Supplementary Table 1a List of residue positions evaluated in mutagenesis screen

Position	Residue	Domain	Variants (/19)
130	K	REC1	19
131	G	REC1	18
132	L	REC1	17
133	F	REC1	19
134	K	REC1	17
135	A	REC1	18
162	F	REC1	19
163	D	REC1	13
164	K	REC1	14
165	F	REC1	18
166	T	REC1	19
168	Y	REC1	12
169	F	REC1	17
171	G	REC1	10
172	F	REC1	17
173	Y	REC1	18
174	E	REC1	15
175	N	REC1	17
176	R	REC1	19
177	K	REC1	19
536	Q	WED-II	15
537	M	WED-II	14
538	P	WED-II	19
539	T	WED-II	18
540	L	WED-II	18
541	A	WED-II	18
542	S	WED-II	19
543	G	WED-II	19
544	W	WED-II	17
545	D	WED-II	17
546	V	WED-II	19
547	N	WED-II	14
548	K	WED-II	19
550	K	WED-II	15
551	N	WED-II	15
552	N	WED-II	16
570	K	WED-II	19
571	Q	WED-II	19
572	K	WED-II	19
573	G	WED-II	19
595	Y	WED-II	16
596	D	WED-II	19
597	Y	WED-II	15
599	P	PI	15
600	D	PI	12
601	A	PI	17
602	A	PI	16
603	K	PI	16
604	M	PI	18
605	I	PI	16
606	P	PI	10
607	K	PI	13
608	C	PI	15
609	S	PI	12
610	T	PI	17
611	Q	PI	12
612	L	PI	11
613	K	PI	18
614	A	PI	18
615	V	PI	13

Supplementary Table 1b List of variants depleted at least 15-fold relative to pUC19

TATC	
K164N	K548E
Y168V	K548A*
G171N	K548V*
G171M	K548G*
G171S	K548Y*
G171L	K548F*
E174L	K548C*
T539R	K548W*
L540F	N551R*
K548N*	N551Y
K548T*	N552G*
K548I*	N552K*
K548S*	N552R*
K548R*	N552S*
K548H*	N552T*
K548Q*	N552Q
K548P	A601C
K548L	A614R

TGTC
A135F
F169Y
F172A
F172I
K177L
K548T
K548M
K548S
K548R
K548H
K548Q
K548A
K548V
K548G
K548Y
K548C
K548W

TTCC	
K130Q	Q571S
K130L	Q571P
G131D	Q571A
G131F	Q571G
K134C	Q571C
F169W	K572P
F169Y	K572R
G171L	G573I
G171Y	G573L
K177R	G573E
Q536R	Y595L
M537R	D596N
S542L	D596S
S542R*	D596A
K548R	D596C
K550T	P599G
K550H	D600M
K550P	A602K
K550R	A602Y
N551I	K607H
N551S	S609G
N551R	A614Q
Q571T	A614L

TCCC
S542R*

* Evaluated in HEK293T cells in this study.

