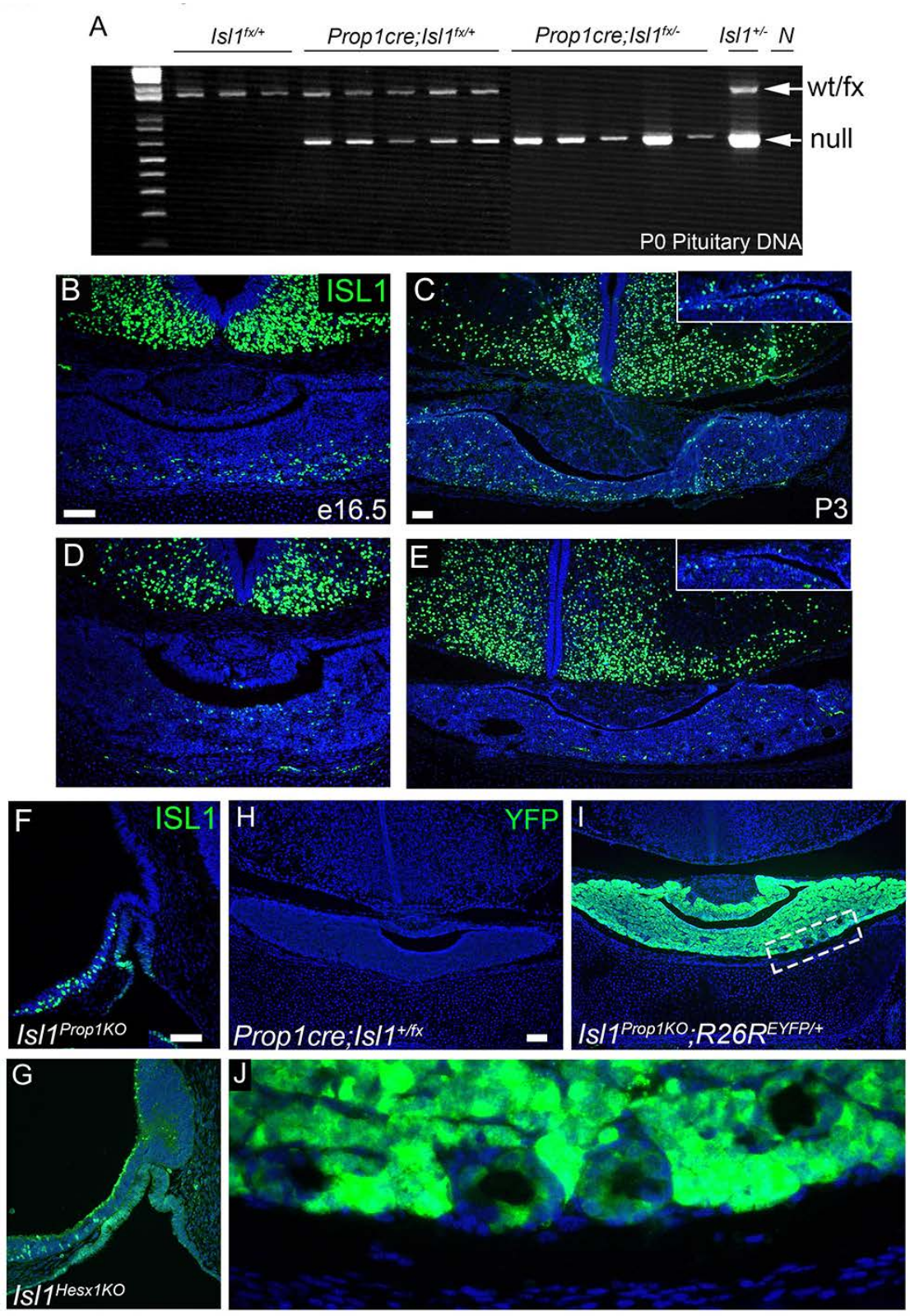
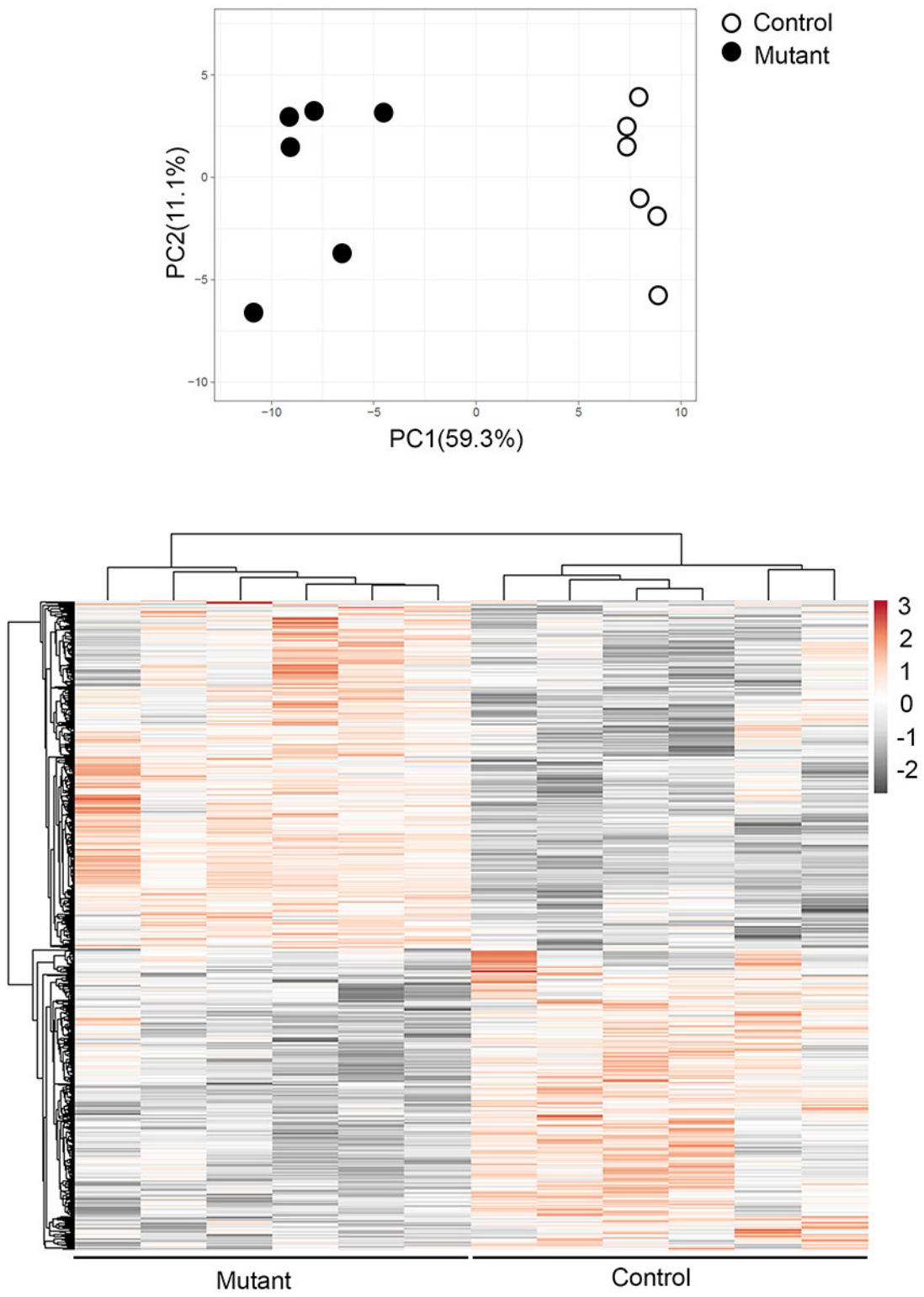
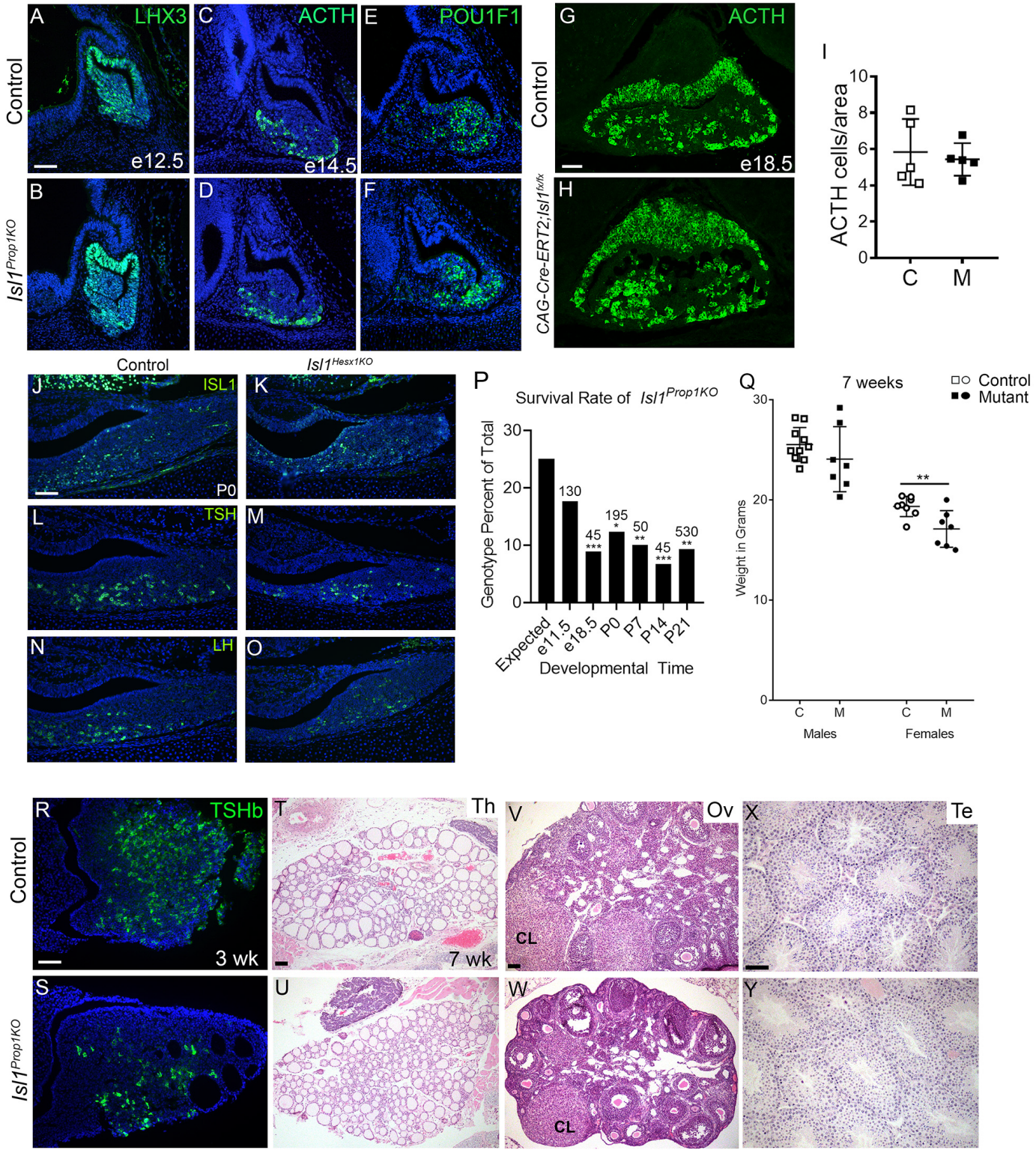


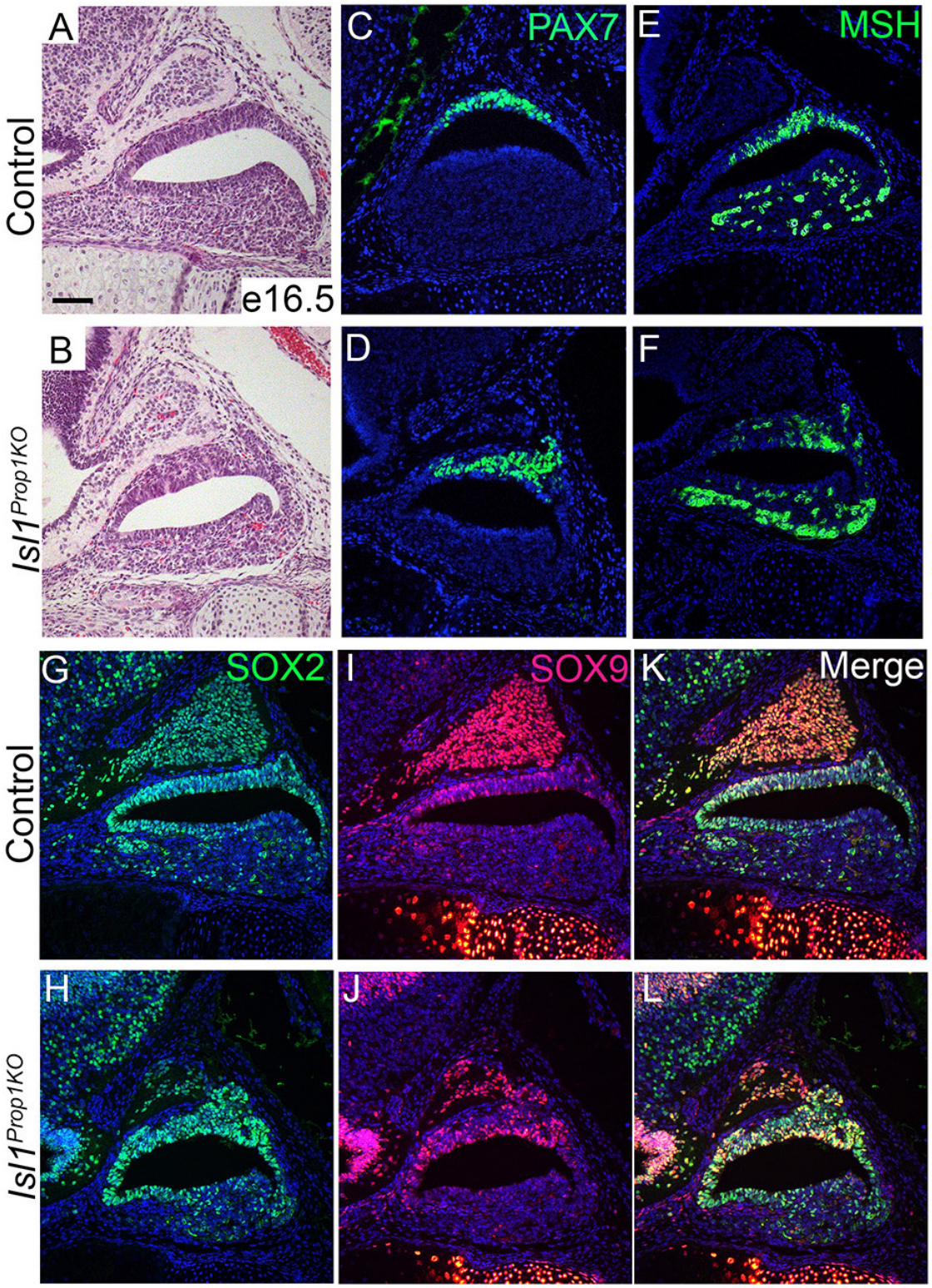
Supplemental Figure 1. Prop1cre effectively deletes Isl1fx in the pituitary gland. (A) PCR on DNA from P0 pituitary glands amplifies an approximately 1600bp fragment representing the *Isl1fx* and *Isl1* wild type alleles plus a 478bp fragment representing the *Isl1null* allele demonstrates the loss of the *Isl1 wt/fx* allele in the *Prop1cre;Isl1*$^{fx/-}$ mutants. **(B-E)** Prominent ISL1 protein expression is detected in control mice at e16.5 and P3. A significant reduction in ISL1 expression is observed at e16.5 progressing to a complete loss at P3 in the *Isl1*^{Prop1KO} mice. **(F, G)** ISL1 protein is reduced in both *Isl1*^{Prop1KO} (F) and *Isl1*^{Hesx1KO} (G) mutants at e11.5. **(H, I)** YFP immunostaining was not detected in control pituitary glands at P0 (H) but was prominent in all cells of *Isl1*^{Prop1KO}*;R26R*$^{EYFP/+}$ mutants (I) including cysts. **(J)** Higher magnification of boxed region in I. The scale bar in panel B and F represents 50μm and is applicable to panels B, D, F, G. The scale bar in panel C represents 50μm and is applicable to panels C, E, H, I.



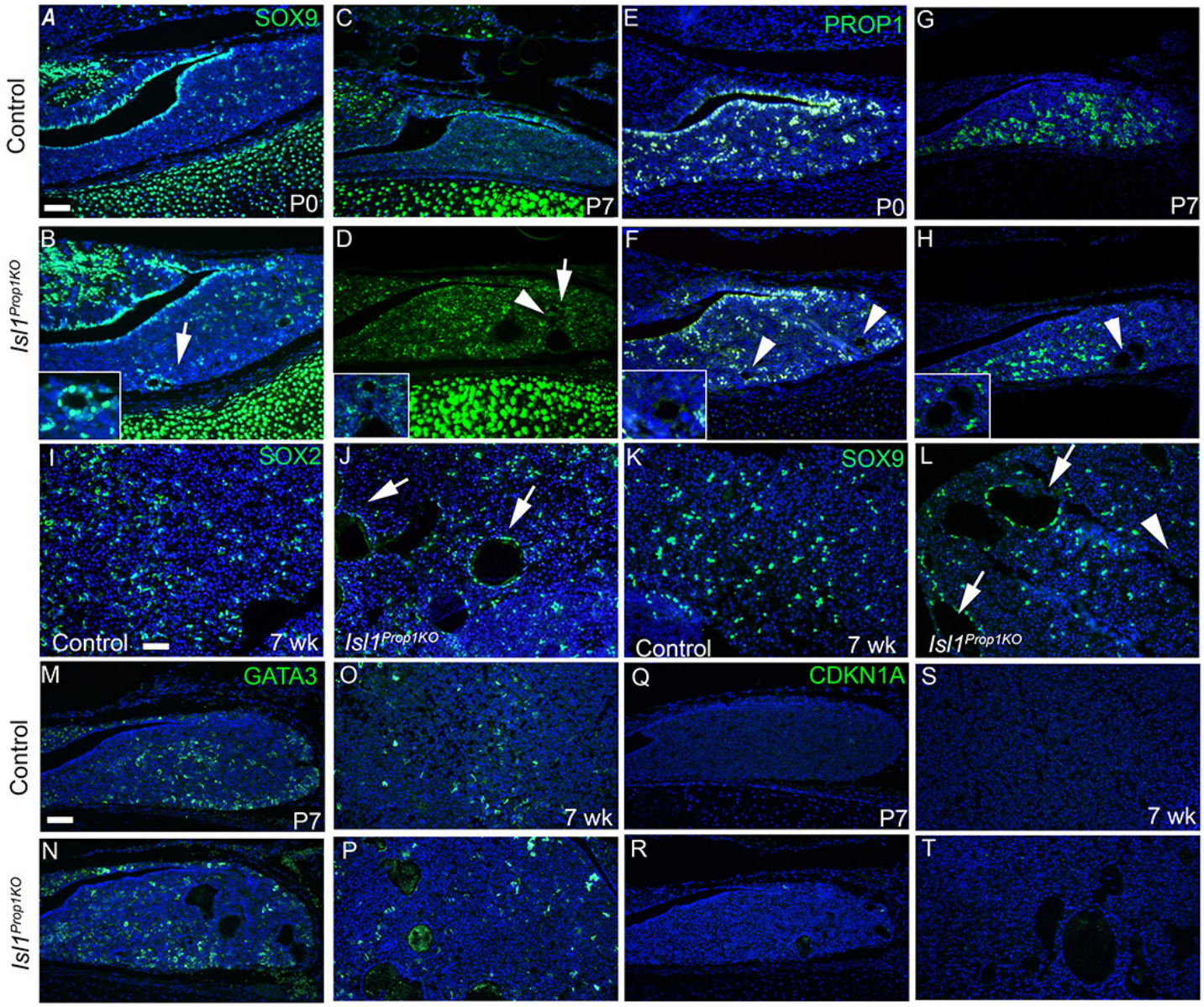
Supplemental Figure 2. Principal Component Analysis and heat map clustering of differentially expressed genes. (A) PCA was performed using ClustVis SVD with imputation and preprocessing ln(x+1) transformation. Principal components 1 and 2 explain 59.3% and 11.1% of the variance, respectively. **(B)** Heat map clustering of differentially expressed genes from 6 mutant and 6 control samples. Red indicates genes with elevated expression and grey indicates genes with reduced expression.



