

Genome editing with the HDR-enhancing DNA-PKcs inhibitor AZD7648 causes large-scale genomic alterations

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Supplemental Table 1

Cell type	Target	Cas9	sgRNA		ssODN		Length (nt)	Mutation type
			Origin	Sequence	Origin	Sequence		
K-562	HBB	Home-made SpCas9-NLS	Alt-R CRISPR-Cas9 sgRNA (IDT)	CTTGCCCCACAGGGCAGTAA	Alt-R HDR Donor oligo (IDT)	TCAGGGCAGAGCCATCTATTGCTTACATTTTGTCTCTGACACAACCTGTGTCTACTAGCAACCTCAACAGACACCATGGTGCACTGACTCCTGTAGAGAAGTCTGCGGTACTGTCCCTGTGGGCAAGGTGAACGTGGATGAAGTTGGTGTGAGGCCCTGGGCA*G*G*T	171	substitution (12nt)
K-562	CCR5	Home-made SpCas9-NLS	Alt-R CRISPR-Cas9 sgRNA (IDT)	GGCAGCATAGTGAGCCAGA	Alt-R HDR Donor oligo (IDT)	TGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCCTCTTACTGTCCCTTTTGGGGcATATGCTGCCGCCAGTGGGACTTTTGGAAATACAATGTCTCAACTCTTGACAGGGCTCTATTTATAG	150	substitution (4 nt)
K-562	HBD	Home-made SpCas9-NLS	Alt-R CRISPR-Cas9 sgRNA (IDT)	CAGGACCAGCATAAAGGCA	Alt-R HDR Donor oligo (IDT)	GGAATAGTGAATGAAGGTTCAITTTTCATTCTCACAACTAATGAACCTGCTTATCTTTAAACCAACCTGCTCACCACACCTGGAGCAGGAGGGCAGGAGCCAGGGCTGGGCATAAAAGGCAGGGCAGAGTGCACTGTGCTTACACTTTCTCTGCATAAACAGTGTTCCTAGCAACCTCAACACAGAC	194	insertion (15 nt) + substitution (2nt)
K-562	TRAC	Home-made SpCas9-NLS	CRISPRRevolution sgRNA EZ Kit (Synthego)	TCAGGGTTCTGGATATCTGT	Microsynth	AAATGAGATCATGTCTCAACCTGATCCTCTTGTCCACACATGATATCCAGAACCCTGACCCCTGCCGTGACACAGCTGAGAG	83	insertion (3 nt)
K-562	GAPDH	Home-made SpCas9-NLS	CRISPRRevolution sgRNA EZ Kit (Synthego)	GGGTCTACATGCCAACTGTG	Alt-R HDR Donor oligo (IDT)	GAAGAGAGAGACCCCTCACTGCTGGGGAGTCCCTGCCACACTCAGTCCCCACCCACACTGAATCTCCCTTGTDBDHVHDDBVGTAGACCCCTTGAAGAGGGGAGGGGCTAGGGAGCCGCACCTTGTCTATGTACCATCAATAAAGTAC	150	substitution barcode (12nt)
K-562	AAVS1	Home-made SpCas9-NLS	CRISPRRevolution sgRNA EZ Kit (Synthego)	TCCTAGTGGCCCCACTGTG	Microsynth	CTCTGGTTCTGGGTACTTTTATCTGTCCCTCCACCCACAGTAGTGGGGCCACTAGGGACAGGATTGGTGACAGAAAGCCC	83	insertion (3 nt)
K-562 FIRE reporter	FIRE reporter	Home-made SpCas9-NLS	CRISPRRevolution sgRNA EZ Kit (Synthego)	CATGAGGGGTCOCATGTTCG	GenExact™ Single-stranded DNA	GCTCTATATAAGCAGAGCTCGTTTGTGAACCTCAGATCGCGCGCCAATTCAGCGGACAGACAAAGGCAGCGCCACATGCTCAGCAAGGGGAGGSCCTCATCAAGGAGTTCTATGCGGTTCAAGGTGCACATGAGGGCTCCATGAACGCTCACAGTTCGAGATCGGAGGCGAAGCGGAGGGCAGGSCCTACGAGCGCCACCAAGCCGCAAGCTGAAGGTGACAAAGGGGCGCCCTGCCCTCTCTCGGACATCCCTGTCCCTCAAGTTCAGTGTACGGCTCCAGGGCTTTCATCAAGCAACCCGCGACATCCCGACACTACACAAGCAGTCTCTCCCGAGGGCTTCAAGTGGGAGAGGGTGTATGAATTCGAGGAGCGGCGCCGCTGACCGTCAACAGGACACCTCCCTGAGGAGCGGCAACCTCTCATCTCAAGGTCAAGCTGCGGGCCACCACTTCCTCCAGAGCGGCCCTCATGCAAGAAACAATGGGCTGGGAGGCTCCACGGAG	528	insertion (228 nt)
						TTCTCTTTGAAGTGGAGAGTGAACACTACAGACTCCCCCGACAGCCCACTCTCTATCAGAGCCTAACCGTACCCCGGGAGCGGAGAGAGACATTCATTCGAGACTGAAGCGCCCTCGGGATGAGGTGAGGTGAGAGGCCCACTG	150	insertion (6 nt)
K-562 eGFP	SMURF1	Home-made SpCas9-NLS	Alt-R CRISPR-Cas9 sgRNA (IDT)	TCTATCAGAGCCTAACCG	Alt-R HDR Donor oligo (IDT)	CAAATTTGGATTTCCTGGGCCCAAGACTTCCAAAGACCTGTAAATGGAGGGATTTACACCTCACATATGTCCAGTTAAACAGTTTGTGGTACTGTAACTCGGGTACCCA GCCCAATGATACACAGTAGTTTATCACTGTATT	150	insertion (6 nt)
K-562 eGFP	IFT22	Home-made SpCas9-NLS	Alt-R CRISPR-Cas9 sgRNA (IDT)	GTGTGATCATTGGGCTGCGA	Alt-R HDR Donor oligo (IDT)	TCAGGGCAGAGCCATCTATTGCTTACATTTGCTCTGACACAACCTGTGTCTACTAGCAACCTCAACAGACACCATGGTGCACTGACTCCTGTAGAGAAGTCTCGGTTACTGTCCCTGTGGGCAAGGTGAACGTGGATGAAGTTGGTGTGAGGCCCTGGCA*G*G*T	171	substitution (12nt)
