Amino Acids and Derivatives

Carbohydrates


Cell Division and Cell Cycle
Drought
Flood
Freeze
Heat
Sporulation initiation inhibitor protein Soj
Rod shape–determining protein RodA
Rod shape–determining protein MreD
Penicillin–binding protein PBP2
MreB–like protein (Mbl protein)
Chromosome (plasmid) partitioning protein ParB
Chromosome (plasmid) partitioning protein ParA
Cell division protein FtsN
Cell division protein FtsL
Uncharacterized protein YppC
Recombination protein RecU
FIG001721: Predicted N6–adenine–specific DNA methylase
Group 2 RNA polymerase sigma factor
Circadian phase modifier
Circadian oscillation regulator KaiB
Circadian input kinase A
Circadian clock protein KaiC
SSU ribosomal protein S21p
Signal recognition particle, subunit Ffh SRP54 (TC 3.A.5.1.1)
Signal recognition particle associated protein
Pseudouridine synthase family protein
Chromosome partition protein smc
Bacterial Cytoskeleton (9/16)
Control of cell elongation – division cycle in Bacilli (3/10)
Cyanobacterial Circadian Clock (5/9)
Macromolecular synthesis operon (1/2)
Two cell division clusters relating to chromosome partitioning (4/6)
−0.00025
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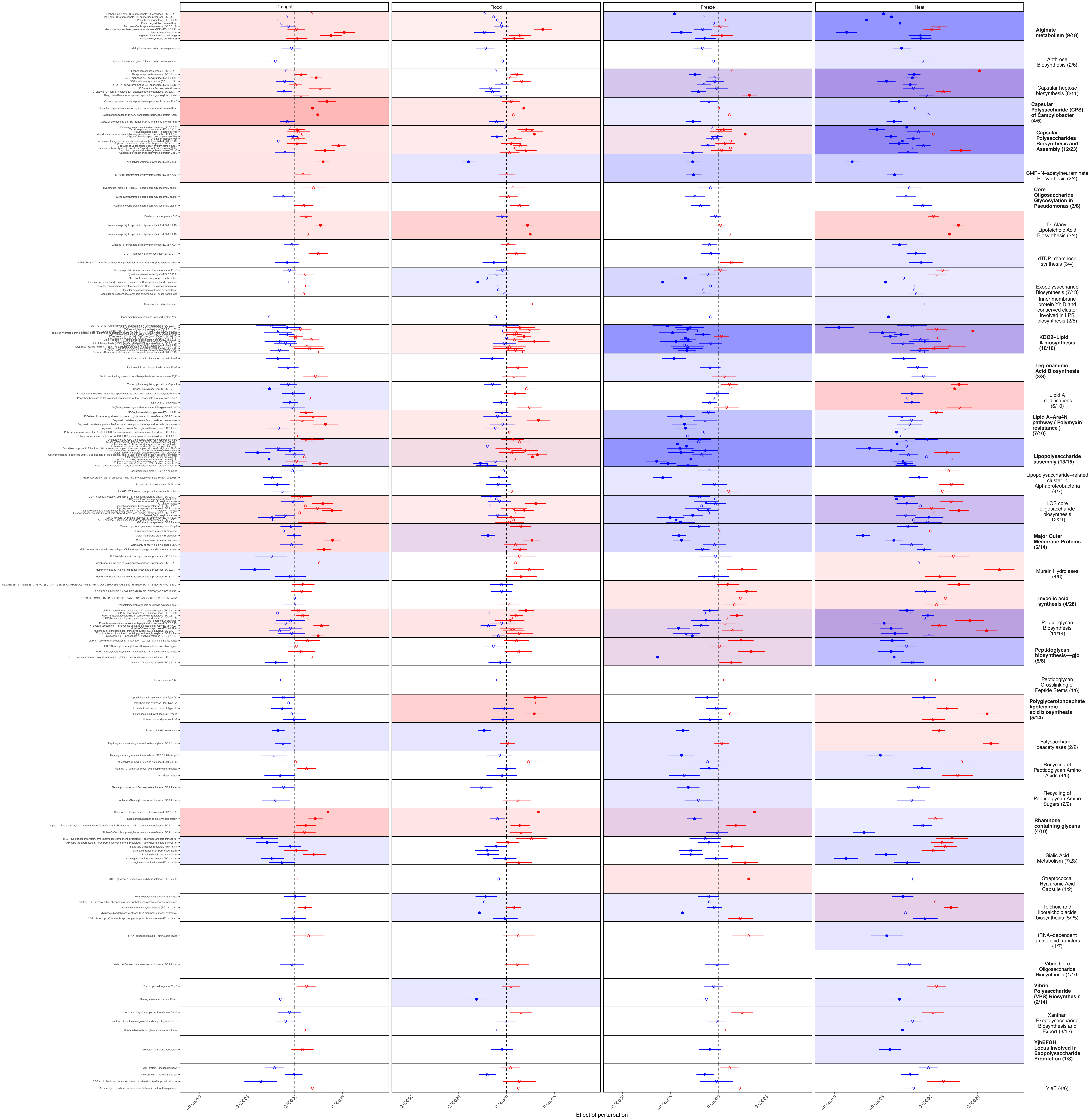
Effect of perturbation

Cell Wall and Capsule




Clustering–based subsystems
Drought
Flood
Freeze
Heat
A Gammaproteobacteria Cluster Relating to Translation (7/9)
A Glutathione–dependent Thiol Reductase Associated with a Step in Lysine Biosynthesis (2/2)
A Gram–positive cluster that relates ribosomal protein L28P to a set of uncharacterized proteins (6/8)
Bacterial Cell Division (19/25)
Bacterial RNA–metabolizing Zn–dependent hydrolases (10/12)
Beta–lactamase cluster in Streptococcus (1/7)
CBSS–138119.3.peg.2719 (3/4)
CBSS–159087.4.peg.2189 (1/4)
CBSS–160492.1.peg.550 (4/4)
CBSS–176279.3.peg.868 (4/5)
CBSS–176280.1.peg.1561 (7/14)
CBSS–176299.3.peg.235 (1/4)
CBSS–176299.4.peg.1292 (7/8)
CBSS–188.1.peg.6170 (4/4)
CBSS–188.1.peg.9880 (4/4)
CBSS–194948.1.peg.143 (1/12)
CBSS–196164.1.peg.1690 (7/9)
CBSS–196164.1.peg.461 (4/4)
CBSS–196620.1.peg.2477 (2/7)
CBSS–198094.1.peg.4426 (3/3)
CBSS–205922.3.peg.1809 (3/5)
CBSS–214092.1.peg.3450 (4/5)
CBSS–216592.1.peg.3534 (4/9)
CBSS–222523.1.peg.1311 (1/4)
CBSS–224911.1.peg.435 (4/4)
CBSS–235.1.peg.567 (5/9)
CBSS–243265.1.peg.198 (2/2)
CBSS–243277.1.peg.4359 (1/4)
CBSS–246196.1.peg.364 (2/2)
CBSS–251221.1.peg.1863 (2/3)
CBSS–257314.1.peg.488 (2/2)
CBSS–257314.1.peg.676 (8/12)
CBSS–257314.1.peg.752 (2/2)
CBSS–258594.1.peg.3339 (3/10)
CBSS–261594.1.peg.2640 (1/7)
CBSS–261594.1.peg.788 (2/3)
CBSS–262316.1.peg.2929 (5/7)
CBSS–262719.3.peg.410 (4/5)
CBSS–265072.7.peg.546 (2/10)
CBSS–266117.6.peg.2476 (2/2)
CBSS–269482.1.peg.1294 (3/3)
CBSS–269799.3.peg.2220 (4/5)
CBSS–269801.1.peg.1715 (5/6)
CBSS–269801.1.peg.1725 (7/10)
CBSS–269801.1.peg.2186 (1/2)
CBSS–280355.3.peg.2835 (2/3)
CBSS–281090.3.peg.464 (1/2)
CBSS–288000.5.peg.1793 (3/6)
CBSS–288681.3.peg.1039 (2/2)
CBSS–290633.1.peg.1906 (2/3)
CBSS–291331.3.peg.3674 (7/12)
CBSS–296591.1.peg.2330 (7/12)
CBSS–306254.1.peg.1508 (1/2)
CBSS–312309.3.peg.1965 (3/4)
CBSS–314267.3.peg.390 (1/1)
CBSS–314269.3.peg.1840 (6/6)
CBSS–316057.3.peg.1308 (6/14)
CBSS–316057.3.peg.3521 (2/2)
CBSS–316057.3.peg.563 (2/3)
CBSS–316057.3.peg.659 (1/1)
CBSS–316273.3.peg.227 (2/3)
CBSS–316273.3.peg.448 (4/5)
CBSS–316273.3.peg.922 (3/6)
CBSS–316279.3.peg.746 (1/4)
CBSS–316407.3.peg.1371 (1/3)
CBSS–316407.3.peg.2816 (1/4)
CBSS–320372.3.peg.6046 (3/3)
CBSS–323097.3.peg.2594 (1/2)
CBSS–323098.3.peg.2823 (2/2)
CBSS–323850.3.peg.3142 (1/1)
CBSS–323850.3.peg.3269 (3/4)
CBSS–323850.3.peg.3284 (5/7)
CBSS–326442.4.peg.1852 (8/12)
CBSS–342610.3.peg.1536 (3/4)
CBSS–342610.3.peg.1794 (3/3)
CBSS–342610.3.peg.283 (2/2)
CBSS–344610.3.peg.2335 (2/5)
CBSS–345072.3.peg.1318 (5/8)
CBSS–350688.3.peg.1509 (10/11)
CBSS–354.1.peg.2917 (2/2)
CBSS–370552.3.peg.1240 (1/3)
CBSS–376686.6.peg.291 (3/8)
CBSS–393121.3.peg.1913 (1/2)
CBSS–393121.3.peg.2760 (4/9)
CBSS–393130.3.peg.129 (4/5)
CBSS–393130.3.peg.794 (2/3)
CBSS–393131.3.peg.612 (1/1)
CBSS–393133.3.peg.2787 (1/2)
CBSS–49338.1.peg.459 (5/8)
CBSS–52598.3.peg.2843 (3/3)
CBSS–562.2.peg.5158 SK3 including (3/7)
CBSS–56780.10.peg.1536 (5/5)
CBSS–630.2.peg.3360 (1/3)
CBSS–69014.3.peg.2094 (2/13)
CBSS–83331.1.peg.3039 (6/6)
CBSS–83332.1.peg.3803 (3/10)
CBSS–84588.1.peg.1247 (3/7)
CBSS–87626.3.peg.3639 (3/4)
CBSS–89187.3.peg.2957 (3/5)
Cell Division Cluster (3/5)
Cell division–ribosomal stress proteins cluster (10/13)
Cluster Ytf and putative sugar transporter (6/9)
Cluster–based Subsystem Grouping Hypotheticals – perhaps Proteosome Related (8/9)
Conserved cluster in Enterobacteriaceae downstream from YqjA, a DedA family protein (3/9)
Conserved gene cluster associated with Met–tRNA formyltransferase (12/16)
EC49–61 (5/5)
EC699–706 (4/5)
GABA and putrescine metabolism from cluters (3/5)
Hypothetical Coupled to RecF (1/1)
KH domain RNA binding protein YlqC (2/3)
LMPTP YfkJ cluster (2/3)
LMPTP YwlE cluster (3/3)
PA0057 cluster (3/3)
Predicted mycobacterial monooxygenase (1/3)
Proteasome subunit alpha archaeal cluster (3/8)
Putative diaminopropionate ammonia–lyase cluster (5/15)
SeqA and Co–occurring Genes (1/3)
Spore Coat (6/20)
Sporulation–related Hypotheticals (2/4)
Staphylococcus aureus hypothetical repetitive gene loci (1/5)
Sulfatases and sulfatase modifying factor 1 (3/4)
Unspecified monosaccharide transport cluster (1/4)
USS–DB–2 (2/5)
USS–DB–4 (1/3)
USS–DB–7 (1/1)
YeiH (1/4)
−1e−03
−5e−04
0e+00
5e−04
1e−03
Effect of perturbation

