

Appendices

Appendix 1. Reactome pathways significantly associated with transcripts upregulated in wild type *S. Typhimurium* infection.

Pathway name	Pathway uploaded gene count	Genes in InnateDB for this entity	% of pathway genes upregulated	Pathway p-value (corrected)
Immune system	236	884	27	1.14E-22
Hemostasis	121	407	30	9.79E-15
Innate immune system	128	450	28	5.29E-14
Immunoregulatory interactions between a lymphoid and a non-lymphoid cell	30	45	67	1.14E-13
Class A/1 (Rhodopsin-like receptors)	87	277	31	5.42E-12
Cytokine signalling in immune system	68	194	35	9.02E-12
Signalling by GPCR	151	616	25	6.06E-11
GPVI-mediated activation cascade	26	42	62	6.84E-11
Interferon gamma signalling	26	43	60	1.27E-10
GPCR downstream signalling	130	524	25	7.25E-10
Interferon signalling	33	72	46	3.09E-09
Cell surface interactions at the vascular wall	36	83	43	3.16E-09
GPCR ligand binding	99	379	26	9.00E-09
Chemokine receptors bind chemokines	28	58	48	1.69E-08
Signal transduction	287	1490	19	4.18E-08
Platelet activation, signalling and aggregation	57	186	31	1.28E-07
Extracellular matrix organisation	63	216	29	1.69E-07
Peptide ligand-binding receptors	55	181	30	3.17E-07
Adaptive immune system	112	484	23	9.01E-07
G alpha (i) signalling events	60	214	28	1.63E-06
PD-1 signalling	11	14	79	2.48E-06
Generation of second messenger molecules	14	22	64	2.91E-06
Toll-like receptor cascades	41	127	32	3.02E-06
DAPI2 interactions	43	138	31	4.45E-06
Signalling by interleukins	34	100	34	8.42E-06
Phosphorylation of CD3 and TCR zeta chains	9	11	82	1.88E-05
G-protein beta:gamma signalling	15	28	54	2.04E-05
G beta:gamma signalling through PI3Kgamma	14	25	56	2.27E-05
Translocation of ZAP-70 to immunological synapse	8	9	89	2.37E-05
TCR signalling	21	52	40	5.48E-05
Other semaphorin interactions	11	18	61	9.49E-05
Interleukin-2 signalling	17	39	44	1.32E-04
Endosomal/vacuolar pathway	7	8	88	1.32E-04
Interleukin receptor SHC signalling	12	22	55	1.66E-04
Co-stimulation by the CD28 family	19	49	39	2.84E-04
DAPI2 signalling	37	131	28	2.89E-04
Initial triggering of complement	10	17	59	3.60E-04
Latent infection of <i>Homo sapiens</i> with <i>Mycobacterium tuberculosis</i>	14	32	44	6.77E-04
Phagosomal maturation (early endosomal stage)	14	32	44	6.77E-04
FCGR activation	8	12	67	6.83E-04

Cross-presentation of particulate exogenous antigens (phagosomes)	6	7	86	6.98E-04
Gastrin-CREB signalling pathway via PKC and MAPK	45	180	25	9.76E-04
Toll-like receptor 4 (TLR4) cascade	31	109	28	1.03E-03
G alpha (q) signalling events	40	156	26	1.29E-03
Semaphorin interactions	20	59	34	1.36E-03
Transport of inorganic cations/anions and amino acids/oligopeptides	23	75	31	2.35E-03
Degradation of the extracellular matrix	28	100	28	2.78E-03
Axon guidance	59	268	22	3.46E-03
Activation of C3 and C5	5	6	83	3.73E-03
Integrin cell surface interactions	19	59	32	3.98E-03
Collagen degradation	17	51	33	4.92E-03
Complement cascade	12	30	40	5.18E-03
Trafficking and processing of endosomal TLR	7	12	58	5.26E-03
Antigen presentation: folding, assembly and peptide loading of class I MHC	9	19	47	6.05E-03
Interleukin-3, 5 and GM-CSF signalling	14	39	36	6.35E-03
FCERI mediated Ca ²⁺ mobilisation	12	31	39	6.91E-03
Binding and uptake of ligands by scavenger receptors	13	36	36	8.92E-03
Formation of fibrin clot (clotting cascade)	12	32	38	9.45E-03
Basigin interactions	10	24	42	9.64E-03
Platelet homeostasis	14	41	34	1.03E-02
Collagen formation	19	65	29	1.22E-02
Signalling by VEGF	26	100	26	1.23E-02
Amino acid transport across the plasma membrane	11	29	38	1.29E-02
Nucleotide-like (purinergic) receptors	7	14	50	1.49E-02
Antigen processing-cross presentation	21	76	28	1.51E-02
VEGFA-VEGFR2 pathway	24	92	26	1.69E-02
Scavenging by class A receptors	8	18	44	1.73E-02
Fc epsilon receptor (FCERI) signalling	34	146	23	1.81E-02
Calcitonin-like ligand receptors	5	8	63	1.99E-02
Downstream TCR signalling	12	35	34	1.99E-02
Activated TLR4 signalling	25	99	25	2.09E-02
Formyl peptide receptors bind formyl peptides and many other ligands	7	15	47	2.27E-02
Transmembrane transport of small molecules	96	518	19	2.34E-02
MyD88:Mal cascade initiated on plasma membrane	21	81	26	3.05E-02
Toll-like receptor 2 (TLR2) cascade	21	81	26	3.05E-02
Toll-like receptor TLR1:TLR2 cascade	21	81	26	3.05E-02
Toll-like receptor TLR6:TLR2 cascade	21	81	26	3.05E-02
Activation of matrix metalloproteinases	12	37	32	3.13E-02
Activation, myristoylation of BID and translocation to mitochondria	5	9	56	3.49E-02
Dissolution of fibrin clot	5	9	56	3.49E-02
Removal of amino-terminal pro-peptides from gamma-carboxylated proteins	5	9	56	3.49E-02
Signal regulatory protein (SIRP) family interactions	5	9	56	3.49E-02
Antigen activates B Cell Receptor (BCR) leading to generation of second messengers	11	33	33	3.55E-02
Classical antibody-mediated complement activation	4	6	67	3.78E-02