RPE-1 +/- p53	HBB	Home-made SpCas9-NLS	Alt-R CRISPR-Cas9 sgRNA (IDT)	CTTGCCCCACAGGGCAGTAA	Alt-R HDR Donor oligo (IDT)	TGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCCTCTTACTGTCCCTTTTGGGGcATATGCTGCCGCCAGTGGGACTTTTGGAAATACAATGTCTCAACTCTTGACAGGGCTCTATTTATAG	150	substitution (4 nt)
RPE-1 +/- p53	CCR5	Home-made SpCas9-NLS	Alt-R CRISPR-Cas9 sgRNA (IDT)	GGCAGCATAGTGAGCCAGA	Alt-R HDR Donor oligo (IDT)	GGAATAGTGAATGAAGGTTCAITTTTCATTCTCACAACTAATGAACCTGCTTATCTTTAAACCAACCTGCTCACCACACCTGGAGCAGGAGGGCAGGAGCCAGGGCTGGGCATAAAAGGCAGGGCAGAGTGCACTGTGCTTACACTTTCTCTGCATAAACAGTGTTCCTAGCAACCTCAACACAGAC	194	insertion (15 nt) + substitution (2nt)
RPE-1 +/- p53	HBD	Home-made SpCas9-NLS	Alt-R CRISPR-Cas9 sgRNA (IDT)	CAGGACCAGCATAAAGGCA	Alt-R HDR Donor oligo (IDT)	AAATGAGATCATGTCTCAACCTGATCCTCTTGTCCACACATGATATCCAGAACCCTGACCCCTGCCGTGACACAGCTGAGAG	83	insertion (3 nt)
RPE-1 +/- p53	TRAC	Home-made SpCas9-NLS	CRISPRRevolution sgRNA EZ Kit (Synthego)	TCAGGGTTCTGGATATCTGT	Microsynth	GAAGAGAGAGACCCCTCACTGCTGGGGAGTCCCTGCCACACTCAGTCCCCACCCACACTGAATCTCCCTTGTDBDHVHDDBVGTAGACCCCTTGAAGAGGGGAGGGCTAGGGAGCCGCACCTTGTCTATGTACCATCAATAAAGTAC	150	substitution barcode (12nt)
RPE-1 +/- p53	GAPDH	Home-made SpCas9-NLS	CRISPRRevolution sgRNA EZ Kit (Synthego)	GGGTCTACATGCCAACTGTG	Alt-R HDR Donor oligo (IDT)	CTCTGGTTCTGGGTACTTTTATCTGTCCCTCCACCCACAGTAGTGGGGCCACTAGGGACAGGATTGGTGACAGAAAGCCC	83	insertion (3 nt)
RPE-1 +/- p53	AAVS1	Home-made SpCas9-NLS	In vitro transcription	TCCTAGTGGCCCCACTGTG	Microsynth	TCAGGGCAGAGCCATCTATTGCTTACATTTGCTCTGACACAACCTGTGTCTACTAGCAACCTCAACAGACACCATGGTGCACTGACTCCTGTAGAGAAGTCTCGGTTACTGTCCCTGTGGGCAAGGTGAACGTGGATGAAGTTGGTGTGAGGCCCTGGGCA*G*G*T	171	substitution (12nt)
HSPC	HBB	It-R™ 5.p. Cas9 Nuclease V3 (IDT)	Alt-R CRISPR-Cas9 sgRNA (IDT)	CTTGCCCCACAGGGCAGTAA	Alt-R HDR Donor oligo (IDT)	TGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCCTCTTACTGTCCCTTTTGGGGcATATGCTGCCGCCAGTGGGACTTTTGGAAATACAATGTCTCAACTCTTGACAGGGCTCTATTTATAG	150	substitution (4 nt)
HSPC	CCR5	It-R™ 5.p. Cas9 Nuclease V3 (IDT)	Alt-R CRISPR-Cas9 sgRNA (IDT)	GGCAGCATAGTGAGCCAGA	Alt-R HDR Donor oligo (IDT)	GGAATAGTGAATGAAGGTTCAITTTTCATTCTCACAACTAATGAACCTGCTTATCTTTAAACCAACCTGCTCACCACACCTGGAGCAGGAGGGCAGGAGCCAGGGCTGGGCATAAAAGGCAGGGCAGAGTGCACTGTGCTTACACTTTCTCTGCATAAACAGTGTTCCTAGCAACCTCAACACAGAC	194	insertion (15 nt) + substitution (2nt)
HSPC	TRAC	Home-made SpCas9-NLS	CRISPRRevolution sgRNA EZ Kit (Synthego)	TCAGGGTTCTGGATATCTGT	Microsynth	AAATGAGATCATGTCTCAACCTGATCCTCTTGTCCACACATGATATCCAGAACCCTGACCCCTGCCGTGACACAGCTGAGAG	83	insertion (3 nt)
RPE-1 +/- p53	GAPDH	Home-made SpCas9-NLS	CRISPRRevolution sgRNA EZ Kit (Synthego)	GGGTCTACATGCCAACTGTG	Alt-R HDR Donor oligo (IDT)	GAAGAGAGAGACCCCTCACTGCTGGGGAGTCCCTGCCACACTCAGTCCCCACCCACACTGAATCTCCCTTGTDBDHVHDDBVGTAGACCCCTTGAAGAGGGGAGGGGCTAGGGAGCCGCACCTTGTCTATGTACCATCAATAAAGTACCTGTGCTC	150	substitution (12nt)
HSPC (scRNA-seq)	GAPDH	Home-made SpCas9-NLS	CRISPRReverseolution sgRNA EZ Kit (Synthego)	GGGTCTACATGCCAACTGTG	Alt-R HDR Donor oligo (IDT)	CAAGAGGAAGAGAGAGACCCCTCACTGCTGGGGAGTCCCTGCCACACTCAGTCCCCACCACTGAATCTCCCTTGTDBDHVHDDBVGTAGACCCCTTGAAGAGGGGAGGGGCTAGGGAGCCGCACCTTGTCTATGTACCATCAATAAAGTACCTGTGCTC	150	substitution barcode (12nt)
Upper airway organoid	GAPDH	Home-made SpCas9-NLS	CRISPRRevolution sgRNA EZ Kit (Synthego)	GGGTCTACATGCCAACTGTG	Alt-R HDR Donor oligo (IDT)	CAAGAGGAAGAGAGAGACCCCTCACTGCTGGGGAGTCCCTGCCACACTCAGTCCCCACCACTGAATCTCCCTTGTDBDHVHDDBVGTAGACCCCTTGAAGAGGGGAGGGGCTAGGGAGCCGCACCTTGTCTATGTACCATCAATAAAGTACCTGTGCTC	150	substitution barcode (12nt)

