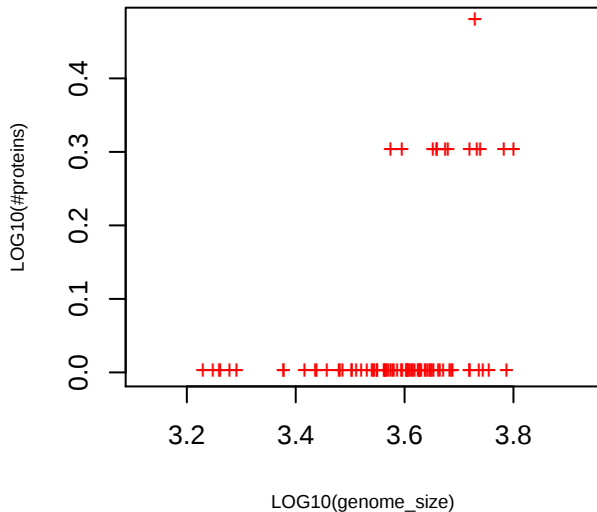
TIGR00328 flhB: flagellar biosynthetic protein FlhB

slope= -0.0072 p_value= 2.2e-08 intercept= 0.0079 p_value= 6.2e-08

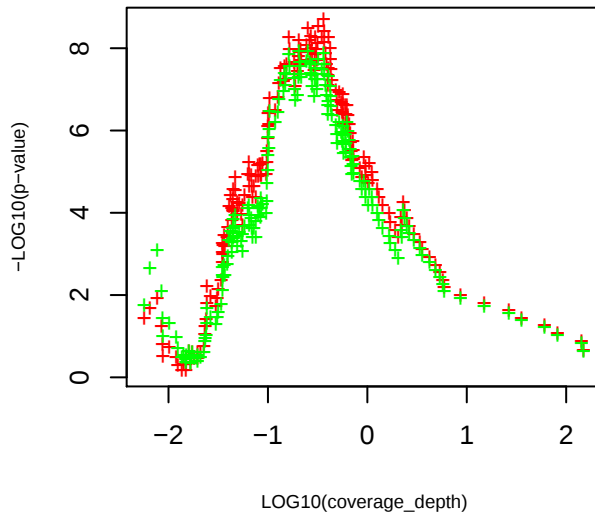


TIGR00328 flhB: flagellar biosynthetic protein FlhB

slope= 2.49 p_value= 0.0043 intercept= -11.13 p_value= 0.00035

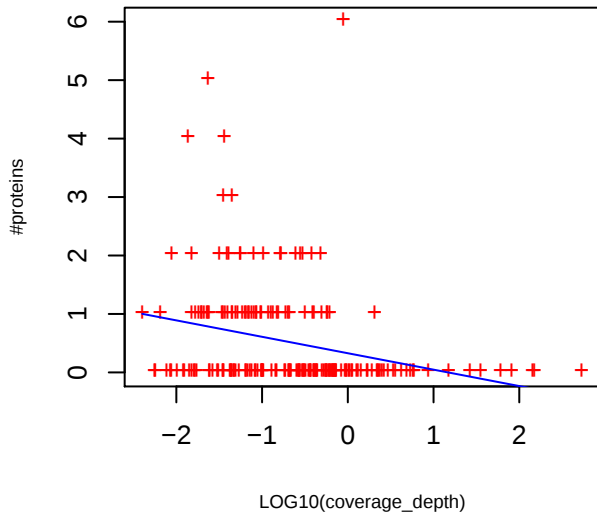


P-value curve ; red (unnorm), green (norm)



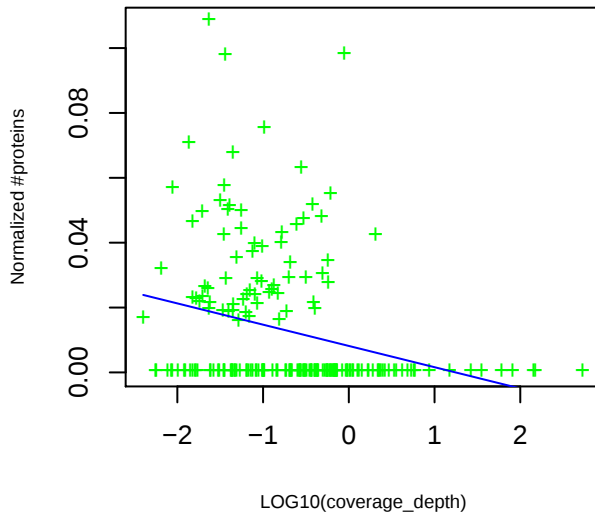
TIGR00711 efflux_EmrB: drug resistance MFS transporter, drug:H+ antiporter-1 (14 Spanner) (DHA2)

slope= -0.28 p_value= 0.00011 intercept= 0.33 p_value= 6.4e-05



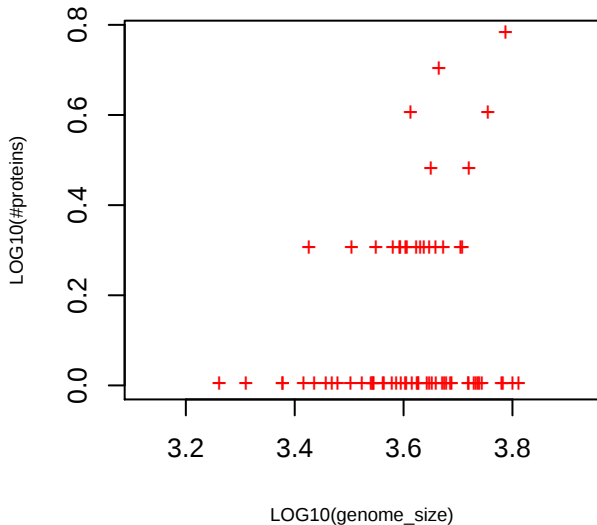
TIGR00711 efflux_EmrB: drug resistance MFS transporter, drug:H+ antiporter-1 (14 Spanner) (DHA2)

slope= -0.0066 p_value= 8.1e-05 intercept= 0.0082 p_value= 1.5e-05

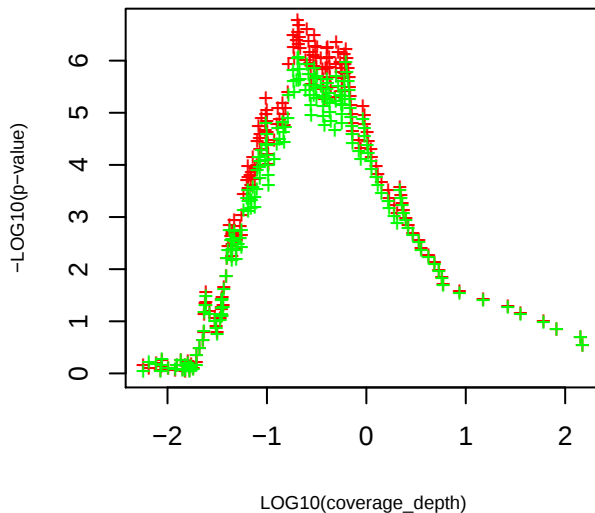


TIGR00711 efflux_EmrB: drug resistance MFS transporter, drug:H+ antiporter-1 (14 Spanner) (DHA2)

slope= 3.64 p_value= 1.7e-05 intercept= -15.47 p_value= 3.4e-07

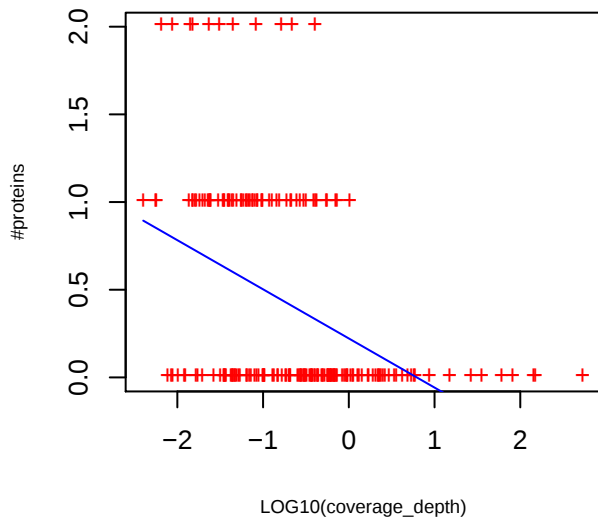


P-value curve : red (unnorm), green (norm)



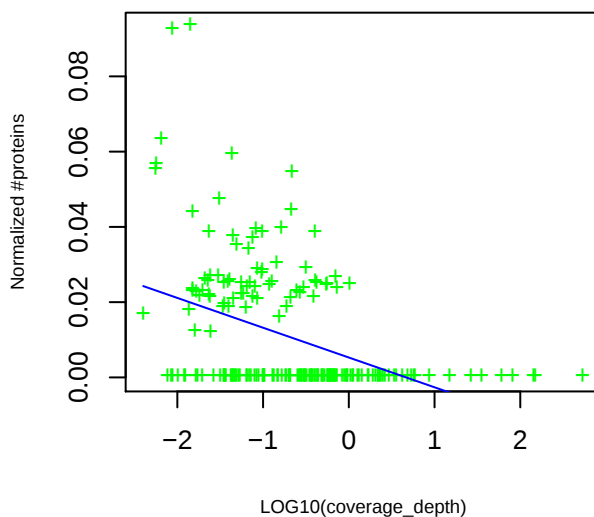
PF01980 UPF0066: Uncharacterised protein family

slope= -0.28 p_value= 8.2e-10 intercept= 0.22 p_value= 1e-05



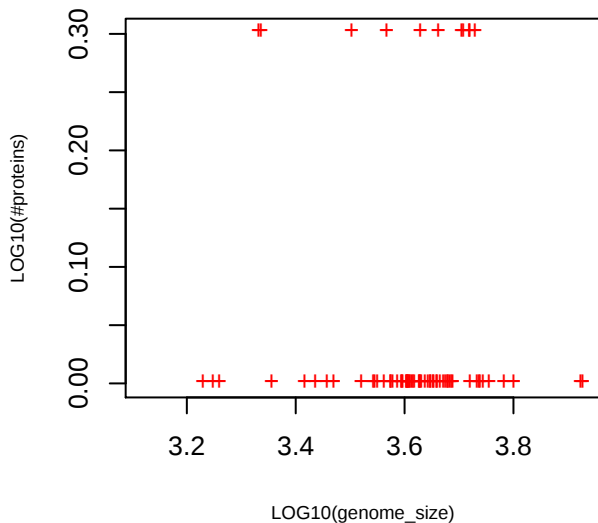
PF01980 UPF0066: Uncharacterised protein family

slope= -0.0079 p_value= 1.3e-09 intercept= 0.0053 p_value= 0.00022

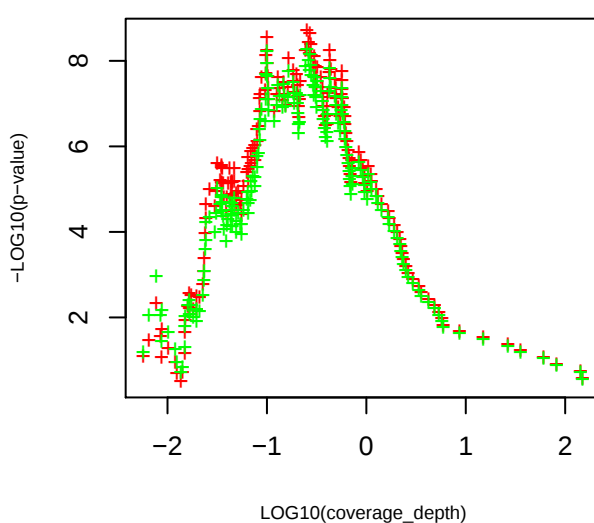


PF01980 UPF0066: Uncharacterised protein family

slope= 3.62 p_value= 1.5e-05 intercept= -15.37 p_value= 3e-07

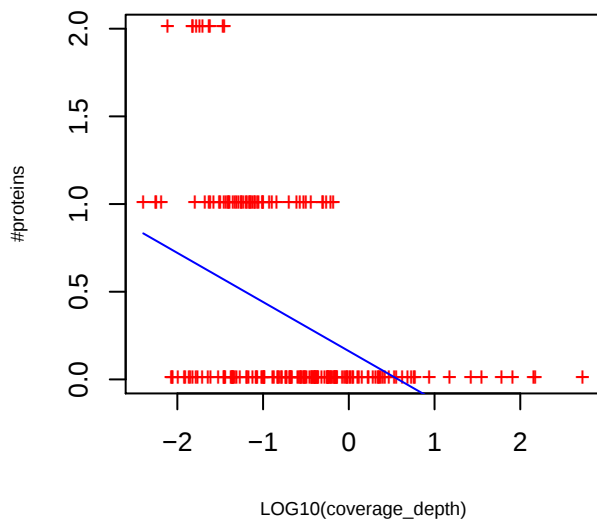


P-value curve ; red (unnorm), green (norm)



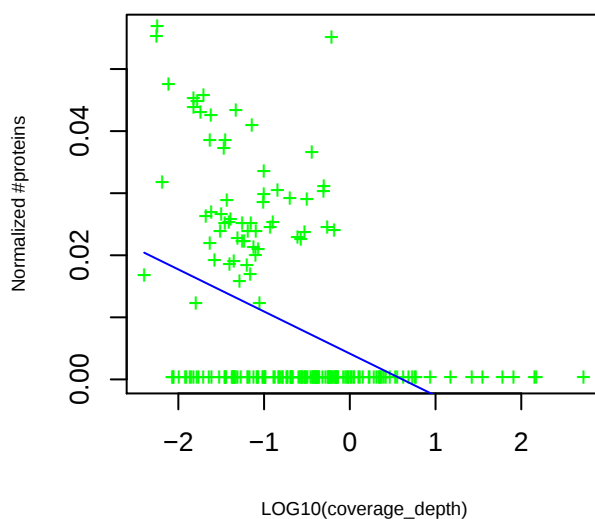
PF08267 Meth_synt_1: Cobalamin-independent synthase, N-terminal domain

slope= -0.28 p_value= 1.8e-10 intercept= 0.16 p_value= 0.00071



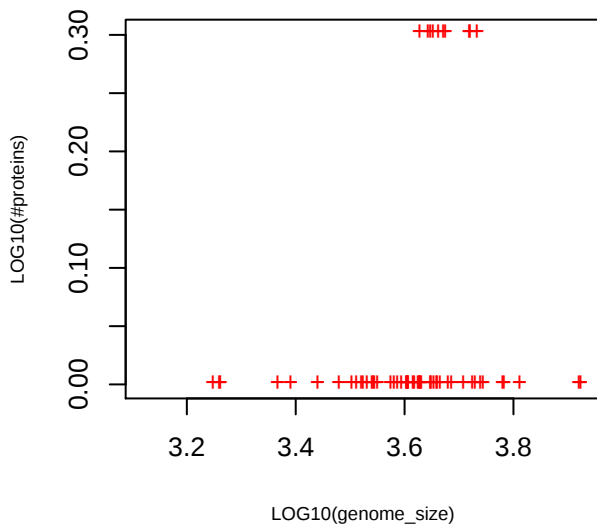
PF08267 Meth_synt_1: Cobalamin-independent synthase, N-terminal domain

slope= -0.0068 p_value= 1.5e-09 intercept= 0.0042 p_value= 0.00068

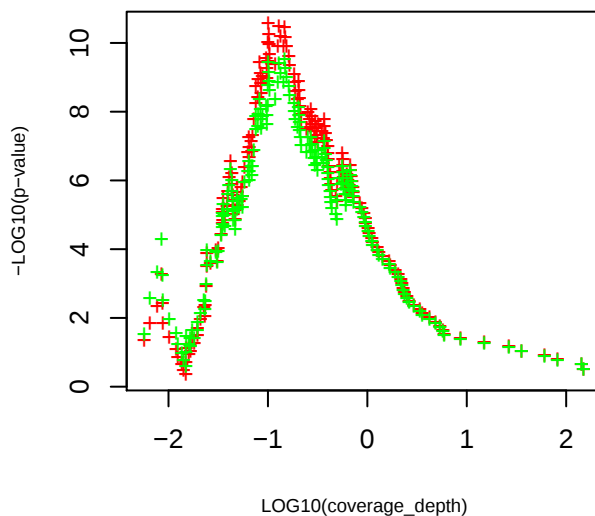


PF08267 Meth_synt_1: Cobalamin-independent synthase, N-terminal domain

slope= 3.25 p_value= 5.5e-05 intercept= -14.29 p_value= 7.6e-07

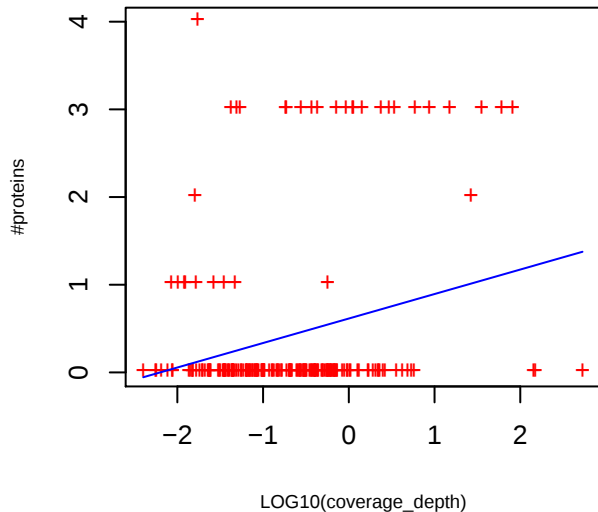


P-value curve ; red (unnorm), green (norm)



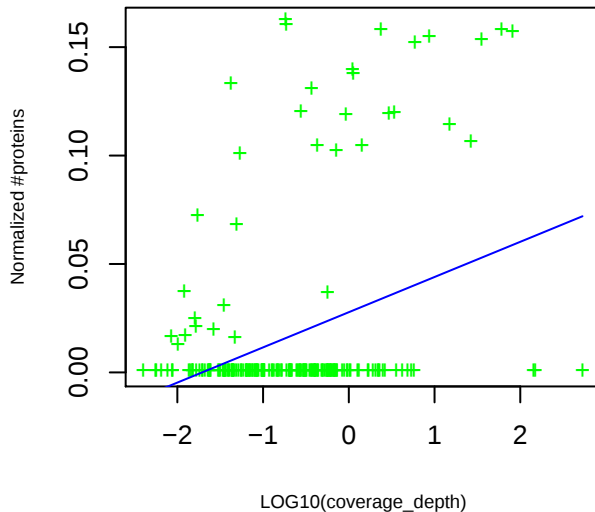
PF05996 Fe_bilin_red: Ferredoxin-dependent bilin reductase

slope= 0.28 p_value= 4e-04 intercept= 0.61 p_value= 3.6e-11



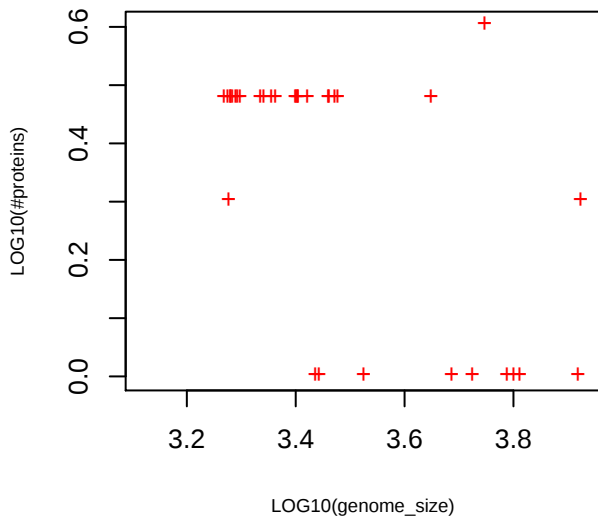
PF05996 Fe_bilin_red: Ferredoxin-dependent bilin reductase

slope= 0.016 p_value= 8.4e-07 intercept= 0.028 p_value= 6.1e-13

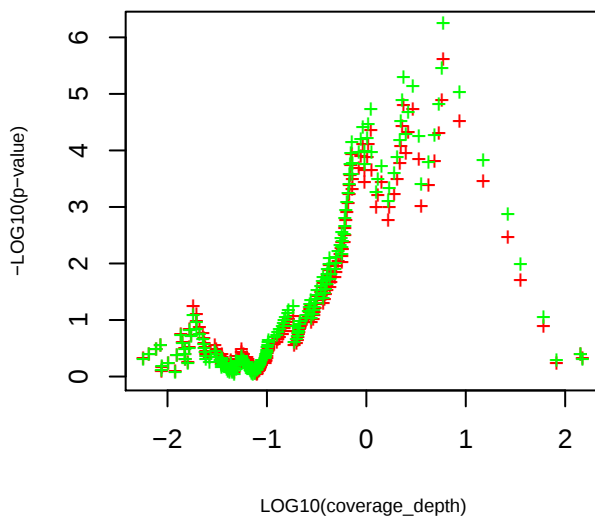


PF05996 Fe_bilin_red: Ferredoxin-dependent bilin reductase

slope= -2.05 p_value= 0.0043 intercept= 4.01 p_value= 0.11

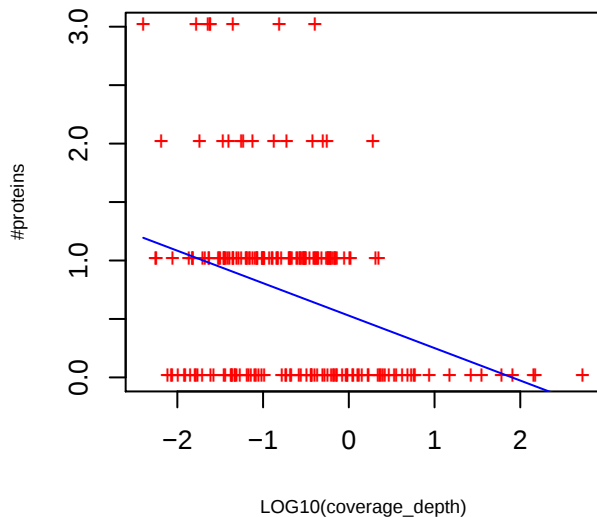


P-value curve ; red (unnorm), green (norm)



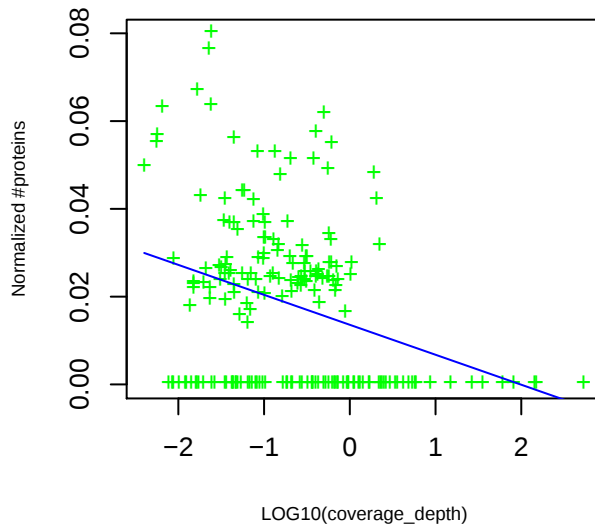
PF01313 Bac_export_3: Bacterial export proteins, family 3

slope= -0.28 p_value= 2.9e-06 intercept= 0.53 p_value= 5.2e-14



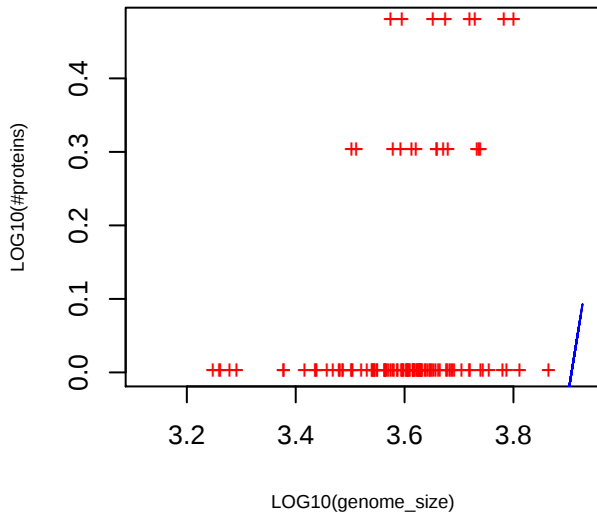
PF01313 Bac_export_3: Bacterial export proteins, family 3

slope= -0.0068 p_value= 3.4e-06 intercept= 0.014 p_value= 7.7e-15

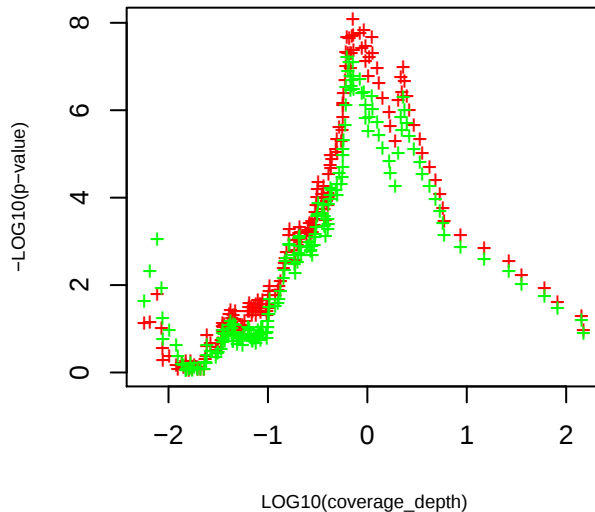


PF01313 Bac_export_3: Bacterial export proteins, family 3

slope= 4.61 p_value= 7.3e-08 intercept= -18.01 p_value= 4.1e-09

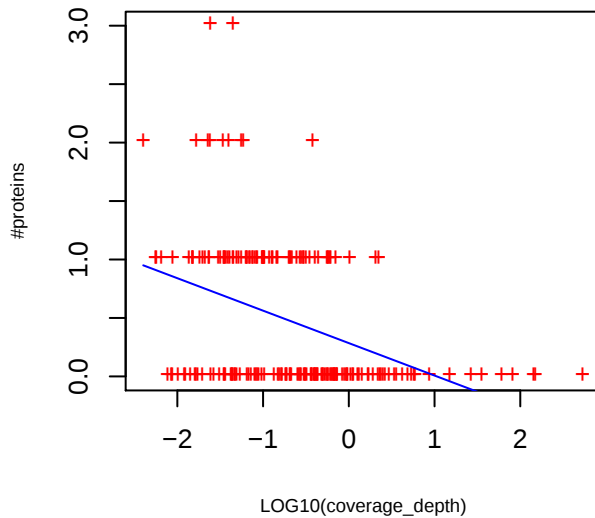


P-value curve ; red (unnorm), green (norm)



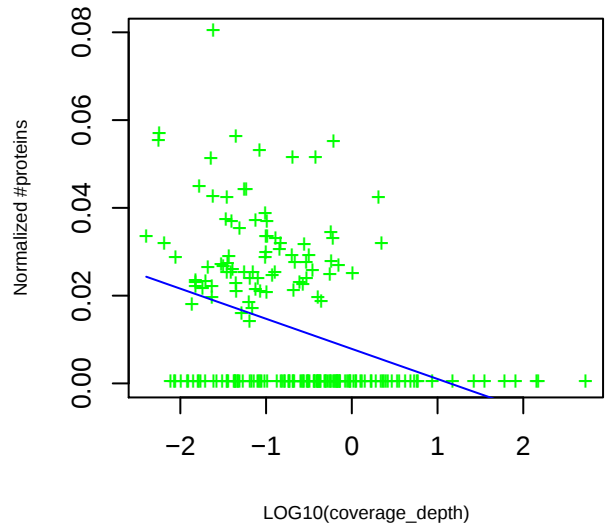
TIGR00205 fliE: flagellar hook-basal body complex protein FliE

slope= -0.28 p_value= 1.4e-08 intercept= 0.29 p_value= 2.0e-07



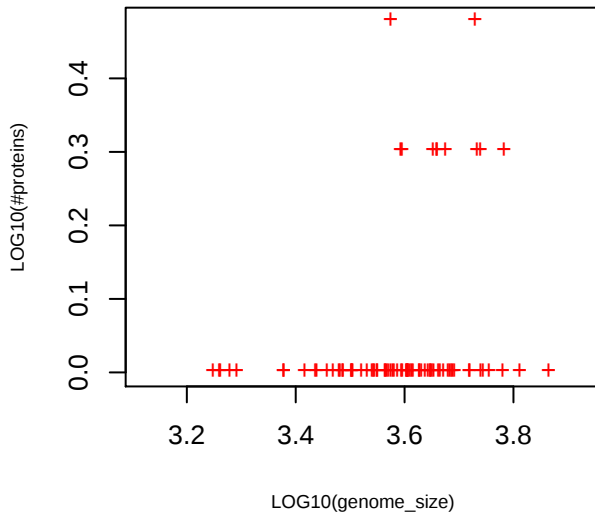
TIGR00205 fliE: flagellar hook-basal body complex protein FliE

slope= -0.0069 p_value= 1.6e-07 intercept= 0.0079 p_value= 1.0e-07

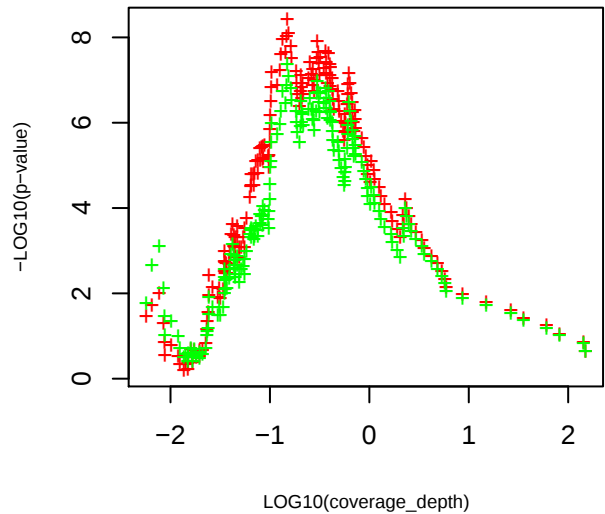


TIGR00205 fliE: flagellar hook-basal body complex protein FliE

slope= 2.56 p_value= 0.0032 intercept= -11.40 p_value= 0.00024

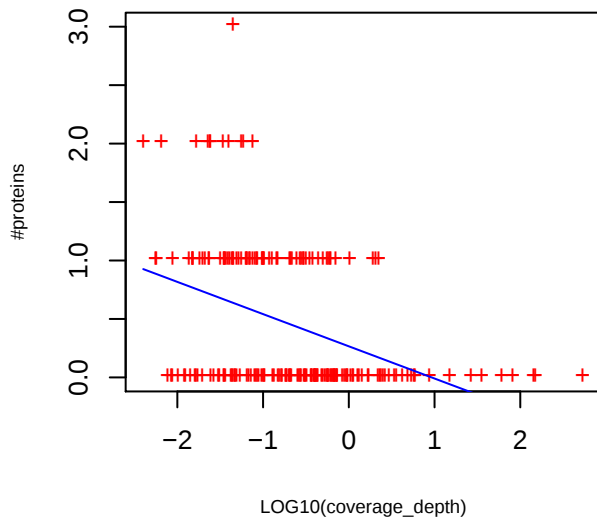


P-value curve : red (unnorm), green (norm)



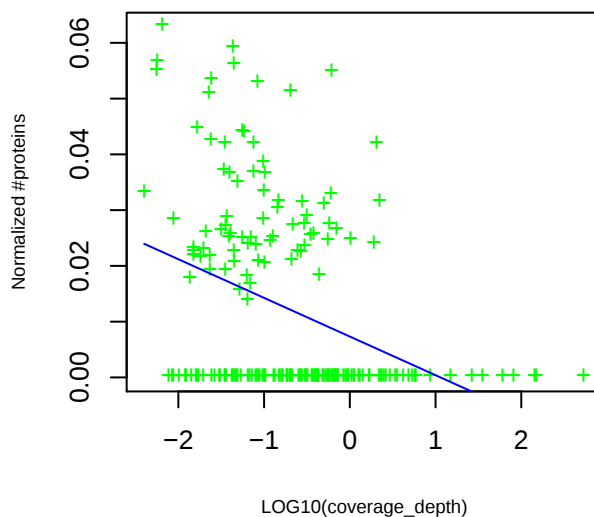
PF07195 FliD_C: Flagellar hook-associated protein 2 C-terminus

slope= -0.28 p_value= 1.1e-08 intercept= 0.27 p_value= 7.6e-07



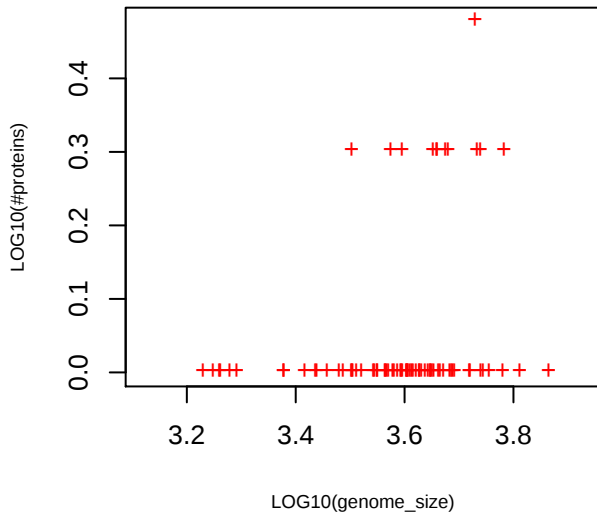
PF07195 FliD_C: Flagellar hook-associated protein 2 C-terminus

slope= -0.007 p_value= 1.1e-07 intercept= 0.0073 p_value= 5.8e-07

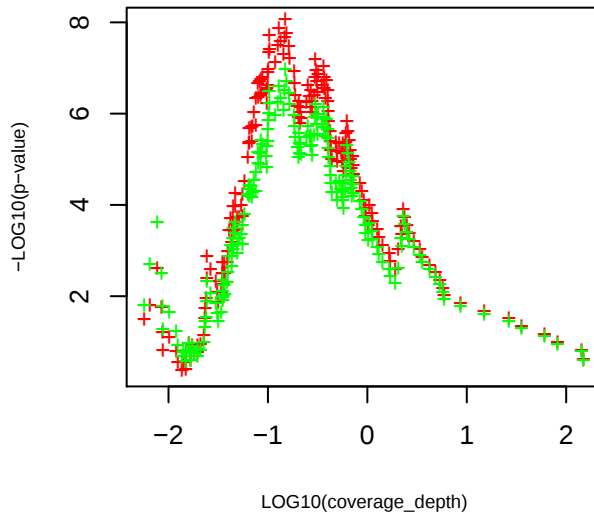


PF07195 FliD_C: Flagellar hook-associated protein 2 C-terminus

slope= 2.45 p_value= 0.0046 intercept= -11.09 p_value= 0.00032

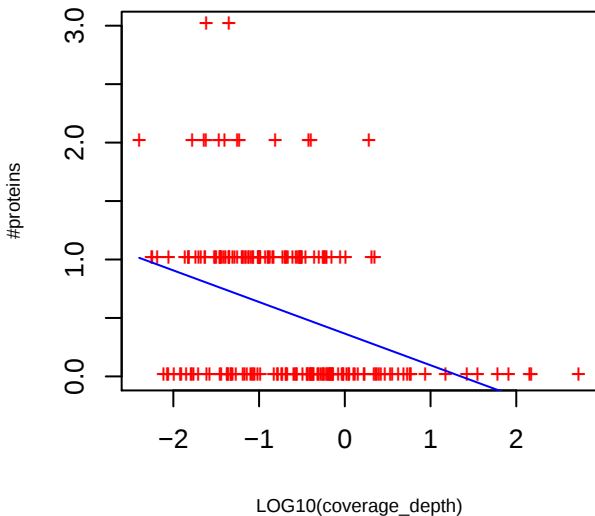


P-value curve ; red (unnorm), green (norm)



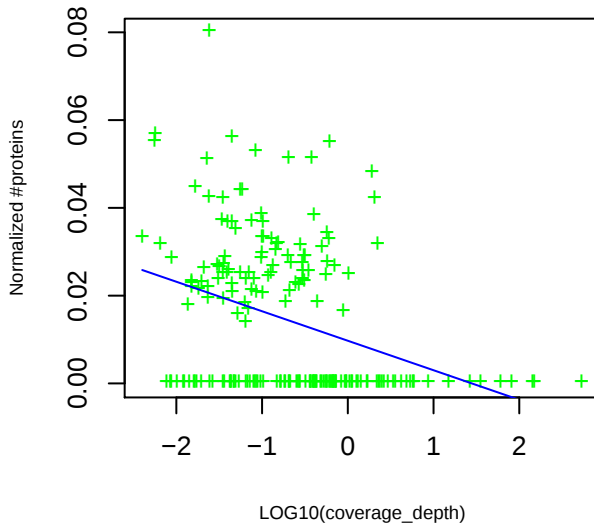
PF02049 FliE: flagellar hook-basal body complex protein FliE

slope= -0.27 p_value= 1.0e-07 intercept= 0.37 p_value= 3.3e-10



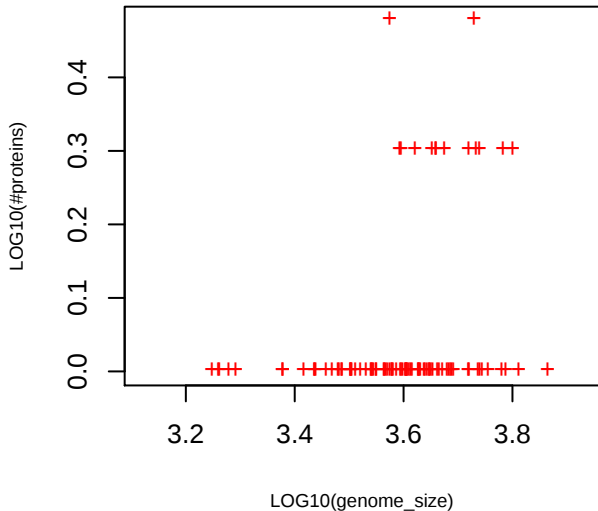
PF02049 FliE: flagellar hook-basal body complex protein FliE

slope= -0.0067 p_value= 4.3e-07 intercept= 0.0097 p_value= 2.1e-10

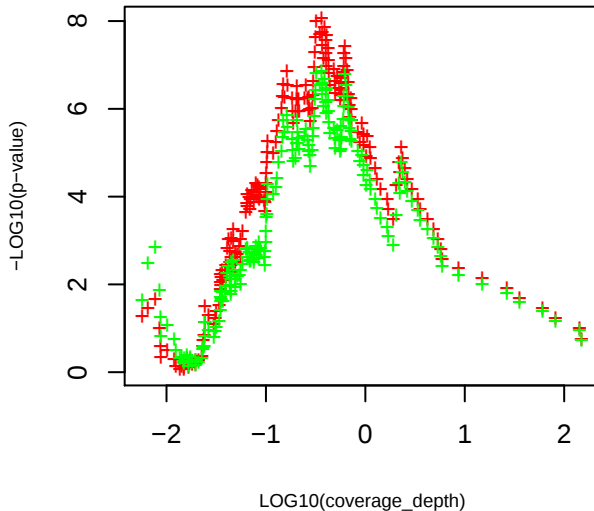


PF02049 FliE: flagellar hook-basal body complex protein FliE

slope= 3.40 p_value= 0.00010 intercept= -14.13 p_value= 6.2e-06

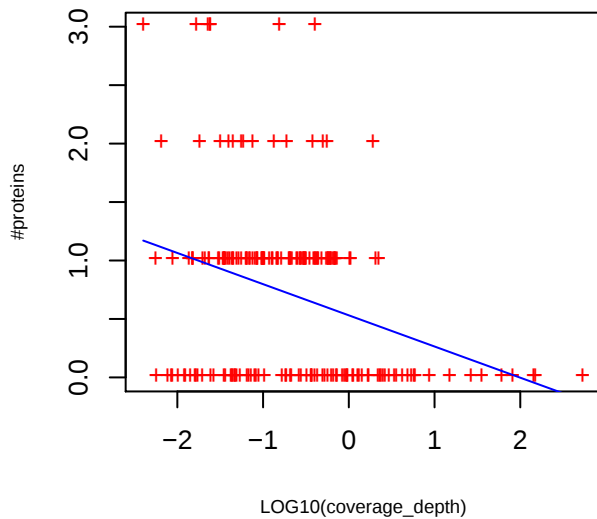


P-value curve : red (unnorm), green (norm)



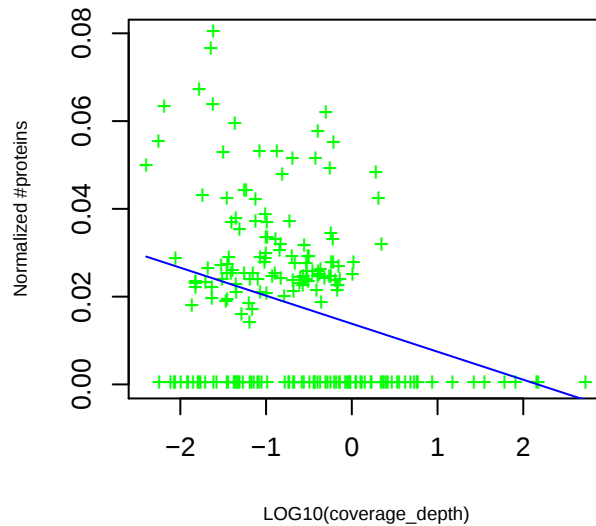
TIGR01026 filI_yscN: ATPase FilI/YscN family

slope= -0.27 p_value= 5.2e-06 intercept= 0.53 p_value= 2.1e-14



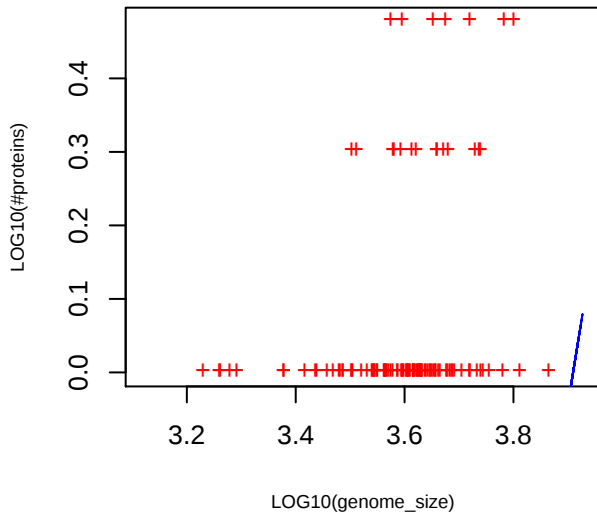
TIGR01026 filI_yscN: ATPase FilI/YscN family

slope= -0.0064 p_value= 1.4e-05 intercept= 0.014 p_value= 3.8e-15

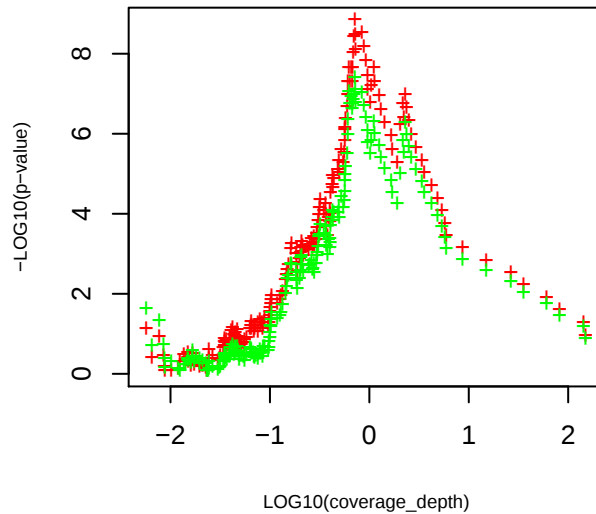


TIGR01026 filI_yscN: ATPase FilI/YscN family

slope= 4.58 p_value= 9.1e-08 intercept= -17.89 p_value= 5.1e-09

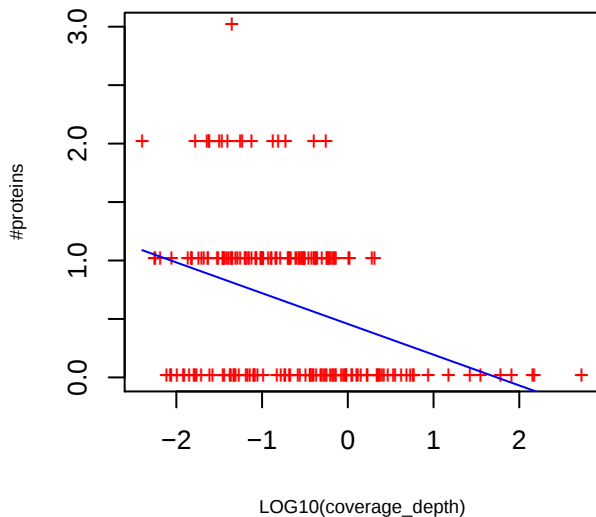


P-value curve ; red (unnorm), green (norm)



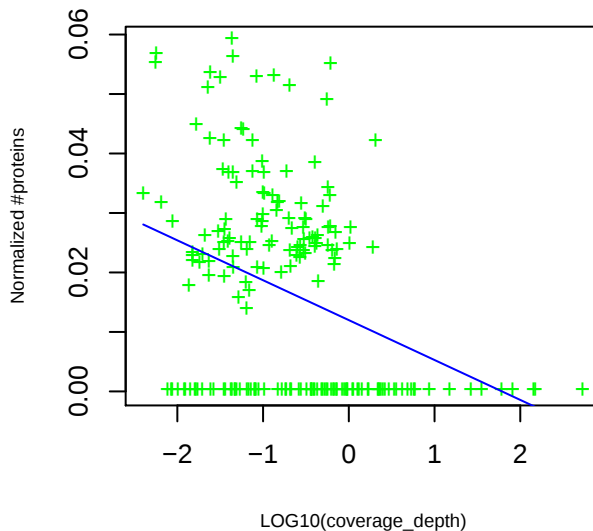
TIGR00206 flIF: flagellar M-ring protein FlIF

slope= -0.26 p_value= 1.9e-07 intercept= 0.46 p_value= 1.6e-14



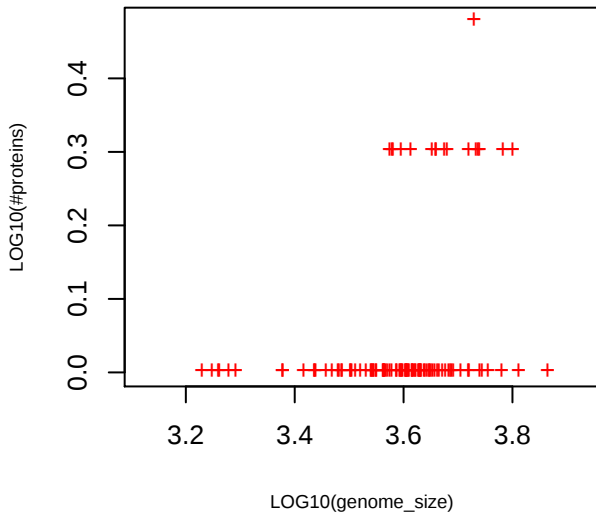
TIGR00206 flIF: flagellar M-ring protein FlIF

slope= -0.0067 p_value= 3.7e-07 intercept= 0.012 p_value= 1.4e-14

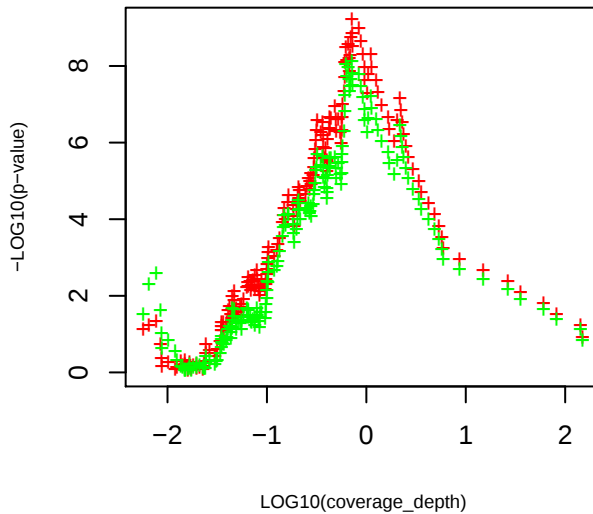


TIGR00206 flIF: flagellar M-ring protein FlIF

slope= 3.84 p_value= 9.3e-06 intercept= -15.41 p_value= 6.6e-07

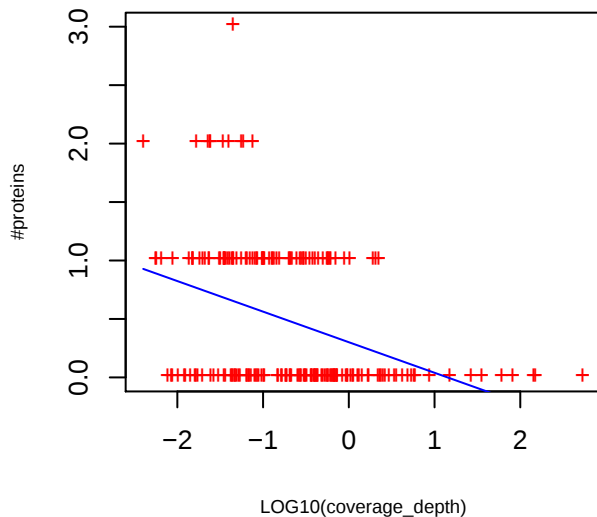


P-value curve ; red (unnorm), green (norm)



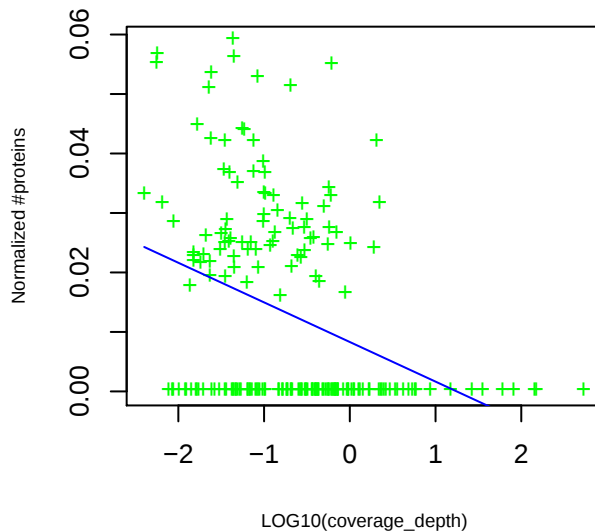
TIGR01400 fliR: flagellar biosynthetic protein FliR

slope= -0.26 p_value= 4.5e-08 intercept= 0.30 p_value= 2.5e-08



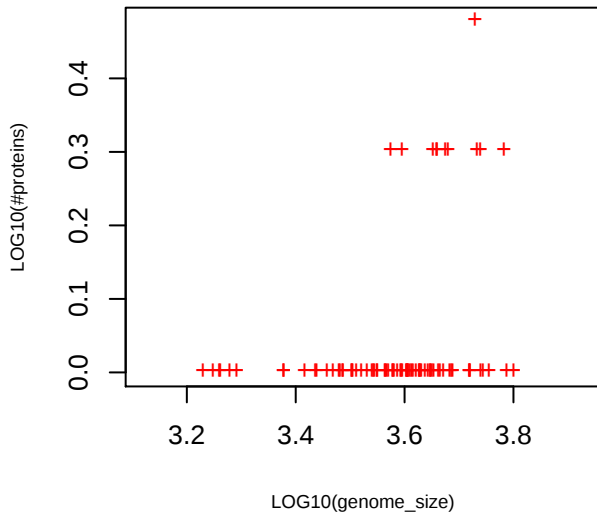
TIGR01400 fliR: flagellar biosynthetic protein FliR

slope= -0.0067 p_value= 2.6e-07 intercept= 0.0083 p_value= 1.6e-08

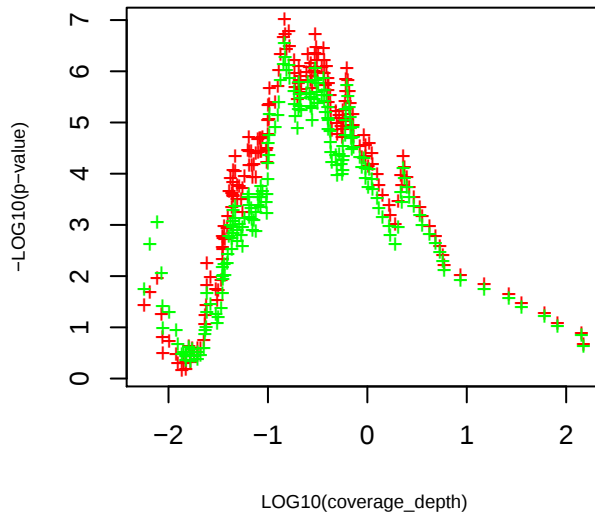


TIGR01400 fliR: flagellar biosynthetic protein FliR

slope= 2.22 p_value= 0.011 intercept= -10.18 p_value= 0.0011

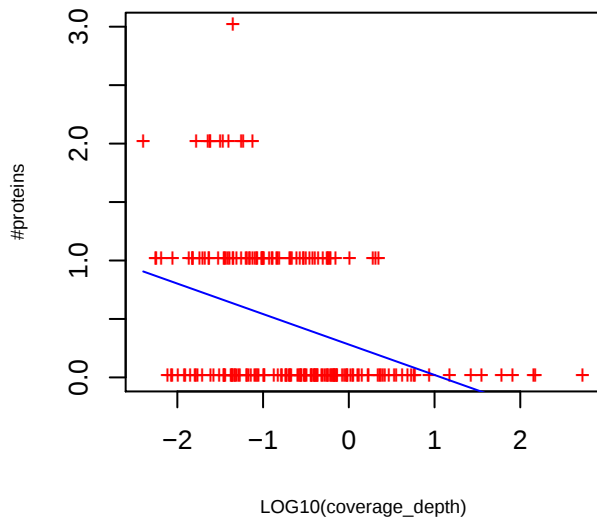


P-value curve ; red (unnorm), green (norm)



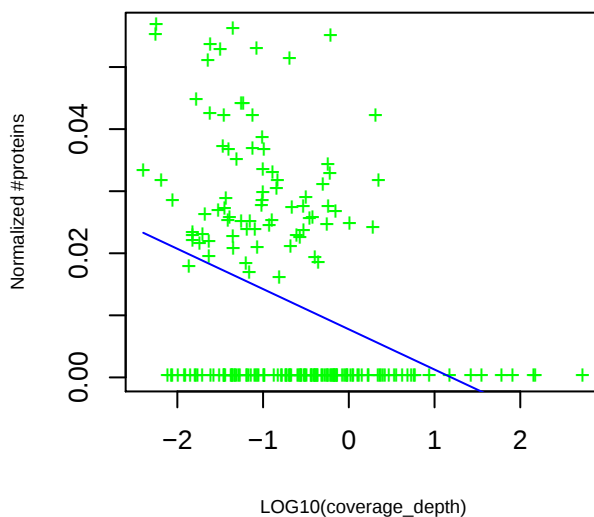
TIGR01396 FlgB: flagellar basal-body rod protein FlgB

slope= -0.26 p_value= 7.4e-08 intercept= 0.28 p_value= 2.4e-07



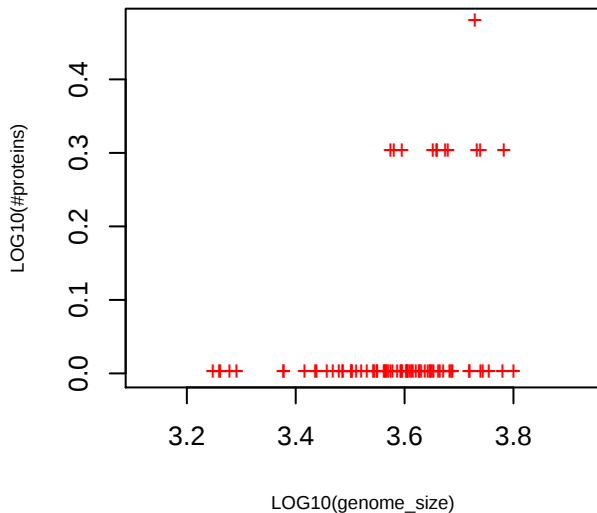
TIGR01396 FlgB: flagellar basal-body rod protein FlgB

slope= -0.0065 p_value= 4.7e-07 intercept= 0.0078 p_value= 1.1e-07

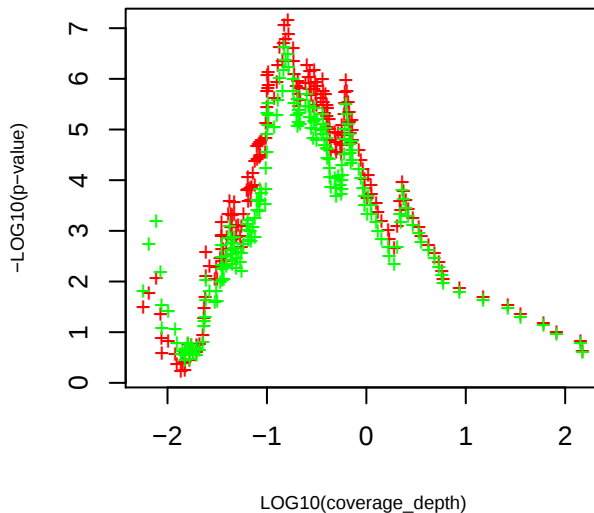


TIGR01396 FlgB: flagellar basal-body rod protein FlgB

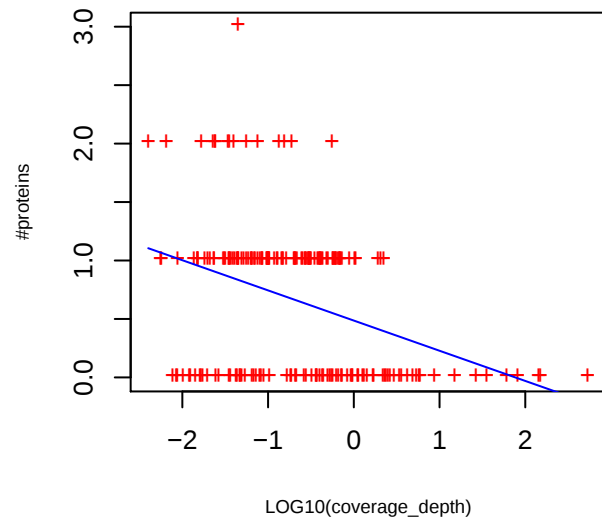
slope= 2.28 p_value= 0.0085 intercept= -10.48 p_value= 7e-04



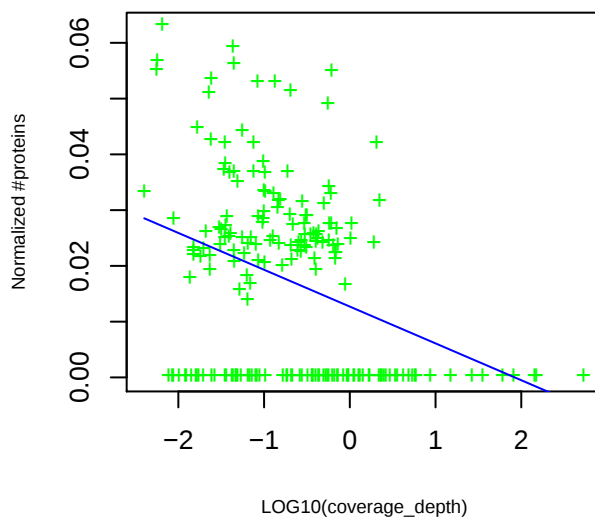
P-value curve ; red (unnorm), green (norm)



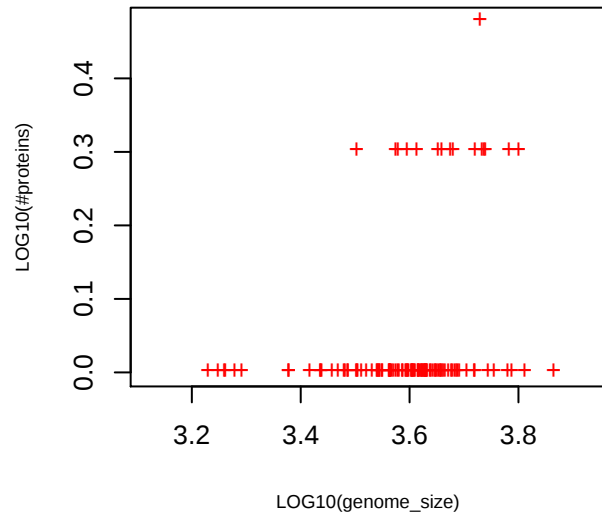
TIGR02492 flgK_ends: flagellar hook-associated protein FlgK
 slope= -0.26 p_value= 1.8e-07 intercept= 0.49 p_value= 1.6e-16



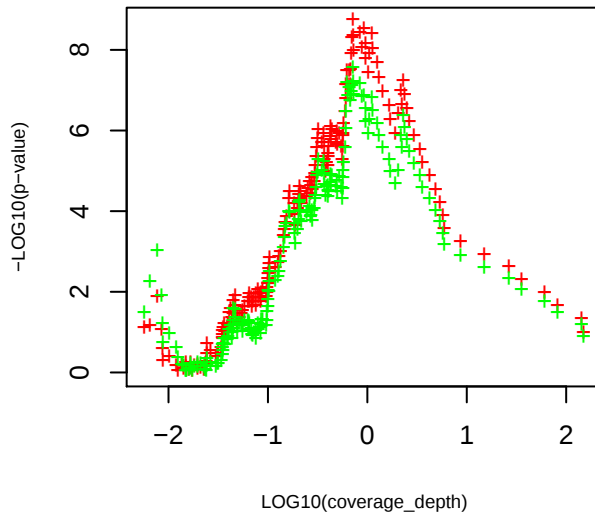
TIGR02492 flgK_ends: flagellar hook-associated protein FlgK
 slope= -0.0066 p_value= 4.2e-07 intercept= 0.013 p_value= 3.3e-16



TIGR02492 flgK_ends: flagellar hook-associated protein FlgK
 slope= 4.21 p_value= 8.4e-07 intercept= -16.58 p_value= 5.6e-08

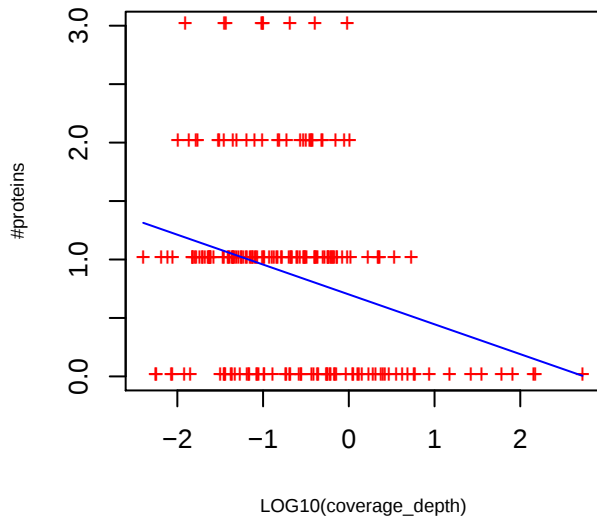


P-value curve ; red (unnorm), green (norm)



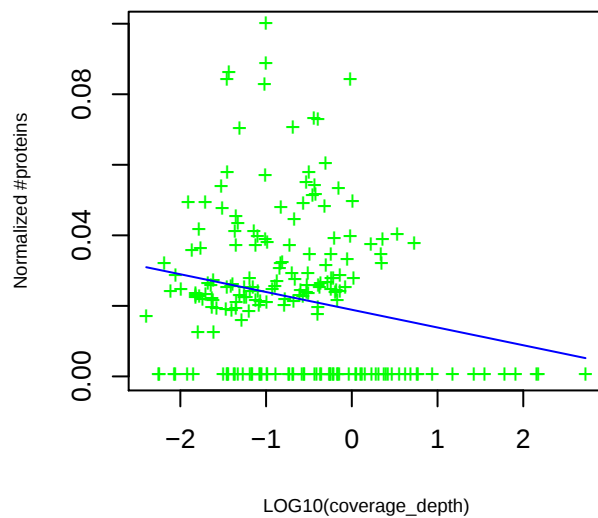
TIGR00765 yihY_not_rbn: YihY family protein

slope= -0.26 p_value= 6.1e-05 intercept= 0.70 p_value= 3.7e-19



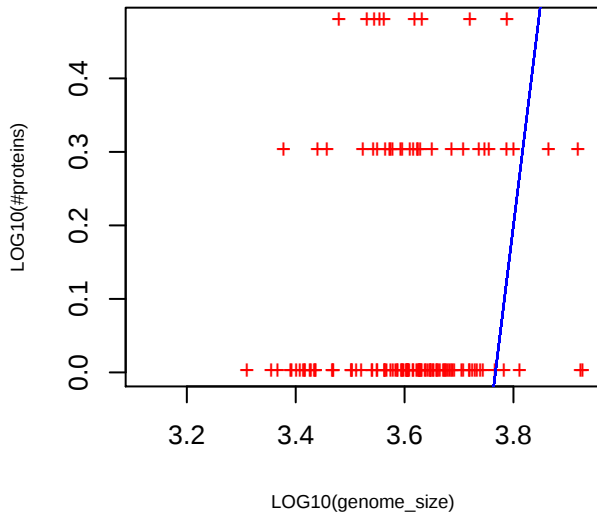
TIGR00765 yihY_not_rbn: YihY family protein

slope= -0.005 p_value= 0.0034 intercept= 0.019 p_value= 7.7e-19

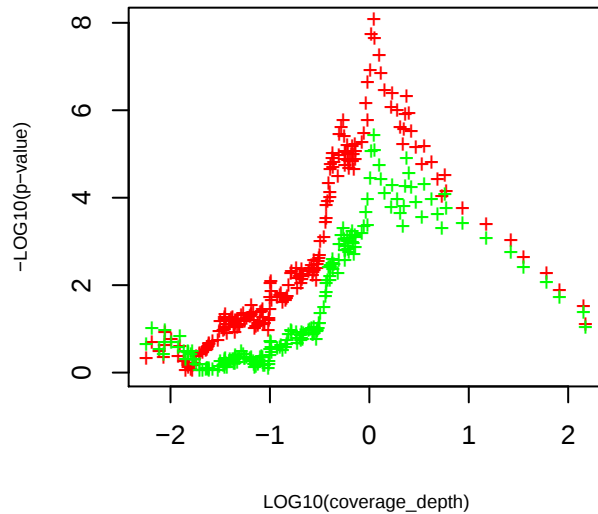


TIGR00765 yihY_not_rbn: YihY family protein

slope= 6.04 p_value= 6.3e-14 intercept= -22.74 p_value= 2.8e-15

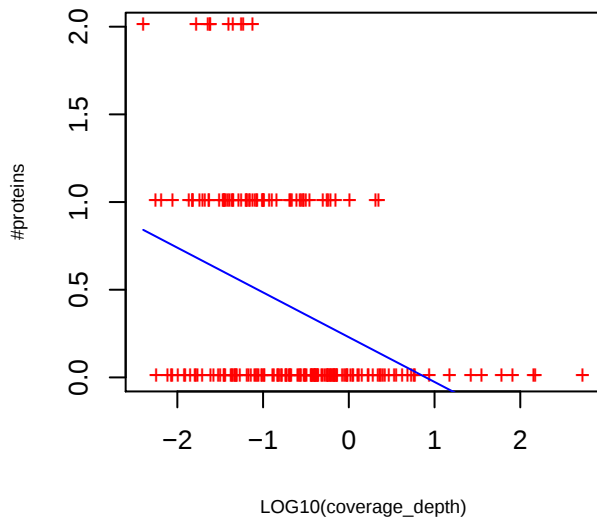


P-value curve ; red (unnorm), green (norm)



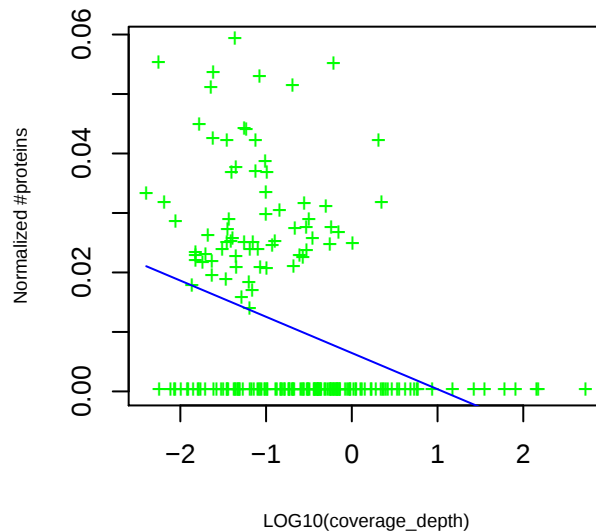
TIGR03496 FliI_clade1: flagellar protein export ATPase FliI

slope= -0.26 p_value= 1.6e-08 intercept= 0.23 p_value= 5.1e-06



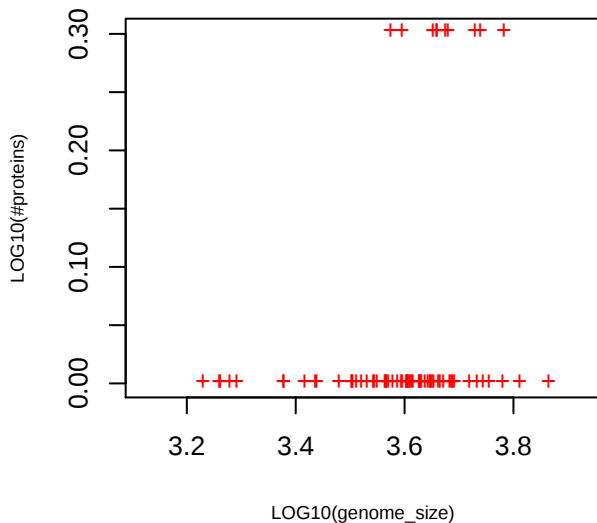
TIGR03496 FliI_clade1: flagellar protein export ATPase FliI

slope= -0.0061 p_value= 6.9e-07 intercept= 0.0065 p_value= 2.8e-06

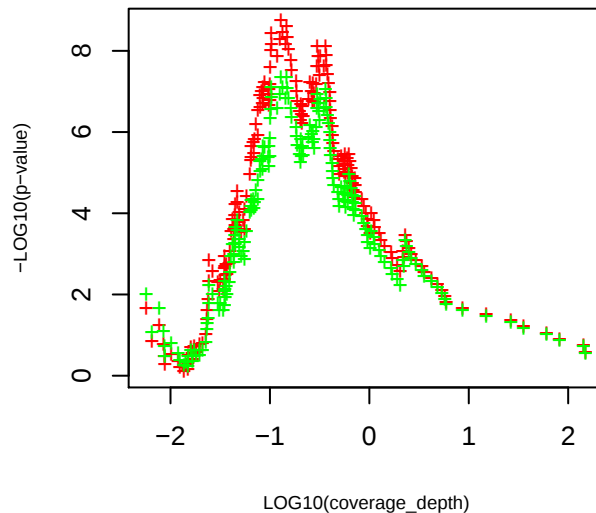


TIGR03496 FliI_clade1: flagellar protein export ATPase FliI

slope= 2.50 p_value= 0.0031 intercept= -11.42 p_value= 0.00015

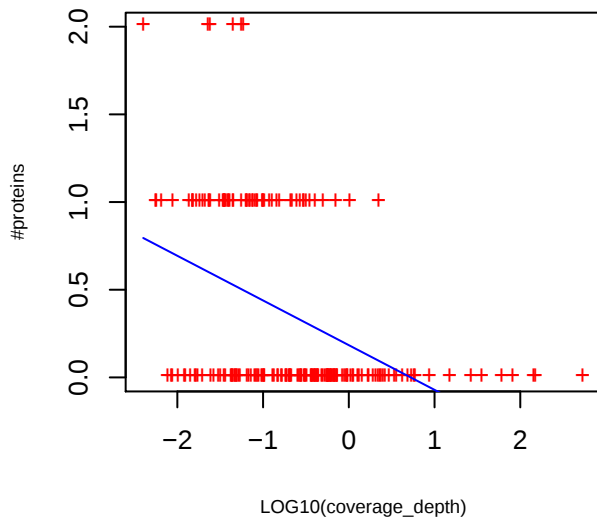


P-value curve ; red (unnorm), green (norm)



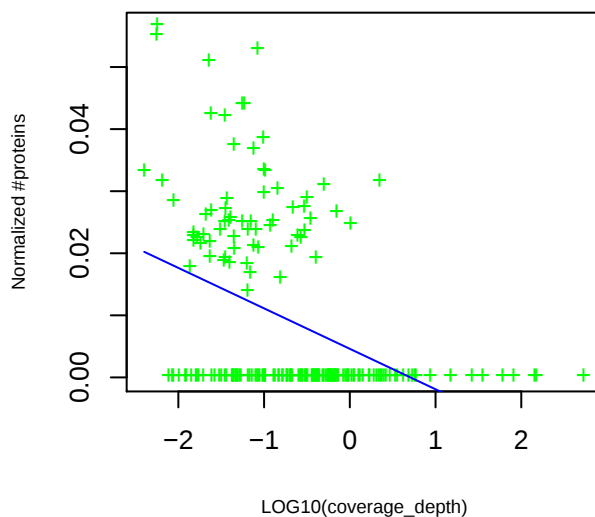
TIGR02473 flagell_FliJ: flagellar export protein FliJ

slope= -0.25 p_value= 7.1e-10 intercept= 0.18 p_value= 5.1e-05



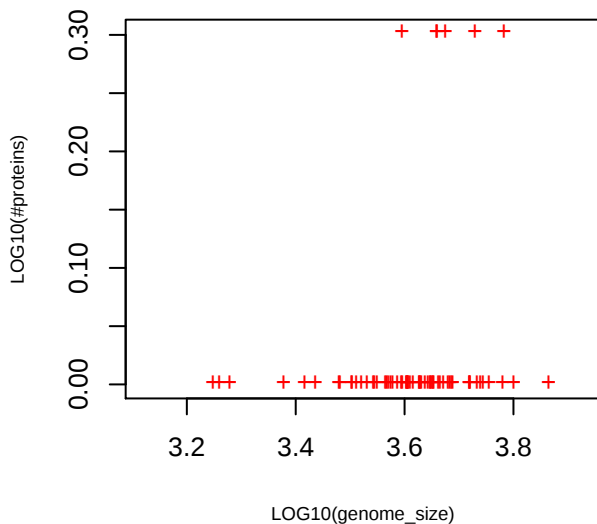
TIGR02473 flagell_FliJ: flagellar export protein FliJ

slope= -0.0065 p_value= 1.6e-09 intercept= 0.0046 p_value= 0.00010

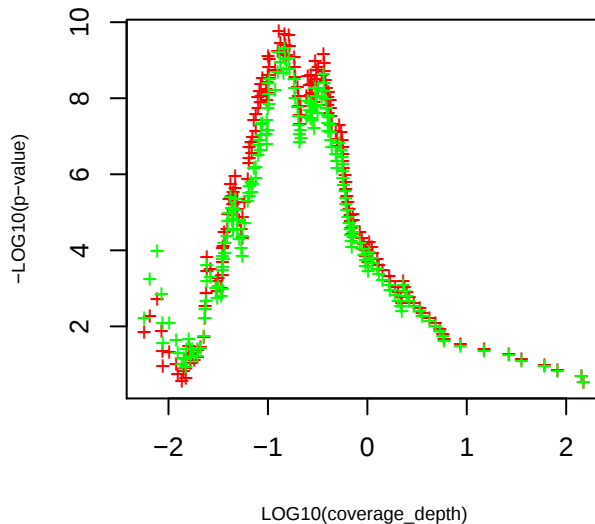


TIGR02473 flagell_FliJ: flagellar export protein FliJ

slope= 3.17 p_value= 0.00011 intercept= -13.92 p_value= 2.2e-06

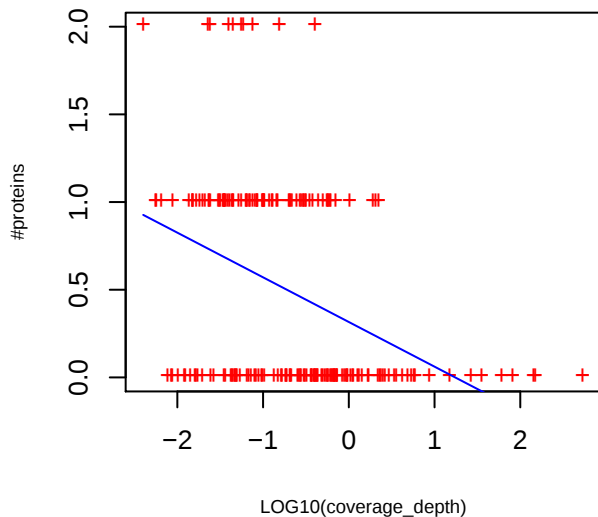


P-value curve ; red (unnorm), green (norm)



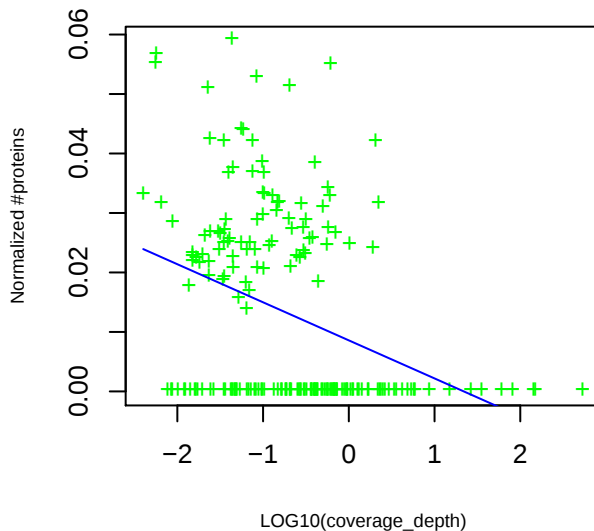
TIGR02480 flhN: flagellar motor switch protein FlhN

slope= -0.25 p_value= 2.7e-08 intercept= 0.32 p_value= 1.4e-09



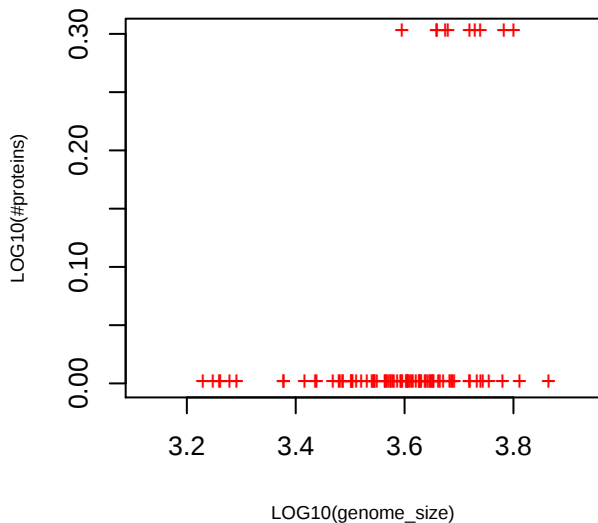
TIGR02480 flhN: flagellar motor switch protein FlhN

slope= -0.0064 p_value= 2.9e-07 intercept= 0.0086 p_value= 1.8e-09

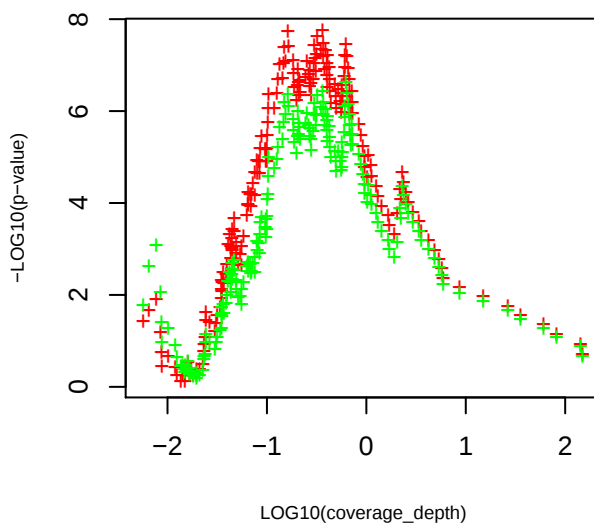


TIGR02480 flhN: flagellar motor switch protein FlhN

slope= 2.88 p_value= 0.00095 intercept= -12.43 p_value= 6.6e-05

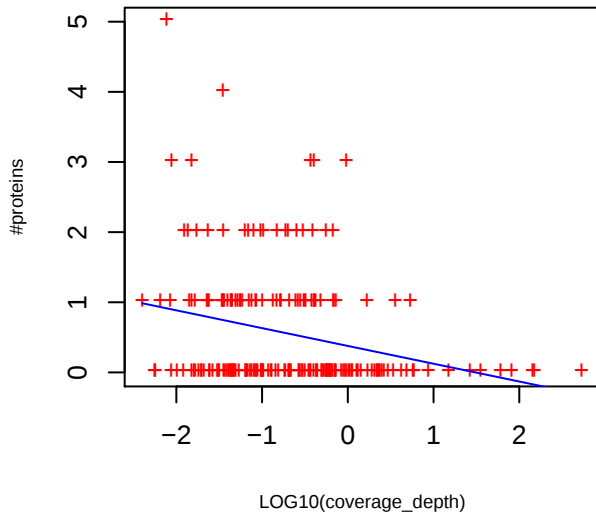


P-value curve ; red (unnorm), green (norm)



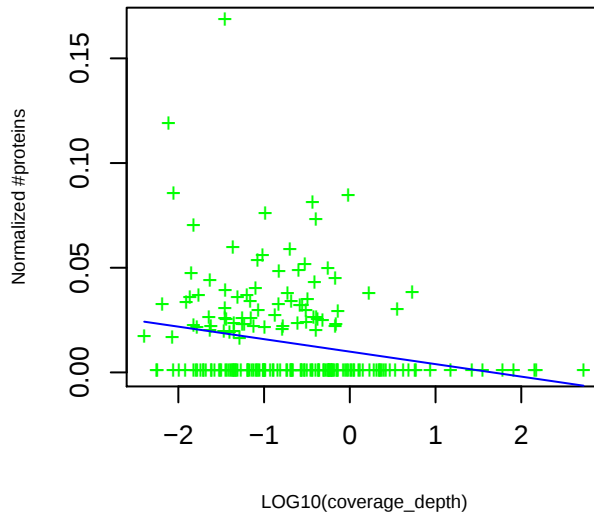
TIGR01512 ATPase-IB2_Cd: cadmium-translocating P-type ATPase

slope= -0.25 p_value= 0.00020 intercept= 0.38 p_value= 1.3e-06



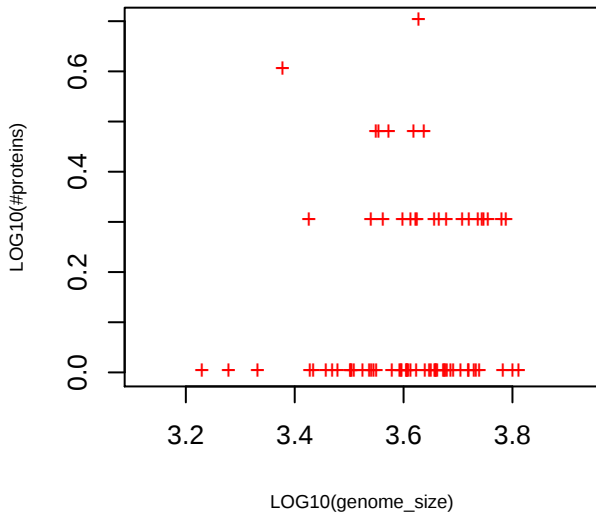
TIGR01512 ATPase-IB2_Cd: cadmium-translocating P-type ATPase

slope= -0.006 p_value= 0.0014 intercept= 0.01 p_value= 3.4e-06

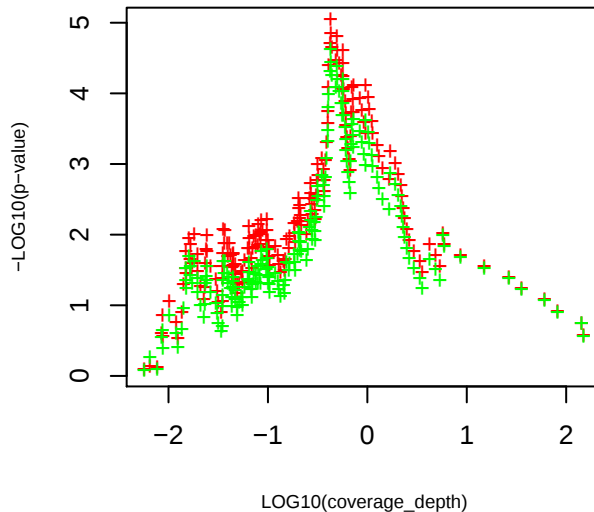


TIGR01512 ATPase-IB2_Cd: cadmium-translocating P-type ATPase

slope= 3.81 p_value= 9.3e-06 intercept= -15.97 p_value= 2.2e-07

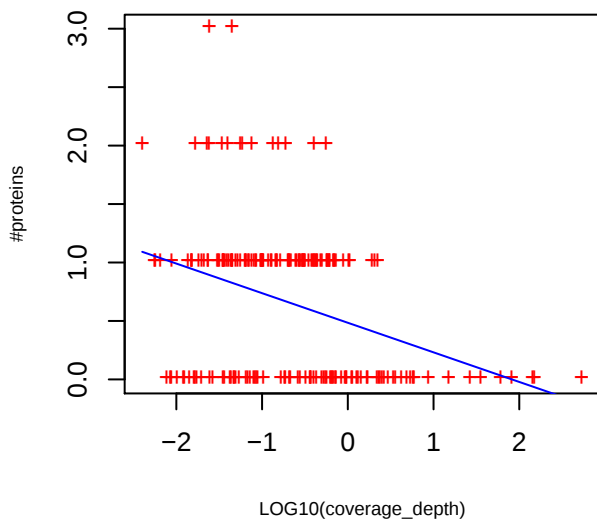


P-value curve ; red (unnorm), green (norm)



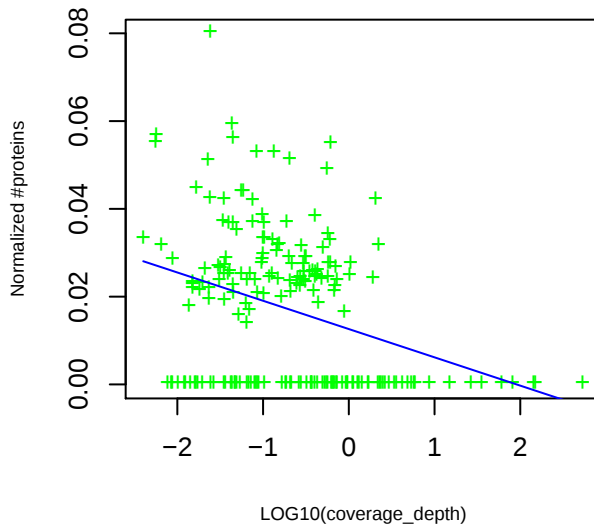
TIGR01103 fliP: flagellar biosynthetic protein FlpP

slope= -0.25 p_value= 6.7e-07 intercept= 0.48 p_value= 1.3e-15



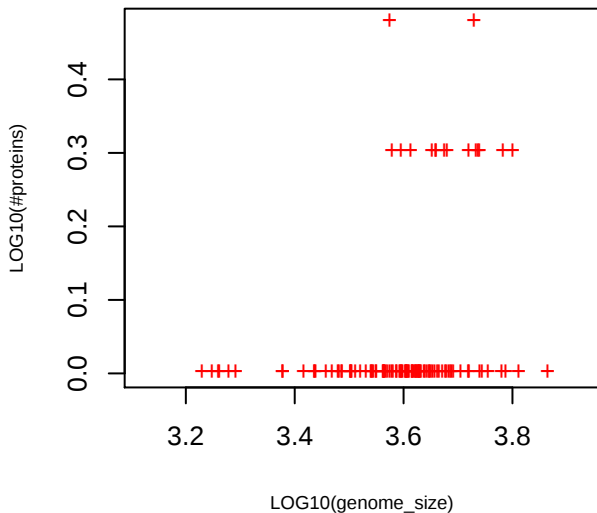
TIGR01103 fliP: flagellar biosynthetic protein FlpP

slope= -0.0064 p_value= 1.2e-06 intercept= 0.013 p_value= 1.7e-15

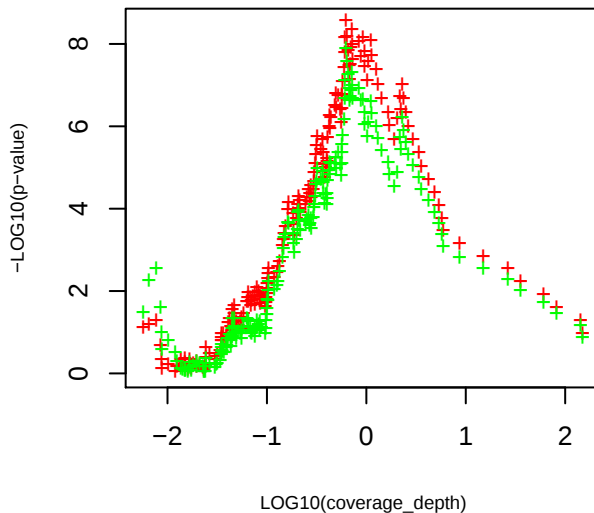


TIGR01103 fliP: flagellar biosynthetic protein FlpP

slope= 4.22 p_value= 8.8e-07 intercept= -16.65 p_value= 5.6e-08

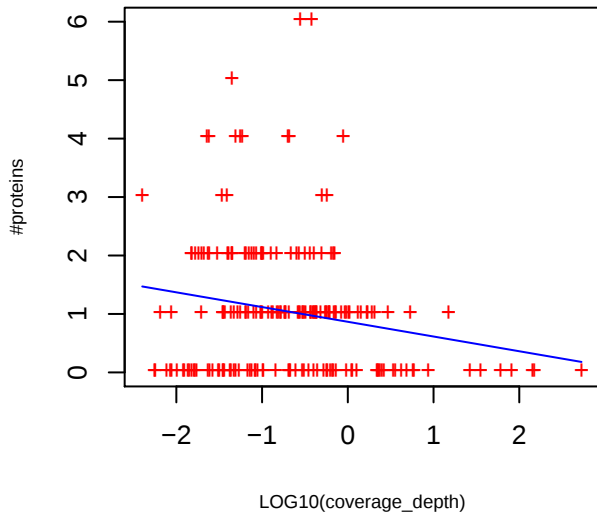


P-value curve : red (unnorm), green (norm)



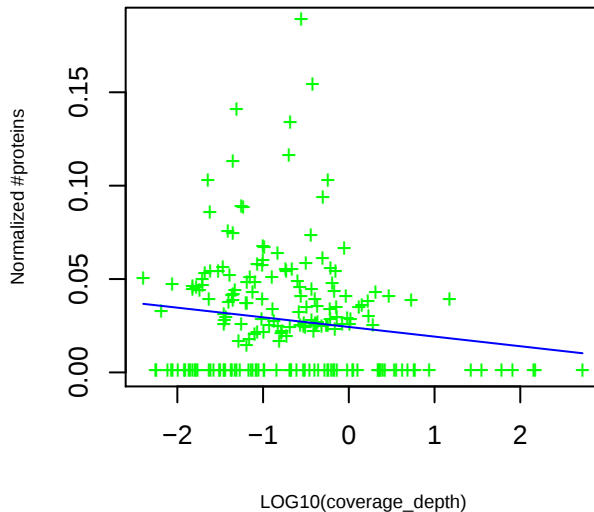
PF05433 Rick_17kDa_Anti: Rickettsia 17 kDa surface antigen

slope= -0.25 p_value= 0.0068 intercept= 0.87 p_value= 1.5e-14



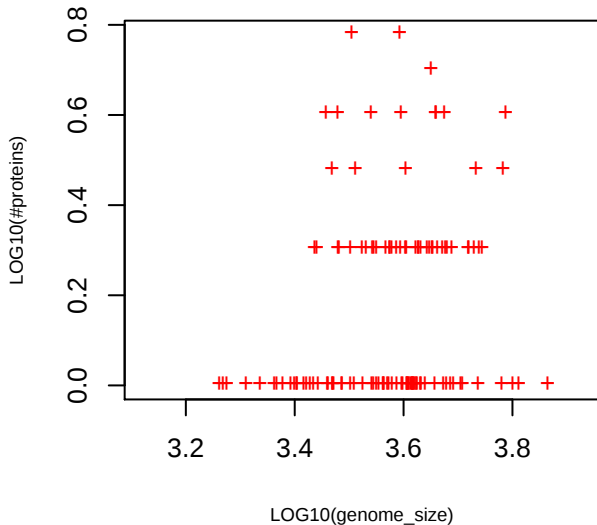
PF05433 Rick_17kDa_Anti: Rickettsia 17 kDa surface antigen

slope= -0.0052 p_value= 0.041 intercept= 0.024 p_value= 2.7e-15

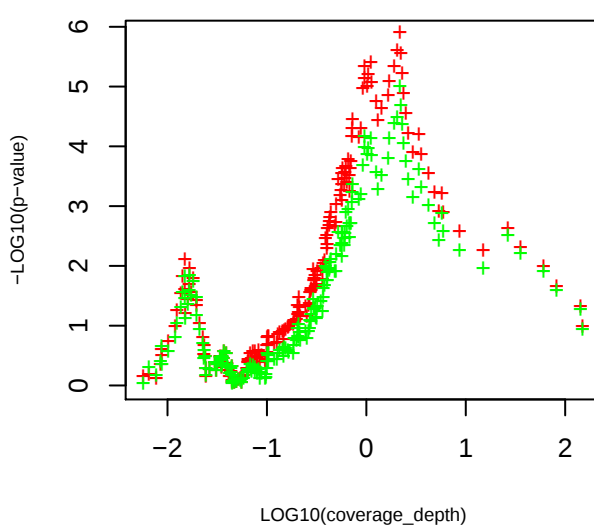


PF05433 Rick_17kDa_Anti: Rickettsia 17 kDa surface antigen

slope= 2.83 p_value= 0.0014 intercept= -11.46 p_value= 0.00028

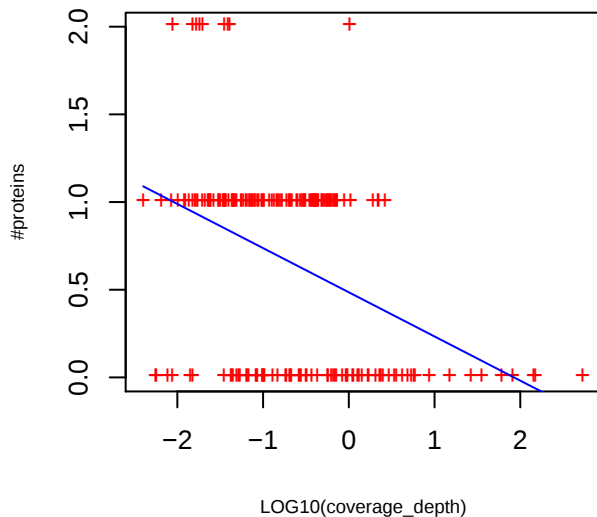


P-value curve ; red (unnorm), green (norm)



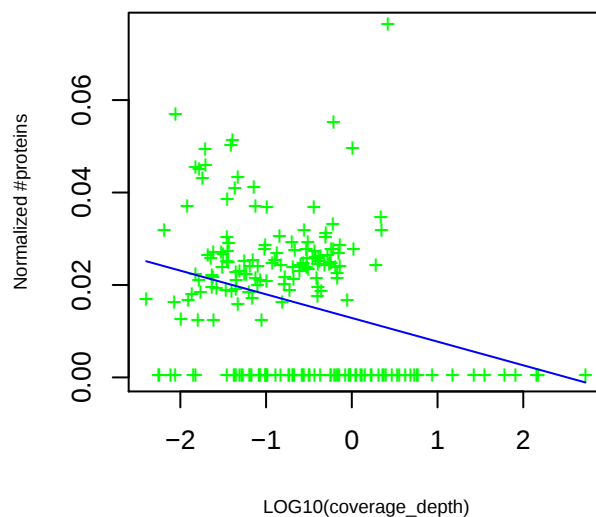
TIGR02141 modB_ABC: molybdate ABC transporter, permease protein

slope= -0.25 p_value= 5.8e-09 intercept= 0.49 p_value= 2e-20



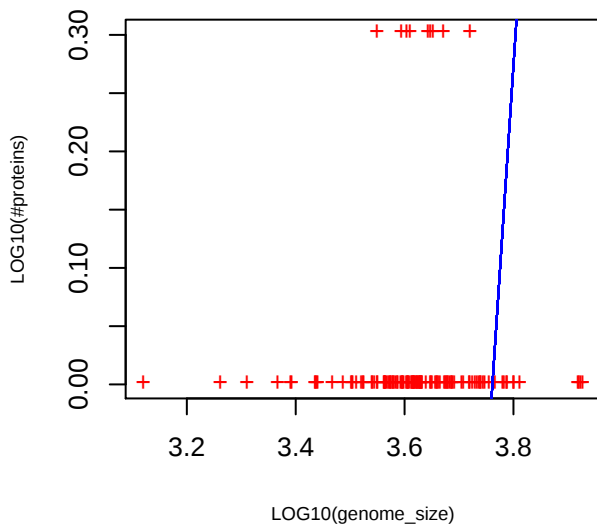
TIGR02141 modB_ABC: molybdate ABC transporter, permease protein

slope= -0.0051 p_value= 1.8e-05 intercept= 0.013 p_value= 1.2e-18

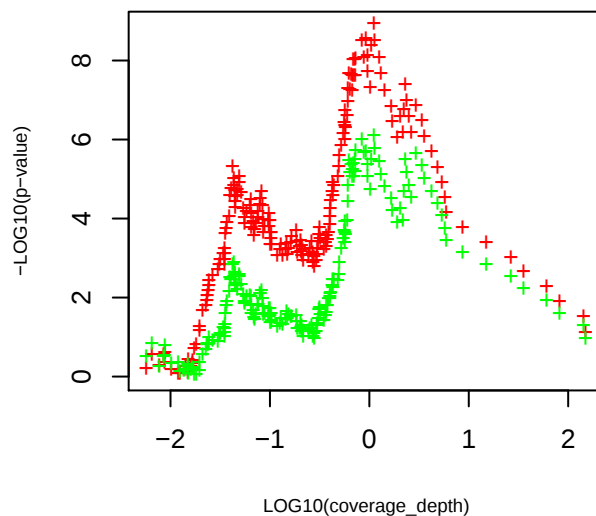


TIGR02141 modB_ABC: molybdate ABC transporter, permease protein

slope= 7.08 p_value= 1.1e-19 intercept= -26.62 p_value= 1.9e-21

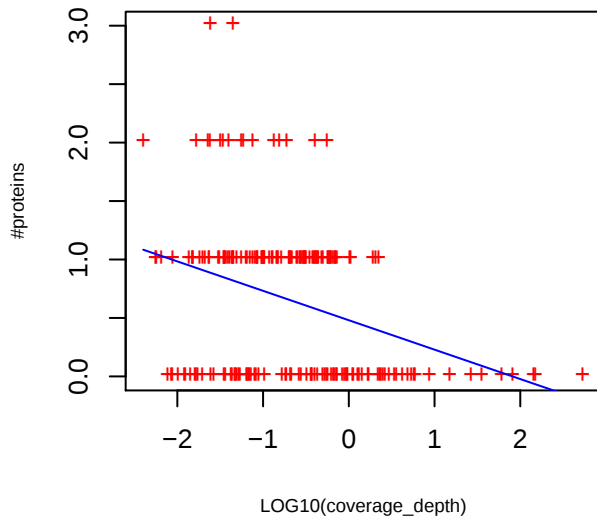


P-value curve ; red (unnorm), green (norm)



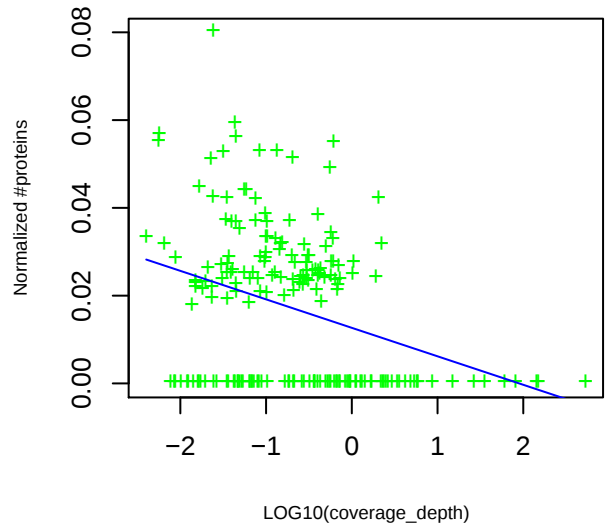
PF08345 YscJ_FliF_C: Flagellar M-ring protein C-terminal

slope= -0.25 p_value= 1.1e-06 intercept= 0.48 p_value= 4.8e-15



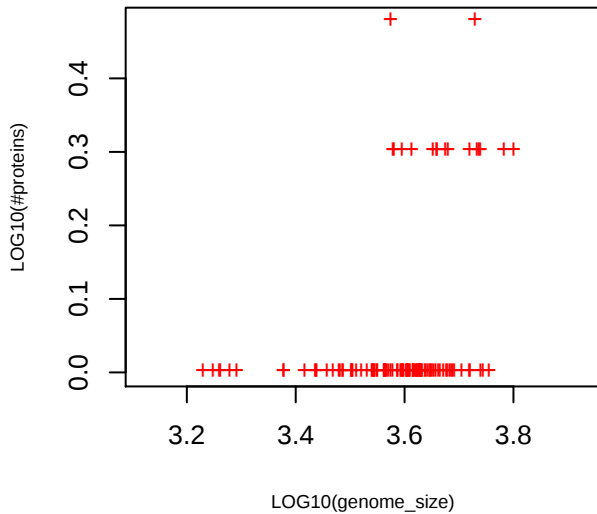
PF08345 YscJ_FliF_C: Flagellar M-ring protein C-terminal

slope= -0.0065 p_value= 1.6e-06 intercept= 0.013 p_value= 3.5e-15

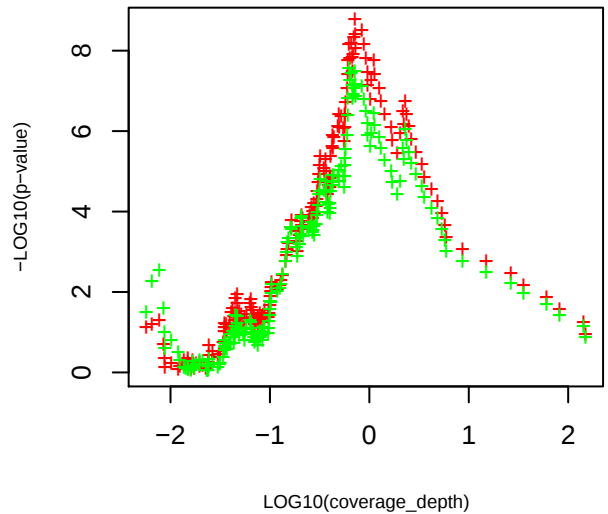


PF08345 YscJ_FliF_C: Flagellar M-ring protein C-terminal

slope= 3.47 p_value= 6.6e-05 intercept= -14.04 p_value= 6.2e-06

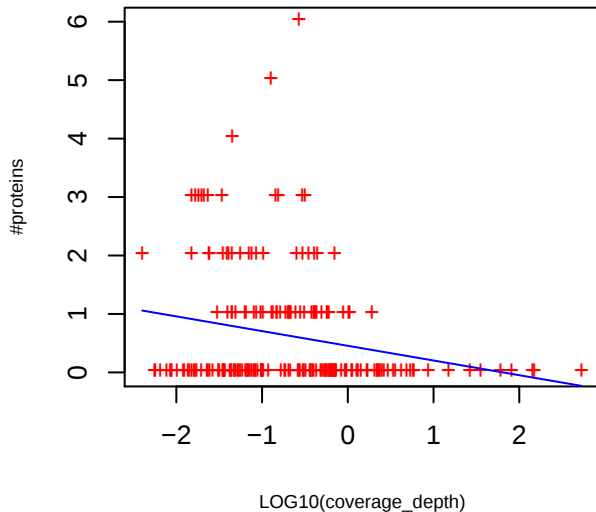


P-value curve ; red (unnorm), green (norm)



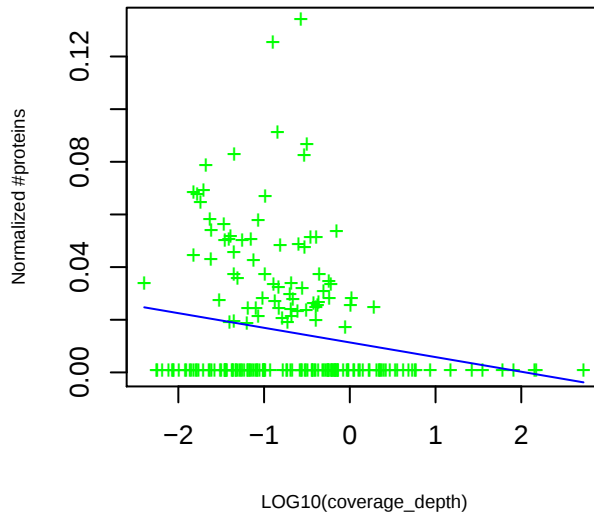
PF06629 MipA: MltA-interacting protein MipA

slope= -0.25 p_value= 0.0023 intercept= 0.46 p_value= 1.5e-06



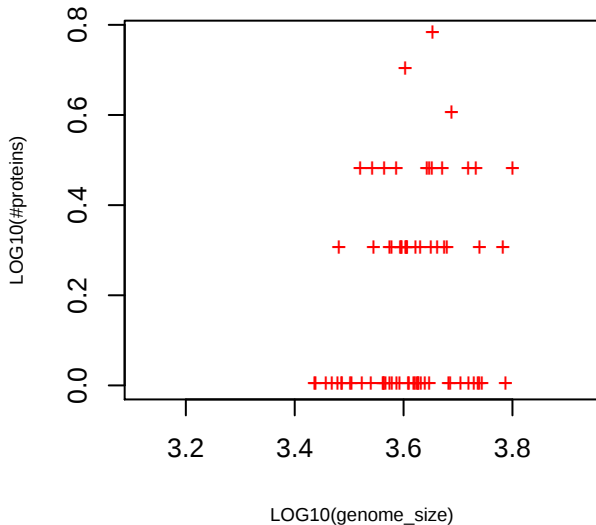
PF06629 MipA: MltA-interacting protein MipA

slope= -0.0056 p_value= 0.0047 intercept= 0.011 p_value= 5.5e-07

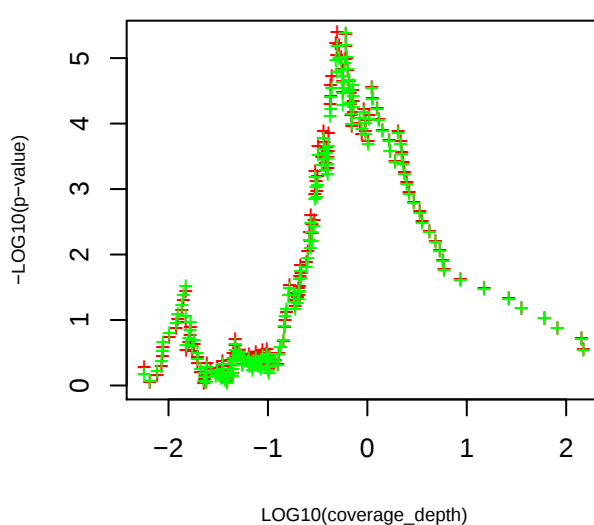


PF06629 MipA: MltA-interacting protein MipA

slope= 3.93 p_value= 5.4e-06 intercept= -16.44 p_value= 1.1e-07

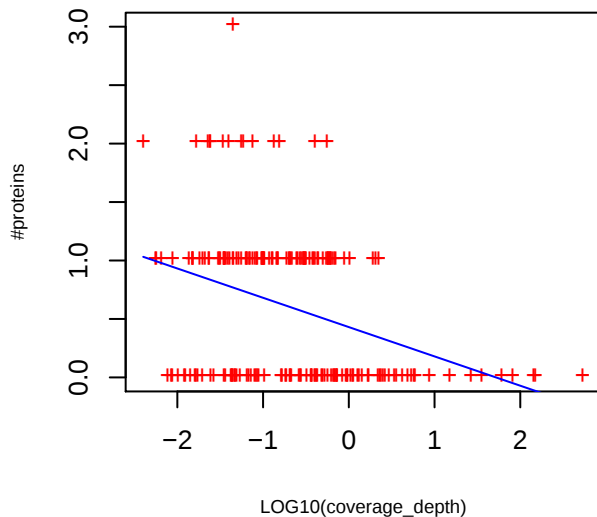


P-value curve ; red (unnorm), green (norm)



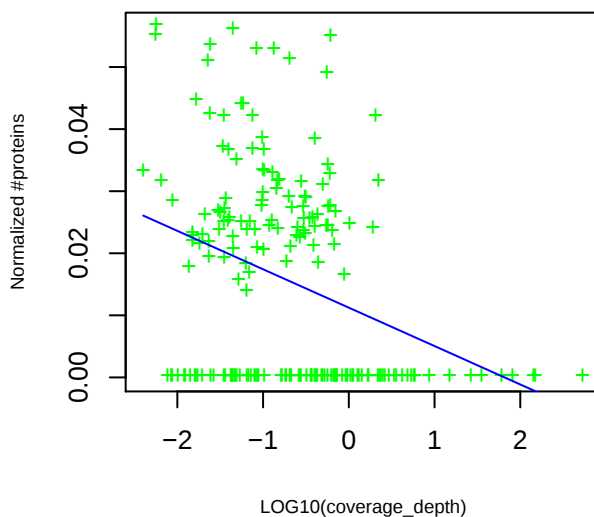
TIGR01395 FlgC: flagellar basal-body rod protein FlgC

slope= -0.25 p_value= 5.2e-07 intercept= 0.43 p_value= 2.0e-13



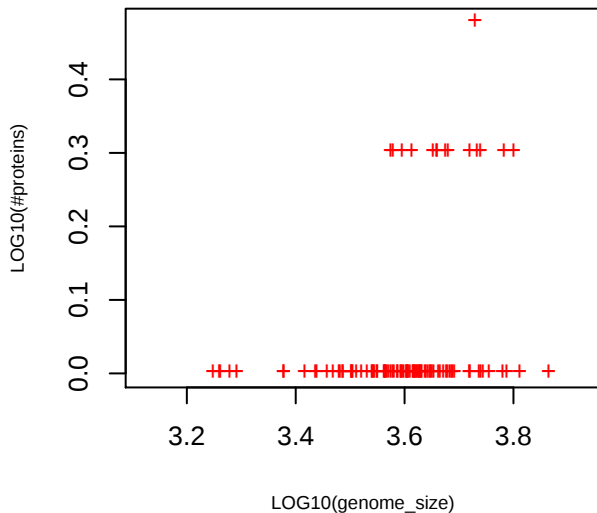
TIGR01395 FlgC: flagellar basal-body rod protein FlgC

slope= -0.0062 p_value= 1.7e-06 intercept= 0.011 p_value= 1.5e-13

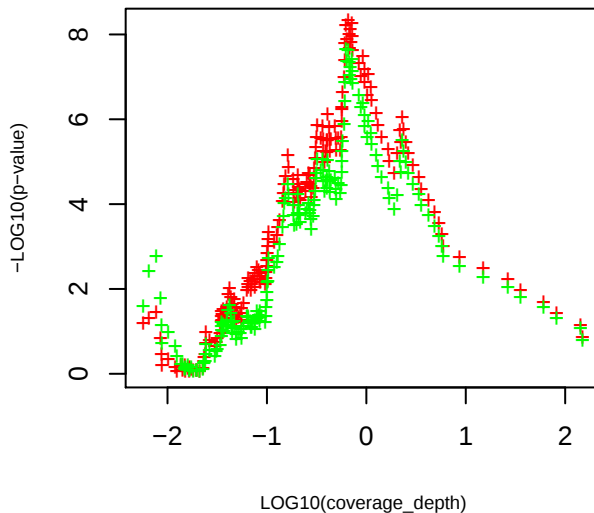


TIGR01395 FlgC: flagellar basal-body rod protein FlgC

slope= 4.10 p_value= 2.3e-06 intercept= -16.41 p_value= 1.2e-07

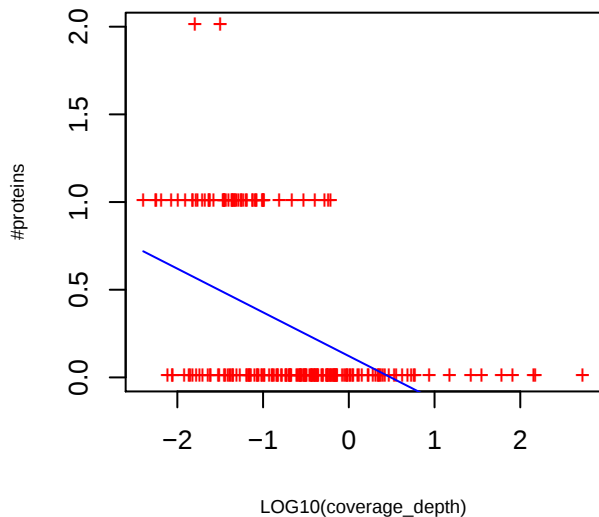


P-value curve : red (unnorm), green (norm)



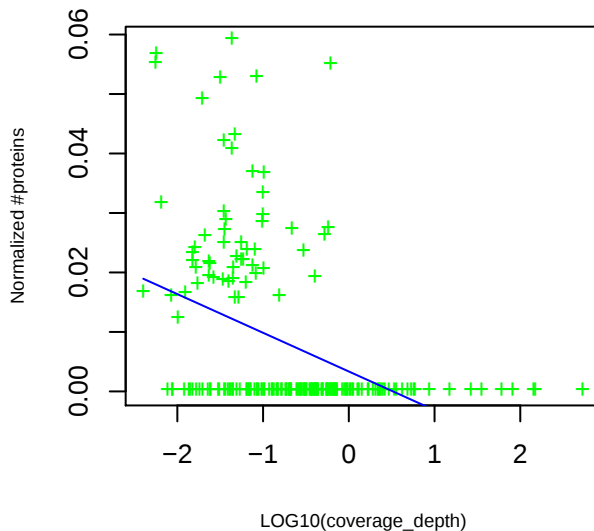
PF03649 UPF0014: Uncharacterised protein family (UPF0014)

slope= -0.25 p_value= 5.5e-12 intercept= 0.12 p_value= 0.0017



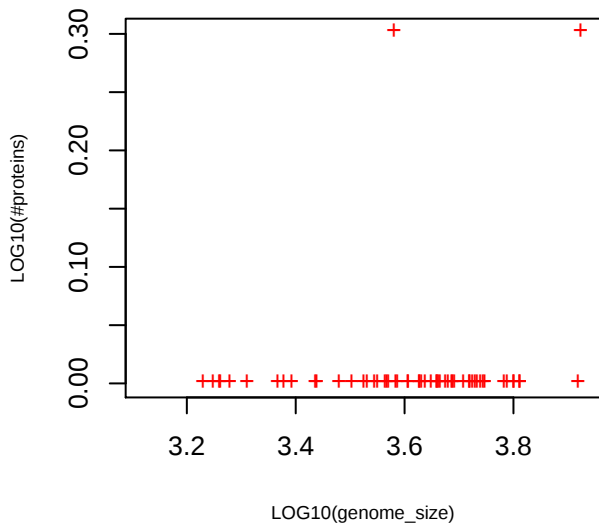
PF03649 UPF0014: Uncharacterised protein family (UPF0014)

slope= -0.0065 p_value= 1.5e-09 intercept= 0.0034 p_value= 0.0042

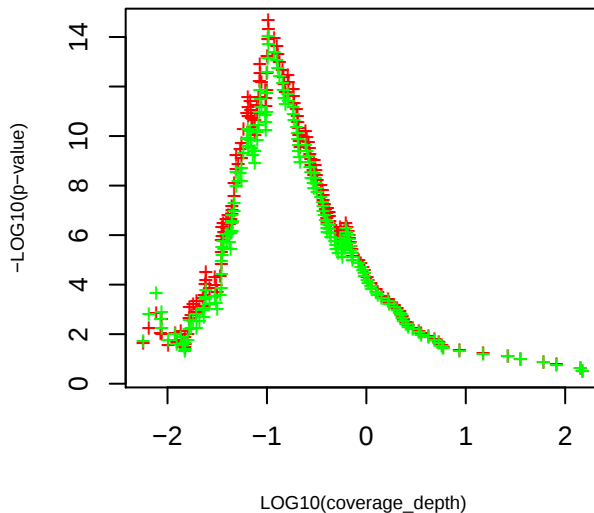


PF03649 UPF0014: Uncharacterised protein family (UPF0014)

slope= 2.55 p_value= 0.0012 intercept= -11.91 p_value= 2.4e-05

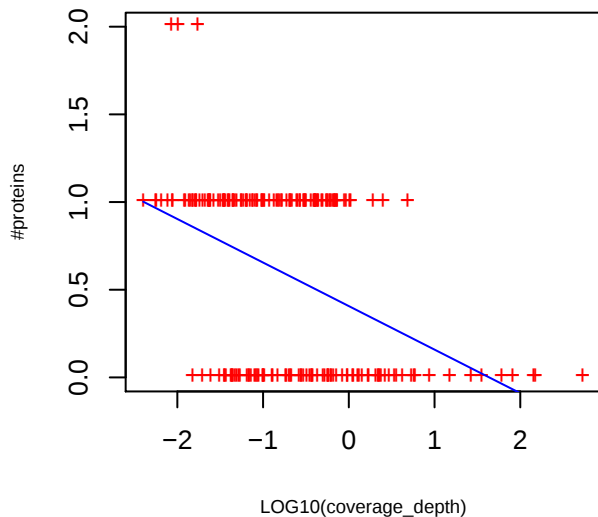


P-value curve ; red (unnorm), green (norm)



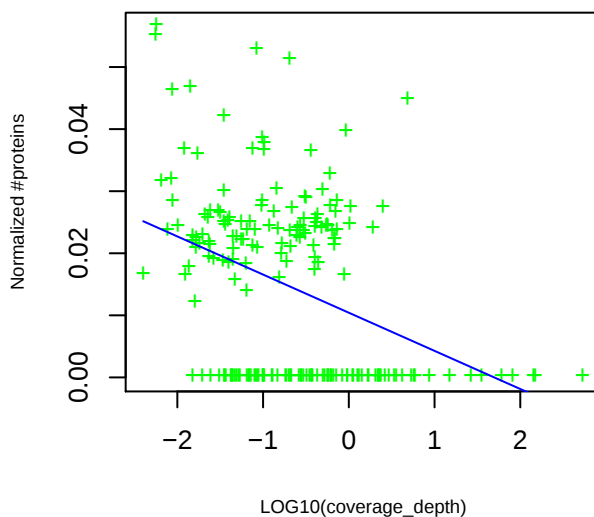
TIGR01091 upp: uracil phosphoribosyltransferase

slope= -0.25 p_value= 5.9e-10 intercept= 0.41 p_value= 1.0e-17



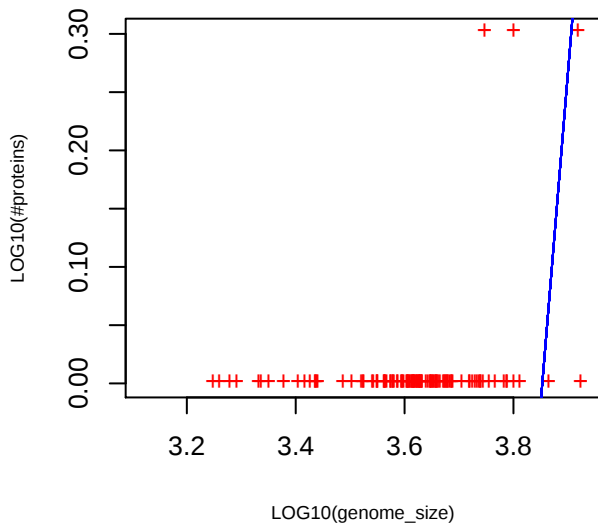
TIGR01091 upp: uracil phosphoribosyltransferase

slope= -0.0061 p_value= 3.2e-08 intercept= 0.010 p_value= 1.9e-15

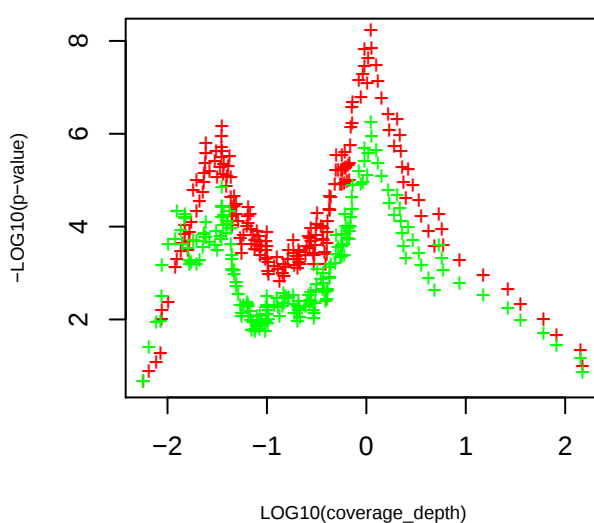


TIGR01091 upp: uracil phosphoribosyltransferase

slope= 5.66 p_value= 7.4e-12 intercept= -21.81 p_value= 1.8e-13

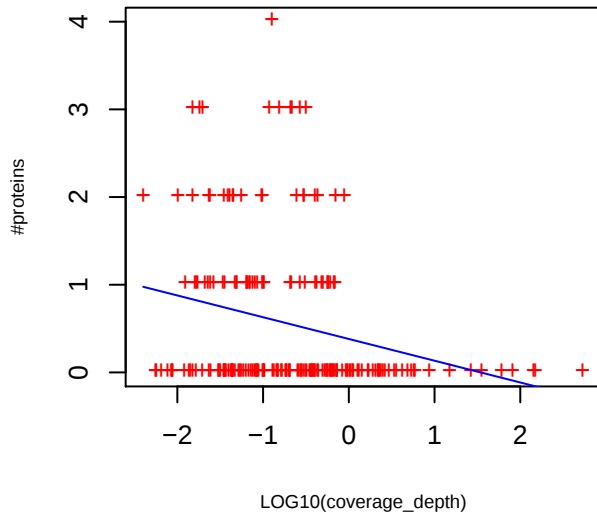


P-value curve ; red (unnorm), green (norm)



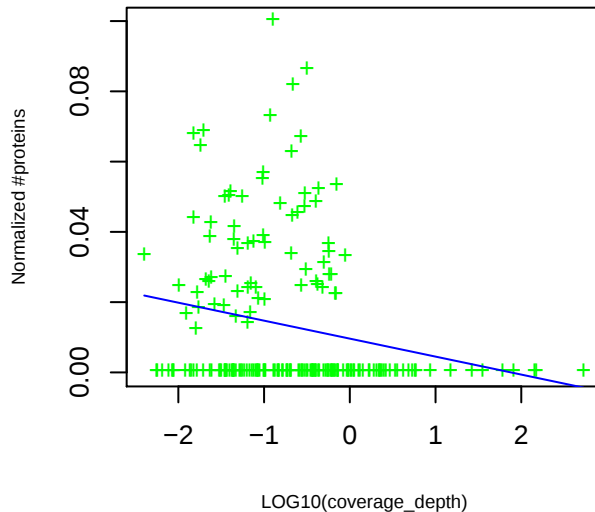
PF03924 CHASE: CHASE domain

slope= -0.25 p_value= 4e-04 intercept= 0.38 p_value= 2.0e-06



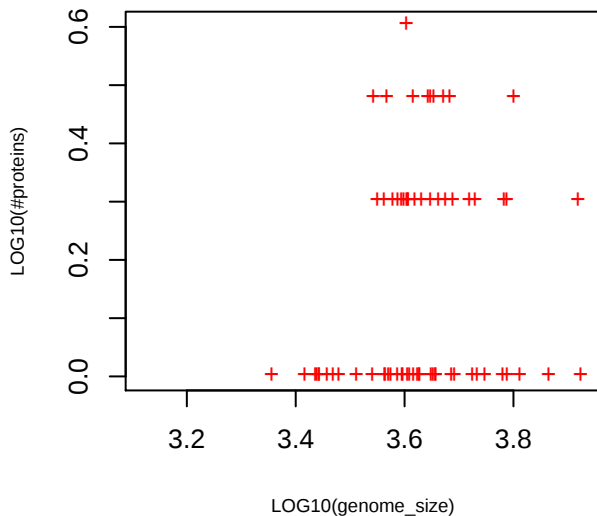
PF03924 CHASE: CHASE domain

slope= -0.0051 p_value= 0.0023 intercept= 0.0096 p_value= 6.6e-07

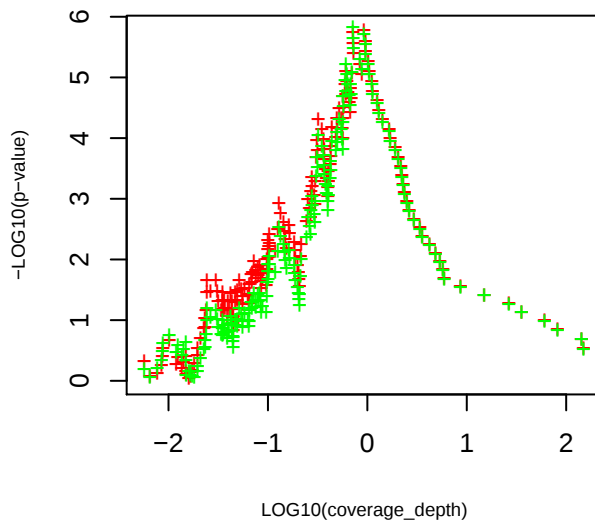


PF03924 CHASE: CHASE domain

slope= 4.52 p_value= 8.2e-08 intercept= -18.58 p_value= 8.2e-10

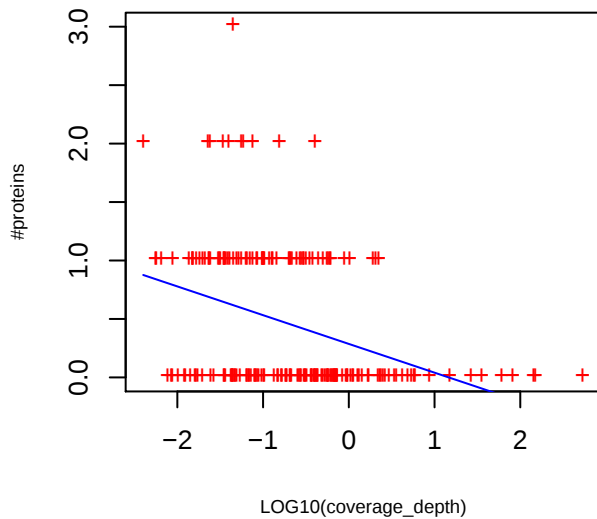


P-value curve ; red (unnorm), green (norm)



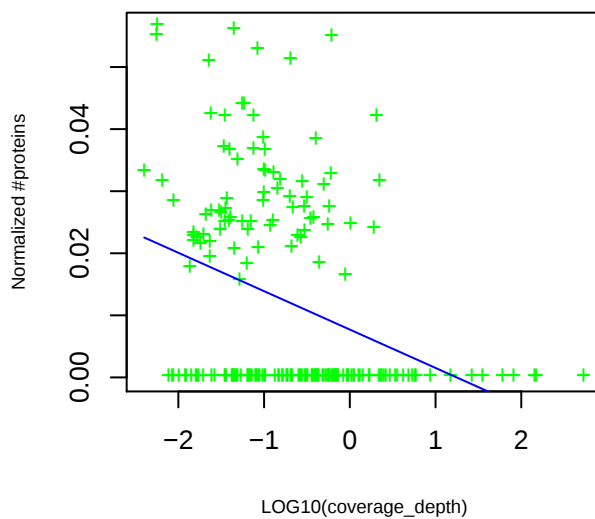
TIGR01402 fliQ: flagellar biosynthetic protein FliQ

slope= -0.25 p_value= 2.9e-07 intercept= 0.29 p_value= 1.3e-07



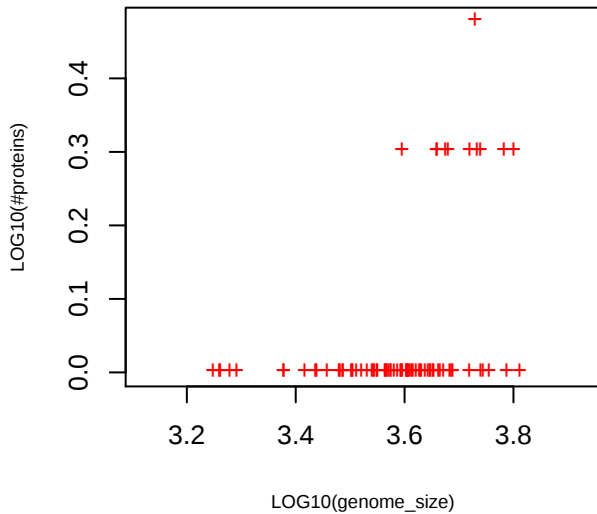
TIGR01402 fliQ: flagellar biosynthetic protein FliQ

slope= -0.0062 p_value= 7.9e-07 intercept= 0.0077 p_value= 6.1e-08

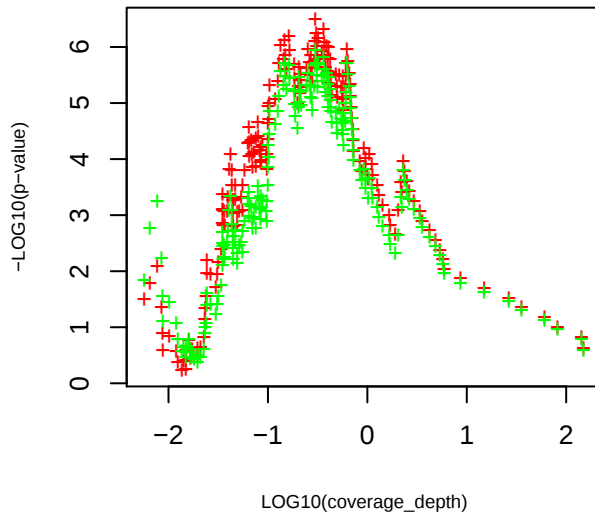


TIGR01402 fliQ: flagellar biosynthetic protein FliQ

slope= 2.44 p_value= 0.0047 intercept= -11.06 p_value= 0.00034

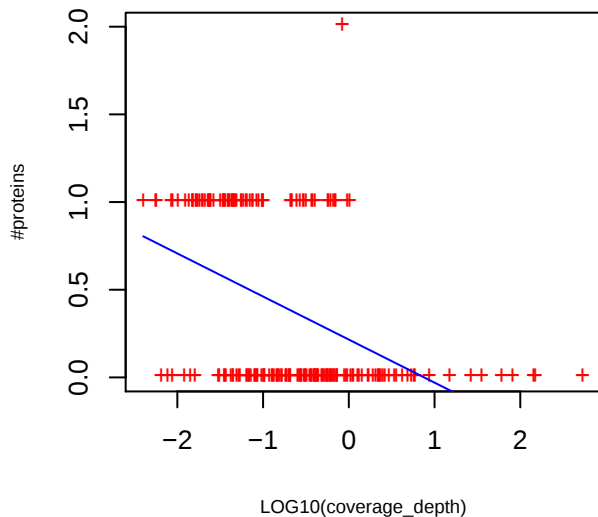


P-value curve ; red (unnorm), green (norm)