Cofactors, Vitamins, Prosthetic Groups, Pigments


DNA Metabolism
Drought
Flood
Freeze
Heat
2–phosphoglycolate salvage (4/6)
Competence in Streptococci (1/5)
CRISP Cmr Cluster (6/13)
CRISPRs (6/16)
DNA Helicase of Unknown Function (2/2)
DNA phosphorothioation (1/5)
DNA processing cluster (6/7)
DNA recombination, archaeal (2/2)
DNA repair and recombination eukaryotic (1/6)
DNA Repair Base Excision (8/10)
DNA repair, bacterial (22/28)
DNA repair, bacterial DinG and relatives (4/4)
DNA repair, bacterial MutL–MutS system (5/8)
DNA repair, bacterial photolyase (2/4)
DNA repair, bacterial RecBCD pathway (7/7)
DNA repair, bacterial RecFOR pathway (5/7)
DNA repair, bacterial UvrD and related helicases (7/16)
DNA repair, UvrABC system (6/7)
DNA replication, archaeal (8/11)
DNA structural proteins, bacterial (8/10)
DNA topoisomerases, Type I, ATP–independent (5/9)
DNA topoisomerases, Type II, ATP–dependent (4/6)
DNA–replication (9/21)
Gram Positive Competence (4/10)
Natural DNA Transformation in Vibrio (1/3)
Nonhomologous End–Joining in Bacteria (1/1)
Nucleoid–associated proteins in Bacteria (1/3)
Plasmid replication (2/2)
Restriction–Modification System (6/8)
Uracil–DNA glycosylase (6/9)
YcfH (2/4)
−5e−04
0e+00
5e−04
Effect of perturbation

Dormancy and Sporulation
Drought
Flood
Freeze
Heat
SinR, regulator of post−exponential−phase responses genes (competence and sporulation)
Signal peptidase SipW (EC 3.4.21.89), required for TasA secretion
Immune inhibitor A metalloprotease
Dipicolinate synthase subunit B
Outer spore coat protein E
HipA protein
Small acid−soluble spore protein, beta−type SASP
Small acid−soluble spore protein, alpha/beta family, SASP_1
Small acid−soluble spore protein, alpha−type SASP
Endopeptidase spore protease Gpr (EC 3.4.24.78)
Spore maturation protein B
Spore maturation protein A−like protein
Spore maturation protein A
Fused spore maturation proteins A and B
Spore germination protein YpeB
Spore germination protein GerYA
Spore germination protein GerSB
Spore germination protein GerSA
Spore germination protein GerN (inosine−dependent germination), Na+/H+ antiporter
Spore germination protein GerKC
Spore germination protein GerKB
Spore germination protein GerKA
Spore germination protein GerD
Spore germination protein GerAA, germination response to L−alanine and related amino acids (earliest stage)
Spore cortex−lytic enzyme, N−acetylglucosaminidase SleL (EC 3.2.1.−)
Spore cortex−lytic enzyme, lytic transglycosylase SleB
Putative peptidoglycan hydrolase YvbX, NOT involved in spore germination
WhiE I protein of unknown function
Polyketide hydroxylase WhiE VIII
Polyketide chain length factor WhiE−CLF paralog
Polyketide beta−ketoacyl synthase WhiE−KS paralog
Stage III sporulation protein AH
Stage III sporulation protein AG
Stage III sporulation protein AF
Stage III sporulation protein AD
Stage III sporulation protein AC
Stage III sporulation protein AB
Stage III sporulation protein AA
Stage V sporulation protein B
spore peptidoglycan hydrolase (N−acetylglucosaminidase) (EC 3.2.1.−)
Spore cortex−lytic enzyme precursor
Stage V sporulation protein whose disruption leads to the production of immature spores (SpoVK)
Stage V sporulation protein T, AbrB family transcriptional regulator (SpoVT)
Stage V sporulation protein involved in spore cortex synthesis (SpoVR)
Stage V sporulation protein AF (SpoVAF)
Stage V sporulation protein AE (SpoVAE)
Stage V sporulation protein AD (SpoVAD)
Stage V sporulation protein AC (SpoVAC)
Stage V sporulation protein AA (SpoVAA)
Stage IV sporulation protein FA (SpoIVFA)
Stage IV sporulation protein B
Stage IV sporulation pro−sigma−K processing enzyme (SpoIVFB)
Stage II sporulation serine phosphatase for sigma−F activation (SpoIIE)
Stage II sporulation protein required for processing of pro−sigma−E (SpoIIR)
Stage II sporulation protein P
Stage II sporulation protein M (SpoIIM)
Stage 0 sporulation two−component response regulator (Spo0A)
Sporulation sigma−E factor processing peptidase (SpoIIGA)
Sporulation kinase B (EC 2.7.13.3)
Sporulation kinase A (EC 2.7.13.3)
Stage III sporulation protein AE
Protein of unknown function identified by role in sporulation (SpoVG)
Bacillus biofilm matrix protein component TasA and homologs (3/15)
Dipicolinate Synthesis (1/1)
Exosporium (1/14)
Persister Cells (1/2)
Small acid−soluble spore proteins (4/10)
Spore Core Dehydration (4/5)
Spore germination (13/49)
Spore pigment biosynthetic cluster in Actinomycetes (4/10)
Sporulation Cluster III A (7/7)
Sporulation draft (3/8)
Sporulation gene orphans (19/29)
Sporulation−associated proteins with broader functions (2/3)
−0.00025
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0.00025
0.00050
Effect of perturbation