Supplementary Table 2 BLISS data

	WT AsCpf1			S542R/K607R			S542R/K548V/N552R				
Target	**BLISS**	**PAM**	**% Indel**	**BLISS**	**PAM**	**% Indel**	**BLISS**	**PAM**	**% Indel**	**PAM**	**Sequence**
VEGFA	0.833	0.88	58 (1.5)	0.988	0.42	54 (1.3)	0.895	0.89	59 (1.6)	TTTG	CTAGGAATATTGAAGGGGGCAGG
OT1	ND	0.00	<0.1	0.025	0.00	<0.1	ND	0.24	<0.1	CATA	GCAGGTATTTTGAAGGGGGCAGG
GRIN2B	0.590	0.88	49 (2.7)	0.664	0.42	51 (1.8)	0.969	0.89	60 (2.1)	TTTG	GTGCTCAATGAAAGGAGATAAGG
DNMT1	0.467	0.88	33 (5.9)	0.042	0.42	12 (2.4)	0.809	0.89	48 (12)	TTTG	AAGAAATATTACAACATATAAAA
OT1	ND	0.00	<0.1	ND	0.00	<0.1	0.030	0.24	<0.1	CATA	AACAAATATCACTAATATATAAAA
OT2	ND	0.00	<0.1	0.030	0.00	<0.1	ND	0.00	<0.1	AGAG	AAGCAGTATCACAACATATTAAA
OT3	ND	0.00	<0.1	0.025	0.00	<0.1	ND	0.00	<0.1	TAAA	GAGAAATATTTCATCATGATAAAA
OT4	0.022	0.00	<0.1	ND	0.02	<0.1	ND	0.10	<0.1	AACA	AAGAAATATTAGAAAATAATTAAA
EMX1	0.738	0.88	44 (0.8)	0.263	0.42	22 (0.6)	0.549	0.89	41 (2.4)	TTTG	TCCTCCGGTTCTGGAACCACACC
OT1	0.187	0.14	4.8 (0.2)	2.958	0.95	32 (1.5)	0.704	0.34	11 (1.3)	TTCA	TCCTCCGGTTCTGGAACCAGATT
OT2	0.048	0.14	3.7 (0.2)	1.173	0.95	40 (1.2)	0.189	0.34	13 (0.9)	TTCA	TCCTCCGGTTCTGGAACCAGATC
OT3	ND	0.14	1.5 (0.2)	0.794	0.95	33 (1.3)	0.026	0.34	6.0 (0.5)	TTCA	TCCTCCGGTTCTGAAACCACACT
OT4	ND	0.14	0.4 (0.1)	0.419	0.95	11 (0.9)	0.045	0.34	1.7 (0.1)	TTCA	TCCTCCGGTTCTGAAACCAGATC
OT5	ND	0.14	0.1 (0.2)	0.040	0.95	1.3 (0.4)	ND	0.34	0.3 (0.4)	TTCA	TCCTCTGGTTCTGGAACCAGGTC
OT6	ND	0.14	<0.1	0.036	0.95	2.8 (0.1)	ND	0.34	0.3 (0.0)	TTCA	TCCTTCGGTTCTGGAACCAGATC

BLISS data represent unique DSB ends per 10^5 reads (ND: not detected). PAM values are normalized cleavage rates from the *in vitro* PAM identification assay shown in **Figure 2d**. Indel values represent mean (std. dev.) of $n = 4$ replicates.

Supplementary Table 3 List of selected Cpf1 orthologs and their predicted PAM-altering mutations

