Supplemental data

Supplementary Figure 1. Analysis of the *Sall1* mutant mice

(A) (A’: higher magnification) Nephrons formed in the *Six2GFPCre;Sall1*$^{flox/flox}$ mice at E14.5 retain Sall1 expression. Sall1 is stained red and Six2 is green. Scale bar=40 μm.
(B)(C) *In situ* hybridization of Etv4 (FGF activity) in *Sall1*$^{+/flox}$ and *Sall1*$^{CreER/flox}$ kidneys at E14.5 (48hr after tamoxifen treatment), showing the intact expression in the progenitors (arrowheads). Expression in ureteric buds reflects Gdnf activity. Scale bar=100 μm.
(D)(E) Immunostaining of Six2 (green) and cytokeratin 8 (red) in *Sall1*$^{flox/flox}$ (D) and *Six2Cre;Sall1*$^{flox/flox}$ (E) kidneys in culture. E12.5 kidneys were treated with FGF2 (50ng/ml) and heparin (1ug/ml) and cultured for 2 days, but the phenotypes of the *Sall1* mutants were not rescued. Scale bar=100 μm.
(F)(G) Immunostaining of Lef1 (Wnt activity) *Sall1*$^{+/flox}$ and *Sall1*$^{CreER/flox}$ kidneys at E14.5 (48hr after tamoxifen treatment). Lef1 is expressed in the differentiating nephrons (arrows) and excluded from the progenitors (arrowheads) in both samples. Scale bar=100 μm.
(H)(I) Whole mount *in situ* hybridization of *Wnt9b* in *Sall1*$^{+/flox}$ (H) and *Sall1*$^{CreER/flox}$ (I) kidneys 48hr after tamoxifen treatment. Scale bar=100 μm.
(J)(K) Whole mount *in situ* hybridization of *Wnt11* in *Sall1*$^{+/flox}$ (J) and *Sall1*$^{CreER/flox}$ (K) kidneys 48hr after tamoxifen treatment. Scale bar=100 μm.
(L) Quantitative RT-PCR of E14.5 kidneys. *Sall1*$^{+/flox}$ mice and *Sall1*$^{CreER/flox}$ mice were treated with tamoxifen at E12.5. The columns represent means ± SD (n=5). Primers are listed in Supplementary Table 4.

Supplementary Figure 2. Sall1 binding to gene loci that are essential for kidney development

(A) Sall1 and Six2 co-occupy *Pax2*, *Wt1*, *Gdnf*, and *Sall1* loci. Asterisk: peaks co-occupied by Sall1 and Six2. Diamond: peaks reported in a study by Park et al.[3]
(B) Sall1 but not Six2 binds to the loci of *Hox* gene clusters.
(C) Six2 but not Sall1 binds to the *Fgf8* and *Bmp7* loci. The peak marked by # is an artifact, which is also detected in the IgG control sample.

Supplementary Figure 3. Generation and analysis of Sall1Flag mouse

(A) Targeting strategy for Sall1Flag knock-in mouse. The stop codon of Sall1 was replaced by the Flag tag. H: *Hind*III; E: *EcoR*V. The genomic DNA was digested with

*EcoR*V or *Hind*III and hybridized with 5’ or 3’ probes, respectively.

(B) Flag and Sall1 immunostaining of Sall1Flag mouse kidneys at E15.5. Scale bar=100 μm.

(C) ChIP-qPCR analysis of the *Six2* locus using Sall1Flag mouse kidneys and the anti-Flag antibody. A binding peak is observed at region 2, which corresponds to the marked peak in Figure 6A. Primers are listed in Supplementary Table 4.

Supplementary Figure 4. Overexpression of Nkx6.1 *in vivo* affects kidney development

(A) Successful overexpression of Nkx6.1 in *Six2Cre: Nkx6.1 OE* kidneys at E14.5, shown by immunostaining using the anti-Nkx6.1 antibody.

(B) A mild size reduction of the *Six2Cre: Nkx6.1 OE* kidneys at P0. Hematoxylin-eosin staining.

(C) Scattered Six2-positive nephron progenitors in the *Six2Cre: Nkx6.1 OE* kidneys at P0. Scale bar=100 μm.

Supplementary Figure 5. *Wnt4Cre*-mediated deletion is not specific to differentiating nascent nephrons

(A) *Wnt4Cre*-mediated *Sall1* deletion at E14.5.

(B) Lineage trace analysis of *Wnt4Cre* analyzed at E14.5. tdTomato is stained by the anti-RFP antibody (blue). Arrowheads: nephron progenitors; arrows: differentiating nephrons; ub: ureteric bud. Scale bar=50 μm.

Supplementary Video 1. Time-lapse analysis of nephron progenitor development in the control kidney

Six2CreGFP kidneys were cultured at E12.5 on Millicell Cell Culture Inserts placed in dishes containing DMEM with 10% serum. The confocal time-lapse images were taken using a CellVoyager CV1000. GFP-positive nephron progenitors expand as the ureteric bud branches.

Supplementary Video 2. Time-lapse analysis of nephron progenitor depletion in Sall1 deficiency

Six2CreGFP; Sall1$^{flox/flox}$ kidneys were cultured at E12.5 on Millicell Cell Culture Inserts placed in glass-bottomed dishes containing DMEM with 10% serum. Confocal time-lapse images were taken using a CellVoyager CV1000. GFP signal decreased rapidly in the absence of Sall1.

Supplementary Table 1. Down-regulated genes in the absence of *Sall1*

Decreased expression of a series of genes in *Sall1* mutant kidneys compared with that in their respective controls. Most of the down-regulated genes in the absence of Sall1 are expressed more abundantly in Six2(+) cells than in Six2(-) cells. Sall1- and Six2-binding peaks detected in our ChIP-Seq analysis were compared with Six2-binding peaks in the study by Park et al.[3] (mm9 coordinates). Asterisks and diamonds correspond to those in Figure 6 and Supplementary Figure 2.

