

Supplemental Information

Genome-wide target specificities of CRISPR-Cas9 nucleases revealed by multiplex Digenome-seq

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Supplemental Figure 1. In vitro DNA cleavage scoring system for Digenome-seq analysis. We assigned a DNA cleavage score to each nucleotide position across the human genome using the following equation and set a cutoff value of 2.5 to identify in vitro DNA cleavage sites. This equation accounts for both blunt ends and cohesive ends ($\alpha = 1$ to 5), unlike the previous method that accounts for blunt ends only. The number of forward sequence reads starting at position i (F_i) is subtracted by one to set the score at >99% of nt positions to zero and then multiplied by the number of reverse sequence reads starting at nearby positions. The equation also accounts for the sequencing depth.

Score at position i =

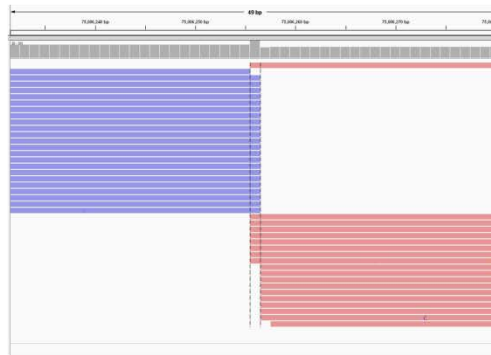
$$\sum_{a=1}^5 \frac{(F_i - 1)}{D_i} \times \frac{(R_{i-4+a} - 1)}{D_{i-4+a}} \times (F_i + R_{i-4+a} - 2) + \sum_{a=1}^5 \frac{(R_{i-1} - 1)}{D_{i-1}} \times \frac{(F_{i-3+a} - 1)}{D_{i-3+a}} \times (R_{i-1} + F_{i-3+a} - 2)$$

F_i : Number of forward sequence reads starting at position i

R_i : Number of reverse sequence reads starting at position i

D_i : Sequencing depth at position i

Example :



		75006253	75006254	75006255	75006256	75006257	75006258	75006259
Count	Reverse	0	0	1	22	0	0	0
	Forward	0	0	0	9	9	1	0
Depth		23	23	23	31	18	19	19

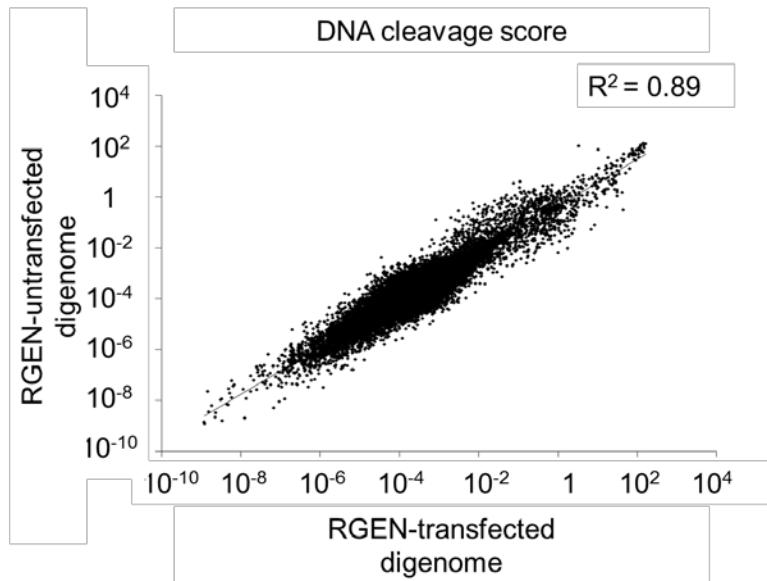
Score at position 75006256

$$= (22-1)/31 * [(0-1)/23 * (22+0-2) + (9-1)/31 * (22+9-2) + (9-1)/18 * (22+9-2) + (1-1)/19 * (22+1-2) + (0-1)/19 * (22+0-2)]$$

$$+ (9-1)/18 * [(0-1)/23 * (9+0-2) + (1-1)/23 * (9+1-2) + (22-1)/31 * (9+22-2) + (0-1)/18 * (9+0-2) + (0-1)/19 * (9+0-2)]$$

$$= 20.66$$

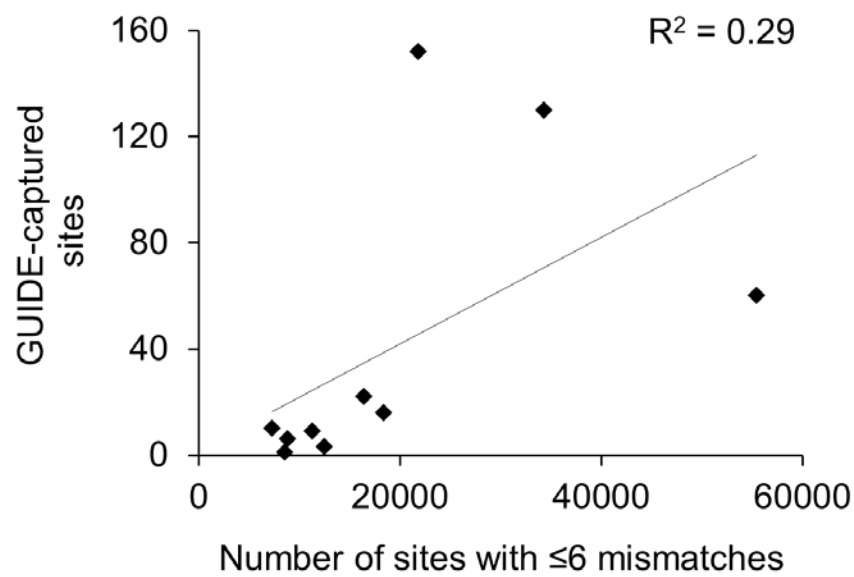
Supplemental Figure 2. Reproducibility of the in vitro DNA cleavage scoring system. We assigned a DNA cleavage score to each nucleotide position using the two independent digenome sequencing datasets we had reported previously (Kim et al. 2015).



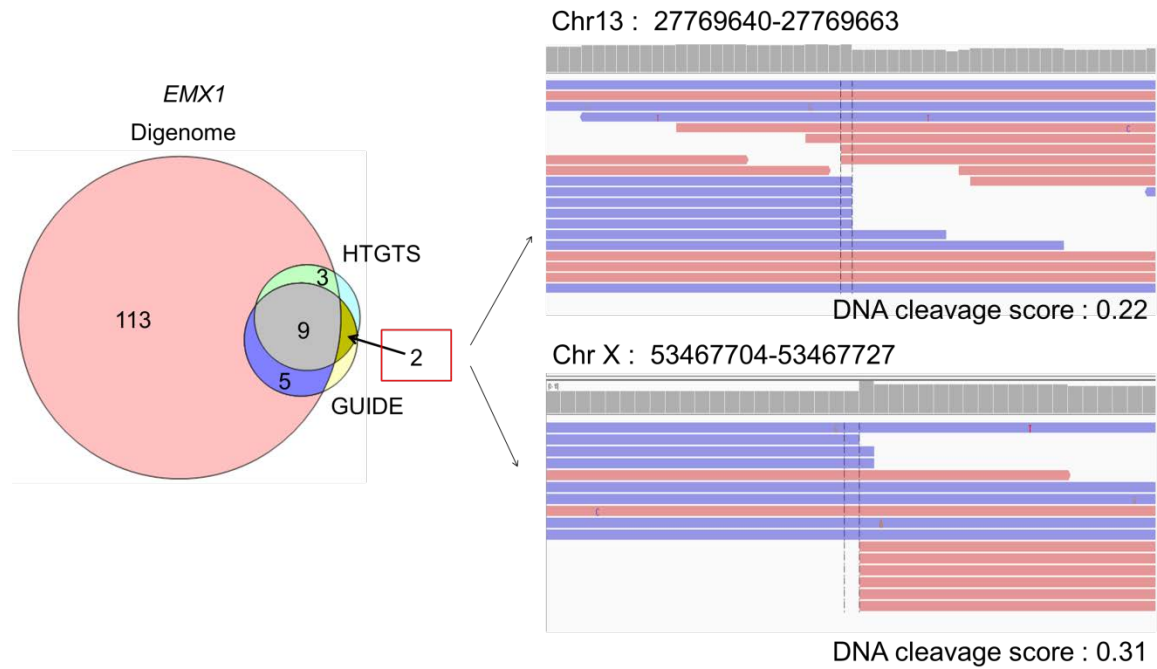
Supplemental Figure 3. Bulge-type off-target sites captured by Digenome-seq using sgRNAs transcribed from an oligonucleotide duplex. Note that most of synthesis-failed oligonucleotides are (n-1) mers, which give rise to RNA-bulge off-target cleavages at sites with a missing nucleotide compared to the on-target sequence.

5' - gTTaCCCC-CAGGGaAGTAtAGG -3' Off-target 1	5' - tgTGCCCCACA-GGCAGTAGATG -3' Off-target 2
5' - CTTGCCCCACAGGGCAGTAACGG -3' On-target sequence	5' - CTTGCCCCACAGGGCAGTAACGG -3' On-target sequence
5' - CgTGCCCCACAGGG-AGTgAGGG -3' Off-target 3	5' - CTT-CCCCAAtatcC-AGTaGGG -3' Off-target 4
5' - CTTGCCCCACAGGGCAGTAACGG -3' On-target sequence	5' - CTTGCCCCACAGGGCAGTAACGG -3' On-target sequence

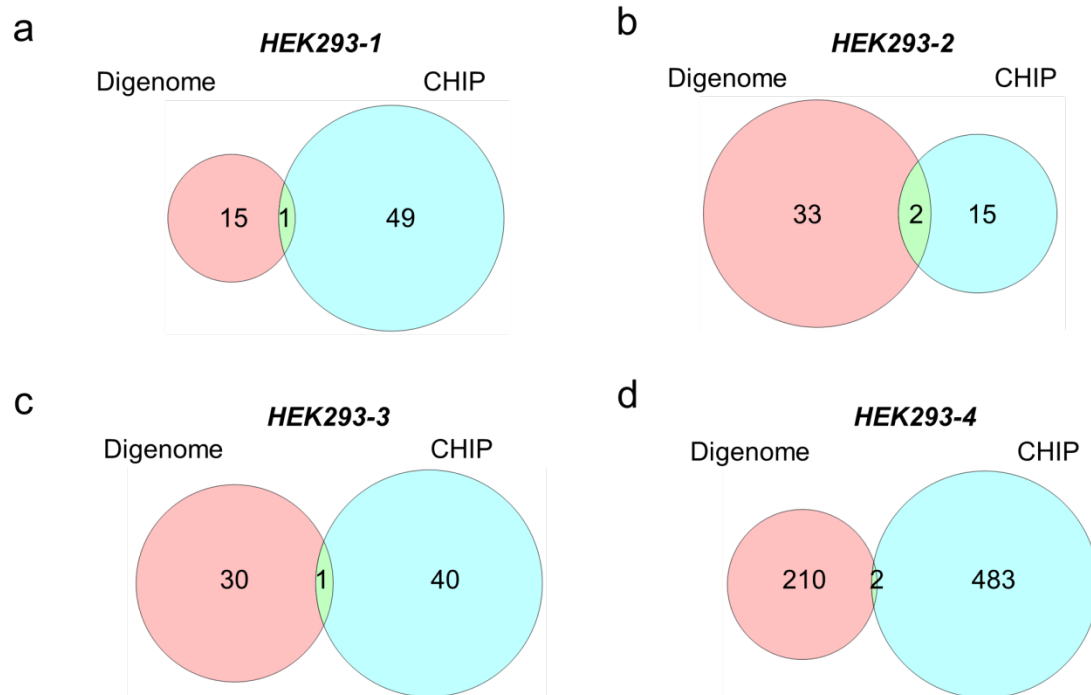
Supplemental Figure 4. Poor correlation between the number of GUIDE-seq positive sites and the number of homologous sites with 6 or fewer mismatches in the human genome.



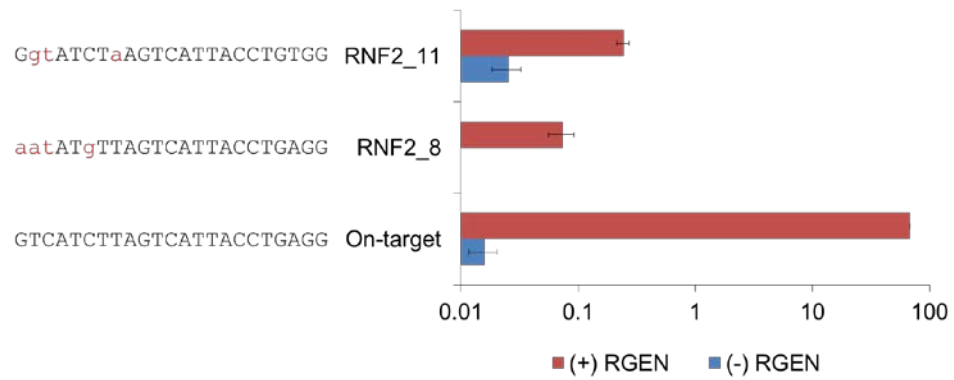
Supplemental Figure 5. Two *EMX1* off-target sites captured by HTGTS and GUIDE-seq but missed by Digenome-seq. The two numbers below the IGV images indicate DNA cleavage scores calculated using the equation in Supplemental Fig. 1, which are smaller than the cutoff value of 2.5.



Supplemental Figure 6. Venn diagrams showing the number of sites captured by Digenome-seq and CHIP -seq.



Supplemental Figure 7. Indel frequencies (log scale) at on-target and off-target sites determined in HeLa cells transfected with the *RNF2*-specific sgRNA.



