

Supplementary information

Gata4 is critical to maintain gut barrier function and mucosal integrity following epithelial injury

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Supplementary Figure legends

Figure S1. Indomethacin does not affect jejunum epithelial cell proliferation in Gata4 mutant mice. PCNA positive cells were detected by immunofluorescence on the jejunum of control (**a**) and *Gata4*^{ΔIEC} (**b**) mice that were sacrificed 24 h after indomethacin injection. Original magnification: 2.5X. (**c**) The ratio of PCNA-positive cells was expressed in percentage of total number of crypt cells and was averaged from 8 individual crypts of a total of 3 different mice per group.

Figure S2. Transcriptomic analysis predicts increased epithelial cell death in the jejunum of Gata4 mutant mice following indomethacin treatment. Total RNA was isolated from the jejunum of control and *Gata4*^{ΔIEC} mice that were sacrificed after indomethacin injection (n=3 per group) and probes for hybridization with Illumina BeadChips were generated. Genes were then filtered for up- or down-regulation of expression of a minimum of 2.0-fold with a *P* value ≤ 0.05 and gene signature datasets were analyzed by the Ingenuity Pathway Analysis tool. (**a**) Categories and functions annotations were associated with a p-value, activation state and number of different

molecules found to be modulated in these categories. **(b)** 26 molecules were found to be modulated (up in red and down in green) and associated with predicted increases of epithelial cell death. The color quantification scale of dotted lines associated with biological functions covers between orange (increased state) and blue (decreased state).

Figure S3. Transcriptomic analysis predicts decreased immune cell trafficking in the jejunum of Gata4 mutant mice following indomethacin treatment. Total RNA was isolated from the jejunum of control and *Gata4*^{ΔIEC} mice that were sacrificed after indomethacin injection (n=3 per group) and probes for hybridization with Illumina BeadChips were generated. Genes were then filtered for up- or down-regulation of expression of a minimum of 2.0-fold with a *P* value ≤ 0.05 and gene signature datasets were analyzed by the Ingenuity Pathway Analysis tool.

(a) Categories and functions annotations were associated with a p-value, activation state and number of different molecules found to be modulated in these categories. **(b)** 34 molecules were found to be modulated (up in red and down in green) and associated with predicted decreases of immune cell trafficking. The color quantification scale of dotted lines associated with biological functions covers between orange (increased state) and blue (decreased state).

Figure S4. ZO-1 localization remains unchanged in the jejunum of *Gata4* mutant mice.

Immunofluorescence detection of ZO-1 on jejunum sections prepared from controls and *Gata4*^{ΔIEC} mice. Original magnification: 10X.

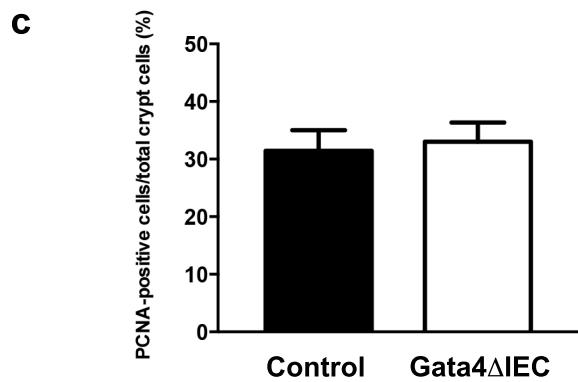
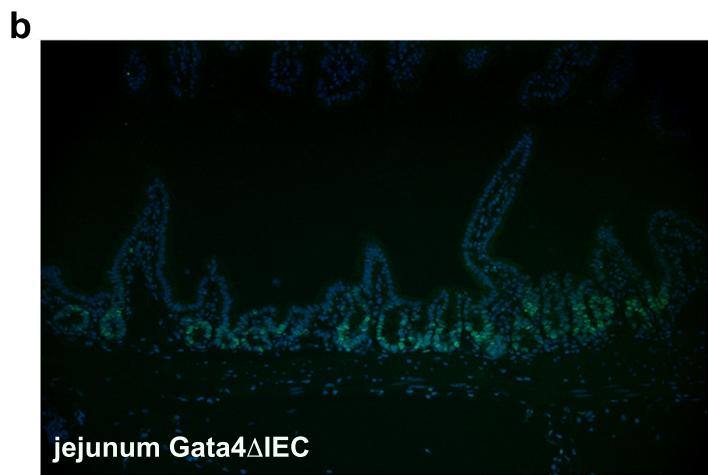
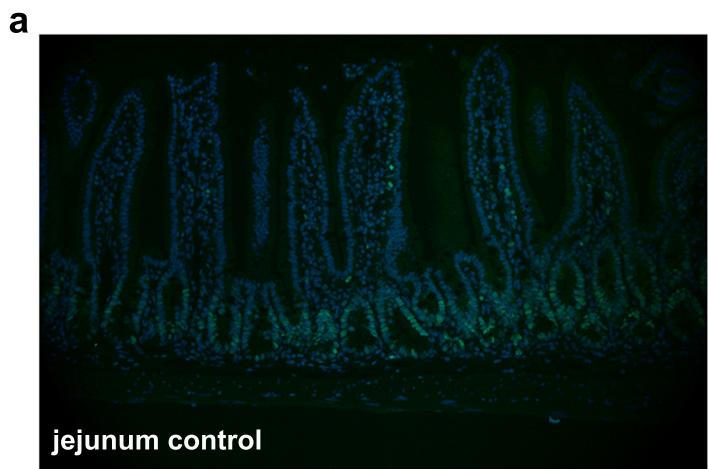
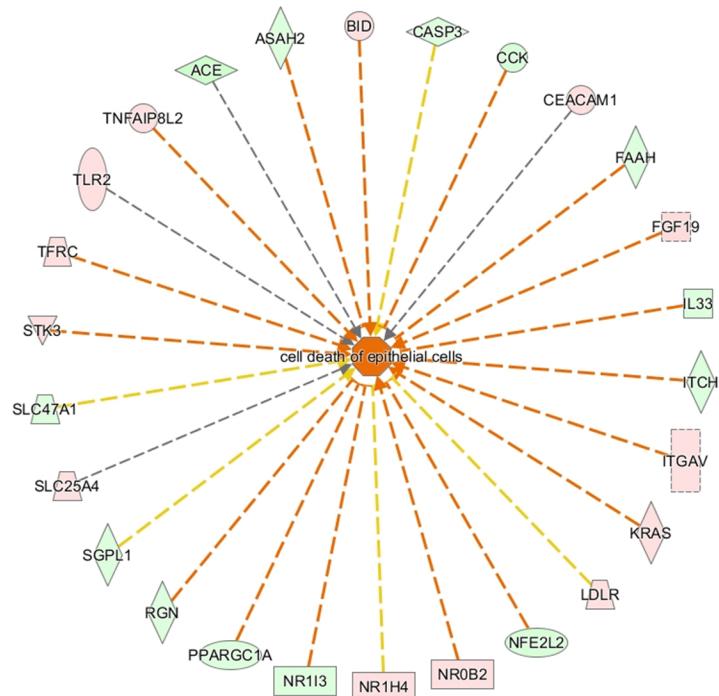


Figure S1. Lepage et al.

