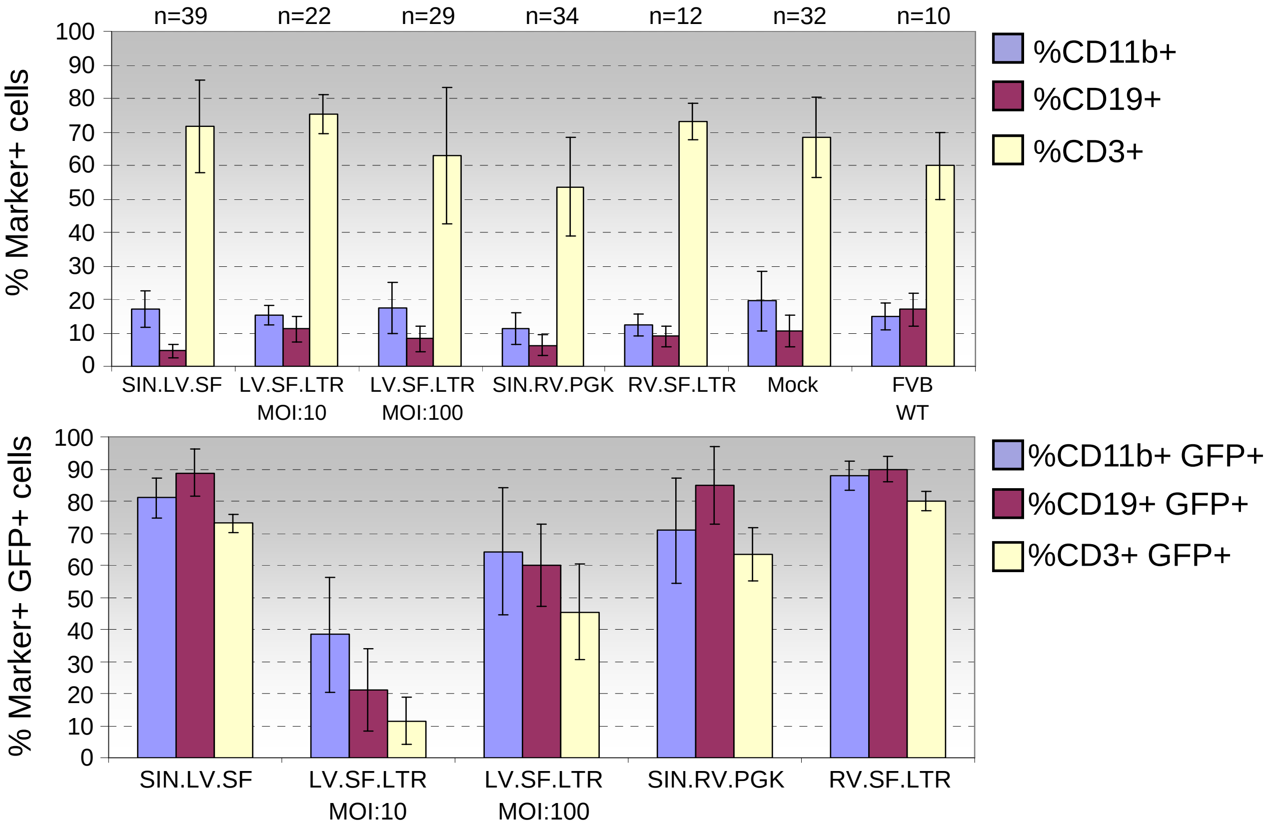
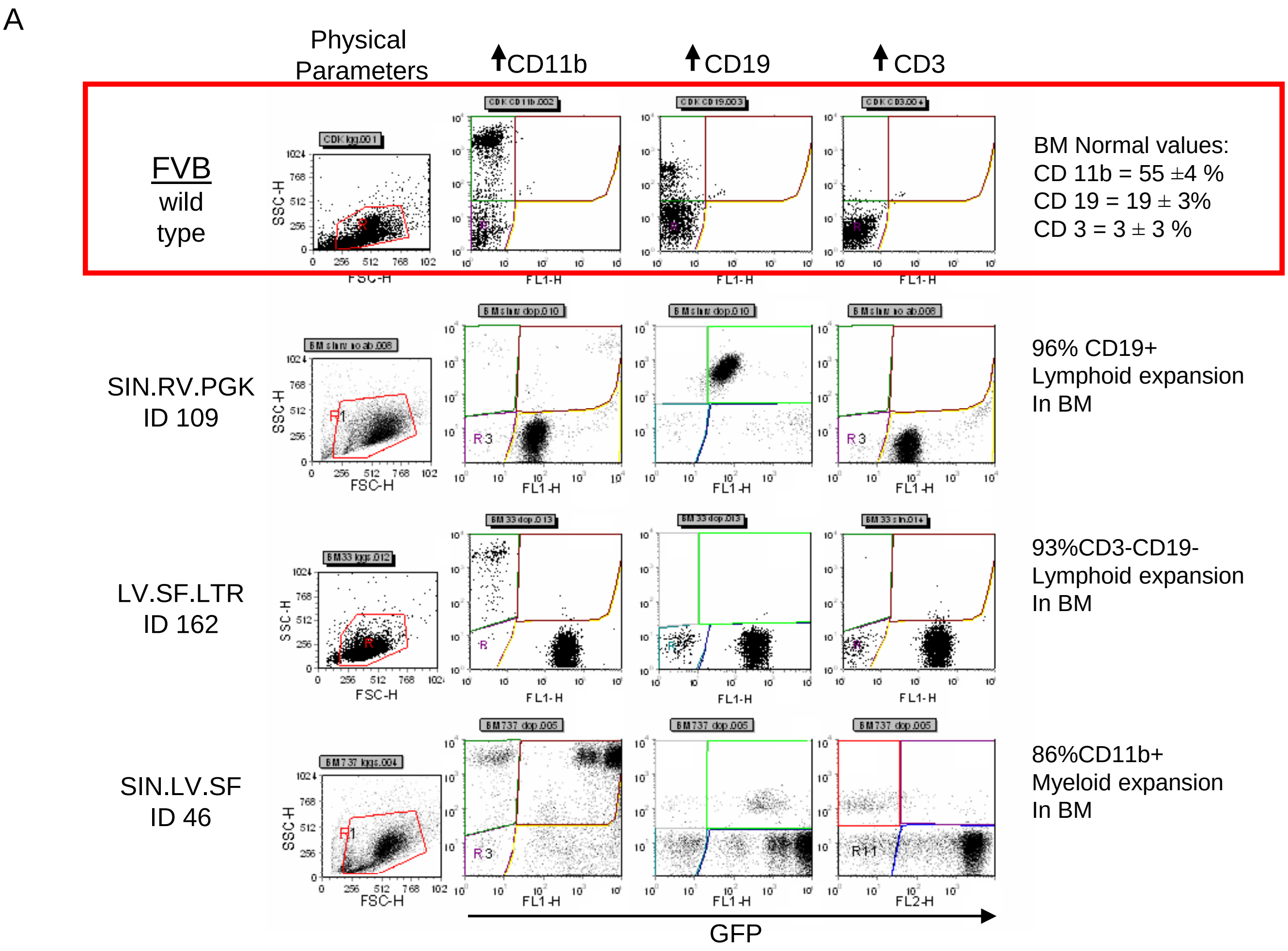
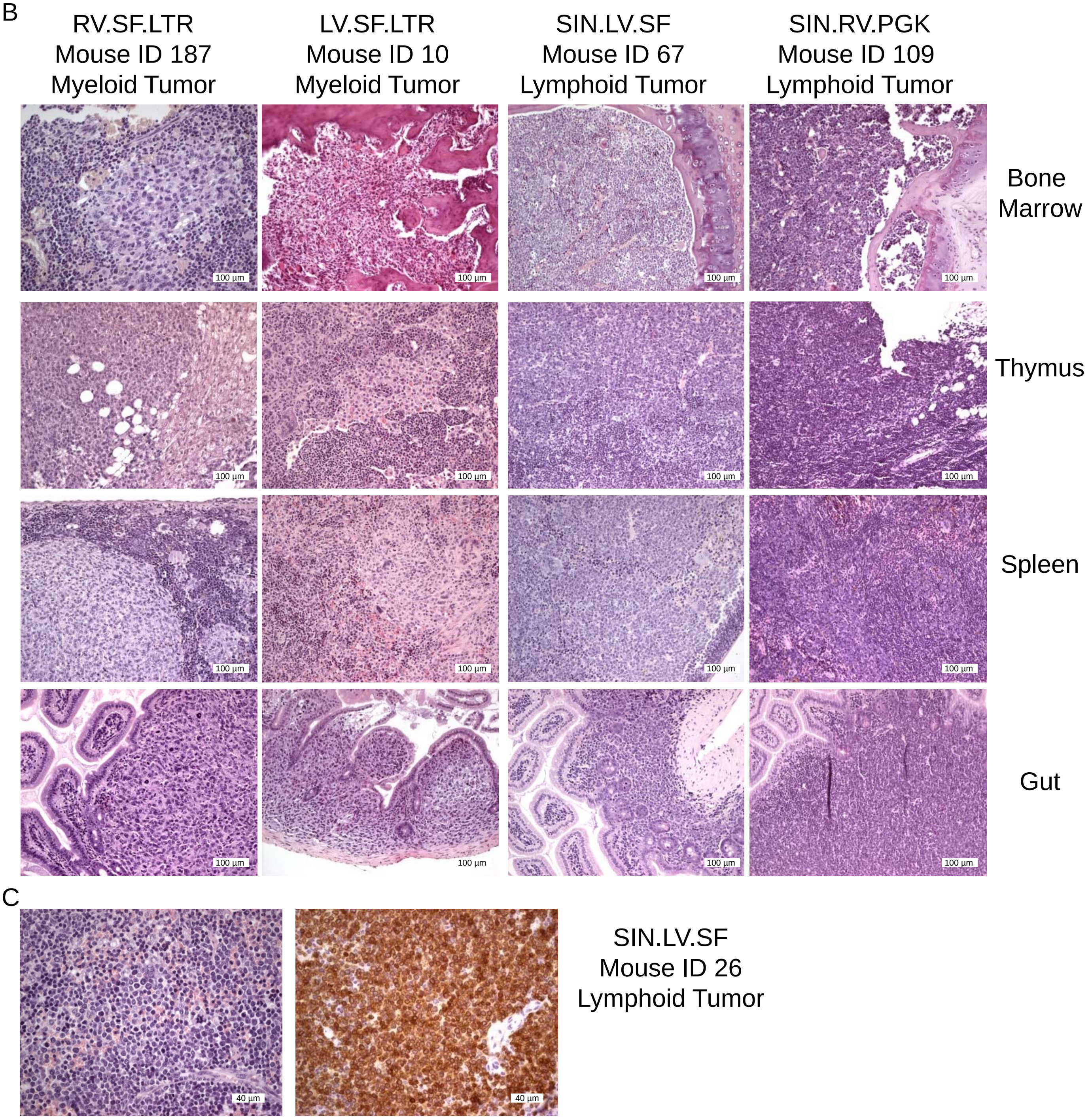


Supplementary figure 1. Blood analysis of mice 6-8 weeks after transplant. Percentage of total CD11b+, CD19+ and CD3+ cells (upper panel) and relative proportion of GFP+ cells in each blood lineage (lower panel) assessed by FACS analysis in the blood of mice of the different experimental groups, as indicated**.**
n= number of mice.


A
Physical Parameters
CD11b
CD19
CD3
FVB wild type
BM Normal values:
CD 11b = 55 ±4 %
CD 19 = 19 ± 3%
CD 3 = 3 ± 3 %
SIN.RV.PGK ID 109
96% CD19+
Lymphoid expansion
In BM
LV.SF.LTR ID 162
93%CD3-CD19-
Lymphoid expansion
In BM
SIN.LV.SF ID 46
86%CD11b+
Myeloid expansion
In BM
SSC-H
FSC-H
FL1-H
FL2-H
R1
R3
R11
GFP



Supplementary figure 2. Representative hematopoietic tumors developed in mice transplanted with transduced Cdkn2a-/- HSPCs

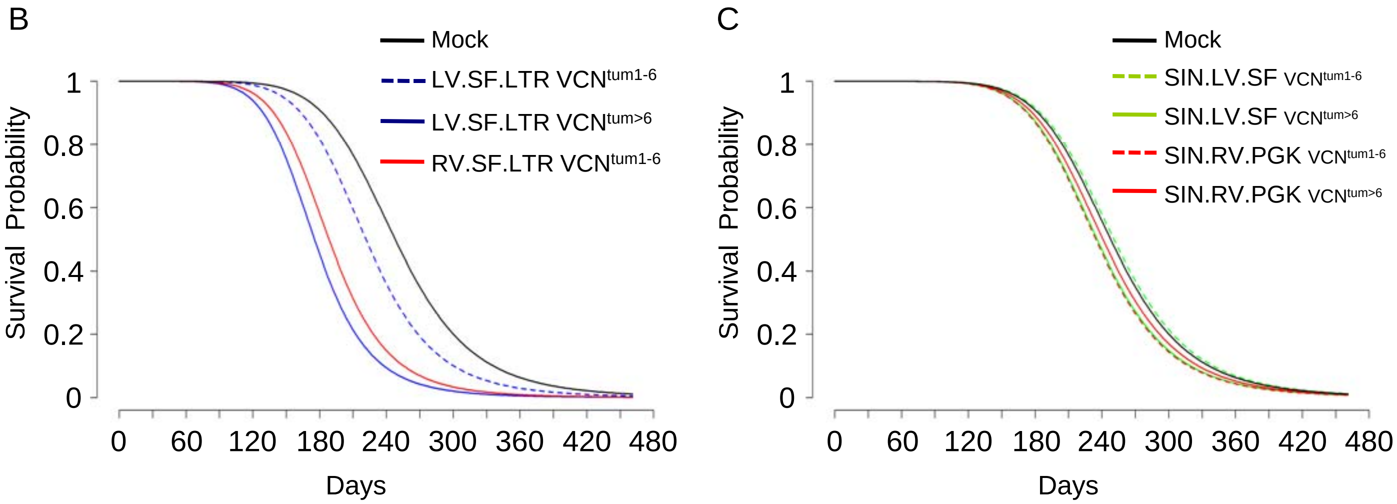
A) Representative FACS analysis of bone marrow cells from a FVB wild-type (WT) mouse (first row) and tumor infiltrated bone marrow cells from mice transplanted with vector transduced *Cdkn2a-/-* cells. In column order, from left to right: physical parameters (SSC vs. FSC), CD11b (myeloid cells), CD19 (B-cells) and CD3 (T-cells) marking (y-axis) versus GFP (x-axis). Vector used and mouse ID are indicated on the left. Average of normal percentages of each lineage are shown on the right. For each pathological sample, marker and percentage of the expanded cell population is indicated.

B) Representative examples of hematoxylin and eosin-stained sections (20x magnifications) of the indicated organ, infiltrated by lymphoid or myeloid cells, as reported.

C) Hematoxylin and eosin-stained section of a splenic lymphoid neoplasia (left panel). Immunohistochemical analysis on a serial section of same tissue reveals cytoplasmic localization of CD3 antigen (right panel). 40x magnifications.

A

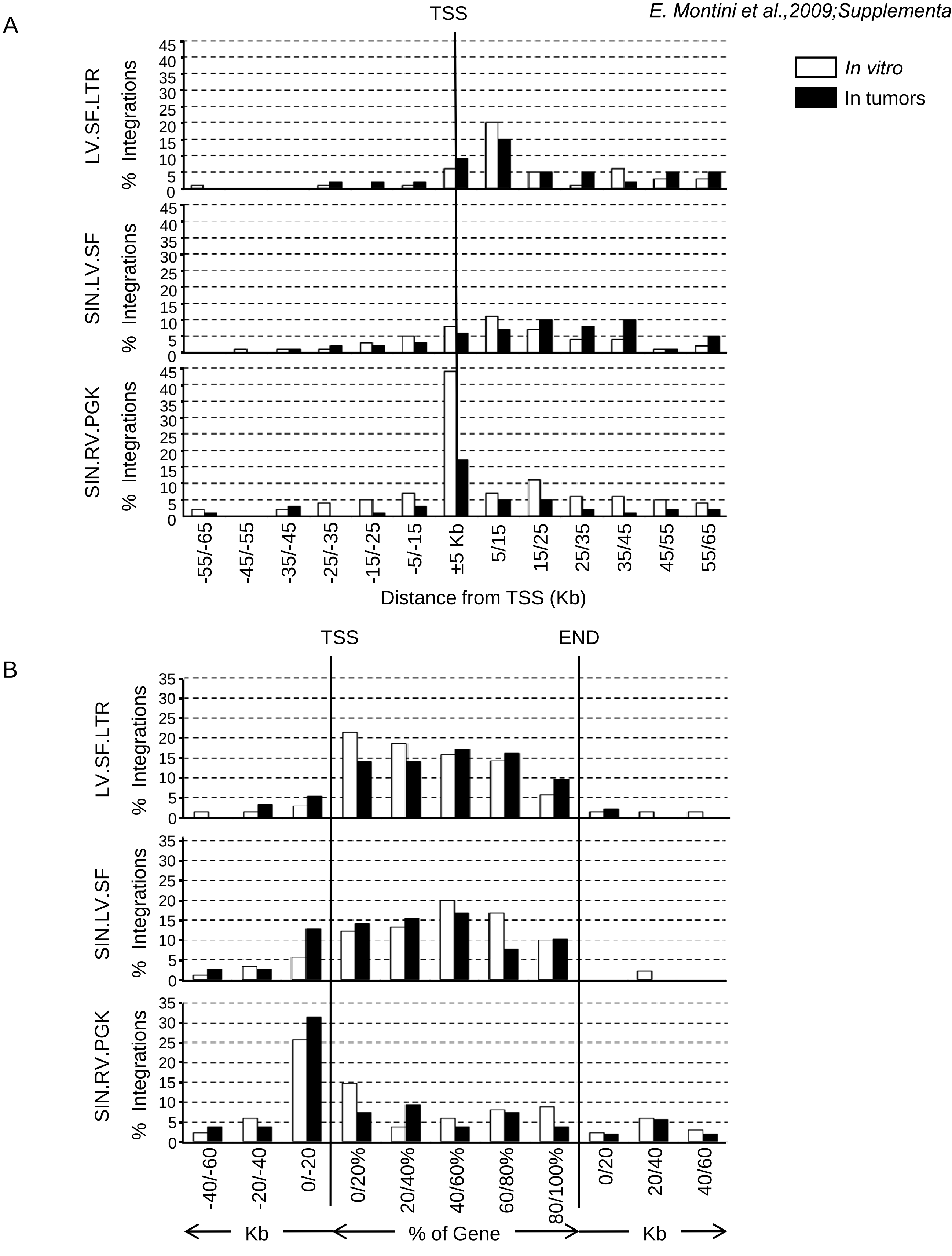
Vector	Stratification Group	n	Log logistic Parameter ±SE	z	p Vs mock
Mock	NA	32	NA	NA	NA
LV.SF.LTR	1 to 6	22	-0.112±0.067	-1.671	9.46 x10^{-2}
	>6	21	-0.346±0.066	-5.216	1.83 x10^{-7}
RV.SF.LTR	1 to 6	10	-0.274±0.083	-3.318	9.08 x10^{-4}
SIN.LV.SF	1 to 6	9	0.012±0.089	0.133	8.94 x10^{-1}
	>6	23	-0.050±0.069	-0.729	4.66 x10^{-1}
SIN.RV.PGK	1 to 6	6	-0.055±0.113	-0.491	6.23 x10^{-1}
	>6	20	-0.028±0.071	-0.397	6.92 x10^{-1}



D

Vector and VCN combined risk	Log logistic Parameter ±SE	z	p Vs Mock
LV.SF.LTR MOI:100+10	-0.019±0.005	-4.058	4.96x10^{-5}
RV.SF.LTR	-0.068±0.024	-2.868	4.13x10^{-3}
SIN.LV.SF	0.001±0.003	0.379	7.05x10^{-1}
SIN.RV.PGK	0.002±0.006	0.396	6.92x10^{-1}

Supplementary Figure 3. Log logistic accelerated failure time analysis of vector treatment groups stratified for VCN^{tum}. A) The log-logistic accelerated failure time model was used to evaluate the impact on the survival probability of all stratified ranging from 1 to 6 or VCN^{tum} > 6 vector groups**.** (Vector and Stratification Group columns). The number of mice of each stratification group are indicated in the n column. LV.SF.LTR-VCN$^{tum>6}$ and RV.SF.LTR-VCN^{tum1-6} show a negative impact on survival, as shown in the Log logistic Parameter values ± SE (Standard Error) and z (Z scores) columns, and are significantly different than the Mock group (column p vs Mock , $p<0.05$ are highlighted in red) **B,C**) Survival probability over time of the VCN^{tum} stratified groups for SF.LTR vectors (B) and SIN.LTR vectors (C) was estimated using the log logistic values of the accelerated failure time model shown in (A). **D)** Impact on survival of VCN^{tum} using the log logistic accelerated failure time model using VCN^{tum} and vector type as covariates. When LV.SF.LTR MOI:100 and MOI: 10 are pooled, the impact on the hazard of failure over time impact varies only slightly with respect to the impact of the LV.SF.LTR MOI:100 group alone (column p vs Mock; p values <0.05 shown in red), as shown by the negative value of the Log logistic Parameter (± SE, Standard Error) and z score (z).

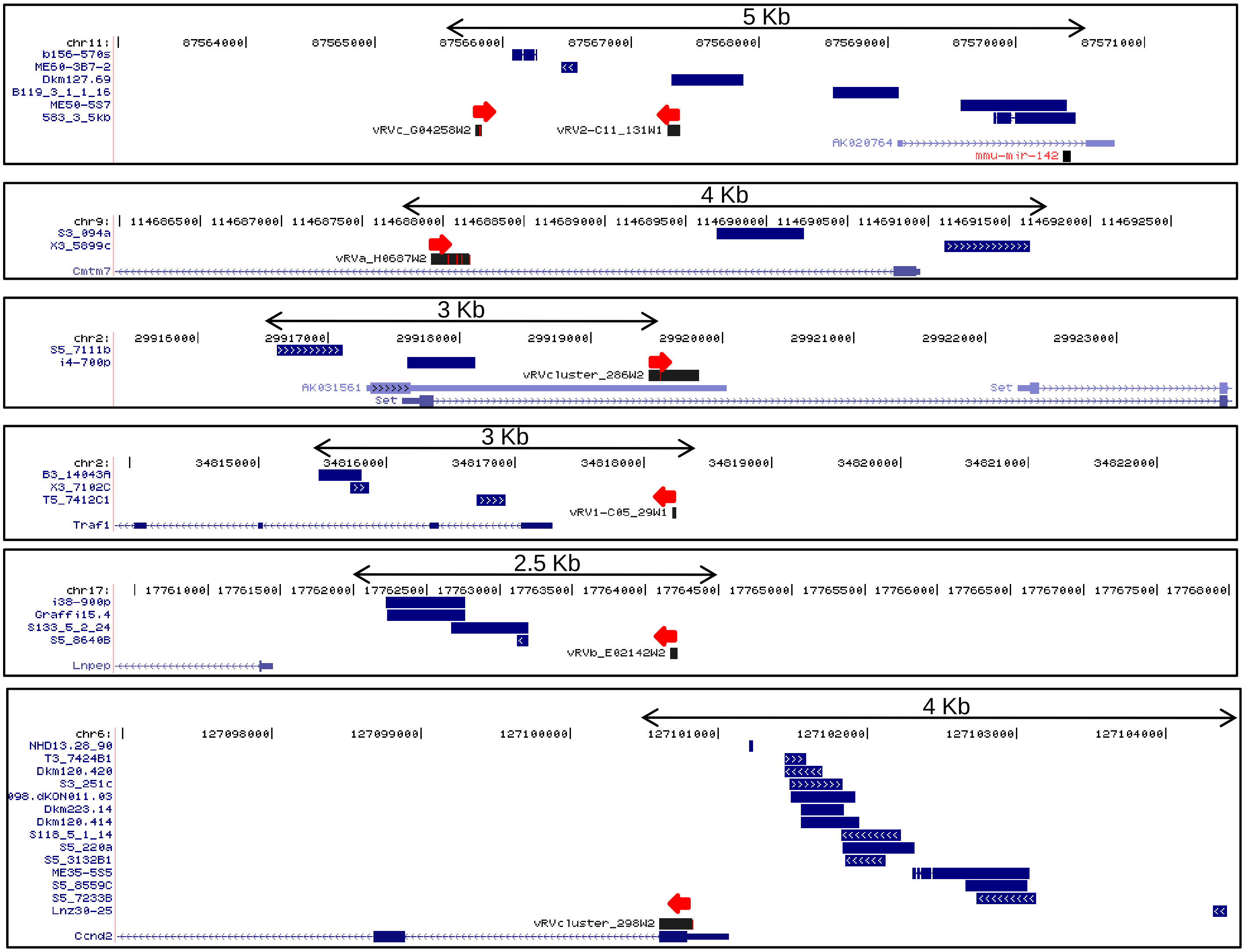


Supplementary figure 4. Vector integration site analysis in cells before transplant and in tumors. A) Integration frequency distribution around the TSS of LV.SF.LTR (upper panel), SIN.LV.SF (middle panel) and SIN.RV.PGK (lower panel) in *in vitro* (white bars) and in tumors (black bars). A 60-kb window centered on the TSS divided in 10-kb intervals is shown. **B)** Integration frequency distribution along the transcription unit (vector order as above). The length of each gene was normalized to 1 and divided in 5 intervals (each 20% of the gene size). Integrations upstream and downstream of genes are shown in 20-kb intervals.

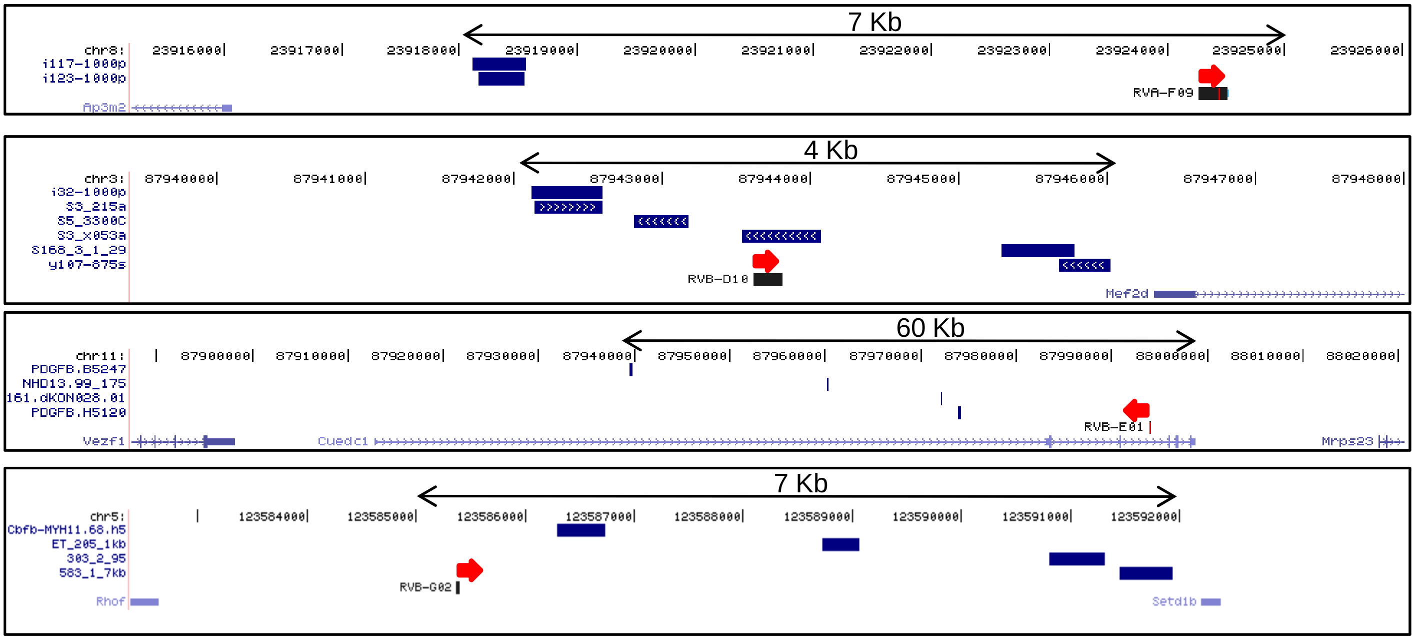
E. Montini et al.,2009;Supplementary Fig. 5