Supplemental Table 2

Target	Cell line	Condition	Total read (rep1)	Total read (rep2)	Category	chr	start	end	reads (rep1)	reads (rep2)	hits (rep1)	hits (rep2)	Annotation	Closest element	Putative target site	Score
HBB	HSCs	Cas9 + ssODN	414'567	596'827	ON	chr11	5'225'112	5'228'549	4'892	11'102	117	122	Promoter (<=1kb)	HBB	CTTGC000CACAGGGCAGTAAAGG	20.5
					Deletion to HBD	chr11	5'234'125	5'234'655	8'946	14'635	32	41	5' UTR	HBD	TTTGC000CACAGGGCAGTAAAGG	14.5
					OMT1	chr9	101'833'332	101'833'859	367	465	6	5	Distal Intergenic	GRIN3A	CTTACG000CACAGGGCAGTAAAGG	17.5
					ON	chr11	5'224'021	5'234'941	60'684	29'959	129	106	Promoter (<=1kb)	HBB	CTTGC000CACAGGGCAGTAAAGG	20.5
					OMT1	chr9	101'832'145	101'834'365	5'803	4'362	67	56	Distal Intergenic	GRIN3A	CTTACG000CACAGGGCAGTAAAGG	17.5
		Cas9 + ssODN + AZD7648	482'138	315'288	OMT2	chr12	124'319'031	124'319'545	2'337	1'082	12	13	Distal Intergenic	MIR6880	CT-G0000CACAGGGCAGCAAGG	15.5
					OMT3	chr17	78'243'303	78'243'814	582	241	7	3	Distal Intergenic	LOC105371910	CTTGC000CACAGGGCAGTAAAGG	17.5
					OMT4	chrX	75'786'171	75'786'671	123	20	2	1	Promoter (<=1kb)	MAGEE2	GTGG000CACAGGGCAGCAATGG	14.5
					ON	chr3	46'363'453	46'378'217	4'352	5'233	195	176	Promoter (<=1kb)	CCR5	GGCAGCATAGTGAGCCACAGAGG	20.5
					OMT1	chr11	16'159'958	16'161'306	155	257	23	37	Intron (intron 5 of 14)	SOX6	AGCAGCATAGTGAGCCACAGGGG	14.5
CCR5	HSCs	Cas9 + ssODN	3'807'449	3'723'426	ON	chr3	46'370'917	46'378'088	2'103	2'669	123	142	Promoter (<=1kb)	CCR5	GGCAGCATAGTGAGCCACAGAGG	20.5
					OMT1	chr11	16'157'300	16'162'682	1'051	748	73	68	Intron (intron 5 of 14)	SOX6	AGCAGCATAGTGAGCCACAGGGG	14.5
					OMT2	chr14	105'852'906	105'853'419	169	93	6	6	Intron (intron 4 of 5)	MIR4539	GACATAGCATATGAGCCACAGGG	10.5
					OMT3	chr3	46'357'499	46'358'069	39	44	5	5	5' UTR	CCR2	TGACGAGATAGTGAGCCACAGATG	13.5
					OMT4	chr14	55'463'094	55'463'599	1	13	1	3	Distal Intergenic	TBPL2	AACAGCATAGTGAAACCCAGGAGG	12.5
		Cas9 + ssODN + AZD7648	3'944'929	5'052'178	OMT5	chr17	44'077'075	44'077'576	16	74	1	2	3' UTR	HDACS	GTGAGCAAGGGAGCCAGAGG	14.5
					OMT6	chr14	91'323'991	91'324'491	17	19	1	1	Intron (intron 12 of 29)	CCDC88C	GGCAGCAGAGCAAGCCAGGAGG	12.5
					ON	chr12	6'533'860	6'540'931	654	352	40	25	Promoter (<=1kb)	GAPDH	GGGTCTACATGGCAACTGTGAGG	20.5
					ON	chr12	6'533'349	6'548'412	984	1'142	83	82	Promoter (<=1kb)	GAPDH	GGGTCTACATGGCAACTGTGAGG	20.5
					OMT1	chr12	53'219'201	53'219'709	223	174	13	6	Intron (intron 2 of 8)	RARG	AGGTCCACATGGC--CTGTGAGG	11.5
GAPDH	HSCs	Cas9 + ssODN + AZD7648	1'101'134	1'707'332	OMT2	chr10	124'473'266	124'473'799	84	33	8	8	Intron (intron 1 of 6)	LHP	GAGGCCACATGGCAACTATGGG	12.5
					OMT3	chr4	107'862'066	107'863'318	14	80	1	6	Intron (intron 2 of 2)	SGM52	GCTCTCATATGGTAACTGTGAGG	12.5
					OMT4	chr1	110'612'401	110'612'905	17	60	2	4	Intron (intron 1 of 4)	KCNJ2	GGGTCTCTATAGCAACTGTGGG	14.5
					OMT5	chr12	726'027	726'542	29	4	4	1	Distal Intergenic	WNK1	AGGTCTCATATGGCA--CTGTGAAG	13.5
					OMT6	chr19	45'372'302	45'372'803	21	48	3	1	Promoter (1-2kb)	ERC22	GGATGTCTAC--TGTCAACTGTGGGG	12.5
					OMT7	chr2	103'803'591	103'804'096	1	19	1	3	Distal Intergenic	LINC01965	GAGCAGCATATGACCAAGTGAAG	12.5
					OMT8	chr14	51'884'315	51'884'816	10	5	2	2	Intron (intron 2 of 3)	GN22	CAGACACATATGGTAACTGTGAGG	10.5
					OMT9	chr13	126'818'682	126'819'183	49	11	2	1	Intron (intron 5 of 7)	CHCHD6	AGGCTCATATGGCAACTGTGAGG	14.5
					OMT10	chr7	101'237'289	101'237'865	20	10	2	1	Promoter (<=1kb)	CLDN15	GCTTCTTCATGGCACTGTGGGG	14.5
HBB	RPE-1 p53-/-	Cas9 + ssODN	1'494'728	1'443'632	ON	chr11	5'221'187	5'242'723	174'049	150'105	518	548	Promoter (<=1kb)	HBB	CTTGC000CACAGGGCAGTAAAGG	20.5
					OMT1	chr9	101'833'341	101'833'859	1'475	349	5	4	Distal Intergenic	GRIN3A	CTTACG000CACAGGGCAGTAAAGG	17.5
					ON	chr11	5'220'728	5'235'876	234'492	133'564	434	405	Promoter (<=1kb)	HBB	CTTGC000CACAGGGCAGTAAAGG	20.5
