

Supplemental Information

Chromatin hinders CRISPR off-target effects

Table of Contents

Supplemental Figures

Supplemental Figure 1. Chromatin states in HEK 293T and HeLa cells confirmed by DNase I assays and real-time quantitative PCR.

Supplemental Figure 2. Tolerance of Cas9 for mismatched sgRNAs at sites in open and closed chromatin regions.

Supplemental Figure 3. Mismatched sgRNAs are sensitive to chromatin states.

Supplemental Figure 4. Comparison of DIG-seq using chromatin DNA and DIG-seq using Nuclei pellet.

Supplemental Figure 5. Comparison of Digenome-seq using histone-free genomic DNA and DIG-seq using chromatin DNA.

Supplemental Figure 6. Venn diagrams showing the number of sites captured by chromatin DNA mediated Digenome-seq and histone-free DNA mediated Digenome-seq with Digenome 2.0 program.

Supplemental Figure 7. Correlation between the Indel frequency and DNA cleavage score identified by histone-free DNA and Chromatin DNA at the VEGFA, FANCE, HEK3, and EMX1 sites.

Supplemental Figure 8. The number of total sites and the number of PAM-containing sites with ten or fewer mismatches depending on a range of DNA cleavage scores.

Supplemental Tables

Supplemental Table 1. Mutation frequencies obtained with Cas9 at endogenous target sites present in both open and closed chromatin regions

Supplemental Table 2. Off-target candidate sites captured by DIG-seq

Supplemental Table 3. Off-target candidate sites captured by DIG-seq aligned to GRCh38.

Supplemental Table 4. Mutation frequencies of Cas9 at on-target and off-target sites captured by DIG-seq.

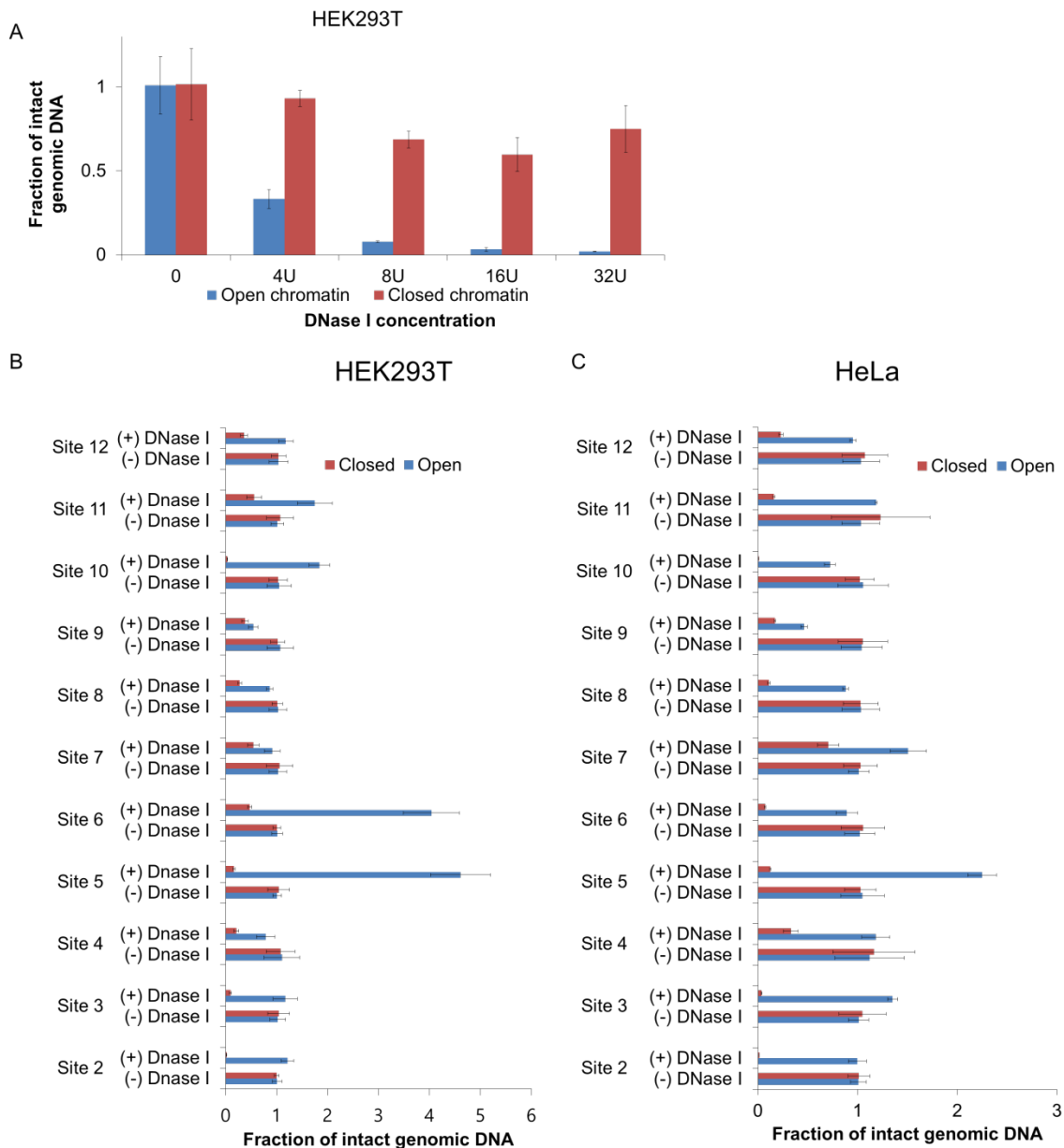
Supplemental Table 5. Mutation frequencies of Cas9 off-target sites captured by Digenome-seq but missed by DIG-seq

Supplemental Table 6. Comparison of off-target candidate sites captured by Digenome-seq and DIG-seq.

Supplemental Table 7. Chromatin accessibility of Cas9 off-target sites captured by Digenome-seq.

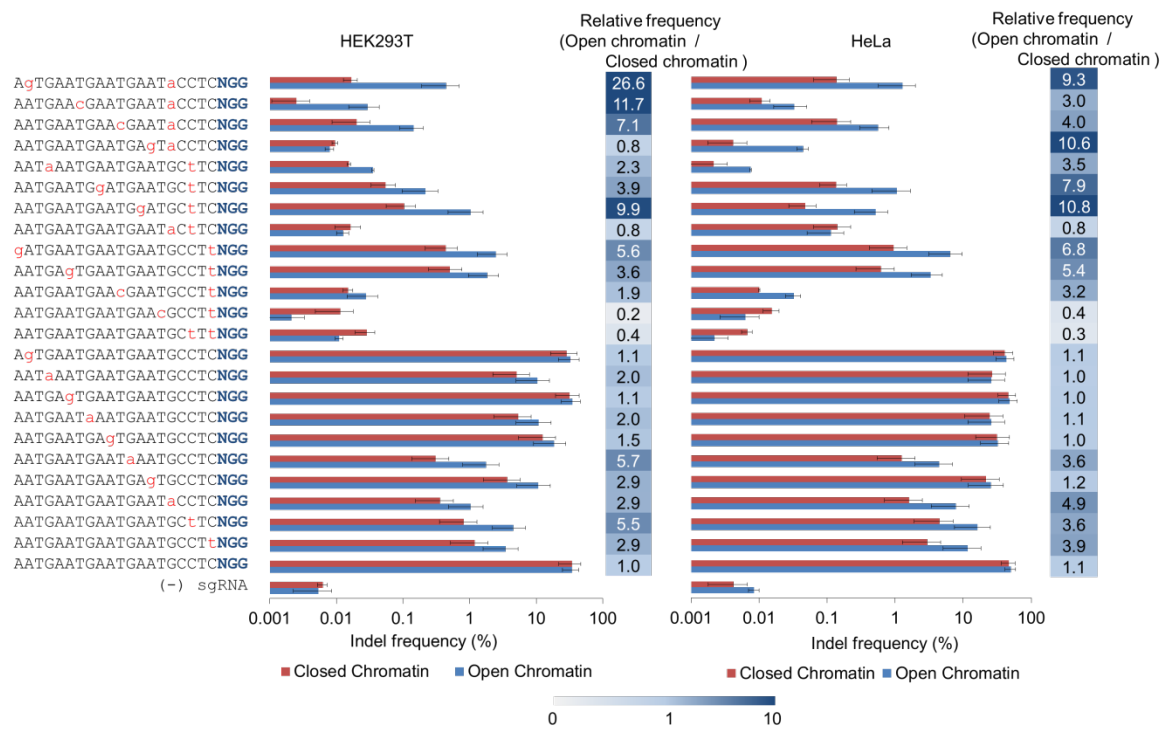
Supplemental Figure 1. Chromatin states in HEK 293T cells confirmed by DNase I assays and real-time quantitative PCR.

(A) Chromatin DNA isolated from HEK 293T cells was treated with DNase I and subjected to real-time quantitative PCR. 0-16U(Unit) represents the concentration of DNase I. Error bars, s.e.m. from at least three independent experiments. (B-C) The fraction of undigested DNA by DNase I was measured by real-time quantitative PCR in HEK293T cells (B) and HeLa cells (C).



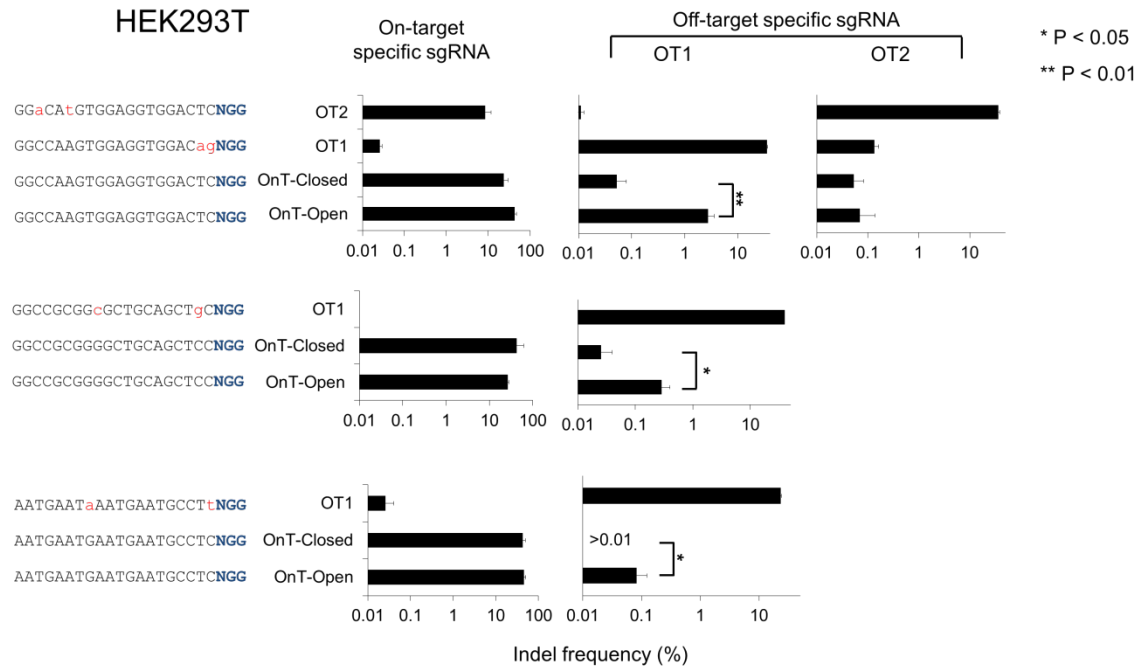
Supplemental Figure 2. Tolerance of Cas9 for mismatched sgRNAs at sites in open and closed chromatin regions.

Mismatched sgRNAs that differed with on-target sequence by 1-2 nucleotides were tested in HEK293T and HeLa cells. Indel frequencies at the open and closed chromatin were measured using targeted deep sequencing. Error bars indicate s.e.m. (n = 3).



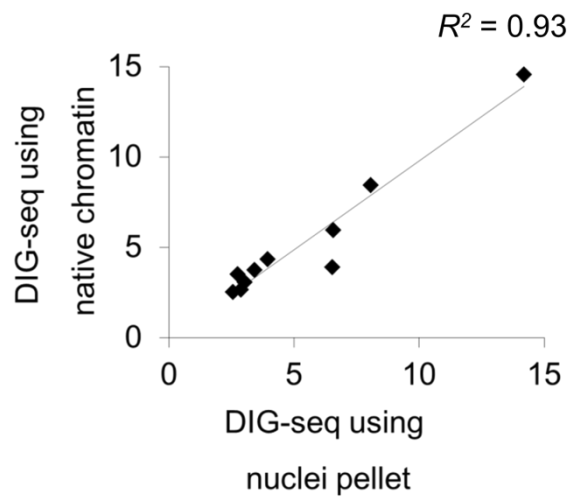
Supplemental Figure 3. Mismatched sgRNAs are sensitive to chromatin states.

Cas9 efficiencies were measured at on-target sites present in open and closed chromatin regions using on-/off-target specific sgRNAs in HEK293T cells. Indel frequencies were measured using targeted deep sequencing. Error bars indicate s.e.m. (n = 3).



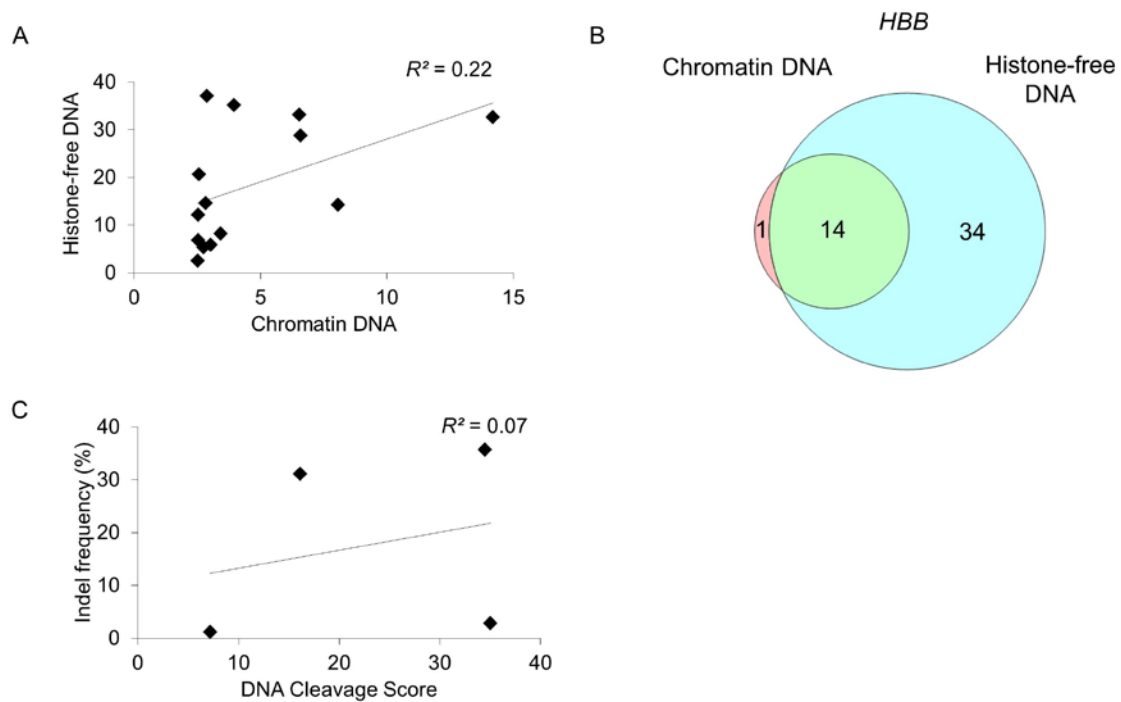
Supplemental Figure 4. Comparison of DIG-seq using chromatin DNA and DIG-seq using Nuclei pellet

Scatterplot of DNA cleavage scores at in vitro cleavage sites identified by DIG-seq using native chromatin DNA vs. DIG-seq using nuclei pellet.