A

SIN.RV.PGK *in vitro*

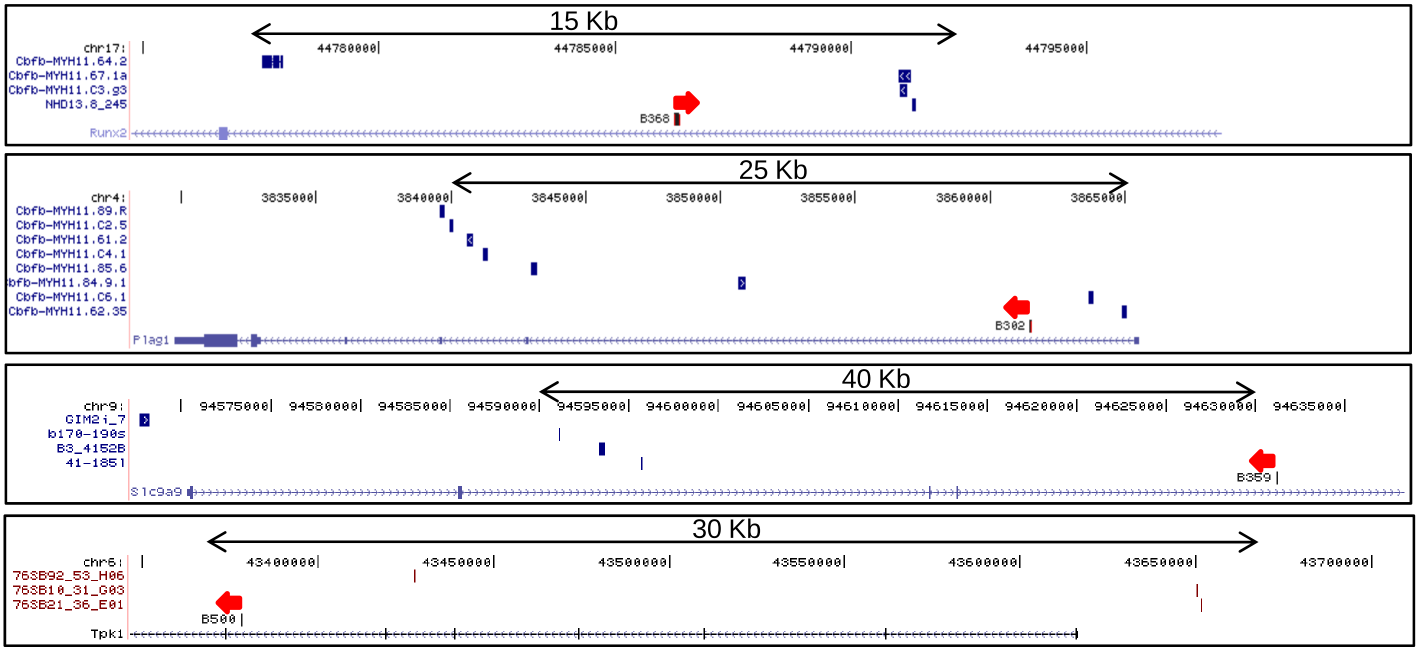


SIN.RV.PGK in tumors

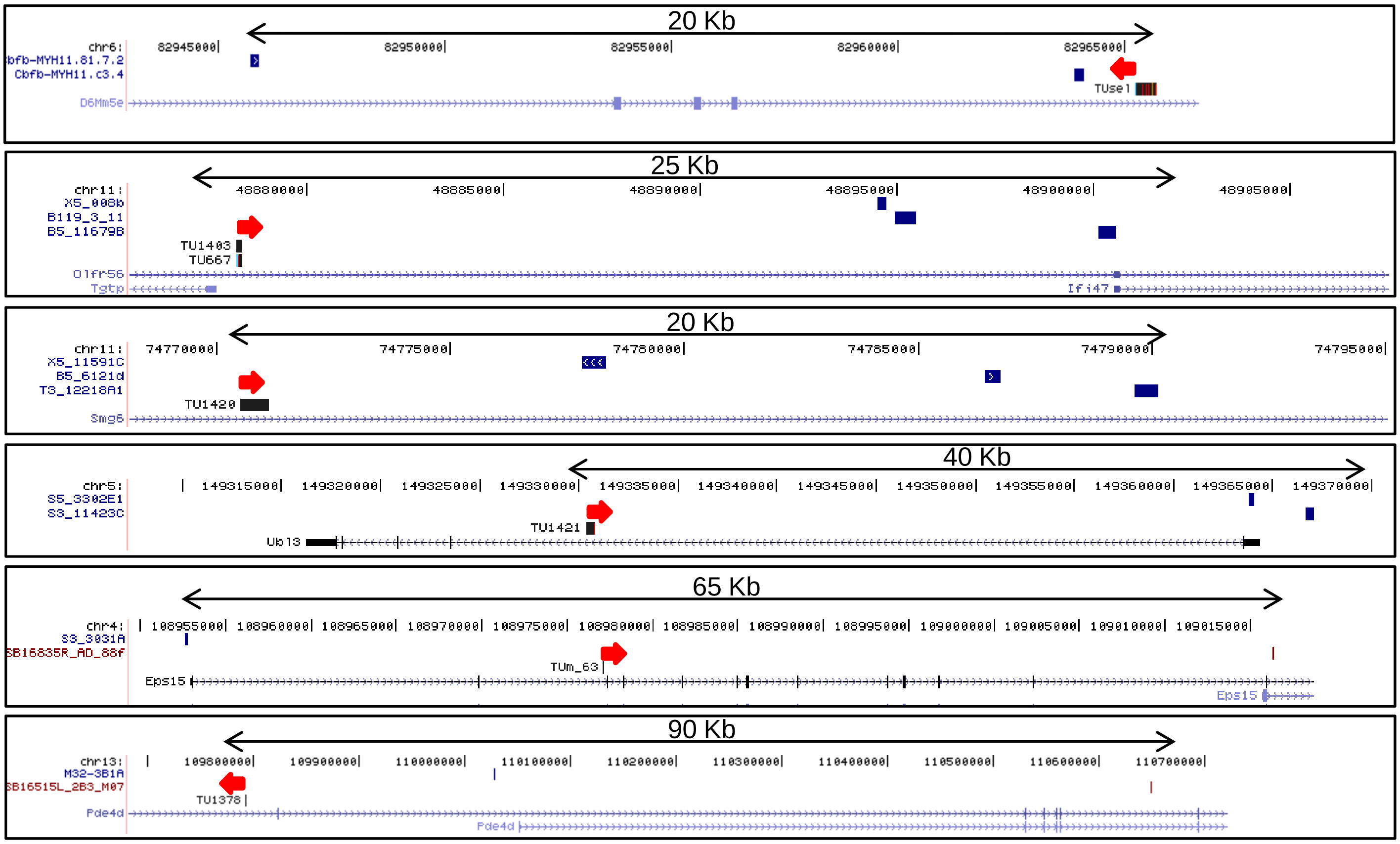


B

LV.SF.LTR *in vitro*



LV.SF.LTR in tumors



Supplementary Figure 5: Representative examples of SIN.RV.PGK and LV.SF.LTR integrations *in vitro* and in tumors at RTCGD CIS genes. UCSC BLAT output: chromosome number (Chr; top left): chromosomal coordinates (numbers on top); genes (bottom; vertical bars represent exons, the direction of transcription is indicated by the direction of the arrows on the genes) retroviral (blue) and Sleeping Beauty integrations (brown) are shown and identified on the left side, vector integrations are indicated by the red arrow (indicating the vector orientation). The minimum interval covering all integrations is shown (double headed arrow on top) **A)** SIN.RV.PGK integrations tend to map near RTCGD retroviral integrations, the interval containing SIN.RV.PGK and the RTCGD integrations is often <10 Kb; **B)** LV.SF.LTR integrations tend to target CIS genes. The interval of the integrations for this vector is often larger with respect to the SIN.RV.PGK intervals.

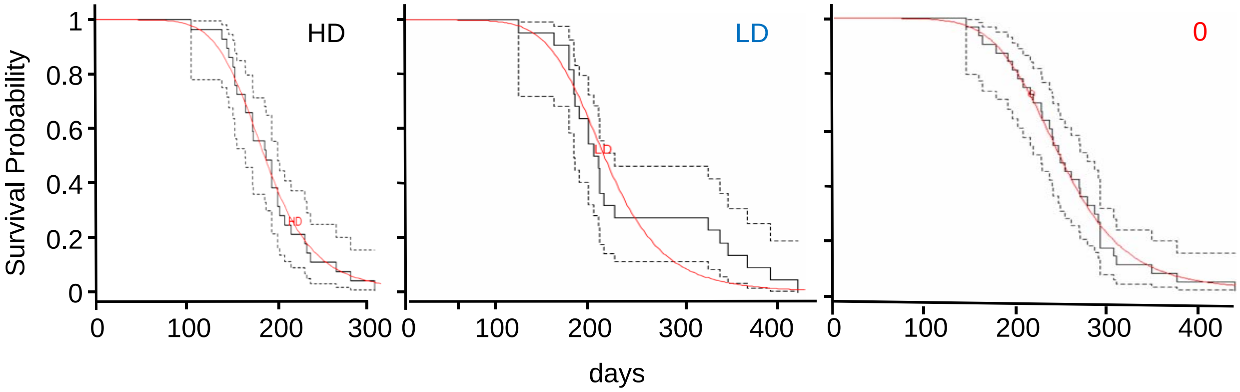
Supplementary Statistical Methods

A) Log Logistic Accelerated Failure Time Model

For survival analysis, a parametric approach was used because smooth continuous estimates of the survivor function were necessary for predictive purposes. The formula describing the log logistic distribution (Cox D.R and D Oakes, “Analysis of Survival Data”, 1998, Chapman and Hall) is:

$(\rho^k\ kt^{\ k-1})/[1+(t\rho)^k]$ in which t is the time; ρ is risk of failure and k the log logistic parameter that determines the effect of the treatment. For further reference see Bradburn et al.“Survival Analysis Part II: Multivariate data analysis - an introduction to concepts and methods”, British Journal of Cancer, 2003; 89: 431-436. Graphical examples of survival probability over time obtained by the log-logistic distribution (red lines) fitting the experimentally generated Kaplan Meier curves are shown below. Dashed lines represent the confidence intervals of each experimental curve.

HD: LV.SF.LTR MOI:100; LD: LV.SF.LTR MOI:10; 0: Mock.



B) VCN^{tum} acts linearly on the log logistic hazard
We addressed whether the impact of the VCN^{tum} covariate within the accelerated failure time model was linear, quadratic, cubic impact. We first tested significance of each form of impact (see below). We then performed a comparison between these models by means of likelihood ratios and testing the null hypothesis of no models difference.
To compare models of different degree in terms of the information provided by the associated likelihood, models must be considered as nested (adding each degree progressively). Introducing a higher degree of impact (from 1 to 3) leads to an enlargement of the parameters set to be estimated, which starts with 6 parameters (linear impact or Degree 1), up to 18 parameters (Degree 3). To evaluate statistically the information provided both from increase of likelihood and increase of parameters, we chose the Akaike information criteria (AIC). The linear impact (model 1) has the lowest AIC, thus is preferred. Results are displayed below.

MODEL 1 (VCN^{tum}) (linear)
Log logistic distribution
Loglik(model)= -1109.2 Loglik(intercept only)= -1127.2
Number of Newton-Raphson Iterations: 4
Chisq= **35.86** on 6 degrees of freedom,
p=2.9e-06

MODEL 2 (VCN^{tum}^2) (quadratic)
Log logistic distribution
Loglik(model)= -1104.6 Loglik(intercept only)= -1127.2
Number of Newton-Raphson Iterations: 4
Chisq= **45.23** on 12 degrees of freedom,
p=9.4e-06

MODEL3 (VCN^{tum}^3) (cubic)
Log logistic distribution
Loglik(model)= -1103.4 Loglik(intercept only)= -1127.2
Number of Newton-Raphson Iterations: 4
Chisq= **47.46** on 18 degrees of freedom,
p=1.8e-04

Akaike's Information Criterion (AIC) is -2*log-likelihood+2**k* where *k* is the number of estimated parameters.

MODEL 1
AIC1= -2*(-1109.12)+2*6=2230.24

MODEL 2
AIC2=-2*(-1104.6)+2*12=2233.2

MODEL 3
AIC3=-2*(-1103.4)+2*18=2242.8

Model 1 (linear) has the lowest AIC

Supplementary Table 1a

Vector (a)	MOI (b)	Mouse ID (c)	Status (d)	Cell Age Days (e)	Tumor VCN (f)	Tumor Type (g)	Bone Marrow (h)						Blood (i)				Spleen (l)					
							Pathol diag.	I.G.	CD11b	CD19	CD3	GFP	CD11b	CD19	CD3	GFP	Pathol diag.	I.G.	CD11b	CD19	CD3	GFP
LV.SF.LTR	100	4	1	105	8.1	LY	NT	0	79	81	10	7	34	49	34	32	NT	0	21	70	20	30
LV.SF.LTR	100	8	1	139	12.6	LY-MY	NT	0	85	5	12	2	48	23	7	26	MY	1	41	37	12	26
LV.SF.LTR	100	10	1	144	17.7	MY	MY	3	93	8	-	19	67	26	25	19	MY	2	82	30	15	14
LV.SF.LTR	100	13	1	146	11.7	LY	LY	3	8	96	1	94	5	95	0	95	LY	2	5	95	2	91
LV.SF.LTR	100	14	1	151	10.3	LY	LY	3	8	94	0	96	11	91	0	96	LY	3	6	96	1	95
LV.SF.LTR	100	16	1	153	10.9	LY	NT	0	77	11	10	6	3	0	27	88	LY	3	22	69	20	24
LV.SF.LTR	100	161	1	153	7.5	LY-MY	-	-	94.3	0.9	1.9	83.8	-	-	-	-	NT	0	-	-	-	-
LV.SF.LTR	100	153	1	155	8.1	LY-MY	-	-	80.5	1.2	3.4	60.9	84.4	31.2	8.8	53.1	LY	3	41.4	29.5	6.5	63.9
LV.SF.LTR	100	22	1	164	9.4	MY	-	-	82	7	4	9	-	-	-	-	NT	0	18	64	24	33
LV.SF.LTR	100	28	1	165	35.3	LY	LY	3	0	99	0	99	22	58	26	35	LY	3	2	95	2	90
LV.SF.LTR	100	163	1	172	5.3	LY-MY	MY	0-1	73.3	12.6	1.8	28.4	23.3	3.8	83.9	26.4	NT	0	14.8	72.1	14.8	25.5
LV.SF.LTR	100	164	1	172	11.2	MY	MY	2	87.8	5.9	4.6	86.8	73.2	9.5	9.7	82.8	MY	3	72.9	21.6	13.8	49.7
LV.SF.LTR	100	24	1	173	5.6	LY-MY	MY	3	64	24	14	35	42	29	2	37	LY	3	-	-	-	-
LV.SF.LTR	100	82	1	185	14.8	LY-MY	MY	3	69.2	28	2.6	46	1	0	22	1	LY	3	14	61	6	27
LV.SF.LTR	100	156	1	187	4.8	LY	NT	0	74.6	7.4	3.4	17.6	8.4	7.8	41.9	6.1	LY	2	9.4	14.9	21.2	8.7
LV.SF.LTR	100	32	1	193	11.4	LY-MY	MY	1	88	8	10	13	64	21	11	13	NT	0	59	30	17	21
LV.SF.LTR	100	154	1	193	7	LY-MY	NT	0	91	4.7	8	34.8	-	-	-	-	MY	3	29	40.7	30.4	39.6
LV.SF.LTR	100	155	1	193	13	LY-MY	MY	2	84.6	20.2	21.8	35.1	-	-	-	-	MY	3	66.6	61.6	18.4	34.6
LV.SF.LTR	100	159	1	200	7.3	LY-MY	LY	3	36.4	90.4	2.1	11.3	-	-	-	-	LY	2	11.5	83.7	7.5	9.7
LV.SF.LTR	100	160	1	200	10.2	LY-MY	NT	0	82.2	8.9	4.4	8.1	-	-	-	-	LY-MY	3	30.1	37.6	24.2	34.1
LV.SF.LTR	100	166	1	202	4.4	LY-MY	MY	2	63.9	66.7	2.2	18.2	46.5	48	10.5	22.5	LY	3	15.4	85.2	4.1	24.9
LV.SF.LTR	100	83	1	207	5	LY	LY	3	4	95	1	96	22	43	21	45	LY	2-3	4	92	5	83
LV.SF.LTR	100	81	1	214	12	LY-MY	MY	3	83	6	78	10	41	15	51	9	MY	3	33	47	10	40

Vector (a)	MOI (b)	Mouse ID (c)	Status (d)	Cell Age Days (e)	Tumor VCN (f)	Tumor Type (g)	Bone Marrow (h)						Blood (i)				Spleen (l)					
							Pathol diag.	I.G.	CD11b	CD19	CD3	GFP	CD11b	CD19	CD3	GFP	Pathol diag.	I.G.	CD11b	CD19	CD3	GFP
LV.SF.LTR	100	84	1	229	16.8	LY-MY	MY	1-2	92	4	4	7	81	8	6	13	MY	3	30	78	9	21
LV.SF.LTR	100	85	1	231	3.9	LY	LY	3	2	98	0	1	29	12	2	88	LY	2-3	3	93	3	9
LV.SF.LTR	100	158	1	235	9	LY	NT	0	75.5	14.8	4.3	54.5	-	-	-	-	NT	0	-	-	-	-
LV.SF.LTR	100	157	1	263	3.3	LY-MY	MY	1	96.5	1.2	1.1	2.4	79.2	45.6	8.6	21.9	NT	0	31.5	52.2	11	8.1
LV.SF.LTR	100	165	1	279	6.2	LY	LY	3	25.1	0.4	0.1	99.8	42.2	1.9	0.3	98.5	LY	2	10.7	3.2	0.6	96.9
LV.SF.LTR	100	162	1	305	5	LY	LY	3	9.3	0.7	0.2	99.4	23.9	15	2.6	85.4	LY	2	13.6	37.2	4.5	63.7
LV.SF.LTR	10	143	1	126	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LV.SF.LTR	10	148	1	165	0.9	LY-MY	LY	1	71.8	17	2.4	20.1	6.7	3.7	10.2	3.2	LY	2	13.3	49	19.7	5
LV.SF.LTR	10	6	1	181	1.2	LY	LY	1-2	9	90	7	89	18	65	15	69	NT	0	11	79	16	65
LV.SF.LTR	10	152	1	181	0.2	LY	LY	2	11.7	90.9	0.5	1.2	35.8	65.8	1.6	19.5	LY	1-2	6.3	94.1	2.1	1.9
LV.SF.LTR	10	145	1	187	0	LY	LY	3	7.4	97.9	1.2	0.4	-	-	-	-	LY	3	7.5	88.1	2.6	2.5
LV.SF.LTR	10	144	1	187	0.2	MY	MY	1	93.5	2.3	3.8	0.4	75.3	13.2	7.2	3.8	NT	0	40.8	59.8	17.5	2.6
LV.SF.LTR	10	7	1	188	1.3	LY-MY	MY	3	94	12	17	11	55	41	22	21	MY	3	49	37	39	18
LV.SF.LTR	10	147	1	193	0.1	LY-MY	LY	3	11.4	97.1	0.9	0.5	34.3	74.1	1	7.3	LY	3	2.5	96.7	1.3	1.4
LV.SF.LTR	10	150	1	202	1.2	LY	NT	0	68.8	19.5	4	20.3	8.4	2.8	55.3	16.4	NT	0	24.6	62.1	19	10.2
LV.SF.LTR	10	149	1	202	2.2	LY-MY	LY	2	20.1	78.8	0.8	86.8	35.8	53.5	7.5	63.1	LY	2	10.8	84.5	5	78.9
LV.SF.LTR	10	142	1	208	0	LY	LY	3	2.9	96.9	0.5	0.5	18.9	70.6	6.6	23.2	LY	3	3.2	93.3	1.5	1.9
LV.SF.LTR	10	18	1	214	1.2	MY	NT	0	97	1	3	36	87	7	6	52	MY	3	72	52	18	21
LV.SF.LTR	10	141	1	215	0.5	LY	LY	3	12.6	88	0.9	0.6	69.8	64.5	6.2	12.5	LY	3	61.4	93.7	2.4	1.8
LV.SF.LTR	10	151	1	215	1.6	LY-MY	NT	0	92.9	2.9	5	17.7	27.3	8.5	14.9	36.7	MY	3	35.6	46.6	11.6	22
LV.SF.LTR	10	21	1	220	1.4	MY	NT	0	81	7	4	12	59	20	22	24	MY	3	43	58	12	3
LV.SF.LTR	10	140	1	231	0.9	MY	MY	0-1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LV.SF.LTR	10	146	1	334	0	LY-MY	LY	3	8.5	98.6	0.5	0.2	18	73.3	0.5	3	LY	2	2.6	93.6	0.5	0.6
LV.SF.LTR	10	72	1	347	1.4	LY	-	-	2.2	97.2	0.4	0.4	-	-	-	-	-	-	-	-	-	-

Vector (a)	MOI (b)	Mouse ID (c)	Status (d)	Cell Age Days (e)	Tumor VCN (f)	Tumor Type (g)	Bone Marrow (h)						Blood (i)				Spleen (l)					
							Pathol diag.	I.G.	CD11b	CD19	CD3	GFP	CD11b	CD19	CD3	GFP	Pathol diag.	I.G.	CD11b	CD19	CD3	GFP
LV.SF.LTR	10	73	1	356	5.3	LY-MY	MY	1	16.8	71.7	2.2	68.3	-	-	-	-	MY	3	42.1	71	15.8	40
LV.SF.LTR	10	74	1	377	1.7	LY-MY	MY	3	85.4	9.1	8.6	34.8	75.6	12.3	8.7	57.7	MY	3	-	-	-	-
LV.SF.LTR	10	71	1	402	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LV.SF.LTR	10	70	1	432	2.6	LY-MY	NT	0	61.7	3.4	5.1	62.9	36.2	10	40.4	58.7	NT	0	21.4	34.6	24.6	36.2
Mock	-	2	1	146	-	LY-MY	MY	2	87.7	5.8	21	0	4	5	15	0	MY	2	56	32	20	0
Mock	-	27	1	160	0	LY	LY	3	4	92	0	0	14	83	3	0	LY	3	7	95	1	0
Mock	-	130	1	164	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mock	-	29	1	179	-	LY	LY	1-2	6	94	0	0	40	66	3	0	LY	1	10	88	4	0
Mock	-	31	1	192	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mock	-	170	1	197	-	LY	LY	3	16.8	83	0.5	0	22.3	78.2	1.7	0	LY	2	10	86.5	3.7	0
Mock	-	128	1	203	-	LY-MY	MY	3	-	-	-	-	-	-	-	-	LY	3	-	-	-	-
Mock	-	135	1	209	-	LY	LY	2	33.7	88.2	6.4	0	-	-	-	-	LY	3	-	-	-	-
Mock	-	126	1	216	-	LY	LY	3	-	-	-	-	-	-	-	-	LY	3	-	-	-	-
Mock	-	139	1	219	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mock	-	169	1	228	-	LY	LY	3	-	-	-	-	-	-	-	-	LY	3	-	-	-	-
Mock	-	124	1	229	-	LY-MY	NT	0	70	17	4	0	43	28	31	0	MY	3	23	62	20	0
Mock	-	131	1	237	-	MY	NT	0	90	3.2	5.5	0	-	-	-	-	-	-	-	-	-	-
Mock	-	129	1	240	-	LY-MY	MY	0-1	43.9	11.1	6.5	0	-	-	-	-	LY	2	-	-	-	-
Mock	-	168	1	241	-	LY	-	-	1.4	93	0.3	0	-	-	-	-	LY	2	-	-	-	-
Mock	-	125	1	247	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mock	-	167	1	249	-	LY	LY	3	3.1	94.7	1.1	0	-	-	-	-	LY	3	-	-	-	-
Mock	-	127	1	254	-	LY-MY	NT	0	40.3	47.6	2.3	0	-	-	-	-	MY	1	-	-	-	-
Mock	-	120	1	261	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mock	-	117	1	270	-	LY	LY	3	5	94	0	0	-	-	-	0	LY	3	3	90	3	0

Vector (a)	MOI (b)	Mouse ID (c)	Status (d)	Cell Age Days (e)	Tumor VCN (f)	Tumor Type (g)	Bone Marrow (h)						Blood (i)				Spleen (l)					
							Pathol diag.	I.G.	CD11b	CD19	CD3	GFP	CD11b	CD19	CD3	GFP	Pathol diag.	I.G.	CD11b	CD19	CD3	GFP
Mock	-	121	1	271	-	MY	-	-	94	1	3	0	52	30	21	0	MY	3	-	-	-	-
Mock	-	138	1	279	-	LY	LY	1	67.9	0.5	8.5	0	-	-	-	-	LY	3	-	-	-	-
Mock	-	137	1	287	-	LY	NT	0	43.2	24.8	12.1	0	-	-	-	-	NT	0	13.6	68.3	9.8	0
Mock	-	115	1	291	-	LY	LY	3	3	98	1	0	4	98	1	0	LY	3	-	-	-	-
Mock	-	136	1	293	-	LY	LY	3	11.1	90.5	10.9	0	-	-	-	-	LY	3	6	82.9	5.2	0
Mock	-	133	1	293	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mock	-	134	1	293	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mock	-	118	1	307	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mock	-	119	1	310	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mock	-	122	1	349	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mock	-	116	1	377	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mock	-	123	1	440	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
RV.SF.LTR	100	191	1	116	4	LY	LY	0-1	-	-	-	-	-	-	-	-	LY	2	-	-	-	-
RV.SF.LTR	100	192	1	158	4.3	LY	LY	3	2.3	97.1	0.4	99.5	34.5	45.8	11	92.2	LY	3	3.3	89	2.1	96.1
RV.SF.LTR	100	195	1	170	3.1	LY	LY	3	1.3	98.9	0.4	98.9	-	-	-	-	LY	3	1.9	95.1	1.6	89.3
RV.SF.LTR	100	188	1	185	1.5	LY	LY	2-3	1.3	93.1	0.3	96.6	-	-	-	-	LY	1	3.8	80.5	3	87
RV.SF.LTR	100	187	1	192	1.7	MY	MY	1	88.1	2	1.2	81.9	-	-	-	-	MY	3	34.1	40.7	5.6	80
RV.SF.LTR	100	190	1	192	5.6	MY	MY	2	90.2	0.4	0.1	99.3	79.3	3.7	0.8	97.7	MY	3	74.8	14.3	2.3	92.8
RV.SF.LTR	100	185	1	197	2.6	LY	LY	3	2.8	97.9	0.3	97.2	-	-	-	-	LY	2	7.5	94.4	1.3	91.8
RV.SF.LTR	100	189	1	205	4.2	LY-MY	LY	3	4.1	94.1	0.3	93.3	-	-	-	-	LY	3	5.5	92.9	0.7	95.2
RV.SF.LTR	100	194	1	221	1.5	LY	LY	3	15.9	98	0.3	0.7	-	-	-	-	LY	2	20.5	96.6	0.6	2.7
RV.SF.LTR	100	186	1	255	2.4	MY	MY	3	64.6	22.2	1.9	69.2	81.8	19	2.2	90.2	MY	3	39.5	52.8	2.7	79.5
RV.SF.LTR	100	184	1	354	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
RV.SF.LTR	100	193	1	354	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Vector (a)	MOI (b)	Mouse ID (c)	Status (d)	Cell Age Days (e)	Tumor VCN (f)	Tumor Type (g)	Bone Marrow (h)						Blood (i)				Spleen (l)					
							Pathol diag.	I.G.	CD11b	CD19	CD3	GFP	CD11b	CD19	CD3	GFP	Pathol diag.	I.G.	CD11b	CD19	CD3	GFP
SIN.LV.SF	100	68	1	133	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.LV.SF	100	1	1	146	11.9	LY	NT	0	67.6	13.8	6	50	8	0	2	11	LY	0-1	15	56	18	60
SIN.LV.SF	100	64	1	153	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.LV.SF	100	3	1	161	17.3	LY	LY	3	0	98	0	99	5	93	28	97	LY	1	2	90	0	94
SIN.LV.SF	100	55	1	162	10.5	LY	LY	3	4	96	0	99	19	80	0	97	LY	1-2	4	91	1	96
SIN.LV.SF	100	60	1	162	11.1	LY	NT	0	79	11	1	71	3	3	1	39	LY	3	11	25	2	30
SIN.LV.SF	100	23	1	171	9.3	LY	LY	3	11	89	0	91	6	95	0	94	LY	0-1	6	87	2	87
SIN.LV.SF	100	26	1	174	4.4	LY	LY	3	5	0	0	94	16	7	8	65	LY	3	4	14	2	87
SIN.LV.SF	100	52	1	184	-	MY	MY	1	-	-	-	-	-	-	-	-	MY	3	-	-	-	-
SIN.LV.SF	100	61	1	192	12	LY	LY	0-1	74	13	6	68	3	1	54	99	LY	1	11	69	23	76
SIN.LV.SF	100	63	1	192	12.5	LY-MY	MY	1	90	1	7	67	37	21	45	84	LY	1	27	34	36	68
SIN.LV.SF	100	66	1	194	10.4	LY	LY	2-3	3	2	15	94	10	19	15	83	LY	3	0	10	30	91
SIN.LV.SF	100	59	1	212	4.4	LY	-	-	-	-	-	-	-	-	-	-	LY	3	-	-	-	-
SIN.LV.SF	100	17	1	214	5	LY-MY	MY	3	61	45	4	81	56	6	33	78	MY	3	63	34	31	64
SIN.LV.SF	100	69	1	217	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.LV.SF	100	25	1	230	1.5	LY	LY	3	1	98	0	99	16	46	7	65	LY	3	1	93	2	95
SIN.LV.SF	100	40	1	230	17.1	ND	NT	0	-	-	-	-	-	-	-	-	NT	0	-	-	-	-
SIN.LV.SF	100	67	1	231	18.2	LY	LY	3	0.3	99.6	0.4	99.6	26.9	64.8	9.4	85.2	LY	3	0.4	98.3	0.8	98.2
SIN.LV.SF	100	53	1	234	22.6	LY	LY	3	-	-	-	-	-	-	-	-	LY	3	-	-	-	-
SIN.LV.SF	100	41	1	238	36.1	LY	LY	3	3	96	1	98	35	61	2	72	LY	2	2	94	3	93
SIN.LV.SF	100	43	1	238	8	LY	LY	2	62	9	9	31	5	3	22	94	LY	3	14	36	18	45
SIN.LV.SF	100	56	1	248	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.LV.SF	100	47	1	254	9.4	LY	LY	3	1	92.3	0.7	97.5	-	-	-	-	LY	3	1	85.2	1.6	92.2
SIN.LV.SF	100	57	1	254	5.5	LY	LY	3	4.5	5.6	53.5	7.4	-	-	-	-	LY	3	6.7	12.8	37.7	15.1