Fatty Acids, Lipids, and Isoprenoids
Drought
Flood
Freeze
Heat
Isohexenylglutaconyl−CoA hydratase
Geranyl−CoA carboxylase carboxyl transferase subunit
Acyclic terpenes utilization regulator AtuR, TetR family
3−hydroxy−3isohexenylglutaryl−CoA:acetate lyase
TesB−like acyl−CoA thioesterase 5
TesB−like acyl−CoA thioesterase 4
TesB−like acyl−CoA thioesterase 3
TesB−like acyl−CoA thioesterase 1
Acyl−CoA thioesterase II (EC 3.1.2.−)
Isopentenyl−diphosphate delta−isomerase, FMN−dependent (EC 5.3.3.2)
Isopentenyl phosphate kinase
Hydroxymethylglutaryl−CoA synthase (EC 2.3.3.10)
Hydroxymethylglutaryl−CoA reductase (EC 1.1.1.34)
Glycerol−1−phosphate dehydrogenase [NAD(P)] (EC 1.1.1.261)
Digeranylgeranylglycerophospholipid reductase
(S)−3−O−geranylgeranylglyceryl phosphate synthase
Electron transfer flavoprotein, alpha subunit FixB
Zeaxanthin glucosyl transferase
Squalene−−hopene cyclase
Pro−zeta−carotene desaturase
Phytoene synthase
Phytoene desaturase
Methoxyneurosporene dehydrogenase
Lycopene beta cyclase
Geranyltransferase (farnesyldiphosphate synthase)
Geranylgeranyl pyrophosphate synthetase
Dehydrosqualene synthase
Beta−carotene ketolase
Beta−carotene hydroxylase
Putative cytochrome P450 IgrA
Lipid carrier protein IgrF
Enoyl coenzyme A hydratase IgrE
Conserved protein IgrD
Acyl−CoA dehydrogenase IgrC
Trans−2,3−enoyl−cozyme A reductase of elongase (EC 1.−.−.−)
Fatty acyl−coenzyme A elongase
Acetyl−coenzyme A carboxyl transferase of ACAC1 (EC 6.4.1.2)
4'−phosphopantetheinyl transferase of FASI (EC 2.7.8.7)
[Acyl−carrier−protein] malonyl transferase of FASI (EC 2.3.1.39)
Malonyl CoA−acyl carrier protein transacylase (EC 2.3.1.39)
Enoyl−[acyl−carrier−protein] reductase [NADPH] (EC 1.3.1.10)
Enoyl−[acyl−carrier−protein] reductase [NADH] (EC 1.3.1.9)
Biotin carboxyl carrier protein of acetyl−CoA carboxylase
Acyl carrier protein phosphodiesterase (EC 3.1.4.14)
Acetyl−coenzyme A carboxyl transferase alpha chain (EC 6.4.1.2)
4'−phosphopantetheinyl transferase (EC 2.7.8.−)
3−oxoacyl−[acyl−carrier−protein] synthase, KASII (EC 2.3.1.41)
3−oxoacyl−[acyl−carrier−protein] synthase, KASIII (EC 2.3.1.41)
3−hydroxydecanoyl−[acyl−carrier−protein] dehydratase (EC 4.2.1.60)
(3R)−hydroxymyristoyl−[acyl carrier protein] dehydratase (EC 4.2.1.−)
Transcriptional regulator for fatty acid degradation FadR, GntR family
Predicted transcriptional regulator for fatty acid degradation FadP, TetR family
Long−chain fatty acid transport protein
2,4−dienoyl−CoA reductase [NADPH] (EC 1.3.1.34)
Phosphatidylserine decarboxylase (EC 4.1.1.65)
Phosphatidylglycerophosphatase A (EC 3.1.3.27)
Phosphate:acyl−ACP acyltransferase PlsX
Glycerol−3−phosphate acyltransferase (EC 2.3.1.15)
CDP−diacylglycerol−−serine O−phosphatidyltransferase (EC 2.7.8.8)
Cardiolipin synthetase (EC 2.7.8.−)
Aldehyde dehydrogenase B (EC 1.2.1.22)
Acyl−phosphate:glycerol−3−phosphate O−acyltransferase PlsY
1−acyl−sn−glycerol−3−phosphate acyltransferase (EC 2.3.1.51)
Phosphomevalonate kinase (EC 2.7.4.2)
Isopentenyl−diphosphate delta−isomerase (EC 5.3.3.2)
Diphosphomevalonate decarboxylase (EC 4.1.1.33)
2−C−methyl−D−erythritol 4−phosphate cytidylyltransferase (EC 2.7.7.60)
2−C−methyl−D−erythritol 2,4−cyclodiphosphate synthase (EC 4.6.1.12)
1−deoxy−D−xylulose 5−phosphate synthase (EC 2.2.1.7)
Putative histidine ammonia−lyase protein
FIGfam138462: Acyl−CoA synthetase, AMP−(fatty) acid ligase
FIG138576: 3−oxoacyl−[ACP] synthase (EC 2.3.1.41)
FIG027190: Putative transmembrane protein
FIG021862: membrane protein, exporter
FIG018329: 1−acyl−sn−glycerol−3−phosphate acyltransferase
FIG002571: 4−hydroxybenzoyl−CoA thioesterase domain protein
Acyl carrier protein (ACP)
3−oxoacyl−[ACP] synthase (EC 2.3.1.41) FabV like
3−oxoacyl−[ACP] reductase (EC 1.1.1.100)
3−hydroxydecanoyl−[ACP] dehydratase (EC 4.2.1.60)
Polyhydroxyalkanoic acid synthase
polyhydroxyalkanoate synthesis repressor PhaR
Polyhydroxyalkanoate granule−associated protein PhaF
Poly(3−hydroxyalkanoate) depolymerase
Intracellular PHB depolymerase (EC 3.1.1.−)
D(−)−3−hydroxybutyrate oligomer hydrolase (EC 3.1.1.22)
D−beta−hydroxybutyrate permease
D−beta−hydroxybutyrate dehydrogenase (EC 1.1.1.30)
Octaprenyl−diphosphate synthase (EC 2.5.1.−)
Heptaprenyl diphosphate synthase component I (EC 2.5.1.30)
Geranylgeranyl reductase (EC 1.3.1.83)
omega−3 polyunsaturated fatty acid synthase subunit, PfaC
omega−3 polyunsaturated fatty acid synthase subunit, PfaA
Enoyl−[acyl−carrier−protein] reductase [FMN] (EC 1.3.1.9), inferred for PFA pathway
4'−phosphopantetheinyl transferase (EC 2.7.8.−), inferred for PFA pathway
Putative fatty acid desaturase (EC 1.14.−.−)
Triacylglycerol lipase precursor (EC 3.1.1.3)
Triacylglycerol lipase (EC 3.1.1.3)
Phospholipase A1 precursor (EC 3.1.1.32, EC 3.1.1.4)
Lysophospholipase (EC 3.1.1.5)
Acyclic terpenes utilization (4/7)
Acyl−CoA thioesterase II (5/6)
Archaeal lipids (7/11)
Carnitine Metabolism in Microorganisms (1/8)
Carotenoids (18/31)
Cholesterol catabolic operon in Mycobacteria (5/6)
Fatty Acid Biosynthesis FASI (5/10)
Fatty Acid Biosynthesis FASII (11/20)
Fatty acid degradation regulons (4/6)
Glycerolipid and Glycerophospholipid Metabolism in Bacteria (9/12)
Isoprenoid Biosynthesis (6/9)
Phospholipid and Fatty acid biosynthesis related cluster (16/22)
Polyhydroxybutyrate metabolism (8/10)
Polyprenyl Diphosphate Biosynthesis (3/8)
Polyunsaturated Fatty Acids synthesis (4/7)
Sphingolipid biosynthesis (1/3)
Triacylglycerol metabolism (4/4)
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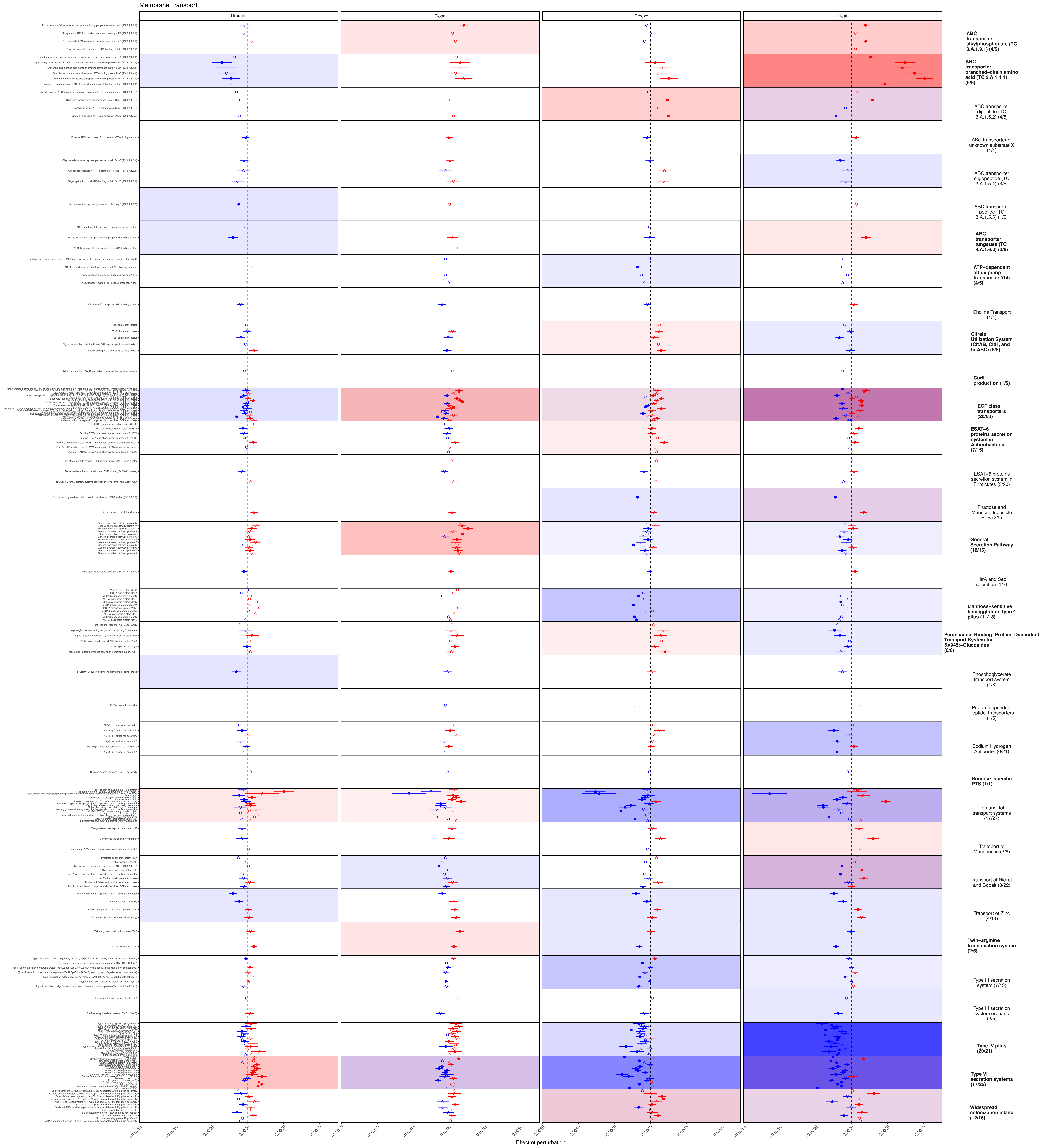
0e+00
5e−04
Effect of perturbation