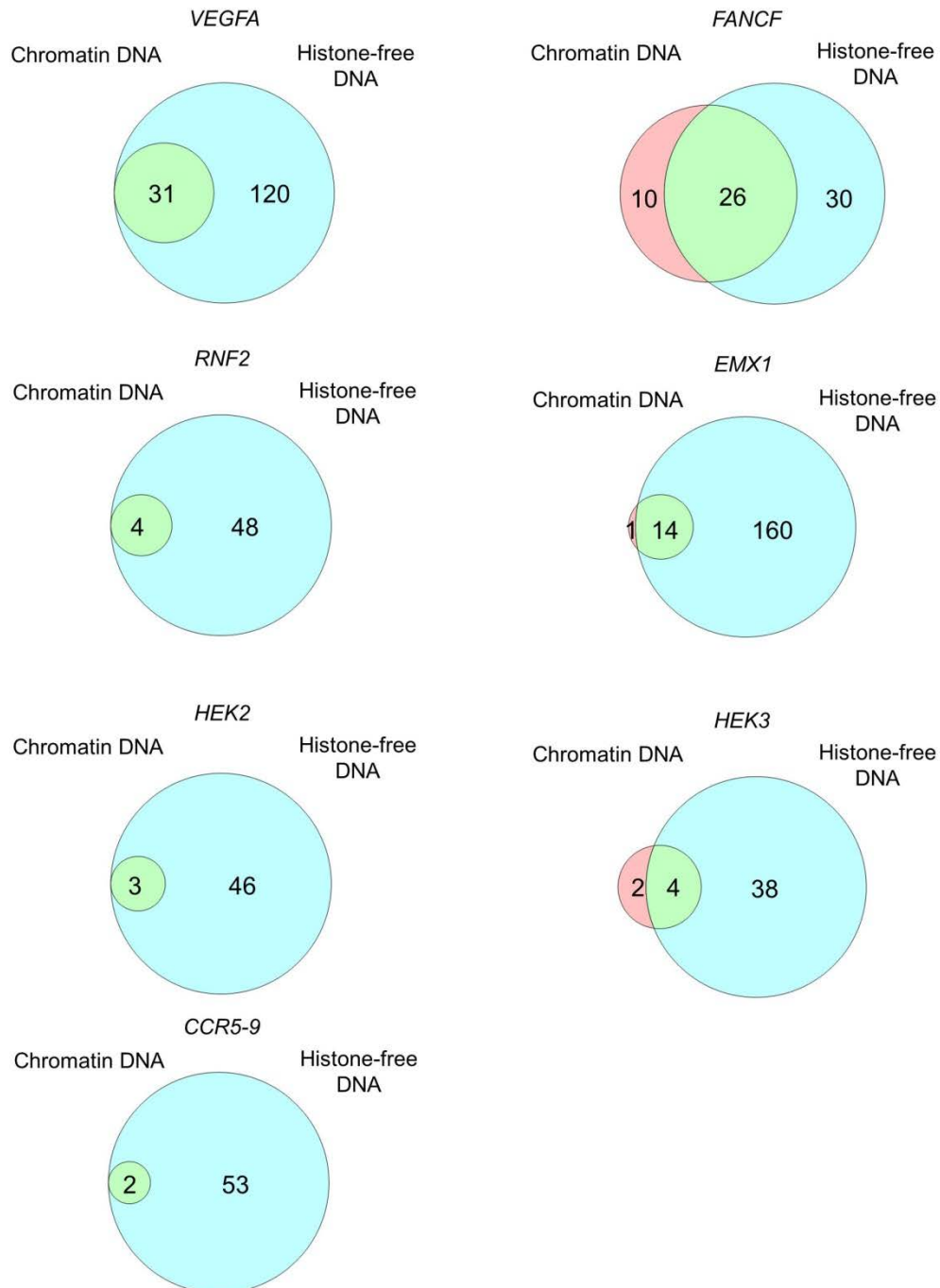


Supplemental Figure 5. Comparison of Digenome-seq using histone-free genomic DNA and DIG-seq using chromatin DNA.

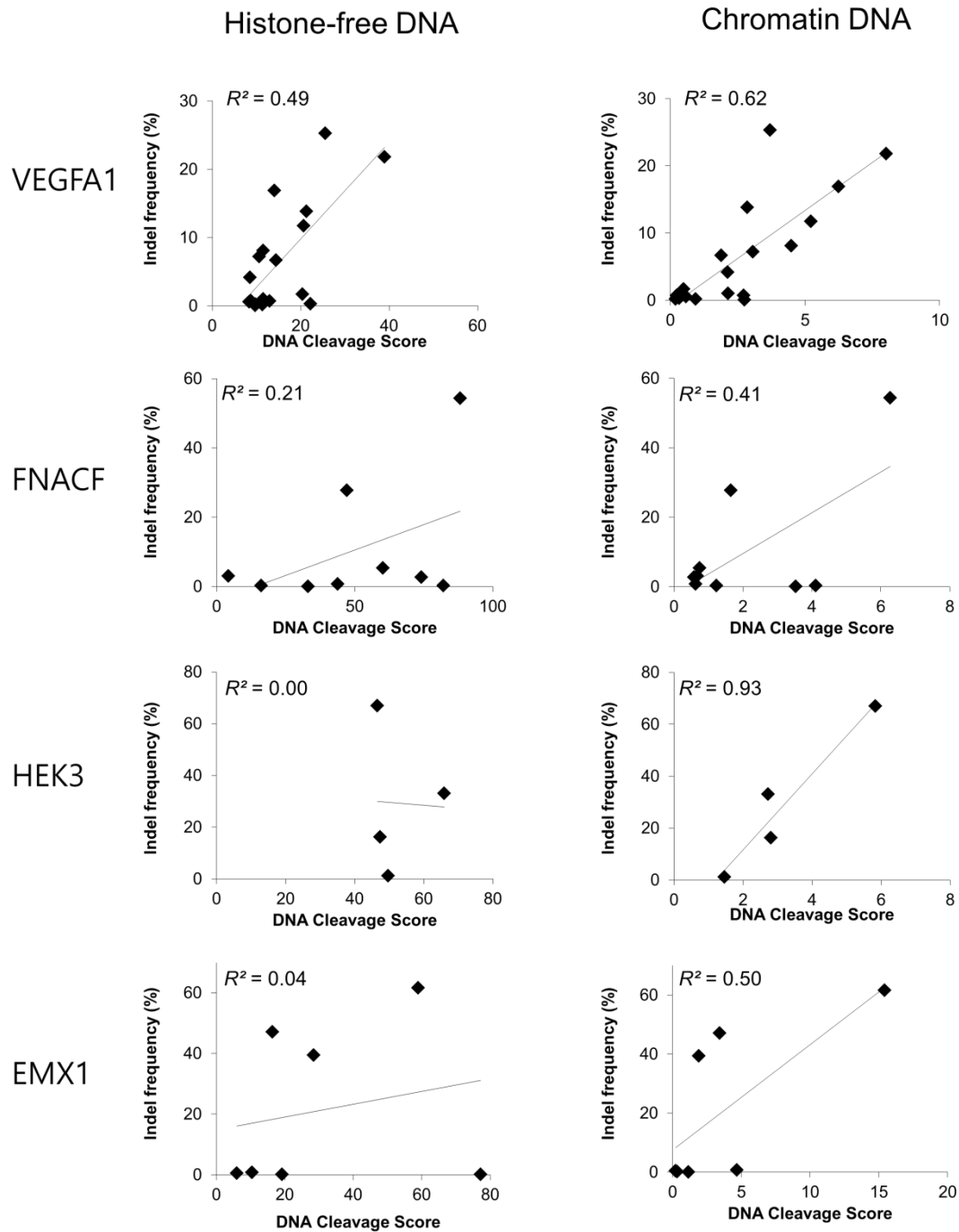
(a) Scatterplot of DNA cleavage scores at in vitro cleavage sites identified by Digenome-seq using chromatin DNA vs. histone-free genomic DNA. (b) Venn diagram showing the number of on-/off-target candidates captured by Digenome-seq using histone-free genomic DNA or chromatin DNA (Digenome 1.0). (c) Scatterplot of DNA cleavage scores at in vitro cleavage sites identified by Digenome-seq using histone-free genomic DNA vs. indel frequencies at these sites in HeLa cells.



Supplemental Figure 6. Venn diagrams showing the number of sites captured by chromatin DNA mediated Digenome-seq and histone-free DNA mediated Digenome-seq with Digenome 2.0 program.

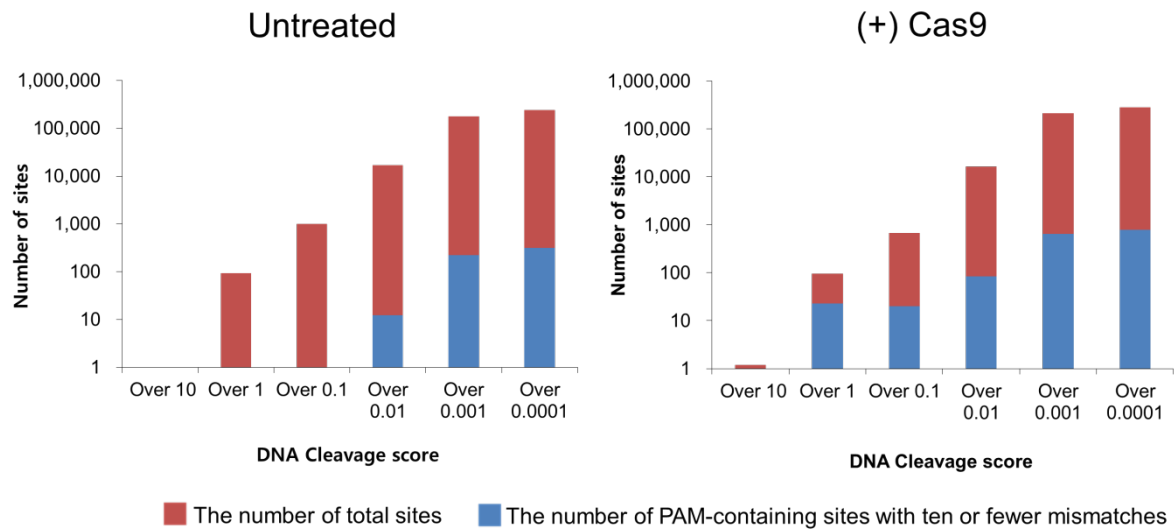


Supplemental Figure 7. Correlation between the Indel frequency and DNA cleavage score identified by histone-free DNA and Chromatin DNA at the VEGFA, FANCF, HEK3, and EMX1 sites.



Supplemental Figure 8. The number of total sites (red) and the number of PAM-containing sites with ten or fewer mismatches (blue) depending on a range of DNA cleavage scores.

Intact human genomic DNA (left) and Cas9 mediated digested DNA (right) were subjected to Digenome-seq.



Supplemental Table 1. Mutation frequencies obtained with SpCas9 at endogenous target sites present in both open and closed chromatin regions

HEK293T			
	Target sites	Indel frequency (%)	
		Open chromatin	Closed chromatin
Site1	AATGAATGAATGAATGCCTCNGG	36.6	30.0
Site2	TCACAGATGCCAAGCAGCTGNNG	45.2	31.6
Site3	GGCCAAGTGGAGGTGGACTCNGG	37.7	35.8
Site4	GGCCGCGGGGCTGCAGCTCCNGG	27.8	28.6
Site5	CCTGGGAGGCCAGGGTCACANGG	52.9	25.7
Site6	TCGGGGAGAGCTTCGAGAAGNNG	64.7	59.2
Site7	AACTCCCCTTCCCCAACACTNNG	54.3	49.1
Site8	TGAAAGGAGATGGAGGAGGGNNG	46.8	41.0
Site9	GAGCCTTGCAGCTTCAGCCTNNG	11.8	4.4
Site10	AAGGGTGGCAGGAGAGTAGCNGG	41.3	31.2
Site11	AAAGCAGCAGCAGCAGCCAGNNG	56.6	44.5
Site12	TGAATTGAGGCAGTAGCCTCNGG	57.4	16.5

HeLa			
	Target sites	Indel frequency (%)	
		Open chromatin	Closed chromatin
Site1	AATGAATGAATGAATGCCTCNGG	39.3	42.2
Site2	TCACAGATGCCAAGCAGCTGNNG	62.4	55.7
Site3	GGCCAAGTGGAGGTGGACTCNGG	37.7	37.2
Site4	GGCCGCGGGGCTGCAGCTCCNGG	29.7	26.4
Site5	CCTGGGAGGCCAGGGTCACANGG	75.4	54.7
Site6	TCGGGGAGAGCTTCGAGAAGNNG	76.4	73.7
Site7	AACTCCCCTTCCCCAACACTNNG	75.5	63.8
Site8	TGAAAGGAGATGGAGGAGGGNNG	65.8	63.8
Site9	GAGCCTTGCAGCTTCAGCCTNNG	24.5	9.7
Site10	AAGGGTGGCAGGAGAGTAGCNGG	71.1	53.8
Site11	AAAGCAGCAGCAGCAGCCAGNNG	77.5	68.7
Site12	TGAATTGAGGCAGTAGCCTCNGG	68.1	29.2

Supplemental Table 2. Off-target candidate sites captured by DIG-seq.

HeLa					Chromatin accessibility (1= DNase I hypersensitive sites, 0 = DNase I non-sensitive sites)			
	Chromosome	Location	DNA Cleavage score	Target sequence	HeLa	HEK293T	K562	H9 cell
On-target	chr11	5248215	14.20	CTTGCCCCACAGGGCAGTAACGG	0	0	0	0
HBB-2	chr9	104595883	8.07	tcaGCCCCACAGGGCAGTAAGGG	0	0	0	0
HBB-3	chr17	8370253	6.58	tTgctCCCACAGGGCAGTAAACG	0	0	0	0
HBB-4	chr12	124803834	6.54	gcTGCCCCACAGGGCAGcAAAGG	0	0	0	0
HBB-5	chr14	94585327	3.96	aTgGCCCCACaAGGCAGaAATGG	0	0	0	0
HBB-6	chr22	17230623	3.43	tgtGCCCCACAGaGCACTAAGGG	0	0	0	0
HBB-7	chr2	121715240	3.04	gTgtCCCCACAGGGCAGgAAAGG	0	0	0	0
HBB-8	chr12	93549202	2.89	aTTGCCCCACgGGGCAGTgACGG	0	0	0	0
HBB-9	chr7	97874171	2.86	CcctCCCCACAGGGCAGTcATGG	0	0	0	0
HBB-10	chr3	19957634	2.82	gcTaCCCCACAGGGCAcTAgGGG	0	0	0	0
HBB-11	chrX	75006257	2.76	gTgGCCCCACAGGGCAGgAATGG	0	0	0	0
HBB-12	chr15	46598129	2.57	gTTGCCCCtCAGGaCAGTAcAGG	0	0	0	0
HBB-13	chr9	96637408	2.54	acaGCCCCACAGGGCAtaAACGG	0	0	0	0
HBB-14	chr5	131423385	2.53	tcTGCCCCACAGGGCAGgAAGGG	0	0	0	0
HBB-15	chr8	24931381	2.52	agTGCCaCACaGCAGTAAGGG	0	0	0	0
HBB-16	chr14	36889538	2.31	gTTatCCCCACAGGaCAGTgAGGG	0	0	0	0
HBB-17	chr20	39992928	2.31	agTgGCCCCCAGGGCAGTgAGGG	0	0	0	0
HBB-18	chr1	177593980	2.15	tcTaCCCCACatGGCAGTAATGG	0	0	0	0
HBB-19	chr6	23709579	1.95	gaaGCCCtACAGGGCAGcAATGG	0	0	0	0
HBB-20	chr4	148531374	1.75	gTTaCCtCACAGaGCAGaAAGGG	0	0	0	0
HBB-21	chr10	72286450	1.47	CaaGCCCCACAGGGCAGacAGGG	0	0	0	0
HBB-22	chr19	8560462	1.31	aaatCCCCACAGGGCAGTAAGGC	0	0	0	0
HBB-23	chr11	76387498	1.18	CTgcccCtcagGgaCAGTAtGGG	0	0	0	0
HBB-24	chr5	14347051	1.08	CaTaCCCCACAGGtCAGTAAGGA	0	0	0	0
HBB-25	chr1	17346702	0.95	ggTCCCCacagGgtCAGTAAGGG	0	0	0	0
HBB-26	chr15	29983547	0.78	CcaGCCCCACAGGGCAGTAAAGC	0	0	0	0
HBB-27	chr19	34262012	0.78	gcTGctCCACAGGGCAGgtATGG	0	0	0	0
HBB-28	chr10	73555691	0.78	CagGCCCCACAGGaCAGgAAGGG	0	0	0	0
HBB-29	chr19	50010010	0.73	aTTGCCCCCAGGtCAGTAAGGG	1	1	1	1
HBB-30	chr15	34059408	0.56	gTTaCCaCACAGaGCAGtTAAGG	0	0	0	0
HBB-31	chr13	44886376	0.54	ggaGCCCCACAGGGCAGagAGGG	0	0	0	0
HBB-32	chr9	134609673	0.50	tTTGCCCCtCAGGGCAGctAAGG	0	0	0	0
HBB-33	chr16	49082904	0.46	gcaGCCCCACAGGtCAGTgAGGG	0	0	0	0
HBB-34	chr3	128713852	0.45	aTaGCCCCACAGGGCAGgtTAGG	0	0	0	0
HBB-35	chr12	27234755	0.44	gaTGCCtCACAGGaCAGgAAGGG	1	1	1	1
HBB-36	chr19	923900	0.37	aaTtaCCCCCAGGGCAGgAAGGG	0	0	0	0
HBB-37	chr8	143699609	0.35	CcaGCCCCacGGGCAGTAgATG	0	0	0	0
HBB-38	chr12	50056756	0.22	aagGCCCCgCAGGGCAGTttGGG	0	0	0	0
HBB-39	chr2	240591539	0.20	acaGCCCCACAGGGCAcTAgAGG	0	0	0	0
HBB-40	chr17	66624245	0.17	CctCtCCCCACAGGGCAGTAAAGG	0	1	1	1
HBB-41	chr9	134994964	0.15	tTTGCCCCtCAGGGCAGctAAGG	0	0	0	0
HBB-42	chr2	43013308	0.15	CcTGCCcagtAagGCAGTAAGGG	0	0	0	0
HBB-43	chr8	41296595	0.14	tcaGCCCCACAGGtCAGcAATGG	0	0	0	0
HBB-44	chr22	35537395	0.14	agTGCCCCACAGGGgAGaAATGG	0	0	0	0