Vector (a)	MOI (b)	Mouse ID (c)	Status (d)	Cell Age Days (e)	Tumor VCN (f)	Tumor Type (g)	Bone Marrow (h)						Blood (i)				Spleen (l)					
							Pathol diag.	I.G.	CD11b	CD19	CD3	GFP	CD11b	CD19	CD3	GFP	Pathol diag.	I.G.	CD11b	CD19	CD3	GFP
SIN.LV.SF	100	44	1	256	8.3	LY	-	-	-	-	-	-	-	-	-	-	LY	2	-	-	-	-
SIN.LV.SF	100	54	1	262	11.3	LY-MY	MY	3	17	75.7	3.1	90.1	43.7	39.6	11.8	93.4	MY	3	17.1	72.5	13.9	89.2
SIN.LV.SF	100	48	1	268	7.1	LY	LY	3	1.3	97.7	0.8	99.2	30.2	46.1	21.9	92.1	LY	3	1.3	97.5	1.2	99.2
SIN.LV.SF	100	33	1	270	27.8	LY	LY	3	2	97	0	98	-	-	-	-	LY	2	2	97	1	96
SIN.LV.SF	100	58	1	277	3.8	LY	NT	0	72.1	16.2	4.5	67.8	50.7	6.6	7.8	97	LY	0-1	11.5	73.6	17.4	87.4
SIN.LV.SF	100	62	1	280	5.2	LY	LY	3	-	-	-	-	-	-	-	-	LY	3	-	-	-	-
SIN.LV.SF	100	51	1	309	5.7	LY	NT	0	48.7	36.9	8.3	87	24.5	25	47.5	78.5	LY	2	8.4	66.1	19.5	80.7
SIN.LV.SF	100	65	1	319	15.7	LY-MY	NT	0	74.1	11.9	4.3	51.9	-	-	-	-	LY	2	34.2	64.4	38.5	25.1
SIN.LV.SF	100	49	1	343	3	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.LV.SF	100	50	1	343	14.7	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.LV.SF	100	39	1	383	13.8	LY-MY	NT	0	92.8	1.5	2	2.3	-	-	-	-	LY	1	-	-	-	-
SIN.LV.SF	100	46	1	385	9.3	MY	NT	0	85.5	5.3	5.6	90.5	68.1	22.9	7.4	94.6	NT	0	-	-	-	-
SIN.LV.SF	100	42	1	461	11.7	MY	MY	1	88.3	2.1	2.2	2.6	-	-	-	-	NT	0	41.6	29	16.8	7
SIN.LV.SF	100	45	1	467	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.LV.SF	100	38	1	486	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.RV.PGK	100	11	1	130	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.RV.PGK	100	12	1	130	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.RV.PGK	100	19	1	144	8	LY	NT	0	76	10	5	78	34	40	3	89	NT	0	9	71	13	83
SIN.RV.PGK	100	107	1	160	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.RV.PGK	100	111	1	160	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.RV.PGK	100	30	1	172	6.4	LY	NT	0	71	14	2	12	4	0	5	0	NT	0	16	46	7	35
SIN.RV.PGK	100	100	1	175	12.6	LY	LY	3	6	0	4	98	28	12	10	93	LY	02-mar	4	14	3	98
SIN.RV.PGK	100	97	1	184	-	LY	LY	3	-	-	-	-	-	-	-	-	LY	2	-	-	-	-
SIN.RV.PGK	100	99	1	184	2.7	LY	LY	3	-	-	-	-	-	-	-	-	LY	3	-	-	-	-

Vector (a)	MOI (b)	Mouse ID (c)	Status (d)	Cell Age Days (e)	Tumor VCN (f)	Tumor Type (g)	Bone Marrow (h)						Blood (i)				Spleen (l)					
							Pathol diag.	I.G.	CD11b	CD19	CD3	GFP	CD11b	CD19	CD3	GFP	Pathol diag.	I.G.	CD11b	CD19	CD3	GFP
SIN.RV.PGK	100	9	1	188	3.7	LY	LY	3	31	98	2	3	43	66	4	52	LY	2	52	97	1	10
SIN.RV.PGK	100	102	1	192	7.2	LY	NT	0	47	41	4	86	-	-	-	-	LY	2	11	70	20	83
SIN.RV.PGK	100	88	1	194	6.9	LY	LY	3	1	100	0	96	-	-	-	-	LY	3	1	98	0	98
SIN.RV.PGK	100	105	1	199	9.4	LY	LY	3	1	99	0	99	37	64	3	84	LY	2	3	96	2	95
SIN.RV.PGK	100	92	1	200	9.7	LY	NT	0	74	13	3	5	33	38	4	12	NT	0	11	68	11	27
SIN.RV.PGK	100	96	1	207	3.8	LY	LY	3	2	97	0	98	18	64	21	60	LY	2	4	92	6	87
SIN.RV.PGK	100	114	1	214	17.1	LY	LY	3	7.6	79.8	0.4	96.6	-	-	-	-	LY	3	11.2	69.2	3.2	91.9
SIN.RV.PGK	100	91	1	221	6.3	LY	LY	3	12	90	3	4	9	90	4	26	LY	0-1	5	83	5	26
SIN.RV.PGK	100	101	1	234	13.9	LY-MY	NT	0	-	-	-	-	-	-	-	-	LY	2	-	-	-	-
SIN.RV.PGK	100	94	1	242	7.9	LY	LY	3	-	-	-	-	-	-	-	-	LY	3	-	-	-	-
SIN.RV.PGK	100	103	1	244	3.5	LY	LY	3	1.7	97.9	0.5	98.9	25.3	45.3	21.3	84.3	LY	2	4.2	87.9	7.2	92
SIN.RV.PGK	100	112	1	256	15.1	LY	NT	0	62.6	22.9	5	57.8	4.9	2.8	1.6	46.3	NT	0	9.4	61.3	23.2	62.2
SIN.RV.PGK	100	104	1	272	10.6	LY-MY	NT	0	69.8	27.8	6.4	69.2	47.6	44.5	17.6	91	MY	2	18.5	71.9	22.1	87
SIN.RV.PGK	100	109	1	299	8.9	LY	LY	3	1.4	97.3	1	99.1	29.9	58.7	12.7	84.2	LY	2	6.9	77.3	11	84.8
SIN.RV.PGK	100	89	1	300	13.3	LY	NT	0	60.9	20.3	9.3	41.4	15.6	32.3	34.6	84.7	LY	3	11.3	74.1	17.7	82.6
SIN.RV.PGK	100	93	1	314	6.8	LY	LY	3	-	-	-	-	-	-	-	-	LY	1	-	-	-	-
SIN.RV.PGK	100	110	1	319	7.7	MY	-	-	83.3	5.5	2.1	62.3	-	-	-	-	MY	2	47.7	50.3	11.6	62.8
SIN.RV.PGK	100	87	1	320	4.9	LY	-	-	2	97	0	100	25	70	0	96	LY	3	2	97	0	100
SIN.RV.PGK	100	98	1	322	8.5	LY	LY	3	11	93.7	0.6	96.8	60.3	80.6	6.8	87.4	LY	3	4.6	93.7	1.3	97.5
SIN.RV.PGK	100	108	1	326	7.7	LY	LY	1	62.6	19.9	7.1	58.6	-	-	-	-	LY	2	-	-	-	-
SIN.RV.PGK	100	113	1	326	3.8	LY	NT	0	57.1	14.9	18.7	12.3	-	-	-	-	LY	1	-	-	-	-
SIN.RV.PGK	100	90	1	347	6.4	LY-MY	MY	2	54.9	25.8	15.4	79.9	-	-	-	-	MY	3	26.5	43.4	32.4	82.8
SIN.RV.PGK	100	95	1	396	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.RV.PGK	100	106	1	412	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Vector (a)	MOI (b)	Mouse ID (c)	Status (d)	Cell Age Days (e)	Tumor VCN (f)	Tumor Type (g)	Bone Marrow (h)						Blood (i)				Spleen (l)					
							Pathol diag.	I.G.	CD11b	CD19	CD3	GFP	CD11b	CD19	CD3	GFP	Pathol diag.	I.G.	CD11b	CD19	CD3	GFP
SIN.RV.PGK	100	86	1	425	-	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Supplementary Table 1a: Tumor phenotype analysis by FACS and histopathology on bone marrow, blood and spleen of all transplanted mice for each treatment group.

In columns are indicated: (a): Vector Treatment on cells which defines the experimental group (SIN.LV.SF, LV.SF.LTR, SIN.RV.PGK, RV.SF.LTR, Mock); (b) MOI: Vector dose (Multiplicity Of Infection, MOI); (c): Mouse Identifier; (d): Status of the mice: 1:dead; 0:alive; (e): Cell age: age in days of the transplanted cells at the time of mouse death; (f): vector copy number in tumors; (g): Tumor Type: Tumor type was defined by merging histopathology and FACS data from all collected tissues: LY, Lymphoid Tumor (highlighted in yellow); MY, Myeloid Tumor (highlighted in red); LY-MY, Double tumors with coexisting lymphoid and myeloid expansions (highlighted in orange); ND, Not determined (highlighted in grey); (h), (i), (l) Histopathological and FACS analysis of bone marrow, blood, spleen. For each tissue hematoxylin and eosin-stained sections were analyzed by a team of pathologists that diagnosed (Pathol diag. columns) if myeloid (MY, highlighted in red), lymphoid (LY, highlighted in yellow) or double tumors with lymphoid and myeloid expansions were present, (LY-MY, highlighted in orange), NT (no tumor, highlighted in green) indicates absence of malignant infiltration in that section; in addition a semiquantitative scoring system (I.G; infiltration grade) was applied to each section (from 0 to 3, from none to the highest level of infiltration). The relative percentages of myeloid (CD11b), B (CD19) T (CD3) and GFP+ cells in BM, blood and spleen was also included. Normal range of myeloid cells in tumor free age-matched mice was 55±4% in BM, 15±6% in blood and 10±6% in spleen. Mice with >80% CD11b+ cells in BM, >40% in blood or >30% in spleen were considered bearing a pathological expansion (highlighted in red). Normal levels of B cells (CD19+) were: 19±3% in BM, 15±4% in blood and 57±10% in spleen. Mice with >35% of CD19+ cells in BM, >30% of CD19+ cells in blood or >70% of CD19+ cells in spleen were diagnosed as lymphoid B-cell tumors (LY, highlighted in yellow). Normal levels of T cells (CD3+) in tumor free controls were 3±3% in BM, 53±10% in blood and 40 ±8% in spleen. Mice with >8% of CD3+ cells in BM, >80% in blood or >70% in spleen were diagnosed as lymphoid T-cell tumors (LY, highlighted in yellow).

Supplementary Table 1b

Vector (a)	MOI (b)	Mouse ID (c)	Cell Age Days (e)	Tumor Type (g)	Thymus (m)						Lymphonode (n)		Liver (o)		Kidney (p)		Lung (q)		Gut (r)		Brain (s)		Heart (t)	
					Pathol diag.	I.G	CD11b	CD19	CD3	GFP	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.
LV.SF.LTR	10	143	126	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LV.SF.LTR	10	148	165	LY-MY	LY	3	10	3.8	36.7	1.7	LY	1	LY	1	LY	3	LY	3	MY	2	NT	0	LY	1
LV.SF.LTR	10	6	181	LY	NT	0	-	-	-	-	LY	3	LY	2	LY	1	LY	0-1	LY	0-1	-	-	-	-
LV.SF.LTR	10	152	181	LY	LY	3	3.3	98.9	0.9	0.1	LY	3	LY	2	NT	0	LY	1-2	NT	0	NT	0	NT	0
LV.SF.LTR	10	145	187	LY	LY	3	-	-	-	-	LY	3	LY	2	NT	0	LY	2	NT	0	LY	1	NT	0
LV.SF.LTR	10	144	187	MY	MY	3	-	-	-	-	MY	3	MY	3	NT	0	MY	1	MY	1	NT	0	NT	0
LV.SF.LTR	10	7	188	LY-MY	MY	3	-	-	-	-	MY	3	MY	2	MY	3	MY	3	NT	0	-	-	-	-
LV.SF.LTR	10	147	193	LY-MY	LY	3	-	-	-	-	MY	3	LY	2	LY	1	NT	0	MY	1	NT	0	NT	0
LV.SF.LTR	10	150	202	LY	LY	1	19	0.4	67.9	0.2	NT	0	NT	0	LY	1	LY	3	NT	0	NT	0	NT	0
LV.SF.LTR	10	149	202	LY-MY	LY	3	0.9	97.9	0.8	97.7	LY	3	MY	2	LY	1	LY	1	NT	0	NT	0	NT	0
LV.SF.LTR	10	142	208	LY	LY	1	1.7	86	11.8	0.7	LY	3	LY	3	NT	0	NT	0	NT	0	NT	0	NT	0
LV.SF.LTR	10	18	214	MY	MY	2	-	-	-	-	MY	3	MY	3	MY	3	MY	3	MY	3	-	-	-	-
LV.SF.LTR	10	141	215	LY	LY	3	-	-	-	-	LY	1	LY	2	NT	0	NT	0	NT	0	NT	0	NT	0
LV.SF.LTR	10	151	215	LY-MY	LY	3	14.5	0.5	14	0.4	-	-	MY	2	Ly-My	2	LY	2-3	NT	0	NT	0	NT	0
LV.SF.LTR	10	21	220	MY	MY	3	-	-	-	-	MY	3	MY	1	MY	1	MY	1	MY	3	-	-	-	-
LV.SF.LTR	10	140	231	MY	MY	3	-	-	-	-	MY	3	NT	0	NT	0	MY	3	MY	3	NT	0	MY	2
LV.SF.LTR	10	146	334	LY-MY	LY	3	22.6	90.6	3.5	0.3	LY	3	LY	3	LY	1	NT	0	MY	2	NT	0	NT	0
LV.SF.LTR	10	72	347	LY	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LV.SF.LTR	10	73	356	LY-MY	MY	2	42.8	23.8	70.2	9	MY	3	MY	1	MY	2	MY	2	NT	0	NT	0	NT	0
LV.SF.LTR	10	74	377	LY-MY	MY	3	-	-	-	-	-	-	MY	3	NT	0	MY	2	NT	0	NT	0	NT	0
LV.SF.LTR	10	71	402	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
LV.SF.LTR	10	70	432	LY-MY	MY	2	-	-	-	-	LY	3	MY	2-3	MY	1	MY	1	NT	0	NT	0	NT	0
LV.SF.LTR	100	4	105	LY	NT	0	-	-	-	-	-	-	NT	0	NT	0	NT	0	NT	0	-	-	-	-

Vector (a)	MOI (b)	Mouse ID (c)	Cell Age Days (e)	Tumor Type (g)	Thymus (m)						Lymphonode (n)		Liver (o)		Kidney (p)		Lung (q)		Gut (r)		Brain (s)		Heart (t)	
					Pathol diag.	I.G	CD11b	CD19	CD3	GFP	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.
LV.SF.LTR	100	8	139	LY-MY	NT	0	-	-	-	-	-	-	MY	1	NT	0	-	-	MY	3	-	-	-	-
LV.SF.LTR	100	10	144	MY	MY	3	-	-	-	-	-	-	MY	2	MY	2	MY	3	MY	3	-	-	-	-
LV.SF.LTR	100	13	146	LY	LY	2	-	-	-	-	LY	3	LY	2	LY	1	LY	1-2	LY	1	-	-	-	-
LV.SF.LTR	100	14	151	LY	LY	3	-	-	-	-	LY	3	LY	3	LY	1-2	LY	2	LY	1-2	-	-	-	-
LV.SF.LTR	100	16	153	LY	LY	3	1	0	22	95	-	-	NT	0	LY	2	LY	3	NT	0	-	-	-	-
LV.SF.LTR	100	161	153	LY-MY	LY	3	-	-	-	-	Ly-My	1	NT	0	NT	0	NT	0	NT	0	NT	0	NT	0
LV.SF.LTR	100	153	155	LY-MY	MY	2	-	-	-	-	MY	3	MY	3	MY	1	NT	0	MY	2	NT	0	NT	0
LV.SF.LTR	100	22	164	MY	NT	0	-	-	-	-	-	-	NT	0	NT	0	NT	0	NT	0	-	-	-	-
LV.SF.LTR	100	28	165	LY	LY	2	-	-	-	-	LY	3	LY	2	NT	0	NT	0	NT	0	-	-	-	-
LV.SF.LTR	100	163	172	LY-MY	LY	3	44.3	0.4	95.6	0.2	MY	2	MY	1	NT	0	LY	2-3	MY	2	NT	0	NT	0
LV.SF.LTR	100	164	172	MY	MY	3	-	-	-	-	MY	3	MY	3	MY	1-2	MY	1	MY	2	NT	0	NT	0
LV.SF.LTR	100	24	173	LY-MY	Ly-My	3	-	-	-	-	LY	2	LY	3	LY	2	MY	2	MY	2	-	-	-	-
LV.SF.LTR	100	82	185	LY-MY	LY	3	1	0	25	0	-	-	MY	2	MY	1	MY	2	NT	0	-	-	-	-
LV.SF.LTR	100	156	187	LY	LY	3	15.7	3.9	15.9	1.3	LY	3	LY	1	LY	3	LY	3	NT	0	NT	0	LY	1
LV.SF.LTR	100	32	193	LY-MY	MY	1	-	-	-	-	-	-	MY	1-2	MY	1	MY	3	MY	2	-	-	-	-
LV.SF.LTR	100	154	193	LY-MY	LY	0-1	-	-	-	-	MY	3	MY	3	MY	1	MY	1	MY	2	NT	0	-	-
LV.SF.LTR	100	155	193	LY-MY	MY	3	-	-	-	-	MY	3	MY	3	NT	0	MY	1-2	MY	1	NT	0	NT	0
LV.SF.LTR	100	159	200	LY-MY	LY	2	-	-	-	-	MY	3	LY	3	NT	0	LY	1	MY	1	NT	0	NT	0
LV.SF.LTR	100	160	200	LY-MY	LY	3	96.4	0.3	2.2	0.2	MY	2	MY	2	LY	1	LY	3	NT	0	NT	0	NT	0
LV.SF.LTR	100	166	202	LY-MY	LY	3	-	-	-	-	MY	2	MY	3	NT	0	MY	1	MY	1	MY	1	NT	0
LV.SF.LTR	100	83	207	LY	LY	2	-	-	-	-	LY	2	LY	1	NT	0	NT	0	NT	0	-	-	-	-
LV.SF.LTR	100	81	214	LY-MY	NT	0	-	-	-	-	-	-	MY	3	MY	2-3	MY	1	MY	1	-	-	-	-
LV.SF.LTR	100	84	229	LY-MY	MY	3	-	-	-	-	-	-	MY	3	MY	1	MY	2	MY	2	-	-	-	-
LV.SF.LTR	100	85	231	LY	LY	3	4	91	8	6	-	-	LY	2-3	LY	1	NT	0	LY	1	-	-	-	-

Vector (a)	MOI (b)	Mouse ID (c)	Cell Age Days (e)	Tumor Type (g)	Thymus (m)						Lymphonode (n)		Liver (o)		Kidney (p)		Lung (q)		Gut (r)		Brain (s)		Heart (t)	
					Pathol diag.	I.G	CD11b	CD19	CD3	GFP	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.
LV.SF.LTR	100	158	235	LY	LY	3	2.4	0.1	0.3	0.3	NT	0	NT	0	LY	3	LY	3	NT	0	NT	0	LY	2
LV.SF.LTR	100	157	263	LY-MY	LY	0-1	9.3	52.1	23.5	6.8	NT	0	NT	0	NT	0	NT	0	NT	0	NT	0	NT	0
LV.SF.LTR	100	165	279	LY	LY	3	19.2	5.2	1.7	95.4	LY	3	LY	3	LY	3	LY	2	LY	1	NT	0	NT	0
LV.SF.LTR	100	162	305	LY	LY	3	-	-	-	-	LY	3	LY	1	LY	1	LY	1	NT	0	NT	0	NT	0
Mock	-	2	146	LY-MY	-	-	-	-	-	-	-	-	LY-MY	3	MY	1	-	-	NT	0	-	-	-	-
Mock	-	27	160	LY	LY	3	-	-	-	-	LY	3	LY	2-3	LY	1	NT	0	-	-	-	-	-	-
Mock	-	130	164	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mock	-	29	179	LY	LY	3	1	99	0	0	LY	3	LY	1-2	LY	1	NT	0	LY	2	-	-	-	-
Mock	-	31	192	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mock	-	170	197	LY	LY	3	5.1	97.5	1.5	0	LY	3	LY	1-2	LY	1	NT	0	NT	0	LY	1	NT	0
Mock	-	128	203	LY-MY	LY	3	-	-	-	-	-	-	LY	2	NT	0	NT	0	NT	0	-	-	-	-
Mock	-	135	209	LY	LY	3	-	-	-	-	LY	3	LY	2	NT	0	LY	1	LY	1	-	-	-	-
Mock	-	126	216	LY	LY	3	-	-	-	-	-	-	LY	3	-	-	-	-	-	-	-	-	-	-
Mock	-	139	219	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mock	-	169	228	LY	NT	0	-	-	-	-	LY	3	LY	2	NT	0	LY	1	NT	0	-	-	NT	0
Mock	-	124	229	LY-MY	MY	3	12	28	32	0	-	-	MY	1	MY	3	MY	3	NT	0	-	-	-	-
Mock	-	131	237	MY	MY	2	-	-	-	-	-	-	MY	2	MY	2	MY	2	NT	0	NT	0	MY	2
Mock	-	129	240	LY-MY	MY	2	-	-	-	-	-	-	LY	2	LY	2	LY	3	NT	0	-	-	-	-
Mock	-	168	241	LY	LY	3	-	-	-	-	LY	3	LY	2	LY	1	NT	0	NT	0	-	-	NT	0
Mock	-	125	247	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mock	-	167	249	LY	-	-	-	-	-	-	LY	3	LY	2-3	NT	0	NT	0	NT	0	-	-	NT	0
Mock	-	127	254	LY-MY	MY	1	-	-	-	-	MY	3	NT	0	MY	1	MY	1	NT	0	NT	0	MY	0-1
Mock	-	120	261	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mock	-	117	270	LY	-	-	-	-	-	-	-	-	LY	1	NT	0	NT	0	NT	0	-	-	-	-

Vector (a)	MOI (b)	Mouse ID (c)	Cell Age Days (e)	Tumor Type (g)	Thymus (m)						Lymphonode (n)		Liver (o)		Kidney (p)		Lung (q)		Gut (r)		Brain (s)		Heart (t)	
					Pathol diag.	I.G	CD11b	CD19	CD3	GFP	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.
Mock	-	121	271	MY	MY	3	-	-	-	-	MY	3	MY	2	MY	3	MY	3	NT	0	-	-	-	-
Mock	-	138	279	LY	LY	3	-	-	-	-	LY	3	LY	2-3	LY	3	LY	3	-	-	NT	0	NT	0
Mock	-	137	287	LY	LY	0-1	-	-	-	-	NT	0	-	-	NT	0	NT	0	NT	0	NT	0	NT	0
Mock	-	115	291	LY	LY	3	-	-	-	-	-	-	LY	2	LY	1	LY	2	NT	0	-	-	-	-
Mock	-	136	293	LY	LY	3	-	-	-	-	-	-	LY	1	NT	0	NT	0	NT	0	NT	0	NT	0
Mock	-	133	293	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mock	-	134	293	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mock	-	118	307	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mock	-	119	310	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mock	-	122	349	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mock	-	116	377	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mock	-	123	440	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
RV.SF.LTR	100	191	116	LY	-	-	-	-	-	-	LY	3	LY	1	-	-	-	-	-	-	-	-	-	-
RV.SF.LTR	100	192	158	LY	LY	3	-	-	-	-	LY	3	LY	2	NT	0	NT	0	NT	0	NT	0	NT	0
RV.SF.LTR	100	195	170	LY	LY	3	2	72.9	15.1	82.6	LY	3	LY	2	NT	0	NT	0	LY	1	NT	0	NT	0
RV.SF.LTR	100	188	185	LY	LY	3	0.4	92.7	1.5	98.4	LY	3	LY	3	LY	3	LY	1	NT	0	LY	1	LY	1
RV.SF.LTR	100	187	192	MY	MY	3	-	-	-	-	MY	3	MY	3	MY	2	MY	3	MY	3	NT	0	NT	0
RV.SF.LTR	100	190	192	MY	MY	3	-	-	-	-	MY	3	MY	2	MY	3	MY	2	MY	3	NT	0	NT	0
RV.SF.LTR	100	185	197	LY	LY	3	3.8	100.2	0.2	99.4	LY	3	LY	2-3	LY	2	NT	0	LY	1	NT	0	NT	0
RV.SF.LTR	100	189	205	LY-MY	LY	2	50.7	52.4	24.1	67.4	LY	3	LY	3	LY	1	MY	1	MY	3	NT	0	NT	0
RV.SF.LTR	100	194	221	LY	LY	2	16.4	95.1	1.5	2.9	LY	3	LY	2-3	LY	2	LY	2	LY	2	LY	1	LY	1
RV.SF.LTR	100	186	255	MY	MY	3	-	-	-	-	-	-	MY	3	MY	3	MY	3	MY	3	LY	2	NT	0
RV.SF.LTR	100	184	354	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
RV.SF.LTR	100	193	354	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Vector (a)	MOI (b)	Mouse ID (c)	Cell Age Days (e)	Tumor Type (g)	Thymus (m)						Lymphonode (n)		Liver (o)		Kidney (p)		Lung (q)		Gut (r)		Brain (s)		Heart (t)	
					Pathol diag.	I.G	CD11b	CD19	CD3	GFP	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.
SIN.LV.SF	100	68	133	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.LV.SF	100	1	146	LY	LY	3	19	0	0	1	-	-	NT	0	LY	1	-	-	NT	0	-	-	-	-
SIN.LV.SF	100	64	153	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.LV.SF	100	3	161	LY	LY	3	-	-	-	-	LY	3	LY	1	LY	1	NT	0	NT	0	-	-	-	-
SIN.LV.SF	100	55	162	LY	LY	3	8	75	7	74	LY	3	LY	1	LY	1	LY	1	NT	0	-	-	-	-
SIN.LV.SF	100	60	162	LY	LY	3	11	10	2	11	-	-	LY	1	LY	2	LY	2	NT	0	-	-	-	-
SIN.LV.SF	100	23	171	LY	LY	3	-	-	-	-	-	-	LY	2	LY	1	NT	0	NT	0	-	-	-	-
SIN.LV.SF	100	26	174	LY	LY	3	1	1	1	99	LY	3	LY	1-2	LY	3	LY	3	NT	0	-	-	-	-
SIN.LV.SF	100	52	184	MY	-	-	-	-	-	-	-	-	MY	3	MY	3	-	-	-	-	-	-	-	-
SIN.LV.SF	100	61	192	LY	LY	3	3	0	7	100	-	-	LY	1	LY	1	LY	2	LY	0-1	-	-	-	-
SIN.LV.SF	100	63	192	LY-MY	LY	2	-	-	-	-	-	-	LY	1	LY	1	LY	2	LY	1	-	-	-	-
SIN.LV.SF	100	66	194	LY	LY	3	-	-	-	-	LY	3	LY	3	LY	3	LY	3	NT	0	-	-	-	-
SIN.LV.SF	100	59	212	LY	LY	3	-	-	-	-	-	-	LY	3	LY	2	LY	1	LY	1	-	-	-	-
SIN.LV.SF	100	17	214	LY-MY	MY	3	-	-	-	-	-	-	MY	3	MY	2	MY	2	MY	2	-	-	-	-
SIN.LV.SF	100	69	217	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.LV.SF	100	25	230	LY	LY	3	-	-	-	-	LY	3	LY	2	LY	1	NT	0	NT	0	-	-	-	-
SIN.LV.SF	100	40	230	ND	NT	0	-	-	-	-	-	-	NT	0	-	-	-	-	-	-	-	-	-	-
SIN.LV.SF	100	67	231	LY	LY	3	0.4	99	1.1	98.6	LY	3	LY	2	LY	1	LY	0-1	LY	2	NT	0	NT	0
SIN.LV.SF	100	53	234	LY	LY	3	-	-	-	-	-	-	LY	2	LY	1	-	-	NT	0	-	-	-	-
SIN.LV.SF	100	41	238	LY	LY	3	1	99	0	100	-	-	LY	2	LY	0-1	NT	0	LY	1	-	-	-	-
SIN.LV.SF	100	43	238	LY	LY	3	0	0	23	100	-	-	LY	0-1	LY	2	LY	3	NT	0	-	-	-	-
SIN.LV.SF	100	56	248	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.LV.SF	100	47	254	LY	LY	2	10	68	11.2	80	LY	3	LY	3	LY	0-1	LY	1	NT	0	NT	0	NT	0
SIN.LV.SF	100	57	254	LY	LY	3	7.5	1.1	55.8	0.8	LY	3	LY	2	LY	2	LY	3	NT	0	NT	0	LY	1

Vector (a)	MOI (b)	Mouse ID (c)	Cell Age Days (e)	Tumor Type (g)	Thymus (m)						Lymphonode (n)		Liver (o)		Kidney (p)		Lung (q)		Gut (r)		Brain (s)		Heart (t)	
					Pathol diag.	I.G	CD11b	CD19	CD3	GFP	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.
SIN.LV.SF	100	44	256	LY	LY	3	-	-	-	-	LY	3	LY	2	NT	0	LY	1-2	NT	0	-	-	-	-
SIN.LV.SF	100	54	262	LY-MY	MY	3	-	-	-	-	MY	3	MY	2	MY	3	MY	2	MY	2	MY	1	MY	2
SIN.LV.SF	100	48	268	LY	LY	3	-	-	-	-	LY	3	LY	2	LY	2	LY	1	NT	0	NT	0	NT	0
SIN.LV.SF	100	33	270	LY	LY	3	-	-	-	82	LY	1	LY	2-3	NT	0	LY	1	LY	1	-	-	-	-
SIN.LV.SF	100	58	277	LY	LY	3	57.7	0.6	3.2	98.6	-	-	NT	0	NT	0	LY	3	NT	0	NT	0	NT	0
SIN.LV.SF	100	62	280	LY	LY	3	-	-	-	-	LY	3	LY	2	LY	1	LY	1	NT	0	NT	0	NT	0
SIN.LV.SF	100	51	309	LY	LY	3	22.1	0.6	94.8	1.3	-	-	NT	0	NT	0	LY	2	NT	0	NT	0	NT	0
SIN.LV.SF	100	65	319	LY-MY	LY	1	-	-	-	-	NT	0	NT	0	NT	0	NT	0	NT	0	NT	0	NT	0
SIN.LV.SF	100	49	343	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.LV.SF	100	50	343	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.LV.SF	100	39	383	LY-MY	-	-	-	-	-	-	LY	1	LY	1	MY	1	MY	1	NT	0	NT	0	NT	0
SIN.LV.SF	100	46	385	MY	MY	2	-	-	-	-	-	-	NT	0	MY	3	MY	1	NT	0	NT	0	-	-
SIN.LV.SF	100	42	461	MY	MY	3	-	-	-	-	NT	0	MY	2-3	NT	0	NT	0	NT	0	NT	0	NT	0
SIN.LV.SF	100	45	467	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.LV.SF	100	38	486	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.RV.PGK	100	11	130	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.RV.PGK	100	12	130	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.RV.PGK	100	19	144	LY	NT	0	-	-	-	-	-	-	NT	0	NT	0	NT	0	NT	0	-	-	-	-
SIN.RV.PGK	100	107	160	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.RV.PGK	100	111	160	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.RV.PGK	100	30	172	LY	LY	3	0	0	2	0	LY	3	NT	0	NT	0	LY	1	NT	0	-	-	-	-
SIN.RV.PGK	100	100	175	LY	LY	3	2	3	7	99	-	-	LY	3	LY	3	LY	3	LY	2	-	-	-	-
SIN.RV.PGK	100	97	184	LY	LY	0-1	-	-	-	-	-	-	LY	2	-	-	-	-	-	-	-	-	-	-
SIN.RV.PGK	100	99	184	LY	LY	3	-	-	-	-	-	-	LY	3	-	-	-	-	-	-	-	-	-	-