#	Accession No.	Organism	Name	"542"	"548"	"552"	"607"
1	WP_013282991	*Butyrivibrio proteoclasticus*	BpCpf1	R527	E535	N540	K590
2	WP_044910712	*Lachnospiraceae bacterium MC2017*	Lb3Cpf1	N520	E528	K533	K582
3	KKR91555	*Candidatus Falkowbacteria bacterium GW2011_GWA2_41_14*		E633	K639	Y643	G705
4	KKP36646	*Candidatus Peregrinibacteria bacterium GW2011_GWA2_33_10*	PeCpf1	G623	K629	N633	K703
5	KKQ36153	*candidate division WS6 bacterium GW2011_GWA2_37_6*		G568	Q574	K578	R619
6	EKE28449	*uncultured bacterium (gcode 4)*		T552	K558	R562	R615
7	KKQ38174	*Candidatus Roizmanbacteria bacterium GW2011_GWA2_37_7*		N592	K598	N602	K660
8	KKT48220	*Parcubacteria group bacterium GW2011_GWC2_44_17*	PbCpf1	K624	K630	F634	R689
9	WP_005398606	*Helcococcus kunzii*		D554	K560	N564	N614
10	WP_028830240	*Proteocatella sphenisci*		K483	K489	N493	K551
11	WP_015504779	*Candidatus Methanomethylophilus alvus*		D515	K521	N525	K577
12	CUP14506	*Lachnospira pectinoschiza*		S548	K554	N558	K614
13	CUM80100	*Eubacterium rectale*		D529	K535	N539	K594
14	WP_012739647	*Eubacterium eligens*	EeCpf1	N535	K541	N545	K601
15	AIZ56868	*Candidatus Methanoplasma termitum*	CMtCpf1	N528	K534	Y538	R591
16	WP_037975888	*Synergistes jonesii*		K539	K545	N549	K602
17	WP_021736722	*Acidaminococcus sp. BV3L6*	**AsCpf1**	S542	K548	N552	K607
18	WP_031492824	*Succinivibrio dextrinosolvens*		E564	K570	C574	K629
19	WP_018359861	*Porphyromonas macacae*	PmCpf1	S559	K565	N569	K623
20	WP_050786240	*Prevotella disiens*		T588	N600	Y604	K674
21	WP_027407524	*Anaerovibrio sp. RM50*		A525	N531	N535	K594
22	KDN25524	*Moraxella bovoculi 237*	MbCpf1	N576	K582	N586	K637
23	AJI61006	*Francisella tularensis subsp. novicida U112*	FnCpf1	N607	K613	N617	K671
24	KUJ74576	*Thiomicrospira sp. XS5*		S575	K581	N585	K658
25	WP_051666128	*Lachnospiraceae bacterium ND2006* (*)	LbCpf1	G550	K556	Y560	K613
26	WP_027109509	*Lachnospiraceae bacterium NC2008*		G511	K517	C521	K574
27	WP_027216152	*Butyrivibrio fibrisolvens*		D510	N516	Y520	N573
28	WP_028248456	*Pseudobutyrivibrio ruminis*		N511	K517	N521	K574
29	WP_049895985	*Oribacterium sp. NK2B42*		D528	K534	N538	K591
30	WP_035798880	*Butyrivibrio sp. NC3005*		N512	K518	N522	K575
31	WP_044919442	*Lachnospiraceae bacterium MA2020*	Lb2Cpf1	N512	K518	N522	K575
32	WP_044910713	*Lachnospiraceae bacterium MC2017*		C537	K543	Y547	K599
33	WP_020988726	*Leptospira inadai*	LiCpf1	K580	R586	N590	R644
34	WP_016301126	*Lachnospiraceae bacterium COE1*		D545	K551	N555	R608
35	KIE18657	*Smithella sp. SC_K08D17*	SsCpf1	G561	K567	N571	K625
36	WP_014085038	*Flavobacterium branchiophilum*		N588	K594	Y598	K649
37	WP_045971446	*Flavobacterium sp. 316*		N586	K592	Y596	K647
38	KXB38146	*Bacteroidales bacterium KA00251*		A550	K556	N560	K613
39	WP_036890108	*Porphyromonas crevioricanis*	PcCpf1	S575	K581	N585	K641
40	WP_044110123	*Prevotella brevis*		D541	K547	N551	K603
41	WP_009217842	*Bacteroidetes oral taxon 274*		D564	K570	N574	K628
42	WP_006283774	*Prevotella bryantii*		G566	K572	N576	K629
43	WP_024988992	*Prevotella albensis*		G561	K567	C571	K624

(*) The version of LbCpf1 we used in in this study has the first 18 residues deleted relative to the NCBI record for accession number WP_051666128, consistent with previous work (Zetsche *et al*. 2015; Yamano *et al*. 2016). The numbering in figures and text is based on the truncated sequence (G532/K538/Y542/K595).