Supplemental Table 1. Digenome-captured sites using oligonucleotide templates and plasmid templates

Oligonucleotide template				
Chromosome	location	DNA sequence at cleavage site	DNA cleavage Score	Bulge
chr11	5248215	CTTGCCCCACAGGGCAGTAACGG	19.1	x
chr1	38230668	CTctgtCtcgcGctgctTttGGG	8.9	x
chr1	177593980	tcTaCCCCACAtGGCAGTAATGG	13.1	x
chr2	112686732	ggTcCCgggaAtaGCgGgtAAGG	6.4	x
chr2	240591539	acaGCCCCACAGGGCAcTAgAGG	12.0	x
chr3	3662556	aaaGCCCCACAGGGtAGTAAGG	23.2	x
chr3	19957634	gcTaCCCCACAGGGCAtTAgGGG	12.3	x
chr4	45763604	gcTGCCCCACAtGaCAGaAATGG	12.4	x
chr4	48091817	acTcgtCtcCgatatccagtTGG	12.5	x
chr4	55979545	ggTGtaaCcCgGaGtgaccAAGG	11.0	x
chr4	55979546	ggTGtaaCcCgGaGtgaccAAGG	3.1	x
chr4	148531374	gTTaCCtCACAGaGCAGaAAGGG	17.4	x
chr4	165593737	taTGctCCAgAGGGtAGTAATGA	3.7	x
chr5	14347051	CaTaCCCCACAGGtCAGTAAGGA	16.4	x
chr5	131423385	tcTGCCCCACAGGcCAGgAAGGG	8.5	x
chr6	50041372	tcTGCCCCACAtGGCAGTAATGA	19.6	x
chr6	80093919	tgaGttCtcCAatatccagtTGG	10.0	x
chr6	85738203	acTGCCCCACAGGGaAGTAATAG	19.7	x
chr8	41296595	tcaGCCCCACAGGtCAGcAATGG	17.1	x
chr9	24439672	ggactCCtcCAatatccTgtTGG	2.6	x
chr9	78341070	gTTaCCCC-CAGGGaAGTAtAGG	5.3	RNA Bulge
chr9	104595883	tcaGCCCCACAGGGCAGTAAGGG	25.4	x
chr9	134609673	tTTGCCCCtCAGGGCAGctAAGG	7.8	x
chr9	134994964	CcTGCCCCACAGGGCAaTtATGG	9.6	x
chr10	71843328	CaTGgCCaggAaGagAaggcTGG	14.9	x
chr10	72286450	CaaGCCCCACAGGGCAGacAGGG	6.8	x
chr10	73555691	CagGCCCCACAGGaCAGgAAGGG	3.4	x
chr11	3125346	agccCCCacagGGcagGTAgGGG	3.5	x
chr11	59611432	CggcCagattcatGgcaatcAGG	21.4	x
chr11	76387498	CTgcCCctcagGgaCAGTAAGGG	11.5	x
chr12	27234755	gaTGCCtCACAGGaCAGgAAGGG	7.8	x
chr12	40327469	gcTatggttCctGaacGgccTGG	13.3	x
chr12	93549202	aTTGCCCCACgGGGCAGTgACGG	31.9	x
chr12	124803834	gcTGCCCCACAGGGCAGcAAAGG	27.7	x
chr13	29005426	tTgGtCaattcGtcgccTtACGG	2.9	x
chr13	44886376	ggaGCCCCACAGGGCAGagAGGG	15.5	x
chr14	36889538	gTTatCCCACAGGaCAGTgAGGG	24.0	x
chr14	59445901	CTT-CCCCAatatcCAGT-AGGG	4.5	RNA Bulge
chr14	94585327	aTgGCCCCACAaGGCAGaAATGG	20.9	x
chr15	29983547	CcaGCCCCACAGGGCAGTAAAGC	12.6	x
chr15	46598129	gTTGCCCCtCAGGaCAGTAAGG	32.5	x
chr15	99709337	tgTGCCCCACAGGG-AGTgAGGG	3.4	RNA Bulge
chr16	49082904	gcaGCCCCACAGGtCAGTgAGGG	13.7	x
chr17	8370253	tgctCCCacagGGcagtaAACGG	18.3	x
chr18	745994	aaaataCCtCgttGattTccAGG	27.3	x
chr18	6663844	gTTGCCCCActGGGgAGaAAAGG	4.3	x
chr19	29880768	tgTGCCCCACAGG-CAGTAATG	11.6	RNA Bulge
chr19	34262013	CTgctCCacagGGcagGTAtGGG	4.3	x
chr19	37539042	CTTGCaCCACAGaGCACTAAGGG	2.9	x
chr20	39992928	agTGgCCCCcAGGGCAGTgAGGG	4.2	x
chr22	17230623	tgTGCCCCACAGaGCACTAAGGG	22.0	x
chr22	35537395	agTGCCCCACAGGGgAGaAATGG	12.1	x
chrX	75006257	gTgGCCCCACAGGGCAGgAATGG	7.0	x
chrX	132429379	gcacCCCCACAGGGCAGTAATGTG	3.3	x

Plasmid template				
Chromosome	location	DNA sequence at cleavage site	DNA cleavage Score	Bulge
chr11	5248215	CTTGCCCCACAGGGCAGTAACGG	17.5	x
chr1	17346702	ggTcCCCacagGGtCAGTAAGGG	4.5	x
chr1	177593980	tcTaCCCCACAtGGCAGTAATGG	14.4	x
chr3	3662556	aaaGCCCCACAGGGtAGTAgAGG	9.9	x
chr3	19957634	gcTaCCCCACAGGGCAtTAgGGG	12.0	x
chr4	148531374	gTTaCCtCACAGaGCAGaAAGGG	13.4	x
chr5	14347051	CaTaCCCCACAGGtCAGTAAGGA	4.3	x
chr5	131423385	tcTGCCCCACAGGcCAGgAAGGG	4.9	x
chr6	23709579	gaaGCCctACAGGGCAGcAATGG	4.6	x
chr6	50041372	tcTGCCCCACAtGGCAGTAATGA	17.7	x
chr8	24931381	agTGCCCaCACaGCAGTAAGGG	6.0	x
chr9	104595883	tcaGCCCCACAGGGCAGTAAGGG	11.1	x
chr9	134994964	CcTGCCCCACAGGGCAaTtATGG	7.3	x
chr10	72286450	CaaGCCCCACAGGGCAGacAGGG	4.8	x
chr10	73555691	CagGCCCCACAGGaCAGgAAGGG	4.3	x
chr11	76387498	CTgcCCCtcagGGaCAGTAtGGG	16.9	x
chr12	27234755	gaTGCCtCACAGGaCAGgAAGGG	5.3	x
chr12	93549202	aTTGCCCCACgGGGCAGTgACGG	35.6	x
chr12	124803834	gcTGCCCCACAGGGCAGcAAAGG	27.6	x
chr13	44886376	ggaGCCCCACAGGGCAGagAGGG	5.0	x
chr14	36889538	gTTatCCCACAGGaCAGTgAGGG	23.0	x
chr14	94585327	aTgGCCCCACAaGGCAGaAATGG	17.0	x
chr15	34059408	gTTaCCaCACAGaGCAGTtAAGG	3.1	x
chr15	46598129	gTTGCCCCtCAGGaCAGTAcAGG	21.2	x
chr16	49082904	gcaGCCCCACAGGtCAGTgAGGG	4.0	x
chr17	8370253	tTgctCCCACAGGGCAGTAAACG	21.1	x
chr19	8560462	aaatCCCCACAGGGCAGTAAGGC	2.6	x
chr20	39992928	agTGgCCCCcAGGGCAGTgAGGG	3.5	x
chr22	17230623	tgTGCCCCACAGaGCAcTAAGGG	15.5	x
chrX	75006257	gTgGCCCCACAGGGCAGgAATGG	4.5	x

Supplemental Table 2. Multiplex Digenome-captured sites

VEGFA1			
Chr	Position	DNA cleavage Score	DNA seq at a cleavage sites
Chr6	43737290	38.9	GGGTGGGGGGAGTTTGCTCCAGG
Chr15	65637537	25.6	GGaTGGaGGGAGTTTGCTCCTGG
Chr5	7067159	22.2	GaGgGtGGGGAGTTTaCTCCTGG
Chr1	99347651	21.3	GGGgaGGGGaAGTTTGCTCCTGG
Chr12	1988077	20.7	cGGgGGaGGGAGTTTGCTCCTGG
Chr22	37215276	20.4	GGGTGGGGGGAGTTTGCCcCAGG
Chr17	32986325	17.8	GGGgGtGGGGAcTTTGCTCCAGG
Chr1	82627648	16.6	GGGTGctGGcAcagTGCTCCTGG
Chr12	26641302	16.5	aGtTtGGGGGAGTTTGCCcCAGG
Chr1	233157354	15.6	GGagGaGGGGAGTcTGCTCCAGG
Chr10	124731416	15.3	aGcTGGaGGGAGTTTGCCcCAGG
Chr12	131690199	14.4	GGGaGGGtGGAGTTTGCTCCTGG
Chr11	71497119	14.3	aGGaaGGaGGAGTTaGCTCCTGG
Chr20	7836107	14.2	caGgtGGGaGAGTTTGCTCCcAG
Chr17	39796328	14.1	taGTGGaGGGAGcTTGCTCCTGG
Chr4	8453803	14.1	GaGTGGGtGGAGTTTGCTaCAGG
Chr9	88657759	14.1	GGaTGGaGGtAGTTTGtTCCTGG
Chr9	93925190	14.1	GGGgGtGGGGAGcaTGCTCCAGG
Chr3	125633992	13.8	aGGaaGGaGGAGTTaGCTCCTGG
Chr16	8763213	13.4	aaGTaaGGGaAGTTTGCTCCTGG
Chr8	140714327	13.1	GGGaGGaGaGAGTTTGCTcCTG
Chr20	56175356	13.0	aGGgaGGaGGAaTTTGCTCCAGG
Chr15	93140401	12.7	GGGgGaGGGaAGTTTcCTCCAGG
Chr2	209437600	11.6	aGGgaGGGaGAaTTTGCTCCTGG
Chr3	128284321	11.6	aGGTGGtGGGAGcTTGtTCCTGG
Chr5	32945275	11.6	GcGTGGGGGGtGTTTGCTCCCGG
Chr6	14316373	11.5	GtGgGGGtaGAGTTTGCTCCAGG
Chr13	26202812	11.4	GGtTGaGGGGAGTcTGCTCCAGG
Chr5	156390	11.3	tGcTcGGGGGAGTTTGCaCCAGG
Chr21	43689878	10.7	GGcccaGGGGAGTTTGCTCCcAG
Chr19	51310920	10.7	GtGcaGGGGGAaTTTGCTtCCGG
Chr5	139263024	10.6	ttGgGGGGGcAGTTTGCTCCTGG
ChrX	82127748	10.5	aGagGGGGaGAGTTTGCCcCCTGG
Chr7	17819097	10.2	acaactGGGGAGTTTGCTCCTGG
Chr22	41676762	10.1	aGtgcaGGGGAGcTTGCTCCTGG
Chr2	96056645	9.9	GGGTGGGGaGAGTTTctTCCTGG
Chr3	195871264	9.8	GGtgGGGGaGAGcTaGCTCCGGG
Chr11	3445204	9.7	aGGaaGGaGGAGTTaGCTCCTGG
Chr6	45554056	9.7	GGGgtGGGaGAGTTTGCTcCTG
Chr18	366714	9.4	GGGgGcaGGGAGaATTGCTCCTGG
Chr3	13580170	9.1	atGgGGGaGaAacTTGCTCCTGG
ChrX	19185601	8.9	GGGaGGGGaGAGTTTGtTCCAGG
Chr11	67574262	8.7	aGGaaGGaGGAGTTaGCTCCTGG
Chr17	47317539	8.5	ctGgtGGGGAGcTTGCTCCAGG
Chr6	91365255	8.4	cccgGGGGGaAGcTTGCTCCAGG
Chr22	18454623	8.4	GGaaaGGaGGAGcTTGCTCCAGG
Chr22	19698463	8.3	GaGgGGGaGcAGTTTGCTCCAGG
Chr3	36358934	8.3	aGtgGGGGaGAGTaTGCTCCGGG
Chr21	37116659	7.7	aaGTGGGaaGAGTTTGtTCCAGG

Chr11	117481208	7.5	GGGcaaGGGGAGgTTGCTCCTGG
Chr7	29081029	7.5	GGagtGGGtGAGcTTGCTCCTGG
Chr17	63035708	7.4	aGGaGGGGGaAGaaTGCTCCAGG
Chr2	181170961	6.7	tGGgGaGGGGAAaTTGCTCCTGG
Chr6	109284989	6.7	tGGaGaGGGGAGTTgGCTCCTGG
Chr11	122583511	6.7	aGaaGaGGGGAAtTTTGCTCCTGG
Chr5	56172079	6.6	GGtgGGGGtGgGTTTGCTCCTGG
Chr1	33643288	6.5	GGGTGGGtGGAGTTTGCTaCTGG
Chr8	28483353	6.4	aaGTGGGaGGAGacTGCTCCAGG
Chr22	38219333	6.0	aGGTcGGGGGAGTTaGaTCCCGG
Chr15	29263777	6.0	GGGatGGGaGAGTcTGCTCCTGG
Chr2	30430777	5.7	aGGgaGaGGGAGcTTGCTCCCAG
Chr12	107832636	5.4	tctTGGGGGGAagTTGCTCCAGG
Chr4	185246171	5.3	GGagGGGGGGcTTTGCTCCAGG
Chr8	10804669	4.8	GaGTGaGGaGAGcTTGCTCCATG
Chr5	95220670	4.6	GGGaGcaGGGAaTTTGCTCCAGG
Chr2	129199817	4.5	tccTGaGGGcAGTTTGCTCCAGG
Chr13	31251013	4.4	tGtaGaGGGagtTTTGCTCCCGG
Chr16	89679839	4.4	GGagGaGGGaAcTTTGCTCCAGG
Chr1	20166440	4.3	GtGgGaGGatAGcTTGCTCCTGG
Chr18	13983474	3.7	GGGTGaaaGaAGTTTaCTCCTGG
Chr6	50485682	3.6	atGTGtGGGGAAaTTTGCTCCAGG
Chr1	205484156	3.6	GtGTGaGtGGAGTTTGCTCtGGG
Chr6	109070771	3.5	GGtgGGGGaaAGTTTGCTCCTGA
Chr15	101813024	3.4	aaGgaGGcGGAGcTTGCTCCTGG
Chr11	11823598	3.1	GGcTGGaGGGGaTTTGCTCCTGG
Chr9	5336085	3.1	tcGTGGtGGGAaTTTaCTCCTGG
Chr4	116853325	2.9	aaagGGGGGaAcTTTGCTCCAGG
Chr11	86695108	2.8	aGGgaaGGGGAAaTTTGCaCCTGG
Chr5	57030871	2.8	ctcTGaGGGGAGTTTGCTCtGGG
Chr15	84047385	2.7	GGagtcaGGGAaTTTGCTCCTGG

