

Appendices

Appendix 2A: Linker sequences from GENEART for the *Vk*hPB* and *Vk*MYC-TA-hPB* constructs

Sequence 1 – *Vk*hPB* linker

GGATCCAGAAATTCTTCTCAGCC**CTCAAC**ggcagcagcctggacgacgagcacatcctgagcgcc
ctgctgcagagcgacgacgagctggtcggcgaggacagcgacagcgagatcagcgacc**cacgtg**

Sequence 2 – *Vk*hMYC-TA-hPB* linker

GAATTCaGGTACCaa**gaaatcgat**gttggttctgtggaaaagaggcaggctcctggcaaaaggtcagagtctggatcac
cttctgctggaggccacagcaaacctcctcacagcccactggtcctcaagagggtccacgtctccacacatcagcacaactacg
cagcgctccctccactcgggaaggactatcctgctgccaagagggtcaagttggacagtgtcagagtctgagacagatcagc
aacaaccgaaaatgcaccagccccaggctcctggacaccgaggagaatgtcaagaggcgaacacacaacgtcttgagcg
ccagaggaggaacgagctaaaacggagctttttgccctgctgaccagatcccggagttgaaaaaacaatgaaaaggcccc
aaggtagtattccttaaaaaagccacagcatacatcctgtccgtccaagcagaggagcaaaagctcatttctgaagaggactgt
tgcggaaacgacgagaacagttgaaacacaaactgaacagctacggaactctgtg**cgagggcagaggaagtcttcta**
acatg**cggtgacgtggaggagaatcccggccct**ggcagcagcctggacgacgagcacatcctgagcgccctgctg
cagagcgacgacgagctggtcggcgaggacagcgacagcgagatcagcgacc**cacgtg**agc

Open reading frame

Restriction sites KpnI = GGTACC, PmlI = CACGTG, EcoRI = GAATTC, ClaI =
ATCGAT, BbvCI = CCTCAGC

From just before start of hMYC

hMYC exon 3 (last) excluding stop codon

T2A linker peptide

mPB from 2nd codon to PmlI site

Appendix 2B: Primers used for TraDIS sequencing

These primer sequences were provided by Iraad Bronner

PiggyBac

Name	Order sequence	temp
PB5pr_1	g*atatacagaccgataaaacacatgctc*a	63
PB5pr_2	a*atgatacggcgaccaccgagatctacaccacgcgattatctttaacgtacgtca*c	65
PB5pr_seq_2	c*accgagatctacaccacgcgattatctttaacgtacgtcacaatatgattatcttt*c	-
PB3pr_1	g*acggattcgcgctatttagaaagaga*g	63
PB3pr_2	a*atgatacggcgaccaccgagatctacacatgctcaattttacgcagactat*c	65
PB3pr_seq_3	c*accgagatctacacatgctcaattttacgcagactatcttt*c	-

Sleeping Beauty

Name	Order sequence	temp
SB5pr_1	t*ttgtaacaagaaatttgaggagtagtt*g	63
SB5pr_2	a*atgatacggcgaccaccgagatctacacaaaaacagagtttaagactccaa*c	65
SB5pr_seq_3	a*aaaacgagtttaagactccaacttaagtgtatgtaaaactcc*g	-
SB3pr_1	a*ctgaccttaagacagggaaactttact*c	63
SB3pr_2	a*atgatacggcgaccaccgagatctacacggaatctttactcggattaaatgtca*g	65
SB3pr_seq_4b	g*tgagtttaaatgtattggctaagggtgatgtaaaactcc*g	-

qPCR primers

Name	sequence (for ordering)	temp
qPCR2.1	a*atgatacggcgaccaccgagat*c	60
qPCR2.2	c*aagcagaagacggcatacagaga*t	60
PB5prseqR1	t*gattatctttaacgtacgtcacaatatgattatcttt*c	60
PB3prseqR1	a*tgctcaattttacgcagactatcttt*c	60
SB5prseqR1	t*gactccaacttaagtgtatgtaaaactcc*g	60
SB3prseqR1	t*ttggctaagggtgatgtaaaactcc*g	60

General Splinkerette primers and adapter primers

Name	Sequence (for ordering)	temp
SplAP1	g*ttcccatggtactactcat*a	63
Spl_rev_seq	t*aatacgaactactataggtgacagcgagcgc*t	-
Spl_tag_seq	a*gcgctcgtgtcacctatagtgagtcgtatt*a	-
Splinkerette V1.2 top strand	g*ttcccatggtactactcatataatacgaactactataggtgacagcgagcgc*t	ND
Splinkerette V1.2 bottom strand	/5Phos/g*cgctcgtgtcacctatagtgagtcgtattataattttttcaaaaa*a	ND

Splinkerette V1.2 index primer sequences

Only the first ten are shown

name	Sequence (for ordering)	Obtained tag sequence
P7_SplAP2_V1.1	c*aagcagaagacggcatacagagatcgggACAAGCTAataacgactcactatag*g	tagcttgt
P7_SplAP2_V1.2	c*aagcagaagacggcatacagagatcgggAAACATCGtaatacgactcactatag*g	cgatgitt
P7_SplAP2_V1.3	c*aagcagaagacggcatacagagatcgggACATTGGCtaatacgactcactatag*g	gccaatgt
P7_SplAP2_V1.4	c*aagcagaagacggcatacagagatcgggACCACTGTtaatacgactcactatag*g	acagtggg
P7_SplAP2_V1.5	c*aagcagaagacggcatacagagatcgggAACGTGATtaatacgactcactatag*g	atcacggt
P7_SplAP2_V1.6	c*aagcagaagacggcatacagagatcgggCGCTGATCtaatacgactcactatag*g	gatcagcg
P7_SplAP2_V1.7	c*aagcagaagacggcatacagagatcgggCAGATCTGtaatacgactcactatag*g	cagatctg
P7_SplAP2_V1.8	c*aagcagaagacggcatacagagatcgggATGCCTAAataacgactcactatag*g	ttaggcat
P7_SplAP2_V1.9	c*aagcagaagacggcatacagagatcgggCTGTAGCCtaatacgactcactatag*g	ggctacag
P7_SplAP2_V1.10	c*aagcagaagacggcatacagagatcgggAGTACAAGtaatacgactcactatag*g	cttgctact

Appendix 3A: Pindel variants detected in the CMML (blue) and AML (grey) samples

Chr	Call start position	Call end position	Variant	Length	Sequence altered	Sum of mapping score	Simple score	Statistical score	Annotation	Repeat number	Start of Repeat	End of Repeat	Number of unique reads called as variant by Pindel and BWA		Pindel variant reads		Total unique read depth					
													Disease	Normal	Disease	Normal	Disease	Normal				
1	2660881 2	2660888 9	D	78	ccagg<db>ggga	116	9	160.45	UBXN11 CCDS41288.1 r.1929_2006de 178 c.1464_1541del78 p.G490_P515d e GPGSPGPGSPGSPGSPGSPGPGP	1	26608811	26608892	2	0	0	2	0	22	3	19	3	
5	1708375 43	1708375 44	I	4	TCTG	250	8	263.64	NP11 CCDS4376.1 r.1104_1105insuc ug c.859_860insTCTG p.W288fs*12	1	1.71E+08	170837548	8	30	0	7	0	69	111	10	12	
5	1708375 47	1708375 48	I	4	TCTG	1374	27	982.50	NP11 CCDS4376.1 r.1108_1109insuc ug c.863_864insTCTG p.W288fs*12	0	1.71E+08	170837548	0	27	0	0	26	0	65	111	10	12
6	8406184 2	8406186 4	DI	23	AAGTAAAAAAA ACCTCTGGA	87	4	0.00	ME1 Coding	0	84061842	84061864	0	3	0	0	3	0	12	22	9	22
11	7675154 3	7675158 5	DI	43	GGAGCGCCCGC CTGGCCCAAGC GCCACAGGGCAT CC	87	4	0.00	B9GN76 Coding	1	76751543	76751585	3	0	0	3	0	0	13	0	7	1
17	4523215 2	4523427 8	DI	2127	G	83	4	0.00	CD27 Coding	1	45232152	45234278	3	0	0	3	0	0	20	101	21	5
17	3924080 3	3924080 4	I	15	ATCTCCAGCTGCTG T	97	4	93.74	KRTAP4- 7 CCDS45673.1 r.402_403insuuccc8 cucgcu c.345_346insATCCACGCTGC TGT p.C115_R116miSSCC	0	39240803	39240804	0	3	0	0	3	0	23	11	20	6
19	3600242 1	3600242 3	D	3	acc	87	4	113.62	DMKN CCDS12463.1 r.985_987delGG U c.808_810delGGT p.G270delG	1	36002418	36002426	7	0	3	0	3	0	13	12	4	9

Chr = Chromosome. Variant D = deletion, I = insertion, DI = complex

Chr	Call start position	Call end position	Variant	Length	Sequence altered	Sum of map score	Simple score	Statistical Score	Annotation	Repeats	Start of Repeat	End of Repeat	Number of unique reads called as variant by Pindel and BWA		Pindel variant reads		Total unique read depth						
													Disease	Normal	Disease	Normal	Disease	Normal	Disease	Normal			
1	109792735	109792736	I	3	CGC	180	4	114.92	CELSR2 CCDS5796.1 r.95_96insccg c.34_35insGGC p.P16_L17insP	5	109792735	109792751	10	3	3	0	0	31	6	27	5		
5	65892767	65892768	I	3	GCC	180	4	115.27	MA514 CCDS47224.1 r.560_563insGCC c.284_285insGCC p.P98_L99insP	3	65892767	65892779	3	3	0	0	0	4	6	0	6		
5	170837547	170837548	I	4	TCTG	1343	27	983.33	NPM1 CCDS4376.1 r.1108_1109insccug c.863_864insTCTG p.W288fs*12	1	170837543	170837548	18	33	0	0	26	0	97	2	12	10	
15	102392941	102392967	DI	27	GAGGCAACCA AGGAGTTCAT	55	5	0.00	AIC1079777.1 Coding	0	102392941	102392967	0	4	0	0	4	0	22	40	24	23	
17	45232152	45232178	DI	2127	G	69	4	0.00	CDC27 Coding	1	45232152	45232178	3	0	0	0	3	0	24	9	10	5	
19	36002419	36002421	D	3	cca	87	4	120.90	DMKN CCDS12463.1 c.987_989delUGG c.810_812delTGG p.G271delG	2	36002418	36002426	8	4	0	3	3	0	15	15	4	9	
19	33793204	33793205	I	2	CG	240	5	156.38	CEBPA ENST00000498907 c.266_267insccg c.116_117insCCG p.Q41fs*120	2	33793199	33793205	0	5	0	0	0	4	0	5	16	5	10
22	20779973	20779974	I	1	G	209	5	159.86	SCARF2 CCDS13779.1 c.2409_2410insc c.2304_2305insCC p.E769fs*9	2	20779973	20779976	4	2	0	1	4	0	4	5	2	1	
X	50350686	50350713	DI	28	CTCCCTCCTC TTCCCT	180	4	0.00	SHROOM4 Coding	0	50350686	50350713	3	0	0	0	3	0	13	14	14	24	
X	104464237	104464282	DI	46	AT	116	8	0.00	TEX13A Coding	1	104464237	104464282	1	3	0	0	1	3	0	35	21	47	10

A
M
L

Appendix 3B: SNV which are unique to either the CMML or AML samples on Caveman call

	GENE	CHR	Position	cDNA	Protein	Type	Allele		Depth		% mutant in	
							WT	MT	Normal	Tumour	Normal	Tumour
CMML	PTCHD2	1	11595708	c.3816+7A>C	p.?	splice	A	C	33	44	0	13.64
	PRG4	1	186276486	c.1635A>C	p.A545A	silent	A	C	132	140	3.79	10
	PRG4	1	186276589	c.1738A>C	p.T580P	missense	A	C	171	145	4.09	8.28
	ITPK8	1	226924822	c.338T>G	p.V113G	missense	A	C	57	53	1.75	11.32
	ARL6IP6	2	153575160	c.22T>G	p.W8G	missense	T	G	97	89	1.03	8.99
	TLK1	2	172017001	Non-coding	r.343u>g	5' UTR	A	C	38	52	10.53	19.23
	SPEG	2	220348806	c.6621A>C	p.A2207A	silent	A	C	30	39	0	15.38
	AGAP1	2	236877171	c.1549G>C	p.D517H	missense	G	C	83	66	3.61	15.15
	CAND2	3	12857461	c.1116T>G	p.G372G	silent	T	G	67	79	2.99	10.13
	TEX264	3	51733561	c.620A>G	p.E207G	missense	A	G	134	156	2.24	5.77
	PLXNA1	3	126708354	c.849T>G	p.G283G	silent	T	G	195	280	2.56	7.14
	SOX2	3	181430812	c.664A>C	p.T222P	missense	A	C	77	88	2.6	7.95
	TBC1D1	4	38016337	c.625T>G	p.S209A	missense	T	G	75	68	5.33	14.71
	SPATA18	4	52938111	c.547G>C	p.A183P	missense	G	C	60	67	5	10.45
	SLC22A23	6	3324119	c.1031T>G	p.V344G	missense	A	C	21	34	0	14.71
	HLA-A	6	29911240	c.539T>A	p.L180*	nonsense	T	A	47	53	4.26	7.55
	HLA-A	6	29911271	c.570G>C	p.E190D	missense	G	C	48	58	2.08	12.07
	WASF1	6	110423242	c.1071A>C	p.P357P	silent	T	G	45	41	0	12.2
	FAM160B2	8	21953856	c.133A>C	p.T45P	missense	A	C	21	28	9.52	17.86
	KIAA1529	9	100071811	c.734T>G	p.V245G	missense	T	G	65	86	6.15	8.14
	RXRA	9	137300857	c.502A>C	p.T168P	missense	A	C	138	171	5.8	7.6
	SYT15	10	46970440	c.7+2T>G	p.?	essential splice	A	C	13	26	0	26.92
	SH2D4B	10	82363515	c.824A>C	p.D275A	missense	A	C	26	24	3.85	16.67
	KRTAP5-2	11	1619378	c.103C>T	p.R35C	missense	G	A	97	100	1.03	7
	KRT83	12	52713016	c.517T>G	p.C173G	missense	A	C	149	161	4.7	6.83
	PTPN11	12	112915523	c.922A>G	p.N308D	missense	A	G	94	92	0	9.78
	ADAMT57	15	79059160	c.3093A>C	p.S1031S	silent	T	G	45	42	0	11.9
	ENSG00000179038	16	21817596	Non-coding	r.2542u>c	5' UTR	A	G	37	42	2.7	9.52
	ZNF646	16	31089685	c.2040T>G	p.G680G	silent	T	G	48	87	0	8.05
	NT5C3L	17	39981891	c.763C>G	p.R255G	missense	G	C	80	85	5	10.59
	HCN2	19	590406	c.461A>G	p.E154G	missense	A	G	14	22	0	22.73
	CYP2A7	19	41387647	c.190T>C	p.C64R	missense	A	G	36	38	2.78	13.16
	CYP2A7	19	41387656	c.181T>A	p.F61I	missense	A	T	30	34	0	8.82
	AP2A1	19	50285864	c.356A>C	p.D119A	missense	A	C	115	128	4.35	8.59
	CCDC106	19	56164006	c.737A>C	p.Y246S	missense	A	C	73	98	9.59	12.24
	NCOA6	20	33331075	c.2985A>C	p.A995A	silent	T	G	34	57	2.94	21.05
	KRTAP10-2	21	45970771	c.571G>A	p.V191I	missense	C	T	128	156	2.34	5.77
	TRIOBP	22	38121786	c.3223T>C	p.S1075P	missense	T	C	65	73	7.69	12.33
	ACRC	X	70830650	c.1731G>T	p.L577F	missense	G	T	68	72	0	8.33

	GENE	CHR	Position	cDNA	Protein	Type	Allele		Depth		% mutant in	
							WT	MT	Normal	Tumour	Normal	Tumour
AML	AL355149.1	1	16863213	Non-coding	r.1449g>c	mRNA	C	G	52	65	3.85	7.69
	AL355149.1	1	16863233	Non-coding	r.1429u>g	mRNA	A	C	70	76	2.86	6.58
	ABCA4	1	94490534	c.4610C>T	p.T1537M	missense	G	A	121	125	0	6.4
	NRAS	1	115258748	c.34G>T	p.G12C	missense	C	A	201	204	0	7.35
	HELT	4	185940170	c.88A>C	p.T30P	missense	A	C	29	40	0	15
	RREB1	6	7231841	c.3509T>G	p.V1170G	missense	T	G	11	18	0	38.89
	UBN2	7	138967815	c.1915G>A	p.A639T	missense	G	A	78	56	0	26.79
	SOX7	8	10583751	c.664T>C	p.S222P	missense	A	G	39	44	2.56	18.18
	PDLIM2	8	22451396	c.1032A>C	p.A344A	silent	A	C	10	22	0	18.18
	FAM171A1	10	15255870	c.1717G>A	p.V573I	missense	C	T	162	165	0	23.03
	FRG2B	10	135438806	c.634C>A	p.R212R	silent	G	T	83	98	3.61	6.12
	API5	11	43344985	c.549A>G	p.L183L	silent	A	G	71	69	0	30.43
	KRT81	12	52681054	c.1079C>A	p.A360D	missense	G	T	77	93	1.3	9.68
	AP451	14	31554147	Non-coding	r.747c>a	3' UTR	C	A	53	50	0	10
	C17orf97	17	263613	c.979C>A	p.P327T	missense	C	A	83	82	2.41	8.54
	TMC4	19	54676732	c.79+2T>G	p.?	essential splice	A	C	116	111	5.17	8.11
	RBBP9	20	18477732	c.80T>G	p.V27G	missense	A	C	30	52	3.33	19.23
	FAM182B	20	25755519	c.437A>C	p.H146P	missense	T	G	32	30	0	13.33
	ARSH	X	2936713	c.901+2T>G	p.?	essential splice	T	G	61	64	1.64	7.81
	GPR50	X	150349621	c.1566G>C	p.K522N	missense	G	C	145	118	4.83	7.63

Appendix 4A: CIS integrations that were identified on only 1 or 2 of the CIS analysis methods used for the 454 analysis.

The gene nearest to the CIS peak, the kernel sizes at which the CIS was identified, the location and height of the peak and the boundaries of the CIS are shown, along with the number of hits, the genes in the CIS and the analysis methods by which the CIS was identified

Gene nearest to CIS peak	Kernel size (x1000)	Chromosome	peak location*	peak height*	start	end	CIS width	Number of hits	P value	Genes in CIS*	Method
Rabgap1	10	2	37312541	4.029030834	37308610	37314507	5898	5	2.514E-05	Rabgap1	GV/NSD7
Nfia	100	4	97485158	8.262911755	97426325	97524380	98056	11	4.388E-05	E130114P18Rik Nfia	NSD7
Gm17091	10	5	10663101	3.910404439	10661145	10663101	1957	6	5.428E-05	intergenic	NSD7
Slco3a1	100	7	81586072	9.96738084	81546748	81586072	39325	17	0.0001721	Slco3a1 Gm7580	GV/NSD7
Akap13	30	7	82869581	6.328003393	82869581	82872522	2942	10	7.384E-05	Akap13	LHC
Cbl	30	9	43994061	5.406177651	43985303	43996980	11678	7	6.278E-05	Cbl	NSD7
Gm12068	60, 100	11	24339451	10.39816394	24280654	24359050	78397	16	9.529E-05	Gm12068	GV
Nsd1	100	13	55400553	7.402812078	55351678	55439654	87977	13	0.0001126	Nsd1 Rab24 Preld1 Mxd3	GV
Fhl1	30	X	53993652	3.952833137	53987836	53993652	5817	6	8.257E-05	Fhl1	NSD7

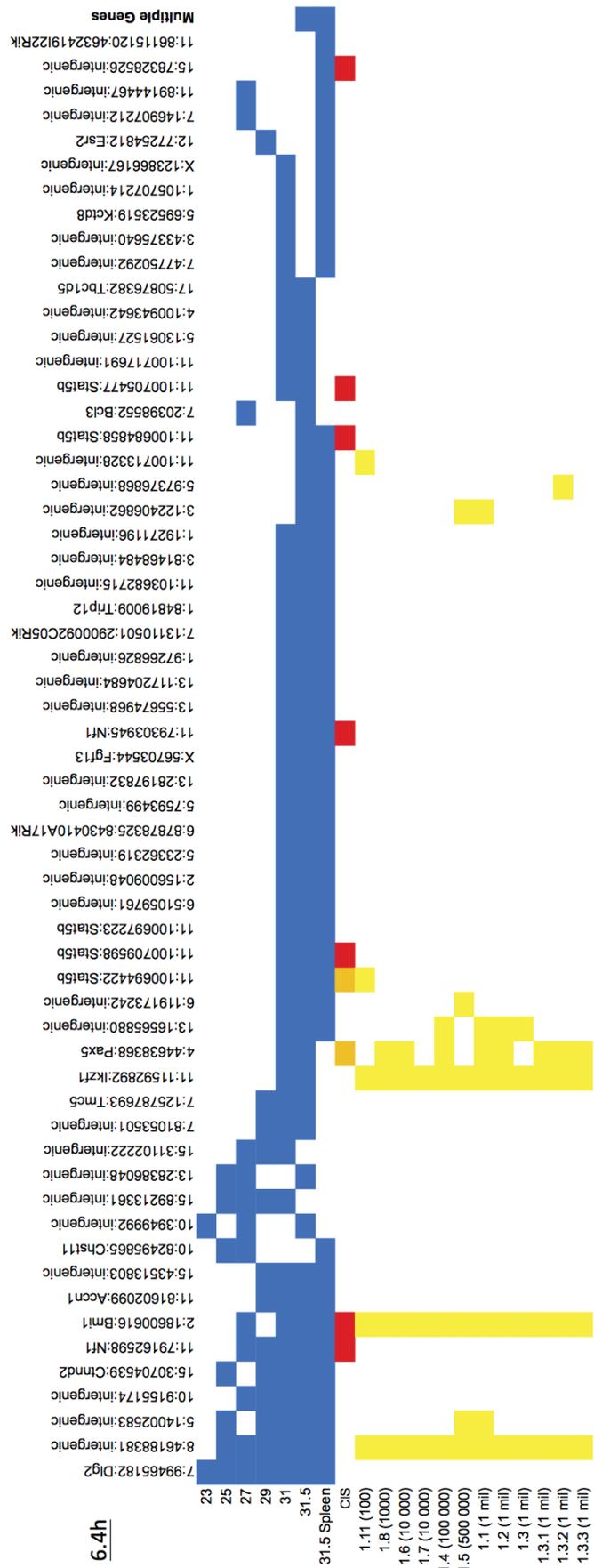
Name	Sex	Genotype		pIpC	Age at death (weeks)	Mouse (g)	Spleen (g)	Liver (g)	Lymph-adenopathy	WBC	Hb	HCT	PII	MCV	Blood film Changes	Tissue involvement	Diagnosis
		Nrm1	Mutagenesis														
6.4a	Male	WT/c	yes	x6	42.9	44	0.7	3.1	yes	398	9.8	36.7	31.3	61	CMML like	Spleen, liver, kidney, heart, thymus, BM, LN, muscle	Myeloid leukaemia with maturation
6.4b	Male	WT (Cre neg)	No (Cre neg)	x2	109.3	50.5	0.3G	2.9G	no	10.2	11.1	38.8	1812	58	Normal	Mass in pancreatic node	?Lymphoma in pancreatic node, Spleen follicular hyperplasia
6.4g	Male	WT/c	yes	x2	85.1	45.4	0.5	2.5	no, tumour on leg	14.1	8.7	32.9	679	48	Normal	Spleen	Angiosarcoma leg, follicular hyperplasia
6.4h	Female	WT/c	yes	x6	31.4	45	0.5	2.3	no	34.5	13	52.6	809	58	Undifferentiated blasts	Spleen, LN, BM, liver	Undifferentiated leukaemia, MPO, B220 and CD3 neg
7.5b	Male	WT/c	yes	x6	50	45.9	1.2	2.4	yes	114	12.3	46	503	59	Blasts present, v high WCC with maturation	Spleen, liver, LN, BM, muscle	Myeloid leukaemia with maturation
7.5c	Male	WT/c	yes	x6	32.4	39.7	3.71	3.9	no	78.3	22.8	75	4930	67	eukerythroblastic, thrombocytosis, giant platelets	Spleen, bone marrow, liver	Myeloid leukaemia, ?MPO with progression
7.5d	Female	WT/c	yes	x6	26	29.2	1.5	4	no	627	18.3	>70	733	62	CMML like	Liver, BM, spleen, LN	Myeloid leukaemia with maturation
7.7a	Male	WT/c	yes	No	115.9	42.8	0.2	1.9	no	14.4	14.4	55.2	>2200	59	Normal	Spleen, lung	Follicular lymphoma, lung adenocarcinoma
7.7b	Male	WT/c	yes	No	73.6	45.2	1.2	2.4	no	32.5	10.1	35.1	145	67	Leukaemia with poorly differentiated blasts	BM, spleen, liver, muscle, papillary adenoma lung	Myeloid leukaemia, very poorly differentiated, MPO positive
16.3b	Male	WT/c	yes	x6	43	54.4	0.6	2.7	No	109	15.8	59	367	56	Neutrophilia, toxic granulation, left shift, ring forms ++, low blast percentage	Spleen, liver, thymus, LN, BM, muscle	Myeloid leukaemia with maturation
16.3c	Female	WT/c	yes	x6	29.4	34	0.7	2.7	yes	131.2	8.8	32.6	147	71	CMML like	Spleen, liver, LN, thymus, lung, BM, muscle	Myeloid leukaemia with maturation
16.3f	Female	WT/c	yes	x6	55.3	45.2	1	2.2	yes	45.8	11.9	47.2	173	59	Left shift, blasts, v high PMN	Spleen, liver, kidney, LN, thymus, BM, Also B cell infiltrate in lung and B and T infiltrate in liver and kidney	Myeloid leukaemia with lymphoma as probable second diagnosis
16.3g	Female	WT/c	yes	x6	33	42.2	0.8	2.9	no	167	14.5	52.8	129	62	CMML like	Spleen, liver, LN, thymus, BM	Myeloid leukaemia with maturation
16.3h	Female	WT/c	yes	x6	20.3	28.3	0.53	1.65	no	58	14.1	54.3	739	56	Undifferentiated blasts	Spleen, liver, BM	Myeloid leukaemia, AMML like
16.3i	Female	WT (Cre neg)	No (Cre neg)	x6	57	37.4	0.2	1.7	no	7.4	10.3	35.7	1219	51	Sick blood, few WBC	Culled due to tail inflammation	Borderline, ?normal
19.2a	Male	WT (sg)	WT	x4	51.6	37.1	0.7	3.1	no, thymomegaly	381	10.9	42.5	427	65	Normal	BM, spleen, LN, liver, kidney	B cell lymphoma, adenoma lung
19.2b	Male	WT/c	yes	x4	27	38.1	1.2	4	yes	221	10.7	41.4	262	79	AMML like	BM, muscle, peritoneal liver, kidney, spleen, LN	Myeloid leukaemia, AMML like
19.2d	Female	WT/c	yes	x4	38.6	28.4	1.5	3	yes	595	5.9	23.8	112	101	AMML like	spleen, LN, liver, lung, BM, muscle	Myeloid leukaemia, AMML like
19.3a	Male	WT/c	No (Cre neg)	x4	49.3	24	0.1	1	no	6.5	13.4	54.2	1357	57	Normal	Culled due to eye lesion	Normal
20.2b	Male	WT	yes	x4	47.8	35.3	1.1	2.4	no, thymomegaly	101	10.9	45.7	671	62	Myeloid with blasts and maturation	Spleen, BM, liver, fat, muscle	Myeloid leukaemia with maturation and numerous blasts
20.4e	Female	WT	No (Cre neg)	No	100.9	24.19	0.63	1.45	no, tumours on kidneys	11.8	20.9	66.1	672	54	Unremarkable	Kidney, liver	B cell lymphoma, adenoma lung
20.4f	Female	WT	No (Cre neg)	No	63.2	42.6	0.2	1.7	no						Normal	Culled due to swollen abdomen, pallor	Normal
20.4g	Female	WT	No (Cre neg)	No	53.3	37.7	<0.1	1.7	no	5.8	14	54.9	696	59	Normal	Culled as pale, slow movement	Normal
21.3j	Male	WT/c	yes	x4	25.1	33.9	0.7	1.7	no	92	14.1	61.7	208	65	Myeloid disease with blasts and some maturation	BM, spleen, muscle, liver, kidney	Myeloid leukaemia with blasts and some maturation
22.2b	Male	WT/c	yes	x4	30.8	39	1.1	2.4	no	281	9.6	36.8	165	61	Very high WCC with many blasts	BM, spleen, liver, muscle	Myeloid leukaemia, with many blasts

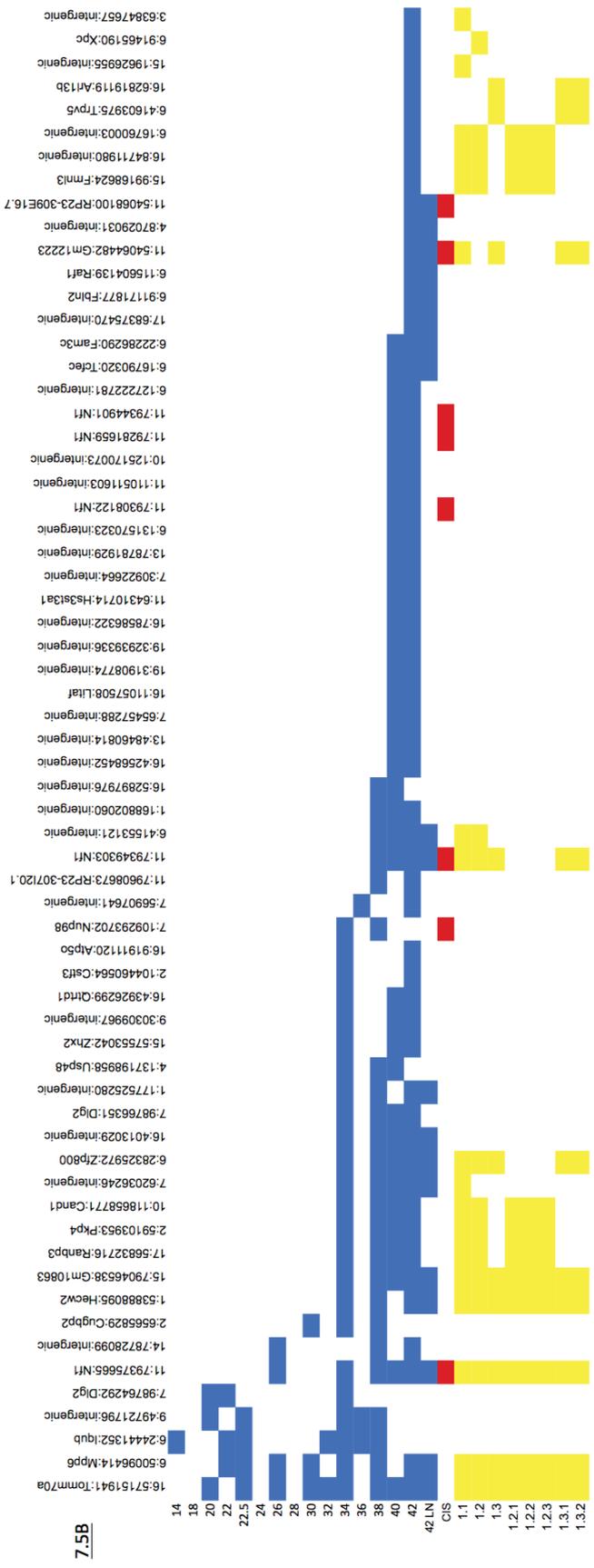
Appendix 4B: Details of the serially bred mice.

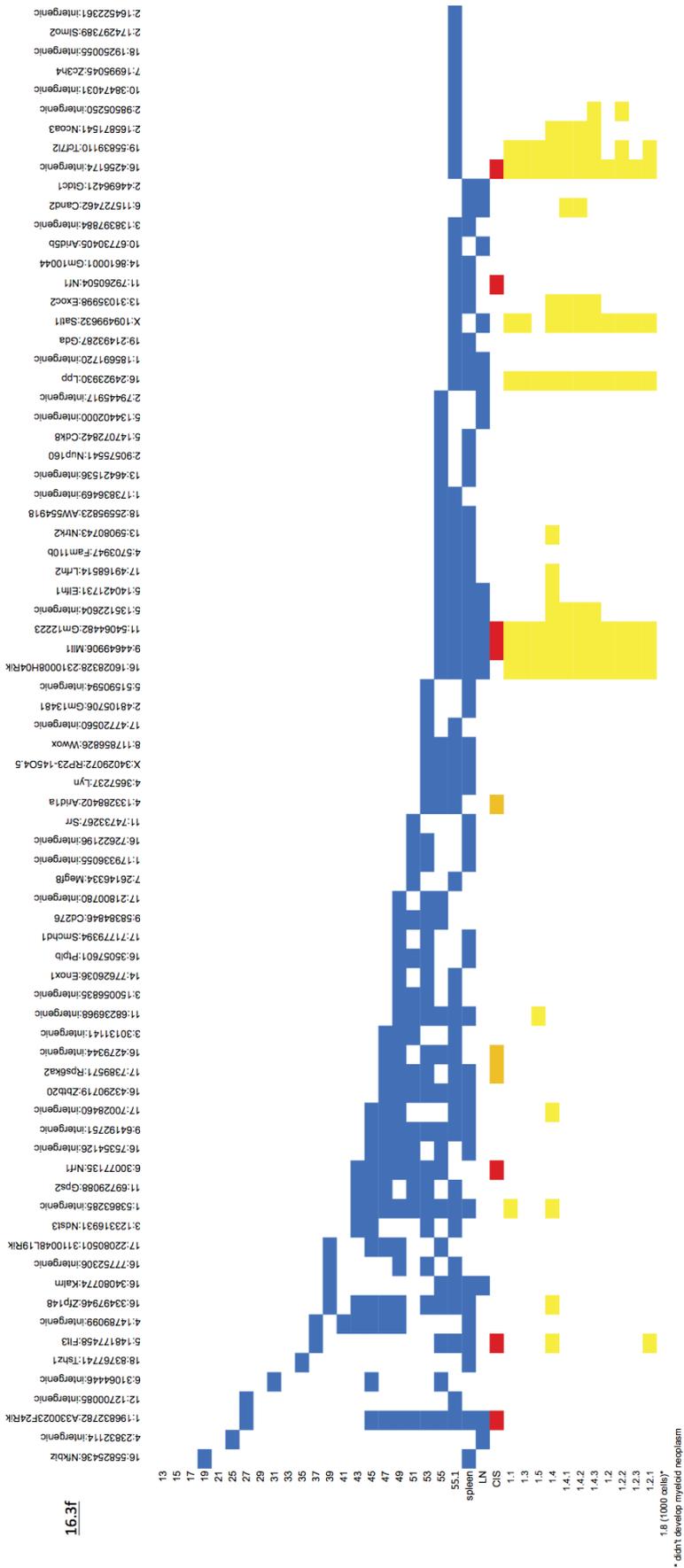
The sex, genotype, number of pIpC injections, age at death, necropsy finding and pathology findings are shown for each mouse.