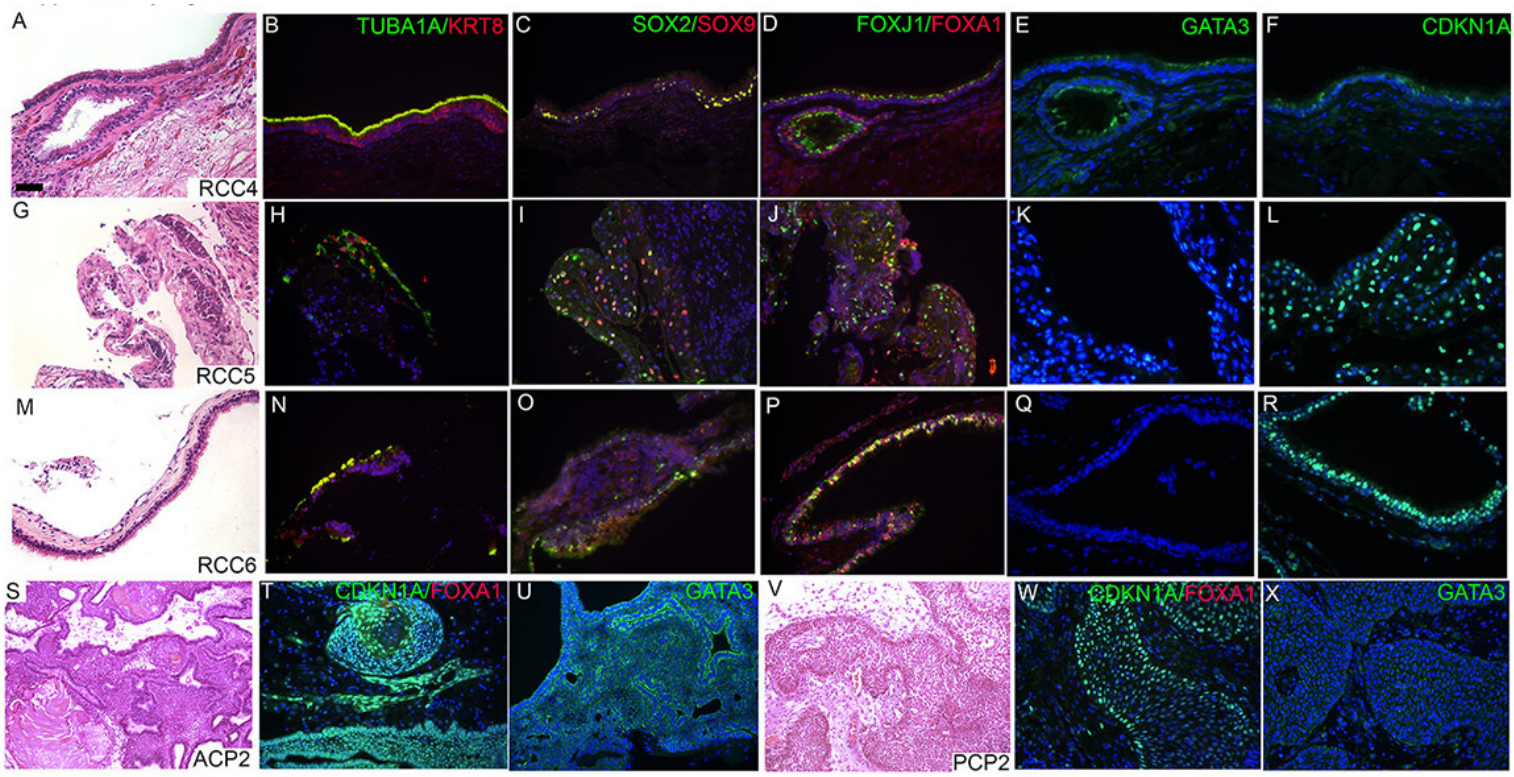
Supplemental Figure 3. Transient decrease in thyrotope and gonadotrope specification does not impact adult thyroid gland, ovary, or testis. **(A-F)** Protein expression of LHX3, ACTH, and POU1F1 were comparable between control and *Isl1*^{Prop1KO} embryos. **(G-I)** Inducible deletion of *Isl1* using the *CAGGCre-ERT2* did not alter specification of the corticotrope cell population. **(J-O)** Deletion of *Isl1*^{fx} using the *Hesx1-cre* resulted in variable deletion of ISL1 and reduced levels of TSH and LH. **(P)** *Isl1*^{Prop1KO} mice have reduced viability beginning in late embryonic stages. Total number of mice analyzed for each time point is listed and Chi Square analysis was used to determine the significance of distribution away from the expected Mendelian ratios. **(Q)** Weights of individual mice, male and female, are graphed for Control (C) and *Isl1*^{Prop1KO} mutants (M) at 7 weeks of age. The significance of weight variance was evaluated using the Student T test with one tail distribution and 2 sample unequal variance, and the female weights were significantly different. **(R,S)** TSHb protein expression is reduced in *Isl1*^{Prop1KO} mutants compared to controls at weaning. **(T-Y)** The transient decrease in thyrotrope and gonadotrope specification does not impact thyroid gland, ovary, or testis development. In addition, female mice are fertile. The scale bars represent 50μm and can be applied to adjacent panels.



Supplemental Figure 4. Cells of the developing intermediate lobe are properly specified in *Isl1*^{Prop1KO} mutants at e16.5. (A, B) H&E staining of sagittal sections highlights the dysmorpology of the developing intermediate lobe in the *Isl1*^{Prop1KO} mice compared to Controls. **(C, D)** PAX7 and **(E, F)** MSH were used as markers of intermediate lobe and are properly specified in *Isl1*^{Prop1KO} mutants. **(G-L)** Co-im-munostaining of SOX2 and SOX9 was used to analyze the pituitary stem cells, demonstrating no changes in *Isl1*^{Prop1KO} mice compared to controls. The scale bar in panel A represents 50μm and is applicable to panels A-L.



Supplemental Figure 5. Developing and mature cysts express a subset of progenitor cell markers. **(A-D)** SOX9 is transiently expressed in the cells lining the walls of forming cysts in *Isl1*^{Prop1KO} mutants at P0, however expression within the cyst wall remains only in a small subset of cells at P7. **(E-H)** PROP1 expression is not detected in the cells lining the cysts of *Isl1*^{Prop1KO} mutants at P0 or P7. **(I-L)** SOX2 and SOX9 expression is abundant in the cells lining the cyst walls in *Isl1*^{Prop1KO} mutants at 7 wks. **(M-P)** GATA3 is not expressed in the maturing *Isl1*^{Prop1KO} cysts at P7 or 7 wks. **(Q-T)** CDNK1A is not expressed in the maturing *Isl1*^{Prop1KO} cysts at P7 or 7 wks. Scale bars represent 50μm and apply to adjacent panels.



Supplemental Figure 6. Additional Human Rathke's Cleft Cysts confirm FOXA1 expression.
(A-R) Classification of human Rathke's cleft cyst samples was confirmed by staining with H&E to detect characteristic RCC morphology (A, G, M) and co-staining with antibodies for cytokeratin8 (KRT8) and acetylated tubulin (TUBA1A) (B, H, N) Co-staining with antibodies for progenitor markers SOX2 and SOX9 detected many positive cells (C, I, O). Co-staining with antibodies FOXJ1 and FOXA1 detected positive cells lining the cysts (D, J, P). Immunostaining for GATA3 was negative in all additional samples (E, K, Q). CDKN1A (F, L, R) detected positive cells lining the cysts in some, but not all additional samples. **(S-X)** Surgical samples from craniopharyngiomas of both the adamantinomatous (ACP) (S-U) and papillary (PCP) (V-X) subtypes were stained with H&E, co-stained for CDKN1A and FOXA1, and immunostained for GATA3. Samples were positive for CDKN1A and negative for both FOXA1 and GATA3. Magnification: scale bar in panel A corresponds to 50μm.

Supplemental Table 1: Stem Cell Markers unchanged in *Isl1*^{Prop1KO}	
Stem Cell Marker	**Fold Change**
Cadherin1, *Cdh1*	1.5x
Cyclin-dependent kinase inhibitor 2a, *Cdkn2a*	1.2x
SRY-box 2, *Sox2*	1.2x
S100 protein, beta peptide, *S100b*	1.2x
Paired related homeobox 2, *Prrx2*	1.1x
Lymphocyte antigen 6 complex locus A, *Ly6a*	1.1x
Beta catenin, *Ctnnb1*	1.0x
Paired like homeodomain factor 1, *Prop1*	1.0x
Caspase 3, *Casp3*	1.0x
SRY-box 9, *Sox9*	1.0x
Coxsackie virus and adenovirus receptor, *Cxadr*	1.0x
Glial cell line derived neurotrophic factor family receptor alpha 1, *Gfra1*	0.9x
Paired related homeobox 1, *Prrx1*	0.9x
Glial cell line derived neurotrophic factor family receptor alpha 2, *Gfra2*	0.9x
Neuronatin, *Nnat*	0.9x
Glial cell line derived neurotrophic factor family receptor alpha 4, *Gfra4*	0.9x
Nestin, *Nes*	0.9x
LIM homeobox protein 3, *Lhx3*	0.9x
Ret proto-oncogene, *Ret*	0.8x

Supplemental Table 2: Gene Ontology Terms Associated With Elevated Gene Expression in *Isl1*^{Prop1KO}

Database ID	Category	#Genes/Total	Fold Change	P Value
GO: 0005576	Extracellular Region	92/351	2.0	1.52-10
GO: 0006811	Ion Transport	47/366	2.5	2.71E-08
GO: 0005886	Plasma Membrane	121/351	1.5	1.31E-06
GO:0030855	**Epithelial Cell Differentiation**	**15/366**	**4.5**	**5.40E-06**
GO:0022803	Passive Transmembrane Transporter Activity	27/363	2.7	7.81E-06
GO:0015267	Channel Activity	27/363	2.7	7.81E-06
GO: 0022838	Substrate Specific Channel Activity	26/363	2.6	1.80E-05
GO: 0030594	Neurotransmitter Receptor Activity	12/363	5.0	2.31E-05
GO: 0006812	Cation Transport	32/366	2.3	2.36E-05
GO: 0030001	Metal Ion Transport	29/366	2.4	2.36E-05
PIRSF001630	Serpin	10/253	6.1	3.06E-05
PIRSF002282	Cytoskeletal Keratin	10/253	6.1	3.06E-05
GO: 0004857	Enzyme Inhibitor Activity	20/363	3.0	3.78E-05
GO: 0060429	**Epithelium Development**	**21/366**	**2.9**	**4.50E-05**
GO: 0042573	Retinoic Acid Metabolic Process	6/366	13.1	6.45E-05
GO: 0030414	Peptidase Inhibitor Activity	16/363	3.3	9.45E-05
GO: 0016324	Apica Plasma Membrane	12/351	4.3	9.85E-05
IPR000215	Protease Inhibitor I4, Serpin	10/493	5.2	1.17E-04
IPR016044	**Filament**	**10/493**	**5.1**	**1.29E-04**
GO: 0046873	Metal Ion Transmembrane Transporter	21/363	2.7	1.37E-04
GO: 0034702	Ion Channel Complex	15/351	3.4	1.40E-04
GO: 0042445	Hormone Metabolic Process	11/366	4.5	1.46E-04
GO: 0003700	**Transcription Factor Activity**	**40/363**	**1.9**	**1.58E-04**
IPR001664	**Intermediate Filament Protein**	**10/493**	**5.0**	**1.60E-04**
IPR001314	Peptidase S1A, Chymotrypsin	14/493	3.5	1.75E-04
GO: 0006833	Water Transport	5/366	15.5	2.14E-04
GO: 0042044	Fluid Transport	5/366	15.5	2.14E-04
GO: 0005216	Ion Channel Activity	23/363	2.4	2.33E-04
GO: 0022836	Gated Channel Activity	20/363	2.6	2.85E-04
GO: 0048568	**Embryonic Organ Development**	**18/366**	**2.8**	**2.81E-04**
GO: 0004867	Serine-Type Endopeptidase Inhibitor Activity	12/363	3.8	2.98E-04
GO:0005261	Cation Channel Activity	18/363	2.7	4.59E-04
IPR001254	Peptidase S1 and S6, Chymotrypsin/Hap	14/493	3.2	4.92E-04
GO: 0008188	Neuropeptide Receptor Activity	7/363	6.7	5.18E-04
GO: 0006776	Vitamin A Metabolic Process	6/366	8.6	5.62E-04
GO: 0043565	Sequence Specific DNA Binding	30/363	2.0	6.28E-04
GO: 0010817	Regulation of Hormone Level	12/366	3.5	6.65E-04
GO: 0008236	Serine-Type Peptidase Activity	16/363	2.8	7.10E-04
GO: 0016101	Diterpenoid Metabolic Process	6/366	8.0	8.03E-04
GO: 0001523	Retinoid Metabolic Process	6/366	8.0	8.03E-04
IPR001846	von Willebrand Factor, Type D	5/493	11.3	8.12E-04
GO: 0048732	**Gland development**	**15/366**	**2.8**	**8.90E-04**
GO: 0006721	Terpenoid Metabolic Process	6/366	7.7	9.50E-04
IPR001766	**Transcription factor, forkhead**	**7/493**	**6.0**	**9.80E-04**
GO: 0044421	Extracellular Region Part	38/351	1.7	9.90E-04
IPR016054	Ly-6 Antigen/uPA Receptor-Like	6/493	1.7	1.09E-03
GO: 0043068	**Postive Regulation of Programmed Cell Death**	**17/366**	**2.5**	**1.20E-03**
GO: 0015672	Monovalent Inorganic Cation Transport	19/366	2.4	1.43E-03
GO:0005929	**Cilium**	**12/351**	**3.2**	**1.40E-03**
GO: 0042277	Peptide Binding	13/363	3.0	1.44E-03
GO: 0045177	Apical Part of Cell	12/351	3.1	1.52E-03
GO: 0004866	Endopeptidase Inhibitor Activity	13/363	3.0	1.52E-03
GO: 0031420	Alkali Metal Ion Binding	15/363	2.7	1.55E-03
GO: 0030216	**Keratinocyte Differentiation**	**7/366**	**5.4**	**1.71E-03**
IPR002957	**Keratin, type I**	**6/493**	**6.8**	**1.70E-03**
GO: 0007605	Sensory Perception of Sound	9/366	4.0	1.85E-03
GO: 0006775	Fat Soluble Vitamin Metabolic Process	6/366	6.6	1.90E-03
GO: 0004252	Serine-type Endopeptidase Activity	14/363	2.7	2.04E-03
GO: 0048878	Chemical Homeostasis	21/366	2.1	2.08E-03
IPR006208	Cystine Knot	4/493	14.4	2.19E-03
GO: 0044447	Axoneme Part	4/351	14.3	2.25E-03
IPR006788	Myelin-Associated Oligodendryocytic Basic Protein	3/493	36.0	2.25E-03
GO: 0009913	**Epidermal Cell Differentiation**	**7/366**	**5.1**	**2.30E-03**

Supplemental Table 3: Differentially Expressed Genes in Pituitaries of *Isl1* ^{Prop1KO} vs Wild Type Mice