VEGFA2

Chr	Position	DNA cleavage Score	DNA seq at a cleavage sites
Chr2	242214607	167.0	attCCCCcCCACCCCGCCTCAGG
Chr9	103599649	105.2	acaCCCCcCCACCCCGCCTCAGG
Chr14	75098723	101.0	cctCaCCcCCACCCCaCCTCTGG
Chr11	31817483	95.2	GggCCCCTCCACCCCGCCTCTGG
Chr17	4358752	72.7	tACCCCCcaCACCCCGCCTCTGG
Chr16	56963429	58.0	tgCCCCCcCCACCCCaCCTCTGG
Chr12	26025095	56.2	cAttCCCcCCACCCCaCCTCAGG
Chr1	111860603	44.5	tAaatCCTCCACCCCaCCTCAGG
Chr18	21359559	40.7	GcCCCCacCCACCCCGCCTCTGG
Chr6	43738562	36.2	GACCCCTCCACCCCGCCTCCGG
Chr10	116294256	35.4	ccCCaCCcCCACCCCGCCTCAGG
Chr22	32532901	35.2	GAgCCaCTgCgCCCgGCCcCCGG
Chr9	27338875	33.9	GACCCctCCACCCCGaCTCCGG
Chr17	40044757	33.4	tgCCCCtCCACCCCGCCTCTGG
Chr12	31812350	31.9	GAtCgaCTCCACCCCGCCTCTGG
Chr13	100546989	30.0	ccCCCCCcCCcCCCCGCCTCAGG
Chr19	13122189	30.0	GcCCCCCaCCACCCCaCCTCGGG
Chr5	6715119	29.4	ctaCCCCTCCACCCCGCCTCCGG
Chr10	72538218	29.3	cAgtCCCcCCACCCCaCCTCTGG
Chr16	13492458	28.6	tcCgCCCcCCACCCCaCCTCCGG
Chr4	38537628	28.1	ctCCCCacCCACCCCGCCTCAGG
Chr6	160552566	27.9	tcagaCCTCCACCCCGCCTCAGG
Chr16	81442194	26.1	ttCaCCaTCaACCCCaCTtCAG
Chr4	182638032	25.1	tcCtttCTCCACCCCaCCTCTGG
Chr10	135149948	24.7	cgCCCTCcCCACCCCGCCTCCGG
Chr11	2686249	23.2	ctCaCCCCcCCACCCCaCCTCTGG
Chr11	83433600	19.4	GtCaCtCcCCACCCCGCCTCTGG
Chr4	148977716	18.8	tcCCgCCcCCACCCCaCCTCCGG
Chr1	198124848	18.8	tgCaaCCTCctCCCCGCCTCGGG
Chr9	131706582	18.6	agCCaaCcCCACCCCGCCTCTGG
Chr17	29983010	15.9	cAtCttCcCCACCCCGCCTCTGG
ChrX	70597642	14.3	ctaCgCtcCacCaCCaCCTCCAG
Chr16	69166711	13.0	agtagCCcCCACCCCGCCTCGGG
Chr4	1496258	12.2	aggCCCCcaCACCCCGCCTCAGG
Chr4	160033153	12.2	tcaCtCCcCCACCCCaCCTCTGG
Chr11	71948805	11.4	GcttCCCTCCACCCCGCaTCCGG
Chr18	19751064	10.7	cgtCtCCcCCACCCCaCCTCAGG
Chr11	374667	9.3	aggCCCCcCCgCCCCGCCTCAGG
Chr14	19361511	8.7	GtCgaggTCCACCCCGCCTCAGG
Chr5	139028257	8.6	ctCCCCCcCtCCCCGCCTCGGG
Chr9	140428961	8.6	ctCCCagaCtcCtCCcCCTCCTC
Chr3	140398801	8.1	cAaCCCCcCCACCCCGCtTCAGG
Chr20	25240252	8.1	ccCaCaCcCCACCCCaCCTCCGG
Chr8	122367964	7.1	ccaCCatcCCACCCCGCCTCTGG
ChrX	118865483	6.1	GtCCtCCaCCACCCCGCCTCTGG
Chr1	5477153	6.0	ctgCCTCctCACCCCGCCTCAGG
Chr6	10882454	5.7	ccCtCtCcaCcCCCacCCTCTGG
Chr13	107367839	5.6	tctCCCCTgtACCCCGCCTCTGG
Chr11	14596970	4.5	ccCtaCCcCCACCCCaCCTCAGG
Chr17	48624779	3.9	ccCttCCcCCACCCCaCCTCCGG

Chr19	42806801	3.9	ttCtCCCTCCtCCCCGCCTCGGG
Chr2	225762279	3.8	ctCCCCtCacCCCaGCCTCCGG
Chr12	101603788	3.8	GcCagCCctCACCCCGCCTCGGG
Chr2	12744776	3.7	GACaCaCcCCACCCCaCCTCAGG
Chr11	45402251	3.3	cgatCCtcttACCCCGCCTCCGG
Chr6	167929803	3.3	GctgtCtCCACCCCGCCTCAGG
Chr21	37111654	3.1	tcttCttTCCACCCCGCCTCAGG
Chr17	41797972	2.9	tcCCCTtcCCACCCCaCCTCCGG
Chr9	13973961	2.9	cAagtaaTCCACCCCaCCTCAGG
Chr1	112708281	2.8	GcCaCCtTCCACCCCaCCTCAGG
Chr5	58336894	2.8	cttCCtCcaCcCCgCagtctATG
Chr17	58404869	2.6	cgCCCaCcCCACCCCaCCTCAGG
Chr4	84744222	2.6	ccagCtCcCCACCCCaCCTCAGG

VEGFA3

Chr	Position	DNA cleavage Score	DNA seq at a cleavage sites
Chr20	2650069	50.1	GGTGtaTGAGTGTGTGCGTcGGA
Chr2	177463426	45.0	GGTGAGTgTGTGTGTGCaTGTGG
Chr5	89440969	43.7	aGaGAGTGAGTGTGTGCaTGAGG
Chr5	98946319	43.2	GGTGtagtgTGTGTGTGcTGTGG
Chr6	39028642	41.2	GGTGtGTGAGTGTGTGCaTtGGG
Chr4	58326608	39.5	aGTGAGTGAGTGaGTGaGTGAGG
Chr19	1716792	36.8	caTGAGTGAGTGTGTGgGTGGGG
Chr16	74898121	31.2	GGTGAGaGAGTGTGTGCGTaGGA
Chr7	152671378	31.0	aGTGAGTGAGTGaGTGaGTGAGG
Chr4	89935133	29.8	tcTGAGTGAGTGTGgGCaTGGGG
Chr16	84032646	28.8	GGTGAAaTGAGTGTGTGcTctGGG
Chr22	37662824	27.8	GcTGAGTGAGTGTaTGCGTGTGG
Chr20	50724405	27.1	cGTGAGTGAGTGTGTaCcTGGGG
Chr6	157078327	27.0	GaTGAGTGAGTGaGTGaGTGGGG
Chr11	79178523	26.9	aGTGAGTGAGTGaGTGgGgtTGG
Chr14	65569159	24.7	aGTGAGTGAGTGTGTGtGTGGGG
Chr20	20178284	24.1	aGTGtGTGAGTGTGTGCGTGTGG
Chr17	33323269	23.8	tGTGAGTGAGTaTGTaCaTGTGG
Chr7	23792987	22.7	taTGAGTGAGTGTGTGgaTGAGG
Chr5	34452076	22.1	tGTGtGaGtGTGTGTGtGcGTGG
Chr5	29367379	21.3	tGTGAGTGAGTGTGTGtaTGGGG
Chr14	98442534	20.6	GGTGAGTgTGTGTGTGaGTGTGG
Chr15	29699015	20.5	GGaGAGcGAGTGTGTGCaTtTGG
Chr8	143890827	20.4	GGTGtaTGAGTGTGTGtGTGAGG
Chr3	10723187	20.4	aGcGAGTGAGTGaGTGCaTtGGG
Chr2	230506241	19.7	GGTGAGcaAGTGTGTGtGTGTGG
Chr2	199628306	18.9	tGTGAGTGAGTGTGTGCagaAGG
Chr10	109378067	18.0	GGTGAGTGAGTGaGTGaGTGAGG
Chr18	43287997	17.9	tGaGAGTGAGTGTGTGtaTaTGG
Chr2	183092036	17.7	GaTGtGTGAGTGTGTGCcTGTGG
Chr15	92864212	16.8	tGTGAGTGAGTGTGTGtGTGTGA
Chr5	115434676	16.2	tGTGgGTGAGTGTGTGCGTGAGG
Chr9	18733635	15.6	aGcGAGTGAGTGTGTGtGTGGGG
Chr17	79111961	15.3	GGTaAGTGTGTGTGTGCaTGTGG
Chr3	10403702	15.1	caTGAGTGgGTGTGTGCaTtGGG
Chr8	48997806	14.7	GtaGAGTGAGTGTGTGtGTGTGG
Chr20	21927847	14.5	GaaGAaTGAGTGTGTGcTGTGG
Chr10	87387984	14.2	GGTGtGTGAGTGTGTGCaTGTTG
Chr10	1684972	14.1	tGTGAGTGgGTGTGTGaGTGAGG
Chr11	7625795	13.5	GGTGAGTagGTGTGTGtGTGGGG
Chr18	75912617	13.4	GGaGAGTgTGTGTGTGaGTGTGG
Chr6	24224744	13.0	GGTGAGcGtGTGTGTGCaTGTGG
Chr2	18696225	13.0	aGTGAGaaAGTGTGTGCaTGCGG
Chr1	203434970	12.9	caTaAGTGAGTGTGTGCGaGTGG
Chr10	130228354	12.8	aGgGAGTGAcTGTGTGCGTGTGG
Chr1	152925734	12.4	tGTGAGTgTGTGTGTGCaTcTGG
Chr3	14430297	12.4	GGTGAagtGTGTGTGCcTGTGG
Chr1	116485644	12.4	aaTGAGTGAGTGTGTGaGTGAAG
Chr6	144458291	12.3	aGgGAGTGAGTGTGaGaGTGCGG
Chr1	32738764	12.0	GGgGtGaGtGTGTGTGtGgGGGG

Chr8	145090503	12.0	tGTGAGTGAAaTGTGTGCaTaTGG
Chr21	26653015	11.9	GGTgtGTgtGTGTGTGCaTGTGG
Chr22	49740001	11.9	GGTgtGTGAGTGTGTgtGTGTGG
Chr19	47732492	11.6	ctgGAGTGAGTGTGTgtGTGTGG
Chr1	181204797	11.6	GGaGAGTGAGTGTGTttGTGTGG
Chr16	49384711	11.4	tGTGtaTGAGTGTGTGCGTtGGG
Chr17	47051410	11.4	aaTGgGTGAGTGTGTGgGTGGGG
Chr15	71796660	11.3	aaTGAaTGAaTGTGTGCaTGTGG
Chr7	158305228	11.3	tGTgtGTGAGTGTGTGCaTGTGG
Chr1	47690894	11.1	tGTGAGaGAGaGTGTGCGTGTGG
Chr8	128556646	10.9	tGTGAGTatGTGTGTGCaTGTGG
Chr6	1587476	10.8	tGTGcaTGAGgGTGTgtGTtGGG
Chr2	74655959	10.7	GGTaAGTatGTGTGTGCaTGGGG
Chr7	51294279	10.6	aGTGAGTaAGTGaGTGaGTGAGG
Chr2	10373473	10.6	tGTGAGTGAAaTGaGTGCaTGTGG
Chr11	63366342	10.6	aGTGAGTatGTGTGTGaGgGTGG
Chr21	44179977	10.5	tGTGAGTGgGTGTGTGCaTGTGG
Chr4	168168030	10.4	GGTgtGTgtGTGTGTgtGTGTGG
Chr19	16569487	10.4	tGTgtGaGtGaGTGTgtGTGTGG
Chr16	87047314	10.4	aGTGAaTGAGTGaGTGaGTGAGG
Chr3	193993884	10.4	aGTGAaTGAGTGTGTgtGTGTGG
Chr8	92645411	10.3	GaTgtGTGAGTGTGTaCaTGAGG
Chr11	78871125	10.3	aaTGAGTGAGTGaGTGCaTGGAG
Chr17	64940809	10.3	aGTGAaTGAGgcTGTGctTcGGG
ChrX	56327306	10.1	tGTGAGTgtGTGTGTGCaTGTGG
Chr22	43939297	10.1	GGTGAGaGAGTGTGTGCacGGGG
Chr4	154005628	10.0	tGTGAGTgtGTGTGTGCaTGCAG
Chr21	43375271	9.8	GtgatGTGAGcGTGTgtGTGTGG
Chr16	46642109	9.8	aGaGAGTGAGTGaGTGaGTGTGG
Chr3	55318919	9.8	aGTGAGTGAAaTGaGTGCaTaGTG
Chr3	10207131	9.7	GGTgtGTgtGTGTGTgtGTGTGG
Chr11	68851139	9.6	GGTGAGTGAGTGcGTGCGgGTGG
Chr1	212639778	9.6	GGgGAaTGAGTGTGTGCaTGGAG
Chr3	43415188	9.5	tcaGAaTGAGTGTGTGCcTGGGG
Chr8	140710487	9.2	GGgagGTGAGTGcaTGCgtGTGG
Chr12	133361327	9.1	GGgGtGTGAGcaTGTGCGTGTGG
Chr17	74046702	8.9	cGTGAGTGAGTGTGTGgtTGGGG
Chr18	6130265	8.9	tGTGAGTGAAaTGTGTgtGTGTGG
Chr14	106029032	8.8	GGTGAGTGAGTGTGTgtGTGAGG
Chr19	47787100	8.7	GaTGAGTgtGTcTGTGCaTGAGG
Chr3	1831002	8.7	acTGAGTGgGTGTGTGCcTGAGG
Chr14	62078773	8.6	tGTGAGTaAGTGTGTgtGTGTGG
Chr1	48691305	8.6	aGTgtGTGAGaGTGTGCaTGTGG
Chr19	40561867	8.4	acTgtGTGAGTGTGTGCGTGAGG
Chr20	39096994	8.3	tGTatGTGAGTGTGTGCGTGTGG
Chr10	45209678	8.3	aGgtAGTGAGTGTGTGCaTGGGT
Chr14	76750082	8.0	tGTGAGTGcGTGTcTgtGTGTGG
Chr16	84532	8.0	taTGAGTgtGTGTGTGaGTGTGG
Chr19	6660674	7.9	tGTGAGTGAGTGaGTGaaTGTGG
Chr22	29329724	7.9	aGTgtGTgtGTGTGTgtGTGGGG
Chr4	5844313	7.8	tGTGAGaGAGTGTGTGaGTGTGG
Chr1	22117219	7.8	aGTGAtgGAGTGTGTGCcTGTGG