Supplementary Table 2. Up-regulated genes in the absence of *Sall1*

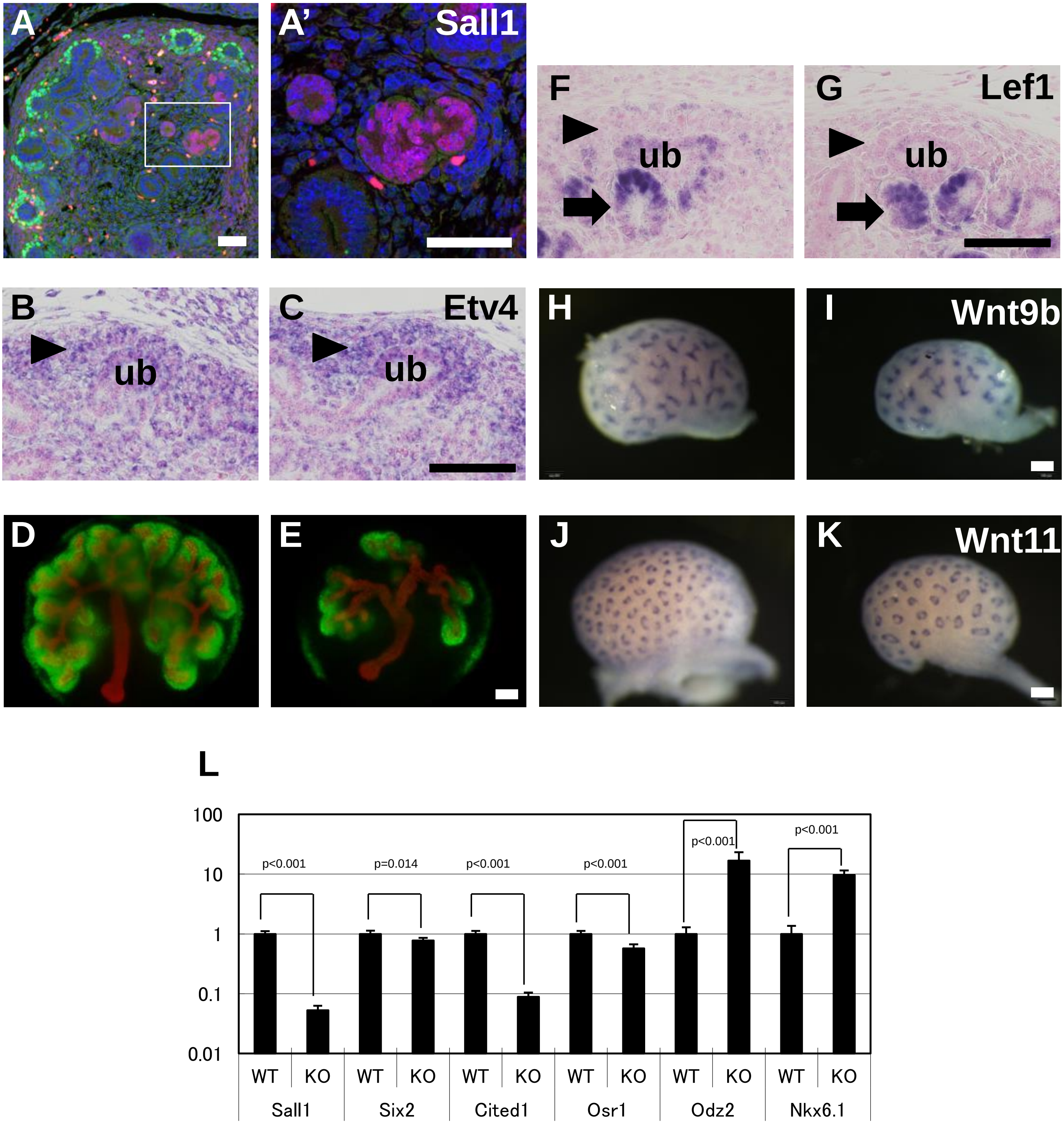
Increased gene expression in a series of *Sall1* mutant kidneys compared with their respective controls. Most of the up-regulated genes are expressed more abundantly in Six2(-) cells than in Six2(+) cells. Sall1- and Six2-binding peaks detected in our ChIP-Seq analysis were compared with Six2-binding peaks in the study by Park et al.[3] (mm9 coordinates).

Supplementary Table 3. Expression and ChIP-seq analysis of kidney developmental genes

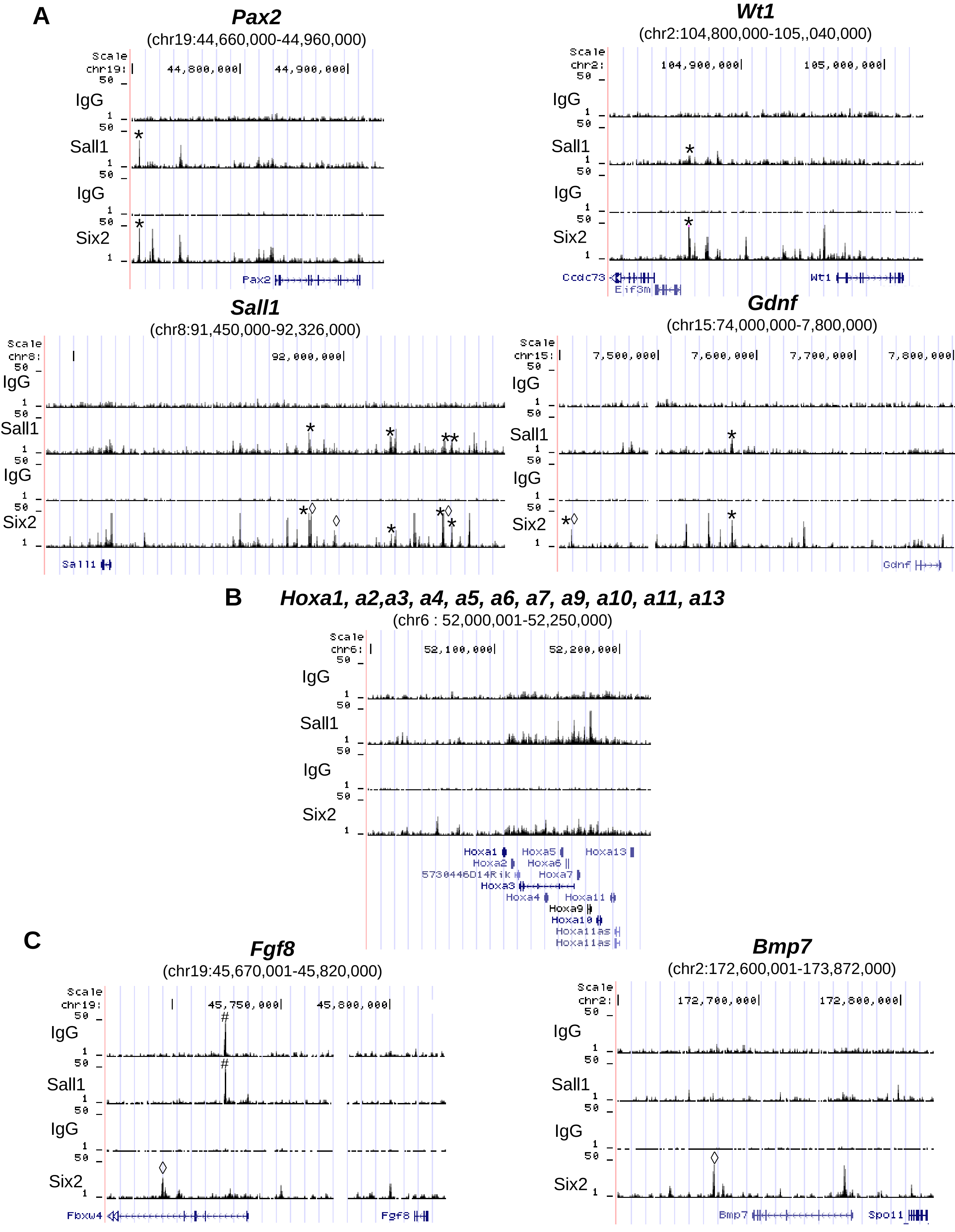
Sall1- and Six2-binding peaks detected in our ChIP-Seq analysis were compared with Six2-binding peaks in the study by Park et al.[3] (mm9 coordinates). Asterisks and diamonds correspond to those in Figure 6 and Supplementary Figure 2.

Supplementary Table 4. Primers for ChIP-qPCR and quantitative RT-PCR, and oligonucleotides for EMSA.

