

Fig. S1. Sall1 expression pattern in mouse gonads.

- A. Immunostainings of SALL1 (red) and FOXL2 and SOX9 (green) as markers of somatic female and male cells, respectively. O: ovary, T: testis, K: kidney. Note the absence of SALL1 positive cells in the embryonic gonads but the specific expression in the adjacent kidney. Scale bars: 50 μm.
- B. RPKMs quantification from RNA-seq data of adult gonads in mouse and mole. Expression levels in mouse are lower compared to mole and not sex specific.



Fig. S2. SALL1 expression in Eulipotyphla species.

A. Immunostaining of SALL1 in transversal sections of an early hedgehog embryo from the *Atelerix albiventris* species. SALL1 is highly expressed in the neural tube, a well-known tissue for SALL1 expression. Scale bar: 100 µm.

B. Immunostaining of SALL1 in adult kidneys from the common shrew, *Sorex araneus*. Note the specificity of the antibody to the nucleus of the renal tubular cells. Scale bar: $20 \mu m$.

C. RT-qPCRs for *SALL1* expression in adult ovaries and kidneys from hedgehogs (*Atelerix albiventris*) and shrews (*Sorex araneus*). Shown is relative *SALL1* expression normalized to *RPS9*. Data is presented as mean ± SD and p-values are indicated as * $p \le 0.05$, ** $p \le 0.01$, *** $p \le 0.001$.

D. RT-qPCRs for *FOXL2* expression in adult ovaries and kidneys from hedgehogs (*Atelerix albiventris*) and shrews (*Sorex araneus*). Shown is relative *FOXL2* expression normalized to *RPS9*. Data is presented as mean ± SD and p-values are indicated as * $p \le 0.05$, ** $p \le 0.01$, *** $p \le 0.001$.



Fig. S3. Hi-C map comparison between limb and ovotestis

- A. Hi-C maps at high resolution from embryonic limbs with the corresponding TAD calling (black bars) underneath.
- B. Hi-C maps from adult ovotestis with the corresponding TAD calling (black bars) underneath. Note the conservation of the *SALL1* TAD domain between tissues.



Fig. S4. Regulatory domain of *Sall1* in mouse.

- A. Hi-C map from Neural Progenitor Cells (NPCs) denotes the domain of *Sall1* in a large gene desert.
- B. Virtual 4C-seq analysis from NPCs Hi-C maps with *SALL1* promoter as viewpoint. Note high interaction frequency between the gene promoter and the surrounding 1Mb desert clearly demarcating the *Sall1* regulatory domain. The domain is strikingly conserved between cell types and species.
- C. ATAC-seq track from mouse embryonic kidneys at E14.5 to identify regulatory regions in this tissue.
- D. Zoom-in on the two equivalent regions where the mole enhancers were identified. Homologous regions are marked as gray bars and labeled as E1-5. Consistent with our enhancer activity results, enhancer 3 (E3) coincides with an ATAC-seq peak in kidneys.

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Fig. S5. Synteny of the enhancer regions.

A. Alignment of syntenic blocks for the enhancer region 1 (E1) against the mouse genome (upper panel) and against the shrew genome (*Sorex araneus*, lower panel). Visualization with Gbrowse⁴⁶.

B. Alignment of syntenic blocks for the cluster of enhancers (E2-E5) against the mouse genome (upper panel) and against the shrew genome (*Sorex araneus*, lower panel). Visualization with Gbrowse⁴⁶.

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Against mouse

Fig. S6. Sequence alignments for the individual enhancers 1 to 3.

The conserved nucleotides are highlighted in blue and capitalized. Light blues nucleotides denote the beginning and end of the homology sequence.