A

Categories	Diseases or Functions Annotation	p-Value	Predicted Activation State	Activation z-score	# Molecules
Cell Death and Survival	necrosis	1.86E-07		1.664	93
Cell Death and Survival, Gastrointestinal Disease, Hepatic System Disease	cell death of hepatocytes	5.66E-07	Increased	2.251	14
Cell Death and Survival	cell death	7.76E-07		1.479	111
Cell Death and Survival, Gastrointestinal Disease, Hepatic System Disease	cell death of liver cells	2.68E-06		1.691	15
Cell Death and Survival, Respiratory Disease	apoptosis of lung cells	6.61E-06		0.896	7
Cell Death and Survival	cell death of epithelial cells	7.60E-06	Increased	2.233	26
Cell Death and Survival, Gastrointestinal Disease, Hepatic System Disease	necrosis of liver	1.06E-05		1.488	16
Cell Death and Survival	necrosis of epithelial tissue	3.00E-05		1.954	28
Cell Death and Survival	apoptosis	3.14E-05		1.594	86
Cell Death and Survival, Gastrointestinal Disease, Hepatic System Disease	apoptosis of hepatocytes	9.71E-05		1.659	10
Cell Death and Survival, Gastrointestinal Disease, Hepatic System Disease	apoptosis of liver cells	9.74E-05		1.052	11
Cell Death and Survival	cell death of enteroendocrine cells	1.44E-04			3
Cell Death and Survival	necrosis of kidney	2.41E-04		1.497	18
Cell Death and Survival	apoptosis of connective tissue cells	3.04E-04		0.375	15
Cell Death and Survival	apoptosis of epithelial cells	3.57E-04		1.392	15
Cell Death and Survival	cell death of kidney cells	3.96E-04		1.332	17
Cell Death and Survival, Respiratory Disease	cell death of pneumocytes	4.04E-04		1.982	4
Cell Death and Survival	cell death of tumor cell lines	6.02E-04		1.561	51
Cell Death and Survival	cell death of splenocytes	6.51E-04		0.447	5
Cell Death and Survival, Cellular Compromise, Reproductive System Development	cytotoxicity of gonadal cell lines	7.89E-04			2
Cell Death and Survival, Respiratory Disease	quantity of apoptotic pneumocytes	7.89E-04			2
Cell Death and Survival	cell death of colon	1.09E-03			3
Cell Death and Survival	apoptosis of tumor cell lines	1.16E-03		1.702	41
Cell Death and Survival	cell death of striatal neurons	1.31E-03		0.468	5
Cell Death and Survival, Embryonic Development	apoptosis of embryonic cell lines	1.32E-03	Increased	2.043	10
Cell Death and Survival, Embryonic Development	cell death of embryonic cell lines	1.49E-03		1.965	12
Cell Death and Survival	cell death of endocrine cells	1.51E-03		1.461	7
Cell Death and Survival	delay in initiation of removal of cells	1.56E-03			2
Cell Death and Survival	necrosis of colon	1.56E-03			2
Cell Death and Survival	cell death of kidney cell lines	1.66E-03		1.595	14
Cell Death and Survival, Respiratory Disease	apoptosis of pneumocytes	2.06E-03			3
Cell Death and Survival	opsonization	2.47E-03			3
Cell Death and Survival	cell death of islet cells	3.19E-03		1.461	6
Cell Death and Survival	quantity of apoptotic cells	3.57E-03		0.6	6
Cell Death and Survival	apoptosis of kidney cell lines	3.90E-03		1.336	11
Cell Death and Survival	cell death of pericytes	6.00E-03			3
Cell Death and Survival	apoptosis of uterine cell lines	6.97E-03			2
Cell Death and Survival	opsonization of cells	6.97E-03			2
Cell Death and Survival	cell death of intestinal cells	8.30E-03			4

B**Figure S2. Lepage et al.**

A

Categories	Diseases or Functions Annotation	p-Value	Predicted Activation State	Activation # Molecules
Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking	cell movement of myeloid cells	1.6E-04	Decreased	-2,183
Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking	influx of leukocytes	1.93E-04		-0.816
Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response, Tissue Development	accumulation of neutrophils	2.44E-04		-1.777
Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response	cell movement of neutrophils	2.57E-04		-1.576
Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response	migration of neutrophils	2.75E-04		-0.656
Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response	adhesion of neutrophils	2.82E-04		-0.883
Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response, Tissue Development	accumulation of phagocytes	4.44E-04		-1.671
Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response	cell movement of phagocytes	5.89E-04		-1.834
Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking	infiltration of granulocytes	6.06E-04		-1.795
Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response	chemotaxis of myeloid cells	7.85E-04		-1.874
Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response	chemotaxis of phagocytes	8.69E-04		-1.835
Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking	cell movement of granulocytes	9.29E-04		-1.695
Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking	homing of leukocytes	9.92E-04		-1.271
Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response	activation of myeloid cells	1.04E-03		-1.087
Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking	migration of myeloid cells	1.06E-03		-0.701
Cellular Movement, Immune Cell Trafficking	leukocyte migration	1.10E-03	Decreased	-2.35
Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response	infiltration by neutrophils	1.27E-03	Decreased	-2.155
Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response	chemotaxis of neutrophils	1.37E-03		-1.466
Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response	chemotaxis of leukocytes	1.55E-03		-1.879
Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking	infiltration of leukocytes	1.60E-03	Decreased	-2.047
Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking	cell movement of leukocytes	1.65E-03		-1.735
Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response, Tissue Development	accumulation of myeloid cells	1.87E-03		-1.887
Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response	chemokinesis of neutrophils	2.89E-03		-2
Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response	activation of neutrophils	4.58E-03		-1.949
Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response	activation of leukocytes	4.59E-03		-0.996
Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response	migration of phagocytes	4.89E-03		-0.636
Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response	activation of phagocytes	5.53E-03		-0.84
Cell-To-Cell Signaling and Interaction, Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking	recruitment of granulocytes	7.09E-03	Decreased	-2,244
Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response	activation of peripheral blood neutrophils	1.20E-02		8
Cellular Movement, Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response	chemokinesis of monocytes	1.20E-02		1

