

Supplemental Table 3. Indel frequencies at Digenome-captured sites in HeLa cells

VEGFA1						
	Chromosome	Location	DNA seq at a Cleavage sites	Indel frequency (%)		Validation
				(-) RGEN	(+) RGEN	
On-Target	Chr6	43737290	GGGTGGGGGAGTTTGCTCCAGG	0.01%	21.77%	validated
VEGFA1_02	Chr15	65637537	GGaTGGaGGGAGTTTGCTCCTGG	0.01%	25.28%	validated
VEGFA1_03	Chr5	7067159	GaGgGtGGGGAGTTTaCTCCTGG	0.01%	0.09%	validated
VEGFA1_04	Chr1	99347651	GGGgaGGGGaAGTTTGCTCCTGG	0.01%	13.84%	validated
VEGFA1_05	Chr12	1988077	cGGgGGaGGGAGTTTGCTCCTGG	0.00%	11.73%	validated
VEGFA1_06	Chr22	37215276	GGGTGGGGGAGTTTGCCcCAGG	0.09%	1.03%	validated
VEGFA1_07	Chr17	32986325	GGGgGtGGGGAcTTTGCTCCAGG	0.04%	0.02%	Invalidated
VEGFA1_08	Chr12	26641302	aGtTtGGGGGAGTTTGCCcCAGG	0.12%	0.12%	Invalidated
VEGFA1_09	Chr1	233157354	GGagGaGGGGAGTcTGCTCCAGG	0.01%	0.05%	validated
VEGFA1_10	Chr10	124731416	aGcTGGaGGGAGTTTGCCcCAGG	0.13%	0.26%	validated
VEGFA1_11	Chr12	131690199	GGGaGGGtGGAGTTTGCTCCTGG	0.00%	6.70%	validated
VEGFA1_12	Chr11	71497119	aGGaaGGaGGAGTTaGCTCCTGG	0.00%	0.02%	Invalidated
VEGFA1_13	Chr17	39796328	taGTGGaGGGAGcTTTGCTCCTGG	0.00%	16.90%	validated
VEGFA1_14	Chr4	8453803	GaGTGGGtGGAGTTTGCTaCAGG	0.01%	0.13%	validated
VEGFA1_15	Chr9	93925190	GGGgGtGGGGAGcaTGCTCCAGG	0.01%	0.02%	validated
VEGFA1_16	Chr3	125633992	aGGaaGGaGGAGTTaGCTCCTGG	0.02%	0.01%	Invalidated
VEGFA1_17	Chr16	8763213	aaGTaaGGGaAGTTTGCTCCTGG	0.01%	0.01%	Invalidated
VEGFA1_18	Chr20	56175356	aGGgaGGaGGaATTTGCTCCAGG	0.00%	0.72%	validated
VEGFA1_19	Chr15	93140401	GGGgGaGGGaAGTTTcCTCCAGG	0.02%	0.01%	Invalidated
VEGFA1_20	Chr3	128284321	aGGTGGtGGGAGcTTGtTCCTGG	0.00%	0.14%	validated
VEGFA1_21	Chr5	32945275	GcGTGGGGGGtGTTTGCTCCCGG	0.03%	1.00%	validated
VEGFA1_22	Chr6	14316373	GtGgGGGtaGAGTTTGCTCCAGG	0.02%	8.10%	validated
VEGFA1_23	Chr13	26202812	GGtTGaGGGGAGTcTGCTCCAGG	0.01%	0.17%	validated
VEGFA1_24	Chr5	139263024	ttGgGGGGGcAGTTTGCTCCTGG	2.33%	7.19%	validated
VEGFA1_25	Chr2	96056645	GGGTGGGGaGAGTTTctTCCTGG	0.00%	0.00%	Invalidated
VEGFA1_26	Chr3	195871264	GGtgGGGGaGAGcTaGCTCCGGG	0.00%	0.20%	validated
VEGFA1_27	Chr11	3445204	aGGaaGGaGGAGTTaGCTCCTGG	0.02%	0.04%	validated
VEGFA1_28	ChrX	19185601	GGGaGGGGaGAGTTTgTCCAGG	0.01%	0.02%	Invalidated
VEGFA1_29	Chr11	67574262	aGGaaGGaGGAGTTaGCTCCTGG	0.01%	0.73%	validated
VEGFA1_30	Chr17	47317539	ctGgtGGGGGAGcTTTGCTCCAGG	1.64%	4.14%	validated
VEGFA1_31	Chr22	19698463	GaGgGGGaGcAGTTTGCTCCAGG	0.01%	0.56%	validated
VEGFA1_32	Chr21	37116659	aaGTGGGaaGAGTTTGtTCAGG	0.03%	0.01%	Invalidated
VEGFA1_33	Chr11	117481208	GGGcaaGGGGAGgTTGCTCCTGG	0.01%	0.35%	validated
VEGFA1_34	Chr5	56172079	GGtgGGGGtGgGTTTGCTCCTGG	0.00%	3.94%	validated
VEGFA1_35	Chr1	33643288	GGGTGGGtGGAGTTTGCTaCTGG	0.00%	0.30%	validated
VEGFA1_36	Chr8	28483353	aaGTGGGaGGAGacTGCTCCAGG	0.01%	0.02%	Invalidated
VEGFA1_37	Chr22	38219333	aGGTcGGGGGAGTTaGaTCCCGG	0.01%	0.02%	Invalidated

