Supplemental Methods

In situ hybridization

Staged E14.5 and E16.5 C57Bl/6J embryos were dissected in DEPC-treated 1X PBS. Isolated gastrointestinal tracts were fixed overnight at 4°C in 4% paraformaldehyde (PFA), embedded in paraffin, and cut into 5 μm sections. In situ hybridization was performed as described previously (Li et al., 2007). Specific probes used for in situ hybridization included: Gata3 (NM_008091.3; 1028-1591 bp), nephrocan (NM_025684.2; 758-1450 bp), Sfrp5 (NM_018780.2; 203-985 bp), Creb3l3 (NM_145365.3; 683-1361 bp), Tcfec (NM_031198.2; 258-789), Grem1 (NM_011824.4; 487-1281), and Axin2 (NM_015732.4; 2227-3358).

Antibodies and immunostaining

Staged E14.5 and E16.5 C57Bl/6J embryos were dissected in 1X PBS. Excised gastrointestinal tracts were fixed for overnight at 4°C in 4% PFA, embedded in paraffin, and cut into 5 μm sections. Vectastain ABC (Vector) was used for Hnf4γ immunohistochemistry, per the manufacturer's instructions. Sox2 immunofluorescence was performed as described previously (Que et al., 2007). Briefly, sections were deparaffinized in xylene, rehydrated through increasing alcohol concentrations, and boiled for 10 minutes either in Antigen Unmasking Solution (Vector Laboratories, CA) (Sox2) or 10 mM sodium citrate, pH 6.0 (Hnf4γ). Slides were allowed to slowly cool down and then washed with 1X PBS. The sections were blocked with 10% donkey serum/0.01% Triton X-100 in 1X PBS for 1 hour at room temperature. Antibodies used were: rabbit polyclonal anti-Sox2 antibody (1:500, Chemicon, MA); goat polyclonal anti-Hnf4γ (1:500, Santa Cruz Biotechnology, CA); biotinylated horse anti-goat IgG (1:200, Vector); and,

Supplemental Table 6. Summary of primer sequences and optimized conditions

Gene Symbol	Forward primer	Reverse primer	Amplicon length (bp)	Temp (deg C)	Cycles	$MgCl_2$ (mM)	DMSO[1]
Barx1	GGAGTCGCACCGTATTCACTGAGC	CCGCCACCTTGCAGCACTATTTTC	187	58	30	2.5	NO
Cdx1	CGGACGCCCTACGAATGGATG	CTGCTGCTGCTGCTGTTTCTTC	276	61	30	1.5	YES
Cdx2	GAAACCTGTGCGAGTGGATGC	TTGTTGCTGCTGCTGCTGTTG	284	58	30	1.5	YES
Creb3l3	CAGTGGCATCTCTGAGGATCTACC	CAGTGAGGTTGAAGCGGGAGG	266	61	30	1.5	YES
Foxa1	GGCATGAGAGCAACGACTGG	TAGGTGTTCATGGAGTTCATAGAGC	115	57	30	2.5	NO
Gli1	CGCCAAGCACCAGAATCGG	CCGAGACACAAGGTCCTTCATCC	419	61	40	6[2]	YES
Hnf4a	GATGCTTCTCGGAGGGTCTGC	TTGGTGGTGATGGCTGTGGAG	200	60	30	1.5	NO
Hnf4g	CGCAGCATTCGGAAGAGTCATG	CCGCTTGTGCCAGAGTGTTTATG	220	60	30	1.5	NO
Hprt	AGTCCCAGCGTCGTGATTAGC	ATAGCCCCCCTTGAGCACACAG	204	61	30	2[2]	YES[3]
Isx	ACTTCACCCATTACCCTGACATCC	TCTTCTCCTGCTTCCTCCACTTG	123	55	30	1.5	YES
Maf	CAACGGCTTCCGAGAAAACG	CCCACGGAGCATTTAACAAGG	111	56	30	2.5	YES
Mafb	GCAACAGCTACCCACTAGCC	AGCTGGTCATCAGAGAAGCG	108	60	30	2.5	YES
Sfrp5	CCCTGGACAACGACCTCTGC	CACAAAGTCACTGGAGCACATCTG	143	59	30	2.5	YES
Sox2	CTCGCAGACCTACATGAACG	AGTGGGAGGAAGAGGTAACC	146	59	28	3	NO
Tcfec	ATGAACCCATGAGCCCAGACAG	AGCATCCGTGAGACCAGCATTAG	173	56	30	2	YES