Vector (a)	MOI (b)	Mouse ID (c)	Cell Age Days (e)	Tumor Type (g)	Thymus (m)						Lymphonode (n)		Liver (o)		Kidney (p)		Lung (q)		Gut (r)		Brain (s)		Heart (t)	
					Pathol diag.	I.G	CD11b	CD19	CD3	GFP	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.
SIN.RV.PGK	100	9	188	LY	LY	1	-	-	-	-	-	-	LY	3	LY	1	NT	0	NT	0	-	-	-	-
SIN.RV.PGK	100	102	192	LY	LY	2	-	-	-	-	-	-	NT	0	NT	0	-	-	NT	0	-	-	-	-
SIN.RV.PGK	100	88	194	LY	LY	3	-	-	-	-	-	-	LY	3	LY	2	LY	1-2	LY	0-1	-	-	-	-
SIN.RV.PGK	100	105	199	LY	LY	3	-	-	-	-	-	-	LY	1	NT	0	NT	0	NT	0	-	-	-	-
SIN.RV.PGK	100	92	200	LY	LY	3	16	12	2	4	NT	0	NT	0	NT	0	LY	3	NT	0	-	-	-	-
SIN.RV.PGK	100	96	207	LY	LY	3	-	-	-	-	-	-	LY	2	NT	0	-	-	NT	0	-	-	-	-
SIN.RV.PGK	100	114	214	LY	-	-	7.7	74	-	96.7	LY	3	LY	2	LY	3	LY	2	LY	2	-	-	-	-
SIN.RV.PGK	100	91	221	LY	LY	1-2	-	-	-	-	-	-	LY	2	LY	1	NT	0	NT	0	-	-	-	-
SIN.RV.PGK	100	101	234	LY-MY	NT	0	-	-	-	-	NT	0	NT	0	MY	1	MY	1	MY	3	-	-	-	-
SIN.RV.PGK	100	94	242	LY	LY	3	-	-	-	-	-	-	LY	2-3	LY	3	LY	3	NT	0	-	-	-	-
SIN.RV.PGK	100	103	244	LY	LY	3	-	-	-	-	-	-	LY	2	LY	1	LY	1	NT	0	NT	0	LY	1
SIN.RV.PGK	100	112	256	LY	LY	3	12	0.5	1.2	0.5	NT	0	NT	0	NT	0	LY	1	NT	0	NT	0	NT	0
SIN.RV.PGK	100	104	272	LY-MY	MY	2	-	-	-	-	MY	3	MY	2	MY	3	MY	3	MY	3	MY	1	NT	0
SIN.RV.PGK	100	109	299	LY	LY	2	-	-	-	-	NT	0	LY	1	NT	0	NT	0	LY	1	NT	0	NT	0
SIN.RV.PGK	100	89	300	LY	LY	3	-	-	-	-	NT	0	LY	2	LY	1	LY	2	NT	0	NT	0	LY	1
SIN.RV.PGK	100	93	314	LY	LY	3	-	-	-	-	LY	3	LY	2	NT	0	LY	2	NT	0	LY	2	NT	0
SIN.RV.PGK	100	110	319	MY	MY	2	-	-	-	-	NT	0	MY	2	NT	0	MY	2	MY	1	NT	0	NT	0
SIN.RV.PGK	100	87	320	LY	-	-	-	-	-	-	LY	3	LY	3	NT	0	NT	0	NT	0	-	-	-	-
SIN.RV.PGK	100	98	322	LY	LY	3	-	-	-	-		3	LY	2	LY	1	NT	0	NT	0	NT	0	NT	0
SIN.RV.PGK	100	108	326	LY	LY	3	1.5	0.2	7.5	99.6	NT	0	NT	0	LY	1	LY	2	NT	0	-	-	NT	0
SIN.RV.PGK	100	113	326	LY	LY	3	0.6	0.2	39.3	0.6	-	-	LY	2	LY	2	LY	3	NT	0	-	-	LY	1
SIN.RV.PGK	100	90	347	LY-MY	MY	3	-	-	-	-	MY	3	MY	3	MY	3	MY	3	NT	0	NT	0	NT	0
SIN.RV.PGK	100	95	396	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SIN.RV.PGK	100	106	412	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Vector (a)	MOI (b)	Mouse ID (c)	Cell Age Days (e)	Tumor Type (g)	Thymus (m)						Lymphonode (n)		Liver (o)		Kidney (p)		Lung (q)		Gut (r)		Brain (s)		Heart (t)	
					Pathol diag.	I.G	CD11b	CD19	CD3	GFP	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.	Pathol diag.	I.G.
SIN.RV.PGK	100	86	425	ND	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Supplementary Table 1b: Tumor phenotype analysis by FACS and histopathology on lymphonodes, liver, kidney, lung, gut, brain and heart from the same mice shown in Table 1a.

Columns from (a) to (g) as in Table 1a. (m), (n), (o), (p), (q), (r), (s), and (t): Histopathological analysis of thymus, lymph nodes, liver, kidney, lung, gut, brain and heart, respectively. For each tissue hematoxilin and eosin-stained sections were analyzed as in 1a. For the thymus the relative percentages of myeloid (CD11b), B (CD19) T (CD3) and GFP+ cells assessed by FACS is also indicated. In tumor free age-matched mice thymus normal levels of myeloid, B- and T-lymphoid cells were 2±2%, 1±3% and 50±8% respectively. Mice with >10% of CD11b+ cells were diagnosed as myeloid tumors (highlighted in red), whereas mice with >20% CD19+ or >65% CD3+ cells were diagnosed as lymphoid tumor (highlighted in yellow).

Supplementary Table 2: LV.SF.LTR, SIN.LV.SF and SIN.RV.PGK integrations and nearest genes *in vitro* and in tumors

Seq ID	Vector	Mouse ID	Chr.	Chr. Position	Identical	Transcript ID	Symbol	Int. type	ORI	Dist to tss	Human Ortholog
iv352	LV.SF.LTR na		1	6 257409		NM_009826.3	Rb1cc1	intra	same	52666	RB1CC1
iv588	LV.SF.LTR na		1	9 9901922		NM_013626.3	Pam	intra	opp	24116	PAM
iv333	LV.SF.LTR na		1	1 65233531		NM_178883.5	Scyl1bp1	intra	same	6785	SCYL1BP1
iv602	LV.SF.LTR na		1	173996818		NM_153555.1	Wdr42a	intra	same	12001	WDR42A
iv351	LV.SF.LTR na		2	1 1100586		NM_008859.2	Prkcq	intra	same	10351	PRKCQ
iv522	LV.SF.LTR na		2	1 4582295		NM_023116.3	Cacnb2	intra	same	60235	CACNB2
iv475	LV.SF.LTR na		2	1 4664073		NM_023116.3	Cacnb2	intra	same	142013	CACNB2
iv344	LV.SF.LTR na		2	4 8081542		NM_007396.3	Acvr2a	ups	opp	-554624	ACVR2A
iv613	LV.SF.LTR na		2	7 9377747		NM_080558.3	Ssfa2	ups	same	-58632	SSFA2
iv418	LV.SF.LTR na		2	1 26619184		NM_023220.1	2010106G01Rik	intra	same	5492	PSL2
iv531	LV.SF.LTR na		3	2 8425325		ENSMUST00000074264	Tnik	ups	same	-28962	TNIK
iv547	LV.SF.LTR na		4	3 432370		NM_028097.3	Tmem68	downs	same	69545	TMEM68
iv302	LV.SF.LTR na		4	3 861558		NM_019969.2	Plag1	intra	same	3971	PLAG1
iv330	LV.SF.LTR na		5	5 189514		NM_011074.1	Pftk1	intra	same	196689	PFTK1
iv555	LV.SF.LTR na		5	6 5911820		NM_001081321.1	Pds5a	intra	same	65171	NP_056015.1
iv349	LV.SF.LTR na		5	8 1384636		NM_198702.2	Lphn3	ups	opp	-711518	LPHN3
iv579	LV.SF.LTR na		5	1 10479865		NM_027922.1	D5Ertd585e	intra	same	8522	KIAA0692
iv526	LV.SF.LTR na		5	1 15412161		NM_175403.2	2410014A08Rik	intra	opp	6984	KIAA0152
iv433	LV.SF.LTR na		6	5 240180		NM_183308.2	Pon2	intra	opp	8193	PON2
iv445	LV.SF.LTR na		6	8 118343		NM_001037865.1	Col28a1	intra	opp	24274	
iv458	LV.SF.LTR na		6	2 3594443		NM_153163.3	Cadps2	intra	same	194859	CADPS2
iv587	LV.SF.LTR na		6	30812215		NM_017478.2	Copg2	intra	opp	14706	TSGA13
iv595	LV.SF.LTR na		6	4 0313251		NM_023538.1	Agk	intra	same	13115	AGK
iv500	LV.SF.LTR na		6	4 3357739		NM_013861.3	Tpk1	intra	same	238043	TPK1

Seq ID	Vector	Mouse ID	Chr.	Chr. Position	Identical	Transcript ID	Symbol	Int. type	ORI	Dist to tss	Human Ortholog
iv505	LV.SF.LTR na		6	53429346		NM_172728.2	Creb5	ups	same	-73606	CREB5
iv424	LV.SF.LTR na		6	56831923		NM_026004.2	Nt5c3	intra	same	21484	NT5C3
iv525	LV.SF.LTR na		6	66017633		NM_027547.2	Prdm5	downs	same	309093	PRDM5
iv589	LV.SF.LTR na		6	146738693		NM_172734.2	Stk38l	downs	opp	56515	STK38L
iv593	LV.SF.LTR na		7	5994799		NM_175247.3	Zfp28	intra	opp	7479	ZFP28
iv470	LV.SF.LTR na		7	55755739		NM_011370.1	Cyfip1	intra	same	45445	CYFIP1
iv338	LV.SF.LTR na		7	68617255		NM_001042592.2	Arrdc4	intra	opp	5496	ARRDC4
iv513	LV.SF.LTR na		7	79921956		NM_175433.4	Zfp710	intra	same	22109	ZNF710
iv607	LV.SF.LTR na		7	97067879		NM_010248.1	Gab2	intra	same	110936	GAB2
iv473	LV.SF.LTR na		7	100337062		NM_001017985.2	AU020772	intra	opp	90746	NP_056346.2
iv306	LV.SF.LTR na		7	106458602		NM_146453.1	Olfr693	downs	opp	13531	OR2AG1
iv440	LV.SF.LTR na		7	111850802		NM_133758.2	Usp47	intra	opp	36115	USP47
iv578	LV.SF.LTR na		7	140826392		NM_026820.2	Ifitm1	downs	opp	7846	XR_018421.1
iv402	LV.SF.LTR na		8	37610989		NM_172911.2	D8Ertd82e	intra	opp	47611	SG223
iv530	LV.SF.LTR na		8	73606542		NM_015816.3	Lsm4	intra	opp	4161	C19orf50
iv450	LV.SF.LTR na		8	74841353		NM_133358.2	Zfp617	ups	same	-10472	
iv430	LV.SF.LTR na		9	28403006		NM_177906.4	Opcml	intra	opp	862291	OPCML
iv401	LV.SF.LTR na		9	85534672		NM_001081282.1	Ibtk	intra	opp	6205	IBTK
iv462	LV.SF.LTR na		9	92388029		NM_011961.2	Plod2	intra	opp	41806	PLOD2
iv359	LV.SF.LTR na		9	94540155		NM_177909.4	Slc9a9	intra	opp	60894	SLC9A9
iv326	LV.SF.LTR na		9	108212000		NM_011678.1	Usp4	intra	opp	6037	USP4
iv599	LV.SF.LTR na		10	74081756		NM_023115.2	Pcdh15	downs	same	864573	PCDH15
iv592	LV.SF.LTR na		10	74492812		NM_029781.3	Rab36	intra	opp	12007	RAB36
iv390	LV.SF.LTR na		10	80267748		NM_175195.3	3110056O03Rik	intra	same	9344	PSL1
iv596	LV.SF.LTR na		10	98380104		NM_026482.1	Atp2b1	intra	same	35246	ATP2B1

Seq ID	**Vector**	**Mouse ID**	**Chr.**	**Chr. Position**	**Identical**	**Transcript ID**	**Symbol**	**Int. type**	**ORI**	**Dist to tss**	**Human Ortholog**
iv582	LV.SF.LTR na		11	8 552613		NM_001083587.1	Tns3	intra	opp	11925	TNS3
iv498	LV.SF.LTR na		12	4 9170323		NM_008241.1	Foxg1	ups	same	-1088811	FOXG1B
iv419	LV.SF.LTR na		12	9 0203953		NM_172544.2	Nrxn3	intra	opp	737075	NRXN3
iv460	LV.SF.LTR na		12	1 11990743		NM_178041.1	Eif5	intra	same	4834	IF5
iv427	LV.SF.LTR na		13	1 2463569		NM_144835.4	Heatr1	intra	same	13861	HEATR1
iv581	LV.SF.LTR na		13	4 6833269		NM_010617.2	Kif13a	intra	opp	107421	KIF13A
iv353	LV.SF.LTR na		14	3 8549169		NM_008734.2	Nrg3	ups	opp	-164202	NRG3
iv474	LV.SF.LTR na		15	5 9242959		NM_026746.2	Nsmce2	intra	same	39031	NSMCE2
iv337	LV.SF.LTR na		15	9 8371824		NM_009833.1	Ccnt1	intra	opp	23846	CCNT1
iv477	LV.SF.LTR na		16	4 9494136		NM_028680.3	Ift57	ups	opp	-124784	IFT57
iv535	LV.SF.LTR na		16	7 8364040		NM_025967.2	D16Ertd472e	downs	opp	95199	C21orf91
iv571	LV.SF.LTR na		16	9 4478301		NM_019543.2	Pigp	intra	opp	1512	PIGP
iv381	LV.SF.LTR na		17	1 7080677		NM_025934.1	Riok2	intra	opp	1483	RIOK2
iv502	LV.SF.LTR na		17	3 0258246		NM_172618.1	Btbd9	intra	opp	44935	BTBD9
iv368	LV.SF.LTR na		17	4 4112356		NM_009820.3	Runx2	intra	opp	165326	RUNX2
iv357	LV.SF.LTR na		17	8 4202515		ENSMUST00000047524	Thada	intra	same	170243	THADA
iv604	LV.SF.LTR na		18	4 2207785		NM_172966.2	Sh3rf2	intra	same	28102	SH3RF2
iv382	LV.SF.LTR na		19	11119412		ENSMUST00000099676	AW112010	ups	opp	-3969	
iv576	LV.SF.LTR na		19	2 6744615		NM_011416.2	Smarca2	intra	opp	72358	SMARCA2
iv384	LV.SF.LTR na		19	4 7671393		NM_009289.2	Slk	intra	same	38063	SLK
iv577	LV.SF.LTR na		X	1 00176340		NM_011276.3	Rnf12	intra	opp	7663	RNF12
1773	LV.SF.LTR 3	12	12	9 6145621		NM_201518.2	Flrt2	intra	same	57536	FLRT2
1581	LV.SF.LTR 2	96	10	6 6559773		ENSMUST00000051446	Jmjd1c	ups	opp	-21564	JMJD1C
1732	LV.SF.LTR 2	95	1	1 84279090		NM_173378.2	Trp53bp2	intra	same	33248	TP53BP2
1675	LV.SF.LTR 2	94	6	8 2981371		NM_033079.1	D6Mm5e	intra	opp	59304	NP_620159.2

Seq ID	Vector	Mouse ID	Chr.	Chr. Position	Identical	Transcript ID	Symbol	Int. type	ORI	Dist to tss	Human Ortholog
1672	LV.SF.LTR 2	94	16	56744537		NM_019631.3	Tmem45a	intra	opp	66577	TMEM45A
1591	LV.SF.LTR 2	77	15	76477239		NM_019396.2	Cyhr1	intra	opp	10077	Q6ZMK1
1759	LV.SF.LTR 2	75	7	51597959		NM_080853.2 Slc1	7a6 d	owns	same	107873	SLC17A6
1162	LV.SF.LTR 2	75	10	45150008		NM_001031772.1	Lin28b	intra	same	8608	LIN28B
1074	LV.SF.LTR 2	75	11	11077025		NM_177033.3	Vwc2	intra	same	63006	VWC2
1159	LV.SF.LTR 2	75	15	51795991		NM_009009.3	Rad21	intra	opp	25645	RAD21
1062	LV.SF.LTR 2	74	1	139976672		NM_011210.2	Ptprc	intra	opp	15005	PTPRC
1056	LV.SF.LTR 2	74	3	10415368		NM_029068.2	Snx16	intra	same	7251	SNX16
1069	LV.SF.LTR 2	74	5	148829188		NM_011908.2	Ubl3	intra	opp	33949	UBL3
1147	LV.SF.LTR 2	74	6	24103671		NM_019481.1 Slc1	3a1 in	tra	same	14423	SLC13A1
1151	LV.SF.LTR 2	74	6	108405127		NM_010585.3	Itpr1	intra	opp	226254	ITPR1
1152	LV.SF.LTR 2	74	15	34437320		NM_008287.2	Hrsp12	intra	same	2459	HRSP12
1067	LV.SF.LTR 2	74	16	23985541		NM_009744.3	bcl6	ups	opp	-81580	BCL6
1070	LV.SF.LTR 2	74	19	55800134		NM_009333.2	Tcf7l2	intra	same	4614	TCF7L2
1593	LV.SF.LTR 2	72	12	94568209		NM_201518.2	Flrt2	ups	same	-1519876	FLRT2
1322	LV.SF.LTR 2	71	8	125859454		NM_001081379.1	Ankrd11	intra	same	68633	ANKRD11
1304	LV.SF.LTR 2	71	13	55270674	261;271	NM_008739.3	Nsd1	intra	same	51270	NSD1
1307	LV.SF.LTR 2	71	14	30877014		NM_030166.3	Galntl2	intra	same	18902	GALNTL2
1283	LV.SF.LTR 2	71	17	81751011	261;271	NM_011406.2	Slc8a1	ups	opp	-104308	SLC8A1
1296	LV.SF.LTR 2	70	1	99721998		NM_013626.3	Pam	intra	opp	204040	PAM
1300	LV.SF.LTR 2	70	6	45639721		NM_001004357.1	Cntnap2	intra	opp	650026	CNTNAP2
1765	LV.SF.LTR 2	70	10	117465466		NM_148922.2	Mdm1	ups	same	-79359	MDM1
1302	LV.SF.LTR 2	70	X 1	09852822		NM_033605.2	Dach2	intra	same	437622	DACH2
1741	LV.SF.LTR 2	69	19	37428297		NM_010615.1	Kif11	ups	same	-13250	KIF11
1818	LV.SF.LTR 2	67	1	7134596		NM_183028.3	Pcmtd1	intra	same	55595	PCMTD1

Seq ID	Vector	Mouse ID	Chr.	Chr. Position	Identical	Transcript ID	Symbol	Int. type	ORI	Dist to tss	Human Ortholog
1268	LV.SF.LTR 2	66	13	76572945		NM_001081352.1	AK129128	intra	same	8209	KIAA0372
1265	LV.SF.LTR 2	66	16	67301540		NM_178721.3	Cadm2	intra	same	237606	CADM2
1648	LV.SF.LTR 2	65	X 1	54605441		NM_148945.1	Rps6ka3	intra	opp	5216	RPS6KA3
1119	LV.SF.LTR 2	64	1	146526930		NM_022881.4	Rgs18	intra	opp	10709	RGS18
1236	LV.SF.LTR 2	64	2	177296167		ENSMUST00000099024	0610010B08Rik	intra	opp	122434	
1105	LV.SF.LTR 2	64	18	38038811		NM_007858.2	Diap1	intra	same	22574	DIAPH1
1102	LV.SF.LTR 2	63	18	89832319		NM_001039173.1	Dok6	intra	opp	71015	DOK6
1607	LV.SF.LTR 2	62	2	52811633		NM_172409.2	Fmnl2	intra	same	131756	FMNL2
1677	LV.SF.LTR 2	62	3	81179207		NM_019971.2	Pdgfc	intra	same	56864	PDGFC
1609	LV.SF.LTR 2	62	13	115954105		NM_008396.2	Itga2	downs	opp	98814	ITGA2
1601	LV.SF.LTR 2	62	19	26884163		NM_011416.2	Smarca2	downs	same	211906	SMARCA2
1041	LV.SF.LTR 2	61	3	20873024		NM_175086.2	Agtr1b	ups	same	-314774	AGTR1
1045	LV.SF.LTR 2	61	11	9798936		NM_178259.3	Abca13	downs	opp	706991	ABCA13
1767	LV.SF.LTR 2	61	13	55270673	261;271	NM_008739.3	Nsd1	intra	same	51269	NSD1
1710	LV.SF.LTR 2	61	17	81751011	261;271	NM_011406.2	Slc8a1	ups	opp	-104308	SLC8A1
1754	LV.SF.LTR 2	59	6	56651316		ENSMUST00000031805	5830411G16Rik	intra	opp	6811	KIAA0241
1799	LV.SF.LTR 2	58	8	36960129		NM_026067.2	Thex1	intra	opp	3869	THEX1
1022	LV.SF.LTR 2	57	1	175645846		BC010546.1/ NM_008329	Ifi204	intra	opp	103708	MNDA
1019	LV.SF.LTR 2	57	3	73797155		NM_009738.3	bche	ups	same	-2814	BCHE
1018	LV.SF.LTR 2	57	3	152228052		NM_174868.3	C030011O14Rik	intra	opp	49724	FAM73A
1097	LV.SF.LTR 2	57	4	39493535		NM_001081095.1	1700009N14Rik	ups	same	-145429	RAN
1091	LV.SF.LTR 2	57	12	5018756		NM_001099628.1	Atad2b	intra	same	75490	ATAD2B
1008	LV.SF.LTR 2	57	13	16993480		NM_138654.2	5033411D12Rik	intra	opp	486401	C7orf10
996	LV.SF.LTR 2	55	2	75776675		NM_001081228.1	Ttc30a2	downs	opp	2343	Q96NE6
979	LV.SF.LTR 2	55	3	65468744		NM_026155.3	Ssr3	intra	opp	11738	SSR3

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1205	LV.SF.LTR 2	55	11	7 4773202		NM_001002764.1	Smg6	intra	same	31135	SMG6
987	LV.SF.LTR 2	55	19	4 3635234		NM_008699.2	Nkx2-3	ups	opp	-30402	NKX2-3
1785	LV.SF.LTR 2	54	11	7 7242436		NM_177710.3	Ssh2	intra	same	209816	SSH2
343	LV.SF.LTR 2	30	2	3 198129		NM_008708.1	Nmt2	ups	opp	-3431	NMT2
278	LV.SF.LTR 2	30	3	1 4569367		NM_007892.2	E2f5	intra	same	13952	E2F5
359	LV.SF.LTR 2	30	4	4 4155103		NM_001038993.2	Rnf38	intra	opp	34336	RNF38
1407	LV.SF.LTR 2	30	4	1 08802429		NM_007943.2	Eps15	intra	same	24194	EPS15
361	LV.SF.LTR 2	30	4	1 09291240		NM_007983.2	Faf1	intra	opp	116681	FAF1
349	LV.SF.LTR 2	30	6	8 163594		NM_145374.1	BC020002	intra	same	4365	NP_061878.3
373	LV.SF.LTR 2	30	8	6 4901967		NM_001081215.1	BC013672	intra	opp	81736	NP_060101.2
353	LV.SF.LTR 2	30	13	5 427461		NM_011803.2	Klf6	ups	opp	-433274	KLF6
335	LV.SF.LTR 2	30	13	1 10123259		NM_011056.2	Pde4d	intra	opp	348218	PDE4D
341	LV.SF.LTR 2	30	15	4 9365978		NM_001081391.1	Csmd3	ups	same	-861992	CSMD3
336	LV.SF.LTR 2	30	17	8 9734701		ENSMUST00000086423	Kpna2	downs	same	83941	KPNA2
662	LV.SF.LTR 2	29	11	1 8422438		NM_010789.2	Meis1	downs	same	496245	MEIS1
565	LV.SF.LTR 2	24	4	1 42475400		NM_001081355.1	Prdm2	intra	same	3996	PRDM2
671	LV.SF.LTR 2	24	12	4 0545660		NM_007487.3	Arl4a	intra	opp	2139	ARL4A
1545	LV.SF.LTR 2	14	1	4 3148311		ENSMUST00000070599	Fhl2	ups	opp	-7004	FHL2
1585	LV.SF.LTR 2	14	1	4 3933476		NM_009418.2	Tpp2	intra	same	54923	TPP2
1826	LV.SF.LTR 2	14	13	5 5268300		NM_008739.3	Nsd1	intra	opp	48896	NSD1
1713	LV.SF.LTR 2	13	8	6 9800035		ENSMUST00000015051	BC053440	intra	opp	10073	NP_612395.1
1825	LV.SF.LTR 2	13	9	5 0349650		NM_025848.2	sdhd	intra	same	6397	SDHD
1638	LV.SF.LTR 2	12	1	1 09325143		NM_011111.3	Serpinb2	ups	same	-17877	SERPINB2
643	LV.SF.LTR 2	12	1	1 75712030		BC010546.1/ NM_008329	Ifi204	intra	opp	37524	MNDA
642	LV.SF.LTR 2	12	6	3 9576935		NM_139294.5	Braf	intra	same	78135	BRAF

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1427	LV.SF.LTR 1	91	4	1 49259496		NM_001085492.1	Rere	intra	same	133780	Rere
1426	LV.SF.LTR 1	91	15	8 4757338		NM_016714.2	Nup50	intra	opp	6144	NUP50
252	LV.SF.LTR 1	84	10	4 0106086	182;184	NM_198164.2	Cdc2l6	intra	same	67333	CDC2L6
614	LV.SF.LTR 1	84	11	4 8908149	182;184	NM_010999.2	Olfr56	intra	same	13993	
1412	LV.SF.LTR 1	84	17	8 0344002	182;184	NM_009231.2	Sos1	intra	opp	44777	SOS1
1409	LV.SF.LTR 1	84	19	5 3627540	182;184	NM_007790.2	Smc3	ups	opp	-26219	SMC3
1823	LV.SF.LTR 1	84	X	164545671	182;184	NM_009707.3 ar	hgap6 in	tra	opp	406467	ARHGAP6
1417	LV.SF.LTR 1	82	3	1 34614561		ENSMUST00000093973	Gm421	ups	same	-4830978	NP_940908.1
717	LV.SF.LTR 1	82	10	4 0106083	182;184	NM_198164.2	Cdc2l6	intra	same	67330	CDC2L6
607	LV.SF.LTR 1	82	11	4 8908149	182;184	NM_010999.2	Olfr56	intra	same	13993	
1416	LV.SF.LTR 1	82	17	8 0344002	182;184	NM_009231.2	Sos1	intra	opp	44777	SOS1
1821	LV.SF.LTR 1	82	19	5 3627540	182;184	NM_007790.2	Smc3	ups	opp	-26219	SMC3
1822	LV.SF.LTR 1	82	X	164545671	182;184	NM_009707.3 ar	hgap6 in	tra	opp	406467	ARHGAP6
1424	LV.SF.LTR 1	80	4	8 4479433		NM_175275.3	D53005L1Rik	intra	same	123875	C9orf39
1425	LV.SF.LTR 1	80	9	8 5492977		NM_001081282.1	lbtk	intra	opp	47900	IBTK
1619	LV.SF.LTR 1	79	4	8 8022787		NM_206870.1	Ifna14	downs	opp	6689	IFNA5
1422	LV.SF.LTR 1	79	16	7 8444089		NM_025967.2	D16Ertd472e	intra	opp	15150	C21orf91
1419	LV.SF.LTR 1	76	5	7 4638097		NM_178672.5	Scfd2	downs	same	175351	SCFD2
1616	LV.SF.LTR 1	73	1	1 41052145		NM_133239.1	Crb1	intra	opp	141307	CRB1
582	LV.SF.LTR 1	73	5	8 6869118		NM_007683.2	Cenpc1	downs	opp	270893	CENPC1
1421	LV.SF.LTR 1	73	10	1 2323047		NM_011682.4	Utrn	intra	same	228878	UTRN
iv257	SIN.LV.SF n	a	1	5 084370		NM_133826.4	Atp6v1h	intra	same	11116	ATP6V1H
iv162	SIN.LV.SF n	a	1	24650586		NM_026719.2 Lm	brd1 in	tra	opp	17767	LMBRD1
iv150	SIN.LV.SF n	a	1	3 4474898		NM_007685.2	Cfc1	ups	opp	-5296	CFC1
iv224	SIN.LV.SF n	a	1	5 2603445		NM_133829.1	2210010L05Rik	intra	opp	50260	NP_060164.3

