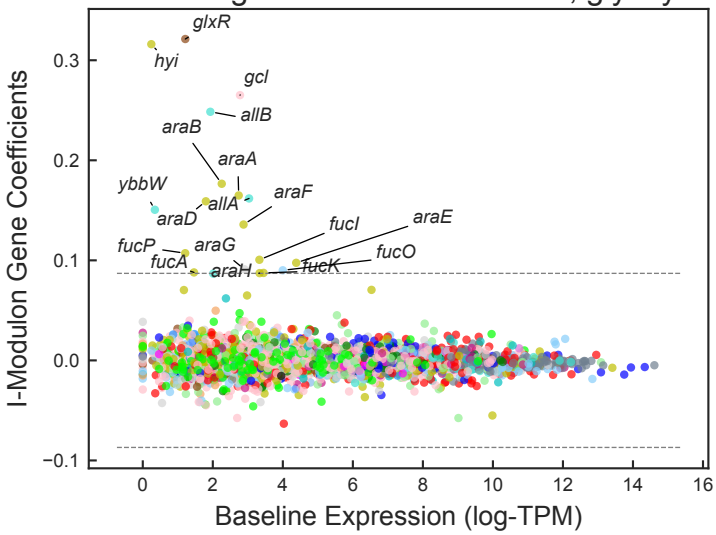
AllR/AraC/FucR I-Modulon

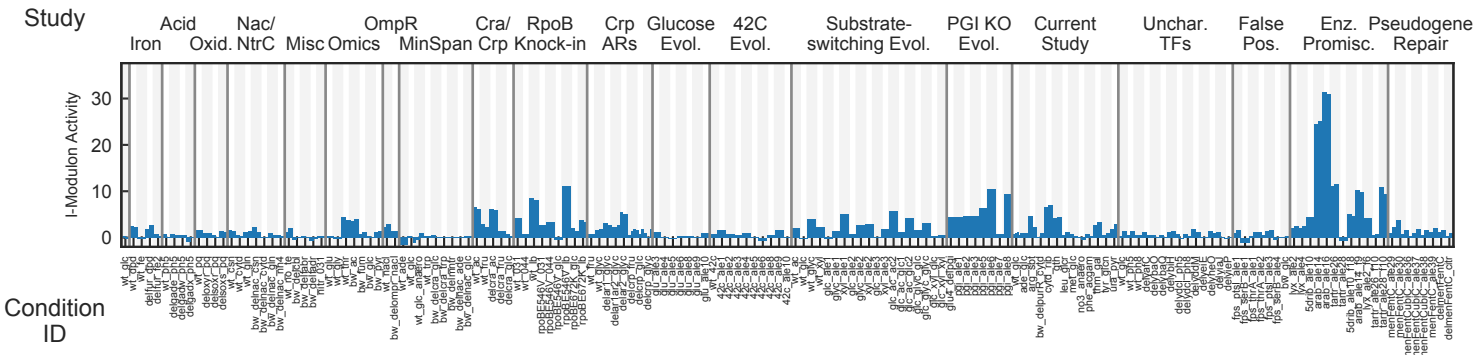
Regulated by: AllR or AraC or FucR

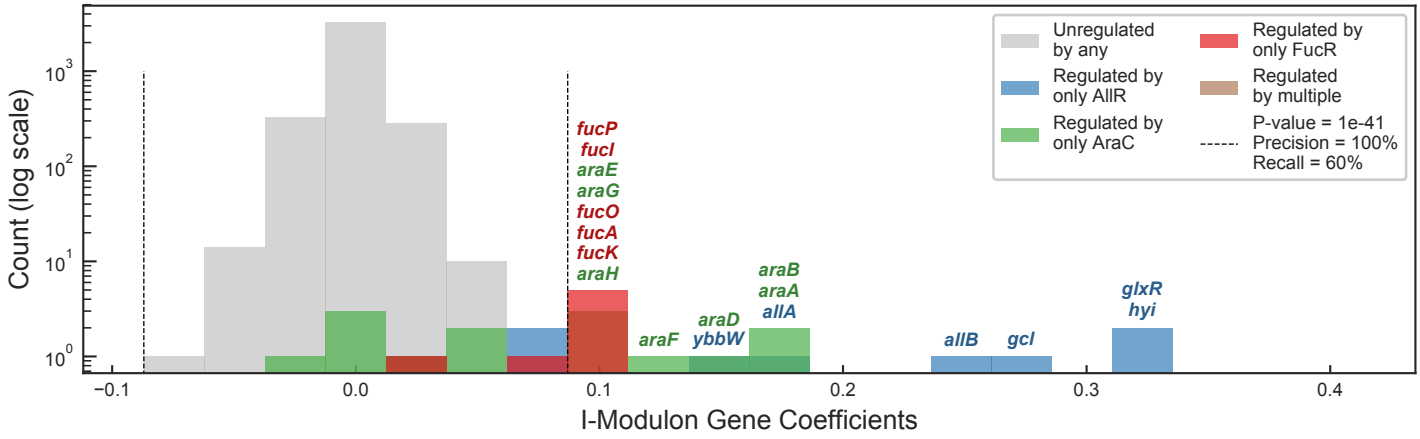
Biological Function: Allantoin, glyoxylate, L-arabinose, and L-fucose catabolism

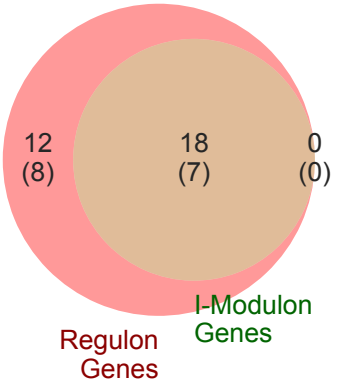


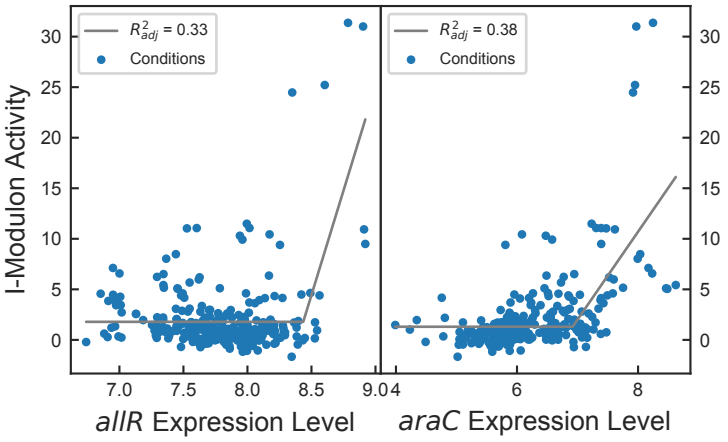
COG Categories

- Carbohydrate transport and metabolism (11): *araA*, *araB*, *araD*, *araE*, *araF*, *araH*, *fucA*, *fucI*, *fucK*, *fucP*, *hyi*
- Nucleotide transport and metabolism (3): *allA*, *allB*, *ybbW*
- Energy production and conversion (1): *fucO*
- Inorganic ion transport and metabolism (1): *araG*
- Lipid transport and metabolism (1): *glxR*
- Function unknown (1): *gcl*





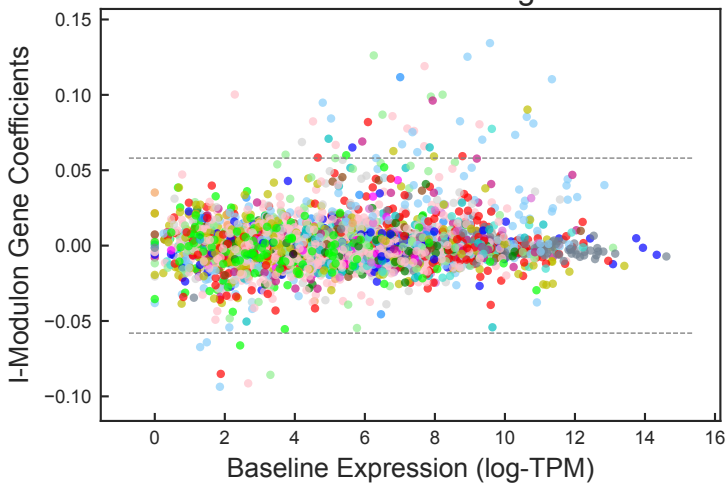




ArcA – 1 I-Modulon

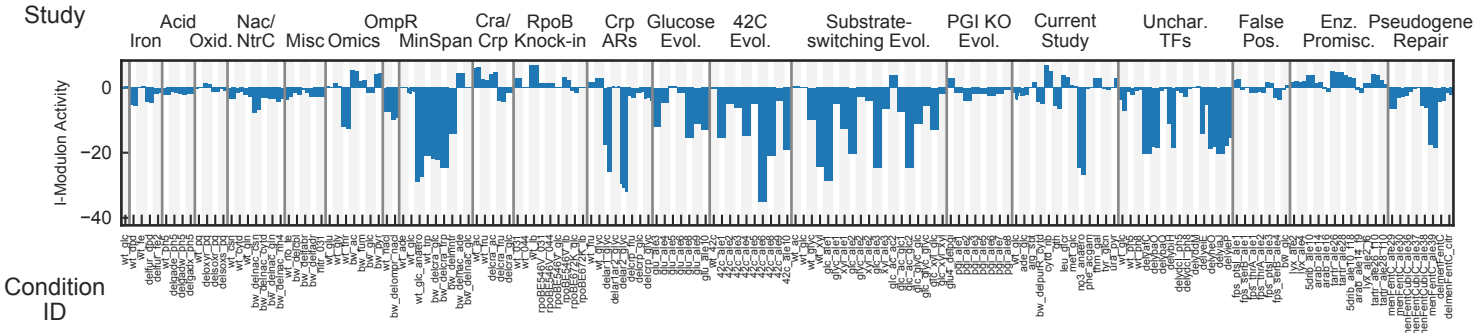
Regulated by: ArcA

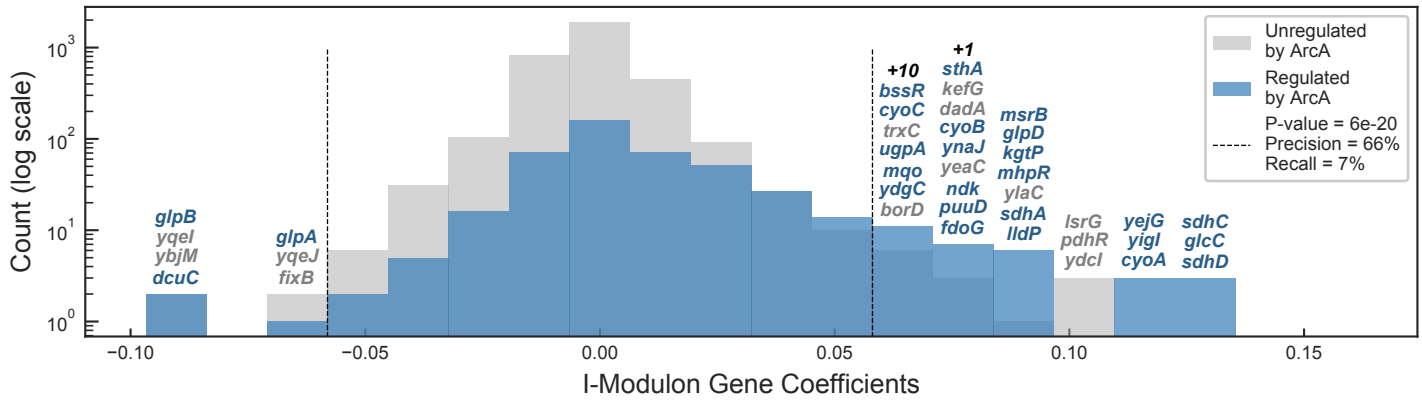
Biological Function: Anaerobic response

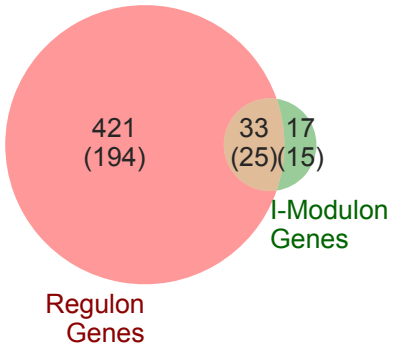


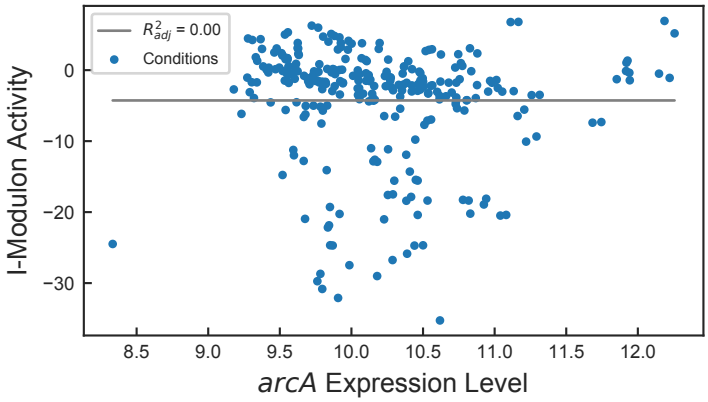
COG Categories

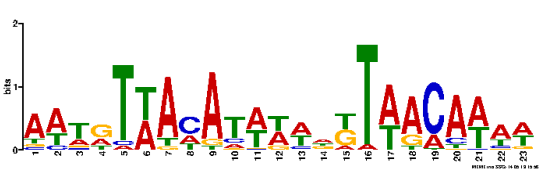
- Energy production and conversion (17): *cyoA*, *cyoB*, *cyoC*, *cyoD*, *dctA*, *dcuC*, *fdoG*, *fixB*, *glpA*, *glpD*, *lldP*, *mqo*, *sdhA*, *sdhB*, *sdhC*, *sdhD*, *sthA*
- Transcription (6): *glcC*, *mhpR*, *pdhR*, *prpR*, *ydcI*, *yqeI*
- Amino acid transport and metabolism (4): *astC*, *dadA*, *glpB*, *puuA*
- Carbohydrate transport and metabolism (3): *gcd*, *kgtP*, *ugpB*
- Other (20): *msrB*, *trxC*, *bssR*, *phoH*, *dadX*, *ugpA*, *ndk*, *yigI*, *borD*, *kefG*, *lsrG*, *puuD*, *ybjM*, *ydgC*, *yeaC*, *yejG*, *ylaC*, *ynaJ*, *mntS*, *yqeJ*





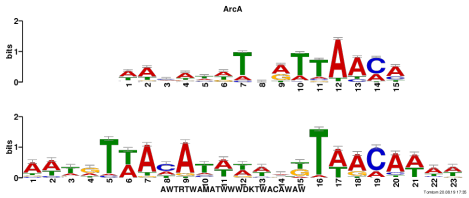






Motif E-value: 1.40e-12

Operons with Upstream Motif: 85%

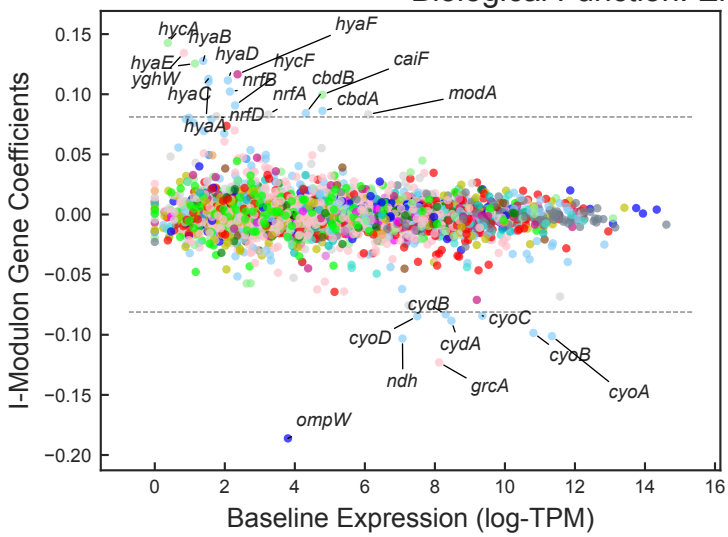


Motif similar to ArcA (E-value: 3.24e-04)

ArcA – 2 I-Modulon

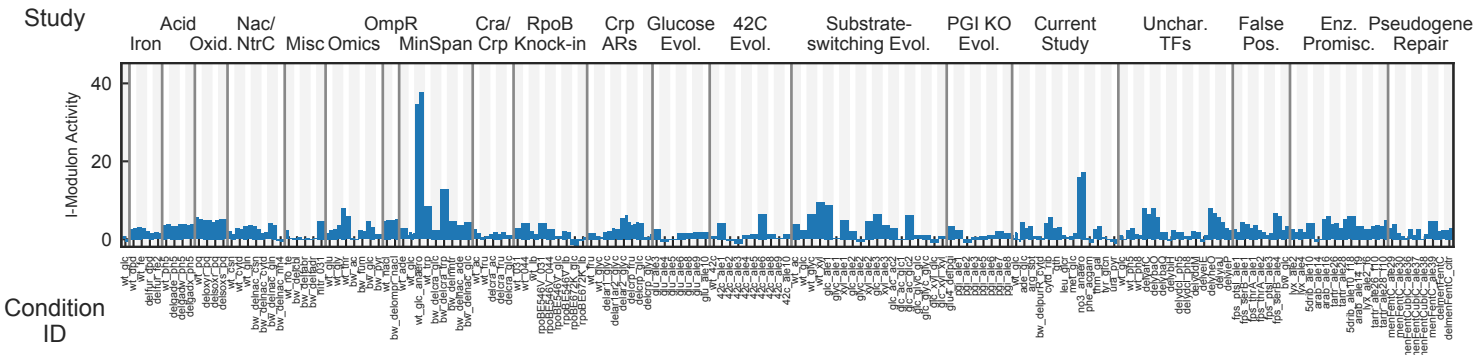
Regulated by: ArcA

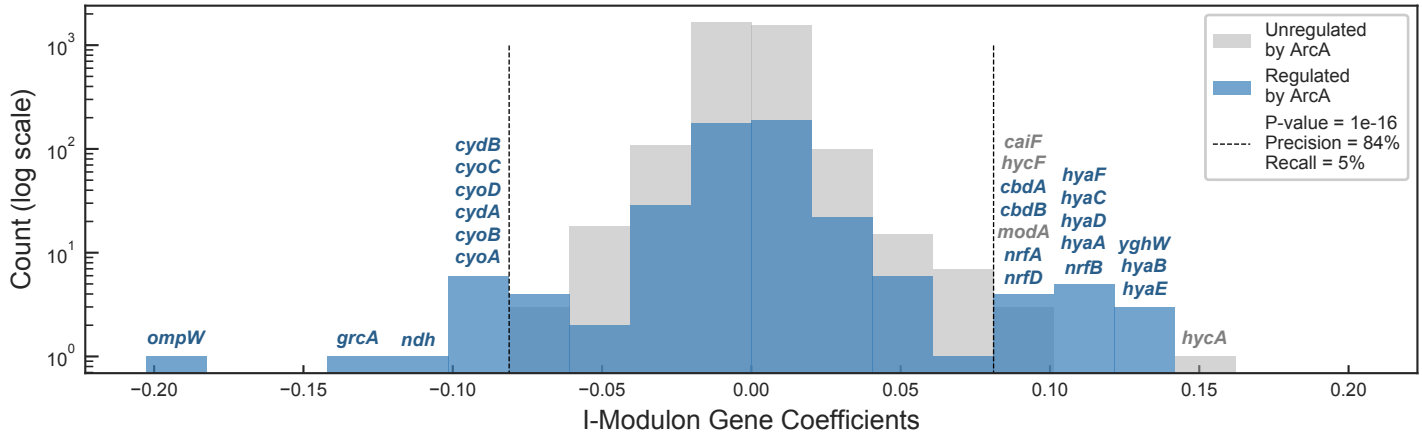
Biological Function: Electron Transport Chain

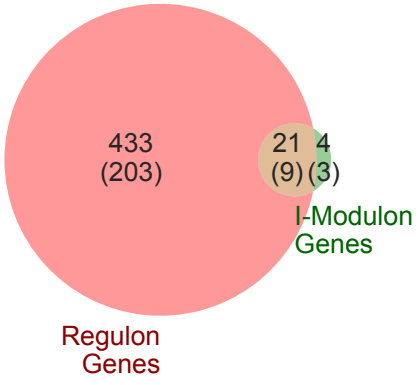


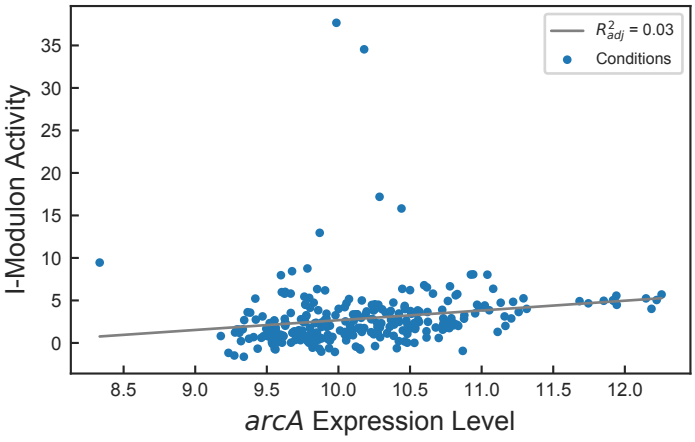
COG Categories

- Energy production and conversion (15): *cbdA*, *cbdB*, *cydA*, *cydB*, *cyoA*, *cyoB*, *cyoC*, *cyoD*, *hyaA*, *hyaB*, *hyaC*, *hyaD*, *hycF*, *ndh*, *nrfB*
- Inorganic ion transport and metabolism (3): *modA*, *nrfA*, *nrfD*
- Transcription (3): *caiF*, *hyaE*, *hycA*
- Cell wall/membrane/envelope biogenesis (1): *ompW*
- Posttranslational modification, protein turnover, chaperones (1): *hyaF*
- Function unknown (2): *grcA*, *yghW*





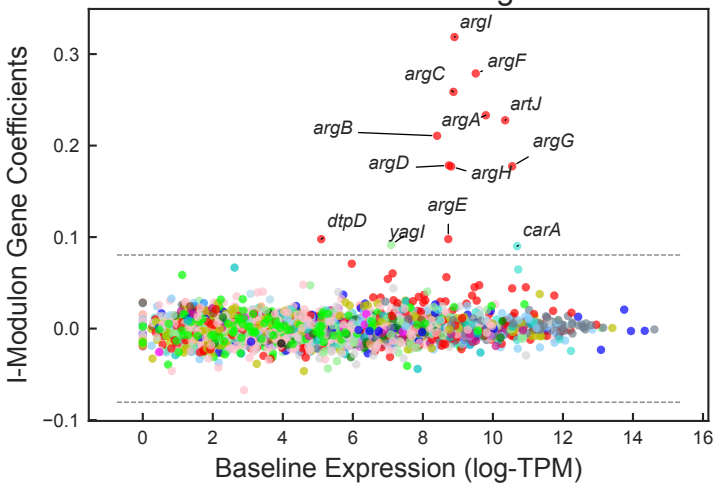




ArgR I-Modulon

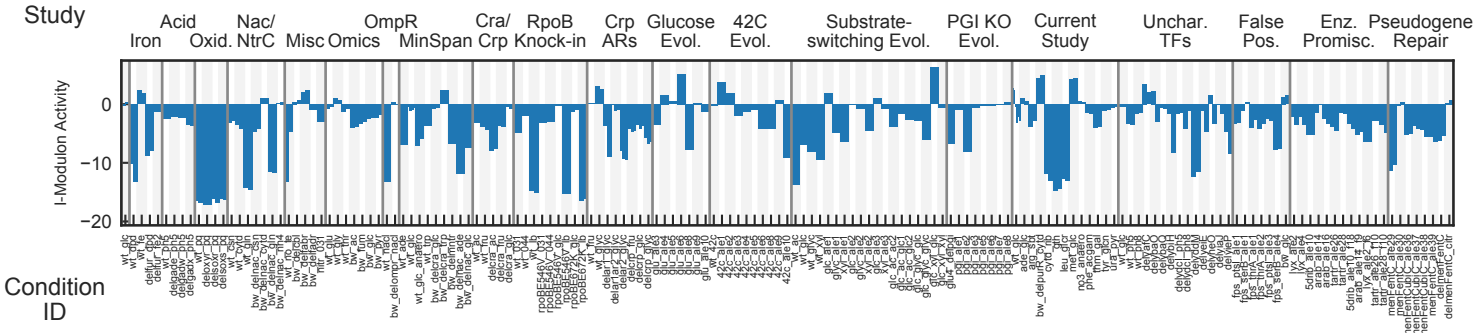
Regulated by: ArgR

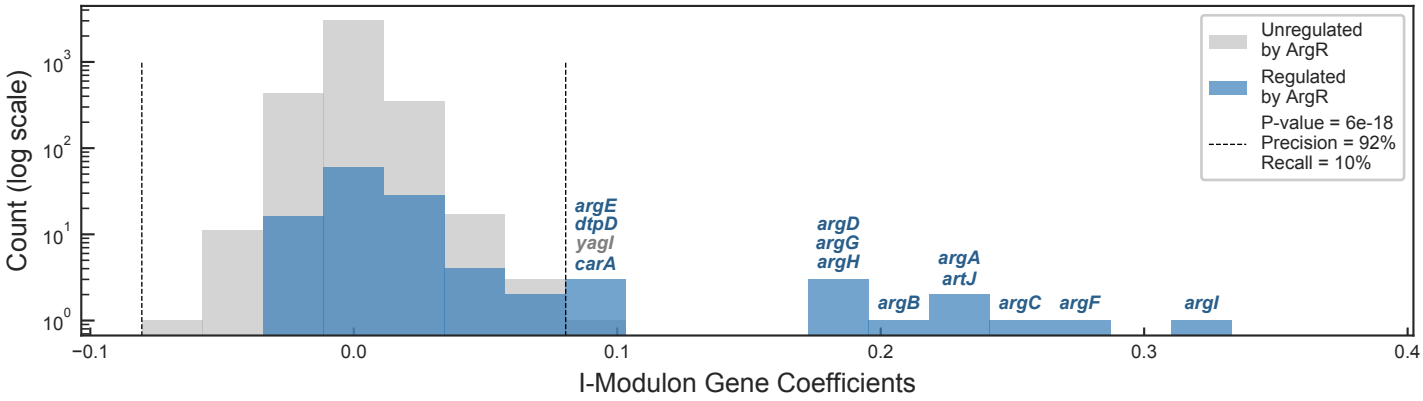
Biological Function: Arginine biosynthesis

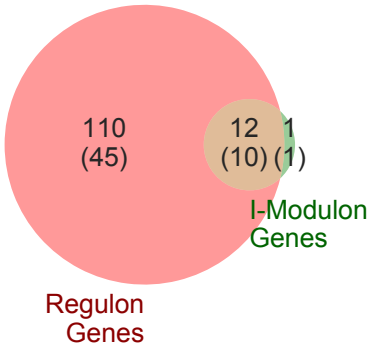


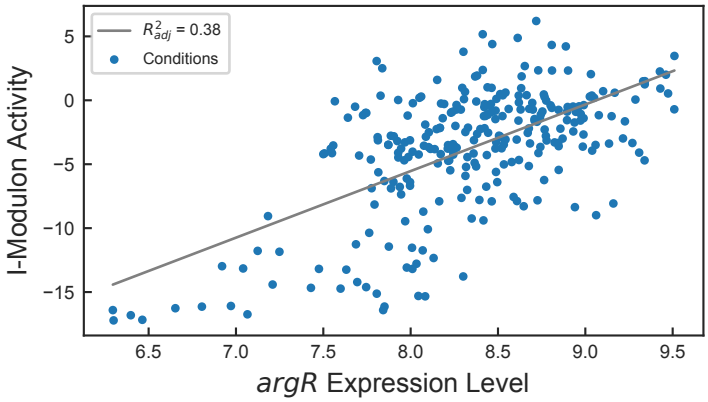
COG Categories

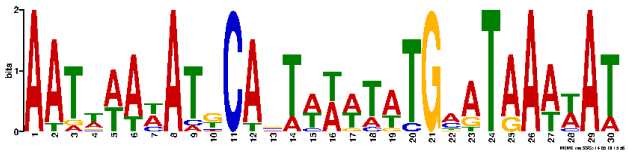
- Amino acid transport and metabolism (11): *argA*, *argB*, *argC*, *argD*, *argE*, *argF*, *argG*, *argH*, *argI*, *artJ*, *dtpD*
- Nucleotide transport and metabolism (1): *carA*
- Transcription (1): *yagI*





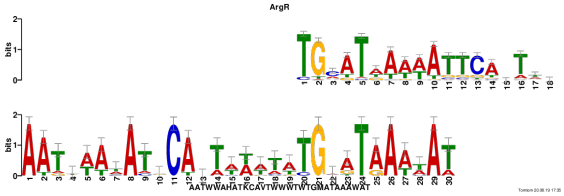






Motif E-value: 9.60e-21

Operons with Upstream Motif: 91%

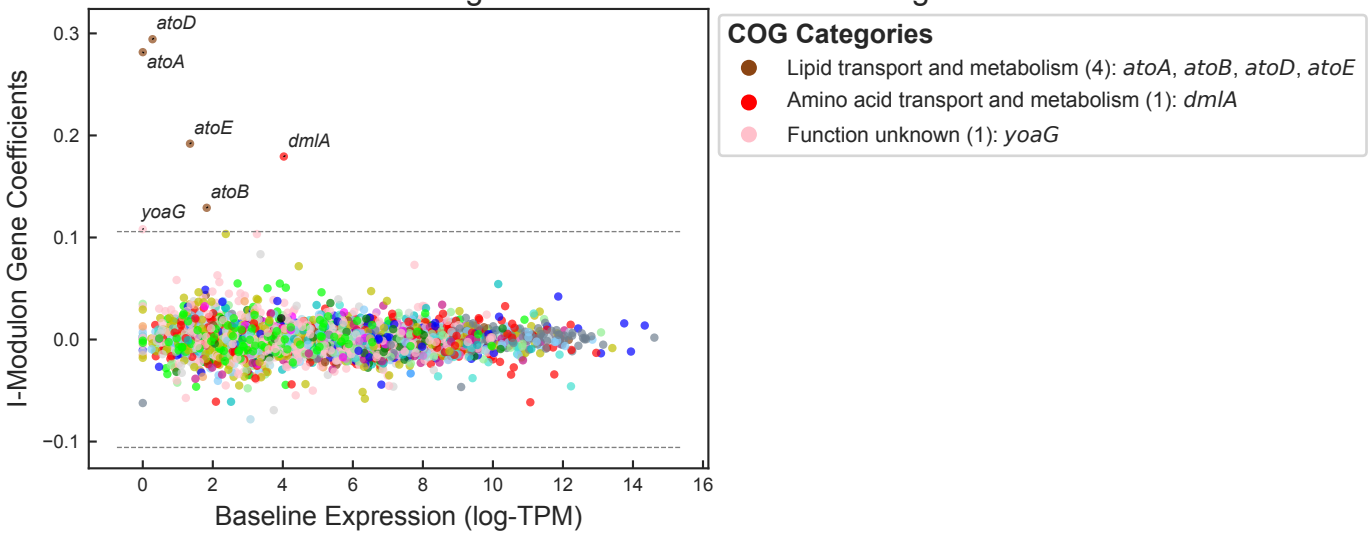


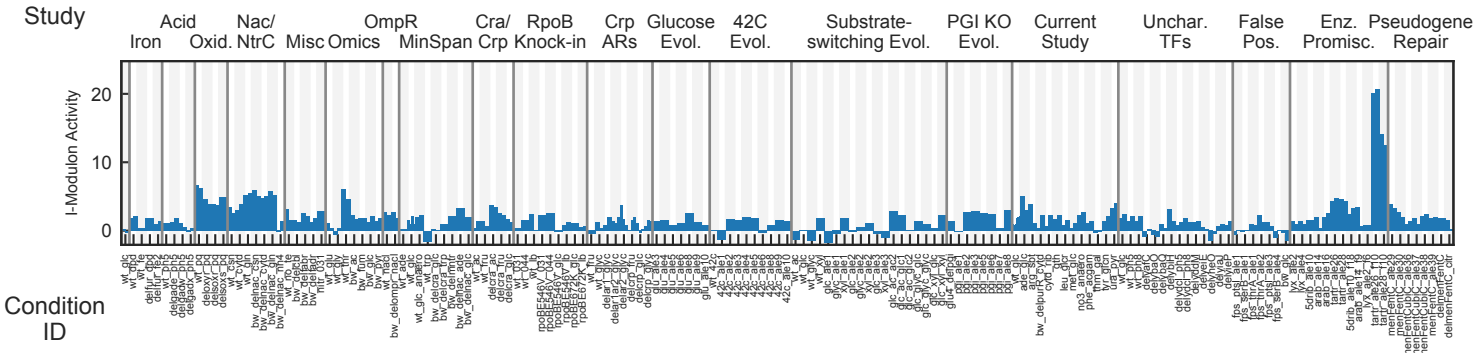
Motif similar to ArgR (E-value: 1.91e-04)

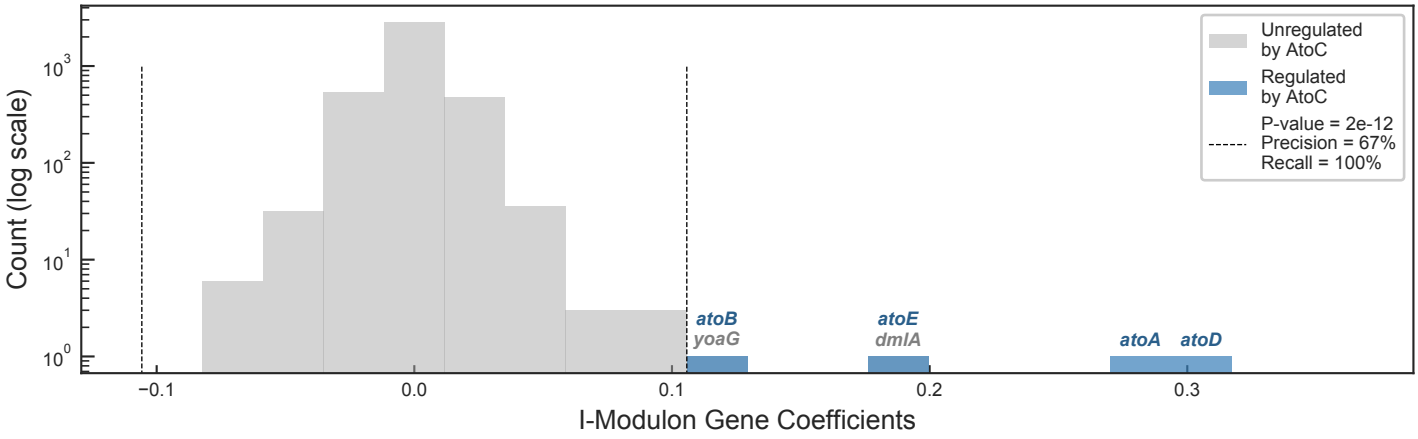
AtoC I-Modulon

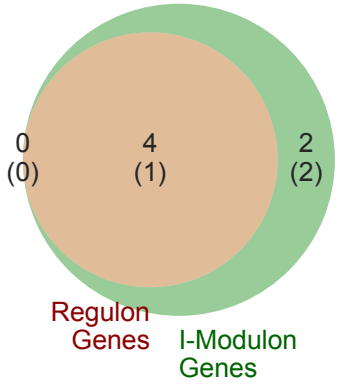
Regulated by: AtoC

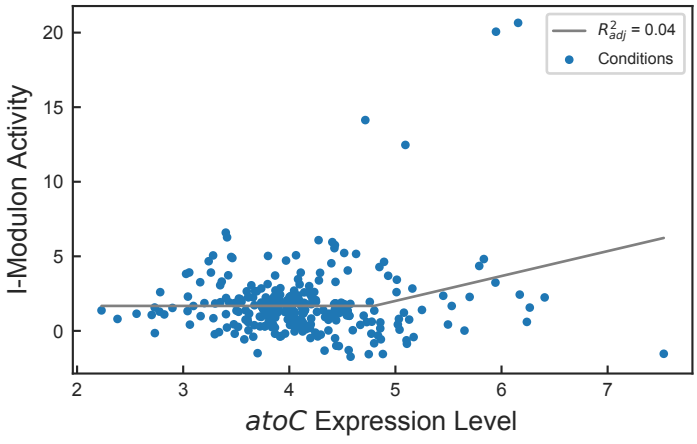
Biological Function: Acetoacetate degradation





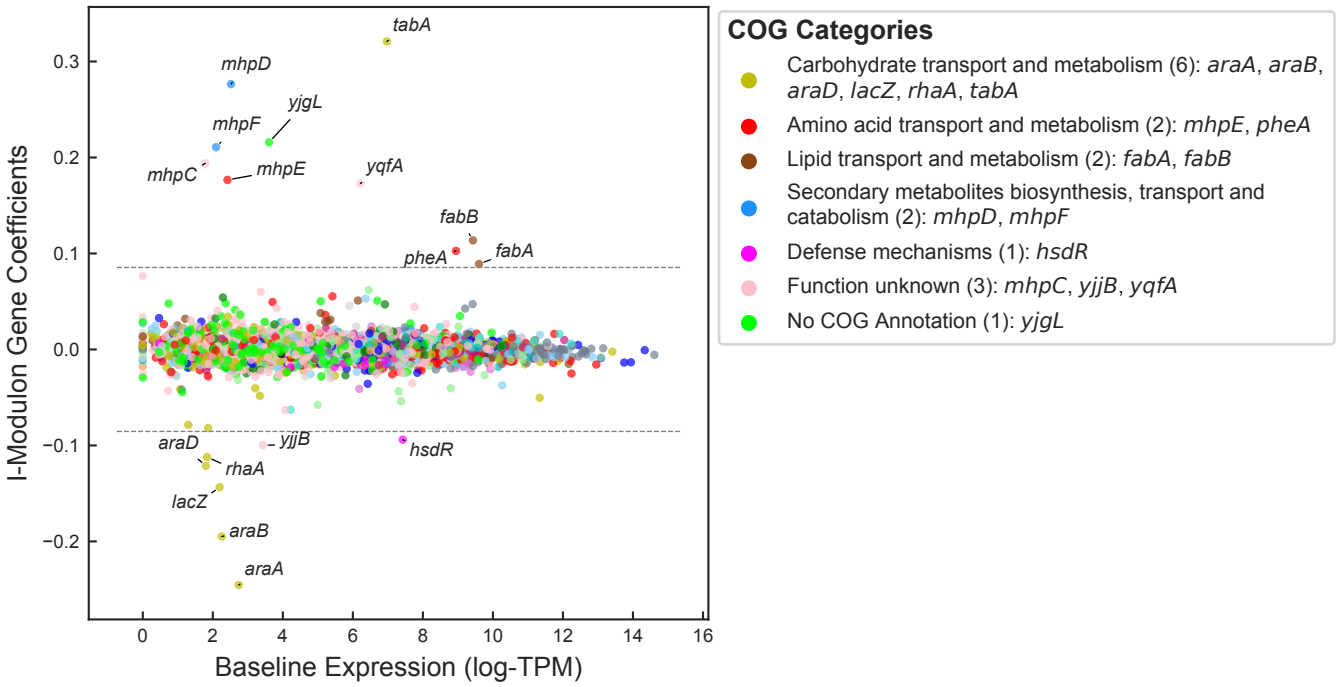


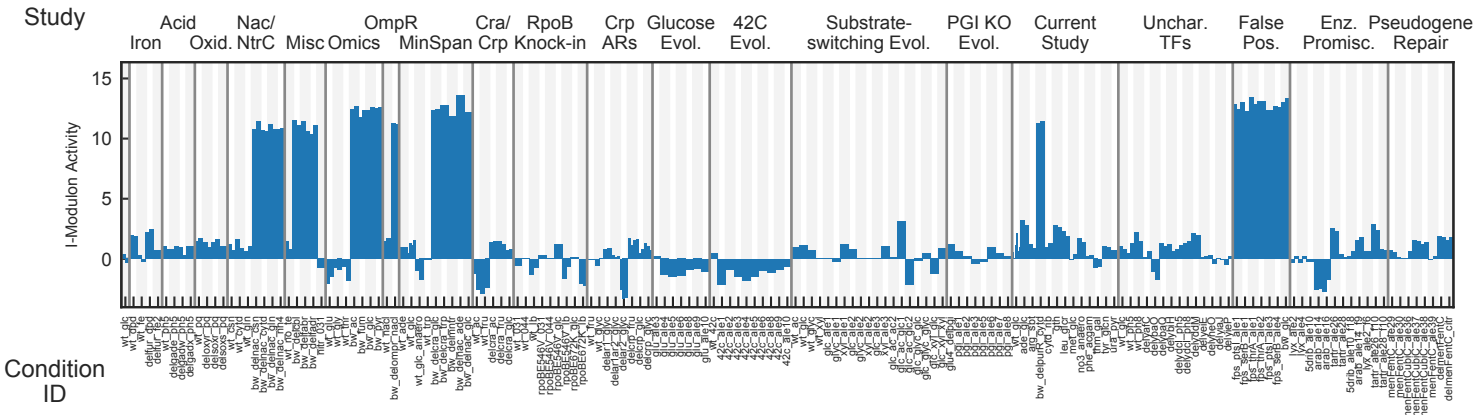


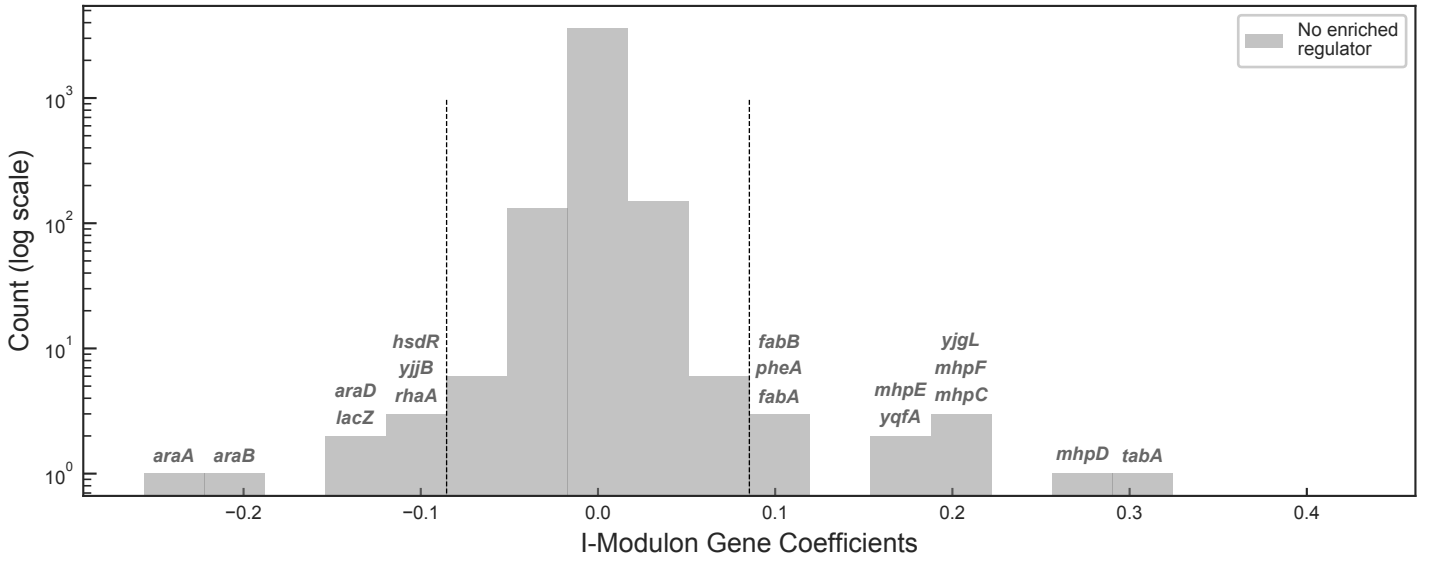


BW25113 I-Modulon

Biological Function: Transcriptional difference between BW25113 and MG1655



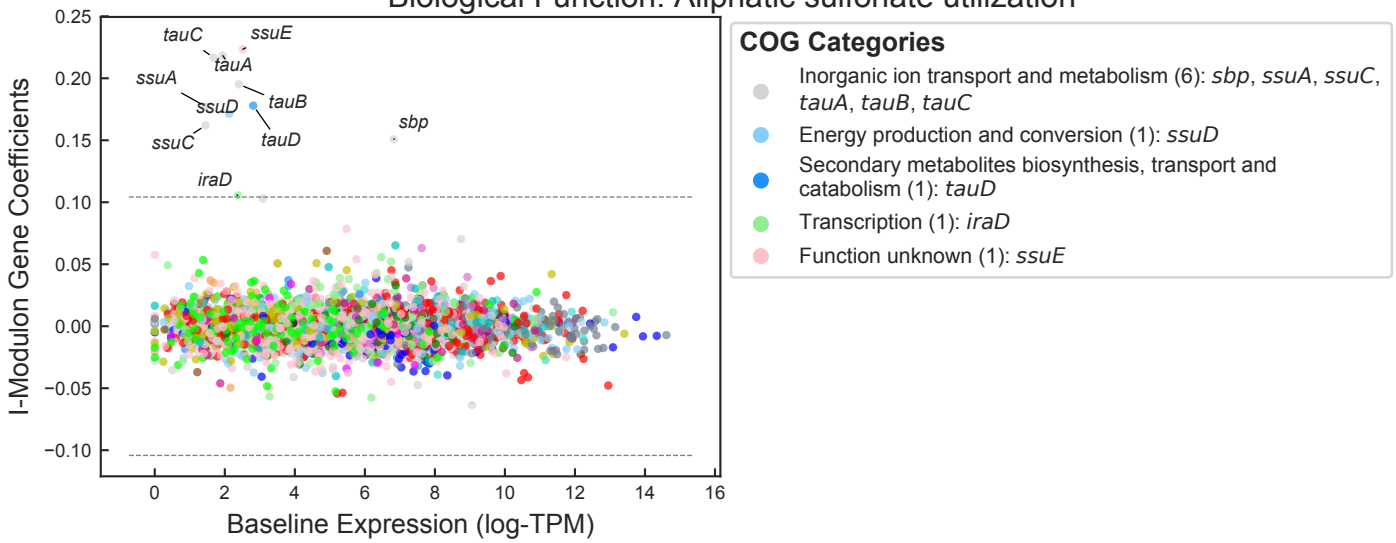


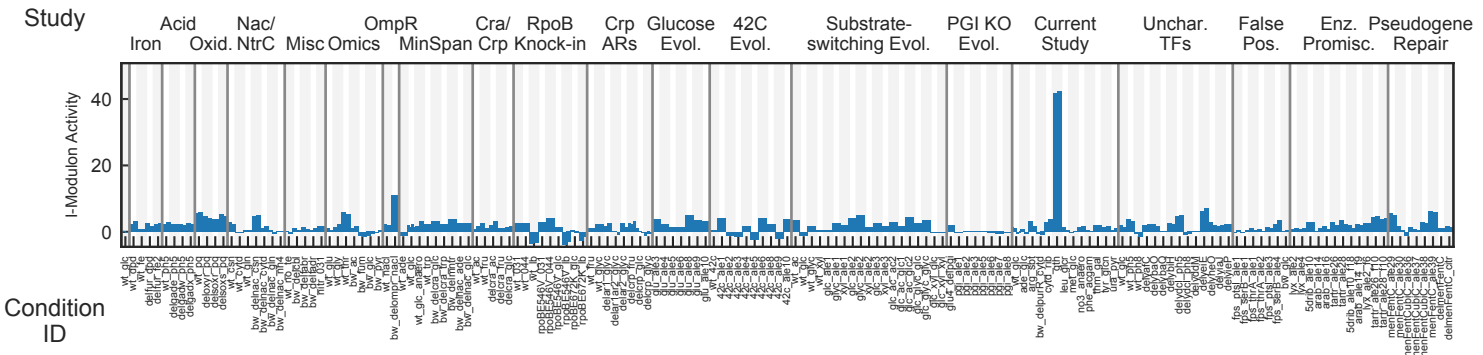


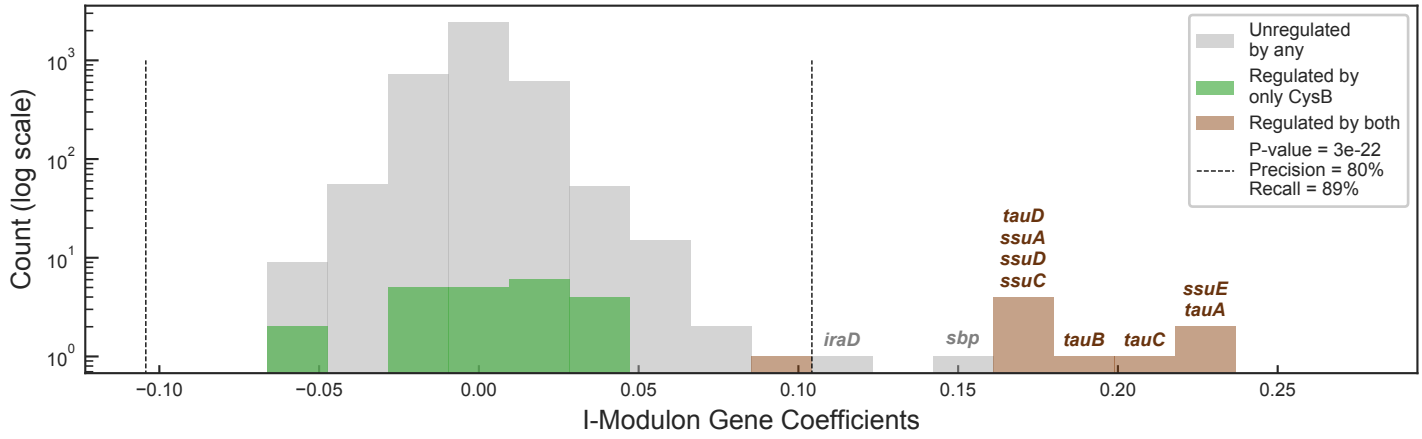
Cbl + CysB I-Modulon

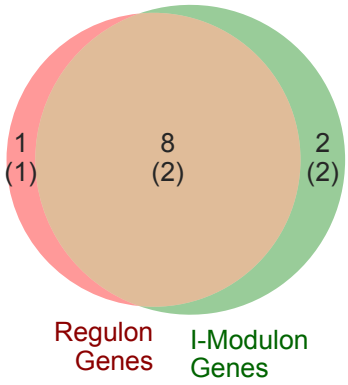
Regulated by: Cbl and CysB

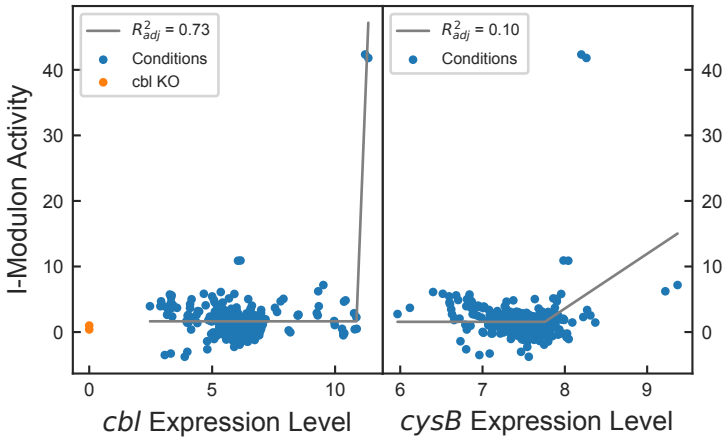
Biological Function: Aliphatic sulfonate utilization







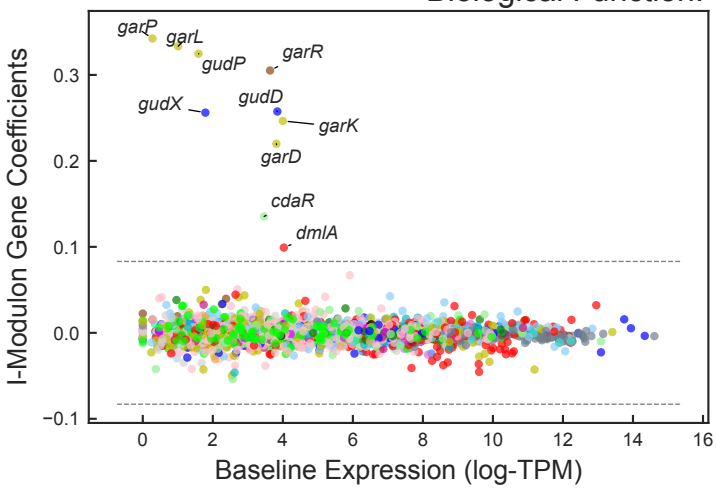




CdaR I-Modulon

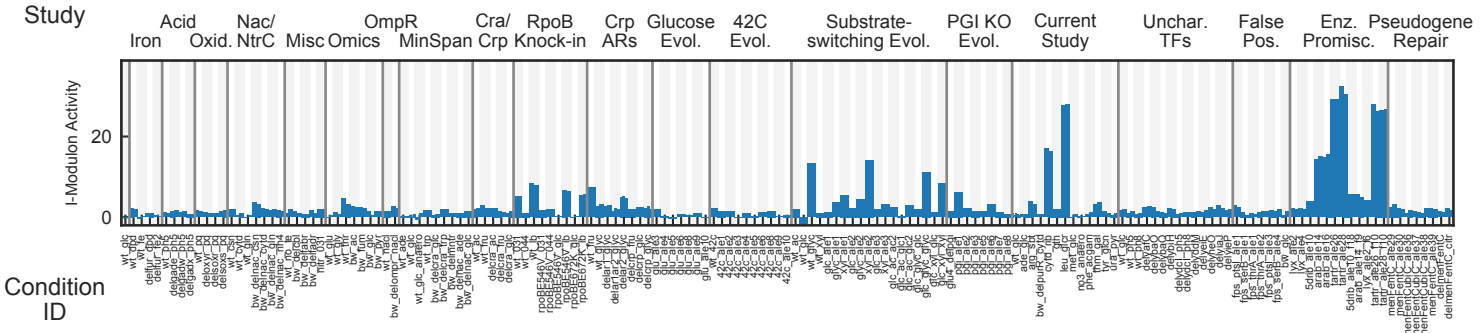
Regulated by: CdaR

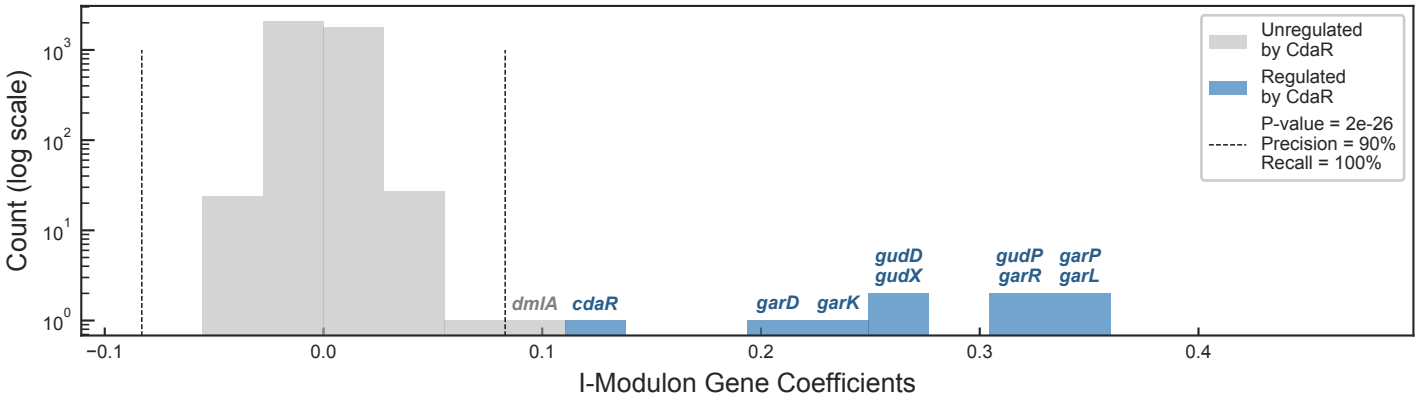
Biological Function: Glucarate catabolism

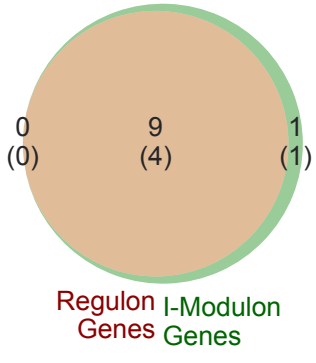


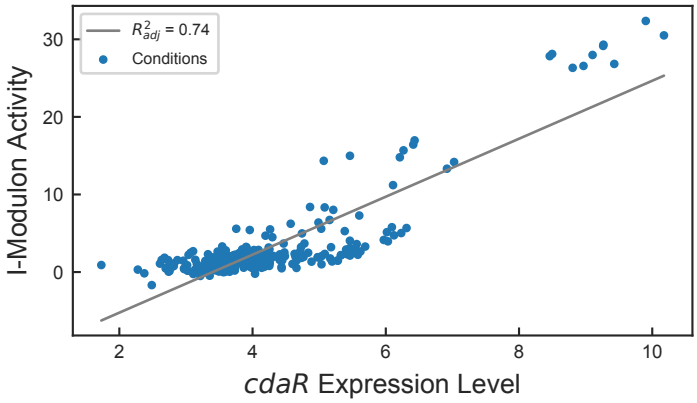
COG Categories

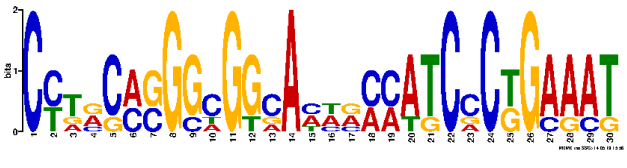
- Carbohydrate transport and metabolism (5): *garD*, *garK*, *garL*, *garP*, *gudP*
- Cell wall/membrane/envelope biogenesis (2): *gudD*, *gudX*
- Amino acid transport and metabolism (1): *dmlA*
- Lipid transport and metabolism (1): *garR*
- Transcription (1): *cdaR*





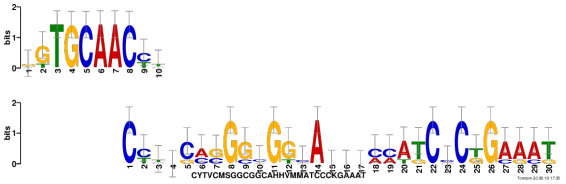






Motif E-value: 2.70e-05

Operons with Upstream Motif: 100%

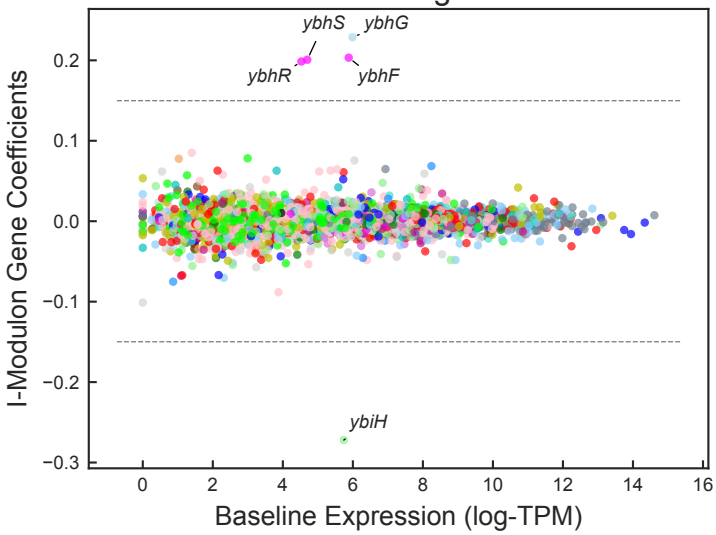


Motif similar to PutA (E-value: 1.53e-04)

CecR I-Modulon

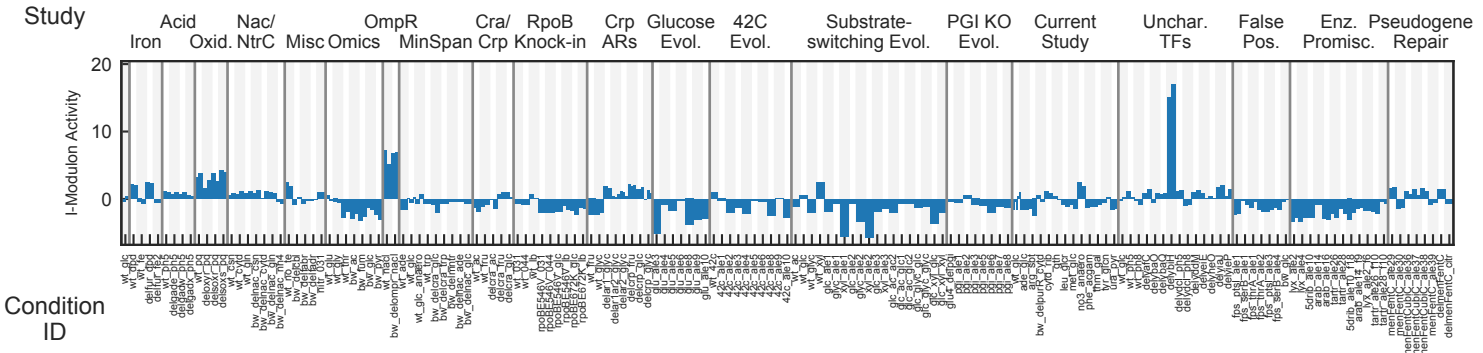
Regulated by: CecR

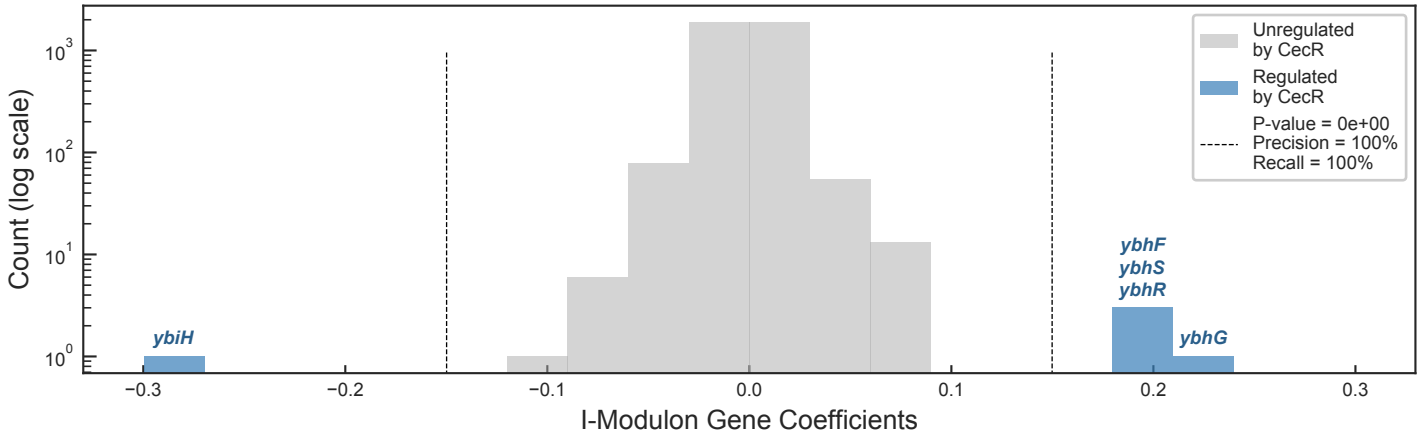
Biological Function: Related to antibiotic sensitivity

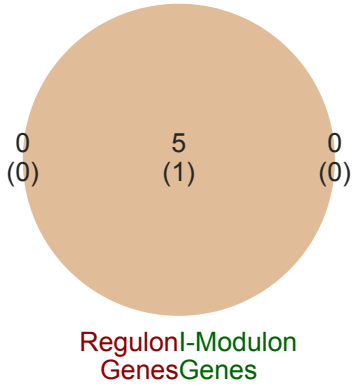


COG Categories

- Defense mechanisms (3): *ybhF*, *ybhR*, *ybhS*
- Intracellular trafficking, secretion, and vesicular transport (1): *ybhG*
- Transcription (1): *ybiH*

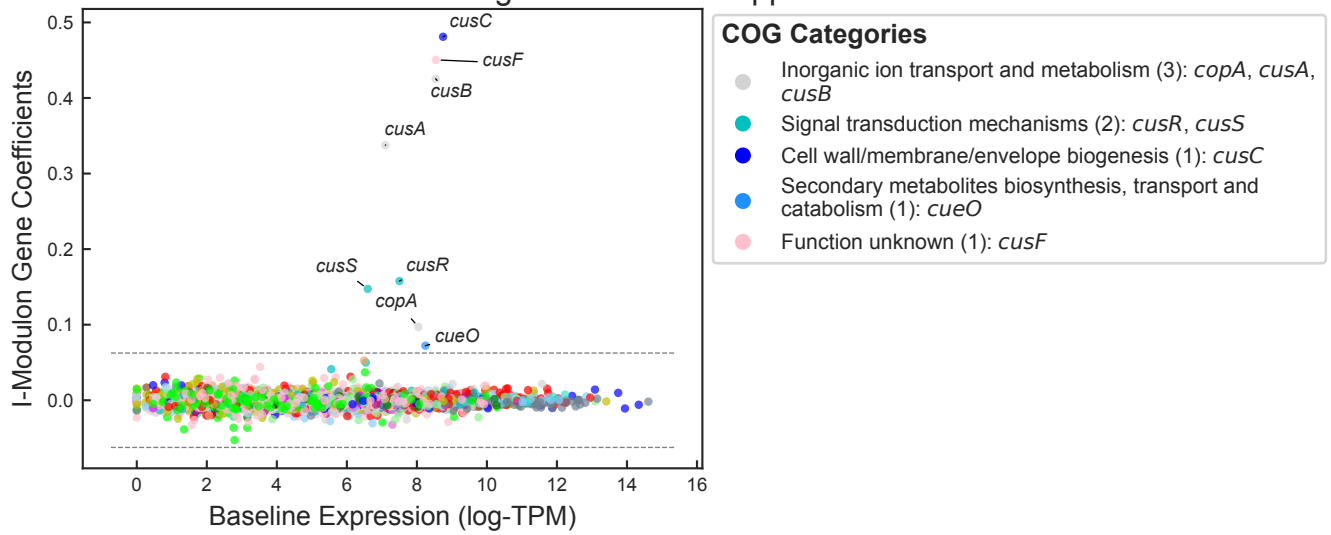


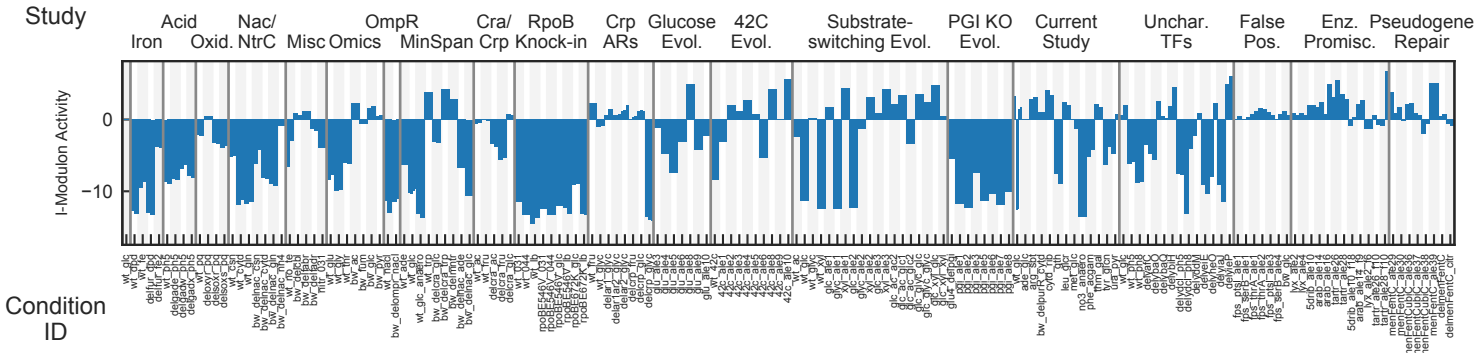


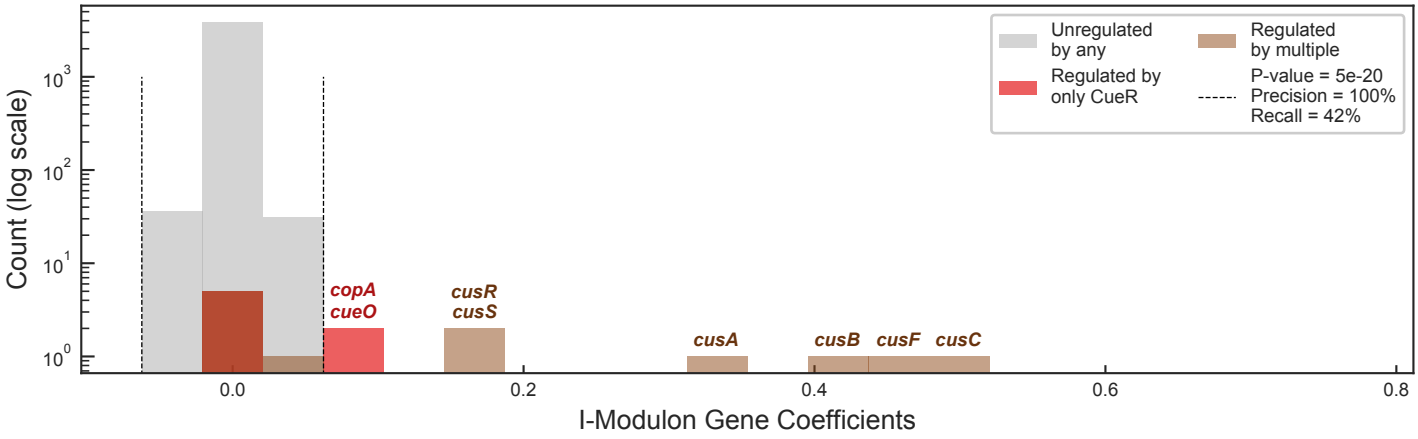


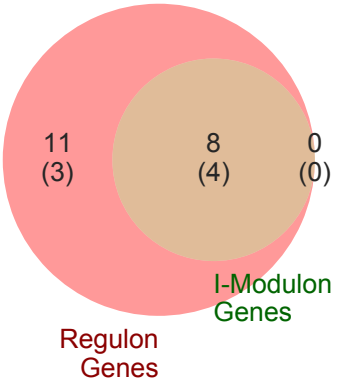
Copper I-Modulon

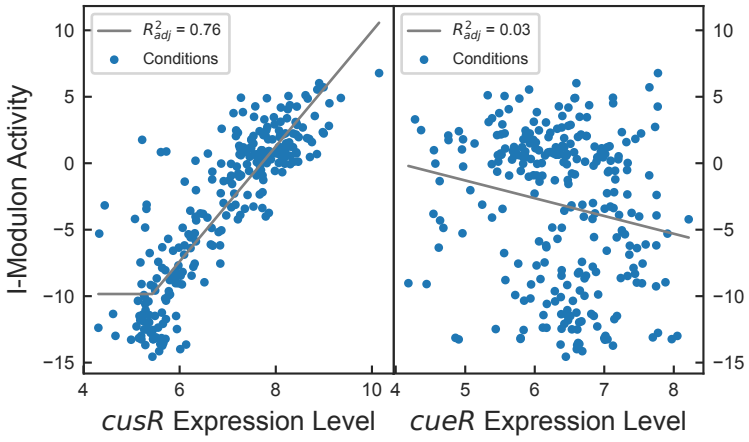
Regulated by: CusR or HprR or CueR
Biological Function: Copper homeostasis







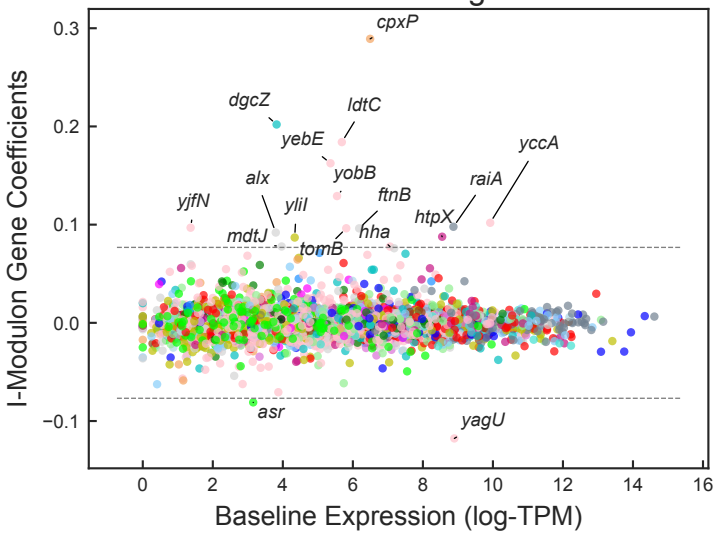




CpxR I-Modulon

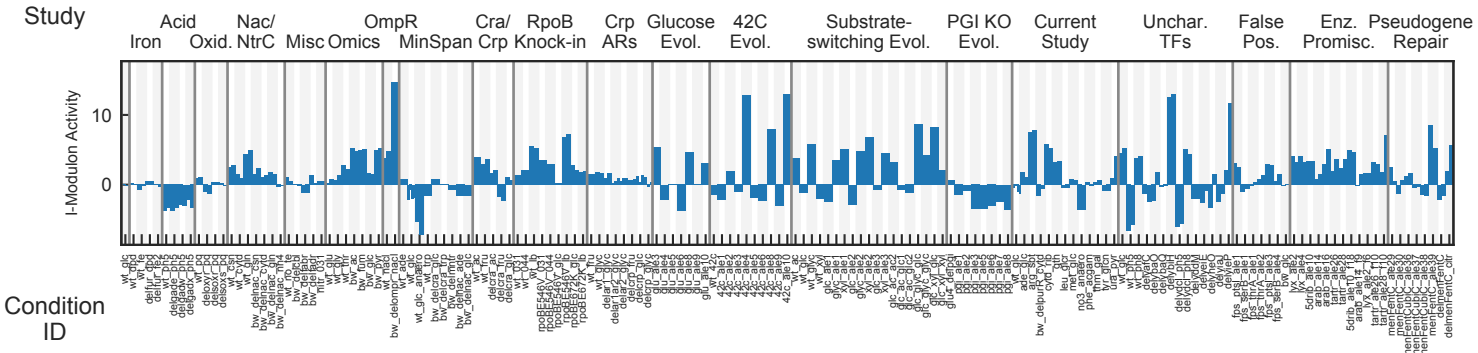
Regulated by: CpxR

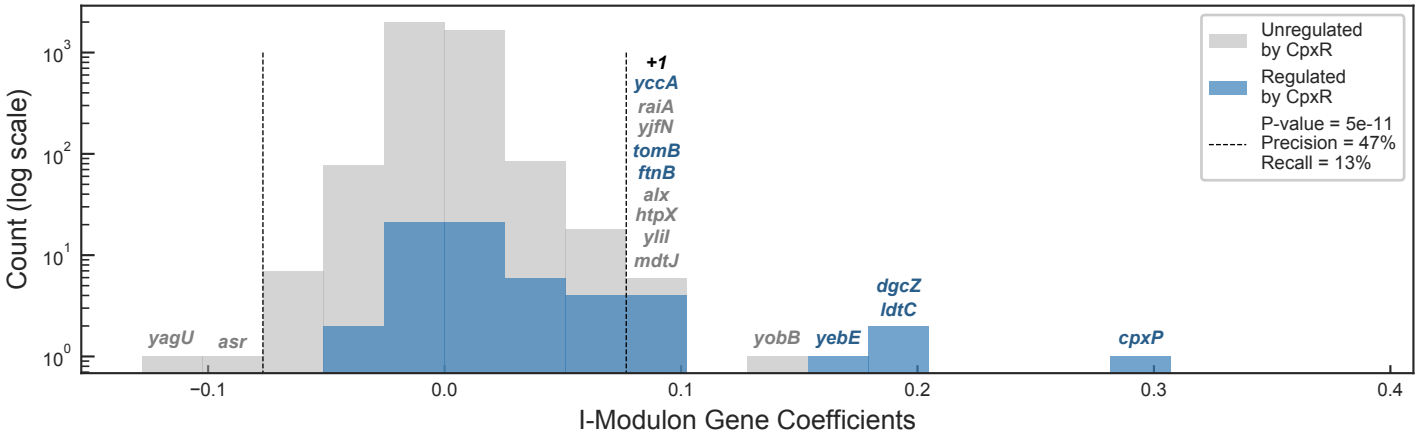
Biological Function: Various stress responses

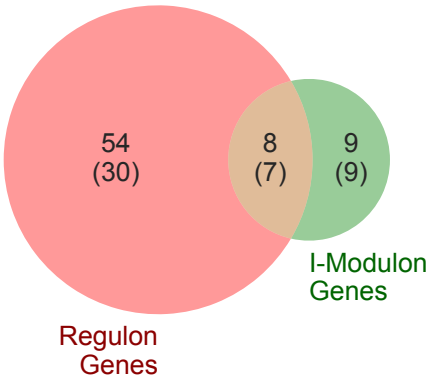


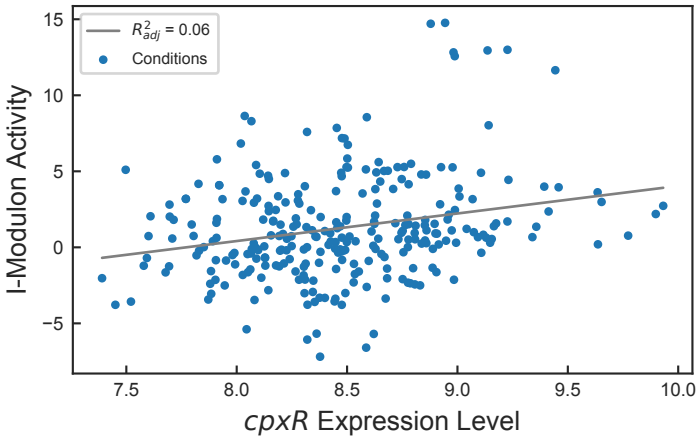
COG Categories

- Inorganic ion transport and metabolism (3): *alx*, *ftnB*, *mdtJ*
- Carbohydrate transport and metabolism (1): *yliI*
- Cell motility (1): *cpxP*
- Posttranslational modification, protein turnover, chaperones (1): *htpX*
- Signal transduction mechanisms (1): *dgcZ*
- Translation, ribosomal structure and biogenesis (1): *raiA*
- Function unknown (8): *hha*, *ldtC*, *tomB*, *yagU*, *yccA*, *yebE*, *yjfN*, *yobB*
- No COG Annotation (1): *asr*





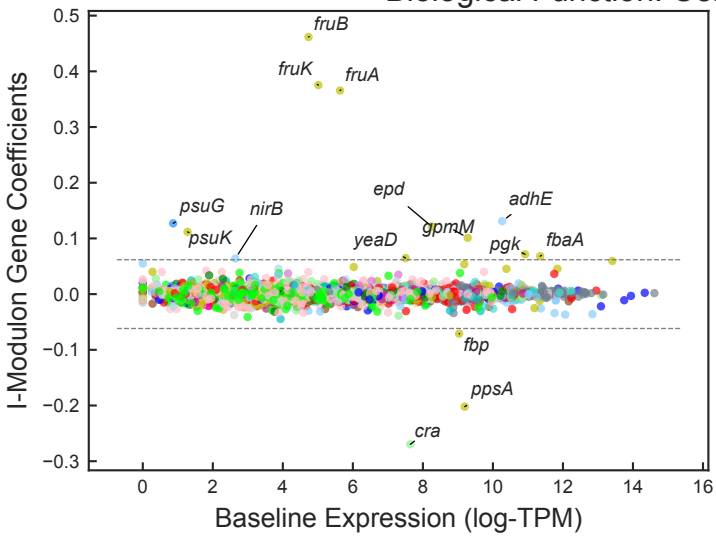




Cra I-Modulon

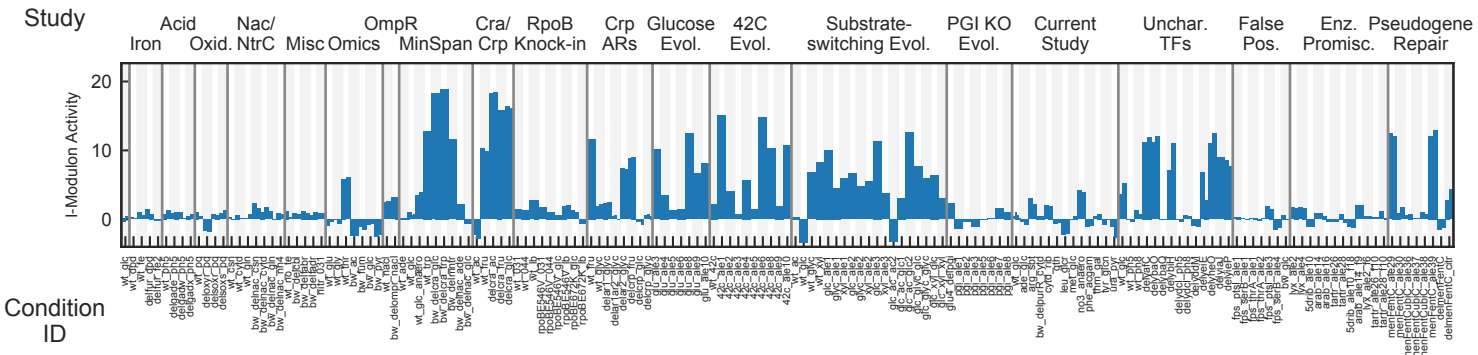
Regulated by: Cra

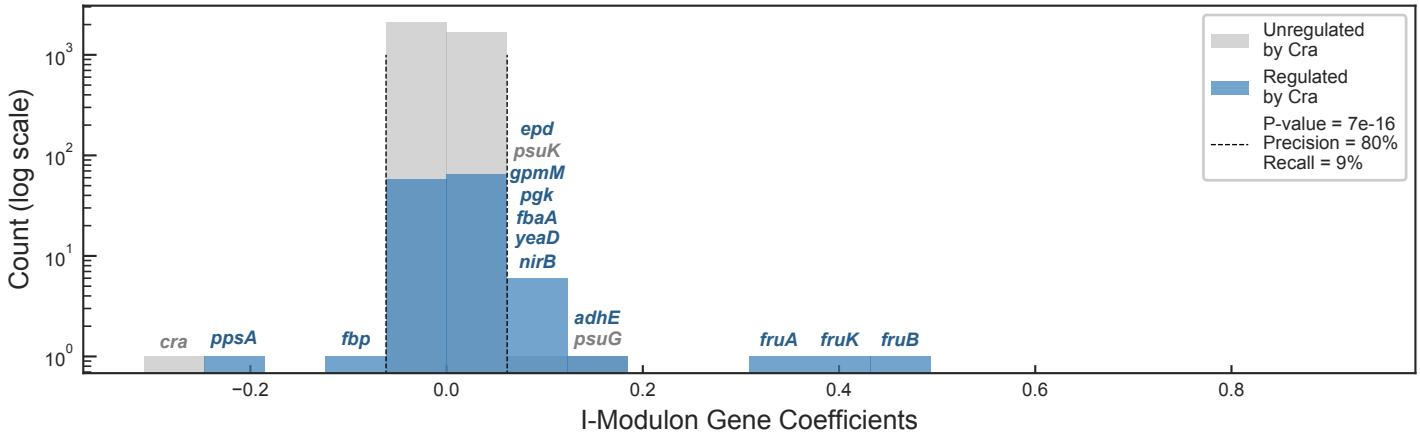
Biological Function: Central carbon metabolism