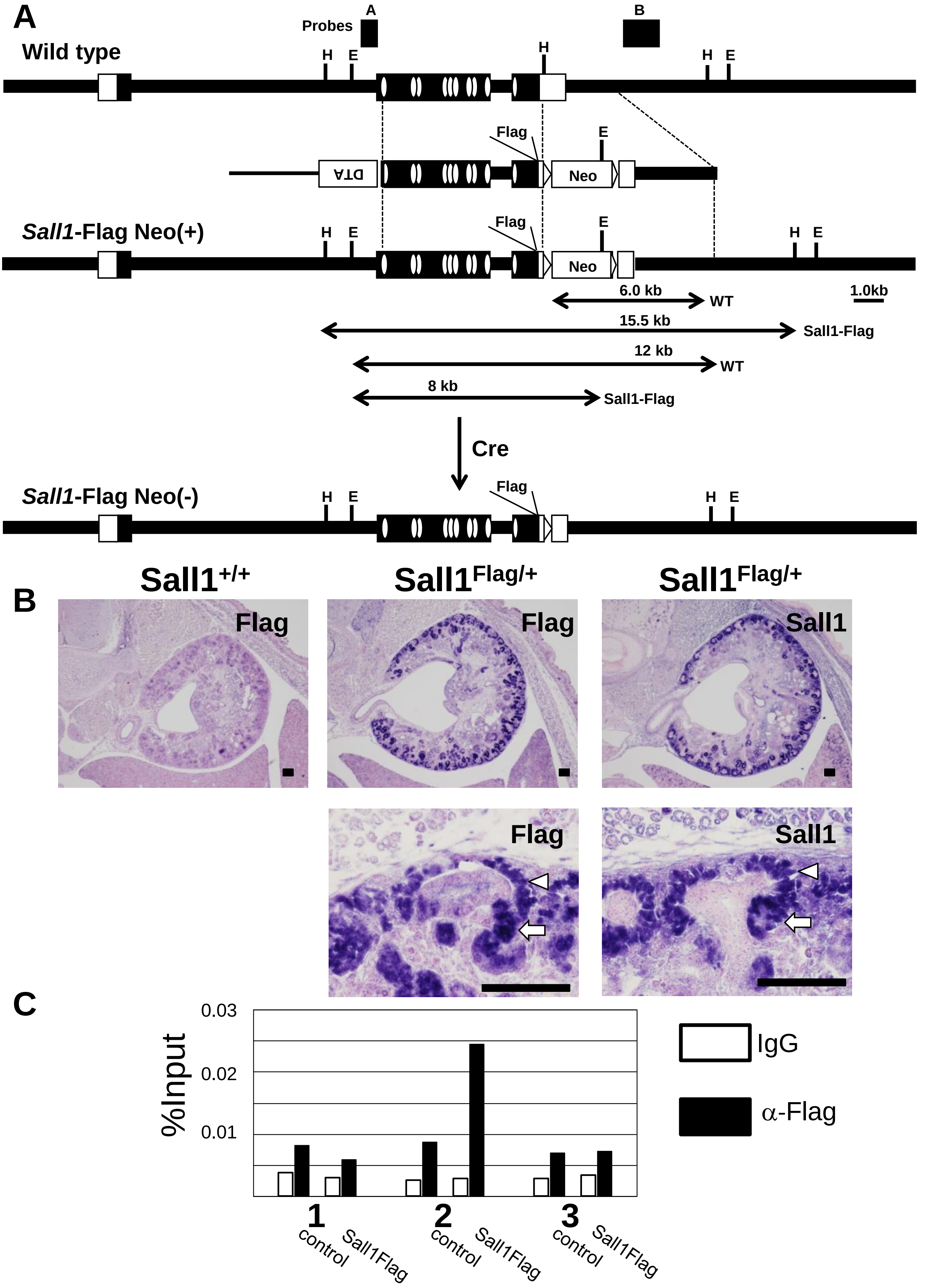
Supplementary Figure 1



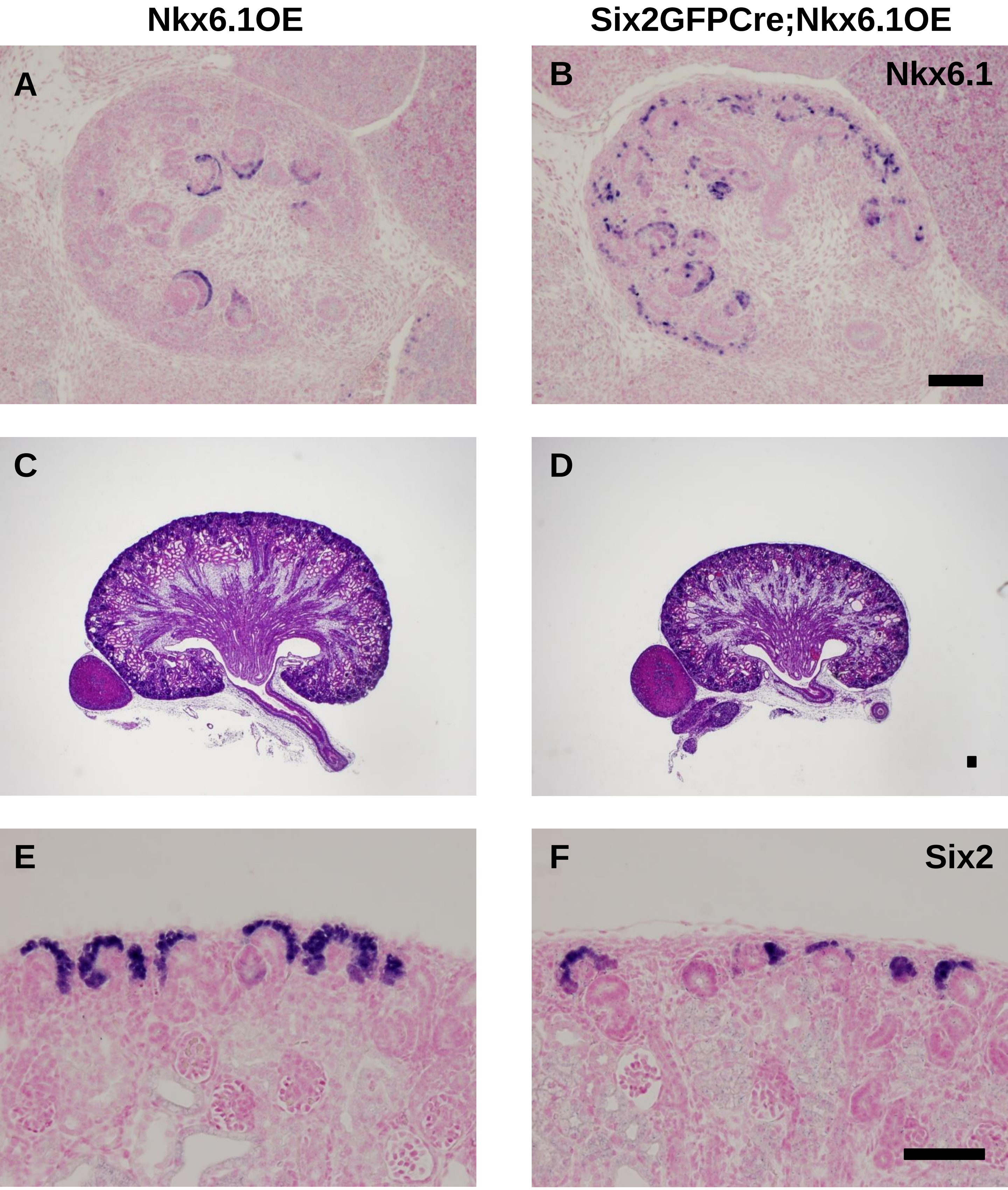
Supplementary Figure 2



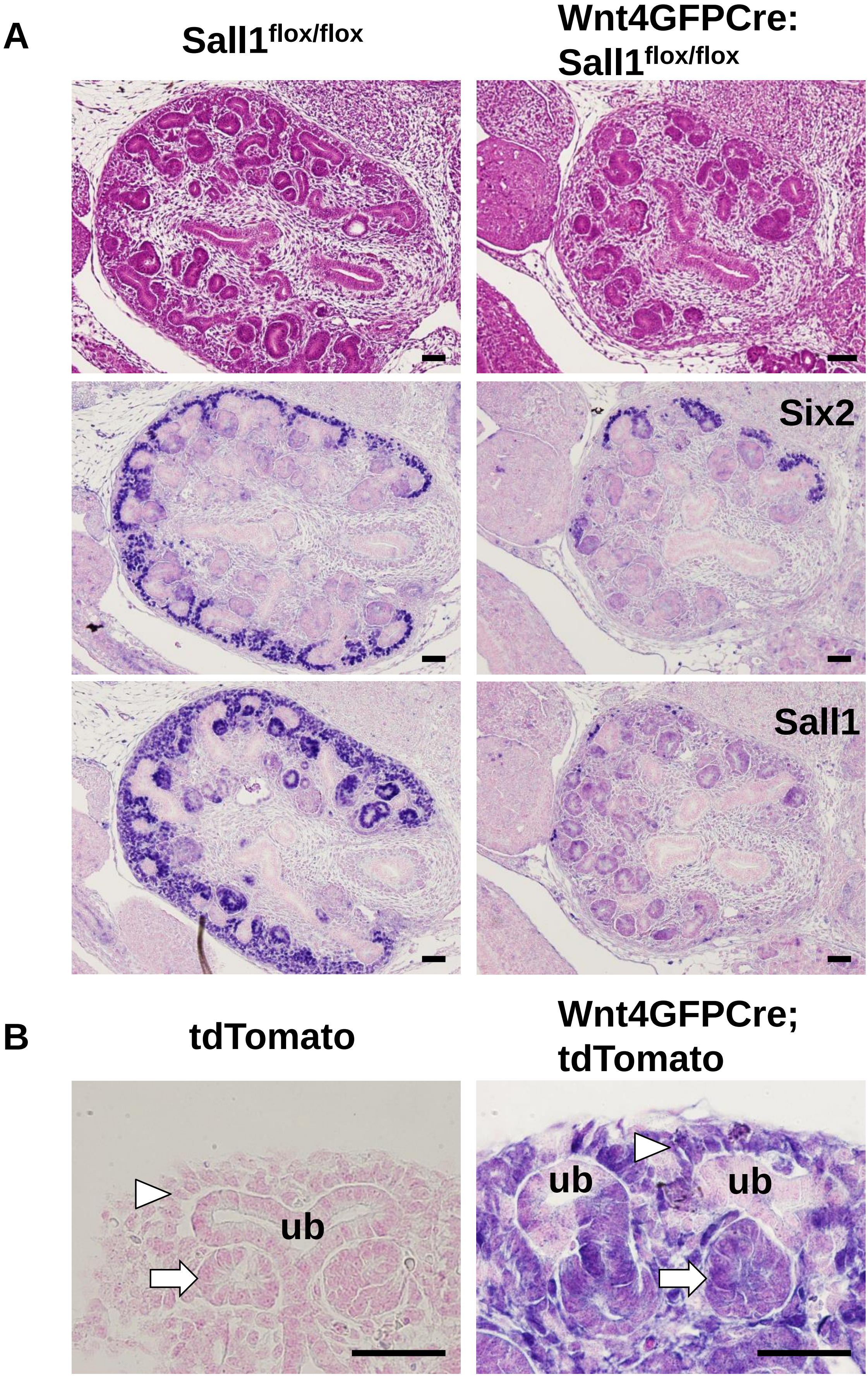
Supplementary Figure 3



Supplementary Figure 4



Supplementary Figure 5



Supplementary Table 1

GeneSymbol	**GeneName**	**Log2 (Sall1$^{CreER/flox}$ 48hr)**	**Log2 (Sall1$^{CreER/flox}$ 24hr)**	**Log2 (Six2Cre; Sall1$^{flox/flox}$)**	**Log2 (Six2 GFP+ vs GFP-)**	**Sall1 binding**	**Six2 binding**	**Six2 binding (Park et al.; ref3)**
Ocm	oncomodulin	-3.78	-2.59	-1.78	7.05	absent	chr5:144,793,500-144,793,600	chr5:144,793,471-144793622
Cited1	Cbp/p300-interacting transactivator with Glu/Asp-rich carboxy-terminal domain 1	-2.85	-2.20	-4.16	4.80	absent	chrX:99,515,160-99,515,460	absent
Sall1	sal-like 1 (Drosophila)	-2.78	-0.74	-1.25	1.64	chr8:91,559,382-91,564,748	chr8:91,569,591-91,571,276	
						chr8:91,910,504-91,914,563	chr8:91,912,350-91,913,805	
						chr8:91,935,147-91,937,179*	chr8:91,935,304-91,937,293*	chr8:91,936,103-91,936,284◊
						chr8:91,962,070-91,964,145	chr8:91,938,409-91,940,376	chr8:91,939,275-91,939,431◊
							chr8:91,982,978-91,984,393	
						chr8:92,085,399-92,088,663	chr8:92,085,787-92,088,204	
						chr8:92,092,399-92,094,667*	chr8:92,129,157-92,130,804*	
						chr8:92,094,825-92,096,530		
						chr8:92,182,190-92,186,278*	chr8:92,182,364-92,184,152*	chr8:92,130,054-92,130,238◊
							chr8:92,184,846-92,186,022	
						chr8:92,197,793-92,199,765*	chr8:92,198,196-92,199,608*	
						chr8:92,239,090-92,242,534	chr8:92,230,587-92,232,637	
Dync1i1	dynein cytoplasmic 1 intermediate chain 1	-2.30	-1.12	-1.65	3.30	absent	chr6:5,683,998-5,685,382	chr6:5,684,379-5,684,728
Dkk1	dickkopf homolog 1 (Xenopus laevis)	-2.15	-1.00	-1.69	-5.32	absent	absent	absent
Dkk1	dickkopf homolog 1 (Xenopus laevis)	-2.03	-1.00	-1.73	-5.57	shown in the other column		
Galntl2	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransferase-like 2	-1.98	-2.46	-2.66	4.14	absent	absent	absent
Pdyn	prodynorphin	-1.93	-1.30	-3.93	5.35	absent	chr2:129,523,851-129,526,042	absent