[1]To be used at a 2% final concentration.

[2]iQ Supermix contains 6 mM $MgCl_2$ (qPCR only).

[3]To be used at a 4% final concentration (qPCR only).

Alexa Fluor 488 donkey anti-rabbit IgG (1:1000, Invitrogen, OR). Primary antibodies were diluted in blocking solution and incubated on slides overnight at 4°C. Slides were washed in 1X PBS prior to incubation with appropriate secondary antibodies and DAPI (1:100, Fisher Scientific, PA) (Sox2) for 30 to 60 minutes at room temperature. After 1X PBS wash, coverslips were mounted with ProLong Gold Antifade Reagent (Invitrogen) (Sox2), or sections were lightly counterstained with hematoxylin, dehydrated with serial alcohol/xylene washes and coverslips were mounted with Permount (Fisher). Imaging was done on a Nikon E800 microscope digital imaging system (Nikon, Japan).

X-gal staining

Staged E14.5 or E16.5 embryos from genetic crosses of villin$^{lacZ/+}$ or Gli1$^{lacZ/+}$ males with C57Bl/6J females were dissected on ice in 1X PBS (Park et al., 2000; Braunstein et al., 2002). The gastrointestinal tract was excised, fixed with 4% PFA for 10 minutes at 4°C, and washed three times in 1X PBS. Tissues were saturated overnight with 30% sucrose (in 1X PBS), embedded and frozen in Optimal Cutting Temperature (OCT) compound (Sakura, Japan), and cut into 5 μm sections. X-gal staining solution was prepared fresh, as follows: 1X PBS (pH 7.5), 2 mM magnesium chloride, 5 mM potassium ferrocyanide, 5 mM potassium ferricyanide, and 1 mg X-gal (from 20 mg/ml stock in DMF). Sectioned tissue was incubated in staining solution at 37°C and monitored periodically to control staining intensity. Sections were then washed three times in 1X PBS, counterstained lightly with eosin and dehydrated with serial alcohol/xylene washes, and coverslips were mounted with Permount. Slides were imaged on an E800 microscope imaging system.

qPCR

Staged E14.5 and E16.5 C57Bl/6J embryos were dissected in 1X PBS. Samples from the duodenum and antrum of individual embryos were collected and RNA was harvested by brief vortexing in MELT (Multi-Enzymatic Liquefaction of Tissue) digestion buffer (Applied Biosystems/Ambion, TX) and purified using the RNeasy kit. A total of eight E14.5 and nine E16.5 samples were obtained (for each tissue). cDNA was prepared with the iScript cDNA Synthesis Kit (Bio-Rad). qPCR reactions were set up using 2X iQ Supermix buffer and iQ iCycler 96-well plates and carried out in an iCycler real-time PCR detection system (Bio-Rad). Data were processed using the iCycler program (Bio-Rad) and imported into Excel (Microsoft, WA) for normalization and statistical analysis. Gli1 Ct values were normalized to Hprt (ΔCt) and then compared to the average ΔCt for E14.5 intestine ($\Delta\Delta$Ct). Average $\Delta\Delta$Ct values were calculated to determine relative fold difference to E14.5 tissue [2^(- $\Delta\Delta$Ct)]. 95% confidence intervals were determined using Excel (CONFIDENCE function). PCR conditions were optimized previously in the lab (i.e.- temperature, DMSO, etc; see Supplemental Table 6).