Against shrew

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Development • Sup

Against human

AGCTAGACTT GAATTTATTC AGCACUTATT TTAAAAATAA TTTCCCCCGAA TTATAAAAAT AATGTTTGTT CAATTTTTTAA ATTAGUTGCC AAUGTATAAA ATTagggatt ttacataaag ttgtcaATTT CAGGTTTCTT TCCAAAACTT AGAATTCTgG AACcagttca acTCATTCCC TCAACcaaca tgtgaccaaa 50 100 150 4 200 ggtagtactg gctgctcatg ggcggggcg tgcattttc ggttcctgg agtctcccTC ACTCCCTga AtCcCTTAGA TtTAGTcCAC ATCTCTCATT tAgATTGTCT GCTGGAAAct ataaaacttt gaatttacaa cccctgactc 250 Enhancer 300 350 tcagccgtat ttttttttt taaagaaaat aaacatttca agttatttca 400 tcagcagta tutttitt taaagaaat aacattica agtiattoa tcaggaagaa gggacattig gggaaagtica actataggca ggaaaagti acagtigott tatgTATTT TCCATCtCaG ATTTTCtott TCTCTTTAG CCCAGiggag caaaaacaaa aagagctgca gataaatgat gocttagga cTCATAAAGT TcAAaGTAAG CAATTATAct tcacttaca agatotatag caaaataaat tgcaatggat tgaatagta aaatattat aaaggcatg 450 500 550 600 650 700 taacttaga tcatcotta aaggagcag tagotacaga gaaggcagag aaggtocact tagtgcaatt ctgtgtcatc tcagtattc agcaatttot taaaagtcat gaaaaaagtt taaaaatact tootgttaaa ggatacottc 750 800 850 taggccaatg tcatcagtga aattaaccaa gaacaaagag aacgagaacc 900 agaaaaggaa tgtccccttc taggaaacga gggtccacag gag

Against shrew

agctacactt	gaatttattc	agcacttatt	ttaaaaataa	tttcccccaa	50
ttataaaaat	aatgtttgtt	caatttttaa	attagttgcc	aatgtataaa	100
attagggatt	ttacataaag	ttgtcaattt	caggtttctt	tccaaaactt	150
agaattctgg	aaccagttca	actcattccc	tcaaccaaca	tgtgaccaaa	200
ggtagtactg	gctgctcatg	ggcgaggccg	tgcattttc	agtttcctgg	250
agtctccctc	actccctgaa	atcccttaga	tttagtccac	atctctcatt	300
tagattgtct	gctggaaact	ataaaacttt	gaatttacaa	cccctgactc	350
tcagccgtat	tttttttt	taaagaaaat	aaacatttca	agttatttca	400
tcaggaagaa	gggacatttg	gggaagttca	actataggca	ggaaaaagtt	450
acagttgctt	tatgtatttt	tccatctcag	attttctctt	tctcttttag	500
cccagaggag	caaaaacaaa	aagagc <mark>TGCA</mark>	GATAAATGaT	GCTCTTAGCA	550
CTCATAAAgt	TCAAAGTaAG	CAATtAtACT	TCACTTTACA	AGATCtATAg	600
CAAAAtAAAT	TGcaATGGAt	TGAATAGTTA	AAATATTTAT	AAAGGCAtAG	650
g GAAAAGACC	AGAAAACAgA	CACACAgACa	cacacacaCA	CACTTtTGTC	700
TTAACTTaga	tcatccttaa	aagggagcag	tagctacaga	gaaggcagag	750
aaggtccact	tagtgcaatt	ctgtgtcatc	tcagtatttc	agcaatttct	800
taaaagtcat	gaaaaaagtt	taaaatact	tcctgttaaa	ggataccttc	850
taggccaatg	tcatcagtga	aattaaccaa	gaacaaagag	aacgagaacc	900
agaaaaggaa	tgtccccttc	taggaaacga	gggtccacag	gag	