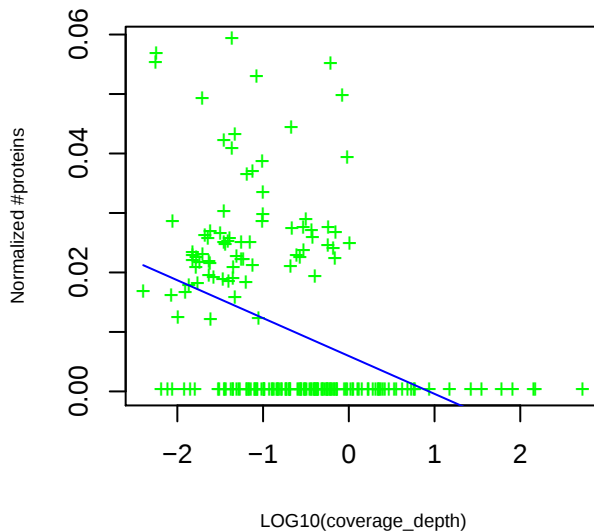
TIGR00619 sbcd: exonuclease SbcCD, D subunit

slope= -0.25 p_value= 9.1e-11 intercept= 0.22 p_value= 2.6e-07



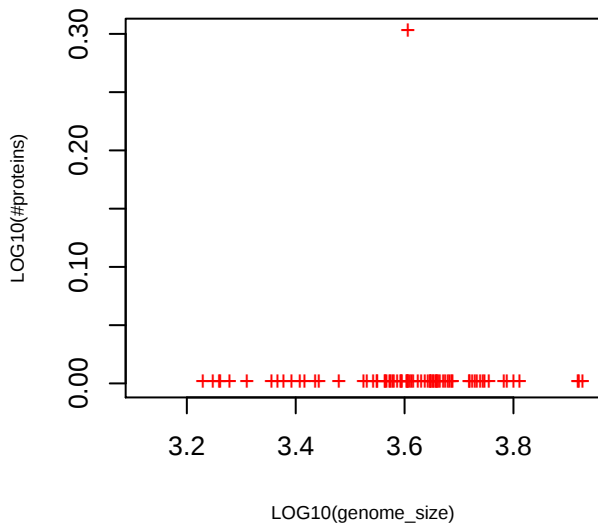
TIGR00619 sbcd: exonuclease SbcCD, D subunit

slope= -0.0064 p_value= 2.8e-08 intercept= 0.006 p_value= 3.3e-06

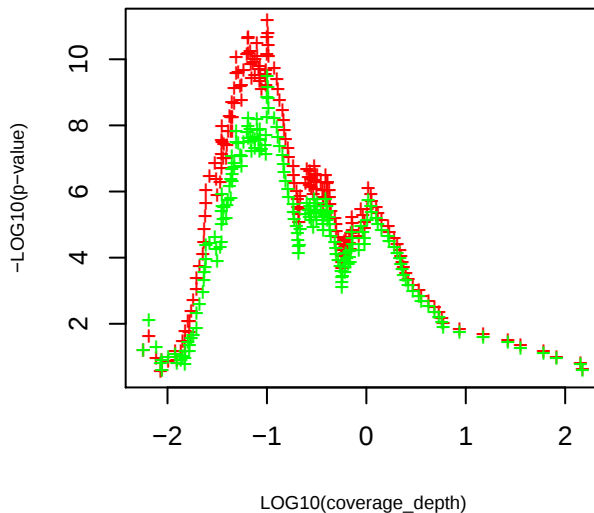


TIGR00619 sbcd: exonuclease SbcCD, D subunit

slope= 3.09 p_value= 0.00024 intercept= -13.44 p_value= 8.3e-06

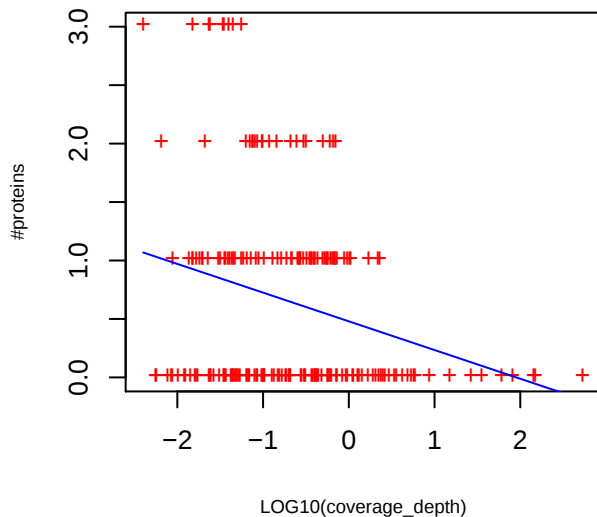


P-value curve ; red (unnorm), green (norm)



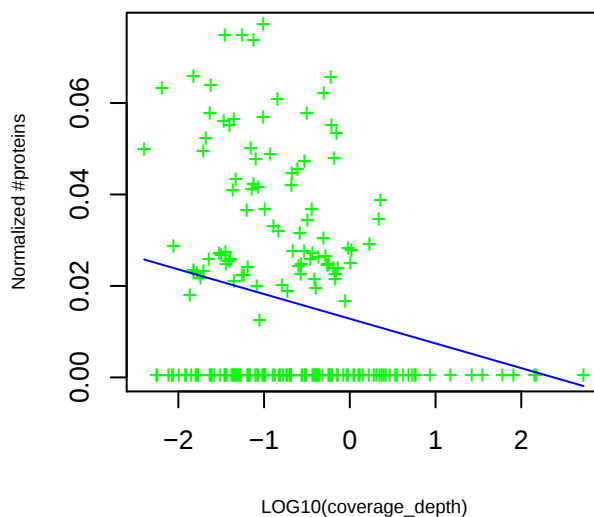
PF03445 DUF294: Putative nucleotidyltransferase DUF294

slope= -0.25 p_value= 0.00021 intercept= 0.48 p_value= 5.6e-10



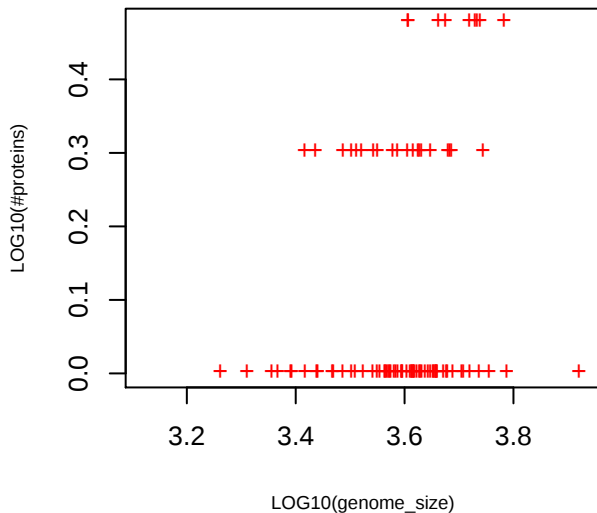
PF03445 DUF294: Putative nucleotidyltransferase DUF294

slope= -0.0054 p_value= 0.0012 intercept= 0.013 p_value= 7e-11

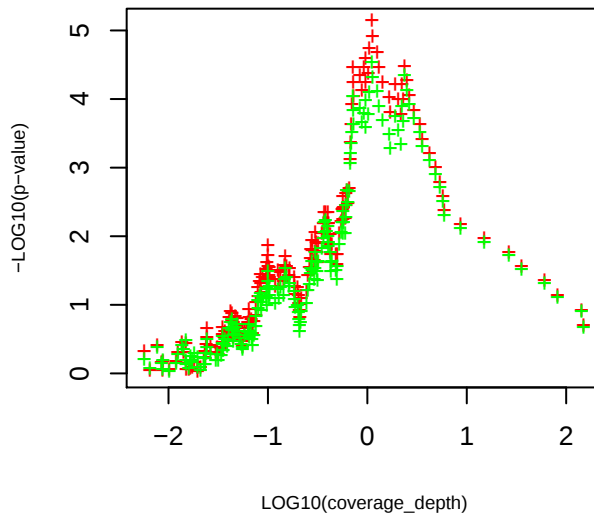


PF03445 DUF294: Putative nucleotidyltransferase DUF294

slope= 3.60 p_value= 4.8e-05 intercept= -14.90 p_value= 2.6e-06

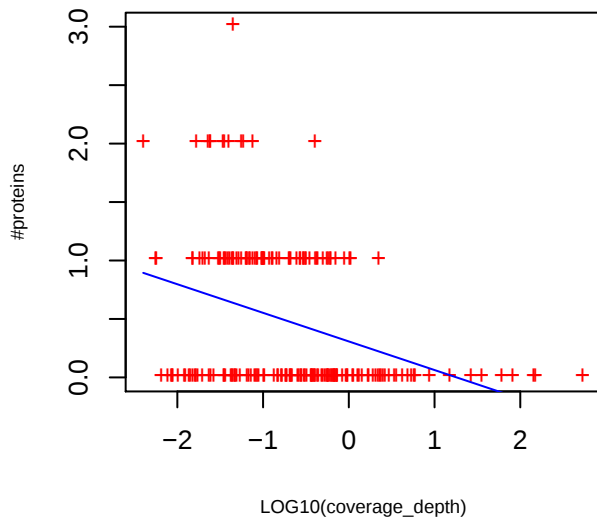


P-value curve ; red (unnorm), green (norm)



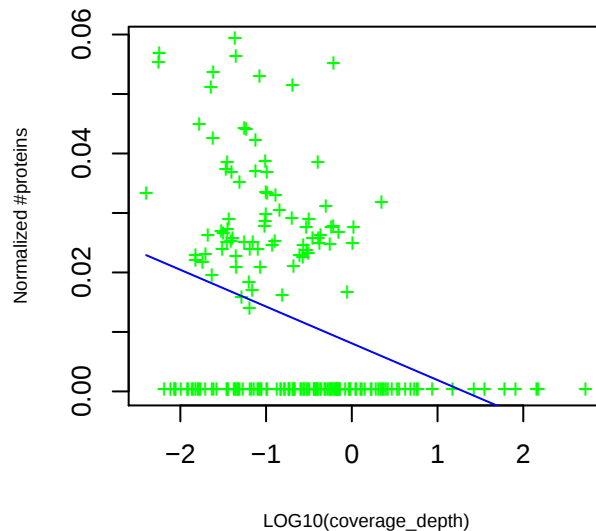
PF07559 FlaE: Flagellar basal body protein FlgE

slope= -0.24 p_value= 7.2e-07 intercept= 0.31 p_value= 4.3e-08



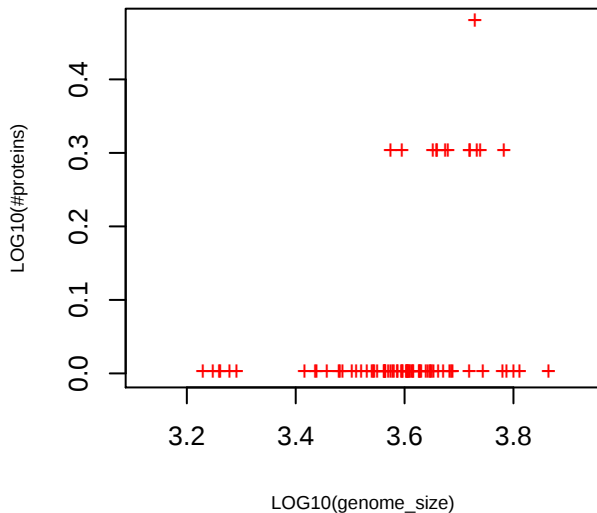
PF07559 FlaE: Flagellar basal body protein FlgE

slope= -0.0062 p_value= 1.5e-06 intercept= 0.0081 p_value= 3.5e-08

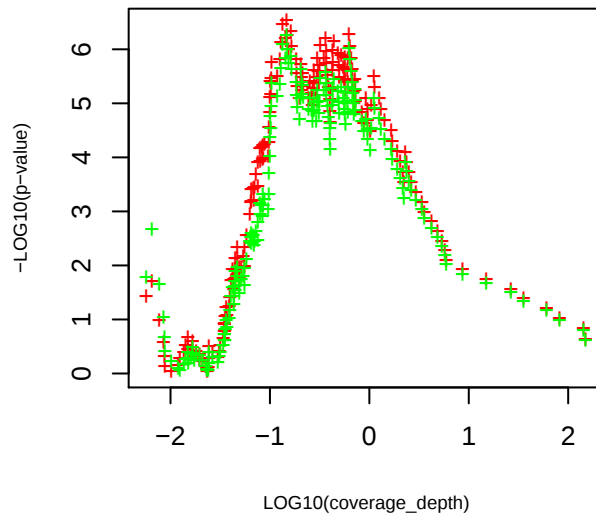


PF07559 FlaE: Flagellar basal body protein FlgE

slope= 3.00 p_value= 0.00053 intercept= -12.98 p_value= 2.7e-05

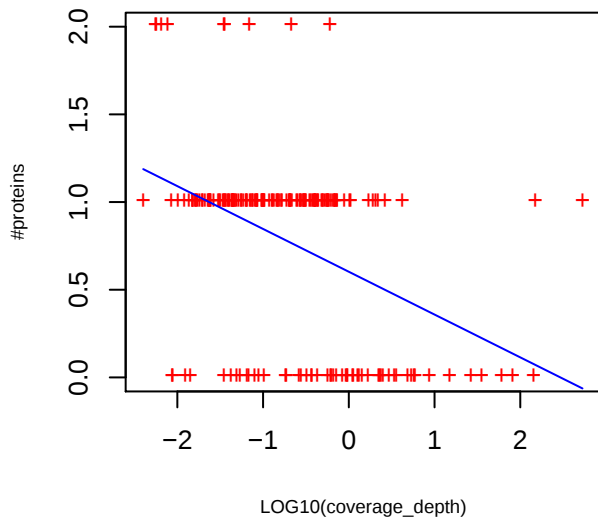


P-value curve : red (unnorm), green (norm)



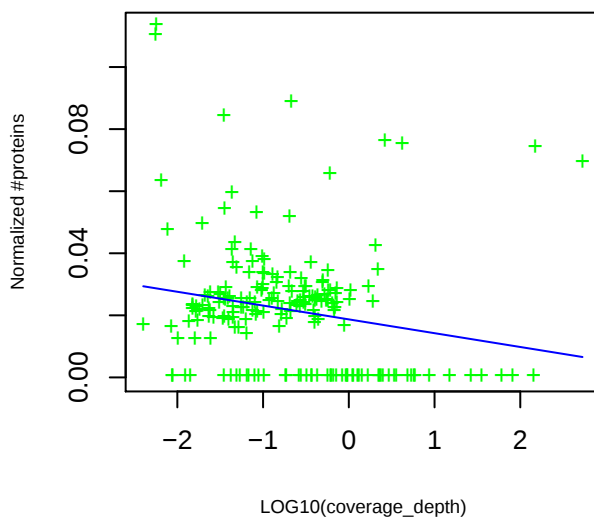
TIGR02135 phoU_full: phosphate transport system regulatory protein PhoU

slope= -0.24 p_value= 7.3e-10 intercept= 0.60 p_value= 8.7e-32



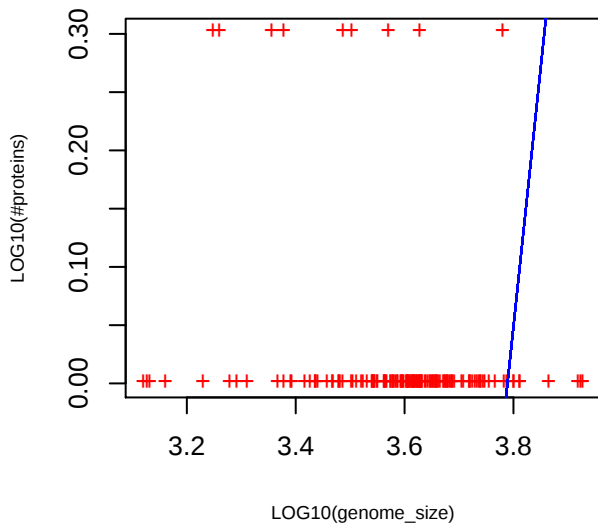
TIGR02135 phoU_full: phosphate transport system regulatory protein PhoU

slope= -0.0044 p_value= 0.0044 intercept= 0.019 p_value= 2.2e-21

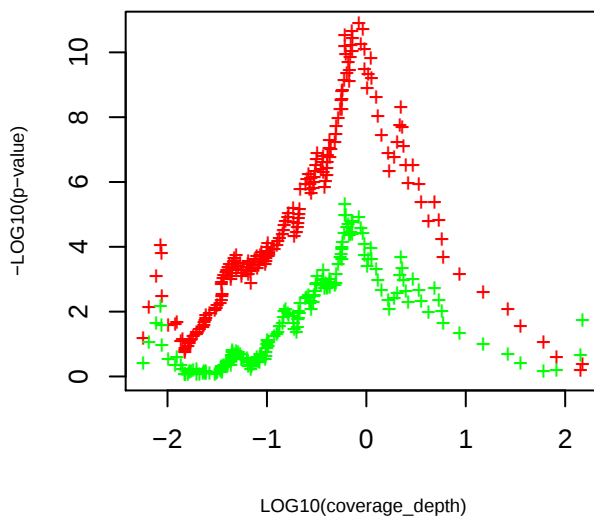


TIGR02135 phoU_full: phosphate transport system regulatory protein PhoU

slope= 4.44 p_value= 4.5e-09 intercept= -16.83 p_value= 4.8e-10

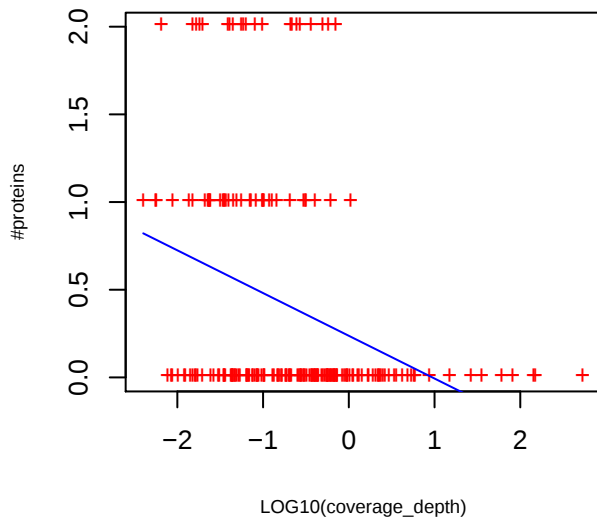


P-value curve ; red (unnorm), green (norm)



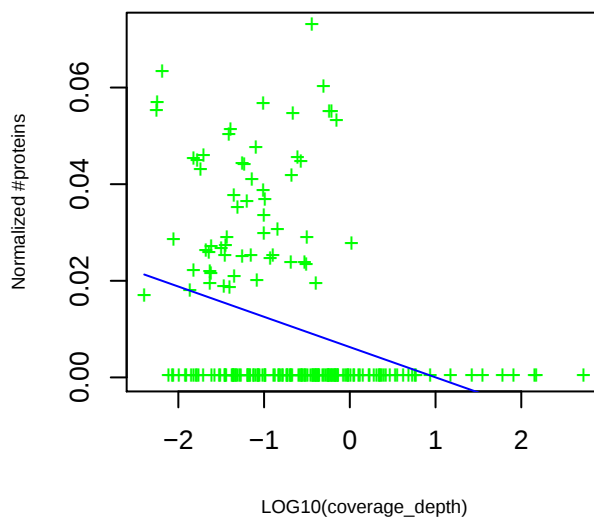
PF04463 DUF523: Protein of unknown function (DUF523)

slope= -0.24 p_value= 3.8e-06 intercept= 0.24 p_value= 6e-05



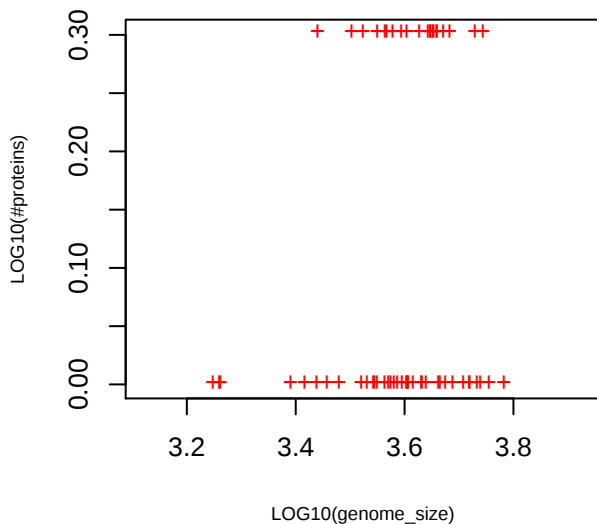
PF04463 DUF523: Protein of unknown function (DUF523)

slope= -0.0063 p_value= 8e-06 intercept= 0.0063 p_value= 6.8e-05

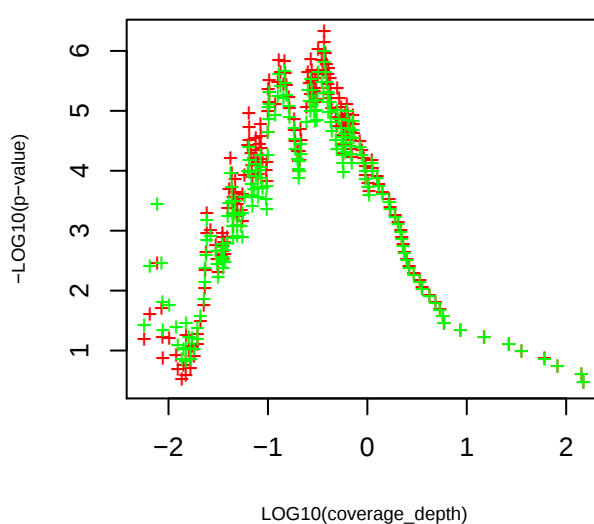


PF04463 DUF523: Protein of unknown function (DUF523)

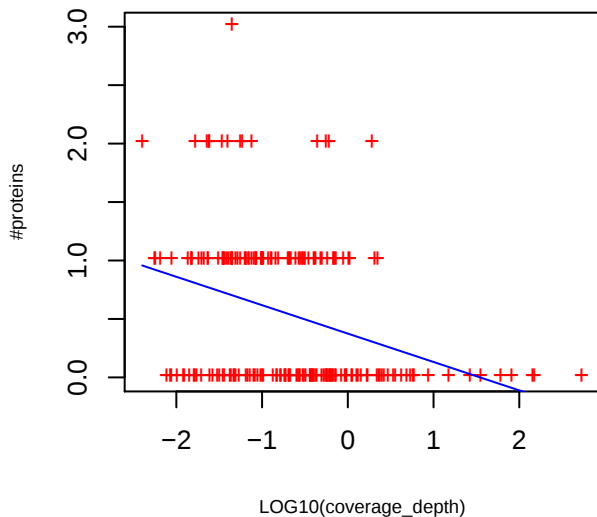
slope= 2.13 p_value= 0.0098 intercept= -10.31 p_value= 0.00046



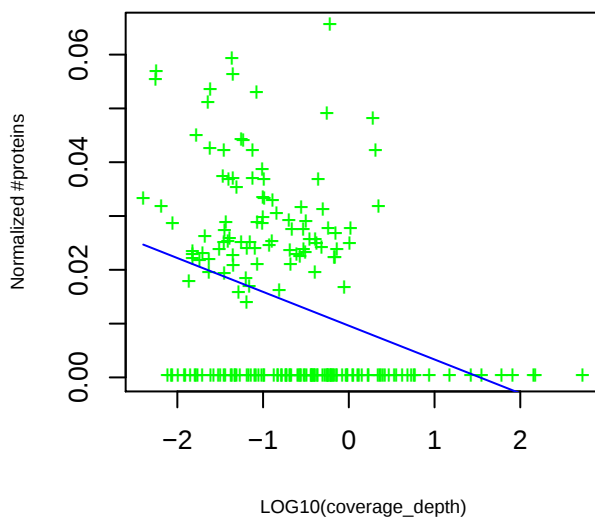
P-value curve ; red (unnorm), green (norm)



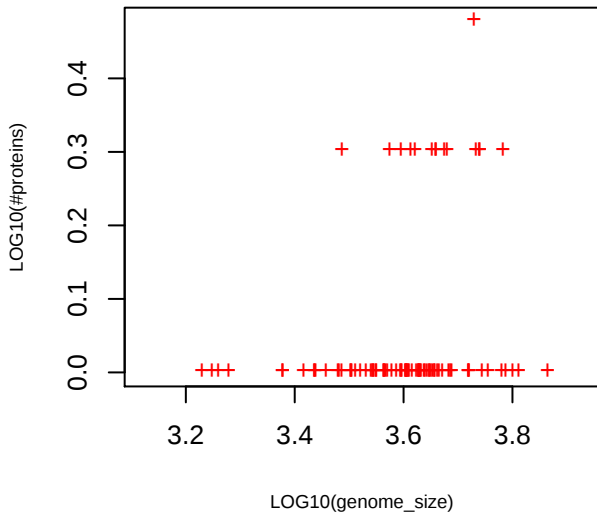
PF02120 Flg_hook: flagellar hook-length control protein
 slope= -0.24 p_value= 1.6e-06 intercept= 0.37 p_value= 1.5e-10



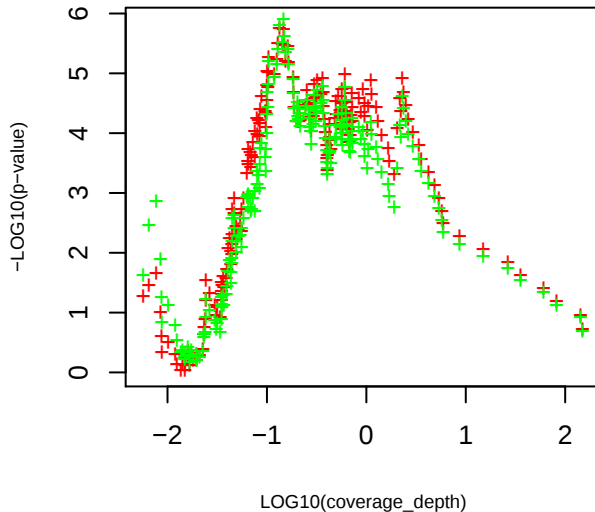
PF02120 Flg_hook: flagellar hook-length control protein
 slope= -0.0063 p_value= 1.8e-06 intercept= 0.0096 p_value= 2.5e-10



PF02120 Flg_hook: flagellar hook-length control protein
 slope= 3.70 p_value= 2.1e-05 intercept= -15.26 p_value= 9.6e-07

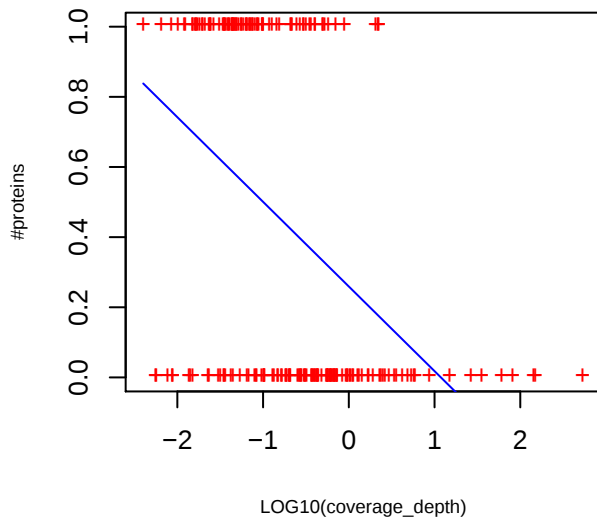


P-value curve ; red (unnorm), green (norm)



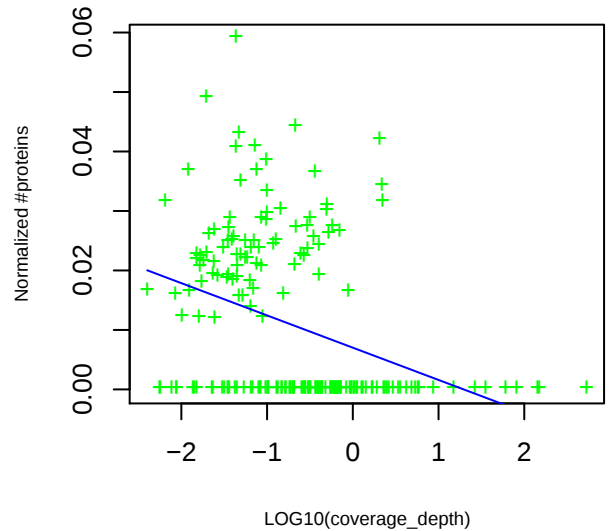
TIGR00252 TIGR00252: conserved hypothetical protein TIGR00252

slope= -0.24 p_value= 1.6e-10 intercept= 0.26 p_value= 1e-09



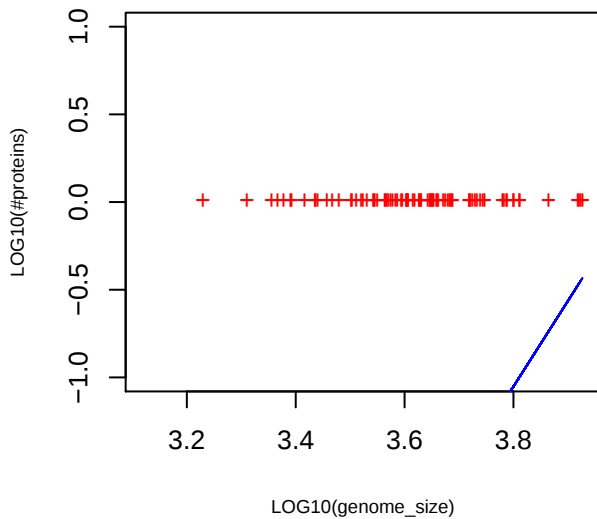
TIGR00252 TIGR00252: conserved hypothetical protein TIGR00252

slope= -0.0054 p_value= 3.6e-07 intercept= 0.007 p_value= 8e-09

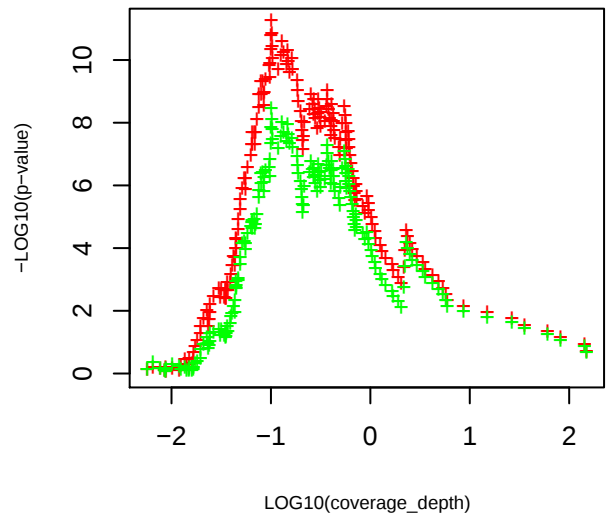


TIGR00252 TIGR00252: conserved hypothetical protein TIGR00252

slope= 4.88 p_value= 5.3e-09 intercept= -19.59 p_value= 6.5e-11

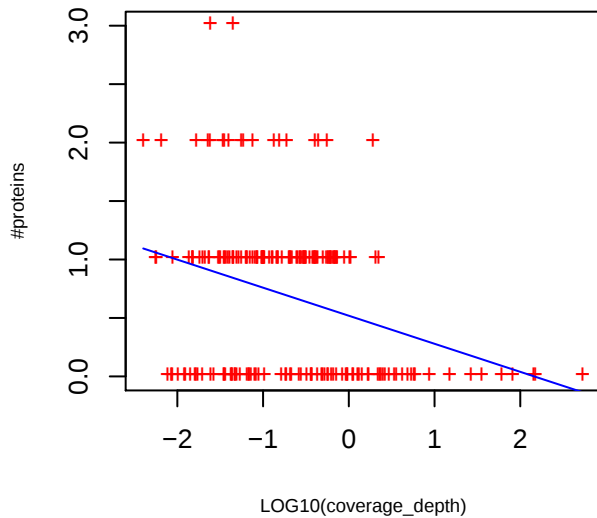


P-value curve ; red (unnorm), green (norm)



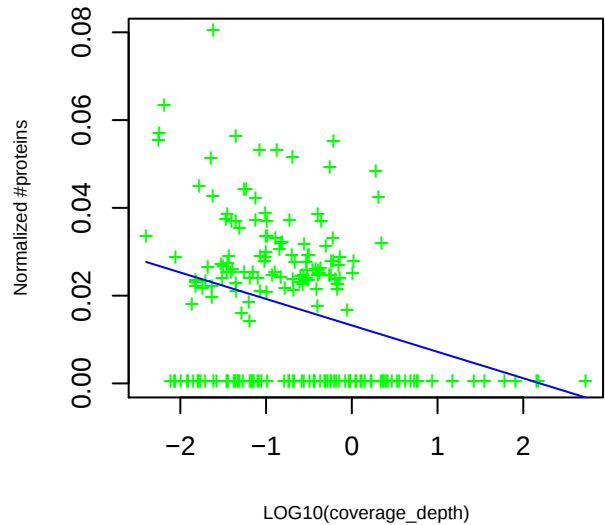
PF03963 FlgD: flagellar hook capping protein

slope= -0.24 p_value= 6.1e-06 intercept= 0.52 p_value= 3.7e-16



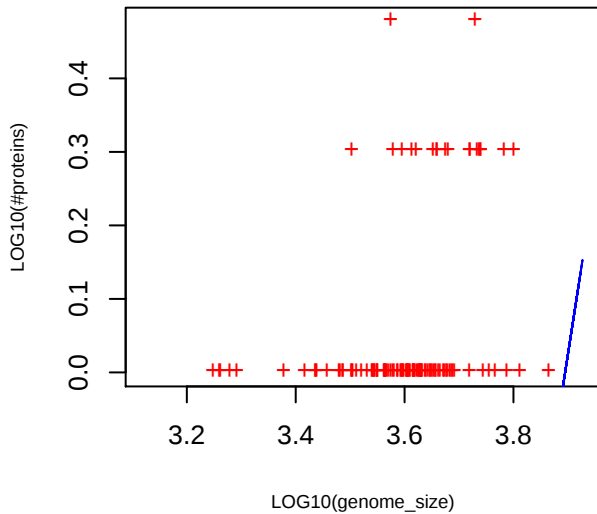
PF03963 FlgD: flagellar hook capping protein

slope= -0.006 p_value= 7.8e-06 intercept= 0.013 p_value= 3.1e-16

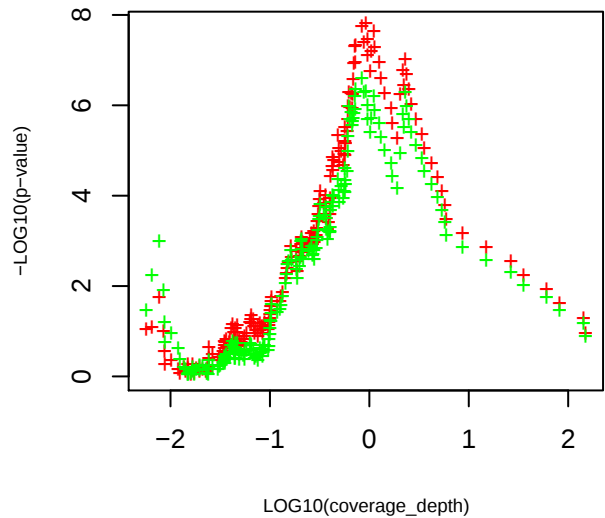


PF03963 FlgD: flagellar hook capping protein

slope= 4.79 p_value= 1.9e-08 intercept= -18.64 p_value= 9e-10

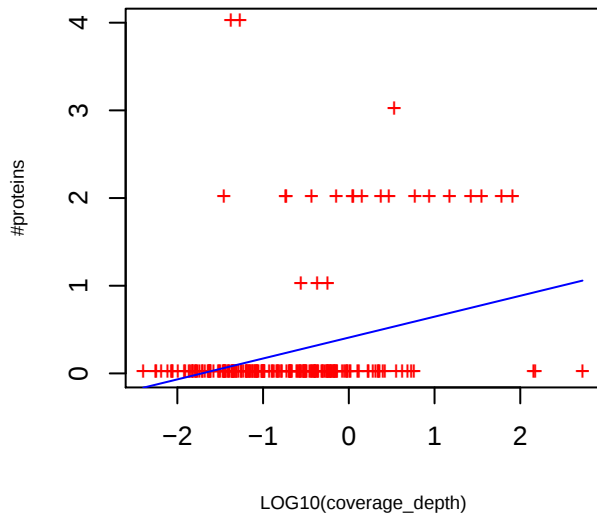


P-value curve ; red (unnorm), green (norm)



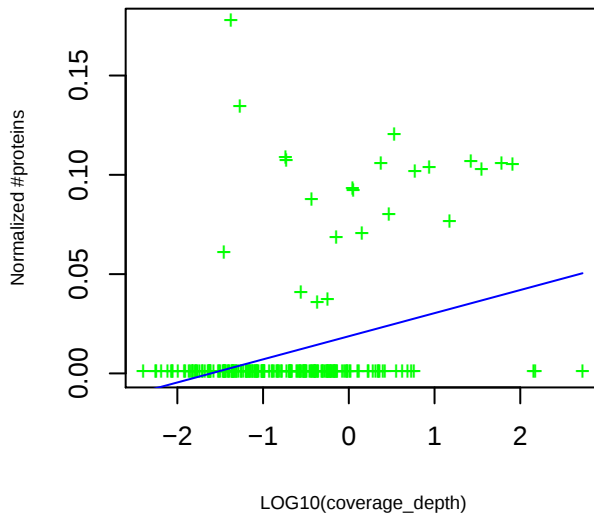
PF07878 DUF1662: Protein of unknown function (DUF1662)

slope= 0.24 p_value= 2.1e-05 intercept= 0.41 p_value= 3.4e-10



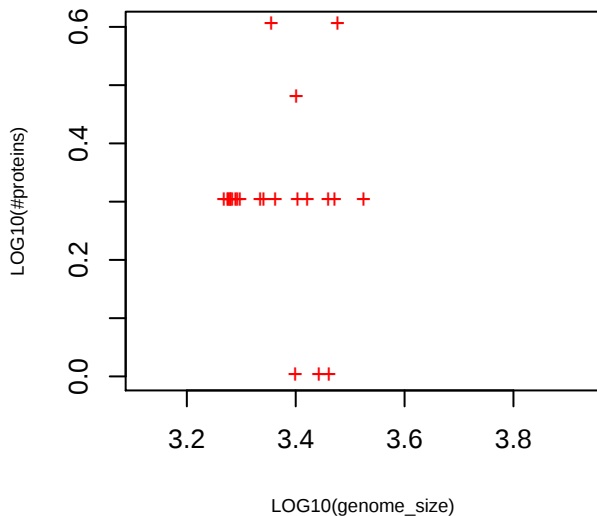
PF07878 DUF1662: Protein of unknown function (DUF1662)

slope= 0.012 p_value= 1.8e-06 intercept= 0.019 p_value= 3.8e-11

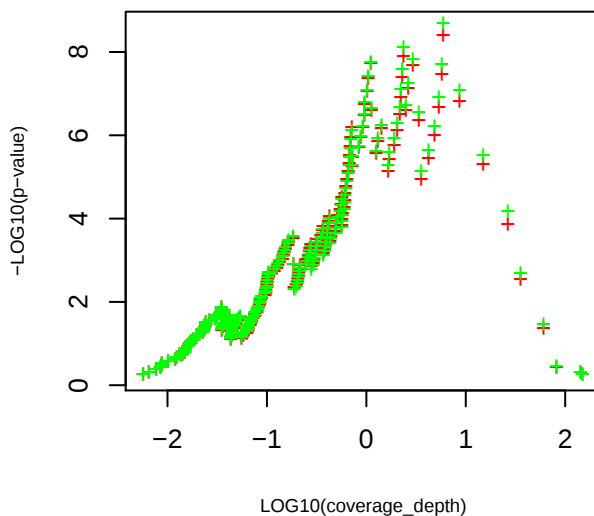


PF07878 DUF1662: Protein of unknown function (DUF1662)

slope= -3.42 p_value= 4.3e-09 intercept= 8.63 p_value= 2e-05

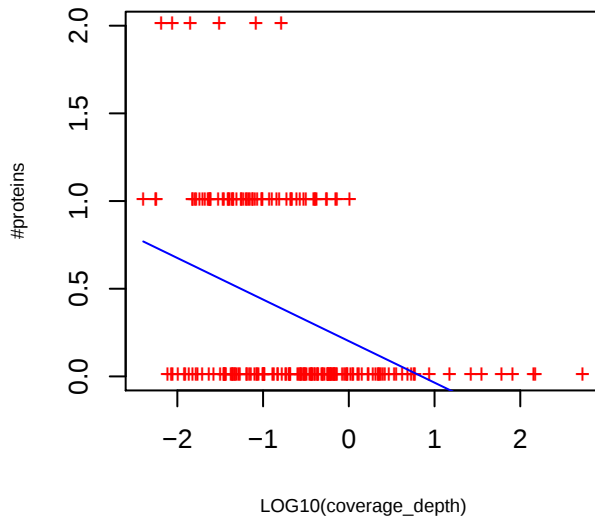


P-value curve ; red (unnorm), green (norm)



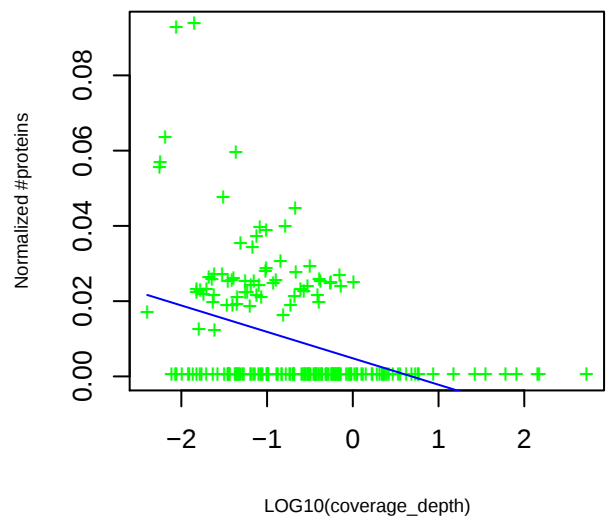
TIGR00104 TIGR00104: conserved hypothetical protein TIGR00104

slope= -0.24 p_value= 1.4e-08 intercept= 0.20 p_value= 1.4e-05



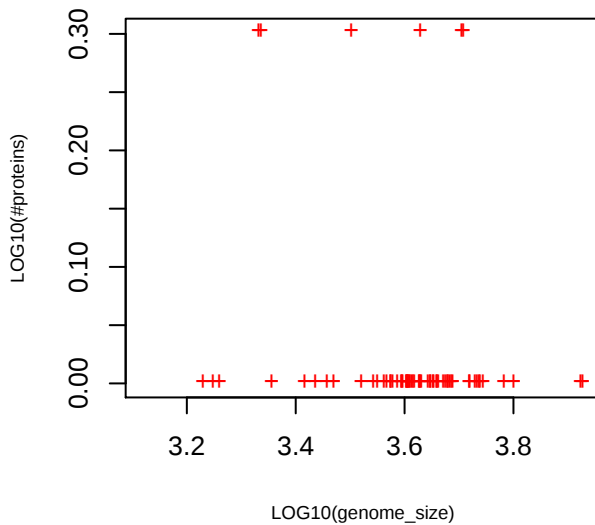
TIGR00104 TIGR00104: conserved hypothetical protein TIGR00104

slope= -0.007 p_value= 2.3e-08 intercept= 0.0048 p_value= 5e-04

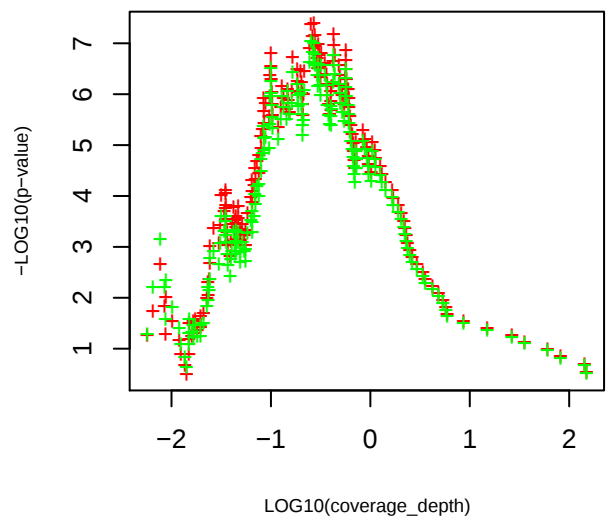


TIGR00104 TIGR00104: conserved hypothetical protein TIGR00104

slope= 3.12 p_value= 0.00015 intercept= -13.73 p_value= 3.3e-06

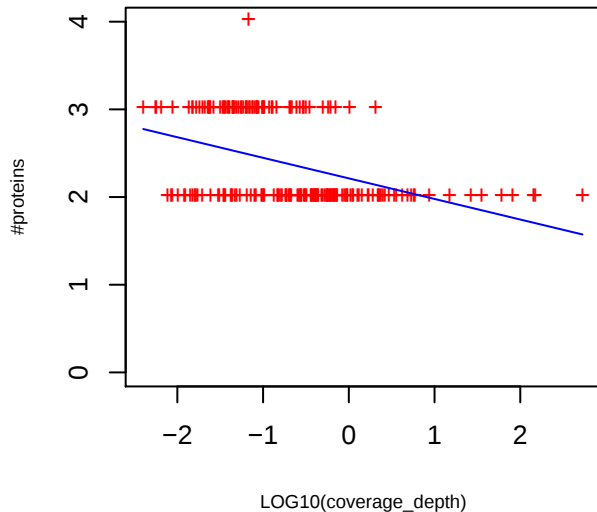


P-value curve ; red (unnorm), green (norm)



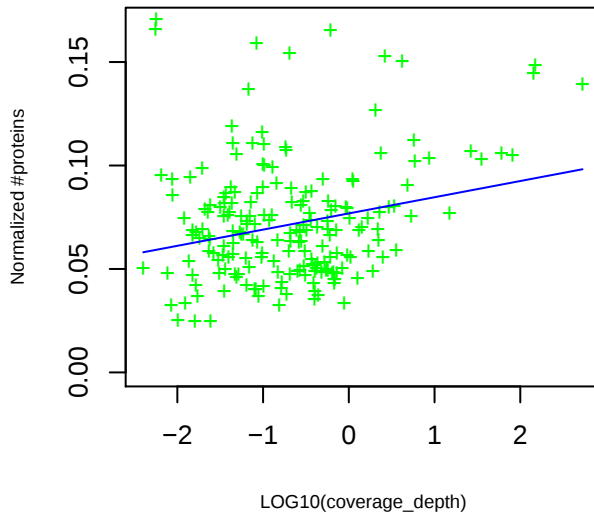
PF00448 SRP54: SRP54-type protein, GTPase domain

slope= -0.23 p_value= 5.8e-10 intercept= 2.21 p_value= 6.2e-120



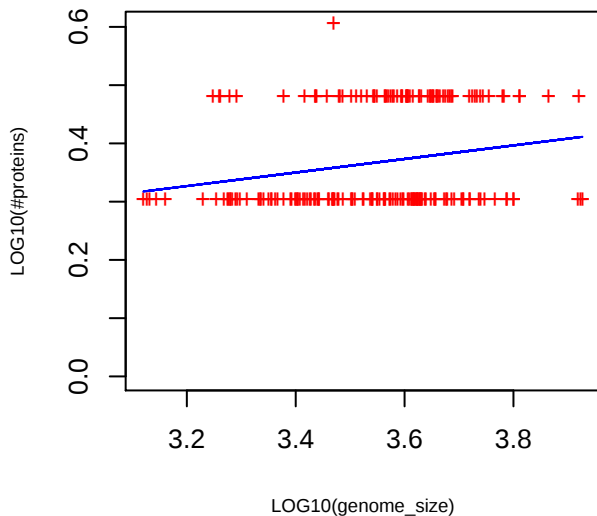
PF00448 SRP54: SRP54-type protein, GTPase domain

slope= 0.0078 p_value= 0.00057 intercept= 0.077 p_value= 5.4e-76

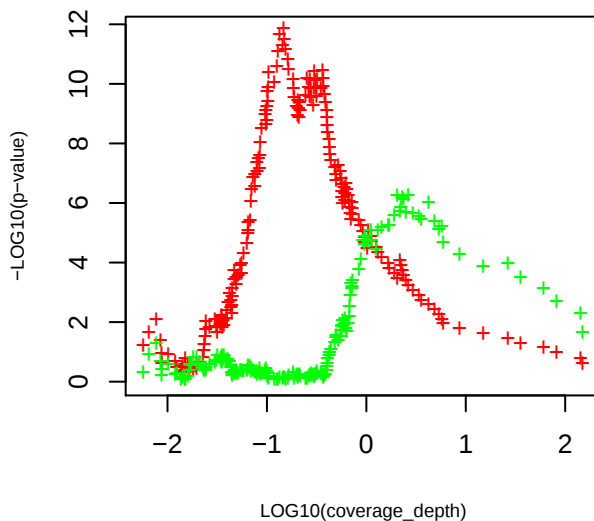


PF00448 SRP54: SRP54-type protein, GTPase domain

slope= 0.12 p_value= 0.0020 intercept= -0.046 p_value= 0.73

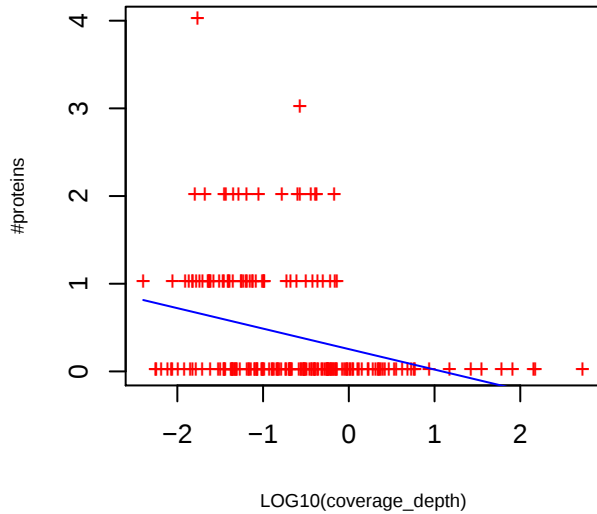


P-value curve ; red (unnorm), green (norm)



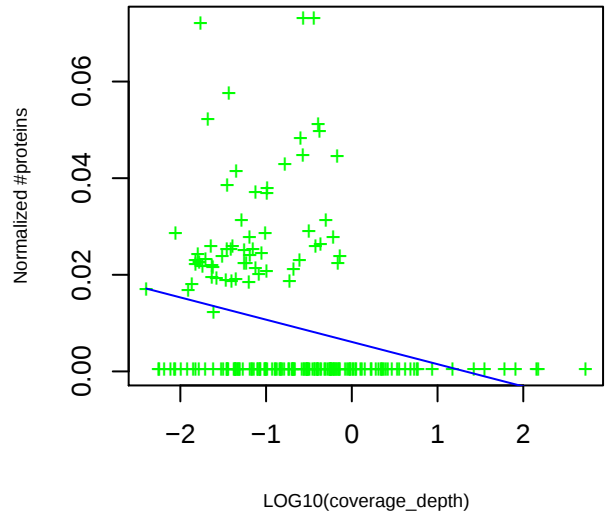
PF00042 Globin: Globin

slope= -0.23 p_value= 2.0e-05 intercept= 0.25 p_value= 3.8e-05



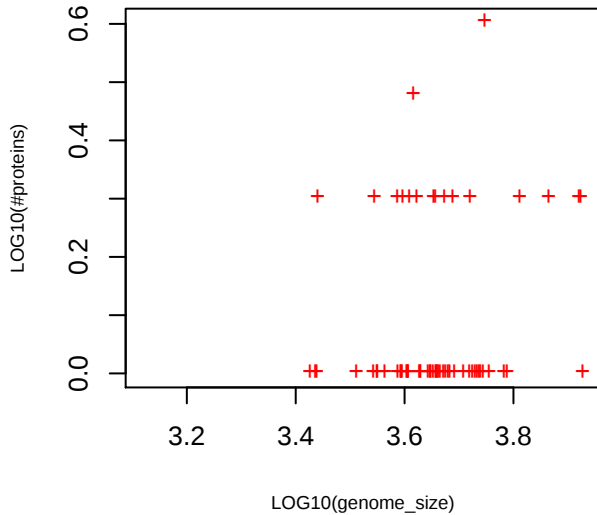
PF00042 Globin: Globin

slope= -0.0046 p_value= 0.00021 intercept= 0.0061 p_value= 1.6e-05

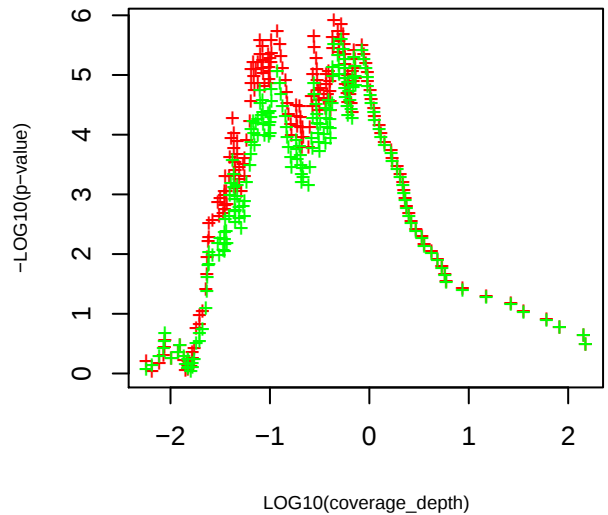


PF00042 Globin: Globin

slope= 5.47 p_value= 4e-12 intercept= -22.12 p_value= 7.8e-15

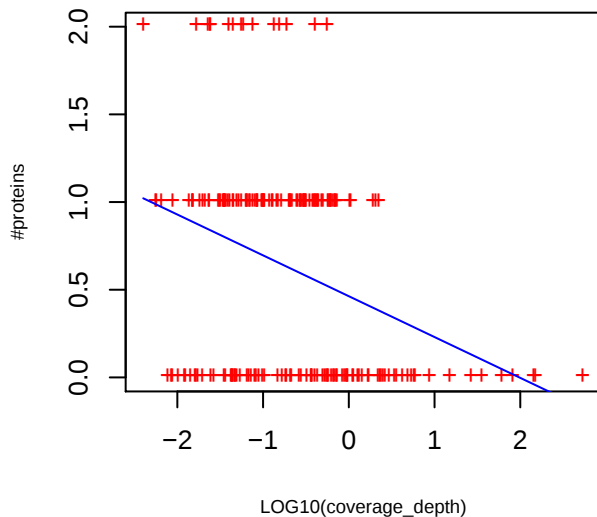


P-value curve ; red (unnorm), green (norm)



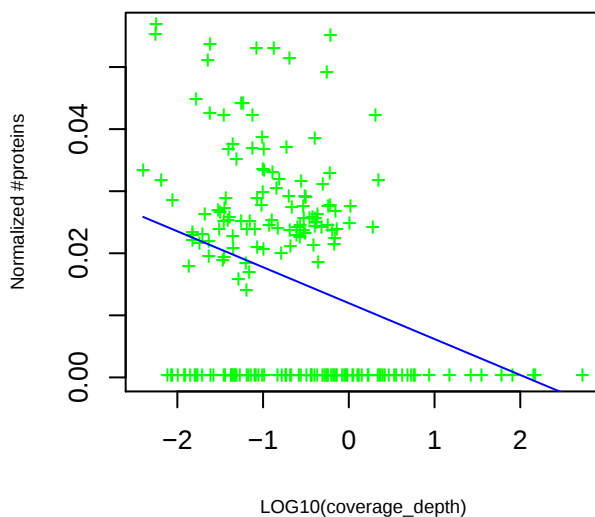
TIGR01398 FlhA: flagellar biosynthesis protein FlhA

slope= -0.23 p_value= 1.6e-06 intercept= 0.46 p_value= 1.3e-15



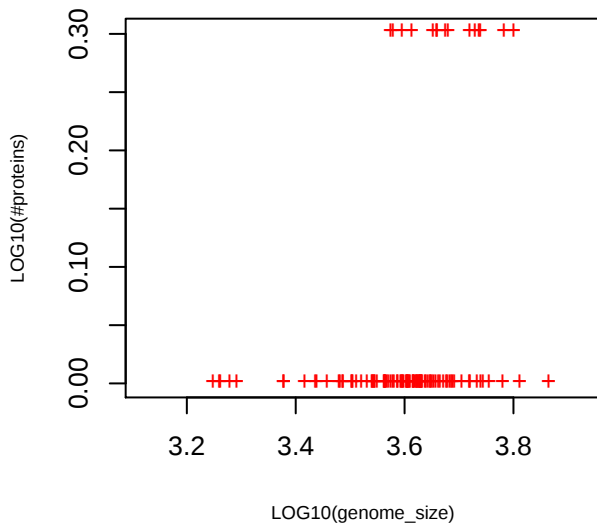
TIGR01398 FlhA: flagellar biosynthesis protein FlhA

slope= -0.0058 p_value= 4.7e-06 intercept= 0.012 p_value= 2.3e-15

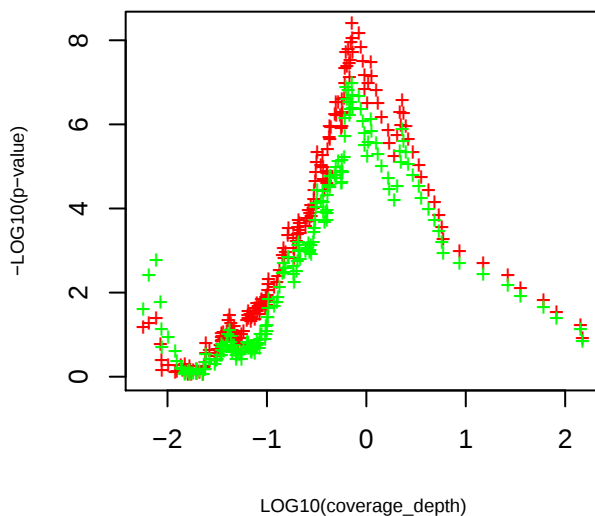


TIGR01398 FlhA: flagellar biosynthesis protein FlhA

slope= 4.49 p_value= 1.6e-07 intercept= -17.72 p_value= 7.5e-09

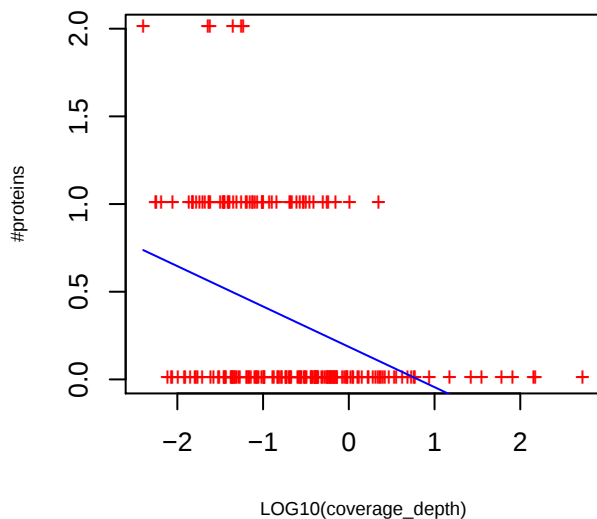


P-value curve : red (unnorm), green (norm)



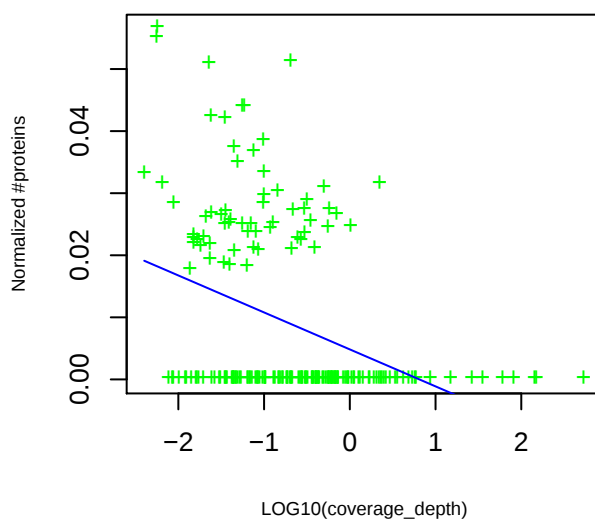
PF04316 FlgM: anti-sigma-28 factor, FlgM

slope= -0.23 p_value= 2.7e-08 intercept= 0.19 p_value= 5.1e-05



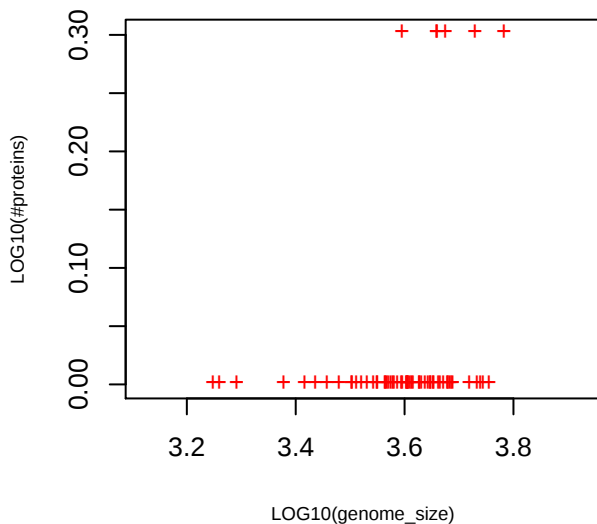
PF04316 FlgM: anti-sigma-28 factor, FlgM

slope= -0.006 p_value= 5.6e-08 intercept= 0.0048 p_value= 7e-05

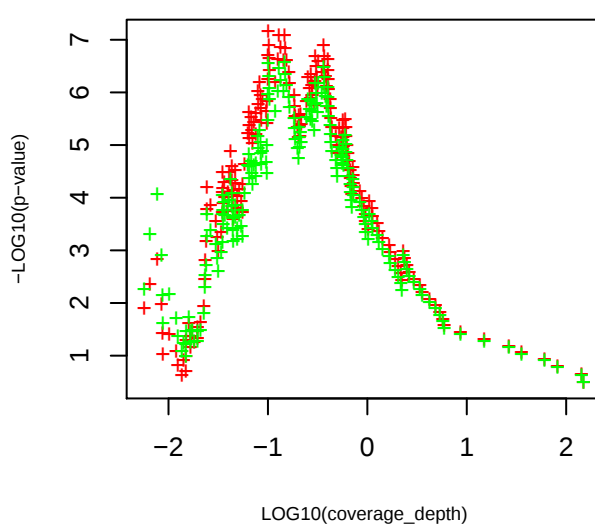


PF04316 FlgM: anti-sigma-28 factor, FlgM

slope= 2.33 p_value= 0.0043 intercept= -10.99 p_value= 0.00017

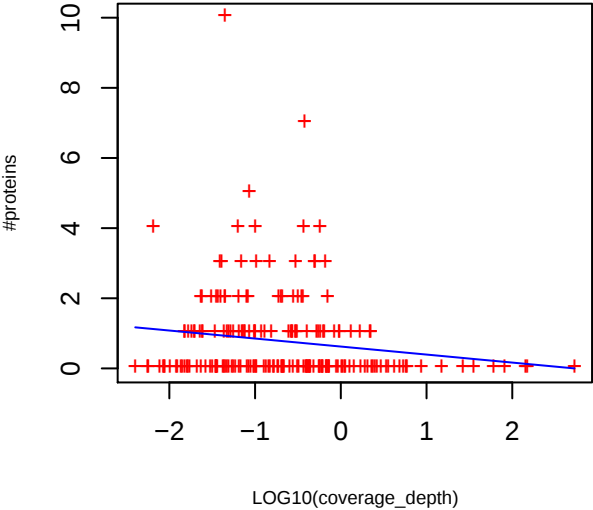


P-value curve ; red (unnorm), green (norm)



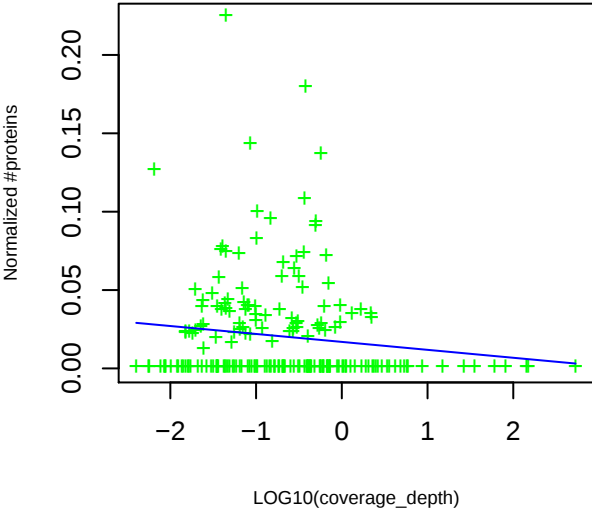
TIGR01845 outer_NodT: efflux transporter, outer membrane factor (OMF) lipoprotein, NodT family

slope= -0.23 p_value= 0.029 intercept= 0.62 p_value= 2.8e-07



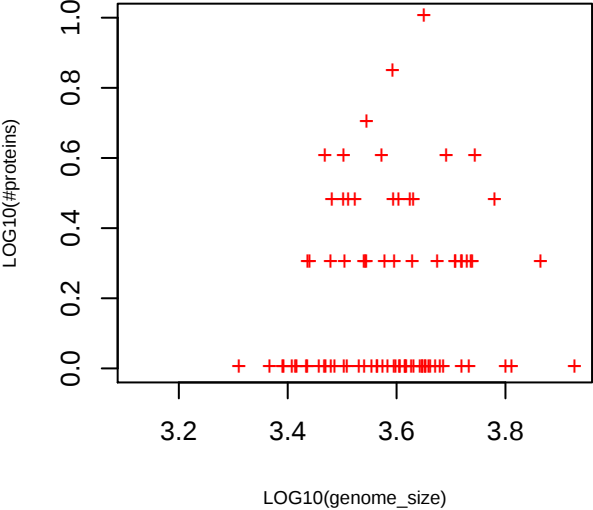
TIGR01845 outer_NodT: efflux transporter, outer membrane factor (OMF) lipoprotein, NodT family

slope= -0.0051 p_value= 0.061 intercept= 0.017 p_value= 8.4e-08

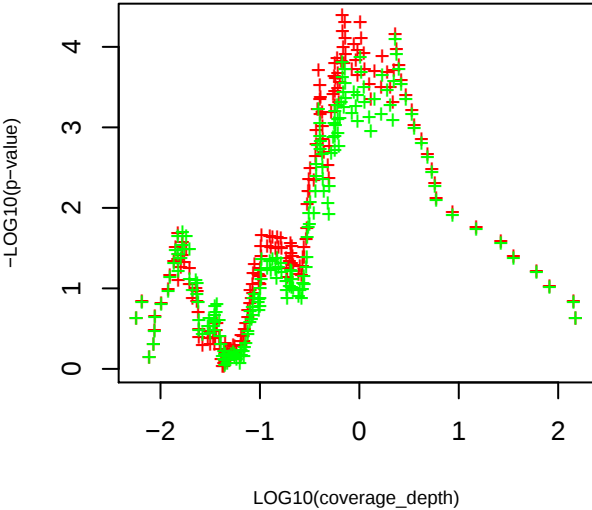


TIGR01845 outer_NodT: efflux transporter, outer membrane factor (OMF) lipoprotein, NodT family

slope= 2.94 p_value= 0.0011 intercept= -12.66 p_value= 8.5e-05

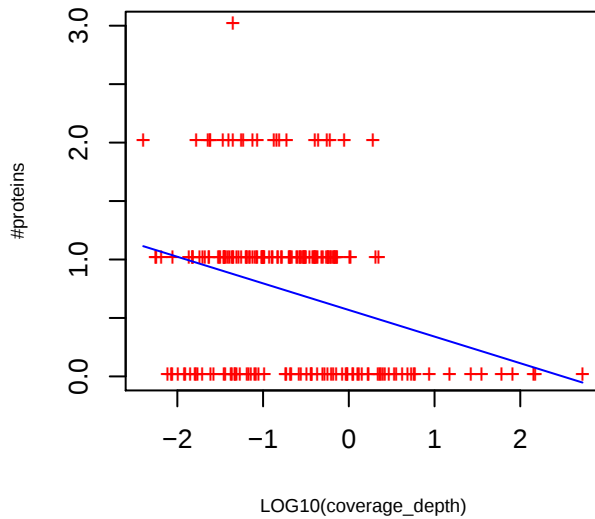


P-value curve ; red (unnorm), green (norm)



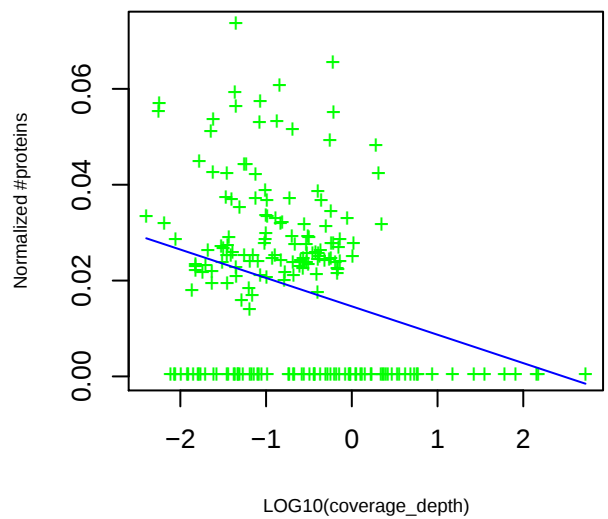
PF01706 FliG_C: FliG C-terminal domain

slope= -0.23 p_value= 1.6e-05 intercept= 0.57 p_value= 1.3e-18



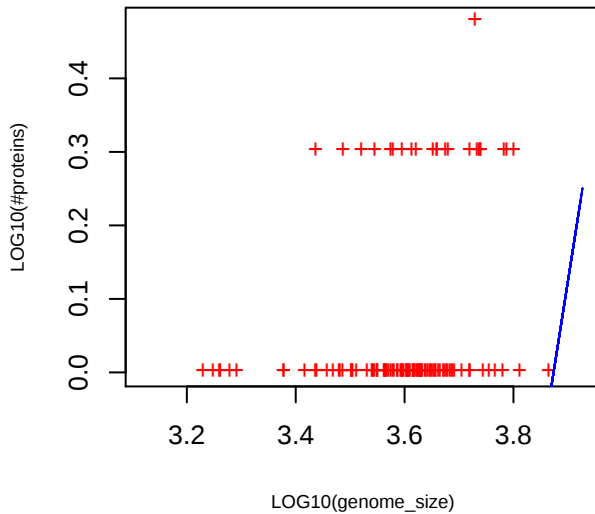
PF01706 FliG_C: FliG C-terminal domain

slope= -0.0059 p_value= 2.1e-05 intercept= 0.015 p_value= 6.5e-18

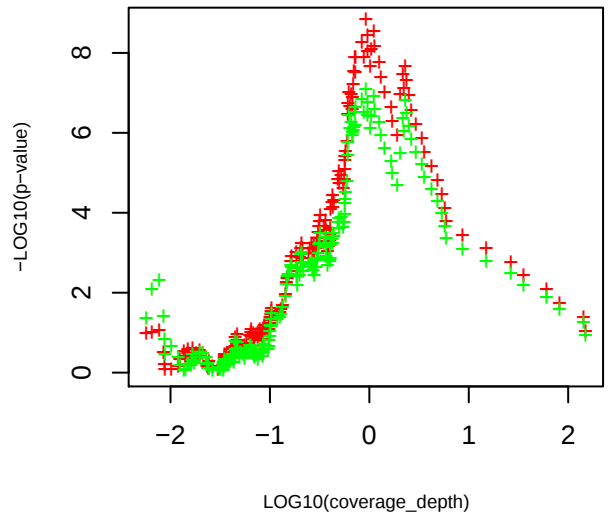


PF01706 FliG_C: FliG C-terminal domain

slope= 4.71 p_value= 2.2e-08 intercept= -18.25 p_value= 1.3e-09

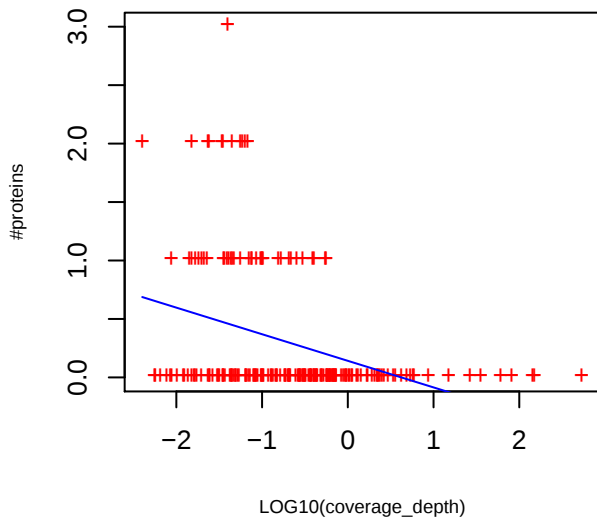


P-value curve ; red (unnorm), green (norm)



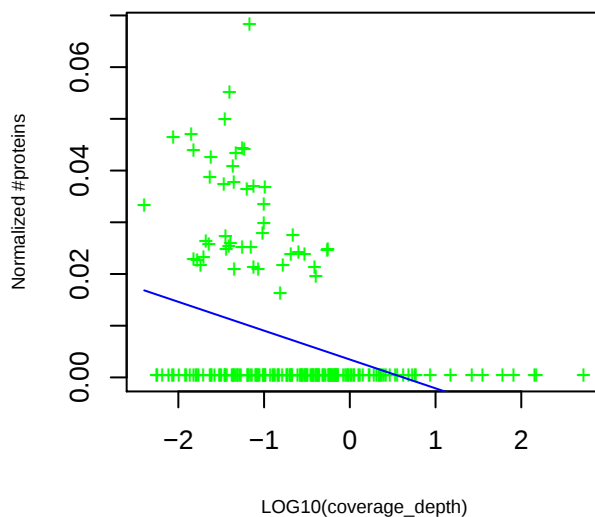
PF03595 C4dic_mal_tran: C4-dicarboxylate transporter/malic acid transport protein

slope= -0.23 p_value= 8.6e-07 intercept= 0.14 p_value= 0.0055



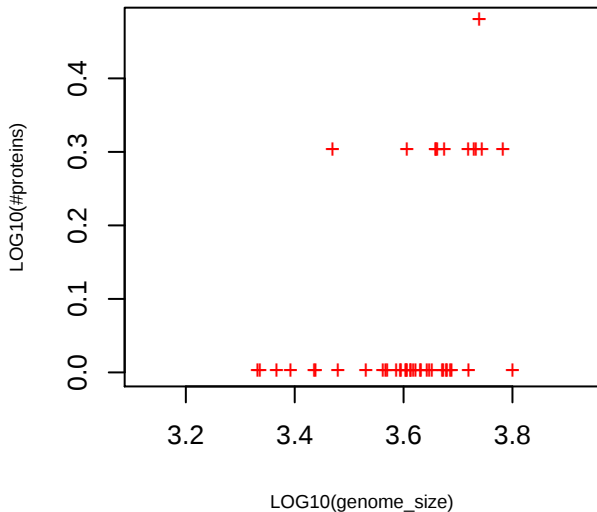
PF03595 C4dic_mal_tran: C4-dicarboxylate transporter/malic acid transport protein

slope= -0.0056 p_value= 5.5e-07 intercept= 0.0035 p_value= 0.0048

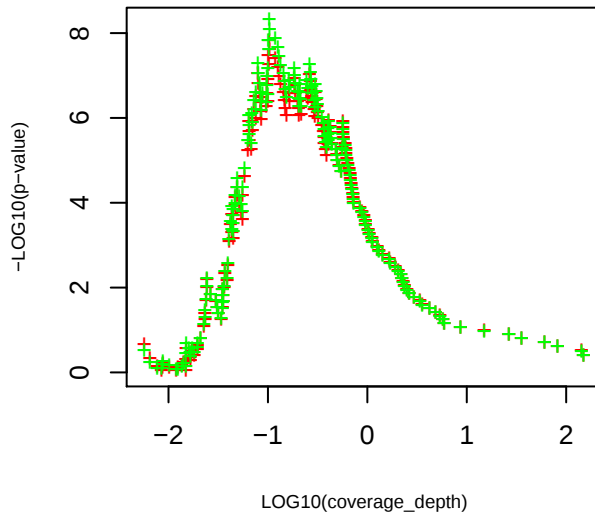


PF03595 C4dic_mal_tran: C4-dicarboxylate transporter/malic acid transport protein

slope= 2.37 p_value= 0.0016 intercept= -11.47 p_value= 2.2e-05

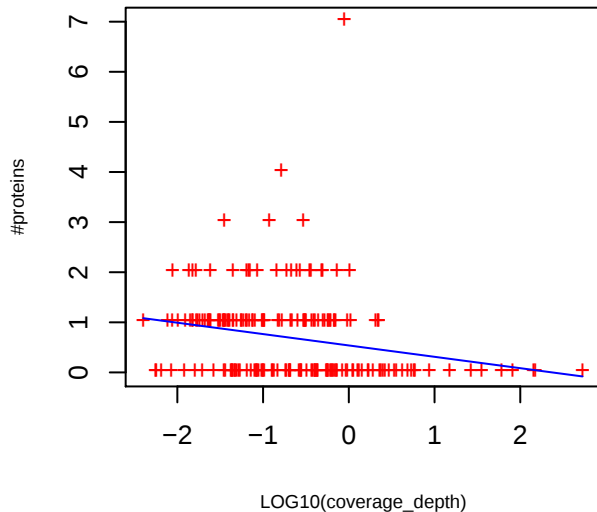


P-value curve ; red (unnorm), green (norm)



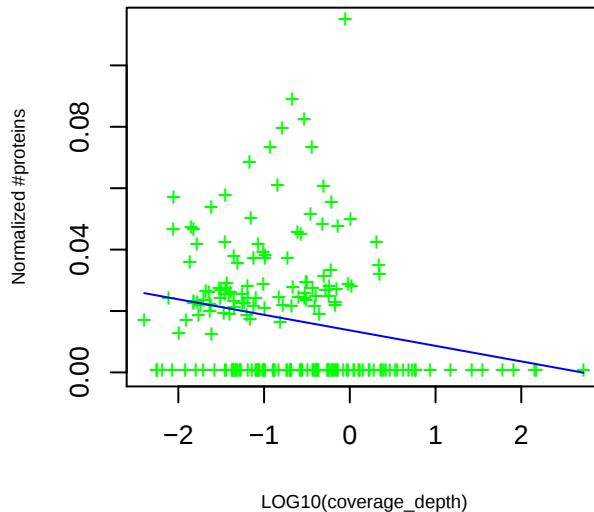
PF08546 ApbA_C: Ketopantoate reductase PanE/ApbA C terminal

slope= -0.23 p_value= 0.0013 intercept= 0.54 p_value= 9e-11



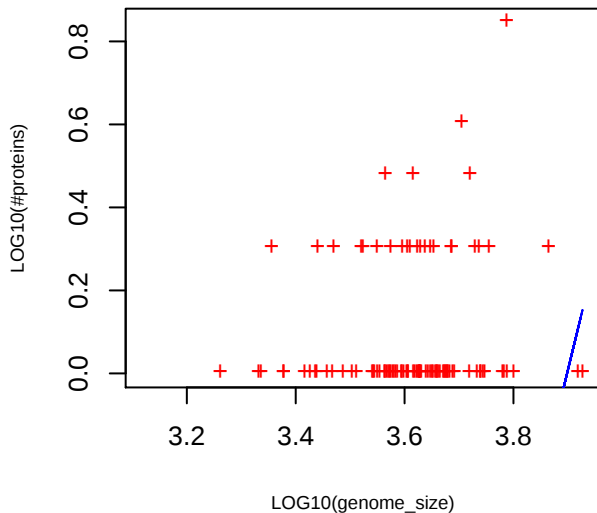
PF08546 ApbA_C: Ketopantoate reductase PanE/ApbA C terminal

slope= -0.0051 p_value= 0.0025 intercept= 0.014 p_value= 5.3e-12

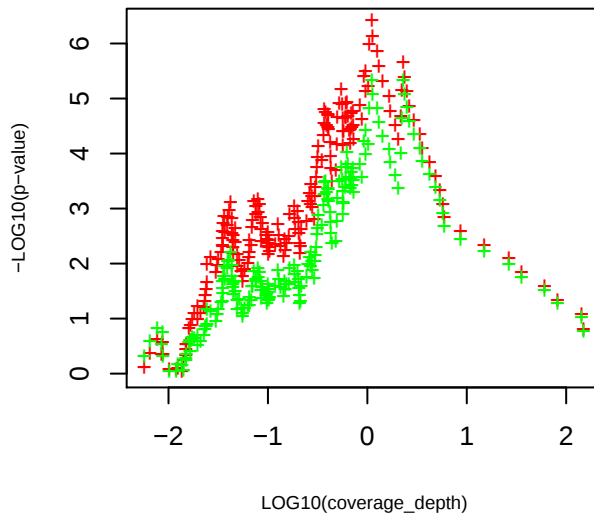


PF08546 ApbA_C: Ketopantoate reductase PanE/ApbA C terminal

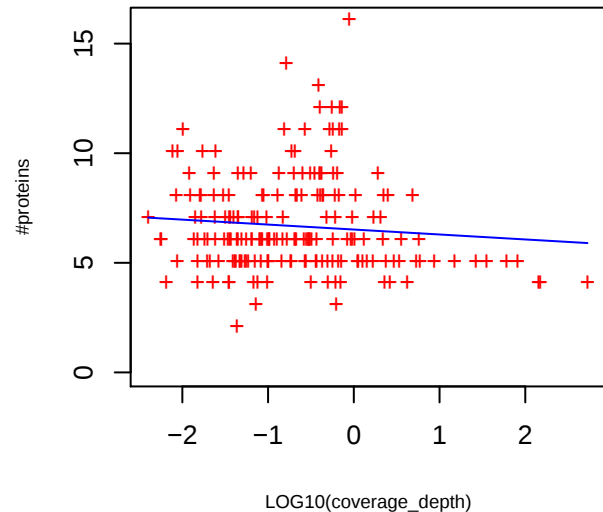
slope= 5.39 p_value= 3.7e-10 intercept= -21.00 p_value= 9.2e-12



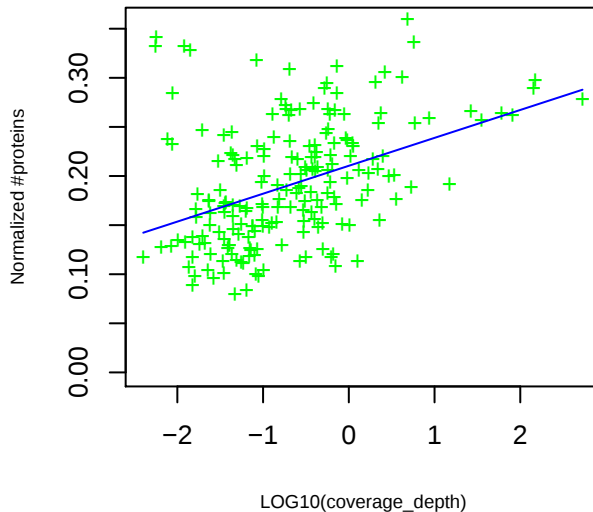
P-value curve ; red (unnorm), green (norm)



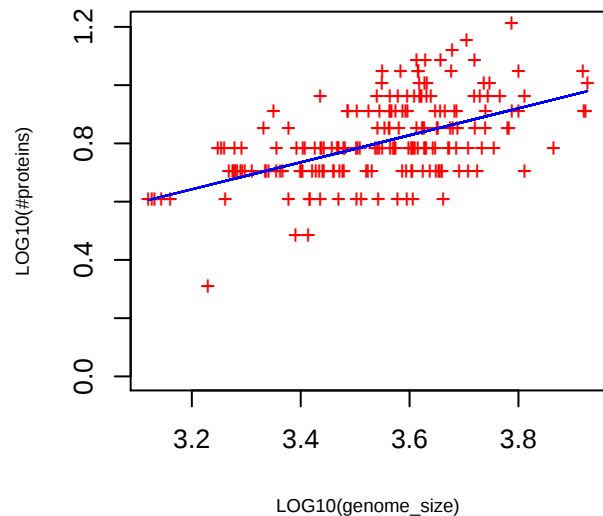
PF00291 PALP: Pyridoxal-phosphate dependent enzyme
slope= -0.23 p_value= 0.20 intercept= 6.52 p_value= 5.4e-81



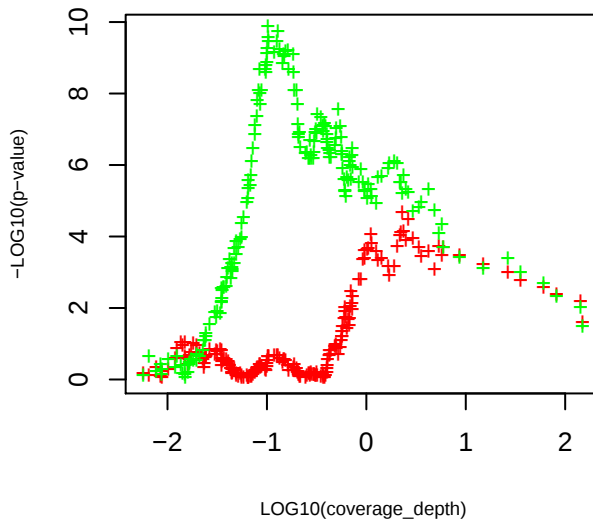
PF00291 PALP: Pyridoxal-phosphate dependent enzyme
slope= 0.028 p_value= 1.9e-09 intercept= 0.21 p_value= 1.9e-98



PF00291 PALP: Pyridoxal-phosphate dependent enzyme
slope= 0.46 p_value= 6.6e-17 intercept= -0.84 p_value= 5.2e-06

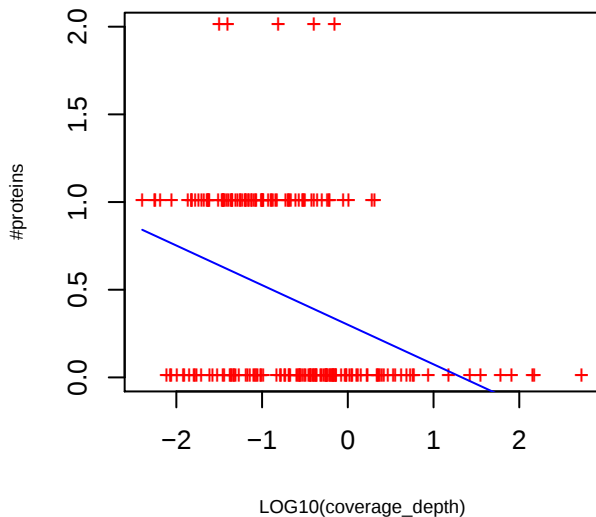


P-value curve ; red (unnorm), green (norm)



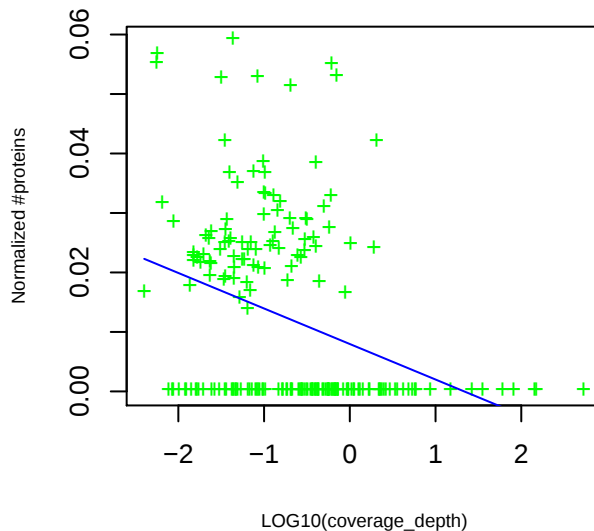
PF02154 FliM: flagellar motor switch protein FliM

slope= -0.23 p_value= 1e-07 intercept= 0.30 p_value= 5.8e-10



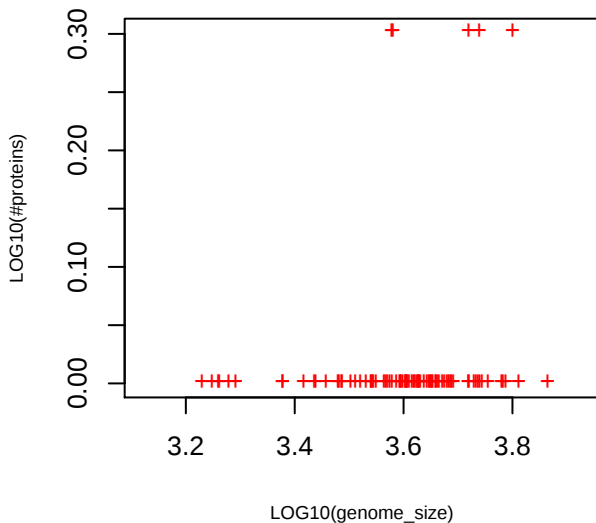
PF02154 FliM: flagellar motor switch protein FliM

slope= -0.006 p_value= 7.1e-07 intercept= 0.008 p_value= 7e-09

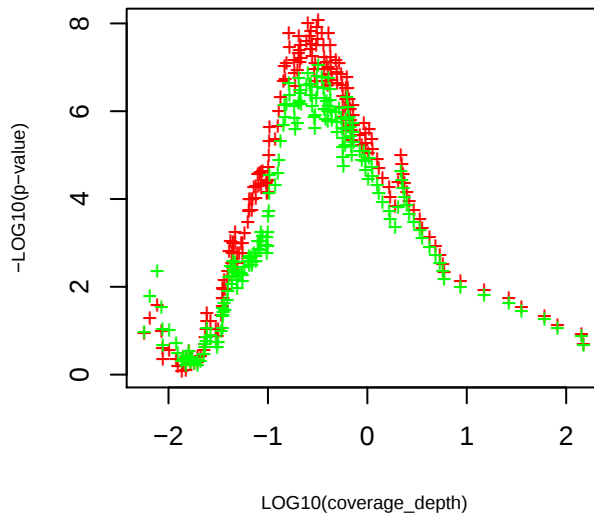


PF02154 FliM: flagellar motor switch protein FliM

slope= 3.23 p_value= 0.00018 intercept= -13.72 p_value= 8.6e-06

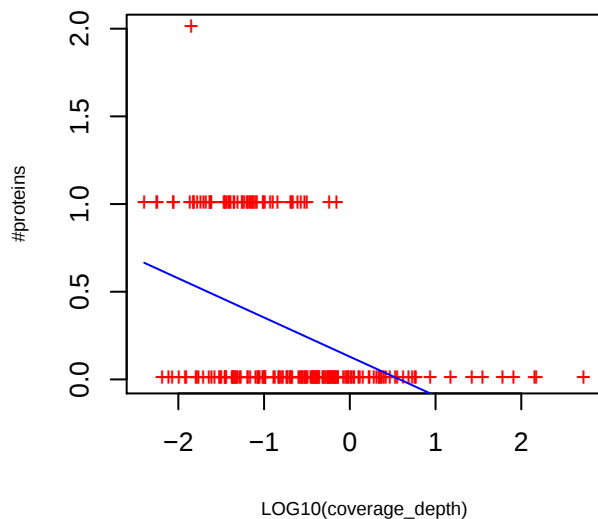


P-value curve ; red (unnorm), green (norm)



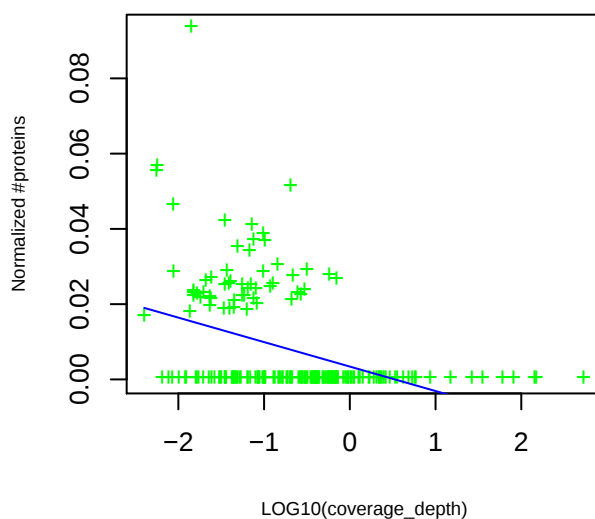
TIGR00342 TIGR00342: thiamine biosynthesis/tRNA modification protein ThiI

slope= -0.22 p_value= 2.6e-10 intercept= 0.13 p_value= 0.00074



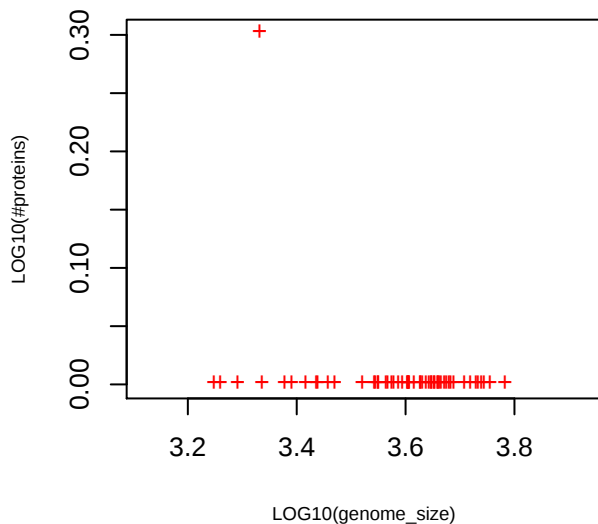
TIGR00342 TIGR00342: thiamine biosynthesis/tRNA modification protein ThiI

slope= -0.0065 p_value= 4.1e-09 intercept= 0.0034 p_value= 0.0046

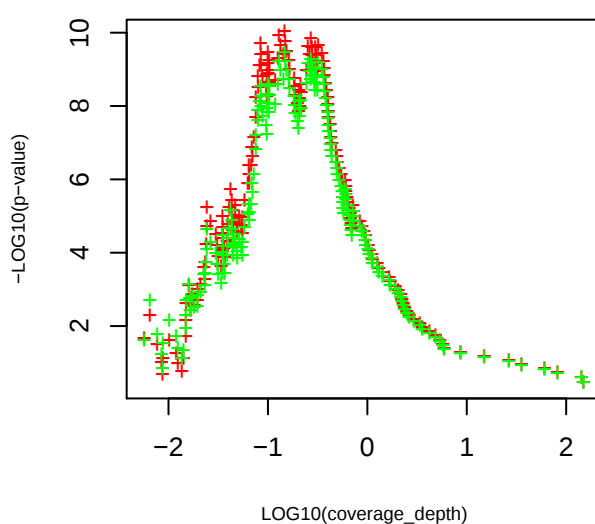


TIGR00342 TIGR00342: thiamine biosynthesis/tRNA modification protein ThiI

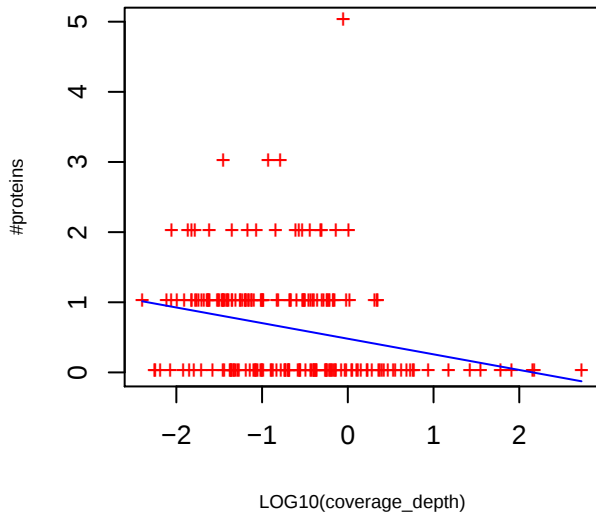
slope= 1.51 p_value= 0.055 intercept= -8.25 p_value= 0.0034



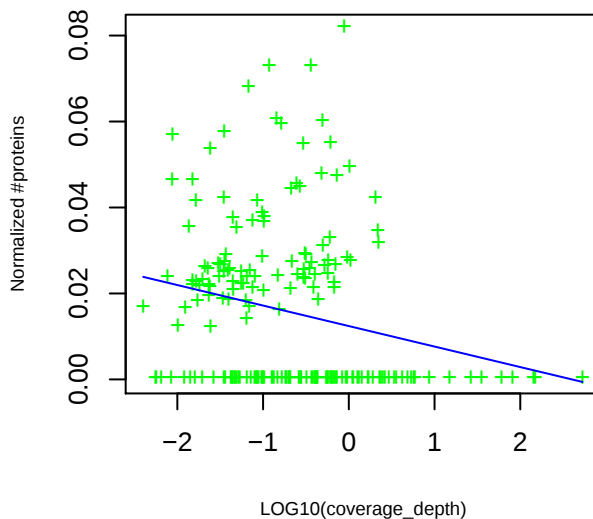
P-value curve ; red (unnorm), green (norm)



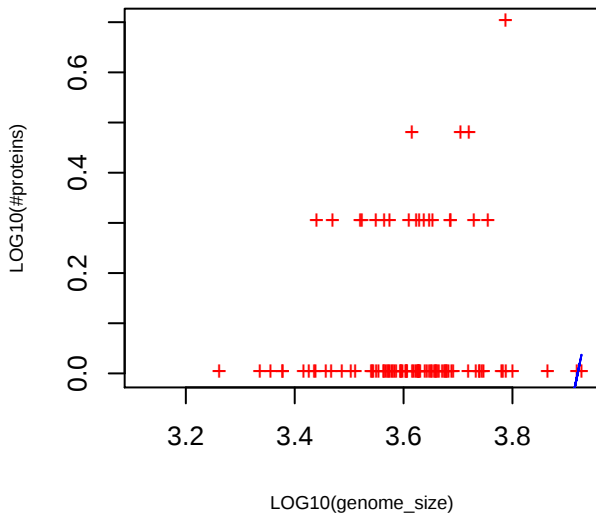
TIGR00745 apbA_panE: 2-dehydroapantoate 2-reductase
 slope= -0.22 p_value= 0.00027 intercept= 0.48 p_value= 2.3e-11



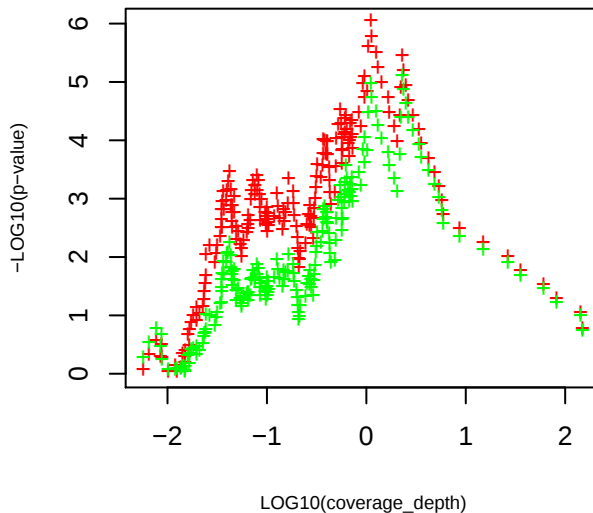
TIGR00745 apbA_panE: 2-dehydroapantoate 2-reductase
 slope= -0.0048 p_value= 0.0014 intercept= 0.012 p_value= 2.8e-12



TIGR00745 apbA_panE: 2-dehydroapantoate 2-reductase
 slope= 5.27 p_value= 8e-10 intercept= -20.65 p_value= 1.8e-11

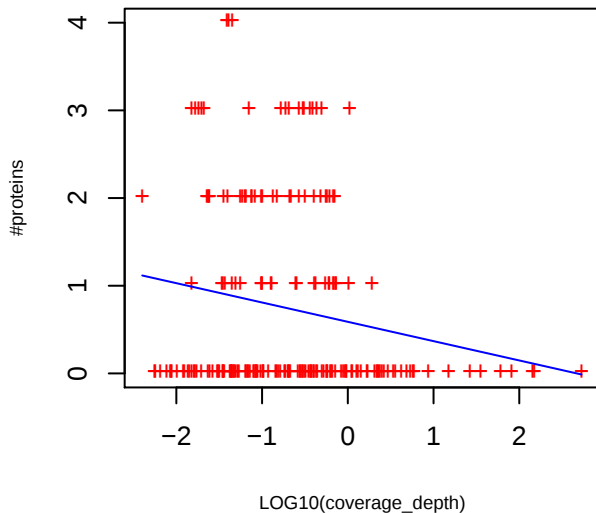


P-value curve ; red (unnorm), green (norm)



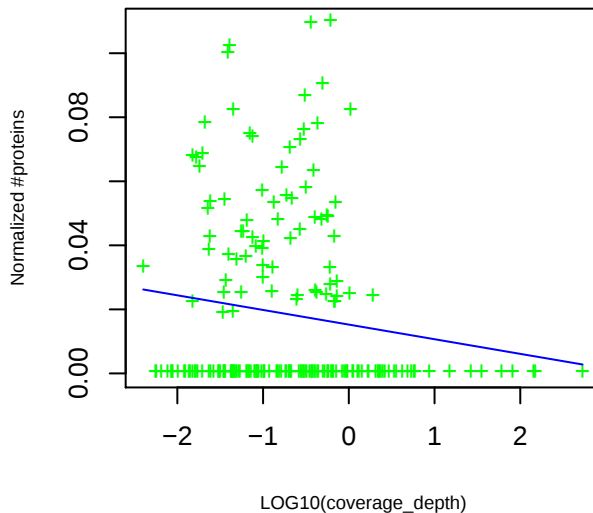
PF04403 PqiA: Paraquat-inducible protein A

slope= -0.22 p_value= 0.011 intercept= 0.59 p_value= 6.9e-09



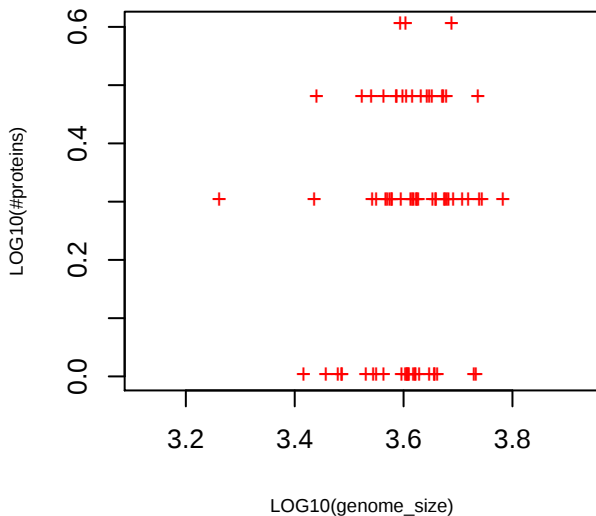
PF04403 PqiA: Paraquat-inducible protein A

slope= -0.0046 p_value= 0.038 intercept= 0.015 p_value= 4.1e-09

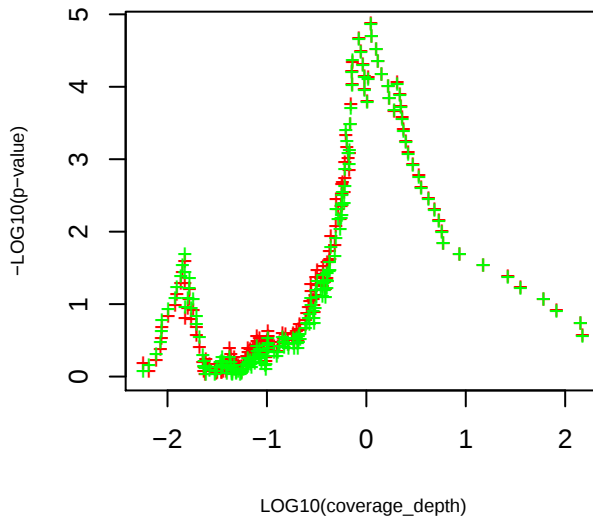


PF04403 PqiA: Paraquat-inducible protein A

slope= 3.86 p_value= 1.4e-05 intercept= -16.09 p_value= 4.1e-07

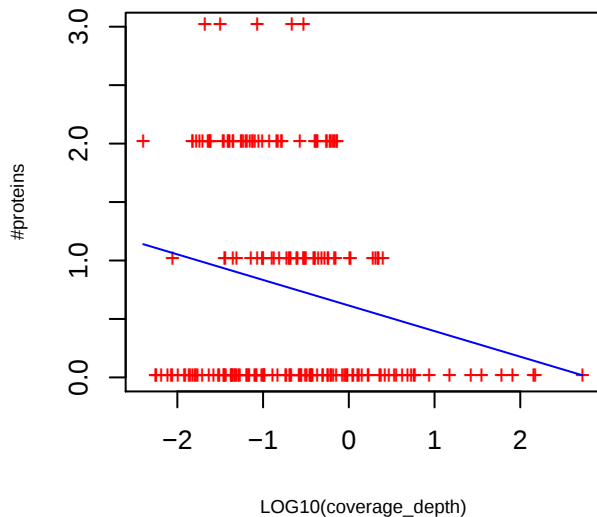


P-value curve ; red (unnorm), green (norm)



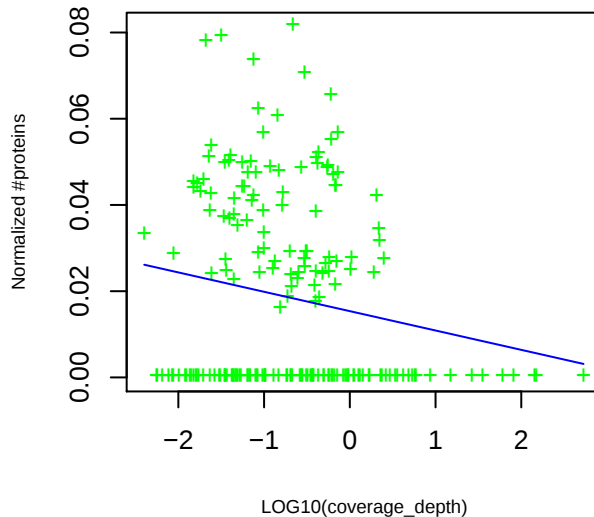
PF02036 SCP2: SCP-2 sterol transfer family

slope= -0.22 p_value= 0.0023 intercept= 0.61 p_value= 7.6e-13



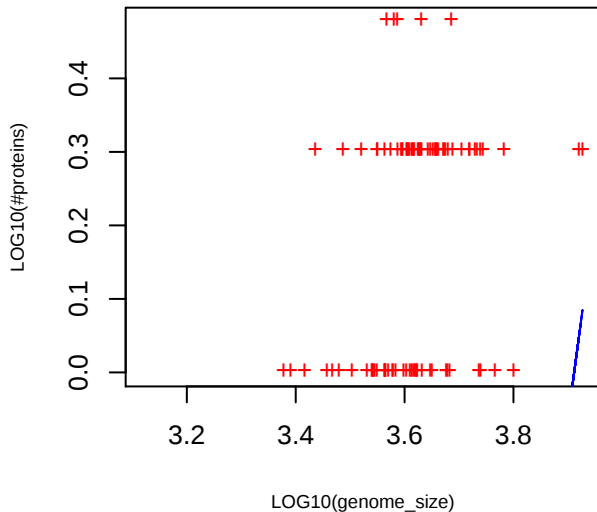
PF02036 SCP2: SCP-2 sterol transfer family

slope= -0.0045 p_value= 0.010 intercept= 0.015 p_value= 2.7e-13

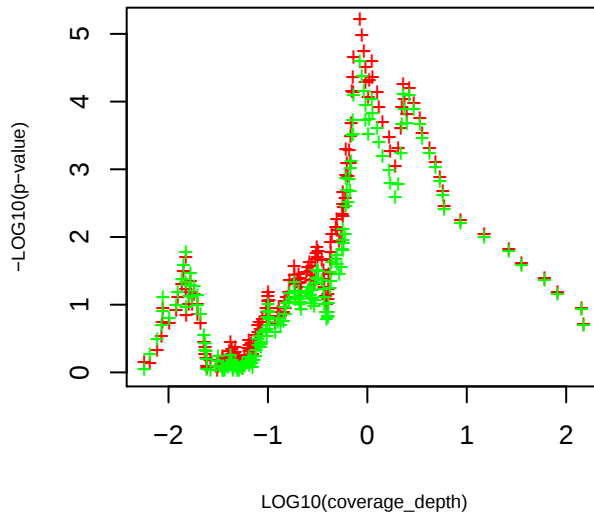


PF02036 SCP2: SCP-2 sterol transfer family

slope= 5.53 p_value= 2.7e-10 intercept= -21.64 p_value= 5.7e-12

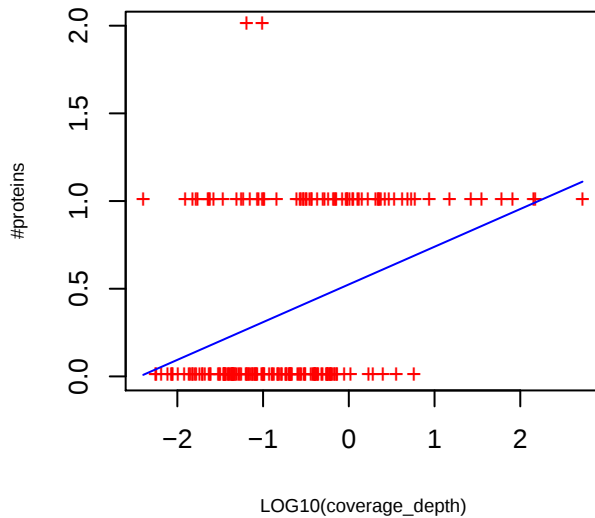


P-value curve ; red (unnorm), green (norm)



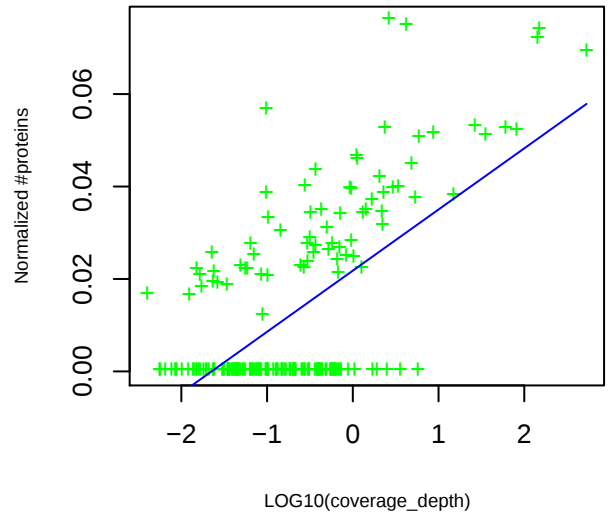
TIGR03643 TIGR03643: conserved hypothetical protein TIGR03643

slope= 0.22 p_value= 3.6e-08 intercept= 0.52 p_value= 2.2e-26



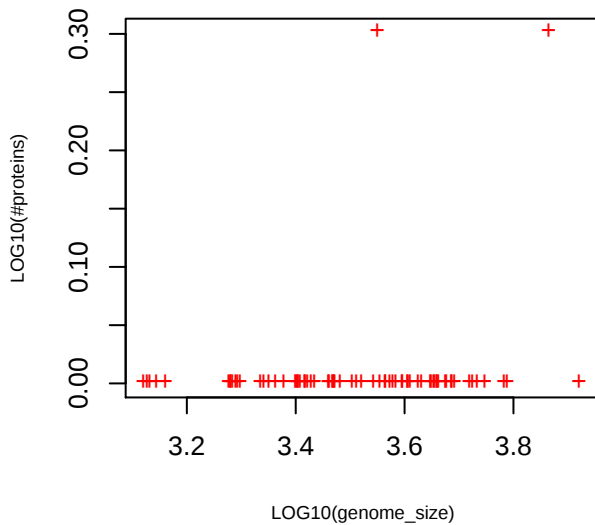
TIGR03643 TIGR03643: conserved hypothetical protein TIGR03643

slope= 0.013 p_value= 1.5e-22 intercept= 0.022 p_value= 5e-38

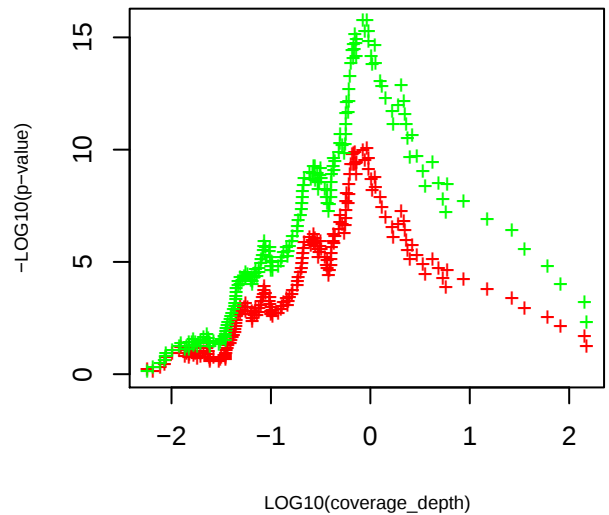


TIGR03643 TIGR03643: conserved hypothetical protein TIGR03643

slope= -2.14 p_value= 0.011 intercept= 5.05 p_value= 0.09

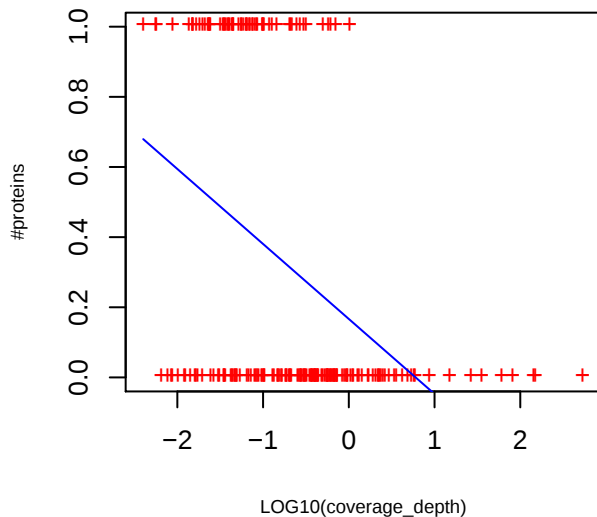


P-value curve ; red (unnorm), green (norm)



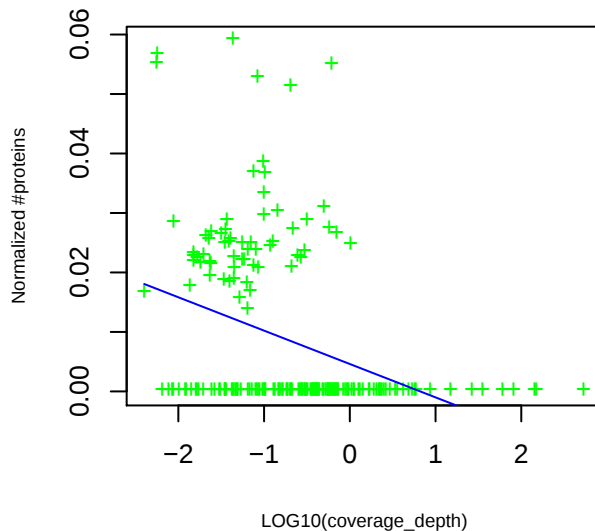
TIGR03499 FlhF: flagellar biosynthetic protein FlhF

slope= -0.21 p_value= 2.0e-09 intercept= 0.17 p_value= 2.3e-05



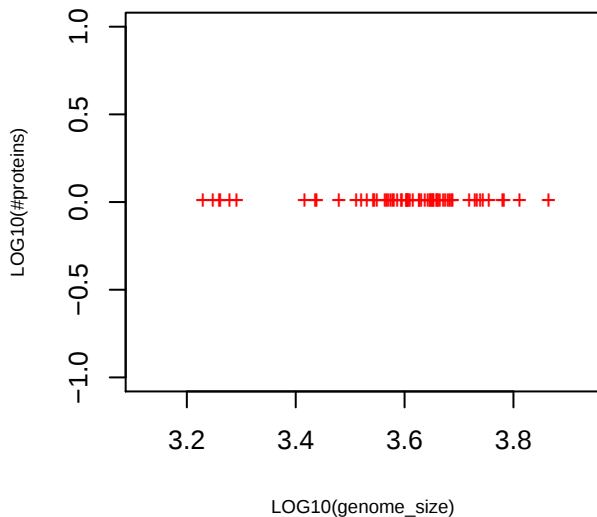
TIGR03499 FlhF: flagellar biosynthetic protein FlhF

slope= -0.0056 p_value= 1.6e-07 intercept= 0.0046 p_value= 0.00011

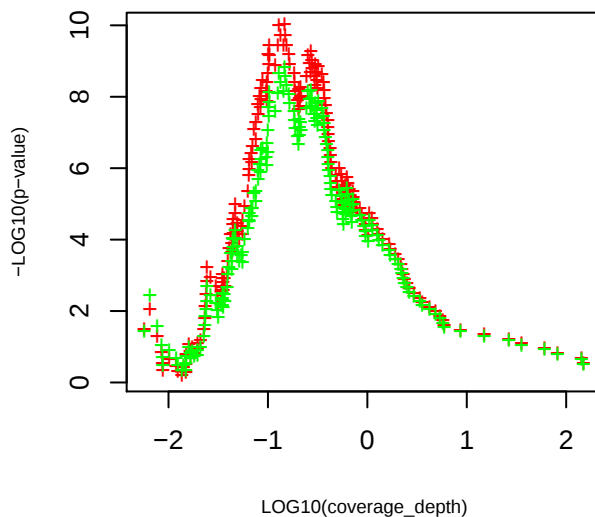


TIGR03499 FlhF: flagellar biosynthetic protein FlhF

slope= 2.29 p_value= 0.0047 intercept= -10.88 p_value= 0.00018

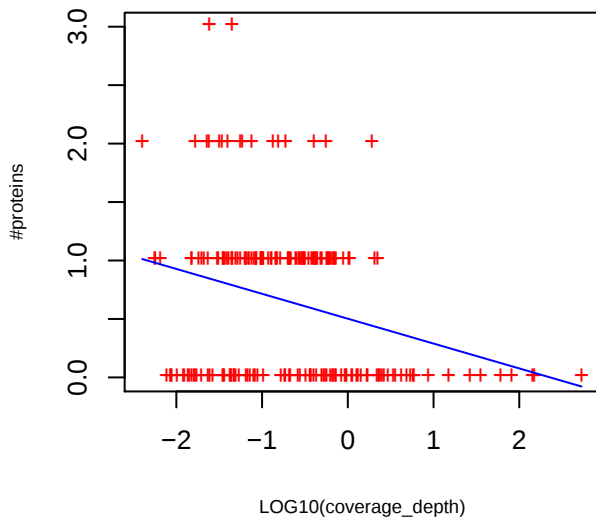


P-value curve ; red (unnorm), green (norm)



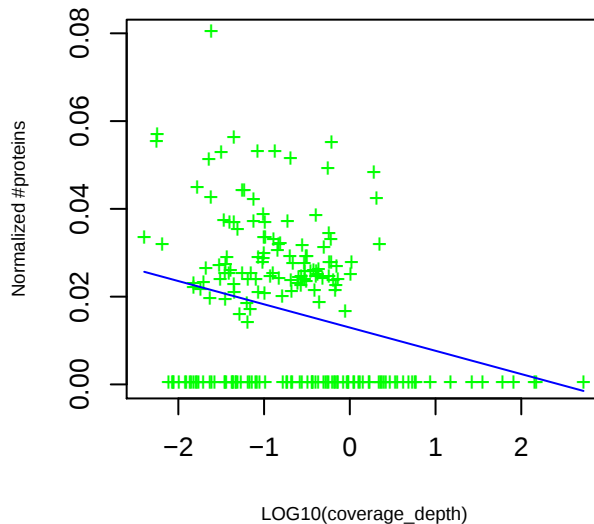
PF02119 FlgI: flagellar P-ring protein FlgI

slope= -0.21 p_value= 5.7e-05 intercept= 0.50 p_value= 2.5e-15



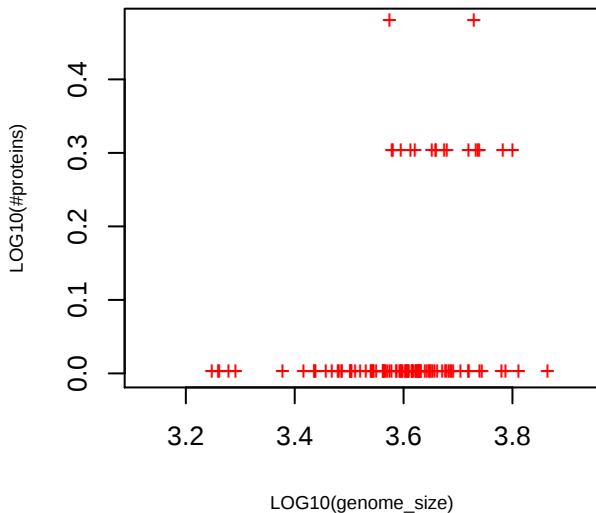
PF02119 FlgI: flagellar P-ring protein FlgI

slope= -0.0053 p_value= 9e-05 intercept= 0.013 p_value= 1.8e-15

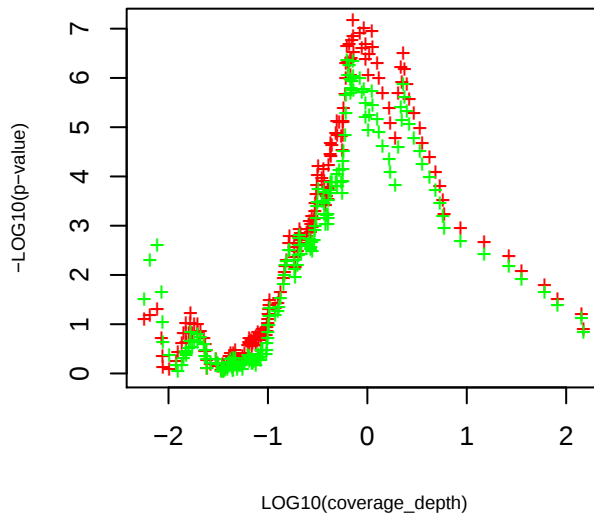


PF02119 FlgI: flagellar P-ring protein FlgI

slope= 4.33 p_value= 5e-07 intercept= -17.14 p_value= 2.7e-08

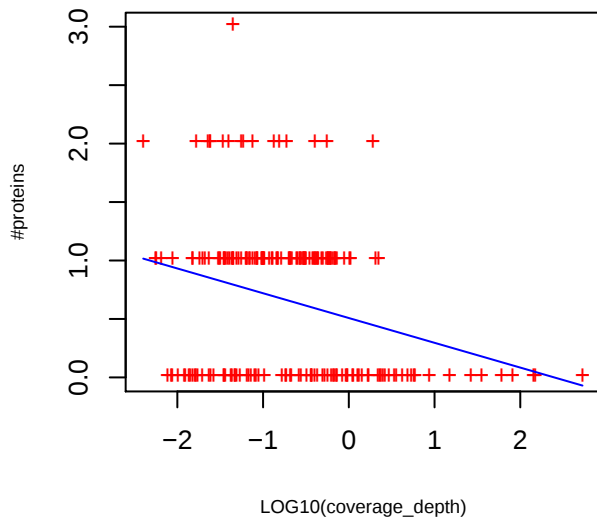


P-value curve ; red (unnorm), green (norm)



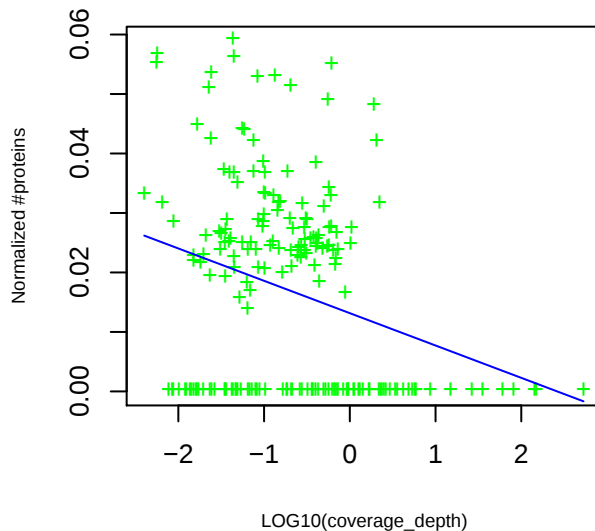
TIGR02488 flgG_G_neg: flagellar basal-body rod protein FlgG

slope= -0.21 p_value= 3.1e-05 intercept= 0.51 p_value= 1.4e-16



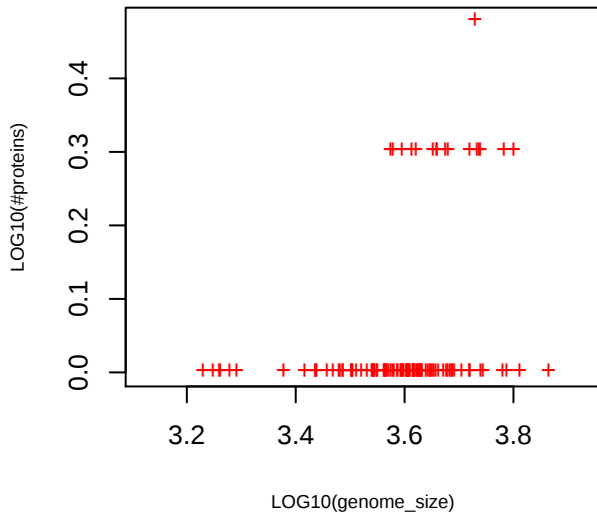
TIGR02488 flgG_G_neg: flagellar basal-body rod protein FlgG

slope= -0.0054 p_value= 3.7e-05 intercept= 0.013 p_value= 1.5e-16

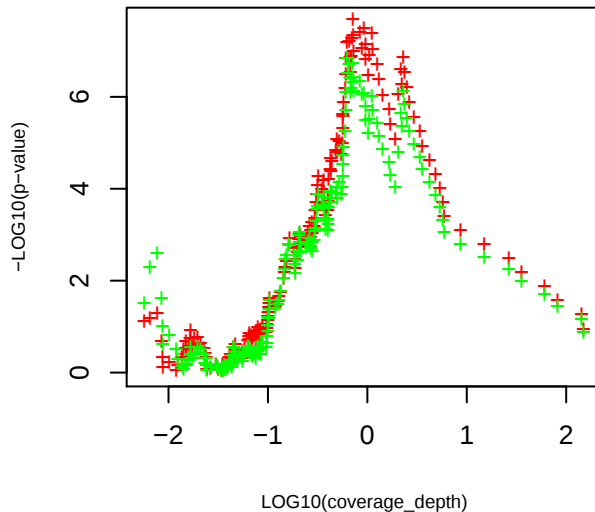


TIGR02488 flgG_G_neg: flagellar basal-body rod protein FlgG

slope= 4.15 p_value= 1.4e-06 intercept= -16.42 p_value= 9.2e-08

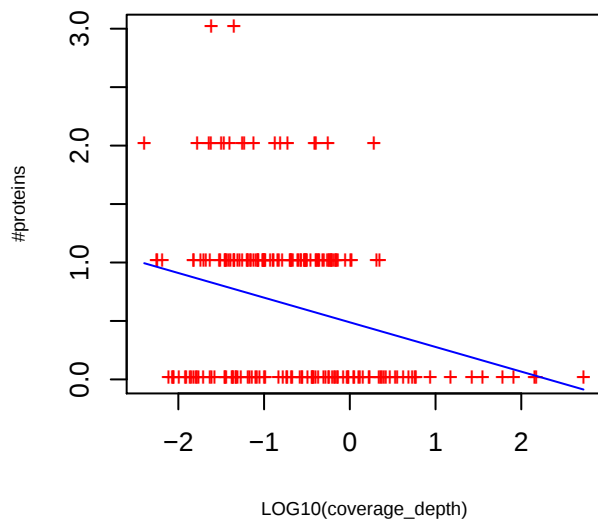


P-value curve : red (unnorm), green (norm)