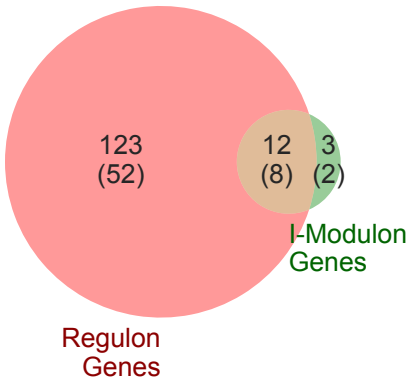


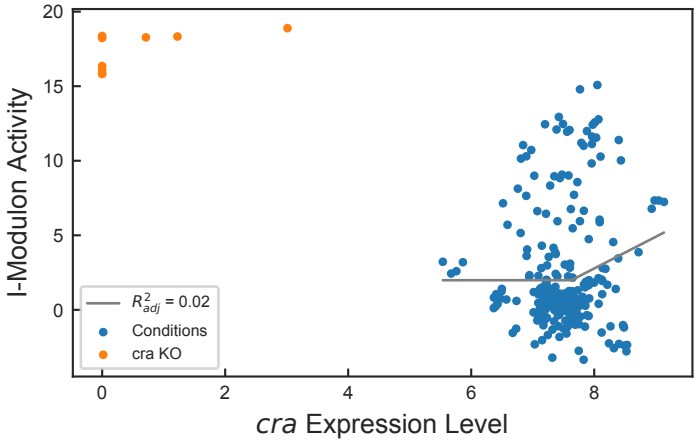
COG Categories

- Carbohydrate transport and metabolism (11): *epd*, *fbaA*, *fbp*, *fruA*, *fruB*, *fruK*, *gpmM*, *pgk*, *ppsA*, *psuK*, *yeaD*
- Energy production and conversion (2): *adhE*, *nirB*
- Secondary metabolites biosynthesis, transport and catabolism (1): *psuG*
- Transcription (1): *cra*





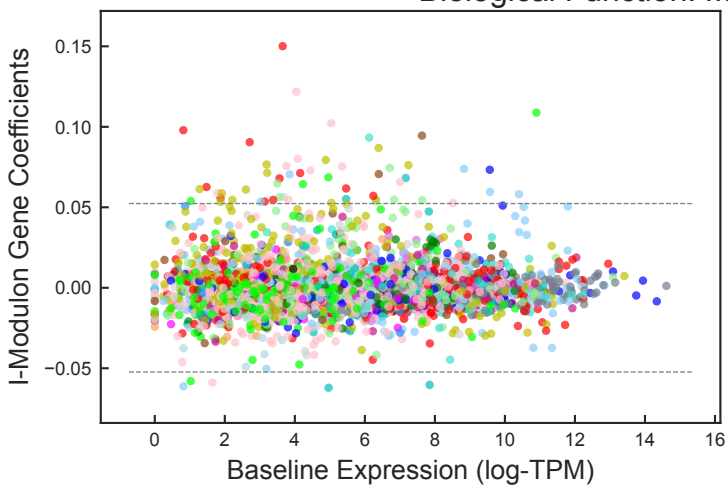




Crp − 1 I-Modulon

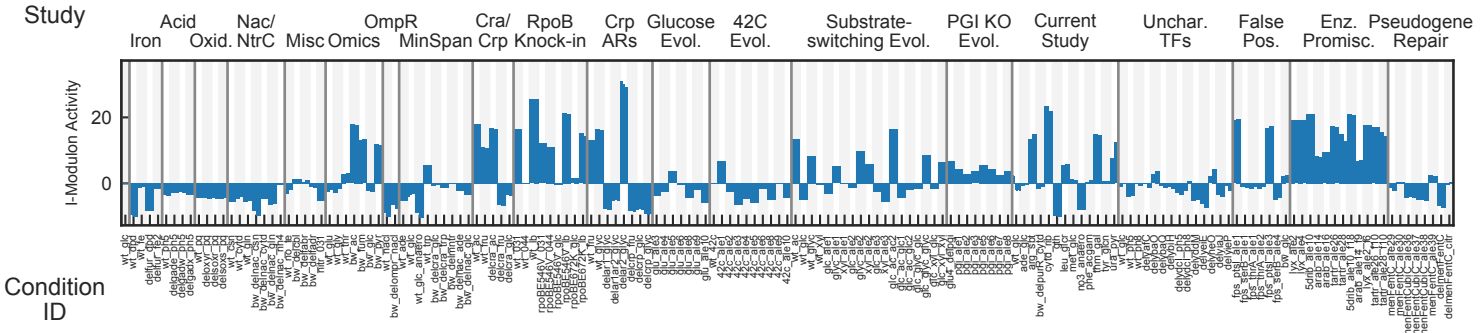
Regulated by: Crp

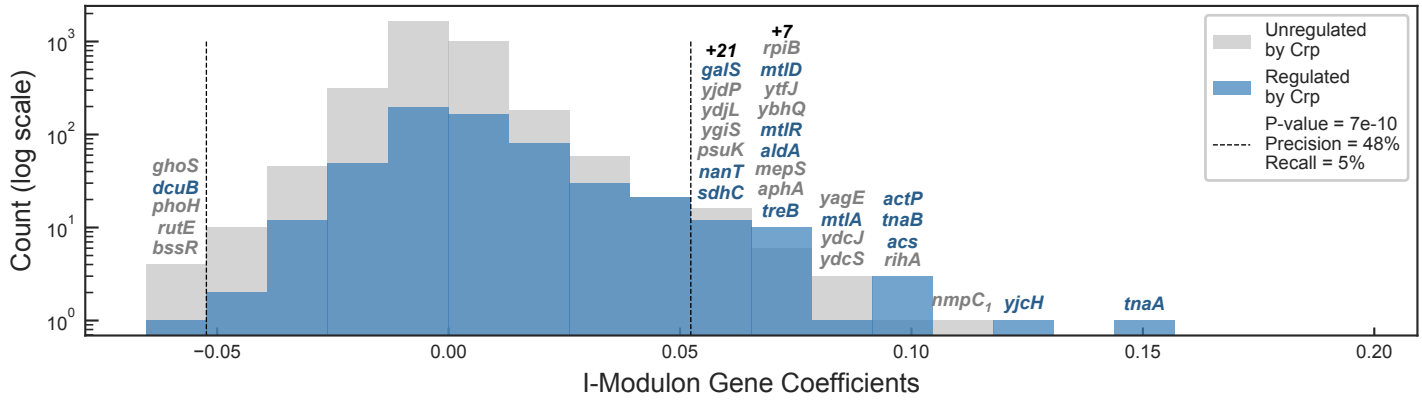
Biological Function: Miscellaneous functions

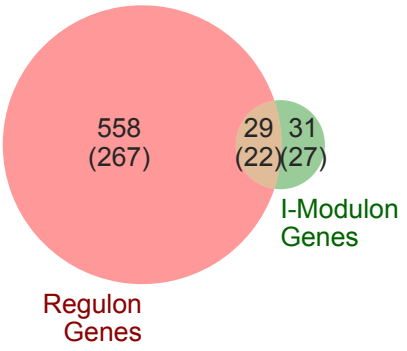


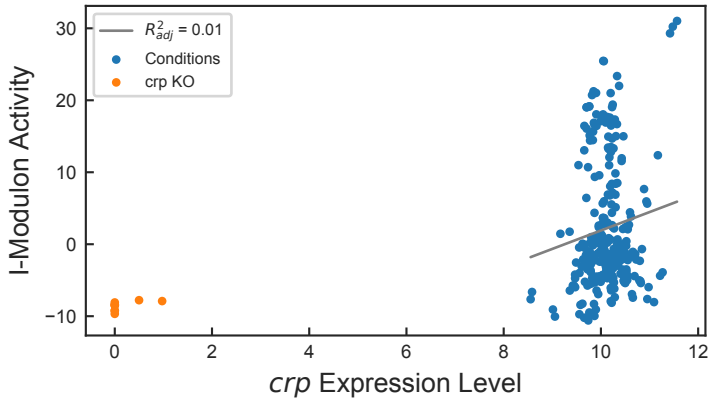
COG Categories

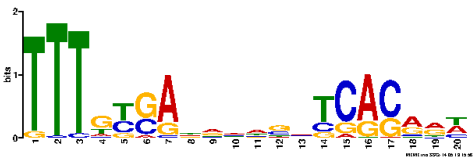
- Carbohydrate transport and metabolism (12): *agaV*, *kbaZ*, *mtlA*, *mtlD*, *nanT*, *psuK*, *rbsD*, *rpiB*, *treB*, *uidA*, *uxaC*, *ydcS*
- Amino acid transport and metabolism (11): *ansB*, *aspA*, *nanA*, *tnaA*, *tnaB*, *yagE*, *yagF*, *ycaM*, *ydcT*, *ydjL*, *ygiS*
- Energy production and conversion (6): *aldA*, *aldB*, *rutE*, *sdhC*, *sucD*, *ykgE*
- Transcription (6): *cra*, *cytR*, *galS*, *mtlR*, *yebK*, *ygeV*
- Other (25): *bssR*, *cstA*, *phoH*, *uspC*, *acs*, *yqeF*, *mepS*, *ydcU*, *rihA*, *actP*, *aphA*, *bax*, *dcuB*, *fadH*, *mtfA*, *ybhQ*, *ydcJ*, *yfbM*, *yjcH*, *ytfJ* + 5





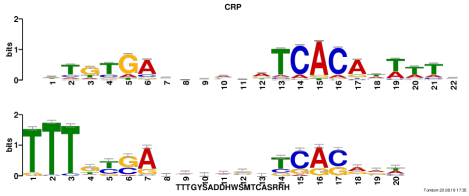






Motif E-value: 5.30e-07

Operons with Upstream Motif: 83%

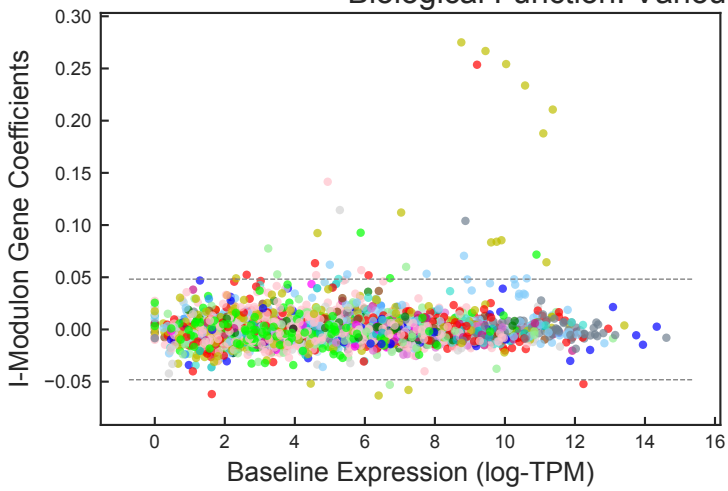


Motif similar to CRP (E-value: 7.82e-09)

Crp – 2 I-Modulon

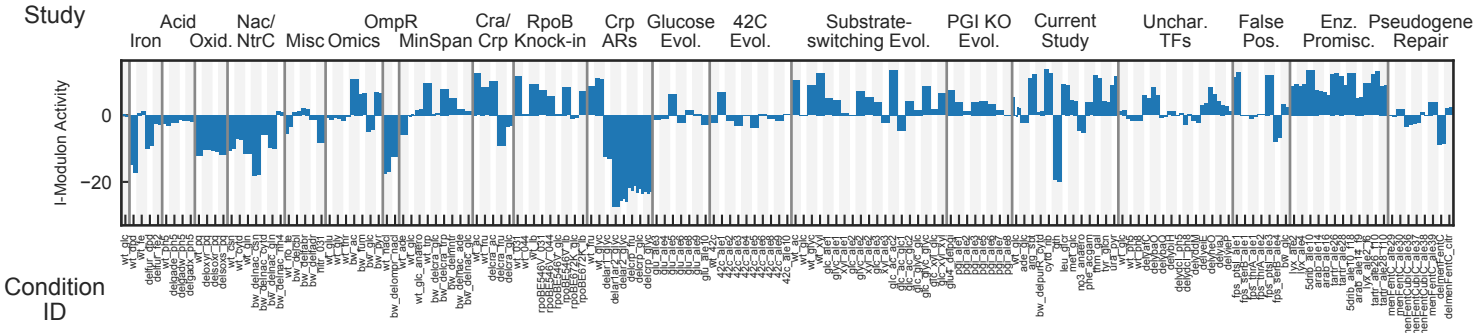
Regulated by: Crp

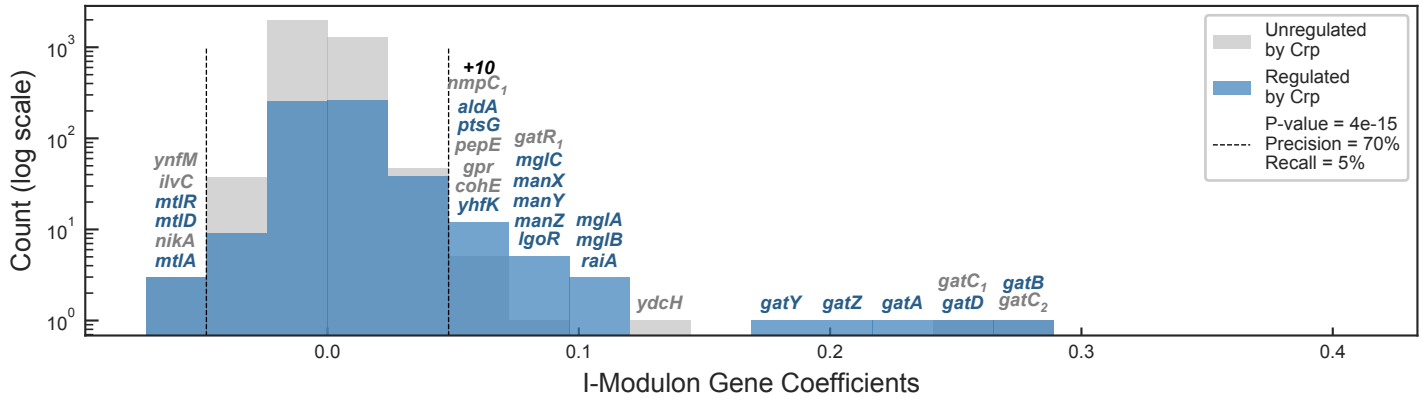
Biological Function: Various carbon source catabolism

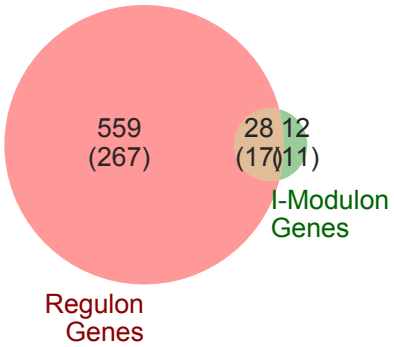


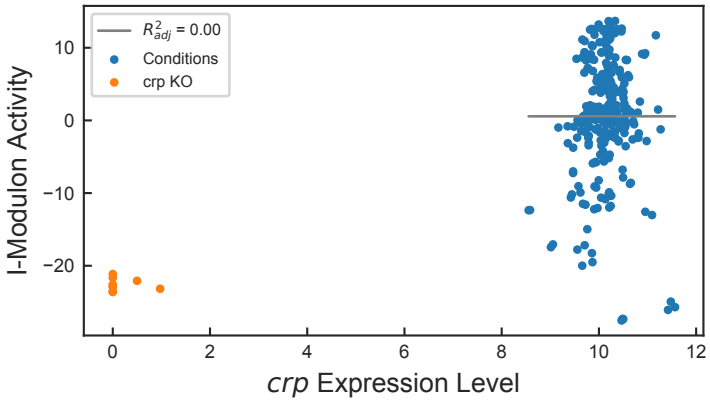
COG Categories

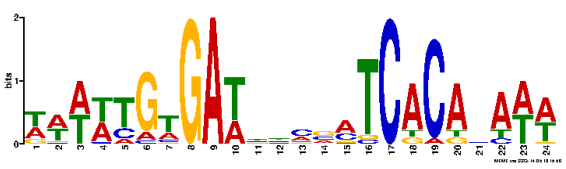
- Carbohydrate transport and metabolism (16): *gatA*, *gatB*, $gatC_1$, $gatC_2$, *gatY*, *gatZ*, *glpT*, *manX*, *manY*, *manZ*, *mglB*, *mglC*, *mtlA*, *mtlD*, *ptsG*, *ynfM*
- Amino acid transport and metabolism (6): *gatD*, *idnD*, *ilvC*, *nikA*, *pepE*, *sdaC*
- Energy production and conversion (5): *aldA*, *glpQ*, *gpr*, *pck*, *sdhA*
- Transcription (4): *cohE*, *galS*, *lgoR*, *mtlR*
- Other (9): *mglA*, *cdd*, *raiA*, *ychH*, *ydcH*, *yhfK*, $gatR_1$, $nmpC_1$, *ymfI*





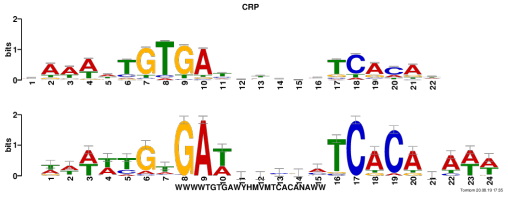






Motif E-value: 1.30e-10

Operons with Upstream Motif: 63%

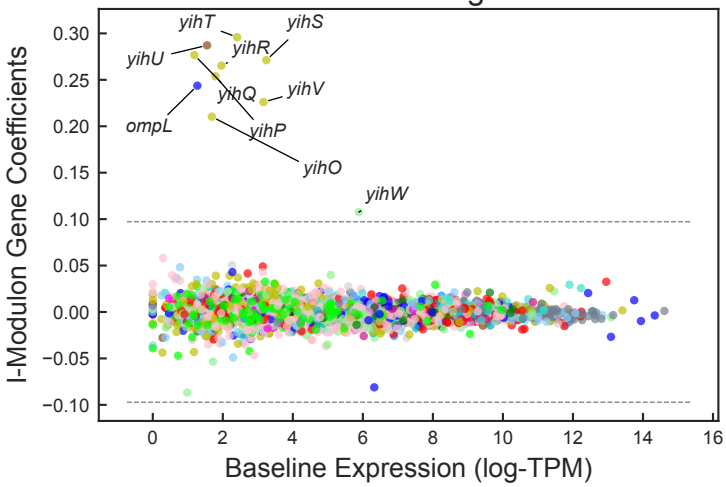


Motif similar to CRP (E-value: 1.14e-09)

CsqR I-Modulon

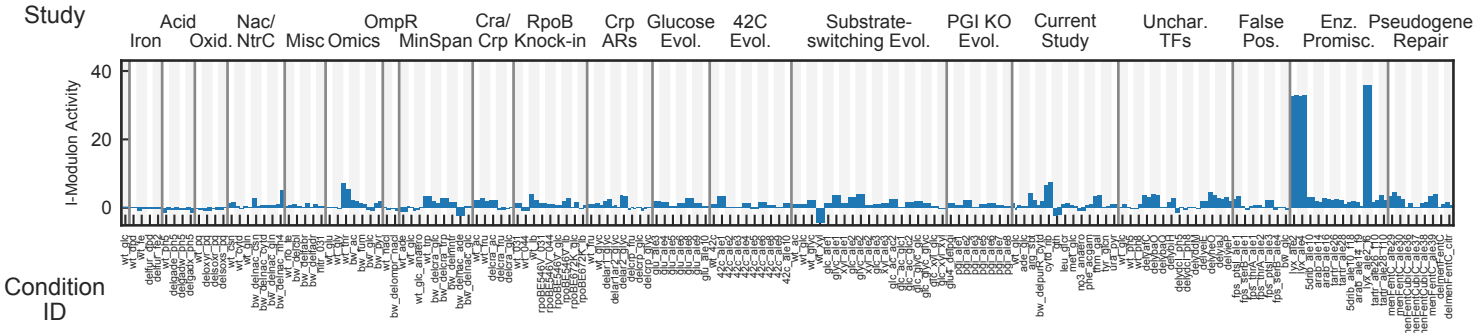
Regulated by: CsqR

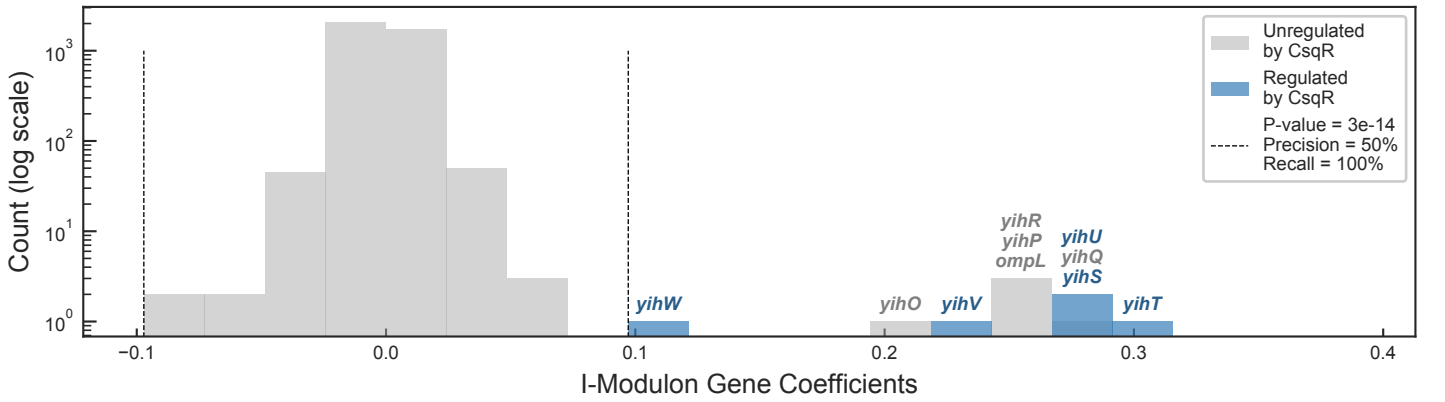
Biological Function: Sulfoquinovose catabolism

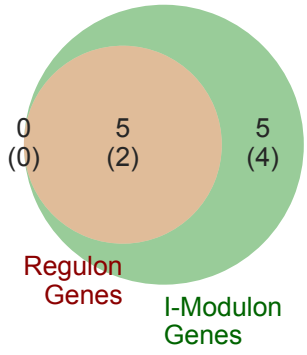


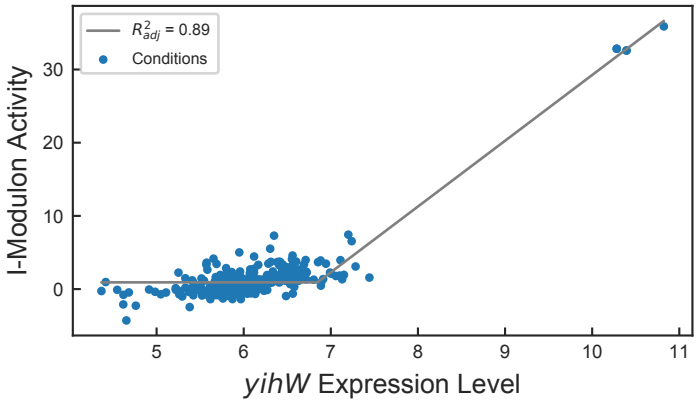
COG Categories

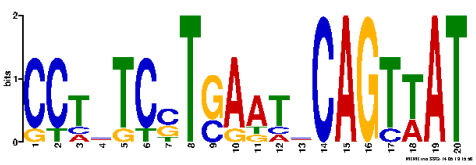
- Carbohydrate transport and metabolism (7): *yihO*, *yihP*, *yihQ*, *yihR*, *yihS*, *yihT*, *yihV*
- Cell wall/membrane/envelope biogenesis (1): *ompL*
- Lipid transport and metabolism (1): *yihU*
- Transcription (1): *yihW*











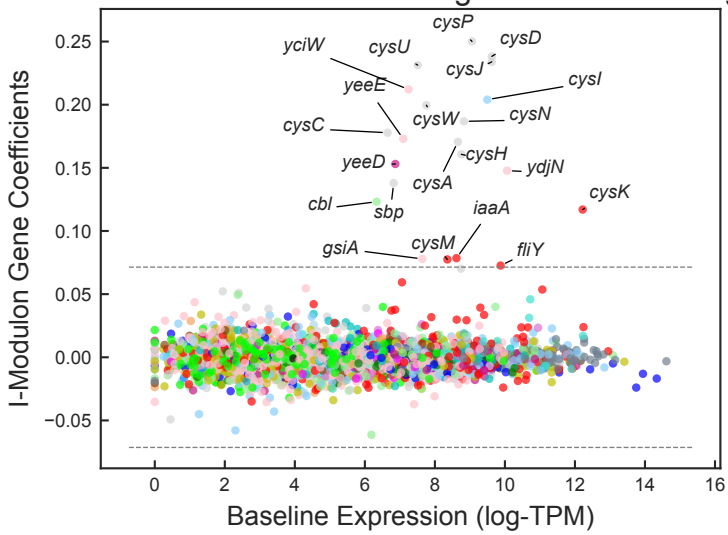
Motif E-value: 4.50e-04

Operons with Upstream Motif: 100%

CysB I-Modulon

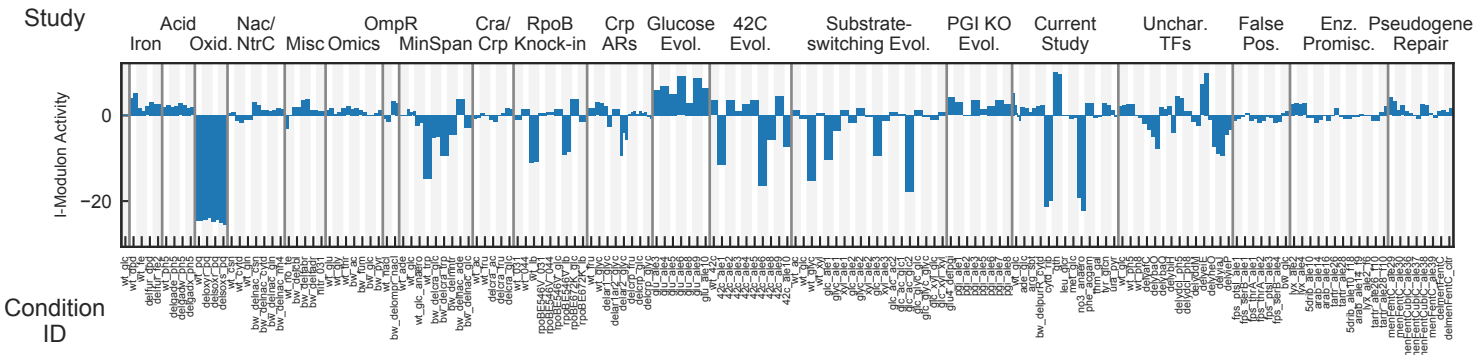
Regulated by: CysB

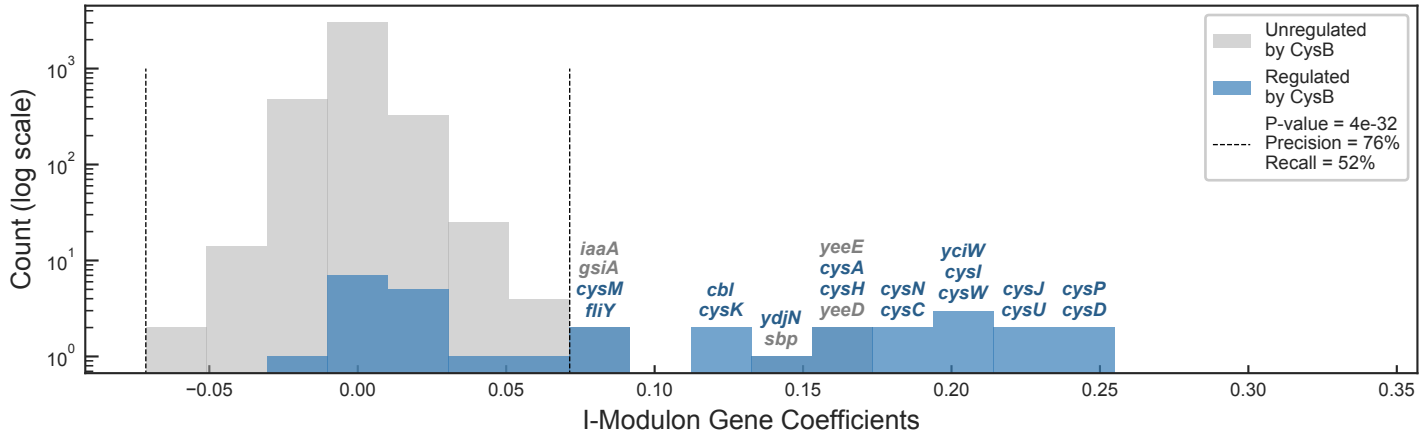
Biological Function: Inorganic sulfate assimilation

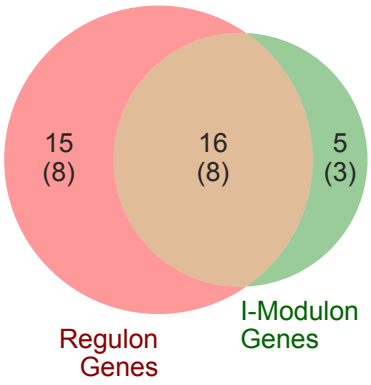


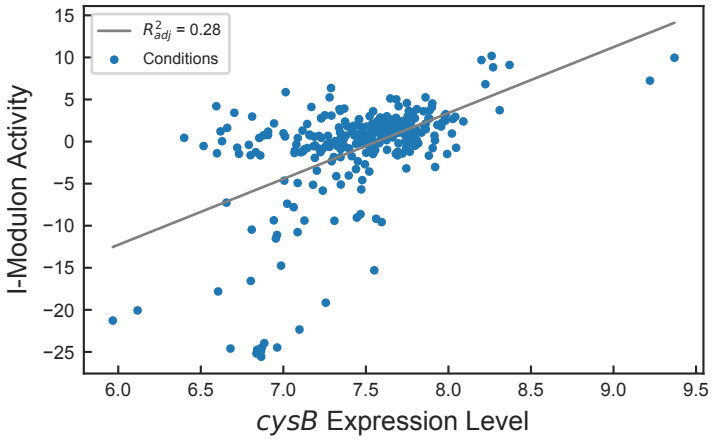
COG Categories

- Inorganic ion transport and metabolism (10): *cysA*, *cysC*, *cysD*, *cysH*, *cysJ*, *cysN*, *cysP*, *cysU*, *cysW*, *sbp*
- Amino acid transport and metabolism (4): *cysK*, *cysM*, *fliY*, *iaaA*
- Energy production and conversion (1): *cysI*
- Posttranslational modification, protein turnover, chaperones (1): *yeeD*
- Transcription (1): *cbl*
- Function unknown (4): *gsiA*, *yciW*, *ydjN*, *yeeE*





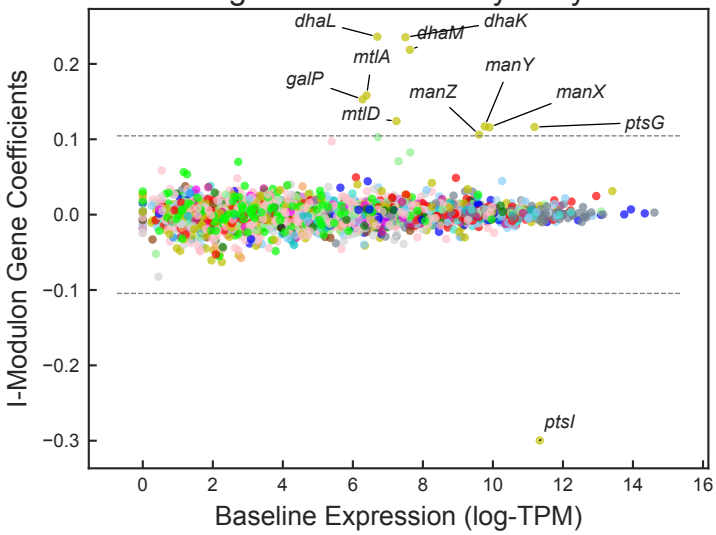




DhaR/Mlc I-Modulon

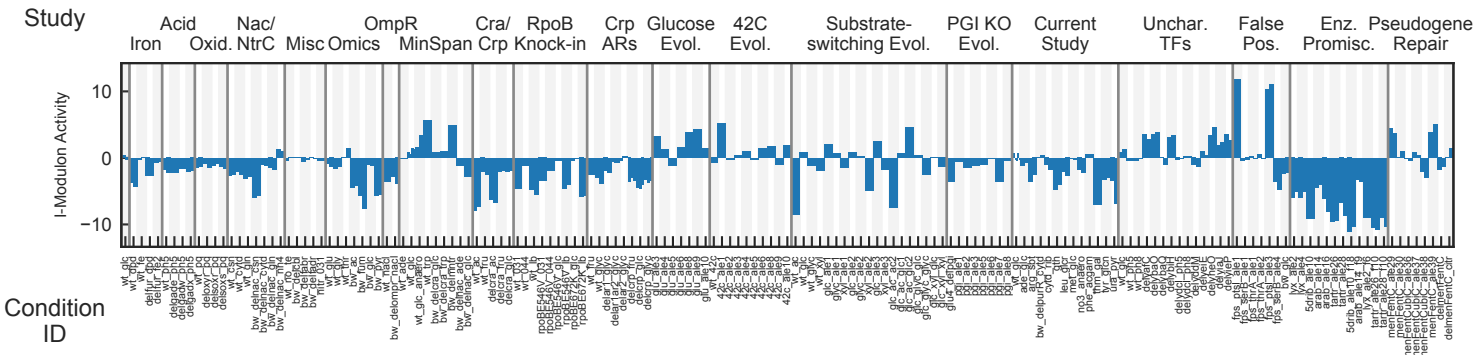
Regulated by: DhaR or Mlc

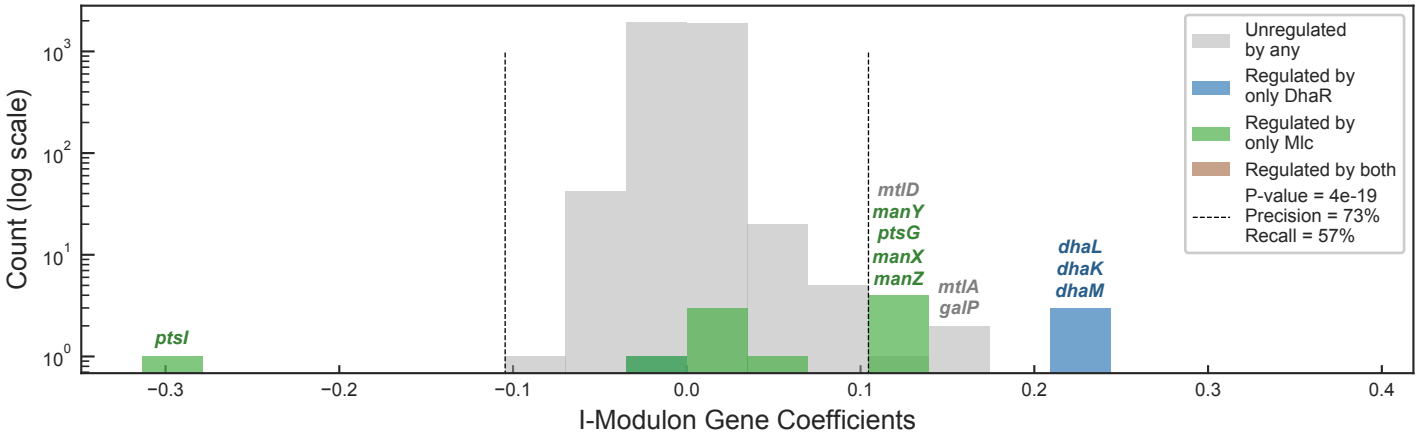
Biological Function: Dihydroxyacetone kinase and phosphotransferase systems

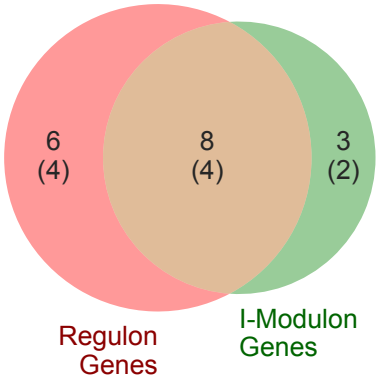


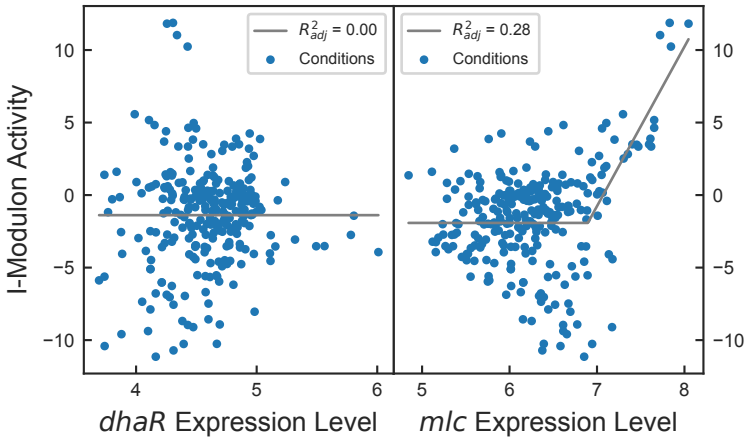
COG Categories

Carbohydrate transport and metabolism (11): *dhaK*, *dhaL*, *dhaM*, *galP*, *manX*, *manY*, *manZ*, *mtlA*, *mtlD*, *ptsG*, *ptsI*





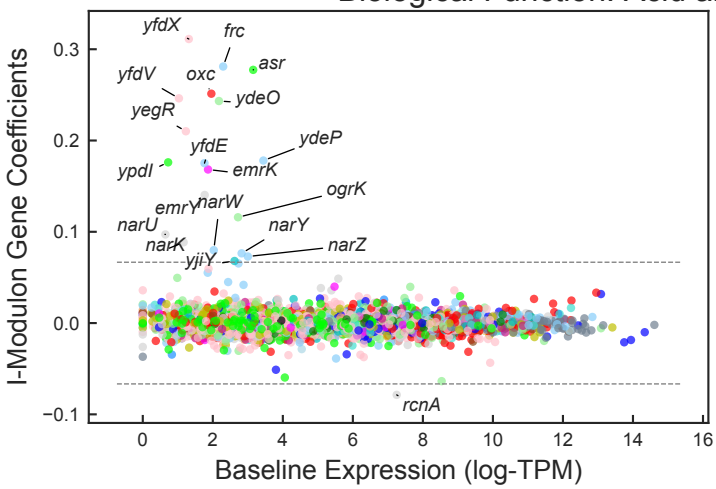




EvgA I-Modulon

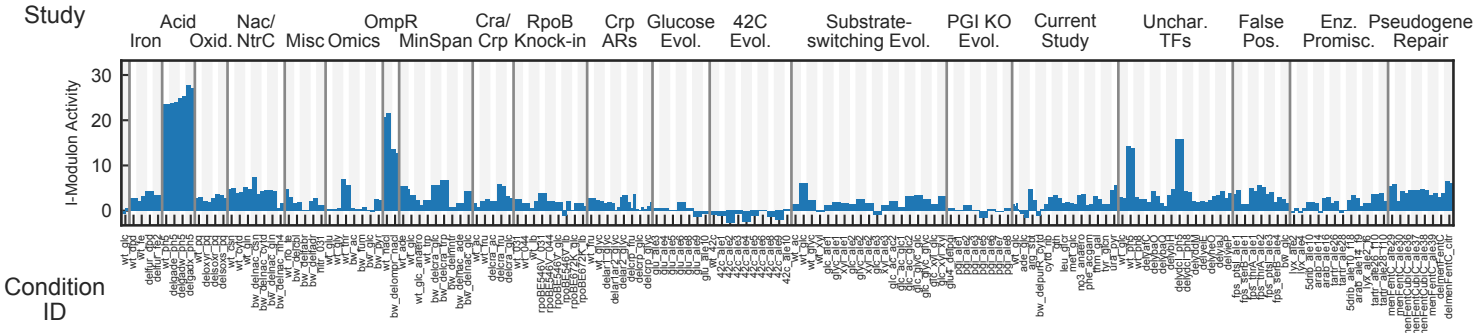
Regulated by: EvgA

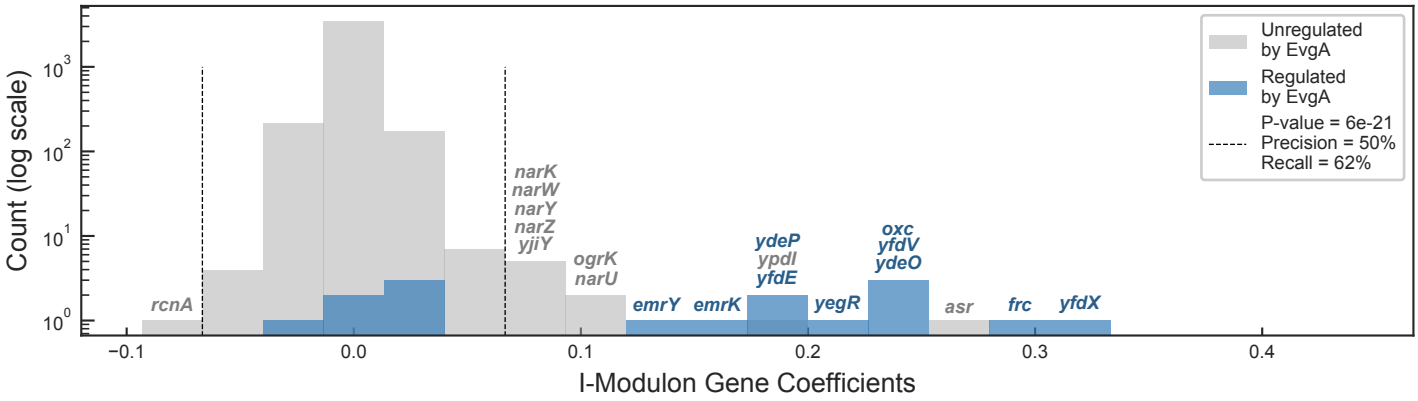
Biological Function: Acid and osmotic stress response

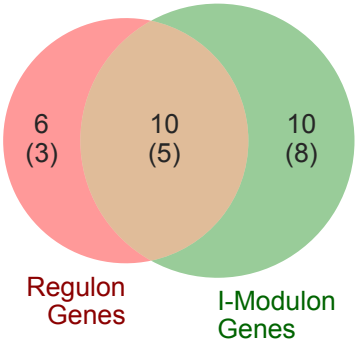


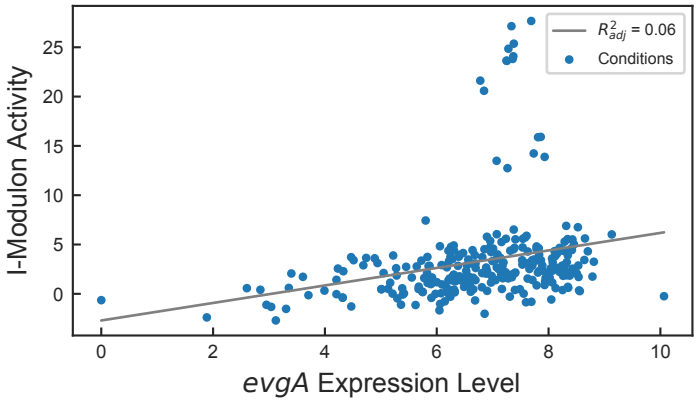
COG Categories

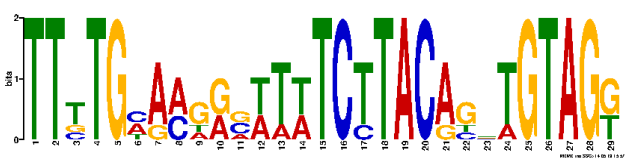
- Energy production and conversion (6): *frc*, *narW*, *narY*, *narZ*, *ydeP*, *yfdE*
- Inorganic ion transport and metabolism (4): *emrY*, *narK*, *narU*, *rcnA*
- Transcription (2): *ogrK*, *ydeO*
- Amino acid transport and metabolism (1): *oxc*
- Defense mechanisms (1): *emrK*
- Signal transduction mechanisms (1): *yjiY*
- Function unknown (3): *yegR*, *yfdV*, *yfdX*
- No COG Annotation (2): *asr*, *ypdI*





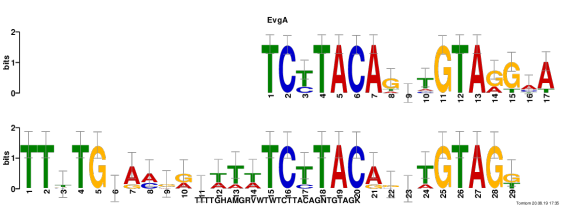






Motif E-value: 2.20e-05

Operons with Upstream Motif: 38%

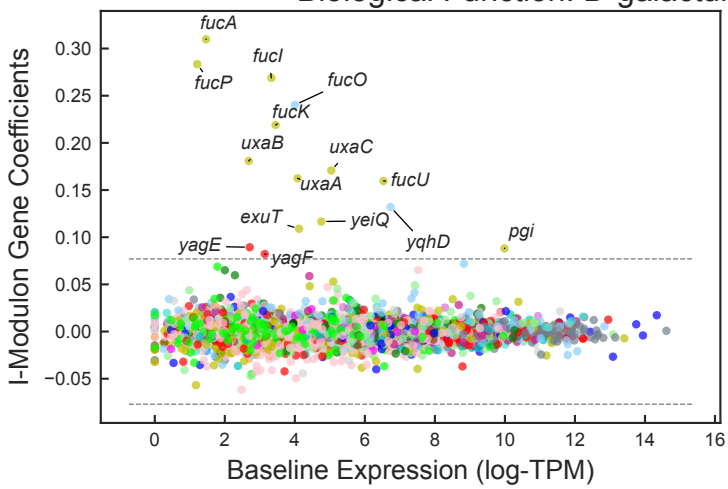


Motif similar to EvgA (E-value: 6.32e-12)

ExuR/FucR I-Modulon

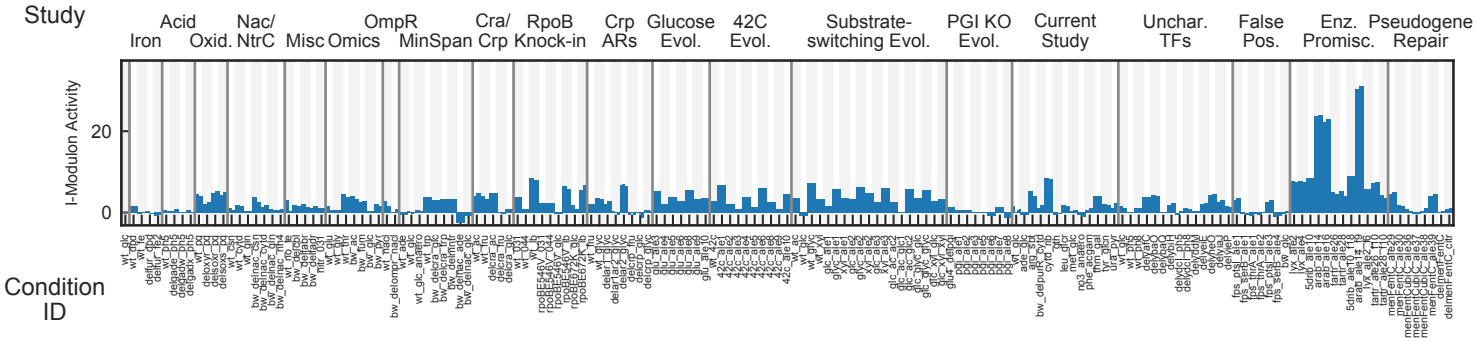
Regulated by: ExuR or FucR

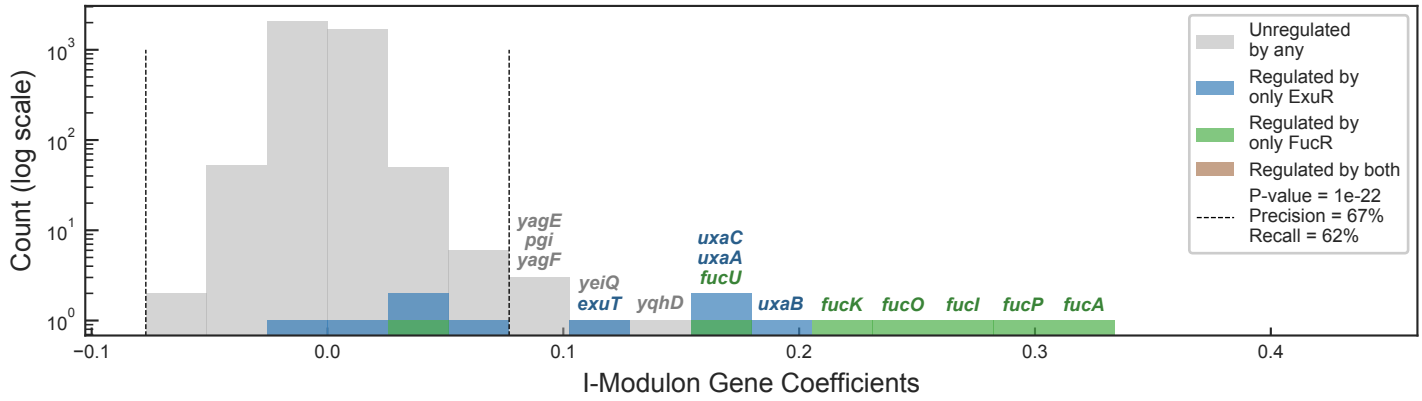
Biological Function: D-galacturonate and L-fucose catabolism

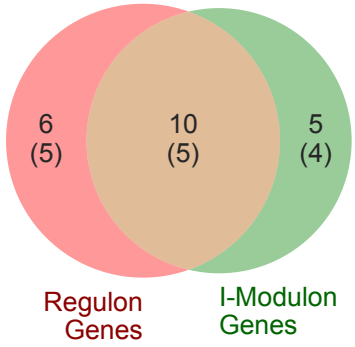


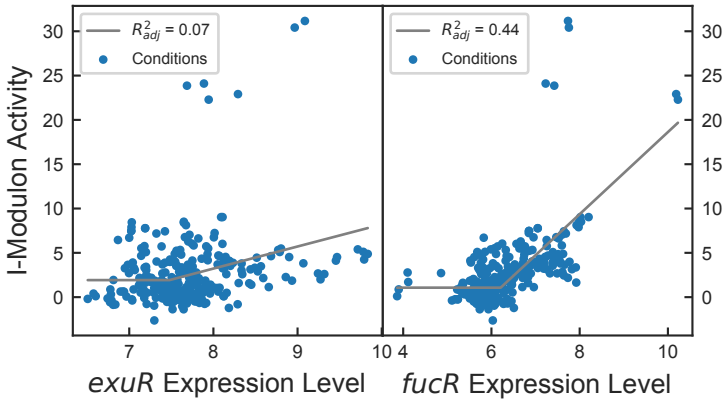
COG Categories

- Carbohydrate transport and metabolism (11): *exuT*, *fucA*, *fucI*, *fucK*, *fucP*, *fucU*, *pgi*, *uxaA*, *uxaB*, *uxaC*, *yeiQ*
- Amino acid transport and metabolism (2): *yagE*, *yagF*
- Energy production and conversion (2): *fucO*, *yqhD*









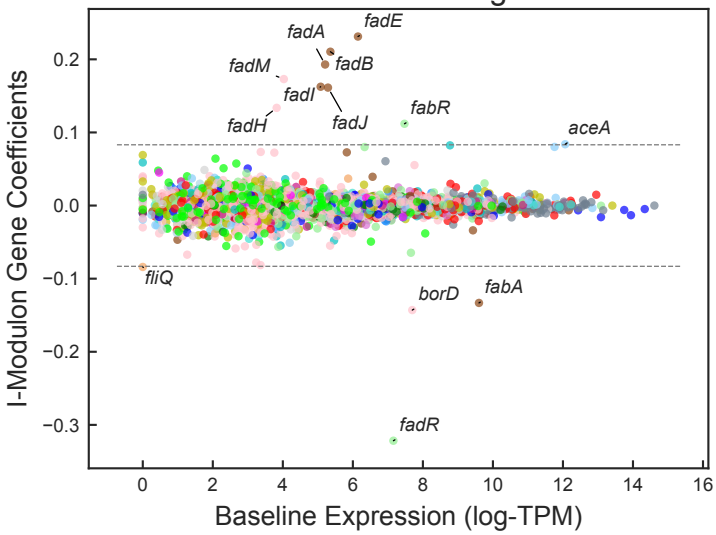
Motif E-value: 1.10e-04

Operons with Upstream Motif: 67%

FadR I-Modulon

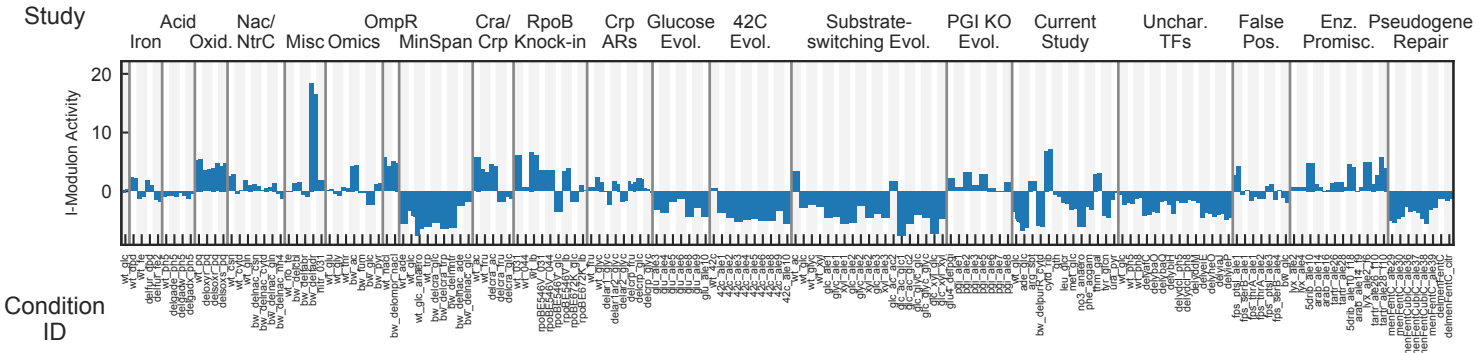
Regulated by: FadR or IclR

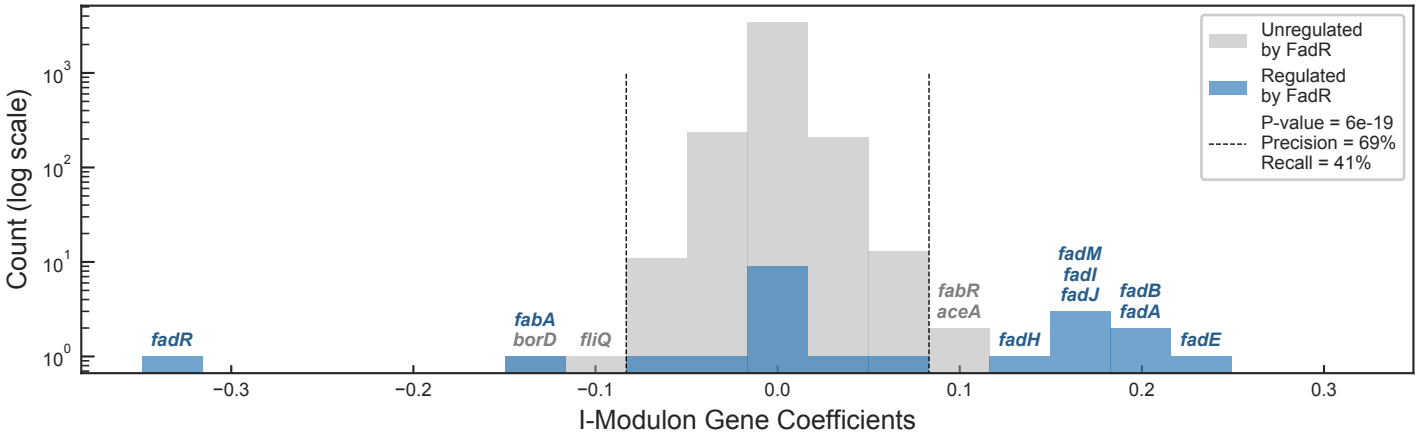
Biological Function: Fatty acid degradation

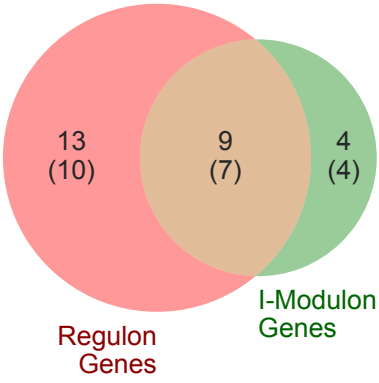


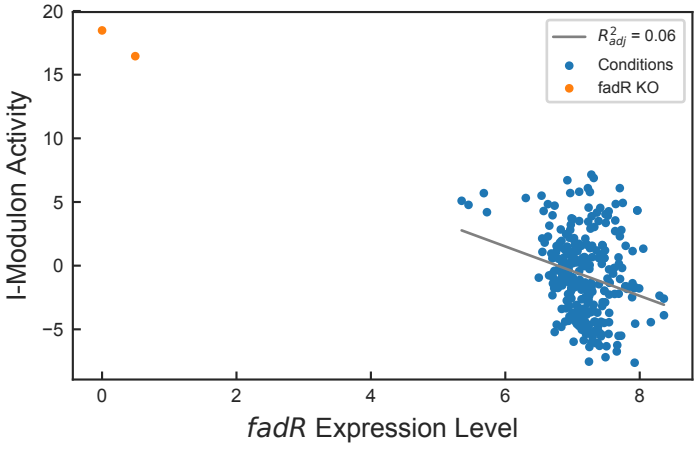
COG Categories

- Lipid transport and metabolism (6): *fabA*, *fadA*, *fadB*, *fadE*, *fadI*, *fadJ*
- Transcription (2): *fabR*, *fadR*
- Cell motility (1): *fliQ*
- Energy production and conversion (1): *aceA*
- Function unknown (3): *borD*, *fadH*, *fadM*





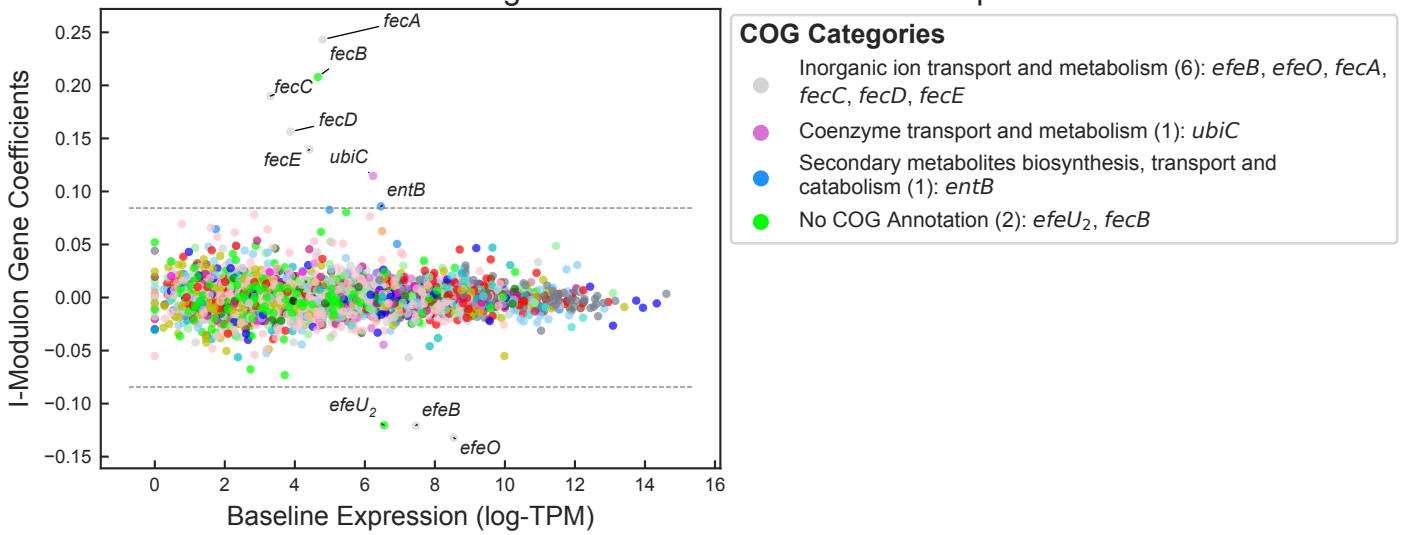


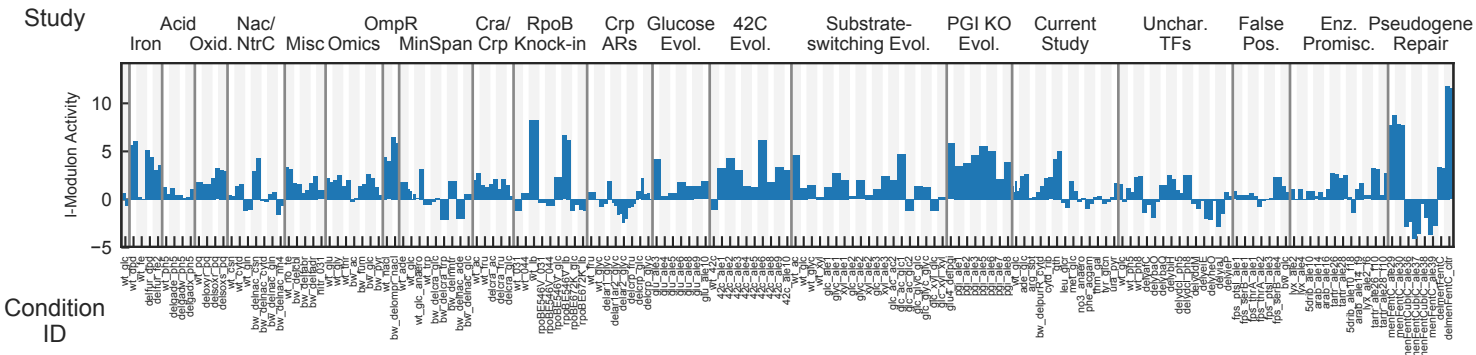


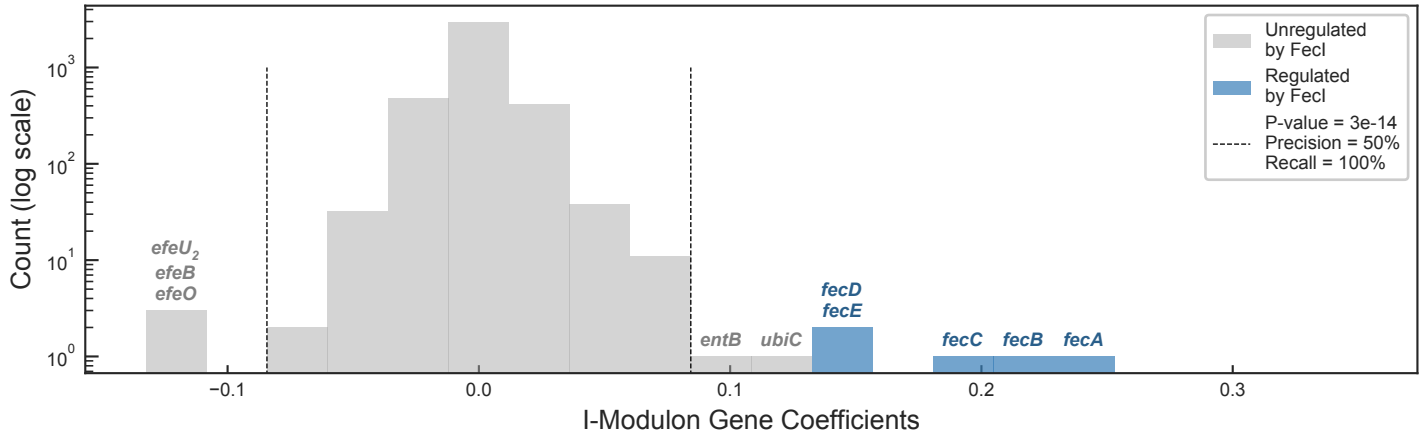
FecI I-Modulon

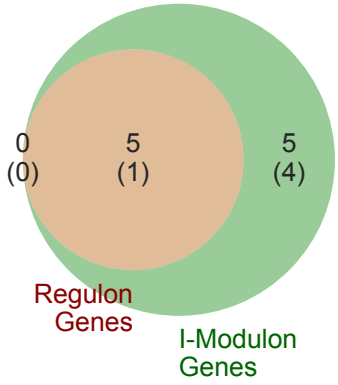
Regulated by: FecI

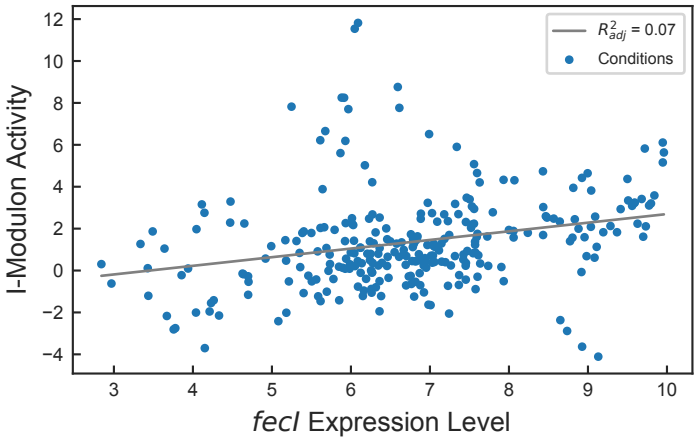
Biological Function: Ferric citrate transport







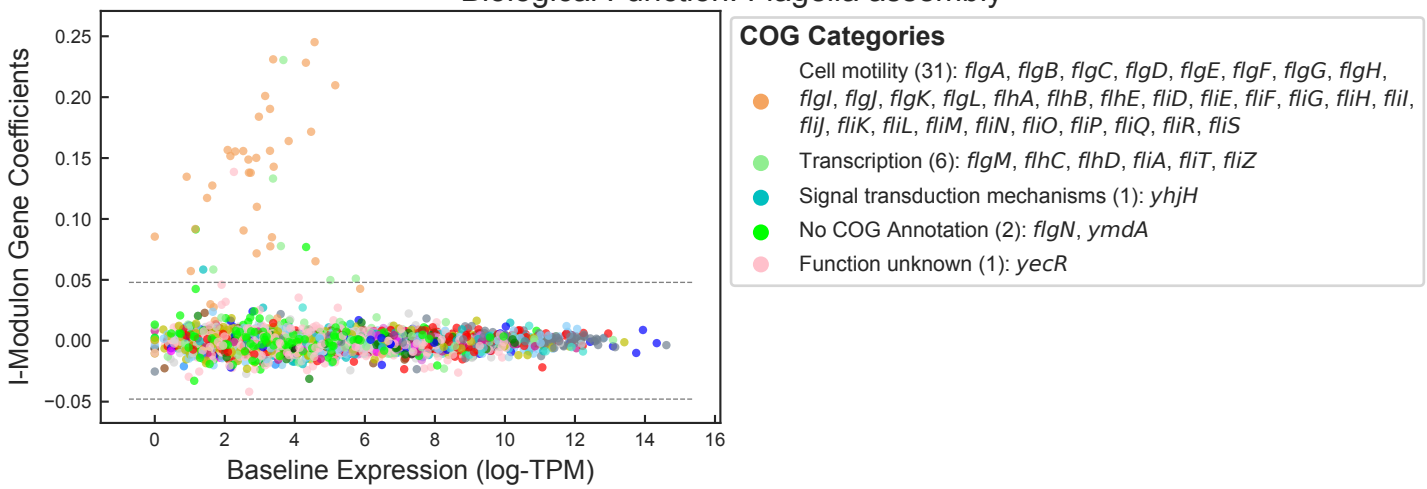


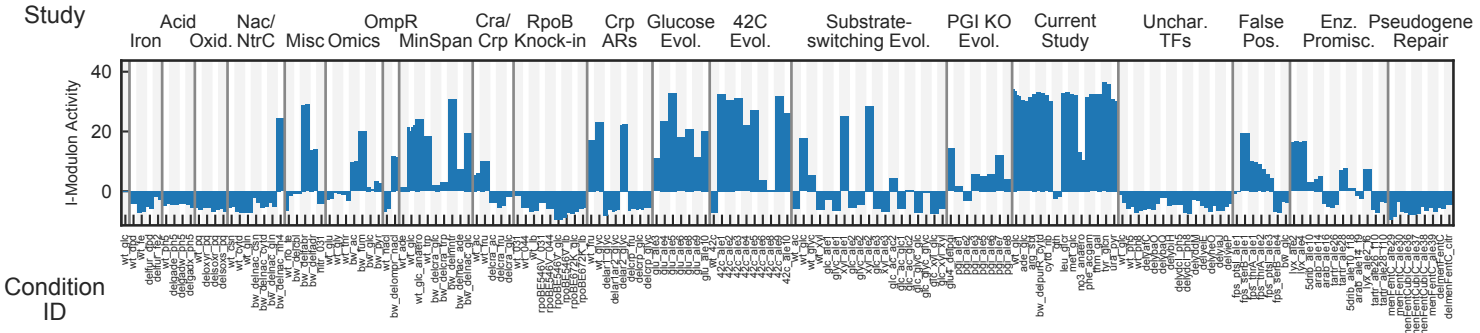


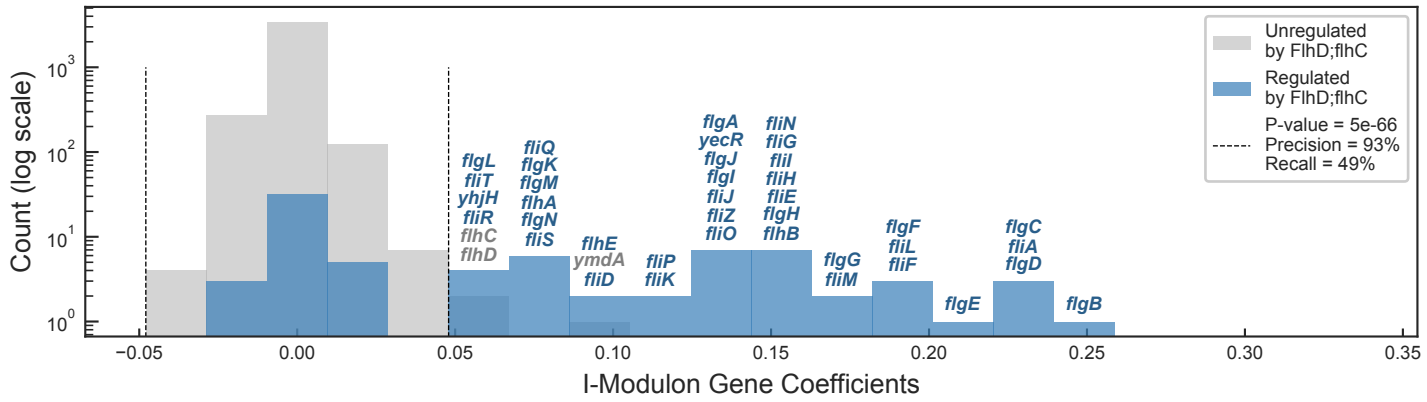
FlhDC I-Modulon

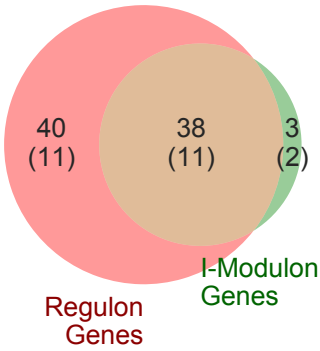
Regulated by: FlhDC

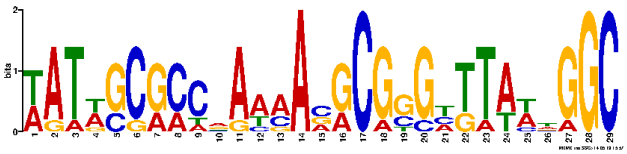
Biological Function: Flagella assembly











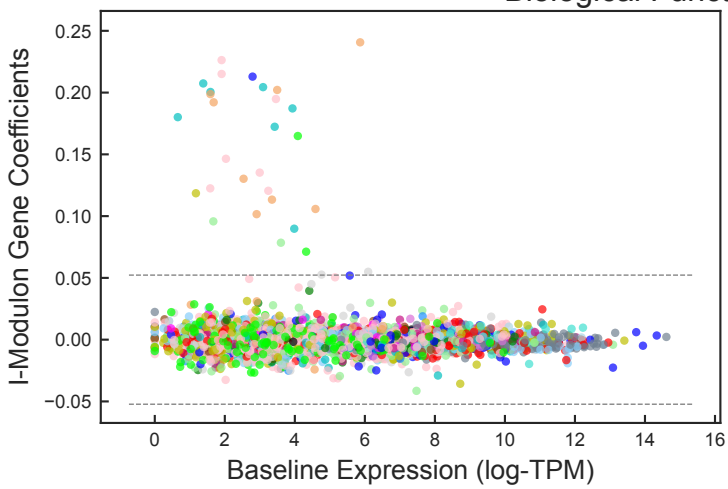
Motif E-value: 7.40e-07

Operons with Upstream Motif: 54%

FliA I-Modulon

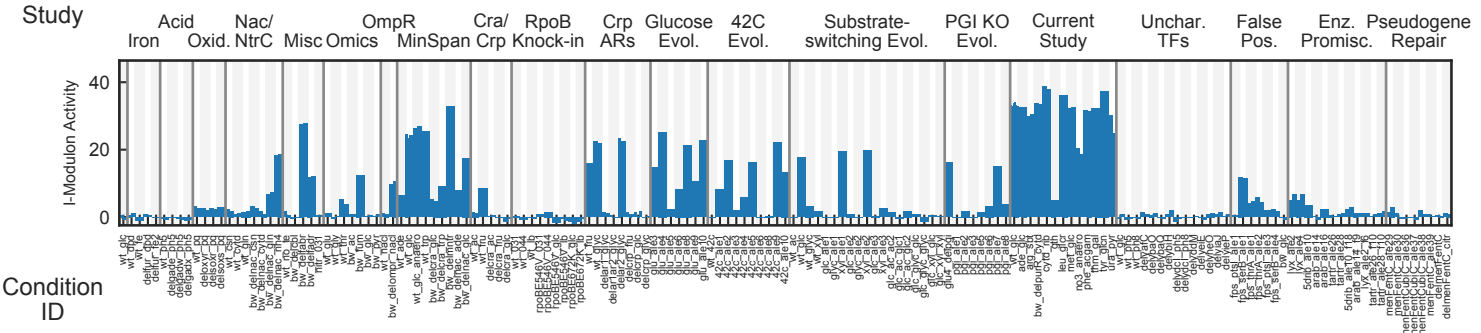
Regulated by: FliA

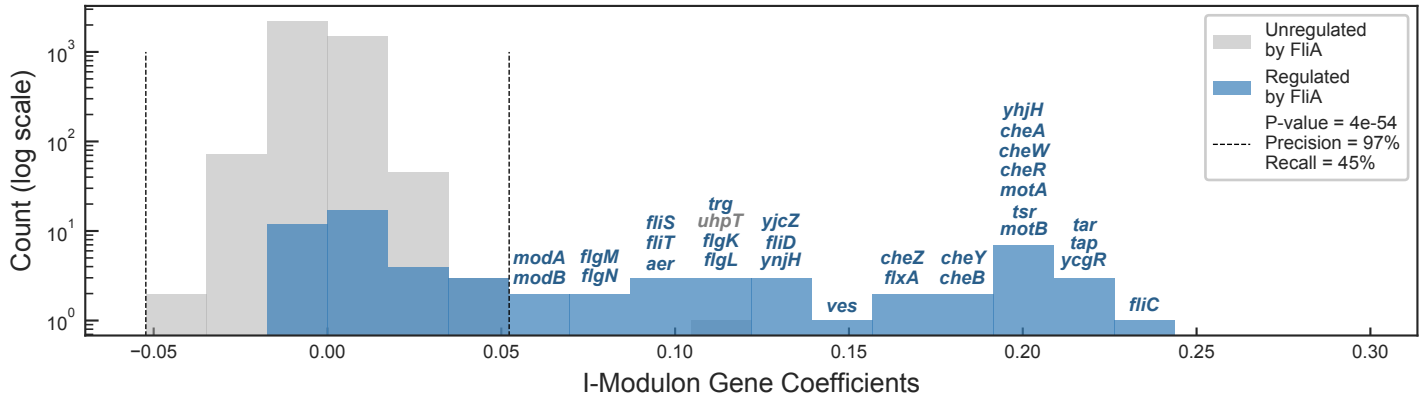
Biological Function: Chemotaxis

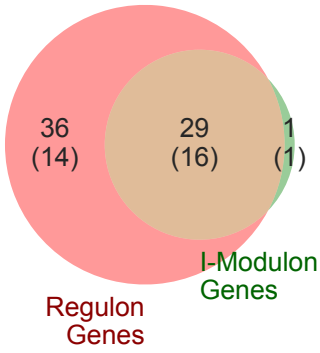


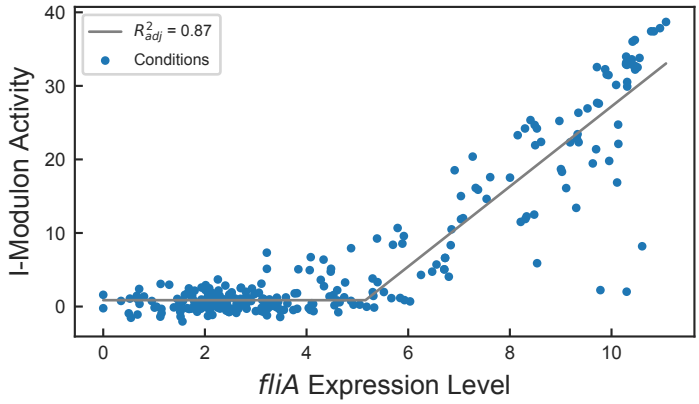
COG Categories

- Cell motility (8): *cheW*, *flgK*, *flgL*, *fliC*, *fliD*, *fliS*, *motA*, *motB*
- Signal transduction mechanisms (7): *aer*, *cheA*, *cheB*, *cheR*, *cheY*, *cheZ*, *yhjH*
- Inorganic ion transport and metabolism (2): *modA*, *modB*
- Transcription (2): *flgM*, *fliT*
- Carbohydrate transport and metabolism (1): *uhpT*
- Cell wall/membrane/envelope biogenesis (1): *ycgR*
- Function unknown (7): *tap*, *tar*, *trg*, *tsr*, *ves*, *yjcZ*, *ynjH*
- No COG Annotation (2): *flgN*, *flxA*