B

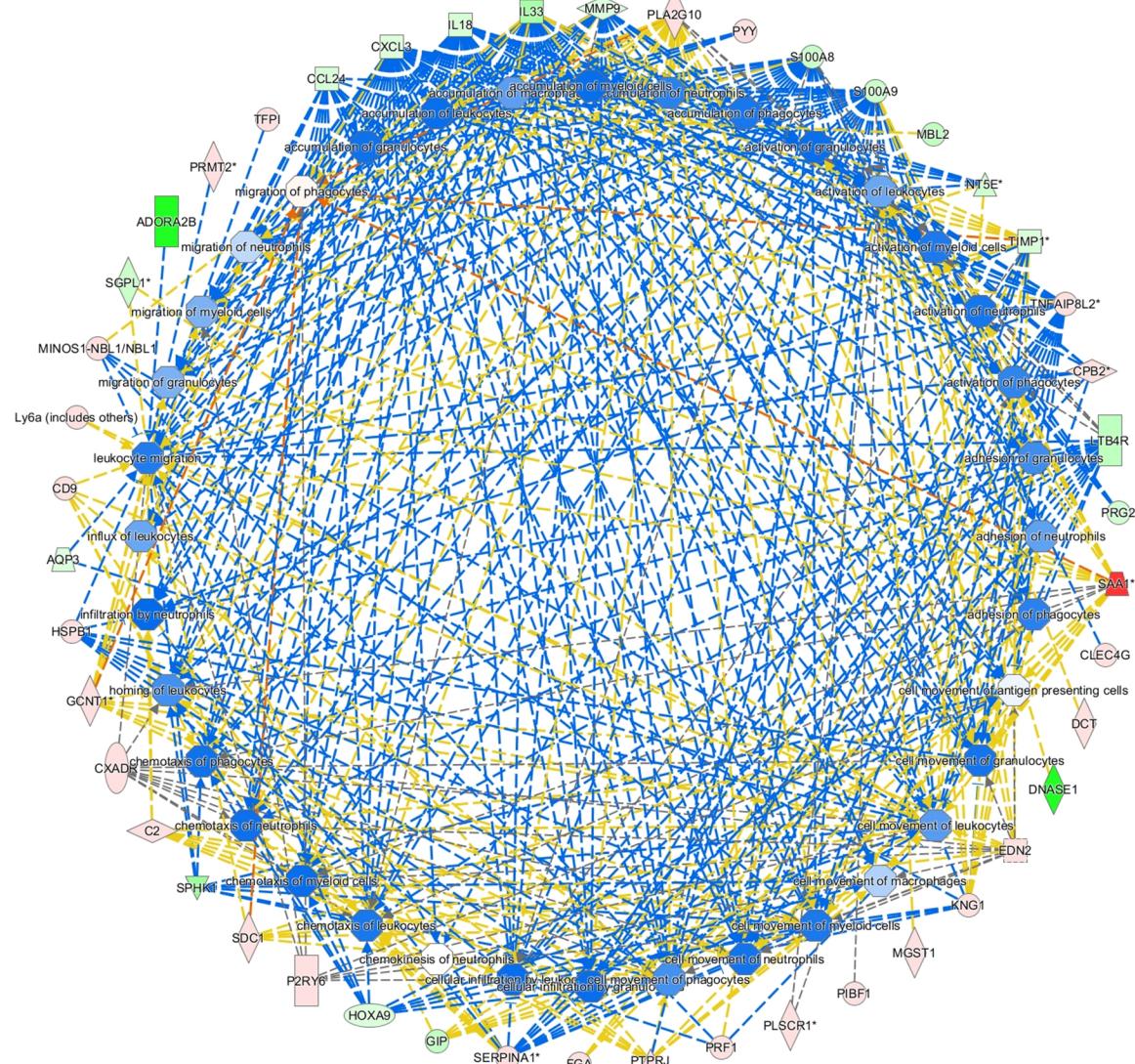
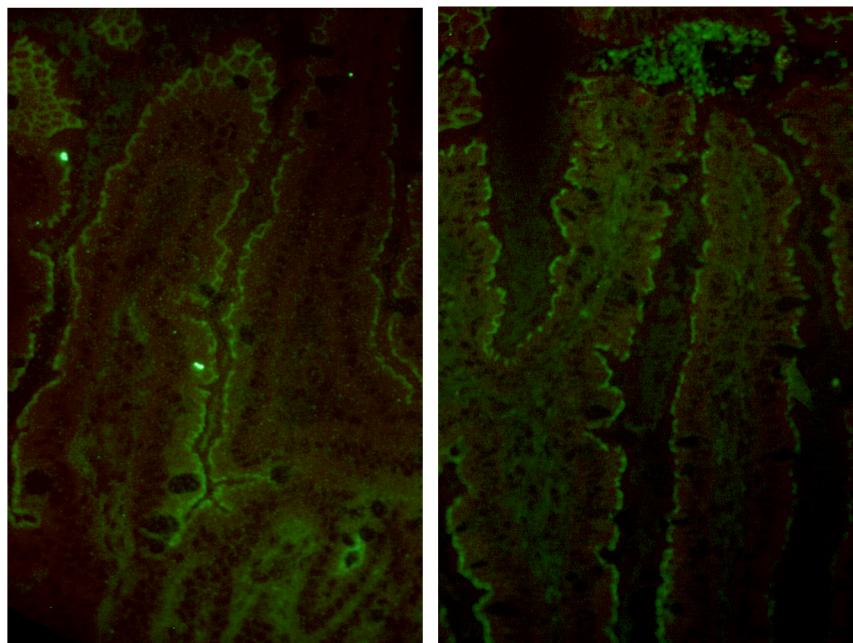


Figure S3. Lepage et al.



Controls

Gata4 Δ IEC

Figure S4. Lepage et al.

Table S1. Comparative gene transcript expression of junctional molecules in the jejunum of *Gata4*^{ΔIEC} and control mice (n=6 for each group).

Gene transcript	Fold difference (<i>Gata4</i> ^{ΔIEC} /control)	P value (Student T-test)
Claudin-1	1.17 ± 0.1	0.16
Claudin-2	6.59 ± 0.52	0.0001
Claudin-3	1.56 ± 0.06	0.0006
ZO-1	1.26 ± 0.07	0.01
JAM-1	1.28 ± 0.08	0.05
Occludin	1.24 ± 0.04	0.02
E-Cadherin	1.45 ± 0.08	0.007

Table S2. Comparative gene transcript expression of inflammatory molecules in the jejunum of *Gata4*^{ΔIEC} and control mice (n=6 for each group).

Gene transcript	Fold difference (<i>Gata4</i> ^{ΔIEC} /control)	P value (Student T-test)
Icam1	1.43 ± 0.12	0.02
Cx3cr1	1.55 ± 0.26	0.05
Il-1β	0.62 ± 0.04	0.08
Cd5	1.67 ± 0.52	0.30
Cd69	1.54 ± 0.34	0.19
Il-1βr	1.15 ± 0.10	0.54
Il-23a	0.64 ± 0.13	0.22
Ccl20	1.19 ± 0.44	0.74
Ccr6	1.06 ± 0.55	0.92
Cxcl1	1.08 ± 0.22	0.82
Il-21	0.46 ± 0.15	0.29
Ccr4	0.46 ± 0.15	0.20
Cd25	1.27 ± 0.26	0.36
Cxcr4	1.39 ± 0.43	0.43
Foxp3	0.79 ± 0.26	0.51
Inf-γ	1.57 ± 0.41	0.33
Il-10	1.11 ± 0.14	0.60
Il-12p35	0.63 ± 0.22	0.60
Il-12p40	1.38 ± 0.22	0.42
Il-13	0.02 ± 0.01	0.15
Il-17	1.72 ± 0.90	0.54
Il-2	0.87 ± 0.21	0.67
Il-23r	1.73 ± 0.38	0.12
Il-24	0.67 ± 0.08	0.17
Tgfβ	1.11 ± 0.16	0.61
Tnfα	1.63 ± 0.34	0.15

