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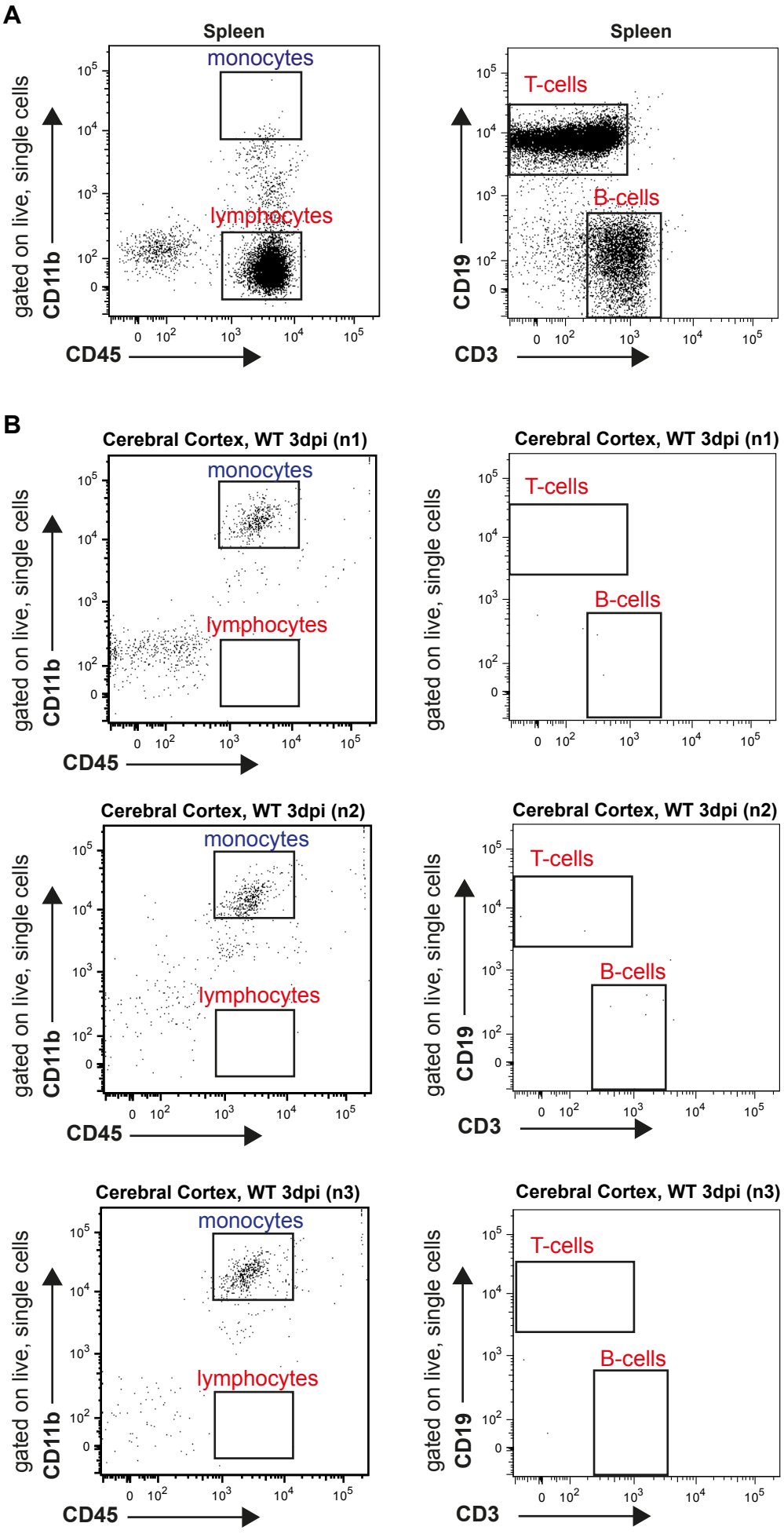
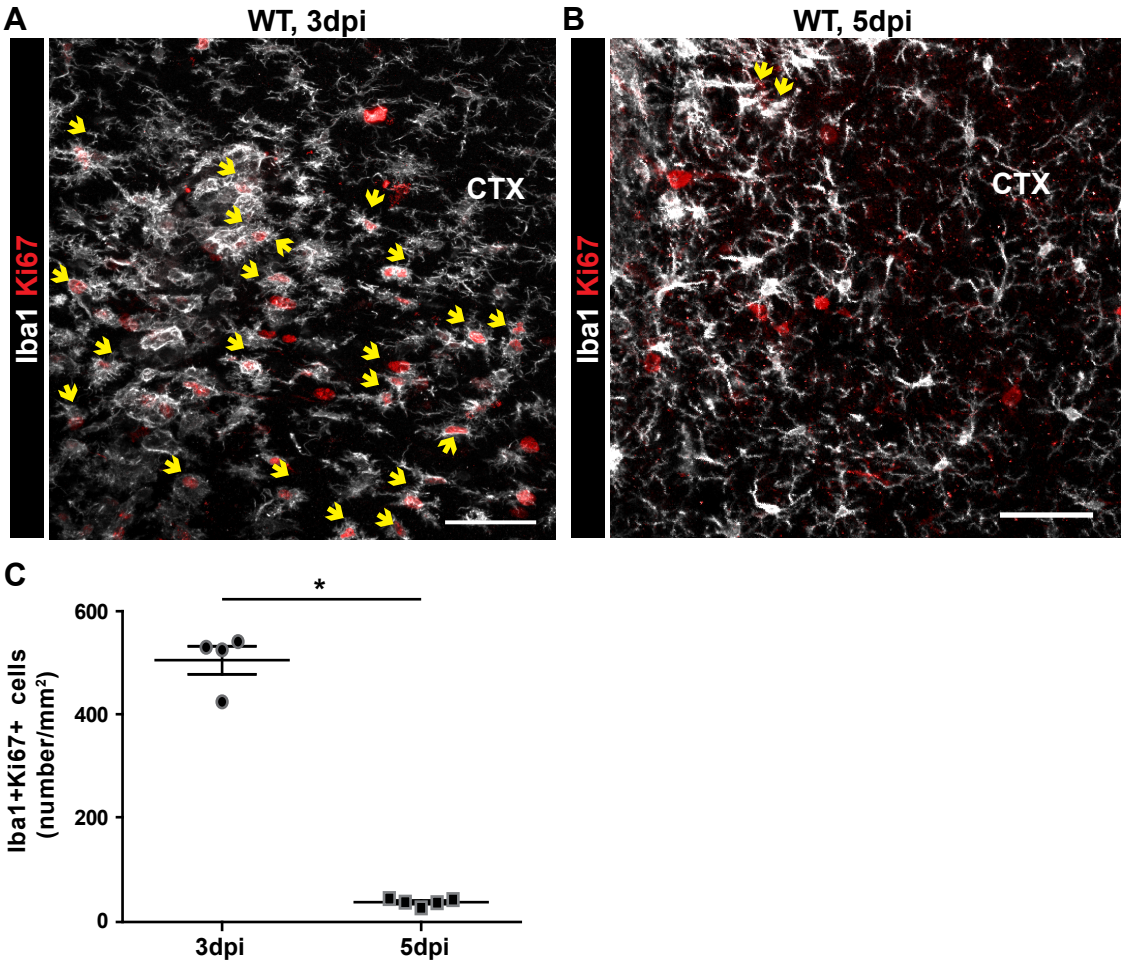
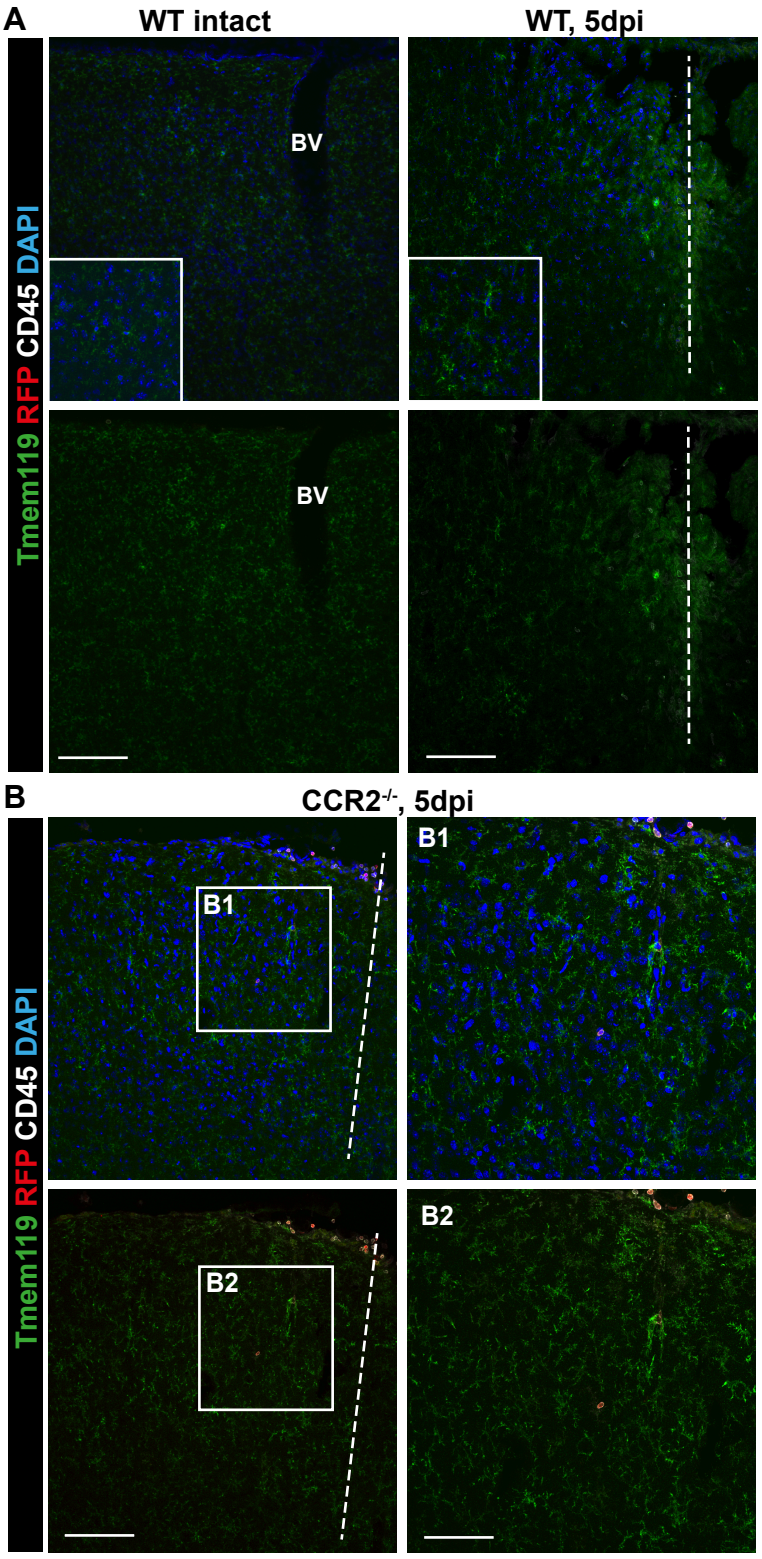