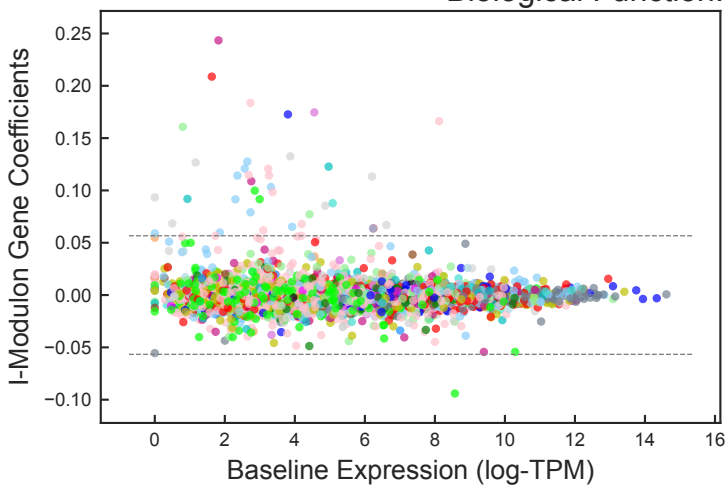
Motif E-value: 2.00e-08

Operons with Upstream Motif: 47%

Fnr I-Modulon

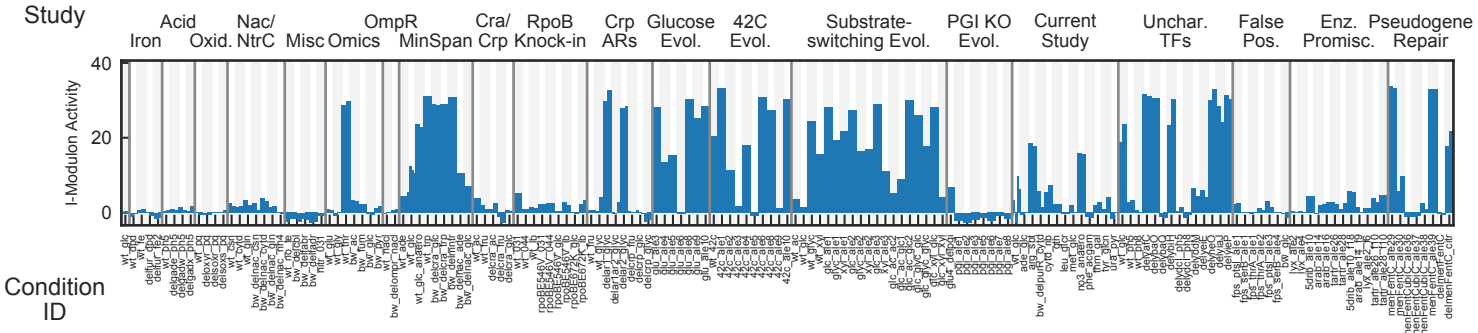
Regulated by: Fnr

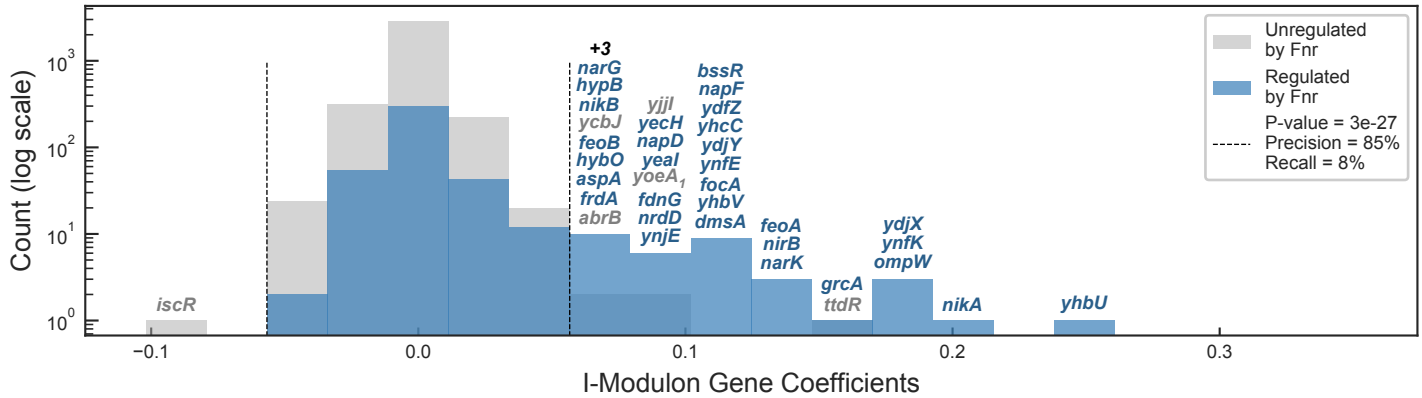
Biological Function: Anaerobic response

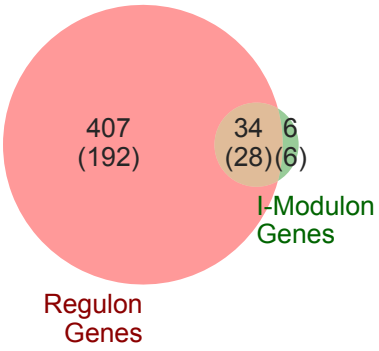


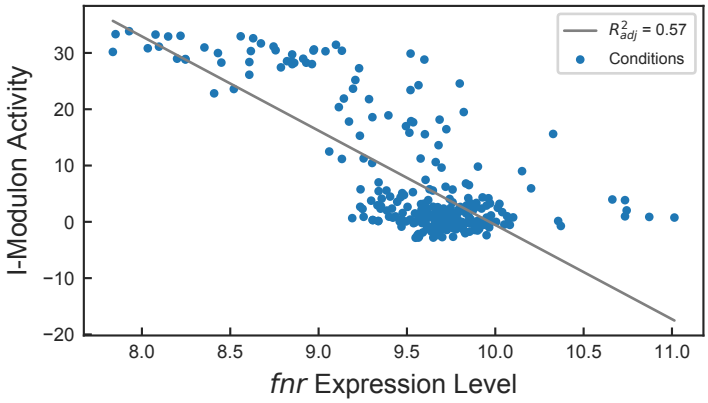
COG Categories

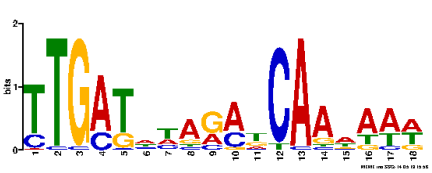
- Energy production and conversion (10): *dcuC*, *dmsA*, *fdnG*, *frdA*, *hybO*, *napF*, *narG*, *nirB*, *nirD*, *ynfE*
- Inorganic ion transport and metabolism (7): *feoA*, *feoB*, *focA*, *napD*, *narK*, *nikB*, *ynjE*
- Amino acid transport and metabolism (2): *aspA*, *nikA*
- Posttranslational modification, protein turnover, chaperones (2): *yhbU*, *yhbV*
- Signal transduction mechanisms (2): *bssR*, *yeaI*
- Other (17): *hypB*, *ttdR*, *ompW*, *ynfK*, *nrdD*, *abrB*, *grcA*, *ycbJ*, *ydfZ*, *ydjX*, *ydjY*, *yecH*, *yfcC*, *yhcC*, *iscR*, *yjjI*, *yoeA*$_1$





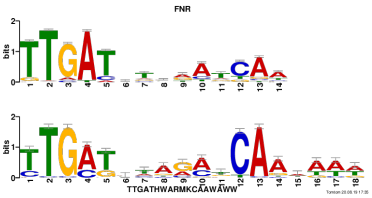






Motif E-value: 4.60e-12

Operons with Upstream Motif: 82%

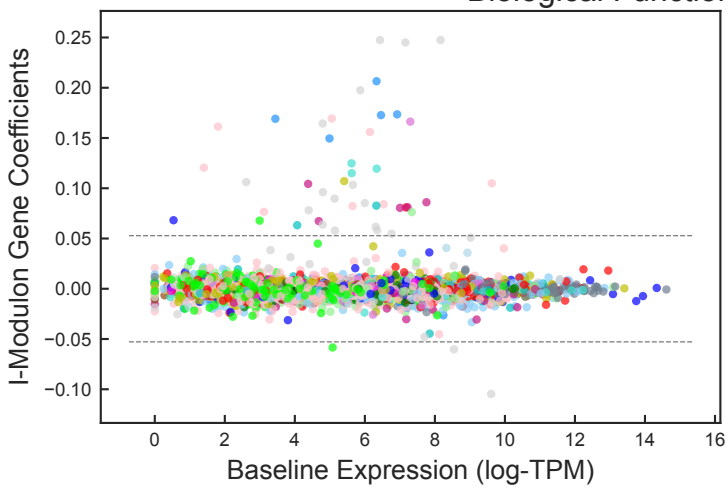


Motif similar to FNR (E-value: 2.98e-06)

Fur − 1 I-Modulon

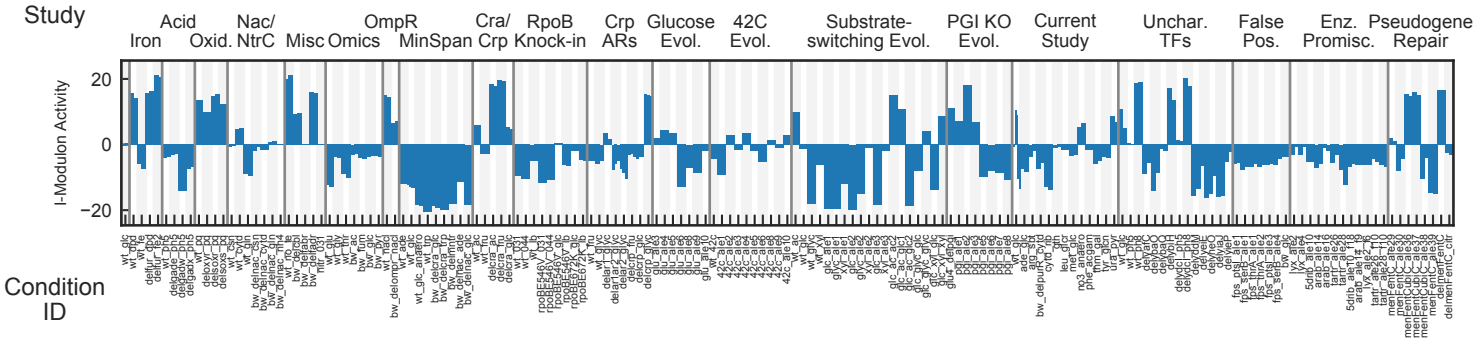
Regulated by: Fur

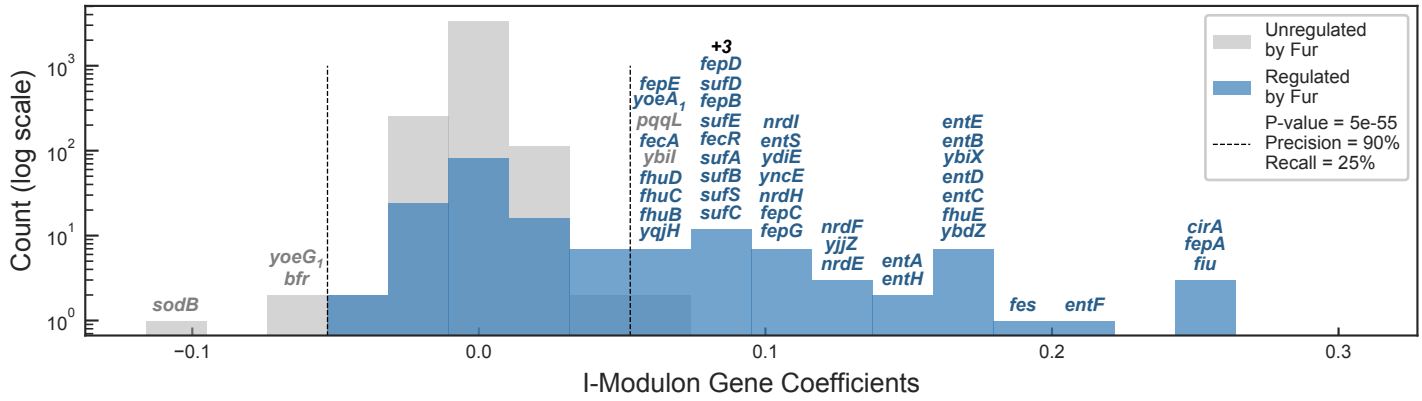
Biological Function: Iron homeostasis

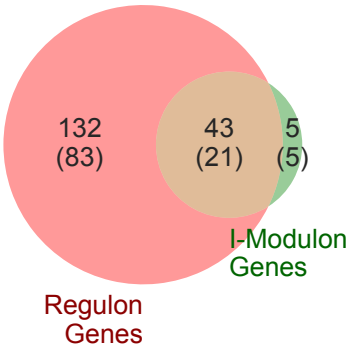


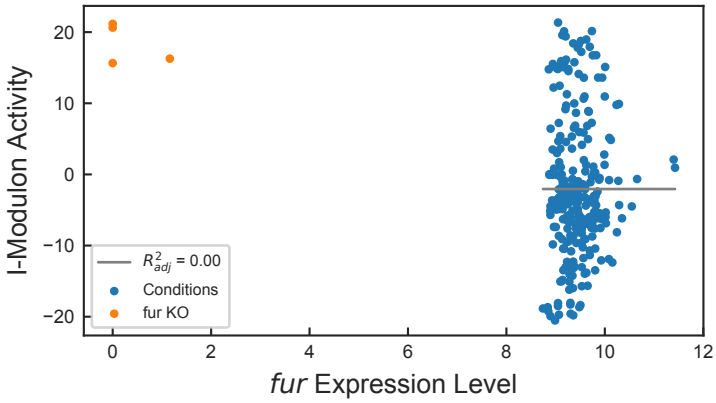
COG Categories

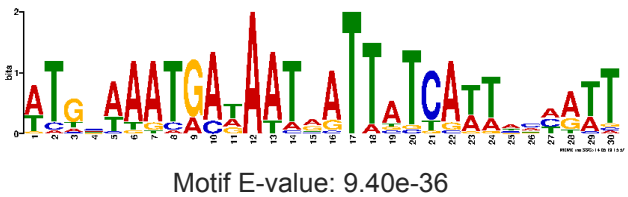
- Inorganic ion transport and metabolism (18): *bfr*, *cirA*, *fecA*, *fepA*, *fepB*, *fepC*, *fepD*, *fepG*, *fes*, *fhuB*, *fhuC*, *fhuD*, *fhuE*, *fiu*, *sodB*, *yddB*, *ydiE*, *yqjH*
- Posttranslational modification, protein turnover, chaperones (5): *nrdH*, *pqqL*, *sufB*, *sufC*, *sufD*
- Secondary metabolites biosynthesis, transport and catabolism (5): *entB*, *entD*, *entE*, *entF*, *entH*
- Nucleotide transport and metabolism (3): *nrdE*, *nrdF*, *nrdI*
- Signal transduction mechanisms (2): *fecR*, *ybiI*
- Other (15): *sufS*, *entS*, *fepE*, *entC*, *fecI*, *entA*, *sufA*, *sufE*, *ybdZ*, *ybiX*, *yddA*, *yjjZ*, *yncE*, *yoeA*$_1$, *yoeG*$_1$





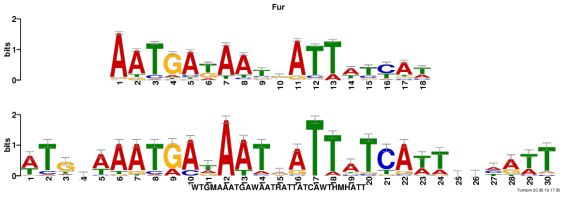






Motif E-value: 9.40e-36

Operons with Upstream Motif: 69%

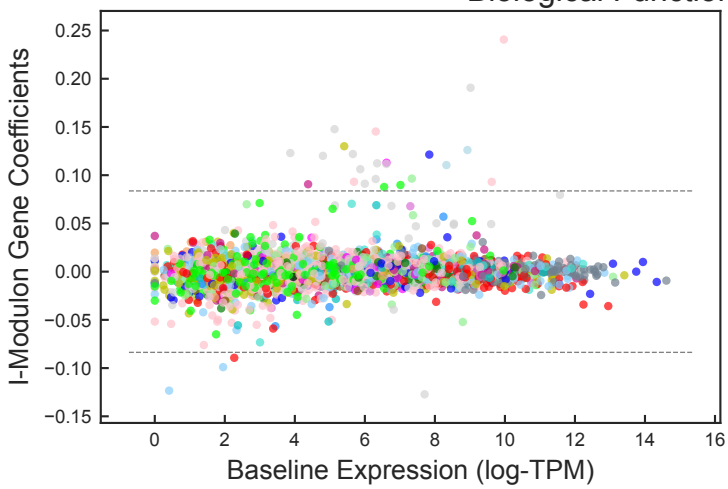


Motif similar to Fur (E-value: 1.75e-10)

Fur – 2 I-Modulon

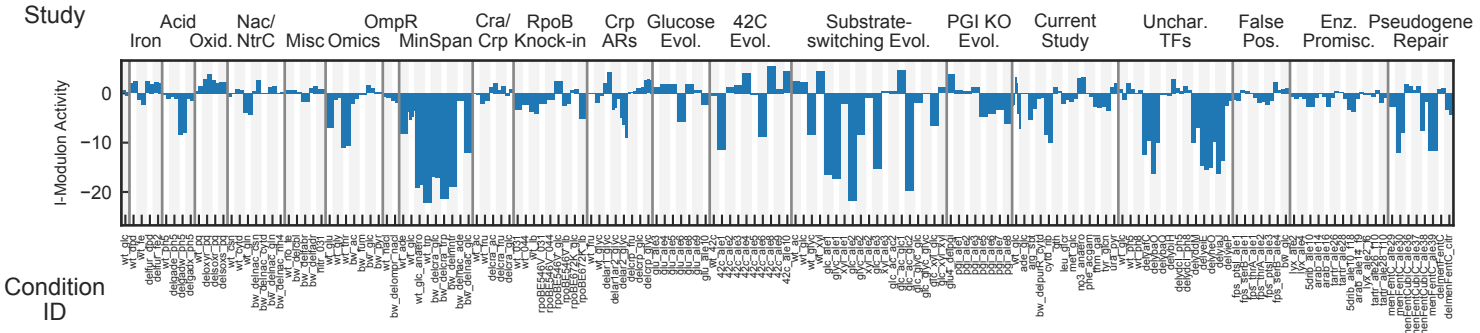
Regulated by: Fur

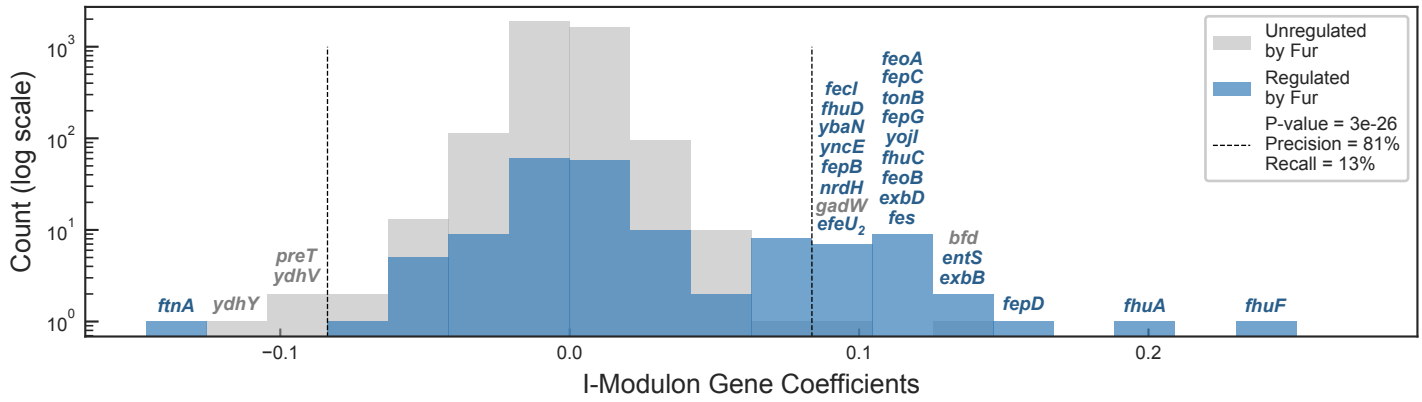
Biological Function: Iron homeostasis

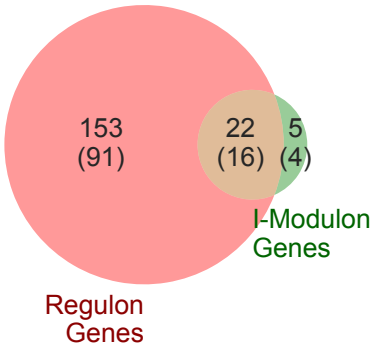


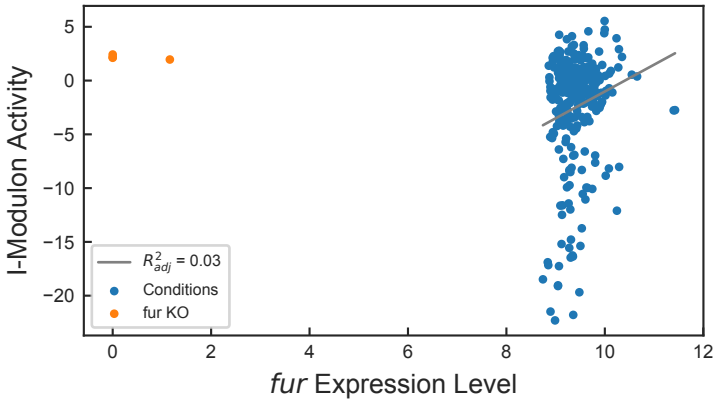
COG Categories

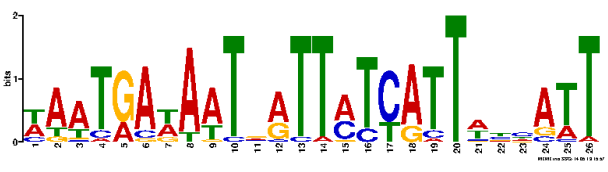
- Inorganic ion transport and metabolism (11): *feoA*, *feoB*, *fepB*, *fepC*, *fepD*, *fepG*, *fes*, *fhuA*, *fhuC*, *fhuD*, *ftnA*
- Energy production and conversion (2): *ydhV*, *ydhY*
- Intracellular trafficking, secretion, and vesicular transport (2): *exbB*, *exbD*
- Amino acid transport and metabolism (1): *preT*
- Carbohydrate transport and metabolism (1): *entS*
- Cell wall/membrane/envelope biogenesis (1): *tonB*
- Other (9): *yojI*, *nrdH*, *fecI*, *bfd*, *fhuF*, *ybaN*, *yncE*, $efeU_2$, *gadW*





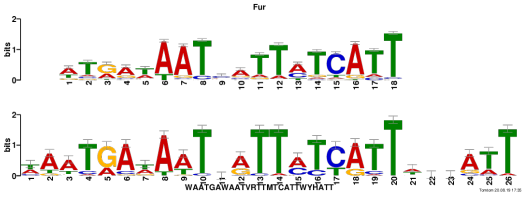






Motif E-value: 3.40e-32

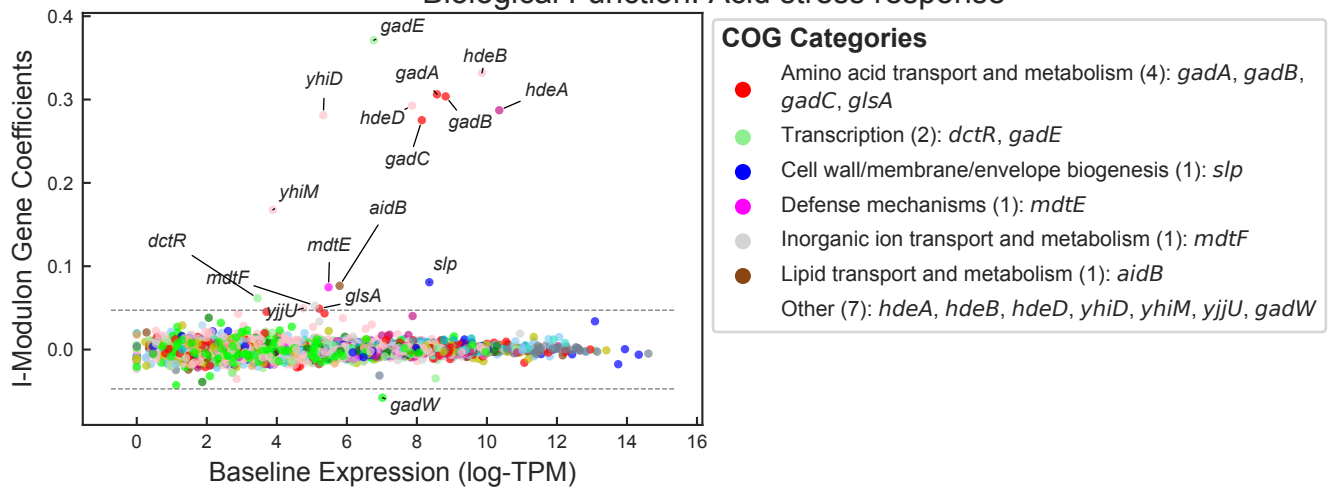
Operons with Upstream Motif: 90%

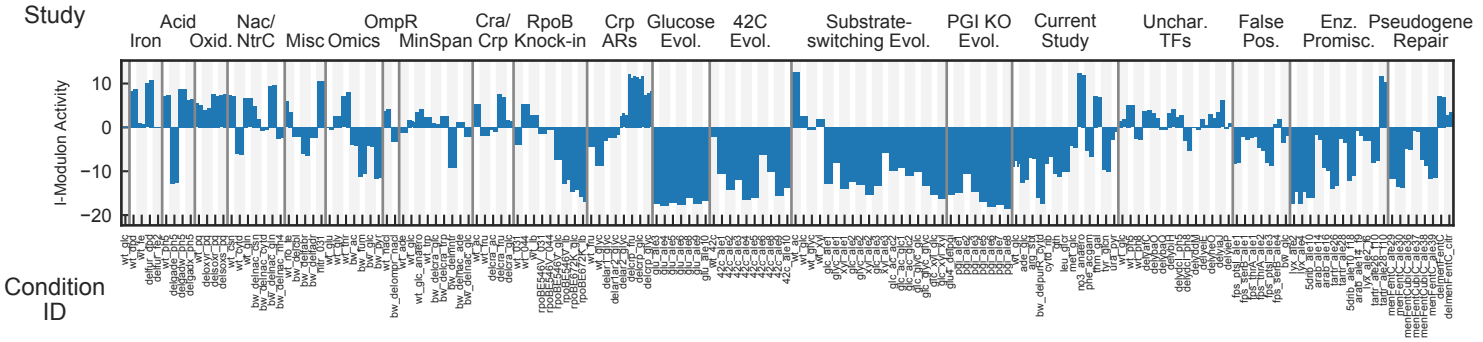


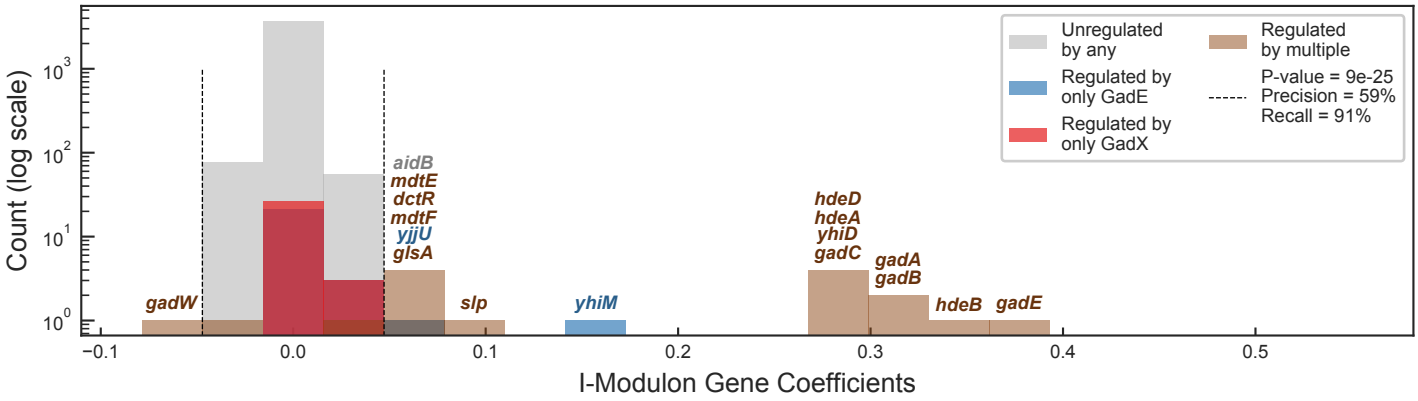
Motif similar to Fur (E-value: 2.42e-11)

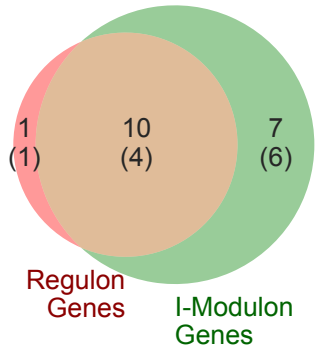
GadEWX I-Modulon

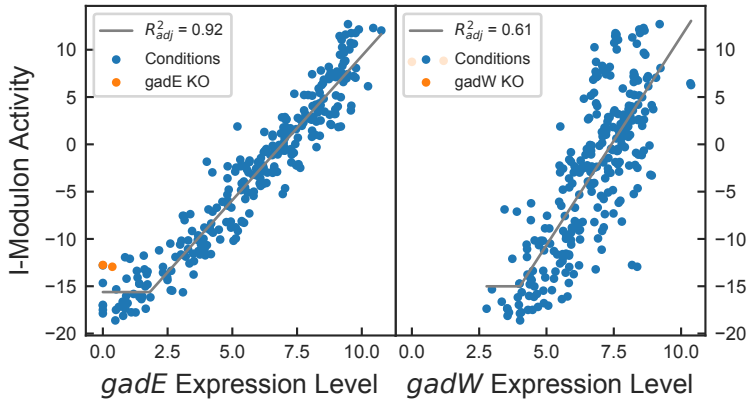
Regulated by: GadE and GadW and GadX
Biological Function: Acid stress response



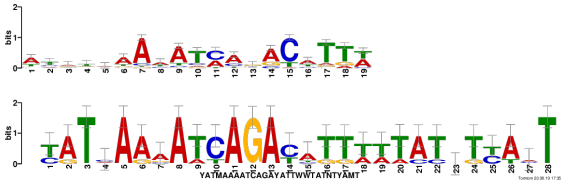








Motif E-value: 8.00e-04
Operons with Upstream Motif: 60%

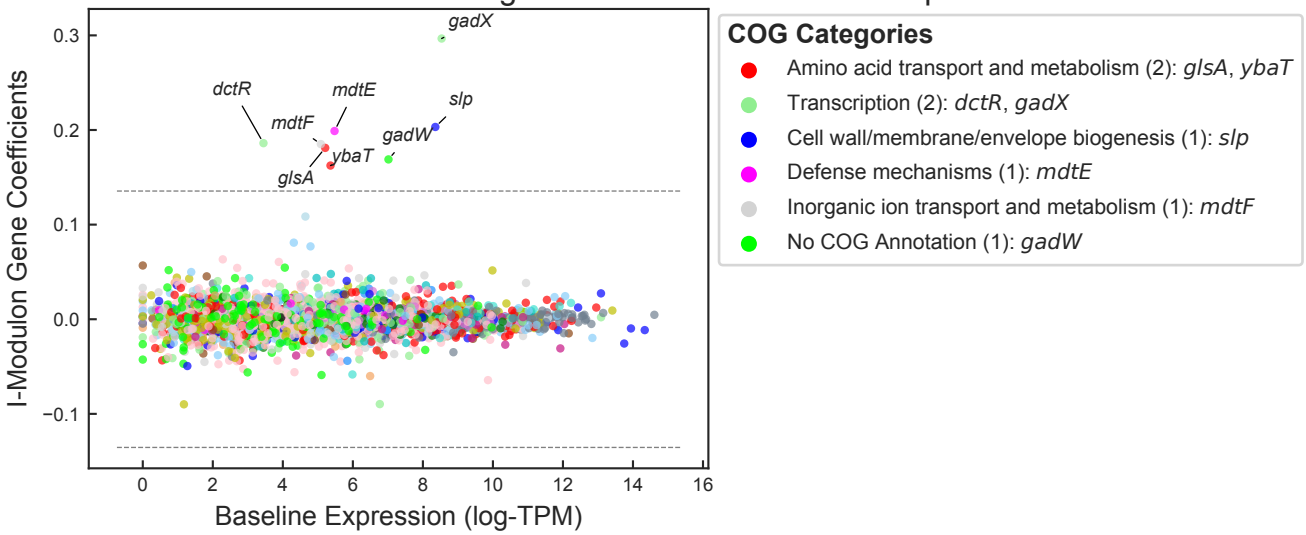


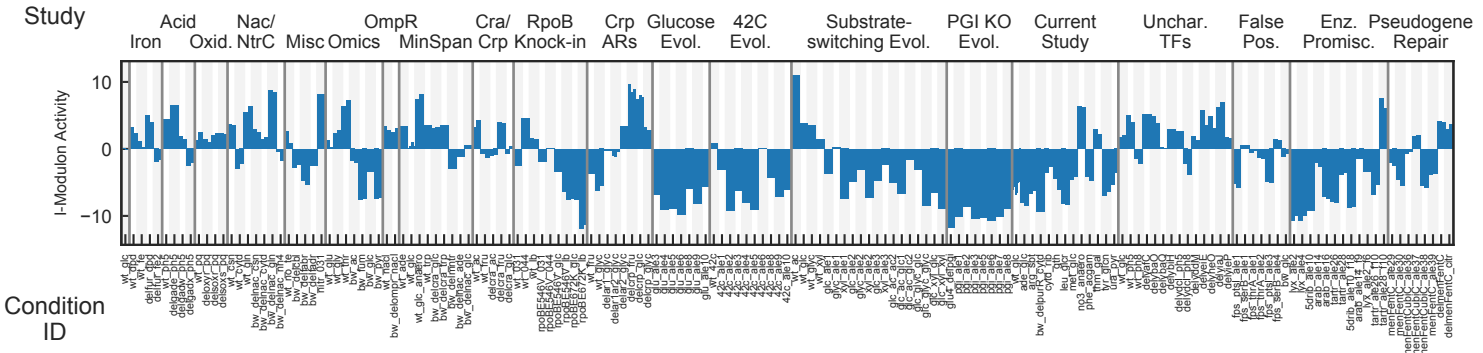
Motif similar to GadX (E-value: 5.32e-04)

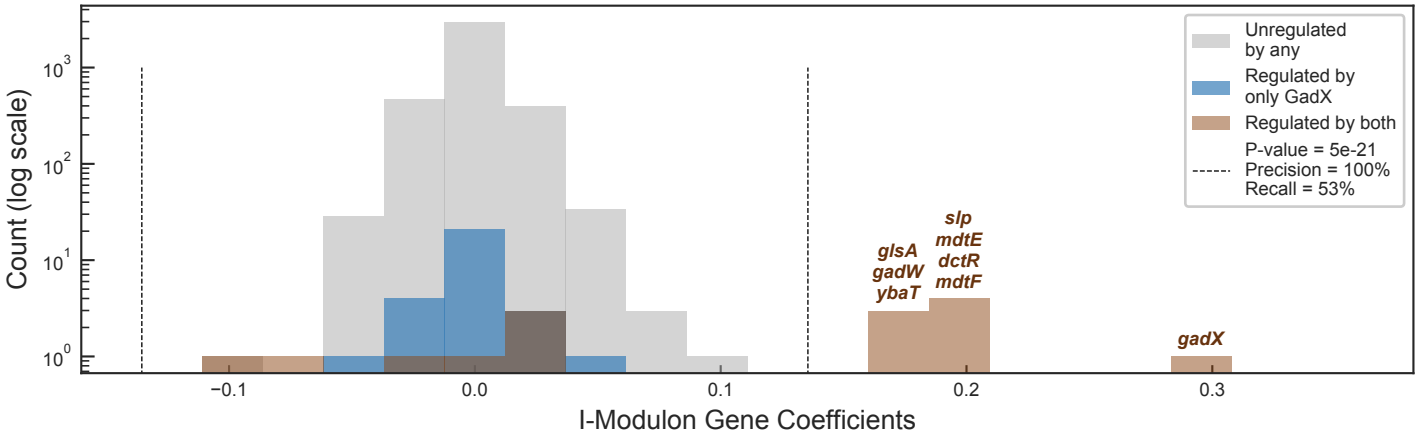
GadWX I-Modulon

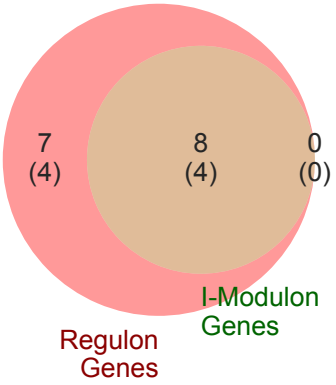
Regulated by: GadW and GadX

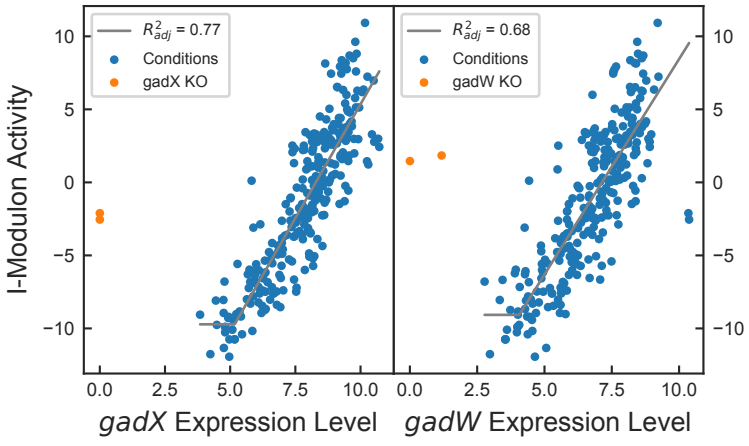
Biological Function: Acid stress response







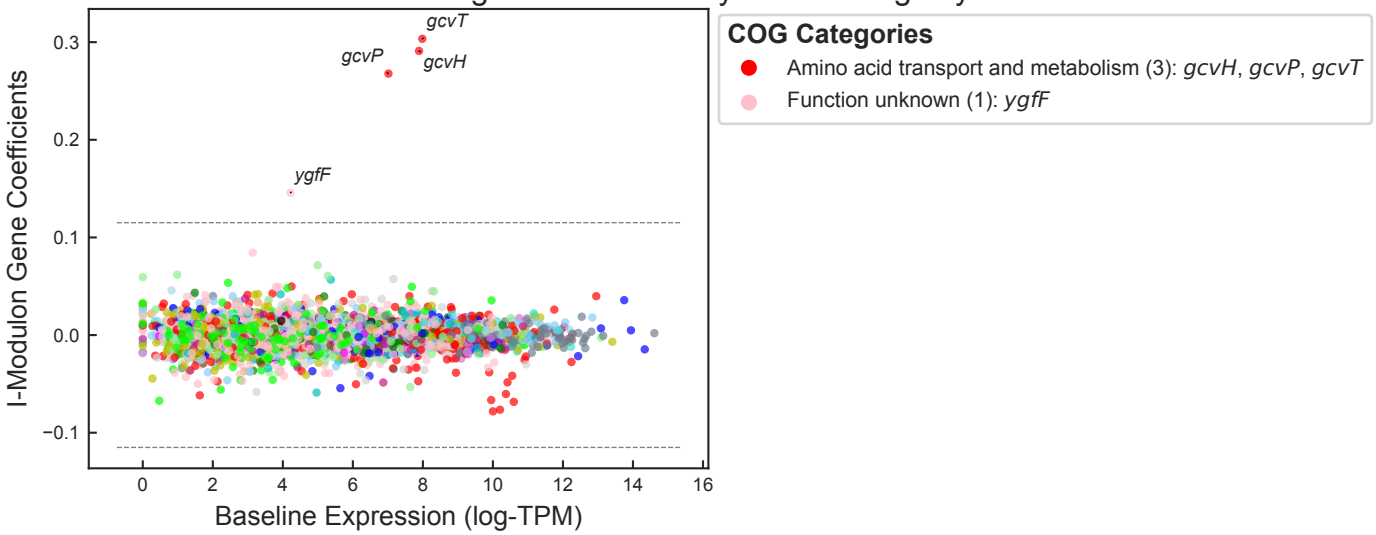


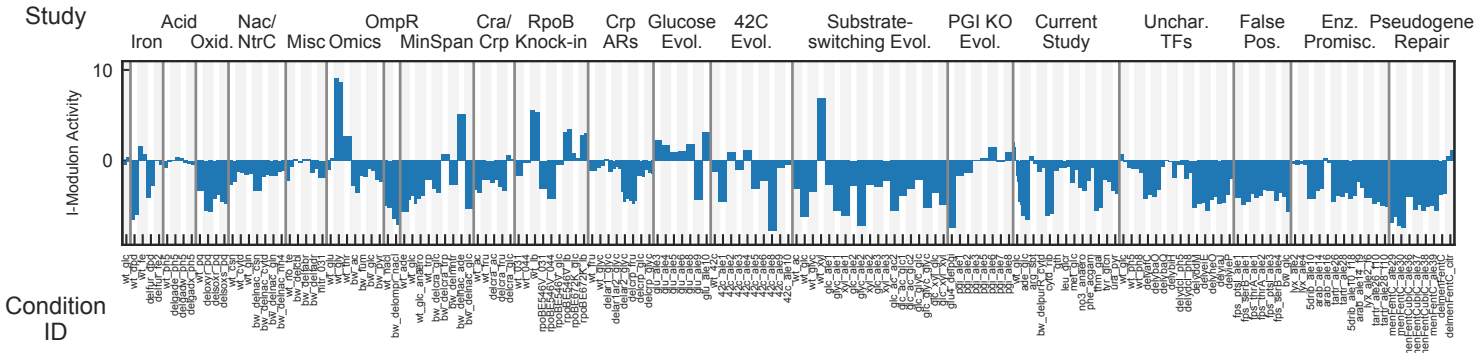


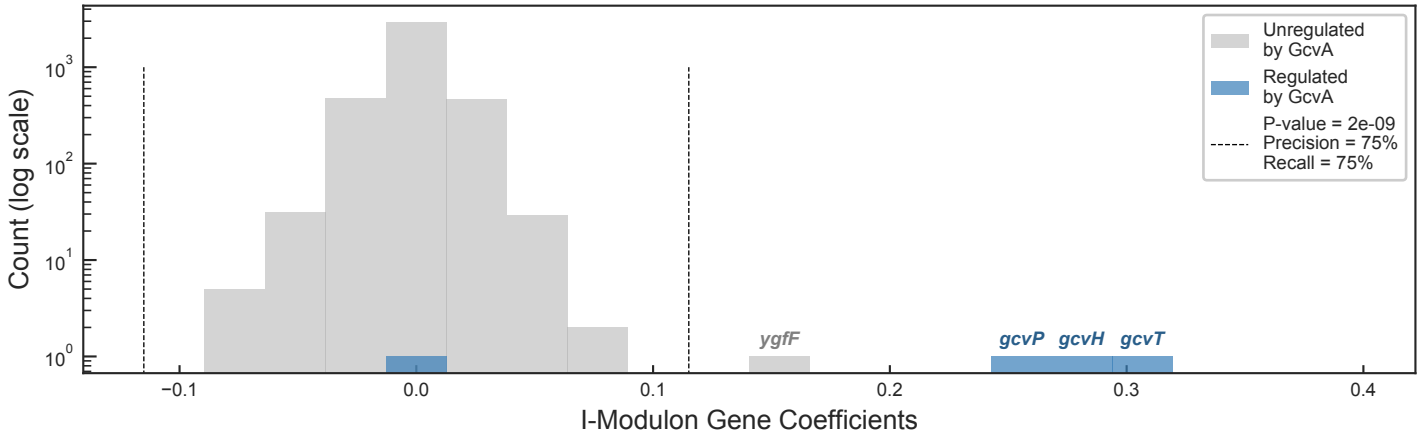
GcvA I-Modulon

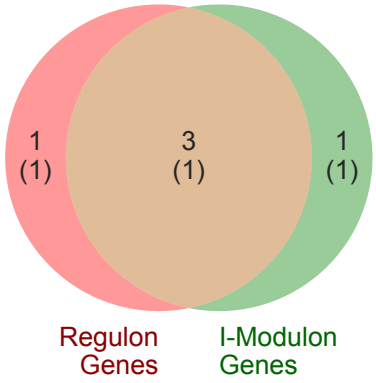
Regulated by: GcvA

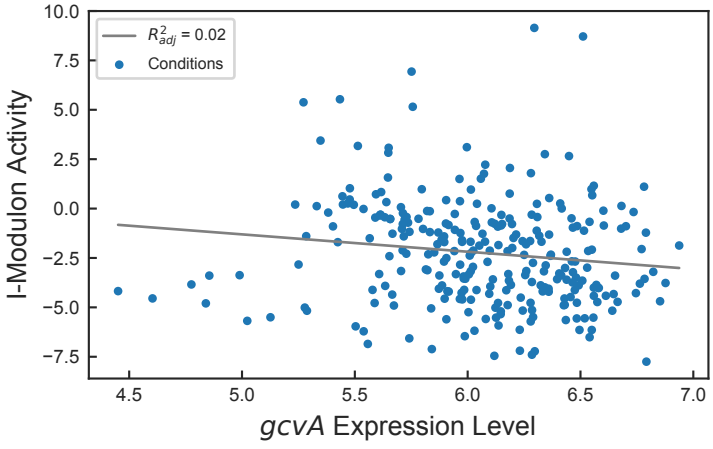
Biological Function: Glycine cleavage system







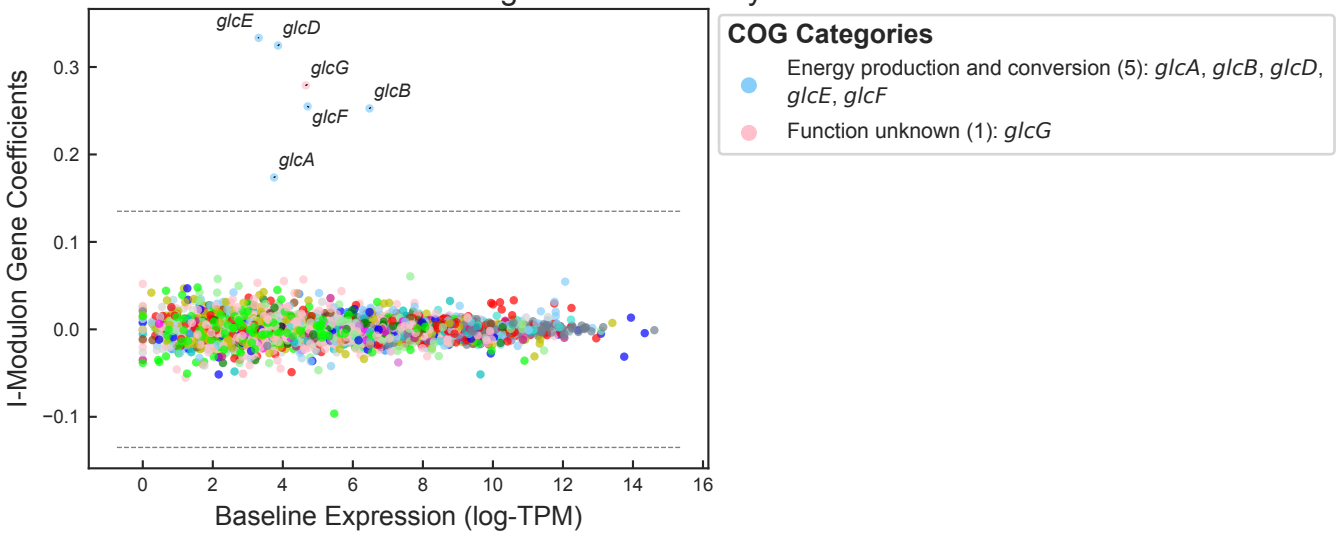


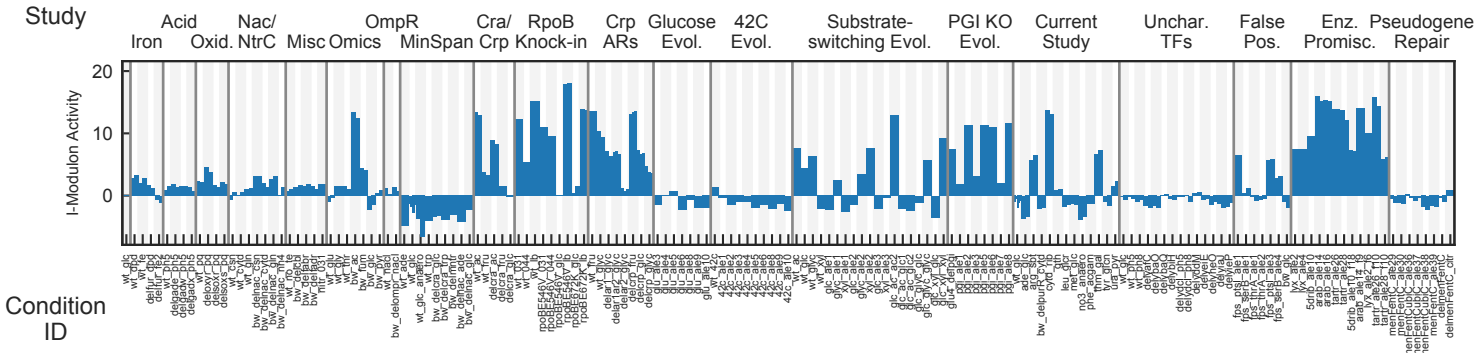


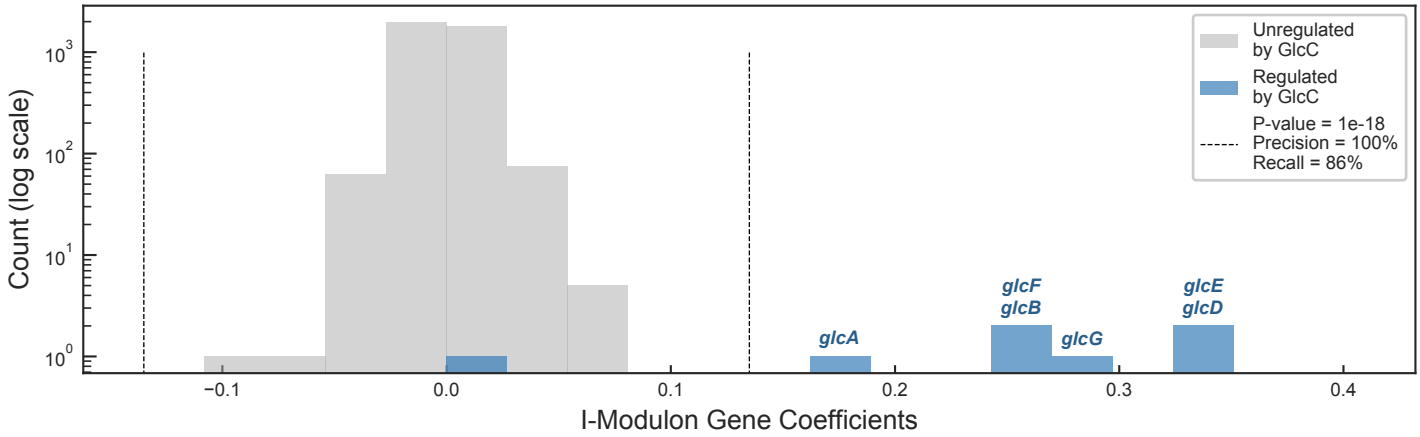
GlcC I-Modulon

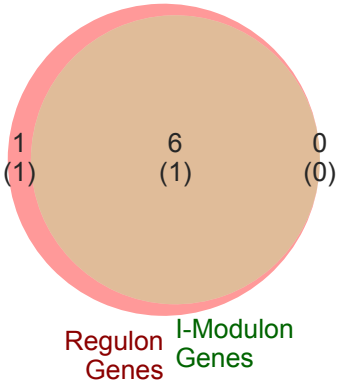
Regulated by: GlcC

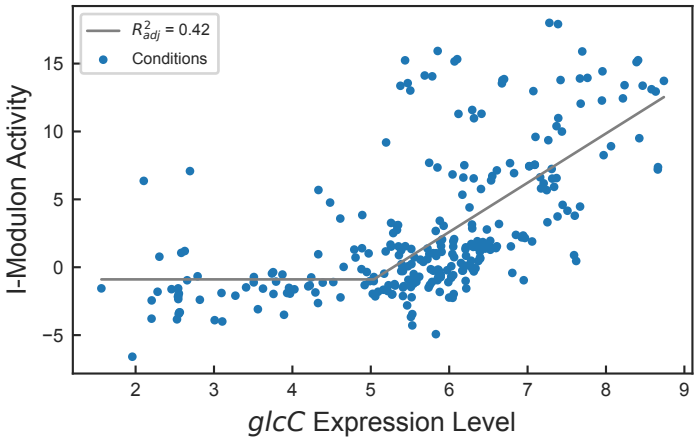
Biological Function: Glycolate catabolism







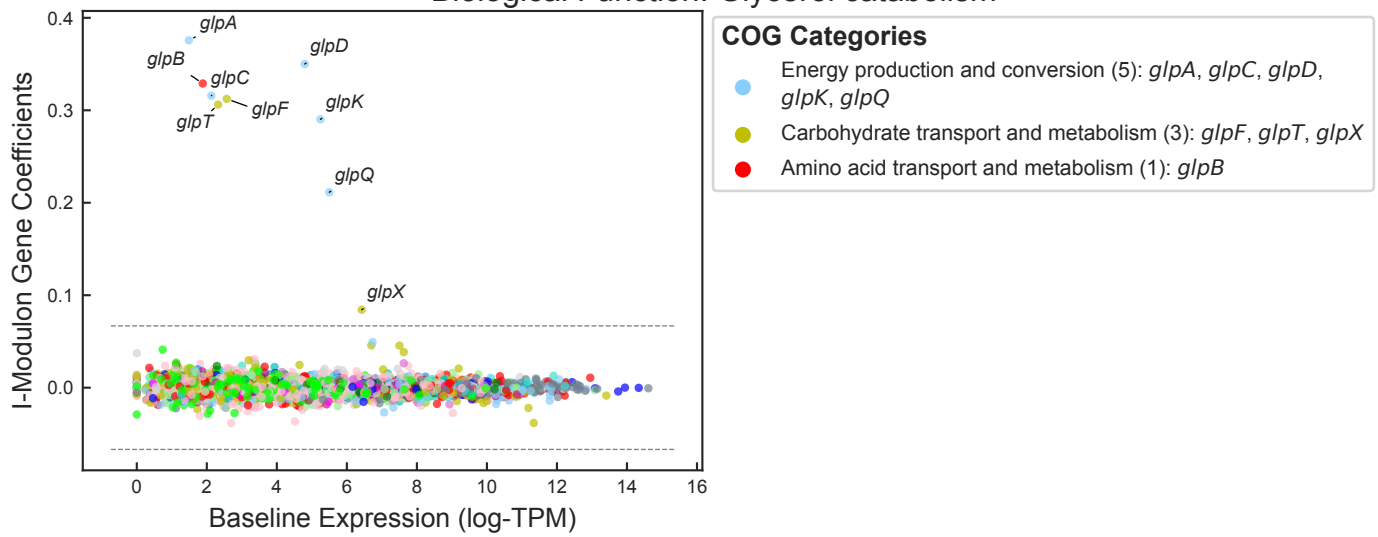


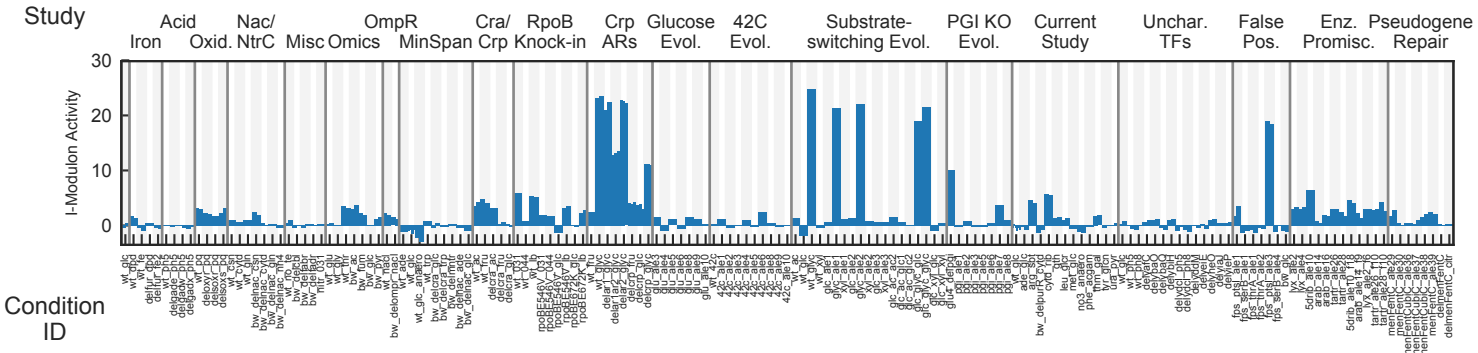


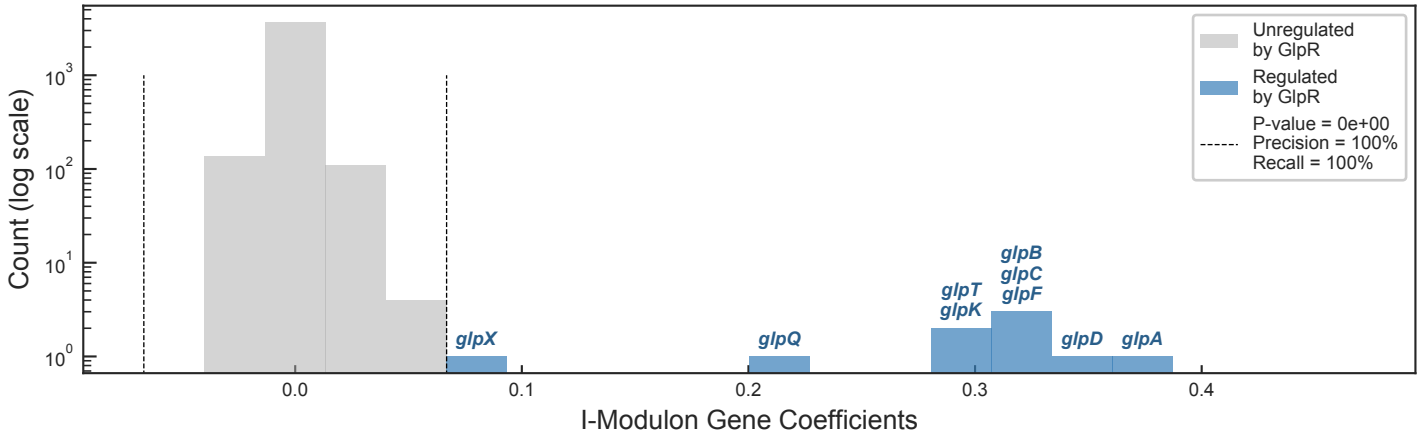
GlpR I-Modulon

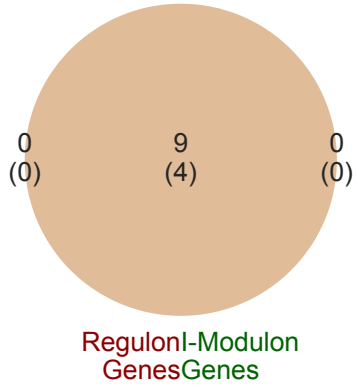
Regulated by: GlpR

Biological Function: Glycerol catabolism





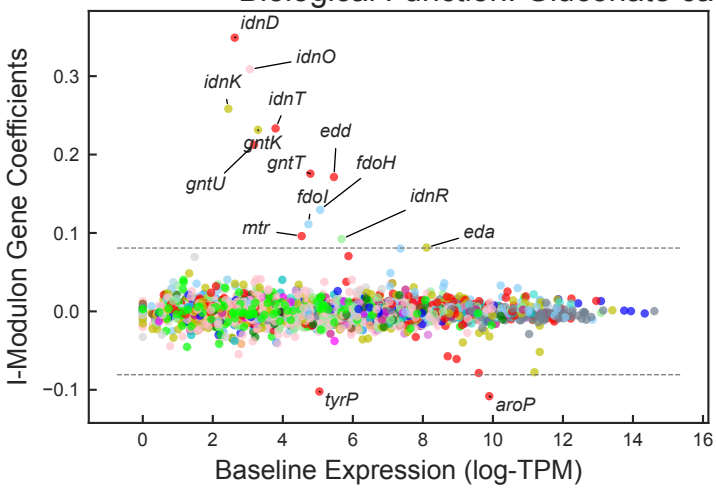




GntR/TyrR I-Modulon

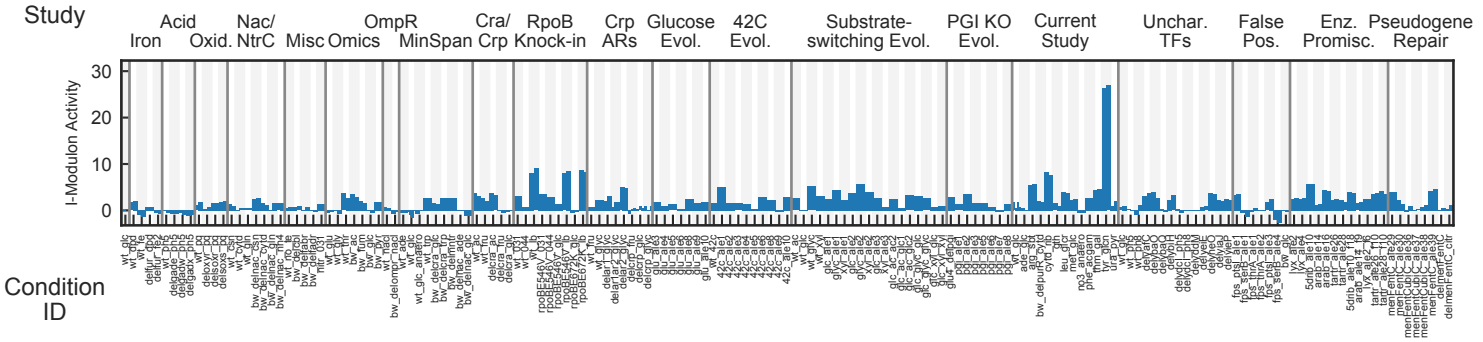
Regulated by: GntR or TyrR

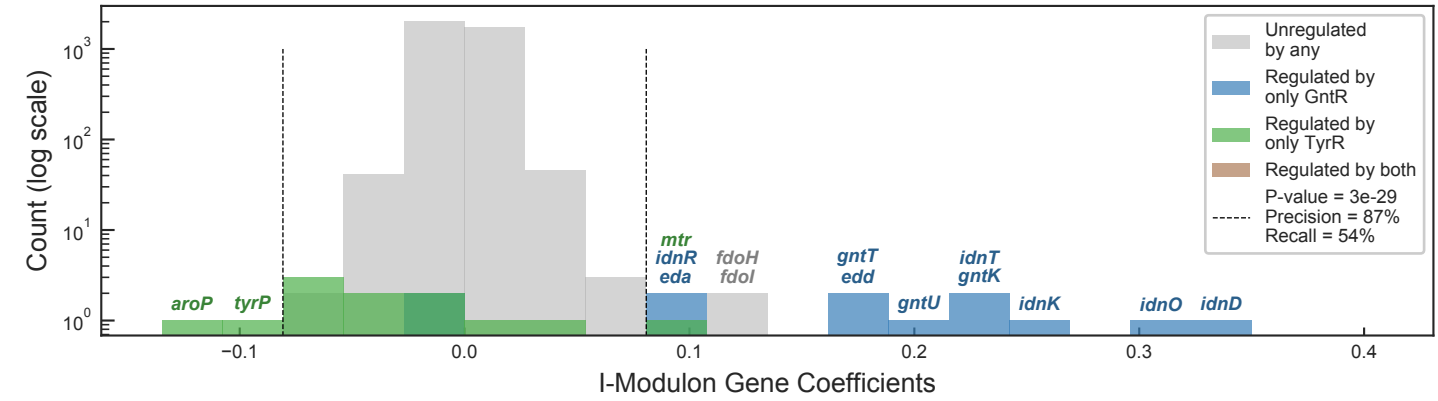
Biological Function: Gluconate catabolism and tyrosine biosynthesis

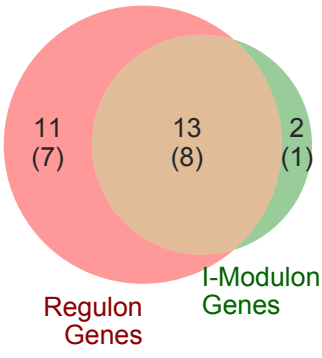


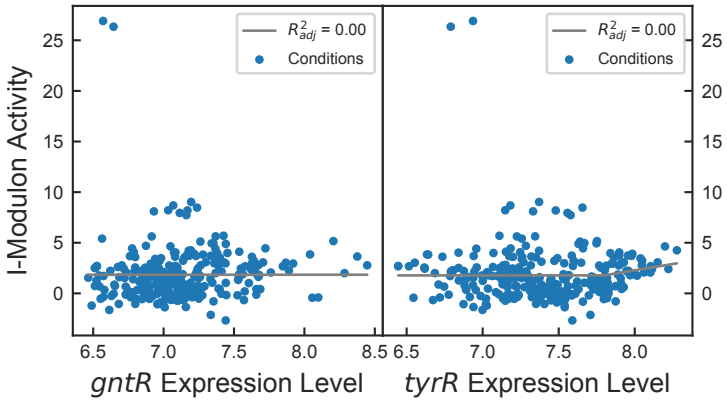
COG Categories

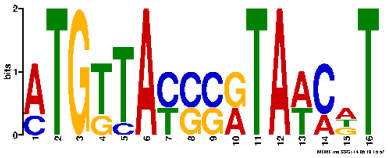
- Amino acid transport and metabolism (8): *aroP*, *edd*, *gntT*, *gntU*, *idnD*, *idnT*, *mtr*, *tyrP*
- Carbohydrate transport and metabolism (3): *eda*, *gntK*, *idnK*
- Energy production and conversion (2): *fdoH*, *fdoI*
- Transcription (1): *idnR*
- Function unknown (1): *idnO*





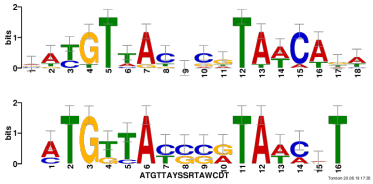






Motif E-value: 4.30e-04

Operons with Upstream Motif: 78%

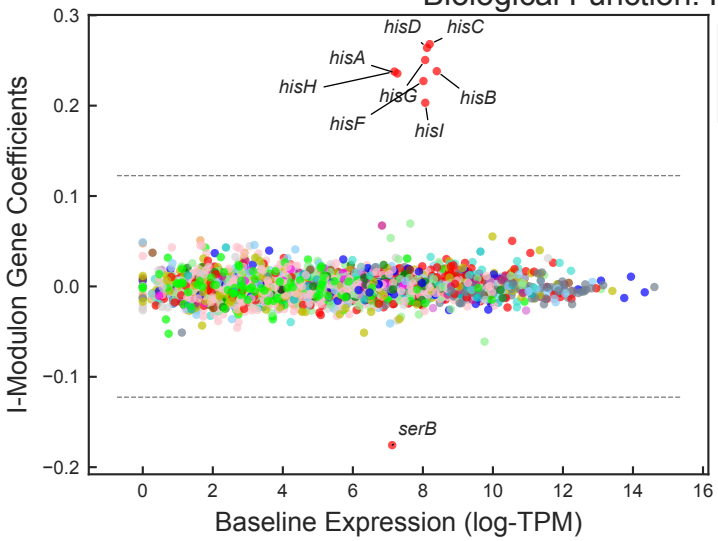


Motif similar to GntR (E-value: 3.25e-06)

His − tRNA I-Modulon

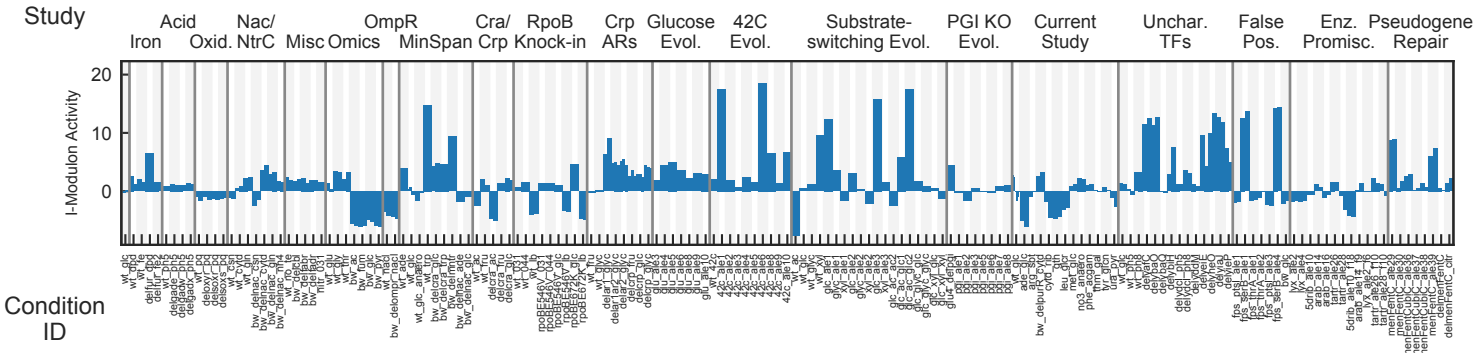
Regulated by: His-tRNA attenuation

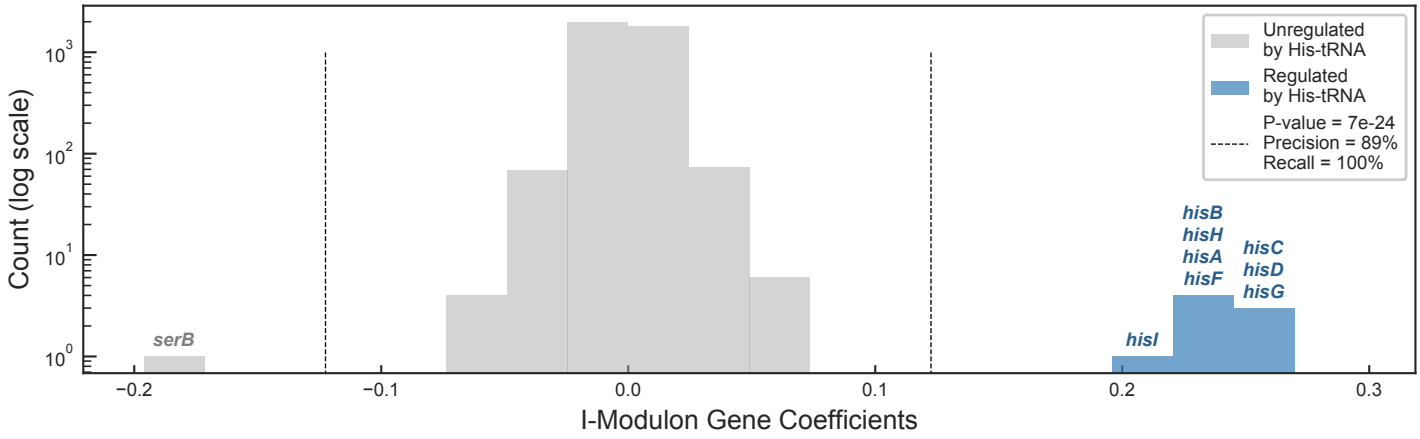
Biological Function: Histidine biosynthesis

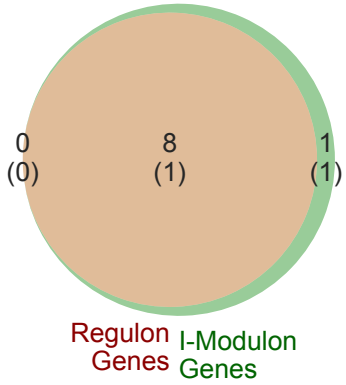


COG Categories

- Amino acid transport and metabolism (9): *hisA*, *hisB*, *hisC*, *hisD*, *hisF*, *hisG*, *hisH*, *hisI*, *serB*

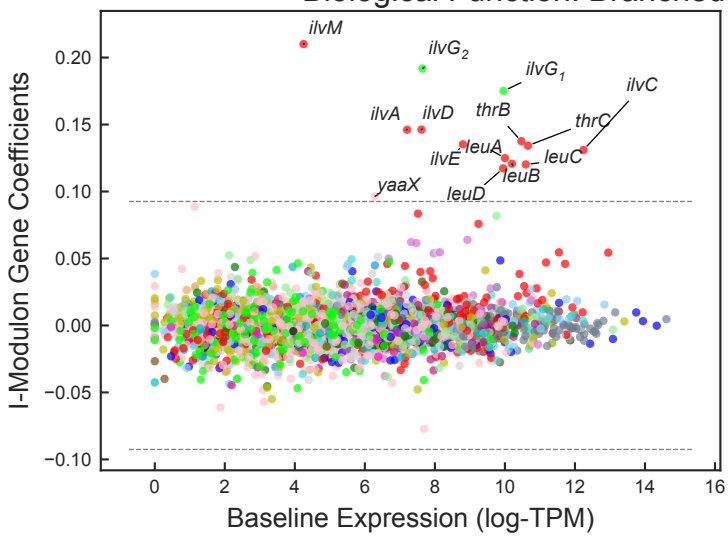






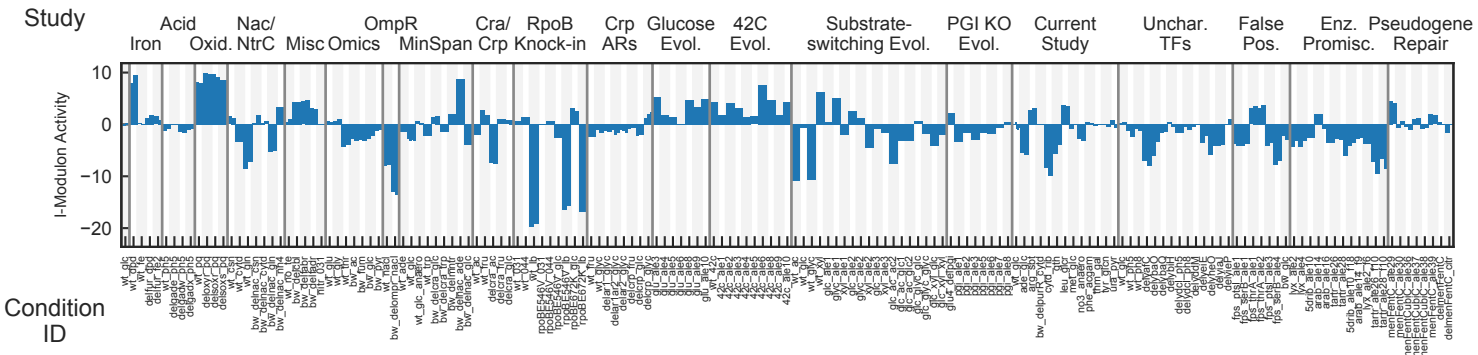
Leu/Ile I-Modulon

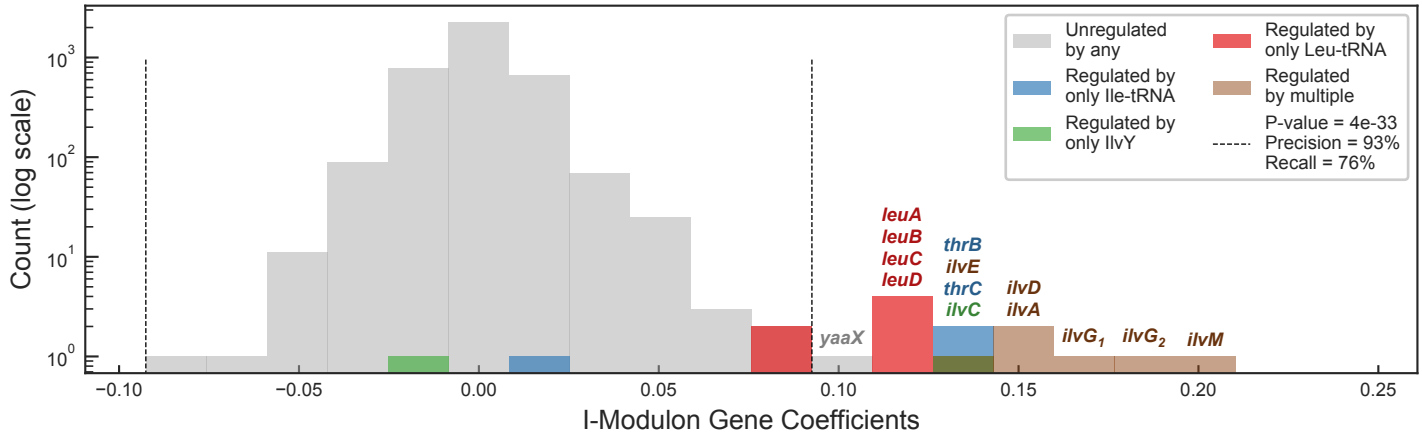
Regulated by: IlvY or leu-tRNA attenuation or ile-tRNA attenuation
Biological Function: Branched-chain amino acid biosynthesis

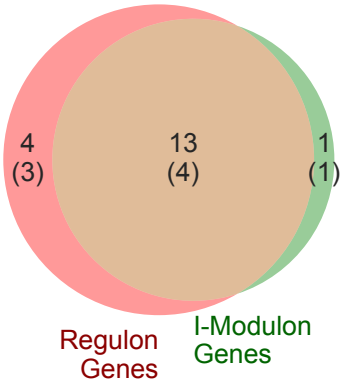


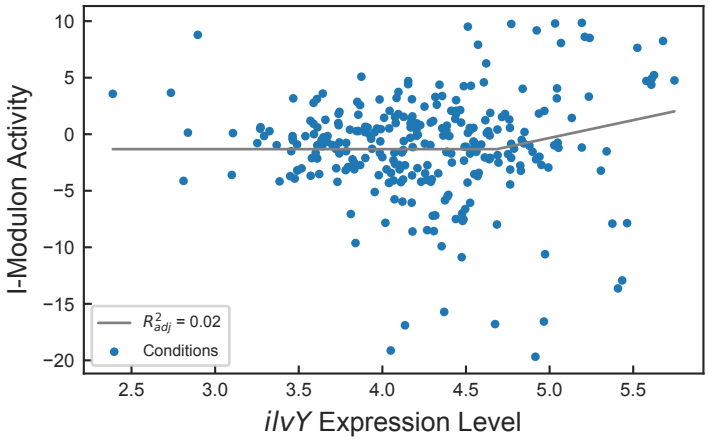
COG Categories

- Amino acid transport and metabolism (11): *ilvA*, *ilvC*, *ilvD*, *ilvE*, *ilvM*, *leuA*, *leuB*, *leuC*, *leuD*, *thrB*, *thrC*
- No COG Annotation (2): $ilvG_1$, $ilvG_2$
- Function unknown (1): *yaaX*





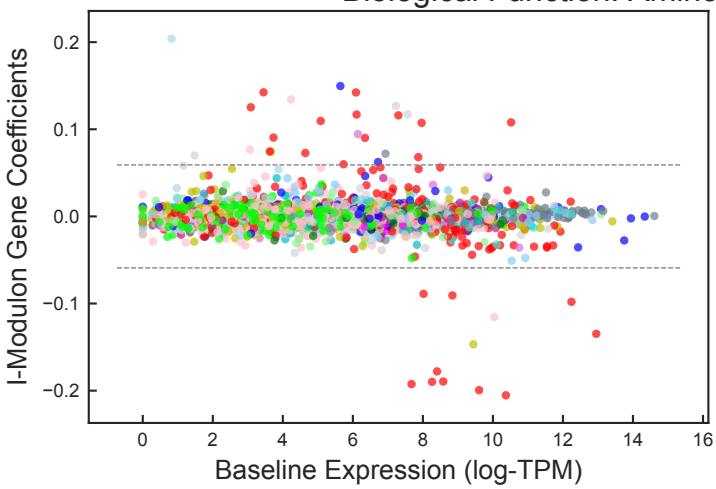




Lrp I-Modulon

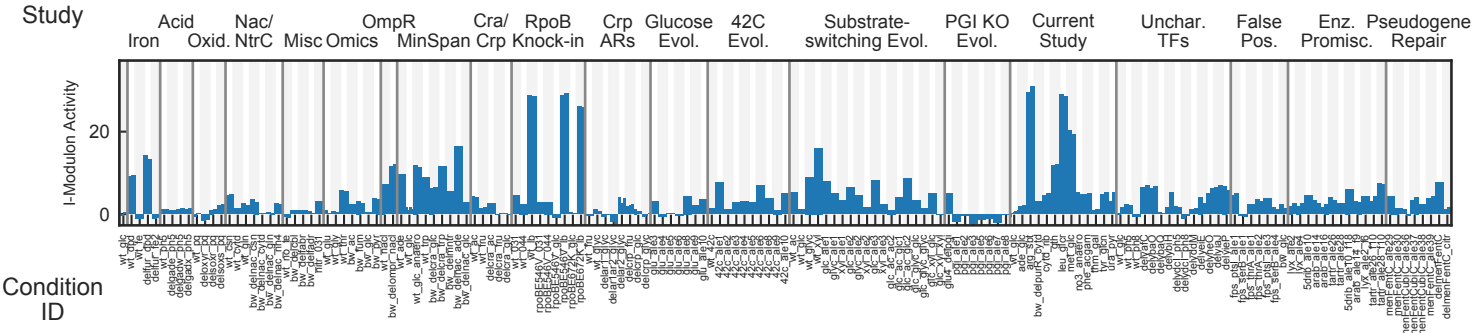
Regulated by: Lrp

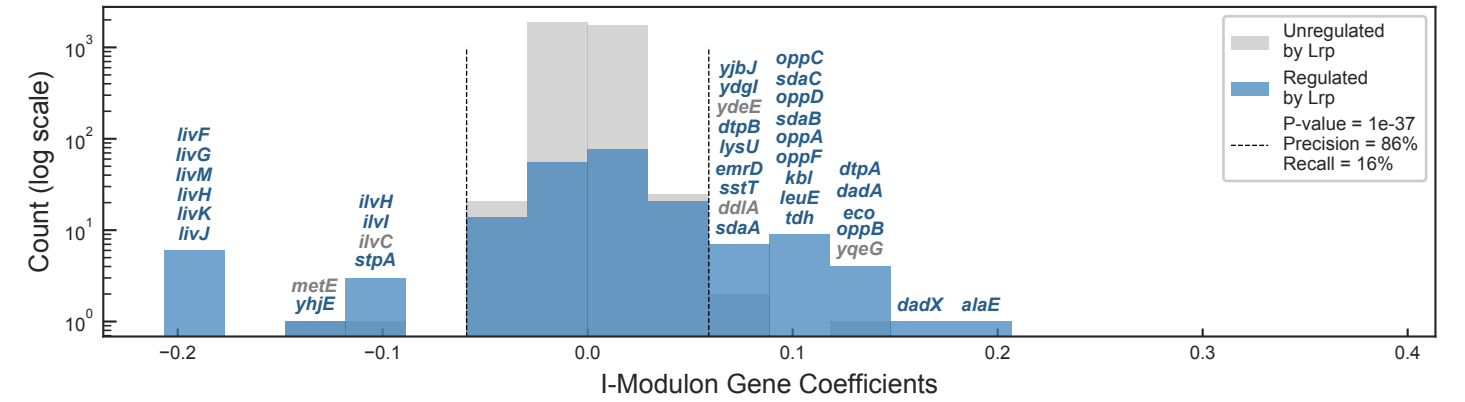
Biological Function: Amino acid and peptide transport