Death receptor signalling	6	13	46	4.25E-02
Eicosanoid ligand-binding receptors	6	13	46	4.25E-02
Extrinsic pathway for apoptosis	6	13	46	4.25E-02
Platelet adhesion to exposed collagen	6	13	46	4.25E-02
Synthesis of leukotrienes (LT) and eoxins (EX)	6	13	46	4.25E-02
G alpha (s) signalling events	22	89	25	4.29E-02
Signalling by PDGF	32	145	22	4.65E-02
Signalling by SCF-KIT	26	112	23	4.87E-02

Appendix 2. Reactome pathways significantly associated with transcripts downregulated in wild type *S. Typhimurium* infection.

Pathway name	Pathway uploaded gene count	Genes in InnateDB for this entity	% of pathway genes downregulated	Pathway p-value (corrected)
Metabolism	275	1414	19	3.19E-27
Biological oxidations	57	146	39	5.49E-18
Phase II conjugation	28	63	44	2.19E-10
Transmembrane transport of small molecules	99	518	19	2.64E-08
Phase 1 - Functionalization of compounds	26	80	33	2.49E-06
Mitochondrial fatty acid beta-oxidation	10	15	67	1.08E-05
Metabolism of lipids and lipoproteins	90	519	17	1.44E-05
Degradation of cysteine and homocysteine	7	8	88	2.98E-05
Ethanol oxidation	7	8	88	2.98E-05
Transport of glucose and other sugars, bile salts and organic acids, metal ions and amine compounds	25	86	29	3.33E-05
The citric acid (TCA) cycle and respiratory electron transport	34	139	24	3.55E-05
Nuclear receptor transcription pathway	16	46	35	1.89E-04
Cytosolic sulfonation of small molecules	8	13	62	2.44E-04
Abacavir transport and metabolism	7	10	70	2.62E-04
Abacavir transmembrane transport	5	5	100	2.66E-04
Regulation of beta-cell development	11	25	44	3.22E-04
Sulfur amino acid metabolism	11	25	44	3.22E-04
SLC-mediated transmembrane transport	44	223	20	3.30E-04
Metabolism of amino acids and derivatives	38	183	21	3.68E-04
Stimuli-sensing channels	23	88	26	3.74E-04
Organic cation transport	6	8	75	5.19E-04
Respiratory electron transport	21	79	27	6.04E-04
Glutathione conjugation	11	27	41	6.41E-04
Fatty acid, triacylglycerol, and ketone body metabolism	34	165	21	9.83E-04
Reversible hydration of carbon dioxide	7	12	58	9.95E-04
Glucuronidation	5	6	83	1.02E-03

Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	24	101	24	1.08E-03
Regulation of gene expression in endocrine-committed (NEUROG3+) progenitor cells	4	4	100	1.59E-03
Synthesis of ketone bodies	4	4	100	1.59E-03
Incretin synthesis, secretion, and inactivation	9	21	43	1.65E-03
Na ⁺ /Cl ⁻ dependent neurotransmitter transporters	8	17	47	1.77E-03
Xenobiotics	10	26	38	1.95E-03
Cytochrome P450 - arranged by substrate type	17	64	27	2.36E-03
Ion channel transport	28	137	20	3.56E-03
Synthesis, secretion, and inactivation of Glucagon-like Peptide-1 (GLP-1)	8	19	42	3.89E-03
Class A/1 (Rhodopsin-like receptors)	47	277	17	4.51E-03
Ketone body metabolism	4	5	80	5.69E-03
Propionyl-CoA catabolism	4	5	80	5.69E-03
Sulfide oxidation to sulfate	4	5	80	5.69E-03
Organic cation/anion/zwitterion transport	6	12	50	6.46E-03
Bile acid and bile salt metabolism	11	36	31	7.11E-03
Pyruvate metabolism and Citric Acid (TCA) cycle	12	42	29	7.77E-03
ABC-family proteins mediated transport	9	26	35	7.82E-03
Beta oxidation of butanoyl-CoA to acetyl-CoA	3	3	100	1.00E-02
GRB7 events in ERBB2 signalling	3	3	100	1.00E-02
Mitochondrial fatty acid beta-oxidation of unsaturated fatty acids	3	3	100	1.00E-02
GPCR ligand binding	58	379	15	1.16E-02
Erythrocytes take up carbon dioxide and release oxygen	4	6	67	1.22E-02
O ₂ /CO ₂ exchange in erythrocytes	4	6	67	1.22E-02
Transport and synthesis of PAPS	4	6	67	1.22E-02
Regulation of gene expression in beta cells	6	14	43	1.46E-02
Retinoid metabolism and transport	11	40	28	1.55E-02
Defective AMN causes hereditary megaloblastic anemia 1	16	72	22	1.58E-02
Defective BTM causes biotinidase deficiency	16	72	22	1.58E-02
Defective CD320 causes methylmalonic aciduria	16	72	22	1.58E-02
Defective CUBN causes hereditary megaloblastic anemia 1	16	72	22	1.58E-02
Defective GIF causes intrinsic factor deficiency	16	72	22	1.58E-02
Defective HLCS causes multiple carboxylase deficiency	16	72	22	1.58E-02
Defective LMBRD1 causes methylmalonic aciduria and homocystinuria type cblF	16	72	22	1.58E-02
Defective MMAA causes methylmalonic aciduria type cblA	16	72	22	1.58E-02
Defective MMAB causes methylmalonic aciduria type cblB	16	72	22	1.58E-02

Defective MMACHC causes methylmalonic aciduria and homocystinuria type cblC	16	72	22	1.58E-02
Defective MMADHC causes methylmalonic aciduria and homocystinuria type cblD	16	72	22	1.58E-02
Defective MTR causes methylmalonic aciduria and homocystinuria type cblG	16	72	22	1.58E-02
Defective MTRR causes methylmalonic aciduria and homocystinuria type cblE	16	72	22	1.58E-02
Defective MUT causes methylmalonic aciduria mut type	16	72	22	1.58E-02
Defective TCN2 causes hereditary megaloblastic anemia	16	72	22	1.58E-02
Defects in biotin (B7) metabolism	16	72	22	1.58E-02
Defects in cobalamin (B12) metabolism	16	72	22	1.58E-02
Defects in vitamin and cofactor metabolism	16	72	22	1.58E-02
Metabolism of vitamins and cofactors	16	72	22	1.58E-02
Metabolism of water-soluble vitamins and cofactors	16	72	22	1.58E-02
Branched-chain amino acid catabolism	6	15	40	1.77E-02
Sialic acid metabolism	9	31	29	2.09E-02
Peptide ligand-binding receptors	31	181	17	2.09E-02
Synthesis, secretion, and inactivation of Glucose-dependent Insulinotropic Polypeptide (GIP)	5	11	45	2.10E-02
Synthesis of bile acids and bile salts	8	26	31	2.34E-02
Aflatoxin activation and detoxification	6	16	38	2.48E-02
O-linked glycosylation of mucins	10	38	26	2.67E-02
Alpha-linolenic (omega3) and linoleic (omega6) acid metabolism	5	12	42	3.07E-02
Alpha-linolenic acid (ALA) metabolism	5	12	42	3.07E-02
Peroxisomal lipid metabolism	7	22	32	3.15E-02
Synthesis of bile acids and bile salts via 7alpha-hydroxycholesterol	7	22	32	3.15E-02
Mitochondrial fatty acid beta-oxidation of saturated fatty acids	4	8	50	3.39E-02
Pyruvate metabolism	7	23	30	4.07E-02
G alpha (i) signalling events	34	214	16	4.12E-02
Inositol phosphate metabolism	10	41	24	4.42E-02

Appendix 3. GO terms significantly associated with transcripts regulated in wild type *S. Typhimurium* infection.

Pathway name	Pathway uploaded gene count	Genes in InnateDB for this entity	Pathway p-value (corrected)
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Upregulated

Biological process

innate immune response	302	718	8.28E-86
inflammatory response	129	249	3.21E-47
immune response	110	237	1.79E-34
response to lipopolysaccharide	71	162	5.72E-20
defence response to Gram-positive bacterium	36	54	2.61E-17
chemotaxis	40	77	5.70E-14
cellular response to lipopolysaccharide	44	93	1.65E-13
cell surface receptor signalling pathway	54	134	4.15E-13
neutrophil chemotaxis	27	41	1.40E-12
cell adhesion	95	329	1.46E-12

Molecular function

protein binding	1433	9494	2.15E-18
transmembrane signalling receptor activity	44	105	2.51E-11
carbohydrate binding	65	203	1.21E-10
receptor binding	81	288	3.75E-10
cytokine activity	56	171	1.36E-09
cytokine receptor activity	18	28	4.14E-08
calcium ion binding	137	642	5.45E-08
integrin binding	31	76	1.20E-07
cysteine-type endopeptidase inhibitor activity	20	40	1.43E-06
chemokine activity	24	55	1.50E-06