VEGFA2

	Chromosome	Location	DNA seq at a Cleavage sites	Indel frequency (%)		Validation
				(-) RGEN	(+) RGEN	
On-Target	Chr6	43738562	GACCCCCTCCACCCCGCCTCCGG	0.00%	96.41%	validated
VEGFA2_02	Chr11	31817483	GggCCCCCTCCACCCCGCCTCTGG	0.04%	2.50%	validated
VEGFA2_03	Chr5	6715119	ctaCCCCCTCCACCCCGCCTCCGG	0.00%	6.24%	validated
VEGFA2_04	Chr17	4358752	tACCCCCcaCACCCCGCCTCTGG	0.01%	0.74%	validated
VEGFA2_05	Chr9	27338875	GACCCCTcCCACCCCGaCTCCGG	0.00%	0.87%	validated
VEGFA2_06	Chr18	21359559	GcCCCCacCCACCCCGCCTCTGG	0.00%	34.17%	validated
VEGFA2_07	ChrX	118865483	GtCctCCaCCACCCCGCCTCTGG	0.00%	0.05%	validated
VEGFA2_08	Chr2	242214607	attCCCCcCCACCCCGCCTCAGG	0.78%	6.77%	validated
VEGFA2_09	Chr9	103599649	acaCCCCcCCACCCCGCCTCAGG	0.00%	3.35%	validated
VEGFA2_10	Chr16	56963429	tgCCCCcCCACCCCaCCTCTGG	0.03%	3.82%	validated
VEGFA2_11	Chr11	71948805	GcttCCCTCCACCCCGCaTCCGG	0.01%	0.44%	validated
VEGFA2_12	Chr17	40044757	tgCCCCtCCACCCCGCCTCTGG	0.00%	0.77%	validated
VEGFA2_13	Chr10	116294256	ccCCCaCCcCCACCCCGCCTCAGG	0.15%	63.43%	validated
VEGFA2_14	Chr10	135149948	cgCCCTcCCACCCCGCCTCCGG	0.01%	8.44%	validated
VEGFA2_15	Chr3	140398801	cAaCCCCcCCACCCCGCtTCAGG	0.03%	1.38%	validated
VEGFA2_17	Chr12	26025095	cAttCCCCcCCACCCCaCCTCAGG	0.03%	16.64%	validated
VEGFA2_18	Chr10	72538218	cAgtCCcCCaCCCCCaCCTCTGG	0.01%	0.57%	validated
VEGFA2_19	Chr9	131706582	agCCaaCcCCACCCCGCCTCTGG	0.01%	0.06%	validated
VEGFA2_22	Chr19	13122189	GcCCCCCaCCACCCCaCCTCGGG	0.00%	1.86%	validated
VEGFA2_33	Chr2	12744776	GACaCaCcCCACCCCaCCTCAGG	0.01%	0.39%	validated
VEGFA2_34	Chr13	100546989	ccCCCCcCCcCCCCGCCTCAGG	4.45%	13.82%	validated
VEGFA2_39	Chr4	38537628	ctCCCCacCCACCCCGCCTCAGG	0.00%	69.10%	validated
VEGFA2_40	Chr12	101603788	GcCagCCctCACCCCGCCTCGGG	0.00%	0.00%	Invalidated
VEGFA2_42	Chr6	10882454	ccCtCtCcaCcCCcCCTCTGG	0.00%	0.00%	Invalidated
VEGFA2_43	Chr16	13492458	tcCgCCcCCACCCCaCCTCCGG	0.04%	0.03%	Invalidated
VEGFA2_44	Chr1	111860603	tAaatCCTCCACCCCaCCTCAGG	0.01%	0.00%	Invalidated
VEGFA2_48	Chr6	167929803	GctgtCtCCACCCCGCCTCAGG	0.00%	0.01%	Invalidated
VEGFA2_50	Chr17	29983010	cAtCtCcCCACCCCGCCTCTGG	0.24%	0.26%	Invalidated
VEGFA2_51	Chr14	75098723	cctCaCCcCCACCCCaCCTCTGG	0.00%	0.00%	Invalidated
VEGFA2_54	Chr20	25240252	ccCaCaCcCCACCCCaCCTCCGG	0.00%	0.01%	Invalidated