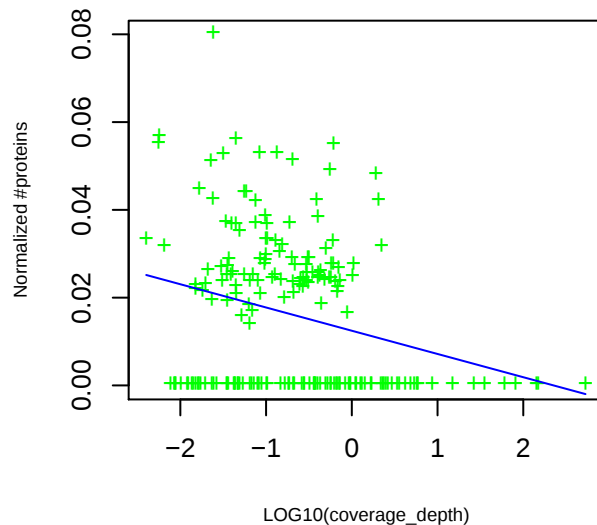
TIGR03170 flgA_c-term: flagella basal body P-ring formation protein FlgA

slope= -0.21 p_value= 8.8e-05 intercept= 0.49 p_value= 2.8e-14



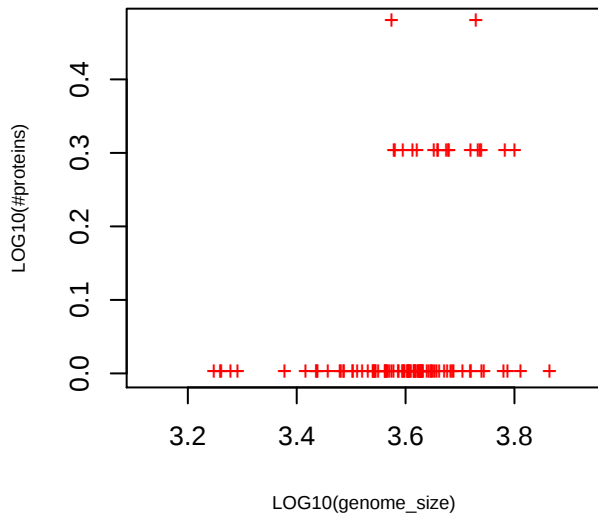
TIGR03170 flgA_c-term: flagella basal body P-ring formation protein FlgA

slope= -0.0053 p_value= 0.00010 intercept= 0.012 p_value= 2.2e-14

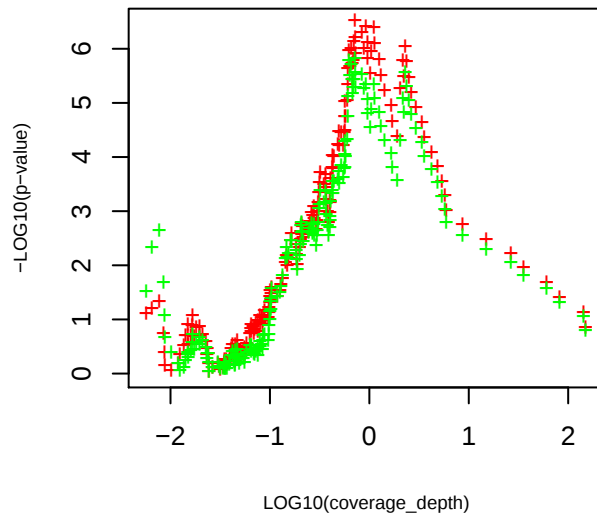


TIGR03170 flgA_c-term: flagella basal body P-ring formation protein FlgA

slope= 4.37 p_value= 4.4e-07 intercept= -17.36 p_value= 2.1e-08

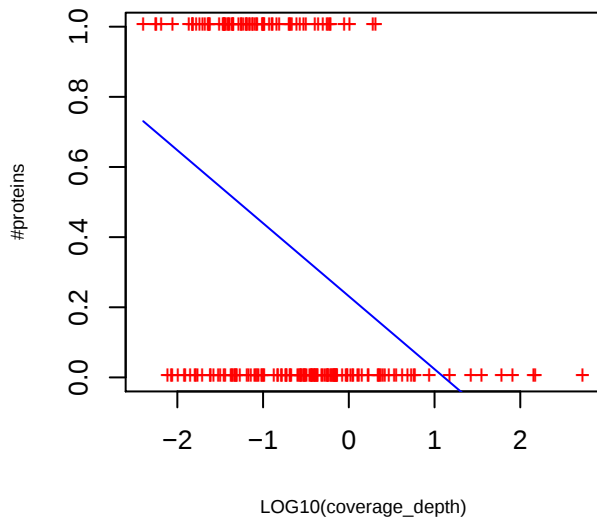


P-value curve ; red (unnorm), green (norm)



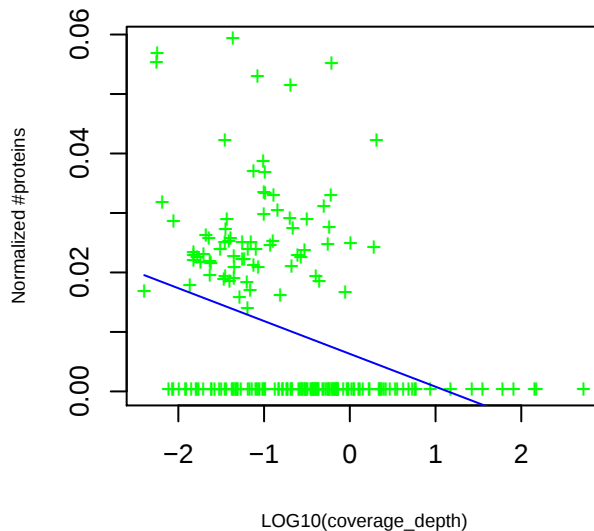
TIGR01397 fliM_switch: flagellar motor switch protein FliM

slope= -0.21 p_value= 2.7e-08 intercept= 0.23 p_value= 4.2e-08



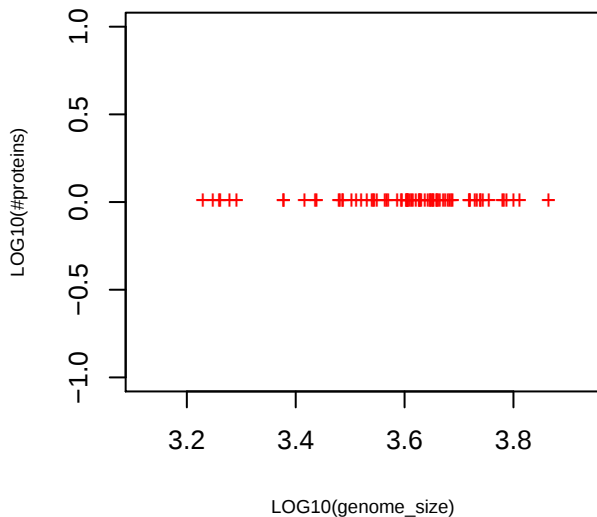
TIGR01397 fliM_switch: flagellar motor switch protein FliM

slope= -0.0055 p_value= 1e-06 intercept= 0.0063 p_value= 7.4e-07

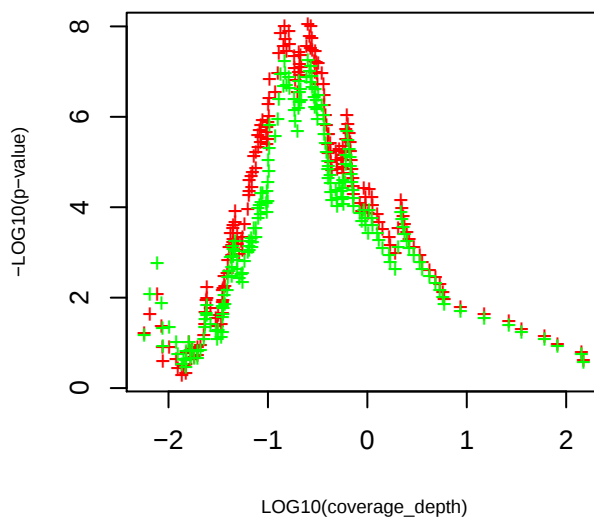


TIGR01397 fliM_switch: flagellar motor switch protein FliM

slope= 2.76 p_value= 0.0011 intercept= -12.28 p_value= 4.6e-05

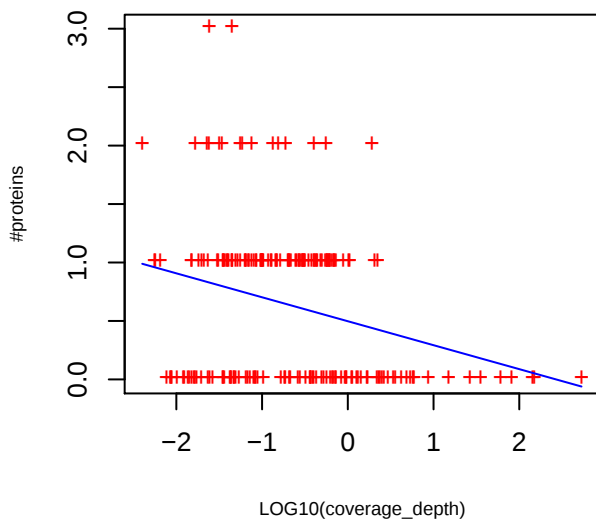


P-value curve ; red (unnorm), green (norm)



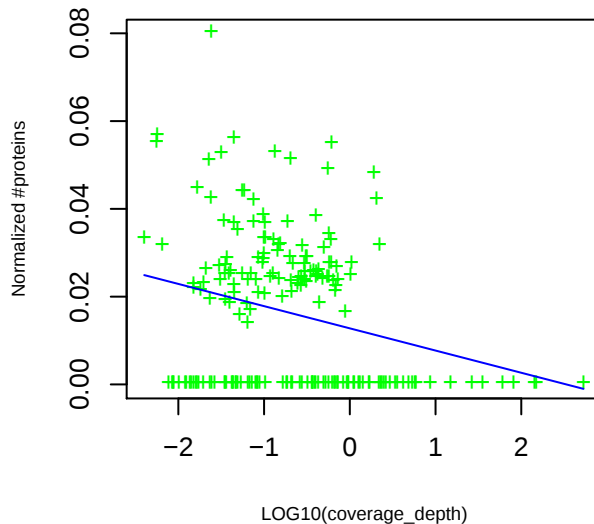
PF02107 FlgH: flagellar L-ring protein FlgH

slope= -0.20 p_value= 9.5e-05 intercept= 0.50 p_value= 3.1e-15



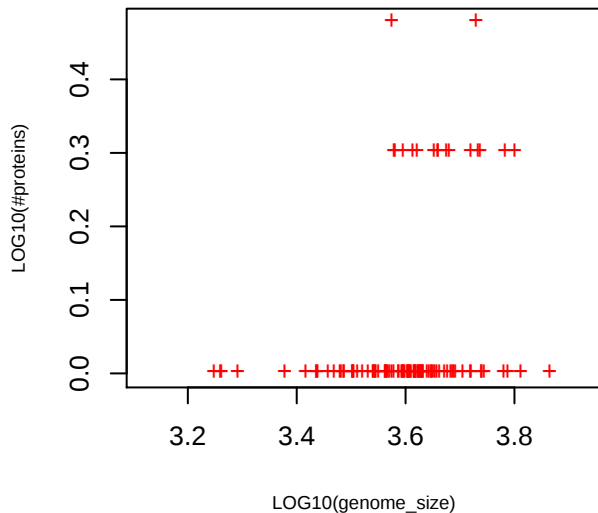
PF02107 FlgH: flagellar L-ring protein FlgH

slope= -0.0051 p_value= 0.00016 intercept= 0.013 p_value= 2.3e-15

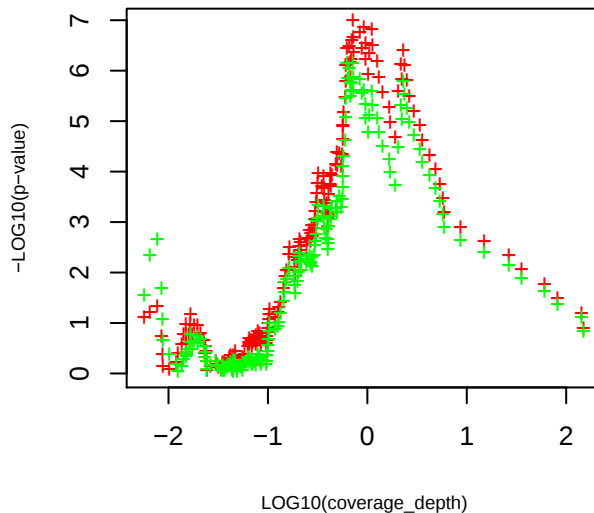


PF02107 FlgH: flagellar L-ring protein FlgH

slope= 4.48 p_value= 1.9e-07 intercept= -17.68 p_value= 9.1e-09

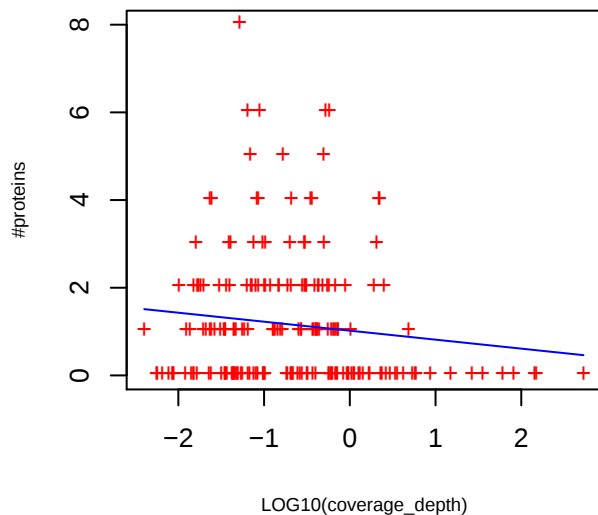


P-value curve ; red (unnorm), green (norm)



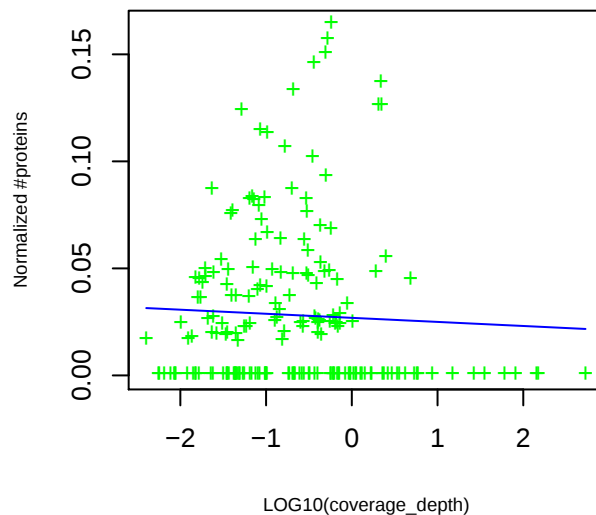
PF07859 Abhydrolase_3: alpha/beta hydrolase fold

slope= -0.20 p_value= 0.088 intercept= 1.02 p_value= 1.5e-12



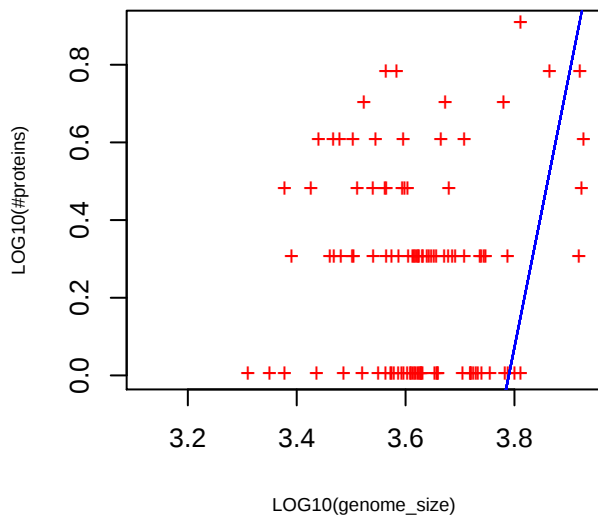
PF07859 Abhydrolase_3: alpha/beta hydrolase fold

slope= -0.0019 p_value= 0.52 intercept= 0.027 p_value= 8.8e-14

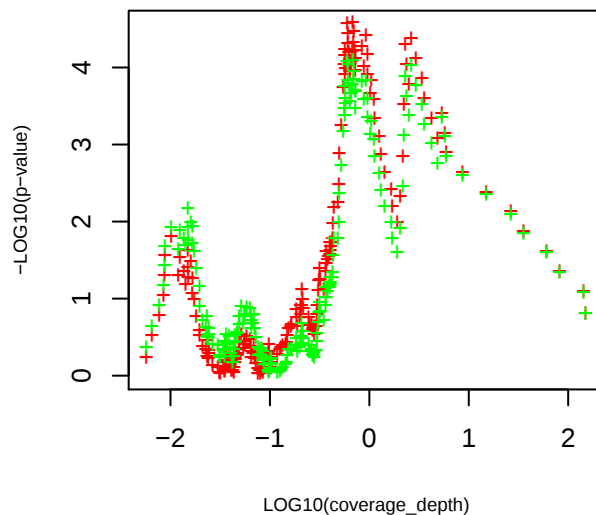


PF07859 Abhydrolase_3: alpha/beta hydrolase fold

slope= 6.99 p_value= 6.6e-16 intercept= -26.50 p_value= 1.4e-17

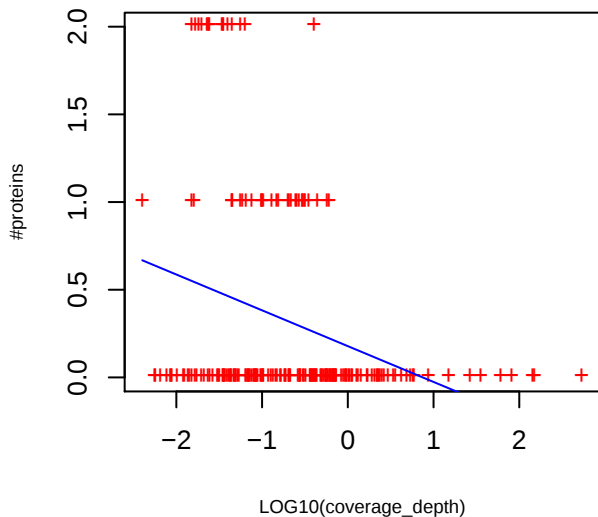


P-value curve ; red (unnorm), green (norm)



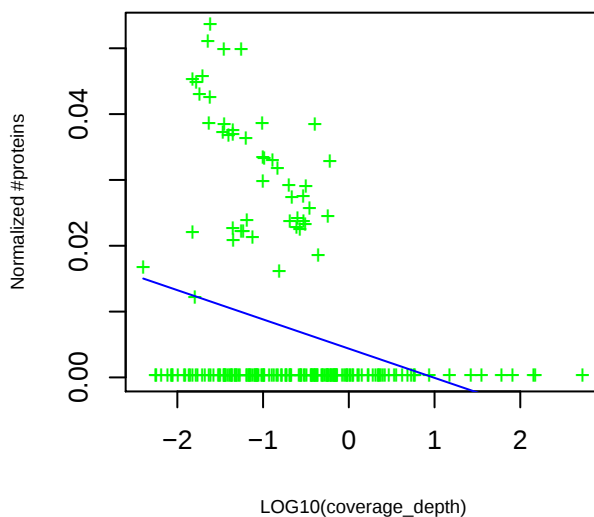
TIGR01785 TonB-hemin: TonB-dependent heme/hemoglobin receptor family protein

slope= -0.20 p_value= 2.5e-05 intercept= 0.18 p_value= 0.001



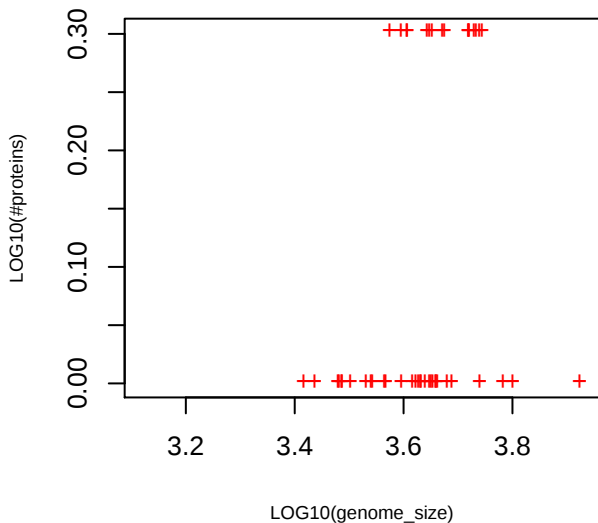
TIGR01785 TonB-hemin: TonB-dependent heme/hemoglobin receptor family protein

slope= -0.0044 p_value= 7.2e-05 intercept= 0.0044 p_value= 0.00051

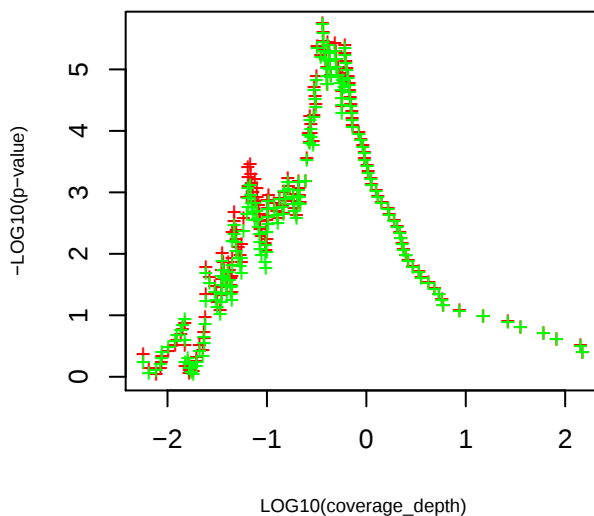


TIGR01785 TonB-hemin: TonB-dependent heme/hemoglobin receptor family protein

slope= 3.26 p_value= 1.6e-05 intercept= -14.56 p_value= 7.7e-08

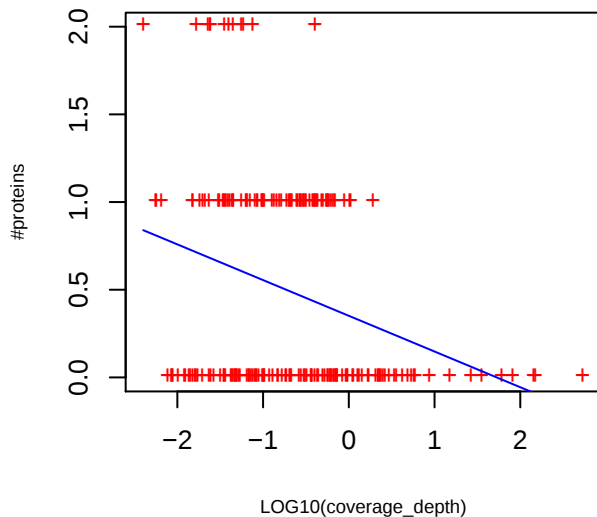


P-value curve ; red (unnorm), green (norm)



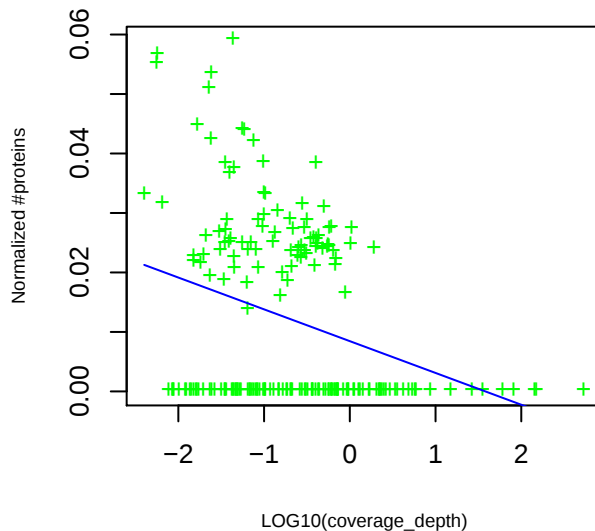
TIGR02490 flgF: flagellar basal-body rod protein FlgF

slope= -0.20 p_value= 2.1e-05 intercept= 0.35 p_value= 2.7e-10



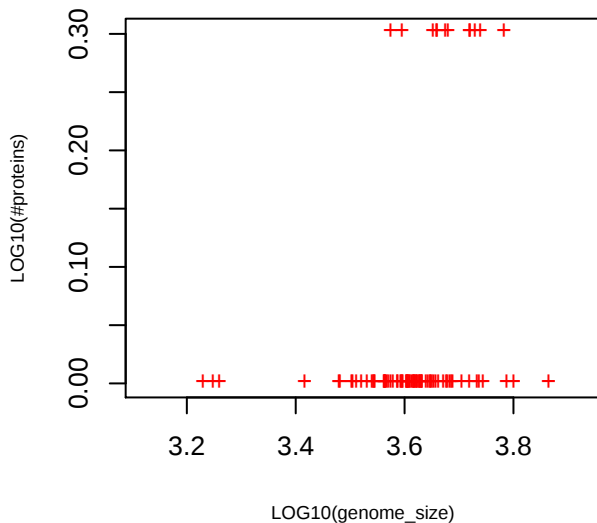
TIGR02490 flgF: flagellar basal-body rod protein FlgF

slope= -0.0053 p_value= 7.3e-06 intercept= 0.0085 p_value= 8.4e-10

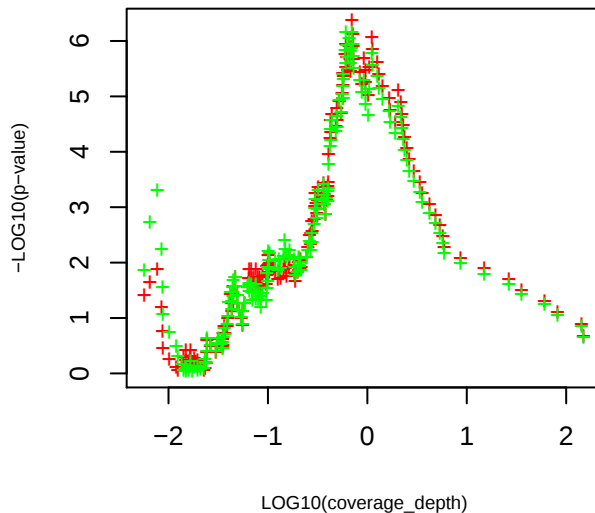


TIGR02490 flgF: flagellar basal-body rod protein FlgF

slope= 4.46 p_value= 1.7e-07 intercept= -18.07 p_value= 3.4e-09

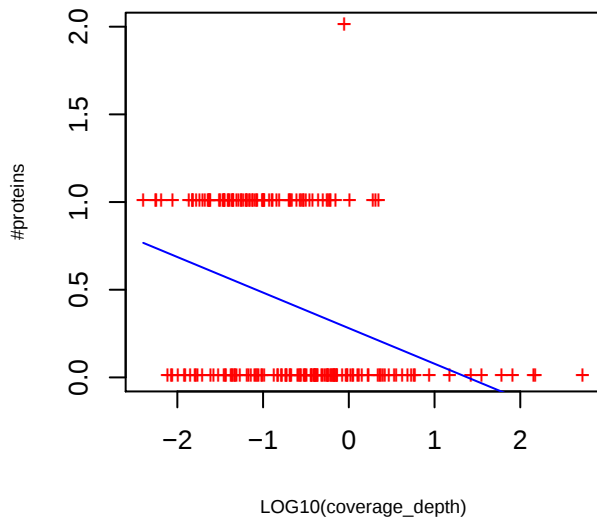


P-value curve ; red (unnorm), green (norm)



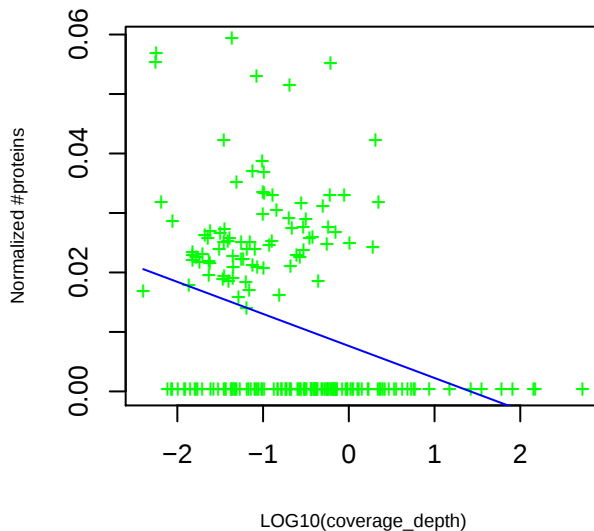
TIGR00207 fliG: flagellar motor switch protein FliG

slope= -0.20 p_value= 2.2e-07 intercept= 0.28 p_value= 4.1e-10



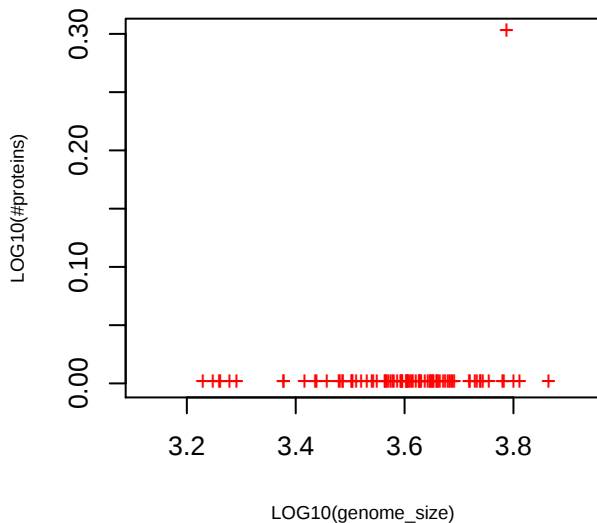
TIGR00207 fliG: flagellar motor switch protein FliG

slope= -0.0054 p_value= 3.4e-06 intercept= 0.0076 p_value= 9.1e-09

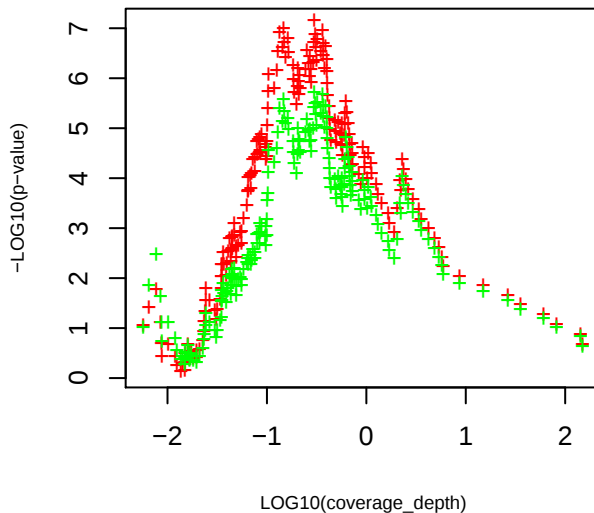


TIGR00207 fliG: flagellar motor switch protein FliG

slope= 2.79 p_value= 0.0012 intercept= -12.21 p_value= 6.9e-05

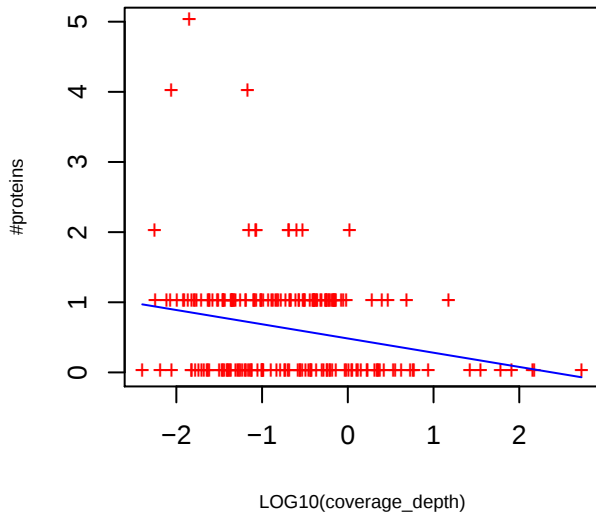


P-value curve ; red (unnorm), green (norm)



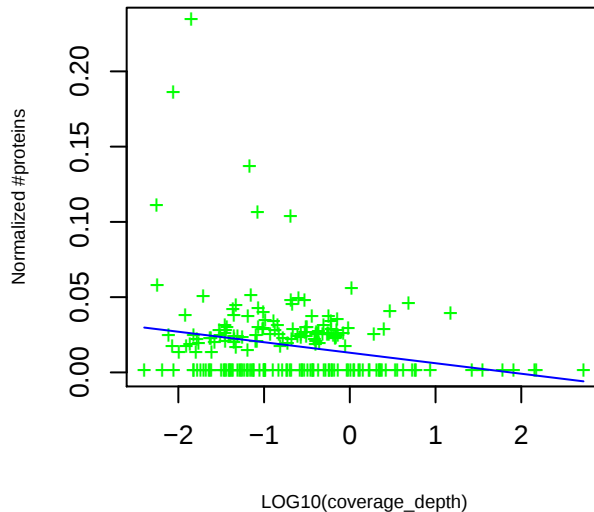
PF04039 MnhB: Domain related to MnhB subunit of Na⁺/H⁺ antiporter

slope= -0.20 p_value= 0.00054 intercept= 0.48 p_value= 3.4e-12



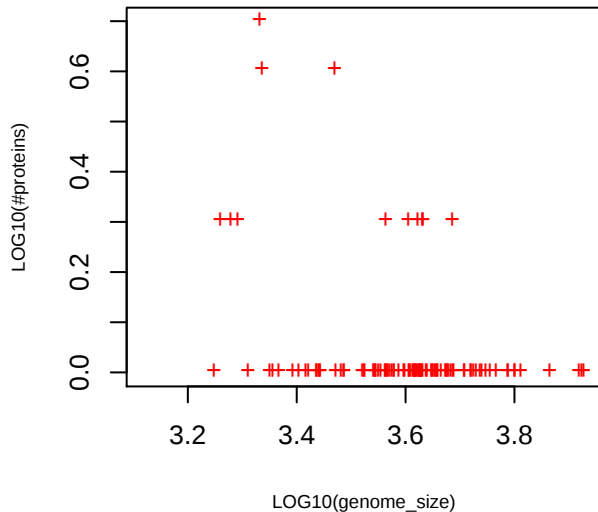
PF04039 MnhB: Domain related to MnhB subunit of Na⁺/H⁺ antiporter

slope= -0.007 p_value= 0.0019 intercept= 0.013 p_value= 4.6e-07

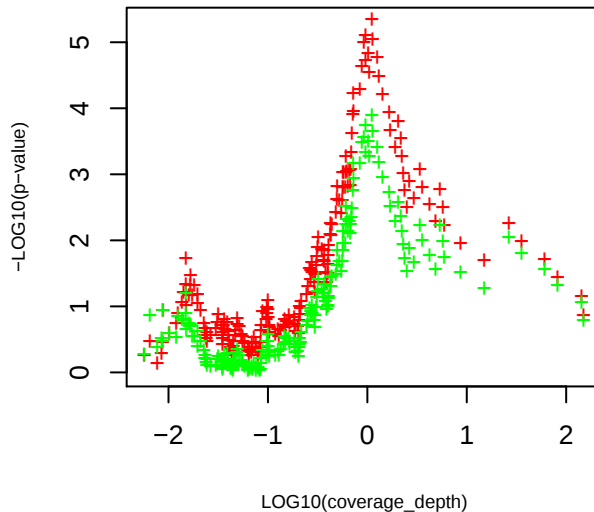


PF04039 MnhB: Domain related to MnhB subunit of Na⁺/H⁺ antiporter

slope= 3.79 p_value= 1.3e-05 intercept= -15.31 p_value= 8.4e-07

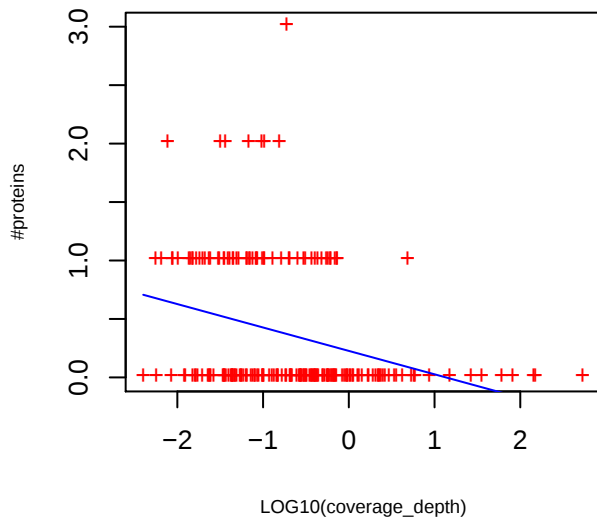


P-value curve ; red (unnorm), green (norm)



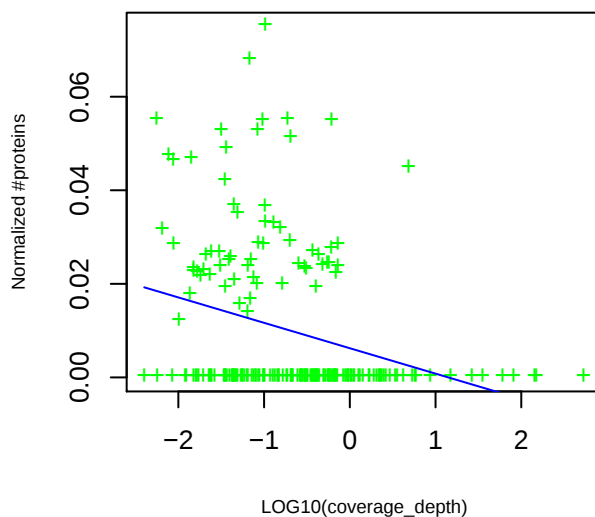
TIGR01460 HAD-SF-IIA: HAD-superfamily hydrolase, subfamily IIA

slope= -0.20 p_value= 9.7e-06 intercept= 0.23 p_value= 9.1e-06



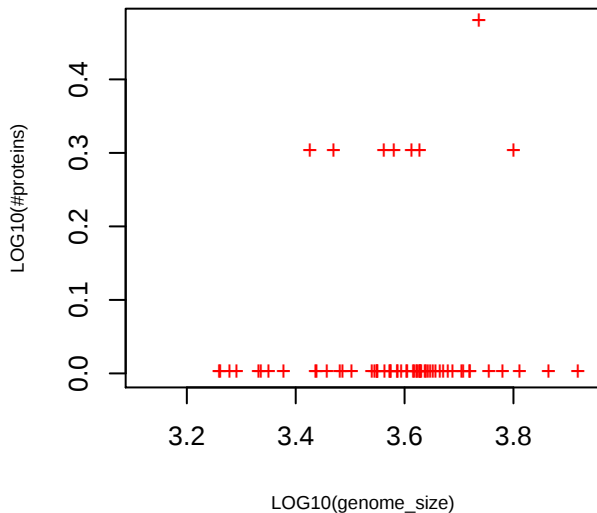
TIGR01460 HAD-SF-IIA: HAD-superfamily hydrolase, subfamily IIA

slope= -0.0054 p_value= 2.8e-05 intercept= 0.0062 p_value= 2.0e-05

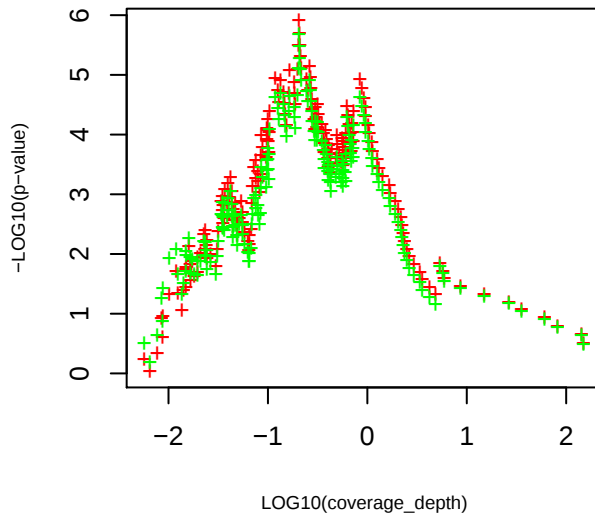


TIGR01460 HAD-SF-IIA: HAD-superfamily hydrolase, subfamily IIA

slope= 1.80 p_value= 0.029 intercept= -9.09 p_value= 0.0021

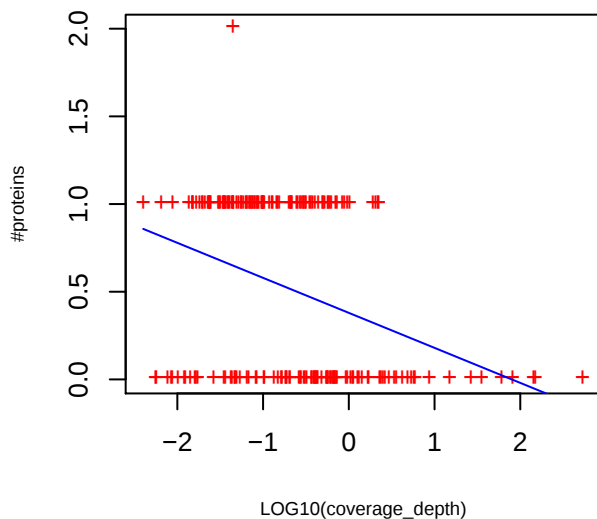


P-value curve ; red (unnorm), green (norm)



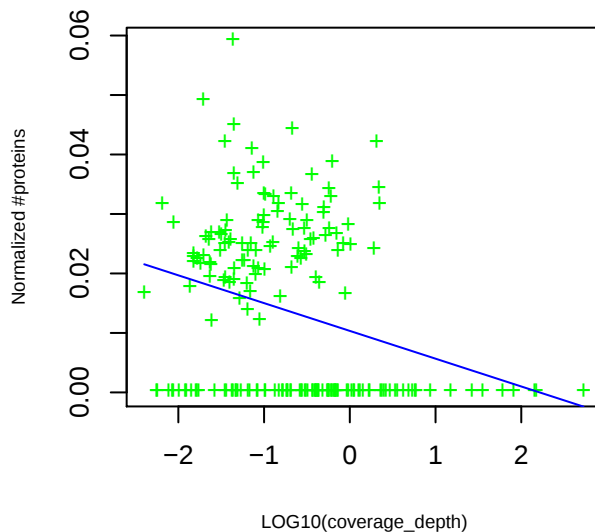
PF00309 Sigma54_AID: sigma-54 factor, Activator interacting domain (AID)

slope= -0.20 p_value= 4.8e-07 intercept= 0.38 p_value= 9e-16



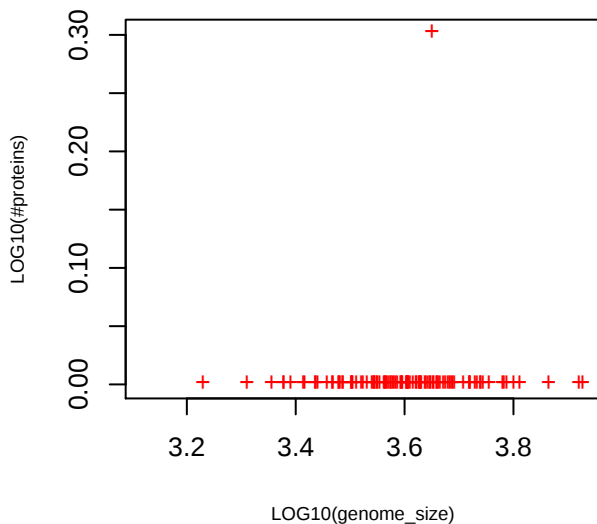
PF00309 Sigma54_AID: sigma-54 factor, Activator interacting domain (AID)

slope= -0.0047 p_value= 3.7e-05 intercept= 0.010 p_value= 1.9e-14

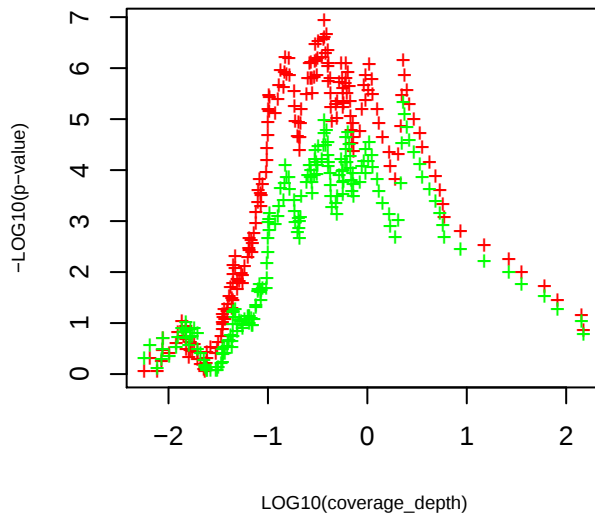


PF00309 Sigma54_AID: sigma-54 factor, Activator interacting domain (AID)

slope= 4.10 p_value= 1.7e-06 intercept= -16.47 p_value= 7.7e-08

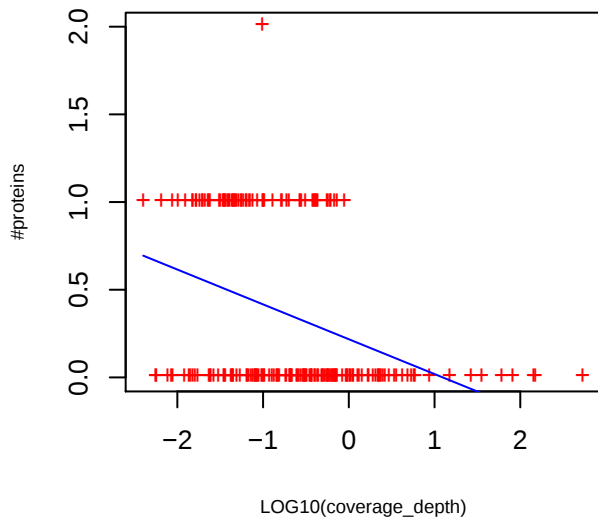


P-value curve : red (unnorm), green (norm)



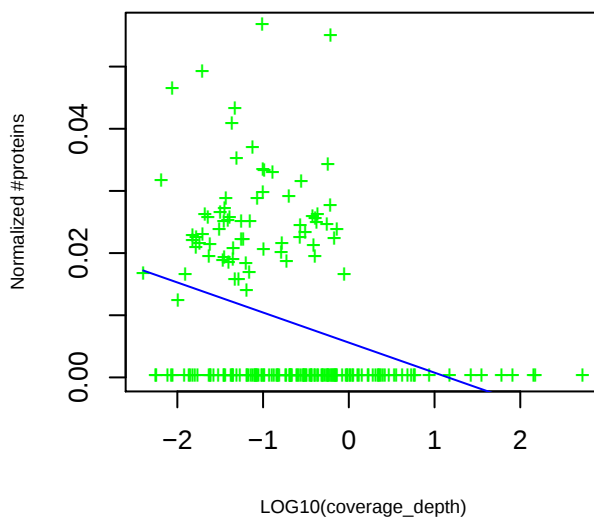
PF02594 DUF167: Uncharacterized ACR, YggU family COG1872

slope= -0.20 p_value= 1.7e-07 intercept= 0.22 p_value= 3.6e-07



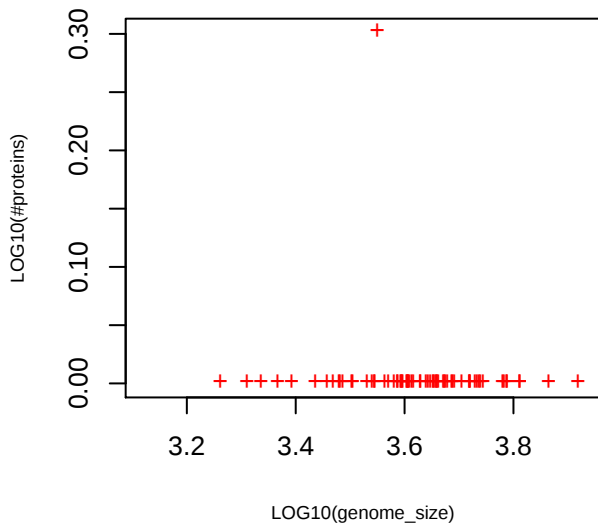
PF02594 DUF167: Uncharacterized ACR, YggU family COG1872

slope= -0.0048 p_value= 3.1e-06 intercept= 0.0056 p_value= 1.8e-06

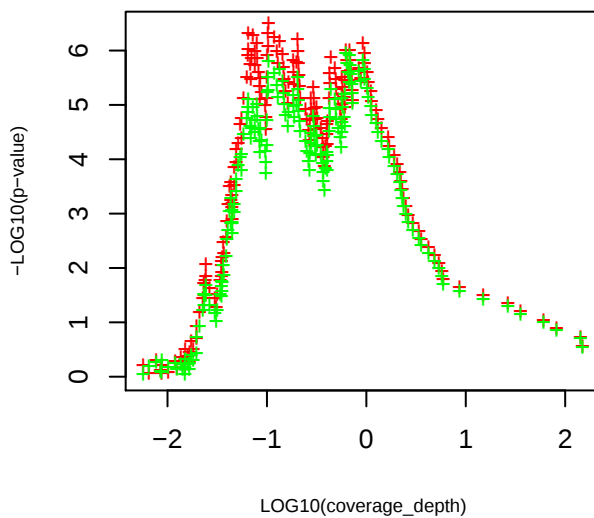


PF02594 DUF167: Uncharacterized ACR, YggU family COG1872

slope= 3.90 p_value= 1.9e-06 intercept= -16.41 p_value= 2.3e-08

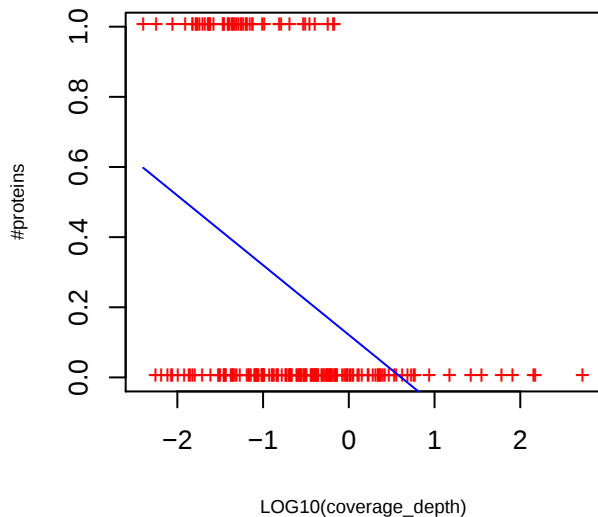


P-value curve ; red (unnorm), green (norm)



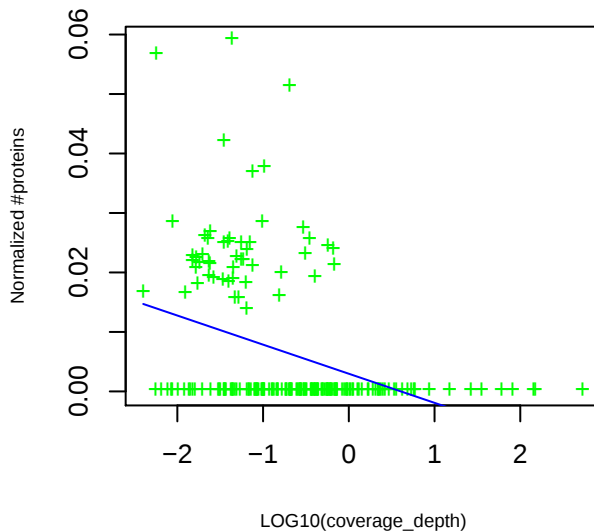
TIGR02152 D_ribokin_bact: ribokinase

slope= -0.20 p_value= 3.7e-09 intercept= 0.12 p_value= 0.001



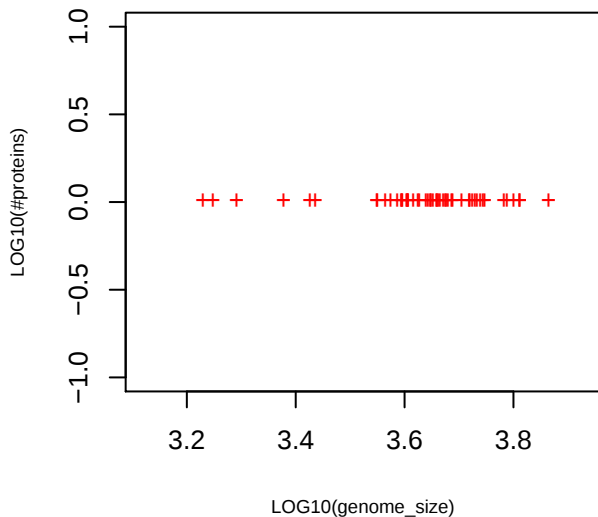
TIGR02152 D_ribokin_bact: ribokinase

slope= -0.0049 p_value= 8.3e-08 intercept= 0.003 p_value= 0.0031

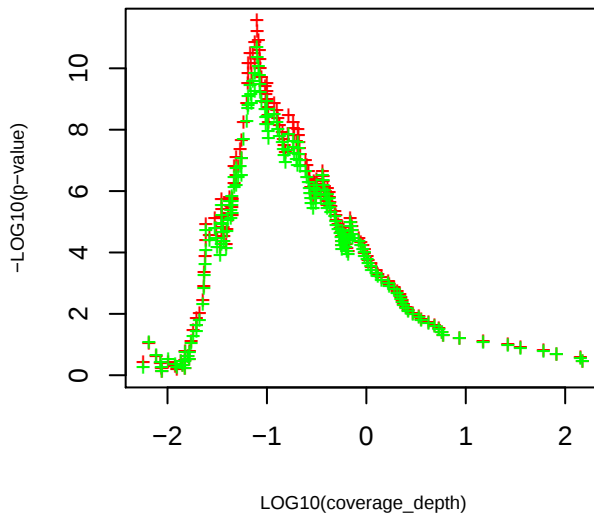


TIGR02152 D_ribokin_bact: ribokinase

slope= 3.43 p_value= 5.2e-06 intercept= -15.12 p_value= 2.3e-08

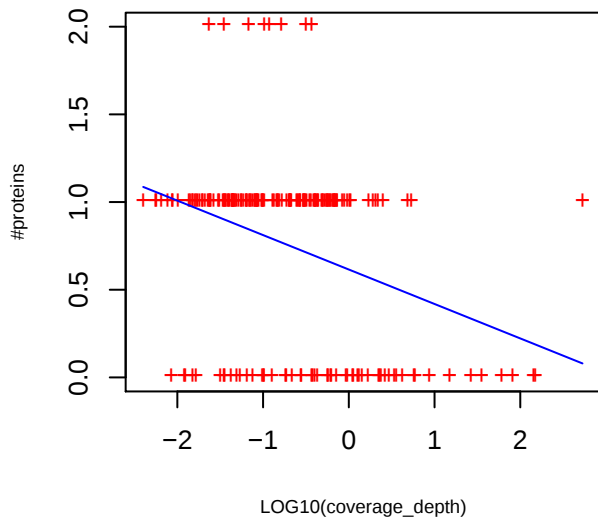


P-value curve ; red (unnorm), green (norm)



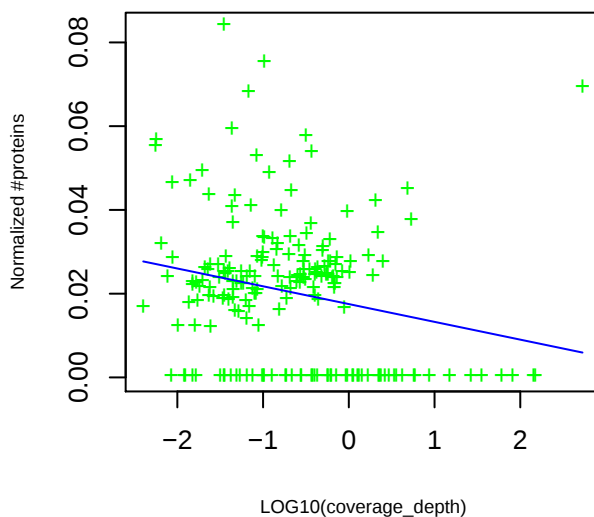
TIGR01311 glycerol_kin: glycerol kinase

slope= -0.20 p_value= 1.1e-06 intercept= 0.62 p_value= 4.5e-31



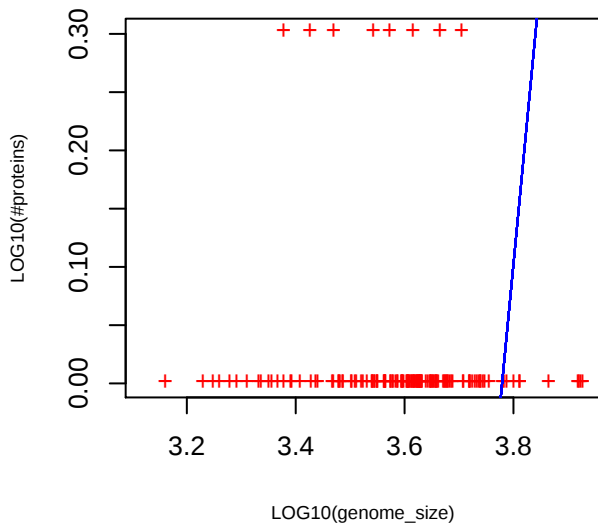
TIGR01311 glycerol_kin: glycerol kinase

slope= -0.0042 p_value= 0.0014 intercept= 0.018 p_value= 1.4e-24

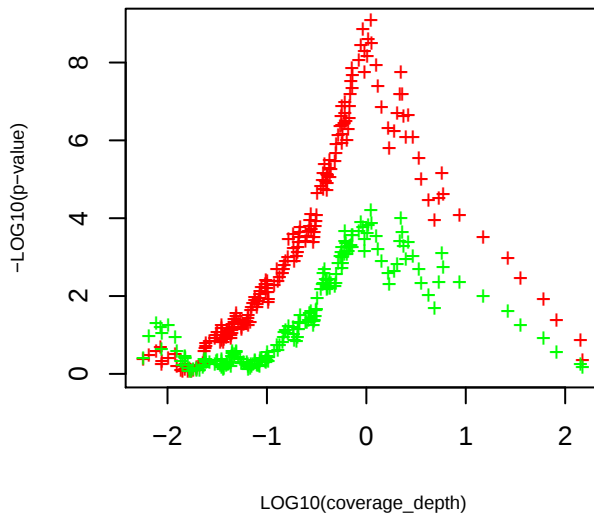


TIGR01311 glycerol_kin: glycerol kinase

slope= 4.90 p_value= 1.4e-10 intercept= -18.51 p_value= 1.1e-11

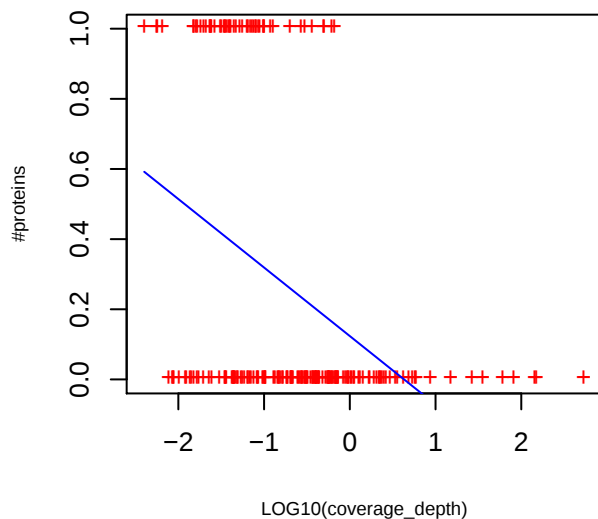


P-value curve ; red (unnorm), green (norm)



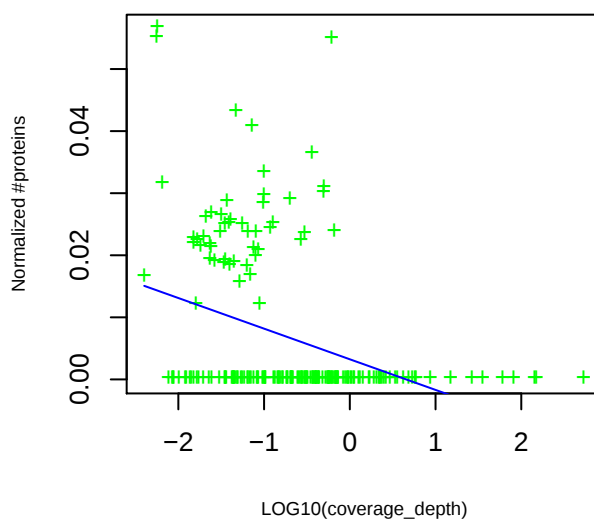
TIGR01371 met_syn_B12ind: 5-methyl/tetrahydropteroyltriglutamate--homocysteine S-methyltransf

slope= -0.20 p_value= 7e-09 intercept= 0.12 p_value= 0.00083



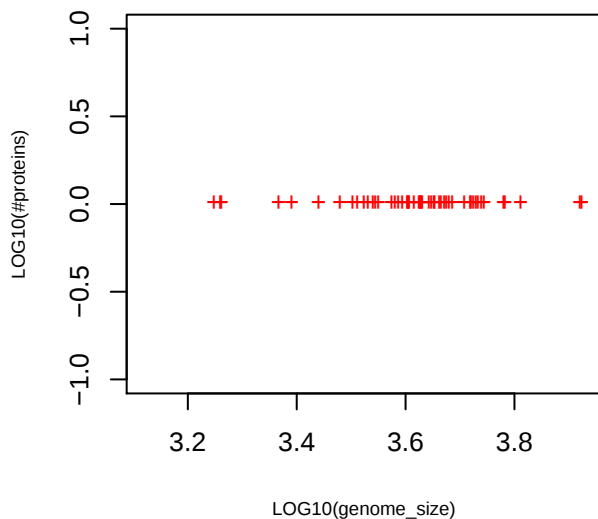
TIGR01371 met_syn_B12ind: 5-methyl/tetrahydropteroyltriglutamate--homocysteine S-methyltransf

slope= -0.0049 p_value= 2.3e-07 intercept= 0.0032 p_value= 0.0021

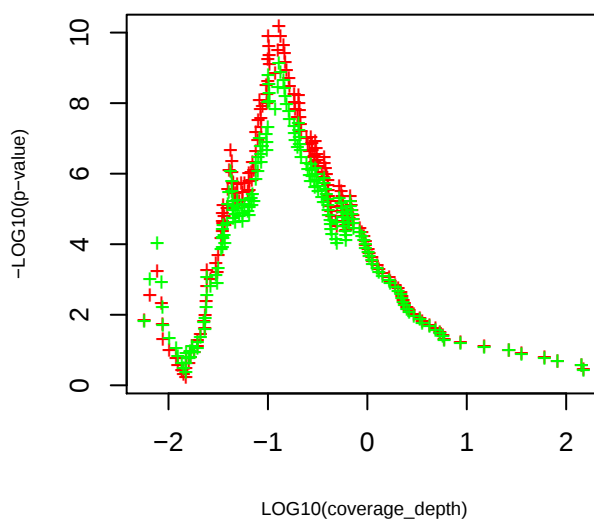


TIGR01371 met_syn_B12ind: 5-methyl/tetrahydropteroyltriglutamate--homocysteine S-methyltransf

slope= 2.70 p_value= 0.00039 intercept= -12.53 p_value= 4.4e-06

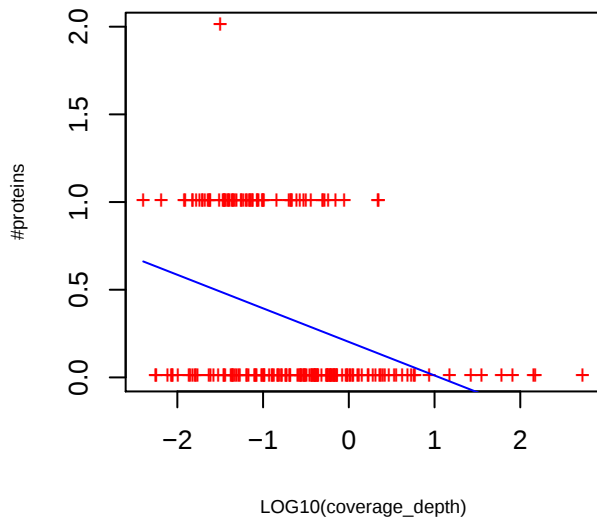


P-value curve ; red (unnorm), green (norm)



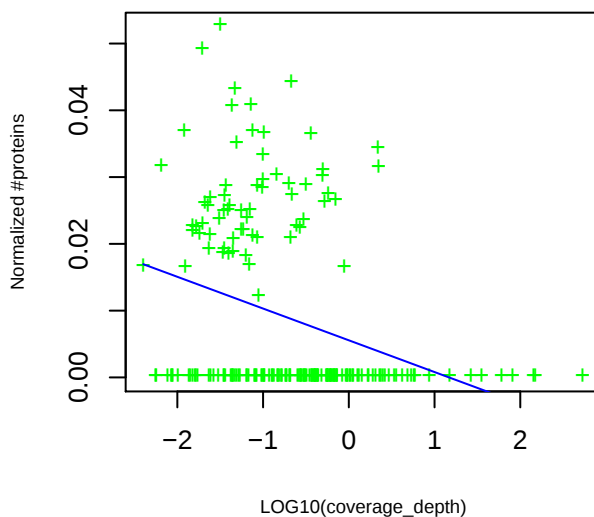
TIGR02199 rfaE_dom_II: bifunctional protein RfaE, domain II

slope= -0.19 p_value= 3.4e-07 intercept= 0.20 p_value= 1.6e-06



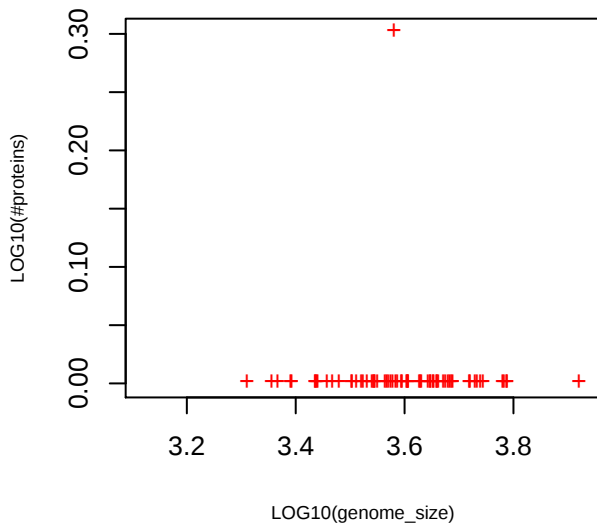
TIGR02199 rfaE_dom_II: bifunctional protein RfaE, domain II

slope= -0.0048 p_value= 6.2e-06 intercept= 0.0056 p_value= 3e-06

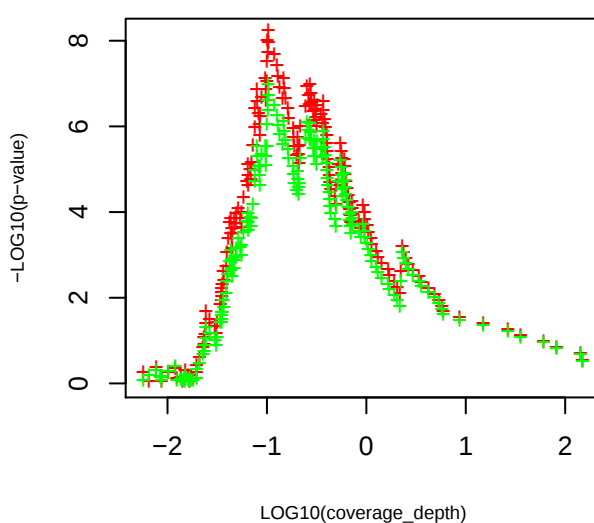


TIGR02199 rfaE_dom_II: bifunctional protein RfaE, domain II

slope= 2.45 p_value= 0.0029 intercept= -11.36 p_value= 0.00011

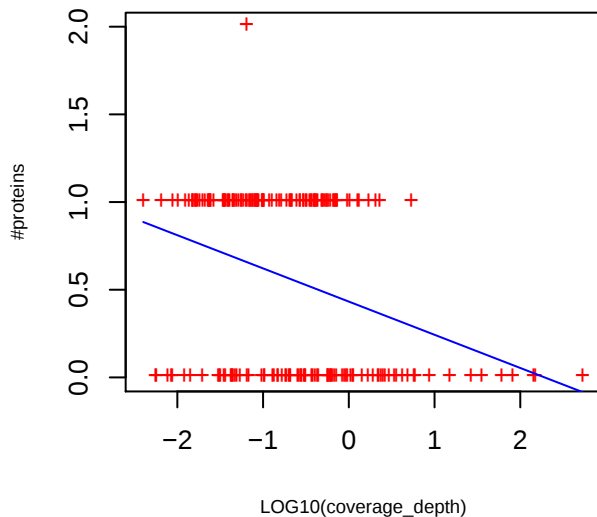


P-value curve : red (unnorm), green (norm)



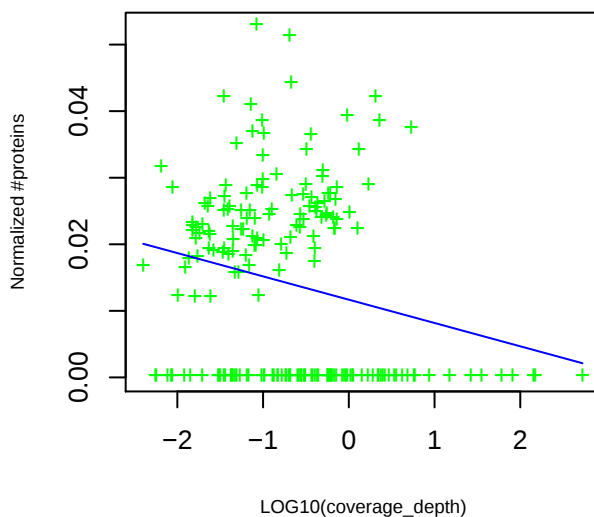
PF09371 Tex_N: Tex-like protein N-terminal domain

slope= -0.19 p_value= 1.7e-06 intercept= 0.43 p_value= 2.9e-19



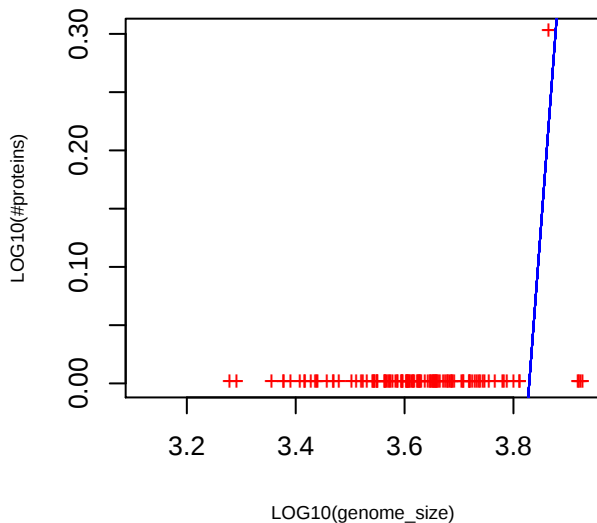
PF09371 Tex_N: Tex-like protein N-terminal domain

slope= -0.0035 p_value= 0.0014 intercept= 0.012 p_value= 4e-18

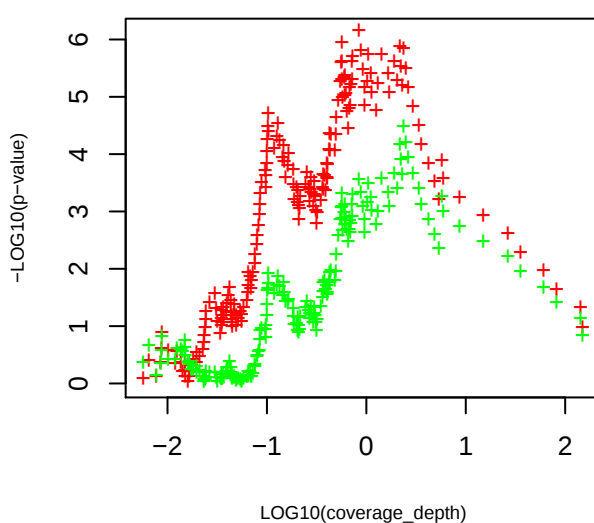


PF09371 Tex_N: Tex-like protein N-terminal domain

slope= 6.22 p_value= 2.2e-14 intercept= -23.82 p_value= 3.7e-16

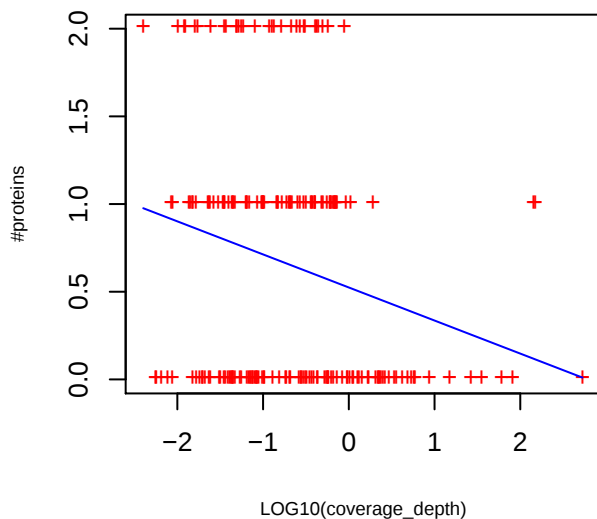


P-value curve ; red (unnorm), green (norm)



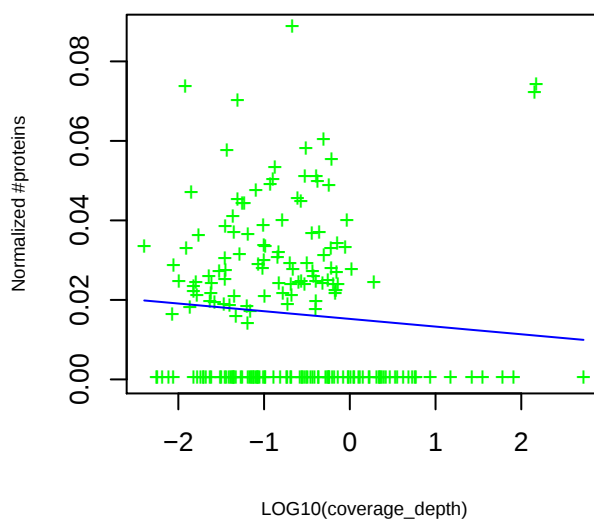
PF06094 AIG2: AIG2-like family

slope= -0.19 p_value= 0.0011 intercept= 0.52 p_value= 4e-14



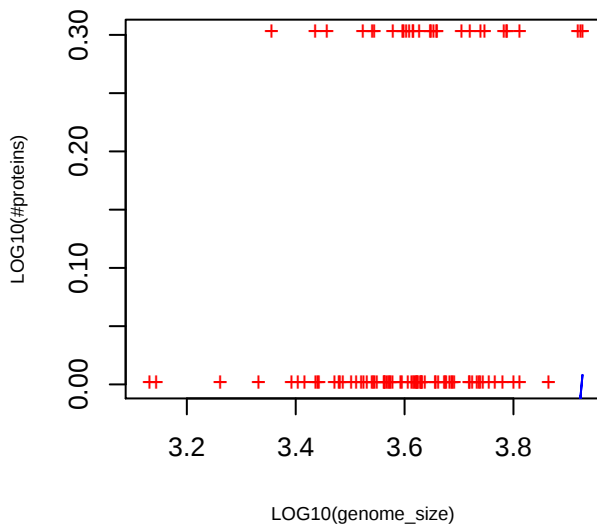
PF06094 AIG2: AIG2-like family

slope= -0.0019 p_value= 0.22 intercept= 0.015 p_value= 1.9e-15

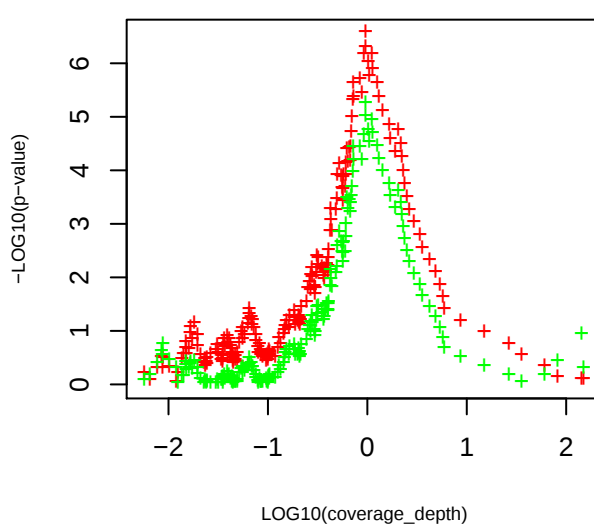


PF06094 AIG2: AIG2-like family

slope= 5.12 p_value= 3.2e-09 intercept= -20.08 p_value= 8.6e-11

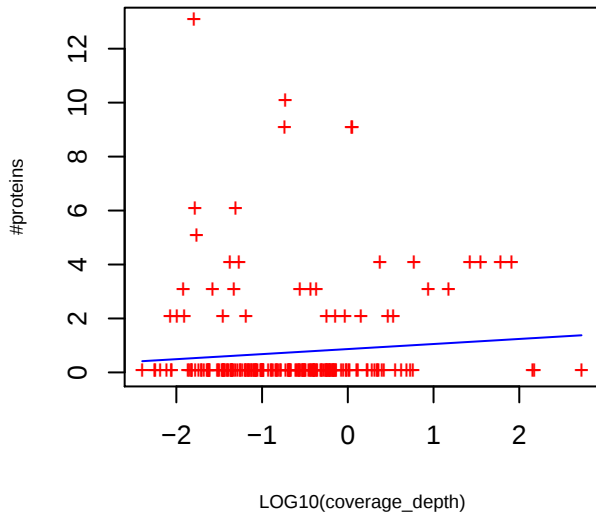


P-value curve ; red (unnorm), green (norm)



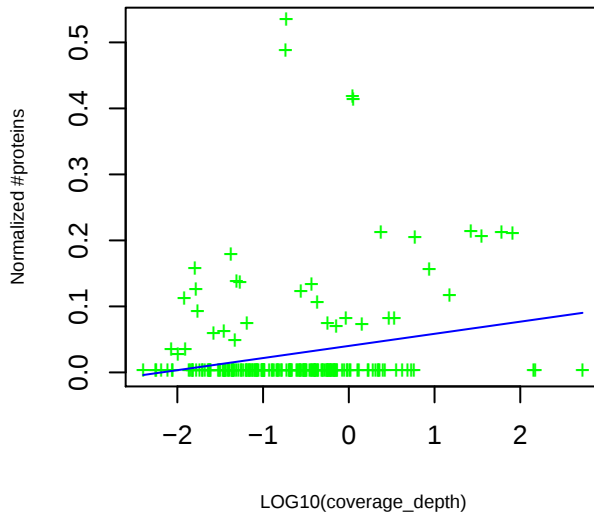
PF00421 PSII: Photosystem II protein

slope= 0.19 p_value= 0.23 intercept= 0.87 p_value= 1.8e-06



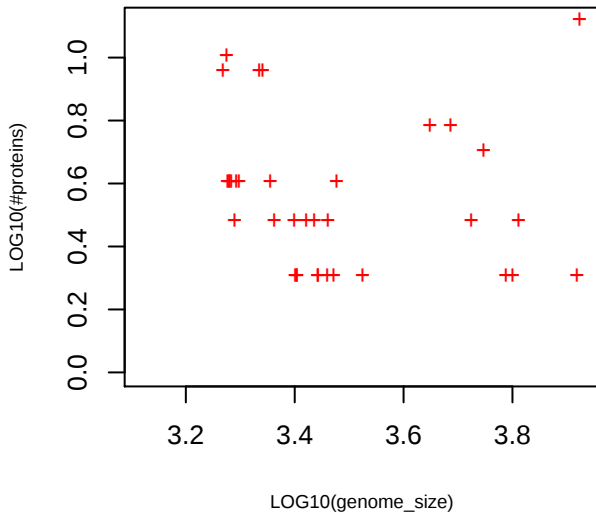
PF00421 PSII: Photosystem II protein

slope= 0.018 p_value= 0.0034 intercept= 0.04 p_value= 3.6e-08

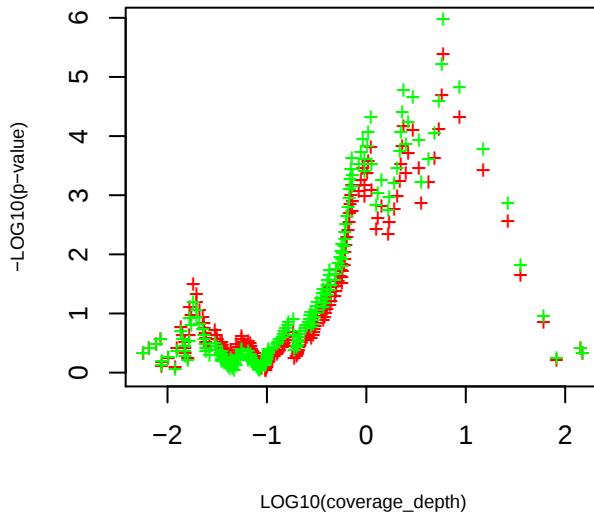


PF00421 PSII: Photosystem II protein

slope= -2.09 p_value= 0.0059 intercept= 4.23 p_value= 0.11

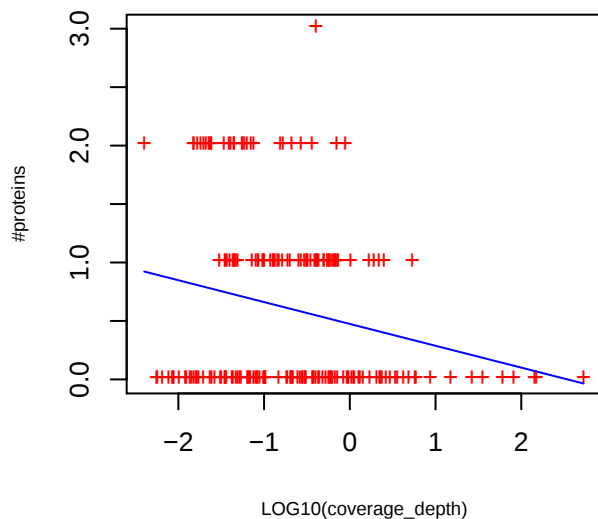


P-value curve ; red (unnorm), green (norm)



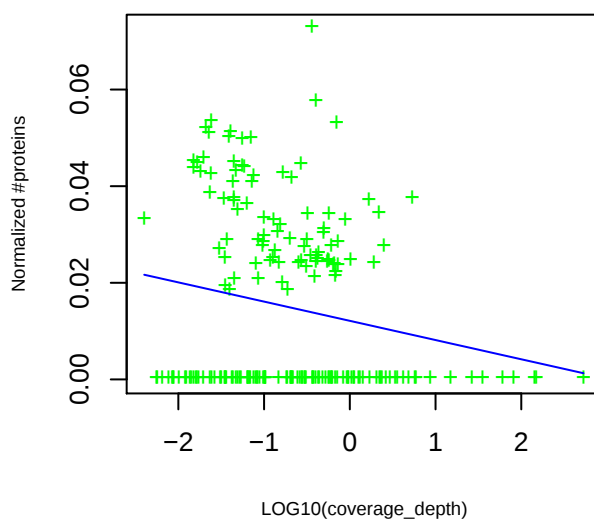
TIGR00932 2a37: transporter, monovalent cation:proton antiporter-2 (CPA2) family

slope= -0.19 p_value= 0.0017 intercept= 0.47 p_value= 1.7e-11



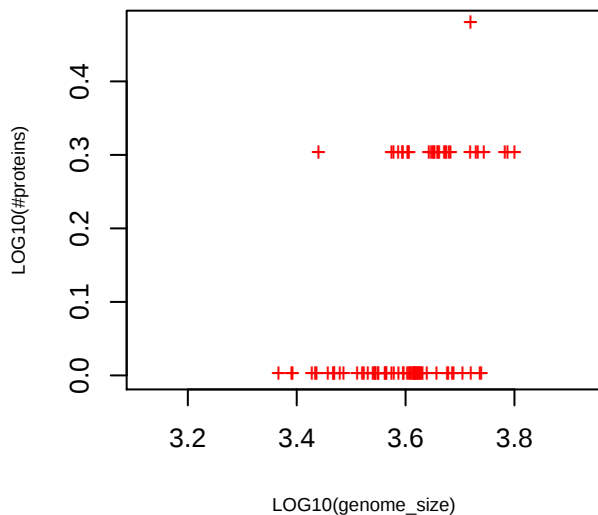
TIGR00932 2a37: transporter, monovalent cation:proton antiporter-2 (CPA2) family

slope= -0.004 p_value= 0.0056 intercept= 0.012 p_value= 1.5e-12

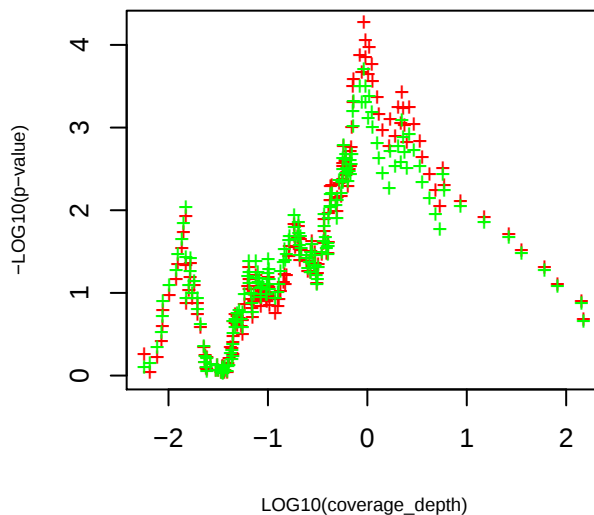


TIGR00932 2a37: transporter, monovalent cation:proton antiporter-2 (CPA2) family

slope= 4.10 p_value= 2.9e-06 intercept= -16.69 p_value= 1.0e-07

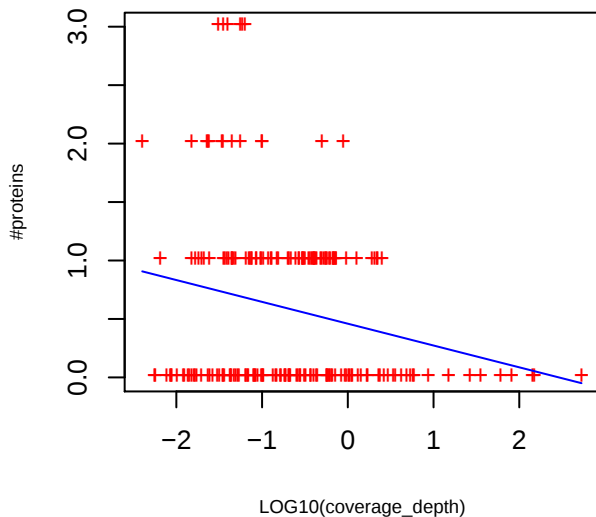


P-value curve ; red (unnorm), green (norm)



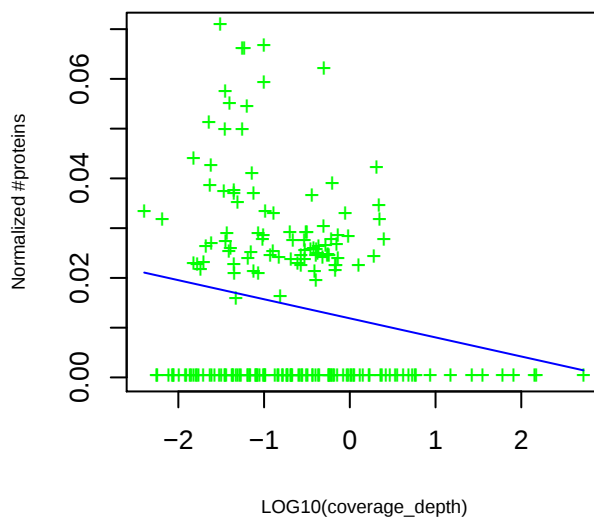
PF05170 AsmA: AsmA family

slope= -0.19 p_value= 0.0016 intercept= 0.46 p_value= 4.8e-11



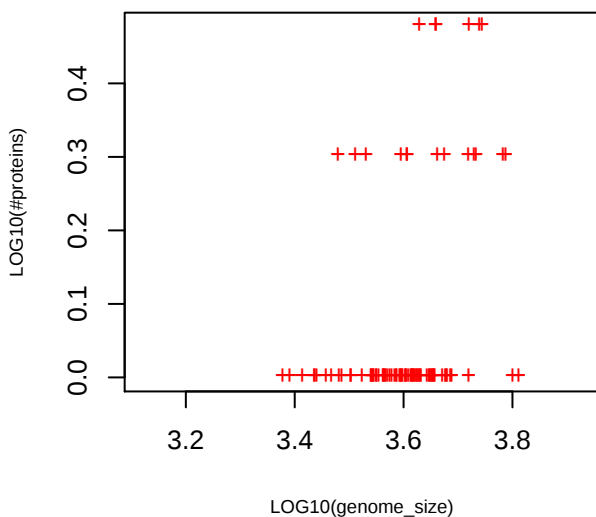
PF05170 AsmA: AsmA family

slope= -0.0038 p_value= 0.0067 intercept= 0.012 p_value= 2e-12

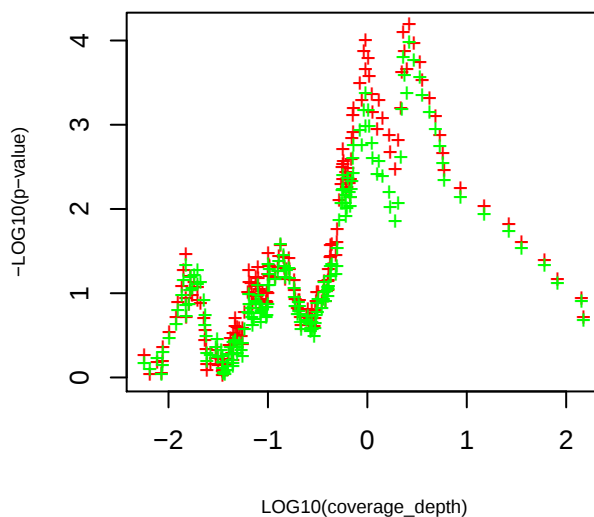


PF05170 AsmA: AsmA family

slope= 4.21 p_value= 1.3e-06 intercept= -17.05 p_value= 4.5e-08

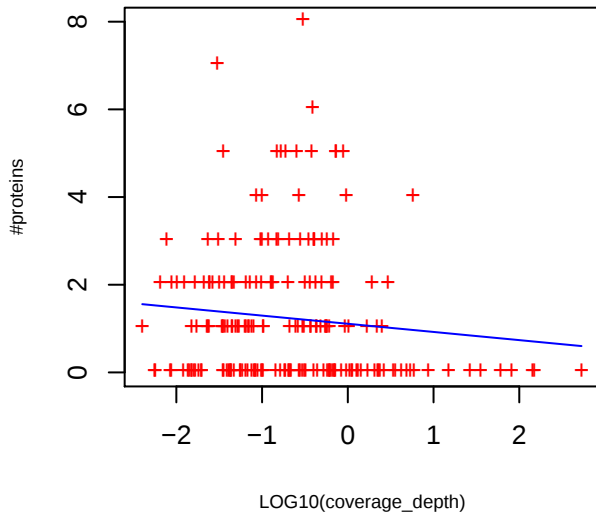


P-value curve ; red (unnorm), green (norm)



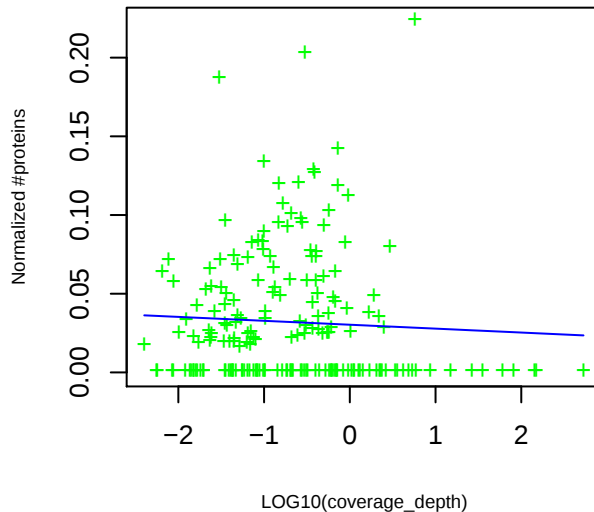
PF07731 Cu-oxidase_2: Multicopper oxidase

slope= -0.19 p_value= 0.14 intercept= 1.11 p_value= 1.9e-13



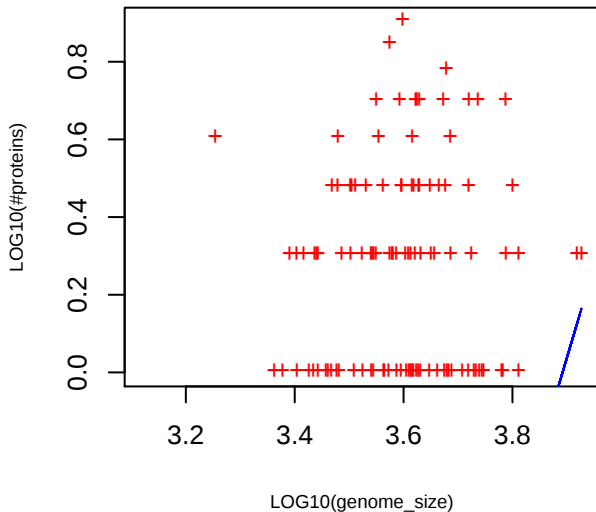
PF07731 Cu-oxidase_2: Multicopper oxidase

slope= -0.0025 p_value= 0.45 intercept= 0.030 p_value= 5.4e-14

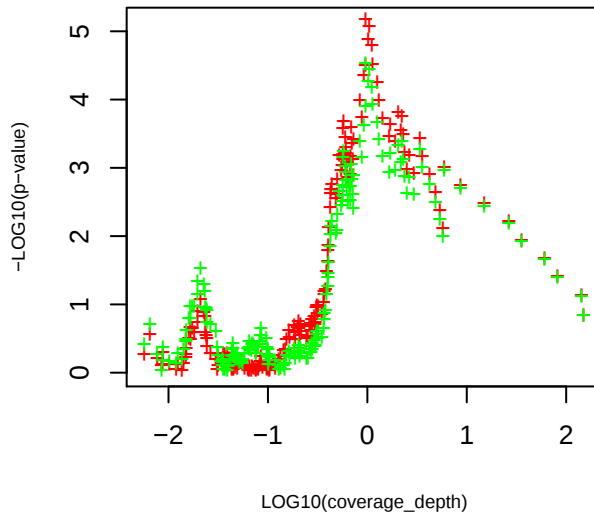


PF07731 Cu-oxidase_2: Multicopper oxidase

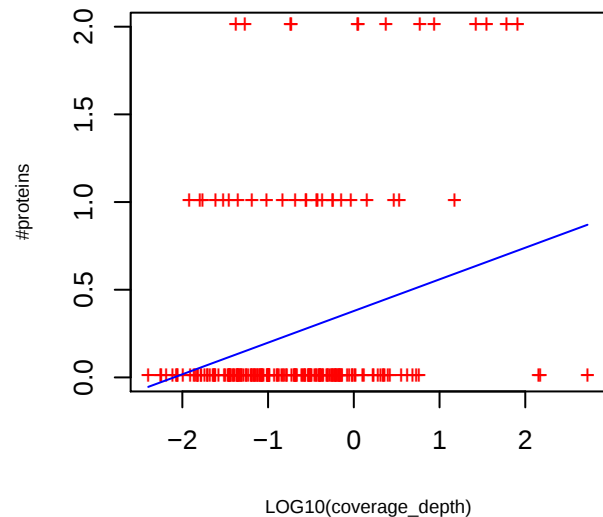
slope= 4.72 p_value= 2e-07 intercept= -18.38 p_value= 1.5e-08



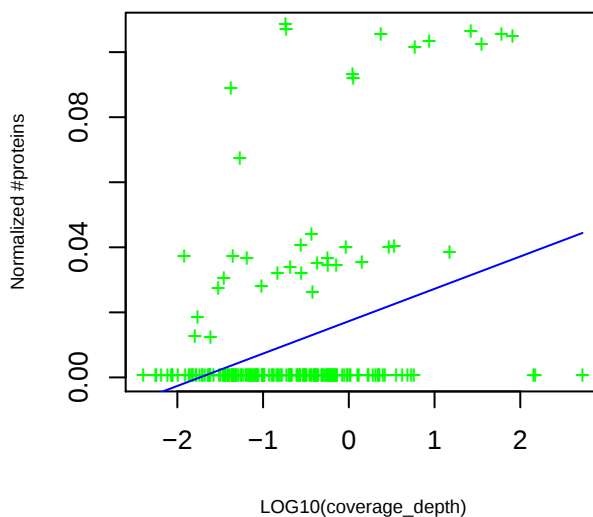
P-value curve ; red (unnorm), green (norm)



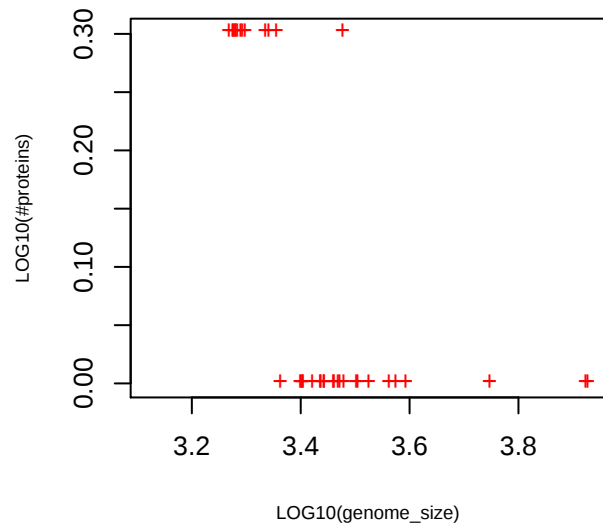
TIGR01790 carotene-cycl: lycopene cyclase family protein
 slope= 0.18 p_value= 5.3e-05 intercept= 0.38 p_value= 7.2e-13



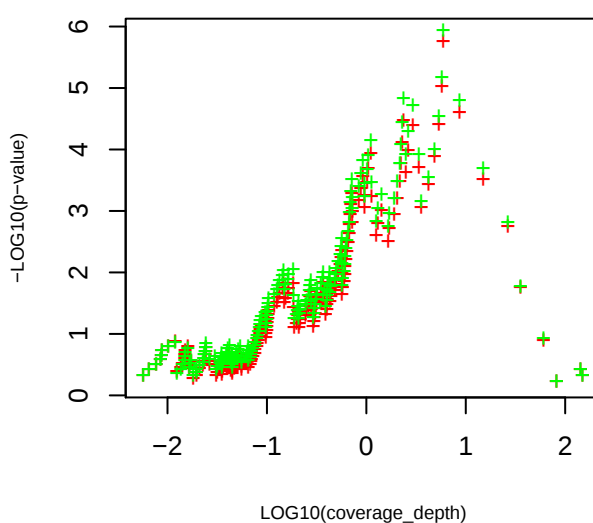
TIGR01790 carotene-cycl: lycopene cyclase family protein
 slope= 0.01 p_value= 8.2e-07 intercept= 0.017 p_value= 2.9e-13



TIGR01790 carotene-cycl: lycopene cyclase family protein
 slope= -3.08 p_value= 8.2e-06 intercept= 7.68 p_value= 0.0015

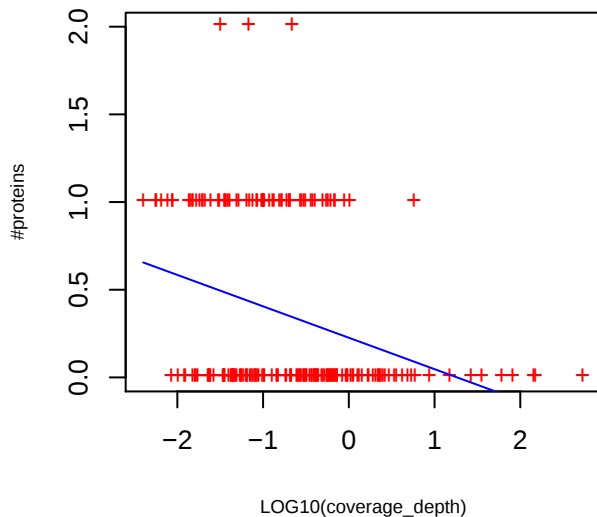


P-value curve ; red (unnorm), green (norm)



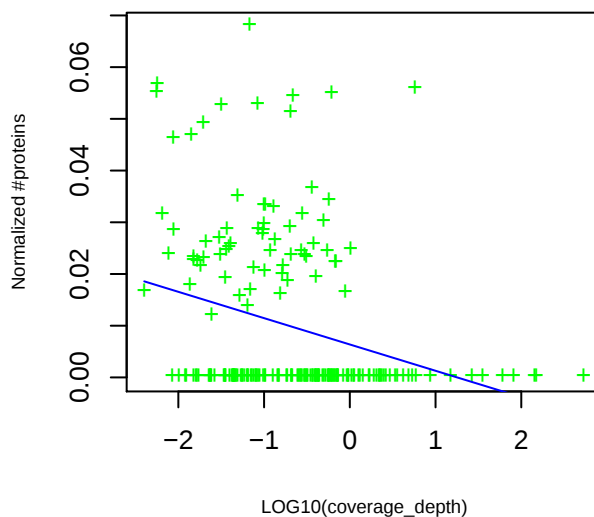
TIGR02258 2_5_ligase: 2'-5' RNA ligase

slope= -0.18 p_value= 6.7e-06 intercept= 0.23 p_value= 5.6e-07



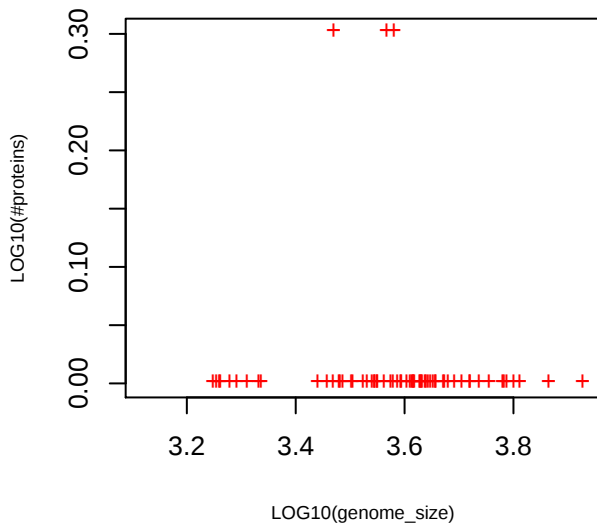
TIGR02258 2_5_ligase: 2'-5' RNA ligase

slope= -0.0051 p_value= 3.9e-05 intercept= 0.0064 p_value= 5.7e-06

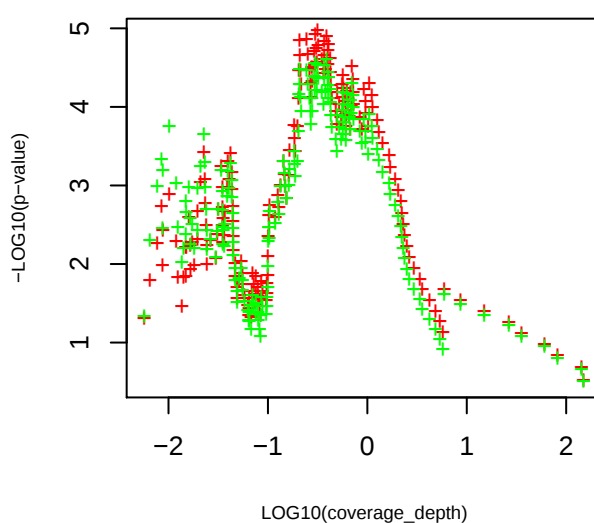


TIGR02258 2_5_ligase: 2'-5' RNA ligase

slope= 1.63 p_value= 0.05 intercept= -8.42 p_value= 0.0045

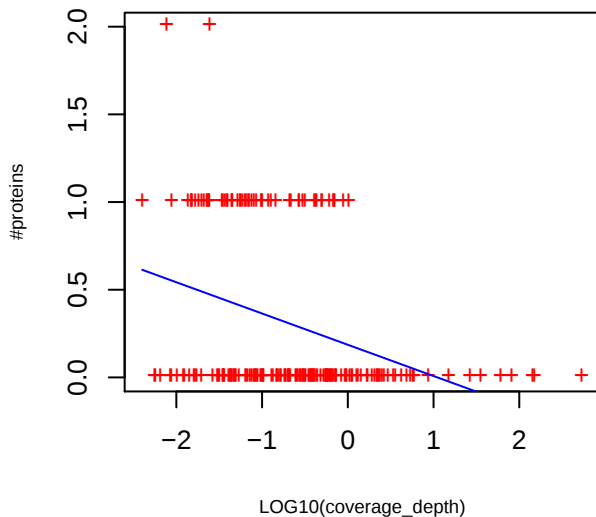


P-value curve ; red (unnorm), green (norm)



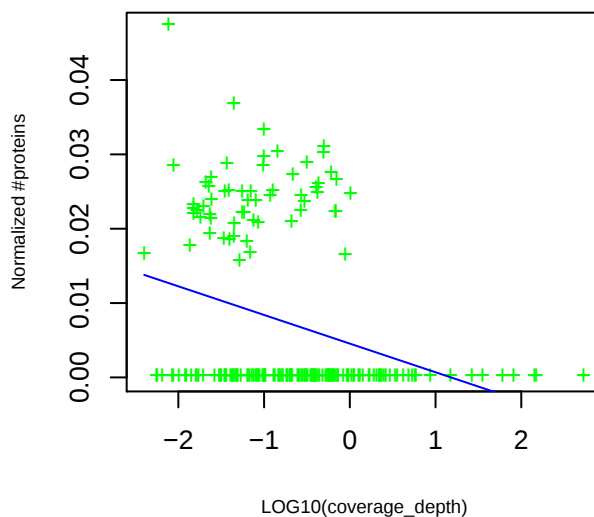
PF08298 AAA_PrkA: PrkA AAA domain

slope= -0.18 p_value= 2.4e-06 intercept= 0.19 p_value= 1.2e-05



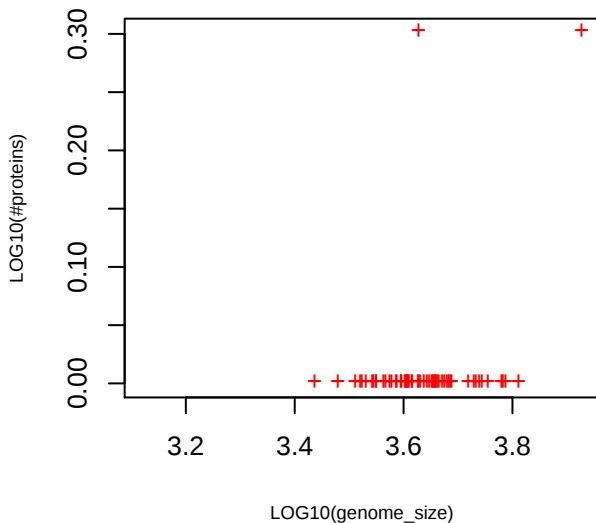
PF08298 AAA_PrkA: PrkA AAA domain

slope= -0.0039 p_value= 1.6e-05 intercept= 0.0045 p_value= 7e-06

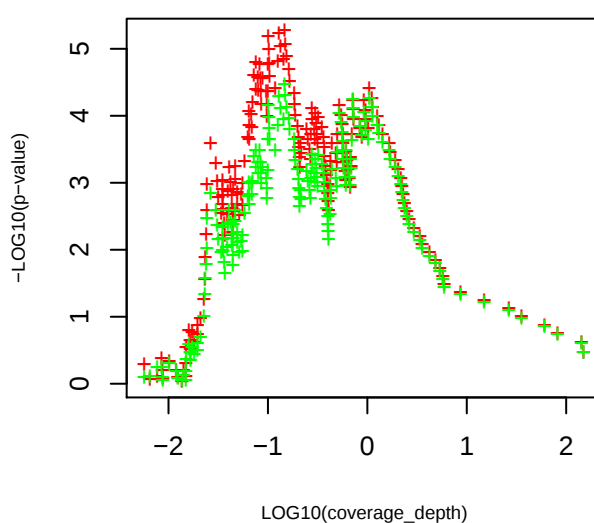


PF08298 AAA_PrkA: PrkA AAA domain

slope= 4.20 p_value= 7.7e-08 intercept= -17.68 p_value= 3.2e-10

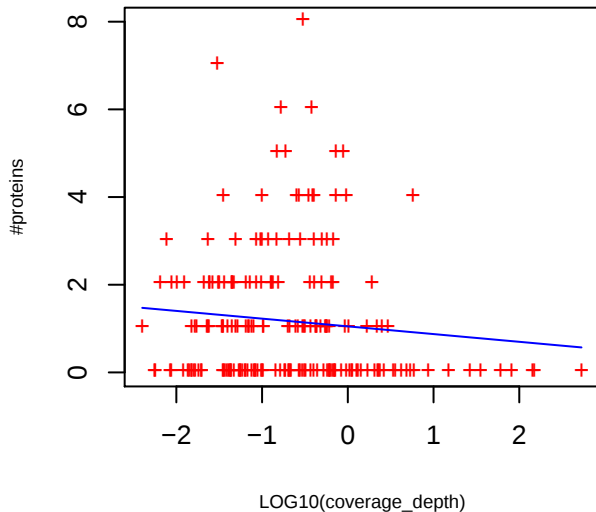


P-value curve ; red (unnorm), green (norm)



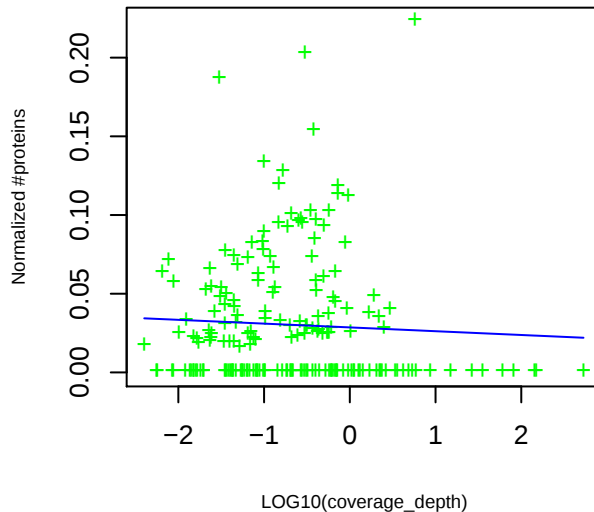
PF07732 Cu-oxidase_3: Multicopper oxidase

slope= -0.18 p_value= 0.15 intercept= 1.05 p_value= 1.1e-12



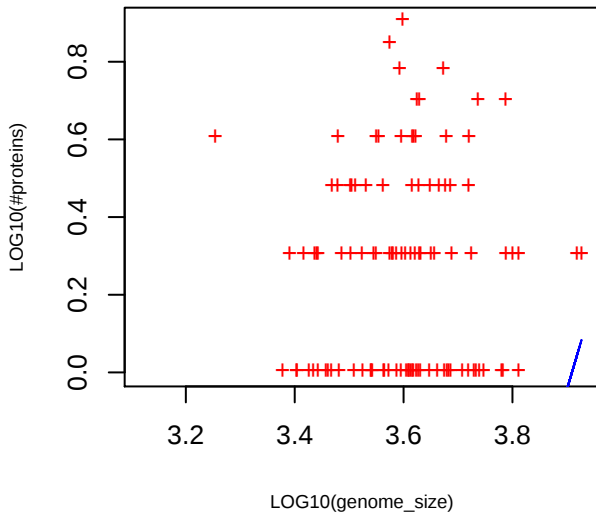
PF07732 Cu-oxidase_3: Multicopper oxidase

slope= -0.0024 p_value= 0.46 intercept= 0.029 p_value= 5.1e-13

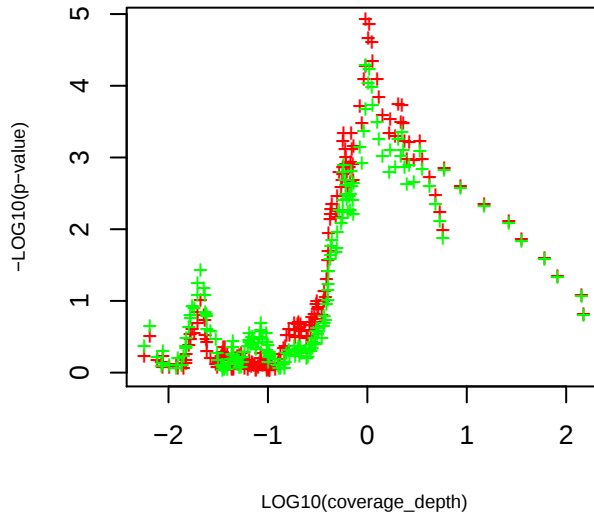


PF07732 Cu-oxidase_3: Multicopper oxidase

slope= 4.75 p_value= 1.8e-07 intercept= -18.56 p_value= 1.1e-08

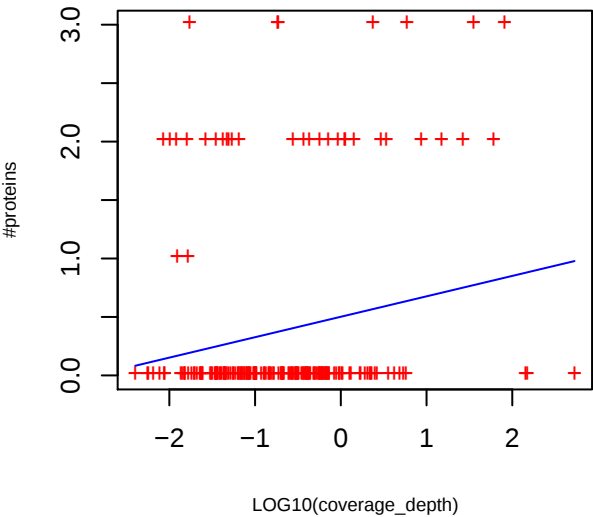


P-value curve ; red (unnorm), green (norm)



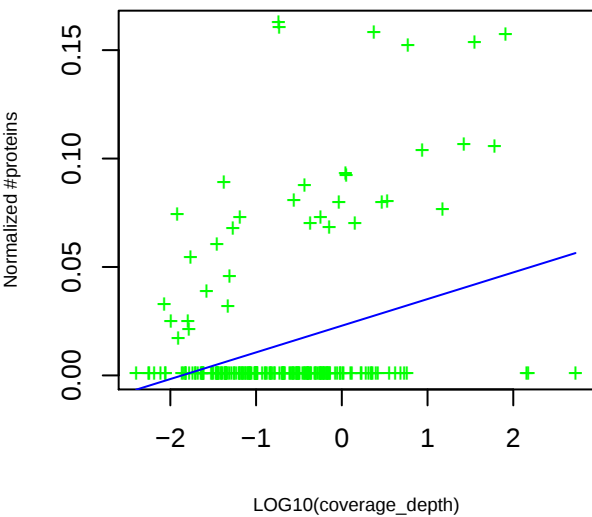
PF00283 Cytochrom_B559: Cytochrome b559, alpha (gene psbE) and beta (gene psbF)subunits

slope= 0.17 p_value= 0.0094 intercept= 0.50 p_value= 2.6e-10



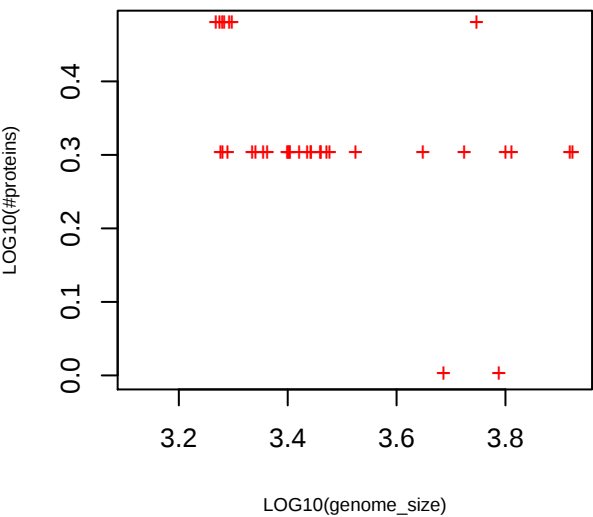
PF00283 Cytochrom_B559: Cytochrome b559, alpha (gene psbE) and beta (gene psbF)subunits

slope= 0.012 p_value= 1.1e-05 intercept= 0.023 p_value= 2.8e-12

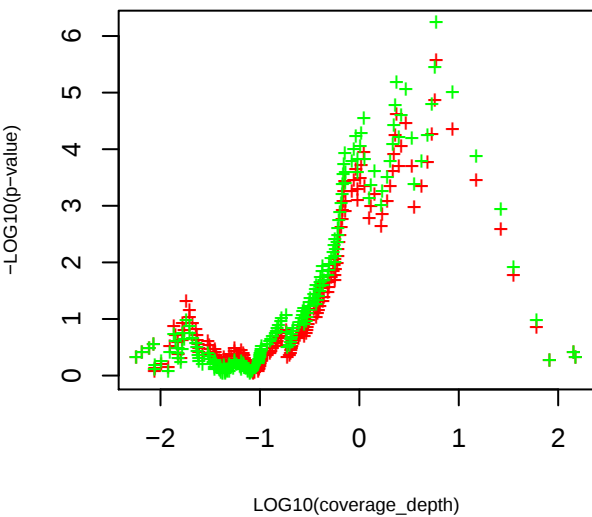


PF00283 Cytochrom_B559: Cytochrome b559, alpha (gene psbE) and beta (gene psbF)subunits

slope= -2.01 p_value= 0.0052 intercept= 3.91 p_value= 0.12

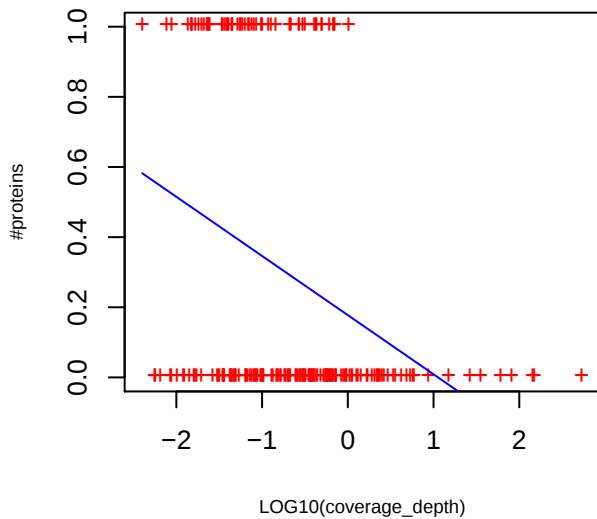


P-value curve ; red (unnorm), green (norm)



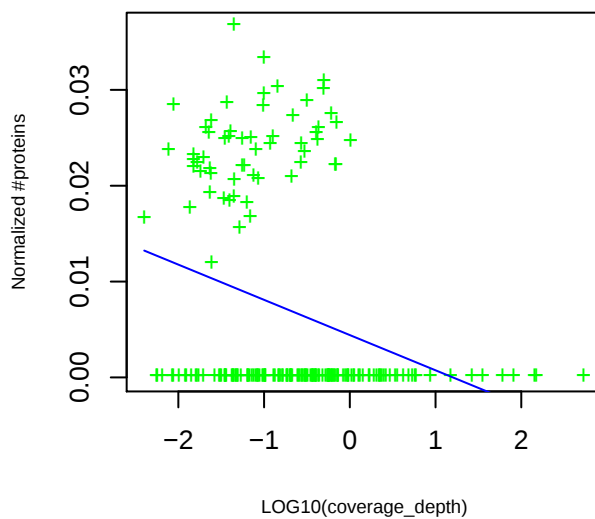
PF04285 DUF444: Protein of unknown function (DUF444)

slope= -0.17 p_value= 2.2e-06 intercept= 0.18 p_value= 9.2e-06



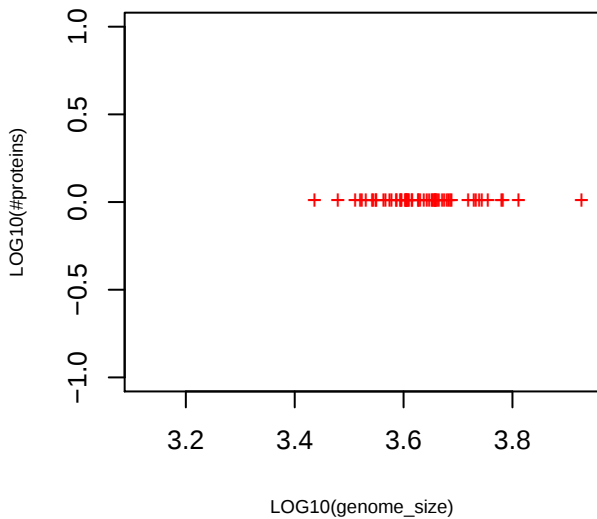
PF04285 DUF444: Protein of unknown function (DUF444)

slope= -0.0037 p_value= 2.3e-05 intercept= 0.0044 p_value= 6.9e-06

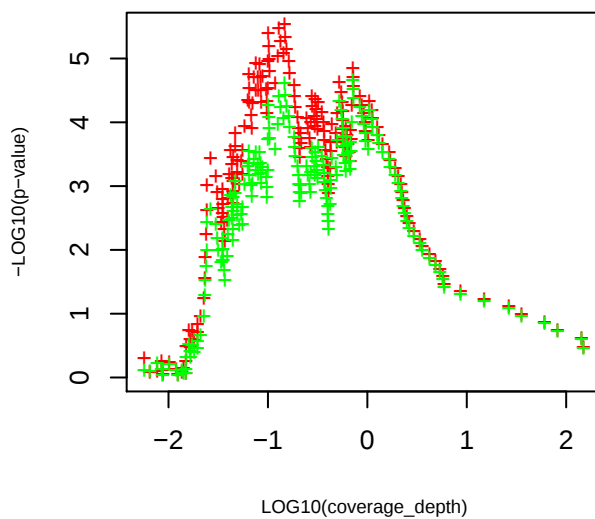


PF04285 DUF444: Protein of unknown function (DUF444)

slope= 3.96 p_value= 3.6e-07 intercept= -16.86 p_value= 1.7e-09

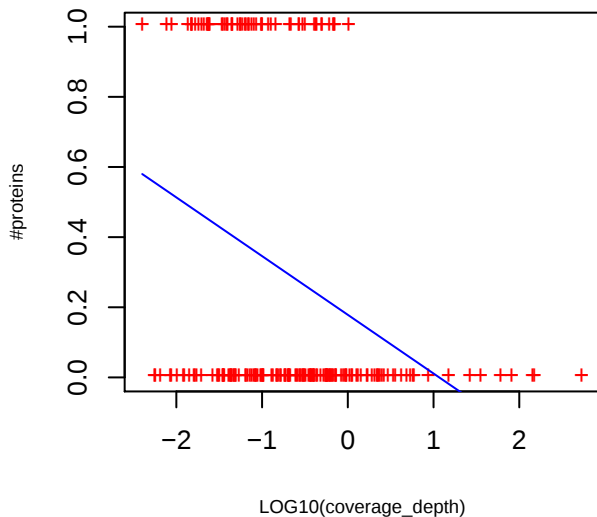


P-value curve ; red (unnorm), green (norm)



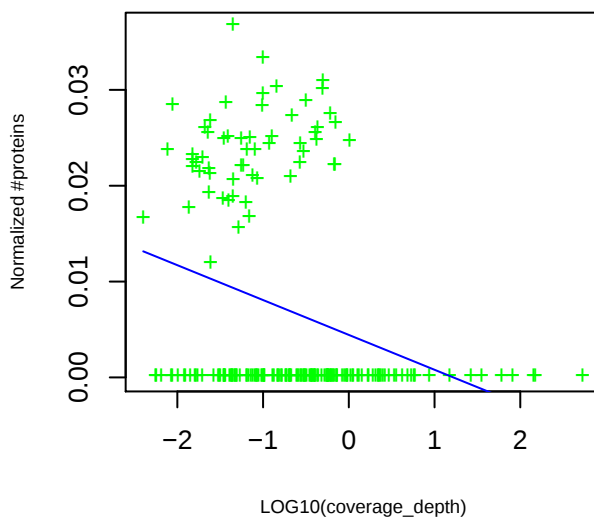
PF06798 PrkA: PrkA serine protein kinase

slope= -0.17 p_value= 2.6e-06 intercept= 0.18 p_value= 8.5e-06



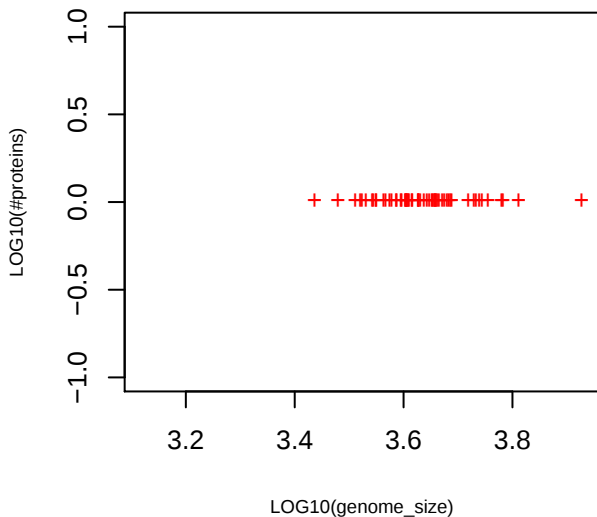
PF06798 PrkA: PrkA serine protein kinase

slope= -0.0036 p_value= 2.7e-05 intercept= 0.0044 p_value= 6.3e-06

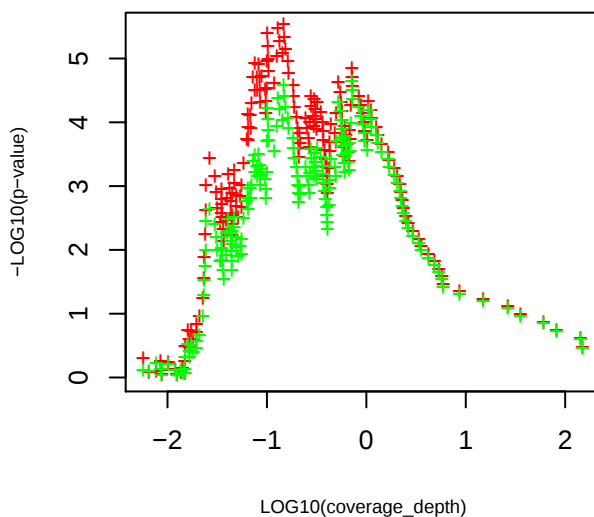


PF06798 PrkA: PrkA serine protein kinase

slope= 3.98 p_value= 3e-07 intercept= -16.95 p_value= 1.4e-09

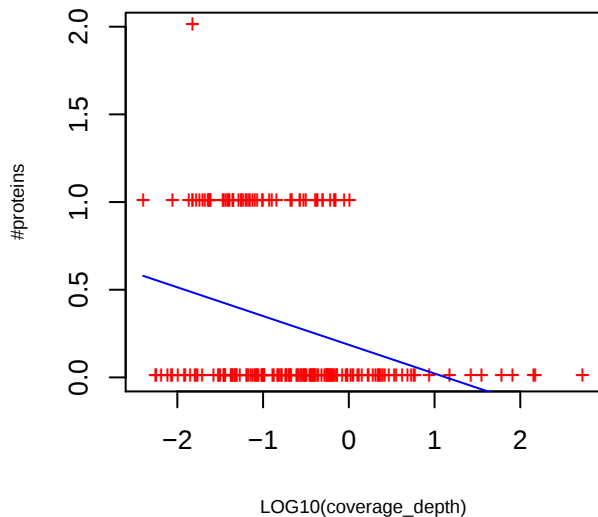


P-value curve ; red (unnorm), green (norm)