HEK293T					Chromatin accessibility (1= DNase I hypersensitive sites, 0 = DNase I non-sensitive sites)			
	Chromosome	Location	DNA Cleavage score	Target sequence	HeLa	HEK293T	K562	H9 cell
On-target	chr11	5248215	14.63	CTTGCCCCACAGGGCAGTAACGG	0	0	0	0
HBB_HEK-2	chr9	104595883	8.17	tcaGCCCCACAGGGCAGTAAGGG	0	0	0	0
HBB_HEK-3	chr17	8370253	3.65	tTgctCCCACAGGGCAGTAAACG	0	0	0	0
HBB_HEK-4	chr12	124803834	2.96	gcTGCCCCACAGGGCAGcAAAGG	0	0	0	0
HBB_HEK-5	chr14	94585327	1.82	aTgGCCCCACaAGGCAGaAATGG	0	0	0	0
HBB_HEK-6	chr12	93549202	1.01	aTTGCCCCACgGGGCAGTgACGG	0	0	0	0
HBB_HEK-7	chr2	121715240	0.88	gTgtCCCCACAGGGCAGgAAAGG	0	0	0	0
HBB_HEK-8	chr12	27234755	0.70	gaTGCCtCACAGGaCAGgAAGGG	1	1	1	1
HBB_HEK-9	chrX	75006257	0.46	gTgGCCCCACAGGGCAGgAATGG	0	0	0	0
HBB_HEK-10	chr14	36889538	0.40	gTTatCCCCACAGGaCAGTgAGGG	0	0	0	0

HBB_HEK-11	chr6	23709579	0.29	gaa GCCCTACAGGGCAGC AAT GG	0	0	0	0
HBB_HEK-12	chr7	97874171	0.28	Ccct CCCCACAGGGCAGT c ATGG	0	0	0	0
HBB_HEK-13	chr10	72286450	0.23	Caa CCCCACAGGGCAG ac AGGG	0	0	0	0
HBB_HEK-14	chr8	24931381	0.19	ag TGCC a CAC Aca GCAGTAAGGG	0	0	0	0

K562								
					Chromatin accessibility (1= DNase I hypersensitive sites, 0 = DNase I non-sensitive sites)			
	Chr	Location	DNA Cleavage Score	DNA sequence at target sites	HeLa	HEK293T	K562	H9 cell
On-target	chr11	5248215	16.29	CTTGCCCCACAGGGCAGTAACGG	0	0	0	0
HBB_K562-2	chr9	104595883	9.41	tca CCCCACAGGGCAGTAAGGG	0	0	0	0
HBB_K562-3	chr17	8370253	3.80	tTgct CCCACAGGGCAGTAAACG	0	0	0	0
HBB_K562-4	chr12	124803834	2.65	gc TGCCCCACAGGGCAG c AAAGG	0	0	0	0
HBB_K562-5	chrX	75006257	2.62	gTg CCCCACAGGGCAG g AATGG	0	0	0	0
HBB_K562-6	chr14	94585327	1.04	aTg CCCCAC a GGCAG a AATGG	0	0	0	0
HBB_K562-7	chr2	121715240	0.56	gTgt CCCCACAGGGCAG g AAAGG	0	0	0	0
HBB_K562-8	chr22	17230623	0.30	tg TGCCCCACAG a GC Ac TAAAGG	0	0	0	0
HBB_K562-9	chr12	93549202	0.28	aTTG CCCCAC g GGGCAGT g ACGG	0	0	0	0
HBB_K562-10	chr1	17346702	0.15	ggTc CCC acag G Gt CAGTAAGGG	0	0	0	0
HBB_K562-11	chr7	97874171	0.14	Ccct CCCCACAGGGCAGT c ATGG	0	0	0	0
HBB_K562-12	chr6	23709579	0.12	gaa GCCCTACAGGGCAGC AAT GG	0	0	0	0

H9 cell								
					Chromatin accessibility (1= DNase I hypersensitive sites, 0 = DNase I non-sensitive sites)			
	Chr	Location	DNA Cleavage Score	DNA sequence at target sites	HeLa	HEK293T	K562	H9 cell
On-target	chr11	5248215	14.63	CTTGCCCCACAGGGCAGTAACGG	0	0	0	0
HBB_H9-2	chr9	104595883	8.17	tca CCCCACAGGGCAGTAAGGG	0	0	0	0
HBB_H9-3	chr17	8370253	3.65	tTgct CCCACAGGGCAGTAAACG	0	0	0	0
HBB_H9-4	chr12	124803834	2.96	gc TGCCCCACAGGGCAG c AAAGG	0	0	0	0
HBB_H9-5	chr14	94585327	1.82	aTg CCCCAC a GGCAG a AATGG	0	0	0	0
HBB_H9-6	chr12	93549202	1.01	aTTG CCCCAC g GGGCAGT g ACGG	0	0	0	0
HBB_H9-7	chr2	121715240	0.88	gTgt CCCCACAGGGCAG g AAAGG	0	0	0	0
HBB_H9-8	chr12	27234755	0.70	ga TGCC t CACAG Ga CAG g AAGGG	1	1	1	1
HBB_H9-9	chrX	75006257	0.46	gTg CCCCACAGGGCAG g AATGG	0	0	0	0
HBB_H9-10	chr14	36889538	0.40	gTTat CCCACAG Ga CAGT g AGGG	0	0	0	0
HBB_H9-11	chr6	23709579	0.29	gaa GCCCTACAGGGCAGC AAT GG	0	0	0	0
HBB_H9-12	chr7	97874171	0.28	Ccct CCCCACAGGGCAGT c ATGG	0	0	0	0
HBB_H9-13	chr10	72286450	0.23	Caa CCCCACAGGGCAG ac AGGG	0	0	0	0
HBB_H9-14	chr8	24931381	0.19	ag TGCC a CAC Aca GCAGTAAGGG	0	0	0	0
HBB_H9-15	chr9	134994964	0.12	tTTG CCCC t CAGGGCAG c TAAAGG	0	0	0	0

T cell				
	Chr	Location	DNA Cleavage Score	DNA sequence at target sites
On-target	chr11	5248215	15.29	CTTGCCCCACAGGGCAGTAACGG
HBB_Tcell-2	chr9	104595883	5.64	tca CCCCACAGGGCAGTAAGGG
HBB_Tcell-3	chr12	124803834	3.78	gc TGCCCCACAGGGCAG c AAAGG
HBB_Tcell-4	chr17	8370253	3.27	tTgct CCCACAGGGCAGTAAACG
HBB_Tcell-5	chr14	94585327	3.03	aTg CCCCAC a GGCAG a AATGG
HBB_Tcell-6	chr12	93549202	1.94	aTTG CCCCAC g GGGCAGT g ACGG
HBB_Tcell-7	chr22	17230623	1.52	tg TGCCCCACAG a GC Ac TAAAGG
HBB_Tcell-8	chrX	75006257	1.46	gTg CCCCACAGGGCAG g AATGG
HBB_Tcell-9	chr6	23709579	1.23	gaa GCCCTACAGGGCAGC AAT GG
HBB_Tcell-10	chr2	121715240	1.06	gTgt CCCCACAGGGCAG g AAAGG
HBB_Tcell-11	chr19	50010010	0.50	aTTG CCCC c CAG Gt CAGTA g GGG
HBB_Tcell-12	chr5	131423385	0.23	tc TGCCCCACAG Gc CAG g AAGGG

Supplemental Table 3. Off-target candidate sites captured by DIG-seq aligned to GRCh38.

HeLa				
	Chromosome	Location	DNA Cleavage score	Target sequence
On-target	chr11	5226985	14.20	CTTGCCCCACAGGGCAGTAACGG
HBB-2	chr9	101833601	8.07	tcaGCCCCACAGGGCAGTAAGGG
HBB-3	chr17	8466935	6.58	tTgctCCCACAGGGCAGTAAACG
HBB-4	chr12	124319288	6.54	gcTGCCCCACAGGGCAGcAAAGG
HBB-5	chr14	94118990	3.96	aTgGCCCCACAAGGCAGaAATGG
HBB-6	chr22	16749733	3.43	tgTGCCCCACAGaGCACTAAGGG
HBB-7	chr2	120957664	3.04	gTgtCCCCACAGGGCAGgAAAGG
HBB-8	chr12	93155426	2.89	ATTGCCCCACgGGGCAGTgACGG
HBB-9	chr7	98244859	2.86	CcctCCCCACAGGGCAGTcATGG
HBB-10	chr3	19916142	2.82	gcTaCCCCACAGGGCAtTAGGGG
HBB-11	chrX	75786422	2.76	gTgGCCCCACAGGGCAGgAATGG
HBB-12	chr15	46305931	2.57	gTTGCCCCtCAGGaCAGTAcAGG
HBB-13	chr9	93875126	2.54	acaGCCCCACAGGGCAtaAACGG
HBB-14	chr5	132087692	2.53	tcTGCCCCACAGGcCAGgAAGGG
HBB-15	chr8	25073866	2.52	agTGCCaCACaCaGCAGTAAGGG

Supplemental Table 4 :Mutation frequencies of Cas9 at on-target and off-target sites captured by DIG-seq.

HBB								
	Chromosome	Location	DNA Cleavage score	Target sequence	Indel frequency (%)			Chromatin accessibility (1= DNase I hypersensitive sites, 0 = DNase I non-sensitive sites)
					Untreated	(+)Cas9		
On-target	chr11	5248215	14.20	CTTCCCCACAGGGCAGTAACGG	0.01	35.70	validated	0
HBB-2	chr9	104595883	8.07	tcaGCCCCACAGGGCAGTAAGGG	0.03	31.18	validated	0
HBB-3	chr17	8370253	6.58	tTgctCCCACAGGGCAGTAACG	0.06	0.06	Not validated	0
HBB-4	chr12	124803834	6.54	gcTCCCCACAGGGCAGCAAGG	0.01	2.90	validated	0
HBB-5	chr14	94585327	3.96	aTgCCCCACAaGGCAGaAATGG	0.02	0.01	Not validated	0
HBB-6	chr22	17230623	3.43	tgTCCCCACAGaGCATAAAGG	0.01	0.01	Not validated	0
HBB-7	chr2	121715240	3.04	gTgtCCCCACAGGGCAGgAAAG	0.05	0.03	Not validated	0
HBB-8	chr12	93549202	2.89	aTTGCCCCaGggGCAGTgACGG	0.07	0.09	Not validated	0
HBB-9	chr7	97874171	2.86	CcctCCCCACAGGGCAGTcATGG	0.01	0.01	Not validated	0
HBB-10	chr3	19957634	2.82	gcTaCCCCACAGGGCAtTAGGG	0.00	0.02	Not validated	0
HBB-11	chrX	75006257	2.76	gTgCCCCACAGGGCAGgAATGG	0.01	1.24	validated	0
HBB-12	chr15	46598129	2.57	gTTGCCctCAGGaCAGTAcAGG	0.00	0.00	Not validated	0
HBB-13	chr9	96637408	2.54	acaGCCCCACAGGGCAtAACGG	0.13	0.10	Not validated	0
HBB-14	chr5	131423385	2.53	tcTgCCCCACAGGcCAGgAAGGG	0.02	0.01	Not validated	0
HBB-15	chr8	24931381	2.52	agTGCCaCACaGCAGTAAGGG	0.01	0.00	Not validated	0
HBB-16	chr14	36889538	2.31	gTTatCCCACAGGaCAGTgAGGG	0.02	0.00	Not validated	0
HBB-17	chr20	39992928	2.31	agTgGCCCCCAGGGCAGTgAGGG	0.01	0.00	Not validated	0
HBB-18	chr1	177593980	2.15	tcTaCCCCACatGGCAGTAATGG	0.08	0.01	Not validated	0
HBB-19	chr6	23709579	1.95	gaagCCctACAGGGCAGcAATGG	0.01	0.03	Not validated	0
HBB-20	chr4	148531374	1.75	gTTaCctCACAGaGCAGaAAGGG	0.01	0.01	Not validated	0
HBB-21	chr10	72286450	1.47	CaagCCCCACAGGGCAGaAGGG	0.00	0.00	Not validated	0
HBB-22	chr19	8560462	1.31	aaatCCCCACAGGGCAGTAAGGC	0.00	0.00	Not validated	0
HBB-23	chr11	76387498	1.18	CTgcCCctcagGGaCAGTatGGG	0.05	0.04	Not validated	0
HBB-24	chr5	14347051	1.08	CaTaCCCCACAGgtCAGTAAGGA	0.02	0.01	Not validated	0
HBB-25	chr1	17346702	0.95	ggTcCCcagGgtCAGTAAGGG	0.01	0.00	Not validated	0
HBB-26	chr15	29983547	0.78	CcaGCCCCACAGGGCAGTAAGC	0.00	0.00	Not validated	0
HBB-27	chr19	34262012	0.78	gcTGctCCACAGGGCAGgtATGG	0.01	0.00	Not validated	0
HBB-28	chr10	73555691	0.78	CagGCCCCACAGGaCAGgAAGGG	0.02	0.01	Not validated	0
HBB-29	chr19	50010010	0.73	aTTGCCCCcAGgtCAGTAGGGG	0.00	0.00	Not validated	1
HBB-30	chr15	34059408	0.56	gTTaCCaCACAGaGCAGTAAAG	0.03	0.03	Not validated	0
HBB-31	chr13	44886376	0.54	ggaGCCCCACAGGGCAGagAGGG	0.01	0.02	Not validated	0
HBB-32	chr9	134609673	0.50	tTTGCCctCAGGGCAGctAAGG	0.00	0.01	Not validated	0
HBB-33	chr16	49082904	0.46	gaGCCCCACAGgtCAGTgAGGG	0.00	0.00	Not validated	0
HBB-34	chr3	128713852	0.45	aTaGCCCCACAGGGCAGgttAGG	0.01	0.01	Not validated	0
HBB-35	chr12	27234755	0.44	gaTGcttCACAGGaCAGgAAGGG	0.02	0.03	Not validated	1
HBB-36	chr19	923900	0.37	aaTtaCCcCAGGGCAGgAAGGG	0.02	0.02	Not validated	0
HBB-37	chr8	143699609	0.35	CcaGCCCCaCgGGGCAGTAgATG	0.01	0.09	Not validated	0
HBB-38	chr12	50056756	0.22	aagGCCCCgCAGGGCAGTttGGG	0.55	0.52	Not validated	0
HBB-39	chr2	240591539	0.20	acaGCCCCACAGGGCActAgAGG	0.14	0.02	Not validated	0
HBB-40	chr17	66624245	0.17	CcTctCCCACAGGGCAGTAAGG	0.00	0.00	Not validated	0
HBB-41	chr9	134994964	0.15	CcTGCCCCACAGGGCAaTtATGG	0.01	0.00	Not validated	0
HBB-42	chr2	43013308	0.15	CcTGCCcagTaaGGCAGTAAGGG	0.13	0.09	Not validated	0
HBB-43	chr8	41296595	0.14	tcaGCCCCACAGgtCAGcAATGG	0.01	0.00	Not validated	0
HBB-44	chr22	35537395	0.14	agTGCCCCACAGGGgAGaAATGG	0.01	0.00	Not validated	0

