

Supplementary figure legends

Supplementary Figure 1 Gene coverage density plot. Representation of the gene coverage generated by the sequenced reads that were obtained for each experimental condition: infection of *Drosophila melanogaster* wild-type adult flies with *Heterorhabditis* axenic nematodes, *Heterorhabditis* symbiotic nematodes, *Photorhabdus* bacteria at 12 h and 30 h post-infection, and uninfected control.

Supplementary Figure 2 Quantitative real-time RT-PCR validation. Seven *Drosophila melanogaster* genes (CG34040, CG64267, CG9468, CG11909, CG6524, CG17571, CG10374) were selected from the RNAseq dataset and qRT-PCR results are shown from flies infected by *Heterorhabditis bacteriophora* symbiotic nematodes for 12 h. Solid bars represent transcript levels obtained from RNAseq; open bars show expression levels obtained from qRT-PCR experiments. Flies used for RNAseq and qRT-PCR assays were subjected to the same experimental conditions.

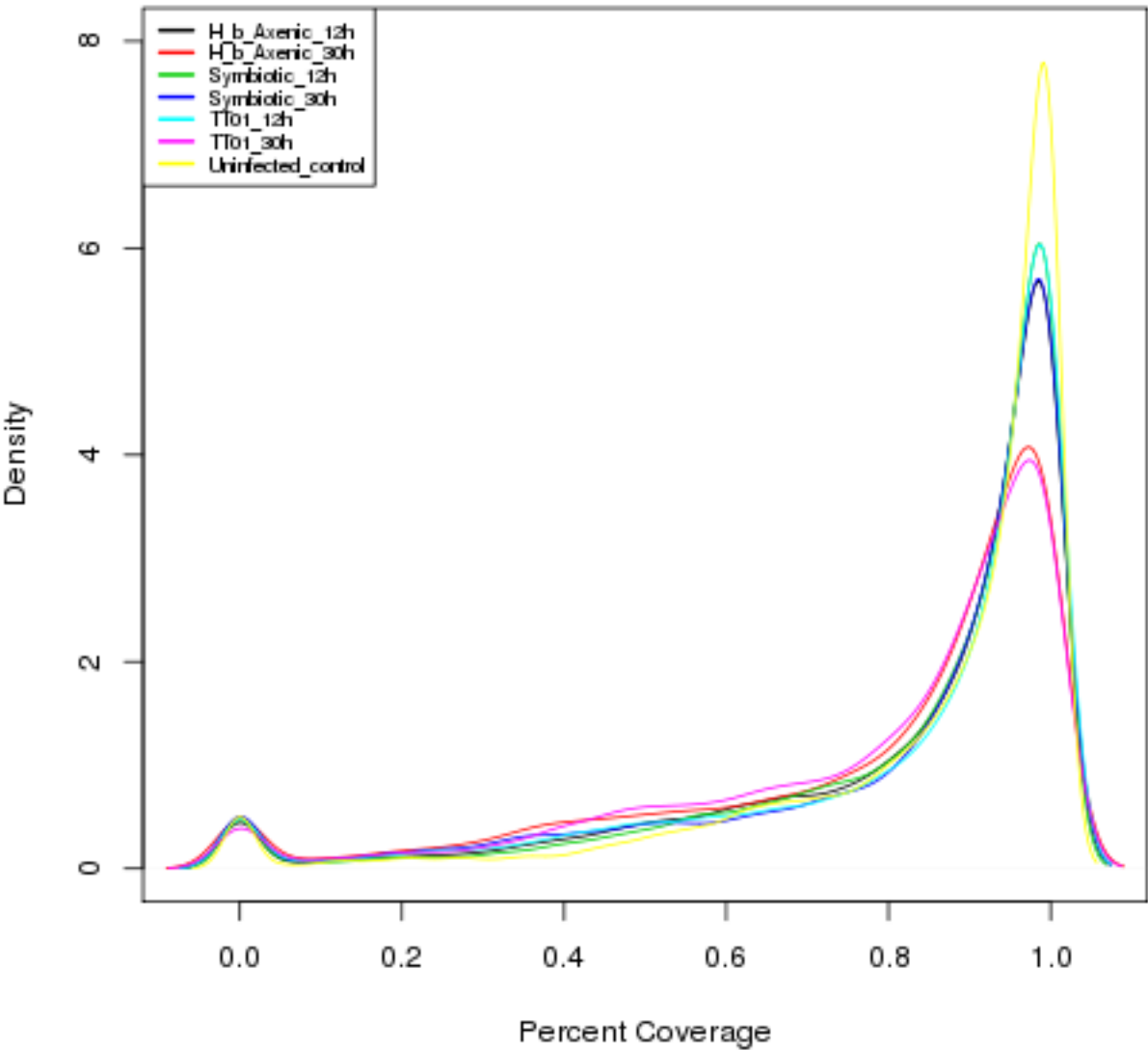
Supplementary Figure 3 Infection of *Drosophila* flies with *Heterorhabditis* nematodes or their *Photorhabdus* bacteria induces diverse physiological responses. Enrichment of pathway specific genes according to the KEGG and PANTHER classification databases. Representative KEGG pathway categories in flies infected by **(A)** axenic *Heterorhabditis* nematodes, **(B)** symbiotic *Heterorhabditis* nematodes, and **(C)** *Photorhabdus* bacteria at 12 h post-infection. The number of genes represents those that were only found associated with a particular pathway. Representative PANTHER pathway categories in flies infected with **(D)** axenic *Heterorhabditis* nematodes, **(E)** symbiotic *Heterorhabditis* nematodes, and **(F)** *Photorhabdus* bacteria at 30 h post-infection.

Supplemental Figure 4 Quadrant plots showing expression patterns in adult flies infected by nematodes or their bacteria. Upper right (UP/UP): genes up-regulated upon infection; Upper left (DOWN/UP): genes up-regulated at 30 h only; Lower right (UP/DOWN): genes up-regulated at 12 h only; Lower left (DOWN/DOWN): genes down-regulated upon infection.