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iv133	SIN.LV.SF n	a	1	56956367		NM_139146.2	Satb2	ups	same	-40488	SATB2
iv103	SIN.LV.SF n	a	1	77110364		NM_007936.3	Epha4	downs	opp	287872	EPHA4
iv10	SIN.LV.SF n	a	1	108430811		NM_009741.3	Bcl2	intra	opp	111026	BCL2
iv47	SIN.LV.SF n	a	1	181943317		ENSMUST00000097452.1	Cdc42bpa	intra	same	107281	CDC42BPA
iv78	SIN.LV.SF n	a	2	3418490		NM_015765.2	Hspa14	intra	same	11596	HSPA14
iv52	SIN.LV.SF n	a	2	91604219		NM_001080754.1	D030051N19Rik	intra	same	73242	NP_060219.2
iv610	SIN.LV.SF n	a	2	102808146		NM_175094.4	Pdhx	downs	same	66204	PDHX
iv26	SIN.LV.SF n	a	2	122135593		NM_172980.2 Slc2	8a2 in	tra	same	17675	SLC28A2
iv614	SIN.LV.SF n	a	3	19342469		NM_028840.2	Armc1	intra	same	12747	ARMC1
iv67	SIN.LV.SF n	a	3	62569276		NM_028136.1	Dhx36	intra	opp	25641	DHX36
iv3	SIN.LV.SF n	a	3	89118202		NM_138679.5	Ash1l	intra	same	66463	ASH1L
iv59	SIN.LV.SF n	a	3	90408624		NM_139304.1	Gatad2b	ups	opp	-18957	GATAD2B
iv235	SIN.LV.SF n	a	3	123406215		NM_201638.1	G430022H21Rik	ups	same	-28245	NP_066012.1
iv274	SIN.LV.SF n	a	3	135242654		NM_027208.1	Bdh2	downs	same	23975	BDH2
iv15	SIN.LV.SF n	a	3	136581586		NM_008913.3	Ppp3ca	ups	opp	-26571	PPP3CA
iv19	SIN.LV.SF n	a	3	137127113		NM_016885.1	Emcn	ups	opp	-151376	EMCN
iv142	SIN.LV.SF n	a	3	149399909		NM_001033772.2	LOC381483	downs	same	157694	
iv172	SIN.LV.SF n	a	4	12909141		NM_173746.2	ENSMUSG00000055963 d	owns	same	75136	Q629K1
iv120	SIN.LV.SF n	a	4	49266539		NM_178756.4	E130309F12Rik	intra	same	185977	NP_060223.2
iv29	SIN.LV.SF n	a	4	96026436		NM_010008.3	Cyp2j6	intra	opp	19233	CYP2J2
iv77	SIN.LV.SF n	a	4	114173223		NM_001085549.1	OTTMUSG00000008561 d	owns	same	268567	
iv277	SIN.LV.SF n	a	5	5182228		NM_011074.1	Pftk1	intra	opp	203975	PFTK1
iv286	SIN.LV.SF n	a	5	42101003		NM_001081422.1	LOC665775	intra	same	31560	FAM44A
iv253	SIN.LV.SF n	a	5	46899628		NM_178142.3	Lcorl	ups	same	-753874	LCORL

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iv93	SIN.LV.SF n	a	5	48471934		NM_178804.2	Slit2	intra	same	198893	SLIT2
iv279	SIN.LV.SF n	a	5	52452817		NM_007839.2	Dhx15	intra	same	25950	DHX15
iv66	SIN.LV.SF n	a	5	96506590		NM_053158.2	Mrpl1	intra	opp	56173	MRPL1
iv202	SIN.LV.SF n	a	5	105711854		NM_001033550.1	Lrrc8b	intra	same	55777	LRRC8B
iv205	SIN.LV.SF n	a	5	116150115		NM_007708.3	Cit	intra	same	43460	CIT
iv584	SIN.LV.SF n	a	5	123149633		NM_001005866.1	Fbxl10	intra	same	99517	FBXL10
iv137	SIN.LV.SF n	a	5	123303113		NM_029112.1	Morn3	intra	opp	4324	MORN3
iv102	SIN.LV.SF n	a	5	139491841		NM_024451.1	Unc84a	intra	same	37529	UNC84A
iv117	SIN.LV.SF n	a	6	11878770		NM_029404.2	Phf14	intra	opp	2889	PHF14
iv282	SIN.LV.SF n	a	6	43481800		NM_013861.3	Tpk1	intra	opp	113982	TPK1
iv161	SIN.LV.SF n	a	6	99369581		NM_053202.1	Foxp1	ups	same	-241100	FOXP1
iv219	SIN.LV.SF n	a	6	108117774		NM_145937.2	Sumf1	intra	opp	33583	SUMF1
iv87	SIN.LV.SF n	a	7	5742020		NM_001013012.1	Zfp787	intra	opp	17038	ZNF787
iv107	SIN.LV.SF n	a	7	88285100		NM_028238.6	Rab38	ups	same	-20365	RAB38
iv216	SIN.LV.SF n	a	8	32693394		NM_134161.2	fut10	intra	opp	40127	FUT10
iv90	SIN.LV.SF n	a	8	48082564		NM_001001184.1	Ccdc111	intra	opp	33453	CCDC111
iv241	SIN.LV.SF n	a	8	48310164		NM_008391.3	Irf2	intra	same	71572	IRF2
iv125	SIN.LV.SF n	a	8	82593636		NM_015751.2	Abce1	intra	opp	14176	ABCE1
iv65	SIN.LV.SF n	a	9	41607449		NM_011436.3	Sorl1	downs	same	267835	SORL1
iv89	SIN.LV.SF n	a	9	69199914		NM_145618.3	Narg2	intra	same	2752	NARG2
iv104	SIN.LV.SF n	a	9	115657576		ENSMUST00000084841	Gadl1	ups	opp	-100577	GADL1
iv79	SIN.LV.SF n	a	10	9473562		NM_001081344.1	Stxbp5	intra	same	117311	STXBP5
iv60	SIN.LV.SF n	a	10	41505155		ENSMUST00000099931.1	Sesn1	intra	same	6166	SESN1
iv244	SIN.LV.SF n	a	10	76741987		NM_001024837.1	Adarb1	intra	same	120002	ADARB1
iv55	SIN.LV.SF n	a	10	85445209		NM_177772.3	Bpil2	ups	same	-3560	FBXO7

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iv170	SIN.LV.SF n	a	10	1 07583981		NM_027892.1	Ppp1r12a	intra	opp	17471	PPP1R12A
iv25	SIN.LV.SF n	a	11	6 079733		NM_173748.3	Nudcd3	intra	same	20432	NUDCD3
iv62	SIN.LV.SF n	a	11	1 8851411		NM_010789.2	Meis1	intra	opp	67272	MEIS1
iv153	SIN.LV.SF n	a	11	97494097		NM_139311.2 Mllt6		intra sam	e	14595	MLLT6
iv239	SIN.LV.SF n	a	11	1 08434070		NM_029606.3	Ccdc46	intra	opp	192714	CCDC46
iv43	SIN.LV.SF n	a	12	3467197		NM_172421.3	Asxl2	intra	opp	40313	ASXL2
iv70	SIN.LV.SF n	a	12	9 1139492		NM_010050.2	Dio2	intra	same	4336	DIO2
iv82	SIN.LV.SF n	a	12	9 1762370		NM_181815.2	4930534B04Rik	intra	same	27565	C14orf145
iv179	SIN.LV.SF n	a	12	1 19560078		NM_177290.3	Itgb8	downs	opp	122300	ITGB8
iv248	SIN.LV.SF n	a	13	21175536		NM_009054.2	Trim27	ups	same	-11888	TRIM27
iv18	SIN.LV.SF n	a	13	2 9806255		NM_144536.2	Cdkal1	intra	opp	56798	CDKAL1
iv255	SIN.LV.SF n	a	13	3 0948688		NM_025588.2	Exoc2	intra	opp	32824	EXOC2
iv57	SIN.LV.SF n	a	13	1 18008088		NM_001081009.1	parp8	intra	same	136709	PARP8
iv122	SIN.LV.SF n	a	14	18209554		NM_001024706.1	EG432825	downs	same	183729	
iv169	SIN.LV.SF n	a	14	20378017		NM_017479.2	Myst4	intra	same	89611	MYST4
iv189	SIN.LV.SF n	a	14	4 9724683		NM_009632.2	Parp2	ups	same	-5214	PARP2
iv204	SIN.LV.SF n	a	14	8 5741880		NM_019670.1	Diap3	intra	opp	230981	DIAPH3
iv222	SIN.LV.SF n	a	14	103921395		NM_134077.4	Rbm26	downs	same	141611	RBM26
iv609	SIN.LV.SF n	a	14	1 22560518		NM_177393.4	Nalcn	intra	opp	201806	NALCN
iv601	SIN.LV.SF n	a	15	6 282443		NM_001008702.1	Dab2	intra	same	35379	DAB2
iv203	SIN.LV.SF n	a	15	9 531478		ENSMUST00000077670.4	ENSMUSG00000063249 in	tra	opp	14201	NP_653323.1
iv263	SIN.LV.SF n	a	15	3 7947473		NM_001081359.1	Edd1	intra	same	75969	EDD1
iv586	SIN.LV.SF n	a	15	57798207		NM_001081396.1	Wdr67	intra	opp	55925	WDR67
iv251	SIN.LV.SF n	a	16	1 7300470		NM_001001983.1	Pik4ca	intra	same	19407	PIK4CA
iv184	SIN.LV.SF n	a	16	9 0916149		ENSMUST00000023698.3	1810007M14Rik	intra	same	16874	C21orf66

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iv237	SIN.LV.SF n	a	17	2 5716668		ENSMUST00000075024	Rab11fip3	intra	same	79550	RAB11FIP3
iv181	SIN.LV.SF n	a	17	5 3094749		NM_020005.3	Pcaf	intra	opp	62505	PCAF
iv22	SIN.LV.SF n	a	17	58634361		NM_027001.1	2610034M16Rik	intra	opp	42345	
iv600	SIN.LV.SF n	a	17	5 9711119		NM_026497.2	Nudt12	downs	opp	1024387	NUTD12
iv198	SIN.LV.SF n	a	17	9 0279927		NM_020252.2	Nrxn1	intra	opp	721194	NRXN1
iv254	SIN.LV.SF n	a	18	4 6672752		NM_173394.2	Ticam2	downs	same	27111	TICAM2
iv45	SIN.LV.SF n	a	18	6 7979968		ENSMUST00000025425	Cep192	intra	opp	498	SEH1L
iv597	SIN.LV.SF n	a	18	7 5782820		NM_201354.2	Gm672	intra	opp	40241	KIAA0427
iv14	SIN.LV.SF n	a	18	8 9146210		NM_175542.3	Rttn	intra	same	40227	RTTN
iv127	SIN.LV.SF n	a	19	3 7035381		NM_001080706.1	Btaf1	intra	opp	44158	BTAF1
iv590	SIN.LV.SF n	a	Un_ran	21495		NM_011515.3	Sybl1	intra	same	17653	SYBL1
iv6	SIN.LV.SF n	a	X	3 8117738		NM_001033422.1	Thoc2	intra	opp	38790	THOC2
1665	SIN.LV.SF 3	11	8	6 4845285	301;311	NM_001081215.1	BC013672	intra	same	25054	NP_060101.2
1486	SIN.LV.SF 3	10	11	4 071240		NM_026175.4	Sf3a1	intra	same	10869	SF3A1
1774	SIN.LV.SF 3	09	10	1 8043031		NM_173390.3	Nhsl1	ups	opp	-54060	NHSL1
1625	SIN.LV.SF 3	06	11	1 15514640		NM_008163.3	Grb2	intra	same	10047	GRB2
1587	SIN.LV.SF 3	05	18	6 229335		NM_008448.2	Kif5b	intra	same	12163	KIF5B
1549	SIN.LV.SF 3	03	6	6 6199140		NM_019499.4	Mad2l1	ups	same	-265906	MAD2L1
1653	SIN.LV.SF 3	03	14	3 1011583		NM_016897.1	Timm23	intra	opp	19297	Q5SRD2
1804	SIN.LV.SF 3	03	15	4 759496		NM_016704.1	C6	downs	same	82284	C6
1553	SIN.LV.SF 3	02	Un_ran 1	257668	207;302	NM_001033326.2	Dhrsx	ups	same	-2347	DHRSX
1724	SIN.LV.SF 3	01	8	6 4845285	301;311	NM_001081215.1	BC013672	intra	same	25054	NP_060101.2
1722	SIN.LV.SF 3	01	9	2 2396737		NM_181316.3	Bbs9	intra	same	170620	BBS9
1720	SIN.LV.SF 3	01	12	7 4113629		NM_008612.2	Mnat1	intra	same	71074	MNAT1
1556	SIN.LV.SF 3	01	X 6	7492014		NM_019926.2	Mtm1	intra	same	16376	MTM1

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1574	SIN.LV.SF 2	99	7	7 9328334		NM_017462.2	Polg	intra	same	11452	POLG
1477	SIN.LV.SF 2	98	4	1 19964347		NM_013883.1	Scmh1	intra	opp	61303	SCMH1
1689	SIN.LV.SF 2	38	2	9 424882		NM_008091.2	Gata3	downs	opp	370747	GATA3
1358	SIN.LV.SF 2	38	16	3 7012585		NM_029977.1	Polq	intra	same	81560	POLQ
1357	SIN.LV.SF 2	38	16	6 4727705		NM_028059.2	Zfp654	intra	opp	818	ZNF654
1368	SIN.LV.SF 2	37	6	6 5017171		NM_007958.1	Smarcad1	intra	opp	44926	SMARCAD1
1360	SIN.LV.SF 2	36	5	5 4460202		NM_001081103.1	Stim2	downs	opp	173384	STIM2
1442	SIN.LV.SF 2	22	2	1 65450012		NM_010165.2	Eya2	intra	opp	103509	EYA2
1395	SIN.LV.SF 2	22	4	4 4825320		NM_177027.3	Zcchc7	intra	opp	47652	
1346	SIN.LV.SF 2	22	13	9 3614055		NM_173392.3	Zfyve16	intra	same	17498	ZFYVE16
1403	SIN.LV.SF 2	20	1	150790935		NM_008869.3 Pla2	g4a d	owns	same	932567	PLA2G4A
190	SIN.LV.SF 2	20	1	1 81262583		NM_027188.3	smyd3	intra	opp	92095	SMYD3
181	SIN.LV.SF 2	20	10	1 25404318		NM_177152.4	Lrig3	intra	opp	35093	LRIG3
192	SIN.LV.SF 2	20	11	2 0108654		NM_008996.3	Rab1	intra	opp	7049	RAB1A
1378	SIN.LV.SF 2	20	13	6 0883763		NM_178098.2	4930486L24Rik	ups	same	-9724	CTSL1
1621	SIN.LV.SF 2	19	8	67120989		NM_009390.2 Tll1		ups opp		-22804	TLL1
1493	SIN.LV.SF 2	19	9	1 3352799		ENSMUST00000034401	Maml2	ups	opp	-17588	MAML2
1370	SIN.LV.SF 2	15	1	8 2578759		NM_007734.2	Col4a3	intra	opp	112814	COL4A3
1373	SIN.LV.SF 2	15	1	1 89741621		NM_011935.2	Esrrg	intra	opp	42974	ESRRG
1372	SIN.LV.SF 2	15	2	9 6131055		NM_178725.4	Lrrc4c	ups	opp	-1137441	LRRC4C
1392	SIN.LV.SF 2	15	5	2 0364878		NM_172992.2	Phtf2	intra	same	28972	PHTF2
1369	SIN.LV.SF 2	15	14	8 6833990		NM_172605.2	Tdrd3	downs	opp	585561	TDRD3
450	SIN.LV.SF 2	10	6	1 22719243		NM_011401.3	Slc2a3	ups	opp	-11105	
1355	SIN.LV.SF 2	10	13	7 6594289		NM_001081352.1	AK129128	intra	same	29553	KIAA0372
1437	SIN.LV.SF 2	10	14	3 9187515		NM_177816.3	Sh2d4b	downs	opp	614163	SH2D4B

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1438	SIN.LV.SF 2	10	16	42792446		BC056446/NM_019778	Zbtb20	ups	opp	-34559	ZBTB20
1356	SIN.LV.SF 2	10	X 7	1898162		NM_175122.4	Rab39b	ups	same	-67238	RAB39B
1667	SIN.LV.SF 2	09	2	58018992		NM_139200.4	Pscdbp	ups	opp	-43484	PSCDBP
1668	SIN.LV.SF 2	09	10	110691113		NM_001003717.1	Osbpl8	intra	opp	122201	OSBPL8
1435	SIN.LV.SF 2	09	X	104012778		NM_025921.2	2610002M06Rik	intra	opp	6222	
1431	SIN.LV.SF 2	07	4	154373542		NM_008142.3	Gnb1	intra	opp	2292	GNB1
1389	SIN.LV.SF 2	07	5	33143972		NM_194340.1	C330019G07Rik	intra	opp	560	C22orf30
1448	SIN.LV.SF 2	07	5	52456831		NM_007839.2	Dhx15	intra	same	21936	DHX15
1447	SIN.LV.SF 2	07	10	30499589		NM_172495.3	Ncoa7	ups	opp	-7235	NCOA7
1352	SIN.LV.SF 2	07	10	79513262		NM_011492.3	Stk11	ups	opp	-6403	STK11
519	SIN.LV.SF 2	07	12	13421078		ENSMUST00000042953	BC072598	intra	same	72102	NP_056993.2
1449	SIN.LV.SF 2	07	14	120048561		NM_023579.4	Ranbp5	intra	opp	2187	RANBP5
1388	SIN.LV.SF 2	07	17	79791884		NM_019717.2	Arl6ip2	intra	same	12470	ARL6IP2
1350	SIN.LV.SF 2	07	17	92710388		NM_001025309.1	Pja2	ups	opp	-361788	PJA2
509	SIN.LV.SF 2	07	Un_ran 1	257668	207;302	NM_001033326.2	Dhrsx	ups	same	-2347	DHRSX
1383	SIN.LV.SF 2	06	1	68632148		NM_010154.1	Erbb4	intra	same	409119	ERBB4
1386	SIN.LV.SF 2	06	2	70528811		NM_172664.2	Tlk1	intra	opp	97508	TLK1
1385	SIN.LV.SF 2	06	2	141965497		NM_001013802.2	LOC433479	intra	opp	1878626	C20orf133
830	SIN.LV.SF 2	06	3	126811114		NM_001025438.1	camk2d	intra	same	222119	CAMK2D
808	SIN.LV.SF 2	06	4	77697427		NM_011211.2	Ptprd	ups	opp	-1631897	PTPRD
1384	SIN.LV.SF 2	06	8	11623901		NM_133971.1	Ankrd10	intra	same	11760	ANKRD10
834	SIN.LV.SF 2	06	12	15594742		NM_144551.5	trib2	downs	same	247593	TRIB2
823	SIN.LV.SF 2	06	17	62987589		ENSMUST00000024761	Fbxl17	intra	same	197173	FBXL17
863	SIN.LV.SF 2	06	19	10595581		NM_172302.2 5730453I16R	ik	intra sam	e	3270	CPSF7
1367	SIN.LV.SF 2	06	X 9	700632		NM_019634.2	Tspan7	intra	opp	58557	TSPAN7

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1398	SIN.LV.SF 1	98	13	6 3246179		NM_028079.2	2010111I01Rik	intra	opp	221622	C9orf3
1	SIN.LV.SF 1	98	13	8 5676081		NM_023243.4	CcnH	intra	same	13494	CCNH
55	SIN.LV.SF 1	98	16	7 0230655		NM_028803.3	Gbe1	intra	opp	33888	GBE1
1381	SIN.LV.SF 1	94	1	8 4711637		NM_133975.4	Trip12	intra	same	6692	TRIP12
1361	SIN.LV.SF 1	94	5	3 736255		NM_001003909	Ankib1	intra	same	72676	ANKIB1
1362	SIN.LV.SF 1	94	13	2 3126631		NM_134239.1	V1rh14	ups	opp	-4436	V1rh14
1348	SIN.LV.SF 1	90	6	6 6381652		NM_019499.4	Mad2l1	ups	same	-83394	MAD2L1
1347	SIN.LV.SF 1	90	X 7	1690124		NM_145956.3	Brcc3	intra	opp	20704	BRCC3
1380	SIN.LV.SF 1	87	15	5 0592163		NM_032000.1	Trps1	intra	opp	127952	TRPS1
1349	SIN.LV.SF 1	86	8	8 2597737		NM_015751.2	Abce1	intra	same	10075	ABCE1
28	SIN.LV.SF 1	74	7	106249746		NM_001001318.2	EG209380	ups	same	-15024	
43	SIN.LV.SF 1	74	9	5 9601618		ENSMUST00000085572	Myo9a	intra	same	23998	MYO9A
86	SIN.LV.SF 1	74	11	25023562		ENSMUST00000044347	4933427E13Rik	ups	same	-206395	
1428	SIN.LV.SF 1	74	11	1 10135208		NM_147219.2	Abca5	intra	opp	18598	ABCA5
310	SIN.LV.SF 1	74	18	6 7807634		NM_008977.2	Ptpn2	intra	opp	42312	PTPN2
1430	SIN.LV.SF 1	74	Un_ran 1	255607		NM_001033326.2	Dhsrx	ups	opp	-4408	DHRSX
317	SIN.LV.SF 1	74	X 1	61831793		NM_019773	rab9	ups	opp	-7998	RAB9A
ivR201	SINRV.PGK n	.a.	1	38720601		NM_010678.2	Aff3	intra	opp	1199	AFF3
ivR208	SINRV.PGK	n.a.	1	135698078			Atp2b4	ups	same	-747	ATP2B4
ivR135	SINRV.PGK n	.a.	1	193398483		NM_029766	Dtl	intra	opp	930	DTL
ivR279	SINRV.PGK n	.a.	2	6629496		NM_001110228,	Cugbp2	intra	opp	176546	CUGBP2
ivR294	SINRV.PGK n	.a.	2	18812842		NM_008845.4	Pip4k2a	intra	same	106906	PIP4K2A
ivR291	SINRV.PGK n	.a.	2	18883468		NM_008845.4	Pip4k2a	intra	opp	36280	PIP4K2A
ivR141	SINRV.PGK n	.a.	2	27333567		NM_080848.1	Wdr5	intra	opp	319797	WDR5
ivR74	SINRV.PGK n	.a.	2	28457034		NM_008114.2	Gfi1b	downs	same	20431	GFI1B

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ivR286	SINRV.PGK n	.a.	2	29919439		NM_023871.3	Set	intra	opp	7875	SET
ivR126	SINRV.PGK n	.a.	2	32349762		NM_194335.2	4933440H19Rik	downs	same	43786	C9orf90
ivR29	SINRV.PGK n	.a.	2	34818251		NM_009421,	Traf1	ups	same	-959	TRAF1
ivR104	SINRV.PGK n	.a.	2	38375816		NM_021606.2	Nek6	intra	opp	8597	NEK6
ivR126	SINRV.PGK n	.a.	2	45134386		NM_007396,	Acvr2a	ups	opp	-3535242	ACVR2A
ivR295	SINRV.PGK n	.a.	2	62295639		NM_008100,	Gcg	downs	opp	26071	GCG
ivR55	SINRV.PGK n	.a.	2	80787464		NM_027091.2	Nup35	downs	opp	308492	NUP35
ivR60	SINRV.PGK n	.a.	2	130952662		NM_028306.3	Hspa12b	ups	same	-485	HSPA12B
ivR16	SINRV.PGK n	.a.	2	144013221		NM_024225.4	Snx5	downs	same	83046	SNX5
ivR183	SINRV.PGK n	.a.	2	160526740		NM_009408.2	Top1	intra	same	55108	TOP1
ivR98	SINRV.PGK n	.a.	2	169979948		NM_001033299.2	Zfp217	ups	opp	-23228	ZNF217
ivR63	SINRV.PGK n	.a.	3	8676945		NM_010423.2	Hey1	ups	opp	-9907	HEY1
ivR259	SINRV.PGK n	.a.	3	65762696		NM_019937,	Ccnl1	ups	opp	-549	CCNL1
ivR127	SINRV.PGK n	.a.	3	95117151		NM_029789.1	Lass2	ups	opp	-2022	LASS2
ivR237	SINRV.PGK n	.a.	3	95755708		NM_023210.3	Anp32e	downs	opp	22495	ANP32E
ivR164	SINRV.PGK n	.a.	3	116136856		NM_001080818.1	Cdc14a	ups	opp	-9906	CDC14A
ivR9	SINRV.PGK n	.a.	3	137618459		NM_011932.2	Dapp1	intra	opp	26054	DAPP1
ivR166	SINRV.PGK n	.a.	3	137625846		NM_011932.2	Dapp1	intra	opp	18667	DAPP1
ivR246	SINRV.PGK n	.a.	3	155624637		NM_001039094.2 NM_177274.3	Negr1	ups	opp	-600120	NEGR1
ivR63	SINRV.PGK	n.a.	4	59449788			LOC634731	intra	same	1694	SUSD1
ivR239	SINRV.PGK n	.a.	4	59817199		NM_172468.2	Snx30	ups	opp	-1322	SNX30
ivR37	SINRV.PGK n	.a.	4	83618214		NM_001081012,	4930473A06Rik	downs	opp	446766	C9orf93
ivR281	SINRV.PGK n	.a.	4	107040197		NM_028355.3	Tmem48	ups	same	-191	TMEM48
ivR275	SINRV.PGK n	.a.	4	109079392		NM_153392.1	4922503N01Rik	ups	opp	-335	C1orf34
ivR110	SINRV.PGK n	.a.	4	132964535		NM_016981.2	Slc9a1	intra	opp	38849	SLC9A1

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ivR161	SINRV.PGK n	.a.	4	135585935		NM_013736.4	Tceb3	ups	same	-8371	TCEB3
ivR224	SINRV.PGK n	.a.	5	76214994		NM_010612.2	Kdr	downs	same	159459	KDR
ivR327	SINRV.PGK n	.a.	5	77564426		NM_175606.2	Hod	ups	same	-20278	HOP
ivR237	SINRV.PGK n	.a.	5	121093218		NM_013832.3	Rasal1	ups	same	-5612	RASAL1
ivR78	SINRV.PGK n	.a.	5	126003610		NM_030210.1	Aacs	downs	opp	47368	AACS
ivR108	SINRV.PGK n	.a.	5	136942203		NM_009986.3 NM_198602.2	Cutl1	intra	opp	101098	CUTL1
ivR290	SINRV.PGK n	.a.	5	148351081		NM_028291.3	Pan3	intra	opp	108617	PAN3
ivR179	SINRV.PGK n	.a.	6	72462181		XM_355785, XM_911211,	4933424C13Rik	downs	opp	8440	SH2D6
ivR271	SINRV.PGK n	.a.	6	122694044		NM_011401.3	Slc2a3	ups	same	-1507	SLC2A14
ivR289	SINRV.PGK n	.a.	6	123200381		NM_020001	Clec4n	downs	same	20490	CLEC4C
ivR298	SINRV.PGK n	.a.	6	127100599		NM_009829.3	Ccnd2	intra	opp	467	CCND2
ivR132	SINRV.PGK	n.a.	6	129165351		NM_053109.2	Clec2d	downs	opp	34712	
ivR33	SINRV.PGK n	.a.	6	140646672		NM_001005605.1 NM_009637.3 NM_178803.2	Aebp2	downs	opp	74463	AEBP2
ivR153	SINRV.PGK n	.a.	7	4690746		NM_146177.1	Suv420h2	ups	same	-982	SUV420H2
ivR287	SINRV.PGK n	.a.	7	20190305		NM_016680,	Sfrs16	ups	opp	-488	SFRS16
ivR228	SINRV.PGK n	.a.	7	26470994		NM_172148,	B9d2	intra	opp	4818	B9D2
ivR96	SINRV.PGK n	.a.	7	52345908		NM_026555.1	Rcn3	intra	opp	1675	RCN3
ivR282	SINRV.PGK n	.a.	7	87721138		NM_173863.2	Crtc3	downs	same	112625	CRTC3
ivR263	SINRV.PGK n	.a.	7	87792421		NM_173863.2	Crtc3	intra	opp	41342	CRTC3
ivR69	SINRV.PGK n	.a.	7	104356148		NM_010248.1	Gab2	intra	same	125888	GAB2
ivR19	SINRV.PGK n	.a.	7	106459560		NM_001043355.2 NM_001048167.1 NM_010837.3	Mtap6	intra	same	42705	MAP6
ivR4	SINRV.PGK n	.a.	7	124548714		NM_175645.3	Xylt1	intra	opp	24222	XYLT1

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ivR96	SINRV.PGK n	.a.	7	124576672		NM_175645.3	Xylt1	intra	opp	52180	XYLT1
ivR274	SINRV.PGK	n.a.	7	149538269		NM_177265.4	6330512M04Rik	intra	same	19895	
ivR91	SINRV.PGK n	.a.	8	26736508		NM_001001735.1 NM_001081269.1	Whsc1 l1	intra	opp	23731	WHSC1L1
ivR173	SINRV.PGK n	.a.	8	89594486		NM_026533,	Rps13	downs	opp	33883162	RPS13
ivR172	SINRV.PGK n	.a.	8	112132958		NM_020046.3	Dhodh	ups	opp	-385	DHODH
ivR247	SINRV.PGK	n.a.	8	124637542		NM_016812.3	Banp I	downs	same	163109	BANP
ivR301	SINRV.PGK n	.a.	9	54430875		NM_029573.2	Idh3a	ups	opp	-3442	IDH3A
ivR288	SINRV.PGK n	.a.	9	75274903		NM_001039522	Leo1	ups	opp	-14428	LEO1
ivR87	SINRV.PGK	n.a.	9	114687929		NM_133978,	Cmtm7	intra	opp	3018	
ivR45	SINRV.PGK n	.a.	9	123858053		NM_009912.4	Ccr1	downs	same	25472	CCR1
ivR86	SINRV.PGK n	.a.	10	18611639		NM_022032.4	Perp	downs	same	46763	PERP
ivR129	SINRV.PGK n	.a.	10	67711896		NM_023598,	arid5b	intra	same	29578	ARID5B
ivR2	SINRV.PGK n	.a.	10	80598159		NM_010731.3	Zbtb7a	ups	opp	-856	ZBTB7A
ivR163	SINRV.PGK n	.a.	10	110557248		NM_001003717.1 NM_175489.3	Osbpl8	ups	same	-44609	OSBPL8
ivR21	SINRV.PGK	n.a.	11	11446942			4930512M02Rik	downs	opp	80899	
ivR59	SINRV.PGK n	.a.	11	22891519		NM_009837.1	Cct4	intra	opp	927	CCT4
ivR302	SINRV.PGK n	.a.	11	49014517		NM_001024846, NM_009562, Zf	p62	ups	opp	-2484	ZFP62
ivR11	SINRV.PGK n	.a.	11	53469058		NM_009012.2	Rad50	intra	same	51763	RAD50
ivR119	SINRV.PGK n	.a.	11	65619651		NM_026107.2	Zfp535	ups	same	-1094	ZNF18
ivR133	SINRV.PGK n	.a.	11	74539018		NM_013625,	Pafah1b1	ups	same	-846	PAFAH1B1
ivR297	SINRV.PGK n	.a.	11	80598389		NM_177390.3	Myo1d	ups	opp	-4862	MYO1D
ivR258	SINRV.PGK	n.a.	11	87565786			mmu-mir-142	ups	same	-4580	
ivR131	SINRV.PGK	n.a.	11	87567380			mmu-mir-142	ups	opp	-2986	
ivR172	SINRV.PGK n	.a.	11	99004882		NM_007719.2	Ccr7	downs	same	11509	CCR7