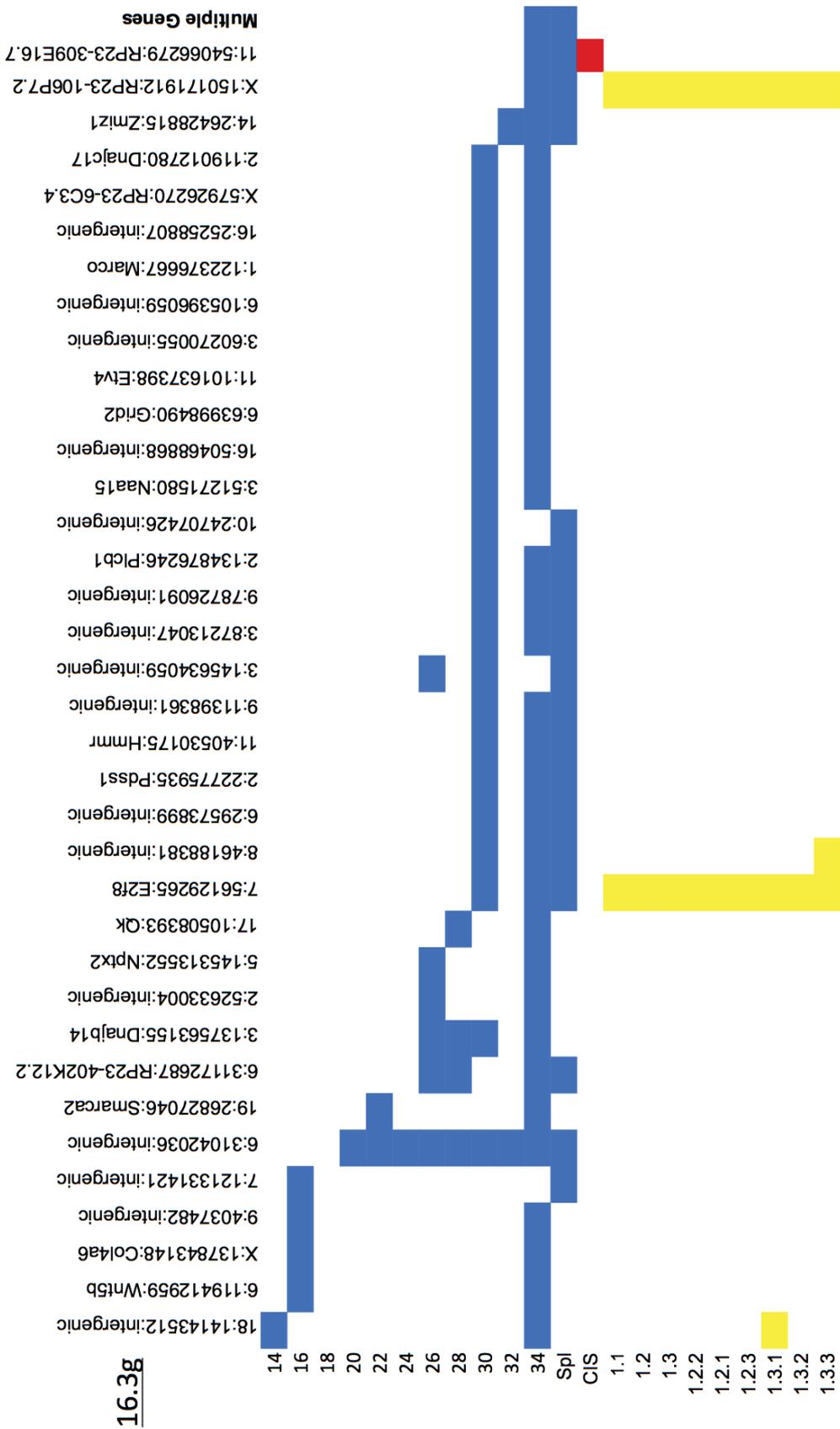
Appendix 4C:

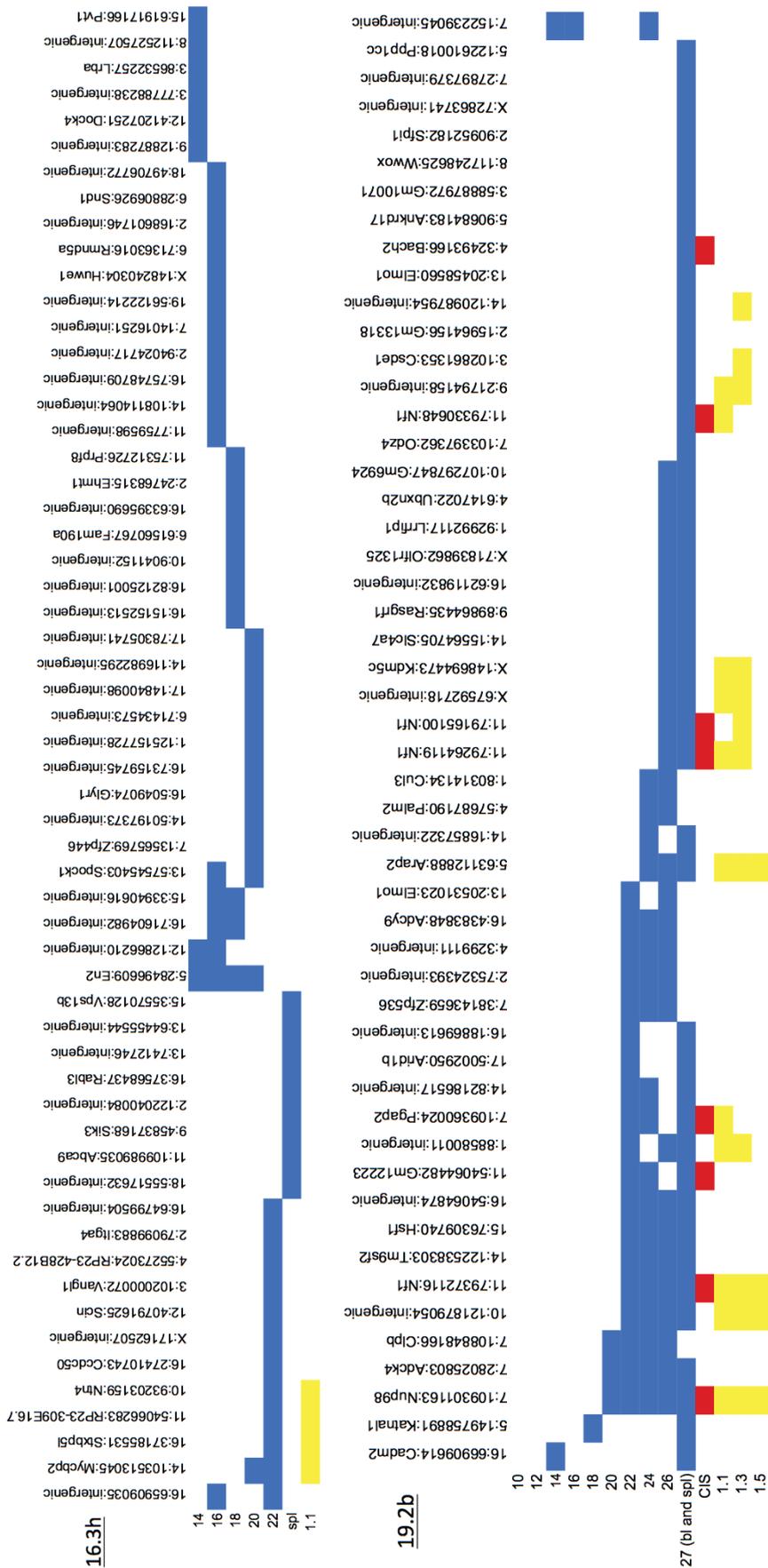
These tables show the shared integrations on blood, primary and recipient tumours for each of the mice that were serially bled. The identity of the mouse is shown at the top left. The precise position of each integration is shown across the top. Integrations in a position are indicated by the coloured squares (blue = serial blood or primary tumour spleen or lymph node, yellow = recipient tumour). The integrations that fall within CISs are indicated in red. The age of the mouse is shown in weeks for the blood samples. IDs of the recipient tumours are indicated. Integrations are shown by the order in which they accumulated and only integrations that persisted on multiple samples are shown. Not all integrations in a given tumour could be represented in these tables.

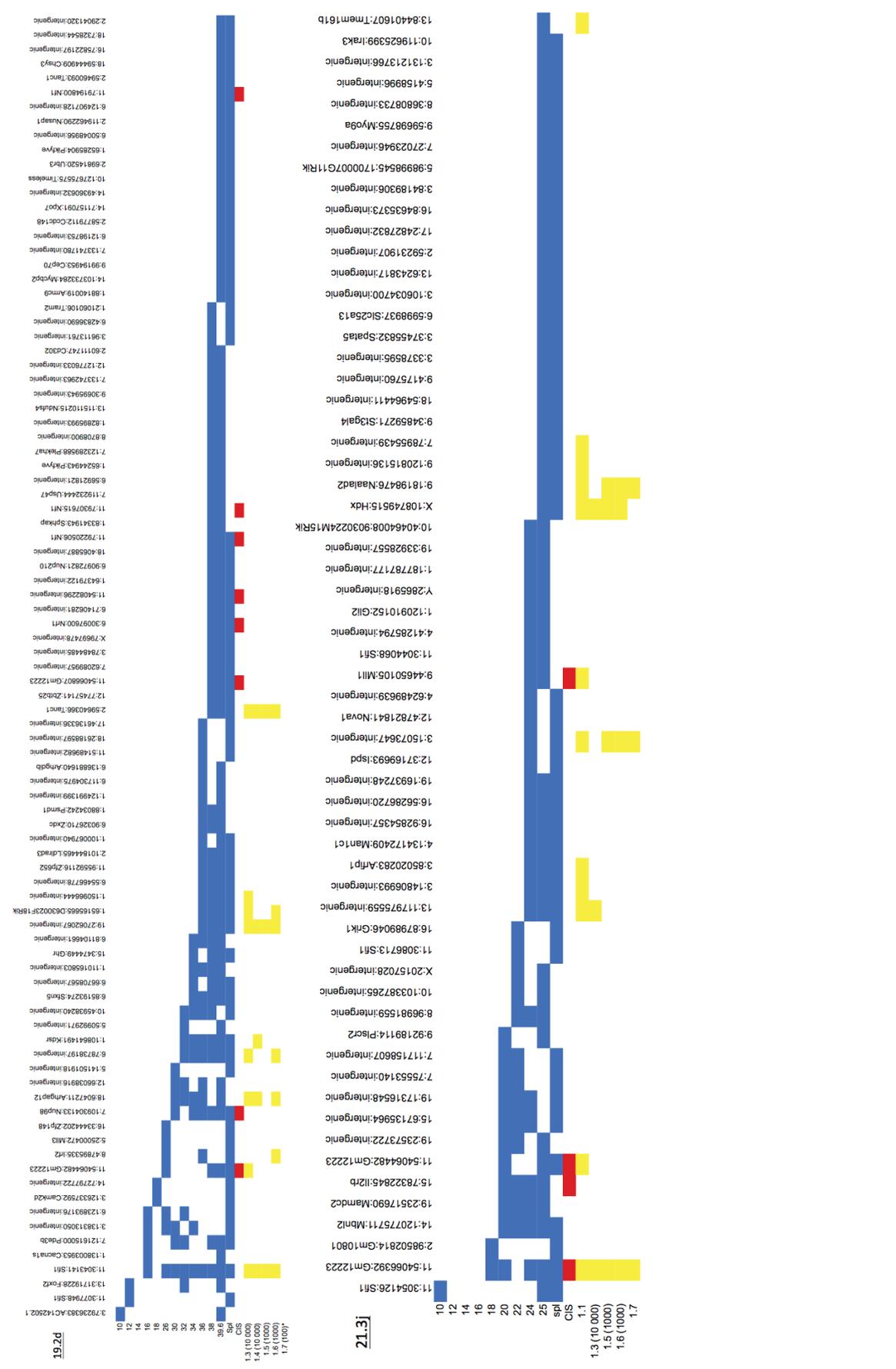


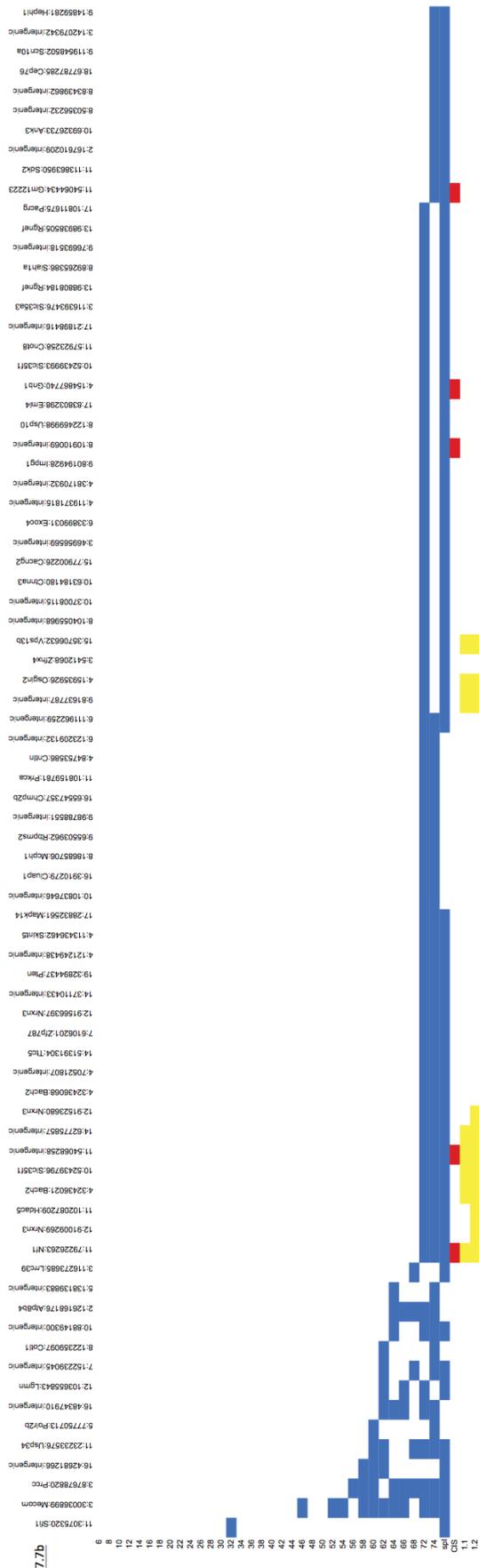
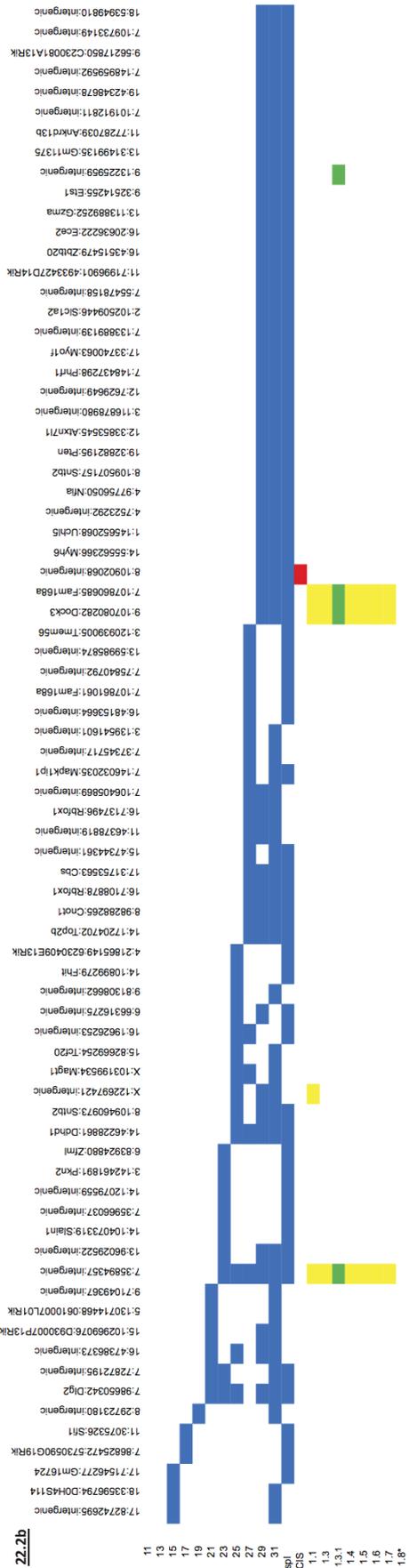












Appendix 4D: Details of the transplant mice

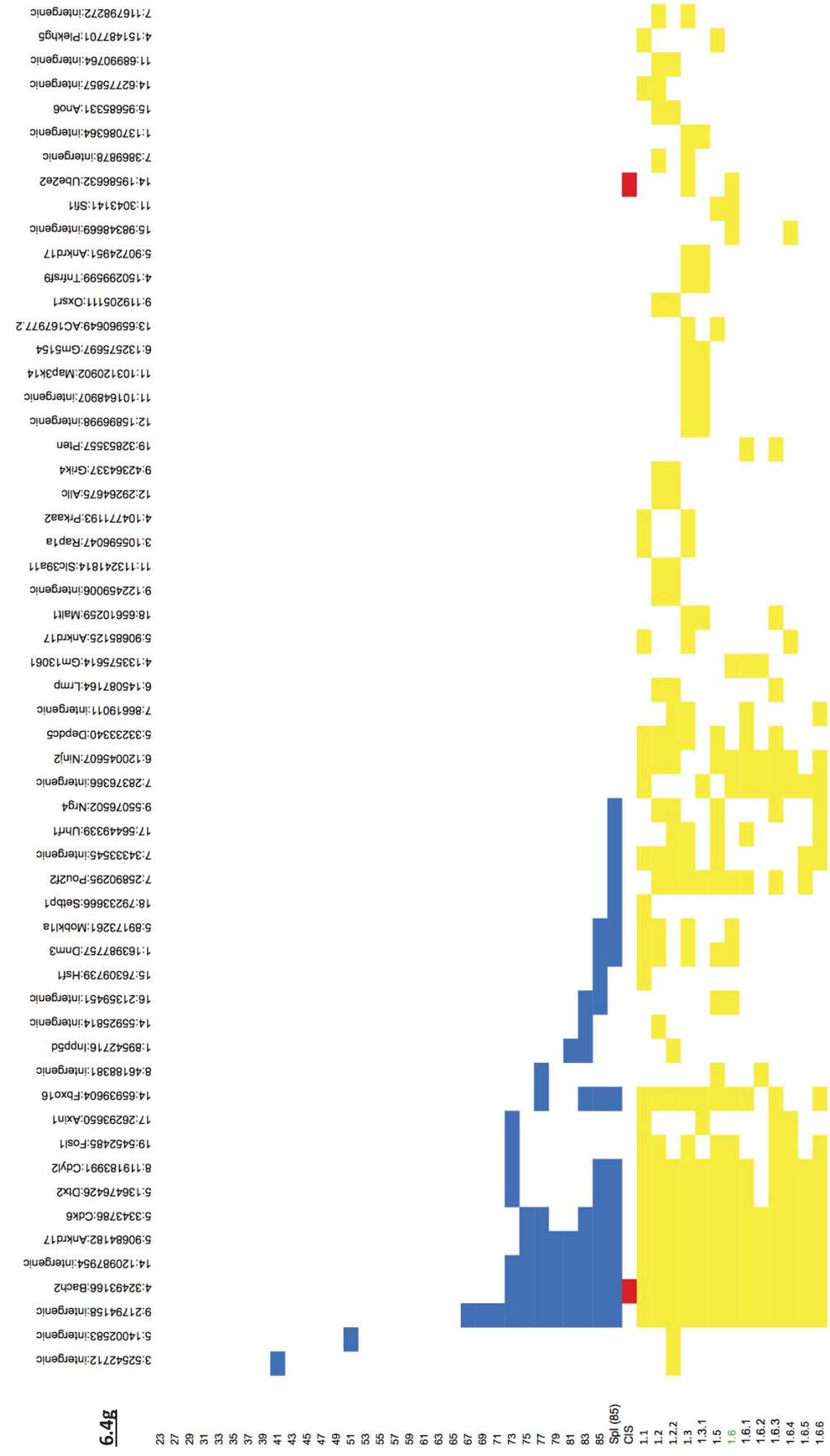
Mouse	Cell Dose	Lifetime (days) post transplant	Necropsy findings	Blood film	Histopath	WCC	Hb	Hct	Plt	MCV	Lymph/blasts	Gran
4.4a		300	spleen 0.7g, liver 3.1g	CMML like	myeloid leukaemia	398	9.8	36.7	313	61	172	173
1.1	1 million	26	spleen 0.5g, liver 1.6g	AMML	myeloid leukaemia in blood, bone marrow, spleen, liver, LN, bone and peritoneum	488	14.1	55.6	575	55	137	288
1.2	1 million	28	spleen 0.5g, liver 2g, 3x pale areas liver, small mesenteric and 1x inguinal LN	AMML	myeloid leukaemia in blood, bone marrow, spleen, liver, kidney, lung, LN, muscle, peritoneum	694	13.3	52.3	557	56	155	462
1.3	1 million	28	spleen 0.6g, liver 2.7g, 7small LN	AMML	myeloid leukaemia in blood, spleen, liver, kidney, lung, lymph node, bone marrow, muscle, meninges and peritoneum	187	12	46.7	485	59	53	112
1.1.1	1 million	24	spleen 0.6g, liver 1.8g	AMML	myeloid leukaemia in blood, liver, spleen, bone marrow, muscle, minor LN only, and meninges.	248	12.4	45.4	523	60	34	192
1.1.2	1 million	37	paraspinal mass left lumbar region 1.3x0.8cm, arising off pelvis, spleen 0.6g, liver 1.7g	AMML	myeloid leukaemia in blood, spleen, liver, lymph nodes, bone marrow, muscles and meninges	266	10	42.6	467	74	230	27
1.1.3	1 million	119	macroscopic tail lesion ~1cm, spleen 0.1g, liver 1.3g	AMML Leukopenia and thrombocytosis	spleen EMH, tail lesion ant injection site myeloid leukaemia in blood, spleen, liver, renal LN, stomach, bone marrow and muscle	2.7	13.7	46.7	1132	56	0.8	1.6
1.2.1	1 million	34	splenomegaly 0.4g, liver 1.5g, LN right axilla	AMML	myeloid leukaemia in blood, spleen, liver, bone marrow and muscle	347	10.4	36.4	232	59	104	197
1.2.2	1 million*	82	rear leg paralysis, spleen 0.1g, liver 1.3g dilated appendix and caecum, no mass lesion, spleen 0.4g, liver 1.7g	Leukopenia, thrombocytosis,	spleen extramedullary haematopoiesis	2	16.7	60	1868	57	0.8	0.8
1.2.3	1 million	27	spleen 0.4g, liver 1.9g	AMML	myeloid leukaemia in blood, spleen, liver, bone marrow and muscle	273	12.5	48.5	482	56	95	140
1.3.3	1 million	25	spleen 0.4g, liver 1.9g	AMML	myeloid leukaemia in blood, spleen, liver, bone marrow, muscle and peritoneal	187	14.2	53.5	629	58	62	98
1.3.2	1 million	26	spleen 0.4g, liver 1.8g	AMML	myeloid leukaemia in blood, spleen, liver, bone marrow and muscle	268	12.5	48	441	56	102	128
1.3.1	1 million	31	spleen 0.6g, liver 2.1g	AMML	myeloid leukaemia in blood, spleen, liver, bone marrow and muscle	150	15.4	57.5	577	58	37	96
1.1.1.1	1 million	19	hunched, thin, weak rear legs, spleen 0.4g, liver 1.6g	AMML	myeloid leukaemia in blood, spleen, liver, bone marrow and muscle and peritoneum	455	14.4	56.5	654	62	150	245
1.1.1.2	1 million	21	dragging hind limbs, piloerection, reduced mobility spleen 0.5g liver 1.9g	AMML	myeloid leukaemia in blood, spleen, liver, bone marrow and muscle and meninges	265	10.8	38.8	548	60	120	110
1.1.1.3	1 million	25	spleen 0.5g, liver 1.3g, no lymphadenopathy	AMML	myeloid leukaemia in blood, spleen, liver, kidney, lung, bone marrow and muscle and meningeal	135	13.5	51.5	658	59	57	62
1.1.1.1.1	1 million	22	spleen 0.6g, liver 1.9g	AMML	myeloid tumour in blood, spleen, liver, bone marrow, muscle and meninges	396	12.5	45.4	426	60	114	222
1.1.1.1.2	1 million	22	spleen 0.7g, liver 2.2g	AMML	myeloid leukaemia in blood, spleen, liver, bone marrow, muscle	384	14.9	55.5	625	62	146	187
1.1.1.1.3	1 million	25	spleen 0.3g, liver 1.9g	AMML	myeloid leukaemia in blood, spleen, liver, bone marrow and muscles and meninges	466	14.2	32.8	533	38	138	252
1.1.2.1	1 million	48	spleen 0.6g, 7small ing LN, liver 1.7g	AML with maturation	myeloid leukaemia in blood, spleen, BM, liver, muscle, kidney	143	15.1	56.5	622	61	37	87
1.1.2.2	1 million	40	intestine full of gas, pale extremities, hunched, piloerect, spleen 0.2g, liver 1.3g	AML with high % blasts	myeloid leukaemia in blood, BM, spleen, muscle, liver	208	15.4	65.5	1074	63	191	13
1.1.2.3	1 million	39	spleen 0.6g, liver 2.1g	AML with maturation	myeloid leukaemia in blood, bone marrow, spleen, liver, muscle	152	13.8	50.8	639	58	70	59
6.4g		596	lump on leg, spleen 0.5g, liver 2.5g		Angiosarcoma leg, follicular hyperplasia spleen	14.1	8.7	32.9	679	48	8.1	4.9
1.1	1 million	99	spleen 0.7g, liver 2.1g, kidney 0.8g, large pale kidneys 2x1x1cm, mesenteric LN	Undifferentiated blasts with high WCC	Leukaemia without maturation (B220 pos) BM, spleen, liver, LN, kidney, lung, muscle, stomach	294	15	56	552	59	196	82
1.2	1 million	91	moribund, rear leg paralysis, liver 4g, spleen 1.3g	AML with some maturation	Leukaemia with minimal myeloid differentiation (B220 pos) BM, spleen, liver, kidney, lung, LN, muscle	247	16.4	60.2	235	56	137	90
1.3	1 million	95	moribund, spleen 0.9g, liver 2.1g, kidney enlarged, large pale kidneys 2x1x1cm	No sample	Leukaemia without maturation (B220 pos) BM, spleen, kidney, liver, muscle							
1.4	1 million	134	spleen 1.8g, liver 4.6g, enlarged pale kidneys 0.7g	AML	Leukaemia with minimal myeloid differentiation (B220 pos) BM, spleen, kidney, liver, lung	68	18.7	>70	1470	61	5.4	1.2
1.5	1 million	91	pale, liver 3.3g, spleen 2g, big lungs	AML	Leukaemia with minimal myeloid differentiation (B220 pos) BM, spleen, kidney, lung, liver, muscle	451	15.4	54.1	515	59	221	194
1.6	1 million	83	spleen 0.9g, liver 2.5g, enlarged kidney 1.2g	Leukaemia	Leukaemia without maturation (B220 pos) spleen, LN, liver, kidney, lung, bone marrow, peritoneal	66.4	17.3	66.9	803	55	38.5	21.8
1.2.1	1 million	29	spleen 1g, liver 2.4g	AML	Leukaemia with minimal myeloid differentiation BM, spleen, LN, liver, lung, kidney	52.7	16.2	63	244	56	11.6	37.7
1.2.2	1 million	33	spleen 0.9g, liver 3.2g, big lungs	AML	Leukaemia with minimal myeloid differentiation BM, spleen, LN, liver, lung, kidney, adrenal	75.1	11.7	51.4	381	62	47.3	23.5
1.3.1	1 million	38	spleen 1g, liver 2.7g	AML	Leukaemia with minimal myeloid differentiation BM, spleen, liver, lung, kidney, muscle	250	11.8	53.6	429	67	204	38
1.3.1	1 million	38	spleen 0.7g, liver 2.6g, found dead 19/11/11 and necropsied 25/11/11	No sample	degenerate, likely tumour present BM, spleen, liver, lung, kidney but degenerate							
1.6.1	1 million	33	spleen 0.9g, liver 2.4g, thymomegaly, big lungs	Leukaemia	Leukaemia without maturation (B220 pos) BM, spleen, liver, lung, kidney, muscle	451	12.1	58.7	399	73	397	39
1.6.2	10 000	39	spleen 0.7g, liver 3.1g, large pale lungs	Leukaemia	Leukaemia without maturation (B220 pos) BM, spleen, liver, kidney, lung, muscle, peritoneal	72	13.1	65.2	504	71	63	7
1.6.3	10 000	48	spleen 0.8g, liver 2.3g, kidney 0.5g and pale with abnormal texture	Leukaemia	Leukaemia without maturation (B220 pos) BM, spleen, liver, kidney, lung	37.1	8.8	33.7	183	51	19.5	13.8
1.6.4	1000	48	spleen 1.1g, liver 2g, kidneys 0.3g and look normal	Leukaemia	Leukaemia without maturation (B220 pos) BM, spleen, liver, kidney, lung, muscle	47.6	14.1	51.8	1027	69	34.6	10.3
1.6.5	1000	49	moribund, agonal breathing, congested vessels, spleen 0.6g, liver 1.8g	AML	Leukaemia with minimal myeloid differentiation BM, spleen, liver, lung, kidney, pancreas	100	12.5	39.5	312	73	61	31
1.6.6	100	61	spleen 1.1g, liver 3g	AML	Myeloid leukaemia BM, spleen, liver, lung, kidney	77	13	50.3	264	54	37	33