VEGFA1								
	Chromosome	Location	DNA Cleavage score	Target sequence	Indel frequency (%)			Chromatin accessibility (1= DNase I hypersensitive sites, 0 = DNase I non-sensitive sites)
					Untreated	(+)Cas9		
On-target	chr6	43737297	8.0	GGGTGGGGGAGTTTGCTCCAGG	0.01	21.77	validated	0
VEGFA1-2	chr17	39796328	6.3	taGTGgaGGGAGcTTGCTCCTGG	0.00	16.90	validated	0
VEGFA1-3	chr12	1988077	5.2	cGGgGgaGGGAGTTTGCTCCTGG	0.00	11.73	validated	0
VEGFA1-4	chr6	14316373	4.5	GtGgGGGtaGAGTTTGCTCCAGG	0.02	8.10	validated	0
VEGFA1-5	chr15	65637537	3.7	GgaTGgaGGGAGTTTGCTCCTGG	0.01	25.28	validated	0
VEGFA1-6	chr16	8763213	3.5	aaGTaaGGGaAGTTTGCTCCTGG	0.01	0.01	Not validated	0
VEGFA1-7	chr11	71497119	3.3	aGGaaGgaGGAGTTaGCTCCTGG	0.00	0.02	Not validated	0
VEGFA1-8	chr12	26641302	3.1	aGtTtGGGGGAGTTTGcCCAGG	0.12	0.12	Not validated	0
VEGFA1-9	chr5	139263024	3.1	ttGgGGGGGcAGTTTGCTCCTGG	2.33	7.19	validated	0
VEGFA1-10	chr1	99347651	2.9	GGGgaGGGgaAGTTTGCTCCTGG	0.01	13.84	validated	0
VEGFA1-11	chr11	3445204	2.8	aGGaaGgaGGAGTTaGCTCCTGG	0.02	0.04	validated	0
VEGFA1-12	chr20	56175356	2.7	aGGgaGgaGGaATTTGCTCCAGG	0.00	0.72	validated	0
VEGFA1-13	chr5	32945275	2.2	GcGTGGGGGgtGTTTGCTCCCGG	0.03	1.00	validated	0
VEGFA1-14	chr17	47317539	2.1	ctGgtGGGGGAGcTTGCTCCAGG	1.64	4.14	validated	0
VEGFA1-15	chr3	125633992	2.1	aGGaaGgaGGAGTTaGCTCCTGG	0.02	0.01	Not validated	0
VEGFA1-16	chr12	131690199	1.9	GGGaGGgtGGAGTTTGCTCCTGG	0.00	6.70	validated	0
VEGFA1-17	chr13	31251013	1.8	tGtaGaGGgagtTTTGCTCCCGG	0.01	0.02	Not validated	1
VEGFA1-18	chr7	17819097	1.8	acaactGGGGAGTTTGCTCCTGG	0.02	0.03	Not validated	0
VEGFA1-19	chr22	18454623	1.6	GGaaGgaGGAGcTTGCTCCAGG	0.01	0.02	Not validated	0
VEGFA1-20	chr3	195871264	0.9	GGtgGGGgaGAGTaGCTCCGGG	0.00	0.20	validated	0
VEGFA1-21	chr22	19698463	0.6	GaGgGGGaGcAGTTTGCTCCAGG	0.01	0.56	validated	0
VEGFA1-22	chr17	32986325	0.5	GGGgGtGGGGAcTTTGCTCCAGG	0.04	0.02	Not validated	0
VEGFA1-23	chr22	37215276	0.5	GGGTGGGGGAGTTTGcCCAGG	0.06	1.69	validated	0

VEGFA1-24	chr13	28075024	0.4	atGaGGaGGGAGTTTGcACCAGG	0.01	0.01	Not validated	0
VEGFA1-25	chr6	50485682	0.4	atGTGtGGGGAAaTTTGCTCCAGG	0.02	0.01	Not validated	0
VEGFA1-26	chr5	7067159	0.3	GaGgGtGGGGAGTTTAcTCTCGG	0.07	0.28	validated	0
VEGFA1-27	chr15	93140401	0.3	GGGgGaGGGaAGTTTcCTCCAGG	0.02	0.01	Not validated	0
VEGFA1-28	chr11	67574262	0.3	aGgaAGaGGAGTTaGCTCTGG	0.01	0.73	validated	0
VEGFA1-29	chr2	129199817	0.2	tccTgaGGGcAGTTTGCTCCAGG	0.01	0.01	Not validated	0
VEGFA1-30	chr7	76022392	0.2	aGgGTGGGccGTTTGCTCCCGG	0.00	0.00	Not validated	1
VEGFA1-31	chr13	26202812	0.2	GGtTgaGGGAGTcTGCTCCAGG	0.01	0.17	validated	0

FANCF								
	Chromosome	Location	DNA Cleavage score	Target sequence	Indel frequency (%)			Chromatin accessibility (1= DNase I hypersensitive sites, 0 = DNase I non-sensitive sites)
On-target	chr11	22647338	6.3	GGAATCCCTTCTGCAGCACCCTGG	0.06	54.37	validated	0
FANCF-2	chr7	102131659	5.5	GtctcCCCTTCTGCAGCACCAGG	Interspersed repeat sequence			0
FANCF-3	chr10	73463136	4.1	tGAATCCCAcTcCAGCACCAGG	0.01	0.34	validated	0
FANCF-4	chr7	102230832	3.8	GtctcCCCTTCTGCAGCACCAGG	Interspersed repeat sequence			0
FANCF-5	chr11	66475045	3.5	GGAAcAcCTTCTGCAGCtCCAGG	0.00	0.07	validated	0
FANCF-6	chr16	28615201	3.2	GGctTCCCTTCTGCAGCcCCAGG	0.11	0.12	Not validated	0
FANCF-7	chr7	44076497	3.0	GtctcCCCTTCTGCAGCACCAGG	Interspersed repeat sequence			0
FANCF-8	chr18	8707528	1.7	GGAAcCCcgTCTGCAGCACCAGG	0.05	27.79	validated	0
FANCF-9	chr19	39405599	1.6	GctgTCCCTTCTGCAGCtCCAGG	0.52	0.69	Not validated	0
FANCF-10	chr9	139891539	1.5	aGttcCCCAcTCTGCAGCACCAGG	0.00	0.01	Not validated	1
FANCF-11	chr17	39675789	1.3	GGgAgTcCAcTCTGCAGCACCAGG	0.01	0.02	Not validated	0
FANCF-12	chrX	86355180	1.2	accATCCCTcCTGCAGCACCAGG	0.02	0.35	validated	0
FANCF-13	chr12	2719895	1.0	acAcTCCCTTCTGCAGCACCATG	0.00	0.01	Not validated	0
FANCF-14	chr10	43410031	0.7	GGAgTCCCTcCTaCAGCACCAGG	0.01	5.41	validated	0
FANCF-15	chr17	78923978	0.7	aGaggCCCCtCTGCAGCACCAGG	0.01	3.09	validated	0
FANCF-16	chr16	49671025	0.6	GGAgTCCCTcCTGCAGCACCTGA	0.00	0.82	validated	0
FANCF-17	chr10	37953200	0.6	GGAgTCCCTcCTaCAGCACCAGG	0.01	2.75	validated	0
FANCF-18	chr7	5013586	0.6	GGtccCtCcTcGCAGCACCCGG	0.01	0.02	Not validated	1
FANCF-19	chr2	133174786	0.5	atccTttCTTCTGCAGCACCCTGG	0.00	0.00	Not validated	0
FANCF-20	chr10	3151994	0.5	ctctgtCCTTCTGCAGCACCTGG	0.01	0.00	Not validated	0
FANCF-21	chr11	47554037	0.4	GGAATCCCTTCTaCAGCAcCTG	0.00	0.00	Not validated	0
FANCF-22	chr17	30452575	0.4	cctgctgCTTCTGCAGCACCTGG	0.00	0.00	Not validated	0
FANCF-23	chrX	153002368	0.3	ccAcTCCCTTCTGCAGCACCTGC	0.01	0.00	Not validated	0
FANCF-24	chr4	53092937	0.2	aatATtCCcTCTGCAGCACCAGG	1.44	1.42	Not validated	0
FANCF-25	chr17	65709672	0.2	atccCCCTTCTGCAGCcCCTGG	0.00	0.02	Not validated	0
FANCF-26	chr22	45871981	0.2	ccccTCCCTcCTGCAGCACCCGG	0.00	0.00	Not validated	0
FANCF-27	chr12	115467808	0.2	aGggTCCCTTCTGCAGCcCCTGG	0.04	0.06	Not validated	0
FANCF-28	chr19	10929976	0.2	aGtAaggCTTCTGCAGCACCTGG	0.00	0.00	Not validated	0
FANCF-29	chr3	35113165	0.2	tGAATCCtaaCTGCAGCACCAGG	0.00	0.00	Not validated	0
FANCF-30	chr2	242473665	0.1	GGgAatCCcTcccAGCACCCGG	0.00	0.00	Not validated	0
FANCF-31	chr20	61912779	0.1	cacATCCCTTCTGCAGCtCCcAG	0.01	0.01	Not validated	0
FANCF-32	chr1	223900677	0.1	GGctTCCcCaCTGCAGCACCCGG	0.03	0.03	Not validated	0
FANCF-33	chr22	26091104	0.1	ccgtcCCCTTCTGCAGCACCTCG	0.00	0.01	Not validated	0
FANCF-34	chr17	34985068	0.1	GGgtCcGCTTCTGCAGCACCTGG	0.00	0.00	Not validated	0
FANCF-35	chr1	27648497	0.1	aGcATCCCTTCTGCAGCcgcGGG	0.00	0.00	Not validated	0
FANCF-36	chr13	114815604	0.1	GgGAaCCCTTccGCAGCACCCAG	0.01	0.01	Not validated	0

HEK3								
	Chromosome	Location	DNA Cleavage score	Target sequence	Indel frequency (%)			Chromatin accessibility (1= DNase I hypersensitive sites, 0 = DNase I non-sensitive sites)
On-target	chr9	110184637	5.8	GGCCcAGACTGAGCAGCTGATGG	0.01	66.99	validated	1
HEK3-2	chr1	47005705	2.8	aGctCAGACTGAGCAaGTGAGGG	0.01	16.23	validated	0
HEK3-3	chr15	79749931	2.7	caCCCAGACTGAGCACGTGcTGG	0.00	33.14	validated	0
HEK3-4	chr10	131593121	1.5	GagCCAGaATGAGCACGTGAGGG	0.00	1.17	validated	0
HEK3-5	chr2	11810044	0.3	GcgCCAGgCTGAGCACGTGgTGG	0.00	0.01	Not validated	0
HEK3-6	chr17	34954539	0.1	cGgCCcACTGAGCAaGTGATGG	0.00	0.01	Not validated	0

RNF2								
	Chromosome	Location	DNA Cleavage score	Target sequence	Indel frequency (%)			Chromatin accessibility (1= DNase I hypersensitive sites, 0 = DNase I non-sensitive sites)
On-target	chr1	185056773	8.41	GTCATCTTAGTCATTACCTGAGG	0.01	68.06	validated	0
RNF2-2	chr5	92036966	1.03	GgtATCTaAGTCATTACCTGTGG	0.07	0.24	validated	0
RNF2-3	chr11	60883789	0.4	aTaaacGtAGTCATTACCTGGGG	0.00	0.00	Not validated	0
RNF2-4	chr8	99451745	0.3	cgtgcaTTAGTCATTACCTGAGG	0.01	0.02	Not validated	0

HEK2								
					Indel frequency (%)			
	Chromosome	Location	DNA Cleavage score	Target sequence	Untreated	(+)Cas9		Chromatin accessibility (1= DNase I hypersensitive sites, 0 = DNase I non-sensitive sites)
On-target	chr5	87240614	4.44	GAACACAAAGCATAGACTGCGGG	0.01	59.05	validated	0
HEK2-2	chr4	90522184	0.27	GAACACAAtGCATAGATTGCCGG	0.01	16.33	validated	0
HEK2-3	chr5	142142325	0.2	tAAacactAaCATAGACTGCAGG	0.00	0.00	Not validated	0

EMX1								
					Indel frequency (%)			
	Chromosome	Location	DNA Cleavage score	Target sequence	Untreated	(+)Cas9		Chromatin accessibility (1= DNase I hypersensitive sites, 0 = DNase I non-sensitive sites)
On-target	chr2	73160999	15.4	GAGTCCGAGCAGAAGAAGAAGGG	0.23	61.61	validated	0
EMX1-2	chr6	9118799	4.7	acGTCTGAGCAGAAGAAGATGG	0.03	0.75	validated	0
EMX1-3	chr5	45359067	3.4	GAGTtaGAGCAGAAGAAGAAAGG	0.02	47.11	validated	0
EMX1-4	chr15	44109764	1.9	GAGTCTaAGCAGAAGAAGAGaG	0.42	39.41	validated	0
EMX1-5	chr5	9227163	1.7	aAGTCTGAGCacAAGAAGATGG	0.02	19.00	validated	0
EMX1-6	chr1	33606480	1.2	GAGcCTGAGCAGAAGgAGAAGGG	0.01	0.08	validated	0
EMX1-7	chr18	34906762	0.8	GAGcCTGAGCgGAAGAGGAAAGG	0.02	0.03	Not validated	0
EMX1-8	chr16	78848850	0.8	aAaTCCaAcCAGAAGAAGAAAGG	0.03	0.06	Not validated	0
EMX1-9	chr4	87256693	0.6	GAGTaaGAGaAGAAGAAGAGGG	0.08	0.09	Not validated	0
EMX1-10	chr11	62365273	0.4	GAaTCCaAGCAGAAGAAGAGaAg	0.02	0.13	validated	0
EMX1-11	chr4	131662222	0.3	agaatCcAagAGAAGAAGATGG	0.00	0.00	Not validated	0
EMX1-12	chr15	61646877	0.2	aAGTCaGAGgAGAAGAAGAAAGGG	0.26	0.47	validated	0
EMX1-13	chr19	1438827	0.2	GAagtaGAGCAGAAGAAGAAAGcG	0.03	0.01	Not validated	0
EMX1-14	chr17	8640230	0.2	GAGaCTGAGaAGAAGAAGAAAGG	0.01	0.01	Not validated	0
EMX1-15	chr14	75723909	0.1	agtTCCaAGCAGAGgGAAGAAGGG	0.03	0.03	Not validated	0

CCR5-9								
					Indel frequency (%)			
	Chromosome	Location	DNA Cleavage score	Target sequence	Untreated	(+)Cas9		Chromatin accessibility (1= DNase I hypersensitive sites, 0 = DNase I non-sensitive sites)
On-target	chr3	46414766	12.2	TCATCCTCCTGACAATCGATAGG	0	86.42	validated	0
CCR5-9-1	chr10	48385259	0.3	aCATCCTtCTGACAATCatTTGG	0	0.85	validated	0

Supplemental Table 5 : Mutation frequencies of Cas9 off-target sites captured by Digenome-seq but missed by DIG-seq