Fgf1	fibroblast growth factor 1	-1.83	-2.48	-1.68	5.40	absent	chr18:39,034,094-39,035,438	chr18:39,034,516-39,034,806
							chr18:39,040,772-39,042,700	chr18:39,041,961-39,042,307
Moxd1	monooxygenase, DBH-like 1	-1.42	-1.11	-1.20	1.57	absent	absent	absent
Fgf1	fibroblast growth factor 1	-1.17	-0.61	-1.62	4.35	shown in the other column		
Gm6213	predicted gene 6213	-1.16	-0.63	-1.65	-5.01	absent	absent	absent
Capn6	calpain 6	-1.10	-0.67	-0.85	2.99	absent	absent	absent
Lbx2	ladybird homeobox homolog 2 (Drosophila)	-1.07	-0.78	-1.29	2.79	absent	absent	absent
Tcfap2c	transcription factor AP-2, gamma	-1.07	-0.69	-0.80	-4.06	absent	absent	absent
Wnt6	wingless-related MMTV integration site 6	-1.04	-1.06	-1.45	-3.01	absent	absent	absent
H2-Eb1	histocompatibility 2, class II antigen E beta	-1.02	-0.65	-1.13	0.49	absent	absent	absent
Osr1	odd-skipped related 1 (Drosophila)	-1.01	-0.85	-0.88	5.15		chr12:9,265,136-9,266,406	
						chr12: 9,583,063-98,855,408		
							chr12:9,663,412-9,665,066	
							chr12:9,9904852-9,906,011*	
							chr12:10,134,583-10,136,241	
							chr12:10,141,956-10,143,714	
							chr12:10,237,565-10,239,324◊	chr12:10,238,413-10,238,627◊
Robo2	roundabout homolog 2 (Drosophila)	-1.00	-0.70	-0.66	3.56	chr16:73,529,347-73,531,168	chr16:73,530,336-73,530,636	
							chr16:73,533,609-73,533,909	
						chr16:74,457,123-74,459,457*	chr16:74,457,244-74,459,474*	chr16:74,458,499-74,458,753◊
							chr16:74,464,261-74,466,231	
							chr16:74,467,369-74,469,755	
						chr16:74,513,516-74,516,223*	chr16:74,514,010-74,516,020*	chr16:74,514,689-74,515,212◊
C2cd4b	C2 calcium-dependent domain containing 4B	-0.99	-1.27	-1.41	5.18	absent	absent	absent
Nefl	neurofilament, light polypeptide	-0.95	-0.79	-0.92	3.70	absent	absent	absent
Stk32a	serine/threonine kinase 32A	-0.95	-1.14	-2.31	3.50	absent	chr18:43,442,666-43,444,253	chr18:43,443,559-43,443,715
Osr1	odd-skipped related 1 (Drosophila)	-0.94	-0.85	-0.82	4.72	shown in the other column		
Snap91	synaptosomal-associated protein 91	-0.93	-1.10	-3.60	3.30	absent	chr9:86,878,689-86,882,629	absent
							chr9:86,891,164-86,893,355	