RT-PCR

Staged E14.5 and E16.5 C57Bl/6J embryos were dissected in 1X PBS. Samples from four independent collections were separated by tissue type and time point (e.g. - E14.5 border, E16.5 duodenum, etc.) and then pooled randomly into two groups for replicate analysis. Additionally, fragments of contiguous tissue spanning the antrum, border and proximal duodenum were collected from E14.5 and E16.5 embryos as an input control. Tissue from each group was homogenized in 1 mL of TRIzol (Invitrogen) by drawing it through a 30-gauge needle. Total RNA was prepared according to the manufacturer's instructions, purified by consecutive phenol-

chloroform (2X) and chloroform (2X) extractions, and quantitated by UV spectrophotometry using a NanoDrop (Thermo). For each RNA sample, two independent cDNA preparations were performed using the iScript cDNA Synthesis Kit and pooled for subsequent analysis. Negative "No RT" controls for genomic contamination were prepared from whole E14.5 and E16.5 RNA in a similar manner. PCR was performed on cDNA samples using qRT-PCR-quality primers created by Beacon Designer (PREMIER Biosoft). Individual primer conditions were optimized (i.e.- temperature, number of cycles, magnesium chloride, DMSO, etc; see Supplemental Table 6) prior to PCR. Products from PCR reactions were resolved under UV light with ethidium bromide-loaded, 2% TBE-agarose gels. The band intensity of experimental genes was compared to the housekeeping gene Hprt.

Supplemental Figure Legends

Supplemental Figure 1. Diagram of microdissection for microarray experiment

A photomicrograph showing E14.5 foregut. The pylorus was identified grossly by its muscular constriction (arrows). Small, contiguous pieces of tissue were dissected from the pylorus and surrounding stomach and duodenum. St = stomach, Py = pylorus and D = duodenum.

Supplemental Figure 2. Independent validation of microarray data by RT-PCR

Semi-quantitative RT-PCR was carried out as described in Supplemental Methods. Hprt is used as a control; it does not vary with time and tissue. Tissue specific regulation of Cdx1, Cdx2, Isx, Barx1, Sox2 and Sfrp5 is set by E14.5 and does not vary with time. Mafb and Hnf4γ are preferentially, but not specifically, expressed in the intestine. Tcfec and Creb3l3 are greatly induced in E16.5 duodenum.

Supplemental Table 3. DAVID analysis of D16 enriched epithelial genes					
Annotation Cluster 1	Enrichment Score: 5.05	Count	P-value	Fold Enrichment	FDR
cellular lipid metabolic process		29	2.0E-7	3.1	0
Annotation Cluster 2	Enrichment Score: 4.64	Count	P-value	Fold Enrichment	FDR
transporter		40	2.4E-15	4.7	0
Annotation Cluster 3	Enrichment Score: 4.1	Count	P-value	Fold Enrichment	FDR
hydrolase activity, acting on glycosyl bonds		13	1.2E-6	6.2	0
Annotation Cluster 4	Enrichment Score: 3.95	Count	P-value	Fold Enrichment	FDR
carbohydrate metabolism		30	2.2E-10	4.2	0
Annotation Cluster 5	Enrichment Score: 3.44	Count	P-value	Fold Enrichment	FDR
acyltransferase activity		12	1.7E-4	4.1	0.3
Annotation Cluster 6	Enrichment Score: 3.18	Count	P-value	Fold Enrichment	FDR
organic acid metabolic process		22	9.3E-5	2.6	0.2

Note: Only the top annotation term is displayed for a given Annotation Cluster.