Chr12	5100948	7.8	tGcatGTGAGTGTGTGtGcGTGG
Chr11	115758116	7.7	aGaGAGTGTGTGTGTGcTGGGG
Chr18	73286082	7.6	caTGAGTGgGTGTGTGCGTGGAG
Chr1	236264583	7.6	taTGAGTGTGTGTGTGaaTGTGG
Chr6	101025624	7.3	aGaGAGTGTGTGTGTGTGTGG
Chr7	101077901	7.2	tGTGAGTGAGTGTGTtgGTGAGG
ChrX	38624688	7.1	taTGAGTGtaTGTGTGCaTaGGG
Chr5	22787253	7.1	GGTGTGTGTGTGTGTGTGTGG
Chr17	66592348	7.1	GGTGTGTGTGTGTGTGTGTGG
Chr10	5749657	7.1	aGTGAGTatGTGTGTGTGTGGGG
Chr2	217617270	7.1	aGgGAGTGAGTGTGTaaGTGTGG
Chr7	20263523	7.0	tGTGAGTGtaTGTGTGTGTGTGG
Chr9	96679964	7.0	tGTGAGTGTGTGTGTGCaTGTGA
Chr3	30904559	7.0	aGaGAGTGAGTGTGTGaGTGTGA
Chr4	62067619	6.9	GaTGAGTGTGTGTGTGTGTGAGG
Chr17	72614843	6.9	GGgtgagGAagGTGTGCGTGGTG
Chr13	30280840	6.9	GaTaAGTGAGTaTGTGTGTGTGG
Chr20	62468987	6.8	aGTGAGTGAGTGaGTGaaTGAGG
Chr11	83585151	6.8	aGaGAGaGAGTGTGTGCGTGTGA
Chr14	74353497	6.8	aGcGAGTGgGTGTGTGCGTGGGG
Chr3	150919004	6.7	aGaGAGaGAGTGTGTGCacGTGG
Chr3	38182513	6.6	tGTGAGTGAAaTGTGTGCcaGGGG
Chr16	23981202	6.6	GGTGTGTGTGTGTGTaCGTGGGG
Chr11	12159168	6.6	tGTGTGaGtGTGTGTGTGgGGGG
Chr12	113240368	6.6	tGTGcGTGAGTGTGTGtaTGTGG
Chr12	57612417	6.6	ctTGAGTGAGaGTGaGCGTGAGG
Chr3	80057064	6.6	GGTGTGTGTGTGTGTGTGTGG
Chr10	107867379	6.6	aGaGAGTGAGTGTGTGTGTtGGG
Chr21	39875948	6.5	aGTGTGTGAGTGTGTGtaTGAGG
Chr10	105307473	6.5	tGaGtGTGAGTGTGTGCGTGGGG
Chr2	126931490	6.5	tGTGTGTGAGTGTGTGTGTGTGG
Chr9	23824554	6.4	tGTGgGTGAGTGTGTGCGTGAGA
Chr1	48305038	6.4	tGTGgGTGAGTGTGTGTGTGTGG
Chr22	33161120	6.2	aGcGAGaGAGTGTGTGaGTGTGG
Chr10	130236827	6.2	GGTGTGTGTGTGTGTGCGTGCGG
Chr8	54584099	6.2	GGTGTGTGTGTGTGTGTGTGG
Chr1	59847610	6.1	acaGAGTGAGTGTaTGTGTGGGG
Chr3	58727139	6.1	tGgtgaTGAGTGTGTGTGTGTGG
Chr2	765652	6.1	taTGAaTGtGTGTGTGCaTGTGG
Chr18	50274481	6.1	GGTGTGTGAGTGaGTGaGTGCGG
Chr11	41554134	6.0	GGTGTGTGTGTGTGTGTGTGG
Chr5	21934229	6.0	tGTGTGTGAGTGTGTGTGTGTGG
Chr1	208239410	6.0	tGTGTGaGtGaGTGTGTGTGTGG
Chr5	150224721	6.0	aGTGAGaGtGTGTGTGTGgGGGG
Chr10	99685339	5.9	tGaGAGTGAGTGTGaGaGTGGGG
Chr6	89076647	5.9	tGTGAGTGTaTGTGTGTGGGG
Chr12	592739	5.9	GGTGtagtgGTGTGTGCcTGTGG
Chr13	90418142	5.8	tGTGTGTGTGaGTGTGTGTaTGG
Chr11	40324874	5.8	tGTGTGTGAGTGTGTGCaTGTGA
Chr18	23286405	5.8	cGTGAGTGTGTGTaTGCGTGTGG
Chr4	7430877	5.8	caTGcGTGAGTGTGTGCaTGGGG
Chr12	114752937	5.8	tGTGAGTGAGTGTGTGCaTGTGA

Chr17	1178800	5.7	aGTGtGTGAGTGTGTGtGTGAGG
Chr3	194073652	5.7	acTGAGTGAGTGTGaGtGTGAGG
Chr14	84459815	5.7	GGgtgagatGTGTGTGCaTGTGG
Chr20	25612568	5.7	GGTGtagtgGTGTGTGCCtTGTGG
Chr15	85046541	5.7	tGTGtGTGAGTGTGTGCaTGTGG
Chr3	169379105	5.6	aGaGAGaGAGaGTGTGtGTGTGG
Chr2	238409544	5.6	GaaGAGTaAGTGTGTGtGTGGGG
Chr2	236425371	5.6	aGTGgaTGAGTGaGTGCaTGCGG
Chr11	8794152	5.6	GtaGAGTGAGTGTGaGaGTGTGG
ChrX	42430834	5.6	aGTGAGTGAGTGTGaGCGTGAAG
Chr2	121087513	5.6	aGaGtGTGAGTGTGTGtGTGGGG
Chr16	86214365	5.5	GGgGtGTGAGTGTGgtgcgtGTG
Chr6	43737471	5.5	GGTGAGTGAGTGTGTGCCGTGTGG
Chr1	238722563	5.4	GGTGtGTGtGTGTGTGCCGTGTGG
Chr17	78954441	5.4	tGTGAGTGAGTGTGTGtGTGTGA
Chr8	20109735	5.4	aGTGtGTaAGTGTGTGaGTGGGG
Chr7	23276732	5.4	aGTGAGTGtGTGTGTGtGTtGGG
Chr2	124275984	5.4	aGTGAaTGtGTGTGTGCaTGTGG
Chr11	131931836	5.4	tGTGAGTGcGTGTGTGtGTGTGG
Chr5	139122257	5.3	tGTGAGTGcGTGTGTGaGTGTGG
Chr5	155118304	5.3	tGTGAGaGAGTGTGTGCaTGTGA
Chr5	159012346	5.3	tGTGtGTGAGTGTGTGtaTGTGG
Chr11	78932523	5.3	GGTGAGTttGTGTGTGgGTGTGG
Chr13	60101377	5.2	GGTaAaTGAGTGTGaGgcatGGG
Chr1	18868939	5.2	GGaGtGTGAGTGTGTGaGTGCGG
Chr5	178746539	5.2	tGTGAGTGAGTGcaTGtGTGTGG
Chr6	129056545	5.1	tGTGtGTGAGTGTGTGtGTGTGG
ChrX	99664994	5.1	GaaGAGTGAGTGTGTGgtgtGGG
Chr11	61485469	5.1	GcaGAGTGAGTGTGTGtGTtGGG
Chr4	187327499	5.0	caTGAGTGtGTGTGTGaGTGTGG
Chr9	95974277	5.0	tGTGAaTGAGTGcGTGaaTGGGG
Chr13	91706956	5.0	aGTGtGTGAGTGTGTGaGTGAGG
Chr2	73317050	4.9	GGTGAGTcAGTGTGTGaGTGAGG
Chr12	6937056	4.9	GGTGgaTGAGTGTGTGtGTGGGG
Chr5	132802864	4.9	tGaGAGTGAGTGTaTGaGTGTGG
Chr1	229141145	4.9	tGTGtGTGAGTGTGTaCaTGAGG
Chr2	123052110	4.8	GGTattTGAGTGTGTaCaTGTGG
Chr2	171597348	4.8	acTGAcTGAGTGTGaGCaTGTGG
Chr5	56989649	4.8	aaTGAGTGtGTGTGTGtaTGGGG
Chr7	117741100	4.8	GGTGtGTGtGTGTGTGCCGTGTGG
Chr1	207097588	4.8	GtaGAGTGtGTGaGTGtGTGGCG
Chr10	28251664	4.7	GaTGAGTGtGcGTGTGCaTGAGG
Chr11	74904632	4.7	accagGTGAGTGTGTGCCGTGGGC
Chr14	28518304	4.6	tGTGAGTatGTGTGTGtGTGTGG
Chr10	95051225	4.6	ccTGAGcGAGTaTGTGCaTGTGG
Chr1	181557204	4.6	GGaGAGTGAGTGTGTGCaTGTGC
Chr10	120245284	4.6	GGTGtGTGAaTGTGTGtGTGTGG
Chr7	87667089	4.5	aGaaAGTGAGTGTGTGtaTaAGG
Chr3	155092668	4.5	aGTGcaTGAGTGTGTatGTGAGG
Chr12	31106567	4.4	GcTGAGTGtGTGTGTGCCGTGTAG
Chr20	2780911	4.4	GGTGAGTGAGcGaagGaGTaGGG
Chr8	107510883	4.3	tGTGAGTGtGTGTGTGaGTGTGG

Chr2	81220097	4.3	tGTGAGTGtaTGTGTGtGTGTGG
Chr20	36039815	4.3	taTGAGTGtGTGTGTGCacGTGG
Chr1	4770493	4.3	tGgGtGTGAGTGTGTGCGTGTGG
Chr14	102953779	4.3	tGTGAGTGtGTGTGTGCGTGCGC
Chr5	23562308	4.2	aGaGAGaGAGTGTGTGtGTGTGG
Chr11	62781473	4.2	caTGAGTGAcTGTGTGtGTGTGG
Chr21	30993730	4.1	GGTGtGTGtGTGTGTGtGTGGGG
Chr19	56497640	4.1	tGTGAGTGtGaGTGTGtGTtGGG
Chr15	37202049	4.1	tGTGtGTGgGgGTGgGgGTGGGG
Chr19	41713254	4.1	aGTGAGTGtGTaTGTGtGTGTGG
Chr3	184590078	4.0	aaTGAGTGtGTaTGTGtGTGTGG
Chr13	101257208	4.0	ttTGAGTGtGTGTGTGCaTGAGG
Chr11	133611177	4.0	tGcGtGTGAGTGTGTGCGTaGGT
Chr10	99306651	4.0	aGaGAGaGAGTGTGTGtGTGAGG
Chr10	61044507	4.0	GGgGtaaGgGTGTGTGtGTGTGG
Chr17	10029642	3.9	tGTGtGTGAGcGTGTGtGTGTGG
Chr5	149501694	3.9	GaTGAGTGAGTGTGTGaGTGAGA
Chr2	174931405	3.9	GGTGtGaGAGTGTGTGCGgaGGC
Chr4	168057437	3.9	tGTGtGTGAGTGTGTGtGTGTGG
Chr2	88996016	3.9	GaTGAGTttGTGTGTGtGTGGGG
Chr11	44999873	3.9	tGTGAGaGAaTGTGTGCGTGTGA
Chr8	135523492	3.9	tGaGAGTGAGaGTGTGtGTGGGG
Chr19	40596585	3.9	GGactGTGAGTGTGTGCGTGAGG
Chr18	60759565	3.8	tGTGAGTGgGTGTGTGtGTGTGG
Chr19	48782757	3.8	tGTGAGTGtGTGTGTGgGTGGGG
ChrX	41726218	3.8	GGTGAGTGAGTGaGTGaGTGAGG
Chr11	1004348	3.8	GGTGtagtgGTGTGTGCcTGTGG
ChrX	105614415	3.8	aGTGAaTGAGTGTGTGCaTGTGA
Chr7	77128126	3.7	tGTGtaTGAGTGTGTGtaTGCGG
Chr2	16837556	3.7	tGTGAGTGgGTGTGTGgGTGTGG
Chr8	121823447	3.7	tGaGtGTGAGTGTGaGCGTGCGG
Chr7	31100113	3.7	tGTGAagGAGTGTGTGtGTGTGG
Chr16	88218507	3.7	atTGtGTGAGTGTGTGCaTGTGG
Chr4	7132480	3.6	tGTGgGTGtGgaTGTGtGTGTGG
Chr12	129149692	3.6	taTGtGTGAGTGTGTGCaTaTGG
Chr4	183729842	3.6	tGTGgGTGgGTGTGTGCGTGTGG
Chr10	98760588	3.6	GtTGAGTGAAaTGTGTGCGTGAGG
Chr3	172121469	3.6	GGgaAGgGAGTGTGTGCaTGGGG
Chr2	4734730	3.6	GGgGAaTGAGTGTGTatGTGAGG
Chr5	31640966	3.5	aGTGAGTGtGTGTGTtgcgGGGG
Chr10	107228008	3.5	GGTGtGTGtGTGTGTGtGTGTGG
Chr16	23869051	3.4	aGaGAGTGtGTGTGTGtGTGTGG
Chr19	54524100	3.4	tGaGtGTGtGTGTGTGCGTGTGG
Chr5	134817941	3.4	caTGAGTGtGTGTGTGCtTGTGG
Chr17	50130332	3.4	GtgagtgatGTGTGTGtGTGTGG
Chr11	75330150	3.3	tGTGtGTGAGTGTGTGCaTGAGG
Chr13	110882529	3.3	tGTGtGTGAGTGTGTGCccGTGG
Chr5	84905674	3.3	tGTGtGTGAGTGTGaGtGTGTGG
Chr8	9768212	3.3	aGaGAGaGAGTGTGTGtGTGTGG
Chr12	124763151	3.2	tGTGAGTGtGTGTGTaCcTGGGG
Chr6	43905520	3.2	GGTGtagGAGTGTGTGtGTGGGG
Chr20	31382040	3.1	GGTGAGgtgGTGTGTGCcTGTGG