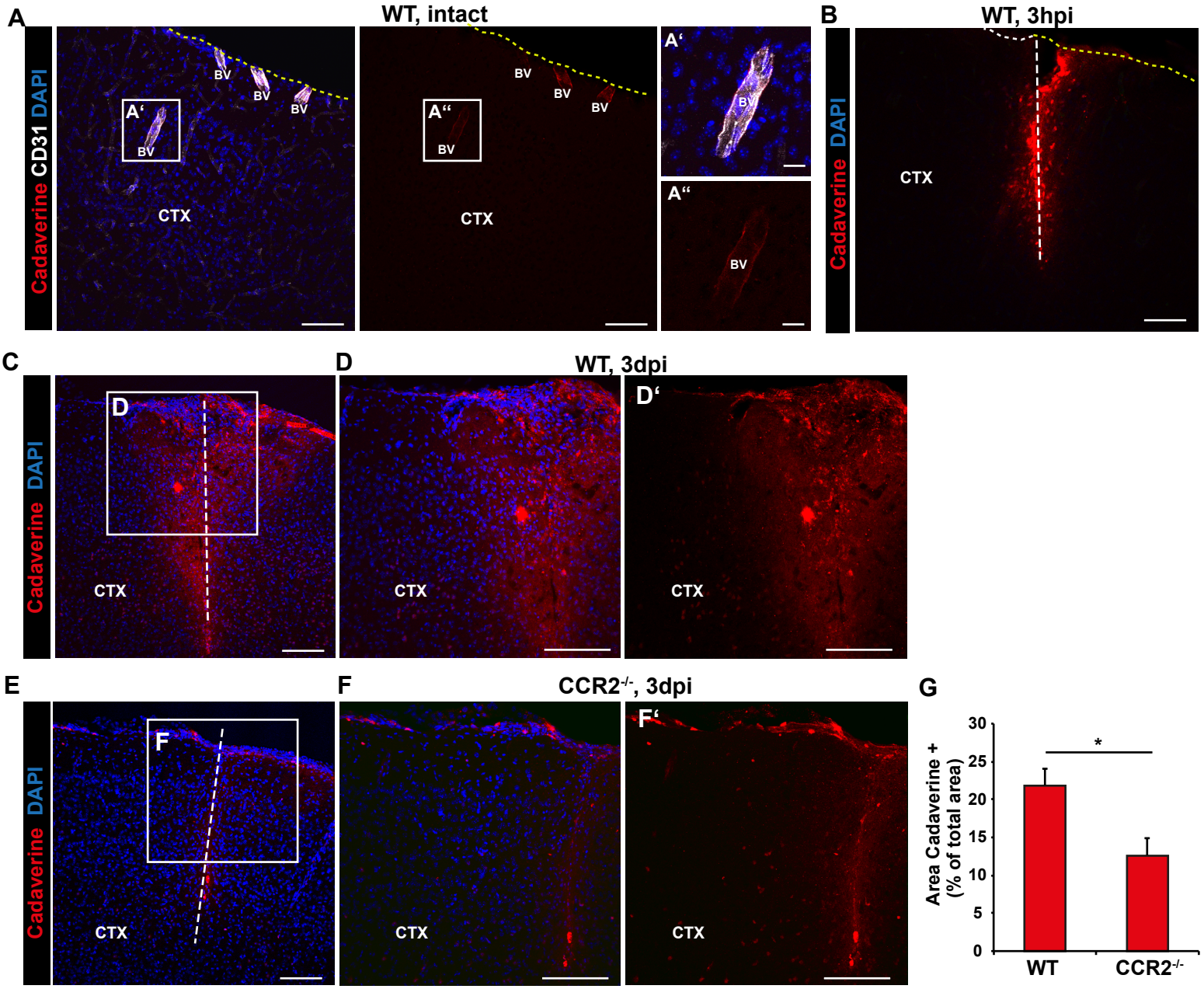
Appendix Figure S1



Appendix Figure S2



Appendix Figure S3



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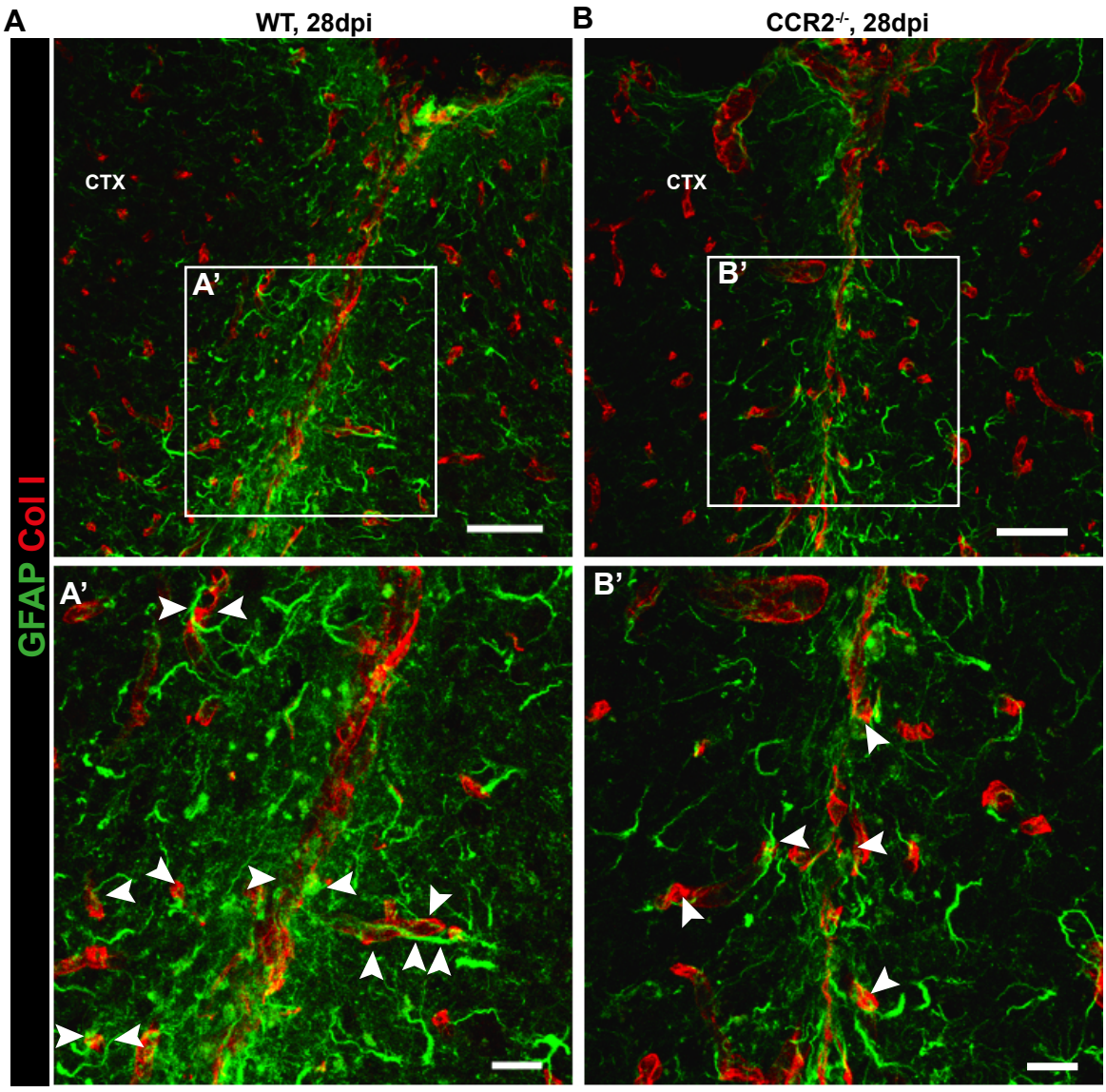
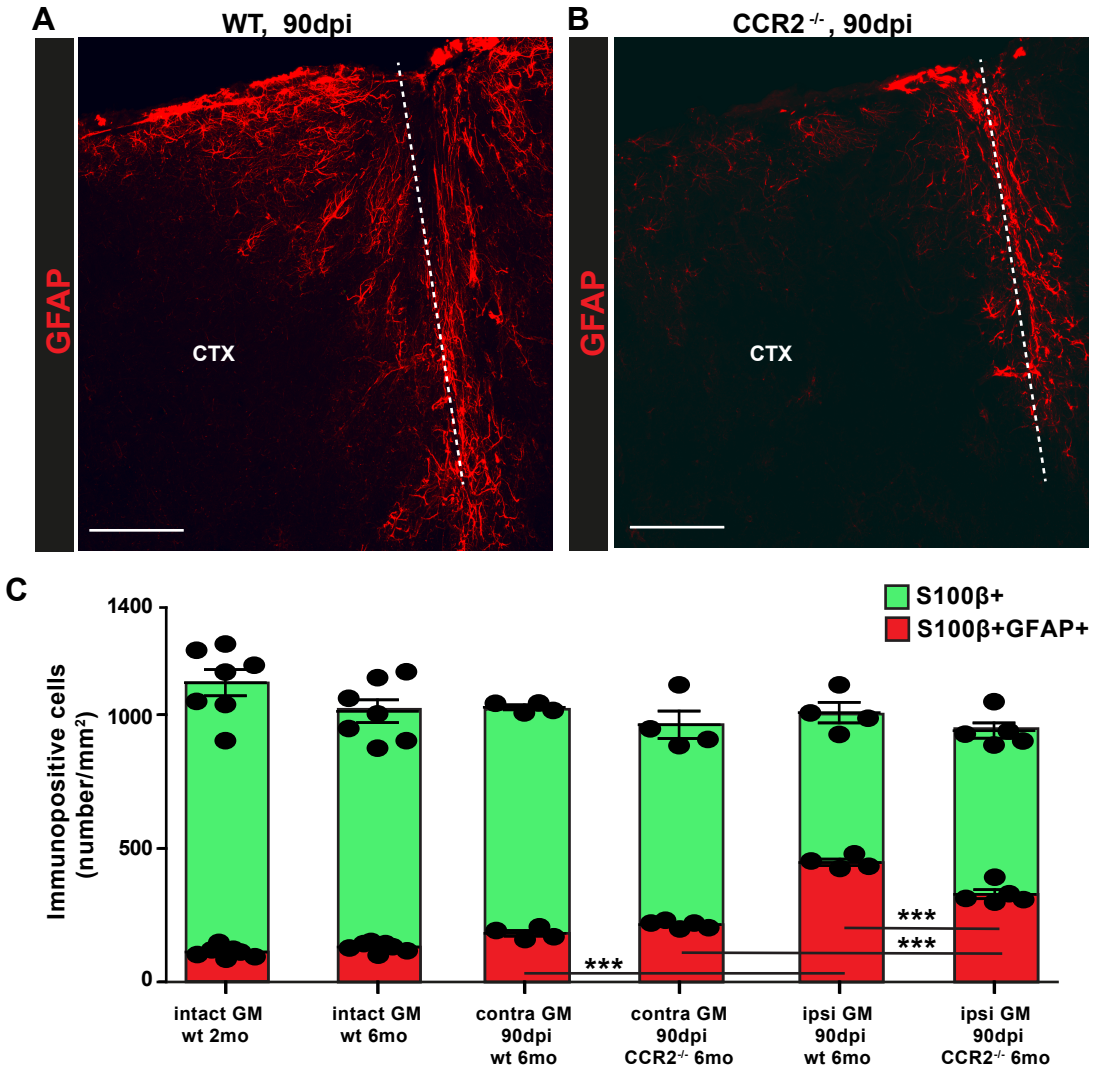


Appendix Figure S5



Appendix Figure S6

Appendix Figure Legends

Appendix Figure S1: Absence of lymphocytes and predominance of CD45$^+$/CD11b$^+$ monocytes/macrophages in the injured GM parenchyma at 3 dpi. Fluorescence-Activated Cell Sorting (FACS) of CD45$^+$ cells (isolated previously by magnetic activated cell sorting) was performed on spleen **(A)** and CD45$^+$ cells from the GM tissue at 3dpi isolated by MACS **(B).** The identity of CD45$^+$ cells was determined by staining with CD11b (high: monocytes/macrophages, see B, n1, left panel; low: lymphocytes, see A), CD19 (T-cells, see A, right panel) and CD3 (B-cells, see A right panel). While lymphocytes were readily detectable in samples taken from spleen **(A)**, they were absent in brain tissue collected from the lesion site where CD45$^+$ cells were exclusively CD11b high monocytes/macrophages.

Appendix Figure S2: Microglia proliferation between 3 and 5 days after injury. Confocal images of Iba1 and Ki67 double-immunostaining in WT GM at 3 dpi **(A)** and 5 dpi **(B).** Arrows point to double-positive cells, the proliferating microglia at the injury site. **(C)** Histogram depicting the number of Iba1$^+$Ki67$^+$ cells in the injured cortical GM of WT mice at 3 dpi and 5 dpi. Of note, there was the steep decline in microglia proliferation at the injury site between 3-5 dpi. Data are represented as mean ± SEM per independent experiments (p=0.0159, n=4 for 3 dpi and n=5 for 5 dpi). Marks represent individual data points. Significance of differences between means was analyzed using Mann-Whitney test. Scale bars: 50µm.

Appendix Figure S3: Tmem119+ microglia around the stab- wound injury site of WT and CCR2$^{-/-}$ mice at 5 dpi. Representative confocal images of Tmem119 immunostaining in the intact (left panel) or injured (right panel) GM of WT **(A)** or CCR2$^{-/-}$ mice **(B)** shown with DAPI staining to visualize nuclei in the upper row and without DAPI in the lower row of panels. Higher magnification views are shown as boxes in **(A)** and as separate panels in B1 and B2 (location is indicated by boxed area in the left panels of B). The dashed lines indicate the injury site. Note the increase in Tmem119 immunostaining at the lesion site. Scale bars: 125µm (A, B), 50µm (B1, B2).

Appendix Figure S4: Faster resealing of the Blood-Brain Barrier (BBB) in the absence of monocyte invasion. Confocal images of the intact GM parenchyma showing restriction of 1-kDa Alexa Fluor 555–Cadaverine exclusively to the cerebral vasculature **(A)**. Higher magnification view of the boxed areas (**A'** and **A''** in **A**) shows Cadaverine within the lumen of blood vessels (BV). Representative images displaying the injury-related extravasation of Cadaverine-Alexa-555 into the GM parenchyma at 3 hours (3hpi) **(B)** and 3 days post stab wound in WT **(C, D)** and CCR2$^{-/-}$ **(E, F)** mice. The dashed lines indicate the site of injury. The cell nuclei were counterstained with DAPI and this staining is omitted in the panels **D'** and **F'**. **(G)** Quantification of Cadaverine labelled area within the injured GM at 3 dpi showed a significant reduction in in CCR2$^{-/-}$ stab wound injured brains (Mann-Whitney test, **p*=0.0376, n=6)**,** suggesting faster resealing of the BBB in the absence of monocyte invasion**.** Data are represented as mean ± SEM per independent experiments. Scale bars: 100µm (A, B, C, D), 30µm (A', A'').

Appendix Figure S5: Collagen I immunostaining in WT and CCR2$^{-/-}$ mice at 28 dpi. Representative confocal images showing Collagen 1- and GFAP-immunoreactivity at the injury site in WT **(A)** and CCR2$^{-/-}$ **(B)** mice at 28dpi. Higher magnification view of the boxed areas (**A'** in **A,** and **B' in B**) showing reduction in collagen I deposits in the center of the lesion (center of boxed areas) and fewer GFAP reactive cells and processes (arrowheads) at the collagen1^{+} structures around the injury site in the CCR2$^{-/-}$ compared to WT mice. Scale bars: 100µm (A, B).

Appendix Figure S6: Reduced astrogliotic scar in CCR2$^{-/-}$ mice at 90 dpi. Confocal images displaying GFAP in the injured GM from WT **(A)** and CCR2$^{-/-}$ **(B)** mice at 90dpi. Histogram in **(C)** depicts the total number of astrocytes (S100β+) and reactive (GFAP+ and S100β+) astrocytes in a comparable region of the cerebral cortex GM at the injury site (ipsilateral) or in the contralateral hemisphere. Note that the increased astrocyte proliferation in CCR2$^{-/-}$ mice does not lead to a permanent increase in astrocyte numbers and rather results in a significant reduction of GFAP+ cells at 90 dpi. All data are represented as mean ± SEM per independent experiments (n=7 for intact 6 months old WT mice, n=4 for WT 90 dpi and n=5 for CCR2 KO mice). Marks depict individual data points (animals). Significance of differences between means was analyzed using one way ANOVA with Tukeys post-hoc test and is indicated based on the *p* value (***p<0.0001). Scale bars: 125µm.

Table S1

Significanlty different proteins in the injured hemisphere of WT mice compared to injured CCR2-/-