	Chromosome	Location	DNA Cleavage score	Target sequence	Indel frequency (%)	
					Untreated	(+)Cas9
Digenome-only-01	chr11	76387498	31.4	CTgcCCcctcagGGaCAGTATGGG	0.01	0.00
Digenome-only-02	chr5	14347051	27.2	CaTaCCCCACAGGtCAGTAAGGA	0.01	0.01
Digenome-only-03	chr14	36889538	25.8	gTTatCCCACAGGaCAGTgAGGG	0.01	0.01
Digenome-only-04	chr9	134994964	24.9	CcTGCCCCACAGGGCaTtATGG	0.00	0.00
Digenome-only-05	chr16	49082904	21.6	gcaGCCCCACAGGtCAGTgAGGG	0.08	0.01
Digenome-only-06	chr9	134609673	21.4	tTTGCCCCtCAGGGCAGctAAGG	0.00	0.01
Digenome-only-07	chr3	3662556	20.2	aaaGCCCCACAGGGtAGTAGAGG	0.00	0.00
Digenome-only-08	chr6	50041372	15.1	tcTGCCCCACatGGCAGTAATGA	0.01	0.00
Digenome-only-09	chr5	37628319	15.1	acTGcACCACAGGcCAGaAATGG	0.07	0.06
Digenome-only-10	chr8	143699609	14.8	CcaGCCCCACcGGGCAGTAGATG	0.07	0.06
Digenome-only-11	chr12	27234755	12.9	gaTGCCtCACAGGaCAGgAAGGG	0.09	0.15
Digenome-only-12	chr2	240591539	12.9	acaGCCCCACAGGGCaCTAgAGG	0.00	0.00
Digenome-only-13	chr15	29983547	12.8	CcaGCCCCACAGGGCAGTAAAGC	0.03	0.03
Digenome-only-14	chr8	41296595	12.7	tcaGCCCCACAGtCAGcAATGG	0.01	0.00
Digenome-only-15	chr10	72286450	12.2	CaaGCCCCACAGGGCAGacAGGG	0.00	0.01
Digenome-only-16	chr19	34262012	12.0	gcTGctCCACAGGGCAGgtATGG	0.00	0.00
Digenome-only-17	chr6	85738203	10.4	acTGCCCCACAGGGaAGTAATAG	0.03	0.00
Digenome-only-18	chr20	39992928	10.1	agTGgCCCcCAGGGCAGTgAGGG	0.02	0.02
Digenome-only-19	chr13	44886376	9.7	ggaGCCCCACAGGGCAGagAGGG	0.02	0.02
Digenome-only-20	chr3	128713852	9.2	aTaGCCCCACAGGGCAGgttAGG	0.01	0.00
Digenome-only-21	chr1	177593980	8.9	tcTaCCCCACatGGCAGTAATGG	0.03	0.03
Digenome-only-22	chr4	45763604	8.5	gcTGCCCCACatGaCAGaAATGG	0.04	0.03
Digenome-only-23	chr15	34059408	7.9	gTTaCCaCACAGaGCAGTtAAGG	0.00	0.01
Digenome-only-24	chr4	148531374	7.9	gTTaCCtCACAGaGCAGaAAGGG	0.00	0.00
Digenome-only-25	chr22	35537395	7.2	agTGCCCCACAGGGgAGaAATGG	0.03	0.03
Digenome-only-26	chr10	73555691	7.0	CagGCCCCACAGGaCAGgAAGGG	0.01	0.02
Digenome-only-27	chr14	89458507	6.9	gaaaCCCCACAGaGCAGTAATGA	0.09	0.09
Digenome-only-28	chr12	50056756	5.3	aagGCCCCgCAGGGCAGTttGGG	0.11	0.08
Digenome-only-29	chr6	23709579	4.4	gaaGCCCCtACAGGGCAGcAATGG	0.02	0.01
Digenome-only-30	chr19	8560462	4.3	aaatCCCCACAGGGCAGTAAGGC	0.00	0.02
Digenome-only-31	chr1	17346702	4.0	ggTcCCCacagGGtCAGTAAGGG	0.00	0.00
Digenome-only-32	chr19	37539042	3.8	CTTGcACCACAGaGCAcTAAGGG	0.02	0.01
Digenome-only-33	chr7	57716477	3.0	tgTGcACCACAGaGCAaTAAGGG	0.00	0.02
Digenome-only-34	chr1	34925501	2.7	agTtgCCCACAGGcCAGTAAGAG	0.00	0.00

Supplemental Table 6. Comparison of off-target candidate sites captured by Digenome-seq and DIG-seq .

HBB				
Chromosome	Location	Target sequence	Captured by Digenome-seq	Captured by DIG-seq
chr11	5248215	CTTGCCCCACAGGGCAGTAACGG	o	o
chr17	8370253	tTgct CCCACAGGGCAGTAAACG	o	o
chr22	17230623	tg TGCCCCACAG aGCAC TAAGGG	o	o
chr8	24931381	ag TGCC aCACa GCAGTAAGGG	o	o
chr15	46598129	g TTGCC ct CAG a CAGT Ac AGG	o	o
chrX	75006257	gTg CCCCACAGGGCAG g AATGG	o	o
chr12	93549202	a TTGCC CCACg GGGCAGT g ACGG	o	o
chr14	94585327	aTg CCCC ACAa GGCAG a AATGG	o	o
chr9	104595883	tca CCCCACAGGGCAGTAAGGG	o	o
chr2	121715240	gTgt CCCCACAGGGCAG g AAAGG	o	o
chr12	124803834	gc TGCC CCACAGGGCAGc AAAGG	o	o
chr3	19957634	gcTa CCCCACAGGG CAt TA g GGG	x	o
chr9	96637408	aca CCCCACAGGG CAta AACGG	x	o
chr7	97874171	Ccct CCCCACAGGGCAGT c ATGG	x	o
chr5	131423385	tc TGCC CCACAGGc CAG g AAGGG	x	o
Chr1	177593980	tcTa CCCC ACAt GGCAGTAATGG	o	x
Chr6	50041372	tc TGCC CCACAt GGCAGTAATGA	o	x
Chr6	23709579	gaa GCC ct ACAGGGCAG c AATGG	o	x
Chr14	36889538	gTTat CCCACAG ga CAGT g AGGG	o	x
Chr1	17346702	Cggt CCCCACAGGG tcagt AAGG	o	x
Chr20	39992928	agTgG CCCC c CAGGGCAGT g AGGG	o	x
Chr10	95791920	acTct CCC ACAa GGCAGTAAGGG	o	x
Chr4	148531374	gTTa C ct CACAG a GCAG a AAGGG	o	x
Chr5	53613387	tcac CCCCACAG Gc CAGTAAGG	o	x

VEGFA1				
Chromosome	Location	Target sequence	Captured by Digenome-seq	Captured by DIG-seq
chr6	43737297	GGGTGGGGGGAGTTTGCTCCAGG	o	o
chr17	39796328	ta GTGG a GGGAG c TTGCTCCTGG	o	o
chr12	1988077	cGGg GG a GGGAGTTTGCTCCTGG	o	o
chr6	14316373	GtGg GGG ta GAGTTTGCTCCAGG	o	o
chr15	65637537	GG a TGG a GGGAGTTTGCTCCTGG	o	o
chr16	8763213	aaGTaa GGG a AGTTTGCTCCTGG	o	o
chr11	71497119	aGGaa GG a GGAGTT a GCTCCTGG	o	o
chr12	26641302	aGtTt GGGGGAGTTTG Cc CCAGG	o	o
chr5	139263024	ttGg GGGG Gc AGTTTGCTCCTGG	o	o
chr1	99347651	GGG ga GGGG a AGTTTGCTCCTGG	o	o
chr11	3445204	aGGaa GG a GGAGTT a GCTCCTGG	o	o
chr20	56175356	aGGga GG a GG a ATTTGCTCCAGG	o	o
Chr5	7067159	GaGgGt GGGGAGTT Ta CTCCTGG	o	x
Chr22	37215276	GGGTGGGGGGAGTTTG Cc CCAGG	o	x
Chr17	32986325	GGG Gt GGGG Ac TTTGCTCCAGG	o	x
Chr1	82627648	GGGT Gct GG c Acag TGCTCCTGG	o	x
Chr1	233157354	GG agGa GGGGAGT c TGCTCCAGG	o	x
Chr10	124731416	aGc TGG a GGGAGTTTG Cc CCAGG	o	x
Chr12	131690199	GGG a GG gt GGAGTTTGCTCCTGG	o	x
Chr20	7836107	caGgt GGG a GAGTTTGCTCCAG	o	x
Chr4	8453803	GAGTGGG t GGAGTTTGCT a CAGG	o	x
Chr9	88657759	GG a TGG a GG t AGTTT gt TCCTGG	o	x
Chr9	93925190	GGG Gt GGGGAG ca TGCTCCAGG	o	x

Chr3	125633992	aGGaaGGaGGAGTTaGCTCCTGG	0	x
Chr8	140714327	GGGaGGaGaGAGTTTGCTCtCTG	0	x
Chr15	93140401	GGGgGaGGGaAGTTTcCTCCAGG	0	x
Chr2	209437600	aGGgaGGGaGAaTTTGCTCCTGG	0	x
Chr3	128284321	aGGTGGtGGGAGcTTGtTCCTGG	0	x
Chr5	32945275	GcGTGGGGGtGTTTGCTCCCGG	0	x
Chr13	26202812	GGtTGaGGGGAGTcTGCTCCAGG	0	x
Chr5	156390	tGcTcGGGGGAGTTTGCaCCAGG	0	x
Chr21	43689878	GGcccaGGGGAGTTTGCTCCAG	0	x
Chr19	51310920	GtGcaGGGGGAaTTTGCTtCCGG	0	x
ChrX	82127748	aGagGGGGaGAGTTTGcCcCTGG	0	x
Chr7	17819097	acaactGGGGAGTTTGCTCCTGG	0	x
Chr22	41676762	aGtgcaGGGGAGcTTTGCTCCTGG	0	x
Chr2	96056645	GGGTGGGGaGAGTTTcTCCTGG	0	x
Chr3	195871264	GGtgGGGGaGAGcTaGCTCCGGG	0	x
Chr6	45554056	GGGgtGGGaGAGTTTGCTcCTG	0	x
Chr18	366714	GGGgGcaGGGAGaTTTGCTCCTGG	0	x
Chr3	13580170	atGgGGGaGaAacTTTGCTCCTGG	0	x
ChrX	19185601	GGGaGGGGaGAGTTTgtTCCAGG	0	x
Chr11	67574262	aGGaaGGaGGAGTTaGCTCCTGG	0	x
Chr17	47317539	ctGgtGGGGAGcTTTGCTCCAGG	0	x
Chr6	91365255	cccgGGGGGaAGcTTTGCTCCAGG	0	x
Chr22	18454623	GGaaaGGaGGAGcTTTGCTCCAGG	0	x
Chr22	19698463	GaGgGGGaGcAGTTTGCTCCAGG	0	x
Chr3	36358934	aGtgGGGGaGAGTaTGCTCCGGG	0	x
Chr21	37116659	aaGTGGGaAGAGTTGtTCCAGG	0	x
Chr11	117481208	GGGcaaGGGGAGgTTTGCTCCTGG	0	x
Chr7	29081029	GGagtGGGtGAGcTTTGCTCCTGG	0	x
Chr17	63035708	aGgaGGGGGaAGaaTGCTCCAGG	0	x
Chr2	181170961	tGGgGaGGGGaaaTTTGCTCCTGG	0	x
Chr6	109284989	tGgaGaGGGGAGTtgGCTCCTGG	0	x
Chr11	122583511	aGaaGaGGGGATTTTGCTCCTGG	0	x
Chr5	56172079	GGtgGGGtGgTTTGCTCCTGG	0	x
Chr1	33643288	GGGTGGgtGGAGTTTGCTaCTGG	0	x
Chr8	28483353	aaGTGGGaGGAGacTGCTCCAGG	0	x
Chr22	38219333	aGGTcGGGGGAGTTaGaTCCCGG	0	x
Chr15	29263777	GGGatGGGaGAGTcTGCTCCTGG	0	x
Chr2	30430777	aGGgaGaGGGAGcTTTGCTCCAG	0	x
Chr12	107832636	tctTGGGGGGAagTTTGCTCCAGG	0	x
Chr4	185246171	GGagGGGGGcTTTGCTCCAGG	0	x
Chr8	10804669	GaGTGaGGaGAGcTTTGCTCCATG	0	x
Chr5	95220670	GGGaGcaGGGAaTTTGCTCCAGG	0	x
Chr2	129199817	tccTGaGGGcAGTTTGCTCCAGG	0	x
Chr13	31251013	tGtaGaGGGagtTTTGCTCCCGG	0	x
Chr16	89679839	GGagGaGGGaAcTTTGCTCCAGG	0	x
Chr1	20166440	GtGgGaGGatAGcTTTGCTCCTGG	0	x
Chr18	13983474	GGGTGaaaGaAGTTTaCTCCTGG	0	x
Chr6	50485682	atGTGtGGGGaTTTGCTCCAGG	0	x
Chr1	205484156	GtGTGaGtGGAGTTTGCTcTGGG	0	x
Chr6	109070771	GGtgGGGGaaAGTTTGCTCCTGA	0	x
Chr15	101813024	aaGgaGGcGGAGcTTTGCTCCTGG	0	x
Chr11	11823598	GGcTGGaGGGgaTTTGCTCCTGG	0	x
Chr9	5336085	tcGTGGtGGGAaTTTaCTCCTGG	0	x
Chr4	116853325	aaagGGGGGaAcTTTGCTCCAGG	0	x
Chr11	86695108	aGGgaaGGGGaATTGCaCCTGG	0	x

Chr5	57030871	ctcTgaGGGGAGTTTGTCTtGGG	0	x
Chr15	84047385	GGagtcaGGGAaTTTGCTCCTGG	0	x

FANCF				
Chromosome	Location	Target sequence	Captured by Digenome-seq	Captured by DIG-seq
chr11	22647338	GGAATCCCTTCTGCAGCACCTGG	0	0
chr7	102131659	GtctcCCCTTCTGCAGCACCAGG	0	0
chr10	73463136	tGAATCCCaTCTcCAGCACCAGG	0	0
chr7	102230832	GtctcCCCTTCTGCAGCACCAGG	0	0
chr11	66475045	GGAAcaCCTTCTGCAGctCCAGG	0	0
chr16	28615201	GGctTCCCTTCTGCAGcCCAGG	0	0
chr7	44076497	GtctcCCCTTCTGCAGCACCAGG	0	0
Chr10	37953200	GGAgTCCCTcCTaCAGCACCAGG	0	x
Chr10	43410031	GGAgTCCCTcCTaCAGCACCAGG	0	x
Chr18	8707528	GGAAcCCCgTCTGCAGCACCAGG	0	x
Chr16	49671025	GGAgTCCCTcCTGCAGCACCTGA	0	x
Chr3	35113165	tGAATCCtaACTGCAGCACCAGG	0	x
Chr20	44903573	tccATCCCTaCTGCcagcaCCAG	0	x
Chr3	10885901	acccTCCCTTCTGCAGgcaCCGG	0	x
Chr10	3151994	ctctgtCCTTCTGCAGCACCTGG	0	x
Chr17	39675789	GGgAgTCCaTCTGCAGCACCAGG	0	x
Chr11	47554037	GGAATCCCTTCTaCAGCatCCTG	0	x
Chr2	54853314	GGAATatCTTCTGCAGcCCAGG	0	x
Chr12	115467808	aGggTCCCTTCTGCAGCcCCTGG	0	x
ChrX	86355180	accATCCCTcCTGCAGCACCAGG	0	x
Chr2	35692938	acttTatCTTCTGCAGCACCTGG	0	x
Chr2	133174786	atccTttCTTCTGCAGCACCTGG	0	x
Chr12	2719895	acAcTCCCTTCTGCAGCACCATG	0	x
ChrX	97566910	tGtATtCCTTCTGCAGgcaCCAG	0	x
Chr17	30452575	cctgctgCTTCTGCAGCACCTGG	0	x
Chr9	113162294	aaAATCCCTTCCGCAGCACCTAG	0	x
Chr4	53092937	aatATtCCcTCTGCAGCACCAGG	0	x
Chr3	97725864	accATttCTTCTGCAGCACCTGG	0	x
Chr17	34985068	GGgtcCgCTTCTGCAGCACCTGG	0	x
Chr9	111467809	aGgAatCCTaCTGCAGCACCCAG	0	x
Chr4	76159966	ttAcTCaCTTCTGCAGgcaCCTG	0	x
Chr5	68338523	ccAcTCctTTCTGCAGCACCCGG	0	x
Chr17	3980376	GGAAcCCCCtCTGCAGcttCTGG	0	x
Chr20	19790626	cattTtCtTTCTGCAGCACCTGG	0	x
Chr17	78923978	aGAggCCCCtCTGCAGCACCAGG	0	x
Chr8	71384404	tttcctgCTTCTGCAGCACCAGG	0	x
Chr17	39655735	GccccCtCcTCTGCAGCACCTGG	0	x
Chr6	41457565	ctccTCCCTcCTGCAGCACCTGG	0	x
Chr13	109802140	aaAATaCCTTCTGCAGtACCAGG	0	x
Chr5	85696042	ctAcTgaCTTCTGCAGCACCTGG	0	x
Chr4	7336836	aGctcCCaTTCTGCAGCACCCGG	0	x
Chr9	139891539	aGttcCCCaTCTGCAGCACCAGG	0	x
Chr10	13436789	ctcATCCCTTCTGCAGcCCAGG	0	x
Chr2	176121765	GccccCtgcTCTGCAGCACCCGG	0	x
Chr13	100011450	acctgCctTctgGCAGCACCAGG	0	x
Chr17	8432606	actgTCatTTCTGCAGCACCTGG	0	x