Test_id	Gene	Description	WT value	MUT value	log2(fold_change)	Test_stat	p_value	q_value	Fold Change	Diff Exp
NM_011260	Reg3g	regenerating islet-derived 3 gamma	0.32113	24.3996	6.25	13.351	5E-05	0.0017	75.98	YES
ENSMUSG00000097554.1	Gm26825		0.12563	6.25452	5.64	6.366	5E-05	0.0017	49.79	YES
NM_010844	Muc5ac	mucin 5, subtypes A and C, tracheobronchial/gastric	0.01751	0.838883	5.58	8.130	5E-05	0.0017	47.90	YES
NM_172905	E030002O03	olfactomedin 5	0.35702	17.0605	5.58	13.920	5E-05	0.0017	47.79	YES
NM_028801	Muc5b	mucin 5, subtype B, tracheobronchial	0.03377	1.58407	5.55	11.895	5E-05	0.0017	46.91	YES
NM_008469	Krt15	keratin 15	0.41957	15.7041	5.23	12.129	5E-05	0.0017	37.43	YES
NM_001164437	Tmem212	transmembrane protein 212	0.20767	6.5558	4.98	8.881	5E-05	0.0017	31.57	YES
NM_027011	Krt5	keratin 5	0.20072	6.30251	4.97	9.559	5E-05	0.0017	31.40	YES
NM_013473	Anxa8	annexin A8	0.15356	4.19007	4.77	7.720	5E-05	0.0017	27.29	YES
NM_177624	Sntn	sentan, cilia apical structure protein	0.09789	2.56887	4.71	7.249	5E-05	0.0017	26.24	YES
NM_001034037	1700024G13	RIKEN cDNA 1700024G13 gene	0.21847	5.26373	4.59	7.843	5E-05	0.0017	24.09	YES
NM_001081284	Gm12695	predicted gene 12695	0.05166	1.1463	4.47	5.207	5E-05	0.0017	22.19	YES
NM_001037914	Gm6320	multiciliate differentiation and DNA synthesis associated cell cycle protein	0.08659	1.72309	4.31	7.056	5E-05	0.0017	19.90	YES
NM_013501	Cryaa	crystallin, alpha A	0.02052	0.408056	4.31	2.564	5E-05	0.0017	19.89	YES
NM_001170705	Gm17384	death domain containing 1	0.02106	0.415556	4.30	3.759	5E-05	0.0017	19.73	YES
NM_001081372	Ces1b	carboxylesterase 1B	0.01293	0.245613	4.25	2.559	5E-05	0.0017	19.00	YES
NM_010742	Ly6d	lymphocyte antigen 6 complex, locus D	0.12164	2.2642	4.22	5.943	5E-05	0.0017	18.61	YES
NM_145423	Slc5a8	solute carrier family 5 (iodide transporter), member 8	0.07029	1.20152	4.10	8.335	5E-05	0.0017	17.09	YES
NM_029306	1700012B09	RIKEN cDNA 1700012B09 gene	0.24907	4.17481	4.07	7.235	5E-05	0.0017	16.76	YES
NM_001195662	Rp1	retinitis pigmentosa 1 (human)	0.01398	0.234045	4.07	1.891	0.002	0.0404	16.74	YES
NM_177629	AU021034	family with sequence similarity 216, member B	0.12397	2.04272	4.04	5.221	5E-05	0.0017	16.48	YES
NM_027077	1700016C15	RIKEN cDNA 1700016C15 gene	0.0367	0.571828	3.96	2.670	5E-05	0.0017	15.58	YES
NM_177702	4833427G06	RIKEN cDNA 4833427G06 gene	0.20863	3.1943	3.94	6.917	5E-05	0.0017	15.31	YES
NM_013688	Tcte1	t-complex-associated testis expressed 1	0.07761	1.14605	3.88	2.564	0.0002	0.0058	14.77	YES
NM_175030	Tctex1d4	Tctex1 domain containing 4	0.16745	2.4697	3.88	2.889	0.0003	0.0082	14.75	YES
NM_010662	Krt13	keratin 13	0.05603	0.800941	3.84	4.220	5E-05	0.0017	14.29	YES
NM_030187	Ak7	adenylate kinase 7	0.20982	2.95103	3.81	8.702	5E-05	0.0017	14.06	YES
NM_008259	Foxa1	forkhead box A1	0.26813	3.51919	3.71	9.283	5E-05	0.0017	13.12	YES
ENSMUSG00000086868.1	Gm15883	predicted gene 15883	0.21424	2.77712	3.70	6.115	5E-05	0.0017	12.96	YES
NM_001013759	Gas2l2	growth arrest-specific 2 like 2	0.04217	0.524458	3.64	4.613	5E-05	0.0017	12.44	YES
NM_007817	Cyp2f2	cytochrome P450, family 2, subfamily f, polypeptide 2	2.53207	30.9566	3.61	11.272	5E-05	0.0017	12.23	YES
NM_009363	Tff2	trefoil factor 2 (spasmolytic protein 1)	0.20092	2.44539	3.61	6.025	5E-05	0.0017	12.17	YES
NM_027997	Serpina9	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, an	0.07185	0.868358	3.60	5.027	5E-05	0.0017	12.09	YES
NM_001013767	Capn11	calpain 11	0.04134	0.497093	3.59	4.223	5E-05	0.0017	12.03	YES
NM_018857	Msln	mesothelin	0.88413	10.5914	3.58	10.845	5E-05	0.0017	11.98	YES
NM_020051	Ascl3	achaete-scute complex homolog 3 (Drosophila)	0.21838	2.60555	3.58	6.320	5E-05	0.0017	11.93	YES
NM_007621	Cbr2	carbonyl reductase 2	7.5602	87.4552	3.53	17.401	5E-05	0.0017	11.57	YES
NM_001029937	Sec14l3	SEC14-like lipid binding 3	0.53677	6.17469	3.52	10.971	5E-05	0.0017	11.50	YES
NM_027963	Wdr16	cilia and flagella associated protein 52	0.2957	3.39214	3.52	3.919	5E-05	0.0017	11.47	YES
NM_009402	Pglyrp1	peptidoglycan recognition protein 1	1.62341	18.5899	3.52	11.419	5E-05	0.0017	11.45	YES
NM_009160	Sftpd	surfactant associated protein D	0.20213	2.29829	3.51	6.093	5E-05	0.0017	11.37	YES
NM_029816	2610028H24	RIKEN cDNA 2610028H24 gene	0.34939	3.80312	3.44	2.120	0.0008	0.0181	10.88	YES
NM_009264	Sprr1a	small proline-rich protein 1A	0.13017	1.41621	3.44	4.744	5E-05	0.0017	10.88	YES
NM_183096	Ttc29	tetratricopeptide repeat domain 29	0.11875	1.2759	3.43	6.312	5E-05	0.0017	10.74	YES
NM_029639	1600029D21	placenta expressed transcript 1	0.48726	5.14635	3.40	7.682	5E-05	0.0017	10.56	YES
NM_153576	Cxcl17	chemokine (C-X-C motif) ligand 17	0.49767	5.25503	3.40	2.644	0.0009	0.0201	10.56	YES
NM_001042715	Ccdc135	dynein regulatory complex subunit 7	0.12529	1.31443	3.39	6.496	5E-05	0.0017	10.49	YES
NM_001040700	BC051019	cDNA sequence BC051019	0.24013	2.45353	3.35	3.404	5E-05	0.0017	10.22	YES
NM_023655	Trim29	tripartite motif-containing 29	0.05855	0.56411	3.27	4.790	5E-05	0.0017	9.64	YES
NM_148935	Foxn4	forkhead box N4	0.09567	0.914988	3.26	5.642	5E-05	0.0017	9.56	YES
NM_001024478	Cdhr3	cadherin-related family member 3	0.20662	1.97392	3.26	7.113	5E-05	0.0017	9.55	YES
NM_001254953	D730048J04	ankyrin repeat domain 66	0.06233	0.580455	3.22	3.833	5E-05	0.0017	9.31	YES
NM_178594	Vtcn1	V-set domain containing T cell activation inhibitor 1	0.06851	0.637727	3.22	4.907	5E-05	0.0017	9.31	YES
NM_008522	Ltf	lactotransferrin	0.5384	4.90931	3.19	9.000	5E-05	0.0017	9.12	YES
NM_207280	Ccdc121	coiled-coil domain containing 121	0.15332	1.38688	3.18	5.705	5E-05	0.0017	9.05	YES
NM_178387	Spata18	spermatogenesis associated 18	0.88704	8.01425	3.18	9.588	5E-05	0.0017	9.03	YES
NM_146017	Gabrp	gamma-aminobutyric acid (GABA) A receptor, pi	0.33786	3.01899	3.16	8.297	5E-05	0.0017	8.94	YES
NM_007812	Cyp2a5	cytochrome P450, family 2, subfamily a, polypeptide 5	0.24792	2.11865	3.10	6.362	5E-05	0.0017	8.55	YES
NM_001081272	Ldlrad1	low density lipoprotein receptor class A domain containing 1	0.08286	0.666719	3.01	3.765	5E-05	0.0017	8.05	YES
NM_172799	Ttll6	tubulin tyrosine ligase-like family, member 6	0.10128	0.803138	2.99	5.430	5E-05	0.0017	7.93	YES
NM_007969	Expi	WAP four-disulfide core domain 18	0.1801	1.42497	2.98	4.728	5E-05	0.0017	7.91	YES
NM_023907	Foxi1	forkhead box I1	0.15225	1.18351	2.96	5.680	5E-05	0.0017	7.77	YES
NM_001012704	Wfdc13	WAP four-disulfide core domain 13	0.09814	0.757104	2.95	4.058	5E-05	0.0017	7.71	YES
NM_029335	1700026D08	cilia and flagella associated protein 161	0.35985	2.74959	2.93	6.337	5E-05	0.0017	7.64	YES
NM_028618	Dmkn	dermokine	0.49323	3.70575	2.91	3.440	5E-05	0.0017	7.51	YES
NM_029638	Abp1	amine oxidase, copper-containing 1	0.05729	0.42529	2.89	2.129	0.0022	0.0436	7.42	YES
NM_175370	Als2cr12	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 12	0.03345	0.247998	2.89	2.835	0.0001	0.0031	7.42	YES
NM_198660	E230008N13	coiled-coil domain containing 180	0.16758	1.21844	2.86	6.623	5E-05	0.0017	7.27	YES
NM_177024	Tmprss11bn	transmembrane protease, serine 11B	0.13613	0.973455	2.84	5.313	5E-05	0.0017	7.15	YES
NM_173052	Serpinb1b	serine (or cysteine) peptidase inhibitor, clade B, member 1b	0.09607	0.672253	2.81	4.210	5E-05	0.0017	7.00	YES
NM_008963	Ptgds	prostaglandin D2 synthase (brain)	13.9987	97.9047	2.81	10.984	5E-05	0.0017	6.99	YES
NM_008475	Krt4	keratin 4	1.11375	7.74191	2.80	8.798	5E-05	0.0017	6.95	YES
NM_009474	Uox	urate oxidase	0.14104	0.96938	2.78	3.920	5E-05	0.0017	6.87	YES
NM_001105252	Tmc5	transmembrane channel-like gene family 5	0.18449	1.26222	2.77	5.840	5E-05	0.0017	6.84	YES
NM_001178038	Fmo6	flavin containing monooxygenase 6	0.08757	0.58073	2.73	4.048	5E-05	0.0017	6.63	YES
NM_029195	Ccdc146	coiled-coil domain containing 146	0.29581	1.96146	2.73	2.761	5E-05	0.0017	6.63	YES
NM_172916	Hydin	HYDIN, axonemal central pair apparatus protein	0.15192	0.996715	2.71	8.004	5E-05	0.0017	6.56	YES
NM_001207021	Al848285	shisa family member 8	0.10914	0.70188	2.69	4.254	5E-05	0.0017	6.43	YES
NM_001165957	Txndc6	NME/NM23 family member 9	0.78359	4.9939	2.67	2.127	0.0017	0.0352	6.37	YES
NM_029309	Morn5	MORN repeat containing 5	0.73231	4.53571	2.63	6.576	5E-05	0.0017	6.19	YES
NM_133365	Dnahc5	dynein, axonemal, heavy chain 5	0.28704	1.76706	2.62	9.352	5E-05	0.0017	6.16	YES
NM_001081369	Ccdc153	coiled-coil domain containing 153	1.77384	10.8497	2.61	8.382	5E-05	0.0017	6.12	YES
NM_175223	Dnali1	dynein, axonemal, light intermediate polypeptide 1	0.70419	4.29088	2.61	2.171	5E-05	0.0017	6.09	YES
NM_172864	Wdr63	WD repeat domain 63	0.5166	3.13371	2.60	7.219	5E-05	0.0017	6.07	YES
NM_027416	Calml3	calmodulin-like 3	0.13352	0.806395	2.59	4.101	5E-05	0.0017	6.04	YES
NM_013588	Lrrc23	leucine rich repeat containing 23	3.06304	18.4099	2.59	10.128	5E-05	0.0017	6.01	YES
NM_029112	Morn3	MORN repeat containing 3	0.3197	1.91045	2.58	5.026	5E-05	0.0017	5.98	YES
NM_010389	H2-Ob	histocompatibility 2, O region beta locus	0.06616	0.385742	2.54	3.723	5E-05	0.0017	5.83	YES
NM_206974	Kcnrg	potassium channel regulator	0.35398	2.05921	2.54	1.954	0.0003	0.007	5.82	YES
NM_017370	Hp	haptoglobin	0.76272	4.41105	2.53	6.696	5E-05	0.0017	5.78	YES
NM_019992	Stap1	signal transducing adaptor family member 1	0.18597	1.05696	2.51	4.216	5E-05	0.0017	5.68	YES
NM_145403	Tmprss4	transmembrane protease, serine 4	0.0898	0.509524	2.50	3.278	5E-05	0.0017	5.67	YES
NM_001081062	Ccno	cyclin O	0.67179	3.79096	2.50	6.858	5E-05	0.0017	5.64	YES
NM_001033461	Lrrc43	leucine rich repeat containing 43	0.18045	0.984172	2.45	4.572	5E-05	0.0017	5.45	YES
NM_001195672	Gm221	coiled-coil domain containing 170	0.12363	0.672357	2.44	4.068	5E-05	0.0017	5.44	YES
NM_011783	Agr2	anterior gradient 2	0.86925	4.72292	2.44	6.299	5E-05	0.0017	5.43	YES
NM_001013022	Odf3b	outer dense fiber of sperm tails 3B	0.99701	5.34818	2.42	6.615	5E-05	0.0017	5.36	YES
NM_001013373	Tmprss13	transmembrane protease, serine 13	0.11724	0.616212	2.39	4.160	5E-05	0.0017	5.26	YES
NM_146117	Lrrc26	leucine rich repeat containing 26	0.55415	2.90021	2.39	2.070	0.0011	0.0243	5.23	YES
NM_030701	Niacr1	hydroxycarboxylic acid receptor 2	0.0859	0.44468	2.37	3.487	5E-05	0.0017	5.18	YES
ENSMUSG00000033731.3	3300002A11	RIKEN cDNA 3300002A11 gene	0.08134	0.419785	2.37	2.899	5E-05	0.0017	5.16	YES
NM_019536	Dnahc10	dynein, axonemal, heavy chain 10	0.37889	1.92848	2.35	8.565	5E-05	0.0017	5.09	YES
NM_001008973	Tmem232	transmembrane protein 232	0.32071	1.61888	2.34	5.524	5E-05	0.0017	5.05	YES
NM_001017419	Tbata	thymus, brain and testes associated	0.11539	0.571014	2.31	2.449	5E-05	0.0017	4.95	YES