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ivR243	SINRV.PGK n	.a.	11	106639774		NM_015810,	Polg2	intra	opp	982	POLG2
ivR270	SINRV.PGK n	.a.	11	115574978		NM_008163.3	Grb2	ups	same	-5067	GRB2
ivR309	SINRV.PGK n	.a.	11	117211272		NM_017380,	Sept9	intra	opp	18244	SEPT9
ivR115	SINRV.PGK n	.a.	11	120410346		NM_026814.3	Dysfip1	downs	same	2100	DYSFIP1
ivR223	SINRV.PGK	n.a.	11	120410346		NM_001033231.2	BC003940	intra	same	695	
ivR213	SINRV.PGK n	.a.	12	85546299		XM_001473233, XM_001477247, C1	3003 9O16Rik	intra	same	13532	C14orf43
ivR299	SINRV.PGK n	.a.	12	88670924		NM_011479.3	Sptlc2	intra	same	58256	SPTLC2
ivR203	SINRV.PGK n	.a.	12	111936626		NM_010480.5	Hsp90aa1	ups	same	-2021	Q58FG1
ivR18	SINRV.PGK n	.a.	12	117521903		NM_028731.5	D12Ertd551e	intra	opp	2209	FAM62B
ivR136	SINRV.PGK n	.a.	13	4255917		NM_001013785.2	Akr1c19	downs	opp	22932	AKR1C1
ivR195	SINRV.PGK	n.a.	13	17004644		NM_138654.2	5033411D12Rik	intra	same	781929	Q4KMW4
ivR145	SINRV.PGK	n.a.	13	34877638			AK007247	downs	same	50919	FAM50B
ivR293	SINRV.PGK n	.a.	13	49284511		NM_013610.2	Ninj1	intra	opp	1596	NINJ1
ivR183	SINRV.PGK n	.a.	13	96457105		NM_027711.1	Iqgap2	intra	opp	204772	IQGAP2
ivR135	SINRV.PGK n	.a.	13	109240926		NM_178683.4	Depdc1b	downs	opp	134396	DEPDC1B
ivR261	SINRV.PGK n	.a.	13	110611561		NM_011056,	Pde4d	intra	opp	1167191	PDE4D
ivR32	SINRV.PGK n	.a.	14	15505837		NM_001033270.2	Slc4a7	ups	opp	-29701	SLC4A7
ivR250	SINRV.PGK n	.a.	14	22419139		NM_017479,	Myst4	intra	opp	100064	MYST4
ivR280	SINRV.PGK n	.a.	14	26283507		NM_183208.2	Zmiz1	intra	same	4730	ZMIZ1
ivR273	SINRV.PGK n	.a.	14	26283507		NM_183208.2	Zmiz1	intra	same	4730	ZMIZ1
ivR42	SINRV.PGK n	.a.	14	37689255		NM_027045.1 NM_028407.3	Gcap14	intra	opp	92695	KIAA1128
ivR128	SINRV.PGK n	.a.	14	122790973		NM_029556.2	Clybl	intra	same	210031	CLYBL
ivR196	SINRV.PGK n	.a.	15	3946506		NM_145930.2	AW549877	ups	opp	-754	NP_787117.3
ivR23	SINRV.PGK	n.a.	15	73697174		NM_001033365.2	Gm628	ups	opp	-27073	

Seq ID	**Vector**	**Mouse ID**	**Chr.**	**Chr. Position**	**Identical**	**Transcript ID**	**Symbol**	**Int. type**	**ORI**	**Dist to tss**	**Human Ortholog**
ivR301	SINRV.PGK n	.a.	15	80430325		NM_010815,	Grap2	ups	same	-23587	GRAP2
ivR306	SINRV.PGK n	.a.	15	96172087		NM_175251.2	Arid2	ups	same	-15118	ARID2
ivR142	SINRV.PGK	n.a.	15	96485041			Slc38a1	ups	opp	-11697	SLC38A1
ivR300	SINRV.PGK n	.a.	16	17253220		NM_178922.3	Hic2	intra	same	19541	HIC2
ivR178	SINRV.PGK n	.a.	16	17761896		NM_145479.4	Klhl22	intra	opp	2183	KLHL22
ivR308	SINRV.PGK n	.a.	16	33748838		NM_172934.4 NM_175256.5	Heg1	downs	opp	64287	
ivR80	SINRV.PGK n	.a.	16	33752526		NM_172934.4 NM_175256.5	Heg1	downs	same	67975	
ivR283	SINRV.PGK n	.a.	16	49770118		NM_028680.3	Ift57	downs	opp	70712	IFT57
ivR9	SINRV.PGK	n.a.	16	93193516			mmu-mir-802	ups	same	-176449	
ivR312	SINRV.PGK n	.a.	17	3492772		NM_011878.1	Tiam2	intra	same	95566	TIAM2
ivR305	SINRV.PGK n	.a.	17	5238429		NM_001085355.1	Arid1b	intra	opp	243356	ARID1B
ivR142	SINRV.PGK n	.a.	17	17764219		NM_172827.3	Lnpep	ups	same	-2766	LNPEP
ivR165	SINRV.PGK n	.a.	17	27926549		NM_001033279.2 NM_001044719.1	D17Wsu92e	intra	opp	30938	C6orf106
ivR1	SINRV.PGK n	.a.	17	34257753		NM_001025387.2 NM_010238.3	Brd2	ups	same	-425	BRD2
ivR178	SINRV.PGK n	.a.	17	35162314		NM_138582.1	D17H6S56E-3	intra	same	8791	C6orf27
ivR304	SINRV.PGK n	.a.	17	52303446		NM_009122.1	Satb1	ups	opp	-331488	SATB1
ivR285	SINRV.PGK n	.a.	17	64205265		NM_001037997.1 NM_008000.1	Fert2	ups	opp	-40107	FER
ivR187	SINRV.PGK n	.a.	17	79778624		NM_026514.2	Cdc42ep3	ups	same	-24193	CDC42EP3
ivR159	SINRV.PGK n	.a.	17	84358269		NM_025325,	Haao	ups	opp	-112139	HAAO
ivR260	SINRV.PGK n	.a.	17	84547795		NM_001001806.2	Zfp36l2	downs	same	39492	ZFP36L2
ivR2	SINRV.PGK n	.a.	17	85245494		NM_028233.2	Lrpprc	ups	opp	-55368	LRPPRC
ivR12	SINRV.PGK n	.a.	17	86584585		NM_011104.1	Prkce	intra	same	16656	PRKCE
ivR303	SINRV.PGK n	.a.	18	38159973		NM_139206.2	Centd3	ups	same	-2745	CENTD3

Seq ID	Vector	Mouse ID	Chr.	Chr. Position	Identical	Transcript ID	Symbol	Int. type	ORI	Dist to tss	Human Ortholog
ivR40	SINRV.PGK n	.a.	18	53310654		NM_026386.1	Snx2	ups	same	-25364	SNX2
ivR278	SINRV.PGK n	.a.	18	84398933		XM_976217, XM_991500,	Zfp407	intra	opp	329382	ZNF407
ivR130	SINRV.PGK n	.a.	19	5729833		NM_023166, NM_181452,	Mtvr2	ups	opp	-200	FAM89B
ivR28	SINRV.PGK n	.a.	19	8850120		NM_146092,	Taf6l	intra	same	10633	TAF6L
ivR26	SINRV.PGK n	.a.	19	10631440		NM_026798.1	2810441K11Rik	ups	opp	-712	NP_057583.2
ivR313	SINRV.PGK n	.a.	19	46529287		NM_001025391.1 NM_015752.2	Sufu	intra	opp	57880	SUFU
ivR51	SINRV.PGK n	.a.	19	47062594		NM_029810.3	Nt5c2	ups	same	-25796	NT5C2
ivR42	SINRV.PGK n	.a.	X	131117678		NM_013482.1	Btk	intra	same	1	BTK
ivR169	SINRV.PGK n	.a.	X	156084656		NM_021389.4	Sh3kbp1	ups	same	-61876	SH3KBP1
ivR297	SINRV.PGK n	.a.	X	158363355		NM_001081052.1	Nhs	intra	same	234367	NHS
RAD02	SINRV.PGK	114	4	145686197		NM_001085522.2	LOC433791	down	same	62812	
RAC11	SINRV.PGK 1	14	X	6889639		NM_016691.2	Clcn5	up	opp	-123827	CLCN5
RCA06	SINRV.PGK 1	13	17	84514402		NM_001001806.2	Zfp36l2	down	opp	72885	ZFP36L2
RAF06	SINRV.PGK 1	12	3	14612200		NM_001099674.1	1810022K09Rik	up	opp	-944	C8orf59
RAF09	SINRV.PGK 1	12	8	23924275		NM_001122820.1	Ap3m2	up	opp	-8149	AP3M2
RBE12	SINRV.PGK	110	5	24745489		NM_144908.3 G	alnt11 in		same	16779	GALNT11
RBF07	SINRV.PGK 1	10	11	88829612		NM_016706.2	Coil	up	same	-5636	COIL
RBA07	SINRV.PGK 1	09	1	184054264		NM_012058.3	srp9	up	same	-603	SRP9
RAH10	SINRV.PGK 1	09	6	22432066		NM_138587.4	D6Wsu176e	up	same	-125985	FAM3C
RAH06	SINRV.PGK 1	09	8	114175914		NM_001037665.2	Zfp1	in	same	8572	ZFP1
RBG02	SINRV.PGK	108	5	123585364		NM_175092.3	Rhof	up	opp	-2726	RHOF
RBH09	SINRV.PGK 1	08	8	122953983		NM_198671.1	Gse1	up	same	-58782	KIAA0182
RBG10	SINRV.PGK 1	08	12	53762737		NM_198111.2	akap6	up	same	-37632	AKAP6
RBG11	SINRV.PGK 1	08	13	94542670		NM_009712.3	Arsb	in	opp	1037	ARSB
RBG08	SINRV.PGK 1	08	17	34777246		NM_019873.2	Fkbpl	up	same	-4581	FKBPL

Seq ID	**Vector**	**Mouse ID**	**Chr.**	**Chr. Position**	**Identical**	**Transcript ID**	**Symbol**	**Int. type**	**ORI**	**Dist to tss**	**Human Ortholog**
RAA01	SINRV.PGK	105	10	117298507		NM_024457.2	Rap1b	up	same	-15477	RAP1B
RAA06	SINRV.PGK 1	05	11	103124521		NM_016896.3	Map3k14	in	same	4194	MAP3K14
RAE02	SINRV.PGK 1	04	4	57050588		NM_019427.2	Epb4.1l4b	down	same	105440	EPB41L4B
RAE06	SINRV.PGK	104	11	53163566		NM_033565.1	Aff4	up	opp	-768	AFF4
RAE08	SINRV.PGK 1	04	15	103125764		NM_019817.1	copz1	in	same	22416	COPZ1
R15D07	SINRV.PGK 1	02	7	4604522		NM_172894.2	Saps1	in	opp	6030	SAPS1
R15A06	SINRV.PGK 1	02	7	29567357		NM_022432.4	Sirt2	in	same	15587	SIRT2
R15A12	SINRV.PGK 1	02	15	63491486		NM_177912.3	AI987692 down		opp	185245	MLZE
R15A08	SINRV.PGK 1	02	17	27958660		NM_001033279.2 NM_001044719.1	D17Wsu92e	up	same	-1173	C6orf106
R15D08	SINRV.PGK 1	02	19	46530764		NM_001025391.1 NM_015752.2	Sufu	in	same	59357	SUFU
RAB08	SINRV.PGK 1	01	2	25390438		NM_009422.2	Traf2	in	same	11976	TRAF2
RAB03	SINRV.PGK 1	01	17	84385935		NM_025325.2	Haao	up	opp	-139805	HAAO
R15F09	SINRV.PGK 1	00	3	65294058		NM_178892.5	Tparp	up	opp	-38310	TIPARP
R15D01	SINRV.PGK 1	00	3	70029586		NM_001018031.1	Gm414	down	same	218052	NP_0010739 09.1
R15F03	SINRV.PGK	100	11	58717912		NM_011758.2	Zfp39	up	opp	-185	
R15G04	SINRV.PGK 1	00	16	32522832		NM_199309.2	Zdhhc19	down	same	26466	ZDHHC19
RCC12	SINRV.PGK	99	1	52636434		NM_133829.2	2210010L05Rik	down	same	147728	NP_060164.3
RCD05	SINRV.PGK 9	9	13	41581251		NM_001111324.1	Nedd9	in	same	1438	NEDD9
RBB07	SINRV.PGK 9	8	2	154252374		NM_009823.1	Cbfa2t2	up	same	-9845	CBFA2T2
RCE12	SINRV.PGK 9	6	2	32389041		NM_153560.4	C230093N12Rik	up	opp	-1837	FAM102A
RCF04	SINRV.PGK 9	6	19	17394305		NM_173442.2	Gcnt1	down	same	36802	GCNT1
RCC04	SINRV.PGK	93	3	96048238		NM_013549.1	Hist2h2aa1	in	opp	1800	
RCB08	SINRV.PGK 9	3	7	31001025		NM_025548.3	Tbcb	down	opp	16023	TBCB
RCB11	SINRV.PGK 9	3	10	76677988		NM_030262.3	Pofut2	up	same	-44056	POFUT2

Seq ID	Vector	Mouse ID	Chr.	Chr. Position	Identical	Transcript ID	Symbol	Int. type	ORI	Dist to tss	Human Ortholog
R15H08	SINRV.PGK 9	2	15	76531370		NM_027122.3	Mfsd3	up	same	-601	MFSD3
R15E07	SINRV.PGK 9	1	1	92955134		NM_008515.3	Lrrfip1	in	opp	5113	LRRFIP1
R15E12	SINRV.PGK 9	1	10	7561098		NM_172785.2	Zc3h12d	in	opp	8831	ZC3H12D
RBD10	SINRV.PGK 9	0	3	87943617		NM_133665.3	mef2d	up	same	-2699	MEF2D
RBD02	SINRV.PGK	90	7	16586555		NM_001081418.1	Gltscr1	up	opp	-1711	GLTSCR1
RBE06	SINRV.PGK 9	0	9	70687687		NM_008280.2	Lipc	in	opp	94928	LIPC
RBE01	SINRV.PGK	90	11	87994013		NM_198013.2	Cuedc1	in	opp	81203	CUEDC1
RBD08	SINRV.PGK	90	17	32249962		NM_008716.2	Notch3	down	same	53835	NOTCH3
R16E02	SINRV.PGK 8	8	5	53881718		NM_001080927.1 NM_001080928.1 NM_009035.4	Rbpsuh	up	same	-100094	RBPJ
RCE08	SINRV.PGK 8	8	7	121210066		NM_025846.2	Rras2	in	same	51229	RRAS2
RCE04	SINRV.PGK	88	15	60669286		NM_001081067.1	A1bg	down	opp	83539	A1BG
RCH11	SINRV.PGK	87	9	107470437		NM_010489.2	Hyal2	up	same	-1056	HYAL2
R16B09	SINRV.PGK 3	0	4	131771664		NM_145393.3	Ythdf2	up	opp	-3493	YTHDF2
R16A02	SINRV.PGK 30		7	31784462		NM_175240.3	Tmem162	down	same	22401	TMEM162
R16A08	SINRV.PGK 3	0	13	55855992		NM_028281.1	Pcbd2	in	opp	27264	PCBD2

Supplementary Table 2. Genomic position of LV.SF.LTR , SIN.LV.SF and SIN.RV.PGK integrations found *in vitro* and in tumors and nearest targeted gene. Sequences obtained from plasmid libraries of cloned LAM PCR products were analyzed for the presence of vector LTR sequences, linker cassette and internal or terminal restriction sites for Tsp509I or HpyCH4IV used in the LAM PCR procedure. Sequences containing the LV LTR end (either full-length or up to 3 nt before the end) and the linker cassette were considered genuine LAM PCR products of provirus/genome junctions or control bands. Sequences contained between LTR sequence and linker cassette were discarded if containing vector or plasmid sequences or if contained a restriction site for the same enzyme used in the LAM PCR in internal position. Linker and vector sequences were subsequently trimmed and the remaining sequence aligned to each other to generate a non redundant dataset of sequences (column Seq ID). Sequences of length >18 bp were mapped on the mouse genome (version Feb 2006) by BLAT analysis at http://genome.ucsc.edu/cgi-bin/hgBlat.

Column Seq ID: ID of integrations retrieved from lin- cells transduced *in vitro* (seq id with the prefix: iv) or tumor infiltrated mouse tissues.
Vector: vector used.
Mouse ID: mouse identifier number.
Chr.: chromosome number.
Chr. Position: LTR position on chromosome in nucleotides.
Identical: IDs of mice sharing identical integration sites are indicated. We excluded sample cross-contamination as the same results were obtained sequencing LAM-PCR products obtained from different tissues including those of secondary transplanted mice. Two pairs of LV.SF.LTR mice transplanted with the same bulk population shared a common set of integrations (5 in one pair of mice and 2 in the other pair). Similarly, two pairs of SIN.LV.SF mice also shared a common integration.
Transcript ID: Mouse RefSeq or ENSEMBL transcripts of genes targeted or near vector integrations are indicated. Genomic coordinates for the indicated transcripts were used for the calculation of distance distribution of the integration around the TSS and the entire gene length.
Symbol: gene symbol targeted or nearest an integration site.
Int Type: intra: intragenic vector integrations between the TSS and cDNA end; ups: upstream the TSS; downs: downstream the gene end.
ORI: orientation of LTR with respect to the direction of transcription of the targeted gene, opposite (opp) and the same are indicated.
Dist. to TSS: distance between TSS and LTR end were calculated based on the genomic coordinates of the targeted transcript and the vector integration site. Distance of integration upstream the TSS is negative whereas the integrations inside and downstream genes are positive.
Human Ortholog: gene symbol of the putative human ortholog genes of the mouse gene datasets were retrieved by searching the biomart human mouse homology databases (http://www.ensembl.org/biomart/martview).

Supplementary Table 3a

DB	CIS Type	LV.SF.LTR S		IN.LV.SF		SIN.RV.PGK	
		in vitro n=70	Tumors n=93	*in vitro* n=90	Tumors n=78	*in vitro* n=135	Tumors n=54
RTCGD	R CIS	**6**	**8**	2 2		**20**	**8**
	SB CIS	**5**	**3**	1 1		1	0
	All CIS	**10**	**11**	3 3		**20**	**8**

Supplementary Table 3b

Dataset S	ystem	Gene Class	n	p Value	Fold
LV.SF.LTR *in vitro*	BP	phosphate metabolic process	11	1.70E-03	4.0
		phosphorus metabolic process	11	2.30E-02	6.4
		phosphorylation 10		1.40E-03	3.3
		protein amino acid phosphorylation	9	2.40E-03	3.7
	MF	phosphotransferase activity, alcohol group as acceptor	8	1.40E-03	3.3
		protein kinase activity	7	1.30E-02	3.1
LV.SF.LTR Tumors	BP	B cell differentiation	3	2.90E-02	4.2
		cell cycle phase	5	3.30E-02	3.3
		mitotic cell cycle	5	1.10E-03	4.2
		regulation of apoptosis	6	5.00E-02	3.0
SIN.LV.SF *in vitro*	BP	chromatin modification	4	2.40E-02	4.5
SIN.LV.SF Tumors	BP	dephosphorylation 4		2.40E-02	4.5
		intracellular protein transport 6		3.60E-02	3.2
		protein amino acid dephosphorylation	4	1.50E-03	3.6
	MF	helicase activity	4	4.50E-02	4.9
		hydrolase activity, acting on acid anhydrides	9	3.90E-02	5.3
		hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	9 1.50	E-02	7.7
		nucleoside-triphosphatase activity	9	1.60E-03	4.0
		phosphoprotein phosphatase activity	4	1.80E-02	7.1
		protein transporter activity	6	1.50E-02	15.8
		protein tyrosine phosphatase activity	4	2.60E-02	4.4
		pyrophosphatase activity	9	4.40E-02	3.7
SIN.RV.PGK *in vitro*	BP	chromatin modification	5	3.60E-02	3.3
		DNA packaging	6	2.00E-02	4.7
		establishment and/or maintenance of chromatin architecture	6 2.60	E-02	3.4
	MF	GTPase activator activity	5	4.00E-02	3.0
		phosphoinositide binding	5	5.80E-03	10.8
SIN.RV.PGK Tumors	BP	establishment of protein localization	6	3.50E-02	3.2
		intracellular protein transport 5		2.00E-02	6.8
		macromolecule localization	6	3.60E-04	9.7
		negative regulation of cellular metabolic process	4	1.50E-03	4.0
		protein localization	6	2.10E-02	3.2

Supplementary Table 3c

DB	Gene Class	LV.SF.LTR SIN		.LV.SF		SIN.RV.PGK	
		in vitro n=70	Tumors n=93	in vitro n=90	Tumors n=78	in vitro n=135	Tumors n=54
Gene Ontology	BP:protein amino acid phosphorylation	9	7	5	5	6	1
	MF:protein kinase activity	7	5	5	6	7	1
	BP:B cell differentiation	0	3	1	0	0	1
	BP:cell cycle phase	1	5	2	3	3	2
	BP:mitotic cell cycle	2	5	2	3	2	2
	BP:regulation of apoptosis	2	7	1	1	4	1
	BP:chromatin modification	0	4	4	3	5	1
	BP:dephosphorylation 1		2	1	4	1	0
	BP:intracellular protein transport	3	6	3	6	4	5
	MF:helicase activity	1	2	3	4	0	0
	MF:phosphoprotein phosphatase activity	1	2	2	4	1	0
	MF:protein transporter activity	1	2	1	6	1	2
	MF:pyrophosphatase activity	1	5	6	9	0	1
	MF:GTPase activator activity	0	2	1	0	5	0
	MF:phosphoinositide binding	0	1	0	1	5	1

***Supplementary Table 3**:* RTCGD CIS and GO DAVID-EASE overrepresentation analysis.
a) Number of retroviral (R) and Sleeping Beauty transposon (SB) and total (All) RTCGD CIS genes targeted in *in vitro* and in tumors by each vector used, as indicated. (n) indicates the total number of integrations in *in vitro* and in tumors datasets. Overall, we compared 520 unique integration sites obtained from 3 different vectors. Numbers significantly higher than the expected frequency ($p<0.05$; χ^2) are highlighted and bold (all significant p values were <0.001). The expected random frequency of each CIS gene class in the mouse genome was: for retroviral CIS 492/25613 mouse genes, (1.9%); for SB CIS 53/25613 (0.2%); for all CIS 535 CIS/25613 (2%).
b) GO DAVID-EASE overrepresentation analysis of gene classes contained in the Biological Process (BP) and Molecular Function (MF) systems (System) for the LV.SF.LTR, SIN.LV.SF and SIN.RV.PGK in *in vitro* and in tumors datasets. Gene Class: overrepresented gene class; n: number of matching genes in the dataset; p Value: Significance; Fold: fold increase with respect to the expected random frequency.
c) Number of occurrences in all datasets for each GO gene class overrepresented in at least one dataset.

Supplementary Table 4

Vector	primary DNA number	Source	Gene Symbol	Entrez ID	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
IV- LV.SF.LTR		IV	2010106G01Rik	66552																													
IV- LV.SF.LTR		IV	2410014A08Rik	109154				x																									
IV- LV.SF.LTR		IV	3110056O003Rik	73218	2		x																										
IV- LV.SF.LTR		IV	Acvr2a	11480								x														x	x						
IV- LV.SF.LTR		IV	Agk	69923																x													
IV- LV.SF.LTR		IV	Arrdc4	66412																													
IV- LV.SF.LTR		IV	Atp2b1	67972																												x	
IV- LV.SF.LTR		IV	AU020772	277939																													
IV- LV.SF.LTR		IV	AW112010	107350																													
IV- LV.SF.LTR		IV	Btbd9	224671																													
IV- LV.SF.LTR		IV	Cacnb2	12296																													
IV- LV.SF.LTR		IV	Cacnb2	12296																													
IV- LV.SF.LTR		IV	Cadps2	320405		3	x																										
IV- LV.SF.LTR		IV	Ccnt1	12455						x	x	x	x							x													
IV- LV.SF.LTR		IV	Col28a1	213945		2	x																										
IV- LV.SF.LTR		IV	Copg2	54160				x																				x					
IV- LV.SF.LTR		IV	Creb5	231991																													
IV- LV.SF.LTR		IV	Cyfip1	20430																													
IV- LV.SF.LTR		IV	D16Ertd472e	67102																													
IV- LV.SF.LTR		IV	D5Ertd585e	71782																													
IV- LV.SF.LTR		IV	D8Ertd82e	244418								x														x							

Vector	**primary DNA number**	**Source**	**Gene Symbol**	**Entrez ID**	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
IV- LV.SF.LTR		IV	Eif5	217869																													
IV- LV.SF.LTR		IV	Foxg1	15228		2	x			x	x		x									x											
IV- LV.SF.LTR		IV	Gab2	14389																													
IV- LV.SF.LTR		IV	Heatr1	217995																													
IV- LV.SF.LTR		IV	Ibtk	108837								x																					
IV- LV.SF.LTR		IV	Ifitm1	68713																													
IV- LV.SF.LTR		IV	Ift57	73916										x	x																		
IV- LV.SF.LTR		IV	Kif13a	16553																													
IV- LV.SF.LTR		IV	Lphn3	319387																													
IV- LV.SF.LTR		IV	Lsm4	50783																													
IV- LV.SF.LTR		IV	Nrg3	18183																													
IV- LV.SF.LTR		IV	Nrxn3	18191																													
IV- LV.SF.LTR		IV	Nsmce2	68501																													
IV- LV.SF.LTR		IV	Nt5c3	107569																													
IV- LV.SF.LTR		IV	Olfr693	258445																													
IV- LV.SF.LTR		IV	Opcml	330908																													
IV- LV.SF.LTR		IV	Pam	18484																													
IV- LV.SF.LTR		IV	Pcdh15	11994																													
IV- LV.SF.LTR		IV	Pds5a	71521							x		x									x	x										
IV- LV.SF.LTR		IV	Pftk1	18647								x														x	x						
IV- LV.SF.LTR		IV	Pigp	56176																													
IV- LV.SF.LTR		IV	Plag1	56711	8		x																										

Vector	**primary DNA number**	**Source**	**Gene Symbol**	**Entrez ID**	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
IV- LV.SF.LTR		IV	Plod2	26432																													
IV- LV.SF.LTR		IV	Pon2	330260																													
IV- LV.SF.LTR		IV	Prdm5	70779																													
IV- LV.SF.LTR		IV	Prkcq	18761								x														x	x						
IV- LV.SF.LTR		IV	Rab36	76877																													
IV- LV.SF.LTR		IV	Rb1cc1	12421						x	x	x	x	x	x																		
IV- LV.SF.LTR		IV	Riok2	67045																						x	x						
IV- LV.SF.LTR		IV	Rnf12	19820																													
IV- LV.SF.LTR		IV	Runx2	12393	4	2	x											x															
IV- LV.SF.LTR		IV	Scyl1bp1	98376																													
IV- LV.SF.LTR		IV	Sh3rf2	269016																													
IV- LV.SF.LTR		IV	Slc9a9	331004	3		x																										
IV- LV.SF.LTR		IV	Slk	20874								x														x	x						
IV- LV.SF.LTR		IV	Smarca2	67155																					x								
IV- LV.SF.LTR		IV	Ssfa2	70599																													
IV- LV.SF.LTR		IV	Stk38l	232533	2		x	x				x														x	x						
IV- LV.SF.LTR		IV	Thada	240174	2		x																										
IV- LV.SF.LTR		IV	Tmem68	72098																													
IV- LV.SF.LTR		IV	Tnik	665113																													
IV- LV.SF.LTR		IV	Tns3	319939																				x									x
IV- LV.SF.LTR		IV	Tpk1	29807		2	x																										
IV- LV.SF.LTR		IV	Usp4	22258																													

Vector	**primary DNA number**	**Source**	**Gene Symbol**	**Entrez ID**	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
IV- LV.SF.LTR		IV	Usp47	74996																													
IV- LV.SF.LTR		IV	Wdr42a	98193																													
IV- LV.SF.LTR		IV	Zfp28	22690																													
IV- LV.SF.LTR		IV	Zfp617	170938																													
IV- LV.SF.LTR		IV	Zfp710	209225																													
IV- SIN. LV.SF		IV	1810007M14Rik	67367																													
IV- SIN. LV.SF		IV	2210010L05Rik	98682																													
IV- SIN. LV.SF		IV	2610034M16Rik	69239				x																									
IV- SIN. LV.SF		IV	4930534B04Rik	75216																													
IV- SIN. LV.SF		IV	Abce1	24015																												x	
IV- SIN. LV.SF		IV	Adarb1	110532																													
IV- SIN. LV.SF		IV	Armc1	74252																													
IV- SIN. LV.SF		IV	Ash1l	192195					x																								
IV- SIN. LV.SF		IV	Asxl2	75302																													
IV- SIN. LV.SF		IV	Atp6v1h	108664																												x	
IV- SIN. LV.SF		IV	Bcl2	12043										x	x																		
IV- SIN. LV.SF		IV	Bdh2	69772																													
IV- SIN. LV.SF		IV	Bpil2	270757																													
IV- SIN. LV.SF		IV	Btaf1	107182																					x							x	
IV- SIN. LV.SF		IV	Ccdc111	408022																													
IV- SIN. LV.SF		IV	Ccdc46	76380																													
IV- SIN. LV.SF		IV	Cdc42bpa	226751								x														x	x						

Vector	primary DNA number	Source	Gene Symbol	Entrez ID	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
IV- SIN. LV.SF		IV	Cdkal1	68916																													
IV- SIN. LV.SF		IV	Cep192	70799																													
IV- SIN. LV.SF		IV	Cfc1	12627																													
IV- SIN. LV.SF		IV	Cit	12704							x	x	x									x	x			x	x						
IV- SIN. LV.SF		IV	Cyp2j6	13110																													
IV- SIN. LV.SF		IV	D030051N19Rik	228361																													
IV- SIN. LV.SF		IV	Dab2	13132																													
IV- SIN. LV.SF		IV	Dhx15	13204																					x							x	
IV- SIN. LV.SF		IV	Dhx36	72162																					x							x	
IV- SIN. LV.SF		IV	Diap3	56419																													
IV- SIN. LV.SF		IV	Dio2	13371																													
IV- SIN. LV.SF		IV	E130309F12Rik	272031																													
IV- SIN. LV.SF		IV	Edd1	70790																													
IV- SIN. LV.SF		IV	EG432825	432825																													
IV- SIN. LV.SF		IV	Emcn	59308																													
IV- SIN. LV.SF		IV	ENSMUSG00000055963	208820																													
IV- SIN. LV.SF		IV	ENSMUSG00000063249																														
IV- SIN. LV.SF		IV	Epha4	13838								x														x	x						
IV- SIN. LV.SF		IV	Exoc2	66482																													
IV- SIN. LV.SF		IV	Fbxl10	30841	6		x		x																								