Accession	Gene symbol	Unique peptides	Confidence score	ratio WT/CCR2$^{-/-}$	T-Test WT/CCR2$^{-/-}$	Description
Q922H4	Gmppa	1	71	0,1	0,001	Mannose-1-phosphate guanyltransferase alpha OS=Mus musculus GN=Gmppa PE=1 SV=1
Q5SP85	Ccdc85a	1	14	0,1	0,032	Coiled-coil domain-containing protein 85A OS=Mus musculus GN=Ccdc85a PE=2 SV=1
Q69ZX8	Ablim3	1	118	0,1	0,029	Actin-binding LIM protein 3 OS=Mus musculus GN=Ablim3 PE=1 SV=2
Q9CYI0	5730455P16Rik	1	76	0,1	0,008	Protein Njmu-R1 OS=Mus musculus PE=1 SV=2
Q61161	Map4k2	1	75	0,1	0,030	Mitogen-activated protein kinase kinase kinase kinase 2 OS=Mus musculus GN=Map4k2 PE=1 SV=1
Q2NL51	Gsk3a	1	269	0,1	0,004	Glycogen synthase kinase-3 alpha OS=Mus musculus GN=Gsk3a PE=1 SV=2
P56546	Ctbp2	1	134	0,2	0,006	C-terminal-binding protein 2 OS=Mus musculus GN=Ctbp2 PE=1 SV=2
Q8C3X4	Guf1	1	24	0,2	0,026	Translation factor Guf1, mitochondrial OS=Mus musculus GN=Guf1 PE=1 SV=1
Q9DBS9	Osbpl3	2	154	0,2	0,015	Oxysterol-binding protein-related protein 3 OS=Mus musculus GN=Osbpl3 PE=1 SV=2
Q9WVS4	Mok	1	16	0,3	0,007	MAPK/MAK/MRK overlapping kinase OS=Mus musculus GN=Mok PE=1 SV=1
Q8VEE1	Lmcd1	1	64	0,3	0,011	LIM and cysteine-rich domains protein 1 OS=Mus musculus GN=Lmcd1 PE=1 SV=1
Q9DAM5	Slc25a19	2	31	0,3	0,022	Mitochondrial thiamine pyrophosphate carrier OS=Mus musculus GN=Slc25a19 PE=1 SV=1
P61967	Ap1s1	1	200	0,3	0,024	AP-1 complex subunit sigma-1A OS=Mus musculus GN=Ap1s1 PE=1 SV=1
Q6P5E8	Dgkq	1	37	0,3	0,042	Diacylglycerol kinase theta OS=Mus musculus GN=Dgkq PE=1 SV=1
Q9JLY7	Dusp14	1	25	0,3	0,020	Dual specificity protein phosphatase 14 OS=Mus musculus GN=Dusp14 PE=2 SV=2
Q8BK26	Fbxo44	1	42	0,3	0,026	F-box only protein 44 OS=Mus musculus GN=Fbxo44 PE=1 SV=1
Q8BUL6	Plekha1	1	31	0,3	0,008	Pleckstrin homology domain-containing family A member 1 OS=Mus musculus GN=Plekha1 PE=1 SV=1
Q91WU5	As3mt	1	17	0,4	0,033	Arsenite methyltransferase OS=Mus musculus GN=As3mt PE=1 SV=2
Q67FY2	Bcl9l	1	17	0,4	0,016	B-cell CLL/lymphoma 9-like protein OS=Mus musculus GN=Bcl9l PE=1 SV=1
Q9WTV7	Rlim	1	13	0,4	0,027	E3 ubiquitin-protein ligase RLIM OS=Mus musculus GN=Rlim PE=1 SV=2
Q9JJL8	Sars2	3	163	0,4	0,032	Serine--tRNA ligase, mitochondrial OS=Mus musculus GN=Sars2 PE=1 SV=2
P19001;P05784	Krt19	3	312	0,4	0,017	Keratin, type I cytoskeletal 19 OS=Mus musculus GN=Krt19 PE=1 SV=1
Q9Z0V1	Kcnd3	1	63	0,4	0,042	Potassium voltage-gated channel subfamily D member 3 OS=Mus musculus GN=Kcnd3 PE=1 SV=1
Q8K296	Mtmr3	1	49	0,4	0,043	Myotubularin-related protein 3 OS=Mus musculus GN=Mtmr3 PE=1 SV=2
P70698	Ctps1	1	102	0,4	0,047	CTP synthase 1 OS=Mus musculus GN=Ctps1 PE=1 SV=2
O54990	Prom1	1	64	0,4	0,011	Prominin-1 OS=Mus musculus GN=Prom1 PE=1 SV=1
Q924K8	Mta3	2	47	0,5	0,009	Metastasis-associated protein MTA3 OS=Mus musculus GN=Mta3 PE=1 SV=1
P26048	Gabra2	2	366	0,5	0,037	Gamma-aminobutyric acid receptor subunit alpha-2 OS=Mus musculus GN=Gabra2 PE=1 SV=1
Q8BWW9	Pkn2	1	15	0,5	0,036	Serine/threonine-protein kinase N2 OS=Mus musculus GN=Pkn2 PE=1 SV=3
G3X9K3	Arfgef1	3	224	0,5	0,015	Brefeldin A-inhibited guanine nucleotide-exchange protein 1 OS=Mus musculus GN=Arfgef1 PE=1 SV=1
Q6P2K6	Ppp4r3a	1	53	0,5	0,017	Serine/threonine-protein phosphatase 4 regulatory subunit 3A OS=Mus musculus GN=Ppp4r3a PE=1 SV=1
P98064	Masp1	1	27	0,5	0,027	Mannan-binding lectin serine protease 1 OS=Mus musculus GN=Masp1 PE=1 SV=2
P50428	Arsa	1	28	0,6	0,041	Arylsulfatase A OS=Mus musculus GN=Arsa PE=1 SV=2
Q8C6B2	Rtkn	3	257	0,6	0,031	Rhotekin OS=Mus musculus GN=Rtkn PE=1 SV=3
Q3ULA2	Btrc	1	21	0,6	0,030	F-box/WD repeat-containing protein 1A OS=Mus musculus GN=Btrc PE=1 SV=2
Q9WVB2	Tle2	1	17	0,6	0,030	Transducin-like enhancer protein 2 OS=Mus musculus GN=Tle2 PE=2 SV=1
Q9JLK7	Cabp1	1	28	0,6	0,007	Calcium-binding protein 1 OS=Mus musculus GN=Cabp1 PE=1 SV=3
Q9D2N9	Vps33a	4	268	0,6	0,045	Vacuolar protein sorting-associated protein 33A OS=Mus musculus GN=Vps33a PE=1 SV=2
Q9EPE9	Atp13a1	1	55	0,6	0,033	Manganese-transporting ATPase 13A1 OS=Mus musculus GN=Atp13a1 PE=1 SV=2
Q8BXA7	Phlpp2	1	16	0,6	0,041	PH domain leucine-rich repeat-containing protein phosphatase 2 OS=Mus musculus GN=Phlpp2 PE=1 SV=3
Q80UY2	Kcmf1	1	143	0,6	0,023	E3 ubiquitin-protein ligase KCMF1 OS=Mus musculus GN=Kcmf1 PE=1 SV=1
Q80XC6	Nrde2	1	16	0,6	0,037	Protein NRDE2 homolog OS=Mus musculus GN=Nrde2 PE=1 SV=3
Q91XD6	Vps36	1	24	0,6	0,008	Vacuolar protein-sorting-associated protein 36 OS=Mus musculus GN=Vps36 PE=1 SV=1
E9Q612	Ptpro	1	44	0,6	0,043	Receptor-type tyrosine-protein phosphatase O OS=Mus musculus GN=Ptpro PE=1 SV=1
Q60790	Rasa3	4	167	0,6	0,046	Ras GTPase-activating protein 3 OS=Mus musculus GN=Rasa3 PE=1 SV=2
Q6V4S5	Sdk2	2	67	0,6	0,014	Protein sidekick-2 OS=Mus musculus GN=Sdk2 PE=1 SV=1
Q5HZI9	Slc25a51	4	126	0,6	0,013	Solute carrier family 25 member 51 OS=Mus musculus GN=Slc25a51 PE=1 SV=1
Q6PAV2	Herc4	2	112	0,6	0,009	Probable E3 ubiquitin-protein ligase HERC4 OS=Mus musculus GN=Herc4 PE=1 SV=2
Q9DCT1	Akr1e2	4	216	0,6	0,025	1,5-anhydro-D-fructose reductase OS=Mus musculus GN=Akr1e2 PE=1 SV=1
O54784	Dapk3	1	41	0,6	0,048	Death-associated protein kinase 3 OS=Mus musculus GN=Dapk3 PE=1 SV=1
Q6P6L0	Filip1l	1	15	0,7	0,020	Filamin A-interacting protein 1-like OS=Mus musculus GN=Filip1l PE=1 SV=2
Q80TL1;Q91WF3	Adcy2	4	223	0,7	0,001	Adenylate cyclase type 2 OS=Mus musculus GN=Adcy2 PE=1 SV=2
P0C7M9	Clec2l	3	81	0,7	0,012	C-type lectin domain family 2 member L OS=Mus musculus GN=Clec2l PE=1 SV=1
Q99PH1	Lrrc4	1	60	0,7	0,016	Leucine-rich repeat-containing protein 4 OS=Mus musculus GN=Lrrc4 PE=1 SV=2
Q9CPQ3	Tomm22	7	606	0,7	0,019	Mitochondrial import receptor subunit TOM22 homolog OS=Mus musculus GN=Tomm22 PE=1 SV=3
Q6PAR5	Gapvd1	6	376	0,7	0,027	GTPase-activating protein and VPS9 domain-containing protein 1 OS=Mus musculus GN=Gapvd1 PE=1 SV=2
Q60900	Elavl3	2	155	0,7	0,004	ELAV-like protein 3 OS=Mus musculus GN=Elavl3 PE=1 SV=1
Q60823	Akt2	4	543	0,7	0,046	RAC-beta serine/threonine-protein kinase OS=Mus musculus GN=Akt2 PE=1 SV=1
Q9CZS1	Aldh1b1	6	476	0,7	0,019	Aldehyde dehydrogenase X, mitochondrial OS=Mus musculus GN=Aldh1b1 PE=1 SV=1
Q9QXX4	Slc25a13	1	459	0,7	0,012	Calcium-binding mitochondrial carrier protein Aralar2 OS=Mus musculus GN=Slc25a13 PE=1 SV=1
Q4PZA2	Ece1	1	20	0,7	0,020	Endothelin-converting enzyme 1 OS=Mus musculus GN=Ece1 PE=1 SV=1
Q8R3P0	Aspa	7	237	0,7	0,007	Aspartoacylase OS=Mus musculus GN=Aspa PE=1 SV=2
Q91YX5	Lpgat1	8	416	0,7	0,047	Acyl-CoA:lysophosphatidylglycerol acyltransferase 1 OS=Mus musculus GN=Lpgat1 PE=1 SV=1
Q9D7B6	Acad8	1	26	0,7	0,035	Isobutyryl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acad8 PE=1 SV=2
Q9CPV9;Q8VHS2	P2ry12	2	56	0,7	0,009	P2Y purinoceptor 12 OS=Mus musculus GN=P2ry12 PE=1 SV=1
A2AVQ5	C1orf177 homolog	1	28	0,7	0,033	Uncharacterized protein C1orf177 homolog OS=Mus musculus PE=2 SV=1
Q8C0L6	Paox	2	58	0,7	0,023	Peroxisomal N(1)-acetyl-spermine/spermidine oxidase OS=Mus musculus GN=Paox PE=1 SV=3
Q9D404	Oxsm	3	138	0,7	0,001	3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial OS=Mus musculus GN=Oxsm PE=1 SV=1
Q9CQM2	Kdelr2	1	115	0,7	0,010	ER lumen protein-retaining receptor 2 OS=Mus musculus GN=Kdelr2 PE=1 SV=1
Q8C996	Tmem163	7	378	0,7	0,005	Transmembrane protein 163 OS=Mus musculus GN=Tmem163 PE=1 SV=1
P50429	Arsb	5	249	0,8	0,014	Arylsulfatase B OS=Mus musculus GN=Arsb PE=1 SV=3
Q6P069	Sri	6	185	0,8	0,034	Sorcin OS=Mus musculus GN=Sri PE=1 SV=1
Q9ESK9	Rb1cc1	1	98	0,8	0,032	RB1-inducible coiled-coil protein 1 OS=Mus musculus GN=Rb1cc1 PE=1 SV=3
P28028	Braf	7	386	0,8	0,006	Serine/threonine-protein kinase B-raf OS=Mus musculus GN=Braf PE=1 SV=3
Q9ES52	Inpp5d	1	13	0,8	0,022	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1 OS=Mus musculus GN=Inpp5d PE=1 SV=2
P35922	Fmr1	4	333	0,8	0,001	Fragile X mental retardation protein 1 homolog OS=Mus musculus GN=Fmr1 PE=1 SV=1
Q9Z110	Aldh18a1	12	634	0,8	0,035	Delta-1-pyrroline-5-carboxylate synthase OS=Mus musculus GN=Aldh18a1 PE=1 SV=2
Q9CQ75	Ndufa2	6	243	0,8	0,017	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 OS=Mus musculus GN=Ndufa2 PE=1 SV=3
P48379	Rfx2	1	25	0,8	0,034	DNA-binding protein RFX2 OS=Mus musculus GN=Rfx2 PE=1 SV=2
Q9D6W8	C17orf59 homolog	1	28	0,8	0,047	Uncharacterized protein C17orf59 homolog OS=Mus musculus PE=1 SV=1
Q9JJ28	Flii	4	105	0,8	0,014	Protein flightless-1 homolog OS=Mus musculus GN=Flii PE=1 SV=1
P97449	Anpep	4	155	0,8	0,030	Aminopeptidase N OS=Mus musculus GN=Anpep PE=1 SV=4
P51855	Gss	9	366	0,8	0,024	Glutathione synthetase OS=Mus musculus GN=Gss PE=1 SV=1
Q80U57	Rims3	1	308	0,8	0,001	Regulating synaptic membrane exocytosis protein 3 OS=Mus musculus GN=Rims3 PE=1 SV=2
Q9CRD2	Emc2	4	190	0,8	0,034	ER membrane protein complex subunit 2 OS=Mus musculus GN=Emc2 PE=1 SV=1
P08414;P58801	Camk4	16	698	0,8	0,006	Calcium/calmodulin-dependent protein kinase type IV OS=Mus musculus GN=Camk4 PE=1 SV=2
P08553	Nefm	59	5289	0,8	0,042	Neurofilament medium polypeptide OS=Mus musculus GN=Nefm PE=1 SV=4
Q9QX60	Dguok	1	17	0,8	0,014	Deoxyguanosine kinase, mitochondrial OS=Mus musculus GN=Dguok PE=1 SV=3
Q9D9V3	Echdc1	3	161	0,8	0,049	Ethylmalonyl-CoA decarboxylase OS=Mus musculus GN=Echdc1 PE=1 SV=2
Q8BGR9	Ublcp1	3	112	0,8	0,046	Ubiquitin-like domain-containing CTD phosphatase 1 OS=Mus musculus GN=Ublcp1 PE=1 SV=1
Q62188	Dpysl3	28	2942	0,8	0,046	Dihydropyrimidinase-related protein 3 OS=Mus musculus GN=Dpysl3 PE=1 SV=1
Q9QXN0	Shroom3	1	15	0,8	0,043	Protein Shroom3 OS=Mus musculus GN=Shroom3 PE=1 SV=2
Q03157	Aplp1	8	344	0,8	0,045	Amyloid-like protein 1 OS=Mus musculus GN=Aplp1 PE=1 SV=1
P26361	Cftr	1	14	0,8	0,035	Cystic fibrosis transmembrane conductance regulator OS=Mus musculus GN=Cftr PE=1 SV=2
P58044	Idi1	4	350	0,8	0,040	Isopentenyl-diphosphate Delta-isomerase 1 OS=Mus musculus GN=Idi1 PE=1 SV=1
Q8BVG4	Dpp9	3	241	0,8	0,046	Dipeptidyl peptidase 9 OS=Mus musculus GN=Dpp9 PE=1 SV=2
P36993	Ppm1b	4	110	0,9	0,042	Protein phosphatase 1B OS=Mus musculus GN=Ppm1b PE=1 SV=1
Q8BYR5	Cadps2	14	1273	0,9	0,021	Calcium-dependent secretion activator 2 OS=Mus musculus GN=Cadps2 PE=1 SV=2
Q80XN0	Bdh1	21	1319	0,9	0,046	D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Mus musculus GN=Bdh1 PE=1 SV=2
O70250	Pgam2	3	318	0,9	0,040	Phosphoglycerate mutase 2 OS=Mus musculus GN=Pgam2 PE=1 SV=3
Q99MX1	Usp26	1	24	0,9	0,021	Ubiquitin carboxyl-terminal hydrolase 26 OS=Mus musculus GN=Usp26 PE=1 SV=2