VEGFA3

	Chromosome	Location	DNA seq at a Cleavage sites	Indel frequency (%)		Validation
				(-) RGEN	(+) RGEN	
On-Target	Chr6	43737471	GGTGAGTGAGTGTGTGCGTGTGG	0.01%	41.88%	validated
VEGFA3_02	Chr14	65569159	aGTGAGTGAGTGTGTGTGTTGGG	0.28%	35.20%	validated
VEGFA3_03	Chr5	89440969	aGaGAGTGAGTGTGTGCaTGAGG	0.00%	18.71%	validated
VEGFA3_04	Chr5	115434676	tGTGgGTGAGTGTGTGCGTGAGG	0.01%	30.88%	validated
VEGFA3_05	Chr22	37662824	GcTGAGTGAGTGTaTGCGTGTGG	0.00%	24.48%	validated
VEGFA3_06	Chr11	68851139	GGTGAGTGAGTGcGTGCGgGTGG	1.79%	11.15%	validated
VEGFA3_07	Chr10	98760588	GtTGAGTGAaTGTGTGCGTGAGG	0.00%	19.92%	validated
VEGFA3_08	Chr3	193993884	aGTGAaTGAGTGTGTGTGTGTGG	0.40%	23.67%	validated
VEGFA3_09	Chr14	62078773	tGTGAGTaAGTGTGTGTGTGTGG	0.57%	20.05%	validated
VEGFA3_10	Chr19	40561867	acTGTGTGAGTGTGTGCGTGAGG	0.02%	0.72%	validated
VEGFA3_11	Chr20	20178284	aGTGTGTGAGTGTGTGCGTGTGG	0.25%	34.58%	validated
VEGFA3_12	Chr9	23824554	tGTGgGTGAGTGTGTGCGTGAGA	0.00%	0.32%	validated
VEGFA3_14	Chr14	106029032	GGTGAGTGAGTGTGTGTGTGAGG	0.03%	2.39%	validated
VEGFA3_15	Chr19	47732492	ctgGAGTGAGTGTGTGTGTGTGG	0.01%	0.00%	Invalidated
VEGFA3_16	Chr9	18733635	aGcGAGTGAGTGTGTGTGTGGGG	0.20%	32.70%	validated
VEGFA3_17	Chr2	73317050	GGTGAGTcAGTGTGTGaGTGAGG	2.29%	2.66%	Invalidated
VEGFA3_18	Chr4	58326608	aGTGAGTGAGTGAaGTGAGG	0.02%	0.00%	Invalidated
VEGFA3_19	Chr8	48997806	GtaGAGTGAGTGTGTGTGTGTGG	0.45%	5.11%	validated
VEGFA3_20	Chr14	74353497	aGcGAGTGgGTGTGTGCGTGGGG	0.01%	12.60%	validated
VEGFA3_21	Chr22	49740001	GGTGTGTGAGTGTGTGTGTGTGG	0.46%	2.89%	validated
VEGFA3_23	Chr16	84032646	GGTGAAaTGAGTGTGTGCTcTGGG	0.01%	0.68%	validated
VEGFA3_24	Chr10	5749657	aGTGAGTatGTGTGTGTGTGGGG	1.31%	1.86%	validated
VEGFA3_27	Chr4	62067619	GaTGAGTGTGTGTGTGTGTGAGG	0.45%	0.36%	Invalidated
VEGFA3_29	Chr2	230506241	GGTGAGCaAGTGTGTGTGTGTGG	0.46%	51.82%	validated
VEGFA3_31	Chr17	33323269	tGTGAGTGAGTaTGTaCaTGTGG	0.00%	0.01%	Invalidated
VEGFA3_32	Chr7	51294279	aGTGAGTaAGTGAaGTGaGTGAGG	0.00%	0.00%	Invalidated
VEGFA3_34	Chr16	73585926	aaTGAGTGAGTGTGTGTGTGTGA	0.77%	0.97%	Invalidated
VEGFA3_36	Chr2	18696225	aGTGAGaaAGTGTGTGCaTGCGG	0.00%	0.16%	validated
VEGFA3_37	Chr19	6660674	tGTGAGTGAGTGAaGTGaaTGTGG	0.06%	0.18%	validated
VEGFA3_39	Chr10	87387984	GGTGTGTGAGTGTGTGCaTGTTG	0.22%	0.23%	Invalidated
VEGFA3_40	Chr12	114752937	tGTGAGTGAGTGTGTGCaTGTGA	0.32%	0.36%	Invalidated
VEGFA3_41	Chr14	98442534	GGTGAGTGTGTGTGTGaGTGTGG	0.00%	0.00%	Invalidated
VEGFA3_42	Chr19	16569487	tGTGTGaGtGaGTGTGTGTGTGG	0.07%	0.22%	validated
VEGFA3_43	Chr5	34452076	tGTGTGaGtGTGTGTGTGcGTGG	0.18%	0.13%	Invalidated
VEGFA3_44	ChrX	41726218	GGTGAGTGAGTGAaGTGaGTGAGG	0.01%	0.03%	Invalidated
VEGFA3_45	Chr10	105307473	tGaGtGTGAGTGTGTGCGTGGGG	0.00%	0.01%	Invalidated
VEGFA3_46	Chr11	12159168	tGTGTGaGtGTGTGTGTGgGGGG	0.40%	0.34%	Invalidated
VEGFA3_47	Chr11	75330150	tGTGTGTGAGTGTGTGCaTGAGG	0.30%	0.32%	Invalidated
VEGFA3_48	Chr18	6130265	tGTGAGTGAaTGTGTGTGTGTGG	0.15%	0.25%	Invalidated
VEGFA3_49	Chr18	73286082	caTGAGTGgGTGTGTGCGTGGAG	0.03%	0.03%	Invalidated
VEGFA3_50	Chr19	40596585	GGactGTGAGTGTGTGCGTGAGG	0.01%	0.00%	Invalidated
VEGFA3_52	Chr2	183092036	GaTGTGTGAGTGTGTGcCtGTGG	0.01%	0.07%	validated
VEGFA3_53	Chr20	2650069	GGTGtaTGAGTGTGTGCGTcGGA	1.26%	1.30%	Invalidated
VEGFA3_54	Chr3	10207131	GGTGTGTGTGTGTGTGTGTGTGG	0.10%	0.09%	Invalidated
VEGFA3_55	Chr5	98946319	GGTGTagtGTGTGTGcTGTGTGG	0.00%	0.00%	Invalidated
VEGFA3_56	Chr6	39028642	GGTGTGTGAGTGTGTGCaTtGGG	0.00%	0.09%	validated