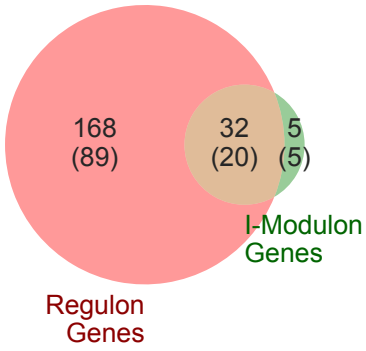


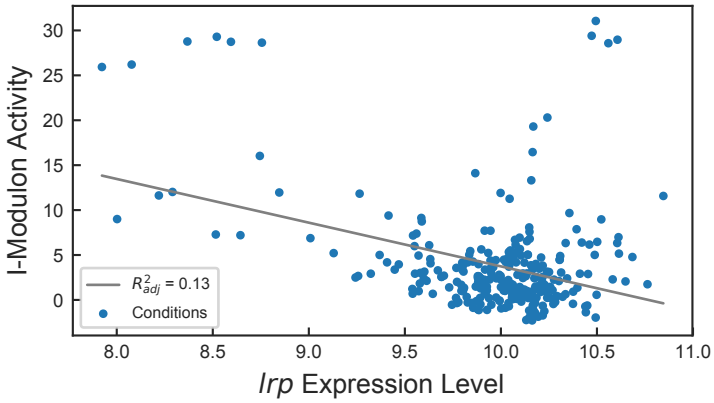
COG Categories

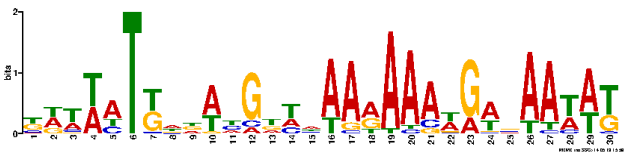
- Amino acid transport and metabolism (24): *dadA*, *dtpA*, *dtpB*, *ilvC*, *ilvH*, *ilvI*, *leuE*, *livF*, *livG*, *livH*, *livJ*, *livK*, *livM*, *metE*, *oppA*, *oppD*, *oppF*, *sdaA*, *sdaB*, *sdaC*, *sstT*, *tdh*, *ydgI*, *yqeG*
- Inorganic ion transport and metabolism (3): *emrD*, *oppB*, *oppC*
- Carbohydrate transport and metabolism (2): *ydeE*, *yhjE*
- Cell wall/membrane/envelope biogenesis (2): *dadX*, *ddlA*
- Coenzyme transport and metabolism (1): *kbl*
- Other (5): *alaE*, *lysU*, *eco*, *stpA*, *yjbJ*











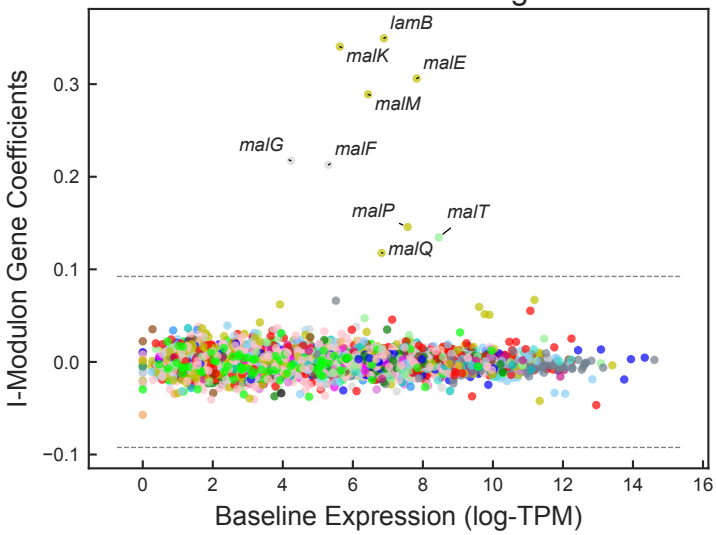
Motif E-value: 1.20e-04

Operons with Upstream Motif: 72%

MalT I-Modulon

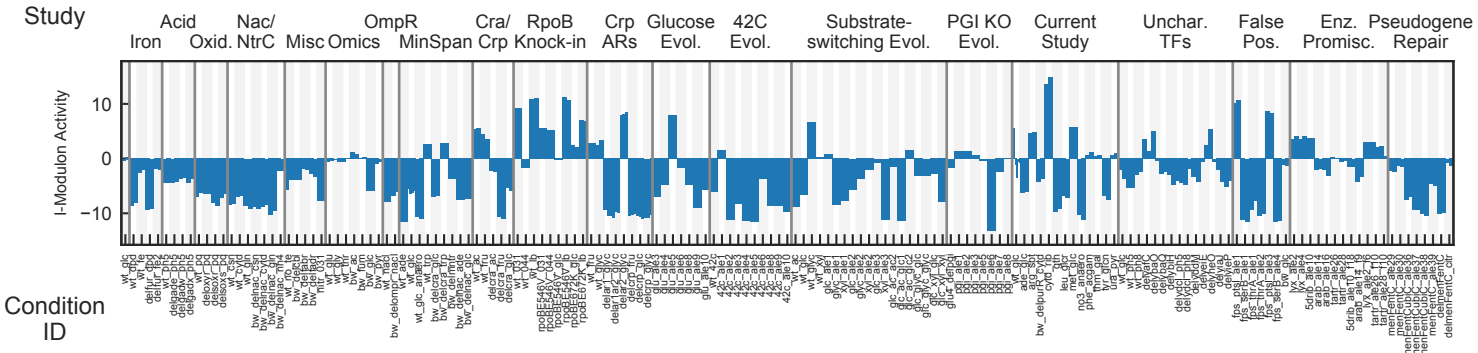
Regulated by: MalT

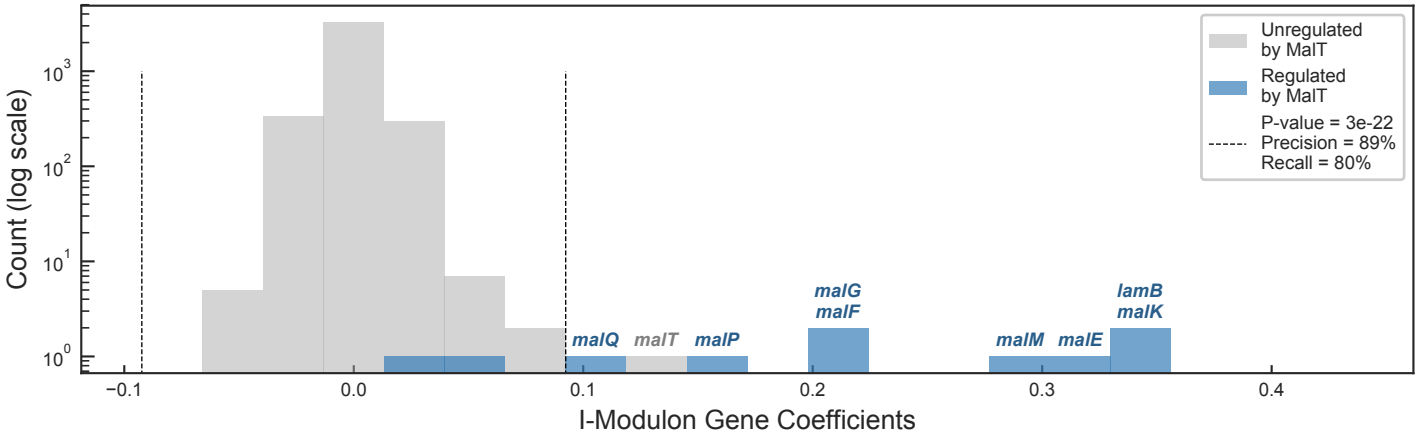
Biological Function: Maltose catabolism

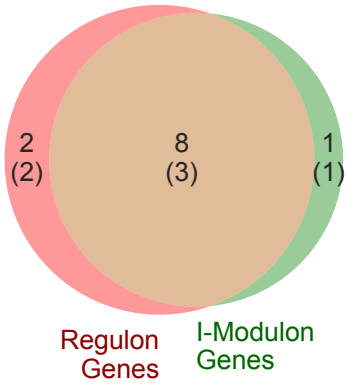


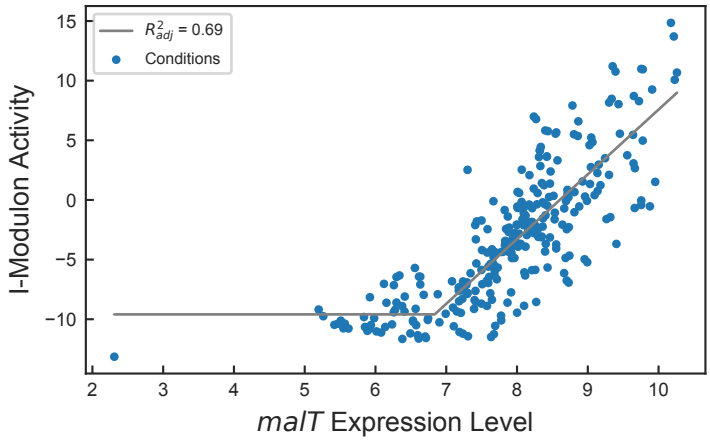
COG Categories

- Carbohydrate transport and metabolism (6): *lamB*, *malE*, *malK*, *malM*, *malP*, *malQ*
- Inorganic ion transport and metabolism (2): *malF*, *malG*
- Transcription (1): *malT*





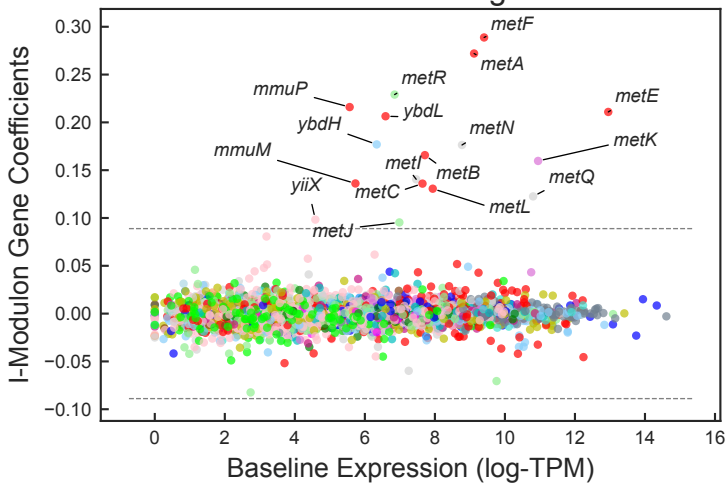




MetJ I-Modulon

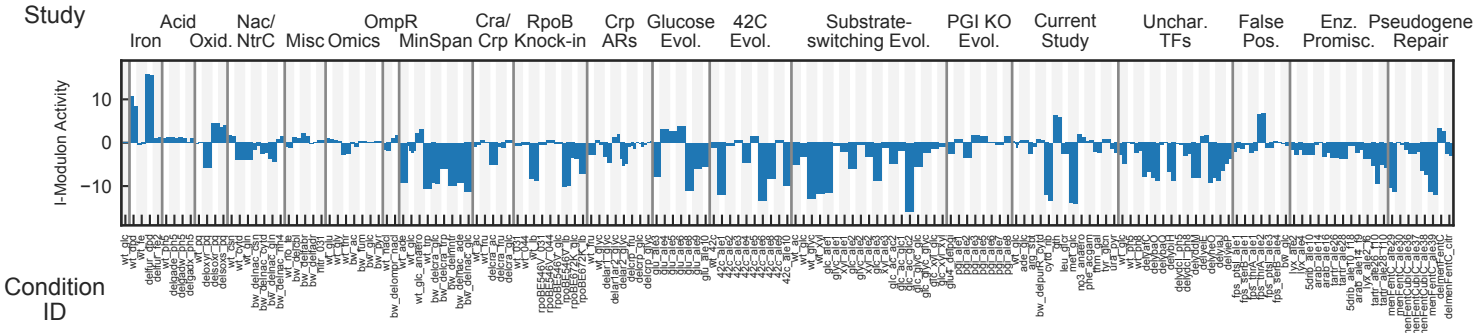
Regulated by: MetJ

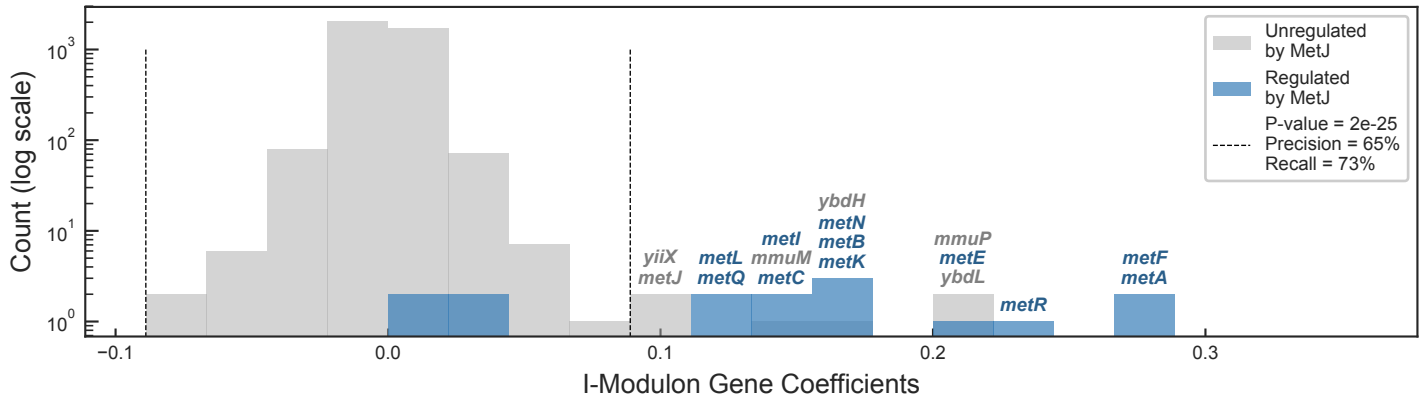
Biological Function: Methionine biosynthesis

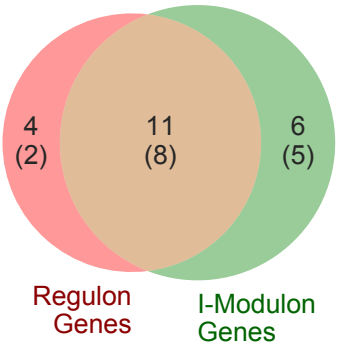


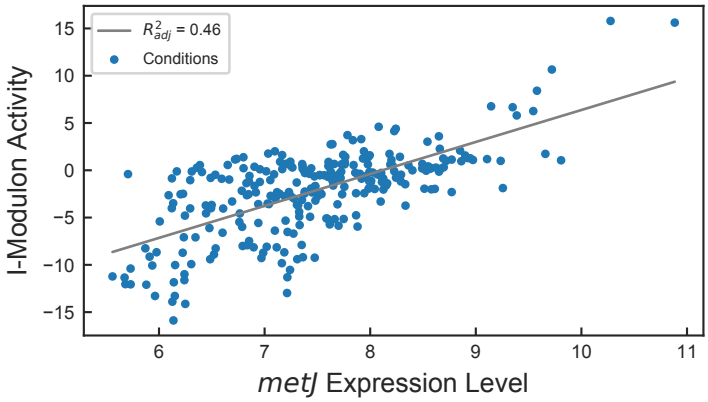
COG Categories

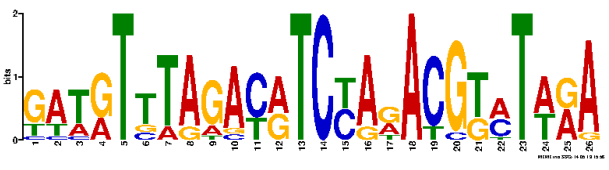
- Amino acid transport and metabolism (9): *metA*, *metB*, *metC*, *metE*, *metF*, *metL*, *mmuM*, *mmuP*, *ybdL*
- Inorganic ion transport and metabolism (3): *metI*, *metN*, *metQ*
- Transcription (2): *metJ*, *metR*
- Coenzyme transport and metabolism (1): *metK*
- Energy production and conversion (1): *ybdH*
- Function unknown (1): *yiiX*





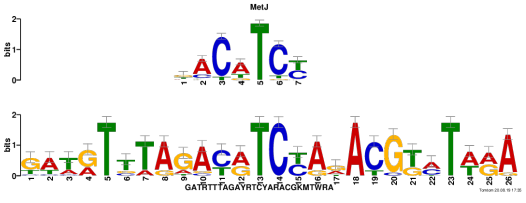






Motif E-value: 1.60e-37

Operons with Upstream Motif: 92%

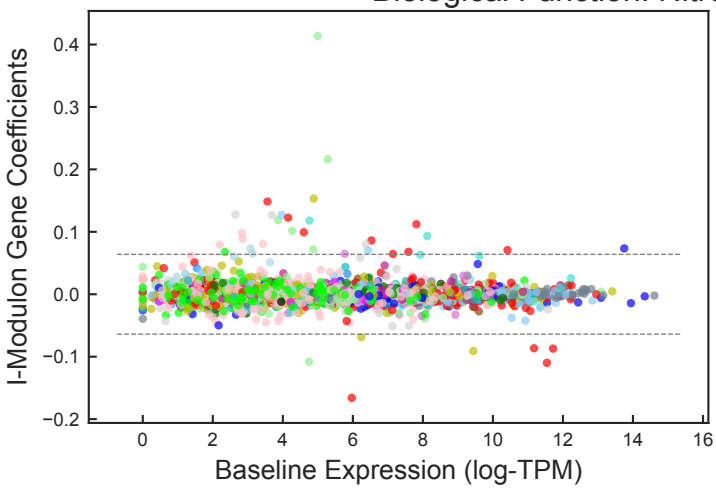


Motif similar to MetJ (E-value: 3.99e-03)

Nac I-Modulon

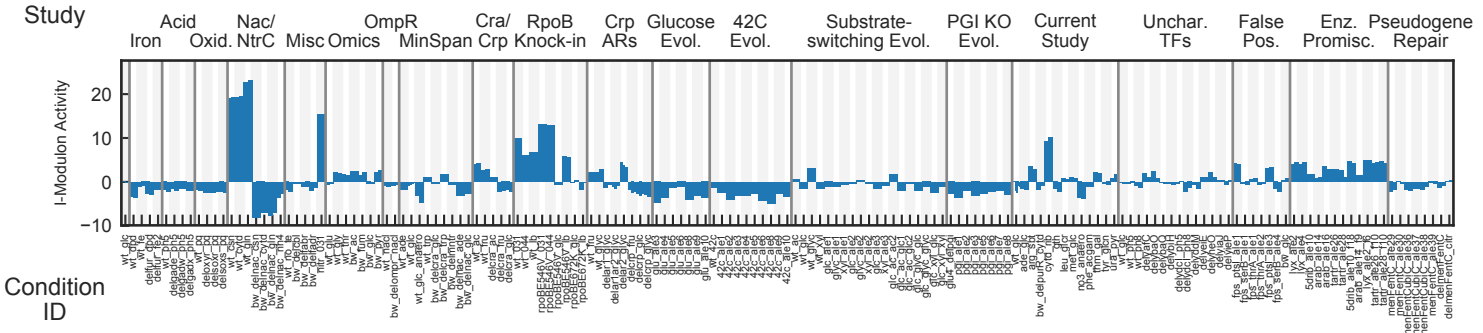
Regulated by: Nac

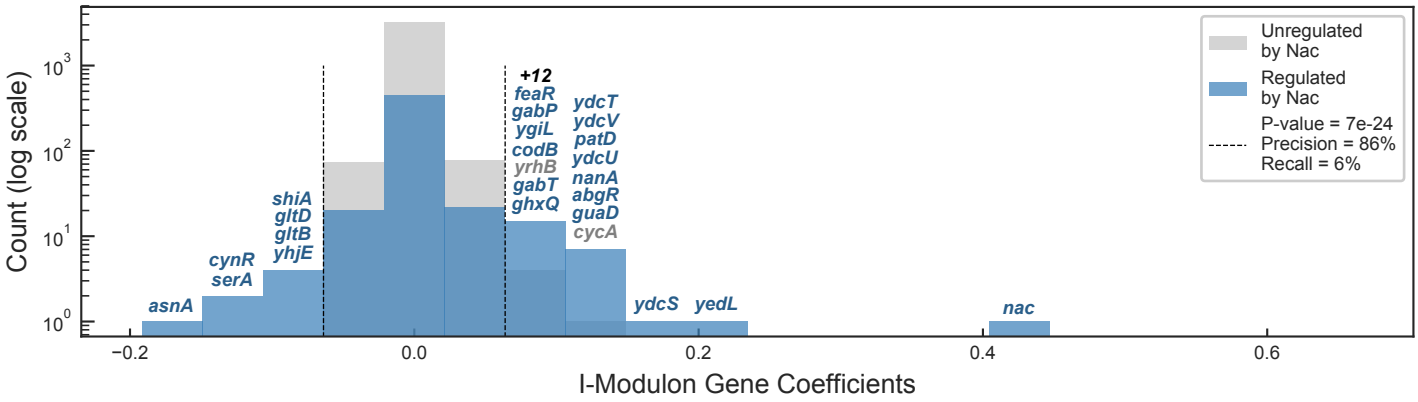
Biological Function: Nitrogen starvation response

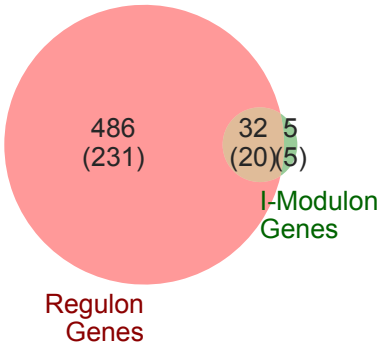


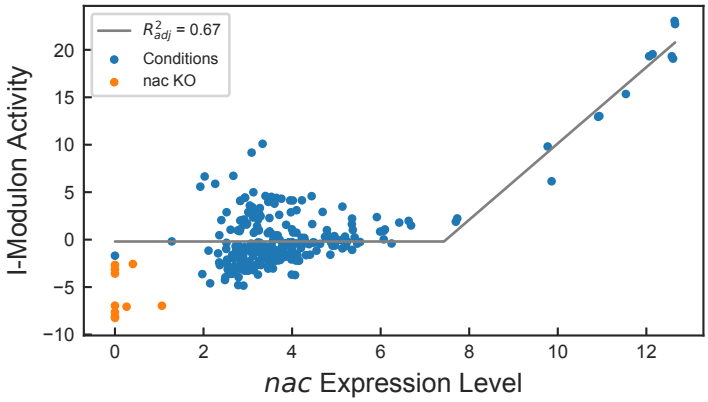
COG Categories

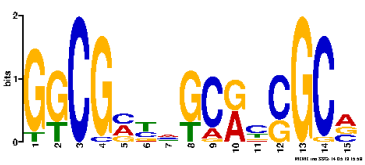
- Amino acid transport and metabolism (12): *asnA*, *cycA*, *dppA*, *dppD*, *dppF*, *gabP*, *gabT*, *gltB*, *gltD*, *nanA*, *serA*, *ydcT*
- Transcription (6): *abgR*, *csiR*, *cynR*, *feaR*, *nac*, *yedL*
- Carbohydrate transport and metabolism (3): *shiA*, *ydcS*, *yhjE*
- Inorganic ion transport and metabolism (3): *dppB*, *ydcU*, *ydcV*
- Energy production and conversion (2): *gabD*, *patD*
- Intracellular trafficking, secretion, and vesicular transport (2): *gspC*, *gspE*
- Other (9): *codB*, *guaD*, *ompF*, *yieE*, *ghxQ*, *ybeQ*, *ygiL*, *yrhB*, *yrdE*$_2$











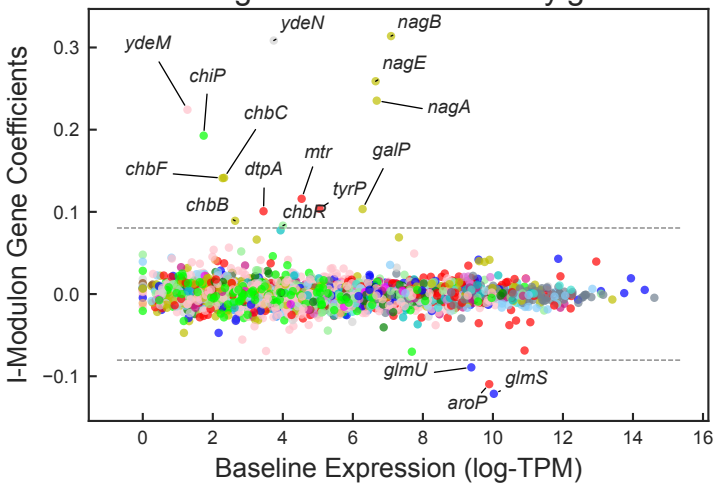
Motif E-value: 2.20e-08

Operons with Upstream Motif: 72%

NagC/TyrR I-Modulon

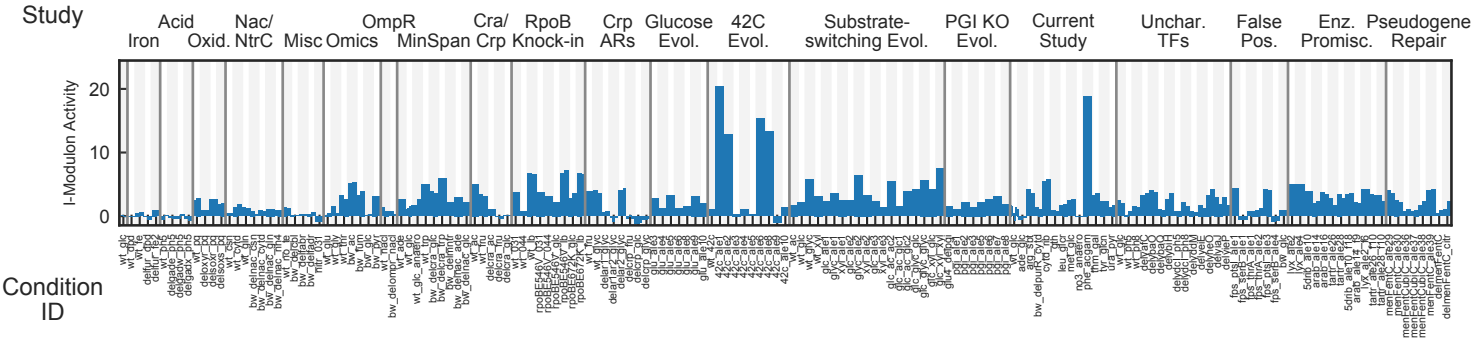
Regulated by: NagC or TyrR

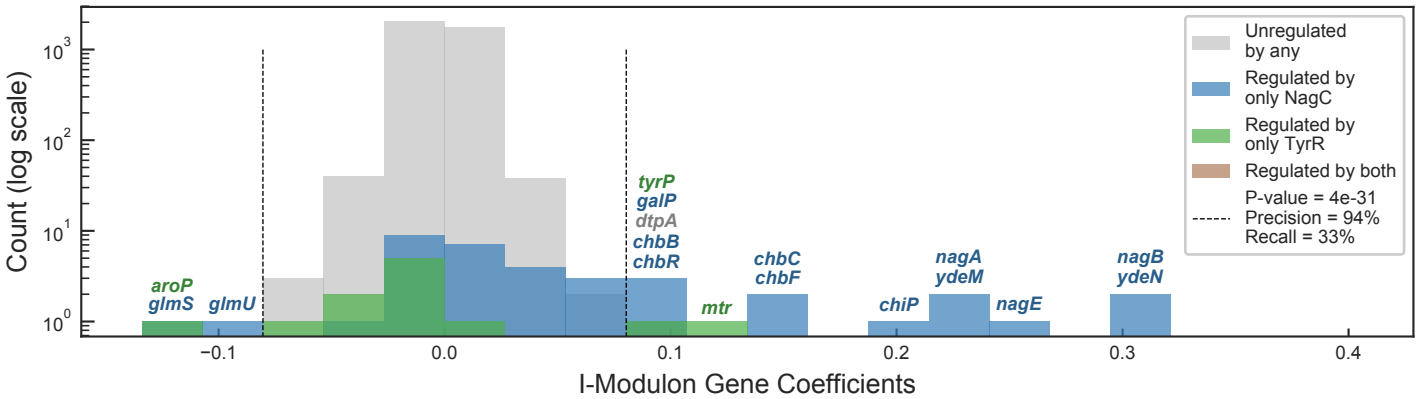
Biological Function: N-acetylglucosamine catabolism and tyrosine biosynthesis

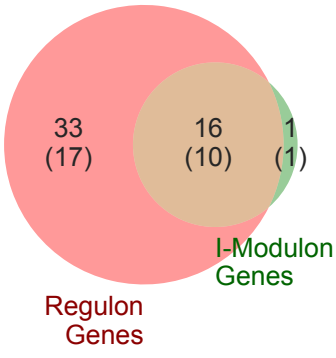


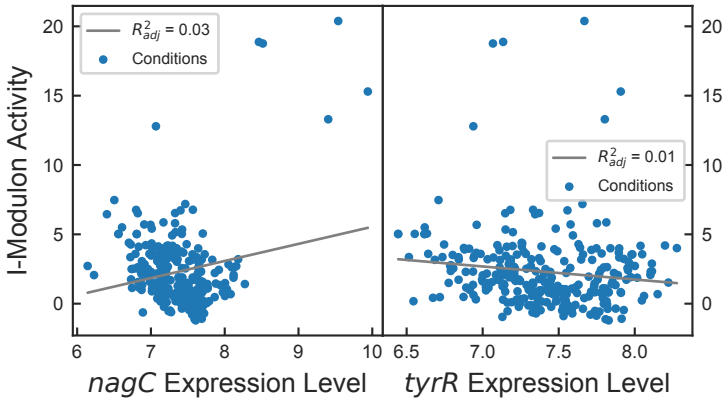
COG Categories

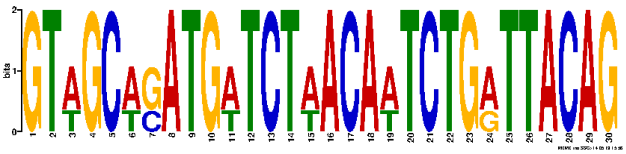
- Carbohydrate transport and metabolism (7): *chbB*, *chbC*, *chbF*, *galP*, *nagA*, *nagB*, *nagE*
- Amino acid transport and metabolism (4): *aroP*, *dtpA*, *mtr*, *tyrP*
- Cell wall/membrane/envelope biogenesis (2): *glmS*, *glmU*
- Inorganic ion transport and metabolism (1): *ydeN*
- Transcription (1): *chbR*
- Function unknown (1): *ydeM*
- No COG Annotation (1): *chiP*











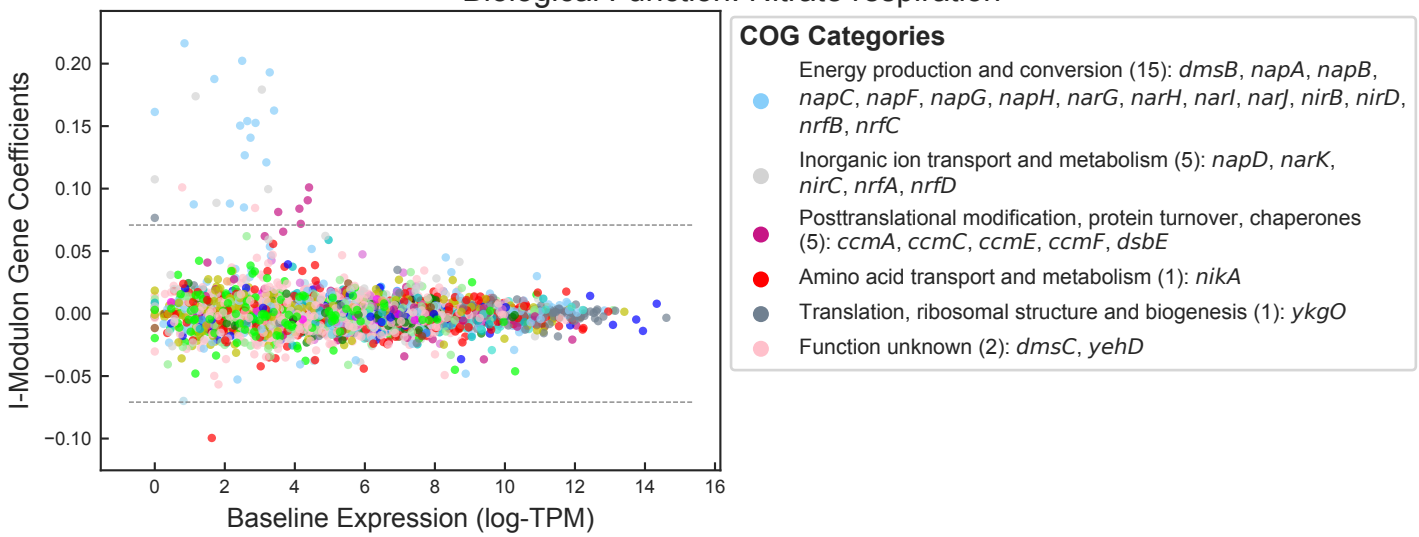
Motif E-value: 1.50e-04

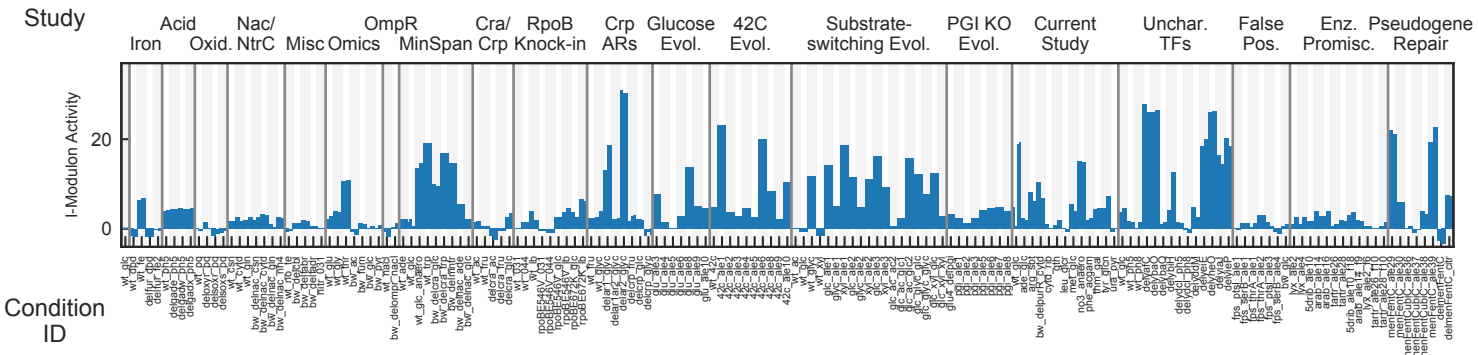
Operons with Upstream Motif: 27%

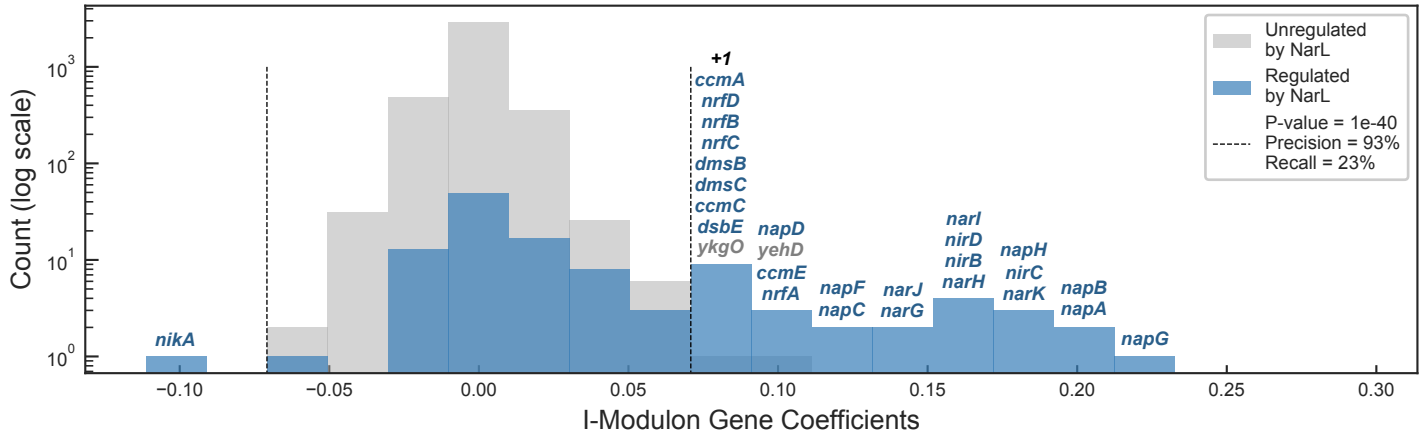
NarL I-Modulon

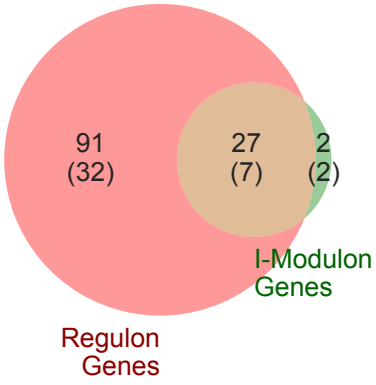
Regulated by: NarL

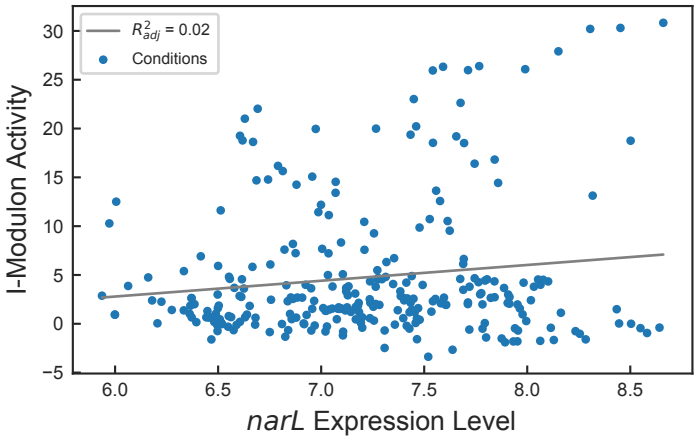
Biological Function: Nitrate respiration







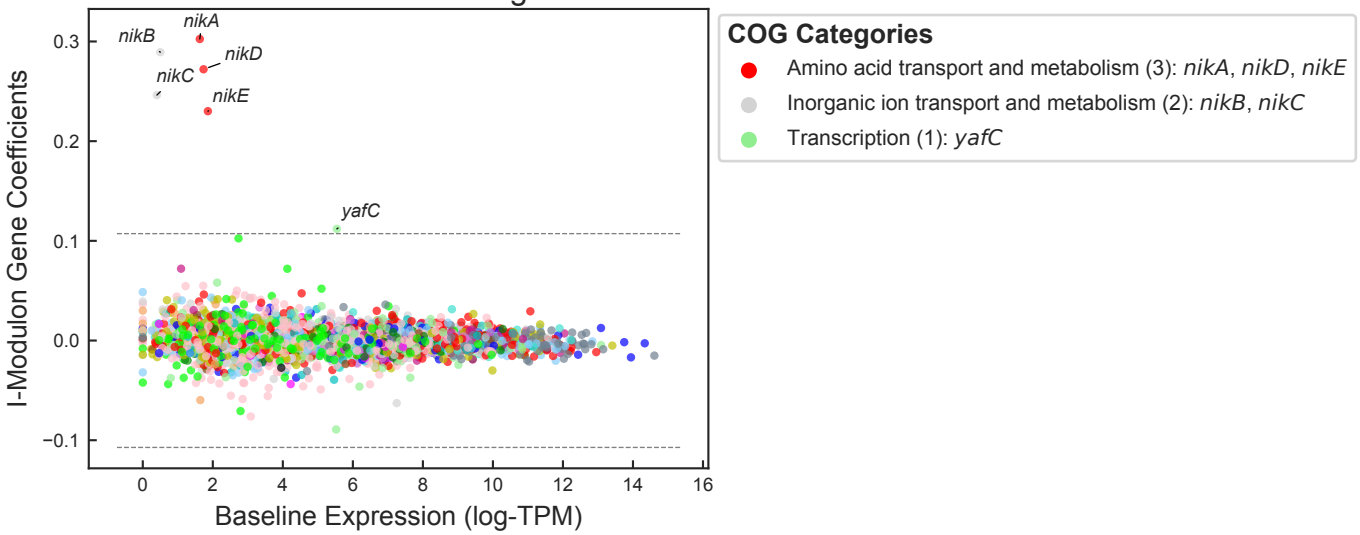


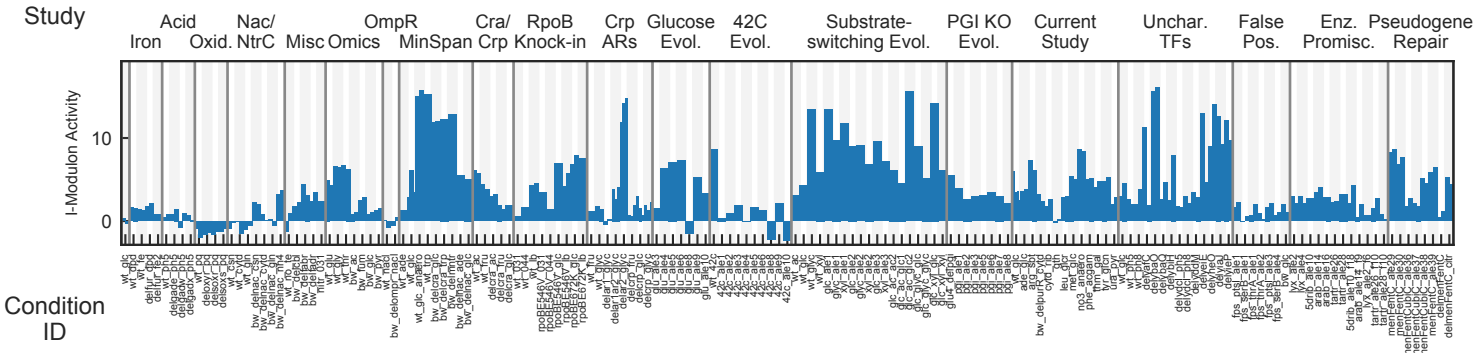


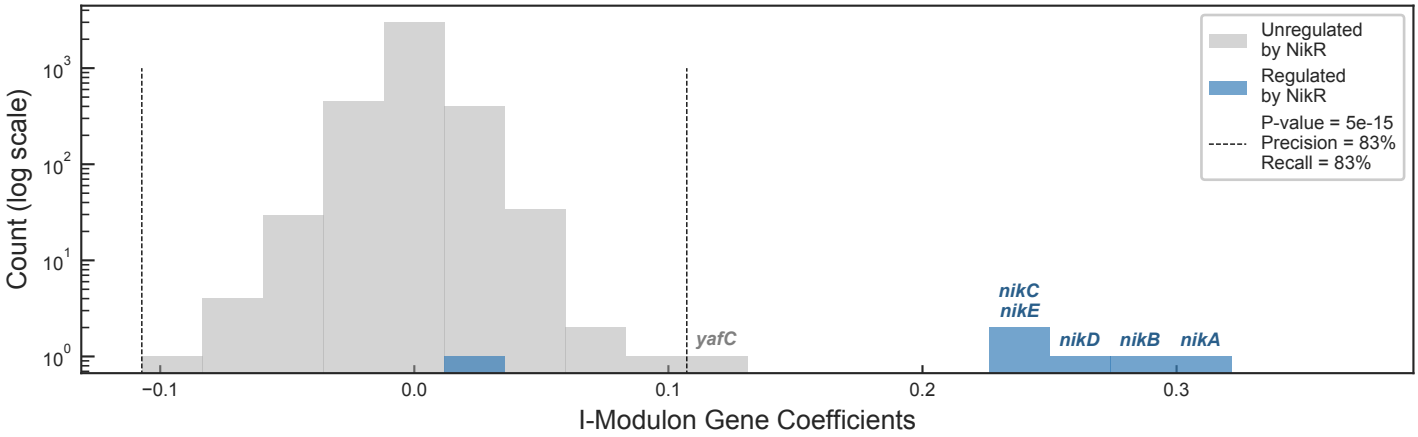
NikR I-Modulon

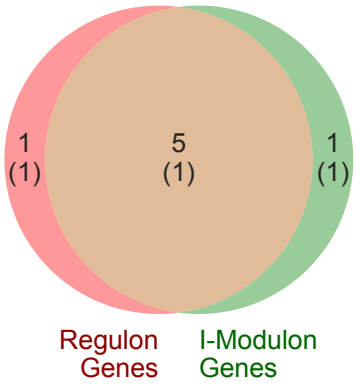
Regulated by: NikR

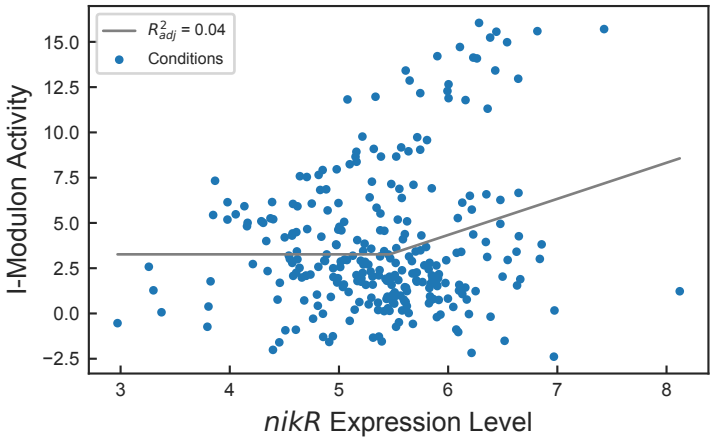
Biological Function: Nickel homeostasis







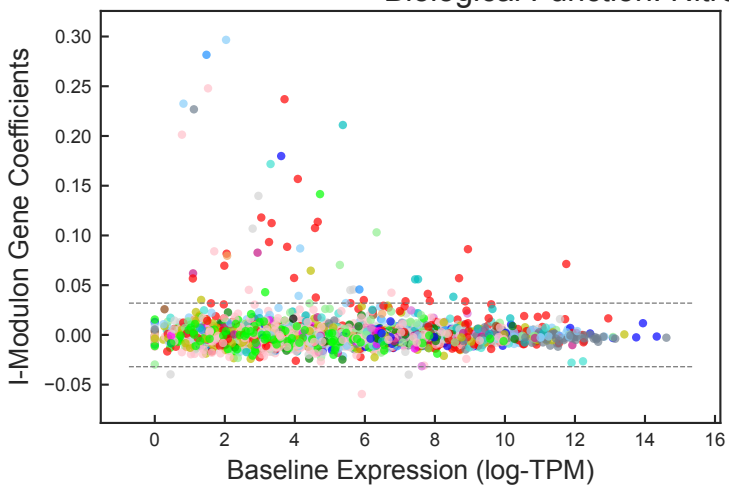




NtrC + RpoN I-Modulon

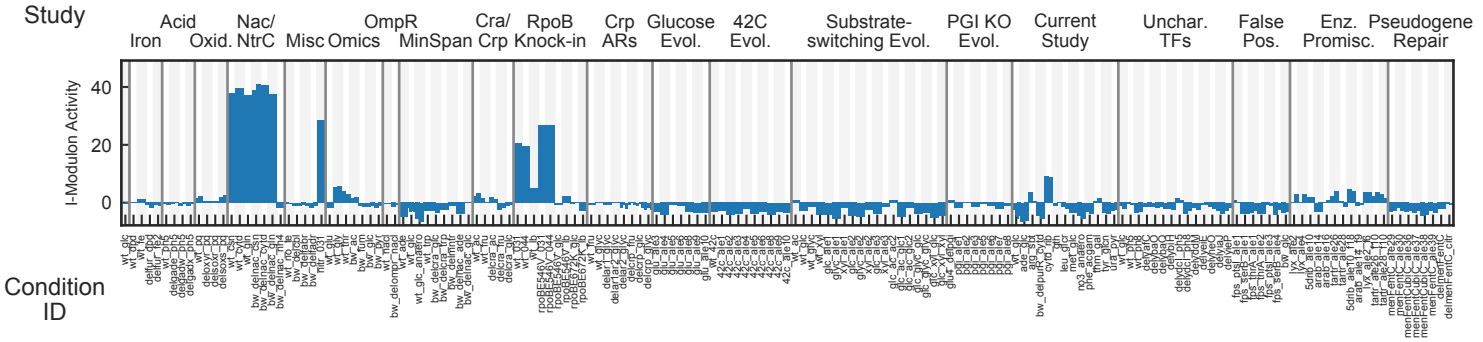
Regulated by: NtrC and RpoN

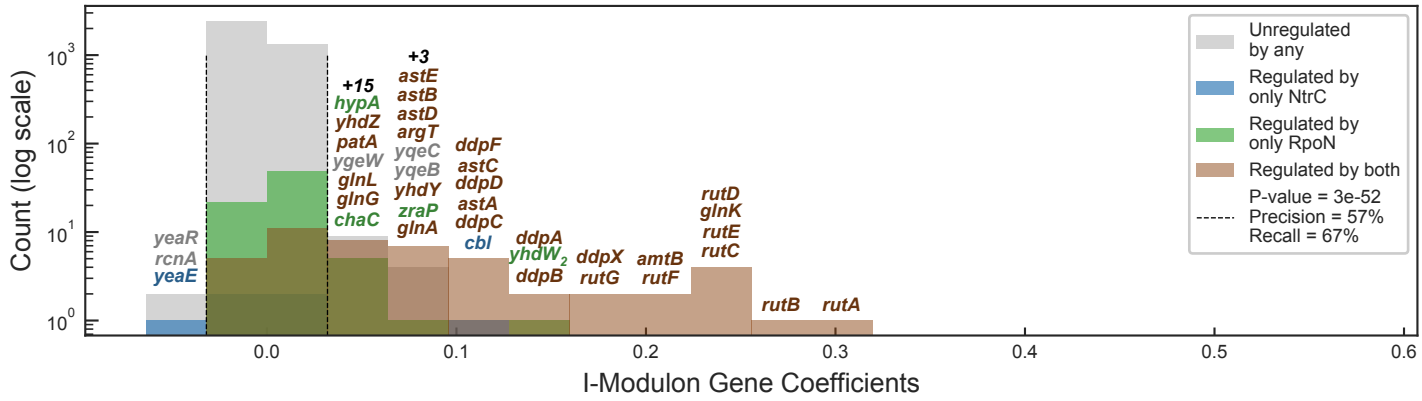
Biological Function: Nitrogen starvation response

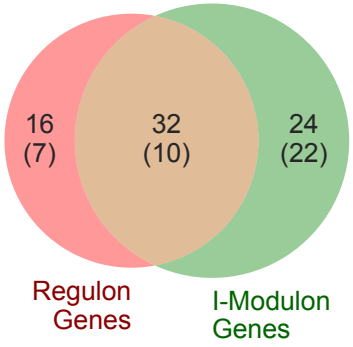


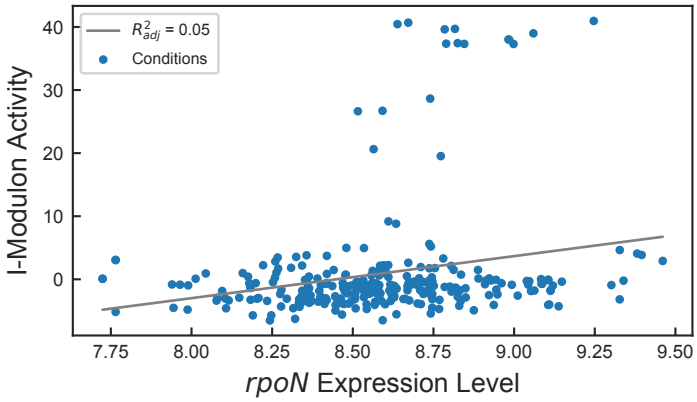
COG Categories

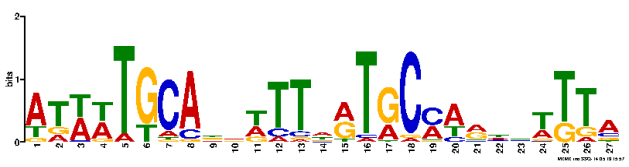
- Amino acid transport and metabolism (21): *argT*, *asnA*, *asnB*, *astA*, *astB*, *astC*, *astE*, *ddpA*, *ddpD*, *ddpF*, *gabP*, *glnA*, *glnK*, *gltI*, *hisP*, *patA*, *potF*, *ygeW*, *yhdX*, *yhdY*, *yhdZ*
- Inorganic ion transport and metabolism (6): *chaC*, *ddpB*, *ddpC*, *mgtA*, *rcnA*, *yeaR*
- Energy production and conversion (5): *astD*, *fdhF*, *lhgO*, *rutA*, *rutE*
- Signal transduction mechanisms (4): *amtB*, *glnG*, *glnL*, *yeaG*
- Carbohydrate transport and metabolism (2): *prpB*, *ynfM*
- Other (18): *hypA*, *yqeB*, *csiD*, *rutB*, *cbl*, *yedL*, *zraP*, *ddpX*, *rutG*, *rutC*, *mgrB*, *rutD*, *rutF*, *yeaE*, *yeaH*, *yqeC*, *asr*, *yhdW*$_2$





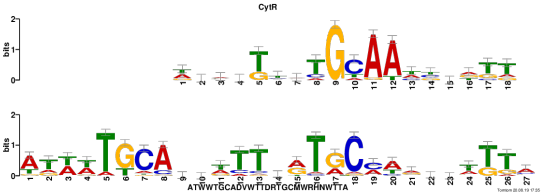






Motif E-value: 1.30e-06

Operons with Upstream Motif: 68%

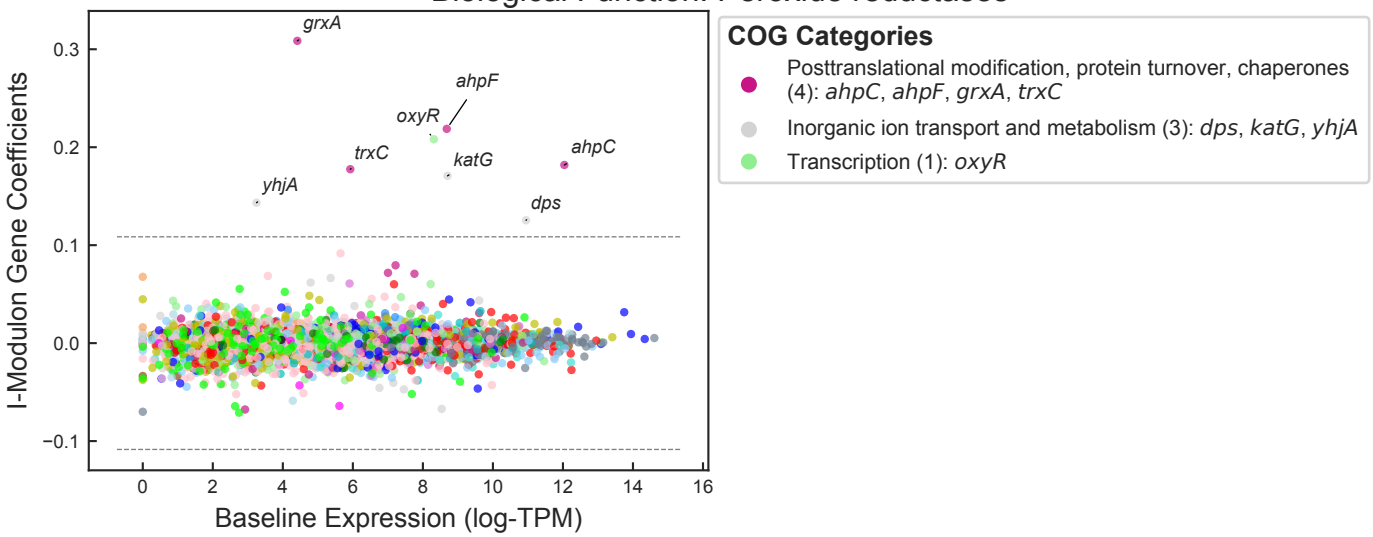


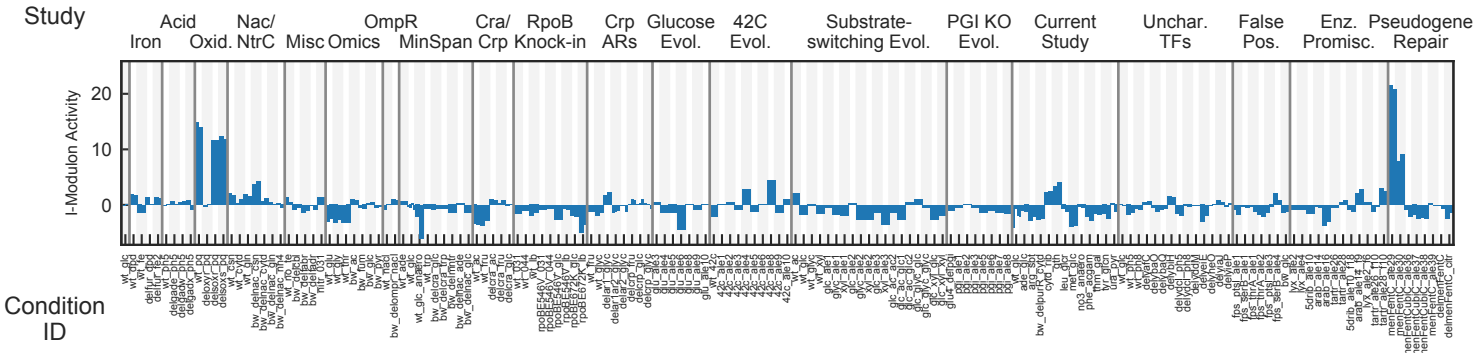
Motif similar to CytR (E-value: 2.29e-03)

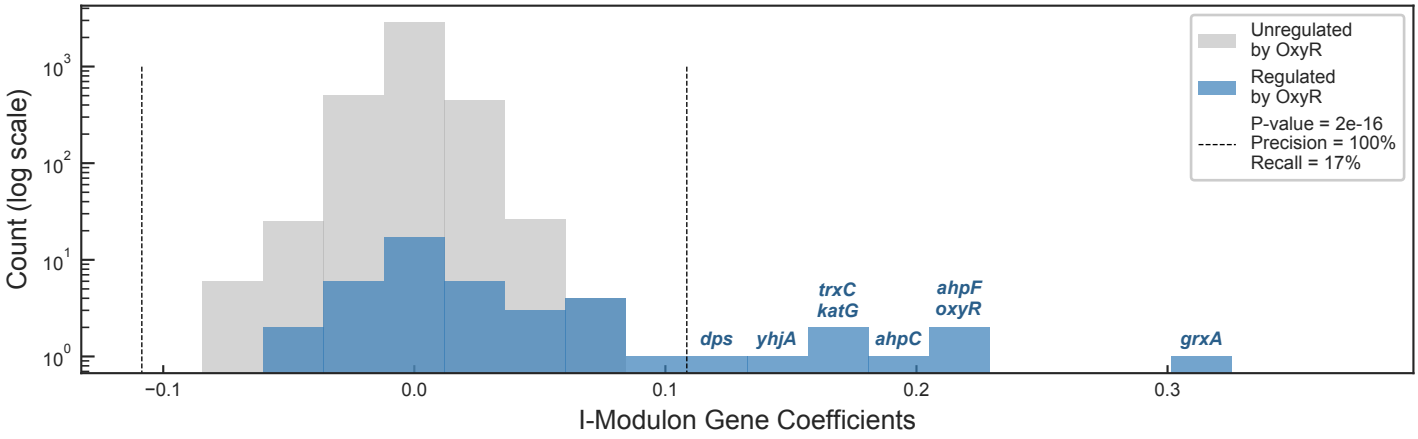
OxyR I-Modulon

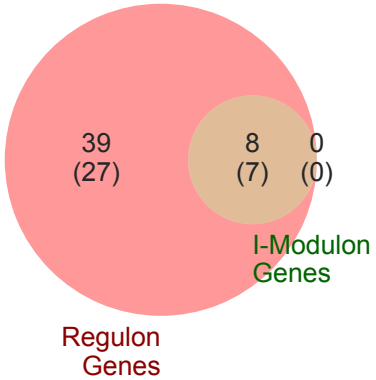
Regulated by: OxyR

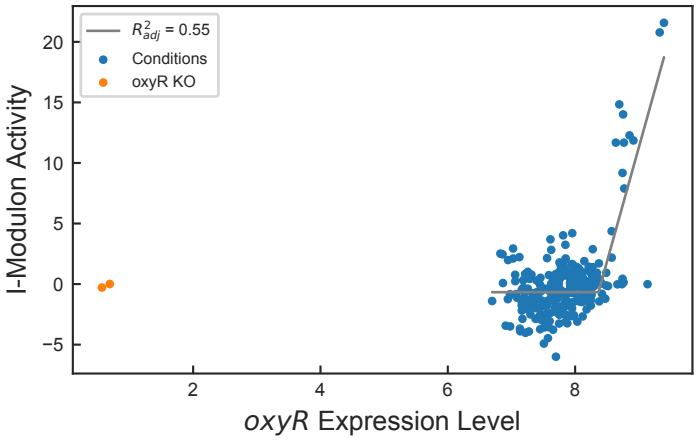
Biological Function: Peroxide reductases







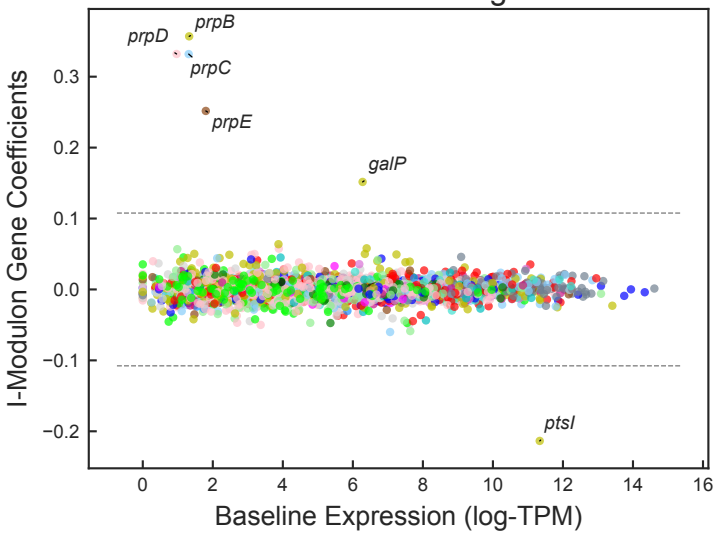




PrpR I-Modulon

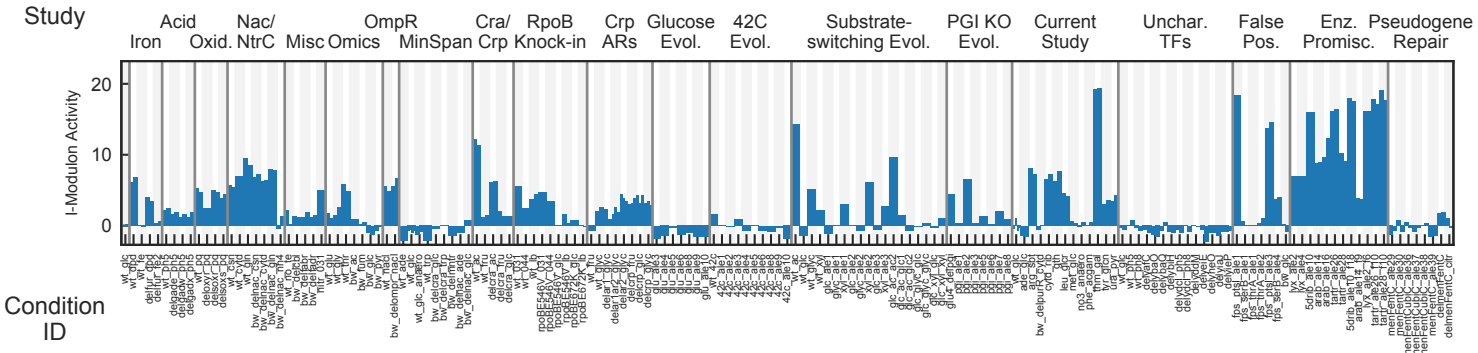
Regulated by: PrpR

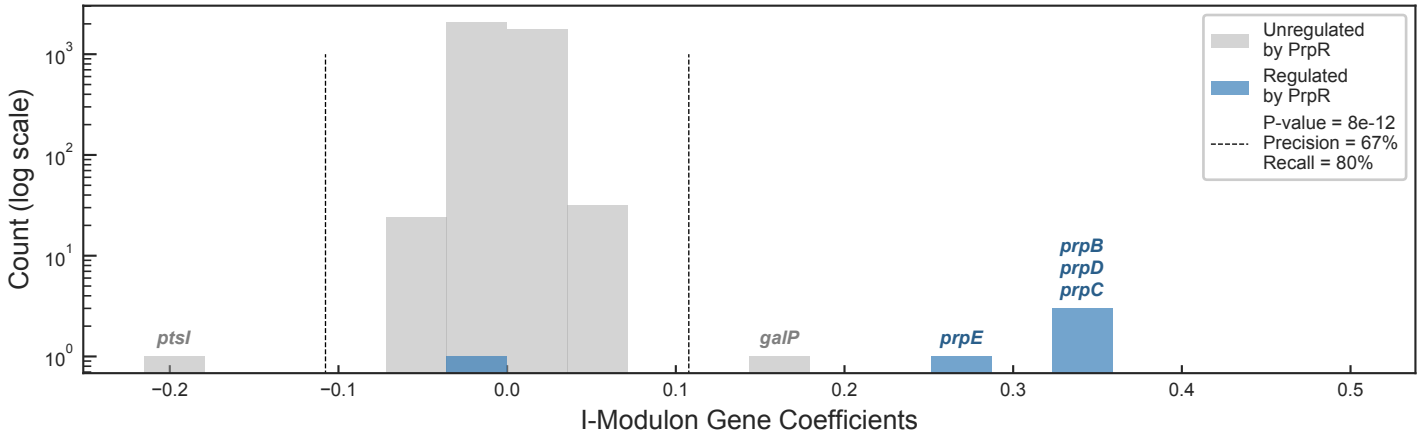
Biological Function: Propionate catabolism

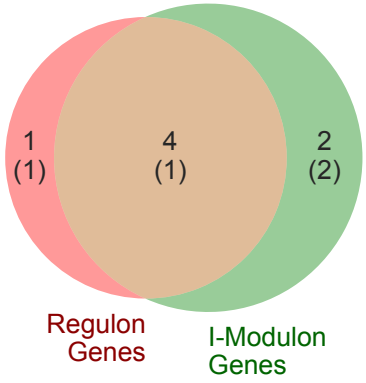


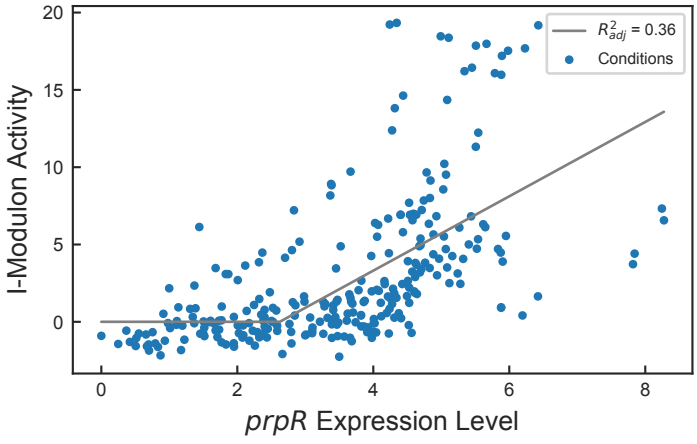
COG Categories

- Carbohydrate transport and metabolism (3): *galP*, *prpB*, *ptsI*
- Energy production and conversion (1): *prpC*
- Lipid transport and metabolism (1): *prpE*
- Function unknown (1): *prpD*





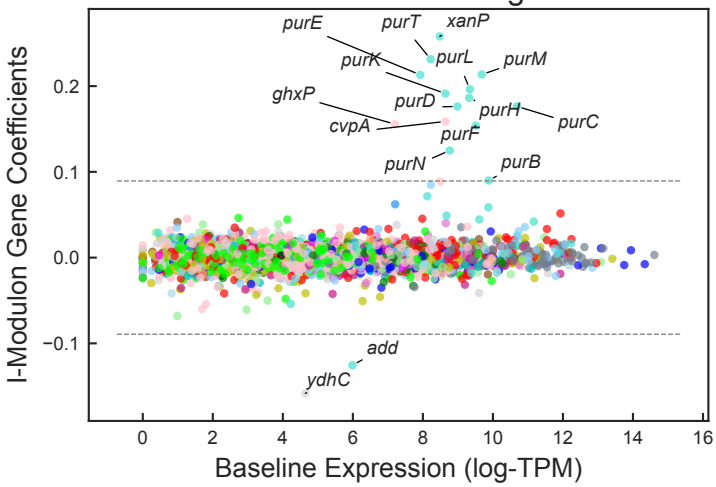




PurR – 1 I-Modulon

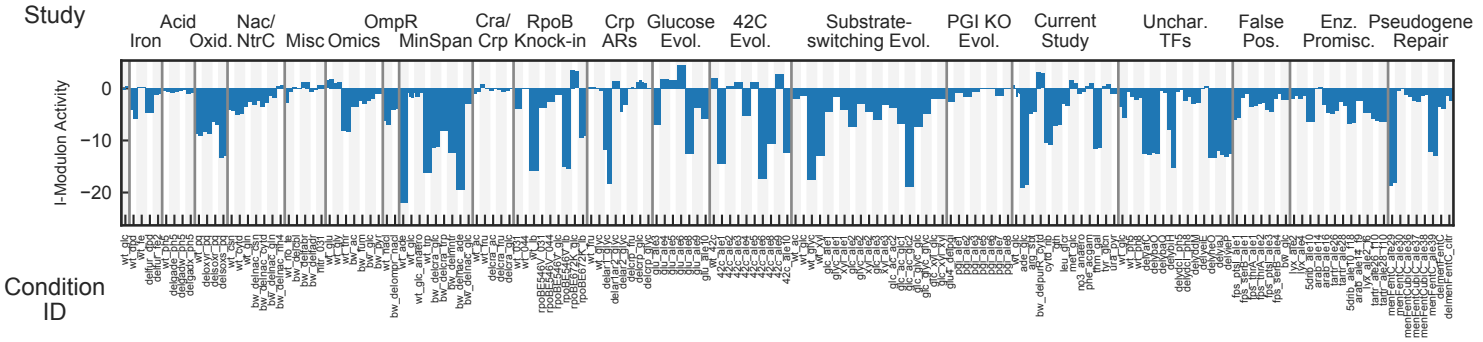
Regulated by: PurR

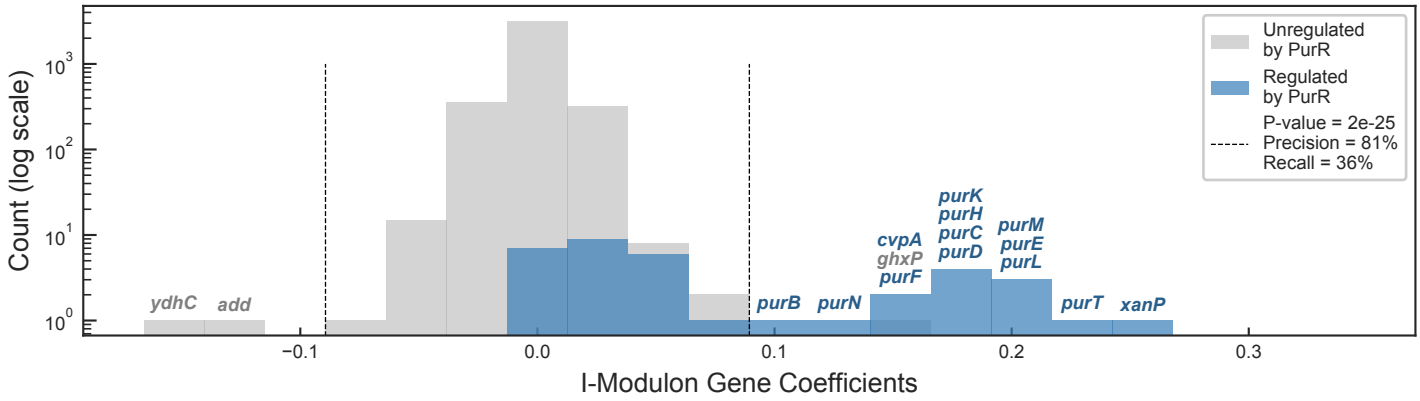
Biological Function: Purine Biosynthesis

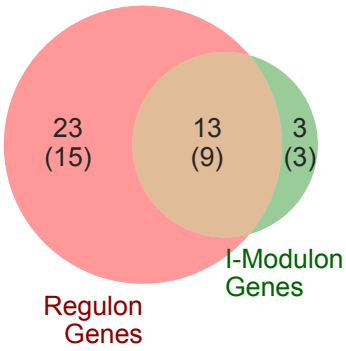


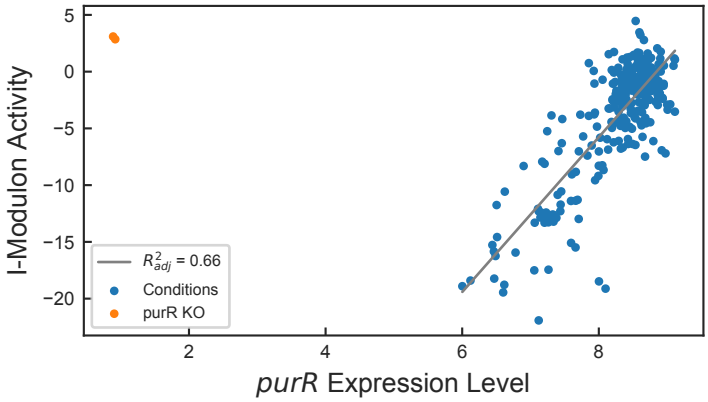
COG Categories

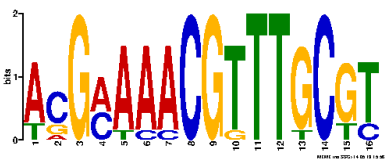
- Nucleotide transport and metabolism (13): *add*, *purB*, *purC*, *purD*, *purE*, *purF*, *purH*, *purK*, *purL*, *purM*, *purN*, *purT*, *xanP*
- Inorganic ion transport and metabolism (1): *ydhC*
- Function unknown (2): *cvpA*, *ghxP*





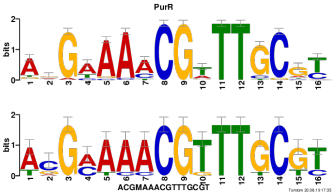






Motif E-value: 2.20e-18

Operons with Upstream Motif: 75%

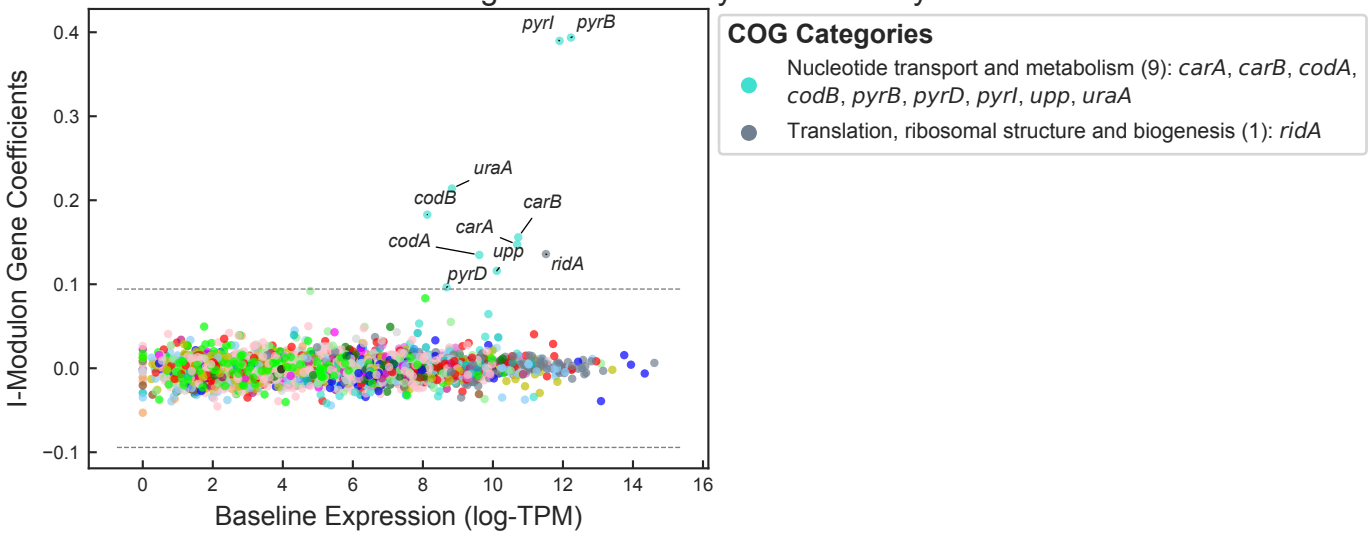


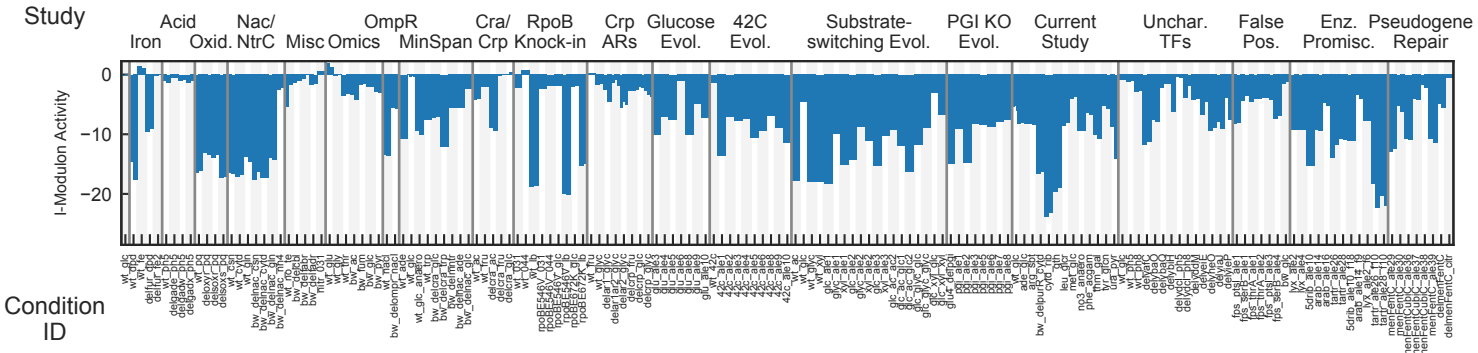
Motif similar to PurR (E-value: 7.38e-12)