Supplementary Table 4a Selected list of plasmids used in study

Construct	Experiments Used	Figures	Addgene #
T7-AsCpf1(library)-T7-crRNA	Bacterial	1C-D	
CMV-AsCpf1(WT)-NLS-3xHA	Indel; lysate	2A-D, 3B-C, S1, S4, S8	69982
CMV-NLS-AsCpf1(WT)-NLS-3xHA	Indel	2E, S5, S10	
CMV-AsCpf1(RR)-NLS-3xHA	Indel; lysate	2A-D, 3B-C, S4	
CMV-NLS-AsCpf1(RR)-NLS-3xHA	Indel	2E, 3D, S5, S10	89351
CMV-AsCpf1(RVR)-NLS-3xHA	Indel; lysate	2A-D, 3B-C, S1	
CMV-NLS-AsCpf1(RVR)-NLS-3xHA	Indel	2E, 3D, S5, S10	89353
CMV-NLS-LbCpf1(WT)-NLS-3xHA	Indel	S10, S11	
CMV-NLS-LbCpf1(RR)-NLS-3xHA	Indel	S10, S11	89355
CMV-NLS-LbCpf1(RVR)-NLS-3xHA	Indel	S10, S11	
U6-crRNA-CBh-NLS-AsCpf1(WT)-NLS-3xHA	BLISS	3A	
U6-crRNA-CBh-NLS-AsCpf1(RR)-NLS-3xHA	BLISS; indel (Neuro2a)	3A, S6	89352
U6-crRNA-CBh-NLS-AsCpf1(RVR)-NLS-3xHA	BLISS	3A	89354
U6-crRNA(As)-CMV-mCherry	Indel	2A, 2E, 3B-D, S1, S4, S5, S8, S10	
U6-crRNA(Lb)-CMV-mCherry	Indel	S10, S11	