Supplemental Table 4. Summary of gene expression changes in Wnt signaling pathway components

Probeset ID	Symbol	Description	D14-S14	D16-S16	S16-S14	D16-D14
1437351_at	Cxxc4	CXXC finger 4	NC (1.15)	S16 (2.25)	NC (1.93)	D14 (5.01)
1438884_at	D830007B15Rik	RIKEN cDNA D830007B15 gene	D14 (3.62)	NC (1.40)	NC (1.36)	D14 (3.70)
1420512_at	Dkk2	dickkopf homolog 2 (Xenopus laevis)	NC (1.06)	S16 (3.01)	S14 (2.05)	D14 (6.56)
1417312_at	Dkk3	dickkopf homolog 3 (Xenopus laevis)	NC (1.24)	S16 (2.29)	NC (1.11)	D14 (2.57)
1437284_at	Fzd1	frizzled homolog 1 (Drosophila)	NC (1.42)	S16 (2.14)	NC (1.04)	D14 (3.15)
1418532_at	Fzd2	frizzled homolog 2 (Drosophila)	NC (1.62)	S16 (4.55)	S14 (2.00)	D14 (5.61)
1449730_s_at	Fzd3	frizzled homolog 3 (Drosophila)	NC (1.12)	NC (1.76)	NC (1.43)	D14 (2.24)
1417301_at	Fzd6	frizzled homolog 6 (Drosophila)	NC (1.45)	S16 (2.59)	NC (1.14)	NC (1.57)
1450044_at	Fzd7	frizzled homolog 7 (Drosophila)	NC (1.19)	NC (1.95)	S14 (2.46)	D14 (4.02)
1451022_at	Lrp6	low density lipoprotein receptor-related protein 6	NC (1.36)	NC (1.19)	S14 (2.02)	NC (1.76)
1417278_a_at	Nkd1	naked cuticle 1 homolog (Drosophila)	NC (1.46)	NC (1.67)	NC (1.14)	D14 (2.14)
1452249_at	Prickle1	prickle like 1 (Drosophila)	NC (1.19)	NC (1.50)	NC (1.51)	D14 (2.70)
1428808_at	Prickle2	prickle-like 2 (Drosophila)	NC (1.62)	NC (1.62)	NC (1.50)	D14 (3.94)
1446780_at	Ror2	Receptor tyrosine kinase-like orphan receptor 2	NC (1.11)	NC (1.52)	S14 (2.07)	NC (1.23)
1423986_a_at	Scotin	scotin gene	NC (1.03)	NC (1.06)	S16 (3.35)	D16 (3.66)
1448395_at	Sfrp1	secreted frizzled-related sequence protein 1	NC (1.29)	S16 (2.17)	S14 (3.24)	D14 (5.45)
1448201_at	Sfrp2	secreted frizzled-related protein 2	NC (1.28)	S16 (6.37)	NC (1.55)	D14 (7.70)
1451031_at	Sfrp4	secreted frizzled-related sequence protein 4	NC (1.91)	S16 (2.52)	S16 (2.13)	NC (1.62)
1436075_at	Sfrp5	secreted frizzled-related sequence protein 5	D14 (31.69)	D16 (10.66)	NC (1.58)	D14 (4.71)
1450117_at	Tcf3	transcription factor 3	NC (1.45)	S16 (5.35)	NC (1.63)	D14 (6.03)
1441756_at	Tcf7l2	Transcription factor 7-like 2, T-cell specific, HMG-box	NC (1.87)	NC (1.43)	S14 (2.45)	NC (1.87)
1423852_at	Tmem46	transmembrane protein 46	D14 (2.79)	NC (1.84)	NC (1.02)	D14 (5.03)
1438426_at	Tmem58	transmembrane protein 58	NC (1.03)	S16 (2.25)	NC (1.64)	D14 (3.61)
1436118_at	Vangl2	vang-like 2 (van gogh, Drosophila)	NC (1.10)	S16 (2.78)	NC (1.81)	D14 (4.56)
1450772_at	Wnt11	wingless-related MMTV integration site 11	NC (1.48)	S16 (2.21)	NC (1.93)	NC (1.29)
1450782_at	Wnt4	wingless-related MMTV integration site 4	NC (1.35)	S16 (4.35)	S16 (6.34)	NC (1.97)
1436791_at	Wnt5a	wingless-related MMTV integration site 5A	S14 (2.34)	S16 (4.38)	NC (1.59)	D14 (2.99)
1436978_at	Wnt9a	wingless-type MMTV integration site 9A	NC (1.22)	NC (1.47)	NC (1.20)	D14 (2.17)

Note: NC means no significant change (significant change is FC≥2 and $p<0.05$). For each comparison, the label (e.g., D14, D16, S14, S16) refers to the time and/or tissue of maximum expression and the number in parentheses is the fold change.