Mouse	Cell Dose	Lifetime (days) post transplant	Necropsy findings	Blood film	Histopath	WCC	Hb	Hct	Plt	MCV	Lymph/blasts	Gran
6.4h		220	spleen 0.5, liver 2.3	Undifferentiated leukaemia	Undifferentiated leukaemia	34.5	13	52.6	809	58	25	7.2
1.1	1 million	49	spleen 0.7, liver 4.3g	Undifferentiated leukaemia	Undifferentiated leukaemia spleen, liver	57.9	8.2	42.5	218	70	41.4	14
1.2	1 million	49	spleen 0.6g, liver 3.4g	Undifferentiated leukaemia	Undifferentiated leukaemia spleen, liver	44.3	9.2	40.6	191	87	30.3	12
1.3	1 million	47	bloody pleural effusion, spleen 0.6g liver 1.7g	Undifferentiated leukaemia	Undifferentiated leukaemia BM, muscle, peritoneum, liver, LN, spleen	13	10	38.6	451	83	7.6	4.7
1.4	1 million	39	spleen 0.2g, liver 1.6g, hydrocephalus	not sent	not sent	16.6	12.6	48.8	860	56	12.6	2.8
1.5	500 000	45	spleen 0.4g, liver 2.6g	Undifferentiated leukaemia	Undifferentiated leukaemia BM, muscle, spleen, liver, lung, destructive of bone	68.1	11.4	42.2	528	57	43.4	18.2
1.6	100 000	41	spleen 0.5g, liver 2.4g	Undifferentiated leukaemia	Undifferentiated leukaemia BM, spleen, liver, muscle, kidney	68.1	12.9	48.6	547	59	12.9	16.4
1.7	10 000	77	spleen 0.3g, liver 2g, left leg mass	Undifferentiated leukaemia	Undifferentiated leukaemia BM, spleen, LN, muscle, liver, destructive of bone, invasive ++ (LN ->thymus?)	20.9	10.7	38.7	474	58	14.2	5.3
1.8	10 000	80	spleen 0.5g, liver 2.7g	Undifferentiated leukaemia	Undifferentiated leukaemia BM, spleen, liver, muscle, kidney and peritoneal, BM patchy replacement but periosteal involvement and into muscle	66.7	12	46.4	233	61	39.7	22
1.9	1000	80	spleen pale, 0.6g, liver 5.7g, bloody ascites	Undifferentiated leukaemia	Undifferentiated leukaemia liver, spleen, BM, kidney, BM surprisingly little invasion	69.4	10.7	41.1	214	71	34.6	27.6
1.10	1000	86										
1.11	100	107	spleen 0.4g, liver 3.4g, mouse 28.9g	Undifferentiated leukaemia	Undifferentiated leukaemia BM, spleen, liver, muscle, kidney +/-	253	9.5	38	234	71	171	63
1.12	100	24	spleen 0.2g, liver 2.3g		no lesion	14.3	11.6	41.5	356	33	4.4	7.8
1.3.1	1 million	36	spleen 0.5g, liver 3.1g, hindlimb paralysis	Undifferentiated leukaemia	Undifferentiated leukaemia BM, spleen, muscle, liver	52.1	11.5	44	522	56	31.6	15.8
1.3.2	1 million	25	spleen 0.6g, liver 2.4g, dragging right hind leg	Undifferentiated leukaemia	Undifferentiated leukaemia BM, spleen, muscle, liver, ovary	80	8.5	31.6	349	61	54	28
1.3.3	1 million	25	spleen 0.8g, liver 2.6g	Undifferentiated leukaemia	Undifferentiated leukaemia BM, spleen, liver, muscle, peritoneum	40.8	6.9	24.3	342	62	22.4	15.4
7.5b		350	spleen 1.2g, liver 2.4g, inguinal LN, splenunculus	High WCC with few blasts	Myeloid leukaemia with maturation; BM, spleen, LN, liver, muscle	114	12.3	46	503	59	22	83
1.1	1 million	63	spleen 0.5, liver 2.2	Myeloid leukaemia with many blasts and maturation	Acute myeloid with some maturation; BM, spl, ln, liver, kidney, peritoneum	446	5.8	23.5	228	82	251	13.8
1.2	1 million	75	spleen 1.1g, liver 3.2g	Myeloid leukaemia with many blasts and maturation	Acute myeloid with some maturation; BM, spleen, liver, kidney, lung, muscle, peritoneum	299	5.4	19.7	211	71	95	164
1.2.1	1 million	46	spleen 0.6g, liver 2.1g	Myeloid leukaemia with >80% blasts	Acute myeloid with minimal differentiation; BM, spleen, LN, liver, kidney	201	6.1	24.4	297	71	171	25
1.2.2	1 million	46	spleen 0.7g, liver 2g	Myeloid leukaemia, mainly blasts with some maturation	Acute myeloid with minimal differentiation; perianal subcutaneous leukaemia, BM, spl, liver, kidney, muscle	129	5.1	21.5	511	70	105	18
1.2.3	1 million	46	spleen 0.7g, liver 2.7g	Myeloid leukaemia with many blasts and maturation	Acute myeloid, virtually undifferentiated; BM, spleen, liver, LN, kidney, fat, ovary, lung, muscle	438	7.1	26.2	222	74	380	62
1.3	1 million	75	spleen 0.9g, liver 2.2g	Myeloid leukaemia with many maturing cells	Myeloid leukaemia with maturation; BM, spleen, liver, muscle, kidney	692	11.9	44.1	375	60	94	526
1.3.1	1 million	28	spleen 0.6g, liver 1.3g	Myeloid leukaemia with many maturing cells	Acute myeloid with maturation; BM, spleen, liver, muscle	429	12.8	45.5	764	56	80	324
1.3.2	1 million	28	spleen 0.1g, liver 1.6g	Myeloid leukaemia with many blasts and maturation	Acute myeloid with maturation; BM, spleen, liver, muscle, kidney	284	11.4	42.2	791	57	45	207
1.3.3	1 million	32	spleen 0.6g, liver 1.6g	Myeloid leukaemia with many blasts and maturation	Acute myeloid with maturation; BM, spl, liver, peritoneum	398	10.6	39.3	661	61	51	306
7.5c		257	spleen pale, 3.7g, liver 3.9g	Myeloproliferative with progression, giant platelets, thrombocytosis, leukoerythroblastia	Myeloid leukaemia with maturation, megakaryocytes +++ in spleen. Involves spleen, liver, bone marrow but not heart, lung or kidney	78.3	22.8	75	4930	67	40.6	34.4
1.1	1 million	273	cultured									
1.2	1 million	273	cultured									
1.3	1 million	273	cultured									
1.4	1 million	210	distended intestine without tumour, spleen 0.1g, liver 1.4g	thrombocytosis, otherwise normal	megakaryocytes increased in spleen	8	12.1	44.5	>2200	53	2.8	4
1.5	1 million	210	stomach distended 4cm, rest normal, spleen <0.1g, liver 1.7g	MPO with eosinophilia	MPO, mild bowel inflammation	5.8	11	40.2	1230	55	2.7	2.6
1.6	1 million	399	pus in bladder/ureter; spleen 0.1g, liver 1.3g	thrombocytosis only	Myeloid leukaemia with maturation, BM, spleen, liver, kidney, not muscle, liver, spleen sclerosis and eosinophilia, megakaryocytes increased and abnormal in BM and spleen	4.3	14.1	54	1980	56	1.9	1.9
1.7	1 million	175	spleen 0.2g, liver 5.5g	None	Myeloid disease							
1.8	1 million	148	spleen <0.1g, liver 1.3g ascites and pleural effusion, pale kidneys, spleen <0.1g, liver 1g	Low WCC otherwise normal	MPO with eosinophilia, megakaryocytes and eosinophilia increase BM, spleen, sclerosis and eosinophilia in lungs and liver	3.8	14.9	54.7	1094	54	1.2	2.3
1.9	1 million	238	not available	not available	sclerotic kidneys with immune deposits in glomeruli	1.2	5.7	15.7	>2200	42	1	0.2
7.5h		182	spleen 1.3g, liver 4g	Myeloid leukaemia with maturation	Myeloid leukaemia with maturation; liver, BM, spleen, LN	627	18.3	>70	733	82	146	411
1.1	1 million	162	Cultured									
1.2	1 million	99	spleen 0.9g, liver 4.2g	Very poorly differentiated, ?myeloid	Myeloid leukaemia with little differentiation; BM, spl, liver, kidney, lung, thymus	233	14.3	50.8	362	57	71	138
1.3	1 million	176	Cultured									
1.4	1 million	330	Cultured									
1.5	1 million	304	Cultured									
1.6	1 million	190	Pus filled mass ~1.2cm diameter right inguinal region, spleen 0.2, liver 2.2		Benign PMNs in liver, abscess in skin	17.5	11	42.3	1890	51	6.4	8.5
1.2.1	1 million	36	peritoneal haemorrhage, kidneys pale and abnormal, spleen 0.6g, liver 3.8g	if+	Acute myeloid leukaemia with little differentiation; BM, Spl, LN, liver, kidney, lung, kidney, muscle	111	12	44.5	387	60	37	62
1.2.2	1 million	36	spleen 1.4g, liver 6g, mouse 32.7g, 7LN thorax	Acute leukaemia with very high blast count, very little differentiation	Acute myeloid leukaemia with little differentiation; BM, Spl, LN, liver, kidney, lung, muscle, peritoneum	357	14.5	56.3	316	71	115	203
1.2.3	1 million	25	spleen 0.8g, liver 2.4g, mouse 30.8g	Acute leukaemia with very high blast count, very little differentiation	Acute myeloid leukaemia with little differentiation; BM, Spl, LN, spleen, liver, kidney, muscle, fat	70.4	14.7	54.6	634	55	21.6	40.8
16.3b		301	Spleen 0.6, liver 2.7	Myeloid leukaemia with few blasts	Myeloid leukaemia with maturation; BM, spleen, LN, liver, muscle	109	15.8	59	367	56	54	43
1.1	1 million	52	Spleen 0.5g, liver 1.8g, small right inguinal LN	Myeloid leukaemia with maturation	Myeloid leukaemia with maturation; BM, spleen, LN, liver, lungs, peritoneum, kidney, muscle	307	14	53.6	409	60	102	156
1.2	1 million	62	spleen 0.5g, liver 1.6	Myeloid leukaemia with numerous blasts and maturation	Acute myeloid leukaemia with some maturation; BM, spleen, LN, liver, muscle, kidney	523	15.5	59.7	525	63	128	325
1.1.1	1 million	24	Hindlimb paralysis, spleen 0.3g, liver 1.5g	Myeloid leukaemia with numerous blasts and maturation	Acute myeloid leukaemia with some maturation; BM, spleen, liver, kidney, & probable benign teratoma	40.9	16.5	59.8	571	55	12.4	22.5
1.1.2	10 000	165	found dead, no masses, pale kidneys, spleen 0.1g, liver 2.7g		there is a bm cytoplasm							
1.1.3	1000	102	bowel prolapse, no mass, spleen <0.1g, liver 1.7g	Reactive? Left shift of myeloid series without elevated count	Normal	6.2	9	33.2	1666	54	2.2	2.8
1.1.4	100	857	Pale, spleen 0.3g, liver 1.6g		Normal	7.7	13.2	52	1979	55	3.8	2.9
1.2.1	1 million	33	spleen 0.9g, liver 3.9g, enlarged lungs spotted with blood	Myeloid blasts with maturation	Undifferentiated leukaemia, BM, spleen, liver, LN, lung +++, muscle +++, some eos in BM							
1.2.2	10 000	54	Spleen 0.8g, liver 2g	Myeloid leukaemia with numerous blasts and maturation	Acute myeloid leukaemia with some maturation; spleen, BM, muscle, liver, kidney, lung	279	10	36.9	990	57	66	183
1.2.3	1000	132	Shaking, inactive, spleen 0.1g, no lymphadenopathy	?	Some increase in myeloid cells in spleen, not diagnostic	8.6	12	41.8	532	55	1.2	69
1.2.4	100	363	Cultured									

Mouse	Cell Dose	Lifetime (days) post transplant	Necropsy Findings	Blood film	Histopath	WCC	Hb	Hct	PLT	MCV	Lymph/blasts	Gran
16.3e		206	spleen 0.7g, liver 2.7g	Myeloid leukaemia with blasts and maturation	Myeloid leukaemia with maturation; BM, spleen, LN, liver, muscle, lung no histopath	131.2	8.8	32.6	147	71	35.4	78.8
1.1	1 million	12	Acute, spl 0.1g, liver 1.5g	Normal	Acute myeloid leukaemia with limited maturation; BM, spl, LN, liver, muscle	193	8.4	32.4	215	59	74	89
1.2	1 million	41	Spleen 0.4g, Liver 1.5g	Myeloid leukaemia with numerous blasts and maturation	Acute myeloid leukaemia with maturation; BM, spleen, liver, muscle	47.8	12.7	39	530	63	13.8	29.3
1.3	1 million	62	Spleen 0.5g, liver 1.6g	Myeloid leukaemia with numerous blasts and maturation	Acute myeloid leukaemia with maturation; BM, spleen, muscle, liver	43.5	10.8	42.3	607	57	23.9	14.7
1.3.1	1 million	39	Hindlimb paralysis, spleen 0.3g, liver 1.3g	Myeloid leukaemia with numerous blasts and maturation	Acute myeloid leukaemia with maturation; BM, spleen, muscle, liver	103	9.7	35.2	640	61	51	40
1.3.2	1 million	39	Hindlimb paralysis, spleen 0.3g, liver 1.4g	Myeloid leukaemia with numerous blasts and maturation	Acute myeloid leukaemia with maturation; BM, spleen, liver, muscle, liver	172	10.1	40	509	60	83	67
1.3.3	1 million	39	spleen 0.5g, liver 1.4g	Myeloid leukaemia with numerous blasts and maturation	Myeloid leukaemia with probable lymphoma as secondary diagnosis; Spleen, liver, kidney, LN, thymus, BM. Also B cell infiltrate in lung and B and T infiltrate in liver and kidney	45.8	11.9	47.2	173	59	15.1	24.5
16.3f		387	spleen 1g, liver 2.2g, inguinal and axillary LN	Myeloid leukaemia with blasts and differentiated cells	Myeloid leukaemia in spleen, BM and blood	37.5	16.1	57.9	79	52	14.8	16.3
1.1	1 million	33	hindlimb paralysis, spleen 0.2g, liver 1.2g	AML or MPD	myeloid leukaemia in blood, spleen, liver, kidney, bone marrow and muscle	566	8.8	35.6	687	69	233	253
1.2	1 million	46	hydrocephalus, piloerection, spleen 0.3g, liver 1.4g	AML	myeloid leukaemia in blood, spleen, liver, LN, bone marrow, muscle, meninges and fat. Probable AML in tail lesion	514	12	45.7	557	61	253	186
1.3	1 million	69	tall mass 2cm x1mm, purpuric and wraps around tail, spleen 0.5g, liver 1.5g	AML	myeloid leukaemia in blood, spleen, liver, kidney, BM and muscles and meninges	362	17.9	68	1025	56	121	200
1.4	1 million	31	spleen 0.5g, liver 1.7g, excreted right eye	AMML	myeloid leukaemia in blood, spleen, liver, kidney, LN, stomach, periosteum, meninges, bone marrow and muscle	11	11.8	41.3	431	52	2.1	7.5
1.5	1 million	32	diarrhoea, dilated U, SI and stomach, no overt mass, spleen 0.2g, liver 1.5g	AML or MPD	Reparing myocardial infarction, extramedullary haematopoiesis, no malignancy	7	12.8	42.9	234	52	1.7	4.5
1.6	1 million	368	culled									
1.7	10 000	292	hindlimb paralysis, piloerect, liver 1.4g, spleen 0.1g	NAD								
1.8	1000	29	moribund, hindlimb paralysis, blood stained urine, two pale areas in right kidney, spleen 0.1g, liver 1.1g	Reactive changes								
1.9	1000	269	culled									
1.10	100	369	culled									
1.11	100	369	culled									
1.2.1	1 million	29	spleen 0.4g, liver 1.7g	AML	myeloid leukaemia in blood, spleen, liver, kidney, bone marrow, muscle and periosteum	303	11.2	43.3	849	59	97	162
1.2.2	1 million	26	spleen 0.4g, liver 1.7g	AMML	myeloid leukaemia in blood, spleen, liver, LN, BM and muscles and may be thymus	309	11.7	45.7	787	57	125	142
1.2.3	1 million	22	spleen 0.4g, liver 2g	AMML	myeloid leukaemia in blood, spleen, liver, kidney, LN, bone marrow and muscle and periosteum	415	12.3	46.6	818	61	285	94
1.4.1	1 million	21	partial hindlimb paralysis, spleen 0.5g, liver 1.5g	AMML	myeloid leukaemia in blood, spleen, liver, kidney, skin, lung, bone marrow and muscles and meninges	340	10.5	39.4	642	60	130	164
1.4.2	1 million	21	spleen 0.4g, liver 1.3g	AMML	myeloid leukaemia in blood, spleen, liver and kidney and marrow and muscle and meninges, great picture	420	13.5	50.9	716	60	209	161
1.4.3	1 million	21	spleen 0.4g, liver 1.8g	AMML	myeloid leukaemia in blood, spleen, liver, kidney, marrow, muscle	377	15.8	61.6	572	60	153	173
16.3G		231	Spleen 0.8g, liver 2.9g, no LN or masses	Myeloid leukaemia CMML like	Myeloid leukaemia with differentiation; Spleen, liver, LN, thymus, BM	167	14.5	52.8	129	62	48	97
1.1	1 million	52	dilated bowel, no mass, spleen 0.4g, liver 1.3g	CMML like	Myeloid leukaemia in blood, spleen, lung, BM, muscle and bone. CMML in and around bone	504	13.9	52.3	983	59	185	247
1.3	1 million	31	spleen 0.6g, liver 2.4g	AMML	myeloid leukaemia in blood, spleen, liver, BM, muscle and periosteum	545	18.9	>70	750	62	272	201
1.2	1 million	37	spleen 0.5g, liver 1.5g, Rt inguinal LN	AMML	myeloid leukaemia in blood, spleen, kidney, spleen, lung, muscle, BM, meninges and periosteum	500	13.3	59.3	953	66	448	39
1.3.1	1 million	18	spleen 0.5g, liver 1.5g, moribund, hindlimb paralysis	AMML	myeloid leukaemia in blood, spleen, liver, bone marrow, muscle	117	15.5	59.5	1199	59	36	64
1.3.2	1 million	19	spleen pale, 0.3g, liver 1.5g, weak rear legs	AMML	myeloid leukaemia in blood, spleen, liver, bone marrow	72.8	15.8	56.7	1008	56	21.7	41.7
1.3.3	1 million	19	spleen 0.3g, liver 1.3g, hindlimb paralysis	AMML	myeloid leukaemia in blood, spleen, liver, bone marrow	259	16	58.4	1031	56	60	16.4
1.2.1	1 million	21	hindlimb paralysis, spleen 0.5g, liver 1.5g	AMML	myeloid leukaemia in blood, spleen, liver; bone marrow and periosteum	162	16.7	61.2	962	55	66	73
1.2.2	1 million	21	spleen 0.5g, liver 1.6g	AMML	myeloid leukaemia in blood, spleen, liver, bone marrow, muscle, bone and periosteum	193	15	55.6	747	58	65	100
1.2.3	1 million	21	hindlimb paralysis, pale spleen 0.5g, liver 1.5g	AMML	myeloid leukaemia in blood, spleen, liver, bone marrow	165	14.8	54.6	456	56	68	72
16.3h		142	Spleen 0.53g, liver 1.65g	AMML	Myeloid leukaemia in blood, spleen, liver, BM	58	14.1	54.3	739	56	12.8	41.1
1.1	1 million	76	Spleen <0.1g and congested ?infarcted, liver 2.3g	NAD	No tumour	3.9	15.3	56.9	1705	54	1.4	2.1
1.2	1 million*	176	culled									
1.3	1 million	176	culled									
1.4	1 million	170	piloerect, spleen <0.1g, liver 1.2g	NAD	No tumour	7.3	22.6	>70	1198	55	3.6	2.6
1.5	1 million	270	piloerect, hunched, NAD									
1.6	1 million	256	spl et. 1g, liver 1.5g									
22.2b		216	spleen 1.1g, liver 2.4g	Myeloid leukaemia with many blasts and maturation	Myeloid leukaemia with blasts, BM, spleen, liver, muscle	281	9.6	36.8	165	61	89	149
1.1	1 million	25	spleen 0.4g, liver 1.5g	Myeloid leukaemia with blasts and maturation, more blasts than 22.2b	Myeloid leukaemia with some maturation; BM, spleen + + +, muscle + +, liver +, kidney/liver-	668	10.8	43.6	714	63	307	261
1.2	1 million	25	spleen 0.5g, liver 2.4g	Myeloid leukaemia with blasts and maturation, more blasts than 22.2b	Myeloid leukaemia with some maturation; BM, spleen + + +, liver, muscle, periosteal + +, kidney, lung-	722	10.1	40	822	64	254	383
1.3	1 million	22	hindlimb paralysis, spleen 0.7g, liver 2.2g	Myeloid leukaemia with maturation	Myeloid leukaemia with maturation, BM, spleen + + +, liver +, kidney +, lung and muscle, periosteal + +	324	14.8	57.4	531	59	178	101
1.4	1 million	33	spleen 0.6g, liver 2.3g, mesenteric LN	Myeloid leukaemia with maturation	Myeloid leukaemia with maturation BM, spleen, ln, liver + + +, kidney +, muscle + +, lung -	544	10.1	37.8	462	60	26.6	19.9
1.5	10 000	53	spleen 0.7g	Myeloid leukaemia with blasts and maturation	Myeloid leukaemia with some maturation; spleen + + +, lung +, kidney?-, no bone or ln or muscle sample, peritoneal + + +	317	16.3	>70	679	66	282	26
1.6	10 000	33	spleen 0.5g, liver 2.1g	Myeloid leukaemia with blasts and maturation	Myeloid leukaemia with some maturation, BM + + +, spleen + + +, liver, muscle + +, kidney, lung-	623	11.3	43.9	677	63	38.3	15.8
1.7	1000	61	spleen 0.5g, liver 1.8g	Myeloid leukaemia with blasts and maturation	Myeloid leukaemia with some maturation, BM + + +, spleen, liver + +, muscle +, kidney, lung -, periosteal + +	171	13.9	63.5	738	67	148	17
1.8	1000	103	antalgic gait favouring right hindlimb, spleen <0.1g, liver 2.3g	Benign monocytosis	Inflammation of knee	19.7	11.5	45.9	802	31	7.2	9.8
1.9	100	180	reduced activity, piloerect, lungs speckled ?patchy haemorrhages, otherwise NAD, spleen <0.1g, liver 2.1g	Unremarkable	Floral arthritis in knees	13	17.4	65.6	1109	54	3.1	8.2
1.3.1	1 million	38	partial hindlimb paralysis, spleen 0.3g, liver 1.3g	Unremarkable	BM, spleen + + +, liver, muscle + + +, kidney-	167	11.9	45.6	802	57	53	89
1.3.2	10000	333	piloerect, swollen abdomen, spleen 0.1g, liver 2.6g	Unremarkable	No tumour seen	1.3	11.4	42.5	37	55	0.8	0.4
1.3.3	1000	333	piloerect, swollen abdomen, spleen 0.3g, liver 2.4g	Unremarkable	No tumour seen	11.6	12.7	47.1	1593	54	4.7	5.3
1.3.4	100	391	piloerect, pale, immobile, spleen <0.1g, liver 0.5g									

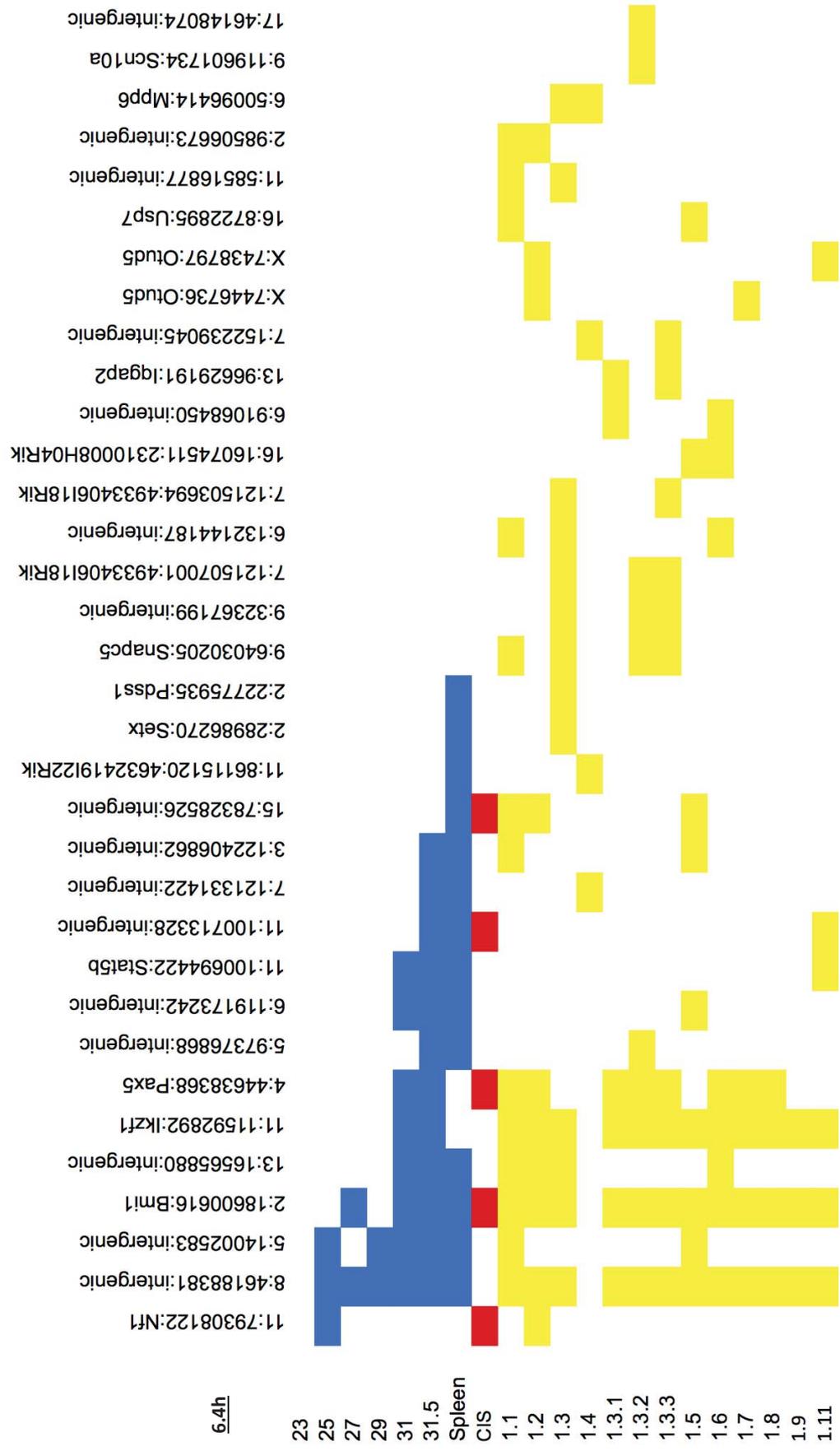
Mouse	Cell Dose	Lifetime (days) post transplant	Necropsy findings	Blood film	Histopath	WCC	Hb	Hct	Ht	MCV	Lymph/blasts	Gran
7.7b		515	spleen blotchy appearance with areas of pallor, 1.2g, liver pale throughout, 2.4g, fat 45.2g mouse	Numerous blasts, virtually undifferentiated, no PMNs	Myeloid disease, MPO positive; BM, spleen, liver, muscle, papillary adenoma lung	32.5	10.1	35.1	145	67	12.6	17.3
1.3	1 million	312	Spleen 0.4g, liver 1.6g	undifferentiated blasts	Myeloid leukaemia; BM, spleen	54.9	4.5	16.9	93	64	27.4	19.9
1.2	1 million	19	spleen 0.3g, liver 1.3g, rear leg paralysis	Myeloid leukaemia with blasts and differentiation	Myeloid leukaemia; BM, spleen, muscle, liver, infarcted bone	28.3	16	57.3	721	56	7.8	16.4
1.1	1 million	30	hindlimb paralysis, spleen 0.3g, liver 1.5g	Myeloid leukaemia with blasts and differentiation	Myeloid leukaemia; BM, spleen, liver, muscle, kidney	32.9	17	59.3	979	54	11.1	16.9
1.4	1 million	22	hindlimb paralysis, spleen 0.3g, liver 1.9g	Myeloid leukaemia with blasts and differentiation	Myeloid leukaemia; BM and spleen, liver, kidney. BM and spleen blasts only	44.8	16.2	60	657	54	14.7	23.4
1.5	1 million	22	spleen 0.2g, liver 1.3g	Myeloid leukaemia with blasts and differentiation	Myeloid leukaemia; BM, spleen (blasts only, no maturing granulocytes), liver, muscle	52.7	14.4	54.3	478	55	21.1	24.3
1.6	1 million	22	spleen 0.4g, liver 1.3g, hindlimb paralysis	Myeloid leukaemia with blasts and differentiation	Myeloid leukaemia; spleen (poorly differentiated only), BM, liver, lung	44.3	16.6	62.9	1032	56	12	26
1.2.1	1 million	27	spleen 0.3g, liver 1.5g	Myeloid leukaemia with blasts and differentiation	Myeloid leukaemia; BM & spleen blasts only, liver, muscle	52.2	17.2	66	1070	57	15.6	28.8
1.2.2	1 million	29	spleen 0.2g, liver 1.5g	Myeloid leukaemia with blasts and differentiation	Myeloid leukaemia; spleen, BM, liver. BM and spleen only blasts	35.7	19	>70	1121	57	13.1	17.2
1.2.3	1 million	29	spleen 0.3g, liver 1.5g, hydrocephalus	Myeloid leukaemia with blasts and differentiation	Myeloid leukaemia; BM & spleen blasts only, liver, kidney, muscle	60	16	59.3	1169	54	22.7	29.2
1.1.1	1 million	23	spleen 0.3g, liver 1.3g, full bladder, hindlimb paralysis	Myeloid leukaemia with blasts and differentiation	Myeloid leukaemia; BM, spleen	58.7	16.5	62.3	1260	55	22	28.4
1.1.2	1 million	23	spleen 0.4g, liver 1.5g, urinary retention and hindlimb paralysis	Myeloid leukaemia with blasts and differentiation	Myeloid leukaemia; BM & spleen blasts only, liver, muscle	44	18.7	>70	1063	55	11.6	26.1
1.1.3	1 million	23	spleen 0.3g, liver 1.3g	Myeloid leukaemia with blasts and differentiation	Myeloid leukaemia; BM & spleen blasts only, liver, kidney, muscle	38.3	16.4	65.3	1392	53	14.6	18
19.2d		277	lymphadenopathy, spleen 1.5g, liver 3g, mouse 28.4g, hydrocephalic, swaying, shallow breathing	AMML	Myeloid leukaemia; blood, spleen, LN, liver, lung, BM, muscle	595	5.9	23.8	112	101	445	117
1.1	1 million	58	found dead, spleen 0.3g, liver 1.6g, thymomegaly	no blood film	Probable leukaemia, autolysed, cannot exclude lymphoma; spleen, liver, kidney, lung, LN, bone marrow and muscle							
1.2	1 million	53	spleen 0.6g, liver 2g	no blood film	presumed myeloid leukaemia; spleen, liver, LN, lung, bone marrow and muscle							
1.3	10000	61	spleen 0.6g, liver 1.6g	AML	myeloid leukaemia; blood, spleen, kidney, liver, fat, lung, lymph node, bone marrow and muscle	39.5	4.5	20.8	211	99	31.2	7.1
1.4	10000	61	spleen 0.4g, liver 1.9g	AML dysplastic background	myeloid leukaemia; blood, spleen, liver, kidney, BM and muscle	86	6.6	30.8	853	68	81	4
1.5	1000	62	spleen 0.5g, liver 2.1g	AML	myeloid leukaemia; blood, spleen, liver, kidney, LN, bone marrow and muscle. Adenoma of lung	47	7.3	30.5	899	63	27.7	15.8
1.6	1000	61	spleen 0.4g, liver 1.6g	Myeloid leukaemia with clumped platelets.	myeloid leukaemia; spleen, liver, kidney, adrenal gland, lung, marrow and muscle	70.8	5.6	24.9	563	65	56.4	12
1.7	100	7	antalgic gait, favouring left hind limb, no masses, spleen <0.1g, liver 1.1g	Normal	Normal	3.8	16.3	58.4	1086	54	1.9	1.6
1.8	100	343	Culled									
21.3j		176	spleen 0.7g, liver 1.7g	Myeloid leukaemia with blasts and maturation	Myeloid leukaemia; BM, spleen, muscle, liver, kidney	92	14.1	61.7	208	65	67	21
1.1	1 million	30	paraspinous mass left lumbar region 1cm diameter, partial hindlimb paralysis, spleen 0.3g, liver 2.1g	Myeloid leukaemia with maturation	Myeloid leukaemia; BM, spleen, LN, liver, muscle, lung, kidney	179	17.5	65.2	248	54	38	124
1.2	1 million	26	hindlimb paralysis, spleen 0.2g, liver 1.7g, pulmonary haemorrhages	Myeloid leukaemia with blasts and maturation	Myeloid leukaemia; BM, spleen, muscle, liver, kidney	16.1	17.2	62.6	331	52	3.4	11.1
1.3	10000	33	urinary retention, 7widening spine, spleen 0.4g, liver 1.5g	Myeloid leukaemia with maturation	Myeloid leukaemia; BM, spleen, muscle, liver, kidney	113	15.4	57.2	883	55	37	61
1.4	10000	343	Culled									
1.5	1000	30	spleen pale, 0.4g, liver 1.5g, abnormal posture hindlimbs	Myeloid leukaemia with maturation	Myeloid leukaemia; BM, spleen, LN, liver, muscle	53.8	14.4	49.1	673	56	16.5	29.8
1.6	1000	26	spleen 0.3g, liver 1.3g, stomach distended lesion at base of tail, hunched, spleen pale, 0.3g, liver 1.3g	Myeloid leukaemia with maturation	Myeloid leukaemia; BM, spleen +++, muscle, periosteum ++, liver +, kidney, liver -	70	16.1	59.6	745	56	18.1	42.4
1.7	100	25	hunched and thin, spleen 0.4g, liver 1.3g	Myeloid leukaemia with blasts and maturation	Myeloid leukaemia; BM, spleen, liver	29.8	16.8	58.5	405	54	5	21.5
1.8	100	343	Culled									
21.3j1	single colony	42	Small inguinal LN, spleen 0.5g, liver 1.8g	Myeloid leukaemia, predominantly blasts	Acute myeloid leukaemia, spinal cord compression; BM, spleen, muscle, liver, kidney, lung	290	12.1	46.1	766	59	118	135
21.3j2	single colony	39	Morbund, spleen 0.4g, liver 1.3g	Myeloid leukaemia with blasts and maturation	Leukaemia poorly differentiated, favour myeloid; BM, spleen, liver, LN, liver, muscle	500	13.9	52.6	804	62	179	252
21.3j3	single colony	36	Hind limb paralysis, spleen 0.5g, inguinal LN, liver 1.6g	Myeloid leukaemia with blasts and maturation	Leukaemia poorly differentiated, favour myeloid; CSF, spleen, BM, LN, liver, muscle	488	17	68.1	486	58	160	266
21.3j4	single colony	36	Partial hind limb paralysis, spleen 0.2g, liver 1.3g	Myeloid leukaemia with blasts and maturation	AML, spinal cord compression; BM, spleen, muscle, liver, blood,	74.3	15.6	57.3	456	55	26.2	36.9
21.3j5	single colony	87	hunched and thin, spleen 0.4, liver 1.4	None	Probable AML; BM, spleen, muscle, liver							
21.3j6	single colony	311	Culled									
21.3j7	single colony	314	Culled									
21.3j8	single colony	209	Culled									
21.3j9	single colony	314	Culled									
21.3j10	single colony	248	Culled									
19.2b		189	Enlarged LN, spleen 1.2g, liver 4g	AMML	Myeloid Leukaemia in blood, BM, infiltrating muscle along nerve, liver, kidney, spleen and LN.	221	10.7	41.4	262	79	159	50
1.1	1 million	33	spleen 0.4g, liver 2.2g, pale liver and kidneys, brown urine, faecal loading.	AMML (less differentiated than 19.2b)	Myeloid leukaemia in blood, kidney, liver, spleen, BM and muscle, meninges of cord and periosteum. Spleen total replacement.	327	10.8	36.8	240	57	14.9	13.9
1.2	1 million	35	venous system dilated, spleen 0.5g, liver 1.5g	AMML	myeloid leukaemia in blood, spleen, kidney, liver, BM	210	11.2	38.7	312	50	88	97
1.3	10000	49	spleen 0.5g, liver 2.1g	AMML less differentiated than 19.2b	Myeloid leukaemia in spleen, kidney, liver, fat, BM, bladder and pleura	133	13.6	62.8	613	66	98	24
1.4	10000	57	spleen 0.4g, liver 2g	AMML less differentiated than 19.2b	Myeloid leukaemia in blood, kidney, spleen, liver, heart, BM. Necrosis in kidney	121	12.5	47.8	483	56	30	76
1.5	1000	48	morbund, spleen 0.3g and pale, solid white mass near bladder, large kidney.	AMML less differentiated than 19.2b	Undifferentiated leukaemia, BM, spleen, liver, kidney, lung, muscle	68	16.6	62.5	887	55	52	1.3
1.6	1000	131	spleen 0.6g, liver 2.4g	Undifferentiated blasts and occasional PMN	Undifferentiated leukaemia, BM, spleen, liver, kidney, lung, muscle	69.4	7.3	28.5	301	65	26.3	34.3
1.7	100	295	Piloerect, spleen 0.1g, liver 2.2g	Normal	No tumour seen	14.9	11.6	41.6	1862	54	4.7	8.1
1.8	100	253	Piloerect, pale and shaly. Pus in fat pad of suprappubic.	Normal	Liver adenoma, kidney pyelonephritis	13.9	12.2	48.2	736	58	4.3	8
19.2b1	single colony	202	Culled									
19.2b2	single colony	314	Culled									
19.2b3	single colony	310	found dead									
19.2b4	single colony	311	Culled									
19.2b5	single colony	176	found dead									
19.2b6	single colony	169	found dead									
19.2b7	single colony	178	found dead									
19.2b8	single colony	314	Culled									
19.2b9	single colony	314	Culled									
19.2b10	single colony	314	Culled									