					OMT1	chr9	101'831'953	101'835'418	2'780	9'955	22	37	Distal Intergenic	GRIN3A	CTTACG000CACAGGGCAGTAAAGG	17.5
					OMT2	chr12	124'319'035	124'319'549	6	677	1	4	Distal Intergenic	MIR6880	CT-G0000CACAGGGCAGCAAGG	15.5
		Cas9 + ssODN + AZD7648	986'117	1'045'525	ON	chr11	5'219'668	5'236'813	31'162	25'314	227	269	Promoter (<=1kb)	HBB	CTTGC000CACAGGGCAGTAAAGG	20.5
					ON	chr11	5'224'830	5'230'761	14'776	11'791	125	106	Promoter (<=1kb)	HBB	CTTGC000CACAGGGCAGTAAAGG	20.5
					OMT1	chr9	101'832'726	101'834'804	8'316	8'136	45	38	Distal Intergenic	GRIN3A	CTTACG000CACAGGGCAGTAAAGG	17.5
					OMT2	chr12	124'319'037	124'319'541	310	1'066	2	5	Distal Intergenic	MIR6880	CT-G0000CACAGGGCAGCAAGG	15.5
					OMT3	chr11	126'115'573	126'116'073	287	548	2	1	Distal Intergenic	LOC105369591	ATTAC000CACAGGGCAGT--GGG	11.5
CCR5	RPE-1 p53-/-	Cas9 + ssODN	1'052'897	985'094	OMT4	chr17	78'243'307	78'243'808	1	562	1	1	Distal Intergenic	LOC105371910	CTTGC000CACAGGGCAGTAAAGG	17.5
					ON	chr3	46'366'228	46'380'887	12'093	23'452	246	338	Promoter (<=1kb)	CCR5	GGCAGCATAGTGAGCCACAGAGG	20.5
					OMT1	chr3	46'356'820	46'358'204	354	145	11	17	Promoter (2-3kb)	CCR2	TGACGAGATAGTGAGCCACAGATG	13.5
					ON	chr3	46'355'973	46'380'234	549'435	482'705	2583	2716	Promoter (<=1kb)	CCR5	GGCAGCATAGTGAGCCACAGAGG	20.5
					OMT1 / HMT	chr14	55'461'620	55'465'727	2'500	12'787	15	51	Distal Intergenic	TBPL2	AACAGCATAGTGAAACCCAGGAGG	12.5
		Cas9 + ssODN + AZD7648	2'126'782	1'865'952	OMT2	chr11	16'160'153	16'161'309	3'270	2'771	16	13	Intron (intron 5 of 14)	SOX6	AGCAGCATAGTGAGCCACAGGGG	14.5
					OMT3	chr13	95'195'150	95'196'765	1'703	914	2	6	intron (intron 8 of 30)	ABCC4	GGAGGCA--AGTGAGCCACAGAGG	15.5
					HMT	chr1	202'169'830	202'174'244	2'674	726	6	5	Promoter (1-2kb)	PTPRVP	-	-
					ON	chr3	46'371'646	46'374'562	95	-	21	-	5' UTR	CCR5AS	GGCAGCATAGTGAGCCACAGAGG	20.5
					HMT	chr22	30'843'750	30'844'253	45	-	3	-	Intron (intron 3 of 14)	OSBP2	-	-
CCR5	RPE-1 p53+/+	Cas9 + ssODN	1'403'331	-	HMT	chr2	112'815'826	112'816'333	57	-	2	-	Distal Intergenic	LOC124907871	-	-
					ON	chr3	46'370'946	46'376'271	37'222	-	359	-	Promoter (<=1kb)	CCR5	GGCAGCATAGTGAGCCACAGAGG	20.5
					OMT1	chr14	55'463'090	55'463'603	4'341	-	29	-	Distal Intergenic	TBPL2	AACAGCATAGTGAAACCCAGGAGG	12.5
					OMT2	chr11	16'160'505	16'162'844	1'805	-	30	-	intron (intron 5 of 14)	SOX6	AGCAGCATAGTGAGCCACAGGGG	14.5
					OMT3	chr13	95'195'159	95'195'667	1'247	-	10	-	intron (intron 8 of 30)	ABCC4	GGAGGCA--AGTGAGCCACAGAGG	15.5
		Cas9 + ssODN + AZD7648	2'284'541	-	OMT4	chr10	77'610'687	77'611'191	493	-	8	-	Intron (intron 1 of 27)	KCNMA1	GGCA-CATCCAGAGAGCCACACAG	10.5
					OMT5	chr18	44'884'270	44'884'770	162	-	4	-	Intron (intron 3 of 5)	SETBP1	GGCAGCATATGGAGCCAG--GGG	13.5
					OMT6	chr10	98'300'072	98'300'573	200	-	3	-	Distal Intergenic	LOXL4	GGACG--ATAATGAGCCACAG--GG	14
					OMT7	chr1	25'236'334	25'236'838	81	-	3	-	Distal Intergenic	SYF2	GG-AGCTTTCAGTGAAGCCACAGATTG	11.5
					OMT8	chr17	43'575'622	43'576'126	453	-	2	-	Intron (intron 24 of 24)	DHX8	GTGAGCATGGTGAGCCACAG--GG	15
CCR5	RPE-1 p53+/+	Cas9 + ssODN + AZD7648	2'284'541	-	OMT9	chr3	73'656'082	73'656'590	432	-	2	-	Distal Intergenic	PDZRN3	TTCAGCATATGAGGCCACAG--GGG	11.5
					OMT10	chr12	69'837'322	69'837'822	343	-	2	-	Intron (intron 4 of 4)	MYRF1	GGCAGGGAAGTGTGCTCCAGAGG	10.5
					OMT11	chr5	57'804'159	57'804'666	67	-	2	-	Distal Intergenic	LINC02225	GACAGCATAGTGAGCC--ACAAGG	13.5
					OMT12	chr3	133'602'863	133'603'363	9	-	2	-	Intron (intron 1 of 1)	TOPBP1	GGCTGCA--GTGAGCCACAGATCG	10.5
					HMT	chr3	46'356'970	46'358'682	519	-	16	-	5' UTR	CCR2	-	-
					HMT	chr3	52'683'469	52'683'976	488	-	3	-	Promoter (2-3kb)	GNL3	-	-
					HMT	chr5	131'146'598	131'147'098	256	-	3	-	Distal Intergenic	LYRM7	-	-
					HMT	chr5	43'013'395	43'013'897	237	-	3	-	Exon (exon 2 of 2)	ANXA2R-OT1	-	-
					HMT	chr22	23'721'321	23'721'821	273	-	2	-	Distal Intergenic	GUSBP11	-	-

