

Table S4. Gene mutants identified enriched or depleted in murine liver after intravenous infection (cutoff: adj. p-Values <= 0.0005)

ID	log ₂ FC	Adj. p-Value	gene	annotation
RSAU_001097	-5.74	0.0000233	def	Peptide deformylase
RSAU_000902	-5.35	0.0000354	ugtP	Processive diacylglycerol glucosyltransferase
RSAU_000586	-5.26	7.42E-07	rsaC	non-coding RNA RsaC
RSAU_000571	-4.64	8.67E-08		Putative membrane protein
RSAU_001052	-3.57	0.0000599	eta	C4-dicarboxylate transporter/malic acid transport family protein
RSAU_000958	-3.22	0.00002	purM	Phosphoribosylformylglycinamide cyclo-ligase
RSAU_002404	-3.19	0.0000223	crtQ	4,4'-diaponeurosporenoate glycosyltransferase
RSAU_000985	-3.02	0.000135	potB	Spermidine/putrescine ABC transporter permease protein
RSAU_002542	-2.79	0.0000219		DNA-binding protein, putative
RSAU_000940	3.44	0.000137	atl	Bifunctional autolysin / N-acetylmuramoyl-L-alanine amidase
RSAU_002096	3.74	5.78E-07	pycA	RND multidrug transporter; Acriflavin resistance protein
RSAU_001615	3.83	0.000134	leuS	Leucyl-tRNA synthetase
RSAU_001480	3.99	0.000131	alaS	Alanyl-tRNA synthetase
RSAU_000981	4.05	0.0000396	pdhD	Dihydrolipoamide dehydrogenase
RSAU_000014	4.06	0.0000659		Phosphoesterase, DHH family protein
RSAU_002342	4.07	0.00002	gntP	Gluconate permease
RSAU_002402	4.18	0.000123	crtN	Squalene/phytoene synthase
RSAU_002410	4.21	0.000084	isaA	Immunodominant antigen A, transglycosylase isaA
RSAU_000222	4.22	0.00000207	lytM	Peptidoglycan hydrolase
RSAU_000494	4.22	0.00000151	rpoB	DNA-directed RNA polymerase subunit beta
RSAU_000758	4.25	0.0000938	rnr	Ribonuclease R
RSAU_001970	4.27	0.0000804		ATP-GRASP domain protein
RSAU_002274	4.34	0.0000386	bcr	Drug resistance transporter protein
RSAU_001152	4.34	0.000135	infB	Translation initiation factor IF-2
RSAU_002241	4.41	0.0000219	fnt	Formate/nitrite transporter family protein
RSAU_000888	4.41	0.000196		Monovalent cation/H ⁺ antiporter-2 family protein
RSAU_002255	4.5	0.000154	gpmA	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase
RSAU_001560	4.51	0.0000317	dnaE	DNA polymerase III subunit alpha
RSAU_000065	4.53	0.0000518		hypothetical protein
RSAU_002302	4.62	0.0000219	opp-1D	Oligopeptide ABC transporter, ATPase domain, putative
RSAU_000266	4.63	0.000151	geh	glycerol ester hydrolase
RSAU_001210	4.63	0.0000451	dhoM	Homoserine dehydrogenase
RSAU_001882	4.68	0.0000219	gcp	Putative DNA-binding/iron metalloprotein/AP endonuclease
RSAU_000168	4.7	0.00018	walK	Sensor histidine kinase protein
RSAU_000943	4.75	0.0000599	nanE	Cell envelope-related transcriptional attenuator domain protein
RSAU_002525	4.83	0.00014	hisZ	ATP phosphoribosyltransferase regulatory subunit
RSAU_002298	4.89	0.000149	gltB2	Ferredoxin-dependent glutamate synthase
RSAU_000666	4.91	0.0000599		Transporter Anion:Sodium Symporter family protein
RSAU_001351	4.94	0.0000354	ebpS	Elastin binding protein
RSAU_002089	4.96	0.0000023	pbuG	Xanthine/uracil permease family protein
RSAU_002272	4.96	0.000123	glxK	Glycerate kinase