Pcnxl2	pecanex-like 2 (Drosophila)	-0.92	-1.09	-1.29	2.75	absent	chr8:128,395,717-128,397,635	chr8:128,396,405-128,396,560
Has2	hyaluronan synthase 2	-0.92	-0.76	-1.16	4.18	absent	chr15:56,349,183-56,350,888	chr15:56,350,004-56,350,207
Nefl	neurofilament, light polypeptide	-0.87	-0.79	-0.89	4.50	shown in the other column		
Spock2	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2	-0.86	-1.08	-1.89	3.74	absent	chr10:59,559,940-59,561,286	chr10:59,568,493-59,569,043
							chr10:59,567,851-59,570,032	
Has2	hyaluronan synthase 2	-0.84	-0.76	-1.30	4.81	shown in the other column		
Gadd45gip1	growth arrest and DNA-damage-inducible, gamma interacting protein 1	-0.83	-0.88	-1.01	0.37	absent	absent	absent
1700024P16Rik	RIKEN cDNA 1700024P16 gene	-0.83	-0.57	-0.70	-1.92	absent	absent	absent
Stk32a	serine/threonine kinase 32A	-0.82	-2.95	-1.87	2.20	shown in the other column		
Robo2	roundabout homolog 2 (Drosophila)	-0.80	-0.49	-0.75	3.93	shown in the other column		
Wnt6	wingless-related MMTV integration site 6	-0.79	-1.06	-1.16	-1.59	shown in the other column		
Pnmt	phenylethanolamine-N-methyltransferase	-0.79	-0.70	-1.78	5.00	absent	absent	absent
Ppm1e	protein phosphatase 1E (PP2C domain containi	-0.75	-0.83	-1.47	3.13	absent	absent	absent
Robo2	roundabout homolog 2 (Drosophila)	-0.72	-0.70	-1.25	3.43	shown in the other column		
2610028E06Rik	RIKEN cDNA 2610028E06 gene	-0.72	-0.63	-3.77	3.74	absent	absent	absent
Spock2	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2	-0.71	-1.08	-1.53	4.30	shown in the other column		
Krt23	keratin 23	-0.66	-1.02	-0.62	-6.09	absent	absent	absent
Megf9	multiple EGF-like-domains 9	-0.63	-0.69	-0.94	1.51	chr4:70,149,257-70,152,337*	chr4:70,149,909-70,151,851*	absent
						chr4:70,157,125-70,159,298*	chr4:70,157,444-70,159,250*	
						chr4:70,160,472-70,162,492	chr4:70,195,594-70,199,117	
						chr4:70,163,076-70,164,382		
						chr4:70,195,701-70,198,887		
B3galt5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	-0.62	-1.01	-1.70	1.04	absent	chr5:150,477,007-150,478,593	chr5:150,477,654-150,477,982

