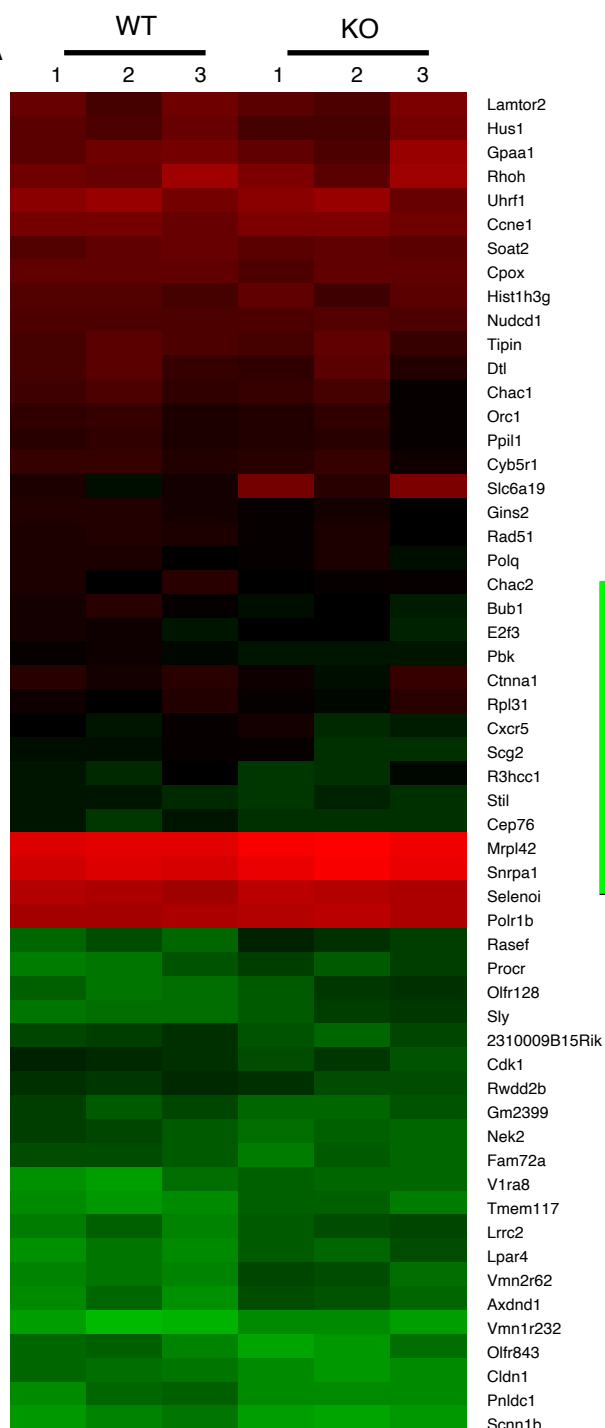


A



B

Fold-Change	P-val	Gene Symbol	Description
3.6	0.0206	Slc6a19	solute carrier family 6 (neurotransmitter transporter), member 19
2.82	0.0313	Axdnd1	axonemal dynein light chain domain containing 1
2.67	0.0303	Rasef	RAS and EF hand domain containing
2.58	0.0264	Olf1r128	olfactory receptor 128
2.51	0.0336	Vmn2r62	vomeronasal 2, receptor 62
2.36	0.0069	Sly	Sycp3 like Y-linked
2.32	0.0423	Lrrc2	leucine rich repeat containing 2
2.12	0.0115	Vmn1r232	vomeronasal 1 receptor 232
2.12	0.0277	V1ra8	vomeronasal 1 receptor, A8
2.05	0.0068	Tmem117	transmembrane protein 117
2.05	0.0462	Procr	protein C receptor, endothelial
2.01	0.0109	Lpar4	lysophosphatidic acid receptor 4
-2.01	0.002	Cldn1	claudin 1
-2.02	0.0136	Polr1b	polymerase (RNA) I polypeptide B
-2.05	0.0095	Gm2399	predicted gene 2399 [Source:MGI Symbol;Acc:MGI:3780567]
-2.05	0.0448	R3hcc1	R3H domain and coiled-coil containing 1
-2.06	0.01	Hist1h3g	histone cluster 1, H3g
-2.1	0.0052	2310009B15Rik	RIKEN cDNA 2310009B15 gene
-2.11	0.0221	Ccne1	cyclin E1
-2.12	0.007	Nudcd1	NudC domain containing 1
-2.12	0.0165	Cep76	centrosomal protein 76
-2.12	0.0265	Rpl31	ribosomal protein L31
-2.12	0.0339	Scn1b	sodium channel, nonvoltage-gated 1 beta
-2.13	0.0266	Rhoh	ras homolog gene family, member H
-2.14	0.0144	Ept1	ethanolaminephosphotransferase 1 (CDP-ethanolamine-specific)
-2.15	0.0133	Fam72a	family with sequence similarity 72, member A
-2.18	0.0044	Rwdd2b	RWD domain containing 2B
-2.2	0.0426	Mrpl42	mitochondrial ribosomal protein L42
-2.24	0.0414	Pnlcd1	poly(A)-specific ribonuclease (PARN)-like domain containing 1
-2.25	0.0029	Cpox	coproporphyrinogen oxidase
-2.26	0.019	Ctnna1	catenin (cadherin associated protein), alpha 1
-2.27	0.0104	Hus1	Hus1 homolog (S. pombe)
-2.28	0.0189	Stil	Sci/Tal1 interrupting locus