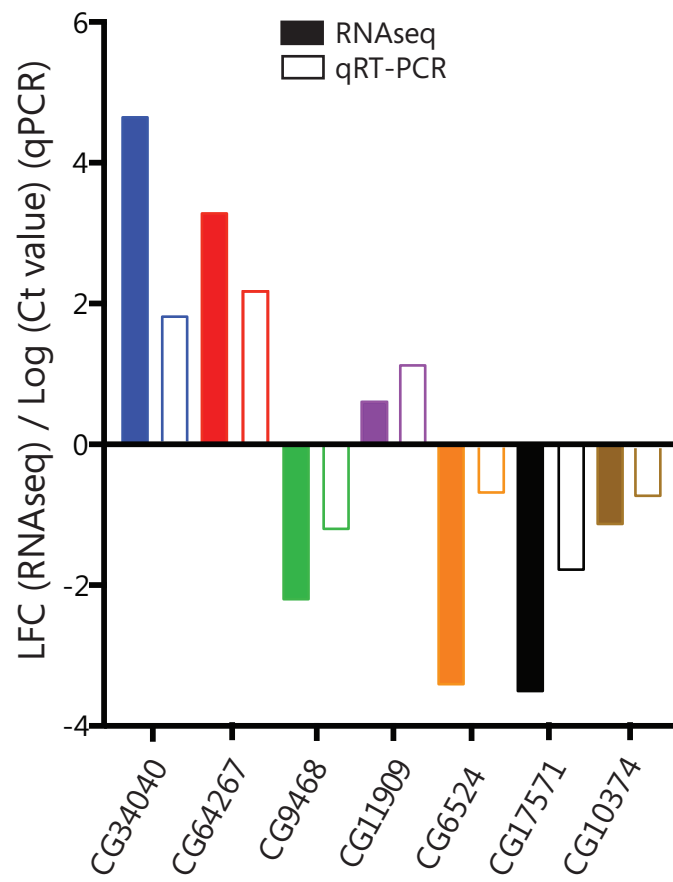
Supplementary Figure 5 Infection of *Drosophila* flies with *Heterorhabditis* or their *Photorhabdus* suppresses the expression of several genes. The 25 most strongly downregulated genes upon infection with **(A)** axenic *Heterorhabditis* nematodes **(B)** symbiotic *Heterorhabditis* nematodes and **(C)** *Photorhabdus* bacteria. X-axis represents the relative Log-Fold Change (LFC) for each gene after normalization against uninfected controls. All genes have a fold change higher than 2 (LFC=0.58 corresponds to 2-fold change difference).

Supplementary Figure 6 Gene Ontology analysis. GO immune response categories identified in *Drosophila melanogaster* wild-type adult flies infected by **(A)** axenic *Heterorhabditis* nematodes, **(B)** symbiotic *Heterorhabditis* nematodes, or **(C)** *Photorhabdus* bacteria at 12 h post-infection. The Y-axis corresponds to the number of genes for each GO category and their relative level of expression (upregulation or down-regulation). All genes have a fold change higher than 2 (Log-Fold Change=0.58 corresponds to 2-fold change difference).

