

Supplementary Data 6: iModulon Dashboards

Machine learning uncovers independently regulated modules in the *Bacillus subtilis* transcriptome

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This PDF contains automatically generated summaries of each iModulon. Note that the gene lists and counts here will include non-coding RNAs, which were usually omitted for simplicity in the main text.

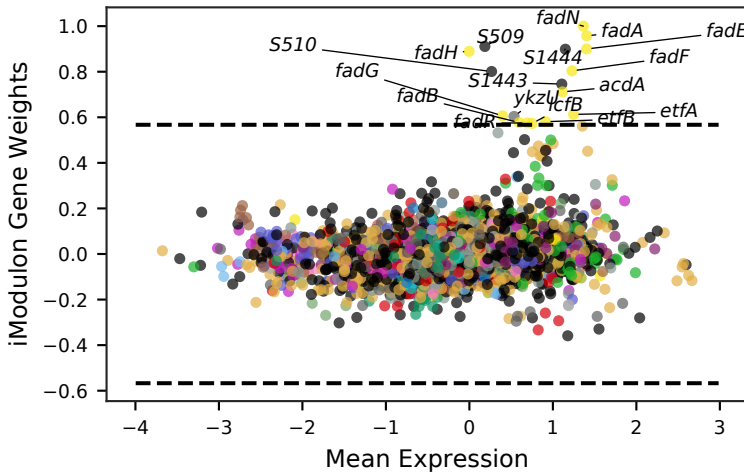
- *Title:* N - Short Name - Long Name. N corresponds to the iModulon number in Supplementary Data 3-5
- *Biological function:* brief description of the function of the iModulon's genes
- *Regulon:* includes the category that the iModulon falls into (see Main Fig. 1c) and the string of regulators. The regulator may be a boolean combination with '/' denoting union of regulons and '+' denoting intersection.
- *Plot 1:* Scatter plot of mean gene expression (Supplementary Data 2) and iModulon gene weight (Supplementary Data 3), with horizontal lines indicating the weight threshold and colors indicating gene category annotations from *SubtiWiki*. Gene categories of iModulon member genes are listed in the legend, with the number of member genes in each category in parentheses.
- *Plot 2:* Semi-log histogram of gene weights. Regulated genes are colored as shown in the legend, and member genes are listed above the appropriate bars.
- *Plot 3:* Activity level of the iModulon across all conditions (mean $\pm$ standard deviation). Stars indicate statistically significant conditions relative to their matched control (FDR < 0.05, Supplementary Data 7, Methods), and shaded backgrounds indicate significant correlation with time (Pearson R > 0.8, FDR < 0.05).
- *Plot 4:* Venn diagram of the known regulon (red), the annotated iModulon genes (green), and the unannotated iModulon genes (blue). Numbers indicate the size of the subset.
- *Plot 5:* Scatter plot(s) of regulator expression and iModulon activity (see Figure 3D-F). A best fit line and adjusted R^2 value is shown. If there are multiple regulators, the adjusted R^2 was computed for all of them and the top 3 regulators are shown, sorted with the highest correlation on the left. Colors of points match those in plot 3 and are listed in Supplementary Data 1.
- *Motifs:* If the iModulon contained genes from four or more operons, the genome sequence was searched for upstream consensus motifs (see Supplementary Methods). If there was a consensus, and if that consensus matches a known motif, the results are shown in the bottom right of the dashboard.

Visit imodulondb.org for more information and interactive versions of these dashboards.

0 - FadR - Fatty Acids

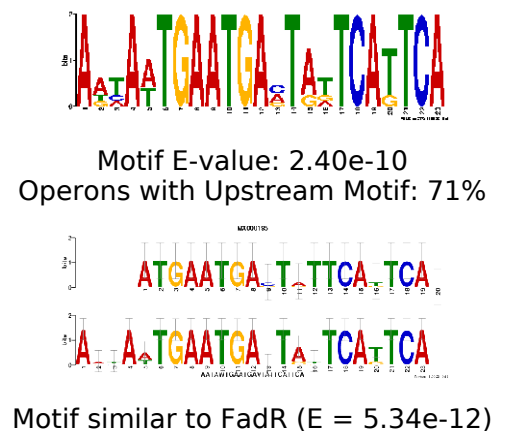
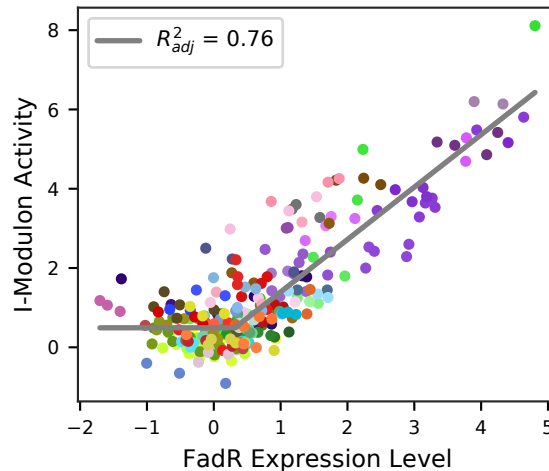
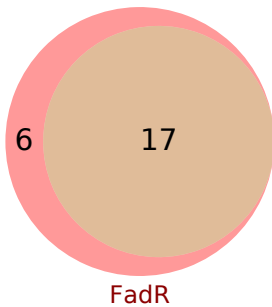
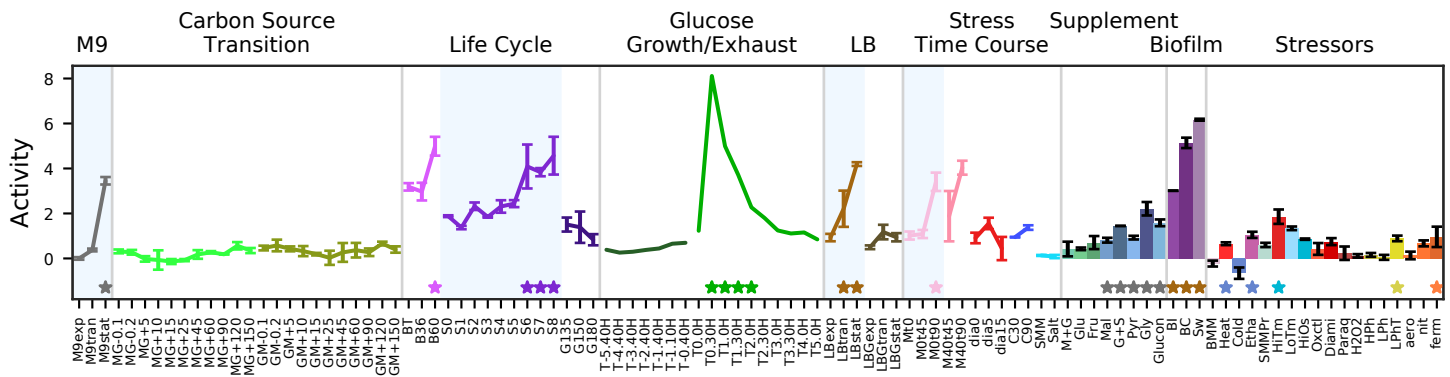
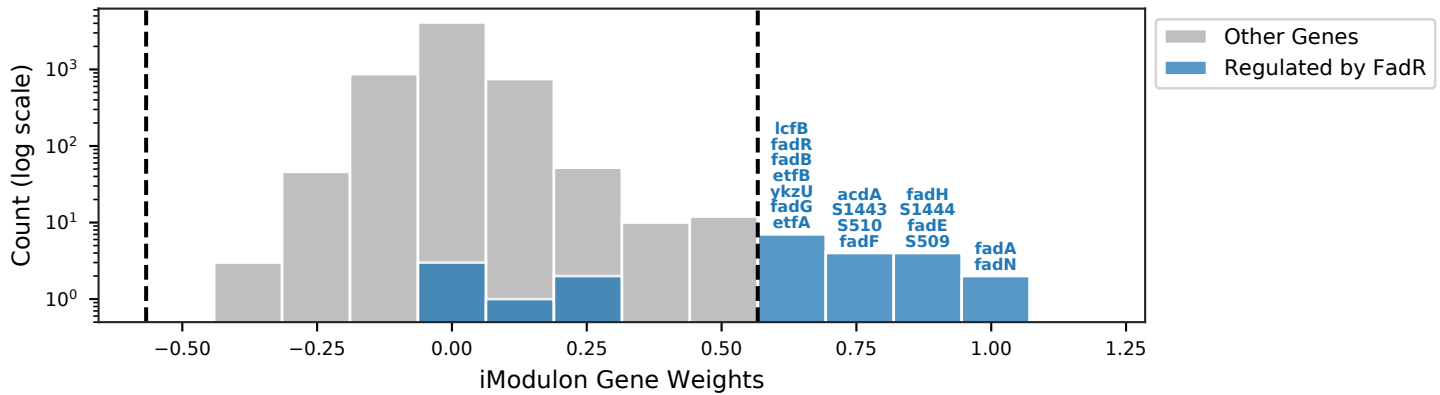
Biological Function:
Fatty acid degradation

Well-defined regulon:
FadR



Gene Categories

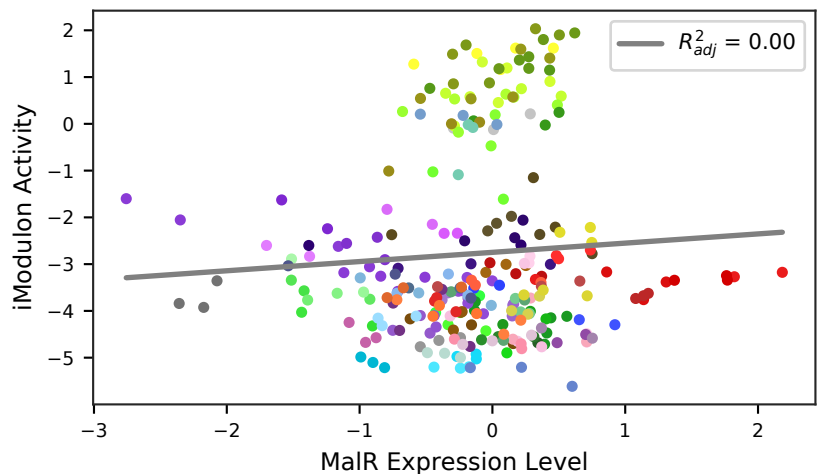
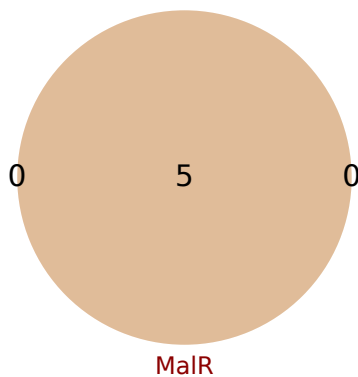
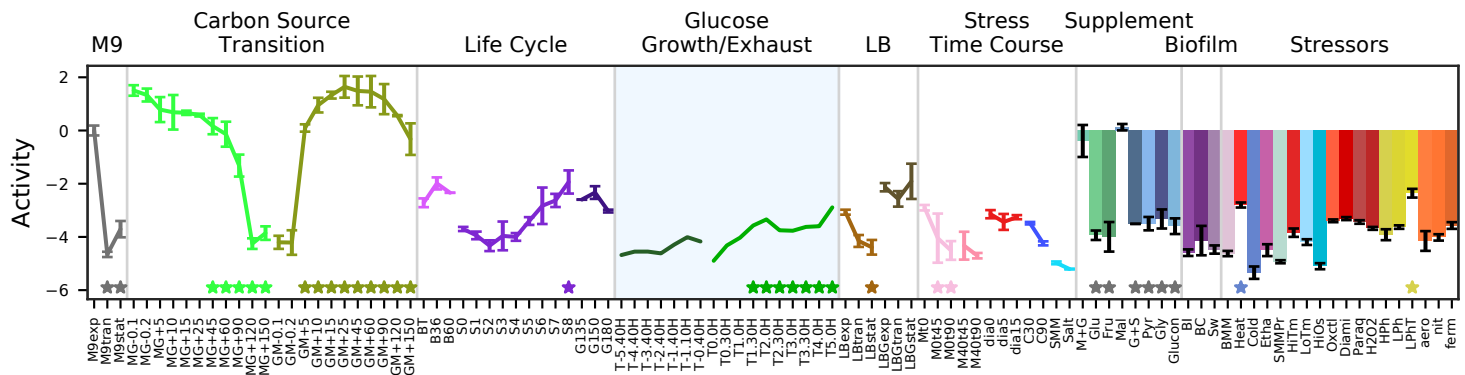
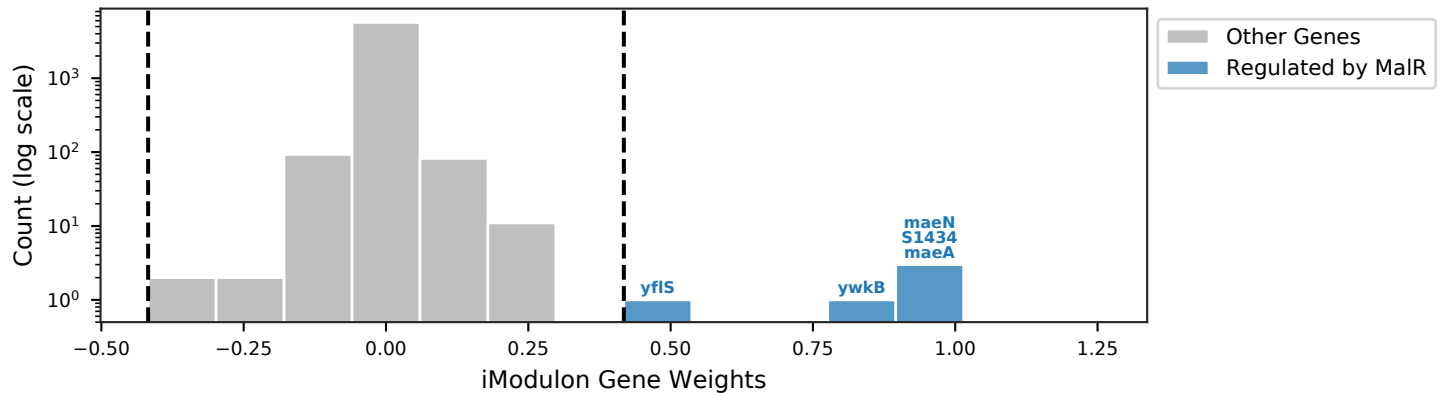
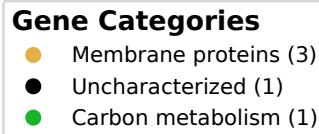
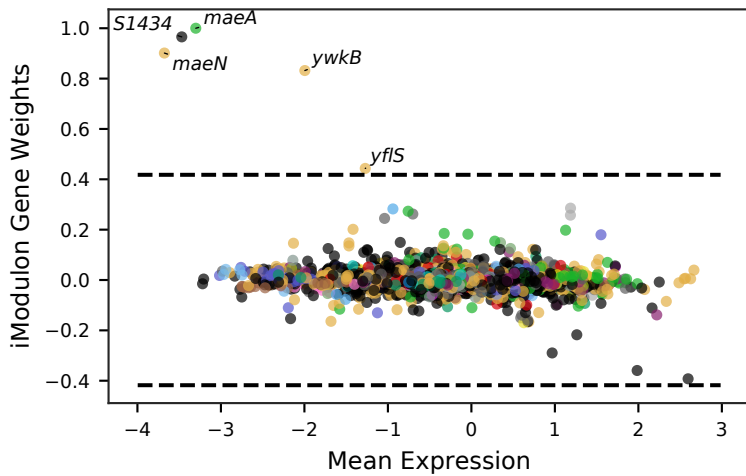
- Lipid metabolism (12)
- Uncharacterized (4)
- Proteins of unknown function (1)



1 - MalR - Malate

Biological Function:
Malate uptake and utilization

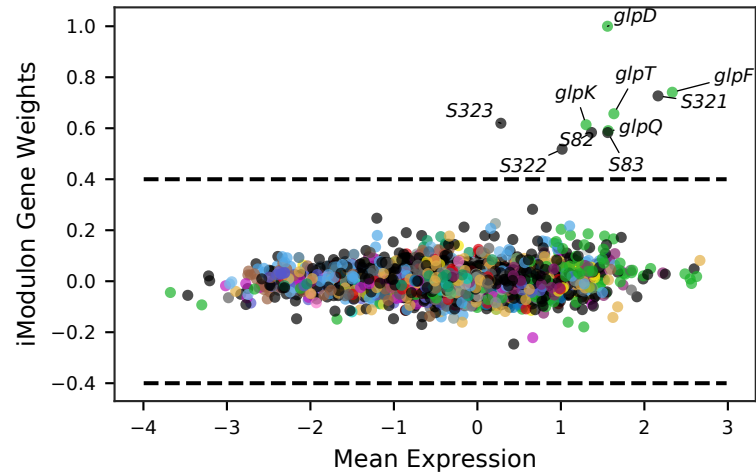
Well-defined regulon:
MalR



2 - GlpP - Glycerol

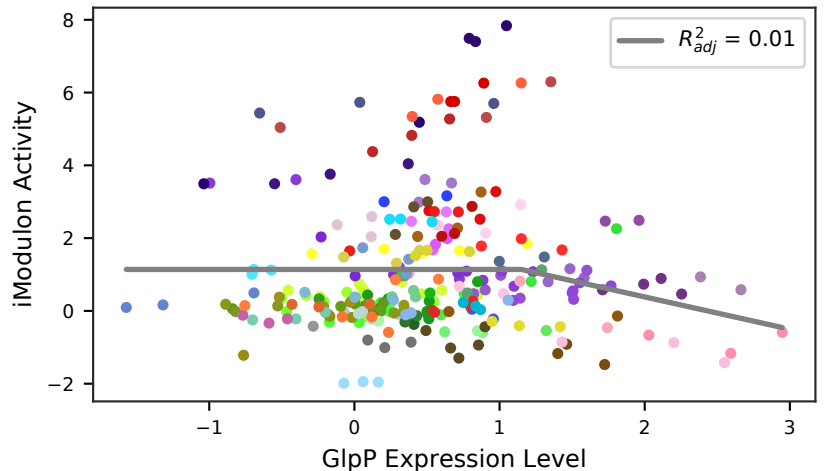
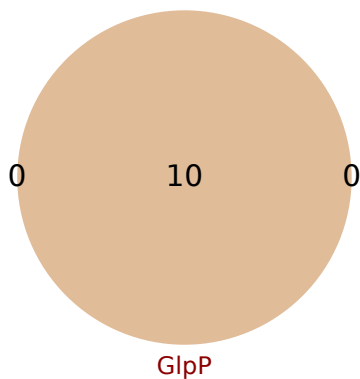
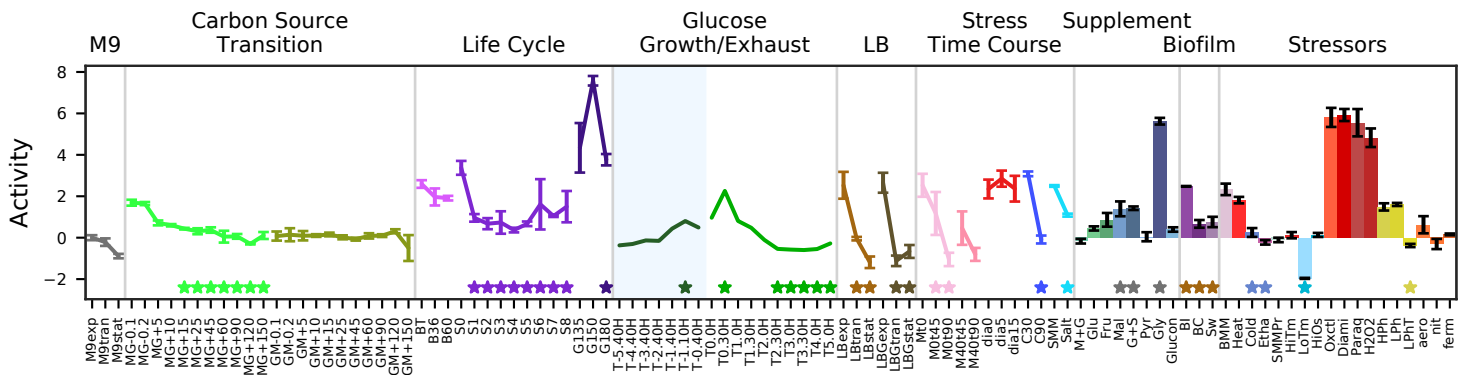
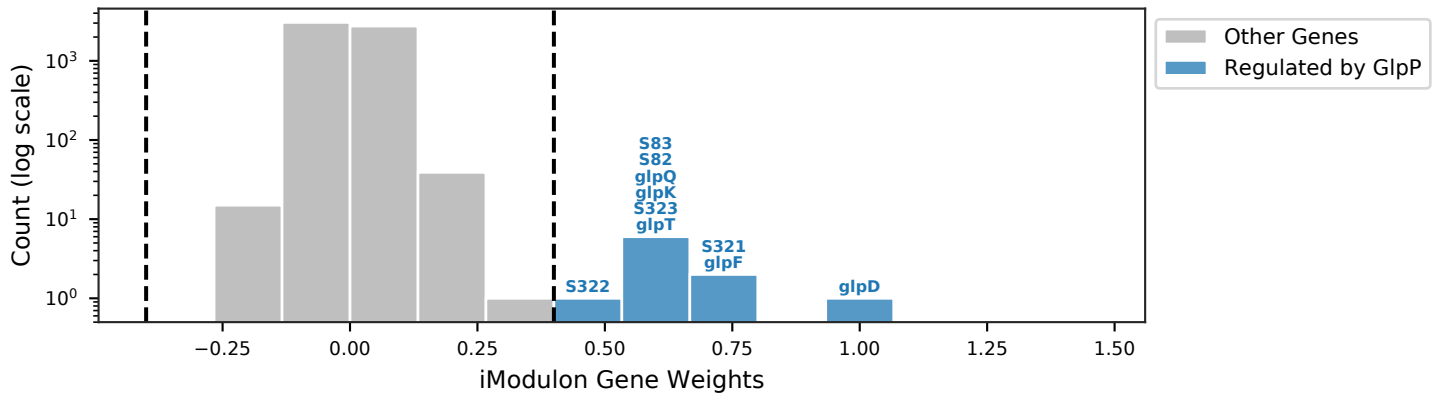
Biological Function:
Glycerol uptake and utilization

Well-defined regulon:
GlpP



Gene Categories

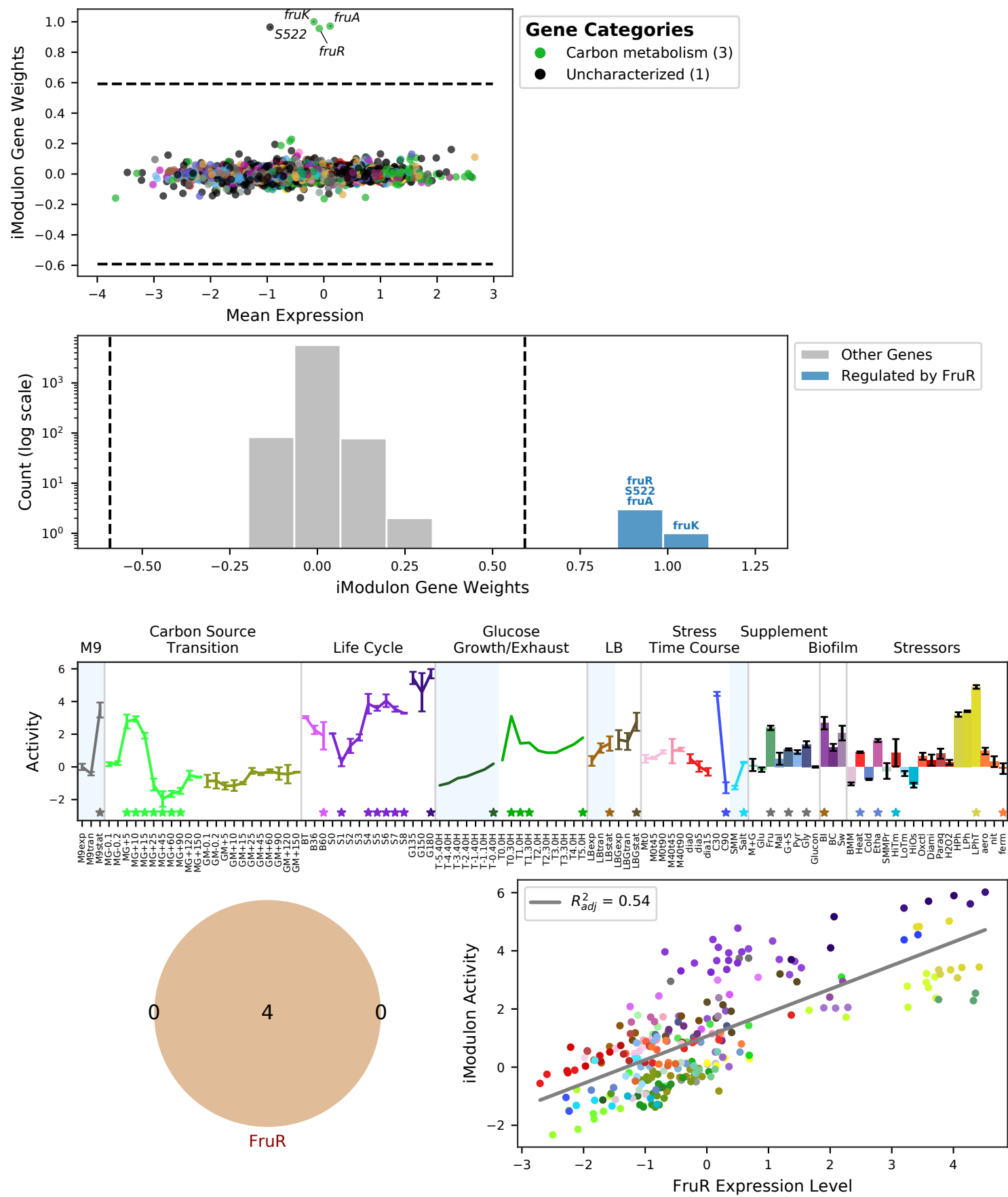
- Uncharacterized (5)
- Carbon metabolism (5)



3 - FruR - Fructose

Biological Function:
Fructose uptake and utilization

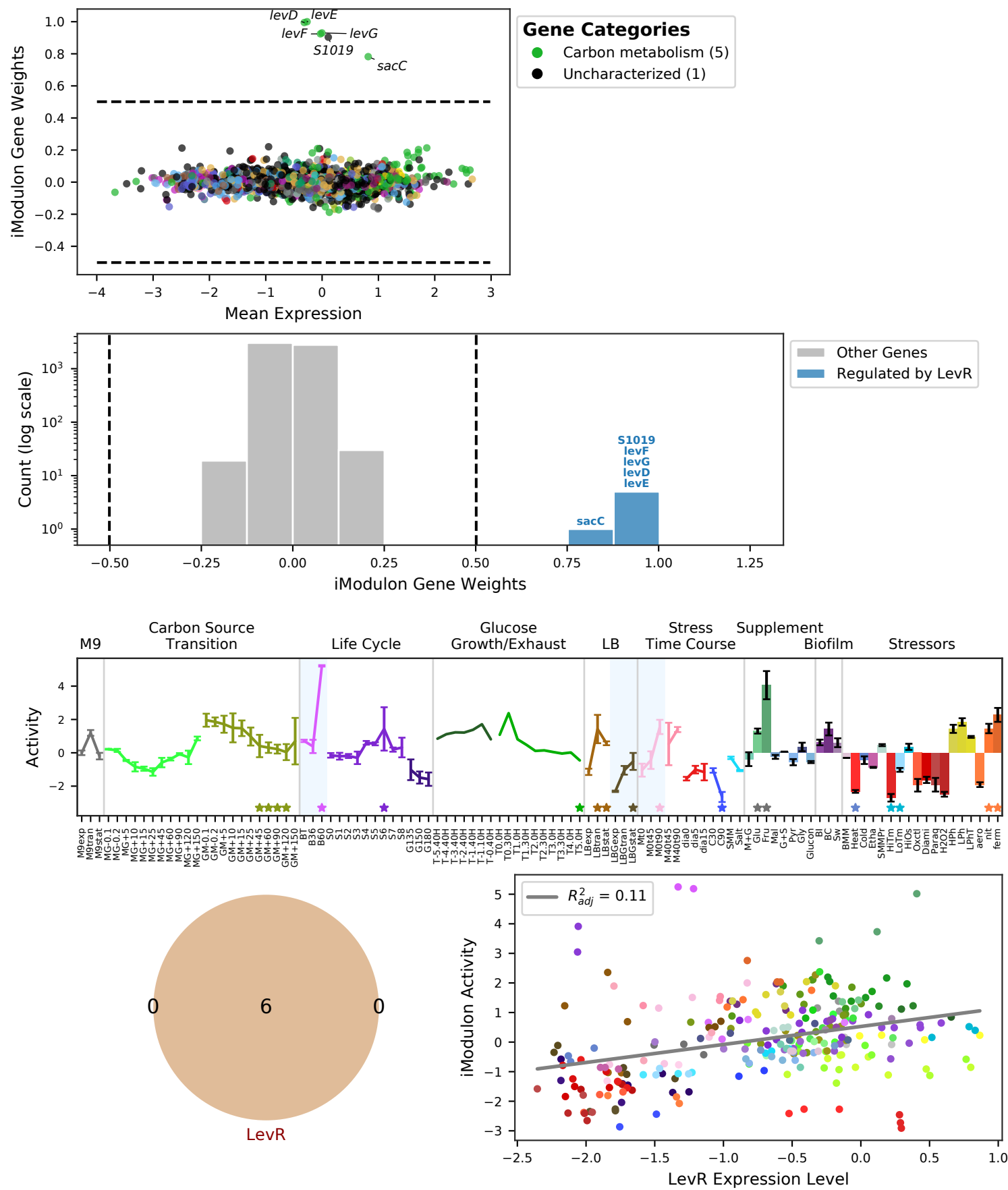
Well-defined regulon:
FruR



4 - LevR - Levan and Fructose

Biological Function:
Fuctose uptake and phosphorylation, degradation of the exopolysaccharide levan into fructose

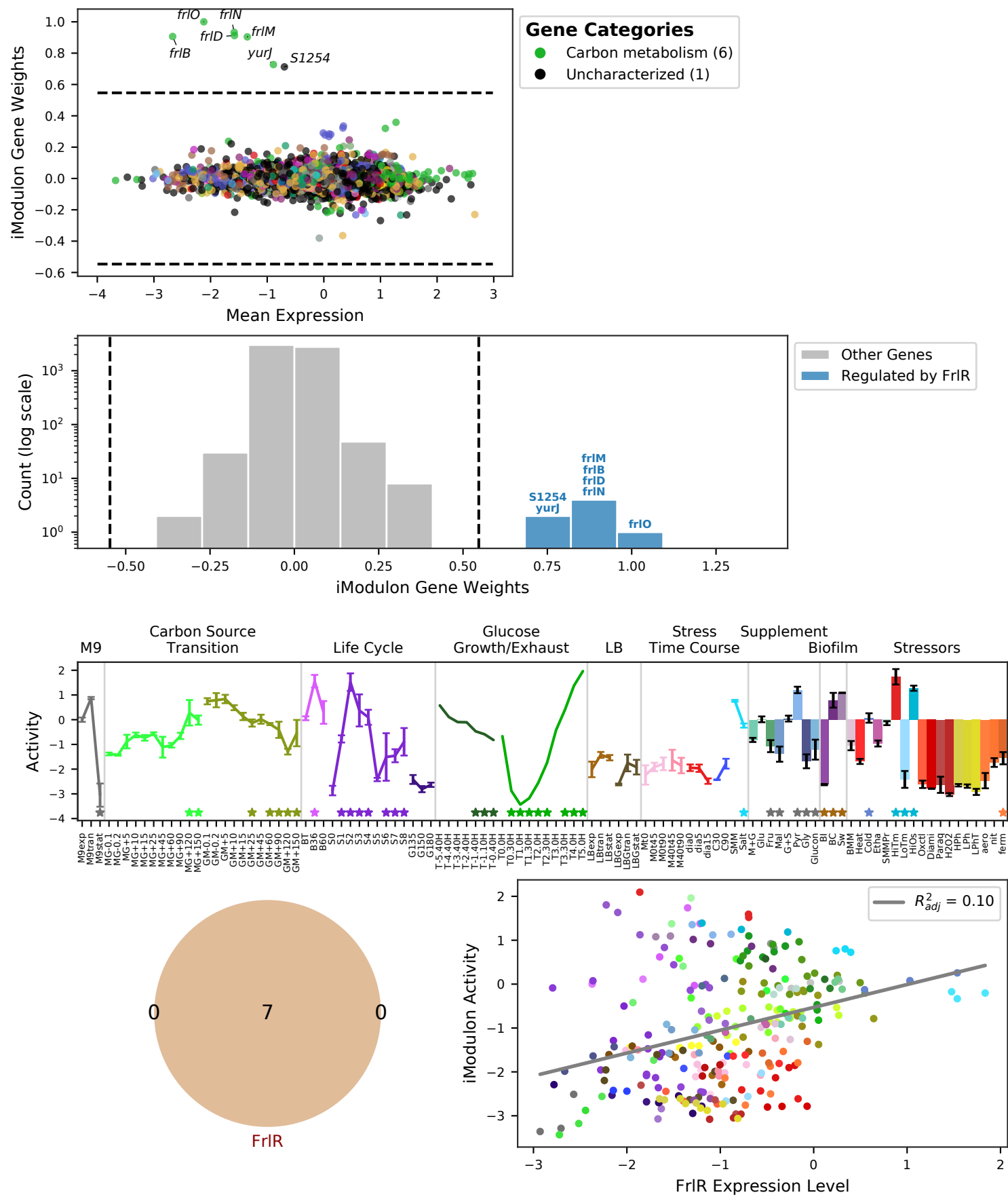
Well-defined regulon:
LevR



5 - FrIR - Amino Sugars

Biological Function:
Amino sugar uptake and metabolism

Well-defined regulon:
FrIR



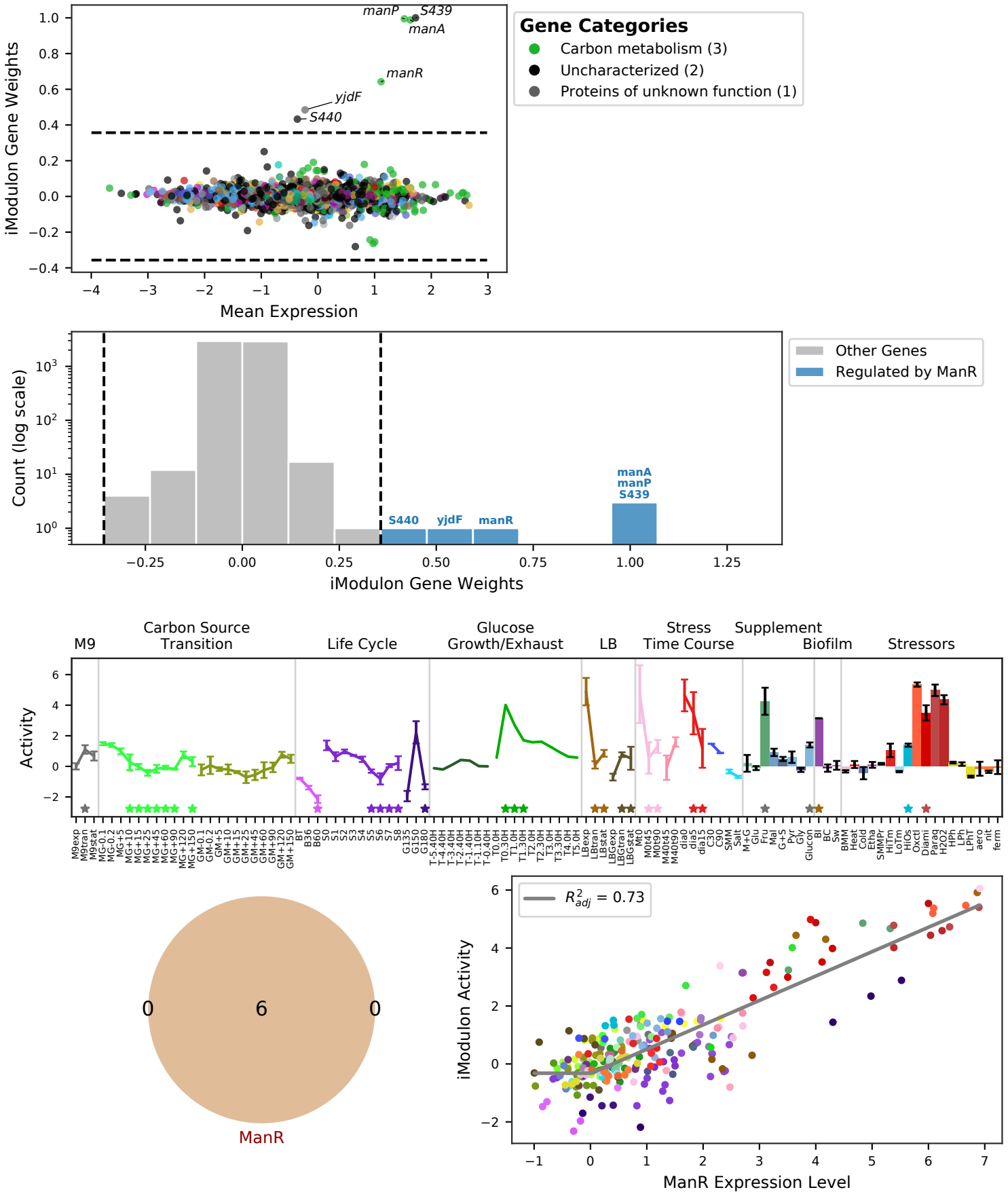
6 - ManR - Mannose

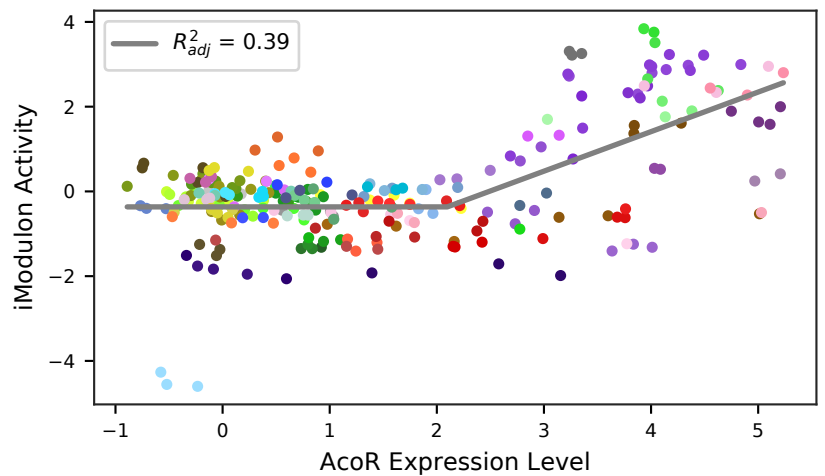
Biological Function:

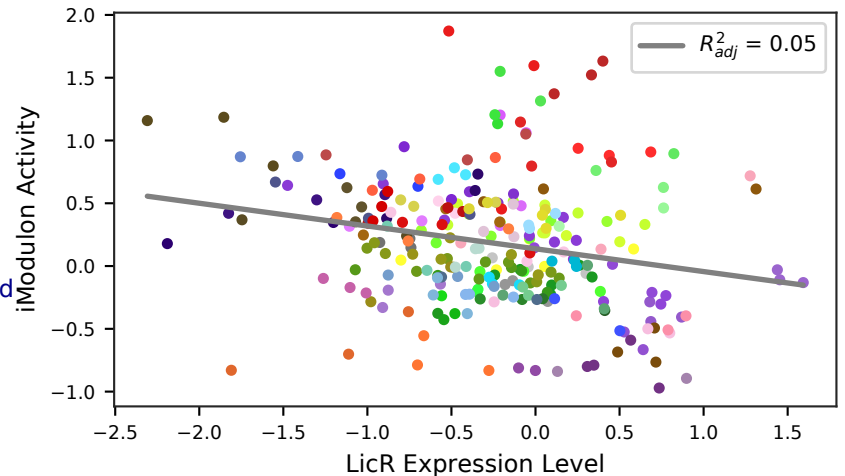
Utilization of mannose for cell wall synthesis. Needed for exponential growth in LB media (absent glucose) or in the presence of fructose

Well-defined regulon:

ManR







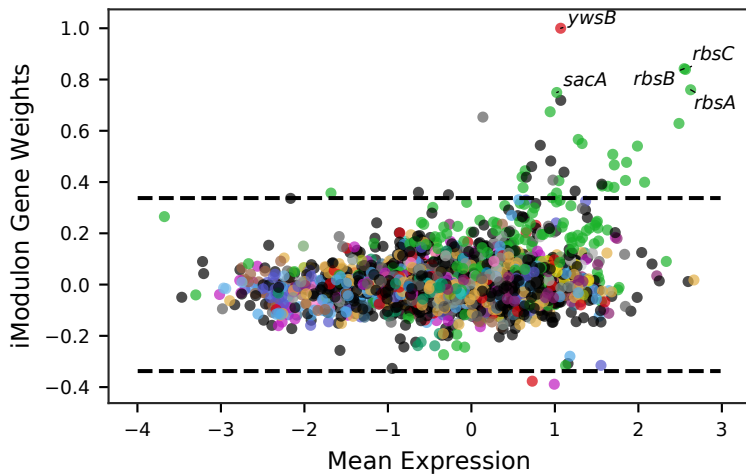
9 - CcpA-1 - Low Glucose 1

Biological Function:

Uptake and utilization of alternative carbon sources: ribose, sucrose, salicin, beta-glucosides, lichenan, glucomannan, trehalose, G3P, etc. High expression in exponential phase on LB media

Subset of known regulon:

CcpA + SigA



Gene Categories

- Carbon metabolism (24)
- Uncharacterized (10)
- Proteins of unknown function (2)
- Coping with stress (2)
- Phosphoproteins (1)

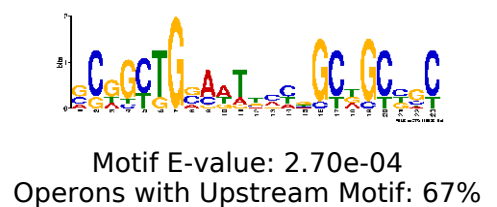
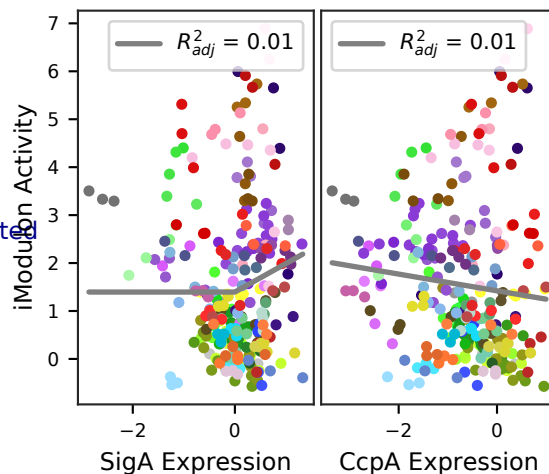
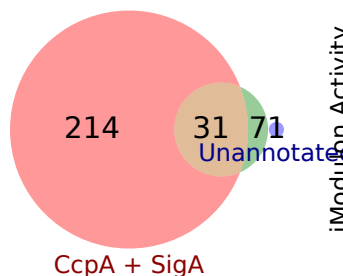
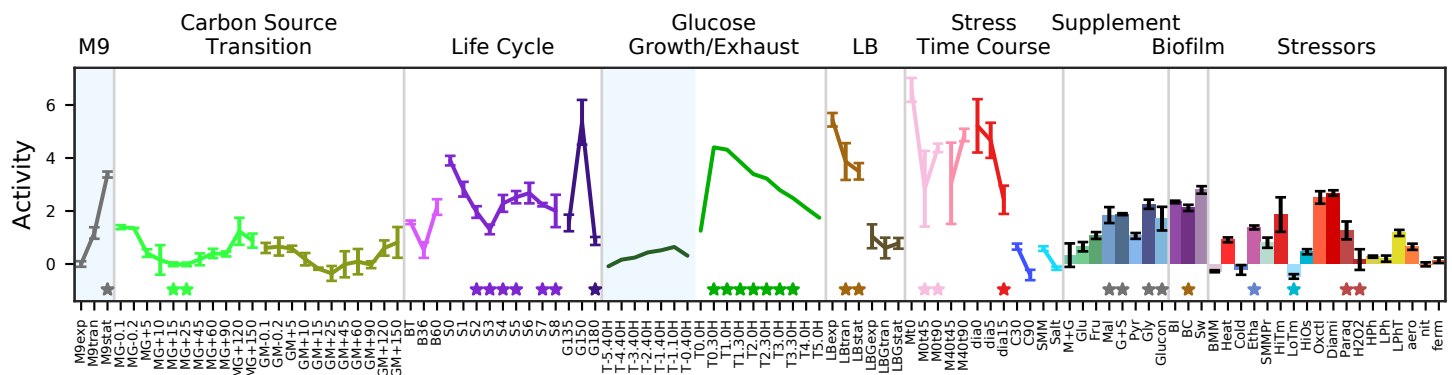
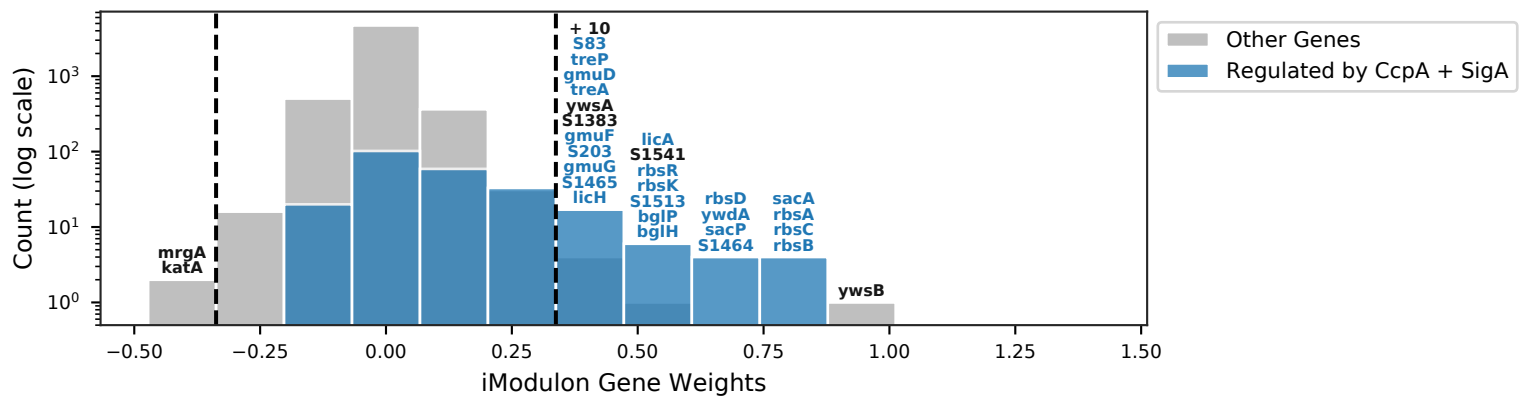


Figure 1: Genes regulated by CcpA and SigA

A Scatter plot showing iModulon Gene Weights (Y-axis, ranging from -0.50 to 1.00) versus Mean Expression (X-axis, ranging from -4 to 3). Data points are colored by Gene Categories: Carbon metabolism (38), Uncharacterized (30), Membrane proteins (7), Regulation of gene expression (2), Proteins of unknown function (2), Sporulation (1), Poorly characterized/ putative enzymes (1), Phosphoproteins (1), Lipid metabolism (1), Genetics (1), and Amino acid/ nitrogen metabolism (1).

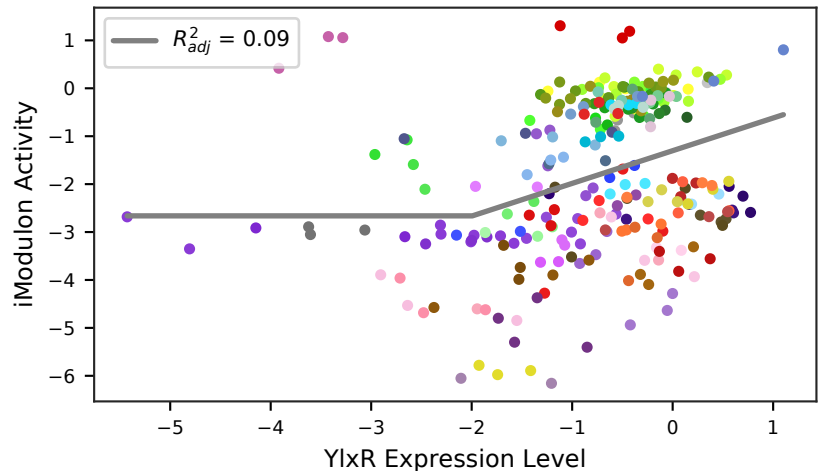
B Histogram showing the Count (log scale) of iModulon Gene Weights (X-axis, ranging from -0.5 to 2.0). The histogram is divided into three categories: Other Genes (grey), Regulated by CcpA + SigA (blue), and Regulated by CcpN (orange). Specific genes are labeled: ptsG, S505, S1302, cggR, glpF, melR, S108, sspH, ywcE, S321, S1470, gntR, cstA, gntK, + 48, + 2, msmX, yibP, S438, S345, S637, S346, rbsA, rbsK, S1098, S476, rbsR, ykoM, rbsD, dctP, S948, yeaA, yrbE, S950, gapB, and sr1.

C Line plot showing Activity (Y-axis, ranging from -2 to 6) versus Time Course (X-axis, showing various conditions: M9, Carbon Source Transition, Life Cycle, Glucose Growth/Exhaust, LB, Stress, Supplement, Biofilm, and Stressors). The plot shows activity levels for various genes across these conditions.

D Venn diagram showing the overlap of genes regulated by CcpA + SigA (red circle, 203 genes) and CcpN (blue circle, 16 genes). The overlap is 52 genes. The unannotated region is 17 genes.

E Scatter plots showing iModulon Activity (Y-axis, ranging from -2 to 6) versus CcpN (X-axis, ranging from -2.5 to 0.0), CcpA (X-axis, ranging from -2.5 to 0.0), and SigA (X-axis, ranging from -2.5 to 0.0). The plots show the relationship between iModulon Activity and the expression of CcpN, CcpA, and SigA. $R^2_{adj} = 0.28$ for CcpN, $R^2_{adj} = 0.16$ for CcpA, and $R^2_{adj} = 0.04$ for SigA.

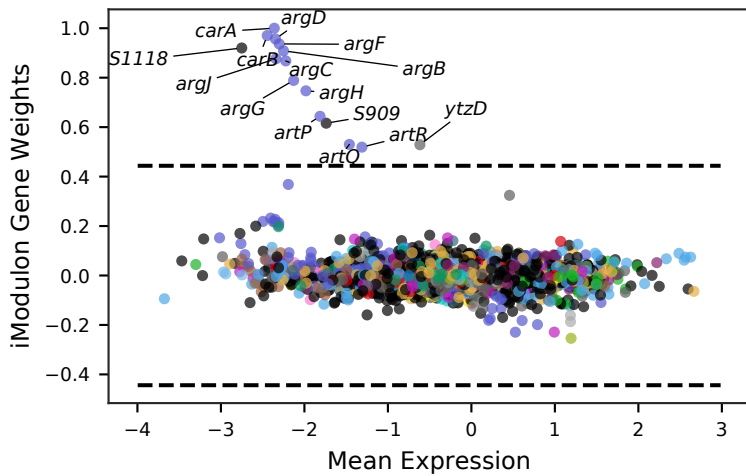
F Motif analysis showing the Motif E-value (8.20e-07) and the percentage of Operons with Upstream Motif (72%). The motif is shown as a sequence logo: ATGTAACGCTTCAAT.



12 - AhrC - Arginine

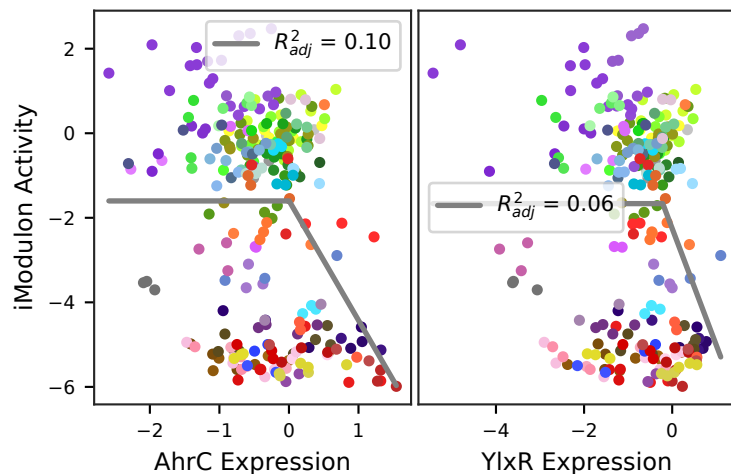
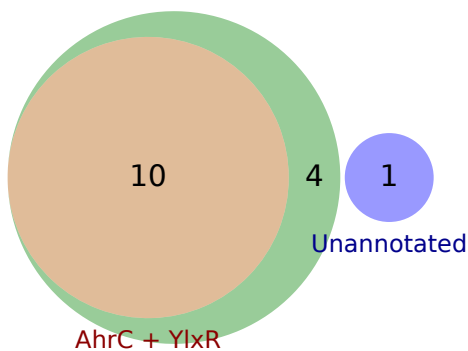
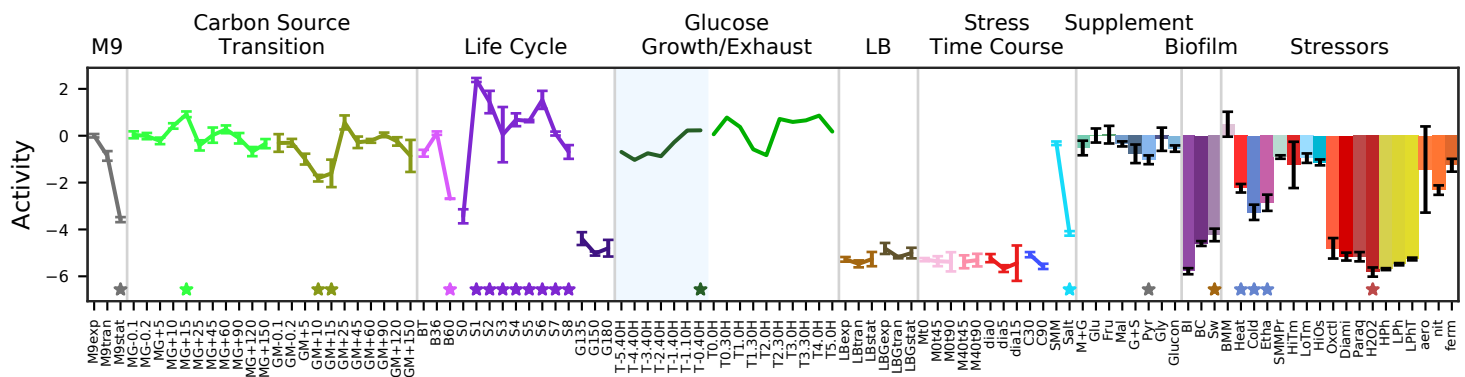
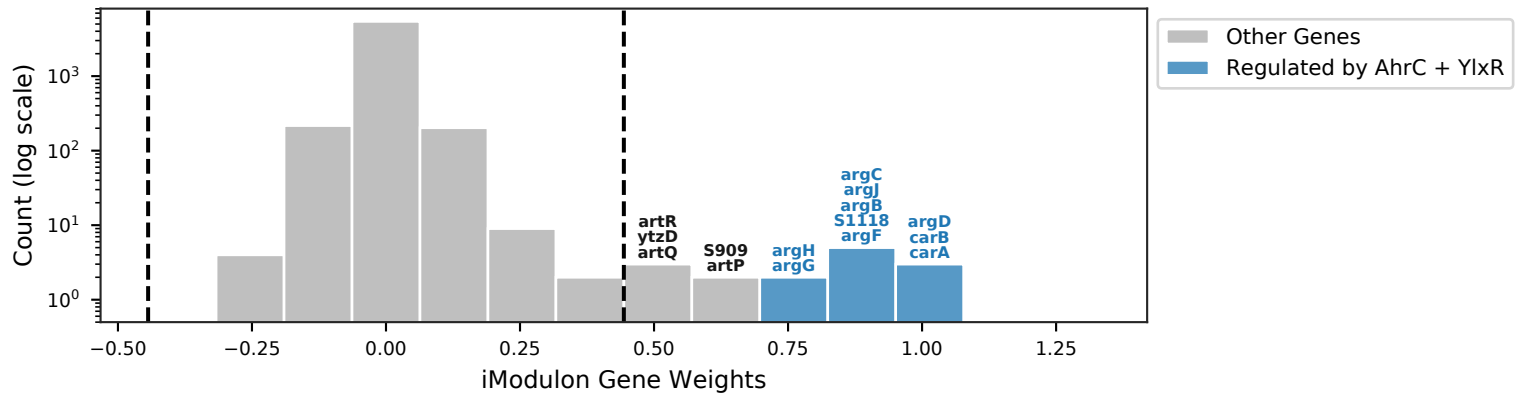
Biological Function:
Uptake and biosynthesis of arginine

Well-defined regulon:
AhrC + YlxR



Gene Categories

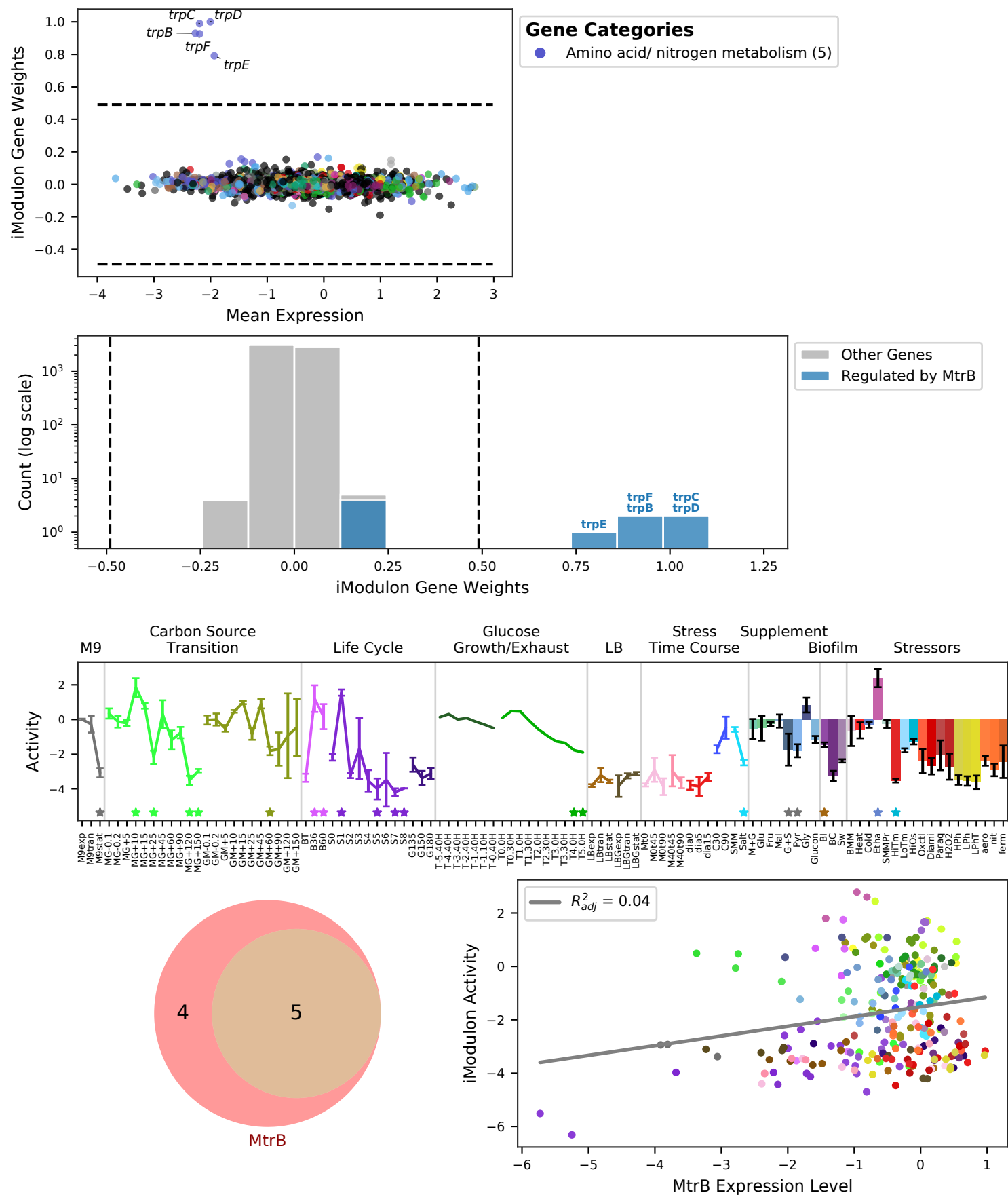
- Amino acid/ nitrogen metabolism (12)
- Uncharacterized (2)
- Proteins of unknown function (1)



13 - MtrB - Tryptophan

Biological Function:
Biosynthesis of tryptophan

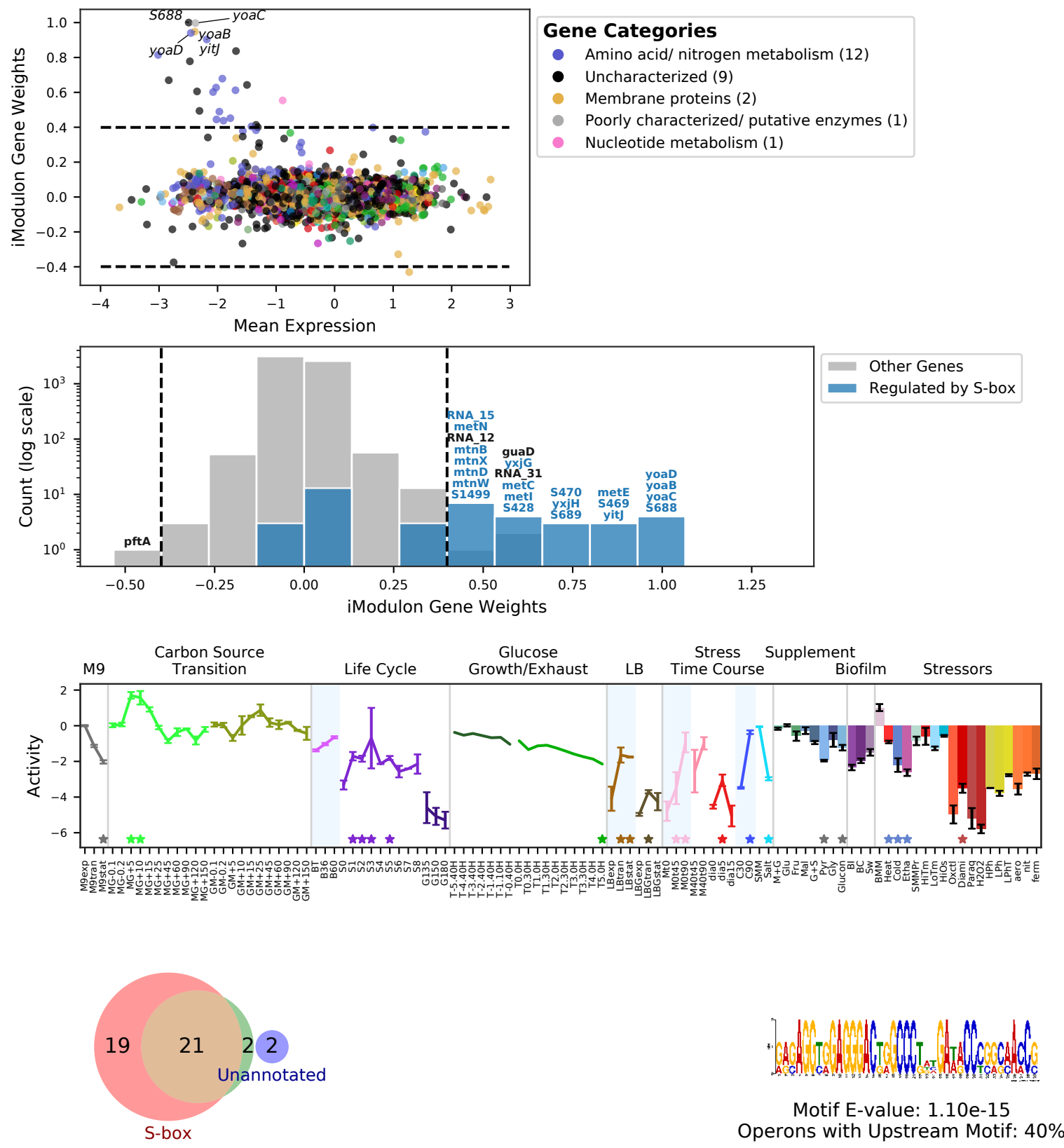
Subset (single operon) of known regulon:
MtrB



14 - S-Box - Methionine

Biological Function:
Methionine salvage and biosynthesis

Subset of known regulon:
S-box



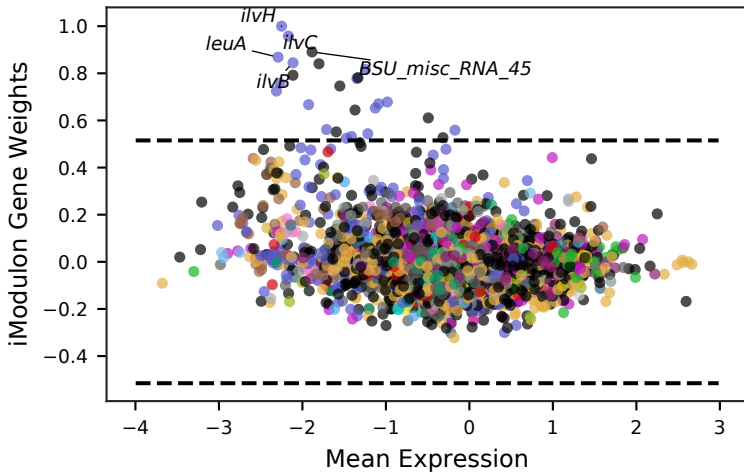
15 - TnrA + CodY - Leucine, Methionine, and Threonine

Biological Function:

Synthesis and salvage of leucine, methionine, threonine

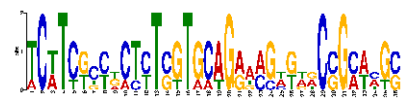
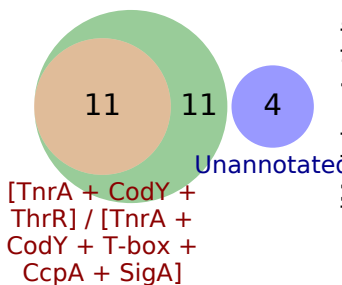
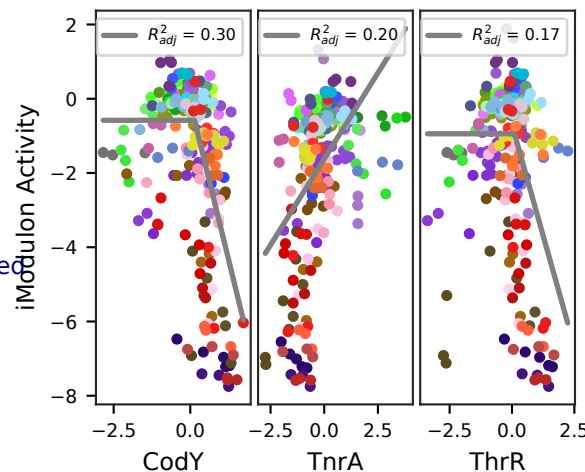
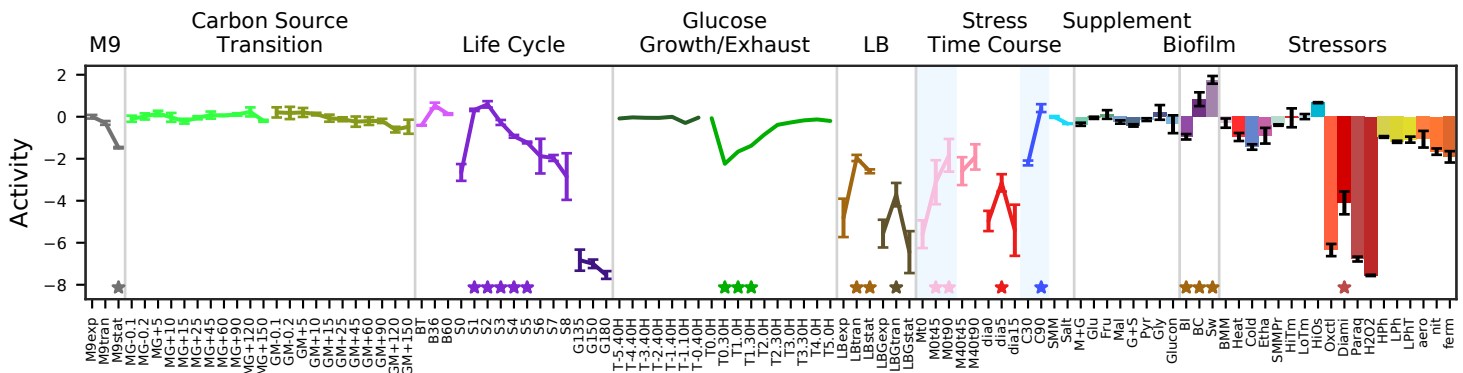
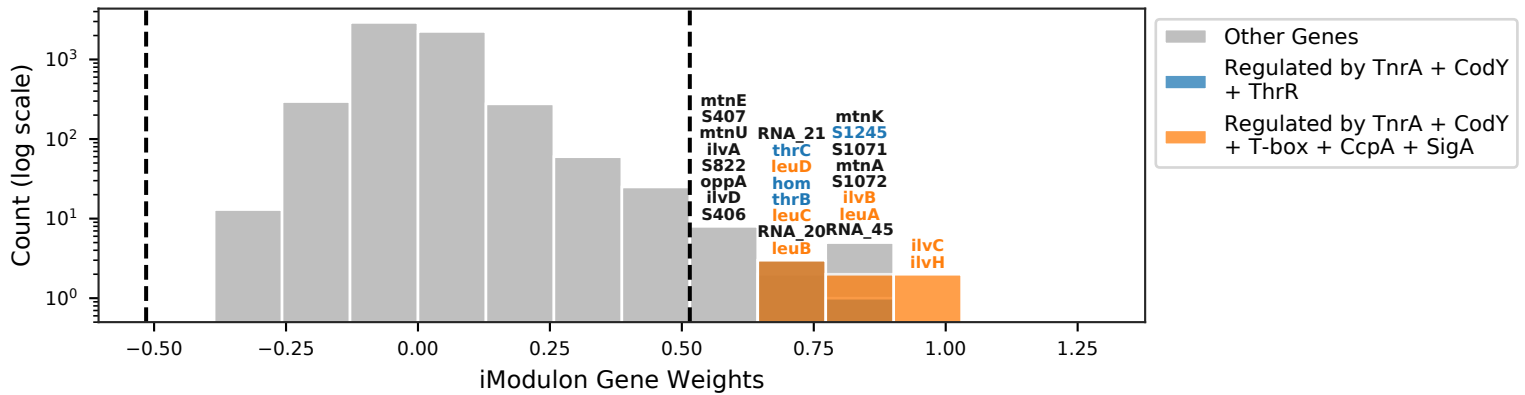
Contains unknown genes and known regulon:

[TnrA + CodY + ThrR] / [TnrA + CodY + T-box + CcpA + SigA]



Gene Categories

- Amino acid/ nitrogen metabolism (17)
- Uncharacterized (9)



Motif E-value: 2.70e-05
Operons with Upstream Motif: 62%

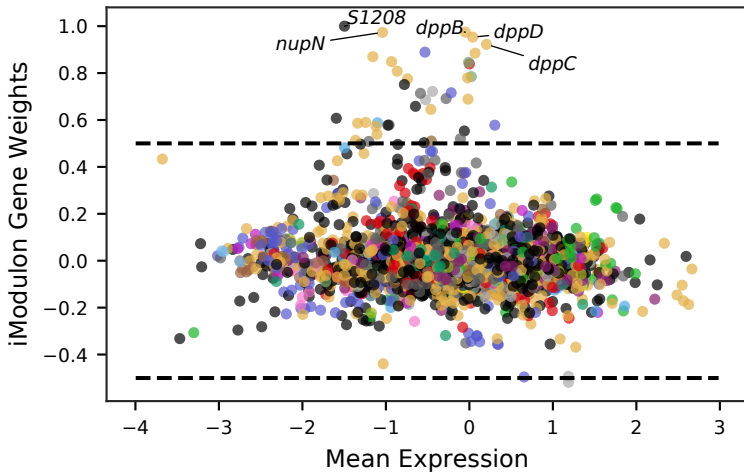
16 - CodY - BCAA Limitation

Biological Function:

Uptake of di-/oligopeptides, uptake of guanosine, cell wall metabolism

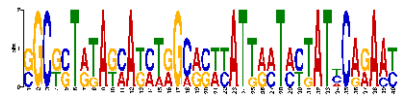
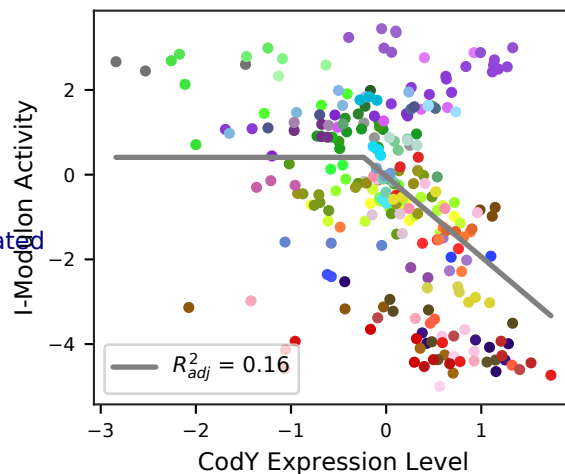
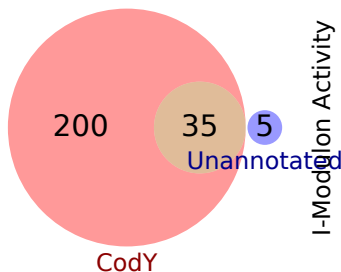
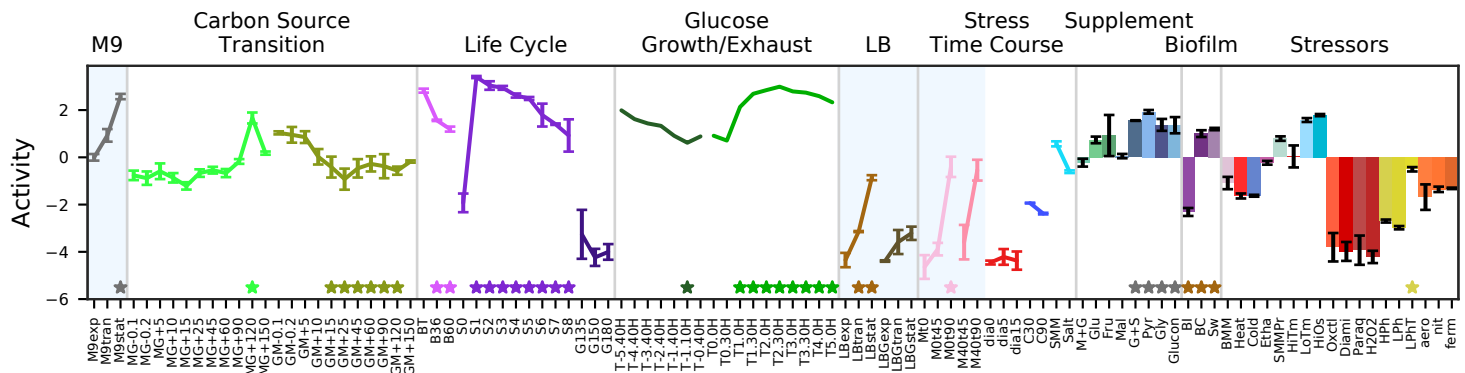
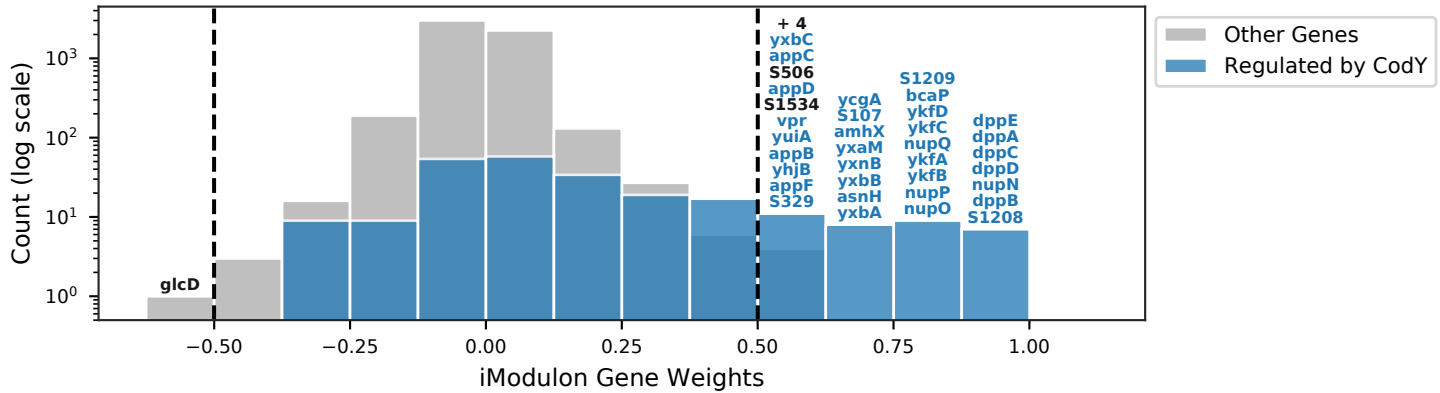
Subset of known regulon:

CodY



Gene Categories

- Membrane proteins (17)
- Uncharacterized (7)
- Proteins of unknown function (5)
- Poorly characterized/ putative enzymes (3)
- Amino acid/ nitrogen metabolism (3)
- Cell envelope and cell division (2)
- Transporters (1)
- Efp-dependent proteins (1)
- Coping with stress (1)

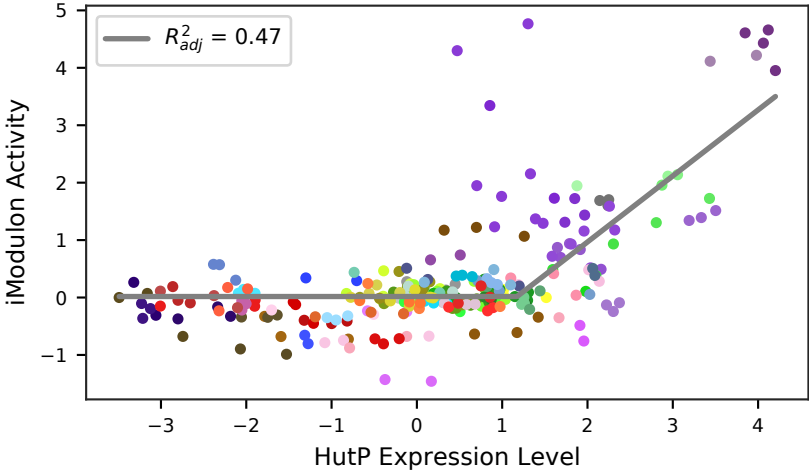
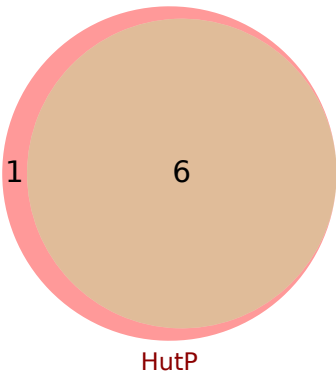
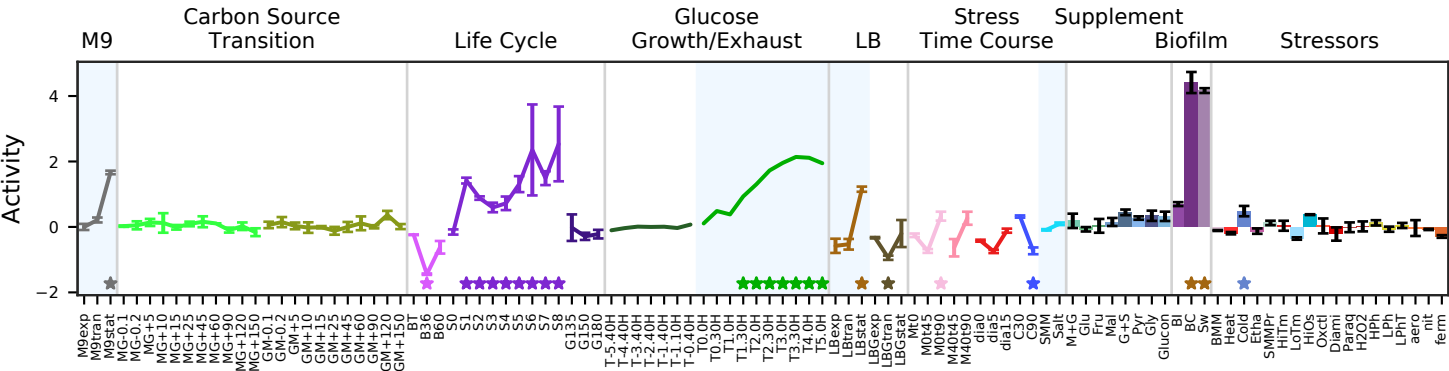
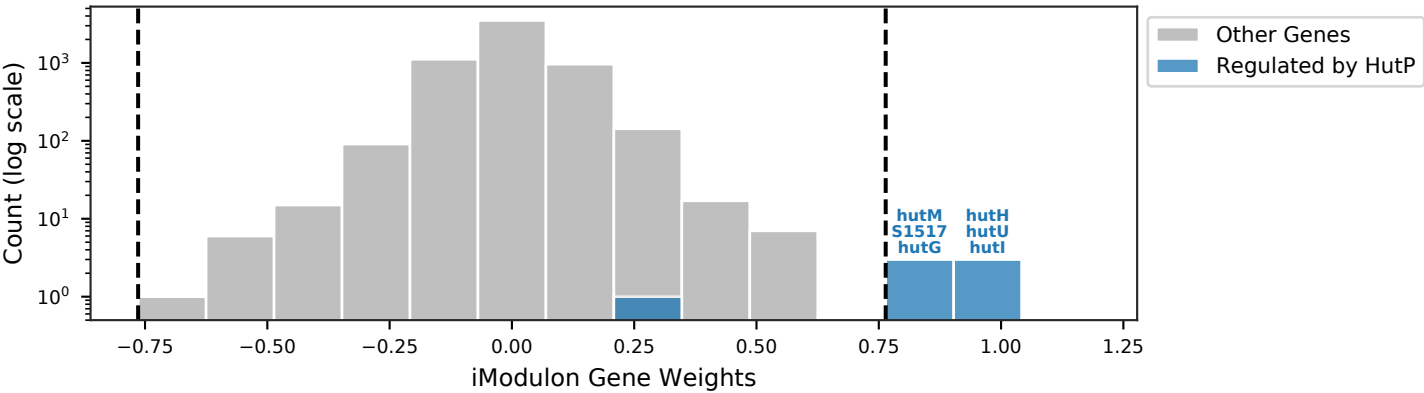
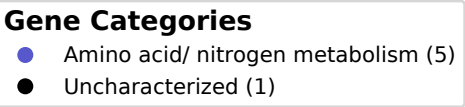
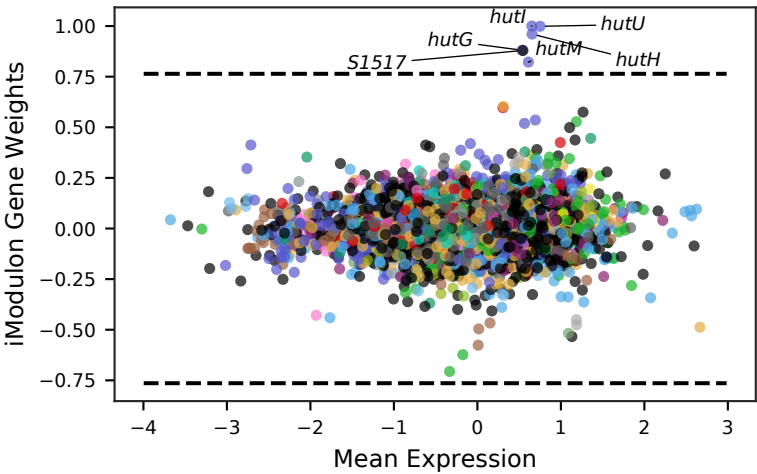


Motif E-value: 2.90e-09
Operons with Upstream Motif: 35%

17 - HutP - Histidine Utilization

Biological Function:
Histidine uptake and utilization

Well-defined regulon:
HutP



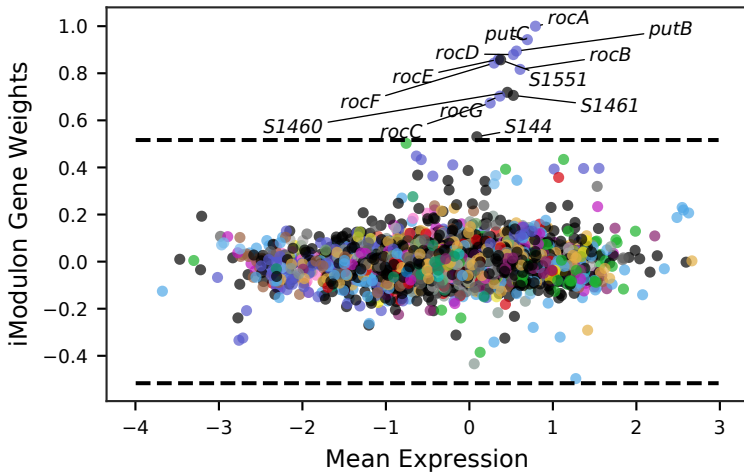
18 - RocR / PutR - Arginine and Proline Utilization

Biological Function:

Utilization of arginine, ornithine, citrulline and proline as carbon and energy sources

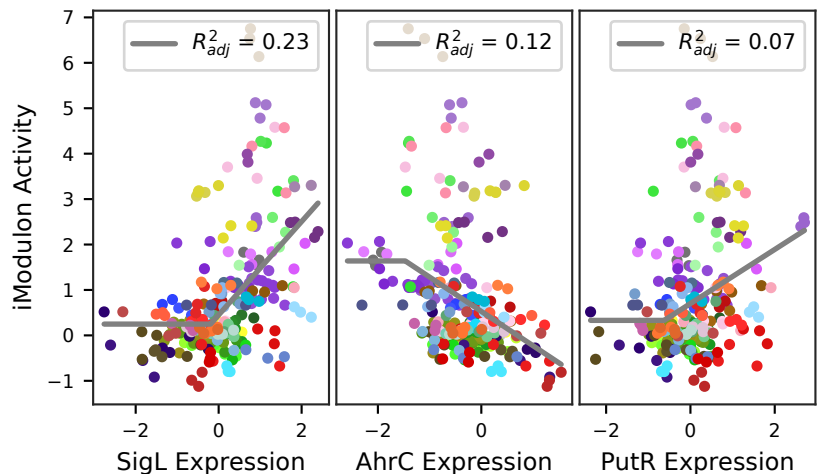
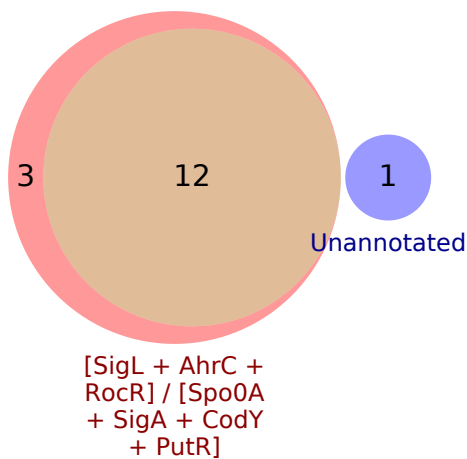
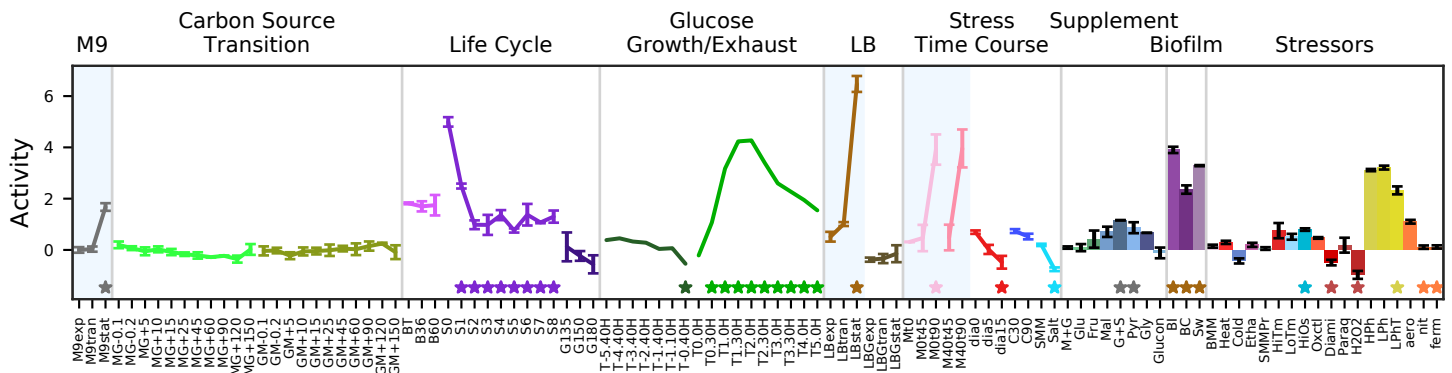
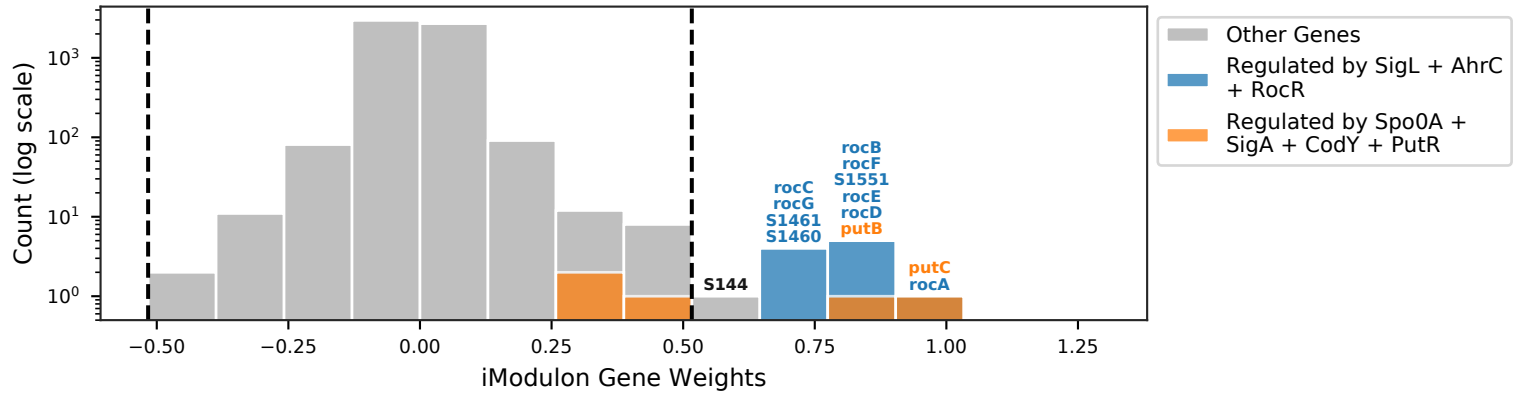
Well-defined regulon:

[SigL + AhrC + RocR] / [Spo0A + SigA + CodY + PutR]



Gene Categories

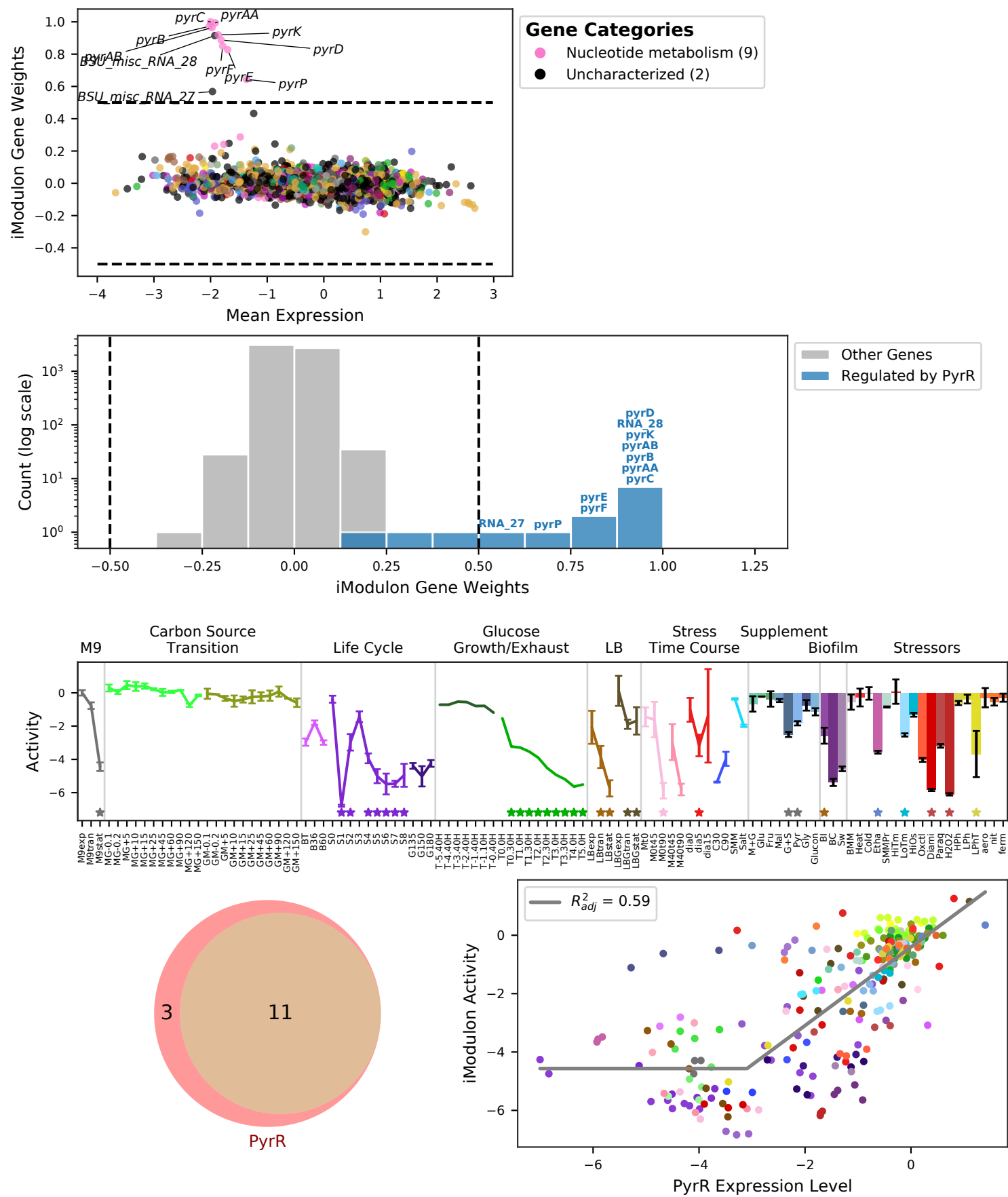
- Amino acid/ nitrogen metabolism (9)
- Uncharacterized (4)



19 - PyrR - Pyrimidines

Biological Function:
Synthesis of pyrimidines

Well-defined regulon:
PyrR



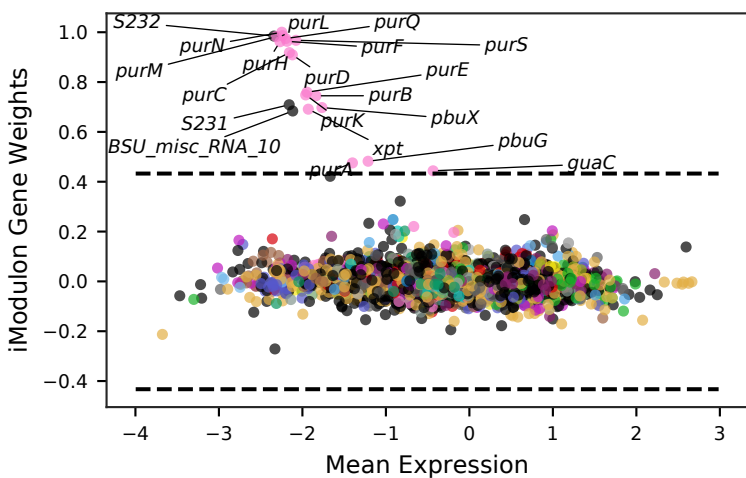
20 - PurR - Purines

Biological Function:

Synthesis of purine, xanthine and guanine uptake and conversion into purines

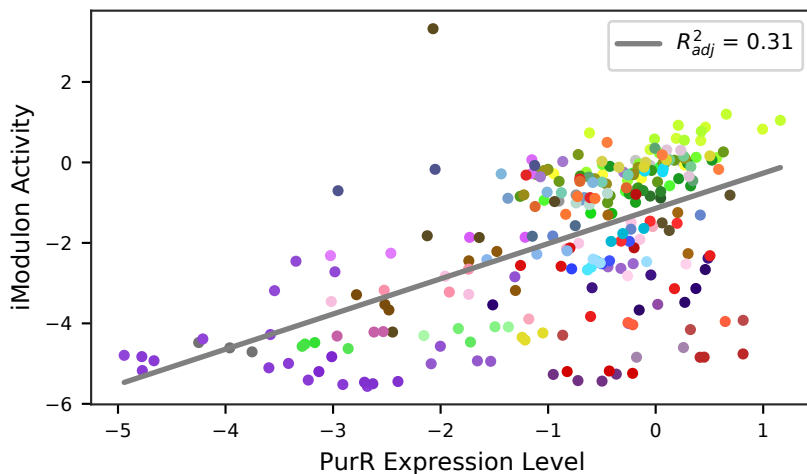
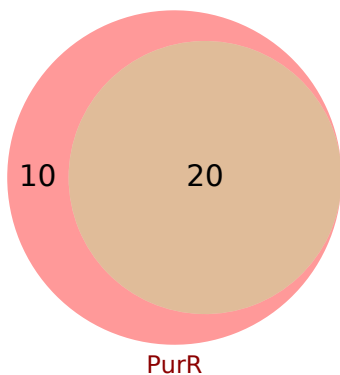
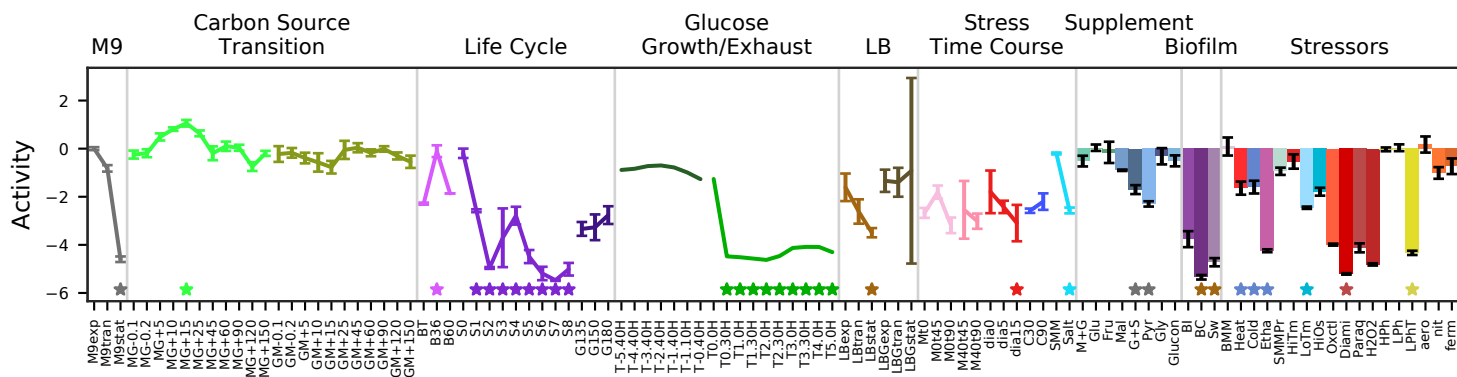
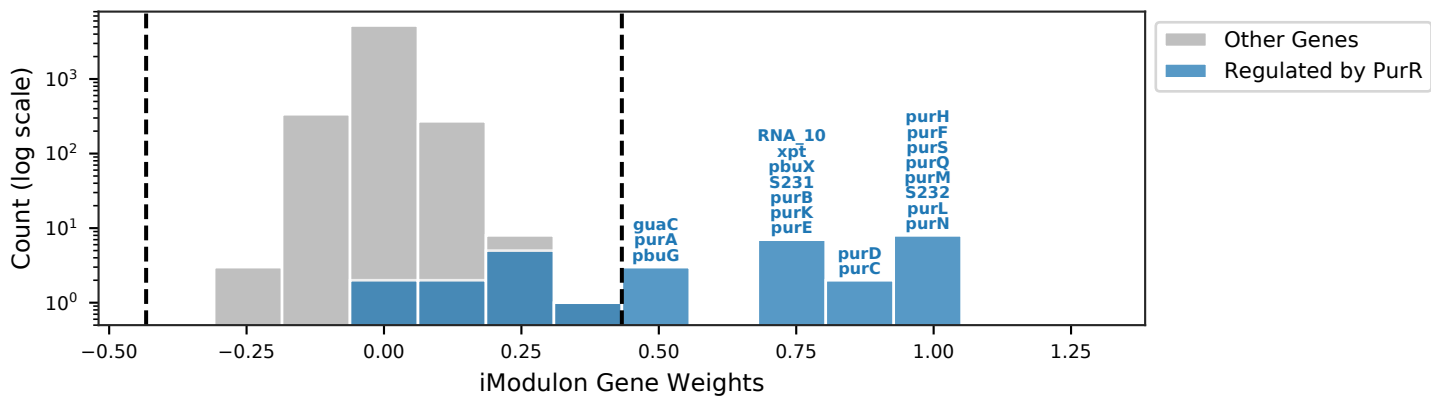
Well-defined regulon:

PurR



Gene Categories

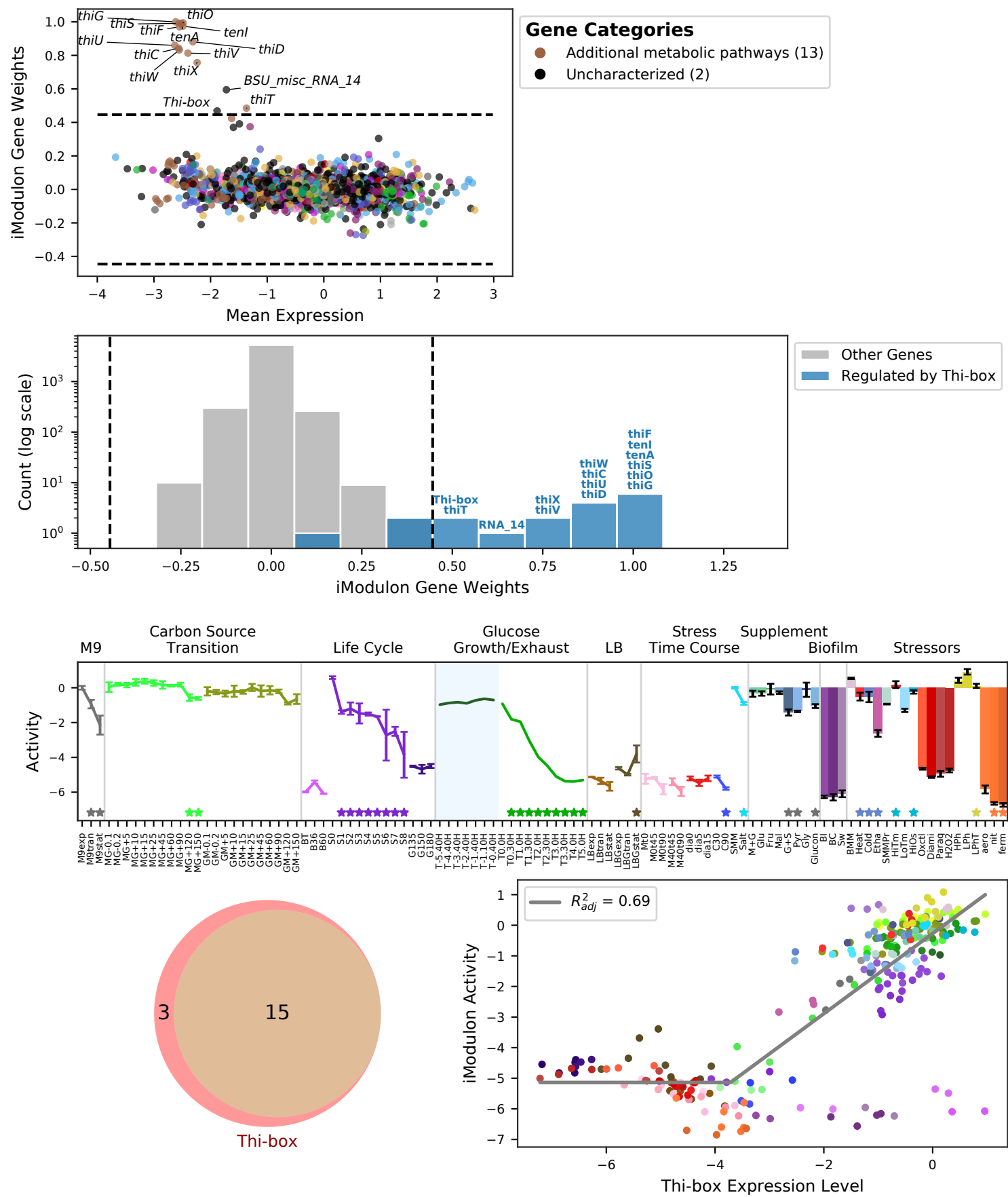
- Nucleotide metabolism (17)
- Uncharacterized (3)



21 - Thi-Box - Thiamine

Biological Function:
Synthesis and uptake of thiamine

Well-defined regulon:
Thi-box



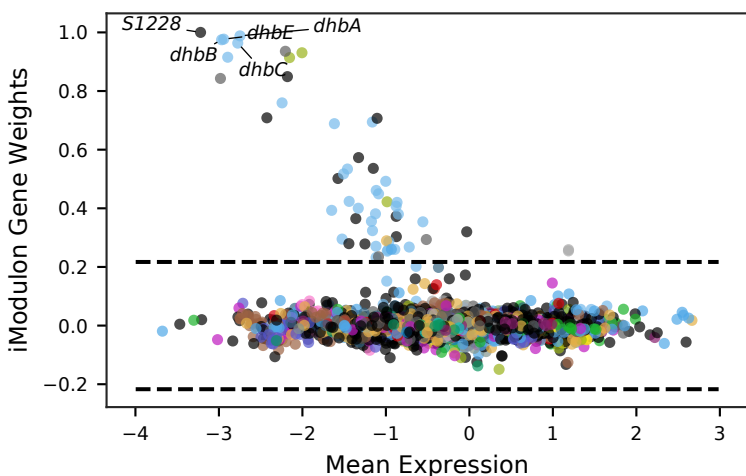
23 - Fur - Iron Limitation

Biological Function:

Production and transport of siderophores for iron chelation, replacement of ferredoxins in the ETC with flavodoxins, RNA chaperones for iron-limited conditions, heme degradation

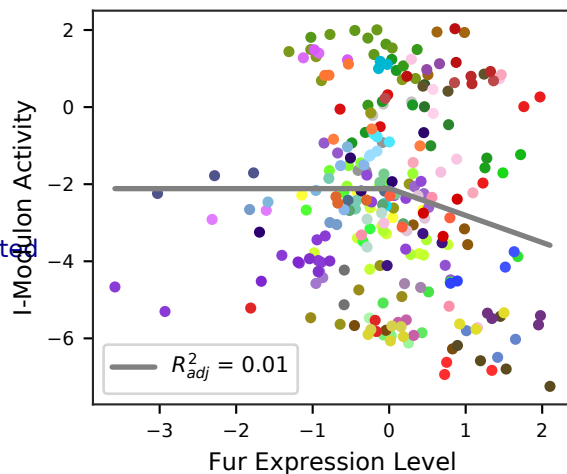
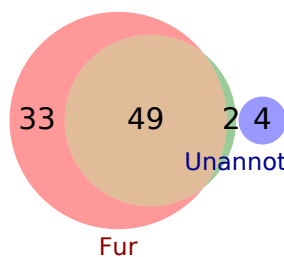
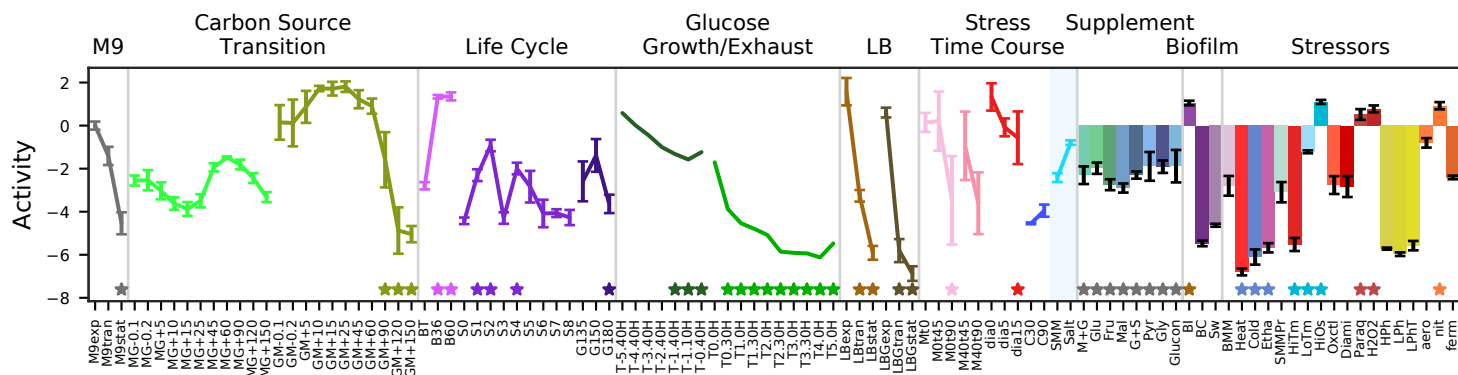
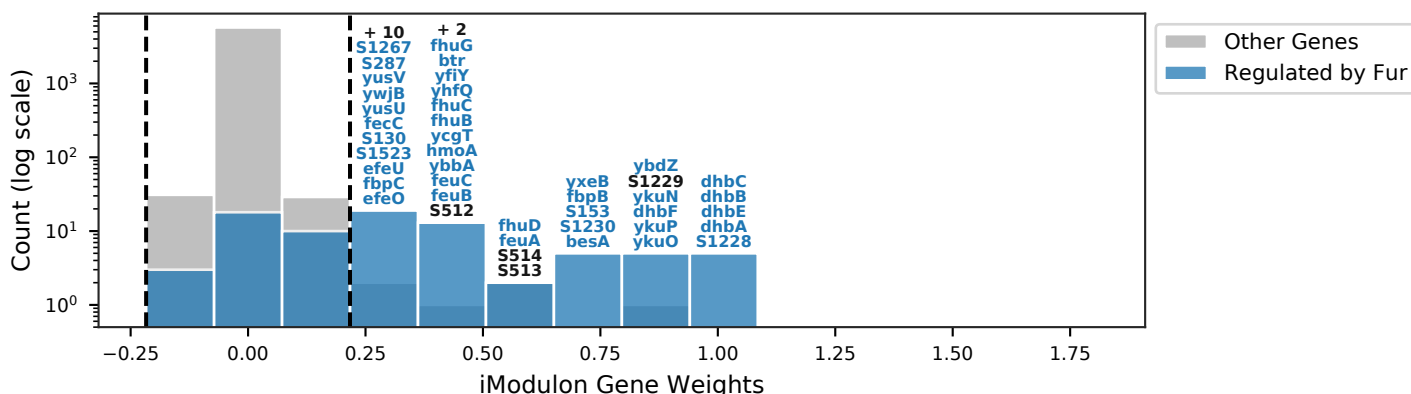
Subset of known regulon:

Fur

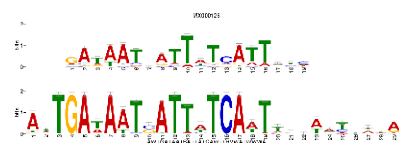


Gene Categories

- Homeostasis (31)
- Uncharacterized (13)
- Proteins of unknown function (4)
- Electron transport and ATP synthesis (3)
- Poorly characterized/ putative enzymes (2)
- Transporters (1)
- Membrane proteins (1)



Motif E-value: 1.20e-66
Operons with Upstream Motif: 78%



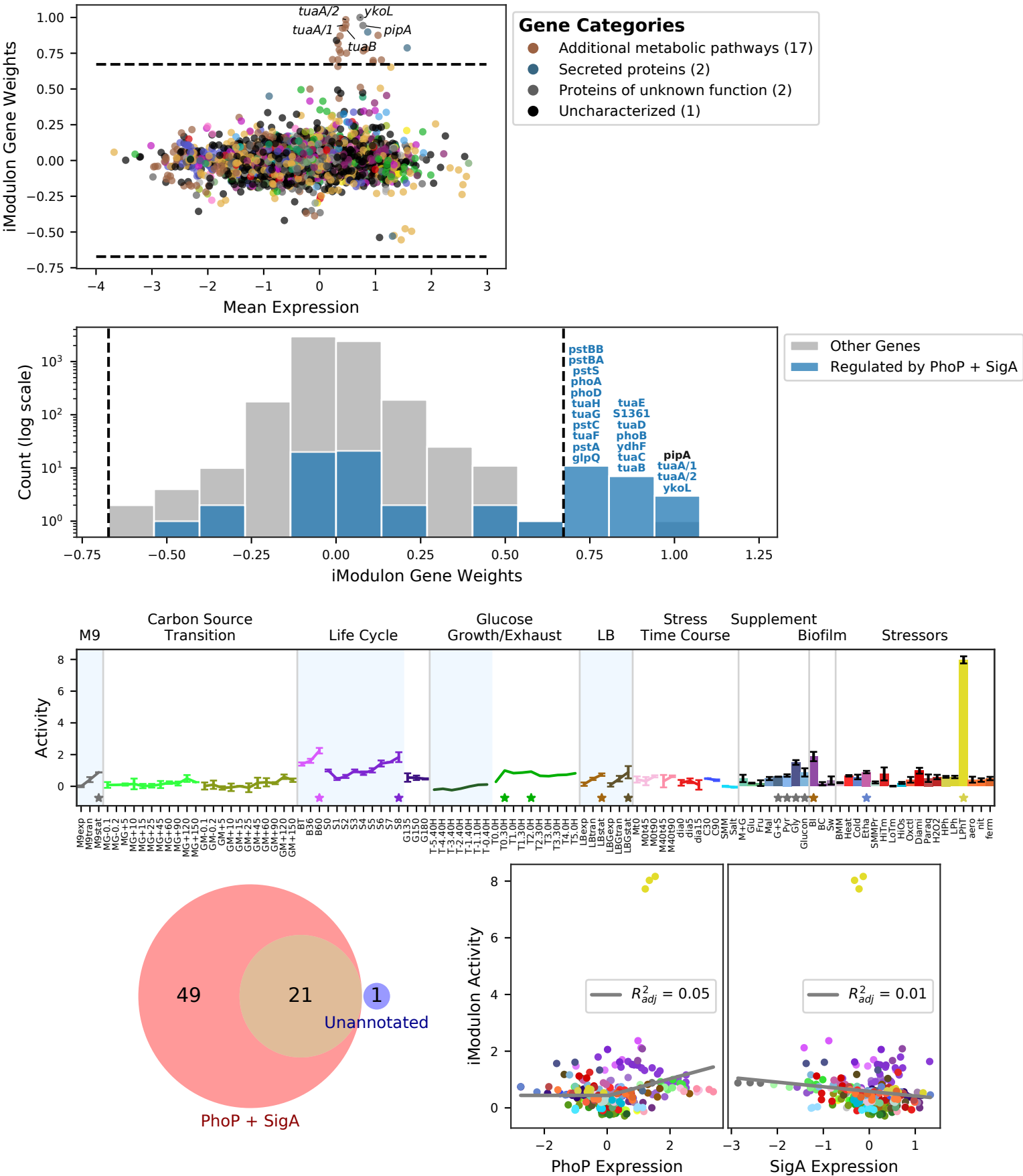
Motif similar to Fur -
E. coli (E = 2.47e-05)

Figure 2 consists of two side-by-side scatter plots. The left plot shows iModulon Activity (y-axis, -1 to 4) versus SigA Expression (x-axis, -3 to 1). A grey regression line indicates a positive correlation, with a legend showing $R^2_{adj} = 0.02$. The right plot shows iModulon Activity (y-axis, -1 to 4) versus PhoP Expression (x-axis, -2 to 2). A horizontal grey regression line indicates no correlation, with a legend showing $R^2_{adj} = 0.00$. Both plots feature a dense cloud of multi-colored data points.

25 - PhoP-2 - Phosphate Limitation 2

Biological Function:
Degradation of wall teichoic acid to salvage phosphate, synthesis of teichuronic acid to replace wall, high-affinity phosphate uptake.

Subset of known regulon:
PhoP + SigA



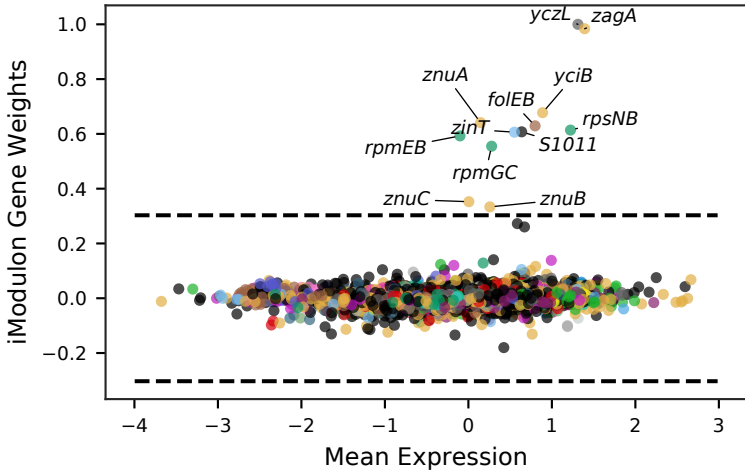
26 - Zur - Zinc Limitation

Biological Function:

Zinc uptake, zinc metallochaperones, alternatives to zinc-containing proteins

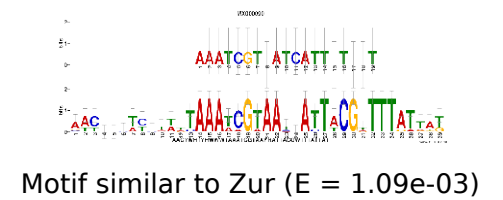
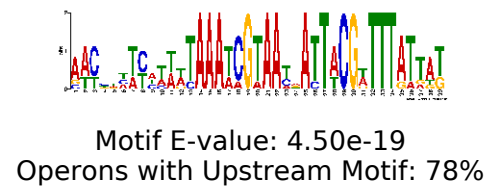
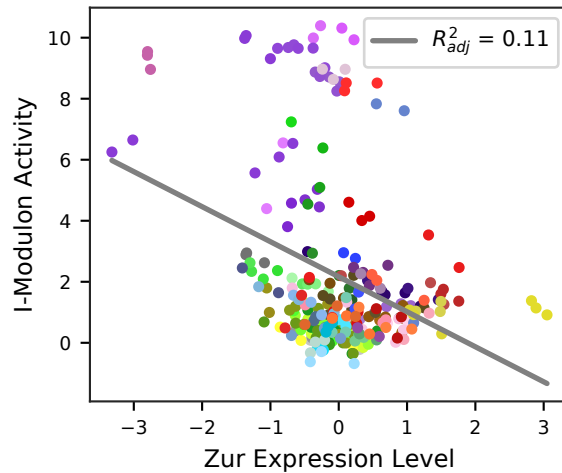
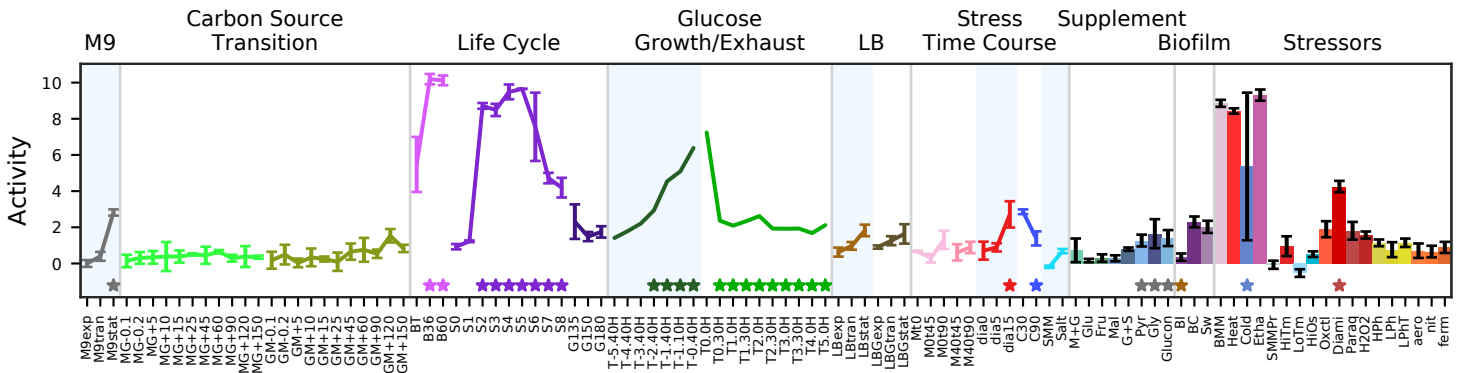
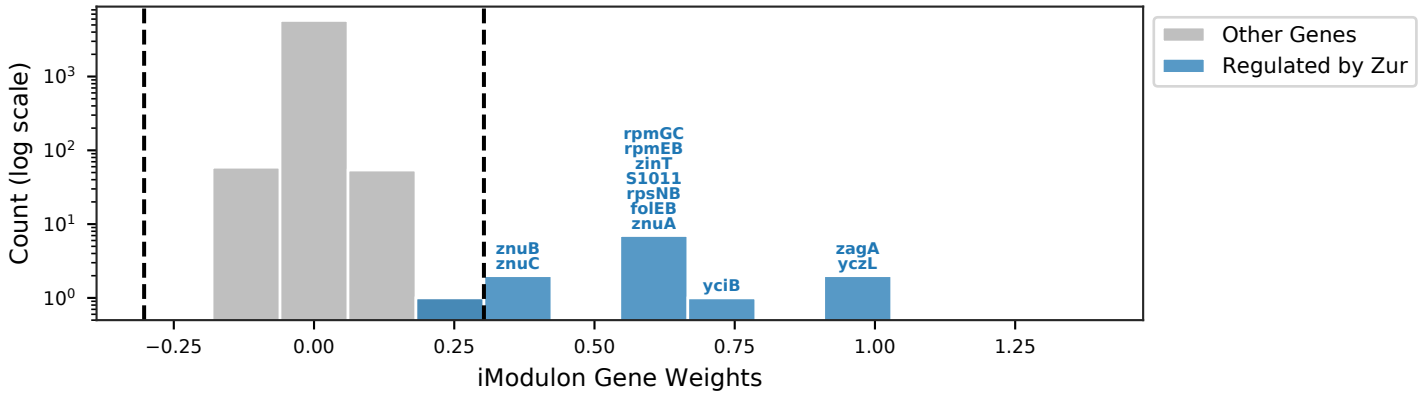
Well-defined regulon:

Zur



Gene Categories

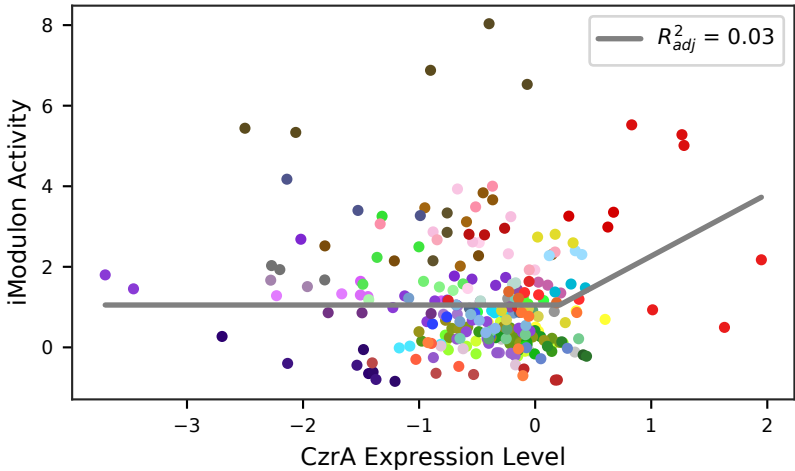
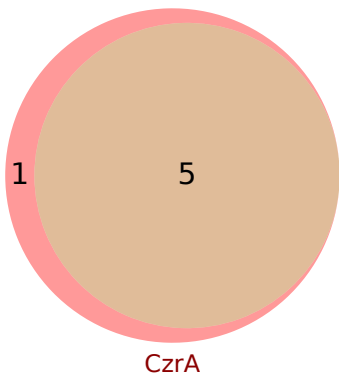
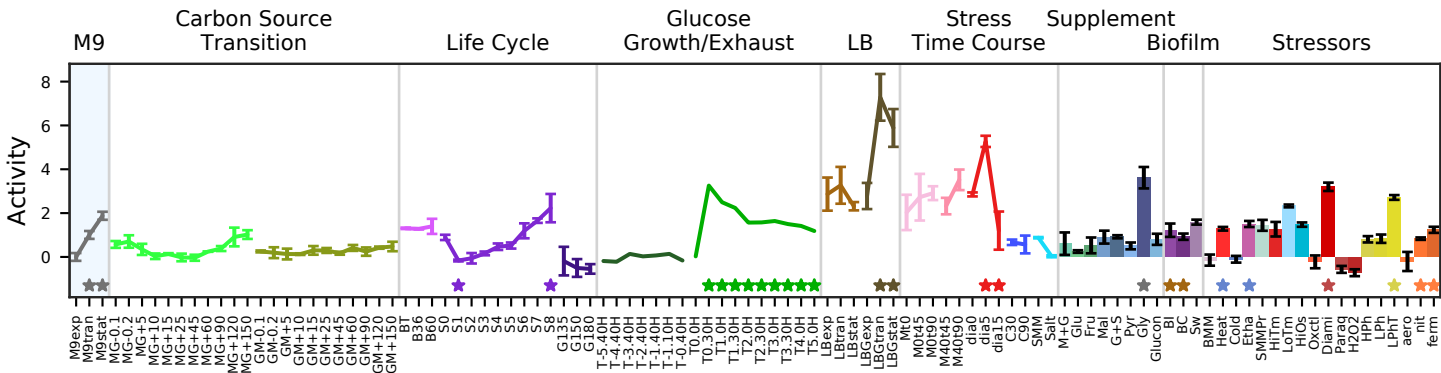
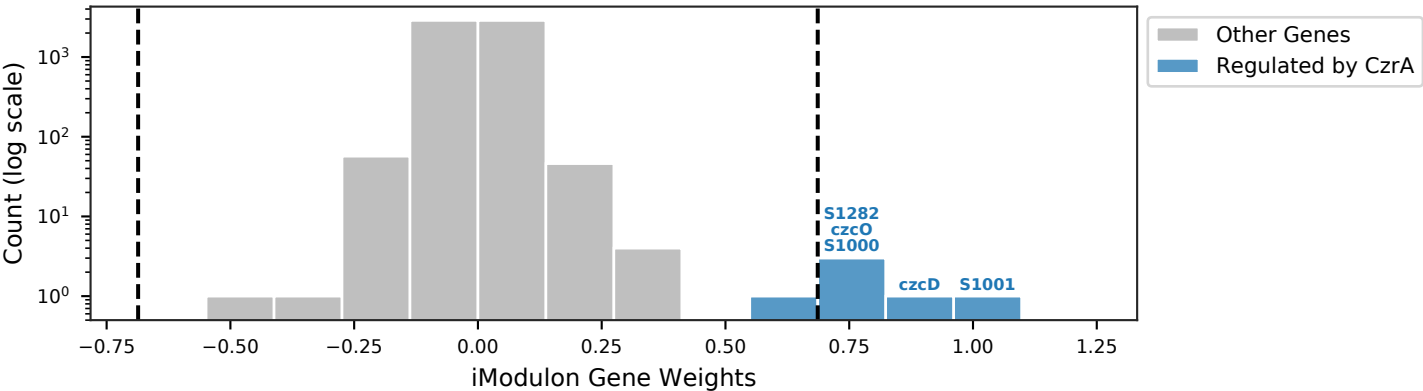
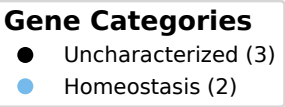
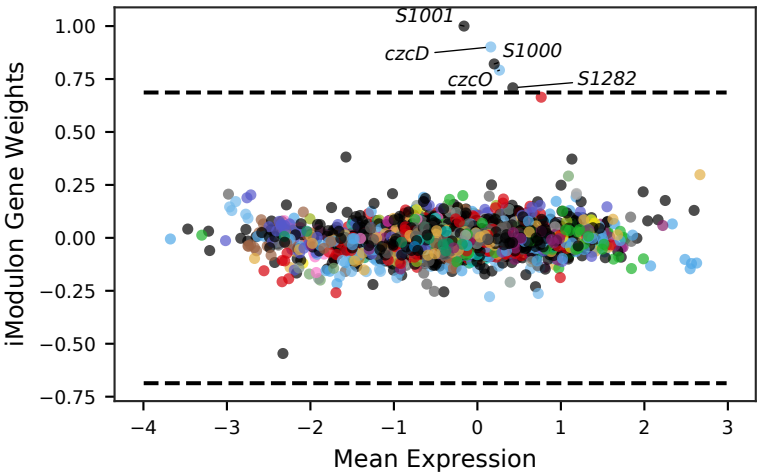
- Membrane proteins (5)
- Protein synthesis, modification and degradation (3)
- Uncharacterized (1)
- Proteins of unknown function (1)
- Homeostasis (1)
- Additional metabolic pathways (1)



27 - CzcA - Toxic Cation Export

Biological Function:
Resistance to Zn, Cu, Co, Ni, and Cd

Well-defined regulon:
CzcA



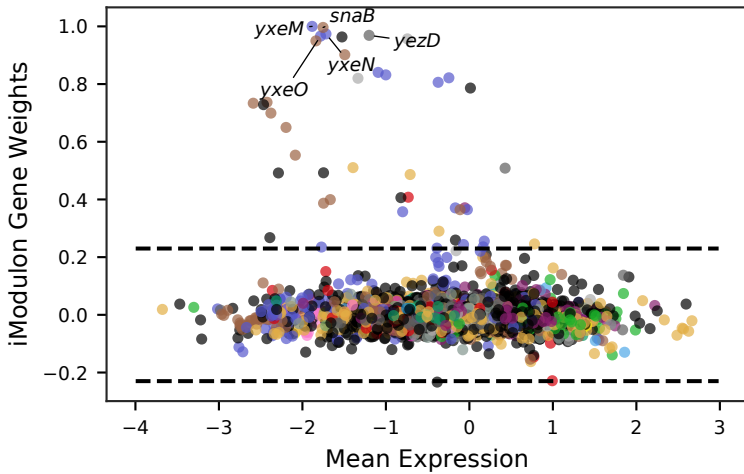
28 - CymR - Sulfur

Biological Function:

Sulfur metabolism in response to oxidative stress. Utilization and detoxification of S-(2-succino)cysteine, methionine-cysteine conversion, siroheme biosynthesis

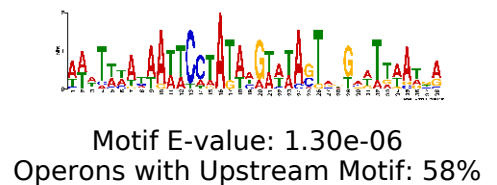
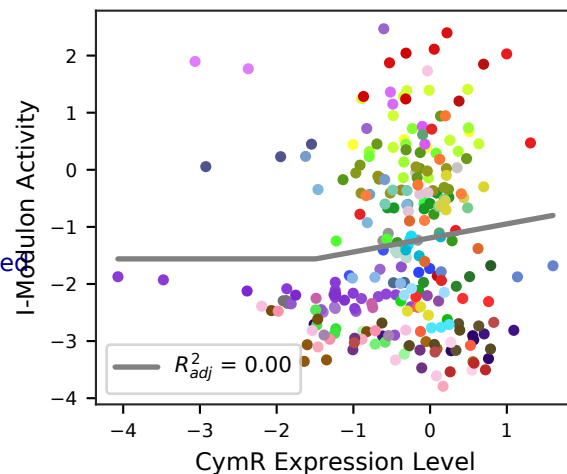
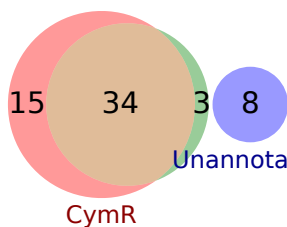
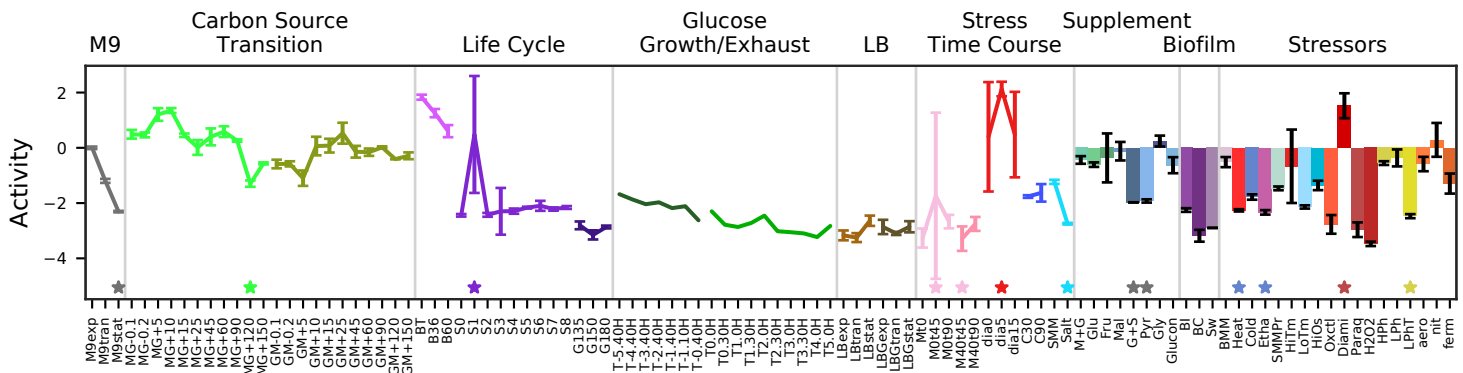
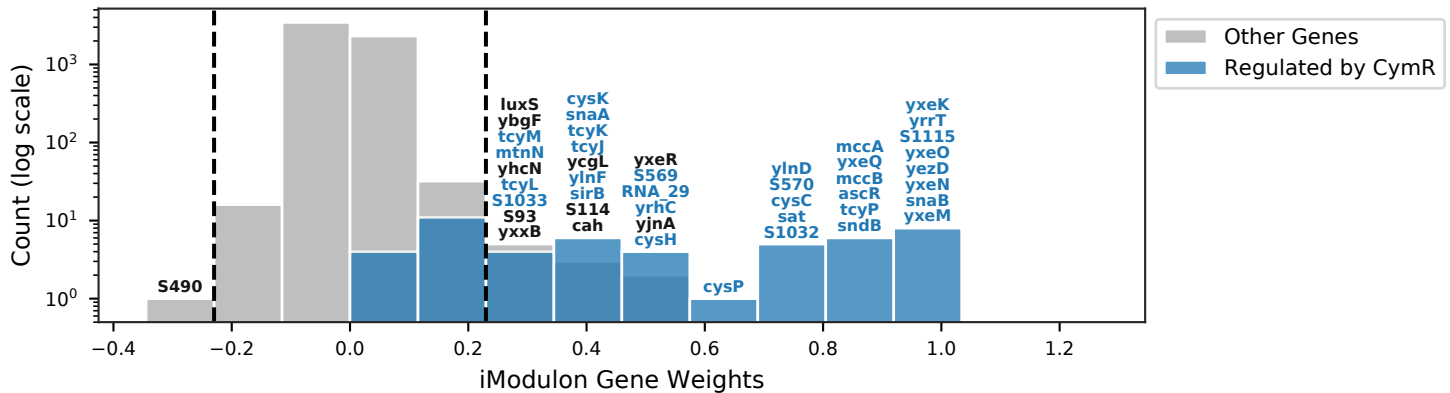
Well-defined regulon:

CymR

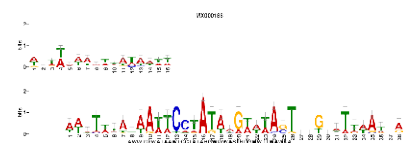


Gene Categories

- Amino acid/ nitrogen metabolism (15)
- Additional metabolic pathways (11)
- Uncharacterized (9)
- Membrane proteins (4)
- Proteins of unknown function (2)
- Poorly characterized/ putative enzymes (2)
- Sporulation (1)
- Coping with stress (1)



Motif E-value: 1.30e-06
Operons with Upstream Motif: 58%

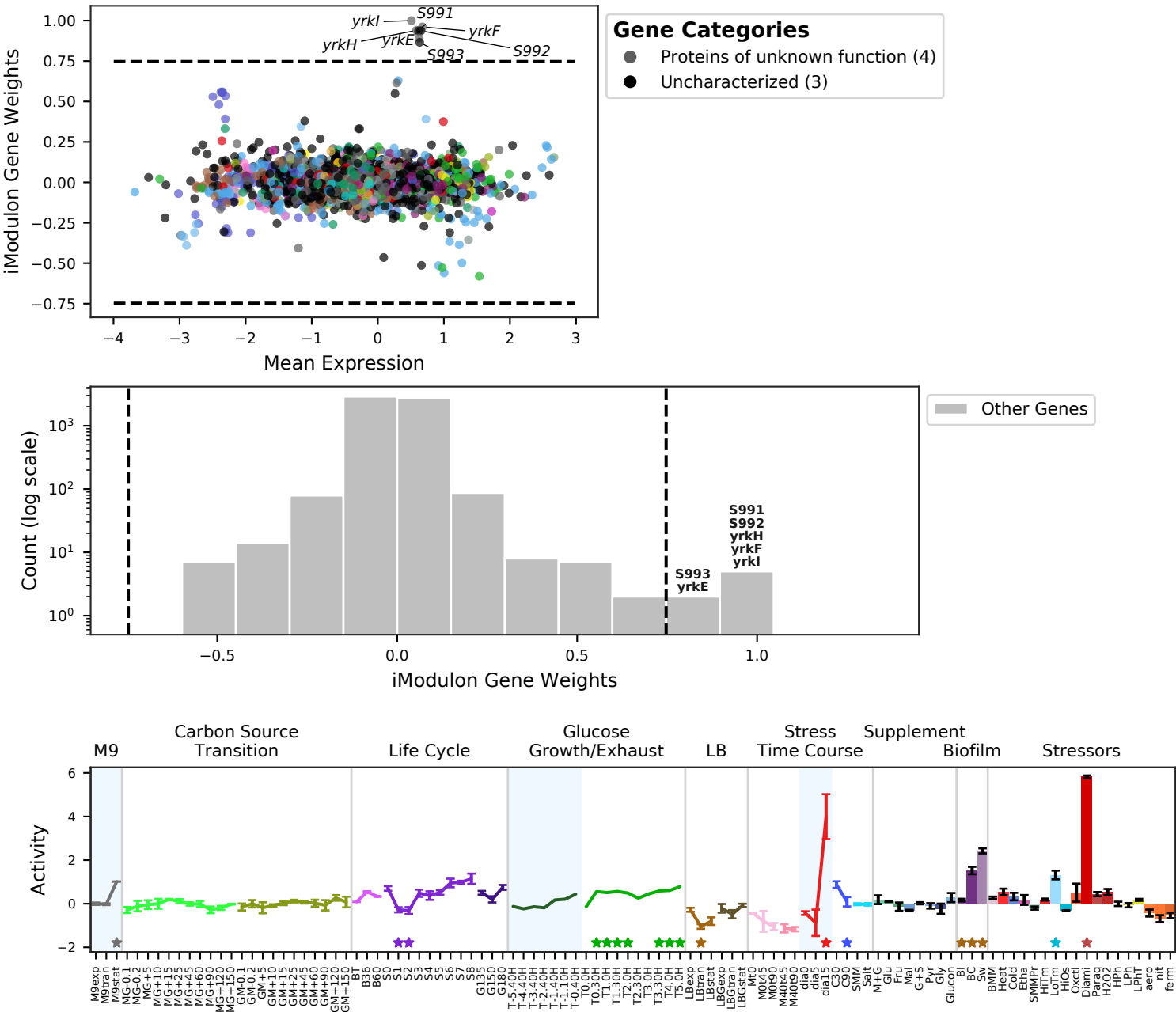


Motif similar to SarA -
S. aureus (E = 2.84e-04)

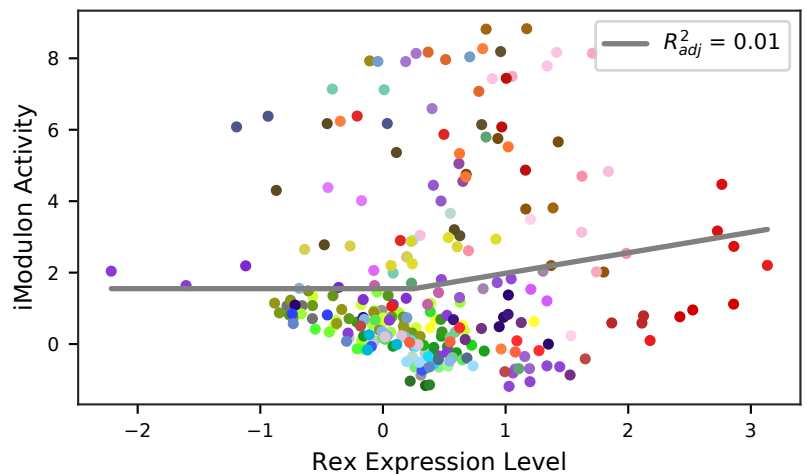
29 - Yrk - Putative Sulfur Carriers

Biological Function:
Putative sulfur carriers. High activity under diamide stress

No known regulator



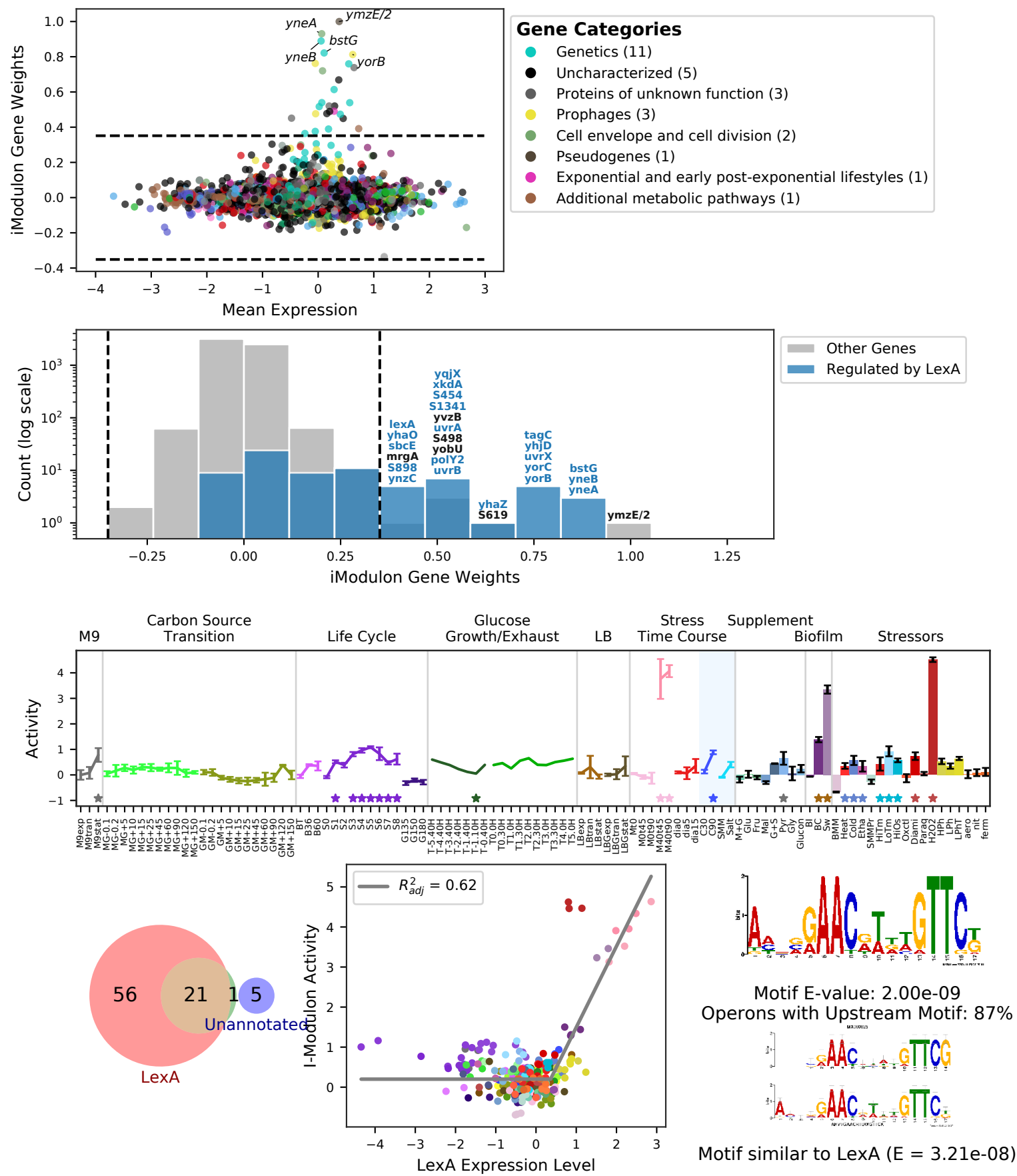
Motif E-value: 9.80e-04
Operons with Upstream Motif: 82%



33 - LexA - DNA Repair

Biological Function:
SOS response for DNA protection and repair

Subset of known regulon:
LexA



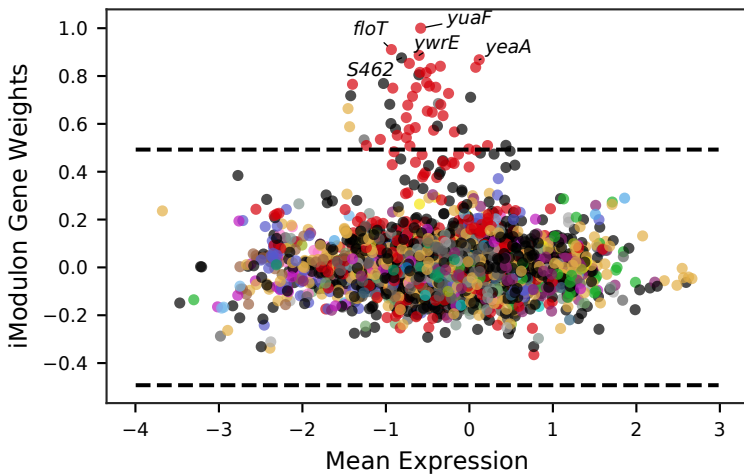
34 - SigW - Cell Wall Stress

Biological Function:

Adaptation to membrane active agents such as cefuroxime, antimicrobials from *B. amyloliquefaciens*, *sdpC*, and nisin. Control of membrane fluidity. Contains many unknown proteins.