NM_001081665	Ccdc129	coiled-coil domain containing 129	0.05773	0.284073	2.30	3.347	5E-05	0.0017	4.92	YES
NM_001033170	Fam83e	family with sequence similarity 83, member E	0.07351	0.359156	2.29	3.336	5E-05	0.0017	4.89	YES
NR_028280	Prr18	proline rich 18	0.34909	1.68387	2.27	2.939	5E-05	0.0017	4.82	YES
NM_001164669	Dnahc6	dynein, axonemal, heavy chain 6	0.34428	1.65556	2.27	7.907	5E-05	0.0017	4.81	YES
NM_009257	Serpinb5	serine (or cysteine) peptidase inhibitor, clade B, member 5	0.13276	0.636574	2.26	4.163	5E-05	0.0017	4.80	YES
NM_024445	Tsnaxip1	translin-associated factor X (Tsnax) interacting protein 1	0.42815	2.02409	2.24	5.395	5E-05	0.0017	4.73	YES
ENSMUSG00000085967.1	Gm12530	predicted gene 12530	0.04941	0.23188	2.23	3.083	5E-05	0.0017	4.69	YES
NM_053259	Prss28	protease, serine 28	0.93893	4.40576	2.23	6.043	5E-05	0.0017	4.69	YES
NM_172564	Tns4	tensin 4	0.08924	0.416757	2.22	4.151	5E-05	0.0017	4.67	YES
NM_001034878	Dnaic2	dynein, axonemal, intermediate chain 2	0.60596	2.79898	2.21	1.645	0.0003	0.0082	4.62	YES
NM_008766	Slc22a6	solute carrier family 22 (organic anion transporter), member 6	0.07205	0.332531	2.21	3.324	5E-05	0.0017	4.62	YES
NM_030677	Gpx2	glutathione peroxidase 2	0.16617	0.765442	2.20	3.527	5E-05	0.0017	4.61	YES
NM_130452	Bbox1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase 1 (gamma-butyrobeta	0.13745	0.62949	2.20	3.593	5E-05	0.0017	4.58	YES
NM_080457	Muc4	mucin 4	0.45223	2.0443	2.18	7.347	5E-05	0.0017	4.52	YES
NM_026907	Sectm1b	secreted and transmembrane 1B	0.13834	0.625026	2.18	3.851	5E-05	0.0017	4.52	YES
NM_145451	Gpx6	glutathione peroxidase 6	0.0832	0.372676	2.16	2.844	5E-05	0.0017	4.48	YES
NM_177243	Slc26a9	solute carrier family 26, member 9	0.04775	0.211421	2.15	3.027	5E-05	0.0017	4.43	YES
ENSMUST00000153562.1	Gm15883	predicted gene 15883	0.72502	3.19683	2.14	2.065	5E-05	0.0017	4.41	YES
NM_001195036	Ect2l	epithelial cell transforming sequence 2 oncogene-like	0.18572	0.814657	2.13	4.327	5E-05	0.0017	4.39	YES
NM_025393	S100a14	S100 calcium binding protein A14	0.92437	3.93443	2.09	4.397	5E-05	0.0017	4.26	YES
NM_144828	Ppp1r1b	protein phosphatase 1, regulatory (inhibitor) subunit 1B	0.48308	2.01603	2.06	4.634	5E-05	0.0017	4.17	YES
NM_033373	Krt23	keratin 23	0.30058	1.24899	2.05	4.108	5E-05	0.0017	4.16	YES
NM_198637	1700016K19	RIKEN cDNA 1700016K19 gene	1.39891	5.71498	2.03	5.911	5E-05	0.0017	4.09	YES
NM_020047	Tacstd2	tumor-associated calcium signal transducer 2	1.21905	4.87371	2.00	6.189	5E-05	0.0017	4.00	YES
NM_001166282	Ccdc33	coiled-coil domain containing 33	0.16815	0.671853	2.00	2.383	5E-05	0.0017	4.00	YES
NM_026648	Lrrc50	dynein, axonemal assembly factor 1	0.36017	1.42913	1.99	2.148	5E-05	0.0017	3.97	YES
NM_027951	Tekt4	tektin 4	0.78843	3.11769	1.98	5.202	5E-05	0.0017	3.95	YES
NM_008471	Krt19	keratin 19	8.09104	31.9352	1.98	9.544	5E-05	0.0017	3.95	YES
NM_028064	Slc39a4	solute carrier family 39 (zinc transporter), member 4	0.38255	1.50261	1.97	4.599	5E-05	0.0017	3.93	YES
NM_001048175	Adam28	a disintegrin and metallopeptidase domain 28	0.15984	0.627238	1.97	3.202	5E-05	0.0017	3.92	YES
NM_001039495	Ccdc108	coiled-coil domain containing 108	1.46773	5.7491	1.97	7.916	5E-05	0.0017	3.92	YES
NM_010730	Anxa1	annexin A1	14.2035	54.5104	1.94	10.629	5E-05	0.0017	3.84	YES
NM_029053	4930451C15	leucine rich repeat containing 74B	0.74044	2.8254	1.93	3.076	5E-05	0.0017	3.82	YES
NM_027972	Ccdc19	cilia and flagella associated protein 45	0.82278	3.12909	1.93	3.257	5E-05	0.0017	3.80	YES
NM_177656	6820408C15	RIKEN cDNA 6820408C15 gene	0.88638	3.36077	1.92	5.228	5E-05	0.0017	3.79	YES
NM_178924	Upk1b	uroplakin 1B	0.18395	0.696552	1.92	3.488	5E-05	0.0017	3.79	YES
NM_001100177	Calcoco2	calcium binding and coiled-coil domain 2	0.11665	0.440448	1.92	2.417	5E-05	0.0017	3.78	YES
NM_008241	Foxg1	forkhead box G1	0.43091	1.6203	1.91	3.642	5E-05	0.0017	3.76	YES
NM_001160265	Cyp2w1	cytochrome P450, family 2, subfamily w, polypeptide 1	0.21615	0.811956	1.91	3.525	5E-05	0.0017	3.76	YES
NM_007843	Defb1	defensin beta 1	0.26872	1.00558	1.90	3.403	5E-05	0.0017	3.74	YES
NM_001145953	Lgals3	lectin, galactose binding, soluble 3	1.28988	4.6955	1.86	1.735	5E-05	0.0017	3.64	YES
NM_197999	Ces2g	carboxylesterase 2G	0.35528	1.28704	1.86	4.436	5E-05	0.0017	3.62	YES
NM_177894	Fam154b	stablizer of axonemal microtubules 2	1.21287	4.3855	1.85	6.295	5E-05	0.0017	3.62	YES
NM_001243018	E030019B06	cilia and flagella associated protein 46	0.33252	1.2011	1.85	3.874	5E-05	0.0017	3.61	YES
NM_001160112	Foxg1	forkhead box G1	0.16028	0.570695	1.83	2.228	5E-05	0.0017	3.56	YES
NM_054037	Scgb3a1	secretoglobin, family 3A, member 1	0.45641	1.61446	1.82	1.719	0.0012	0.0262	3.54	YES
NM_001145874	Muc20	mucin 20	0.15255	0.539492	1.82	1.622	0.0008	0.0191	3.54	YES
NM_153156	Stoml3	stomatin (Epb7.2)-like 3	0.23837	0.814031	1.77	2.980	5E-05	0.0017	3.42	YES
NM_027158	2310043J07	uroplakin 3B-like	0.36827	1.25669	1.77	3.526	5E-05	0.0017	3.41	YES
NM_007677	Psg17	pregnancy specific glycoprotein 17	0.26111	0.890421	1.77	3.466	5E-05	0.0017	3.41	YES
NM_133689	Ppp1r32	protein phosphatase 1, regulatory subunit 32	0.92524	3.15414	1.77	4.696	5E-05	0.0017	3.41	YES
NM_008491	Lcn2	lipocalin 2	2.69556	9.16571	1.77	6.072	5E-05	0.0017	3.40	YES
NM_001163103	Ppp1r36	protein phosphatase 1, regulatory subunit 36	0.72311	2.45798	1.77	4.465	5E-05	0.0017	3.40	YES
NM_026188	1700028P14	RIKEN cDNA 1700028P14 gene	0.68016	2.29884	1.76	4.105	5E-05	0.0017	3.38	YES
NM_198029	Fermt1	fermitin family homolog 1 (Drosophila)	0.14404	0.483998	1.75	3.716	5E-05	0.0017	3.36	YES
NM_007695	Chi3l1	chitinase-like 1	0.37445	1.24908	1.74	3.713	5E-05	0.0017	3.34	YES
NM_177921	E230019M04	PIH1 domain containing 3B	0.31134	1.03203	1.73	3.537	5E-05	0.0017	3.31	YES
NM_009701	Aqp5	aquaporin 5	0.10704	0.350709	1.71	2.508	5E-05	0.0017	3.28	YES
NM_178774	Prr18	proline rich 18	0.30764	1.00082	1.70	1.762	0.0003	0.0082	3.25	YES
NM_001163267	Ccdc147	cilia and flagella associated protein 58	0.19859	0.644161	1.70	3.452	5E-05	0.0017	3.24	YES
NM_001201332	2410004P03	RIKEN cDNA 2410004P03 gene	1.37081	4.43387	1.69	4.433	5E-05	0.0017	3.23	YES
NM_008557	Fxyd3	FXYD domain-containing ion transport regulator 3	1.37246	4.39927	1.68	1.598	0.0011	0.0243	3.21	YES
NM_007689	Chad	chondroadherin	1.30015	4.15601	1.68	1.804	5E-05	0.0017	3.20	YES
NM_011921	Aldh1a7	aldehyde dehydrogenase family 1, subfamily A7	0.94255	3.00495	1.67	4.857	5E-05	0.0017	3.19	YES
ENSMUSG00000089653.1	Gm15841		0.11271	0.355596	1.66	1.560	0.0005	0.0129	3.15	YES
NM_009759	Bmx	BMX non-receptor tyrosine kinase	0.32824	1.0284	1.65	3.910	5E-05	0.0017	3.13	YES
NM_013590	Lyz1	lysozyme 1	0.60629	1.86035	1.62	3.800	5E-05	0.0017	3.07	YES
NM_029659	Styxl1	serine/threonine/tyrosine interacting-like 1	0.39021	1.19626	1.62	3.516	5E-05	0.0017	3.07	YES
NM_001165929	Ccdc78	coiled-coil domain containing 78	1.20404	3.67993	1.61	2.269	5E-05	0.0017	3.06	YES
NM_001081643	Xlr3b	X-linked lymphocyte-regulated 3B	0.28164	0.857844	1.61	2.919	5E-05	0.0017	3.05	YES
NM_172641	9930023K05	pleckstrin homology domain containing, family S member 1	0.38201	1.15766	1.60	2.036	5E-05	0.0017	3.03	YES
NM_145551	Slc5a9	solute carrier family 5 (sodium/glucose cotransporter), member 9	0.16202	0.488446	1.59	3.352	5E-05	0.0017	3.01	YES
NM_007914	Ehf	ets homologous factor	1.83443	5.47669	1.58	6.488	5E-05	0.0017	2.99	YES
NM_018751	Sult1c1	sulfotransferase family, cytosolic, 1C, member 1	0.52285	1.54252	1.56	3.527	5E-05	0.0017	2.95	YES
NM_011359	Sftpc	surfactant associated protein C	0.76552	2.25109	1.56	3.724	5E-05	0.0017	2.94	YES
NR_033450	Serpina3h	serine (or cysteine) peptidase inhibitor, clade A, member 3H	0.11557	0.337889	1.55	2.235	5E-05	0.0017	2.92	YES
ENSMUST00000181713.1	Gm26717	predicted gene, 26717	0.15886	0.462628	1.54	1.758	0.0002	0.0058	2.91	YES
NM_001115074	Gm101	cilia and flagella associated protein 221	0.18363	0.53169	1.53	2.918	5E-05	0.0017	2.90	YES
NM_029946	Efcab6	EF-hand calcium binding domain 6	0.1823	0.52672	1.53	2.780	5E-05	0.0017	2.89	YES
NM_027948	1700003E16	RIKEN cDNA 1700003E16 gene	0.81447	2.34469	1.53	4.140	5E-05	0.0017	2.88	YES
NM_028892	Spag17	sperm associated antigen 17	0.36252	1.0416	1.52	2.073	5E-05	0.0017	2.87	YES
NM_001081393	Armc4	armadillo repeat containing 4	0.57454	1.64514	1.52	4.213	5E-05	0.0017	2.86	YES
NM_029821	1190003J15	urate (5-hydroxyiso-) hydrolase	0.35337	1.00828	1.51	2.314	0.0013	0.029	2.85	YES
NM_011139	Pou2f3	POU domain, class 2, transcription factor 3	0.09917	0.280962	1.50	2.373	5E-05	0.0017	2.83	YES
NM_001198835	Coch	coagulation factor C homolog (Limulus polyphemus)	1.21393	3.43158	1.50	4.237	5E-05	0.0017	2.83	YES
NM_008009	Fgfbp1	fibroblast growth factor binding protein 1	1.61943	4.5746	1.50	4.372	5E-05	0.0017	2.82	YES
NM_027041	1700003M02	cilia and flagella associated protein 206	1.90127	5.32968	1.49	4.979	5E-05	0.0017	2.80	YES
NM_001013761	Gm606	geminin coiled-coil domain containing	0.17404	0.48531	1.48	3.161	5E-05	0.0017	2.79	YES
NM_026789	Wdr65	cilia and flagella associated protein 57	0.61336	1.70519	1.48	4.164	5E-05	0.0017	2.78	YES
NM_026862	Cd177	CD177 antigen	0.41604	1.15574	1.47	3.427	5E-05	0.0017	2.78	YES
NM_026671	Lypd2	Ly6/Plaur domain containing 2	16.4509	45.6535	1.47	8.514	5E-05	0.0017	2.78	YES
NM_001037916	Ccdc17	coiled-coil domain containing 17	2.27174	6.28581	1.47	1.658	5E-05	0.0017	2.77	YES
NM_001081957	Gm11428	WAP four-disulfide core domain 17	1.72371	4.75817	1.46	4.611	5E-05	0.0017	2.76	YES
NM_144512	Slc6a13	solute carrier family 6 (neurotransmitter transporter, GABA), member 13	0.91719	2.51715	1.46	3.943	5E-05	0.0017	2.74	YES
NM_001029988	Fat2	FAT tumor suppressor homolog 2 (Drosophila)	0.1606	0.439964	1.45	3.938	5E-05	0.0017	2.74	YES
NR_045078	Gm3716	predicted gene 3716	0.10835	0.294337	1.44	2.222	5E-05	0.0017	2.72	YES
NM_016958	Krt14	keratin 14	2.29113	6.20689	1.44	4.939	5E-05	0.0017	2.71	YES
NM_009625	Adcyap1	adenylate cyclase activating polypeptide 1	0.11213	0.303099	1.43	2.291	5E-05	0.0017	2.70	YES
NM_026922	Atp2c2	ATPase, Ca++ transporting, type 2C, member 2	0.31998	0.864446	1.43	3.312	5E-05	0.0017	2.70	YES
NM_183193	Foxi2	forkhead box I2	0.08304	0.220722	1.41	2.125	5E-05	0.0017	2.66	YES
NM_146125	Itpka	inositol 1,4,5-trisphosphate 3-kinase A	0.23705	0.626292	1.40	2.596	5E-05	0.0017	2.64	YES
NM_010705	Lgals3	lectin, galactose binding, soluble 3	2.47832	6.5472	1.40	2.065	0.0001	0.0031	2.64	YES
NM_001081416	Fndc1	fibronectin type III domain containing 1	1.04987	2.763	1.40	5.085	5E-05	0.0017	2.63	YES
NM_010125	Elf5	E74-like factor 5	0.41245	1.08468	1.39	2.426	5E-05	0.0017	2.63	YES
NM_144945	Lgi2	leucine-rich repeat LGI family, member 2	2.22619	5.82146	1.39	4.961	5E-05	0.0017	2.61	YES
NM_030682	Tlr1	toll-like receptor 1	0.22891	0.597755	1.38	2.747	5E-05	0.0017	2.61	YES