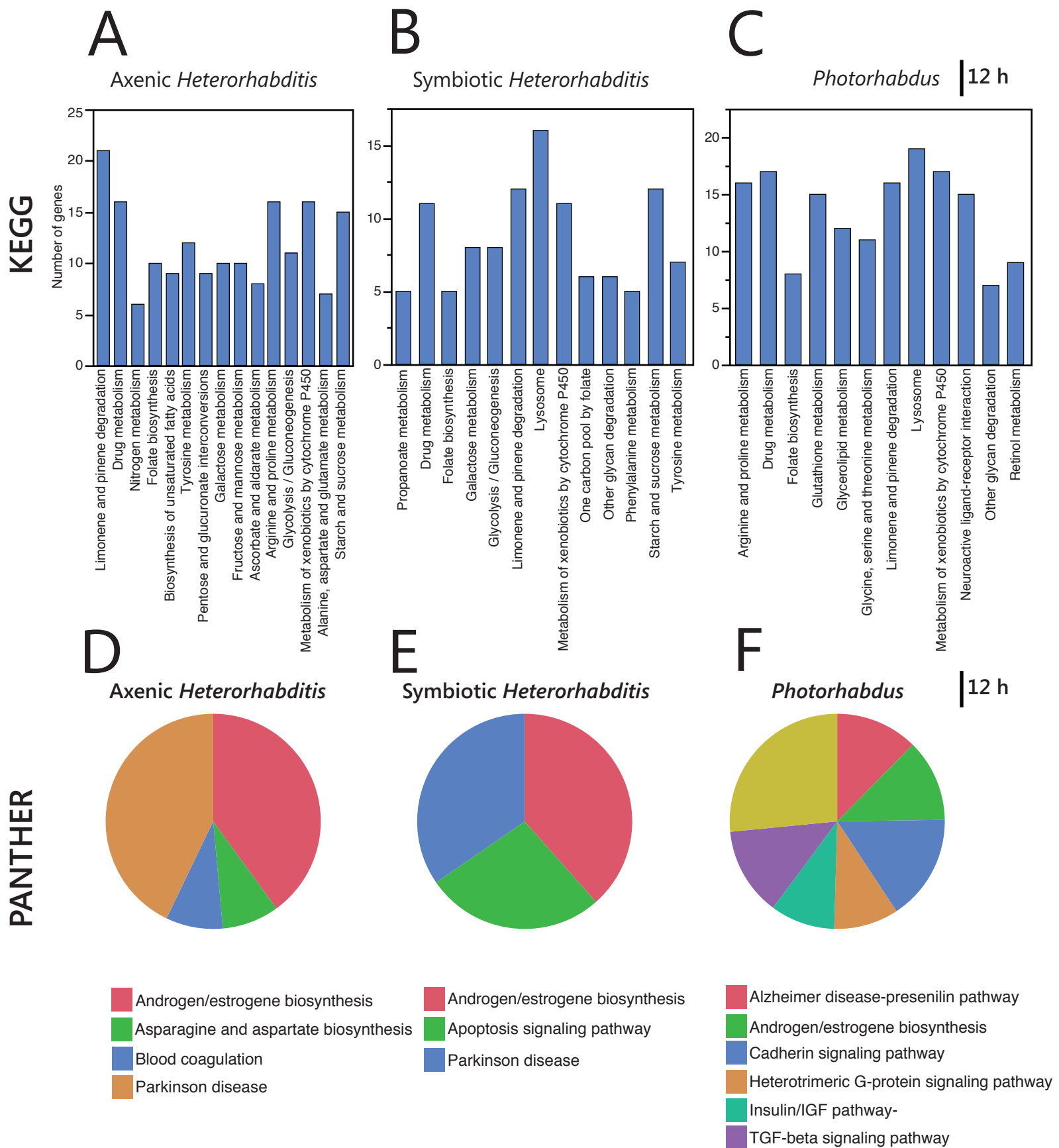
Supplementary Fig. S1



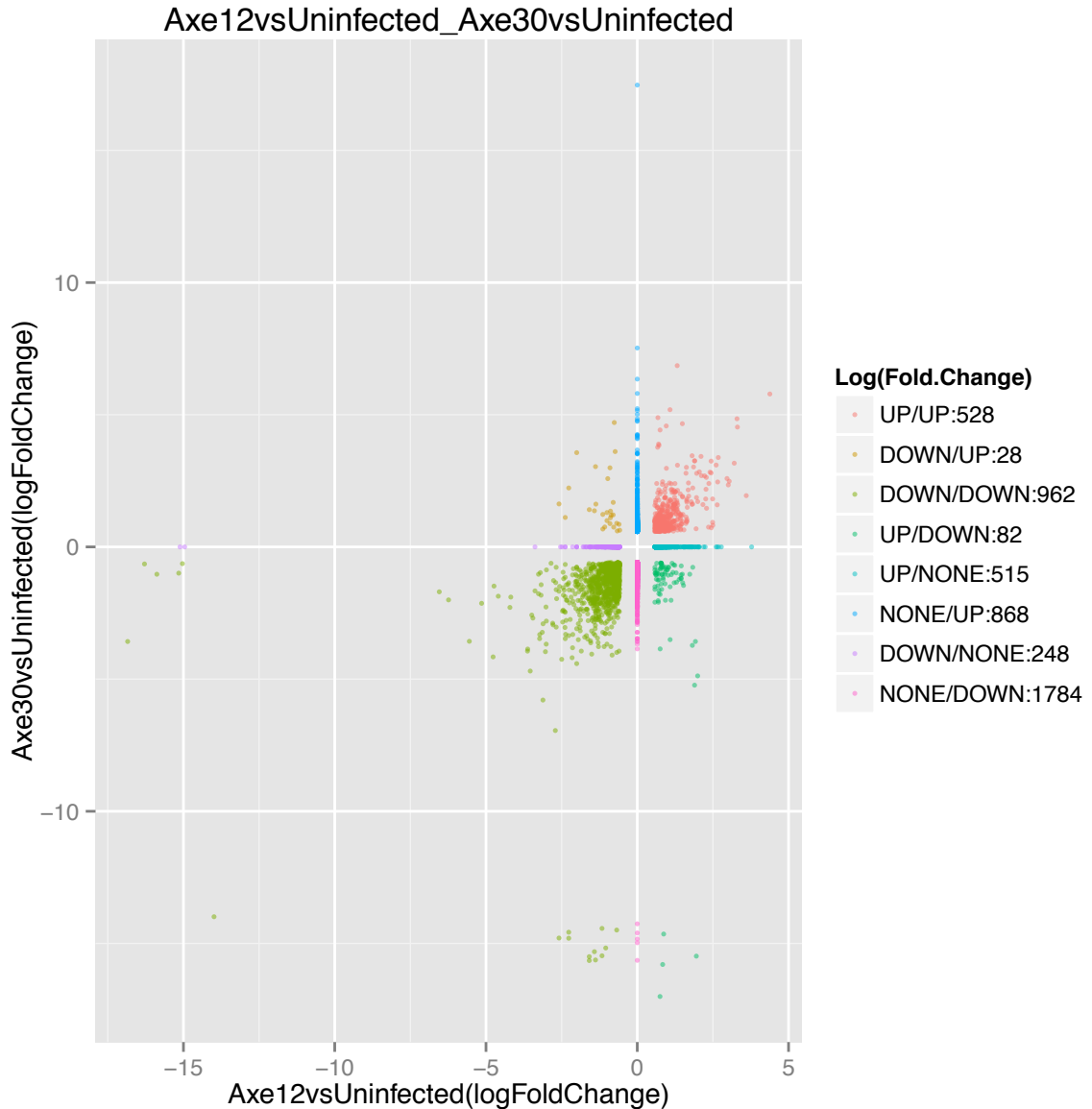
Supplementary Fig. S2

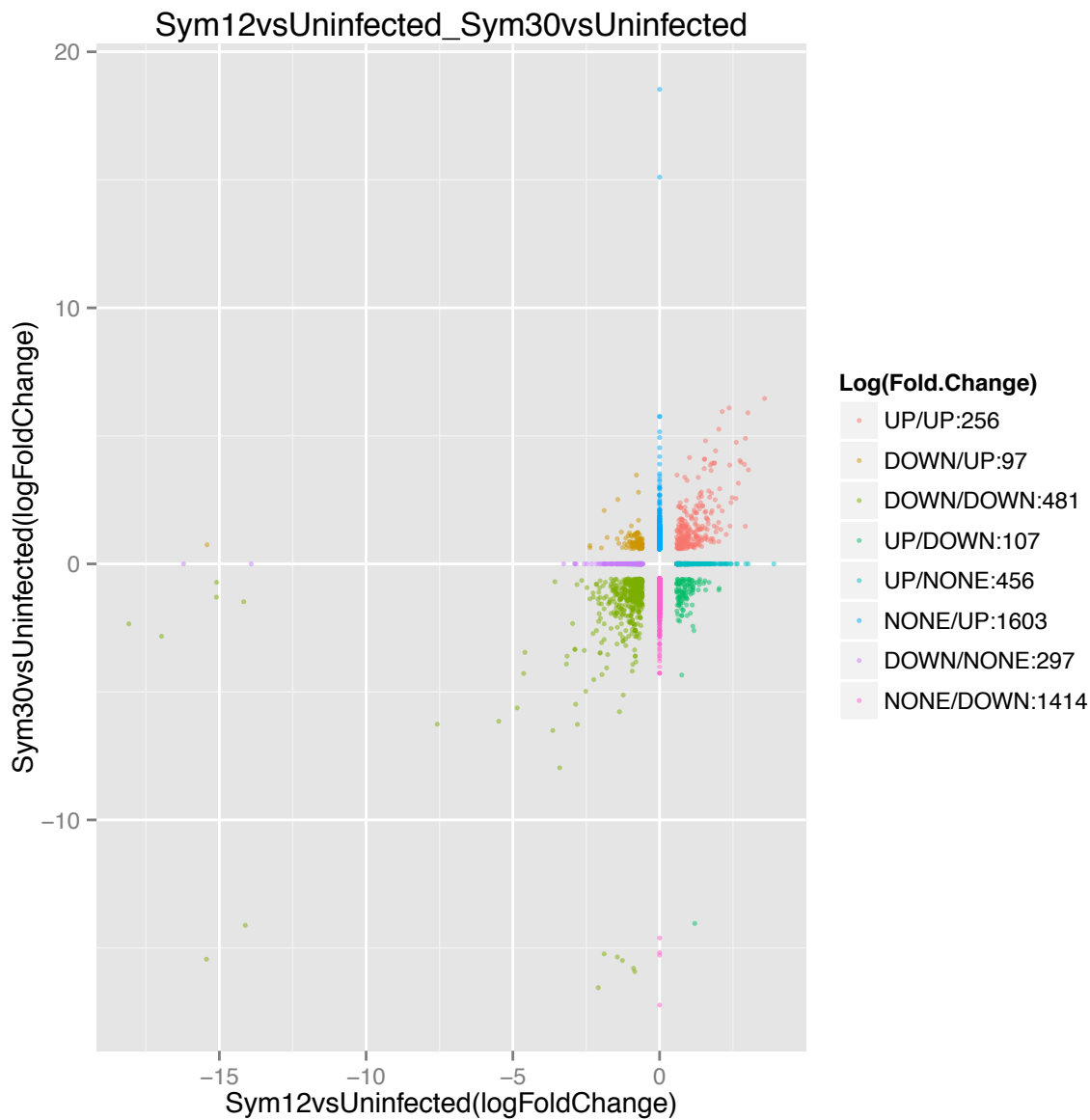