Q80YQ2	Med23	1	17	0,9	0,027	Mediator of RNA polymerase II transcription subunit 23 OS=Mus musculus GN=Med23 PE=1 SV=2
Q6P1B1	Xpnpep1	12	572	0,9	0,045	Xaa-Pro aminopeptidase 1 OS=Mus musculus GN=Xpnpep1 PE=1 SV=1
P61971	Nutf2	5	226	0,9	0,007	Nuclear transport factor 2 OS=Mus musculus GN=Nutf2 PE=1 SV=1
P70188	Kifap3	8	477	0,9	0,048	Kinesin-associated protein 3 OS=Mus musculus GN=Kifap3 PE=1 SV=1
Q9R1P3	Psmb2	8	427	0,9	0,016	Proteasome subunit beta type-2 OS=Mus musculus GN=Psmb2 PE=1 SV=1
Q922J6	Tspan2	9	710	0,9	0,010	Tetraspanin-2 OS=Mus musculus GN=Tspan2 PE=1 SV=1
Q8K4R4	Pitpnc1	14	713	0,9	0,040	Cytoplasmic phosphatidylinositol transfer protein 1 OS=Mus musculus GN=Pitpnc1 PE=1 SV=1
Q8BRT1	Clasp2	33	1556	0,9	0,045	CLIP-associating protein 2 OS=Mus musculus GN=Clasp2 PE=1 SV=1
Q9JI46	Nudt3	7	524	0,9	0,017	Diphosphoinositol polyphosphate phosphohydrolase 1 OS=Mus musculus GN=Nudt3 PE=1 SV=1
P22723;Q9R0Y8	Gabrg2	9	342	0,9	0,036	Gamma-aminobutyric acid receptor subunit gamma-2 OS=Mus musculus GN=Gabrg2 PE=1 SV=3
Q61885	Mog	14	1004	0,9	0,033	Myelin-oligodendrocyte glycoprotein OS=Mus musculus GN=Mog PE=1 SV=1
Q9D2V7	Coro7	10	484	0,9	0,016	Coronin-7 OS=Mus musculus GN=Coro7 PE=1 SV=2
P97300	Nptn	21	1255	0,9	0,032	Neuroplastin OS=Mus musculus GN=Nptn PE=1 SV=3
Q58A65	Spag9	11	572	0,9	0,016	C-Jun-amino-terminal kinase-interacting protein 4 OS=Mus musculus GN=Spag9 PE=1 SV=2
P59648	Fxyd7	1	40	0,9	0,043	FXYD domain-containing ion transport regulator 7 OS=Mus musculus GN=Fxyd7 PE=3 SV=1
Q6P5F9	Xpo1	22	1073	0,9	0,047	Exportin-1 OS=Mus musculus GN=Xpo1 PE=1 SV=1
Q6ZWR6;Q5NCY0	Syne1	16	939	0,9	0,041	Nesprin-1 OS=Mus musculus GN=Syne1 PE=1 SV=2
P03888	Mtnd1	6	318	0,9	0,024	NADH-ubiquinone oxidoreductase chain 1 OS=Mus musculus GN=Mtnd1 PE=1 SV=3
Q9D1M4	Eef1e1	1	86	0,9	0,027	Eukaryotic translation elongation factor 1 epsilon-1 OS=Mus musculus GN=Eef1e1 PE=1 SV=1
Q8C0M9	Asrgl1	13	1220	0,9	0,003	Isoaspartyl peptidase/L-asparaginase OS=Mus musculus GN=Asrgl1 PE=1 SV=1
Q8BUK6	Hook3	14	678	0,9	0,035	Protein Hook homolog 3 OS=Mus musculus GN=Hook3 PE=1 SV=2
Q99JY0	Hadhb	14	1006	0,9	0,004	Trifunctional enzyme subunit beta, mitochondrial OS=Mus musculus GN=Hadhb PE=1 SV=1
P10605	Ctsb	11	1008	0,9	0,022	Cathepsin B OS=Mus musculus GN=Ctsb PE=1 SV=2
Q8VCW8	Acsf2	13	802	0,9	0,012	Acyl-CoA synthetase family member 2, mitochondrial OS=Mus musculus GN=Acsf2 PE=1 SV=1
P19157;P46425	Gstp1	19	1219	0,9	0,019	Glutathione S-transferase P 1 OS=Mus musculus GN=Gstp1 PE=1 SV=2
P49615;P06240	Cdk5	13	713	0,9	0,048	Cyclin-dependent-like kinase 5 OS=Mus musculus GN=Cdk5 PE=1 SV=1
P70175	Dlg3	21	1313	0,9	0,043	Disks large homolog 3 OS=Mus musculus GN=Dlg3 PE=1 SV=1
P28660	Nckap1	46	2624	1,0	0,044	Nck-associated protein 1 OS=Mus musculus GN=Nckap1 PE=1 SV=2
P14231	Atp1b2	26	1445	1,0	0,042	Sodium/potassium-transporting ATPase subunit beta-2 OS=Mus musculus GN=Atp1b2 PE=1 SV=2
P39053	Dnm1	79	7112	1,0	0,047	Dynamin-1 OS=Mus musculus GN=Dnm1 PE=1 SV=2
P35564	Canx	28	1652	1,0	0,048	Calnexin OS=Mus musculus GN=Canx PE=1 SV=1
Q6ZPJ3	Ube2o	32	1877	1,0	0,026	(E3-independent) E2 ubiquitin-conjugating enzyme UBE2O OS=Mus musculus GN=Ube2o PE=1 SV=3
Q80TJ1	Cadps	62	4680	1,1	0,024	Calcium-dependent secretion activator 1 OS=Mus musculus GN=Cadps PE=1 SV=3
Q8C167	Prepl	19	1332	1,1	0,036	Prolyl endopeptidase-like OS=Mus musculus GN=Prepl PE=1 SV=1
Q9WV18	Gabbr1	16	1177	1,1	0,023	Gamma-aminobutyric acid type B receptor subunit 1 OS=Mus musculus GN=Gabbr1 PE=1 SV=1
P27773	Pdia3	31	2327	1,1	0,022	Protein disulfide-isomerase A3 OS=Mus musculus GN=Pdia3 PE=1 SV=2
Q9R1Q9;Q6ZPJ0	Atp6ap1	6	122	1,1	0,038	V-type proton ATPase subunit S1 OS=Mus musculus GN=Atp6ap1 PE=1 SV=1
Q8CAQ8	Immt	51	3892	1,1	0,004	MICOS complex subunit Mic60 OS=Mus musculus GN=Immt PE=1 SV=1
Q11136	Pepd	10	510	1,1	0,035	Xaa-Pro dipeptidase OS=Mus musculus GN=Pepd PE=1 SV=3
Q9D8N0	Eef1g	18	1397	1,1	0,011	Elongation factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 SV=3
Q920P5	Ak5	14	656	1,1	0,021	Adenylate kinase isoenzyme 5 OS=Mus musculus GN=Ak5 PE=1 SV=2
Q8R326	Pspc1	8	554	1,1	0,038	Paraspeckle component 1 OS=Mus musculus GN=Pspc1 PE=1 SV=1
Q64455	Ptprj	8	308	1,1	0,024	Receptor-type tyrosine-protein phosphatase eta OS=Mus musculus GN=Ptprj PE=1 SV=2
P60122	Ruvbl1	11	852	1,1	0,032	RuvB-like 1 OS=Mus musculus GN=Ruvbl1 PE=1 SV=1
P80317	Cct6a	25	1971	1,1	0,006	T-complex protein 1 subunit zeta OS=Mus musculus GN=Cct6a PE=1 SV=3
Q64487	Ptprd	24	1880	1,1	0,010	Receptor-type tyrosine-protein phosphatase delta OS=Mus musculus GN=Ptprd PE=1 SV=3
P48722	Hspa4l	47	3050	1,1	0,020	Heat shock 70 kDa protein 4L OS=Mus musculus GN=Hspa4l PE=1 SV=2
O08553	Dpysl2	84	8601	1,1	0,033	Dihydropyrimidinase-related protein 2 OS=Mus musculus GN=Dpysl2 PE=1 SV=2
P05064;Q91Y97	Aldoa	54	5342	1,1	0,050	Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2
Q6PDM2	Srsf1	12	491	1,1	0,044	Serine/arginine-rich splicing factor 1 OS=Mus musculus GN=Srsf1 PE=1 SV=3
P48678	Lmna	30	1794	1,1	0,011	Prelamin-A/C OS=Mus musculus GN=Lmna PE=1 SV=2
Q07076	Anxa7	10	742	1,1	0,015	Annexin A7 OS=Mus musculus GN=Anxa7 PE=1 SV=2
Q8CC86	Naprt	1	47	1,1	0,005	Nicotinate phosphoribosyltransferase OS=Mus musculus GN=Naprt PE=1 SV=1
Q8BL66	Eea1	32	1870	1,1	0,023	Early endosome antigen 1 OS=Mus musculus GN=Eea1 PE=1 SV=2
Q91W50	Csde1	22	1218	1,1	0,016	Cold shock domain-containing protein E1 OS=Mus musculus GN=Csde1 PE=1 SV=1
P40124	Cap1	29	2381	1,1	0,011	Adenylyl cyclase-associated protein 1 OS=Mus musculus GN=Cap1 PE=1 SV=4
Q60737	Csnk2a1	15	1106	1,1	0,028	Casein kinase II subunit alpha OS=Mus musculus GN=Csnk2a1 PE=1 SV=2
P62317	Snrpd2	7	293	1,1	0,028	Small nuclear ribonucleoprotein Sm D2 OS=Mus musculus GN=Snrpd2 PE=1 SV=1
Q9ER00	Stx12	9	809	1,1	0,009	Syntaxin-12 OS=Mus musculus GN=Stx12 PE=1 SV=1
Q9JKR6	Hyou1	29	1762	1,1	0,003	Hypoxia up-regulated protein 1 OS=Mus musculus GN=Hyou1 PE=1 SV=1
P62821;Q8CG50	Rab1A	7	1718	1,1	0,013	Ras-related protein Rab-1A OS=Mus musculus GN=Rab1A PE=1 SV=3
Q9EQU5	Set	11	1014	1,1	0,011	Protein SET OS=Mus musculus GN=Set PE=1 SV=1
Q91V41	Rab14	14	1188	1,1	0,024	Ras-related protein Rab-14 OS=Mus musculus GN=Rab14 PE=1 SV=3
Q9WU78	Pdcd6ip	25	1364	1,1	0,010	Programmed cell death 6-interacting protein OS=Mus musculus GN=Pdcd6ip PE=1 SV=3
Q9JKK7;Q9JHJ0	Tmod2	16	900	1,1	0,015	Tropomodulin-2 OS=Mus musculus GN=Tmod2 PE=1 SV=2
P31938	Map2k1	15	1096	1,1	0,024	Dual specificity mitogen-activated protein kinase kinase 1 OS=Mus musculus GN=Map2k1 PE=1 SV=2
Q6NZL0	Soga3	21	1200	1,1	0,048	Protein SOGA3 OS=Mus musculus GN=Soga3 PE=1 SV=2
Q9D6K5	Synj2bp	4	327	1,1	0,048	Synaptojanin-2-binding protein OS=Mus musculus GN=Synj2bp PE=1 SV=1
P09103;Q8CII2	P4hb	24	1646	1,1	0,024	Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=1 SV=2
Q9D8X1	Cutc	1	148	1,1	0,030	Copper homeostasis protein cutC homolog OS=Mus musculus GN=Cutc PE=1 SV=1
Q61137	Astn1	25	1511	1,1	0,043	Astrotactin-1 OS=Mus musculus GN=Astn1 PE=1 SV=4
P98084	Apba2	4	201	1,1	0,013	Amyloid beta A4 precursor protein-binding family A member 2 OS=Mus musculus GN=Apba2 PE=1 SV=2
P16054	Prkce	32	1911	1,1	0,017	Protein kinase C epsilon type OS=Mus musculus GN=Prkce PE=1 SV=1
P35803	Gpm6b	21	1086	1,1	0,008	Neuronal membrane glycoprotein M6-b OS=Mus musculus GN=Gpm6b PE=1 SV=2
P13020	Gsn	17	793	1,1	0,010	Gelsolin OS=Mus musculus GN=Gsn PE=1 SV=3
Q9R1V7	Adam23	14	883	1,1	0,041	Disintegrin and metalloproteinase domain-containing protein 23 OS=Mus musculus GN=Adam23 PE=1 SV=1
Q61335	Bcap31	8	420	1,1	0,035	B-cell receptor-associated protein 31 OS=Mus musculus GN=Bcap31 PE=1 SV=4
Q9DAR7	Dcps	10	427	1,1	0,011	m7GpppX diphosphatase OS=Mus musculus GN=Dcps PE=1 SV=1
Q9Z204	Hnrnpc	11	605	1,1	0,035	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Mus musculus GN=Hnrnpc PE=1 SV=1
Q8R0A7	Kiaa0513	16	994	1,1	0,021	Uncharacterized protein KIAA0513 OS=Mus musculus GN=Kiaa0513 PE=1 SV=1
Q8BI08	Mal2	2	135	1,1	0,036	Protein MAL2 OS=Mus musculus GN=Mal2 PE=1 SV=1
Q61545	Ewsr1	4	284	1,1	0,010	RNA-binding protein EWS OS=Mus musculus GN=Ewsr1 PE=1 SV=2
O55100	Syngr1	2	140	1,2	0,012	Synaptogyrin-1 OS=Mus musculus GN=Syngr1 PE=1 SV=2
Q64332	Syn2	39	4245	1,2	0,035	Synapsin-2 OS=Mus musculus GN=Syn2 PE=1 SV=2
O70310	Nmt1	8	810	1,2	0,050	Glycylpeptide N-tetradecanoyltransferase 1 OS=Mus musculus GN=Nmt1 PE=1 SV=1
Q8BGC4	Zadh2	3	124	1,2	0,022	Zinc-binding alcohol dehydrogenase domain-containing protein 2 OS=Mus musculus GN=Zadh2 PE=1 SV=1
P55012	Slc12a2	17	701	1,2	0,032	Solute carrier family 12 member 2 OS=Mus musculus GN=Slc12a2 PE=1 SV=2
Q61699	Hsph1	53	3712	1,2	0,023	Heat shock protein 105 kDa OS=Mus musculus GN=Hsph1 PE=1 SV=2
Q8R1B4	Eif3c	13	544	1,2	0,020	Eukaryotic translation initiation factor 3 subunit C OS=Mus musculus GN=Eif3c PE=1 SV=1
O55091	Impact	9	464	1,2	0,048	Protein IMPACT OS=Mus musculus GN=Impact PE=1 SV=2
Q62420	Sh3gl2	23	1859	1,2	0,001	Endophilin-A1 OS=Mus musculus GN=Sh3gl2 PE=1 SV=2
Q8BG39	Sv2b	22	1675	1,2	0,002	Synaptic vesicle glycoprotein 2B OS=Mus musculus GN=Sv2b PE=1 SV=1
P61226	Rap2b	6	874	1,2	0,004	Ras-related protein Rap-2b OS=Mus musculus GN=Rap2b PE=1 SV=1
Q8BH57	Wdr48	14	739	1,2	0,007	WD repeat-containing protein 48 OS=Mus musculus GN=Wdr48 PE=1 SV=1
Q9Z1D1	Eif3g	4	261	1,2	0,045	Eukaryotic translation initiation factor 3 subunit G OS=Mus musculus GN=Eif3g PE=1 SV=2
Q80U63	Mfn2	12	644	1,2	0,047	Mitofusin-2 OS=Mus musculus GN=Mfn2 PE=1 SV=3
Q8BYI8	Kiaa1467	8	436	1,2	0,029	Uncharacterized protein KIAA1467 OS=Mus musculus GN=Kiaa1467 PE=1 SV=1
P63094;Q6R0H7	Gnas	13	991	1,2	0,006	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Mus musculus GN=Gnas PE=1 SV=1
Q61672	Slc29a2	2	73	1,2	0,009	Equilibrative nucleoside transporter 2 OS=Mus musculus GN=Slc29a2 PE=1 SV=2
P49817;P51637	Cav1	4	127	1,2	0,016	Caveolin-1 OS=Mus musculus GN=Cav1 PE=1 SV=1
Q99P58;Q9ERI2	Rab27b	3	113	1,2	0,004	Ras-related protein Rab-27B OS=Mus musculus GN=Rab27b PE=1 SV=3
Q9EP69	Sacm1l	20	904	1,2	0,031	Phosphatidylinositide phosphatase SAC1 OS=Mus musculus GN=Sacm1l PE=1 SV=1
Q61481;Q64338	Pde1a	14	1076	1,2	0,042	Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1A OS=Mus musculus GN=Pde1a PE=1 SV=2
P37040	Por	14	662	1,2	0,021	NADPH--cytochrome P450 reductase OS=Mus musculus GN=Por PE=1 SV=2
P62715	Ppp2cb	2	2012	1,2	0,043	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Mus musculus GN=Ppp2cb PE=1 SV=1