NM_001100184	Cyp2t4	cytochrome P450, family 2, subfamily t, polypeptide 4	0.93724	2.44481	1.38	3.738	5E-05	0.0017	2.61	YES
NM_029948	Pramef12	PRAME family member 12	0.11426	0.297214	1.38	2.031	5E-05	0.0017	2.60	YES
NM_001033349	Gm410	ankrin repeat and ubiquitin domain containing 1	0.2122	0.550869	1.38	2.536	5E-05	0.0017	2.60	YES
NM_025744	4933404M02	glutamate rich 2	0.59711	1.54227	1.37	1.894	0.0002	0.0045	2.58	YES
NM_001166207	Dpy19l2	dpy-19-like 2 (C. elegans)	0.1376	0.355198	1.37	2.476	5E-05	0.0017	2.58	YES
NM_027053	Lrrc51	leucine rich repeat containing 51	1.04105	2.68303	1.37	1.407	0.0011	0.0252	2.58	YES
NM_001037928	Gm11992	predicted gene 11992	0.79058	2.02879	1.36	3.431	5E-05	0.0017	2.57	YES
NM_011313	S100a6	S100 calcium binding protein A6 (calcyclin)	9.13553	23.3636	1.35	6.349	5E-05	0.0017	2.56	YES
NM_134157	Atp6v1b1	ATPase, H+ transporting, lysosomal V1 subunit B1	0.87689	2.23474	1.35	3.633	5E-05	0.0017	2.55	YES
NM_027399	Steap1	six transmembrane epithelial antigen of the prostate 1	0.50421	1.28056	1.34	2.949	5E-05	0.0017	2.54	YES
NM_153527	Dnajb13	DnaJ (Hsp40) related, subfamily B, member 13	1.2988	3.29491	1.34	3.738	5E-05	0.0017	2.54	YES
NM_001143765	Syce1	synaptonemal complex central element protein 1	0.09853	0.248423	1.33	1.749	0.001	0.0233	2.52	YES
NM_008240	Foxj1	forkhead box J1	7.34648	18.3632	1.32	6.634	5E-05	0.0017	2.50	YES
NM_029674	Got1l1	glutamic-oxaloacetic transaminase 1-like 1	0.14619	0.364663	1.32	2.011	0.0001	0.0031	2.49	YES
NM_175532	Nlrp10	NLR family, pyrin domain containing 10	0.16055	0.399691	1.32	2.739	5E-05	0.0017	2.49	YES
NM_001145637	Gm1661	predicted gene 1661	0.43803	1.08971	1.31	2.088	5E-05	0.0017	2.49	YES
NM_172553	Alx1	ALX homeobox 1	0.0987	0.244194	1.31	2.050	0.0001	0.0031	2.47	YES
NM_001254761	Rnf128	ring finger protein 128	1.4999	3.71078	1.31	2.018	5E-05	0.0017	2.47	YES
NM_172658	Slco4c1	solute carrier organic anion transporter family, member 4C1	0.46727	1.14182	1.29	3.175	5E-05	0.0017	2.44	YES
NM_008365	Il18r1	interleukin 18 receptor 1	0.16933	0.412385	1.28	2.115	5E-05	0.0017	2.44	YES
NM_177697	Vwa3a	von Willebrand factor A domain containing 3A	0.96631	2.35285	1.28	4.305	5E-05	0.0017	2.43	YES
NM_027559	Wdr96	cilia and flagella associated protein 43	1.01851	2.47531	1.28	4.656	5E-05	0.0017	2.43	YES
NM_053253	Zmynd10	zinc finger, MYND domain containing 10	3.06494	7.44665	1.28	4.771	5E-05	0.0017	2.43	YES
NM_177384	Ttc16	tetratricopeptide repeat domain 16	0.94503	2.29337	1.28	1.749	5E-05	0.0017	2.43	YES
NM_013667	Slc22a2	solute carrier family 22 (organic cation transporter), member 2	0.18041	0.437656	1.28	2.322	5E-05	0.0017	2.43	YES
NM_029345	2310007L24	proline rich 29	1.25006	3.0316	1.28	3.362	5E-05	0.0017	2.43	YES
NM_027035	1700001L19	RIKEN cDNA 1700001L19 gene	0.37938	0.919146	1.28	2.721	5E-05	0.0017	2.42	YES
NM_054058	Psg20	pregnancy-specific glycoprotein 20	0.26925	0.649796	1.27	2.342	5E-05	0.0017	2.41	YES
NM_153786	Vgll2	vestigial like 2 homolog (Drosophila)	0.32174	0.773952	1.27	2.472	5E-05	0.0017	2.41	YES
NM_028624	1110017D15	RIKEN cDNA 1110017D15 gene	1.06602	2.55957	1.26	1.466	0.0019	0.0396	2.40	YES
NM_177082	Sp8	trans-acting transcription factor 8	0.58704	1.40836	1.26	3.855	5E-05	0.0017	2.40	YES
NM_017372	Lyz2	lysozyme 2	6.26412	14.8649	1.25	5.277	5E-05	0.0017	2.37	YES
NM_177922	Mapk15	mitogen-activated protein kinase 15	2.2844	5.41597	1.25	4.404	5E-05	0.0017	2.37	YES
NM_175512	Dhrs9	dehydrogenase/reductase (SDR family) member 9	0.31833	0.754574	1.25	2.781	5E-05	0.0017	2.37	YES
NM_177222	Casc1	cancer susceptibility candidate 1	0.89025	2.07953	1.22	2.798	5E-05	0.0017	2.34	YES
NM_177822	Mslnl	mesothelin-like	0.52513	1.22574	1.22	3.037	5E-05	0.0017	2.33	YES
NM_018754	Sfn	stratifin	1.51919	3.53413	1.22	3.672	5E-05	0.0017	2.33	YES
NM_027366	Ly6g6e	lymphocyte antigen 6 complex, locus G6E	0.18869	0.438632	1.22	1.937	0.0004	0.0105	2.32	YES
NM_029415	Slc10a6	solute carrier family 10 (sodium/bile acid cotransporter family), member 6	0.46605	1.08302	1.22	2.603	5E-05	0.0017	2.32	YES
NM_008623	Mpz	myelin protein zero	3.66851	8.51428	1.21	3.908	5E-05	0.0017	2.32	YES
NM_029122	Iqca	IQ motif containing with AAA domain	0.76692	1.7681	1.21	3.454	5E-05	0.0017	2.31	YES
NM_027548	Serpinb7	serine (or cysteine) peptidase inhibitor, clade B, member 7	0.48508	1.11727	1.20	2.799	5E-05	0.0017	2.30	YES
NM_027941	Lrrc34	leucine rich repeat containing 34	1.22492	2.82062	1.20	3.518	5E-05	0.0017	2.30	YES
NM_009141	Cxcl5	chemokine (C-X-C motif) ligand 5	0.15218	0.348939	1.20	2.006	0.0003	0.0082	2.29	YES
NM_018803	Syt10	synaptotagmin X	0.59955	1.37105	1.19	2.850	5E-05	0.0017	2.29	YES
NM_011737	Ysk4	mitogen-activated protein kinase kinase kinase 19	0.64107	1.46364	1.19	3.352	5E-05	0.0017	2.28	YES
NM_010762	Mal	myelin and lymphocyte protein, T cell differentiation protein	0.88361	2.00383	1.18	2.001	5E-05	0.0017	2.27	YES
NM_001195074	Kcnmb3	potassium large conductance calcium-activated channel, subfamily M, beta	0.82038	1.85326	1.18	2.756	5E-05	0.0017	2.26	YES
NM_001081257	Hpse2	heparanase 2	0.21684	0.489232	1.17	2.235	5E-05	0.0017	2.26	YES
NM_007539	Bdkrb1	bradykinin receptor, beta 1	0.23238	0.520939	1.16	2.070	0.0001	0.0031	2.24	YES
NM_001040086	Sytl2	synaptotagmin-like 2	0.11839	0.26397	1.16	1.460	0.001	0.0233	2.23	YES
NR_024257	4930412O13	RIKEN cDNA 4930412O13 gene	0.09194	0.204198	1.15	1.812	0.0001	0.0031	2.22	YES
NM_009528	Wnt7b	wingless-type MMTV integration site family, member 7B	0.49484	1.09608	1.15	2.221	5E-05	0.0017	2.22	YES
NM_013624	Otog	otogelin	0.17204	0.379225	1.14	2.702	5E-05	0.0017	2.20	YES
ENSMUSG00000085693.1	Gm13371		1.3905	3.05583	1.14	2.062	5E-05	0.0017	2.20	YES
NM_010168	F2	coagulation factor II	0.11726	0.257213	1.13	1.699	0.0004	0.0094	2.19	YES
NM_019738	Nupr1	nuclear protein transcription regulator 1	5.64004	12.3692	1.13	4.480	5E-05	0.0017	2.19	YES
NM_001039646	Gbp10	guanylate-binding protein 10	0.18483	0.403283	1.13	2.122	5E-05	0.0017	2.18	YES
NM_172892	Slc13a4	solute carrier family 13 (sodium/sulfate symporters), member 4	0.41002	0.888113	1.12	2.666	5E-05	0.0017	2.17	YES
NM_008243	Mst1	macrophage stimulating 1 (hepatocyte growth factor-like)	0.27881	0.602074	1.11	2.222	5E-05	0.0017	2.16	YES
NM_177577	Dcdc2a	doublecortin domain containing 2a	0.42741	0.918127	1.10	3.191	5E-05	0.0017	2.15	YES
NM_172515	Zbbx	zinc finger, B-box domain containing	0.30681	0.657483	1.10	2.304	5E-05	0.0017	2.14	YES
NM_007628	Ccna1	cyclin A1	3.92349	8.3912	1.10	4.291	5E-05	0.0017	2.14	YES
NM_001162957	Rsph4a	radial spoke head 4 homolog A (Chlamydomonas)	1.69483	3.61394	1.09	4.006	5E-05	0.0017	2.13	YES
ENSMUST00000137756.1	Gm13371		5.59056	11.8924	1.09	1.722	0.0002	0.0058	2.13	YES
NM_207268	Ccdc87	coiled-coil domain containing 87	0.46208	0.981448	1.09	2.741	5E-05	0.0017	2.12	YES
NM_212452	Rxfp1	relaxin/insulin-like family peptide receptor 1	0.24813	0.526847	1.09	2.022	0.0001	0.0031	2.12	YES
NM_001162970	Aim1l	absent in melanoma 1-like	0.14759	0.313121	1.09	2.139	5E-05	0.0017	2.12	YES
ENSMUSG00000097209.1	AU022754	expressed sequence AU022754	0.11079	0.234461	1.08	1.963	5E-05	0.0017	2.12	YES
NM_001111023	Runx1	runt related transcription factor 1	0.97764	2.06239	1.08	2.671	5E-05	0.0017	2.11	YES
NM_001001179	BC048546	cDNA sequence BC048546	0.3514	0.739379	1.07	2.736	5E-05	0.0017	2.10	YES
NM_025619	1700019L03	cilia and flagella associated protein 157	1.15727	2.41671	1.06	2.122	5E-05	0.0017	2.09	YES
NM_030025	Ccdc150	coiled-coil domain containing 150	0.25685	0.536239	1.06	2.326	5E-05	0.0017	2.09	YES
NM_007860	Dio1	deiodinase, iodothyronine, type I	0.15589	0.325192	1.06	1.645	0.0004	0.0094	2.09	YES
NM_001081083	Armc3	armadillo repeat containing 3	1.23402	2.57384	1.06	3.408	5E-05	0.0017	2.09	YES
NM_007559	Bmp8b	bone morphogenetic protein 8b	0.26642	0.552034	1.05	1.976	5E-05	0.0017	2.07	YES
NM_130861	Slco1a5	solute carrier organic anion transporter family, member 1a5	0.36146	0.747019	1.05	2.187	5E-05	0.0017	2.07	YES
NM_022886	Scel	sciellin	0.58014	1.19745	1.05	2.719	5E-05	0.0017	2.06	YES
NM_009253	Serpina3m	serine (or cysteine) peptidase inhibitor, clade A, member 3M	0.29032	0.598729	1.04	1.874	5E-05	0.0017	2.06	YES
NM_001033233	Tmprss11a	transmembrane protease, serine 11a	0.1264	0.260389	1.04	1.761	0.0004	0.0105	2.06	YES
NM_023842	Dsp	desmoplakin	3.4515	7.10353	1.04	5.542	5E-05	0.0017	2.06	YES
NM_025867	Serpinb11	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 11	2.81575	5.79283	1.04	3.786	5E-05	0.0017	2.06	YES
NM_080450	Gjc3	gap junction protein, gamma 3	0.30298	0.622895	1.04	2.029	0.0001	0.0031	2.06	YES
NM_021050	Cftr	cystic fibrosis transmembrane conductance regulator	0.35403	0.727149	1.04	2.637	5E-05	0.0017	2.05	YES
NM_177087	Fam179a	family with sequence similarity 179, member A	1.0758	2.19675	1.03	3.188	5E-05	0.0017	2.04	YES
NM_181816	Ccdc67	coiled-coil domain containing 67	3.10147	6.31221	1.03	4.216	5E-05	0.0017	2.04	YES
NM_027298	Ccdc89	coiled-coil domain containing 89	0.75442	1.5097	1.00	2.664	5E-05	0.0017	2.00	YES
NM_016689	Aqp3	aquaporin 3	2.43673	4.85947	1.00	3.488	5E-05	0.0017	1.99	YES
NM_029696	Mdh1b	malate dehydrogenase 1B, NAD (soluble)	1.14202	2.26885	0.99	2.760	5E-05	0.0017	1.99	YES
NM_010801	Mlf1	myeloid leukemia factor 1	7.75741	15.3677	0.99	3.585	5E-05	0.0017	1.98	YES
NM_010755	Maff	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)	5.99189	11.8575	0.98	4.368	5E-05	0.0017	1.98	YES
NM_007511	Atp7b	ATPase, Cu++ transporting, beta polypeptide	0.7431	1.46923	0.98	3.052	5E-05	0.0017	1.98	YES
NM_026146	Eps8l1	EPS8-like 1	3.04443	6.00007	0.98	2.651	5E-05	0.0017	1.97	YES
NM_029314	1700013F07	RIKEN cDNA 1700013F07 gene	1.65265	3.23998	0.97	2.726	5E-05	0.0017	1.96	YES
NM_029044	Lrrc48	leucine rich repeat containing 48	5.95621	11.6207	0.96	4.298	5E-05	0.0017	1.95	YES
NM_019645	Pkp1	plakophilin 1	0.64256	1.24916	0.96	2.786	5E-05	0.0017	1.94	YES
NM_007752	Cp	ceruloplasmin	1.73799	3.37559	0.96	2.200	5E-05	0.0017	1.94	YES
NM_173427	Klhdc7a	kelch domain containing 7A	0.6227	1.20941	0.96	2.952	5E-05	0.0017	1.94	YES
NM_013891	Spdef	SAM pointed domain containing ets transcription factor	0.4784	0.928116	0.96	2.116	5E-05	0.0017	1.94	YES
NM_001162979	Ccdc81	coiled-coil domain containing 81	0.89723	1.73591	0.95	2.649	5E-05	0.0017	1.93	YES
NM_177117	Dlec1	deleted in lung and esophageal cancer 1	1.425	2.74977	0.95	3.574	5E-05	0.0017	1.93	YES
NM_007440	Alox12	arachidonate 12-lipoxygenase	1.35061	2.60253	0.95	3.085	5E-05	0.0017	1.93	YES
NM_001033345	Gm216	ciliogenesis associated TTC17 interacting protein	1.07685	2.0727	0.94	2.671	5E-05	0.0017	1.92	YES
NM_001007463	Spag8	sperm associated antigen 8	2.6242	5.04193	0.94	3.145	5E-05	0.0017	1.92	YES
ENSMUST00000160264.1	Gm16136	predicted gene 16136	2.90719	5.58173	0.94	1.735	0.0015	0.0316	1.92	YES
NM_010903	Nfe2l3	nuclear factor, erythroid derived 2, like 3	1.42571	2.73703	0.94	3.057	5E-05	0.0017	1.92	YES

NM_133681	Tspan1	tetraspanin 1	3.6789	7.05822	0.94	3.781	5E-05	0.0017	1.92	YES
NM_009259	Spn	sialophorin	0.18305	0.350516	0.94	1.651	5E-05	0.0017	1.91	YES
NM_028735	Ttc21a	tetratricopeptide repeat domain 21A	1.41997	2.70758	0.93	3.312	5E-05	0.0017	1.91	YES
NM_001014394	Gpr113	adhesion G protein-coupled receptor F3	0.28126	0.533873	0.92	1.984	5E-05	0.0017	1.90	YES
NM_172535	Iqub	IQ motif and ubiquitin domain containing	0.88665	1.6825	0.92	2.842	5E-05	0.0017	1.90	YES
NM_029297	Dynlrb2	dynein light chain roadblock-type 2	22.6215	42.912	0.92	5.479	5E-05	0.0017	1.90	YES
NM_026385	Pllp	plasma membrane proteolipid	0.93848	1.77746	0.92	2.529	5E-05	0.0017	1.89	YES
NM_009252	Serpina3n	serine (or cysteine) peptidase inhibitor, clade A, member 3N	4.85169	9.16611	0.92	3.445	5E-05	0.0017	1.89	YES
NM_009027	Rasgrf2	RAS protein-specific guanine nucleotide-releasing factor 2	0.13456	0.253481	0.91	1.887	5E-05	0.0017	1.88	YES
NM_010362	Gsto1	glutathione S-transferase omega 1	16.7714	31.5309	0.91	5.001	5E-05	0.0017	1.88	YES
NM_013605	Muc1	mucin 1, transmembrane	3.81196	7.1503	0.91	3.719	5E-05	0.0017	1.88	YES
NM_010642	Klk1b21	kallikrein 1-related peptidase b21	0.40433	0.757399	0.91	1.721	0.0015	0.0316	1.87	YES
NM_172469	Clic6	chloride intracellular channel 6	9.25147	17.2917	0.90	4.992	5E-05	0.0017	1.87	YES
NM_146050	Oit1	oncoprotein induced transcript 1	0.96146	1.79557	0.90	2.238	5E-05	0.0017	1.87	YES
NM_007738	Col7a1	collagen, type VII, alpha 1	1.14369	2.12709	0.90	3.524	5E-05	0.0017	1.86	YES
NM_001008419	Aox3l1	aldehyde oxidase 2	0.56163	1.04163	0.89	1.800	5E-05	0.0017	1.85	YES
NM_001198914	Myb	myeloblastosis oncogene	0.83941	1.5542	0.89	1.465	0.0013	0.029	1.85	YES
NM_026428	Dcxr	dicarbonyl L-xylulose reductase	5.43342	10.0487	0.89	3.484	5E-05	0.0017	1.85	YES
NM_033652	Lmx1a	LIM homeobox transcription factor 1 alpha	0.18848	0.348564	0.89	1.703	0.0003	0.007	1.85	YES
NM_001033460	Ccdc164	dynein regulatory complex subunit 1	3.01784	5.57982	0.89	3.314	5E-05	0.0017	1.85	YES
NM_133663	Itgb4	integrin beta 4	1.01514	1.87338	0.88	1.776	0.0001	0.0031	1.85	YES
NM_007882	Dsc3	desmocollin 3	1.10215	2.02736	0.88	3.145	5E-05	0.0017	1.84	YES
NM_207281	4832428D23	methyltransferase like 21E	1.4986	2.75119	0.88	3.001	5E-05	0.0017	1.84	YES
NM_026619	Gsto2	glutathione S-transferase omega 2	1.36482	2.50028	0.87	1.523	0.0016	0.0335	1.83	YES
NM_025290	Rsph1	radial spoke head 1 homolog (Chlamydomonas)	9.11339	16.6889	0.87	3.975	5E-05	0.0017	1.83	YES
NM_009700	Aqp4	aquaporin 4	1.70275	3.11675	0.87	3.517	5E-05	0.0017	1.83	YES
NM_028430	Ppil6	peptidylprolyl isomerase (cyclophilin)-like 6	4.53842	8.27989	0.87	3.322	5E-05	0.0017	1.82	YES
NM_152947	Ovol2	ovo-like 2 (Drosophila)	1.06311	1.93948	0.87	1.806	0.0004	0.0105	1.82	YES
NM_023224	Cblc	Casitas B-lineage lymphoma c	0.9014	1.64106	0.86	1.935	5E-05	0.0017	1.82	YES
ENSMUST00000144718.2	4930526F13	RIKEN cDNA 4930526F13 gene	1.55727	2.82963	0.86	2.101	5E-05	0.0017	1.82	YES
NM_029698	Ttc18	cilia and flagella associated protein 70	1.03165	1.87008	0.86	1.767	5E-05	0.0017	1.81	YES
NM_133485	Ppp1r14c	protein phosphatase 1, regulatory (inhibitor) subunit 14c	0.8501	1.5339	0.85	2.090	5E-05	0.0017	1.80	YES
NM_008579	Meig1	meiosis expressed gene 1	3.85404	6.95299	0.85	3.047	5E-05	0.0017	1.80	YES
NM_001102615	Kif19a	kinesin family member 19A	1.17176	2.10533	0.85	2.666	5E-05	0.0017	1.80	YES
NM_001033247	Wdr52	cilia and flagella associated protein 44	2.88785	5.17068	0.84	3.975	5E-05	0.0017	1.79	YES
NM_011642	Trp73	transformation related protein 73	0.36904	0.660483	0.84	1.351	0.0021	0.0429	1.79	YES
NM_027040	1700007K13	RIKEN cDNA 1700007K13 gene	3.76569	6.73903	0.84	2.935	5E-05	0.0017	1.79	YES
NM_019587	Plxnb3	plexin B3	0.44155	0.788994	0.84	2.341	5E-05	0.0017	1.79	YES
NM_008484	Lamb3	laminin, beta 3	2.50883	4.47971	0.84	3.421	5E-05	0.0017	1.79	YES
NM_011324	Scnn1a	sodium channel, nonvoltage-gated 1 alpha	3.82676	6.81655	0.83	3.693	5E-05	0.0017	1.78	YES
NM_021451	Pmaip1	phorbol-12-myristate-13-acetate-induced protein 1	1.72194	3.06396	0.83	2.861	5E-05	0.0017	1.78	YES
NR_015521	1700030C10	RIKEN cDNA 1700030C10 gene	0.4297	0.762996	0.83	1.694	0.0002	0.0058	1.78	YES
NM_022983	Lpar3	lysophosphatidic acid receptor 3	0.2804	0.497451	0.83	1.727	0.0004	0.0105	1.77	YES
NM_010663	Krt17	keratin 17	5.25987	9.3255	0.83	3.317	5E-05	0.0017	1.77	YES
NM_010827	Msc	musculin	0.28488	0.503602	0.82	1.535	0.0017	0.036	1.77	YES
NM_177006	3110047P20	NACHT and WD repeat domain containing 2	0.37106	0.654345	0.82	2.410	5E-05	0.0017	1.76	YES
NM_172838	Slc16a12	solute carrier family 16 (monocarboxylic acid transporters), member 12	0.51131	0.900904	0.82	2.223	5E-05	0.0017	1.76	YES
ENSMUSG00000089635.1	Gm16559	predicted gene 16559	0.54767	0.96494	0.82	3.025	5E-05	0.0017	1.76	YES
NM_013589	Ltbp2	latent transforming growth factor beta binding protein 2	0.77421	1.36157	0.81	2.640	5E-05	0.0017	1.76	YES
NM_172914	Ccdc113	coiled-coil domain containing 113	3.14885	5.53627	0.81	2.784	5E-05	0.0017	1.76	YES
NM_001195681	Gm684	predicted gene 684	1.20655	2.11755	0.81	2.188	0.0001	0.0031	1.76	YES
NM_013467	Aldh1a1	aldehyde dehydrogenase family 1, subfamily A1	3.92564	6.87163	0.81	3.244	5E-05	0.0017	1.75	YES
NM_001081169	Aspg	asparaginase homolog (S. cerevisiae)	0.48534	0.849555	0.81	1.781	5E-05	0.0017	1.75	YES
NM_023755	Tfcp2l1	transcription factor CP2-like 1	2.38076	4.16666	0.81	4.028	5E-05	0.0017	1.75	YES
NM_001005422	Gm1574	stathmin domain containing 1	1.50123	2.62595	0.81	2.291	5E-05	0.0017	1.75	YES
NM_007409	Adh1	alcohol dehydrogenase 1 (class I)	8.34965	14.5869	0.80	2.771	5E-05	0.0017	1.75	YES
NM_194263	Tbx20	T-box 20	0.32889	0.574508	0.80	2.087	5E-05	0.0017	1.75	YES
NM_175430	Ccdc40	coiled-coil domain containing 40	2.54317	4.44212	0.80	3.402	5E-05	0.0017	1.75	YES
NM_001098789	Ndufa4l2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	12.6139	21.9938	0.80	2.079	0.0003	0.007	1.74	YES
NM_027026	Lrrc46	leucine rich repeat containing 46	5.21039	9.08058	0.80	3.226	5E-05	0.0017	1.74	YES
NM_028216	Psca	prostate stem cell antigen	0.55176	0.961419	0.80	1.649	0.0019	0.0396	1.74	YES
NM_021610	Gpa33	glycoprotein A33 (transmembrane)	1.2937	2.25406	0.80	2.409	5E-05	0.0017	1.74	YES
NR_015605	2900052N01	RIKEN cDNA 2900052N01 gene	0.25193	0.437102	0.79	1.586	0.0002	0.0045	1.74	YES
NM_008113	Arhgdig	Rho GDP dissociation inhibitor (GDI) gamma	2.58029	4.47184	0.79	2.523	5E-05	0.0017	1.73	YES
NM_026357	Ribc2	RIB43A domain with coiled-coils 2	0.63341	1.09752	0.79	1.827	0.0002	0.0045	1.73	YES
NM_001101519	4932443I19	RIKEN cDNA 4932443I19 gene	1.23393	2.13791	0.79	2.027	0.0005	0.0117	1.73	YES
NM_022025	Slc5a7	solute carrier family 5 (choline transporter), member 7	2.83663	4.91459	0.79	3.668	5E-05	0.0017	1.73	YES
NM_001081275	1700009P17	cilia and flagella associated protein 126	9.61014	16.6027	0.79	3.605	5E-05	0.0017	1.73	YES
NM_030192	4930562C15	RIKEN cDNA 4930562C15 gene	0.30628	0.526654	0.78	1.762	0.0002	0.0045	1.72	YES
NM_026481	Tppp3	tubulin polymerization-promoting protein family member 3	23.1217	39.7294	0.78	4.387	5E-05	0.0017	1.72	YES
NM_007627	Cckbr	cholecystokinin B receptor	0.32511	0.557277	0.78	1.641	0.0006	0.0139	1.71	YES
NM_031170	Krt8	keratin 8	31.3305	53.6628	0.78	4.762	5E-05	0.0017	1.71	YES
NM_178259	Abca13	ATP-binding cassette, sub-family A (ABC1), member 13	0.25835	0.441313	0.77	2.439	5E-05	0.0017	1.71	YES
NM_001127353	9130014G24	androglobin	1.98059	3.38204	0.77	3.147	5E-05	0.0017	1.71	YES
ENSMUSG00000084866.1	A930006K02	RIKEN cDNA A930006K02 gene	0.5515	0.941014	0.77	1.865	5E-05	0.0017	1.71	YES
NM_018881	Fmo2	flavin containing monooxygenase 2	16.4598	27.9876	0.77	4.637	5E-05	0.0017	1.70	YES
NM_024204	Ankrd22	ankyrin repeat domain 22	0.95737	1.62598	0.76	1.756	5E-05	0.0017	1.70	YES
NM_080575	Acss1	acyl-CoA synthetase short-chain family member 1	1.05799	1.79457	0.76	2.365	5E-05	0.0017	1.70	YES
NM_001081025	4932425I24	MYCBP-associated, testis expressed 1	1.8015	3.04957	0.76	2.481	5E-05	0.0017	1.69	YES
NM_012016	Ern2	endoplasmic reticulum (ER) to nucleus signalling 2	0.26202	0.443192	0.76	1.541	0.0006	0.0139	1.69	YES
NM_198192	Qrfpr	pyroglutamylated RFamide peptide receptor	0.44209	0.747421	0.76	1.657	0.0006	0.015	1.69	YES
NM_010848	Myb	myeloblastosis oncogene	3.31101	5.58631	0.75	2.490	5E-05	0.0017	1.69	YES
NR_027893	BB123696	expressed sequence BB123696	0.76694	1.29268	0.75	1.907	5E-05	0.0017	1.69	YES
NM_172461	Nek11	NIMA (never in mitosis gene a)-related expressed kinase 11	1.04106	1.75108	0.75	2.008	5E-05	0.0017	1.68	YES
NM_016861	Pdlim1	PDZ and LIM domain 1 (elfin)	5.90988	9.93411	0.75	3.171	5E-05	0.0017	1.68	YES
NM_021459	Isl1	ISL1 transcription factor, LIM/homeodomain	14.8296	24.8966	0.75	4.382	5E-05	0.0017	1.68	YES
NM_001013771	Gm973	predicted gene 973	1.59171	2.66668	0.74	2.543	5E-05	0.0017	1.68	YES
NM_145489	AI661453	expressed sequence AI661453	1.23479	2.06654	0.74	2.474	5E-05	0.0017	1.67	YES
NM_026200	Kcnv1	potassium channel, subfamily V, member 1	0.19046	0.318439	0.74	1.556	0.0007	0.016	1.67	YES
NM_001164201	Lass3	ceramide synthase 3	0.24647	0.411364	0.74	1.546	0.0004	0.0105	1.67	YES
NR_037693	2700046A07	RIKEN cDNA 2700046A07 gene	0.24346	0.406301	0.74	1.386	0.0022	0.0445	1.67	YES
NM_145218	Wbscr17	Williams-Beuren syndrome chromosome region 17 homolog (human)	1.48885	2.47758	0.73	2.621	5E-05	0.0017	1.66	YES
ENSMUSG00000086765.1	Gm11827	predicted gene 11827	1.16626	1.93759	0.73	1.912	5E-05	0.0017	1.66	YES
NM_008416	Junb	jun B proto-oncogene	37.0179	61.3719	0.73	4.433	5E-05	0.0017	1.66	YES
NM_001037927	Wdr93	WD repeat domain 93	1.14091	1.88724	0.73	2.121	5E-05	0.0017	1.65	YES
NM_027153	Pir	pirin	2.96218	4.89632	0.73	2.568	5E-05	0.0017	1.65	YES
NM_010858	Myl4	myosin, light polypeptide 4	2.90559	4.79522	0.72	2.132	5E-05	0.0017	1.65	YES
NM_053015	Mlph	melanophilin	1.29853	2.13845	0.72	2.507	5E-05	0.0017	1.65	YES
NM_177230	Ccdc158	coiled-coil domain containing 158	0.35639	0.585531	0.72	1.648	0.0002	0.0058	1.64	YES
NM_183187	Fam107a	family with sequence similarity 107, member A	12.9827	21.3233	0.72	3.947	5E-05	0.0017	1.64	YES
NM_008773	P2ry2	purinergic receptor P2Y, G-protein coupled 2	0.36605	0.600906	0.72	1.610	0.0003	0.007	1.64	YES
NM_001080944	Atp8b4	ATPase, class I, type 8B, member 4	0.21675	0.355171	0.71	1.615	0.0003	0.0082	1.64	YES
NM_021387	Vstm2b	V-set and transmembrane domain containing 2B	1.5792	2.58493	0.71	2.098	5E-05	0.0017	1.64	YES
ENSMUSG00000038408.7	1700018A04	RIKEN cDNA 1700018A04 gene	0.28303	0.462568	0.71	2.255	5E-05	0.0017	1.63	YES
NM_144854	ORF63	Map3k7 C-terminal like	1.15707	1.89036	0.71	1.956	5E-05	0.0017	1.63	YES
NM_029961	Abcb5	ATP-binding cassette, sub-family B (MDR/TAP), member 5	0.21123	0.345034	0.71	1.381	0.0012	0.027	1.63	YES

