

Supplementary Table 1: Gene identification and insertion site

ROSA	ref seq	Symbol	Name	chr	insertion	CDS
72	NM_009551	Zfand5	zinc finger, AN1-type domain 5	19	1st intron	upstream
73	NM_001024708	BC058969	BC058969 (similar to cdh11 precursor)	8	1st intron	upstream
74	NM_181072	Myole	myosin IE	9	1st intron	1 aa
75	NM_023598	Arid5b	AT rich interactive domain 5B	10	4th intron	283 aa
76	NM_001001737	BC055757	cDNA sequence BC055757	19	1st intron	1 aa
77	NM_013928	Schip1	schwannomin interacting protein 1	3	2nd intron	134 aa
78	NM_009163	Sgpl1	sphingosine phosphate lyase 1	10	2nd intron	9 aa
79	NM_178892	Tiparp	TCDD-inducible poly(ADP-ribose) polymerase	3	1st intron	upstream
80	NM_153287	Axud1	AXIN1 up-regulated 1	9	2nd intron	67 aa
81	AY149175	Mzf6d	KRAB zinc finger protein 6D	13	unknown ¹	upstream ¹
82	NM_133942	Plekha1	pleckstrin homology domain family A1	7	3rd intron	82 aa
83	NM_023719	Txnip	thioredoxin interacting protein ²	3	8th intron ²	unknown ²

Consistent with previous gene trap mutations generated in our laboratory, all mutations are designated as ROSA (Reverse Orientation Splice Aceptor; <http://www.fhcr.org/science/labs/soriano/trap.html>). Following the mouse nomenclature committee guidelines, the mutation in *Zfand5* is thus referred to as *Zfand5*^{Gt(ROSA)72Sor}, or ROSA72 for short. The insertion of gene trap construct is noted relative to intron number and the coding start site (CDS). ¹The intron/exon structure of the *Mzf6d* gene is unknown due to repetitive sequences in this region of chromosome 13. However, the 3' RACE product of *Mzf6d* overlaps with the start of the predicted coding start site, indicating that the insertion site is likely upstream of the coding sequence. ²The insertion into the 8th intron of *Txnip* is actually in the reverse orientation for this gene, indicating that the trapped gene may be a novel gene anti-sense to *Txnip*.