Supplementary Fig. S3



Supplementary Fig. S4

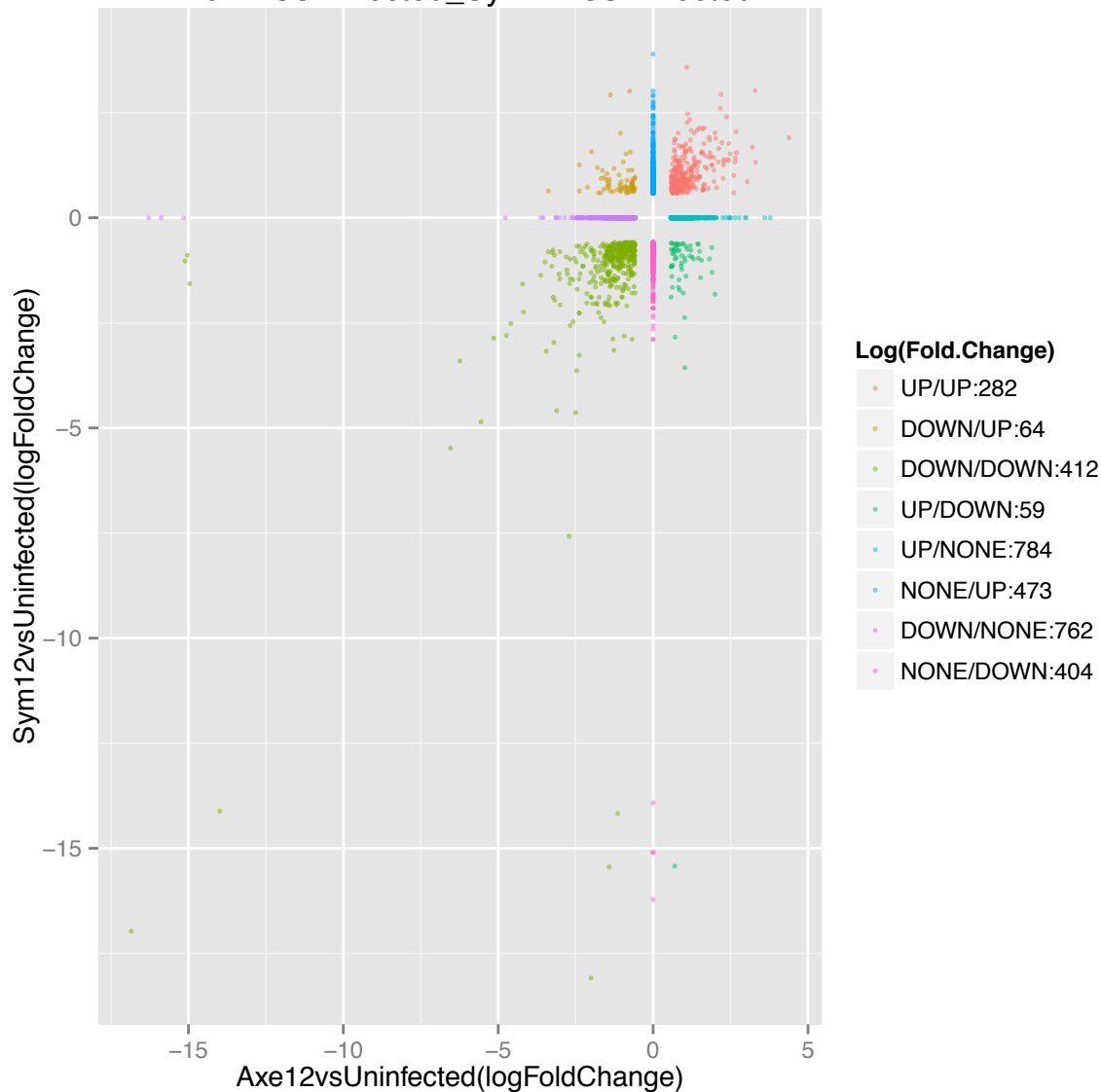




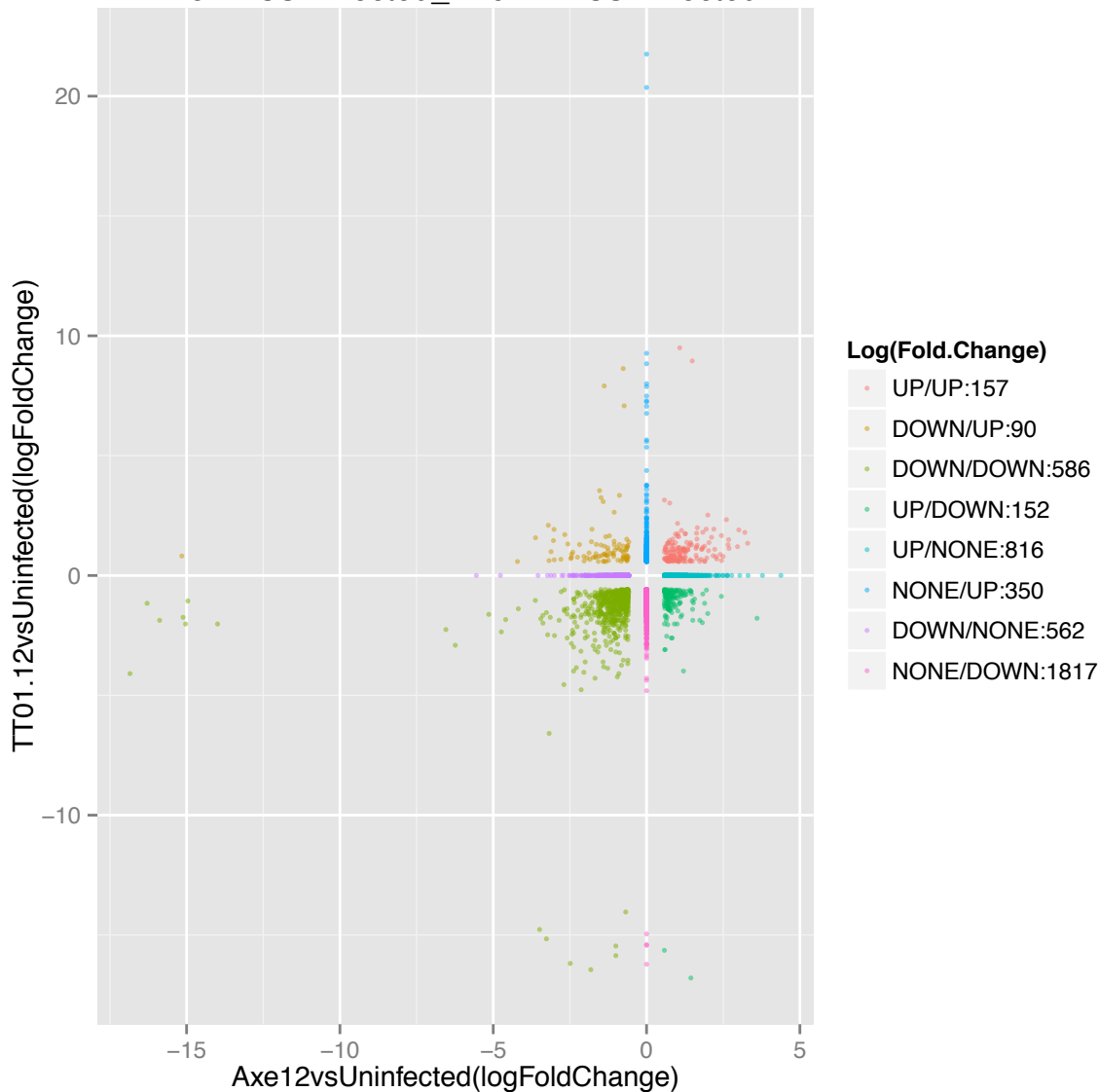
TT01.12vsUninfected_TT01.30vsUninfected