EMX1

	Chromosome	Location	DNA seq at a Cleavage sites	Indel frequency (%)		Validation
				(-) RGEN	(+) RGEN	
On-Target	Chr2	73160999	GAGTCCGAGCAGAAGAAGAAGGG	0.23%	61.61%	validated
EMX1_02	Chr5	45359067	GAGTtaGAGCAGAAGAAGAAAGG	0.02%	47.11%	validated
EMX1_03	Chr15	44109764	GAGTCtaAGCAGAAGAAGAAGAG	0.42%	39.41%	validated
EMX1_04	Chr2	219845073	GAGgCCGAGCAGAAGAAgACGG	0.01%	6.38%	validated
EMX1_05	Chr8	128801260	GAGTCCtAGCAGgAGAAGAAGAG	0.03%	6.67%	validated
EMX1_06	Chr5	146833190	GAGcCgGAGCAGAAGAAGgAGGG	0.03%	0.78%	validated
EMX1_07	Chr1	23720618	aAGTCCGAGgAGAgGAAGAAAGG	0.03%	0.06%	Invalidated
EMX1_08	Chr6	9118799	acGTCTgAGCAGAAGAAGAATGG	0.03%	0.75%	validated
EMX1_09	Chr15	100292479	aAGTCCcgGCAGAgGAAGAAGGG	0.01%	0.09%	validated
EMX1_10	Chr10	58848729	GAGcaCGAGCAAgAGAAGAAGGG	0.00%	0.00%	Invalidated
EMX1_11	Chr2	218378108	GAGTCTaAGCAGgAGAAatAAAGG	0.06%	0.14%	validated
EMX1_12	Chr3	95690186	tcaTCCaAGCAGAAGAAGAAGAG	0.45%	0.51%	Invalidated
EMX1_15	Chr14	48932120	GAGTCCcAGCAaAAGAAGAAAAG	0.05%	0.03%	Invalidated
EMX1_16	Chr1	113741471	GAGgtaGAGCAGAAGAAGAAGCG	0.06%	0.06%	Invalidated
EMX1_17	Chr1	231750743	GAGTCaGAGCAaAAGAAGtAGTG	0.00%	0.00%	Invalidated
EMX1_18	Chr1	234492864	GAagtaGAGCAGAAGAAGAAGCG	0.07%	0.06%	Invalidated
EMX1_19	Chr2	172374203	GAagtaGAGCAGAAGAAGAAGCG	0.07%	0.07%	Invalidated
EMX1_20	Chr11	62365273	GAaTCCaAGCAGAAGAAGAgAAG	0.02%	0.13%	validated
EMX1_21	Chr3	16077518	GAGgCaGAGagaAAGAAGAAGAG	0.01%	0.01%	Invalidated
EMX1_22	Chr1	33606480	GAGcCTgAGCAGAAGgAGAAGGG	0.01%	0.08%	validated
EMX1_23	Chr1	221522625	GAGTttGAGtAGAAGAAGAAGAG	0.72%	0.70%	Invalidated
EMX1_24	Chr3	34042974	GAGTtCaAGCAGAgAgaAAGGG	1.09%	1.10%	Invalidated
EMX1_25	Chr4	44622977	aAGTCTgAGaAGAAGAAGAAAGA	0.02%	0.03%	Invalidated
EMX1_26	Chr4	87256692	GAGTaaGAGaAGAAGAAGAAGGG	0.08%	0.09%	Invalidated
EMX1_28	Chr15	61646878	aAGTCaGAGgAGAAGAAGAAGGG	0.26%	0.47%	validated
EMX1_30	Chr17	54421043	GAGTCCcAGgAGAAGAAGAgAGG	0.01%	0.01%	Invalidated
EMX1_31	Chr19	24250503	GAGTCCaAGCAGtAGAgGAAGGG	0.01%	0.02%	Invalidated
EMX1_33	Chr20	6653999	aAGTCCagaCAGAAGAAGAAGGA	0.11%	0.14%	Invalidated