Against mouse

	ggagcgatga	tgtgagaggg	agagagaggg	gtgggatgca	atctctgaaa	50
	acgctcatca	acatatttcc	agtctgcaaa	aggacaggtc	acgctggagg	100
	aacacttgtg	gaagactctc	ctccagtcgg	gcagcagccc	ctgagcaaac	150
	aacagccttc	cctaggggcc	agacccacac	ctccacgggc	cccttggggg	200
	ccaggcctct	tgagggccca	tgtagttctg	tcccccaagc	tatgttgttc	250
	atgggcagcg	ccatgctggt	tggcctaggg	agagcgtggt	gaagaagcat	300
	catctctggt	cctctcgtgc	gcagaggcag	tgccagctga	cctcgccccg	350
	gccacagctc	ctcccgggac	tgcagagtgc	ccacggcagg	attctgaacc	400
	agccaccggt	cagtggaagc	caggactggg	tctgagtctt	ctccccttcc	450
	agaggtgaaa	agagatcgaa	gggaagggga	gaggcacaga	gccagagaga	500
	gaaaaggggg	gtctggaagg	aagcactgca	ggatggaaat	cacagcttgc	550
	aaaaggcact	tgggagtgga	tgtcccagca	cagccttgaa	aatgagttgc	600
L)	agataacact	cgatcctgcg	ttcccgtgag	gccctccccg	aagagtaatg	650
	gccgcctcct	tggtccattt	agcttgcgcc	gtttgcagtt	tatcagcgat	700
	gagccccctg	aaatctggga	ccccggacaa	ggcagggtgg	aagtacgcag	750
θ	aagtagctga	tggcatttcc	cccgtccccg	acttctgccc	tcgtgggggc	800
υ	ctccctgcac	tgattcctgg	accctattgt	ggacagacag	cgccccagtg	850
Ē	tctccaaaag	cactgctgcc	tcctccctat	acccccgctg	ccccctccc	900
=	caaggcagac	agacaggaga	cgaattaacc	tggcccccc	gacggcgggt	950
σ	gttccaggat	ggcgcccact	gcacccctaa	aagcagcccc	cagaacccgg	1000
_	tgcaagacaa	ggtggttaag	aggcagtgtt	ttatagcccg	caagaaagaa	1050
-	gggaaaacaa	ccctttactg	gggatgcaaa	taaactccgc	ttcacctcta	1100
<u> </u>	gtgctggaaa	cctgtgccct	tggcaggacg	gccgggccgg	ctccagaggt	1150
ш	attaatcttc	cctcttctac	atgtgaaaca	ggccttggga	gggtttcccg	1200
	ggcagggctg	tctctctcca	gcacagccgc	cctctcttcc	ctctggtgca	1250
	gtcagagctc	cccagcagca	gggagcccca	ggggaccagg	tcgggaaccc	1300
	aagccagcgg	atggcagggg	cgccgggccg	cggggccctc	tcggggtgcc	1350
	aggccggccg	gcaggtggcg	ctgccccgcg	cgctatggcc	cctcgcgtgc	1400
	ccggccggcg	ccgcagccag	aggcttcaag	tttctTGTGC	CATTCCTGGa	1450
	cccaaacaAA	TGTTTGTGGA	ATTAAGtAGT	GATTTCCTTT	AGTCTGcGCg	1500
	ACTCtcaCTG	GCTGTGTttt	caggctctag	atgtcaacct	atgccaagta	1550
	ttgcttttcg	ggtgaaatca	ggggtttcca	tgcacactta	aacctgttcc	1600
	aactgcccag	GTCAGCTAGC	AaAGGTCTGC	CTTTTCTGAT	aAAATagCcc	1650
	aTaaAaCTTC	CATAtcAtCA	<pre>GctAgagtGa</pre>	TTTGGagGAC	AAAGAAGTGC	1700
	TGAGAAAtGT	AAGTAAacaG	AgCACCTAAG	ATTTTttTT	CTttctaaat	1750
	aaaaagaagg	gagggcgggt	gtgtttaaac	caggcttaaa	agcgaaggct	1800
	gcaagtgagc	aggagggaaa				