HEK3				
Chromosome	Location	Target sequence	Captured by Digenome-seq	Captured by DIG-seq
chr9	110184637	GGCCCAGACTGAGCACGTGATGG	0	0
chr1	47005705	aGcTcAGACTGAGCAaGTGAGGG	0	0
chr15	79749931	caCCCAGACTGAGCACGTGcTGG	0	0
Chr10	131593121	GagCCAGAAcTGAGCACGTGAGGG	0	x
Chr7	66968042	GaCaCAGACcGgGCACGTGAGGG	0	x
Chr11	134582415	GGCgCAGACaGAGCACGTGACGA	0	x
ChrX	114764149	aGaCCAGACTGAGCAaGaGAGGG	0	x
Chr4	72203005	atatCAGACTGAGCACcgtgAGG	0	x
Chr6	103918240	aaataAGACTGAGCACGTGgTGG	0	x
Chr17	7594610	agCCagactgagGCAaGTGAGGG	0	x
Chr3	160129761	aGgCCAGACTGAaCACGatgAGG	0	x
Chr15	35402774	cctaaAGACTGAGCAaGTGAAGG	0	x
Chr9	137039236	cagCCAGACaGAGCACGTGgAGG	0	x
Chr6	79958440	aaCaaAGACTGAGCACGTtAGGG	0	x
Chr2	130402896	GaCCCAGAAcTGAGCACaaaAGGG	0	x
Chr1	34163192	attCtAGACTGAGCACGTGcAAG	0	x
Chr2	97163211	ccCatgGACTGAGCACatGAAGG	0	x
Chr17	79043523	tGgCCAGACTGAGcTCGTGAGTG	0	x
Chr10	22896606	GaaggAGACTGAGCATtGTGAGGG	0	x
Chr8	20947876	tctCCAGACTGAGCcCaTGAGGG	0	x
Chr19	19169358	GGaCCAGgCTGAGCACatGgAGG	0	x
Chr6	112273496	aagCCAGACTGAGCACGTtcAGG	0	x
Chr1	229294224	GGtCatcACTGAGCACGTGAGGT	0	x
Chr2	240026760	GGcTcAGACTGAGCACcTGAGAG	0	x
Chr15	94188821	attCCAGAAcTGAGCACaTGAAGG	0	x
Chr2	131090691	acCCaAGACaGAGCACGTGgAGG	0	x
Chr11	60830962	tcCCagaACTaAGCACGTGAATG	0	x
Chr14	102917106	ctCggAGACTGAcCACGTGAGGG	0	x
Chr10	23135503	actCCAGACTGAGCAacTGAGGG	0	x
ChrX	16606309	ttCCAGACaaAGCACGcGAAGG	0	x
Chr14	78070357	aaCCagactgGAGCACGTGgTGG	0	x

RNF2				
Chromosome	Location	Target sequence	Captured by Digenome-seq	Captured by DIG-seq
chr1	185056773	GTCATCTTAGTCATTACCTGAGG	0	0
Chr12	131619805	aTCAcCTTAGcCATTACcAGGGG	0	x
Chr18	62061226	aTtATtTTAGTCATTACCTtTGG	0	x
Chr8	99451745	cgtgcaTTAGTCATTACCTGAGG	0	x
Chr7	43967267	acttatTTAGTCATTACCTGTAG	0	x
Chr6	143212079	GTaATaTTAGTCATTACcGTGG	0	x
Chr4	171989625	taacaCaTAGTCaCTACCTGGTG	0	x
Chr8	5745882	aatATgTTAGTCATTACCTGAGG	0	x
Chr4	189725512	aTgcTtcTtGTCATTACCTtGGG	0	x
Chr9	138721895	acttcagTAGTCATTACCTaGGG	0	x
Chr5	92036966	GgtATCTaAGTCATTACCTGTGG	0	x
Chr15	25135467	catcTaaTAGTaATTACCTGGGG	0	x
Chr17	53928586	GTCATCTTAGTCATTAC - TGAGG	0	x

HEK2				
Chromosome	Location	Target sequence	Captured by Digenome-seq	Captured by DIG-seq
chr5	87240614	GAACACAAAGCATAGACTGCGGG	0	0
Chr4	90522184	GAACACAAtGCATAGAtTGCCGG	0	x
Chr10	43159340	aAcacaAAGaCATAGACcaCTGG	0	x
Chr1	40461425	tAcacacAAGCAcAGACTGCAGG	0	x
Chr2	19844956	aActcCAAAGCATAtACTGCTGG	0	x
Chr15	93557679	agAacacAtGCATAGACTGCTAG	0	x
Chr11	128508577	GAAttCAAAGCATAGAtTGCAGG	0	x
Chr5	131174461	aAAtACAAtGCATAGACTGCTAG	0	x
Chr19	30112719	tAcacaAAAcataAGACTGCTGG	0	x
Chr20	97641	GAAttCAAAGCATAGAtTGCAGG	0	x
Chr4	53536210	GAAtACTaAGCATAGACTcCAGG	0	x
Chr13	113428467	cAAtACAAAGgATAGACTGCAGG	0	x
Chr18	22360702	GgAatCAAAGCAcAGACTGCAGG	0	x
ChrX	36949815	GAAaACAAAaCATAGAgTGCTGG	0	x
Chr7	83764327	actatatAAGCATAGACTGtTGG	0	x
Chr5	126385455	ccACACcAAGCATAGACTtCTGG	0	x
Chr5	142142325	tAAacactAaCATAGACTGCAGG	0	x
Chr18	56307003	aAgAACAAAaCATAGACTGCAGG	0	x
Chr1	36097073	GtAaACAAAGCATAGACTGaGGG	0	x
Chr3	81710854	ctcCtaAAGcatTAGACTGCAGG	0	x
Chr5	7625837	GgtacacAAtaATAGACTGCAGG	0	x
Chr18	5596266	cctacagAAGCATAGACTGCAGG	0	x
Chr6	139353018	ccAaACAAAaCATAGACTGCTGG	0	x
Chr22	28895718	attaAgAtAGCATAGACTGCAGG	0	x
Chr1	77190607	tcACACAAAcCATAGACTGaGGG	0	x
Chr6	40925010	aAcaAgtAtGCATAGACTGCTGG	0	x
Chr9	97332609	GtAattAAAGCAcAGACTGCTGG	0	x
Chr18	68431104	tgtgtaAgAGCATAGACTGCTGG	0	x
Chr20	23101380	atACACAgAGCAaAGACTGCAGG	0	x
Chr8	97317605	GAACACAgtaCATAGACTGgCAG	0	x
Chr9	290168	aACATAAAGaATAGACTGCAAG	0	x
Chr6	152710071	tActctAtAtCATAGACTGCTGG	0	x
Chr4	31157435	tgAttgAgtGCATAGACTGCTGG	0	x
Chr1	108869935	agtatagcAGCATAGACTGCAGG	0	x
Chr15	65377019	GAgCgataAGCAcAGACTGCTGG	0	x

EMX1				
Chromosome	Location	Target sequence	Captured by Digenome-seq	Captured by DIG-seq
chr2	73160999	GAGTCCGAGCAGAAGAAGAAGGG	0	0
chr6	9118799	acGTctGAGCAGAAGAAGAATGG	0	0
chr5	45359067	GAGTtaGAGCAGAAGAAGAAAGG	0	0
Chr11	62365273	GAaTCCaAGCAGAAGAAGAgaAAG	0	x
Chr19	1438827	GAagtaGAGCAGAAGAAGAAGCG	0	x
Chr1	234492864	GAagtaGAGCAGAAGAAGAAGCG	0	x
Chr2	172374203	GAagtaGAGCAGAAGAAGAAGCG	0	x
Chr2	219845073	GAGgCCGAGCAGAAGAAgACGG	0	x
Chr1	23720618	aAGTCCGAGgAGAgGAAGAAAGG	0	x
Chr12	106646091	aAGTCCatGCAGAAGAgGAAGGG	0	x
Chr15	44109764	GAGTctaAGCAGAAGAAGAAGAG	0	x
Chr8	128801260	GAGTCCtAGCAGgAGAAGAAGAG	0	x
Chr15	22366622	GgagtaGAGCAGAgGAAGAAGGG	0	x
Chr9	127309505	aAGcCCaAGCAaAtGAAGAATGG	0	x
Chr11	43747949	aAGcCCGAGCAaAgGAAGAAAGG	0	x

Chr5	9227163	aAGT Ct GAGCA c AAGAAGAATGG	0	x
Chr10	128080196	GAGT a CaAGCAGAT t GAA a AACGG	0	x
Chr1	33606480	GAG c Ct GAGCAGAAG g AGAAGGG	0	x
Chr3	34042974	GAGT t CaAGCAG Aga A gaa AGGG	0	x
Chr21	24667742	ccc TCC a AGCAGAAGAAG t GAG	0	x
Chr14	38654666	aAGT Ct GAG a AGAAGAAG c ATG	0	x
Chr18	68861321	agag ta GA a CAGAAGAAG g AAAG	0	x
Chr4	87256692	GAGT aa GAG a AGAAGAAGAAGGG	0	x
Chr10	58848729	GAG ca CGAGCA ag AGAAGAAGGG	0	x
Chr8	74634212	aAGTCC a aaa AGAAG aaa AAAGG	0	x
Chr19	24250503	GAGTCC a AGCAG t AG g GAAGGG	0	x
Chr8	105164126	GAG c CC a AG a AGAAGAAGAAGGA	0	x
Chr14	43156807	GAG g CC a AGCAG aa AAAATGG	0	x
Chr11	30301809	c AGT Ct GAG t AGAAG aaa AAGGG	0	x
Chr4	58838593	aAGTCC c AG a AGAAG aa tATGG	0	x
Chr15	65614525	GAG agg GAGCAG ggag A g AAGG	0	x
ChrX	149010707	Ggag t CaAG g AGAAGAAGAAGAG	0	x
Chr7	111475449	GAG c CC a AGC a CA aa AAGAATGG	0	x
Chr14	48932120	GAGTCC c AGCA aa AAGAAGAAAAG	0	x
Chr10	91416162	at GTCC a AGCAGAAGAAG tc TGG	0	x
Chr12	102743729	t AGT Ca GAGCAG t GAAG g AAAG	0	x
Chr3	95690186	tca TCC a AGCAGAAGAAGAAGAG	0	x
Chr3	16077518	GAG g CaGAG aga AAGAAGAAAGG	0	x
Chr12	73504675	GAGT ta GAGCAG aa AAAATGG	0	x
Chr5	141129457	aAGT Cac AG g AG c AGAA g AAGA	0	x
Chr7	31901077	GAG g CC a AGCAG aa g A aa AGG	0	x
Chr1	209931600	tt aTCCGAG a AGAAGAAG t AAGG	0	x
Chr6	106901799	GAG c C g GAGCAG ggag A g AAGG	0	x
Chr22	34858917	GAG c Ct GAGCAG g A g A g AAGA	0	x
Chr6	29806752	tgtc Ca ag GCAG g AGAAGAAGGG	0	x
Chr15	36839471	c AG aga GAG g AG c AGAAA aa AGA	0	x
Chr5	134375867	c AG g Ct GAGCAG aa g A g AAAG	0	x
Chr2	199919487	GAGT Ca GAGCAG aa ct AGAAGGG	0	x
Chr20	6653999	aAGTCC aga CAGAAGAAGAAGGA	0	x
Chr8	135098073	c AGTCC agcag GAAGAAG g AGG	0	x
Chr11	131106371	G cc TCC a AGCAGAAG g AGAAATG	0	x
Chr9	2513258	GAG aga GAGCA aa AG g A g AATG	0	x
Chr17	72057114	GAG gagagcaga AAGAAGAAGGG	0	x
Chr16	56184077	aAGT Ca GAG a AG g A g A g AAAG	0	x
Chr5	146833190	GAG c C g GAGCAGAAGAAG g AGGG	0	x
Chr5	120294736	at GTCC a AGC a AGAG g GAATGG	0	x
Chr1	113741471	GAG g ta GAGCAGAAGAAGAAGCG	0	x
ChrX	38971206	GAGTCC c AG a AGAAG aa g AAAG	0	x
Chr4	2181662	cctct CGAGCA aa AG g A g AAGG	0	x
Chr14	75723908	agt TCC a AGCAG g GAAGAAGGG	0	x
Chr4	155734338	tgc T tt GAGCAG aa g A g AAAG	0	x
Chr4	122686219	aAGT aa GA ag AG c AG g A g AAGA	0	x
Chr12	4927416	t AGTCC t AGCA ag A at A g AATG	0	x
Chr3	5031614	GA a TCC a AGCAG g AGAAGAAGGA	0	x
Chr2	106719739	tAa T ga GAGCAG aa g A g AATG	0	x
Chr7	142597224	GA caga GA ag AGAAGAAG g AAGA	0	x
Chr1	27913391	ag GT Ca GAGCAGAAG aaa g AGG	0	x
Chr7	73602675	G caaagagcag GAAGAAGAAGGG	0	x
Chr18	34906762	GAG c Ct GAGC g GAAG g GAAAGG	0	x
Chr2	45607957	tAa TCC c AG agc A g GAAGAAGAA	0	x

Chr18	1677040	agtcCaGAGCAaAAtAAGAAGGG	0	X
Chr4	44622977	aAGTCtGAGaAGAAGAAGAAAGA	0	X
Chr12	2873991	GctaaaGAGCAGAAGgAagAAGG	0	X
Chr2	239393515	cAGTaCGAGCAGAgGAAGgAAGA	0	X
Chr8	102244552	agtTCCaAGCAGAAGAAGcATGG	0	X
Chr2	66582071	atGgCaGAGCAGAAgAagAAAG	0	X
Chr11	69660352	cAGTCCatGCAGAgGgAagAAGG	0	X
Chr11	130764292	GcaTtaGAGCAGAAGgAagAAGG	0	X
Chr1	231750743	GAGTCaGAGCAaAAGAAGtAGTG	0	X
Chr6	36604882	GgcagaGAGCAGAAGgAagAAAG	0	X
Chr15	61646878	aAGTCaGAGgAGAAGAAGAAGGG	0	X
Chr7	141972562	aAGTCCGgGCAaAAGAgGAAAGG	0	X
Chr12	111418051	GAGaggGAGCAaAAGAAGgAAGG	0	X
Chr9	72899757	cAGaatGAGCAGgAagAagAACa	0	X
Chr17	8640231	GAGaCtGAGaAGAAGAAGAAAGG	0	X
Chr1	84869216	GAGTCaGctgAGcAGAAGgAAGA	0	X
Chr4	41187173	GAaggaGAGCAGAAgAagAAAG	0	X
Chr9	130107853	GttTgaGAGCAGAAGgAagAAGA	0	X
Chr11	118816273	attTCCaAGCAGAgagAagAATG	0	X
Chr8	72482455	GAGTCCGAGaAGAAGAAgAAAA	0	X
Chr1	221522625	GAGTttGAGtAGAAGAAGAAGAG	0	X
Chr21	37132446	tgGcCaGAGCAGAAGgAagAAGG	0	X
Chr2	217972073	tgtcCgagGCAGtAGAAgAACG	0	X
Chr5	35927682	aAGcCCGAGCtagAagAaAtAGG	0	X
Chr3	157623637	aAGgggagcagGAAGAAGAAAGG	0	X
Chr20	14924870	aAGaagGAGCAGgAagAagAAAG	0	X
Chr4	48639408	cAcTCCaAGtAGAAGAAGAAAAG	0	X
Chr9	91487902	GAGgCaGAGagaAgaAAGAAGGG	0	X
Chr2	105425353	agaTCCaAaCAGAAGgAagAATG	0	X
Chr7	100895242	cgcTCCGAGCAGAAGAAagTGg	0	X
Chr7	93390477	agtcCtGAGCAGAgGAAGgAATG	0	X
Chr1	179024805	GAGTCCaAGaAGAAGAAGccAGG	0	X
Chr17	54421043	GAGTCCcAGgAGAAGAAGAgAGG	0	X
Chr8	108409228	tgtTgaGAGCAGAAgAagAAAG	0	X
Chr15	68455211	GtccaaagGCAGgAGAAGAAGGG	0	X
Chr14	88550473	GAGggaGAGagcAgGAAGAAGAA	0	X
Chr12	124551806	ttGTtgagcagGAAGAAGAATGG	0	X
Chr18	32722290	tgtcCaGAGCAGAtGAAGAATGG	0	X
Chr7	97319990	GAaTCCaAGCAGAAGAAaAtGGA	0	X
Chr7	3812781	GAGTCCtAGaAaAAGAAGAgAGG	0	X
Chr11	36270410	GAGagaGAGCAGAAGAAGtAGAG	0	X
Chr18	25950253	agGcCtGAGCAGAAGgAagAAGG	0	X
Chr15	100292479	aAGTCCcgGCAGAgGAAGAAGGG	0	X
Chr3	169381222	GAGggaGAGCAaAAGAAGgAAAG	0	X
Chr5	74513307	GtccatagcaAGAAaAAGAAGGG	0	X
Chr2	238373187	agtGCaGAGCAGAAGAAGgAAAG	0	X
Chr7	70109967	GAaTCaGAGCAaAAGgAGAAAGG	0	X
Chr6	110491414	aAGTCaGAGCAGAAaAAGAgAGG	0	X
Chr1	151027598	ttcTCCaAGCAGAAGAAGAAGAG	0	X
Chr9	135663404	cAGTCCaAaCAGAAGAgGAATGG	0	X
Chr6	147955462	tgGcCaGAGCAGAAGgAagAAAG	0	X
Chr9	140936012	GAGTCaaAGCAGAAGAAgAACG	0	X
Chr14	35092801	tAtcCaagcagGAAGAAGcAAGG	0	X
Chr17	73339913	tgcaCgagcagGgAGAAGAAGG	0	X
Chr4	82567700	tAtTtacAGagcAgGAAGAAGAG	0	X