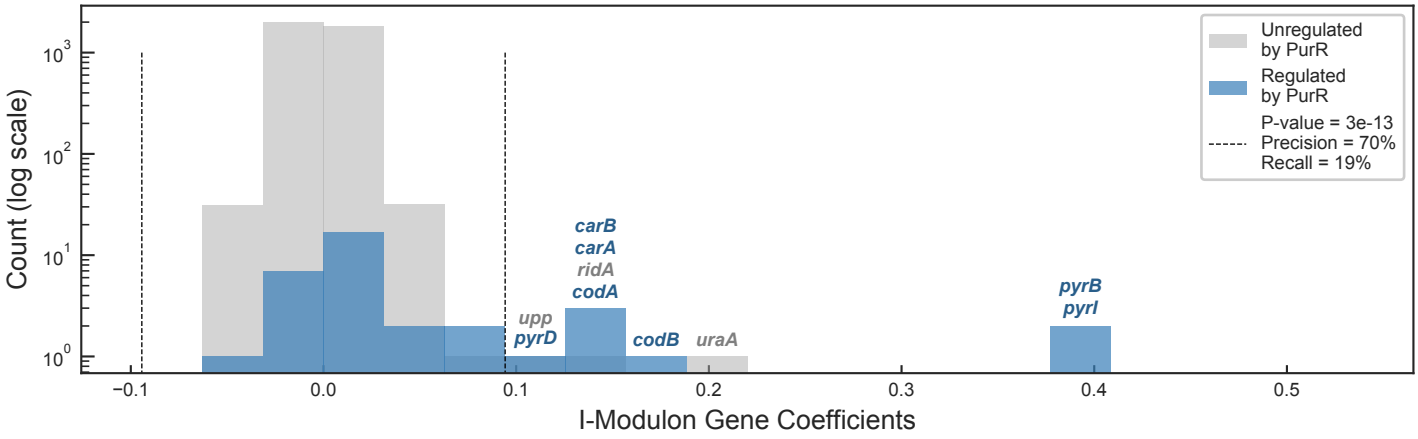
PurR – 2 I-Modulon

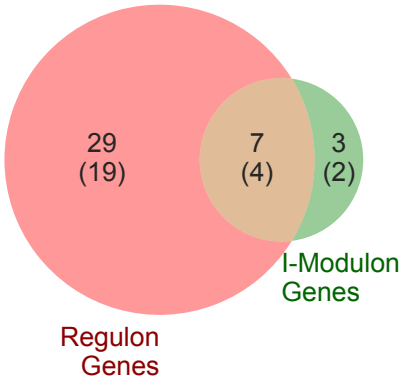
Regulated by: PurR

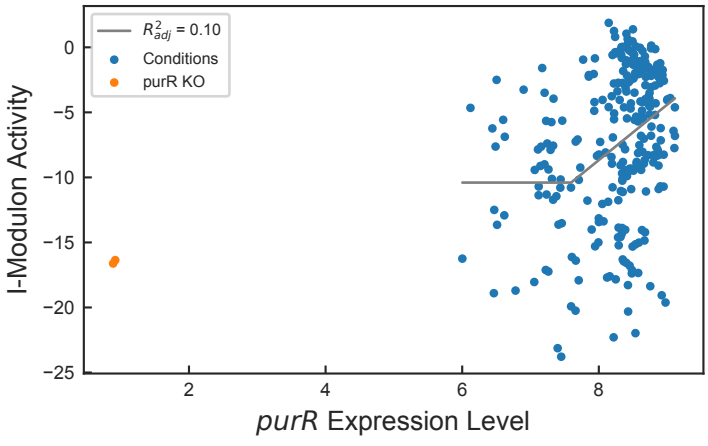
Biological Function: Pyrimidine biosynthesis







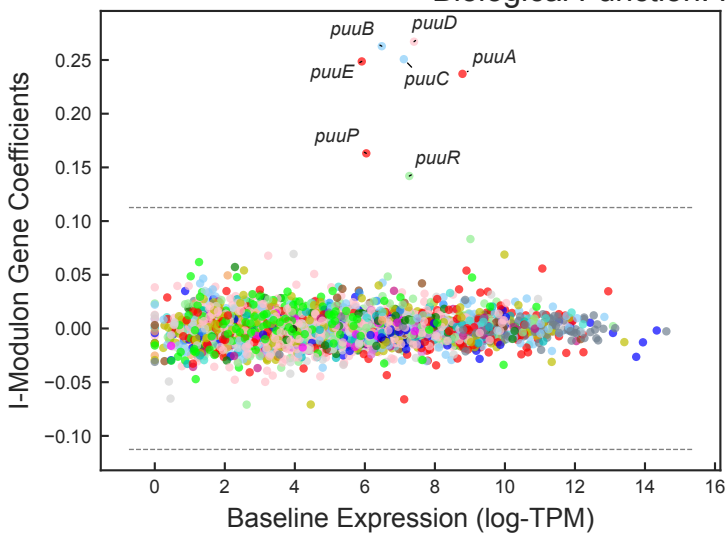




PuuR I-Modulon

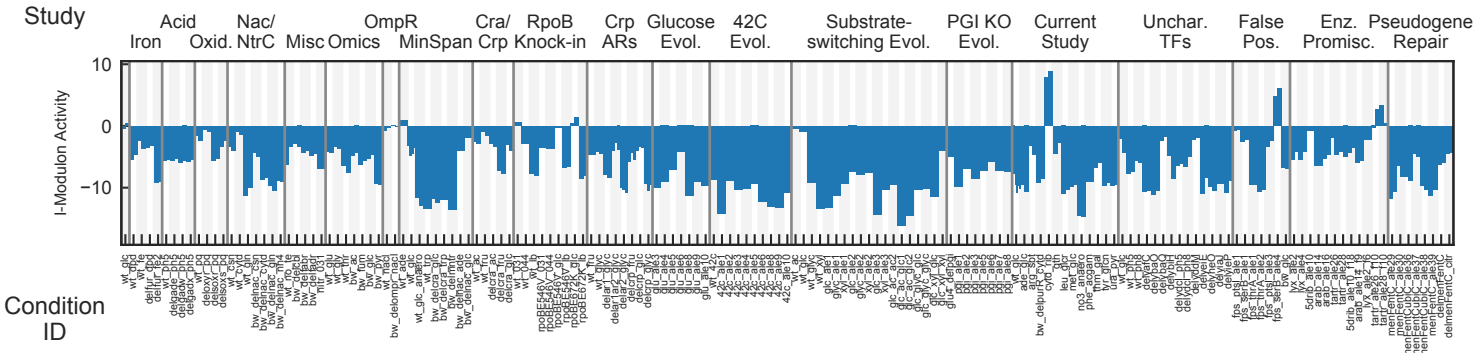
Regulated by: PuuR

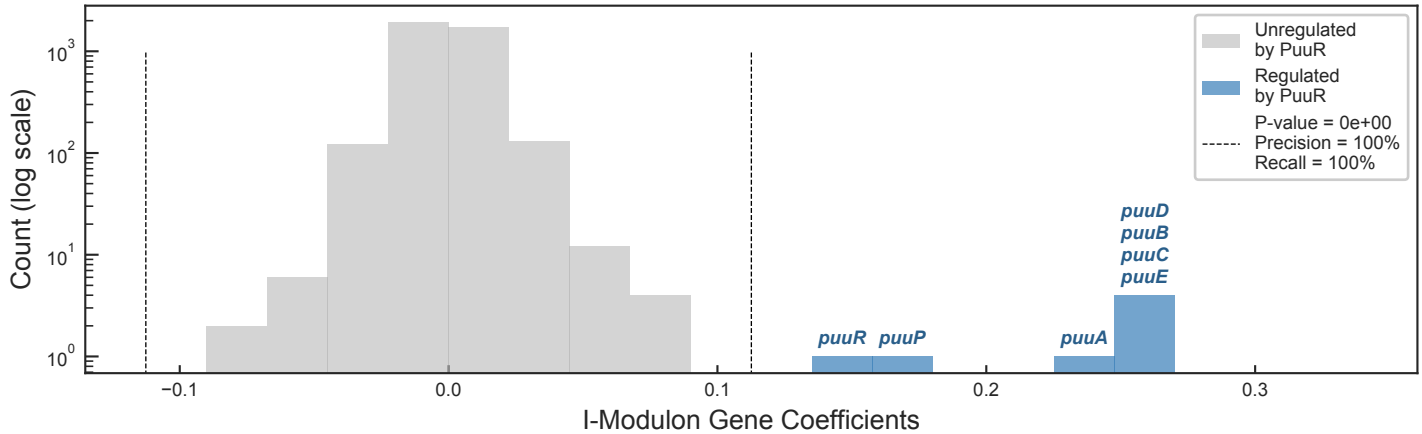
Biological Function: Putrescine catabolism

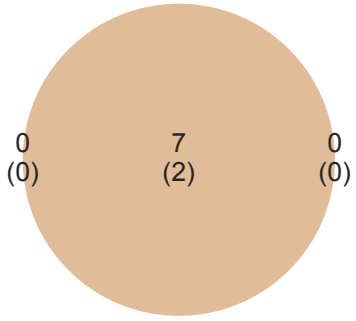


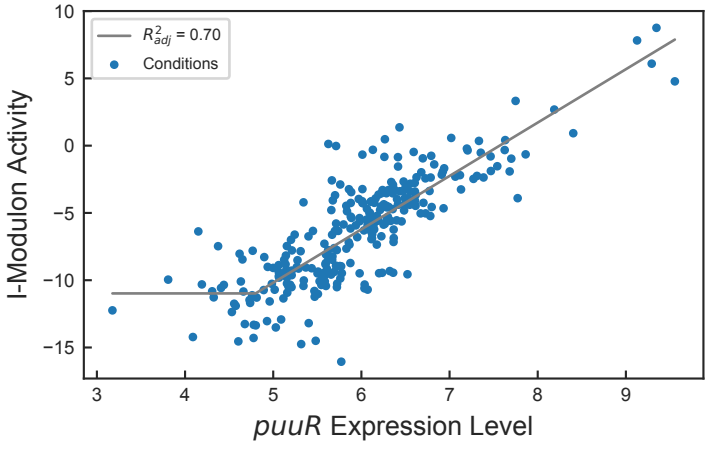
COG Categories

- Amino acid transport and metabolism (3): *puuA*, *puuE*, *puuP*
- Energy production and conversion (2): *puuB*, *puuC*
- Transcription (1): *puuR*
- Function unknown (1): *puuD*





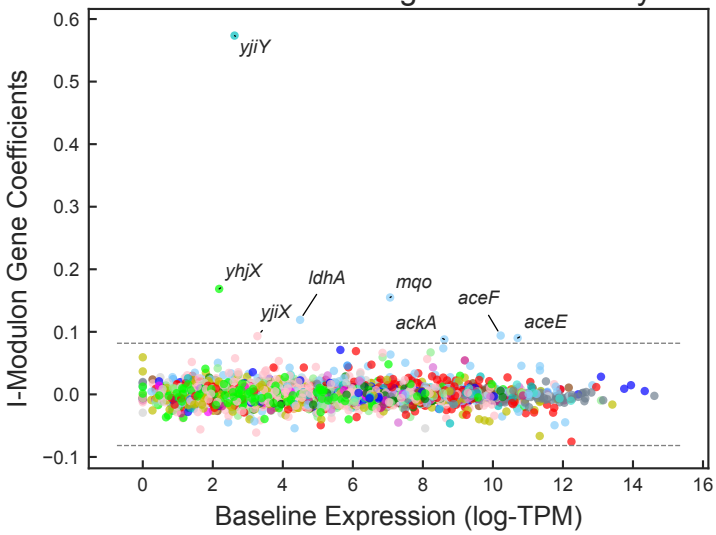




Pyruvate I-Modulon

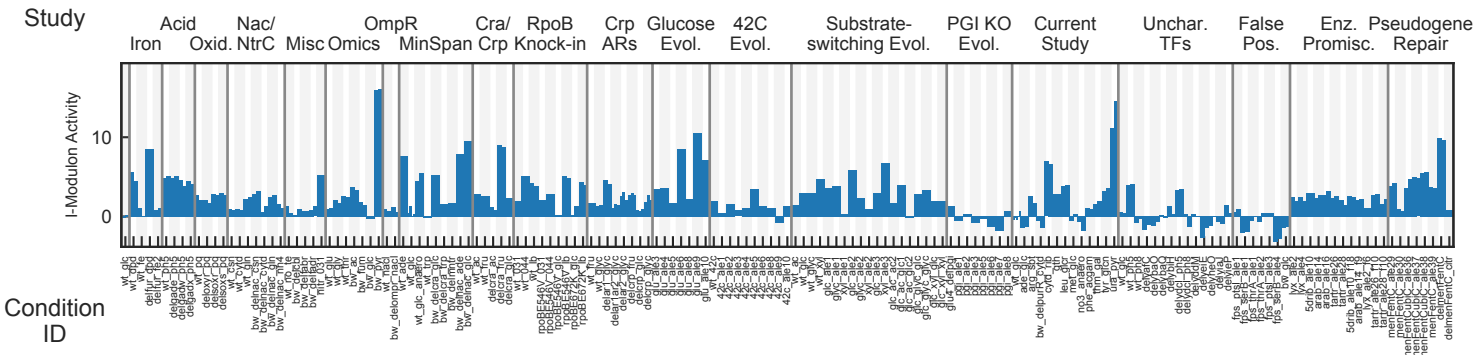
Regulated by: BtsR or YpdB or PdhR

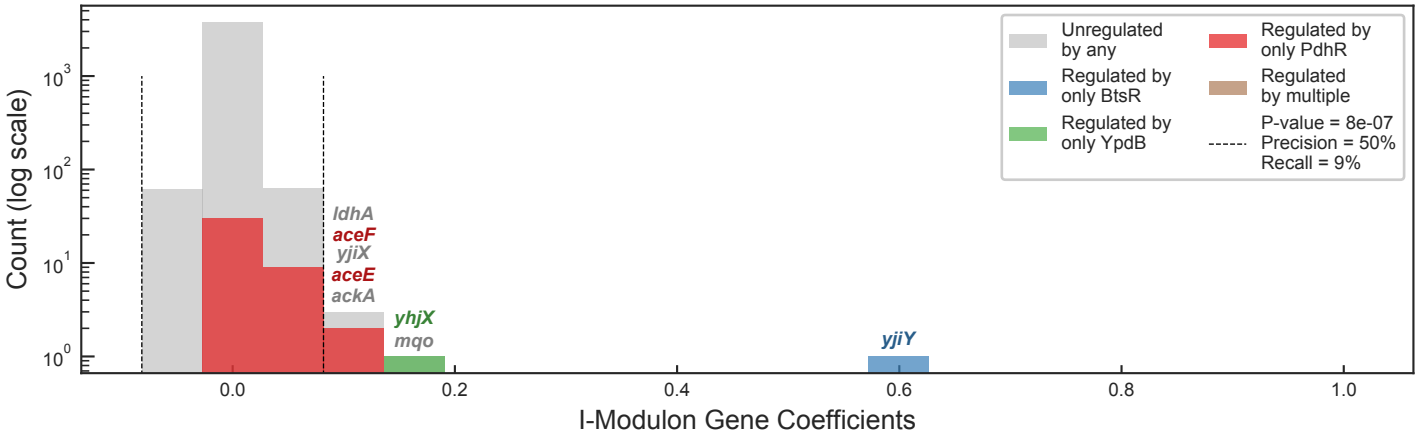
Biological Function: Pyruvate transport and metabolism

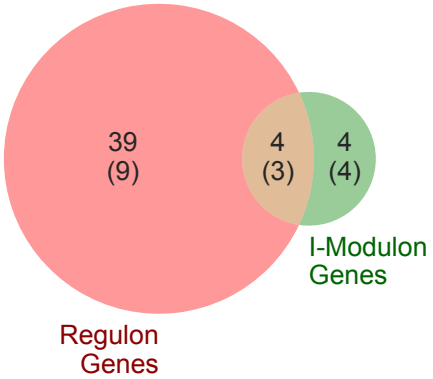


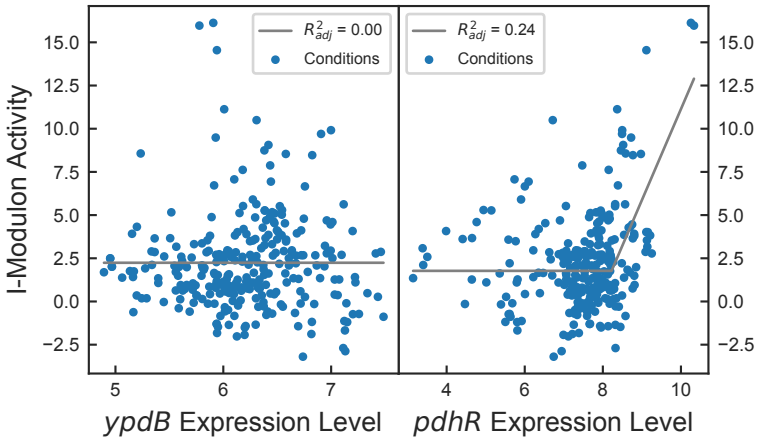
COG Categories

- Energy production and conversion (5): *aceE*, *aceF*, *ackA*, *ldhA*, *mqo*
- Signal transduction mechanisms (1): *yjiY*
- Function unknown (1): *yjiX*
- No COG Annotation (1): *yhjX*





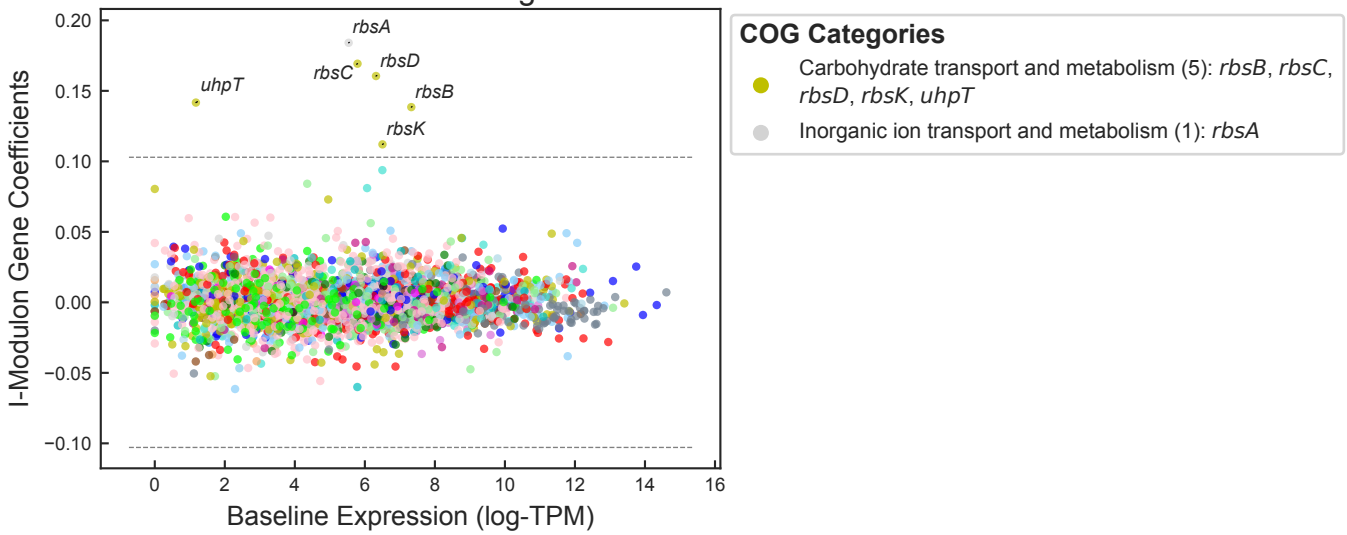


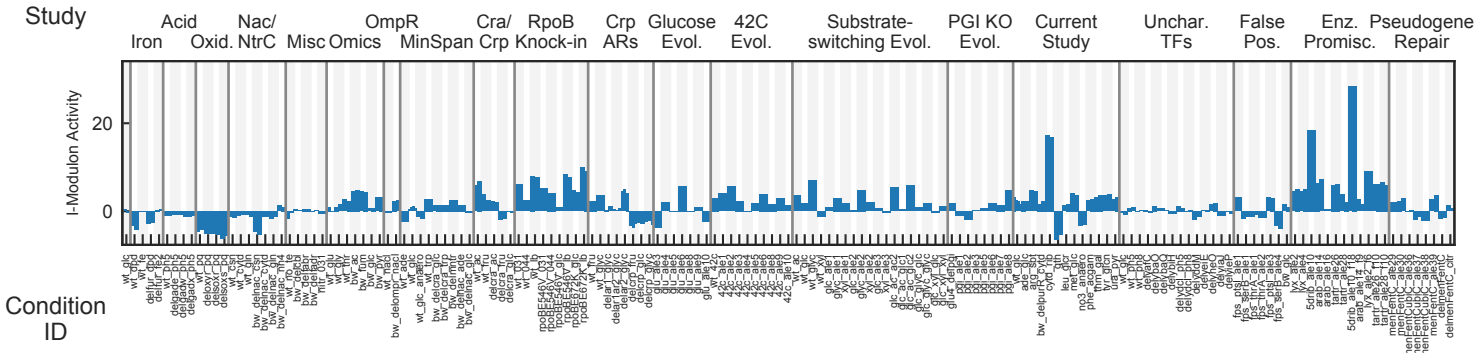


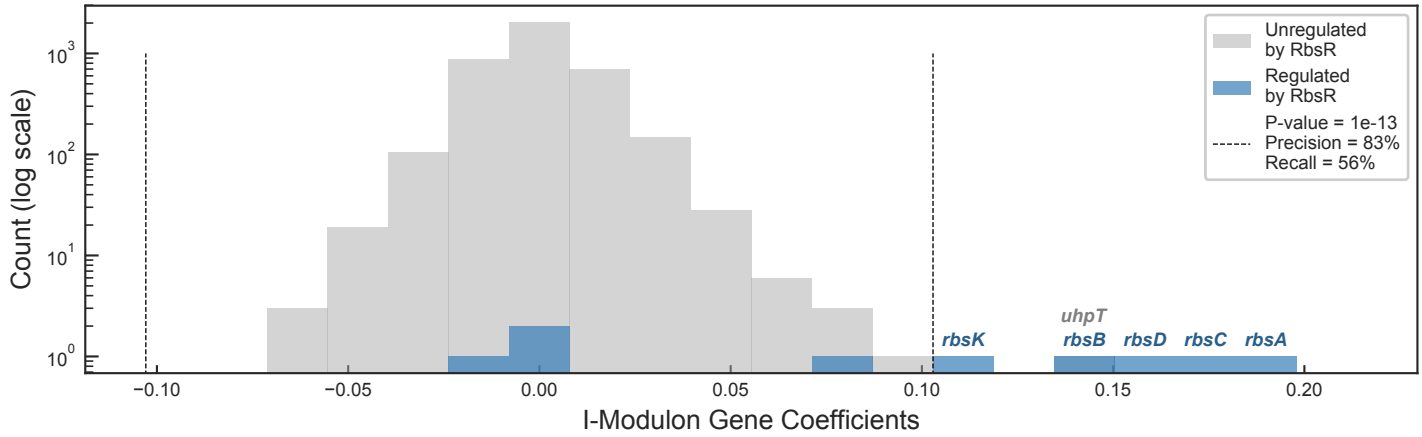
RbsR I-Modulon

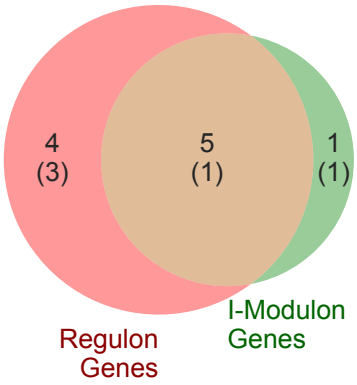
Regulated by: RbsR

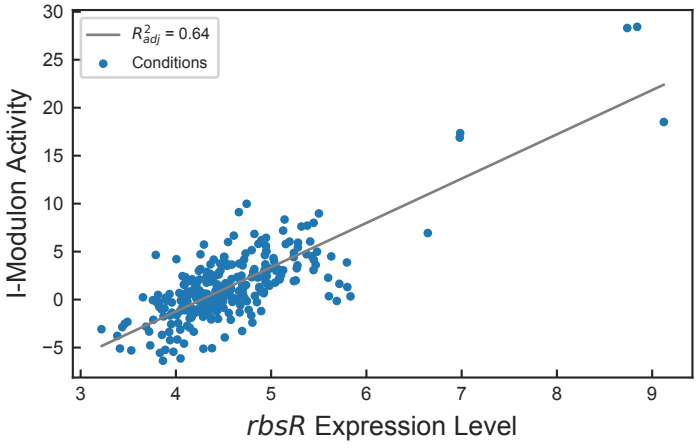
Biological Function: D-ribose catabolism







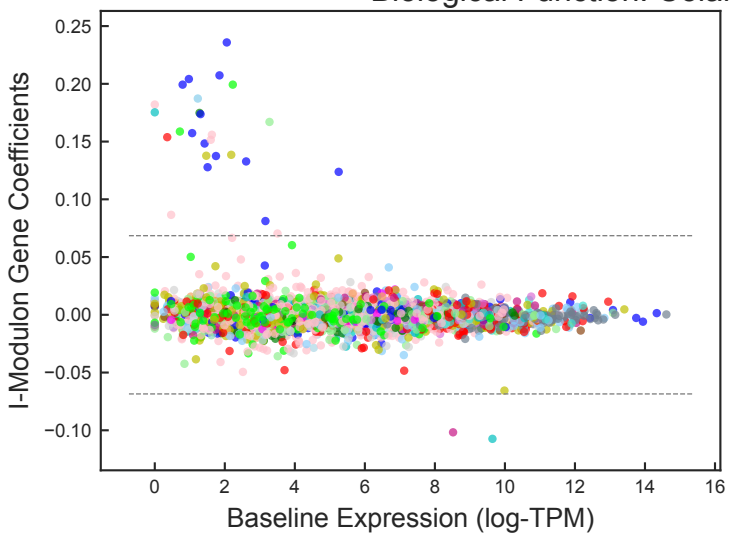




RcsAB I-Modulon

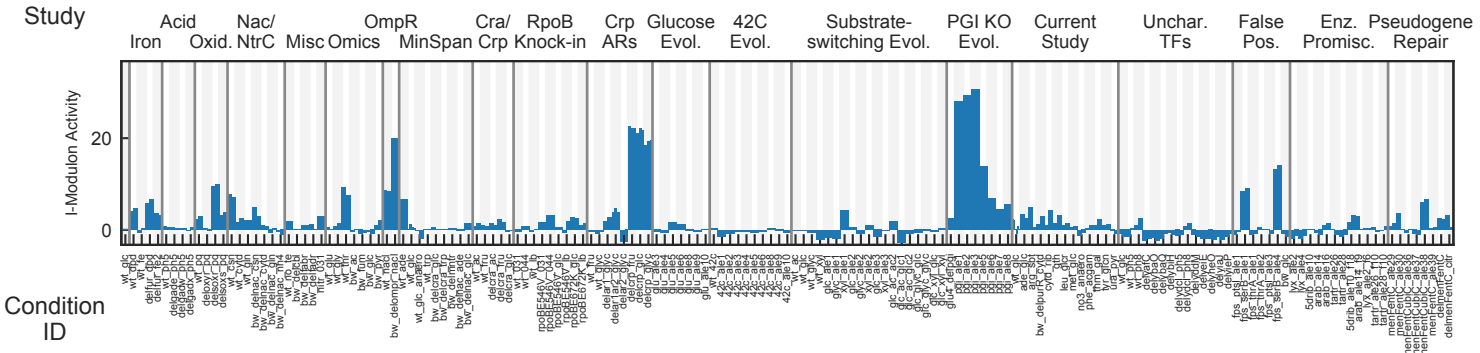
Regulated by: RcsAB

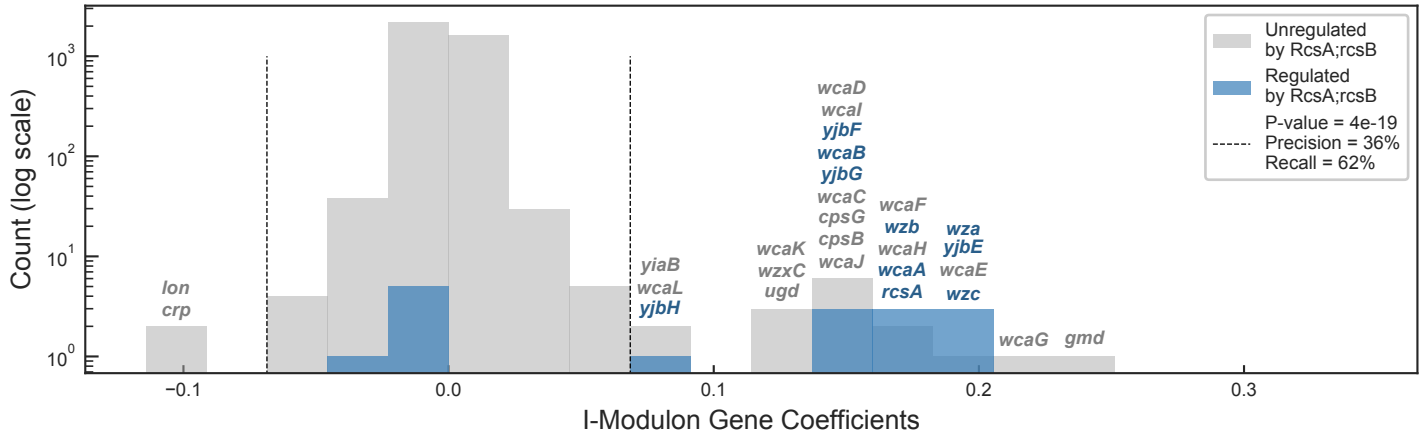
Biological Function: Colanic acid capsule formation

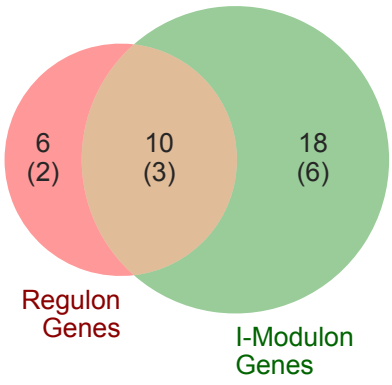


COG Categories

- Cell wall/membrane/envelope biogenesis (12): *gmd*, *ugd*, *wcaA*, *wcaC*, *wcaE*, *wcaG*, *wcaI*, *wcaJ*, *wcaK*, *wcaL*, *wza*, *wzxC*
- Carbohydrate transport and metabolism (2): *cpsB*, *cpsG*
- Signal transduction mechanisms (2): *crp*, *wzb*
- Amino acid transport and metabolism (1): *wcaB*
- Cell cycle control, cell division, chromosome partitioning (1): *wzc*
- Other (10): *lon*, *wcaH*, *rcsA*, *wcaF*, *yiaB*, *yjbF*, *yjbG*, *yjbH*, *wcaD*, *yjbE*



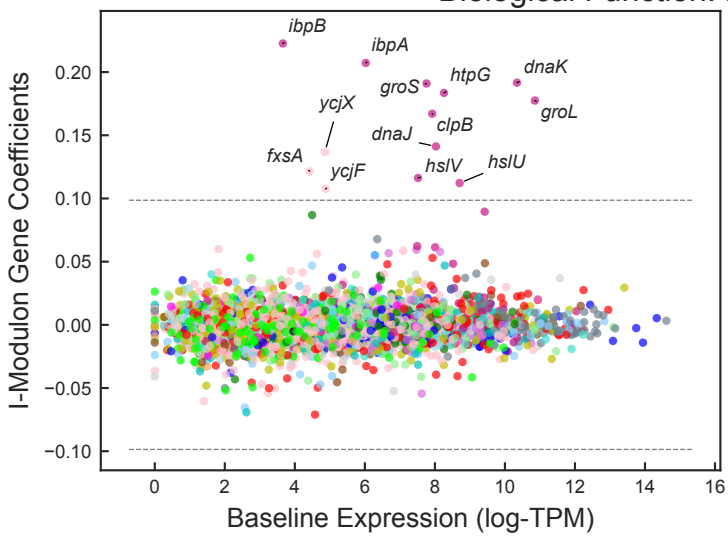




RpoH I-Modulon

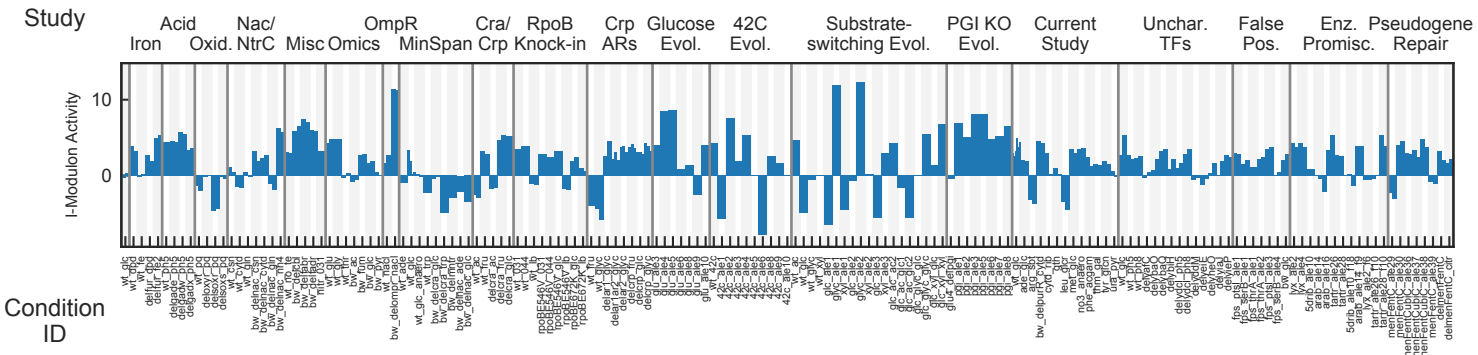
Regulated by: RpoH

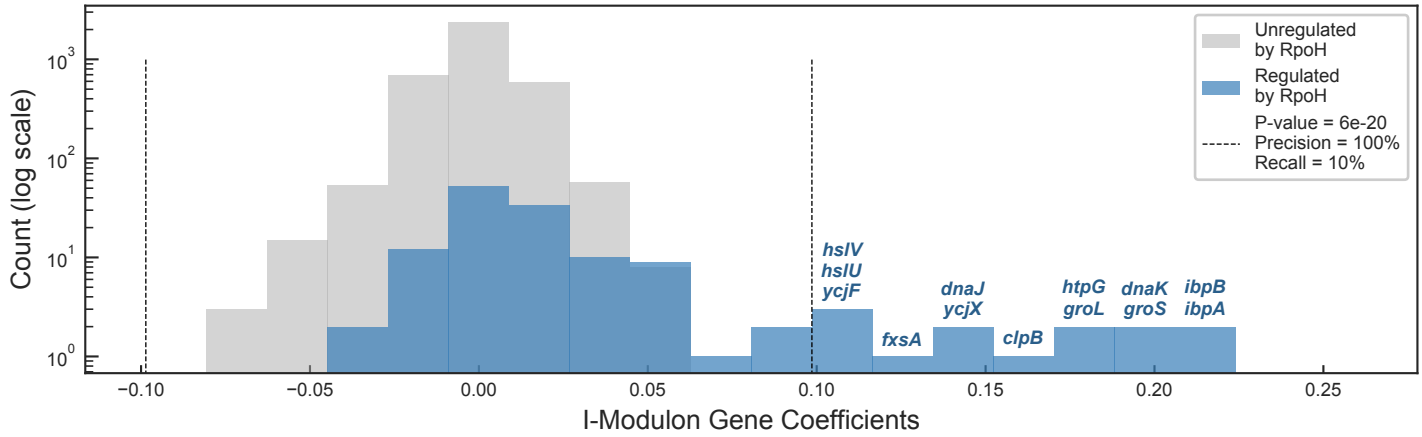
Biological Function: Heat shock response

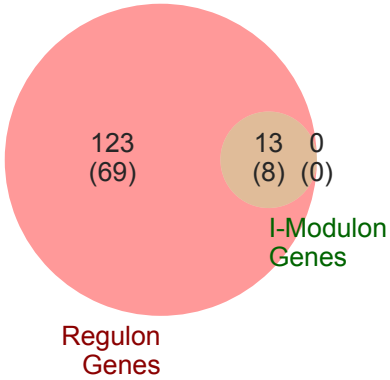


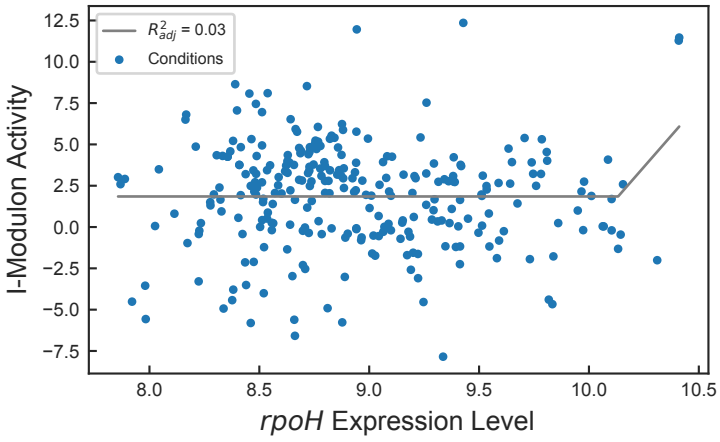
COG Categories

- Posttranslational modification, protein turnover, chaperones (10): *clpB*, *dnaJ*, *dnaK*, *groL*, *groS*, *hslU*, *hslV*, *htpG*, *ibpA*, *ibpB*
- Function unknown (3): *fxsA*, *ycjF*, *ycjX*





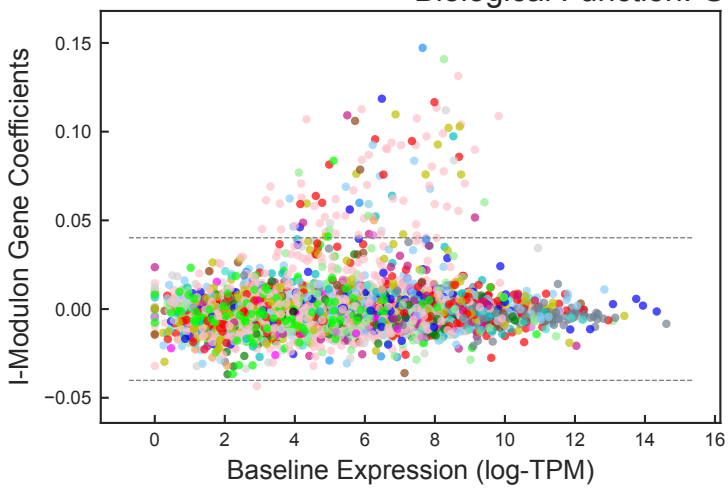




RpoS I-Modulon

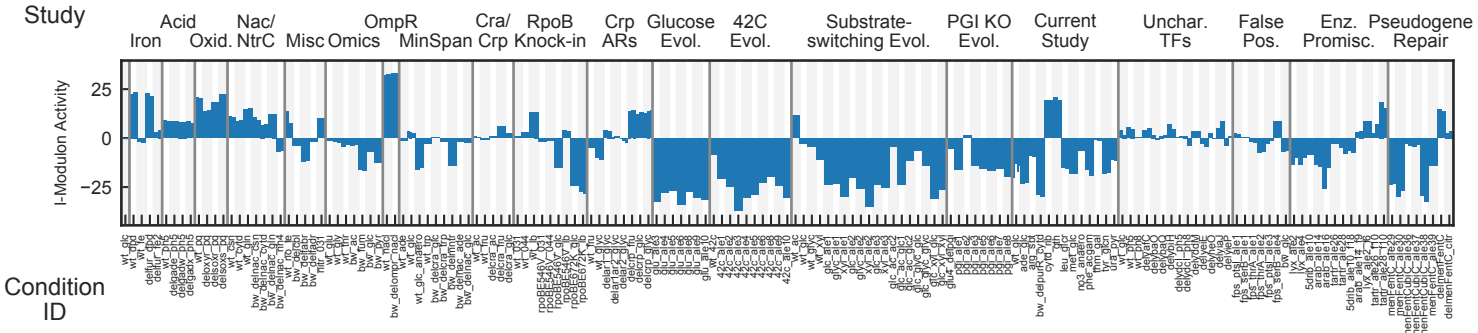
Regulated by: RpoS

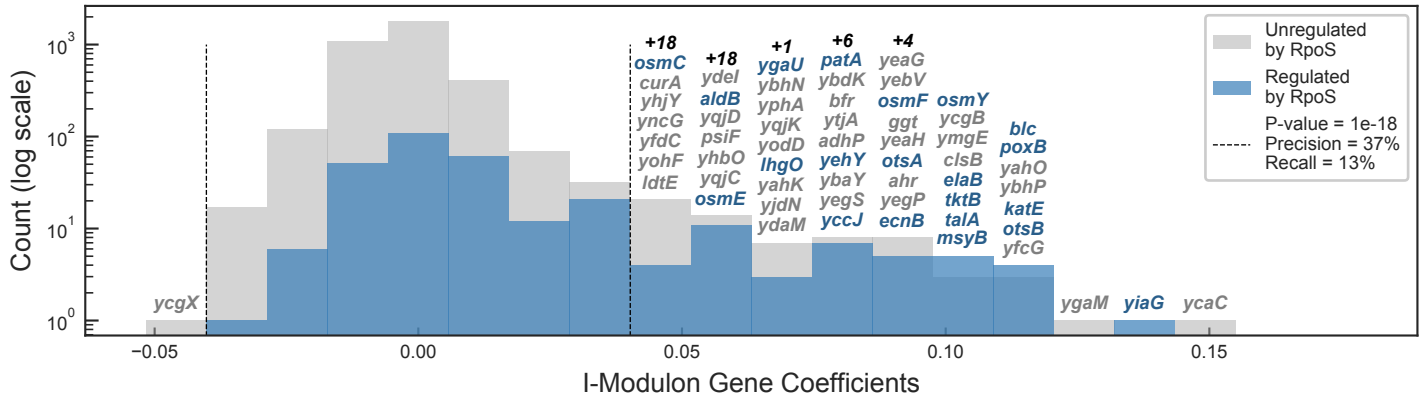
Biological Function: General stress response

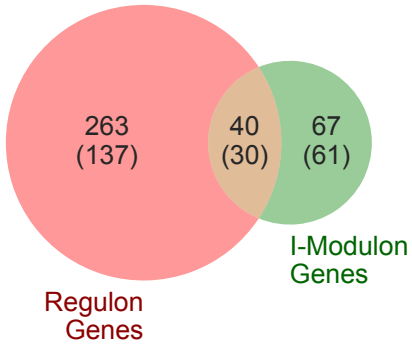


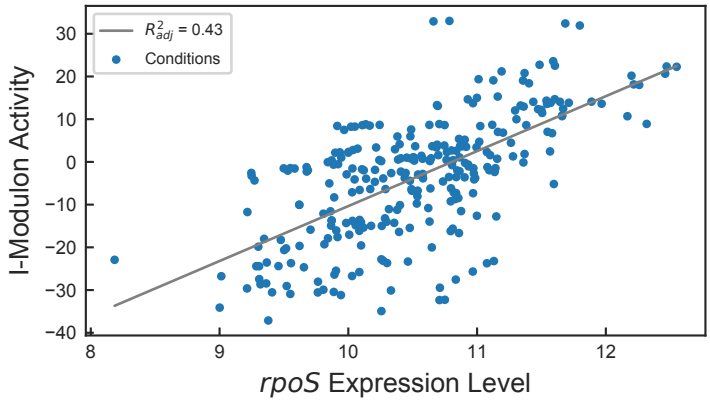
COG Categories

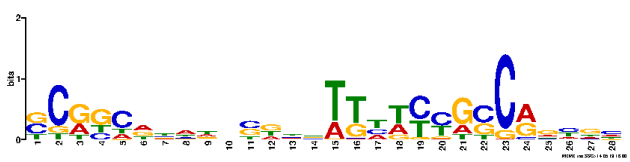
- Carbohydrate transport and metabolism (10): *amyA*, *fbaB*, *otsA*, *otsB*, *talA*, *tktB*, *treA*, *ydcS*, *ylil*, *yniA*
- Amino acid transport and metabolism (9): *gabP*, *gabT*, *ggt*, *osmF*, *patA*, *poxB*, *yehW*, *yehX*, *yehY*
- Energy production and conversion (7): *adhP*, *ahr*, *aldB*, *gabD*, *lhgO*, *rclA*, *yahK*
- Transcription (5): *mcbR*, *mlrA*, *osmE*, *yhcO*, *yiaG*
- Inorganic ion transport and metabolism (4): *bfr*, *katE*, *sodC*, *yfdC*
- Other (72): *osmC*, *yfcG*, *yncG*, *yqjG*, *blc*, *ybiO*, *yhjG*, *gmr*, *ydaM*, *yeaG*, *clsB*, *yegS*, *csiD*, *ycaC*, *fic*, *yhjY*, *ubiC*, *curA*, *ecnB*, *elaB* + 52











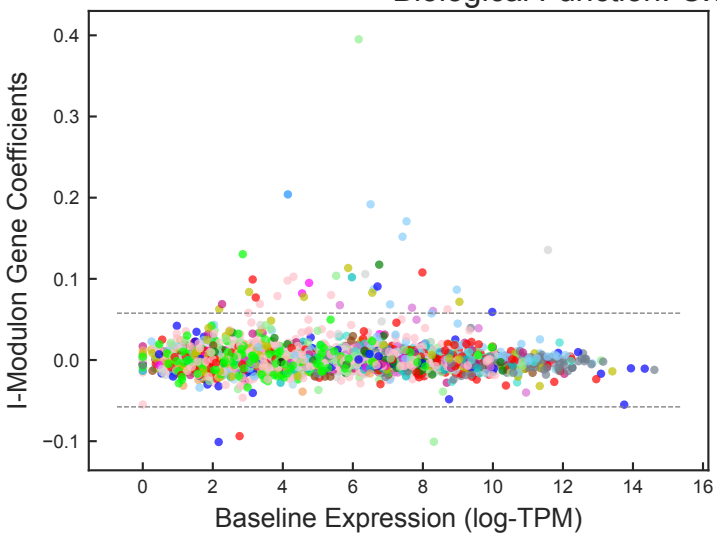
Motif E-value: 3.00e-05

Operons with Upstream Motif: 98%

SoxS I-Modulon

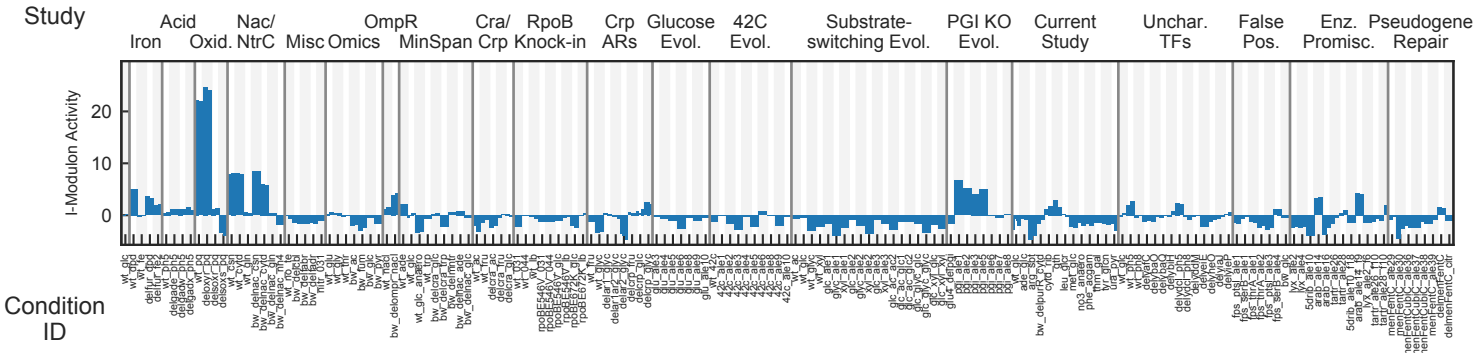
Regulated by: SoxS

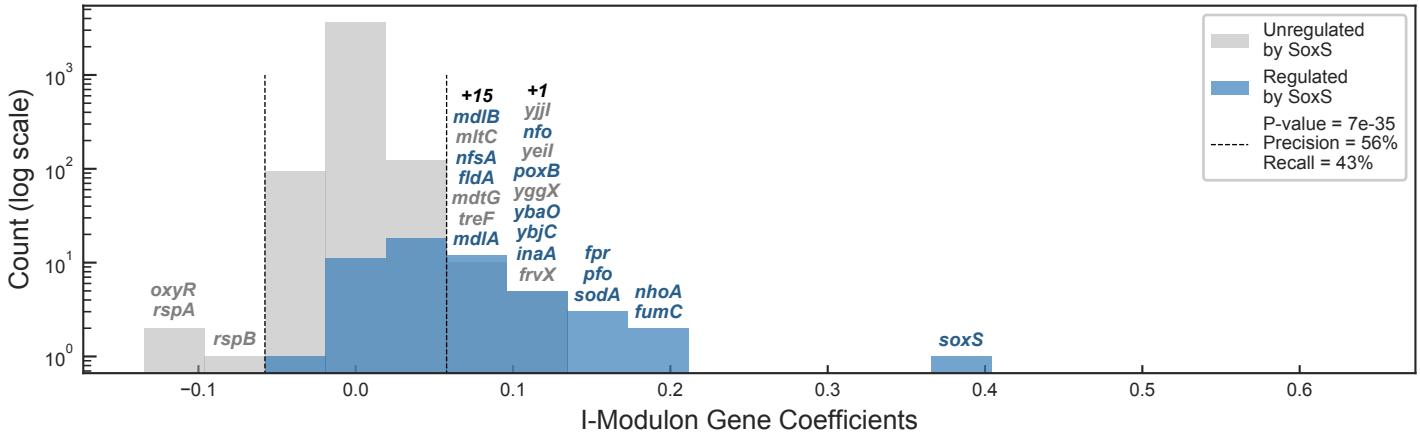
Biological Function: Oxidative stress response

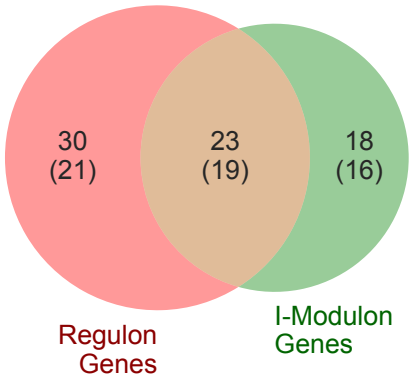


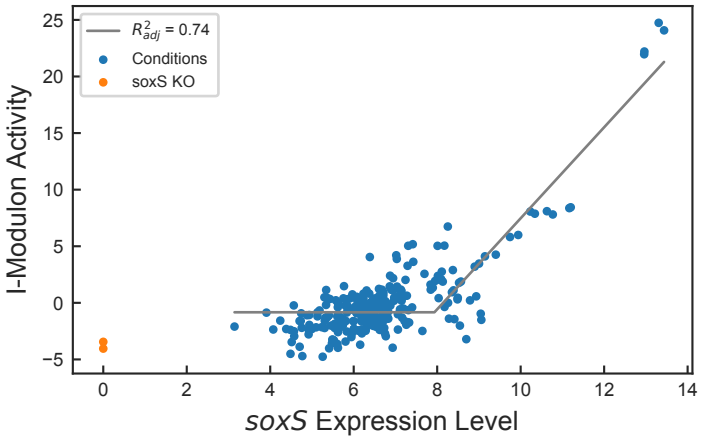
COG Categories

- Carbohydrate transport and metabolism (6): *cpsG*, *mdtG*, *nepI*, *treF*, *yeiI*, *zwf*
- Energy production and conversion (6): *fldA*, *fldB*, *fpr*, *fumC*, *nfsA*, *pfo*
- Amino acid transport and metabolism (4): *aegA*, *frvX*, *poxB*, *rspB*
- Cell wall/membrane/envelope biogenesis (3): *lpxC*, *mltC*, *rspA*
- Other (22): *lipA*, *ribA*, *rimK*, *oxyR*, *soxS*, *ybaO*, *mdlA*, *mdlB*, *sodA*, *yggX*, *yjjW*, *nfo*, *nhoA*, *inaA*, *ariR*, *yaiA*, *ybjC*, *ygfZ*, *yhcN*, *ymgA* + 2





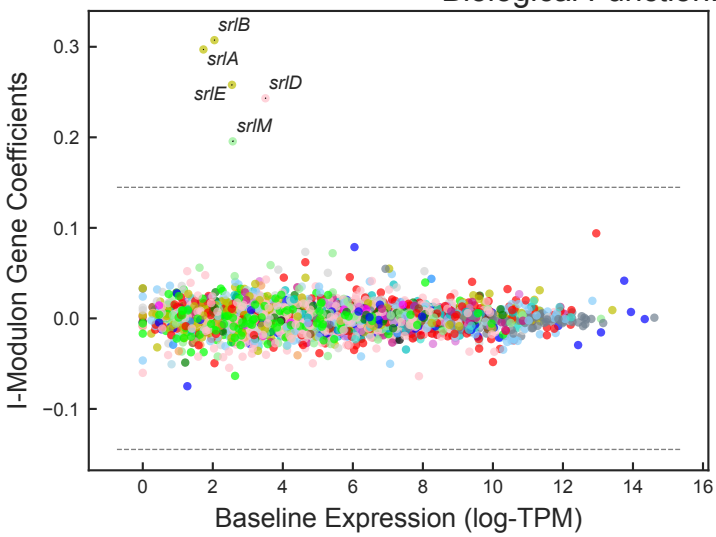




SrlR + GutM I-Modulon

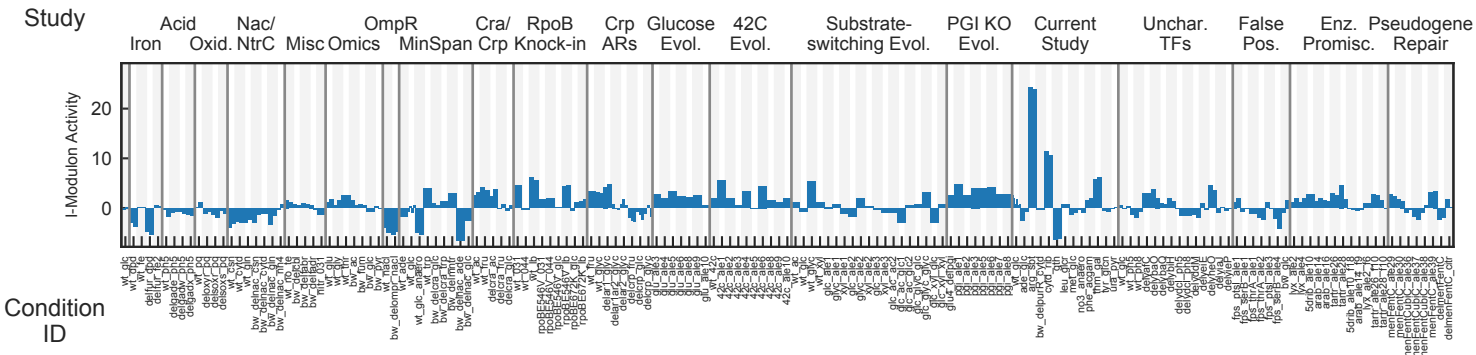
Regulated by: SrlR and GutM

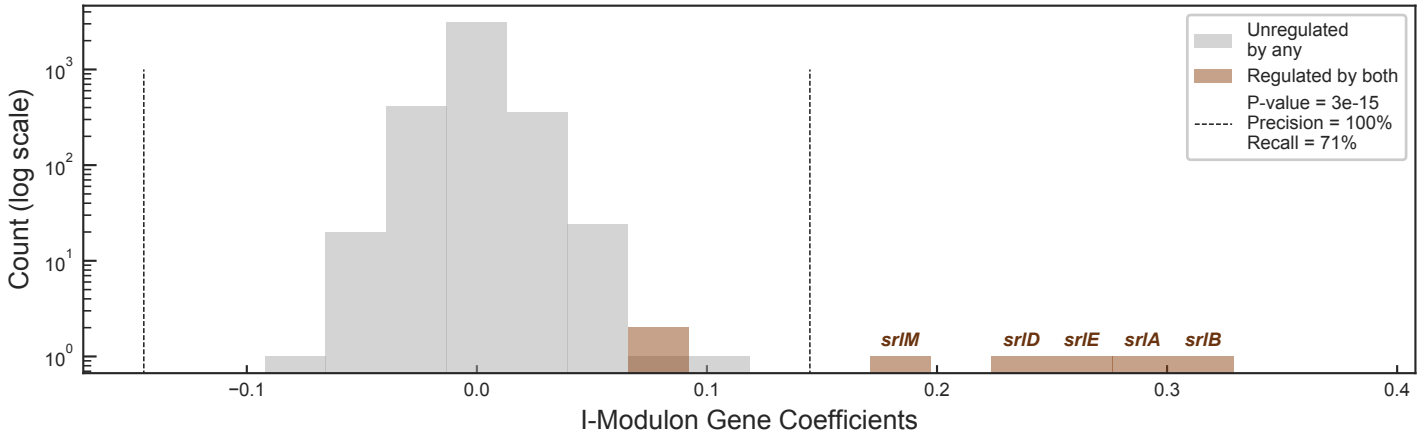
Biological Function: Sorbitol catabolism

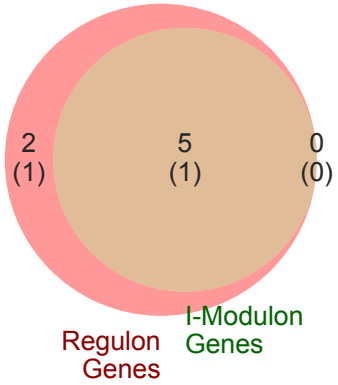


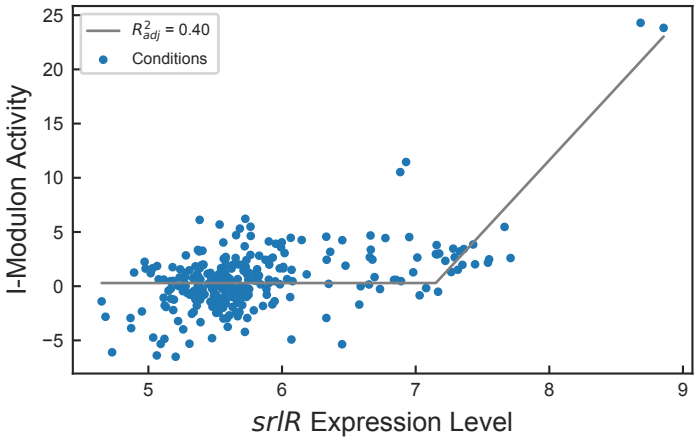
COG Categories

- Carbohydrate transport and metabolism (3): *srlA*, *srlB*, *srlE*
- Transcription (1): *srlM*
- Function unknown (1): *srlD*





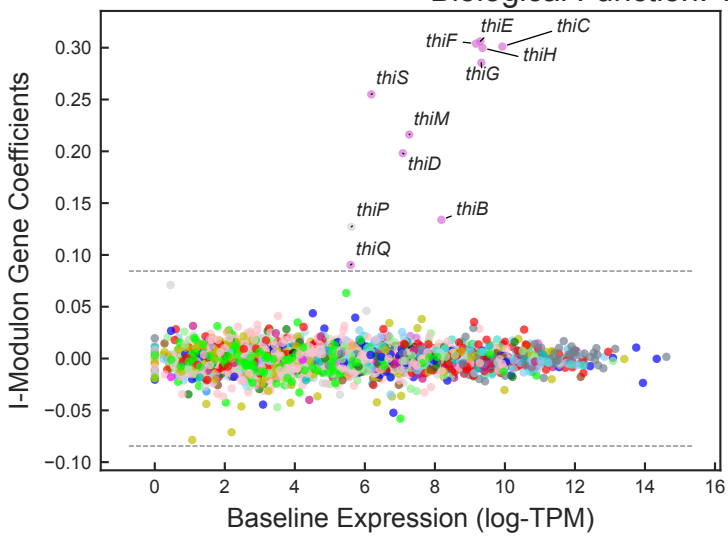




Thiamine I-Modulon

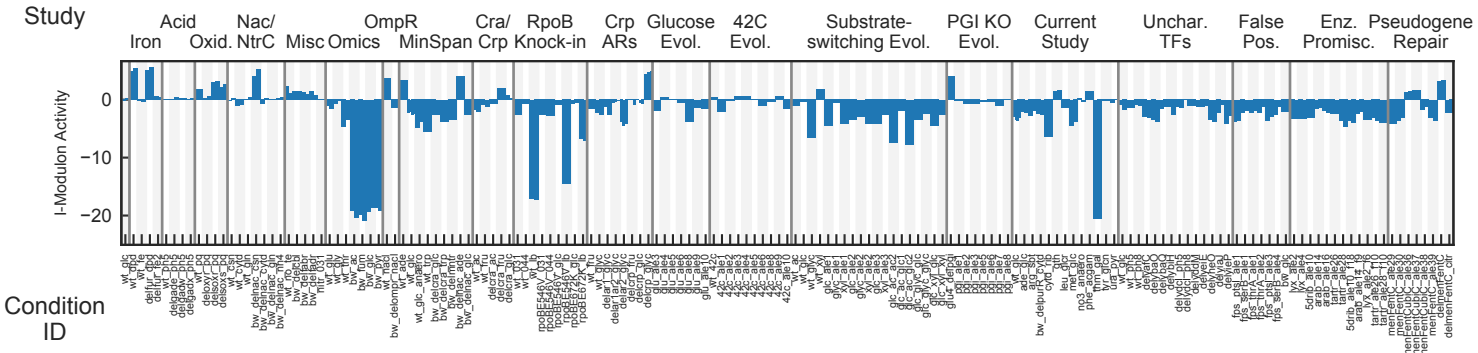
Regulated by: Thiamine

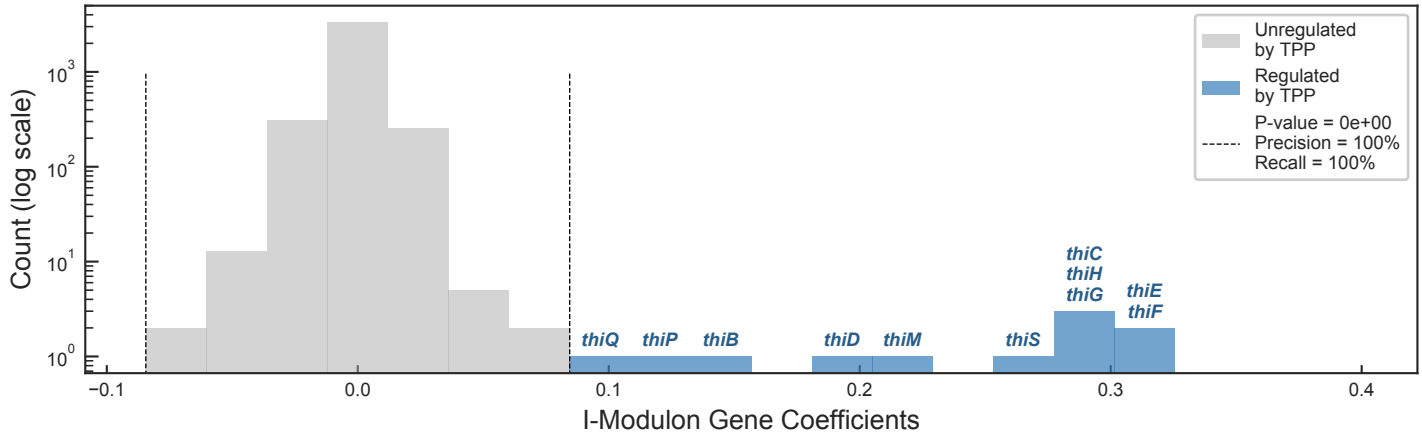
Biological Function: Thiamine biosynthesis

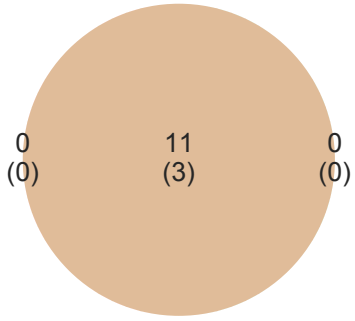


COG Categories

- Coenzyme transport and metabolism (10): *thiB*, *thiC*, *thiD*, *thiE*, *thiF*, *thiG*, *thiH*, *thiM*, *thiQ*, *thiS*
- Inorganic ion transport and metabolism (1): *thiP*



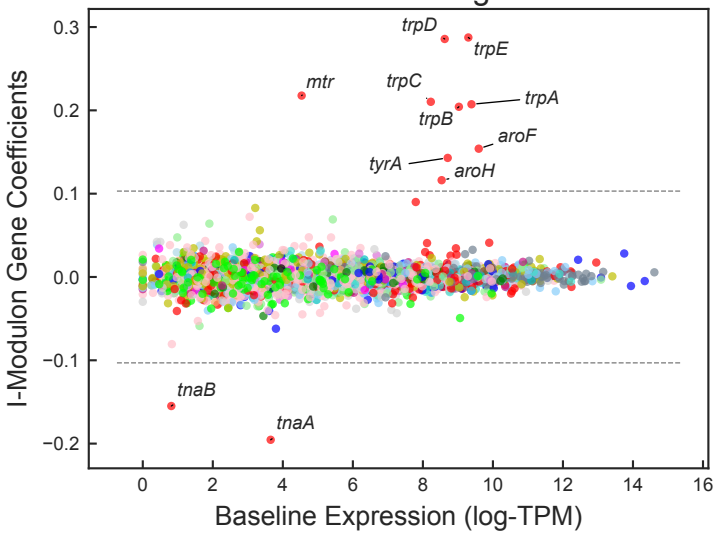




Tryptophan I-Modulon

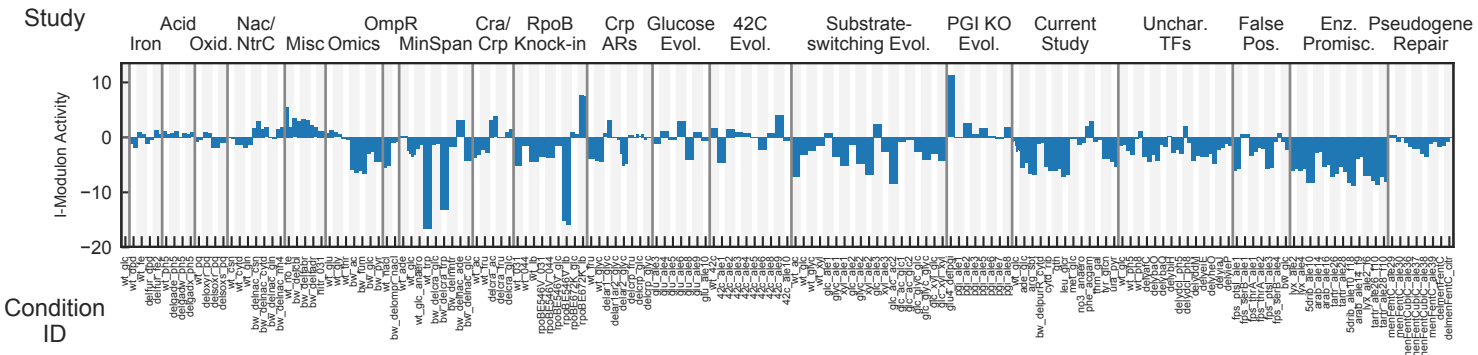
Regulated by: TrpR or trp-tRNA attenuation or Tryptophan attenuation

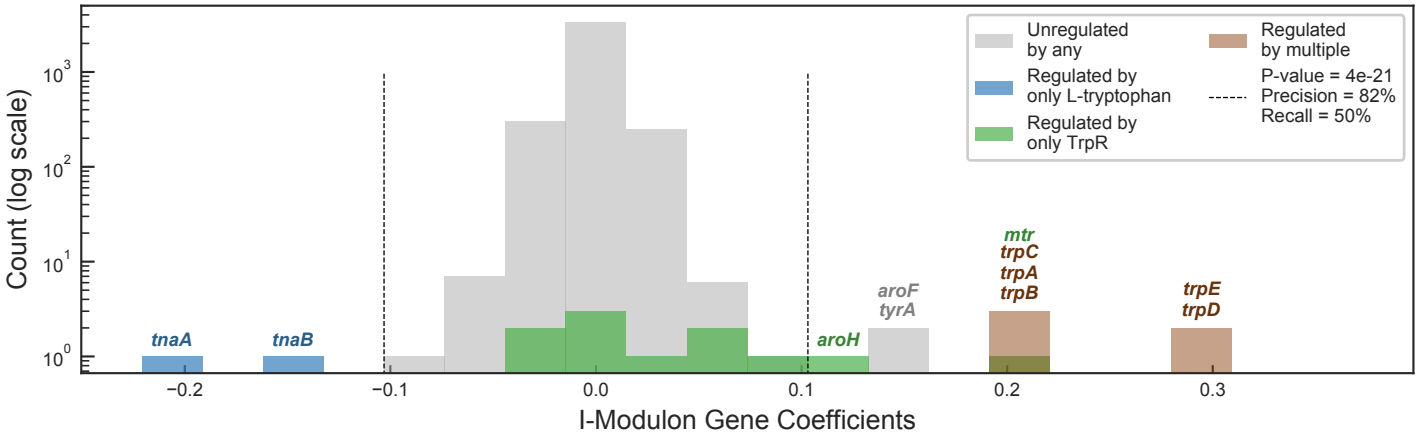
Biological Function: Tryptophan Biosynthesis

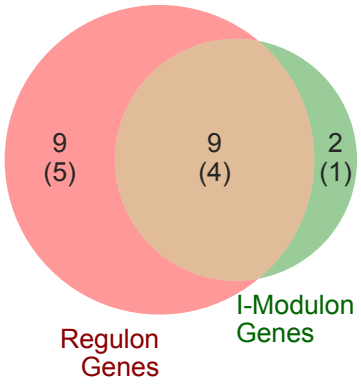


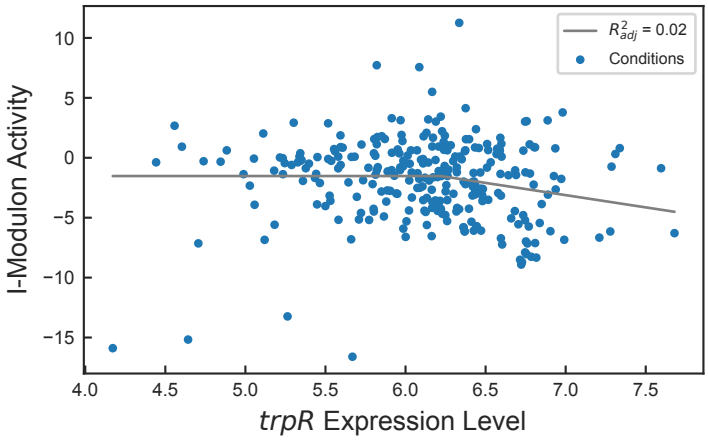
COG Categories

Amino acid transport and metabolism (11): *aroF*, *aroH*, *mtr*, *tnaA*, *tnaB*, *trpA*, *trpB*, *trpC*, *trpD*, *trpE*, *tyrA*





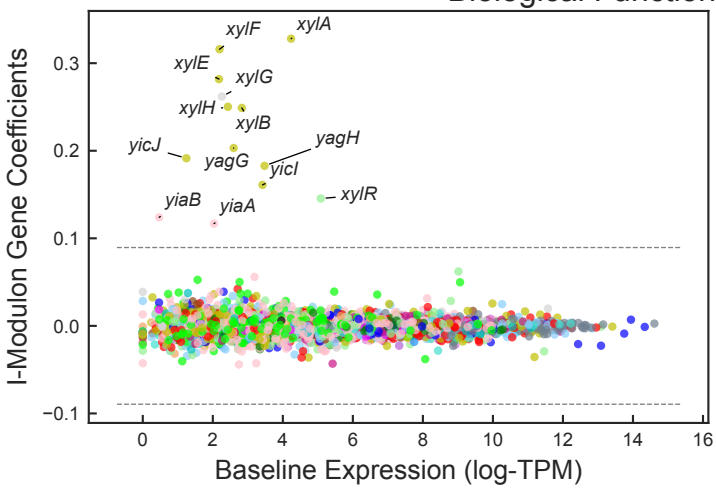




XylR I-Modulon

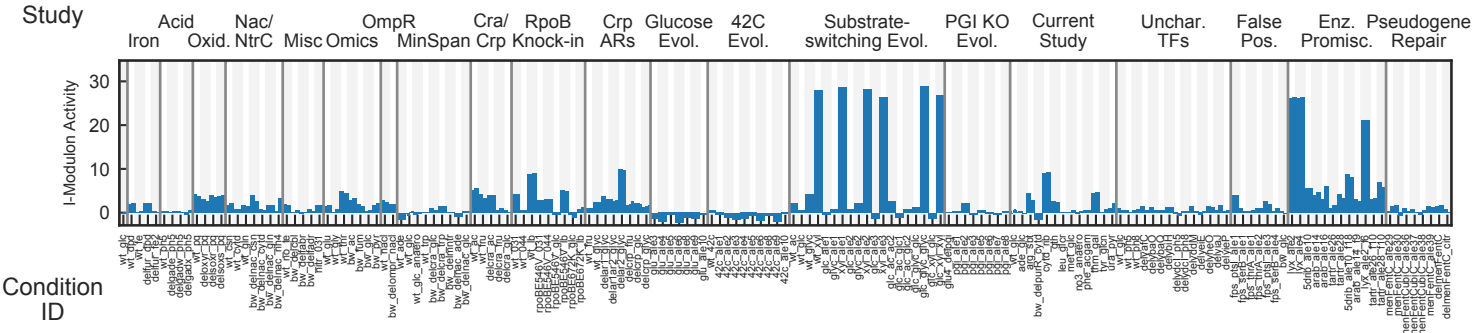
Regulated by: XylR

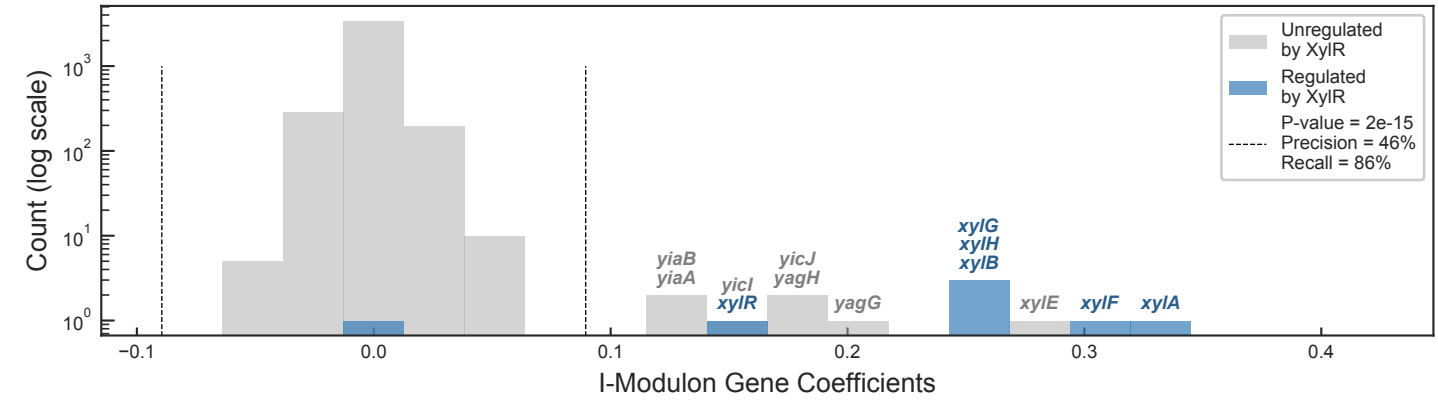
Biological Function: Xylose catabolism

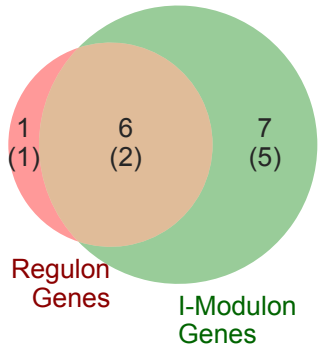


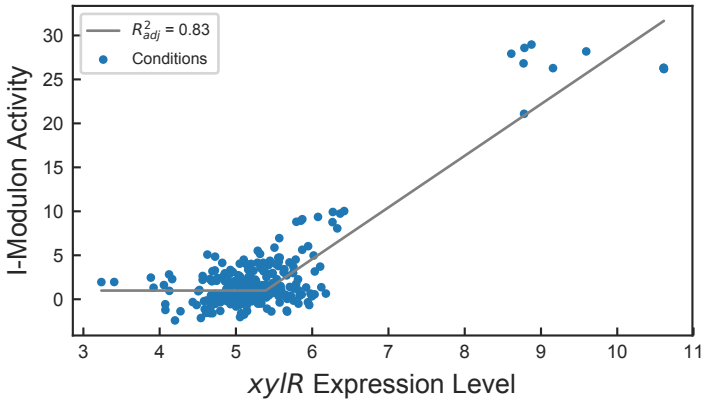
COG Categories

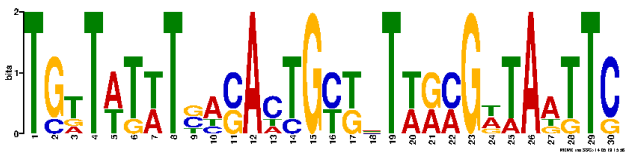
- Carbohydrate transport and metabolism (9): *xylA*, *xylB*, *xylE*, *xylF*, *xylH*, *yagG*, *yagH*, *yicI*, *yicJ*
- Inorganic ion transport and metabolism (1): *xylG*
- Transcription (1): *xylR*
- Function unknown (2): *yiaA*, *yiaB*