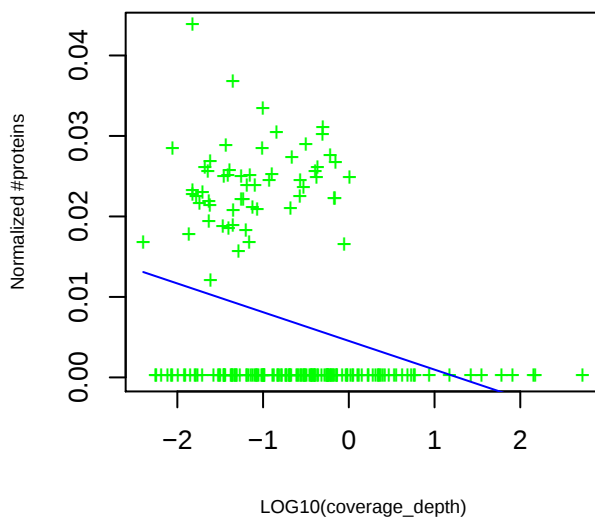
PF04293 SpoVR: SpoVR like protein

slope= -0.16 p_value= 8.1e-06 intercept= 0.19 p_value= 7.5e-06



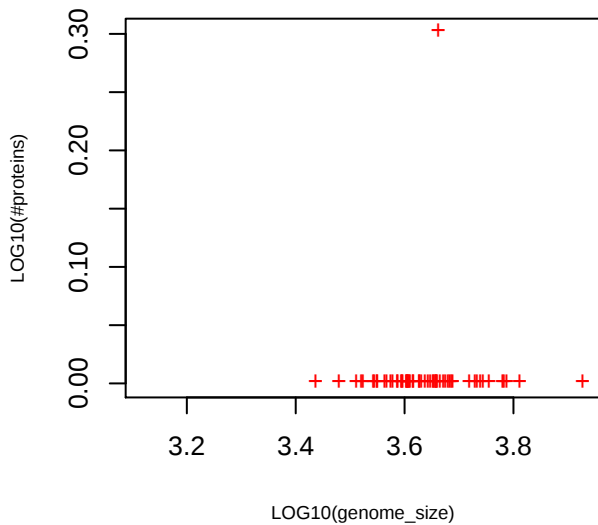
PF04293 SpoVR: SpoVR like protein

slope= -0.0036 p_value= 5.2e-05 intercept= 0.0045 p_value= 5.9e-06

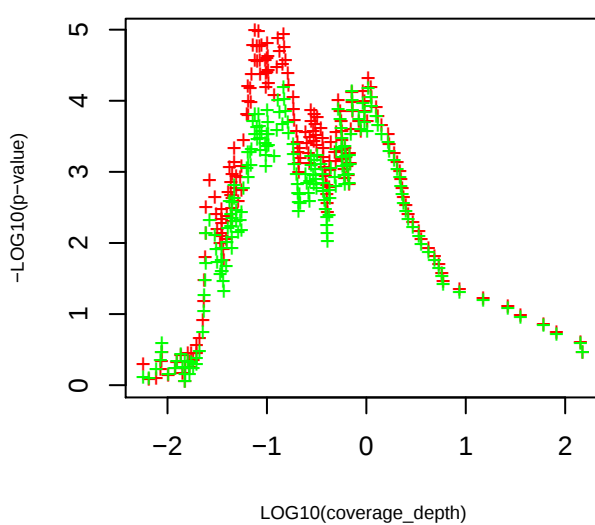


PF04293 SpoVR: SpoVR like protein

slope= 4.16 p_value= 8.2e-08 intercept= -17.57 p_value= 3.2e-10

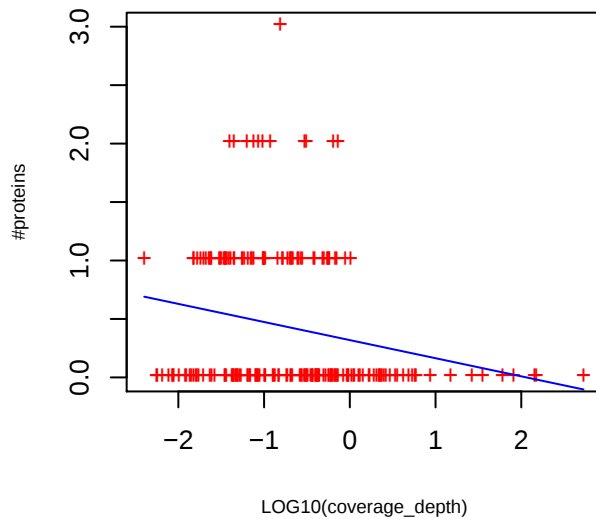


P-value curve ; red (unnorm), green (norm)



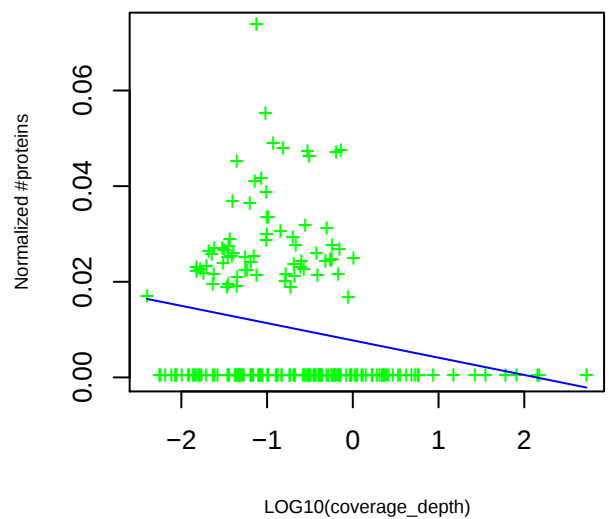
TIGR01449 PGP_bact: phosphoglycolate phosphatase, bacterial

slope= -0.15 p_value= 0.0017 intercept= 0.32 p_value= 2.6e-08



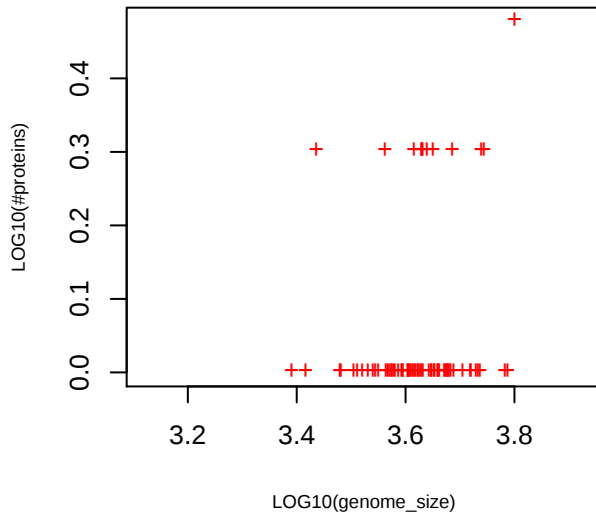
TIGR01449 PGP_bact: phosphoglycolate phosphatase, bacterial

slope= -0.0036 p_value= 0.0024 intercept= 0.0077 p_value= 2.2e-08

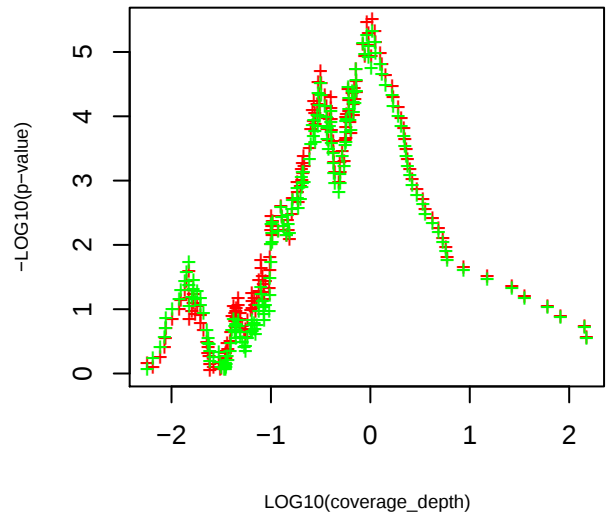


TIGR01449 PGP_bact: phosphoglycolate phosphatase, bacterial

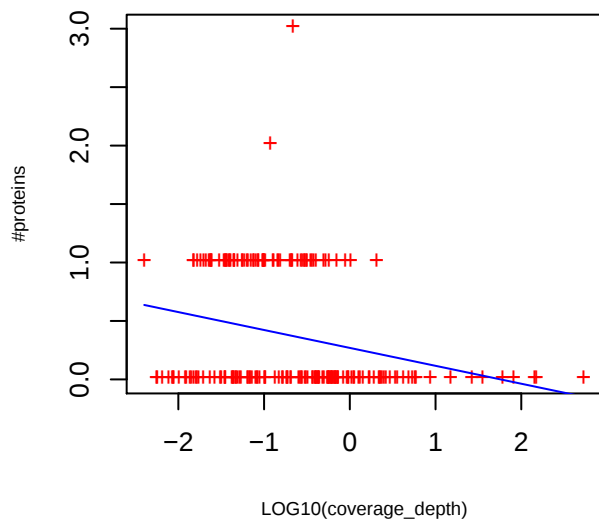
slope= 4.27 p_value= 2.6e-07 intercept= -17.69 p_value= 2.9e-09



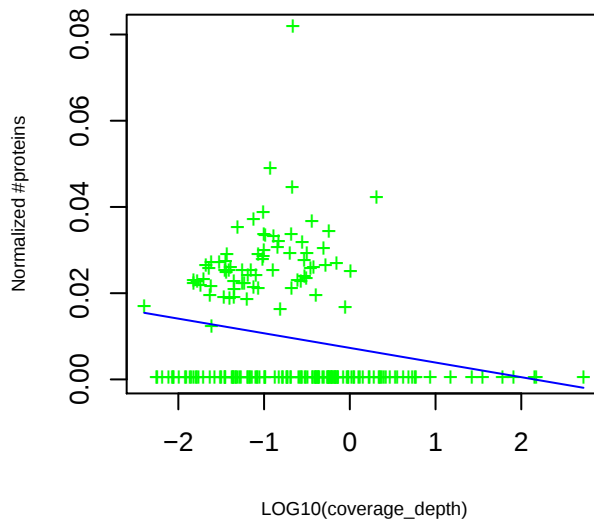
P-value curve ; red (unnorm), green (norm)



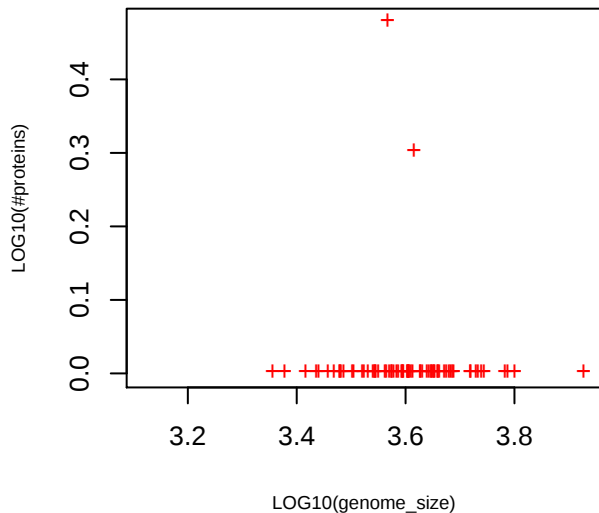
PF05088 Bac_GDH: Bacterial NAD-glutamate dehydrogenase
 slope= -0.15 p_value= 0.00022 intercept= 0.27 p_value= 1.8e-08



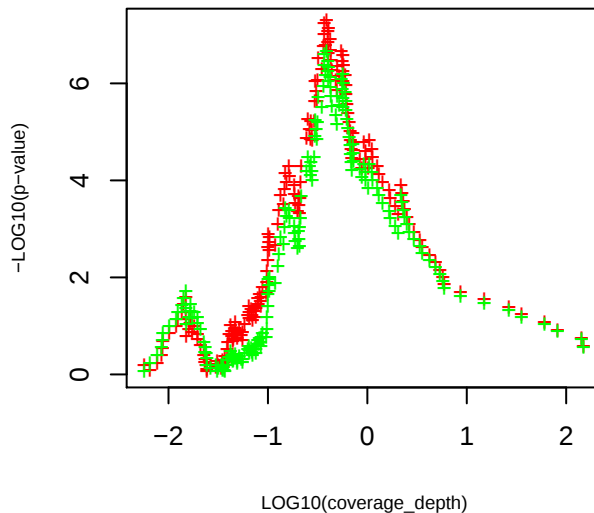
PF05088 Bac_GDH: Bacterial NAD-glutamate dehydrogenase
 slope= -0.0034 p_value= 0.0023 intercept= 0.0073 p_value= 1.7e-08



PF05088 Bac_GDH: Bacterial NAD-glutamate dehydrogenase
 slope= 3.10 p_value= 0.00021 intercept= -13.53 p_value= 6e-06

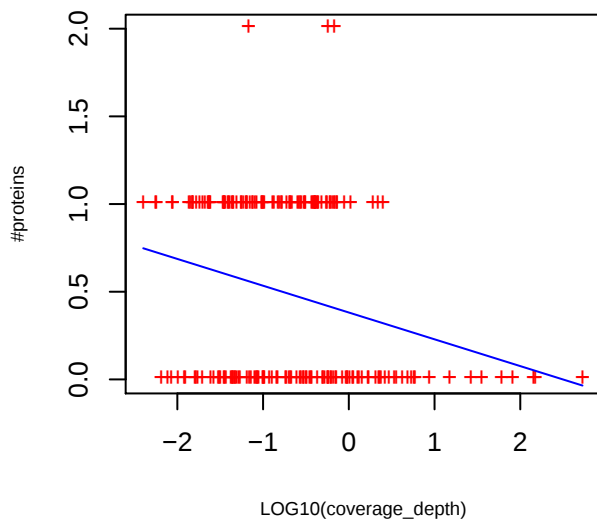


P-value curve ; red (unnorm), green (norm)



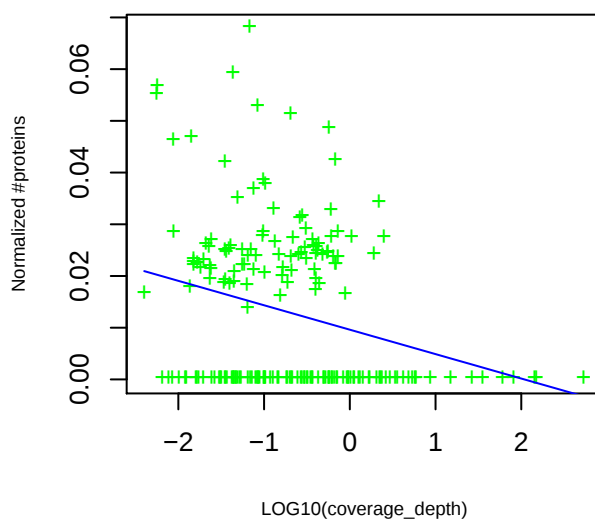
PF07831 PYNP_C: Pyrimidine nucleoside phosphorylase C-terminal domain

slope= -0.15 p_value= 0.00026 intercept= 0.38 p_value= 2.7e-14



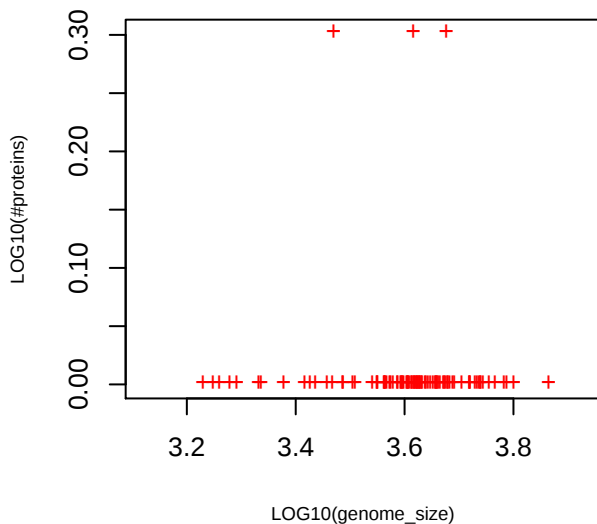
PF07831 PYNP_C: Pyrimidine nucleoside phosphorylase C-terminal domain

slope= -0.0047 p_value= 9.6e-05 intercept= 0.0096 p_value= 1.4e-11

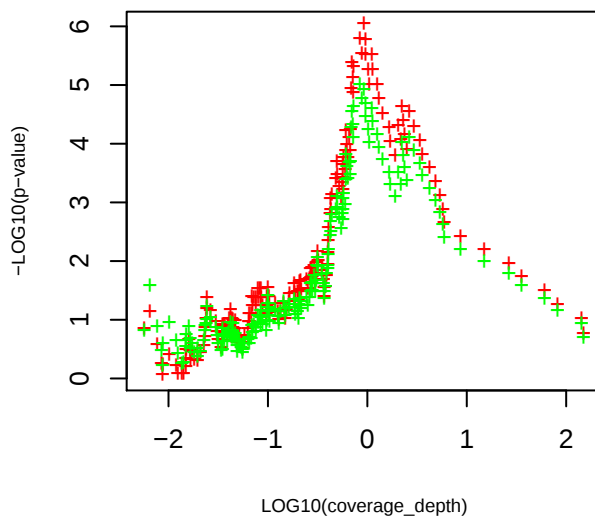


PF07831 PYNP_C: Pyrimidine nucleoside phosphorylase C-terminal domain

slope= 3.75 p_value= 1.3e-05 intercept= -15.41 p_value= 5.8e-07

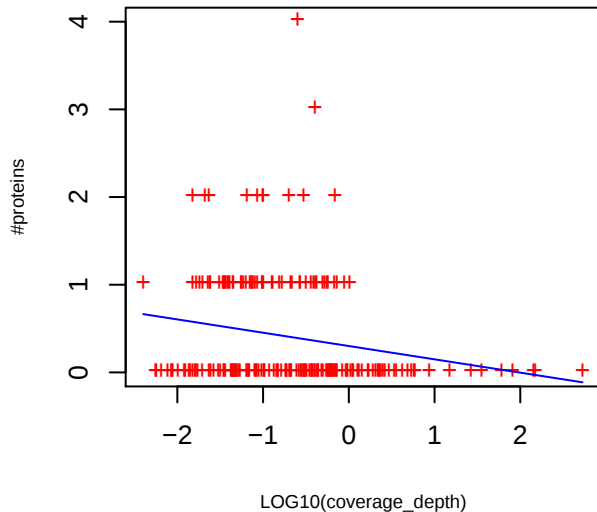


P-value curve ; red (unnorm), green (norm)



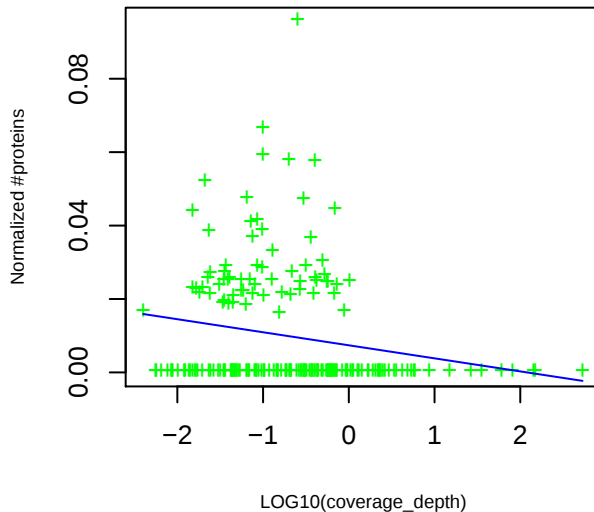
PF05940 NnrS: NnrS protein

slope= -0.15 p_value= 0.0038 intercept= 0.30 p_value= 6.3e-07



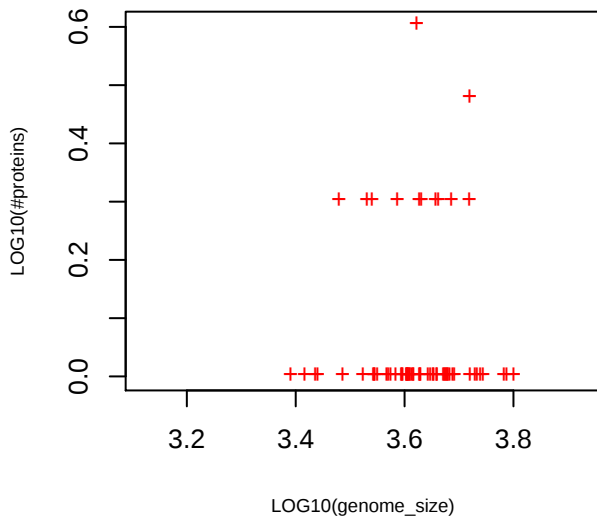
PF05940 NnrS: NnrS protein

slope= -0.0036 p_value= 0.0058 intercept= 0.0074 p_value= 6.7e-07

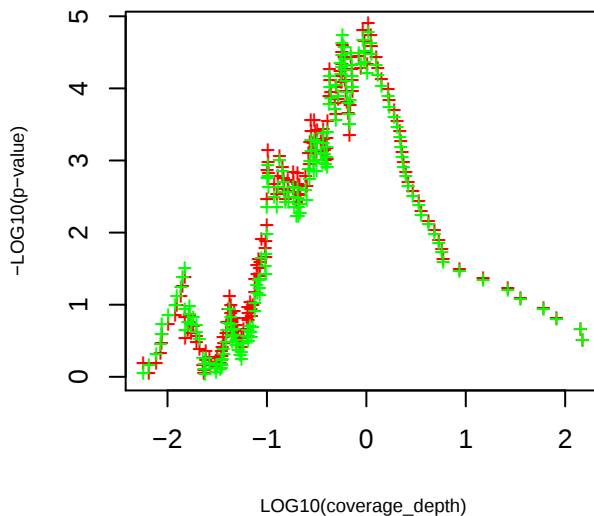


PF05940 NnrS: NnrS protein

slope= 3.91 p_value= 1.8e-06 intercept= -16.51 p_value= 2.0e-08

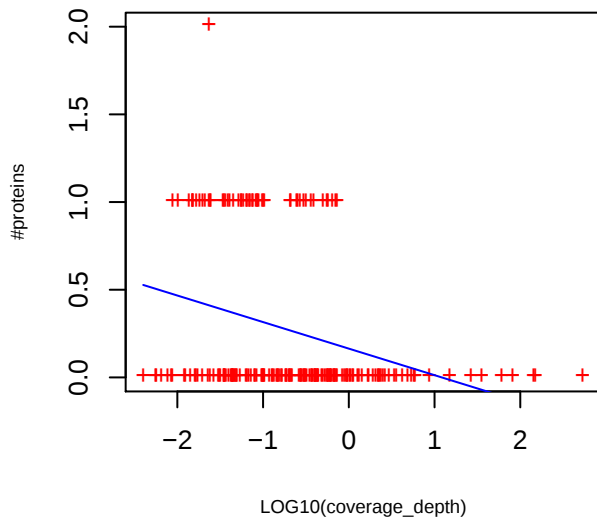


P-value curve ; red (unnorm), green (norm)



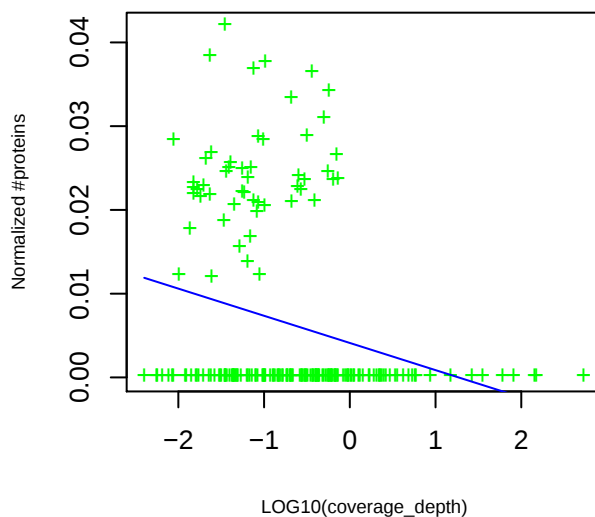
PF06961 DUF1294: Protein of unknown function (DUF1294)

slope= -0.15 p_value= 2.2e-05 intercept= 0.16 p_value= 4.6e-05



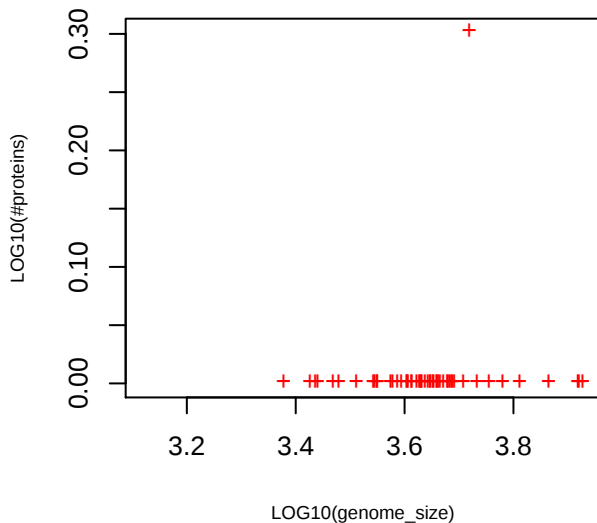
PF06961 DUF1294: Protein of unknown function (DUF1294)

slope= -0.0032 p_value= 0.00023 intercept= 0.0041 p_value= 3.7e-05

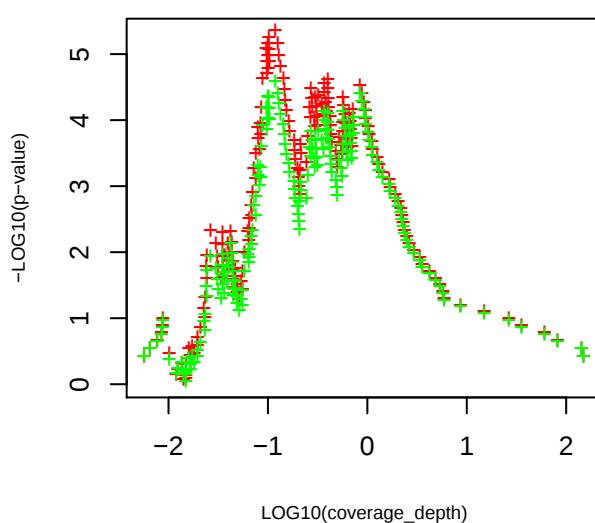


PF06961 DUF1294: Protein of unknown function (DUF1294)

slope= 3.79 p_value= 5e-07 intercept= -16.37 p_value= 1.6e-09

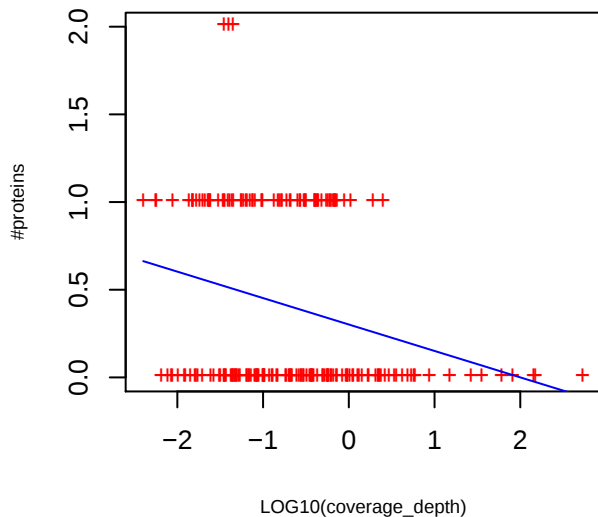


P-value curve ; red (unnorm), green (norm)



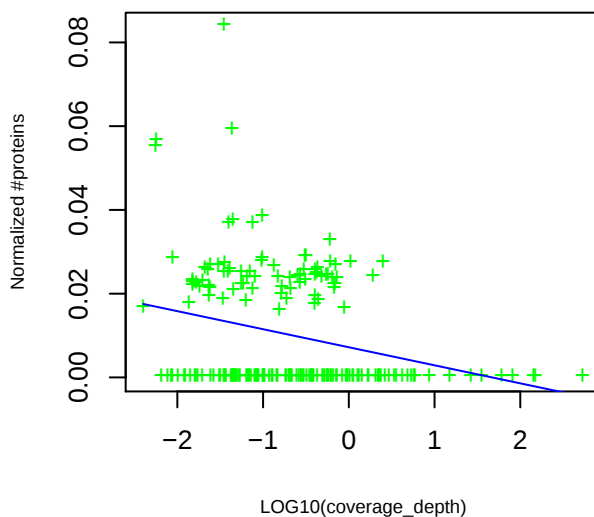
PF08342 PPM_N: Phosphopentomutase N-terminal

slope= -0.15 p_value= 0.00025 intercept= 0.30 p_value= 3.6e-10



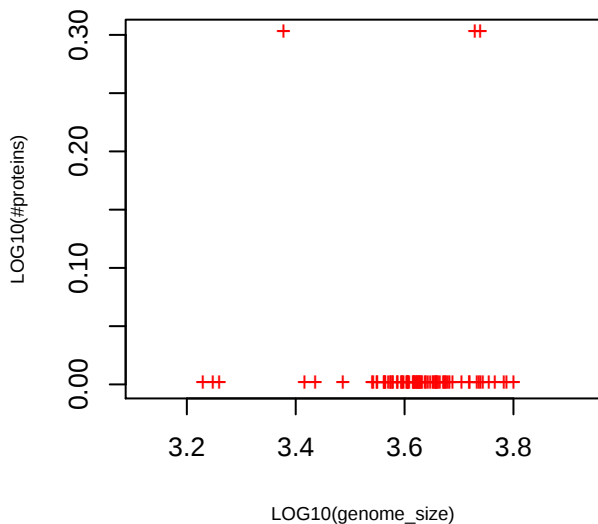
PF08342 PPM_N: Phosphopentomutase N-terminal

slope= -0.0043 p_value= 0.00012 intercept= 0.0072 p_value= 2.6e-08

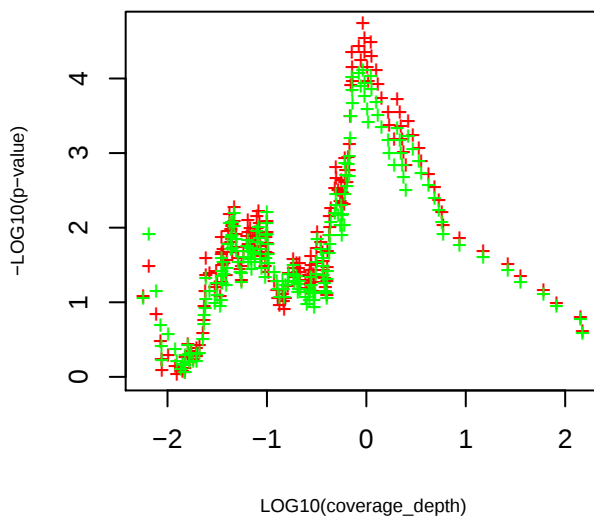


PF08342 PPM_N: Phosphopentomutase N-terminal

slope= 4.24 p_value= 4e-07 intercept= -17.45 p_value= 5.8e-09

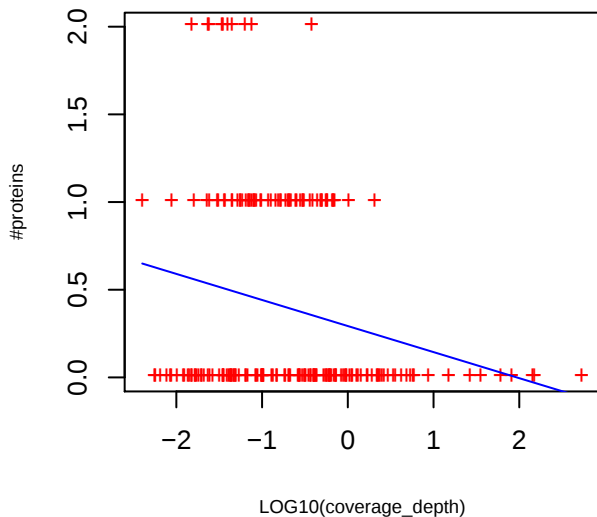


P-value curve ; red (unnorm), green (norm)



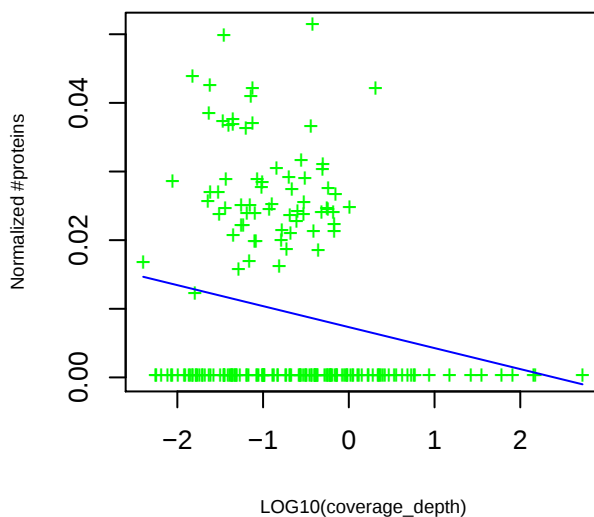
TIGR02374 nitri_red_nirB: nitrite reductase [NAD(P)H], large subunit

slope= -0.15 p_value= 0.0013 intercept= 0.29 p_value= 4.7e-08



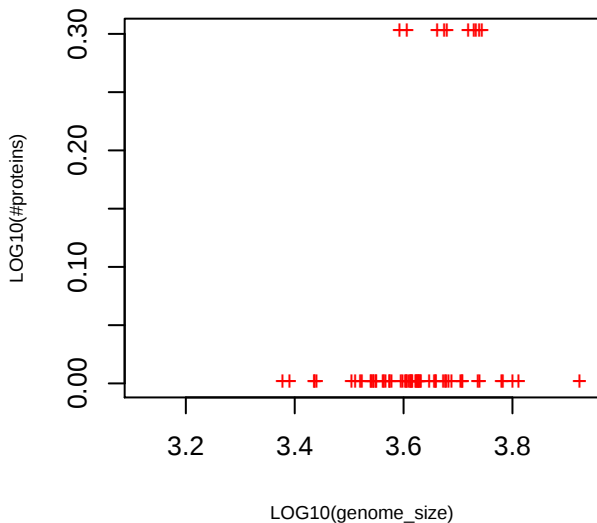
TIGR02374 nitri_red_nirB: nitrite reductase [NAD(P)H], large subunit

slope= -0.0031 p_value= 0.0056 intercept= 0.0073 p_value= 1.2e-08

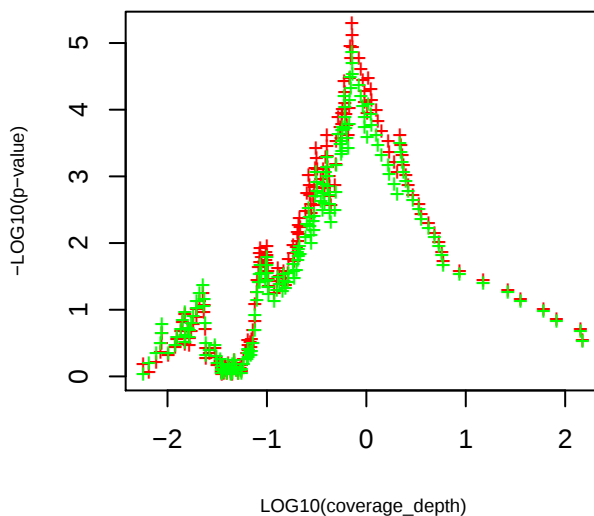


TIGR02374 nitri_red_nirB: nitrite reductase [NAD(P)H], large subunit

slope= 4.26 p_value= 2.1e-07 intercept= -17.69 p_value= 1.9e-09

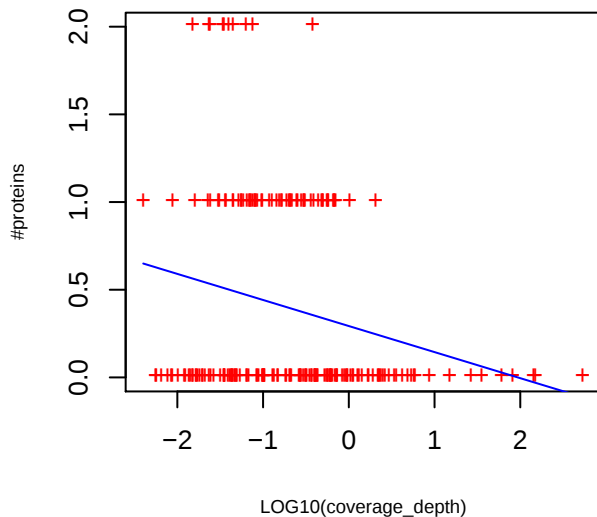


P-value curve ; red (unnorm), green (norm)



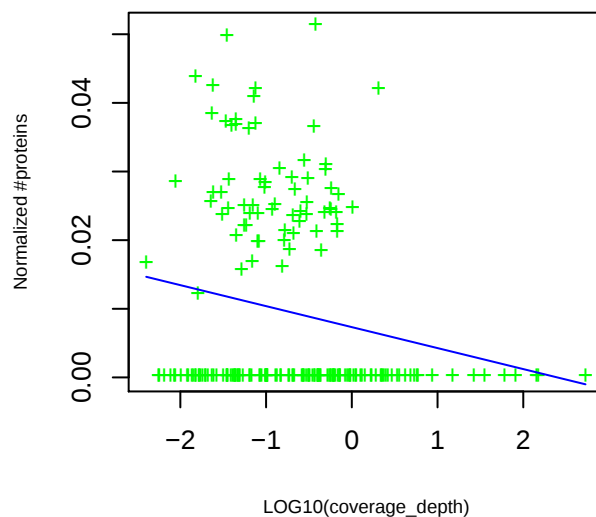
TIGR02378 nirD_assim_sml: nitrite reductase [NAD(P)H], small subunit

slope= -0.15 p_value= 0.0013 intercept= 0.29 p_value= 4.7e-08



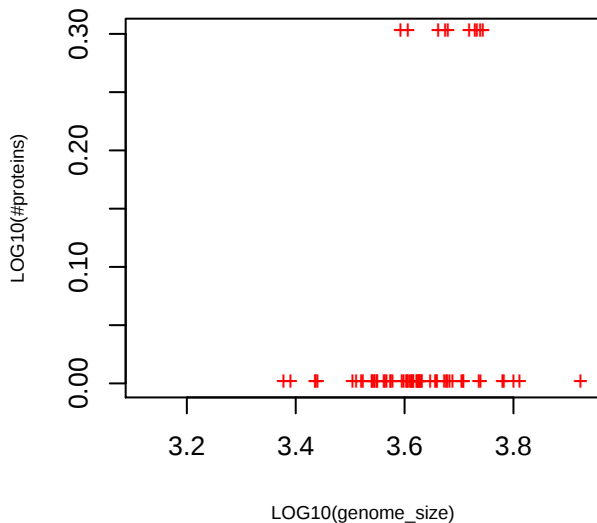
TIGR02378 nirD_assim_sml: nitrite reductase [NAD(P)H], small subunit

slope= -0.0031 p_value= 0.0056 intercept= 0.0073 p_value= 1.2e-08

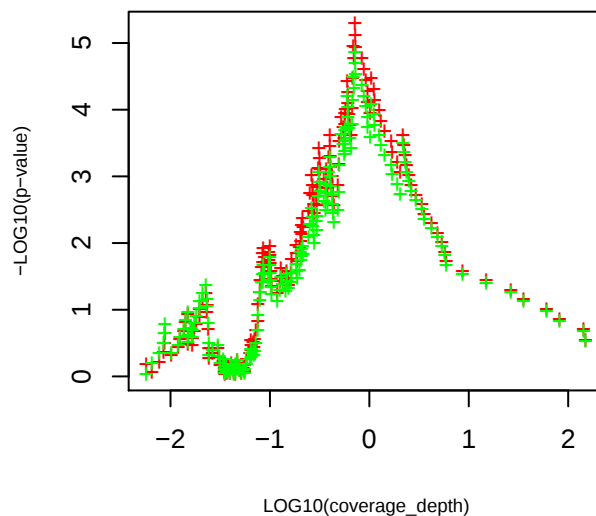


TIGR02378 nirD_assim_sml: nitrite reductase [NAD(P)H], small subunit

slope= 4.26 p_value= 2.1e-07 intercept= -17.69 p_value= 1.9e-09

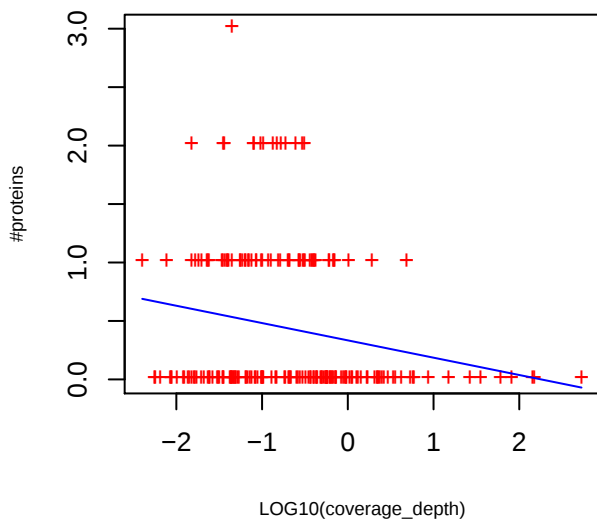


P-value curve ; red (unnorm), green (norm)



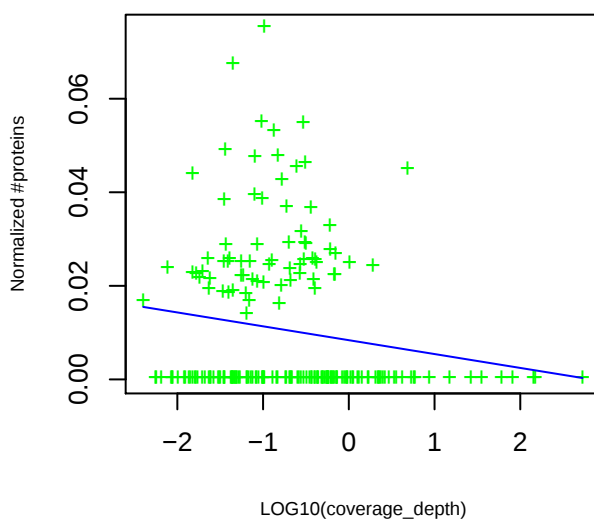
PF08021 FAD_binding_9: Siderophore-interacting FAD-binding domain

slope= -0.15 p_value= 0.004 intercept= 0.33 p_value= 2.4e-08



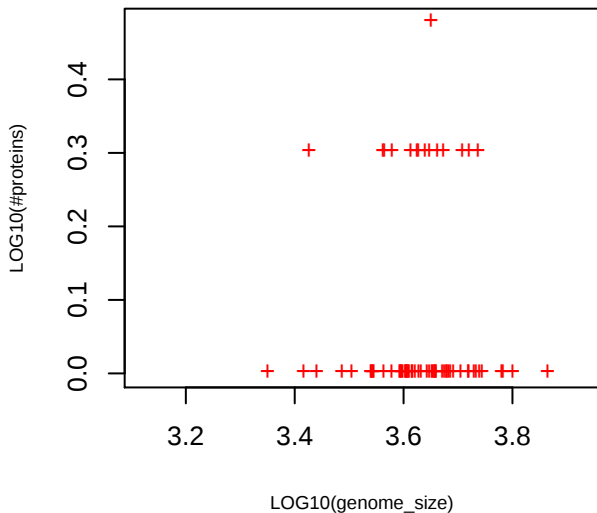
PF08021 FAD_binding_9: Siderophore-interacting FAD-binding domain

slope= -0.0030 p_value= 0.019 intercept= 0.0084 p_value= 1.5e-08

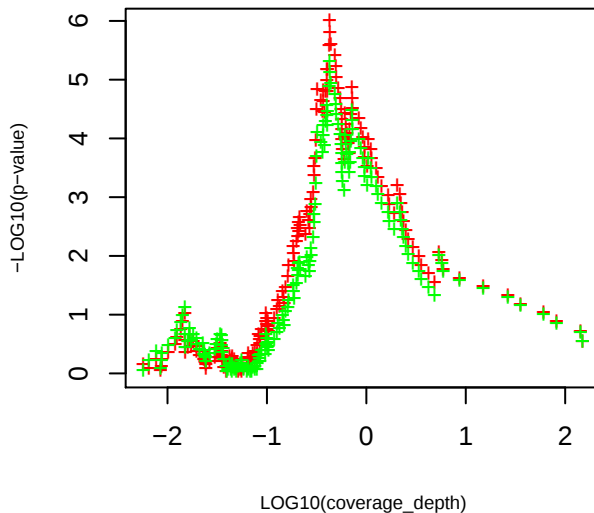


PF08021 FAD_binding_9: Siderophore-interacting FAD-binding domain

slope= 4.64 p_value= 1.8e-08 intercept= -19.02 p_value= 1.4e-10

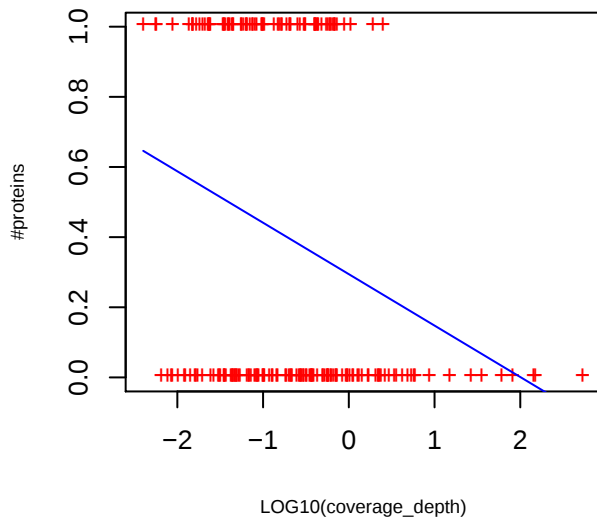


P-value curve ; red (unnorm), green (norm)



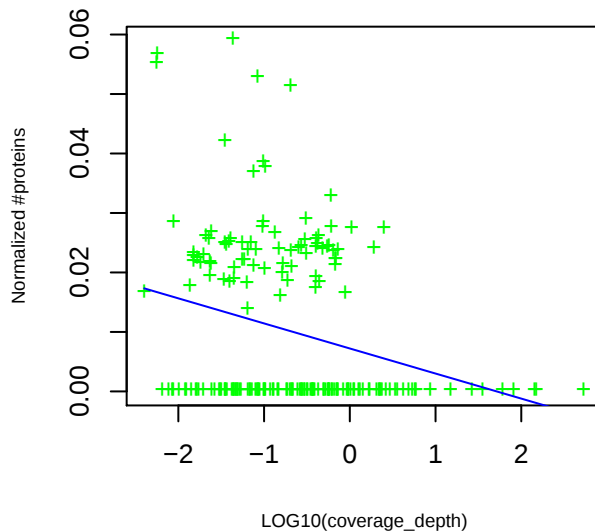
TIGR02644 Y_phosphoryl: pyrimidine-nucleoside phosphorylase

slope= -0.15 p_value= 0.00014 intercept= 0.29 p_value= 7.4e-11



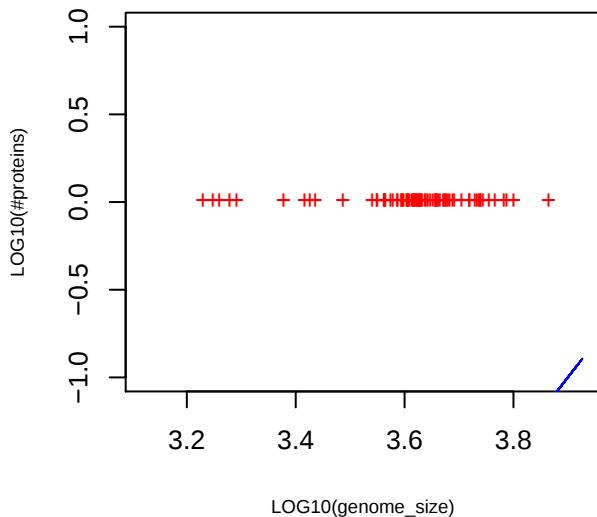
TIGR02644 Y_phosphoryl: pyrimidine-nucleoside phosphorylase

slope= -0.0042 p_value= 0.00010 intercept= 0.0072 p_value= 8.7e-09

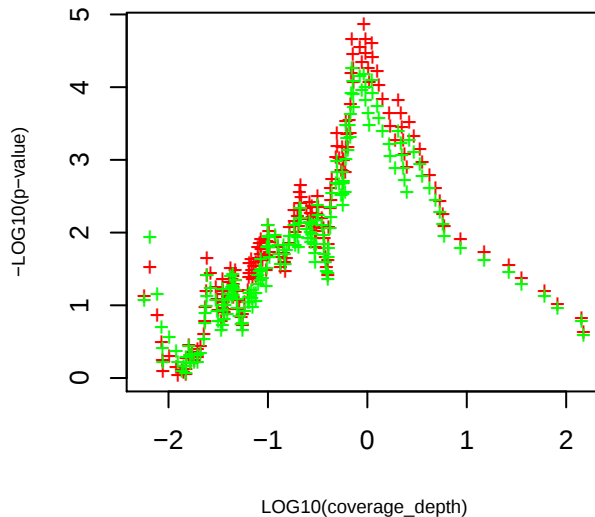


TIGR02644 Y_phosphoryl: pyrimidine-nucleoside phosphorylase

slope= 3.99 p_value= 1.9e-06 intercept= -16.58 p_value= 3.4e-08

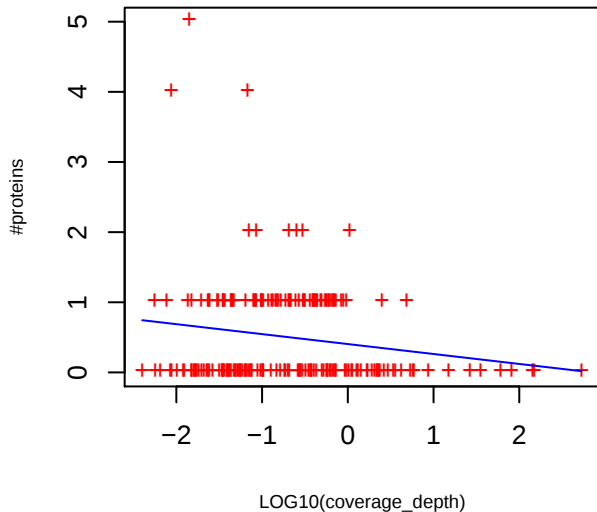


P-value curve ; red (unnorm), green (norm)



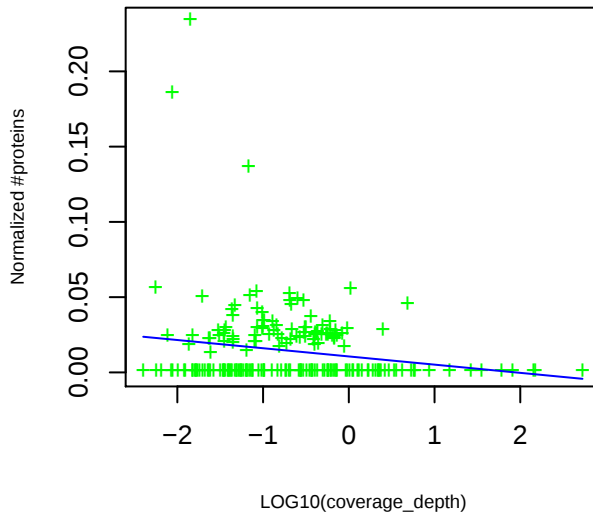
TIGR01300 CPA3_mnhG_phaG: monovalent cation/proton antiporter, MnhG/PhaG subunit

slope= -0.14 p_value= 0.015 intercept= 0.40 p_value= 3.4e-09



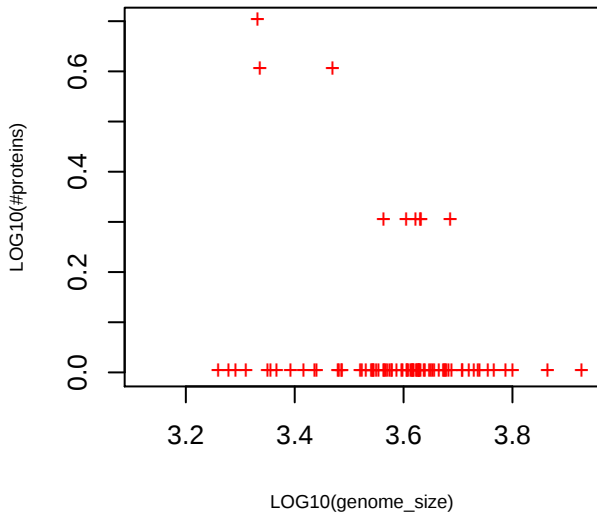
TIGR01300 CPA3_mnhG_phaG: monovalent cation/proton antiporter, MnhG/PhaG subunit

slope= -0.0055 p_value= 0.01 intercept= 0.011 p_value= 1.3e-05

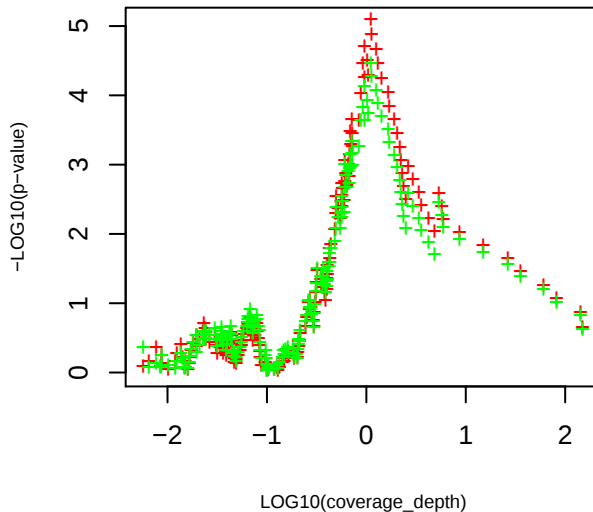


TIGR01300 CPA3_mnhG_phaG: monovalent cation/proton antiporter, MnhG/PhaG subunit

slope= 2.45 p_value= 0.005 intercept= -10.98 p_value= 0.00043

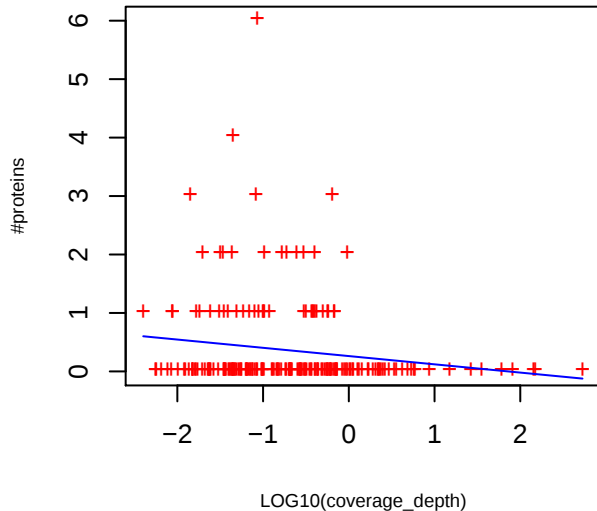


P-value curve ; red (unnorm), green (norm)



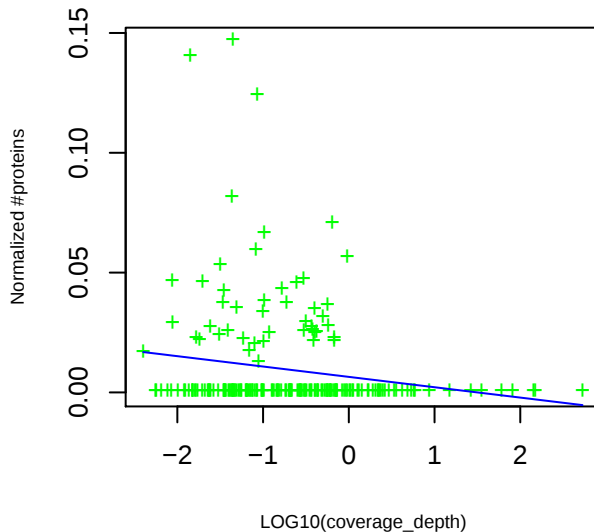
PF08843 DUF1814: Domain of unknown function (DUF1814)

slope= -0.14 p_value= 0.028 intercept= 0.26 p_value= 0.00034



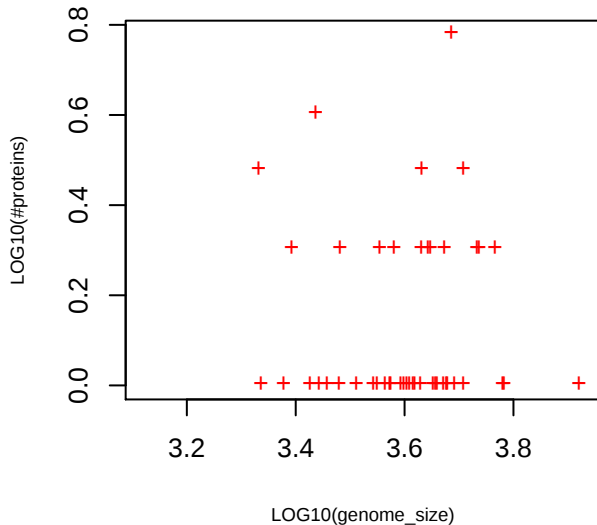
PF08843 DUF1814: Domain of unknown function (DUF1814)

slope= -0.0043 p_value= 0.015 intercept= 0.0065 p_value= 0.0013

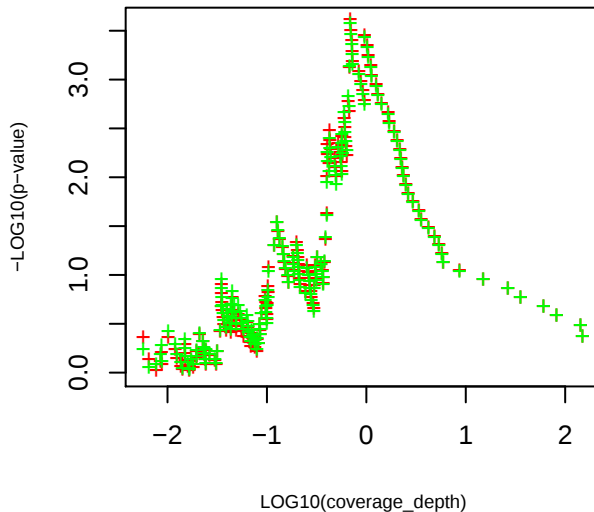


PF08843 DUF1814: Domain of unknown function (DUF1814)

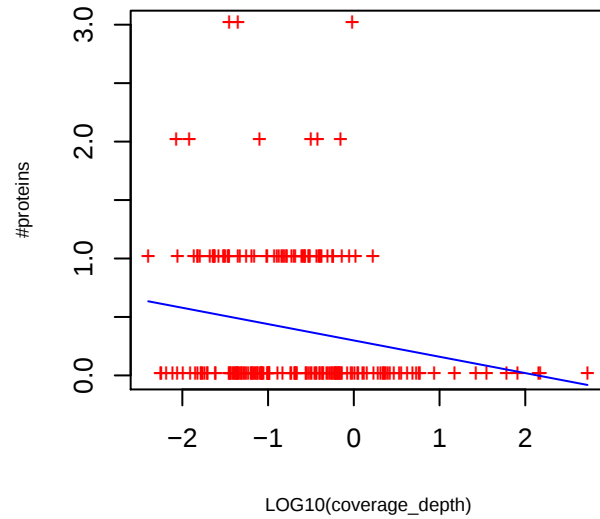
slope= 2.00 p_value= 0.0091 intercept= -10.11 p_value= 0.00022



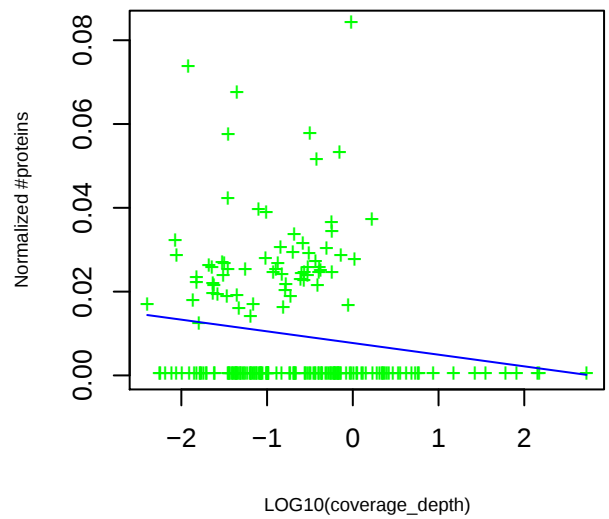
P-value curve ; red (unnorm), green (norm)



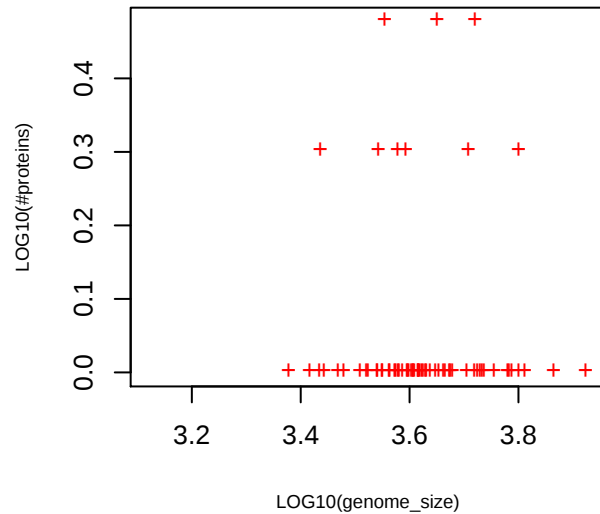
PF02308 MgtC: putative Mg²⁺ transporter-C (MgtC) family
 slope= -0.14 p_value= 0.005 intercept= 0.30 p_value= 2.1e-07



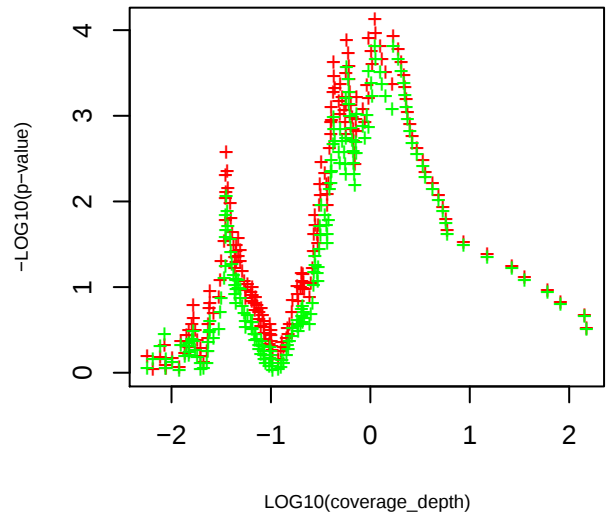
PF02308 MgtC: putative Mg²⁺ transporter-C (MgtC) family
 slope= -0.0028 p_value= 0.027 intercept= 0.0077 p_value= 1.3e-07



PF02308 MgtC: putative Mg²⁺ transporter-C (MgtC) family
 slope= 4.11 p_value= 4.8e-07 intercept= -17.21 p_value= 4.4e-09

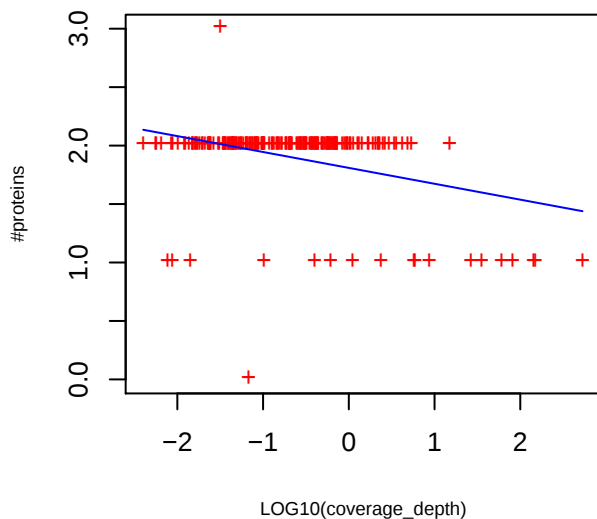


P-value curve : red (unnorm), green (norm)



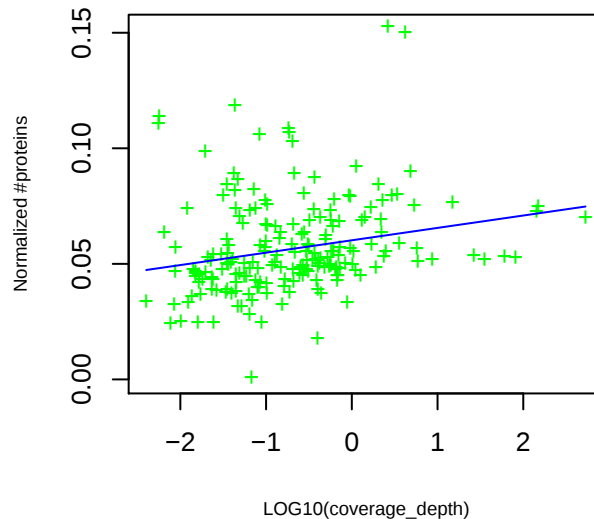
PF00814 Peptidase_M22: glycoprotease family

slope= -0.14 p_value= 8.8e-08 intercept= 1.81 p_value= 8.7e-135



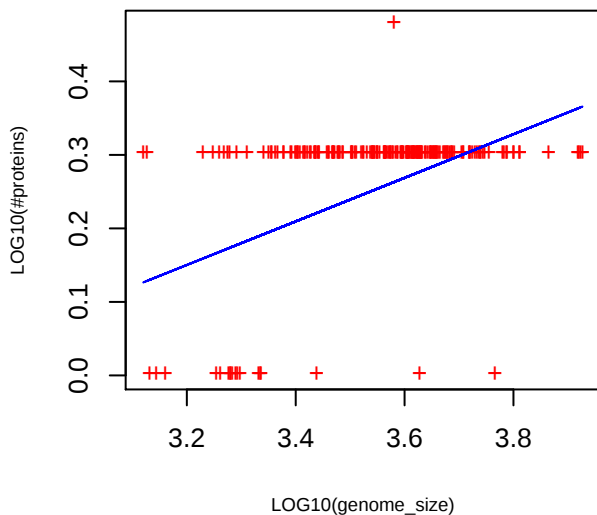
PF00814 Peptidase_M22: glycoprotease family

slope= 0.0054 p_value= 0.0013 intercept= 0.06 p_value= 9.2e-81

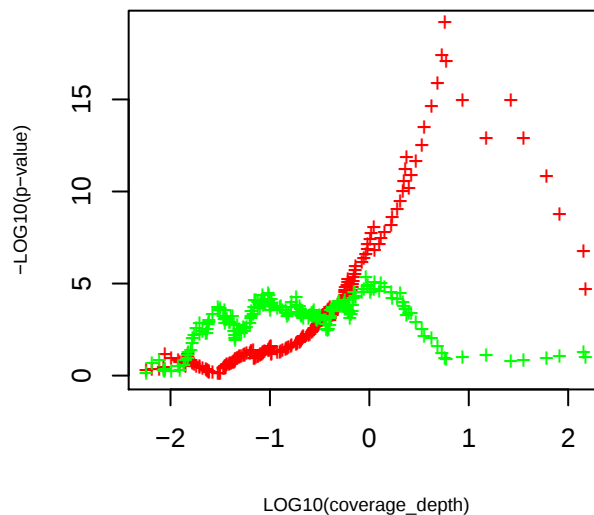


PF00814 Peptidase_M22: glycoprotease family

slope= 0.30 p_value= 0.032 intercept= -0.80 p_value= 0.10

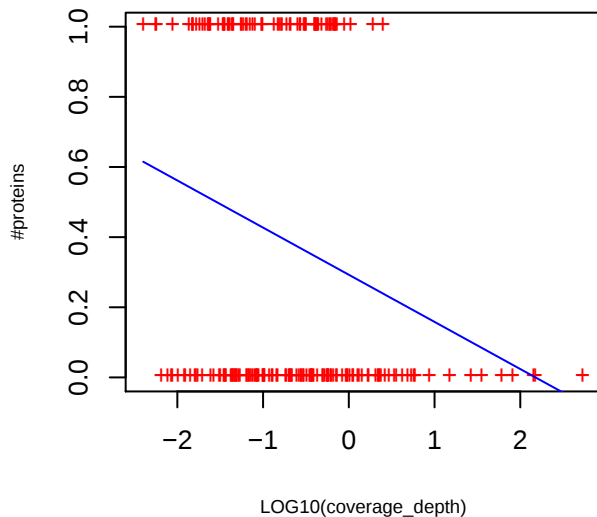


P-value curve ; red (unnorm), green (norm)



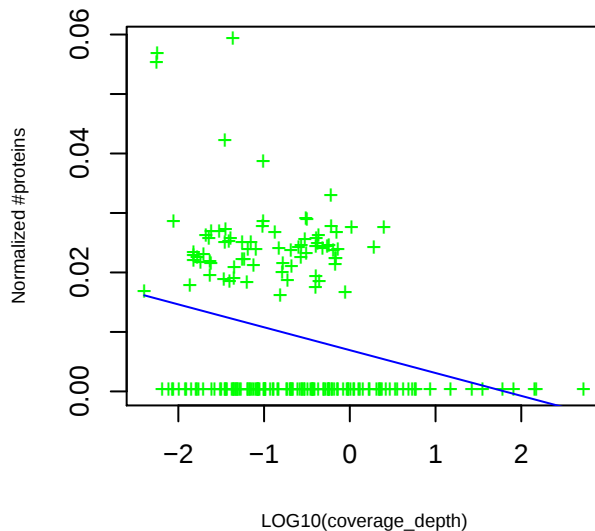
TIGR01696 deoB: phosphopentomutase

slope= -0.13 p_value= 0.00048 intercept= 0.29 p_value= 9.7e-11



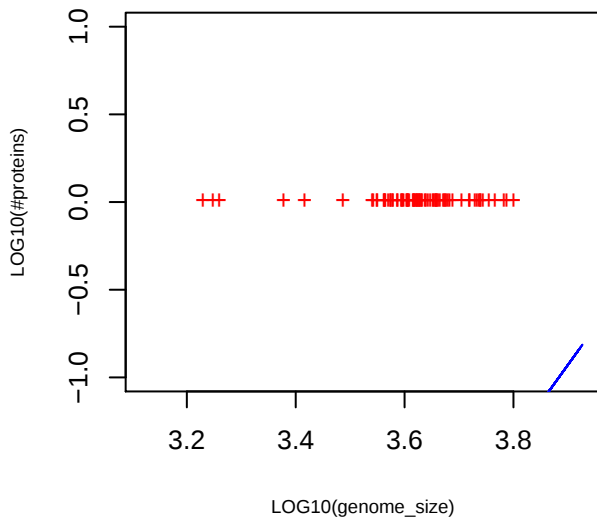
TIGR01696 deoB: phosphopentomutase

slope= -0.0038 p_value= 0.00019 intercept= 0.007 p_value= 6.1e-09

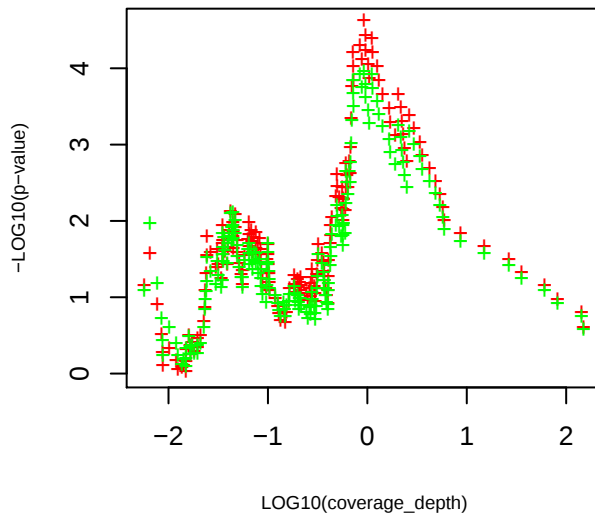


TIGR01696 deoB: phosphopentomutase

slope= 4.31 p_value= 2.1e-07 intercept= -17.73 p_value= 2.6e-09

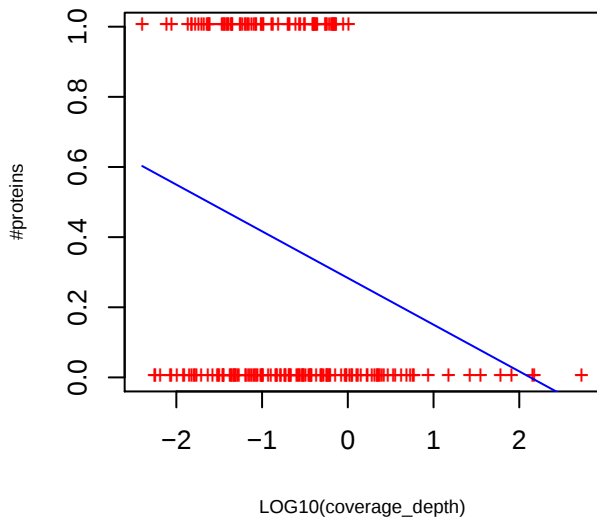


P-value curve ; red (unnorm), green (norm)



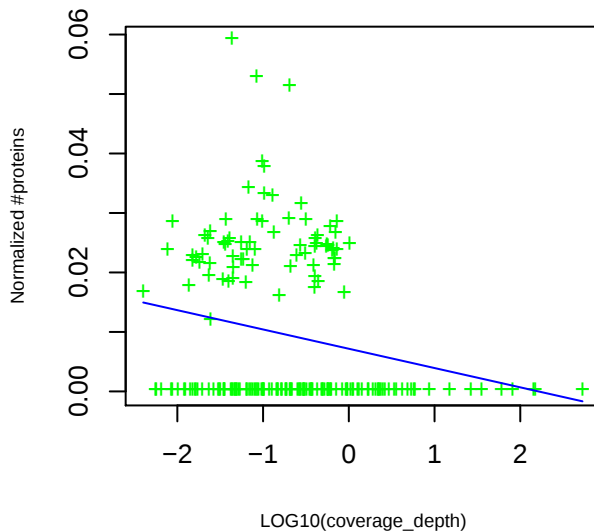
TIGR01228 hutU: urocanate hydratase

slope= -0.13 p_value= 0.00051 intercept= 0.28 p_value= 2.7e-10



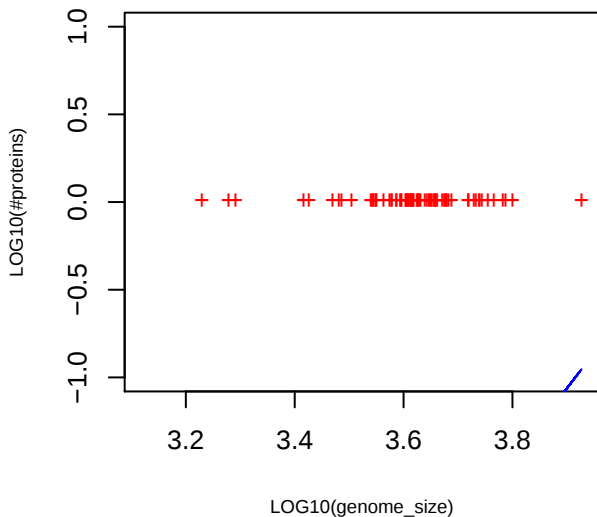
TIGR01228 hutU: urocanate hydratase

slope= -0.0032 p_value= 0.0017 intercept= 0.0072 p_value= 2.7e-09

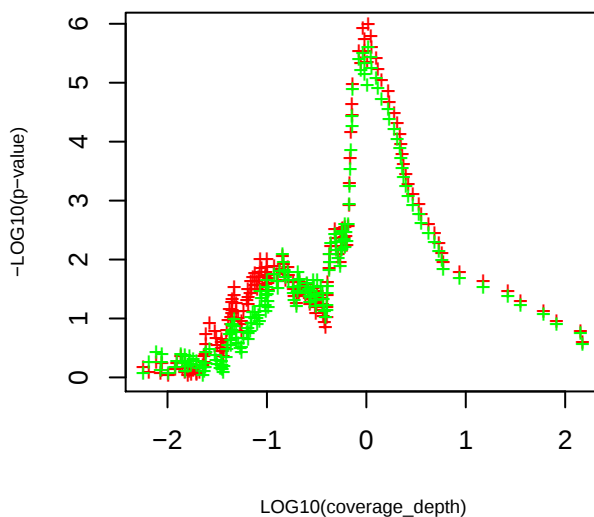


TIGR01228 hutU: urocanate hydratase

slope= 4.05 p_value= 1.0e-06 intercept= -16.84 p_value= 1.5e-08

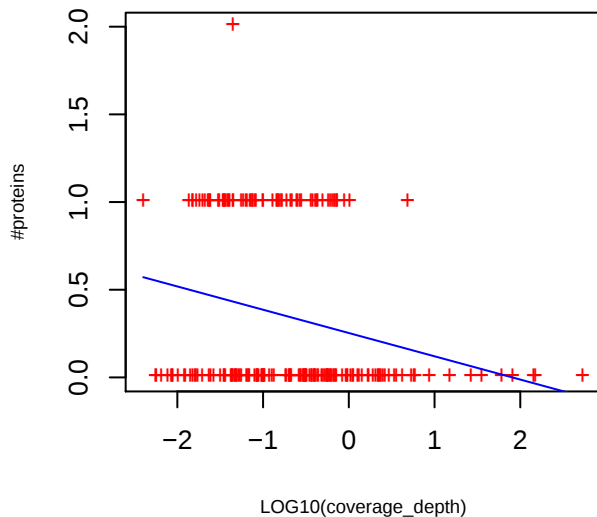


P-value curve ; red (unnorm), green (norm)



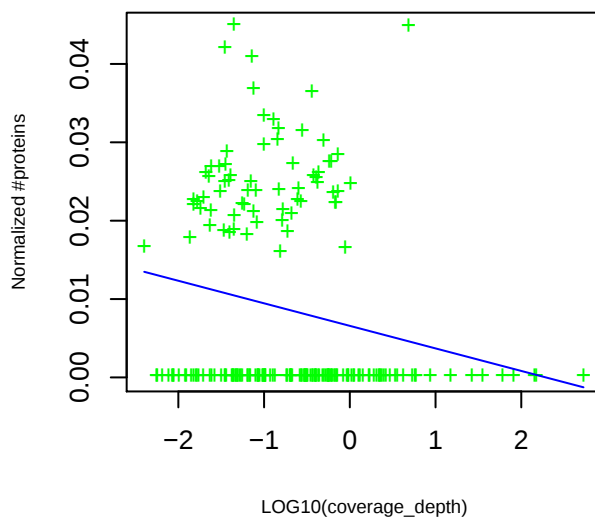
PF04304 DUF454: Protein of unknown function (DUF454)

slope= -0.13 p_value= 0.00056 intercept= 0.25 p_value= 1.4e-08



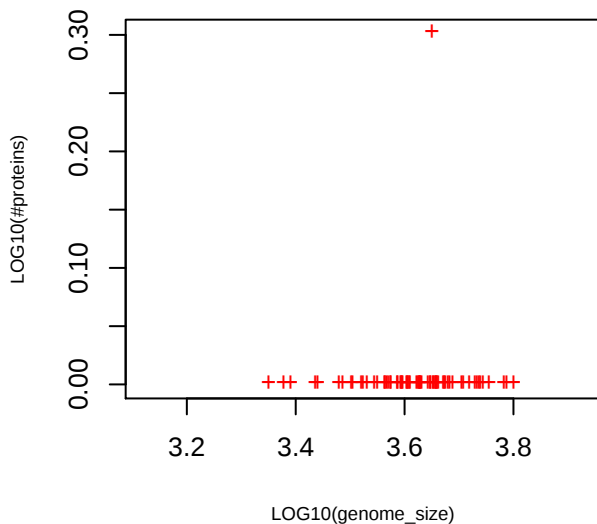
PF04304 DUF454: Protein of unknown function (DUF454)

slope= -0.0029 p_value= 0.0038 intercept= 0.0066 p_value= 1.3e-08

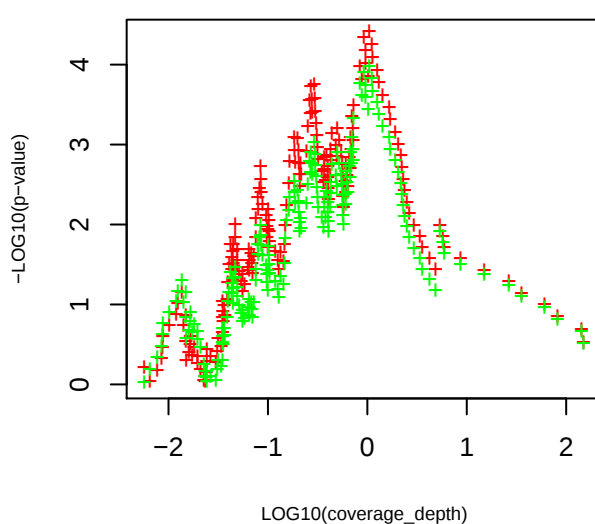


PF04304 DUF454: Protein of unknown function (DUF454)

slope= 3.60 p_value= 1.0e-05 intercept= -15.41 p_value= 1.4e-07

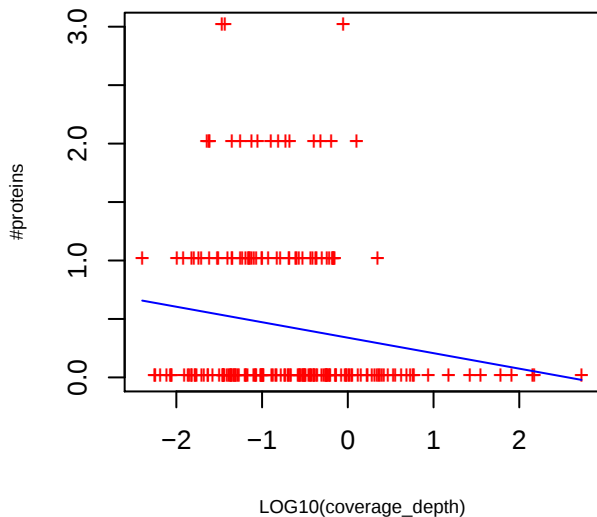


P-value curve ; red (unnorm), green (norm)



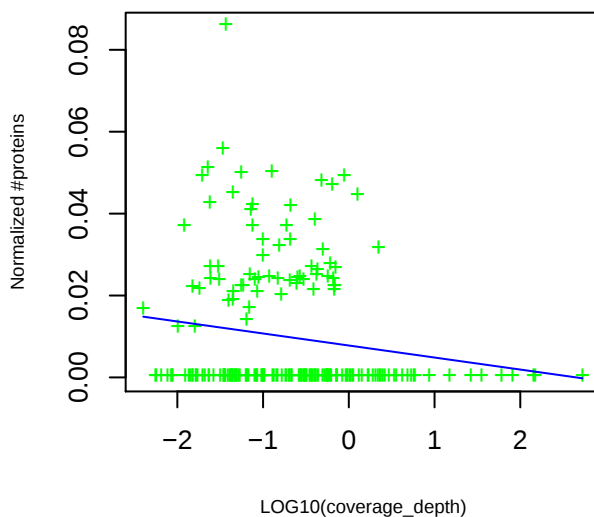
PF04965 GPW_gp25: Gene 25-like lysozyme

slope= -0.13 p_value= 0.018 intercept= 0.34 p_value= 1.6e-07



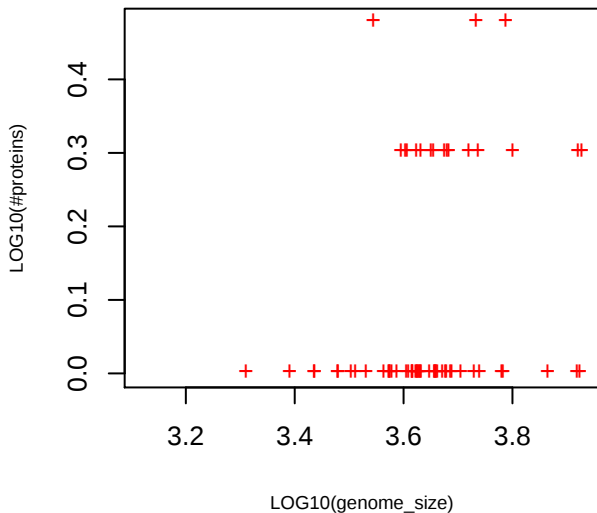
PF04965 GPW_gp25: Gene 25-like lysozyme

slope= -0.0029 p_value= 0.021 intercept= 0.0078 p_value= 1.4e-07

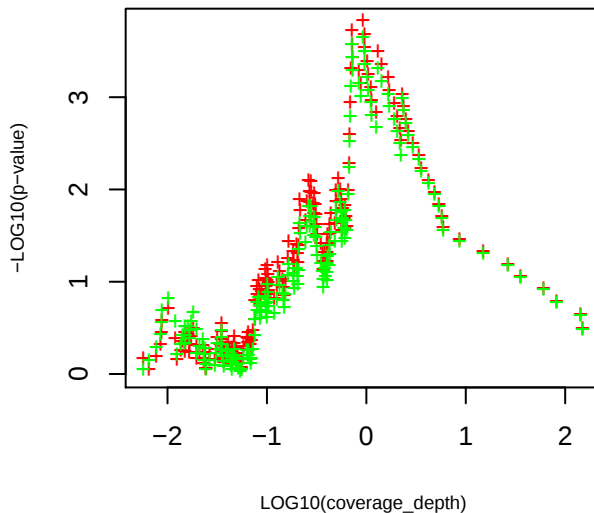


PF04965 GPW_gp25: Gene 25-like lysozyme

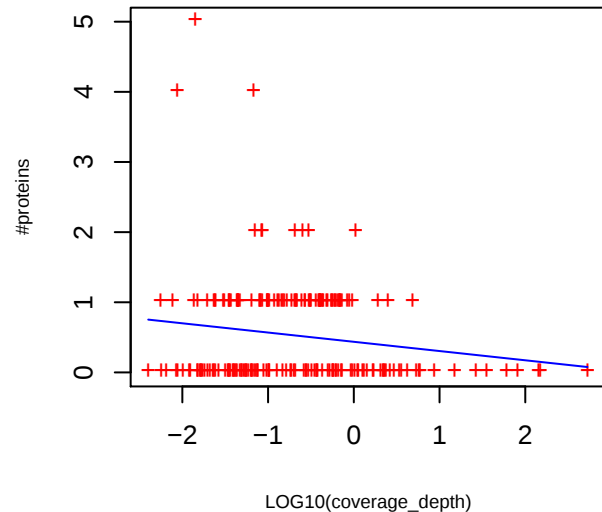
slope= 5.11 p_value= 2.1e-10 intercept= -20.79 p_value= 7e-13



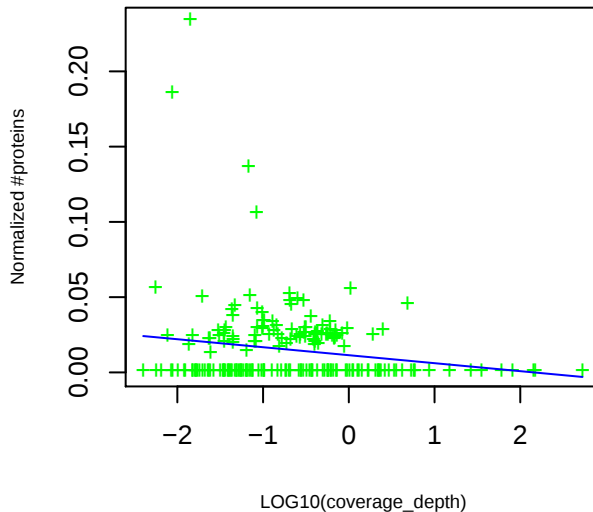
P-value curve ; red (unnorm), green (norm)



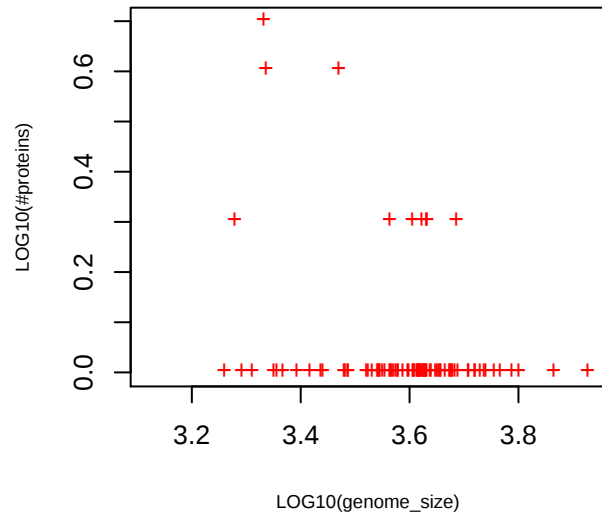
PF03334 PhaG_MnhG_YufB: Na⁺/H⁺ antiporter subunit
slope= -0.13 p_value= 0.025 intercept= 0.44 p_value= 3.5e-10



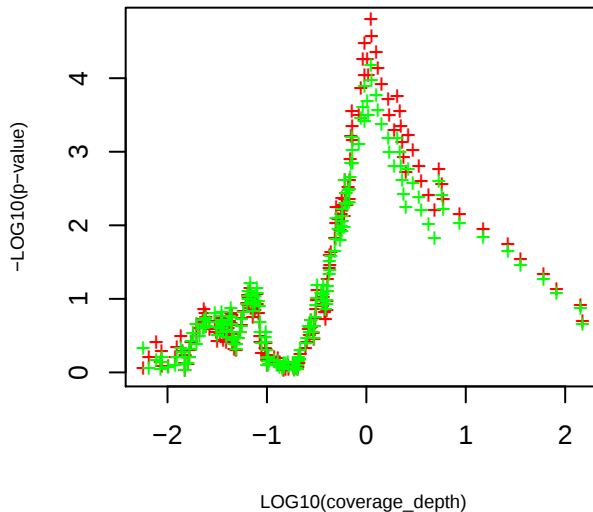
PF03334 PhaG_MnhG_YufB: Na⁺/H⁺ antiporter subunit
slope= -0.0053 p_value= 0.014 intercept= 0.011 p_value= 4.5e-06



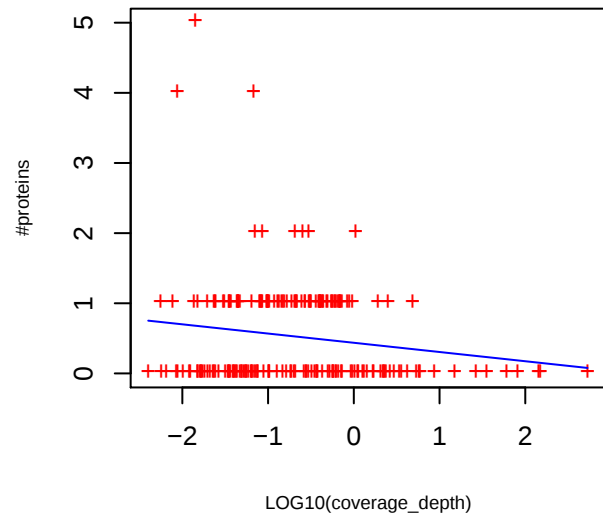
PF03334 PhaG_MnhG_YufB: Na⁺/H⁺ antiporter subunit
slope= 2.76 p_value= 0.0016 intercept= -12.01 p_value= 0.00012



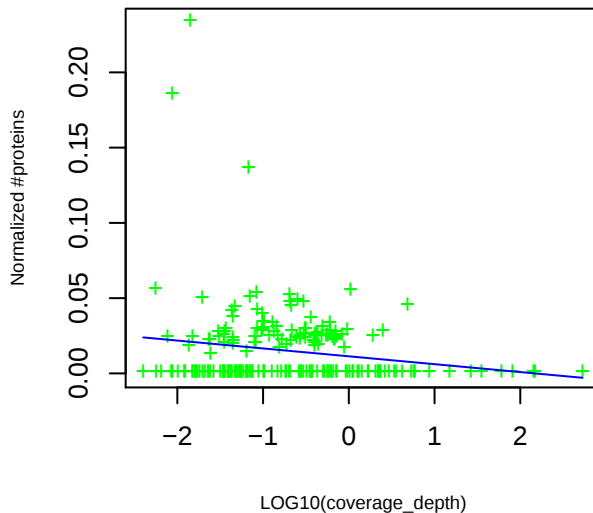
P-value curve ; red (unnorm), green (norm)



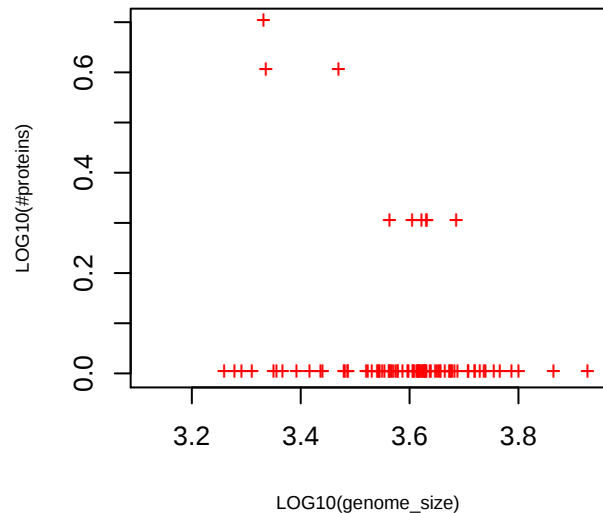
PF01899 MNHE: Na⁺/H⁺ ion antiporter subunit
 slope= -0.13 p_value= 0.024 intercept= 0.44 p_value= 2.4e-10



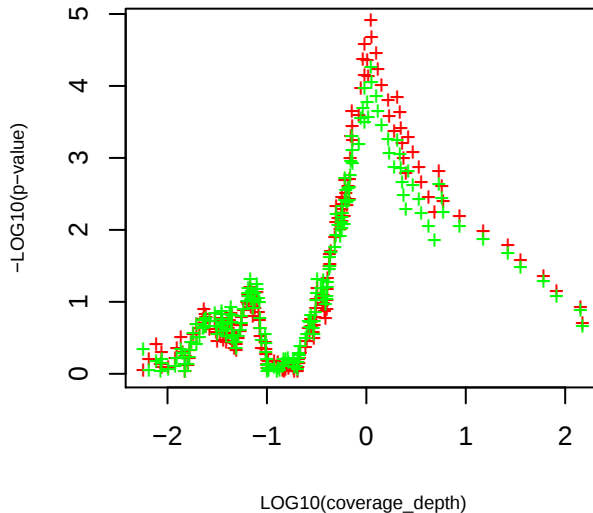
PF01899 MNHE: Na⁺/H⁺ ion antiporter subunit
 slope= -0.0052 p_value= 0.013 intercept= 0.011 p_value= 3.1e-06



PF01899 MNHE: Na⁺/H⁺ ion antiporter subunit
 slope= 2.79 p_value= 0.0014 intercept= -12.10 p_value= 0.00011

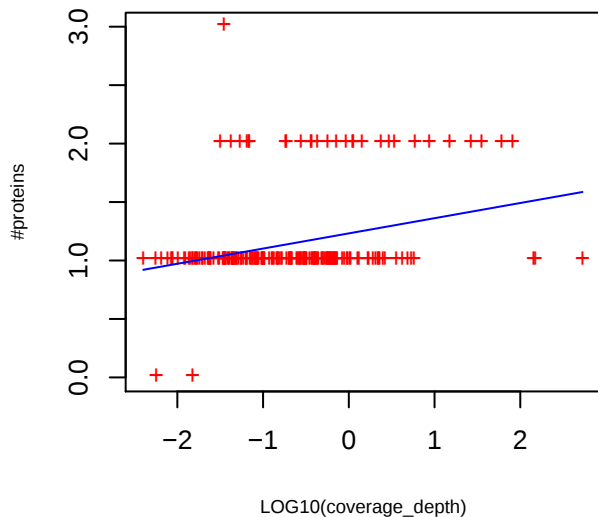


P-value curve ; red (unnorm), green (norm)



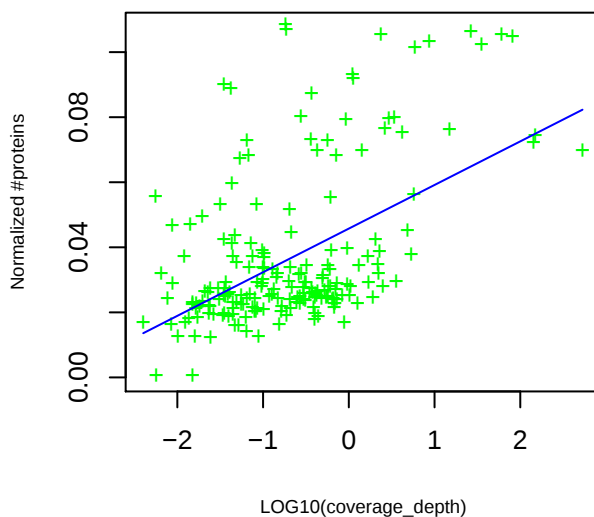
PF01725 Ham1p_like: Ham1 family

slope= 0.13 p_value= 2.3e-05 intercept= 1.23 p_value= 5.1e-89



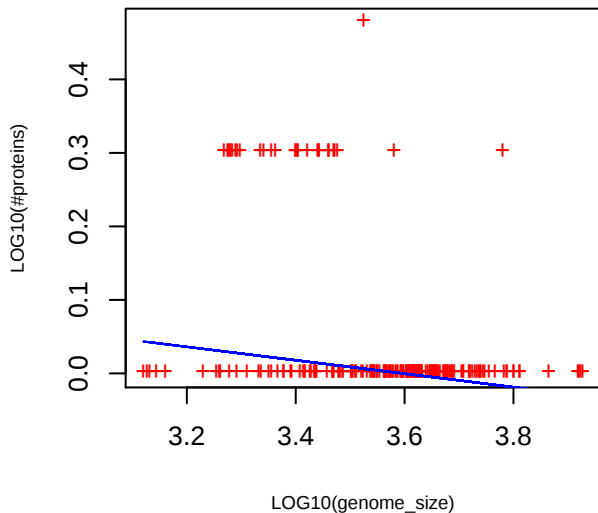
PF01725 Ham1p_like: Ham1 family

slope= 0.013 p_value= 3.3e-14 intercept= 0.046 p_value= 4.3e-62

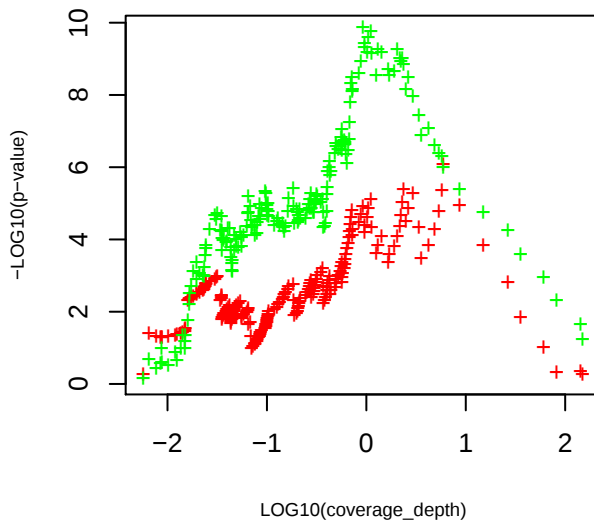


PF01725 Ham1p_like: Ham1 family

slope= -0.091 p_value= 0.62 intercept= 0.33 p_value= 0.62

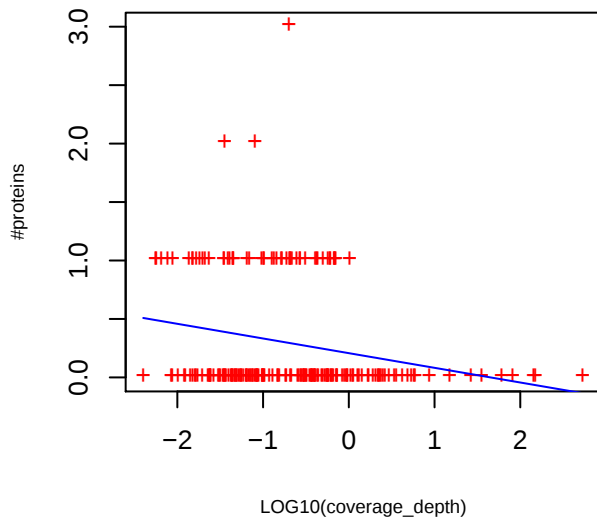


P-value curve ; red (unnorm), green (norm)



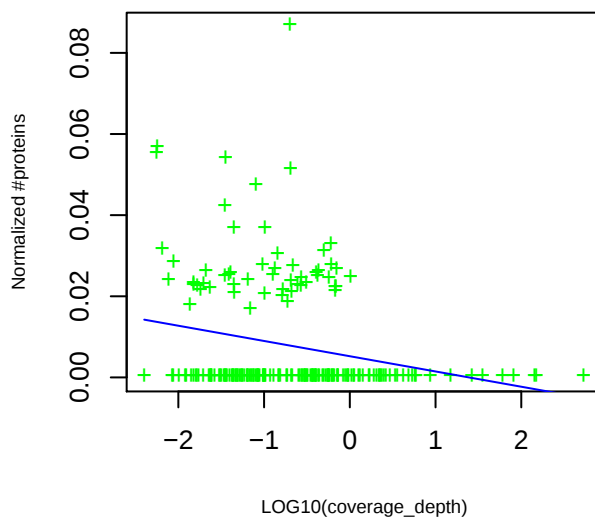
PF03975 CheD: CheD

slope= -0.13 p_value= 0.0019 intercept= 0.21 p_value= 7.1e-06



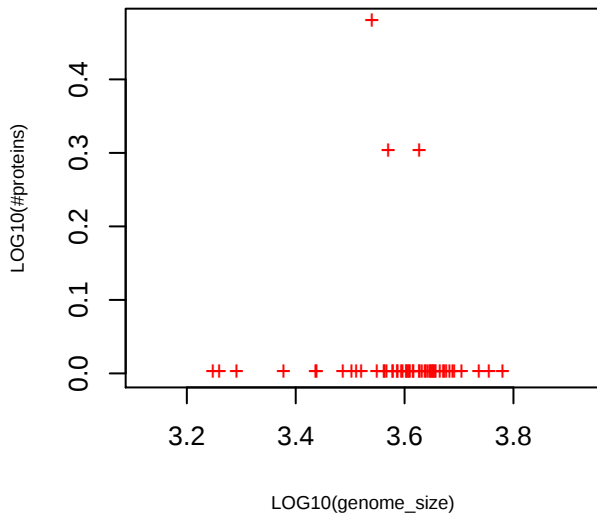
PF03975 CheD: CheD

slope= -0.0038 p_value= 0.00088 intercept= 0.0052 p_value= 4.8e-05

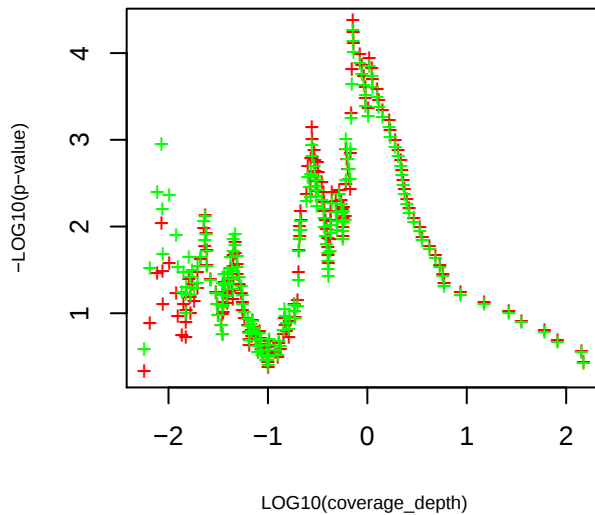


PF03975 CheD: CheD

slope= 1.91 p_value= 0.015 intercept= -9.68 p_value= 0.00057

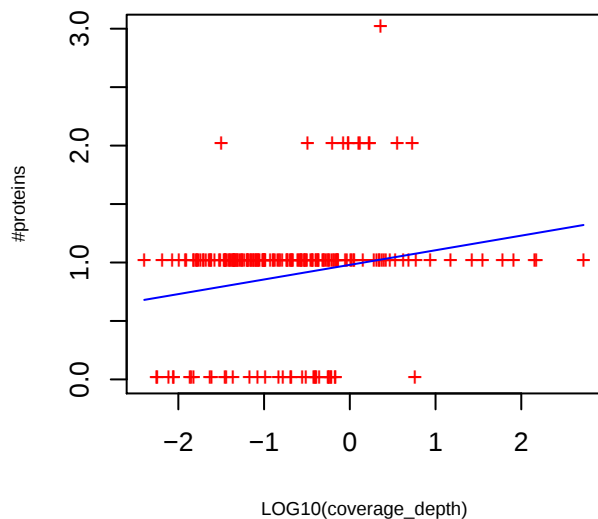


P-value curve ; red (unnorm), green (norm)



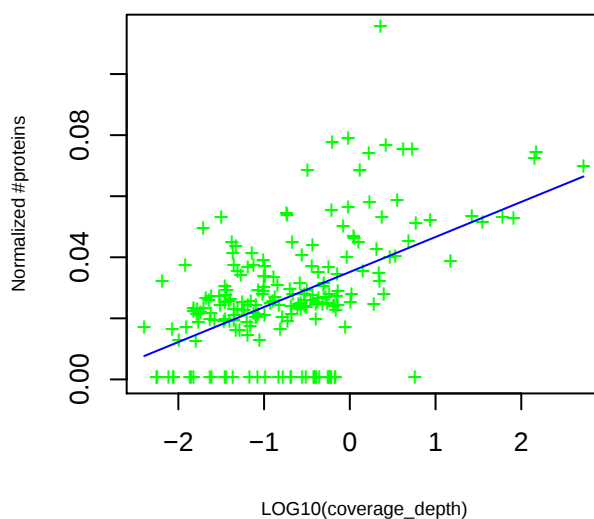
TIGR01853 lipid_A_lpxD: UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase

slope= 0.13 p_value= 0.0015 intercept= 0.98 p_value= 1.5e-55



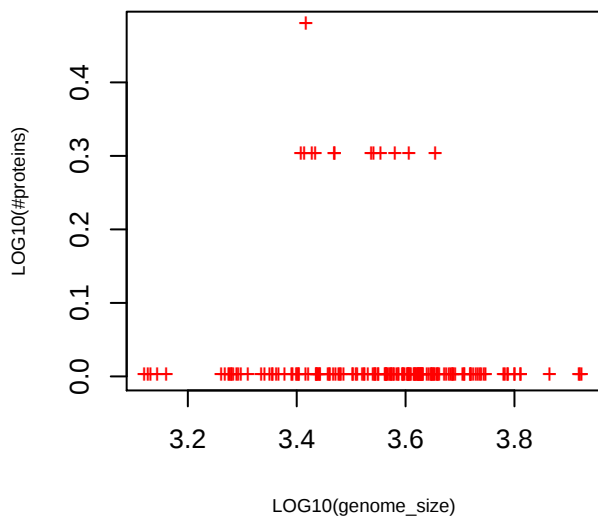
TIGR01853 lipid_A_lpxD: UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase

slope= 0.011 p_value= 4.5e-15 intercept= 0.035 p_value= 9.3e-58

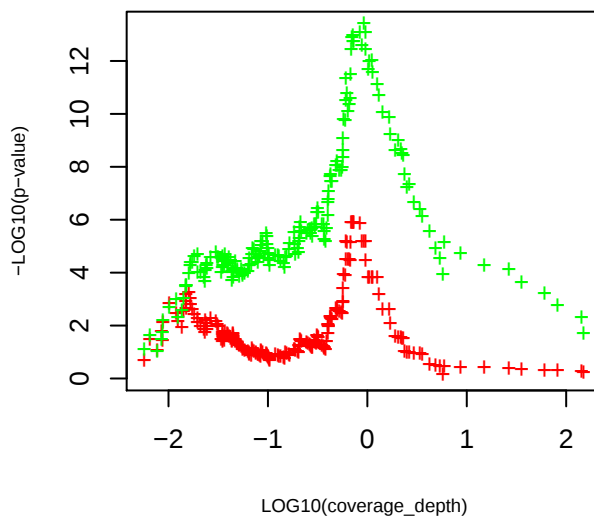


TIGR01853 lipid_A_lpxD: UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase

slope= 0.47 p_value= 0.49 intercept= -2.34 p_value= 0.33

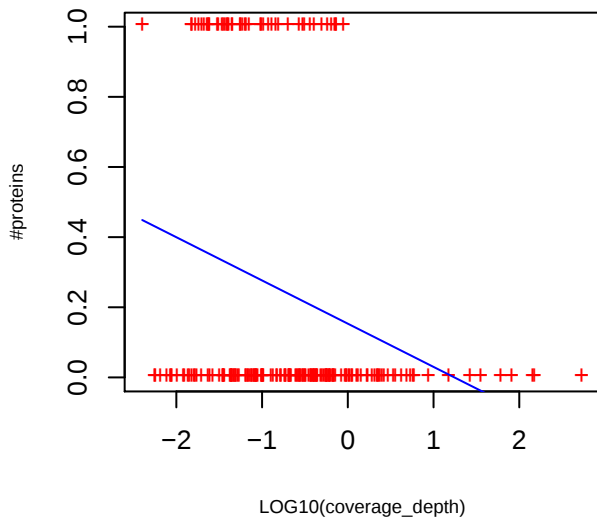


P-value curve ; red (unnorm), green (norm)



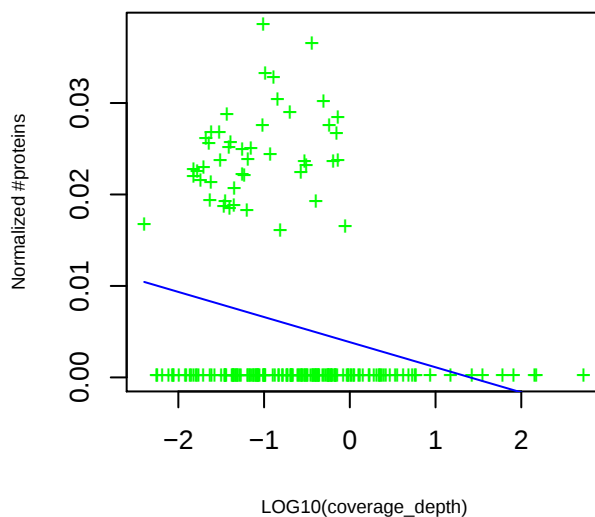
TIGR01419 nitro_reg_IIA: PTS IIA-like nitrogen-regulatory protein PtsN

slope= -0.12 p_value= 0.00025 intercept= 0.15 p_value= 5.9e-05



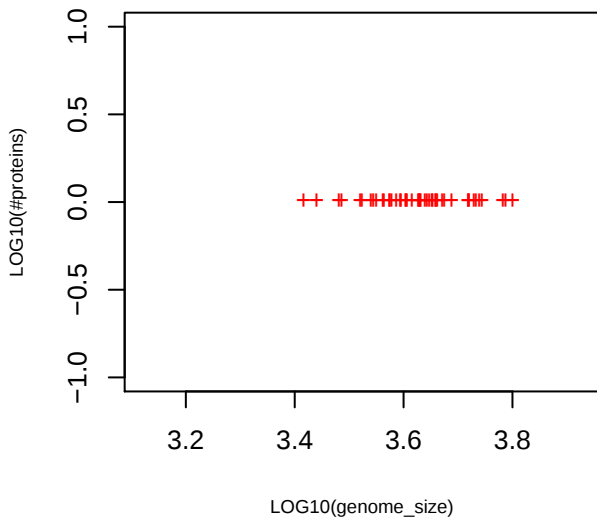
TIGR01419 nitro_reg_IIA: PTS IIA-like nitrogen-regulatory protein PtsN

slope= -0.0027 p_value= 0.0010 intercept= 0.0039 p_value= 5.2e-05

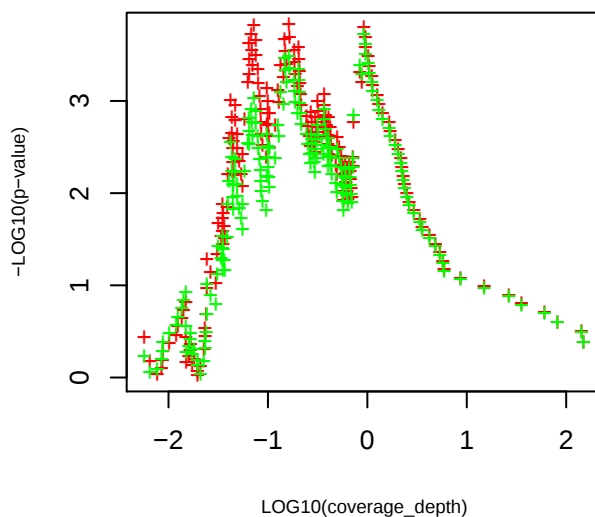


TIGR01419 nitro_reg_IIA: PTS IIA-like nitrogen-regulatory protein PtsN

slope= 2.92 p_value= 7.5e-05 intercept= -13.39 p_value= 4.3e-07

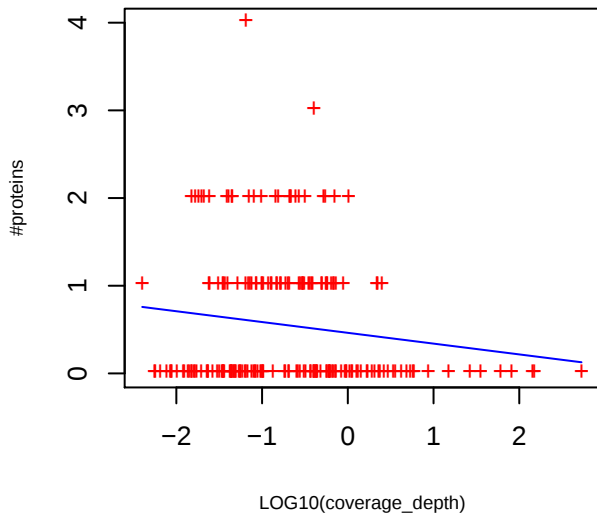


P-value curve ; red (unnorm), green (norm)



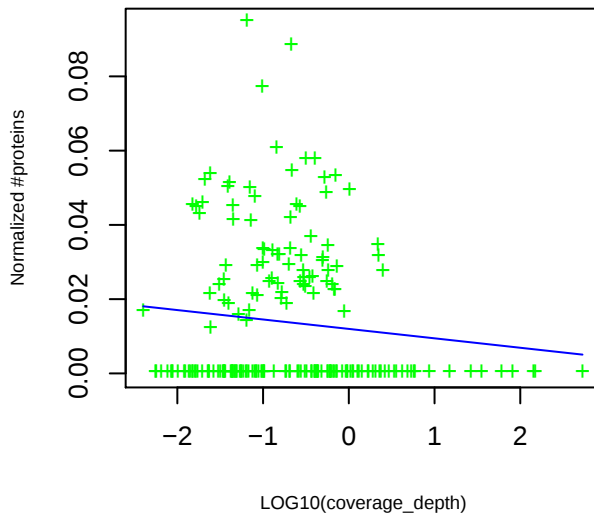
TIGR00754 bfr: bacterioferritin

slope= -0.12 p_value= 0.046 intercept= 0.46 p_value= 2.2e-10



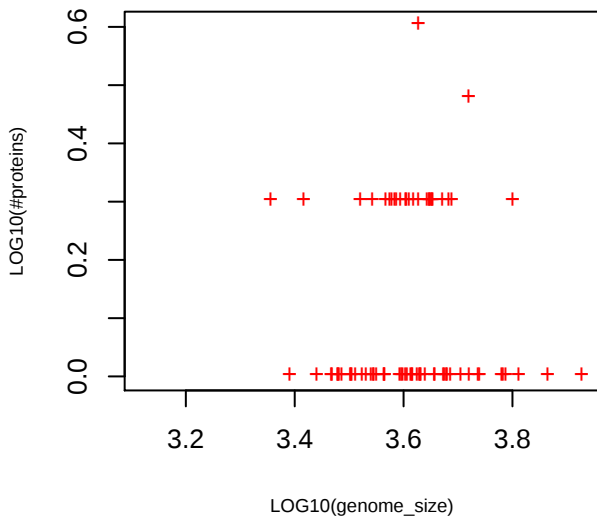
TIGR00754 bfr: bacterioferritin

slope= -0.0025 p_value= 0.11 intercept= 0.012 p_value= 1.7e-10

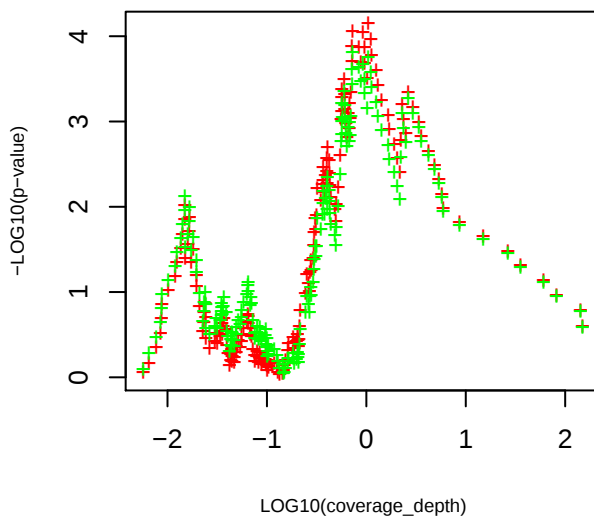


TIGR00754 bfr: bacterioferritin

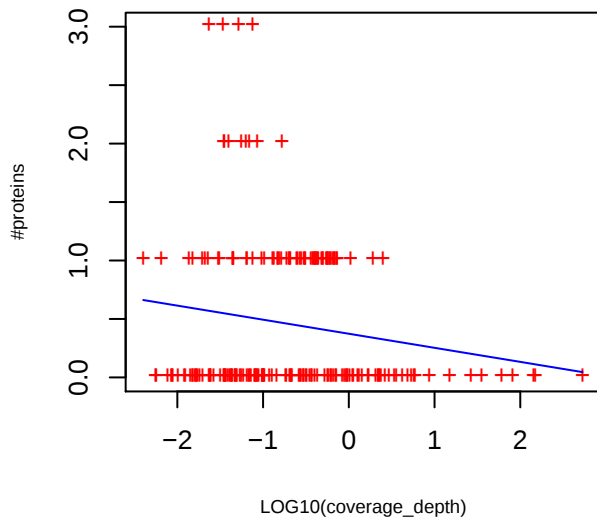
slope= 4.04 p_value= 2.8e-06 intercept= -16.71 p_value= 6.5e-08



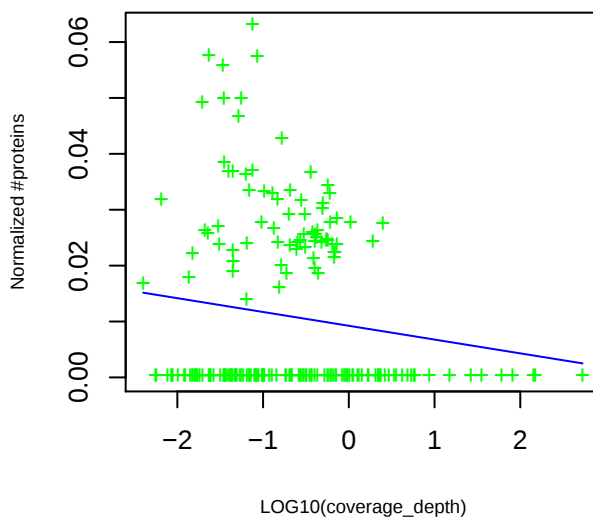
P-value curve ; red (unnorm), green (norm)



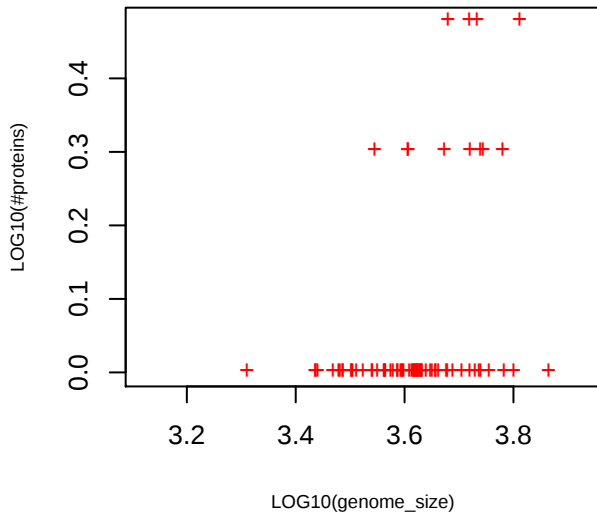
TIGR03177 pilus_cpaB: Flp pilus assembly protein CpaB
 slope= -0.12 p_value= 0.025 intercept= 0.37 p_value= 3.1e-09



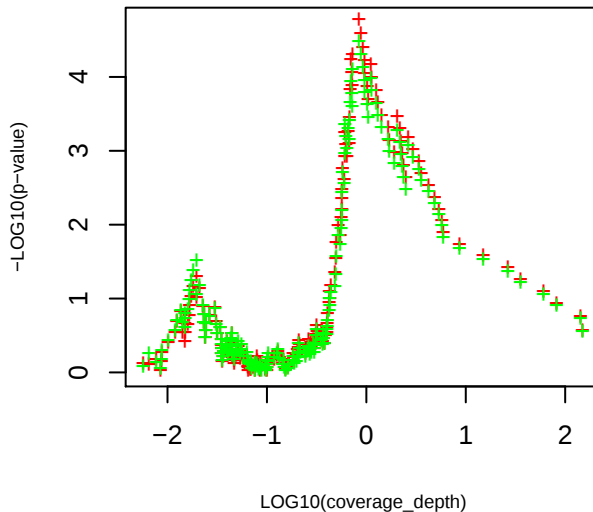
TIGR03177 pilus_cpaB: Flp pilus assembly protein CpaB
 slope= -0.0025 p_value= 0.046 intercept= 0.0092 p_value= 2.7e-10



TIGR03177 pilus_cpaB: Flp pilus assembly protein CpaB
 slope= 4.18 p_value= 6.4e-07 intercept= -17.31 p_value= 9.4e-09

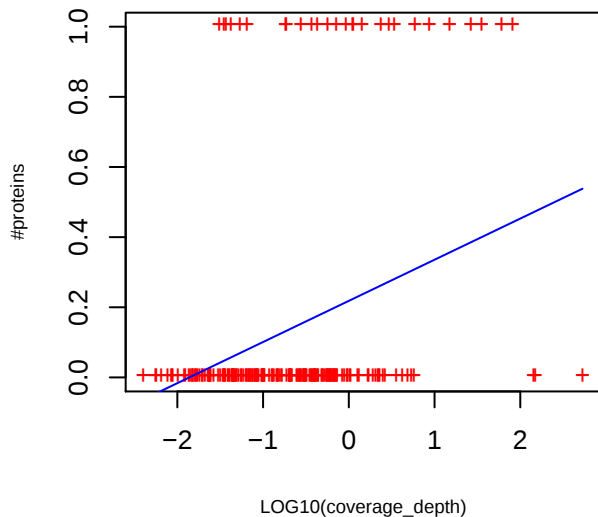


P-value curve ; red (unnorm), green (norm)



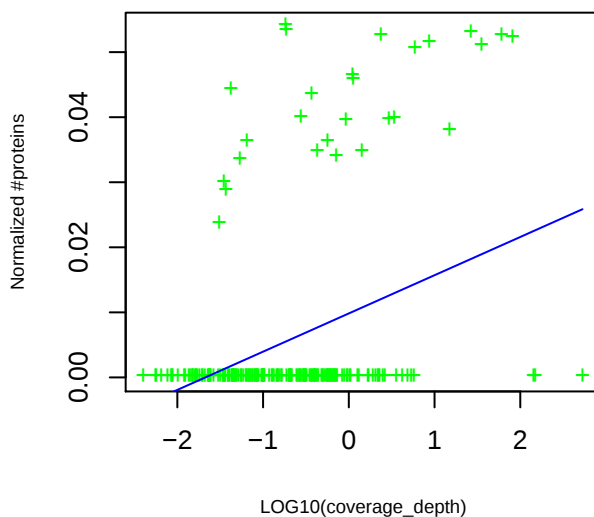
PF08936 CsoSCA: Carboxysome Shell Carbonic Anhydrase

slope= 0.12 p_value= 1.4e-05 intercept= 0.22 p_value= 5.3e-12



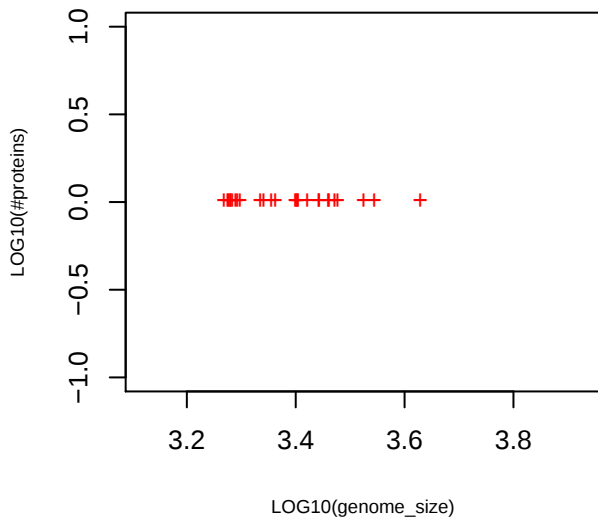
PF08936 CsoSCA: Carboxysome Shell Carbonic Anhydrase

slope= 0.0059 p_value= 3.4e-07 intercept= 0.0098 p_value= 3.1e-13

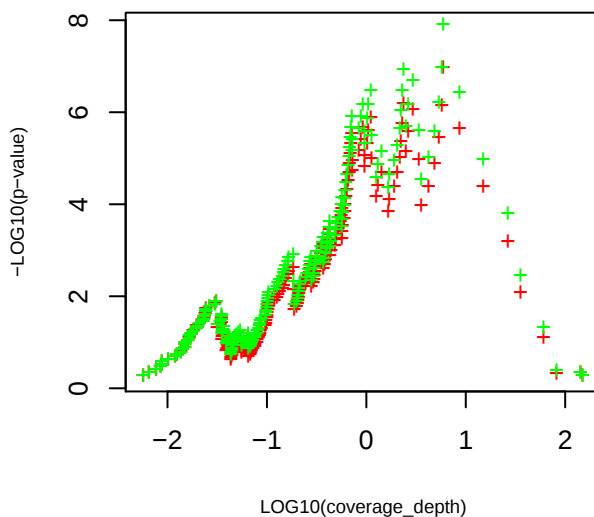


PF08936 CsoSCA: Carboxysome Shell Carbonic Anhydrase

slope= -3.31 p_value= 1.4e-08 intercept= 8.27 p_value= 4.4e-05

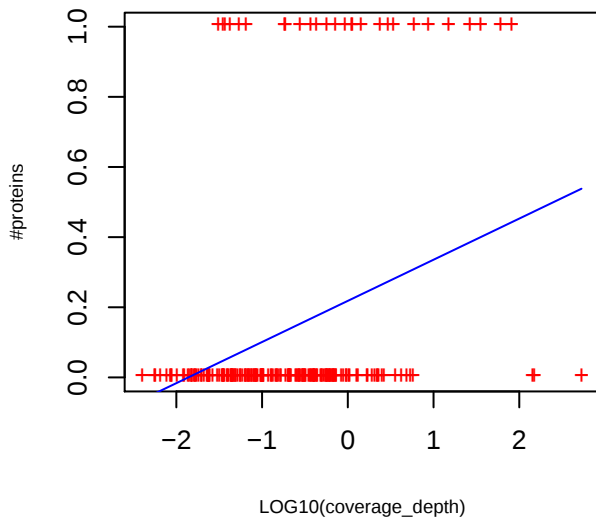


P-value curve ; red (unnorm), green (norm)



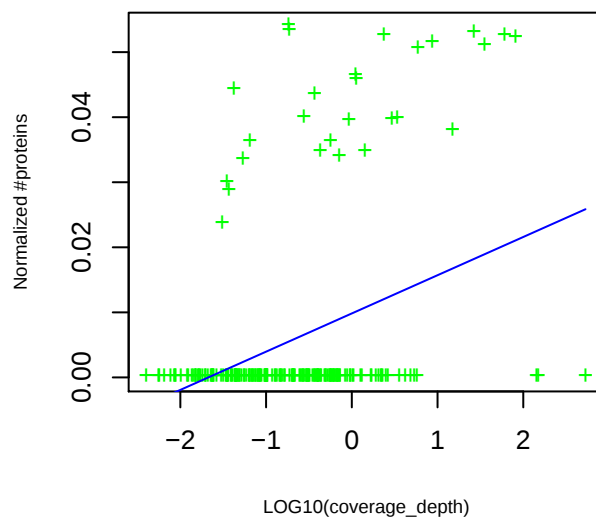
TIGR02701 shell_carb_anhy: carboxysome shell carbonic anhydrase

slope= 0.12 p_value= 1.4e-05 intercept= 0.22 p_value= 5.3e-12



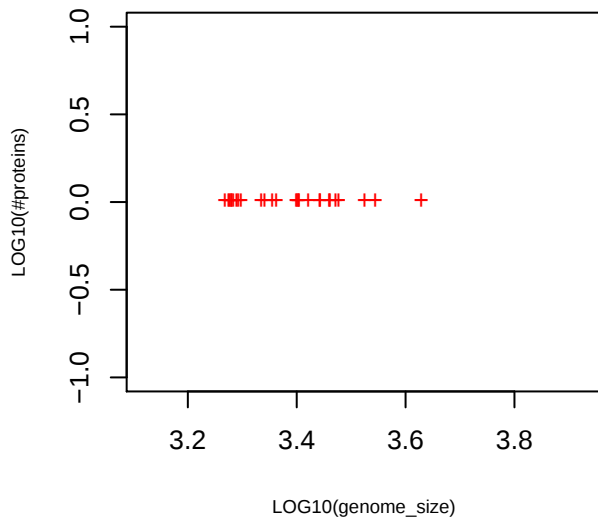
TIGR02701 shell_carb_anhy: carboxysome shell carbonic anhydrase

slope= 0.0059 p_value= 3.4e-07 intercept= 0.0098 p_value= 3.1e-13

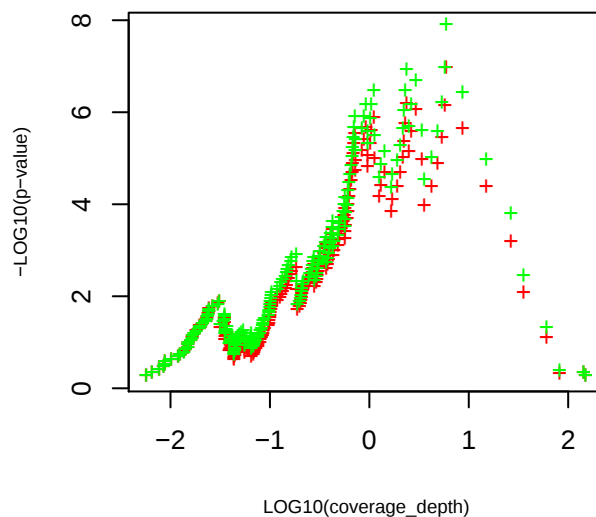


TIGR02701 shell_carb_anhy: carboxysome shell carbonic anhydrase

slope= -3.31 p_value= 1.4e-08 intercept= 8.27 p_value= 4.4e-05

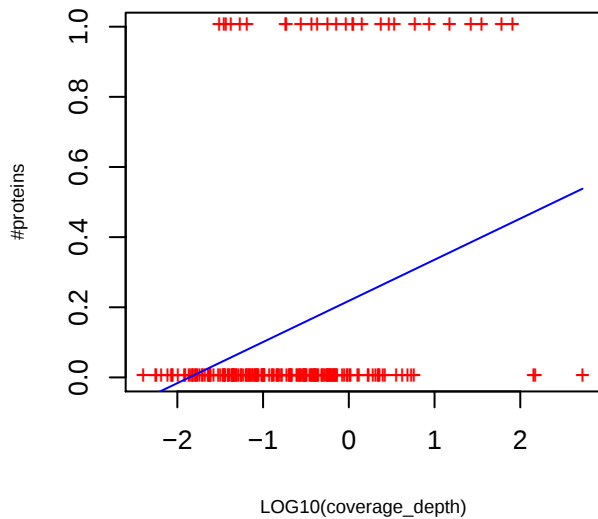


P-value curve ; red (unnorm), green (norm)



