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cyaA adenylate cyclase fliZ predicted regulator of FliA activity trxB thioredoxin reductase monomer acrR AcrR transcriptional repressor typA protein possibly involved in LPS biosynthesis and host colonization trkH TrkH potassium ion Trk Transporter fre FMN reductase ubiD 3-octaprenyl-4-hydroxybenzoate carboxy-lyase monomer pitA PitA slyD FKBP-type peptidyl prolyl cis-trans isomerase trkA NAD-binding component of TrK potassium transporter rpoN RNA polymerase, sigma 54 (sigma N) factor greA transcription elongation factor GreA speA arginine decarboxylase, biosynthetic ptsI PTS enzyme I ptsH HPr sixA phosphohistidine phosphatase spex arginine decarboxylase, biosynthetic ptsI PTS enzyme I ptsH HPr sixA phosphohistidine phosphatase gnd 6-phosphogluconate dehydrogenase (decarboxylating) filA RNA polymerase, sigma 28 (sigma F) factor zwf glucose 6-phosphate-1-dehydrogenase pro fail-specific protease indoD glucan biosynthesis protein D sapC peptide uptake ABC transporter sapD peptide uptake ABC transporter sapC aspartate aminotransferase, PLP-dependent Irp Lrp transcriptional dual regulator dcd dCTP deaminase fiiG flagellar motor switch protein FliG cdd cyftdine deaminase udk uridine kinase / cyftdine kinase figC flagellar basal-body rod protein FligC ptsN phosphotransferase system enzyme IIA, regulates N metabolism dnaJ chaperone with DnaK; heat shock protein ftB flagellar biosynthesis protein FliB fligJ flagJ feoA ferrous iron transport protein A ygbE putative cytochrome oxidase subunit gcvT aminomethyltransferase flhD FlhDC transcriptional dual regulator rcsC RcsC-P his flhC Flagellar mice glucan (MDO) biosynthesis protein rcsC RcsC-P his flhC FlhDC transcriptional dual regulator arcB ArcB-P his292 fliN flagellar motor switch protein FliM mdoH membrane glycosyttransferase; synthesis of membrane-derived The FIND Transcriptional dual regulator arcB ArcB-P his292 filN flagellar motor switch protein FIIN mdoH membrane glycosyltransferase; synthesis of membrane-derived oligosaccharide (MDO) figG flagellar basal-body rod protein FIgG lon DNA-binding, ATP-dependent protease La flgF flagellar basal-body rod protein FIgF flgE flagellar book protein FIgE flgD flagellar biosynthesis, initiation of hook assembly flgM anti-sigma factor for FIIA (sigma 28) afpD ATP synthase, F1 complex, beta; subunit elbB isoprenoid biosynthesis protein with amidotransferase-like domain kdsD D-arabinose 5-phosphate isomerase gevP glycine decarboxylase mPA MprA transcriptional repressor fliR flagellar biosynthesis protein FIIA flig flagellar biosynthesis protein FIIA hyp murein lipoprotein pykF pyruvate kinase I monomer mtA Mic titration factor fliD flagellar cop protein FID; filament capping protein; enables filament assembly dhaR DhaR transcriptional dual regulator pyrD dihydroorotate oxidase fepA FepA, outer membrane receptor for ferric enterobactin (enterochelin) and colicins B and D rfaP lipopolysaccharide core biosynthesis; phosphorylation of core heptose dhaB primosome wzzE ipredicted Wzy protein involved in ECA polysaccharide chain elongation wzzE ipredicted transcriptional regulator rsmD 16S rRNA m 20966 methyltransferase yeP predicted transcriptional regulator smD 16S rRNA m 20966 methyltransferase yeP predicted racemase gedA_conserved inner membrane protein Key yeA predicted racemase dedA_conserved inner membrane protein Z-score ygeA predicted racemase dedA conserved inner membrane protein rbsR RbsR transcriptional repressor barA BarA-P his 7-score rosk kosk transcriptional repressor barA BarA-P his damX predicted membrane-anchored protein, interferes with cell division ftsP cell division protein required during stress conditions yfgC predicted peptidase ydpG conserved protein ompC outer membrane porin C anmK anhydro-N-acetylmuramic acid kinase rcsF RcsF-P rob Rob transcriptional activator stt soluble lytic murein transglycosylase ampC beta, lactamase, penicillin resistance degQ serine endoprotease, periplasmic mtB membrane-bound lytic murein transglycosylase B ampG AmpG muropeptide MFS transporter phoP PhoP-Phosphorylated transcriptional dual regulator acrB AcrB RND-type permease rfbA dTDP-glucose pyrophosphorylase yecR predicted protein rffA dTDP-4-oxo-6-deoxy-D-glucose transaminase rhB degradosome

Figure S9. Loci whose disruption was significant in at least one β -lactam.

Yellow (blue) indicates that transposon insertions in or near a gene were beneficial (deleterious). Black indicates no significant effect. Z-scores were calculated as described in *Materials and Methods*. Note that this set of loci is distinct from the set of loci whose disruption caused significant changes in all the β -lactams tested (Table S2).