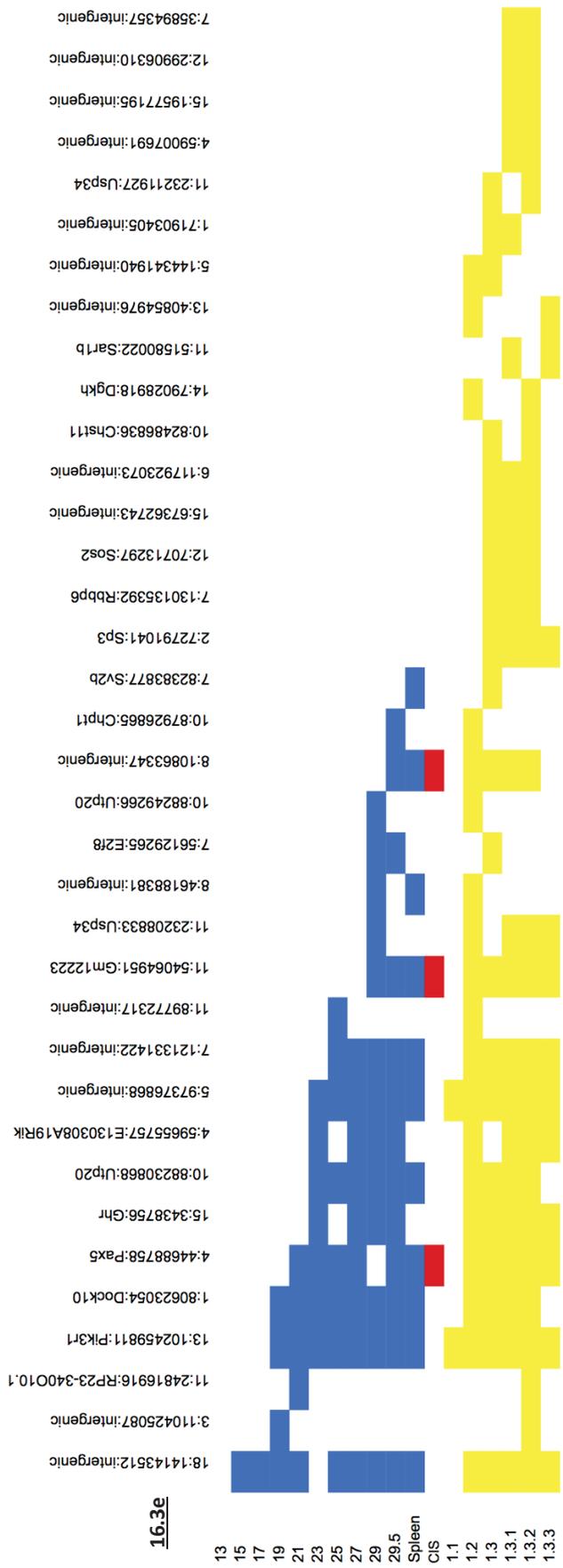
Mouse	Cell Dose	Lifetime (days) post transplant	Necropsy findings	Blood film	Histopath	WCC	Hb	Hct	Plt	MCV	Lymph/blasts	Gran
7.1a		322	Spleen 1.3g, liver 3g	Megakaryoblastic, low count	Megakaryoblastic leukaemia with some myeloid features							
1.1	1 million	103	swollen abdomen, spl 0.4, liver 1.6, mouse 33.3	Myeloid leukaemia with blasts and some maturation	Myeloid leukaemia without much maturation; spleen, BM, liver, kidney	28.5	3.7	11.8	434	65	12.3	13.6
1.2	1 million	103	swollen abdo, spleen 0.8g, liver 2g, mouse 24.2g	Myeloid leukaemia with blasts and some maturation	Myeloid leukaemia without much maturation; BM, spleen, liver	33	2.1	6.4	376	70	8.5	23.4
1.3	100 000	101	spleen 1.4g, liver 5.3g, gelatinous texture to both	Myeloid leukaemia with maturation	Myeloid leukaemia with maturation; BM, spleen, LN, liver, kidney, lung, renal capsule, small LN, megakaryocytes increased ++	588	7.6	32.4	>2200	69	114	390
1.4	100000	111	spleen pale, gelatinous, 1.4g, liver pale, 3.7g	remarkable film, no histo	Myeloid leukaemia with maturation; BM, spleen, liver, LN, lung, megakaryocytes increased +++	131	6.5	27.7	>2200	60	43	77
1.5	10 000	111	spleen 0.4g, liver 2.5g	Myeloid leukaemia with blasts and maturation	Could be megakaryoblastic, megakaryocytes increased ++ but not PMNs, immature blasts; BM, spleen, liver, lung	6.3	10.4	38.4	163	56	2.7	2.9
1.6	10 000	323	Culled									
1.7	1000	323	Culled									
1.8	1000	311	Unwell, moribund, piloerect and immobile. Splenomegaly. Mouse - 31.7, spleen 0.8, liver 2.3 and kidney 0.4	Myeloid leukaemia with some blasts and lots of maturation	AML; BM, spleen, liver, kidney, muscle	685	7.7	31.2	563	95	271	325
1.9	100	169	spleen 0.3g, liver 2.8g, mouse 37.1g, tumour mass in the urogenital system haemorrhax, retroperitoneal haematoma, mesenteric mass, thickening pleural and inner sternum, spleen 0.1g, liver 1.2g	Left shift only Unremarkable, but haemorrhax fluid high WCC with blasts, 7myeloid	Myeloid leukaemia with blasts and differentiation; spleen looks malignant but nowhere else, spleen unusual geographic pattern, megakaryocytes increased ++	10.2	8.1	27.4	375	50	1	8.7
1.10	100	132	found dead	PMN+++	Undifferentiated blasts, pericardium, paraspleen, BM, apoptosis +++ autolysed, septic or CML; BM, liver and kidney PMNs ++	4	11.7	43.9	1626	54	2	1.4
1.11	10	214	found dead									
1.12	10	323	Culled									
7.1m		165		Leukocytosis with blasts	MPO with blasts and eosinophilia	600.00	15.00		423	66	400.00	150.00
1.1	1 million	323	piloerect, heavy breathing, spleen 0.1g, liver 1.3g		no malignancy	17.1	12.8	49.7	>2200	52	4.3	10.2
1.2	1 million	323	culled									
1.3	10000	323	culled									
1.4	10000	323	culled									
1.5	1000	323	culled									
1.6	1000	268	Found dead, small bowel obstruction cut off at caecum but no obvious masses. Liver necrotic, spleen <0.1g	No sample	no lesion seen, no gut section							
1.7	100	323	culled									
1.8	100	323	culled									
19.2a		361	Thymomegaly, spleen 0.7g, liver 3.1g	Normal	B cell lymphoma; BM, spleen, LN, liver, kidney, adenoma of lung	361	10.9	42.5	427	65	249	88
1.1	1 million	13	spleen 0.3g, liver 1.8g, mouse 27.8g	Undifferentiated blasts with no other white cells	Undifferentiated leukaemia BM, spleen, liver, lung, kidney, muscle	119	13.9	62.8	883	65	93	22
1.2	1 million	12	hindlimb paralysis, spleen 0.3g, liver 2g	Undifferentiated leukaemia	Undifferentiated blasts BM, spleen, liver, muscle, kidney	117	14.4	56.2	952	57	88	23
1.3	1 million	13	spleen 0.3g, liver 1.5g	Undifferentiated leukaemia	Undifferentiated blasts BM, spleen, LN, liver, kidney, lung, muscle	79.4	13.3	57.6	866	64	57	18.9
20.2b		335	Spleen 1.1g, Liver 2.4g, Thymomegaly	Myeloid leukaemia with blasts and maturation	Myeloid leukaemia; spleen, BM, liver, fat	101	10.9	45.7	671	62		26
1.1	1 million	59	spleen 0.8g, liver 2.2g, cervical, thoracic, axillary, mesenteric and inguinal LN	Myeloid leukaemia with blasts and maturation	Myeloid leukaemia, poorly differentiated, little maturation; BM, spleen, liver, kidney, LN, muscle, salivary gland, lung	351	13.1	48	514	62	85	224
1.2	1 million	59	spleen 1g, liver 2.5g, cervical, thoracic LN	Myeloid leukaemia with blasts and maturation	Myeloid leukaemia, poorly differentiated; BM, spleen, LN, liver, kidney, lung, muscle, salivary gland	190	9.8	34.7	1034	66	56	115
1.3	1 million	50	spleen 0.7g, liver 2.2g	Myeloid leukaemia with blasts and maturation	Myeloid leukaemia with blasts and little maturation; BM, spleen, LN, kidney, muscle, liver, lung, fat, most infiltrate undifferentiated	318	12.3	44.5	1394	63	118	177
1.4	1 million	22	head tilt, spleen 0.2g, liver 1.8g	Myeloid increased	Moderate myeloid infiltrate with maturation; BM, spleen	13.7	12.9	48.9	91	53	4.4	7.7

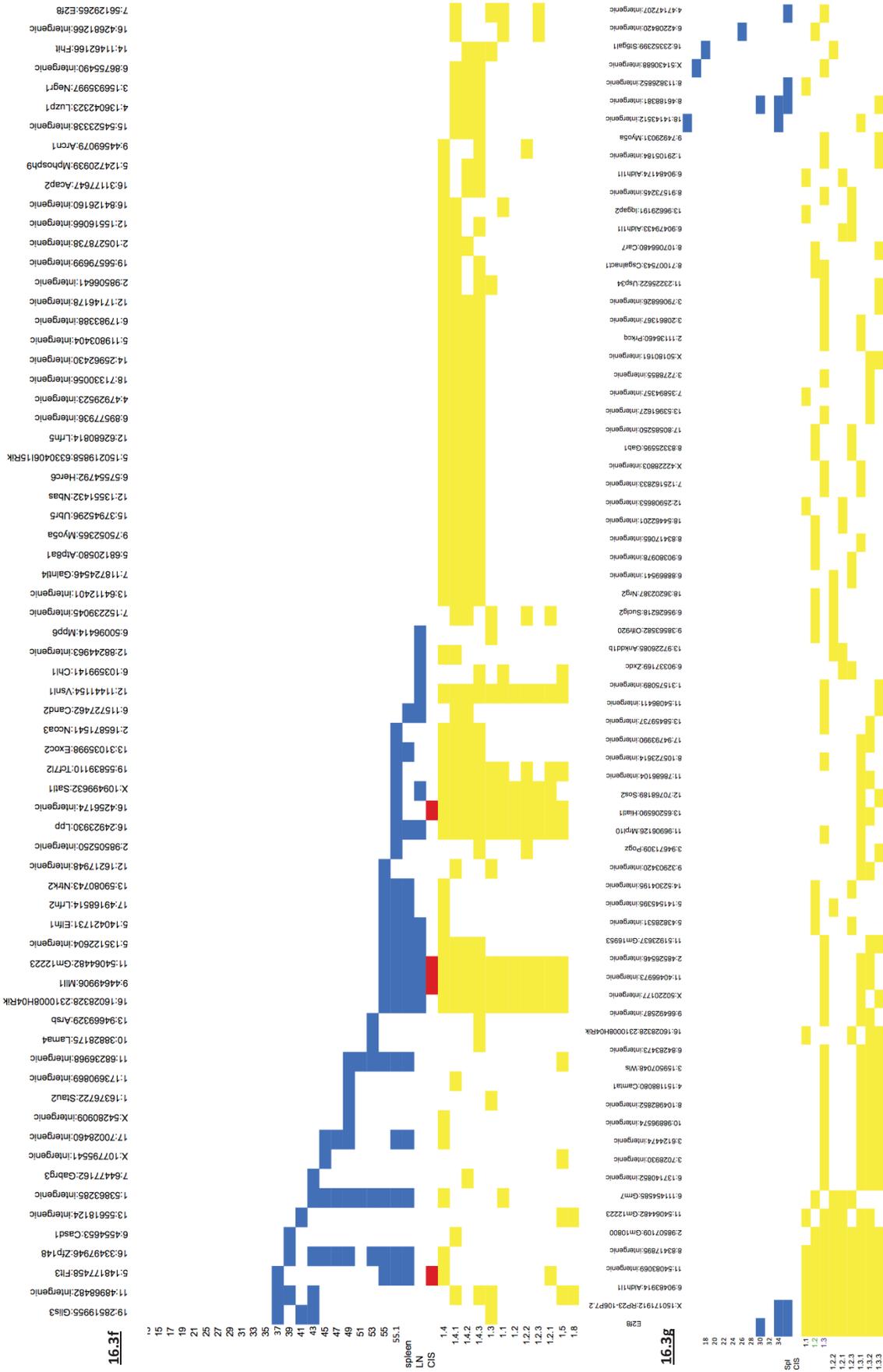


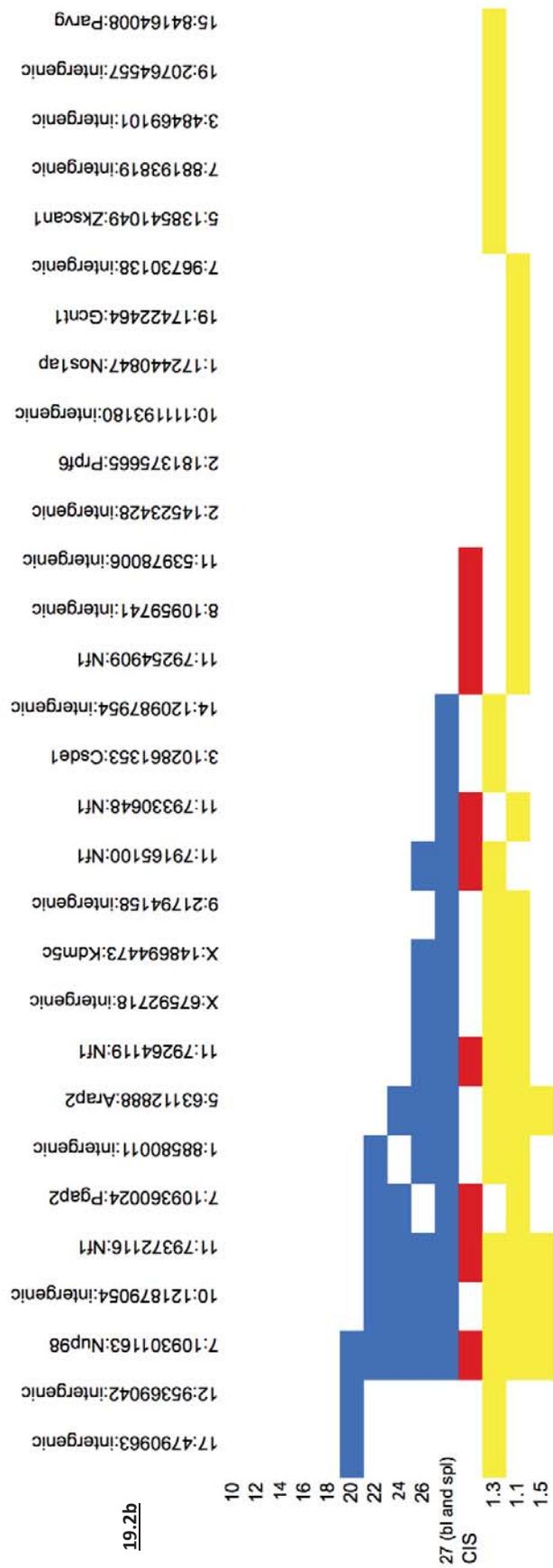
Appendix 4E: Transposon integrations ordered by their presence in multiple transplant recipients

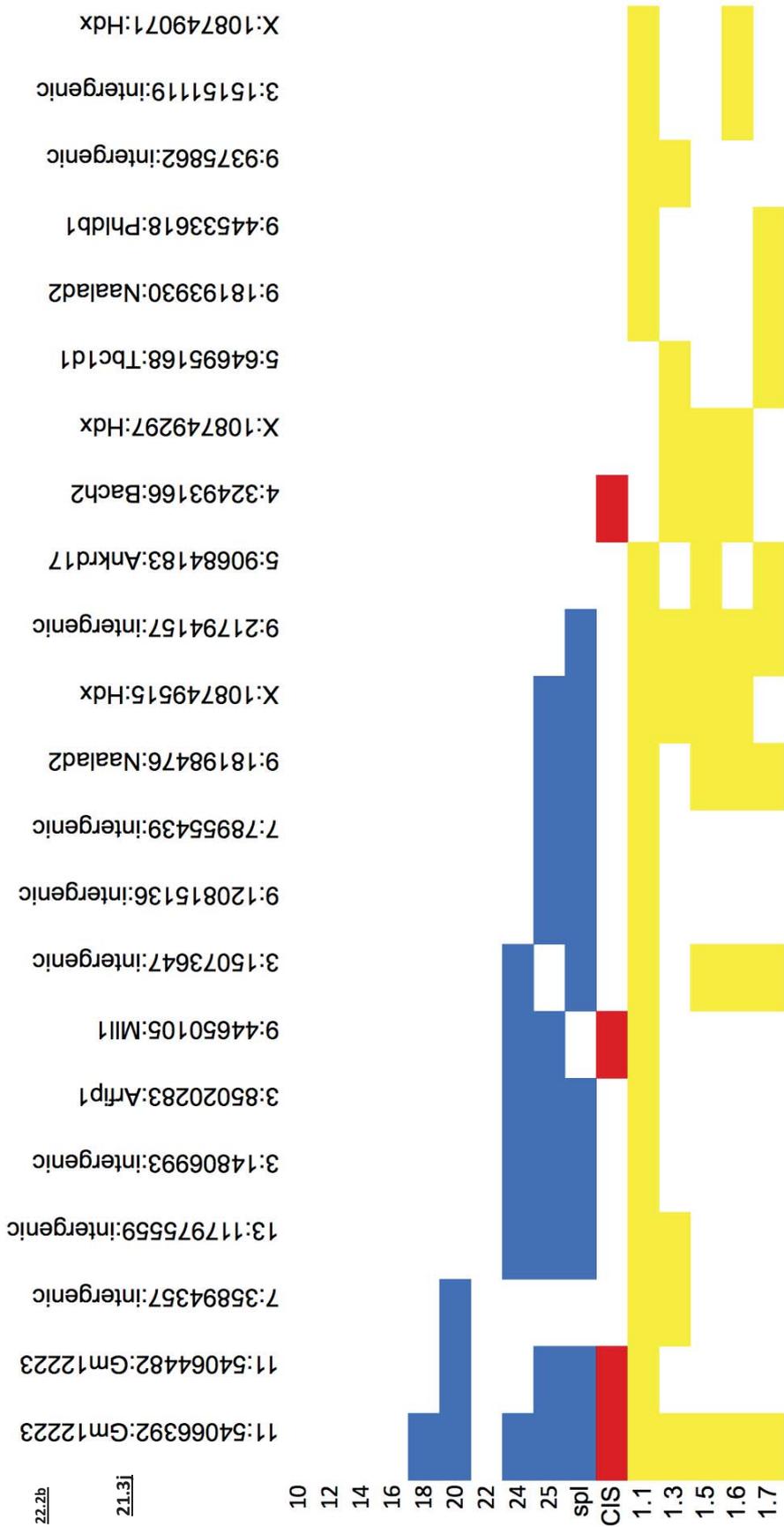
The identity of the mouse is shown at the top left.











Appendix 4F: CIS results for the analysis on serial blood sample

CIS which were found in the tumour analysis of the whole cohort are shown in red. CIS which were excluded in that analysis are shown in blue. The number of samples, and the time at which the blood samples were taken relative to the onset of leukaemia are shown for each table.

Final Tumour					
Number samples in analysis = 15					
Gene nearest peak	Genes in CIS	Chr	Start	End	Kernel size (kb)
A330023F24Rik	A330023F24Rik	1	196821188	196835909	30
Dnajc17	Gchfr Dnajc17 Gm14137 Gm14138	2	119002990	119018636	10,30
Ndufc1	Elf2 4930583H14Rik Ndufc1 Naa15	3	51127253	51254938	60, 100
Cpsf3l	Aurkaip1 Gm10562 Mxra8 Dvl1 Tas1r3 Gltpd1 Cpsf3l	4	155205032	155254034	100
Kdm3a	Rnf103 Vps24 Kdm3a	6	71429134	71586550	10, 30, 60, 100
Gm13834	Gm13834 Gm13833 Gm13835 AB041803	6	31032284	31120830	10, 30, 60, 100
Nrf1	Nrf1	6	30079561	30083481	10, 30
Tet3	Tet3	6	83356893	83359834	10
9330179D12Rik	9330179D12Rik	6	127134776	127176029	60
Nup98	Art1 Chrna10 Nup98 Pgap2	7	109251626	109386388	10, 30, 60, 100
Copb1	intergenic	7	121321414	121327261	10
Il27	intergenic	7	133739132	133742056	10
Mtnr1a	intergenic	8	46184160	46190938	10
Mll1	Mll1	9	44646167	44651018	10
Sik3	Sik3	9	45808700	45832010	10, 30, 60
Gm12223	4933405E24Rik Gm12222 Csf2 Gm12223 Il3 Acsf6 Gm9964 Nf1 Gm11198	11	53987119	54145289	10, 30, 60, 100
Nf1	Gm11199 AU040972 Omg Evi2b Evi2a Rab11fip4 U6 Gm11202 U6 U6	11	79092975	79454961	10, 30, 60, 100
Sfi1	Pisd-ps1 Sfi1 Gm11399 Gm11400	11	3026257	3078900	10, 30, 60, 100
1700012B15Rik	1700012B15Rik	12	3102877	3239602	100
Nedd9	Nedd9	13	41556525	41564300	10
Foxf2	Foxf2	13	31712954	31722673	10
Abcc1	Abcc1 U6	16	14372427	14395263	10, 30, 60
Gtf2h5	Synj2 Serac1 Gtf2h5 Tulp4 Gm5812	17	6005254	6129776	100
Gm3395	intergenic	Y	2825028	2911516	10, 30, 60, 100
Zfy2	intergenic	Y	1307754	1317818	10, 30

24-33 days pre-tumour					
Number samples in analysis = 15					
Gene nearest peak	Genes in CIS	Chr	Start	End	Kernel size (kb)
Hecw2	Hecw2	1	53868275	53880081	30
Dock10	Dock10	1	80659185	80700544	60, 100
Commd3	intergenic	2	18576689	18582557	30
Pax5	Pax5 Gm12462	4	44681807	44692561	10
En2	En2	5	28486080	28504626	10, 30, 60
U2	intergenic	5	97371820	97379629	10
Mpp6	Mpp6	6	50087883	50102556	10, 30
Zfp800	Zfp800	6	28322835	28326747	10
Tjp1	Tjp1	7	72421068	72548749	30, 60, 100
Nup98	Nup98	7	109281340	109337165	30, 60, 100
Sntb2	Sntb2	8	109454987	109465693	10, 30
Mtnr1a	Mtnr1a	8	46164323	46193550	10, 30, 60
Cand1	Cand1	10	118654797	118661578	10
Chst11	Chst11	10	82420512	82488615	100
Sfi1	Pisd-ps1 Sfi1 Gm11399 Gm11400 Drg1 Gm12735 Fau-ps2 Eif4enif1	11	2986289	3144475	10, 30, 60, 100
Gm12223	Csf2 Gm12223	11	54059597	54067389	10
Nf1	Nf1 Gm11198 Gm11199 AU040972 Omg Evi2b Evi2a	11	79157294	79382335	60, 100
Foxf2	Foxf2	13	31714003	31722694	10

51-61 days pre-tumour					
Number samples in analysis = 14					
Gene nearest peak	Genes in CIS	Chr	Start	End	Kernel size (kb)
Lrba	Lrba Gm3788	3	86446015	86514337	100
Bach2	Bach2	4	32458140	32481575	30, 60
En2	En2 Cnpy1	5	28414611	28572578	10, 30, 60, 100
9330179D12Rik	9330179D12Rik	6	127120888	127170674	30, 60, 100
Sfi1	Pisd-ps1 Sfi1 Gm11399 Gm11400 Drg1 Gm12735 Fau-ps2 Eif4enif1	11	2986176	3161941	10, 30, 60, 100
Gphn	Gphn	12	79709137	79749966	60, 100
Foxf2	Foxf2	13	31712297	31723901	10, 30
6720401G13Rik	6720401G13Rik	X	47919483	47924376	10, 30
Gm6026	intergenic	Y	1623173	1687462	30, 60

79-88 days pre-tumour Number samples in analysis = 11					
Gene nearest peak	Genes in CIS	Chr	Start	End	Kernel size (kb)
En2	En2	5	28482111	28508451	10, 30, 60, 100
U3	intergenic	7	71118825	71157003	30, 60, 100
Nrbf2	intergenic	10	66783554	66905150	100
Sfi1	Pisd-ps1 Sfi1 Gm11399 Gm11400 Drg1	11	3011148	3088662	10, 30, 60, 100
Gm3395	intergenic	Y	2873260	2881485	10, 30, 60, 100

98-113 days pre-tumour Number samples in analysis = 11					
Gene nearest peak	Genes in CIS	Chr	Start	End	Kernel size (kb)
En2	En2	5	28478970	28512057	10, 30, 60, 100
Sfi1	Pisd-ps1 Sfi1 Gm11399 Gm11400 Drg1 Gm12735 Fau-ps2 Eif4enif1	11	3020557	3123527	10, 30, 60, 100
Gm3395	intergenic	Y	2882416	2903328	10, 30, 60, 100

Appendix 4G: Results of the splinkerette analysis out of the blunt end of PB.

Integrations which shared an insertion site in the SB analysis are highlighted in red

Sample	Read Name	Chr	Transposon Integration Site	Query Start-Stop (length)	Alignment % Identity	Reads per Cluster	Hit	Hit Start-Stop	Transposon Ori	Hit Strand
10.1D (transposase neg)	HS0580M02C05T0	8	71584302	36 - 57 (22)	100.00%	50	Slc18a1	71584281-71584302	+	-
16.3B	HS0580M02EQ9X4	1	26092751	36 - 69 (34)	100.00%	42	Intergenic	26092751-26092784	-	+
16.3B	HS0580M02D8GX6	5	28496561	36 - 289 (254)	99.61%	1	En2	28496561-28496813	-	+
16.3B	HS0580M02D8809	6	118402713	36 - 51 (16)	100.00%	12	Zfp248	118402698-118402713	+	-
16.3B	HS0580M02D18GH	9	59783750	36 - 61 (26)	100.00%	222	Intergenic	59783725-59783750	+	-
16.3B	HS0580M02EXZ4D	13	117356737	36 - 51 (16)	100.00%	2	Intergenic	117356722-117356737	+	-
16.3B	HS0580M02DD7BB	15	47496863	37 - 66 (30)	96.67%	37	Csmd3	47496834-47496863	+	-
16.3B	HS0580M02DRY10	16	7330576	39 - 128 (90)	98.89%	25	Rbfox1	7330488-7330576	+	-
16.3B	HS0580M02EU7S5	16	16754611	36 - 79 (44)	100.00%	114	Spag6	16754568-16754611	+	-
16.3B	HS0580M02D19T	16	21101741	37 - 100 (64)	100.00%	42	Intergenic	21101741-21101804	-	+
16.3B	HS0580M02DGKN7	16	78764476	39 - 126 (88)	100.00%	4	Intergenic	78764476-78764563	-	+
16.3B	HS0580M02EXM45	17	4671285	39 - 263 (225)	99.56%	1	Intergenic	4671285-4671509	-	+
16.3B	HS0580M02DQSIK	X	134134562	39 - 58 (20)	100.00%	8	Il1rapl2	134134562-134134581	-	+
16.3D (cre neg)	HS0580M02ED2OY	1	75813529	39 - 62 (24)	100.00%	39	Intergenic	75813506-75813529	+	-
16.3D (cre neg)	HS0580M02DTSES	1	156588715	39 - 57 (19)	100.00%	1	Intergenic	156588697-156588715	+	-
16.3D (cre neg)	HS0580M02DGIJQ	5	50570301	39 - 64 (26)	100.00%	11	Intergenic	50570301-50570326	-	+
16.3D (cre neg)	HS0580M02CZV8D	7	129061296	36 - 56 (21)	100.00%	36	Scnn1b	129061276-129061296	+	-
16.3D (cre neg)	HS0580M02D780F	9	52999816	36 - 58 (23)	100.00%	26	Ddx10	52999816-52999838	-	+
16.3D (cre neg)	HS0580M02C2HCN	10	108585724	36 - 66 (31)	100.00%	35	Intergenic	108585724-108585754	-	+
16.3D (cre neg)	HS0580M02C82CD	12	95013247	36 - 69 (34)	100.00%	36	Intergenic	95013247-95013280	-	+
16.3D (cre neg)	HS0580M02EISWI	13	42714334	38 - 108 (71)	98.59%	2	Intergenic	42714334-42714403	-	+
16.3D (cre neg)	HS0580M02EEYIU	13	113569285	34 - 57 (24)	100.00%	8	Intergenic	113569285-113569308	-	+
16.3D (cre neg)	HS0580M02C241F	14	83946367	40 - 56 (17)	100.00%	6	Intergenic	83946351-83946367	+	-
16.3D (cre neg)	HS0580M02DTJL7	15	6203029	40 - 129 (90)	100.00%	1	Intergenic	6202940-6203029	+	-
16.3D (cre neg)	HS0580M02D45JX	19	17873784	36 - 54 (19)	100.00%	71	Pesks5	17873784-17873802	-	+
16.3E	HS0580M02DUOWA	1	134034978	38 - 69 (32)	100.00%	2	Cdk18	134034947-134034978	+	-
16.3E	HS0580M02EJDJU	1	140134035	37 - 137 (101)	100.00%	15	Intergenic	140133935-140134035	+	-
16.3E	HS0580M02EUUSM	2	30082528	40 - 140 (101)	100.00%	3	Intergenic	30082428-30082528	+	-
16.3E	HS0580M02ELTGU	2	163468418	36 - 75 (40)	92.50%	32	Serinc3	163468418-163468457	-	+
16.3E	HS0580M02D507U	3	31655677	39 - 122 (84)	97.62%	2	Intergenic	31655593-31655677	+	-
16.3E	HS0580M02D088K	5	85253057	38 - 184 (147)	99.32%	4	Intergenic	85252912-85253057	+	-
16.3E	HS0580M02DCHJG	6	34699904	34 - 63 (30)	100.00%	1	Cald1	34699904-34699933	-	+
16.3E	HS0580M02CAAJN	7	112858521	40 - 59 (20)	95.00%	8	Intergenic	112858521-112858540	-	+
16.3E	HS0580M02EOAW0	7	122827036	36 - 71 (36)	100.00%	29	Sox6	122827036-122827071	-	+
16.3E	HS0580M02DUBTB	8	30054315	39 - 128 (90)	100.00%	1	Unc5d	30054226-30054315	+	-
16.3E	HS0580M02EDTMJ	11	27303463	38 - 165 (128)	100.00%	68	Intergenic	27303336-27303463	+	-
16.3E	HS0580M02DPPIM	13	105321414	39 - 201 (163)	98.77%	407	Intergenic	105321414-105321577	-	+
16.3E	HS0580M02DRCIJ	14	111547518	39 - 77 (39)	100.00%	8	Intergenic	111547518-111547556	-	+
16.3E	HS0580M02DCT36	15	7303833	38 - 125 (88)	100.00%	40	Egflam	7303833-7303920	-	+
16.3E	HS0580M02DCCOKS	16	8984646	38 - 69 (32)	100.00%	203	Intergenic	8984615-8984646	+	-
16.3E	HS0580M02DTLTK	16	19094622	39 - 182 (144)	98.61%	12	Intergenic	19094480-19094622	+	-
16.3E	HS0580M02DHD791	16	19110639	38 - 107 (70)	98.57%	47	Intergenic	19110639-19110708	-	+
16.3E	HS0580M02D051H	16	23827477	38 - 231 (194)	99.48%	1	Intergenic	23827477-23827671	-	+
16.3E	HS0580M02C3NRW	16	41664747	39 - 90 (52)	100.00%	2	Lsmp	41664696-41664747	+	-
16.3E	HS0580M02DDL97	16	43352874	33 - 59 (27)	100.00%	313	Zbtb20	43352874-43352900	-	+
16.3E	HS0580M02EBYK4	16	82519045	38 - 80 (43)	97.67%	114	Intergenic	82519004-82519045	+	-
16.3E	HS0580M02ESKOK	16	89105941	37 - 201 (165)	99.39%	6	Intergenic	89105941-89106106	-	+
16.3E	HS0580M02DDM2J	18	14665047	35 - 138 (104)	99.04%	16	Intergenic	14664933-14665047	+	-
16.3E	HS0580M02C63KR	19	52617444	39 - 177 (139)	100.00%	5	Intergenic	52617306-52617444	+	-
16.3F	HS0580M02ESNUL	17	22090796	37 - 249 (213)	99.53%	17	Zfp942	22090583-22090796	+	-