Supplemental Table 3

Component	End Concentration	Company	Catalog number
A83-01 (5 mM)	500 nM	Tocris	2939
Advanced DMEM/F12 +++		Gibco	12634010
B27 (50x)	1x	Thermo Fisher Scientific	17504044
FGF-10	100 ng / mL	PeproTech	100-26
FGF-7	25 ng / mL	PeproTech	100-19
N-Acetylcysteine (500 mM)	1.25 mM	Sigma-Aldrich	A9165-5G
Nicotinamide (1 M)	5 mM	Sigma-Aldrich	N0636-100G
Noggin Conditioned Medium (100%)	5%	Own production	N/A
R-Spondin Conditioned Medium (100%)	5%	Own production	N/A
SB202190 / p38i (30 mM)	500 nM	Sigma-Aldrich	S7067-5MG
Wnt3a Conditioned Medium (100%)	5%	Own production	N/A

Supplemental Table 4

Cell type	Cas9	sgRNA	ssODN	# of nucleofected cells	Format	Kit	Program
K-562	100 pmol	120 pmol	100 pmol	200'000	20 µL Nucleocuvette Strips	SF	FF-120
K-562 FIRE reporter	200 pmol	240 pmol	90 pmol	8'000'000	100 µL single Nucleocuvette	SF	FF-120
K-562 eGFP	100 pmol	120 pmol	100 pmol	200'000	20 µL Nucleocuvette Strips	SF	FF-120
RPE-1 +/- p53	200 pmol	240 pmol	300 pmol	2'000'000	100 µL single Nucleocuvette	P3	EA-104
HSPC	100 pmol	120 pmol	100 pmol	200'000	20 µL Nucleocuvette Strips	P3	ER-100
HSPC (scRNA-seq)	500 pmol	600 pmol	500 pmol	1'000'000	100 µL single Nucleocuvette	P3	ER-100
Upper airway organoid	500 pmol	600 pmol	500 pmol	1'000'000	100 µL single Nucleocuvette	SE	EW-100

Supplemental Table 5

Sanger sequencing			
Target	Primer	Sequence (5' to 3')	
FIRE reporter	Forward	GAGAACCATCAGATGTTTCCA	
	Reverse	ACGGTGTAGTCCTCGTTGTG	
Short-read sequencing			
Target	Primer	Sequence (5' to 3')	
HBB	1st PCR - Forward	ACCCGTGTTACTTATCCCCTTCC	
	1st PCR - Reverse	TCCATCTACATATCCCAAAGCTGA	
	2nd nested PCR - Forward	CTTTCCCTACACGACGCTCTTCCGATCTTTCTCTGTCTCCACATGCC	
	2nd nested PCR - Reverse	GGAGTTCAGACGTGTGCTCTTCCGATCTACTGTGTTCACTAGCAACCTCAA	
CCR5	Forward	CTTTCCCTACACGACGCTCTTCCGATCTAACTGCAAAAGGCTGAAGAGC	
	Reverse	GGAGTTCAGACGTGTGCTCTTCCGATCTCAAACACAGCATGGACGACAG	
HBD	Forward	CTTTCCCTACACGACGCTCTTCCGATCTCACACATGACAGAACGCCAATCTCAG	
	Reverse	GGAGTTCAGACGTGTGCTCTTCCGATCTGAAGAAAGTGAAGCAACAGTCGACTCTG	
TRAC	Forward	CTTTCCCTACACGACGCTCTTCCGATCTGCAAGAGGGGAAATGAGATCAT	
	Reverse	GGAGTTCAGACGTGTGCTCTTCCGATCTATGTCTAGCACAGTTTGTGCTG	
GAPDH	Forward	CTTTCCCTACACGACGCTCTTCCGATCTGGCCTCCAAGGAGTAAGACC	
	Reverse	GGAGTTCAGACGTGTGCTCTTCCGATCTCCAGACCTAGAATAAGACAGG	
AAVS1	Forward	CTTTCCCTACACGACGCTCTTCCGATCTGGGACCACCTTATATTTCCAGG	
	Reverse	GGAGTTCAGACGTGTGCTCTTCCGATCTATCCTCTCTGGCTCCATCGT	
SMURF1	Forward	CTTTCCCTACACGACGCTCTTCCGATCTCATCCTGTGTCTCATTACCAT	
	Reverse	GGAGTTCAGACGTGTGCTCTTCCGATCTATACCACCACCAGGAAAATCAG	
IFT22	Forward	CTTTCCCTACACGACGCTCTTCCGATCTTTCATCTCAGACCATCTGTGCTC	
	Reverse	GGAGTTCAGACGTGTGCTCTTCCGATCTGAATGAAAATCACATTCAAGCC	
Long-read sequencing			
Target	Primer	Amplification size (bp)	Sequence (5' to 3')
FIRE reporter	Forward	3802	TTTCTGTTGGTGCTGATATTGCGAGAACCATCAGATGTTTCCA
	Reverse		ACTTGCCGTGTCGCTCTATCTTCGAAGGCGATAGAAGGCGATG
HBB	Forward	4627	TTTCTGTTGGTGCTGATATTGCTCAAGCTACAAAAGCCGCC
	Reverse		ACTTGCCGTGTCGCTCTATCTTCCCTTGAAGCCAGGATGATGGT
CCR5	Forward	4545	TTTCTGTTGGTGCTGATATTGCTTTGGCAAACACCAAGTGCTC
	Reverse		ACTTGCCGTGTCGCTCTATCTTCCCCCTTTGCTATTGACGG
HBD	Forward	4710	TTTCTGTTGGTGCTGATATTGCTCTCATGGCCTTAAGAATTTACCT
	Reverse		ACTTGCCGTGTCGCTCTATCTTCTGAGGCACAGTAGGCATGTA
TRAC	Forward	5942	TTTCTGTTGGTGCTGATATTGCGGCACATGCAAAGTAGCCTAAG
	Reverse		ACTTGCCGTGTCGCTCTATCTTCCGGCCACTTTCAGGAGGAGG
GAPDH	Forward	4690	TTTCTGTTGGTGCTGATATTGCCCCAGTCTCTGTCCCTTTTG
	Reverse		ACTTGCCGTGTCGCTCTATCTTCAGTGCCGTCGGTCTTCAG
AAVS1	Forward	3972	TTTCTGTTGGTGCTGATATTGCCGACCTACTCTCTTCCGCAT
	Reverse		ACTTGCCGTGTCGCTCTATCTTCTGCAAACAGGAAGTGAACGG
SMURF1	Forward	4051	TTTCTGTTGGTGCTGATATTGCAGGAACAGACAGACACGCAG
	Reverse		ACTTGCCGTGTCGCTCTATCTTCATAACCGGTGCGCAAAGAAA
Digital Droplet PCR			
Target	Primer	Sequence (5' to 3')	
U5Psi	Forward	TAGTGTGTGCCCCGTCTGTTG	
	Reverse	CCTCTGGTTTCCCTTTTCGCT	
	Probe (5' 6-FAM/ZEN/3' IBFQ)	TCTCTAGCAGTGGCGCCCGA	
RPP30	Forward	TGTAAGTGGTAGTGCATAGACTTTA	
	Reverse	GTCAAGAGTAGGAGGACATTTGA	
	Probe (5' 6-FAM/ZEN/3' IBFQ)	AGGCAGACTGACACTAGAGTTCAC	
eGFP	Forward	GCCACAACATCGAGGAC	
	Reverse	CTTTACTCAGCTTGGACTGG	
	Probe (5' 6-FAM/ 3' BHQ-1)	TCGCCGACCACTACCAGCA	
KMT2C	Forward	CGCAGTACCGGAAGATG	
	Reverse	GCTTCAGATTGCTAGACTCC	
	Probe (5' 6-FAM/ 3' BHQ-1)	AAATCCAATGTGTATCTGGCACGGT	
chr3:46,270,956-46,271,086 - used as reference	Forward	AGTAGCATCCAGGCAGGT	
	Reverse	ACAGAGAGGCACATTCAAGG	
	Probe (5' HEX/ 3' BHQ-1)	TGCCACTGTGCCCTTCCAACAAAC	
CAST-sequencing			
Target	Function	Sequence (5' to 3')	
HBB	CAST-seq PCR I	bait	GTTTCTATTGGTCTCCTTAAACC
		decoy 1	CCATGGTGTCTGTTTGAGG
		decoy 2	CATCTGACTCCTGAGGAGAAG
		decoy ssODN	CACCTGACTCCTGTAGAGAAG
	CAST-seq PCR II	bait nested	GACTGGAGTTCAGACGTGTGCTCTTCCGATCTGGTCTCCTTAAACCTGTCTTGTAACC
CCR5	CAST-seq PCR I	bait	GAAGAAGATTCCAGAGAAGAAGC
		decoy 1	CTCTGACCTGTTTTTCCTTC
		decoy 2	AGGTTGAGCAGGTAGATGTC
	CAST-seq PCR II	bait nested	GACTGGAGTTCAGACGTGTGCTCTTCCGATCTTAGAGCCCTGTCAAGAGTTGACAC
Linker prey primers	CAST-seq PCR I	initial PCR	GTAATACGACTCACATATAGGGC
	CAST-seq PCR II	nested PCR	ACACTCTACACTCTTTCCCTACACGACGCTCTTCCGATCTAGGGCTCCGCTTAAGGGAC
Linker oligo		positive strand	GTAATACGACTCACATATAGGGCTCCGCTTAAGGGACT
		negative strand	P-GTCCCTTAAGCGGAGC-NH3

