

Supplementary Table S1. gRNAs designed for gene reactivation by CRISPRa technology.

The genomic annotations for each designed gRNA are from the Genome Reference Consortium Human Build 38 (GRCh38/hg38). The distance from the TSS is expressed in base pairs. PAM protospacer-adjacent motif, Chr chromosome, - negative or antisense DNA strand, + positive or sense DNA strand, TSS transcription start site.

Target gene	gRNA name	gRNA sequence	PAM sequence	DNA strand targeted	Distance from the TSS	Genomic annotation (start)	Genomic annotation (end)
<i>CDKN2A</i>	G1	CTTCCGGCTGGTGCCCCCGG	GGG	Chr9 -	+9	21975105	21975124
<i>CDKN2A</i>	G2	CCAACCTGGGGCGACTTCAG	GGG	Chr9 -	+36	21975078	21975097
<i>CDKN2A</i>	G3	CGCCGTGAGCGAGTGCTCGG	AGG	Chr9 +	+119	21975015	21975034
<i>CDKN2A</i>	G4	CCTTGCTGGAAAGATACCG	CGG	Chr9 -	+122	21974992	21975011
<i>CDKN2A</i>	G5	ATTTGAGGGACAGGGTCGGA	GGG	Chr9 -	+157	21974957	21974976
<i>CPS1</i>	G1	GGCCTAAGTTTGTCTTCTG	AGG	Chr2 +	-69	210477613	210477632
<i>CPS1</i>	G2	AAAGAGCAAACCTGGGTGTG	GGG	Chr2 -	+7	210477669	210477688
<i>CPS1</i>	G3	AATTCATGAAGATTTAGCCG	AGG	Chr2 +	+56	210477738	210477757
<i>CPS1</i>	G4	TCCAGCTTAAGACTACCAT	GGG	Chr2 -	+102	210477764	210477783
<i>HHIP</i>	G1	GCGAGAAGCGGTGACGTCAA	GGG	Chr4 +	+74	144646070	144646089
<i>HHIP</i>	G2	TTTTAACTAGCGCGCGGGG	AGG	Chr4 -	+136	144646112	144646131
<i>HHIP</i>	G3	GCTGAGGTCTCCTCTGCCGG	CGG	Chr4 -	+209	144646185	144646204
<i>HHIP</i>	G4	AGGAACAGAAACGGCGACCG	CGG	Chr4 -	+277	144646253	144646272
<i>miR-122-5p</i>	G1	TTTATCGATTCAGTGGGGGA	GGG	Chr18 +	+391	58446160	58446179
<i>miR-122-5p</i>	G2	CTGGATCCCATAAAGGGAGA	GGG	Chr18 +	+437	58446225	58446244
<i>miR-122-5p</i>	G3	GAGCTGACTGGGGGTAAGTG	CGG	Chr18 +	+537	58446325	58446344
<i>miR-122-5p</i>	G4	AAGAACGGCCTGATCACTCA	GGG	Chr18 -	+606	58446375	58446394
<i>MT1E</i>	G1	CGAGCGAACGGGCTCCAAAG	GGG	Chr16 +	-97	56625576	56625595
<i>MT1E</i>	G2	GCTGCTCTATTTATAGACGG	AGG	Chr16 -	+93	56625746	56625765
<i>MT1E</i>	G3	AGTGAGACGAACAAGCAGTC	AGG	Chr16 -	+148	56625801	56625820
<i>MT1E</i>	G4	CGCAGAGCTTCCCTTACCAG	TGG	Chr16 -	+224	56625877	56625896
<i>MT1M</i>	G1	GCGGTGCGAACCAGCCGGG	CGG	Chr16 +	-62	56632560	56632579
<i>MT1M</i>	G2	GCGGCTGCTTTTCTACTCAG	GGG	Chr16 -	+22	56632624	56632643
<i>MT1M</i>	G3	GCTCCACCACGCCGTCCGGG	TGG	Chr16 +	+32	56632654	56632673
<i>MT1M</i>	G4	AATGGGATTCCTAGGGCGCA	GGG	Chr16 -	+175	56632777	56632796
<i>PTGR1</i>	G1	TGAACGTGAAGCTAAGTCGT	TGG	Chr9 +	-529	111600385	111600404
<i>PTGR1</i>	G2	GGTGTTACGAGGGCGGACTG	GGG	Chr9 -	-363	111600199	111600218
<i>PTGR1</i>	G3	CGGTGCTGGCTCCGATCCCT	GGG	Chr9 +	-240	111600096	111600115
<i>PTGR1</i>	G4	CGGCGGAAATATGCCCCGTG	GGG	Chr9 +	-137	111599993	111600012
<i>PZP</i>	G1	GTTGAAGGTTTCTTATCAGG	AGG	Chr12 -	-268	9208619	9208638
<i>PZP</i>	G2	AAAAGGGTCATTACTCTCAG	TGG	Chr12 +	-126	9208497	9208516
<i>PZP</i>	G3	TGGGGCTTGTGTACATAG	TGG	Chr12 -	-81	9208432	9208451
<i>PZP</i>	G4	GAGATTTATCCCTCACAATG	CGG	Chr12 -	+12	9208339	9208358
<i>TMEM106A</i>	G1	TCGGTAACGTTTGAAGAGC	TGG	Chr17 +	-98	43211729	43211748
<i>TMEM106A</i>	G2	GCACTGAGTCAAAGCTTGAG	GGG	Chr17 +	+10	43211837	43211856
<i>TMEM106A</i>	G3	GAGAGTGAATCGAAAATGC	GGG	Chr17 -	+66	43211873	43211892
<i>TMEM106A</i>	G4	TAGGTATAAAGGGTCTAGGG	AGG	Chr17 -	+126	43211933	43211952
<i>TTC36</i>	G1	ATCCAGCTTCAGCCTTAAGG	TGG	Chr11 -	-243	118527232	118527251
<i>TTC36</i>	G2	CCAAGTAGTCTGCCAAGCCA	GGG	Chr11 +	-200	118527295	118527314
<i>TTC36</i>	G3	GGGAGACACTCCTCACGAAG	GGG	Chr11 +	-131	118527364	118527383
<i>TTC36</i>	G4	TTTTGGAGTTGAGCACCATG	GGG	Chr11 +	-17	118527478	118527497