Chr16	73585926	3.1	aaTGAGTGAGTGTGTGtGTGTGA
Chr11	69518904	3.1	GGgGtGTGAGTGgGTGtGTGCGG
Chr12	131196667	3.1	GGTGgGTGAGTGaGTGaGTGAGG
Chr4	158621598	3.1	aGTGtaTGAGTGTtTGCaTGGGG
Chr7	134234248	3.1	aGTGAGTGAGTGaGTGaaTGTGG
ChrX	30439128	3.0	tGTGAGTGtGTGTGTGtaTGTGG
Chr5	73855632	3.0	GGTGtGTGAGaGTGTGtaTGTGG
Chr5	146520400	3.0	GGTGtGTGgGTGTGTGtGTGGGG
Chr12	125156261	3.0	GaTGAGTGtGTGTGTGtGTGCGG
Chr15	80907957	3.0	tGTGAGTGtGTaTGTGtGTGTGG
Chr14	78443706	3.0	tGTGtGTGtGTGTGTGtGTGTGG
Chr1	18837923	3.0	GGTGtGTGtGTGTGTGtGTGTGG
Chr1	35189392	3.0	tGTGtGTGAGTGTGTGtGTGGGG
Chr18	6110703	3.0	aGgatGTGAGTGTGTGCaTGTGG
Chr12	33270686	2.9	GGaGAaTagGTGTGTGCGTGGGG
Chr8	141037928	2.9	aGTGAGTGtGTGTGTGaagGAGG
Chr16	26809933	2.9	GaTGAGTaAGTGTcTGaGTGGGG
Chr8	21494840	2.9	tGTGAGTGtGTGTaTGCGTGTGA
Chr7	121687676	2.9	tGTGtGTGAGTGTGTGtGTGTGG
Chr9	29602720	2.9	GGgGtGTGtGTGTGTGtGTGTGG
Chr6	105265269	2.9	aGaGAGaGAGTGTGTGCaaGGGG
Chr10	43251651	2.9	GtaGgGTGgGaGTGTGtGTGTGG
Chr8	139883090	2.8	tGTGAGTGgGTGTGTatGTGAGG
Chr16	10276764	2.8	GGcGAGTGtGTGTGTGaGTGTGG
Chr14	90885641	2.8	GaTGtGTGtGTGTGTGCGTGTGG
Chr6	33999846	2.8	tGTtAGTGAGTGTGTGCagGTGG
ChrX	39606149	2.8	GaTGAGcGAGTGTGTGtGTaTGG
Chr17	6891149	2.7	GGTGAaaGAGTaTGTGtGTGTGG
Chr2	240564198	2.7	GGTGtGTatGTGTGgGgGTGTGG
Chr1	3325807	2.7	GGTGtGaGAGTGTGTGaGTGGGG
Chr12	2469347	2.7	GGgGtGTGtGTGTGTGtGTGTGG
Chr6	24574540	2.7	GGTGtagtgGTGTGTGCCtGTGG
Chr1	175049116	2.7	tGTGAGTGtGTGTGTGtGTGTGG
Chr3	3697106	2.7	GGTGtGTGtGTGTGTGtGTGTGG
Chr7	39341125	2.6	GGTGtGTGAGTGTGTGtGTGTGA
Chr20	23960933	2.6	GGTatGTGAGTGTGaGtGTGGGG
Chr19	54375904	2.6	GGTGtGgtgGTGTGTGCGTGTGG
Chr7	31353825	2.6	ccaGAaTGAGTGTGTGtGTGTGG
Chr3	79455732	2.6	tGTGtGTGAGTaTGTGtGTGTGG
Chr2	126515435	2.6	tGTGAGTGAAaTaTGTGtaTGTGG
Chr4	82574191	2.6	GGTatGTGAGTGTGTGtaTaTGG
Chr1	3002774	2.5	GGTGAGctcGTGaGTGCGTGAGG
Chr17	43132890	2.5	aagtgagGAGTGTGTGCCtGTGG
Chr18	74103175	2.5	GGTGAGTaAGTGTGaGCGTaAGG

EMX1			
Chr	Position	DNA cleavage Score	DNA seq at a cleavage sites
Chr11	62365273	77.2	GAaTCCaAGCAGAAGAAGAgAAG
Chr19	1438827	59.7	GAagtaGAGCAGAAGAAGAAGCG
Chr2	73160999	58.9	GAGTCCGAGCAGAAGAAGAAGGG
Chr1	234492864	49.5	GAagtaGAGCAGAAGAAGAAGCG
Chr2	172374203	40.3	GAagtaGAGCAGAAGAAGAAGCG
Chr2	219845073	38.3	GAGgCCGAGCAGAAGAAgACGG
Chr1	23720618	37.5	aAGTCCGAGgAGAgGAAGAAAGG
Chr12	106646091	29.5	aAGTCCatGCAGAAGAgGAAGGG
Chr15	44109764	28.4	GAGTCtaAGCAGAAGAAGAAGAG
Chr8	128801260	27.9	GAGTCctAGCAGgAGAAGAAGAG
Chr15	22366622	23.3	GgagtaGAGCAGAgGAAGAAGGG
Chr9	127309505	22.3	aAGcCCaAGCAaAtGAAGAATGG
Chr11	43747949	21.7	aAGcCCGAGCAaAgGAAGAAAGG
Chr5	9227163	21.3	aAGTCtGAGCAcAAGAAGAATGG
Chr10	128080196	19.6	GAGTaCaAGCAGAtGAaAaACGG
Chr1	33606480	19.2	GAGcCtGAGCAGAAGgAGAAGGG
Chr3	34042974	17.8	GAGTtCaAGCAGAgAgaAAGGG
Chr21	24667742	16.7	cccTCCaAGCAGAAGAAGAtGAG
Chr14	38654666	16.5	aAGTCtGAGaAGAAGAAGAcATG
Chr5	45359067	16.3	GAGTtaGAGCAGAAGAAGAAAGG
Chr18	68861321	16.0	agagtaGAaCAGAAGAAGgAAAG
Chr4	87256692	15.9	GAGTaaGAGaAGAAGAAGAAGGG
Chr10	58848729	15.7	GAGcaCGAGCAagAGAAGAAGGG
Chr8	74634212	15.5	aAGTCCaAaaAGAAGAAaAAAGG
Chr19	24250503	14.7	GAGTCCaAGCAGtAGAgGAAGGG
Chr8	105164126	14.3	GAGcCCaAGaAGAAGAAGAAGGA
Chr14	43156807	14.1	GAGgCCaAGCAGAAaAAaAATGG
Chr11	30301809	14.0	cAGTCtGAGtAGAAGAAaAAGGG
Chr4	58838593	13.8	aAGTCCcAGaAGAAGAAatATGG
Chr15	65614525	13.6	GAGaggGAGCAGggagAagAAGG
ChrX	149010707	13.5	GgagtCaAGgAGAAGAAGAAGAG
Chr7	111475449	13.0	GAGcCCaAGCAcAAaAAGAATGG
Chr14	48932120	12.9	GAGTCCcAGCAaAAGAAGAAAAG
Chr10	91416162	12.8	atGTCCaAGCAGAAGAAGtcTGG
Chr12	102743729	12.2	tAGTCaGAGCAGAtGAAGgAAAG
Chr3	95690186	11.8	tcaTCCaAGCAGAAGAAGAAGAG
Chr3	16077518	11.7	GAGgCaGAGagaAAGAAGAAAGG
Chr12	73504675	10.6	GAGTtaGAGCAGAAaAAaAATGG
Chr6	9118799	10.4	acGTCTGAGCAGAAGAAGAATGG
Chr5	141129457	10.4	aAGTCacAGgAGcAGAAagAAGA
Chr7	31901077	10.3	GAGgCCaAGCAGAAagAaAAAGG
Chr1	209931600	10.3	ttaTCCGAGaAGAAGAAGtAAGG
Chr6	106901799	10.2	GAGcCgGAGCAGggagAagAAGG
Chr22	34858917	10.2	GAGcCtGAGCAGgAagAagAAGA
Chr6	29806752	10.2	tgctCaagGCAGgAGAAGAAGGG
Chr15	36839471	10.0	cAGagaGAGgAGcAGAAaAAAGA
Chr5	134375867	9.6	cAGgCtGAGCAGAAagAagAAAG
Chr2	199919487	9.6	GAGTCaGAGCAGAActAGAAGGG
Chr20	6653999	9.6	aAGTCCagaCAGAAGAAGAAGGA
Chr8	135098073	9.5	cAGTCCagcagGAAGAAGAgAGG

Chr11	131106371	9.0	GccTCCaAGCAGAAGgAGAAATG
Chr9	2513258	9.0	GAGagaGAGCAaAAGgAagAATG
Chr17	72057114	9.0	GAGgagagcagaAAGAAGAAGGG
Chr16	56184077	8.9	aAGTCaGAGaAGgAagAagAAAG
Chr5	146833190	8.9	GAGcCgGAGCAGAAGAAGgAGGG
Chr5	120294736	8.8	atGTCCaAGCAcAAGAgGAATGG
Chr1	113741471	8.7	GAGgtaGAGCAGAAGAAGAAGCG
ChrX	38971206	8.7	GAGTCCcAGaAGAAGAAgAAAG
Chr4	2181662	8.6	cctctCGAGCAaAAGgAagAAGG
Chr14	75723908	7.8	agtTCCaAGCAGAgGAAGAAGGG
Chr4	155734338	7.7	tgcTttGAGCAGAAgAagAAAG
Chr4	122686219	7.7	aAGTaaGAagAGcAGgAagAAGA
Chr12	4927416	7.5	tAGTCCtAGCAagAatAagAATG
Chr3	5031614	7.4	GAaTCCaAGCAGgAGAAGAAGGA
Chr2	106719739	7.3	tAaTgaGAGCAGAAgAagAATG
Chr7	142597224	7.3	GAcagaGAagAGAAGAAGgAAGA
Chr1	27913391	7.2	agGTCaGAGCAGAAGAAaAgAGG
Chr7	73602675	7.2	GcaaagagcagGAAGAAGAAGGG
Chr18	34906762	7.1	GAGcCtGAGCgGAAGAgGAAAGG
Chr2	45607957	7.0	tAaTCCcAGagcAgGAAGAAGAA
Chr18	1677040	6.9	agtcCaGAGCAaAAAtAAGAAGGG
Chr4	44622977	6.9	aAGTCtGAGaAGAAGAAGAAAGA
Chr12	2873991	6.9	GctaaaGAGCAGAAGgAagAAGG
Chr2	239393515	6.8	cAGTaCGAGCAGAgGAAGgAAGA
Chr8	102244552	6.6	agtTCCaAGCAGAAGAAGcATGG
Chr2	66582071	6.6	atGgCaGAGCAGAAgAagAAAG
Chr11	69660352	6.3	cAGTCCatGCAGAgGgAagAAGG
Chr11	130764292	6.3	GcaTtaGAGCAGAAGgAagAAGG
Chr1	231750743	6.2	GAGTCaGAGCAaAAGAAGtAGTG
Chr6	36604882	6.1	GgcagaGAGCAGAAGgAagAAAG
Chr15	61646878	6.0	aAGTCaGAGgAGAAGAAGAAGGG
Chr7	141972562	5.9	aAGTCCGgGCAaAAGAgGAAAGG
Chr12	111418051	5.9	GAGaggGAGCAaAAGAAGgAAGG
Chr9	72899757	5.8	cAGaatGAGCAGgAagAagAACA
Chr17	8640231	5.7	GAGaCtGAGaAGAAGAAGAAAGG
Chr1	84869216	5.7	GAGTCaGctgAGcAGAAGgAAGA
Chr4	41187173	5.7	GAaggaGAGCAGAAgAagAAAG
Chr9	130107853	5.4	GttTgaGAGCAGAAGgAagAAGA
Chr11	118816273	5.3	attTCCaAGCAGAgagAagAATG
Chr8	72482455	5.3	GAGTCCGAGaAGAAGAAgAAAA
Chr1	221522625	5.1	GAGTttGAGtAGAAGAAGAAGAG
Chr21	37132446	4.9	tgGcCaGAGCAGAAGgAagAAGG
Chr2	217972073	4.9	tgtcCgagGCAGtAGAAgAACG
Chr5	35927682	4.8	aAGcCCGAGCtagAagAaAtAGG
Chr3	157623637	4.7	aAGgggagcagGAAGAAGAAAGG
Chr20	14924870	4.6	aAGaagGAGCAGgAagAagAAAG
Chr4	48639408	4.4	cAcTCCaAGtAGAAGAAGAAAAAG
Chr9	91487902	4.4	GAGgCaGAGagaAgaAAGAAGGG
Chr2	105425353	4.3	agaTCCaAaCAGAAGgAagAATG
Chr7	100895242	4.3	cgcTCCGAGCAGAAGAAaAgTGG
Chr7	93390477	4.3	agtcCtGAGCAGAgGAAGgAATG
Chr1	179024805	4.2	GAGTCCaAGaAGAAGAAGccAGG