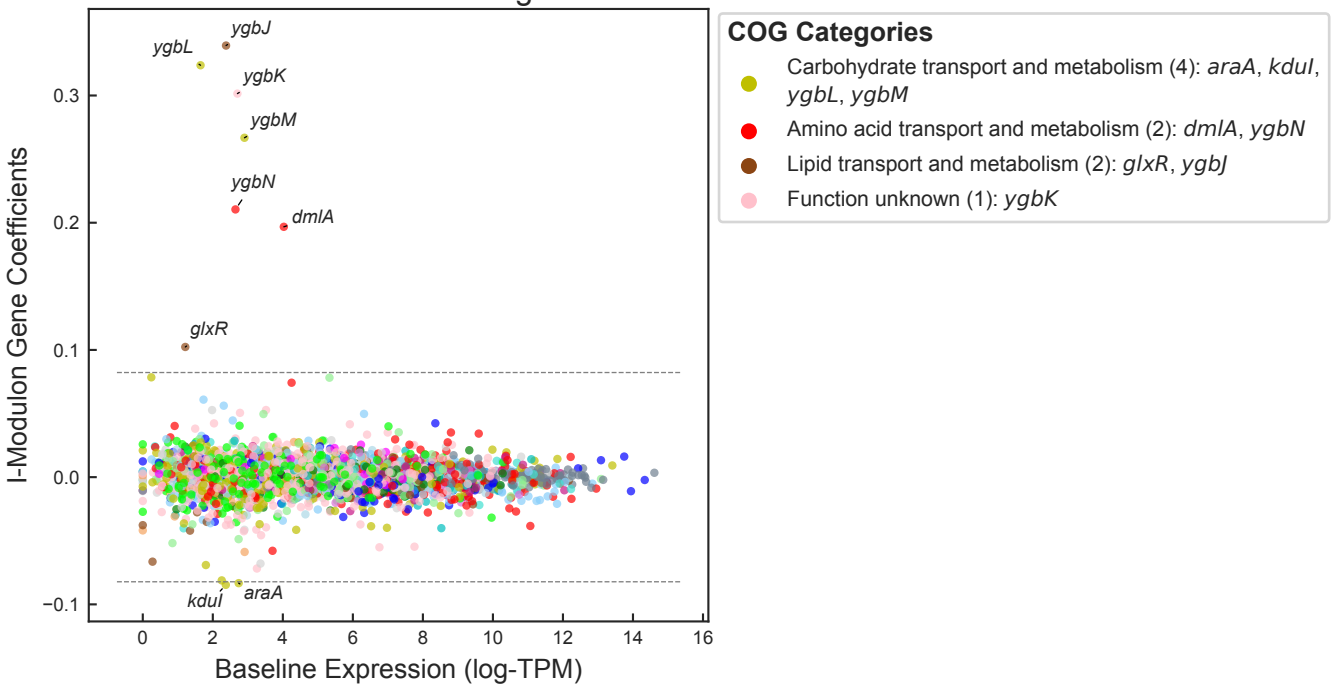
Motif E-value: 3.70e-04

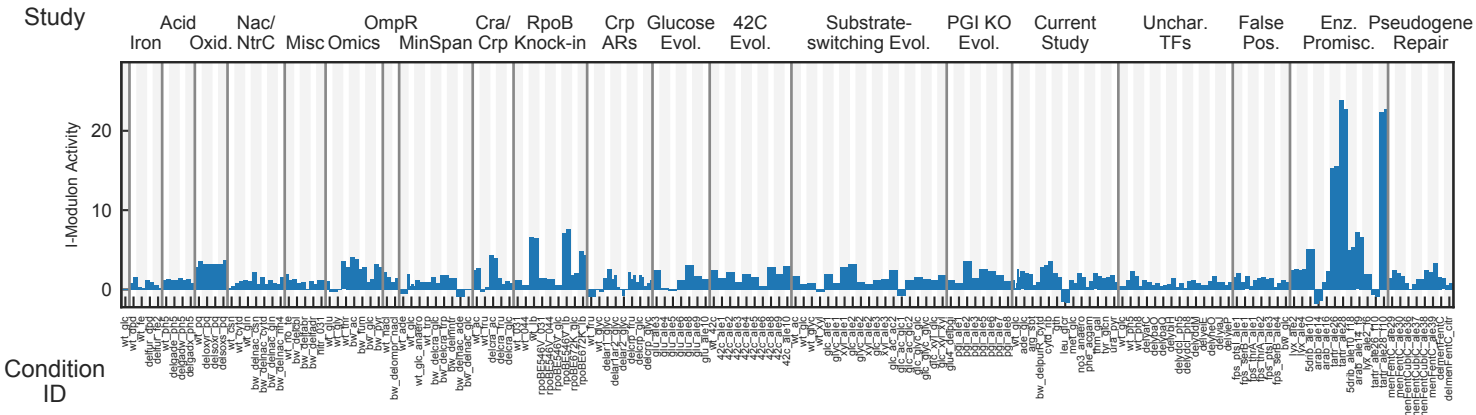
Operons with Upstream Motif: 71%

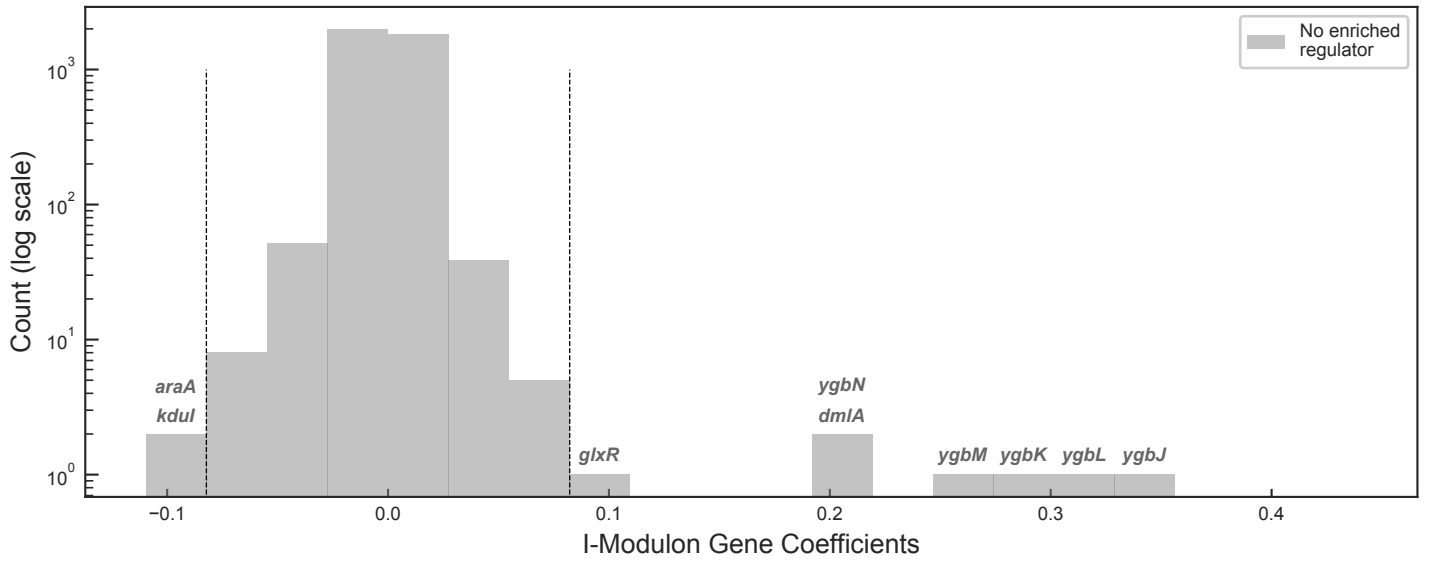
YgbI I-Modulon

Regulated by: YgbI

Biological Function: Unknown Function



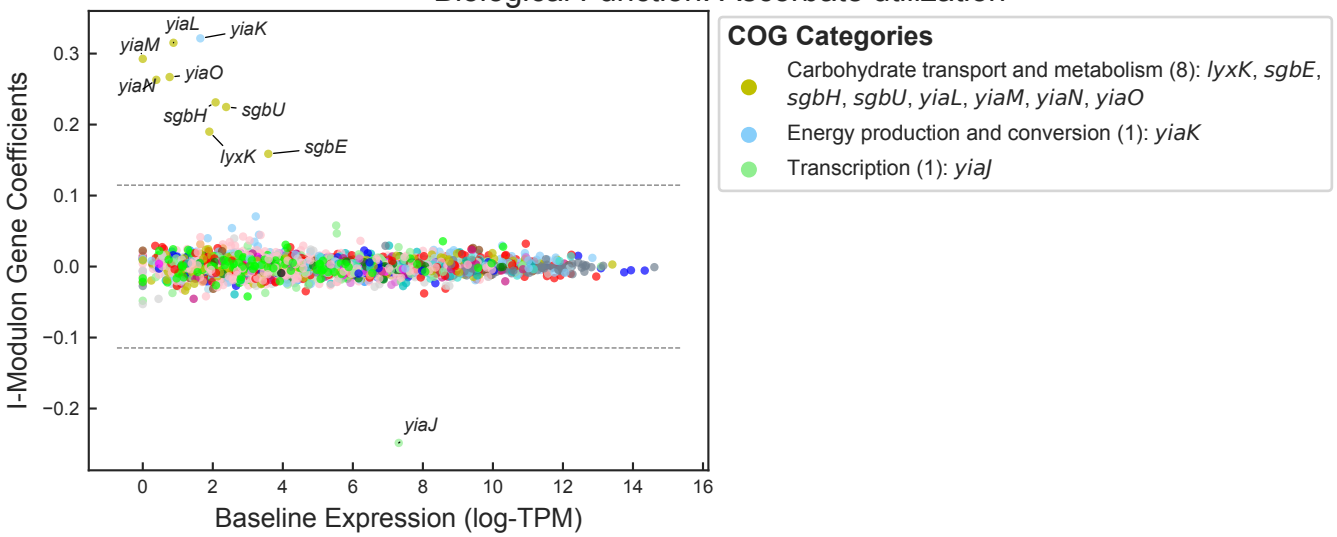


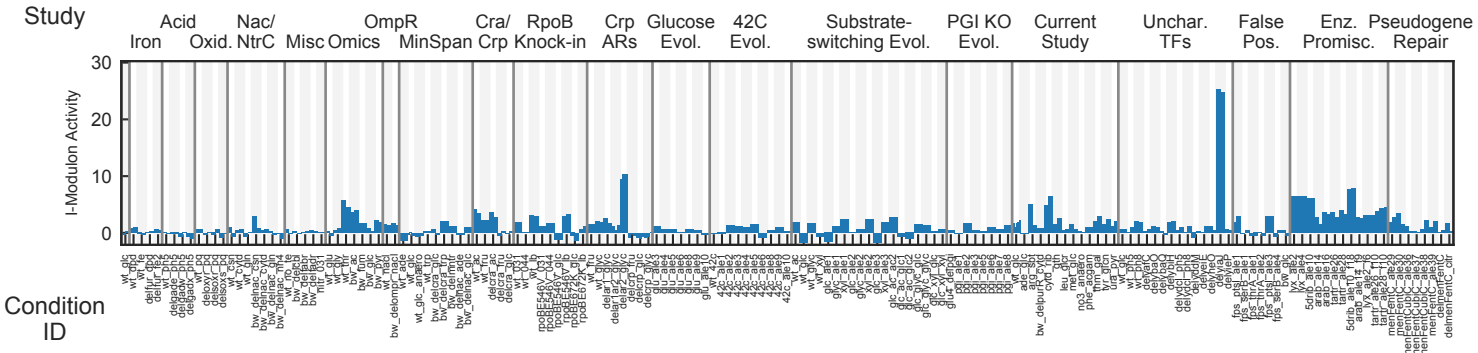


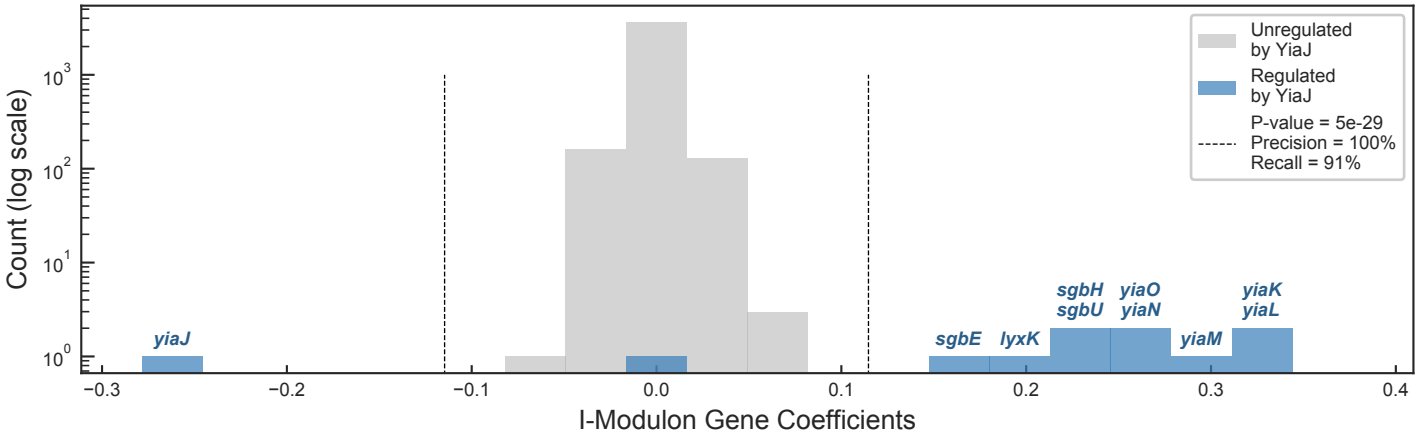
YiaJ I-Modulon

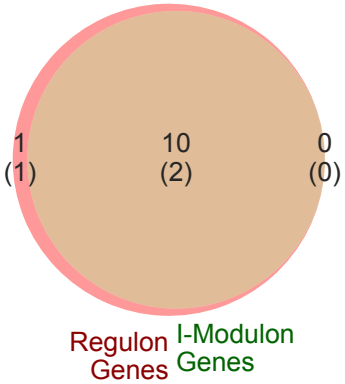
Regulated by: YiaJ

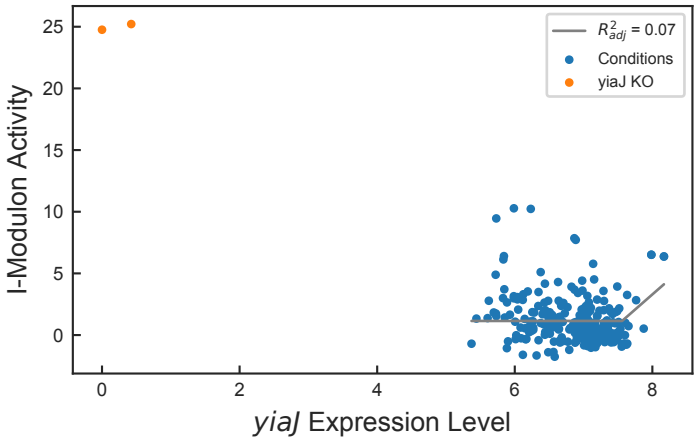
Biological Function: Ascorbate utilization







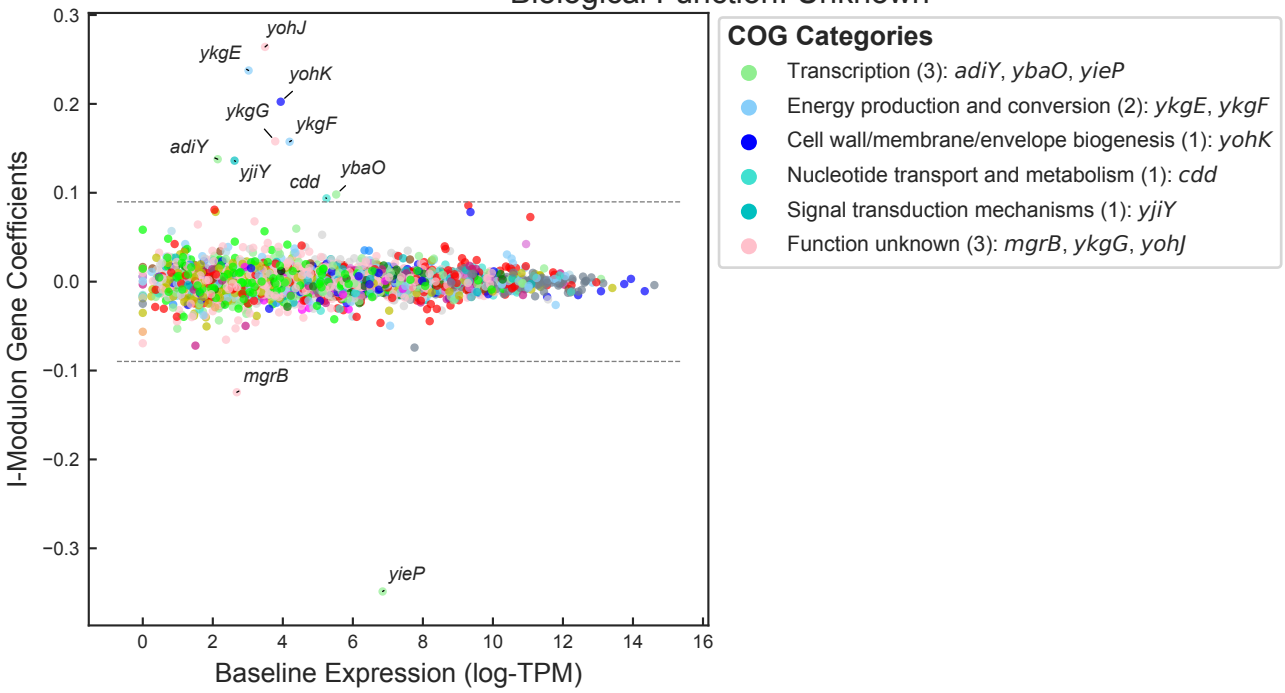


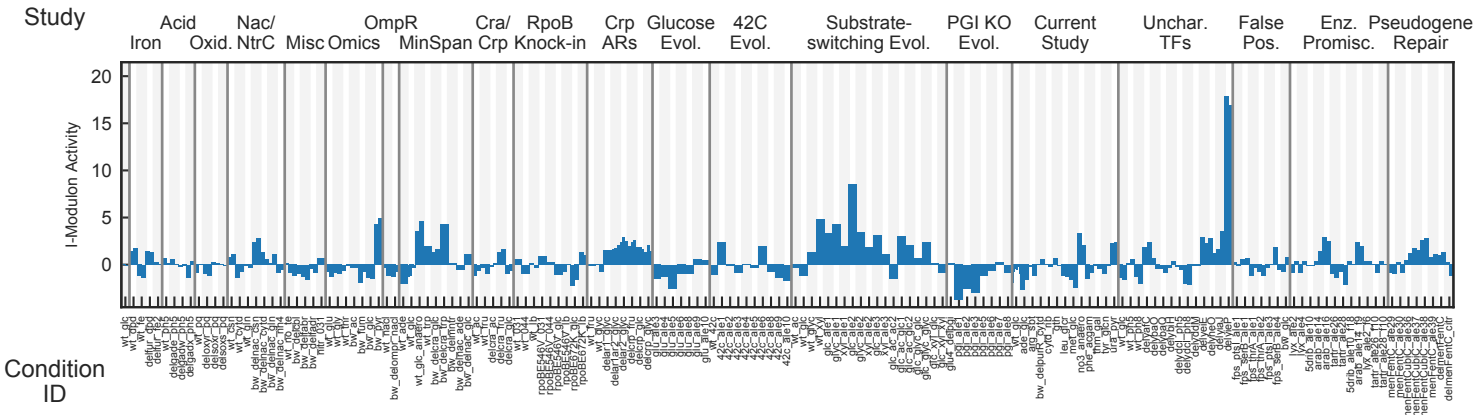


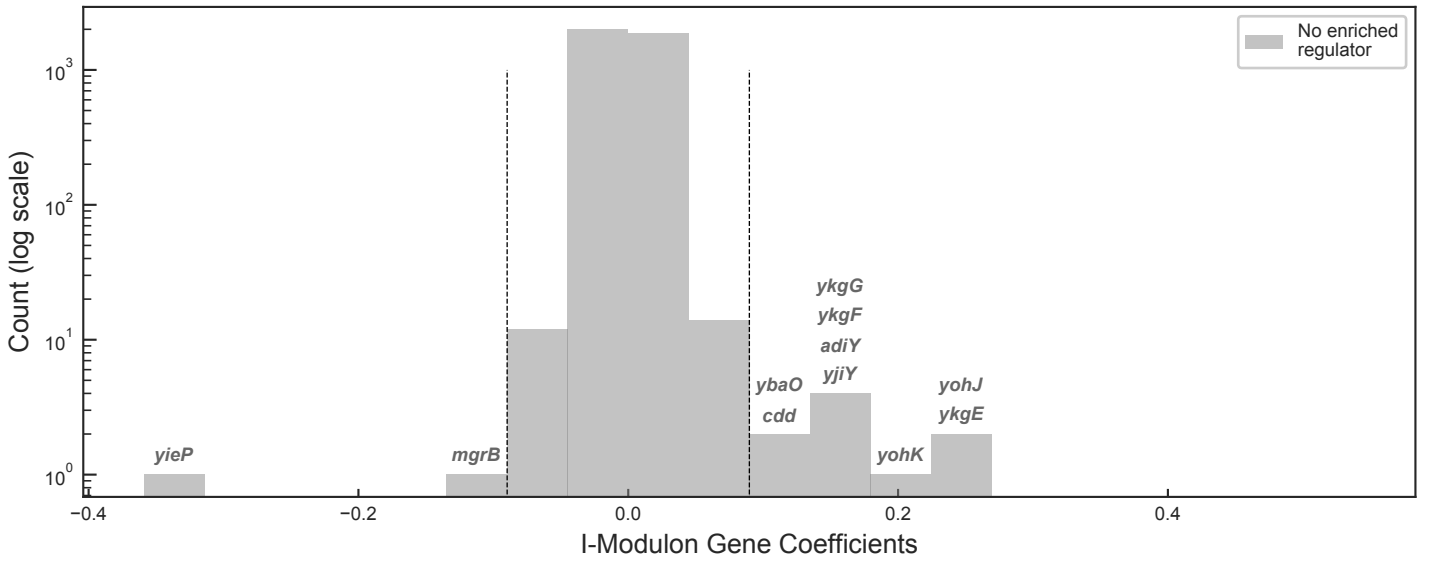
YieP I-Modulon

Regulated by: YieP

Biological Function: Unknown



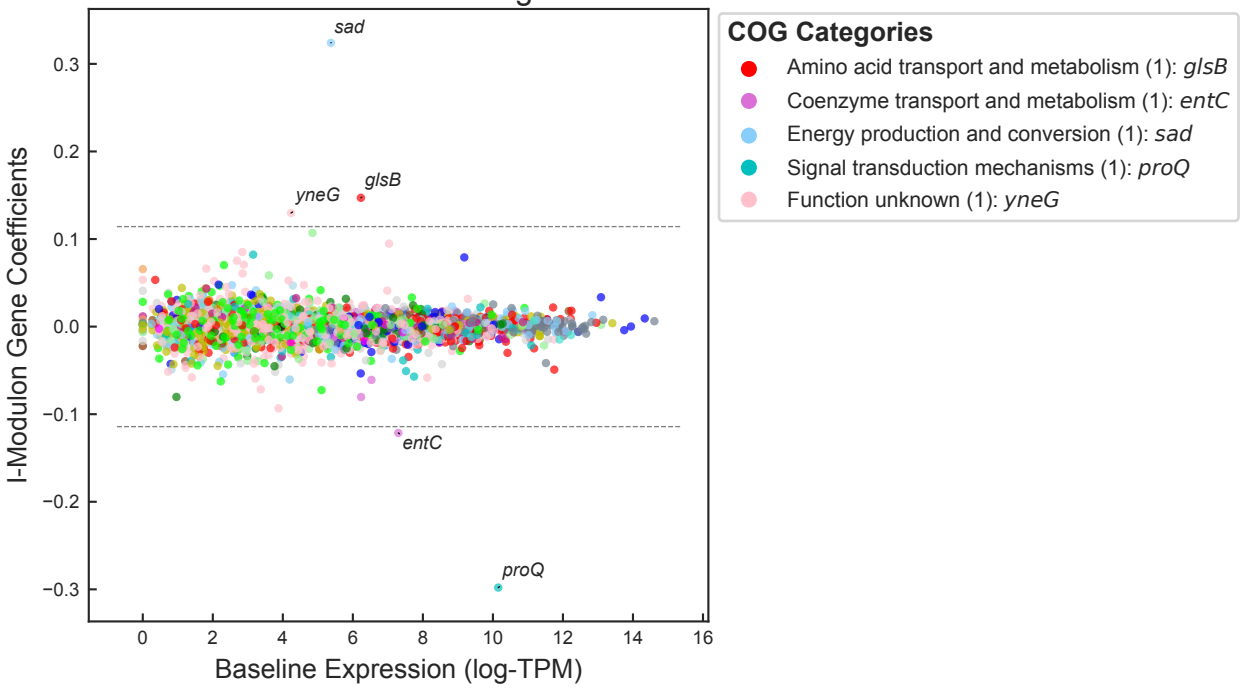


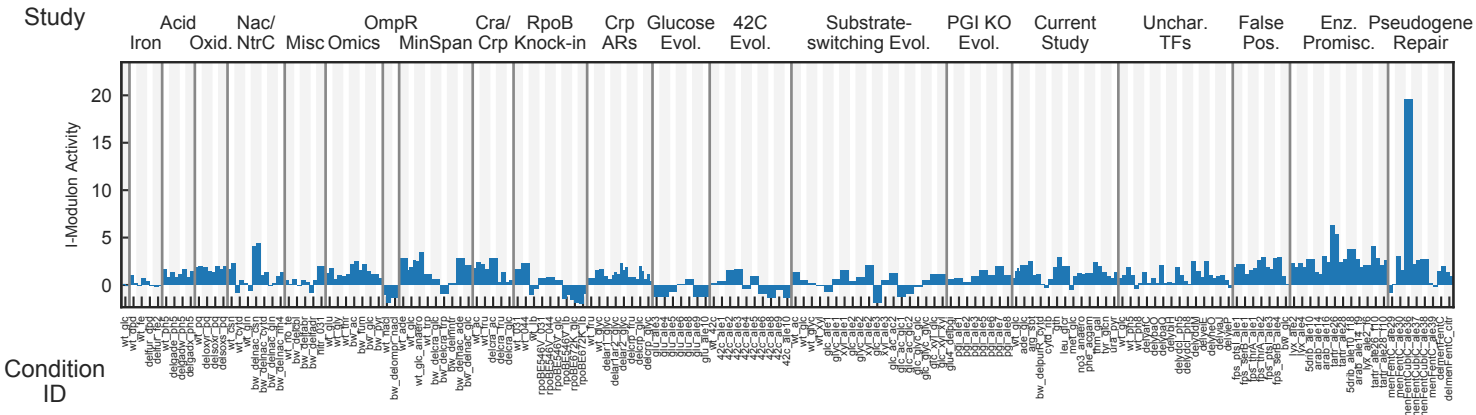


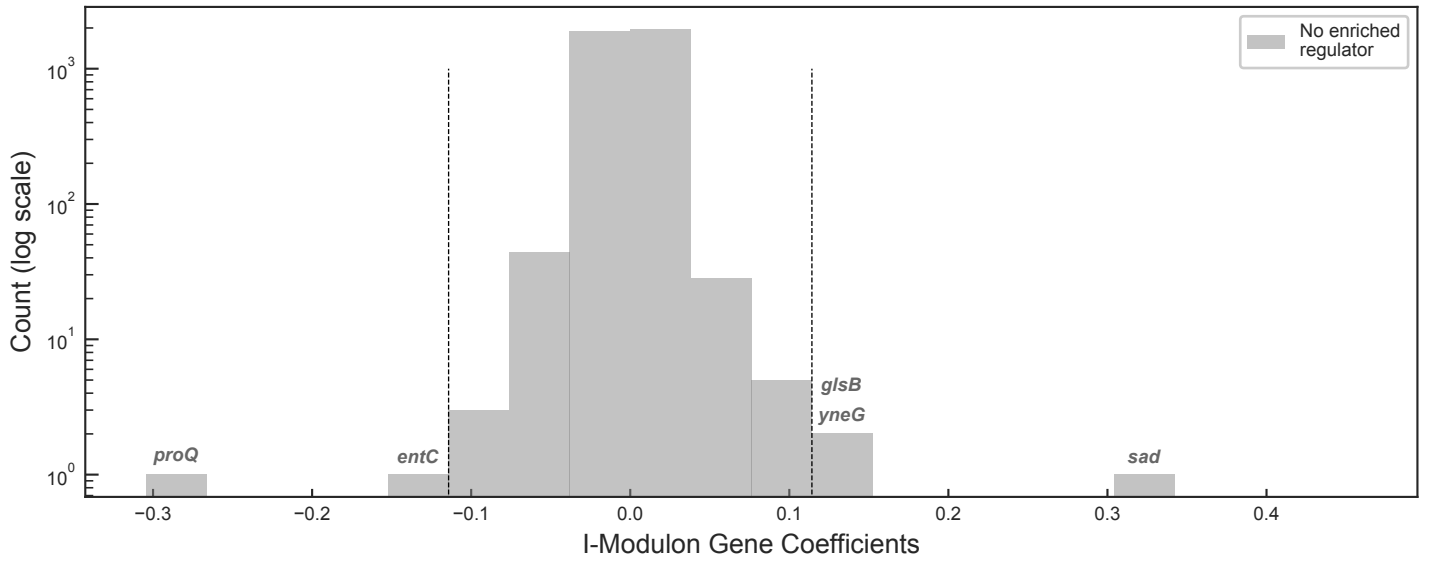
YneJ I-Modulon

Regulated by: YneJ

Biological Function: Unknown Function



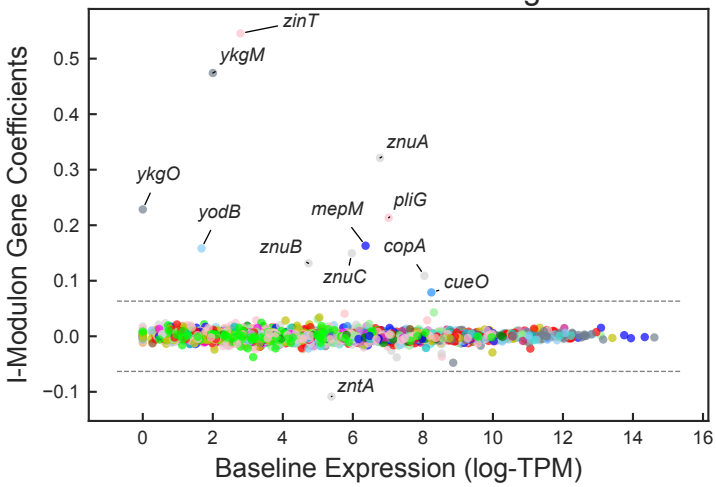




Zinc I-Modulon

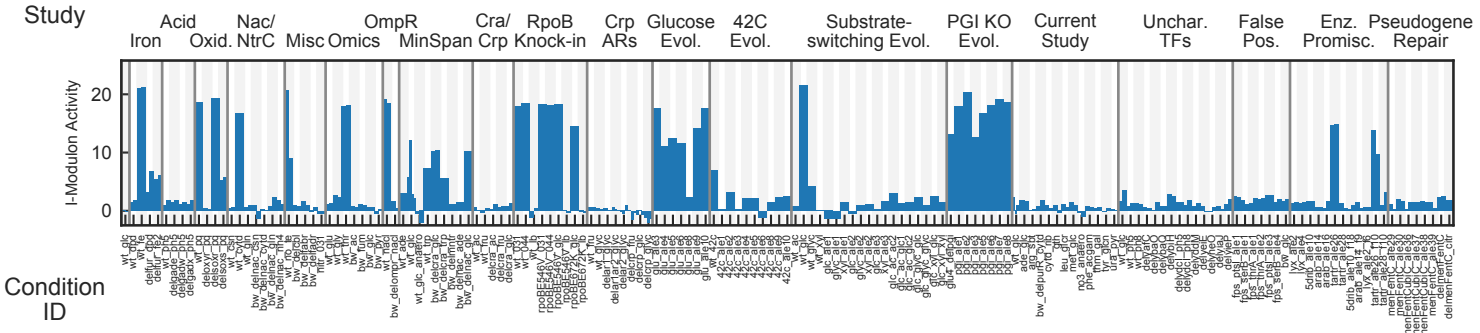
Regulated by: ZntR or Zur

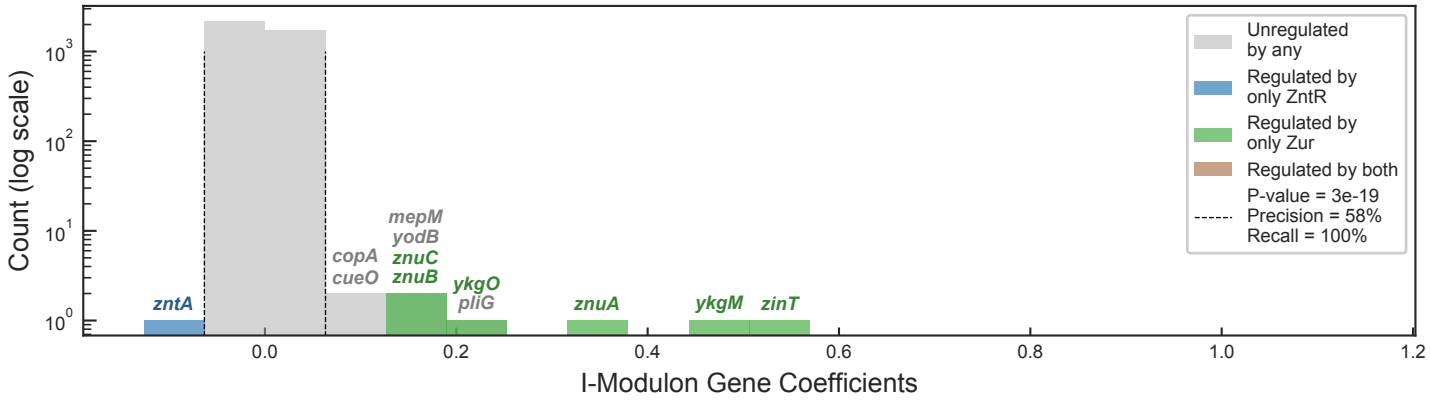
Biological Function: Zinc homeostasis

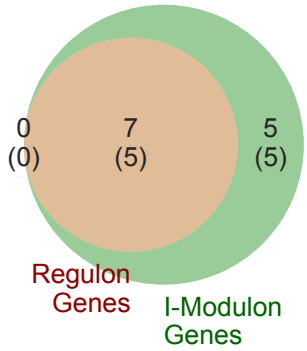


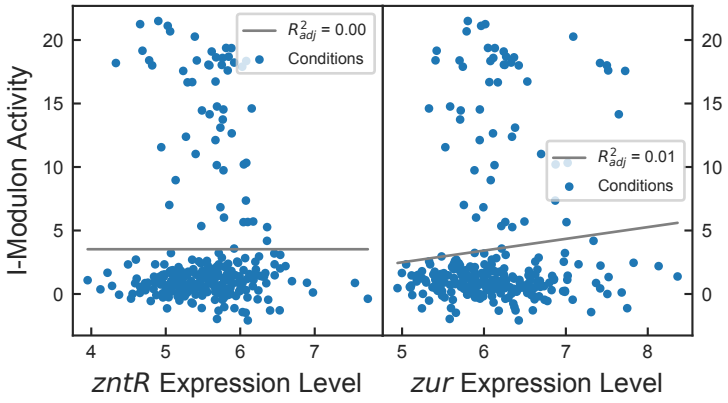
COG Categories

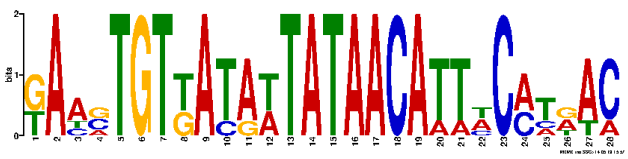
- Inorganic ion transport and metabolism (5): *copA*, *zntA*, *znuA*, *znuB*, *znuC*
- Translation, ribosomal structure and biogenesis (2): *ykgM*, *ykgO*
- Cell wall/membrane/envelope biogenesis (1): *mepM*
- Energy production and conversion (1): *yodB*
- Secondary metabolites biosynthesis, transport and catabolism (1): *cueO*
- Function unknown (2): *pliG*, *zinT*









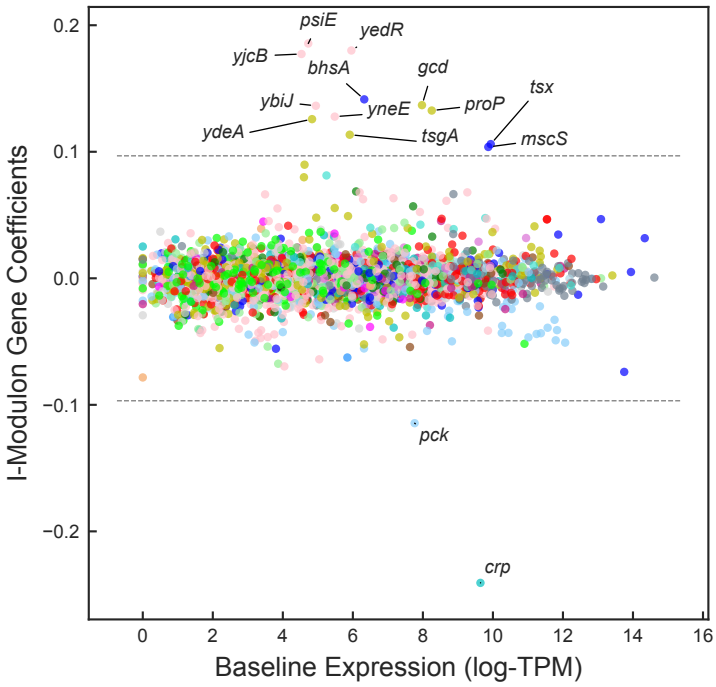


Motif E-value: 4.50e-06

Operons with Upstream Motif: 50%

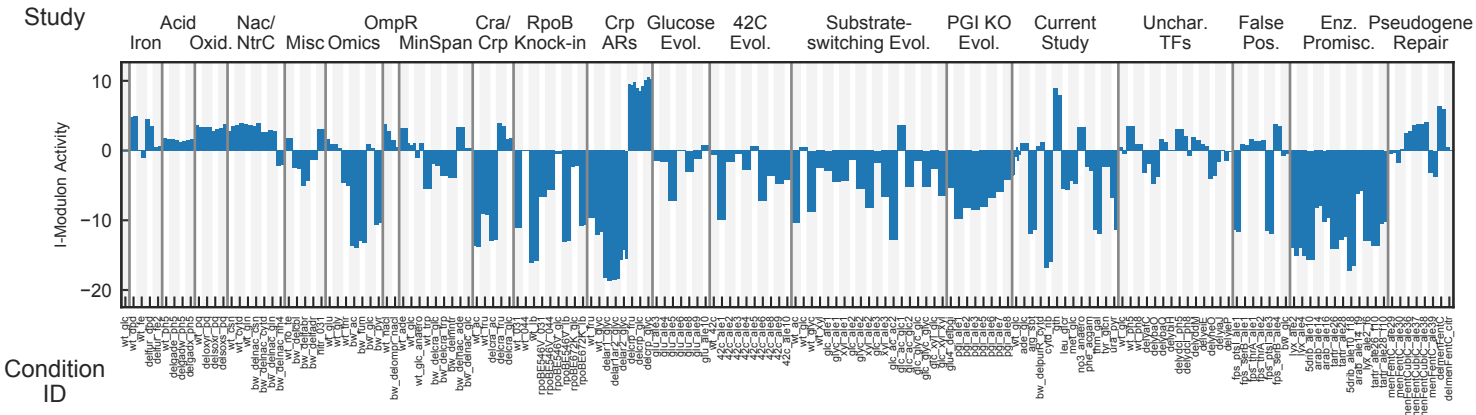
crp − KO I-Modulon

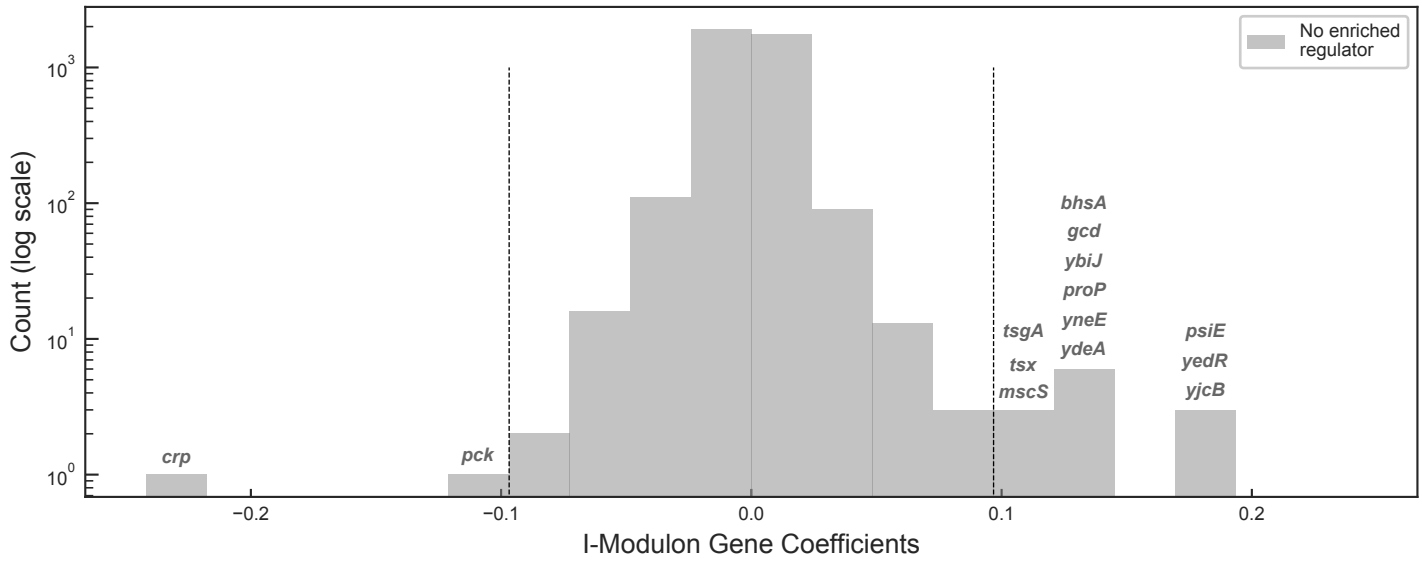
Biological Function: Accounts for crp knock-out



COG Categories

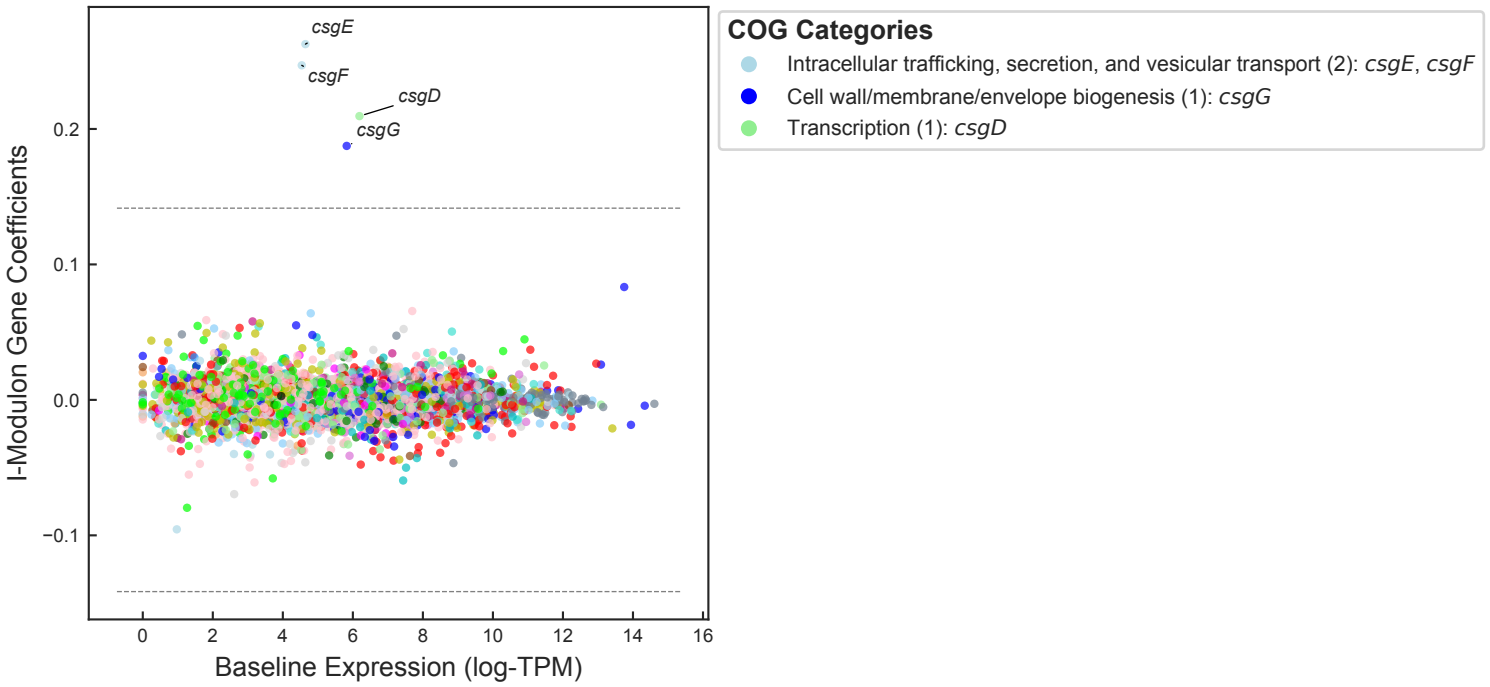
- Carbohydrate transport and metabolism (4): *gcd*, *proP*, *tsgA*, *ydeA*
- Cell wall/membrane/envelope biogenesis (3): *bhsA*, *mscS*, *tsx*
- Energy production and conversion (1): *pck*
- Signal transduction mechanisms (1): *crp*
- Function unknown (5): *psiE*, *ybiJ*, *yedR*, *yjcB*, *yneE*

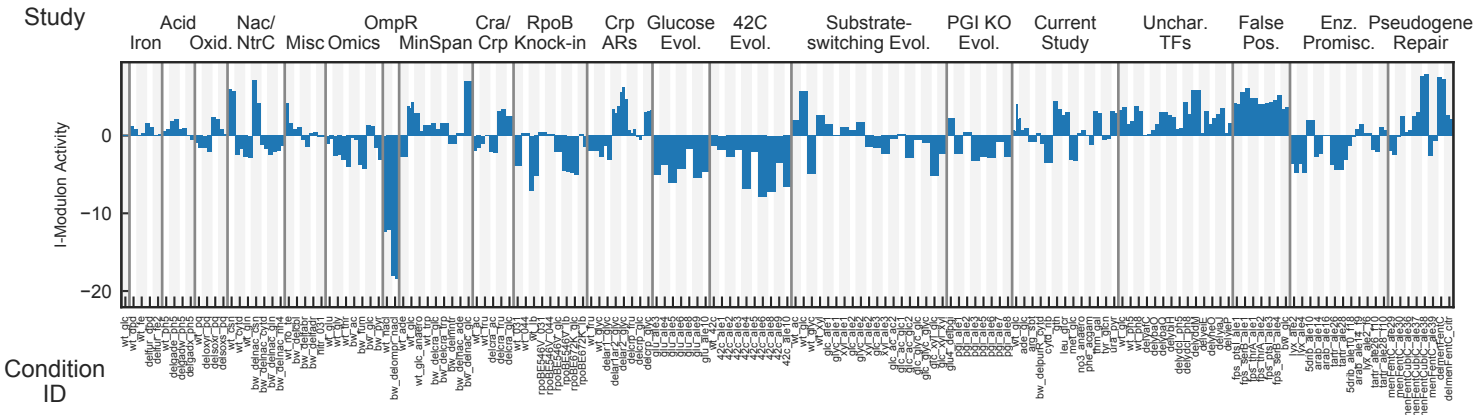


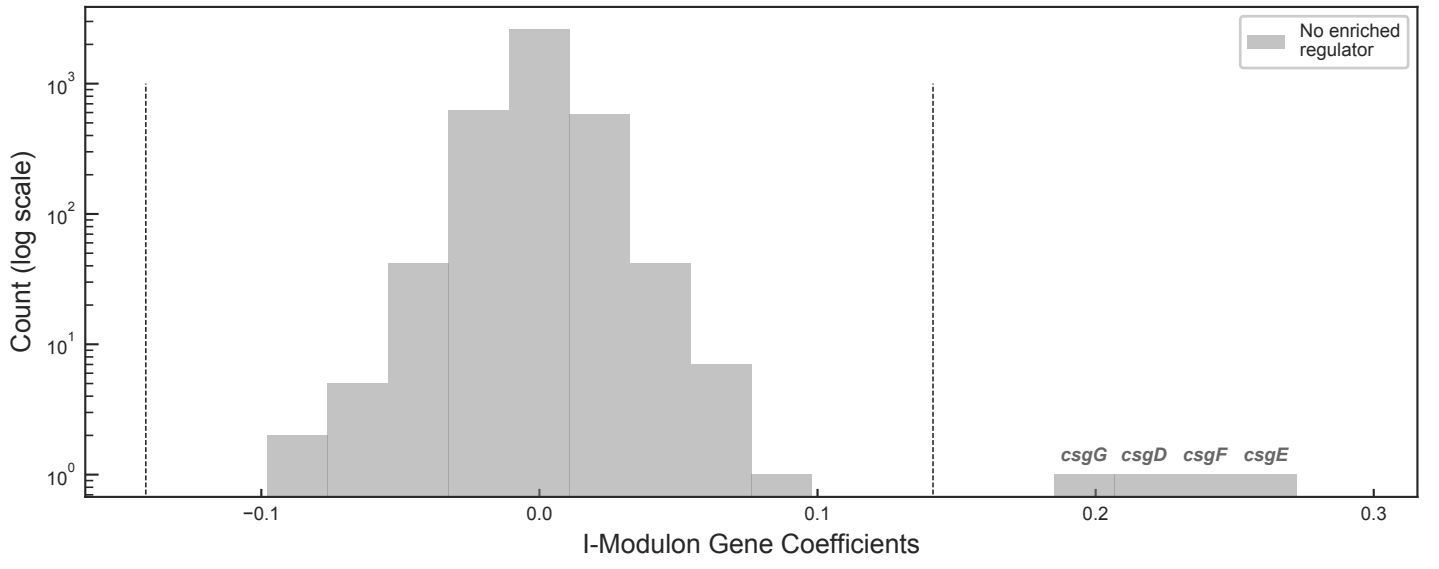


curli I-Modulon

Biological Function: Curli assembly

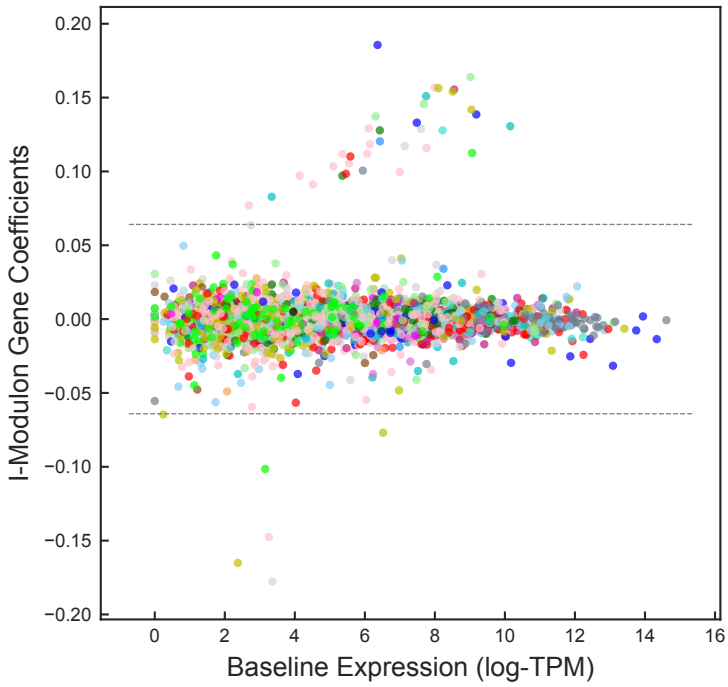






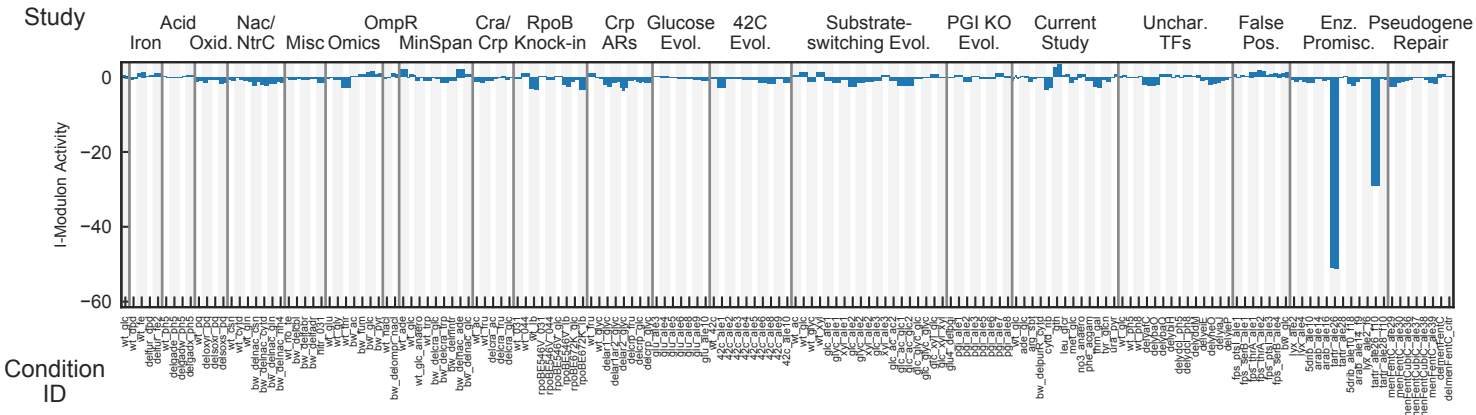
deletion − 1 I-Modulon

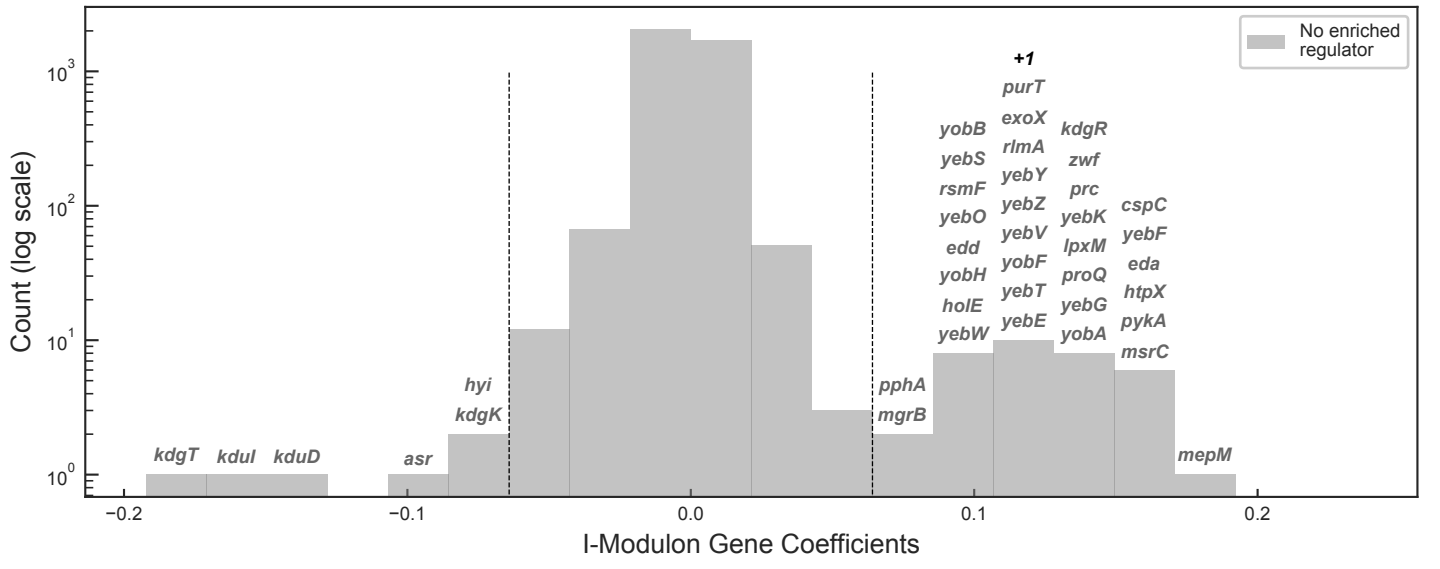
Biological Function: Large deletion of 39 genes during evolution



COG Categories

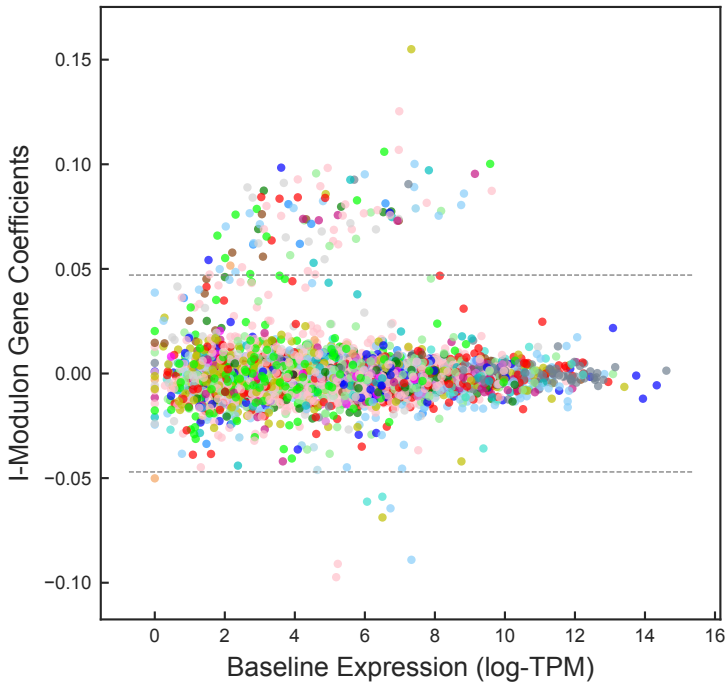
- Carbohydrate transport and metabolism (6): *eda*, *hyi*, *kdgK*, *kduI*, *pykA*, *zwf*
- Cell wall/membrane/envelope biogenesis (3): *lpxM*, *mepM*, *prc*
- Inorganic ion transport and metabolism (3): *kdgT*, *yebZ*, *yobA*
- Signal transduction mechanisms (3): *msrC*, *pphA*, *proQ*
- Other (26): *cspC*, *kdgR*, *yebK*, *edd*, *ptrB*, *exoX*, *holE*, *purT*, *htpX*, *rlmA*, *rsmF*, *kduD*, *mgrB*, *yebE*, *yebF*, *yebG*, *yebO*, *yebS*, *yebT*, *yebV* + 6





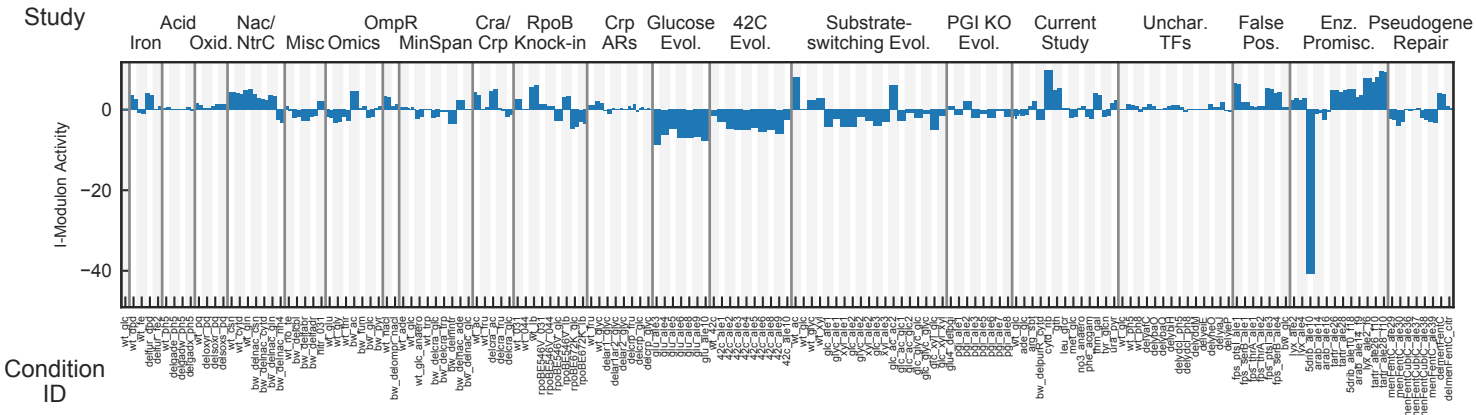
deletion − 2 I-Modulon

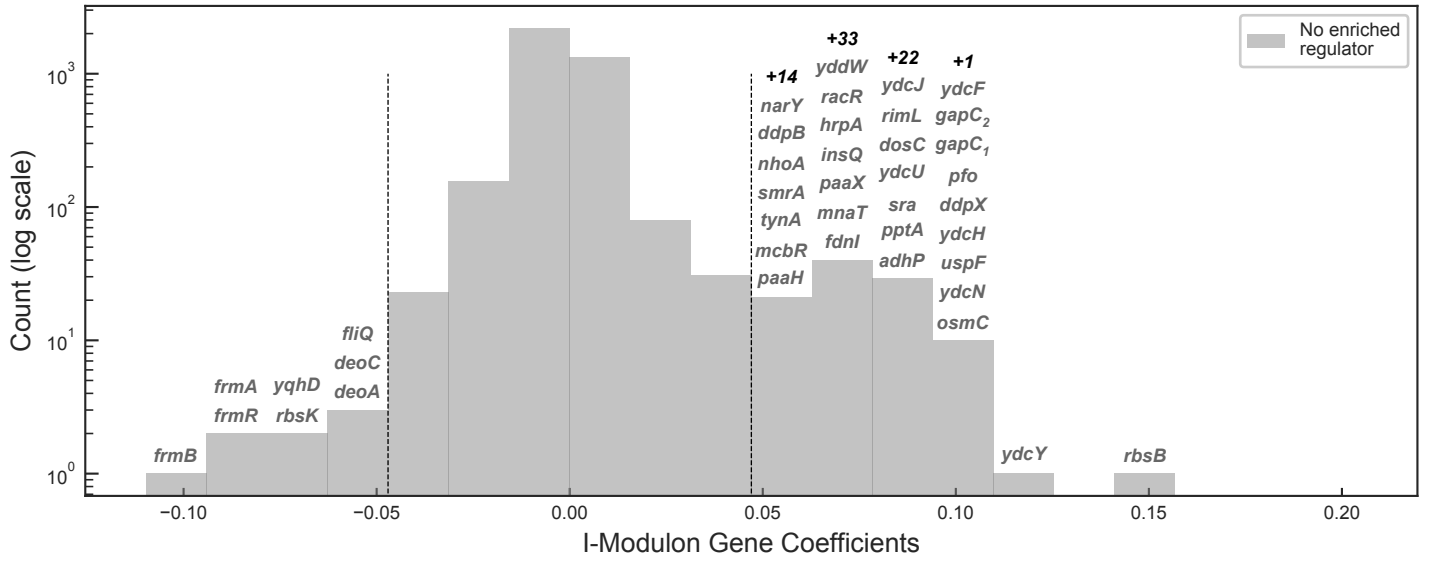
Biological Function: Large deletion of 171 genes during evolution



COG Categories

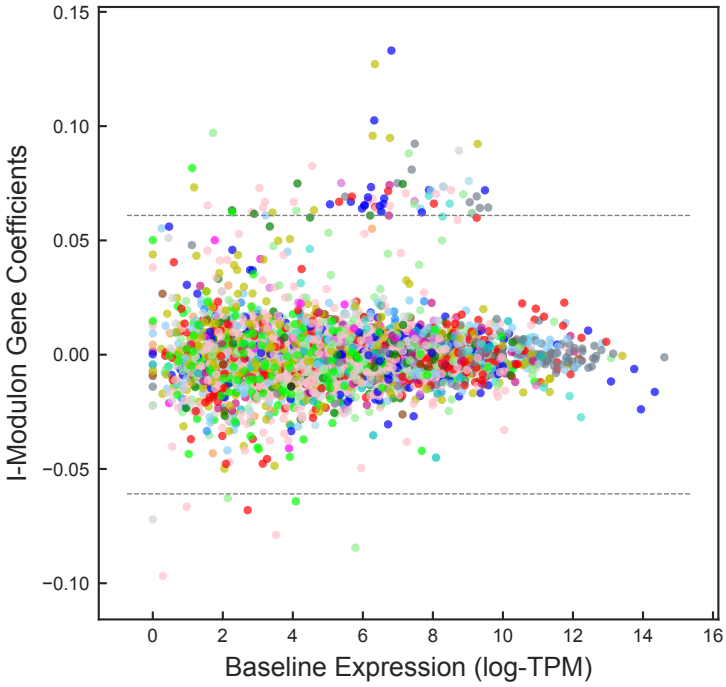
- Energy production and conversion (16): *adhP*, *aldA*, *cybB*, *fdnG*, *fdnI*, *feaB*, *frmA*, *maeA*, *narV*, *narW*, *narY*, *narZ*, *patD*, *pfo*, *ydbC*, *yqhD*
- Inorganic ion transport and metabolism (11): *ddpB*, *ddpC*, *opgD*, *tehA*, *trkG*, *ydaN*, *ydcU*, *ydcV*, *yddB*, *ydeN*, *yncD*
- Transcription (7): *abgR*, *feaR*, *mcbR*, *paaX*, *racR*, *ydcN*, *ydcR*
- Amino acid transport and metabolism (5): *ddpA*, *ddpD*, *ddpF*, *ydcT*, *yddG*
- Other (71): *azoR*, *paaH*, *paaJ*, *ynbC*, *ynbD*, *hslJ*, *osmC*, *pqqL*, *ydcP*, *yncG*, *dbpA*, *hrpA*, *insQ*, *intR*, *recT*, *nhoA*, *paaK*, *tehB*, *tynA*, *ydcO* + 51





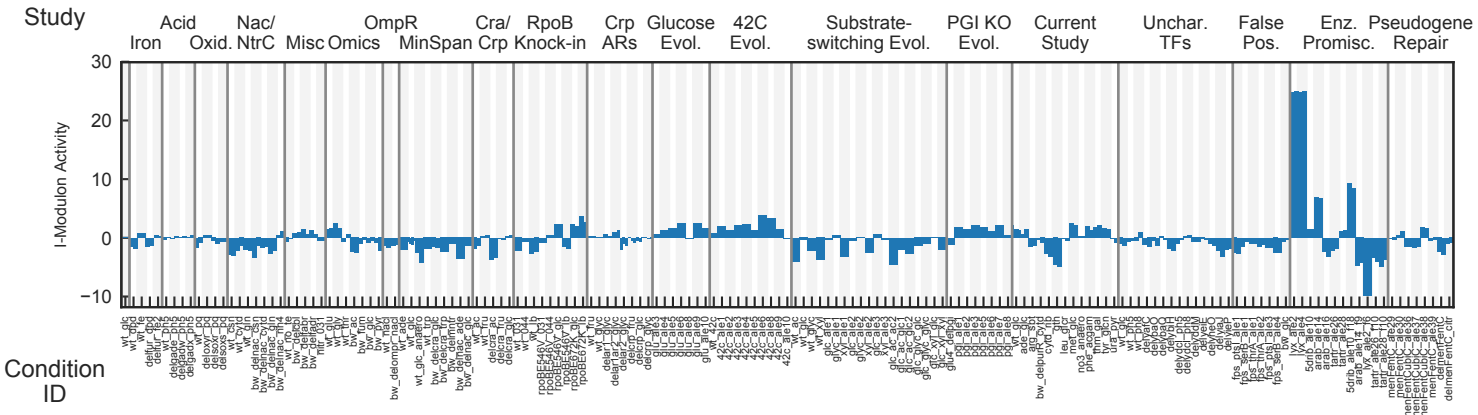
duplication − 1 I-Modulon

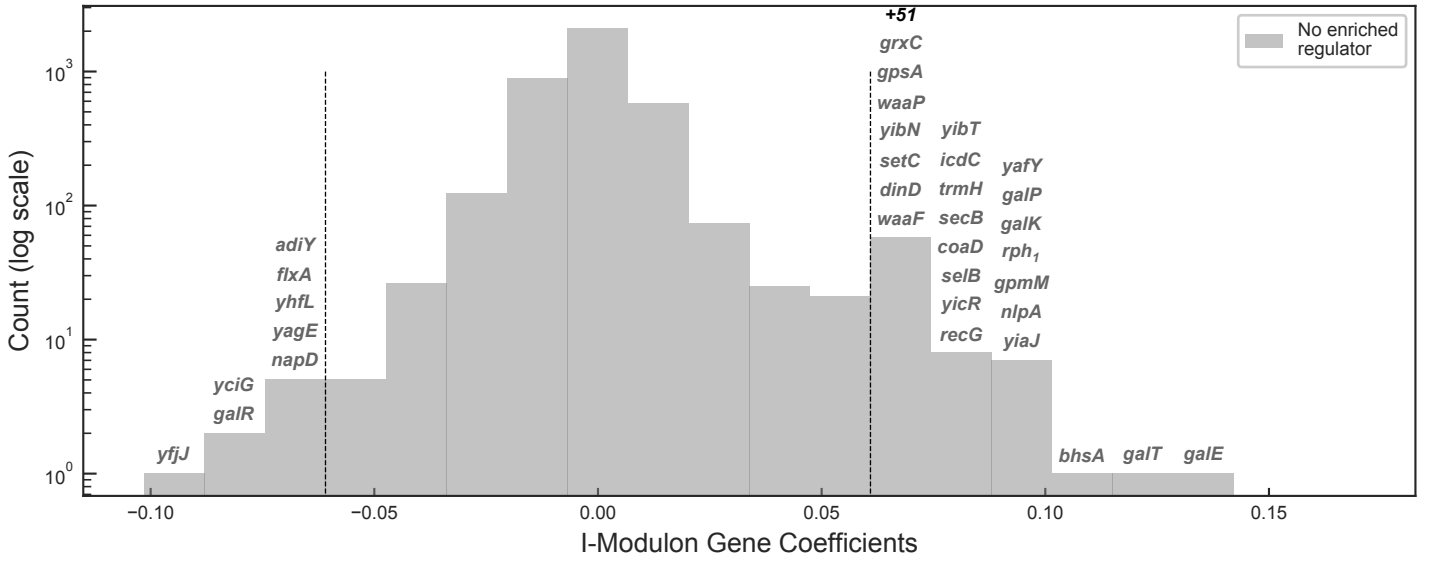
Biological Function: Large duplication of 129 genes during evolution



COG Categories

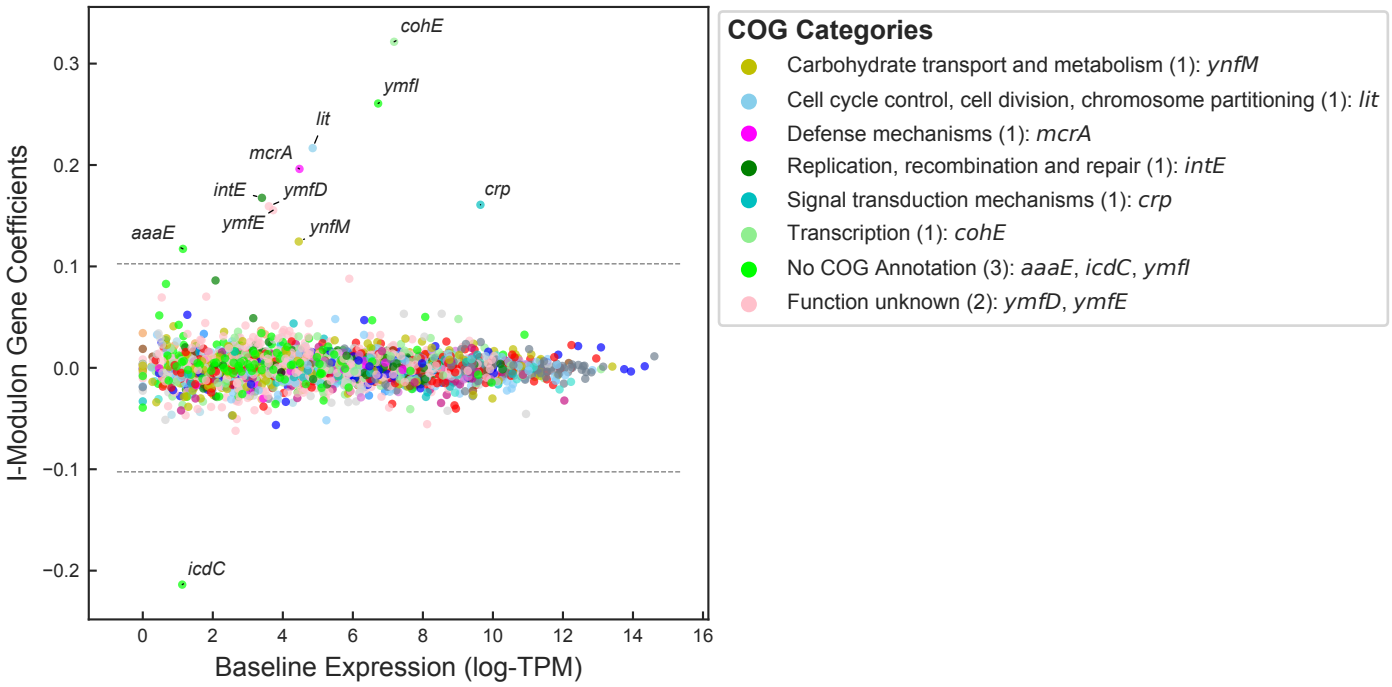
- Cell wall/membrane/envelope biogenesis (16): *bhsA*, *galE*, *hldD*, *waaA*, *waaB*, *waaC*, *waaF*, *waaG*, *waaO*, *waaP*, *waaQ*, *waaR*, *waaU*, *waaY*, *waaZ*, *yiaD*
- Carbohydrate transport and metabolism (8): *galK*, *galM*, *galP*, *galT*, *gpmM*, *nepI*, *setC*, *yicI*
- Translation, ribosomal structure and biogenesis (8): *glyQ*, *glyS*, *rph*$_1$, *rpmB*, *rpmG*, *selB*, *trmH*, *trmL*
- Other (52): *adiY*, *galR*, *rpoZ*, *spoT*, *yafY*, *yiaJ*, *yiaU*, *cysE*, *gltS*, *selA*, *tdh*, *yagE*, *yicL*, *bisC*, *ghrB*, *gpsA*, *ysaA*, *insK*, *ligB*, *recG* + 32