FANCF

	Chromosome	Location	DNA seq at a Cleavage sites	Indel frequency (%)		Validation
				(-) RGEN	(+) RGEN	
On-Target	Chr11	22647338	GGAATCCCTTCTGCAGCACCTGG	0.06%	54.37%	validated
FANCF_02	Chr18	8707528	GGAACCCCGTCTGCAGCACCAGG	0.05%	27.79%	validated
FANCF_03	Chr10	43410031	GGAgTCCCTcCTaCAGCACCAGG	0.01%	5.41%	validated
FANCF_04	Chr17	78923978	aGAggCCCcTCTGCAGCACCAGG	0.01%	3.09%	validated
FANCF_05	ChrX	86355180	accATCCCTcCTGCAGCACCAGG	0.02%	0.35%	validated
FANCF_06	Chr10	73463136	tGAATCCCaTCTcCAGCACCAGG	0.01%	0.34%	validated
FANCF_07	Chr10	37953200	GGAgTCCCTcCTaCAGCACCAGG	0.01%	2.75%	validated
FANCF_08	Chr16	49671025	GGAgTCCCTcCTGCAGCACCTGA	0.00%	0.82%	validated
FANCF_11	Chr16	28615201	GGctTCCCTTCTGCAGCcCCAGG	0.11%	0.12%	Invalidated
FANCF_12	Chr11	66475045	GGAAcaCCTTCTGCAGCtCCAGG	0.00%	0.07%	validated
FANCF_15	Chr17	39675789	GGgAgtCCaTCTGCAGCACCAGG	0.01%	0.02%	Invalidated
FANCF_16	Chr17	34985068	GGgtcCgCTTCTGCAGCACCTGG	0.00%	0.00%	Invalidated
FANCF_17	Chr17	3980376	GGAACCCcTCTGCAGCttCTGG	0.00%	0.00%	Invalidated
FANCF_18	Chr13	109802140	aaAATaCCTTCTGCAGtACCAGG	0.02%	0.01%	Invalidated
FANCF_19	Chr12	115467808	aGggTCCCTTCTGCAGCcCCTGG	0.04%	0.06%	Invalidated
FANCF_21	Chr12	2719895	acAcTCCCTTCTGCAGCACCATG	0.00%	0.01%	Invalidated

RNF2						
	Chromosome	Location	DNA seq at a Cleavage sites	Indel frequency (%)		Validation
				(-) RGEN	(+) RGEN	
On-Target	Chr1	185056773	GTCATCTTAGTCATTACCTGAGG	0.01%	68.06%	validated
RNF2_02	Chr12	131619805	aTCAcCTTAGcCATTACCaGGGG	0.02%	0.03%	Invalidated
RNF2_03	Chr18	62061226	aTtATtTTAGTCATTACCTtTGG	0.05%	0.03%	Invalidated
RNF2_04	Chr8	99451745	cgtgcaTTAGTCATTACCTGAGG	0.01%	0.02%	Invalidated
RNF2_05	Chr7	43967267	acttatTTAGTCATTACCTGTAG	0.02%	0.01%	Invalidated
RNF2_06	Chr6	143212079	GTaATaTTAGTCATTACCgGTGG	0.02%	0.02%	Invalidated
RNF2_07	Chr4	171989625	taacaCaTAGTCAcTACCTGGTG	0.01%	0.01%	Invalidated
RNF2_08	Chr8	5745882	aatATgTTAGTCATTACCTGAGG	0.01%	0.09%	validated
RNF2_09	Chr4	189725512	aTgcTtcTtGTCATTACCTtGGG	0.02%	0.03%	Invalidated
RNF2_10	Chr9	138721895	acttcagTAGTCATTACCTaGGG	0.03%	0.01%	Invalidated
RNF2_11	Chr5	92036966	GgtATCTaAGTCATTACCTGTGG	0.07%	0.24%	validated
RNF2_12	Chr15	25135467	catcTaaTAGTaATTACCTGGGG	0.01%	0.01%	Invalidated
RNF2_13	Chr17	53928586	GTCATCTTAGTCATTAC-TGAGG	0.00%	0.00%	Invalidated