ENSMUSG00000087574.1	C030037D0	RIKEN cDNA C030037D09 gene	0.45928	0.749746	0.71	1.640	0.0003	0.0082	1.63	YES
NM_028567	1700094D03	RIKEN cDNA 1700094D03 gene	3.61535	5.89411	0.71	3.054	5E-05	0.0017	1.63	YES
NM_153518	Ccdc65	coiled-coil domain containing 65	3.27836	5.33851	0.70	2.598	5E-05	0.0017	1.63	YES
NM_007403	Adam8	a disintegrin and metallopeptidase domain 8	2.75837	4.48921	0.70	1.839	5E-05	0.0017	1.63	YES
NM_173775	Ccdc37	cilia and flagella associated protein 100	1.06904	1.73917	0.70	1.931	5E-05	0.0017	1.63	YES
NM_007418	Adra2c	adrenergic receptor, alpha 2c	0.49489	0.804371	0.70	1.764	0.0001	0.0031	1.63	YES
NM_207668	Acpp	acid phosphatase, prostate	1.08667	1.76465	0.70	2.204	5E-05	0.0017	1.62	YES
NM_145831	Dmrt2	doublesex and mab-3 related transcription factor 2	0.65271	1.0597	0.70	1.742	0.0002	0.0045	1.62	YES
ENSMUSG00000086245.1	Gm16170	predicted gene 16170	0.36582	0.593812	0.70	2.048	5E-05	0.0017	1.62	YES
NM_029056	Tdrd9	tudor domain containing 9	0.30883	0.501014	0.70	1.651	0.0004	0.0105	1.62	YES
NM_133731	Prss22	protease, serine 22	1.00213	1.6202	0.69	1.768	0.0003	0.0082	1.62	YES
NM_001033361	Pgr15l	G protein-coupled receptor 15-like	0.87213	1.40893	0.69	2.320	5E-05	0.0017	1.62	YES
NM_016867	Gipc2	GIPC PDZ domain containing family, member 2	0.65404	1.05605	0.69	1.532	0.0014	0.0299	1.61	YES
NM_172883	Mfsd7a	major facilitator superfamily domain containing 7A	0.77971	1.25837	0.69	1.855	0.0001	0.0031	1.61	YES
NM_001099310	Gm8787	predicted gene 8787	0.92747	1.49561	0.69	1.766	0.0004	0.0105	1.61	YES
NM_007419	Adrb1	adrenergic receptor, beta 1	0.271	0.436649	0.69	1.402	0.0025	0.0492	1.61	YES
NM_182807	Fam19a2	family with sequence similarity 19, member A2	1.05075	1.69269	0.69	1.569	0.0006	0.0139	1.61	YES
NM_144557	Myrip	myosin VIIA and Rab interacting protein	3.39675	5.45959	0.68	3.029	5E-05	0.0017	1.61	YES
NM_007763	Crip1	cysteine-rich protein 1 (intestinal)	21.7546	34.9399	0.68	4.096	5E-05	0.0017	1.61	YES
ENSMUSG00000086425.1	F730016J06	RIKEN cDNA F730016J06 gene	1.20508	1.93413	0.68	2.960	5E-05	0.0017	1.60	YES
NM_178257	Il22ra1	interleukin 22 receptor, alpha 1	0.52801	0.846372	0.68	1.967	5E-05	0.0017	1.60	YES
NM_029604	1700027A23	primary cilia formation	6.63581	10.6305	0.68	2.127	5E-05	0.0017	1.60	YES
NM_008091	Gata3	GATA binding protein 3	0.44776	0.716596	0.68	1.555	0.0005	0.0129	1.60	YES
NM_001081322	Myo5c	myosin VC	1.26873	2.02751	0.68	2.575	5E-05	0.0017	1.60	YES
NM_028848	Spata17	spermatogenesis associated 17	0.94822	1.5133	0.67	1.371	0.0013	0.029	1.60	YES
NR_027636	Wdr69	dynein assembly factor with WDR repeat domains 1	1.13025	1.80255	0.67	1.311	0.0022	0.0436	1.59	YES
NM_010628	Kif9	kinesin family member 9	1.862	2.96043	0.67	1.527	0.0005	0.0129	1.59	YES
NM_033073	Krt7	keratin 7	11.7313	18.6115	0.67	3.340	5E-05	0.0017	1.59	YES
NM_010338	Gpr37	G protein-coupled receptor 37	1.18458	1.87915	0.67	2.121	5E-05	0.0017	1.59	YES
NM_001039048	Trim63	tripartite motif-containing 63	1.92885	3.05947	0.67	2.120	5E-05	0.0017	1.59	YES
NM_021301	Slc15a2	solute carrier family 15 (H+/peptide transporter), member 2	7.97443	12.6264	0.66	3.354	5E-05	0.0017	1.58	YES
NM_012038	Vsnl1	visinin-like 1	1.23385	1.9518	0.66	1.894	5E-05	0.0017	1.58	YES
NM_001164056	Pld1	phospholipase D1	1.32963	2.09845	0.66	1.218	0.0025	0.0484	1.58	YES
NM_011326	Scnn1g	sodium channel, nonvoltage-gated 1 gamma	0.49002	0.770554	0.65	1.565	0.0004	0.0105	1.57	YES
NM_001033220	AU021092	expressed sequence AU021092	2.12711	3.3435	0.65	2.021	0.0001	0.0031	1.57	YES
NM_001164565	Acnat1	acyl-coenzyme A amino acid N-acyltransferase 1	0.97689	1.53288	0.65	2.216	5E-05	0.0017	1.57	YES
ENSMUSG00000097923.1	Gm26577		0.74302	1.16529	0.65	1.677	5E-05	0.0017	1.57	YES
NM_028903	Scara5	scavenger receptor class A, member 5 (putative)	8.86689	13.9034	0.65	3.337	5E-05	0.0017	1.57	YES
NM_001014900	Zmynd12	zinc finger, MYND domain containing 12	0.96049	1.50422	0.65	1.644	0.0003	0.0082	1.57	YES
NM_139200	Cytip	cytohesin 1 interacting protein	0.20686	0.3239	0.65	1.479	0.0006	0.0139	1.57	YES
NM_013560	Hspb1	heat shock protein 1	16.924	26.4924	0.65	3.396	5E-05	0.0017	1.57	YES
NM_020268	Klk1b27	kallikrein 1-related peptidase b27	1.26414	1.97882	0.65	1.643	0.0017	0.0352	1.57	YES
ENSMUSG00000078607.3	1810010H24	RIKEN cDNA 1810010H24 gene	1.35888	2.11762	0.64	1.476	0.0003	0.0082	1.56	YES
NM_008970	Pthlh	parathyroid hormone-like peptide	1.11443	1.73633	0.64	1.698	0.0003	0.0082	1.56	YES
NM_009437	Tst	thiosulfate sulfurtransferase, mitochondrial	10.3345	16.0818	0.64	2.953	5E-05	0.0017	1.56	YES
NM_001013756	Grhl3	grainyhead-like 3 (Drosophila)	0.47041	0.72957	0.63	1.470	0.0008	0.0191	1.55	YES
NM_001195730	Dcdc2b	doublecortin domain containing 2b	1.4139	2.19236	0.63	1.682	0.0017	0.0352	1.55	YES
NM_007669	Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)	14.6343	22.6819	0.63	3.049	5E-05	0.0017	1.55	YES
NM_011023	Otx1	orthodenticle homolog 1	0.82942	1.28455	0.63	1.774	0.0004	0.0094	1.55	YES
NM_145825	Cetn4	centrin 4	5.66524	8.77223	0.63	2.535	5E-05	0.0017	1.55	YES
NM_133995	Upb1	ureidopropionase, beta	0.85103	1.31729	0.63	1.499	0.0017	0.036	1.55	YES
NM_026278	Lrp2bp	Lrp2 binding protein	1.03299	1.59605	0.63	1.993	5E-05	0.0017	1.55	YES
NM_001163559	Lrriq1	leucine-rich repeats and IQ motif containing 1	0.83223	1.28496	0.63	1.836	5E-05	0.0017	1.54	YES
NM_007987	Fas	Fas (TNF receptor superfamily member 6)	1.81198	2.7954	0.63	1.583	0.0003	0.007	1.54	YES
NM_026271	Fibin	fin bud initiation factor homolog (zebrafish)	8.53917	13.1574	0.62	3.051	5E-05	0.0017	1.54	YES
NM_001122603	Fcgbp	Fc fragment of IgG binding protein	0.22228	0.342398	0.62	1.528	0.0006	0.015	1.54	YES
NM_027442	Ddo	D-aspartate oxidase	1.97312	3.03803	0.62	2.233	5E-05	0.0017	1.54	YES
NM_177260	Tmem154	transmembrane protein 154	0.96487	1.48459	0.62	1.876	5E-05	0.0017	1.54	YES
NM_175173	Wdr27	WD repeat domain 27	0.42534	0.653694	0.62	1.424	0.0011	0.0252	1.54	YES
NM_023821	Cmya5	cardiomyopathy associated 5	0.25577	0.39291	0.62	1.629	0.0002	0.0045	1.54	YES
NM_009397	Tnfaip3	tumor necrosis factor, alpha-induced protein 3	3.85613	5.9233	0.62	1.646	0.0001	0.0031	1.54	YES
NM_009313	Tacr1	tachykinin receptor 1	0.50102	0.769574	0.62	1.697	0.0001	0.0031	1.54	YES
NM_027990	Lypd6b	LY6/PLAUR domain containing 6B	0.97797	1.50136	0.62	1.706	0.0001	0.0031	1.54	YES
NM_028021	Myh14	myosin, heavy polypeptide 14	7.55517	11.5803	0.62	3.439	5E-05	0.0017	1.53	YES
NM_008998	Rab17	RAB17, member RAS oncogene family	2.71844	4.16024	0.61	1.564	5E-05	0.0017	1.53	YES
NM_178278	Caps2	calcyphosphine 2	1.31729	2.01513	0.61	1.950	5E-05	0.0017	1.53	YES
NM_023478	Upk3a	uroplakin 3A	2.9212	4.46721	0.61	2.012	5E-05	0.0017	1.53	YES
NM_010357	Gsta4	glutathione S-transferase, alpha 4	22.6594	34.5815	0.61	3.410	5E-05	0.0017	1.53	YES
NM_027728	Enkur	enkurin, TRPC channel interacting protein	6.53812	9.97519	0.61	2.540	5E-05	0.0017	1.53	YES
NM_172770	Ttc12	tetratricopeptide repeat domain 12	1.99016	3.03385	0.61	2.245	5E-05	0.0017	1.52	YES
ENSMUSG00000089713.1	Gm16564		0.42315	0.644483	0.61	1.709	5E-05	0.0017	1.52	YES
NM_010171	F3	coagulation factor III	7.8093	11.8889	0.61	2.847	5E-05	0.0017	1.52	YES
NM_024228	Gdpd3	glycerophosphodiester phosphodiesterase domain containing 3	1.78306	2.71266	0.61	1.637	0.0014	0.0308	1.52	YES
NM_001162950	Hif3a	hypoxia inducible factor 3, alpha subunit	17.6358	26.7224	0.60	2.344	5E-05	0.0017	1.52	YES
NM_001033324	Zbtb16	zinc finger and BTB domain containing 16	14.6935	22.2458	0.60	3.241	5E-05	0.0017	1.51	YES
NM_009180	St6galnac2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosa	3.45713	5.2303	0.60	2.273	5E-05	0.0017	1.51	YES
NM_008935	Prom1	prominin 1	7.06276	10.6808	0.60	2.303	5E-05	0.0017	1.51	YES
NM_133643	Edaradd	EDAR (ectodysplasin-A receptor)-associated death domain	0.19126	0.288724	0.59	1.413	0.0007	0.016	1.51	YES
NM_029152	Efcab10	EF-hand calcium binding domain 10	7.70917	11.6317	0.59	2.519	5E-05	0.0017	1.51	YES
NM_001166705	1700101E01	cilia and flagella associated protein 77	3.79832	5.72695	0.59	1.580	0.0001	0.0031	1.51	YES
NM_001099307	Gm7173	predicted gene 7173	0.60627	0.913844	0.59	1.522	0.0012	0.0262	1.51	YES
ENSMUSG00000093619.1	4930535L15	RIKEN cDNA 4930535L15 gene	0.34793	0.524336	0.59	1.278	0.0018	0.0369	1.51	YES
NM_001081162	Slc4a11	solute carrier family 4, sodium bicarbonate transporter-like, member 11	1.57537	2.36825	0.59	1.990	5E-05	0.0017	1.50	YES
NM_145100	Lypd1	Ly6/Plaur domain containing 1	2.86577	4.30806	0.59	1.929	5E-05	0.0017	1.50	YES
NR_040291	6430706D22	RIKEN cDNA 6430706D22 gene	25.0635	37.6655	0.59	2.061	5E-05	0.0017	1.50	YES
NM_025285	Stmn2	stathmin-like 2	5.65401	8.49497	0.59	2.555	5E-05	0.0017	1.50	YES
ENSMUST00000135687.1	A730046J19	RIKEN cDNA A730046J19 gene	2.36152	3.54274	0.59	2.331	5E-05	0.0017	1.50	YES
NM_001195258	Gm14378	transforming growth factor, beta receptor III-like	29.1079	19.3036	-0.59	-3.294	5E-05	0.0017	0.66	YES
NM_001002927	Penk	preproenkephalin	17.3609	11.509	-0.59	-2.680	5E-05	0.0017	0.66	YES
NR_040648	1700003M07	RIKEN cDNA 1700003M07 gene	4.61872	3.0598	-0.59	-1.357	0.0006	0.0139	0.66	YES
NM_001033212	Rprml	reprimo-like	2.35834	1.55848	-0.60	-1.668	0.0011	0.0243	0.66	YES
NM_011589	Timeless	timeless circadian clock 1	11.521	7.61191	-0.60	-2.182	5E-05	0.0017	0.66	YES
NM_009380	Thrb	thyroid hormone receptor beta	5.08598	3.34339	-0.61	-1.934	5E-05	0.0017	0.66	YES
NM_008901	Pou3f4	POU domain, class 3, transcription factor 4	2.5159	1.6471	-0.61	-1.712	0.0009	0.0201	0.65	YES
NM_033610	Sncb	synuclein, beta	2.75015	1.79134	-0.62	-1.765	0.0002	0.0058	0.65	YES
NM_153564	Gbp5	guanylate binding protein 5	1.15818	0.753262	-0.62	-1.692	0.0001	0.0031	0.65	YES
NM_001033399	Gfod1	glucose-fructose oxidoreductase domain containing 1	3.13974	2.03767	-0.62	-2.728	5E-05	0.0017	0.65	YES
NM_001165940	Tshb	thyroid stimulating hormone, beta subunit	348.838	226.286	-0.62	-2.716	5E-05	0.0017	0.65	YES
NM_175519	Kctd8	potassium channel tetramerisation domain containing 8	0.84005	0.54462	-0.63	-1.579	0.0003	0.0082	0.65	YES
NM_009518	Wnt10a	wingless-type MMTV integration site family, member 10A	1.52772	0.986852	-0.63	-1.685	0.0001	0.0031	0.65	YES
NM_173385	Cilp	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	2.37174	1.53171	-0.63	-2.244	5E-05	0.0017	0.65	YES
NM_015783	Isg15	ISG15 ubiquitin-like modifier	12.2088	7.87809	-0.63	-2.656	5E-05	0.0017	0.65	YES
NM_009513	Nrsn1	neurensin 1	6.13001	3.94504	-0.64	-2.574	5E-05	0.0017	0.64	YES
NM_019662	Rrad	Ras-related associated with diabetes	2.33659	1.49431	-0.64	-1.828	0.0002	0.0058	0.64	YES
NM_199021	Dpp10	dipeptidylpeptidase 10	7.6789	4.90841	-0.65	-3.275	5E-05	0.0017	0.64	YES
NM_145922	Kcnc4	potassium voltage gated channel, Shaw-related subfamily, member 4	0.87919	0.561936	-0.65	-1.627	5E-05	0.0017	0.64	YES