Q91Z67	Srgap2	12	612	1,2	0,026	SLIT-ROBO Rho GTPase-activating protein 2 OS=Mus musculus GN=Srgap2 PE=1 SV=2
Q64213	Sf1	9	417	1,2	0,024	Splicing factor 1 OS=Mus musculus GN=Sf1 PE=1 SV=6
Q9WTT4	Atp6v1g2	7	769	1,2	0,037	V-type proton ATPase subunit G 2 OS=Mus musculus GN=Atp6v1g2 PE=1 SV=1
O70228	Atp9a	16	702	1,2	0,002	Probable phospholipid-transporting ATPase IIA OS=Mus musculus GN=Atp9a PE=1 SV=3
Q5SWU9	Acaca	10	429	1,2	0,005	Acetyl-CoA carboxylase 1 OS=Mus musculus GN=Acaca PE=1 SV=1
Q62082	Myl10	1	22	1,2	0,031	Myosin regulatory light chain 10 OS=Mus musculus GN=Myl10 PE=2 SV=1
Q6WVG3	Kctd12	9	624	1,2	0,004	BTB/POZ domain-containing protein KCTD12 OS=Mus musculus GN=Kctd12 PE=1 SV=1
Q3TWW8	Srsf6	2	141	1,2	0,042	Serine/arginine-rich splicing factor 6 OS=Mus musculus GN=Srsf6 PE=1 SV=1
P70290	Mpp1	9	293	1,2	0,040	55 kDa erythrocyte membrane protein OS=Mus musculus GN=Mpp1 PE=1 SV=1
Q9WVJ2	Psmd13	13	731	1,2	0,011	26S proteasome non-ATPase regulatory subunit 13 OS=Mus musculus GN=Psmd13 PE=1 SV=1
Q3TY86	Aifm3	6	177	1,2	0,037	Apoptosis-inducing factor 3 OS=Mus musculus GN=Aifm3 PE=1 SV=1
Q4QQM4	Trp53i11	3	125	1,2	0,049	Tumor protein p53-inducible protein 11 OS=Mus musculus GN=Trp53i11 PE=1 SV=1
Q9CXS4	Cenpv	9	590	1,2	0,027	Centromere protein V OS=Mus musculus GN=Cenpv PE=1 SV=2
Q99JN2	Klhl22	1	20	1,2	0,000	Kelch-like protein 22 OS=Mus musculus GN=Klhl22 PE=1 SV=1
Q9CSN1	Snw1	2	53	1,2	0,009	SNW domain-containing protein 1 OS=Mus musculus GN=Snw1 PE=1 SV=3
Q9CQV5	Mrps24	1	30	1,2	0,022	28S ribosomal protein S24, mitochondrial OS=Mus musculus GN=Mrps24 PE=1 SV=1
Q6P2L7	Casc4	6	274	1,3	0,009	Protein CASC4 OS=Mus musculus GN=Casc4 PE=1 SV=1
O89106	Fhit	2	37	1,3	0,049	Bis(5'-adenosyl)-triphosphatase OS=Mus musculus GN=Fhit PE=1 SV=3
Q6NSQ7	Ltv1	1	14	1,3	0,000	Protein LTV1 homolog OS=Mus musculus GN=Ltv1 PE=1 SV=2
Q9EQZ7	Rims2	5	282	1,3	0,019	Regulating synaptic membrane exocytosis protein 2 OS=Mus musculus GN=Rims2 PE=1 SV=1
P20108	Prdx3	13	1026	1,3	0,045	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Mus musculus GN=Prdx3 PE=1 SV=1
Q3UXZ6;P97299	Fam81a	5	113	1,3	0,015	Protein FAM81A OS=Mus musculus GN=Fam81a PE=1 SV=2
O08579	Emd	4	225	1,3	0,012	Emerin OS=Mus musculus GN=Emd PE=1 SV=1
Q6PGB6	Naa50	2	55	1,3	0,042	N-alpha-acetyltransferase 50 OS=Mus musculus GN=Naa50 PE=1 SV=1
Q08331	Calb2	6	321	1,3	0,045	Calretinin OS=Mus musculus GN=Calb2 PE=1 SV=3
P21300	Akr1b7	1	87	1,3	0,011	Aldose reductase-related protein 1 OS=Mus musculus GN=Akr1b7 PE=1 SV=4
O09172	Gclm	4	160	1,3	0,035	Glutamate--cysteine ligase regulatory subunit OS=Mus musculus GN=Gclm PE=1 SV=1
Q9Z2V5	Hdac6	8	424	1,3	0,028	Histone deacetylase 6 OS=Mus musculus GN=Hdac6 PE=1 SV=3
Q6PB44	Ptpn23	10	585	1,3	0,003	Tyrosine-protein phosphatase non-receptor type 23 OS=Mus musculus GN=Ptpn23 PE=1 SV=2
P28658	Atxn10	5	274	1,3	0,044	Ataxin-10 OS=Mus musculus GN=Atxn10 PE=1 SV=2
Q6P1J0	Maneal	1	21	1,3	0,046	Glycoprotein endo-alpha-1,2-mannosidase-like protein OS=Mus musculus GN=Maneal PE=2 SV=1
Q8R3T5	Stxbp6	7	296	1,3	0,028	Syntaxin-binding protein 6 OS=Mus musculus GN=Stxbp6 PE=1 SV=1
Q99JF8	Psip1	9	607	1,3	0,031	PC4 and SFRS1-interacting protein OS=Mus musculus GN=Psip1 PE=1 SV=1
Q9ES28	Arhgef7	12	648	1,3	0,022	Rho guanine nucleotide exchange factor 7 OS=Mus musculus GN=Arhgef7 PE=1 SV=2
P50153	Gng4	4	187	1,3	0,026	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-4 OS=Mus musculus GN=Gng4 PE=1 SV=1
A2AG50	Map7d2	8	509	1,3	0,039	MAP7 domain-containing protein 2 OS=Mus musculus GN=Map7d2 PE=1 SV=1
P21619	Lmnb2	24	1603	1,4	0,034	Lamin-B2 OS=Mus musculus GN=Lmnb2 PE=1 SV=2
Q9ERR1	Ndel1	3	74	1,4	0,044	Nuclear distribution protein nudE-like 1 OS=Mus musculus GN=Ndel1 PE=1 SV=2
Q3UIA2	Arhgap17	1	21	1,4	0,043	Rho GTPase-activating protein 17 OS=Mus musculus GN=Arhgap17 PE=1 SV=1
Q8BXR1	Slc7a14	6	378	1,4	0,012	Probable cationic amino acid transporter OS=Mus musculus GN=Slc7a14 PE=1 SV=1
Q6PAM0	Prkab2	2	139	1,4	0,032	5'-AMP-activated protein kinase subunit beta-2 OS=Mus musculus GN=Prkab2 PE=1 SV=1
Q8K3A6	Armcx6	2	15	1,4	0,017	Protein ARMCX6 OS=Mus musculus GN=Armcx6 PE=2 SV=1
Q8BGY7	Fam210a	3	120	1,4	0,038	Protein FAM210A OS=Mus musculus GN=Fam210a PE=1 SV=1
Q6ZPY5	Znf507	2	40	1,4	0,013	Zinc finger protein 507 OS=Mus musculus GN=Znf507 PE=2 SV=2
Q80U30	Clec16a	1	72	1,4	0,001	Protein CLEC16A OS=Mus musculus GN=Clec16a PE=1 SV=2
P09925	Surf1	2	116	1,4	0,019	Surfeit locus protein 1 OS=Mus musculus GN=Surf1 PE=1 SV=3
Q3UUQ7	Pgap1	3	117	1,4	0,022	GPI inositol-deacylase OS=Mus musculus GN=Pgap1 PE=1 SV=3
Q8R1N4	Nudcd3	5	253	1,4	0,027	NudC domain-containing protein 3 OS=Mus musculus GN=Nudcd3 PE=1 SV=3
Q3ZRW6	Clul1	1	21	1,4	0,019	Clusterin-like protein 1 OS=Mus musculus GN=Clul1 PE=2 SV=1
Q9Z2D6	Mecp2	13	951	1,4	0,017	Methyl-CpG-binding protein 2 OS=Mus musculus GN=Mecp2 PE=1 SV=1
Q8BP71	Rbfox2	2	242	1,4	0,009	RNA binding protein fox-1 homolog 2 OS=Mus musculus GN=Rbfox2 PE=1 SV=2
Q923S9	Rab30	1	265	1,4	0,029	Ras-related protein Rab-30 OS=Mus musculus GN=Rab30 PE=1 SV=1
Q8BXZ1	Tmx3	12	649	1,4	0,001	Protein disulfide-isomerase TMX3 OS=Mus musculus GN=Tmx3 PE=1 SV=2
Q921I1	Tf	42	2995	1,5	0,029	Serotransferrin OS=Mus musculus GN=Tf PE=1 SV=1
Q99K01	Pdxdc1	4	183	1,5	0,032	Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Mus musculus GN=Pdxdc1 PE=1 SV=2
O88845	Akap10	3	146	1,5	0,039	A-kinase anchor protein 10, mitochondrial OS=Mus musculus GN=Akap10 PE=1 SV=3
Q9ERU9	Ranbp2	6	208	1,5	0,030	E3 SUMO-protein ligase RanBP2 OS=Mus musculus GN=Ranbp2 PE=1 SV=2
P70699	Gaa	6	329	1,5	0,023	Lysosomal alpha-glucosidase OS=Mus musculus GN=Gaa PE=1 SV=2
Q9D7V2	Lysmd2	1	46	1,5	0,042	LysM and putative peptidoglycan-binding domain-containing protein 2 OS=Mus musculus GN=Lysmd2 PE=1 SV=2
A4Q9E8	Ttll6	1	13	1,5	0,002	Tubulin polyglutamylase TTLL6 OS=Mus musculus GN=Ttll6 PE=2 SV=1
O09005	Degs1	2	90	1,5	0,039	Sphingolipid delta(4)-desaturase DES1 OS=Mus musculus GN=Degs1 PE=1 SV=1
Q99K30	Eps8l2	1	16	1,5	0,024	Epidermal growth factor receptor kinase substrate 8-like protein 2 OS=Mus musculus GN=Eps8l2 PE=1 SV=1
P21661	Pcsk2	2	37	1,5	0,006	Neuroendocrine convertase 2 OS=Mus musculus GN=Pcsk2 PE=1 SV=1
Q8JZW4;Q9DC53	Cpne5	4	405	1,6	0,005	Copine-5 OS=Mus musculus GN=Cpne5 PE=1 SV=1
O35609	Scamp3	3	126	1,6	0,030	Secretory carrier-associated membrane protein 3 OS=Mus musculus GN=Scamp3 PE=1 SV=3
Q8BG18	Necab1	3	214	1,6	0,036	N-terminal EF-hand calcium-binding protein 1 OS=Mus musculus GN=Necab1 PE=1 SV=1
Q3TES0	Iqsec3	3	226	1,6	0,029	IQ motif and SEC7 domain-containing protein 3 OS=Mus musculus GN=Iqsec3 PE=1 SV=1
Q9JKF1	Iqgap1	3	221	1,6	0,024	Ras GTPase-activating-like protein IQGAP1 OS=Mus musculus GN=Iqgap1 PE=1 SV=2
Q8BXK8	Agap1	5	562	1,7	0,011	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 1 OS=Mus musculus GN=Agap1 PE=1 SV=1
O35691	Pnn	5	163	1,7	0,030	Pinin OS=Mus musculus GN=Pnn PE=1 SV=4
Q9CQA1	Trappc5	1	83	1,7	0,030	Trafficking protein particle complex subunit 5 OS=Mus musculus GN=Trappc5 PE=1 SV=1
Q1HKZ5	Map3k13	1	15	1,7	0,016	Mitogen-activated protein kinase kinase kinase 13 OS=Mus musculus GN=Map3k13 PE=1 SV=1
Q9QUN9	Dkk3	1	47	1,7	0,038	Dickkopf-related protein 3 OS=Mus musculus GN=Dkk3 PE=2 SV=1
Q01279	Egfr	4	185	1,7	0,033	Epidermal growth factor receptor OS=Mus musculus GN=Egfr PE=1 SV=1
Q9WVC3	Cav2	1	63	1,8	0,016	Caveolin-2 OS=Mus musculus GN=Cav2 PE=1 SV=1
P56695	Wfs1	8	295	1,8	0,040	Wolframin OS=Mus musculus GN=Wfs1 PE=1 SV=1
Q8C008	Dzank1	4	157	1,8	0,034	Double zinc ribbon and ankyrin repeat-containing protein 1 OS=Mus musculus GN=Dzank1 PE=1 SV=2
Q810I2	Trim50	1	13	1,9	0,013	E3 ubiquitin-protein ligase TRIM50 OS=Mus musculus GN=Trim50 PE=2 SV=1
Q00897	Serpina1d	3	1185	1,9	0,045	Alpha-1-antitrypsin 1-4 OS=Mus musculus GN=Serpina1d PE=1 SV=1
P32261	Serpinc1	9	323	1,9	0,036	Antithrombin-III OS=Mus musculus GN=Serpinc1 PE=1 SV=1
Q64337	Sqstm1	3	215	1,9	0,005	Sequestosome-1 OS=Mus musculus GN=Sqstm1 PE=1 SV=1
P21614	Gc	8	403	1,9	0,036	Vitamin D-binding protein OS=Mus musculus GN=Gc PE=1 SV=2
Q6KAU4	Mvb12b	1	23	2,0	0,035	Multivesicular body subunit 12B OS=Mus musculus GN=Mvb12b PE=1 SV=2
Q64362	Aktip	4	169	2,0	0,035	AKT-interacting protein OS=Mus musculus GN=Aktip PE=1 SV=1
Q61324	Arnt2	1	46	2,0	0,047	Aryl hydrocarbon receptor nuclear translocator 2 OS=Mus musculus GN=Arnt2 PE=1 SV=2
Q9D5R3	Cep83	2	36	2,0	0,035	Centrosomal protein of 83 kDa OS=Mus musculus GN=Cep83 PE=1 SV=2
Q8R0W6	Ndfip1	1	13	2,1	0,028	NEDD4 family-interacting protein 1 OS=Mus musculus GN=Ndfip1 PE=1 SV=1
Q8K215	Lyrm4	1	46	2,1	0,038	LYR motif-containing protein 4 OS=Mus musculus GN=Lyrm4 PE=1 SV=1
Q9DCF9	Ssr3	2	160	2,1	0,017	Translocon-associated protein subunit gamma OS=Mus musculus GN=Ssr3 PE=1 SV=1
Q8K0X8	Fez1	1	57	2,1	0,001	Fasciculation and elongation protein zeta-1 OS=Mus musculus GN=Fez1 PE=1 SV=2
Q8R1F1	Fam129b	1	32	2,2	0,014	Niban-like protein 1 OS=Mus musculus GN=Fam129b PE=1 SV=2
Q61704	Itih3	5	157	2,3	0,013	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Mus musculus GN=Itih3 PE=1 SV=3
Q8BJZ4	Mrps35	1	93	2,3	0,024	28S ribosomal protein S35, mitochondrial OS=Mus musculus GN=Mrps35 PE=1 SV=2
Q8CBX0	Tmem63c	1	21	2,6	0,001	Calcium permeable stress-gated cation channel 1 OS=Mus musculus GN=Tmem63c PE=1 SV=1
Q8CGV9	Tshz3	1	14	2,7	0,020	Teashirt homolog 3 OS=Mus musculus GN=Tshz3 PE=1 SV=2
Q8CJF8	Ago4	1	140	2,8	0,039	Protein argonaute-4 OS=Mus musculus GN=Ago4 PE=2 SV=2
P29391;P49945	Ftl1	3	244	3,2	0,004	Ferritin light chain 1 OS=Mus musculus GN=Ftl1 PE=1 SV=2
Q8VHL0	Slc14a1	1	15	3,5	0,001	Urea transporter 1 OS=Mus musculus GN=Slc14a1 PE=1 SV=2
Q9WVB3	Tle6	1	33	3,8	0,042	Transducin-like enhancer protein 6 OS=Mus musculus GN=Tle6 PE=1 SV=1
Q61781;A1L317;Q	Krt14	4	1326	3,9	0,025	Keratin, type I cytoskeletal 14 OS=Mus musculus GN=Krt14 PE=1 SV=2
Q8CGK7	Gnal	1	417	5,4	0,038	Guanine nucleotide-binding protein G(olf) subunit alpha OS=Mus musculus GN=Gnal PE=1 SV=1
P59270	B3gat2	1	15	7,9	0,008	Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 2 OS=Mus musculus GN=B3gat2 PE=2 SV=1
Q8CI85	Ca12	1	25	8,3	0,000	Carbonic anhydrase 12 OS=Mus musculus GN=Ca12 PE=1 SV=1
D3Z6Q9	Bin2	1	50	11,2	0,010	Bridging integrator 2 OS=Mus musculus GN=Bin2 PE=1 SV=1
Q91YJ3	Thyn1	1	15	12,7	0,003	Thymocyte nuclear protein 1 OS=Mus musculus GN=Thyn1 PE=1 SV=1