Supplementary Table 4b List of guide sequences used in study

Figure				Gene	PAM	Guide Sequence (5' to 3')
1C	1D			[Plasmid]	Varies	CCGATGGTCCATGTCTGTTACTCGCCTGTC
2A				*DNMT1*	TCCC site 1	GTCACCCCTGTTTCTGGCACCAG
2A				*DNMT1*	TTCC site 1	TGGTGCCAGAAACAGGGGTGACG
2A				*VEGFA*	TTCC site 2	AAAGCCCATTCCCTCTTTAGCCA
2A	S1			*VEGFA*	TATC site 1	AAATTCCAGCACCGAGCGCCCTG
2A				*DNMT1*	TATA site 1	GGAGAGATTTATTTGAAGAAATA
2B	2C	2D		[Plasmid]	NNNN	GAGAAGTCATTTAATAAGGCCACT
2E		S5A	S10B	*TSPYL6*	TTTG	ATGGCCGCTTGGAGCCAATCGTG
2E		S5A	S10B	*PRMT1*	TTTG	ACGATCTTCACCGCATAATCAGA
2E		S5A	S10B	*WNT8A*	TTTC	CCCAAATTCCACATTGTCGCTGC
2E		S5A	S10B	*FANCF*	TTTG	CACTATGACCTTCAGAAAGGCAT
2E		S5A	S10B	*PRCC*	TTTG	TCACCTGCAGGGCAGCACTCTTG
2E		S5A	S10B	*THAP10*	TTTG	ACGTCTCTTCGGTTATCCAGAAG
2E		S5A	S10B	*FASTKD1*	TTTC	TTCGAAATGTTAGATATCGTTAT
2E		S5A	S10B	*AGO1*	TTTG	ATGCAGGCATCACGAATGGCCAG
2E		S5A	S10B	*RBM11*	TTTG	CTGAATGGAATTCGTTTATATGG
2E		S5A	S10B	*PROM2*	TTTC	AGGCTCTGCAACTCCTGCCGTAG
2E		S5A	S10B	*GRN*	TTTA	CGTGTGACACGCAGAAGGGTACC
2E		S5A	S10B	*RUNX1*	TTTC	ACATTTGCTTCTCTTTACCATAG
2E		S5A	S10B	*ESAM*	TTTC	TCCTGGAGACCCTCCAGCCGCAG
2E		S5A	S10B	*RRAGA*	TTTC	CAGTTCGCGGCTCTCCACGTCAA
2E		S5A	S10B	*APOB*	TTTC	AGTGGATATTTCTGTTGCCACAT
2E		S5A	S10B	*ERBB2*	TTTG	TGGAAGGACATCTTCCACAAGAA
2E		S5A	S10B	*LIPF*	TTTC	CTCTGCTGTTGCCCAGCCACACA
2E		S5A	S10B	*FXN*	TTTC	CCAGTCCAGTCATAACGCTTAGG
2E		S5A	S10B	*FAP*	TTTC	GGTCCTGTCTATATGTGACTTCA
2E		S5A	S10B	*DNMT2*	TTTC	CAGAACACTGTATGCTGCCATCA
2E		S5A	S10B	*HOTTIP*	TTTC	CCTGAGAGCTGGGCCGAACGGGG
2E		S5A	S10B	*XIST*	TTTA	CCCTTGGCATTGCTGATCTTCAG
2E		S5A	S10B	*HIST1H4C*	TTTC	CGGTCTTATCTATGAGGAGACTC
2E	3D	S5B	S10B	*TSPYL6*	TCCA	AGCGGCCATCAAACATATCTGCC
2E	3D	S5B	S10B	*PRMT1*	TTCA	CCGCATAATCAGAGATACTGGAA
		S5B		*WNT8A*	CCCC	AAATTCCACATTGTCGCTGCAGC
2E	3D	S5B	S10B	*FANCF*	TCCA	ACCCAAATGCCTTTCTGAAGGTC
2E	3D	S5B	S10B	*PRCC*	TTCC	TGCGTGATCTGCTTTGTCACCTG
2E	3D	S5B	S10B	*THAP10*	TCCC	AGCGCCTGAGGCTGGTGGCAGGC
2E	3D	S5B	S10B	*FASTKD1*	TTCG	AAATGTTAGATATCGTTATCAAC
2E	3D	S5B	S10B	*AGO1*	TCCA	GTTTGATGCAGGCATCACGAATG
2E	3D	S5B	S10B	*RBM11*	TTCG	TTTATATGGAAGACCAATTAACG
2E	3D	S5B	S10B	*PROM2*	TTCA	GGCTCTGCAACTCCTGCCGTAGC
		S5B		*GRN*	CCCC	GCGGGACAGCAGTGTATGTGGTC
2E	3D	S5B	S10B	*RUNX1*	TCCC	TATGGTAAAGAGAAGCAAATGTG
2E	3D	S5B	S10B	*ESAM*	TTCC	GGGAGGGCATGGAGTAGACCAAG
2E	3D	S5B	S10B	*RRAGA*	TTCC	AGTTCGCGGCTCTCCACGTCAAA
		S5B		*APOB*	CCCC	AGGTCTCTTTCAGTGGATATTTC
2E	3D	S5B	S10B	*ERBB2*	TTCC	ACAAGAACAACCAGCTGGCTCTC
2E	3D	S5B	S10B	*LIPF*	TTCC	TCTGCTGTTGCCCAGCCACACAT

Supplementary Table 4b (continued)