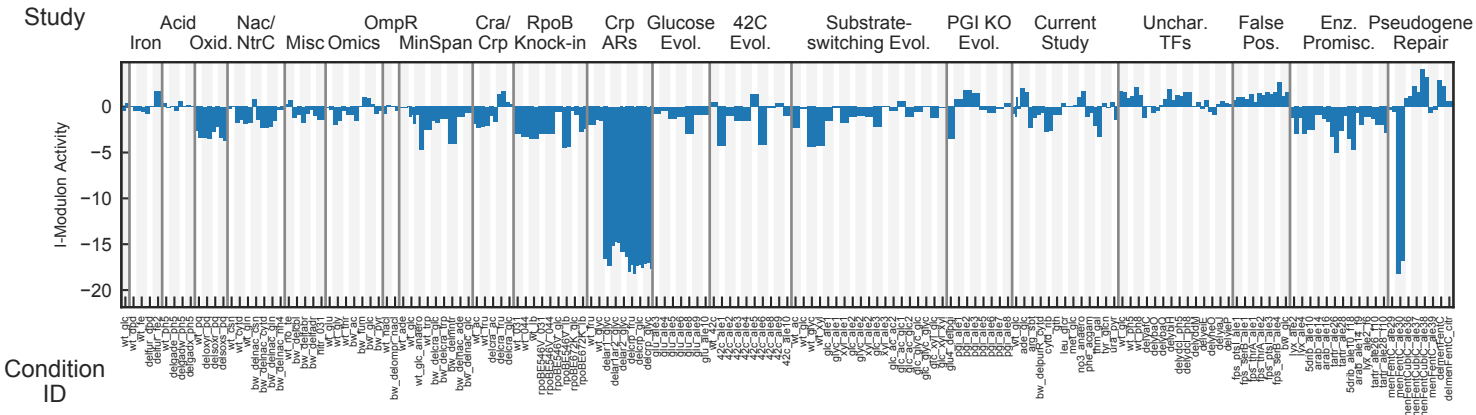


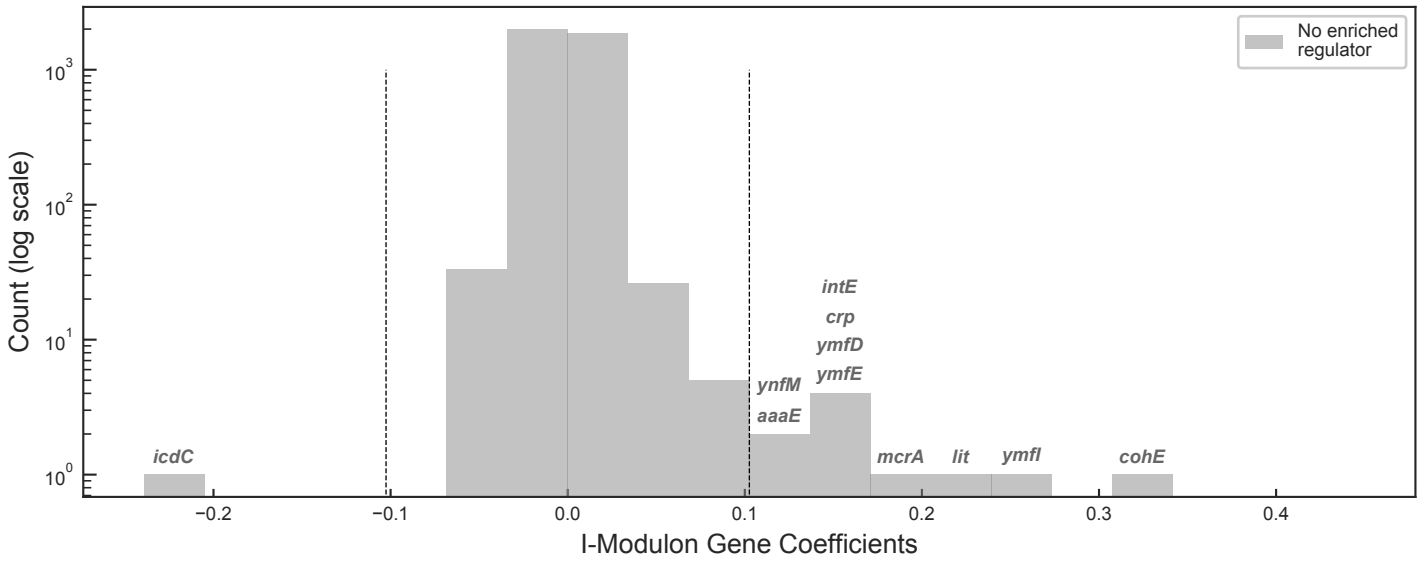


e14 – deletion I-Modulon

Biological Function: Removal of e14 prophage

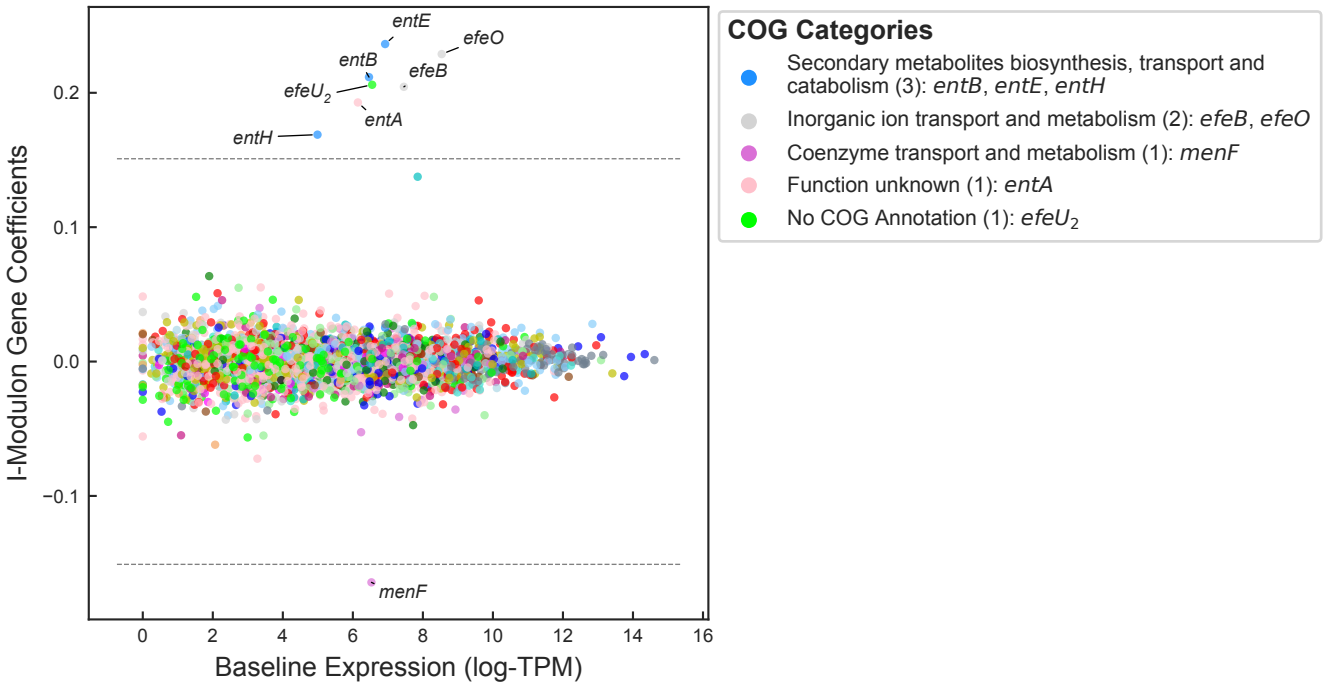


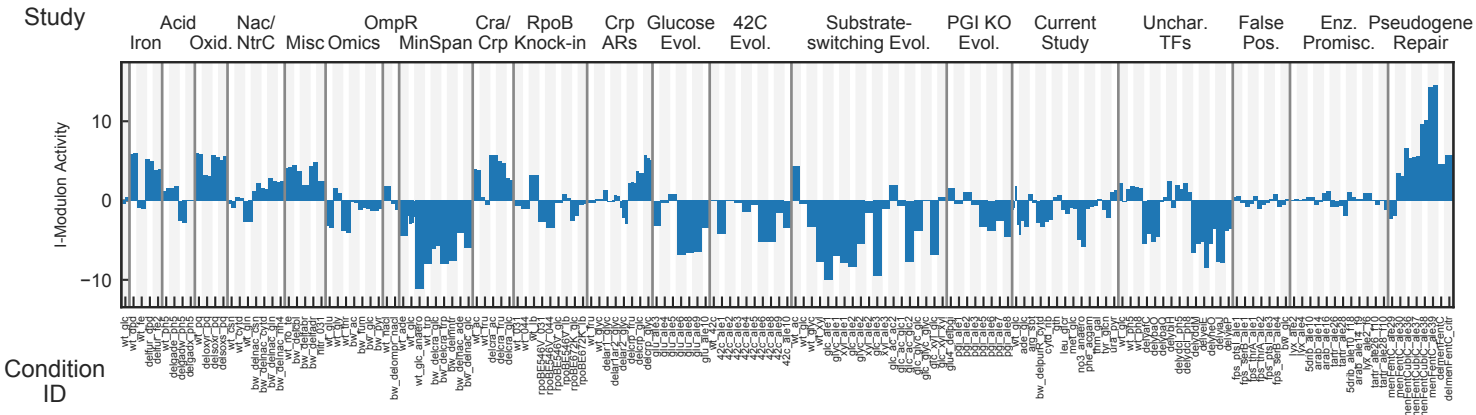


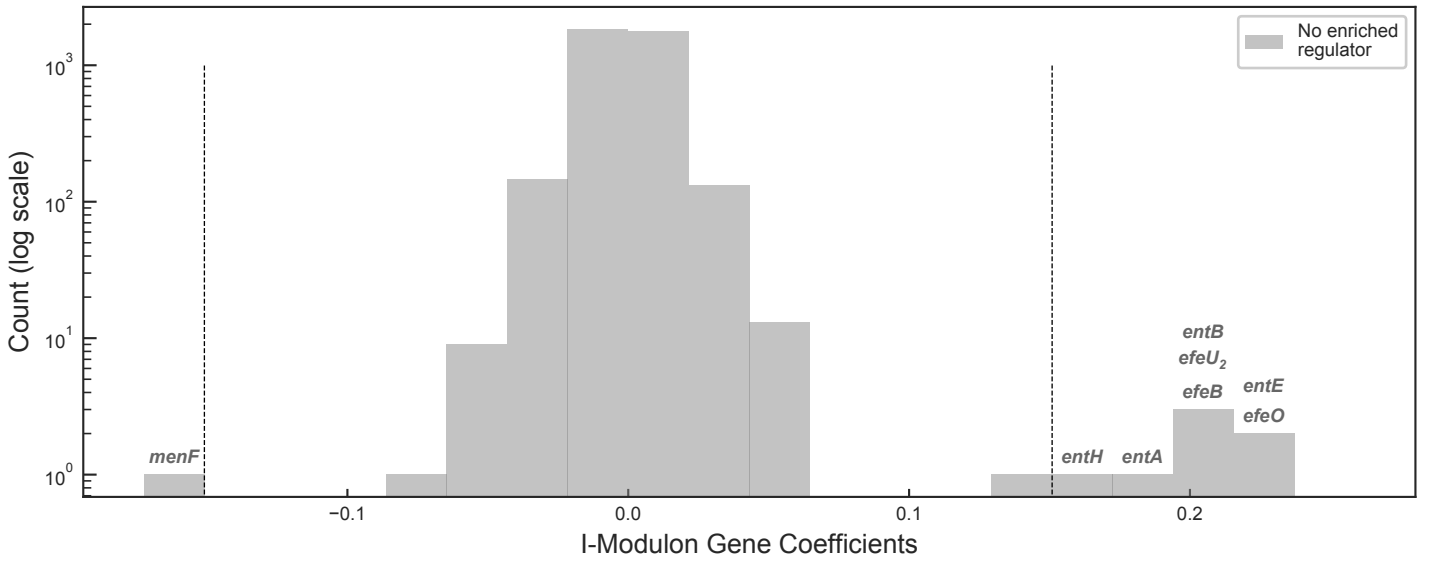


efeU – repair I-Modulon

Biological Function: Accounts for repair and expression of efeU operon

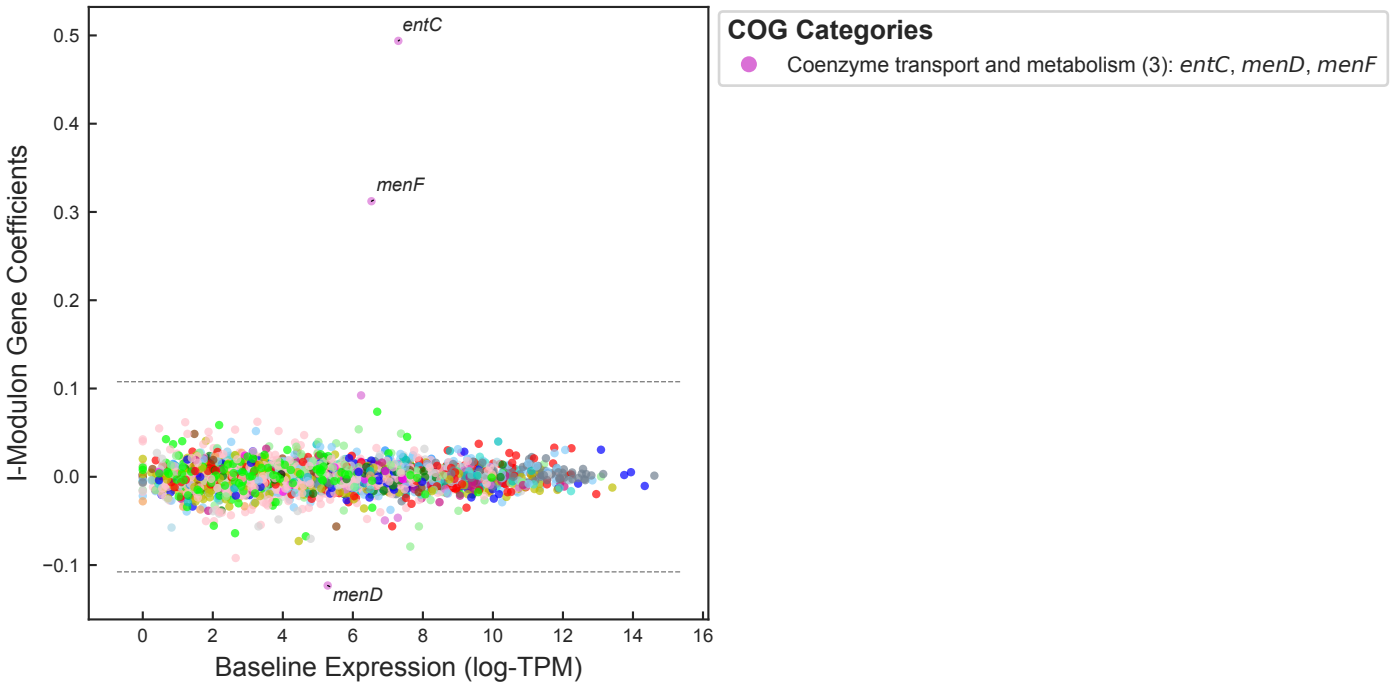


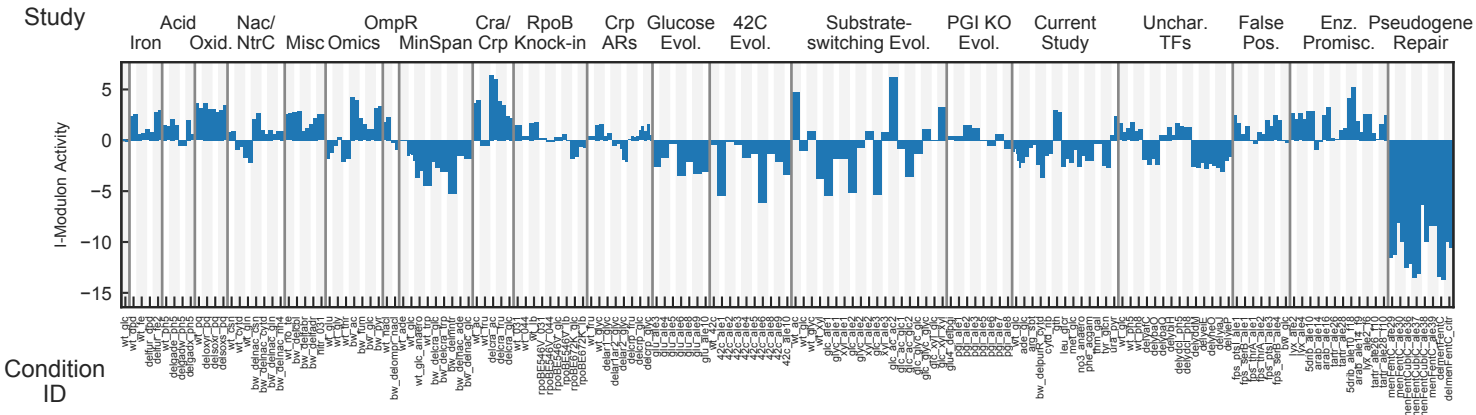


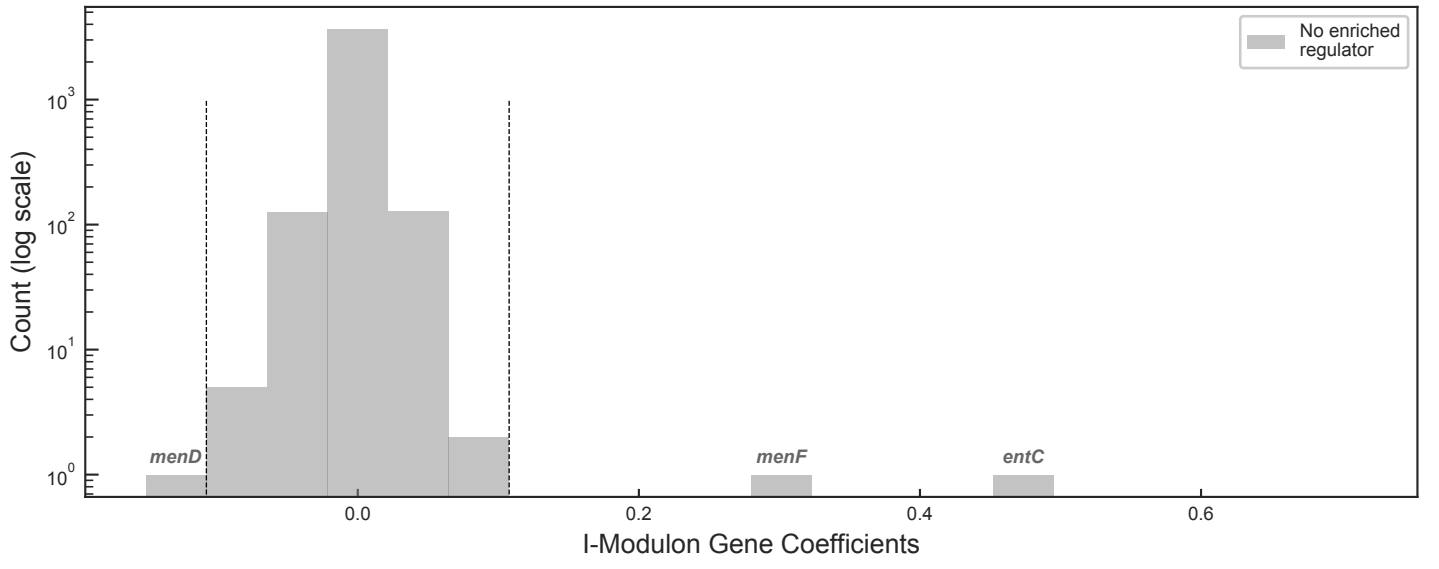


entC − menF − KO I-Modulon

Biological Function: Accounts for entC and menF knock-outs

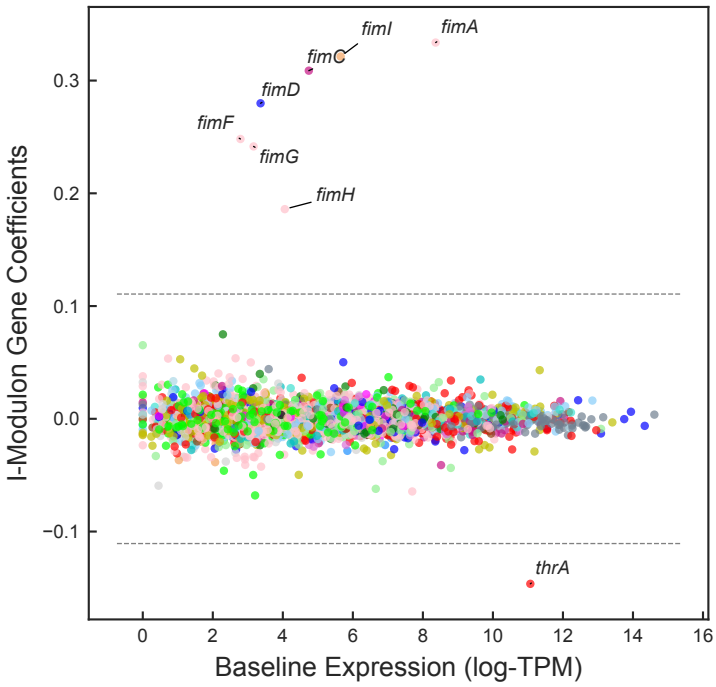






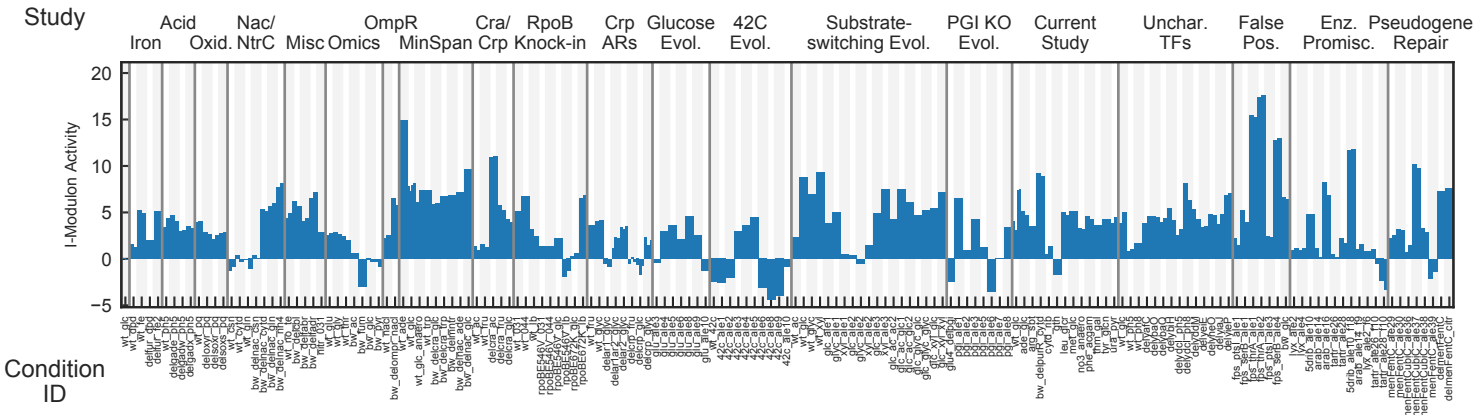
fimbriae I-Modulon

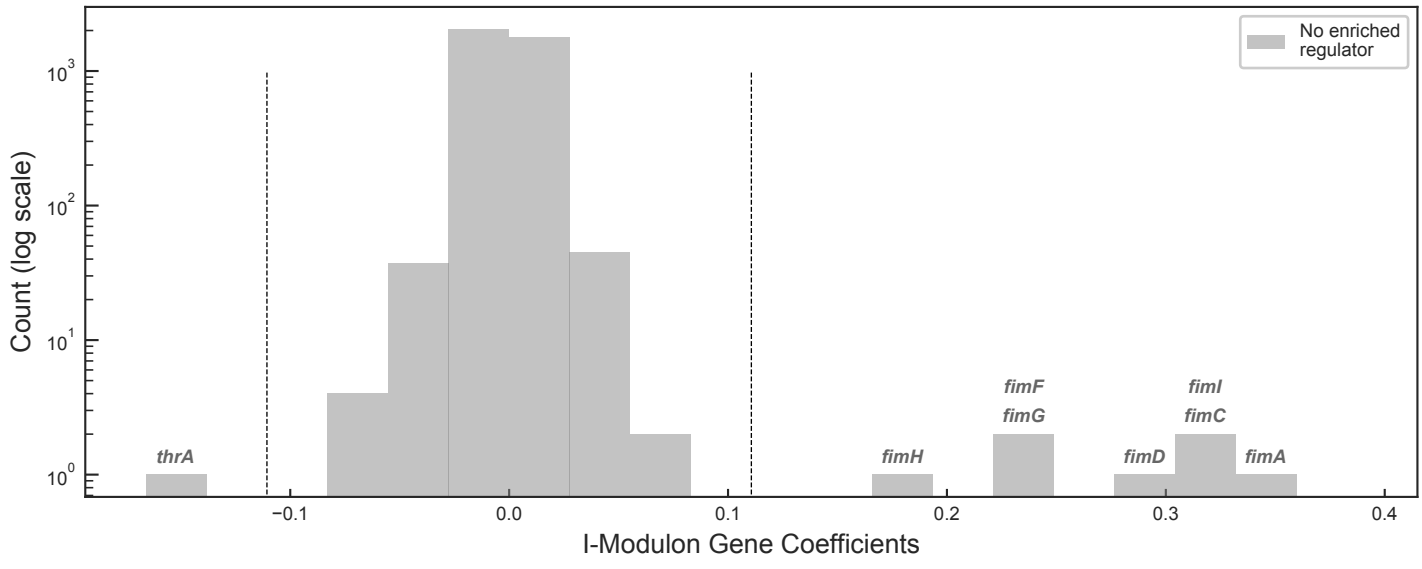
Biological Function: Fimbriae assembly



COG Categories

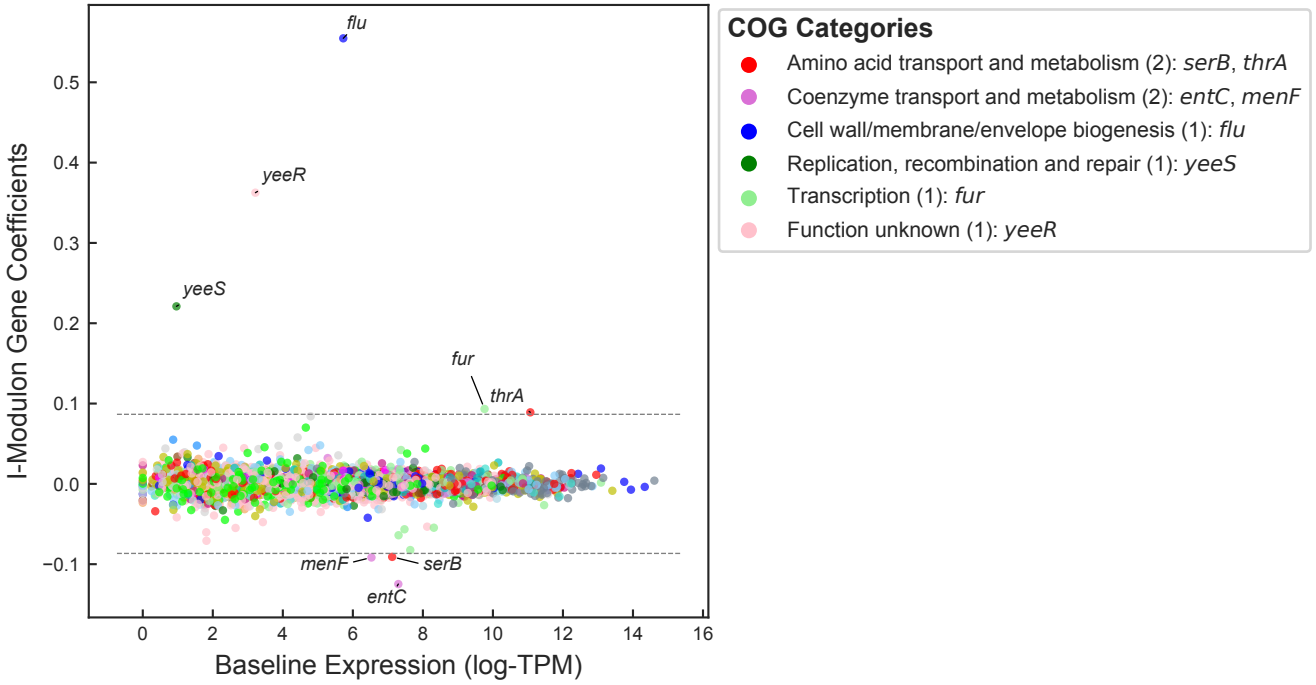
- Amino acid transport and metabolism (1): *thrA*
- Cell motility (1): *fimI*
- Cell wall/membrane/envelope biogenesis (1): *fimD*
- Posttranslational modification, protein turnover, chaperones (1): *fimC*
- Function unknown (4): *fimA*, *fimF*, *fimG*, *fimH*

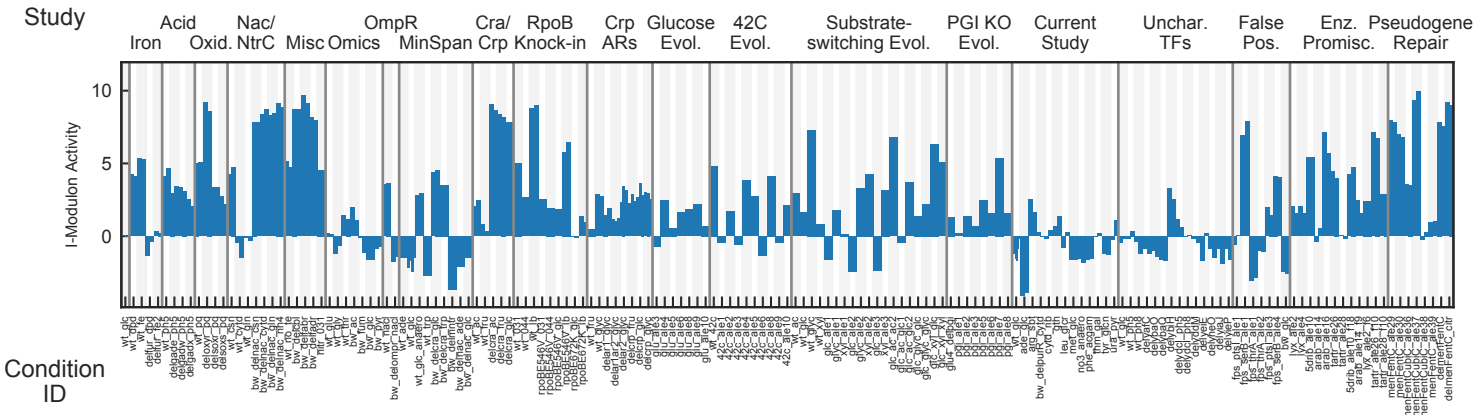


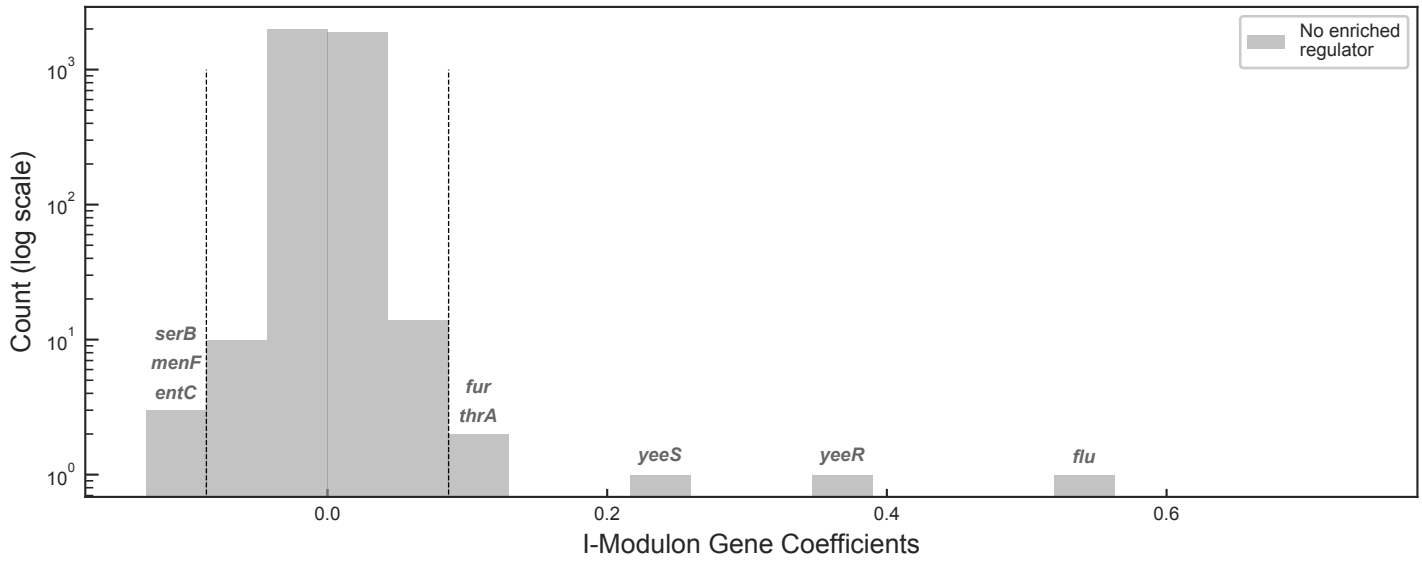


flu – yeeRS I-Modulon

Biological Function: Genes in CP4-44 prophage

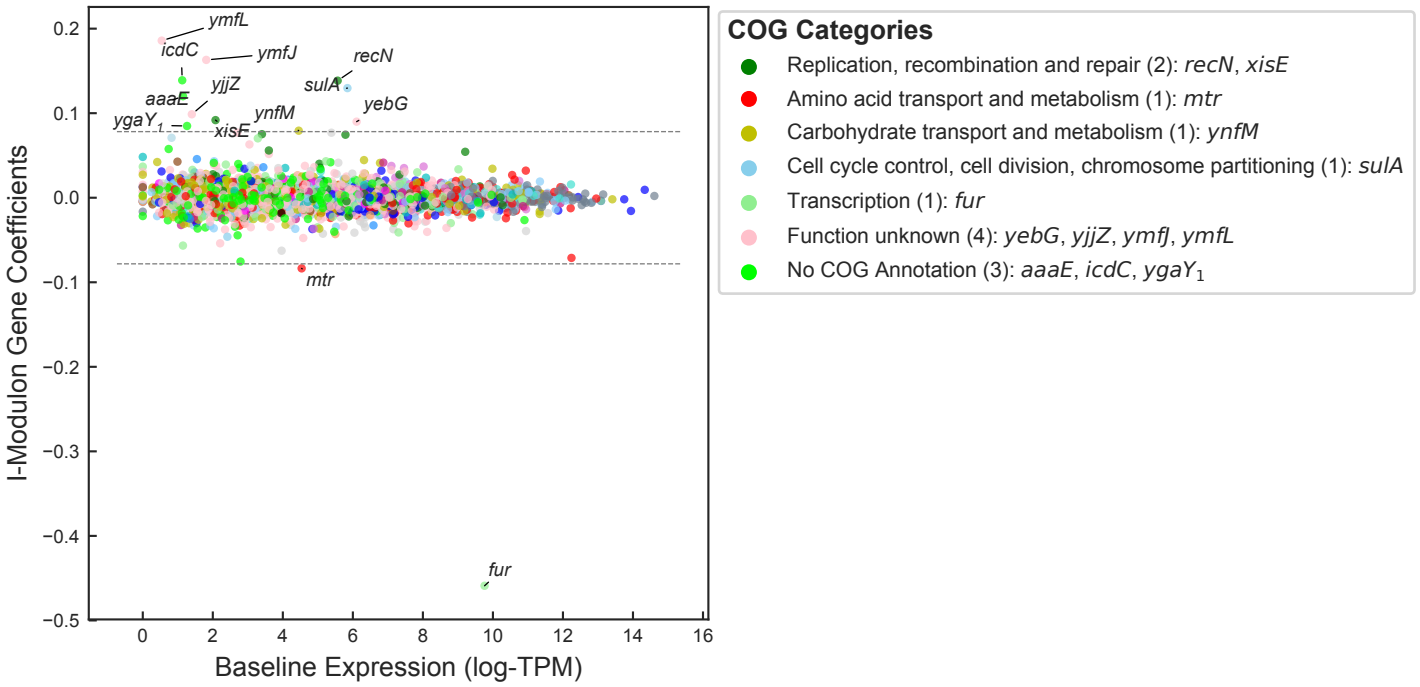


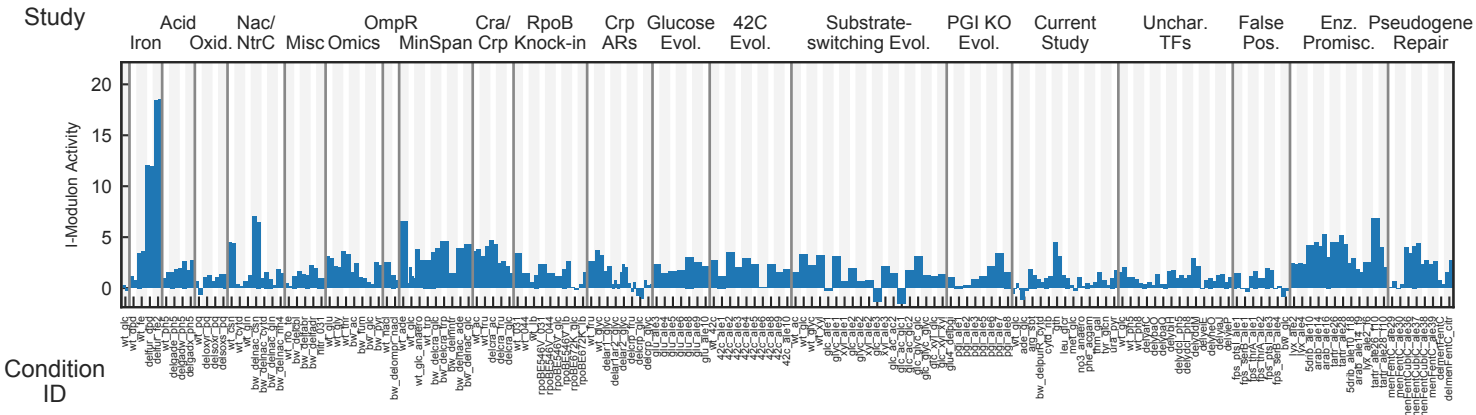


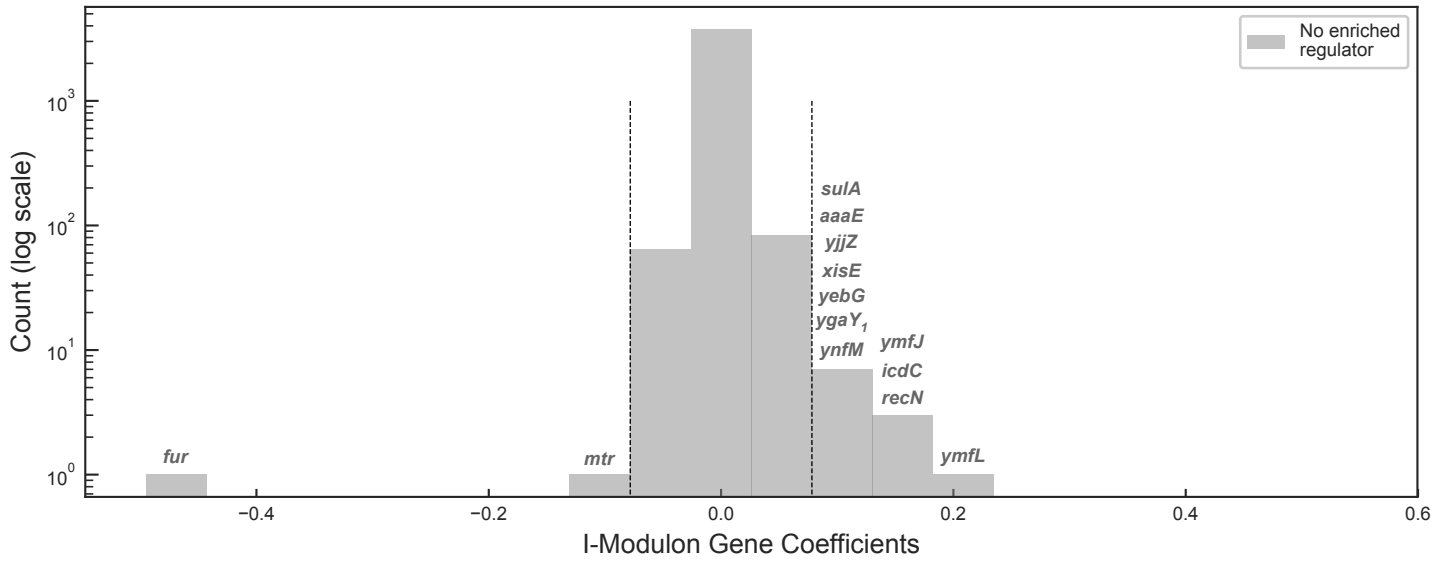


fur – KO I-Modulon

Biological Function: Accounts for fur knock-out

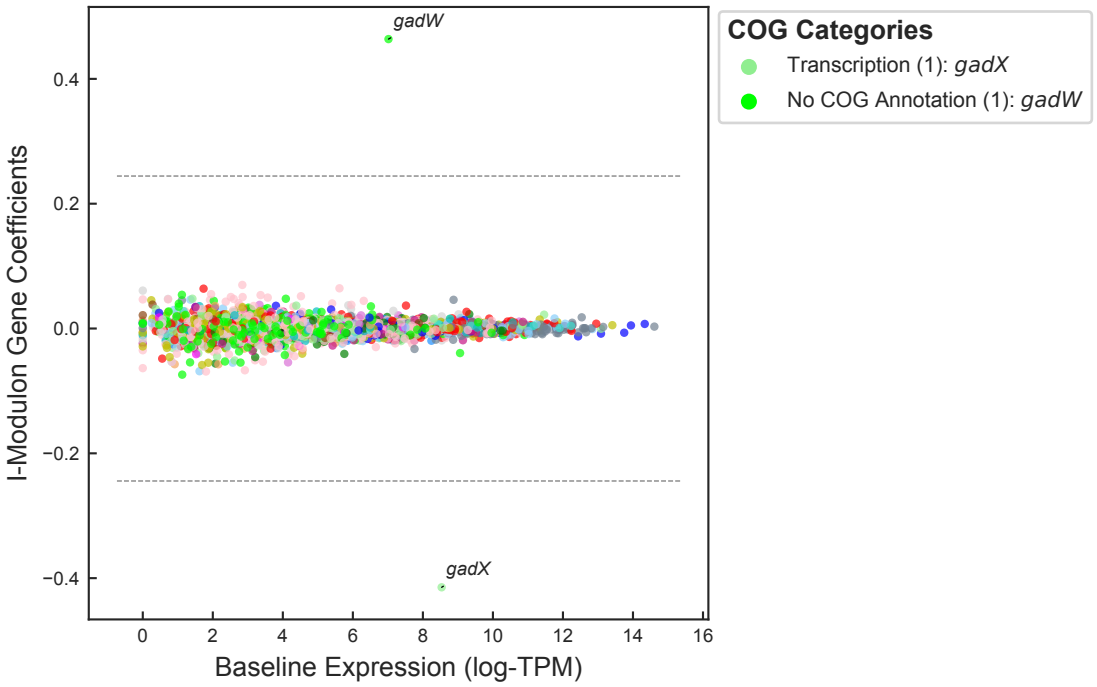


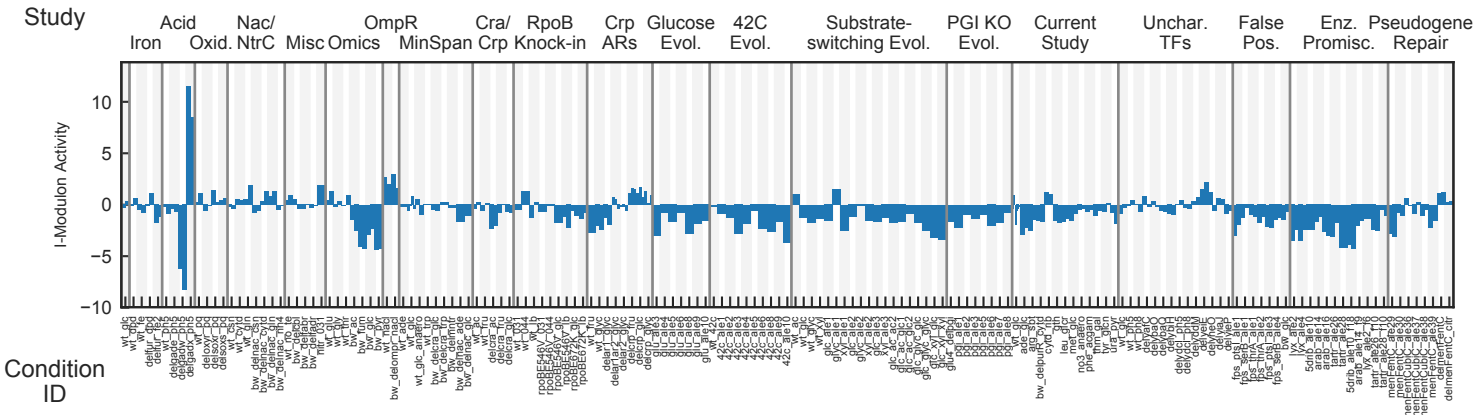


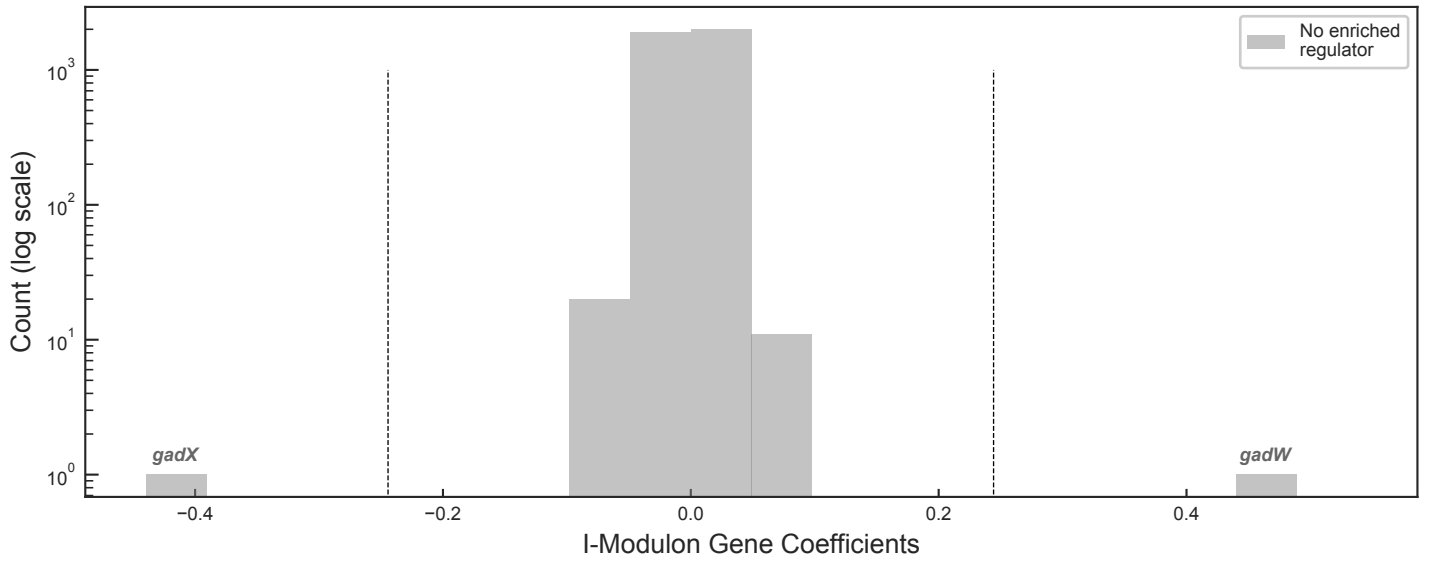


gadWX − KO I-Modulon

Biological Function: Accounts for gadW and gadX knock-outs

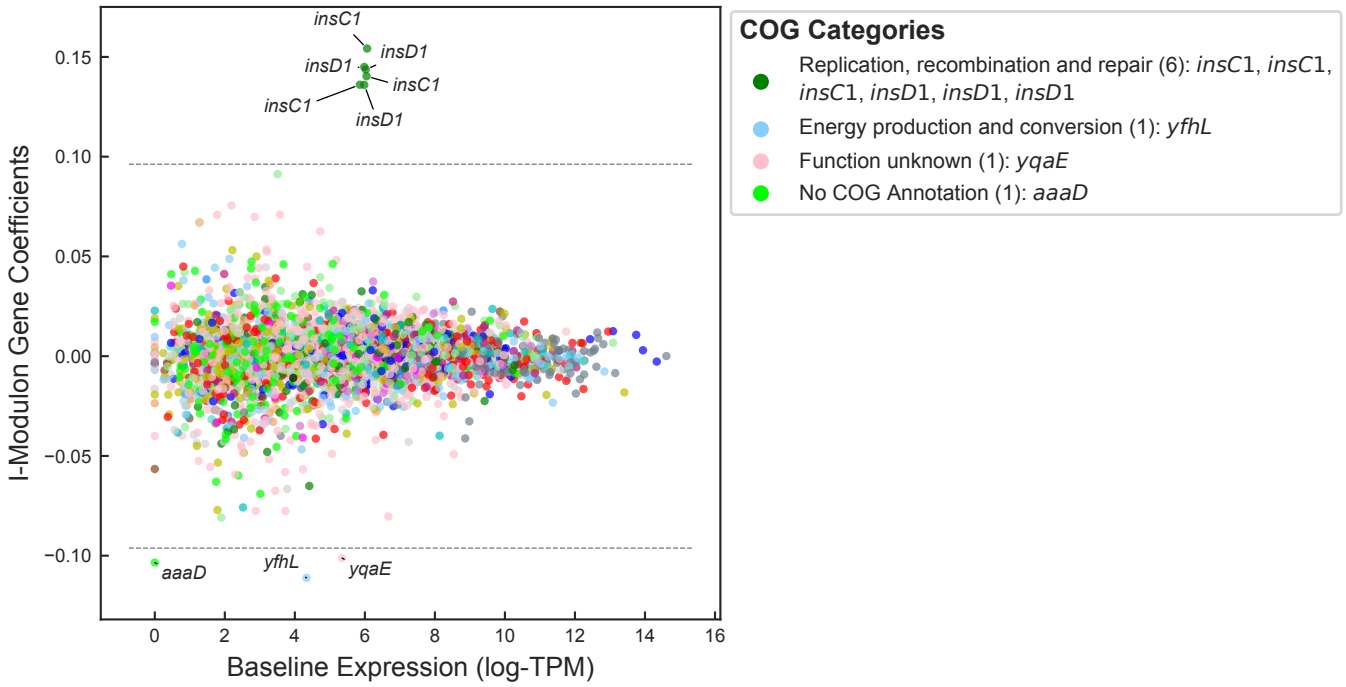


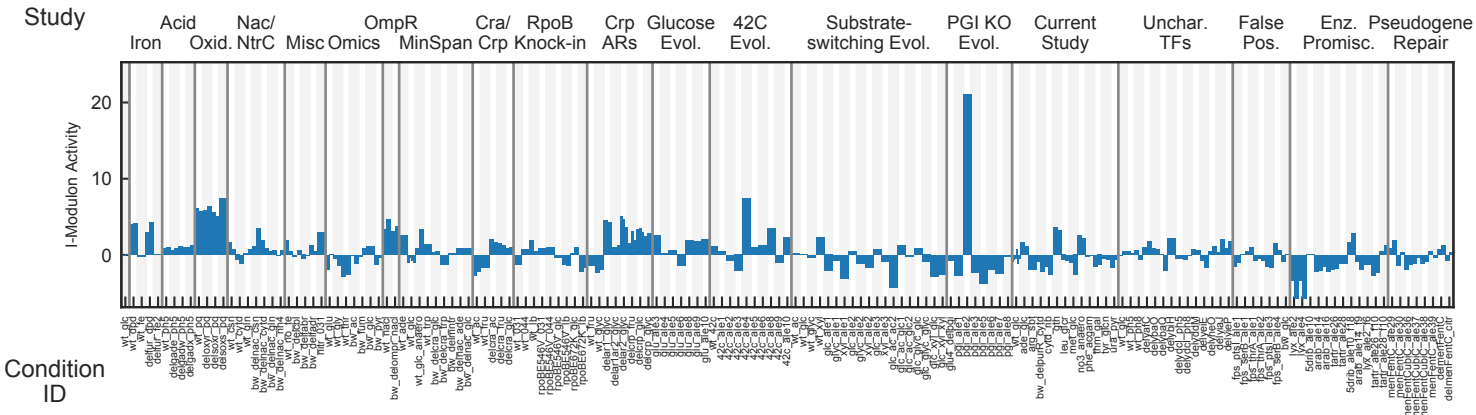


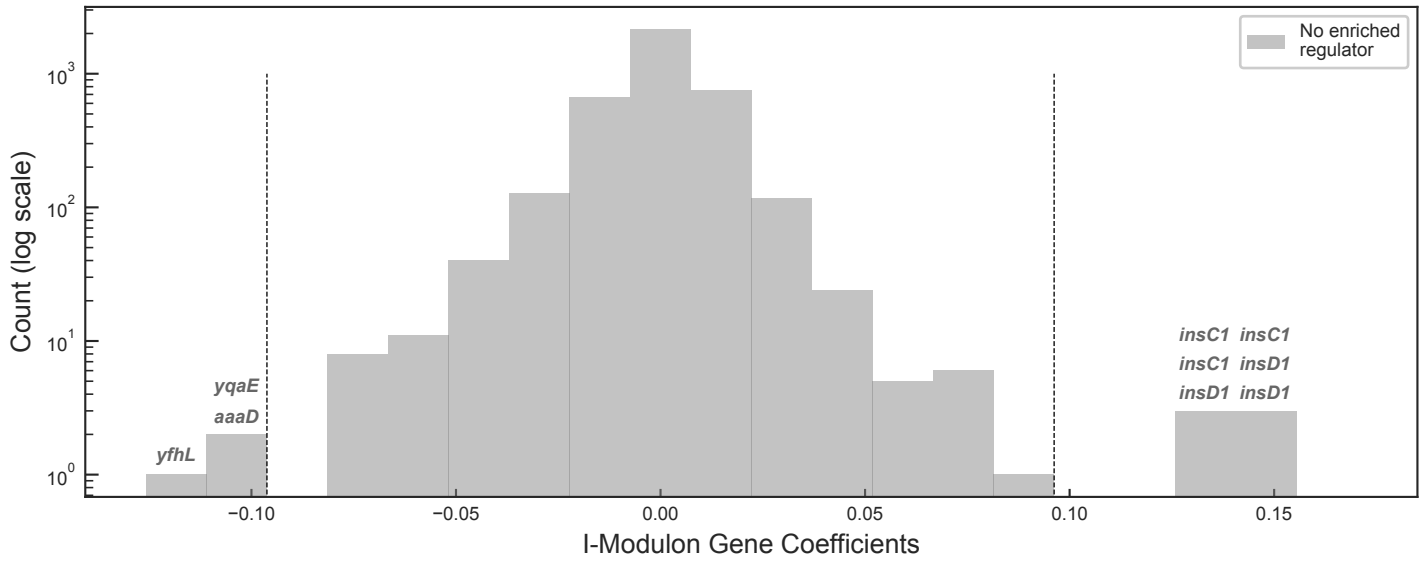


insertion I-Modulon

Biological Function: IS2 insertion element after laboratory evolution

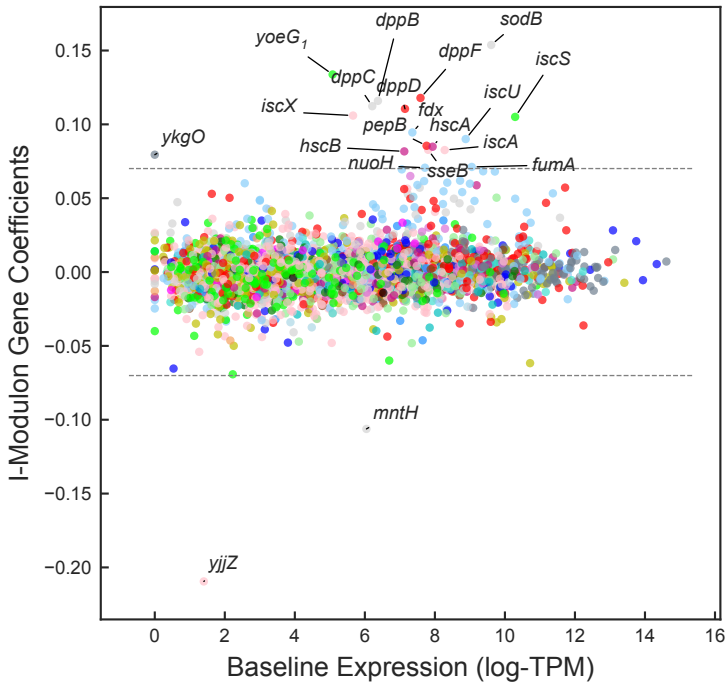






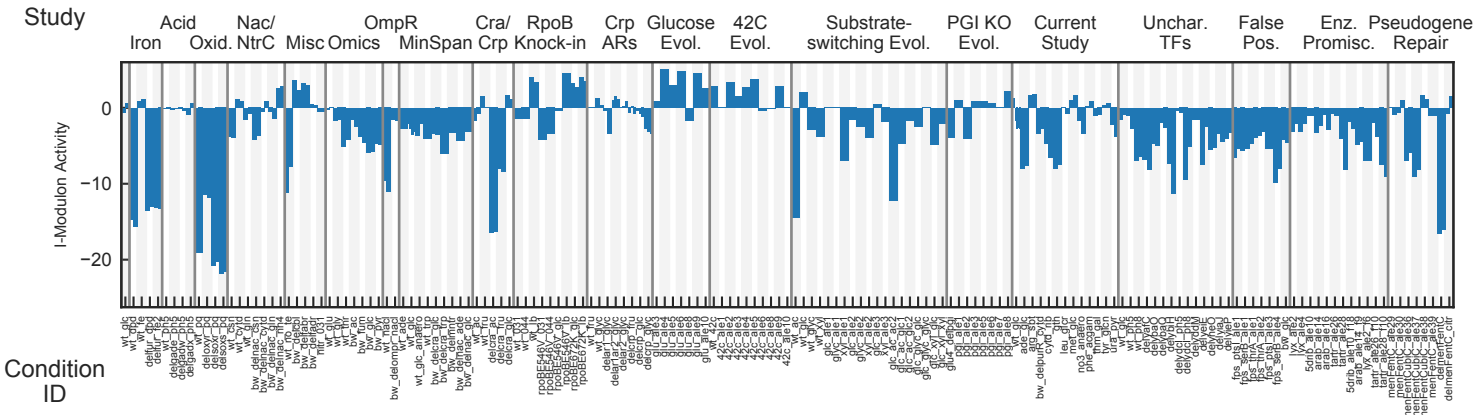
iron − related I-Modulon

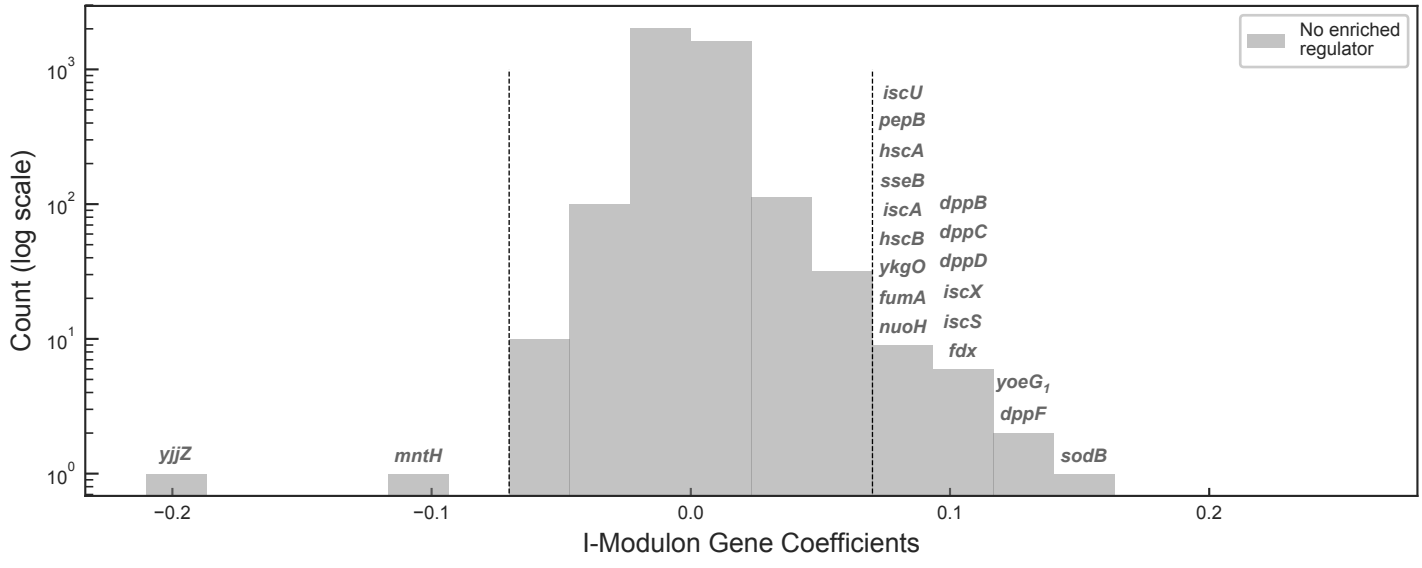
Biological Function: Related to iron metabolism



COG Categories

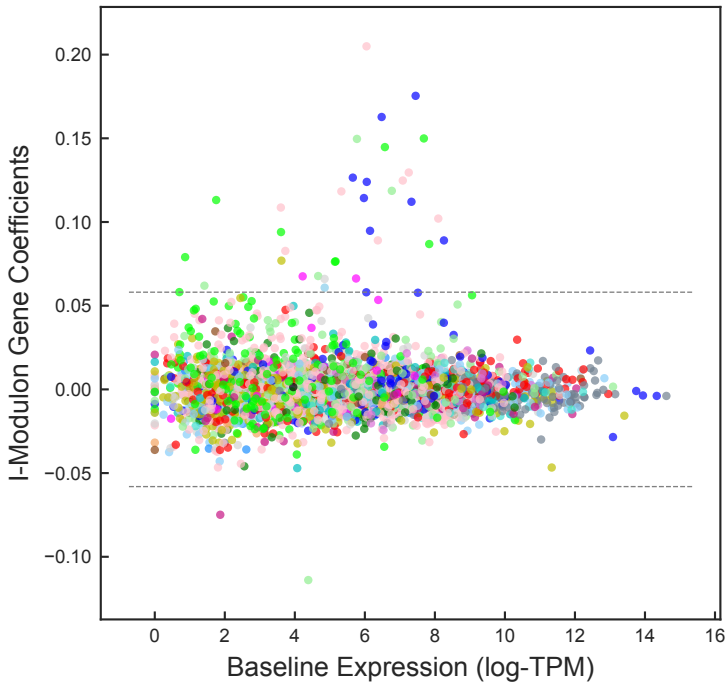
- Energy production and conversion (4): *fdx*, *fumA*, *iscU*, *nuoH*
- Inorganic ion transport and metabolism (4): *dppB*, *dppC*, *mntH*, *sodB*
- Amino acid transport and metabolism (3): *dppD*, *dppF*, *pepB*
- Posttranslational modification, protein turnover, chaperones (2): *hscA*, *hscB*
- Translation, ribosomal structure and biogenesis (1): *ykgO*
- Function unknown (4): *iscA*, *iscX*, *sseB*, *yjjZ*
- No COG Annotation (2): *iscS*, *yoeG*$_1$





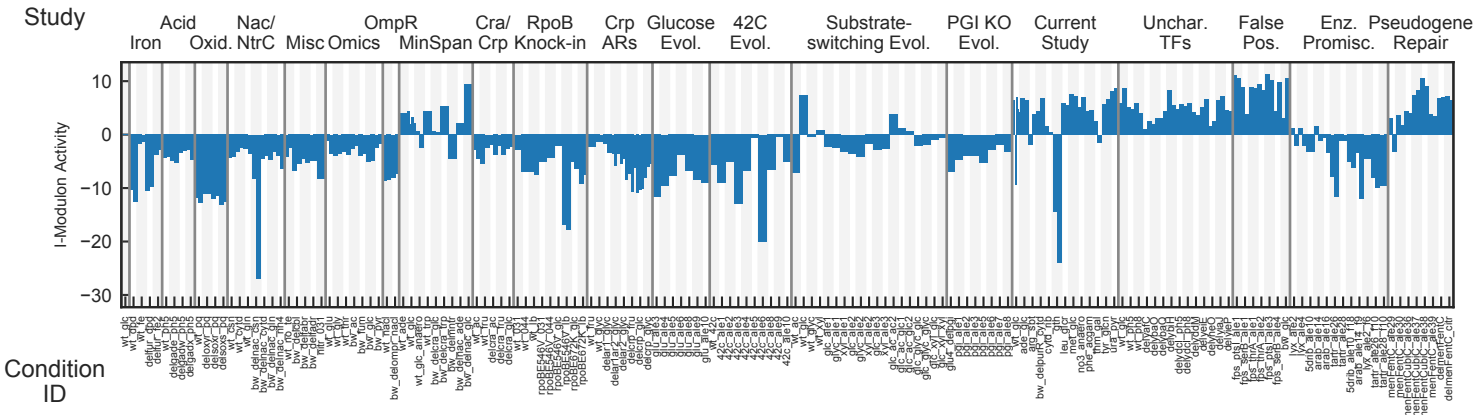
lipopolysaccharide I-Modulon

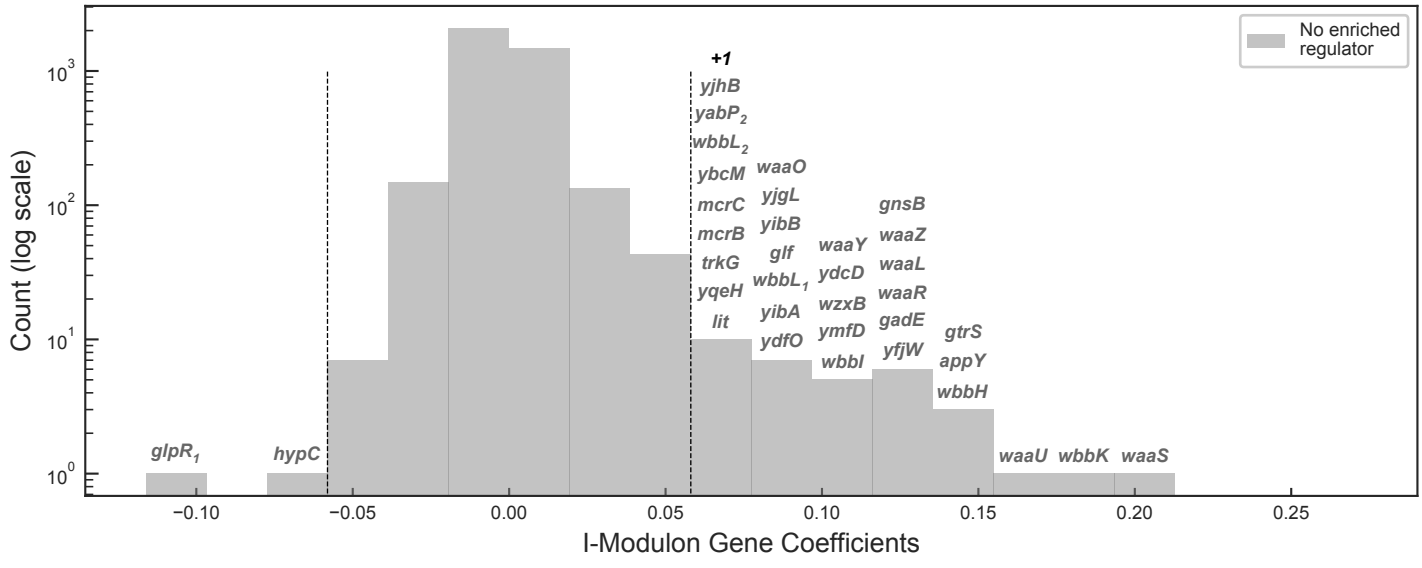
Biological Function: Lipopolysaccharide biosynthesis



COG Categories

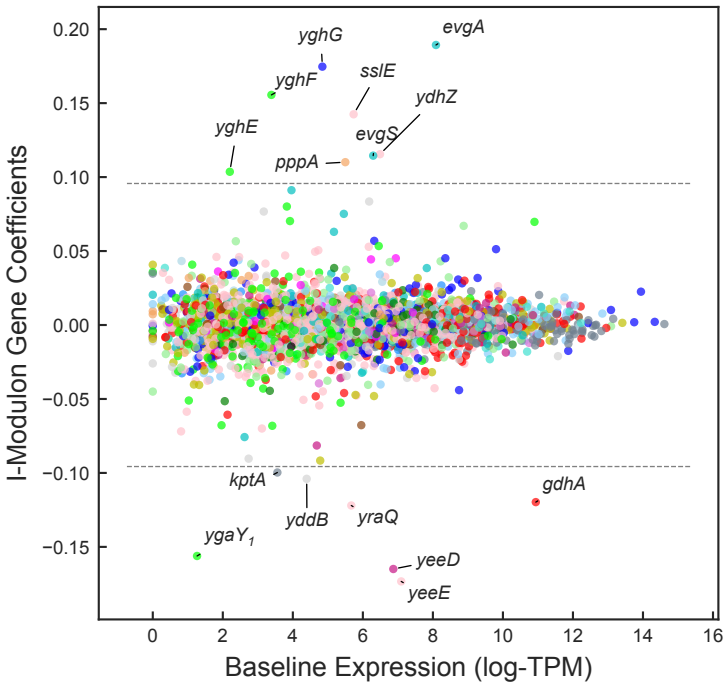
- Cell wall/membrane/envelope biogenesis (8): *glf*, *waaO*, *waaR*, *waaU*, *waaY*, *waaZ*, *wbbK*, *wzxB*
- Transcription (5): *appY*, *gadE*, *glpR*$_1$, *ybcM*, *yqeH*
- Defense mechanisms (2): *mcrB*, *mcrC*
- Carbohydrate transport and metabolism (1): *yjhB*
- Cell cycle control, cell division, chromosome partitioning (1): *lit*
- Other (19): *trkG*, *hypC*, *gtrS*, *wbbH*, *wbbL*$_1$, *wbbL*$_2$, *yabP*$_2$, *ydcD*, *ydfO*, *yjbI*$_3$, *yjgL*, *gnsB*, *waaL*, *waaS*, *wbbI*, *yfjW*, *yibA*, *yibB*, *ymfD*





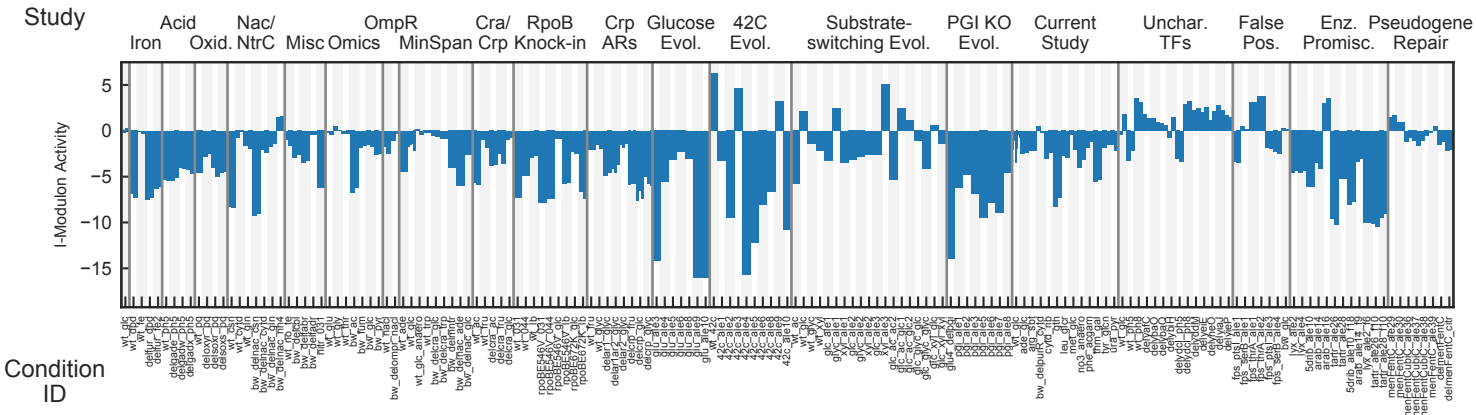
membrane I-Modulon

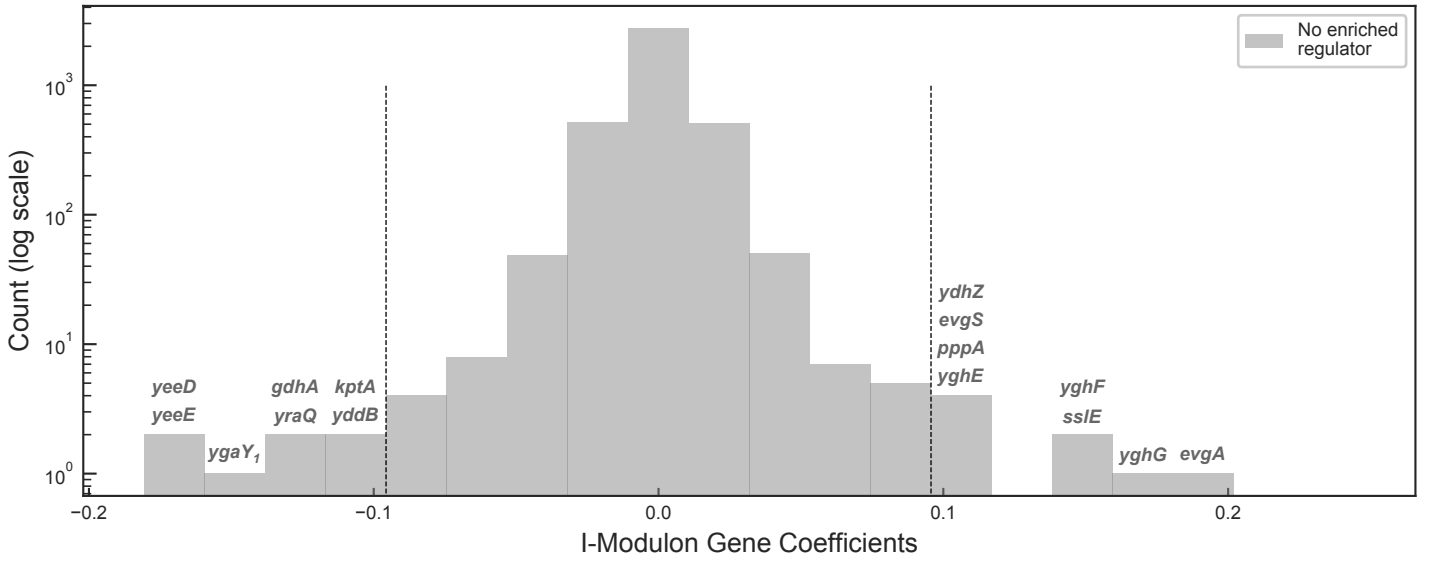
Biological Function: Enriched in membrane-bound proteins



COG Categories

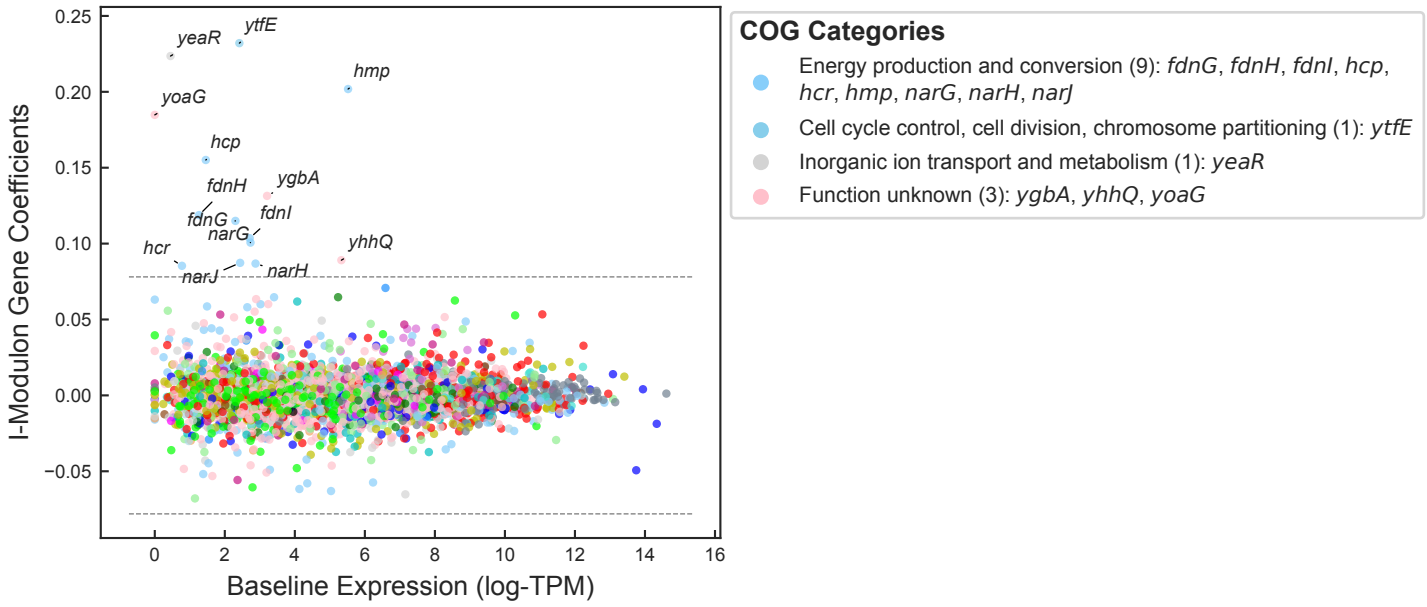
- Signal transduction mechanisms (2): *evgA*, *evgS*
- Amino acid transport and metabolism (1): *gdhA*
- Cell motility (1): *pppA*
- Cell wall/membrane/envelope biogenesis (1): *yghG*
- Inorganic ion transport and metabolism (1): *yddB*
- Posttranslational modification, protein turnover, chaperones (1): *yeeD*
- Translation, ribosomal structure and biogenesis (1): *kptA*
- Function unknown (4): *sslE*, *ydhZ*, *yeeE*, *yraQ*
- No COG Annotation (3): $ygaY_1$, *yghE*, *yghF*

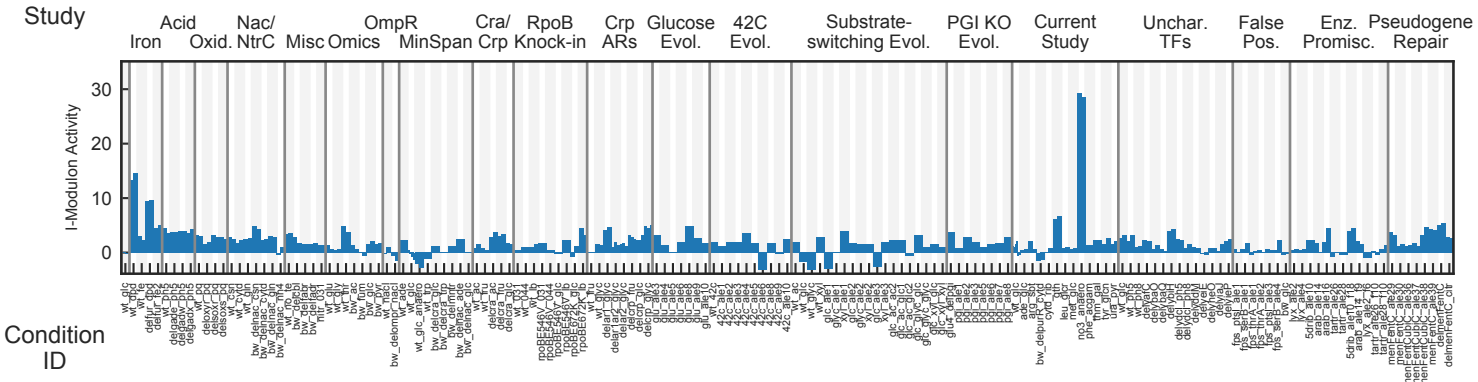


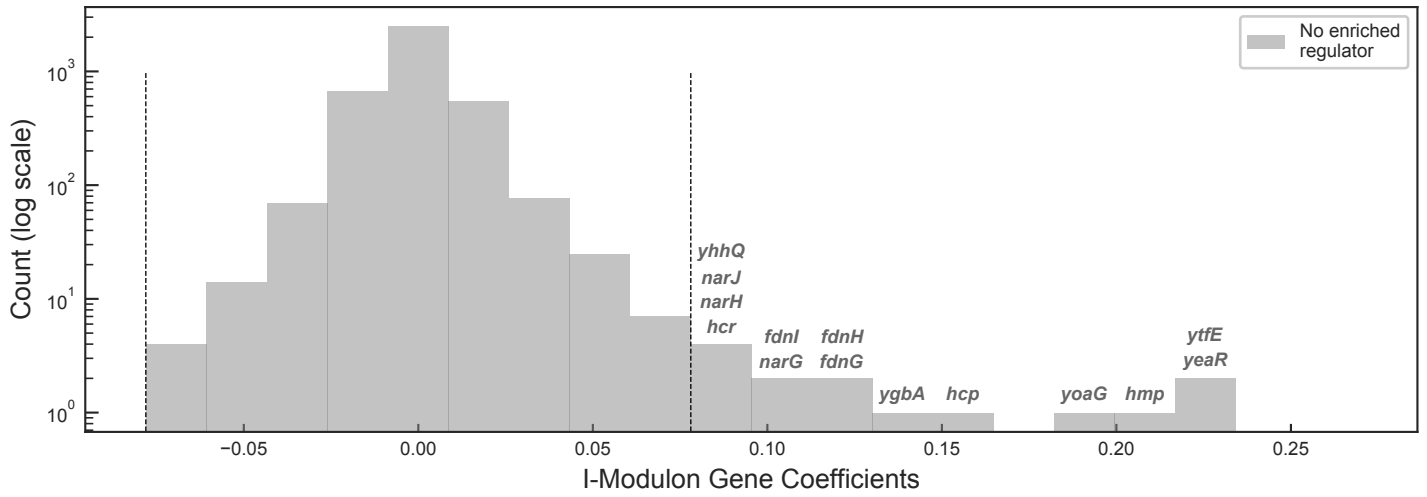


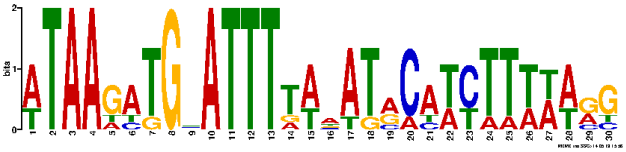
nitrate − related I-Modulon

Biological Function: Nitric oxide response







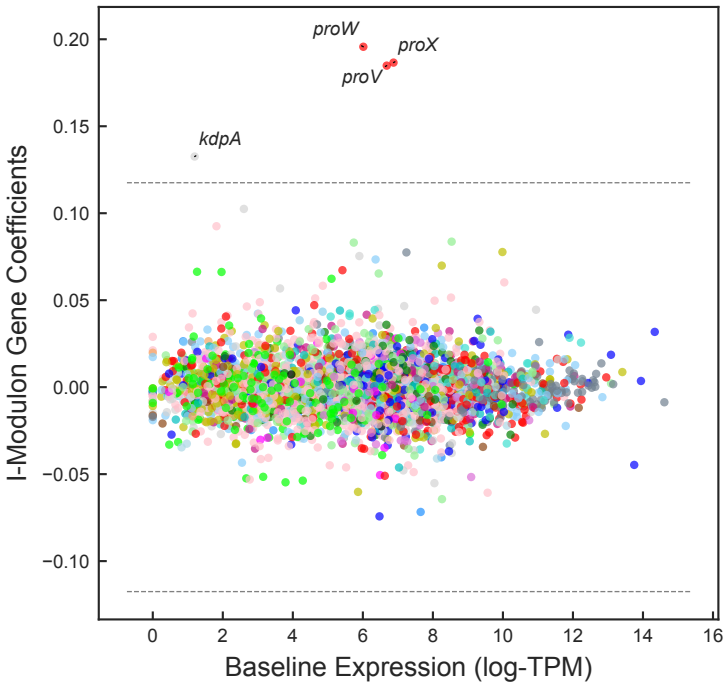


Motif E-value: 5.30e-05

Operons with Upstream Motif: 75%

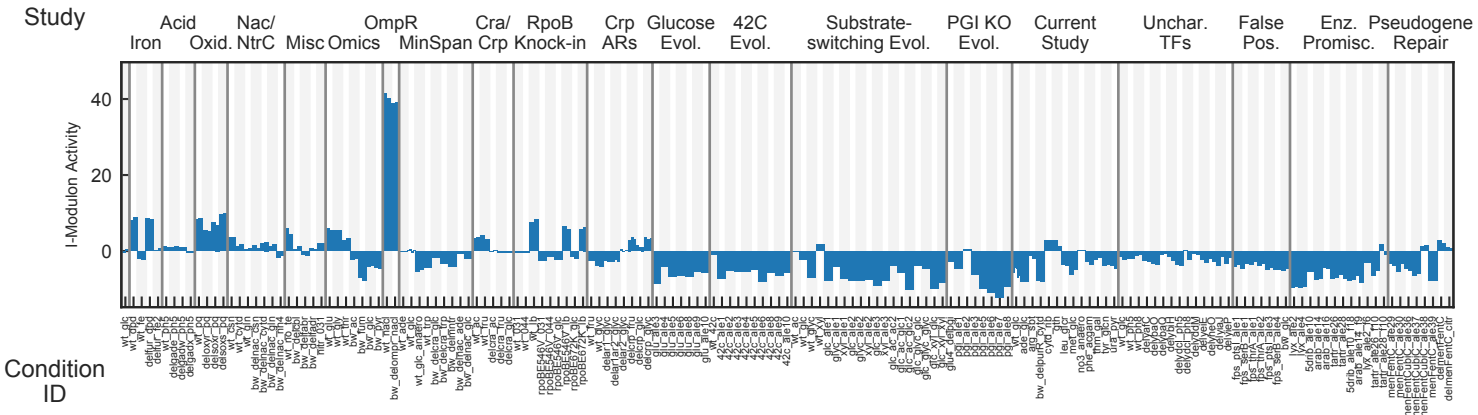
proVWX I-Modulon

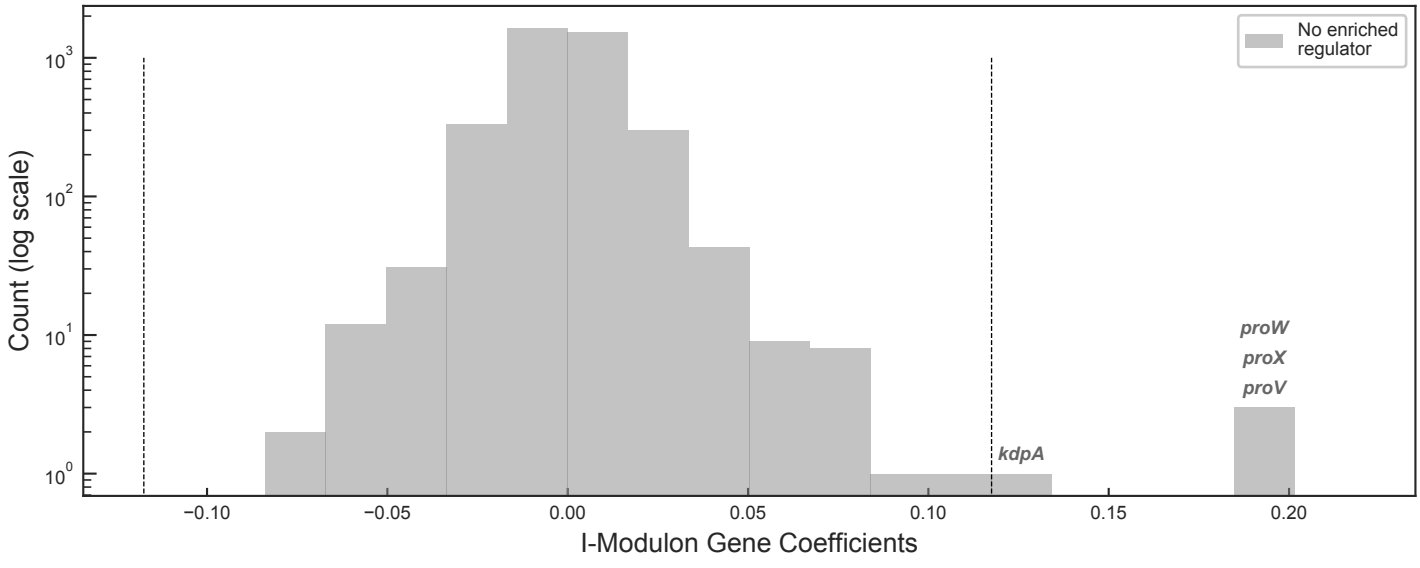
Biological Function: Glycine betaine transport



COG Categories

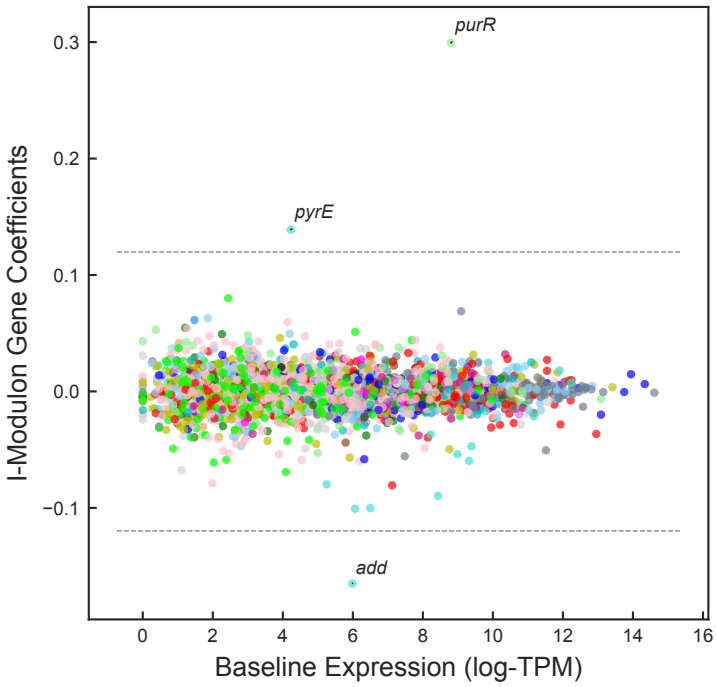
- Amino acid transport and metabolism (3): *proV*, *proW*, *proX*
- Inorganic ion transport and metabolism (1): *kdpA*