Iron acquisition and metabolism
Drought
Flood
Freeze
Heat
Siderophore [Alcaligin] biosynthesis complex, long chain
Bacillibactin synthetase component F (EC 2.7.7.−)
Putative high−affinity iron permease
Periplasmic protein p19 involved in high−affinity Fe2+ transport
Ferrous iron transport protein B
Ferric iron ABC transporter, iron−binding protein
Ferrous iron transport peroxidase EfeB
Ferrous iron transport permease EfeU, N−terminal extended
Ferrous iron transport permease EfeU
Ferrous iron transport periplasmic protein EfeO, contains peptidase−M75 domain and (frequently) cupredoxin−like domain
Zn−dependent hydrolase (beta−lactamase superfamily)
Uncharacterized iron compound ABC uptake transporter, permease protein
Uncharacterized iron compound ABC uptake transporter, ATP−binding protein
Two−component response regulator SA14−24
Sortase A, LPXTG specific
Iron−dependent repressor IdeR/DtxR
Iron compound ABC uptake transporter substrate−binding protein PiaA
Iron compound ABC uptake transporter substrate−binding protein
Iron compound ABC uptake transporter permease protein
Iron compound ABC uptake transporter ATP−binding protein
Hypothetical, distant similarity with heme−degrading oxygenase IsdG
Hemoglobin, heme−dependent two component system sensory histidine kinase ChrS
Hemoglobin, heme−dependent two component system response regulator ChrA
Hemoglobin−dependent two component system, sensory histidine kinase HrrS
Hemin transport protein HmuS
Heme ABC type transporter HtsABC, permease protein HtsC
Heme ABC transporter, permease protein HmuU
Heme ABC transporter, cell surface heme and hemoprotein receptor HmuT
Heme ABC transporter, ATPase component HmuV
Heme ABC transporter (Streptococcus), permease protein
Heme ABC transporter (Streptococcus), ATP−binding protein
Periplasmic hemin−binding protein
Outer membrane receptor proteins, mostly Fe transport
Hemin uptake protein
Hemin transport protein
Hemin ABC transporter, permease protein
heme uptake transmembrane sensor
Haemin uptake system outer membrane receptor
Ferric siderophore transport system, periplasmic binding protein TonB
ABC−type hemin transport system, ATPase component
Two−component response regulator, associated with ferric iron transporter, SPy1062 homolog
Ferric iron ABC transporter, permease protein
Ferric iron ABC transporter, ATP−binding protein
TonB−dependent receptor
Ferrous iron transport protein A
Probable thiol oxidoreductase with 2 cytochrome c heme−binding sites
Iron siderophore sensor protein
Iron siderophore receptor protein
Petrobactin ABC transporter, permease protein II
Glycosyltransferase IroB
Iron−siderophore [Alcaligin−like] transport system, substrate−binding component
Putative achromobactin biosynthesis protein, related to 2−demethylmenaquinone methyltransferase
Ferric hydroxamate ABC transporter (TC 3.A.1.14.3), permease component FhuB
Ferric hydroxamate ABC transporter (TC 3.A.1.14.3), periplasmic substrate binding protein FhuD
Ferric hydroxamate ABC transporter (TC 3.A.1.14.3), ATP−binding protein FhuC
TonB−dependent siderophore receptor
TonB−dependent hemin , ferrichrome receptor
Siderophore transport protein
Siderophore synthetase small component, acetyltransferase
Siderophore synthetase large component, acetyltransferase
Siderophore synthetase component, ligase
Siderophore biosynthesis protein, monooxygenase
Siderophore biosynthesis non−ribosomal peptide synthetase modules
Siderophore biosynthesis L−2,4−diaminobutyrate decarboxylase
Siderophore biosynthesis diaminobutyrate−−2−oxoglutarate aminotransferase (EC 2.6.1.76)
Iron−siderophore transport system, permease component
ABC−type Fe3+−siderophore transport system, permease component
ABC−type Fe3+−siderophore transport system, ATPase component
Putative Desferrioxamine E transporter
Desferrioxamine E biosynthesis protein DesD
Desferrioxamine E biosynthesis protein DesC
Desferrioxamine E biosynthesis protein DesB
Desferrioxamine E biosynthesis protein DesA
Proofreading thioesterase in enterobactin biosynthesis EntH
Enterobactin synthetase component F, serine activating enzyme (EC 2.7.7.−)
2,3−dihydro−2,3−dihydroxybenzoate dehydrogenase (EC 1.3.1.28) [enterobactin] siderophore
Enantio−pyochelin synthetase PchF, non−ribosomal peptide synthetase module
ABC efflux pump, fused inner membrane and ATPase subunits in pyochelin gene cluster
Pyoverdine sidechain non−ribosomal peptide synthetase PvdJ
Pyoverdine sidechain non−ribosomal peptide synthetase PvdI
Pyoverdine sidechain non−ribosomal peptide synthetase PvdD
Pyoverdine chromophore precursor synthetase PvdL
Pyoverdin biosynthesis protein PvdN, putative aminotransferase, class V
PvdO, pyoverdine responsive serine/threonine kinase (predicted by OlgaV)
Probable thioesterase involved in non−ribosomal peptide biosynthesis, PA2411 homolog
Pirin−related protein, coexpressed with pyoverdine biosynthesis regulon
Non−ribosomal peptide synthetase modules, pyoverdine??
Non−ribosomal peptide synthetase modules, pyoverdine
Hypothetical MbtH−like protein, PA2412 homolog
Cation ABC transporter, periplasmic cation−binding protein, PA2407 homolog
Antisigma transmembrane sensor FpvR
Acyl−homoserine lactone acylase PvdQ (EC 3.5.1.−), quorum−quenching
ABC transporter in pyoverdin gene cluster, permease component
ABC transporter in pyoverdin gene cluster, ATP−binding component
Siderophore staphylobactin biosynthesis protein SbnH
iron aquisition yersiniabactin synthesis enzyme (YbtT,resembles thioesterases)
iron aquisition yersiniabactin synthesis enzyme (Irp2)
iron aquisition yersiniabactin synthesis enzyme (Irp1,polyketide synthetase)
Iron−regulated protein A precursor
Ferrichrome−iron receptor
Vibrioferrin decarboxylase protein PvsE
Alcaligin Siderophore (1/9)
Bacillibactin Siderophore (1/11)
Campylobacter Iron Metabolism (4/16)
Ferrous iron transporter EfeUOB, low−pH−induced (4/4)
Heme, hemin uptake and utilization systems in GramPositives (21/62)
Hemin transport system (9/14)
Iron acquisition in Streptococcus (3/4)
Iron acquisition in Vibrio (2/37)
Iron Scavenging cluster in Thermus (1/3)
Iron siderophore sensor & receptor system (2/3)
Petrobactin−mediated iron uptake system (1/4)
Salmochelin−mediated Iron Acquisition (1/5)
Siderophore [Alcaligin−like] (1/10)
Siderophore Achromobactin (1/18)
Siderophore Aerobactin (3/12)
Siderophore assembly kit (13/20)
Siderophore Desferrioxamine E (5/6)
Siderophore Enterobactin (3/18)
Siderophore pyochelin (2/22)
Siderophore Pyoverdine (16/39)
Siderophore Staphylobactin (1/16)
Siderophore Yersiniabactin Biosynthesis (3/7)
Transport of Iron (2/5)
Vibrioferrin synthesis (1/11)
−0.002
−0.001
0.000
0.001
Effect of perturbation


Membrane Transport
Drought
Flood
Freeze
Heat
ABC transporter alkylphosphonate (TC 3.A.1.9.1) (4/5)
ABC transporter branched−chain amino acid (TC 3.A.1.4.1) (6/6)
ABC transporter dipeptide (TC 3.A.1.5.2) (4/5)
ABC transporter of unknown substrate X (1/4)
ABC transporter oligopeptide (TC 3.A.1.5.1) (3/5)
ABC transporter peptide (TC 3.A.1.5.5) (1/5)
ABC transporter tungstate (TC 3.A.1.6.2) (3/6)
ATP−dependent efflux pump transporter Ybh (4/5)
Choline Transport (1/4)
Citrate Utilization System (CitAB, CitH, and tctABC) (5/6)
Curli production (1/5)
ECF class transporters (20/50)
ESAT−6 proteins secretion system in Actinobacteria (7/15)
ESAT−6 proteins secretion system in Firmicutes (3/20)
Fructose and Mannose Inducible PTS (2/9)
General Secretion Pathway (12/15)
HtrA and Sec secretion (1/7)
Mannose−sensitive hemagglutinin type 4 pilus (11/18)
Periplasmic−Binding−Protein−Dependent Transport System for α−Glucosides (6/6)
Phosphoglycerate transport system (1/8)
Proton−dependent Peptide Transporters (1/6)
Sodium Hydrogen Antiporter (6/21)
Sucrose−specific PTS (1/1)
Ton and Tol transport systems (17/27)
Transport of Manganese (3/8)
Transport of Nickel and Cobalt (8/22)
Transport of Zinc (4/14)
Twin−arginine translocation system (2/5)
Type III secretion system (7/13)
Type III secretion system orphans (2/5)
Type IV pilus (20/21)
Type VI secretion systems (17/25)
Widespread colonization island (12/16)
−0.0015
−0.0010
−0.0005
0.0000
0.0005
0.0010
Effect of perturbation