Chr17	54421043	4.2	GAGTCCcAGgAGAAGAAGAgAGG
Chr8	108409228	4.2	tgtTgaGAGCAGAAgAagAAAG
Chr15	68455211	4.2	GtccaaagGCAGgAGAAGAAGGG
Chr14	88550473	4.2	GAGggaGAGagcAgGAAGAAGAA
Chr12	124551806	4.1	ttGTtgagcagGAAGAAGAATGG
Chr18	32722290	4.1	tgtcCaGAGCAGAtGAAGAATGG
Chr7	97319990	4.1	GAaTCCaAGCAGAAGAAaAtGGA
Chr7	3812781	4.1	GAGTCCtAGaAaAAGAAGAgAGG
Chr11	36270410	3.9	GAGagaGAGCAGAAGAAGtAGAG
Chr18	25950253	3.9	agGcCtGAGCAGAAGgAagAAGG
Chr15	100292479	3.8	aAGTCCcgGCAGAgGAAGAAGGG
Chr3	169381222	3.8	GAGggaGAGCAaAAGAAGgAAAG
Chr5	74513307	3.8	GtccatagcaAGAAaAAGAAGGG
Chr2	238373187	3.8	agtgCaGAGCAGAAGAAGgAAAG
Chr7	70109967	3.7	GAaTCaGAGCAaAAGgAGAAAGG
Chr6	110491414	3.7	aAGTCaGAGCAGAAaAAGAgAGG
Chr1	151027598	3.6	ttcTCCaAGCAGAAGAAGAAGAG
Chr9	135663404	3.6	cAGTCCaAaCAGAAGAgGAATGG
Chr6	147955462	3.5	tgGcCaGAGCAGAAGgAagAAAG
Chr9	140936012	3.4	GAGTCaaAGCAGAAGAAgAACG
Chr14	35092801	3.4	tAtCaagcagGAAGAAGcAAGG
Chr17	73339913	3.3	tgcaCgagcagGgAGAAGAAAGG
Chr4	82567700	3.3	tAtTtacAGagcAgGAAGAAGAG
Chr14	98020018	3.3	cAtTCCaAGCAGAAGgAagAGAG
Chr9	119853407	3.3	tAccagGAGCAGgAaAAagAAGG
Chr7	29268537	3.2	GAGcggGAGCAaAAGgAagAATG
Chr3	9802191	3.1	GtacCCaAGCAGAAGgAagAAGG
Chr18	24570836	3.1	cctgaaGAGCAGAAGgAGgAAGG
Chr13	101018849	2.8	GtcTgaGcagAaAgGAAGAAGGG
Chr10	8337281	2.8	GAagtCagaCAGAAGAAGAAGAG
Chr15	68619369	2.8	GAGaaaGAGCAGAAGgAagAAGT
Chr2	218378108	2.8	GAGTCtaAGCAGgAGAAaAAAGG
Chr1	2744291	2.8	GgtcCaGAGagaAAGAAGAAAGG
Chr16	78848850	2.7	aAaTCCaAcCAGAAGAAGAAAGG
Chr10	5401788	2.7	tAaTCCaAtCAGAAGAAGAAGGG
Chr11	30490142	2.7	GAGagaagcagaAAGAAGAAAGG
Chr17	21133222	2.7	GAaTCCcAGCAGAAaggaAgAAA
Chr6	12210833	2.6	atGaatGAGCAGAAGgAGgAAAG
Chr7	43259054	2.6	GAtaCCGAGCtaAAGAAGgAAGG
Chr22	47725583	2.6	GAagagGAGCAGAAGgAGgAAGG
Chr11	56910170	2.6	accTggGAGCAGgAaAAagAAGG

FANCF			
Chr	Position	DNA cleavage Score	DNA seq at a cleavage sites
Chr7	102131659	114.4	GtctcCCCTTCTGCAGCACCAGG
Chr11	22647338	88.1	GGAATCCCTTCTGCAGCACCTGG
Chr10	73463136	82.0	tGAATCCCaTCTcCAGCACCAGG
Chr10	37953200	74.1	GGAgTCCCTcCTaCAGCACCAGG
Chr10	43410031	60.2	GGAgTCCCTcCTaCAGCACCAGG
Chr7	44076497	56.5	GtctcCCCTTCTGCAGCACCAGG
Chr18	8707528	47.1	GGAACCCcGtTCTGCAGCACCAGG
Chr16	49671025	43.8	GGAgTCCCTcCTGCAGCACCTGA
Chr3	35113165	40.8	tGAATCCtaaCTGCAGCACCAGG
Chr7	102230832	34.0	GtctcCCCTTCTGCAGCACCAGG
Chr20	44903573	33.8	tccATCCCTaCTGCcagcaCCAG
Chr11	66475045	33.1	GGAACAaCCTTCTGCAGCtCCAGG
Chr3	10885901	31.7	acccTCCCTTCTGCAGgcaCCGG
Chr10	3151994	27.9	ctctgtCCTTCTGCAGCACCTGG
Chr17	39675789	26.8	GGgAgtCCaTCTGCAGCACCAGG
Chr11	47554037	19.3	GGAATCCCTTCTaCAGCAtCCTG
Chr2	54853314	17.4	GGAATatCTTCTGCAGCcCCAGG
Chr12	115467808	17.2	aGggTCCCTTCTGCAGCcCCTGG
ChrX	86355180	16.2	accATCCCTcCTGCAGCACCAGG
Chr2	35692938	13.1	acttTatCTTCTGCAGCACCTGG
Chr2	133174786	11.4	atccTttCTTCTGCAGCACCTGG
Chr12	2719895	10.6	acAcTCCCTTCTGCAGCACCATG
Chr16	28615201	10.0	GGctTCCCTTCTGCAGCcCCAGG
ChrX	97566910	9.8	tGtATtCCTTCTGCAGgcaCCAG
Chr17	30452575	8.9	cctgctgCTTCTGCAGCACCTGG
Chr9	113162294	8.9	aaAATCCCTTCCcGCAGCACCTAG
Chr4	53092937	7.1	aatATtCCcTCTGCAGCACCAGG
Chr3	97725864	6.9	accATttCTTCTGCAGCACCTGG
Chr17	34985068	6.8	GGgtcCgCTTCTGCAGCACCTGG
Chr9	111467809	5.3	aGgAatCCTaCTGCAGCACCCAG
Chr4	76159966	4.9	ttAcTCaCTTCTGCAGgcaCCTG
Chr5	68338523	4.7	ccAcTCCtTTCTGCAGCACCCGG
Chr17	3980376	4.6	GGAACCCcTCTGCAGCtTCTGG
Chr20	19790626	4.2	cattTtCtTTCTGCAGCACCTGG
Chr17	78923978	4.2	aGAggCCCcTCTGCAGCACCAGG
Chr8	71384404	4.0	tttcctgCTTCTGCAGCACCAGG
Chr17	39655735	3.8	GccccCtCcTCTGCAGCACCTGG
Chr6	41457565	3.4	ctccTCCCTcCTGCAGCACCTGG
Chr13	109802140	3.2	aaAATaCCTTCTGCAGtACCAGG
Chr5	85696042	3.1	ctAcTgaCTTCTGCAGCACCTGG
Chr4	7336836	3.0	aGctcCCaTTCTGCAGCACCCGG
Chr9	139891539	3.0	aGttcCCCaTCTGCAGCACCAGG
Chr10	13436789	2.9	ctcATCCCTTCTGCAGCcCCAGG
Chr2	176121765	2.7	GccccCtgcTCTGCAGCACCCGG
Chr13	100011450	2.7	acctgCCtTctgGCAGCACCAGG
Chr17	8432606	2.5	actgTCatTTCTGCAGCACCTGG

RNF2			
Chr	Position	DNA cleavage Score	DNA seq at a cleavage sites
Chr1	185056773	69.6	GTCATCTTAGTCATTACCTGAGG
Chr12	131619805	12.3	aTCAcCTTAGcCATTACCaGGGG
Chr18	62061226	9.8	aTtATtTTAGTCATTACCTtTGG
Chr8	99451745	8.2	cgtgcaTTAGTCATTACCTGAGG
Chr7	43967267	7.0	acttatTTAGTCATTACCTGTAG
Chr6	143212079	6.7	GTaATaTTAGTCATTACCGGTGG
Chr4	171989625	5.9	taacaCaTAGTCaCTACCTGGTG
Chr8	5745882	5.8	aatATgTTAGTCATTACCTGAGG
Chr4	189725512	3.5	aTgcTtcTtGTCATTACCTtGGG
Chr9	138721895	3.2	acttcagTAGTCATTACCTaGGG
Chr5	92036966	3.0	GgtATCTaAGTCATTACCTGTGG
Chr15	25135467	3.5	catcTaaTAGTaATTACCTGGGG
Chr17	53928586	3.2	GTCATCTTAGTCATTAC-TGAGG

HEK293-1			
Chr	Position	DNA cleavage Score	DNA seq at a cleavage sites
Chr1	201992441	98.3	GGGAAAGtCCCAGCATCCtTTGG
Chr9	110103705	84.0	GGGAAAGACCCAGCATCCGTGGG
Chr22	47970525	77.3	GGaAAAGACCaAGCATCaGTGGG
Chr8	21121524	66.3	GGGAAgGACCCAGCATCCtgGGG
Chr9	129621088	61.9	GGGAAAtACCCAGCATCCaaTGG
Chr10	123094947	31.7	GGGAAAagCCCAGCATCCcTTGG
Chr10	86303625	26.1	tGGAAAGAAaCAGCATCCGTACG
Chr11	75956264	20.4	ttatAAGACCCAGCATCCGTAAG
Chr12	5555206	19.8	GGagAAagaCCAGCATCCaTAGG
Chr4	8541711	11.6	GGGAAAtcCCCAGCATCtcTAGG
Chr5	65217522	8.9	GGaAAgtACaCAGCATCCaTCGG
Chr1	3488120	7.9	GGGgAAGACCCAGCAcCCtTGGG
Chr13	31633478	7.4	atGAAAGACCCAGCATCCaTTGA
Chr19	30027761	3.1	aGGAttccCCaAGCATCCGTGGG
Chr8	48879627	2.8	GaGAAAagCCCAGCATCCtTAGG
Chr2	85388185	2.6	GGGAAtacaCCAGCATCCGTAGA

HEK293-2			
Chr	Position	DNA cleavage Score	DNA seq at a cleavage sites
Chr5	87240614	48.7	GAACACAAAGCATAGACTGCGGG
Chr4	90522184	37.7	GAACACAAtGCATAGAtTGCCGG
Chr10	43159340	33.6	aAcacaAAgaCATAGACcaCTGG
Chr1	40461425	30.0	tAcacacAAGCAcAGACTGCAGG
Chr2	19844956	25.2	aActcCAAAGCATAtACTGCTGG
Chr15	93557679	24.8	agAacacAtGCATAGACTGCTAG
Chr11	128508577	24.4	GAAttCAAAGCATAGAtTGCAGG
Chr5	131174461	21.2	aAAtACAAtGCATAGACTGCTAG
Chr19	30112719	21.0	tAcacaAAAcataAGACTGCTGG
Chr20	97641	19.2	GAAttCAAAGCATAGAtTGCAGG
Chr4	53536210	18.0	GAAtACTAAGCATAGACTcCAGG
Chr13	113428467	17.1	cAAtACAAAGgATAGACTGCAGG
Chr18	22360702	16.7	GgAatCAAAGCAcAGACTGCAGG
ChrX	36949815	15.5	GAAaACAAAaCATAGAgTGCTGG
Chr7	83764327	11.3	actatatAAGCATAGACTGtTGG
Chr5	126385455	10.7	ccACACcAAGCATAGACTtCTGG
Chr5	142142325	10.7	tAAacactAaCATAGACTGCAGG
Chr18	56307003	8.5	aAgaACAAAaCATAGACTGCAGG
Chr1	36097073	8.5	GtAaACAAAGCATAGACTGaGGG
Chr3	81710854	8.5	ctcCtaAAgcatTAGACTGCAGG
Chr5	7625837	6.4	GgtacacAAtaATAGACTGCAGG
Chr18	5596266	5.9	cctacagAAGCATAGACTGCAGG
Chr6	139353018	5.8	ccAaACAAAaCATAGACTGCTGG
Chr22	28895718	5.1	attaAgAtAGCATAGACTGCAGG
Chr1	77190607	5.1	tcACACAAAcCATAGACTGaGGG
Chr6	40925010	4.7	aAcaAgtAtGCATAGACTGCTGG
Chr9	97332609	3.9	GtAattAAAGCAcAGACTGCTGG
Chr18	68431104	3.6	tgtgtaAgAGCATAGACTGCTGG
Chr20	23101380	3.4	atACACAgAGCAaAGACTGCAGG
Chr8	97317605	3.0	GAACACAgtaCATAGACTGgCAG
Chr9	290168	3.0	aAACAtAAAGaATAGACTGCAAG
Chr6	152710071	3.0	tActctAtAtCATAGACTGCTGG
Chr4	31157435	2.8	tgAttgAgtGCATAGACTGCTGG
Chr1	108869935	2.8	agtatagcAGCATAGACTGCAGG
Chr15	65377019	2.6	GAgCgatAAGCAcAGACTGCTGG

HEK293-3

Chr	Position	DNA cleavage Score	DNA seq at a cleavage sites
Chr15	79749931	65.9	caCCCAGACTGAGCACGTGcTGG
Chr10	131593121	49.7	GagCCAGAAaTGAGCACGTGAGGG
Chr1	47005705	47.4	aGcTcAGACTGAGCAaGTGAGGG
Chr7	66968042	47.1	GaCaCAGACcGgGCACGTGAGGG
Chr9	110184637	46.5	GGCCCAGACTGAGCACGTGATGG
Chr11	134582415	44.5	GGCgCAGACaGAGCACGTGACGA
ChrX	114764149	27.2	aGaCCAGACTGAGCAaGaGAGGG
Chr4	72203005	23.0	atatCAGACTGAGCACcgtgAGG
Chr6	103918240	23.0	aaataAGACTGAGCACGTGgTGG
Chr17	7594610	23.0	aGCCagactgagGCAaGTGAGGG
Chr3	160129761	18.3	aGgCCAGACTGAaCACGatgAGG
Chr15	35402774	16.3	cctaaAGACTGAGCAaGTGAAGG
Chr9	137039236	15.9	cagCCAGACaGAGCACGTGgAGG
Chr6	79958440	14.7	aaCaaAGACTGAGCACGTtAGGG
Chr2	130402896	10.5	GaCCCAGAAaTGAGCACaaaAGGG
Chr1	34163192	10.0	attCtAGACTGAGCACGTGcAAG
Chr2	97163211	9.3	ccCatgGACTGAGCACaTGAAGG
Chr17	79043523	7.2	tGgCCAGACTGAGCtCGTGAGTG
Chr10	22896606	6.5	GaaggAGACTGAGCAtGTGAGGG
Chr8	20947876	5.7	tctCCAGACTGAGCcCaTGAGGG
Chr19	19169358	5.2	GGaCCAGgCTGAGCACaTGgAGG
Chr6	112273496	5.1	aagCCAGACTGAGCACGTtAGG
Chr1	229294224	4.6	GGtCatcACTGAGCACGTGAGGT
Chr2	240026760	4.3	GGCtCAGACTGAGCACcTGAGAG
Chr15	94188821	4.3	attCCAGAAaTGAGCACaTGAAGG
Chr2	131090691	4.1	acCCaAGACaGAGCACGTGgAGG
Chr11	60830962	3.9	tcCCagaACTaAGCACGTGAATG
Chr14	102917106	3.7	ctCggAGACTGAcCACGTGAGGG
Chr10	23135503	3.2	actCCAGACTGAGCAacTGAGGG
ChrX	16606309	3.1	ttCCCAGACaaAGCACGcGAAGG
Chr14	78070357	2.6	aaCCagactgGAGCACGTGgTGG