Supplemental Table 5. Summary of pyloric genes

Probeset ID	Symbol	Description	P14-S14	P14-D14	P16-S16	P16-D16
1459266_at	---	---	P14 (2.05)	P14 (2.08)	NC (1.53)	NC (1.47)
1429286_at	1190003M12Rik	RIKEN cDNA 1190003M12 gene	NC (1.12)	NC (1.64)	P16 (2.48)	P16 (12.56)
1424439_at	1810065E05Rik	RIKEN cDNA 1810065E05 gene	NC (1.76)	NC (1.67)	P16 (4.51)	P16 (6.56)
1425233_at	2210407C18Rik	RIKEN cDNA 2210407C18 gene	P14 (5.01)	P14 (2.87)	NC (1.00)	P16 (17.46)
1427437_at	2610203C20Rik	RIKEN cDNA 2610203C20 gene	NC (1.54)	P14 (2.87)	P16 (2.40)	P16 (2.20)
1432556_a_at	3100002J23Rik	RIKEN cDNA 3100002J23 gene	P14 (6.30)	NC (1.46)	P16 (2.65)	P16 (2.19)
1438798_at	4931406P16Rik	RIKEN cDNA 4931406P16 gene	NC (1.62)	NC (1.75)	P16 (2.92)	P16 (2.18)
1435163_at	9030612M13Rik	RIKEN cDNA 9030612M13 gene	P14 (2.19)	P14 (2.45)	P16 (3.37)	NC (1.75)
1438531_at	A730054J21Rik	RIKEN cDNA A730054J21 gene	NC (1.69)	P14 (2.65)	P16 (2.47)	P16 (3.95)
1415927_at	Actc1	actin, alpha, cardiac	NC (1.91)	NC (1.24)	P16 (2.04)	P16 (2.58)
1451675_a_at	Alas2	aminolevulinic acid synthase 2, erythroid	P14 (3.26)	P14 (2.03)	P16 (2.89)	P16 (3.41)
1416649_at	Ambp	alpha 1 microglobulin/bikunin	P14 (2.20)	NC (1.33)	P16 (8.72)	P16 (2.39)
1459253_at	Arrdc3	Arrestin domain containing 3	P14 (2.57)	P14 (2.84)	NC (1.27)	NC (1.08)
1443801_at	AW822216	Expressed sequence AW822216	NC (1.55)	NC (1.84)	P16 (3.37)	P16 (2.10)
1438663_at	Bat2d	BAT2 domain containing 1	NC (1.32)	n/1 (1.87)	P16 (2.34)	P16 (2.28)
1440990_at	BC056349	cDNA sequence BC056349	NC (1.83)	P14 (2.34)	P16 (2.25)	P16 (3.26)
1457458_at	BC057627	cDNA sequence BC057627	NC (1.50)	NC (1.77)	P16 (2.14)	P16 (2.10)
1450624_at	Bhmt	betaine-homocysteine methyltransferase	NC (1.96)	NC (1.64)	P16 (2.56)	P16 (2.89)
1439040_at	Cenpe	centromere protein E	NC (1.40)	NC (1.55)	P16 (2.25)	P16 (3.42)
1427767_a_at	Cftr	cystic fibrosis transmembrane conductance regulator homolog	NC (1.40)	NC (1.04)	P16 (3.73)	P16 (2.33)
1436343_at	Chd4	chromodomain helicase DNA binding protein 4	NC (1.37)	NC (1.63)	P16 (2.46)	P16 (2.19)
1439427_at	Cldn9	claudin 9	NC (1.32)	NC (1.41)	P16 (2.53)	P16 (2.67)
1428571_at	Col9a1	procollagen, type IX, alpha 1	P14 (2.76)	P14 (2.48)	P16 (4.63)	P16 (10.41)
1448326_a_at	Crabp1	cellular retinoic acid binding protein I	NC (1.63)	P14 (5.02)	P16 (2.14)	P16 (5.53)
1424598_at	Ddx6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	NC (1.49)	P14 (2.13)	P16 (2.68)	P16 (3.54)
1437403_at	E130306M17Rik	RIKEN cDNA E130306M17 gene	P14 (2.30)	P14 (2.23)	P16 (2.80)	P16 (4.29)
1456319_at	EG665081	predicted gene, EG665081	P14 (2.19)	P14 (2.36)	NC (1.58)	NC (1.72)