Against shrew

ggagcgatga	tgtgagaggg	agagagaggg	gtgggatgca	atctctgaaa	50
acgctcatca	acatatttcc	agtctgcaaa	aggacaggtc	acgctggagg	100
aacacttgtg	gaagactctc	ctccagtcgg	gcagcagccc	ctgagcaaac	150
aacagccttc	cctaggggcc	agacccacac	ctccacgggc	cccttggggg	200
ccaggcctct	tgagggccca	tgtagttctg	tcccccaagc	tatgttgttc	250
atgggcagcg	ccatgctggt	tggcctaggg	agagcgtggt	gaagaagcat	300
catctctggt	cctctcgtgc	gcagaggcag	tgccagctga	cctcgccccg	350
gccacagctc	ctcccgggac	tgcagagtgc	ccacggcagg	attctgaacc	400
agccaccggt	cagtggaagc	caggactggg	tctgagtctt	ctccccttcc	450
agaggtgaaa	agagatcgaa	gggaagggga	gaggcacaga	gccagagaga	500
gaaaaggggg	gtctggaagg	aagcactgca	ggatggaaat	cacagcttgc	550
aaaaggcact	tgggagtgga	tgtcccagca	cagccttgaa	aatgagttgc	600
agataacact	cgatcctgcg	ttcccgtgag	gccctccccg	aagagtaatg	650
gccgcctcct	tggtccattt	agcttgcgcc	gtttgcagtt	tatcagcgat	700
gagccccctg	aaatctggga	ccccggacaa	ggcagggtgg	aagtacgcag	750
aagtagctga	tggcatttcc	cccgtccccg	acttctgccc	tcgtgggggc	800
ctccctgcac	tgattcctgg	accctattgt	ggacagacag	cgccccagtg	850
tctccaaaag	cactgctgcc	tcctccctat	acccccgctg	ccccctccc	900
caaggcagac	agacaggaga	cgaattaacc	tggcccccc	gacggcgggt	950
gttccaggat	ggcgcccact	gcacccctaa	aagcagcccc	cagaacccgg	1000
tgcaagacaa	ggtggttaag	aggcagtgtt	ttatagcccg	caagaaagaa	1050
gggaaaacaa	ccctttactg	gGGATGCAAA	TAAACTCcGC	TTCACCTcTa	1100
gTGCTGgAAA	CcTGTGCCCt	t <mark>GGC</mark> ag <mark>GA</mark> cg	gcc <mark>GGG</mark> cCgG	cTCCAGAgGT	1150
ATTAATCTTC	CctCtTcTAC	ATGT gaaaca	ggccttggga	gggtttcccg	1200
ggcagggctg	tctctctcca	gcacagccgc	cctctcttcc	ctctggtgca	1250
gtcagagctc	cccagcagca	gggagcccca	ggggaccagg	tcgggaaccc	1300
aagccagcgg	atggcagggg	cgccgggccg	cggggccctc	tcggggtgcc	1350
aggccggccg	gcaggtggcg	ctgccccgcg	cgctatggcc	cctcgcgtgc	1400
ccggccggcg	ccgcagccag	aggcttcaag	TTTCTtGTGC	Cattcctgga	1450
CCCAAaCAAA	TGTTTgTGGA	ATTAAGTAGT	GATTTCCTTT	AGTCTGCGCG	1500
ACTCTCACTG	GCTGTGTTTT	CAgGCTCTAG	ATGTCAaCCT	ATGCCAagtA	1550
TTGCTTTTCg	GGTGAAATCA	gGGGTTTCCA	TGCACACTTA	AaCCtgTtCc	1600
AACtGCcCAg	GTCagCtAGC	AAAGGTCTGC	cttttctgat	aaaatagccc	1650
ataaaacttc	catatcatca	gctagagtga	tttggaggac	AAAGAAGTGC	1700
TGAGAaATGT	AAGTAAACAG	AGCACCTAAG	ATtttttTTT	CTTTCTAAAT	1750
AAAAAGAAGG	GAGGgcgggt	gtgtttaaac	caggcttaaa	agcgaaggct	1800
gcaagtgagc	aggagggaaa				

Fig. S7. Sequence alignments of the individual enhancers 4 and 5.

The conserved nucleotides are highlighted in blue and capitalized. Light blues nucleotides denote the beginning and end of the homology sequence. Note that for enhancer 4 there was no homology in the sequence compared to mouse, human was used instead.