Supplementary Table 2

GeneSymbol	GeneName	Log2 (Sall1$^{CreER/flox}$ 48hr)	Log2 (Sall1$^{CreER/flox}$ 24hr)	Log2 (Six2Cre; Sall1$^{flox/flox}$)	Log2 (Six2 GFP+ vs GFP-)	Sall1 binding	Six2 binding	Six2 binding (Park et al.; ref3)
Odz2	odd Oz/ten-m homolog 2 (Drosophila)	3.70	2.48	2.13	-1.53	absent	chr11:36,685,840-36,687,519	chr11:36,686,562-36,686,793
Odz2	odd Oz/ten-m homolog 2 (Drosophila)	3.62	2.48	2.10	-1.42	absent	chr11:36,810,638-36,812,020	
Odz2	odd Oz/ten-m homolog 2 (Drosophila)	3.47	2.48	1.47	0.18	absent		
Nkx6-1	NK6 homeobox 1	3.10	2.14	1.53	-1.47	absent	absent	absent
3110082D06Rik	RIKEN cDNA 3110082D06 gene	2.68	1.54	2.40	-2.74	absent	absent	absent
Trhr	thyrotropin releasing hormone receptor	2.64	1.07	1.86	0.12	chr15:44,020,317-44,022,935	absent	absent
Krt36	keratin 36	2.32	2.08	2.65	2.07	absent	chr11:99,964,150-99,964,350	absent
3110082D06Rik	RIKEN cDNA 3110082D06 gene	2.31	1.54	2.32	-1.56	absent	absent	absent
Krt36	keratin 36	2.13	1.99	2.67	2.00	shown in the other column	shown in the other column	shown in the other column
Gm6792	predicted gene 6792	2.04	0.61	0.63	-3.21	absent	absent	absent
Rnf152	ring finger protein 152	1.81	1.33	1.68	-1.26	absent	absent	absent
Kera	keratocan	1.78	1.97	2.05	-1.90	absent	chr10:97,053,826-97,055,372	chr10:97,054,393-97,054,612
Pcdh8	protocadherin 8	1.66	0.78	1.02	4.37	absent	absent	absent
Rnf152	ring finger protein 152	1.47	1.33	1.76	-0.86	shown in the other column	shown in the other column	shown in the other column
Ccl21a	chemokine (C-C motif) ligand 21A	1.45	1.30	1.48	-1.39	absent	absent	absent
Lrrc4c	leucine rich repeat containing 4C	1.42	0.60	1.68	-0.86	absent	absent	absent
Slitrk6	SLIT and NTRK-like family, member 6	1.40	1.40	0.69	-5.30	absent	absent	absent
Saa2	serum amyloid A 2	1.36	0.98	0.75	5.13	absent	absent	absent
Ebf2	early B-cell factor 2	1.36	0.66	0.69	-1.03	absent	absent	absent
Fap	fibroblast activation protein	1.34	0.76	0.89	-0.37	absent	absent	absent
Fap	fibroblast activation protein	1.34	0.76	1.56	-5.15	shown in the other column	shown in the other column	shown in the other column
Krt15	keratin 15	1.30	0.87	2.08	2.63	absent	absent	absent
Rnf152	ring finger protein 152	1.28	1.33	1.93	-0.65	shown in the other column	shown in the other column	shown in the other column
Snph	syntaphilin	1.24	1.01	1.02	1.46	absent	absent	absent
Vegfc	vascular endothelial growth factor C	1.24	0.62	1.17	-1.20	absent	absent	absent
Gdpd2	glycerophosphodiester phosphodiesterase domai	1.24	0.89	0.74	-0.03	absent	absent	absent
Angptl1	angiopoietin-like 1	1.21	1.45	0.88	-2.97	absent	absent	absent
Gabrb3	gamma-aminobutyric acid (GABA) A receptor, su	1.20	0.63	0.72	-1.77	absent	absent	absent
Oit3	oncoprotein induced transcript 3	1.18	0.84	1.09	-3.46	absent	absent	absent
Foxp2	forkhead box P2	1.18	1.09	1.36	-3.50	absent	absent	absent
Lypd1	Ly6/Plaur domain containing 1	1.16	0.87	0.82	-0.05	absent	absent	absent
Egfl6	EGF-like-domain, multiple 6	1.12	0.78	0.97	-1.57	chrX:162,947,271-162,948,745	absent	absent
Aspn	asporin	1.09	2.14	1.52	-5.27	absent	absent	absent
5430435G22Rik	RIKEN cDNA 5430435G22 gene	1.05	0.67	0.68	-1.45	absent	absent	absent
Dtna	dystrobrevin alpha	1.05	0.83	0.80	2.06	absent	absent	absent
Napsa	napsin A aspartic peptidase	1.05	0.47	0.98	-2.72	absent	absent	absent
1700028P14Rik	RIKEN cDNA 1700028P14 gene	1.04	0.61	0.73	-0.46	absent	absent	absent
Epha5	Eph receptor A5	0.99	1.37	1.32	-0.59	chr5:84,813,557-84,815,455	absent	absent
						chr5:85,097,634-85,099,671		
Rspo2	R-spondin 2 homolog (Xenopus laevis)	0.97	1.90	1.51	-0.42	absent	absent	absent
Ebf3	early B-cell factor 3	0.96	0.62	1.77	-3.46	absent	absent	absent
Foxp2	forkhead box P2	0.95	0.78	1.36	-2.18	shown in the other column	shown in the other column	shown in the other column
Dtna	dystrobrevin alpha	0.95	0.83	0.70	1.90	shown in the other column	shown in the other column	shown in the other column
Shisa9	shisa homolog 9 (Xenopus laevis)	0.95	0.85	0.74	-2.70	absent	absent	absent
Ebf3	early B-cell factor 3	0.94	0.62	1.38	0.00	shown in the other column	shown in the other column	shown in the other column
Sfrp4	secreted frizzled-related protein 4	0.92	1.26	1.95	-4.32	absent	absent	absent
Htr2b	5-hydroxytryptamine (serotonin) receptor 2B	0.90	0.80	0.62	1.60	absent	chr1:88,015,600-88,017,322	absent
Fibin	fin bud initiation factor homolog (zebrafish)	0.87	0.75	1.18	-4.77	absent	absent	absent
Ryr3	ryanodine receptor 3	0.86	0.60	0.75	-2.07	absent	absent	absent
Nov	nephroblastoma overexpressed gene	0.84	1.41	1.30	-2.10	chr15:54,477,140-54,478,129	absent	absent
Dtna	dystrobrevin alpha	0.82	0.83	0.73	0.71	shown in the other column	shown in the other column	shown in the other column
Col5a3	collagen, type V, alpha 3	0.76	0.64	1.17	-3.92	chr9:20,557,700-20,558,700	absent	absent
Ddx4	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	0.76	1.01	0.64	-0.20	absent	absent	absent
Sema3a	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	0.75	0.93	1.16	-4.17	chr5:13,325,149-13,327,960	absent	absent
						chr5:13,397,505-13,402,459		
						chr5:13,402,643-13,406,956		
						chr5:13,426,453-13,427,898		
Bmp5	bone morphogenetic protein 5	0.75	0.72	0.86	-2.33	absent	absent	absent
Oit3	oncoprotein induced transcript 3	0.75	0.84	0.77	-0.83	shown in the other column	shown in the other column	shown in the other column
Cldn1	claudin 1	0.75	1.30	1.55	-4.40	absent	absent	absent
Tbx1	T-box 1	0.75	0.72	1.03	-3.54	absent	absent	absent
Trem2	triggering receptor expressed on myeloid cells 2	0.72	0.61	0.68	0.06	absent	absent	absent
Ms4a7	membrane-spanning 4-domains, subfamily A, member 7	0.72	0.66	1.38	0.71	absent	absent	absent
Fxyd7	FXYD domain-containing ion transport regulator	0.70	0.68	1.22	-0.78	absent	absent	absent
Cldn1	claudin 1	0.69	1.30	1.28	-5.01	shown in the other column	shown in the other column	shown in the other column
Ms4a7	membrane-spanning 4-domains, subfamily A, member 7	0.69	0.66	1.43	0.75	shown in the other column	shown in the other column	shown in the other column
Col12a1	collagen, type XII, alpha 1	0.68	0.74	0.81	-4.30	absent	absent	absent
Trem2	triggering receptor expressed on myeloid cells 2	0.65	0.61	0.77	-0.00	shown in the other column	shown in the other column	shown in the other column
Sema3a	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	0.64	0.83	1.26	-5.00	shown in the other column	shown in the other column	shown in the other column
Pcdh20	protocadherin 20	0.64	0.88	1.37	-3.22	absent	absent	absent
March11	membrane-associated ring finger (C3HC4) 11	0.62	0.72	0.66	-4.09	absent	absent	absent
Parm1	prostate androgen-regulated mucin-like protein 1	0.61	0.64	1.13	-1.91	absent	absent	absent
Bmp5	bone morphogenetic protein 5	0.61	0.72	0.75	0.44	shown in the other column	shown in the other column	shown in the other column
Figf	c-fos induced growth factor	0.60	0.82	1.18	-4.93	absent	absent	absent
Ccdc113	coiled-coil domain containing 113	0.60	0.91	1.13	-4.03	absent	absent	absent
Slurp1	secreted Ly6/Plaur domain containing 1	0.59	0.49	1.25	-0.70	absent	absent	absent