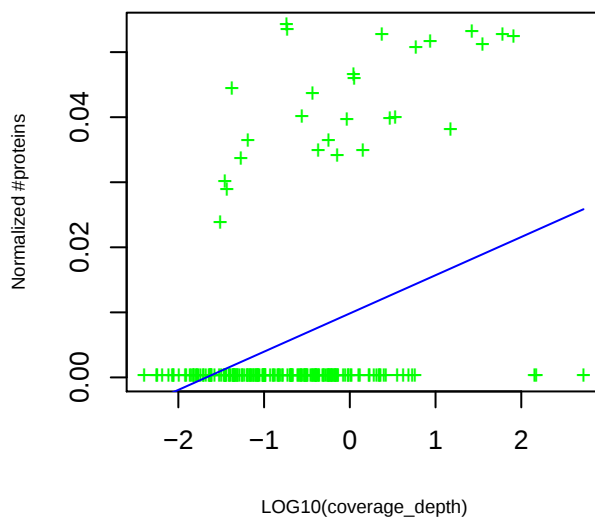
TIGR02703 carboxysome_A: carboxysome peptide A

slope= 0.12 p_value= 1.4e-05 intercept= 0.22 p_value= 5.3e-12



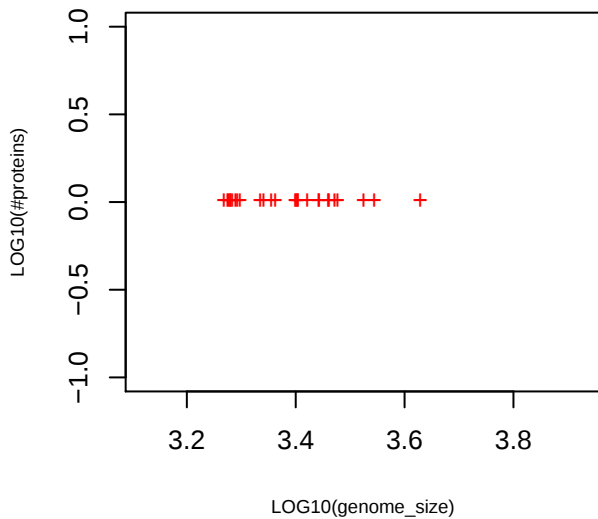
TIGR02703 carboxysome_A: carboxysome peptide A

slope= 0.0059 p_value= 3.4e-07 intercept= 0.0098 p_value= 3.1e-13

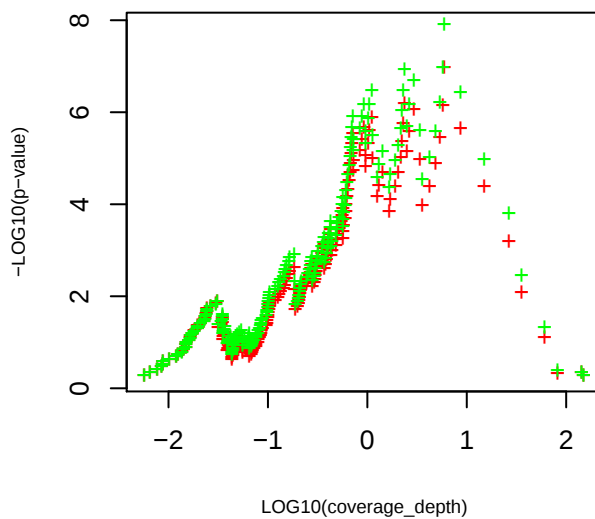


TIGR02703 carboxysome_A: carboxysome peptide A

slope= -3.31 p_value= 1.4e-08 intercept= 8.27 p_value= 4.4e-05

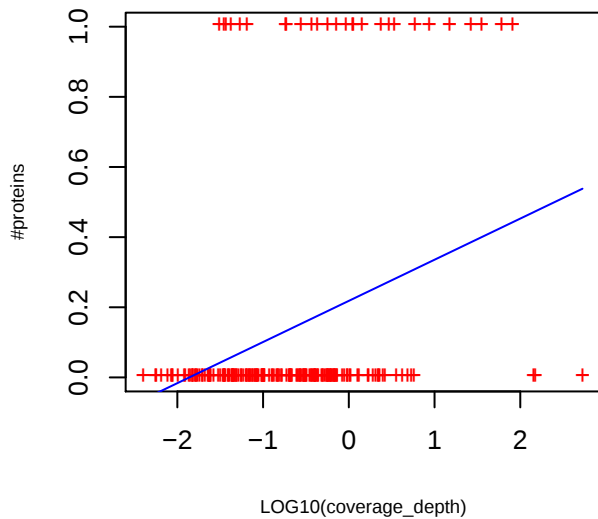


P-value curve ; red (unnorm), green (norm)



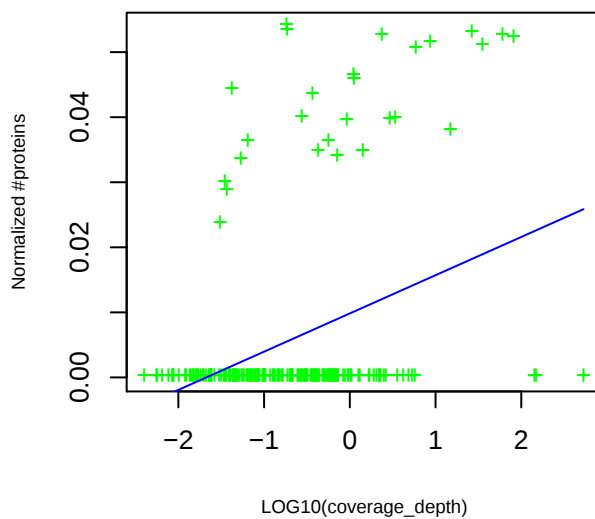
TIGR02704 carboxysome_B: carboxysome peptide B

slope= 0.12 p_value= 1.4e-05 intercept= 0.22 p_value= 5.3e-12



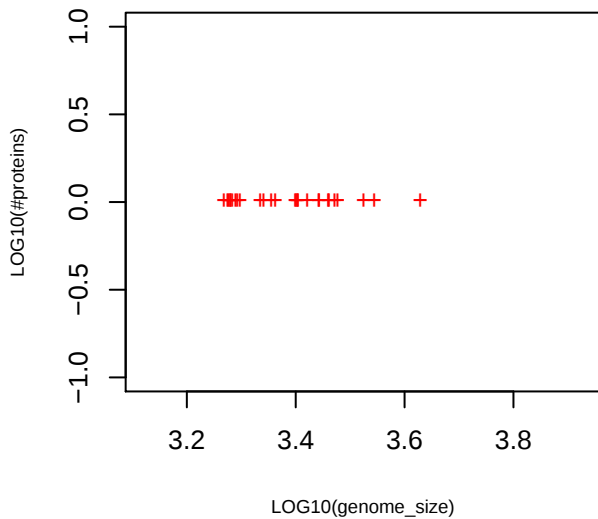
TIGR02704 carboxysome_B: carboxysome peptide B

slope= 0.0059 p_value= 3.4e-07 intercept= 0.0098 p_value= 3.1e-13

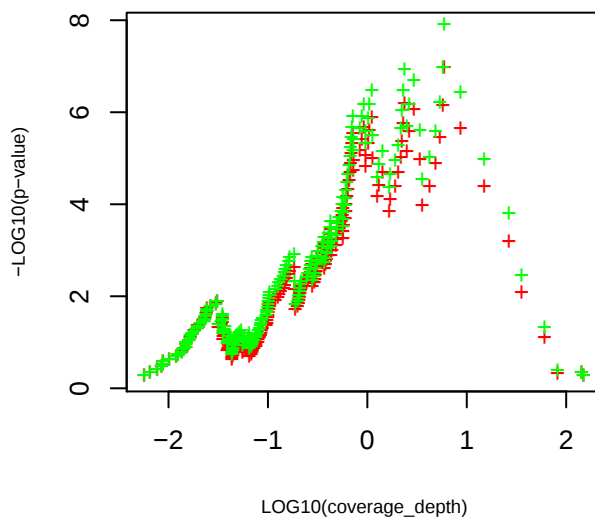


TIGR02704 carboxysome_B: carboxysome peptide B

slope= -3.31 p_value= 1.4e-08 intercept= 8.27 p_value= 4.4e-05

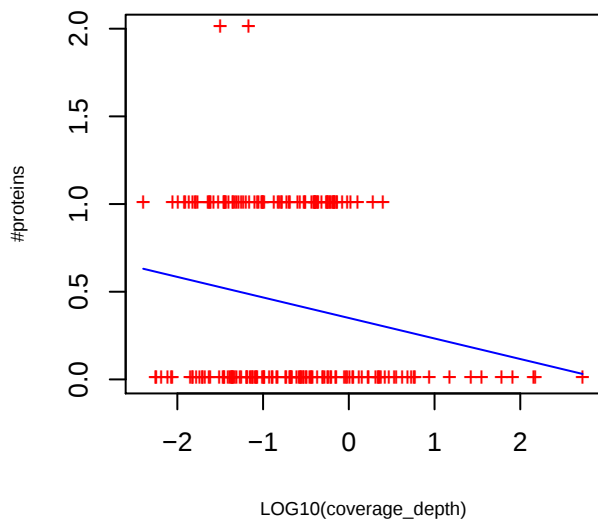


P-value curve ; red (unnorm), green (norm)



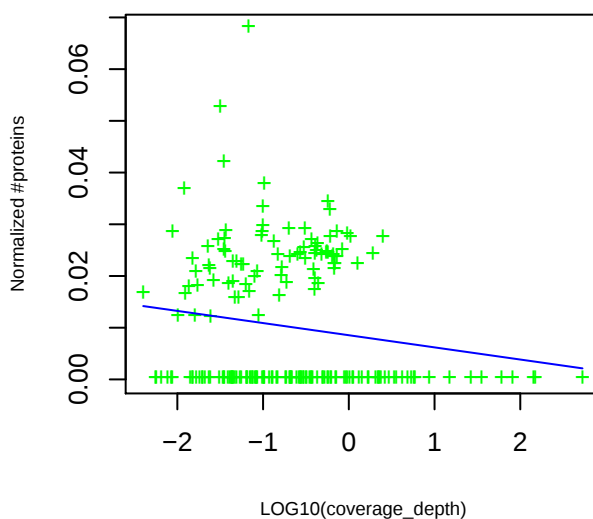
PF04095 NAPRTase: Nicotinate phosphoribosyltransferase (NAPRTase) family

slope= -0.12 p_value= 0.0043 intercept= 0.35 p_value= 8.5e-13



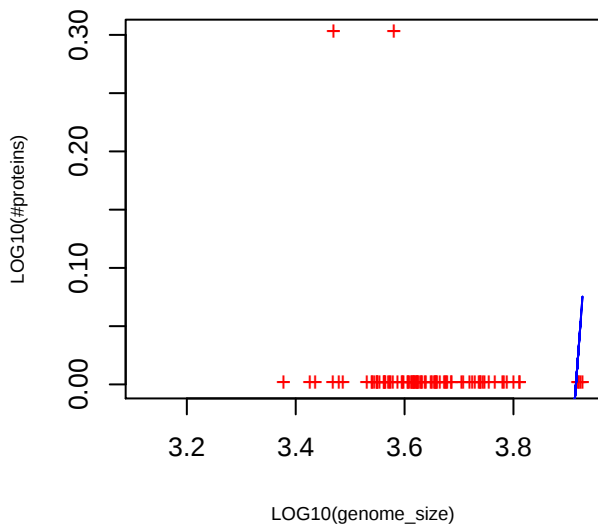
PF04095 NAPRTase: Nicotinate phosphoribosyltransferase (NAPRTase) family

slope= -0.0024 p_value= 0.024 intercept= 0.0085 p_value= 5.5e-12

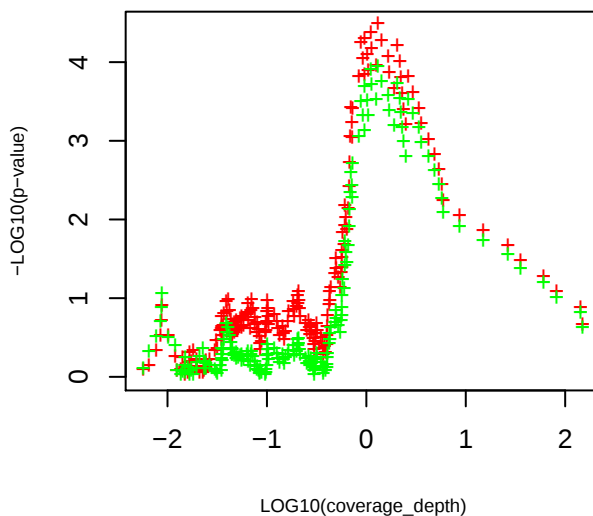


PF04095 NAPRTase: Nicotinate phosphoribosyltransferase (NAPRTase) family

slope= 6.26 p_value= 1.1e-14 intercept= -24.49 p_value= 4.5e-17

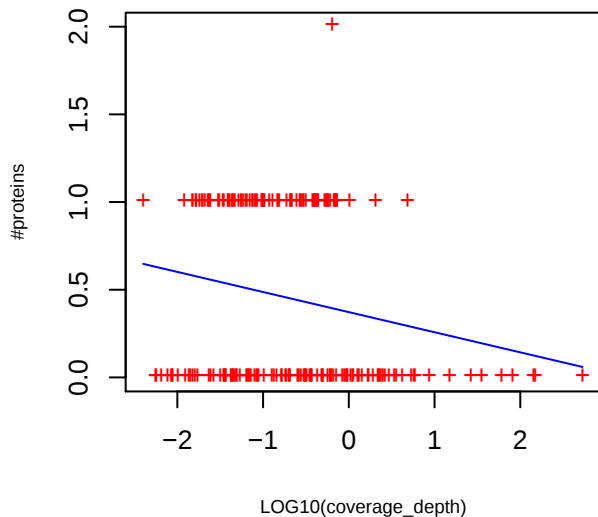


P-value curve ; red (unnorm), green (norm)



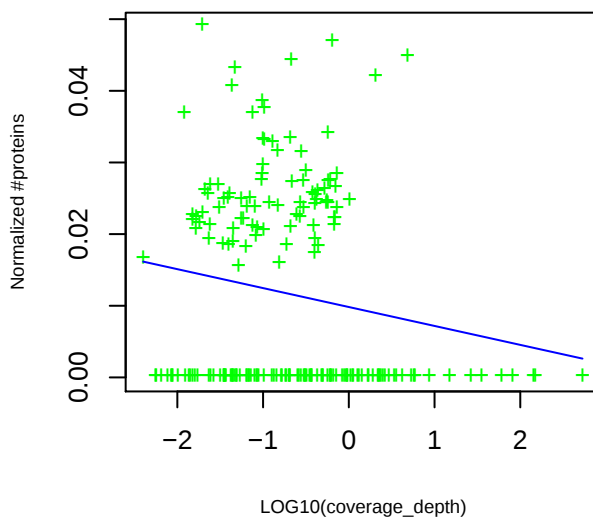
TIGR00553 pabB: aminodeoxychorismate synthase, component I

slope= -0.11 p_value= 0.0045 intercept= 0.37 p_value= 2.2e-14



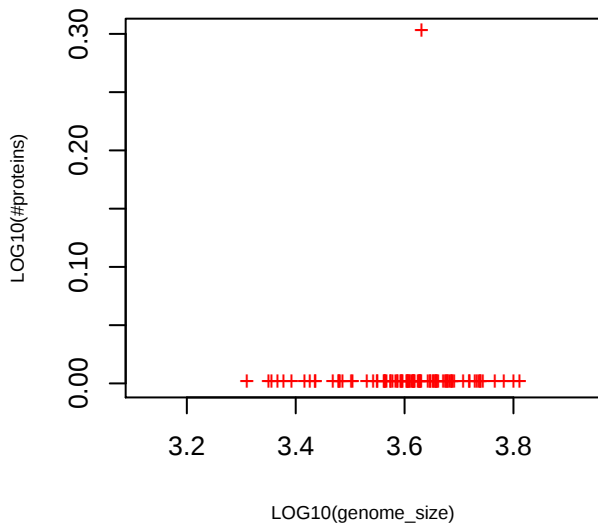
TIGR00553 pabB: aminodeoxychorismate synthase, component I

slope= -0.0026 p_value= 0.017 intercept= 0.0098 p_value= 1.5e-13

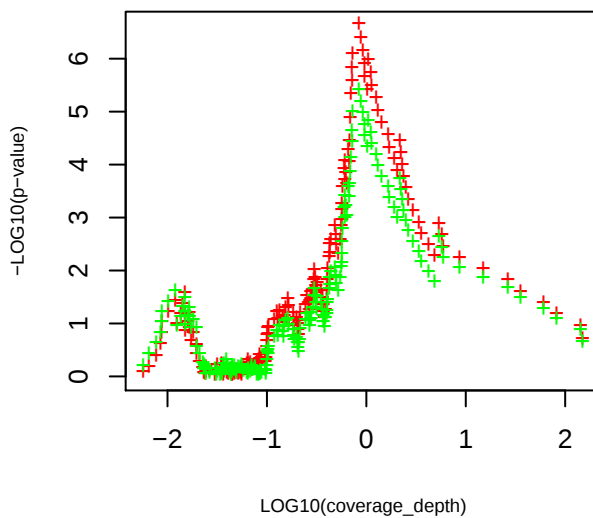


TIGR00553 pabB: aminodeoxychorismate synthase, component I

slope= 3.81 p_value= 8.7e-06 intercept= -15.71 p_value= 2.9e-07

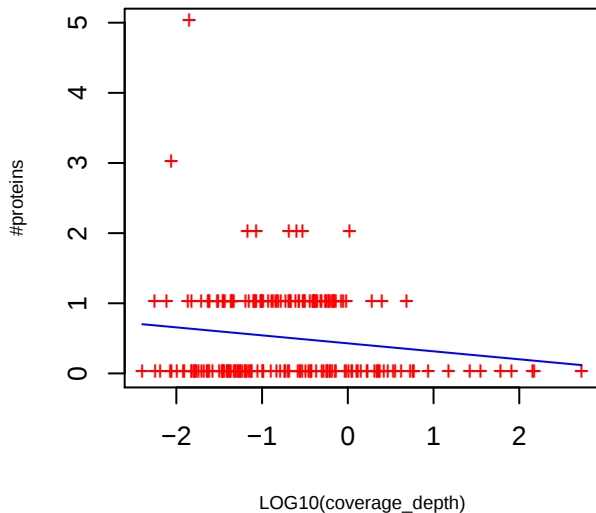


P-value curve ; red (unnorm), green (norm)



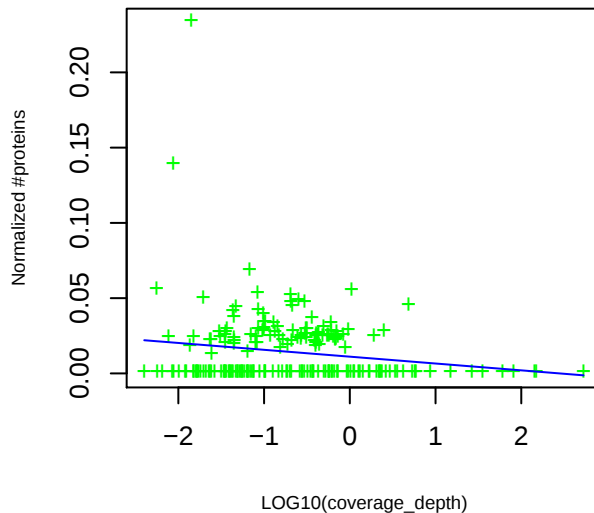
PF04066 MrpF_PhaF: Multiple resistance and pH regulation protein F (MrpF / PhaF)

slope= -0.11 p_value= 0.032 intercept= 0.43 p_value= 1.3e-11



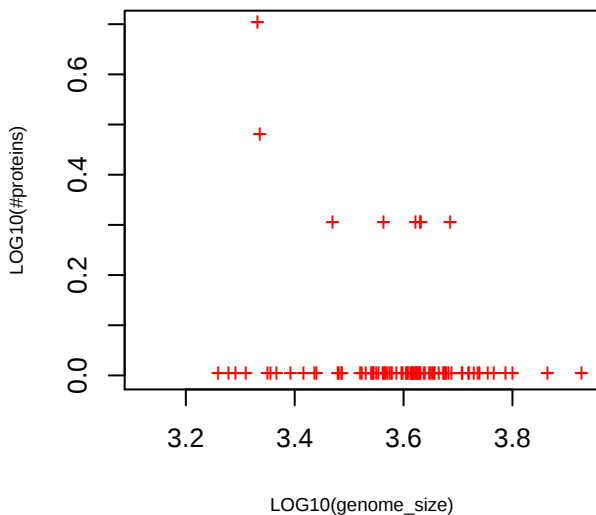
PF04066 MrpF_PhaF: Multiple resistance and pH regulation protein F (MrpF / PhaF)

slope= -0.0046 p_value= 0.017 intercept= 0.011 p_value= 4.5e-07

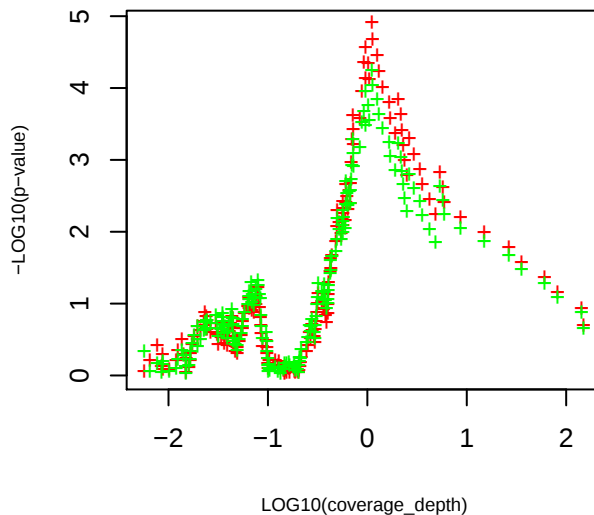


PF04066 MrpF_PhaF: Multiple resistance and pH regulation protein F (MrpF / PhaF)

slope= 2.80 p_value= 0.0014 intercept= -12.12 p_value= 0.00010

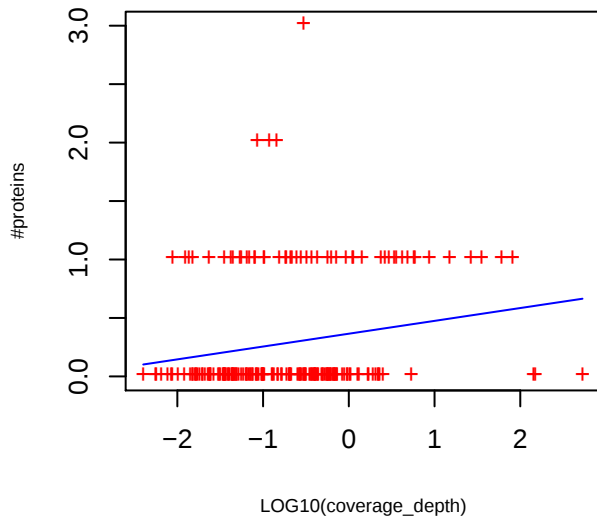


P-value curve ; red (unnorm), green (norm)



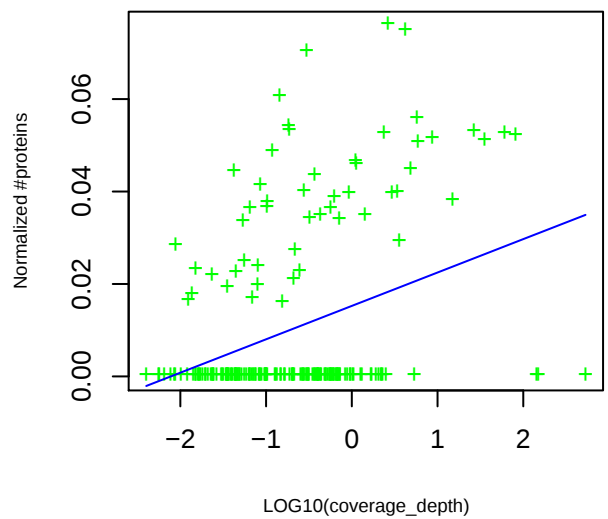
PF06039 Mqo: Malate:quinone oxidoreductase (Mqo)

slope= 0.11 p_value= 0.0076 intercept= 0.37 p_value= 1.5e-13



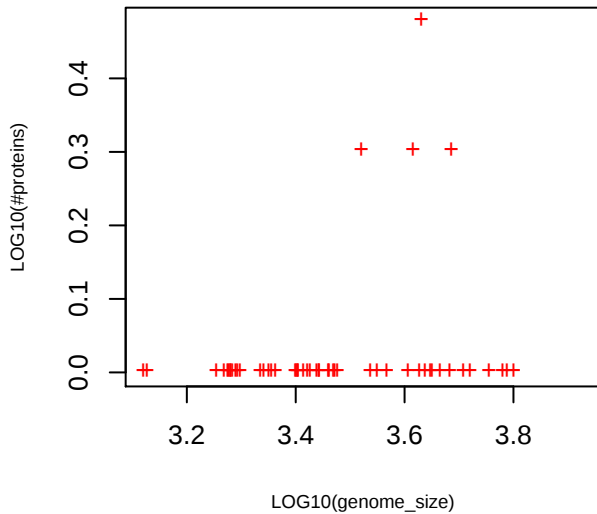
PF06039 Mqo: Malate:quinone oxidoreductase (Mqo)

slope= 0.0072 p_value= 7.4e-07 intercept= 0.015 p_value= 5e-18

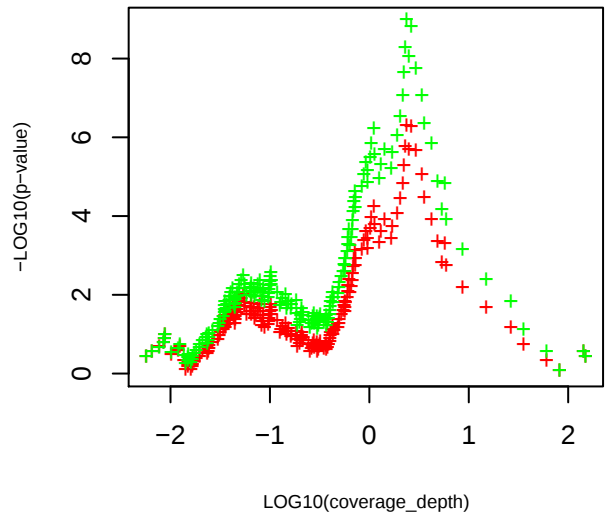


PF06039 Mqo: Malate:quinone oxidoreductase (Mqo)

slope= -2.95 p_value= 0.00012 intercept= 7.52 p_value= 0.0054

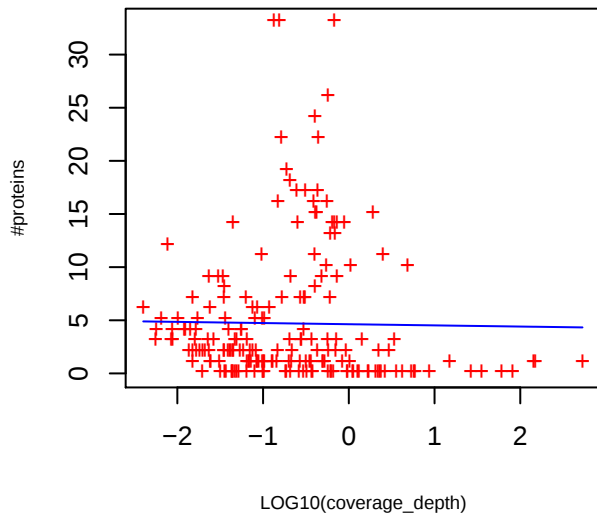


P-value curve ; red (unnorm), green (norm)



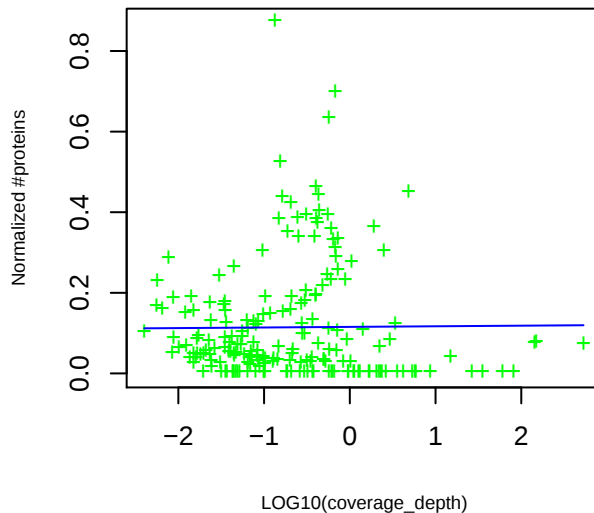
PF08402 TOBE_2: TOBE domain

slope= -0.11 p_value= 0.83 intercept= 4.63 p_value= 2.1e-13



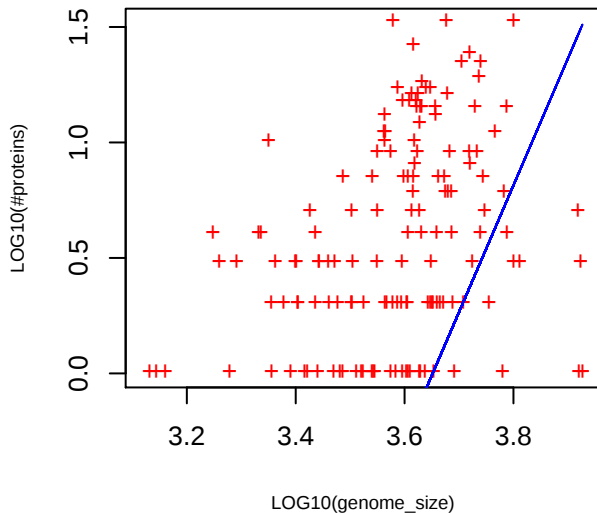
PF08402 TOBE_2: TOBE domain

slope= 0.0015 p_value= 0.90 intercept= 0.12 p_value= 7.5e-16

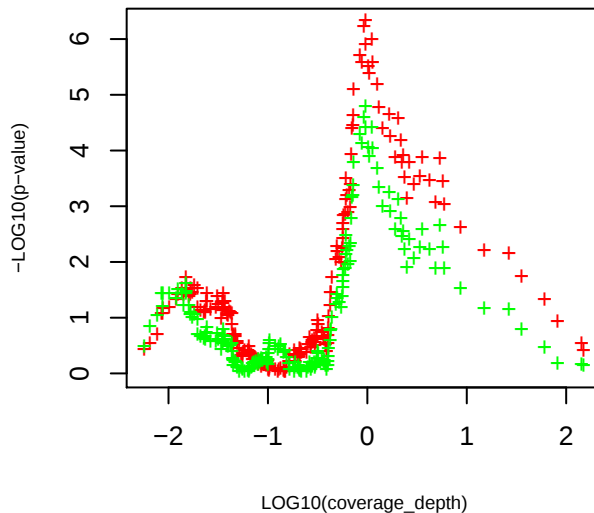


PF08402 TOBE_2: TOBE domain

slope= 5.49 p_value= 9.9e-11 intercept= -20.04 p_value= 3.2e-11

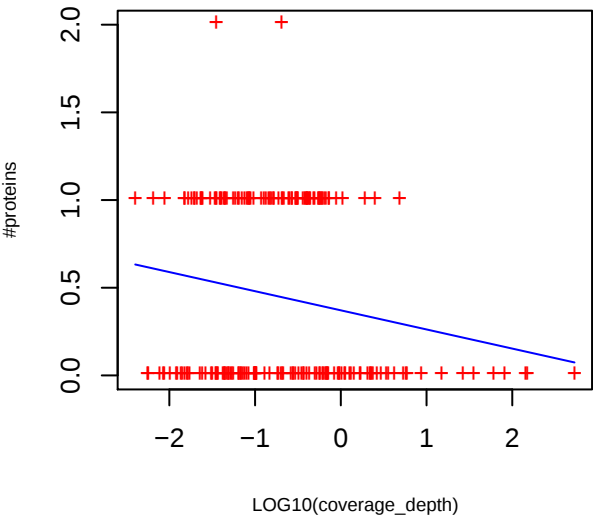


P-value curve ; red (unnorm), green (norm)



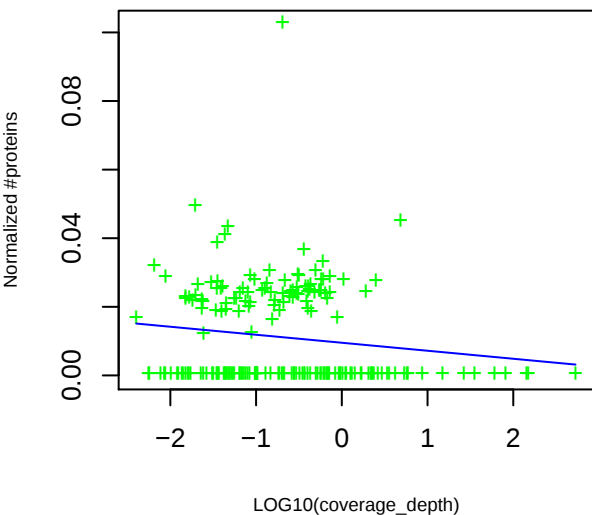
TIGR03160 cobT_DBIPRT: nicotinate-nucleotide--dimethyl/benzimidazole phosphoribosyltransferase

slope= -0.11 p_value= 0.0081 intercept= 0.37 p_value= 7.4e-14



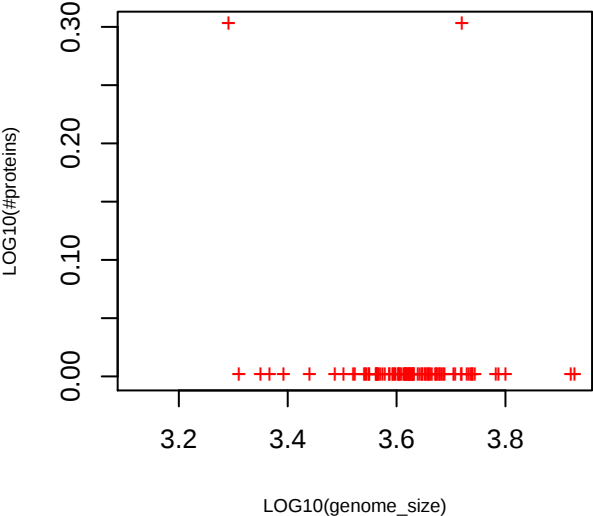
TIGR03160 cobT_DBIPRT: nicotinate-nucleotide--dimethyl/benzimidazole phosphoribosyltransferase

slope= -0.0023 p_value= 0.043 intercept= 0.0095 p_value= 4.4e-12

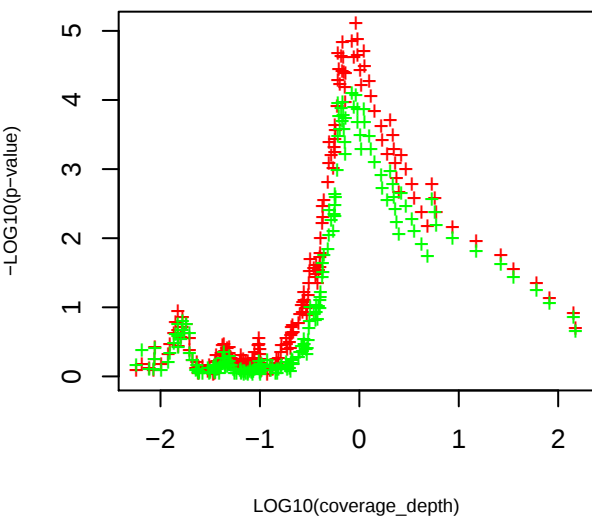


TIGR03160 cobT_DBIPRT: nicotinate-nucleotide--dimethyl/benzimidazole phosphoribosyltransferase

slope= 4.98 p_value= 2.8e-09 intercept= -19.92 p_value= 3.6e-11

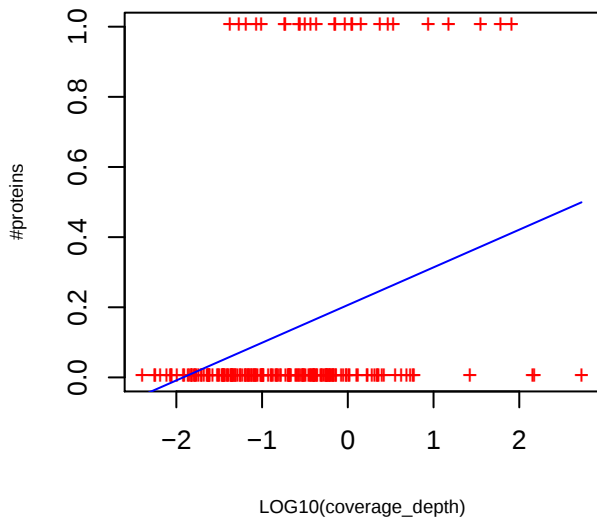


P-value curve ; red (unnorm), green (norm)



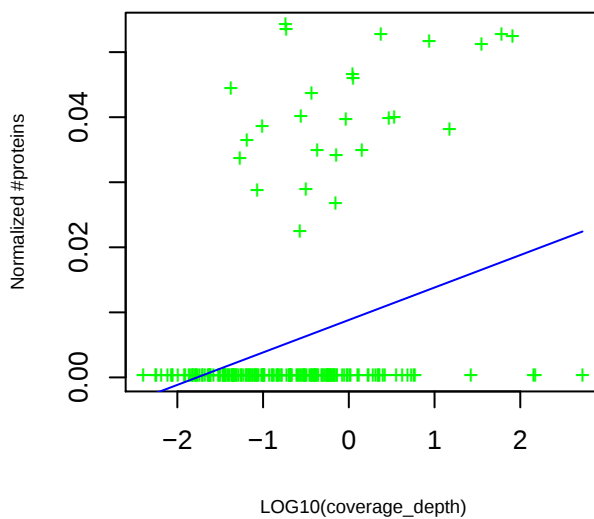
PF07566 DUF1543: Domain of Unknown Function (DUF1543)

slope= 0.11 p_value= 5.5e-05 intercept= 0.21 p_value= 3.7e-11



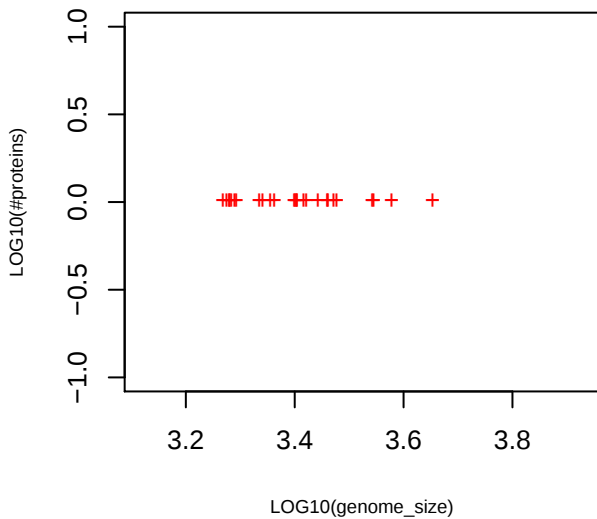
PF07566 DUF1543: Domain of Unknown Function (DUF1543)

slope= 0.005 p_value= 6.9e-06 intercept= 0.0088 p_value= 9.8e-12

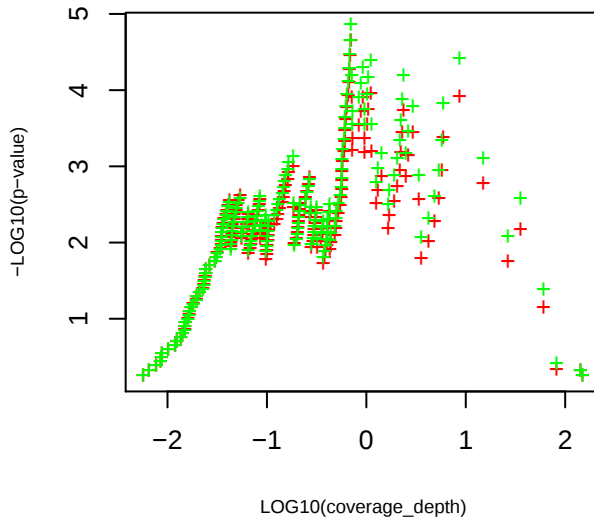


PF07566 DUF1543: Domain of Unknown Function (DUF1543)

slope= -2.87 p_value= 7e-07 intercept= 6.71 p_value= 0.00088

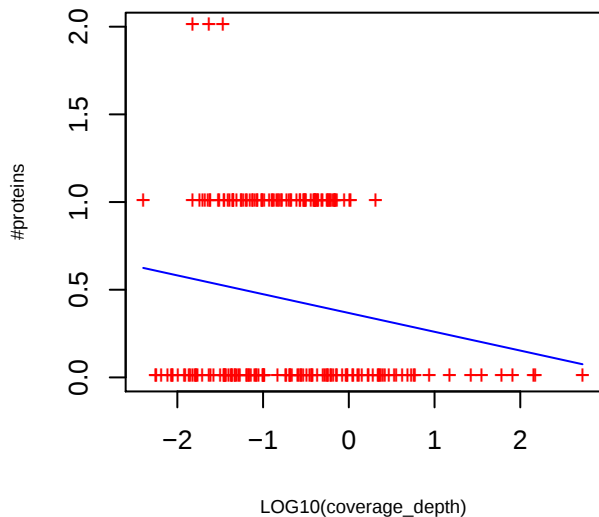


P-value curve ; red (unnorm), green (norm)



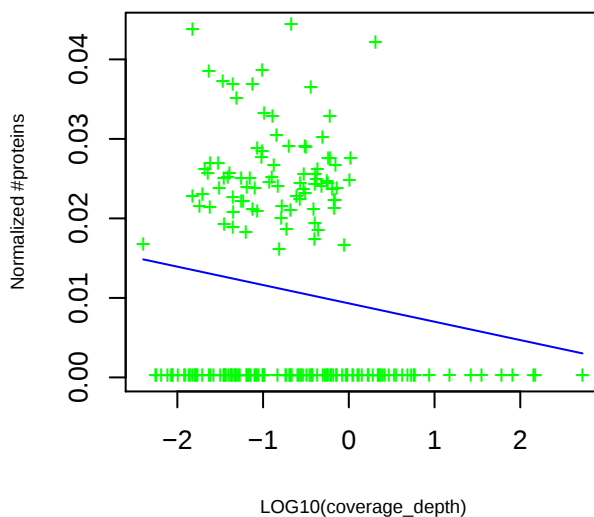
PF04378 DUF519: Protein of unknown function (DUF519)

slope= -0.11 p_value= 0.011 intercept= 0.37 p_value= 3.0e-13



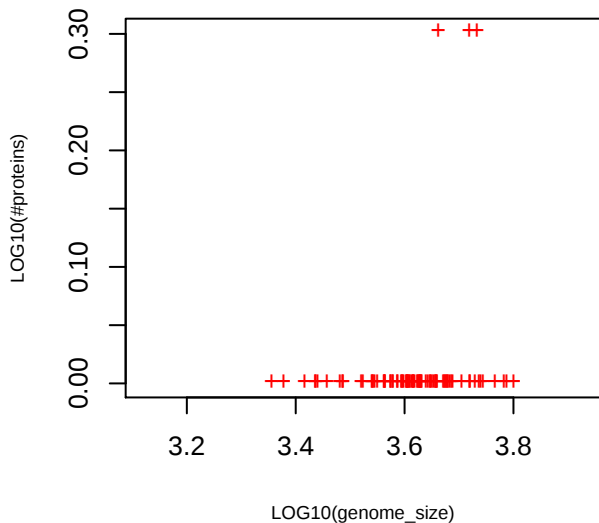
PF04378 DUF519: Protein of unknown function (DUF519)

slope= -0.0023 p_value= 0.029 intercept= 0.0093 p_value= 2.8e-13

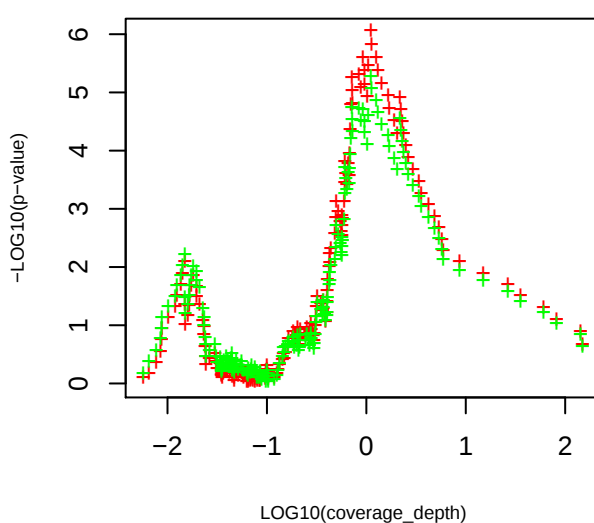


PF04378 DUF519: Protein of unknown function (DUF519)

slope= 4.45 p_value= 1.4e-07 intercept= -18.05 p_value= 2.5e-09

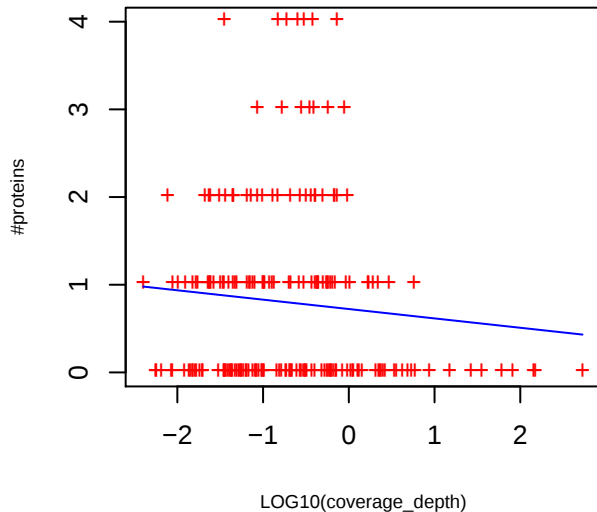


P-value curve ; red (unnorm), green (norm)



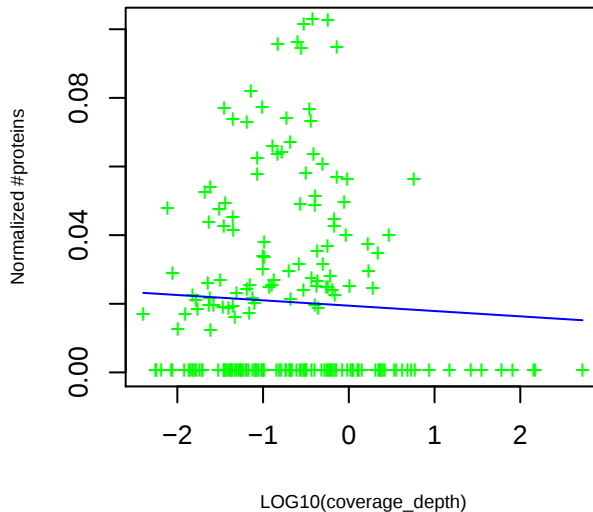
PF00394 Cu-oxidase: Multicopper oxidase

slope= -0.11 p_value= 0.20 intercept= 0.72 p_value= 4.7e-13



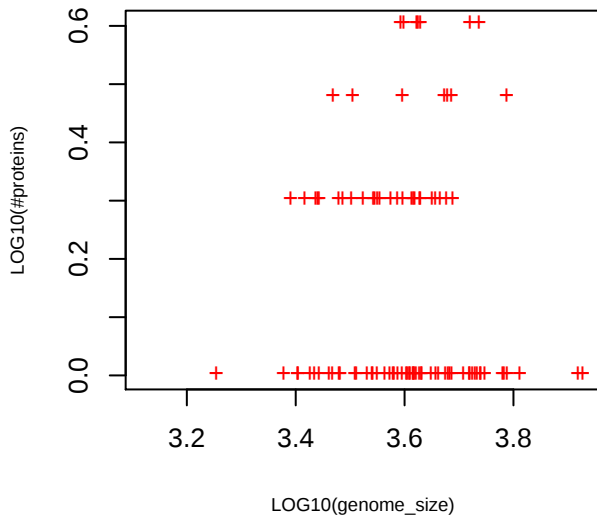
PF00394 Cu-oxidase: Multicopper oxidase

slope= -0.0016 p_value= 0.47 intercept= 0.019 p_value= 9.7e-14

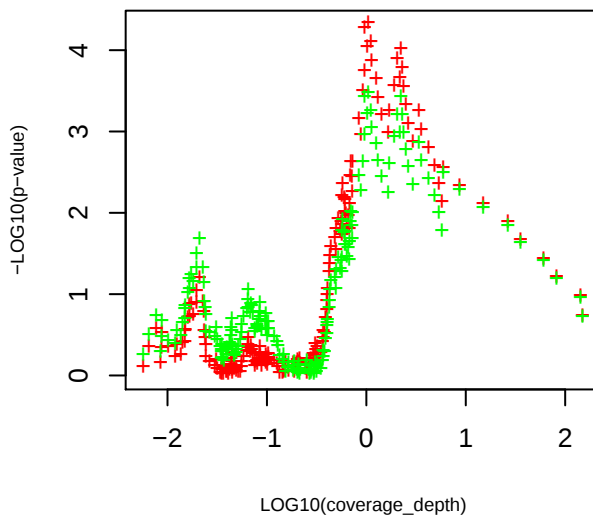


PF00394 Cu-oxidase: Multicopper oxidase

slope= 4.30 p_value= 1.4e-06 intercept= -17.23 p_value= 6.7e-08

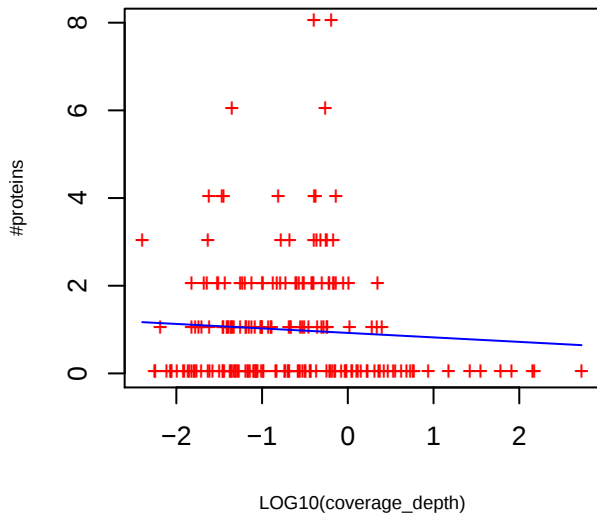


P-value curve ; red (unnorm), green (norm)



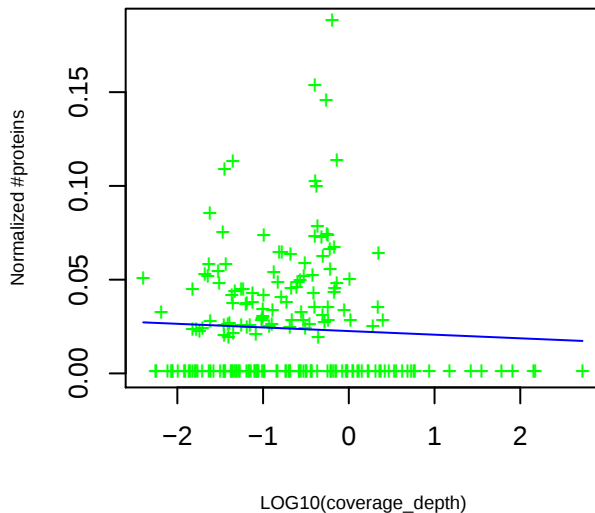
TIGR01843 type_I_hlyD: type I secretion membrane fusion protein, HlyD family

slope= -0.10 p_value= 0.36 intercept= 0.92 p_value= 6.1e-12



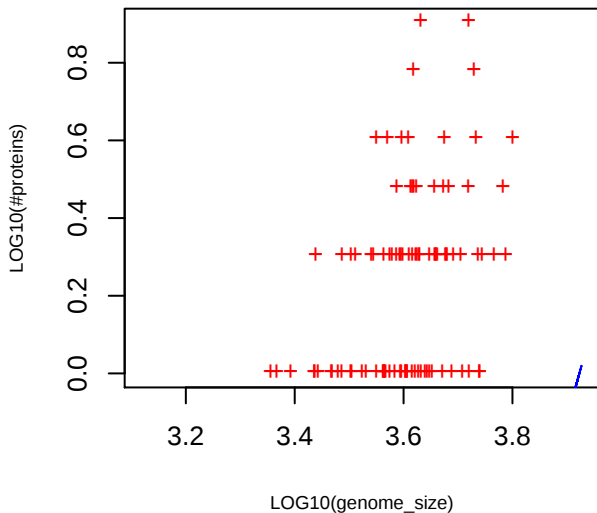
TIGR01843 type_I_hlyD: type I secretion membrane fusion protein, HlyD family

slope= -0.0019 p_value= 0.45 intercept= 0.023 p_value= 2.9e-13

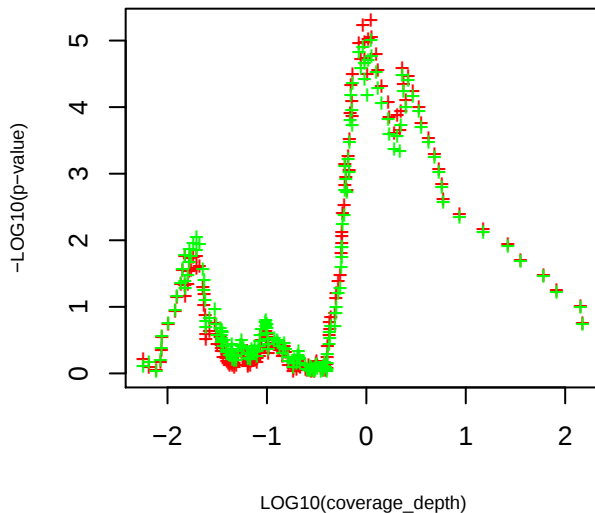


TIGR01843 type_I_hlyD: type I secretion membrane fusion protein, HlyD family

slope= 5.02 p_value= 2.3e-08 intercept= -19.70 p_value= 9e-10

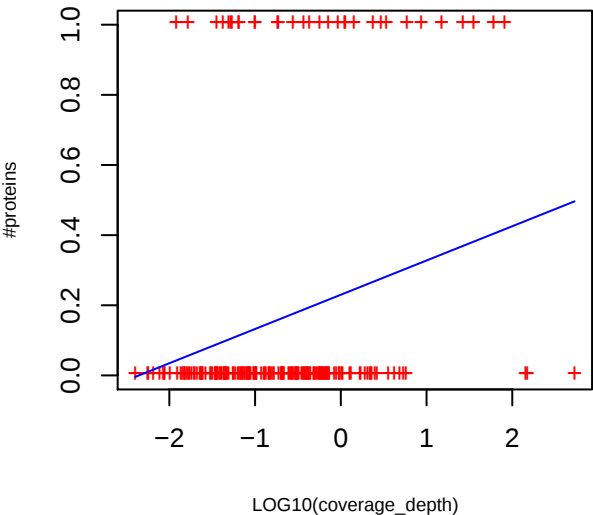


P-value curve ; red (unnorm), green (norm)



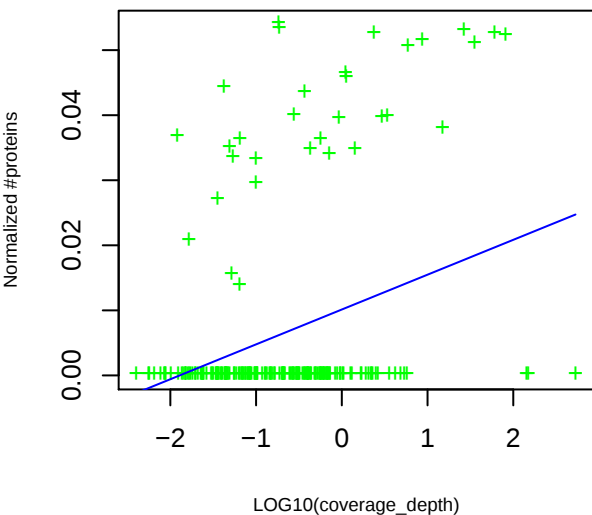
TIGR02472 sucP_syn_N: sucrose-phosphate synthase, putative, glycosyltransferase domain

slope= 0.098 p_value= 0.00083 intercept= 0.23 p_value= 2.5e-11



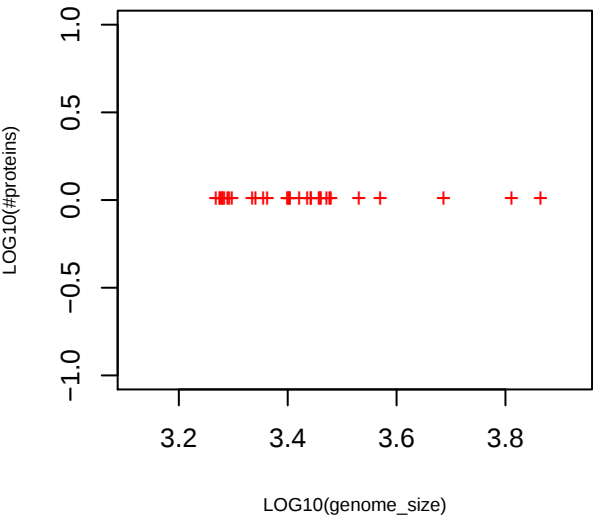
TIGR02472 sucP_syn_N: sucrose-phosphate synthase, putative, glycosyltransferase domain

slope= 0.0054 p_value= 6.8e-06 intercept= 0.010 p_value= 5.1e-13

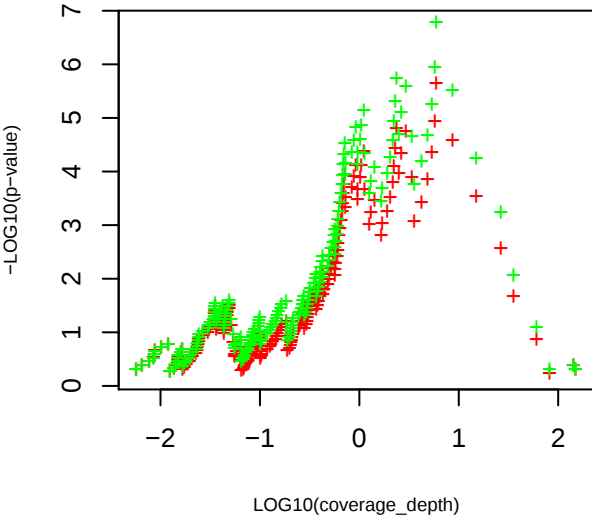


TIGR02472 sucP_syn_N: sucrose-phosphate synthase, putative, glycosyltransferase domain

slope= -2.99 p_value= 2.3e-06 intercept= 7.25 p_value= 0.0010

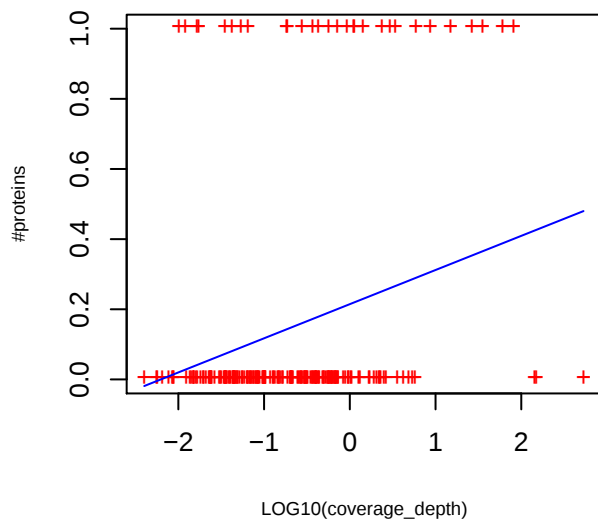


P-value curve ; red (unnorm), green (norm)



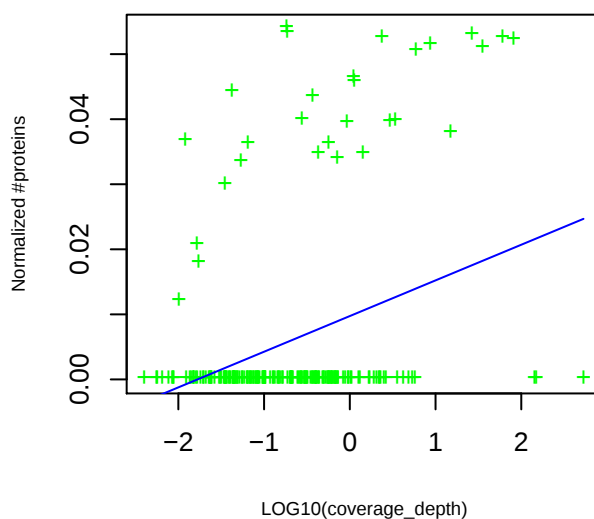
TIGR02505 RTPR: ribonucleoside-triphosphate reductase, adenosylcobalamin-dependent

slope= 0.097 p_value= 0.00052 intercept= 0.21 p_value= 7.4e-11



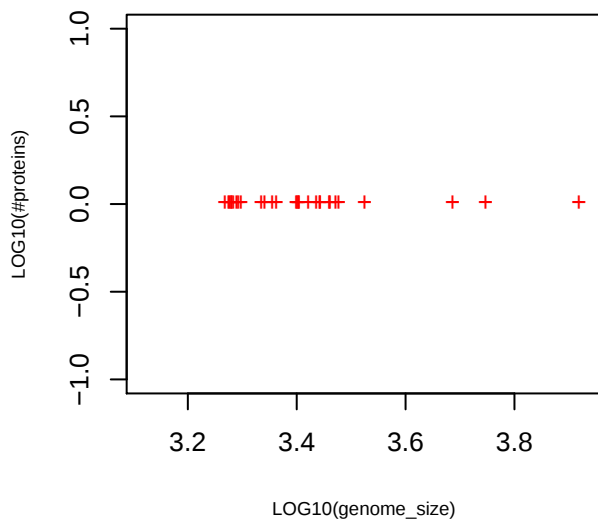
TIGR02505 RTPR: ribonucleoside-triphosphate reductase, adenosylcobalamin-dependent

slope= 0.0055 p_value= 2.5e-06 intercept= 0.0097 p_value= 9.7e-13

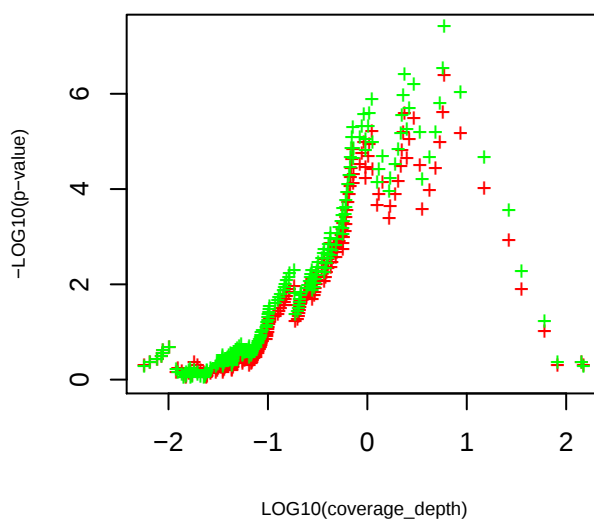


TIGR02505 RTPR: ribonucleoside-triphosphate reductase, adenosylcobalamin-dependent

slope= -2.90 p_value= 1.7e-06 intercept= 6.88 p_value= 0.0012

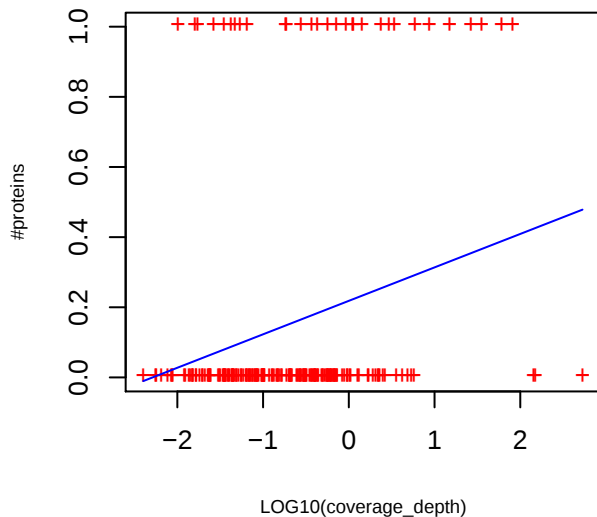


P-value curve ; red (unnorm), green (norm)



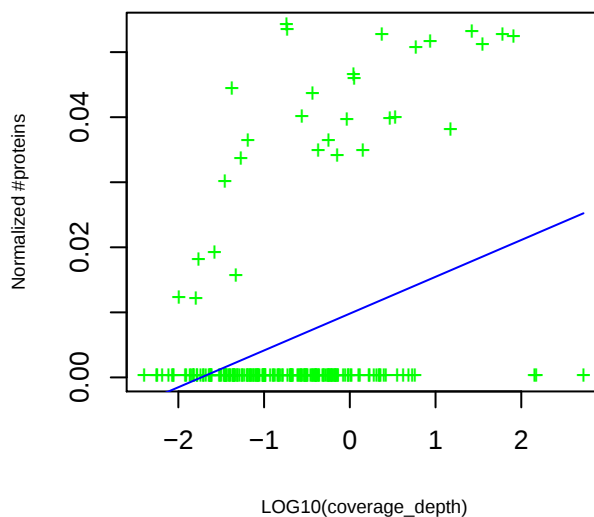
PF09506 Salt_to_Pase: Glucosylglycerol-phosphate phosphatase (Salt_to_Pase)

slope= 0.095 p_value= 8e-04 intercept= 0.22 p_value= 7.1e-11



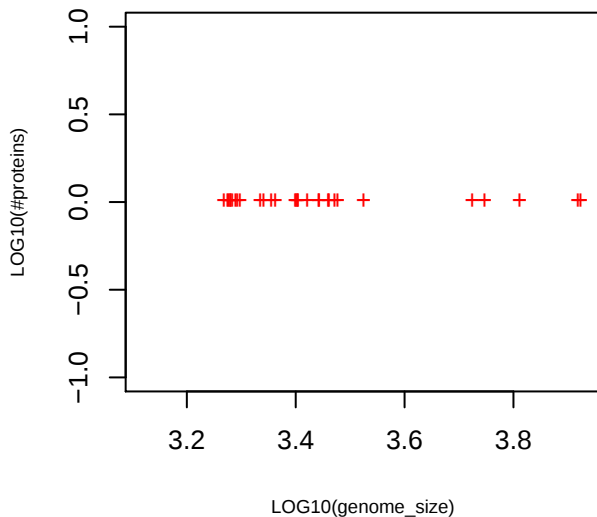
PF09506 Salt_to_Pase: Glucosylglycerol-phosphate phosphatase (Salt_to_Pase)

slope= 0.0057 p_value= 8.4e-07 intercept= 0.0098 p_value= 3.4e-13

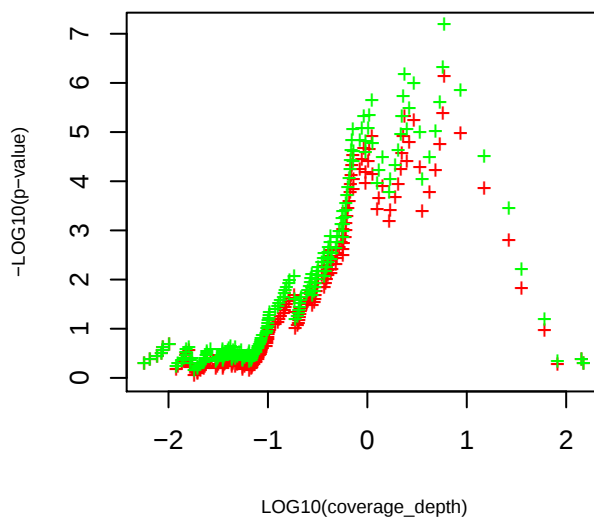


PF09506 Salt_to_Pase: Glucosylglycerol-phosphate phosphatase (Salt_to_Pase)

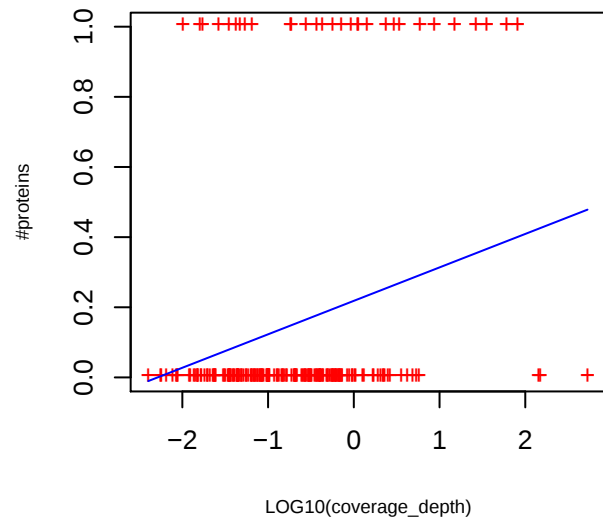
slope= -2.30 p_value= 0.00023 intercept= 4.75 p_value= 0.03



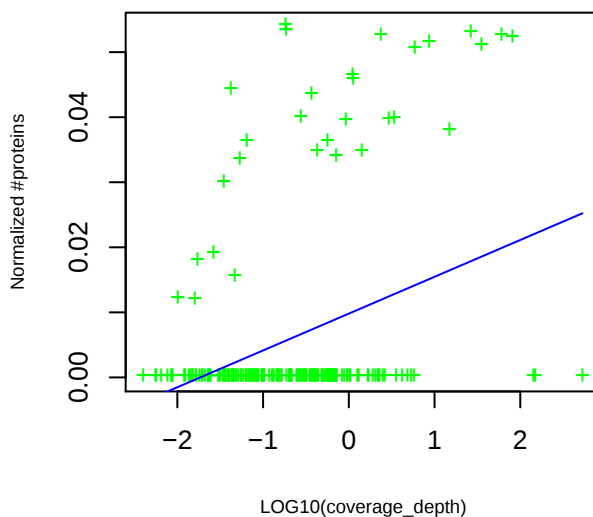
P-value curve ; red (unnorm), green (norm)



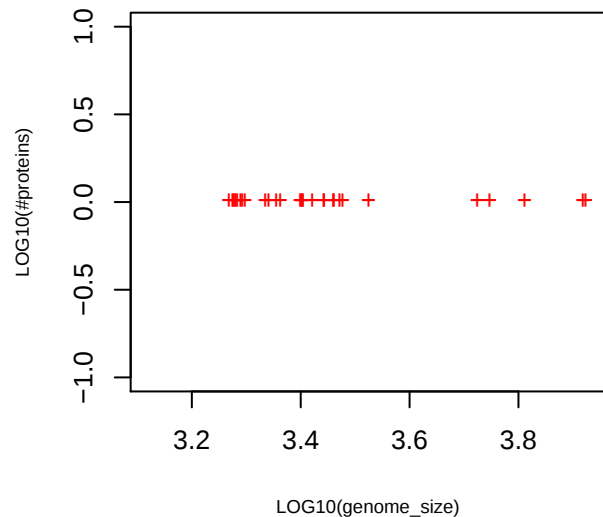
TIGR02399 salt_tol_Pase: glucosylglycerol 3-phosphatase
 slope= 0.095 p_value= 8e-04 intercept= 0.22 p_value= 7.1e-11



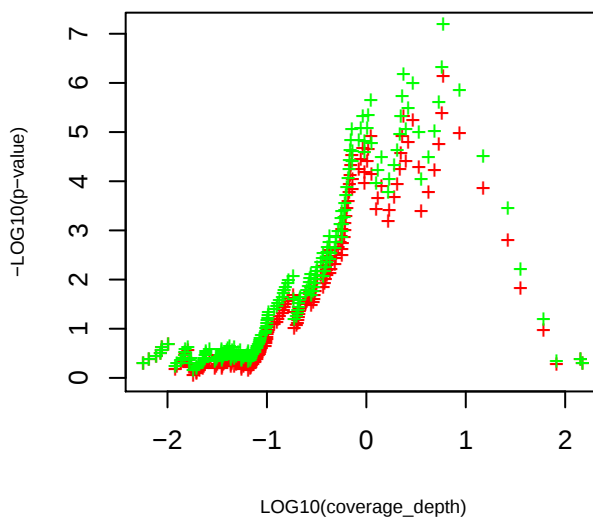
TIGR02399 salt_tol_Pase: glucosylglycerol 3-phosphatase
 slope= 0.0057 p_value= 8.4e-07 intercept= 0.0098 p_value= 3.4e-13



TIGR02399 salt_tol_Pase: glucosylglycerol 3-phosphatase
 slope= -2.30 p_value= 0.00023 intercept= 4.75 p_value= 0.03

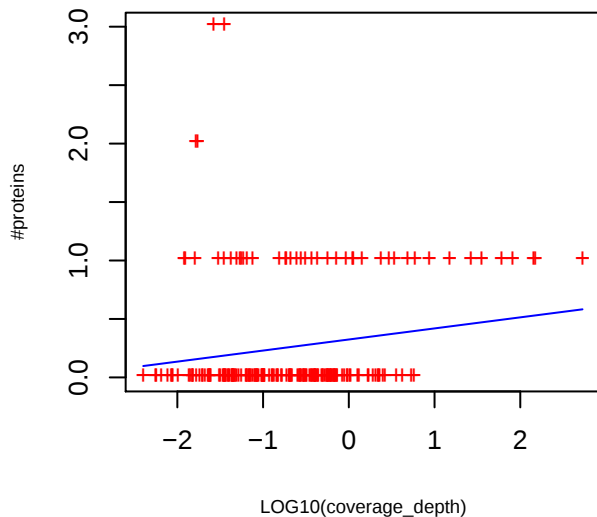


P-value curve ; red (unnorm), green (norm)



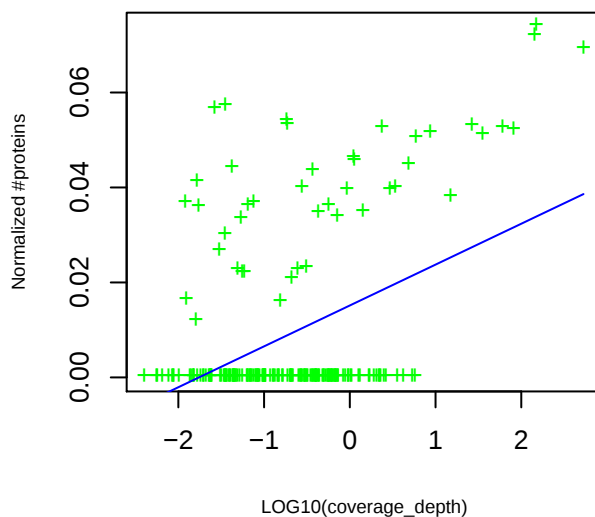
PF05992 SbmA_BacA: SbmA/BacA-like family

slope= 0.095 p_value= 0.023 intercept= 0.32 p_value= 5.6e-11



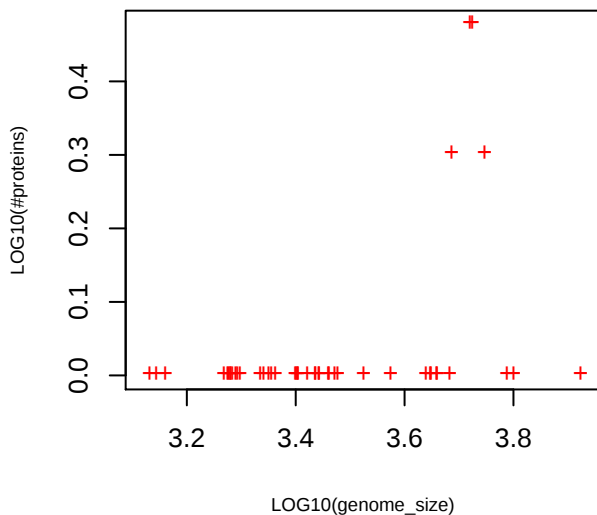
PF05992 SbmA_BacA: SbmA/BacA-like family

slope= 0.0086 p_value= 7.4e-10 intercept= 0.015 p_value= 1.5e-19

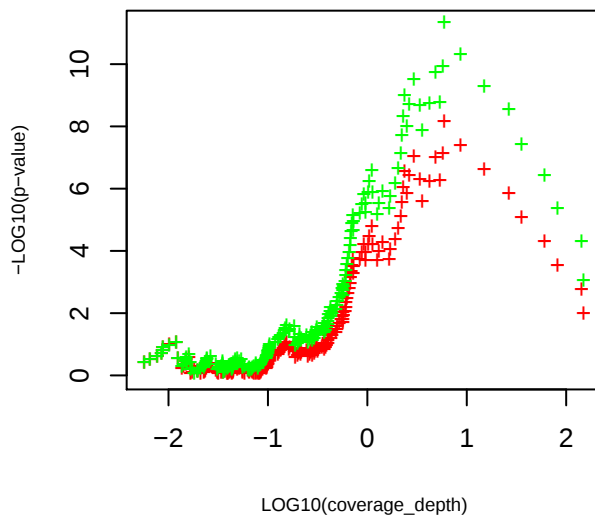


PF05992 SbmA_BacA: SbmA/BacA-like family

slope= -2.82 p_value= 0.00012 intercept= 6.90 p_value= 0.0074

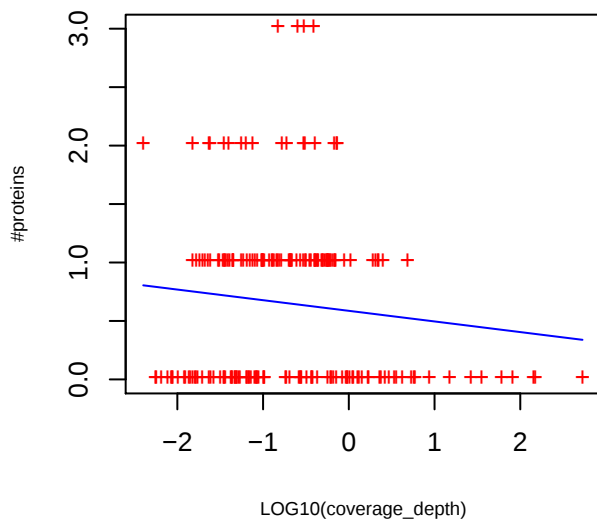


P-value curve ; red (unnorm), green (norm)



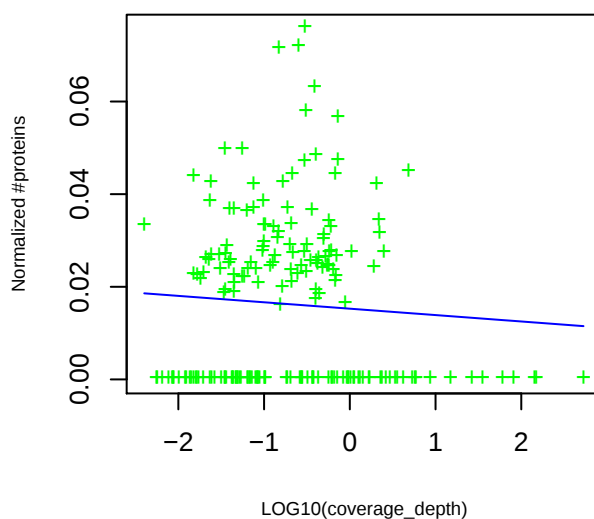
TIGR00385 dsbE: periplasmic protein thiol:disulfide oxidoreductases, DsbE subfamily

slope= -0.091 p_value= 0.12 intercept= 0.59 p_value= 1.8e-16



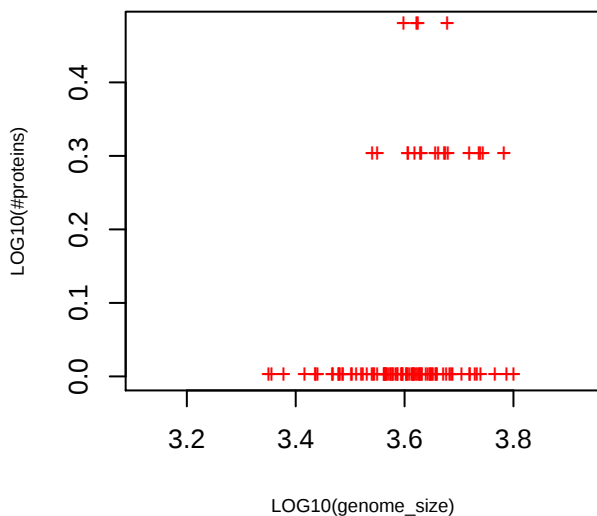
TIGR00385 dsbE: periplasmic protein thiol:disulfide oxidoreductases, DsbE subfamily

slope= -0.0014 p_value= 0.33 intercept= 0.015 p_value= 6.5e-18

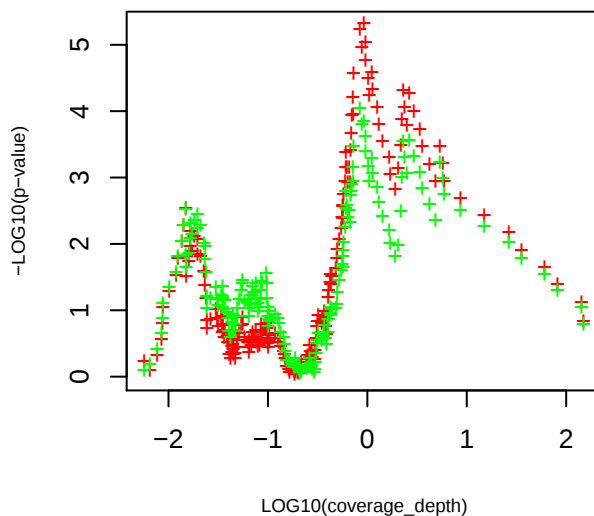


TIGR00385 dsbE: periplasmic protein thiol:disulfide oxidoreductases, DsbE subfamily

slope= 4.63 p_value= 8.6e-08 intercept= -18.29 p_value= 3.4e-09

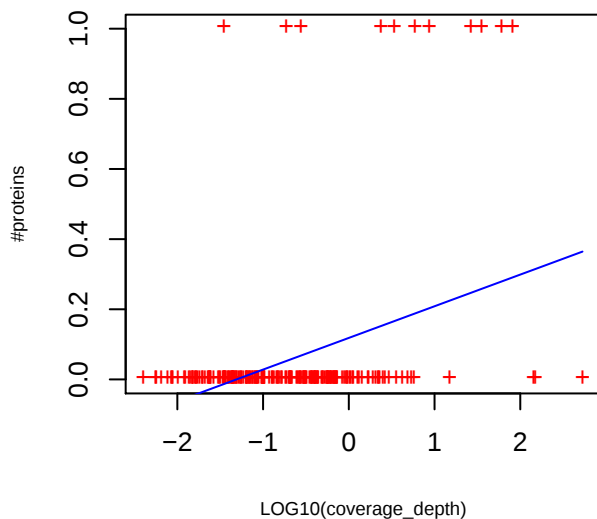


P-value curve ; red (unnorm), green (norm)



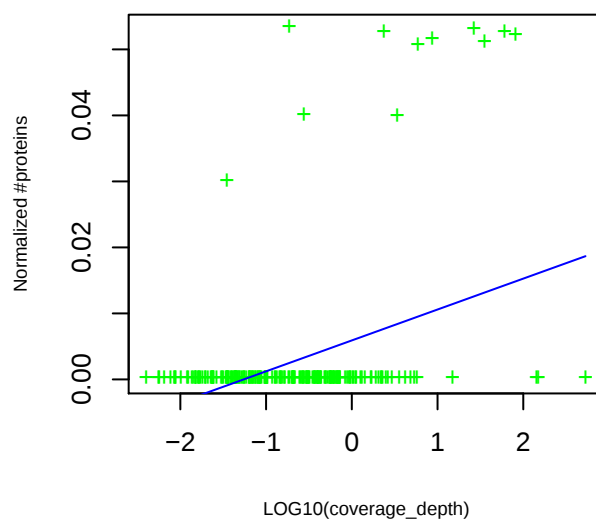
TIGR02463 MPGP_rel: mannosyl-3-phosphoglycerate phosphatase homolog

slope= 0.09 p_value= 4.3e-07 intercept= 0.12 p_value= 6.5e-09



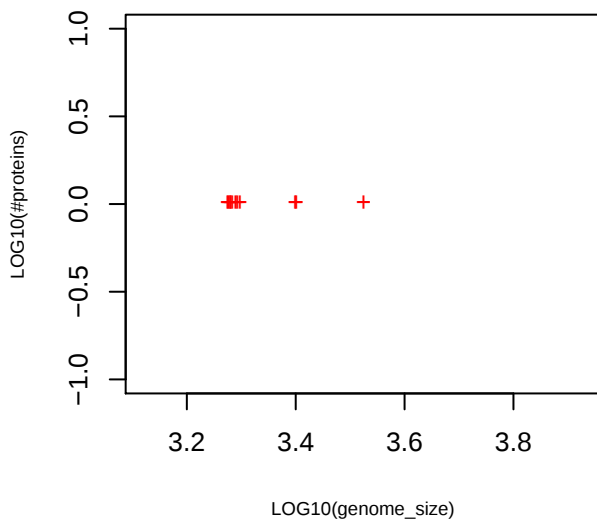
TIGR02463 MPGP_rel: mannosyl-3-phosphoglycerate phosphatase homolog

slope= 0.0047 p_value= 5e-08 intercept= 0.0059 p_value= 1.6e-09

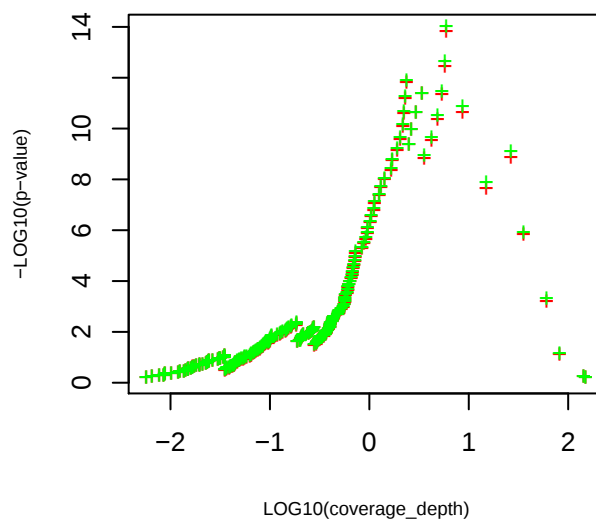


TIGR02463 MPGP_rel: mannosyl-3-phosphoglycerate phosphatase homolog

slope= -1.84 p_value= 2.9e-06 intercept= 2.75 p_value= 0.044

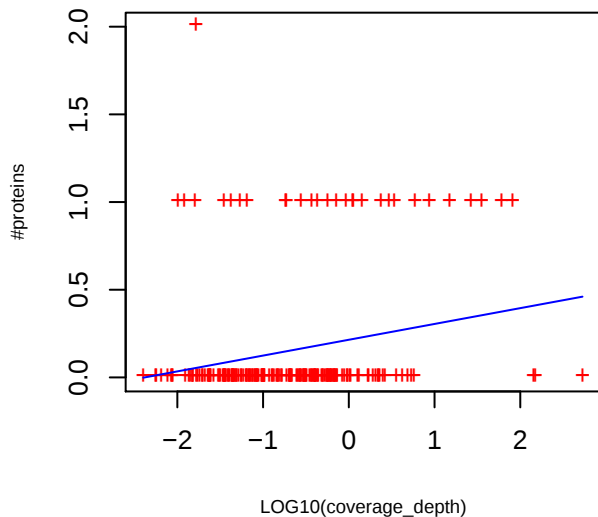


P-value curve ; red (unnorm), green (norm)



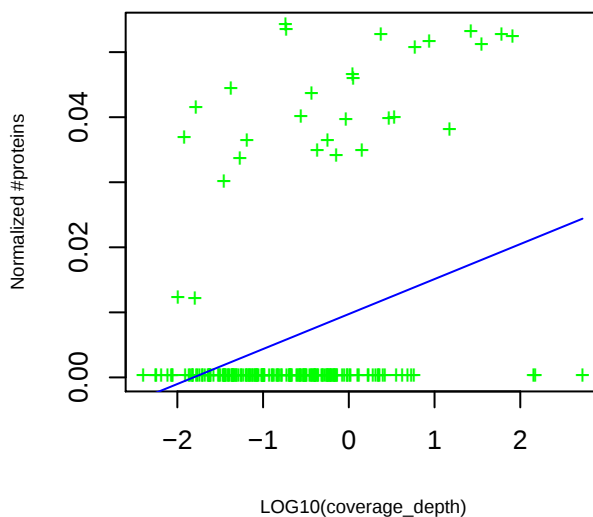
PF04853 Invertase_neut: Plant neutral invertase

slope= 0.09 p_value= 0.0023 intercept= 0.21 p_value= 6.5e-10



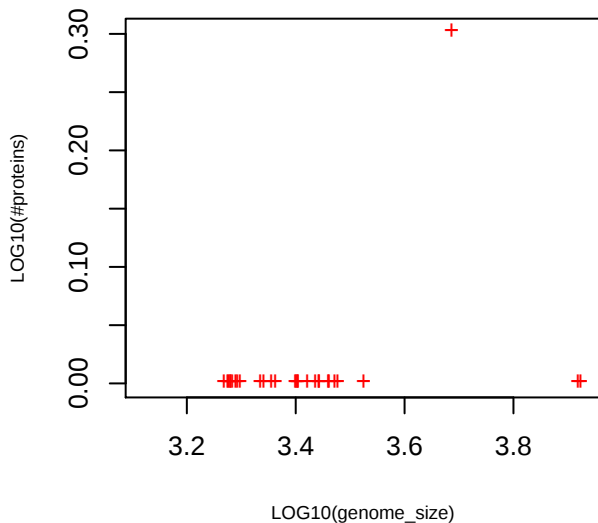
PF04853 Invertase_neut: Plant neutral invertase

slope= 0.0054 p_value= 5e-06 intercept= 0.0097 p_value= 1.8e-12

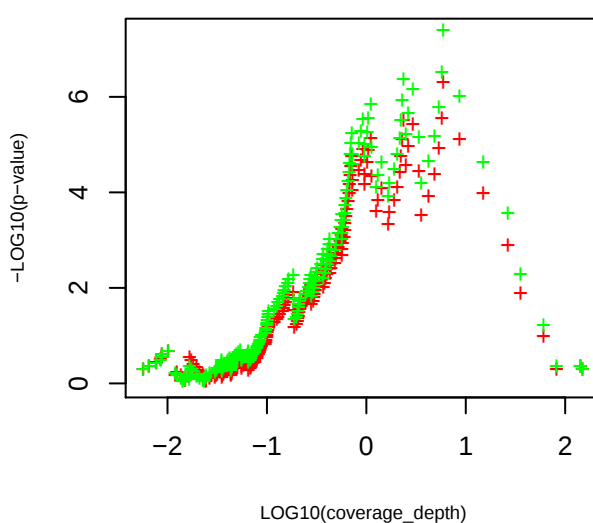


PF04853 Invertase_neut: Plant neutral invertase

slope= -2.76 p_value= 6.2e-06 intercept= 6.37 p_value= 0.0028

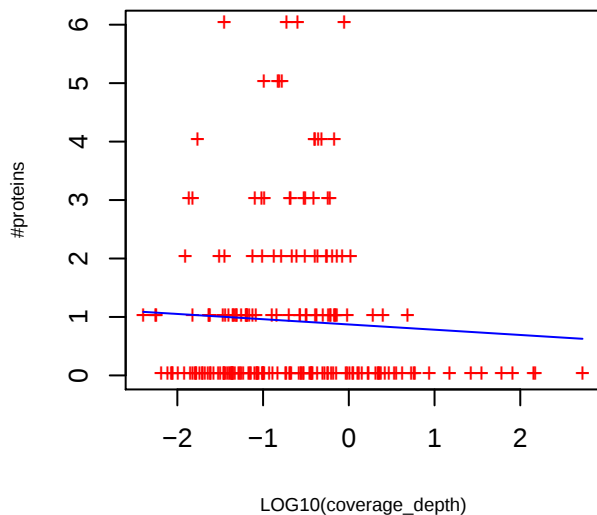


P-value curve ; red (unnorm), green (norm)



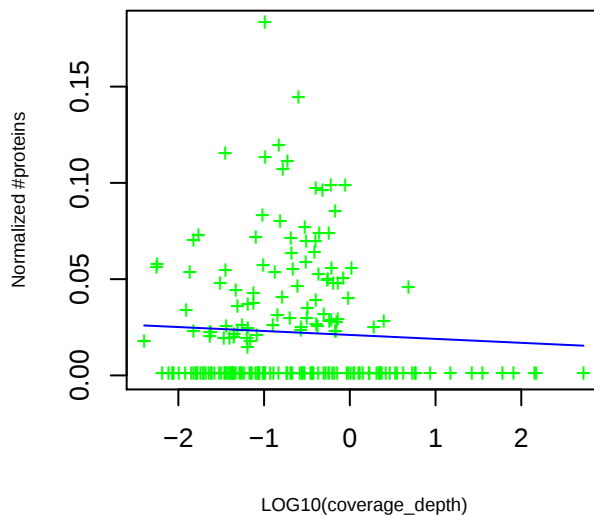
PF09084 NMT1: NMT1/THI5 like

slope= -0.09 p_value= 0.43 intercept= 0.87 p_value= 1.1e-10



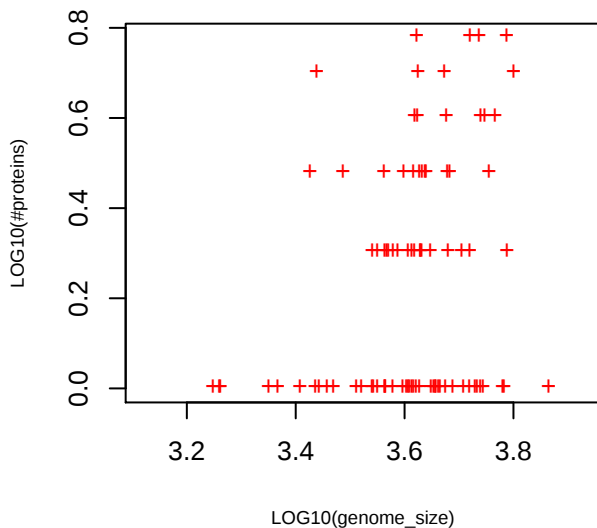
PF09084 NMT1: NMT1/THI5 like

slope= -0.0020 p_value= 0.44 intercept= 0.021 p_value= 2.5e-11

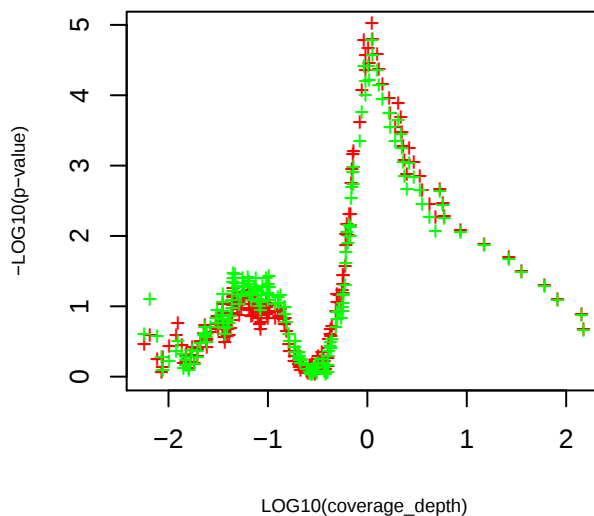


PF09084 NMT1: NMT1/THI5 like

slope= 4.84 p_value= 6.8e-08 intercept= -19.28 p_value= 2e-09

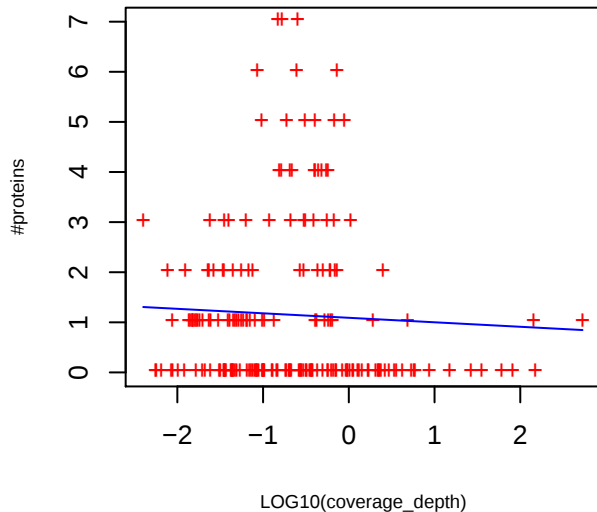


P-value curve ; red (unnorm), green (norm)



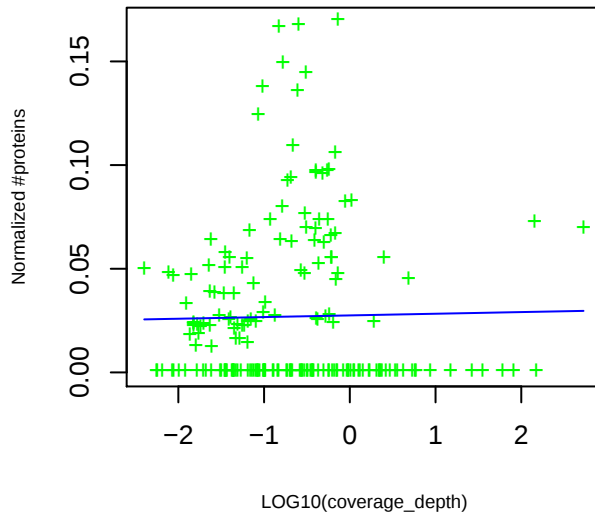
TIGR02122 TRAP_TAXI: TRAP transporter solute receptor, TAXI family

slope= -0.09 p_value= 0.50 intercept= 1.09 p_value= 8.2e-12



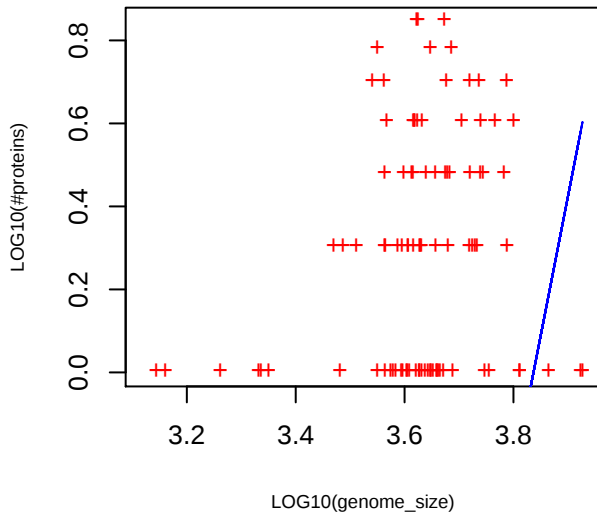
TIGR02122 TRAP_TAXI: TRAP transporter solute receptor, TAXI family

slope= 8e-04 p_value= 0.79 intercept= 0.027 p_value= 1.8e-13

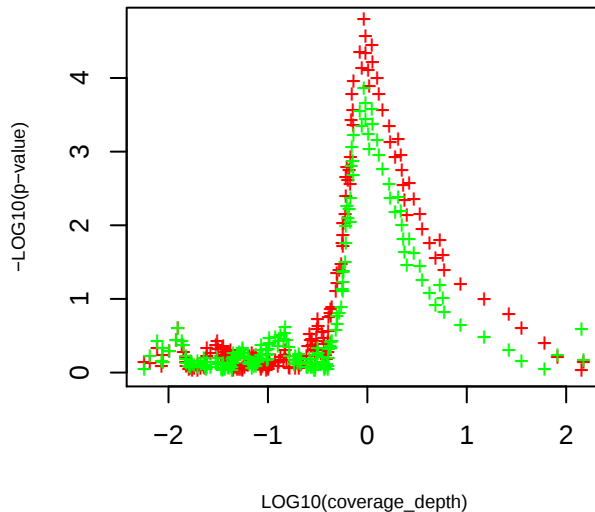


TIGR02122 TRAP_TAXI: TRAP transporter solute receptor, TAXI family

slope= 6.70 p_value= 3.2e-14 intercept= -25.70 p_value= 4.9e-16

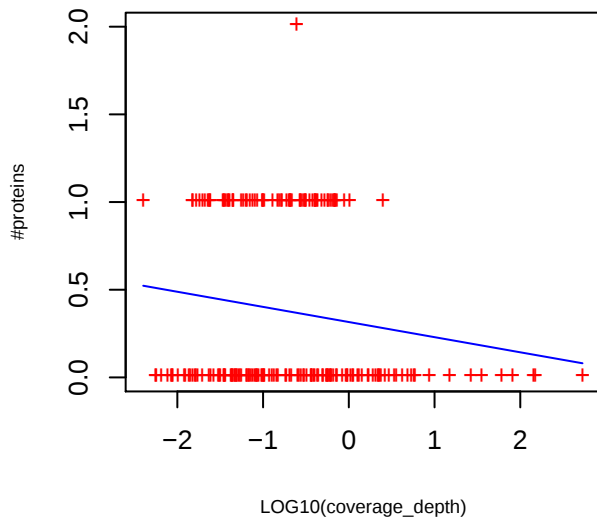


P-value curve ; red (unnorm), green (norm)



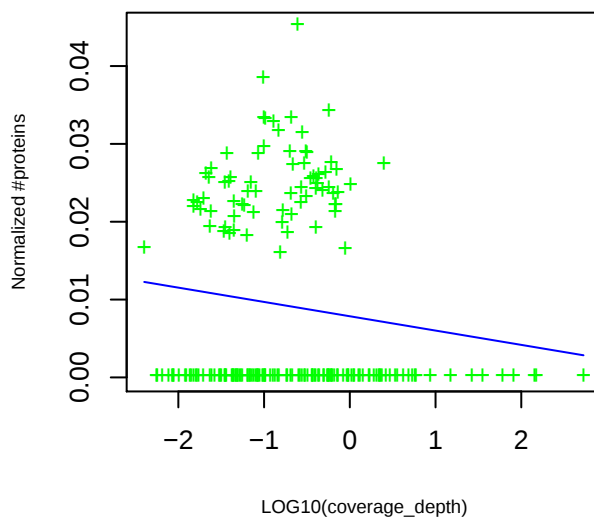
TIGR01262 maiA: maleylacetoacetate isomerase

slope= -0.086 p_value= 0.029 intercept= 0.32 p_value= 1.9e-11



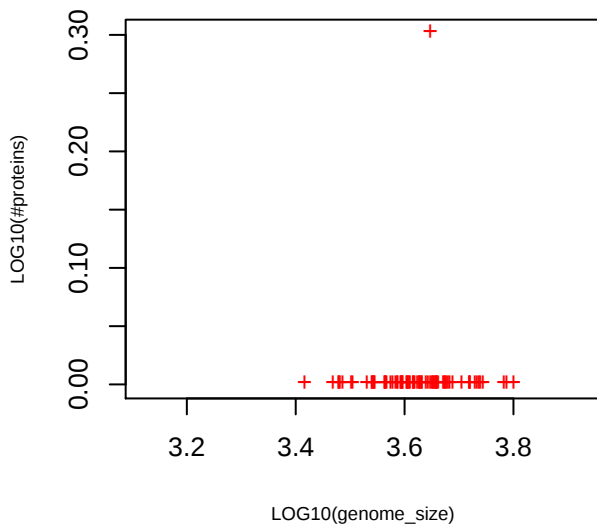
TIGR01262 maiA: maleylacetoacetate isomerase

slope= -0.0018 p_value= 0.062 intercept= 0.0079 p_value= 2.1e-11

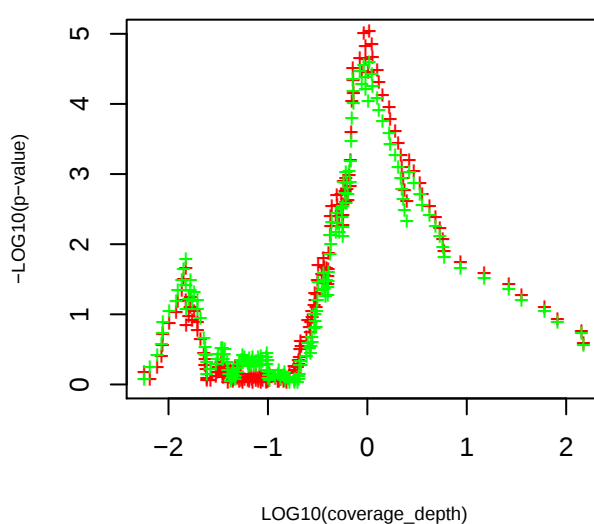


TIGR01262 maiA: maleylacetoacetate isomerase

slope= 4.26 p_value= 2.4e-07 intercept= -17.61 p_value= 2.7e-09

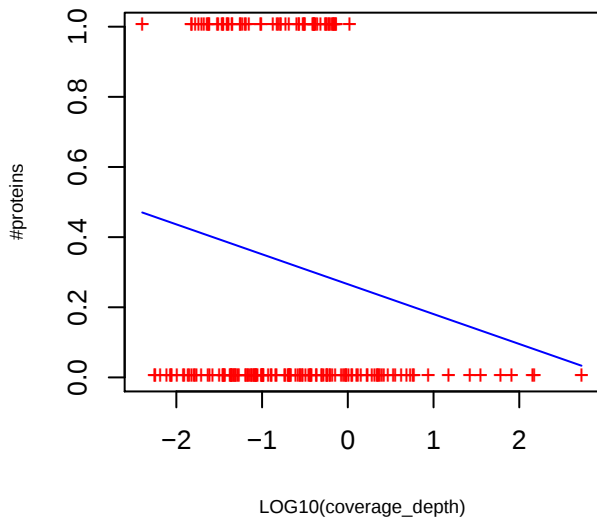


P-value curve ; red (unnorm), green (norm)



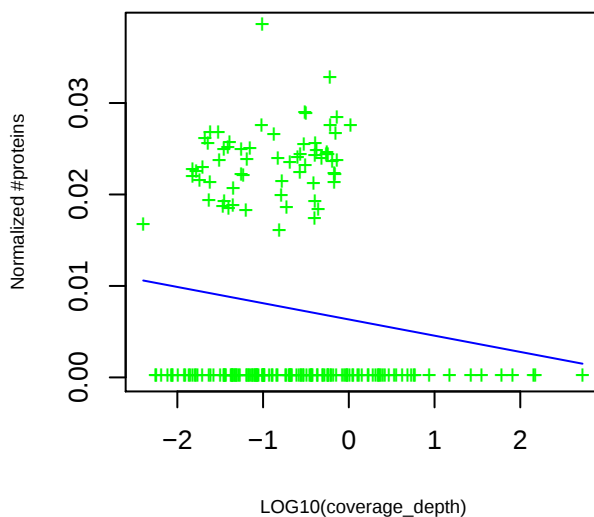
TIGR01620 hyp_HI0043: conserved hypothetical protein TIGR01620

slope= -0.085 p_value= 0.023 intercept= 0.27 p_value= 1.5e-09



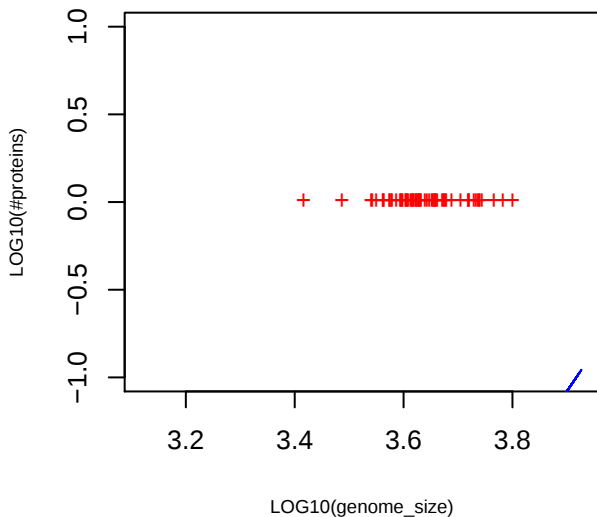
TIGR01620 hyp_HI0043: conserved hypothetical protein TIGR01620

slope= -0.0018 p_value= 0.046 intercept= 0.0063 p_value= 1.5e-09

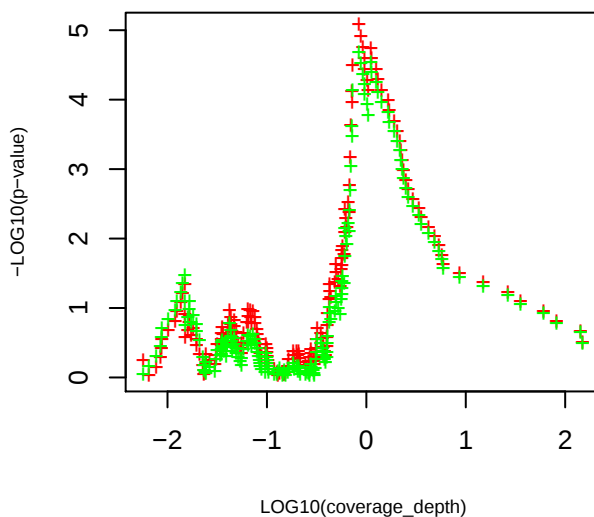


TIGR01620 hyp_HI0043: conserved hypothetical protein TIGR01620

slope= 4.57 p_value= 7.8e-09 intercept= -18.91 p_value= 3.3e-11

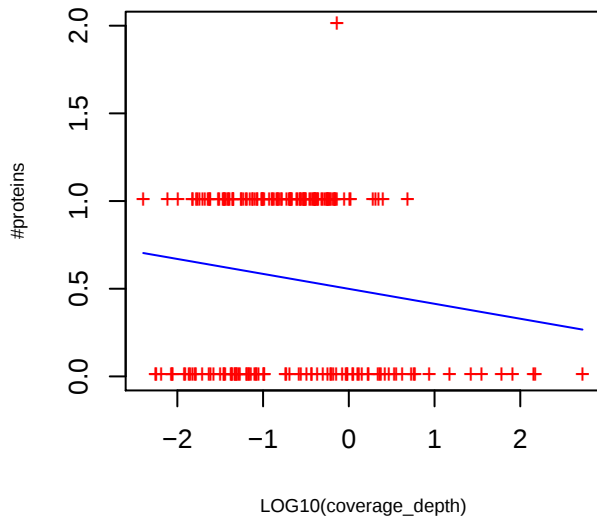


P-value curve ; red (unnorm), green (norm)



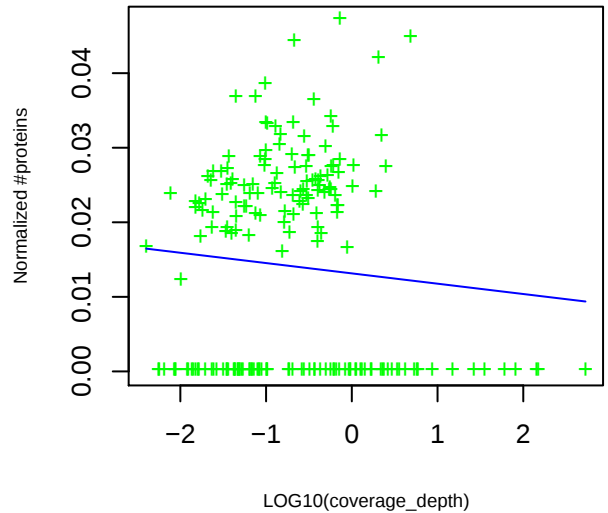
TIGR01189 ccmA: heme ABC exporter, ATP-binding protein CcmA

slope= -0.085 p_value= 0.035 intercept= 0.50 p_value= 3.4e-22



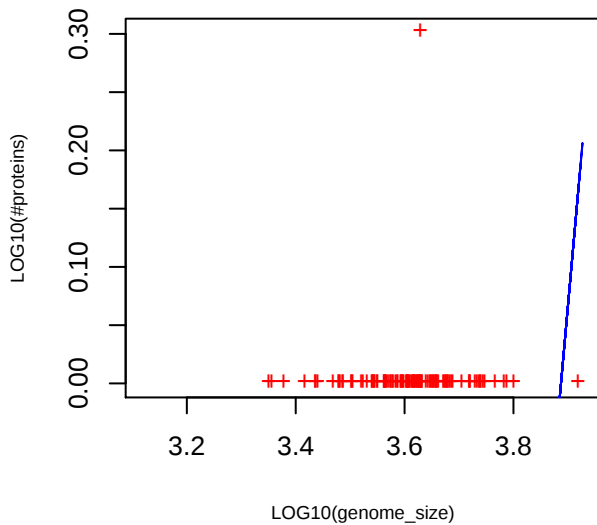
TIGR01189 ccmA: heme ABC exporter, ATP-binding protein CcmA

slope= -0.0014 p_value= 0.20 intercept= 0.013 p_value= 1.0e-21

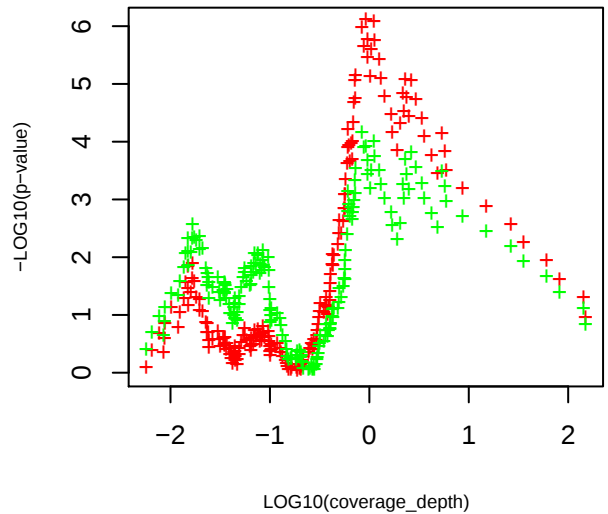


TIGR01189 ccmA: heme ABC exporter, ATP-binding protein CcmA

slope= 5.22 p_value= 4.1e-10 intercept= -20.29 p_value= 1.2e-11

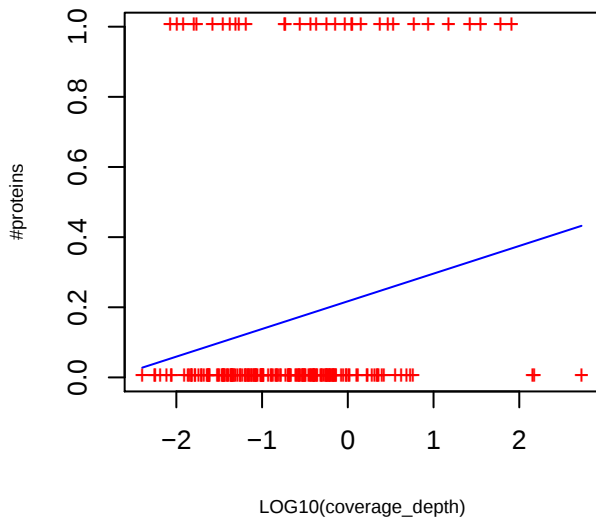


P-value curve ; red (unnorm), green (norm)



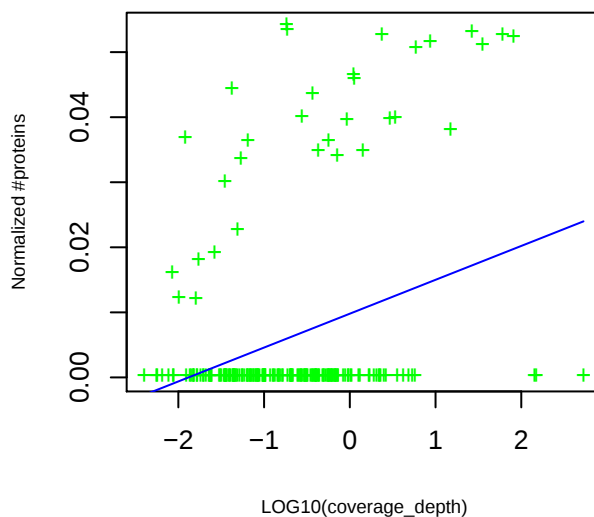
PF02419 PsbL: PsbL protein

slope= 0.079 p_value= 0.0072 intercept= 0.22 p_value= 3.5e-10



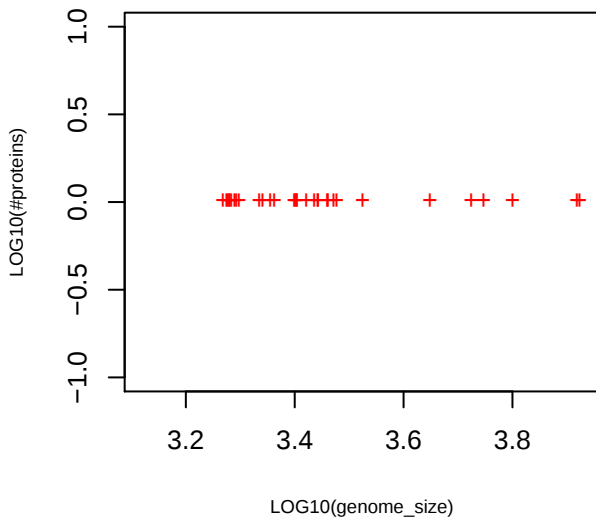
PF02419 PsbL: PsbL protein

slope= 0.0052 p_value= 8.7e-06 intercept= 0.0098 p_value= 1.1e-12

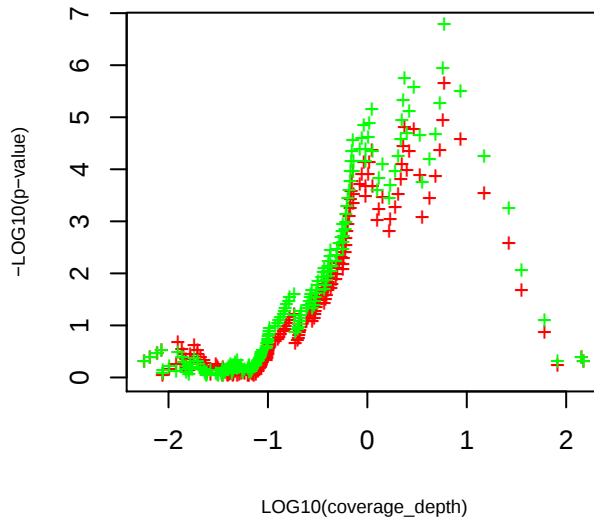


PF02419 PsbL: PsbL protein

slope= -2.31 p_value= 0.00031 intercept= 4.83 p_value= 0.031

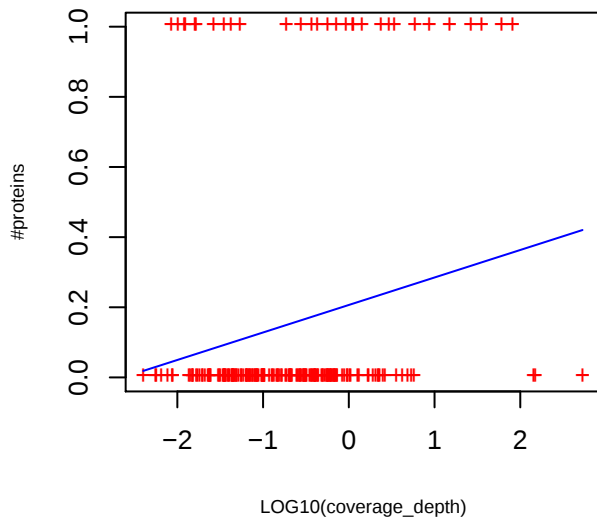


P-value curve ; red (unnorm), green (norm)



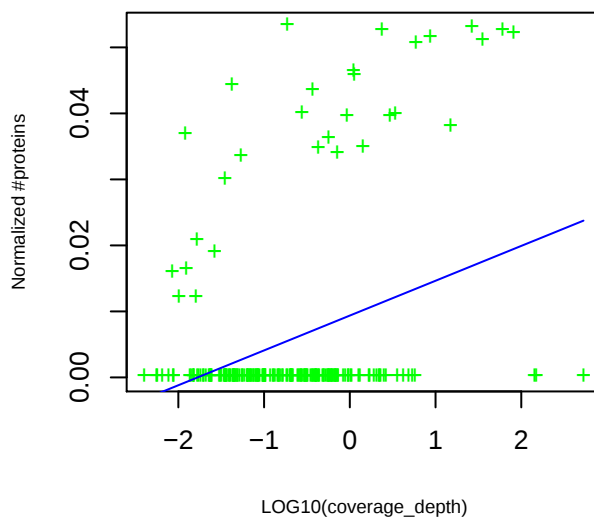
PF05151 PsbM: Photosystem II reaction centre M protein (PsbM)

slope= 0.078 p_value= 0.0061 intercept= 0.21 p_value= 7.9e-10



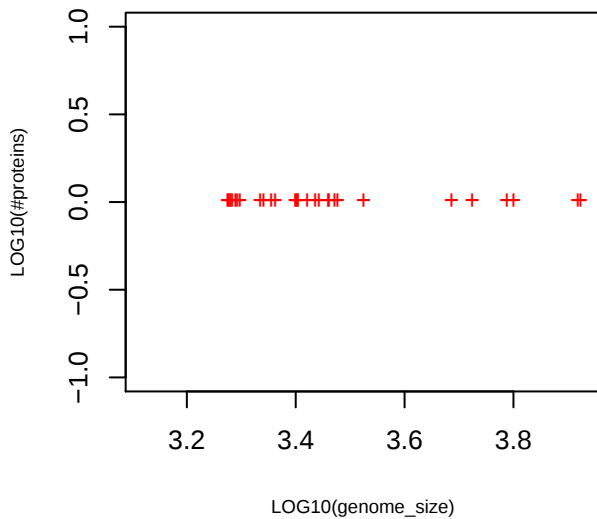
PF05151 PsbM: Photosystem II reaction centre M protein (PsbM)

slope= 0.0053 p_value= 2.6e-06 intercept= 0.0094 p_value= 1.1e-12

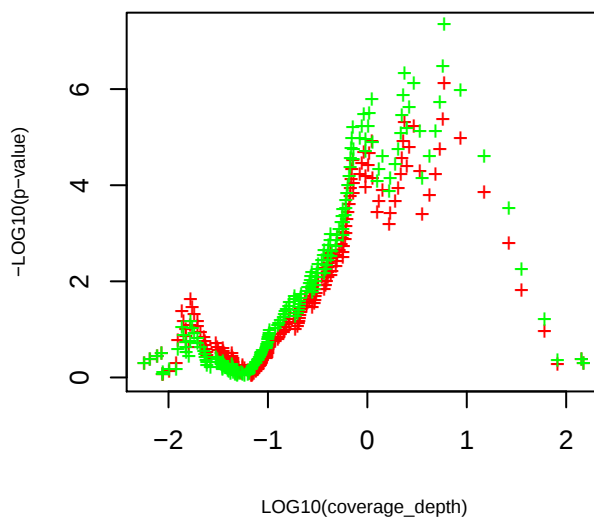


PF05151 PsbM: Photosystem II reaction centre M protein (PsbM)

slope= -1.96 p_value= 0.0018 intercept= 3.54 p_value= 0.11

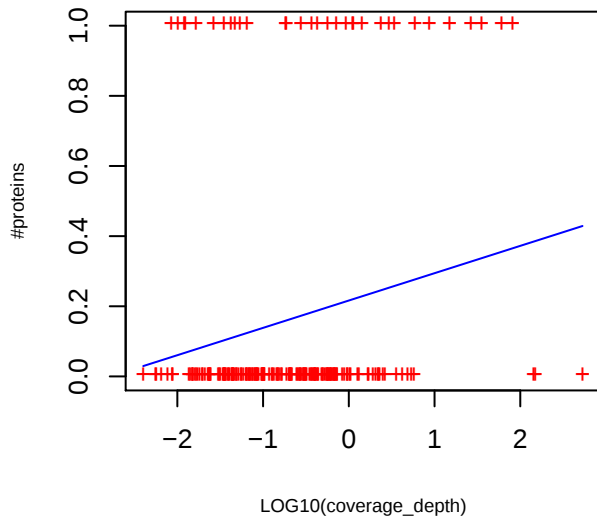


P-value curve ; red (unnorm), green (norm)



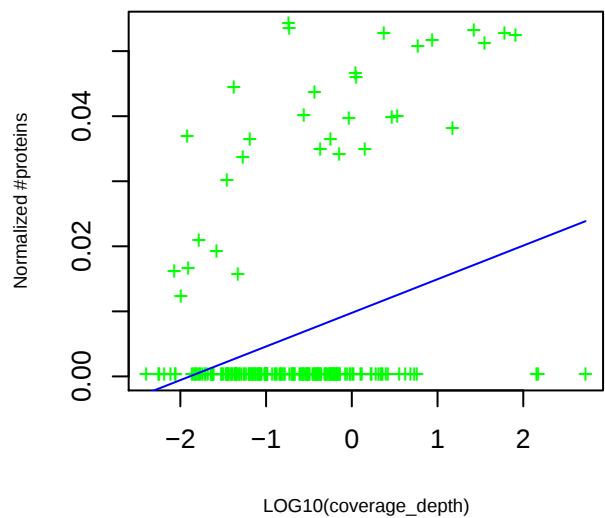
PF08854 DUF1824: Domain of unknown function (DUF1824)

slope= 0.078 p_value= 0.008 intercept= 0.22 p_value= 4e-10



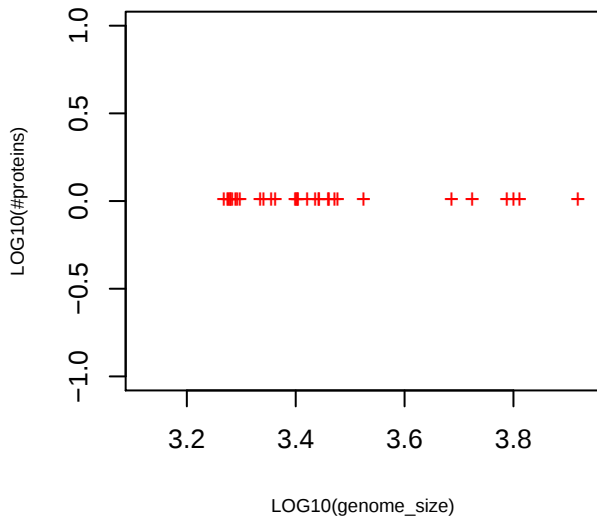
PF08854 DUF1824: Domain of unknown function (DUF1824)

slope= 0.0052 p_value= 1e-05 intercept= 0.0098 p_value= 1.3e-12

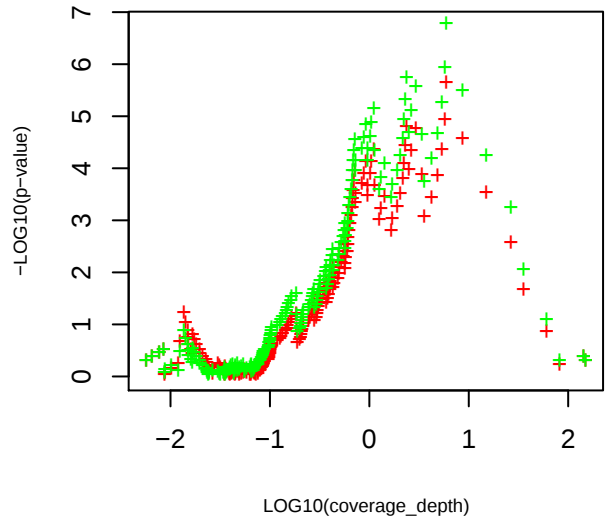


PF08854 DUF1824: Domain of unknown function (DUF1824)

slope= -2.33 p_value= 0.00026 intercept= 4.92 p_value= 0.028

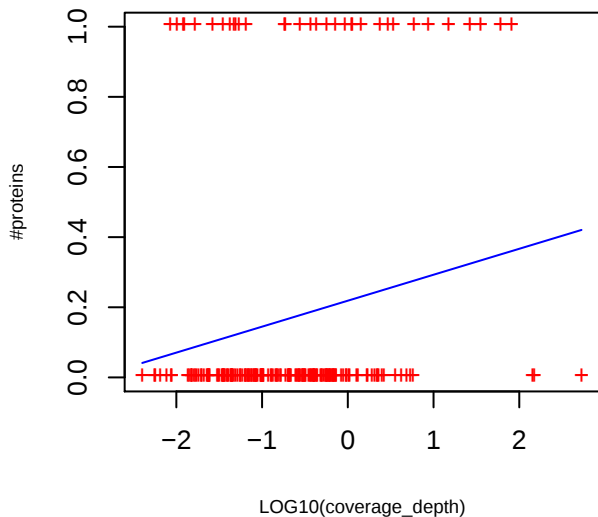


P-value curve ; red (unnorm), green (norm)