HEK293-1

	Chromosome	Location	DNA seq at a Cleavage sites	Indel frequency (%)		Validation
				(-) RGEN	(+) RGEN	
On-Target	Chr9	110103705	GGGAAAGACCCAGCATCCGTGGG	0.04%	48.67%	validated
HEK1_02	Chr1	201992441	GGGAAAGtCCCAGCATCCtTTGG	0.05%	42.78%	validated
HEK1_03	Chr8	21121524	GGGAAgGACCCAGCATCCtgGGG	0.01%	21.48%	validated
HEK1_04	Chr9	129621088	GGGAAAtACCCAGCATCCaaTGG	0.01%	1.81%	validated
HEK1_05	Chr8	48879627	GaGAAAgCCCAGCATCCtTAGG	0.02%	0.26%	validated
HEK1_06	Chr22	47970525	GGaAAAGACCaAGCATCaGTGGG	0.00%	0.08%	validated
HEK1_07	Chr13	31633478	atGAAAGACCCAGCATCCaTTGA	0.00%	0.01%	Invalidated
HEK1_08	Chr10	123094947	GGGAAAgCCCAGCATCCcTTGG	1.62%	17.98%	validated
HEK1_14	Chr12	5555206	GGagAAagaCCAGCATCCaTAGG	0.00%	0.01%	Invalidated
HEK1_15	Chr11	75956264	ttatAAGACCCAGCATCCGTAAG	0.01%	0.09%	validated
HEK1_16	Chr10	86303625	tGGAAAGaaCAGCATCCGTACG	0.00%	0.01%	Invalidated

HEK293-2

	Chromosome	Location	DNA seq at a Cleavage sites	Indel frequency (%)		Validation
				(-) RGEN	(+) RGEN	
On-Target	Chr5	87240614	GAACACAAAGCATAGACTGCGGG	0.01%	59.05%	validated
HEK2_02	Chr4	90522184	GAACACAAtGCATAGAtTGCCGG	0.01%	16.33%	validated
HEK2_04	Chr4	53536210	GAAAtACtAAGCATAGACTcCAGG	0.01%	0.03%	Invalidated
HEK2_05	Chr11	128508577	GAAttCAAAGCATAGAtTGCAGG	0.00%	0.01%	Invalidated
HEK2_06	Chr13	113428467	cAAtACAAAGgATAGACTGCAGG	0.01%	0.02%	Invalidated
HEK2_07	Chr20	97641	GAAttCAAAGCATAGAtTGCAGG	0.01%	0.01%	Invalidated
HEK2_08	ChrX	36949815	GAAaACAAaCATAGAgTGCTGG	0.00%	0.00%	Invalidated
HEK2_09	Chr1	77190607	tcACACAAAcCATAGACTGaGGG	0.00%	0.00%	Invalidated
HEK2_10	Chr5	126385455	ccACACcAAGCATAGACTtCTGG	0.00%	0.01%	Invalidated
HEK2_11	Chr5	131174461	aAAtACAAtGCATAGACTGCTAG	0.53%	0.52%	Invalidated
HEK2_12	Chr6	139353018	ccAaACAAaCATAGACTGCTGG	0.00%	0.01%	Invalidated
HEK2_13	Chr9	290168	aAACAtAAAGaATAGACTGCAAG	0.00%	0.00%	Invalidated
HEK2_16	Chr18	22360702	GgAatCAAAGCAcAGACTGCAGG	0.00%	0.00%	Invalidated
HEK2_17	Chr18	56307003	aAgaACAAaCATAGACTGCAGG	0.01%	0.04%	validated
HEK2_19	Chr20	23101380	atACACAgAGCAaAGACTGCAGG	0.00%	0.00%	Invalidated
HEK2_20	Chr9	97332609	GtAattAAAGCAcAGACTGCTGG	0.00%	0.00%	Invalidated
HEK2_21	Chr2	19844956	aActcCAAAGCATAtACTGCTGG	0.01%	0.01%	Invalidated
HEK2_22	Chr15	65377019	GAgCgatAAGCAcAGACTGCTGG	0.00%	0.00%	Invalidated