Field Change	P-value	Symbol	Entrez Gene Name	Location	Type(s)
-3.03	0.000058	Aldo2b	aldose reductase 2	Plasma Membrane	G-protein coupled receptor
-3.473	4.35E-05	Skl2a2	SLC2A2	Plasma Membrane	transporter
9.335	5.74E-05	Skl2a8i	SLC2A8I	Plasma Membrane	transporter
-3.888	1.34E-04	Gm798	Gm798	Other	other
-6.223	6.30E-04	Apcoc2	APOC2	Extracellular Space	transporter
-5.888	4.92E-05	Sphk1	SPHK1	Cytoplasm	kinase
-5.334	4.92E-05	Bst1	BST1	Plasma Membrane	enzyme
-5.301	3.22E-05	Apcoc2	APOC2	Extracellular Space	transporter
-4.871	9.15E-05	Car2	CA2	Cytoplasm	transporter
-4.841	8.02E-05	Rec8	REC8	Plasma Membrane	enzyme
-4.723	3.47E-05	Egrp7	EMR9P7	Cytoplasm	enzyme
-4.645	2.82E-04	Apoa4	APOA4	Nucleus	other
-4.552	1.01E-04	Trim38	TRIM38	Plasma Membrane	other
-4.523	6.70E-05	Rbp2	RBP2	Extracellular Space	transporter
-4.107	2.78E-04	Skl2a2	SLC2A2	Plasma Membrane	transporter
-4.047	6.12E-05	Rbp2	RBP2	retinol binding protein 2, cellular	transporter
-3.924	2.04E-04	Astd11	ASXL1	Nucleus	transcription regulator
-3.809	2.76E-03	Fam151a	FAM151A	Extracellular Space	other
-3.777	6.40E-04	Caps13	CAPN13	Other	other
-3.731	3.71E-04	Lbd41	LBD41	Plasma Membrane	G-protein coupled receptor
-3.611	1.75E-04	Trim38	TRIM38	Other	other
-3.434	3.52E-03	Fam151a	FAM151A	Extracellular Space	other
-3.379	4.79E-04	Astd11	ASXL1	Other	other
-3.335	4.83E-04	Cyp2b23	CYP2B23	cytochrome P450, family 2, subfamily b, polypeptide 23	enzymes
-3.233	2.47E-04	Adh1c	ADH1C	alcohol dehydrogenase 1C (class 1), gamma polypeptide	enzymes
-3.220	2.47E-04	Skl2a8i	SLC2A8I	solute carrier family 2 (facilitated glucose transporter), member 8	transporter
-3.148	1.78E-04	Tnfr2	TLC202	TLC domain containing	other
-3.181	7.12E-04	Pcsk6	PCSK6	proprotein convertase subtilisin/kexin type 6	enzymes
-3.160	6.02E-05	Sect1c	SEC14L	SEC14-like 1 (S. cerevisiae)	transporter
-3.159	1.83E-04	Skl2a8i	SLC2A8	cytochrome P450, family 2, subfamily A, polypeptide 8	enzymes
-3.127	5.09E-04	Skl2a2	SLC2A2	solute carrier family 2 (facilitated glucose transporter), member 2	transporter
-3.095	8.96E-04	Skl3a3	SLC1A3	solute carrier family 1 (galactosuria, glutamate transporter), member 3	transporter
-3.031	2.10E-04	Skl2a8i	SLC2A8	cytochrome P450, family 2, subfamily A, polypeptide 8	enzymes
-3.002	1.70E-03	Bdh2	BHD2	3-hydroxybutyrate dehydrogenase, type 2	enzymes
-2.991	3.49E-04	Gltph2	GLTPD2	glutathione transfer protein domain containing 2	enzymes
-2.992	5.20E-05	Gm202	ELMO2	engulfment and cell motility 2	transporter
-2.931	1.08E-03	Apoa4	APOA4	apolipoprotein A-IV	transporter
-2.929	8.07E-03	Ltb4r2	LTB4R2	leukotriene B4 receptor 2	receptor
-2.920	4.02E-04	Nbs1	NTSE	neurofibromatosis 1 (neurofibromatosis 1, CD73)	transporter
-2.878	1.34E-04	Cda	CDA	cytidine deaminase	enzymes
-2.833	2.02E-04	Lmd1	LMCD1	LIM and cysteine-rich domains 1	transporter
-2.821	2.21E-04	Codt114	CCDC114	coiled-coil domain containing 114	transporter
-2.810	2.90E-04	Cyp2c27	CYP2C18	cytochrome P450, family 2, subfamily C, polypeptide 18	enzymes
-2.795	3.02E-04	Prrs12	PRRS12	primate-specific protein 12 (primate-specific, missense)	transporter
-2.783	8.01E-05	Plekbf1	PLEKH1	pleckstrin homology domain containing, family F (with FYVE domain) member 1	transporter
-2.762	8.14E-05	Lmd1	LMCD1	LIM and cysteine-rich domains 1	transporter
-2.719	2.60E-04	Cyp2b26	CYP2B26	cytochrome P450, family 2, subfamily b, polypeptide 26	enzymes
-2.711	4.03E-04	Tnfr2	TLC202	TLC domain containing	other
-2.688	1.01E-03	Tgsv5	TGTV5	T cell receptor gamma, variable 5	transporter
-2.688	6.18E-05	Vav1	VSN1	visual system homeobox	other
-2.684	1.03E-03	Unc93a	UNC93A	unc-93 homolog (Caenorhabditis elegans)	transporter
-2.680	1.43E-04	Apoa4	APOA4	apolipoprotein A-IV	transporter
-2.661	1.36E-04	Cress3	CREB3L3	AMPK responsive element binding protein 3-like 3	transporter
-2.659	1.36E-04	Codt2	CCDC2	coiled-coil domain containing 2	transporter
-2.642	5.54E-04	Trp10471C18Rik	2210407C18Rik	cytochrome P450, family 2, subfamily C, polypeptide 18	enzymes
-2.627	8.23E-04	Gpr151	GPR151	G protein-coupled receptor 151	transporter
-2.623	8.23E-04	Cht1	CHT1	chitinase 1, ubiquitous	transporter
-2.603	1.41E-03	Sklct6a8	SLC16A8	solute carrier family 16, member 8	transporter
-2.596	7.26E-05	Gde1	GDE1	glycerophosphodiester phosphodiesterase 1	transporter
-2.592	8.73E-05	Prg2	PRG2	protein required for growth (insect killer cell activator, eosinophil granule major basic protein)	transporter
-2.579	1.51E-04	Trif22	TRIF22/Infra23	tumor necrosis factor receptor-associated factor 2	transporter
-2.524	1.02E-04	Gde1	GDE1	glycerophosphodiester phosphodiesterase 1	transporter
-2.498	1.02E-04	Scd2	SCD2	scd-2 (Caenorhabditis elegans)	transporter
-2.485	1.61E-04	Tnfr2	TLL2	tubulin tyrosine ligase-like family, member 2	transporter
-2.481	1.40E-04	Mdh2	MDH2	malate dehydrogenase 2, NAD (mitochondrial)	enzymes
-2.468	9.20E-04	Cyp2b26	CYP2B26	cytochrome P450, family 2, subfamily b, polypeptide 26	enzymes
-2.458	1.11E-04	Lyst1	LPD1	lysophosphatidylserine lytic membrane protein	transporter
-2.453	1.04E-02	Cyp2d26	CYP2D26	cytochrome P450, family 2, subfamily d, polypeptide 26	enzymes
-2.441	3.40E-04	Pmp7	PMP7	progestin and adrenocorticotropin receptor family member VII	transporter
-2.407	2.15E-04	Tmem68a	TMEM68A	transmembrane protein 68A	transporter
-2.391	4.78E-04	Usp18	USP18	ubiquitin specific peptidase 18	transporter