HEK293-4

Chr	Position	DNA cleavage Score	DNA seq at a cleavage sites
Chr15	75632142	79.5	GcacCTGCGGCTGGAGGTGGCAG
Chr1	201067378	65.7	GGCACTGCTgCTaGAGGTGcAGG
Chr16	50300347	64.9	aGCACTGtGGCTGGgGgaGGGGG
Chr4	56815199	64.9	GGCAaTGCGGCTGGAGGcGGAGG
Chr11	528949	64.7	GGCtCTGCGtCcGGAGGTGaGAG
Chr9	139522901	64.5	GcCACaGCGGCcGGAGGTGGCAG
Chr20	60895671	64.3	GGCACaGCaGCTGGAGGTGcTGG
Chr16	28266968	61.8	GGCtCTtCGGCTGGAGGTaGCGG
Chr15	41044242	61.3	GGCgCTGCGGCgGGAGGTGGAGG
Chr7	134872032	59.3	aGCACTGtGGCTGGgGgaGGCGG
Chr14	21993455	58.0	GGtACaGCGGCTGGgGgaGGCGG
Chr5	141232854	57.7	GGCACTGCGGCaGGgaGgaGGGG
Chr12	113935461	57.1	GGCcCTGCGGCTGGAGaTatGGG
Chr7	1397399	56.2	aGCACTGCaGCTGGgaGTGGAGG
Chr18	37194558	55.8	GGCACTGCGGgTGGAGGcGGGGG
Chr10	126694875	55.8	GGCACgaCGGCTGGAGGTGGGGG
Chr3	51725452	54.6	GGCtCTGtGGCTGGAGGaAGGTGG
Chr22	23284036	51.7	GGCcCTGCTGCTGGAGGTGcTGG
Chr15	80601340	50.4	GaCACctCGGCTGGAGGTGcAGG
Chr13	39262929	50.3	aGCAgTGCGGCTaGAGGTGGTGG
Chr19	33382081	50.3	GGCtCTGCGGCTGGAGGgGGTGG
Chr20	1151854	49.7	GGCACTGtGGCTGcAGGTGGAGG
Chr17	16982386	49.5	cagACTGCGGCaGGgGGTGGCGG
Chr7	139244407	49.4	GcCACTGCGaCTGGAGGaGGGGG
Chr7	54561438	49.1	aGgACTGCGGCTGGgGGTGGTGG
Chr1	32471660	48.4	GGCACTtCaGCTGGAGGcaGAGG
Chr19	1295087	47.5	GaCACTGaGGCaGGAGGTGGGGG
Chr20	31349773	46.5	GGCACTGCGGCTGGAGGTGGGGG
Chr1	171018460	45.9	GcCACTGgGGCTGGgGGTGGGGG
Chr10	52054245	45.7	GGCcCTGCTaCTGGgGGTGGTGG
Chr3	123863990	45.4	tGCcCaGCaGCTGGAGGTGaGGG
Chr20	60080554	45.3	aGCACTGCaGaTGGAGGaGGCGG
Chr9	133039176	45.2	GtCACTGCaGCTGGAGGaGGGGG
Chr20	60010563	44.9	tGCACTGCGGCcGGAGGaGGTGG
Chr3	130508525	44.8	GaCACTGtGGCTGGAaGTGGAAG
Chr19	41220525	44.0	GGCAaTGtGGCTGaAGGTGGGGG
Chr22	35746283	44.0	GaCACTagGGCaGGAGGTGGAGG
Chr6	51500473	43.4	GaCACaGtGGCTGGAGGTGtGGG
Chr15	60790562	42.6	GGCACTGCaaCTGGAaGTGaTGG
Chr13	27629410	42.3	GGCACTGgGGtTGGAGGTGGGGG
Chr9	5020591	41.7	tGCACTGCaGCTGcAGGTGGAGG
Chr19	38616186	41.6	GGCACTGaGaCTGGgGGTGGGGG
Chr22	30130865	41.3	GGCtgTGCGGCcaGAGGTGGAGG
Chr8	144997514	41.1	aaCACTGCGGCTGcAGcTGGAGG
Chr10	45317434	40.9	GGCtCTGCaGCTGtAGGaGGAGG
Chr2	241640854	40.7	GGggCTGCGGCcGGAGGTGGTGG
Chr20	37471343	40.3	aGCACTGtGcCTGGgGGTGGGGG
Chr10	127971444	40.2	GGaACTGgGGCTGGgGGTGGGGG
Chr8	11479079	39.9	GGCcCTGCaGCTGGAGaTGGAAAG
Chr15	71686928	39.7	tGcTCTGCGGCaGGAGGaGGAGG

Chr12	54977735	39.6	GaCACTGCctCTGGgGGTGGGGG
Chr20	24376057	39.4	GGCACTGaGaCcaGAGGTGGTGG
Chr5	177676326	39.3	GcCACTGtGGCTGGAGGTGGGGA
Chr3	23651530	38.8	GGCACaGCaGgTGGAGGTGGAGG
Chr7	110143151	38.7	GcCACTGCaGCTaGAGGTGGAGG
Chr2	25348467	38.4	GGaACTGtGGCTGGAGGTGGCAG
Chr19	56125854	37.6	GGCcCaGCGGCgGGAGGTGGGGG
Chr10	1285239	37.5	GGCcCTtCGGCTGGAGGTGGCAG
Chr8	119227146	37.0	GGCACaatGGCTGGAGGTGaAGG
Chr20	45343011	36.3	GGCACTGaGGgTGGAGGTGGGGG
Chr5	3606830	36.2	GaCACaaCGGCaGGAGGTGGCGG
Chr10	126752487	35.4	GGCACTGCaGCctGgGGgtGGGG
Chr20	61810739	35.2	GtCACTGCGGCTGcAGaTGGCGG
Chr22	41620073	34.6	GGgcaTGCGGCTGGAaGTGGTGG
Chr8	20854500	34.1	GGCACTGgGGCTGGAGacGGGGG
Chr22	49132903	34.0	aGCACaGCaGCTGcAGGTGGGGG
Chr1	230193260	33.7	GaCtCTGCaGCTGaAGGTGGGGG
Chr11	118950338	32.6	GtCACTGaGGCTGGAGtgGaGGG
Chr20	22805414	31.9	aGCACTGttaCaGGAGGTGGGGG
Chr6	158452389	31.8	aGcTCTGtGGCTGGAGGTGtGAG
Chr19	46887174	31.6	GaggCTGCGGCTGGgGGTGGAGG
Chr22	43768275	30.9	aGCACTGCGctTGGgGGTGGGGG
Chr15	34081546	30.6	aGCACTGtaGCaaGAGGTGGAGG
Chr3	53375995	30.6	GGCtCTGaGGCcaGAGGTGGTGG
Chr10	77103120	30.4	GGCAtcaCGGCTGGAGGTGGAGG
Chr10	73435248	30.3	GtaACTGCGGCTGGcGGTGGTGG
Chr5	96338759	30.0	aGCACTGgGGaTGGAGGTGtAGG
Chr1	44397932	29.9	aGaACTGcTgCTGGAGGTGGTGG
Chr5	1832938	28.6	GGCtCTGtGGCcGGAGGaGGCGG
Chr6	160517881	28.4	GGCACTGcTgCTGGgGGTGGTGG
Chr9	140205577	28.1	GGCcCTGgGGCTGGAGGTGtTGG
Chr6	33950129	27.3	GGCtCTGaGGCTGGtGGTGGGGG
Chr1	53336192	26.5	GGCACgcgGctgGGAGGTGGAGG
Chr3	128301954	25.9	tGCACTGCaGCTGGgGcTGGAGG
Chr12	104739609	25.8	ccttCTGCGGCTGGAaGTGGTGG
Chr10	60003488	25.6	GGCACgcgGctgGGAGGTGGAGG
Chr17	69519133	25.3	aGCAaTaCGGaTGGAGGTGGAGG
Chr2	152827915	25.2	GGCACTtCGGtTGGgGGTGGGGG
Chr15	41803379	25.0	tGCACTGCGGgcGGAGGcGGCGG
Chr3	10418956	25.0	GGCtCcGCaGCTGGAGGTGGGGG
Chr7	139631	24.9	tGCACcGCGGCTGGgGcTGGAGG
Chr16	22690928	24.3	tcCACTGaAGGCTGGgGGTGGTGG
Chr11	65326667	24.3	ctggCaGCGGCTGGgGGTGGGGG
ChrX	70836550	23.2	GGCcaTGCGGCTGGtGGTGGTGG
Chr13	88900992	22.9	caCACTGCaGCTGGAGGTGGTGG
Chr12	104234592	22.9	ctgcCTGCGGCTGGgGGTGTGGG
Chr17	75429280	22.6	GaCACcaCGGCTGGAGaTGGTGG
Chr14	101945036	22.4	GGgACTGCaaCTGGAGGTGGGGG
Chr9	74103955	22.1	GGCACTGCaGCaGGgGaTGGGGG
Chr3	9039864	21.8	GGCtCTGtaGCTGGgGGTGGTGG
Chr1	204463911	20.9	GGCgCTGCGGCTGGAGccGGCGG
Chr2	8817154	20.7	tGCACaGCGGaTGGAGGgGGGGG

Chr17	40693639	20.4	GGCACTGCaGgcaGgaGgtGAGT
ChrX	152805653	20.1	GcCACTGaGGCcGGAGGTGGAGA
Chr6	41374185	20.1	GGgcacGCGGCTGGAGGaGGGGG
Chr2	6961256	20.1	aGctCTGCGGCaGGAGtTGGAGG
Chr10	13692637	19.9	GGCACTGgGGCTGGgGGaGGGGG
Chr17	75325331	19.7	GGCcCTGCaGCTGGAGagGGAGG
Chr7	43256545	19.6	taCACTGCaGCTGGgaGTGGTGG
Chr14	88773031	19.5	aGCACTGgGGCTGGgGGaGGGGG
Chr14	63796588	19.4	GaCACTaaGGCTGGAGGTGGGGA
Chr17	42152617	19.1	tGCACTGCaGCTGGgGGTcGGGG
Chr7	29233956	18.7	GcCACTGgGGCTGGAGGgGGAGG
ChrX	104846030	17.8	cagctctgcGCTGGAGGaGGGGG
Chr4	19769425	17.7	aGctCTGctGCTGGAGGaGGTGG
Chr3	52035832	17.5	GGCACTGaatCTGGAGGTGGGGG
Chr7	55344186	17.3	atCACTGCGcCTGGtGGTGGGGG
Chr17	73501168	17.0	GcacCTGCGGCcaGgGGTGGGGG
Chr9	136602370	16.8	GGCACTGgGGCaGGAGaTGGGGG
Chr16	88716134	16.7	aGCACgGCaGCTGGAGGaGGGGG
Chr14	95761249	16.4	GGCACTctGGCTGGAGcTGGGGG
Chr6	151886088	16.2	GGCcCTGctGCTGGAGaaGGTGG
Chr10	36109441	15.9	GGCAtTGctGCTGGtGGTGGTGG
Chr1	228559256	15.8	GcacCgcgtGCTGGAGGaGGAGG
Chr21	36453434	15.5	aGctCTGctatTGGAGGTGGAGG
Chr9	19933045	15.1	aGCcCTGgGGCaGGAGGTGGGGG
Chr7	150498859	15.0	GctgCTGCGGCTGGAGGTGGGGA
Chr16	1072626	14.8	GGCcCTGCaGCaGGgGGTGGAGG
Chr5	41968123	14.8	GGaAgTGCGGCaGGAGGTGGAGG
Chr2	45247404	14.3	GaCACcGtGaCTGGAGGTGGAGG
Chr18	60646595	14.3	GcagCTGCGGCTGGAGcTgaGGG
Chr1	18954894	14.2	GGaACTGtGGCTGGgGaTGGGGG
Chr2	231467380	14.1	GGCACTGCaGCTGGgGGTtGGTG
Chr4	7686554	13.3	aaCACTGgGGCTGGtGGTGGTGG
Chr17	25735157	13.1	tGCACTcCGaCTGGAaGTGGTGG
Chr2	149402504	13.1	tGCACTGaGGaaGGAGGTGGAGG
Chr12	53453557	12.8	tGgACTGCGGCTGGAGagGGAGG
Chr17	29815563	12.6	GGCgCTGCGGCcGGAGGTGGGGC
Chr8	145730111	12.6	GGCACatgGGCTGGgGGTGGGGG
Chr12	55427953	12.5	GGCACTGaGaaaGGAGGTGGAGG
Chr19	32836900	12.4	tGCcCTGCaGCTGGgGGTGGGGG
Chr20	49771524	12.1	tGCACTGCaGaTGgtGgtGGGG
Chr17	38478448	12.1	GGCACcttGGCTGaAGGTGGGGG
Chr3	128169624	12.0	acCACTGtGGCTGGcaGgtGGTG
Chr1	12259808	11.8	aGCACTGCaGCgGGAGGTGaGAG
Chr7	157443393	11.8	GGCACTGgGtCTGaAGGTGGAGG
Chr17	31790791	11.2	tGCACTGCaGCTGGgGGcaGAGG
Chr12	101718339	10.7	GGCACTctGGCTGGAcGTGGTGG
Chr8	1241128	10.6	GGCACTGttGCTGGAGGaGGCAG
Chr13	27530813	10.5	GGCACTGctGactagGGgtGGTG
Chr16	49777696	10.3	tGCACTGCGaCTGGAGGgaGAGG
Chr3	193847797	10.1	GcactgcaaaCTGGAGGTGGGGG
Chr20	60174571	9.9	ccCACTGtGGCTGGAGGTGtGGG
Chr8	145543672	9.7	aGCcCTGCGGCcGGgGGaGGCGG