HEK293-3

	Chromosome	Location	DNA seq at a Cleavage sites	Indel frequency (%)		Validation
				(-) RGEN	(+) RGEN	
On-Target	Chr9	110184637	GGCCCAGACTGAGCACGTGATGG	0.01%	66.99%	validated
HEK3_02	Chr1	34163192	attCtAGACTGAGCACGTGcAAG	0.01%	0.02%	validated
HEK3_03	Chr11	134582415	GGCgCAGACaGAGCACGTGACGA	0.00%	0.00%	Invalidated
HEK3_04	Chr1	47005705	aGCtCAGACTGAGCAaGTGAGGG	0.01%	16.23%	validated
HEK3_05	Chr10	131593121	GagCCAGAA TGAGCACGTGAGGG	0.00%	1.17%	validated
HEK3_06	Chr15	79749931	caCCCAGACTGAGCACGTGcTGG	0.00%	33.14%	validated
HEK3_07	Chr6	103918240	aaataAGACTGAGCACGTGgTGG	0.01%	0.02%	Invalidated
HEK3_08	Chr7	66968042	GaCaCAGACcGgGCACGTGAGGG	0.01%	0.15%	validated
HEK3_09	ChrX	114764149	aGaCCAGACTGAGCAaGaGAGGG	0.01%	0.20%	validated
HEK3_10	Chr15	35402774	cctaaAGACTGAGCAaGTGAAGG	0.01%	0.01%	Invalidated
HEK3_11	Chr9	137039236	cagCCAGACaGAGCACGTGgAGG	0.02%	0.02%	Invalidated
HEK3_12	Chr6	79958440	aaCaaAGACTGAGCACGTtAGGG	0.01%	0.01%	Invalidated
HEK3_13	Chr2	130402896	GaCCCAGAA TGAGCACaaaAGGG	0.10%	0.10%	Invalidated
HEK3_14	Chr2	97163211	ccCatgGACTGAGCACaTGAAGG	0.06%	0.08%	Invalidated
HEK3_15	Chr10	22896606	GaaggAGACTGAGCAtGTGAGGG	0.00%	0.00%	Invalidated
HEK3_16	Chr8	20947876	tctCCAGACTGAGCcCaTGAGGG	0.04%	0.03%	Invalidated
HEK3_17	Chr2	240026760	GGCtCAGACTGAGCACcTGAGAG	0.01%	0.11%	validated
HEK3_18	Chr14	102917106	ctCggAGACTGAcCACGTGAGGG	0.04%	0.05%	Invalidated
HEK3_19	Chr10	23135503	actCCAGACTGAGCAacTGAGGG	0.01%	0.01%	Invalidated
HEK3_20	ChrX	16606309	ttCCCAGACaaAGCACGcGAAGG	2.26%	2.14%	Invalidated