-2.390	3.30E-04	Gm202	SLC2A8	cytochrome P450, family 2, subfamily A, polypeptide 2	enzymes
-2.387	1.31E-04	Soco3	SOOC	short coiled-coil protein	transporter
-2.379	1.03E-04	Muc4	MUC4	mucin 4, cell surface associated	transporter
-2.378	1.55E-04	Prss12	PRRS12	muclin 4, cell surface associated	transporter
-2.365	1.83E-04	Apcoc1	APOC1	Rap guanosine triphosphate-activating factor (GEF) 6	transporter
-2.362	1.77E-04	Tgsv4	TGTV4	transmembrane 4-like ion family member 5	transporter
-2.354	1.95E-04	Hibch	HIBCH	3-hydroxyisobutyryl-CoA hydrolase	transporter
-2.339	3.33E-04	Gsk1	GSK1	glutathione S-transferase kappa 1	transporter
-2.310	1.20E-04	Galt	GALT	galactose-1-phosphate uridylyltransferase	transporter
-2.309	3.45E-04	Gsk1	GSK1	glutathione S-transferase kappa 1	transporter
-2.309	1.08E-04	Scamp5	SCAMP5	secretory carrier membrane protein 5	transporter
-2.279	1.08E-04	Cmpk1	CMPK1	guanosine triphosphate kinase 1	transporter
-2.258	2.30E-04	Pld3	PLCD3	phospholipase C, delta 3	transporter
-2.254	1.81E-04	Muc4	MUC4	muclin 4, cell surface associated	transporter
-2.244	3.02E-04	Rpp46	RPP46	Rap guanosine triphosphate-activating factor (GEF) 6	transporter
-2.228	1.03E-04	Tmfd5	TMFSD5	transmembrane 4-like ion family member 5	transporter
-2.220	2.22E-04	Sytl2	SYTL2	synaptophysin-170/260 kDa gene	transporter
-2.218	1.28E-04	Tmfd5018Rik	TMFSD5018Rik	transmembrane 4-like ion family member 50	transporter
-2.198	3.82E-04	Plekbf1	PLEKH1	pleckstrin homology domain containing, family F (with FYVE domain) member 1	transporter
-2.184	7.91E-04	Tim1	TM1P1	TIMP metallopeptidase inhibitor 1	transporter
-2.184	2.24E-04	Thaf1	THAF1	matrix metalloproteinase inhibitor 1	transporter
-2.157	2.95E-04	Nudt5	NUDT5	nudt5 (nudt5-like 1)	transporter
-2.155	1.77E-03	Cxcl3	CXCL3	chemokine (C-X-C motif) ligand 3	transporter
-2.149	1.22E-03	Skl2a8i	SLC2A8	solute carrier family 2 (concentrative nucleoside transporter), member 2	transporter
-2.136	1.00E-03	Hoxa4	HOXA4	homeobox protein HOXA4	transporter
-2.117	3.96E-04	Unc93a	UNC93A	unc-93 homolog (Caenorhabditis elegans)	transporter
-2.115	1.22E-03	Aldh1a1	ALDH1A1	aldehyde dehydrogenase 1, family, member 1	transporter
-2.113	2.00E-04	Skl2a8i	SLC2A8	solute carrier family 2 (concentrative nucleoside transporter), member 8	transporter
-2.113	6.93E-03	Snrp8	SNRP8	small nuclear ribonucleoprotein polypeptides B and B1	transporter
-2.109	1.91E-03	Hvcn1	HVCN1	hydrogen voltage-gated channel 1	transporter
-2.108	1.00E-03	Nov1	NOV1	novelty 1	transporter
-2.095	1.19E-02	B3galt5	B3GALT5	UDP-Gal beta:GalNAc beta 1,3-galactosyltransferase, polypeptide 5	transporter
-2.077	1.22E-02	Nbel1	NEAL1	neuroblastoma 1	transporter
-2.073	1.07E-02	Tmem3	TMEM3	transmembrane protein 3	transporter
-2.072	4.30E-04	Cyp2d22	CYP2D22	cytochrome P450, family 2, subfamily d, polypeptide 22	enzymes
-2.071	5.56E-03	Ofl1221	OFL1221	olfactory receptor 1221	transporter
-2.070	1.77E-02	Hpd1	HPD1	heme oxygenase 1 protein kinase 2	transporter
-2.067	3.10E-03	Hdpb	HDPB1	high density lipoprotein binding protein 2	transporter
-2.049	2.53E-03	Necab1	NECAB1	N-terminal EF-hand calcium binding protein 1	transporter
-2.048	1.00E-03	Mir61	MIR61	microRNA 61	transporter
-2.040	3.01E-03	49334229Rik	49334229Rik	microRNA 49334229	transporter
-2.034	2.08E-04	Soco3	SOOC	short coiled-coil protein	transporter
-2.038	1.22E-02	Girk2	GIRK2	glycogen receptor, alpha 3	transporter
-2.029	1.07E-02	Tim1	TM1P1	TIMP metallopeptidase inhibitor 1	transporter
-2.022	4.70E-02	Drl1	DR1	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	transporter
-2.022	3.93E-04	Pmkv	PMKV	phosphomimetic kinase	transporter
-2.020	2.79E-02	Vntr2	VNTR2	VNTR repeat 2	transporter
-2.020	8.87E-04	Sklct1a2	SLC11A2	solute carrier family 11 (proton-coupled diacid metal ion transporter), member 2	transporter
-2.032	2.22E-02	Igb2	IGB2	integrin beta 2/4	transporter
-2.032	7.62E-03	Gm798	Gm798	glutathione (S-acyl) transferase 2, 1, branching enzyme 1 (blood group)	transporter
-2.032	1.01E-02	Cdh11	CDH11	cadherin 11, type 2, C9-cadherin (osteoblast)	transporter
-2.135	1.84E-03	Nbt1	MINOS1-NBL1/NBL1	neuroblastoma 1, DAN family BMP antagonist	transporter
-2.137	2.56E-02	Cyp2d9	CYP2D9	cytochrome P450, family 2, subfamily D, polypeptide 6	enzymes
-2.141	1.77E-02	Aldh1a1	ALDH1A1	aldehyde dehydrogenase 8 family, member A1	transporter
-2.145	3.12E-04	Deg2	DG2	desmogelin 2	transporter
-2.150	1.07E-04	Afg2	AFG2	AFGAP with FG repeats 2	transporter
-2.150	1.23E-04	Lts5	LTS5	luteinizing hormone-releasing hormone 5	transporter
-2.155	6.04E-04	Tns4	TNS4	transferrin 4	transporter
-2.159	2.38E-02	Cyp2c37	CYP2C18	olfactory receptor 38	transporter
-2.126	1.90E-03	Ofl25	OFL25	cytochrome P450, family 2, subfamily C, polypeptide 18	enzymes
-2.132	2.02E-02	B007785	B007785	cDNA sequence B007785	transporter
-2.135	1.01E-02	Cdh11	CDH11	cadherin 11, type 2, C9-cadherin (osteoblast)	transporter
-2.135	1.84E-03	Nbt1	MINOS1-NBL1/NBL1	neuroblastoma 1, DAN family BMP antagonist	transporter
-2.137	2.56E-02	Cyp2d9	CYP2D9	cytochrome P450, family 2, subfamily D, polypeptide 6	enzymes
-2.180	1.69E-02	483341D3Rik	483341D3Rik	cytochrome P450, family 2, subfamily D, polypeptide 6	enzymes
-2.180	5.06E-03	Gas1	GAS1	glucosidase, alpha 1, beta-1,4-glucanase/callinectin translocase), member 20	transporter
-2.189	8.33E-04	Skl2a20	SLC2A20	mitogen-activated protein kinase 4	transporter
-2.191	3.63E-04	Makp4	MAPK4	mitogen-activated protein kinase 4	kinase