Vector	**primary DNA number**	**Source**	**Gene Symbol**	**Entrez ID**	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
IV- SIN. LV.SF		IV	Foxp1	108655												x	x	x	x		x								x				
IV- SIN. LV.SF		IV	fut10	171167																													
IV- SIN. LV.SF		IV	G430022H21Rik	210529																													
IV- SIN. LV.SF		IV	Gadl1	73748																													
IV- SIN. LV.SF		IV	Gatad2b	229542																													
IV- SIN. LV.SF		IV	Gm672	269037																													
IV- SIN. LV.SF		IV	Hspa14	50497																													
IV- SIN. LV.SF		IV	Irf2	16363																													
IV- SIN. LV.SF		IV	Itgb8	320910																													
IV- SIN. LV.SF		IV	Lcorl	209707																													
IV- SIN. LV.SF		IV	Lmbrd1	68421																													
IV- SIN. LV.SF		IV	LOC381483	381483																													
IV- SIN. LV.SF		IV	LOC665775	665775																													
IV- SIN. LV.SF		IV	Lrrc8b	433926																													
IV- SIN. LV.SF		IV	Meis1	17268	27		x																										
IV- SIN. LV.SF		IV	Mllt6	246198																													
IV- SIN. LV.SF		IV	Morn3	74890																													
IV- SIN. LV.SF		IV	Mrpl1	94061																													
IV- SIN. LV.SF		IV	Myst4	54169					x									x											x				
IV- SIN. LV.SF		IV	Nalcn	338370																													
IV- SIN. LV.SF		IV	Narg2	93697																													
IV- SIN. LV.SF		IV	Nrxn1	18189																													

Vector	primary DNA number	Source	Gene Symbol	Entrez ID	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
IV- SIN. LV.SF		IV	Nudcd3	209586																													
IV- SIN. LV.SF		IV	Nudt12	67993																												x	
IV- SIN. LV.SF		IV	OTTMUSG00000008561	666048																													
IV- SIN. LV.SF		IV	Parp2	11546																													
IV- SIN. LV.SF		IV	parp8	52552																													
IV- SIN. LV.SF		IV	Pcaf	18519					x																								
IV- SIN. LV.SF		IV	Pdhx	27402																													
IV- SIN. LV.SF		IV	Pftk1	18647								x														x	x						
IV- SIN. LV.SF		IV	Phf14	75725																													
IV- SIN. LV.SF		IV	Pik4ca	224020																													
IV- SIN. LV.SF		IV	Ppp1r12a	17931																													x
IV- SIN. LV.SF		IV	Ppp3ca	19055				x			x		x									x	x	x									x
IV- SIN. LV.SF		IV	Rab11fip3	215445																													
IV- SIN. LV.SF		IV	Rab38	72433								x														x							
IV- SIN. LV.SF		IV	Rbm26	74213																													
IV- SIN. LV.SF		IV	Rttn	246102																													
IV- SIN. LV.SF		IV	Satb2	212712																													
IV- SIN. LV.SF		IV	Sesn1	140742						x	x		x																				
IV- SIN. LV.SF		IV	Slc28a2	269346																													
IV- SIN. LV.SF		IV	Slit2	20563																													
IV- SIN. LV.SF		IV	Sorl1	20660																													

Vector	**primary DNA number**	**Source**	**Gene Symbol**	**Entrez ID**	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
IV- SIN. LV.SF		IV	Stxbp5	78808																													
IV- SIN. LV.SF		IV	Sumf1	58911																													
IV- SIN. LV.SF		IV	Sybl1	20955				x																				x					
IV- SIN. LV.SF		IV	Thoc2	331401																													
IV- SIN. LV.SF		IV	Ticam2	225471																													
IV- SIN. LV.SF		IV	Tpk1	29807		2	x																										
IV- SIN. LV.SF		IV	Trim27	19720														x															
IV- SIN. LV.SF		IV	Unc84a	77053																													
IV- SIN. LV.SF		IV	Wdr67	210544																												x		
IV- SIN. LV.SF		IV	Zfp787	67109																													
IV- SIN. RV.PGK		IV	4922503N01Rik	230603																													
IV- SIN. RV.PGK		IV	4930473A06Rik	320226																													
IV- SIN. RV.PGK		IV	4930512M02Rik	75110																													
IV- SIN. RV.PGK		IV	4933424C13Rik	71130																													
IV- SIN. RV.PGK		IV	4933440H19Rik	71254																													
IV- SIN. RV.PGK		IV	5033411D12Rik	192136																													
IV- SIN. RV.PGK		IV	6330512M04Rik	320802																													
IV- SIN. RV.PGK		IV	Aacs	78894																													
IV- SIN. RV.PGK		IV	Acvr2a	11480								x														x	x						
IV- SIN. RV.PGK		IV	Aebp2	11569																									x				
IV- SIN. RV.PGK		IV	Aff3	16764																													
IV- SIN. RV.PGK		IV	AK007247	108161																													

Vector	primary DNA number	Source	Gene Symbol	Entrez ID	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
IV- SIN. RV.PGK		IV	Akr1c19	432720																													
IV- SIN. RV.PGK		IV	Anp32e	66471																													
IV- SIN. RV.PGK		IV	Arid1b	239985																													
IV- SIN. RV.PGK		IV	Arid2	77044																													
IV- SIN. RV.PGK		IV	arid5b	71371																													
IV- SIN. RV.PGK		IV	Atp2b4	100038692																													
IV- SIN. RV.PGK		IV	AW549877	106064																													
IV- SIN. RV.PGK		IV	B9d2	232987																													
IV- SIN. RV.PGK		IV	Banp I	53325					x				x																				
IV- SIN. RV.PGK		IV	BC003940	192173																													
IV- SIN. RV.PGK		IV	Brd2	14312	2		x																			x	x						
IV- SIN. RV.PGK		IV	Btk	12229								x														x	x						
IV- SIN. RV.PGK		IV	C130039O16Rik	238317																													
IV- SIN. RV.PGK		IV	Ccnd2	12444	22		x			x	x		x																				
IV- SIN. RV.PGK		IV	Ccnl1	56706						x	x		x																				
IV- SIN. RV.PGK		IV	Ccr1	12768	3		x									x	x		x														
IV- SIN. RV.PGK		IV	Ccr7	12775	7		x																										
IV- SIN. RV.PGK		IV	Cct4	12464																													
IV- SIN. RV.PGK		IV	Cdc14a	229776									x											x									x
IV- SIN. RV.PGK		IV	Cdc42ep3	260409																													
IV- SIN. RV.PGK		IV	Centd3	106952																										x	x		

Vector	**primary DNA number**	**Source**	**Gene Symbol**	**Entrez ID**	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
IV- SIN. RV.PGK		IV	Clec2d	93694										x	x	x	x		x														
IV- SIN. RV.PGK		IV	Clec4n	56620																													
IV- SIN. RV.PGK		IV	Clybl	69634																													
IV- SIN. RV.PGK		IV	Cmtm7	102545	3		x																										
IV- SIN. RV.PGK		IV	Crtc3	70461																													
IV- SIN. RV.PGK		IV	Crtc3	70461																													
IV- SIN. RV.PGK		IV	Cugbp2	14007																													
IV- SIN. RV.PGK		IV	Cutl1	13047	4		x											x											x				
IV- SIN. RV.PGK		IV	D12Ertd551e	52635																													
IV- SIN. RV.PGK		IV	D17H6S56E-3	27762																													
IV- SIN. RV.PGK		IV	D17Wsu92e	224647																													
IV- SIN. RV.PGK		IV	Dapp1	26377																													
IV- SIN. RV.PGK		IV	Dapp1	26377																													
IV- SIN. RV.PGK		IV	Depdc1b	218581																												x		
IV- SIN. RV.PGK		IV	Dhodh	56749																													
IV- SIN. RV.PGK		IV	Dtl	76843																													
IV- SIN. RV.PGK		IV	Dysfip1	68701																													
IV- SIN. RV.PGK		IV	Fert2	320004																													
IV- SIN. RV.PGK		IV	Gab2	14389																													
IV- SIN. RV.PGK		IV	Gcap14	72972																													
IV- SIN. RV.PGK		IV	Gcg	14526																													
IV- SIN. RV.PGK		IV	Gfi1b	14582																													

Vector	**primary DNA number**	**Source**	**Gene Symbol**	**Entrez ID**	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
IV- SIN. RV.PGK		IV	Gm628	268816																													
IV- SIN. RV.PGK		IV	Grap2	17444																													
IV- SIN. RV.PGK		IV	Grb2	14784																													
IV- SIN. RV.PGK		IV	Haao	107766																													
IV- SIN. RV.PGK		IV	Heg1	77446																													
IV- SIN. RV.PGK		IV	Heg1	77446																													
IV- SIN. RV.PGK		IV	Hey1	15213																													
IV- SIN. RV.PGK		IV	Hic2	58180																													
IV- SIN. RV.PGK		IV	Hod	74318																x											x				
IV- SIN. RV.PGK		IV	Hsp90aa1	15519												x	x		x														
IV- SIN. RV.PGK		IV	Hspa12b	72630																													
IV- SIN. RV.PGK		IV	Idh3a	67834																													
IV- SIN. RV.PGK		IV	Ift57	73916										x	x																		
IV- SIN. RV.PGK		IV	Iqgap2	544963																												x		
IV- SIN. RV.PGK		IV	Kdr	16542	8		x					x				x	x		x							x	x						
IV- SIN. RV.PGK		IV	Klhl22	224023																													
IV- SIN. RV.PGK		IV	Lass2	76893																													
IV- SIN. RV.PGK		IV	Leo1	235497																													
IV- SIN. RV.PGK		IV	Lnpep	240028	5		x																										
IV- SIN. RV.PGK		IV	LOC634731	634731																													
IV- SIN. RV.PGK		IV	Lrpprc	72416																													
IV- SIN. RV.PGK		IV	mmu-mir-142	387160	8		x																										

Vector	**primary DNA number**	**Source**	**Gene Symbol**	**Entrez ID**	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
IV- SIN. RV.PGK		IV	mmu-mir-142	387160	8		x																										
IV- SIN. RV.PGK		IV	mmu-mir-802	791074																													
IV- SIN. RV.PGK		IV	Mtap6	17760																													
IV- SIN. RV.PGK		IV	Mtvr2	17826																													
IV- SIN. RV.PGK		IV	Myo1d	338367																													
IV- SIN. RV.PGK		IV	Myst4	54169					x									x											x				
IV- SIN. RV.PGK		IV	Negr1	320840																										x			
IV- SIN. RV.PGK		IV	Nek6	59126						x	x	x	x									x	x			x	x						
IV- SIN. RV.PGK		IV	Nhs	195727																													
IV- SIN. RV.PGK		IV	Ninj1	18081																													
IV- SIN. RV.PGK		IV	Nt5c2	76952																													
IV- SIN. RV.PGK		IV	Nup35	69482				x																									
IV- SIN. RV.PGK		IV	Osbpl8	237542																													
IV- SIN. RV.PGK		IV	Pafah1b1	18472							x		x									x	x										
IV- SIN. RV.PGK		IV	Pan3	72587								x														x							
IV- SIN. RV.PGK		IV	Pde4d	238871	1		x																										
IV- SIN. RV.PGK		IV	Perp	64058										x	x																		
IV- SIN. RV.PGK		IV	Pip4k2a	18718																													
IV- SIN. RV.PGK		IV	Pip4k2a	18718																													
IV- SIN. RV.PGK		IV	Polg2	50776																													
IV- SIN. RV.PGK		IV	Prkce	18754								x														x	x						
IV- SIN. RV.PGK		IV	Rad50	19360							x		x										x										

Vector	**primary DNA number**	**Source**	**Gene Symbol**	**Entrez ID**	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
IV- SIN. RV.PGK		IV	Rasal1	19415																											x		
IV- SIN. RV.PGK		IV	Rcn3	52377																													
IV- SIN. RV.PGK		IV	Rps13	68052																													
IV- SIN. RV.PGK		IV	Satb1	20230	2		x		x																								
IV- SIN. RV.PGK		IV	Sept9	53860	7		x						x																				
IV- SIN. RV.PGK		IV	Set	56086	5		x																										
IV- SIN. RV.PGK		IV	Sfrs16	53609																													
IV- SIN. RV.PGK		IV	Sh3kbp1	58194																													
IV- SIN. RV.PGK		IV	Slc2a3	20527																													
IV- SIN. RV.PGK		IV	Slc38a1	105727	2		x																										
IV- SIN. RV.PGK		IV	Slc4a7	218756																													
IV- SIN. RV.PGK		IV	Slc9a1	20544																													
IV- SIN. RV.PGK		IV	Snx2	67804				x																				x		x			
IV- SIN. RV.PGK		IV	Snx30	209131																										x			
IV- SIN. RV.PGK		IV	Snx5	69178	2		x																							x			
IV- SIN. RV.PGK		IV	Sptlc2	20773																													
IV- SIN. RV.PGK		IV	Sufu	24069				x										x															
IV- SIN. RV.PGK		IV	Suv420h2	232811					x																								
IV- SIN. RV.PGK		IV	Taf6l	225895																													
IV- SIN. RV.PGK		IV	Tceb3	27224																													
IV- SIN. RV.PGK		IV	Tiam2	24001																											x		
IV- SIN. RV.PGK		IV	Tmem138	72982																													

Vector	**primary DNA number**	**Source**	**Gene Symbol**	**Entrez ID**	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
IV- SIN. RV.PGK		IV	Tmem48	72787				x																									
IV- SIN. RV.PGK		IV	Top1	21969																													
IV- SIN. RV.PGK		IV	Traf1	22029	3		x							x	x																		
IV- SIN. RV.PGK		IV	Wdr5	140858																													
IV- SIN. RV.PGK		IV	Whsc1 l1	234135					x																								
IV- SIN. RV.PGK		IV	Xylt1	233781																													
IV- SIN. RV.PGK		IV	Xylt1	233781																													
IV- SIN. RV.PGK		IV	Zbtb7a	16969														x											x				
IV- SIN. RV.PGK		IV	Zfp217	228913	5		x																										
IV- SIN. RV.PGK		IV	Zfp36l2	12193	4		x																										
IV- SIN. RV.PGK		IV	Zfp407	240476																													
IV- SIN. RV.PGK		IV	Zfp535	52712																													
IV- SIN. RV.PGK		IV	Zfp62	22720																													
IV- SIN. RV.PGK		IV	Zmiz1	328365	9	3	x																										
Tum- SIN. RV.PGK	290	BM	1810022K09Rik	69126																													
Tum- SIN. RV.PGK	218	BM	2210010L05Rik	98682																													
Tum- SIN. RV.PGK	221	BM	A1bg	117586																													
Tum- SIN. RV.PGK	289	BM	Aff4	93736																													
Tum- SIN. RV.PGK	208	BM	AI987692	331063																													
Tum- SIN. RV.PGK	344	BM	akap6	238161																													
Tum- SIN. RV.PGK	290	BM	Ap3m2	64933	2		x	x																				x					
Tum- SIN. RV.PGK	344	BM	Arsb	11881																													

Vector	**primary DNA number**	**Source**	**Gene Symbol**	**Entrez ID**	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
Tum- SIN. RV.PGK	223	BM	C230093N12Rik	98952																													
Tum- SIN. RV.PGK	341	BM	Cbfa2t2	12396														x											x				
Tum- SIN. RV.PGK	288	BM	Clcn5	12728																													
Tum- SIN. RV.PGK	343	BM	Coil	12812																													
Tum- SIN. RV.PGK	289	BM	copz1	56447				x																				x					
Tum- SIN. RV.PGK	342	BM	Cuedc1	103841	3		x																										
Tum- SIN. RV.PGK	208	BM	D17Wsu92e	224647																													
Tum- SIN. RV.PGK	293	BM	D6Wsu176e	27999																													
Tum- SIN. RV.PGK	289	BM	Epb4.1l4b	54357																													
Tum- SIN. RV.PGK	344	BM	Fkbpl	56299																													
Tum- SIN. RV.PGK	343	BM	Galnt11	231050																													
Tum- SIN. RV.PGK	223	BM	Gcnt1	14537																													
Tum- SIN. RV.PGK	342	BM	Gltscr1	243842																													
Tum- SIN. RV.PGK	225	BM	Gm414	229389																													
Tum- SIN. RV.PGK	344	BM	Gse1	382034	2		x																										
Tum- SIN. RV.PGK	287	BM	Haao	107766																													
Tum- SIN. RV.PGK	346	BM	Hist2h2aa1	15267																													
Tum- SIN. RV.PGK	239	BM	Hyal2	15587																											x			
Tum- SIN. RV.PGK	342	BM	Lipc	15450																													
Tum- SIN. RV.PGK	288	BM	LOC433791	433791																													
Tum- SIN. RV.PGK	211	BM	Lrrfip1	16978																													
Tum- SIN. RV.PGK	286	BM	Map3k14	53859								x														x	x						

Vector	**primary DNA number**	**Source**	**Gene Symbol**	**Entrez ID**	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
Tum- SIN. RV.PGK	342	BM	mef2d	17261	6		x																										
Tum- SIN. RV.PGK	216	BM	Mfsd3	69572																													
Tum- SIN. RV.PGK	218	BM	Nedd9	18003							x		x									x	x										
Tum- SIN. RV.PGK	342	BM	Notch3	18131																													
Tum- SIN. RV.PGK	228	BM	Pcbd2	72562																													
Tum- SIN. RV.PGK	346	BM	Pofut2	80294																													
Tum- SIN. RV.PGK	286	BM	Rap1b	215449	4		x																										
Tum- SIN. RV.PGK	221	BM	Rbpsuh	19664												x	x		x		x												
Tum- SIN. RV.PGK	344	BM	Rhof	23912	4		x	x																									
Tum- SIN. RV.PGK	221	BM	Rras2	66922	32		x																									x	
Tum- SIN. RV.PGK	208	BM	Saps1	243819																													
Tum- SIN. RV.PGK	208	BM	Sirt2	64383					x	x	x		x					x				x	x										
Tum- SIN. RV.PGK	293	BM	srp9	27058				x																									
Tum- SIN. RV.PGK	208	BM	Sufu	24069				x										x															
Tum- SIN. RV.PGK	346	BM	Tbcb	66411																													
Tum- SIN. RV.PGK	228	BM	Tmem162	76415																													
Tum- SIN. RV.PGK	225	BM	Tparp	99929																													
Tum- SIN. RV.PGK	287	BM	Traf2	22030										x	x																		
Tum- SIN. RV.PGK	228	BM	Ythdf2	213541																													
Tum- SIN. RV.PGK	211	BM	Zc3h12d	237256																													
Tum- SIN. RV.PGK	225	BM	Zdhhc19	245308																													
Tum- SIN. RV.PGK	293	BM	Zfp1	22640																													

Vector	**primary DNA number**	**Source**	**Gene Symbol**	**Entrez ID**	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
Tum- SIN. RV.PGK	345	BM	Zfp36l2	12193	4		x																										
Tum- SIN. RV.PGK	225	BM	Zfp39	22698																													
Tum-LV.SF.LTR	264	BM	0610010B08Rik	627932																													
Tum-LV.SF.LTR	257	BM	1700009N14Rik	75471				x			x		x									x	x					x				x	
Tum-LV.SF.LTR	257	BM	5033411D12Rik	192136																													
Tum-LV.SF.LTR	259	T	5830411G16Rik	78937																													
Tum-LV.SF.LTR	261	BM	Abca13	268379				x																								x	
Tum-LV.SF.LTR	261	BM	Agtr1b	11608										x	x																		
Tum-LV.SF.LTR	266	BM	AK129128	218343																													
Tum-LV.SF.LTR	271	BM	Ankrd11	77087																													
Tum-LV.SF.LTR	184	BM	arhgap6	11856																											x		
Tum-LV.SF.LTR	224	BM	Arl4a	11861				x																								x	
Tum-LV.SF.LTR	257	BM	Atad2b	320817																													
Tum-LV.SF.LTR	230	BM	BC013672	234311																					x							x	
Tum-LV.SF.LTR	230	BM	BC020002	252875																													
Tum-LV.SF.LTR	213	T	BC053440	234344																													
Tum-LV.SF.LTR	257	BM	bche	12038																													
Tum-LV.SF.LTR	274	BM	bcl6	12053	5		x							x	x	x	x	x	x		x								x				
Tum-LV.SF.LTR	212	BM	Braf	109880		27	x					x														x	x						
Tum-LV.SF.LTR	257	BM	C030011O14Rik	215708																													
Tum-LV.SF.LTR	266	BM	Cadm2	239857																													

Vector	**primary DNA number**	**Source**	**Gene Symbol**	**Entrez ID**	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
Tum-LV.SF.LTR	184	BM	Cdc2l6	78334								x														x	x						
Tum-LV.SF.LTR	173	BM	Cenpc1	12617																													
Tum-LV.SF.LTR	270	BM	Cntnap2	66797																													
Tum-LV.SF.LTR	173	SP	Crb1	170788																													
Tum-LV.SF.LTR	230	BM	Csmd3	239420		3	x																										
Tum-LV.SF.LTR	277	BM	Cyhr1	54151																													
Tum-LV.SF.LTR	179	SP	D16Ertd472e	67102																													
Tum-LV.SF.LTR	180	SP	D53005L1Rik	338349																													
Tum-LV.SF.LTR	294	T	D6Mm5e	110958	2		x																										
Tum-LV.SF.LTR	270	BM	Dach2	93837	2		x																										
Tum-LV.SF.LTR	264	BM	Diap1	13367																													
Tum-LV.SF.LTR	263	BM	Dok6	623279																													
Tum-LV.SF.LTR	230	BM	E2f5	13559						x	x		x									x	x										
Tum-LV.SF.LTR	230	BM	Eps15	13858		2	x																										
Tum-LV.SF.LTR	230	BM	Faf1	14084				x						x	x																		
Tum-LV.SF.LTR	214	SP	Fhl2	14200																													
Tum-LV.SF.LTR	272	BM	Flrt2	399558								x														x	x						
Tum-LV.SF.LTR	312	BM	Flrt2	399558								x														x	x						
Tum-LV.SF.LTR	262	BM	Fmnl2	71409																													
Tum-LV.SF.LTR	271	BM	Galntl2	78754																													
Tum-LV.SF.LTR	182	BM	Gm421	242235																													
Tum-LV.SF.LTR	274	BM	Hrsp12	15473																													

Vector	**primary DNA number**	**Source**	**Gene Symbol**	**Entrez ID**	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
Tum-LV.SF.LTR	180	SP	Ibtk	108837								x																					
Tum-LV.SF.LTR	212	BM	Ifi204	15951										x	x																		
Tum-LV.SF.LTR	257	BM	Ifi204	15951										x	x																		
Tum-LV.SF.LTR	179	SP	Ifna14	404549																													
Tum-LV.SF.LTR	262	BM	Itga2	16398																													
Tum-LV.SF.LTR	274	BM	Itpr1	16438																													
Tum-LV.SF.LTR	296	BM	Jmjd1c	108829					x																								
Tum-LV.SF.LTR	269	SP	Kif11	16551							x		x									x	x										
Tum-LV.SF.LTR	230	BM	Klf6	23849																													
Tum-LV.SF.LTR	230	BM	Kpna2	16647				x																				x					
Tum-LV.SF.LTR	275	BM	Lin28b	380669																													
Tum-LV.SF.LTR	270	T	Mdm1	17245																													
Tum-LV.SF.LTR	229	BM	Meis1	17268	27		x																										
Tum-LV.SF.LTR	255	BM	Nkx2-3	18089												x	x		x		x												
Tum-LV.SF.LTR	230	BM	Nmt2	18108																													
Tum-LV.SF.LTR	261	T	Nsd1	18193					x									x											x				
Tum-LV.SF.LTR	214	BM	Nsd1	18193					x									x											x				
Tum-LV.SF.LTR	191	SP	Nup50	18141																													
Tum-LV.SF.LTR	184	BM	Olfr56	18356																													
Tum-LV.SF.LTR	270	BM	Pam	18484																													
Tum-LV.SF.LTR	267	BM	Pcmtd1	319263																													
Tum-LV.SF.LTR	230	BM	Pde4d	238871	1		x																										

Vector	**primary DNA number**	**Source**	**Gene Symbol**	**Entrez ID**	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
Tum-LV.SF.LTR	262	T	Pdgfc	54635						x	x	x	x							x													
Tum-LV.SF.LTR	224	BM	Prdm2	110593																													
Tum-LV.SF.LTR	274	BM	Ptprc	19264						x	x		x	x	x	x	x		x	x	x			x									x
Tum-LV.SF.LTR	275	BM	Rad21	19357							x		x									x	x										
Tum-LV.SF.LTR	191	SP	Rere	68703	3		x		x																								
Tum-LV.SF.LTR	264	BM	Rgs18	64214																											x		
Tum-LV.SF.LTR	230	BM	Rnf38	73469																													
Tum-LV.SF.LTR	265	BM	Rps6ka3	110651								x														x	x						
Tum-LV.SF.LTR	176	BM	Scfd2	212986																													
Tum-LV.SF.LTR	213	BM	sdhd	66925																													
Tum-LV.SF.LTR	212	SP	Serpinb2	18788																													
Tum-LV.SF.LTR	274	BM	Slc13a1	55961																													
Tum-LV.SF.LTR	275	T	Slc17a6	140919																													
Tum-LV.SF.LTR	261	T	Slc8a1	20541																													
Tum-LV.SF.LTR	262	BM	Smarca2	67155																					x								
Tum-LV.SF.LTR	184	BM	Smc3	13006							x		x									x	x									x	
Tum-LV.SF.LTR	255	BM	Smg6	103677	9		x																										
Tum-LV.SF.LTR	274	BM	Snx16	74718																										x			
Tum-LV.SF.LTR	184	BM	Sos1	20662																													
Tum-LV.SF.LTR	254	BM	Ssh2	237860																				x									x
Tum-LV.SF.LTR	255	BM	Ssr3	67437				x																									
Tum-LV.SF.LTR	274	BM	Tcf7l2	21416																													

Vector	**primary DNA number**	**Source**	**Gene Symbol**	**Entrez ID**	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
Tum-LV.SF.LTR	258	BM	Thex1	67276																													
Tum-LV.SF.LTR	294	T	Tmem45a	56277																													
Tum-LV.SF.LTR	214	SP	Tpp2	22019																													
Tum-LV.SF.LTR	295	SP	Trp53bp2	209456									x	x	x																		
Tum-LV.SF.LTR	255	BM	Ttc30a2	620631																													
Tum-LV.SF.LTR	274	BM	Ubl3	24109	3		x																										
Tum-LV.SF.LTR	173	SP	Utrn	22288																													
Tum-LV.SF.LTR	275	BM	Vwc2	319922																													
Tum-SIN. LV.SF	198	BM	2010111I01Rik	72061																													
Tum-SIN. LV.SF	209	SP	2610002M06Rik	67028																													
Tum-SIN. LV.SF	220	BM	4930486L24Rik	214639																													
Tum-SIN. LV.SF	174	BM	4933427E13Rik	71234																													
Tum-SIN. LV.SF	206	BM	5730453I16Rik	269061																													
Tum-SIN. LV.SF	174	SP	Abca5	217265																												x	
Tum-SIN. LV.SF	186	BM	Abce1	24015																												x	
Tum-SIN. LV.SF	210	BM	AK129128	218343																													
Tum-SIN. LV.SF	194	BM	Ankib1	70797																													
Tum-SIN. LV.SF	206	BM	Ankrd10	102334																													
Tum-SIN. LV.SF	207	BM	Arl6ip2	56298																												x	
Tum-SIN. LV.SF	301	T	Bbs9	319845																													
Tum-SIN. LV.SF	311	T	BC013672	234311																					x							x	
Tum-SIN. LV.SF	207	BM	BC072598	71169																													

Vector	**primary DNA number**	**Source**	**Gene Symbol**	**Entrez ID**	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
Tum-SIN. LV.SF	190	BM	Brcc3	210766																													
Tum-SIN. LV.SF	207	BM	C330019G07Rik	215476																													
Tum-SIN. LV.SF	303	BM	C6	12274																													
Tum-SIN. LV.SF	206	BM	camk2d	108058	5		x				x	x	x									x	x			x	x						
Tum-SIN. LV.SF	198	BM	CcnH	66671						x	x		x													x	x						
Tum-SIN. LV.SF	215	BM	Col4a3	12828										x	x																		
Tum-SIN. LV.SF	302	BM	Dhsrx	236082																													
Tum-SIN. LV.SF	174	SP	Dhsrx	236082																													
Tum-SIN. LV.SF	207	T	Dhx15	13204																					x							x	
Tum-SIN. LV.SF	174	BM	EG209380	209380	2		x																										
Tum-SIN. LV.SF	206	BM	Erbb4	13869								x														x							
Tum-SIN. LV.SF	215	BM	Esrrg	26381																													
Tum-SIN. LV.SF	222	SP	Eya2	14049																				x									x
Tum-SIN. LV.SF	206	BM	Fbxl17	50758																													
Tum-SIN. LV.SF	238	SP	Gata3	14462																													
Tum-SIN. LV.SF	198	BM	Gbe1	74185																													
Tum-SIN. LV.SF	207	SP	Gnb1	14688																												x	
Tum-SIN. LV.SF	306	BM	Grb2	14784																													
Tum-SIN. LV.SF	305	BM	Kif5b	16573																													
Tum-SIN. LV.SF	206	BM	LOC433479	72899																													
Tum-SIN. LV.SF	220	BM	Lrig3	320398																													
Tum-SIN. LV.SF	215	BM	Lrrc4c	241568																													

Vector	**primary DNA number**	**Source**	**Gene Symbol**	**Entrez ID**	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
Tum-SIN. LV.SF	190	BM	Mad2l1	56150						x	x		x									x	x										
Tum-SIN. LV.SF	303	BM	Mad2l1	56150						x	x		x									x	x										
Tum-SIN. LV.SF	219	SP	Maml2	270118																													
Tum-SIN. LV.SF	301	T	Mnat1	17420									x																				
Tum-SIN. LV.SF	301	BM	Mtm1	17772																				x									x
Tum-SIN. LV.SF	174	BM	Myo9a	270163																													
Tum-SIN. LV.SF	207	T	Ncoa7	211329																													
Tum-SIN. LV.SF	309	BM	Nhsl1	215819																													
Tum-SIN. LV.SF	209	T	Osbpl8	237542																													
Tum-SIN. LV.SF	215	BM	Phtf2	68770																													
Tum-SIN. LV.SF	207	BM	Pja2	224938																													
Tum-SIN. LV.SF	220	BM	Pla2g4a	18783																													
Tum-SIN. LV.SF	299	BM	Polg	18975																													
Tum-SIN. LV.SF	238	BM	Polq	77782																					x							x	
Tum-SIN. LV.SF	209	T	Pscdbp	227929																													
Tum-SIN. LV.SF	174	BM	Ptpn2	19255																				x									x
Tum-SIN. LV.SF	206	BM	Ptprd	19266																				x									x
Tum-SIN. LV.SF	220	BM	Rab1	19324				x																				x				x	
Tum-SIN. LV.SF	210	BM	Rab39b	67790				x																				x					
Tum-SIN. LV.SF	174	BM	rab9	56382				x																				x				x	
Tum-SIN. LV.SF	207	T	Ranbp5	70572				x																				x					
Tum-SIN. LV.SF	298	BM	Scmh1	29871														x											x				

Vector	**primary DNA number**	**Source**	**Gene Symbol**	**Entrez ID**	RV cis	SB cis	All cis	BP:intracellular protein transport	BP: chromatin modification	BP:regulation of cell cycle	BP: cell cycle process	BP: protein amino acid phosphorylation	BP:cell cycle	BP: regulation of programmed cell death	BP:regulation of apoptosis	BP:immune system development	BP:hemopoietic or lymphoid organ dev.	BP:negative regulation of transcri	BP:hemopoiesis	BP:regulation of kinase activity	BP:B cell differentiation	BP:mitotic cell cycle	BP:cell cycle phase	BP:dephosphorylation	MF:helicase activity	MF:protein kinase activity	MF:protein serine-threonine kinase	MF:protein transporter activity	MF:transcription repressor activity	MF:phosphoinositide binding	MF:GTPase activator activity	MF:pyrophosphatase activity	MF:phosphoprotein phosphatase activity
Tum-SIN. LV.SF	310	BM	Sf3a1	67465																													
Tum-SIN. LV.SF	210	SP	Sh2d4b	328381																													
Tum-SIN. LV.SF	210	BM	Slc2a3	20527																													
Tum-SIN. LV.SF	237	BM	Smarcad1	13990					x																x								
Tum-SIN. LV.SF	220	BM	smyd3	69726		3	x		x																								
Tum-SIN. LV.SF	236	BM	Stim2	116873																													
Tum-SIN. LV.SF	207	BM	Stk11	20869						x	x	x	x													x	x						
Tum-SIN. LV.SF	215	BM	Tdrd3	219249																													
Tum-SIN. LV.SF	303	T	Timm23	53600				x																				x					
Tum-SIN. LV.SF	206	BM	Tlk1	228012					x			x	x													x	x						
Tum-SIN. LV.SF	219	SP	Tll1	21892																													
Tum-SIN. LV.SF	206	BM	trib2	217410								x									x					x							
Tum-SIN. LV.SF	194	BM	Trip12	14897																													
Tum-SIN. LV.SF	187	BM	Trps1	83925															x										x				
Tum-SIN. LV.SF	206	BM	Tspan7	21912																													
Tum-SIN. LV.SF	194	BM	V1rh14	171273																													
Tum-SIN. LV.SF	210	SP	Zbtb20	56490																													
Tum-SIN. LV.SF	222	BM	Zcchc7	319885																													
Tum-SIN. LV.SF	238	BM	Zfp654	72020																													
Tum-SIN. LV.SF	222	BM	Zfyve16	218441				x																				x		x			

Supplementary Table 4. CIS genes and overrepresented GO gene classes targeted by LV.SF.LTR, SIN.LV.SF and SIN.RV.PGK integrations *in vitro* and in tumors.