Supplemental Table 6

Cell type	Target	Condition	inputReads	readsPass Cutadapt1	readsPass Cutadapt2	readsPass Cutadapt3
Figure 1						
RPE-1 p53 -/-	HBB	Unedited	51448	36384	21479	21330
		Cas9	40059	32701	23091	22826
		Cas9 + ssODN	30848	22422	13006	12233
		Cas9 + AZD7648	45519	36806	25405	24743
		Cas9 + ssODN + AZD7648	32522	22654	12601	12272
RPE-1 p53 -/-	CCR5	Unedited	23353	19828	18574	18472
		Cas9	67067	56905	52614	52379
		Cas9 + ssODN	21409	18301	17248	15377
		Cas9 + AZD7648	137854	120057	110917	109484
		Cas9 + ssODN + AZD7648	31405	27155	25496	24870
RPE-1 p53 -/-	GAPDH	Unedited	36680	32493	25177	24984
		Cas9 + ssODN	36264	31627	22117	18288
		Cas9 + ssODN + AZD7648	42306	37588	28255	27464
HSPC Donor #1	HBB	Mock	107130	86953	51442	51369
		Mock + AZD7648	109645	86336	56129	56055
		Cas9 + ssODN	122430	97743	59076	57949
HSPC Donor #1	CCR5	Cas9 + ssODN + AZD7648	104867	82023	45918	45520
		Mock	136455	117142	106409	106085
		Mock + AZD7648	77278	64842	58849	58651
HSPC Donor #1	GAPDH	Cas9 + ssODN	125143	104810	92994	90862
		Cas9 + ssODN + AZD7648	80874	69228	61580	60947
		Mock	96553	70926	50518	50365
HSPC Donor #2	HBB	Mock + AZD7648	64766	44731	33487	33373
		Cas9 + ssODN	113171	82474	58746	55640
		Cas9 + ssODN + AZD7648	133949	97246	58650	58099
HSPC Donor #2	CCR5	Mock	1096814	452380	339529	338373
		Cas9 + ssODN	753991	304903	244185	239220
		Cas9 + ssODN + AZD7648	834930	345025	275192	272499
HSPC Donor #2	GAPDH	Mock	290478	244355	227526	226248
		Cas9 + ssODN	309536	263293	244349	239144
		Cas9 + ssODN + AZD7648	348343	297473	276758	273600
HSPC Donor #2	GAPDH	Mock	834930	343752	282107	280419
		Cas9 + ssODN	792373	334239	271949	258465
		Cas9 + ssODN + AZD7648	757618	307853	246678	244147
Figure 2 and Supplemental Figure 7						
RPE-1 p53 -/-	HBB	Unedited	340866	268001	197215	195644
		Cas9	314815	248458	184497	180268
		Cas9 + PolQ12	339826	259338	185116	182739
		Cas9 + AZD7648	310637	237655	172336	166340
		Cas9 + AZD7648 + PolQ12	301809	210172	123445	122285
		Cas9 + ssODN	159385	120681	89584	82400
		Cas9 + ssODN + PolQ12	165899	121628	83577	79298
		Cas9 + ssODN + AZD7648	328924	247922	173878	164849
		Cas9 + ssODN + AZD7648 + PolQ12	218457	167092	112803	111392
		Unedited	342684	286704	271040	269855
RPE-1 p53 -/-	CCR5	Cas9	174978	145221	137362	135817
		Cas9 + PolQ12	199338	167401	158270	157094
		Cas9 + AZD7648	251690	215655	203992	200481
		Cas9 + AZD7648 + PolQ12	253656	217968	206103	205087
		Cas9 + ssODN	296829	248854	235098	215462
		Cas9 + ssODN + PolQ12	509624	435905	412306	381743
		Cas9 + ssODN + AZD7648	198386	168252	158608	153064
		Cas9 + ssODN + AZD7648 + PolQ12	260642	215564	203894	201854
		Unedited	116065	98080	85608	68970
		Cas9	121258	102898	90351	77032
RPE-1 p53 -/-	GAPDH	Cas9 + PolQ12	129139	107848	93413	79752
		Cas9 + AZD7648	157395	135695	117325	114839
		Cas9 + AZD7648 + PolQ12	187184	164246	142601	140572
		Cas9 + ssODN	149607	127733	110604	81617
		Cas9 + ssODN + PolQ12	135976	111437	96977	69689
		Cas9 + ssODN + AZD7648	192984	170424	146961	132534
		Cas9 + ssODN + AZD7648 + PolQ12	104285	78335	67915	55814
		Unedited	424351	318215	213162	211290
		Cas9	509553	391824	282866	278235
		Cas9 + PolQ12	262685	191808	127289	125821
RPE-1 p53 +/-	HBB	Cas9 + AZD7648	354675	256980	165911	161885
		Cas9 + AZD7648 + PolQ12	383608	243404	122085	120822
		Cas9 + ssODN	500698	369989	257152	235274
		Cas9 + ssODN + PolQ12	224238	152245	100262	93514
		Cas9 + ssODN + AZD7648	743518	504721	280215	268141
		Cas9 + ssODN + AZD7648 + PolQ12	227724	158232	88194	86493
		Unedited	308372	258391	243790	242754
		Cas9	417016	358507	339378	336668
		Cas9 + PolQ12	352687	298278	283366	281876
		Cas9 + AZD7648	341542	291152	276364	272653
RPE-1 p53 +/-	CCR5	Cas9 + AZD7648 + PolQ12	376608	324801	308353	307004
		Cas9 + ssODN	323025	269569	255380	234559
		Cas9 + ssODN + PolQ12	200295	165362	156702	145200
		Cas9 + ssODN + AZD7648	372164	318863	302075	294286
		Cas9 + ssODN + AZD7648 + PolQ12	376756	325198	308954	305919
		Unedited	116065	98080	85608	68970
		Cas9	111580	95241	82926	68940
		Cas9 + PolQ12	113727	95551	83162	69407