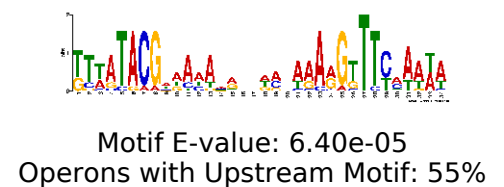
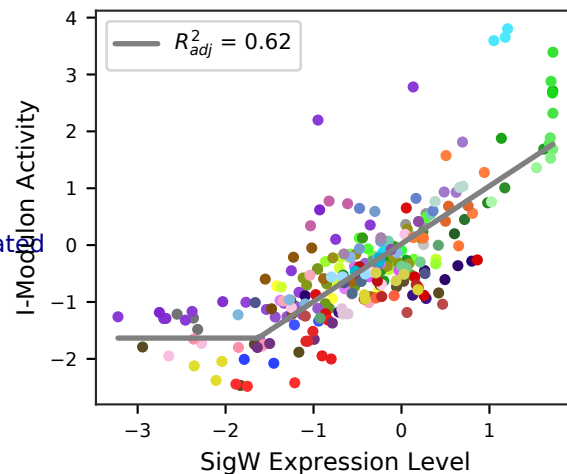
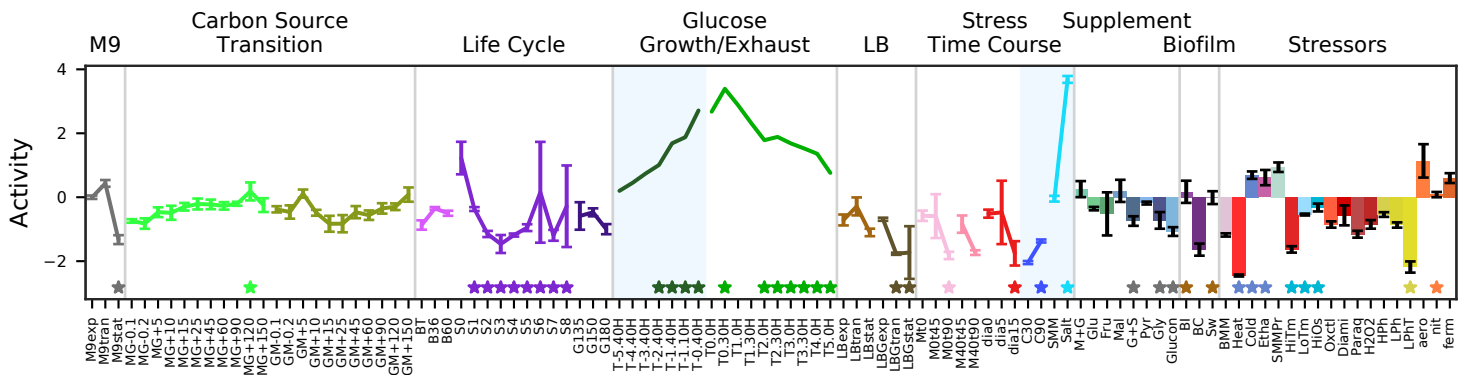
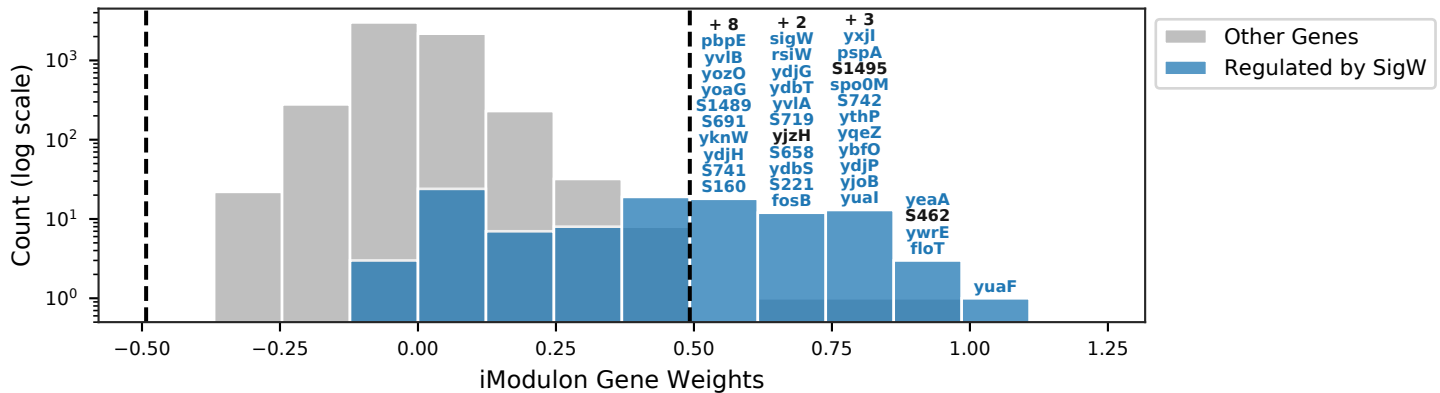
Subset of known regulon:

SigW

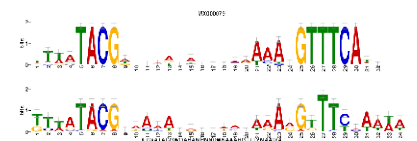


Gene Categories

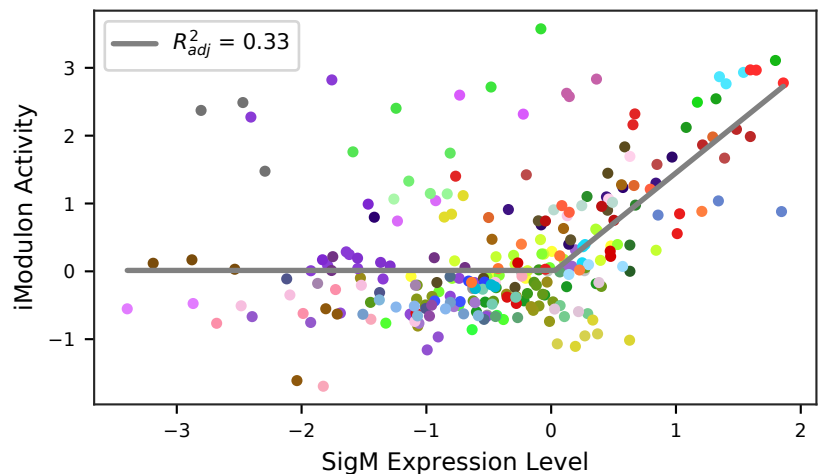
- Coping with stress (35)
- Uncharacterized (11)
- Proteins of unknown function (2)
- Membrane proteins (2)



Motif E-value: 6.40e-05
Operons with Upstream Motif: 55%



Motif similar to SigW (E = 1.51e-15)

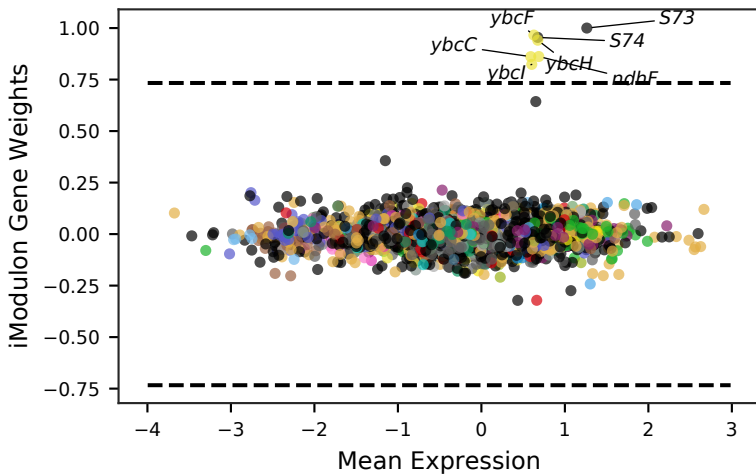


36 - Ybc - Uncharacterized Operon

Biological Function:

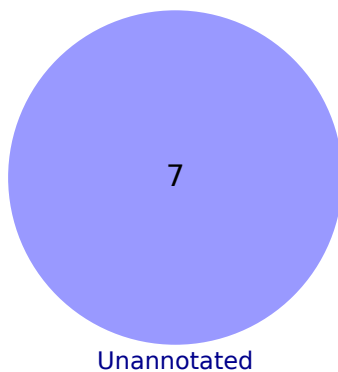
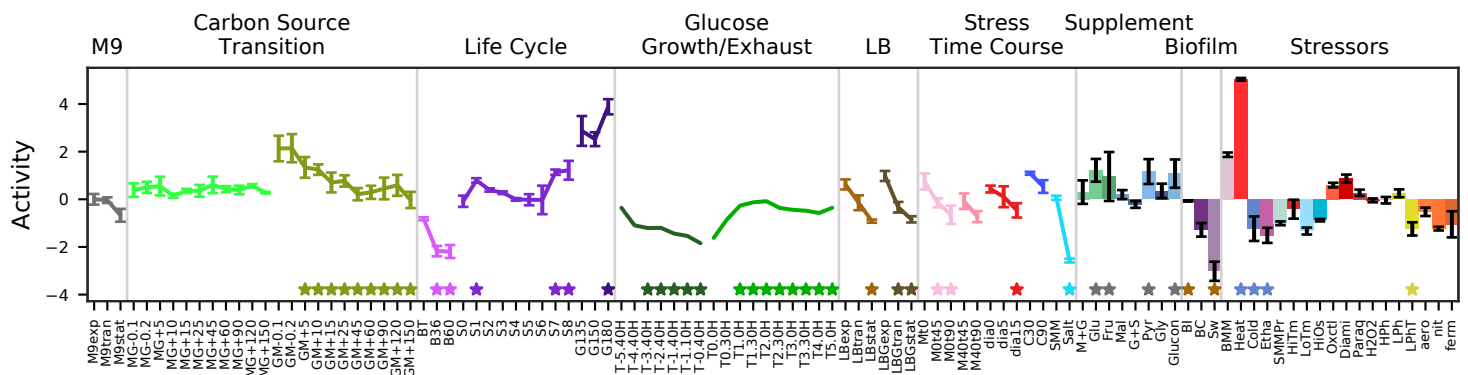
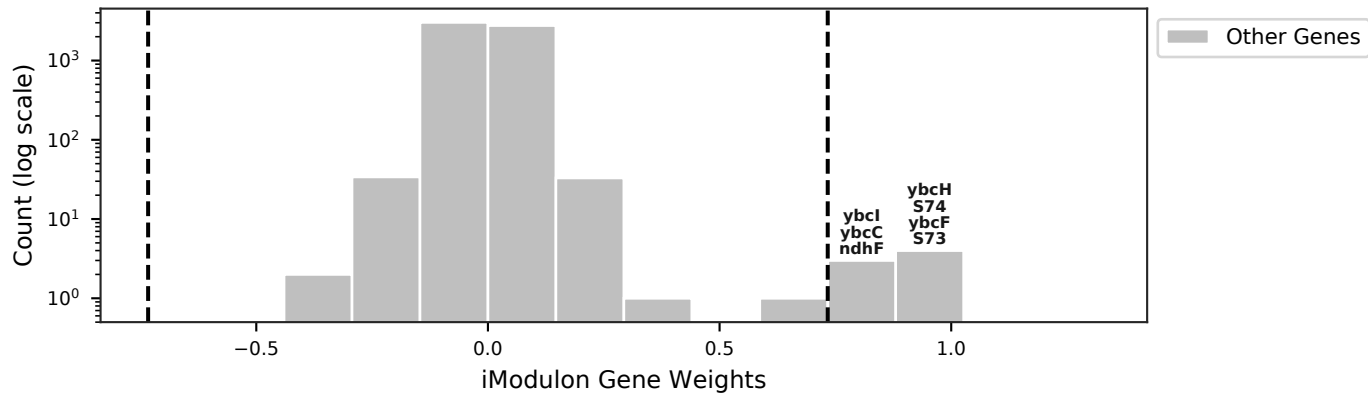
Contains one subunit of NADH dehydrogenase with several unknown genes. Categorized as prophage. Responds to heat shock.

No known regulator



Gene Categories

- Prophages (5)
- Uncharacterized (2)



Motif similar to SigB (32-mer) (E = 8.65e-05)

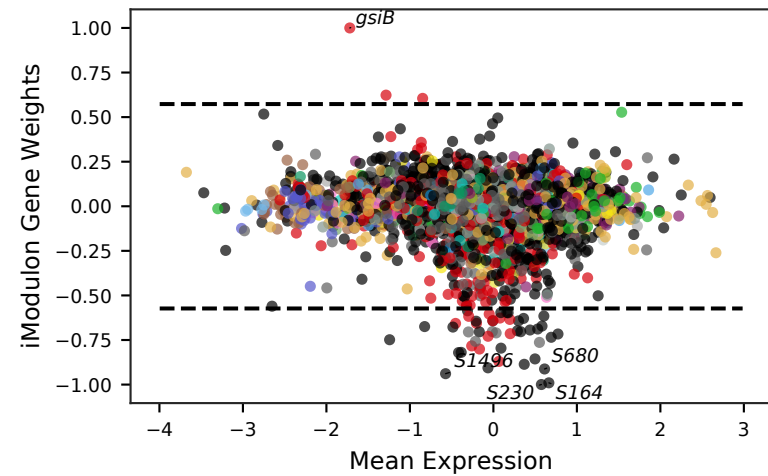
38 - SigB-2 - General Stress 2

Biological Function:

Likely accounting for microarray saturation in the ethanol condition of the SigB-1 iModulon by negatively weighting highly expressed ethanol genes

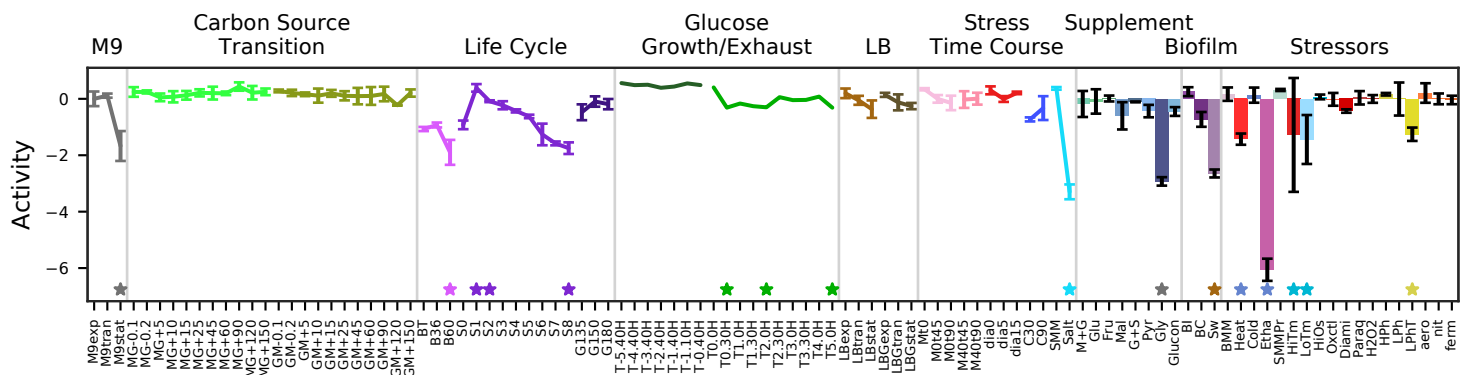
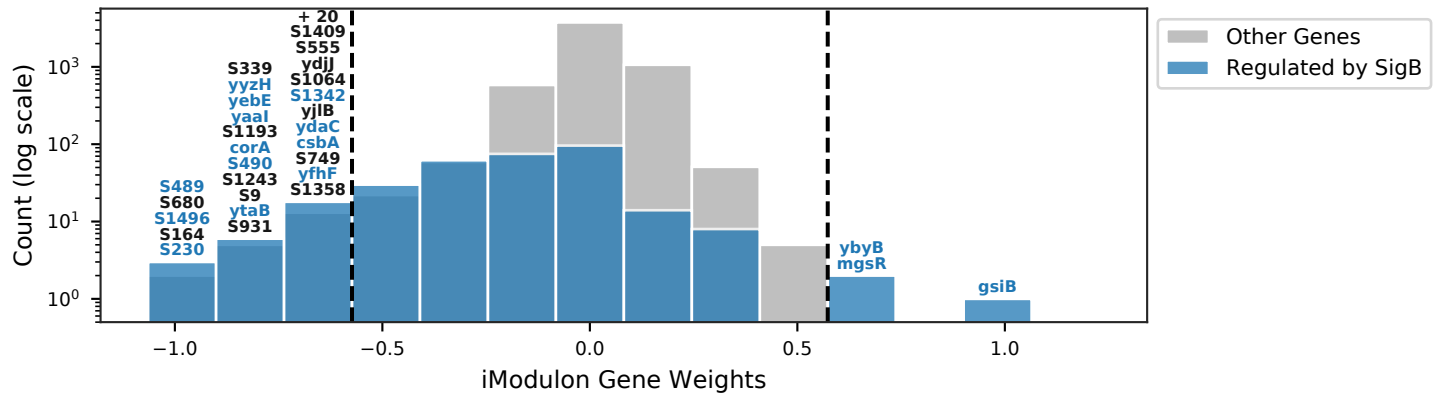
Enriched for known regulon:

SigB



Gene Categories

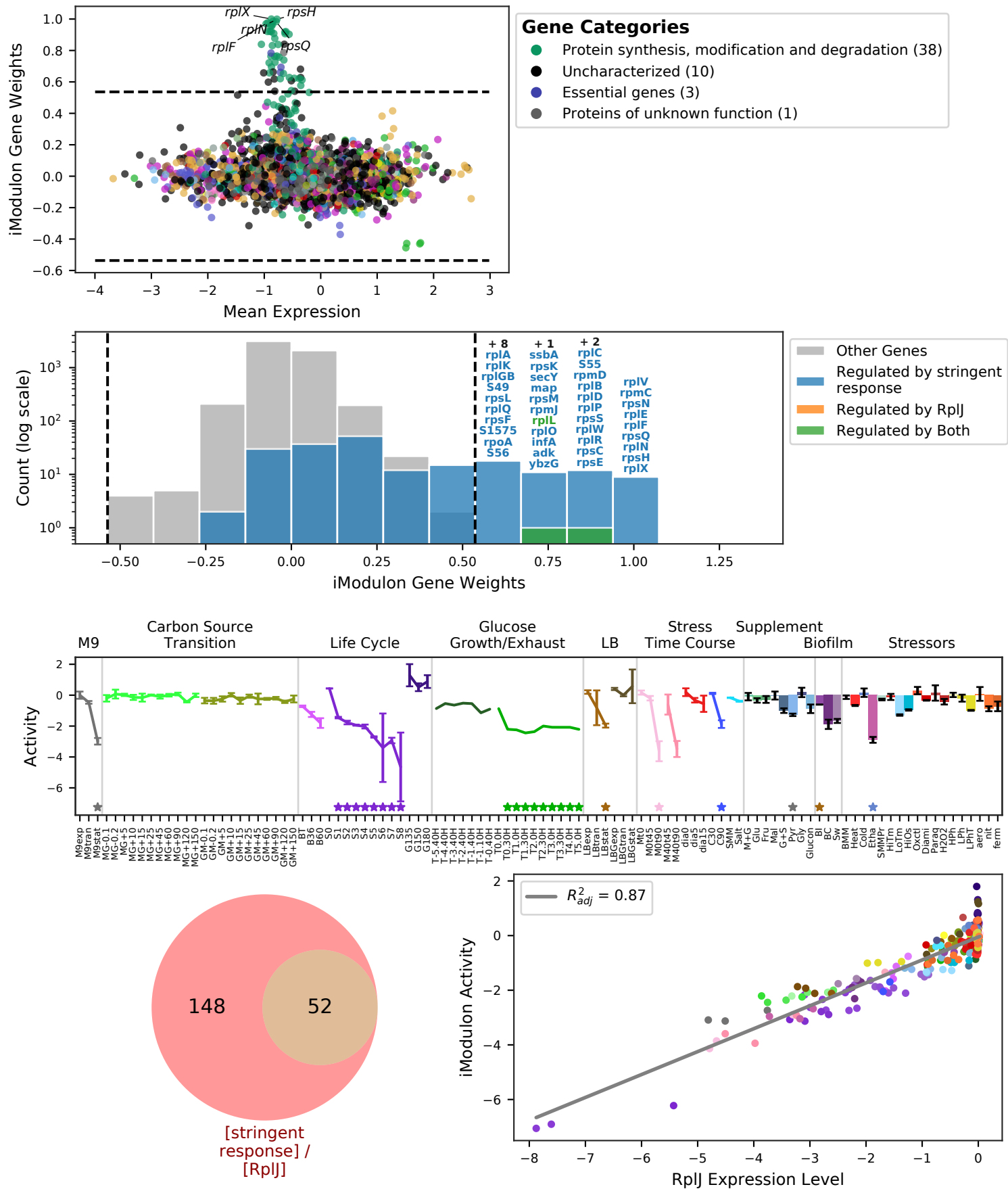
- Uncharacterized (30)
- Coping with stress (15)
- Proteins of unknown function (5)



39 - StrRes - Translation

Biological Function:
Production of ribosomes, translation initiation factors, ADP formation, protein processing and secretory machinery, DNA replication, RNA polymerase

Subset of known regulon:
[stringent response] / [RplJ]



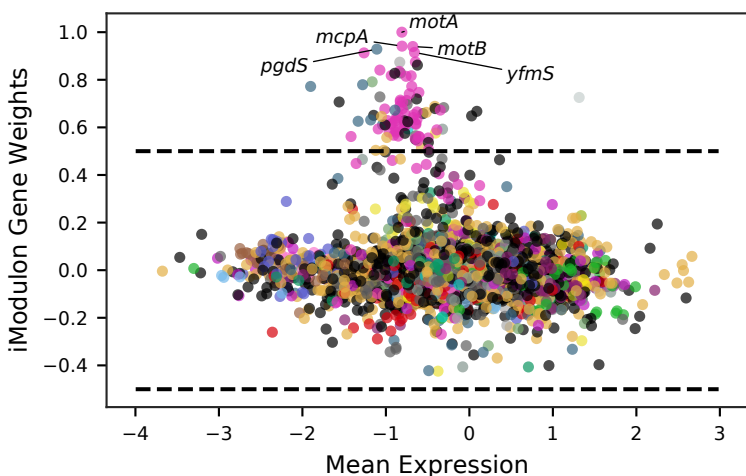
40 - SigD - Motility

Biological Function:

Production of flagella components and export machinery, chemotaxis receptors, use of extracellular energy (polyglutamic acid), regulation of swarming, sporulation inhibitors, cell wall turnover

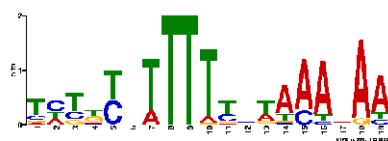
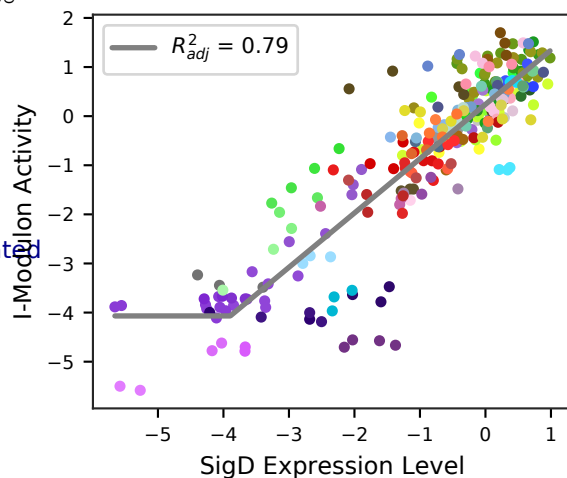
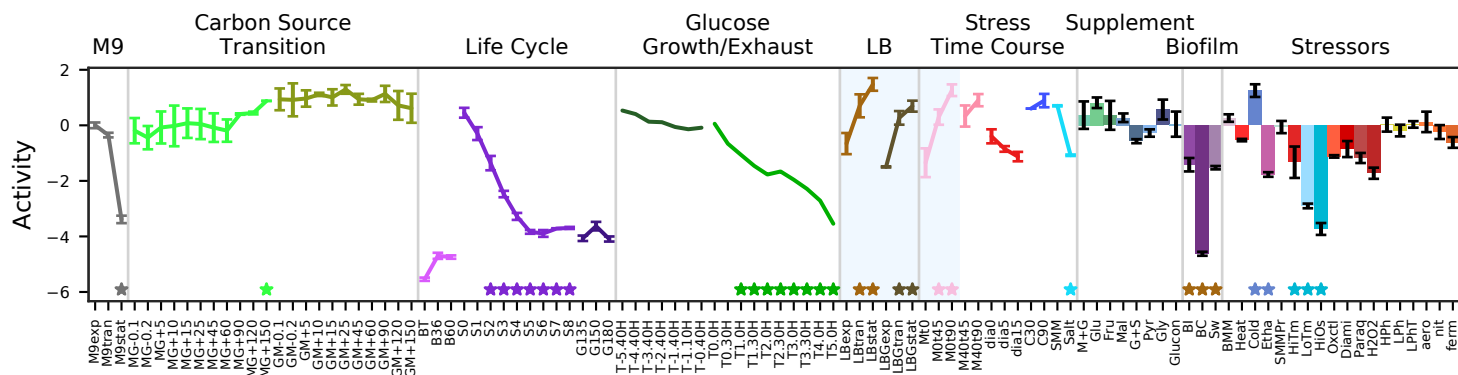
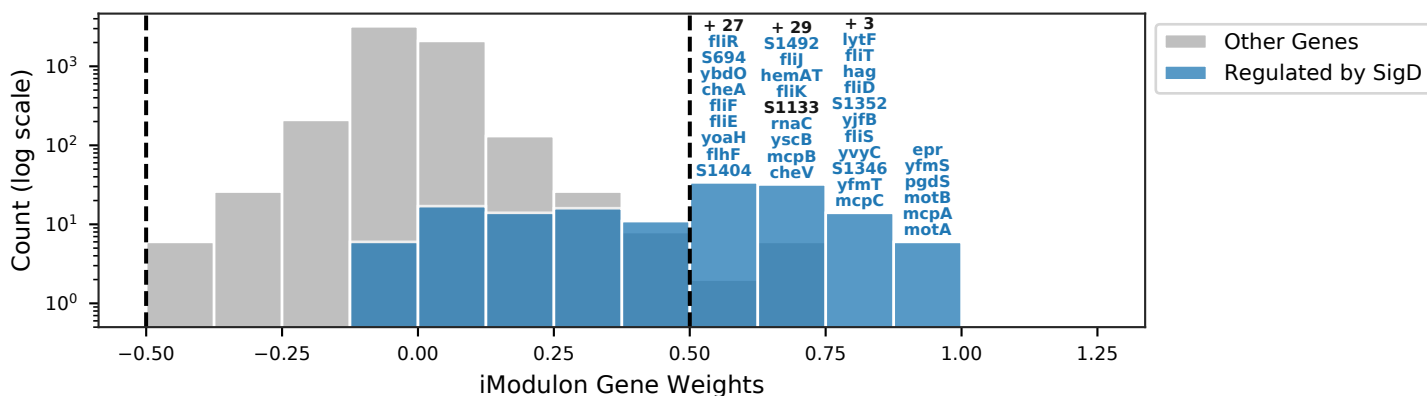
Subset of known regulon:

SigD

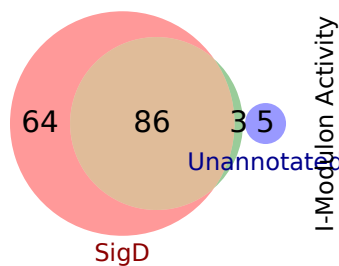


Gene Categories

- Exponential and early post-exponential lifestyles (54)
- Uncharacterized (15)
- Secreted proteins (7)
- Membrane proteins (7)
- Proteins of unknown function (5)
- Regulation of gene expression (1)
- Prophages (1)
- Poorly characterized/ putative enzymes (1)
- ncRNA (1)
- Genetics (1)
- Cell envelope and cell division (1)



Motif E-value: 1.30e-05
Operons with Upstream Motif: 85%



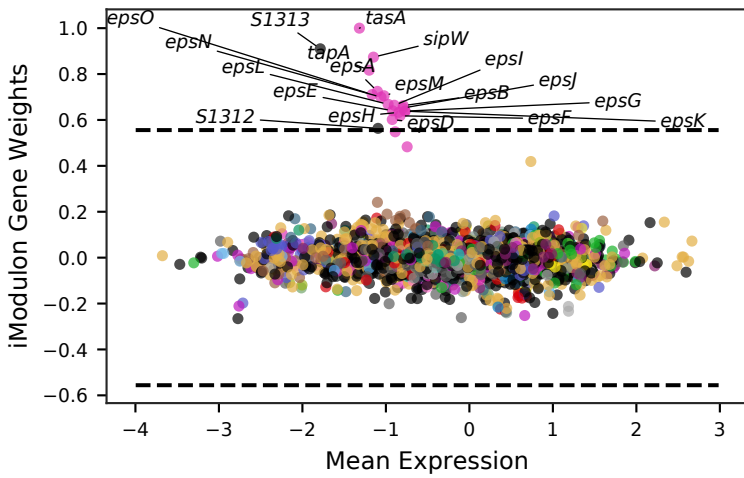
41 - Eps - Exopolymeric Substances

Biological Function:

Biosynthesis of *tasA* and extracellular polysaccharides, the major components of the biofilm

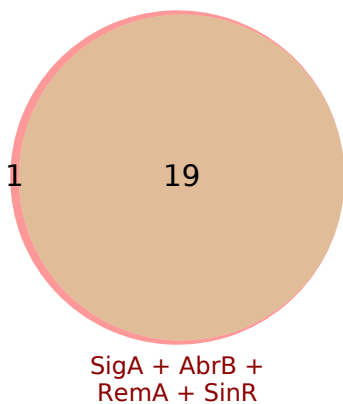
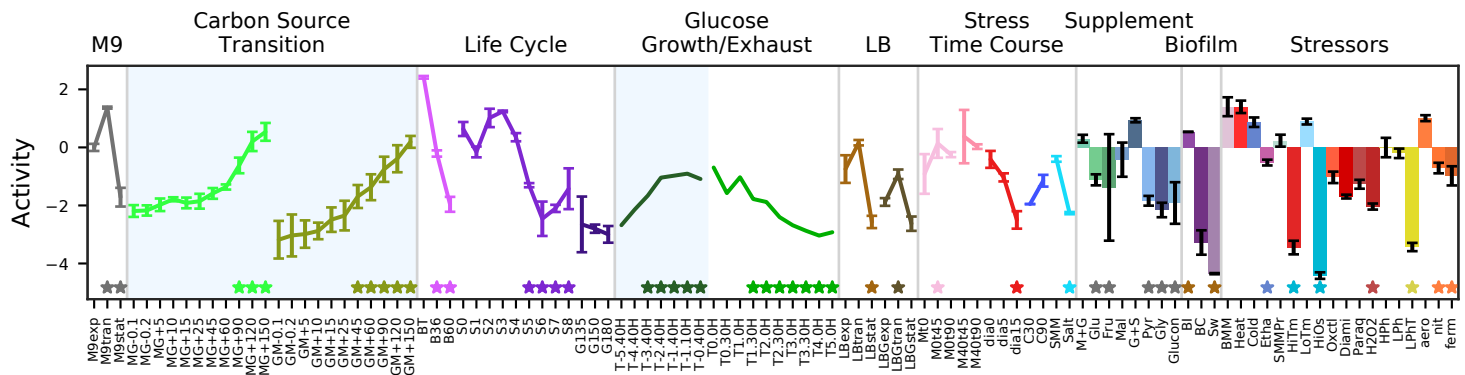
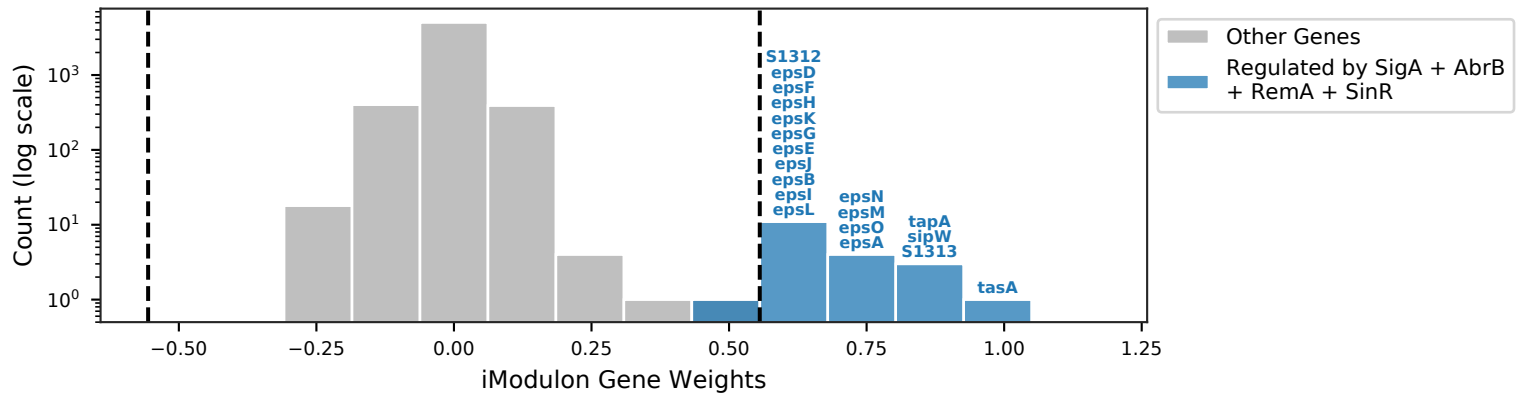
Well-defined regulon:

SigA + AbrB + RemA + SinR

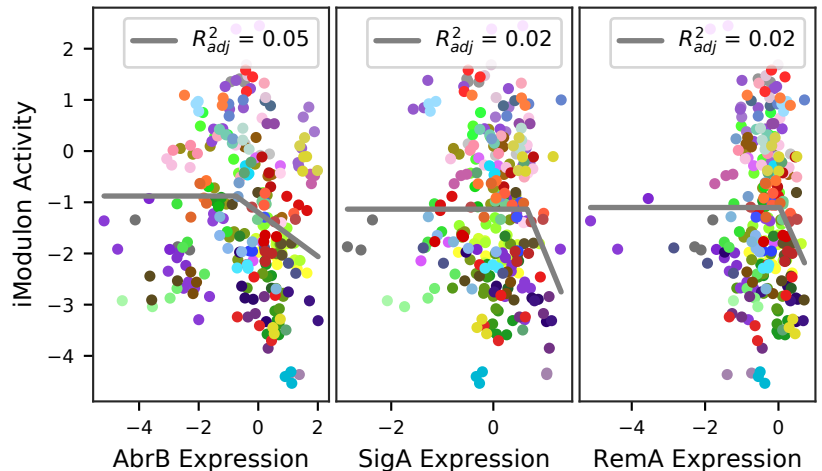


Gene Categories

- Exponential and early post-exponential lifestyles (17)
- Uncharacterized (2)



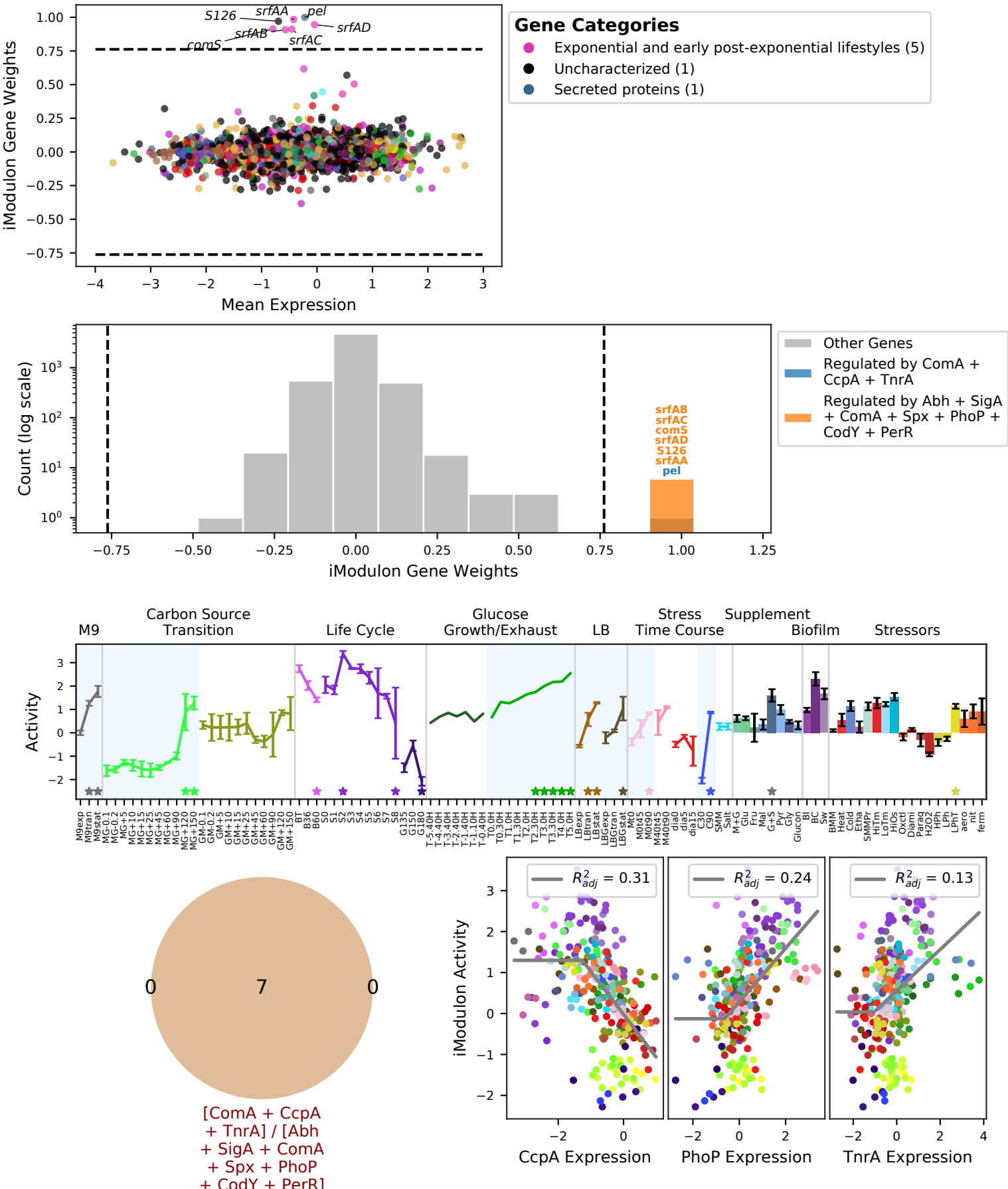
SigA + AbrB +
RemA + SinR



42 - ComA - Surfactants

Biological Function:
Activated during transition to stationary phase (quorum sensing), production of surfactant and exoenzymes to improve nutrient delivery in the biofilm, ComS for activation of competence

Well-defined regulon:
[ComA + CcpA + TnrA] / [Abh + SigA + ComA + Spx + PhoP + CodY + PerR]



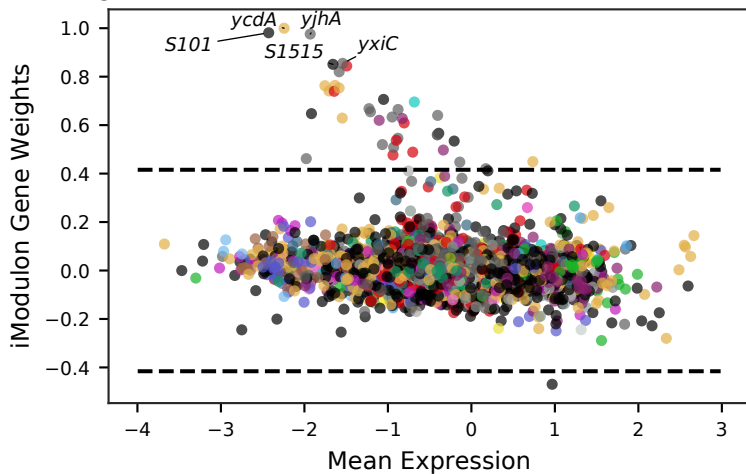
43 - DegU - Toxins and Colony Establishment

Biological Function:

Response to arrested flagellar motor. Secretion of yukE, a homolog of virulence factor EsxA. Production of antitoxins and putative toxin y-genes. Production of hydrophobic biofilm layer and lipoproteins for motility. Many unknown proteins.