2.193	1.67E-02	Mael	MAEL	maelstrom spermatogenic transposon silencer protein-like 1, membrane protein, receptor type, D glutamate receptor interacting protein 1	Cytoplasm	phosphatase
2.194	4.13E-04	Gata1	GATA1	ATPase, Ca++ transporting, plasma membrane 1	Plasma Membrane	transcription regulator
2.198	1.63E-04	Alpb1	ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	Plasma Membrane	transporter
2.200	3.38E-02	Hmgb2	HMBG2	5-hydroxy-3-methyl-CoA reductase	Nucleus	transporter
2.202	3.88E-04	Ghrl	GHRL	ghrelin/oxyntomodulin receptor	Cytoplasm	enzyme
2.210	1.84E-02	Pes1st2	PSORS1C2	psoriasis susceptibility 1 candidate 2	Extracellular Space	growth factor
2.212	1.00E-03	Syng1-ps1	SYNG1-PS1	synapsin 1-associated protein 1, pseudogene 1	Extracellular Space	other
2.216	3.77E-04	Gata4	GATA4	protein complex protein 1, pseudogene 1	Other	other
2.224	4.53E-04	Cap1	CAP2	CAP, adenylate cyclase-associated protein, 2 (yeast)	Plasma Membrane	kinase
2.235	7.27E-04	Tst	TST	thiosulfinate sulfurtransferase (rhodanese)	Plasma Membrane	other
2.239	1.80E-04	Ede1b	EIF4EB	edefitinib resistance mutation factor 4E family member 1B	Cytoplasm	kinase
2.243	1.86E-04	Adk	ADK	adenosine kinase	Nucleus	kinase
2.244	4.73E-04	Mtt	MTE	metallothionein 1	Cytoplasm	other
2.247	1.77E-04	Gata1	GHRL	ghrelin/oxyntomodulin receptor	Extracellular Space	growth factor
2.249	3.51E-03	Akr1c19	Akr1c19	aldo-keto reductase family 1, member C19	Other	other
2.255	1.97E-04	Adldc	ALDLOC	aldolase C, fructose-bisphosphate	Cytoplasm	enzyme
2.258	1.77E-04	Tot12	TOT12	transferrin receptor 12	Nucleus	transcription regulator
2.268	2.78E-03	4930430A15Rik	4930430A15Rik	RIKEN cDNA 4930430A15 gene	Nucleus	transcription regulator
2.271	2.39E-02	Fbxo32	FBXO32	F-box protein 32	Cytoplasm	enzyme
2.273	5.83E-02	4930430B00Rik	4930430B00Rik	RIKEN cDNA 4930430B00 gene	Extracellular Space	peptidase
2.280	1.82E-04	Hed17b7	HSD17B7	hydroxysteroid (17-beta) dehydrogenase 7	Plasma Membrane	G-protein coupled receptor
2.283	1.72E-02	F8	F8	coagulation factor VIII, procoagulant component	Cytoplasm	enzyme
2.286	1.00E-02	Otx382	Otx382	otx382	Cytoplasm	other
2.287	3.54E-04	Ugt1a5b	UGT1A6	UDP glucuronosyltransferase 1 family, polypeptide A6	Extracellular Space	peptidase
2.290	1.64E-04	Papss1	PAPS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	Cytoplasm	enzyme
2.295	1.00E-04	Pst1	PST1	polymerase sigma factor 1	Extracellular Space	G-protein coupled receptor
2.298	3.65E-04	Wdr16	WDR16	WD repeat domain 16	Cytoplasm	enzyme
2.302	1.03E-03	Atdn1a1	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	Cytoplasm	enzyme
2.309	1.00E-04	Gut1	GUT1	GUT1 (GTPase homomeric complex), member 1	Extracellular Space	other
2.313	1.07E-04	Tsp1	TSP1	GUT1 (GTPase homomeric complex), member 1	Nucleus	transcription regulator
2.314	1.39E-02	Taf7	TAF7	TAF7L RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa	Nucleus	transcription regulator
2.324	1.20E-04	Hoxb7	HOBX7	homeobox B7	Nucleus	enzymes
2.340	1.00E-04	Dnm2	DNM2	dynamin 2	Cytoplasm	kinase
2.350	1.27E-04	Tmem65	TMEM65	transmembrane protein 65	Cytoplasm	enzyme
2.354	1.29E-02	Dct	DCT	dopachrome tautomerase	Cytoplasm	enzyme
2.358	7.38E-04	Atp3	ATG3	ubiquitin thioesterase	Cytoplasm	enzyme
2.368	1.09E-04	Paps1	PAPS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	Extracellular Space	other
2.369	3.76E-02	Spns3pk	SPNS3PK	serine (or cysteine) peptidase inhibitor clade A, member 3K	Plasma Membrane	ion channel
2.380	4.00E-04	Skt2a	ITPR1	inositol triphosphate receptor type 2	Extracellular Space	peptidase
2.383	1.97E-03	Skt2a0b	SKT2A0B	solute carrier family 6 (neurotransmitter transporter), member 20B	Plasma Membrane	transporter
2.410	1.29E-02	Cpt2	CPT2	carboxyptoleipidase B (plasma)	Extracellular Space	peptidase
2.411	8.00E-04	Cmtc2a	CMTCA	calcium/calmodulin-dependent protein kinase II alpha	Cytoplasm	kinase
2.420	2.42E-02	Off292	OFFC92	olfactory receptor 297	Extracellular Space	peptidase
2.427	1.09E-03	Inmt	INMT	indolethylamine N-methyltransferase	Cytoplasm	G-protein coupled receptor
2.430	1.00E-04	Qar771	QAR771	alpha-1,3-fucosidase	Plasma Membrane	kinase
2.494	3.39E-02	Ank1	ANKK1	ankyrin repeat and kinasin domain containing 1	Plasma Membrane	kinase
2.509	1.13E-04	Ttyh3	TTYH3	tufted hair cell member 3	Plasma Membrane	ion channel
2.510	7.38E-04	Satn4	STFR	saturnin 4	Plasma Membrane	G-protein coupled receptor
2.512	4.72E-02	Abim1	ABLM1	actin binding LIM protein 1	Cytoplasm	enzyme
2.518	1.32E-03	Fab1	FA2H	fatty acid 2-hydroxylase	Cytoplasm	enzyme
2.519	1.72E-02	Tim23	TMEM23	Fab1 protein 32	Extracellular Space	peptidase
2.537	3.25E-02	Tim2	TIM2	T-cell immunoglobulin and mucin domain containing 2	Plasma Membrane	other
2.543	7.77E-03	Cpt2c	CPT2C	carboxyptoleipidase B2 (plasma)	Extracellular Space	peptidase
2.564	3.07E-02	Cyp26t0	CYP26T0	cytochrome P450, family 2, subfamily C, polypeptide 70	Cytoplasm	enzyme
2.579	2.27E-02	Emr1	ERMR1	endoplasmic reticulum membrane protein 1	Cytoplasm	kinase
2.581	3.60E-02	Serpina10	SERPINA10	serpin peptidase inhibitor, clade A (alpha-1 antitrypsin), member 10	Extracellular Space	other
2.584	9.17E-04	Mst1	MSTP	mercaptopeptide sulfotransferase	Cytoplasm	enzyme
2.634	1.92E-04	Pmp22	PMP22	peripheral myelin protein 22	Plasma Membrane	other
2.634	1.44E-02	Skt2b	SLCO1B3	solute carrier organic anion transporter family, member 1B3	Plasma Membrane	transporter
2.653	1.92E-04	Krt4	KRT4	keratin 4	Cytoplasm	peptidase
2.654	1.40E-04	Arpc2b	ARPC2B	45S ribosomal protein (aminopeptidase P) 2, membrane-bound	Plasma Membrane	peptidase
2.678	1.05E-04	Ugt2z3b	UGT2Z7	UDP glucuronosyltransferase 2 family, polypeptide B7	Plasma Membrane	peptidase
2.686	1.54E-04	Otf12b	OTF12B	olfactory receptor 12B	Extracellular Space	G-protein coupled receptor
2.696	1.00E-04	Bna1	ITPR1	inositol triphosphate receptor heavy chain, family 1	Nucleus	transcription regulator