NM_019944	Mnx1	motor neuron and pancreas homeobox 1	1.72165	1.09421	-0.65	-1.733	0.0007	0.0171	0.64	YES
NM_201367	Gpr176	G protein-coupled receptor 176	0.4197	0.266355	-0.66	-1.401	0.0009	0.0201	0.63	YES
NM_010050	Dio2	deiodinase, iodothyronine, type II	31.0885	19.6994	-0.66	-3.860	5E-05	0.0017	0.63	YES
NM_019697	Kcnd2	potassium voltage-gated channel, Shal-related family, member 2	3.77647	2.39151	-0.66	-2.762	5E-05	0.0017	0.63	YES
NM_001146329	Sbk2	SH3-binding domain kinase family, member 2	1.44311	0.91363	-0.66	-1.584	0.0013	0.029	0.63	YES
NM_053080	Aldh1a3	aldehyde dehydrogenase family 1, subfamily A3	2.33716	1.47564	-0.66	-2.229	5E-05	0.0017	0.63	YES
NM_145841	Sgcz	sarcoglycan zeta	0.57792	0.363263	-0.67	-1.315	0.0014	0.0308	0.63	YES
NM_011440	Sox14	SRY (sex determining region Y)-box 14	1.58808	0.99351	-0.68	-1.852	5E-05	0.0017	0.63	YES
NM_176933	Dusp4	dual specificity phosphatase 4	10.8395	6.76687	-0.68	-3.252	5E-05	0.0017	0.62	YES
NM_001165939	Tshb	thyroid stimulating hormone, beta subunit	95.7612	59.5822	-0.68	-1.610	5E-05	0.0017	0.62	YES
NM_011836	Lamc3	laminin gamma 3	2.13647	1.32924	-0.68	-2.415	5E-05	0.0017	0.62	YES
NM_139310	Otoa	otoancorin	0.53082	0.329963	-0.69	-1.548	0.0004	0.0094	0.62	YES
NM_010501	Ifit3	interferon-induced protein with tetratricopeptide repeats 3	2.00737	1.23475	-0.70	-1.989	5E-05	0.0017	0.62	YES
NM_178906	AI593442	expressed sequence AI593442	16.4615	10.1105	-0.70	-4.275	5E-05	0.0017	0.61	YES
NM_010350	Grin2c	glutamate receptor, ionotropic, NMDA2C (epsilon 3)	0.7321	0.446514	-0.71	-1.902	5E-05	0.0017	0.61	YES
NM_001033360	Gpr101	G protein-coupled receptor 101	0.26996	0.16348	-0.72	-1.519	0.0007	0.016	0.61	YES
NM_177129	Cntn2	contactin 2	1.13936	0.686947	-0.73	-2.580	5E-05	0.0017	0.60	YES
NM_007424	Acan	aggrecan	1.72561	1.03941	-0.73	-2.366	5E-05	0.0017	0.60	YES
NM_001077425	Cntnap5a	contactin associated protein-like 5A	0.56855	0.342409	-0.73	-1.715	5E-05	0.0017	0.60	YES
NM_018734	Gbp3	guanylate binding protein 3	5.55923	3.33823	-0.74	-2.949	5E-05	0.0017	0.60	YES
NM_011648	Tshr	thyroid stimulating hormone receptor	1.16833	0.699642	-0.74	-2.053	5E-05	0.0017	0.60	YES
NR_037698	1500009C09	RIKEN cDNA 1500009C09 gene	6.53811	3.91061	-0.74	-2.424	5E-05	0.0017	0.60	YES
NM_011579	Tgtp1	T cell specific GTPase 1	0.37605	0.223694	-0.75	-1.452	0.0009	0.0211	0.59	YES
ENSMUSG00000086686.1	F630206G17	RIKEN cDNA F630206G17 gene	2.32096	1.38017	-0.75	-3.707	5E-05	0.0017	0.59	YES
NM_001081134	Kcng1	potassium voltage-gated channel, subfamily G, member 1	5.61729	3.33535	-0.75	-2.967	5E-05	0.0017	0.59	YES
NM_021382	Tacr3	tachykinin receptor 3	0.54835	0.3255	-0.75	-1.756	0.0003	0.007	0.59	YES
NM_007694	Chgb	chromogranin B	355.044	210.717	-0.75	-3.154	5E-05	0.0017	0.59	YES
NM_153107	Cpz	carboxypeptidase Z	6.03458	3.58022	-0.75	-2.858	5E-05	0.0017	0.59	YES
NM_026180	Abcg8	ATP-binding cassette, sub-family G (WHITE), member 8	0.22452	0.133034	-0.76	-1.348	0.0019	0.0396	0.59	YES
NM_001113180	Gria4	glutamate receptor, ionotropic, AMPA4 (alpha 4)	2.66073	1.57637	-0.76	-1.812	5E-05	0.0017	0.59	YES
NM_001015046	Rap1gap2	RAP1 GTPase activating protein 2	21.4057	12.6735	-0.76	-4.472	5E-05	0.0017	0.59	YES
NM_173395	Fam132b	family with sequence similarity 132, member B	2.16422	1.27577	-0.76	-2.400	5E-05	0.0017	0.59	YES
NM_001142734	Gm8994	predicted gene 8994	1.22765	0.715016	-0.78	-1.764	0.0003	0.0082	0.58	YES
NM_001033415	Shisa3	shisa family member 3	4.02636	2.34219	-0.78	-3.006	5E-05	0.0017	0.58	YES
NM_009504	Vdr	vitamin D receptor	4.60371	2.67603	-0.78	-3.309	5E-05	0.0017	0.58	YES
NM_080853	Slc17a6	solute carrier family 17 (sodium-dependent inorganic phosphate cotranspo	1.37648	0.796355	-0.79	-2.444	5E-05	0.0017	0.58	YES
NM_021408	Ush2a	Usher syndrome 2A (autosomal recessive, mild)	0.21073	0.121886	-0.79	-2.001	5E-05	0.0017	0.58	YES
NM_173422	Colec10	collectin sub-family member 10	1.78019	1.02566	-0.80	-2.669	5E-05	0.0017	0.58	YES
NM_007392	Acta2	actin, alpha 2, smooth muscle, aorta	5.7023	3.28208	-0.80	-2.964	5E-05	0.0017	0.58	YES
NM_011109	Pla2g2d	phospholipase A2, group IID	1.22981	0.700003	-0.81	-2.079	5E-05	0.0017	0.57	YES
NM_008331	Ifit1	interferon-induced protein with tetratricopeptide repeats 1	2.45497	1.3948	-0.82	-2.581	5E-05	0.0017	0.57	YES
NM_010608	Kcnk3	potassium channel, subfamily K, member 3	10.748	6.09076	-0.82	-3.830	5E-05	0.0017	0.57	YES
NM_001145927	C530028O2	PILR alpha associated neural protein	10.9612	6.20411	-0.82	-1.596	0.0001	0.0031	0.57	YES
NM_025734	Kcng4	potassium voltage-gated channel, subfamily G, member 4	0.2488	0.140042	-0.83	-1.541	0.0004	0.0105	0.56	YES
NM_016687	Sfrp4	secreted frizzled-related protein 4	2.65824	1.49552	-0.83	-2.257	5E-05	0.0017	0.56	YES
NM_023689	Spock3	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 3	3.29976	1.85605	-0.83	-2.169	5E-05	0.0017	0.56	YES
NM_178758	Acsm5	acyl-CoA synthetase medium-chain family member 5	0.33042	0.18585	-0.83	-1.445	0.0012	0.027	0.56	YES
NM_007524	Nkx3-2	NK3 homeobox 2	0.4487	0.250148	-0.84	-1.486	0.0019	0.0388	0.56	YES
NM_001081333	Plekhg4	pleckstrin homology domain containing, family G (with RhoGef domain) me	1.48145	0.824402	-0.85	-2.558	5E-05	0.0017	0.56	YES
NM_010378	H2-Aa	histocompatibility 2, class II antigen A, alpha	1.6573	0.920723	-0.85	-2.066	0.0001	0.0031	0.56	YES
ENSMUSG00000097072.1	Foxl2os	forkhead box L2, opposite strand	3.00873	1.66587	-0.85	-2.665	5E-05	0.0017	0.55	YES
ENSMUST00000181706.1	Foxl2os	forkhead box L2, opposite strand	5.63864	3.10261	-0.86	-2.848	5E-05	0.0017	0.55	YES
NM_183224	Fam19a3	family with sequence similarity 19, member A3	1.17559	0.644718	-0.87	-2.476	5E-05	0.0017	0.55	YES
NM_175696	C530028O2	PILR alpha associated neural protein	11.5223	6.23899	-0.89	-2.319	5E-05	0.0017	0.54	YES
NM_001198561	H2-Q7	histocompatibility 2, Q region locus 7	2.41364	1.29688	-0.90	-1.705	0.0001	0.0031	0.54	YES
NM_012020	Foxl2	forkhead box L2	11.5042	6.17728	-0.90	-4.362	5E-05	0.0017	0.54	YES
NM_020279	Ccl28	chemokine (C-C motif) ligand 28	0.59342	0.317236	-0.90	-2.107	5E-05	0.0017	0.53	YES
NM_027790	Dhrs2	dehydrogenase/reductase member 2	1.83404	0.974834	-0.91	-2.293	5E-05	0.0017	0.53	YES
NM_001033876	Kcnk9	potassium channel, subfamily K, member 9	5.58157	2.9585	-0.92	-3.210	5E-05	0.0017	0.53	YES
NM_015730	Chrna4	cholinergic receptor, nicotinic, alpha polypeptide 4	1.41084	0.743662	-0.92	-2.792	5E-05	0.0017	0.53	YES
NM_009062	Rgs4	regulator of G-protein signaling 4	14.5143	7.56594	-0.94	-4.844	5E-05	0.0017	0.52	YES
NM_007799	Ctse	cathepsin E	0.22999	0.118984	-0.95	-1.368	0.0022	0.0445	0.52	YES
NM_001024138	Gpr139	G protein-coupled receptor 139	0.8349	0.431372	-0.95	-1.936	0.0004	0.0105	0.52	YES
NM_172750	Adprhl1	ADP-ribosylhydrolase like 1	0.68251	0.3444	-0.99	-1.909	0.0002	0.0058	0.50	YES
NM_027551	Klhl30	kelch-like 30	0.40904	0.205241	-0.99	-1.953	5E-05	0.0017	0.50	YES
NM_008780	Pax1	paired box 1	1.84944	0.91943	-1.01	-2.610	5E-05	0.0017	0.50	YES
NM_010781	Tpsb2	tryptase beta 2	1.31383	0.645675	-1.02	-1.995	0.0001	0.0031	0.49	YES
NM_029489	Samd7	sterile alpha motif domain containing 7	0.29519	0.144114	-1.03	-1.502	0.0011	0.0243	0.49	YES
NM_009251	Serpina3g	serine (or cysteine) peptidase inhibitor, clade A, member 3G	2.8381	1.37454	-1.05	-2.706	5E-05	0.0017	0.48	YES
NM_001033426	Grxcr2	glutaredoxin, cysteine rich 2	0.92194	0.440275	-1.07	-2.189	5E-05	0.0017	0.48	YES
NM_001195413	Cngb1	cyclic nucleotide gated channel beta 1	2.69695	1.27922	-1.08	-3.734	5E-05	0.0017	0.47	YES
NM_008639	Mtnr1a	melatonin receptor 1A	5.77357	2.62562	-1.14	-4.024	5E-05	0.0017	0.45	YES
NM_023114	Apoc3	apolipoprotein C-III	4.33889	1.95199	-1.15	-3.559	5E-05	0.0017	0.45	YES
NM_007753	Cpa3	carboxypeptidase A3, mast cell	1.43308	0.640445	-1.16	-2.337	5E-05	0.0017	0.45	YES
NM_001081104	Chrna9	cholinergic receptor, nicotinic, alpha polypeptide 9	0.43407	0.190864	-1.19	-2.071	5E-05	0.0017	0.44	YES
NM_001039124	Kncn	kinocilin	0.4244	0.186004	-1.19	-1.802	0.0015	0.0316	0.44	YES
NM_020626	Tmem27	transmembrane protein 27	1.12001	0.474484	-1.24	-2.227	5E-05	0.0017	0.42	YES
NR_040690	Gm6329	predicted gene 6329	1.94103	0.794423	-1.29	-3.176	5E-05	0.0017	0.41	YES
NM_007562	Bnc1	basonuclin 1	0.21246	0.086507	-1.30	-2.224	5E-05	0.0017	0.41	YES
NM_139051	Nr5a1	nuclear receptor subfamily 5, group A, member 1	4.21453	1.69683	-1.31	-4.545	5E-05	0.0017	0.40	YES
NM_010780	Cma1	chymase 1, mast cell	1.57236	0.627012	-1.33	-2.517	5E-05	0.0017	0.40	YES
NM_021306	Ece1	endothelin converting enzyme-like 1	1.40392	0.554666	-1.34	-3.472	5E-05	0.0017	0.40	YES
NM_146538	Olfr315	olfactory receptor 315	0.9197	0.359918	-1.35	-2.613	5E-05	0.0017	0.39	YES
NM_001101640	Tmem207	transmembrane protein 207	0.28862	0.100919	-1.52	-2.084	5E-05	0.0017	0.35	YES
NM_010280	Gfra3	glial cell line derived neurotrophic factor family receptor alpha 3	0.26627	0.092918	-1.52	-2.208	5E-05	0.0017	0.35	YES
NM_177597	March11	membrane-associated ring finger (C3HC4) 11	0.91266	0.312823	-1.54	-3.151	5E-05	0.0017	0.34	YES
NM_013553	Hoxc4	homeobox C4	0.27818	0.093819	-1.57	-2.304	5E-05	0.0017	0.34	YES
NM_021369	Chrna6	cholinergic receptor, nicotinic, alpha polypeptide 6	0.92019	0.271773	-1.76	-3.917	5E-05	0.0017	0.30	YES
NM_007430	Nr0b1	nuclear receptor subfamily 0, group B, member 1	1.27334	0.365368	-1.80	-3.954	5E-05	0.0017	0.29	YES
NM_001037842	Cml3	camello-like 3	0.26539	0.058315	-2.19	-2.422	5E-05	0.0017	0.22	YES
ENSMUST00000149572.1	2410114N07	pluripotency associated transcript 9	92.6846	18.922	-2.29	-6.790	5E-05	0.0017	0.20	YES
NM_009889	Cga	glycoprotein hormones, alpha subunit	629.492	127.933	-2.30	-13.237	5E-05	0.0017	0.20	YES
NM_008045	Fshb	follicle stimulating hormone beta	27.1335	5.39097	-2.33	-9.427	5E-05	0.0017	0.20	YES
NM_008497	Lhb	luteinizing hormone beta	54.0695	7.53118	-2.84	-12.250	5E-05	0.0017	0.14	YES
NM_010323	Gnrhr	gonadotropin releasing hormone receptor	7.54035	0.941784	-3.00	-8.650	5E-05	0.0017	0.12	YES
NM_001113356	C1rb	complement component 1, r subcomponent B	0.33316	0.012642	-4.72	-2.870	0.0003	0.007	0.04	YES