Cellular component

external side of plasma membrane	120	237	1.50E-42
extracellular space	298	1104	1.89E-36
extracellular region	282	1217	1.86E-22
cell surface	128	409	1.77E-20
extracellular matrix	68	214	6.07E-11
membrane raft	57	170	3.50E-10
integral component of plasma membrane	125	546	3.34E-09
proteinaceous extracellular matrix	61	217	1.32E-07
plasma membrane	581	3699	2.14E-07
neuronal cell body	74	302	1.45E-06

Downregulated

Biological process

metabolic process	230	1034	3.60E-31
oxidation-reduction process	175	770	2.56E-24
lipid glycosylation	21	28	2.49E-13
transmembrane transport	105	513	5.39E-11

steroid hormone mediated signalling pathway	20	57	4.80E-05
fatty acid biosynthetic process	18	51	1.62E-04
drug transmembrane transport	10	17	1.77E-04
sodium ion transport	27	103	2.65E-04
acyl-CoA metabolic process	11	22	3.75E-04
fatty acid metabolic process	20	65	3.84E-04
response to starvation	14	35	3.93E-04

Molecular function

oxidoreductase activity	90	327	3.21E-17
catalytic activity	114	646	8.54E-08
heme binding	45	181	1.09E-06
acyl-CoA dehydrogenase activity	13	20	1.14E-06
transferase activity, transferring hexosyl groups	22	57	2.06E-06
carboxylic ester hydrolase activity	16	32	2.67E-06
oxidoreductase activity, acting on the CH-CH group of donors	14	25	3.24E-06
glutathione transferase activity	15	29	3.84E-06
steroid hormone receptor activity	20	55	2.56E-05
iron ion binding	45	209	6.09E-05

Cellular component

mitochondrion	247	1510	3.20E-14
mitochondrial inner membrane	80	306	4.93E-14
apical plasma membrane	62	231	4.26E-11
peroxisome	36	111	1.84E-08
mitochondrial matrix	39	147	1.49E-06
brush border membrane	15	45	1.75E-03
extracellular vesicular exosome	257	2080	2.08E-03
endoplasmic reticulum membrane	88	584	2.43E-03
basolateral plasma membrane	31	151	4.96E-03
brush border	11	30	6.58E-03

Appendix 4. Reactome pathways significantly associated with genes upregulated at the RNA and protein level in wild type *S. Typhimurium* infection.

Pathway name	Upregulated gene count	% of pathway genes upregulated	Pathway p-value (corrected)	Gene Symbols
Regulation of complement cascade	4	22	3.77E-05	C3, C4b, Cfb, Cfh
Activation of C3 and C5	3	50	4.12E-05	C3, C4b, Cfb
Endosomal/vacuolar pathway	3	38	9.17E-05	B2m, Ctss, H2-K1
Complement cascade	4	13	1.62E-04	C3, C4b, Cfb, Cfh
Interferon signalling	5	7	2.42E-04	B2m, Gbp2, H2-K1, Isg15, Ptpn6
Antigen processing-cross presentation	5	7	2.52E-04	B2m, Ctss, H2-K1, Psmb8, Tapbp
Interferon gamma signalling	4	9	3.79E-04	B2m, Gbp2, H2-K1, Ptpn6
Initial triggering of complement	3	18	4.49E-04	C3, C4b, Cfb

Antigen presentation: folding, assembly and peptide loading of class I MHC	3	16	5.87E-04	B2m, H2-K1, Tapbp
Alternative complement activation	2	50	7.42E-04	C3, Cfb
Immune system	13	1	1.26E-03	B2m, C3, C4b, Cd74, Cfb, Cfh, Ctss, Gbp2, H2-K1, Isg15, Psmb8, Ptpn6, Tapbp
ER-phagosome pathway	4	6	1.32E-03	B2m, H2-K1, Psmb8, Tapbp
Amyloids	4	5	3.12E-03	B2m, Ltf, Lyz2, Tgfb1
Binding and uptake of ligands by scavenger receptors	3	8	3.12E-03	Apoe, Fth1, Hp
Iron uptake and transport	3	8	3.81E-03	Cp, Fth1, Lcn2
Immunoregulatory interactions between a lymphoid and a non-lymphoid cell	3	7	4.86E-03	B2m, C3, H2-K1
HDL-mediated lipid transport	2	14	6.93E-03	A2m, Apoe
Adaptive immune system	8	2	7.58E-03	B2m, C3, Cd74, Ctss, H2-K1, Psmb8, Ptpn6, Tapbp
Cytokine signaling in immune system	5	3	7.97E-03	B2m, Gbp2, H2-K1, Isg15, Ptpn6
Class I MHC mediated antigen processing & presentation	5	2	8.95E-03	B2m, Ctss, H2-K1, Psmb8, Tapbp
Scavenging by class A receptors	2	11	9.38E-03	Apoe, Fth1
Intrinsic pathway	2	10	1.04E-02	A2m, Kng1
Extracellular matrix organization	5	2	1.05E-02	A2m, Col18a1, Ctss, Itgad, Serpinh1
Collagen formation	3	5	1.05E-02	Col18a1, Ctss, Serpinh1
Platelet degranulation	3	4	1.36E-02	A2m, Kng1, Psap
Lipoprotein metabolism	2	8	1.40E-02	A2m, Apoe
Response to elevated platelet cytosolic Ca ²⁺	3	4	1.48E-02	A2m, Kng1, Psap
Formation of fibrin clot (clotting cascade)	2	6	2.31E-02	A2m, Kng1
Peptide ligand-binding receptors	4	2	2.53E-02	Anxa1, C3, Kng1, Psap
Degradation of the extracellular matrix	3	3	2.67E-02	A2m, Col18a1, Ctss
Assembly of collagen fibrils and other multimeric structures	2	5	3.17E-02	Col18a1, Ctss
Lipid digestion, mobilization, and transport	2	5	3.17E-02	A2m, Apoe
Collagen biosynthesis and modifying enzymes	2	4	4.04E-02	Col18a1, Serpinh1
Innate immune system	6	1	4.10E-02	B2m, C3, C4b, Cfb, Cfh, Ctss