Table S2

Biological processes overrepresented with proteins more abundant in WT

Biological processes (GO-Term)	GO-Term id	P-value	Fold enrichment	# Genes (observed)	# Genes (expected)	# Genes (total)	List of observed genes
one-carbon compound transport	GO:0019755	0,0001	175,0	2	0,0	14	Slc14a1, Car12
mucopolysaccharide metabolic process	GO:1903510	0,0010	43,0	2	0,0	57	Itih3, B3galt2
kidney smooth muscle cell differentiation	GO:0072195	0,0016	612,6	1	0,0	2	Tshz3
glycosaminoglycan metabolic process	GO:0030203	0,0022	28,8	2	0,1	85	Itih3, B3galt2
kidney smooth muscle tissue development	GO:0072194	0,0024	408,4	1	0,0	3	Tshz3
negative regulation of isotype switching to IgE isotypes	GO:0048294	0,0024	408,4	1	0,0	3	Ndfip1
aminoglycan metabolic process	GO:0006022	0,0029	24,8	2	0,1	99	Itih3, B3galt2
sensory perception of touch	GO:0050975	0,0033	306,3	1	0,0	4	Tshz3
negative regulation of isotype switching	GO:0045829	0,0033	306,3	1	0,0	4	Ndfip1
urea transmembrane transport	GO:0071918	0,0041	245,0	1	0,0	5	Slc14a1
ureter smooth muscle cell differentiation	GO:0072193	0,0041	245,0	1	0,0	5	Tshz3
ureter smooth muscle development	GO:0072191	0,0041	245,0	1	0,0	5	Tshz3
establishment of centrosome localization	GO:0051660	0,0041	245,0	1	0,0	5	Cep83
intermediate filament bundle assembly	GO:0045110	0,0049	204,2	1	0,0	6	Krt14
urea transport	GO:0015840	0,0049	204,2	1	0,0	6	Slc14a1
isotype switching to IgE isotypes	GO:0048289	0,0057	175,0	1	0,0	7	Ndfip1
negative regulation of interleukin-4 production	GO:0032713	0,0057	175,0	1	0,0	7	Ndfip1
regulation of isotype switching to IgE isotypes	GO:0048293	0,0057	175,0	1	0,0	7	Ndfip1
miRNA loading onto RISC involved in gene silencing by miRNA	GO:0035280	0,0057	175,0	1	0,0	7	Ago4
negative regulation of B cell mediated immunity	GO:0002713	0,0065	153,1	1	0,0	8	Ndfip1
negative regulation of immunoglobulin mediated immune response	GO:0002890	0,0065	153,1	1	0,0	8	Ndfip1
small RNA loading onto RISC	GO:0070922	0,0065	153,1	1	0,0	8	Ago4
carbon dioxide transport	GO:0015670	0,0065	153,1	1	0,0	8	Car12
negative regulation of autophagosome assembly	GO:1902902	0,0073	136,1	1	0,0	9	Fez1
chloride ion homeostasis	GO:0055064	0,0081	122,5	1	0,0	10	Car12
peristalsis	GO:0030432	0,0081	122,5	1	0,0	10	Tshz3
negative regulation of immunoglobulin production	GO:0002638	0,0081	122,5	1	0,0	10	Ndfip1
SRP-dependent cotranslational protein targeting to membrane	GO:0006614	0,0089	111,4	1	0,0	11	Ssr3
positive regulation of smooth muscle cell differentiation	GO:0051152	0,0089	111,4	1	0,0	11	Tshz3
monovalent inorganic anion homeostasis	GO:0055083	0,0089	111,4	1	0,0	11	Car12
negative regulation of type 2 immune response	GO:0002829	0,0089	111,4	1	0,0	11	Ndfip1
regulation of isotype switching to IgG isotypes	GO:0048302	0,0098	102,1	1	0,0	12	Ndfip1
adenylate cyclase-activating dopamine receptor signaling pathway	GO:0007191	0,0098	102,1	1	0,0	12	Gnal
urinary tract smooth muscle contraction	GO:0014848	0,0098	102,1	1	0,0	12	Tshz3
fluid transport	GO:0002087	0,0106	94,2	1	0,0	13	Tshz3
isotype switching to IgG isotypes	GO:0048291	0,0106	94,2	1	0,0	13	Ndfip1
transport	GO:0006810	0,0108	2,4	8	3,3	4087	Bin2, Slc14a1, Fez1, Tmem63c, Cep83, Ssr3, Ndfip1, Car12
organelle assembly	GO:0070925	0,0110	6,3	3	0,5	579	Bin2, Fez1, Cep83
ureter development	GO:0072189	0,0114	87,5	1	0,0	14	Tshz3
membrane tubulation	GO:0097320	0,0114	87,5	1	0,0	14	Bin2
establishment of mitochondrion localization	GO:0051654	0,0114	87,5	1	0,0	14	Fez1
pre-miRNA processing	GO:0031054	0,0114	87,5	1	0,0	14	Ago4
response to caffeine	GO:0031000	0,0114	87,5	1	0,0	14	Gnal
miRNA mediated inhibition of translation	GO:0035278	0,0122	81,7	1	0,0	15	Ago4
cotranslational protein targeting to membrane	GO:0006613	0,0122	81,7	1	0,0	15	Ssr3
ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway	GO:0043162	0,0122	81,7	1	0,0	15	Ndfip1
regulation of translation, ncRNA-mediated	GO:0045974	0,0130	76,6	1	0,0	16	Ago4
regulation of respiratory system process	GO:0044065	0,0130	76,6	1	0,0	16	Tshz3
negative regulation of translation, ncRNA-mediated	GO:0040033	0,0130	76,6	1	0,0	16	Ago4
gas transport	GO:0015669	0,0130	76,6	1	0,0	16	Car12
establishment of localization	GO:0051234	0,0133	2,3	8	3,5	4232	Bin2, Slc14a1, Fez1, Tmem63c, Cep83, Ssr3, Ndfip1, Car12
chondroitin sulfate proteoglycan biosynthetic process	GO:0050650	0,0138	72,1	1	0,0	17	B3galt2
water transport	GO:0006833	0,0138	72,1	1	0,0	17	Slc14a1
activation of adenylate cyclase activity	GO:0007190	0,0138	72,1	1	0,0	17	Gnal
protein targeting to ER	GO:0045047	0,0146	68,1	1	0,0	18	Ssr3
response to amphetamine	GO:0001975	0,0146	68,1	1	0,0	18	Gnal
response to amine	GO:0014075	0,0154	64,5	1	0,0	19	Gnal
phasic smooth muscle contraction	GO:0014821	0,0162	61,3	1	0,0	20	Tshz3
podosome assembly	GO:0071800	0,0170	58,3	1	0,0	21	Bin2
synaptonemal complex assembly	GO:0007130	0,0170	58,3	1	0,0	21	Ago4
protein localization to centrosome	GO:0071539	0,0170	58,3	1	0,0	21	Cep83
miRNA metabolic process	GO:0010586	0,0170	58,3	1	0,0	21	Ago4
regulation of smooth muscle cell differentiation	GO:0051150	0,0170	58,3	1	0,0	21	Tshz3
negative regulation of organelle assembly	GO:1902116	0,0178	55,7	1	0,0	22	Fez1
establishment of protein localization to endoplasmic reticulum	GO:0072599	0,0178	55,7	1	0,0	22	Ssr3
centrosome localization	GO:0051642	0,0178	55,7	1	0,0	22	Cep83
negative regulation of DNA recombination	GO:0045910	0,0178	55,7	1	0,0	22	Ndfip1
regulation of respiratory gaseous exchange	GO:0043576	0,0186	53,3	1	0,0	23	Tshz3
chondroitin sulfate metabolic process	GO:0030204	0,0186	53,3	1	0,0	23	B3galt2
fluid transport	GO:0042044	0,0194	51,0	1	0,0	24	Slc14a1
intermediate filament organization	GO:0045109	0,0194	51,0	1	0,0	24	Krt14
negative regulation of macroautophagy	GO:0016242	0,0194	51,0	1	0,0	24	Fez1
synaptonemal complex organization	GO:0070193	0,0194	51,0	1	0,0	24	Ago4
hyaluronan metabolic process	GO:0030212	0,0202	49,0	1	0,0	25	Itih3
regulation of type 2 immune response	GO:0002828	0,0210	47,1	1	0,0	26	Ndfip1
anion homeostasis	GO:0055081	0,0210	47,1	1	0,0	26	Car12
smooth muscle tissue development	GO:0048745	0,0218	45,4	1	0,0	27	Tshz3
regulation of isotype switching	GO:0045191	0,0226	43,8	1	0,0	28	Ndfip1
chondroitin sulfate proteoglycan metabolic process	GO:0050654	0,0226	43,8	1	0,0	28	B3galt2
production of miRNAs involved in gene silencing by miRNA	GO:0035196	0,0226	43,8	1	0,0	28	Ago4
regulation of interleukin-4 production	GO:0032673	0,0234	42,2	1	0,0	29	Ndfip1
negative regulation of production of molecular mediator of immune response	GO:0002701	0,0234	42,2	1	0,0	29	Ndfip1
production of small RNA involved in gene silencing by RNA	GO:0070918	0,0234	42,2	1	0,0	29	Ago4
dsRNA fragmentation	GO:0031050	0,0234	42,2	1	0,0	29	Ago4
positive regulation of adenylate cyclase activity	GO:0045762	0,0242	40,8	1	0,0	30	Gnal
protein localization to microtubule cytoskeleton	GO:0072698	0,0250	39,5	1	0,0	31	Cep83
negative regulation of adaptive immune response based on somatic recombination of immu	GO:0002823	0,0250	39,5	1	0,0	31	Ndfip1
negative regulation of B cell activation	GO:0050869	0,0250	39,5	1	0,0	31	Ndfip1
single-organism transport	GO:0044765	0,0256	2,5	6	2,4	2946	Bin2, Slc14a1, Tmem63c, Ssr3, Ndfip1, Car12
regulation of autophagosome assembly	GO:2000785	0,0258	38,3	1	0,0	32	Fez1
respiratory system process	GO:0003016	0,0258	38,3	1	0,0	32	Tshz3
type 2 immune response	GO:0042092	0,0258	38,3	1	0,0	32	Ndfip1
regulation of developmental process	GO:0050793	0,0271	2,8	5	1,8	2175	Ago4, Tle6, Fez1, Tshz3, Ndfip1
negative regulation of adaptive immune response	GO:0002820	0,0274	36,0	1	0,0	34	Ndfip1
one-carbon metabolic process	GO:0006730	0,0274	36,0	1	0,0	34	Car12
mitochondrion localization	GO:0051646	0,0282	35,0	1	0,0	35	Fez1
protein localization to cytoskeleton	GO:0044380	0,0282	35,0	1	0,0	35	Cep83
dopamine receptor signaling pathway	GO:0007212	0,0290	34,0	1	0,0	36	Gnal
interleukin-4 production	GO:0032633	0,0290	34,0	1	0,0	36	Ndfip1
cellular component assembly	GO:0022607	0,0297	2,8	5	1,8	2227	Krt14, Bin2, Ago4, Fez1, Cep83
establishment of organelle localization	GO:0051656	0,0304	7,3	2	0,3	337	Fez1, Cep83
positive regulation of lyase activity	GO:0051349	0,0306	32,2	1	0,0	38	Gnal
protein localization to endoplasmic reticulum	GO:0070972	0,0306	32,2	1	0,0	38	Ssr3
negative regulation of lymphocyte mediated immunity	GO:0002707	0,0306	32,2	1	0,0	38	Ndfip1
cellular iron ion homeostasis	GO:0006879	0,0306	32,2	1	0,0	38	Ndfip1
cell differentiation involved in kidney development	GO:0061005	0,0306	32,2	1	0,0	38	Tshz3
positive regulation of cyclase activity	GO:0031281	0,0306	32,2	1	0,0	38	Gnal
male meiosis	GO:0007140	0,0314	31,4	1	0,0	39	Ago4
regulation of vacuole organization	GO:0044088	0,0314	31,4	1	0,0	39	Fez1
intermediate filament cytoskeleton organization	GO:0045104	0,0330	29,9	1	0,0	41	Krt14
proteoglycan biosynthetic process	GO:0030166	0,0330	29,9	1	0,0	41	B3galt2
single-organism localization	GO:1902578	0,0335	2,3	6	2,6	3130	Bin2, Slc14a1, Tmem63c, Ssr3, Ndfip1, Car12
intermediate filament-based process	GO:0045103	0,0337	29,2	1	0,0	42	Krt14
synapsis	GO:0007129	0,0345	28,5	1	0,0	43	Ago4
isotype switching	GO:0045190	0,0345	28,5	1	0,0	43	Ndfip1
somatic recombination of immunoglobulin genes involved in immune response	GO:0002204	0,0345	28,5	1	0,0	43	Ndfip1
somatic diversification of immunoglobulins involved in immune response	GO:0002208	0,0345	28,5	1	0,0	43	Ndfip1
positive regulation of neuron differentiation	GO:0045666	0,0359	6,6	2	0,3	369	Tle6, Fez1
multicellular organismal movement	GO:0050879	0,0361	27,2	1	0,0	45	Tshz3
RNA secondary structure unwinding	GO:0010501	0,0361	27,2	1	0,0	45	Ago4
cellular response to dsRNA	GO:0071359	0,0361	27,2	1	0,0	45	Ago4
musculoskeletal movement	GO:0050881	0,0361	27,2	1	0,0	45	Tshz3
cellular developmental process	GO:0048869	0,0363	2,1	7	3,3	4089	Krt14, Ago4, Tle6, Fez1, Tshz3, Cep83, Ndfip1
positive regulation of cell differentiation	GO:0045597	0,0370	4,0	3	0,7	918	Tle6, Fez1, Tshz3
glycosaminoglycan biosynthetic process	GO:0006024	0,0377	26,1	1	0,0	47	B3galt2
single-organism process	GO:0044699	0,0385	1,4	15	10,8	13200	Krt14, Bin2, Ago4, Gnal, Slc14a1, Tle6, Fez1, Tshz3, Tmem63c, Cep83, Ssr3, Ndfip1, Fam129b, B3galt2, Car12
regulation of adenylate cyclase activity	GO:0045761	0,0385	25,5	1	0,0	48	Gnal
negative regulation of leukocyte mediated immunity	GO:0002704	0,0385	25,5	1	0,0	48	Ndfip1
somatic recombination of immunoglobulin gene segments	GO:0016447	0,0393	25,0	1	0,0	49	Ndfip1
regulation of cell differentiation	GO:0045595	0,0393	3,0	4	1,3	1624	Tle6, Fez1, Tshz3, Ndfip1
carbohydrate derivative metabolic process	GO:1901135	0,0400	3,9	3	0,8	947	Itih3, Gnal, B3galt2
immunoglobulin production involved in immunoglobulin mediated immune response	GO:0002381	0,0400	24,5	1	0,0	50	Ndfip1
aminoglycan biosynthetic process	GO:0006023	0,0408	24,0	1	0,0	51	B3galt2
cellular component biogenesis	GO:0044085	0,0412	2,5	5	2,0	2430	Krt14, Bin2, Ago4, Fez1, Cep83
regulation of immunoglobulin mediated immune response	GO:0002889	0,0416	23,6	1	0,0	52	Ndfip1
vesicle docking	GO:0048278	0,0416	23,6	1	0,0	52	Cep83
negative regulation of autophagy	GO:0010507	0,0416	23,6	1	0,0	52	Fez1
regulation of B cell mediated immunity	GO:0002712	0,0416	23,6	1	0,0	52	Ndfip1
homologous chromosome segregation	GO:0045143	0,0424	23,1	1	0,0	53	Ago4
negative regulation of transporter activity	GO:0032410	0,0424	23,1	1	0,0	53	Ndfip1
somatic diversification of immunoglobulins	GO:0016445	0,0432	22,7	1	0,0	54	Ndfip1
respiratory gaseous exchange	GO:0007585	0,0432	22,7	1	0,0	54	Tshz3
organelle localization	GO:0051640	0,0434	6,0	2	0,3	410	Fez1, Cep83
regulation of immunoglobulin production	GO:0002637	0,0447	21,9	1	0,0	56	Ndfip1
regulation of cyclase activity	GO:0031279	0,0455	21,5	1	0,0	57	Gnal
phagocytosis, engulfment	GO:0006911	0,0463	21,1	1	0,0	58	Bin2
chromosome organization involved in meiotic cell cycle	GO:0070192	0,0463	21,1	1	0,0	58	Ago4
somatic diversification of immune receptors via germline recombination within a single locus	GO:0002562	0,0463	21,1	1	0,0	58	Ndfip1
somatic cell DNA recombination	GO:0016444	0,0463	21,1	1	0,0	58	Ndfip1
regulation of lyase activity	GO:0051339	0,0471	20,8	1	0,0	59	Gnal
negative regulation of T cell proliferation	GO:0042130	0,0471	20,8	1	0,0	59	Ndfip1
localization	GO:0051179	0,0484	1,8	8	4,3	5316	Bin2, Slc14a1, Fez1, Tmem63c, Cep83, Ssr3, Ndfip1, Car12
smooth muscle cell differentiation	GO:0051145	0,0487	20,1	1	0,0	61	Tshz3
membrane docking	GO:0022406	0,0487	20,1	1	0,0	61	Cep83

Table S3

Biological processes overrepresented with proteins more abundant in CCR2 $^{-/-}$ mutant