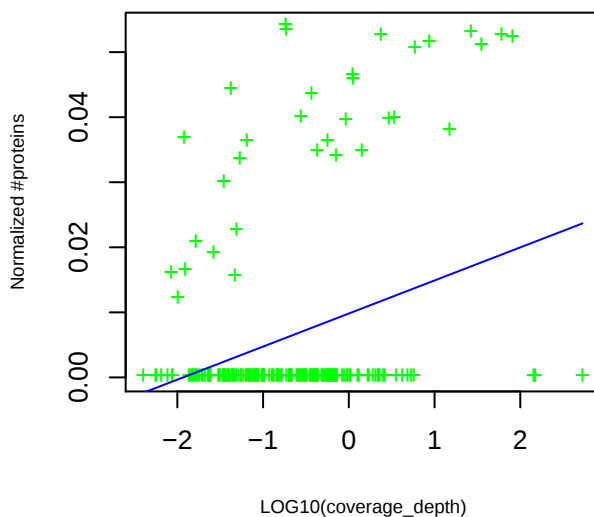
PF07444 Ycf66_N: Ycf66 protein N-terminus

slope= 0.074 p_value= 0.013 intercept= 0.22 p_value= 4.6e-10



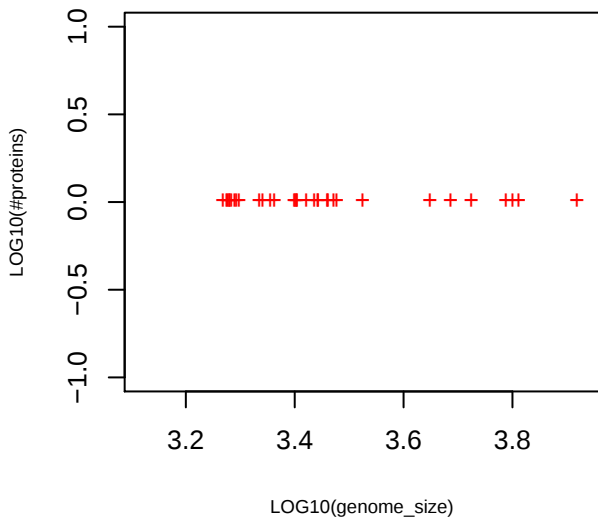
PF07444 Ycf66_N: Ycf66 protein N-terminus

slope= 0.0051 p_value= 1.5e-05 intercept= 0.0098 p_value= 1.2e-12

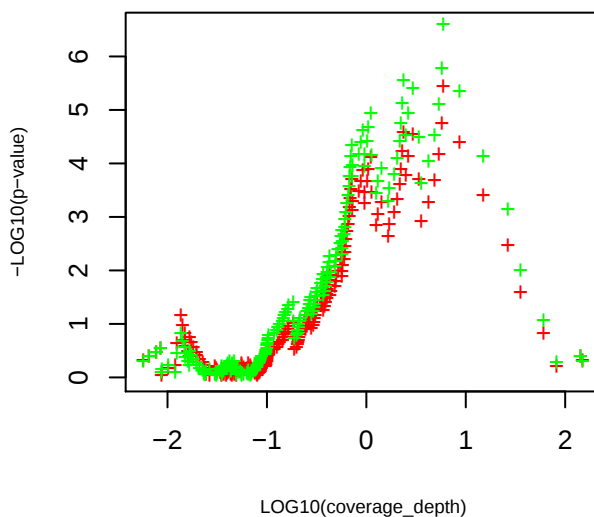


PF07444 Ycf66_N: Ycf66 protein N-terminus

slope= -2.25 p_value= 0.00051 intercept= 4.66 p_value= 0.041

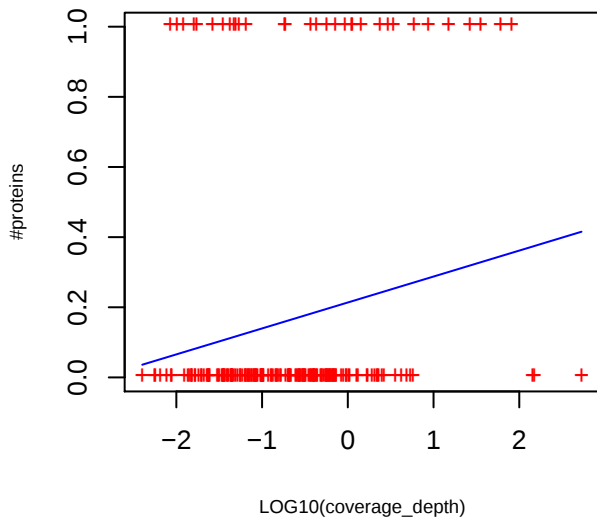


P-value curve ; red (unnorm), green (norm)



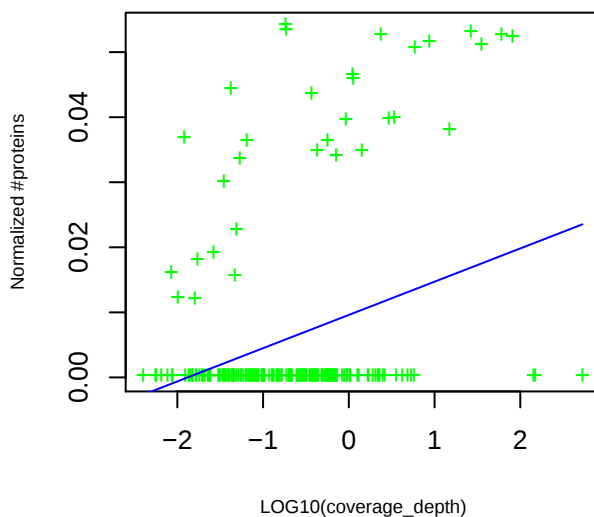
PF02532 Psbl: Photosystem II reaction center I protein (PSII 4.8 kDa protein)

slope= 0.074 p_value= 0.012 intercept= 0.21 p_value= 6.7e-10



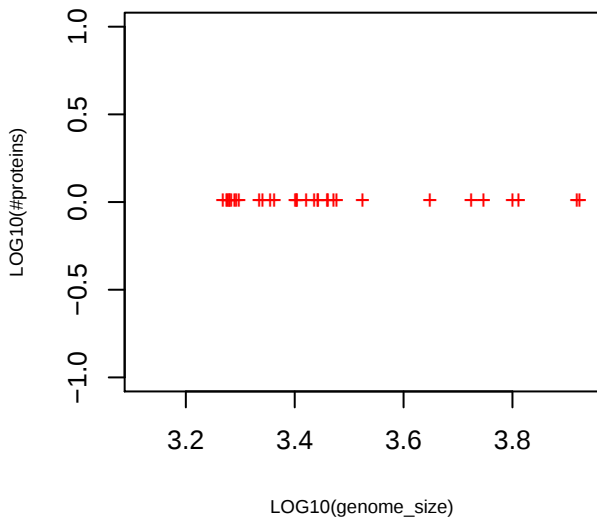
PF02532 Psbl: Photosystem II reaction center I protein (PSII 4.8 kDa protein)

slope= 0.0051 p_value= 1e-05 intercept= 0.0096 p_value= 1.6e-12

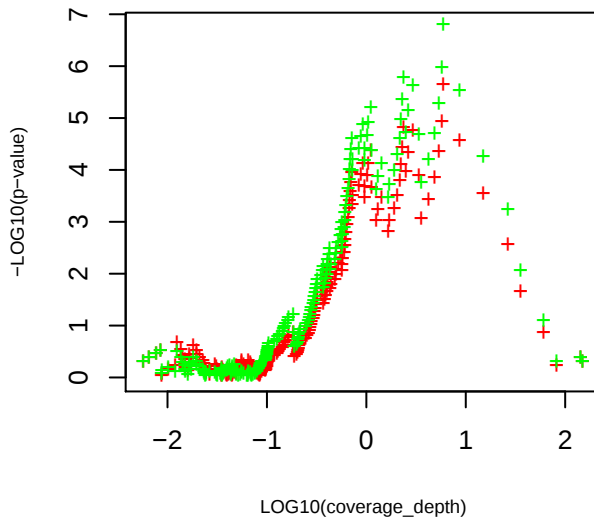


PF02532 Psbl: Photosystem II reaction center I protein (PSII 4.8 kDa protein)

slope= -1.99 p_value= 0.0019 intercept= 3.71 p_value= 0.10

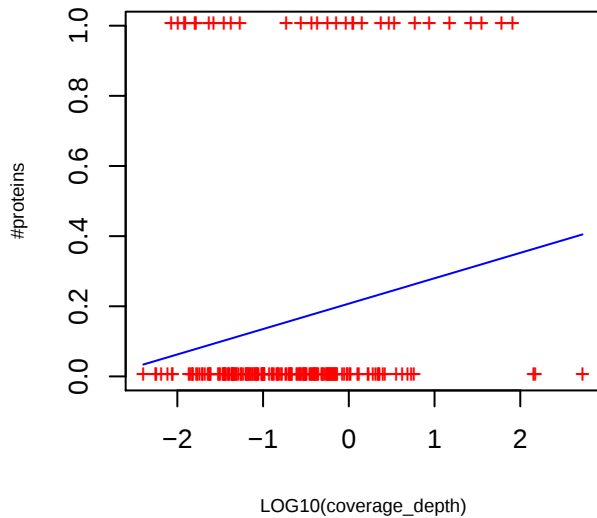


P-value curve ; red (unnorm), green (norm)



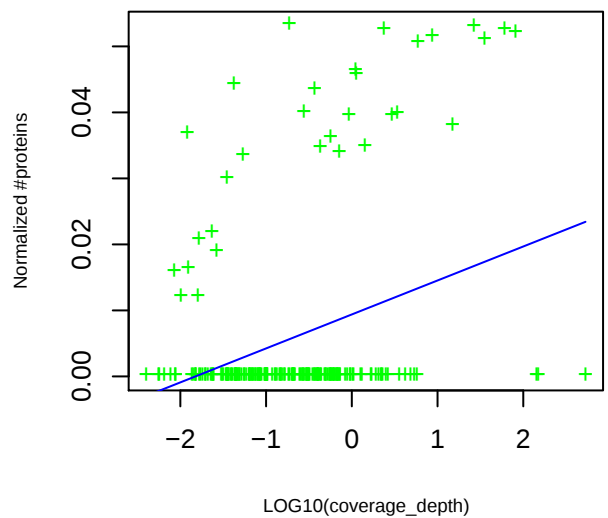
TIGR03038 PS_II_psbM: photosystem II reaction center protein PsbM

slope= 0.072 p_value= 0.013 intercept= 0.21 p_value= 1.2e-09



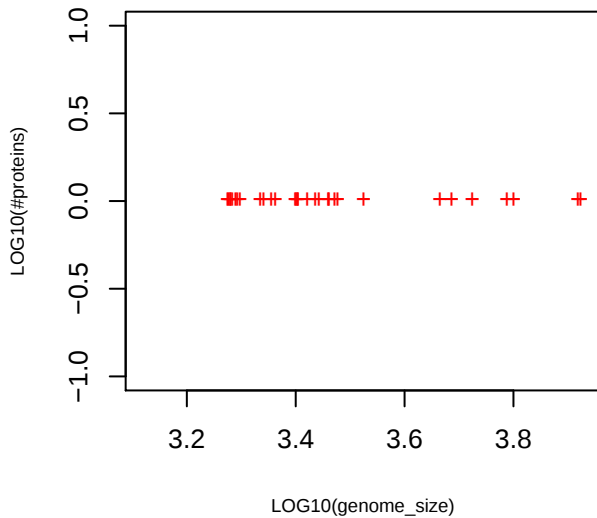
TIGR03038 PS_II_psbM: photosystem II reaction center protein PsbM

slope= 0.0051 p_value= 5.1e-06 intercept= 0.0094 p_value= 1.4e-12

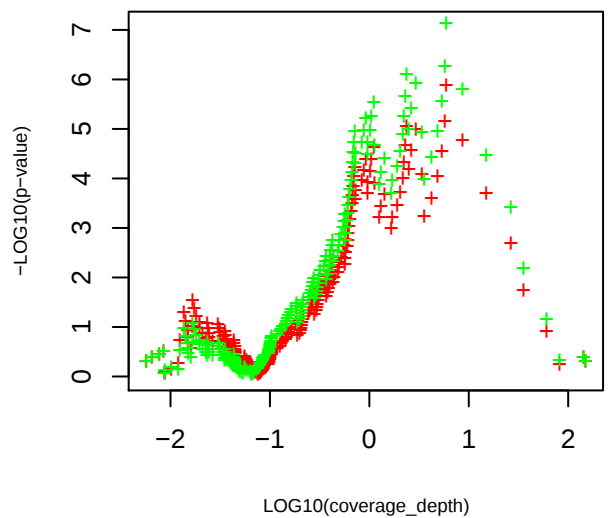


TIGR03038 PS_II_psbM: photosystem II reaction center protein PsbM

slope= -1.86 p_value= 0.0033 intercept= 3.24 p_value= 0.15

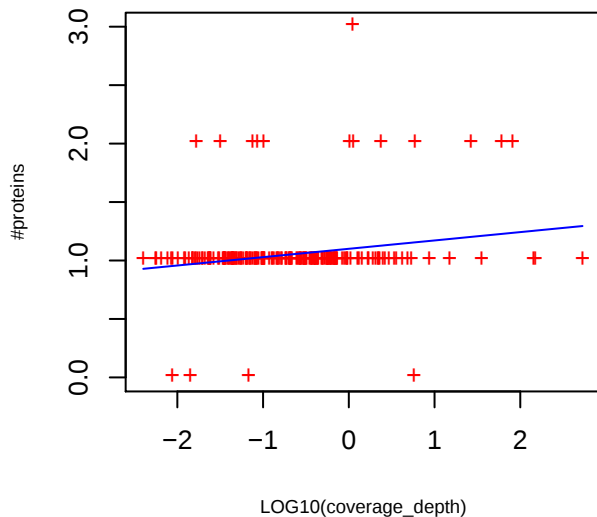


P-value curve ; red (unnorm), green (norm)



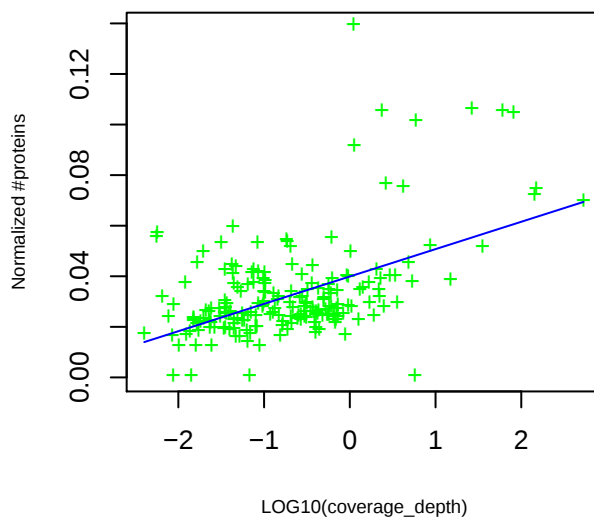
PF01653 DNA_ligase_aden: NAD-dependent DNA ligase adenylation domain

slope= 0.071 p_value= 0.0043 intercept= 1.10 p_value= 8.4e-95



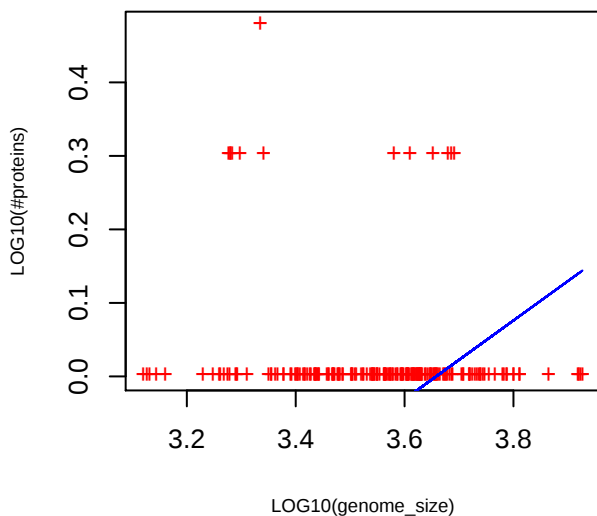
PF01653 DNA_ligase_aden: NAD-dependent DNA ligase adenylation domain

slope= 0.011 p_value= 6.8e-14 intercept= 0.04 p_value= 3e-66

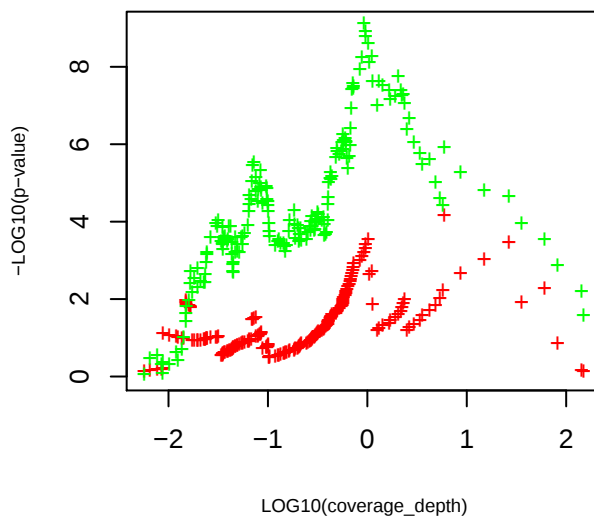


PF01653 DNA_ligase_aden: NAD-dependent DNA ligase adenylation domain

slope= 0.54 p_value= 0.033 intercept= -1.96 p_value= 0.028

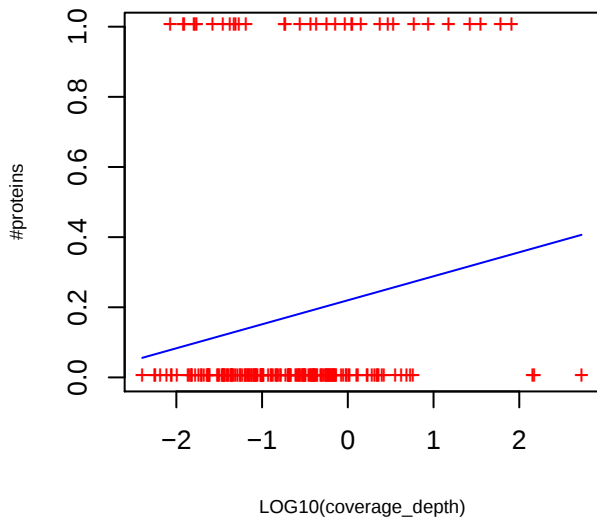


P-value curve ; red (unnorm), green (norm)



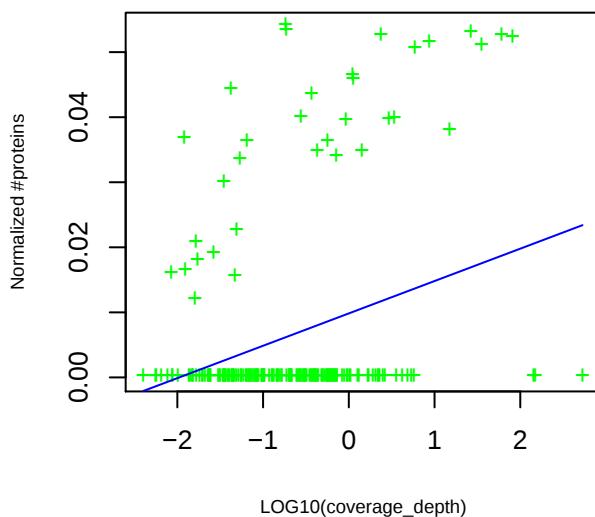
TIGR03039 PS_II_CP47: photosystem II chlorophyll-binding protein CP47

slope= 0.068 p_value= 0.023 intercept= 0.22 p_value= 6.3e-10



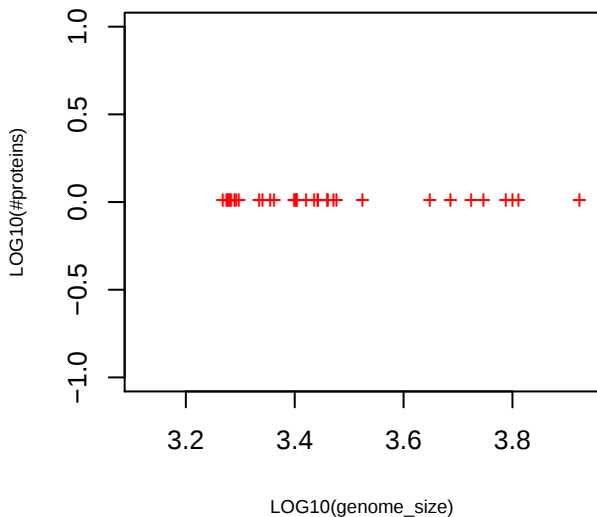
TIGR03039 PS_II_CP47: photosystem II chlorophyll-binding protein CP47

slope= 0.005 p_value= 2.4e-05 intercept= 0.0098 p_value= 1.3e-12

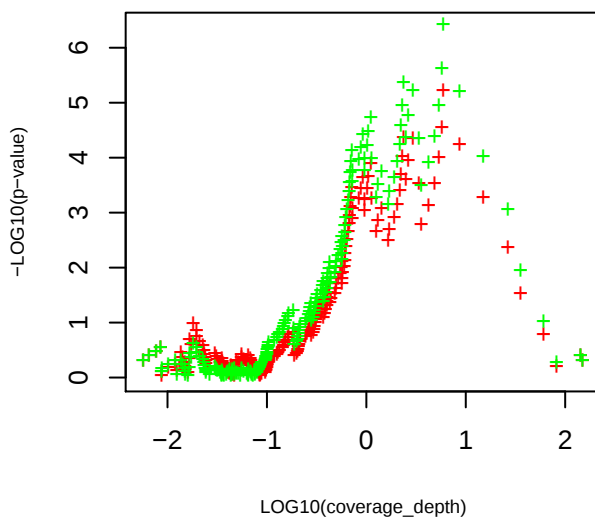


TIGR03039 PS_II_CP47: photosystem II chlorophyll-binding protein CP47

slope= -2.10 p_value= 0.0014 intercept= 4.12 p_value= 0.075

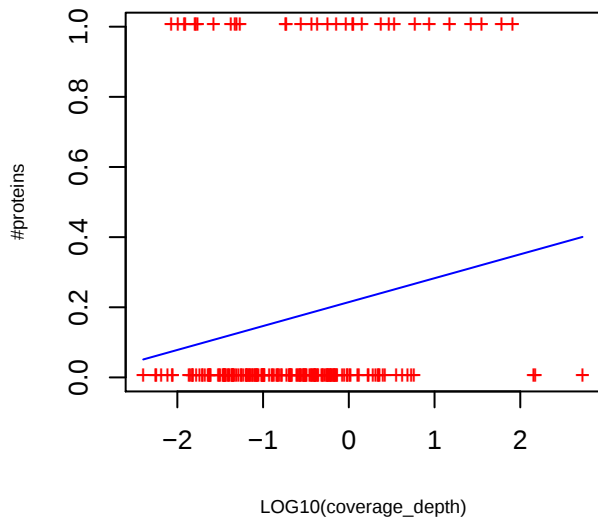


P-value curve ; red (unnorm), green (norm)



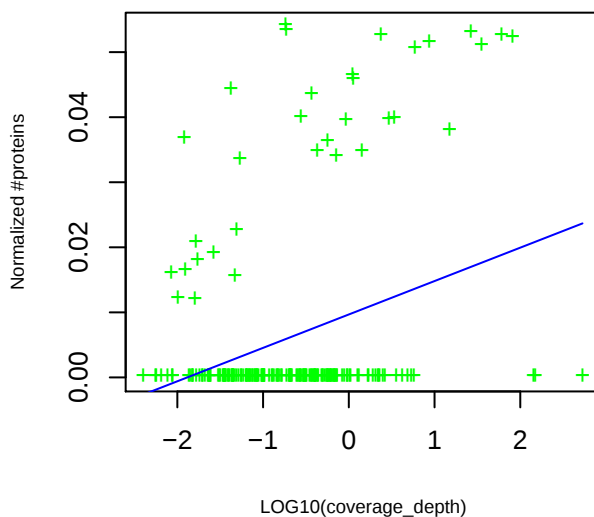
PF08848 DUF1818: Domain of unknown function (DUF1818)

slope= 0.068 p_value= 0.022 intercept= 0.21 p_value= 9.7e-10



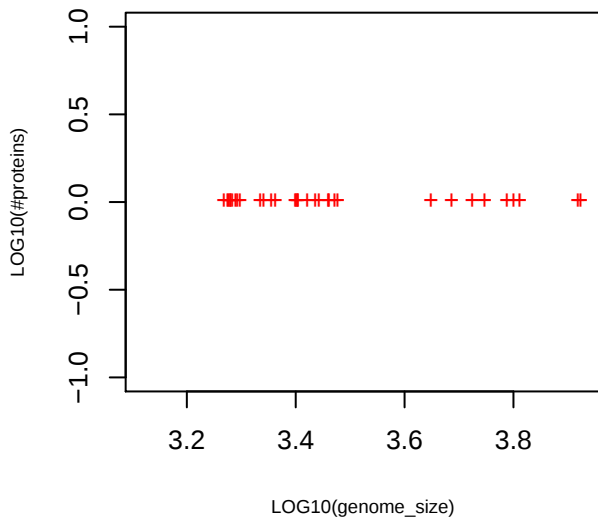
PF08848 DUF1818: Domain of unknown function (DUF1818)

slope= 0.0051 p_value= 8.9e-06 intercept= 0.0097 p_value= 1.1e-12

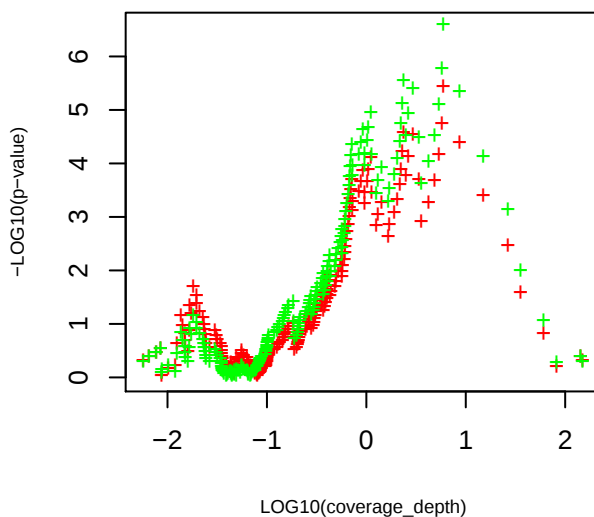


PF08848 DUF1818: Domain of unknown function (DUF1818)

slope= -1.71 p_value= 0.0086 intercept= 2.75 p_value= 0.23

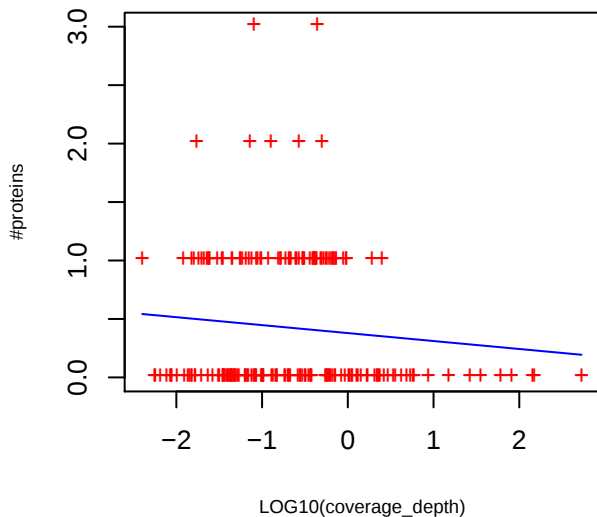


P-value curve ; red (unnorm), green (norm)



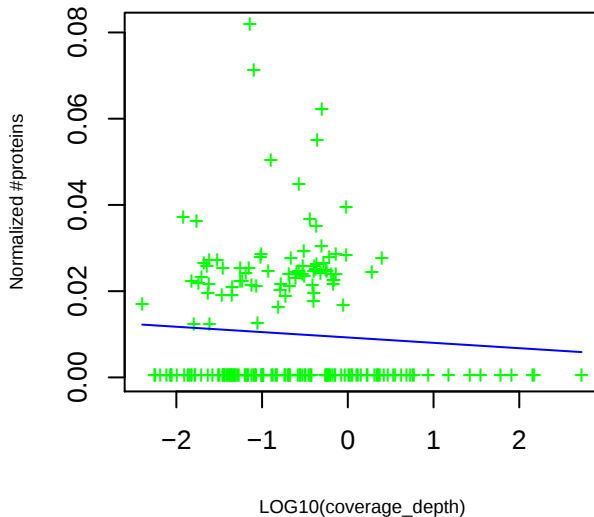
PF06537 DUF1111: Protein of unknown function (DUF1111)

slope= -0.068 p_value= 0.16 intercept= 0.38 p_value= 3.1e-11



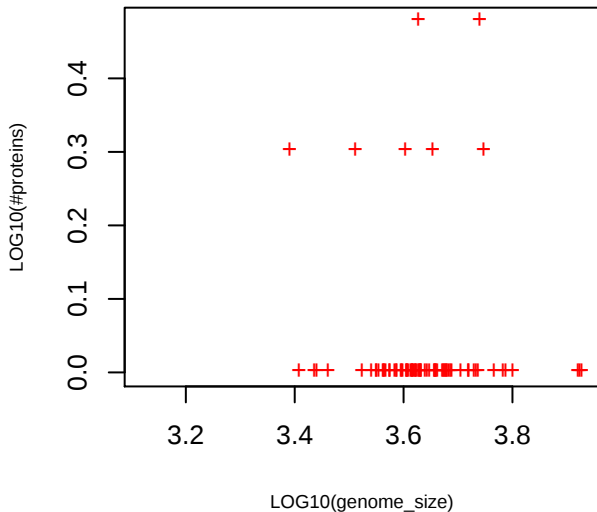
PF06537 DUF1111: Protein of unknown function (DUF1111)

slope= -0.0012 p_value= 0.30 intercept= 0.0093 p_value= 6.2e-11

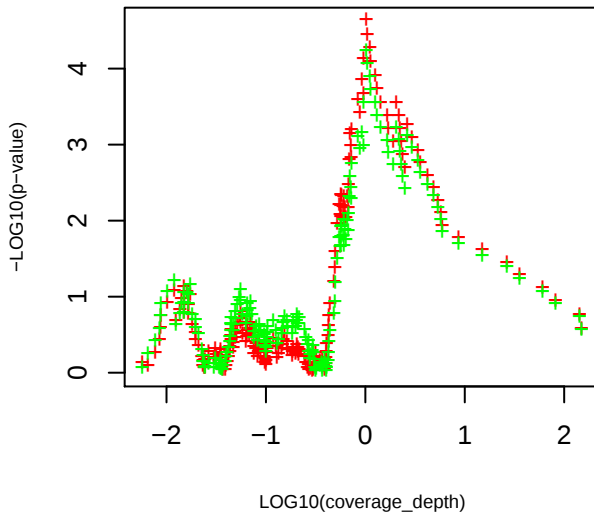


PF06537 DUF1111: Protein of unknown function (DUF1111)

slope= 5.33 p_value= 7.7e-11 intercept= -21.35 p_value= 4.3e-13

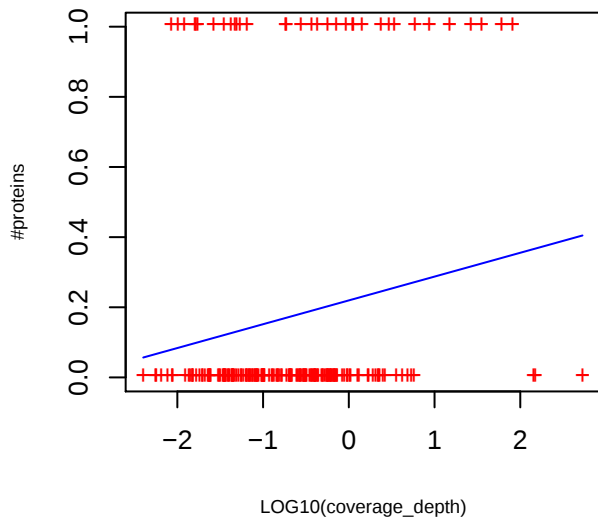


P-value curve ; red (unnorm), green (norm)



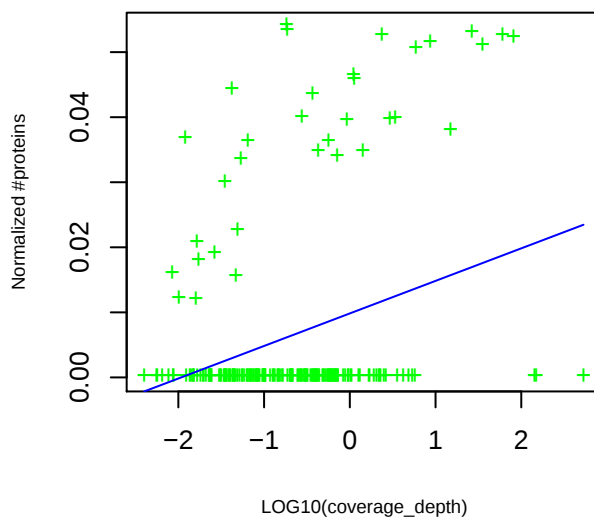
PF01788 PsbJ: PsbJ

slope= 0.068 p_value= 0.024 intercept= 0.22 p_value= 6.8e-10



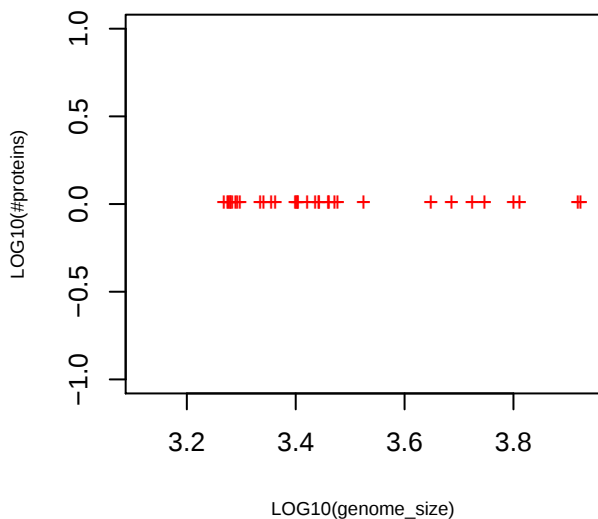
PF01788 PsbJ: PsbJ

slope= 0.005 p_value= 2.1e-05 intercept= 0.0098 p_value= 1.3e-12

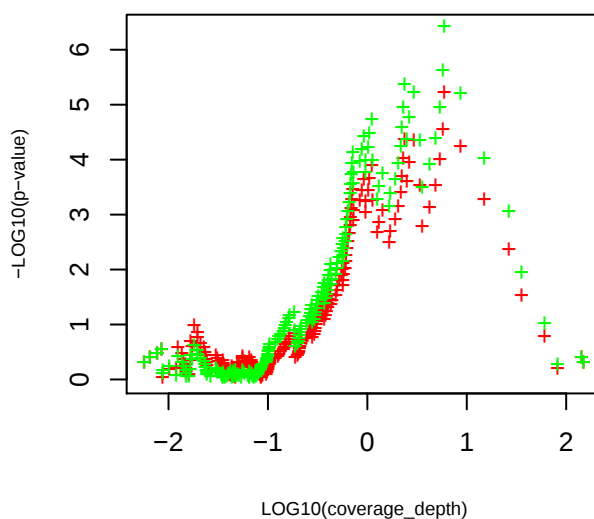


PF01788 PsbJ: PsbJ

slope= -2.00 p_value= 0.0024 intercept= 3.77 p_value= 0.10

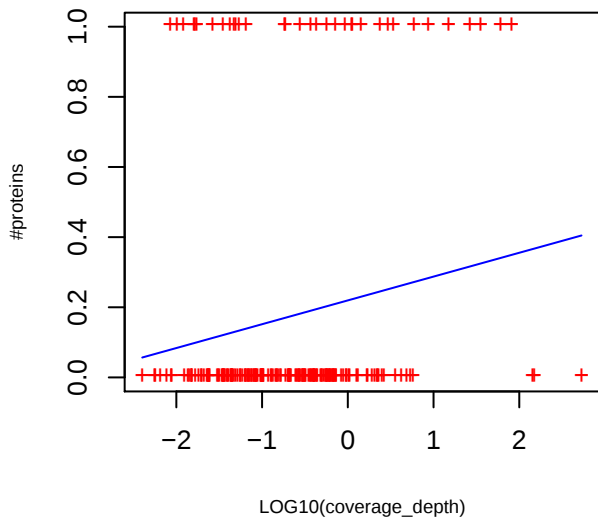


P-value curve ; red (unnorm), green (norm)



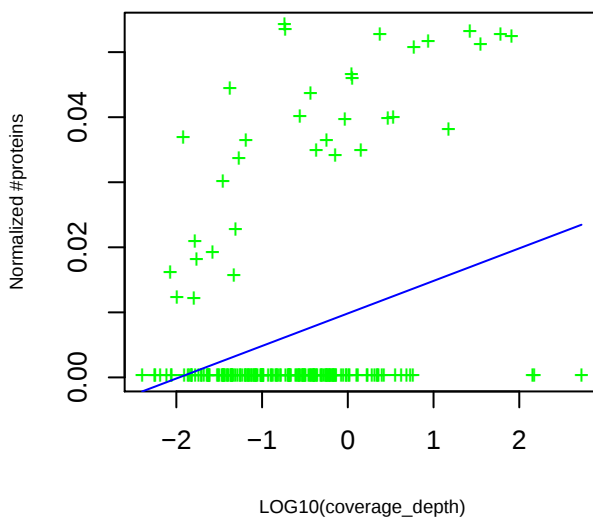
PF05421 DUF751: Protein of unknown function (DUF751)

slope= 0.068 p_value= 0.024 intercept= 0.22 p_value= 6.8e-10



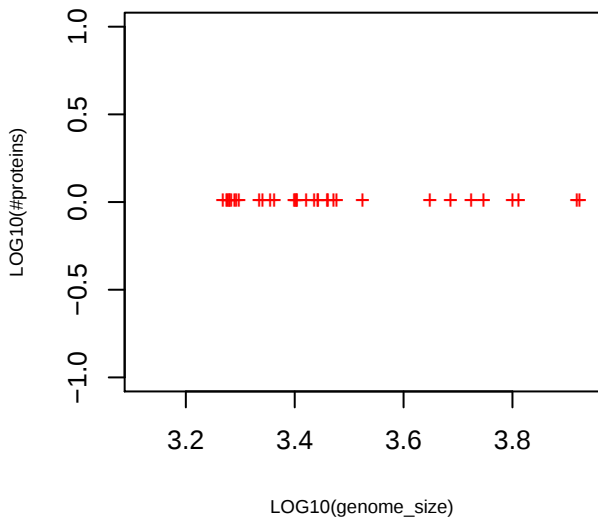
PF05421 DUF751: Protein of unknown function (DUF751)

slope= 0.005 p_value= 2.1e-05 intercept= 0.0098 p_value= 1.3e-12

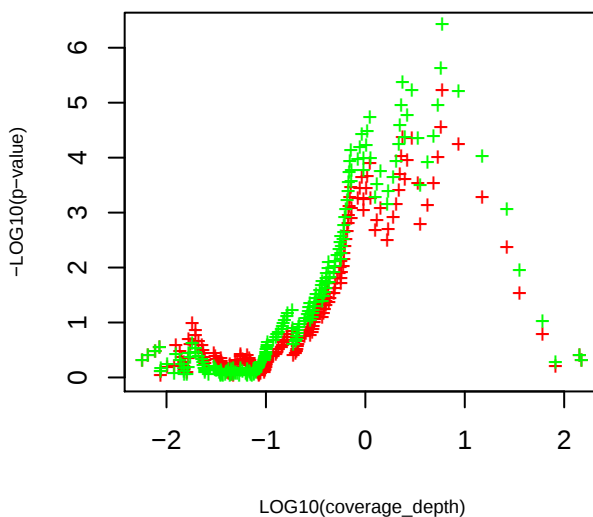


PF05421 DUF751: Protein of unknown function (DUF751)

slope= -2.00 p_value= 0.0024 intercept= 3.77 p_value= 0.10

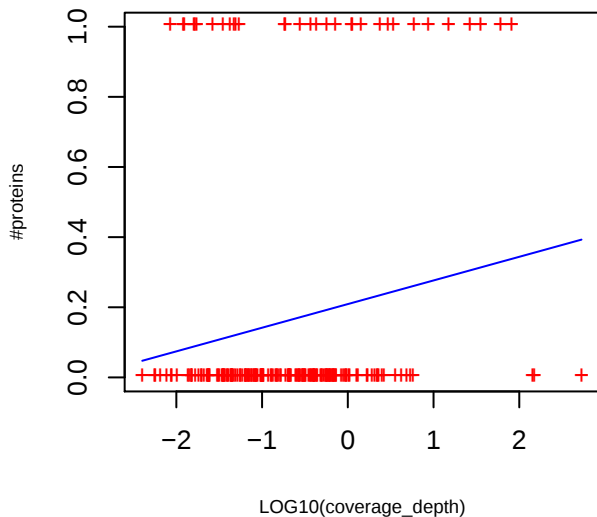


P-value curve ; red (unnorm), green (norm)



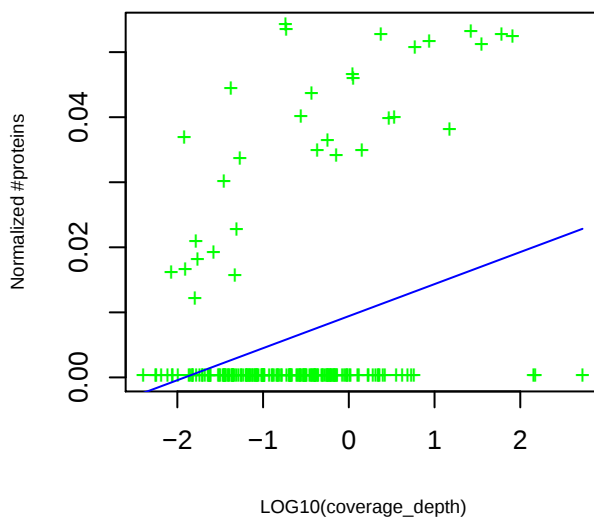
TIGR02656 cyanin_plasto: plastocyanin

slope= 0.067 p_value= 0.022 intercept= 0.21 p_value= 1.6e-09



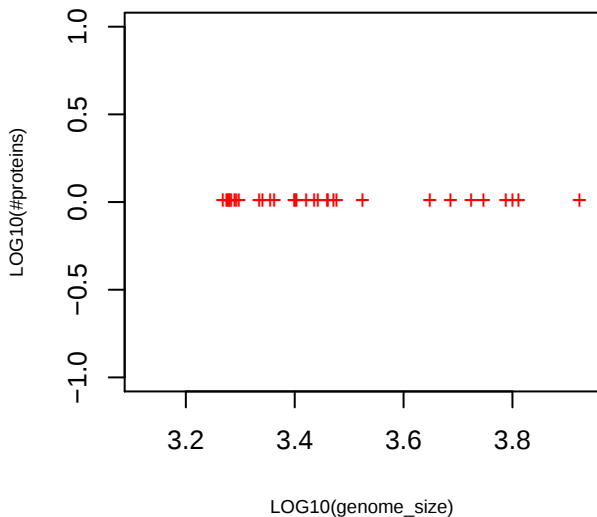
TIGR02656 cyanin_plasto: plastocyanin

slope= 0.0049 p_value= 1.9e-05 intercept= 0.0094 p_value= 3.2e-12

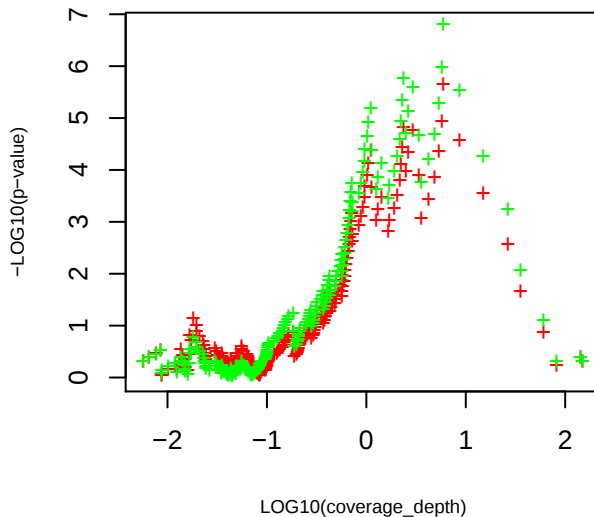


TIGR02656 cyanin_plasto: plastocyanin

slope= -1.91 p_value= 0.003 intercept= 3.42 p_value= 0.13

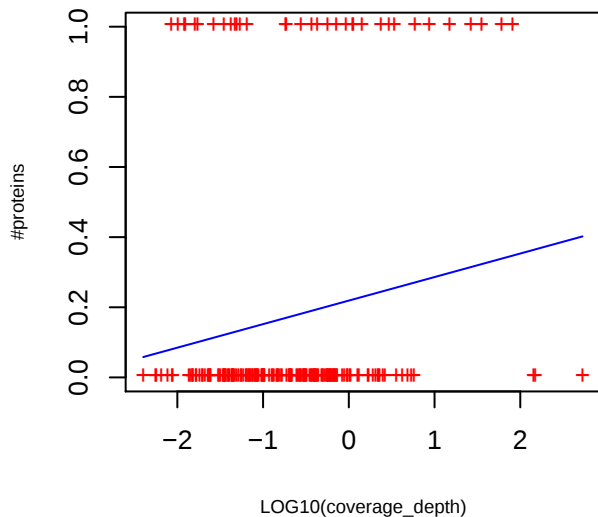


P-value curve ; red (unnorm), green (norm)



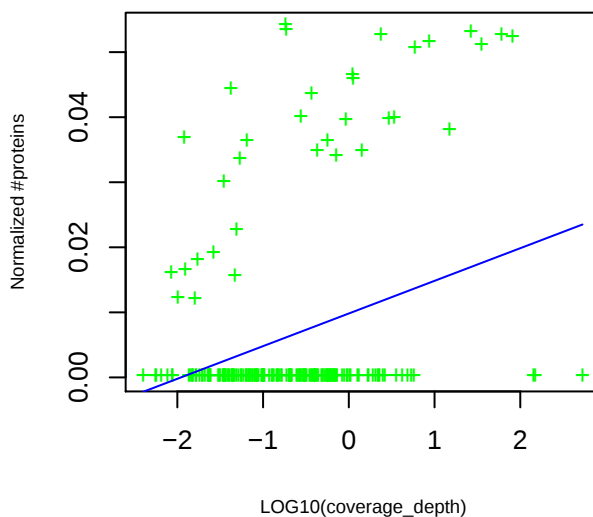
PF02392 Ycf4: Ycf4

slope= 0.067 p_value= 0.026 intercept= 0.22 p_value= 7.5e-10



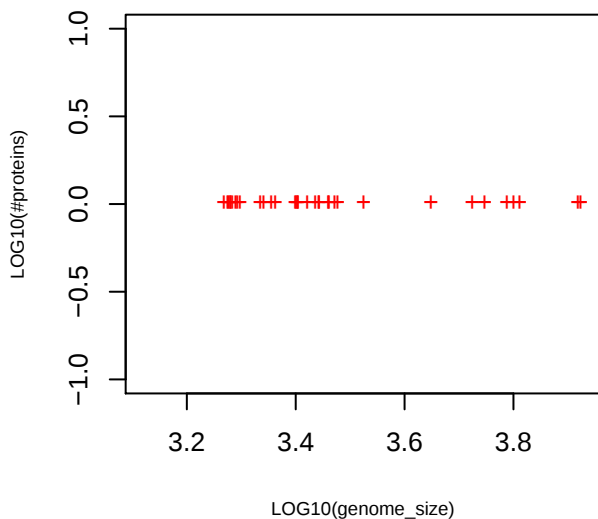
PF02392 Ycf4: Ycf4

slope= 0.005 p_value= 1.9e-05 intercept= 0.0098 p_value= 1.2e-12

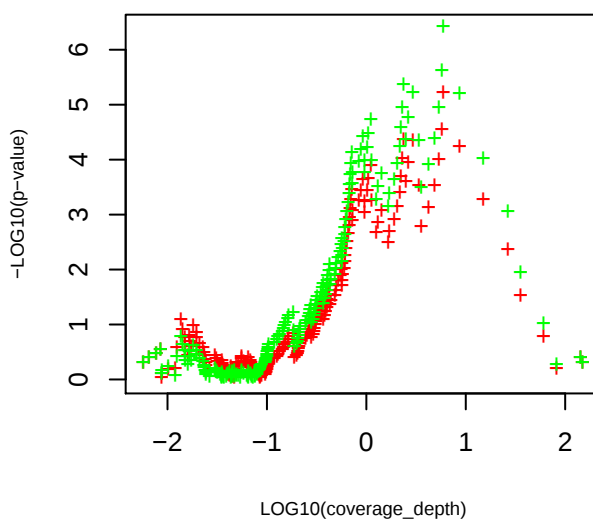


PF02392 Ycf4: Ycf4

slope= -1.92 p_value= 0.0036 intercept= 3.49 p_value= 0.13

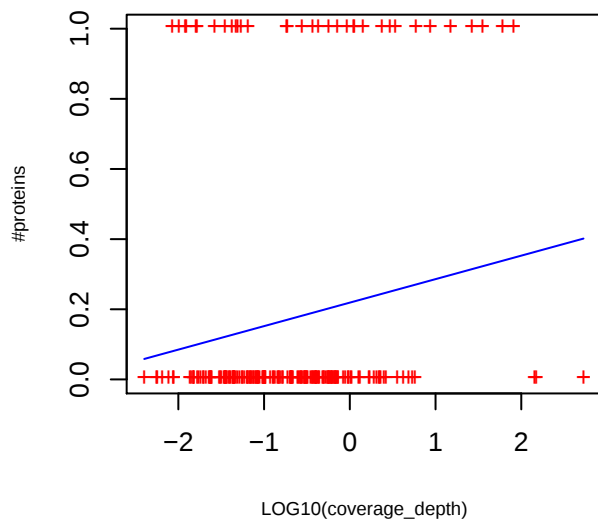


P-value curve ; red (unnorm), green (norm)



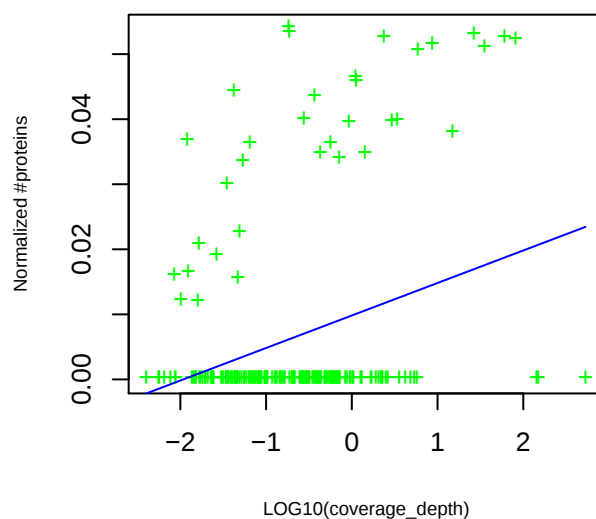
PF04839 PSRP-3_Ycf65: Plastid and cyanobacterial ribosomal protein (PSRP-3 / Ycf65)

slope= 0.067 p_value= 0.026 intercept= 0.22 p_value= 7.6e-10



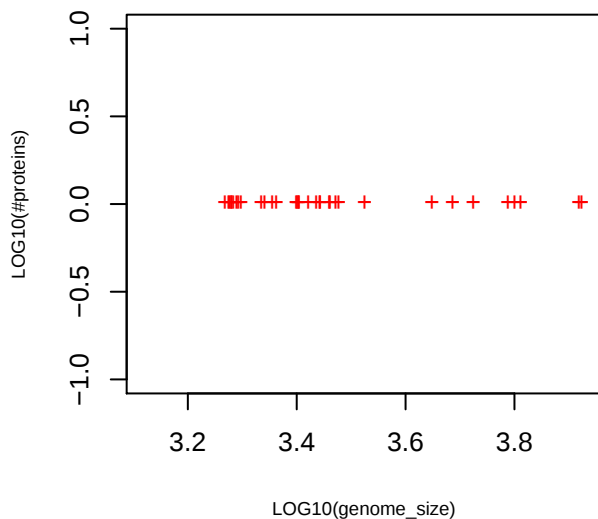
PF04839 PSRP-3_Ycf65: Plastid and cyanobacterial ribosomal protein (PSRP-3 / Ycf65)

slope= 0.005 p_value= 2.1e-05 intercept= 0.0098 p_value= 1.3e-12

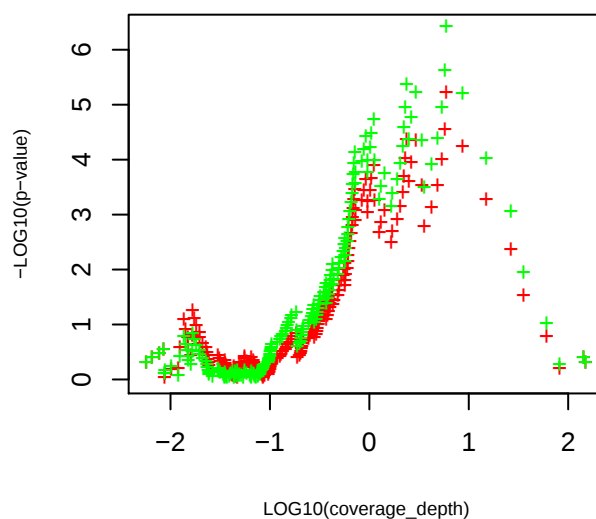


PF04839 PSRP-3_Ycf65: Plastid and cyanobacterial ribosomal protein (PSRP-3 / Ycf65)

slope= -1.96 p_value= 0.0029 intercept= 3.65 p_value= 0.12

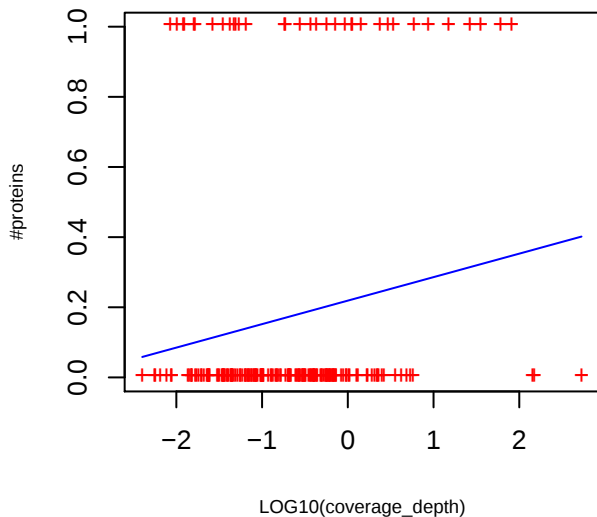


P-value curve ; red (unnorm), green (norm)



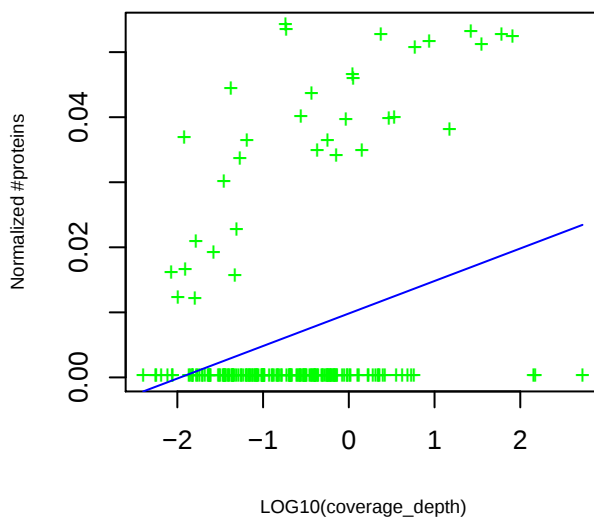
TIGR02730 carot_isom: carotene isomerase

slope= 0.067 p_value= 0.026 intercept= 0.22 p_value= 7.6e-10



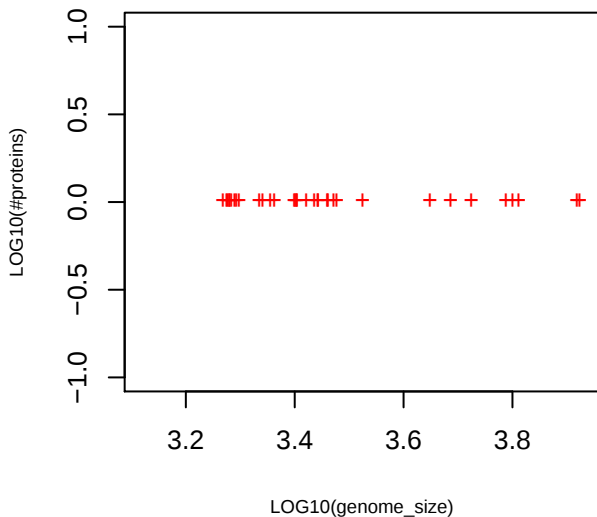
TIGR02730 carot_isom: carotene isomerase

slope= 0.005 p_value= 2.1e-05 intercept= 0.0098 p_value= 1.3e-12

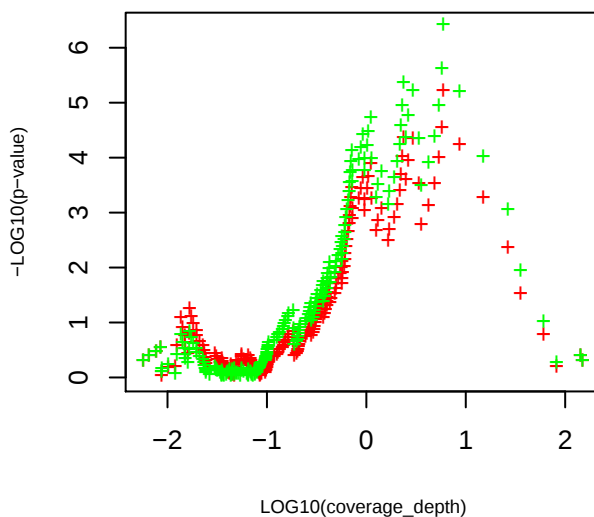


TIGR02730 carot_isom: carotene isomerase

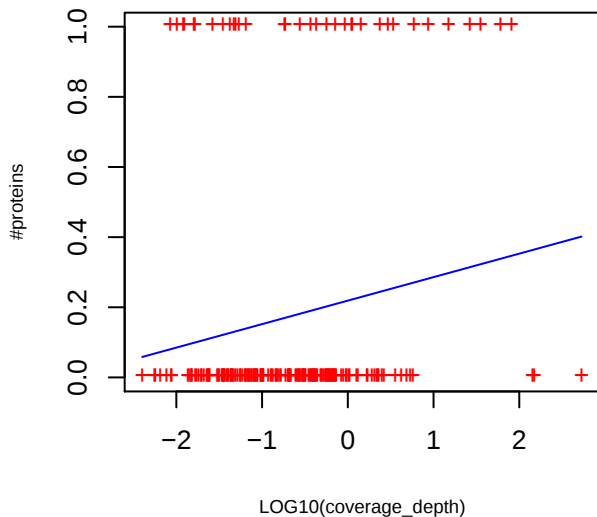
slope= -1.96 p_value= 0.0029 intercept= 3.65 p_value= 0.12



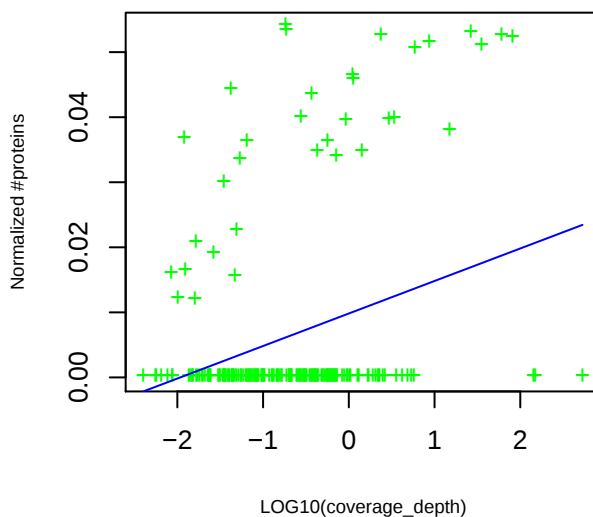
P-value curve ; red (unnorm), green (norm)



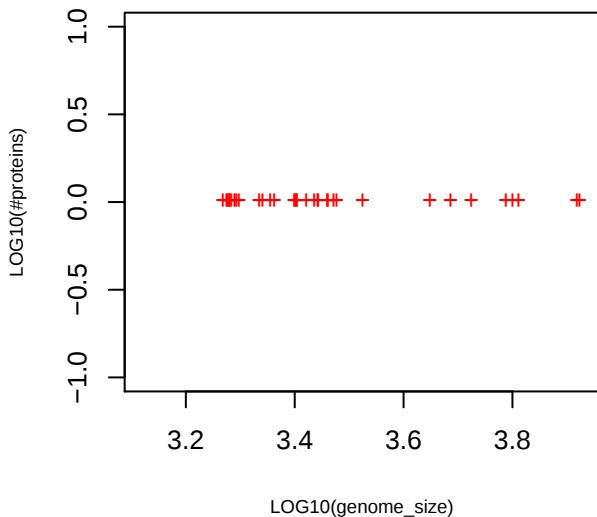
TIGR02731 phytoene_desat: phytoene desaturase
 slope= 0.067 p_value= 0.026 intercept= 0.22 p_value= 7.6e-10



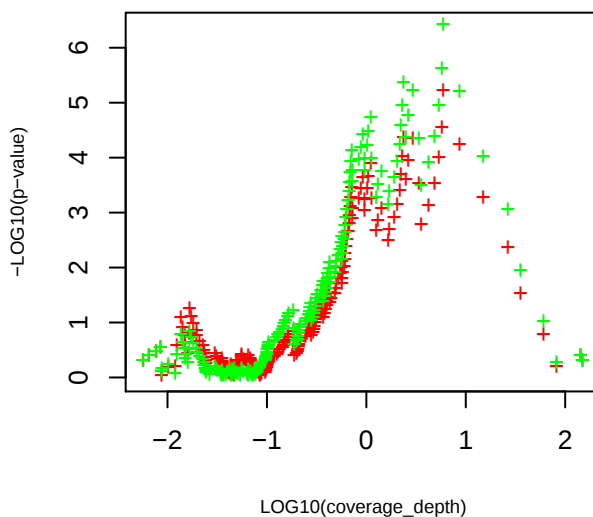
TIGR02731 phytoene_desat: phytoene desaturase
 slope= 0.005 p_value= 2.1e-05 intercept= 0.0098 p_value= 1.3e-12



TIGR02731 phytoene_desat: phytoene desaturase
 slope= -1.96 p_value= 0.0029 intercept= 3.65 p_value= 0.12

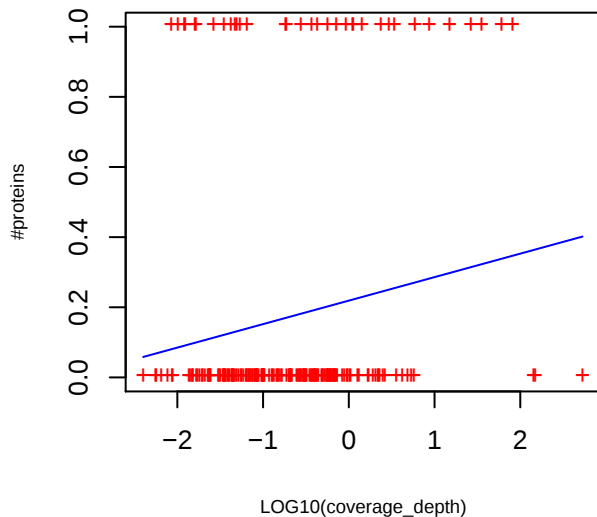


P-value curve ; red (unnorm), green (norm)



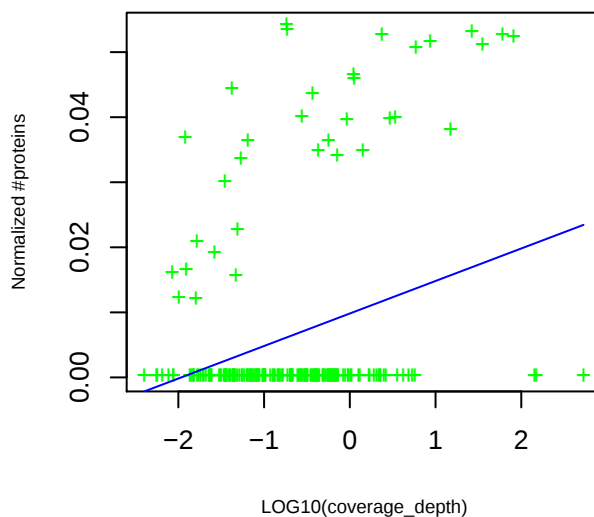
TIGR02732 zeta_caro_desat: carotene 7,8-desaturase

slope= 0.067 p_value= 0.026 intercept= 0.22 p_value= 7.6e-10



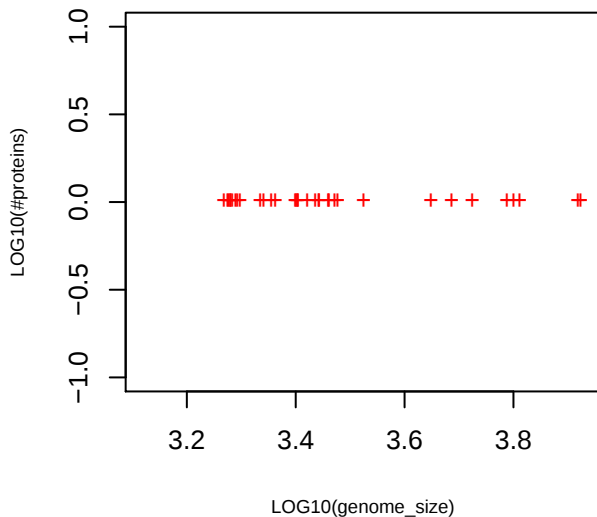
TIGR02732 zeta_caro_desat: carotene 7,8-desaturase

slope= 0.005 p_value= 2.1e-05 intercept= 0.0098 p_value= 1.3e-12

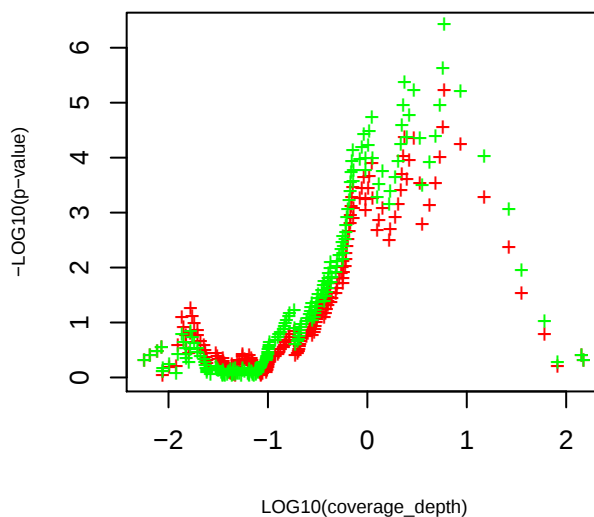


TIGR02732 zeta_caro_desat: carotene 7,8-desaturase

slope= -1.96 p_value= 0.0029 intercept= 3.65 p_value= 0.12

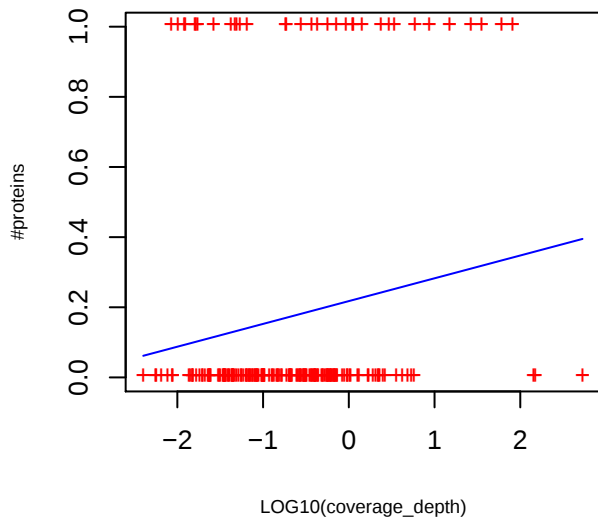


P-value curve ; red (unnorm), green (norm)



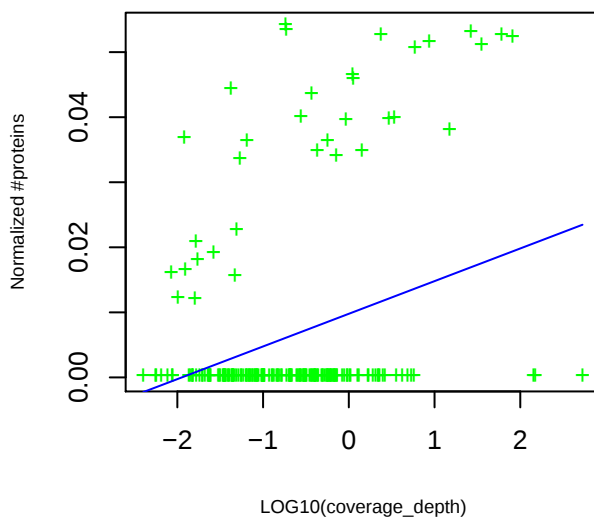
TIGR02654 circ_KaiB: circadian clock protein KaiB

slope= 0.065 p_value= 0.031 intercept= 0.22 p_value= 9.7e-10



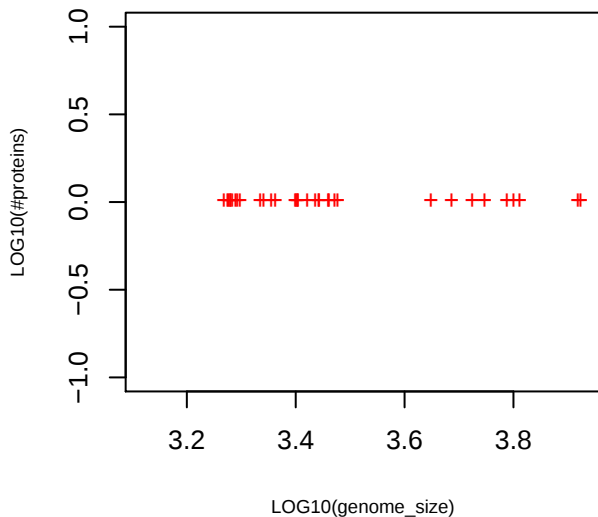
TIGR02654 circ_KaiB: circadian clock protein KaiB

slope= 0.005 p_value= 1.8e-05 intercept= 0.0098 p_value= 1.2e-12

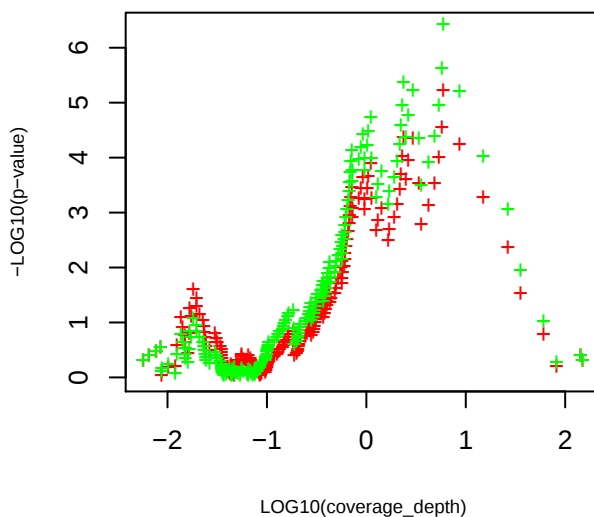


TIGR02654 circ_KaiB: circadian clock protein KaiB

slope= -1.79 p_value= 0.0066 intercept= 3.05 p_value= 0.19

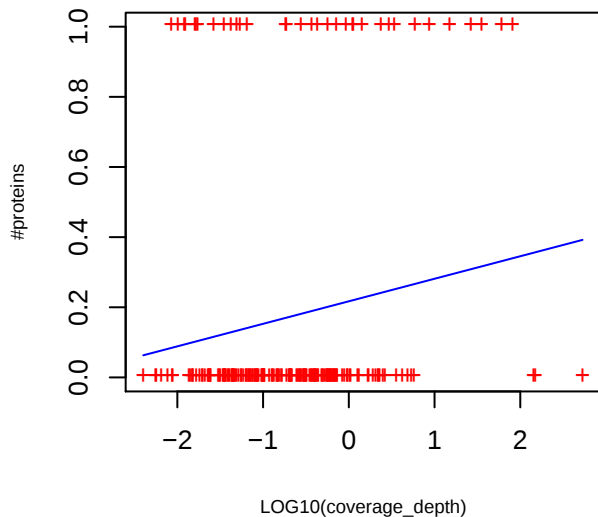


P-value curve : red (unnorm), green (norm)



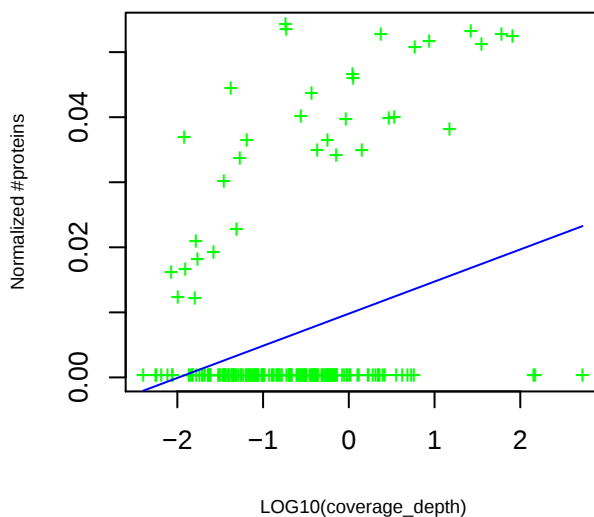
TIGR03279 cyano_FeS_chp: putative FeS-containing Cyanobacterial-specific oxidoreductase

slope= 0.064 p_value= 0.033 intercept= 0.22 p_value= 1.1e-09



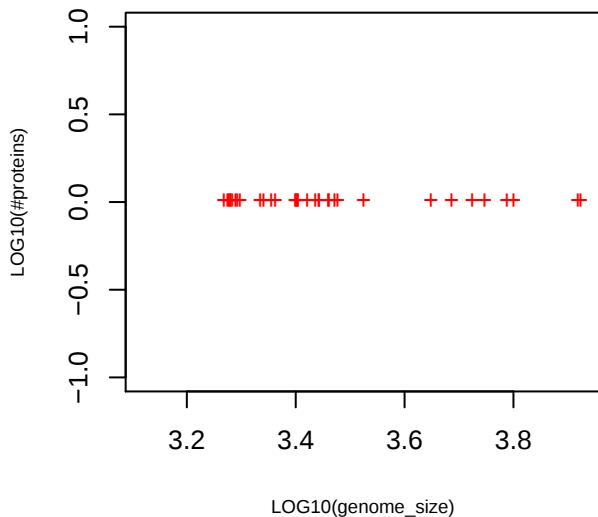
TIGR03279 cyano_FeS_chp: putative FeS-containing Cyanobacterial-specific oxidoreductase

slope= 0.0049 p_value= 2.7e-05 intercept= 0.0098 p_value= 1.6e-12

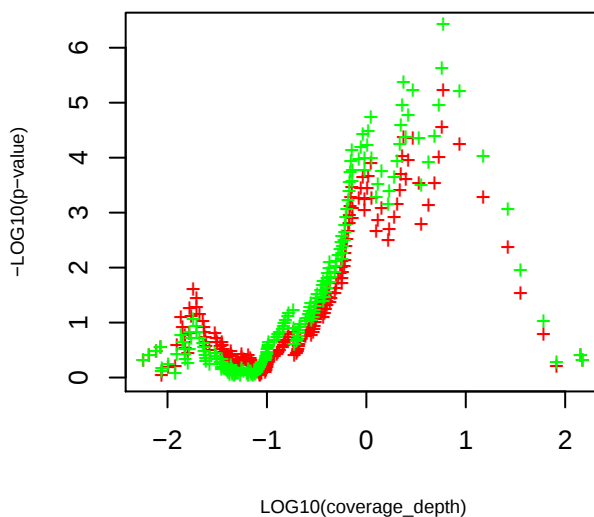


TIGR03279 cyano_FeS_chp: putative FeS-containing Cyanobacterial-specific oxidoreductase

slope= -2.01 p_value= 0.0022 intercept= 3.83 p_value= 0.099

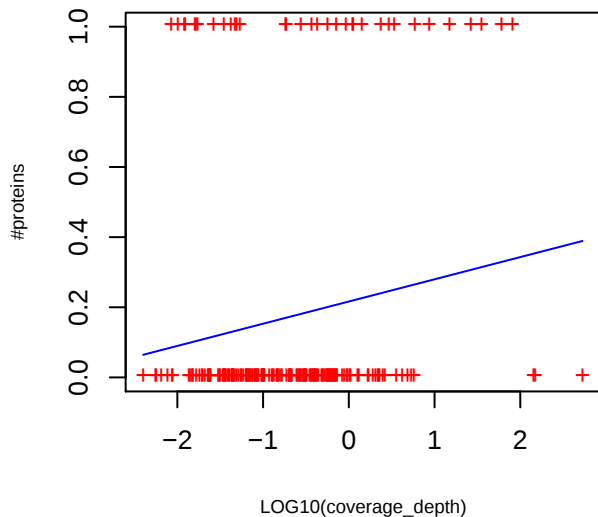


P-value curve ; red (unnorm), green (norm)



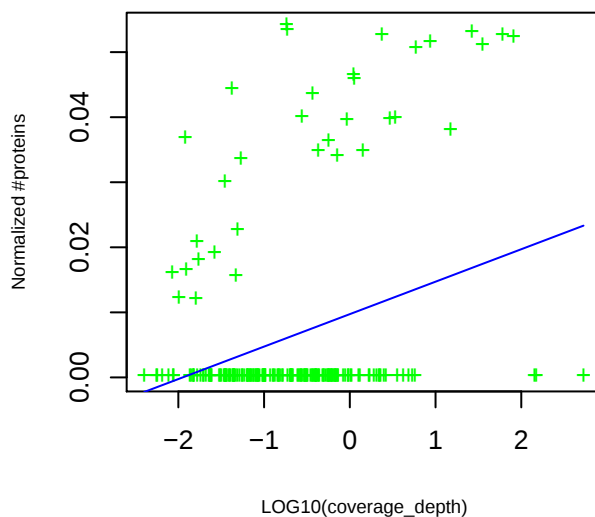
TIGR03060 PS_II_psb29: photosystem II biogenesis protein Psp29

slope= 0.063 p_value= 0.036 intercept= 0.22 p_value= 1.2e-09



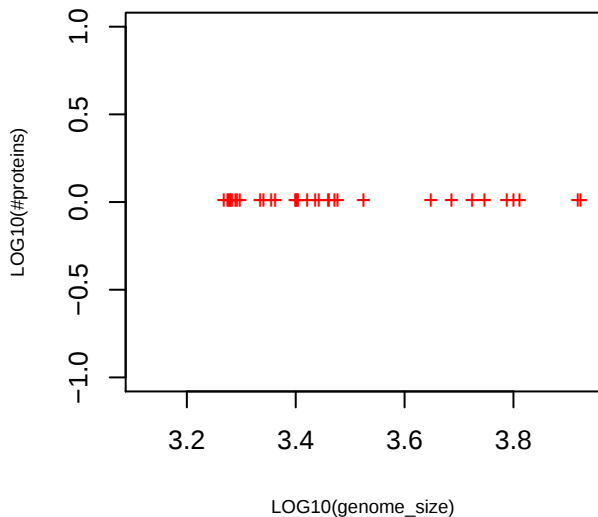
TIGR03060 PS_II_psb29: photosystem II biogenesis protein Psp29

slope= 0.005 p_value= 1.8e-05 intercept= 0.0097 p_value= 1.4e-12

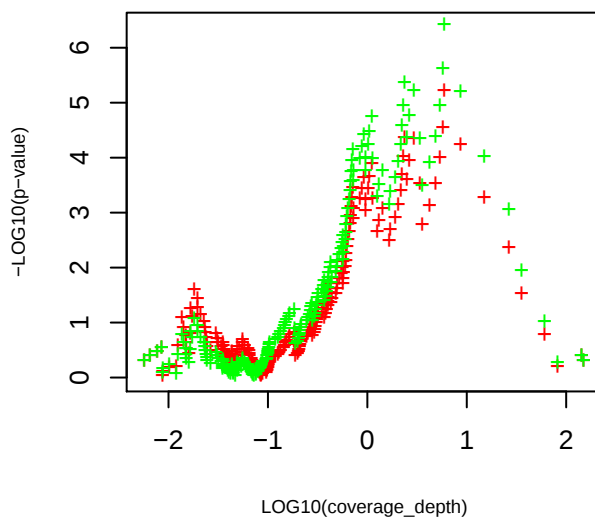


TIGR03060 PS_II_psb29: photosystem II biogenesis protein Psp29

slope= -1.73 p_value= 0.0088 intercept= 2.83 p_value= 0.23

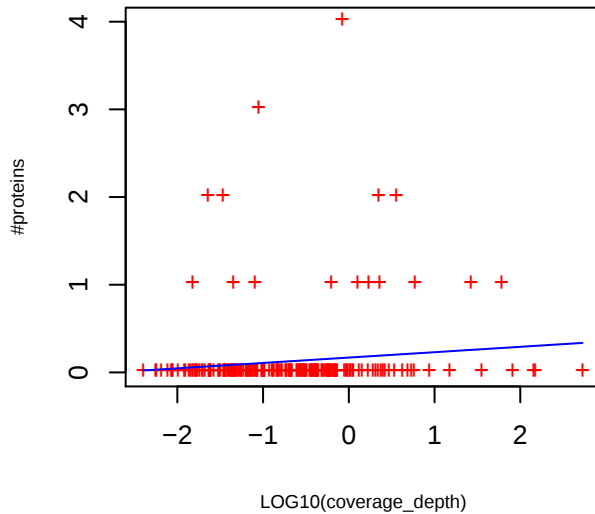


P-value curve ; red (unnorm), green (norm)



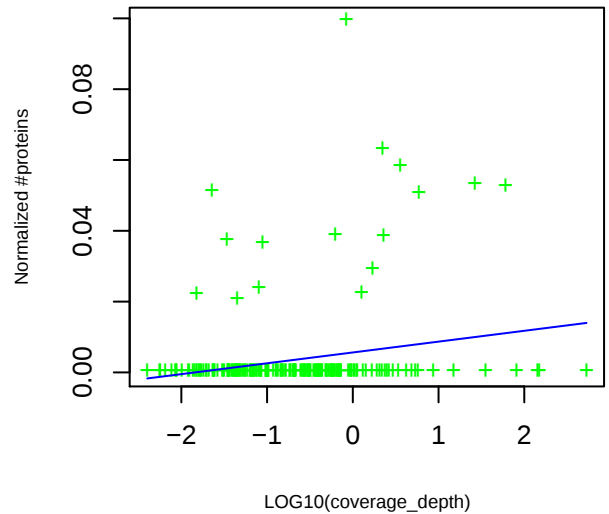
PF03382 DUF285: Mycoplasma protein of unknown function, DUF285

slope= 0.061 p_value= 0.12 intercept= 0.17 p_value= 0.00018



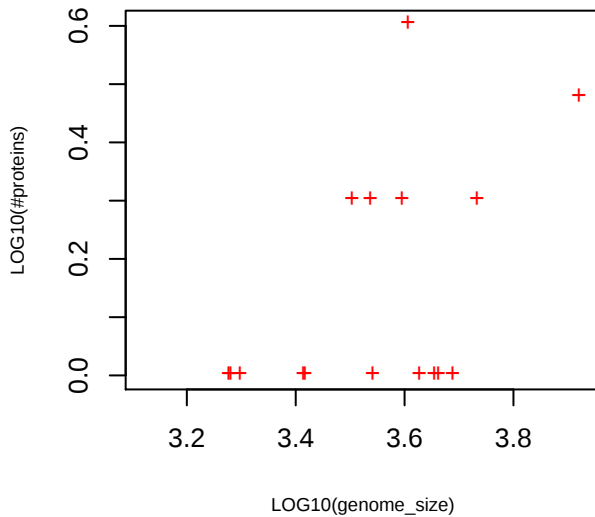
PF03382 DUF285: Mycoplasma protein of unknown function, DUF285

slope= 0.0031 p_value= 0.0033 intercept= 0.0056 p_value= 2.4e-06

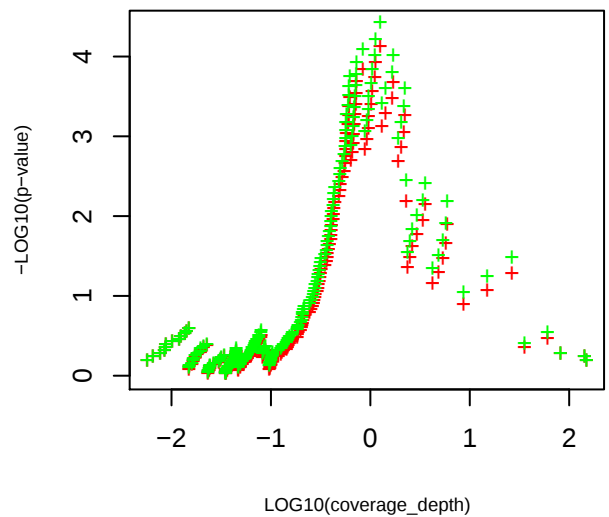


PF03382 DUF285: Mycoplasma protein of unknown function, DUF285

slope= 0.074 p_value= 0.88 intercept= -3.92 p_value= 0.028

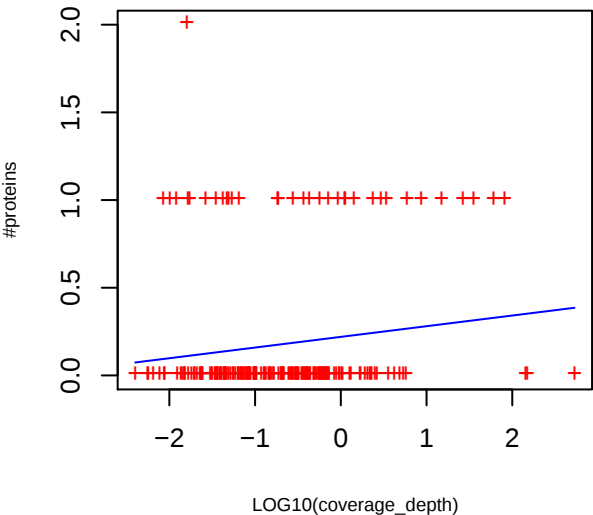


P-value curve ; red (unnorm), green (norm)



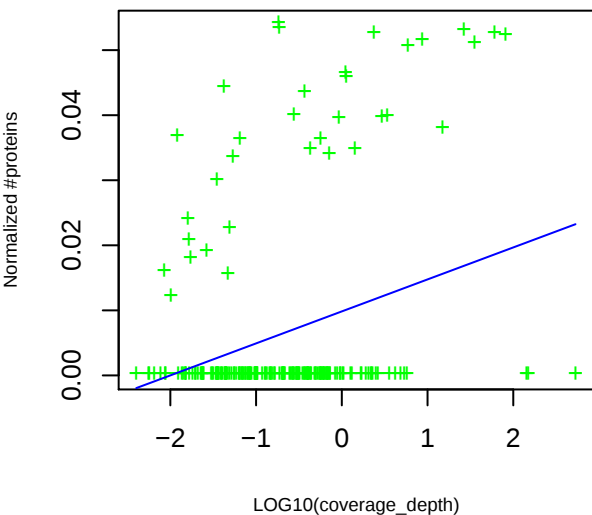
PF00284 Cytochrom_B559a: Luminal portion of Cytochrome b559, alpha (gene psbE) subunit

slope= 0.061 p_value= 0.054 intercept= 0.22 p_value= 3.4e-09



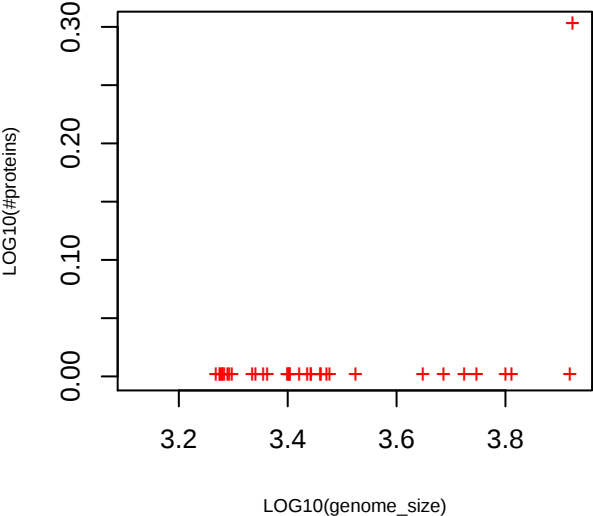
PF00284 Cytochrom_B559a: Luminal portion of Cytochrome b559, alpha (gene psbE) subunit

slope= 0.0049 p_value= 3.1e-05 intercept= 0.0098 p_value= 1.6e-12

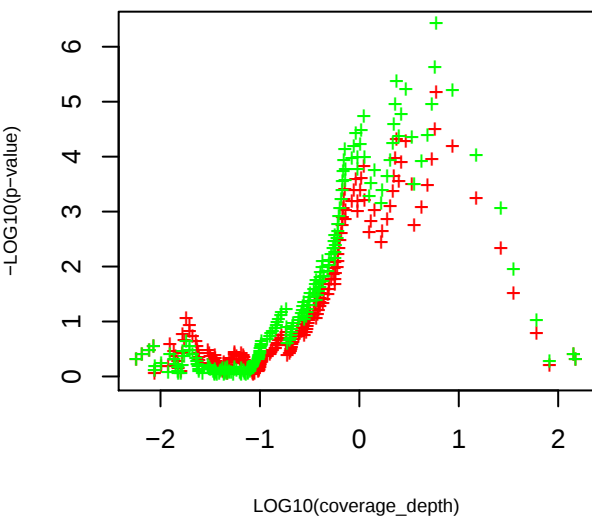


PF00284 Cytochrom_B559a: Luminal portion of Cytochrome b559, alpha (gene psbE) subunit

slope= -1.97 p_value= 0.0028 intercept= 3.69 p_value= 0.11

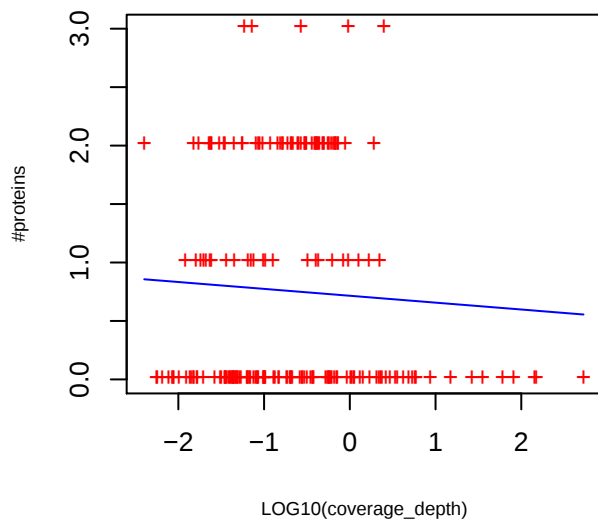


P-value curve : red (unnorm), green (norm)



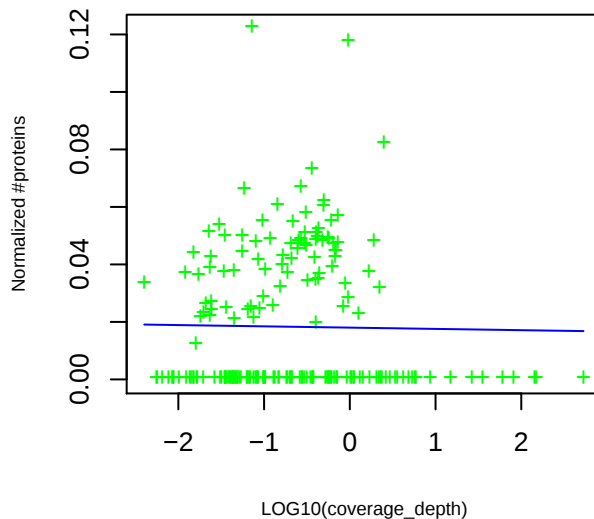
PF09375 Peptidase_M75: Imelysin

slope= -0.059 p_value= 0.44 intercept= 0.72 p_value= 1.2e-14



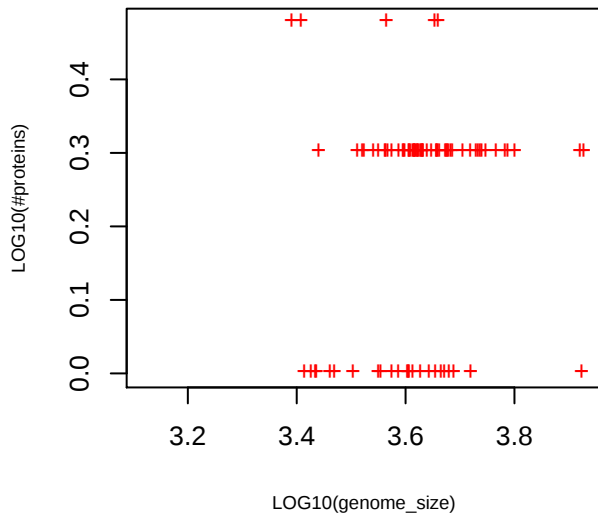
PF09375 Peptidase_M75: Imelysin

slope= -0.00044 p_value= 0.82 intercept= 0.018 p_value= 3e-14

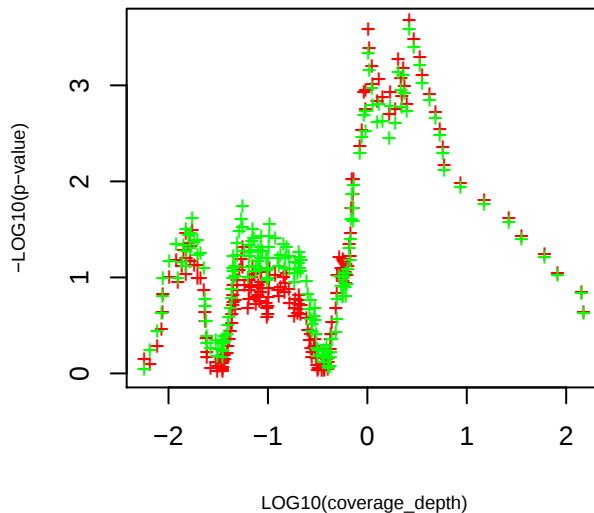


PF09375 Peptidase_M75: Imelysin

slope= 5.48 p_value= 4.5e-10 intercept= -21.61 p_value= 6.9e-12

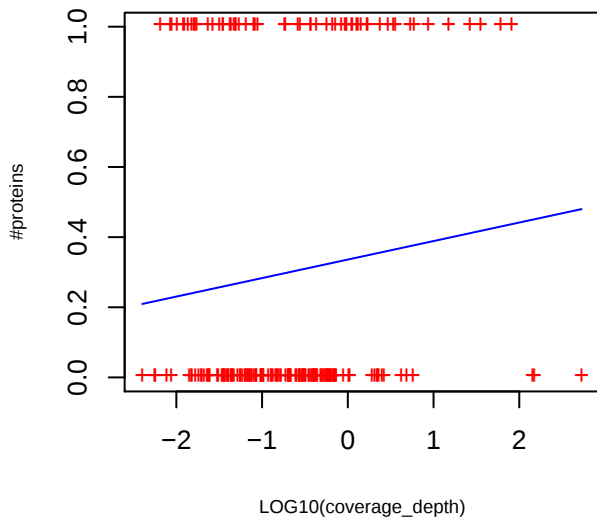


P-value curve ; red (unnorm), green (norm)



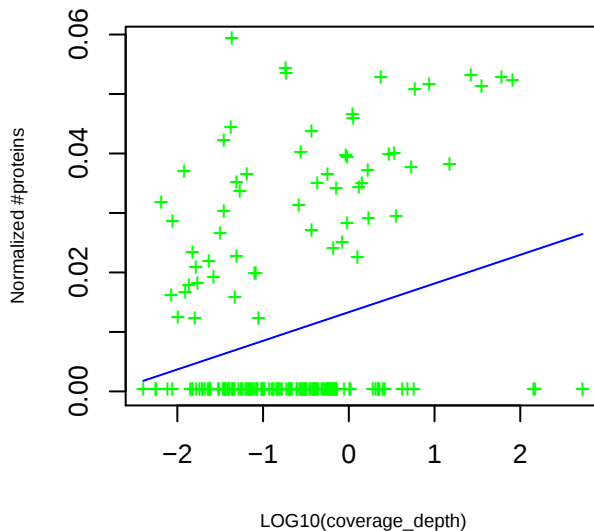
TIGR00159 TIGR00159: conserved hypothetical protein TIGR00159

slope= 0.053 p_value= 0.15 intercept= 0.34 p_value= 4.7e-14



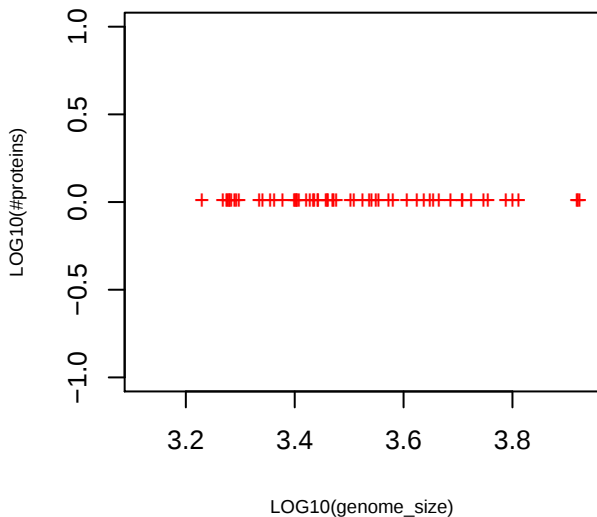
TIGR00159 TIGR00159: conserved hypothetical protein TIGR00159

slope= 0.0048 p_value= 0.00027 intercept= 0.013 p_value= 1.1e-16

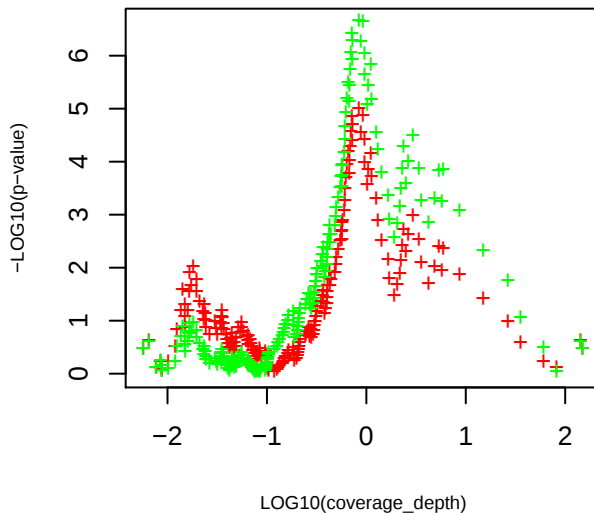


TIGR00159 TIGR00159: conserved hypothetical protein TIGR00159

slope= -1.55 p_value= 0.054 intercept= 2.68 p_value= 0.35

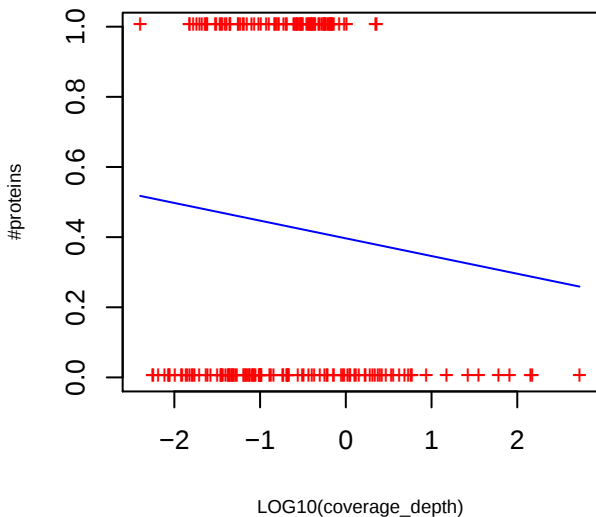


P-value curve ; red (unnorm), green (norm)



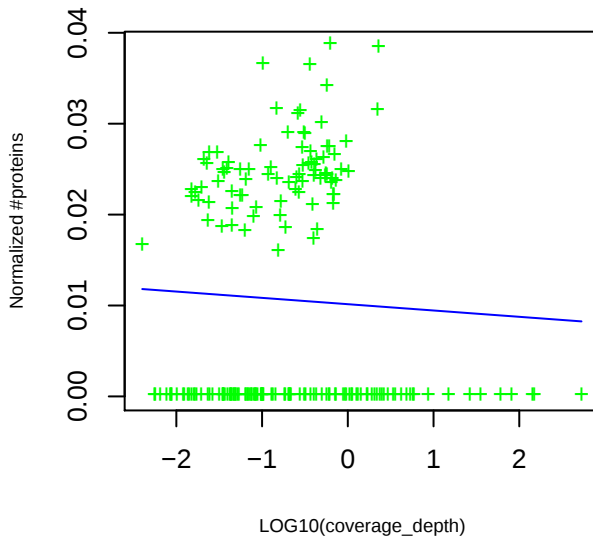
PF05661 DUF808: Protein of unknown function (DUF808)

slope= -0.05 p_value= 0.20 intercept= 0.40 p_value= 4.7e-16



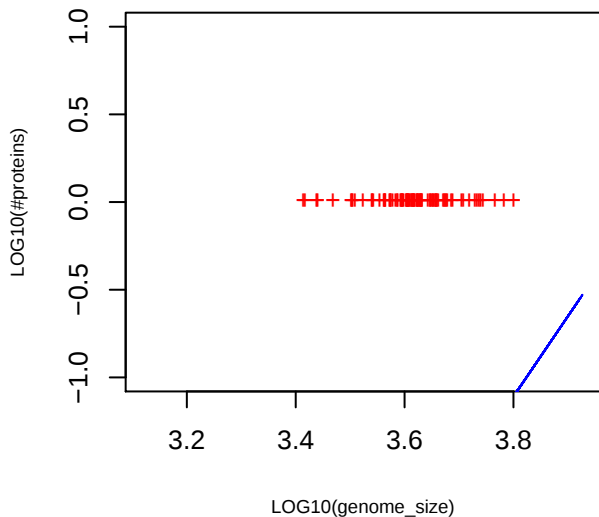
PF05661 DUF808: Protein of unknown function (DUF808)

slope= -7e-04 p_value= 0.49 intercept= 0.010 p_value= 3.2e-16

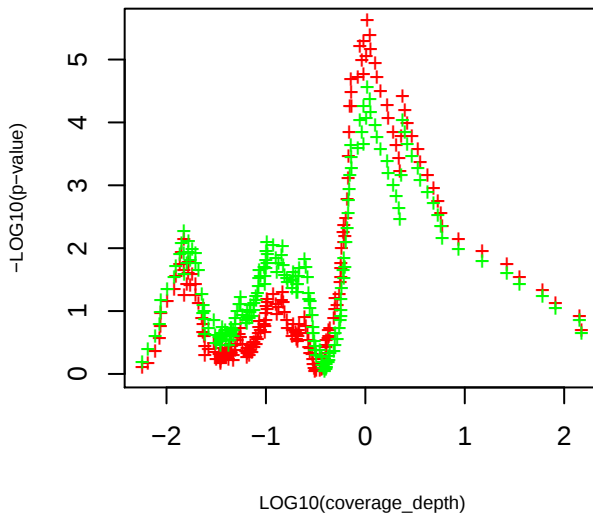


PF05661 DUF808: Protein of unknown function (DUF808)

slope= 4.57 p_value= 5.4e-08 intercept= -18.49 p_value= 9e-10

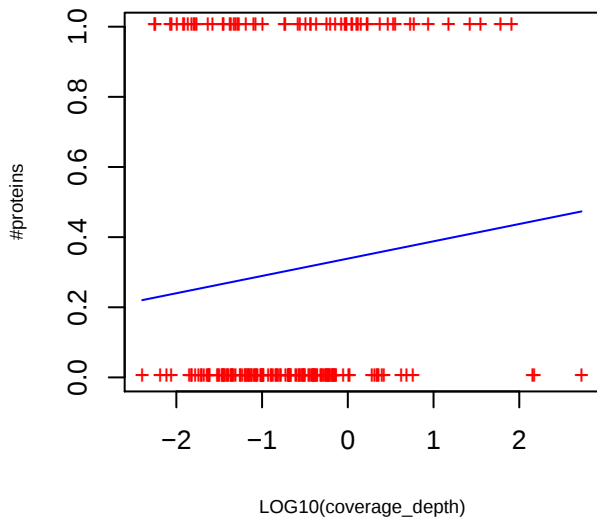


P-value curve ; red (unnorm), green (norm)



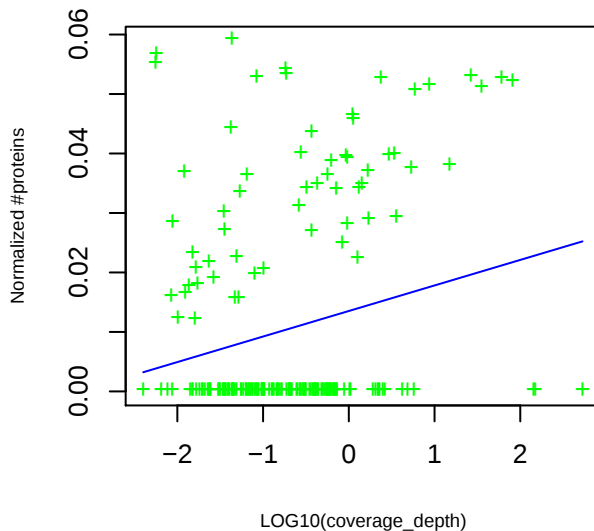
PF07698 7TM-7TMR_HD: 7TM receptor with intracellular HD hydrolase

slope= 0.049 p_value= 0.18 intercept= 0.34 p_value= 4.1e-14



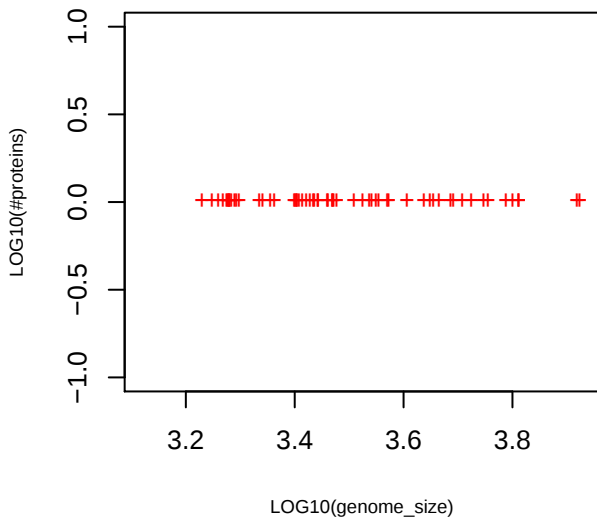
PF07698 7TM-7TMR_HD: 7TM receptor with intracellular HD hydrolase

slope= 0.0043 p_value= 0.0020 intercept= 0.014 p_value= 1e-15

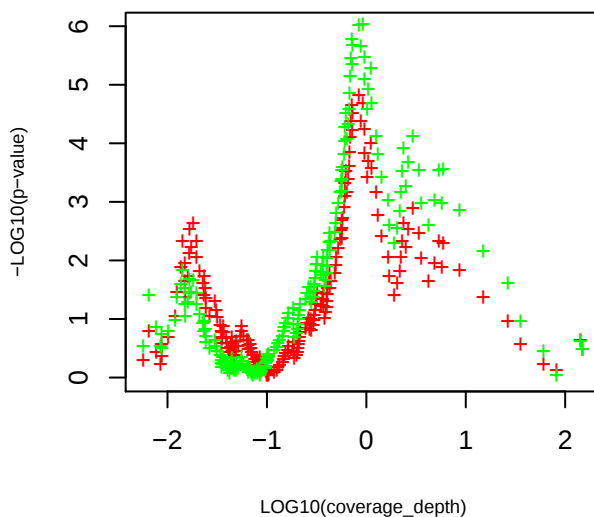


PF07698 7TM-7TMR_HD: 7TM receptor with intracellular HD hydrolase

slope= -2.30 p_value= 0.0043 intercept= 5.36 p_value= 0.059

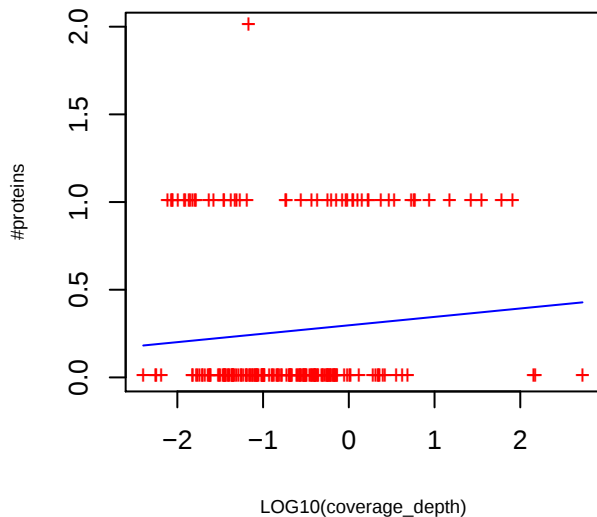


P-value curve ; red (unnorm), green (norm)



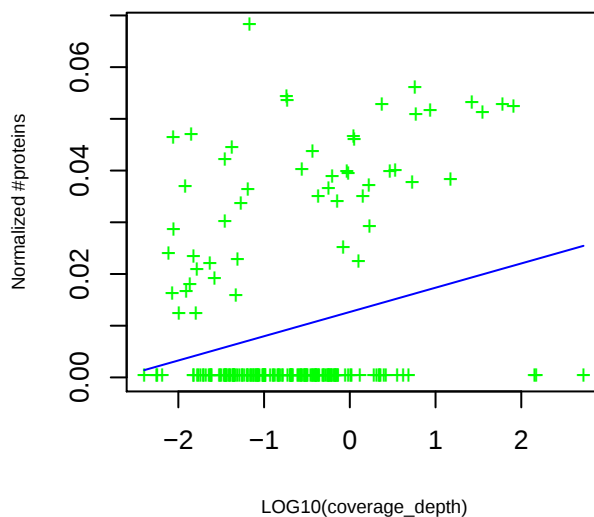
TIGR02651 RNase_Z: ribonuclease Z

slope= 0.048 p_value= 0.19 intercept= 0.30 p_value= 7.8e-12



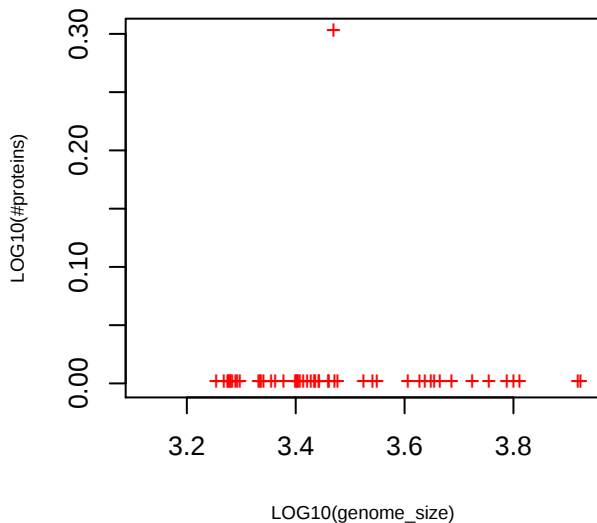
TIGR02651 RNase_Z: ribonuclease Z

slope= 0.0047 p_value= 6e-04 intercept= 0.013 p_value= 1.4e-14

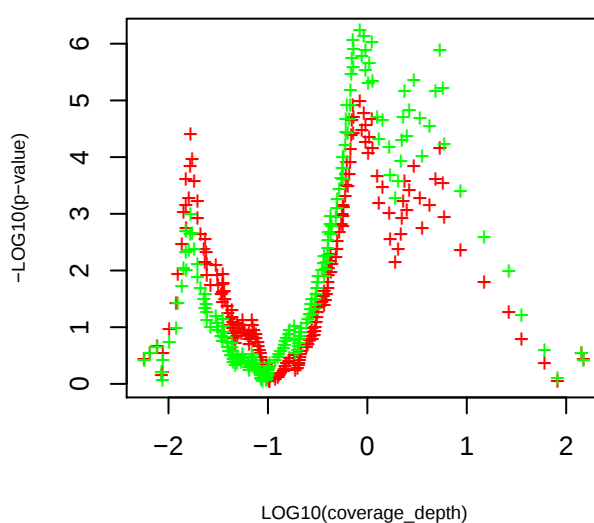


TIGR02651 RNase_Z: ribonuclease Z

slope= -2.57 p_value= 0.00076 intercept= 6.14 p_value= 0.022

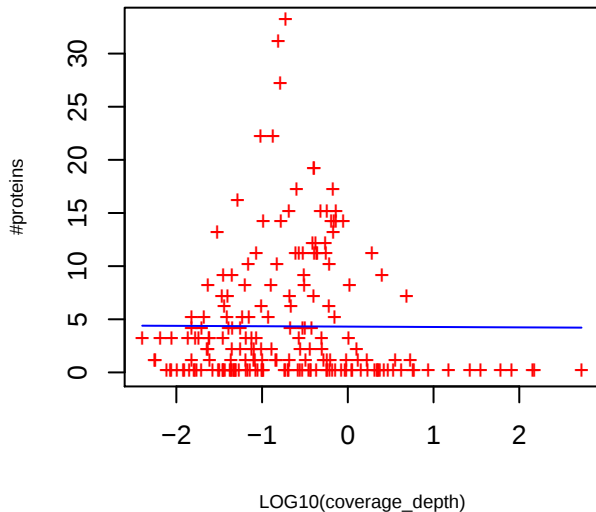


P-value curve ; red (unnorm), green (norm)



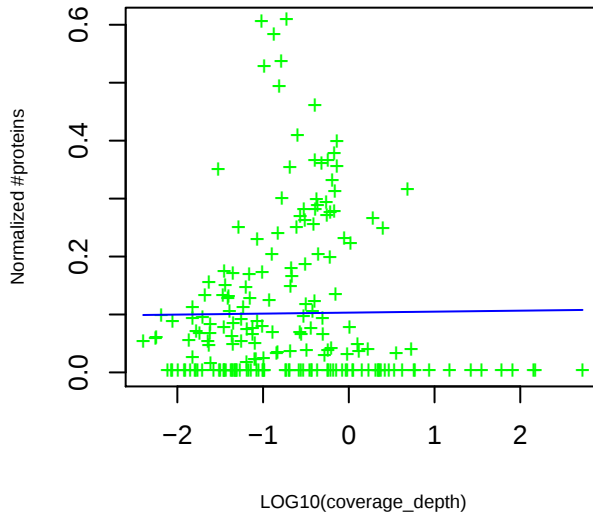
PF07729 FCD: FCD domain

slope= -0.036 p_value= 0.94 intercept= 4.31 p_value= 4.6e-13



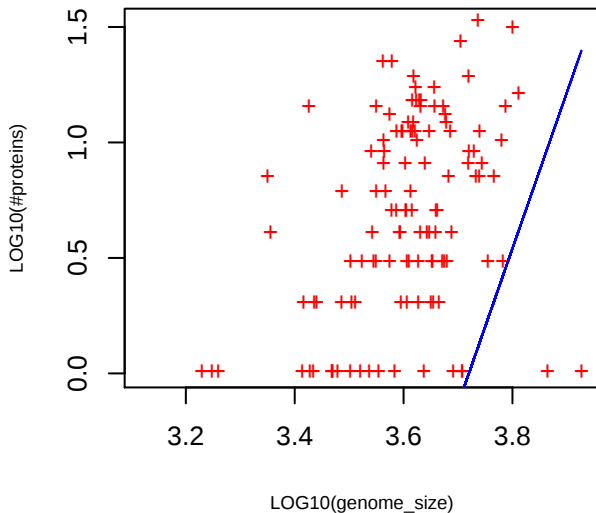
PF07729 FCD: FCD domain

slope= 0.0017 p_value= 0.88 intercept= 0.10 p_value= 1.7e-14

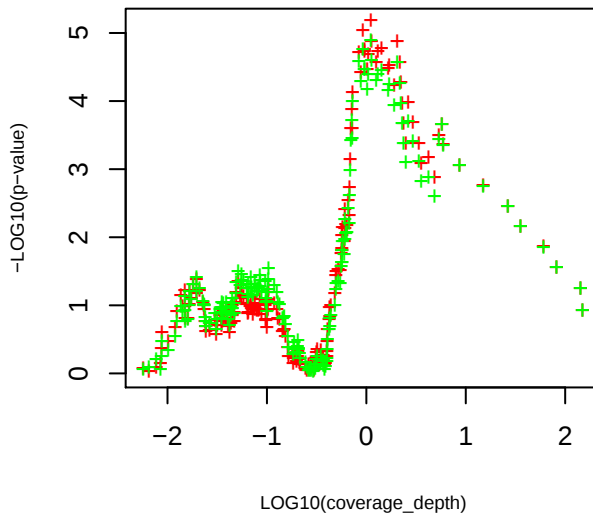


PF07729 FCD: FCD domain

slope= 6.76 p_value= 1.5e-12 intercept= -25.13 p_value= 1.7e-13

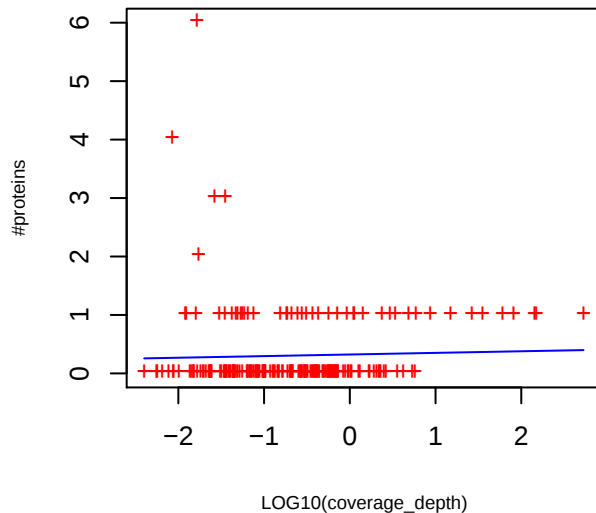


P-value curve ; red (unnorm), green (norm)



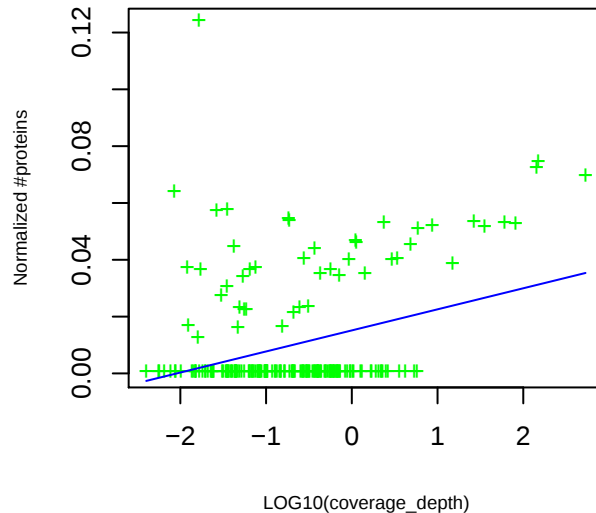
PF06472 ABC_membrane_2: ABC transporter transmembrane region 2

slope= 0.028 p_value= 0.63 intercept= 0.32 p_value= 9e-07



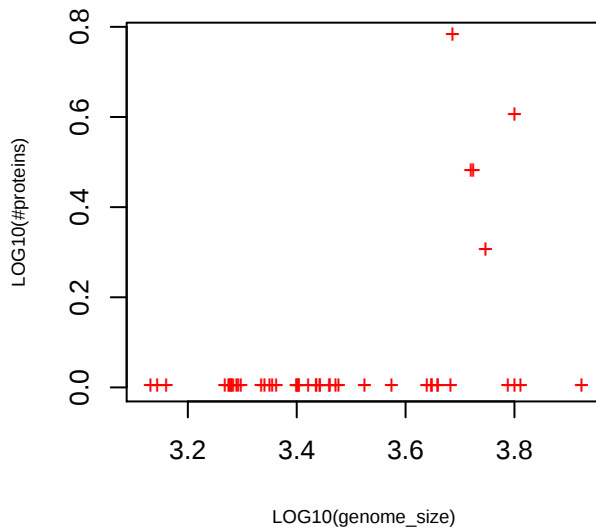
PF06472 ABC_membrane_2: ABC transporter transmembrane region 2

slope= 0.0074 p_value= 2.6e-06 intercept= 0.015 p_value= 9.6e-16

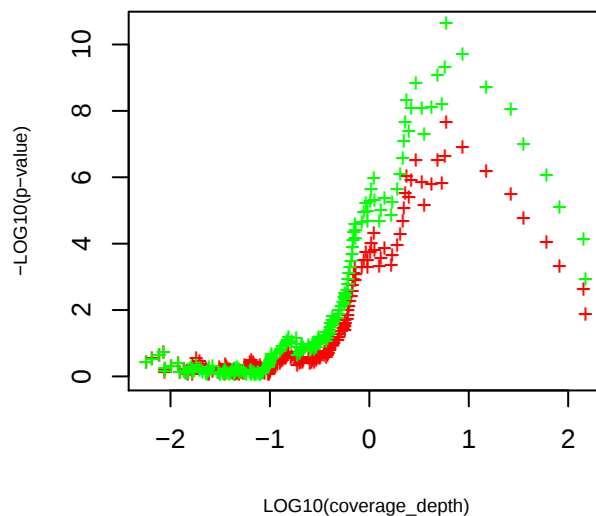


PF06472 ABC_membrane_2: ABC transporter transmembrane region 2

slope= -2.37 p_value= 0.0016 intercept= 5.38 p_value= 0.043

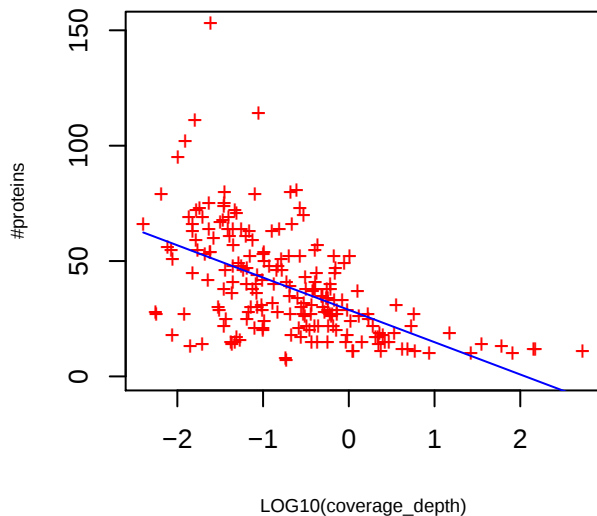


P-value curve ; red (unnorm), green (norm)



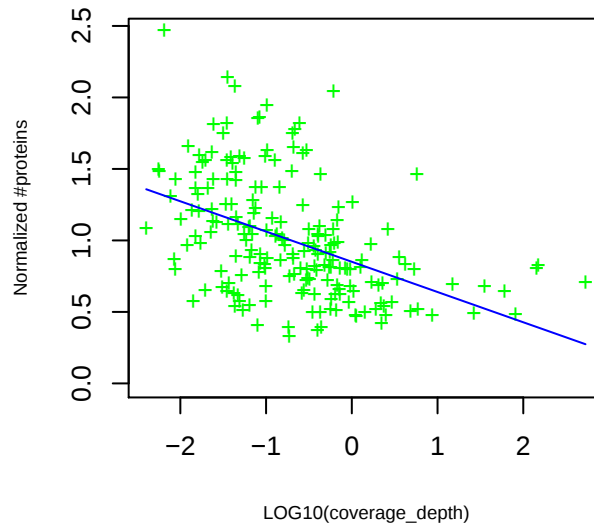
Clan MO

slope= -14.00 p_value= 1.1e-16 intercept= 28.83 p_value= 4.1e-39



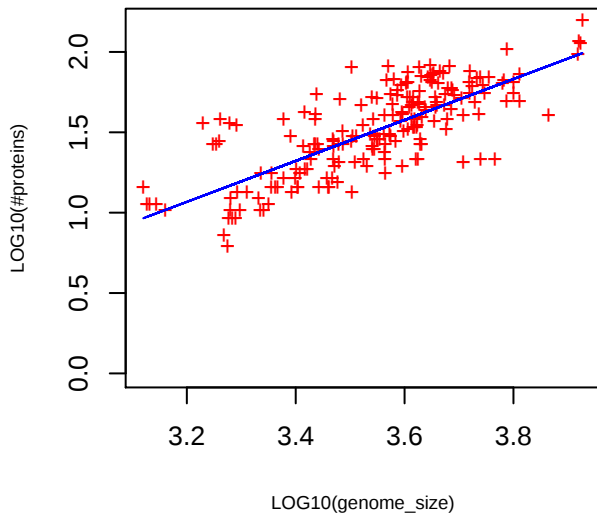
Clan MO

slope= -0.21 p_value= 1.6e-11 intercept= 0.85 p_value= 5.1e-64

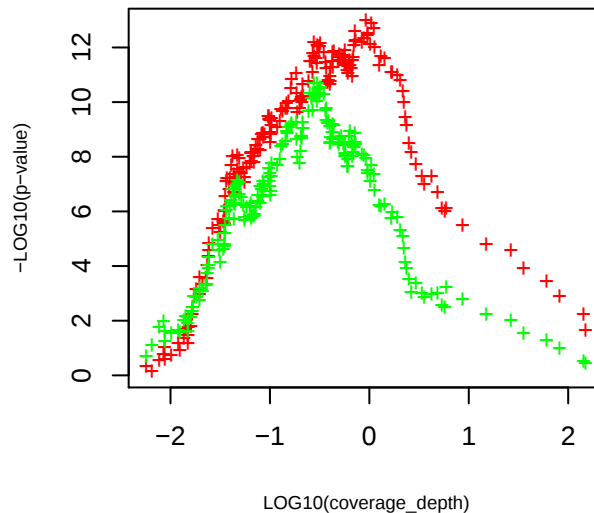


Clan MO

slope= 1.27 p_value= 1e-38 intercept= -3.01 p_value= 4.6e-22

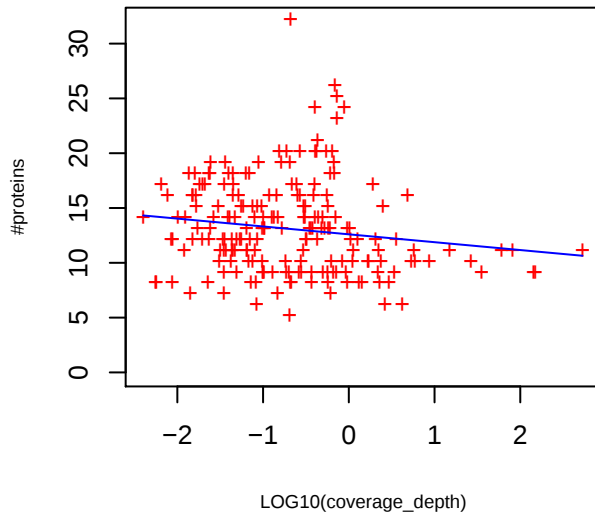


P-value curve ; red (unnorm), green (norm)