Metabolism of Aromatic Compounds


Miscellaneous
Drought
Flood
Freeze
Heat
Archease
Hypothetical nudix hydrolase YeaB
FIG017823: ATPase, MoxR family
FIG003620: Proteophosphoglycan precursor (Fragment)
Transcription regulator [contains diacylglycerol kinase catalytic domain]
Aspartyl–tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6)
YrbA protein
YbbL ABC transporter ATP–binding protein
UPF0234 protein YajQ
Putative oxidoreductase YncB
Thiazole biosynthesis protein ThiG
Thiamin biosynthesis protein ThiC
Sulfur carrier protein ThiS
Predicted thiazole transporter ThiU
Hydroxymethylpyrimidine ABC transporter, substrate–binding component
Hydroxyethylthiazole kinase (EC 2.7.1.50)
TrmH family tRNA/rRNA methyltransferase YacO (EC 2.1.1.–)
Small protein similar to cysteinyl–tRNA synthetase
Serine acetyltransferase (EC 2.3.1.30)
Hypothetical protein DUF901, similar to C–terminal domain of ribosome protection–type Tc–resistance proteins
Cysteinyl–tRNA synthetase (EC 6.1.1.16)
tRNA delta(2)–isopentenylpyrophosphate transferase (EC 2.5.1.8)
Nicotinate–nucleotide adenylyltransferase (EC 2.7.7.18)
Nicotinamide–nucleotide adenylyltransferase, NadM family (EC 2.7.7.1)
Nicotinamidase (EC 3.5.1.19)
N–acetylglucosamine–1–phosphate uridyltransferase (EC 2.7.7.23)
LSU m3Psi1915 methyltransferase RlmH
Inorganic pyrophosphatase (EC 3.6.1.1)
Hydrolase (HAD superfamily), YqeK
Glutamate 5–kinase (EC 2.7.2.11)
Gamma–glutamyl phosphate reductase (EC 1.2.1.41)
FIGfam135315: Iojap–related protein
FIG004454: RNA binding protein
LuxB, luciferase beta chain (EC 1.14.14.3)
N–acylamino acid racemase
Similar to non–heme chloroperoxidase, sll5080 homolog
prolyl oligopeptidase family protein
Menaquinone biosynthesis related protein, putative DHNA–CoA thioesterase
Lysophospholipase L2 (EC 3.1.1.5)
Lipase (EC 3.1.1.3) family protein, sll1969 homolog
UPF0246 protein YaaA
Putative stomatin/prohibitin–family membrane protease subunit YbbK
Putative stomatin/prohibitin–family membrane protease subunit aq_911
Putative membrane–bound ClpP–class protease associated with aq_911
Uncharacterized ATP–dependent helicase MJ0294
Tyrosine–specific transport protein
RNase L inhibitor
Putative permease often clustered with de novo purine synthesis
Putative membrane protein YfcA
Putative heat shock protein YegD
Putative GTP–binding protien TM0445
Protein of unknown function YceH
Protein of unknown function DUF81
Pole remodelling regulatory diguanylate cyclase
Phosphocarrier protein kinase/phosphorylase, nitrogen regulation associated
Phosphatidyl–N–methylethanolamine N–methyltransferase (EC 2.1.1.71)
Mitochondrial processing peptidase–like protein (EC 3.4.24.64)
Lipid A export ATP–binding/permease protein MsbA
GTP–binding protein RBG1
Cephalosporin hydroxylase
Archease2 (1/3)
At2g33980 At1g28960 (3/3)
At3g21300 (2/5)
Broadly distributed proteins not in subsystems (4/10)
COG2363 (6/10)
Conserved gene cluster possibly involved in RNA metabolism (5/8)
Iojap (12/13)
Luciferases (1/6)
Muconate lactonizing enzyme family (1/2)
Synechocystis experimental (5/23)
YaaA (1/1)
YbbK (3/4)
ZZ gjo need homes (16/34)
−5e−04
0e+00
5e−04
−5e−04
0e+00
5e−04
−5e−04
0e+00
5e−04
−5e−04
0e+00
5e−04
Effect of perturbation


Motility and Chemotaxis
Drought
Flood
Freeze
Heat
Flagella−related protein FlaH
Signal transduction histidine kinase CheA (EC 2.7.3.−)
Ribose ABC transporter, periplasmic ribose−binding protein RbsB (TC 3.A.1.2.1)
Positive regulator of CheA protein activity (CheW)
Methyl−accepting chemotaxis protein IV (dipeptide chemoreceptor protein)
Methyl−accepting chemotaxis protein II (aspartate chemoreceptor protein)
Methyl−accepting chemotaxis protein I (serine chemoreceptor protein)
Galactose/methyl galactoside ABC transport system, D−galactose−binding periplasmic protein MglB (TC 3.A.1.2.3)
Flagellar motor switch protein FliN
Flagellar motor switch protein FliM
Flagellar motor switch protein FliG
Chemotaxis response regulator protein−glutamate methylesterase CheB (EC 3.1.1.61)
Chemotaxis response − phosphatase CheZ
Chemotaxis regulator − transmits chemoreceptor signals to flagelllar motor components CheY
Chemotaxis protein methyltransferase CheR (EC 2.1.1.80)
Chemotaxis protein CheX
Chemotaxis protein CheV (EC 2.7.3.−)
Chemotaxis protein CheD
Chemotaxis protein CheC −− inhibitor of MCP methylation
Aerotaxis sensor receptor protein
RNA polymerase sigma factor for flagellar operon
Flagellum−specific ATP synthase FliI
Flagellar synthesis regulator FleN
Flagellar motor rotation protein MotA
Flagellar biosynthesis protein FlhF
Flagellar biosynthesis protein FlhA
Negative regulator of flagellin synthesis
Flagellin protein FlaG
Flagellar transcriptional activator FlhD
Flagellar transcriptional activator FlhC
Flagellar trans−acting factor FliX
Flagellar sensor histidine kinase FleS
Flagellar regulatory protein FleQ
Flagellar protein FliJ
Flagellar protein FlbB
Flagellar P−ring protein FlgI
Flagellar hook−length control protein FliK
Flagellar hook−associated protein FliD
Flagellar hook−associated protein 3
Flagellar hook protein FlgE
Flagellar biosynthesis protein FliT
Flagellar biosynthesis protein FliS
Flagellar biosynthesis protein FliP
Flagellar biosynthesis protein FliO
Flagellar biosynthesis protein FliL
Flagellar biosynthesis protein FliC
Flagellar basal−body P−ring formation protein FlgA
Flagellar assembly protein FliH
Flagellin protein FlaB
Flagellin protein FlaA
Flagellar hook−basal body complex protein FliE
Flagellar hook subunit protein
Flagellar basal−body rod protein FlgB
−1e−03
−5e−04
0e+00
5e−04
Effect of perturbation
Archaeal Flagellum (1/6)
Bacterial Chemotaxis (19/20)
Flagellar motility (6/15)
Flagellum (22/38)
Flagellum in Campylobacter (5/6)