Biological processes (GO-Term)	GO-Term id	P-value	Fold enrichment	# Genes (observed)	# Genes (expected)	# Genes (total)	List of observed genes
positive regulation of nephron tubule epithelial cell differentiation	GO:2000768	0.0025	401,3	1	0,0	2	Prom1
seryl-tRNA aminoacylation	GO:0006434	0.0025	401,3	1	0,0	2	Sars2
positive regulation of adrenergic receptor signaling pathway	GO:0071879	0.0037	267,6	1	0,0	3	Gsk3a
positive regulation of epithelial cell differentiation involved in kidney development	GO:2000698	0.0037	267,6	1	0,0	3	Prom1
regulation of dosage compensation by inactivation of X chromosome	GO:1900095	0.0037	267,6	1	0,0	3	Rlim
cellular response to interleukin-3	GO:0036016	0.0050	200,7	1	0,0	4	Gsk3a
response to interleukin-3	GO:0036015	0.0050	200,7	1	0,0	4	Gsk3a
regulation of adrenergic receptor signaling pathway	GO:0071877	0.0062	160,5	1	0,0	5	Gsk3a
hypermethylation of CpG island	GO:0044027	0.0062	160,5	1	0,0	5	Gsk3a
positive regulation of glycogen (starch) synthase activity	GO:2000467	0.0062	160,5	1	0,0	5	Gsk3a
negative regulation of cell growth involved in cardiac muscle cell development	GO:0061052	0.0062	160,5	1	0,0	5	Gsk3a
positive regulation of retinoic acid receptor signaling pathway	GO:0048386	0.0062	160,5	1	0,0	5	Ctbp2
DNA hypermethylation	GO:0044026	0.0075	133,8	1	0,0	6	Gsk3a
regulation of glycogen (starch) synthase activity	GO:2000465	0.0087	114,7	1	0,0	7	Gsk3a
positive regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	GO:1901030	0.0099	100,3	1	0,0	8	Gsk3a
negative regulation of cardiac muscle cell differentiation	GO:2000726	0.0099	100,3	1	0,0	8	Gsk3a
CTP metabolic process	GO:0046036	0.0112	89,2	1	0,0	9	Ctps
thrombin receptor signaling pathway	GO:0070493	0.0112	89,2	1	0,0	9	Dgkq
CTP biosynthetic process	GO:0006241	0.0112	89,2	1	0,0	9	Ctps
negative regulation of cardiocyte differentiation	GO:1905208	0.0124	80,3	1	0,0	10	Gsk3a
positive regulation of chromatin binding	GO:0035563	0.0124	80,3	1	0,0	10	Ctbp2
positive regulation of calcineurin-NFAT signaling cascade	GO:0070886	0.0124	80,3	1	0,0	10	Lmcd1
pyrimidine ribonucleoside triphosphate biosynthetic process	GO:0009209	0.0124	80,3	1	0,0	10	Ctps
Leydig cell differentiation	GO:0033327	0.0136	73,0	1	0,0	11	Plekha1
toxin metabolic process	GO:0009404	0.0136	73,0	1	0,0	11	As3mt
regulation of nephron tubule epithelial cell differentiation	GO:0072182	0.0136	73,0	1	0,0	11	Prom1
renal filtration cell differentiation	GO:0061318	0.0136	73,0	1	0,0	11	Prom1
glomerular epithelium development	GO:0072010	0.0136	73,0	1	0,0	11	Prom1
glomerular visceral epithelial cell differentiation	GO:0072112	0.0136	73,0	1	0,0	11	Prom1
pyrimidine ribonucleoside triphosphate metabolic process	GO:0009208	0.0136	73,0	1	0,0	11	Ctps
glomerular epithelial cell differentiation	GO:0072311	0.0136	73,0	1	0,0	11	Prom1
potassium ion export	GO:0071435	0.0136	73,0	1	0,0	11	Kcnd3
cellular response to lithium ion	GO:0071285	0.0149	66,9	1	0,0	12	Gsk3a
dosage compensation by inactivation of X chromosome	GO:0009048	0.0161	61,7	1	0,0	13	Rlim
nephron tubule epithelial cell differentiation	GO:0072160	0.0161	61,7	1	0,0	13	Prom1
pyrimidine nucleoside triphosphate biosynthetic process	GO:0009148	0.0161	61,7	1	0,0	13	Ctps
response to lithium ion	GO:0010226	0.0161	61,7	1	0,0	13	Gsk3a
luteinization	GO:0001553	0.0161	61,7	1	0,0	13	Plekha1
white fat cell differentiation	GO:0050872	0.0161	61,7	1	0,0	13	Ctbp2
regulation of epithelial cell differentiation involved in kidney development	GO:2000696	0.0161	61,7	1	0,0	13	Prom1
pyrimidine ribonucleotide biosynthetic process	GO:0009220	0.0173	57,3	1	0,0	14	Ctps
pyrimidine ribonucleoside biosynthetic process	GO:0046132	0.0173	57,3	1	0,0	14	Ctps
negative regulation of cardiac muscle hypertrophy	GO:0010614	0.0173	57,3	1	0,0	14	Gsk3a
pyrimidine nucleoside triphosphate metabolic process	GO:0009147	0.0185	53,5	1	0,0	15	Ctps
regulation of cell growth involved in cardiac muscle cell development	GO:0061050	0.0185	53,5	1	0,0	15	Gsk3a
regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	GO:1901028	0.0185	53,5	1	0,0	15	Gsk3a
regulation of retinoic acid receptor signaling pathway	GO:0048385	0.0185	53,5	1	0,0	15	Ctbp2
dosage compensation	GO:0007549	0.0185	53,5	1	0,0	15	Rlim
pyrimidine ribonucleotide metabolic process	GO:0009218	0.0198	50,2	1	0,0	16	Ctps
pyrimidine nucleoside biosynthetic process	GO:0046134	0.0198	50,2	1	0,0	16	Ctps
negative regulation of muscle hypertrophy	GO:0014741	0.0198	50,2	1	0,0	16	Gsk3a
positive regulation of G2/M transition of mitotic cell cycle	GO:0010971	0.0198	50,2	1	0,0	16	Mta3
estrogen metabolic process	GO:0008210	0.0210	47,2	1	0,0	17	Plekha1
positive regulation of cell cycle G2/M phase transition	GO:1902751	0.0210	47,2	1	0,0	17	Mta3
cardiac left ventricle morphogenesis	GO:0003214	0.0210	47,2	1	0,0	17	Gsk3a
retina layer formation	GO:0010842	0.0210	47,2	1	0,0	17	Prom1
response to arsenic-containing substance	GO:0046685	0.0222	44,6	1	0,0	18	As3mt
regulation of gene expression by genetic imprinting	GO:0006349	0.0222	44,6	1	0,0	18	Gsk3a
negative regulation of cardiac muscle tissue growth	GO:0055022	0.0222	44,6	1	0,0	18	Gsk3a
androgen metabolic process	GO:0008209	0.0222	44,6	1	0,0	18	Plekha1
negative regulation of heart growth	GO:0061117	0.0222	44,6	1	0,0	18	Gsk3a
vesicle targeting	GO:0006903	0.0234	42,2	1	0,0	19	Map4k2
negative regulation of glucose import	GO:0046325	0.0234	42,2	1	0,0	19	Gsk3a
pyrimidine ribonucleoside metabolic process	GO:0046131	0.0246	40,1	1	0,0	20	Ctps
peptidyl-tyrosine dephosphorylation	GO:0035335	0.0246	40,1	1	0,0	20	Dusp14
regulation of chromatin binding	GO:0035561	0.0246	40,1	1	0,0	20	Ctbp2
regulation of cardiac muscle hypertrophy	GO:0010611	0.0013	38,2	2	0,1	42	Gsk3a, Lmcd1
regulation of calcineurin-NFAT signaling cascade	GO:0070884	0.0258	38,2	1	0,0	21	Lmcd1
regulation of muscle hypertrophy	GO:0014743	0.0014	36,5	2	0,1	44	Gsk3a, Lmcd1
negative regulation of glucose transport	GO:0010829	0.0271	36,5	1	0,0	22	Gsk3a
pyrimidine nucleotide biosynthetic process	GO:0006221	0.0283	34,9	1	0,0	23	Ctps
phosphatidylinositol dephosphorylation	GO:0046856	0.0283	34,9	1	0,0	23	Mtmr3
gamma-aminobutyric acid signaling pathway	GO:0007214	0.0283	34,9	1	0,0	23	Gabra2
physiological muscle hypertrophy	GO:0003298	0.0295	33,4	1	0,0	24	Gsk3a
glutamine metabolic process	GO:0006541	0.0295	33,4	1	0,0	24	Ctps
mitochondrial outer membrane permeabilization	GO:0097345	0.0295	33,4	1	0,0	24	Gsk3a
regulation of DNA methylation	GO:0044030	0.0295	33,4	1	0,0	24	Gsk3a
camera-type eye photoreceptor cell differentiation	GO:0060219	0.0295	33,4	1	0,0	24	Prom1
physiological cardiac muscle hypertrophy	GO:0003301	0.0295	33,4	1	0,0	24	Gsk3a
negative regulation of cardiac muscle tissue development	GO:0055026	0.0295	33,4	1	0,0	24	Gsk3a
response to ATP	GO:0033198	0.0295	33,4	1	0,0	24	Dgkq
cell growth involved in cardiac muscle cell development	GO:0061049	0.0295	33,4	1	0,0	24	Gsk3a
protein kinase C-activating G-protein coupled receptor signaling pathway	GO:0007205	0.0307	32,1	1	0,0	25	Dgkq
positive regulation of peptidyl-threonine phosphorylation	GO:0010800	0.0307	32,1	1	0,0	25	Gsk3a
positive regulation of mitochondrial membrane permeability involved in apoptotic process	GO:1902110	0.0319	30,9	1	0,0	26	Gsk3a
mitochondrial outer membrane permeabilization involved in programmed cell death	GO:1902686	0.0319	30,9	1	0,0	26	Gsk3a
epithelial cell differentiation involved in kidney development	GO:0035850	0.0319	30,9	1	0,0	26	Prom1
adrenergic receptor signaling pathway	GO:0071875	0.0331	29,7	1	0,0	27	Gsk3a
negative regulation of striated muscle cell differentiation	GO:0051154	0.0331	29,7	1	0,0	27	Gsk3a
pyrimidine nucleoside metabolic process	GO:0006213	0.0331	29,7	1	0,0	27	Ctps
positive regulation of G-protein coupled receptor protein signaling pathway	GO:0045745	0.0331	29,7	1	0,0	27	Gsk3a
positive regulation of viral genome replication	GO:0045070	0.0331	29,7	1	0,0	27	Pkn2
cellular response to glucose starvation	GO:0042149	0.0343	28,7	1	0,0	28	Mtmr3
regulation of cardiac muscle cell differentiation	GO:2000725	0.0343	28,7	1	0,0	28	Gsk3a
calcineurin-NFAT signaling cascade	GO:0033173	0.0343	28,7	1	0,0	28	Lmcd1
pyrimidine-containing compound biosynthetic process	GO:0072528	0.0343	28,7	1	0,0	28	Ctps
negative regulation of organ growth	GO:0046621	0.0355	27,7	1	0,0	29	Gsk3a
positive regulation of mitochondrial membrane permeability	GO:0035794	0.0355	27,7	1	0,0	29	Gsk3a
retinoic acid receptor signaling pathway	GO:0048384	0.0367	26,8	1	0,0	30	Ctbp2
positive regulation of cytokinesis	GO:0032467	0.0367	26,8	1	0,0	30	Pkn2
protein kinase C signaling	GO:0070528	0.0367	26,8	1	0,0	30	Dgkq
negative regulation of dendrite development	GO:2000171	0.0391	25,1	1	0,0	32	Gsk3a
regulation of autophagosome assembly	GO:2000785	0.0391	25,1	1	0,0	32	Mtmr3
pyrimidine nucleotide metabolic process	GO:0006220	0.0391	25,1	1	0,0	32	Ctps
cell differentiation involved in embryonic placenta development	GO:0060706	0.0391	25,1	1	0,0	32	Krt19
membrane repolarization	GO:0086009	0.0391	25,1	1	0,0	32	Kcnd3
activation of JUN kinase activity	GO:0007257	0.0391	25,1	1	0,0	32	Map4k2
genetic imprinting	GO:0071514	0.0403	24,3	1	0,0	33	Gsk3a
regulation of mitochondrial membrane permeability involved in apoptotic process	GO:1902108	0.0403	24,3	1	0,0	33	Gsk3a
positive regulation of epithelial to mesenchymal transition	GO:0010718	0.0403	24,3	1	0,0	33	Bcl9l
regulation of muscle adaptation	GO:0043502	0.0032	23,6	2	0,1	68	Gsk3a, Lmcd1
negative regulation of TOR signaling	GO:0032007	0.0415	23,6	1	0,0	34	Gsk3a
phospholipid dephosphorylation	GO:0046839	0.0415	23,6	1	0,0	34	Mtmr3
inositol phosphate-mediated signaling	GO:0048016	0.0415	23,6	1	0,0	34	Lmcd1
regulation of cardiocyte differentiation	GO:1905207	0.0415	23,6	1	0,0	34	Gsk3a
cardiac muscle hypertrophy	GO:0003300	0.0035	22,6	2	0,1	71	Gsk3a, Lmcd1
face morphogenesis	GO:0060325	0.0439	22,3	1	0,0	36	Plekha1
negative regulation of insulin receptor signaling pathway	GO:0046627	0.0439	22,3	1	0,0	36	Gsk3a
regulation of peptidyl-threonine phosphorylation	GO:0010799	0.0439	22,3	1	0,0	36	Gsk3a
striated muscle hypertrophy	GO:0014897	0.0038	21,7	2	0,1	74	Gsk3a, Lmcd1
sarcomere organization	GO:0045214	0.0451	21,7	1	0,0	37	Krt19
positive regulation of heart contraction	GO:0045823	0.0451	21,7	1	0,0	37	Gsk3a
muscle hypertrophy	GO:0014896	0.0040	21,1	2	0,1	76	Gsk3a, Lmcd1
cell differentiation involved in kidney development	GO:0061005	0.0463	21,1	1	0,0	38	Prom1
regulation of mitophagy	GO:1903146	0.0463	21,1	1	0,0	38	Gsk3a
regulation of vacuole organization	GO:0044088	0.0475	20,6	1	0,0	39	Mtmr3
negative regulation of cellular response to insulin stimulus	GO:1900077	0.0475	20,6	1	0,0	39	Gsk3a
positive regulation of protein targeting to mitochondrion	GO:1903955	0.0044	20,3	2	0,1	79	Ablim3, Gsk3a
positive regulation of calcium-mediated signaling	GO:0050850	0.0487	20,1	1	0,0	40	Lmcd1
photoreceptor cell maintenance	GO:0045494	0.0487	20,1	1	0,0	40	Prom1
negative regulation of protein kinase B signaling	GO:0051898	0.0487	20,1	1	0,0	40	Plekha1
positive regulation of establishment of protein localization to mitochondrion	GO:1903749	0.0046	19,8	2	0,1	81	Ablim3, Gsk3a
regulation of protein targeting to mitochondrion	GO:1903214	0.0055	18,0	2	0,1	89	Ablim3, Gsk3a
muscle adaptation	GO:0043500	0.0059	17,4	2	0,1	92	Gsk3a, Lmcd1
regulation of establishment of protein localization to mitochondrion	GO:1903747	0.0059	17,4	2	0,1	92	Ablim3, Gsk3a
xenophagy	GO:0098792	0.0076	15,3	2	0,1	105	Lmcd1, Slc25a19
positive regulation of defense response to virus by host	GO:0002230	0.0095	13,6	2	0,1	118	Lmcd1, Slc25a19
regulation of defense response to virus by host	GO:0050691	0.0109	12,6	2	0,2	127	Lmcd1, Slc25a19
positive regulation of mitotic cell cycle	GO:0045931	0.0116	12,3	2	0,2	131	Mta3, Pkn2
protein targeting to mitochondrion	GO:0006626	0.0121	12,0	2	0,2	134	Ablim3, Gsk3a
positive regulation of mitochondrion organization	GO:0010822	0.0124	11,8	2	0,2	136	Ablim3, Gsk3a
establishment of protein localization to mitochondrion	GO:0072655	0.0138	11,1	2	0,2	144	Ablim3, Gsk3a
protein localization to mitochondrion	GO:0070585	0.0149	10,7	2	0,2	150	Ablim3, Gsk3a
regulation of defense response to virus	GO:0050688	0.0153	10,6	2	0,2	152	Lmcd1, Slc25a19
striated muscle cell development	GO:0055002	0.0155	10,5	2	0,2	153	Gsk3a, Krt19
muscle cell development	GO:0055001	0.0185	9,6	2	0,2	168	Gsk3a, Krt19
cellular amino acid metabolic process	GO:0006520	0.0224	8,6	2	0,2	186	Ctps, Sars2
mitophagy	GO:0000422	0.0231	8,5	2	0,2	189	Gsk3a, Lmcd1
mitochondrion disassembly	GO:0061726	0.0231	8,5	2	0,2	189	Gsk3a, Lmcd1
regulation of mitochondrion organization	GO:0010821	0.0233	8,4	2	0,2	190	Ablim3, Gsk3a
regulation of muscle system process	GO:0090257	0.0233	8,4	2	0,2	190	Gsk3a, Lmcd1
regulation of autophagy	GO:0010506	0.0235	8,4	2	0,2	191	Mtmr3, Gsk3a
regulation of viral process	GO:0050792	0.0055	8,3	3	0,4	290	Pkn2, Lmcd1, Slc25a19
macroautophagy	GO:0016236	0.0058	8,2	3	0,4	295	Mtmr3, Lmcd1, Slc25a19
positive regulation of cell cycle process	GO:0090068	0.0254	8,1	2	0,2	199	Mta3, Pkn2
regulation of response to biotic stimulus	GO:0002831	0.0273	7,8	2	0,3	207	Lmcd1, Slc25a19
organelle disassembly	GO:1903008	0.0275	7,7	2	0,3	208	Gsk3a, Lmcd1
mitochondrial transport	GO:0006839	0.0278	7,7	2	0,3	209	Ablim3, Gsk3a
second-messenger-mediated signaling	GO:0019932	0.0280	7,6	2	0,3	210	Dgkq, Lmcd1
regulation of symbiosis, encompassing mutualism through parasitism	GO:0043903	0.0072	7,5	3	0,4	320	Pkn2, Lmcd1, Slc25a19
protein dephosphorylation	GO:0006470	0.0290	7,5	2	0,3	214	Mtmr3, Dusp14
ribonucleotide biosynthetic process	GO:0009260	0.0316	7,2	2	0,3	224	Gsk3a, Ctps
autophagy	GO:0006914	0.0023	7,1	4	0,6	452	Mtmr3, Gsk3a, Lmcd1, Slc25a19
ribose phosphate biosynthetic process	GO:0046390	0.0323	7,1	2	0,3	227	Gsk3a, Ctps
positive regulation of intracellular protein transport	GO:0090316	0.0355	6,7	2	0,3	239	Ablim3, Gsk3a
regulation of gene expression, epigenetic	GO:0040029	0.0394	6,3	2	0,3	253	Gsk3a, Rlim
defense response to virus	GO:0051607	0.0426	6,1	2	0,3	264	Lmcd1, Slc25a19
striated muscle cell differentiation	GO:0051146	0.0426	6,1	2	0,3	264	Gsk3a, Krt19
nucleotide biosynthetic process	GO:0009165	0.0434	6,0	2	0,3	267	Gsk3a, Ctps
peptidyl-serine phosphorylation	GO:0018105	0.0446	5,9	2	0,3	271	Pkn2, Gsk3a
positive regulation of intracellular transport	GO:0032388	0.0452	5,9	2	0,3	273	Ablim3, Gsk3a
nucleoside phosphate biosynthetic process	GO:1901293	0.0458	5,8	2	0,3	275	Gsk3a, Ctps
regulation of multi-organism process	GO:0043900	0.0152	5,7	3	0,5	422	Pkn2, Lmcd1, Slc25a19
regulation of protein targeting	GO:1903533	0.0482	5,7	2	0,4	283	Ablim3, Gsk3a
peptidyl-serine modification	GO:0018209	0.0491	5,6	2	0,4	286	Pkn2, Gsk3a
viral process	GO:0016032	0.0232	4,9	3	0,6	495	Pkn2, Lmcd1, Slc25a19
multi-organism cellular process	GO:0044764	0.0235	4,8	3	0,6	498	Pkn2, Lmcd1, Slc25a19
interspecies interaction between organisms	GO:0044419	0.0291	4,5	3	0,7	541	Pkn2, Lmcd1, Slc25a19
symbiosis, encompassing mutualism through parasitism	GO:0044403	0.0291	4,5	3	0,7	541	Pkn2, Lmcd1, Slc25a19
organelle assembly	GO:0070925	0.0346	4,2	3	0,7	579	Mtmr3, Ablim3, Krt19
muscle structure development	GO:0061061	0.0395	3,9	3	0,8	610	Gsk3a, Bcl9l, Krt19
mitochondrion organization	GO:0007005	0.0401	3,9	3	0,8	614	Ablim3, Gsk3a, Lmcd1
translation	GO:0006412	0.0484	3,6	3	0,8	662	Guf1, Slc25a19, Sars2
organonitrogen compound biosynthetic process	GO:1901566	0.0167	3,3	5	1,5	1227	Gsk3a, Ctps, Guf1, Slc25a19, Sars2
regulation of transcription from RNA polymerase II promoter	GO:0006357	0.0044	3,3	7	2,2	1726	Dgkq, Ablim3, Gsk3a, Bcl9l, Lmcd1, Ctbp2, Rlim
transcription from RNA polymerase II promoter	GO:0006366	0.0054	3,1	7	2,2	1788	Dgkq, Ablim3, Gsk3a, Bcl9l, Lmcd1, Ctbp2, Rlim
positive regulation of transcription from RNA polymerase II promoter	GO:0045944	0.0366	3,1	4	1,3	1022	Ablim3, Gsk3a, Bcl9l, Ctbp2
negative regulation of transcription, DNA-templated	GO:0045892	0.0409	3,0	4	1,3	1059	Mta3, Lmcd1, Ctbp2, Rlim
negative regulation of nucleic acid-templated transcription	GO:1903507	0.0428	3,0	4	1,3	1074	Mta3, Lmcd1, Ctbp2, Rlim
negative regulation of RNA biosynthetic process	GO:1902679	0.0445	3,0	4	1,4	1088	Mta3, Lmcd1, Ctbp2, Rlim
cellular nitrogen compound biosynthetic process	GO:0044271	0.0008	2,5	13	5,2	4214	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Ctps, Lmcd1, Ctbp2, Guf1, Slc25a19, Rlim, Sars2
phosphate-containing compound metabolic process	GO:0006796	0.0152	2,4	8	3,4	2713	Dgkq, Mtmr3, Pkn2, Gsk3a, Mok, Dusp14, Ctps, Map4k2
regulation of transcription, DNA-templated	GO:0006355	0.0097	2,4	9	3,8	3054	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Lmcd1, Ctbp2, Rlim
phosphorus metabolic process	GO:0006793	0.0154	2,4	8	3,4	2718	Dgkq, Mtmr3, Pkn2, Gsk3a, Mok, Dusp14, Ctps, Map4k2
regulation of nucleic acid-templated transcription	GO:1903506	0.0100	2,4	9	3,8	3069	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Lmcd1, Ctbp2, Rlim
regulation of RNA biosynthetic process	GO:2001141	0.0101	2,3	9	3,8	3076	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Lmcd1, Ctbp2, Rlim
transcription, DNA-templated	GO:0006351	0.0113	2,3	9	3,9	3128	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Lmcd1, Ctbp2, Rlim
nucleic acid-templated transcription	GO:0097659	0.0116	2,3	9	3,9	3143	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Lmcd1, Ctbp2, Rlim
RNA biosynthetic process	GO:0032774	0.0119	2,3	9	3,9	3157	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Lmcd1, Ctbp2, Rlim
nucleobase-containing compound biosynthetic process	GO:0034654	0.0077	2,3	10	4,4	3514	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Ctps, Lmcd1, Ctbp2, Rlim
cellular macromolecule biosynthetic process	GO:0034645	0.0031	2,3	12	5,3	4236	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Lmcd1, Ctbp2, Guf1, Slc25a19, Rlim, Sars2
regulation of RNA metabolic process	GO:0051252	0.0126	2,3	9	4,0	3185	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Lmcd1, Ctbp2, Rlim
heterocycle biosynthetic process	GO:0018130	0.0086	2,3	10	4,4	3566	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Ctps, Lmcd1, Ctbp2, Rlim
aromatic compound biosynthetic process	GO:0019438	0.0089	2,2	10	4,5	3583	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Ctps, Lmcd1, Ctbp2, Rlim
macromolecule biosynthetic process	GO:0009059	0.0040	2,2	12	5,4	4359	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Lmcd1, Ctbp2, Guf1, Slc25a19, Rlim, Sars2
organic cyclic compound biosynthetic process	GO:1901362	0.0106	2,2	10	4,6	3679	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Ctps, Lmcd1, Ctbp2, Rlim
biosynthetic process	GO:0009058	0.0022	2,1	14	6,6	5286	Mta3, Dgkq, Gmppa, Ablim3, Pkn2, Gsk3a, Bcl9l, Ctps, Lmcd1, Ctbp2, Guf1, Slc25a19, Rlim, Sars2
regulation of cellular macromolecule biosynthetic process	GO:2000112	0.0205	2,1	9	4,3	3445	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Lmcd1, Ctbp2, Rlim
RNA metabolic process	GO:0016070	0.0155	2,1	10	4,8	3885	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Lmcd1, Ctbp2, Rlim, Sars2
regulation of nucleobase-containing compound metabolic process	GO:0019219	0.0233	2,1	9	4,4	3520	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Lmcd1, Ctbp2, Rlim
cellular biosynthetic process	GO:0044249	0.0050	2,0	13	6,4	5104	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Ctps, Lmcd1, Ctbp2, Guf1, Slc25a19, Rlim, Sars2
regulation of macromolecule biosynthetic process	GO:0010556	0.0246	2,0	9	4,4	3550	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Lmcd1, Ctbp2, Rlim
gene expression	GO:0010467	0.0088	2,0	12	6,0	4793	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Lmcd1, Ctbp2, Guf1, Slc25a19, Rlim, Sars2
organic substance biosynthetic process	GO:1901576	0.0060	2,0	13	6,5	5204	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Ctps, Lmcd1, Ctbp2, Guf1, Slc25a19, Rlim, Sars2
regulation of cellular biosynthetic process	GO:0031326	0.0319	1,9	9	4,6	3712	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Lmcd1, Ctbp2, Rlim
cellular protein metabolic process	GO:0044267	0.0253	1,9	10	5,2	4186	Mtmr3, Pkn2, Gsk3a, Mok, Dusp14, Map4k2, Guf1, Slc25a19, Rlim, Sars2
regulation of biosynthetic process	GO:0009889	0.0351	1,9	9	4,7	3774	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Lmcd1, Ctbp2, Rlim
regulation of nitrogen compound metabolic process	GO:0051171	0.0363	1,9	9	4,7	3795	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Lmcd1, Ctbp2, Rlim
regulation of gene expression	GO:0010468	0.0377	1,9	9	4,8	3821	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Lmcd1, Ctbp2, Rlim
cellular nitrogen compound metabolic process	GO:0034641	0.0110	1,9	13	6,9	5578	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Ctps, Lmcd1, Ctbp2, Guf1, Slc25a19, Rlim, Sars2
nucleic acid metabolic process	GO:0090304	0.0319	1,8	10	5,4	4341	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Lmcd1, Ctbp2, Rlim, Sars2
nucleobase-containing compound metabolic process	GO:0006139	0.0267	1,8	11	6,1	4866	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Ctps, Lmcd1, Ctbp2, Rlim, Sars2
heterocycle metabolic process	GO:0046483	0.0306	1,8	11	6,2	4963	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Ctps, Lmcd1, Ctbp2, Rlim, Sars2
nitrogen compound metabolic process	GO:0006807	0.0175	1,8	13	7,3	5897	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Ctps, Lmcd1, Ctbp2, Guf1, Slc25a19, Rlim, Sars2
cellular macromolecule metabolic process	GO:0044260	0.0063	1,8	16	9,1	7271	Mta3, Dgkq, Mtmr3, Ablim3, Pkn2, Gsk3a, Mok, Dusp14, Bcl9l, Lmcd1, Ctbp2, Map4k2, Guf1, Slc25a19, Rlim, Sars2
cellular aromatic compound metabolic process	GO:0006725	0.0334	1,8	11	6,3	5027	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Ctps, Lmcd1, Ctbp2, Rlim, Sars2
cellular metabolic process	GO:0044237	0.0027	1,7	19	11,1	8923	Mta3, Dgkq, Mtmr3, Ablim3, Pkn2, As3mt, Gsk3a, Mok, Dusp14, Bcl9l, Ctps, Lmcd1, Plekha1, Ctbp2, Map4k2, Guf1, Slc25a19, Rlim, Sars2
organic cyclic compound metabolic process	GO:1901360	0.0416	1,7	11	6,5	5193	Mta3, Dgkq, Ablim3, Pkn2, Gsk3a, Bcl9l, Ctps, Lmcd1, Ctbp2, Rlim, Sars2
metabolic process	GO:0008152	0.0041	1,6	20	12,4	9984	Mta3, Dgkq, Gmppa, Mtmr3, Ablim3, Pkn2, As3mt, Gsk3a, Mok, Dusp14, Bcl9l, Ctps, Lmcd1, Plekha1, Ctbp2, Map4k2, Guf1, Slc25a19, Rlim, Sars2
macromolecule metabolic process	GO:0043170	0.0184	1,6	16	10,0	8057	Mta3, Dgkq, Mtmr3, Ablim3, Pkn2, Gsk3a, Mok, Dusp14, Bcl9l, Lmcd1, Ctbp2, Map4k2, Guf1, Slc25a19, Rlim, Sars2
primary metabolic process	GO:0044238	0.0230	1,5	17	11,2	8996	Mta3, Dgkq, Mtmr3, Ablim3, Pkn2, Gsk3a, Mok, Dusp14, Bcl9l, Ctps, Lmcd1, Ctbp2, Map4k2, Guf1, Slc25a19, Rlim, Sars2
organic substance metabolic process	GO:0071704	0.0177	1,5	18	11,9	9539	Mta3, Dgkq, Mtmr3, Ablim3, Pkn2, As3mt, Gsk3a, Mok, Dusp14, Bcl9l, Ctps, Lmcd1, Ctbp2, Map4k2, Guf1, Slc25a19, Rlim, Sars2