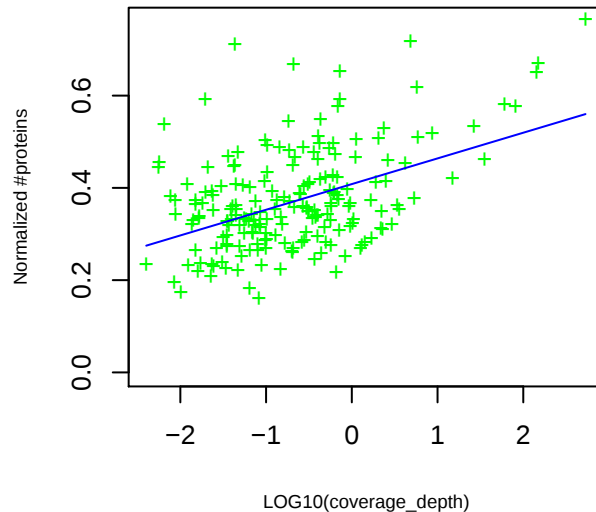
Clan PC

slope= -0.72 p_value= 0.034 intercept= 12.60 p_value= 3.9e-82



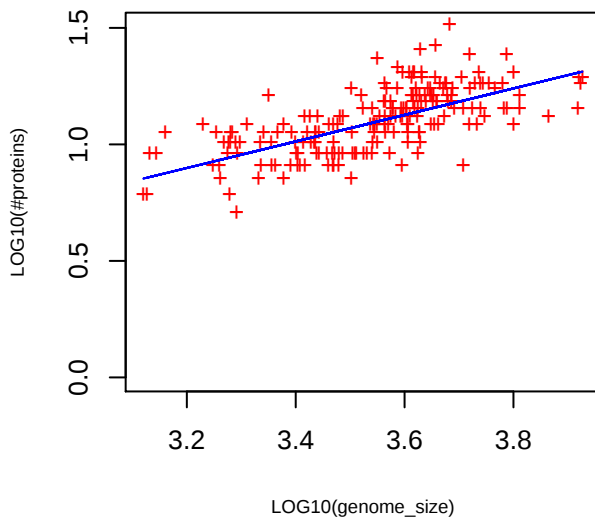
Clan PC

slope= 0.056 p_value= 1.7e-11 intercept= 0.41 p_value= 2.5e-107

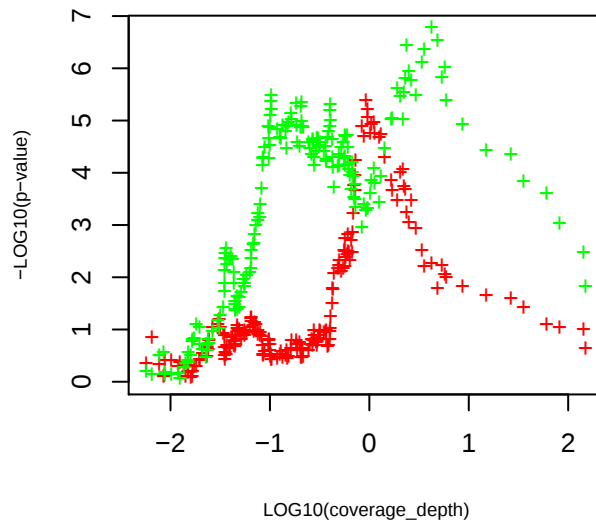


Clan PC

slope= 0.57 p_value= 4.5e-27 intercept= -0.92 p_value= 3.2e-08

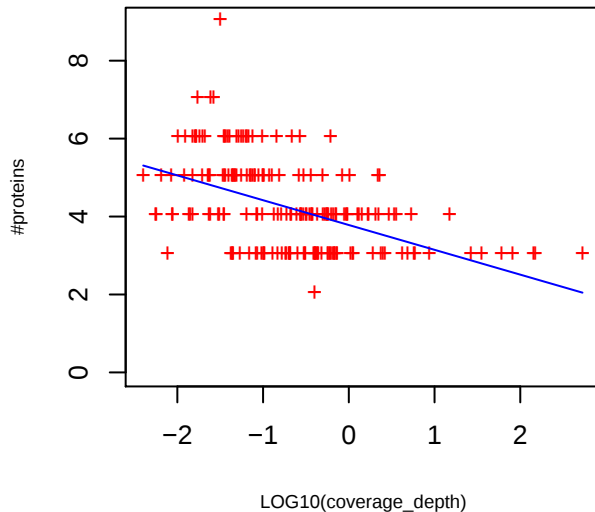


P-value curve ; red (unnorm), green (norm)



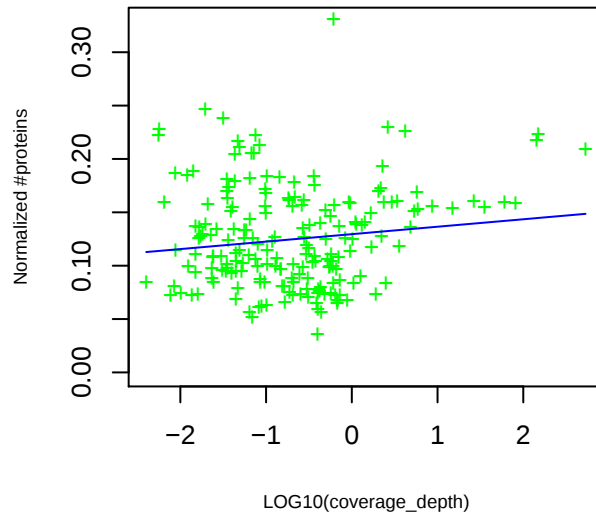
Clan MK

slope= -0.64 p_value= 1.2e-13 intercept= 3.78 p_value= 1.3e-99



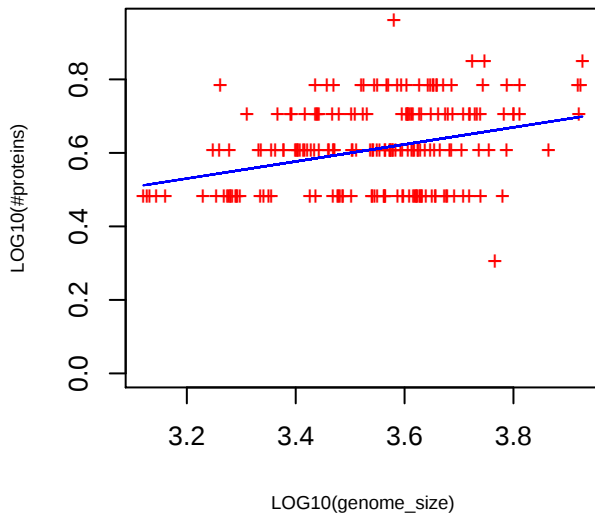
Clan MK

slope= 0.007 p_value= 0.065 intercept= 0.13 p_value= 3e-76

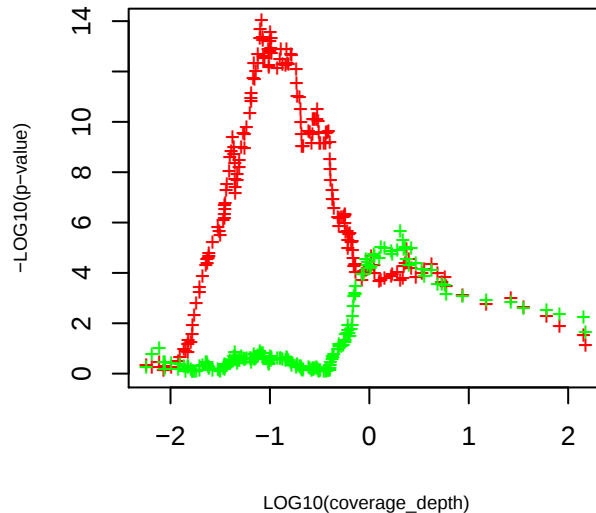


Clan MK

slope= 0.23 p_value= 2.3e-06 intercept= -0.21 p_value= 0.21

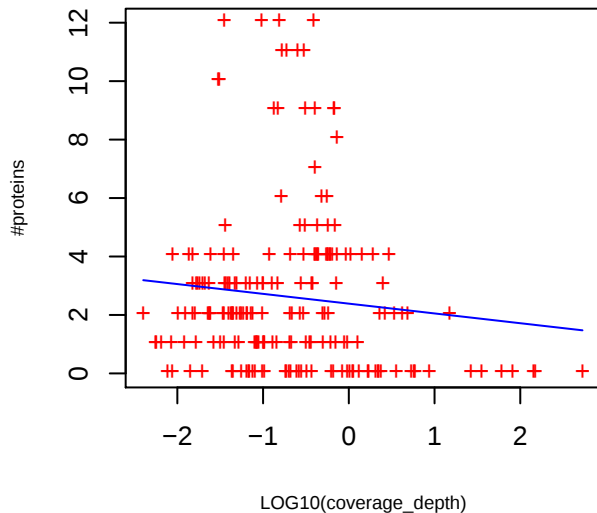


P-value curve ; red (unnorm), green (norm)



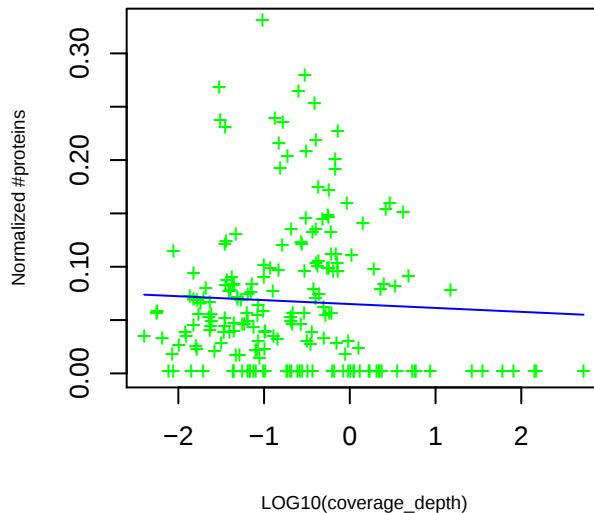
Clan CL

slope= -0.33 p_value= 0.14 intercept= 2.39 p_value= 2.5e-17



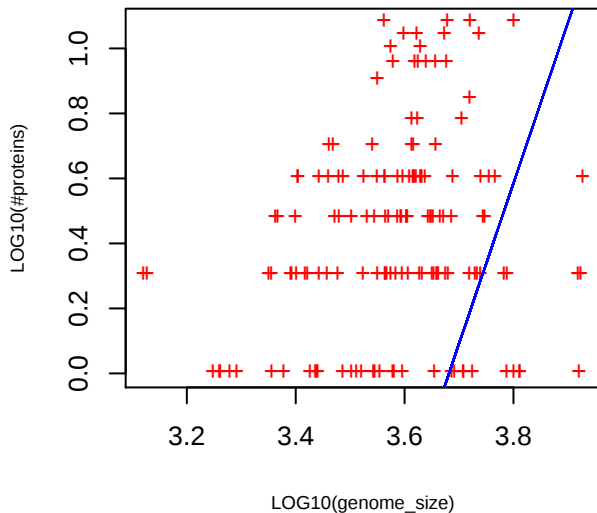
Clan CL

slope= -0.0037 p_value= 0.50 intercept= 0.065 p_value= 7.3e-21

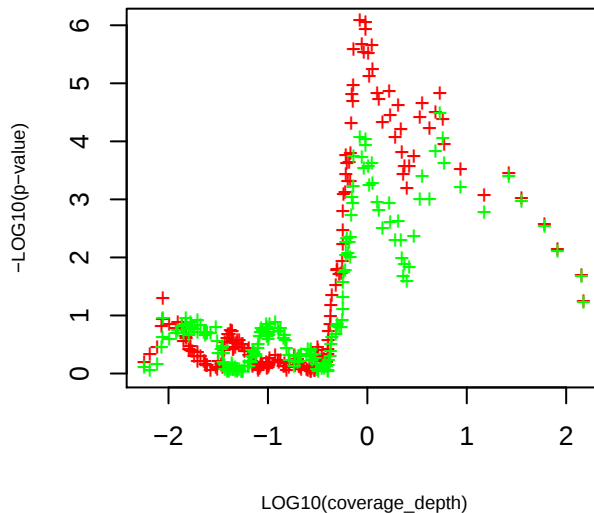


Clan CL

slope= 4.94 p_value= 1.3e-09 intercept= -18.18 p_value= 3.5e-10

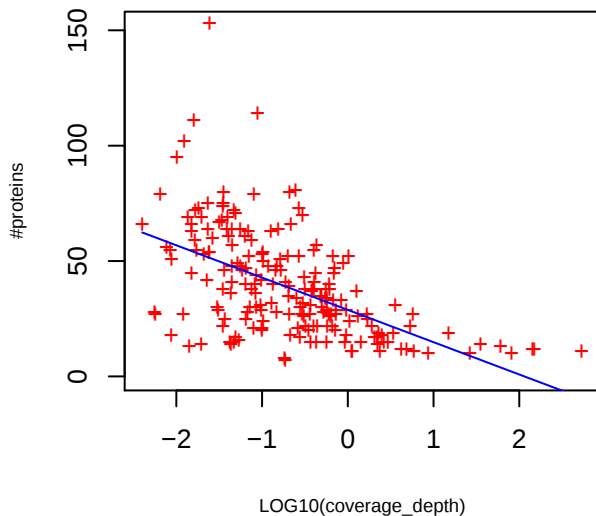


P-value curve ; red (unnorm), green (norm)



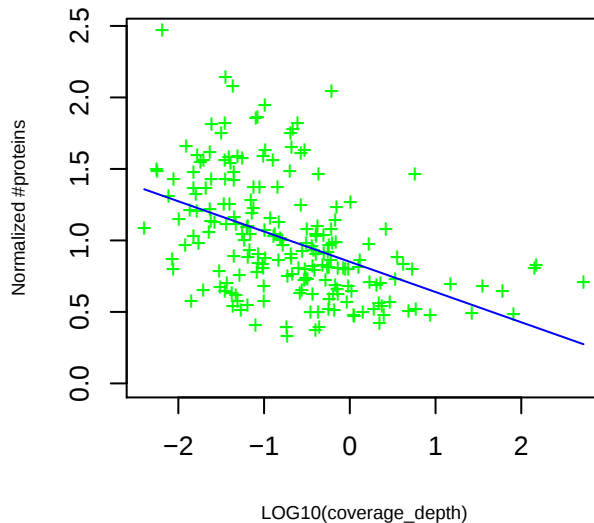
Family M23

slope= -14.00 p_value= 1.1e-16 intercept= 28.83 p_value= 4.1e-39



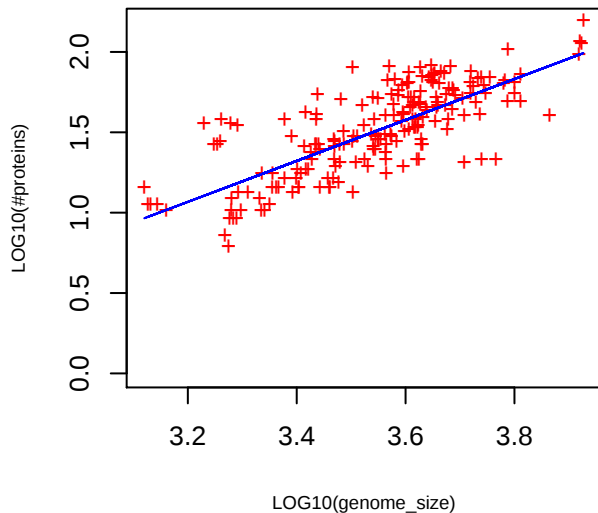
Family M23

slope= -0.21 p_value= 1.6e-11 intercept= 0.85 p_value= 5.1e-64

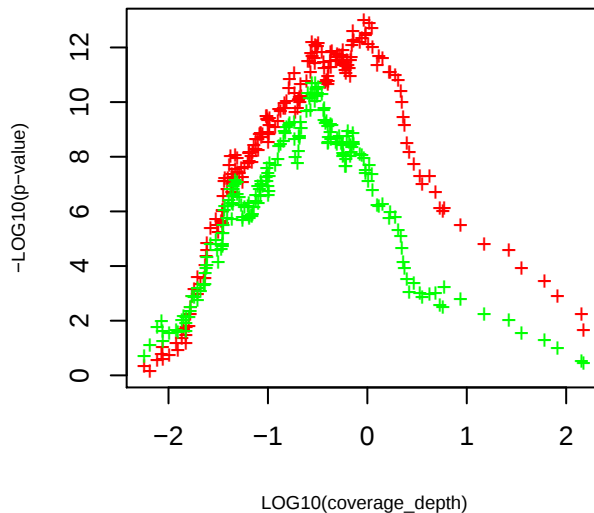


Family M23

slope= 1.27 p_value= 1e-38 intercept= -3.01 p_value= 4.6e-22

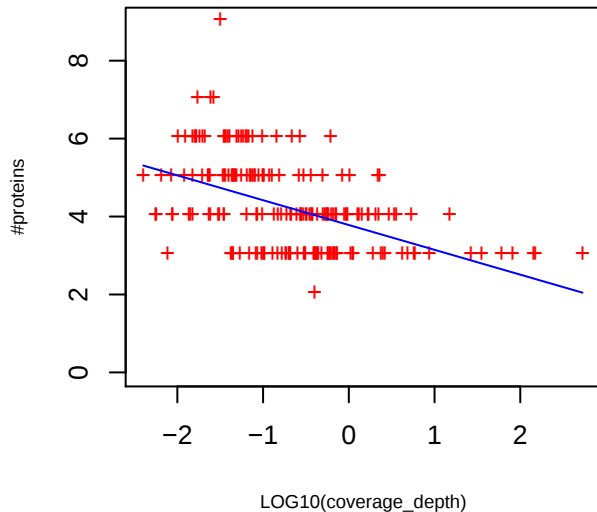


P-value curve ; red (unnorm), green (norm)



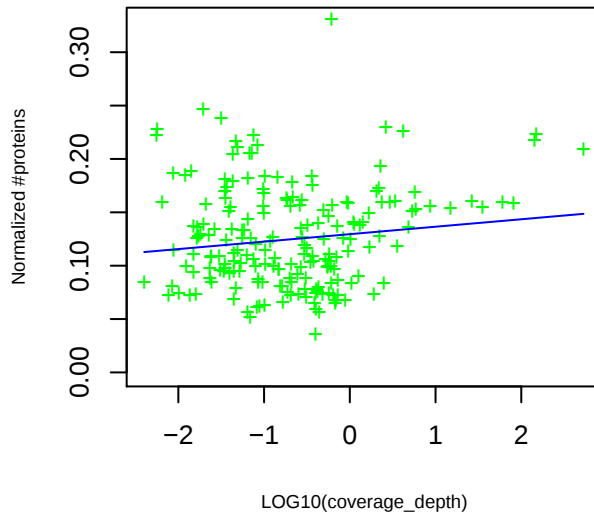
Family M22

slope= -0.64 p_value= 1.2e-13 intercept= 3.78 p_value= 1.3e-99



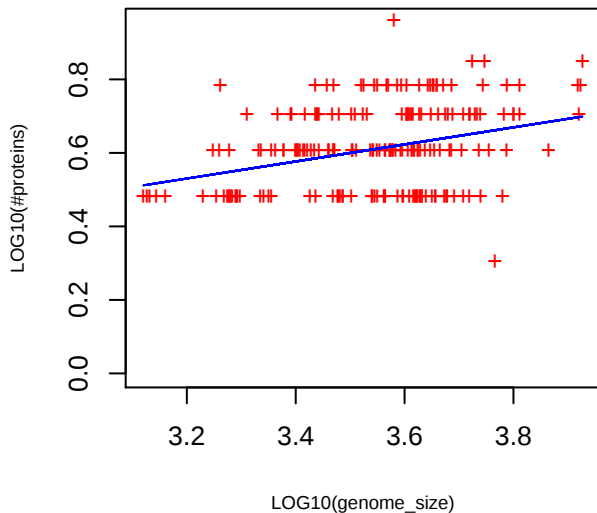
Family M22

slope= 0.007 p_value= 0.065 intercept= 0.13 p_value= 3e-76

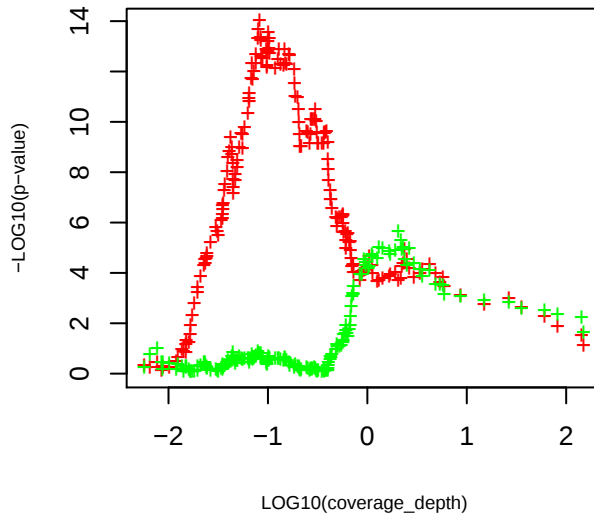


Family M22

slope= 0.23 p_value= 2.3e-06 intercept= -0.21 p_value= 0.21

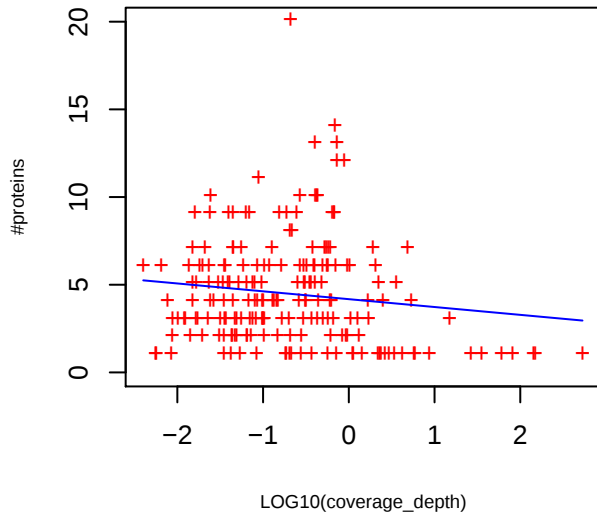


P-value curve ; red (unnorm), green (norm)



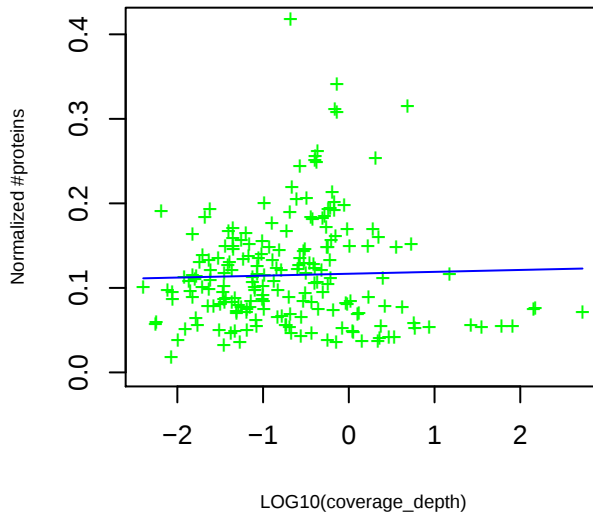
Family C56

slope= -0.45 p_value= 0.067 intercept= 4.18 p_value= 4.2e-35



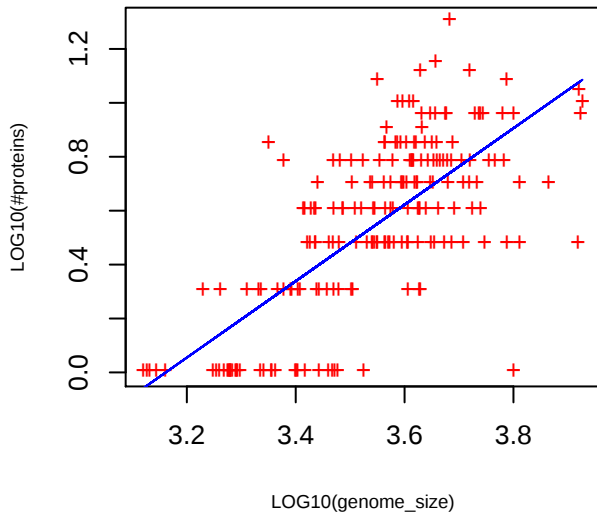
Family C56

slope= 0.0023 p_value= 0.66 intercept= 0.12 p_value= 2.9e-50

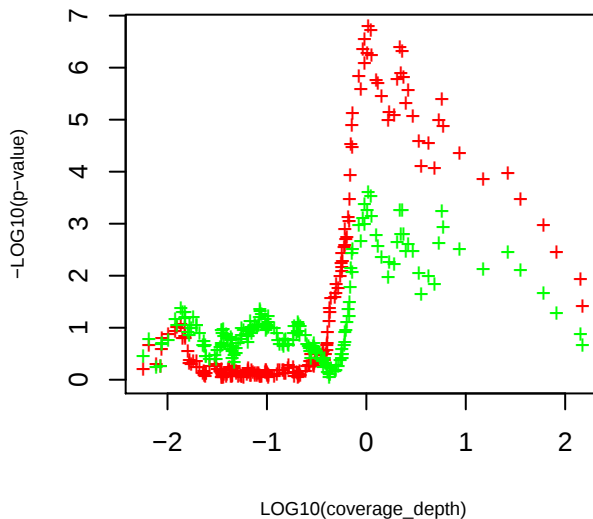


Family C56

slope= 1.42 p_value= 6.5e-32 intercept= -4.48 p_value= 3.5e-27

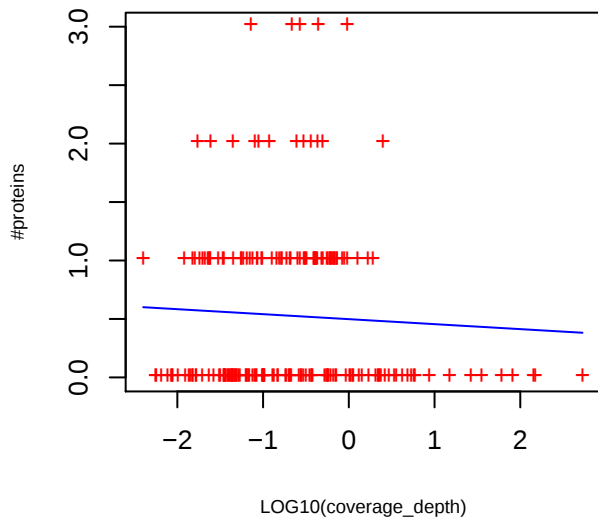


P-value curve ; red (unnorm), green (norm)



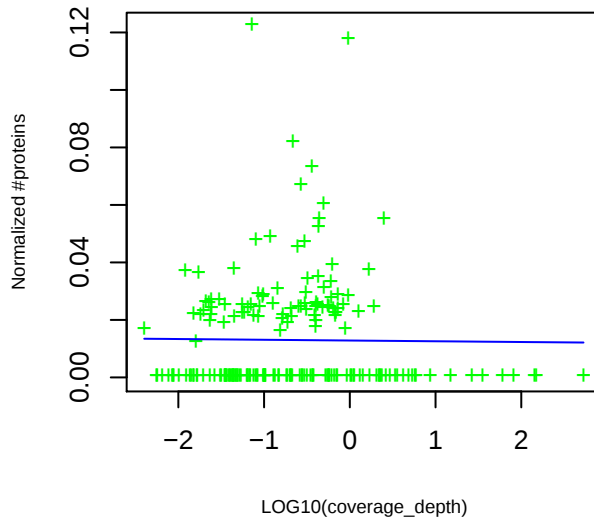
Family M75

slope= -0.043 p_value= 0.46 intercept= 0.50 p_value= 1.1e-12



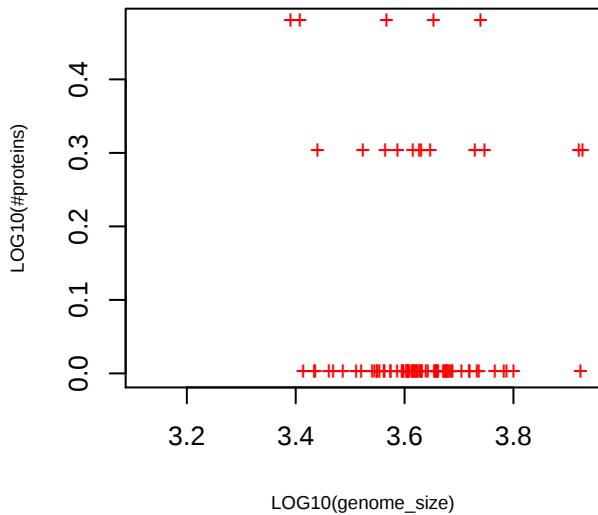
Family M75

slope= -0.00026 p_value= 0.87 intercept= 0.013 p_value= 1.3e-11

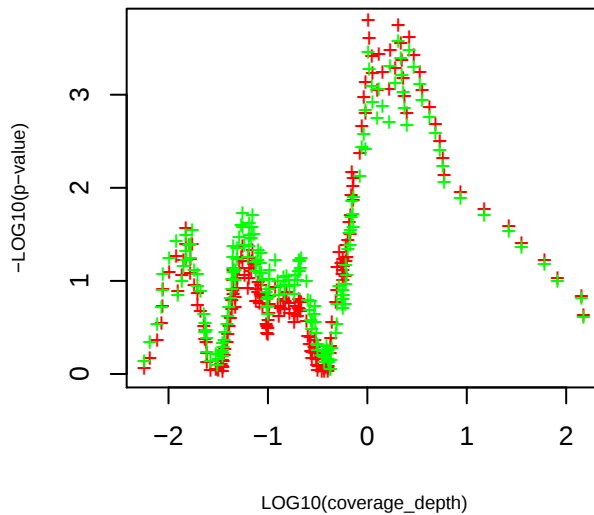


Family M75

slope= 5.17 p_value= 9.7e-10 intercept= -20.63 p_value= 1.1e-11

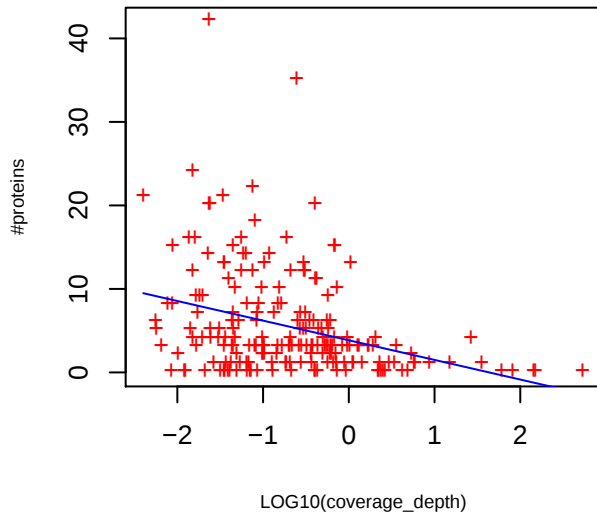


P-value curve ; red (unnorm), green (norm)



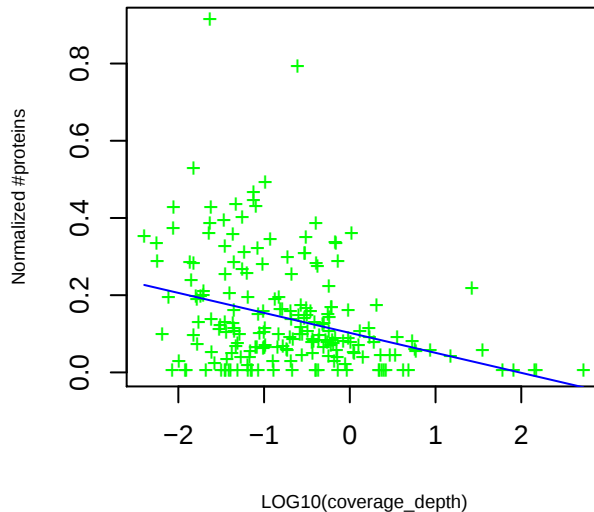
M00370 Complex Module Iron complex transport system

slope= -2.35 p_value= 2.1e-06 intercept= 3.85 p_value= 2.4e-11



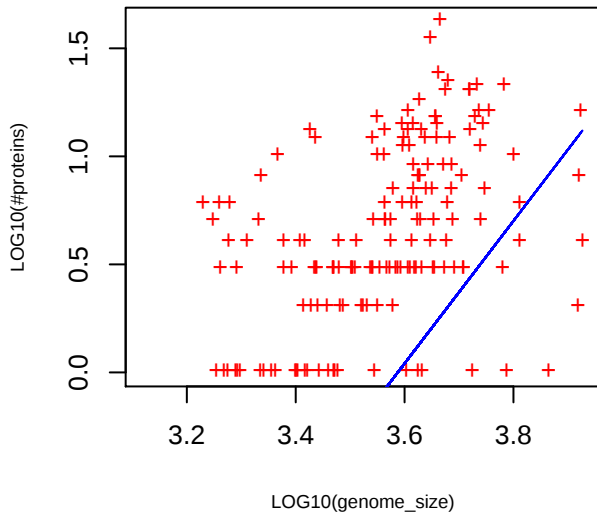
M00370 Complex Module Iron complex transport system

slope= -0.052 p_value= 3.9e-06 intercept= 0.10 p_value= 1.5e-14

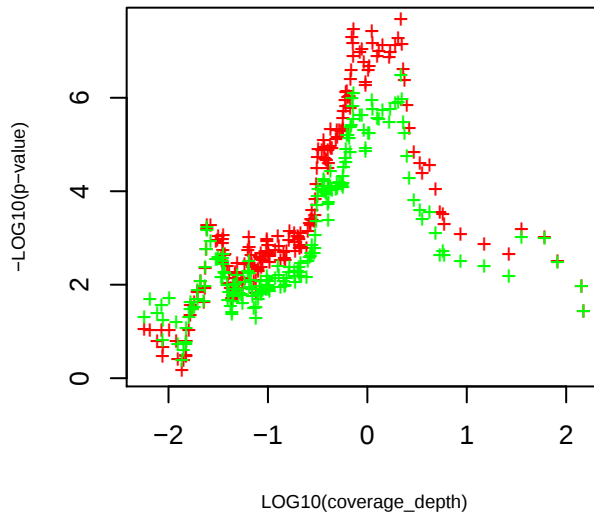


M00370 Complex Module Iron complex transport system

slope= 3.30 p_value= 1.5e-05 intercept= -11.83 p_value= 1.2e-05

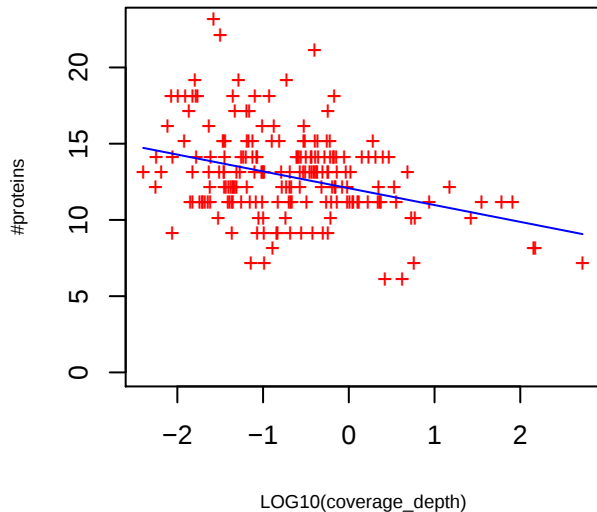


P-value curve ; red (unnorm), green (norm)



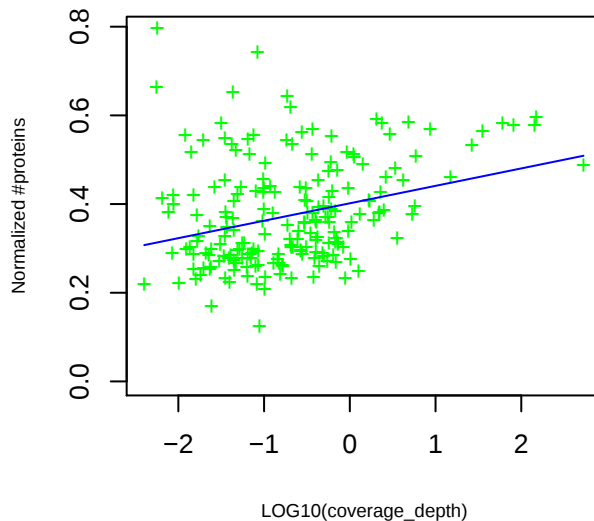
M00001 Pathway Module Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate

slope= -1.10 p_value= 4.9e-07 intercept= 12.08 p_value= 6.9e-114



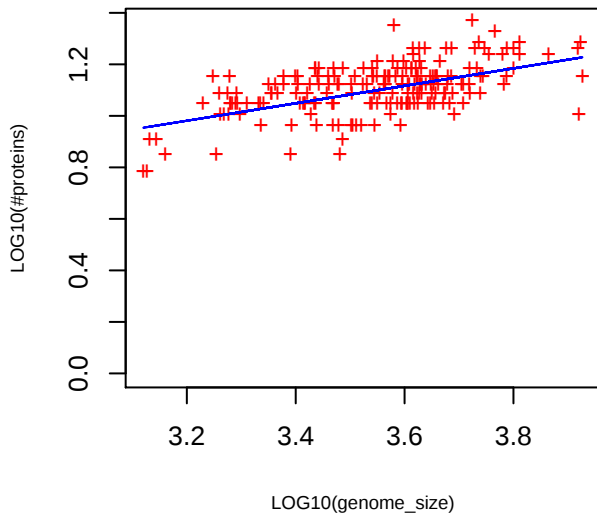
M00001 Pathway Module Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate

slope= 0.039 p_value= 2.1e-05 intercept= 0.40 p_value= 6.2e-95

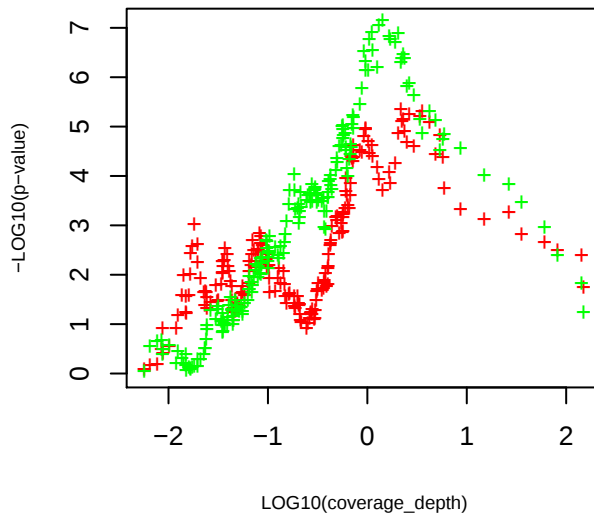


M00001 Pathway Module Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate

slope= 0.34 p_value= 3.7e-18 intercept= -0.10 p_value= 0.41

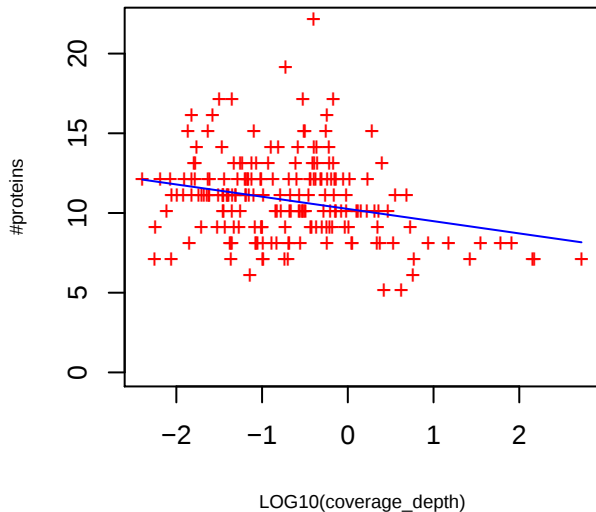


P-value curve : red (unnorm), green (norm)



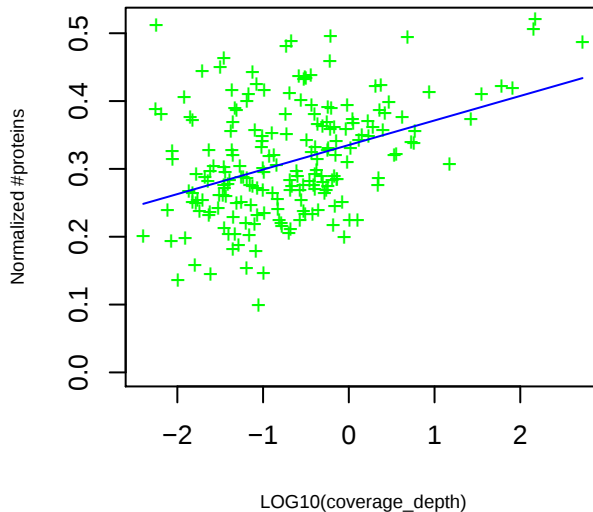
M00003 Pathway Module Gluconeogenesis, oxaloacetate => fructose-6P

slope= -0.77 p_value= 0.00017 intercept= 10.26 p_value= 1.6e-105



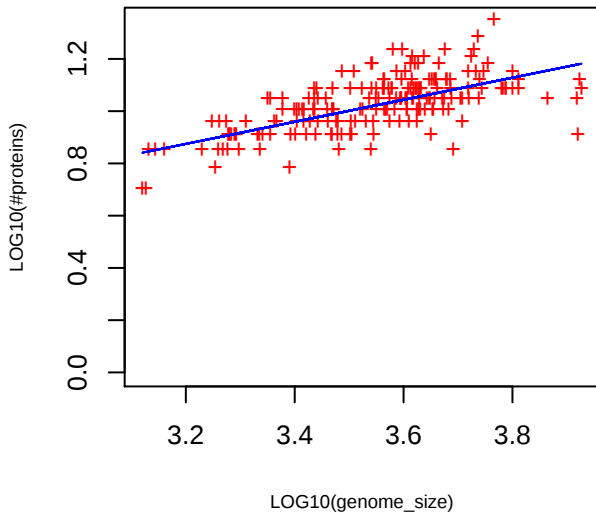
M00003 Pathway Module Gluconeogenesis, oxaloacetate => fructose-6P

slope= 0.036 p_value= 1.3e-08 intercept= 0.34 p_value= 3.8e-111

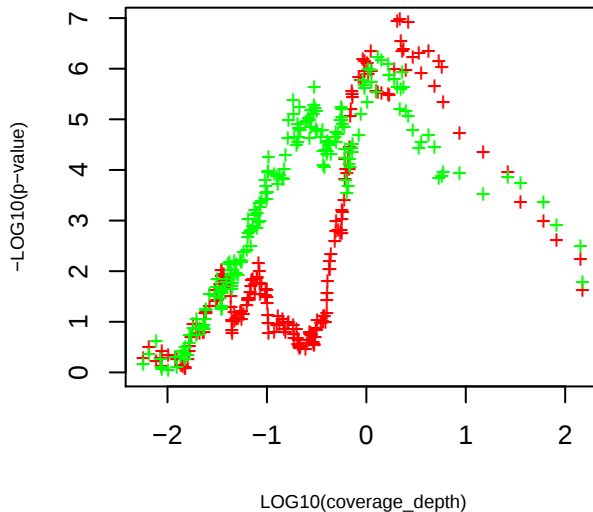


M00003 Pathway Module Gluconeogenesis, oxaloacetate => fructose-6P

slope= 0.42 p_value= 5.8e-26 intercept= -0.48 p_value= 0.00013

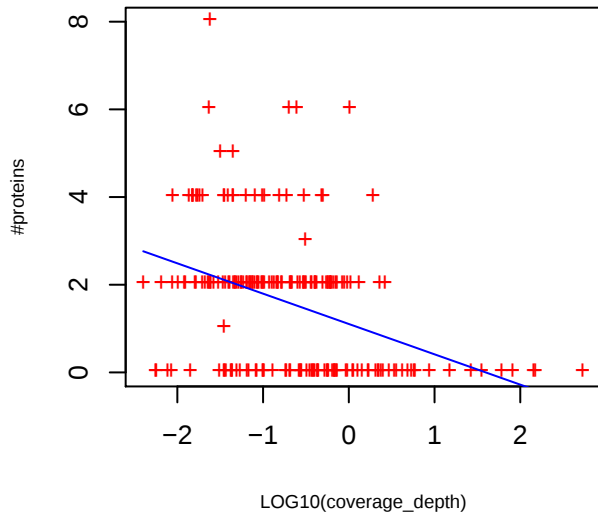


P-value curve ; red (unnorm), green (norm)



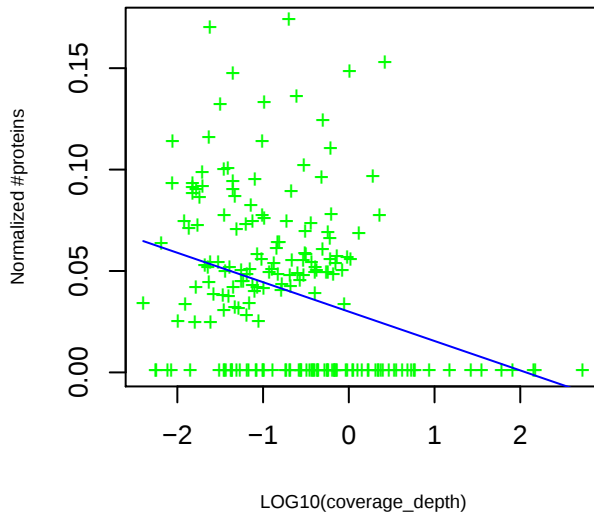
M00282 Complex Module Cytochrome bd complex

slope= -0.69 p_value= 1.7e-08 intercept= 1.10 p_value= 1.5e-14



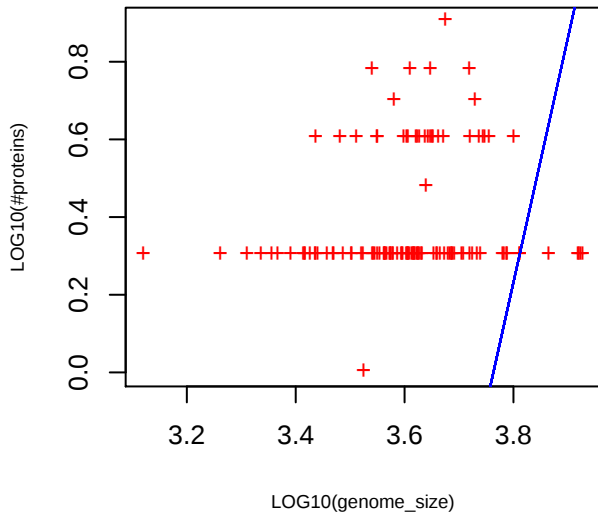
M00282 Complex Module Cytochrome bd complex

slope= -0.014 p_value= 5.8e-06 intercept= 0.03 p_value= 3.9e-15

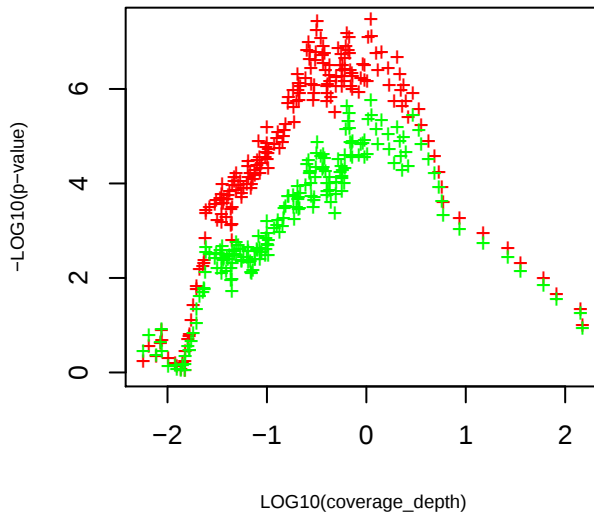


M00282 Complex Module Cytochrome bd complex

slope= 6.29 p_value= 1.8e-12 intercept= -23.68 p_value= 1.2e-13

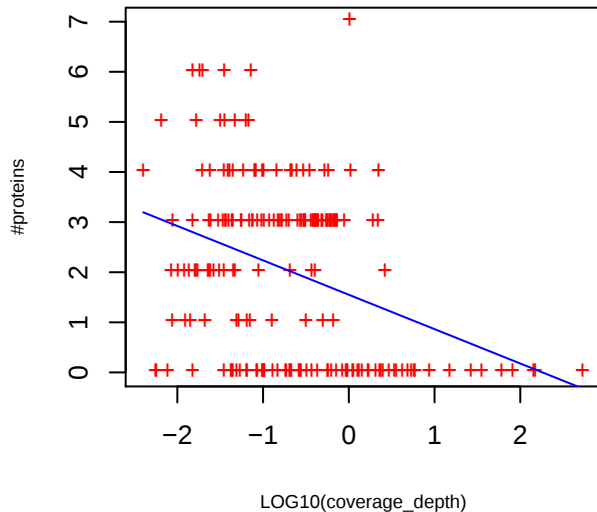


P-value curve ; red (unnorm), green (norm)



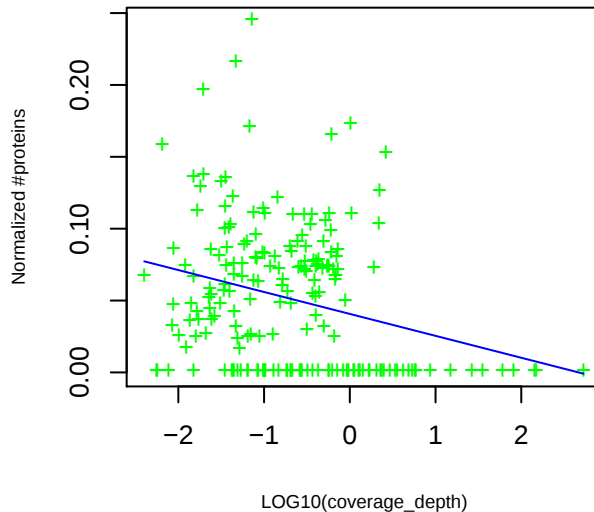
M00319 Complex Module Molybdate transport system

slope= -0.69 p_value= 4.8e-07 intercept= 1.55 p_value= 1.8e-20



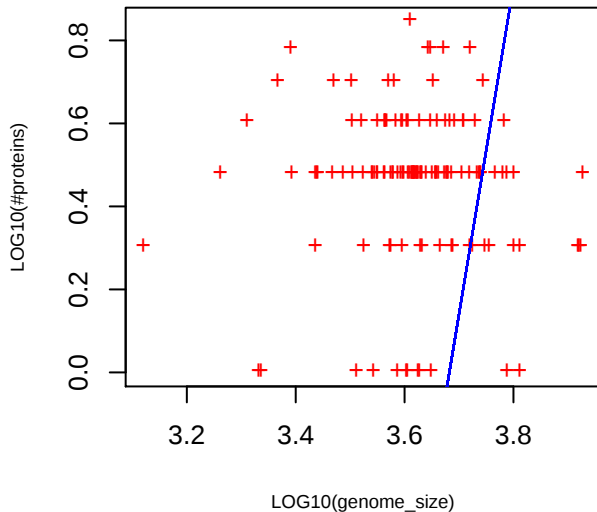
M00319 Complex Module Molybdate transport system

slope= -0.015 p_value= 8.3e-05 intercept= 0.041 p_value= 8e-18

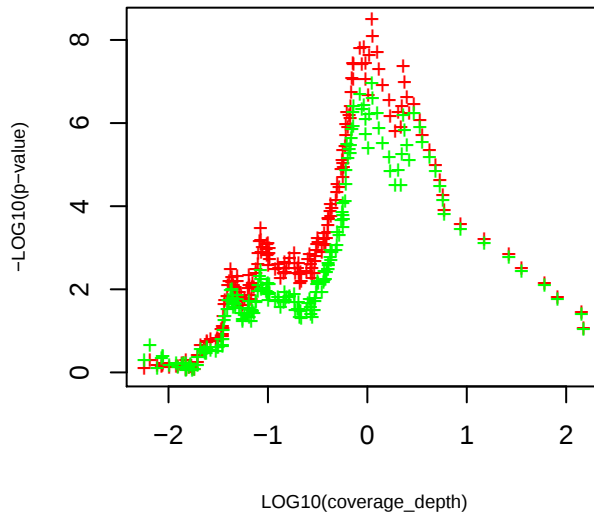


M00319 Complex Module Molybdate transport system

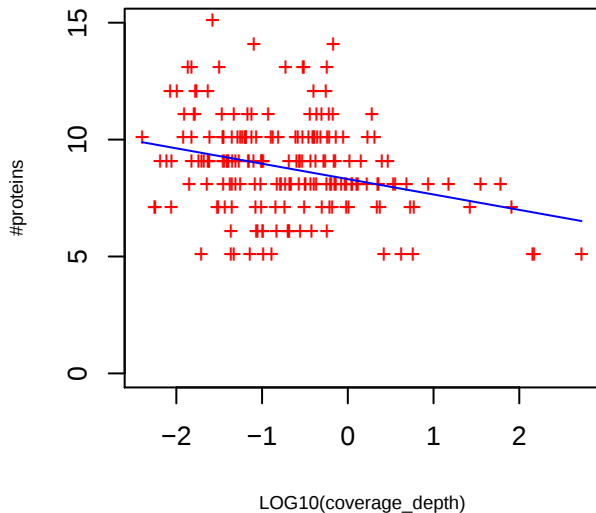
slope= 7.91 p_value= 4.2e-21 intercept= -29.12 p_value= 2.7e-22



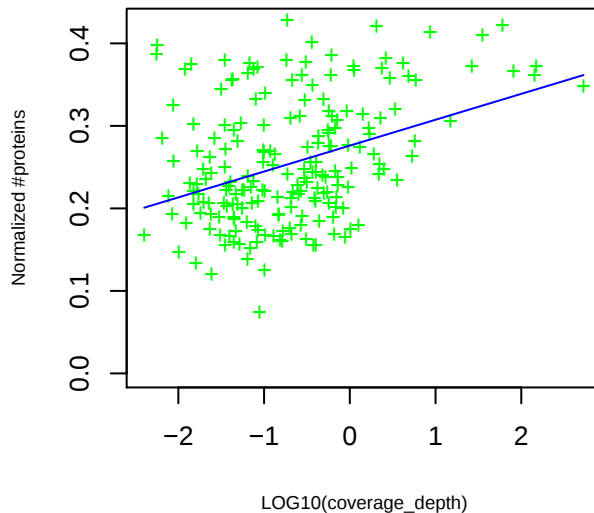
P-value curve ; red (unnorm), green (norm)



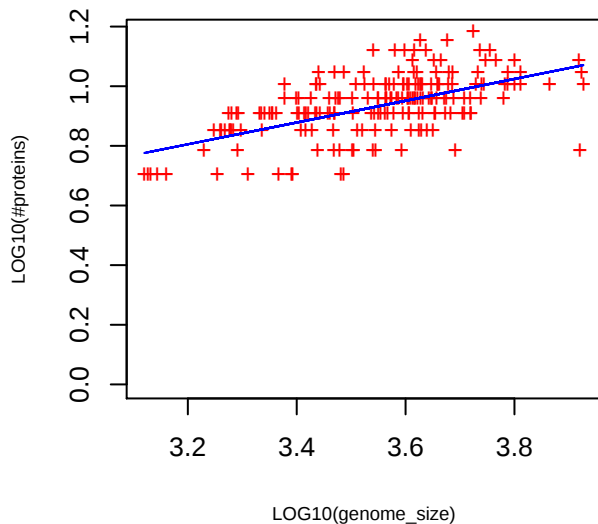
slope= -0.66 p_value= 2.5e-05 intercept= 8.31 p_value= 1.8e-110



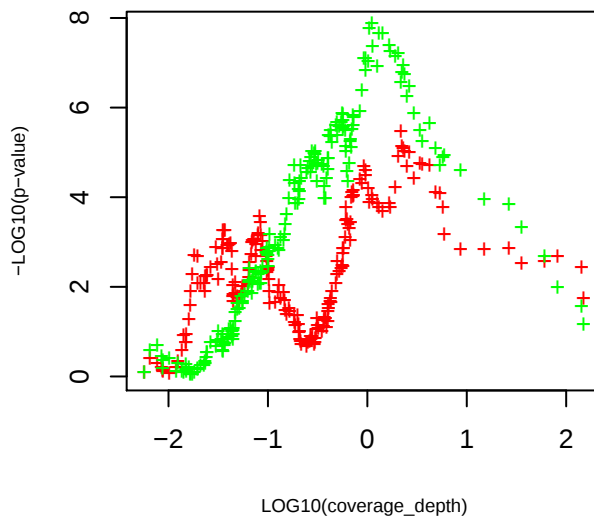
slope= 0.031 p_value= 6.8e-08 intercept= 0.28 p_value= 9.1e-103



slope= 0.36 p_value= 1.9e-19 intercept= -0.36 p_value= 0.0053

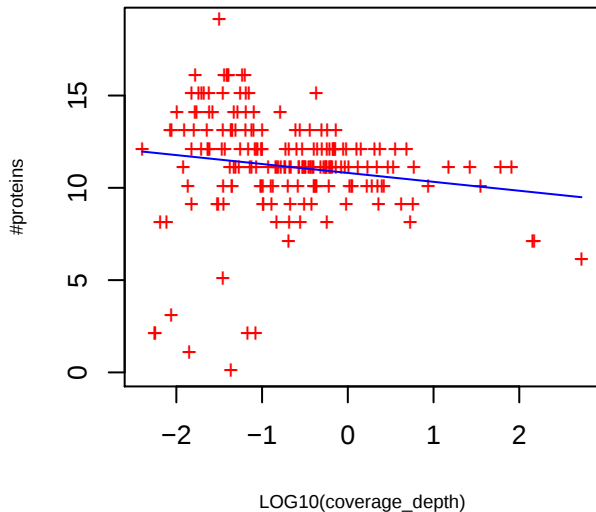


P-value curve ; red (unnorm), green (norm)



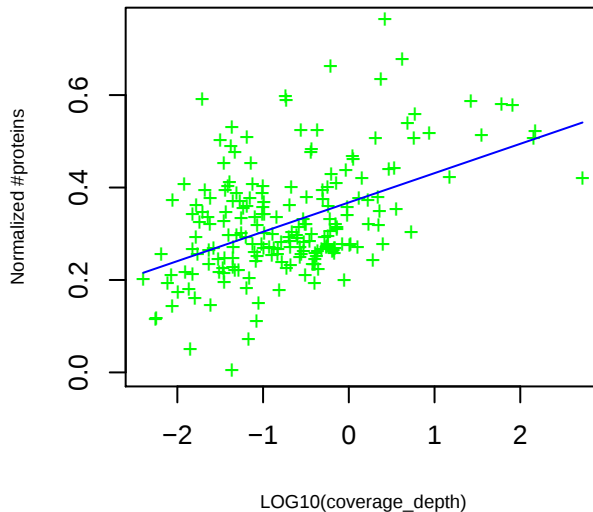
M00246 Pathway Module Heme biosynthesis, glutamate => protoheme/siroheme

slope= -0.48 p_value= 0.027 intercept= 10.81 p_value= 1.2e-103



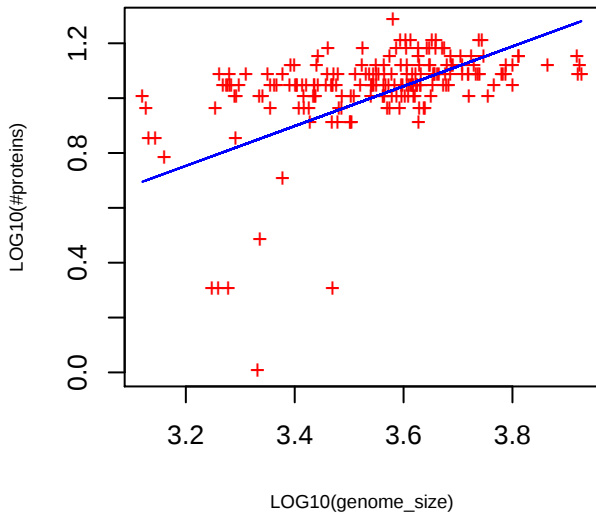
M00246 Pathway Module Heme biosynthesis, glutamate => protoheme/siroheme

slope= 0.063 p_value= 3.2e-12 intercept= 0.37 p_value= 2.1e-92

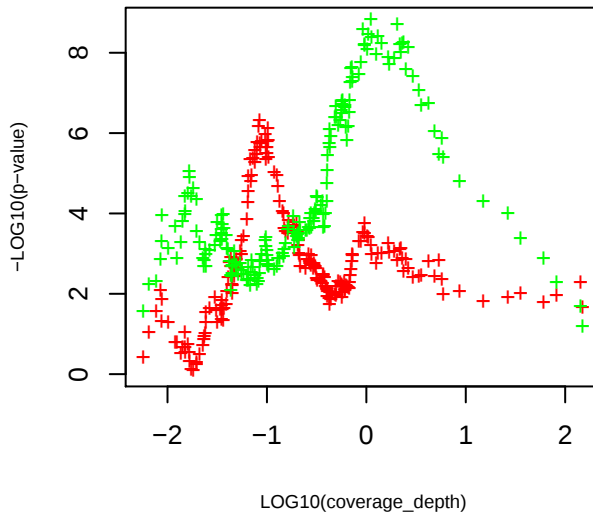


M00246 Pathway Module Heme biosynthesis, glutamate => protoheme/siroheme

slope= 0.73 p_value= 1.6e-05 intercept= -1.57 p_value= 0.0075

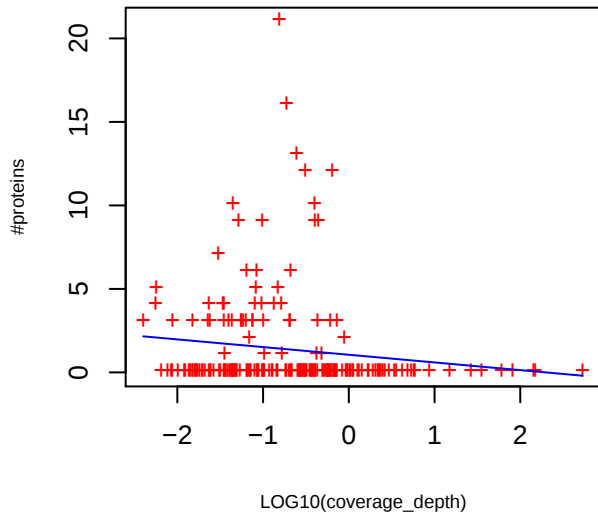


P-value curve ; red (unnorm), green (norm)



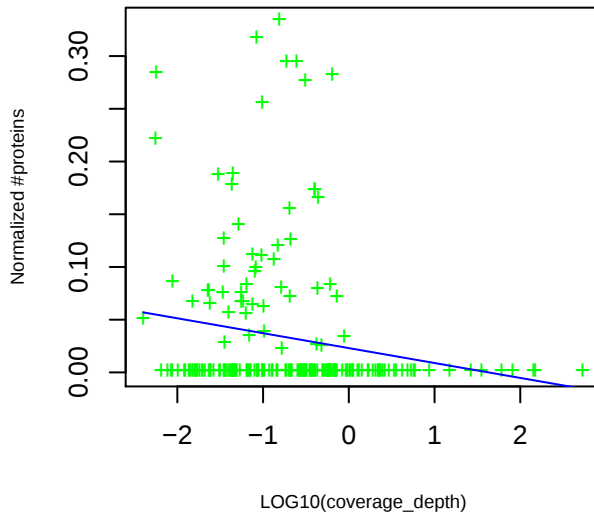
M00342 Complex Module Ribose transport system

slope= -0.46 p_value= 0.061 intercept= 1.06 p_value= 0.00017



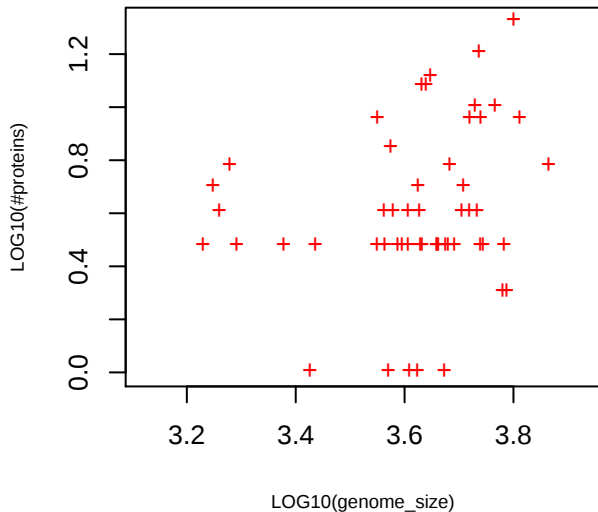
M00342 Complex Module Ribose transport system

slope= -0.014 p_value= 0.011 intercept= 0.023 p_value= 0.00027

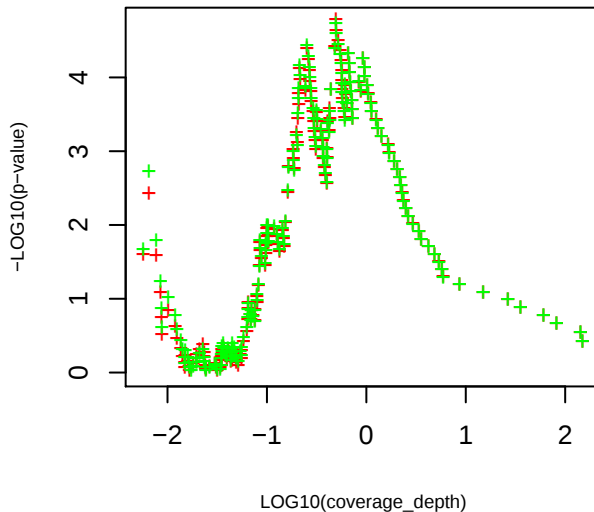


M00342 Complex Module Ribose transport system

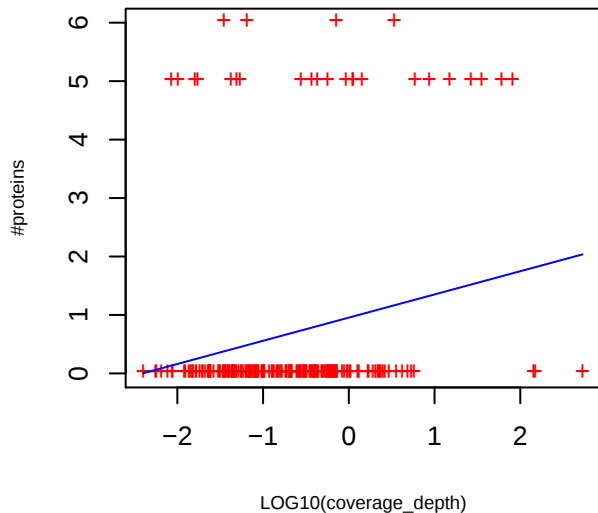
slope= 3.54 p_value= 6.3e-05 intercept= -15.30 p_value= 1.4e-06



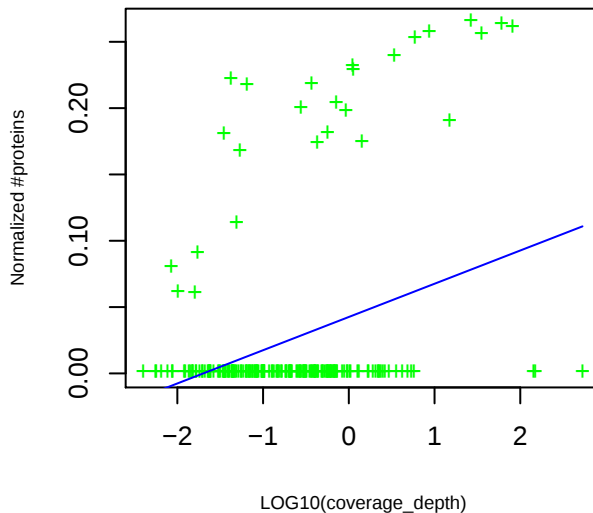
P-value curve ; red (unnorm), green (norm)



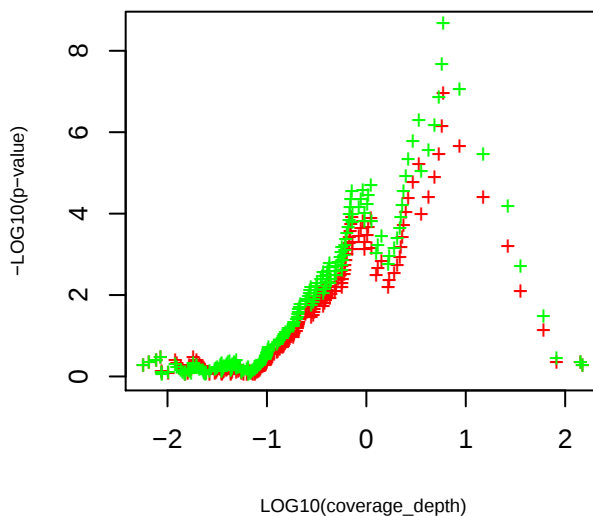
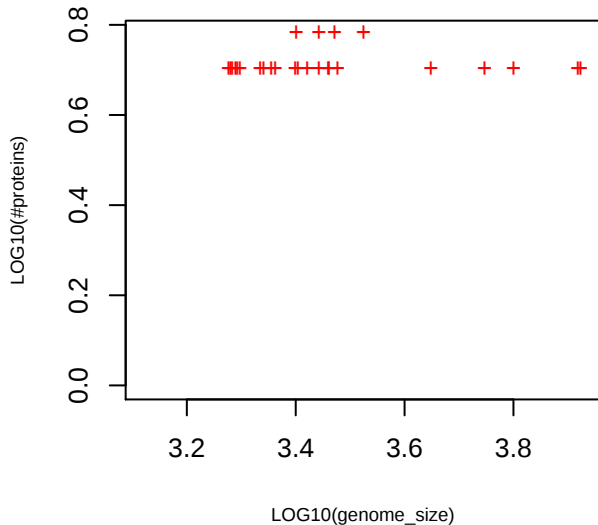
slope= 0.40 p_value= 0.0044 intercept= 0.95 p_value= 4.3e-09



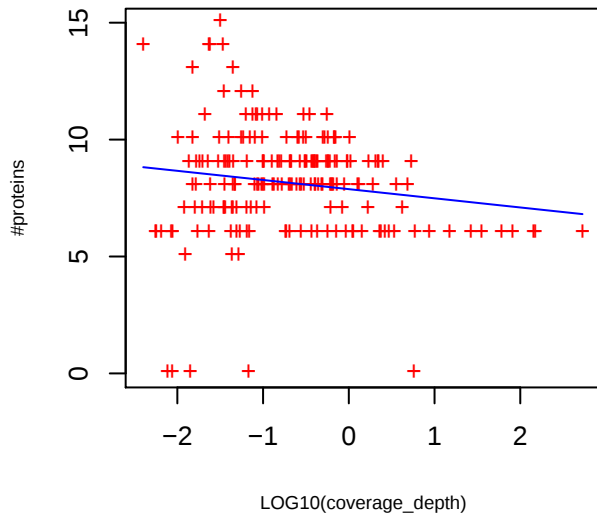
slope= 0.025 p_value= 2.8e-06 intercept= 0.043 p_value= 9.2e-12



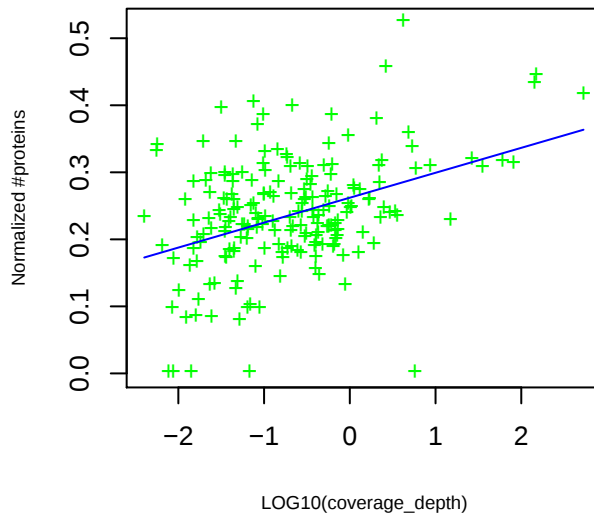
slope= -1.92 p_value= 0.0058 intercept= 3.43 p_value= 0.16



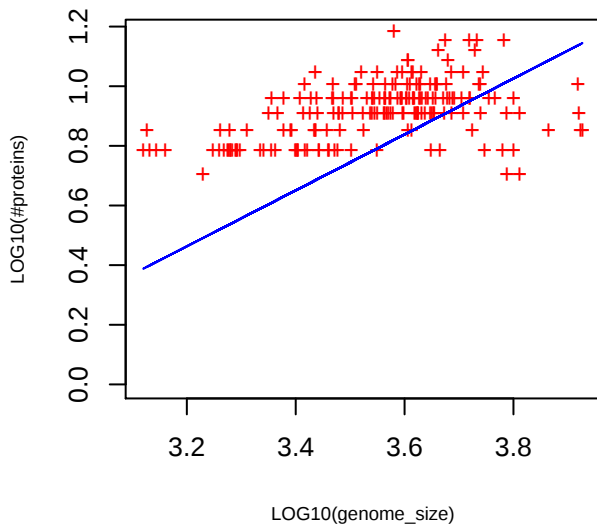
M00597 Complex Module DNA polymerase III complex
 slope= -0.39 p_value= 0.033 intercept= 7.88 p_value= 1.2e-92



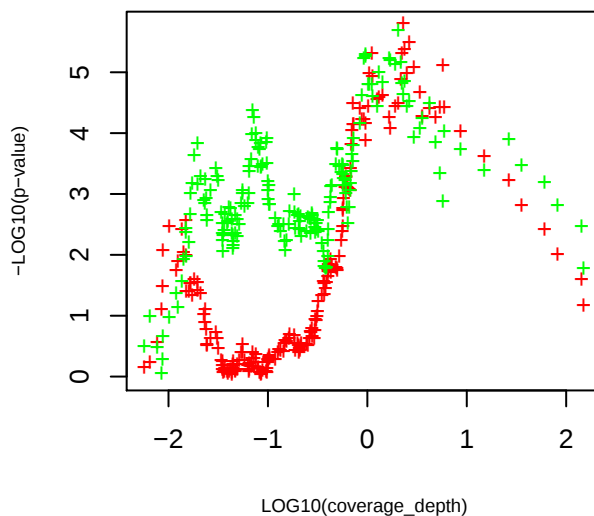
M00597 Complex Module DNA polymerase III complex
 slope= 0.037 p_value= 5e-09 intercept= 0.26 p_value= 1.9e-92



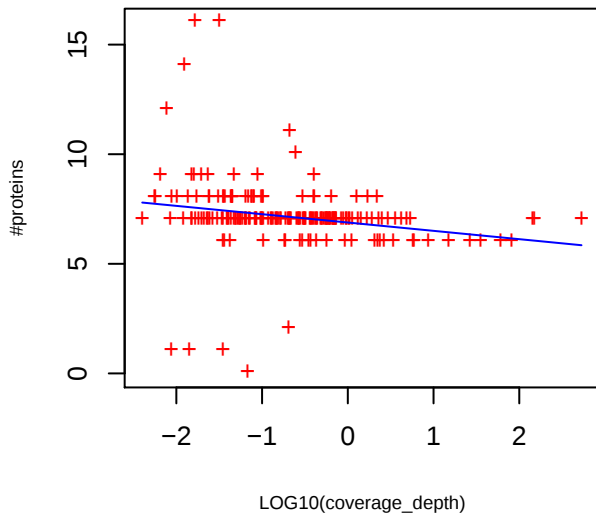
M00597 Complex Module DNA polymerase III complex
 slope= 0.94 p_value= 0.0058 intercept= -2.54 p_value= 0.035



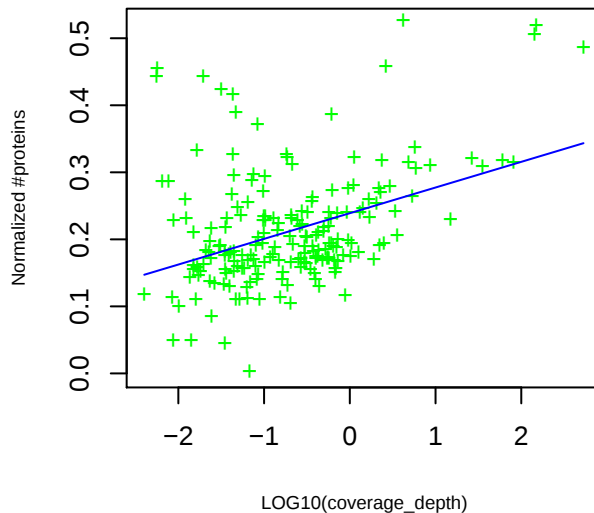
P-value curve ; red (unnorm), green (norm)



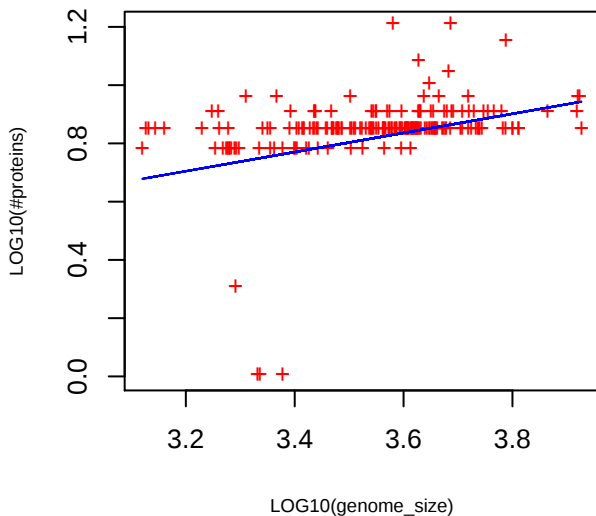
slope= -0.38 p_value= 0.0036 intercept= 6.88 p_value= 8.6e-109



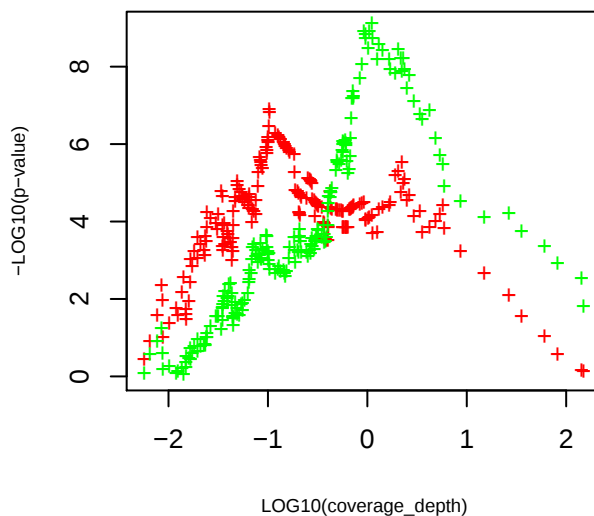
slope= 0.038 p_value= 1.0e-08 intercept= 0.24 p_value= 6.4e-82



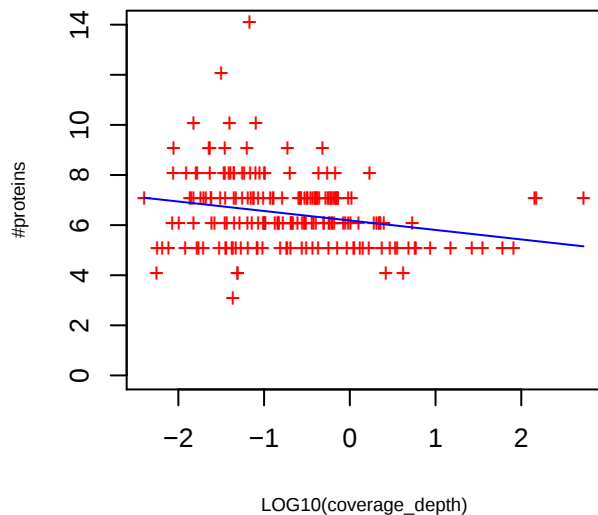
slope= 0.33 p_value= 0.041 intercept= -0.35 p_value= 0.54



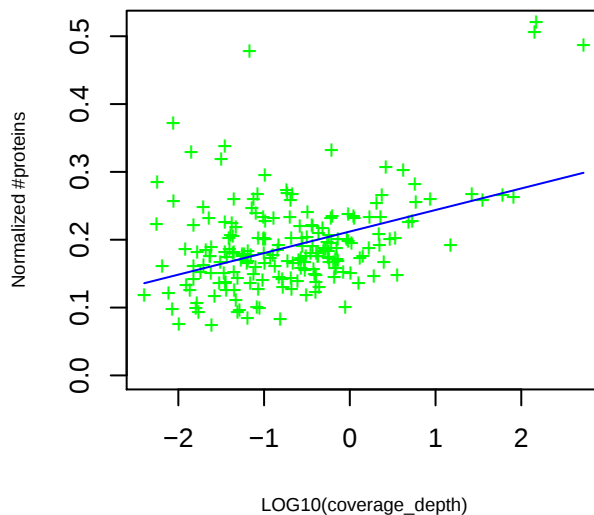
P-value curve ; red (unnorm), green (norm)



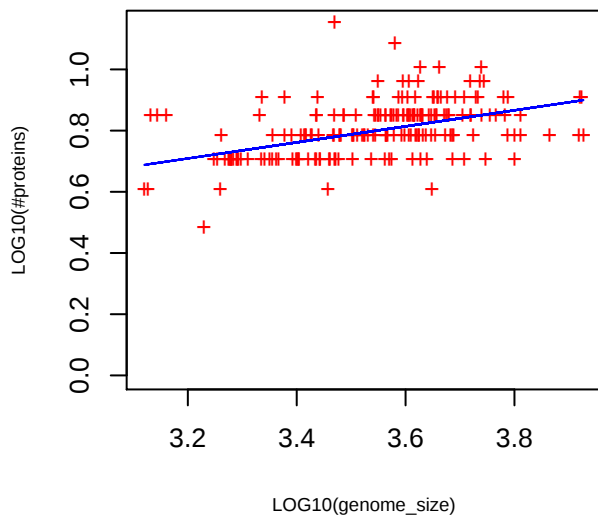
slope= -0.38 p_value= 0.00074 intercept= 6.18 p_value= 1.4e-112



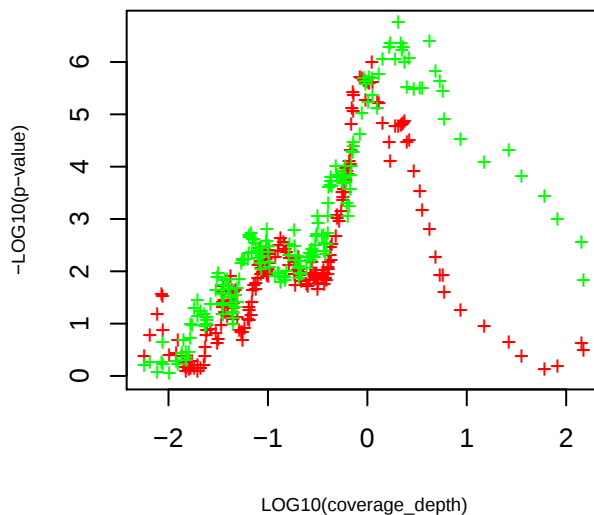
slope= 0.032 p_value= 2.0e-09 intercept= 0.21 p_value= 1.8e-90



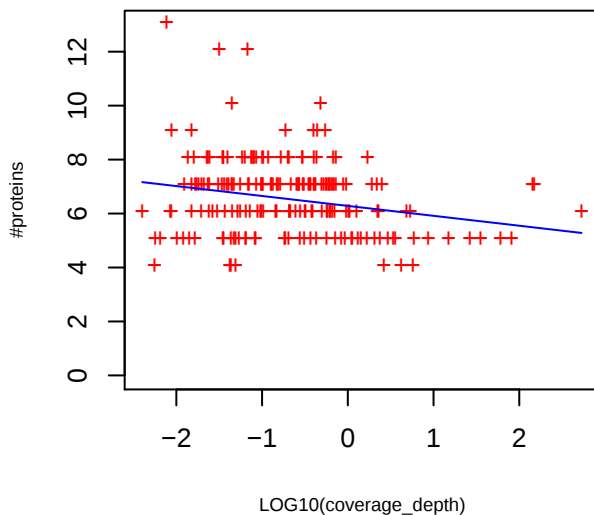
slope= 0.26 p_value= 4.8e-12 intercept= -0.13 p_value= 0.30



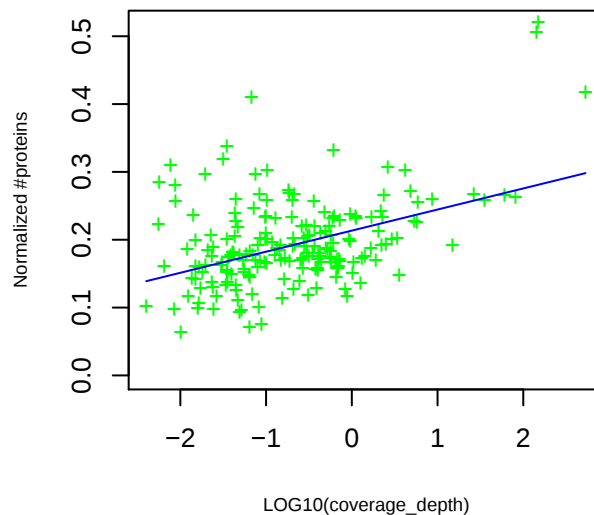
P-value curve ; red (unnorm), green (norm)



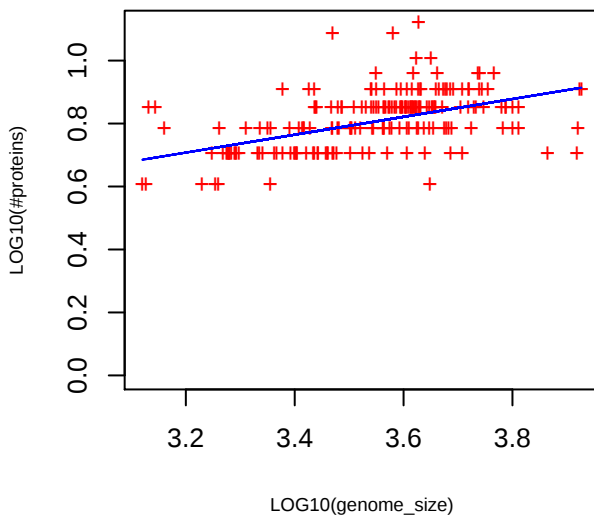
slope= -0.37 p_value= 0.0011 intercept= 6.28 p_value= 3.0e-113



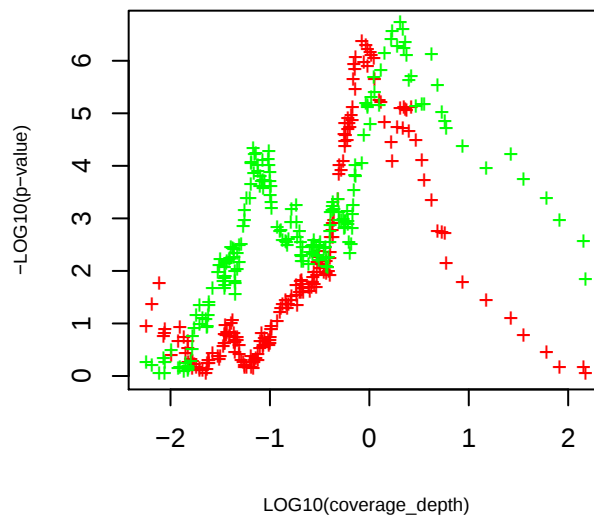
slope= 0.031 p_value= 4.3e-10 intercept= 0.21 p_value= 6e-96



slope= 0.28 p_value= 4.1e-14 intercept= -0.20 p_value= 0.11

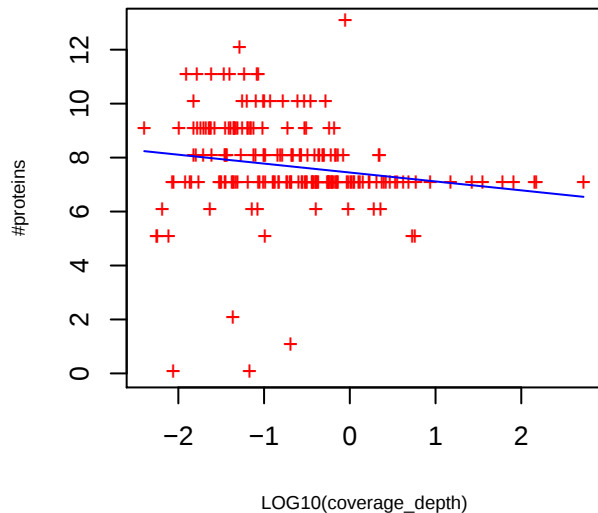


P-value curve : red (unnorm), green (norm)



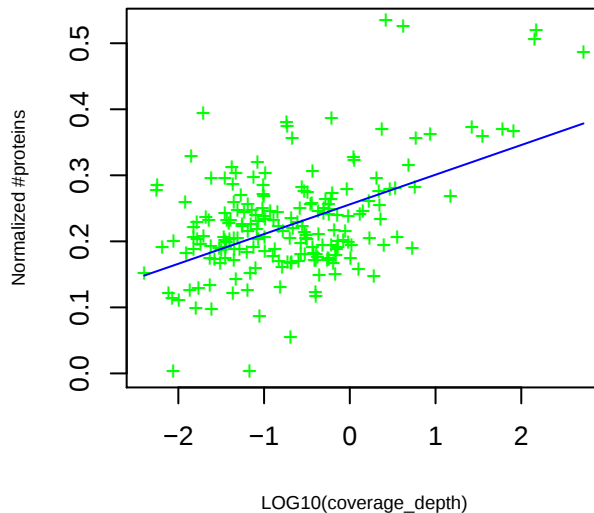
M00033 Pathway Module Chorismate biosynthesis, phosphoenolpyruvate + erythrose-4P =>

slope= -0.33 p_value= 0.014 intercept= 7.45 p_value= 2.1e-112



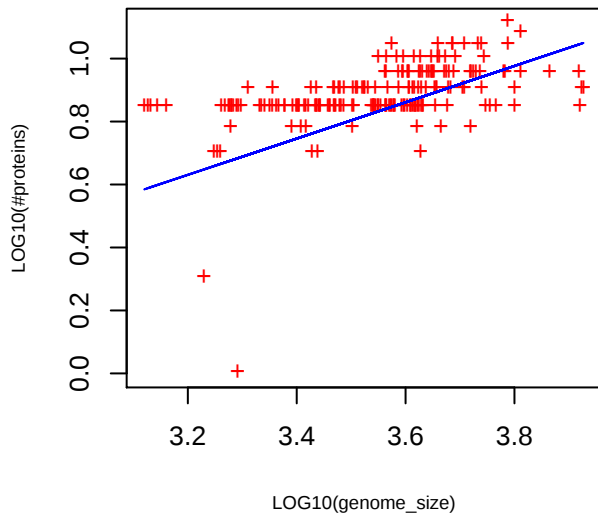
M00033 Pathway Module Chorismate biosynthesis, phosphoenolpyruvate + erythrose-4P =>

slope= 0.045 p_value= 1.1e-13 intercept= 0.26 p_value= 1.8e-96

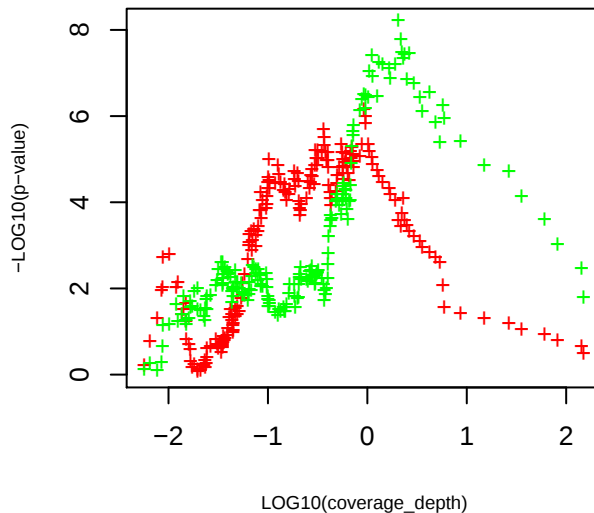


M00033 Pathway Module Chorismate biosynthesis, phosphoenolpyruvate + erythrose-4P =>

slope= 0.58 p_value= 0.0084 intercept= -1.21 p_value= 0.12

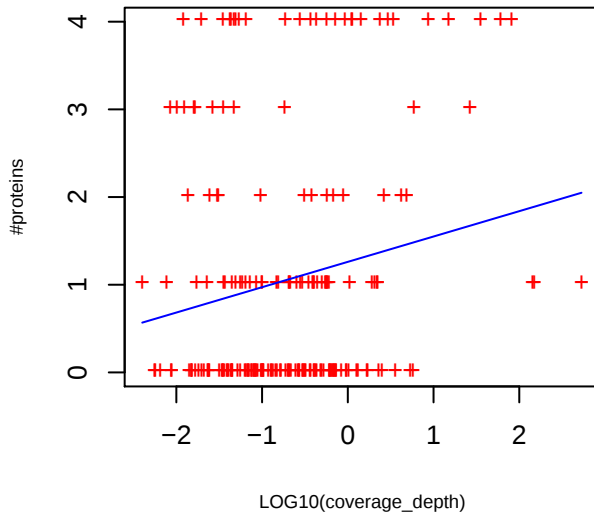


P-value curve ; red (unnorm), green (norm)



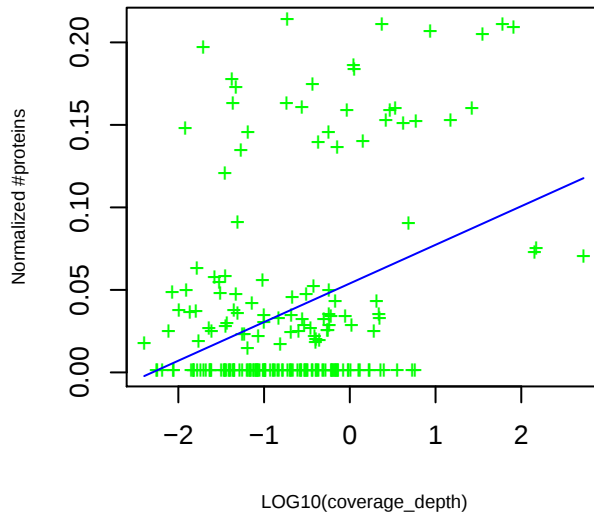
M00197 Pathway Module C40 isoprenoid biosynthesis, GGAP => lycopene

slope= 0.29 p_value= 0.011 intercept= 1.26 p_value= 6.2e-19



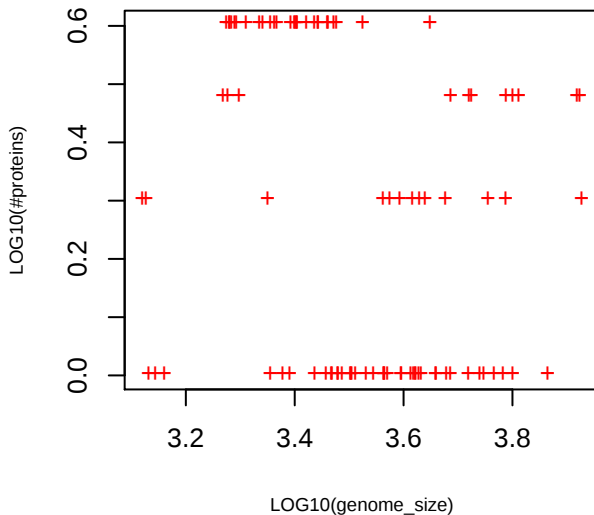
M00197 Pathway Module C40 isoprenoid biosynthesis, GGAP => lycopene

slope= 0.023 p_value= 4.5e-07 intercept= 0.054 p_value= 3.4e-21

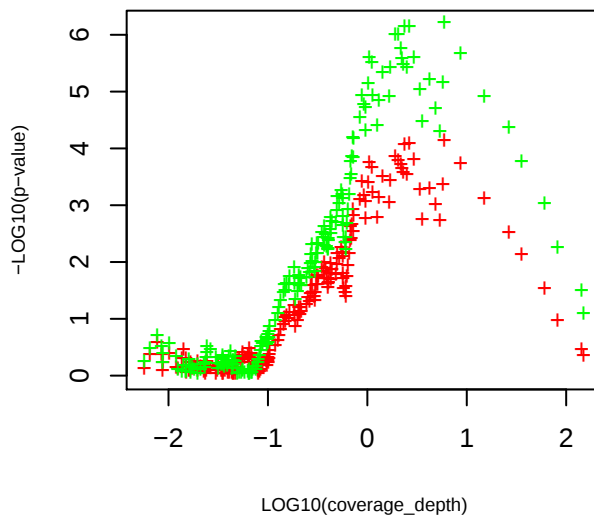


M00197 Pathway Module C40 isoprenoid biosynthesis, GGAP => lycopene

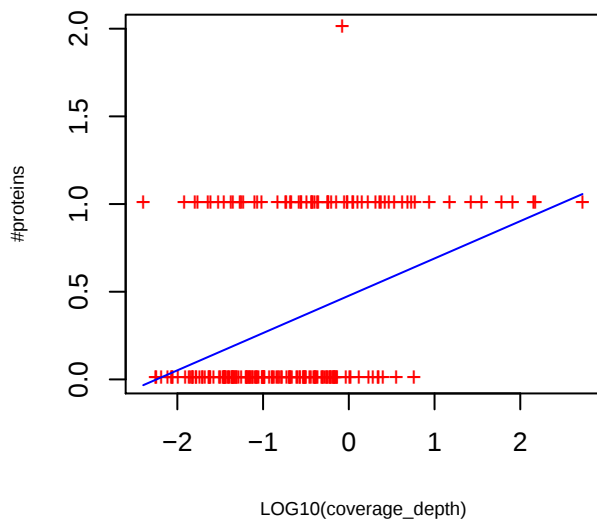
slope= -2.17 p_value= 0.021 intercept= 5.72 p_value= 0.085



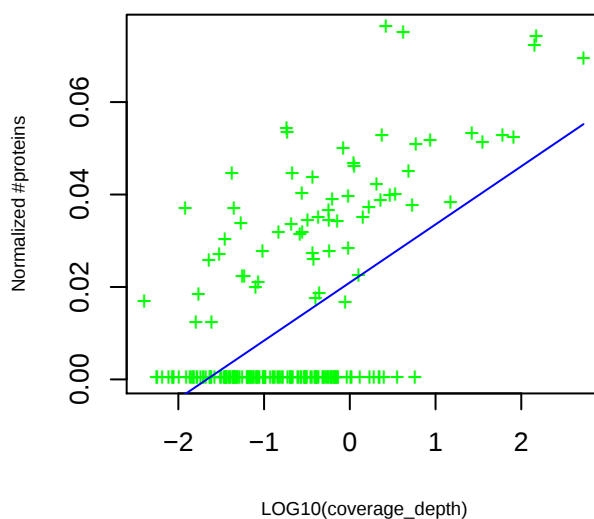
P-value curve ; red (unnorm), green (norm)



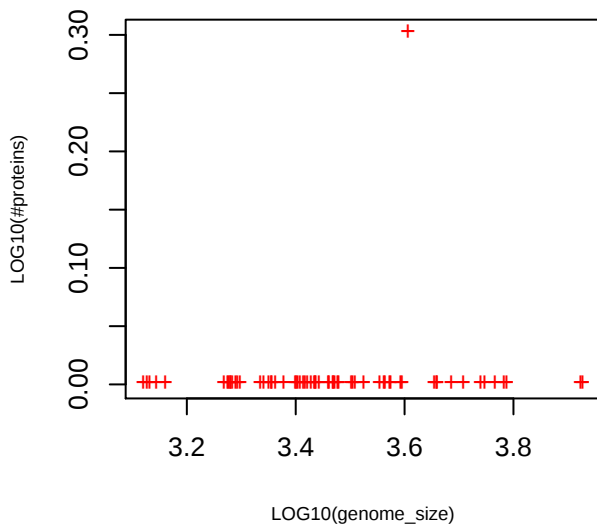
slope= 0.21 p_value= 9.5e-09 intercept= 0.48 p_value= 6e-25



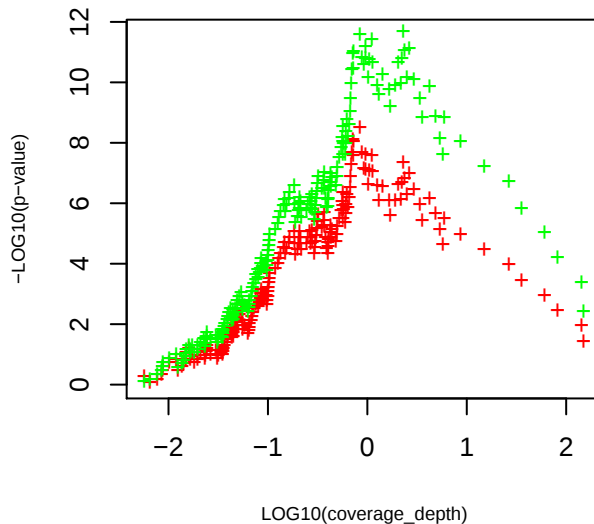
slope= 0.013 p_value= 2.1e-18 intercept= 0.021 p_value= 2.9e-32



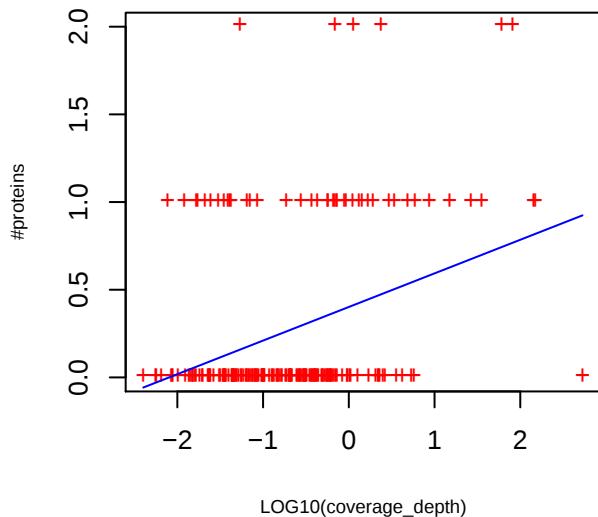
slope= -3.97 p_value= 7.6e-07 intercept= 11.36 p_value= 5.4e-05



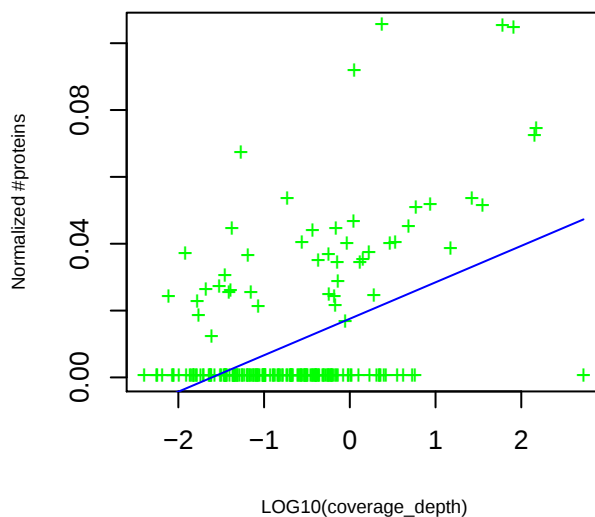
P-value curve ; red (unnorm), green (norm)



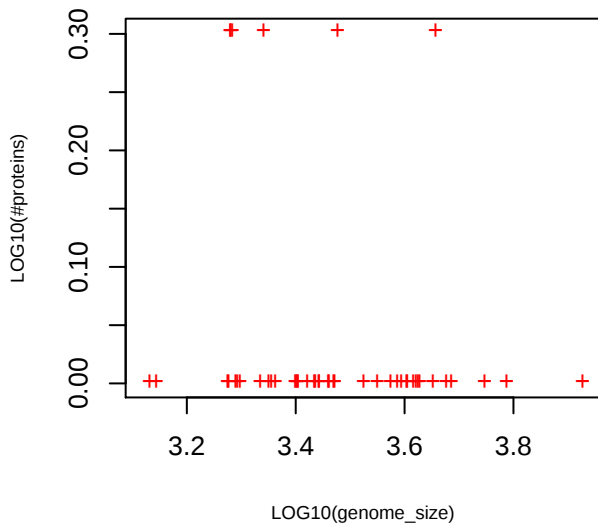
slope= 0.19 p_value= 1.3e-06 intercept= 0.40 p_value= 3.5e-17



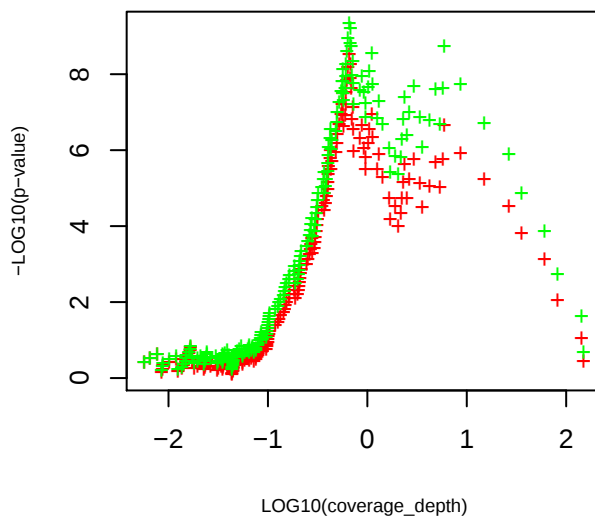
slope= 0.011 p_value= 7e-12 intercept= 0.018 p_value= 1.9e-20



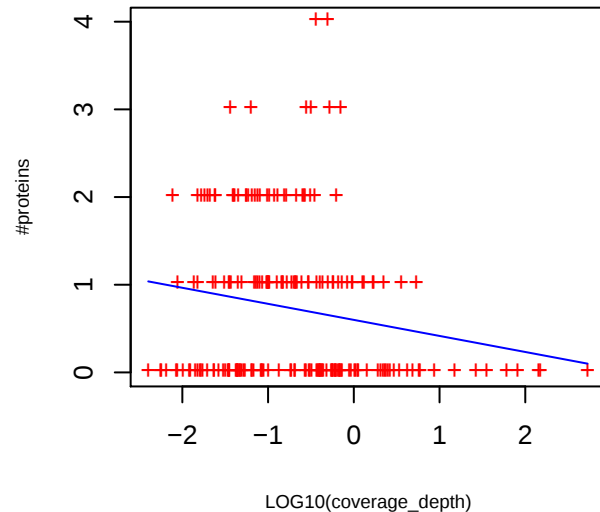
slope= -2.78 p_value= 0.00019 intercept= 6.83 p_value= 0.0092



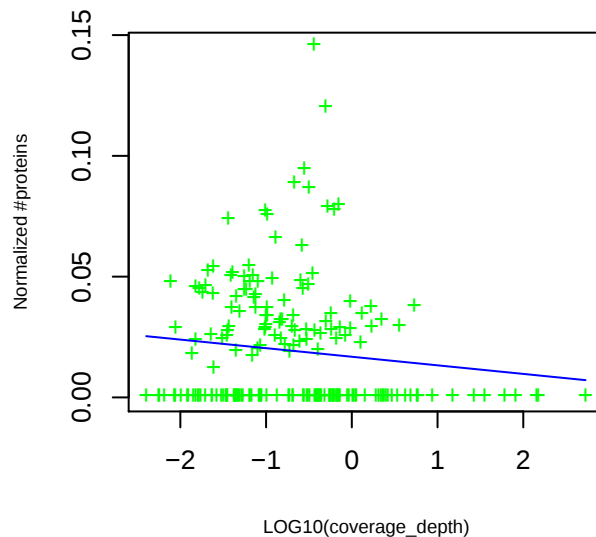
P-value curve ; red (unnorm), green (norm)



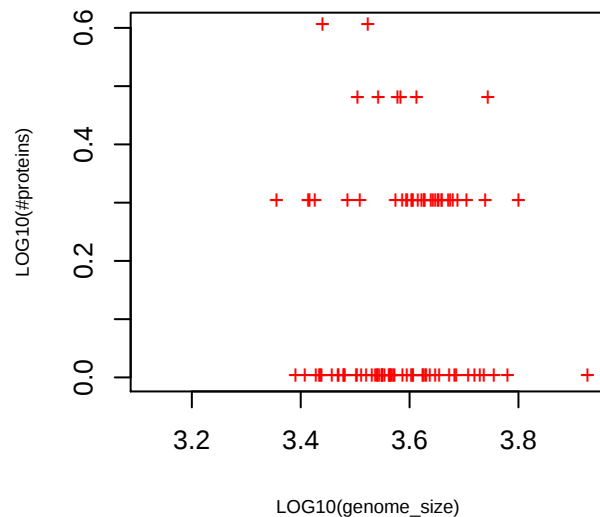
slope= -0.18 p_value= 0.012 intercept= 0.60 p_value= 4.4e-12



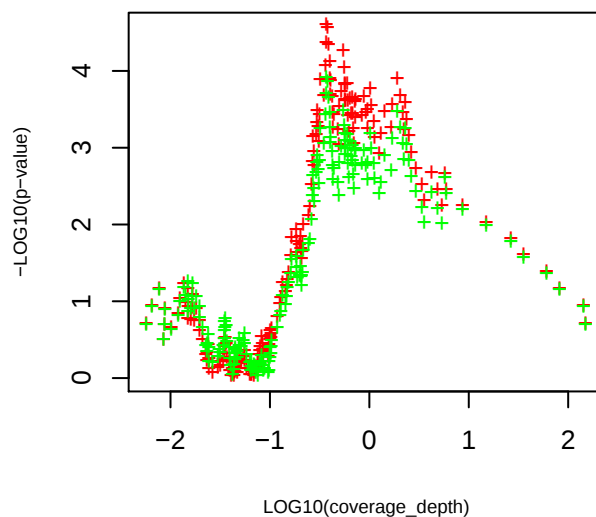
slope= -0.0036 p_value= 0.082 intercept= 0.017 p_value= 5.6e-12



slope= 3.01 p_value= 0.00083 intercept= -12.73 p_value= 7.6e-05

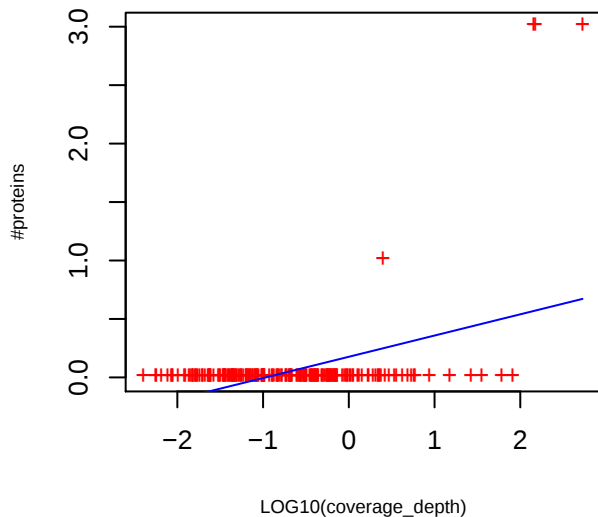


P-value curve ; red (unnorm), green (norm)



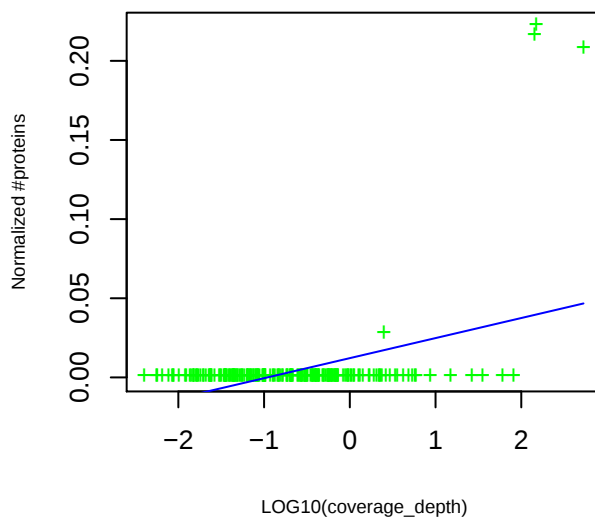
M00361 Complex Module Octopine/nopaline transport system

slope= 0.18 p_value= 1.9e-10 intercept= 0.18 p_value= 2.8e-08



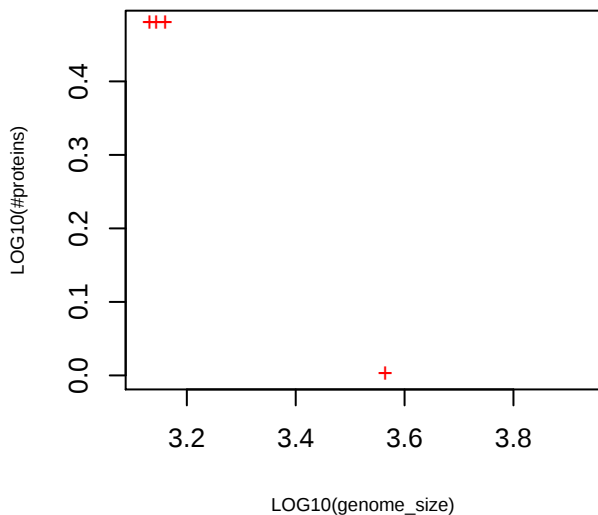
M00361 Complex Module Octopine/nopaline transport system

slope= 0.013 p_value= 3.3e-10 intercept= 0.012 p_value= 5.8e-08

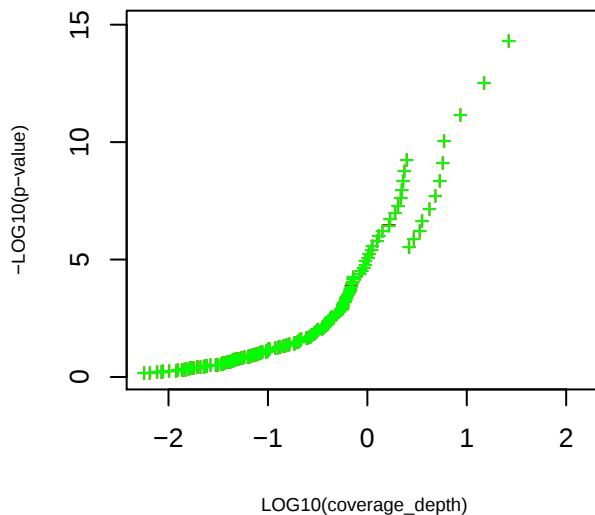


M00361 Complex Module Octopine/nopaline transport system

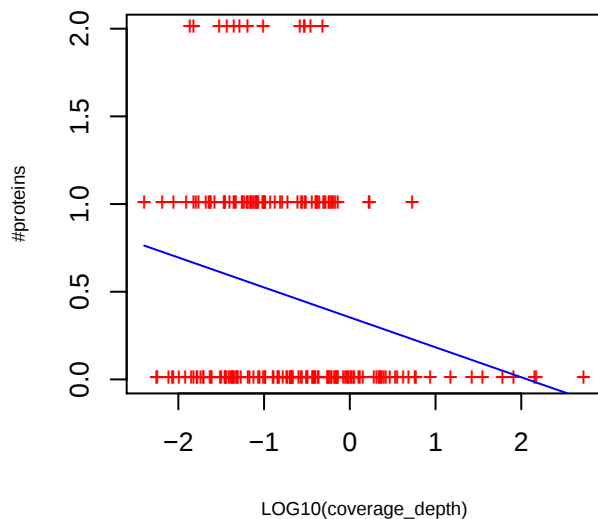
slope= -1.02 p_value= 0.00014 intercept= -0.31 p_value= 0.74



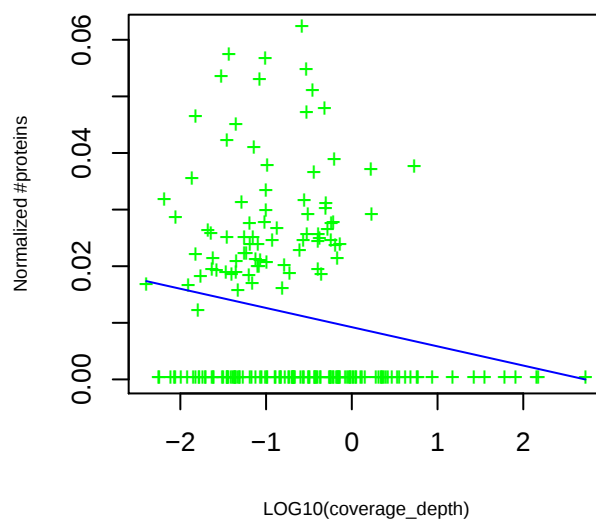
P-value curve ; red (unnorm), green (norm)



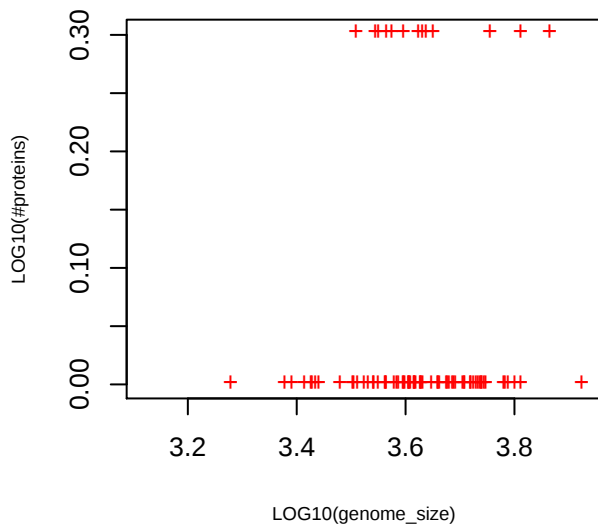
slope= -0.17 p_value= 0.00048 intercept= 0.35 p_value= 5.7e-10



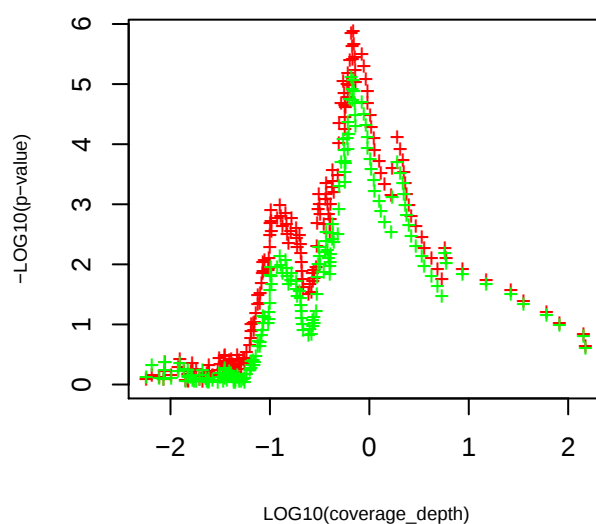
slope= -0.0034 p_value= 0.0069 intercept= 0.0092 p_value= 4.1e-10



slope= 4.87 p_value= 6.8e-09 intercept= -19.63 p_value= 7.9e-11

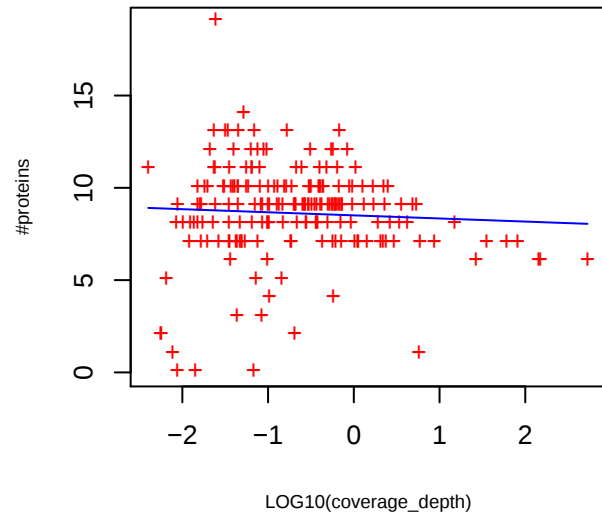


P-value curve ; red (unnorm), green (norm)



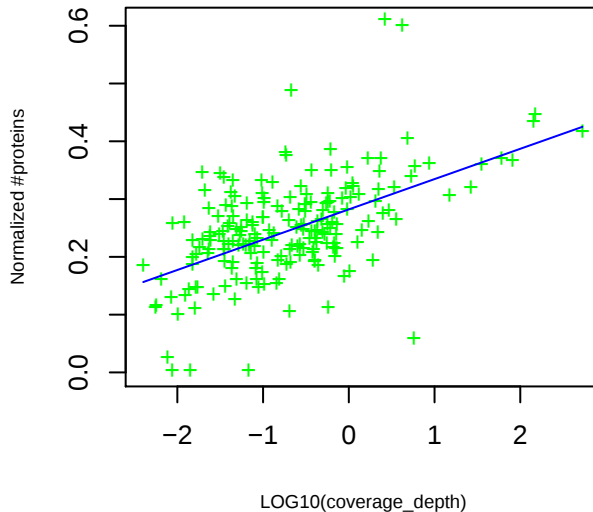
M00159 Pathway Module Fatty acid biosynthesis, initiation

slope= -0.17 p_value= 0.41 intercept= 8.51 p_value= 1.2e-89



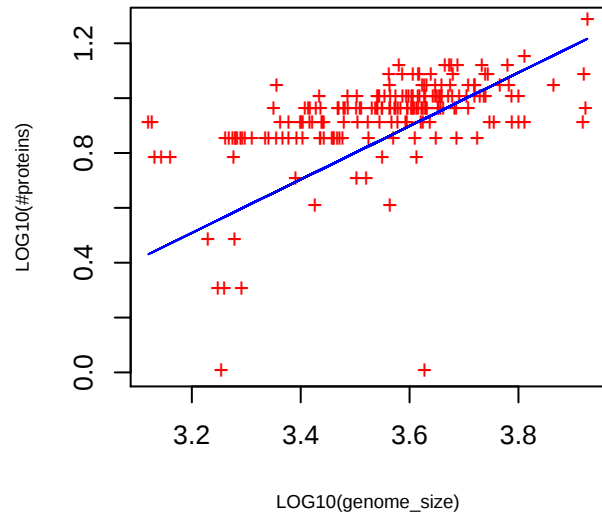
M00159 Pathway Module Fatty acid biosynthesis, initiation

slope= 0.052 p_value= 1.5e-16 intercept= 0.28 p_value= 1.2e-101

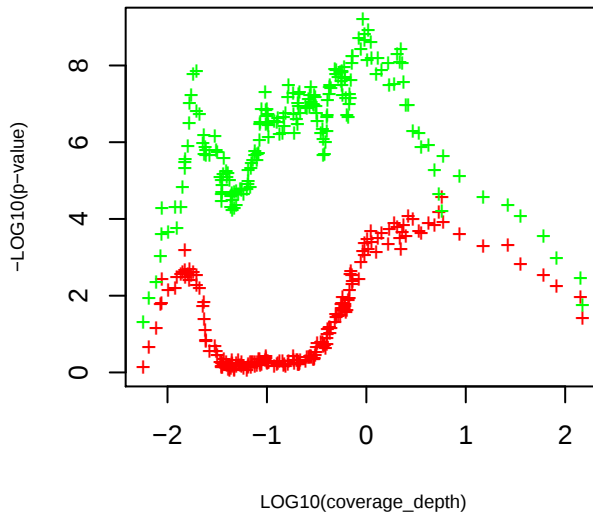


M00159 Pathway Module Fatty acid biosynthesis, initiation

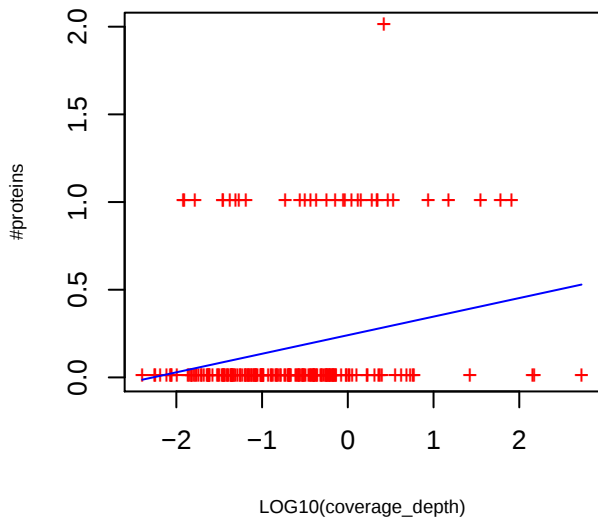
slope= 0.97 p_value= 0.00032 intercept= -2.61 p_value= 0.0062



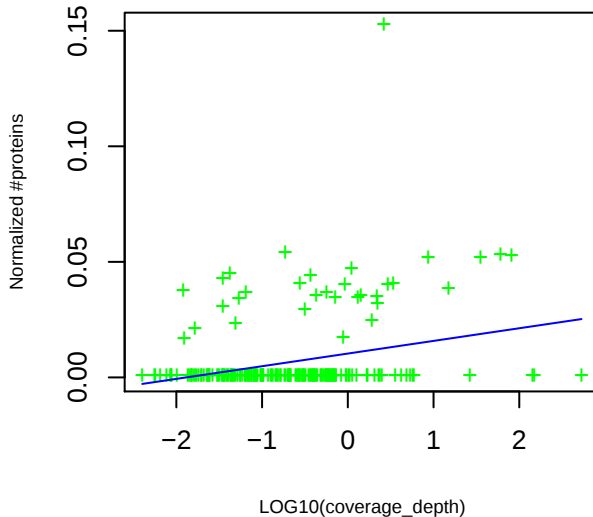
P-value curve ; red (unnorm), green (norm)



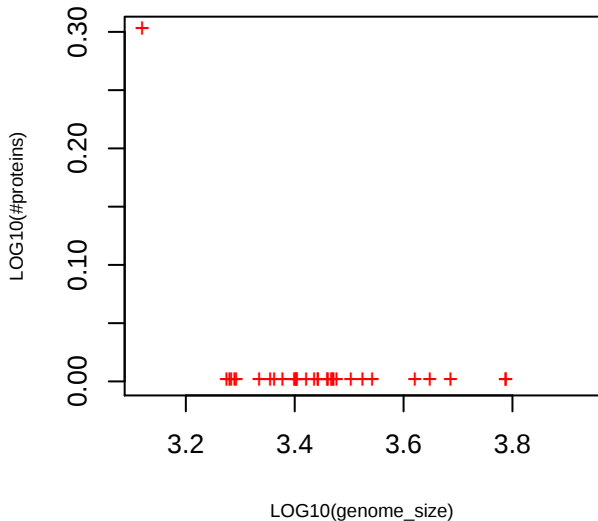
M00203 Pathway Module Glycero glycolipid biosynthesis
 slope= 0.11 p_value= 0.00054 intercept= 0.24 p_value= 2.5e-11



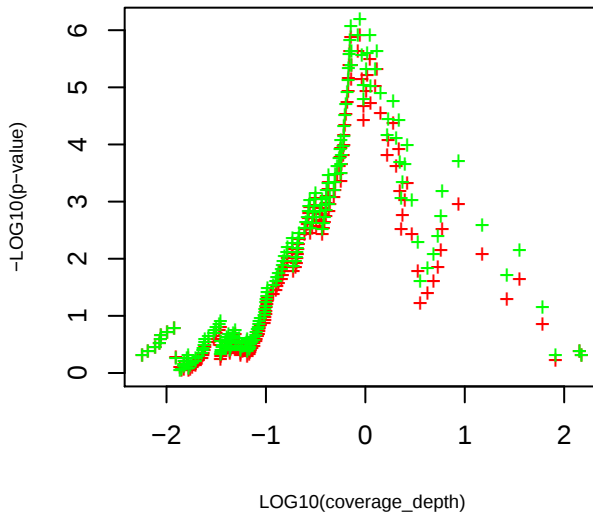
M00203 Pathway Module Glycero glycolipid biosynthesis
 slope= 0.0055 p_value= 6e-05 intercept= 0.010 p_value= 9.7e-11



M00203 Pathway Module Glycero glycolipid biosynthesis
 slope= -2.50 p_value= 9.4e-05 intercept= 5.51 p_value= 0.014

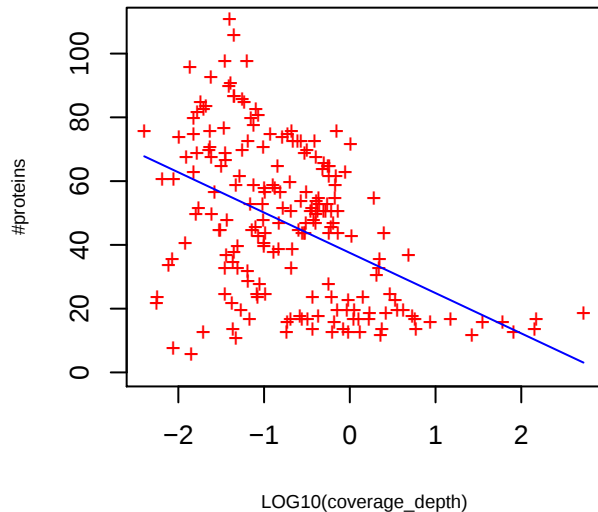


P-value curve ; red (unnorm), green (norm)