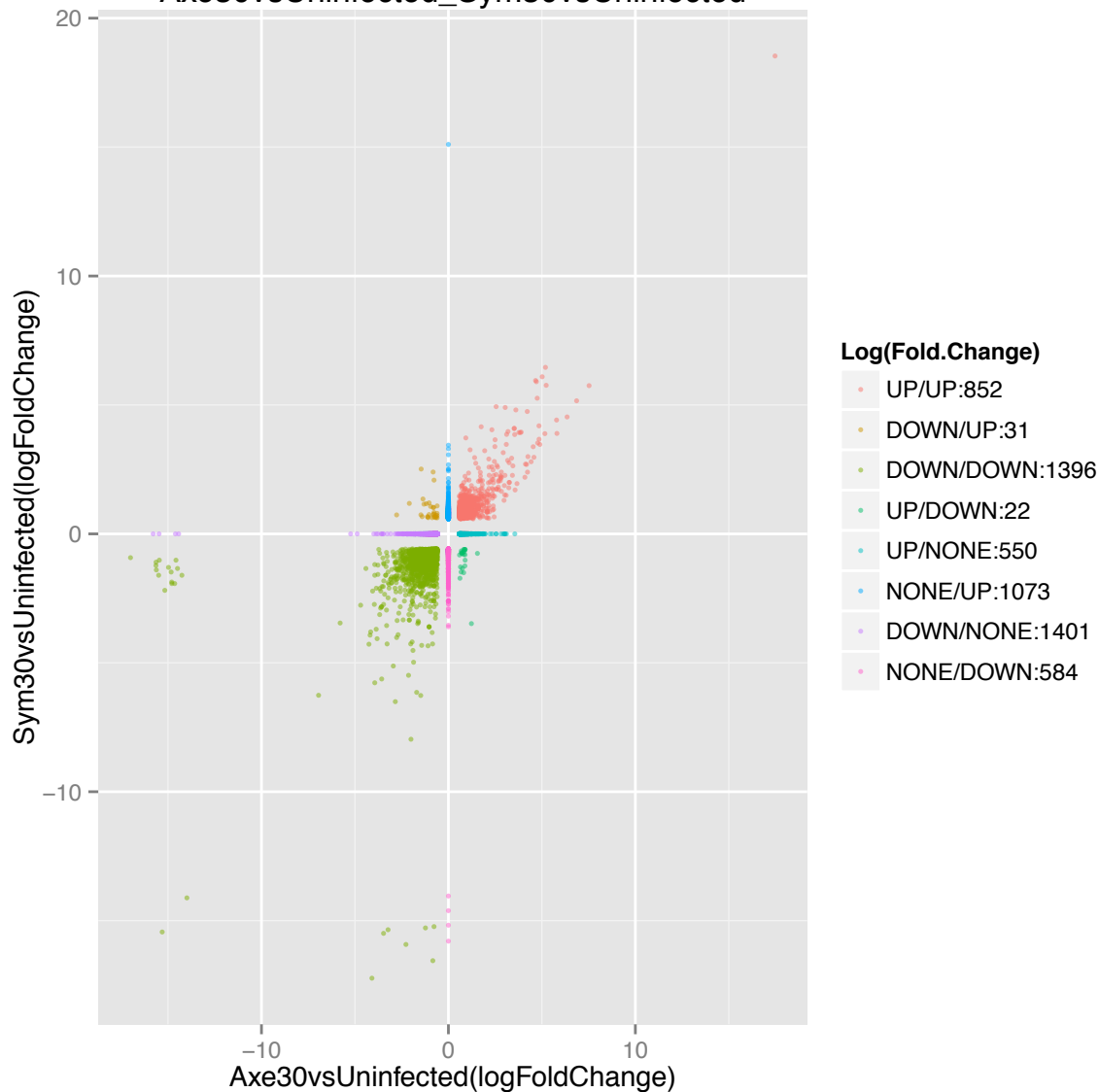
Axe12vsUninfected_Sym12vsUninfected



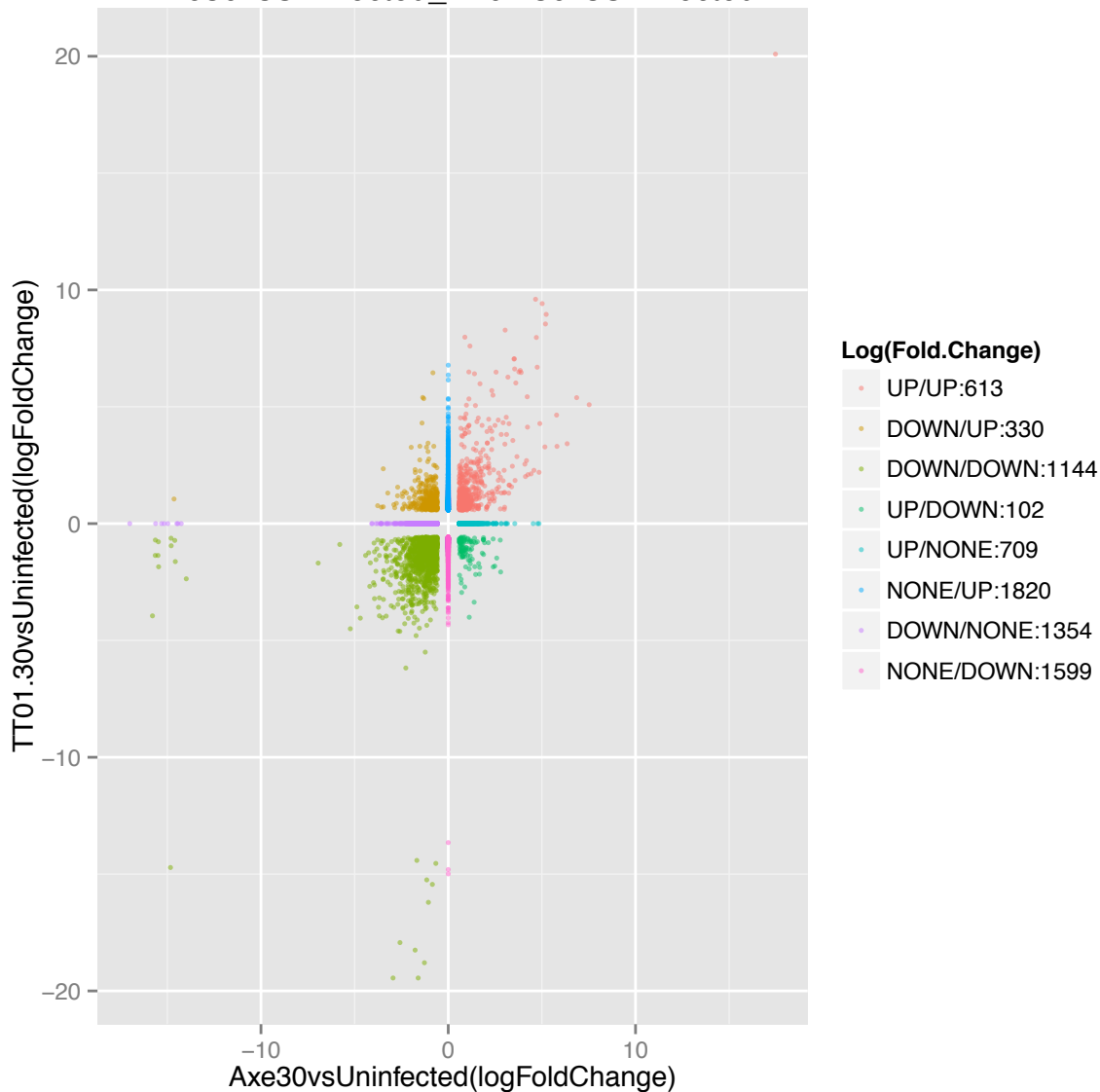
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