1449077_at	Eraf	erythroid associated factor	P14 (2.46)	NC (1.71)	P16 (2.88)	P16 (3.60)
1456326_at	Gm784	gene model 784, (NCBI)	NC (1.46)	NC (1.04)	P16 (2.24)	P16 (4.08)
1423436_at	Gsta3	glutathione S-transferase, alpha 3	P14 (4.12)	NC (1.01)	P16 (2.97)	P16 (2.24)
1423016_a_at	Gypa	glycophorin A	P14 (2.86)	NC (1.96)	P16 (4.00)	P16 (4.59)
1448716_at	Hba-x	hemoglobin X, alpha-like embryonic chain in Hba complex	P14 (2.14)	NC (1.33)	P16 (2.17)	P16 (2.70)
1427866_x_at	Hbb-b1	hemoglobin, beta adult major chain	P14 (2.46)	NC (1.92)	P16 (2.44)	P16 (3.60)
1418199_at	Hemgn	Hemogen	P14 (3.02)	P14 (2.07)	P16 (3.14)	P16 (3.79)
1426114_at	Hnrpab	heterogeneous nuclear ribonucleoprotein A/B	NC (1.39)	NC (1.29)	P16 (2.67)	P16 (2.00)
1458492_x_at	Hnt	Neurotrimin	NC (1.26)	P14 (2.59)	P16 (2.32)	P16 (3.77)
1423276_at	Ildr1	immunoglobulin-like domain containing receptor 1	NC (1.41)	NC (1.41)	P16 (2.85)	P16 (2.07)
1442368_at	Kctd12b	potassium channel tetramerisation domain containing 12b	NC (1.72)	NC (1.80)	P16 (2.49)	P16 (3.28)
1460258_at	Lect1	leukocyte cell derived chemotaxin 1	P14 (4.27)	P14 (4.45)	NC (1.06)	NC (1.52)
1422071_at	Lgals6	lectin, galactose binding, soluble 6	P14 (7.12)	P14 (4.57)	P16 (2.79)	P16 (2.29)
1421278_s_at	LOC630963	similar to spectrin alpha 1	P14 (4.19)	NC (1.50)	P16 (5.80)	P16 (5.54)
1418188_a_at	Malat1	Metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	NC (1.27)	P14 (2.21)	P16 (3.23)	P16 (4.01)
1451989_a_at	Mapre2	microtubule-associated protein, RP/EB family, member 2	NC (1.31)	NC (1.01)	P16 (2.13)	P16 (2.14)
1422643_at	Moxd1	monooxygenase, DBH-like 1	P14 (2.12)	NC (1.07)	P16 (2.30)	P16 (3.95)
1437250_at	Mreg	Melanoregulin	S14 (3.33)	D14 (3.12)	S16 (-4.30)	NC (1.01)
1435521_at	Msi2	Musashi homolog 2 (Drosophila)	NC (1.51)	P14 (2.03)	P16 (2.25)	P16 (3.03)
1436309_at	Neto2	neuropilin (NRP) and tolloid (TLL)-like 2	P14 (2.36)	NC (1.00)	P16 (2.24)	P16 (2.98)
1448290_at	Pap	pancreatitis-associated protein	P14 (2.67)	D14 (2.09)	P16 (63.15)	P16 (2.80)
1428952_at	Pdia2	protein disulfide isomerase associated 2	NC (1.41)	NC (1.07)	S16 (5.69)	D16 (2.88)
1460332_at	Pln	Phospholamban	NC (1.91)	NC (1.60)	P16 (2.00)	P16 (3.63)
1448186_at	Pnliprp2	pancreatic lipase-related protein 2	P14 (2.49)	NC (1.50)	P16 (23.05)	P16 (2.39)
1449876_at	Prkg1	protein kinase, cGMP-dependent, type I	NC (1.82)	NC (1.19)	P16 (2.33)	P16 (2.97)
1460633_at	Prpf19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	NC (1.81)	NC (1.66)	P16 (2.02)	P16 (2.12)
1454791_a_at	Rbbp4	retinoblastoma binding protein 4	NC (1.94)	P14 (2.11)	P16 (2.56)	P16 (2.44)

