Supplementary Table S2: Insertion sites recovered from gamma–retroviral LSK and LK EGFP progeny (DBISA)

recipient	**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									
LSK#11									
#11	11	PB	Vwf	1	22371	6 F3	Von Willebrand factor homolog	-5126 bp	F
#11	11	PB	Bex6	1	328660	16 B2	Brain expressed X-linked 6	4929 bp	F
#11	11	PB	Tlr1	0	21897	5 C3.1	toll-like receptor 1	-1754 bp	R
#11	16	PB	Mpzl1	2	68481	1 H2.3	myelin protein zero-like 1	23321 bp	R
#11	16	PB	Adck1	0	72113	12 E	aarF domain containing kinase 1	68741 bp (i3)	R
#11	16, 27	PB	Stk17b	0	98267	1 C1.1	serine / threonine kinase 17b	10466 bp (i2)	F
#11	16, 27	PB, BM	Mafg*	0	17134	11 E2	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G	2600 bp (i1)	R
#11	16, 27	PB, BM	Tbc1d10c*	0	108995	19 A	TBC1 domain family, member 10c	4518 bp (i6)	F
#11	16	PB	Diap1	0	13367	18 B3	diaphanous homolog 1 (Drosophila): Rho GTPase binding	56600 bp (i16)	R
#11	16, 27	PB, BM	Ppm1h	2	319468	10D2	protein phosphatase 1H	121292 bp (i2)	F
#11	16	PB	LOC100046630	0	100046630	14 A3	similar to CDC28 protein kinase 1b	-41178 bp	R
#11	16	PB	EG665934	0	665934	5 B	predicted gene	-16189 bp	R
#11	27	PB	Cldn14	0	56173	16 C4	claudin 14	-24027 bp	R
#11	27	BM	Arhgef7	0	54126	54126	Rho guanine nucleotide exchange factor	20098 bp (i1)	F
#11	27	BM	Crsp2	1	26896	X A1.1	cofactor required for Sp1 transcriptional activation, subunit 2	1665 bp (i1)	F
#11	27	BM	5330437I02Rik	0	319888	18 E1	endopeptidase inhibitor activity	-1769 bp	R
LSK#12									
#12	5, 16, 23, 27	PB, BM	Brd7	0	26992	8 C4	bromodomain containing 7	-490 bp	F
#12	5, 16, 23, 27	PB, BM	Evi1	24	14013	3 A3	ecotropic viral integration site 1	-205054 bp	R
#12	5, 11, 27	PB	Ccdc21*	0	70012	4 D3	coiled-coil domain containing 21	27671 bp (i3)	R
#12	5, 11	PB	Pim1*	38	18712	17 A3.3	proviral integration site 1	4864 bp (e3)	F
#12	5	PB	Tex14	0	83560	11 C	testis expressed gene 14: protein / tyrosine kinase	36445 bp (i14)	R
#12	11, 16, 27	PB, BM	Patz1*	1	56218	11 A1	POZ (BTB) and AT hook containing zinc finger 1	21443 bp	F
#12	11, 16	PB	2610018G03Rik	0	70415	X A3.3	protein kinase activity	-6022 bp	F
#12	11	PB	Nox1*	0	237038	X E3	NADPH oxidase 1	636 bp	F
#12	16, 23, 27	PB, BM	Ak2	2	11637	4 D2.2	adenylate kinase 2:	32904 bp	F
#12	16	PB	Zfp160	0	224585	17 A3.2	zinc finger protein 160	872 bp (i1)	R
#12	23	PB	LOC671336	0	671336	1 G3	hypothetical	5846 bp	R
LSK#13									
#13	5	PB	Gpr146*	0	80290	5 G1	G protein-coupled receptor 146: signal transduction	1722 bp (i1)	F
#13	5	PB	LOC664909	0	664909	18 A1	similar to carbohydrate sulfotransferase 10	17509 bp	R