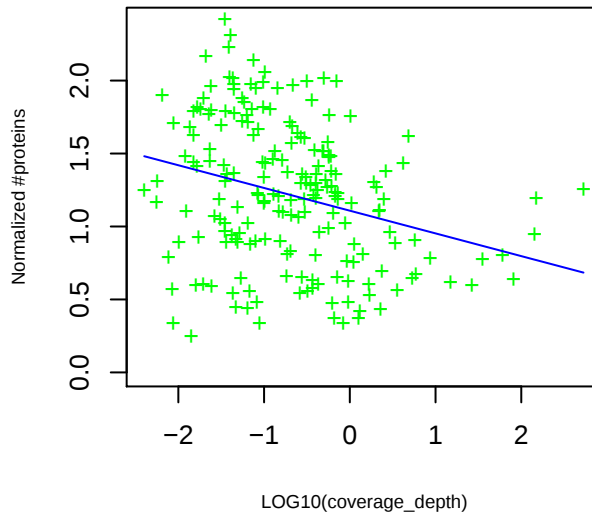
Envi_15 Signal Transduction Two-component system [PATH:ko02020]

slope= -12.63 p_value= 6e-12 intercept= 37.50 p_value= 5e-47



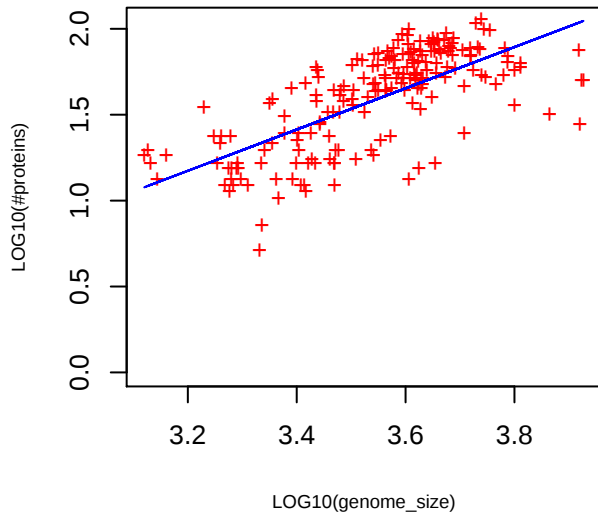
Envi_15 Signal Transduction Two-component system [PATH:ko02020]

slope= -0.16 p_value= 4.8e-05 intercept= 1.11 p_value= 7.2e-66

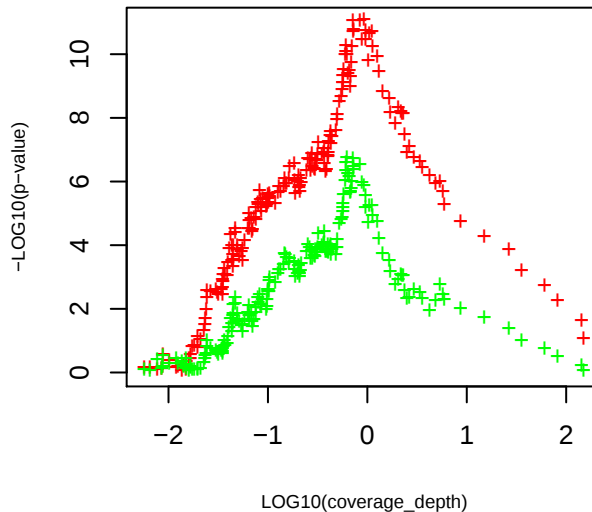


Envi_15 Signal Transduction Two-component system [PATH:ko02020]

slope= 1.20 p_value= 8.6e-30 intercept= -2.67 p_value= 6.3e-15

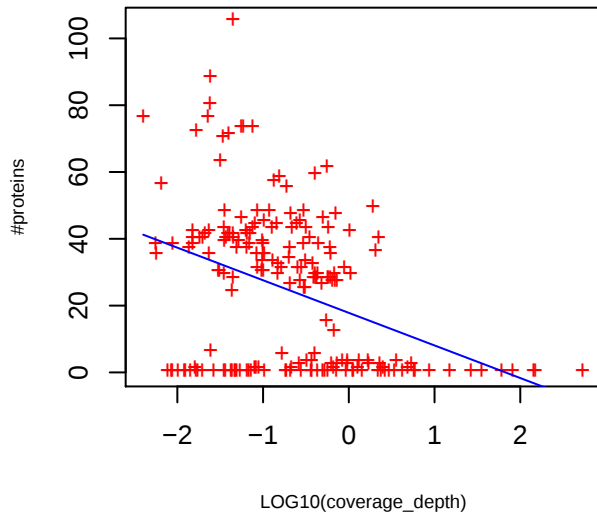


P-value curve ; red (unnorm), green (norm)



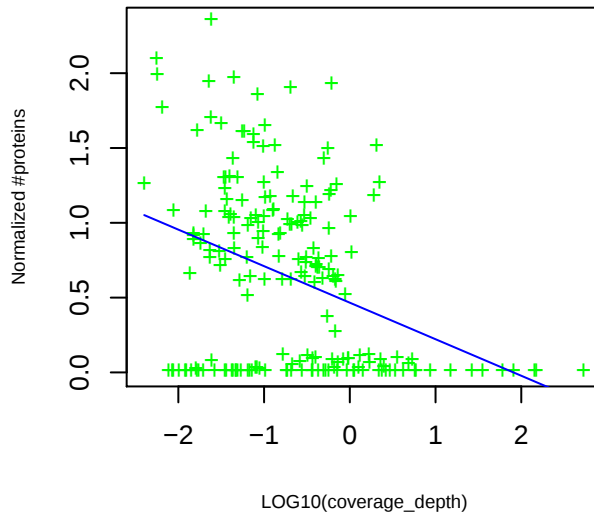
Cell_11 Cell Motility Flagellar assembly [PATH:ko02040]

slope= -9.76 p_value= 4.3e-08 intercept= 17.83 p_value= 4.6e-17



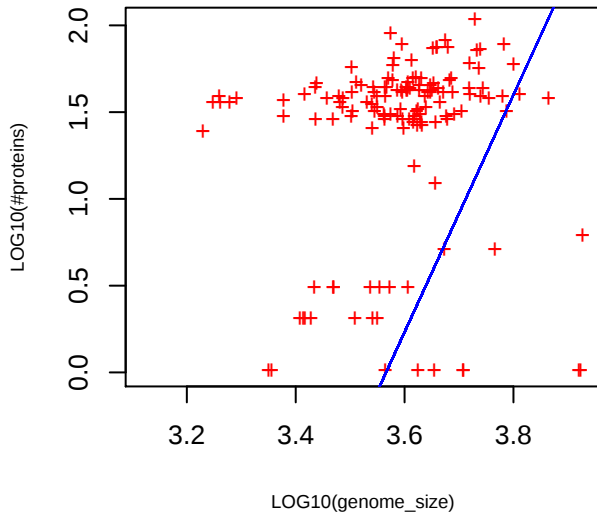
Cell_11 Cell Motility Flagellar assembly [PATH:ko02040]

slope= -0.24 p_value= 1.5e-07 intercept= 0.47 p_value= 5.1e-17

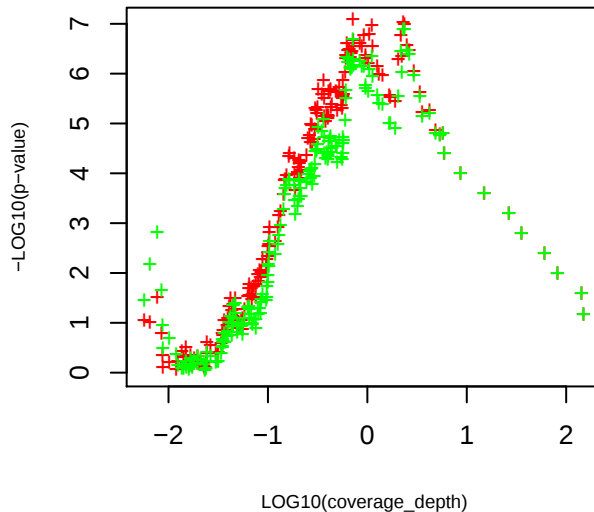


Cell_11 Cell Motility Flagellar assembly [PATH:ko02040]

slope= 6.84 p_value= 1.8e-11 intercept= -24.38 p_value= 1.5e-11

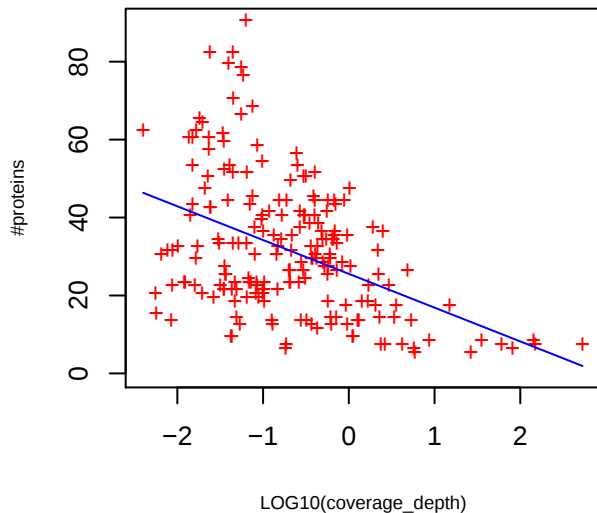


P-value curve : red (unnorm), green (norm)



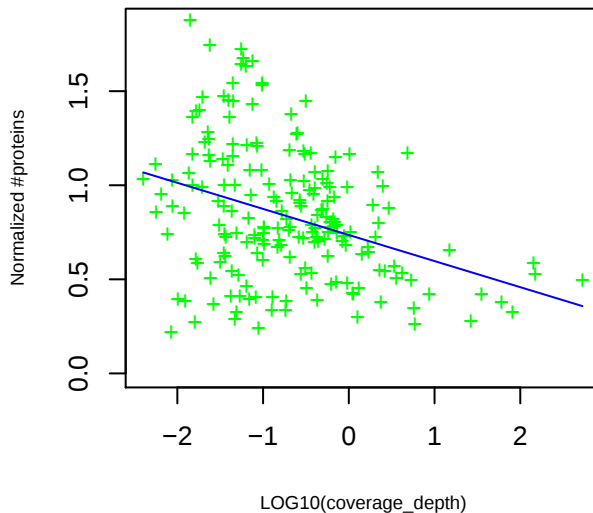
Envi_3 Membrane Transport Other ion-coupled transporters

slope= -8.67 p_value= 8.7e-11 intercept= 25.55 p_value= 4.7e-43



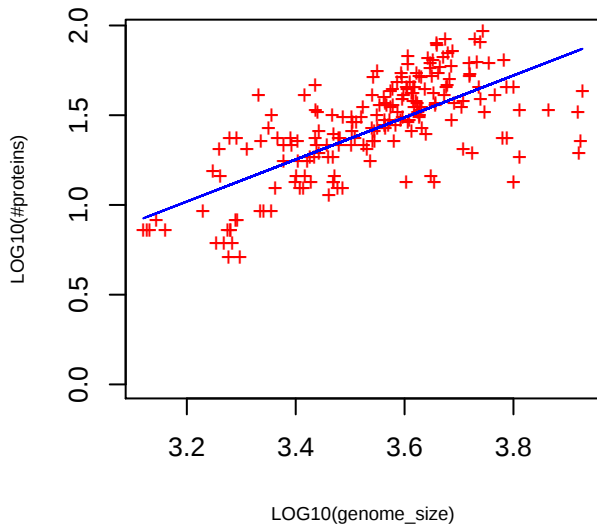
Envi_3 Membrane Transport Other ion-coupled transporters

slope= -0.14 p_value= 3.7e-07 intercept= 0.74 p_value= 5.2e-62

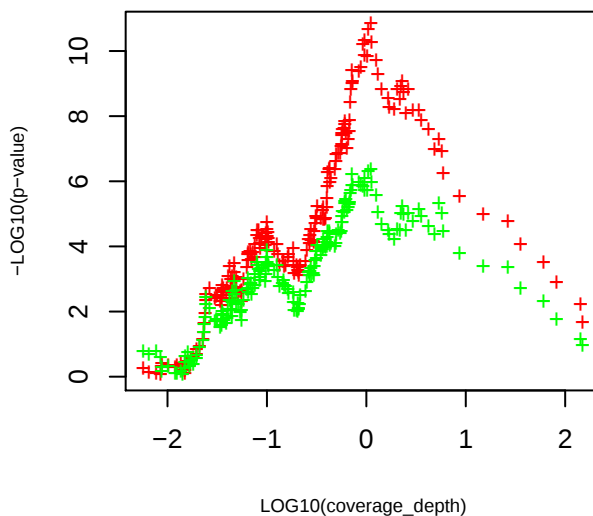


Envi_3 Membrane Transport Other ion-coupled transporters

slope= 1.17 p_value= 7e-30 intercept= -2.73 p_value= 4.2e-16

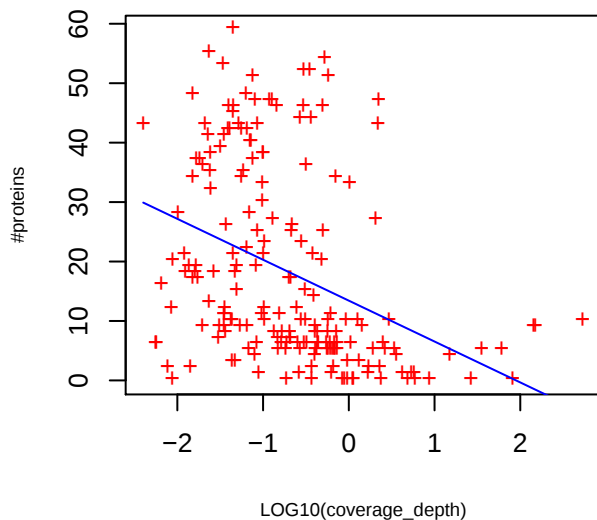


P-value curve ; red (unnorm), green (norm)



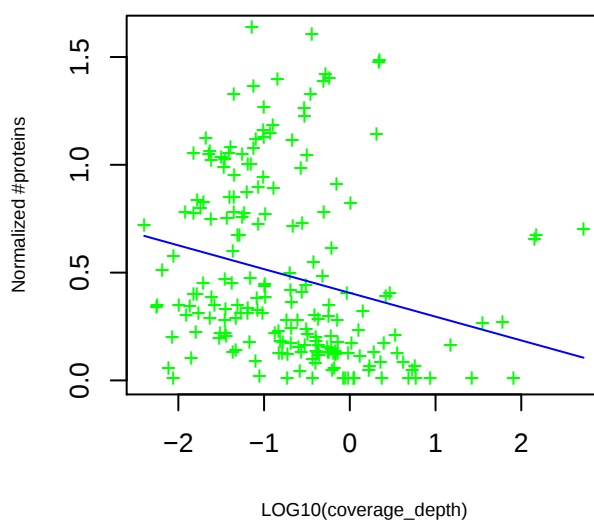
Gene_5 Folding, Sorting and Degradation Type II secretion system [PATH:ko03090]

slope= -6.88 p_value= 6.4e-08 intercept= 13.42 p_value= 1.9e-18



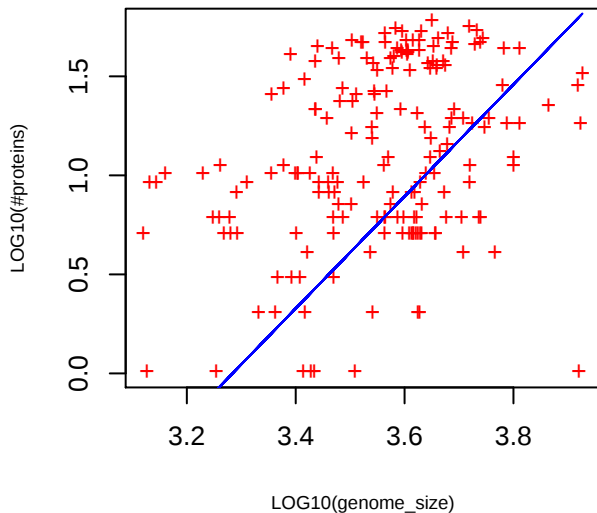
Gene_5 Folding, Sorting and Degradation Type II secretion system [PATH:ko03090]

slope= -0.11 p_value= 0.00091 intercept= 0.41 p_value= 3.6e-22

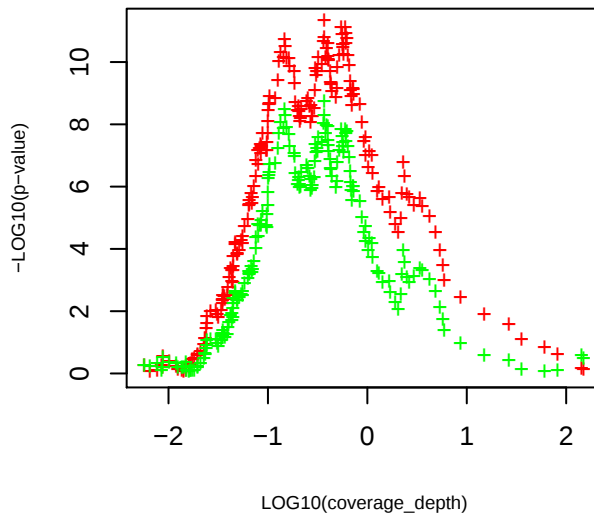


Gene_5 Folding, Sorting and Degradation Type II secretion system [PATH:ko03090]

slope= 2.83 p_value= 1.7e-06 intercept= -9.28 p_value= 8.9e-06

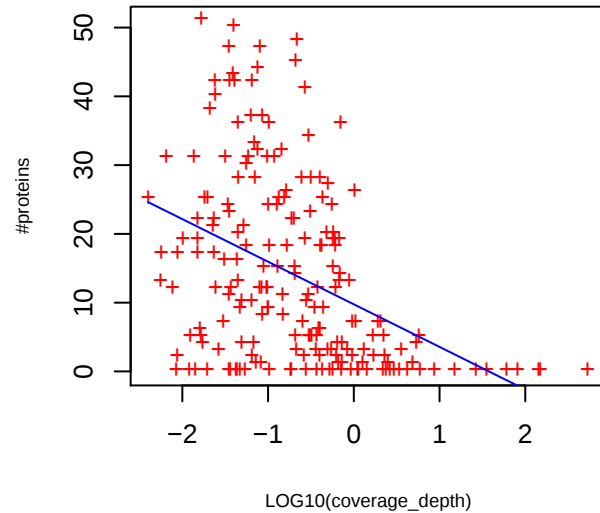


P-value curve ; red (unnorm), green (norm)



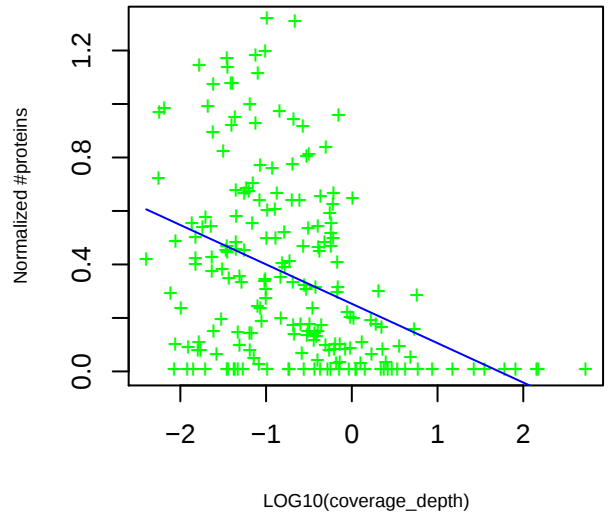
Cell_10 Cell Motility Bacterial chemotaxis [PATH:ko02030]

slope= -6.19 p_value= 3e-09 intercept= 9.76 p_value= 1.6e-15



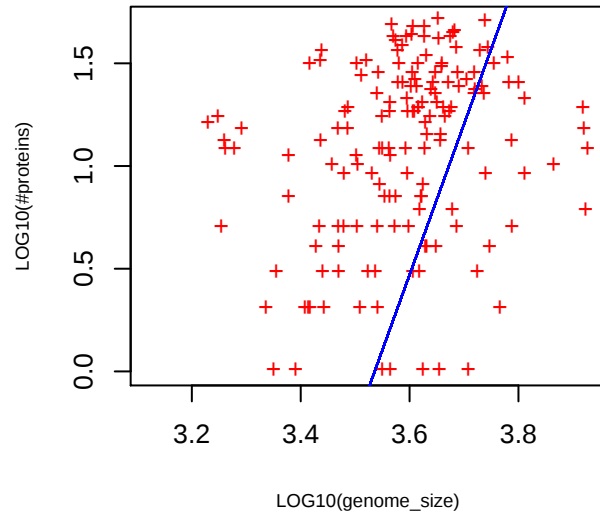
Cell_10 Cell Motility Bacterial chemotaxis [PATH:ko02030]

slope= -0.15 p_value= 2.6e-08 intercept= 0.25 p_value= 6.1e-16

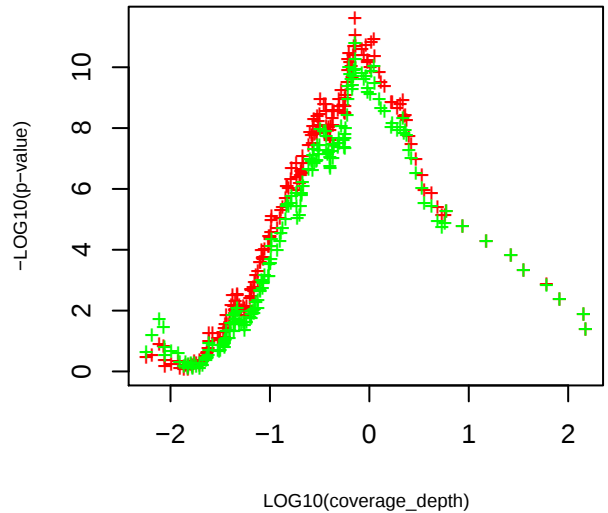


Cell_10 Cell Motility Bacterial chemotaxis [PATH:ko02030]

slope= 7.33 p_value= 5e-19 intercept= -25.93 p_value= 6.4e-19

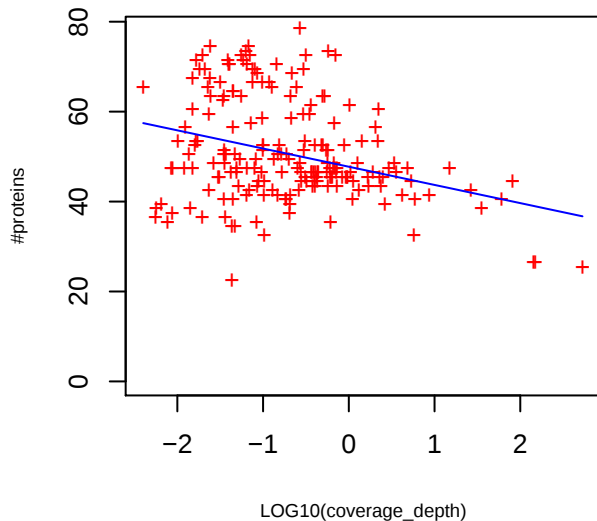


P-value curve ; red (unnorm), green (norm)



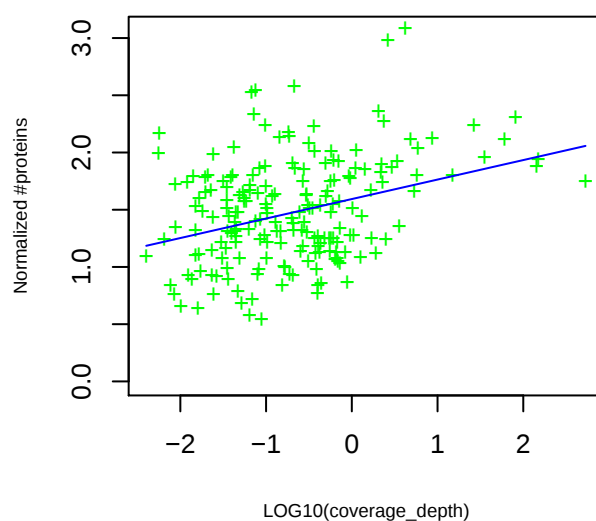
Gene_18 Translation Other translation proteins

slope= -4.05 p_value= 4.6e-06 intercept= 47.75 p_value= 5e-112



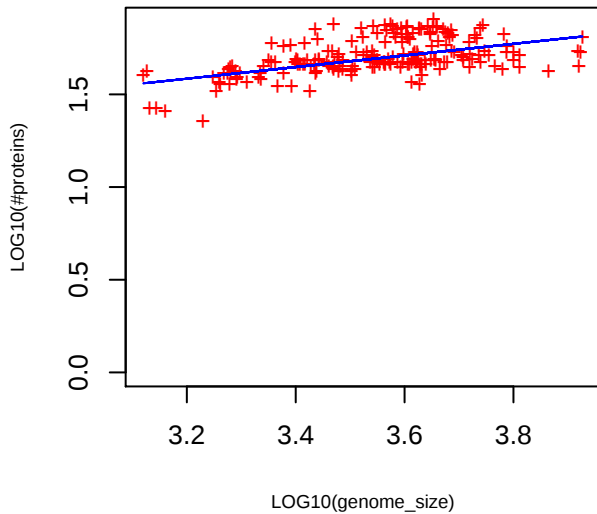
Gene_18 Translation Other translation proteins

slope= 0.17 p_value= 1.4e-06 intercept= 1.59 p_value= 2.5e-98

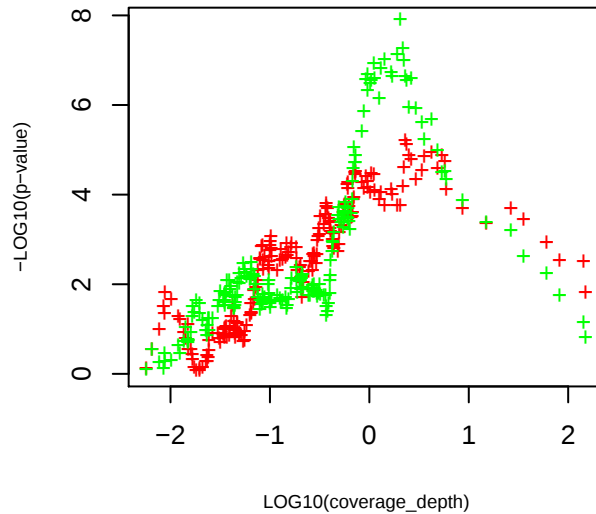


Gene_18 Translation Other translation proteins

slope= 0.31 p_value= 4.4e-15 intercept= 0.58 p_value= 1.4e-05

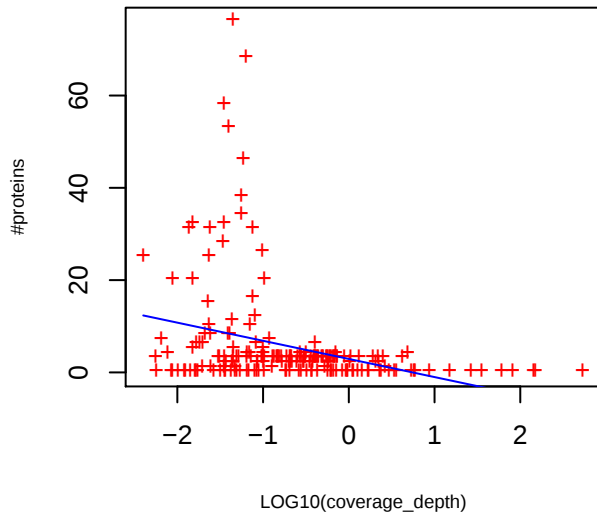


P-value curve ; red (unnorm), green (norm)



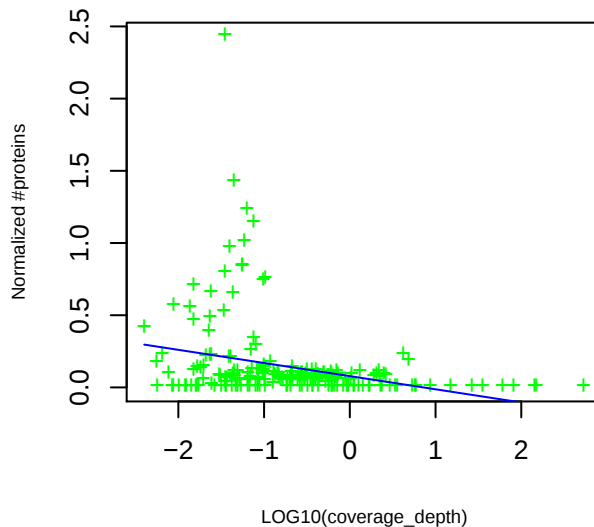
Envi_5 Membrane Transport Phosphotransferase system (PTS) [PATH:ko02060]

slope= -3.93 p_value= 1.4e-05 intercept= 2.92 p_value= 0.0037



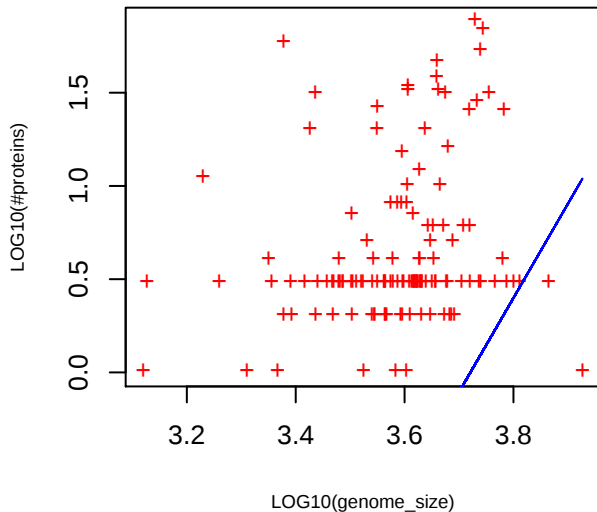
Envi_5 Membrane Transport Phosphotransferase system (PTS) [PATH:ko02060]

slope= -0.091 p_value= 5.3e-05 intercept= 0.078 p_value= 0.0019

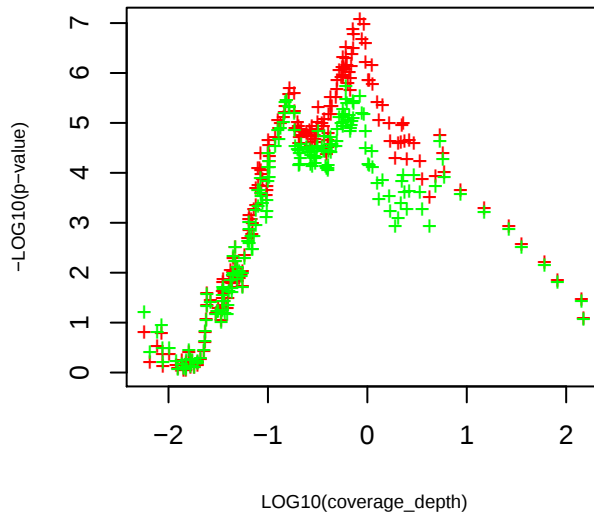


Envi_5 Membrane Transport Phosphotransferase system (PTS) [PATH:ko02060]

slope= 5.05 p_value= 8e-08 intercept= -18.78 p_value= 2.0e-08

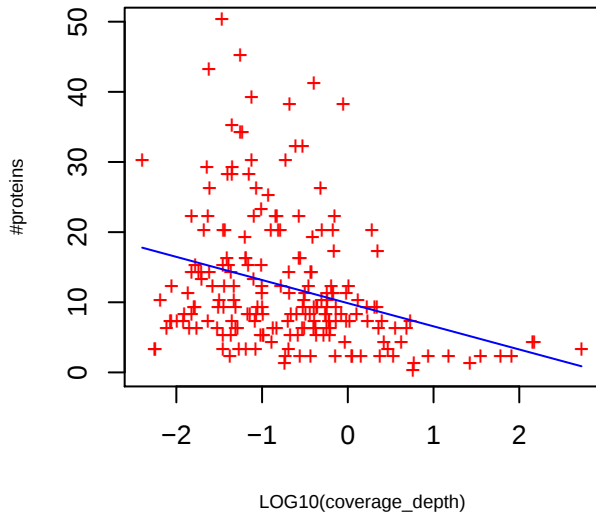


P-value curve ; red (unnorm), green (norm)



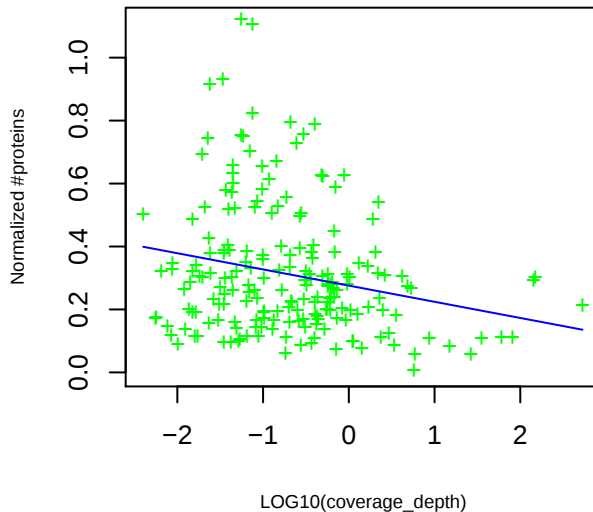
Envi_4 Membrane Transport Other transporters

slope= -3.30 p_value= 1.5e-05 intercept= 9.87 p_value= 1.5e-24



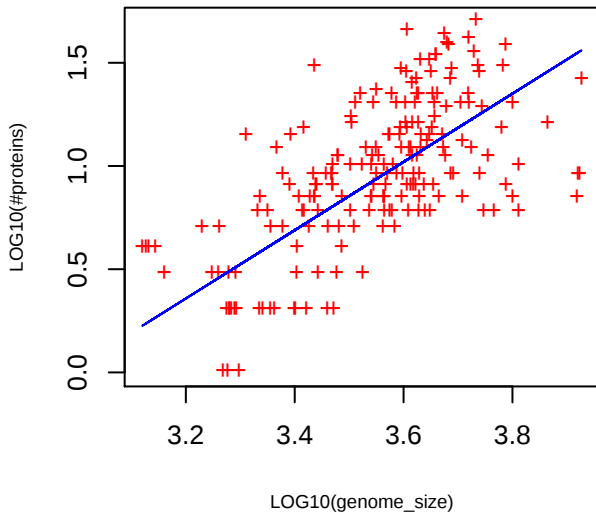
Envi_4 Membrane Transport Other transporters

slope= -0.051 p_value= 0.0016 intercept= 0.28 p_value= 7.2e-35

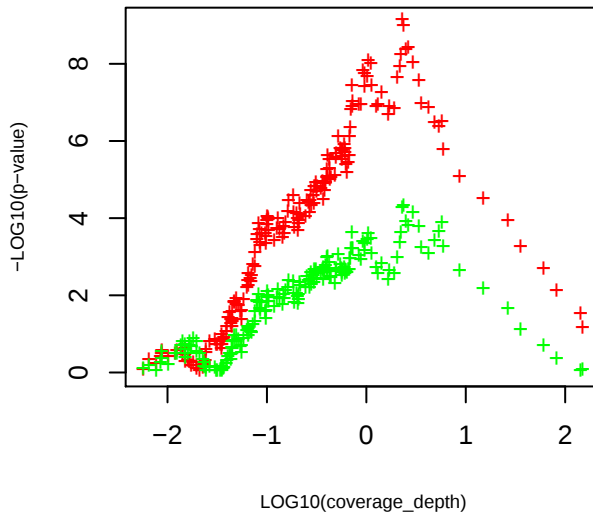


Envi_4 Membrane Transport Other transporters

slope= 1.65 p_value= 3.5e-16 intercept= -4.93 p_value= 2.2e-12

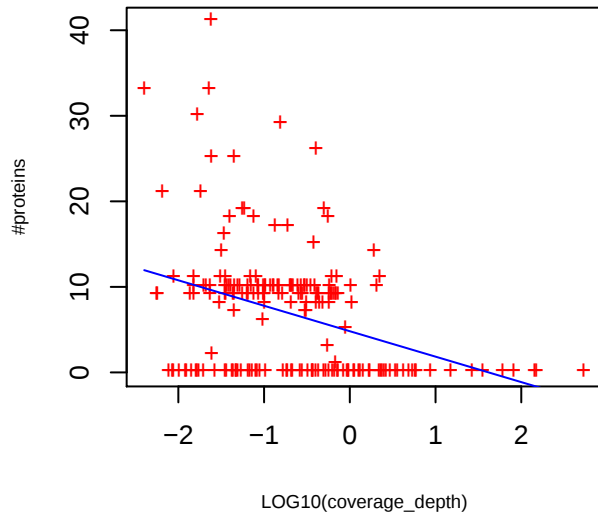


P-value curve ; red (unnorm), green (norm)



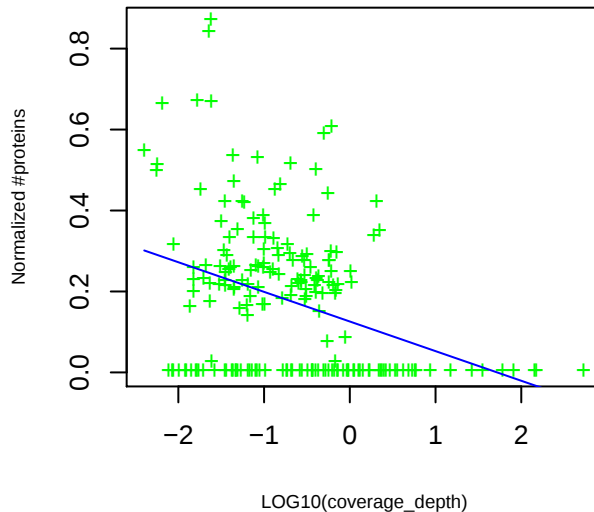
Gene_4 Folding, Sorting and Degradation Type III secretion system [PATH:ko03070]

slope= -2.98 p_value= 2.2e-07 intercept= 4.82 p_value= 6.7e-13



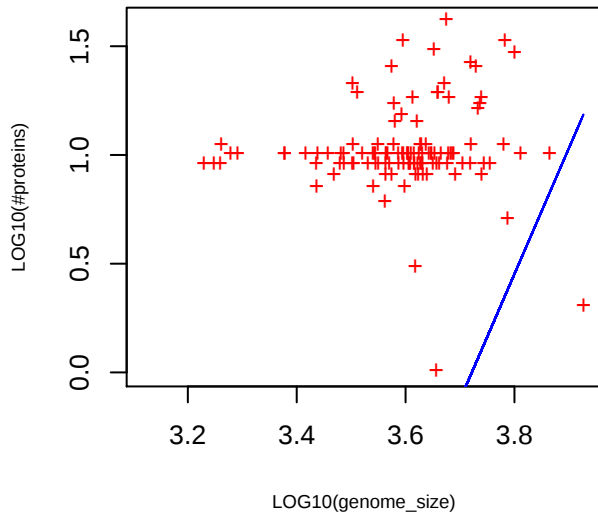
Gene_4 Folding, Sorting and Degradation Type III secretion system [PATH:ko03070]

slope= -0.073 p_value= 3.2e-07 intercept= 0.13 p_value= 7.8e-14

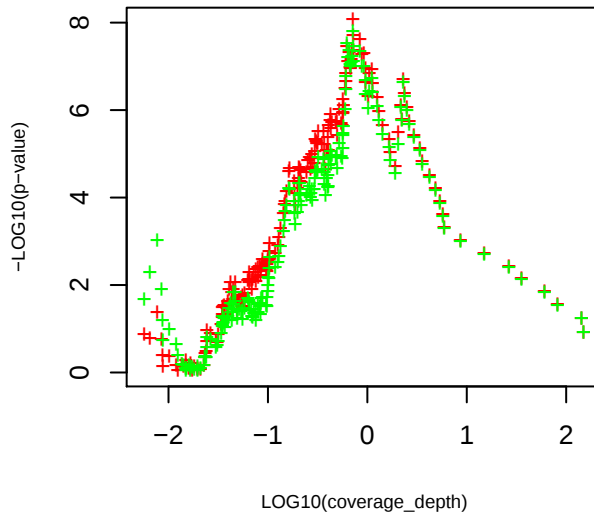


Gene_4 Folding, Sorting and Degradation Type III secretion system [PATH:ko03070]

slope= 5.78 p_value= 3.4e-08 intercept= -21.52 p_value= 8e-09

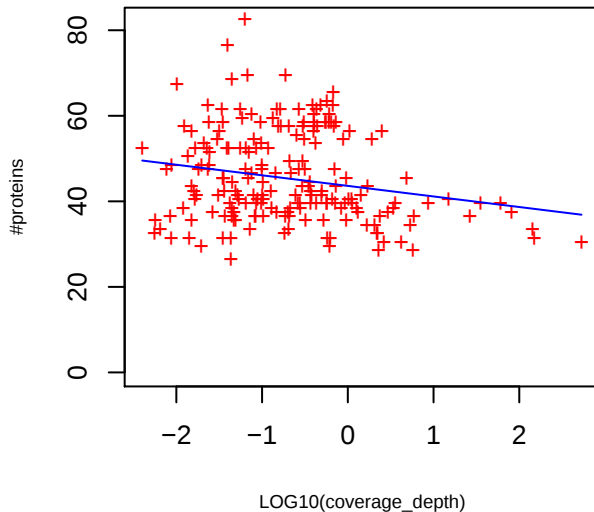


P-value curve ; red (unnorm), green (norm)



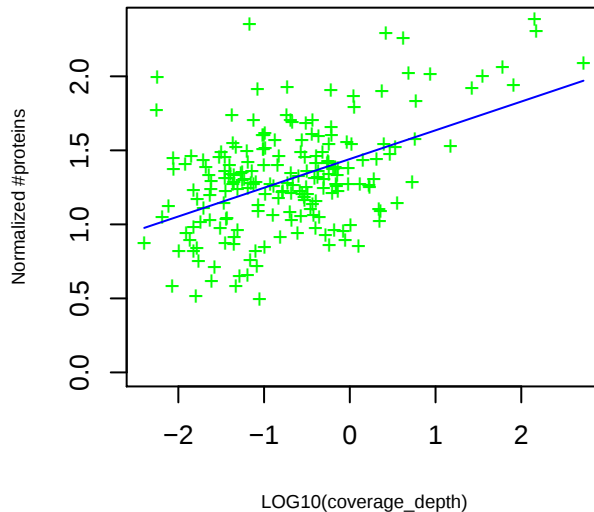
Meta_112 Nucleotide Metabolism Purine metabolism [PATH:ko00230]

slope= -2.47 p_value= 0.0035 intercept= 43.61 p_value= 5.5e-107



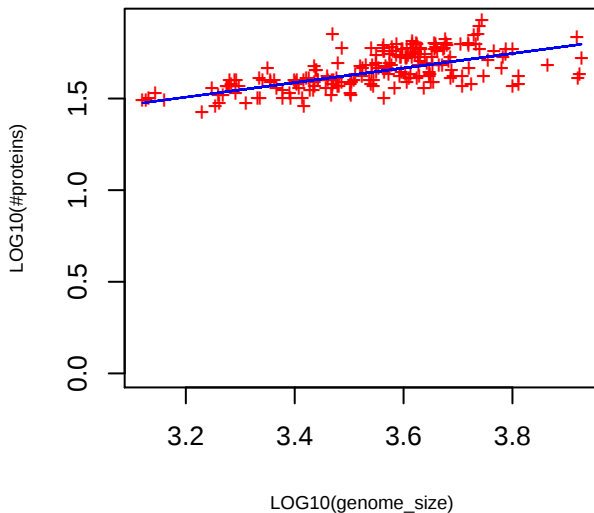
Meta_112 Nucleotide Metabolism Purine metabolism [PATH:ko00230]

slope= 0.19 p_value= 4.1e-13 intercept= 1.44 p_value= 5.5e-115

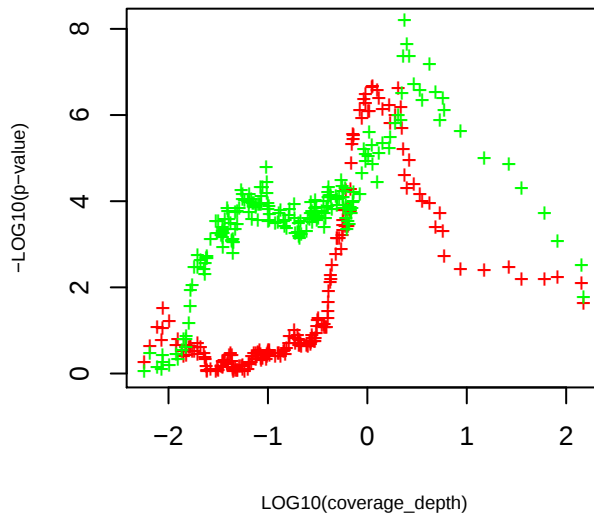


Meta_112 Nucleotide Metabolism Purine metabolism [PATH:ko00230]

slope= 0.40 p_value= 1.9e-24 intercept= 0.24 p_value= 0.05

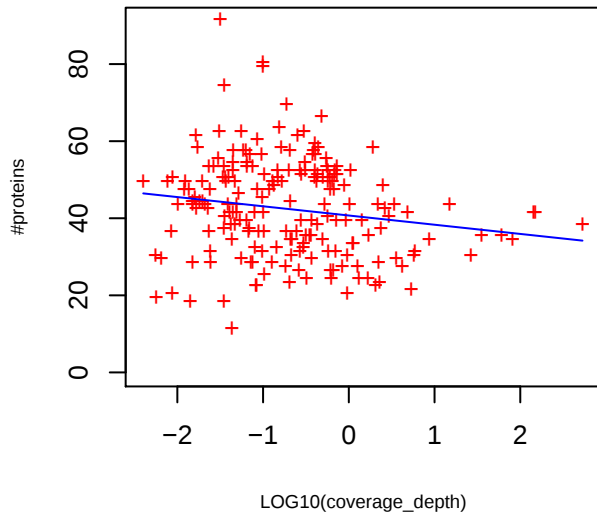


P-value curve ; red (unnorm), green (norm)



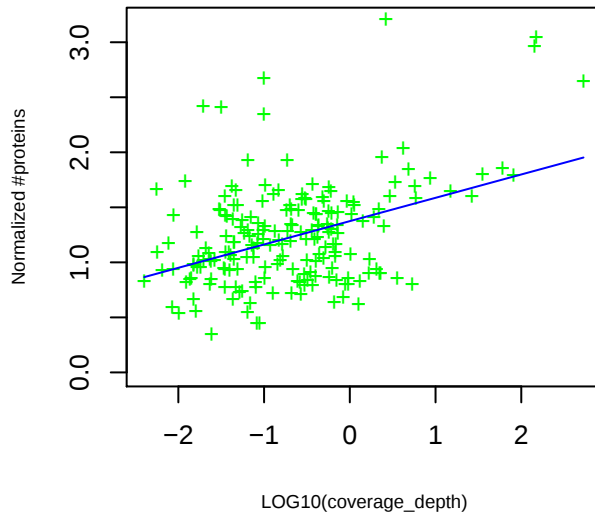
Meta_59 Energy Metabolism Oxidative phosphorylation [PATH:ko00190]

slope= -2.39 p_value= 0.019 intercept= 40.72 p_value= 1.3e-87



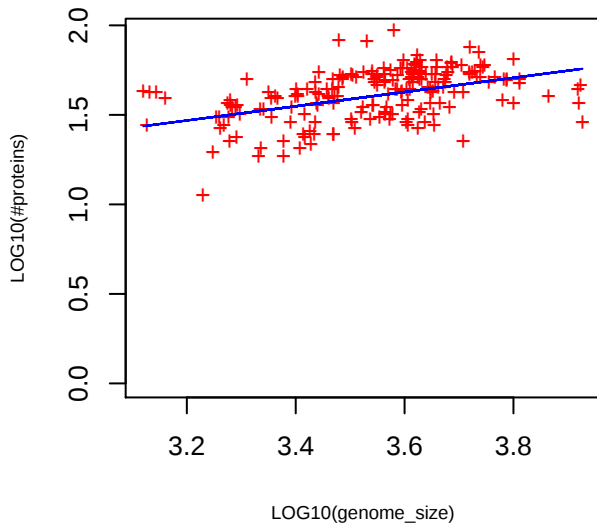
Meta_59 Energy Metabolism Oxidative phosphorylation [PATH:ko00190]

slope= 0.21 p_value= 1.9e-09 intercept= 1.37 p_value= 1.8e-88

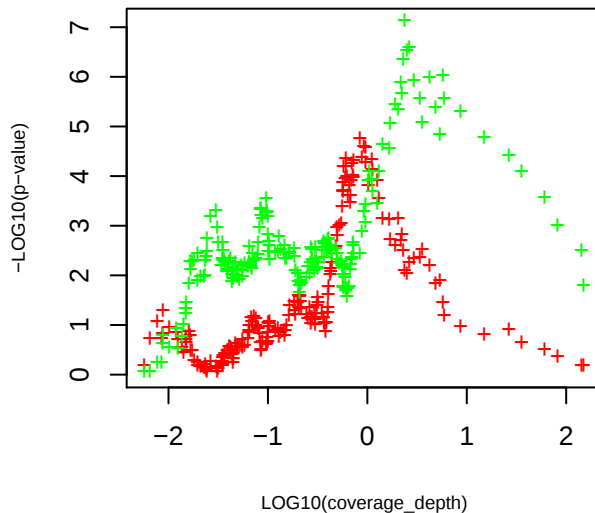


Meta_59 Energy Metabolism Oxidative phosphorylation [PATH:ko00190]

slope= 0.40 p_value= 8.6e-12 intercept= 0.20 p_value= 0.31

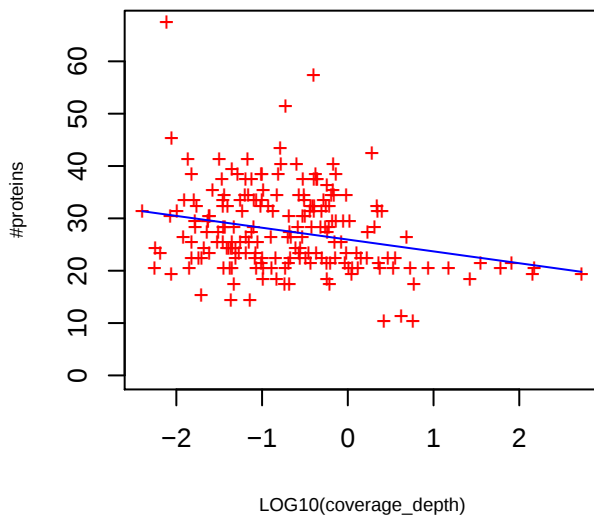


P-value curve ; red (unnorm), green (norm)



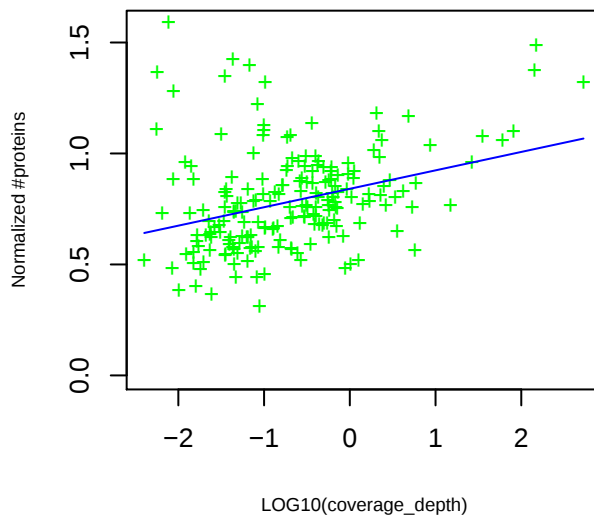
Meta_46 Carbohydrate Metabolism Glycolysis / Gluconeogenesis [PATH:ko00010]

slope= -2.26 p_value= 0.00033 intercept= 25.95 p_value= 2.1e-90



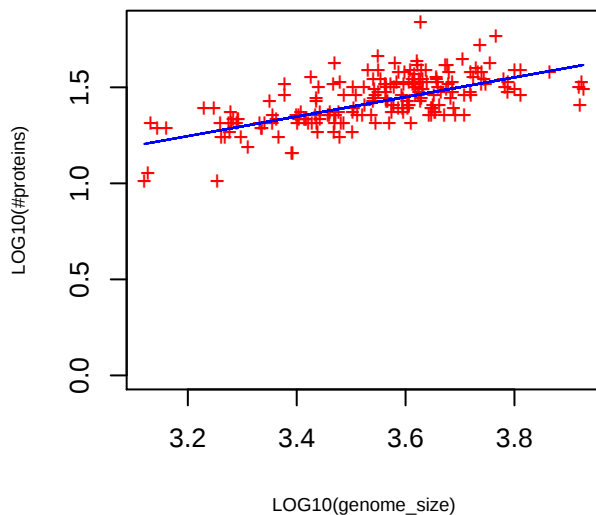
Meta_46 Carbohydrate Metabolism Glycolysis / Gluconeogenesis [PATH:ko00010]

slope= 0.083 p_value= 2.3e-06 intercept= 0.84 p_value= 1.5e-102

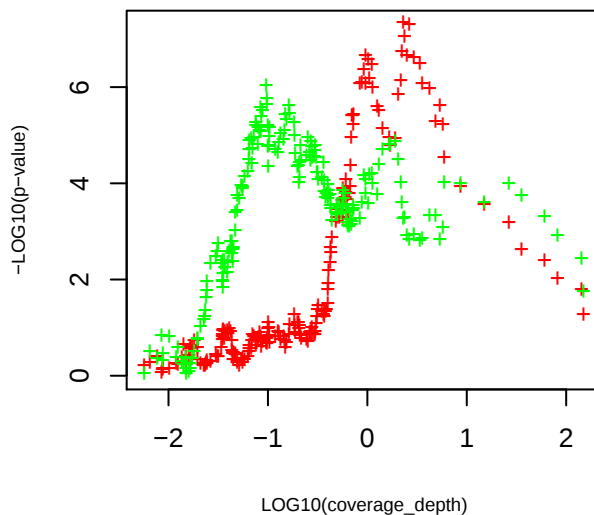


Meta_46 Carbohydrate Metabolism Glycolysis / Gluconeogenesis [PATH:ko00010]

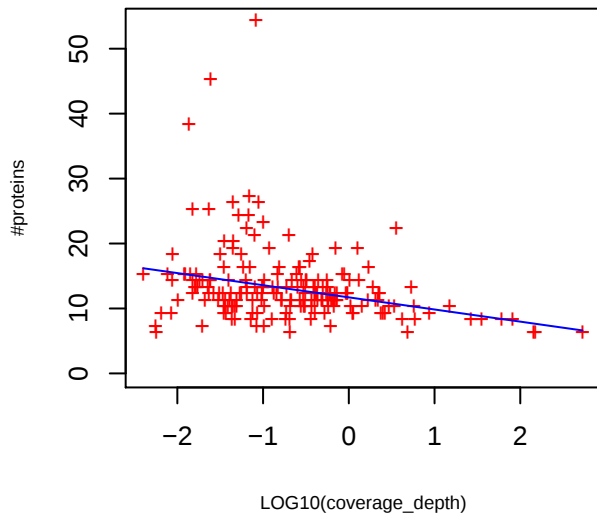
slope= 0.51 p_value= 2.9e-26 intercept= -0.38 p_value= 0.0093



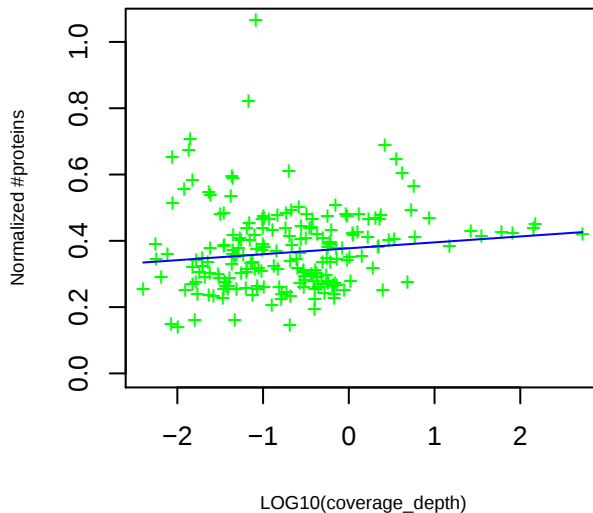
P-value curve ; red (unnorm), green (norm)



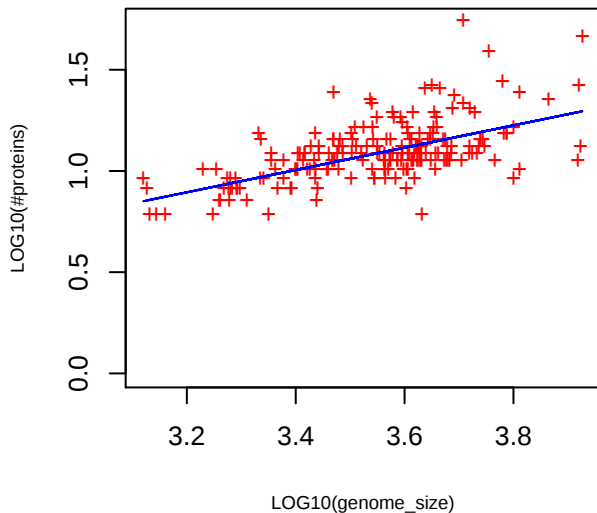
Gene_16 Transcription RNA polymerase [PATH:ko03020]
slope= -1.87 p_value= 4.3e-05 intercept= 11.71 p_value= 4.4e-58



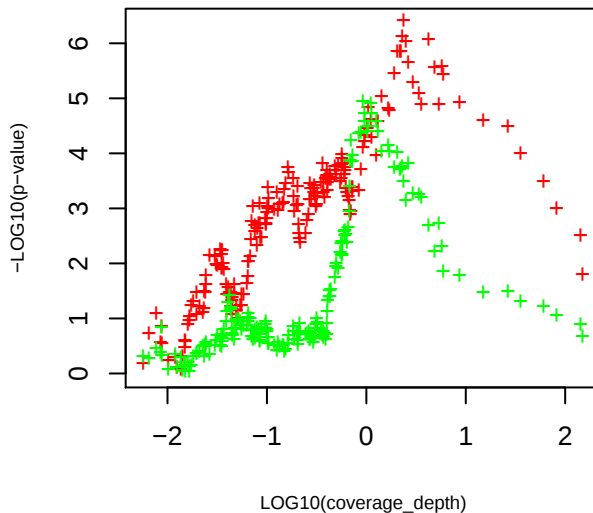
Gene_16 Transcription RNA polymerase [PATH:ko03020]
slope= 0.018 p_value= 0.07 intercept= 0.38 p_value= 6.2e-84



Gene_16 Transcription RNA polymerase [PATH:ko03020]
slope= 0.55 p_value= 1.5e-20 intercept= -0.87 p_value= 6.5e-06

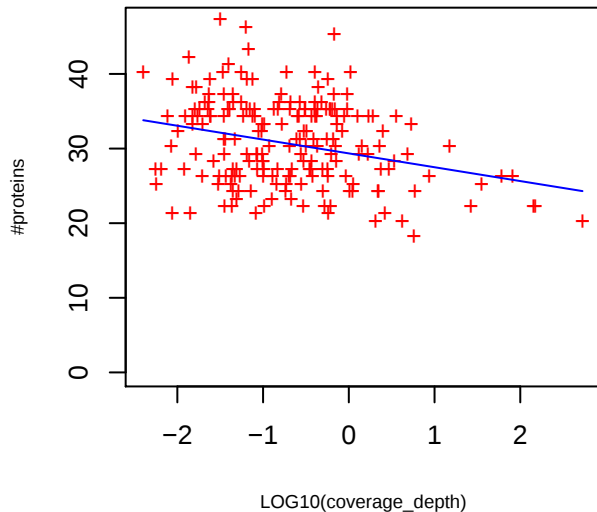


P-value curve ; red (unnorm), green (norm)



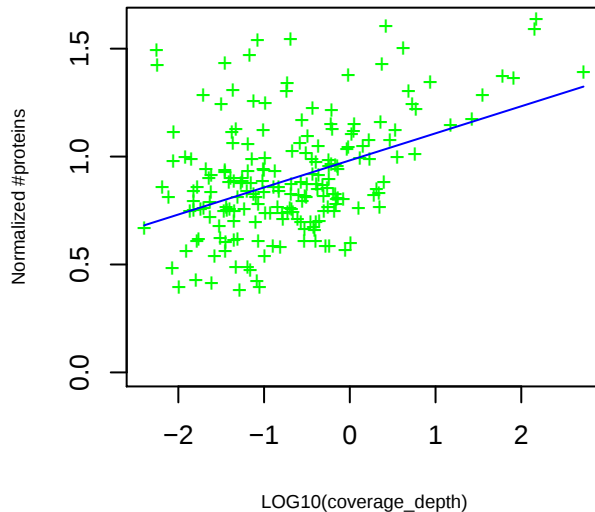
Meta_113 Nucleotide Metabolism Pyrimidine metabolism [PATH:ko00240]

slope= -1.85 p_value= 3.9e-05 intercept= 29.35 p_value= 2.4e-126



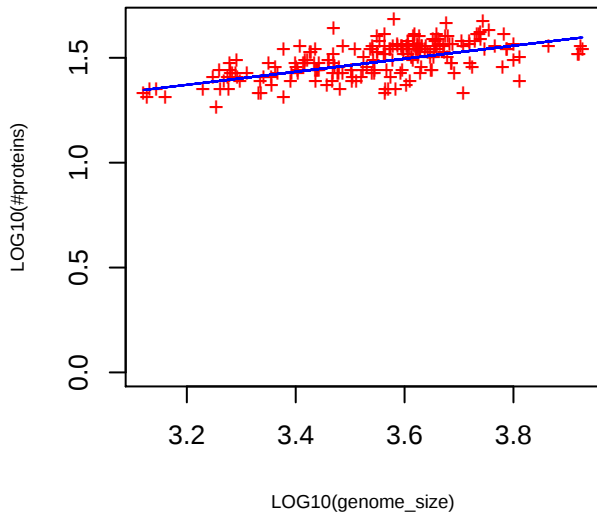
Meta_113 Nucleotide Metabolism Pyrimidine metabolism [PATH:ko00240]

slope= 0.13 p_value= 4.5e-10 intercept= 0.98 p_value= 6.7e-106

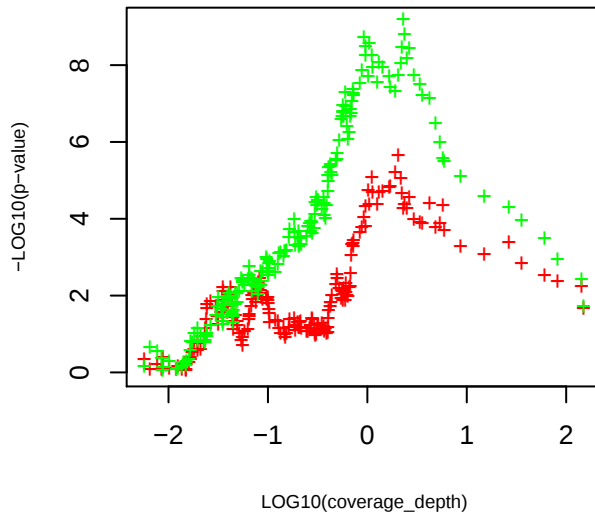


Meta_113 Nucleotide Metabolism Pyrimidine metabolism [PATH:ko00240]

slope= 0.31 p_value= 1.9e-21 intercept= 0.38 p_value= 0.00030

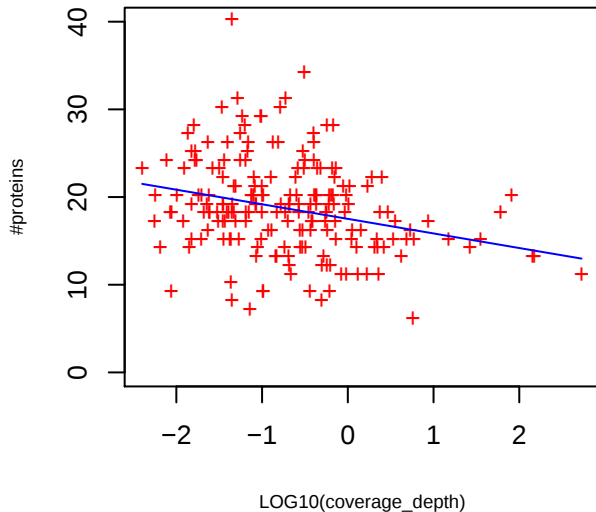


P-value curve ; red (unnorm), green (norm)



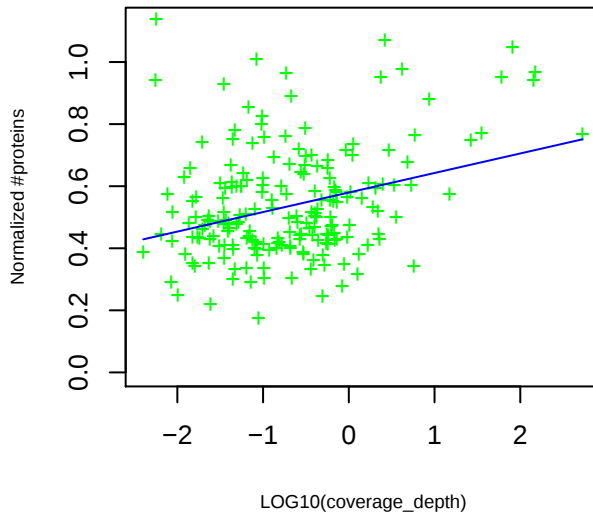
Meta_51 Carbohydrate Metabolism Pentose phosphate pathway [PATH:ko00030]

slope= -1.66 p_value= 8.4e-05 intercept= 17.51 p_value= 5.3e-91



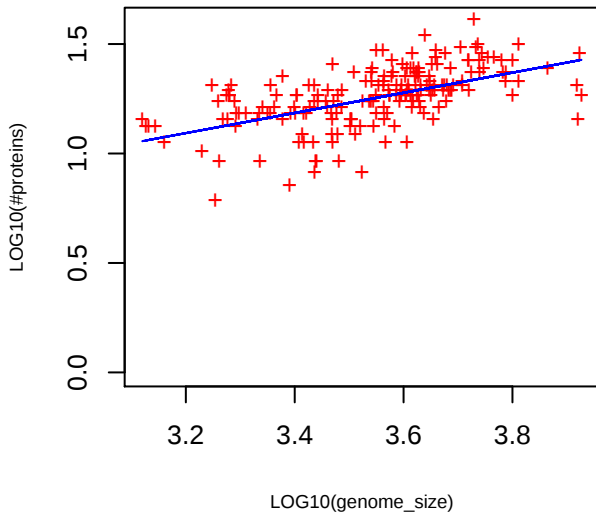
Meta_51 Carbohydrate Metabolism Pentose phosphate pathway [PATH:ko00030]

slope= 0.063 p_value= 5.3e-06 intercept= 0.58 p_value= 1.7e-92

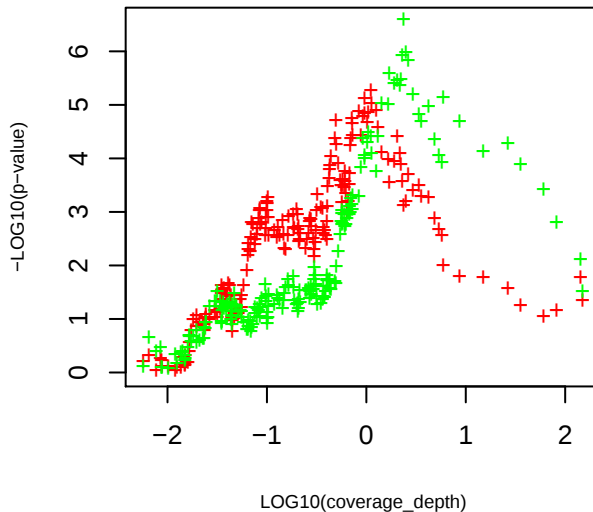


Meta_51 Carbohydrate Metabolism Pentose phosphate pathway [PATH:ko00030]

slope= 0.46 p_value= 3e-18 intercept= -0.38 p_value= 0.026

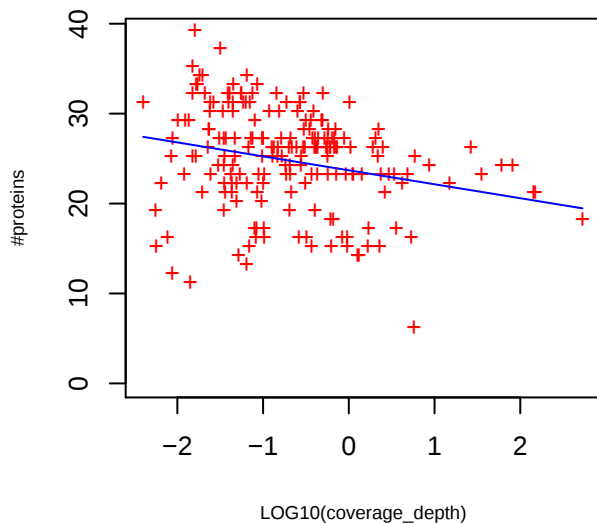


P-value curve ; red (unnorm), green (norm)



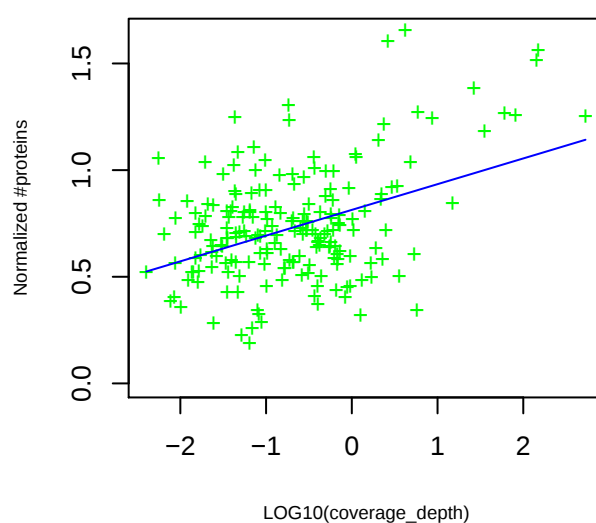
Cell_6 Cell Growth and Death Cell division

slope= -1.55 p_value= 0.00032 intercept= 23.70 p_value= 2.2e-112



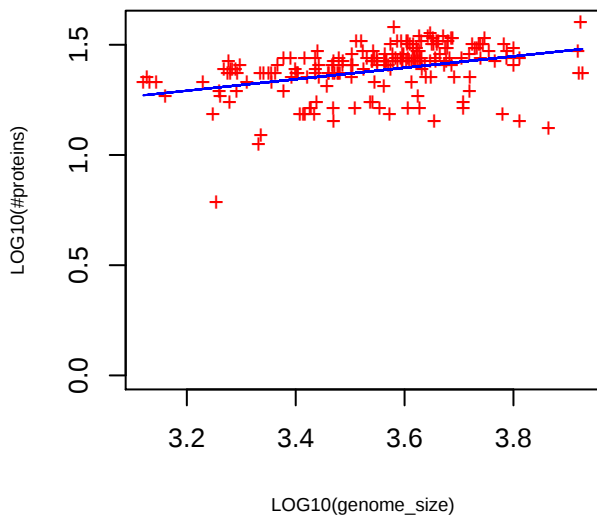
Cell_6 Cell Growth and Death Cell division

slope= 0.12 p_value= 9.7e-10 intercept= 0.81 p_value= 7.4e-93

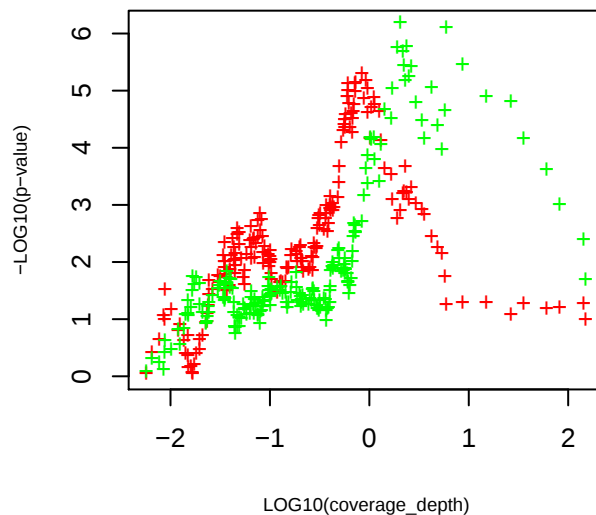


Cell_6 Cell Growth and Death Cell division

slope= 0.26 p_value= 2.7e-08 intercept= 0.46 p_value= 0.0044

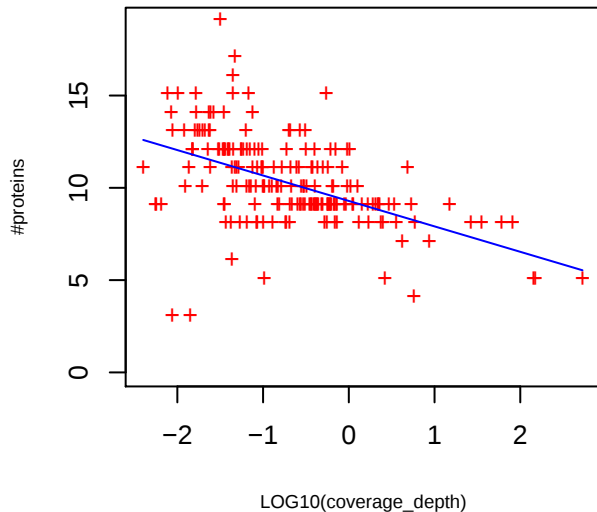


P-value curve ; red (unnorm), green (norm)



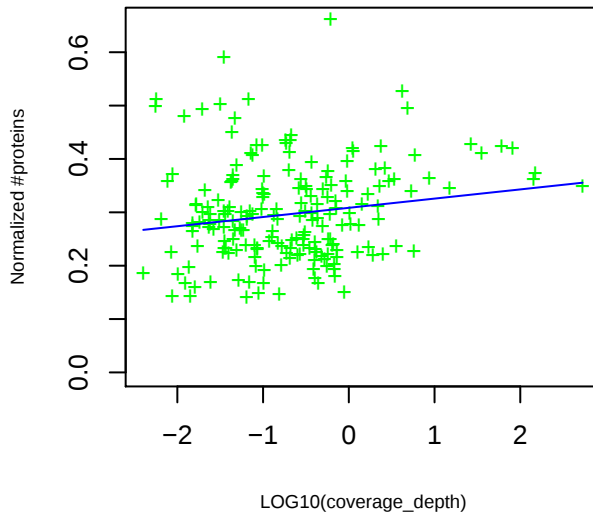
Gene_10 Replication and Repair Mismatch repair [PATH:ko03430]

slope= -1.38 p_value= 1.1e-14 intercept= 9.29 p_value= 4.2e-113



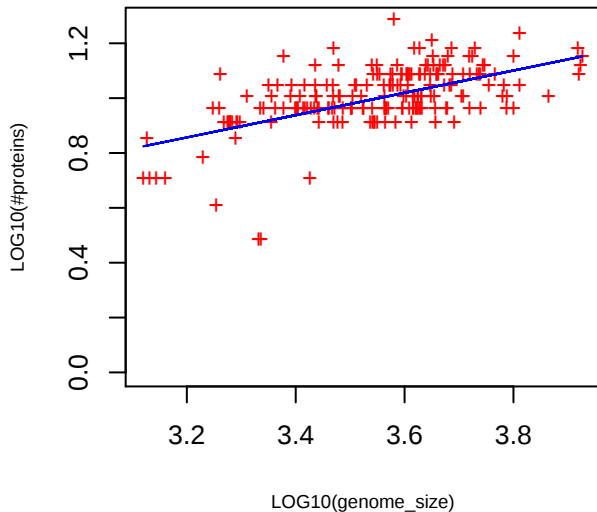
Gene_10 Replication and Repair Mismatch repair [PATH:ko03430]

slope= 0.017 p_value= 0.018 intercept= 0.31 p_value= 1.3e-91

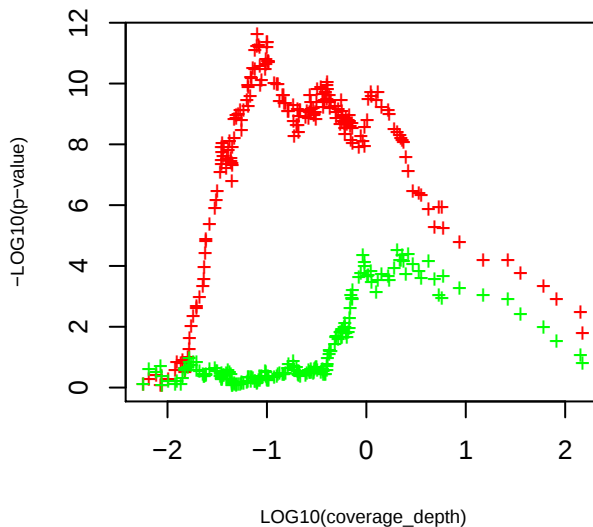


Gene_10 Replication and Repair Mismatch repair [PATH:ko03430]

slope= 0.41 p_value= 1.5e-19 intercept= -0.44 p_value= 0.0022

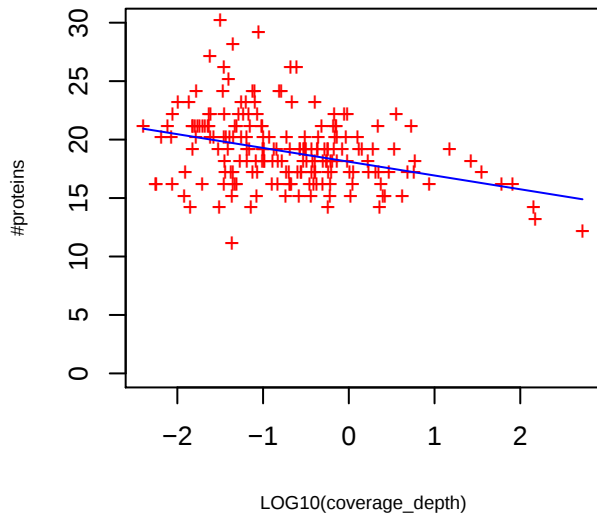


P-value curve ; red (unnorm), green (norm)



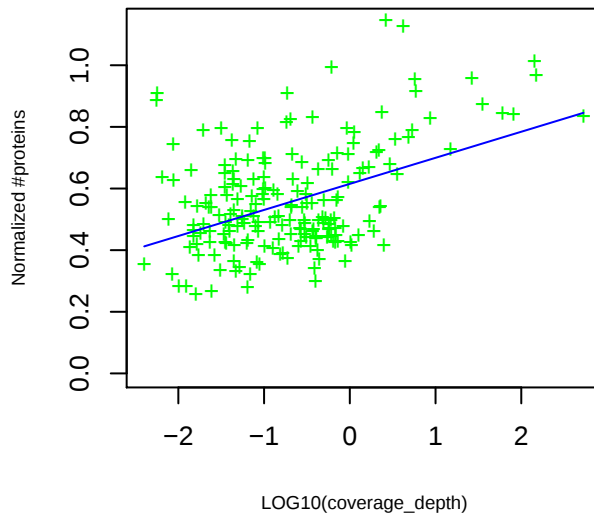
Meta_1 Amino Acid Metabolism Alanine and aspartate metabolism [PATH:ko00252]

slope= -1.18 p_value= 7e-07 intercept= 18.11 p_value= 7e-140



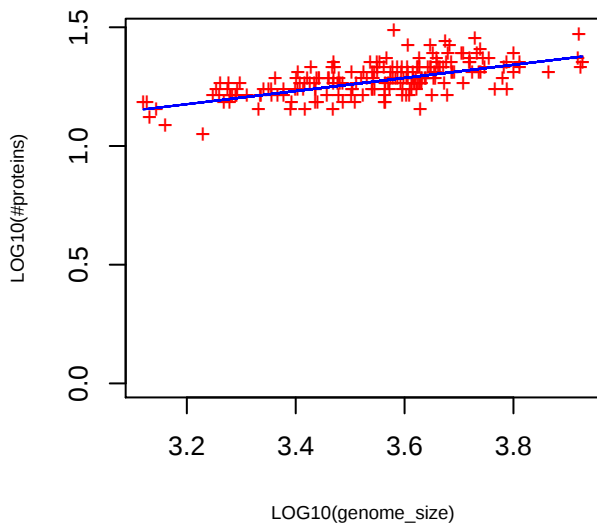
Meta_1 Amino Acid Metabolism Alanine and aspartate metabolism [PATH:ko00252]

slope= 0.085 p_value= 7e-11 intercept= 0.62 p_value= 5.6e-104

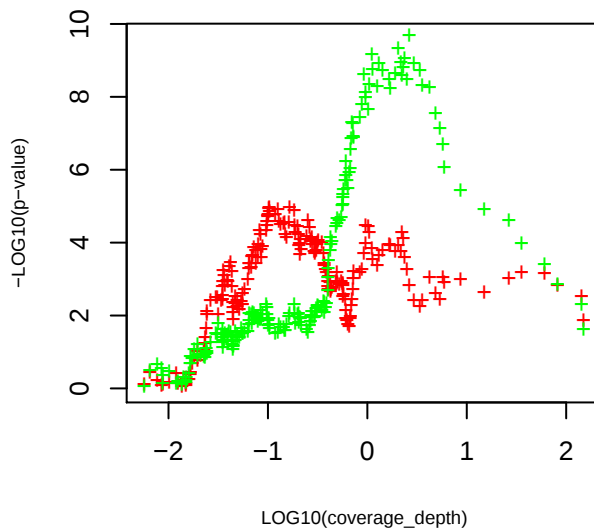


Meta_1 Amino Acid Metabolism Alanine and aspartate metabolism [PATH:ko00252]

slope= 0.28 p_value= 3.6e-25 intercept= 0.29 p_value= 0.00047

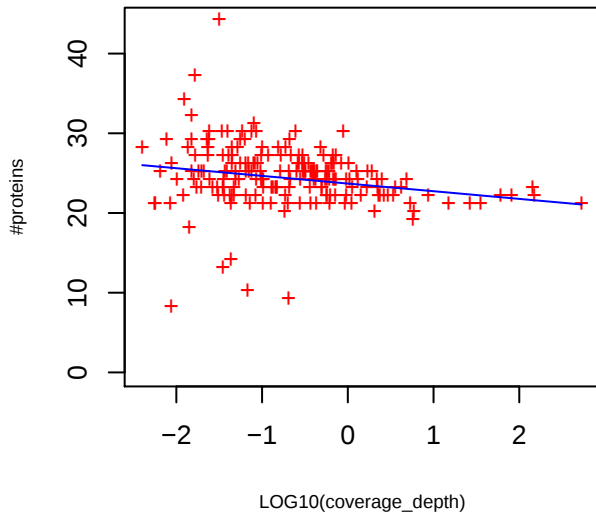


P-value curve ; red (unnorm), green (norm)



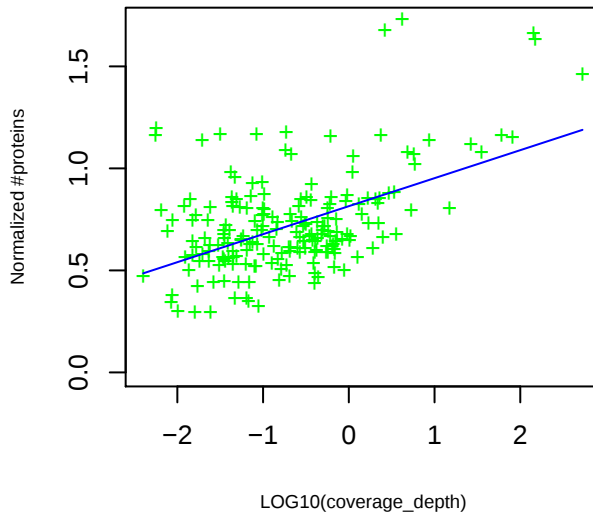
Meta_11 Amino Acid Metabolism Phenylalanine, tyrosine and tryptophan biosynthesis [PATH:ko004

slope= -0.96 p_value= 0.0016 intercept= 23.69 p_value= 3.9e-140



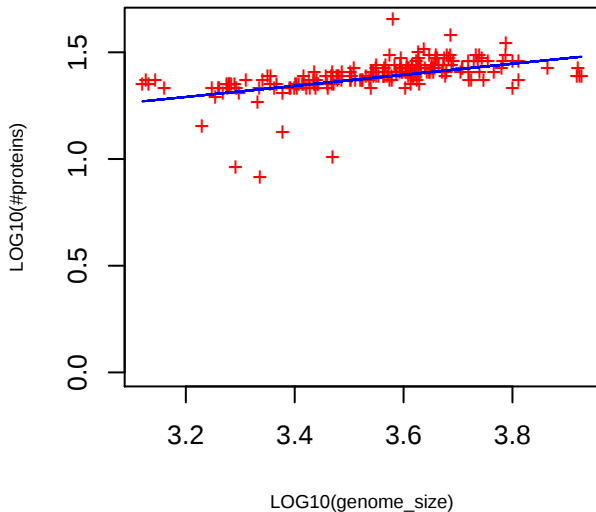
Meta_11 Amino Acid Metabolism Phenylalanine, tyrosine and tryptophan biosynthesis [PATH:ko004

slope= 0.14 p_value= 3.7e-14 intercept= 0.81 p_value= 2.2e-101

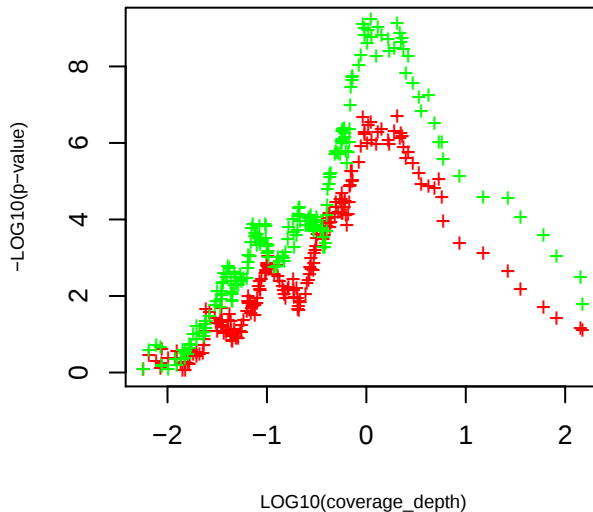


Meta_11 Amino Acid Metabolism Phenylalanine, tyrosine and tryptophan biosynthesis [PATH:ko004

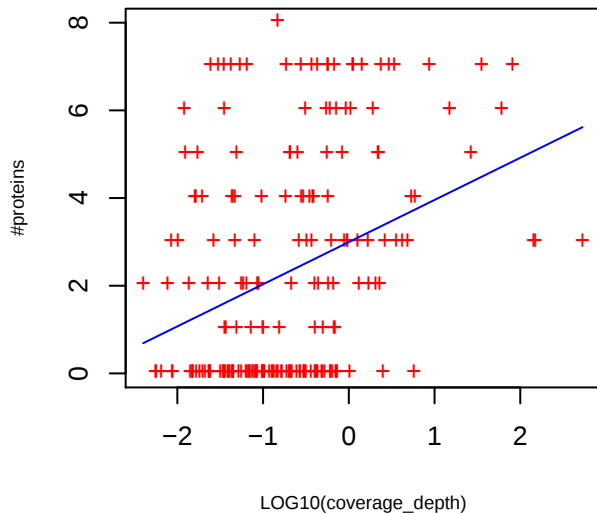
slope= 0.26 p_value= 4.2e-16 intercept= 0.46 p_value= 1.5e-05



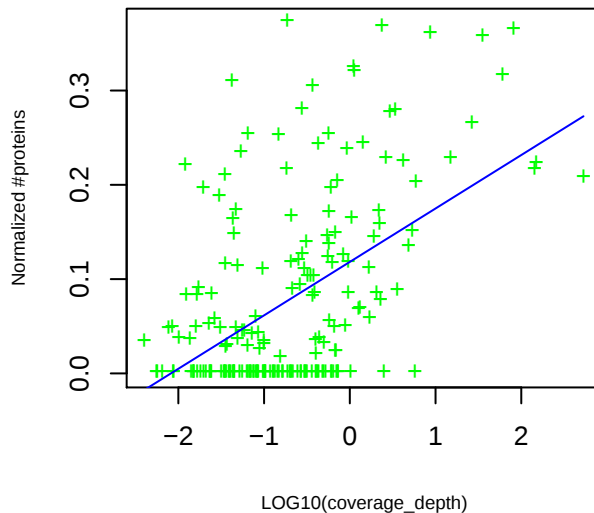
P-value curve : red (unnorm), green (norm)



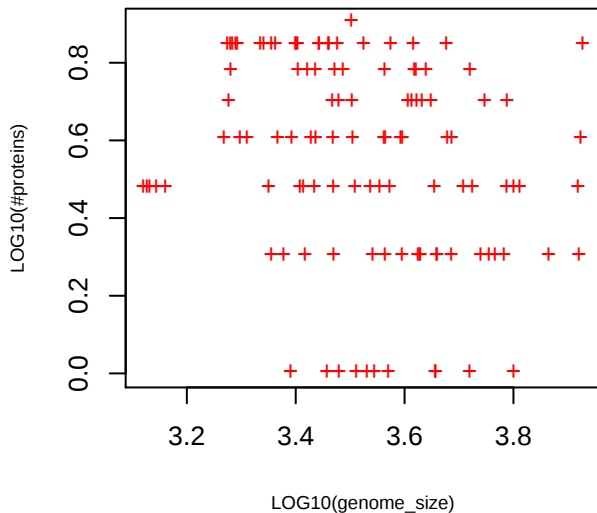
slope= 0.96 p_value= 1.3e-06 intercept= 3.00 p_value= 1.2e-30



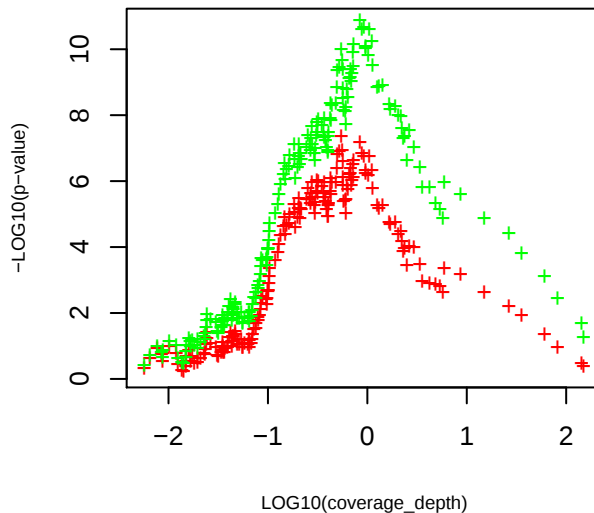
slope= 0.057 p_value= 3.4e-14 intercept= 0.12 p_value= 9.8e-35



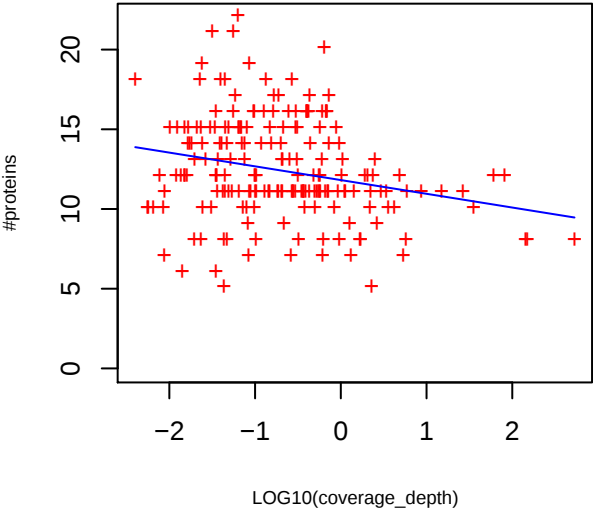
slope= -2.12 p_value= 0.032 intercept= 6.10 p_value= 0.082



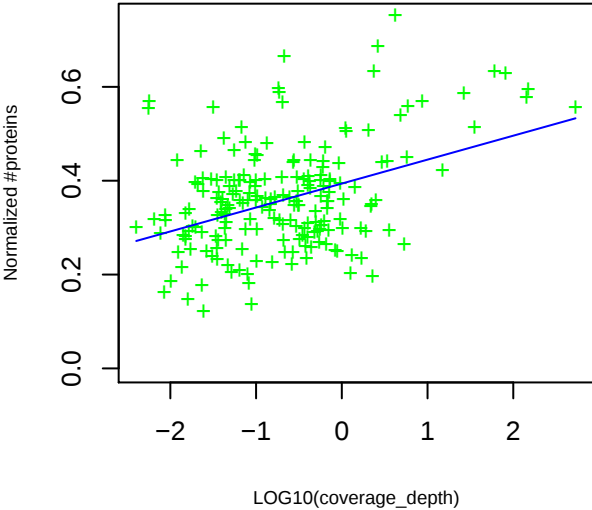
P-value curve ; red (unnorm), green (norm)



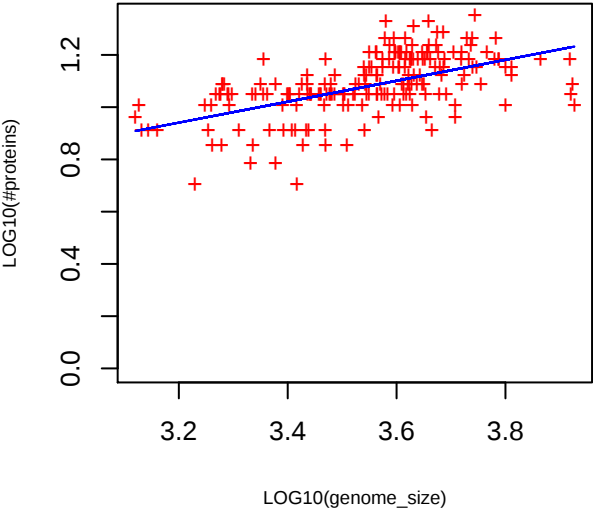
slope= -0.86 p_value= 0.00055 intercept= 11.81 p_value= 8e-101



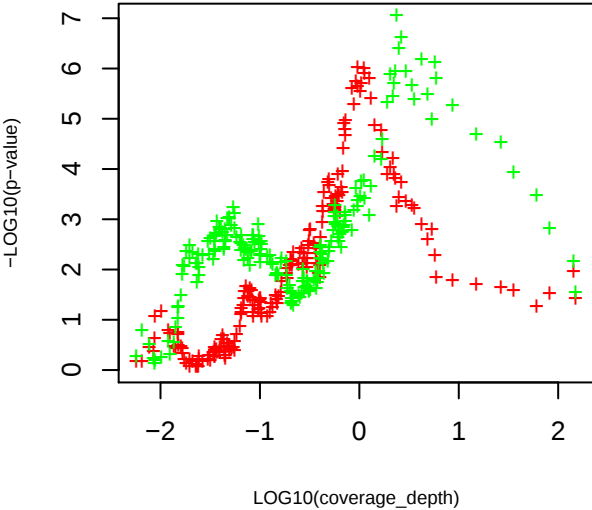
slope= 0.051 p_value= 2.1e-09 intercept= 0.39 p_value= 2.1e-101



slope= 0.40 p_value= 5.6e-18 intercept= -0.34 p_value= 0.023

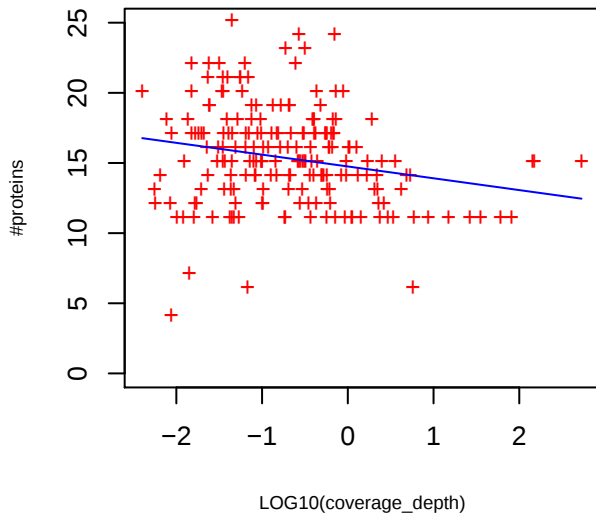


P-value curve ; red (unnorm), green (norm)



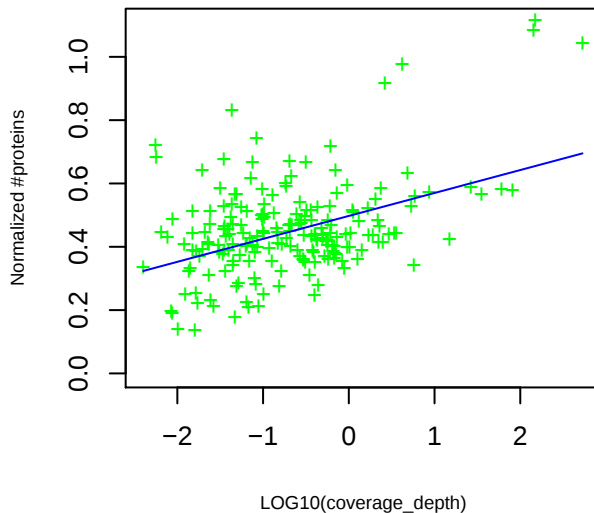
Meta_7 Amino Acid Metabolism Lysine biosynthesis [PATH:ko00300]

slope= -0.84 p_value= 0.0023 intercept= 14.75 p_value= 6.4e-110



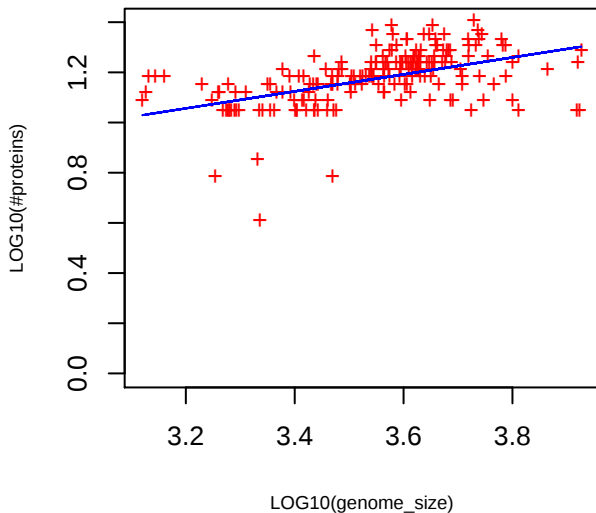
Meta_7 Amino Acid Metabolism Lysine biosynthesis [PATH:ko00300]

slope= 0.072 p_value= 1.3e-10 intercept= 0.50 p_value= 2.3e-98

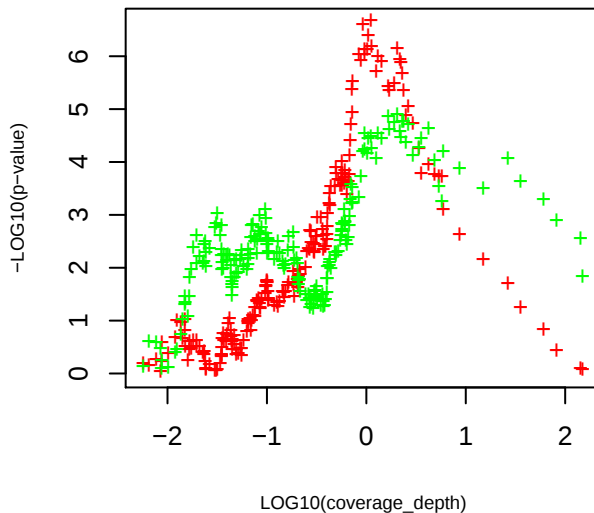


Meta_7 Amino Acid Metabolism Lysine biosynthesis [PATH:ko00300]

slope= 0.34 p_value= 1.9e-14 intercept= -0.026 p_value= 0.86

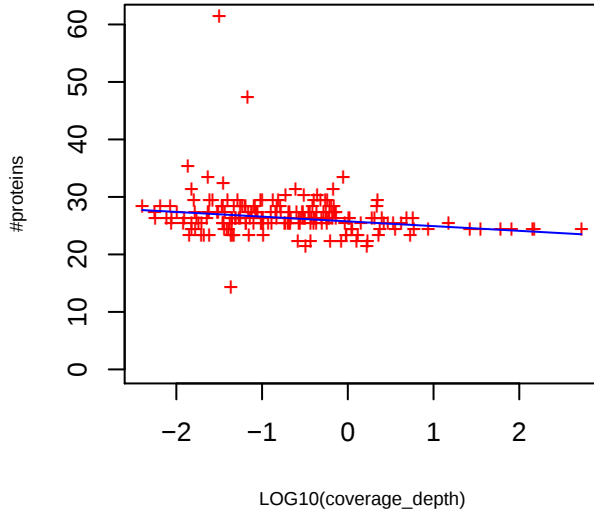


P-value curve ; red (unnorm), green (norm)



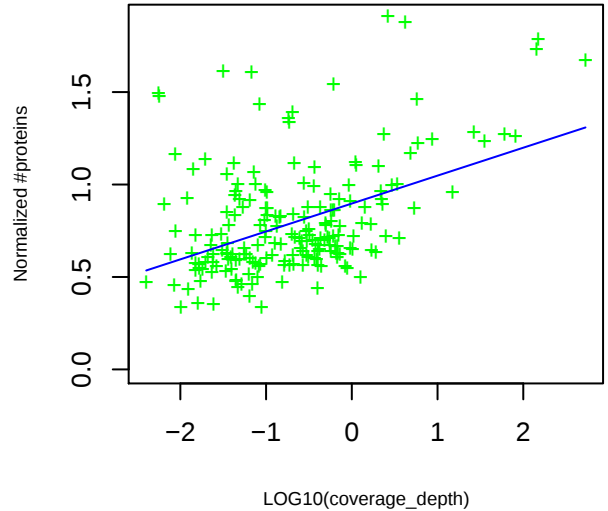
Gene_17 Translation Aminoacyl-tRNA biosynthesis [PATH:ko00970]

slope= -0.82 p_value= 0.0057 intercept= 25.75 p_value= 1.5e-148



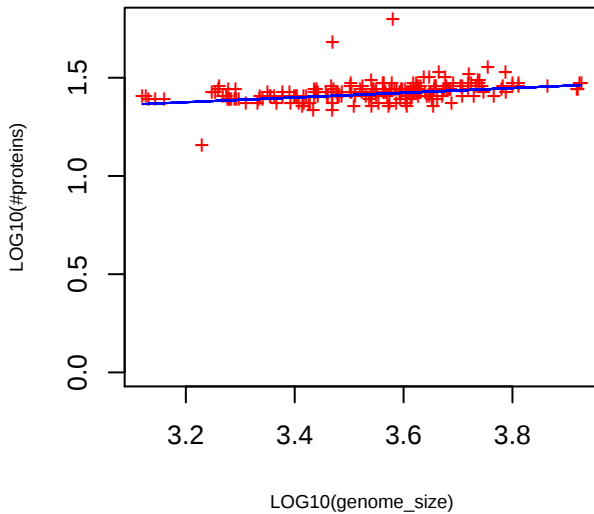
Gene_17 Translation Aminoacyl-tRNA biosynthesis [PATH:ko00970]

slope= 0.15 p_value= 6.9e-11 intercept= 0.90 p_value= 9.1e-89

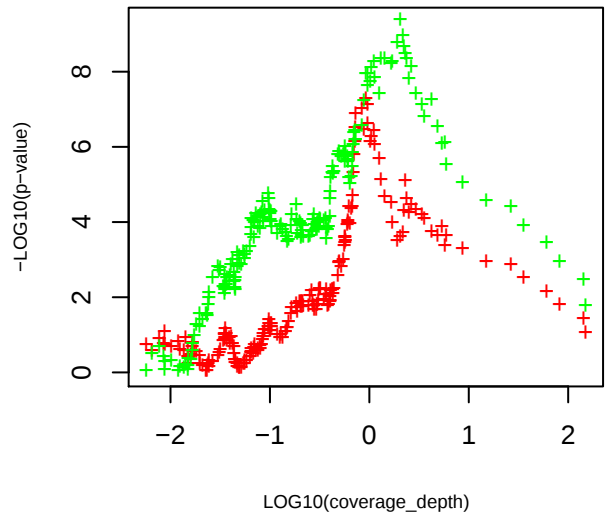


Gene_17 Translation Aminoacyl-tRNA biosynthesis [PATH:ko00970]

slope= 0.12 p_value= 5.5e-08 intercept= 0.99 p_value= 8.4e-29

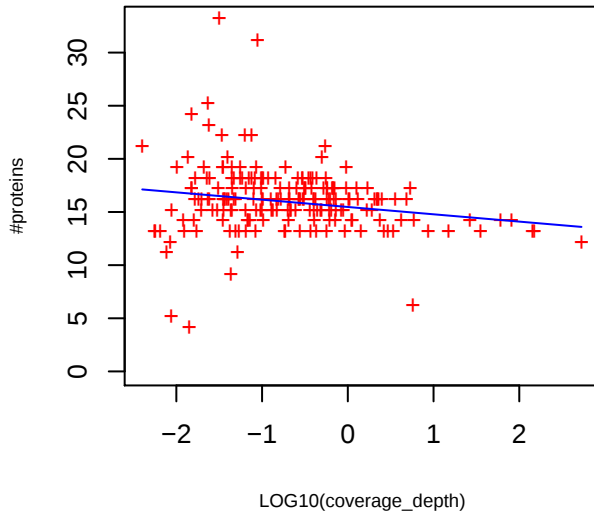


P-value curve ; red (unnorm), green (norm)



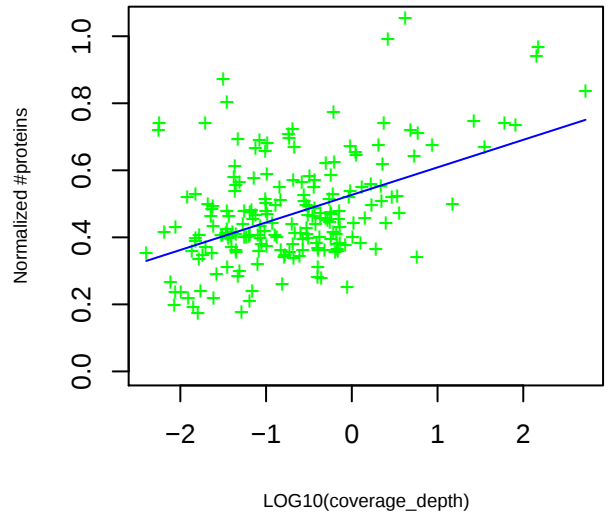
Gene_8 Replication and Repair DNA replication [PATH:ko03030]

slope= -0.69 p_value= 0.006 intercept= 15.47 p_value= 3.3e-121



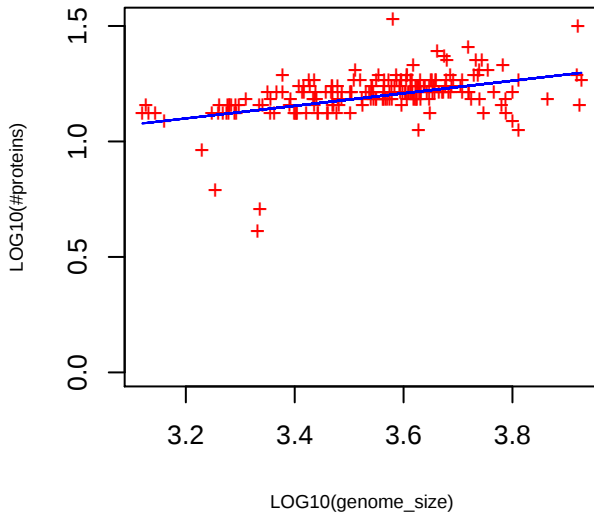
Gene_8 Replication and Repair DNA replication [PATH:ko03030]

slope= 0.082 p_value= 3.6e-12 intercept= 0.53 p_value= 8.4e-100

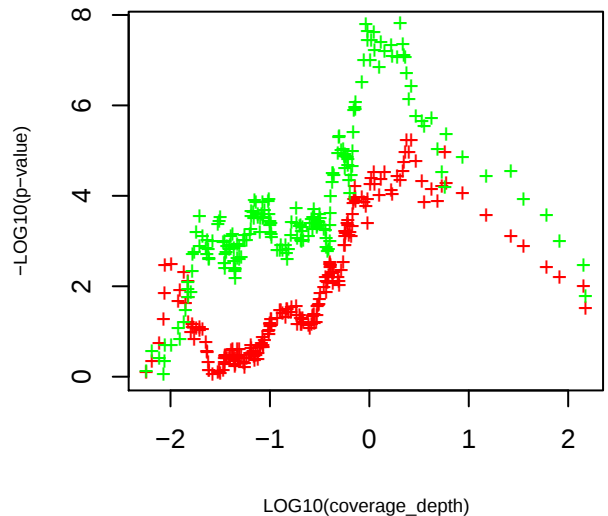


Gene_8 Replication and Repair DNA replication [PATH:ko03030]

slope= 0.27 p_value= 3.0e-12 intercept= 0.23 p_value= 0.077

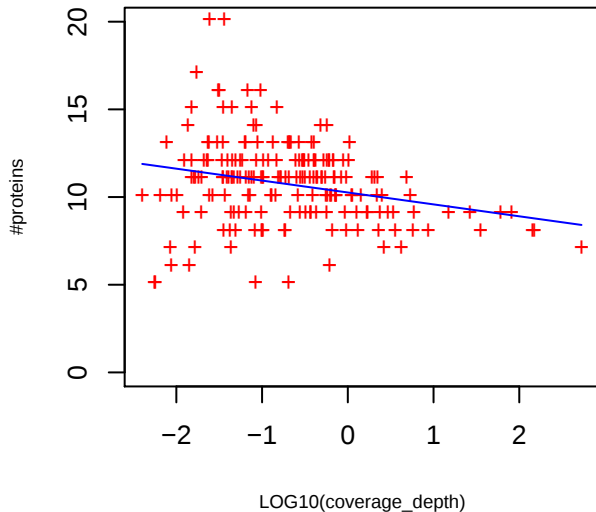


P-value curve ; red (unnorm), green (norm)



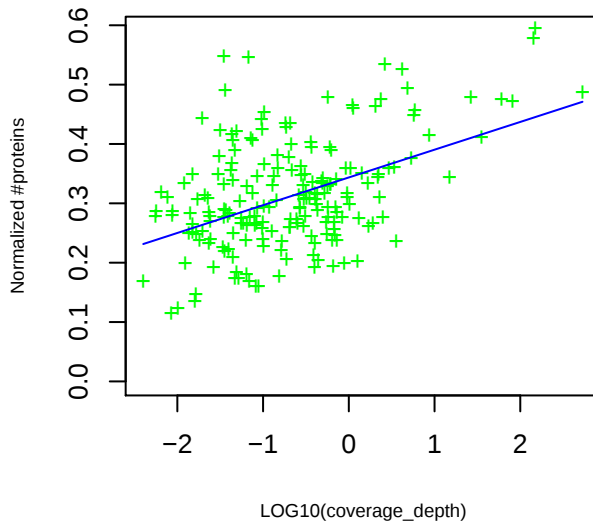
Gene_7 Replication and Repair Base excision repair [PATH:ko03410]

slope= -0.68 p_value= 0.00033 intercept= 10.26 p_value= 1.9e-111



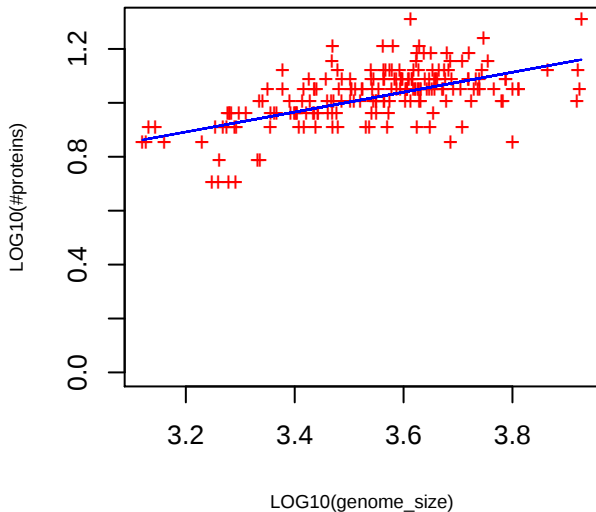
Gene_7 Replication and Repair Base excision repair [PATH:ko03410]

slope= 0.047 p_value= 1.2e-11 intercept= 0.34 p_value= 3.3e-108

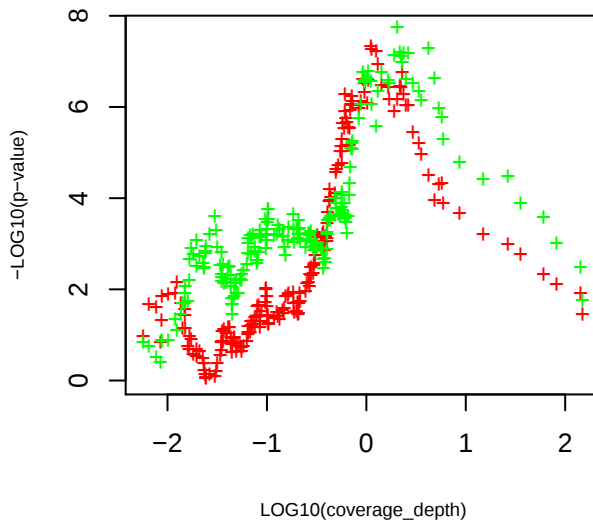


Gene_7 Replication and Repair Base excision repair [PATH:ko03410]

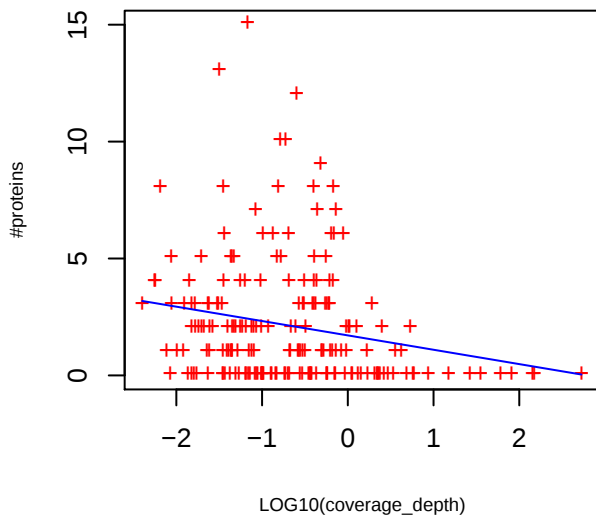
slope= 0.37 p_value= 1.4e-20 intercept= -0.29 p_value= 0.022



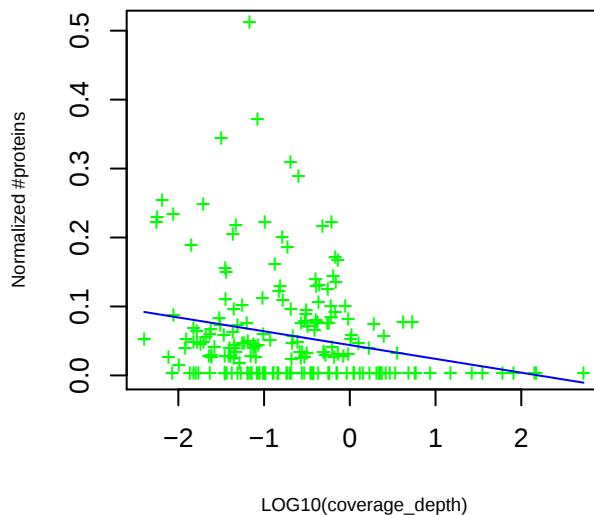
P-value curve ; red (unnorm), green (norm)



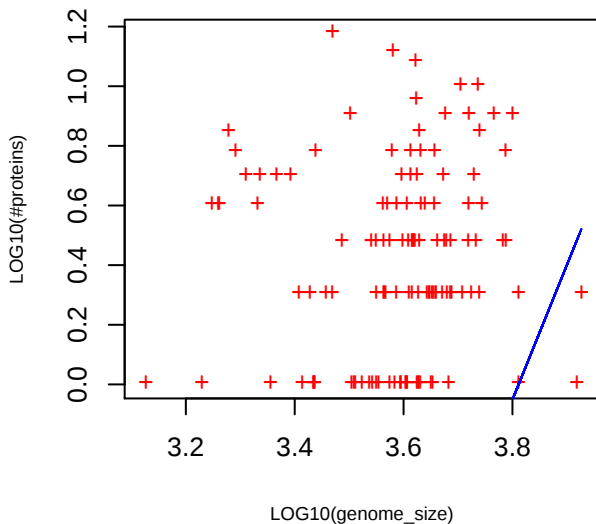
slope= -0.61 p_value= 0.0038 intercept= 1.71 p_value= 1.1e-11



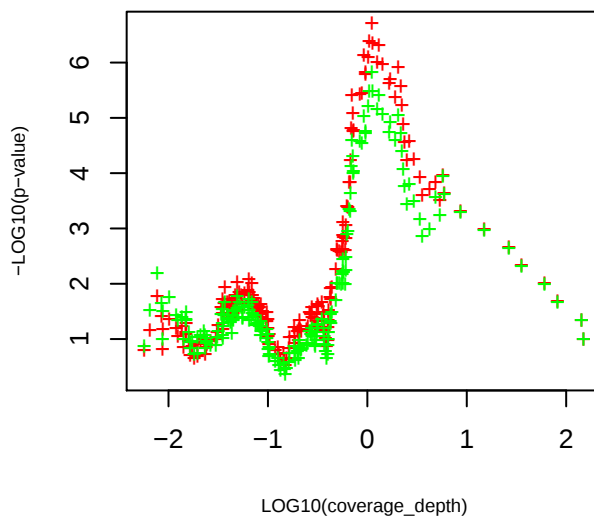
slope= -0.02 p_value= 0.0013 intercept= 0.044 p_value= 1.5e-09



slope= 4.51 p_value= 7.9e-07 intercept= -17.21 p_value= 1.3e-07

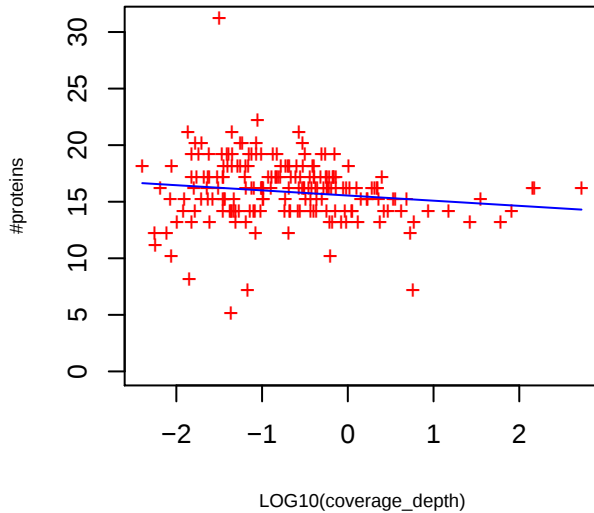


P-value curve ; red (unnorm), green (norm)



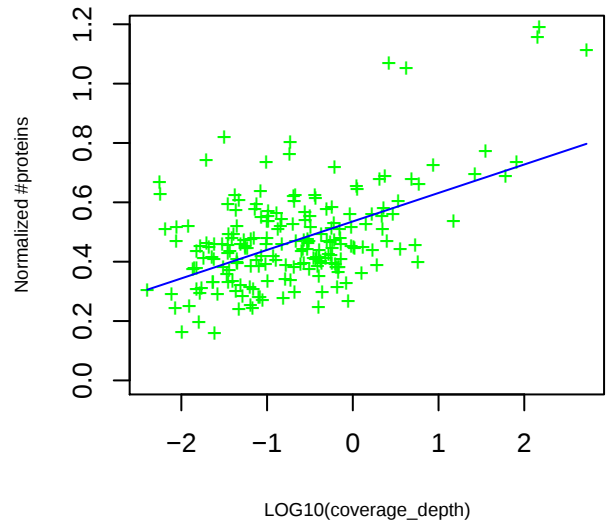
Gene_2 Folding, Sorting and Degradation Protein export [PATH:ko03060]

slope= -0.46 p_value= 0.038 intercept= 15.55 p_value= 8.7e-132



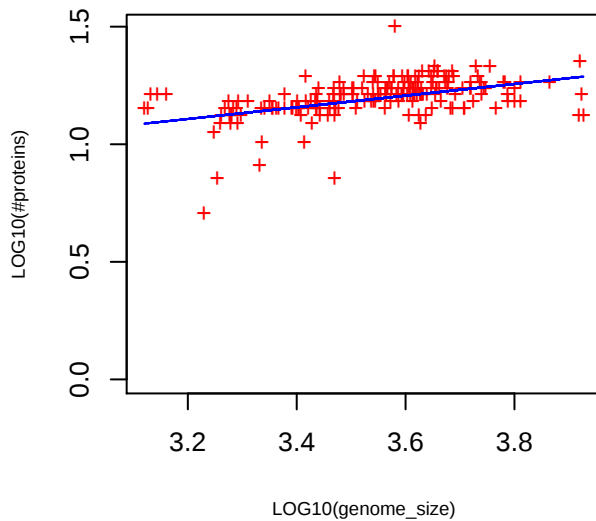
Gene_2 Folding, Sorting and Degradation Protein export [PATH:ko03060]

slope= 0.096 p_value= 2.6e-15 intercept= 0.54 p_value= 1.5e-100

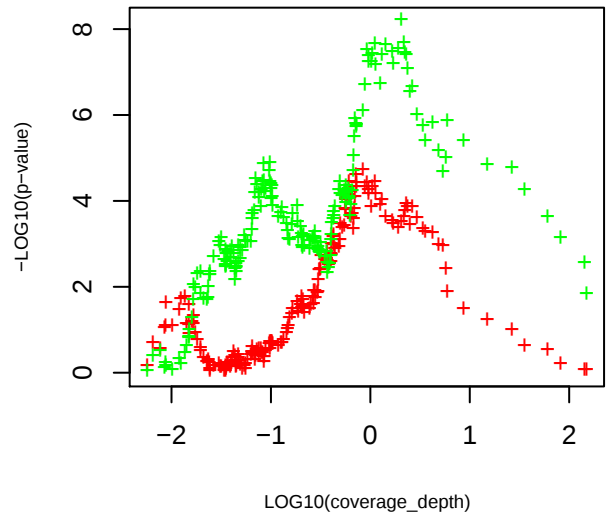


Gene_2 Folding, Sorting and Degradation Protein export [PATH:ko03060]

slope= 0.25 p_value= 5.9e-13 intercept= 0.31 p_value= 0.0066

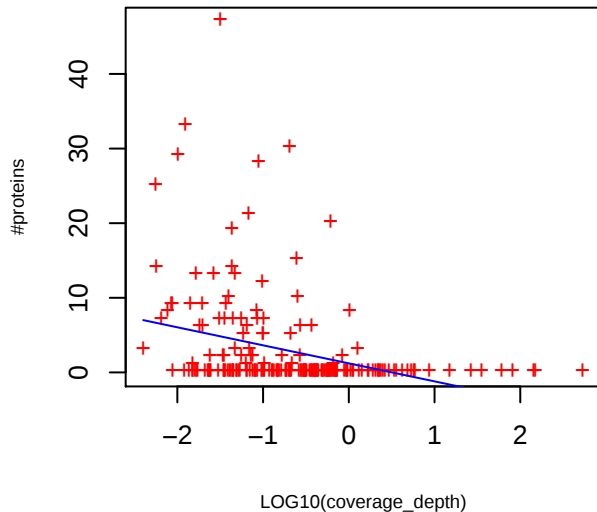


P-value curve ; red (unnorm), green (norm)



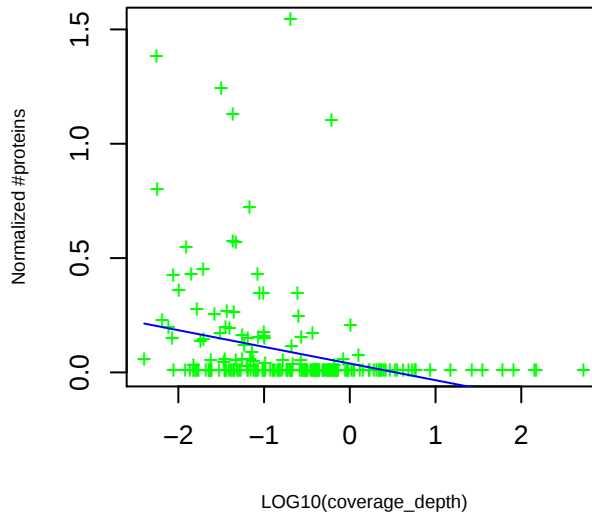
cnt_prot

slope= -2.42 p_value= 3.7e-06 intercept= 1.22 p_value= 0.035



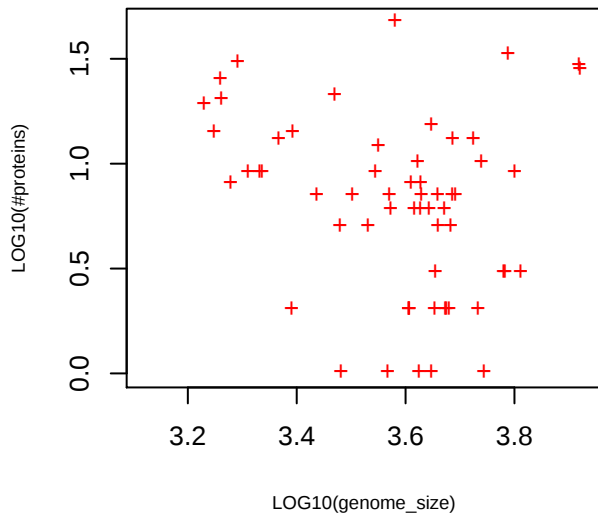
cnt_prot

slope= -0.073 p_value= 7.3e-05 intercept= 0.039 p_value= 0.058

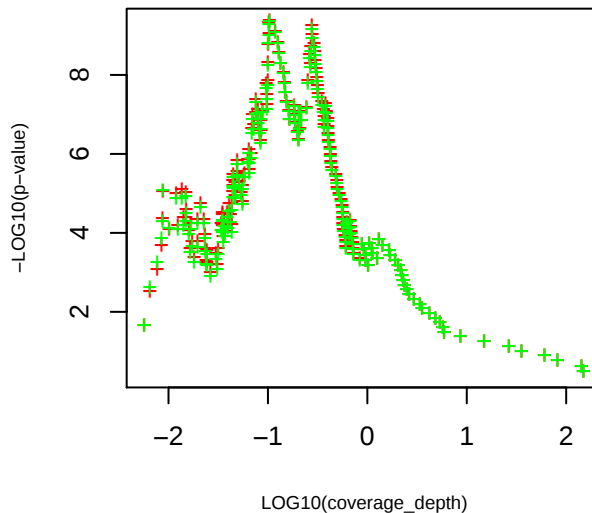


cnt_prot

slope= 1.83 p_value= 0.06 intercept= -9.02 p_value= 0.0093

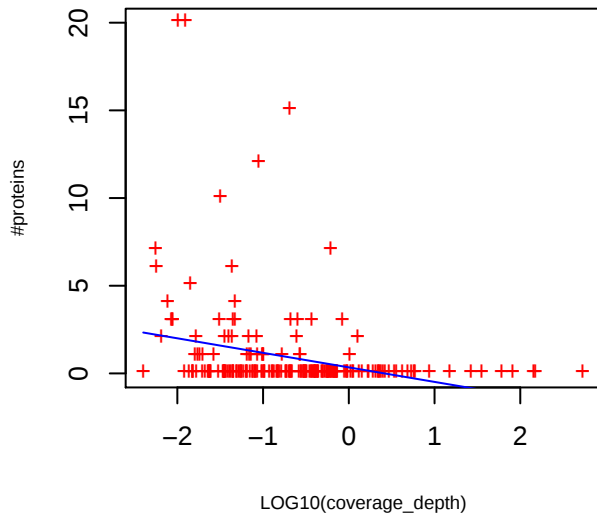


P-value curve ; red (unnorm), green (norm)



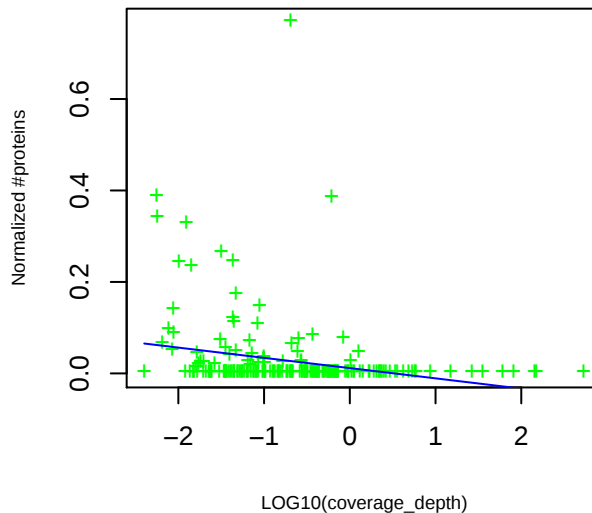
cnt_arr

slope= -0.83 p_value= 0.00012 intercept= 0.35 p_value= 0.15



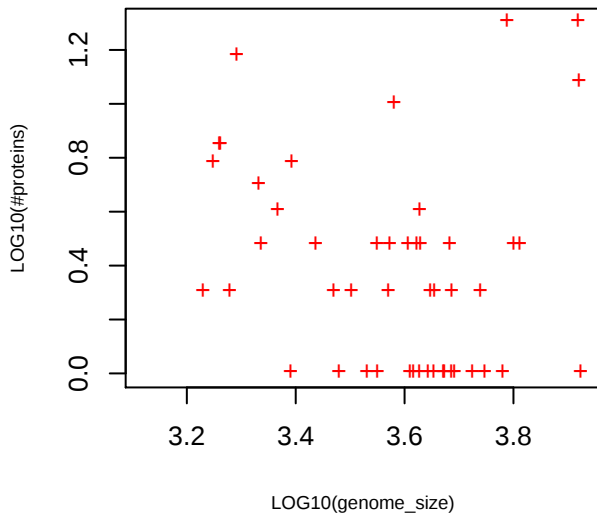
cnt_arr

slope= -0.022 p_value= 0.00072 intercept= 0.012 p_value= 0.12



cnt_arr

slope= 1.28 p_value= 0.12 intercept= -7.47 p_value= 0.012



P-value curve ; red (unnorm), green (norm)