Chr3	49055364	9.6	GGgACTGCGGCTGGAGGTGGGAA
Chr4	156491955	9.4	ttCACTGtGGCTGGAGGTGGGGA
Chr2	3610377	8.6	aGCACTatGgATaGAGGTGGAGG
Chr9	138465751	8.6	taCACTGCGGCcGGgaGTGGTGG
Chr16	26710087	8.5	tGCACTGaaGCTGGAGGTGGAGA
Chr9	35349204	8.2	aGtACTGCGGCTGGgcGTGGTGG
Chr22	18663160	8.1	aGCACTagGGCaGGAGaTGGGGG
Chr18	75260893	8.1	GaCACTGaGGCTGGAAaGaGGTGG
Chr12	90804707	8.0	GGCAtgcgGctgGGAGGTGGAGG
Chr6	167276293	7.9	cGttCTGCGGCgGGAGGTGGCGG
Chr7	17979718	7.7	GcactgGCaGCcGGAGGTGGTGG
Chr17	64544877	7.6	GGCAggGCGGCTGGAGGaGGTGG
Chr10	132972512	7.6	aGCACTGgGGCaGGAGGgtGGTG
Chr1	229619193	7.4	ttgcaTGCGGCTGGAaGTGGTGG
Chr6	36761680	7.4	ccCACTGgGGCTGGAGGTGGGGG
Chr14	77678312	7.3	cagACTGCaGCTGGtaGgtGGTG
Chr11	3159715	6.9	GGCAgTGCaGCTGGAGGcaGGGG
ChrX	26910569	6.9	GGCtCTGCcaCTGGAGGgGGTGG
Chr20	61989531	6.8	GaCACTGaGGCTGGAGGTctGGG
Chr1	2933843	6.6	GGCcCTGaGaCTGcAGcTGGAGG
Chr15	77121510	6.6	aGCACTGtGGaTGGAGtTGGAGG
Chr9	11158273	6.6	cttcCTaCGGCaGGAGGTGGGGG
Chr3	16815640	6.3	cGCACTGgGGCTGcAGGTGGAGG
Chr6	159190938	6.0	GGCcCTGCaGCTGGAGGaGGAGA
Chr2	71786040	5.8	aGCACTGCaGtgaGAGGTGGAGG
Chr10	128864484	5.6	GaCACcGCaGCTGGgGGcGGCGG
Chr7	48144881	5.6	aGCACTGgGGCTGGAGcTaGAGG
Chr16	50334859	5.2	GGttCTGCGGtTGGgGGTGGGGG
Chr15	25425088	5.1	GGCtCTGCattTGGAGGTGtGCG
Chr17	176302	5.0	tGCACTGtGGCTGGAGaTGGGGG
Chr16	1029978	4.9	GGCACTGCaGacGGAGGTGtGGG
Chr13	29913424	4.8	GaCACTGcTgCTGGAGagtGGAG
Chr16	89469252	4.7	GGCACTGCGGgaGGAGGTGGGCG
Chr6	157547859	4.5	aGaACTGgGGCTGGgGGTGGGGG
Chr20	56668028	4.4	GGgcCTGCaGCTGGgGGTGGGGG
Chr16	78413349	4.4	GGtACaGtGGCTGGAGGTGGAAG
Chr5	177928896	4.4	ccCACTGCGGgTGGAGGTGGAAG
ChrX	101411055	4.3	cGCAgTGCGGCaGGAGGgtGGGG
Chr11	20409041	4.3	aaCcCTGCGGCaGGAGGaGGCGG
Chr14	99286477	4.2	GatACTGgGGCTGGgGGTGGAGG
Chr11	78127585	4.2	tGCACTGCaGCTGGAGGcaaCGG
Chr1	183596713	4.1	GcactTGcTgCTGGAGGaGtAGG
Chr11	17538892	4.1	tGCACTGCGGtcaGgaGgaGGCG
Chr22	18854922	3.6	aGCACTagGGCaGGAGaTGGGGG
Chr12	21742959	3.4	aGCcCTGcTaCTGGgGGTGGGGG
Chr8	144781302	3.3	GaCACTGCaGCTGGAGGTGGGGT
Chr2	59012462	3.3	tGCACTGCaaCTGGgGGTGGCAG
Chr1	908980	3.3	GaCcCTGCGGtgGGAGGTGGCGG
Chr15	43601412	3.2	GGCcCTGaGGCaGGAaGTGGGGG
Chr1	176665050	3.1	acCACTGaGGAaTGGgGGTGGAGG
Chr20	19620239	3.1	cGCACTGgGGCTGcAGGTGGAGG
Chr5	171087054	3.1	GGgACTGCaGCTGGgGaTGGGGG

Chr15	26125549	3.1	caaACTGCaGCTGGAGaTGGGAG
Chr12	114150540	2.9	ctgACTGCaGCTGGAGGTGGAGA
Chr7	157889941	2.9	GGCACTGgGGaaGGAGGTGGAGG
Chr22	44625614	2.9	GaCACTGCtaCTGGAGGctGGGG
Chr18	60805450	2.8	GcactgGCGGCTGGgaGTGGTGG
Chr22	18743056	2.7	aGCACTagGGCaGGAGaTGGGGG
Chr12	130859964	2.6	GagAaTGCGGaTGGAGGTGGTGG
Chr14	24740271	2.5	GGCACTGCcaCTGGgGGTGaGGG
Chr5	54469282	2.5	GcCACcGCGGCaGGAGGcGGAGG
Chr4	6094150	2.5	GagcCTGCGGCTGcAGGTGGGTG

HBB			
Chr	Position	DNA cleavage Score	DNA seq at a cleavage sites
Chr12	124803834	141.1	gcTGCCCCACAGGGCAGcAAAGG
Chr15	46598129	110.7	gTTGCCCCtCAGGaCAGTAcAGG
Chr22	17230623	97.4	tgTGCCCCACAGaGCACtAAGGG
Chr9	104595883	92.4	tcaGCCCCACAGGGCAGTAAGGG
Chr17	8370253	87.7	tTgtCCCACAGGGCAGTAAACG
Chr14	94585327	83.7	aTgGCCCCACAaGGCAGaAATGG
Chr11	5248215	81.8	CTTGCCCCACAGGGCAGTAACGG
Chr12	93549202	58.4	aTTGCCCCACgGGGCAGTgACGG
Chr1	177593980	22.9	tcTaCCCCACAtGGCAGTAATGG
ChrX	75006257	16.6	gTgGCCCCACAGGGCAGgAATGG
Chr6	50041372	14.2	tcTGCCCCACAtGGCAGTAATGA
Chr6	23709579	11.5	gaaGCCcTACAGGGCAGcAATGG
Chr2	121715240	9.8	gTgtCCCCACAGGGCAGgAAAGG
Chr8	24931381	9.7	agTGCCaCACaCaGCAGTAAGGG
Chr14	36889538	5.3	gTTatCCCACAGGaCAGTgAGGG
Chr1	17346702	5.2	CggtCCCCACAGGGtcaagtAAGG
Chr20	39992928	4.9	agTGgCCCCcCAGGGCAGTgAGGG
Chr10	95791920	4.8	acTctCCCACAaGGCAGTAAGGG
Chr4	148531374	3.8	gTTaCCtCACAGaGCAGaAAGGG
Chr5	53613387	3.2	tcacCCCCACAGGcCAGTAAAGG

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	GGGTGGGGGGAGTTTGCTCCAGG	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	GGGTGGGGGGAGTTTGCCcCAGG	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	aaGTGGGaaGAGTTTgTCCAGG	0.03%	0.01%	Invalidated
VEGFA1_33	Chr11	117481208	GGGcaaGGGGAGgTTTGCTCCTGG	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	cAgtCCcCCACCCCaCCTCTGG	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	ccCtCtCcaCcCCCacCCTCTGG	0.00%	0.00%	Invalidated
VEGFA2_43	Chr16	13492458	tcCgCCCCcCCACCCCaCCTCCGG	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	aGTGAGTGAGTGTGTGTGGGG	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	aGTGAaTGAGTGTGTGTGTGG	0.40%	23.67%	validated
VEGFA3_09	Chr14	62078773	tGTGAGTaAGTGTGTGTGTGG	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	ctgGAGTGAGTGTGTGTGTGG	0.01%	0.00%	Invalidated
VEGFA3_16	Chr9	18733635	aGcGAGTGAGTGTGTGTGGGG	0.20%	32.70%	validated
VEGFA3_17	Chr2	73317050	GGTGAGTcAGTGTGTGaGTGAGG	2.29%	2.66%	Invalidated
VEGFA3_18	Chr4	58326608	aGTGAGTGAGTGaGTGaGTGAGG	0.02%	0.00%	Invalidated
VEGFA3_19	Chr8	48997806	GtaGAGTGAGTGTGTGTGTGG	0.45%	5.11%	validated
VEGFA3_20	Chr14	74353497	aGcGAGTGgGTGTGTGCGTGGGG	0.01%	12.60%	validated
VEGFA3_21	Chr22	49740001	GGTGTGTGAGTGTGTGTGTGG	0.46%	2.89%	validated
VEGFA3_23	Chr16	84032646	GGTGAAaTGAGTGTGTGcTtGGG	0.01%	0.68%	validated
VEGFA3_24	Chr10	5749657	aGTGAGTatGTGTGTGTGGGG	1.31%	1.86%	validated
VEGFA3_27	Chr4	62067619	GaTGAGTGTGTGTGTGTGAGG	0.45%	0.36%	Invalidated
VEGFA3_29	Chr2	230506241	GGTGAGcaAGTGTGTGTGTGG	0.46%	51.82%	validated
VEGFA3_31	Chr17	33323269	tGTGAGTGAGTaTGTaCaTGTGG	0.00%	0.01%	Invalidated
VEGFA3_32	Chr7	51294279	aGTGAGTaAGTGaGTGaGTGAGG	0.00%	0.00%	Invalidated
VEGFA3_34	Chr16	73585926	aaTGAGTGAGTGTGTGTGTGA	0.77%	0.97%	Invalidated
VEGFA3_36	Chr2	18696225	aGTGAGaaAGTGTGTGCaTGCGG	0.00%	0.16%	validated
VEGFA3_37	Chr19	6660674	tGTGAGTGAGTGaGTGaaTGTGG	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	tGTGTGaGtGaGTGTGTGTGG	0.07%	0.22%	validated
VEGFA3_43	Chr5	34452076	tGTGTGaGtGTGTGTGTGcGTGG	0.18%	0.13%	Invalidated
VEGFA3_44	ChrX	41726218	GGTGAGTGAGTGaGTGaGTGAGG	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	tGTGAGTGAaTGTGTGTGTGG	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	GaTGTGTGAGTGTGTGcTGTGG	0.01%	0.07%	validated
VEGFA3_53	Chr20	2650069	GGTGtaTGAGTGTGTGCGTcGGA	1.26%	1.30%	Invalidated
VEGFA3_54	Chr3	10207131	GGTGTGTGTGTGTGTGTGTGG	0.10%	0.09%	Invalidated
VEGFA3_55	Chr5	98946319	GGTgtagtGTGTGTGcTGTGG	0.00%	0.00%	Invalidated
VEGFA3_56	Chr6	39028642	GGTGTGTGAGTGTGTGCaTGGG	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

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	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	tGGAAAGAaaCAGCATCCGTACG	0.00%	0.01%	Invalidated

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	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	GAAaACAAaACATAGAgTGCTGG	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	ccAaACAAaACATAGACTGCTGG	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	aAgaACAAaACATAGACTGCAGG	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

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	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	aGCAgTGCGGCTaGAGGTGGTGG	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	GGCAaTtGGCTGaAGGTGGGGG	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	aAgaACAAAaCATAGACTGCAGG	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

Supplemental Table 5. Orthogonal target sites.

Gene	Exon	No. of PAM (NGG) -containing sites	No. of sites with no homologous sites harboring up to 2 mismatch in the human genome & No. of sites with fewer than 13,000 homologous sites harboring up to 6 mismatches
VEGFA	Exon1	235	79
	Exon2	8	0
	Exon3	26	18
	Exon4	6	0
	Exon5	1	0
	Exon6	14	5
	Exon7	8	4
	Exon8	252	34
	Total	550	140
EMX1	Exon1	238	73
	Exon2	29	8
	Exon3	245	37
	Total	512	118
FANCF	Exon1	373	90
	Total	373	90
RNF2	Exon1	50	12
	Exon2	4	0
	Exon3	8	0
	Exon4	14	0
	Exon5	21	0
	Exon6	10	0
	Exon7	173	8
	Total	280	20
Total		1715	368

Supplemental Table 6. Calculation of an off-target score assigned to the *EMX1* target sequence (5'-GAGTCCGAGCAGAAGAAGAANGG-3') in the human genome.

No. of mismatches	No. of mismatches in the seed region	No. of sites ^a	Fraction captured ^b	Median indel frequency ^c	No. of sites x Fraction captured x Median indel frequency
0	-	0	1.0	1.0	0.0
1 or 2	-	1	1.0	0.15	0.15
3	0	7	0.56	0.030	0.12
	1	7	0.44	0.0077	0.024
	2	4	0.12	0.0030	0.0014
	3	0	0.0020	0.00010	0.0
4	0	68	0.22	0.030	0.45
	1	73	0.062	0.0039	0.018
	2	115	0.010	0.00088	0.0010
	3	16	0.0013	0.00088	0.000018
	4	4	0.0	0.0	0.0
5	0	136	0.010	0.00067	0.00091
	1	674	0.010	0.00067	0.0045
	2	888	0.0015	0.00067	0.00089
	3	521	0.00025	0.00067	0.000087
	4	91	0.0	0.0	0.0
	5	3	0.0	0.0	0.0
6	0	426	0.0067	0.00026	0.00074
	1	2641	0.0017	0.00026	0.0012
	2	5673	0.000047	0.00026	0.000069
	3	4954	0.000047	0.00026	0.000061
	4	1846	0.0	0.0	0.0
	5	197	0.0	0.0	0.0
	6	10	0.0	0.0	0.0
Off-target score:					0.77

^a No. of sites was obtained using Cas-OFFinder.

^b Fraction captured was experimentally determined and shown in Fig. 3b.

^c Median indel frequency was determined using targeted deep sequencing (Fig. 5a).

Supplemental Note 1

Off-target effect index (OTI) of HBB sgRNA and VEGFA 1 sgRNA

HBB sgRNA

On-target indel frequency : 33.142%

Sum of indel frequencies at off-target sites: 85.541% + 3.143% + 0.088% + 2.292% = 91.064%

Off-target effect index (OTI) : $91.064\% / 33.142\% = 2.75$

VEGFA 1 sgRNA

On-target indel frequency: 42.688%

Sum of indel frequencies at off-target sites: 45.501% + 5.430% + 0.035% + 18.633% + 18.383% + 52.792% + 45.392% + 3.265% = 189.431%

Off-target effect index (OTI): $189.431\% / 42.688\% = 4.44$