

Supplementary Table 1. Table of efficiency of mESC embryo derivation by cell type, cell source and aggregation technique.

Method	Parental ES cell line	Source	# of ESC clones tested	# embryos transferred	# decidua	Implantation rate	# embryos recovered	# completely ES cell derived	% complete ES cell derived
Diploid aggregation	E14	Bay Genomics	24	2737	1091	0.399	942	440	0.467
	E14	SIGTR	17	2126	972	0.423	582	299	0.514
	R1	CMHD	1*	283	102	0.398	78	35	0.449
TOTAL			41	5146	2165	0.407	1602	774	0.477
Tetraploid aggregation	E14	GCTC	7	953	396	0.475	214	198	0.94
	D3H	MFGC	2	105	49	0.426	47	47	1
	R1	CMHD	1*	74	57	0.77	51	37	0.725
	R1	GCTC	2	48	10	0.208	2	6	1
	TBV-2	GCTC	14	813	354	0.435	211	160	0.758
...	IDG_3.2-F1	GCTC	6	485	212	0.437	154	154	1
TOTAL			31	2478	1078	0.458	679	602	0.904
OVERALL			71	7624	3242	0.4325	2281	1376	0.691

* the same clone (179B2-3)

Supplementary table 3. Primer sequences for wild type and gene trap allele specific RT-PCR.

Gene Symbol	Clone ID	Primer Sequence Fwd	Primer Sequence Rev	Gene trap primer 1
<i>Fam122b/4632404H2</i>	AZ0548	TGAGGCTGACACATCTGAGG	TATCTGCATCCCTGCTTG	ATTCAGGCTGCGCAACTGTTGGG
<i>2Rik</i>				
<i>4932441K18Rik</i>	RRJ292	TGGCGAAAGGGGGATGTG	TTCCATTGTGCCAATTTCAA	GACTCGGCTTGAGGAGGTAA
<i>Ccdc160/6330534C20</i>	CMHD-	GTGGTGGCTAGCACTGAACA	GCTTCCTGAAAATCGTGCTC	GCTATCAGGACATAGCGTTGGCTAC
<i>Rik</i>	GT_179B2-3			
<i>A830080D01Rik</i>	W069B04	TTTGGTTGCTATTGGCAAAAC		ATATCCTGATCTTCCAGATAAAGTCCG
<i>A830080D01Rik</i>	P078F05	TCTGGTGACGACTTCTCTGA		ATATCCTGATCTTCCAGATAAAGTCCG
<i>Alg13</i>	P035H04	GCAGGTGCAGGAAGCTGTT		ATATCCTGATCTTCCAGATAAAGTCCG
<i>Alg13</i>	P088H08	GCAGGTGCAGGAAGCTGTT		ATATCCTGATCTTCCAGATAAAGTCCG
<i>Ammecr1</i>	XK571	ACCAATGACAAGGGATGAGC	CAACCTCCGGTAGGTAGGTG	ATTCAGGCTGCGCAACTGTTGGG
<i>Apool</i>	AC0470	CCACTAGGACTGGCCACATT	TTCCTTTGGTTCAGGGAGTG	ATTCAGGCTGCGCAACTGTTGGG
<i>Atp11c</i>	RRM203	CGAGCTAGCTGTCCGCTTT	GAAATGGGATGATTGCCAAC	ATTCAGGCTGCGCAACTGTTGGG
<i>Sfrs17b/</i>	RR1131	GACCAGGAGGGTTGATCCTT	AACTCTTCATGGCGAGCACT	ATTCAGGCTGCGCAACTGTTGGG
<i>B230333C21Rik</i>				
<i>Bcor</i>	XE541	ACTCCGAGGTGTGCAAATTC	AGGTGGCCTCTCCAAGAAAT	ATTCAGGCTGCGCAACTGTTGGG
<i>Bcor</i>	DBO053	ACTCCGAGGTGTGCAAATTC	AGGTGGCCTCTCCAAGAAAT	ATTCAGGCTGCGCAACTGTTGGG
<i>Bcor</i>	P101H07			
<i>Bcor</i>	A20062	TGATGCGCTTCTCAGAGTTG		ATATCCTGATCTTCCAGATAAAGTCCG
<i>Bcor</i>	W096D07	TGATGCGCTTCTCAGAGTTG		ATATCCTGATCTTCCAGATAAAGTCCG
<i>Brwd3</i>	RHA090	CAATGCACACATTCCTCCAG	GCCTGGCTGAGGTGATATTC	ATTCAGGCTGCGCAACTGTTGGG
<i>C330007P06Rik</i>	RRG250	AGCTATGCCGAAAGTCGTGT	GTTTGGCAGCATCGATCAC	ATTCAGGCTGCGCAACTGTTGGG
<i>C330007P06Rik</i>	AWO613	TGACTCTTACGCGCAGAATG	TAAATCCGACCTGAGCCATC	TGGCGAAAGGGGGATGTG
<i>Chic1</i>	XQO221	AGGCTCTCCCTGTCAATGTG	TCCTTTTAGTCAGTTCCAGTGC	ATTCAGGCTGCGCAACTGTTGGG
<i>Cova1</i>	RRJ357	ACCCCTGCAGTTTGGTAGTG	GTTGTCCAGCAATCCCAGT	ATTCAGGCTGCGCAACTGTTGGG
<i>Cox7b</i>	XH290	GCAGTTCCATCTTCGTCTCC	AAGATGGCTCCACCTGCTAA	ATTCAGGCTGCGCAACTGTTGGG
<i>Med14/Ctps2</i>	AS1012	GATGCAACTGGCAGTGATTG	CCCCAGTCTCATTGTTCTCTC	ATTCAGGCTGCGCAACTGTTGGG
<i>Cul4b</i>	M119G06	GGATGTCACGTTCAACTAGGT		ATATCCTGATCTTCCAGATAAAGTCCG
<i>Hdx/D030011N01Rik</i>	CDO231	GGACCTCATTGCATACAGCA	ACCCTGTAATCCAAGGCACA	ATTCAGGCTGCGCAACTGTTGGG
<i>Diap2</i>	W005C03	TGGGGGAGTTTTTCTCTCC		ATATCCTGATCTTCCAGATAAAGTCCG
<i>Diap2</i>	E093H05	GCCTGAAAAACAGCAAACAT		ATATCCTGATCTTCCAGATAAAGTCCG
<i>Flna</i>	F015B06	TCCCACGAGAGAATGGCATC		ATATCCTGATCTTCCAGATAAAGTCCG
<i>Ftsj1</i>	RRD143	CTTCCACTGCCAAGGAGAT	CCACATCATGGAGACCAGTG	ATTCAGGCTGCGCAACTGTTGGG

