## NAL

rfal UDP-D-glucose:(glucosyl)LPS alpha;-1,3-glucosyltransferase radA DNA recombination protein geB QseB-Phosphorylated transcriptional activator pspF PspF transcriptional dual regulator potH putrescine ABC transporter potH putrescine ABC transporter pntA pyridine nucleotide transhydrogenase, alpha; subunit pepT peptidase T mapG ferredoxin-type protein mutT dGTP pyrophosphohydrolase mtD mannitol-1-phosphate 5-dehydrogenase hyfA hydrogenase 4, component A hyaD protein involved in processing of HyaA and HyaB proteins hyaA hydrogenase 1, small subunit gltJ GltJJKL glutamate ABC transporter focA FocA formate FNT transporter flgD flagellar biosynthesis, initiation of hook assembly flgC flagellar basal-body rod protein FlgC fepB Ferric Enterobactin Transport System efp protein chain elongation factor EF-P dusB tRNA dihydrouridine synthase dcuS DcuS-P his349 cyoB cytochrome bo terminal oxidase subunit 1 crl Crl transport parts cyoB cytochrome bo terminal oxidase subunit I crl transcriptional regulator ampE predicted inner membrane protein yraM putative glycosylase yobD conserved inner membrane protein yhiD conserved inner membrane protein yfiD yh[D conserved inner membrane protein
yf[C)
yf[C) predicted peptidase
yf[C] predicted hydrolase, inner membrane
ybDA YbbA/YbbP ABC transporter
wzzxE lipid III flippase
sfsB Nip transcriptional regulator
rffA dT DP-4-oxo-6-deoxy-D-glucose transaminase
rfaQ lipopolysaccharide core biosynthesis protein; heptosyl transferase III
rfaP lipopolysaccharide core biosynthesis: phosphorylation of core heptose
phoP PhoP-Phosphorylated transcriptional dual regulator
envZ EnvZ
rfaG lipopolysaccharide glucosyltransferase I
recN protein used in recombination and DNA repair
ybgS conserved protein
rvbB predicted NTP-binding protein
yrbE YrbF/YrbE ABC transporter
rfaB UDP-D-galactose:(glucosyl)lipopolysaccharide-1,6-D-galactosyltransferase ompC outer membrane porin C
yghD predicted DNA-binding transcriptional regulator
ygeR putative lipoprotein; predicted DNA-binding transcriptional regulator
ygeR putative lipoprotein; predicted DNA-binding transcriptional regulator
yfgP conserved protein
yfb redicted DNA-binding transcriptional regulator
yfgP predicted DNA-binding transcriptional regulator
yfgP conserved protein
yfb conserved protein
yfb conserved protein 

 yfgl putative membrane protein

 yfgl putative membrane protein

 yfaD conserved protein

 yeiU protein with low undecaprenyl pyrophosphate phosphatase activity

 yegT YegT MFS transporter

 yecR predicted protein with FAD/NAD(P)-binding domain

 ydcL conserved protein with FAD/NAD(P)-binding domain

 ydcL conserved protein

 ybil FMN phosphatase

 ybil conserved protein

 ybiA conserved protein

 ydb conserved protein
 4.0101004 Key rob Rob transcriptional activator rhIE DEAD-box-containing ATP-dependent RNA helicase family member rcsF RcsF-P mile DEAD-box-containing ATP-dependent RNA helicase family member rcsF RcsF-P proA gamma;-glutamyl kinase-GP-reductase multienzyme complex norR NorR transcriptional dual regulator melB MelB GPH transporter exuR ExuR transcriptional repressor ebgR EbgR transcriptional repressor dinI DNA damage-inducible protein I cyoA cytochrome bo terminal oxidase subunit II cls cardiolipin synthase cbpA CbpA monomer aroG 2-dehydro-3-deoxyphosphoheptonate aldolase agaR AgaR transcriptional repressor acrB AcrB RND-type permease ypdB predicted response regulator in two-component system with YpdA ymdB putative polyprotein yilS conserved protein yilS conserved protein yhcD predicted outer membrane protein rsgA ribosome small subunit-dependent GTPase A ppk degradosome ppc phosphoenolpyruvate carboxylase pabB pra-aminohenzoate synthase multi-enzyme complex rsgA ribosome small subunit-dependent GTPase A ppk degradosome pabB para-aminobenzoate synthase multi-enzyme complex miaA delta;(2)-isopentenylpyrophosphate tRNA-adenosine transferase dnaJ chaperone with DnaK; heat shock protein yidi predicted inner membrane protein ybjE predicted transporter usg predicted semialdehyde dehydrogenase truA tRNA pseudouridine synthase I trKH TrKH potassium ion TrK Transporter trKA NAD-binding component of TrK potassium transporter sapE peptide uptake ABC transporter sapB peptide uptake ABC transporter gpsA glycerol-3-phosphate-dehydrogenase-[NAD+] acrR AcrR transcriptional repressor fIX putative GTPase; possible regulator of HfIKC fbaA fructose bisphosphate aldolase monomer cyaA adenylate cyclase aroH 2-dehydro-3-deoxyphosphoheptonate aldolase yhdX YhdW/YhdX/YhdY/YhdZ ABC transporter ycBD conserved protein ycaB predicted phosphoting transcriptional regulator LYSB-type

ynA predicted phosphotransterase/kinase yhdX YhdW/YhdX/YhdZ ABC transporter ycjD conserved protein yahB predicted DNA-binding transcriptional regulator LYSR-type tusC sulfur transfer protein complex, TusC subunit sgcQ putative nucleoside triphosphatase nadB L-aspartate oxidase metL aspartate kinase / homoserine dehydrogenase mtoH membrane glycosyltransferase; synthesis of membrane-derived oligosaccharide (MDO) mdoG periplasmic glucan (MDO) biosynthesis protein

## Figure S4. Loci whose disruption was significant in at least one quinolone.

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*.