		Cas9 + AZD7648	127254	111378	97959	91329
		Cas9 + AZD7648 + PolQ12	161277	140679	123055	106820
RPE-1 p53 +/-	GAPDH	Cas9 + ssODN	81895	69885	61661	45476
		Cas9 + ssODN + PolQ12	131711	113714	99788	74569
		Cas9 + ssODN + AZD7648	209864	178478	155909	124748
		Cas9 + ssODN + AZD7648 + PolQ12	123136	101612	89837	71184

Cell type	Target	Condition	inputReads	readsPass Cutadapt1	readsPass Cutadapt2	readsPass Cutadapt3	
Supplemental Figure 3							
K-562 FIRE reporter	FIRE reporter	Unedited	66843	57069	45326	45292	
		Cas9	82766	68164	53254	53031	
		Cas9 + ssODN	64571	52260	41244	39904	
		Cas9 + AZD7648	35532	30613	23083	23043	
		Cas9 + ssODN + AZD7648	114446	91807	71064	64557	
RPE-1 p53 -/-	TRAC	Unedited	68052	53961	47368	47131	
		Cas9	60885	49743	43282	42772	
		Cas9 + ssODN	57603	46804	40333	38877	
		Cas9 + AZD7648	43409	34258	29546	29341	
		Cas9 + ssODN + AZD7648	57801	46855	40474	39921	
RPE-1 p53 -/-	HBD	Unedited	26275	22908	20116	20055	
		Cas9	43028	34632	30502	30355	
		Cas9 + ssODN	17568	15233	13569	12388	
		Cas9 + AZD7648	38904	32341	28518	27938	
		Cas9 + ssODN + AZD7648	21214	18610	16570	15287	
RPE-1 p53 -/-	AAV51	Unedited	161323	138279	125341	124767	
		Cas9	100047	84219	73136	72851	
		Cas9 + ssODN	97640	77980	66538	66039	
		Cas9 + AZD7648	171397	140654	113993	113665	
		Cas9 + ssODN + AZD7648	125999	105121	90196	89899	
RPE-1 p53 +/-	TRAC	Unedited	68810	55834	49042	48785	
		Cas9	42565	33734	29166	28958	
		Cas9 + ssODN	103386	55110	34935	34368	
		Cas9 + AZD7648	98580	42871	27069	26937	
		Cas9 + ssODN + AZD7648	140568	59506	24126	23871	
RPE-1 p53 +/-	HBD	Unedited	23812	20647	18768	18704	
		Cas9	75056	62784	54774	54479	
		Cas9 + ssODN	20393	17771	15557	13500	
		Cas9 + AZD7648	75986	64715	57173	56214	
		Cas9 + ssODN + AZD7648	29981	26271	23386	22321	
RPE-1 p53 +/-	AAV51	Unedited	105879	89664	80389	80019	
		Cas9	103377	86794	77122	76940	
		Cas9 + ssODN	62674	50276	43638	43279	
		Cas9 + AZD7648	119915	102005	90846	90573	
		Cas9 + ssODN + AZD7648	413319	168496	31512	31222	
RPE-1 p53 +/-	CCR5	Unedited	21820	18440	17401	17316	
		Cas9	42694	35672	33040	32918	
		Cas9 + ssODN	23975	20308	19053	17139	
		Cas9 + AZD7648	56005	47685	43963	43539	
		Cas9 + ssODN + AZD7648	13633	11466	10797	10638	
RPE-1 p53 +/-	GAPDH	Unedited	16393	13849	7383	7338	
		Cas9 + ssODN	37675	33155	24929	21586	
		Cas9 + ssODN + AZD7648	24531	21555	11651	11330	
		Unedited	20999	15815	9798	9742	
		Cas9	32130	19654	8385	8279	
RPE-1 p53 +/-	HBB	Cas9 + ssODN	76478	48307	27400	25959	
		Cas9 + AZD7648	32034	19839	10189	10087	
		Cas9 + ssODN + AZD7648	62967	38735	19718	19306	
		Unedited	89588	71210	62236	62061	
		Cas9	68840	55795	48212	47919	
K-562	TRAC	Cas9 + ssODN	63456	49706	42274	42024	
		Cas9 + AZD7648	70081	57883	49032	48798	
		Cas9 + ssODN + AZD7648	75074	60530	52383	52248	
		Unedited	25965	20977	19148	19080	
		Cas9	11933	9455	8581	8498	
K-562	HBD	Cas9 + ssODN	28471	23314	21159	20193	
		Cas9 + AZD7648	20699	17104	15575	15446	
		Cas9 + ssODN + AZD7648	17555	14252	12965	12244	
		Unedited	209972	178609	158824	158085	
		Cas9	133925	112911	98519	97778	
K-562	AAV51	Cas9 + ssODN	226210	187480	157990	156459	
		Cas9 + AZD7648	299531	255529	221310	220386	
		Cas9 + ssODN + AZD7648	210163	178485	154425	153026	
		Unedited	36936	31264	29471	29360	
		Cas9	21863	18477	17291	17180	
K-562	CCR5	Cas9 + ssODN	21959	18642	17585	17083	
		Cas9 + AZD7648	30152	25917	24327	24165	
		Cas9 + ssODN + AZD7648	24630	20873	19594	19286	
		Cas9	241722	181173	159998	159024	
		Cas9 + ssODN	145456	111209	99030	96229	
K-562	GAPDH	Cas9 + AZD7648	82207	60928	51789	51482	
		Cas9 + ssODN + AZD7648	132470	112029	103640	102838	
		Supplemental Figure 8					
		Unedited	492713	389666	357719	356306	
		Cas9	480658	394176	362323	358711	
K-562 eGFP	SMURF1	Cas9 + PolQ12	428690	333268	300036	297324	
		Cas9 + AZD7648	327643	250865	218636	216392	
		Cas9 + AZD7648 + PolQ12	440311	224618	140036	138789	
		Cas9 + ssODN	196277	142150	121060	116910	
		Cas9 + ssODN + PolQ12	213659	156587	137737	133407	
		Cas9 + ssODN + AZD7648	498222	387963	347064	342931	
		Cas9 + ssODN + AZD7648 + PolQ12	242463	180790	160195	158458	