Vector: Integrations of LV.SF.LTR, SIN.LV.SF and SIN.RV.PGK *in vitro* have the prefix "IV-", in tumors "Tum-".
Primary DNA number: Tumor DNA ID number.
Source: Tissue used for DNA extraction. IV, in vitro; BM, bone marrow; SP, spleen; T, thymus.
Closest Gene Symbol: Symbol of the closest gene to the integration site.
Entrez ID: Gene Entrez Identification Number
Retroviral CIS, Sleeping Beauty transposon CIS, All CIS: genes targeted by LV.SF.LTR, SIN.LV.SF and SIN.RV.PGK integrations that matched CIS genes of RTCGD (http://rtcgd.abcc.ncifcrf.gov). The number indicates how many times the gene was hit by independent integrations of previous studies using retroviruses (Retroviral CIS), Sleeping Beauty transposon (SB transposon CIS) or both (All CIS, x highlighted in red).
All remaining columns indicate the genes belonging to GO gene classes (indicated by an x highlighted in red) that were significantly overrepresented by the DAVID-EASE analysis, had a fold increase ≥3 and were represented by ≥3genes in the dataset analyzed. Biological Processes (prefix BP: highlighted in blue) and Molecular Function (prefix MF: highlighted in yellow).

Supplementary Table 5a

Function	Dataset		n	P-value range	Molecules
Cancer	**LV.SF.LTR**	In vitro	14	1.05E-03-4.86E-02	GAB2,PRKCQ,PAM,PRDM5,PFTK1,TPK1,RUNX2,NRG3,KIF13A,SMARCA2,RB1CC1,AGK,TNIK,ACVR2A
		Tumors	35	2.37E-04-3.88E-02	EPS15,FLRT2,IFI16,KPNA2,KLF6,RPS6KA3 (includes EG:6197),MEIS1,BCL6,PDGFC,PDE4D,SERPINB2,BRAF,PTPRC,DIAPH1,FHL2,IFNA7,SOS1,RAD21,SMC3,PAM,ITGA2,NSD1,ITPR1,CNTNAP2,TPP2,TP53BP2,FAF1,SMARCA2,SDHD,CDC2L6,TCF7L2,KIF11
	SIN.LV.SF	In vitro	12	3.11E-03-4.35E-02	PCAF,NUDCD3,FOXP1,DAB2,CYP2J2,PFTK1,MEIS1,SLIT2,ITGB8,VAMP7,IRF2,BCL2
		Tumors	13	4.07E-03-4.78E-02	PLA2G4A,ESRRG,MAD2L1,NCOA7,PSCDBP,ZNF654,GRB2,COL4A3 (includes EG:1285),STK11,ERBB4,MNAT1,GATA3
	SIN.RV.PGK	In vitro	31	2.66E-04-3.16E-02	GAB2,BRD2,NEGR1,SEPT9,PDE4D,SET,RAD50,SLC2A3,CCT4,TOP1,IQGAP2,RASAL1,SUFU,NEK6,PRKCE,HEY1,CCR1,BANP,GRB2,PERP (includes EG:64065),BTK,CUX1,HOPX,WHSC1L1,CCND2,KDR,HSP90AA1,ZFP36L2,GCG,CCR7,ACVR2A
		Tumors	9	2.86E-03-4.75E-02	MAP3K14,TRAF2,RRAS2,SIRT2,NOTCH3,SUFU,GCNT1,HIST2H2AA3,AFF4
Cell Cycle	**LV.SF.LTR**	In vitro	10	1.05E-03-4.88E-02	GAB2,PRKCQ,RUNX2,SMARCA2,PRDM5,RB1CC1,IFITM1,PFTK1,AGK,FOXG1
		Tumors	18	7.58E-05-3.88E-02	SMC3,IFI16,KPNA2,ITGA2,KLF6,CENPC1,RPS6KA3 (includes EG:6197),BCL6,TP53BP2,PTPRC,BRAF,SMARCA2,E2F5,CDC2L6,TCF7L2,KIF11,RAD21
	SIN.LV.SF	In vitro	8	4.93E-03-4.35E-02	PCAF,SESN1,NUDCD3,PARP2,CIT,PFTK1,IRF2,BCL2
		Tumors	10	4.07E-03-4.78E-02	ESRRG,MAD2L1,CAMK2D,PTPN2,GRB2,STK11,ERBB4,BRCC3,MNAT1
	SIN.RV.PGK	In vitro	17	2.77E-03-3.16E-02	GAB2,BANP,GRB2,SEPT9,TMEM48,CCT4,BTK,GFI1B,TOP1,CCND2,TCEB3,KDR,NEK6,HSP90AA1,PRKCE,CDC14A,PAFAH1B1
		Tumors	1	2.86E-03-1.14E-02	COIL
Cell Death	**LV.SF.LTR**	In vitro	8	7.08E-03-4.63E-02	GAB2,PRKCQ,RB1CC1,CADPS2,TPK1,CACNB2,ACVR2A
		Tumors	18	2.37E-04-3.88E-02	AGTR1B,IFI16,KLF6,ITGA2,MEIS1,ITPR1,BCL6,TPP2,TP53BP2,SERPINB2,PTPRC,FAF1,FHL2,SMARCA2,IFNA7,SLC8A1,RAD21
	SIN.LV.SF	In vitro	10	1.8E-03-4.35E-02	ALX3,FOXP1,TICAM2,CIT,DAB2,MEIS1,CYP2J2,IRF2,PPP3CA,BCL2
		Tumors	18	4.07E-03-4.39E-02	MAML2,GRB2,COL4A3 (includes EG:1285),STK11,BRCC3,MNAT1,GNB1,MAD2L1,PLA2G4A,CAMK2D,ERBB4,TRIB2,TRPS1,C6,EYA2,ZFYVE16,ABCE1
	SIN.RV.PGK	In vitro	27	3.01E-03-3.16E-02	GAB2,BRD2,CENTD3,SLC9A1,RAD50,TOP1,IQGAP2,NEK6,PRKCE,SH3KBP1,TRAF1,HEY1,CCR1,GRB2,IFT57,PERP (includes EG:64065),BTK,GFI1B,CCND2,GRAP2,KDR,SATB1,HSP90AA1,GCG,PAFAH1B1,ZFP36L2,ACVR2A
		Tumors	2	1.42E-02-4.48E-02	TRAF2,RRAS2
Molecular Transport	**LV.SF.LTR**	In vitro	7	7.08E-03-4.71E-02	PRKCQ,NRXN3,PAM,ATP2B1,CACNB2,AGK
		Tumors	13	4.93E-03-3.63E-02	EPS15,SMG6,SLC17A6,AGTR1B,KPNA2,ITGA2,NUP50,SLC13A1,ITPR1,PDE4D,PTPRC,FAF1,SLC8A1
	SIN.LV.SF	In vitro	7	2.37E-04-3.4E-02	SLC28A2,EXOC2,STXBP5,DIO2,PPP3CA,PI4KA,BCL2
		Tumors	9	4.07E-03-4.77E-02	PLA2G4A,RAB1A,TLK1,KIF5B,ERBB4,MTM1,RAB9A,TIMM23,SLC2A3
	SIN.RV.PGK	In vitro	16	1.81E-03-3.16E-02	CCR1,GAB2,GRB2,XYLT1,SLC38A1,SLC9A1,NT5C2,BTK,LNPEP,GRAP2,SATB1,KDR,PRKCE,GCG,CCR7
		Tumors	4	2.86E-03-3.93E-02	CLCN5,LIPC,AP3M2,ARSB
Protein	**LV.SF.LTR**	In vitro	2	3.49E-02-3.49E-02	PRKCQ,PAM

Function	Dataset		n	P-value range	Molecules
Trafficking		Tumors	3	1.47E-02-2.92E-02	FAF1,EPS15,KPNA2
	SIN.LV.SF	In vitro	2	2.44E-02-3.4E-02	STXBP5,BCL2
		Tumors	5	2.81E-02-4.24E-02	RAB1A,TLK1,ERBB4,TIMM23,ZFYVE16
	SIN.RV.PGK	In vitro	1	3.16E-02-3.16E-02	SATB1
		Tumors	2	8.54E-03-3.93E-02	CLCN5,SUFU
Post-Translational Modification	**LV.SF.LTR**	In vitro	4	3.32E-02-3.84E-02	CCNT1,PRKCQ,STK38L,ACVR2A
		Tumors	1	9.84E-03-1.96E-02	NMT2
	SIN.LV.SF	In vitro	3	1.8E-03-3.4E-02	PCAF,MYST4,BCL2
		Tumors	5	4.31E-03-1.62E-02	PTPRD,PTPN2,ERBB4,MTM1,EYA2
	SIN.RV.PGK	In vitro	12	1.92E-04-2.54E-02	CCT4,BTK,CCR1,WHSC1L1,CCND2,SUV420H2,MYST4,KDR,SATB1,HSP90AA1,PRKCE,SET
		Tumors	3	1.7E-02-3.65E-02	SIRT2,PCBD2,TIPARP
Cell Signaling	**LV.SF.LTR**	In vitro	5	1.06E-02-3.84E-02	ATP2B1,STK38L,CACNB2,ACVR2A
		Tumors	7	4.93E-03-3.88E-02	PTPRC,FAF1,KLF6,ITGA2,ITPR1,SLC8A1,PDE4D
	SIN.LV.SF	In vitro	7	4.93E-03-3.4E-02	UBR5,EXOC2,STXBP5,DIO2,PPP3CA,IRF2,BCL2
		Tumors	8	1.75E-02-4.34E-02	GNB1,PTPRD,PSCDBP,TSPAN7,GRB2,COL4A3 (includes EG:1285),ERBB4,RANBP5
	SIN.RV.PGK	In vitro	10	6.55E-03-3.16E-02	BTK,CCR1,GAB2,GRB2,GRAP2,KDR,GCG,PDE4D,CCR7,NT5C2
		Tumors	5	2.54E-02-4.56E-02	RAP1B,TRAF2,RRAS2,SUFU,RHOF
Cell-To-Cell Signaling and Interaction	**LV.SF.LTR**	In vitro	4	1.06E-02-2.46E-02	OPCML,PCDH15,CACNB2
		Tumors	13	1.88E-03-3.88E-02	BRAF,PTPRC,SMC3,DIAPH1,IFI16,IFNA7,KLF6,ITGA2,UTRN,BCL6,PDGFC,CRB1
	SIN.LV.SF	In vitro	9	3.11E-03-4.17E-02	FOXP1,DAB2,EMCN,CYP2J2,EPHA4,ITGB8,SLIT2,VAMP7,BCL2
		Tumors	6	4.07E-03-4.39E-02	PTPRD,KIF5B,GRB2,ERBB4,GATA3,MNAT1
	SIN.RV.PGK	In vitro	7	6.4E-03-3.16E-02	CCR1,BTK,PRKCE,PAFAH1B1,GCG,SLC9A1,CCR7
		Tumors	3	5.7E-03-3.93E-02	TRAF2,LIPC,AP3M2
Cellular Growth and Proliferation	**LV.SF.LTR**	In vitro	9	2.44E-03-4.86E-02	GAB2,PRKCQ,SMARCA2,KIF13A,NRG3,RUNX2,FOXG1,ACVR2A,PLAG1
		Tumors	22	2.48E-03-3.88E-02	EPS15,IFI16,ITGA2,KLF6,RPS6KA3 (includes EG:6197),NKX2-3,MEIS1,ITPR1,BCL6,PDGFC,PDE4D,TPP2,SERPINB2,BRAF,PTPRC,DIAPH1,FHL2,SMARCA2,SOS1,CDC2L6,KIF11
	SIN.LV.SF	In vitro	8	4.93E-03-3.88E-02	DAB2,MEIS1,CYP2J2,ITGB8,SLIT2,IRF2,PPP3CA,BCL2
		Tumors	7	4.07E-03-4.78E-02	MAML2,MAD2L1,RAB1A,GRB2,KIF5B,ERBB4
	SIN.RV.PGK	In vitro	27	2.14E-03-3.16E-02	GAB2,SEPT9,PDE4D,TOP1,RASAL1,SUFU,TCEB3,PRKCE,HEY1,TRAF1,DTL,CCR1,ARID5B,GRB2,BTK,GFI1B,HOPX,CCND2,GRAP2,KDR,CLEC2D (includes EG:93694),CDC14A,GCG,PAFAH1B1,ZFP36L2,ACVR2A,CCR7
		Tumors	2	2.86E-03-3.38E-02	SIRT2,RBPJ
Hematological Disease	**LV.SF.LTR**	In vitro	4	2.44E-03-4.86E-02	NT5C3,GAB2,NRG3,RUNX2
		Tumors	15	1.13E-03-3.88E-02	ITGA2,NSD1,MEIS1,ITPR1,BCL6,PDE4D,SERPINB2,BRAF,PTPRC,FAF1,DIAPH1,IFNA7,CDC2L6,RAD21

Function	Dataset		n	P-value range	Molecules
	SIN.LV.SF	In vitro	5	4.93E-03-4.35E-02	FOXP1,DAB2,MEIS1,IRF2,BCL2
		Tumors	1	4.39E-02-4.39E-02	PLA2G4A
	SIN.RV.PGK	In vitro	15	4.71E-03-3.16E-02	CCR1,GAB2,PERP (includes EG:64065),SEPT9,PDE4D,BTK,GFI1B,WHSC1L1,TOP1,CCND2,GRAP2,KDR,SATB1,HSP90AA1,TRAF1
		Tumors	4	5.7E-03-3.38E-02	MAP3K14,TRAF2,LIPC,NOTCH3
Gene Expression	**LV.SF.LTR**	In vitro	9	3.55E-03-4.98E-02	CCNT1,GAB2,PRKCQ,RUNX2,SMARCA2,EIF5,FOXG1,ACVR2A,PLAG1
		Tumors	20	4.93E-03-3.88E-02	RGS18,AGTR1B,JMJD1C,KPNA2,IFI16,ITGA2,KLF6,NSD1,MEIS1,SLC13A1,BCL6,TP53BP2,HRSP12,FHL2,SMARCA2,SOS1,E2F5,TCF7L2
	SIN.LV.SF	In vitro	5	9.84E-03-4.35E-02	PCAF,DAB2,BTAF1,IRF2,BCL2
		Tumors	12	1.91E-03-3.86E-02	GNB1,PLA2G4A,ESRRG,CCNH,CAMK2D,PSCDBP,GRB2,ERBB4,TRPS1,GATA3,MNAT1,EYA2
	SIN.RV.PGK	In vitro	22	6.4E-03-3.16E-02	ARID5B,GAB2,ZBTB7A,CRTC3,MYST4,GFI1B,HOPX,CUX1,TAF6L,TOP1,AFF3,CCND2,SUFU,KDR,TCEB3,SATB1,NEK6,AEBP2,PRKCE,GCG,HEY1
		Tumors	13	2.81E-04-4.75E-02	MAP3K14,NOTCH3,AFF4,TRAF2,SIRT2,SUFU,MEF2D,LRRFIP1,PCBD2,RBPJ,ZFP36L2,CBFA2T2,NEDD9
Immunological Disease	**LV.SF.LTR**	In vitro	1	2.46E-02-3.84E-02	GAB2
		Tumors	7	2.74E-03-3.88E-02	PTPRC,DIAPH1,ITGA2,MEIS1,BCL6,KIF11,TPP2
	SIN.LV.SF	In vitro	7	4.93E-03-4.35E-02	CFC1,MEIS1,EPHA4,SLIT2,IRF2,PPP3CA,BCL2
		Tumors	3	8.12E-03-4.39E-02	PLA2G4A,COL4A3 (includes EG:1285),C6
	SIN.RV.PGK	In vitro	9	1.41E-03-3.16E-02	CCR1,BTK,GAB2,BRD2,CCND2,GRAP2,SATB1,PERP (includes EG:64065),TRAF1
		Tumors	1	5.7E-03-3.38E-02	MAP3K14
Immune Response	**LV.SF.LTR**	In vitro	2	3.55E-03-4.21E-02	CCNT1,PRKCQ
		Tumors	5	4.73E-03-3.88E-02	PTPRC,FHL2,IFNA7,MEIS1,BCL6
	SIN.LV.SF	In vitro	5	4.93E-03-4.31E-02	MEIS1,EPHA4,IRF2,PPP3CA,BCL2
		Tumors	6	8.12E-03-4.57E-02	PLA2G4A,PTPN2,GRB2,COL4A3 (includes EG:1285),C6,GATA3
	SIN.RV.PGK	In vitro	7	1.55E-03-3.16E-02	CCR1,BTK,GAB2,GRAP2,PRKCE,PAFAH1B1,CCR7
		Tumors	4	5.7E-03-4.48E-02	MAP3K14,TRAF2,GCNT1,NEDD9
Immune and Lymphatic System Development and Function	**LV.SF.LTR**	In vitro	1	3.55E-03-3.15E-02	PRKCQ
		Tumors	10	4.93E-03-3.88E-02	PTPRC,DIAPH1,IFI16,IFNA7,MEIS1,NKX2-3,BCL6,PDGFC,PDE4D
	SIN.LV.SF	In vitro	5	1.53E-03-4.35E-02	FOXP1,MEIS1,EPHA4,IRF2,BCL2
		Tumors	3	8.12E-03-4.78E-02	PTPN2,C6,GATA3
	SIN.RV.PGK	In vitro	12	1.55E-03-3.16E-02	CCR1,BTK,GFI1B,GAB2,GRAP2,SATB1,KDR,PRKCE,PAFAH1B1,GCG,PDE4D,CCR7
		Tumors	5	1.7E-02-3.93E-02	MAP3K14,TRAF2,NOTCH3,RBPJ,NEDD9

Supplementary Table 5b

Function	LV.SF.LTR		SIN.LV.SF		SIN.RV.PGK	
	In vitro	**Tumors**	**In vitro**	**Tumors**	**In vitro**	**Tumors**
Cancer	14 35	12	13	31		9
Cell Cycle	10	18	8	10	17	1
Cell Death	8	18 10	18	27		2
Molecular Transport	7	13	7	9	16	4
Protein Trafficking	2 3 2 5	1 2				
Post-Translational Modification	4	1	3	5	12	3
Cell Signaling	5 7 7 8				10	5
Cell-To-Cell Signaling and Interaction	4	13	9	6	7	3
Cellular Growth and Proliferation	9	22	8	7	27	2
Hematological Disease	4	15	5	1	15	4
Gene Expression	9 20		5 12		22	13
Immunological Disease	1	7	7	3	9	1
Immune Response	2 5	5	6	7	4	
Immune and Lymphatic System Development and Function	1	10	5	3	12	5

Supplementary Table 5: Ingenuity Pathways Analysis (IPA) overrepresentation results for LV.SF.LTR, SIN.LV.SF and SIN.RV.PGK datasets *in vitro* and in tumors. **a)** IPA Overrerepresented molecular pathways (Function) obtained from the six datasets (Dataset). The number of occurrences is given (n). Significance of each overrepresented pathway is provided as a range of significant p values (p-value range). Some genes targeted by two independent integrations are indicated in red. Targeted genes belonging to each pathway are listed (Molecules). **b)** Number of occurrences in each dataset of the above mentioned functional classes.

Supplementary Table 6

ID	Gene Name	Int. Type	Chr	Dist to TSS	ORI LTR gene	Function/ CIS	Tiss.	Average fold increase ± SD				Mann Whitney
								INT	n	NO INT	n	
212	*Braf*	I	6	78135	+	Cancer	BM	0.91	1	0.88 ± 0.31	3	
214	*Nsd1*	I	13	48896	-	Cancer	BM	0.48	1	0.72 ± 0.27	3	
271		I		51269	+			0.41	1	0.86 ± 0.19	2	
230	*Faf1*	I	4	116681	-	Apoptosis	BM	0.88	1	1	1	
	E2f5	I	3	13952	+	Cell Cycle	BM	0.71	1	1	1	
	Eps15	I	4	24194	+	Cancer	BM	5.44 ± 1.99	3	1.56 ± 0.33	11	0,0128
							SP	1.23 ± 1.02	3	1.11 ± 0.29	12	
	Pde4d	I	13	348218	-	CIS/Cancer	BM	0.05 ± 0.03	3	0.67 ± 0.29	11	0,0293
							SP	0.37 ± 0.42	3	1.57 ± 0.64	12	0,0253
	Rnf38	I	4	34336	-	Metal ion binding	BM	1.27 ± 0.24	3	0.95 ± 0.29	11	
							SP	1.18 ± 0.81	3	1.42 ± 0.38	12	
182 184	*Arhgap6*	I	X	406467	-	Signaling	BM	13.77 ± 13.04	5	1.62 ± 0.99	9	0,019
							SP	1.72 ± 1.64	6	1.19 ± 0.91	12	
	Cdc2l6	I	10	67333	+	Cell cycle/ Apoptosis	SP	2.00 ± 0.49	6	1.52 ± 0.53	12	
	Cdkl4	D	17	-128158	-	Kinase	SP	1.28 ± 0.69	6	0.97 ± 0.54	11	
	Sos1	I	17	44777	-	Cancer	BM	6.30 ± 3.79	5	1.31 ± 0.27	9	0,001
							SP	5.23 ± 3.25	6	1.71 ± 0.69	12	0,0032
	Gm941	D	17	88136	-	Signaling	SP	3.13 ± 3.08	2	8.64 ± 10.81	2	
	Ifi47	U	11	-22321	+	CIS	SP	2.42 ± 1.60	6	1.27 ± 0.57	12	0,0218
	Orf56	I	11	13993	+	CIS	SP	9.61 ± 11.68	2	9.90 ± 12.58	2	
	Tgtp	U	11	-530	-	GTPase	BM	24.69 ± 3.11	5	0.78 ± 0.49	9	0,001
							SP	9.49 ± 5.44	6	1.02 ± 0.58	12	0,0009
	EG432555	U	11	13492	-	Hydrolase	SP	6.49 ± 6.46	2	6.80 ± 8.21	2	

Supplementary Table 6: Gene expression analysis on a selected number of genes targeted or near LV.SF.LTR integrations in different tumors. Analysis was performed by Q-PCR using the $^{\Delta\Delta}$Ct method corrected for the amplification efficiency of each Taqman probe. The expression level of each tested gene was normalized to the expression of the endogenous control *Hprt*, and is presented as fold change relative to phenotype-matched tumor samples obtained from the mock-transduced groups. The relative expression level for each gene was determined by the qBase software. The amplification efficiency of each Taqman system was calculated by the Real-time PCR Miner software (available on line: http://www.miner.ewindup.info). See Methods for details.

In columns are indicated:

ID: Mouse DNA Identifier
Day: age of transplanted cells at the time of death
Phen: Tumor phenotype defined by histopathology and FACS analysis. MY: myeloid; LY: lymphoid
Gene Name: gene symbol of genes tested for expression. The genomic region surrounding two integration sites are represented below (a,b,)
Int. Type: intragenic, between TSS and cDNA end (I); upstream the TSS (U); downstream the gene end (D)
Dist to TSS: distances between TSS and LTR end
ORI LTR gene: orientation of LTR with respect to the direction of transcription of the targeted gene. Opposite (-); Same (+).
Chr: chromosome number
Tiss.: tissue on which the expression was measured. Bone marrow (BM); spleen (SP).
Average fold increase ± SD: fold change in expression levels of tumor samples with or without the integration (INT and NO INT respectively) and relative to a phenotype-matched tumor from mock transduced control ± Standard Deviation (SD). n= number of biological replicates with or without the integration.
Mann-Whitney: p-value calculated by Mann-Whitney test by comparing the expression levels of the selected gene in the group of mice that harbor the vector integration against controls.

Supplemental Methods

A) QPCR oligonucleotide and probe sequences used for vector copy number quantification and measurement of the engraftment levels using genomic DNA as template

Murine Genomic DNA oligonucleotides and probes
Primers and probe have been designed on the murine β-actin gene.

β-act. Forward: 5’ AGA GGG AAA TCG TGC GTG AC 3’
β-act. Reverse: 5’ CAA TAG TGA TGA CCT GGC CGT 3’
β-act. Probe: 5’ CAC TGC CGC ATC CTC TTC CTC CC 3’

GFP oligonucleotides and probes
Primers and probe have been designed on the GFP cDNA sequence.

GFP Forward: 5’ CAG CTC GCC GAC CAC TA 3’
GFP Reverse: 5’ GGG CCG TCG CCG AT 3’
GFP Probe: 5’ CCA GCA GAA CAC CCC C 3’

NEO oligonucleotides and probes
Primers and probe have been designed on the neomycin resistance gene.

NEO Forward: 5’ CGG TGC CCT GAA TGA ACT G 3’
NEO Reverse: 5’ CAC AGC TGC GCA AGG AA 3’
NEO Probe: 5’ CAG CGC GGC TAT CGT 3’

B) Gene expression assay identification code from Applied Biosystems (Assay ID) and nucleotide sequence of the probe(Probe Sequence 5’ to 3’) used for each tested gene (gene symbol)

Assay ID	Probe Sequence 5’ to 3’	Gene Symbol
Mm00492605_m1	TTCTTGGATCTGAGCTTCCCTGGTA	Ifi47
Mm00446968_m1	GGTTAAGGTTGCAAGCTTGCTGGTG	Hprt1
Mm00446953_m1	CCGCTACGGGAGTCGGGCCCAGTCT	Gusb
Mm00441941_m1	TTCTCTAACTTGTTTGGTGGGGAAC	Tfrc
Mm00436730_m1	GGCAAGCCCTTTTCATTCAAGATCT	Sos1
Mm01165846_m1	ATTCCTGAAGAGGTATGGAATATCA	Braf
Mm00468175_m1	GAAGTATCTTCAGGATCTATTAGTG	E2f5
Mm01181822_m1	CGGATTATCAGCATTCCAGTTCTCG	Cdc2l6
Mm01295120_m1	CACCACTGCTGAGCTTCTACCATAC	Tgtp
Mm01226858_m1	TACATCTGCAGAATGTTCTGAAGTT	Gm941
Mm01294180_s1	TATGCTCGCATCTTGGGGGCTGTGC	Olfr56
Mm01258460_m1	TTGCTAACTTCAGTGCTTATCCCTC	Eps15
Mm01304777_m1	ATCAATACAAACTCGGAACTCGCTC	Pde4d
Mm01263618_m1	TAGGAGAGATGTAACTCAGCTAGAC	Faf1
Mm01349458_m1	AAATGAAAGTTGCCAATAGGAGGCC	Nsd1
Mm02528568_g1	ATCCGGGGGCCTCTCTAGTGAGACT	9930111J21Rik
Mm01136809_m1	TTGGAAAAGAAATGTCAGAGGAGCC	Arhgap6