Supplementary Table S5: Insertion sites recovered from lentiviral LTHSC and STHSC EGFP progeny (DBISA).

Mouse ID	weeks after BMT	Source	locus: within gene or nearest gene	RTCGD (hits N°)	gene ID	chromo-some	(proposed) function	pos. to TSS (i, intron; e, exon)	orien-tation
1° BMT									
LT#41									
# 41	32	BM	6030408C04Rik	0	217558	12 C1	RIKEN cDNA 6030408C04 gene: G2/M phase-specific E3 ubiquitin-protein ligase-like	5 kb (i2)	F
# 41	32	BM	Vmn2r58	0	628422	7 B3	vomeronasal 2, receptor 58	-14 kb	R
# 41	8	PB	hit into repeat region	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
# 41	8	PB	hit into repeat region	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
LT#42									
#42	32	BM	hit into repeat region	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
#42	32	PB, BM	hit into repeat region	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
#42	8	PB	Herc2	0	15204	7 B5	hect domain and RCC1 (CHC1)-like domain (RLD) 2: zink ion binding	8 kb (i2)	R
#42	8	PB	F8*	0	14069	X A7-B	coagulation factor VIII	6 kb (i1)	R
#42	8	PB	no s.h.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
#42	32	PB	hit into repeat region	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
LT#43									
#43	32	PB, BM	LOC100042510	0	100042510	10 D1	predicted gene	31 kb	F
#43	32	PB, BM	no s.h.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
#43	32	PB, BM	hit into repeat region	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
#43	8, 32	PB, BM	EG627543	0	627543	16 B5	predicted gene	-117 kb	F
#43	32	PB	hit into repeat region	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
LT#44									
#44	32	BM	Pde3a	0	54611	6 G1	phosphodiesterase 3A, cGMP inhibited: Insulin signaling pathway	190 kb (i2)	R
#44	8, 32	PB, BM	Rab30	0	75985	7 E1	RAB30, member RAS oncogene family	94 kb (i4)	R
#44	8, 32	PB	hit into repeat region	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
#44	32	BM	V1rc30	0	171203	6 B3	vomeronasal 1 receptor, C30: pheromone receptor activity	8 kb	R
LT#45									
#45	32	BM	hit into repeat region	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
#45	32	BM	hit into repeat region	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
#45	8	PB	LOC100040685	0	100040685	1 D	predicted gene	66 kb	F
#45	8	PB	hit into repeat region	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
#45	8	PB	hit into repeat region	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
#45	8	PB	Glra2	0	237213	X F5	glycine receptor, alpha 2 subunit	106 kb (i7)	F
#45	8	PB	Gramd1b	0	235283	9 B	GRAM domain containing 1B	93 kb (i2)	F
#45	8	PB	Dach1	0	13134	14 E3	dachshund 1 (Drosophila): TF, development	385 kb	R
#45	32	PB	hit into repeat region	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.

#45	32	PB, BM	Atp5f1*	0	11950	3 F2.2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1: transport	11 kb (i6)	F
ST#46									
#46	32	BM	hit into repeat region	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
#46	32	BM	Magi3	0	99470	3 F2.2	membrane associated guanylate kinase, WW and PDZ domain containing 3	17 kb (i1)	F
#46	32	BM	Irak1bp1	0	65099	9 E2	interleukin-1 receptor-associated kinase 1 binding protein 1: I-kappa B kinase	7 kb (i1)	R
ST#47									
# 47	32	BM	hit into repeat region	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
# 47	32	BM	non coding +/- 150 kb	n.a.	n.a.	11A1	n.a.	n.a.	n.a.
ST#48									
#48	32	BM	non coding +/- 150 kb	n.a.	n.a.	15B3.2	n.a.	n.a.	n.a.
#48	32	PB, BM	Rfc1	0	19687	5 C3.1	replication factor C (activator 1) 1: replication, transcription	50 kb (i11)	F
ST#49									
#49	32	BM	non coding +/- 150 kb	n.a.	n.a.	2C1.1	n.a.	n.a.	n.a.
#49	32	BM	no s.h.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
#49	32	PB	no s.h.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
ST#50									
# 50	32	PB, BM	LOC100043741	0	100043741	17 E5	predicted gene, 100043741	-120 kb	F
# 50	32	BM	Serbp1	0	66870	6 C1	Serpine1: mRNA binding protein 1	13 kb (i5)	F
# 50	32	PB, BM	Tnc	0	21923	4 C1	tenascin C: signal transduction	-79 kb	R
# 50	32	PB	no s.h.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.

Insertional coordinates are given based on the NCBI database, July 2008; RTCGD membership is given based on the database's information accessible on July 2008;

PB, total peripheral blood; BM, total bone marrow; TSS, transcriptional start site (NCBI definition); *, located in gene dense region: more than 3 genes wihtin of 50 kb from each RVIS side; n.a., not applicable; no s.h., no significant homlogy found.