Chr14	98020018	cAtTCCaAGCAGAAGgAagAGAG	0	x
Chr9	119853407	tAccagGAGCAGgAaAAagAAGG	0	x
Chr7	29268537	GAGcggGAGCAaAAGgAagAATG	0	x
Chr3	9802191	GtacCCaAGCAGAAGgAagAAGG	0	x
Chr18	24570836	cctgaaGAGCAGAAGgAGgAAGG	0	x
Chr13	101018849	GtcTgaGcagAaAgGAAGAAGGG	0	x
Chr10	8337281	GAagtCagaCAGAAGAAGAAGAG	0	x
Chr15	68619369	GAGaaaGAGCAGAAGgAagAAGT	0	x
Chr2	218378108	GAGTctaAGCAGgAGAAtAAAGG	0	x
Chr1	2744291	GgtcCaGAGagaAAGAAGAAAGG	0	x
Chr16	78848850	aAaTCCaACcAGAAGAAGAAAGG	0	x
Chr10	5401788	tAaTCCaAtCAGAAGAAGAAGGG	0	x
Chr11	30490142	GAGagaagcagaAAGAAGAAAGG	0	x
Chr17	21133222	GAaTCCcAGCAGAAaggaAgAAA	0	x
Chr6	12210833	atGaatGAGCAGAAGgAGgAAAG	0	x
Chr7	43259054	GAtaCCGAGCtaAAGAAGgAAGG	0	x
Chr22	47725583	GAagagGAGCAGAAGgAGgAAGG	0	x
Chr11	56910170	accTggGAGCAGgAaAAagAAGG	0	x

Supplemental Table 7. Chromatin accessibility of Cas9 off-target sites captured by Digenome-seq

HBB			
Chromosome	Location	Target sequence	Chromatin accessibility (1= DNase I hypersensitive sites, 0 = Dnase I non-sensitive sites)
chr11	5248215	CTTGCCCCACAGGGCAGTAACGG	0
chr17	8370253	tTgctCCCACAGGGCAGTAAACG	0
chr22	17230623	tgTGCCCCACAGaGCaCTAAGGG	0
chr8	24931381	agTGCCaCACACaGCAGTAAGGG	0
chr15	46598129	gTTGCCCCtCAGGaCAGTAcAGG	0
chrX	75006257	gTgGCCCCACAGGGCAGgAATGG	0
chr12	93549202	aTTGCCCCACgGGGCAGTgACGG	0
chr14	94585327	aTgGCCCCACAaGGCAGaAATGG	0
chr9	104595883	tcaGCCCCACAGGGCAGTAAGGG	0
chr2	121715240	gTgtCCCCACAGGGCAGgAAAGG	0
chr12	124803834	gcTGCCCCACAGGGCAGcAAAGG	0
Chr1	177593980	tcTaCCCCACATtGGCAGTAATGG	0
Chr6	50041372	tcTGCCCCACATtGGCAGTAATGA	0
Chr6	23709579	gaaGCCctACAGGGCAGcAATGG	0
Chr14	36889538	gTTatCCCACAGGaCAGTgAGGG	0
Chr1	17346702	CggtCCCCACAGGGtcagtAAGG	0
Chr20	39992928	agTGgCCCCcAGGGCAGTgAGGG	0
Chr10	95791920	acTctCCCACAaGGCAGTAAGGG	0
Chr4	148531374	gTTacCtCACAGaGCAGaAAGGG	0
Chr5	53613387	tcacCCCCACAGGcCAGTAAAGG	0

VEGFA1			
Chromosome	Location	Target sequence	Chromatin accessibility (1= DNase I hypersensitive sites, 0 = Dnase I non-sensitive sites)
chr6	43737297	GGGTGGGGGAGTTTGCTCCAGG	0
chr17	39796328	taGTGgaGGGAGcTTGCTCCTGG	0
chr12	1988077	cGGgGgaGGGAGTTTGCTCCTGG	0
chr6	14316373	GtGgGGGtaGAGTTTGCTCCAGG	0
chr15	65637537	GGaTGGaGGGAGTTTGCTCCTGG	0
chr16	8763213	aaGTaaGGGaAGTTTGCTCCTGG	0
chr11	71497119	aGGaaGgaGGGAGTTaGCTCCTGG	0
chr12	26641302	aGtTtGGGGGAGTTTGcCCAGG	0
chr5	139263024	ttGgGGGGGcAGTTTGCTCCTGG	0
chr1	99347651	GGGgaGGGGaAGTTTGCTCCTGG	0
chr11	3445204	aGGaaGgaGGGAGTTaGCTCCTGG	0
chr20	56175356	aGGgaGgaGGAaTTTGCTCCAGG	0
Chr5	7067159	GaGgGtGGGGAGTTTaCTCCTGG	0
Chr22	37215276	GGGTGGGGGAGTTTGcCCAGG	0
Chr17	32986325	GGGgGtGGGGAcTTTGCTCCAGG	0
Chr1	82627648	GGGTGctGGcAcagtGCTCCTGG	0
Chr1	233157354	GGagGaGGGGAGTcTGCTCCAGG	0
Chr10	124731416	aGcTGgaGGGAGTTTGcCCAGG	0

Chr12	131690199	GGGaGGGtGGAGTTTGCTCCTGG	0
Chr20	7836107	caGgtGGGaGAGTTTGCTCCCAG	0
Chr4	8453803	GaGTGGGtGGAGTTTGCTaCAGG	0
Chr9	88657759	GGaTGGaGGtAGTTTGtTCCTGG	0
Chr9	93925190	GGGgTtGGGGAGcaTGCTCCAGG	0
Chr3	125633992	aGGaaGGaGGAGTTaGCTCCTGG	0
Chr8	140714327	GGGaGGaGaGAGTTTGCTCtCTG	0
Chr15	93140401	GGGgGaGGGaAGTTTcTCCAGG	0
Chr2	209437600	aGGgaGGGaGAaTTTGCTCCTGG	0
Chr3	128284321	aGGTGGtGGGAGcTTGtTCCTGG	0
Chr5	32945275	GcGTGGGGGGtGTTTGCTCCCGG	0
Chr13	26202812	GGtTGaGGGGAGTcTGCTCCAGG	0
Chr5	156390	tGcTcGGGGGAGTTTGCaCCAGG	0
Chr21	43689878	GGcccaGGGGAGTTTGCTCCCAG	0
Chr19	51310920	GtGcaGGGGGAaTTTGCTtCCGG	0
ChrX	82127748	aGagGGGGaGAGTTTGCCcCTGG	0
Chr7	17819097	acaactGGGGAGTTTGCTCCTGG	0
Chr22	41676762	aGtgcaGGGGAGcTTGCTCCTGG	0
Chr2	96056645	GGGTGGGgAGAGTTTctTCCTGG	0
Chr3	195871264	GGtgGGGGaGAGcTaGCTCCGGG	0
Chr6	45554056	GGGgtGGGaGAGTTTGCTCtCTG	0
Chr18	366714	GGGgGcaGGGAGaTTGCTCCTGG	0
Chr3	13580170	atGgGGGaGaAacTTGCTCCTGG	0
ChrX	19185601	GGGaGGGGaGAGTTTGtTCCAGG	0
Chr11	67574262	aGGaaGGaGGAGTTaGCTCCTGG	0
Chr17	47317539	ctGgtGGGGGAGcTTGCTCCAGG	0
Chr6	91365255	cccgGGGGGaAGcTTGCTCCAGG	0
Chr22	18454623	GGaaaGGaGGAGcTTGCTCCAGG	0
Chr22	19698463	GaGgGGGaGcAGTTTGCTCCAGG	0
Chr3	36358934	aGtgGGGGaGAGTaTGCTCCGGG	0
Chr21	37116659	aaGTGGGaaGAGTTTGtTCCAGG	0
Chr11	117481208	GGGcaAGGGGAGgTTGCTCCTGG	0
Chr7	29081029	GGagtGGGtGAGcTTGCTCCTGG	0
Chr17	63035708	aGGaGGGGGaAGaaTGCTCCAGG	0
Chr2	181170961	tGGgGaGGGGAAaTTGCTCCTGG	0
Chr6	109284989	tGGaGaGGGGAGTTgGCTCCTGG	0
Chr11	122583511	aGaaGaGGGGAtTTTGCTCCTGG	0
Chr5	56172079	GGtgGGGgtGgGTTTGCTCCTGG	0
Chr1	33643288	GGGTGGGtGGAGTTTGCTaCTGG	0
Chr8	28483353	aaGTGGGaGGAGacTGCTCCAGG	0
Chr22	38219333	aGGTcGGGGGAGTTaGaTCCCGG	0
Chr15	29263777	GGGatGGGaGAGTcTGCTCCTGG	0
Chr2	30430777	aGGgaGaGGGAGcTTGCTCCCAG	0
Chr12	107832636	tctTGGGGGGaagTTGCTCCAGG	0
Chr4	185246171	GGagGGGGGGctTTTGCTCCAGG	0
Chr8	10804669	GaGTGaGGaGAGcTTGCTCCATG	0
Chr5	95220670	GGGaGcaGGGAaTTTGCTCCAGG	0

Chr2	129199817	tccTGaGGGcAGTTTGCTCCAGG	0
Chr13	31251013	tGtaGaGGGagtTTTGCTCCCGG	1
Chr16	89679839	GGagGaGGGAcTTTGCTCCAGG	0
Chr1	20166440	GtGgGaGGatAGcTTGCTCCTGG	0
Chr18	13983474	GGGTGaaaGaAGTTTactCCTGG	0
Chr6	50485682	atGTGtGGGGAaTTTGCTCCAGG	0
Chr1	205484156	GtGTGaGtGGAGTTTGCTCtGGG	0
Chr6	109070771	GGtgGGGGaaAGTTTGCTCCTGA	0
Chr15	101813024	aaGgaGGcGGAGcTTGCTCCTGG	0
Chr11	11823598	GGcTGGaGGGgaTTTGCTCCTGG	0
Chr9	5336085	tcGTGGtGGGAaTTTactCCTGG	0
Chr4	116853325	aaagGGGGGaAcTTTGCTCCAGG	0
Chr11	86695108	aGGgaAGGGGAaTTTGCaCCTGG	0
Chr5	57030871	ctcTGaGGGGAGTTTGCTCtGGG	0
Chr15	84047385	GGagtcaGGGAaTTTGCTCCTGG	0

FANCF			
Chromosome	Location	Target sequence	Chromatin accessibility (1= DNase I hypersensitive sites, 0 = Dnase I non-sensitive sites)
chr11	22647338	GGAATCCCTTCTGCAGCACCTGG	0
chr7	102131659	GtctcCCCTTCTGCAGCACCAGG	0
chr10	73463136	tGAATCCCatCTcCAGCACCAGG	0
chr7	102230832	GtctcCCCTTCTGCAGCACCAGG	0
chr11	66475045	GGAAcacCTTCTGCAGctCCAGG	0
chr16	28615201	GGctTCCCTTCTGCAGcCCAGG	0
chr7	44076497	GtctcCCCTTCTGCAGCACCAGG	0
Chr10	37953200	GGAgTCCCTcCTaCAGCACCAGG	0
Chr10	43410031	GGAgTCCCTcCTaCAGCACCAGG	0
Chr18	8707528	GGAAcCCCgTCTGCAGCACCAGG	0
Chr16	49671025	GGAgTCCCTcCTGCAGCACCTGA	0
Chr3	35113165	tGAATCCTaaCTGCAGCACCAGG	0
Chr20	44903573	tccATCCCTactGCcagcaCCAG	0
Chr3	10885901	acccTCCCTTCTGCAGgcaCCGG	0
Chr10	3151994	ctctgtCCTTCTGCAGCACCTGG	0
Chr17	39675789	GGgAgTCCaTCTGCAGCACCAGG	0
Chr11	47554037	GGAATCCCTTCTaCAGCatCCTG	0
Chr2	54853314	GGAATatCTTCTGCAGcCCAGG	0
Chr12	115467808	aGggTCCCTTCTGCAGcCCTGG	0
ChrX	86355180	accATCCCTcCTGCAGCACCAGG	0
Chr2	35692938	acttTatCTTCTGCAGCACCTGG	0
Chr2	133174786	atccTttCTTCTGCAGCACCTGG	0
Chr12	2719895	acAcTCCCTTCTGCAGCACCATG	0
ChrX	97566910	tGtATtCCTTCTGCAGgcaCCAG	0
Chr17	30452575	cctgctgCTTCTGCAGCACCTGG	0
Chr9	113162294	aaAATCCCTTcGCAGCACCTAG	0
Chr4	53092937	aatATtCCcTCTGCAGCACCAGG	0

Chr3	97725864	accATttCTTCTGCAGCACCTGG	0
Chr17	34985068	GGgtcCgCTTCTGCAGCACCTGG	0
Chr9	111467809	aGgAatCCTaCTGCAGCACCCAG	0
Chr4	76159966	ttAcTCaCTTCTGCAGgcaCCTG	0
Chr5	68338523	ccAcTCctTTCTGCAGCACCCGG	0
Chr17	3980376	GGAACCCCcTCTGCAGCttCTGG	0
Chr20	19790626	cattTtCtTTCTGCAGCACCTGG	0
Chr17	78923978	aGAggCCCCtCTGCAGCACCAGG	0
Chr8	71384404	tttcctgCTTCTGCAGCACCAGG	0
Chr17	39655735	GccccCtCcTCTGCAGCACCTGG	0
Chr6	41457565	ctccTCCCTcTCTGCAGCACCTGG	0
Chr13	109802140	aaAATaCCTTCTGCAGtACCAGG	0
Chr5	85696042	ctActgaCTTCTGCAGCACCTGG	0
Chr4	7336836	aGctcCCaTTCTGCAGCACCCGG	0
Chr9	139891539	aGttcCCCaTCTGCAGCACCAGG	1
Chr10	13436789	ctcATCCCTTCTGCAGCcCCAGG	0
Chr2	176121765	GccccCtgcTCTGCAGCACCCGG	0
Chr13	100011450	acctgCctTctgGCAGCACCAGG	0
Chr17	8432606	actgTCatTTCTGCAGCACCTGG	0

HEK3			
Chromosome	Location	Target sequence	Chromatin accessibility (1= DNase I hypersensitive sites, 0 = Dnase I non-sensitive sites)
chr9	110184637	GGCCCAGACTGAGCACGTGATGG	1
chr1	47005705	aGctCAGACTGAGCAaGTGAGGG	0
chr15	79749931	caCCCAGACTGAGCACGTGcTGG	0
Chr10	131593121	GagCCAGAaTGAGCACGTGAGGG	0
Chr7	66968042	GaCaCAGACcGgGCACGTGAGGG	0
Chr11	134582415	GGCgCAGACaGAGCACGTGACGA	0
ChrX	114764149	aGACCAGACTGAGCAaGaGAGGG	0
Chr4	72203005	atatCAGACTGAGCACcgtgAGG	0
Chr6	103918240	aaataAGACTGAGCACGTGgTGG	0
Chr17	7594610	aGCCagactgagGCAaGTGAGGG	0
Chr3	160129761	aGgCCAGACTGAaCACgatgAGG	0
Chr15	35402774	cctaaAGACTGAGCAaGTGAAGG	0
Chr9	137039236	cagCCAGACaGAGCACGTGgAGG	0
Chr6	79958440	aaCaaAGACTGAGCACGTtAGGG	0
Chr2	130402896	GaCCCAGAaTGAGCACaaaAGGG	0
Chr1	34163192	attCtAGACTGAGCACGTGcAAG	0
Chr2	97163211	ccCatgGACTGAGCACaTGAAGG	0
Chr17	79043523	tGgCCAGACTGAGCtCGTGAGTG	0
Chr10	22896606	GaaggAGACTGAGCaTGTGAGGG	0
Chr8	20947876	tctCCAGACTGAGCcCaTGAGGG	0
Chr19	19169358	GGaCCAGgCTGAGCACaTGgAGG	0
Chr6	112273496	aagCCAGACTGAGCACGTtcAGG	0
Chr1	229294224	GGtCatcACTGAGCACGTGAGGT	0