Appendix 5. Reactome pathways significantly associated with genes downregulated at the RNA and protein level in wild type *S. Typhimurium* infection.

Pathway name	Down-regulated gene count	% of pathway genes upregulated	Pathway p-value (corrected)	Gene Symbols
Metabolism	50	4	3.08E-15	Abcb1a, Acads, Acat1, Acox1, Ahcy, Akr1c13, Aldh1a1, Aldh2, Atp5a1, Bdh1, Bsg, Cbr1, Cmpk1, Cox4i1, Cox6c, Cth, Cyc1, Cyp2c55, Echs1, Eci1, Eno3, Etfa, Etfb, Ethel, Gna11, Gstm1, Gstm2, Gstm3, Hadh, Hmgcs2, Hsd3b3, Maa, Mdh1, Mgst3, Papss2, Pfk1, Sdha, Slc16a1, Slc25a10, Sqrdl, Suclg2, Sult1b1, Sult1d1, Tst, Ugdh, Ugt1a1, Ugt1a7c, Uqcr10, Uqcr1, Uqcr2
Biological oxidations	15	10	3.50E-10	Ahcy, Aldh1a1, Aldh2, Cyp2c55, Gstm1, Gstm2, Gstm3, Maa, Mgst3, Papss2, Sult1b1, Sult1d1, Ugdh, Ugt1a1, Ugt1a7c
Phase II conjugation	11	17	5.10E-10	Ahcy, Gstm1, Gstm2, Gstm3, Mgst3, Papss2, Sult1b1, Sult1d1, Ugdh, Ugt1a1, Ugt1a7c
The citric acid (TCA) cycle and respiratory electron transport	13	9	1.83E-08	Atp5a1, Bsg, Cox4i1, Cox6c, Cyc1, Etfa, Etfb, Sdha, Slc16a1, Suclg2, Uqcr10, Uqcr1, Uqcr2
Degradation of cysteine and homocysteine	5	63	5.69E-08	Cth, Ethel, Slc25a10, Sqrdl, Tst
Sulfide oxidation to sulfate	4	80	4.51E-07	Ethel, Slc25a10, Sqrdl, Tst
Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	10	10	5.77E-07	Atp5a1, Cox4i1, Cox6c, Cyc1, Etfa, Etfb, Sdha, Uqcr10, Uqcr1, Uqcr2
Respiratory electron transport	9	11	7.42E-07	Cox4i1, Cox6c, Cyc1, Etfa, Etfb, Sdha, Uqcr10, Uqcr1, Uqcr2
Sulfur amino acid metabolism	6	24	9.91E-07	Ahcy, Cth, Ethel, Slc25a10, Sqrdl, Tst
Beta oxidation of butanoyl-CoA to acetyl-CoA	3	100	5.98E-06	Acads, Echs1, Hadh
Synthesis of ketone bodies	3	75	2.03E-05	Acat1, Bdh1, Hmgcs2
Beta oxidation of hexanoyl-CoA to butanoyl-CoA	3	60	4.56E-05	Acads, Echs1, Hadh
Ketone body metabolism	3	60	4.56E-05	Acat1, Bdh1, Hmgcs2
Mitochondrial Fatty Acid Beta-Oxidation	4	27	5.51E-05	Acads, Echs1, Eci1, Hadh,