Nitrogen Metabolism


Nucleosides and Nucleotides
Drought
Flood
Freeze
Heat
S−adenosylhomocysteine nucleosidase (EC 3.2.2.9)
Purine nucleoside phosphorylase (EC 2.4.2.1)
hypothetical protein Bcep3774, commonly clustered with carotenoid biosynthesis
5'−methylthioadenosine/S−adenosylhomocysteine nucleosidase related protein VF1653
Ribulose bisphosphate carboxylase (EC 4.1.1.39)
Ribose−1,5−bisphosphate isomerase
PurR: transcription regulator associated with purine metabolism
Possible subunit variant of phosphoribosylaminoimidazolecarboxamide formyltransferase [alternate form]
Phosphoribosylglycinamide formyltransferase 2 (EC 2.1.2.−)
Phosphoribosylformylglycinamidine synthase, synthetase subunit (EC 6.3.5.3)
Phosphoribosylformylglycinamidine synthase, PurS subunit (EC 6.3.5.3)
Phosphoribosylformylglycinamidine synthase, glutamine amidotransferase subunit (EC 6.3.5.3)
Phosphoribosylformylglycinamidine cyclo−ligase (EC 6.3.3.1)
Phosphoribosylaminoimidazolecarboxamide formyltransferase [alternate form]
Phosphoribosylaminoimidazole carboxylase ATPase subunit (EC 4.1.1.21)
Amidophosphoribosyltransferase (EC 2.4.2.14)
Adenylosuccinate lyase (EC 4.3.2.2)
Uracil phosphoribosyltransferase (EC 2.4.2.9)
Uracil permease
Orotidine 5'−phosphate decarboxylase (EC 4.1.1.23)
Orotate phosphoribosyltransferase (EC 2.4.2.10)
Dihydroorotate dehydrogenase (EC 1.3.3.1)
Dihydroorotase (EC 3.5.2.3)
Carbamoyl−phosphate synthase large chain A (EC 6.3.5.5)
Aspartate carbamoyltransferase regulatory chain (PyrI)
Deoxyuridine 5'−triphosphate nucleotidohydrolase (EC 3.6.1.23)
N−methylhydantoinase B (EC 3.5.2.14)
N−methylhydantoinase (ATP−hydrolyzing) (EC 3.5.2.14)
N−carbamoyl−L−amino acid hydrolase (EC 3.5.1.87)
Hydantoin racemase (EC 5.1.99.−)
Hydantoin permease
Dihydropyrimidinase (EC 3.5.2.2)
Deacetylases, including yeast histone deacetylase and acetoin utilization protein
Uridine kinase (EC 2.7.1.48)
Urease gamma subunit (EC 3.5.1.5)
Urease beta subunit (EC 3.5.1.5)
Urease alpha subunit (EC 3.5.1.5)
Urea carboxylase (EC 6.3.4.6)
Possible pyrimidine−degrading protein DUF1688
GTP cyclohydrolase II homolog
Allophanate hydrolase (EC 3.5.1.54)
Thiamin−phosphate pyrophosphorylase−like protein
Pyrimidine deoxynucleoside triphosphate (dYTP) pyrophosphohydrolase YfoO
Nudix−like NDP and NTP phosphohydrolase YmfB
Nudix hydrolase family protein YffH
NADH pyrophosphatase (EC 3.6.1.22)
Mutator mutT protein (7,8−dihydro−8−oxoguanine−triphosphatase) (EC 3.6.1.−)
Low G+C gram positive nudix hydrolase YtkD (EC 3.6.−.−)
GDP−mannose pyrophosphatase YffH
Adenosine (5')−pentaphospho−(5'')−adenosine pyrophosphohydrolase (EC 3.6.1.−)
5−methyl−dCTP pyrophosphohydrolase (EC 3.6.1.−)
Ribosomal small subunit pseudouridine synthase A (EC 4.2.1.70)
Pseudouridine kinase (EC 2.7.1.83)
Pseudouridine 5'−phosphate glycosidase
Probable pyrimidine nucleoside transport protein associated with pseudouridine catabolism
Xanthine phosphoribosyltransferase (EC 2.4.2.22)
putative Adenosine kinase (EC 2.7.1.20)
preQ1−regulated inosine−uridine nucleoside hydrolase (EC 3.2.2.1)
Possible hypoxanthine oxidase XdhD (EC 1.−.−.−)
Nucleotide pyrophosphatase (EC 3.6.1.9)
Nucleoside diphosphate kinase (EC 2.7.4.6)
Inosine−uridine preferring nucleoside hydrolase (EC 3.2.2.1)
Inosine−5'−monophosphate dehydrogenase (EC 1.1.1.205)
IMP dehydrogenase related 2 (EC 1.7.1.7)
GMP synthase [glutamine−hydrolyzing] (EC 6.3.5.2)
GMP reductase (EC 1.7.1.7)
Deoxyguanosinetriphosphate triphosphohydrolase (EC 3.1.5.1)
Deoxyguanosine kinase (EC 2.7.1.113)
Adenosine deaminase (EC 3.5.4.4)
Adenine deaminase (EC 3.5.4.2)
5'−nucleotidase family protein in cluster with NagD−like phosphatase
5'−nucleotidase (EC 3.1.3.5)
2',3'−cyclic−nucleotide 2'−phosphodiesterase (EC 3.1.4.16)
Purine nucleotide synthesis repressor
XdhC protein (assists in molybdopterin insertion into xanthine dehydrogenase)
Xanthine/uracil/thiamine/ascorbate permease family protein
Xanthine/uracil transporter
Xanthine transporter,putative
Xanthine permease
Xanthine dehydrogenase, molybdenum binding subunit (EC 1.17.1.4)
Xanthine dehydrogenase, iron−sulfur cluster and FAD−binding subunit A (1.17.1.4)
Xanthine dehydrogenase iron−sulfur subunit (EC 1.17.1.4)
Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF family
Periplasmic aromatic aldehyde oxidoreductase, FAD binding subunit YagS
Guanine−hypoxanthine permease
Guanine deaminase (EC 3.5.4.3)
Uridine phosphorylase (EC 2.4.2.3)
Uridine kinase (EC 2.7.1.48) [C1]
Deoxycytidine triphosphate deaminase (EC 3.5.4.13)
CTP synthase (EC 6.3.4.2)
Transcriptional regulator RutR of pyrimidine catabolism (TetR family)
Pyrimidine ABC transporter, transmembrane component 2
Pyrimidine ABC transporter, transmembrane component 1
Pyrimidine ABC transporter, substrate−binding component
Pyrimidine ABC transporter, ATP−binding protein
Pyridine nucleotide−disulphide oxidoreductase associated with reductive pyrimidine catabolism
Possible pyrimidine permease in reductive pathway
Dihydropyrimidine dehydrogenase [NADP+] (EC 1.3.1.2)
Ribonucleotide reductase transcriptional regulator NrdR
Ribonucleotide reductase of class III (anaerobic), large subunit (EC 1.17.4.2)
Ribonucleotide reductase of class III (anaerobic), activating protein (EC 1.97.1.4)
Ribonucleotide reductase of class Ib (aerobic), beta subunit (EC 1.17.4.1)
Ribonucleotide reductase of class Ib (aerobic), alpha subunit (EC 1.17.4.1)
Ribonucleotide reductase of class Ia (aerobic), beta subunit (EC 1.17.4.1)
Ribonucleotide reductase of class Ia (aerobic), alpha subunit (EC 1.17.4.1)
Hypoxanthine/guanine permease PbuG
Xanthosine permease
Adenosyl nucleosidases (4/7)
AMP to 3−phosphoglycerate (2/4)
De Novo Purine Biosynthesis (11/17)
De Novo Pyrimidine Synthesis (8/12)
Housecleaning nucleoside triphosphate pyrophosphatases (1/6)
Hydantoin metabolism (7/11)
Novel non−oxidative pathway of Uracil catabolism (8/9)
Nudix proteins (nucleoside triphosphate hydrolases) (10/27)
Pseudouridine Metabolism (4/6)
Purine conversions (18/26)
Purine nucleotide synthesis regulator (1/1)
Purine Utilization (12/16)
pyrimidine conversions (4/7)
Pyrimidine utilization (8/14)
Ribonucleotide reduction (7/9)
Xanthine Metabolism in Bacteria (1/1)
Xanthosine utilization (xap region) (1/5)
−5e−04
0e+00
5e−04
−5e−04
0e+00
5e−04
−5e−04
0e+00
5e−04
−5e−04
0e+00
5e−04
Effect of perturbation