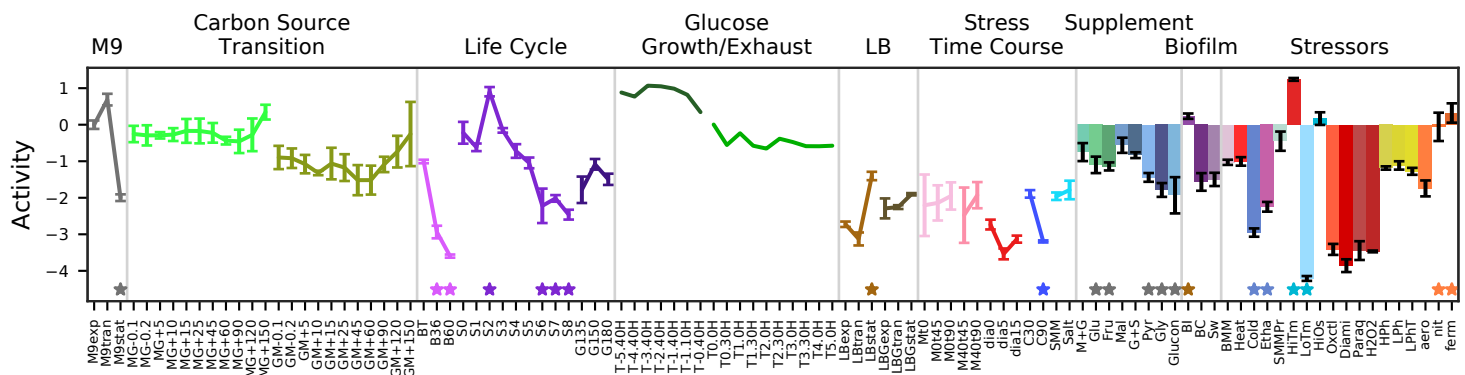
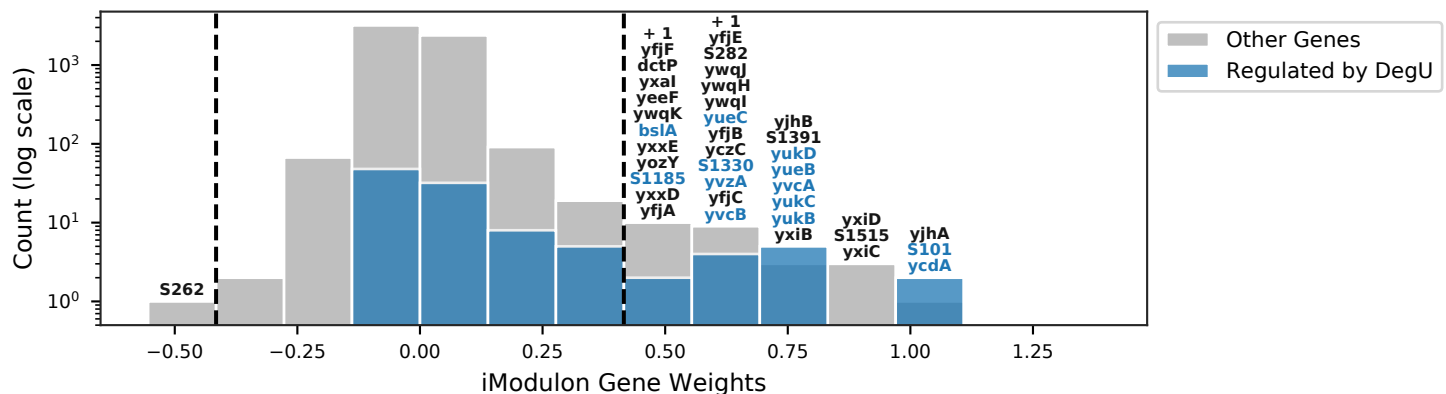
Enriched for known regulon:

DegU



Gene Categories

- Proteins of unknown function (16)
- Uncharacterized (7)
- Membrane proteins (7)
- Coping with stress (6)
- Sporulation (3)
- Genetics (1)



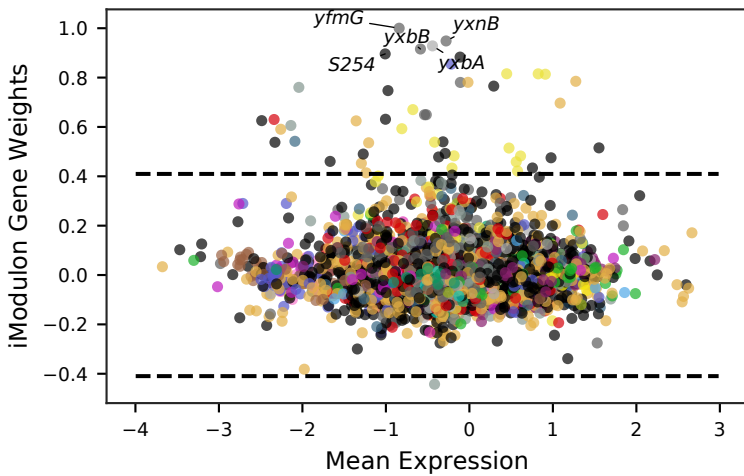
44 - AbrB - Transition State

Biological Function:

Various transition state roles: spore killing, antibiotic resistance, toxin production, metabolism, protein modification, and unknown proteins.

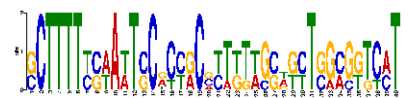
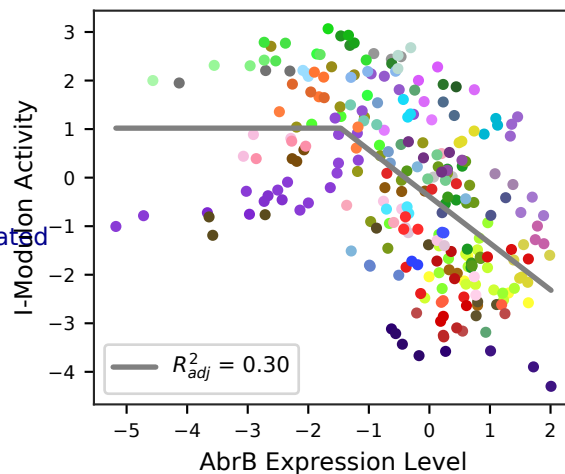
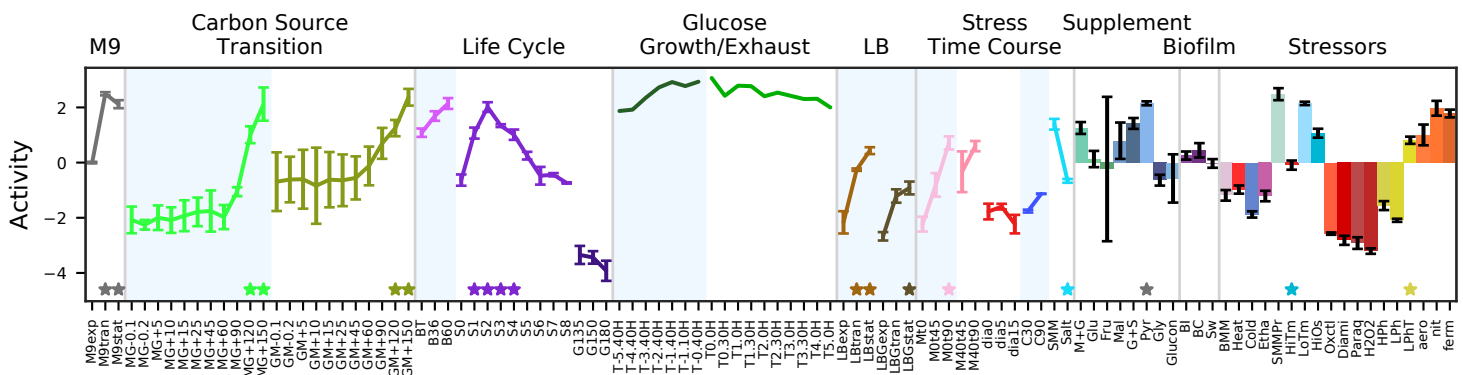
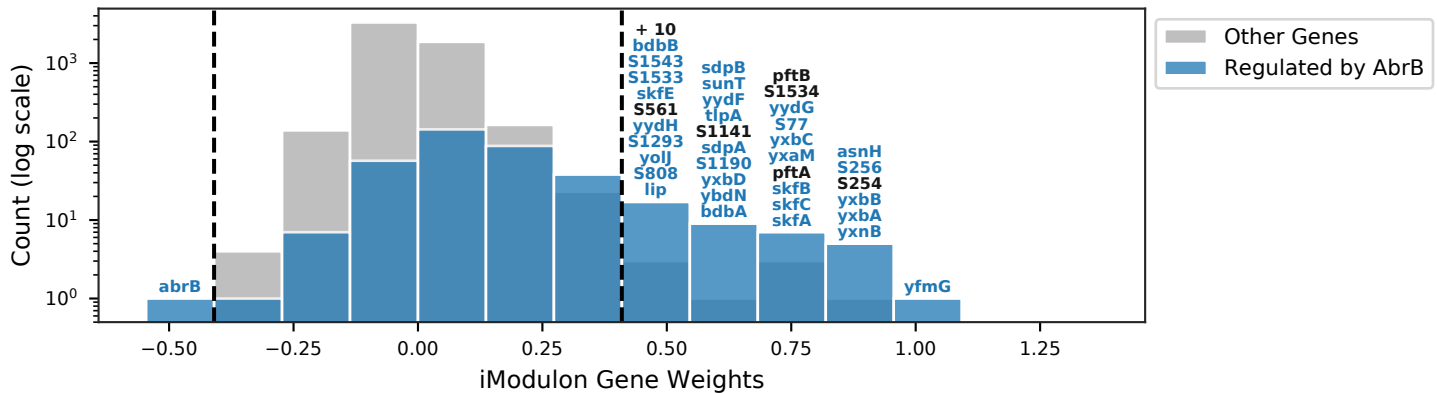
Subset of known regulon:

AbrB



Gene Categories

- Uncharacterized (15)
- Prophages (12)
- Membrane proteins (8)
- Proteins of unknown function (6)
- Regulation of gene expression (3)
- Secreted proteins (1)
- Poorly characterized/ putative enzymes (1)
- Coping with stress (1)
- Amino acid/ nitrogen metabolism (1)



Motif E-value: 2.00e-06
Operons with Upstream Motif: 81%

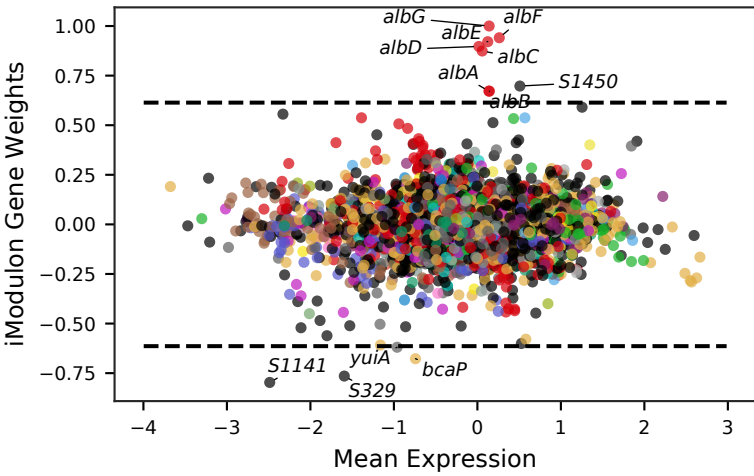
45 - Alb - Antilisterial Bacteriocin

Biological Function:

Produces and exports subtilisin, which kills anaerobic listeria bacteria

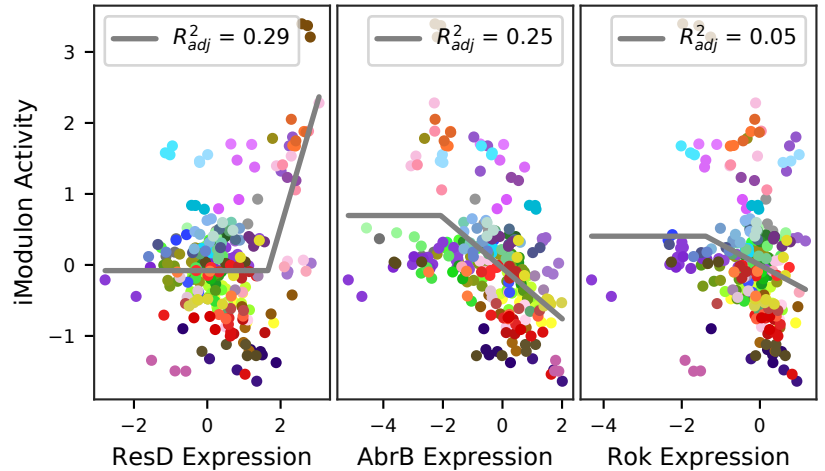
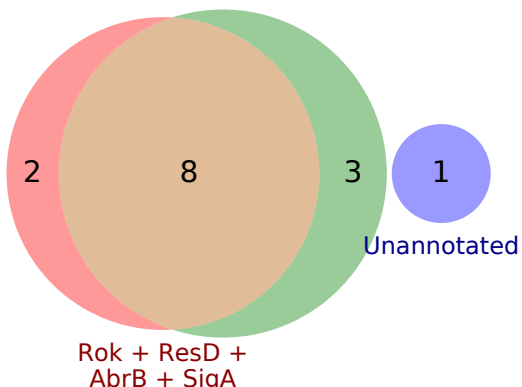
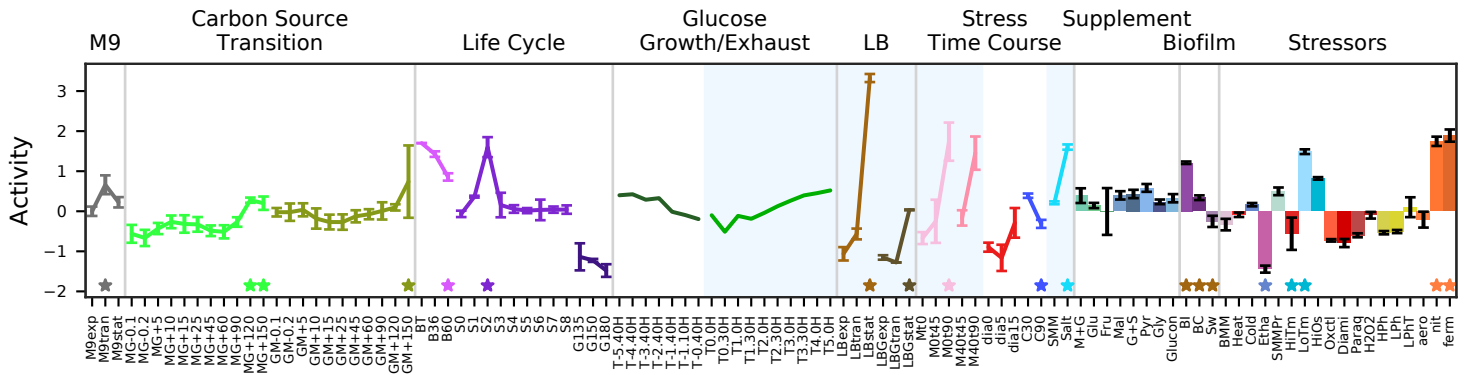
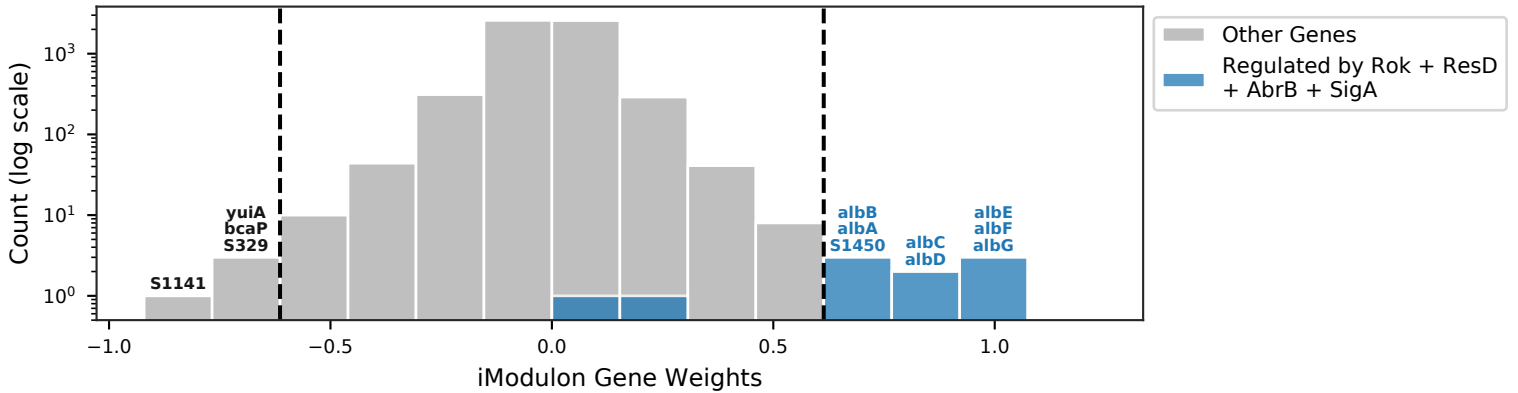
Well-defined regulon:

Rok + ResD + $\bar{\Delta}$ brB + SigA



Gene Categories

- Coping with stress (7)
- Uncharacterized (3)
- Proteins of unknown function (1)
- Membrane proteins (1)



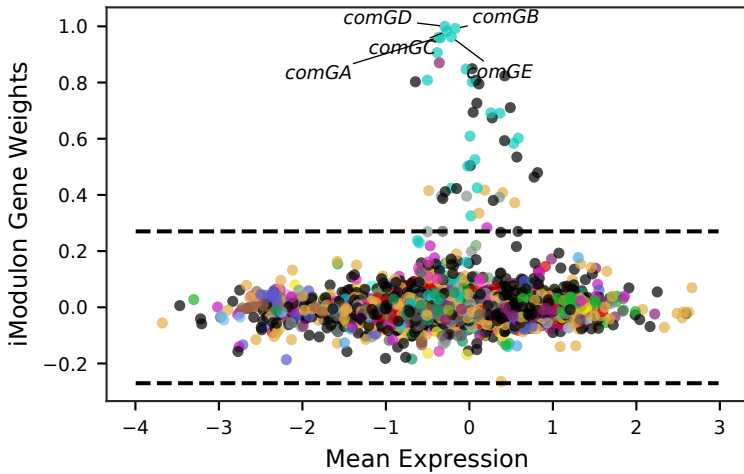
47 - ComK - Competence

Biological Function:

DNA transport, pseudopilus, recombination machinery, and regulatory proteins for competence

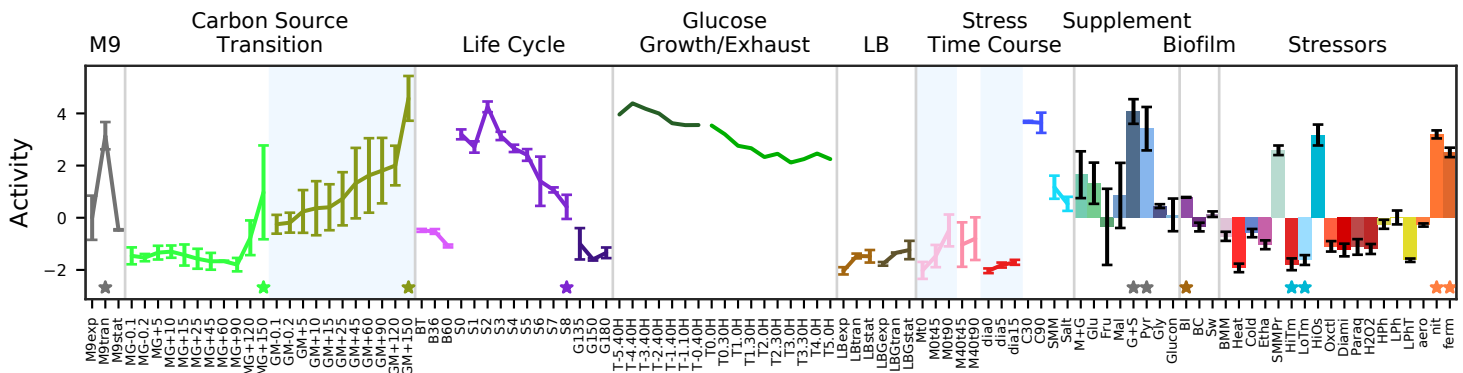
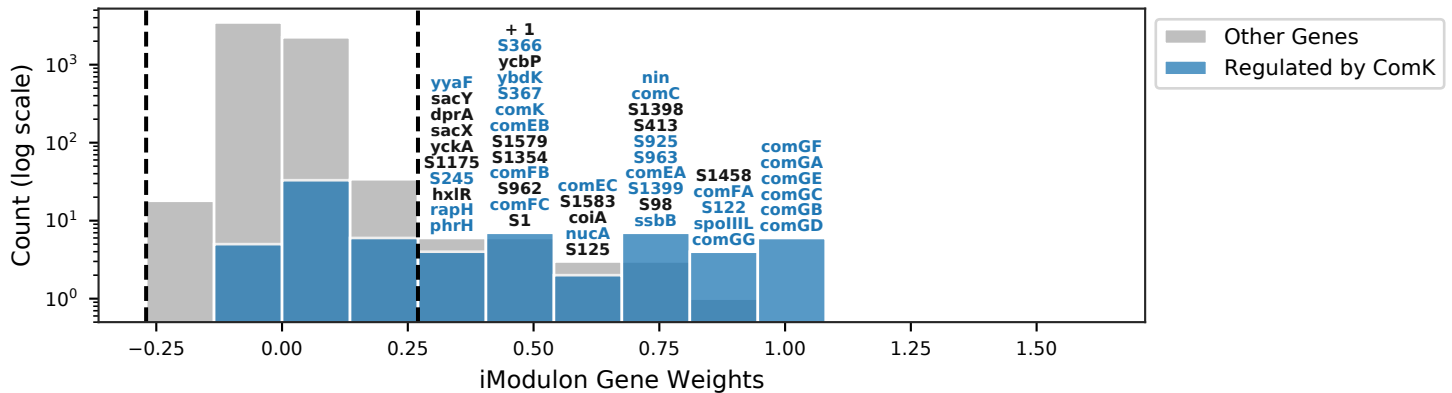
Enriched for known regulon:

ComK



Gene Categories

- Genetics (20)
- Uncharacterized (18)
- Membrane proteins (5)
- Regulation of gene expression (3)
- Sporulation (1)
- Proteins of unknown function (1)
- Phosphoproteins (1)



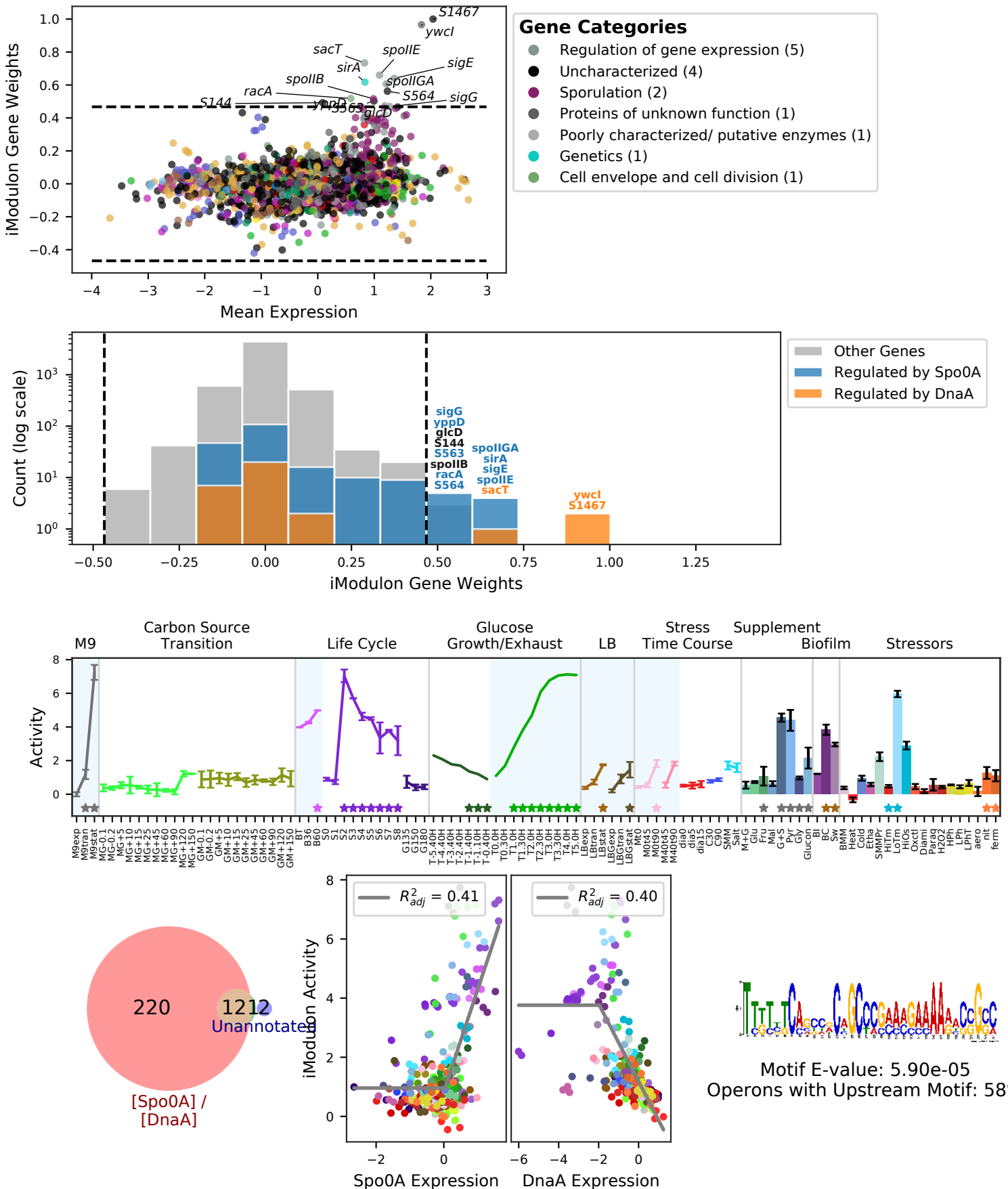
48 - Spo0A - Sporulation 1

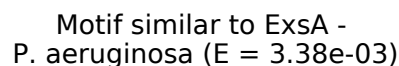
Biological Function:

Initiation of sporulation through sigma factor, transcription factor, and regulatory protein expression, as well as septum formation and chromosome anchoring

Subset of known regulon:

[Spo0A] / [DnaA]





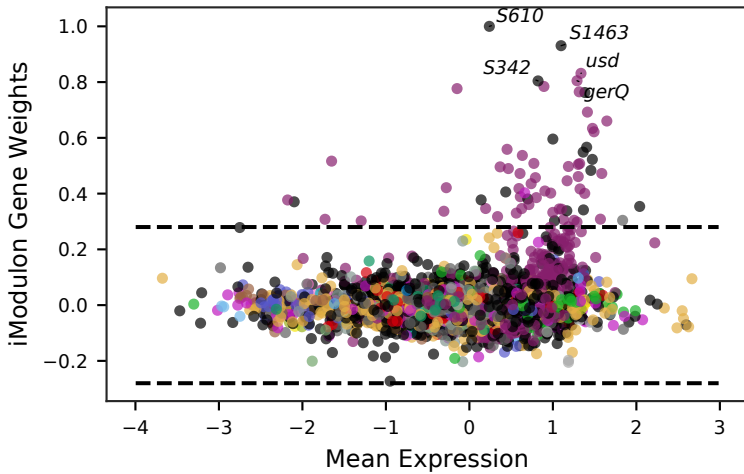
50 - SigE / G - Sporulation 3

Biological Function:

Spore coat production, transcription factor and regulator expression, spore DNA protection, spore stress resistance

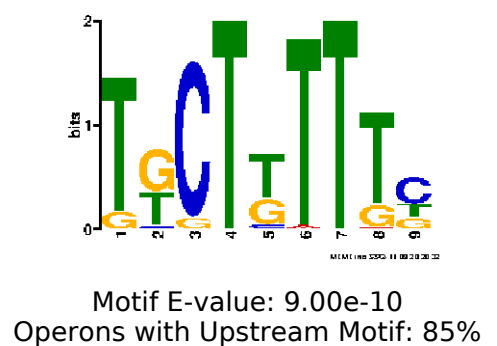
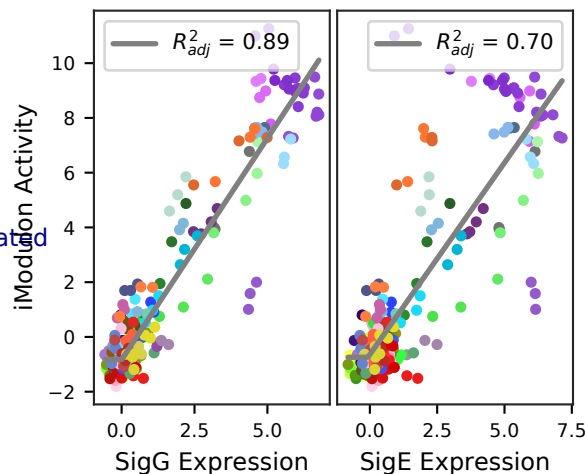
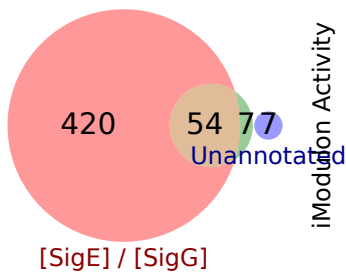
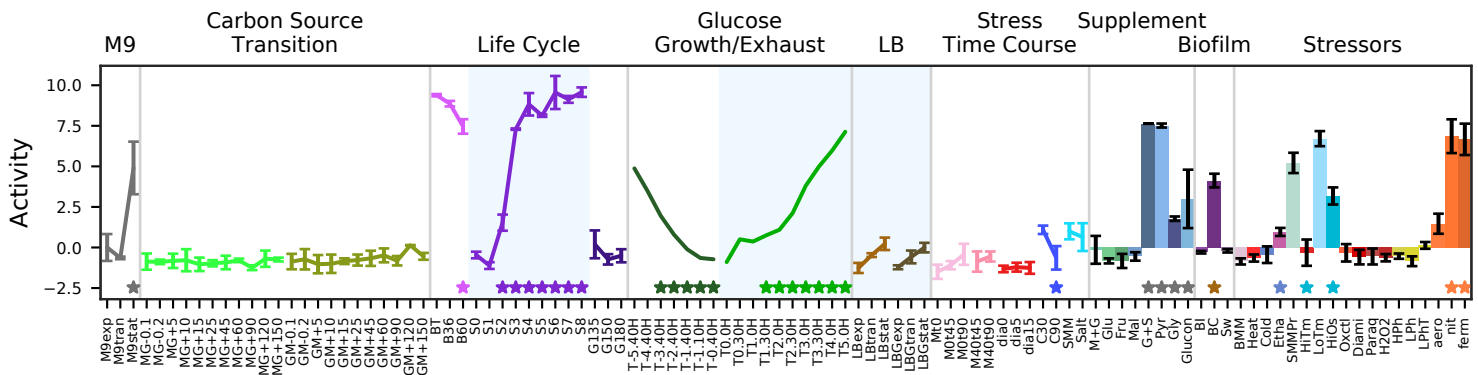
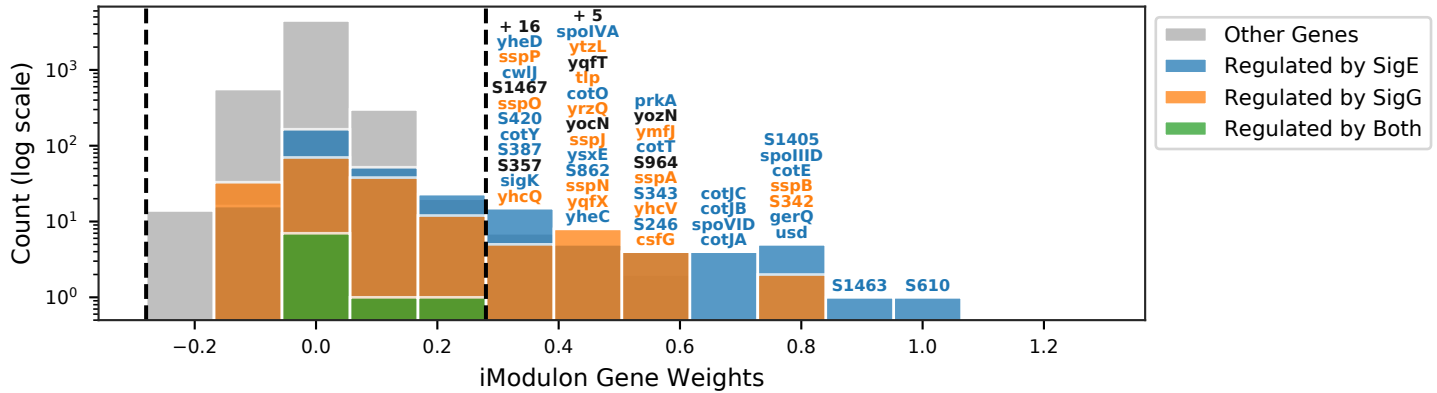
Subset of known regulon:

[SigE] / [SigG]



Gene Categories

- Sporulation (49)
- Uncharacterized (17)
- Proteins of unknown function (1)
- Phosphoproteins (1)

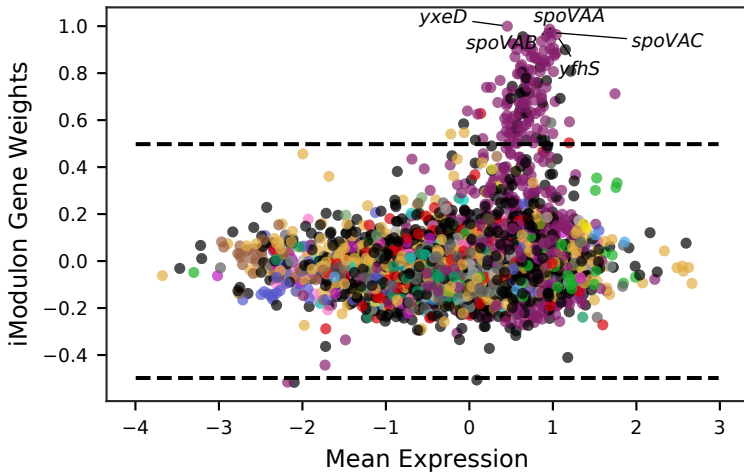


51 - SigG - Sporulation 4

Biological Function:

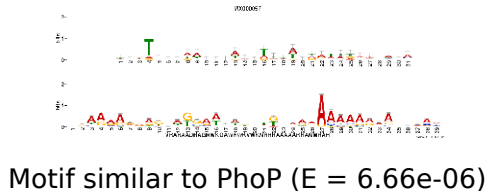
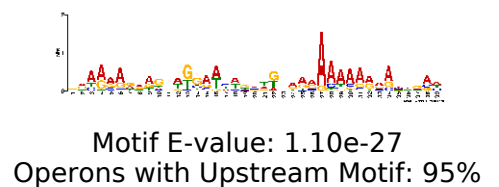
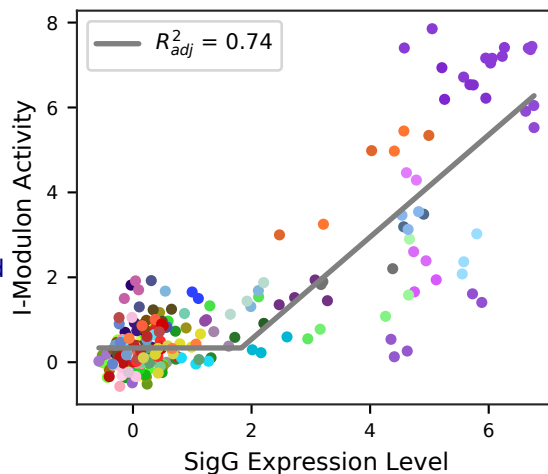
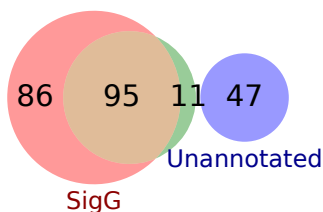
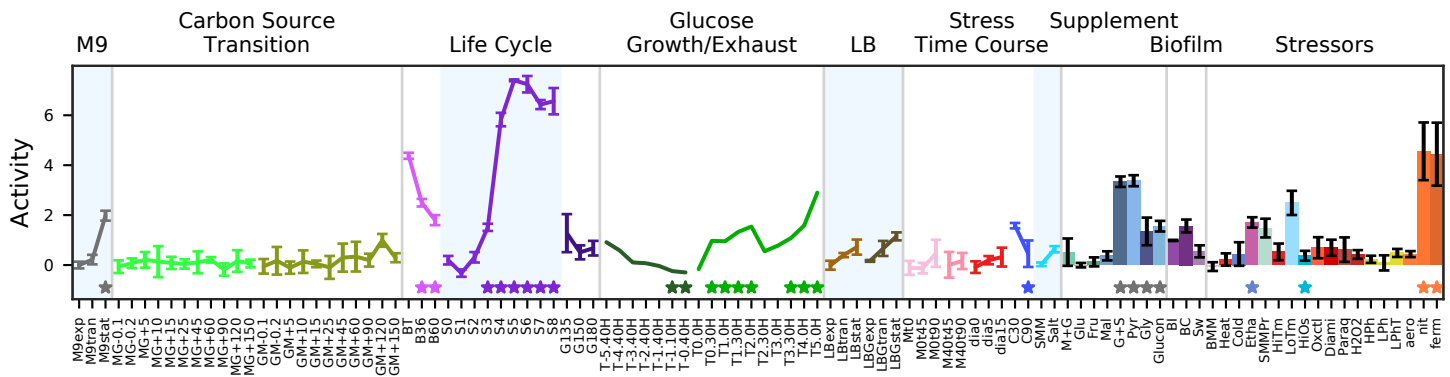
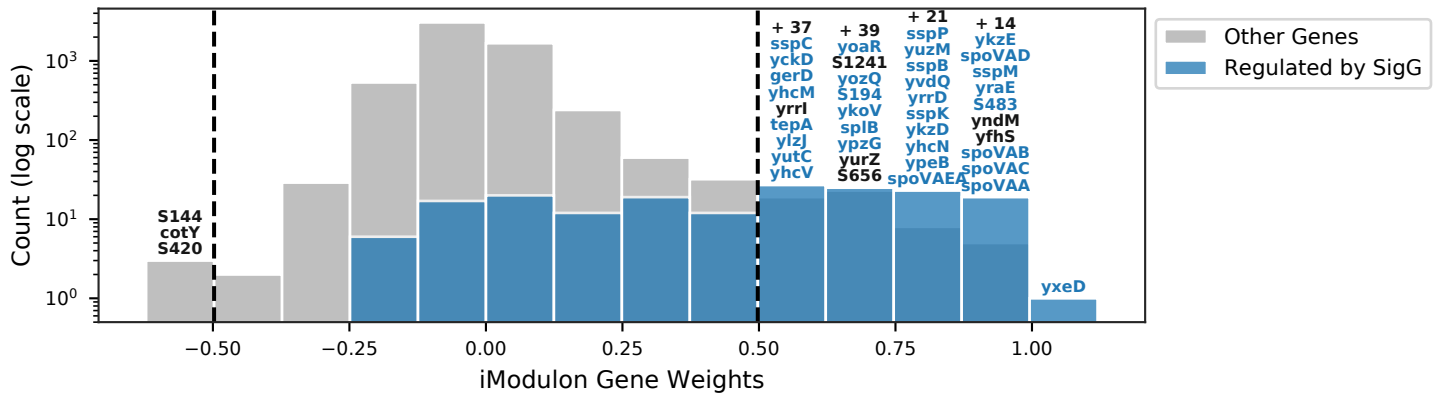
Calcium and nutrient delivery to the spore, endospore cortex maturation, lipoproteins, forespore-specific metabolic proteins, many unknown sporulation proteins, stress resistance, proteins required for germination

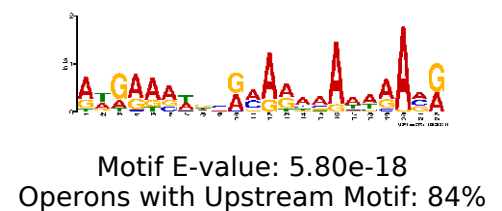
Enriched for known regulon:
SigG



Gene Categories

- Sporulation (116)
- Uncharacterized (32)
- Membrane proteins (2)
- Coping with stress (2)
- Proteins of unknown function (1)





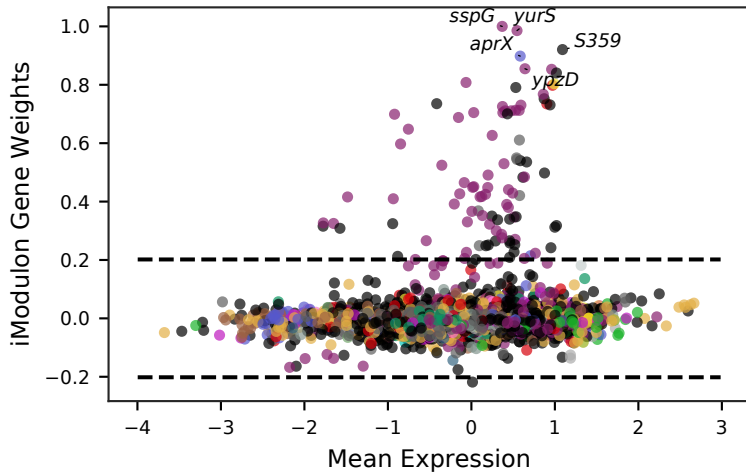
53 - SigK-2 - Sporulation 6

Biological Function:

Production of outermost spore coat and crust proteins, mother cell lysis

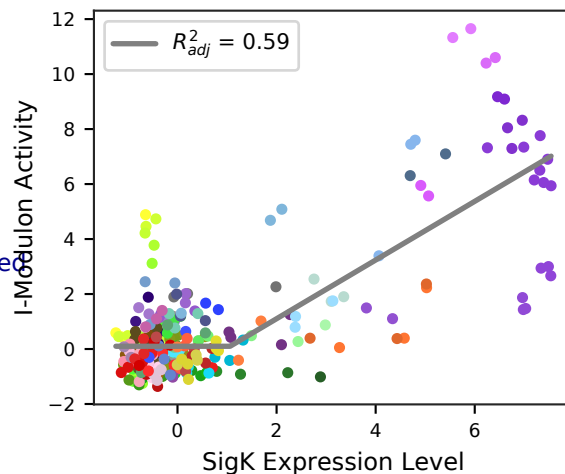
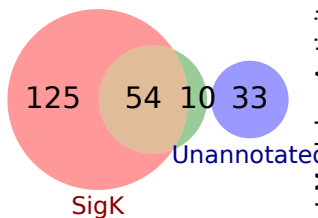
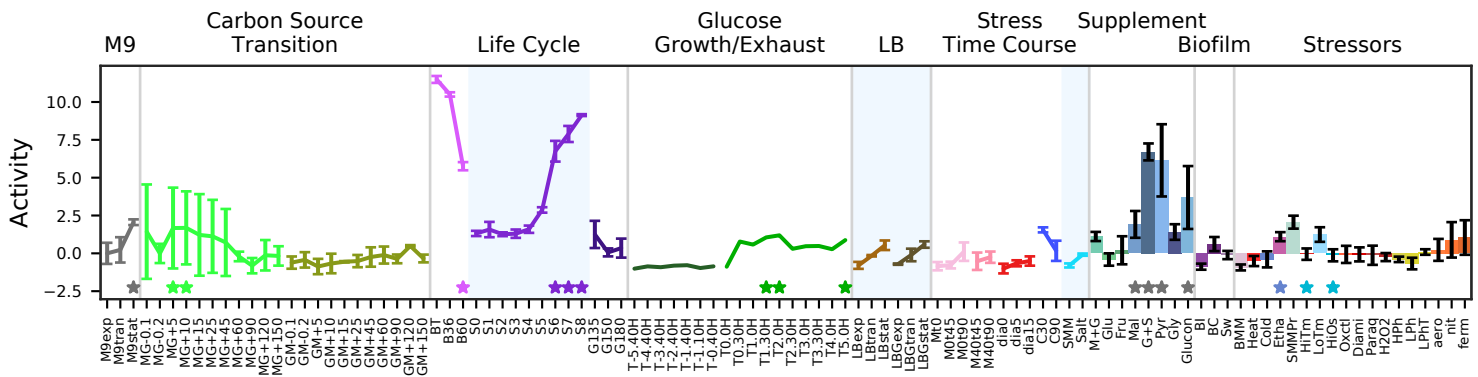
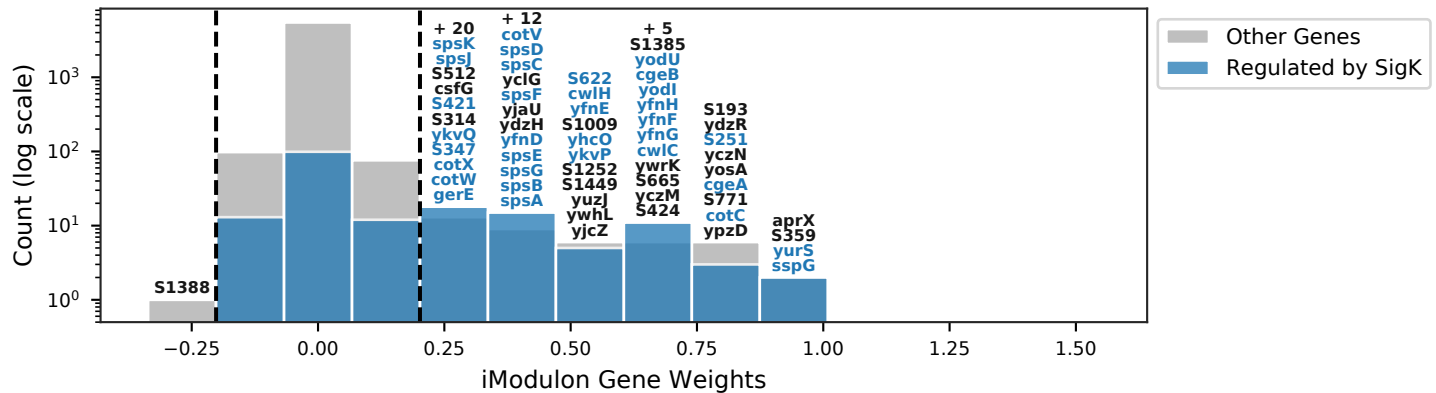
Enriched for known regulon:

SigK

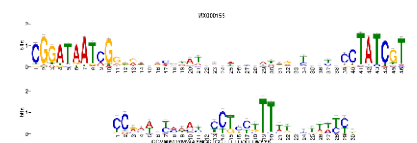


Gene Categories

- Sporulation (54)
- Uncharacterized (32)
- Proteins of unknown function (6)
- Coping with stress (2)
- Amino acid/ nitrogen metabolism (2)
- Prophages (1)



Motif E-value: 1.20e-10
Operons with Upstream Motif: 64%



Motif similar to OxyR -
E. coli (E = 5.60e-03)

89 13 4
Unannotated

[SigK + GerE] /
[SigK + GerR]

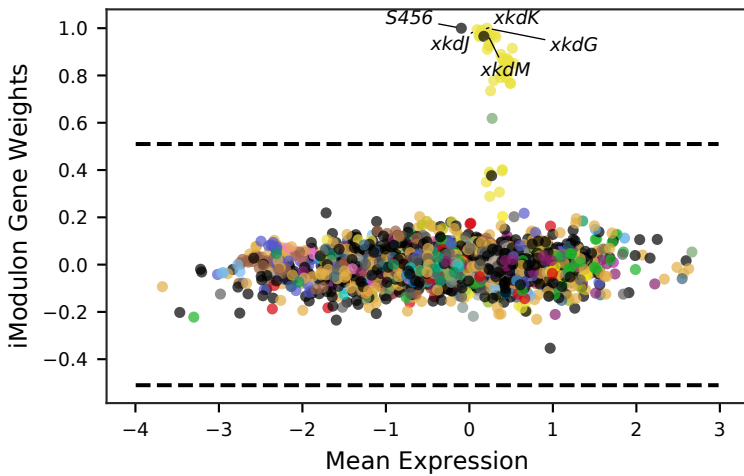
55 - Xpf - PBSX Prophage

Biological Function:

Prophage element that induces production of bacteriocin and cell lysis in response to DNA-damaging agents

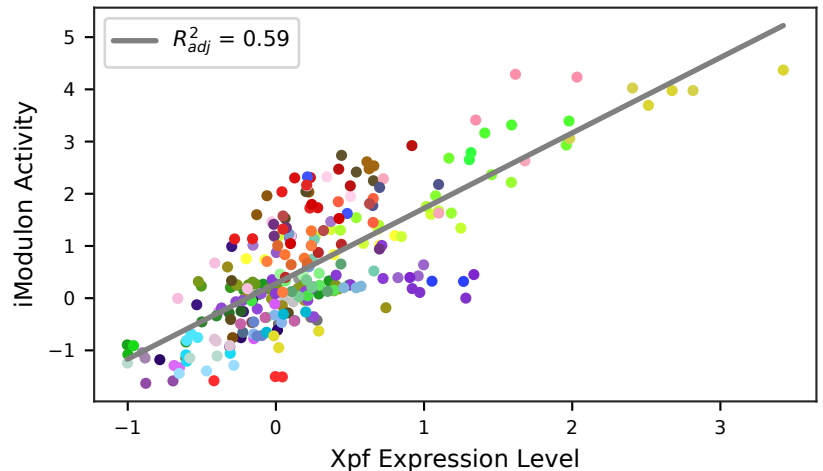
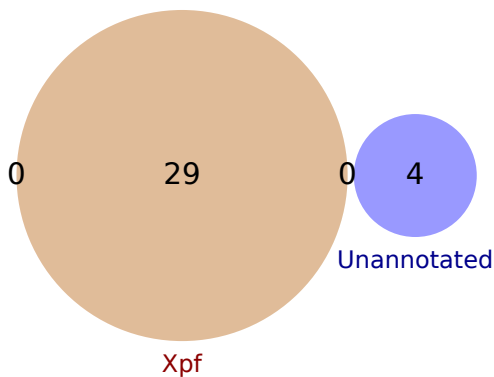
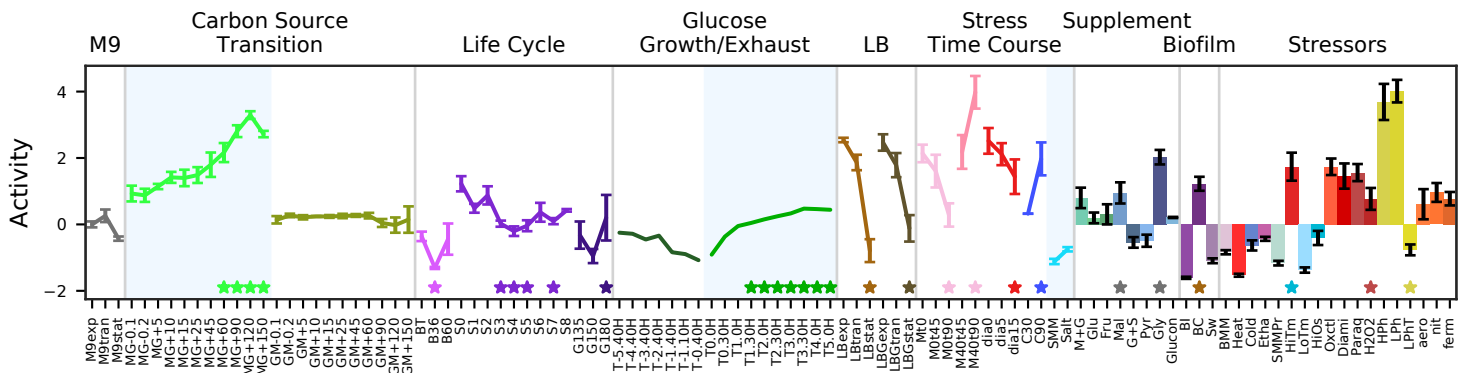
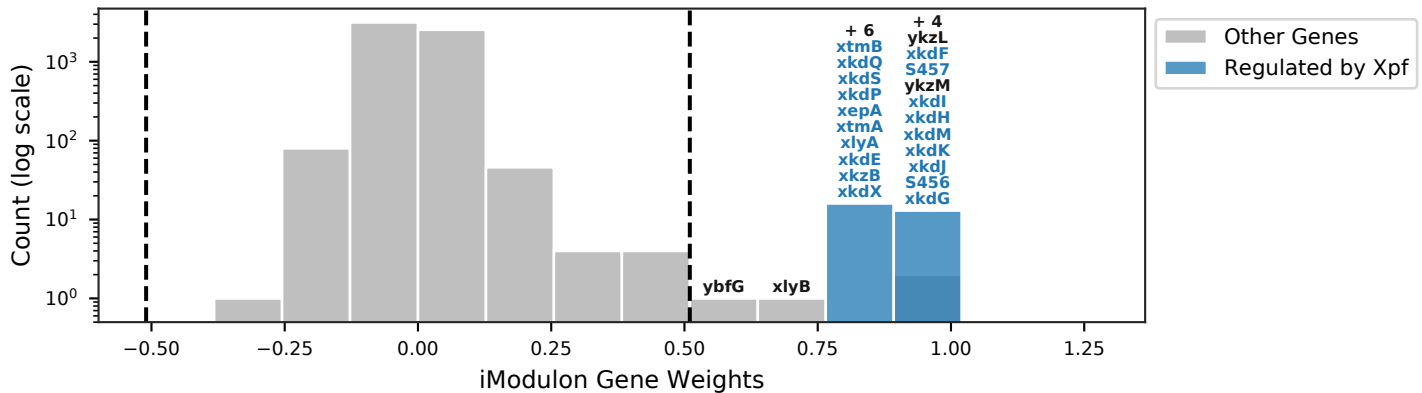
Well-defined regulon:

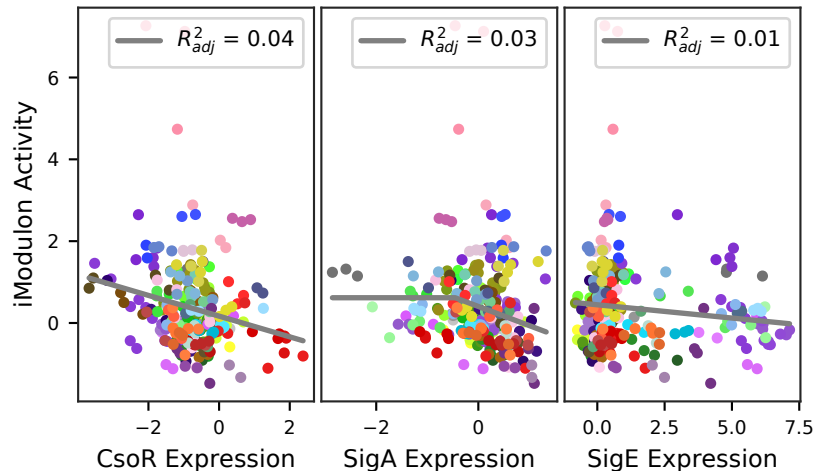
Xpf

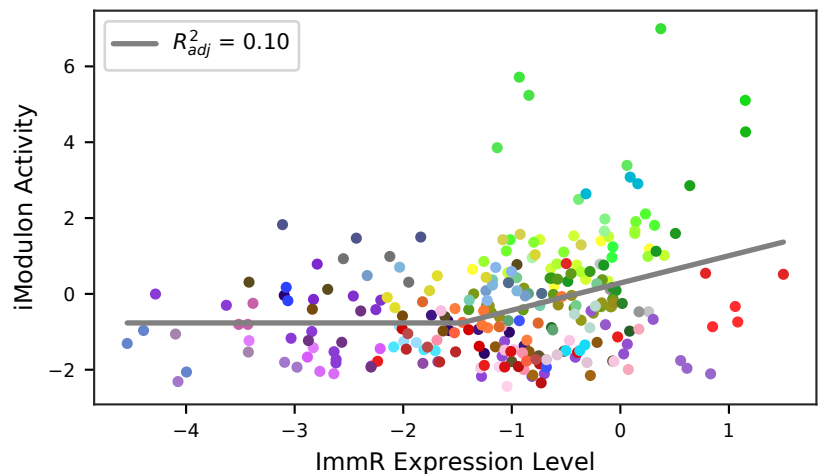


Gene Categories

- Prophages (30)
- Uncharacterized (2)
- Cell envelope and cell division (1)





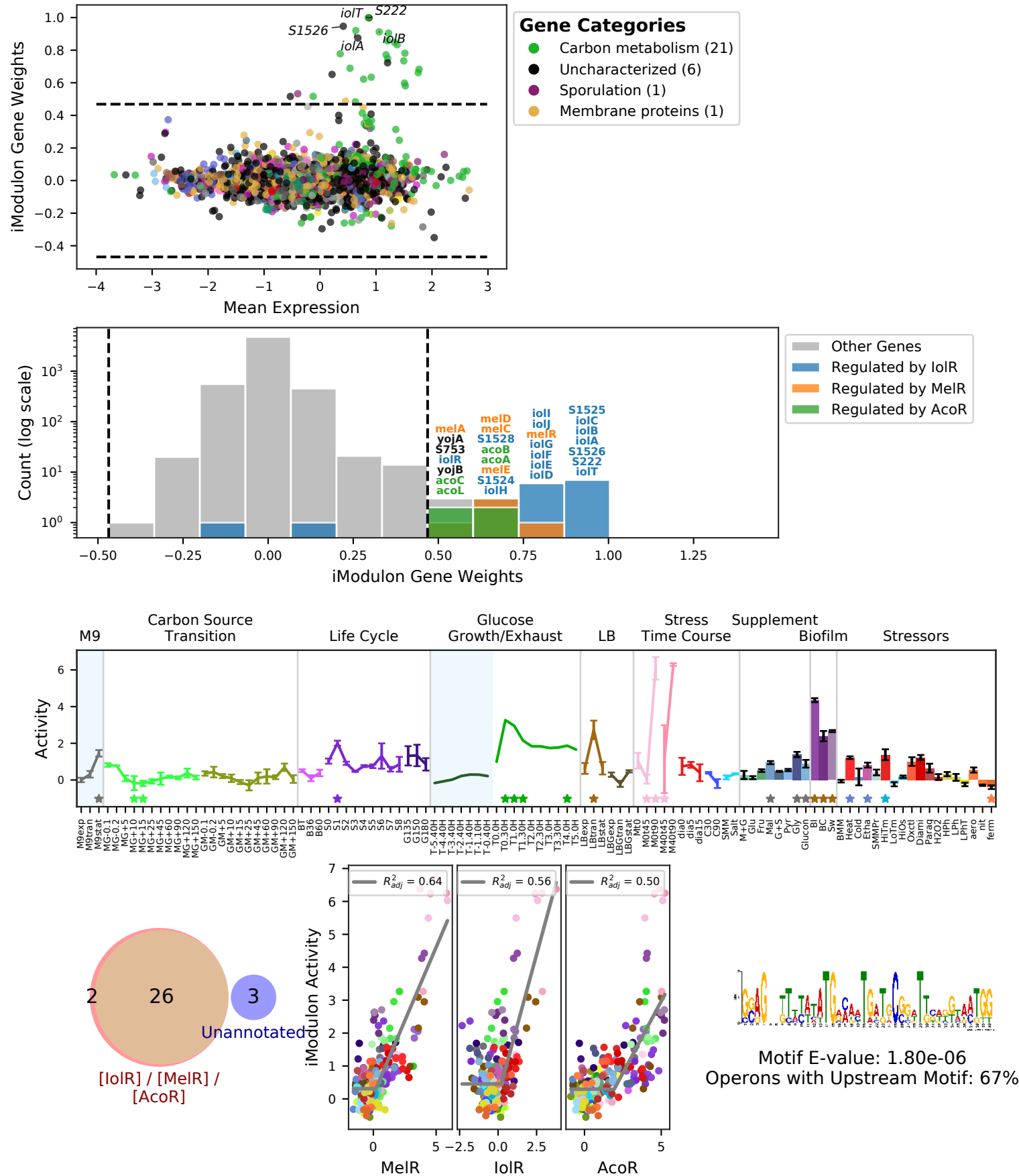


A scatter plot showing the relationship between iModulon Activity (Y-axis) and SknR Expression Level (X-axis). The Y-axis ranges from -2.0 to 0.5, and the X-axis ranges from -4 to 1. The plot includes a regression line and a legend indicating $R^2_{adj} = 0.23$. Data points are colored by cluster, showing a positive correlation between SknR expression and iModulon activity.

60 - IoIR / MeIR - Inositol, Melibiose, and Acetoin

Biological Function:
Uptake and utilization of inositol, melibiose/raffinose, and acetoin

Well-defined regulon:
[IoIR] / [MeIR] / [AcoR]



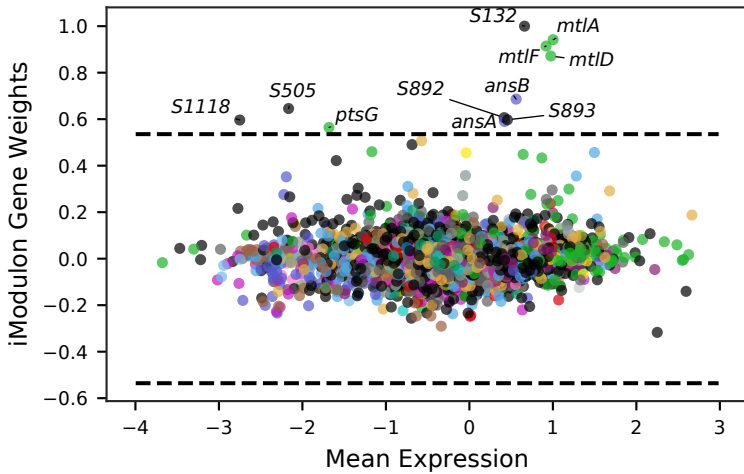
62 - MtIR / AnsR - Mannitol, Asparagine, and Aspartate

Biological Function:

Uptake and utilization of mannitol, degradation of asparagine and aspartate

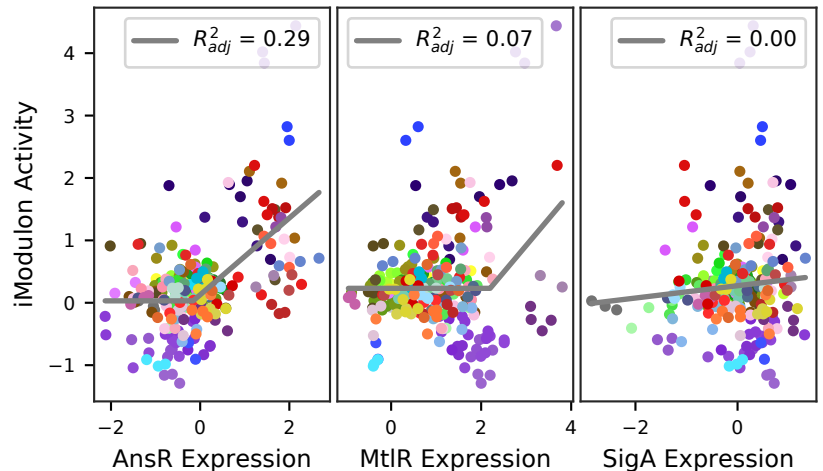
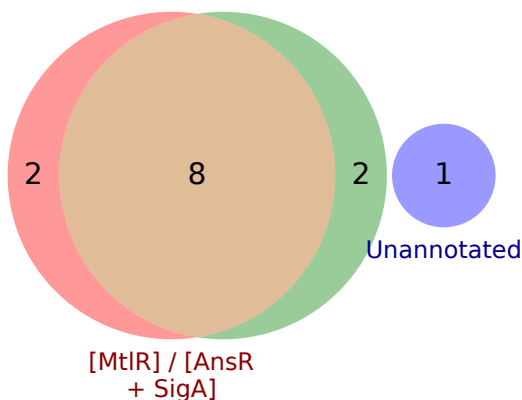
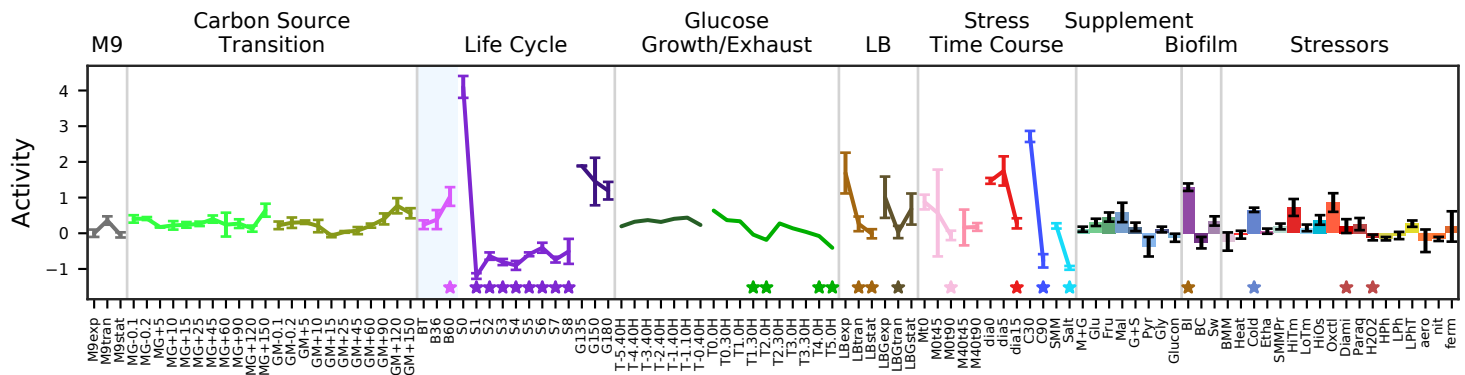
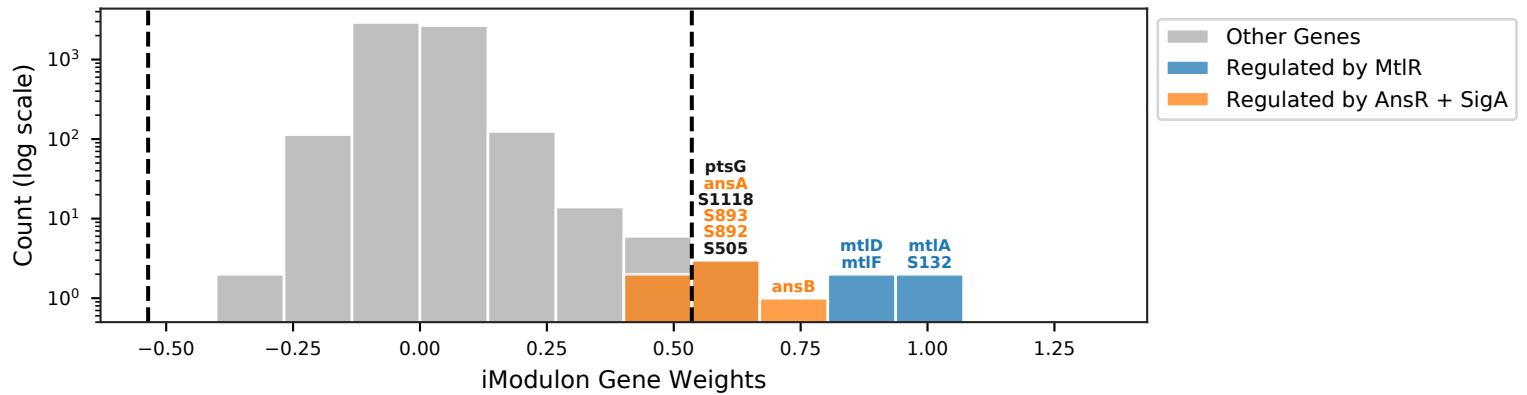
Well-defined regulon:

[MtIR] / [AnsR + SigA]



Gene Categories

- Uncharacterized (5)
- Carbon metabolism (4)
- Amino acid/ nitrogen metabolism (2)

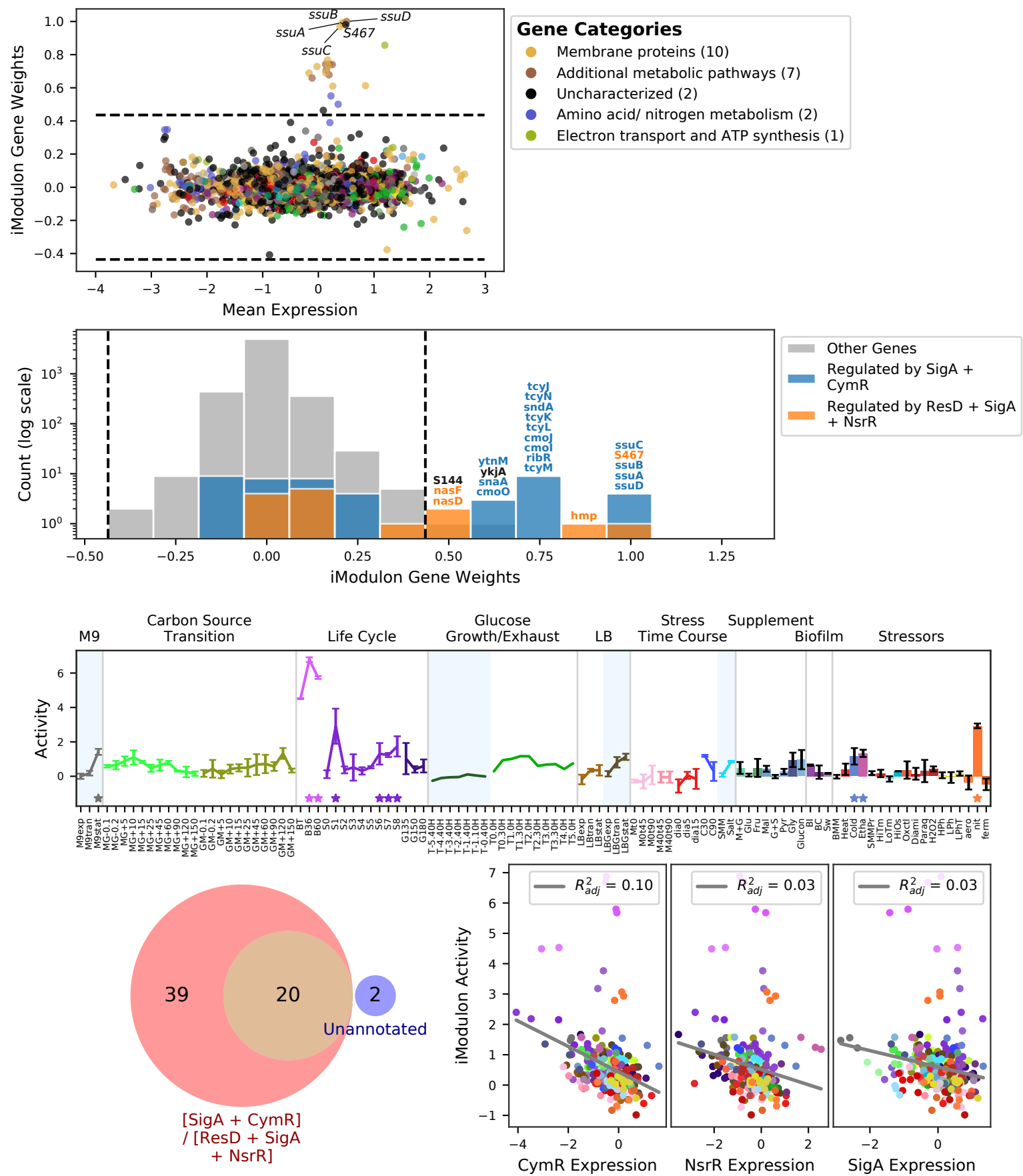


Motif E-value: 5.60e-07
Operons with Upstream Motif: 100%

64 - CymR / NsrR - Sulfur and Nitrate Respiration

Biological Function:
Import and utilization of sulfonate and cystine for cysteine production. Nitrite reduction