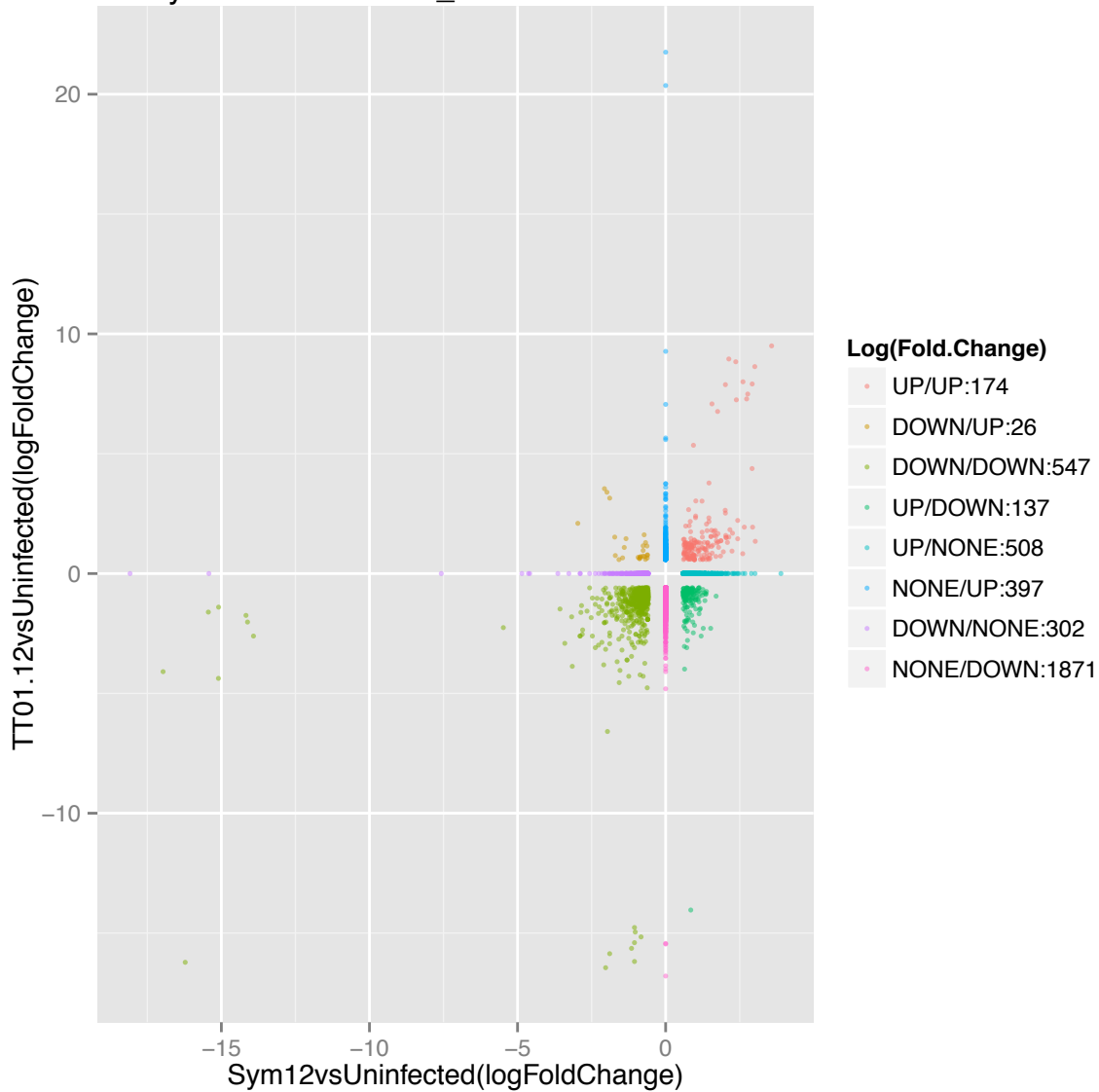
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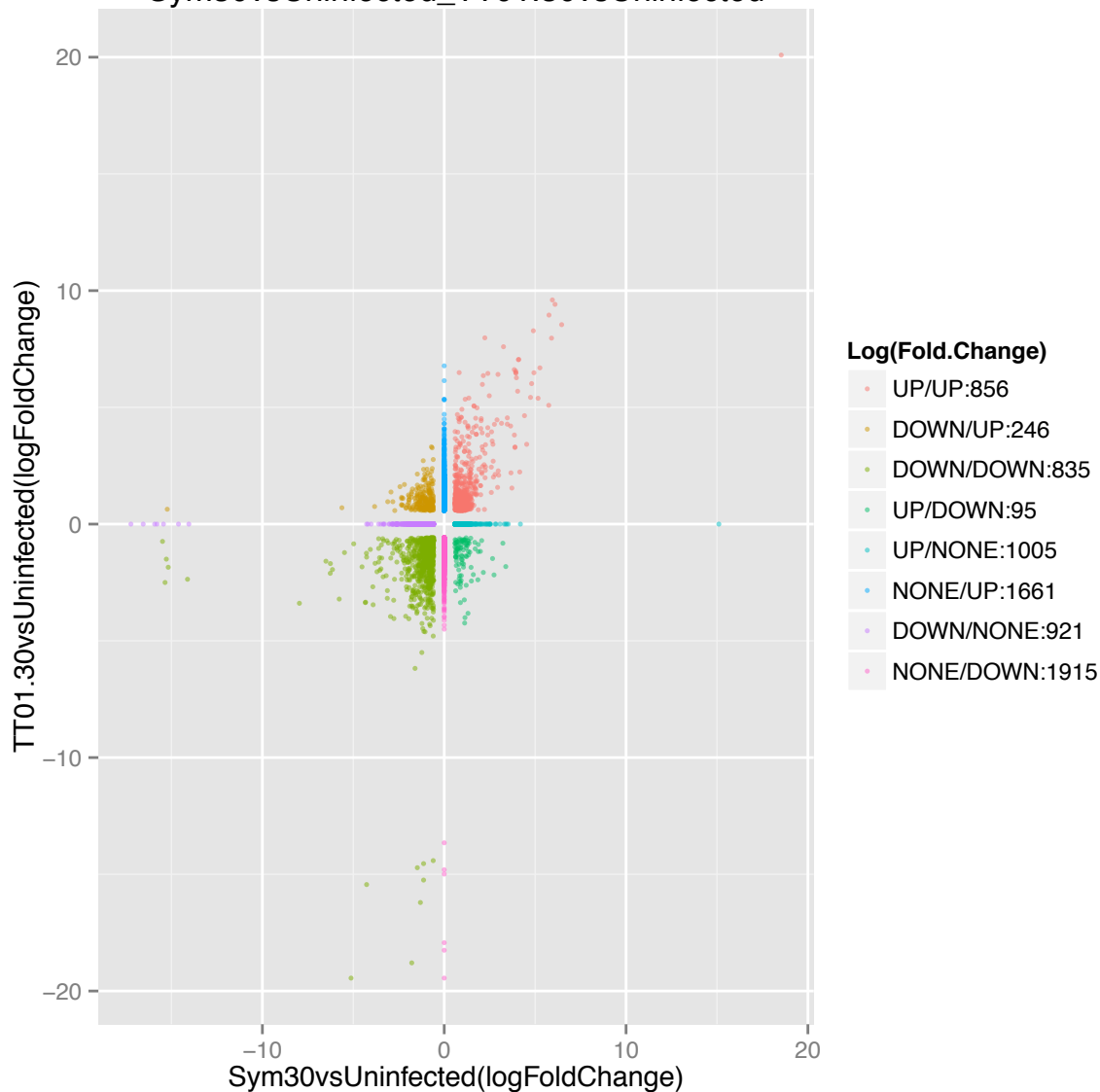
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