2E	3D	S5B	S10B	*FXN*	TCCC	AGTCCAGTCATAACGCTTAGGTC
2E	3D	S5B	S10B	*FAP*	TCCC	TGAAGTCACATATAGACAGGACC
2E	3D	S5B	S10B	*DNMT2*	TCCA	GAACACTGTATGCTGCCATCAAA
2E	3D	S5B	S10B	*HOTTIP*	TTCG	GCCCAGCTCTCAGGGAAACGAAG
2E	3D	S5B	S10B	*XIST*	TCCG	TTTACCCTTGGCATTGCTGATCT
2E	3D	S5B	S10B	*HIST1H4C*	TTCC	GGTCTTATCTATGAGGAGACTCG
2E	3D	S5C	S10B	*TSPYL6*	TATC	TGCCATTACCTCTGTCGCCTTGC
2E	3D	S5C	S10B	*PRMT1*	TATC	TCTGATTATGCGGTGAAGATCGT
2E	3D	S5C	S10B	*WNT8A*	TATA	TAGGAGGCCATGGCTGGATCTGG
2E	3D	S5C	S10B	*FANCF*	TATC	TGGGTCTGCTAACAGACTGGGGT
2E	3D	S5C	S10B	*PRCC*	TATC	AAGGCTGCTGCCAAGAGTGCTGC
2E	3D	S5C	S10B	*THAP10*	TATC	CAGAAGAACCTGCGCTTCTCCCA
2E	3D	S5C	S10B	*FASTKD1*	TATC	TAACATTTCGAAGAAACTTTGCT
2E	3D	S5C	S10B	*AGO1*	TATG	AGCTACTGGCCATTCGTGATGCC
2E	3D	S5C	S10B	*RBM11*	TATG	CCATAGCTTTGCTGAATGGAATT
2E	3D	S5C	S10B	*PROM2*	TATA	CCAACAAGCTACGGCAGGAGTTG
2E	3D	S5C	S10B	*GRN*	TATG	TGGTCCTCACAGCACACAGCCTA
2E	3D	S5C	S10B	*RUNX1*	TATG	GTAAAGAGAAGCAAATGTGAAAC
2E	3D	S5C	S10B	*ESAM*	TATC	CTTGGTCTACTCCATGCCCTCCC
2E	3D	S5C	S10B	*RRAGA*	TATC	TTCCGTAACGTGGAAGTTTTGAT
2E	3D	S5C	S10B	*APOB*	TATC	CACTGAAAGAGACCTGGGGCAGT
2E	3D	S5C	S10B	*ERBB2*	TATC	AGTGTGAGAGCCAGCTGGTTGTT
2E	3D	S5C	S10B	*LIPF*	TATG	ATGTGTGGCTGGGCAACAGCAGA
2E	3D	S5C	S10B	*FXN*	TATG	ACTGGACTGGGAAAAACTGGGTG
2E	3D	S5C	S10B	*FAP*	TATA	TGTGACTTCAGGGAAGACTGGCA
2E	3D	S5C	S10B	*DNMT2*	TATG	CTGCCATCAAAGCTAATATTTGG
2E	3D	S5C	S10B	*HOTTIP*	TATC	AAAAGTTCTTACTGAGCGCTTCG
2E	3D	S5C	S10B	*XIST*	TATA	CTGGGATATTCCGTTTACCCTTG
2E	3D	S5C	S10B	*HIST1H4C*	TATC	TATGAGGAGACTCGAGGTGTGCT
3A				*VEGFA*	TTTG	CTAGGAATATTGAAGGGGGCAGG
3A				*GRIN2B*	TTTG	GTGCTCAATGAAAGGAGATAAGG
3A				*DNMT1*	TTTG	AAGAAATATTACAACATATAAAA
3A	3C	S8		*EMX1*	TTTG	TCCTCCGGTTCTGGAACCACACC
3B				*RPL32P3*	TTTG	GGGTGATCAGACCCAACAGCAGG
S4A				*EMX1*	TTTG	GGGAGGCCTGGAGTCATGGCCCC
S4A				*EMX1*	TTTG	TGGTTGCCCACCCTAGTCATTGG
S4A				*DNMT1*	TTTC	CCTTCAGCTAAAATAAAGGAGGA
S4A				*DNMT1*	TTTG	AGGAGTGTTCAGTCTCCGTGAAC
S4A				*CFTR*	TTTA	ATGGTGCCAGGCATAATCCAGGA
S4A				*VEGFA*	TTTA	GCCAGAGCCGGGGTGTGCAGACG
S4A				*DNMT1*	TTTC	CTGATGGTCCATGTCTGTTACTC
S4A				*VEGFA*	TTTC	CAAAGCCCATTCCCTCTTTAGCC
S4A				*DNMT1*	TTTA	GCTGAAGGGAAATAAAAGGAAAA
S4A				*CFTR*	TCTC	AGTTTTCCTGGATTATGCCTGGC
S4A				*EMX1*	TCTG	GCCACTCCCTGGCCAGGCTTTGG
S4A				*CFTR*	TCTA	TATTCATCATAGGAAACACCAAA
S4A				*VEGFA*	TCTC	TGTACATGAAGCAACTCCAGTCC
S4A				*DNMT1*	TCTG	CCCTCCCGTCACCCCTGTTTCTG
S4A				*VEGFA*	TCTA	TTGGAATCCTGGAGTGACCCCTG