Subset of known regulon:
[SigA + CymR] / [ResD + SigA + NsrR]



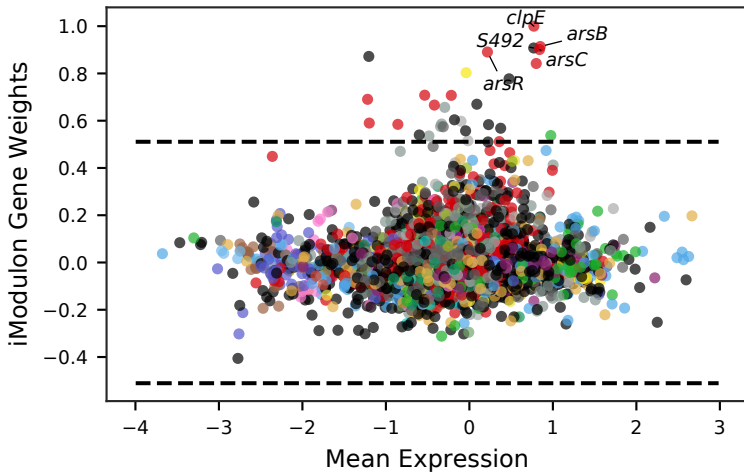
65 - ArsR+ - Diamide Stress

Biological Function:

Detoxification in response to: oxidative protein damage, arsenic, catechol, copper, toxic quinones

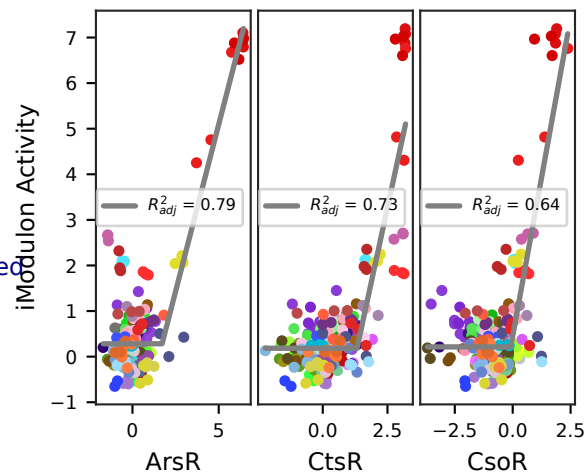
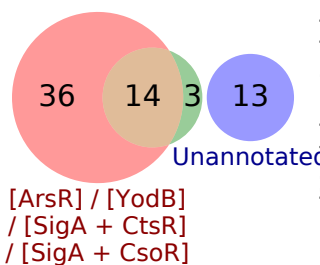
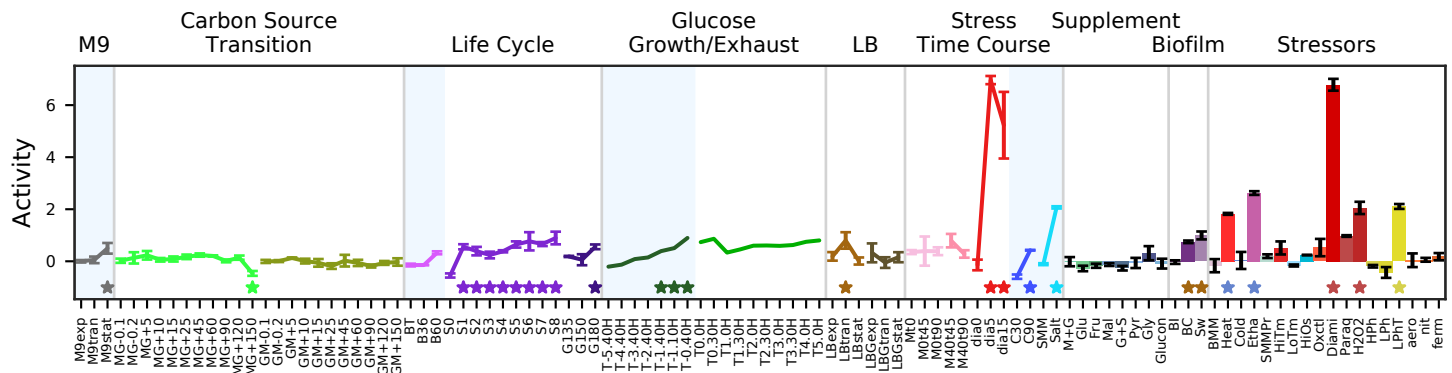
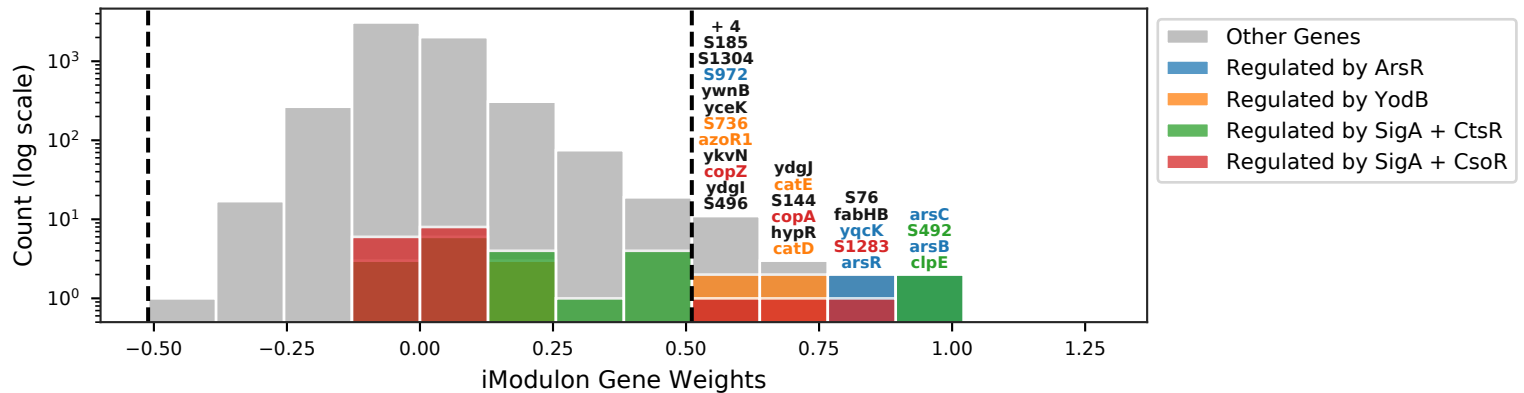
Enriched for known regulon:

[ArsR] / [YodB] / [SigA + CtsR] / [SigA + CsoR]

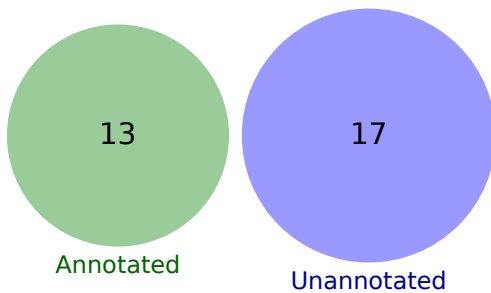


Gene Categories

- Coping with stress (12)
- Uncharacterized (9)
- Regulation of gene expression (4)
- Poorly characterized/ putative enzymes (2)
- Proteins of unknown function (1)
- Lipid metabolism (1)
- Carbon metabolism (1)



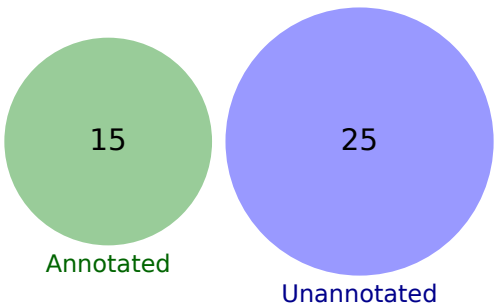
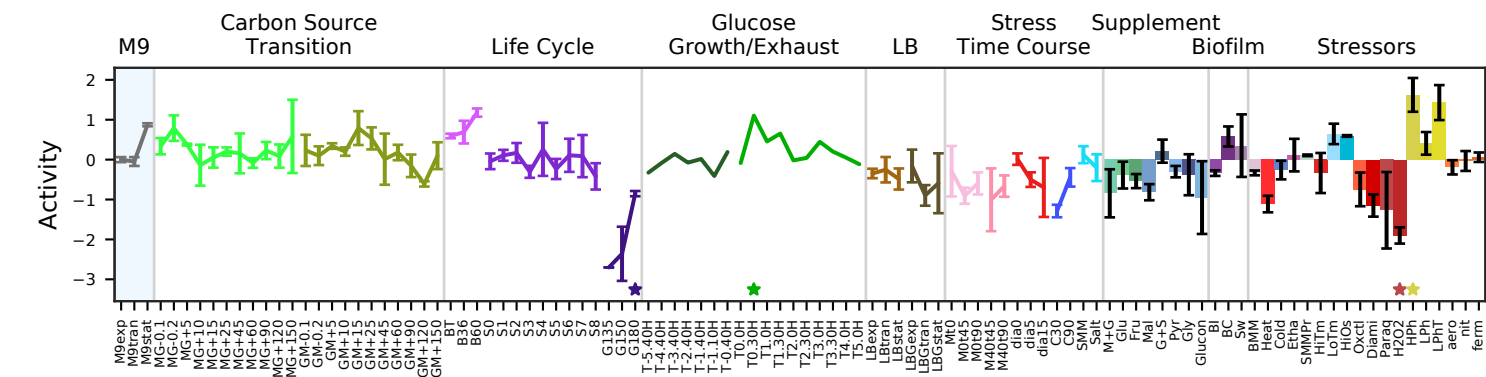
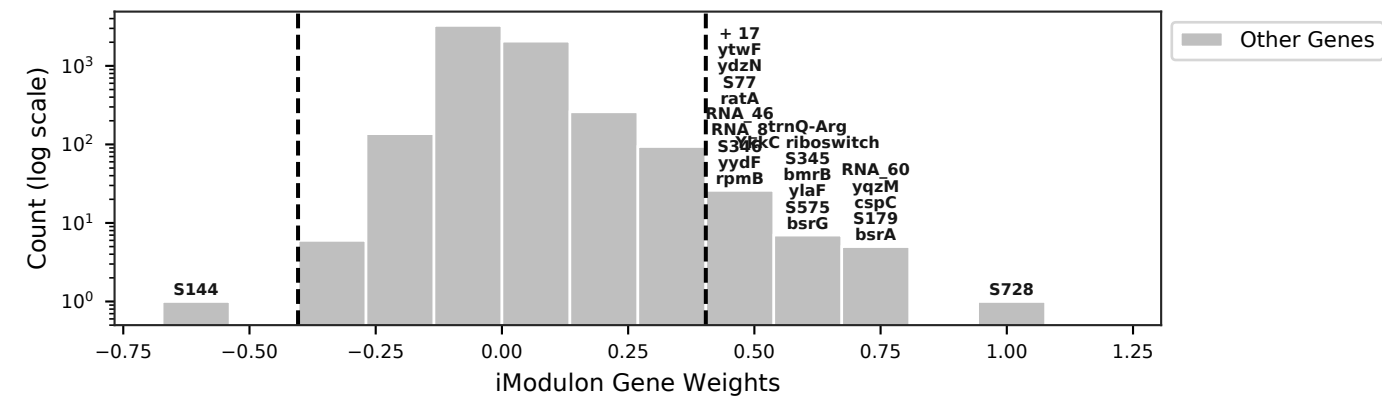
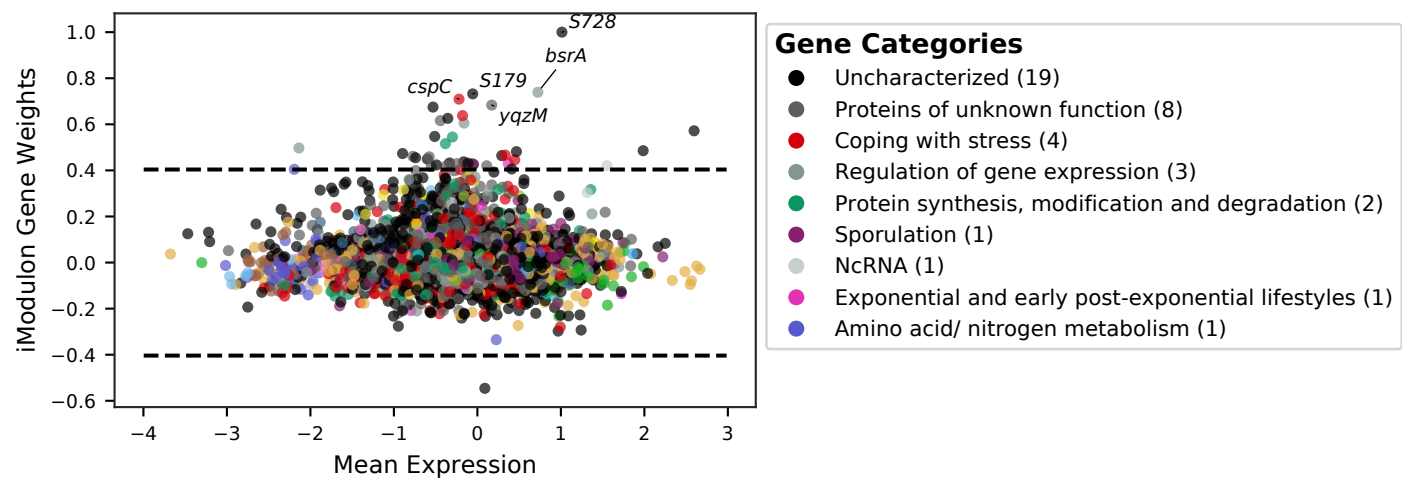
Motif E-value: 1.90e-05
Operons with Upstream Motif: 31%



67 - Uncharacterized 2

Biological Function:
Contains cold shock, sporulation onset, toxin, amino acid homeostasis, translataional, other proteins, many RNAs

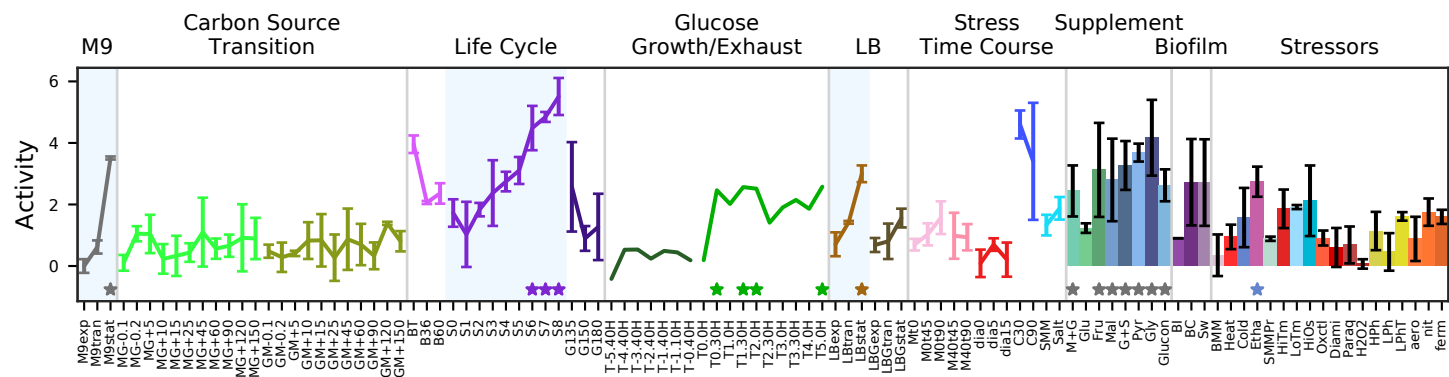
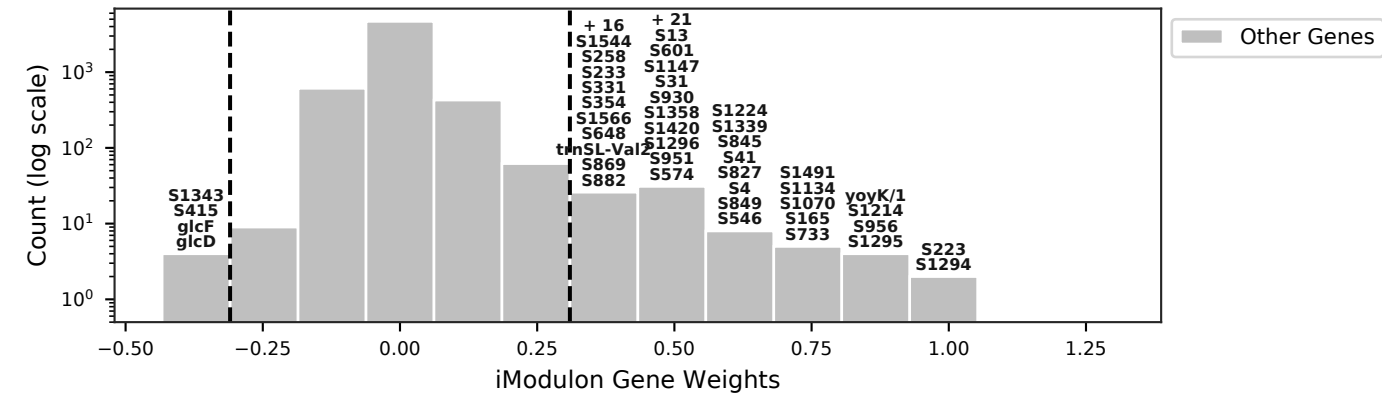
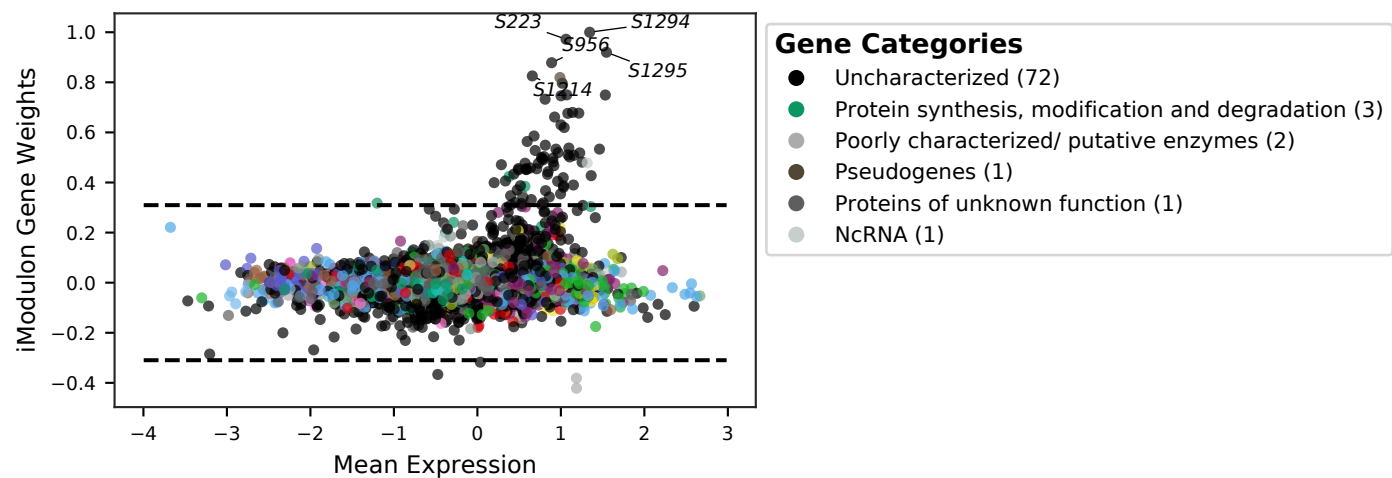
No known regulator



68 - Uncharacterized 3

Biological Function:
Contains many poorly characterized RNAs with noisy activity but clear time correlations, especially in sporulation. May be indicative of overall decreased translational activity

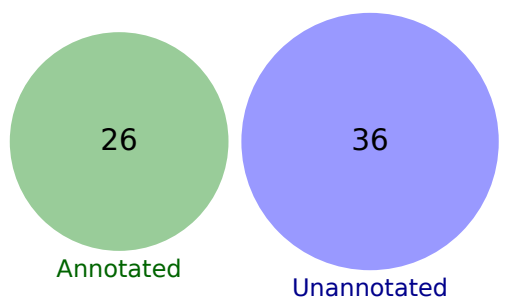
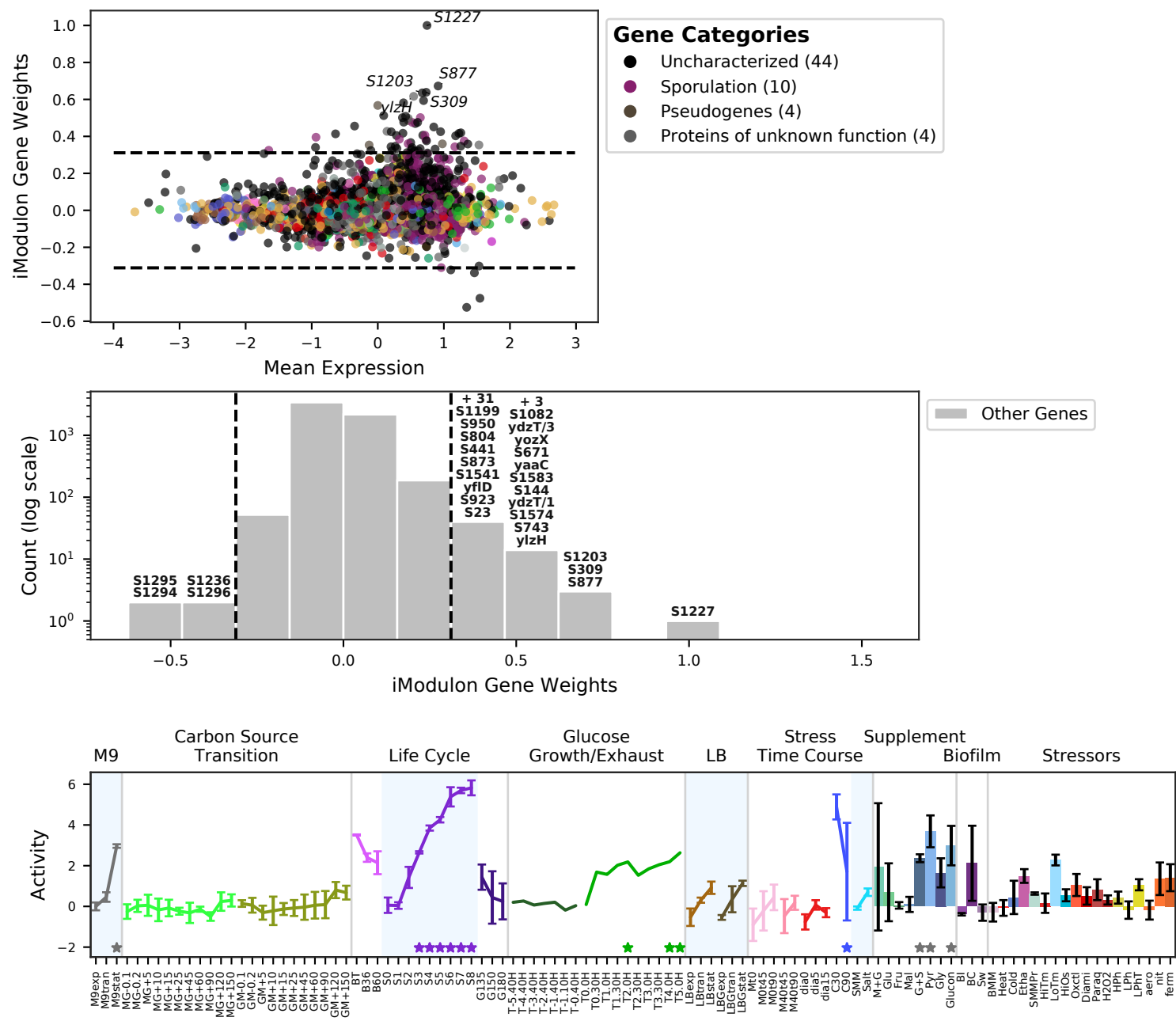
No known regulator

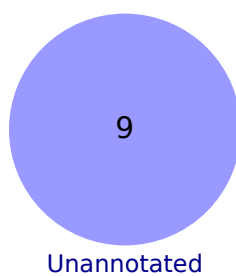


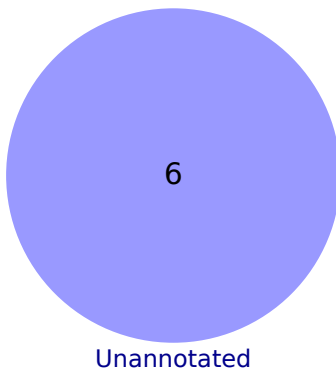
69 - Uncharacterized 4

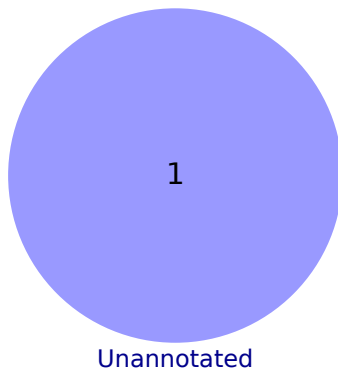
Biological Function:
Contains many poorly characterized RNAs with noisy activity

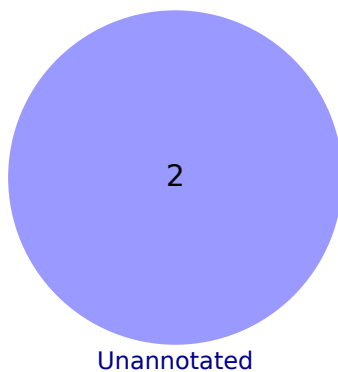
No known regulator



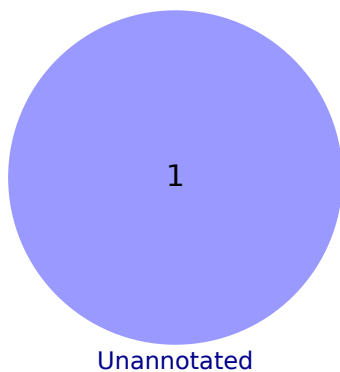








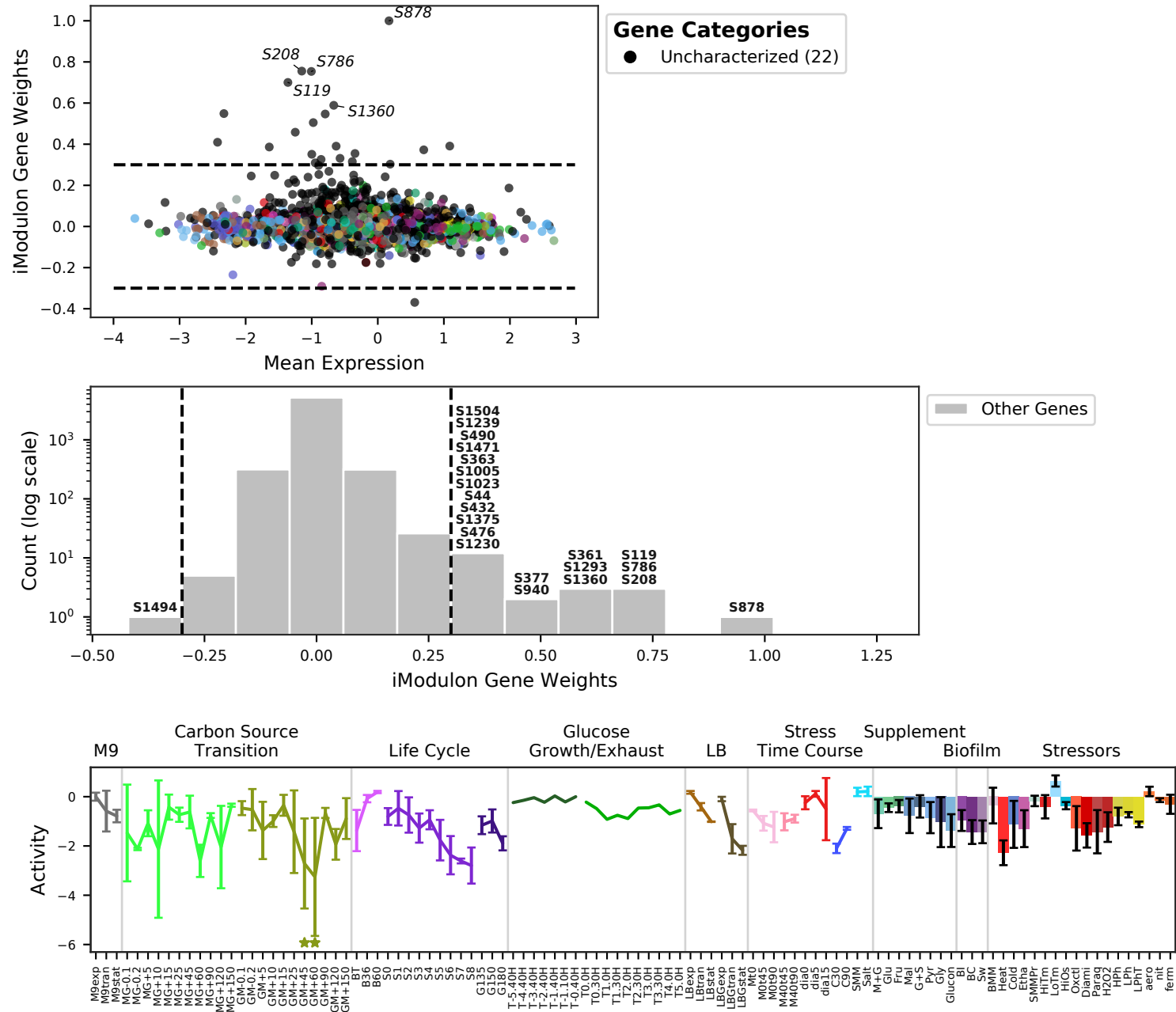
Unannotated

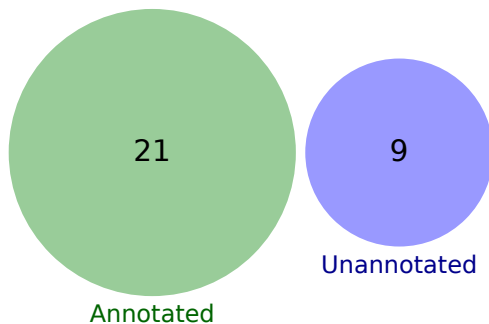


76 - Noise - Carbon Source Transition 1

Biological Function:
Likely accounting for noise in the carbon source transition experiments

No known regulator



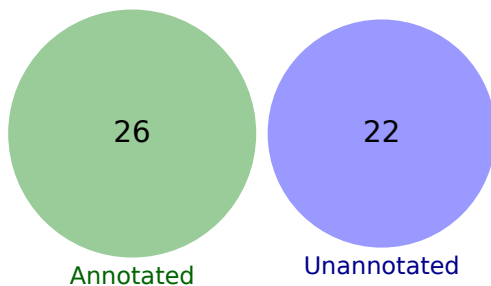
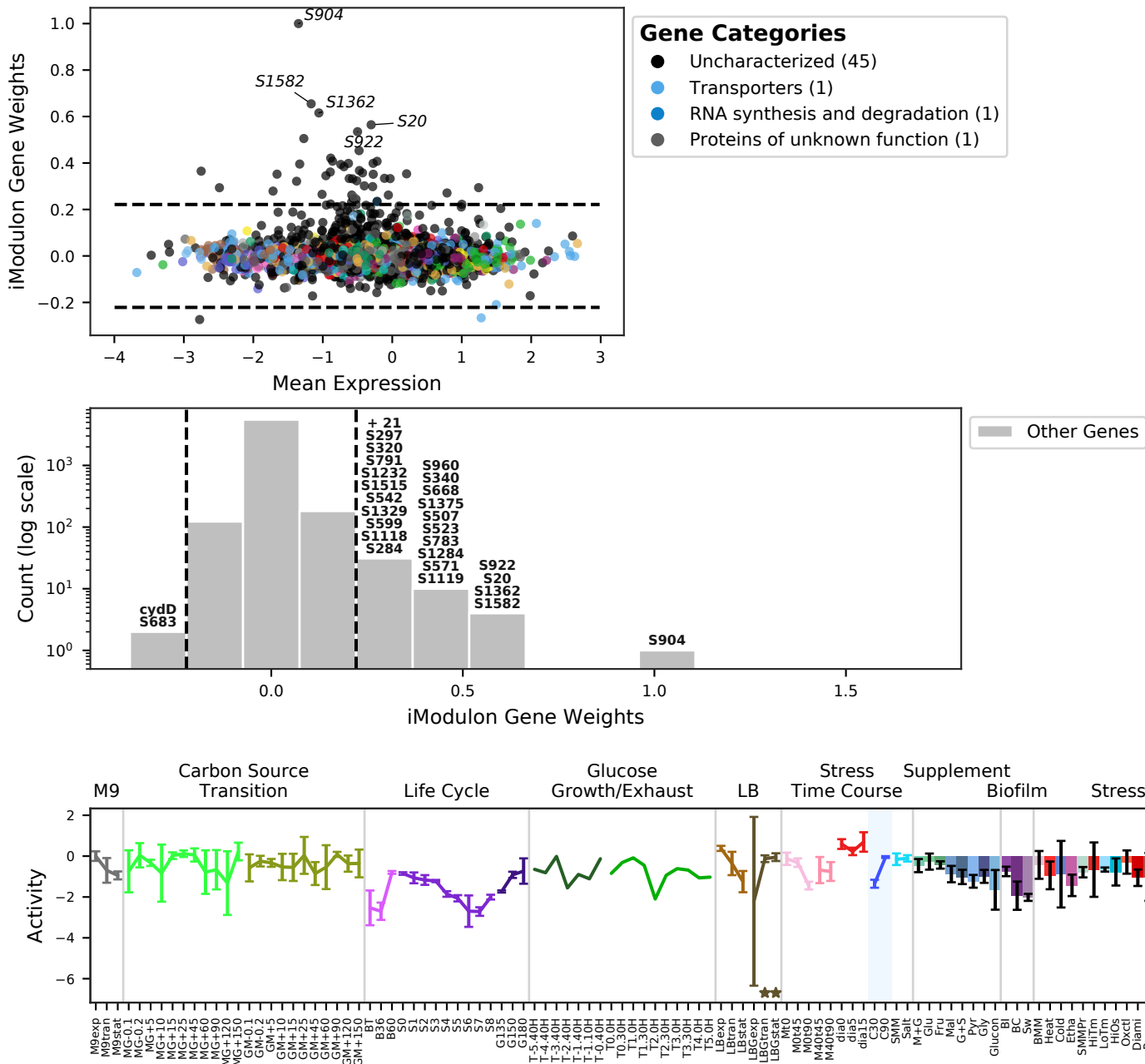


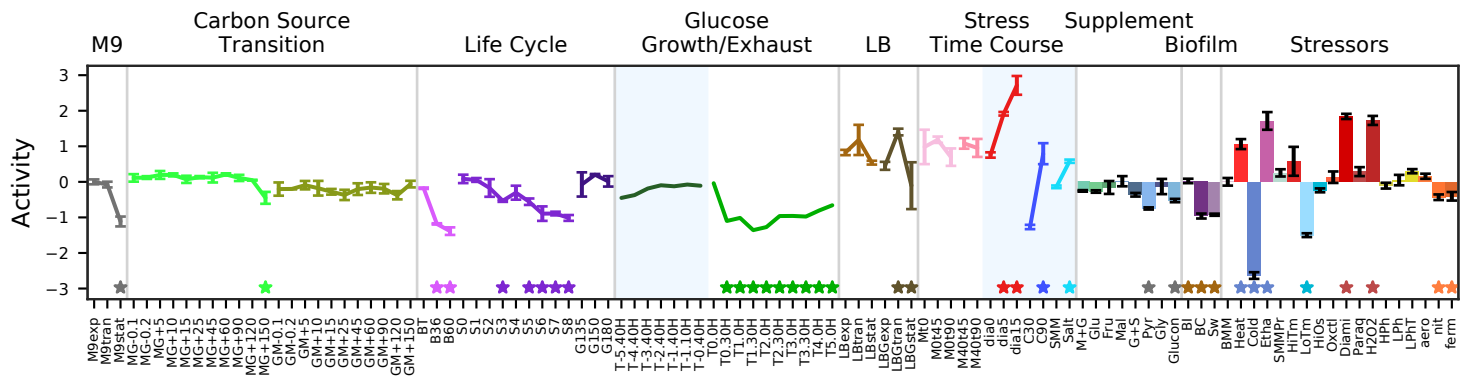
78 - Noise - LBGexp_1

Biological Function:

Likely accounting for noise in the first sample of LBG_exp. Top few RNAs are 5' UTRs of glucose metabolism genes

No known regulator





81 - Empty 2

Biological Function:
Contains no genes

No known regulator