Sample	Read Name	Chr	Transposon Integration Site	Query Start-Stop (length)	Alignment % Identity	Reads per Cluster	Hit	Hit Start-Stop	Transposon Ori	Hit Strand
16.3G	HS0580M02D10NT	1	8739687	39 - 97 (59)	100.00%	27	Sntg1	8739687-8739745	-	+
16.3G	HS0580M02EHHTT	1	69154365	37 - 56 (20)	100.00%	148	ErbB4	69154346-69154365	+	-
16.3G	HS0580M02D47D2	2	5955067	37 - 75 (39)	100.00%	3	Upf2	5955029-5955067	+	-
16.3G	HS0580M02DX5W7	2	19708818	39 - 151 (113)	100.00%	2	Intergenic	19708818-19708930	-	+
16.3G	HS0580M02EVCR5	2	21788192	36 - 223 (188)	97.87%	502	Intergenic	21788006-21788192	+	-
16.3G	HS0580M02E0036	2	95416344	132 - 223 (92)	100.00%	1	Intergenic	95416344-95416435	-	+
16.3G	HS0580M02DVMYV	4	5950694	39 - 209 (171)	100.00%	3	Fam110b	5950524-5950694	+	-
16.3G	HS0580M02D93LG	5	79264814	36 - 63 (28)	100.00%	2	Intergenic	79264787-79264814	+	-
16.3G	HS0580M02EMUUA	5	152179031	32 - 53 (22)	100.00%	92	1700028E10Rik	152179010-152179031	+	-
16.3G	HS0580M02DWDTN	7	13854052	38 - 199 (162)	99.38%	3	6330408A02Rik	13853891-13854052	+	-
16.3G	HS0580M02EW60U	7	55294174	39 - 164 (126)	100.00%	12	Intergenic	55294049-55294174	+	-
16.3G	HS0580M02DQIL3	7	79092022	39 - 152 (114)	98.25%	8	Intergenic	79092022-79092137	-	+
16.3G	HS0580M02DKSP6	8	109813511	40 - 75 (36)	100.00%	3	Intergenic	109813511-109813546	-	+
16.3G	HS0580M02ENWVW	12	88796809	39 - 204 (166)	99.40%	2	Snw1	88796809-88796974	-	+
16.3G	HS0580M02DTY8V	14	120714936	39 - 100 (62)	98.39%	18	Mbnl2	120714936-120714997	-	+
16.3G	HS0580M02DK5E0	16	19627197	39 - 242 (204)	100.00%	1	Intergenic	19626994-19627197	+	-
16.3G	HS0580M02DW96A	16	25110430	37 - 112 (76)	98.68%	13	Intergenic	25110354-25110430	+	-
16.3G	HS0580M02EKIU0	16	25390065	37 - 88 (52)	98.08%	68	Tprg	25390014-25390065	+	-
16.3G	HS0580M02EVDQH	16	40199206	40 - 279 (240)	99.58%	1	Intergenic	40198966-40199206	+	-
16.3G	HS0580M02EGNET	16	47432829	39 - 230 (192)	98.96%	2	Intergenic	47432636-47432829	+	-
16.3G	HS0580M02DR96J	16	54576055	39 - 235 (197)	97.97%	1	Intergenic	54576055-54576248	-	+
16.3G	HS0580M02EQ00Q	16	56686612	36 - 195 (160)	100.00%	3	Abi3bp	56686453-56686612	+	-
16.3G	HS0580M02EHEIR	16	60850001	39 - 104 (66)	100.00%	36	Intergenic	60849936-60850001	+	-
16.3G	HS0580M02ETFFL	16	65372390	38 - 229 (192)	98.96%	4	Intergenic	65372390-65372582	-	+
16.3G	HS0580M02C29KB	16	75281053	39 - 154 (116)	100.00%	17	Intergenic	75281053-75281168	-	+
16.3G	HS0580M02C7WH3	16	83410954	35 - 69 (35)	97.14%	103	Intergenic	83410921-83410954	+	-
16.3G	HS0580M02DUNZ8	17	50860488	36 - 75 (40)	97.50%	79	Intergenic	50860449-50860488	+	-
16.3G	HS0580M02DIVUA	17	52031231	38 - 63 (26)	100.00%	27	Intergenic	52031206-52031231	+	-
16.3G	HS0580M02EZ4LJ	19	30553273	39 - 125 (87)	100.00%	3	Intergenic	30553187-30553273	+	-
16.3G	HS0580M02C7AFO	X	5587469	38 - 60 (23)	100.00%	97	Intergenic	5587469-5587491	-	+
16.3H	HS0580M02DNUIL	1	32570577	38 - 88 (51)	100.00%	1	Khdrbs2	32570527-32570577	+	-
16.3H	HS0580M02DQPUA	1	173570213	39 - 54 (16)	100.00%	5	Slamf7	173570198-173570213	+	-
16.3H	HS0580M02DVNOK	2	3968183	38 - 99 (62)	98.39%	161	FrmD4a	3968183-3968244	-	+
16.3H	HS0580M02C84RT	2	16720779	36 - 54 (19)	100.00%	5	Intergenic	16720761-16720779	+	-
16.3H	HS0580M02E09KS	2	94591245	39 - 69 (31)	100.00%	3	Intergenic	94591245-94591275	-	+
16.3H	HS0580M02EX7E6	2	163468418	39 - 78 (40)	92.50%	112	Serinc3	163468418-163468457	-	+
16.3H	HS0580M02DUSOP	4	51709280	36 - 173 (138)	99.28%	8	Intergenic	51709280-51709417	-	+
16.3H	HS0580M02D8G9W	5	130707211	39 - 198 (160)	100.00%	7	0610007L01Rik	130707052-130707211	+	-
16.3H	HS0580M02EUCT2	6	36069436	37 - 60 (24)	100.00%	313	Intergenic	36069413-36069436	+	-
16.3H	HS0580M02ESYT1	7	32329601	39 - 158 (120)	98.33%	1	Intergenic	32329601-32329718	-	+
16.3H	HS0580M02EM1LG	7	109858915	38 - 116 (79)	98.73%	7	Olf558	109858837-109858915	+	-
16.3H	HS0580M02EOMSH	8	19718602	38 - 88 (51)	100.00%	70	Intergenic	19718602-19718652	-	+
16.3H	HS0580M02C0TJP	8	28601941	38 - 88 (51)	100.00%	1	Poteg	28601941-28601991	-	+
16.3H	HS0580M02E00XQ	9	73847250	39 - 205 (167)	100.00%	1	Intergenic	73847084-73847250	+	-
16.3H	HS0580M02DPOQ8	11	3067893	38 - 173 (136)	98.53%	13	Sfi1	3067757-3067893	+	-
16.3H	HS0580M02EKWZX	12	116074732	39 - 155 (117)	95.73%	14	Intergenic	116074732-116074848	-	+
16.3H	HS0580M02C3LSL	13	62232047	39 - 220 (182)	99.45%	12	Zfp808	62232047-62232227	-	+
16.3H	HS0580M02EJ47H	15	70370066	39 - 200 (162)	98.77%	2	Intergenic	70370066-70370228	-	+
16.3H	HS0580M02C8UUN	16	3586910	38 - 178 (141)	99.29%	17	Intergenic	3586910-3587050	-	+
16.3H	HS0580M02C5KLD	16	39765263	37 - 57 (21)	100.00%	8	Intergenic	39765263-39765283	-	+
16.3H	HS0580M02DWOKY	16	61860006	40 - 170 (131)	100.00%	1493	Intergenic	61859876-61860006	+	-
16.3H	HS0580M02ET2IT	16	65028054	39 - 234 (196)	98.98%	8	Htr1f	65027859-65028054	+	-
16.3H	HS0580M02D6GM7	16	82225648	39 - 64 (26)	96.15%	798	Intergenic	82225623-82225648	+	-
16.3H	HS0580M02EUMFP	17	11767955	35 - 56 (22)	100.00%	1	Park2	11767955-11767976	-	+
16.3H	HS0580M02D2DJR	X	36767695	37 - 214 (178)	100.00%	38	Intergenic	36767518-36767695	+	-
16.3H	HS0580M02ESAX1	X	162471395	37 - 88 (52)	100.00%	2	Intergenic	162471395-162471446	-	+

16.3I (cre neg)

Sample	Read Name	Chr	Transposon Integration Site	Query Start-Stop (length)	Alignment % Identity	Reads per Cluster	Hit	Hit Start-Stop	Transposon Ori	Hit Strand
19.2A	HS0580M02E13BV	1	147328949	36 - 178 (143)	98.60%	2	Intergenic	147328806-147328949	+	-
19.2A	HS0580M02E1JLG	2	163468410	39 - 86 (48)	89.58%	1	Serinc3	163468410-163468457	-	+
19.2A	HS0580M02EK0CU	2	163468418	39 - 78 (40)	92.50%	19	Serinc3	163468418-163468457	-	+
19.2A	HS0580M02DRYUX	2	173532393	36 - 83 (48)	100.00%	3	Rab22a	173532346-173532393	+	-
19.2A	HS0580M02D1951	3	56227096	38 - 101 (64)	95.31%	1	Intergenic	56227030-56227096	+	-
19.2A	HS0580M02DL9DB	3	128515804	38 - 101 (64)	100.00%	2	Intergenic	128515804-128515867	-	+
19.2A	HS0580M02DC7ZT	3	151561995	37 - 89 (53)	100.00%	2	Intergenic	151561995-151562047	-	+
19.2A	HS0580M02D75D8	4	109623985	39 - 65 (27)	96.30%	43	Faf1	109623985-109624011	-	+
19.2A	HS0580M02DHYRJ	5	50955421	37 - 58 (22)	100.00%	5	Intergenic	50955421-50955442	-	+
19.2A	HS0580M02DOC03	8	17238476	39 - 163 (125)	100.00%	4	Csmd1	17238352-17238476	+	-
19.2A	HS0580M02DOZDJ	8	45534346	38 - 144 (107)	100.00%	8	Intergenic	45534240-45534346	+	-
19.2A	HS0580M02D3Z9D	10	144450043	37 - 81 (45)	100.00%	5	Intergenic	144449999-14450043	+	-
19.2A	HS0580M02COWWC	10	27108953	37 - 110 (74)	97.30%	14	Lama2	27108880-27108953	+	-
19.2A	HS0580M02EURLX	10	71642681	37 - 96 (60)	100.00%	11	Intergenic	71642681-71642740	-	+
19.2A	HS0580M02DKFM2	11	15356413	39 - 135 (97)	100.00%	2	Intergenic	15356317-15356413	+	-
19.2A	HS0580M02EEHGG	11	49339650	39 - 104 (66)	100.00%	4	Intergenic	49339585-49339650	+	-
19.2A	HS0580M02E0GQE	13	42714334	38 - 107 (70)	100.00%	3615	Intergenic	42714334-42714403	-	+
19.2A	HS0580M02E0E5B	14	10329333	39 - 114 (76)	100.00%	15	Intergenic	10329333-10329408	-	+
19.2A	HS0580M02E05N8	14	40662076	38 - 143 (106)	100.00%	2	Intergenic	40661971-40662076	+	-
19.2A	HS0580M02DLP0V	14	67436099	38 - 161 (124)	100.00%	3	Dpysl2	67436099-67436222	-	+
19.2A	HS0580M02DAGDO	15	33840224	36 - 62 (27)	100.00%	1	Intergenic	33840224-33840250	-	+
19.2A	HS0580M02D2CLJ	16	6526810	38 - 258 (221)	98.64%	1	Intergenic	6526590-6526810	+	-
19.2A	HS0580M02EHYV	16	6549591	39 - 100 (62)	100.00%	2	Intergenic	6549591-6549652	-	+
19.2A	HS0580M02C8NOY	16	9590199	39 - 58 (20)	100.00%	25	Grin2a	9590180-9590199	+	-
19.2A	HS0580M02D0D1C	16	19665188	39 - 100 (62)	98.39%	64	Lamp3	19665127-19665188	+	-
19.2A	HS0580M02DA6FC	16	26554577	40 - 84 (45)	100.00%	26	Intergenic	26554577-26554621	-	+
19.2A	HS0580M02D0G07	16	28072402	37 - 81 (45)	100.00%	19	Intergenic	28072358-28072402	+	-
19.2A	HS0580M02CZ199	16	38645261	38 - 58 (21)	100.00%	3	Arhgap31	38645261-38645281	-	+
19.2A	HS0580M02DZPA2	16	39182854	39 - 67 (29)	100.00%	1	Intergenic	39182854-39182882	-	+
19.2A	HS0580M02C73CR	16	43333520	39 - 114 (76)	100.00%	1	Zbtb20	43333520-43333595	-	+
19.2A	HS0580M02DKD09	16	49683571	36 - 59 (24)	100.00%	53	Intergenic	49683571-49683594	-	+
19.2A	HS0580M02EURPO	16	54014611	39 - 88 (50)	100.00%	4	Intergenic	54014611-54014660	-	+
19.2A	HS0580M02D3MW8	16	54797206	39 - 117 (79)	100.00%	2	Intergenic	54797128-54797206	+	-
19.2A	HS0580M02C61EA	16	59572139	40 - 105 (66)	95.45%	1	AC154473.2	59572139-59572205	-	+
19.2A	HS0580M02DDK9I	16	66515349	39 - 90 (52)	100.00%	11	Intergenic	66515298-66515349	+	-
19.2A	HS0580M02DUYRM	16	75476168	38 - 56 (19)	100.00%	5	Intergenic	75476168-75476186	-	+
19.2A	HS0580M02DVEAO	16	75598126	35 - 52 (18)	100.00%	2	Rbm11	75598109-75598126	+	-
19.2A	HS0580M02DH612	17	10392822	37 - 89 (53)	98.11%	31	Intergenic	10392771-10392822	+	-
19.2A	HS0580M02C1NBG	17	17058324	38 - 53 (16)	100.00%	1	Intergenic	17058324-17058339	-	+
19.2A	HS0580M02C1J0M	17	59927151	36 - 192 (157)	98.73%	1	Intergenic	59926995-59927151	+	-
19.2A	HS0580M02D0DB4	18	46451797	38 - 221 (184)	99.46%	1	Ccdc112	46451615-46451797	+	-
19.2A	HS0580M02D1XEH	19	30377479	39 - 98 (60)	98.33%	36	Intergenic	30377420-30377479	+	-
19.2B	HS0580M02ESW17	1	42759589	40 - 56 (17)	100.00%	1	Intergenic	42759573-42759589	+	-
19.2B	HS0580M02DWLVC	2	82815045	38 - 54 (17)	100.00%	1	Fsp12	82815045-82815061	-	+
19.2B	HS0580M02C2CQM	2	98502693	37 - 223 (187)	98.40%	20	Gm10801	98502693-98502879	-	+
19.2B	HS0580M02D3DW2	2	179808696	38 - 76 (39)	97.44%	73	Gtpbp5	179808696-179808734	-	+
19.2B	HS0580M02C6VKP	4	37214216	38 - 93 (56)	100.00%	32	Gm12374	37214161-37214216	+	-
19.2B	HS0580M02DMZQ3	5	17319892	38 - 136 (99)	100.00%	15	Cd36	17319892-17319990	-	+
19.2B	HS0580M02DA3DX	5	106008974	38 - 52 (15)	100.00%	1	Lrrcc8c	106008974-106008988	-	+
19.2B	HS0580M02D6HC8	6	131259374	38 - 272 (235)	99.15%	1	Styk1	131259138-131259374	+	-
19.2B	HS0580M02DBJGB	6	149004591	38 - 55 (18)	100.00%	970	Dennd5b	149004574-149004591	+	-
19.2B	HS0580M02C71LG	8	40743439	131 - 234 (104)	99.04%	10	Intergenic	40743439-40743542	-	+
19.2B	HS0580M02EN7B4	9	76605868	39 - 57 (19)	100.00%	12	Intergenic	76605850-76605868	+	-
19.2B	HS0580M02ELW1C	10	44369476	39 - 86 (48)	100.00%	16	Intergenic	44369476-44369523	-	+
19.2B	HS0580M02E01ZL	10	85827031	41 - 55 (15)	100.00%	1	Syn3	85827017-85827031	+	-
19.2B	HS0580M02D305S	10	101394292	36 - 55 (20)	100.00%	1	Mgat4c	101394292-101394311	-	+
19.2B	HS0580M02DTJ5O	16	72239704	38 - 168 (131)	97.71%	12	Intergenic	72239704-72239834	-	+
19.2B	HS0580M02EGDIH	16	79792058	39 - 183 (145)	99.31%	843	Intergenic	79791915-79792058	+	-
19.2B	HS0580M02C2LR8	16	88455299	38 - 55 (18)	100.00%	2	Intergenic	88455299-88455316	-	+
19.2B	HS0580M02EDXDJ	19	23517690	39 - 156 (118)	100.00%	2	Mamdc2	23517690-23517807	-	+
19.2B	HS0580M02ED34D	X	7251668	40 - 55 (16)	100.00%	1	Magix	7251668-7251683	-	+
19.2D	HS0580M02CZSRB	4	126288565	34 - 104 (71)	100.00%	2	5730409E04Rik	126288565-126288635	-	+
19.2D	HS0580M02C419Y	5	18843593	39 - 238 (200)	100.00%	154	Magi2	18843394-18843593	+	-
19.2D	HS0580M02DF3WV	5	18863009	39 - 231 (193)	99.48%	1	Magi2	18863009-18863201	-	+
19.2D	HS0580M02DC6RL	8	4115969	39 - 141 (103)	100.00%	36	Intergenic	4115867-4115969	+	-
19.2D	HS0580M02DD7N7	9	6395060	38 - 171 (134)	100.00%	40	Intergenic	6395060-6395193	-	+
19.2D	HS0580M02ECD1Z	11	5764450	38 - 211 (174)	99.43%	6	Aebp1	5764450-5764623	-	+
19.2D	HS0580M02E0V82	12	13723420	35 - 215 (181)	100.00%	1	Intergenic	13723420-13723420	+	-
19.2D	HS0580M02EIN52	12	19158376	37 - 285 (249)	99.60%	53	Intergenic	19158129-19158376	+	-
19.2D	HS0580M02C909F	14	25548996	37 - 82 (46)	100.00%	1	Intergenic	25548996-25549041	-	+
19.2D	HS0580M02EB1UL	16	3833368	38 - 162 (125)	97.60%	48	Intergenic	3833245-3833368	+	-
19.2D	HS0580M02C8JQT	16	16419796	39 - 216 (178)	100.00%	124	Fgd4	16419796-16419973	-	+
19.2D	HS0580M02DSRGP	16	19540845	35 - 179 (145)	100.00%	16	Intergenic	19540701-19540845	+	-
19.2D	HS0580M02EV5HM	16	25589941	39 - 207 (169)	99.41%	13	Intergenic	25589941-25590110	-	+
19.2D	HS0580M02EWW9P	16	27253525	39 - 138 (100)	99.00%	76	Intergenic	27253525-27253625	-	+
19.2D	HS0580M02DQ0F5	16	51800123	40 - 110 (71)	100.00%	1	Intergenic	51800123-51800193	-	+
19.2D	HS0580M02DW8AV	16	53151578	35 - 186 (152)	98.68%	47	Intergenic	53151578-53151729	-	+
19.2D	HS0580M02DUPFD	16	62191056	39 - 171 (133)	100.00%	15	Intergenic	62190924-62191056	+	-
19.2D	HS0580M02C9U28	16	70643263	40 - 211 (172)	97.67%	1	Intergenic	70643095-70643263	+	-
19.2D	HS0580M02DAGUM	19	49242998	37 - 245 (209)	98.09%	4	Intergenic	49242790-49242998	+	-
19.3A (cre neg)	HS0580M02DZ4G2	2	133338268	157 - 193 (37)	97.30%	4	Intergenic	133338233-133338268	+	-
19.3A (cre neg)	HS0580M02D8IMU	7	116692993	39 - 67 (29)	100.00%	293	St5	116692993-116693021	-	+

Sample	Read Name	Chr	Transposon Integration Site	Query Start-Stop (length)	Alignme nt % Identity	Reads per Cluster	Hit	Hit Start-Stop	Transpos on Ori	Hit Strand
20.2B	HS0580M02DW9FD	1	106253307	38 - 63 (26)	100.00%	1	Intergenic	106253307-106253332	-	+
20.2B	HS0580M02EVWPI	1	117283578	39 - 215 (177)	100.00%	30	Intergenic	117283578-117283754	-	+
20.2B	HS0580M02C36TQ	1	165393355	38 - 95 (58)	98.28%	283	Intergenic	165393355-165393412	-	+
20.2B	HS0580M02DBX0E	1	173533432	39 - 102 (64)	98.44%	4	Ly9	173533369-173533432	+	-
20.2B	HS0580M02EBOOI	2	60200295	37 - 211 (175)	100.00%	3	Ly75	60200295-60200469	-	+
20.2B	HS0580M02DHGJZ	2	107802949	37 - 58 (22)	100.00%	2	Intergenic	107802949-107802970	-	+
20.2B	HS0580M02DG98V	3	57233833	36 - 61 (26)	96.15%	2	Tm4sf4	57233808-57233833	+	-
20.2B	HS0580M02DAIH0	3	119165312	37 - 126 (90)	100.00%	41	Intergenic	119165223-119165312	+	-
20.2B	HS0580M02C9IWX	3	133691878	38 - 51 (14)	100.00%	1	AC123608.1	133691878-133691891	-	+
20.2B	HS0580M02ECZS2	4	44718860	36 - 54 (19)	100.00%	4	Pax5	44718842-44718860	+	-
20.2B	HS0580M02C6HDN	4	97960998	39 - 116 (78)	100.00%	7	Intergenic	97960998-97961075	-	+
20.2B	HS0580M02DCBUT	4	121772016	38 - 57 (20)	100.00%	23	Intergenic	121772016-121772035	-	+
20.2B	HS0580M02EIZL5	5	45181043	33 - 201 (169)	99.41%	7	Ldb2	45180875-45181043	+	-
20.2B	HS0580M02CZ7Q4	5	110101254	36 - 84 (49)	97.96%	2	Intergenic	110101254-110101302	-	+
20.2B	HS0580M02D2YLL5	5	127140010	37 - 85 (49)	100.00%	1	Intergenic	127139962-127140010	+	-
20.2B	HS0580M02DD8ZK	6	108031992	37 - 200 (164)	95.73%	1	Intergenic	108031992-108032156	-	+
20.2B	HS0580M02D7A5T	7	50205478	39 - 64 (26)	100.00%	1	Intergenic	50205453-50205478	+	-
20.2B	HS0580M02DKFPJ	7	83792656	38 - 153 (116)	100.00%	7	Agbl1	83792541-83792656	+	-
20.2B	HS0580M02EM8QW	7	89600876	39 - 168 (130)	98.46%	8	Intergenic	89600876-89601004	-	+
20.2B	HS0580M02DKITP	8	116207218	39 - 56 (18)	100.00%	4	Intergenic	116207218-116207235	-	+
20.2B	HS0580M02EF5Z2	10	21728722	38 - 61 (24)	100.00%	2	Intergenic	21728722-21728745	-	+
20.2B	HS0580M02EMO3A	10	100687183	39 - 66 (28)	100.00%	2	Intergenic	100687183-100687210	-	+
20.2B	HS0580M02EE84I	10	102594934	38 - 117 (80)	100.00%	2	Lrriq1	102594855-102594934	+	-
20.2B	HS0580M02DAEWW	10	105349232	38 - 183 (146)	100.00%	1	Intergenic	105349232-105349377	-	+
20.2B	HS0580M02EZKWW	10	107454791	37 - 237 (201)	97.51%	2	Intergenic	107454791-107454993	-	+
20.2B	HS0580M02C4U8N	11	22982250	36 - 290 (255)	99.22%	2	Intergenic	22982250-22982504	-	+
20.2B	HS0580M02D7AKV	11	63544256	38 - 64 (27)	100.00%	489	Intergenic	63544256-63544282	-	+
20.2B	HS0580M02DURI6	11	80093184	37 - 85 (49)	100.00%	5	Intergenic	80093184-80093232	-	+
20.2B	HS0580M02EVKDG	12	10032983	38 - 161 (124)	100.00%	43	Intergenic	10032860-10032983	+	-
20.2B	HS0580M02ECYK8	13	75983773	40 - 110 (71)	100.00%	48	Glrx	75983703-75983773	+	-
20.2B	HS0580M02E0L6F	13	117285171	36 - 72 (37)	100.00%	405	Intergenic	117285171-117285207	-	+
20.2B	HS0580M02EL9Z2	14	17557982	36 - 57 (22)	100.00%	10	Rarb	17557982-17558003	-	+
20.2B	HS0580M02D5OZ9	14	29682040	38 - 249 (212)	100.00%	2	Intergenic	29682040-29682251	-	+
20.2B	HS0580M02DDEJE	14	48390123	39 - 144 (106)	99.06%	28	Intergenic	48390118-48390123	+	-
20.2B	HS0580M02EU4TL	15	3543609	39 - 99 (61)	100.00%	12	Intergenic	3543549-3543609	+	-
20.2B	HS0580M02D20WG	15	29245583	38 - 203 (166)	100.00%	29	Intergenic	29245418-29245583	+	-
20.2B	HS0580M02DU38Q	15	33149006	39 - 66 (28)	100.00%	5	Pgcp	33148979-33149006	+	-
20.2B	HS0580M02DCG0G	15	81845285	37 - 187 (151)	100.00%	4	Xrcc6	81845285-81845435	-	+
20.2B	HS0580M02D2JWK	16	9168411	39 - 120 (82)	100.00%	83	Intergenic	9168411-9168492	-	+
20.2B	HS0580M02CZM0O	16	16096611	39 - 153 (115)	99.13%	16	2310008H04Rik	16096611-16096726	-	+
20.2B	HS0580M02C8GNM	16	19570419	38 - 147 (110)	99.09%	7	Intergenic	19570419-19570529	-	+
20.2B	HS0580M02EB1GI	16	26640284	39 - 156 (118)	98.31%	3	Il1rap	26640284-26640400	-	+
20.2B	HS0580M02DGYKN	16	27660993	39 - 83 (45)	97.78%	266	Intergenic	27660949-27660993	+	-
20.2B	HS0580M02DOAZ2	16	36447389	37 - 257 (221)	99.55%	3	Intergenic	36447389-36447609	-	+
20.2B	HS0580M02D080C	16	42791093	39 - 73 (35)	100.00%	261	Gm10809	42791093-42791127	-	+
20.2B	HS0580M02DG9X7	16	68678851	37 - 155 (119)	100.00%	12	Intergenic	68678733-68678851	+	-
20.2B	HS0580M02D85IT	16	74924402	38 - 112 (75)	98.67%	27	Intergenic	74924402-74924477	-	+
20.2B	HS0580M02CZJKS	16	78123502	37 - 115 (79)	100.00%	7	Intergenic	78123424-78123502	+	-
20.2B	HS0580M02ENPLJ	16	79161176	40 - 82 (43)	97.67%	55	Intergenic	79161134-79161176	+	-
20.2B	HS0580M02D4KV7	16	82969846	39 - 207 (169)	97.63%	2	Intergenic	82969846-82970014	-	+
20.2B	HS0580M02CZMII	16	86065632	38 - 99 (62)	98.39%	1	Intergenic	86065571-86065632	+	-
20.2B	HS0580M02EA7C6	17	55023225	37 - 99 (63)	100.00%	18	Intergenic	55023225-55023287	-	+
20.2B	HS0580M02EWS93	18	8678137	37 - 67 (31)	100.00%	70	Intergenic	8678107-8678137	+	-
20.2B	HS0580M02EJZNE	X	50304573	38 - 207 (170)	100.00%	9	Phf6	50304404-50304573	+	-
20.2B	HS0580M02DP0ZE	X	76474443	37 - 58 (22)	100.00%	1	Intergenic	76474422-76474443	+	-
20.2B	HS0580M02DJXUF	X	135664800	39 - 66 (28)	100.00%	1	Intergenic	135664800-135664827	-	+
20.2B	HS0580M02DZ549	X	149754908	36 - 61 (26)	96.15%	1	Klf8	149754908-149754933	-	+

Sample	Read Name	Chr	Transposon Integration Site	Query Start-Stop (length)	Alignment % Identity	Reads per Cluster	Hit	Hit Start-Stop	Transposon on Ori	Hit Strand
21.3J	HS0580M02ECE1M	1	51123327	39 - 321 (283)	94.35%	5	Tmeff2	51123327-51123597	-	+
21.3J	HS0580M02D93SP	2	121805444	37 - 54 (18)	100.00%	1	Ctdspl2	121805444-121805461	-	+
21.3J	HS0580M02DESAC	3	30811966	38 - 54 (17)	100.00%	3	Phc3	30811950-30811966	+	-
21.3J	HS0580M02DORLC	3	135974132	38 - 58 (21)	100.00%	1313	Bank1	135974112-135974132	+	-
21.3J	HS0580M02EPEY1	3	158138176	39 - 186 (148)	100.00%	6	Lrrc7	158138029-158138176	+	-
21.3J	HS0580M02D3Z6C	4	96082556	39 - 229 (191)	99.48%	12	Intergenic	96082365-96082556	+	-
21.3J	HS0580M02D38VB	5	43293053	37 - 116 (80)	100.00%	10	Intergenic	43293053-43293132	-	+
21.3J	HS0580M02EMJNW	5	98725575	38 - 92 (55)	98.18%	689	Intergenic	98725575-98725629	-	+
21.3J	HS0580M02CORPF	5	119162831	39 - 136 (98)	98.98%	55	Med13l	119162831-119162929	-	+
21.3J	HS0580M02EXKQ7	6	112258528	37 - 53 (17)	100.00%	3	Lmcd1	112258512-112258528	+	-
21.3J	HS0580M02C9B0R	8	130458544	39 - 247 (209)	99.52%	1	Intergenic	130458544-130458752	-	+
21.3J	HS0580M02COGPZ	9	81111188	38 - 79 (42)	97.62%	9	Intergenic	81111147-81111188	+	-
21.3J	HS0580M02EOBJQ	10	8341153	39 - 63 (25)	92.00%	1	Intergenic	8341129-8341153	+	-
21.3J	HS0580M02EJSHL	10	53576357	38 - 148 (111)	100.00%	44	Intergenic	53576247-53576357	+	-
21.3J	HS0580M02DXAVH	10	90439024	39 - 133 (95)	100.00%	62	Intergenic	90438930-90439024	+	-
21.3J	HS0580M02C4EIX	11	26860241	36 - 55 (20)	95.00%	1	Intergenic	26860222-26860241	+	-
21.3J	HS0580M02EBP3Y	12	68349381	39 - 198 (160)	99.38%	1	Intergenic	68349381-68349540	-	+
21.3J	HS0580M02D4LNM	14	16024868	38 - 106 (69)	100.00%	74	Intergenic	16024800-16024868	+	-
21.3J	HS0580M02ESW9K	14	41907467	38 - 183 (146)	100.00%	16	Intergenic	41907467-41907612	-	+
21.3J	HS0580M02DRU6S	14	104585092	37 - 196 (160)	96.88%	1	Intergenic	104585092-104585250	-	+
21.3J	HS0580M02EYFKF	15	24848603	37 - 206 (170)	99.41%	11	Intergenic	24848434-24848603	+	-
21.3J	HS0580M02E0VR2	15	55046643	36 - 52 (17)	100.00%	1	Deptor	55046643-55046659	-	+
21.3J	HS0580M02EXJZQ	16	3463251	38 - 62 (25)	100.00%	3	Intergenic	3463251-3463275	-	+
21.3J	HS0580M02D63CP	16	4004245	37 - 273 (237)	98.73%	9	Intergenic	4004245-4004480	-	+
21.3J	HS0580M02EZ24P	16	6042397	37 - 156 (120)	100.00%	4	Intergenic	6042278-6042397	+	-
21.3J	HS0580M02DCNCG	16	9403649	36 - 51 (16)	100.00%	2	Intergenic	9403649-9403664	-	+
21.3J	HS0580M02C9DKA	16	12369247	38 - 154 (117)	100.00%	3	Intergenic	12369247-12369247	+	-
21.3J	HS0580M02DZ05Z	16	13608066	36 - 65 (30)	100.00%	49	Parn	13608037-13608066	+	-
21.3J	HS0580M02D77AC	16	21661481	39 - 158 (120)	99.17%	3	2510009E07Rik	21661481-21661600	-	+
21.3J	HS0580M02C73KM	16	25442835	36 - 93 (58)	98.28%	62	Intergenic	25442778-25442835	+	-
21.3J	HS0580M02EQVQJ	16	40069096	39 - 122 (84)	100.00%	3	Intergenic	40069013-40069096	+	-
21.3J	HS0580M02EQADJ	16	40608595	38 - 81 (44)	100.00%	13	Intergenic	40608552-40608595	+	-
21.3J	HS0580M02ELNG4	16	43317069	40 - 57 (18)	100.00%	2	Zbtb20	43317052-43317069	+	-
21.3J	HS0580M02DN9FQ	16	49833054	39 - 105 (67)	100.00%	26	Intergenic	49833054-49833120	-	+
21.3J	HS0580M02DN9HUE	16	51842026	37 - 128 (92)	98.91%	62	Intergenic	51841935-51842026	+	-
21.3J	HS0580M02DPH5K	16	52817899	39 - 188 (150)	98.00%	7	Intergenic	52817899-52818047	-	+
21.3J	HS0580M02ECT0Q	16	54701737	39 - 58 (20)	100.00%	11	Intergenic	54701737-54701756	-	+
21.3J	HS0580M02DIWHJ	16	55238751	39 - 199 (161)	100.00%	1	Zpld1	55238591-55238751	+	-
21.3J	HS0580M02DDWEG	16	65312290	39 - 129 (91)	98.90%	122	Intergenic	65312200-65312290	+	-
21.3J	HS0580M02DK04B	16	65714484	38 - 226 (189)	100.00%	1	Intergenic	65714484-65714672	-	+
21.3J	HS0580M02EPAZV	16	70631184	35 - 182 (148)	100.00%	59	Intergenic	70631037-70631184	+	-
21.3J	HS0580M02EE01P	17	9661791	39 - 116 (78)	97.44%	109	Intergenic	9661791-9661868	-	+
21.3J	HS0580M02C5BNY	17	15696636	39 - 134 (96)	100.00%	84	Prdm9	15696541-15696636	+	-
21.3J	HS0580M02DIO9S	17	93192409	36 - 53 (18)	100.00%	2	Intergenic	93192409-93192426	-	+
21.3J	HS0580M02EYF5V	19	23517692	36 - 151 (116)	100.00%	610	Mamdc2	23517692-23517807	-	+