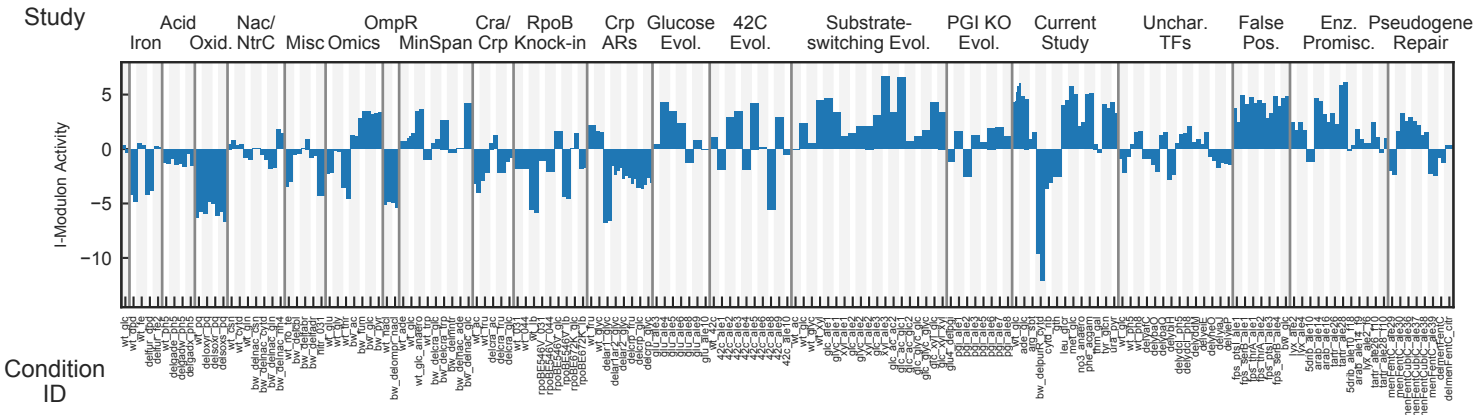


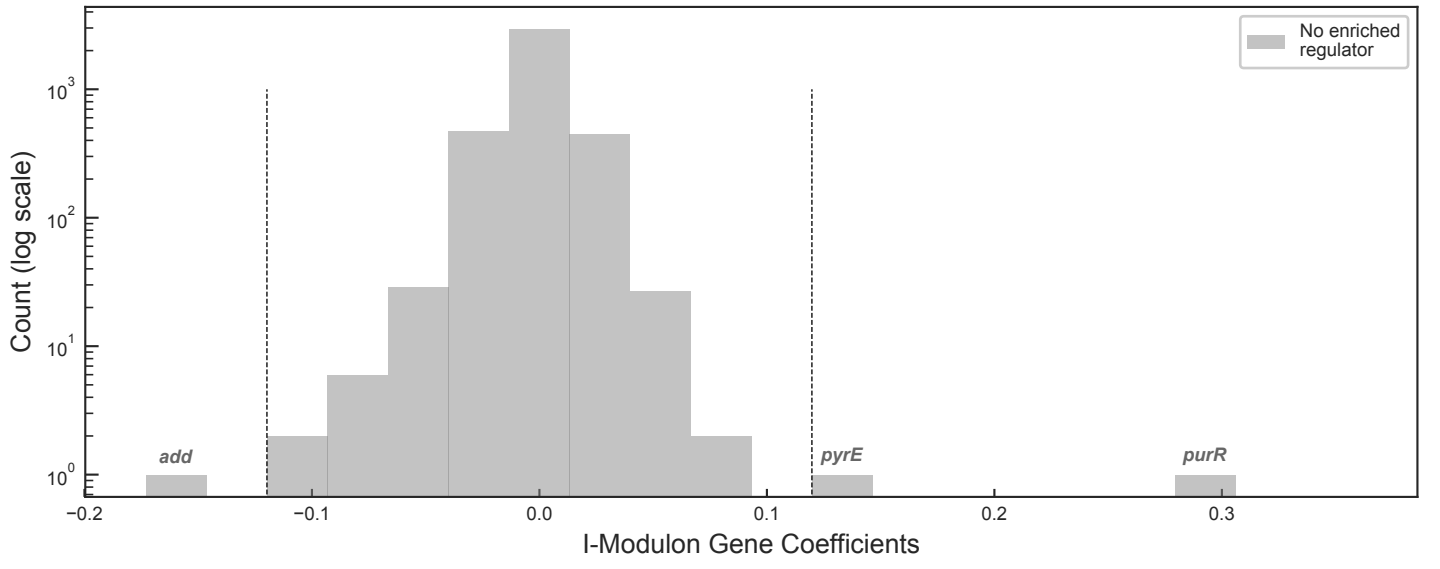


purR − KO I-Modulon

Biological Function: Accounts for purR knock-out

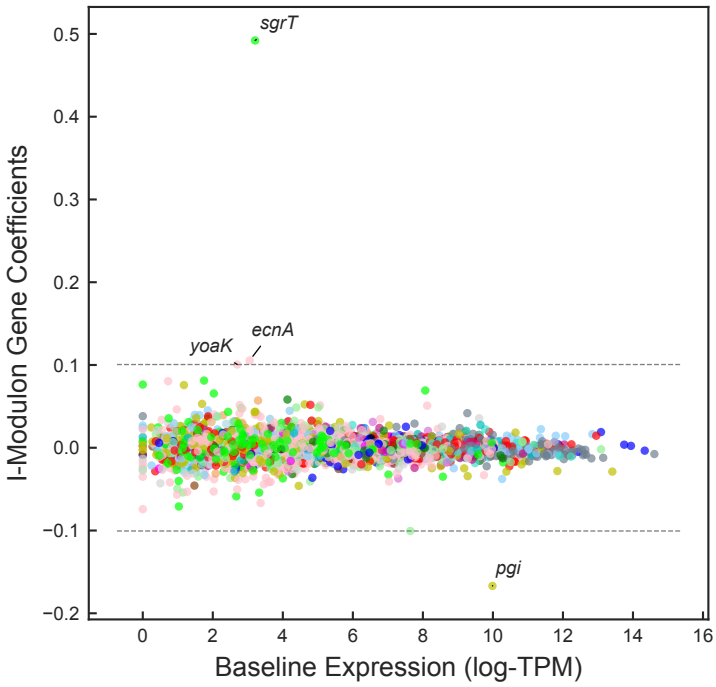


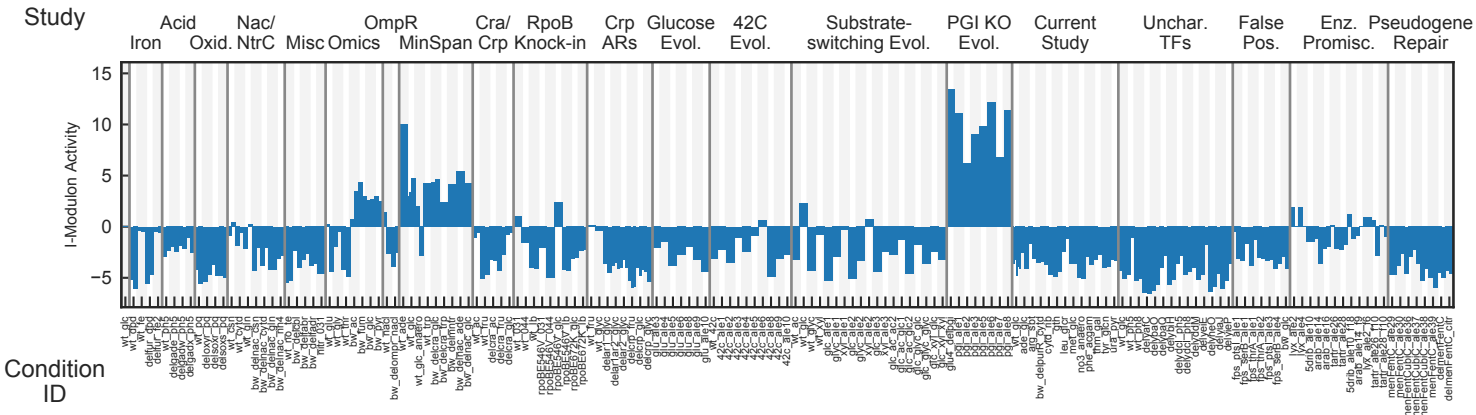


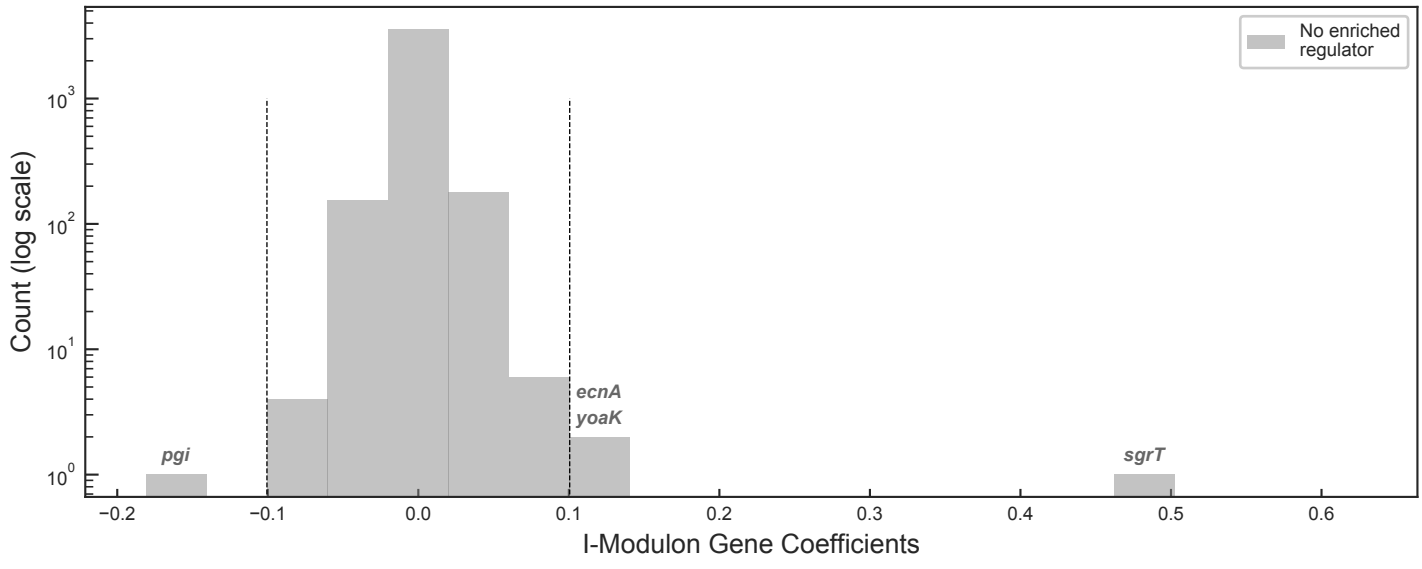


sgrT I-Modulon

Biological Function: Contains single dominating gene: sgrT

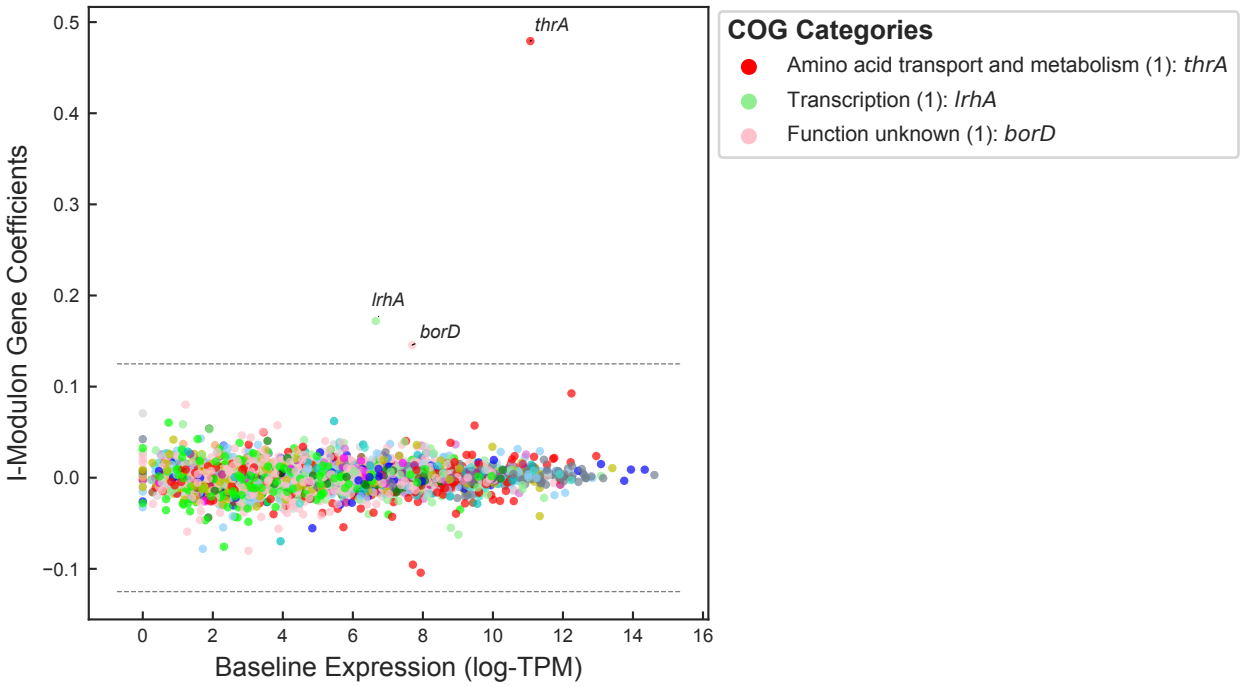


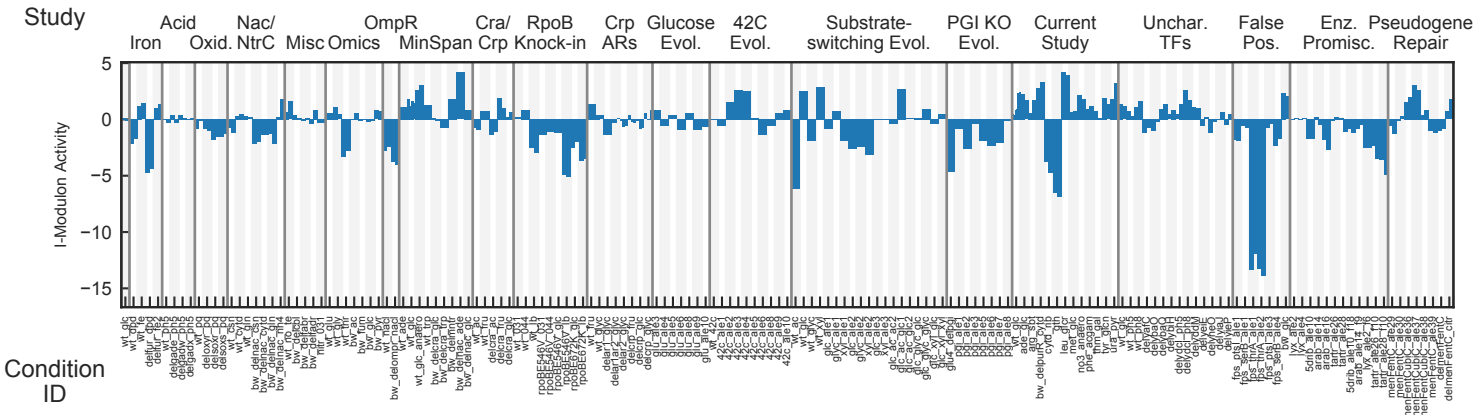


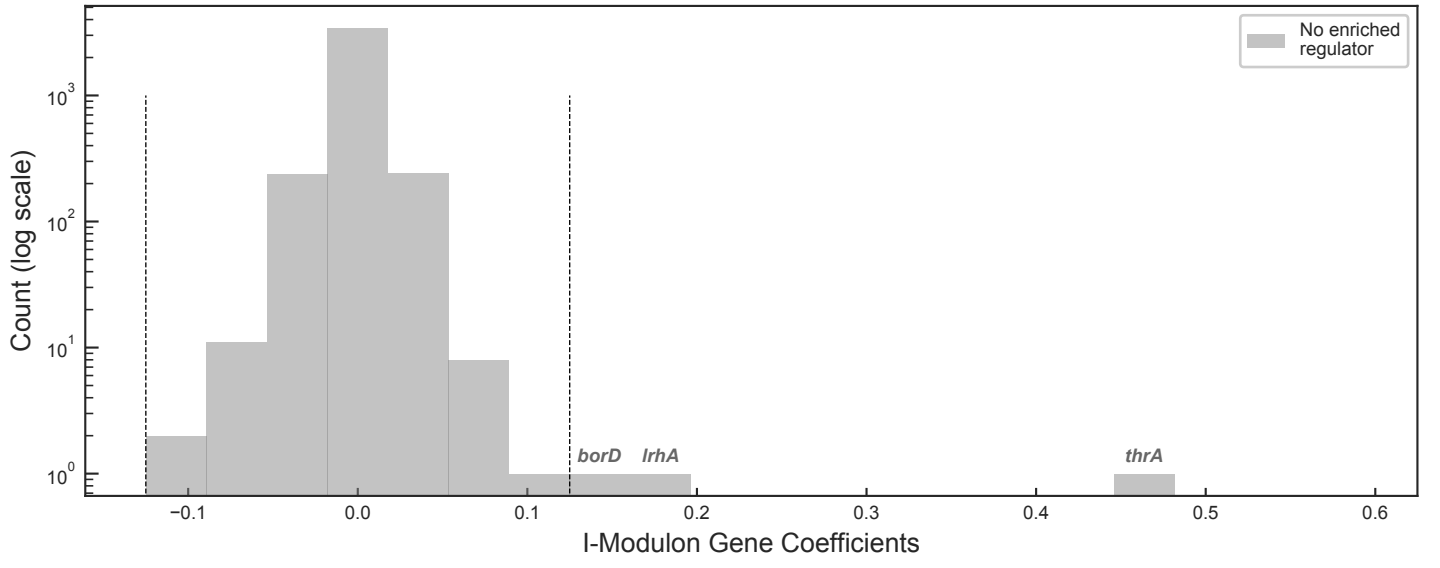


thrA − KO I-Modulon

Biological Function: Accounts for thrA knock-out

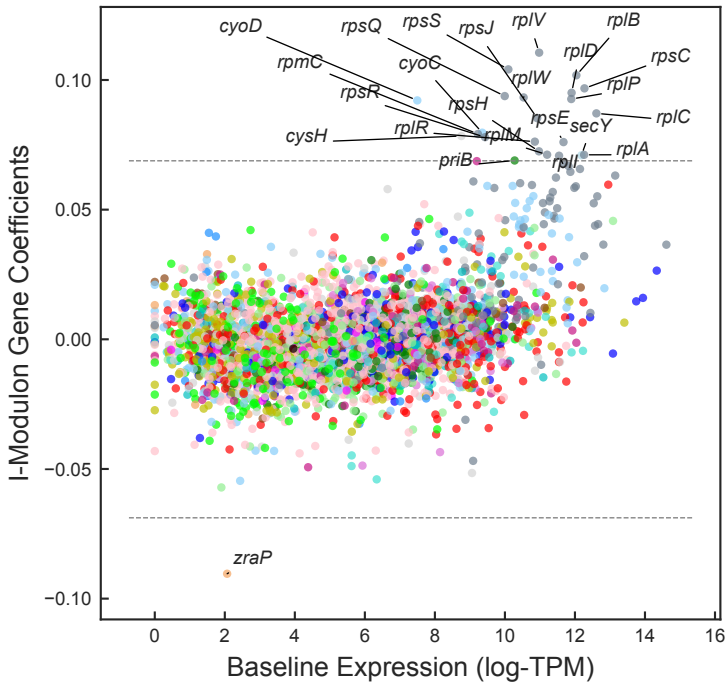






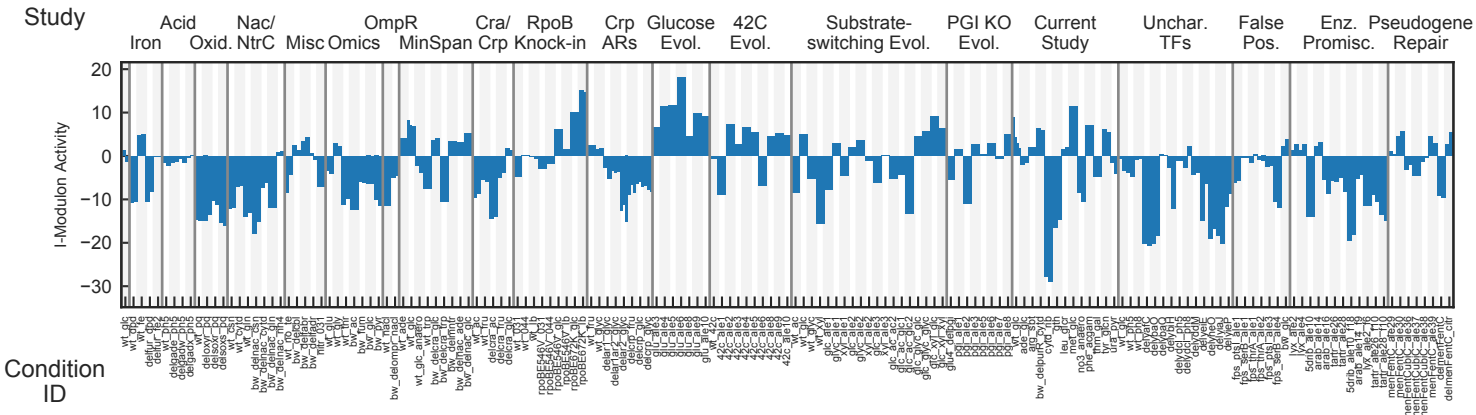
translation I-Modulon

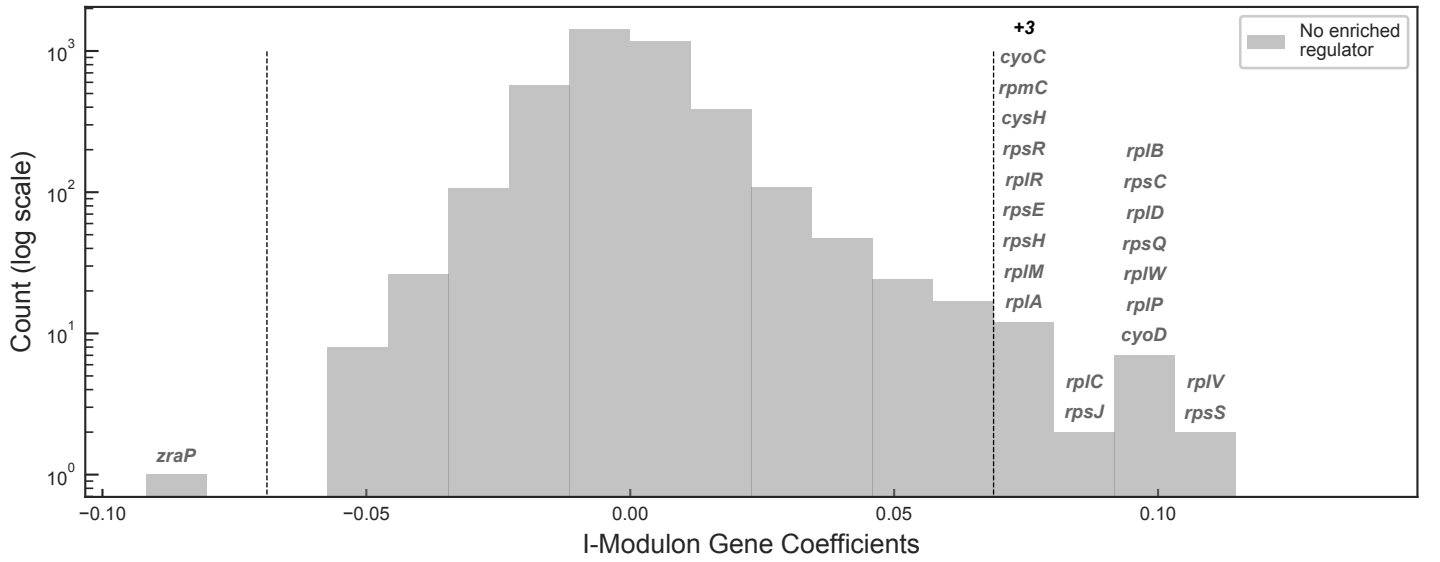
Biological Function: Enriched in translation machinery



COG Categories

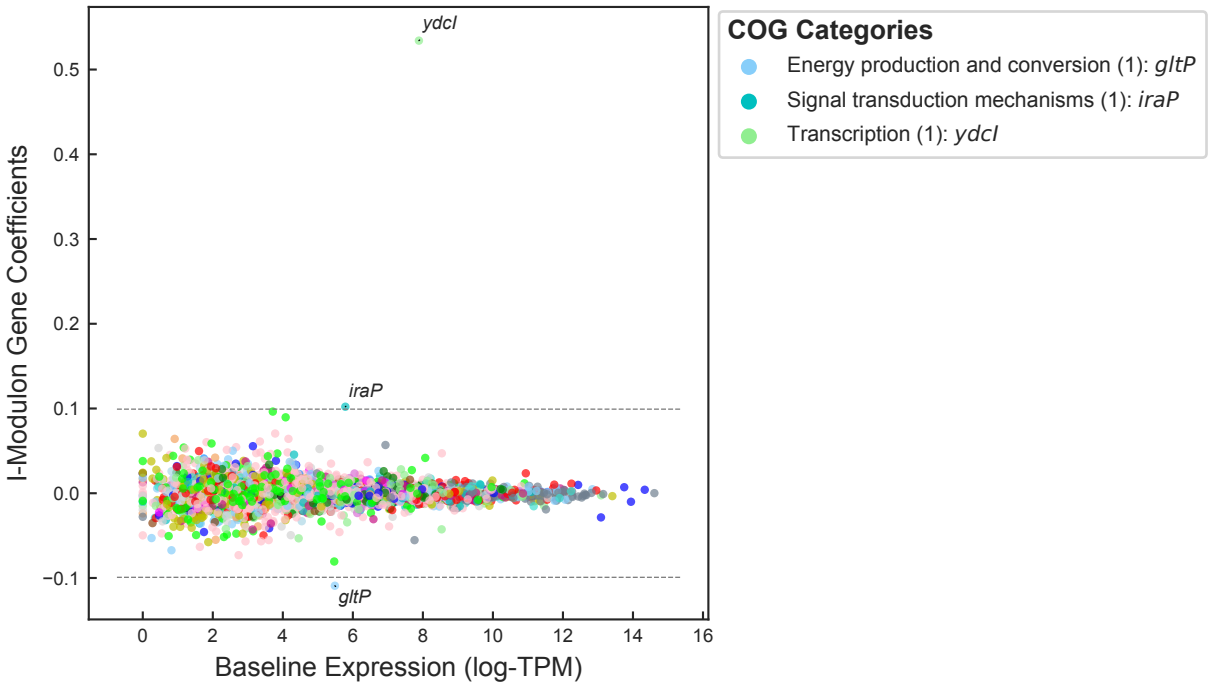
- Translation, ribosomal structure and biogenesis (18): *rplA*, *rplB*, *rplC*, *rplD*, *rplI*, *rplM*, *rplP*, *rplR*, *rplV*, *rplW*, *rpmC*, *rpsC*, *rpsE*, *rpsH*, *rpsJ*, *rpsQ*, *rpsR*, *rpsS*
- Energy production and conversion (2): *cyoC*, *cyoD*
- Cell motility (1): *zraP*
- Inorganic ion transport and metabolism (1): *cysH*
- Intracellular trafficking, secretion, and vesicular transport (1): *secY*
- Replication, recombination and repair (1): *priB*

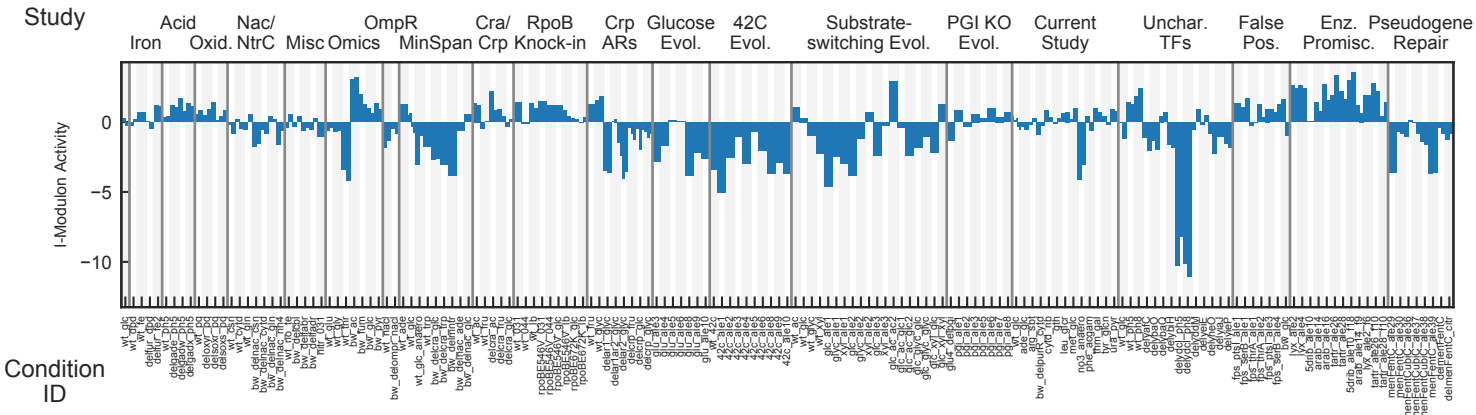


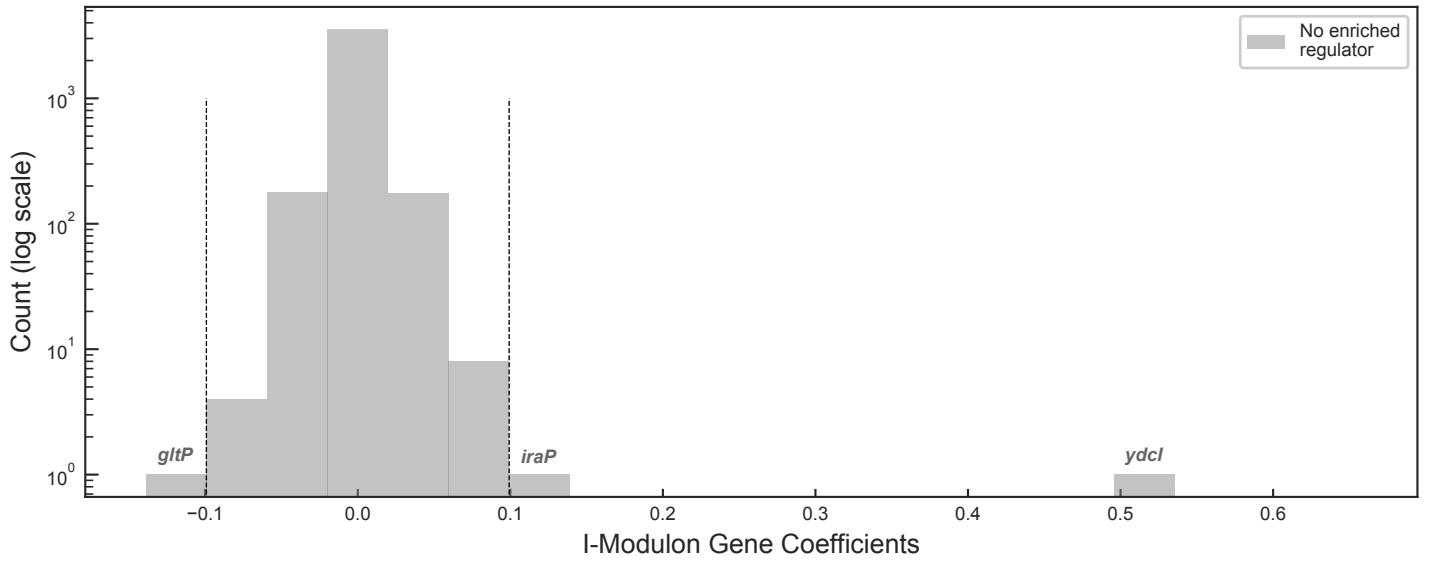


ydcI − KO I-Modulon

Biological Function: Accounts for ydcI knock-out

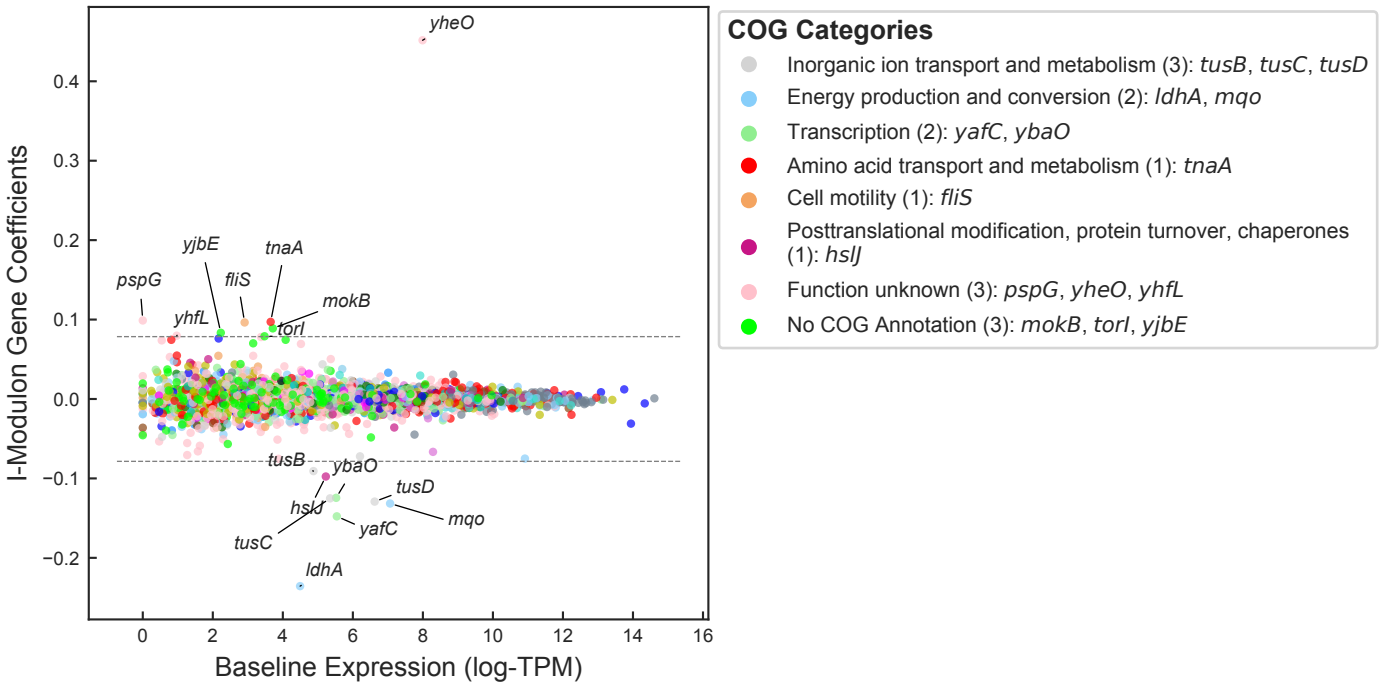


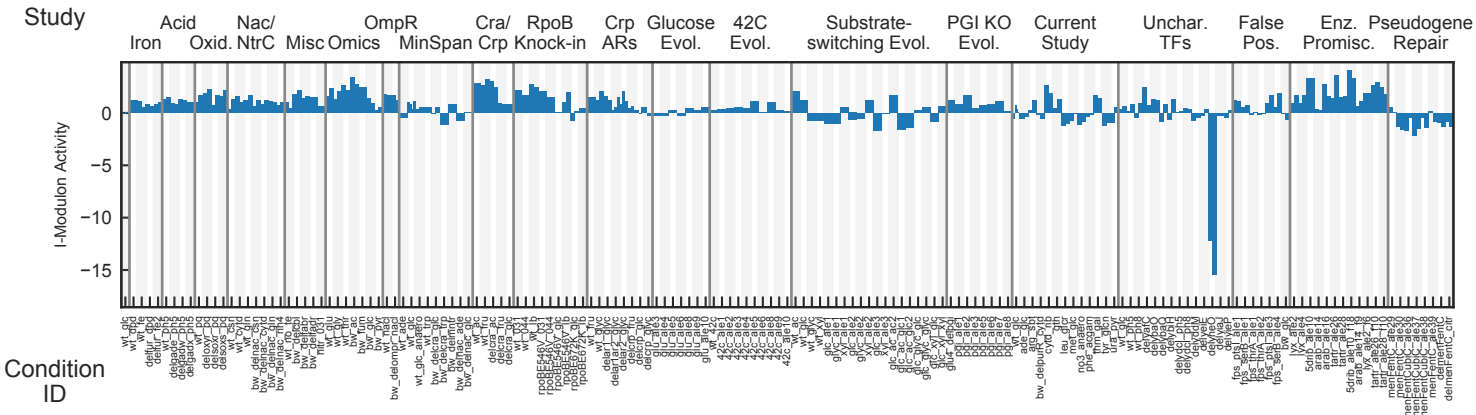


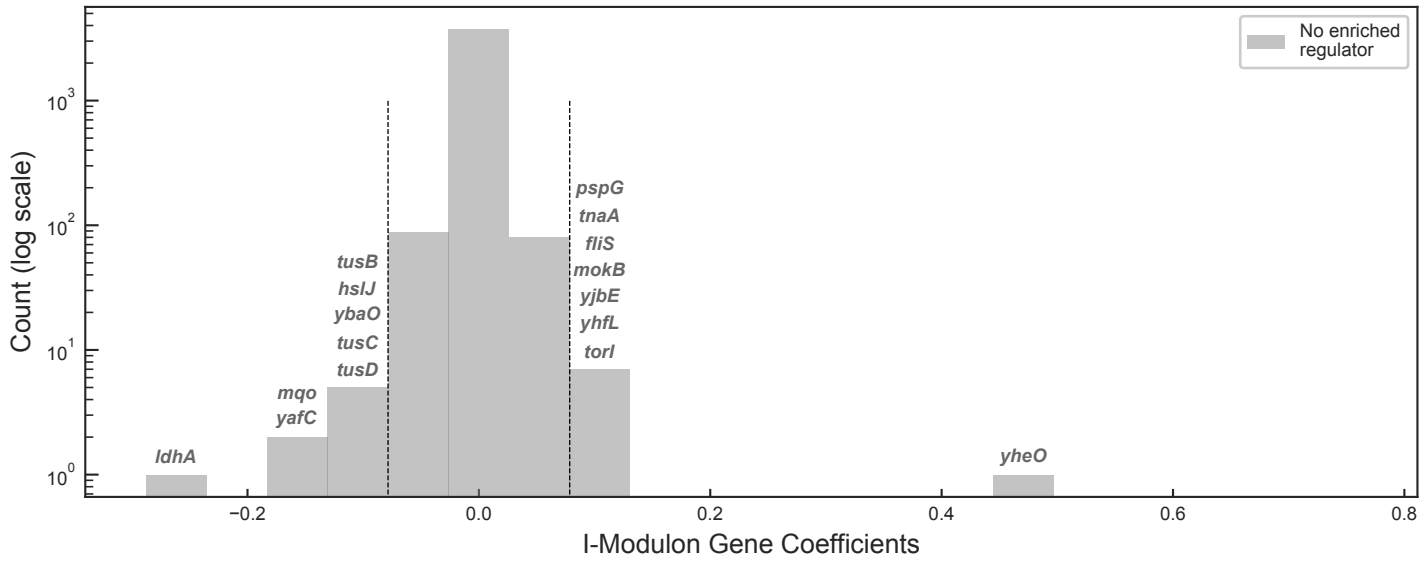


yheO – KO I-Modulon

Biological Function: Accounts for yheO knock-out

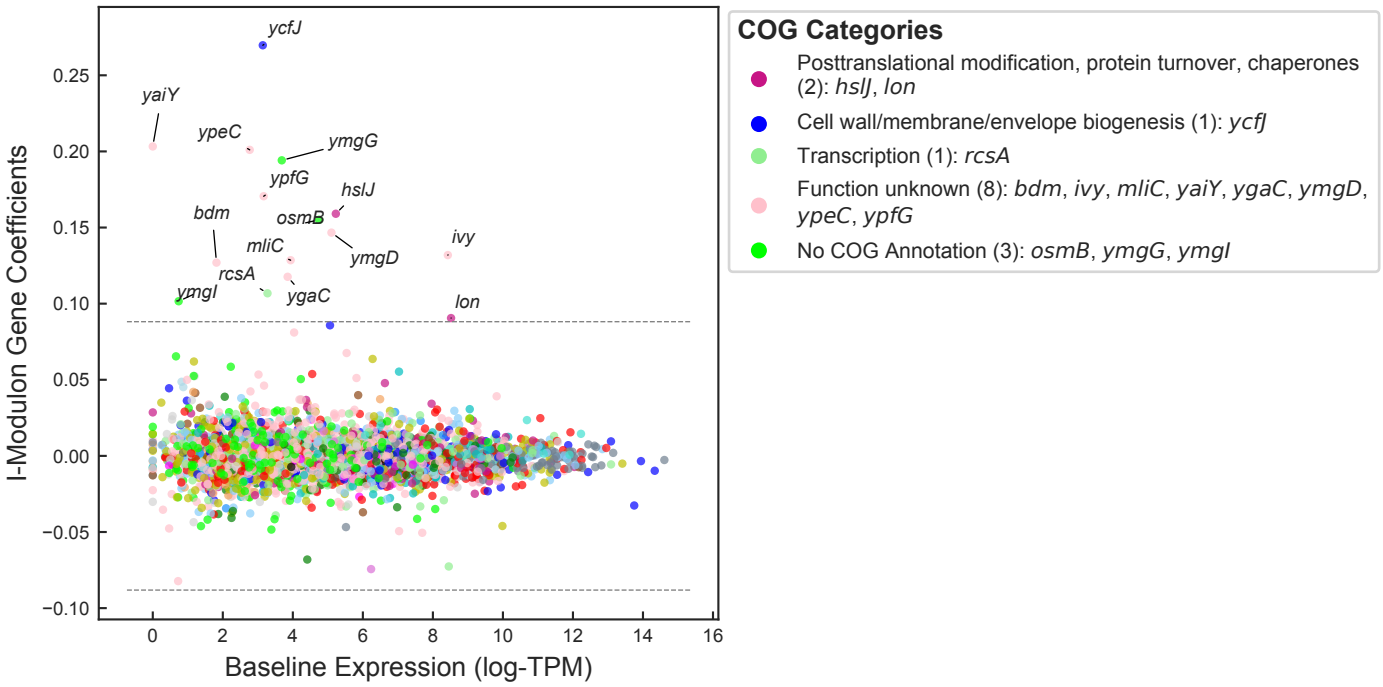


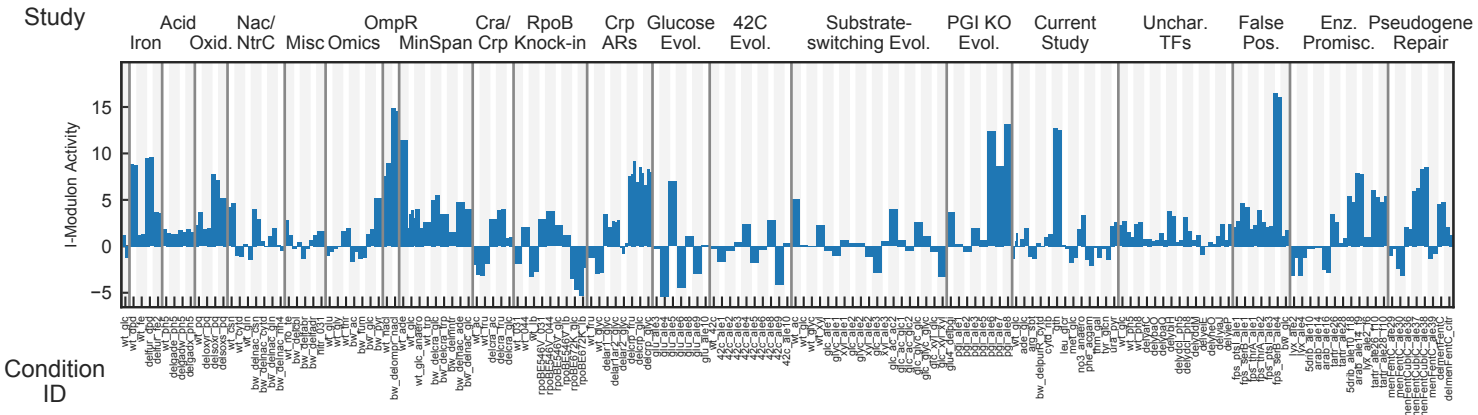


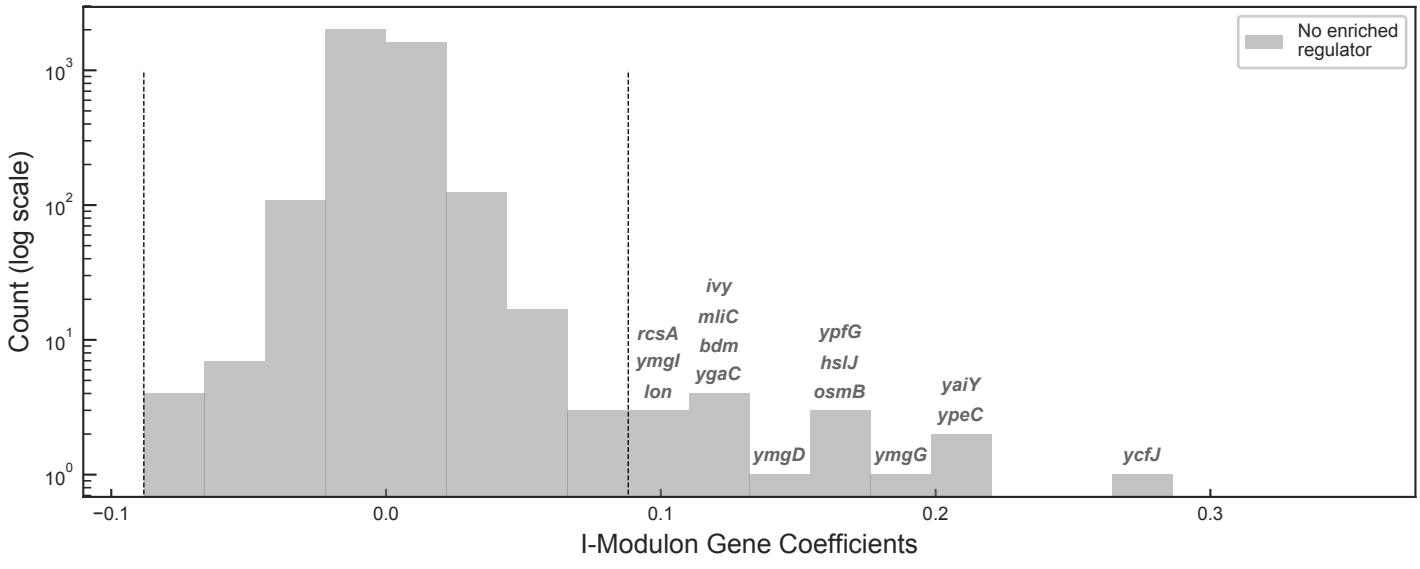


Uncharacterized I-Modulon #1

Biological Function: Unknown Function

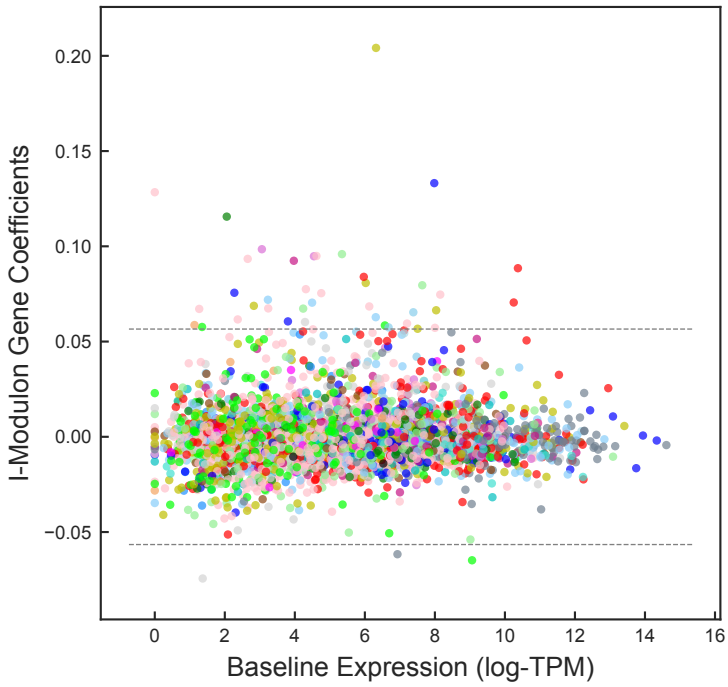






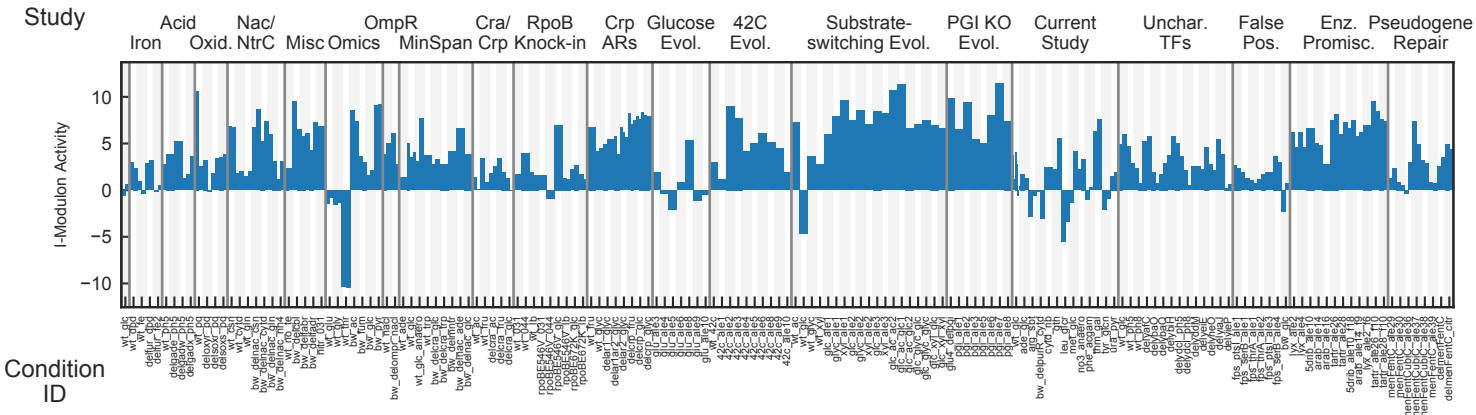
Uncharacterized I-Modulon #2

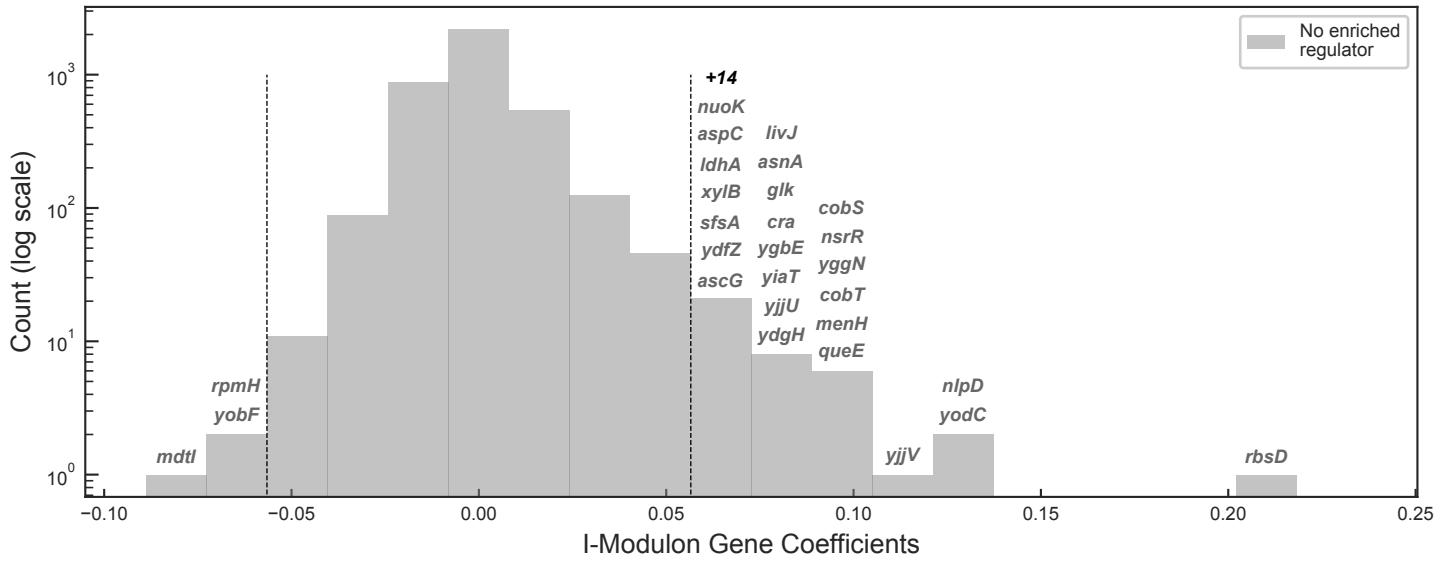
Biological Function: Unknown Function



COG Categories

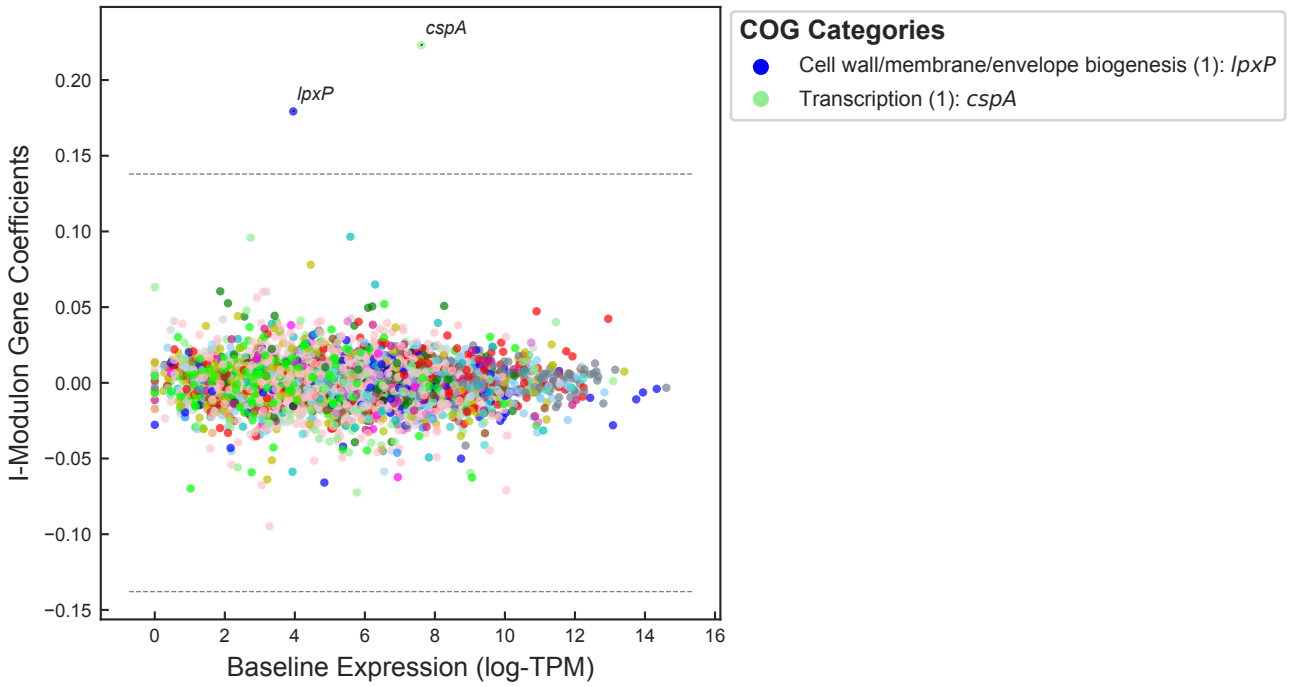
- Carbohydrate transport and metabolism (5): *glk*, *rbsD*, *xylB*, *ybhC*, *yeaD*
- Amino acid transport and metabolism (3): *asnA*, *aspC*, *livJ*
- Cell wall/membrane/envelope biogenesis (3): *nlpD*, *ompW*, *yiaT*
- Energy production and conversion (3): *ldhA*, *nuoJ*, *nuoK*
- Transcription (3): *ascG*, *cra*, *nsrR*
- Other (25): *ftsE*, *mrp*, *cobS*, *cobT*, *mdtI*, *potH*, *yggR*, *queE*, *yjjV*, *rpmH*, *erpA*, *ghxP*, *menH*, *sfsA*, *ydfZ*, *ydgH*, *yfiM*, *ygbE*, *yggN*, *yhjR* + 5

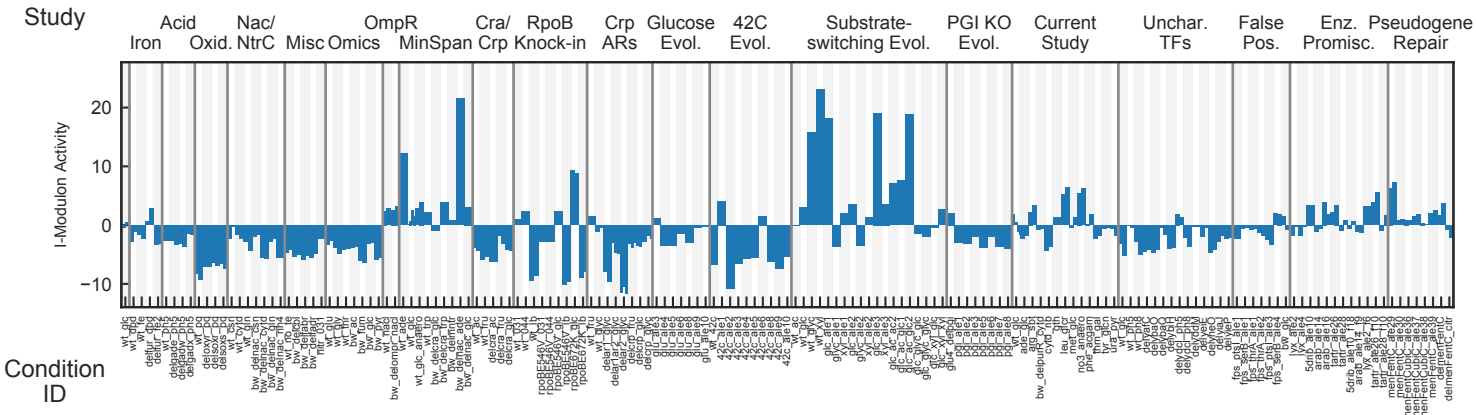


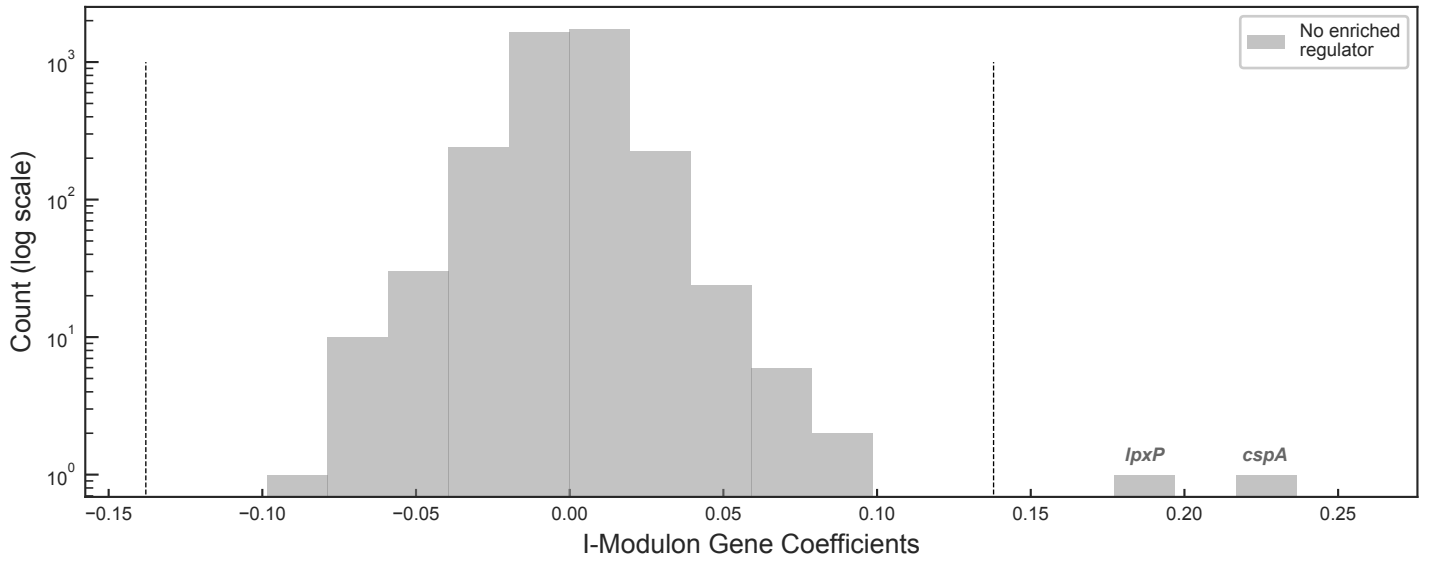


Uncharacterized I-Modulon #3

Biological Function: Unknown Function

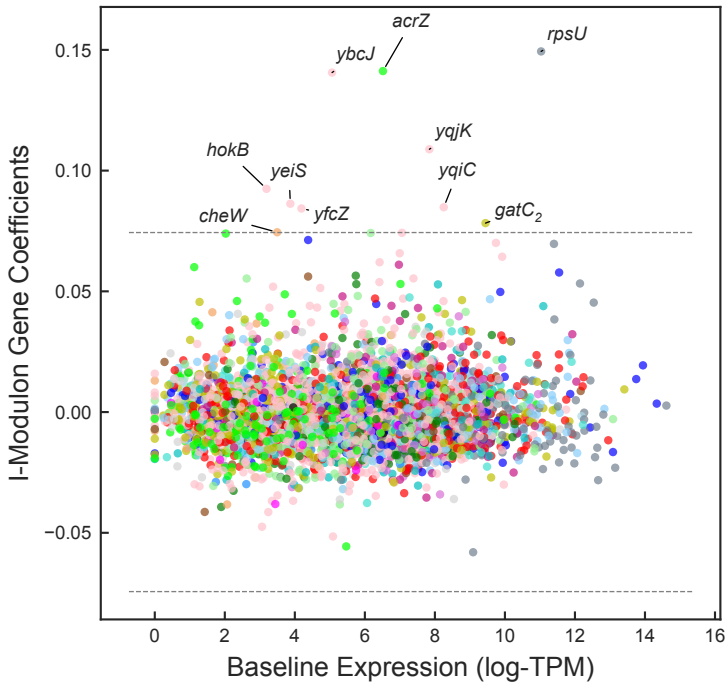






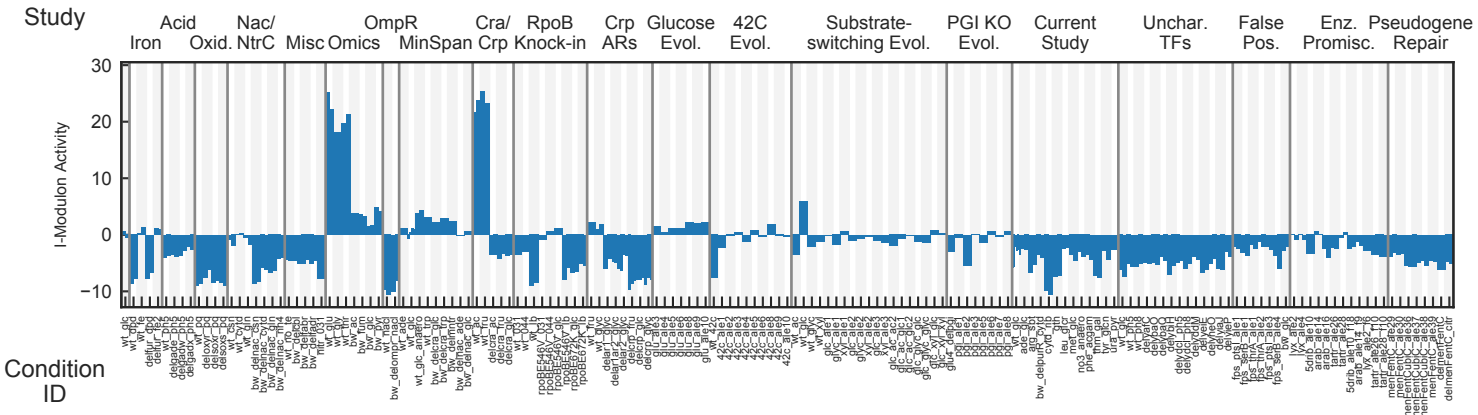
Uncharacterized I-Modulon #4

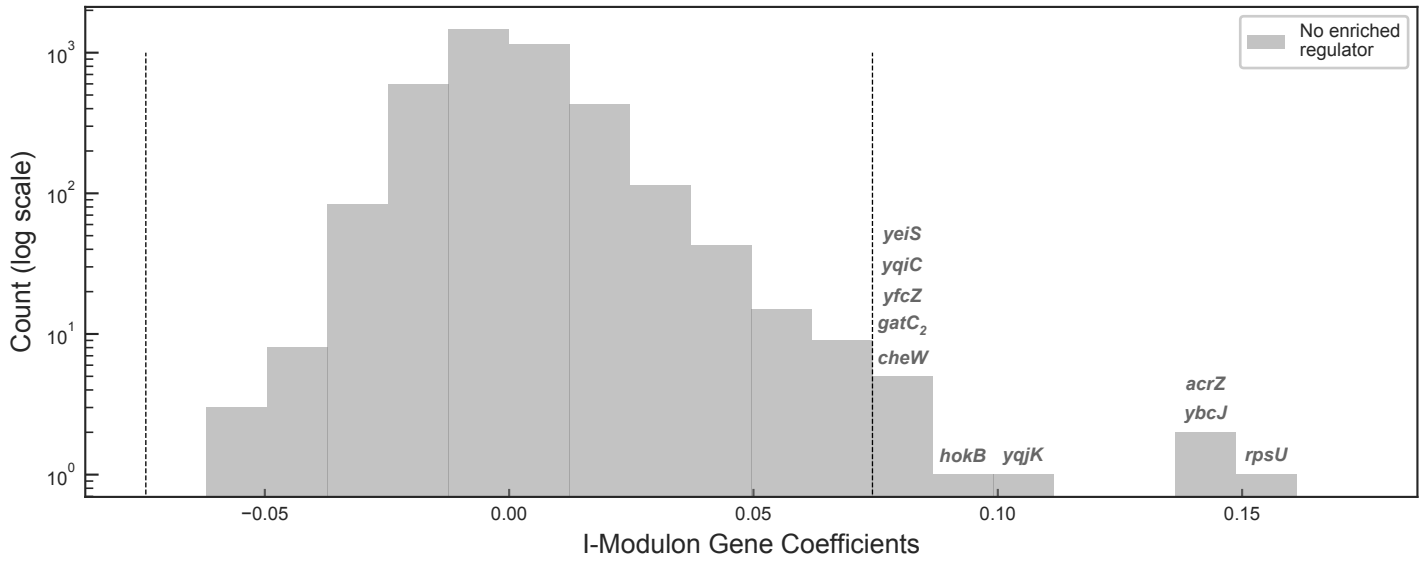
Biological Function: Unknown Function



COG Categories

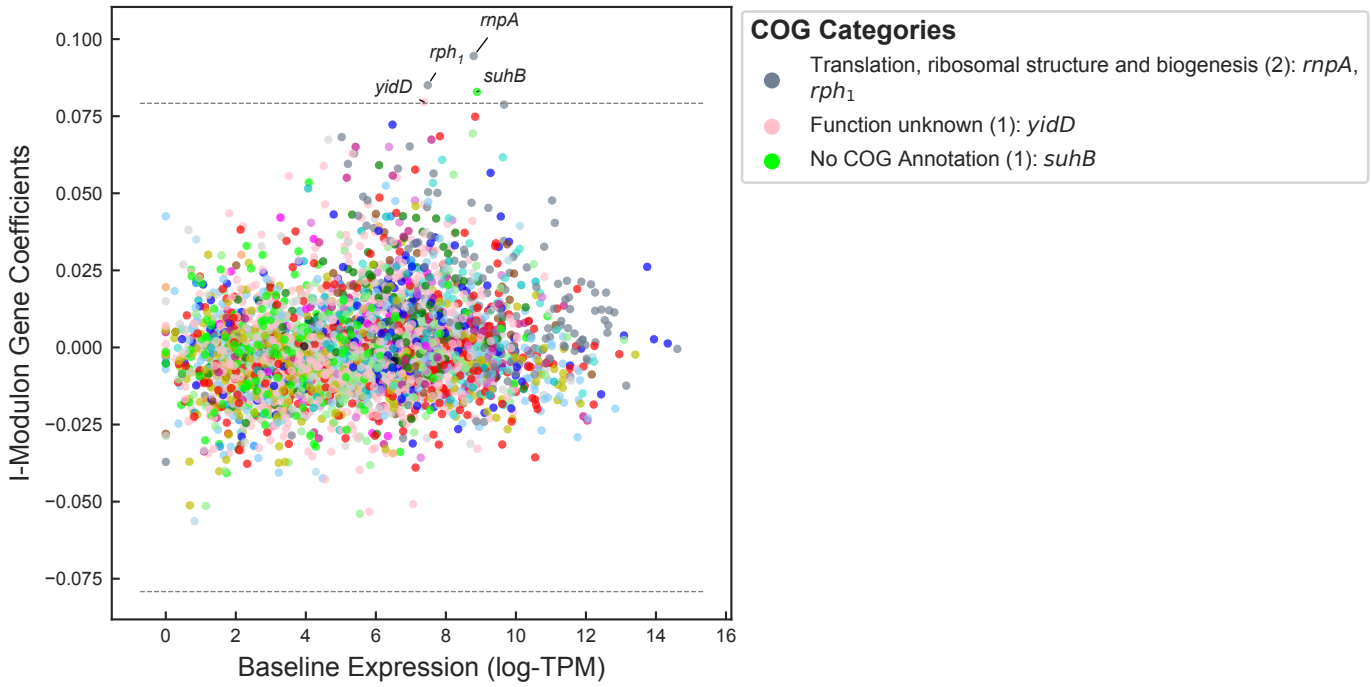
- Carbohydrate transport and metabolism (1): *gatC*$_2$
- Cell motility (1): *cheW*
- Translation, ribosomal structure and biogenesis (1): *rpsU*
- Function unknown (6): *hokB*, *ybcJ*, *yeiS*, *yfcZ*, *yqiC*, *yqjK*
- No COG Annotation (1): *acrZ*

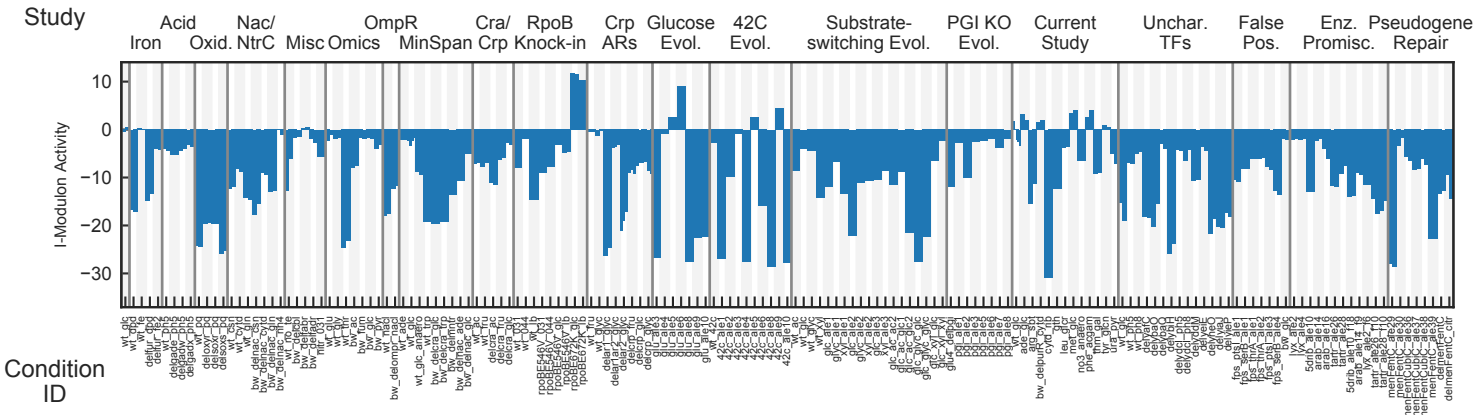


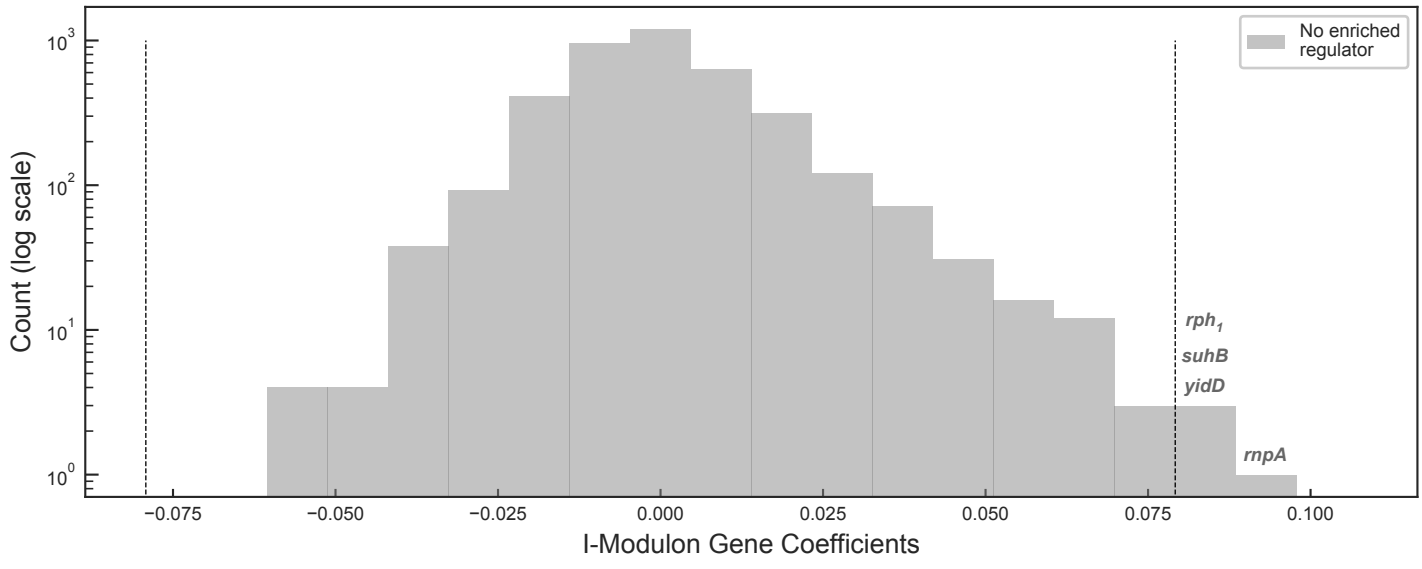


Uncharacterized I-Modulon #5

Biological Function: Unknown Function

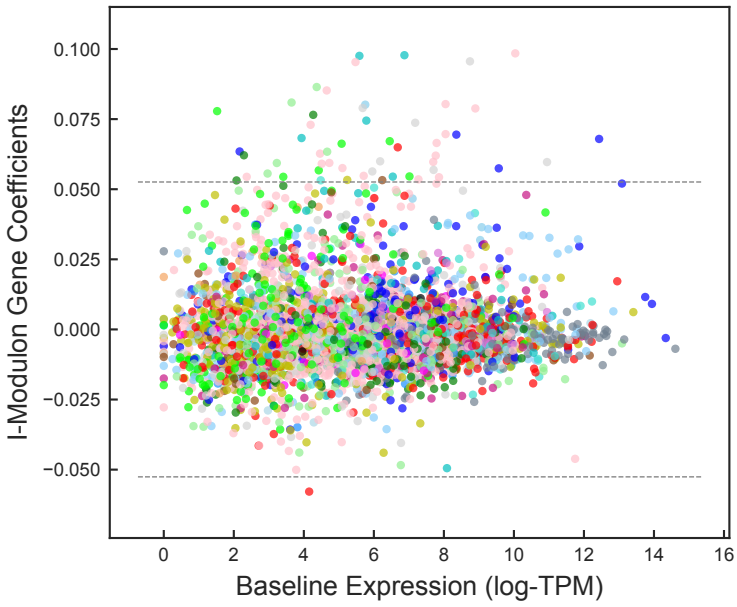






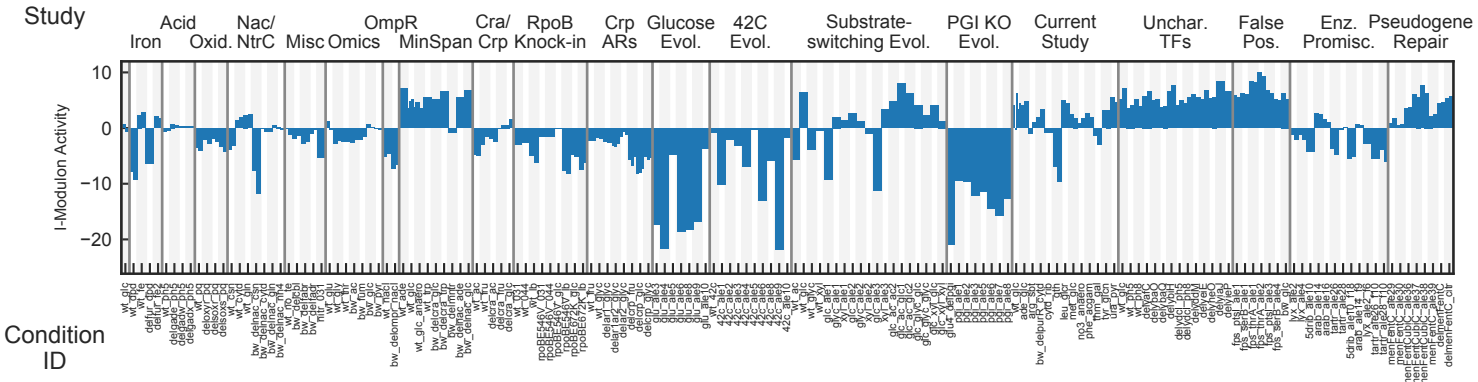
Uncharacterized I-Modulon #6

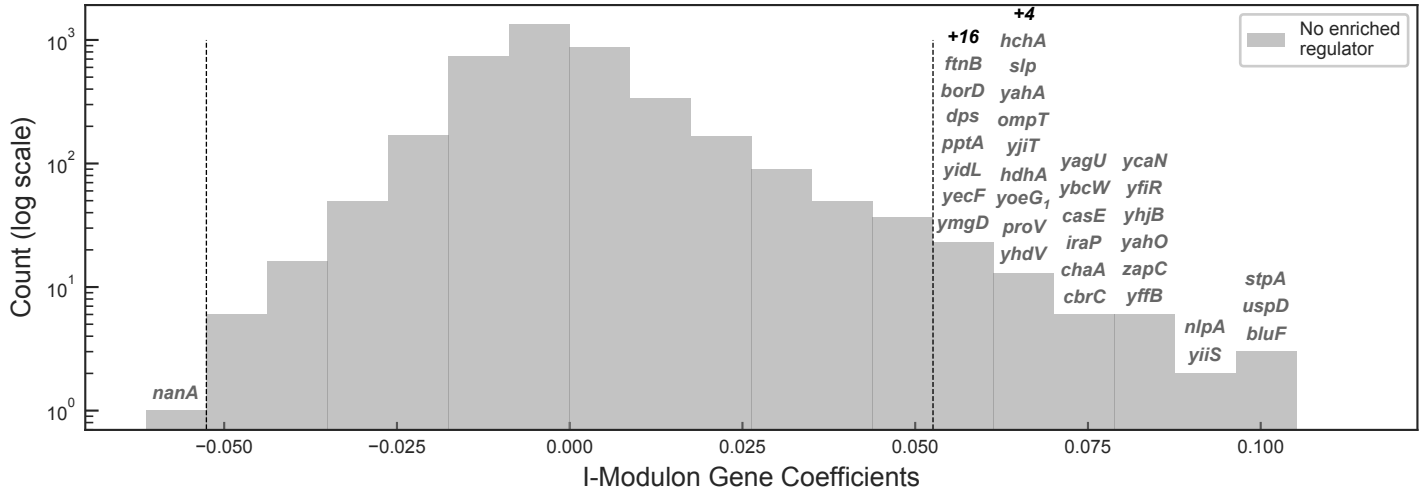
Biological Function: Unknown Function

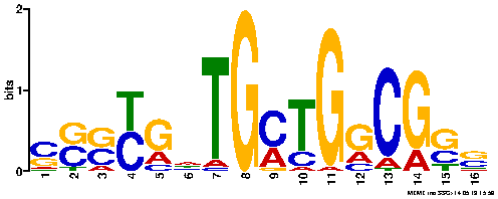


COG Categories

- Inorganic ion transport and metabolism (7): *chaA*, *dps*, *ftnA*, *ftnB*, *nlpA*, *ybjL*, *yffB*
- Signal transduction mechanisms (5): *bluF*, *iraP*, *uspD*, *yahA*, *yedW*
- Transcription (5): *cadC*, *ybcM*, *ycaN*, *yhjB*, *yidL*
- Cell wall/membrane/envelope biogenesis (4): *mepS*, *ompT*, *slp*, *yhdV*
- Other (33): *casE*, *fimE*, *xisE*, *nanA*, *proV*, *mdfA*, *zapC*, *ybjG*, *adeD*, *borD*, *cbrC*, *ecpA*, *hchA*, *hdeD*, *hdhA*, *iap*, *pptA*, *stpA*, *yagU*, *yahO* + 13







Motif E-value: 1.30e-05

Operons with Upstream Motif: 53%