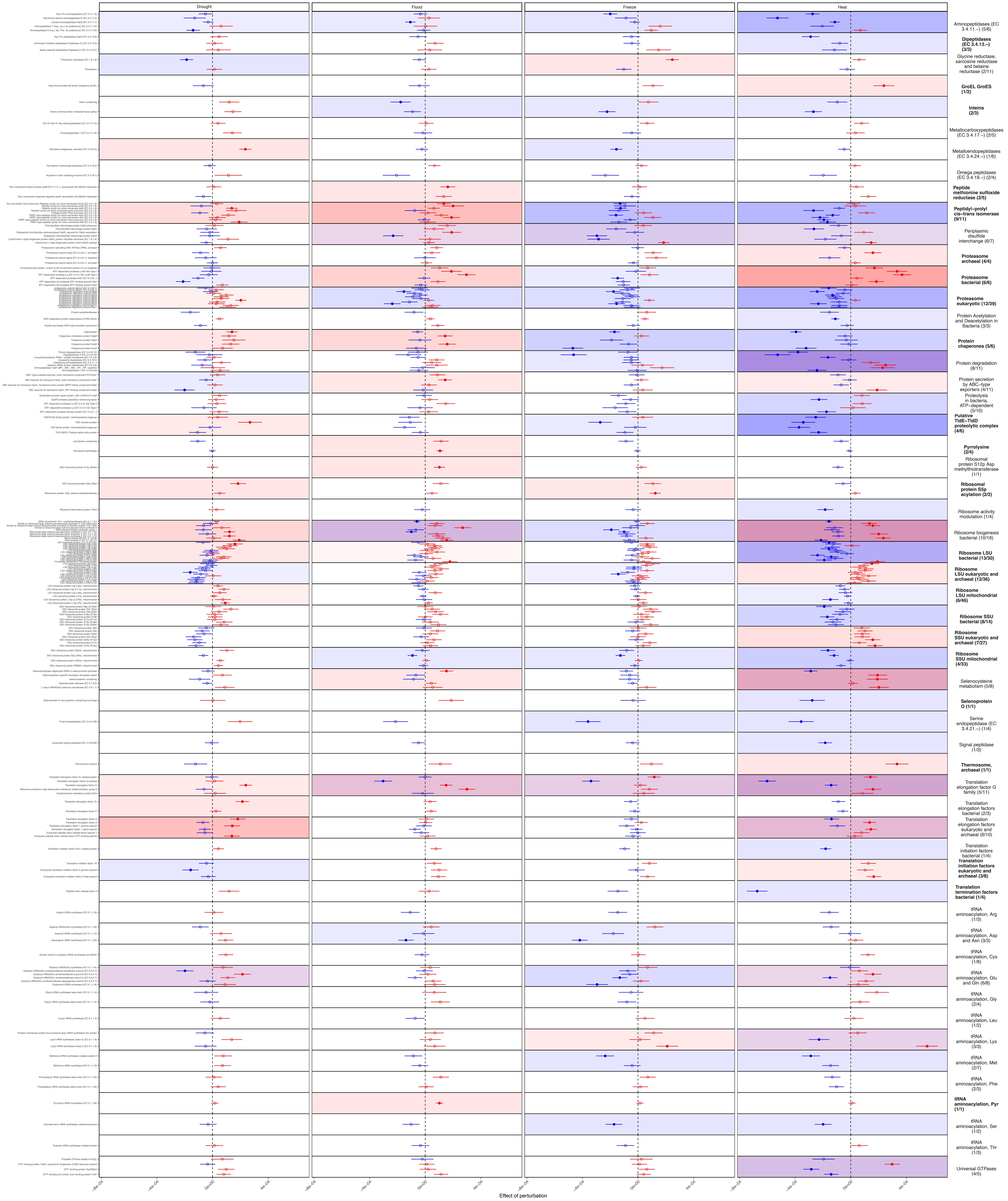

Phages, Prophages, Transposable elements, Plasmids
Drought
Flood
Freeze
Heat
Transposase OrfAB, subunit B
TniB NTP−binding protein
Segregation and condensation protein B
Resolvase/Integrase TniR protein
protein of unknown function DUF1612
protein of unknown function DUF1403
Predicted nucleotidyltransferases
Plasmid replication protein RepA
ISPsy4, transposition helper protein
ISPsy4, transposase
Integrase/recombinase clustered with segregation and condensation protein B
Putative mobilization protein BF0133
Putative conjugative transposon mobilization protein BF0132
Conjugative transposon protein TraN
Conjugative transposon protein TraK
Conjugative transposon protein TraJ
Conjugative transposon protein TraI
Conjugative transposon protein TraG
Conjugative transposon protein TraF
Conjugative transposon protein TraE
Integron integrase IntIPac
Integron integrase IntI1
Integron integrase
Zinc metalloproteinase precursor (EC 3.4.24.29)
Phage capsid and scaffold
Phage portal
Site−specific tyrosine recombinase
Site−specific recombinase
Integrase
Phage terminase, large subunit
Phage terminase small subunit
Phage terminase large subunit
Phage portal protein
Phage DNA packaging
Phage DNA binding protein
Phage tail fiber protein
Phage tape measure
Phage tail assembly
Phage minor tail protein
Outer membrane and periplasm component of type IV secretion of T−DNA complex, has secretin−like domain, VirB9
Phage−associated cell wall hydrolase
Degenerate integrase, superantigen−encoding pathogenicity islands SaPI
T7−like phage primase/helicase protein
T7−like phage endonuclease (EC 3.1.21.2)
CBSS−203122.12.peg.188 (11/17)
transposon, Bacteroidales (9/17)
Integrons (3/5)
Pathogenicity Island LIPI−1 extended (1/6)
Phage capsid proteins (1/11)
Phage entry and exit (1/9)
Phage integration and excision (3/14)
Phage packaging machinery (6/9)
Phage tail fiber proteins (1/4)
Phage tail proteins 2 (3/13)
Plasmid−encoded T−DNA transfer (1/20)
Prophage lysogenic conversion modules (1/2)
Staphylococcal pathogenicity islands SaPI (1/12)
T7−like phage core proteins (2/5)
−4e−04
−2e−04
0e+00
2e−04
4e−04
Effect of perturbation


Phosphorus Metabolism
Drought
Flood
Freeze
Heat
Protein RcsF
PhnI protein
PhnH protein
Metal−dependent hydrolase involved in phosphonate metabolism
Putative periplasmic phosphate−binding protein PstS (Catenulisporaceae type)
Phosphate transport system regulatory protein PhoU
Phosphate transport system permease protein PstA (TC 3.A.1.7.1)
Phosphate transport ATP−binding protein PstB (TC 3.A.1.7.1)
Phosphate regulon transcriptional regulatory protein PhoB (SphR)
Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3)
Phosphate ABC transporter, periplasmic phosphate−binding protein PstS (TC 3.A.1.7.1)
Soluble pyridine nucleotide transhydrogenase (EC 1.6.1.1)
Sodium−dependent phosphate transporter
secreted alkaline phosphatase
response regulator in two−component regulatory system with PhoQ
Pyrophosphate−energized proton pump (EC 3.6.1.1)
Putative periplasmic phosphate−binding protein PstS (Mycoplasma type)
Probable low−affinity inorganic phosphate transporter
Predicted ATPase related to phosphate starvation−inducible protein PhoH
Polyphosphate kinase (EC 2.7.4.1)
NAD(P) transhydrogenase subunit beta (EC 1.6.1.2)
NAD(P) transhydrogenase alpha subunit (EC 1.6.1.2)
Integral membrane protein YggT, involved in response to extracytoplasmic stress (osmotic shock)
Inorganic pyrophospatase PpaX (EC 3.1.3.18)
Exopolyphosphatase (EC 3.6.1.11)
Distant similarity with phosphate transport system regulator
Alkaline phosphatase like protein
2−aminoethylphosphonate:pyruvate aminotransferase (EC 2.6.1.37)
Phosphonoacetate hydrolase (EC 3.11.1.2)
2−aminoethylphosphonate uptake and metabolism regulator
2−aminoethylphosphonate ABC transporter permease protein I (TC 3.A.1.9.1)
Alkylphosphonate utilization (4/13)
High affinity phosphate transporter and control of PHO regulon (7/9)
Phosphate metabolism (16/27)
Phosphoenolpyruvate phosphomutase (1/3)
Phosphonate metabolism (3/8)
−6e−04
−4e−04
−2e−04
0e+00
2e−04
Effect of perturbation


Photosynthesis
Drought
Flood
Freeze
Heat
Light–harvesting LHI, beta subunit
Light–harvesting LHI, alpha subunit
photosystem I biogenesis protein BtpA
photosystem II protein D1 (PsbA)
Photosystem II CP43 protein (PsbC)
Photosynthetic reaction center cytochrome c subunit
Spheroidene monooxygenase
Bacterial light–harvesting proteins (2/12)
Photosystem I (1/16)
Photosystem II (2/23)
Photosystem II–type photosynthetic reaction center (1/5)
Proteorhodopsin (1/2)
−1e−04
0e+00
1e−04
Effect of perturbation


Potassium metabolism
Drought
Flood
Freeze
Heat
Trk system potassium uptake protein TrkA
Glutathione−regulated potassium−efflux system protein KefB
Glutathione−regulated potassium−efflux system ATP−binding protein
Glutathione−regulated potassium−efflux system ancillary protein KefF
Potassium uptake protein, integral membrane component, KtrB
Potassium uptake protein, integral membrane component, KtrA
Trk system potassium uptake protein TrkG
Potassium voltage−gated channel subfamily KQT
Potassium uptake protein TrkH
Potassium efflux system KefA protein
Potassium channel protein
Possible potassium−efflux system protein
Osmosensitive K+ channel histidine kinase KdpD (EC 2.7.3.−)
Kup system potassium uptake protein
Kef−type transport system 2 (probable substrate potassium), subunit 2
Kef−type K+ transport systems (NAD−binding component fused to domain related to exopolyphosphatase)
Glutathione−regulated potassium−efflux system protein KefC
Glutathione−regulated potassium−efflux system and associated functions (4/6)
Hyperosmotic potassium uptake (2/3)
Potassium homeostasis (11/25)
−4e−04
−2e−04
0e+00
2e−04
4e−04
Effect of perturbation