-2.28	0.0405	Snrpa1	small nuclear ribonucleoprotein polypeptide A; small nuclear ribonucleoprotein polypeptide A'
-2.31	0.0342	Olf1r843	olfactory receptor 843
-2.33	0.0159	Ppil1	peptidylprolyl isomerase (cyclophilin)-like 1
-2.34	0.0025	Soat2	sterol O-acyltransferase 2
-2.34	0.0207	Orc1	origin recognition complex, subunit 1
-2.39	0.0058	Nek2	NIMA (never in mitosis gene a)-related expressed kinase 2
-2.4	0.0351	E2f3	E2F transcription factor 3
-2.47	0.0223	Tipin	timeless interacting protein
-2.47	0.0279	Chac1	ChaC, cation transport regulator 1
-2.5	0.0329	Polq	polymerase (DNA directed), theta
-2.56	0.0439	Cxcr5	chemokine (C-X-C motif) receptor 5
-2.58	0.028	Cyb5r1	cytochrome b5 reductase 1
-2.6	0.0051	Chac2	ChaC, cation transport regulator 2
-2.69	0.0128	Scg2	secretogranin II
-2.71	0.0436	Dtl	denticleless homolog (Drosophila)
-2.73	0.0283	Lamtor2	late endosomal/lysosomal adaptor, MAPK and MTOR activator 2
-2.76	0.003	Rad51	RAD51 homolog
-2.77	0.0015	Pbk	PDZ binding kinase
-2.83	0.0015	Cdk1	cyclin-dependent kinase 1
-2.93	0.0314	Gpaa1	GPI anchor attachment protein 1
-2.99	0.0324	Uhrf1	ubiquitin-like, containing PHD and RING finger domains, 1
-3.01	0.0025	Bub1	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)
-3.02	0.0027	Gins2	GINS complex subunit 2 (Psf2 homolog)

Figure S5

C

Pathway	# Up DEGs ↑	# Down DEGs ↓	Significance	p-value	
Purine metabolism	4	10	Pde1b, Gucy2e, Gucy1b2, Pde5a	3.27	0.0005
Cell cycle	0	9	Mcm6, Mcm5, Mcm4, Bub1b, Bub1, Ccne1, Ccnb1, E2f3, Plk1	2.92	0.0012
Electron Transport Chain	0	8	Atp5j2, Atp5o, Ndufs5, Atp5g1, Ndufab1, Ndufc2, Atp5d, Ndufb8	1.96	0.011
DNA Replication	0	8	Prim1, Mcm6, Mcm5, Mcm4, Mcm10, Rfc5, Rfc2, Pold2	4.64	2E-05
Oxidative phosphorylation	0	7	Atp5d, Atp5g1, Atp5j2, Atp5o, Ndufb8, Ndufs5, Ndufc2	2.85	0.0014
G1 to S cell cycle control	0	6	E2f3, Ccne1, Mcm4, Mcm5, Mcm6, Prim1	2	0.01

D