Glucuronidation	3	50	8.25E-05	Ugdh, Ugt1a1, Ugt1a7c
Fatty acid, triacylglycerol, and ketone body metabolism	9	5	1.87E-04	Acads, Acat1, Acox1, Bdh1, Echs1, Eci1, Hadh, Hmgcs2, Ugt1a7c
Mitochondrial fatty acid beta-oxidation of saturated fatty acids	3	38	2.04E-04	Acads, Echs1, Hadh
Metabolism of serotonin	2	100	3.42E-04	Aldh2, Maoa
Serotonin clearance from the synaptic cleft	2	100	3.42E-04	Aldh2, Maoa
Glutathione conjugation	4	15	4.94E-04	Gstm1, Gstm2, Gstm3, Mgst3
Cytosolic sulfonation of small molecules	3	23	8.45E-04	Papss2, Sult1b1, Sult1d1
Utilization of ketone bodies	2	67	9.07E-04	Acat1, Bdh1
Pyruvate metabolism and Citric Acid (TCA) cycle	4	10	2.45E-03	Bsg, Sdha, Slc16a1, Suclg2
Beta oxidation of decanoyl-CoA to octanoyl-CoA-CoA	2	40	2.64E-03	Echs1, Hadh
Beta oxidation of lauroyl-CoA to decanoyl-CoA-CoA	2	40	2.64E-03	Echs1, Hadh
Beta oxidation of octanoyl-CoA to hexanoyl-CoA	2	40	2.64E-03	Echs1, Hadh
Neurotransmitter clearance in the synaptic cleft	2	33	3.86E-03	Aldh2, Maoa
Basigin interactions	3	13	4.34E-03	Atp1b1, Bsg, Slc16a1
Ethanol oxidation	2	25	6.07E-03	Aldh1a1, Aldh2
Metabolism of amino acids and derivatives	7	4	6.14E-03	Acat1, Ahcy, Cth, Ethe1, Slc25a10, Sqrdl, Tst
Gluconeogenesis	3	10	7.42E-03	Eno3, Mdh1, Slc25a10
Glucose metabolism	4	6	8.90E-03	Eno3, Mdh1, Pfkf, Slc25a10
Metabolism of lipids and lipoproteins	12	2	1.43E-02	Acads, Acat1, Acox1, Akr1c13, Bdh1, Cbr1, Echs1, Eci1, Hadh, Hmgcs2, Hsd3b3, Ugt1a7c
Phase I - Functionalization of compounds	4	5	1.79E-02	Aldh1a1, Aldh2, Cyp2c55, Maoa
Cell surface interactions at the vascular wall	4	5	2.01E-02	Atp1b1, Bsg, Ceacam1, Slc16a1
Synthesis of Prostaglandins (PG) and Thromboxanes (TX)	2	13	2.12E-02	Akr1c13, Cbr1
Citric acid cycle (TCA cycle)	2	12	2.29E-02	Sdha, Suclg2
Thrombin signalling through proteinase activated receptors (PARs)	2	12	2.29E-02	Gna11, Mapk3
Pyruvate metabolism	2	9	3.89E-02	Bsg, Slc16a1
Glycolysis	2	8	4.49E-02	Eno3, Pfkf

Appendix 6. Differentially expressed genes in caecal tissue from mutant versus wild type mice, as determined by RNAseq. Changes with an adjusted p-value < 0.05 were deemed statistically significant. Up to 50 genes with the largest increase and decrease in expression are listed (log2 fold change < -1 or > 1). Transcript abundance is the baseMean output from DESeq2 (the average of the normalised count values over all samples).

***IL10rb^{tm1a/tm1a}* (S. Typhimurium-infected)**

Gene symbol	Transcript abundance	log2 Fold change	Adjusted p-value
Upregulated			
EN2	21	2.02	4.65E-07
ERMN	111	1.95	3.75E-07
CD40LG	26	1.89	2.55E-07
SEMA3E	209	1.86	2.27E-08
HPX	56	1.71	9.92E-05
NLRP10	444	1.70	3.26E-05
TMPRSS11G	14	1.62	2.62E-04
CD200R2	39	1.61	4.13E-07
2210407C18RIK	9192	1.60	2.71E-14
ATP12A	81	1.56	5.44E-04
GAL3ST2	404	1.50	3.58E-05
HAPLN1	41	1.49	1.32E-03
RASSF10	71	1.47	1.18E-07
NMU	4	1.46	1.88E-03
IGLC2	754	1.46	2.31E-03
TRGJ1	24	1.45	2.00E-04
CYP2E1	17	1.43	2.52E-03
AQP3	27	1.42	1.03E-03
ST6GALNAC1	4	1.41	3.53E-03
TRBV15	19	1.40	2.09E-03
TFF1	4	1.39	3.45E-03
FGG	18	1.39	6.29E-04
LAT	438	1.38	1.54E-04
EAR1	11	1.37	4.06E-03
IGLV2	685	1.35	6.58E-03
SERPINA10	248	1.34	3.58E-05
ITIH4	14	1.33	8.07E-03
MCPT9	12	1.32	8.11E-03
ACTN2	58	1.31	3.00E-03
1700008I05RIK	7	1.31	1.02E-02
SERPINA1E	8	1.30	1.03E-02
KNDC1	17	1.29	7.58E-04
2010109A12RIK	7	1.29	6.38E-03