HEK293-4

	Chromosome	Location	DNA seq at a Cleavage sites	Indel frequency (%)		Validation
				(-) RGEN	(+) RGEN	
On-Target	Chr20	31349773	GGCACTGCGGCTGGAGGTGGGGG	0.00%	82.90%	validated
HEK4_02	Chr19	33382081	GGCtCTGCGGCTGGAGGgGGTGG	0.14%	2.84%	validated
HEK4_03	Chr10	126694875	GGCACgaCGGCTGGAGGTGGGGG	0.06%	11.61%	validated
HEK4_04	Chr15	41044242	GGCgCTGCGGCgGGAGGTGGAGG	0.02%	5.25%	validated
HEK4_05	Chr6	160517881	GGCACTGCTGCTGGgGGTGGTGG	0.15%	5.38%	validated
HEK4_06	Chr13	27629410	GGCACTGgGGtTGGAGGTGGGGG	0.02%	2.16%	validated
HEK4_07	Chr20	45343011	GGCACTGaGGgTGGAGGTGGGGG	0.02%	1.56%	validated
HEK4_08	Chr20	1151854	GGCACTGtGGCTGcAGGTGGAGG	0.01%	1.44%	validated
HEK4_10	Chr4	56815199	GGCAaTGCGGCTGGAGGcGGAGG	0.02%	11.90%	validated
HEK4_11	Chr20	60010563	tGCACTGCGGCcGGAGGaGGTGG	0.01%	2.83%	validated
HEK4_12	Chr10	77103120	GGCAAtcaCGGCTGGAGGTGGAGG	0.04%	5.09%	validated
HEK4_13	Chr19	38616186	GGCACTGaGaCTGGgGGTGGGGG	0.02%	17.00%	validated
HEK4_14	Chr13	39262929	aGCAgTGCGGCTaAGGTGGTGG	0.03%	12.34%	validated
HEK4_15	Chr10	13692637	GGCACTGgGGCTGGgGGaGGGGG	0.14%	0.25%	Invalidated
HEK4_16	Chr7	54561438	aGgACTGCGGCTGGgGGTGGTGG	0.24%	8.72%	validated
HEK4_17	Chr19	41220525	GGCAaTgTGGCTGaAGGTGGGGG	0.01%	0.68%	validated
HEK4_18	Chr20	60895671	GGCACaGCaGCTGGAGGTGcTGG	0.02%	0.59%	validated
HEK4_19	Chr1	171018460	GcCACTGgGGCTGGgGGTGGGGG	0.26%	2.32%	validated
HEK4_20	Chr17	176302	tGCACTGtGGCTGGAGaTGGGGG	0.01%	1.02%	validated
HEK4_21	Chr13	88900992	caCACTGCaGCTGGAGGTGGTGG	0.55%	0.80%	validated
HEK4_25	Chr16	89469252	GGCACTGCGGgaGGAGGTGGGCG	0.06%	0.09%	Invalidated
HEK4_31	Chr14	24740271	GGCACTGCcaCTGGgGGTGaGGG	0.40%	0.46%	Invalidated
HEK4_41	Chr10	1285239	GGCcCTtCGGCTGGAGGTGGCAG	0.02%	0.01%	Invalidated
HEK4_42	Chr10	60003488	GGCACgcgGctgGGAGGTGGAGG	0.07%	0.07%	Invalidated
HEK4_43	Chr12	90804707	GGCAtgcgGctgGGAGGTGGAGG	0.03%	0.03%	Invalidated
HEK4_45	Chr15	75632142	GcacCTGCGGCTGGAGGTGGCAG	0.02%	0.01%	Invalidated
HEK4_46	Chr1	2933843	GGCcCTGaGaCTGcAGcTGGAGG	0.01%	0.02%	Invalidated
HEK4_48	Chr3	16815640	cGCACTGgGGCTGcAGGTGGAGG	0.66%	0.74%	Invalidated
HEK4_50	Chr4	156491955	ttCACTGtGGCTGGAGGTGGGGA	0.12%	0.10%	Invalidated
HEK4_51	Chr5	41968123	GGaAgTGCGGCaGGAGGTGGAGG	0.02%	0.02%	Invalidated
HEK4_52	Chr5	177928896	ccCACTGCGGgTGGAGGTGGAAG	0.02%	0.02%	Invalidated
HEK4_53	Chr6	33950129	GGCtCTGaGGCTGGtGGTGGGGG	0.48%	0.42%	Invalidated
HEK4_54	Chr6	159190938	GGCcCTGCaGCTGGAGGaGGAGA	0.06%	0.05%	Invalidated
HEK4_55	Chr7	157889941	GGCACTGgGGaaGGAGGTGGAGG	1.81%	1.90%	Invalidated
HEK4_56	Chr8	1241128	GGCACTGttGCTGGAGGaGGCAG	0.01%	0.00%	Invalidated
HEK4_57	Chr8	11479079	GGCcCTGCaGCTGGAGaTGAAG	0.67%	0.72%	Invalidated
HEK4_58	Chr8	145730111	GGCACatgGGCTGGgGGTGGGGG	0.06%	0.07%	Invalidated
HEK4_59	Chr10	36109441	GGCAtTGCTGCTGGtGGTGGTGG	0.00%	0.00%	Invalidated
HEK4_60	Chr10	127971444	GGaACTGgGGCTGGgGGTGGGGG	0.01%	0.20%	validated

Supplemental Table 4. Indel frequencies in HEK 293T cells

HEK293-1							
	Chromosome	Location	DNA seq at a Cleavage sites	Indel frequency (%)		Validation	P-value
				(-) RGEN	(+) RGEN		
On-Target	Chr1	185056773	GGGAAAGACCCAGCATCCGTGGG	0.08%	57.29%	validated	< 0.0001
HEK1_15	Chr11	75956264	ttatAAGACCCAGCATCCGTAAG	0.00%	0.02%	validated	0.0020
HEK293-2							
	Chromosome	Location	DNA seq at a Cleavage sites	Indel frequency (%)		Validation	P-value
				(-) RGEN	(+) RGEN		
On-Target	Chr5	87240614	GAACACAAAGCATAGACTGCGGG	0.00%	52.02%	validated	< 0.0001
HEK2_17	Chr18	56307003	aAgaACAAaCATAGACTGCAGG	0.01%	0.01%	invalidated	0.55
HEK293-3							
	Chromosome	Location	DNA seq at a Cleavage sites	Indel frequency (%)		Validation	P-value
				(-) RGEN	(+) RGEN		
On-Target	Chr9	110184637	GGCCCAGACTGAGCACGTGATGG	0.02%	70.53%	validated	< 0.0001
HEK3_02	Chr1	34163192	attCtAGACTGAGCACGTGcAAG	0.01%	0.05%	validated	0.00011
HEK3_17	Chr2	240026760	GGCtCAGACTGAGCACcTGAGAG	0.01%	0.03%	validated	0.049
HEK293-4							
	Chromosome	Location	DNA seq at a Cleavage sites	Indel frequency (%)		Validation	P-value
				(-) RGEN	(+) RGEN		
On-Target	Chr20	31349773	GGCACTGCGGCTGGAGGTGGGGG	0.03%	38.84%	validated	< 0.0001
HEK4_60	Chr10	127971444	GGaACTGgGGCTGGgGGTGGGGG	0.03%	0.20%	validated	< 0.0001