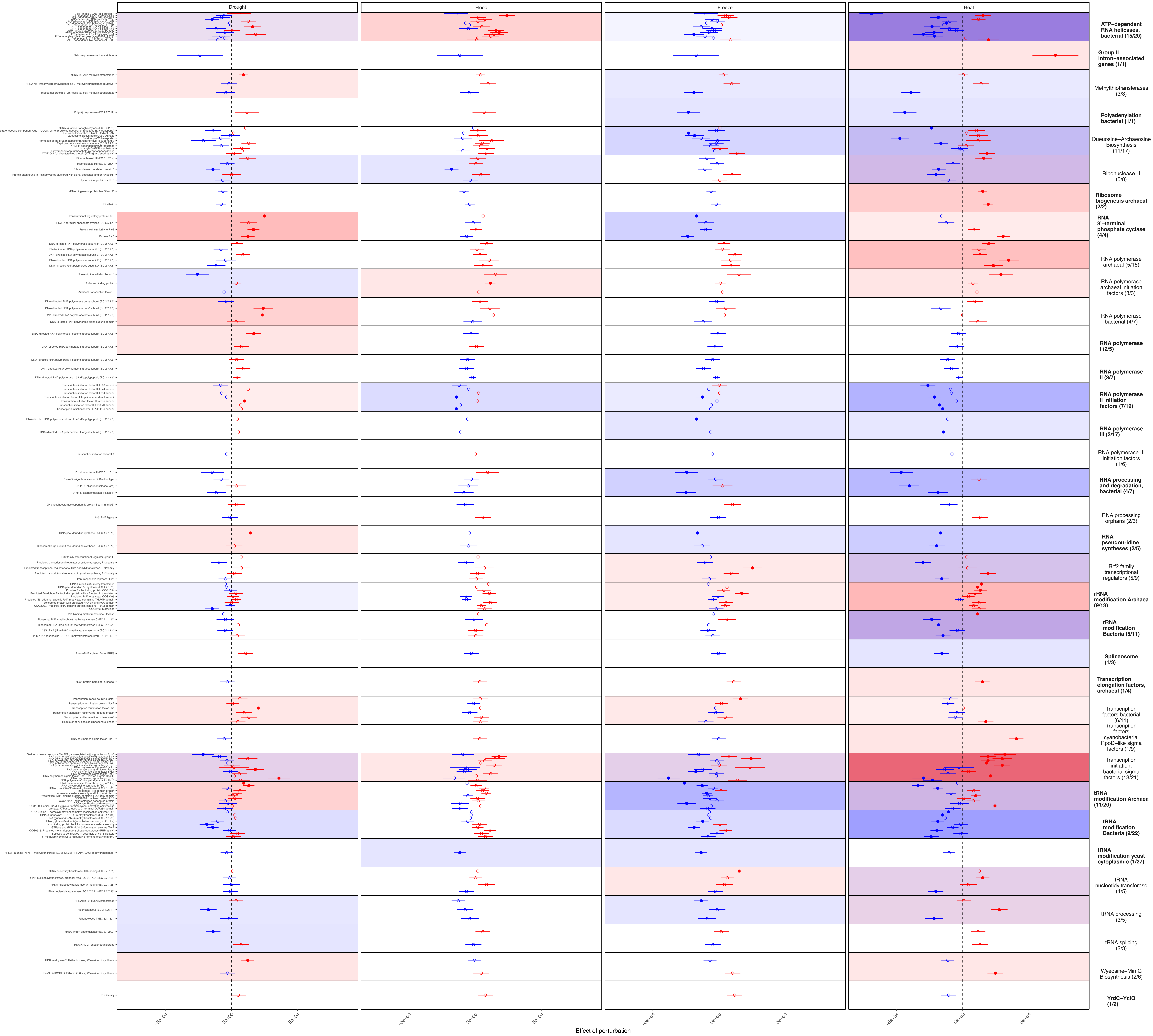
Protein Metabolism



Regulation and Cell signaling


Respiration
Drought
Flood
Freeze
Heat
Anaerobic respiratory reductases (25/44)
Biogenesis of c−type cytochromes (12/26)
Biogenesis of cbb3−type cytochrome c oxidases (2/2)
Biogenesis of cytochrome c oxidases (7/10)
Carbon monoxide dehydrogenase maturation factors (4/5)
Carbon monoxide induced hydrogenase (9/23)
CO Dehydrogenase (6/6)
Coenzyme F420 hydrogenase (1/9)
Coenzyme F420−H2 dehydrogenase (methanophenazine) (1/14)
Energy−conserving hydrogenase (ferredoxin) (6/6)
F0F1−type ATP synthase (7/10)
Formate hydrogenase (24/44)
Hydrogenases (30/55)
Na(+)−translocating NADH−quinone oxidoreductase and rnf−like group of electron transport complexes (6/14)
Na+ translocating decarboxylases and related biotin−dependent enzymes (6/13)
NiFe hydrogenase maturation (5/8)
Quinone oxidoreductase family (3/7)
Respiratory Complex I (12/33)
Respiratory dehydrogenases 1 (3/9)
Soluble cytochromes and functionally related electron carriers (10/16)
Succinate dehydrogenase (6/14)
Terminal cytochrome C oxidases (14/26)
Terminal cytochrome d ubiquinol oxidases (4/7)
Terminal cytochrome O ubiquinol oxidase (3/4)
Terminal cytochrome oxidases (4/4)
Tetrathionate respiration (6/6)
trimethylamine N−oxide (TMAO) reductase (5/11)
Ubiquinone Menaquinone−cytochrome c reductase complexes (4/6)
V−Type ATP synthase (4/10)
−4e−04
0e+00
4e−04
Effect of perturbation

RNA Metabolism




Secondary Metabolism
Drought
Flood
Freeze
Heat
Pleiotropic negative regulator for morphological and physiological development in Streptomyces, BldD
Inducers of aerial mycelium formation biosynthesis protein BldG
Deoxyhypusine synthase
Isoflavone reductase homolog P3 (EC 1.3.1.–)
Tryptophan synthase beta chain (EC 4.2.1.20)
Tryptophan synthase alpha chain (EC 4.2.1.20)
Phosphoribosylanthranilate isomerase (EC 5.3.1.24)
Nitrilase 2 (EC 3.5.5.1)
Nitrilase 1 (EC 3.5.5.1)
Anthranilate phosphoribosyltransferase (EC 2.4.2.18)
Peroxidase (EC 1.11.1.7)
Dihydroflavonol–4–reductase (EC 1.1.1.219)
Cinnamoyl–CoA reductase (EC 1.2.1.44)
Monoglyceride lipase (EC 3.1.1.23)
3–phenylpropionate dioxygenase ferredoxin subunit
3–(3–hydroxy–phenyl)propionate hydroxylase (EC 1.14.13.–)
2,3–dihydroxy–2,3–dihydro–phenylpropionate dehydrogenase (EC 1.3.1.–)
Chalcone synthase (EC 2.3.1.74)
4–coumarate––CoA ligase 1 (EC 6.2.1.12)
NRPS module 4 PG–Ser–Gly–Thr
NRPS module 3 PG–PG
NRPS module 2 PG–PG–Asn
NRPS loading module Thr–PG–PG–Thr
Phenazine biosynthesis protein PhzF
flavonoid 7–O–methyltransferase (EC 2.1.1.75)
6–Methyl salicylic acid synthase
−2e−04
0e+00
2e−04
4e−04
Effect of perturbation
and other bacterial
morphogens (2/5)
biosynthesis from
L–lysine (1/2)
Apigenin
derivatives (1/1)
Auxin biosynthesis
(6/11)
Auxin degradation
(1/3)
Biflavanoid
biosynthesis (1/3)
Caffeic acid
derivatives (1/1)
Cannabinoid
biosynthesis (1/2)
Cinnamic Acid
Degradation (3/9)
Flavanone
biosynthesis (2/4)
(NRPS) in Frankia
sp. Ccl3 (4/4)
Phenazine
biosynthesis (1/8)
Phytoalexin
biosynthesis (1/4)
acid biosynthesis?
(1/2)


Stress Response
Drought
Flood
Freeze
Heat
Acid resistance mechanisms (4/6)
Bacterial hemoglobins (6/7)
Carbon Starvation (5/9)
Choline and Betaine Uptake and Betaine Biosynthesis (13/27)
Cold shock, CspA family of proteins (4/8)
Dimethylarginine metabolism (1/3)
Ectoine biosynthesis and regulation (2/6)
Flavohaemoglobin (1/3)
Glutaredoxins (6/12)
Glutathione analogs: mycothiol (10/10)
Glutathione-dependent pathway of formaldehyde detoxification (2/5)
Glutathione: Biosynthesis and gamma-glutamyl cycle (7/9)
Glutathione: Non-redox reactions (12/24)
Glutathione: Redox cycle (1/2)
Glutathionylspermidine and Trypanothione (2/3)
Heat shock dnaK gene cluster extended (17/19)
Hfl operon (5/6)
O-antigen capsule important for environmental persistence (2/10)
Osmoprotectant ABC transporter YehZYXW of Enterobacteriales (1/4)
Osmoregulation (3/3)
Oxidative stress (20/38)
Periplasmic Stress Response (5/5)
Phage shock protein (psp) operon (3/7)
Protection from Reactive Oxygen Species (1/1)
Redox-dependent regulation of nucleus processes (1/4)
Regulation of Oxidative Stress Response (3/4)
Rubrerythrin (5/5)
SigmaB stress responce regulation (4/7)
Synthesis of osmoregulated periplasmic glucans (6/9)
Universal stress protein family (6/13)
Uptake of selenate and selenite (5/8)
-5e-04
0e+00
5e-04
Effect of perturbation

Sulfur Metabolism


Virulence, Disease and Defense
Drought
Flood
Freeze
Heat
β–Fimbriae (2/3)
σ–Fimbriae (2/5)
Acyl Homoserine Lactone (AHL) Autoinducer Quorum Sensing (2/10)
Adaptation to d–cysteine (2/4)
Adhesion of Campylobacter (1/8)
Aminoglycoside adenylyltransferases (1/2)
Arsenic resistance (5/6)
Bacitracin Stress Response (10/14)
Bacterial cyanide production and tolerance mechanisms (6/14)
Beta–lactamase (10/16)
BlaR1 Family Regulatory Sensor–transducer Disambiguation (6/10)
C jejuni colonization of chick caeca (4/8)
Cadmium resistance (1/3)
Cobalt–zinc–cadmium resistance (8/21)
Copper homeostasis (8/14)
Erythromycin resistance (1/2)
Fosfomycin resistance (1/3)
Listeria surface proteins: Internalin–like proteins (6/33)
Marinocine, a broad–spectrum antibacterial protein (1/2)
Mediator of hyperadherence YidE in Enterobacteria and its conserved region (2/7)
Mercuric reductase (2/2)
Mercury resistance operon (1/7)
Methicillin resistance in Staphylococci (3/12)
MexE–MexF–OprN Multidrug Efflux System (3/4)
MLST (1/2)
Multidrug efflux pump in Campylobacter jejuni (CmeABC operon) (3/4)
Multidrug Resistance Efflux Pumps (9/15)
Multidrug Resistance Operon mdtRP of Bacillus (1/2)
Pertussis toxin (1/2)
Polymyxin Synthetase Gene Cluster in Bacillus (1/4)
Resistance to chromium compounds (4/5)
Resistance to fluoroquinolones (1/2)
Resistance to Vancomycin (4/6)
Streptococcus pneumonae Vancomycin Tolerance Locus (1/5)
Streptococcus pyogenes recombinatorial zone (2/6)
Streptothricin resistance (1/1)
The mdtABCD multidrug resistance cluster (2/6)
Tolerance to colicin E2 (4/5)
Type 1 pili (mannose–sensitive fimbriae) (2/8)
Type 4 secretion and conjugative transfer (32/61)
Zinc resistance (2/3)
−0.0015
−0.0010
−0.0005
0.0000
0.0005
0.0010
Effect of perturbation