2.701	1.11E-02	Tbx15	TBX15	T-box 15	Other	other
2.738	9.84E-05	Tess8	TCEAL8	transcription elongator factor A (SII) like 8	Plasma Membrane	phosphatase
2.742	5.32E-04	Pip6	PIP6	endo-lysosomal phosphoinositide receptor type, D	Extracellular Space	other
2.784	5.39E-04	Fht1	FHL1	four and a half LIM domains 1	Plasma Membrane	phosphatase
2.785	1.99E-04	Nsdhl	NSDHL	(NAD(P)) dependent steroid dehydrogenase-like	Cytoplasm	enzyme
2.791	1.99E-04	Ocm	OCM	(NAD(P)) dependent steroid dehydrogenase-like	Cytoplasm	enzyme
2.800	7.07E-05	Pfd1	PIBF1	(NAD(P)) dependent steroid dehydrogenase-like	Nucleus	other
2.807	1.82E-02	Vep1	VEPH1	inter-alpha-trypsin inhibitor heavy chain 1	Plasma Membrane	peptidase
2.814	3.72E-04	Cpt1	CPT1	X-prolyl aminopeptidase (aminopeptidase P) 1, membrane-bound	Extracellular Space	peptidase
2.814	4.73E-04	Ptd	PPTD	carboxyptoleipidase A, membrane-bound	Plasma Membrane	peptidase
2.835	4.57E-04	330005D01Rik	330005D01Rik	RIKEN cDNA 330005D01 gene	Cytoplasm	phosphatase
2.867	4.45E-04	Fht1	FHT1	four and a half LIM domains 1	Extracellular Space	other
2.869	1.00E-04	Nsdhl	NSDHL	(NAD(P)) dependent steroid dehydrogenase-like	Cytoplasm	enzyme
2.877	1.46E-02	Cyp2e1	CYP2E1	cytochrome P450, family 2, subfamily E, polypeptide 1	Cytoplasm	enzyme
2.880	1.50E-04	Hoxb7	HOBX7	homeobox B7	Nucleus	transcription regulator
2.901	1.00E-04	Nsdhl	NSDHL	(NAD(P)) dependent steroid dehydrogenase-like	Cytoplasm	enzyme
2.907	1.82E-02	Ihh1	ITIH1	inter-alpha-trypsin inhibitor heavy chain 1	Extracellular Space	other
2.924	5.19E-02	Xpm2	XPM2	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	Plasma Membrane	peptidase
2.924	5.59E-02	513024f1Rik	513024f1Rik	RIKEN cDNA 513024f1 gene	Other	other
2.973	7.95E-05	Pscr1	PLSCR1	phospholipid scramblase 1	Plasma Membrane	enzyme
3.016	3.91E-03	Mtnr6	MTMR6	myotubularin related protein 6	Cytoplasm	enzyme
3.029	1.00E-04	Cpt2c5	CPT2C5	carboxyptoleipidase C, polypeptide 9	Extracellular Space	peptidase
3.189	1.73E-04	Epb414a	EPB414A	erythrocyte membrane protein band 4.1 like 4A	Plasma Membrane	transporter
3.208	7.38E-05	Slt13a2	SLC13A2	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2	Extracellular Space	other
3.208	3.72E-02	Fgd7	FGF7	fibroblast growth factor 7	Cytoplasm	enzyme
3.217	1.28E-04	Ugt2z3b	UGT2Z7	UDP glucuronosyltransferase 2 family, polypeptide B7	Cytoplasm	enzyme
3.220	1.14E-04	Rasd2	RASD2	RASD family, member 2	Cytoplasm	enzyme
3.230	4.52E-04	Cyp51	CYP51A1	CYP51A1 (CYP51) family 21, subfamily A, polypeptide 1	Cytoplasm	enzyme
3.237	4.42E-05	Cables1	CABLES1	Cdc42 and Arf6 enzyme substrate	Nucleus	other
3.310	5.48E-03	Ttr	TRT	transferrin	Extracellular Space	transporter
3.338	4.72E-02	4725465J04Rik	4725465J04Rik	RIKEN cDNA 4725465J04 gene	Other	other
3.379	9.45E-04	Abi3bp	AB3BP	ABI3 family member 3 (NEST1) binding protein	Plasma Membrane	other
3.423	2.58E-04	Prnp	PNLIP	T cell immunoglobulin and mucin domain containing 2	Extracellular Space	enzyme
3.437	3.44E-02	Ugt2z2	Tim2	UDP glucuronosyltransferase 2 family, polypeptide A3	Plasma Membrane	peptidase
3.569	4.16E-02	Mut1	MUT1	mutator protein 1	Extracellular Space	other
3.573	8.08E-05	Bex4	BEX4	brain expressed, X-linked 4	Cytoplasm	other
3.587	3.56E-02	Bhd4	BDNF	brain-derived neurotrophic factor	Extracellular Space	other
3.601	9.73E-04	Ptds4	PCMV9	prostaglandin D2 synthase	Cytoplasm	peptidase
3.624	1.41E-04	Eif4elp3	EIF4EBP3	eukaryotic translation initiation factor 4E binding protein 3	Cytoplasm	other
3.640	3.29E-04	Fgr5	KNG1	kininogen 1	Extracellular Space	other
3.649	5.36E-05	Slt13a1	SLC13A1	solute carrier family 13 (sodium/sulfate symporter), member 1	Plasma Membrane	transporter
4.063	3.79E-05	Lamb3	LAMB3	laminin, beta 3	Extracellular Space	other
4.065	4.70E-02	Pmp22	PMP22	pancreatic membrane protein 22	Extracellular Space	enzyme
4.353	4.15E-02	Prnp	PRNP	glucosaminyl (N-acetyl) transferase 1, core 2	Extracellular Space	other
4.355	2.99E-05	Zdhhc19	ZDHHC19	zinc finger, DHHC-type containing 19	Extracellular Space	transporter
4.433	4.43E-04	Hprt	Hprt	hypoxanthine-guanine phosphoribosyltransferase	Extracellular Space	other
4.620	3.75E-02	Mup2	MUP1	Mup1 (mucin 1)	Extracellular Space	other
4.938	1.34E-04	Hmgcs2	HMGCS2	3-hydroxy-3-methyl-CoA lyCoA synthase 2 (mitochondrial)	Cytoplasm	enzyme
5.033	1.00E-04	Cdk2	CDK2	heat shock 27kDa protein 1	Cytoplasm	enzyme
5.087	4.04E-05	Hspb1	HSPB1	heat shock 27kDa protein 1	Cytoplasm	other
5.338	3.60E-05	Ptk2ap1	PTK2AP1	phosphotyrosine-3-kinase adaptor protein 1	Cytoplasm	other
5.361	6.33E-05	Gst3	GST3	glutathione S-transferase alpha 3	Cytoplasm	enzyme
5.408	3.93E-05	Bex4	BEX4	synexin	Cytoplasm	other
5.445	4.93E-03	Synd	SYCN	syndecan 1	Extracellular Space	other
5.446	1.00E-05	Gmt1	GMT1	glucosaminyl (N-acetyl) transferase 1, core 2	Cytoplasm	enzyme
5.544	4.42E-04	Seprin1b	SPRN1B	serpin peptidase inhibitor, clade A (alpha-1 antitrypsin, antitrypsin), member 1	Extracellular Space	other
6.632	5.88E-04	Seprin1d	SPRN1D	serpin peptidase inhibitor, clade A (alpha-1 antitrypsin, antitrypsin), member 1	Extracellular Space	enzyme
6.893	1.00E-05	Gmt1	GMT1	glucosaminyl (N-acetyl) transferase 1, core 2	Cytoplasm	other
7.573	3.13E-04	Slat4d	SLAT4D	SLAT4D	Extracellular Space	other
7.755	2.40E-04	Seprin1b	SPRN1B	serpin peptidase inhibitor, clade A (alpha-1 antitrypsin, antitrypsin), member 1	Extracellular Space	other
7.870	1.85E-04	Seprin1b	SPRN1B	serpin peptidase inhibitor, clade A (alpha-1 antitrypsin, antitrypsin), member 1	Extracellular Space	other
7.935	2.00E-04	Cubn	CUBN	claudin 14 (face-cockamaine receptor)	Plasma Membrane	transporter
9.371	6.31E-03	Slt001	SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1	Plasma Membrane	transporter
12.336	6.94E-04	Defb37	DEFB37	defensin beta 37	Extracellular Space	other