RSAU_001253	4.98	0.0000748	trpB	Tryptophan synthase beta chain
RSAU_002290	4.99	0.000137		Amino acid transporter permease
RSAU_000117	5.06	0.000125	capO	Capsular polysaccharide synthesis UDP-N-acetyl-D dehydrogenase
RSAU_000844	5.13	0.00000323	addA	ATP-dependent helicase/nuclease subunit A
RSAU_002453	5.13	0.0000023	gbsA	Glycine betaine aldehyde dehydrogenase
RSAU_001518	5.14	0.000166		hypothetical protein
RSAU_000906	5.15	0.000193	terC	Toxic anion resistance membrane protein
RSAU_000937	5.15	0.0000712	aspC	Putative aminotransferase
RSAU_001219	5.18	0.000052	guaC	Guanosine monophosphate reductase
RSAU_000592	5.19	0.000123	tagA	Teichoic acid biosynthesis protein
RSAU_000600	5.19	0.000162	nupC2	Na ⁺ dependent nucleoside transporter protein
RSAU_001943	5.19	0.000135	atpA	FOF1 ATP synthase subunit alpha
RSAU_000994	5.22	5.78E-07	typA	GTP-binding protein TypA/BipA
RSAU_002485	5.22	0.0000599	pmi	Mannose-6-phosphate isomerase
RSAU_001860	5.24	0.00000798	groEL	60 kDa chaperonin GroEL
RSAU_002334	5.24	0.0000451	pgcA	Phosphoglucomutase/phosphomannomutase
RSAU_000265	5.28	0.0000283	sirA	Nucleoside recognition domain protein
RSAU_002372	5.32	0.000156	sdaAA	L-serine dehydratase, iron-sulfur-dependent, alpha subunit
RSAU_002291	5.34	0.0000668	pnbA	Para-nitrobenzyl esterase chain A
RSAU_000450	5.36	0.000123	ftsH	Cell division protein FtsH, putative
RSAU_000794	5.37	0.0000651	sufS	Cysteine desulfurase, SufS subfamily
RSAU_001157	5.39	0.00000436	pnpA	Polyribonucleotide nucleotidyltransferase
RSAU_002278	5.45	0.000162	cycA	Amino acid permease, putative
RSAU_002357	5.45	0.00013	fbp	Fructose-1,6-bisphosphatase class 3
RSAU_001388	5.49	0.0000124	ispA	Geranyltranstransferase
RSAU_000974	5.51	0.000032	rnjA	Ribonuclease J 1
RSAU_001991	5.55	0.0000451	glmS	Glucosamine--fructose-6-phosphate aminotransferase
RSAU_002484	5.65	0.0000389	manP	PTS system, fructose-specific IIABC component
RSAU_002100	5.65	0.000128		Major facilitator transporter
RSAU_000062	5.69	0.00000243		67 kDa myosin-cross-reactive antigen
RSAU_001080	5.69	0.0000932	rluD	Ribosomal large subunit pseudouridine synthase
RSAU_001786	5.71	0.00000788	gatB	Aspartyl/glutamyl-tRNA amidotransferase subunit B
RSAU_000693	5.72	0.0000599	ltaS	Glycerol phosphate lipoteichoic acid synthase
RSAU_002444	5.72	0.00000207		Amino acid permease family protein
RSAU_000739	5.75	0.0000733	trxB	Thioredoxin reductase
RSAU_001145	5.82	0.0000497	proS	Prolyl-tRNA synthetase
RSAU_000718	5.86	7.42E-07	pepT	Peptidase T
RSAU_000864	5.88	0.000117	oppA	Oligopeptide ABC transporter-binding protein OppA
RSAU_000833	5.9	0.000135	cls	Family NADH-dependent flavin oxidoreductase, putative
RSAU_002020	5.96	0.0000606	htsB	Iron ABC transporter, permease protein
RSAU_000289	5.99	0.00000791	efeB	Dyp-type peroxidase family protein
RSAU_002289	6	0.00000748	rpsP	Bacteriocin-protection, YdeI/OmpD-Associated family protein
RSAU_002442	6.05	0.000137	budA	Alpha-acetolactate decarboxylase
RSAU_000420	6.12	0.000159	ribA	Protein from nitrogen regulatory protein P-II family YAAQ
RSAU_001032	6.12	0.00000436	sdhA	Succinate dehydrogenase flavoprotein subunit
RSAU_001394	6.14	0.0000233	accB	Biotin carboxyl carrier protein of acetyl-CoA carboxylase

RSAU_002041	6.14	0.0000466	cobB	NAD-dependent protein deacetylase SIR2 family
RSAU_001189	6.18	0.000117	hflX	GTP-binding protein HflX
RSAU_002276	6.31	5.91E-07		Peptidase C39 like family protein
RSAU_002432	6.32	0.000126		Adenine nucleotide alpha hydrolases superfamily protein
RSAU_000300	6.47	0.0000194		Cyclase family protein
RSAU_002165	6.5	3.46E-07	hipO2	N-L-amino acid amidohydrolase
RSAU_000093	6.54	0.0000219	drm	Phosphopentomutase
RSAU_000497	6.56	0.000195	rpsL	30S ribosomal protein S12
RSAU_001643	6.56	0.0000213	metK	S-adenosylmethionine synthetase
RSAU_001034	6.69	0.0000451	murI	Glutamate racemase
RSAU_000566	6.84	0.0000314	btuF	Iron ABC transporter binding protein
RSAU_000534	6.92	0.000117		putative Membrane protein
RSAU_000505	7	0.0000147	capD	NAD dependent epimerase/dehydratase family protein
RSAU_000506	7.03	0.0000354	ilvE	Branched-chain amino acid aminotransferase
RSAU_001527	7.03	0.0000512	hemB	Delta-aminolevulinic acid dehydratase
RSAU_000498	7.25	0.000117	rpsG	30S ribosomal protein S7
RSAU_000427	7.38	0.00000243	metG	Methionyl-tRNA synthetase
RSAU_002292	7.91	1.21E-09	rimM	Major facilitator transporter, chloramphenicol