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NET
NOX
           rob Rob transcriptional activator
        phoP PhoP-Phosphorylated transcriptional dual regulator rfaP lipopolysaccharide core biosynthesis; phosphorylation of core heptose rfaB UDP-D-galactose:(glucosyl)lipopolysaccharide-1,6-D-galactosyltransferase yrbE YrbF/YrbE ABC transporter yrbB predicted NTP-binding protein qseB QseB-Phosphorylated transcriptional activator rseB anti-sigma factor.
          rseB anti-sigma factor
         yphD YphD/YphE/YphF ABC transporter
yfgC predicted peptidase
dedA conserved inner membrane protein
          arnF putative transport/receptor protein
          yeiU protein with low undecaprenyl pyrophosphate phosphatase activity
         motJ MotJ SMR protein
potl putrescine ABC transporter
ybiS conserved protein
glpF GlpF - glycerol MIP channel
yihS predicted glucosamine isomerase
          rfe undecaprenyl-phosphate alpha;-N-acetylglucosaminyl transferase rfaQ lipopolysaccharide core biosynthesis protein; heptosyl transferase III
         rad lipopolysaccharide core biosyntransferase II quef NADPH-dependent nitrile oxidoreductase monomer yfdQ CPS-53 (KpLE1) prophage; predicted protein maly bifunctional: repressor of maltose regulon uspE universal stress protein with a role in resistance to UV irradiation yjhU KpLE2 phage-like element; predicted DNA-binding transcriptional regulator rbsC ribose ABC transporter
         yhhL conserved inner membrane protein
ygeY predicted peptidase
acrB AcrB RND-type permease
cyaA adenylate cyclase
         yagW predicted receptor
trkA NAD-binding component of TrK potassium transporter
acrR AcrR transcriptional repressor
         sapD peptide uptake ABC transporter trxB thioredoxin reductase monomer
          Ion DNA-binding, ATP-dependent protease La
          ppk degradosome
          gnd 6-phosphogluconate dehydrogenase (decarboxylating)
         pykF pyruvate kinase I monomer
dnaT primosome
yjiA P-loop guanosine triphosphatase
lexA LexA transcriptional repressor
                                                                                                               dgkA diacylglycerol kinase
                                                                                                                                                            Key
          metA homosérine O-succinyltransferase
         trkH TrkH potassium ion Trk Transporter
hemC hydroxymethylbilane synthase
wzxE lipid III flippase
                                                                                                                                      Z-scores
          wzki lipia in imposos
ptsN phosphotransferase system enzyme IIA, regulates N metabolism
gcvH H-protein-(dihydrolipoyl)lysine
          sixA phosphohistidine phosphatase rcsC RcsC-P his
          ccmD CcmABCDEFGH cytochrome c biogenesis system
        ccmD CcmABCDEFGH cytochrome c biogenesis system sufA Fe-S cluster assembly protein sufB component of SufB-SufC-SufD cysteine desulfurase (SufS) activator complex sufD component of SufB-SufC-SufD cysteine desulfurase (SufS) activator complex sufS L-selenocysteine lyase (and L-cysteine desulfurase) monomer sapB peptide uptake ABC transporter sapF peptide uptake ABC transporter mdoH membrane glycosyltransferase; synthesis of membrane-derived oligosaccharide (MDO) mdoG periplasmic glucan (MDO) biosynthesis protein aspC aspartate aminotransferase, PLP-dependent bioC predicted methyltransferase, enzyme of biotin synthesis kefA KefA ompR OmpR transcriptional dual regulator
          ompR OmpR transcriptional dual regulator
          yagE predicted protein
          wza lipoprotein required for capsular polysaccharide translocation through the outer membrane
          slyB outer membrane lipoprotein
ompF The Colicin A Import System
apaH diadenosine tetraphosphatase
          cysQ affects pool of 3'-phosphoadenosine-5'-phosphosulfate in pathway of sulfite synthesis purH AICAR transformylase / IMP cyclohydrolase glnA adenylyl-[glutamine synthetase]
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Figure S5. Loci whose disruption was significant in at least one tetracycline.

Yellow (blue) indicates that transposon insertions in or near a gene were beneficial (deleterious). Black indicates no significant effect; gray indicates missing data. Z-scores were calculated as described in *Materials and Methods*.