#13	16	PB	Enpp4	0	224794	17 B3	ectonucleotide pyrophosphatase / phosphodiesterase 4: metabolic	4361 bp (i3)	R
#13	16, 27	PB, BM	Gm969	0	381229	19 D1	gene model	-221 bp	F
#13	16, 27	PB, BM	D17Wsu92e*	0	224647	17 A3.3	DNA segment, Chr 17, Wayne State University 92, expressed	-4979 bp	F
#13	16	PB	Rab27a*	0	11891	9 D	member RAS oncogene family	10375 bp (i1)	R
#13	16, 27	PB	Rpl38	1	67671	11 G1	ribosomal protein L38	-103663 bp	F
#13	27	PB	Irf2	5	16363	8 B2	interferon regulatory factor 2: transcription factor	6481 bp (i1)	F
#13	27	PB	LOC100040725	0	100040725	13 D2.2	hypothetical	-3934 bp	F
#13	27	BM	Kbtbd7*	0	211255	14 D3	kelch repeat and BTB (POZ) domain containing 7	15258 bp	R
LSK#14									
#14	5	PB	LOC623327	0	623327	1 E4	hypothetical	39641 bp (i1)	R
#14	11, 27	PB	Zmiz1	9	328365	14 A3	retinoic acid induced 17: transcription factor, zinc finger, MIZ-type containing 1	69880 bp (i2)	R
#14	11	PB	Commd7	0	99311	2 H1	COMM domain containing 7	24038 bp	F
#14	11	PB	Col11a2*	0	12815	17 B1	procollagen, type XI, alpha 2: a novel retinoic acid-response element	18355 bp (i36)	F
#14	11, 16	PB	Reep5	1	13476	18 B1	receptor accessory protein 5	466 bp	R
#14	16	PB	Hemgn	0	93966	4 B1	hemogen: unknown; cell diff.	116 bp (e1)	R
#14	16	PB	Skap2	2	54353	6 B3	src family associated phosphoprotein 2: B cell activation; signaling	-1168 bp	R
LSK#15									
#15	11	PB	Nek10	0	238944	14 A1	NIMA (never in mitosis gene a)- related kinase 10	279370 bp	R
#15	11	PB	LOC668840	0	668840	3 G3	60S ribosomal protein L7a pseudogene	24882 bp	F
#15	11	PB	Fnbp1	5	14269	2 B	formin binding protein 1: RNA binding	-1802 bp	F
#15	11	PB	Reep5	1	13476	18 B1	receptor accessory protein 5	466 bp	R
#15	11, 16, 23, 27	PB, BM	Sox7	0	20680	14 C3	SRY-box containing gene 7: repression of Wnt signaling	-639 bp	F
#15	27	BM	Rhoh	0	74734	5 D	ras homolog gene family, member H	20329 bp	R
#15	27	BM	Olfr56*	0	18356	11 B1.2	olfactory receptor 56	26114 bp (i1)	F
#15	27	BM	Scarb2	0	12492	5 E3	scavenger receptor class B, member 2	29826 bp (i2)	F
LK#16									
#16	11	PB	hit into repeat region	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
#16	11	PB	hit into repeat region	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
#16	11	PB	no s.h.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
#16	16	PB	hit into repeat region	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
LK#17									
#17	5	PB	Zfp458	0	238690	13 B3	zinc finger protein 458	37 kb	R
#17	5	PB	hit into repeat region	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
#17	11	PB	Pus7	0	78697	5A3	pseudouridylate synthase 7 homolog (S. cerevisiae)	74 kb	F
#17	16	PB	no s.h.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
LK#18									

#18	5	PB	Ldoc1l	0	223732	15 E2	leucine zipper, down-regulated in cancer 1-like	8474 bp	F
#18	5	PB	no s.h.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
#18	11	PB	Stat5b	9	20851	11D	signal transducer and activator of transcription 5B	-2854 bp	R
#18	11	PB	LOC434047	0	434047	5 A3	heat shock protein 8 pseudogene	5988 bp	F
#18	11	PB	Pus7	0	78697	5A3	pseudouridylate synthase 7 homolog (S. cerevisiae)	74 kb	F
#18	11	PB	Serinc3	8	26943	2 H3	serine incorporator 3:TDE1 inhibits apoptosis and stimulates tumorigenesis	2475 bp (i1)	R
#18	11	PB	no s.h.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
#18	16	PB	Sorl1	2	20660	9 A5	sortilin-related receptor, LDLR class A repeats-containing: signaling	211846 bp	F
#18	16	PB	hit into repeat region	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
LK#19									
#19	5	PB	Cd300lb	0	217304	11 E2	receptor activity	17810 bp	R
#19	5	PB	BC017647	0	216971	11 B5	hypothetical protein	4561 bp (i1)	F
#19	11	PB	Zfp458	0	238690	13 B3	zinc finger protein 458	37 kb	R
#19	11	PB	Ccdc21	0	70012	4 D3	coiled-coil domain containing 21:Chromosome segregation ATPases [Cell division and chromo	27659 bp (i3)	R
#19	16	PB	Btrc	0	12234	19 D1	beta-transducin repeat containing protein: ubiquitin; Wnt signaling	174326 bp	R
LK#20									
#20	5	PB	Ccdc21	0	70012	4 D3	coiled-coil domain containing 21:Chromosome segregation ATPases [Cell division and chromo	27659 bp (i3)	R
#20	16	PB	Sorl1	2	20660	9 A5	sortilin-related receptor, LDLR class A repeats-containing: signaling	211846 bp	F
#20	16	PB	Zfp458	0	238690	13 B3	zinc finger protein 458	37 kb	R

Insertional coordinates are given based on the NCBI database, June-December 2007; RTCGD membership is given based on the database's information accessible between June-December, 2007;

PB, total peripheral blood; BM, total bone marrow; TSS, transcriptional start site (NCBI definition); *, located in gene dense region: more than 3 genes within 50 kb from each RVIS side; n.a., not applicable

no s.h., no significant homlogy found.