Sample	Read Name	Chr	Transposon Integration Site	Query Start-Stop (length)	Alignment % Identity	Reads per Cluster	Hit	Hit Start-Stop	Transposon on Ori	Hit Strand
22.2B	HS0580M02D5TCC	1	38105937	36 - 54 (19)	100.00%	13	Eif5b	38105937-38105955	-	+
22.2B	HS0580M02DZLOP	2	98506401	39 - 92 (54)	100.00%	31	Intergenic	98506401-98506454	-	+
22.2B	HS0580M02DY3M4	5	57870912	35 - 74 (40)	97.50%	39	Intergenic	57870912-57870951	-	+
22.2B	HS0580M02EHYW9	5	122111705	34 - 49 (16)	100.00%	1	Brap	122111690-122111705	+	-
22.2B	HS0580M02DLA33	6	85074275	40 - 58 (19)	100.00%	2	Gm5878	85074257-85074275	+	-
22.2B	HS0580M02DKT7Z	7	102501575	40 - 121 (82)	100.00%	1	Intergenic	102501575-102501656	-	+
22.2B	HS0580M02C2E0U	7	110424128	39 - 172 (134)	99.25%	3	Intergenic	110424128-110424261	-	+
22.2B	HS0580M02EUTQC	7	116692993	39 - 67 (29)	100.00%	9717	St5	116692993-116693021	-	+
22.2B	HS0580M02E0M01	10	9114194	35 - 50 (16)	100.00%	1	Intergenic	9114179-9114194	+	-
22.2B	HS0580M02C7EJT	10	104323595	39 - 175 (137)	100.00%	1	Intergenic	104323595-104323731	-	+
22.2B	HS0580M02EPU3Q	11	3062113	40 - 159 (120)	99.17%	5	Sfr1	3062113-3062231	-	+
22.2B	HS0580M02EOHQJ	12	79432277	37 - 165 (129)	99.22%	1	Gphn	79432277-79432404	-	+
22.2B	HS0580M02DXU6F	14	51238090	38 - 64 (27)	100.00%	48	Olf744	51238064-51238090	+	-
22.2B	HS0580M02ETLZP	16	26249551	37 - 132 (96)	98.96%	1	Intergenic	26249456-26249551	+	-
22.2B	HS0580M02DAMWM	16	51403077	36 - 160 (125)	98.40%	1	Intergenic	51402953-51403077	+	-
22.2B	HS0580M02D8AVF	17	13966972	38 - 91 (54)	98.15%	11	Mllt4	13966919-13966972	+	-

Sample	Read Name	Chr	Transposon Integration Site	Query Start-Stop (length)	Alignment % Identity	Reads per Cluster	Hit	Hit Start-Stop	Transposon Ori	Hit Strand
6.4A	HS0580M02D4DWH	1	34524182	38 - 55 (18)	100.00%	1	Ptpn18	34524165-34524182	+	-
6.4A	HS0580M02DIU38	1	48163143	39 - 86 (48)	100.00%	4	Intergenic	48163096-48163143	+	-
6.4A	HS0580M02DDX3J	2	73757777	36 - 55 (20)	100.00%	2	Intergenic	73757777-73757796	-	+
6.4A	HS0580M02EBCPM	4	61647717	34 - 54 (21)	100.00%	4	Intergenic	61647697-61647717	+	-
6.4A	HS0580M02DGGNO	6	14082895	34 - 70 (37)	100.00%	1	Intergenic	14082859-14082895	+	-
6.4A	HS0580M02D7PDR	7	18937967	37 - 84 (48)	100.00%	17	Psg18	18937967-18938014	-	+
6.4A	HS0580M02DGFUB	7	110190119	37 - 200 (164)	98.78%	234	Olfir582	110189956-110190119	+	-
6.4A	HS0580M02EW7OH	7	110881235	36 - 233 (198)	97.98%	2	Olfir628	110881038-110881235	+	-
6.4A	HS0580M02EEDTM	8	34333155	34 - 57 (24)	100.00%	1	Intergenic	34333155-34333178	-	+
6.4A	HS0580M02DSD52H	11	89853085	35 - 59 (25)	96.00%	3	Pctp	89853085-89853109	-	+
6.4A	HS0580M02EZBLY	13	58220730	39 - 55 (17)	100.00%	1	Intergenic	58220714-58220730	+	-
6.4A	HS0580M02DSFJN	13	93073855	38 - 55 (18)	100.00%	1	Msh3	93073838-93073855	+	-
6.4A	HS0580M02EZ7I5	16	14535626	37 - 132 (96)	100.00%	20	Intergenic	14535626-14535721	-	+
6.4A	HS0580M02DPPRF	16	87225379	38 - 113 (76)	98.68%	231	Intergenic	87225304-87225379	+	-
6.4G	HS0580M02C3MIP	1	155361934	36 - 58 (23)	91.30%	4	Npl	155361912-155361934	+	-
6.4G	HS0580M02DTJ4P	6	134958884	37 - 58 (22)	95.45%	3	Intergenic	134958884-134958905	-	+
6.4G	HS0580M02ERL7V	7	12740209	39 - 105 (67)	100.00%	10	Intergenic	12740209-12740275	-	+
6.4G	HS0580M02DH19E	12	31687642	39 - 56 (18)	100.00%	1	Intergenic	31687625-31687642	+	-
6.4G	HS0580M02D4F1U	12	100359583	131 - 247 (117)	98.29%	1	Intergenic	100359583-100359699	-	+
6.4G	HS0580M02EZ015	14	120987953	39 - 77 (39)	97.44%	5309	Intergenic	120987953-120987992	-	+
6.4G	HS0580M02DBFZZ	16	68806219	36 - 176 (141)	100.00%	5	Intergenic	68806219-68806359	-	+
6.4G	HS0580M02DNMY3	16	95487752	39 - 108 (70)	100.00%	3	Kcnj15	95487683-95487752	+	-
6.4H	HS0580M02DSXBC	1	181044763	36 - 57 (22)	95.45%	6	Smyd3	181044742-181044763	+	-
6.4H	HS0580M02C2M42	1	196740788	36 - 60 (25)	100.00%	14	Intergenic	196740788-196740812	-	+
6.4H	HS0580M02DVTIB	3	36833534	39 - 162 (124)	100.00%	6	4932438A13Rik	36833411-36833534	+	-
6.4H	HS0580M02DXMIM	3	61281675	39 - 112 (74)	100.00%	117	Intergenic	61281675-61281748	-	+
6.4H	HS0580M02DEOLS	6	43966176	36 - 88 (53)	98.11%	28	Intergenic	43966176-43966228	-	+
6.4H	HS0580M02DELND	6	137809512	36 - 63 (28)	100.00%	74	Intergenic	137809512-137809539	-	+
6.4H	HS0580M02C87ZL	7	147104540	35 - 66 (32)	100.00%	1	Kndc1	147104509-147104540	+	-
6.4H	HS0580M02DFBXT	10	9534007	39 - 174 (136)	99.26%	5	Stxbp5	9534007-9534141	-	+
6.4H	HS0580M02EGMCA	10	18096044	39 - 262 (224)	99.11%	2	Intergenic	18096044-18096265	-	+
6.4H	HS0580M02DOP85	10	27496908	39 - 148 (110)	98.18%	26	Intergenic	27496908-27497017	-	+
6.4H	HS0580M02DH5OZ	11	3028725	37 - 212 (176)	99.43%	13	Pisd-ps1	3028725-3028900	-	+
6.4H	HS0580M02D72Y2	11	33951526	36 - 59 (24)	100.00%	65	4930469K13Rik	33951526-33951549	-	+
6.4H	HS0580M02C4KTP	11	61726553	37 - 67 (31)	100.00%	2	Akap10	61726523-61726553	+	-
6.4H	HS0580M02C8BG0	12	37673080	37 - 98 (62)	100.00%	11	Intergenic	37673019-37673080	+	-
6.4H	HS0580M02DH98N	12	37891329	38 - 151 (114)	100.00%	22	Meox2	37891216-37891329	+	-
6.4H	HS0580M02EA9DN	12	46755152	37 - 88 (52)	100.00%	198	Intergenic	46755152-46755203	-	+
6.4H	HS0580M02DCKHK	13	27445337	40 - 234 (195)	100.00%	591	Prl8a2	27445337-27445531	-	+
6.4H	HS0580M02DMXRF	14	56205311	39 - 68 (30)	100.00%	20	Intergenic	56205311-56205340	-	+
6.4H	HS0580M02EQ5MV	16	9940260	39 - 73 (35)	100.00%	94	Grin2a	9940260-9940294	-	+
6.4H	HS0580M02C00TG	16	47861517	38 - 150 (113)	100.00%	8	Intergenic	47861405-47861517	+	-
6.4H	HS0580M02DH26N	16	62189451	38 - 145 (108)	100.00%	8	Intergenic	62189451-62189558	-	+
6.4H	HS0580M02DL4N1	16	85434890	40 - 188 (149)	100.00%	1	Intergenic	85434890-85435038	-	+
6.4H	HS0580M02D7VXX	18	7177104	37 - 64 (28)	100.00%	1	Armc4	7177077-7177104	+	-
6.4H	HS0580M02EVHQX	X	20069287	35 - 113 (79)	100.00%	33	Phf16	20069209-20069287	+	-

Sample	Read Name	Chr	Transposon Integration Site	Query Start-Stop (length)	Alignment % Identity	Reads per Cluster	Hit	Hit Start-Stop	Transposon Ori	Hit Strand
7.5B	HS0580M02DLWWS	1	181165067	40 - 56 (17)	100.00%	1	Smyd3	181165067-181165083	-	+
7.5B	HS0580M02EUU60	2	163468418	36 - 75 (40)	92.50%	61	Serinc3	163468418-163468457	-	+
7.5B	HS0580M02EG9XC	5	28402713	36 - 69 (34)	100.00%	44	Insig1	28402713-28402746	-	+
7.5B	HS0580M02DQEV	9	29834781	39 - 280 (242)	99.59%	1	Intergenic	29834541-29834781	+	-
7.5B	HS0580M02D48U1	9	91934272	36 - 161 (126)	99.21%	2	Intergenic	91934148-91934272	+	-
7.5B	HS0580M02EQ3EM	14	28172683	40 - 54 (15)	100.00%	160	Arhgef3	28172683-28172697	-	+
7.5B	HS0580M02EJNXU	16	67517810	39 - 97 (59)	100.00%	24	Cadm2	67517752-67517810	+	-
7.5C	HS0580M02C0E80	1	16377410	36 - 208 (173)	98.27%	19	Stau2	16377410-16377582	-	+
7.5C	HS0580M02D3PV1	2	13426662	38 - 61 (24)	95.83%	1	Intergenic	13426662-13426685	-	+
7.5C	HS0580M02DBJ35	2	14335073	39 - 167 (129)	100.00%	29	Sic39a12	14335073-14335201	-	+
7.5C	HS0580M02DNW7Z	3	120706403	38 - 76 (39)	100.00%	97	Intergenic	120706403-120706441	-	+
7.5C	HS0580M02DDST1	5	9483845	37 - 196 (160)	100.00%	2	Intergenic	9483845-9484004	-	+
7.5C	HS0580M02DGGJR	7	46526510	38 - 97 (60)	98.33%	1	Intergenic	46526451-46526510	+	-
7.5C	HS0580M02DV08W	9	23351310	39 - 258 (220)	98.64%	1	Intergenic	23351310-23351529	-	+
7.5C	HS0580M02ET5E9	9	65507968	38 - 61 (24)	100.00%	1	Rbpms2	65507968-65507991	-	+
7.5C	HS0580M02DWF5P	10	9425236	39 - 176 (138)	100.00%	68	Intergenic	9425099-9425236	+	-
7.5C	HS0580M02DUTQG	12	84845364	37 - 56 (20)	100.00%	1	Intergenic	84845345-84845364	+	-
7.5C	HS0580M02C30Z4	12	101838265	37 - 58 (22)	100.00%	1	Rps6ka5	101838265-101838286	-	+
7.5C	HS0580M02D8V89	13	117356737	36 - 51 (16)	100.00%	3	Intergenic	117356722-117356737	+	-
7.5C	HS0580M02DY8LB	16	28724887	37 - 213 (177)	100.00%	3	Intergenic	28724887-28725063	-	+
7.5C	HS0580M02DND1C	16	48508091	39 - 182 (144)	100.00%	103	Morc1	48508091-48508234	-	+
7.5C	HS0580M02EB100	16	54099065	39 - 125 (87)	98.85%	25	Intergenic	54098980-54099065	+	-
7.5C	HS0580M02DNHN1	16	56169105	39 - 146 (108)	100.00%	2	Senp7	56169105-56169212	-	+
7.5C	HS0580M02DB1HV	16	69126300	37 - 71 (35)	100.00%	32	Intergenic	69126300-69126334	-	+
7.5C	HS0580M02C8BEK	16	71424798	39 - 302 (264)	98.86%	1	Intergenic	71424798-71425062	-	+
7.5C	HS0580M02EU0FE	16	80527692	36 - 140 (105)	89.52%	18	Intergenic	80527595-80527692	+	-
7.5C	HS0580M02ENZ6S	17	17058324	38 - 53 (16)	100.00%	4	Intergenic	17058324-17058339	-	+
7.5H	HS0580M02DBXZX	1	26794463	37 - 151 (115)	100.00%	27	Intergenic	26794349-26794463	+	-
7.5H	HS0580M02DQOCK	1	141255311	39 - 128 (90)	98.89%	1	Crb1	141255223-141255311	+	-
7.5H	HS0580M02EWHQX	1	149681088	35 - 108 (74)	98.65%	10	Intergenic	149681015-149681088	+	-
7.5H	HS0580M02EQ84U	1	152145196	37 - 110 (74)	98.65%	124	Intergenic	152145123-152145196	+	-
7.5H	HS0580M02DUF8S	1	152448908	39 - 79 (41)	100.00%	60	Hmcn1	152448868-152448908	+	-
7.5H	HS0580M02D6LL	2	60907768	37 - 54 (18)	100.00%	59	Intergenic	60907751-60907768	+	-
7.5H	HS0580M02DQ4P8	2	101705017	36 - 54 (19)	100.00%	1	Prr5l	101704999-101705017	+	-
7.5H	HS0580M02C3N5T	2	163468418	39 - 78 (40)	92.50%	95	Serinc3	163468418-163468457	-	+
7.5H	HS0580M02DZTV6	3	75350388	38 - 105 (68)	100.00%	68	Pdcd10	75350388-75350455	-	+
7.5H	HS0580M02EBYEI	3	75905868	36 - 53 (18)	100.00%	1	Fstl5	75905868-75905885	-	+
7.5H	HS0580M02EA6GH	5	28496774	38 - 77 (40)	100.00%	4	En2	28496774-28496813	-	+
7.5H	HS0580M02EE3TM	8	75325174	39 - 188 (150)	99.33%	18	Intergenic	75325025-75325174	+	-
7.5H	HS0580M02D0GY	10	53252437	39 - 162 (124)	98.39%	14	Intergenic	53252437-53252560	-	+
7.5H	HS0580M02DFESI	11	3067893	40 - 175 (136)	98.53%	10	Sfi1	3067757-3067893	+	-
7.5H	HS0580M02DUUYS	11	112634790	38 - 102 (65)	100.00%	227	BC006965	112634726-112634790	+	-
7.5H	HS0580M02EKHWG	11	116757245	38 - 136 (99)	100.00%	2	Intergenic	116757147-116757245	+	-
7.5H	HS0580M02ETWPD	12	45484485	37 - 55 (19)	100.00%	2	Nrcam	45484467-45484485	+	-
7.5H	HS0580M02EKSDJ	14	25548996	37 - 82 (46)	100.00%	48	Intergenic	25548996-25549041	-	+
7.5H	HS0580M02C8ZW2	15	56095373	40 - 138 (99)	100.00%	37	Intergenic	56095275-56095373	+	-
7.5H	HS0580M02C6A09	15	81218977	38 - 193 (156)	100.00%	2	St13	81218977-81219132	-	+
7.5H	HS0580M02DSVAJ	16	3988504	38 - 118 (81)	98.77%	60	Slx4	3988424-3988504	+	-
7.5H	HS0580M02D2APG	16	7392723	38 - 75 (38)	97.37%	95	Rbfox1	7392686-7392723	+	-
7.5H	HS0580M02D1CLK	16	12385827	37 - 176 (140)	99.29%	1	Intergenic	12385827-12385967	-	+
7.5H	HS0580M02EEMXI	16	16193405	38 - 202 (165)	100.00%	1	Intergenic	16193405-16193569	-	+
7.5H	HS0580M02DJZJN3	16	27873374	39 - 59 (21)	100.00%	102	Intergenic	27873374-27873394	-	+
7.5H	HS0580M02DU9Z5	16	41293954	37 - 99 (63)	100.00%	193	Intergenic	41293954-41294016	-	+
7.5H	HS0580M02DGL9A	16	46720946	39 - 170 (132)	99.24%	6	Intergenic	46720815-46720946	+	-
7.5H	HS0580M02EAOSF	16	61860006	40 - 170 (131)	99.24%	701	Intergenic	61859876-61860006	+	-
7.5H	HS0580M02COHSE	16	70016908	39 - 101 (63)	100.00%	108	Intergenic	70016908-70016970	-	+
7.5H	HS0580M02EPL5B	16	74917820	36 - 222 (187)	100.00%	3	Intergenic	74917634-74917820	+	-
7.5H	HS0580M02DGBBB	16	79815100	38 - 103 (66)	100.00%	5	Intergenic	79815035-79815100	+	-
7.5H	HS0580M02DO80U	18	25410073	36 - 185 (150)	99.33%	6	AW554918	25409924-25410073	+	-
7.5H	HS0580M02D5WEK	18	51216844	36 - 90 (55)	100.00%	1	Intergenic	51216844-51216898	-	+
7.5H	HS0580M02D5KP9	X	99382099	36 - 52 (17)	100.00%	1	Rps4x	99382083-99382099	+	-

Appendix5A: Results of the CIS analysis performed using all integrations with 2 or more reads on TraDIS

Chromosome	Minimum Peak Location	Maximum Peak Location	Peak Height (range)	Start	End	Number of Insertions	Smallest p Value	CIS Analysis Scales	Genes in CIS	Gene Nearest Peak
11	54325853	5437445	41.33-48	5403070	5477021	49	0	10-100	Pallid4 P4aa2 Gm12221 4833405248Rik Gm12222 Cuz2 Gm12223 I3 Aca18 Gm12224 493040410Rik Gm12226 Gm12225 Phip1 Gm24198	Gm12223
11	79361616	79857057	16.76-36.01	79221934	7990789	43	0	10-100	Wb1 Gm9564 N1 Gm11198 A10040972 Omg Gm21975 EN2b EV2b Rabi11p4 Gm23203 Gm11202 Gm23867 Gm24887 493054202Rik	N1
2	86651681	86670460	29.76-29.97	86655575	86675787	31	0	10-100	Gm13806 Gm10801 Gm10800	Gm10801
5	20160140	20174630	20.56-22.93	27977161	28376051	25	0	10-100	AC156021.1 Inag1 En2 Cyp1f Rom33	En2
7	102158068	102179487	10.83-16.86	101988901	102342775	18	0	10-100	Numa1 I18bp Rrf121 Tmp2 Av15 Av11 Chrm10 Nup88 Pap22 Rimg Slim1	Nup88
9	44835970	44841958	12.32-15.85	44603945	44969751	16	0	10-100	Treh Phd1b1 Gm24168 Arcm1 Ith46 Trmm25 Tlc36 Mif1 Gm26249 Apg5l Ube4a Cds3 Cdsb	Mif1
11	100832721	100841602	9.83-14.57	100872030	100874832	15	0	10-100	Zp1a3a5 Gm1547 Dhs48 Kat2a Hap89 Rabc10 Hart Ghd2 Gm24358 Stat5b Stat5a Stat3 Prf	Stat5b
6	30864745	31242679	2.16-6.21	30813113	31227202	11	0	10-100	Copp2 4800412F09Rik Toga13 Klf4 Mir29a Mir29b-1 RP23-459L 16.5 Gm13834 Gm13833 Gm13835 AB041803	Gm13833
9	32697818	32704766	8.62-10.61	32585676	32629752	11	0	10-100	Ets1	Ets1
15	3486652	3481150	7.02-9.75	3378660	3657659	11	0	10-100	Ghr Gm20231	Ghr
16	4219767	4227802	3.28-6.64	4132652	4277644	10	2.20E-16	20-100	Cnrbp Gm5766 Gm4107	Cnrbp
4	44457140	4456027	5.27-8.85	44500918	4474213	9	0	10-100	Pav5 Mir120 Gm12482 Gm12483 Zcoch7	Pav5
5	147303448	147373807	7.93-8.90	147236918	147491140	9	0	10-100	Z51001911Rik Pkrt1 RP24-51055.4 Cc2d Phomb1 Ff1b AC134441.1 Gm6054 Pam3	Ff1b
8	10565322	10915507	5.31-8.51	10732788	11003860	8	0	10-100	Rp1a-p1 Sfr1 Gm17399 Gm17400 Dgr1 Gm17395 Fwp62 Efkfep1	Sfr1
16	3747746	3750284	6.73-7.02	3697665	3738794	6	0.000134814	10-100	Prkac1	Prkac1
10	10565322	10915507	5.31-8.51	10732788	11003860	8	0	10-100	Prkac1	Prkac1
4	32197414	32197414	2.86-4.58	32051740	32145446	7	0	10-100	Prkac1	Prkac1
4	101233700	101260741	2.66-6.68	10116402	101841224	7	0	10-100	Rew2c1 Jak1 Gm24468 Gm12785 Gm25124 Gm12801 Gm12786	Jak1
6	103687051	103694028	6.99-7.02	103560360	103748054	7	0	10-100	Ch1 Gm23184	Ch1
7	75712853	75732567	3.4-8.77	75693253	7575748	7	5.53E-05	30-100	Akap13	Akap13
15	78485400	78496467	5.06-6.34	78328070	78522258	7	0	10-100	Gm20233 Tbx33 Tst Mpat Kcid17 Tmpras6 Ikb2b C1qtnf6 Stat3 Gm0723 Rac2	Ikb2b
15	86819465	86826368	2.03-3.75	86762929	8682523	7	2.87E-07	20, 40-80, 100	Wnt1 Dcn AC116185.1 Pkag1 M12	Pkag1
18	52138115	52143388	4.33-5.31	52115955	52159821	7	1.99E-15	10-70	Cbb	Cbb
1	19497427	195025139	3.59-5.24	19470487	195098073	6	0	20-100	Ct34 AC16282.1 rmmu-mir-206-2 Mir206-2 Mir206-2 C446	rmmu-mir-206-2
2	117248438	117259913	3.48-5.03	117272135	117408410	6	0	10-100	Ragrp1	Ragrp1
3	103040284	103074742	3.13-4.55	102975203	103182730	6	0	10-100	Ske1 Ccd1f Nras Amp1 Gm23820 Dnm2c2-Box2 RP24-408D4.2	Ccd1f
4	83759992	83781226	2.91-4.78	83672218	83835833	6	0	20-100	Pfgr1 Pkrt1 Dlx39 C9f7 Gm23024	Gm23024
8	97907260	97910254	3.04-3.77	97823285	97846346	5	0.000116716	60-100	Nfia	Nfia
5	136337299	136357721	3.064-3.32	136291620	136418050	5	1.64E-07E-06	50-100	Cux1	Cux1
6	30125308	30138281	2.43-4.03	30083144	30198385	5	0	10-100	Nr1 Gm25980 Mir162 Mir163	Nr1
6	41588237	41602388	3.04-4.85	41508104	41658720	5	0	10-100	Pra2 Tnfr1 Tnfr1-1 Tnfr1-2 Tnfr1-3 Tnfr1-4 Tnfr1-5 Tnfr1-6 Tnfr1-7 Tnfr1-8 Tnfr1-9 Tnfr1-10 Tnfr1-11 Tnfr1-12 Tnfr1-13 Tnfr1-14 Tnfr1-15 Tnfr1-16 Tnfr1-17 Tnfr1-18 Tnfr1-19 Tnfr1-20 Tnfr1-21 Tnfr1-22 Tnfr1-23 Tnfr1-24 Tnfr1-25 Tnfr1-26 Tnfr1-27 Tnfr1-28 Tnfr1-29 Tnfr1-30 Tnfr1-31 Tnfr1-32 Tnfr1-33 Tnfr1-34 Tnfr1-35 Tnfr1-36 Tnfr1-37 Tnfr1-38 Tnfr1-39 Tnfr1-40 Tnfr1-41 Tnfr1-42 Tnfr1-43 Tnfr1-44 Tnfr1-45 Tnfr1-46 Tnfr1-47 Tnfr1-48 Tnfr1-49 Tnfr1-50 Tnfr1-51 Tnfr1-52 Tnfr1-53 Tnfr1-54 Tnfr1-55 Tnfr1-56 Tnfr1-57 Tnfr1-58 Tnfr1-59 Tnfr1-60 Tnfr1-61 Tnfr1-62 Tnfr1-63 Tnfr1-64 Tnfr1-65 Tnfr1-66 Tnfr1-67 Tnfr1-68 Tnfr1-69 Tnfr1-70 Tnfr1-71 Tnfr1-72 Tnfr1-73 Tnfr1-74 Tnfr1-75 Tnfr1-76 Tnfr1-77 Tnfr1-78 Tnfr1-79 Tnfr1-80 Tnfr1-81 Tnfr1-82 Tnfr1-83 Tnfr1-84 Tnfr1-85 Tnfr1-86 Tnfr1-87 Tnfr1-88 Tnfr1-89 Tnfr1-90 Tnfr1-91 Tnfr1-92 Tnfr1-93 Tnfr1-94 Tnfr1-95 Tnfr1-96 Tnfr1-97 Tnfr1-98 Tnfr1-99 Tnfr1-100	Ephb6
7	145650270	145650270	3.95-4.88	145650270	145650270	5	0	10-100	Ccnd1	Ccnd1
6	87900724	8794888	2.18-4.82	87856599	88025359	5	0	10-100	Zfp423	Zfp423
10	116519759	116530075	2.07-4.11	116442399	116593658	5	9.83E-05E-09	10, 30, 50-100	Prnk	Prnk
11	68419862	68428512	3.00-4.96	68379515	68461441	5	0	10-100	Irf3	Irf3
14	103116920	103116920	3.34-12	103029789	103184648	5	9.87E-07E-07	10-100	Irf3	Irf3
17	62957784	62991033	2.4-1	62913269	63013452	5	4.76E-08E-09	10, 30-100	Inte1n3	Inte1n3
18	67483061	67498164	2.00-3.68	67402091	67537864	5	5.74394E-11	10-30, 50-100	Alp32 Gm24900 Slnm1 Spn1	Spn1
4	11023693	11024092	2.95-3.14	110094417	110201100	4	0.000320338	10-100	Prnk	Prnk
6	142620596	14263460	2.75-3.80	142516202	145324194	4	0	10-100	Prnk	Prnk
8	95797297	95797297	3.123-3.89	95799880	95807192	4	0	10-100	Prnk	Prnk
9	3002184	3004020	2.07-4.03	2984170	3057684	4	0	10-100	Prnk	Prnk
10	88755802	88771056	2.61-3.37	8872427	88802305	4	1.77948E-05	20, 30, 50-80	Gm4925 A1 U200	U200
12	16008880	16012184	2.74-3.33	16031935	16059546	4	8.672E-06	70-100	Roc2 Gm23203	Roc2
15	67247259	67247259	2.91-3.94	67260966	67267226	4	0	10, 30, 50-100	Inte1n3	Inte1n3
16	5006914	5006914	3.29-3.65	4898951	5014844	4	6.22E-11E-05	20, 30	Sep13 Gm5480 Rop1	Sep13
16	42874226	42874226	3.13	42888448	42976152	4	0.000158646	10, 30	Zbn200	Zbn200
16	92031944	92031944	3.4	92032372	92031944	4	0.000160277	10, 30	Rum1	Rum1
16	76226579	76226579	2.96	75178401	76255486	4	8.30327E-10	10, 20, 50-100	Prnk	Prnk
X	107101017	107124183	2.6-3.41	107024321	107166221	4	2.88417E-07	40-80, 80-100	Fg Gm6039	Fg
1	5920611	5930395	2.05-2.97	59379541	59444694	3	5.01393E-11	10, 20, 50-90	Hevw2	Hevw2
2	135444222	135444222	2.07-2.97	135429546	135472217	3	9.31145E-08	10, 30	Ubc93	Ubc93
3	135444222	135444222	2.07-2.97	135429546	135472217	3	9.31145E-08	10, 30	Ubc93	Ubc93
4	90958567	90958567	2.56	90959596	9118664	3	0.000235472	60000	Ebak14b	Ebak14b
4	155310215	155310215	2.56-2.94	90948856	90989140	3	8.87457E-05	20, 50, 60	Gmb1 Gm13171	Gmb1
6	115694757	115694757	2.42-2.97	115646088	115672308	3	1.12359E-13	30-80	Gmb1 Gm13171	Gmb1
6	115694757	115694757	2.42-2.97	115646088	115672308	3	1.12359E-13	30-80	Gmb1 Gm13171	Gmb1
7	15987752	15987752	2.85-2.99	15974141	15995764	3	1.81672E-09	10, 30, 50-90	Raf1 Gm14335	Raf1

Chromosome	Minimum Peak Location	Maximum Peak Location	Peak Height (range)	Start	End	Number of Insertions	Smallest p Value	CIS Analysis Scales	Genes in CIS	Gene Nearest Peak
7	48324569	48324622	3	48322638	48341114	3	2.22045E-16	Oct-30	Nav2	Nav2
8	80323151	80323215	2-2,91	80299568	80339557	3	1.30381E-05	10, 40-60	intergenic	Cyba
8	122116152	122116151	2,95-3,01	122163555	122245982	3	0	10, 50-70	Gm20388	Gm20388
10	37297358	37297482	2,83-2,97	37298681	37298681	3	3.77762E-10	20, 50-70	intergenic	AC153356.1
11	97070698	97070873	2,35-2,98	96976175	97192539	3	1.10222E-16	10, 20, 40-70	intergenic	Bcl1
11	31048317	31048317	2,99-3	31048317	31048317	3	0.000272749	10, 20, 40-70	intergenic	Gm9075
12	72723233	72723359	2,01-2,97	72717200	72784403	3	5.10954E-05	10, 20, 40, 60-100	Ppm1a	Ppm1a
14	8217741	8226082	2,98-3	8198385	8252371	3	0	10, 40, 60-100	Kctd6 Acox2	Kctd6
14	34710585	34710578	2,89-2,98	34673490	34781180	3	1.71759E-08	30, 40, 60-90	Wspal	Wspal
14	50304868	50304868	2,01-2,37	50285463	50320428	3	0.744105E-06	20, 40	Chfr33 Chr734	Chfr33
14	64583584	64583584	2,82-3,1	64583584	64583584	3	0.000103667	40, 60-100	Chfr33 Chr734	Chfr33
16	48885889	48885889	2,82-2,89	48879749	48886486	3	1.29603E-07	10000	intergenic	Il181
17	45435422	45436336	2,30-2,69	45445684	45444821	3	0.000430267	30, 50	Cdcs1 AC163077.1	AC163077.1
17	71139887	71139887	2,83	71139886	71143215	3	0.000186088	50	AC126842.1 Myom1	AC126842.1
17	78984521	78984521	2,92-2,98	78980035	78993934	3	2.1765E-05	30-60	Er2kac AC154274.1 Suibs1	AC154274.1
18	35597442	35597442	2,07-2,93	35597442	35597442	3	1.6197E-07	10, 30-70	AC121621.1 Mrr949 Sncra74a Matr3	AC121621.1
19	32795732	32795732	2,85-2,75	32785563	32813594	3	6.90739E-05	30, 40	Plen	Plen
19	32795732	32795732	2,85-2,75	32785563	32813594	3	6.90739E-05	30, 40	Plen	Plen
X	57213371	57213371	2,73-3	57227130	57305672	3	0	10, 30-50, 80-100	Arhgef6	Arhgef6
X	106128203	106130078	2,8-2,83	106099296	106147474	3	0.000354245	90, 100	Ad7a Tr13	Ad7a
X	152259733	152273471	2,07-2,77	152252933	152319742	3	1.23124E-13	40-70, 100	Kom5c	Kom5c
1	131263176	131263176	1,99	131263176	131263176	3	1.10222E-16	10, 30	Mapk4	Mapk4
1	156687469	156687469	2	156687469	156687469	2	1.10222E-16	10, 30	Mapk4	Mapk4
2	6923332	6923332	2	69231276	6923332	2	1.90536E-12	10	Abpb6	Abpb6
2	12417075	12417075	2	124168520	12417075	2	4.47474E-05	10	intergenic	Gm13321
2	16771983	16771983	1,05-1,91	16771983	16771983	2	4.3096E-05	10	intergenic	Abcb11
3	24865151	24865151	2	24863184	24865151	2	0	10	Sema6d	Sema6d
3	30180433	30180433	1,99-2	30187489	30190433	2	1.40837E-05	10, 20	Nrg1	Nrg1
3	55588343	55588343	2	55584581	55588478	2	0	10, 20	intergenic	Nras
3	10519569	10519569	2	10519569	10519569	2	1.2449E-07	10, 20	Mapk1	Mapk1
4	58026575	58026575	2	5819601	58260575	2	0	10, 20	Vav1	Vav1
4	59755049	59755049	2	5978475	59795049	2	3.76289E-10	10	Ikkap	Ikkap
4	95019762	95019762	2	95018788	95019762	2	6.47301E-05	10	Stk4a1	Stk4a1
5	30363908	30363908	2	30364018	30368387	2	0	10-30	Gm12684	Gm12684
5	3687217	3687217	2	3687217	3687217	2	3.9878E-08	10, 20	Dct1	Dct1
5	62223309	62223309	2	62223309	62223309	2	3.99222E-05	10, 20	Nr6e679e	Nr6e679e
6	24491388	24491388	2	2449437	24491388	2	1.92209E-06	10	intergenic	Igfbp7
6	28375684	28375684	2	28373732	28375684	2	4.05108E-05	10	Igfbp7	Igfbp7
6	54681780	54681780	2	54679628	54681780	2	1.44314E-08	10	Zfp800	Zfp800
6	117951212	117951212	2	11795355	117951212	2	1.53175E-07	20	Znr2	Znr2
7	59278094	59278094	2	59272234	59278094	2	0.00029071	20	intergenic	Zfp239
7	10142938	10142938	2	10140982	10142938	2	0	10, 20	Ubc3a	Ubc3a
7	101387707	101387707	2	101384866	101387707	2	5.81851E-05	10	intergenic	Lip2
7	126897980	126897980	2	126896536	126897980	2	3.1073E-13	10	Arp1	Arp1
8	59571642	59571642	1,99	59520071	59571642	2	8.99809E-08	10	intergenic	Iz27
8	105600606	105600606	2	105600606	105600606	2	1.28516E-05	10	Gaint6	Gaint6
9	11491181	11491181	2	114908167	11491181	2	4.80898E-11	10, 20	intergenic	Chnab5a
9	115001159	115001159	2	11500281	115002133	2	2.19714E-10	10	Gtcl1	Gtcl1
10	11580769	11580769	2	11587616	11580769	2	2.39003E-07	10	Obcd10	Obcd10
10	13381280	13381280	2	13380308	13381280	2	2.4114E-06	10	Phacr2	Phacr2
12	31043009	31043009	2	31040100	31043009	2	1.90797E-05	10	intergenic	Gm25408
12	70516433	70516433	2	70511985	70516433	2	4.29815E-08	10, 20	Phacr2	Phacr2
12	70516433	70516433	2	70511985	70516433	2	4.29815E-08	10, 20	Phacr2	Phacr2
13	93968906	93968906	2	93968880	93968906	2	1.077183E-10	10, 20	Arab	Arab
14	39481146	39481146	1,99	39480177	39481146	2	0.000118864	10	intergenic	Gm24842
14	69737317	69737317	2	69734405	69737317	2	6.22907E-05	10	intergenic	AC162936.1
14	78215343	78215343	2	7821468	78217270	2	3.34415E-10	10, 20	Gm10863	Gm10863
17	20446424	20446424	2	20442722	20446424	2	0.000103667	10, 20	AC163026.1	AC163026.1
17	50116147	50116147	2	50116245	50116275	2	1.11022E-16	10, 20	Rtn1	Rtn1
17	56698150	56698150	1,81	56697199	56705752	2	0.000248063	10	Ranb3	Ranb3
17	57821404	57821404	2	57820453	57821404	2	0.00033417	10	Chnab5c	Chnab5c
17	60765331	60765331	2	60762981	60765331	2	6.38379E-14	10	intergenic	Gm23447
17	64583584	64583584	2	64583584	64583584	2	0.000103667	10, 20	intergenic	Gm23447
18	34510826	34510826	2	34517904	34510826	2	6.4433E-10	10, 20	Wtbs	Wtbs
18	68825584	68825584	2	68822715	68825584	2	0.000163073	10	intergenic	483546C10RK
18	80527711	80527711	2	80511735	80549508	2	0	10-40	Nfalc1	Nfalc1
19	47154357	47154357	2	47150617	47157938	2	5.74687E-09	10, 40	Calhm3	Calhm3
19	50945830	50945830	2	50941269	50945830	2	0	10	intergenic	Gm25469
X	10872882	10872882	2	10872009	10874685	2	6.66134E-16	10, 30	Brwd3	Brwd3
X	143483582	143483582	2	143483582	143483582	2	0.00029448	20	intergenic	Brwd3
Y	1172264	1172264	1,05-1,99	1168013	1300813	2	0	10, 30-100	Uty Docy3	Uty

Appendix5A: CIS analysis using all integrations with 2 or more reads from the duplicate filtered analysis of the TraDIS data.