All embryos analyzed for this enhancer are depicted. Entire embryos at E13.5 as well as the dissected urogenital tracts are displayed. me: mesonephros, te: testes, ov: ovaries, ki: kidneys. Four out of five embryos showed mesonephros-specific staining. Black scale bars: $1000 \mu m$, white scale bars: $100 \mu m$.

Fig. S9. LacZ enhancer reporter assay for Enhancer 2.

All embryos analyzed for this enhancer are depicted. Entire embryos at E13.5 as well as the dissected urogenital tracts are displayed. Me: mesonephros, te: testes, ov: ovaries, ki: kidneys. Seven out of ten embryos showed mesonephros-specific staining. Black scale bars: 1000 μ m, white scale bars: 100 μ m.

Fig. S10. LacZ enhancer reporter assay for Enhancer 3.

All embryos analyzed for this enhancer are depicted. Entire embryos at E13.5 as well as dissected urogenital tracts are displayed. Me: mesonephros, te: testes, ov: ovaries, ki: kidneys. Three out of five embryos showed kidney-specific staining. Black scale bars: 1000 μ m, white scale bars: 100 μ m.

Fig. S11. LacZ enhancer reporter assay for Enhancer 4.

All embryos analyzed for this enhancer are depicted. Entire embryos at E13.5 as well as the dissected urogenital tracts are displayed. Me: mesonephros, te: testes, ov: ovaries, ki: kidneys. Three out of five embryos showed mesonephros-specific staining. Black scale bars: 1000 μ m, white scale bars: 100 μ m.

Fig. S12. LacZ enhancer reporter assay for Enhancer 5.

All embryos analyzed for this enhancer are depicted. Entire embryos at E13.5 as well as the dissected urogenital tracts are displayed. Me: mesonephros, te: testes, ov: ovaries, ki: kidneys. Two out of five embryos showed mesonephros-specific staining. Black scale bars: 1000 μ m, white scale bars: 100 μ m.

Fig. S13. SALL1 expression in mesonephros

SALL1 is detected in the mesonephros duct of mouse at E14.5 and at equivalent stages in moles (s5c). Scale bars: 20 μ m.

Fig. S14. Comparative analyses of transcription factor binding motifs and expression.

A. Venn diagram showing the number of shared transcription factor binding motifs among the top 50 motifs found in mole, shrew and mouse sequences (**Supplementary Table 2**). Note the limited conservation, emphasizing the sequence divergence observed among species.

B, C. Expression levels in RPKM of transcription factors with top-ranked motif bindings sites in the mole enhancer sequences. The mole TP (testicular part) of the female ovotestis at P7 is compared with the mouse ovary and testis at E13.5. Note the upregulation of these 5 transcription factors when compared to mouse gonads. Data is presented as mean \pm SD and p-values are indicated as $*p \le 0.05$, $**p \le 0.01$, $***p \le 0.001$.

Fig. S15. Morphology of *Sall1*-overexpressing testes during gonad development.

Hematoxylin-eosin stanning of mutant overexpressing-*Sall1* and wildtype controls testes before and after birth. There are no differences in size, tissue structure or cell composition between mutants and controls. Scale bars: $200 \mu m$.