Supplemental Table 4. Antibody Conditions

Experiment	Citric Acid Antigen Retrieval	CH_3OH: H_2O_2	Block	Primary Antibody	Secondary Antibody and Detection	Biotin Block	Second Primary Antibody	Second Secondary Antibody and Detection	Reference
ACTH	No	No	NGD	1:1000, National Hormone and Peptide Program	Anti-rabbit Biotin, Strep Cy2	No			
ACTH	No	No	NGD	1:1000, AFP-156102789, National Hormone and Peptide Program	Anti-rabbit Alexa Fluor 488 (Invitrogen)	No			
Caspase 3	10 min	Yes	TNB	1:50, Cell Signaling Technology 9661	Anti-rabbit Biotin, Strep Cy2	No			
CCND1	10 min	Yes	M.O.M., TNB	1:200, Santa Cruz, sc-8396, A-12	Anti-Mouse Biotin, Perkin Elmer TSA-FITC or Biotium TSA-CF488	No			
CDKN1A	10 min	Yes	M.O.M., TNB	1:100, BD Pharmingen, 556431, SXM30	Anti-Mouse Biotin, Perkin Elmer TSA-FITC or Biotium TSA-CF488	No			
CDKN1A/FOXA1	10 min	Yes	M.O.M., TNB	1:100, BD Pharmingen, 556431, SXM30, anti-CDKN1A	Anti-Mouse Biotin, Perkin Elmer Biotium TSA-CF488	Yes	1:100, ThermoFisher PA5-18168, anti-FOXA1	Anti-goat Biotin, Biotium TSA-CF543	
CGA	No	No	NGD	1:1000, National Hormone and Peptide Program	Anti-rabbit Biotin, Strep Cy2	No			
FOXA1	10 min embryo, 15 min postnatal	Yes	TNB	1:100, ThermoFisher PA5-18168	Anti-goat Biotin, Perkin Elmer TSA-FITC or Biotium TSA-CF488	No			
FOXJ1	10 min embryo, 15 min postnatal	Yes	M.O.M., TNB	1:100, ThermoFisher 14-9965-80	Anti-mouse Biotin, Perkin Elmer TSA-FITC	No			
FOXJ1/FOXA1	10 min	Yes	M.O.M., TNB	1:100, ThermoFisher 14-9965-80, Anti-FOXJ1	Anti-mouse Biotin, Perkin Elmer TSA-FITC	Yes	1:100, ThermoFisher PA5-18168, Anti-FOXA1	Anti-goat Biotin, Perkin Elmer TSA-TRITC	
FOXL2	10 min	Yes	TNB	1:100, Novus Bio NB100-1277	Anti-goat Biotin, Perkin Elmer TSA-FITC	No			
FSHb	No	No	NGD	1:250, National Hormone and Peptide Program	Anti-rabbit AlexaFluor 488 (Invitrogen)	No			
GATA3	10 min embryo, 15 min postnatal	Yes	M.O.M., TNB	1:100, BD Biosciences 558686	Anti-mouse Biotin, Biotium TSA-CF488	No			
GH	No	No□	NGD	1:600, National Hormone and Peptide Program	Anti-human Biotin, Strep Cy2	No			
ISL1	10 min embryo, 15 min postnatal	Yes	M.O.M., TNB	1:100, Developmental Studies Hybridoma Bank (DSHB) 40.2D6, Anti-ISL1	Anti-mouse Biotin, Perkin Elmer TSA-FITC	No			
ISL1/FOXA1	10 min	Yes	M.O.M., TNB	1:100, DSHB, 40.2D6, Anti-ISL1	Anti-mouse Biotin, Perkin Elmer TSA-FITC	Yes	1:100, ThermoFisher PA5-18168, Anti-FOXA1	Anti-goat Biotin, Perkin Elmer TSA-TRITC	
ISL1/PROP1	15 min	Yes	M.O.M., TNB	1:100, Dr. Aimee Ryan, Anti-PROP1	Anti-guinea pig biotin, Perkin Elmer TSA-FITC	Yes	1:100, DSHB 40.2D6, Anti-ISL1	Anti-mouse Biotin, Perkin Elmer TSA-TRITC	7
ISL1/SOX2	15 min	Yes	M.O.M., TNB	1:100, DSHB, 40.2D6, Anti-ISL1	Anti-mouse Biotin, Perkin Elmer TSA-FITC	Yes	1:250, Neuromics GT15098, Anti-SOX2	Anti-goat Biotin, Perkin Elmer TSA-TRITC	
KRT8	10 min	Yes	TNB	1:100, Abcam ab5940	Anti-rabbit Biotin, Perkin Elmer TSA-FITC	No			
LHb	No	No	NGD	1:1000, National Hormone and Peptide Program	Anti-guinea pig Biotin, Strep Cy2	No			
LHX3	10 min	Yes	M.O.M., TNB	1:100 DSHB, 67.4E12	Anti-mouse Biotin, Perkin Elmer TSA-FITC or Biotium TSA-CF488	No			
MSH	No	No	NGD	1:100, MilliporeSigma AB5087	Anti-sheep Biotin, StrepCy2	No			
NR5A1	Yes	Yes	TNB	1:500, Dr. Gary Hammer	Anti-rabbit Biotin, Perkin Elmer TSA-FITC	No			8
PAX7	10 min	Yes	M.O.M., TNB	1:100, DSHB	Anti-mouse Biotin, Perkin Elmer TSA-FITC	No			
PITX1	10 min	Yes	TNB	1:250, Dr. Jacques Drouin	Anti-rabbit Biotin, Perkin Elmer TSA-FITC	No			9
POU1F1	10 min	Yes	NGD	1:100, Dr. Simon Rhodes	Anti-rabbit Biotin, Strep Cy2	No			10
PROP1	10 min embryo, 15 min postnatal	Yes	TNB	1:100, Dr. Aimee Ryan	Anti-guinea pig biotin, Perkin Elmer TSA-FITC	No			7
SHH	10 min	Yes	M.O.M., TNB	1:100 DSHB, 5E1	Anti-mouse Biotin, Biotium TSA-CF488	No			
SOX2	10 min embryo, 15 min postnatal	Yes	TNB	1:100, Neuromics GT15098	Anti-goat Biotin, Perkin Elmer TSA-FITC	No			
SOX2/SOX9	10 min	Yes	TNB	1:250, Neuromics GT15098, Anti-SOX2	Anti-goat Biotin, Perkin Elmer TSA-FITC	Yes	1:50, Millipore AB5535, Anti-SOX9	Anti-rabbit Biotin, Perkin Elmer TSA-TRITC	
SOX9	10 min embryo, 15 min postnatal	Yes	TNB	1:100, Abcam ab185966	Anti-rabbit Biotin, Perkin Elmer TSA-FITC	No			
TSHb	No	No	NGS	1:1000, National Hormone and Peptide Program	Anti-guinea pig AlexaFluor 555 (Invitrogen) or anti-guinea pig TRITC (Invitrogen)	No			
TSHb	No	No	NGD	1:1000, National Hormone and Peptide Program	Anti-rabbit Biotin, Strep Cy2	No			
TUBA1A	10 min	Yes	M.O.M., TNB	1:200, Sigma T6793	Anti-mouse Biotin, Perkin Elmer TSA-FITC	No			
TUBA1A/KRT8	10 min	Yes	M.O.M., TNB	1:100, Sigma T6793, Anti-TUBA1A	Anti-mouse Biotin, Perkin Elmer TSA-FITC	Yes	1:100, Abcam ab5940, Anti-KRT8	Anti-rabbit Biotin, Perkin Elmer TSA-TRITC	
YFP	10 min	Yes	TNB	1:100, Abcam ab6556	Anti-rabbit Biotin, Perkin Elmer TSA-FITC or Biotium TSA-CF488	No			

*NGD= Normal Goat Diluent
*M.O.M= Mouse on Mouse Blocking Kit, Vector Labs
*TNB= 0.1M Tris HCl, pH 7.5; 0.15M NaCl, 0.5% Blocking Reagent

Supplemental Methods

Mouse sources and genotyping. *Isl1*^{tm2Gan} mice were a generous gift from Dr. Lin Gan, Dept. of Neuroscience and Regenerative Medicine, Medical College of Georgia, Augusta University, Augusta, GA (1). These mice, referred to here as *Isl1*^{fl}, have loxP sites flanking exon 2. The *Isl1*$^{+/-}$ mice were generated by breeding the *Isl1*^{fl} to B6.C-*Tg(CMV-cre)*$^{1Cgn/J}$ mice (stock number 006054; The Jackson Laboratory) (2). *Tg(Prop1-cre)*^{432Sac}, referred to here as *Prop1-cre,* were generated at University of Michigan (3). The cre reporter strain, B6.129X1-*Gt(ROSA)26Sor*$^{tm1(EYFP)Cos}$/J, referred to as R26R-EYFP, were purchased from the Jackson Laboratory, Stock no. 006148, and genotyped according to the Jackson Laboratory recommended primers and conditions (4). The tamoxifen inducible cre strain, B6.Cg-Tg(CAG-cre;Esr1*)5Amc/J stock 004682 (5), *CAG-Cre-ERT2* was purchased from the Jackson Laboratory. The B6-*Hesx1-cre* strain was generously donated by Dr. Juan Pedro Martinez-Barbera, Developmental Biology and Cancer, Birth Defect Research Centre, GOS Institute of Child Health, University of College London, London, UK (6).

Isl1 and *Prop1-cre* mice were genotyped as previously described (2, 3). *Hesx1-cre* mice were genotyped with oligos specific to the cre recombinase: forward 5'-GCATAACCAGTGAAACAGCATTGCTG-3' and reverse 5'-GGACATGTTCAGGGATCGCCAGGCG-3' using the following conditions: 94°C for 3 min followed by 33 cycles of 94°C 30 sec, 60°C 45 sec, 72°C 90 sec then ending with a final extension of 72°C for 10 min. *CAG-Cre-ERT2* mice were genotyped as described (5), using the following conditions: 94°C for 5 min followed by 35 cycles of 94°C 30 sec, 55°C 30 sec, 72°C 30 sec and a final extension of 72°C for 5 min.

Tissue Preparation. Staged embryos were established using timed pregnancy breeding with the observance of the copulation plug documented at E0.5. Embryos were collected and fixed in 4% buffered formaldehyde with time of fixation depending on the age of the embryo. E11.5 and

E12.5 were fixed for 45 mins and E13.5 thru E16.5 were fixed for 1 hr. After fixation the embryos were washed in 1xPBS then dehydrated through a series of ethanol solutions to 70%. For analysis of neonatal pituitary glands, P0, P3, and P7 heads were dissected and the skin, lower jaw, and skull removed to aid in the penetration of the fixative solutions. P0 and P3 heads were fixed for 4 hours and P7 heads were fixed overnight at 4°C. After fixation, the heads were fixed and treated with 10% EDTA 24-36 hrs to soften the bone and aid in sectioning. Heads were dehydrated through a series of ethanol solutions to 70%. Dissected pituitaries from 3 wk – 1 yr old mice were fixed overnight in 4% buffered formaldehyde, rinsed in 1xPBS, then treated for 24 hrs in 10% EDTA. Pituitaries were then dehydrated through a series of ethanol solutions to 70%. All tissues were processed in the Miles Scientific Tissue-Tek VP Model #20 embedding machine and the Shandon Histocentre 2 Model #64000012 embedding station. Embedded tissues were sectioned to 6μm thickness on an American Optical Microtome and mounted onto SuperFrost Plus microscope slides (Fisher Scientific). Sections from a minimum of 3 animals per genotype per time point were processed by Hematoxylin and Eosin staining or used for immunohistochemistry. Relative Rathke's pouch size was determined by expressing the average Rathke's pouch area as a percentage of the average head area. Areas were calculated with Image J software from five hematoxylin and eosin stained sections per embryo in 7 controls and 10 *Isl1*^{Prop1KO} samples.

For the analysis of *CAG-Cre-ERT2; Isl1*$^{fl/fl}$ conditional mutant embryos, pregnant females were injected with tamoxifen at e12.5 and embryos were extracted at e18.5. *CAG-Cre-ERT2; Isl1*$^{fl/fl}$ embryos were compared to their *Isl1*$^{fl/fl}$ siblings, which served as negative controls. Embryo heads were fixed in 4% paraformaldehyde for 5 hrs and cryoprotected in 10% sucrose/PBS overnight at 4°C. The following day, heads were embedded in 10% gelatin (Sigma-Aldrich) in 10% sucrose/PBS solution, frozen in isopentane at -60°C and stored at -80°C

until use. Gelatin-embedded heads were sliced in 20µm cryosections using a cryostat (Microm 505n).

Immunohistochemistry. Prior to immunohistochemistry paraffin was removed from tissue sections using xylene and sections were rehydrated using a series of ethanol solutions and 1 x PBS. Single and double immunochemistry was performed as previously described (7). Specific antibody information, dilutions, and detection methods are listed in Supplemental Table 4. The ISL1 antibody, 40.2D6, was deposited to the Developmental Studies Hybridoma Bank (DSHB) by Jessell, T.M./Brenner-Morton, S.). The PROP1 antibody was a generous gift from Dr. Aimee K. Ryan, Department of Human Genetics, McGill University, Montreal, QC (7). The LHX3 antibody, 67.4E12, was deposited to the DSHB by Jessell, T.M./Brenner-Morton, S.). The NR5A1 antibody was a generous gift from Dr. Gary Hammer, Cell and Developmental Biology, University of Michigan (8). The PAX7 antibody was deposited to the DSHB by Kawakami, A. (DSHB Hybridoma Product PAX7). The PITX1 antibody was a generous gift from Dr. Jacques Drouin, Laboratoire de Genetique Moleculaire, Institut de recherches cliniques de Montreal, Montreal, QC (9). This POU1F1 antibody was a kind gift from Dr. Simon Rhodes, University of North Florida, Jacksonville, FL (10). The SHH antibody, 5E1, was deposited to the DSHB by Jessell, T.M./Brenner-Morton, S.). The number of LH positive and TSH positive cells per unit area was determined using the Image J software and counting the number of immunopositive cells per unit area in an average of 4 slides per sample across 5 control and 4 $Isl1^{Prop1KO}$ neonates. The area of the cysts was excluded from the overall pituitary area in $Isl1^{Prop1KO}$ samples. The number of FSH and TSH cells in *CAG-Cre-ERT2;* $Isl1^{fl/fl}$ pituitaries was determined by counting immunopositive cells per unit area using FIJI (Image J) software in an average of 6 slides per sample across 5 control and 5 mutant embryos.

Alcian Blue/PAS staining. Prior to Alcian Blue/PAS staining, paraffin was removed from tissue sections using Xylene and sections were rehydrated to 95% ethanol, then rinsed in distilled water. Sections were then incubated in 3% acetic acid for 3 mins then incubated for 15 mins in Alcian Blue, pH 2.5. Sections were then rinsed in running tap water for 2 mins, followed by a 5-min incubation in 0.5% periodic acid. Sections were again rinsed for 2 mins under gently running tap water then incubated for 10 mins in Schiff's Reagent. Sections were then washed for 5 mins in lukewarm tap water, dehydrated to 100% ethanol, cleared with xylene and mounted with Permount Mounting Media.

In Situ Hybridization. The *Gata2* cDNA clone K7B20006K16 was from an E14.5 mouse pituitary cDNA library (11). The *Gata2* plasmid was linearized with *Xho*I and transcribed with T3 polymerase to generate the antisense probe and linearized with *Sfi*I and transcribed with T7 to generate the sense control probe. The probes were diluted 1:100 in hybridization solution and the ISH protocol was performed as previously described (12).

RNAseq. P0 pituitaries were harvested from 6 control mice and 6 $Isl1^{Prop1KO}$ mice. RNA was prepared using the RNA Micro Kit (Ambion). Libraries were prepared from the RNA using the TruSeq RNA Library Prep Kit v2 (Illumina) by the University of Michigan Sequencing Core. The quality of the library preps was confirmed using the Bioanalyzer 2200 (Agilent, Santa Clara, CA). 50 bp single-end sequencing was performed on Illumina HiSeq 4000, each sample was barcoded and pooled and the samples were run across two lanes. Sequencing reads were analyzed by the University of Michigan Bioinformatics Core. The quality of the raw reads data for each sample was confirmed using FastQC (version 0.10.1) to identify features of the data that may indicate quality problems (e.g. low quality scores, over-represented sequences, inappropriate GC content, etc.). The reads were trimmed based on these quality scores. The Tuxedo Suite software package was utilized for alignment, differential expression analysis, and

post-analysis diagnostics (13-15). Briefly, reads were aligned to the combined reference mRNA and lncRNA total transcriptome (UCSC mm10) (http://genome.ucsc.edu/) using TopHat (version 2.0.9) and Bowtie (version 2.1.0.). Default parameter settings were used for alignment, with the exception of: "--b2-very-sensitive" telling the software to spend extra time searching for valid alignments. FastQC was used for a second round of quality control (post-alignment), to ensure that only high-quality data would be input to expression quantitation and differential expression analysis. Cufflinks/CuffDiff (version 2.1.1) was used for expression quantitation, normalization, and differential expression analysis, using UCSC mm10.fa as the reference genome sequence. For this analysis, the parameter settings: "--multi-read-correct" were used to adjust expression calculations for reads that map in more than one locus, as well as "--compatible-hits-norm" and "--upper-quartile –norm" for normalization of expression values. Diagnostic plots were generated using the CummeRbund package. We used locally developed scripts to format and annotate the differential expression data output from CuffDiff. Briefly, we identified genes and transcripts as being differentially expressed based on three criteria: test status = "OK", FDR $\leq$ 0.05 and fold change $\geq \pm$ 1.5. We annotated genes and isoforms with NCBI Entrez GeneIDs and text descriptions. We further annotated differentially expressed genes with Gene Ontology (GO) (http://www.geneontology.org/) terms using NCBI annotation. We used Gene Sequence Enrichment Analysis software (GSEA_4.0.3) for enrichment analysis of the set of differentially expressed genes to identify significantly enriched functional categories. Principal Component Analysis was performed using ClustVis (16). Data from the RNAseq has been deposited in NCBI's Gene Expression Omnibus (17) and is accessible through the Geo accession number GSE149019.

CAG-Cre-ERT2; Isl1$^{fl/fl}$ tamoxifen injection. Tamoxifen (T56648, Sigma-Aldrich) was dissolved in sesame oil (S3547, Sigma-Aldrich) at 10 mg/ml. A single dose of tamoxifen (75μg per gram of body weight) was administered to the mother by intraperitoneal injection at e12.5.

Serum T4 analysis. Blood was collected from 7 control male mice and 7 *Isl1*^{Prop1KO} mutant male mice at 3 wks of age. Blood was allowed to coagulate at room temperature for 20 mins and serum was isolated by centrifugation at 1000rpm for 30 mins. Free T4 levels were analyzed using 25ul of serum with the Total T4 EIA Kit (MP Biomedical).

Statistics. Significance of normalized Rathke's pouch size, LH, TSH, and FSH cells/area, and T4 serum analysis were determined using the Student's T-Test, one tail distribution, 2 sample unequal variance.

Study approval. All mouse studies were approved by the University of Michigan IACUC (PRO00008714) or by the FCEN-University of Buenos Aires CICUAL (protocol no. 68). Mice were housed in an AALAC approved animal facility at University of Michigan and at the Bioterio Central of FCEN-UBA.

Informed consent for collection of human pituitary specimens was approved by the ethical committee of Kagoshima University (reference no. 180135). Anonymized specimens were sent to University of Michigan for immunostaining, which was classified as exempt by the IRB-MED.

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