Probeset ID	Symbol	Description	P14-S14	P14-D14	P16-S16	P16-D16
(continued)						
1438069_a_at	Rbm5	RNA binding motif protein 5	NC (1.75)	P14 (2.16)	P16 (3.15)	P16 (2.88)
1442263_at	Rgs13	regulator of G-protein signaling 13	NC (1.03)	NC (1.01)	P16 (3.50)	P16 (2.90)
1419014_at	Rhag	Rhesus blood group-associated A glycoprotein	P14 (2.84)	P14 (2.01)	P16 (2.12)	P16 (2.33)
1422552_at	Rprm	reprimo, TP53 dependent G2 arrest mediator candidate	NC (1.76)	P14 (5.06)	P16 (2.14)	P16 (3.67)
1460623_at	Skap2	src family associated phosphoprotein 2	P14 (2.56)	P14 (2.06)	NC (1.19)	NC (1.04)
1447517_at	Skiv2l2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)	P14 (3.88)	P14 (3.84)	NC (1.31)	NC (1.51)
1420334_at	Slc12a8	solute carrier family 12 (potassium/chloride transporters), member 8	NC (1.22)	NC (1.22)	P16 (2.77)	P16 (2.04)
1434502_x_at	Slc4a1	solute carrier family 4 (anion exchanger), member 1	P14 (2.69)	NC (1.71)	P16 (4.11)	P16 (5.28)
1436853_a_at	Snca	synuclein, alpha	NC (1.90)	NC (1.72)	P16 (2.40)	P16 (3.87)
1421277_at	Spna1	spectrin alpha 1	P14 (2.96)	NC (1.22)	P16 (2.73)	P16 (2.09)
1441858_at	Uck2	Uridine-cytidine kinase 2	NC (1.23)	P14 (2.03)	P!6 (2.19)	P16 (2.42)
1439174_at	Unc5c	Unc-5 homolog C (C. elegans)	NC (1.77)	NC (1.09)	P16 (2.48)	P16 (2.28)
1426305_at	Upk1a	uroplakin 1A	P14 (2.73)	NC (1.27)	P16 (4.91)	P16 (4.09)
1446886_at	Usp3	Ubiquitin specific peptidase 3	P14 (2.23)	P14 (2.86)	P16 (2.56)	NC (1.20)
1419195_at	Wfdc15	WAP four-disulfide core domain 15	P14 (2.50)	NC (1.20)	P16 (2.90)	P16 (2.34)

Note: NC means no significant change (significant change is FC≥2.0 and $p<0.05$). For each comparison, the label (e.g., P14, P16, D14, D16, S14, S16) refers to the time and/or tissue of maximum expression and the number in parentheses is the fold change.