<i>Glod5</i>	CMHD-GT_111.1G4-3	CCTGCCTCCAGTCTACCAG	TGCCCAGGATCTTGAATAA	GCTATCAGGACATAGCGTTGGCTAC
<i>Huwe1</i>	DCO732	TAGTGCTCCGTGAGGTTGTG	TGATTTGCTGCAGTTCCAAG	ATTCAGGCTGCGCAACTGTTGGG
<i>Huwe1</i>	P125E01			
<i>Huwe1</i>	P036B01	TAGTGCTCCGTGAGGTTGTG		ATATCCTGATCTTCCAGATAACTGCCG
<i>Kdm5c/Jarid1c</i>	E008C01			
<i>Kdm5c/Jarid1c</i>	P026G11	AGGGCCTAGACTCCGAGAAG		ATATCCTGATCTTCCAGATAACTGCCG
<i>Kif4</i>	AA0042	GTCTGAGTGAGGCAGCTGGT	CCAATGTCTCCACGAGCTTT	ATTCAGGCTGCGCAACTGTTGGG
<i>Klf8</i>	AD0932	TGGTTCGATGCAGGTATTCA	CTGCTCTCGAGAAGGATCT	ATTCAGGCTGCGCAACTGTTGGG
<i>LOC434808 (Nono)</i>	P030B07			
<i>Lrch2</i>	RRI232	AGAGGAGACGAAGCAAGCAG	GCCATCAGAGCGGTCATATT	AGTATCGGCCTCAGGAAGATCG
<i>Tab3/Map3k7ip3</i>	RRK351	CAACATTGACTCTGGCATGG	GGCTCGACAACAGGCTTCTA	ATTCAGGCTGCGCAACTGTTGGG
<i>Med14</i>	A055C04	CGGGCCTACTCGGAGCTTAT		ATATCCTGATCTTCCAGATAACTGCCG
<i>Mtap7d2</i>	AFO577	GCAAAAAGAGAAGGCTGAGGA	CTCTCCAGTCGTTCTGCTC	ATTCAGGCTGCGCAACTGTTGGG
<i>Nono</i>	E086B07			
<i>Nono</i>	E089G04			
<i>Ogt</i>	BGA526	CTCCGTGGGTTGAGAGTCAT	AGGAACAAGGGCAAATCTCA	ATTCAGGCTGCGCAACTGTTGGG
<i>Orf34</i>	AP0628	TGGCGAAAGGGGGATGTG	AAGACATCCTTGCCAACCAC	GGACCAGAACATCCTCTTGC
<i>Otud5</i>	A021B07	CCAGTCCGGAACGTGAAGAG		ATATCCTGATCTTCCAGATAACTGCCG
<i>Pdzd4</i>	RRO278	CTCTTCCCCTCTCCTCTTT	GTCCACCAGCTGAAGGTCAT	ATTCAGGCTGCGCAACTGTTGGG
<i>Phf16</i>	XTO269	GCATAGACCTGTCAGCAGCA	TGGCTGGTACTTGGACTCCT	ATTCAGGCTGCGCAACTGTTGGG
<i>Pir</i>	AW0646	GATCATCCACACCGAGGATT	GCCCCCTCCAGAAGATAAG	ATTCAGGCTGCGCAACTGTTGGG
<i>Pola1</i>	CSG241	TGAAGAAGTTGATGAAGAGCAG	TCCACAGGTGTCAAGTGCAT	ATTCAGGCTGCGCAACTGTTGGG
<i>Porcn</i>	CSD256	GACCACGGCTTCCTTTCTG	GGCGAAGCAGATGGTAAGAA	ATTCAGGCTGCGCAACTGTTGGG
<i>Rab9</i>	W255D06	CCGGAGTCTCTGGCCTTCTT		ATATCCTGATCTTCCAGATAACTGCCG
<i>Rbbp7</i>	Q017B06			
<i>Rbm10</i>	W081D04	TAGAGGTGGTCGTGGTGACA		ATATCCTGATCTTCCAGATAACTGCCG
<i>Rbm3</i>	PST5643-NL	TCTTCGTAGGAGGGCTCAAC		CAGGTCGGTCTTGACAAAAAGAAC
<i>Rbm3</i>	PST7787-NL	TCTTCGTAGGAGGGCTCAAC		CAGGTCGGTCTTGACAAAAAGAAC
<i>Rbm41</i>	W007A05	GCCAGCGCATCCTTTACCT		ATATCCTGATCTTCCAGATAACTGCCG
<i>Rlim/Rnf12</i>	AD0035	GAGCCGGACTAATCCAAACA	CCAGAAGCTGCAAAAAGACC	ATTCAGGCTGCGCAACTGTTGGG
<i>Rps6ka6</i>	RRS057	GGTTGATGAGCCAATGGAAG	TCCAAAAGATCCCTGACCAA	ATTCAGGCTGCGCAACTGTTGGG
<i>Snx12</i>	AY0032	GCAAGGCCTCGAACAGTTTA	ACACTGAGGTGGGTTCCAAG	ATTCAGGCTGCGCAACTGTTGGG
<i>Syap1</i>	AF0128	CTCCGTGGGTTGAGAGTCAT	AGGAACAAGGGCAAATCTCA	ATTCAGGCTGCGCAACTGTTGGG