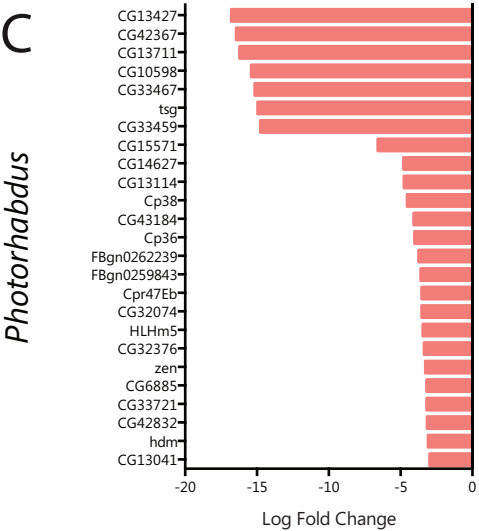
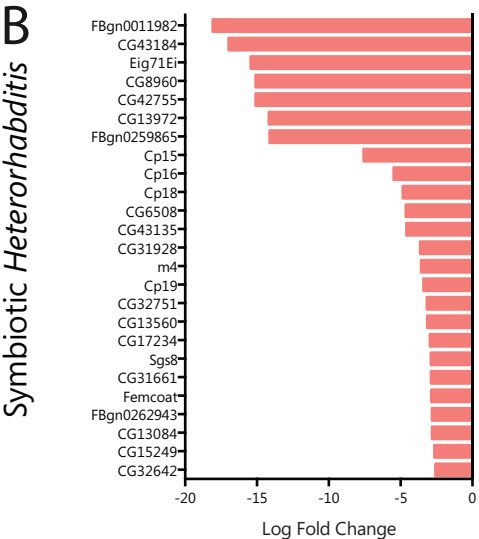
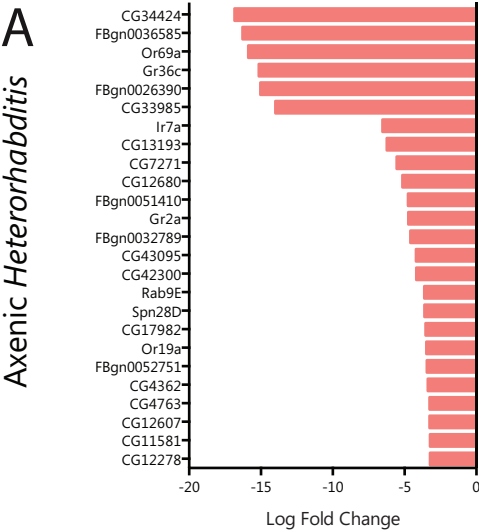
Sym12vsUninfected_TT01.12vsUninfected