Table S4. Primers used for qPCR analysis of gene transcripts

Claudin-1	
Up	5'-GCCATCTACGAGGGACTGTGGA-3'
Dw	5'-TGCCAATTACCATCAAGGCTCGG-3'
Claudin-2	
Up	5'-GCCACCCACAGATACTTGTAAAGGAG-3'
Dw	5'-TTCGGAGCCTGTTGCTTGTGCG-3'
Claudin-3	
Up	5'-CCTTGCTGTGTTGCTCCTGCC-3'
Dw	5'-CTCAGACGTAGTCCTGCCGGTC-3'
ZO-1 (TJP1)	
Up	5'-TGCAGAGACAATAGCATTCTCCCAC-3'
Dw	5'-TAGCTCACGGGCTTCAGGAAC-3'
Jam-1 (F11R)	
Up	5'-TGGATATGGGACAGCCATGAGGT-3'
Dw	5'-GCTATAGGCAAACCAGACGCCA-3'
Occludin	
Up	5'-GGAACACATTATGATGAACAGCCCCC-3'
Dw	5'-CGCTTGCCATTCACTTGCCAT-3'
E-cadherin	
Up	5'-ACCAAAGTGACGCTGAAGTCCAT-3'
Dw	5'-GATGGGAGGGATGACCCAGTCT-3'
Icam1	
Up	5'-CTGCTACCTGCACTTGCCCTG-3'
Dw	5'-AGGCTTCTCTGGGATGGATGGAT-3'
Cx3cr1	
Up	5'-GAGTATGACGATTCTGCTGAGG-3'
Dw	5'-CAGACCGAACGTGAAGACGAG-3'
Il-1β	
Up	5'-TAGCCCGCACTGAGGTCTT-3'
Dw	5'-AGCAATGTGCTGGTGCTTCA-3'
Cd5	
Up	5'-CCCCACAGGAGTGAACCAGAAC-3'
Dw	5'-TGGATAAGCAGACAGGTGAGAGTTCC-3'
Cd69	
Up	5'-ACTTCTTCTCCACCACAAACCAAGAGT-3'
Dw	5'-GCCCAATCCAATGTTCCAGTTCAACC-3'
Il-1βr	
Up	5'-TCGCTATCCGTTATCTGTGTTGTTAAGAA-3'
Dw	5'-TGTAGCCGTGAGGATGATAAAGCCC-3'

Il-23a		
Up	5'-CCCGTATCCAGTGTGAAGATGGTTGT-3'	
Dw	5'-TCCCCTTGAAAGATGTCAGAGTCAAGC-3'	
Ccl20		
Up	5'-GCCTCTCGTACATACAGACGC-3'	
Dw	5'-CCAGTTCTGCTTGGATCAGC-3'	
Cer6		
Up	5'-CCTGGGCAACATTATGGTGGT-3'	
Dw	5'-CAGAACGGTAGGGTGAGGACA-3'	
Cxcl1		
Up	5'-CTGGGATTCACCTCAAGAACATC-3'	
Dw	5'-CAGGGTCAAGGCAAGCCTC-3'	
Il-21		
Up	5'-GGACCCTTGTCTGTCTGGTAG-3'	
Dw	5'-TGTGGAGCTGATAGAAGTTCAGG-3'	
Ccr4		
Up	5'-TCCCCTCGTGCTCTGCA-3'	
Dw	5'-TGC GTGTAAGAGGGAGCTGGAC-3'	
Cd25		
Up	5'-TTGTCGGGCAGAACTGTGTCT-3'	
Dw	5'-GCTCCAGGAGTTCCCTAACCAA-3'	
Cxcr4		
Up	5'-AGCATGACGGACAAGTACC-3'	
Dw	5'-GATGATATGGACAGCCTTACAC-3'	
Foxp3		
Up	5'-GGCCCTTCTCCAGGACAGA-3'	
Dw	5'-GCTGATCATGGCTGGTTGT-3'	
Ifn-γ		
Up	5'-CAGCAACAGCAAGGCGAAA-3'	
Dw	5'-GCTGGATTCCGGCAACAG-3'	
Il-10		
Up	5'-TTTGAATTCCCTGGGTGAGAAG-3'	
Dw	5'-TGCTCCACTGCCTTGCTCTT-3'	
Il-12p35		
Up	5'-CACGCTACCTCCTTTTG-3'	
Dw	5'-TTTCTCTGCCGTCTCAC-3'	
Il-12p40		
Up	5'-GGTGCAAAGAACATGGACTTG-3'	
Dw	5'-GACAGAGACGCCATTCCACAT-3'	
Il-13		
Up	5'-GTGTCTCTCCCTCTGACCCTTAA-3'	
Dw	5'-GAGATGTTGGTCAGGGAATCC-3'	

Il-17		
Up	5'-TCCAGAAGGCCCTCAGACTAC-3'	
Dw	5'-TGTGGTGGTCCAGCTTCC-3'	
Il-2		
Up	5'-CCCAGGATGCTCACCTCAA-3'	
Dw	5'-CCGCAGAGGTCCAAGTTCAT-3'	
Il-23r		
Up	5'-GCCAAGAACCAATTCCGA-3'	
Dw	5'-TCAGTGCTACAATCTTCTTCAGAGGACA-3'	
Il-24		
Up	5'-CTCCACTCTGGCCAACAACTT-3'	
Dw	5'-CACCAAAGCGACTTCTGTATCC-3'	
Tgfβ		
Up	5'-GGACCCTGCCCTATATTG-3'	
Dw	5'-GCTTGCGACCCACGTAGTAG-3'	
Tnfα		
Up	5'-AGGCGGTGCCTATGTCTCA-3'	
Dw	5'-GGGTCTGGGCCATAGAACTG-3'	

Table S5. Primers used for qPCR analysis of ChIPs experiments

Site 1

mClau2prom-331up1	5'-TGACATTTGGCTCTACTTCCA-3'
mClau2prom-157dw1	5'CAGGCTCAAGAAGGCATCTA-3'

Site 2

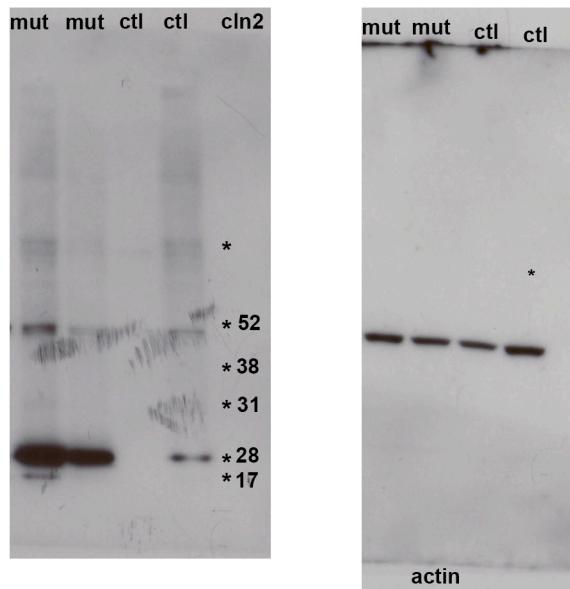
mClau2prom-1706up3	5'-ATTACCCCAGGGATGTTGGT-3'
mClau2prom-1528dw3	5'-GGAGGGGGTTAGGATTAGC-3'

Site 3 (-1775 to -1762)

mClau2prom-18186up5	5'-TGGTGGAAATGAGAACACAA-3'
mClau2prom-1707dw5	5'-CCTTGACACCCCTGTGCCTAT-3'

Negative region

mouseIL1β(-398)-FWD	5'-CCAAACTCCAACTGCAAAGC-3'
mouseIL1β(-197)-REV	5'-TGGTGGAAATGGGCATTATT-3'



Full length gels for claudin-2 and actin blots displayed in Figure 2b.