А	Mus musculus (REF)		<u>u</u>	<u>ipload_1</u> (▼ <u>Hierar</u>	chy	_ NEW! (?)	
GO biological process complete	<u>#</u>	<u>#</u>	expected	Fold Enrichment	<u>+/-</u>	raw P value	<u>FDR</u>
metanephric nephron morphogenesis	<u>18</u>	<u>3</u>	.04	67.89	+	1.79E-05	4.03E-02
•metanephros morphogenesis	<u>24</u>	<u>3</u>	.06	50.92	+	3.89E-05	4.09E-02
<u> </u>	<u>3306</u>	<u>20</u>	8.12	2.46	+	6.24E-05	4.68E-02
<mark> </mark>	<u>3813</u>	<u>25</u>	9.36	2.67	+	8.56E-07	1.35E-02
•multicellular organism development	<u>4559</u>	<u>26</u>	11.19	2.32	+	1.01E-05	2.64E-02
<u> </u>	<u>368</u>	<u>7</u>	.90	7.75	+	3.46E-05	4.20E-02
<mark> </mark>	<u>1057</u>	<u>11</u>	2.59	4.24	+	4.59E-05	4.02E-02
4anatomical structure morphogenesis	<u>2337</u>	<u>19</u>	5.74	3.31	+	1.50E-06	1.18E-02
<u> </u>	<u>136</u>	<u>5</u>	.33	14.98	+	2.45E-05	3.51E-02
positive regulation of branching involved in ureteric bud morphogenesis	<u>23</u>	<u>3</u>	.06	53.13	+	3.47E-05	3.90E-02
regulation of branching involved in ureteric bud morphogenesis	<u>25</u>	<u>3</u>	.06	48.88	+	4.35E-05	4.04E-02
regulation of morphogenesis of a branching structure	<u>66</u>	<u>4</u>	.16	24.69	+	2.61E-05	3.43E-02
regulation of multicellular organismal process	<u>2989</u>	<u>19</u>	7.34	2.59	+	5.28E-05	4.38E-02
ventricular septum development	<u>82</u>	<u>4</u>	.20	19.87	+	5.88E-05	4.63E-02
<u> </u>	<u>145</u>	<u>6</u>	.36	16.86	+	1.84E-06	9.66E-03
<u> </u>	<u>192</u>	<u>6</u>	.47	12.73	+	8.77E-06	2.76E-02
developmental growth involved in morphogenesis	<u>153</u>	<u>5</u>	.38	13.31	+	4.22E-05	4.16E-02
anatomical structure formation involved in morphogenesis	<u>980</u>	<u>11</u>	2.41	4.57	+	2.32E-05	3.65E-02
negative regulation of multicellular organismal process	<u>1154</u>	<u>12</u>	2.83	4.24	+	1.96E-05	3.87E-02
epithelium development	<u>1161</u>	<u>12</u>	2.85	4.21	+	2.08E-05	3.65E-02
<u> •tissue development</u>	<u>1785</u>	<u>16</u>	4.38	3.65	+	3.88E-06	1.53E-02
B <u>Mus musculus</u> (REF) <u>up</u>	<u>load_1</u> (▼ <u>Hierarchy</u> N	IEW	(?)				
GO cellular component complete # # expected F	Fold Enrichment +/- ra	w P	value F	-DR			

extracellular region 2875 20 7.06 2.83 + 7.91E-06 1.61E-02

Fig. S16. Gene ontology enrichment of commonly upregulated genes in female mole testis part and mouse *Sall1*-overexpressing mutant ovaries.

- A. GO terms for biological processes.
- B. GO terms for cellular components.

Gene	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
Lhx1	76,0142476	0,416247256	0,45549231	0,91384036	0,36080074	0,99999929
Fgf9	34,7898814	-0,34199249	0,64606248	-0,5293489	0,59656341	0,99999929
Cxcr4	269,917075	0,363473378	0,24191365	1,50249224	0,13297003	0,99999929
Cxcl12	867,206005	-0,400398642	0,1872609	-2,138186	0,03250165	0,99999929
Spry2	246,127611	0,017530695	0,24731929	0,07088285	0,943491	0,99999929
Mmp14	2980,353	-0,004484855	0,11824949	-0,0379271	0,96974584	0,99999929

Fig. S17. Expression of migration markers in *Sall1*-overexpressing ovaries.

A, B. Immunostaining for PDGFRa in female mutant and male wildtype controls at E13.5. There is no signal for PDGFRa in mutant ovaries, denoting the absence of migration. Scale bars: 100 μ m

C. Differential gene expression between female mutant and controls for several genes involved in cell migration. Note, there are no significant differences between both conditions.

Table S1. Ranking of enhancer regions.

Click here to download Table S1

Table S2. Ranking of transcription factors by significance of binding affinity to the five *SALL1* enhancer sequences.

Click here to download Table S2

Table S3. Differential gene expression between Sall1-overexpressing mutant and wildtype ovaries.