IL2RA	1628	1.29	1.06E-03
GM9994	264	1.28	3.64E-03
SLC17A4	1230	1.27	2.52E-03
TRGV2	91	1.27	2.66E-04
IGHG2B	867	1.26	1.49E-02
PMP22	8838	1.26	1.78E-06
9430041J12RIK	174	1.25	1.54E-03
TMPRSS3	2	1.24	1.61E-02
UBD	23136	1.24	5.05E-05
TCRG-V6	44	1.23	1.94E-02
TCRG-C1	237	1.23	3.66E-03
BLK	131	1.23	8.95E-03
UGT8A	39	1.21	2.42E-02
H19	79	1.21	2.49E-02
5830411N06RIK	65	1.21	3.15E-03
SERPINA1D	4	1.19	3.02E-02
IGKV4-68	433	1.19	2.94E-02

Downregulated

IL10RB	2873	-4.32	1.05E-243
PRSS27	178	-2.97	1.56E-19
GNA14	635	-2.93	8.03E-21
KRT36	166	-2.67	7.00E-35
GATA4	111	-2.57	4.75E-12
REG3G	2851	-2.41	1.06E-10
AQP4	891	-2.24	2.27E-08
B3GALT5	4551	-2.22	3.15E-10
MAL	478	-2.15	8.06E-10
BCL2L15	468	-2.11	3.53E-08
CHST4	464	-1.93	9.29E-07
PLA2G2A	158	-1.91	5.80E-06
BMP3	111	-1.86	2.88E-07
GM8540	58	-1.82	1.76E-05
PLA2G5	260	-1.72	1.16E-07
SP5	36	-1.71	9.36E-08
SEC1	158	-1.67	9.29E-07
M5C1000I18RIK	102	-1.65	3.49E-08
GM5689	47	-1.62	6.80E-05
CNKSR2	12	-1.62	1.89E-05
C2CD4B	149	-1.54	9.29E-07
PPEF1	48	-1.54	7.07E-04
FUT2	6901	-1.54	1.70E-05
9130204K15RIK	32	-1.53	1.06E-03
GM21860	21	-1.52	3.02E-04
CSTA	381	-1.49	5.60E-04

SLC5A9	402	-1.47	1.88E-04
EPGN	31	-1.46	1.65E-03
GM9458	64	-1.46	2.15E-03
Gm21742	56	-1.43	1.71E-03
SPRR2D	12	-1.43	1.53E-03
REG3B	4127	-1.38	4.23E-04
SAA1	2840	-1.36	2.12E-03
RDH18-PS	15	-1.35	1.97E-03
PLA2G12B	217	-1.35	1.46E-03
GGT1	461	-1.33	1.65E-03
SLC7A9	116	-1.33	8.07E-03
TAT	2330	-1.32	4.43E-04
GM26917	3027	-1.32	8.13E-03
GM21970	1905	-1.32	2.96E-16
LYPD3	27	-1.32	3.40E-03
GM21748	23	-1.30	1.09E-02
SPRR2F	33	-1.28	1.35E-02
1700007E05Rik	17	-1.27	6.20E-03
ST8SIA1	118	-1.27	3.29E-03
HOXD11	85	-1.26	1.49E-02
DMBT1	28655	-1.26	1.61E-02
PLA2G2E	67	-1.26	9.75E-03
2210011K15Rik	5	-1.25	1.49E-02
RDH16	466	-1.25	1.03E-02

***IL22ra1*^{tm1a/tm1a} (*S. Typhimurium*-infected)**

Gene symbol	Transcript abundance	log2 Fold change	Adjusted p-value
Upregulated			
CCL20	108	-3.03	1.49E-37
PRSS27	178	-2.55	1.97E-14
GNA14	635	-2.50	4.08E-15
PLA2G2A	158	-2.44	1.39E-10
REG3G	2851	-2.37	1.07E-10
PPEF1	48	-2.30	1.35E-09
KRT36	166	-2.25	7.91E-25
PLA2G5	260	-2.22	1.10E-13
GATA4	111	-2.22	2.58E-09
GM8540	58	-2.18	9.82E-09
SLC5A9	402	-1.92	1.82E-08
AQP4	891	-1.86	3.32E-06
B3GALT5	4551	-1.76	9.59E-07
GM2539	10	-1.75	2.01E-06

SLC1A1	211	-1.69	2.30E-06
CHI3L3	13158	-1.68	4.22E-05
ST8SIA1	118	-1.65	4.26E-06
CHI3L4	439	-1.64	6.54E-05
BCL2L15	468	-1.64	2.78E-05
ADCY2	212	-1.58	3.59E-07
CCIN	6	-1.56	1.50E-04
PLAT	1177	-1.56	5.96E-09
SEC1	158	-1.55	2.68E-06
SPRR2F	33	-1.52	2.89E-04
AOX3	21	-1.52	6.59E-05
CNKSR2	12	-1.52	2.14E-05
PLA2G2E	67	-1.51	1.51E-04
SLC12A3	10	-1.51	1.36E-04
MAL	478	-1.51	3.67E-05
GM5689	47	-1.51	8.74E-05
RS1	13	-1.47	3.64E-04
GM15726	78	-1.46	4.93E-04
GM9458	64	-1.45	5.84E-04
CSTA	381	-1.45	2.37E-04
MT3	64	-1.44	6.77E-04
NTN5	7	-1.43	4.74E-04
KCNA4	8	-1.43	8.28E-04
MT2	5723	-1.43	4.74E-04
EPGN	31	-1.42	6.21E-04
DMGDH	14	-1.42	9.14E-04
NPTX2	170	-1.42	3.18E-05
TMEM119	3443	-1.41	4.26E-04
MEG3_2	5	-1.41	9.38E-04
CHST4	464	-1.40	5.92E-04
MT1	4635	-1.40	2.09E-04
1500009C09RIK	92	-1.40	5.20E-05
ESM1	82	-1.40	4.74E-04
AI747448	53150	-1.38	1.97E-04
REG3B	4127	-1.37	1.13E-04
PLAGL1	402	-1.36	2.95E-04