Chromosome	Minimum Peak Location	Maximum Peak Location	Peak Height (range)	CIS Start	CIS End	Number of hits	Number of tumours	Smallest p Value	Kernel scales	Genes - largest CIS	Genes - smallest CIS	Gene Nearest Peak
7	28006812	28006812	2.064574125	28002630	28006812	2	2	1.3715E-06	20	RP23-73F23.2 Gm4636		RP23-73F23.2
7	132961846	132961846	2.080201475	132961846	132965731	2	2	0.001057654	40	Fgf2 Zmap1		Fgf2
2	91868251	91868251	2.048959164	91879444	91868251	2	1	9.97792E-07	50	Ambr1		Ambr1
2	98662180	98668789	4.064.12	98554936	98756369	4	4	0	10-100	Gm13808 Gm10801 Gm10800	intergenic	Gm10800
5	28162028	28165870	2.73-3.16	28081357	28228777	3	3	0	20, 30, 50-100	Enz Chp1	Enz	Enz
11	3142056	3143290	3.31-3.54	3087203	3196490	3	3	0	10-100	Piss-ps1 Sfr1 Gm11399 Gm1400 Drg1 Gm12735 Fau-ps2	Sfr1 Gm11399	Sfr1
1	33366572	33366695	2	33353487	33376659	2	2	3.37952E-13	40, 80	intergenic		Gm23453
2	180204639	180206513	2.06	180171548	180259930	2	2	0	10-80, 100	Lama5 Res21 Mir3091 Cabes2	Lama5	Lama5
4	9507313	95020995	2.37	95012411	95020995	2	2	7.84138E-05	40, 60, 80	Gm12694	Gm12694	Gm12694
8	13773819	1377535	2.04	13759401	13782034	2	2	0	10, 50, 80	Cdc16	Cdc16	Cdc16
9	41123336	41124635	2.21-2.33	41087192	41138651	2	2	0	20, 40, 70	Ubash3b	Ubash3b	Ubash3b
9	114910254	114911668	2.21	11489109	114914083	2	2	0	20, 40	Gpd11	Gpd11	Gpd11
9	115059581	115060843	2.21	11504037	115074897	2	2	0	20, 40	Osbp10	Osbp10	Osbp10
10	20487361	20490989	2.05-2.16	20467002	20497836	2	2	0	10-30, 50-80	Pde7b	Pde7b	Pde7b
14	37011641	37014879	2.13	36993625	37014879	2	2	0	10-40, 80	intergenic	intergenic	Rgr
18	35566754	35567381	2.05-2.06	35541192	35562636	2	2	1.66533E-15	10, 20, 50, 60	AC121821.1 Mir1949 Snora74a Matr3	AC121821.1 Snora74a	AC121821.1
19	9880120	9881128	2.3-2.4	9871905	9885738	3	2	0	10, 20, 50, 70	Incnp	Incnp	Incnp
11	16791417	16790445	2.234595157	16790445	16791417	2	0	0.000112297	10	Egfr		Egfr
11	67563688	67561923	2.253451297	67561923	67563688	2	0	0.000263611	20	Gas7		Gas7
X	143066829	143066829	1.061163139	143065001	143066829	1	0	9.52668E-07	20	intergenic		Rosa1
13	55457979	55514966	1.03-1.14	55376537	55525126	1	1	0	40, 80-100	Rgs14 Sic34a1 Phn3 F12 Gk6 Pr7 Dbm1 Pdlim7 Dok3	Pdlim7	Pdlim7
14	70657965	70632810	1.07-1.26	70574426	70632810	1	1	1.47458E-05	40-60	Nudt18 Fam160b2 Epb4.9	Fam160b2	Epb4.9
7	100142866	100142862	2.06	100138984	100142862	2	0	3.1881E-06	10, 20	intergenic	intergenic	Lprt2
10	11688263	11589033	2.05-2.16	11577306	11589033	2	0	1.95399E-14	10, 40, 60	intergenic	intergenic	Gm9797
2	93639136	93641370	1.48-2.02	93604888	93654700	2	1	2.13984E-05	20, 60, 80	intergenic	intergenic	Akt4

Appendix 5Bi: CIS integrations excluded from the 'top 25 analysis' of the TraDIS data.

Chromosome	Minimum Peak Location	Maximum Peak Location	Peak Height (range)	CIS Start	CIS End	Number of hits	Number of tumours	Smallest p Value	Kernel scales	Genes - largest CIS	Genes - smallest CIS	Gene Nearest Peak
1	138127240	138127240	2.06059912	138125314	138127240	2	1	5.60106E-05	10	Ptprc		Ptprc
1	155607294	155606257	2.067228491	155606331	155606257	2	2	5.39318E-06	10	Acb6b		Acb6b
1	157506974	157506974	2.067318122	157505047	157506974	2	0	0.000112811	10	Gm15486 Sec1fb		Gm15486
2	26465024	26465024	2.135048324	26463968	26465024	2	0	5.13779E-05	20	Notch1		Notch1
2	52593402	52593402	2.111468975	52592425	52593402	2	0	8.64194E-05	10	Ccamb4		Ccamb4
3	55598343	55598343	2.074297935	55585408	55598321	2	1	0	10	intergenic		Nbsa
3	16801693	16801693	2.941214149	16801693	16804623	4	1	0.000342162	30	intergenic		Tksa
6	50146867	50144715	2.134692326	50144715	50146867	2	2	2.80009E-05	10	Mpp6		Mpp6
10	42680164	42680164	2.089281061	426802374	42680162	2	2	1.1029E-15	20	Ikzf1 Gm12000		Chusp2
11	1189442	1189442	2.892341426	11891350	11893559	3	2	5.27104E-06	10	intergenic		Ikzf1
15	75066350	75066350	2.113341364	75066427	75066350	2	0	1.18033E-05	10	Six4		Six4
16	4001456	4001456	2.469487774	3995721	4003368	3	1	4.83297E-05	10	Zbnb20		Zbnb20
16	42964600	42964600	3.616228678	42966861	42966813	5	2	0.000116398	20	AC163629.1		AC163629.1
17	29464041	29464041	2.118708164	29452910	29465006	2	2	1.11022E-16	10	Rarb3		Rarb3
17	98897917	98897917	2.071612787	98892121	98701781	2	1	2.67698E-12	20	Lidrad4		Lidrad4
18	67999404	67999404	2.053698266	67996510	68000368	2	2	1.9929E-08	10	Gm26312 Fh1		Fh1
X	98737693	98737693	2.251475302	98740744	98744306	3	1	0.000183604	70	intergenic		Pak3
X	143463102	143463102	2.091404193	143479273	143463102	2	2	1.46892E-09	20	intergenic		Pak3
2	98661681	98670460	20.96521.95	98485185	98628371	29	20	Excluded as recurrent CIS on multiple screens	10-100	Gm13806 Gm10801 Gm10800	Gm10801 Gm10800	Gm10801
5	28166020	28170958	16.41-18.64	27990953	28332290	24	17	0	10-100	AC156021.1 Ine1g1 En2 Cnpy1 Rbm33	AC156021.1 Ine1g1 En2 Cnpy1	En2
9	3002184	3012785	3.2-4.37	2984170	3050992	5	4	0	10-100	AC131780.1 Gm10722 Gm11168 Gm10721 Gm10720 Gm10719 Gm10718 Gm10717 Gm17635 Gm10715	AC131780.1 Gm10722 Gm11168 Gm10721 Gm10720 Gm10719 Gm10718 Gm10717 Pisd-ps1 Sfl1 Gm11389 Gm11400	AC131780.1
11	3141162	3152417	4.57-5.38	3086874	3167873	5	4	0	10-70, 100	Pisd-ps1 Sfl1 Gm11389 Gm11400	Pisd-ps1 Sfl1 Gm11389 Gm11400	Sfl1
10	118512112	118520686	2.35-3.98	118488614	118546557	4	2	8.96386E-05	20, 50-90	intergenic	intergenic	lflg
16	5012733	5012733	2.437303221	5006042	5016556	4	2	2.69012E-05	10	Gm5480 Rogd1 Gyr1		Rogd1
18	35565423	35566843	2.83-3.14	35544102	35565705	3	2	0.000197264	30, 50-70	AC121821.1 Mr1948 Snon74a Mair3	Mair3	Mair3
19	9880044	9880044	2.139481557	9876283	9880044	3	0	0.000389883	20	Incnp		Incnp
2	180206483	180206483	2.113283703	180204528	180207461	2	2	0	10	Lama5		Lama5
3	65474764	65474633	2.09-2.15	65468961	65474833	2	2	1.11022E-16	10, 20	intergenic	intergenic	4931440P22Rik
4	85018075	85018075	2.18050821	85015482	85021322	2	2	4.10707E-05	20	Gm12684		Gm12684
5	124384575	124417649	3.15-4.24	124355318	124417649	5	1	0.000272089	60, 80, 100	Sno1	Sno1	Sno1
8	80322470	8032874	2.07-3.15	80314222	80332874	4	1	0.000135844	10, 50-60	intergenic	intergenic	Cypa
6	415893447	41602368	2.16-3.23	41575888	41602920	5	0	4.75914E-06	10, 20, 50, 60	intergenic	intergenic	Eplb6
15	50846847	50846847	3.06-3.34	50844123	50855768	5	0	0.000339393	40, 30	Trps1	Trps1	Trps1

Appendix5Bii: Excluded CIS integrations from the 'top 100 analysis' of the TraDIS data.

Appendix 6A: CIS analysis in the *Vk**hPB** and *Vk**MYC-TA-hPB** cohorts

Chr	Start	End	Genes in CIS	Gene nearest to peak	Number insertions	Number insertions (no hop)	p value	Scale
13	37616615	38065245	Rreb1 Ssr1 Cage1 Riek1	Rreb1	30	23	0	10-100
16	23824481	24294739	Sst Rtp2 Bcl6	Bcl6	11	10	0	10-100
4	44508363	44855905	Pax5 Mir5120 Gm12462 Gm12463 Zcchc7	Gm12463/Zcchc7	7	6	0	10-100
2	18612595	18866281	Gm13355 Gm13352 Commd3 Bmi1					
6	98995326	99242513	Gm13334 BC061194 Gm20539	BC061194	4	4	0	30, 60-80, 100
4	32301533	32489946	Gm13333 RP23-396N6.8 Pip4k2a Foxp1 Bach2	Bach2	4	3	0	30, 50-100
7	24979620	25265769	Atp1a3 Grik5 Zfp574 Pou2f2 D930028M14Rik Dedd2 Zfp526 Gsk3a 9130221H12Rik Erf	Pou2f2	3	3	0	10-100
11	44638767	44754313	Ebf1 Gm12158	Ebf1	3	3	0.0001634	70
16	24137274	24252092	intergenic (Sst Rtp2 Bcl6) Ndst1 Rps14 Gm8731 Cd74 Mir5107 Tcof1 Arsl Camk2a	AC116484.1	3	3	0	10-80
18	60661919	60934217	Nfatc1 Atp9b	Cd74	3	3	0	10-100
18	80498405	80737697	Nfatc1 Atp9b	Nfatc1	3	3	0	10-100
5	147329096	147392896	Fli3	Fli3	3	2	0	30-60, 80, 90
11	17161778	17185094	Ppp3r1 Wdr92	Ppp3r1	3	2	0.000129	20, 80
11	62439680	62439680	Ncor1	Ncor1	3	2	0.0036251	80
1	39896022	40131226	Map4k4 AC161534.1 Il1r2	Il1r2	2	2	1.119E-06	10, 80, 90
1	58669859	58767732	Als2cr12 Cflar	Cflar	2	2	0	20, 40, 50, 70, 80, 100
2	163159736	163357047	Tox2 Jph2	Tox2	2	2	0	10-100
4	138025236	138076416	Eif4g3	Eif4g3	2	2	0	10, 40, 60, 70, 80, 100
5	23441479	23521061	Mil5 Gm25219 Srpk2	Mil5	2	2	0.0041463	70
5	72795165	72867478	Tec	Tec	2	2	1.13E-08	30, 60, 80, 90
6	113054963	113131765	Thumpd3 Gm22591 Gt(ROSA)26Sor Setd5	Setd5	2	2	7.965E-05	30, 70
9	44343501	44526252	Hmbs Vps11 Gm22141 Gm10080 Hyou1 Gm26306 Slc37a4 Trappc4 Rpe25 Ccdc84 Foxr1 Upk2 Gm9830 Gm22540 C030014123Rik Bol9l Cxcr5	Gm9830	2	2	1.295E-06	40, 60-80, 100
17	47686315	47825200	Usp49 Tomm6 Gm21981 Gm14872 Prickle4 Frs3 Gm14873 Pgc Tfeb Mdfi	Tfeb	2	2	1.11E-16	30, 40, 60, 70, 90, 100
17	80405710	80451144	Sos1	Sos1	2	2	2.22E-16	10, 30, 50, 60, 80
18	49990796	50042738	Tnfrsf8 C030005K06Rik	Tnfrsf8	2	2	1.11E-16	30-50, 90
18	65406503	65484149	Gm22567 Malt1	Malt1	2	2	0	10, 40, 50, 80-100
X	52866989	52931935	Rps2-ps13 Phf6	Phf6	2	2	0	20-40, 60-80, 100
2	163620641	163623882	Serinc3	Serinc3	1	1	0.0016047	40
3	94960845	94962472	Rfx5 B230398E01Rik	B230398E01Rik	1	1	9.259E-14	20
3	100478262	100483152	Fam46c	Fam46c	1	1	0.0017189	60
3	101273850	101275477	intergenic	Cd2	1	1	1.945E-11	20
6	129180775	129181687	Clec2d	Clec2d	1	1	0.0011947	10
7	35636231	35639797	Ankrd27	Ankrd27	1	1	0.0030711	50
7	81522887	81523599	mmu-mir-1839	mmu-mir-1839	1	1	0.0012525	10
8	82317320	82318723	intergenic	Il15	1	1	0.0008985	10
8	87859028	87866085	Zfp423	Zfp423	1	1	0.0003767	100
10	17875614	17876319	intergenic	Heca	1	1	0.0002276	10
10	78379851	78386225	intergenic	Gm10146	1	1	1.239E-08	90
12	107858133	107865517	intergenic	Bcl11b	1	1	0	60
13	93170173	93170893	Papd4	Papd4	1	1	0.0015046	10
14	15046049	15048455	intergenic	Nek10	1	1	0.0051263	30
14	75188183	75190589	Lcp1	Lcp1	1	1	6.09E-05	30
15	97720057	97728761	Endou	Endou	1	1	1.11E-16	10, 70
16	8642452	8643767	Pmm2	Pmm2	1	1	0.0019735	20
16	10485822	10487137	intergenic	Ctla	1	1	0.0009845	20
17	45553024	45555498	intergenic	Nfkbi	1	1	0.0006535	30
19	32766562	32767221	Pten	Pten	1	1	4.816E-05	10

CIS analysis using the top 10 hits in the *hPB* cohort. The start and end boundaries encompass all analysis windows in which each locus was identified as a CIS. The gene shown as nearest to peak was the central gene in the majority of kernel windows (scales) detecting the CIS, but is not necessarily the target gene for the CIS. Due to local hopping the total number of insertions occasionally included multiple integrations from the same tumour, so both the total number and the number after correction for local hopping are shown. The smallest p value identified at any scale is shown along with the analysis scales at which the CIS was detected (x1000).

Chr	Start	End	Genes in CIS	Gene nearest to peak	Number insertions	Number insertions (no hop)	p value	Scale
13	37624377	38058475	Rreb1 Ser1 Caga1 Rlok1	Rreb1	28	25	0	10-100
16	23863733	24281043	Sat Rip2 Bcl6	Bcl6	9	9	0	10-100
4	32237229	32561406	Bach2 D130062J21Rik Gm11932 Gm24371 BC024582	Bach2	9	7	0	10-100
11	3056838	3302391	Piad-ps1 Sfl1 Gm11399 Gm11400 Drg1 Gm12735 Fau-ps2 Eif4enif1 Patz1	Sfl1	8	7	0	10-100
1	58578786	58869374	Fam126b Ndufb3 Gm10068 Als2or12 Cflar Casp8	Cflar	7	7	0	10-100
5	147214584	147483494	221001911Rik Pdx1 RP24-510G5.4 Cdx2 Pihoxnb Fil3 AC134441.1 Gm6054 Pan3	Fil3	5	5	0	10-100
9	32500946	32758851	Fil1 Ets1	Ets1	5	5	0	10, 30-100
3	102947840	103164316	Nr1h5 Gm22826 Sike1 Cde1	Cde1	4	4	0	10-100
3	135562444	135765833	Nras Ampd1 Gm23820 Dennd2c Manba Nfkb1 Gm9799	Nfkb1	4	4	0	10-100
16	36537254	36700550	Casr Cj88 lldr1	Cd86	4	3	0	20-80, 100
6	98539472	99085985	Foxp1	Foxp1	3	3	0	10, 30, 50-70, 90, 100
6	99249196	99440799	Foxp1 Gm20696 Gm20705	Foxp1	3	3	0	30-100
11	109337893	109443336	Gm11696 Gna13 9930022D16Rik	Gna13	3	3	5.19E-08	80
15	61885470	62063475	Amz2 Gm15642 Myc Pvt1	Myc	3	3	0	10-100
17	46748591	46933407	CT030702.1 Cnpy3 Ptcra 2310039H08Rik Rpl71l Gltscr1l A330017A19Rik Tbcc Gm23797	Gltscr1l	3	3	0	10-100
17	75376145	75544280	Prph2 Ubr2	Rasgrp3	3	3	0	10, 20, 40, 50, 70-100
18	65353747	65532750	Ltbp1 Rasgrp3 Fam98a	Mall1	3	3	0	10-100
19	34157427	34309421	Alpk2 Gm22567 Mall1 Gm26114	Acta2	3	3	3.79E-08	60-100
2	33384683	33402619	Ankrd22 Stambpl1 Acta2 Fas intergenic	Zbtb34	3	2	3.86E-06	100
3	88452532	88605074	Sema4a Lmna Mex3a Mir1905	Sar2/Lmna	3	2	1.17E-08	100
7	110216552	110256898	Rab25 Lamtor2 Ubqln4 Gm10704 Ser2	Swap70	3	2	0	10, 40, 60, 90
14	115008961	115058395	Swap70 Gm22185 Mir17hg Mir17 Mir18 Mir19a Mir20a Mir19b-1 Mir92-1 Cdc42bpg Men1 Map4k2 Gm14966 Gm22278 Sfl1 Pygm Rasgrp2 Gm14965 Nrxn2	Mir17hg	3	2	0	30-60, 80, 90
19	6313428	6474630	Gm26470	Rasgrp2	3	2	0	10-100
X	11932951	12160660	Gm14512 Bcor 2908C10Rik	Bcor	3	2	0	10-100
1	11328348	11358325	intergenic	A830018L16Rik	2	2	1.935E-11	10, 30, 50, 80
2	167431388	167440338	Sic9a8	Sic9a8	2	2	0.0012557	100
3	95480560	95511013	Arnt Ctak	Ctsk	2	2	0.0004163	60
8	72215060	72407694	Fam32a Gm25027 Ap1m1 Gm10282 Klf2 Eps15l1	Klf2	2	2	0	30, 40, 60, 70, 90
8	105150849	105189744	Ctbf Gm22063	Ctbf	2	2	0	20-40, 60-100
9	88439642	88460300	Gm20537 4932427H20Rik Syncr1p	Gm20537	2	2	4.766E-08	10, 30
14	121822642	121961940	Ubac2 Gpr18 Gpr183	Ubac2	2	2	0.0002112	40, 80, 100
16	10462546	10571037	Cilia Dexi Clec16a	Cilia	2	2	0	10, 30-50, 70-100
16	55787944	55825832	Nfkbiz	Nfkbiz	2	2	0	10-80, 100
17	23564304	23837450	Zfp13 Zscan10 Mmp25	Zfp13	2	2	0	60
18	34906925	34963881	Elf1 Hspa9 Gm22200 Gm26109	Hspa9	2	2	0	10, 20, 50-80, 100
19	4375007	4410643	Kdm2a	Kdm2a	2	2	4.001E-05	20, 50, 70, 90
2	27325880	27331253	Vav2 AA645442	Vav2	1	1	0.0009574	60
2	167356401	167399416	intergenic	B4galt5	1	1	0.0011415	80
2	167449600	167542799	Sic9a8 Spata2 Rnf114 Gm11474	Rnf114	1	1	1.141E-06	80
3	95517352	95525796	intergenic	Ctss	1	1	0.0014022	20
3	101275162	101276006	Cd2	Cd2	1	1	2.068E-06	10
3	13122519	131227508	intergenic	Lef1	1	1	0.0001973	20
7	101398641	101405368	Arap1	Arap1	1	1	1.798E-06	70
7	125595408	125597326	intergenic	Il21r	1	1	0.0013434	20
12	76932603	76934474	intergenic	Max	1	1	7.882E-07	20
12	111168866	111174492	4930595D18Rik Traf3	4930595D18Rik	1	1	0.0008736	60
17	31073581	31074510	Abcg1	Abcg1	1	1	0.0003779	10

CIS analysis using the top 10 hits in the *Vk*MYC-TA-hPB* cohort. The start and end boundaries encompass all analysis windows in which each locus was identified as a CIS. The gene shown as nearest to peak was the central gene in the majority of kernel windows (scales) detecting the CIS, but is not necessarily the target gene for the CIS. Due to local hopping the total number of insertions occasionally included multiple integrations from the same tumour, so both the total number and the number after correction for local hopping are shown. The smallest p value identified at any scale is shown along with the analysis scales at which the CIS was detected (x1000).

Chr	Start	End	Genes in CIS	Gene nearest to peak	Number insertions	Number insertions (no hop)	p value	Scale
13	37631296	38046935	Rreb1 Ssr1 Cage1 Rlok1	Rreb1	43	26	0	10-100
16	23859243	24291463	Sst Rtp2 Bcl6	Bcl6	30	17	0	10-100
16	17001356	17231874	Ypel1 Gm9974 Ppil2 Gm15585 2610318N02Rik Mir130b Mir301b Sdf2l1 Ccdc116 Gm15646 Ydjc Ube2l3	Ube2l3	14	12	0	10-100
4	32162214	32543477	Gm11929 Bach2 D130062J21Rik Gm11932 Gm24371	Bach2	18	11	0	10-100
4	44528816	44968734	Pax5 Mir5120 Gm12462 Gm12463 Zcchc7 Gm22639 Gm12678 Gm12493	Zcchc7	14	11	0	10-100
8	98989496	99390113	Foxp1 Gm20696 Gm20705	Foxp1	12	10	9.533E-11	20, 30, 80-100
11	3083642	3295850	Plsd-ps1 Sfi1 Gm11399 Gm11400 Drg1 Gm12735 Fau-ps2 Elf4enif1 Patz1	Sfi1	14	9	0	10-100
11	44623794	44731292	Ebf1 Gm12158	Ebf1	11	9	0.0002058	80, 100
10	13971899	14219779	Hivep2 AC158608.1	Hivep2	9	8	0	40-100
1	58564955	58830706	Fam126b Ndufb3 Gm10068 Als2cr12 Cflar Casp8	Cflar	8	8	0	10-100
11	86626041	86753084	Vmp1 Gm11478 Pth2 Cltc	Cltc	8	8	0.0002	40, 70, 90, 100
18	49873916	50106787	Dmx1 Tnfai8 C030005K06Rik Tnfai8	Tnfai8	8	8	0	10-100
2	170003847	170239141	Tshz2 AL731822.1 Zfp217 AL844576.1	Zfp217	13	7	0	10-100
18	65351617	65534873	Alpk2 Gm22567 Malt1 Gm26114 Gm14607 Gm6539 Rps2-ps13 Phf6	Malt1	9	7	0	10-100
X	52807880	53036994	Hprt	Phf6	9	7	0	10-100
1	138043905	138289970	Ptprc Alp6v1g3	Ptprc	8	7	0	30-100
11	62351127	62497715	Ncor1 Pigl Gm12278	Ncor1	11	6	0	10-100
4	6822900	7008859	Tox	Tox	9	6	0	10, 20, 40-100
1	54785399	54949545	Ankrd44	Ankrd44	7	6	0	20-100
3	135540681	135779228	Manba Nfk1 Gm9799	Nfk1	6	6	0	10-100
14	76575405	76760351	intergenic	Serp2	6	6	0	10-40, 60-100
18	60673300	60906171	Ndst1 Rps14 Gm8731 Cd74 Mir5107 Tcof1	Cd74	6	6	0	10-100
13	44678280	44858001	Jarid2 Gm22213 2210019111Rik Pdx1 RP24-510G5.4 Cdx2 Phoxnb Flt3 AC134441.1	Jarid2	10	5	0	10, 30-100
5	147260198	147465893	Gm6054 Pan3	Flt3	9	5	0	10-100
18	80554647	80736453	Nfatc1	Nfatc1	9	5	0	10-100
2	61553867	61858017	Tank	Tank	6	5	2.978E-10	30-100
3	60426844	60627224	Mbnl1	Mbnl1	6	5	0	20, 30, 80-100
3	138908972	139118893	Rap1gds1	Rap1gds1	6	5	0	20-80, 80-100
6	129092979	129263511	Clec2e Klrb1-ps1 Gm26160 Clec2d AC142191.1	AC142191.1	6	5	0	10-30, 50-100
2	163987014	164124206	Ywhab Pabpc1 Tomm34 Stk4 Man1c1 Ldlrap1 Gm25751 Tmem57 Rhd	Tomm34	5	5	0	10, 30-100
4	134673032	134878328	Ldlrap1	Ldlrap1	5	5	0	10-100
7	24983081	25236202	Atp1a3 Griks Zfp574 Pou2f2 D930028M14Rik Dedd2 Zfp526 Gsk3a 9130221H12Rik	Pou2f2	5	5	0	10-100
7	80075460	80326626	Zfp710 Idh2 Gm24012 Mir1965 Sema4b Cib1 Gdppp1 Gm15504 Tlll13 Ngm Vps33b Prc1 AC109232.1 Rccod1 Uno45a	Sema4b	5	5	0	10-100
9	44441602	44657005	Upk2 Gm9830 Gm22540 C030014I23Rik Bcl9l Cxcr5 Ddx6	Cxcr5	5	5	5.709E-11	60-100
10	18900904	19101115	Tnfai3p3	Tnfai3p3	5	5	0	10-100
10	68086087	68276764	Arid5b	Arid5b	5	5	1.012E-11	20, 50-100
11	20026387	20128287	Actr2	Actr2	5	5	0	10-100
15	63961054	64090574	Fam49b Gm25628 Asap1	Fam49b	5	5	0	10, 20, 40-100
15	96315030	96463187	Arid2 Gm25397 Scaf11	Arid2	5	5	5.926E-05	50-100
16	20082219	20110676	Klh24	Klh24	5	5	1.677E-08	10, 30, 40, 90
17	17503487	17647345	Lnpnp	Lnpnp	5	5	0	20, 30, 50-100
17	34134185	34294435	H2-DMa H2-DMb2 H2-DMb1 Psmb9 Tap1 Psmb8 Gm20496 Tap2 Gm15621 H2-Ob Gm20506 H2-Ab1 H2-Aa Gm20513	H2-Ob	5	5	3.095E-05	60-100
X	38484044	38657041	Cul4b Mct5 C1galt1c1	Cul4b	5	5	0	30, 50-100
2	98607167	98709956	Gm10801 Gm10800	Gm10800	7	4	0	10, 20, 40-100
3	101161215	101361595	Gm12486 Tpt1-ps1 Gm12490 Cd2 Gm10355	Cd2	6	4	0	10-100
11	17140025	17202381	Ppp3r1 Wdr92	Ppp3r1	5	4	0	10-70
1	80285208	80382419	Cul3	Cul3	4	4	0.0001432	20, 40-100
2	18855573	19008456	Pip4k2a 4930426L09Rik	Pip4k2a	4	4	1.067E-07	20, 30, 50-90
2	45004516	45130230	Zeb2 Gm13476	Zeb2	4	4	0	40-80, 100
2	57218345	57304521	A930012O16Rik Gpd2 Gm13535	Gpd2	4	4	4.677E-05	20, 30, 50-100
2	163565840	163712631	Hnf4a Ttpal Serinc3 0610039K10Rik Pklg Gm16316	0610039K10Rik	4	4	0	20-100
2	165936596	166077663	Gm11462 Gm11463 Gm11464 Ncoa3 Sulf2	Ncoa3	4	4	0	10-100
5	23425205	23549291	5031425E22Rik Mli5 Gm25219 Srpk2	Mli5	4	4	2.115E-08	20, 50, 70-100
6	98951802	98999201	Foxp1	Foxp1	4	4	1E-06	20-80
7	27460972	27852163	Blvrb Pgam1-ps2 Seritad3 Sertad1 Prx Gm15541 Hlpk4 Pld3 2310022A10Rik Akt2	Akt2	4	4	0	10-100
7	128366459	128521590	Rgs10 Gm15503 Tial1 Gm24365 Taar8c Taar9 Gm15137 Stx7 Gm23051	Tial1	4	4	1.447E-05	40, 50, 70-100
10	24096858	24230332	Moxd1	Stx7	4	4	0	10-100
11	115841082	115887895	Grb2 Gm11702	Grb2	4	4	0.0001701	50, 60
12	76317716	76446880	Mthfd1 Akap5 Gm23809 Zbtb25 Zbtb1 AC124453.1 Hspa2 Ppp1r36 Gm25563 Gm10451	Zbtb1	4	4	0	10-100
13	13562664	13661221	Lyst	Lyst	4	4	0.0002391	60-100
14	31337607	31453720	Capn7 Sh3bp5	Sh3bp5	4	4	0	10-100