Click here to download Table S3

Table S4. Primer list.

	RT-qPCRs
Hedgehog-qPCR-Sall1-Fwd	GAAGCAAGCGAAGCCTCAAC
Hedgehog-qPCR-Sall1-Rev	TGCTCTTAGTGGGGCGATTT
Hedgehog-qPCR-Foxl2-Fwd	CAGAAGCCGCCCTATTCGT
Hedgehog-qPCR-Foxl2-Rev	GGGAACTTGGCGATGATGT
Hedgehog-qPCR-Rps9-Fwd	GCCAAGTCCATCCACCAC
Hedgehog-qPCR-Rps9-Rev	CCAGGCGGACAATGAAGG
Shrew-qPCR-Sall1-Fwd	AGAGCGTTCACAACAAAGG
Shrew-qPCR-Sall1-Rev	TGGGGCCATCCACAGAGA
Shrew-qPCR-Foxl2-Fwd	CATCGCCAAGTTCCCCTTCT
Shrew-qPCR-Foxl2-Rev	GCACTCGTTGAGGCTGAGGT
Shrew-qPCR-Rps9-Fwd	GAGTCCAGGCGAACAATGAA
Shrew-qPCR-Rps9-Rev	GGCCAAGTCCATCCACCA

4C-seq experiments			
Sall1-4C-Fwd	TCAGTGGGCTGACATTTTA		
Sall1-4C-Rev	TCAGTGGGCTGACATTTTA		
5ITR-4C-Fwd	gctgcacctacagtttggat		
5ITR-4C-Rev	gctgcacctacagtttggat		
3ITR-4C-Fwd	gctgcacctacagtttggat		
3ITR-4C-Rev	gctgcacctacagtttggat		

Amplification of the Enhancers			
Sall1-E1-Fwd	TCTGGAGAACACTCACACCC		
Sall1-E1-Rev	GCAAGCCAGTAGATACCGCA		
Sall1-E2-Fwd	ACTCTTTCACATGTGCCAAA		
Sall1-E2-Rev	TCCAGCACAAGAAATCCTGC		
Sall1-E3-Fwd	GAAAAAAAATCTTAGGTGC		
Sall1-E3-Rev	GAGCAAACAACAGCCTTCCC		
Sall1-E4-Fwd	GTTTGTTCAATTTTTAAATT		
Sall1-E4-Rev	ACATTGGCCTAGAAGGTATC		
Sall1-E5-Fwd	CAGGGGAAGGAAGGCAGGCT		
Sall1-E5-Rev	GTGGGACCCTTGCCGGTGGC		

PiggyBac Wt1-Sall1-BAC Cloning				
Sall1-CDS-attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTTTTGAGCCAGCATGTCGCGG			
Sall1-CDS-attB2	GGGGACCACTTTGTACAAGAAAGCTGGGTTCTGGCAGCTTTAGCTTGTG			
	TGGGTAAGGCAGTGATGACAGATCAAAAGTAAAAGGTCTCACCCAGTCTACTCGACTGC			
Neo-Rec-Fwd	ACGCGTTATATAG			
	TAAATAACCCCTCCTTTGTGTTCCTCTAACCCACTTAAATTTATTGCTTCATGTACCTGA			
Neo-Rec-Rev	CTGATGAAGTTC			

Genotyping Sall1-BAC insertion into ES cells			
Sex-PCR-Fwd	CTGAAGCTTTTGGCTTTGAG		
Sex-PCR-Rev	CCACTGCCAAATTCTTTGG		
5'ITR-BAC-Fwd	gacgcatgcattcttgaaat		
5'ITR-BAC-Rev	atgcgtcattttgactcacg		
3'ITR-BAC-Fwd	gaagaaattttgagtttttgttttt		
3'ITR-BAC-Rev	cgcatgtgttttatcggtct		
bck-BAC-Fwd	GGCGGTGTTGATACAGCGGGTAA		
bck-BAC-Rev	CCGGCGTTCGGTCGAAGAGTATC		