<i>Taf9b</i>	TEA124	CAATTCTGGACGATGCAAAG OR ATCAAGAACGCTCCGAGAGA	GTGGCTGTGTTCTGTGAGGA	ATTCAGGCTGCGCAACTGTTGGG
<i>Usp9x</i>	XK141	CATGGCAGTTCTGAGGATGA	TTGCAAGGTCAGAGCTTTTTTC	ATTCAGGCTGCGCAACTGTTGGG
<i>Usp9x</i>	W059E04	CAAATGGGTCATTCCTGCACT		ATATCCTGATCTTCCAGATAACTGCCG
<i>Kdm6a/Utx</i>	RRA094	TGTTTCGCTGCTACGAATCTC	AAAAGGCAGCATTCTCCAG	ATTCAGGCTGCGCAACTGTTGGG
<i>Vbp1</i>	BA0243	AGCAGCCTGGGAATGAGACT	CGGCCAGTAAGAATCTCGTC	ATTCAGGCTGCGCAACTGTTGGG
<i>Wdr44</i>	RRE018	CCTATAAATGGCGTCGGAAA	AGGGGACTCATTTCAGCTT	ATTCAGGCTGCGCAACTGTTGGG
<i>Wnk3</i>	RRU456	TAGAGCTGGGAAGAGGAGCA	TGGAGGCCTTTCAACATCTC	ATTCAGGCTGCGCAACTGTTGGG
<i>Zdhhc15</i>	AH0619	ACCTGAGGTCCAGAAGCAGA	GGCAGTGATGGTCCATTTTT	ATTCAGGCTGCGCAACTGTTGGG