Supplementary Table 8: Common Insertion Sites retrieved from hematopoietic tumors derived from *Cdkn2a*^{-/-} HSPCs transduced with the different vector

Mouse Treatment ^(a)	Vector ^(b)	CIS gene ^(c)	CIS power ^(d)	Span (Kb) ^(e)
Cdkn2a-/- HSPCs	SINLV.SF.GFP.PRE	Tas2r143	5	5
		Vegfc	5 5 5	117
		Tmem47	5	17
		Braf	4	3
		Senp8	4	0.1
		Lyst	4	95
		Rasa1	4	57
		Pcmtd1	3 3 3 3 3 3 3 3 3 4	27
		Lrrc4c	3	5
		Macrod2	3	0.2
		Slc35d1	3	1
		Atp10d	3	13
		Phf14	3	6
		Kif5b	3	7
		Tpk1	3	16
		Smarcad1	3	0.1
		Ankrd10	3	0.1
		Dhsrx	3	2
	LV.SF.LTR	Nsd1	5	94
		Braf		
		Thrb	4	55
		Cdc216	4	31
		Hrsp12	3 3 3	15
		Diap1	3	36
		Fxyd5	3	0.1
		Smc3		21
		Rsu1	3	44

- a) **Mouse Treatment**: These CIS were identified by analyzing LV integrations from tumor derived from Wild type mice transplanted with $Cdkn2a^{-/-}$ HSPCs transduced with the indicated vector
- b) Vector: Vector treatment group
- c) **CIS gene**: gene identified as CIS by the algorithm described by Abel et al based on MonteCarlo simulation
- d) **CIS power**: number of times that the indicated gene is targeted by vector integration
- e) **Span**: Genomic window in Kb where are clustered all the different vector integrations that constitute the CIS.

^{*}Highlighted in red are gene that are repeated in the table