Top 100 CIS analysis for the *Vk** *hPB* cohort

Chr	Start	End	Genes in CIS	Gene nearest to peak	Number insertions	Number insertions (no hop)	p value	Scale
14	52047277	52150505	Gm22354 Hnmpc Rpgrip1	Rpgrip1	4	4	0.0001649	30, 40, 60-100
14	121885297	122001108	Ubac2 Gpr18 Gpr183	Ubac2	4	4	5.035E-08	10, 30, 70-100
16	44183346	44237757	Gm608	Gm608	4	4	0	10-60
X	11966280	12186907	Gm14512 Bcor 2900008C10Rik Gm14521	Bcor	4	4	0	10-40, 80-100
8	84805604	84864152	Dand5 Gadd45gjp1 Rad23a Calr 1700122E12Rik Farsa	Calr	4	3	0.0004937	100
12	3762122	3790779	Dtnb Gm20448	Dtnb	4	3	0.0004999	60
14	114996533	115062680	Mir17hg Mir17 Mir18 Mir19a Mir20a Mir19b-1 Mir92-1	Mir17hg	4	3	0	10-40, 60-100
17	35949636	36002251	Gm8801 Abcf1 Mir877 Prr3 Gnl1 Gm20508 A930015D03Rik Gm17414	Gnl1/A930015D03Rik	4	3	1.62E-05	10, 60
17	88025946	88082349	Fbxo11	Fbxo11	4	3	2.503E-09	10, 30, 50-70
X	77573612	77685726	Tbl1x Gm23121 Gm6927	Tbl1x	4	3	0	20-100
1	86441861	86521838	Intergenic	Ptma	3	3	0	10-100
1	178297668	178344854	B230369F24Rik Cox20 Gm16586 Hnmpu	Hnmpu	3	3	3.443E-05	40, 60-80
2	44316687	44350842	Arhgap15	Arhgap15	3	3	2.755E-06	10-30, 50-70
2	163206247	163294322	Tox2	Tox2	3	3	7.55E-15	10-90
3	22125657	22201992	Tbl1xr1	Tbl1xr1	3	3	1.135E-05	20, 30, 50, 70-100
4	154850558	155000070	Ttc34 Gm13112 Mmel1 Fam213b Tnfrsf14 Gm20421 Hes5 Pank4 Plch2	Tnfrsf14	3	3	0	10-100
5	124462994	124551113	Rlip2 Gm15621 Snmp35 Rlip1 Tmed2 Adap1 Cox19 Cyp2w1 3110082117Rik Mir339 Gpr146 D830046C22Rik	Rlip1	3	3	0	10, 20, 40, 50, 80-100
5	139319937	139408057	C130050O18Rik	3110082117Rik	3	3	0.0003036	80-100
6	31047063	31118227	Mir29a Mir29b-1 RP23-459L15.5 Gm13834 Gm13833	Gm13834	3	3	0	10-50, 70-100
6	88441116	88524981	Eefsec Ruvbl1 Sec61a1	Ruvbl1	3	3	6.439E-15	10-100
6	108622048	108713537	O610040F04Rik Gm17055 Bhlhe40	Bhlhe40	3	3	2.859E-13	10-100
6	113074509	113127878	GI(ROSA)26Sor Seld5	Seld5	3	3	0.0002616	70-90
6	127161199	127272713	AC163747.1 Gm4968	AC163747.1	3	3	0	10-50, 70-100
7	55870242	55819848	Cyfp1 Gm17907	Cyfp1	3	3	9.933E-05	40, 90
7	88266311	88310521	Ctsc AC124322.1	Ctsc	3	3	0	10-40, 60, 80, 90
7	101408504	101530885	Arap1 Pde2a Mir139	Pde2a	3	3	0	10-60, 80-100
7	121961555	122022388	Cog7 Gga2	Gga2	3	3	0.0005918	90000
9	32678274	32756584	Ets1	Ets1	3	3	0	10-30, 50-100
10	121385462	121478759	Gns Rassf3	Rassf3	3	3	5.016E-05	40, 70-90
11	22822155	22849435	Gm12057 Comm1d B3gnl2 Gm20456 Gm23772	Gm12057	3	3	4.406E-13	20-50
11	54759778	54783161	Cdc42se2	Cdc42se2	3	3	0.0001665	40
11	69062925	69089813	Tmem107 Snord118 Gm12306 Gm25371 Vamp2	Tmem107	3	3	0.0003239	40, 50
11	103217667	103267541	Spata32 Map3k14	Map3k14	3	3	0	10-50
12	71015257	71055377	3110056K07Rik Arid4a	Arid4a	3	3	4.547E-06	30, 40, 60-80
12	84167783	84225068	Elmsan1	Elmsan1	3	3	0	10-90
13	24600626	24660044	Fam65b Gm11346 AL513014.1	Fam65b	3	3	3.824E-05	30, 40, 60, 70
13	55225968	55282527	Nsd1	Nsd1	3	3	0.0002778	60-90
13	114114766	114182636	Arl15	Arl15	3	3	6.406E-06	10, 20, 40-90
15	12141435	12152927	Zfr	Zfr	3	3	0.0004746	60
15	80525645	80600344	Enthd1	Grap2	3	3	0	10-90
15	96723871	96769541	Intergenic	Gm8888	3	3	5.586E-05	40, 60
15	103216952	103285905	Cbx5 Hnmpa1 Nfe2 Copz1 Mir148b Gm10232 Gm16569 Gm5479	Nfe2	3	3	4.462E-12	10, 20, 40-90
17	3031580	3104904	Gm25909 Plsd-ps2	Plsd-ps2	3	3	0	10, 30-80
17	5045583	5098593	Arid1b	Arid1b	3	3	2.709E-08	30-70
17	80422760	80462242	Sos1	Sos1	3	3	1.042E-08	10-70
17	83383941	83417783	Eml4	Eml4	3	3	1.188E-08	10-70
18	4303849	4350385	Map3k8	Map3k8	3	3	5.229E-06	30-70
18	34497513	34505233	Fam13b	Fam13b	3	3	8.306E-10	20
18	56892100	56743580	Lmn1	Lmn1	3	3	0	10-80
19	5658200	5756891	Sipa1 Pcnx13 Map3k11 Kcnk7 Ehbp11 Gm16538 Fam89b Ssca1 Ltbp3	Ehbp11	3	3	0	10, 30-60, 80-100
19	47394832	47480281	Sh3pxd2a	Sh3pxd2a	3	3	0	10-80
1	138297320	138299284	Intergenic	Atp6v1g3	2	2	4.725E-06	10
2	29633002	29840825	Rappel1	Rappel1	2	2	4.848E-05	40
2	128139757	128141764	Bcl2l11	Bcl2l11	2	2	1.478E-07	10, 20
4	3679034	3682930	Lyn AL772401.1	Lyn	2	2	1.289E-12	10
4	89278557	89282652	Cdkn2a	Cdkn2a	2	2	4.21E-08	10-30
4	138050803	138054699	Eif4g3	Eif4g3	2	2	2.22E-16	10, 20
5	148326668	148330577	Slc7a1	Slc7a1	2	2	2.029E-07	40, 20
6	72510858	72529870	Sh2d6	Sh2d6	2	2	0	10, 20, 50
7	19809875	19825853	Bcl3 Gm16175 Gm16174	Bcl3	2	2	0	10, 40
7	28408589	28417957	Samd4b	Samd4b	2	2	8.882E-14	10, 30, 40
8	13094016	13108003	Pcid2 Cul4a	Pcid2	2	2	3.21E-11	10-50
8	25585755	25593539	Letm2	Letm2	2	2	0.0001626	40
8	45988083	45991971	Ufsp2	Ufsp2	2	2	5.249E-05	10, 20
8	105998484	106008218	Dus2l	Dus2l	2	2	1.668E-07	30-50
9	66421892	66422824	Herc1	Herc1	2	2	2.247E-12	10
9	72017621	72022328	Tcf12	Tcf12	2	2	0.0002163	10, 20
14	101462295	101469824	Tbc1d4	Tbc1d4	2	2	3.746E-08	10, 30
15	38077393	38078348	Ubr5	Ubr5	2	2	0	10
17	19433362	19435236	Intergenic	Vmn2r-ps121	2	2	9.739E-05	10
17	45548216	45565129	Nfkbia Slc35b2	Nfkbia	2	2	0	10, 20
17	46856114	46858924	Intergenic	Gltscr1l	2	2	2.442E-15	10
18	67240763	67242692	Mppe1	Mppe1	2	2	6.867E-06	10
X	18184384	18256541	Kdm6a	Kdm6a	2	2	0	20-80, 100
X	48390733	48444672	Bcor1l Eif4	Eif4	2	2	0	10-30, 70, 80, 100
X	134572730	134577437	Btk	Btk	2	2	0.0003822	50
1	75476608	75477590	Chpf	Chpf	1	1	6.157E-09	10
8	94999314	95000286	Gpr56	Gpr56	1	1	1.518E-06	10
14	25530577	25533869	Zmiz1	Zmiz1	1	1	1.11E-16	20, 30
14	31155243	31156159	Stab1	Stab1	1	1	1.354E-14	10

CIS identified using the top 100 integrations in the *Vk*^hPB* cohort

Chr	Start	End	Genes in CIS	Gene nearest to peak	Number insertions	Number insertions (no hop)	p value	Scale
13	37406200	38068534	Ly86 Rreb1 Ssr1 Cage1 Rlok1 Pisd-ps1 Sfi1 Gm11399 Gm11400 Drg1 Gm12735 Fau-ps2 Eif4enif1 Patz1	Rreb1	94	56	0	10-100
11	3016121	3354935	Gm12592 Gm11944 Pik3ip1 Limk2	Sfi1	53	33	0	10-100
16	23850461	24316468	Sst Rtp2 Bcl6 Gm11929 Bach2 D130062J21Rik Gm11932 Gm24371 BC024582	Bcl6	47	25	0	10-100
4	32157117	32578306	Gm20696 Gm20705 Gm22328	Bach2	40	25	0	10-100
6	98908797	99565200	Foxp1 Gm24556 2210019111Rik Pdx1 RP24-510G5.4 Cdx2 Prhoxnb Flt3 AC134441.1 Gm6054 Pan3	Foxp1	37	24	0	10-100
5	147180300	147522254	Gm15834 Fam126b Ndufb3 Gm10068 Als2cr12 Cflar Casp8	Flt3	34	19	0	10-100
1	58521691	58888508	Myc Pvt1 H2afy3	Cflar	32	25	0	10-100
15	61862678	62244510	Kcnj12 Tnfrsf13b Gm12269 Usp22 Rps13-ps5 Aldh3a1 Aldh3a2	Myc	21	14	0	10-100
11	61013919	61238882	Gtdc1 Zeb2 Mir5129 Gm13476	Tnfrsf13b	21	10	0	10-100
2	44886061	45190365	Fli1 Ets1	Zeb2	20	16	0	10-100
9	32472788	32781639	Tshz2 AL731822.1 Zfp217 AL844576.1	Ets1	19	13	0	10-100
2	170004430	170269470	Manba Oaz2-ps Nfkb1 Gm9799	Zfp217	18	12	0	10-100
3	135525355	135795415	Zfp143 Wee1 Swap70 Gm22185 Sbf2	Nfkb1	18	11	0	10-100
7	110068190	110323094	Adora2b Zswim7 Ttc19 Gm12275 Ncor1 Gm12276 Pigl Gm12278	Swap70	14	12	0	10-100
11	62265887	62490850	Bcor 2900008C10Rik	Ncor1	13	11	0	10-100
X	119961100	12154043	Sycp1 Nr1h5 Gm22826 Sike1 Csd1 Nras Ampd1 Gm23820 Dennd2c	Bcor	13	4	9.992E-16	10-100
3	102913279	103164714	Gm13806 Gm10801 Gm10800	Csd1	12	11	0	10-100
2	98551691	98757833	Kcnh4 Hcrt Ghdc Gm24358 Stat5b Stat5a Stat3 Ptrf	Gm10800	12	10	0	10-100
11	100754115	100959516	Lpp	Stat5a	12	9	0	10-100
16	24472671	24490144	Rtkn2 Gm16212 Arid5b Gm24073 Mir17hg Mir17 Mir18 Mir19a	Lpp	12	5	0.000274	60
10	68021190	68285437	Mir20a Mir19b-1 Mir92-1 Gpc5	Arid5b	11	10	0	10-100
14	114929360	115151053	Casr Cd86 Ildr1	Mir17hg	11	9	0	10-100
16	36549167	36714211	Zbtb20 Zbtb20	Cd86	11	9	4.754E-09	10-100
16	43529572	43638277	Kif11 Hhex Gm23026 Exoc6 Fam60a 3010003L21Rik Gm23395 Gm25539 Dennd5b AC140327.1 Gm15779 Gm15781 Gm22578 Gm15780 Gm23462 Gm10203 Mettl20 Gm10011	Zbtb20	11	8	0.0001117	30, 40, 80-100
19	37366712	37564885	Dennd5b	Gm23026	11	8	0	10-100
6	148913009	149148138	Tnfaip3	Dennd5b	10	10	1.11E-16	10-100
10	18890914	19125800	Rnf145 4930597A21Rik Ebf1 Ebf1 Gm12158 Arid1b Tmem242 Gm22475	Tnfaip3	10	10	0	10-100
11	44493813	44699214	4930405P13Rik Scep1 Gm26471 Gm15698 Coil 2210409E12Rik Gm11496 Trim25 Dgke Gm24974	Rnf145	10	9	1.11E-16	10, 20, 50-100
17	5185325	5424715	Rgs9 Gm11696 Gna13 9930022D16Rik Amz2 Gm15642 Slc16a6 Gm25540 Slc9a7 Gm9083 Gm14529 Rp2h Gm9085 Gm14537 Zcchc7 Gm22639 Gm12678 Gm12493 Gm12679 Grhrp Zbtb5	Arid1b	10	9	9.601E-06	50-100
11	88928888	89056041	Trim25	Trim25	10	8	5.525E-05	50-100
11	109292926	109468984	Gna13	Gna13	10	8	0	10-100
X	20125306	20398134	Slc9a7	Slc9a7	10	8	0	10-100
4	44846231	45006757	Pawr Gm23105	Gm12678	9	9	0	10, 30-100
10	108333463	108392184	Cd47 Cd47	Pawr	9	9	0.0002443	90, 100
16	49830383	50005136	Msi2	Cd47	9	9	3.31E-06	10-100
11	88459400	88664801	Rasgrp3	Msi2	9	8	0	20-100
17	75374410	75527620	Comm3 Bmi1 Gm13334	Rasgrp3	9	7	0	10-100
2	18656976	18698107	Ywhab Pabpc1 Tomm34 Stk4 Tgs1 Gm22541 2210414B05Rik Lyn AL772401.1 Gm11805 Gm22781	Bmi1	9	4	0	10-50
2	163977231	164134292	Hivep2 AC158608.1 Mli2 Rheb1 Dhh Lmbr1l Tuba1b Tuba1a AC157610.1 Gm8973 Tuba1c AC163629.1 Pim1 Gm17657 Tmem217 Tbc1d22b Ftsjd2 Gm25932	Stk4	8	8	0	20-100
4	3614197	3800304	Lyn	Lyn	8	8	0	10-100
10	13948526	14124690	Hivep2	Hivep2	8	8	0	20-100
15	98837538	99032605	Tuba1a	Tuba1a	8	8	0	10, 30-100
17	29382845	29574357	AC163629.1	AC163629.1	8	8	3.423E-08	30-100
18	65347674	65590538	Mall1 Gm26114 Zfp532	Mall1	8	8	0	10-100
19	44208392	44434875	Scd3 Gm25573 Scd2 Mir5114 Scd4 Scd1	Scd4	8	8	0	10-100
4	46506937	46702839	Trim14 Gm16731 Coro2a Tbc1d2 Gabbr2 Myom3 Gm13000 Srsf10 Pnrc2 Gm13006 Cnr2 Fuca1 Hmgcl	Tbc1d2	8	7	0	10-100
4	135789267	135955784	Gm13006	Gm13006	8	7	0	10-100
11	115601670	115689699	Gga3 Gm25364 Mrps7 Mif4gd Slc25a19 AL645470.1 Grb2 Gm11702 2610301G19RIK 9930012K11RIK Pdlim2	Grb2	8	7	0	10-100
14	70138277	70326278	Sorbs3 AC151836.1 Ppp3cc Slc39a14	PPP3CC	8	7	2.524E-05	20, 40-100
15	97316019	97442812	Pced1b Tap1 Psmb8 Gm20496 Tap2 Gm15821 H2-Ob Gm20506 H2-Ab1 H2-Aa Gm20513 H2-Eb1 H2-Eb2 H2-Ea-ps Btlnl2	Pced1b	8	7	0	10-100
17	34189792	34362152	Gm20513	Gm20513	8	7	0	10-100
19	4243544	4407802	Ssh3 Ankrd13d Adrbk1 Kdm2a	Kdm2a	8	7	0	10-40, 70-100
8	72222010	72408911	Gm25027 Ap1m1 Gm10282 Klf2 Eps151	Gm10282	8	6	0	10, 30-100
1	175806574	175914455	Wdr64 Exo1	Exo1	7	7	5.696E-05	10-100

Top 100 CIS analysis for the *Vk** MYC-TA-hPB cohort

Chr	Start	End	Genes in CIS	Gene nearest to peak	Number insertions	Number insertions (no hop)	p value	Scale
2	30976385	31182527	BC005624 Usp20 Fnbp1 D330023K18Rik Gpr107	Fnbp1	7	7	0	20-100
3	89959710	90155271	Atp8b2 Gm24046 Hax1 Ubap2l Gm24608 4933434E20Rik Gm16540 1700094D03Rik Mir190b Tpm3 Nup210l Gm23723 Raver2 Jak1 Gm24468 Gm12785 Gm25124 Gm12801	Tpm3	7	7	0	30-100
4	101144001	101287620	Acot6 Dnalc1 Pnma1 Elmsan1 Gm5436 Gm23399	Jak1	7	7	0	10-100
12	84095746	84281330	Srl Gm15885 Tfp4 Glis2 Pam16 Coro7	Elmsan1	7	7	0	10-100
16	4501438	4656774	Vasn Dnaja3	Glis2	7	7	0	10, 30-100
16	55790823	55878971	Nfkbiz Nxpe3	Nxpe3	7	7	2.204E-09	20-100
18	53602766	53700860	Cep120	Cep120	7	7	0	10-100
18	56701712	56857145	Lmnbl March3 Gm15345	March3	7	7	1.086E-06	20-100
19	32706826	32805685	Atad1 Pten	Pten	7	7	7.519E-11	10-90
16	38430619	38523703	Pla1a Adprh AC209577.1 Cd80 Timmdc1 Gm15953	Cd80	7	6	6.68E-05	60-90
13	32996598	33035439	Serpinb9 Serpinb9b	Serpinb9	7	5	9.119E-05	30-50
2	33384539	33431562	Zbtb34	Zbtb34	7	4	2.253E-08	10-50
2	131953952	132074305	Rassf2 Slc23a2	Rassf2	6	6	0	10-100
4	154821145	155023699	Gm13113 Ttc34 Gm13112 Mmel1 Fam213b Tnfrsf14 Gm20421 Hes5 Pank4 Plch2	Tnfrsf14	6	6	0	10-100
5	64574032	64671733	Gm25306	Gm25306	6	6	1.365E-05	40-100
7	24998900	25194979	D930028M14Rik	Pou2f2	6	6	0	10-100
7	73469866	73616926	Chd2	Chd2	6	6	0	10, 20, 40-100
7	101156356	101283808	Fchs2 Gm15673	Fchs2	6	6	0	10-100
8	126758661	126914832	Intergenic	Tomm20	6	6	0	10, 40-100
10	67047049	67117244	Reep3 Jmjd1c	Reep3	6	6	4.538E-05	30-50
10	116485957	116613186	Cnot2 Gm25190 5330438D12Rik	Cnot2	6	6	0	10-100
13	112757086	112834352	Ppap2a	Ppap2a	6	6	4.074E-06	20-100
16	10471364	10608079	Ciita Dexi Clec16a	Ciita	6	6	7.764E-12	10-30, 60-100
19	41490594	41509467	Lcor	Lcor	6	6	0.0007105	100
X	48282962	48509619	AL672246.1 Gm22528 Gm7212 Gm22612 Bcor1 Gm23868 Elf4 Aifm1	Elf4	6	6	0	10-100
3	15092332	15147922	Intergenic CT030702.1 Ptca 2310039H08Rik Rpl71l	RP23-3D20.1	6	5	9.803E-14	10-70
17	46762543	46867707	Gltscr1l	Gltscr1l	6	5	0	10, 30-100
11	103232095	103270106	Map3k14 1700028N14Rik	Map3k14	6	4	2.958E-06	20-50
19	23122809	23149458	2410080I02Rik Klf9	2410080I02Rik	6	3	1.862E-07	10-30
1	130766427	130864401	Fcamr Gm15848 Plgr	Plgr	5	5	0	10-100
1	131939530	131947248	Intergenic	Nucks1	5	5	0.0001735	80
2	165965542	166071525	Gm11463 Gm11464 Ncoa3	Ncoa3	5	5	2.794E-05	30-100
4	24481982	24547094	Mms22l	Mms22l	5	5	0	10, 30-70
9	44188518	44256803	Cbl Ccdc153 Pdcd3 Nlrp1	Cbl	5	5	0.0001421	10, 30, 40, 90, 100
9	82937551	82977892	Phip	Phip	5	5	0	20-50
11	98430738	98497056	Erbp2 Mien1 Gm12352 Grb7 Ikzf3 Gm25106	Ikzf3	5	5	0	10-100
14	74857270	74997034	Lrch1	Lrch1	5	5	2.461E-08	20, 40-100
15	85680301	85826601	Mirlet7c-2 Mirlet7b Ppara Cdpf1 Pkdrej	Ppara	5	5	0	10-100
16	66106665	6643072	Intergenic	Rbfox1	5	5	0.0001292	30, 40, 60
17	87981043	88042082	Msh6 Fbxo11	Fbxo11	5	5	3.515E-05	30-100
18	2965325	3061432	Vmn1r-ps151	Vmn1r-ps151	5	5	0	10-100
18	4258355	4351005	Map3k8	Map3k8	5	5	2.712E-05	10, 30-100
X	18117256	18272468	Dusp21 Kdm6a	Kdm6a	5	5	0	10, 30-100
8	84877039	84987478	Syce2 Gcdh Klf1 Dnase2a Mast1 Gm24197 Rltdn Rnaseh2a Prdx2 Junb	Rltdn	5	4	1.11E-16	10, 20, 40-100
14	121889438	121941085	Ubac2 Gpr18	Ubac2	5	4	0.0001779	40-70
15	10041942	10076929	Gm26350	Gm26350	5	4	0.0002286	10, 40
17	24269479	24395191	Abca17 Gm24427 Abca3 Gm25618	Abca3	5	4	0	10-100
6	145237661	145253240	Kras	Kras	5	3	0	10-30
9	89807593	89823131	Intergenic	Mir184	5	3	3.527E-06	10
11	86586697	86592542	Vmp1	Vmp1	5	3	0.0001278	20
12	58996936	59020305	Sec23a Gemin2	Sec23a	5	3	0	10, 20, 40, 50
12	111195708	111213225	Traf3	Traf3	5	3	0.0002902	30
17	35189651	35232539	Ltb Tnf Lta Nfkbil1 Gm16181	Nfkbil1	5	3	6.264E-05	30, 40
X	75068539	75111147	Gab3 Dkc1 Gm25520	Dkc1	5	3	0	10-80
1	152856551	152895091	Smg7	Smg7	4	4	8.055E-05	30-50
1	156614107	156637231	Abl2	Abl2	4	4	0.0001158	40
1	180339684	180407148	Itpkb	Itpkb	4	4	0	10-90
2	75638412	75667388	Gm24574 Hnrpa3	Gm24574	4	4	4.82E-06	10-40
3	51391351	51437818	Mgarp Ndufc1 Naa15	Naa15	4	4	9.383E-05	10, 40-60
3	95469842	95534896	Arnt Ctsk Ctss Hmgb1-ps5	Ctsk	4	4	9.465E-09	10-90
5	115191991	115253307	Cabp1 Gm13828 Pop5 Rnf10	Pop5	4	4	0	10-70
5	123379752	123397309	Gm15747 Mixip	Gm15747	4	4	0.000215	60
6	83898801	83932150	Zfml	Zfml	4	4	1.226E-07	10, 30-50
6	115630869	115704194	Raf1 Gm14335 D830050J10Rik	Raf1	4	4	0	10-90
7	45029512	45119443	Prr12 Prrg2 Nosip Rcn3 Fcgrt	Nosip	4	4	1.417E-06	10, 40-100
7	80002302	80048301	Zfp710	Zfp710	4	4	0	10-60
7	90110130	90168806	AC130210.1 Picalm	Picalm	4	4	1.432E-14	10-60
7	125566031	125656085	Il4ra Il21r Gtf3c1	Il21r	4	4	0	10-100

Chr	Start	End	Genes in CIS	Gene nearest to peak	Number insertions	Number insertions (no hop)	p value	Scale
8	81828232	81857377	Inpp4b Gm17072	Inpp4b	4	4	0.0002971	60
8	105632825	105734280	RP24-242N1.1 Ctcf Gm5915 Gm24324 Rltpr Acid Pard6a Enkd1 4933405L10Rik Gfod2	Rltpr	4	4	0	10-100
8	111787035	111811148	Cfdp1	Cfdp1	4	4	0.000321	30, 50, 70
9	36750164	36777397	Stt3a AC155921.1	Stt3a	4	4	0.0001403	40
9	51179551	51241797	Pou2af1	Pou2af1	4	4	0	10-70
10	59551903	59590940	Mcu	Mcu	4	4	0.0001301	30-50
11	97124004	97156168	Tbkbp1	Tbkbp1	4	4	3.906E-05	10-40
12	54949179	55022245	Baz1a RP23-454K24.2 Gm20403 Gm24296	Baz1a	4	4	0	20, 40-80
12	98631007	98677794	Spata7 Ptpn21	Spata7	4	4	0.0001923	50, 60
13	30704965	30741259	Dusp22 Gm11370	Gm11370	4	4	2.315E-05	20-50
14	54611840	54703924	Psmb5 Mir686 Psmb11 Cdh24 Gm20726 Gm17606 Acin1 4930579G18Rik 1700123O20Rik	Acin1	4	4	4.694E-05	40
14	101675585	101686647	Uchl3	Uchl3	4	4	0.0003306	60
16	3331981	3361784	Gm22862	Gm22862	4	4	3.136E-12	10-30
16	75890059	75913298	Samsn1	Samsn1	4	4	3.744E-05	10-40
17	23554762	23592911	AC154766.1 Zfp213 Zfp13	Zfp13	4	4	0.0001529	30-50
17	24125845	24221601	Pdpk1 Amdhd2 Atp6v0c Tbc1d24 Ntn3 BC028777 1602H07Rik	Pdpk1	4	4	0.0002129	40, 50, 100
17	80422683	80465661	Sos1	Sos1	4	4	8.291E-10	10-50
19	44349092	44416617	Scd1	Scd1	4	4	1.11E-16	10-40
X	38446906	38556678	Lamp2 Gm7598 Cul4b	Cul4b	4	4	2.914E-13	10, 40, 60-100
18	80623833	80691754	Nfatc1	Nfatc1	4	3	3.973E-09	40
19	6389763	6411265	Pygm Rasgrp2 Gm14965	Rasgrp2	4	2	0	10-30
1	46850357	46859983	Slc39a10	Slc39a10	3	3	1.11E-16	10
1	85929740	85967303	4933407L21Rik Gpr55	Gpr55	3	3	1.891E-06	30, 40
1	170859704	170874151	Atf6 Gm9929 Dusp12	Gm9929	3	3	3.815E-05	30, 40
1	172142625	172159962	Gm10171 Dcaf8	Dcaf8	3	3	4.282E-05	30, 40
2	168570953	168609146	Nfatc2	Nfatc2	3	3	2.335E-09	20, 30
2	180692870	180716374	Dido1 Gm22502 Gld8	Dido1	3	3	0	10-40
4	40839296	40852965	B4galt1 Mir5123 Gm24112 Gm25931	B4galt1	3	3	7.815E-05	20, 30
4	89270241	89288424	Gm12606 Cdkn2a	Cdkn2a	3	3	2.998E-15	10, 30, 40
4	131869305	131889818	Srsf4	Srsf4	3	3	5.38E-05	30, 40
4	133152527	133176240	Wasf2 Gm24636	Wasf2	3	3	6.894E-07	10-40
5	128987750	129030633	Stx2 Ran	Ran	3	3	0	10, 20, 40-60
6	37726166	37740819	intergenic	Gm15487	3	3	3.042E-06	10-40
6	70715778	70735561	Igkj1 Igkj2 Igkj3 Igkj4 Igkj5 Igkc	Igkc	3	3	4.441E-16	10-40
6	128981486	129002969	Clec2g BC064078	BC064078	3	3	9.626E-14	10-40
7	19569930	19618847	Gemin7 Zfp296 Claspr AC149052.1 Relb	Claspr	3	3	0.0001263	10, 30, 50
7	27558164	27607168	2310022A10Rik Akt2 Plekha4 Gm16022 Hsd17b14	Akt2	3	3	0	10-70
7	45540241	45591093	0610005C13Rik Bcal2	0610005C13Ri	3	3	2.22E-16	10, 30-60
7	84672736	84687489	Zfand6	Zfand6	3	3	4.203E-09	10, 20, 40
8	106936921	106961196	Sntb2	Sntb2	3	3	0.0002554	40, 50
9	2983343	3024328	AC131780.1 Gm10722 Gm11168 Gm10721 Gm10720 Gm10719 Gm10718	AC131780.1	3	3	0	10-60, 80, 100
10	81374496	81414705	Fzr1 Dohh 2210404O07Rik Nfic Gm16104	Dohh	3	3	0	20, 30, 50
11	34031196	34044834	4930469K13Rik	930469K13Ri	3	3	1.016E-09	10, 20
12	92873788	92890209	intergenic	Gm23249	3	3	4.856E-13	10, 20, 40
13	20131395	20147778	Elmo1	Elmo1	3	3	1.388E-08	10, 30
13	43781816	43793456	Cd83	Cd83	3	3	5.217E-05	20
13	52624650	52657631	Syk	Syk	3	3	7.327E-15	10-30
14	7888640	7947574	Flnb	Flnb	3	3	5.329E-15	20-50
14	27279241	27310905	Arhgef3	Arhgef3	3	3	0.000158	40, 50
14	72652782	72658298	Fndc3a	Fndc3a	3	3	3.491E-06	10
14	75183309	75209092	Lcp1 Gm15629	Lcp1	3	3	0.000152	40
14	79397052	79404419	Mtrf1	Mtrf1	3	3	0.0002793	40
15	80724280	80743766	Tnrc6b	Tnrc6b	3	3	0.000233	30, 40
16	8563262	8569071	Abat	Abat	3	3	0.0001961	20
17	3069051	3086207	Pisd-ps2	Pisd-ps2	3	3	8.654E-11	10, 30
17	46755239	46758099	CT030702.1 Ptcra	CT030702.1	3	3	0.0003076	30
17	49994748	50017622	Rftn1	Rftn1	3	3	0	10-40
19	60131251	60153735	E330013P04Rik Gripap1 Kend1 Otud5 Pim2 Slc35a2 Pqbp1	330013P04Ri	3	3	0	10-30
X	7817728	7934754	Timm17b Gm10491 Gm10490 Pcsk1n	Otud5	3	3	0	10-100
Y	90690526	90840981	Gm21860 Gm21857 Erdr1 Gm21748	Erdr1	3	3	0	20-100
1	37079612	37080574	intergenic	Vwa3b	2	2	8.187E-07	10
1	85598375	85601263	Sp110 Gm16094 Sp140	Sp140	2	2	1.078E-06	10
1	86501238	86504125	intergenic	Ptma	2	2	0	10
2	6209267	6212203	Echdc3 A230108P19Rik	Echdc3	2	2	4.935E-12	10
2	49516360	49519296	Epc2	Epc2	2	2	3.433E-05	10
2	152828225	152831161	Bcl2l1	Bcl2l1	2	2	4.418E-08	10
2	173270207	173271185	Pmepa1	Pmepa1	2	2	9.517E-05	10
3	27454968	27457752	Fndc3b	Fndc3b	2	2	3.086E-05	10
3	90110557	90121695	Nup210l	Nup210l	2	2	8.203E-05	20
4	130984054	130988934	Gm12973	Gm12973	2	2	2.065E-11	10
5	27340	27341947	Dpp6	Dpp6	2	2	3.618E-05	10
5	29368625	29371545	Lmbr1	Lmbr1	2	2	1.529E-05	10
5	116954811	116957731	intergenic	Suds3	2	2	2.126E-10	10

Chr	Start	End	Genes in CIS	Gene nearest to peak	Number insertions	Number insertions (no hop)	p value	Scale
5	124010717	124016560	Vps37b	Vps37b	2	2	2.029E-11	10, 20
6	85433259	85435212	Smyd5	Smyd5	2	2	8.111E-05	20
7	43351349	43354279	Siglec5	Siglec5	2	2	3.969E-07	10
7	142550850	142583108	Nctc1 H19 Mir675	Nctc1	2	2	0	10-40
9	35303218	35305161	intergenic	Gm5614	2	2	4.79E-05	10
9	75434947	75436889	intergenic	(130057D12Ri	2	2	5.613E-05	10
10	12919478	12921427	AL691505.1	AL691505.1	2	2	1.138E-05	10
10	21080184	21082133	Ahi1	Ahi1	2	2	1.126E-05	10
10	60160497	60164397	intergenic	Chst3	2	2	2.419E-05	20
10	117904515	117906464	intergenic	Rap1b	2	2	4.946E-05	10
12	79464884	79466829	Rad51b	Rad51b	2	2	7.865E-06	10
12	107864502	107865474	intergenic	Bcl11b	2	2	5.481E-08	10
13	51730278	51736098	Sema4d	Sema4d	2	2	9.598E-07	10-20
13	55197182	55199122	intergenic	Nsd1	2	2	1.356E-05	20
13	59655460	59657400	Golm1	Golm1	2	2	0.0001651	20
14	63501275	63503114	Tdh	Tdh	2	2	0.0001257	10
15	27930407	27932348	Trio	Trio	2	2	3.537E-05	10
15	59292264	59295175	intergenic	Sqle	2	2	9.555E-06	10
15	83189091	83191031	intergenic	Cyb5r3	2	2	0.0001275	10
18	36148244	36154037	Nrg2	Nrg2	2	2	3.242E-14	10, 20
18	60802736	60820157	Cd74 Mir5107	Cd74	2	2	0	10-30
18	65581279	65587075	Zfp532	Zfp532	2	2	5.142E-08	20
19	5841548	5849035	Neat1 Gm9783	Neat1	2	2	5.675E-05	20
19	40990396	40991330	Blink	Blink	2	2	7.674E-05	10
19	57332933	57335738	AC131756.1	AC131756.1	2	2	1.923E-07	10
2	27748312	27749291	Rxra	Rxra	1	1	3.517E-13	10