Supplementary Table 4b (continued)

S4A				*DNMT1*	TCTC	CGTGAACGTTCCCTTAGCACTCT
S4A				*VEGFA*	TCTG	GCTAAAGAGGGAATGGGCTTTGG
S4A				*EMX1*	TTCT	TCTTCTGCTCGGACTCAGGCCCT
S4A				*DNMT1*	TTCT	GCCCTCCCGTCACCCCTGTTTCT
S4A				*VEGFA*	TTCT	GACCTCCCAAACAGCTACATATT
S4A				*DNMT1*	TCCT	GGTGCCAGAAACAGGGGTGACGG
S4A				*DNMT1*	TCCT	GATGGTCCATGTCTGTTACTCGC
S4B	S4A			*CFTR*	TTCG	GCGATGTTTTTTCTGGAGATTTA
S4B	S4A			*DNMT1*	TTCA	GCTAAAATAAAGGAGGAGGAAGC
S4B	S4A			*DNMT1*	TCCC	GTCACCCCTGTTTCTGGCACCAG
S4B	S4A			*DNMT1*	TTCC	TGGTGCCAGAAACAGGGGTGACG
S4B	S4A			*DNMT1*	TTCA	GTCTCCGTGAACGTTCCCTTAGC
S4B	S4A			*DNMT1*	TTCA	CGGAGACTGAACACTCCTCAAAC
S4B	S4A			*EMX1*	TTCG	TGGCAATGCGCCACCGGTTGATG
S4B	S4A			*VEGFA*	TTCC	CTGTGGTGGCCGAGCGCCCCCTA
S4B	S4A			*VEGFA*	TCCA	GTCCCAAATATGTAGCTGTTTGG
S4B	S4A			*VEGFA*	TCCG	CACGTAACCTCACTTTCCTGCTC
S4B	S4A			*VEGFA*	TCCG	CCCCCGGAAACTCTGTCCAGAGA
S4B	S4A			*VEGFA*	TCCG	GGGGCGGATGGGTAATTTTCAGG
S4B	S4A			*VEGFA*	TCCC	TCTTTAGCCAGAGCCGGGGTGTG
S4B	S4A			*VEGFA*	TCCA	ATAGATCTGTGTGTCCCTCTCCC
S4B	S4A			*VEGFA*	TTCC	AAAGCCCATTCCCTCTTTAGCCA
S4B	S4A			*VEGFA*	TCCC	CCCACCCCCTTTCCAAAGCCCAT
S4B				*CFTR*	GTCG	AAAATTTTACACCACAAAATGTT
S4B				*CFTR*	ACCA	AAGATGATATTTTCTTTAATGGT
S4B				*CFTR*	ACCA	TTAAAGAAAATATCATCTTTGGT
S4B				*CFTR*	ATCC	TAAACTCATTAATGCCCTTCGGC
S4B				*CFTR*	ATCC	AGGAAAACTGAGAACAGAATGAA
S4B				*EMX1*	ATCA	CATCAACCGGTGGCGCATTGCCA
S4B				*EMX1*	GTCC	TCCCCATTGGCCTGCTTCGTGGC
S4B				*EMX1*	CCCG	GGCTTCAAGCCCTGTGGGGCCAT
S4B				*EMX1*	ATCG	ATGTCACCTCCAATGACTAGGGT
S4B				*EMX1*	ATCG	ATGTCCTCCCCATTGGCCTGCTT
S4B				*VEGFA*	CCCA	TTCCCTCTTTAGCCAGAGCCGGG
S4B				*VEGFA*	CTCG	GCCACCACAGGGAAGCTGGGTGA
S4B				*VEGFA*	GTCC	CAAATATGTAGCTGTTTGGGAGG
S4B				*VEGFA*	GCCG	AGCGCCCCCTAGTGACTGCCGTC
S4B				*VEGFA*	GCCC	ATTCCCTCTTTAGCCAGAGCCGG
S4B				*VEGFA*	CCCG	GCTCTGGCTAAAGAGGGAATGGG
S4B				*VEGFA*	GCCA	GAGCCGGGGTGTGCAGACGGCAG
S4B				*VEGFA*	CTCG	CTCCATTCACCCAGCTTCCCTGT
S4B				*VEGFA*	GCCC	TGGGCTCTCTGTACATGAAGCAA
S4B				*VEGFA*	CTCC	AGTCCCAAATATGTAGCTGTTTG
S4B				*VEGFA*	GTCA	GAAATAGGGGGTCCAGGAGCAAA
S4B				*VEGFA*	ACCC	CGGCTCTGGCTAAAGAGGGAATG
S4B				*VEGFA*	ACCA	CAGGGAAGCTGGGTGAATGGAGC
S4B				*VEGFA*	CCCA	GCTTCCCTGTGGTGGCCGAGCGC
S4B				*VEGFA*	GCCG	TCTGCACACCCCGGCTCTGGCTA
S4B				*VEGFA*	GCCC	CCTAGTGACTGCCGTCTGCACAC