Appendix Table S4 Primary and secondary antibodies used for immunohistological analysis

Antibody	Provider	Catalog Nr	Dilution
Primary antibody:			
anti AhR rabbit polyclonal IgG	US Bio	031714.200	1:300
anti CD11b rat monoclonal IgG_{2b}	BIORAD	MCA74GA	1:250
anti CD31 rat monoclonal IgG_{2b}	BD Biosciences	550274	1:100
anti CD45 rat monoclonal IgG_{2b}	BD Biosciences	550539	1:500
anti Collagen Type I rabbit polyclonal IgG	Rockland	600-401-103-0.5	1:200
anti Collagen Type IV rabbit polyclonal IgG	Millipore	AB8201	1:40
anti CSPG (CS-56) mouse monoclonal IgM	Abcam	ab11570	1:250
anti GFAP mouse monoclonal IgG_1 rabbit polyclonal IgG	Sigma Aldrich Dako	G3893 Z0334	1:500 1:500
anti Iba1 rabbit polyclonal IgG	Wako	019-19741	1:500
anti Ki67 rat monoclonal IgG_{2a} rabbit monoclonal IgG	eBioscience Thermo Fisher Scientific	14-5698-82 MA5-14520	1:300 1:100
anti NG2 (CSPG4) rabbit polyclonal	Millipore	AB5320	1:400
anti NeuN mouse monoclonal IgG_1	Millipore	MAB377	1:100
anti RFP rabbit polyclonal IgG	Rockland	600-401-379	1:500
anti S100(β-Subunit) mouse monoclonal IgG_1	Sigma Aldrich	S2532	1:250
anti TMEM119 rabbit monoclonal IgG	Abcam	ab209064	1:200
Secondary antibody:			
anti-mouse IgG_1 Alexa Fluor 488	Thermo Fisher Scientific	A-21121	1:500
anti-mouse IgM Alexa Fluor 488	Thermo Fisher Scientific	A-21042	1:500
anti-rabbit IgG Alexa Fluor 488	Thermo Fisher Scientific	A-21206	1:500
anti-rabbit IgG Alexa Fluor 647	Thermo Fisher Scientific	A-31573	1:500
anti-rat IgG Alexa Fluor 647	Thermo Fisher Scientific	A-21247	1:500
anti-mouse IgG CY3	Dianova	115-165-166	1:500
anti-rabbit IgG CY3	Dianova	111-165-144	1:500
anti-rat IgG CY3	Dianova	112-165-167	1:500