Supplemental Table 7

Target	cutadapt1_ForwardStrand	cutadapt1_ReverseStrand	cutadapt2_ForwardStrand	cutadapt2_ReverseStrand	PCR products size (bp)		
	stubForward	stubReverse	stubForward	stubReverse	w/o stub	w/ stub	w/o stub & gDNA primer
HB	TTTCTGTTGGTGCTGATAT TGCTCAAGCTACAAAAGC GGC	ACCATCATCTGGCTTCAA GGGAAGATAGAGCGACAGG CAGT	ACTTGCCGTGCGCTCTATC TTCCCTTGAAGCCAGGATG ATGGT	GGCGGCTTTTGTAGCTTG AGCAATATCAGCACCAACA GAA	4583	4627	4542
HB	TTTCTGTTGGTGCTGATAT TGCTCAAGCTACAAAAGC GGC	ACCATCATCTGGCTTCAA GGGAAGATAGAGCGACAGG CAGT	ACTTGCCGTGCGCTCTATC TTCCCTTGAAGCCAGGATG ATGGT	GGCGGCTTTTGTAGCTTG AGCAATATCAGCACCAACA GAA	4583	4627	4542
HBD	TTTCTGTTGGTGCTGATAT TGCTCAAGCTACAAAAGC GGC	ACCATCATCTGGCTTCAA GGGAAGATAGAGCGACAGG CAGT	ACTTGCCGTGCGCTCTATC TTCCCTTGAAGCCAGGATG ATGGT	GGCGGCTTTTGTAGCTTG AGCAATATCAGCACCAACA GAA	4583	4627	4542
CCR5	TTTCTGTTGGTGCTGATAT TGCTCAAGCTACAAAAGC GGC	ACCATCATCTGGCTTCAA GGGAAGATAGAGCGACAGG CAGT	ACTTGCCGTGCGCTCTATC TTCCCTTGAAGCCAGGATG ATGGT	GGCGGCTTTTGTAGCTTG AGCAATATCAGCACCAACA GAA	4583	4627	4542
GAPDH	TTTCTGTTGGTGCTGATAT TGCTCAAGCTACAAAAGC GGC	ACCATCATCTGGCTTCAA GGGAAGATAGAGCGACAGG CAGT	ACTTGCCGTGCGCTCTATC TTCCCTTGAAGCCAGGATG ATGGT	GGCGGCTTTTGTAGCTTG AGCAATATCAGCACCAACA GAA	4583	4627	4542
TRAC	TTTCTGTTGGTGCTGATAT TGCTCAAGCTACAAAAGC GGC	ACCATCATCTGGCTTCAA GGGAAGATAGAGCGACAGG CAGT	ACTTGCCGTGCGCTCTATC TTCCCTTGAAGCCAGGATG ATGGT	GGCGGCTTTTGTAGCTTG AGCAATATCAGCACCAACA GAA	4583	4627	4542
AAVS1	TTTCTGTTGGTGCTGATAT TGCTCAAGCTACAAAAGC GGC	ACCATCATCTGGCTTCAA GGGAAGATAGAGCGACAGG CAGT	ACTTGCCGTGCGCTCTATC TTCCCTTGAAGCCAGGATG ATGGT	GGCGGCTTTTGTAGCTTG AGCAATATCAGCACCAACA GAA	4583	4627	4542
FIRE reporter	TTTCTGTTGGTGCTGATAT TGCTCAAGCTACAAAAGC GGC	ACCATCATCTGGCTTCAA GGGAAGATAGAGCGACAGG CAGT	ACTTGCCGTGCGCTCTATC TTCCCTTGAAGCCAGGATG ATGGT	GGCGGCTTTTGTAGCTTG AGCAATATCAGCACCAACA GAA	4583	4627	4542
SMURF1	TTTCTGTTGGTGCTGATAT TGCTCAAGCTACAAAAGC GGC	ACCATCATCTGGCTTCAA GGGAAGATAGAGCGACAGG CAGT	ACTTGCCGTGCGCTCTATC TTCCCTTGAAGCCAGGATG ATGGT	GGCGGCTTTTGTAGCTTG AGCAATATCAGCACCAACA GAA	4583	4627	4542