Chr2	240026760	GGCTCAGACTGAGCACCTGAGAG	0
Chr15	94188821	attCCAGAAATGAGCACATGAAGG	0
Chr2	131090691	acCCaAGACaGAGCACGTGgAGG	0
Chr11	60830962	tCCagaACTaAGCACGTGAATG	0
Chr14	102917106	ctCggAGACTGACACGTGAGGG	0
Chr10	23135503	actCCAGACTGAGCAacTGAGGG	0
ChrX	16606309	ttCCCAGACaaAGCACGcGAAGG	0
Chr14	78070357	aaccagactgGAGCACGTGgTGG	0

RNF2			
Chromosome	Location	Target sequence	Chromatin accessibility (1= DNase I hypersensitive sites, 0 = Dnase I non-sensitive sites)
chr1	185056773	GTCATCTTAGTCATTACCTGAGG	0
Chr12	131619805	aTCaCCTTAGcCATTACcAGGGG	0
Chr18	62061226	aTtATtTTAGTCATTACCTtTGG	0
Chr8	99451745	cgtgcaTTAGTCATTACCTGAGG	0
Chr7	43967267	acttatTTAGTCATTACCTGTAG	0
Chr6	143212079	GTaATATTAGTCATTACCgGTGG	0
Chr4	171989625	taacaCaTAGTCaCTACCTGGTG	0
Chr8	5745882	aatATgTTAGTCATTACCTGAGG	0
Chr4	189725512	aTgcTtcTtGTCATTACCTtGGG	0
Chr9	138721895	acttcagTAGTCATTACCTaGGG	0
Chr5	92036966	GgtATCTaAGTCATTACCTGTGG	0
Chr15	25135467	catcTaaTAGTaATTACCTGGGG	0
Chr17	53928586	GTCATCTTAGTCATTAC - TGAGG	0

HEK2			
Chromosome	Location	Target sequence	Chromatin accessibility (1= DNase I hypersensitive sites, 0 = Dnase I non-sensitive sites)
chr5	87240614	GAACACAAAGCATAGACTGCGGG	0
Chr4	90522184	GAACACAAtGCATAGaTTGCCGG	0
Chr10	43159340	aAcacaAAgaCATAGACcACTGG	0
Chr1	40461425	tAcacacAAGCAcAGACTGCAGG	0
Chr2	19844956	aActcCAAAGCATaTACTGCTGG	0
Chr15	93557679	agAacacATGCATAGACTGCTAG	0
Chr11	128508577	GAAttCAAAGCATAGaTTGCAGG	0
Chr5	131174461	aAAtACAAtGCATAGACTGCTAG	0
Chr19	30112719	tAcacaaaaataAGACTGCTGG	0
Chr20	97641	GAAttCAAAGCATAGaTTGCAGG	0
Chr4	53536210	GAAtACTaAGCATAGACTcCAGG	0
Chr13	113428467	cAAtACAAAgATAGACTGCAGG	0
Chr18	22360702	GgAatCAAAGCAcAGACTGCAGG	0
ChrX	36949815	GAAaACAAAaCATAGaGTGCTGG	0
Chr7	83764327	actatatAAGCATAGACTGtTGG	0
Chr5	126385455	ccACACcAAGCATAGACTtCTGG	0
Chr5	142142325	tAAacactAaCATAGACTGCAGG	0

Chr18	56307003	aAgaACAAAaCATAGACTGCAGG	0
Chr1	36097073	GtAaACAAAGCATAGACTGaGGG	0
Chr3	81710854	ctcCtaAAgcatTAGACTGCAGG	0
Chr5	7625837	GgtacacAAtaATAGACTGCAGG	0
Chr18	5596266	cctacagaAGCATAGACTGCAGG	0
Chr6	139353018	ccAaACAAAaCATAGACTGCTGG	0
Chr22	28895718	attaAgAtAGCATAGACTGCAGG	0
Chr1	77190607	tcACACAAAcCATAGACTGaGGG	0
Chr6	40925010	aAcaAgtAtGCATAGACTGCTGG	0
Chr9	97332609	GtAattAAAGCaAGACTGCTGG	0
Chr18	68431104	tgtgtaAgAGCATAGACTGCTGG	0
Chr20	23101380	atACACAgAGCAaAGACTGCAGG	0
Chr8	97317605	GAACACAgtaCATAGACTGgCAG	0
Chr9	290168	aAACATAAAGaATAGACTGCAAG	0
Chr6	152710071	tActctAtAtCATAGACTGCTGG	0
Chr4	31157435	tgAttgAgtGCATAGACTGCTGG	0
Chr1	108869935	agtatagcAGCATAGACTGCAGG	0
Chr15	65377019	GAgcgatAAGCaAGACTGCTGG	0

EMX1			
Chromosome	Location	Target sequence	Chromatin accessibility (1= DNase I hypersensitive sites, 0 = Dnase I non-sensitive sites)
chr2	73160999	GAGTCCGAGCAGAAGAAGAAGGG	0
chr6	9118799	acGTCTGAGCAGAAGAAGAATGG	0
chr5	45359067	GAGTtaGAGCAGAAGAAGAAAGG	0
Chr11	62365273	GAaTCCaAGCAGAAGAAGAgAAG	0
Chr19	1438827	GAagtaGAGCAGAAGAAGAAGCG	0
Chr1	234492864	GAagtaGAGCAGAAGAAGAAGCG	0
Chr2	172374203	GAagtaGAGCAGAAGAAGAAGCG	0
Chr2	219845073	GAGgCCGAGCAGAAGAAgACGG	0
Chr1	23720618	aAGTCCGAGgAGAgGAAGAAAGG	0
Chr12	106646091	aAGTCCatGCAGAAGAgGAAGGG	0
Chr15	44109764	GAGTCTaAGCAGAAGAAGAAGAG	0
Chr8	128801260	GAGTCCtAGCAGgAGAAGAAGAG	0
Chr15	22366622	GgagtaGAGCAGAgGAAGAAGGG	0
Chr9	127309505	aAGcCCaAGCAaAtGAAGAATGG	0
Chr11	43747949	aAGcCCGAGCAaAgGAAGAAAGG	0
Chr5	9227163	aAGTCTGAGCAcAAGAAGAATGG	0
Chr10	128080196	GAGTaCaAGCAGAtGAaAaACGG	0
Chr1	33606480	GAGcCTGAGCAGAAGgAGAAGGG	0
Chr3	34042974	GAGTtCaAGCAGAgAgaAAGGG	0
Chr21	24667742	cccTCCaAGCAGAAGAAGAtGAG	0
Chr14	38654666	aAGTCTGAGaAGAAGAAGAcATG	0
Chr18	68861321	agagtaGAaCAGAAGAAGgAAAG	0
Chr4	87256692	GAGTaaGAGaAGAAGAAGAAGGG	0
Chr10	58848729	GAGcaCGAGCAagAGAAGAAGGG	0

Chr8	74634212	aAGTCCaAaaAGAAGAAaAAAGG	0
Chr19	24250503	GAGTCCaAGCAGtAGAgGAAGGG	0
Chr8	105164126	GAGcCCaAGaAGAAGAAGAAGGA	0
Chr14	43156807	GAGgCCaAGCAGAAaAAaAATGG	0
Chr11	30301809	cAGTCTGAGtAGAAGAAaAAGGG	0
Chr4	58838593	aAGTCCcAGaAGAAGAAatATGG	0
Chr15	65614525	GAGaggGAGCAGggagAagAAGG	0
ChrX	149010707	GgagtCaAGgAGAAGAAGAAGAG	0
Chr7	111475449	GAGcCCaAGCACaAaAAGAATGG	0
Chr14	48932120	GAGTCCcAGCAaAAGAAGAAAAG	0
Chr10	91416162	atGTCCaAGCAGAAGAAGtcTGG	0
Chr12	102743729	tAGTCaGAGCAGAtGAAGgAAAG	0
Chr3	95690186	tcaTCCaAGCAGAAGAAGAAGAG	0
Chr3	16077518	GAGgCaGAGagaAAGAAGAAAGG	0
Chr12	73504675	GAGTtaGAGCAGAAaAAaAATGG	0
Chr5	141129457	aAGTCacAGgAGcAGAAagAAGA	0
Chr7	31901077	GAGgCCaAGCAGAAagAaAAAGG	0
Chr1	209931600	ttaTCCGAGaAGAAGAAGtAAGG	0
Chr6	106901799	GAGcCgGAGCAGggagAagAAGG	0
Chr22	34858917	GAGcCTGAGCAGgAagAagAAGA	0
Chr6	29806752	tgtcCaagGCAGgAGAAGAAGGG	0
Chr15	36839471	cAGagaGAGgAGcAGAAaAAAGA	0
Chr5	134375867	cAGgCTGAGCAGAAgAagAAAG	0
Chr2	199919487	GAGTCaGAGCAGAActAGAAGGG	0
Chr20	6653999	aAGTCCagaCAGAAGAAGAAGGA	0
Chr8	135098073	cAGTCCagcagGAAGAAGAgAGG	0
Chr11	131106371	GccTCCaAGCAGAAGgAGAAATG	0
Chr9	2513258	GAGagaGAGCAaAAGgAagAATG	0
Chr17	72057114	GAGgagagcagaAAGAAGAAGGG	0
Chr16	56184077	aAGTCaGAGaAGgAagAagAAAG	0
Chr5	146833190	GAGcCgGAGCAGAAGAAGgAGGG	0
Chr5	120294736	atGTCCaAGCACaAGAgGAATGG	0
Chr1	113741471	GAGgtaGAGCAGAAGAAGAAGCG	0
ChrX	38971206	GAGTCCcAGaAGAAGAAgAAAG	0
Chr4	2181662	cctctCGAGCAaAAGgAagAAGG	0
Chr14	75723908	agtTCCaAGCAGAgGAAGAAGGG	0
Chr4	155734338	tgcTttGAGCAGAAgAagAAAG	0
Chr4	122686219	aAGTaaGAagAGcAGgAagAAGA	0
Chr12	4927416	tAGTCctAGCAagaAtAagAATG	0
Chr3	5031614	GAaTCCaAGCAGgAGAAGAAGGA	0
Chr2	106719739	tAaTgaGAGCAGAAgAagAATG	0
Chr7	142597224	GAcagaGAagAGAAGAAGgAAGA	0
Chr1	27913391	agGTCaGAGCAGAAGAAgAGG	0
Chr7	73602675	GcaaagagcagGAAGAAGAAGGG	0
Chr18	34906762	GAGcCTGAGCgGAAGAgGAAAGG	0
Chr2	45607957	tAaTCCcAGagcAGgAAGAAGAA	0
Chr18	1677040	agtcCaGAGCAaAAtAAGAAGGG	0

Chr4	44622977	aAGTCTGAGaAGAAGAAGAAAGA	0
Chr12	2873991	GctaaagAGCAGAAGgAagAAGG	0
Chr2	239393515	cAGTaCGAGCAGAGGAAGgAAGA	0
Chr8	102244552	agtTCCaAGCAGAAGAAGcATGG	0
Chr2	66582071	atGgCaGAGCAGAAagAagAAAG	0
Chr11	69660352	cAGTCCatGCAGAGgGAagAAGG	0
Chr11	130764292	GcaTtaGAGCAGAAGgAagAAGG	0
Chr1	231750743	GAGTCaGAGCAaAAGAAGtAGTG	0
Chr6	36604882	GgcagaGAGCAGAAGgAagAAAG	0
Chr15	61646878	aAGTCaGAGgAGAAGAAGAAGGG	0
Chr7	141972562	aAGTCCGgGCAaAAGAgGAAAGG	0
Chr12	111418051	GAGaggGAGCAaAAGAAGgAAGG	0
Chr9	72899757	cAGaatGAGCAGgAagAagAACA	0
Chr17	8640231	GAGaCTGAGaAGAAGAAGAAAGG	0
Chr1	84869216	GAGTCaGctgAGcAGAAGgAAGA	0
Chr4	41187173	GAaggagAGCAGAAagAagAAAG	0
Chr9	130107853	GttTgaGAGCAGAAGgAagAAGA	0
Chr11	118816273	attTCCaAGCAGAgagAagAATG	0
Chr8	72482455	GAGTCCGAGaAGAAGAAgAAAA	0
Chr1	221522625	GAGTttGAGtAGAAGAAGAAGAG	0
Chr21	37132446	tgGcCaGAGCAGAAGgAagAAGG	0
Chr2	217972073	tgtcCgagGCAGtAGAAagAACG	0
Chr5	35927682	aAGcCCGAGCtagAagAaTAgG	0
Chr3	157623637	aAGgggagcagGAAGAAGAAAGG	0
Chr20	14924870	aAGaagGAGCAGgAagAagAAAG	0
Chr4	48639408	cAcTCCaAGtAGAAGAAGAAAAG	0
Chr9	91487902	GAGgCaGAGagaAgaAAGAAGGG	0
Chr2	105425353	agaTCCaAaCAGAAGgAagAATG	0
Chr7	100895242	cgcTCCGAGCAGAAGAAAgTGG	0
Chr7	93390477	agtcCTGAGCAGAGGAAGgAATG	0
Chr1	179024805	GAGTCCaAGaAGAAGAAGccAGG	0
Chr17	54421043	GAGTCCcAGgAGAAGAAGAgAGG	0
Chr8	108409228	tgtTgaGAGCAGAAagAagAAAG	0
Chr15	68455211	GtccaaagGCAGgAGAAGAAGGG	0
Chr14	88550473	GAGggaGAGagcAgGAAGAAGAA	0
Chr12	124551806	ttGTtgagcagGAAGAAGAATGG	0
Chr18	32722290	tgtcCaGAGCAGAtGAAGAATGG	0
Chr7	97319990	GAaTCCaAGCAGAAGAAaTGGa	0
Chr7	3812781	GAGTCCTAGaAaAAGAAGAgAGG	0
Chr11	36270410	GAGagaGAGCAGAAGAAGtAGAG	0
Chr18	25950253	agGcCTGAGCAGAAGgAagAAGG	0
Chr15	100292479	aAGTCCcgGCAGAGGAAGAAGGG	0
Chr3	169381222	GAGggaGAGCAaAAGAAGgAAAG	1
Chr5	74513307	GtccatagcaAGAAaAAGAAGGG	0
Chr2	238373187	agtgCaGAGCAGAAGAAGgAAAG	0
Chr7	70109967	GAaTCaGAGCAaAAGgAGAAAGG	0
Chr6	110491414	aAGTCaGAGCAGAAaAAGAgAGG	0

Chr1	151027598	ttcTCCaAGCAGAAGAAGAAGAG	0
Chr9	135663404	cAGTCCaAaCAGAAGAgGAATGG	0
Chr6	147955462	tgGcCaGAGCAGAAGgAagAAAG	0
Chr9	140936012	GAGTCaaAGCAGAAGAAgAACG	0
Chr14	35092801	tAtcCaagcagGAAGAAGcAAGG	0
Chr17	73339913	tgcaCgagcagGgAGAAGAAAGG	0
Chr4	82567700	tAtTtacAGagcAgGAAGAAGAG	0
Chr14	98020018	cAtTCCaAGCAGAAGgAagAGAG	0
Chr9	119853407	tAccagGAGCAGgAaaaagAAGG	0
Chr7	29268537	GAGcggGAGCAaAAGgAagAATG	0
Chr3	9802191	GtaccCaAGCAGAAGgAagAAGG	0
Chr18	24570836	cctgaaGAGCAGAAGgAggAAGG	0
Chr13	101018849	GtcTgaGcagAaAgGAAGAAGGG	0
Chr10	8337281	GAagtCagaCAGAAGAAGAAGAG	0
Chr15	68619369	GAGaaaGAGCAGAAGgAagAAGT	0
Chr2	218378108	GAGTCtaAGCAGgAGAAtAAAGG	0
Chr1	2744291	GgtcCaGAGagaAAGAAGAAAGG	0
Chr16	78848850	aAaTCCaAccAGAAGAAGAAAGG	0
Chr10	5401788	tAaTCCaAtCAGAAGAAGAAGGG	0
Chr11	30490142	GAGagaagcagaAAGAAGAAAGG	0
Chr17	21133222	GAaTCCcAGCAGAAaggAagAAA	0
Chr6	12210833	atGaatGAGCAGAAGgAGgAAAG	0
Chr7	43259054	GAtaCCGAGCtaAAGAAGgAAGG	0
Chr22	47725583	GAagagGAGCAGAAGgAGgAAGG	0
Chr11	56910170	accTggGAGCAGgAaaaagAAGG	0