Supplementary Table 3

	Gene Symbol	Log2 (Sall1$^{CreER/flox}$ 48hr)	Log2 (Sall1$^{CreER/flox}$ 24hr)	Log2 (Six2Cre; Sall1$^{flox/flox}$)	Log2 (Six2 GFP+ vs GFP-)	Sall1 binding	Six2 binding	Six2 binding (Park et al.; ref3)
Progenitor-related	Sall1	-2.8	-0.72	-1.27	1.65	chr8:91,559,382-91,564,748	chr8:91,569,591-91,571,276	
						chr8:91,910,504-91,914,563	chr8:91,912,350-91,913,805	
						chr8:91,935,147-91,937,179*	chr8:91,935,304-91,937,293*	chr8:91,936,103-91,936,284◊
						chr8:91,962,070-91,964,145	chr8:91,938,409-91,940,376	chr8:91,939,275-91,939,431◊
							chr8:91,982,978-91,984,393	
						chr8:92,085,399-92,088,663	chr8:92,085,787-92,088,204	
						chr8:92,092,399-92,094,667*	chr8:92,129,157-92,130,804*	
						chr8:92,094,825-92,096,530		
						chr8:92,182,190-92,186,278*	chr8:92,182,364-92,184,152*	chr8:92,130,054-92,130,238◊
							chr8:92,184,846-92,186,022	
						chr8:92,197,793-92,199,765*	chr8:92,198,196-92,199,608*	
						chr8:92,239,090-92,242,534	chr8:92,230,587-92,232,637	
	Six2	-0.52	-0.5	-1.62	5.87		chr17:86,087,020-86,088,664◊	chr17:86,087,682-86,087,809◊
						chr17:86,145,975-86,149,207*	chr17:86,146,706-86,149,340*	chr17:86,147,979-86,148,273◊
							chr17:86,196,249-86,200,295◊	chr17:86,198,467-86,198,745◊
	Pax2	0.29	0.17	-0.57	1.22	chr19:44,706,202-44,707,935*	chr19:44,705,424-44,708,047*	
						chr19:44,743,902-44,746,867	chr19:44,718,402-44,720,395	
							chr19:44,743,623-44,745,539	
							chr19:44,827,480-44,829,598	
								chr19:44,978,154-44,978,284
	Eya1	-0.35	0.09	-1.09	0.04		chr1:14,234,375-14,235,693◊	chr1:14,235,103-14,235,289◊
							chr1:14,451,499-14,453,661	
						chr1:14,558,658-14,561,609		chr1:14,560,514-14,560,929
							chr1:14,577,583-14,579,048	
							chr1:14,616,816-14,618,109	
						chr1:14,624,565-14,627,013*	chr1:14,624,969-14,626,797*	chr1:14,625,742-14,625,927◊
							chr1:14,662,024-14,663,490	
								chr1:14,706,626-14,706,934
	Wt1	0.15	0.09	-0.49	1.15	chr2:104,863,154-104,864,824*	chr2:104,862,758-104,865,023*	absent
						chr2:104,882,731-104,886,149		
							chr2:104,867,037-104,868,414	
							chr2:104,902,608-104,904,049	
							chr2:104,928,528-104,931,383	
							chr2:104,957,226-104,958,678	
	Cited1	-2.87	-2.18	-4.18	4.8	absent	chrX:99514,619-99,515,712	absent
	Osr1	-0.99	-0.82	-0.87	5.11		chr12:9,265,136-9,266,406	
						chr12: 9,583,063-98,855,408		
							chr12:9,663,412-9,665,066	
							chr12:9,9904852-9,906,011*	
							chr12:10,134,583-10,136,241	
							chr12:10,141,956-10,143,714	
							chr12:10,237,565-10,239,324◊	chr12:10,238,413-10,238,627◊
	FGF1	-1.52	-1.52	-1.67	5.52	absent	chr18:39,034,094-39,035,438	chr18:39,034,516-39,034,806
							chr18:39,040,772-39,042,700	chr18:39,041,961-39,042,307
	FGF2	0.07	0.14	-0.15	-0.47	absent	absent	absent
	FGF9	0.04	-0.1	-0.68	1.7	absent	chr14:59,107,122-59,108,879	chr14:59,107,730-59,108,069
							chr14:59,134,560-59,136,448	chr14:59,135,528-59,135,796
	FGF20	-0.34	-0.4	-0.32	6.85	absent	chr8:41,324,122-41,326,059	chr8:41,325,166-41,325,419
	BMP7	-1.08	-0.27	-0.74	1.15	absent	chr2:172,667,102-172,668,820◊	chr2:172,667,933-172,668,149◊
							chr2:172,758,882-172,762,510	chr2:172,760,469-172,760,754
	Hoxa2					chr6:52,112,980-52,116,365	absent	absent
	Hoxa5					chr6:52,159,318-52,165,129		
	Hoxa9					chr6:52,175,369-52,182,159		
Diffrentiation	Wnt9b	-0.01	-0.06	0.5	-3.52	absent	absent	absent
	Wnt4	0.37	-0.02	-0.71	-1.59	absent	chr4:136,777,571-136,774,226◊	chr4:136,773,187-136,773,353◊
	LEF1	0.19	-0.1	0.29	-4.26	absent	absent	chr3:130440576-130440757
	Dkk1	-2.1	-0.98	-1.73	-5.71	absent	absent	absent
	FGF8	0.14	-0.13	-1.05	1.3	absent	chr19:45,695,222-45,697,760◊	chr19:45695446-45695814◊
	Jag1	-0.07	0.06	-0.83	-3.87	absent	chr2:136,990,923-136,992,487	absent
	Notch1	0.16	0.29	-0.75	-0.41	absent	chr2:26,396,629-26,398,109	absent
	Notch2	0.07	0.22	-0.14	0.24	absent	chr3:97,740,586-97,742,523	absent
	Hnf1b	-0.14	0.37	-0.82	-3.62	chr11:83,629,065-83,631,720	absent	absent
Adhesion/repulsion	Integrin α3	0.18	0.13	0.05	0.84	absent	absent	absent
	Integrin α8	-0.12	-0.31	-0.82	2.28	absent	chr2:11,940,289-11,942,124	chr2:11,941,243-11,941,615
	Integrin β1	-0.26	-0.03	0.05	-0.67	absent	chr8:130,948,221-130,949,370	chr8:130,948,920-130,949,219
							chr8:131,011,518-131,013,343	
	Robo2	-0.75	-0.57	-1.01	3.42	chr16:73,529,347-73,531,168	chr16:73,530,336-73,530,636	
							chr16:73,533,609-73,533,909	
						chr16:74,457,123-74,459,457*	chr16:74,457,244-74,459,474*	chr16:74,458,499-74,458,753◊
							chr16:74,464,261-74,466,231	
							chr16:74,467,369-74,469,755	
						chr16:74,513,516-74,516,223*	chr16:74,514,010-74,516,020*	chr16:74,514,689-74,515,212◊
	Slit2	0.01	-0.05	-0.01	-0.4	chr5:47,947,543-47,949,658	chr5:47,947,543-47,949,658	chr5:47,948,014-47,948,303
Extracellular matrix	Nephronectin	0.16	-0.1	-0.84	-2.71	absent	absent	absent
	Laminin alpha1	-0.28	0	-1.17	-2.95	absent	absent	chr17:67982218-67982477
	laminin alpha5	0.05	0.07	-0.31	0.03	absent	absent	absent
	laminin beta1	0.12	0.14	-0.06	-1.56	absent	absent	absent
	laminin beta2	0.22	0.17	0.2	0.04	absent	absent	absent
	laminin gamma1	0.08	0.18	-0.22	-1.1	absent	absent	absent
	COL4A3	0.94	0.25	0.38		absent	absent	absent
	COL4A4	0.45	0.07	0.58	-1.56	absent	absent	absent
	COL4A5	0.05	-0.01	0.58	-0.2	absent	absent	absent
Ureteric bud attraction	Gdnf	-0.76	-0.66	-0.06	1.11		chr15:7,411,984-7,413,234◊	chr15:7,412,321-7,412,817◊
						chr15:7,463,342-7,465,268		
						chr15:7,472,514-7,474,370		
							chr15:7,551,156-7,552,891	
							chr15:7,562,479-7,563,621	
						chr15:7,573,709-7,576,260*	chr15:7,574,199-7,575,862*	
							chr15:7,647,427-7,648,858	
	Ret	-0.5	-0.25	-0.24	-6.67	absent	absent	absent
	Etv4	-0.06	-0.27	-1.22	1.37	absent	chr11:101,632,947-101,634,979	chr11:101,633,863-101,634,122
	Etv5	0.04	-0.1	-1.3	0.49	absent	absent	absent
	Sprouty1	-0.12	-0.15	-0.6	-0.46	absent	absent	chr3:37,538,702-37,538,895
	FGF10	0.04	-0.07	-0.3	2.19	absent	absent	absent
	BMP4	-0.15	0.23	-0.21	-1.06	absent	chr14:47,195,029-47,195,717	chr14:47,195,735-47,195,901
						absent	chr14:47,213,357-47,215,049	chr14:47,213,638-47,214,076
						absent	chr14:47,337,540-47,338,880	chr14:47,338,153-47,338,279
	Gremlin	-0.43	0.05	-1.38	-0.83	absent	absent	absent
	Kif26b	-0.29	-0.32	-1.67	2.85	chr1:180,457,002-180,459,602		
							chr1:180,613,106-180,614,972	chr1:180,613,939-180,614,184