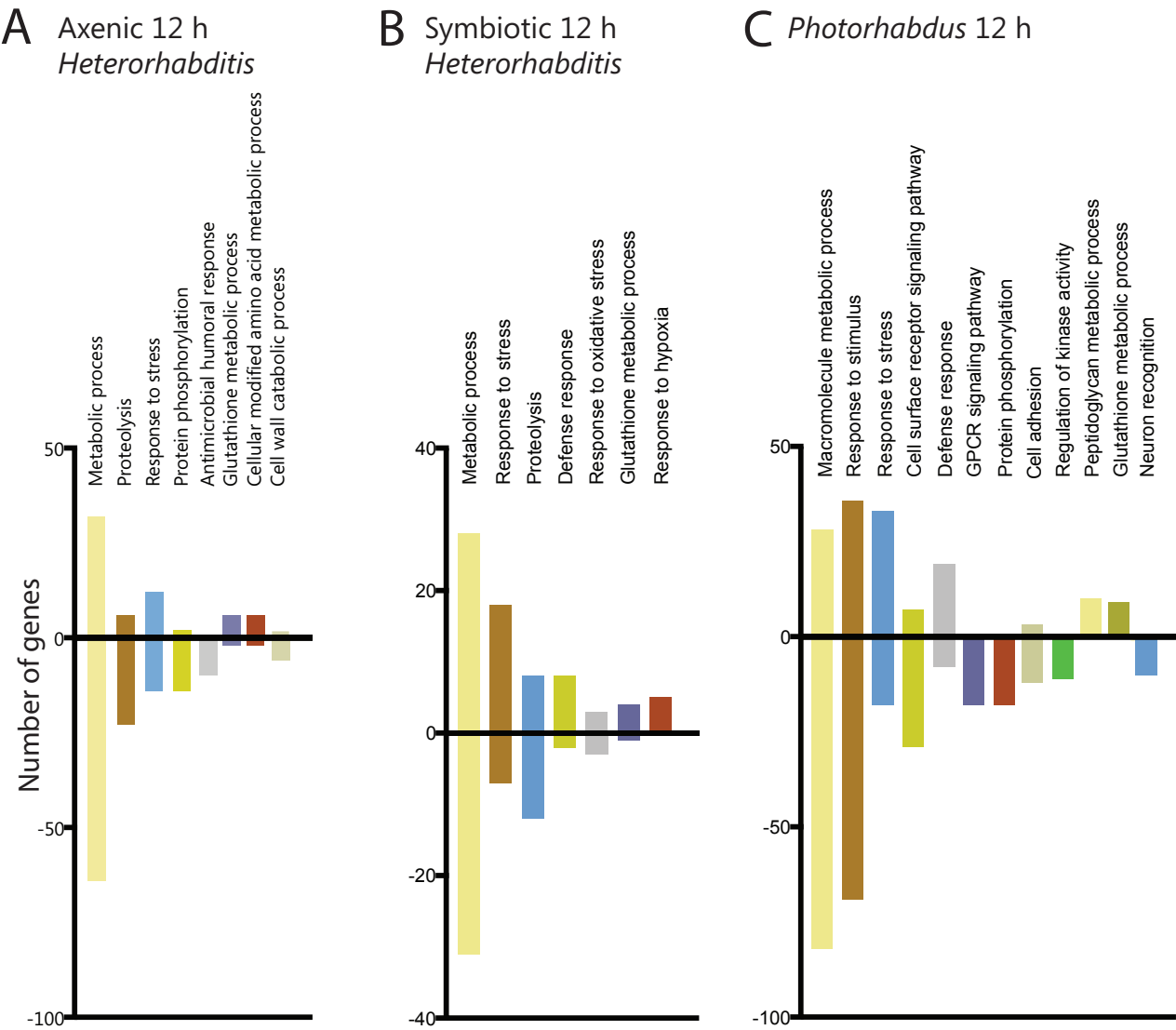
Sym30vsUninfected_TT01.30vsUninfected



Supplementary Fig. S5



Supplementary Fig. S6



Supplementary Table 1 List of primers used for quantitative real-time RT-PCR validation.

Gene Name	Accession no	Comments	Sequence
Unknown	CG34040	Unknown function DUF753	Forward 5'-TCGGGATATAAACTGCCAAAGGAG-3' Reverse 5'-GTTAGTAGCCCGGGAGATTCAGC-3'
Unknown	CG64267	Unknown function	Forward 5'-TGTTCCGCATTATCGCTGTGA-3' Reverse 5'-AAAATTTAACCGTGGTAGATGTGG-3'
Unknown	CG9468	Glycoside hydrolase family	Forward 5'-GCCCCGTCCCCGCATTGGTT-3' Reverse 5'-CCGCAGTGGACATCGAAGCAGTAG-3'
<i>Tobi</i>	CG11909	Aldolase-type TIM barrel; Glycoside hydrolase	Forward 5'-TGCAGGCGGTGGGCGACTAC-3' Reverse 5'-GCAGGGCGGGCATAAAGACG-3'
<i>Cp19</i>	CG6524	Chorion protein	Forward 5'-GGAGCCGAGGGTCAGCAGCGTTAT-3' Reverse 5'-TGGAGCAGCAGGGCGGATGG-3'
Unknown	CG17571	Trypsin-like cysteine/serine peptidase	Forward 5'-CTCCTCCCCCGACACCCTTCA-3' Reverse 5'-GCTGGCGACATCGGCATAGACG-3'
<i>Lsd-1</i>	CG10374	Perilipin domain, lipid mobilization	Forward 5'-TGAGCCGGCGACAGCAACAGT-3' Reverse 5'-CGTAGGCGGCCGAAATGGTG-3'