Downregulated

SLC17A1	24	2.81	2.77E-16
SLC17A4	1230	2.80	1.29E-18
GAL3ST2	404	2.78	3.46E-20
SLC34A2	39	2.59	1.12E-13
GM9994	264	2.48	1.93E-13
ATP12A	81	2.34	5.23E-10
DIO1	161	2.32	1.33E-11

FABP2	3356	2.28	8.19E-10
EN2	21	2.27	1.53E-09
CPN1	251	2.20	9.50E-09
RBP2	315	2.11	3.10E-09
PMP22	8838	2.08	2.44E-19
PBP2	43	2.03	2.87E-08
2210407C18RIK	9192	2.01	2.48E-23
CNPY1	75	2.00	1.50E-10
NLRP10	444	1.98	8.47E-08
UPK1A	147	1.87	1.80E-08
MYO3A	29	1.87	1.02E-10
BCAS1	290	1.86	2.49E-06
TGM5	77	1.85	7.37E-08
IL1F8	42	1.83	5.36E-07
GM15368	18	1.81	2.26E-07
CYP2C55	152	1.81	3.36E-06
GM14259	50	1.80	7.09E-06
CLCN1	51	1.77	3.21E-09
SH3D21	415	1.76	1.96E-12
UPB1	32	1.71	3.73E-06
FAM189A2	986	1.70	2.67E-07
KCNU1	14	1.69	5.42E-07
SYT7	637	1.68	2.54E-11
HSD3B2	47	1.66	4.79E-05
9430041J12RIK	174	1.65	6.58E-07
REP15	81	1.64	1.57E-05
PPFIA3	1306	1.64	2.88E-09
TRIM58	11	1.64	4.99E-05
ABCB1A	2050	1.60	3.21E-09
ANG4	154	1.58	1.48E-04
1810065E05RIK	4819	1.56	1.77E-04
SLC9A2	4482	1.56	4.23E-06
GM13412	9	1.55	4.43E-05
GM20478	38	1.54	2.26E-06
SYTL2	738	1.54	1.50E-07
GM23800	7	1.53	1.25E-04
LGALS2	198	1.53	2.57E-04
MS4A18	256	1.53	2.84E-05
RAPGEFL1	407	1.52	4.87E-07
HSD11B2	734	1.52	2.68E-05
XPNPEP2	177	1.51	2.58E-08
BTNL7-PS	190	1.51	1.98E-06
GM26859	34	1.51	3.34E-05

***IL22ra1*^{tm1a/tm1a} (naïve)**

Gene symbol	Transcript abundance	log2 Fold change	Adjusted p-value
Upregulated			
RPRM	67	1.00	4.85E-03
AOC1	15530	1.01	3.58E-06
TFRC	26067	1.02	7.53E-04
CYP2E1	103	1.05	6.10E-04
GM26697	555	1.07	1.08E-04
B3GALT2	227	1.10	4.23E-06
SLC17A2	281	1.11	1.44E-04
IGKV5-48	989	1.25	2.06E-04
GRIN3A	118	1.26	1.79E-04
IGHV7-1	249	1.30	9.21E-05
MT2	6292	1.34	5.68E-14
CES2A	14332	1.38	2.03E-05
CYP4B1-PS1	78	1.48	2.21E-06
CYP4B1	5572	1.74	2.35E-10
CYP4B1-PS2	44	1.76	1.23E-10
Downregulated			
GM15726	98	-1.89	2.28E-10
MID1	886	-1.83	1.23E-10
MS4A10	677	-1.75	2.35E-11
GM21857	221	-1.62	6.32E-09
IL22RA1	1036	-1.61	1.59E-08
CYP2D9	629	-1.31	6.83E-06
PRSS16	75	-1.26	5.89E-11
RHOX5	67	-1.24	4.34E-05
MYOM3	52	-1.20	8.60E-05
GM8540	129	-1.19	5.47E-04
IGFBP2	1546	-1.18	4.13E-04
GM21742	73	-1.18	5.57E-04
3930402G23RIK	83	-1.18	1.56E-04
PCSK9	683	-1.18	1.79E-05
REG3B	52	-1.17	1.44E-04
MMP10	52	-1.15	9.47E-04
ASB11	115	-1.13	1.49E-04
EREG	747	-1.11	5.51E-04
FAM167B	40	-1.09	9.30E-04
ETV4	150	-1.02	5.06E-04