Supplementary Table 4

Primers for ChIP-qPCR

Six2-1F	5’-CAG CAG CTG TAT CCA GGT CA-3
Six2-1R	5’-CAA TGG GCA CAT GAA CAA AG-3’
Six2-2F	5’-GGG GTT TAT GGT TCA CAA CG-3’
Six2-2R	5’-GGG AAG AAA AAC CAT GTC CA-3’
Six2-3F	5’-CCA TGA GAG ATT CCC TTC CA-3’
Six2-3R	5’-CCG GAG TAC TGA AGC CAG AG-3’

Primers for qRT-PCR

b-actin F	5’-CATCCGTAAAGACCTCTATGCCAAC-3’
b-actin R	5’-ATGGAGCCACCGATCCACA-3’
Sall1 F	5’-TGTCAAGTTCCCAGAAATGTTCCA-3’
Sall1 R	5’-ATGCCGCCGTTCTGAATGA-3’
Six2 F	5’-GCAACTTCCGCGAGCTCTAC-3’
Six2 R	5’-GCCTTGAGCCACAACTGCTG-3’
Osr1 F	5’-ACTGATGAGCGACCTTACACCTG-3’
Osr1 R	5’-ACTTGTGAGTGTAGCGTCTTGTGGA-3’
Cited1 F	5’-GTCGAGGCCTGCACTTGATG-3’
Cited1 R	5’-CCAAGGTTGGAGTAGGCCAGAG-3’
Odz2 F	5’-GAGGTCCCAGATTCACATCAGTCA-3’
Odz2 R	5’-TTTCCATCCAGGCGTTCCA-3’
Nkx6.1 F	5’-AGCACGCTTGGCCTATTCTC-3’
Nkx6.1 R	5’-CACTTGGTCCTGCGGTTCTG-3’

Oligonucleotides for EMSA

	Name	Sequence	Position of Sall1 probe	Position of Six2 binding motif	Six2 consensus GNAACNNNANNC	
1	Osr1-Wt-Fw	5’-GTATAT**ATTAT**CCTGCAAAAGAAAAGCATAAC-3’	chr12:9,905,826-9,905,856	chr12:9,905,421-9,905,432	GGAACCTGACAC	394bp up stream of Sall1 binding motif
2	Osr1-Mt-Fw	5’-GTATATATTgTCCTGCAAAAGAAAAGCAcAAC-3’				
3	Six2-Wt-Fw	5’-CTGGAGAA**ATAAA**ACTGAGTTATTGTTTCC-3’	chr17:86,147,858-86,147,887	chr17:86,148,253-86,148,264	GAAACCCGACCC	366bp down stream of Sall1 binding motif
4	Six2-Mt-Fw	5’-CTGGAGAAAcAAAACTGAGTTgTTGTTTCC-3’				
5	Eya1-Wt-Fw	5’-C**ATAAAT**AGAGTAAATACATTTAATTTTCATTTCTATATTATC-3’	chr1:14,625,520-14625562	chr1:14,625,819-14,625,830	GTAACTACTCCC	257bp down stream of Sall1 binding motif
6	Eya1-Mt-Fw	5’-CAccAAcAGAGTAggTACATTTggccTTCATccCTATATggTC-3’				
7	Robo2-Wt-Fw	5’-CAGATAGTTTC**ATAAT**GAAATTTTCTTTTATGTTGAATCC-3’	chr16:74,514,526-74,514,565	chr16:74,515,053-74,515,063	GTTTGAGTTAC (complementary)	435bp down stream of Sall1 binding motif
8	Robo2-Mt-Fw	5’-CAGATAGccTCAcAATGGGATTcTCTTctgTGTTGggTCC-3’				
9	Megf9-Wt-Fw	5’-GGCACTAAATAAAACGGCAAAGTC**ATAAAAAT**TTAATTTG-3’	chr4:70,150,276-70,150,315	chr4:70,150,664-70,150,675	GTTTTCAGTTCC (complementary)	349bp down stream of Sall1 binding motif
10	Megf9-Mt-Fw	5’-GGCACTAgAcAggACGGCAAAGTCAcAccAATcTccTTTG-3’				
11	Cited1-Wt-Fw	5’-TTACAAGCA**ATTAAAAT**ACACTAAAATAGATTTATACAGG -3’	chrX:99,515,395-99,515,434	chrX:99,515,343-99,515,353	GGAAATGACTC	42bp up stream of Sall1 binding motif
12	Cited1-Mt-Fw	5’-TTACAAGCAAccAggATACACTAggATAGAggTcTACAGG -3’				