Supplementary Table 4b (continued)

S4B				*VEGFA*	GCCA	CCACAGGGAAGCTGGGTGAATGG
S4B				*VEGFA*	GTCA	CTAGGGGGCGCTCGGCCACCACA
S4B				*VEGFA*	GTCC	TCACTCTCGAAGACGCTGCTCGC
S4B				*VEGFA*	GCCG	GGGTGTGCAGACGGCAGTCACTA
S4B				*VEGFA*	CCCG	CTCCAACGCCCTCAACCCCACAC
S4B				*VEGFA*	CTCG	AAGACGCTGCTCGCTCCATTCAC
S4B				*VEGFA*	CTCC	TGGACCCCCTATTTCTGACCTCC
S4B				*VEGFA*	ATCC	TGGAGTGACCCCTGGCCTTCTCC
S4B				*VEGFA*	ACCC	CCTTTCCAAAGCCCATTCCCTCT
S4B				*VEGFA*	CCCC	CCACCCCCTTTCCAAAGCCCATT
S6				*PCSK9* (mouse)	TCCC	GTCCCAGGAGGATGGCCTGGCTG
S6				*PCSK9* (mouse)	TCCC	AGGAGGATGGCCTGGCTGATGAG
S6				*PCSK9* (mouse)	TTCA	ATCTGTAGCCTCTGGGTCTCCTC
S6				*PCSK9* (mouse)	TCCC	TGGCTTCTTGGTGAAGATGAGCA
S6				*PCSK9* (mouse)	TTCC	TCAATGTACTCCACATGGGGCAA
S6				*PCSK9* (mouse)	TCCA	TGGGATGCTCTGGGCGAAGACAA
S6				*PCSK9* (mouse)	TTCC	TCTGTCTGGTGCCATGCTGGGAT
S6				*PCSK9* (mouse)	TCCC	GATGGGCACCCTGGATGCTGGTA
S6				*PCSK9* (mouse)	TCCC	GGCCGCTGACCACACCTGCCAGG