

BEST1 Mutation	Location	WT	MT	sgRNA candidates	Position	Strand	Sequence	PAM	Specificity Score	Efficiency Score	Comp eff at WT	ASE score	Position	Guide	Guide Strand	Edited 5'->3' Sequence	Edit Scores	Efficiency Score	scarless repair
					61951902	1	AGCATcCAAGCTGCTATA	TGG	75.8	41.4	68.3	0.10	61951896	ACTCGCCATATAGCAGCTTG	-1	CAAGCTGTATATAACAAAT	22.4, 13.4, 21.7, 2.5	77.5443088	0
BEST1 Mutation	Location	WT	MT	sgRNA candidates	Position	Strand	Sequence	PAM	Specificity Score	Efficiency Score	Comp eff at WT	ASE score	Position	Guide	Guide Strand	Edited 5'->3' Sequence	Edit Scores	Efficiency Score	scarless repair
K30Arg		61951895	TGCTGGCGGGGAGCAGCATACAAAGCTGCTATATGGCGAGTTCTTA	61951891	1	GCTGGCGGGGAGCAGCATCTAC	AgG	79.4	46.6	100	0.00	61951891	GCTGGCGGGGAGCAGCATCTAC	1	GTTGGTGGGGAGCAGCATCTAC	0.4, 13.4	79.4233066	0	
				61951902	1	AGCATCTACAgGCTGCTATA	TGG	74.4	41.4	55.5	0.14	61951902	AGCATCTACAgGCTGCTATA	1	AGTATTACAgGCTGCTATA	0.5, 26.6	74.3911217	0	
BEST1 Mutation	Location	WT	MT	sgRNA candidates	Position	Strand	Sequence	PAM	Specificity Score	Efficiency Score	Comp eff at WT	ASE score	Position	Guide	Guide Strand	Edited 5'->3' Sequence	Edit Scores	Efficiency Score	scarless repair
K30N		61951896	GCTGGCGGGGAGCAGCATACAACTGCTATATGGCGAGTTCTTAA	61951902	1	AGCATCTACAAcCTGCTATA	TGG	75.2	40.7	49.2	0.16	61951902	AGCATCTACAAcCTGCTATA	1	AGTATTACAAcCTGCTATA	0.5, 26.6	75.180543	0	
				61951902	-1	TTAAGAACTCGCCATATAGC	AgG	76.9	55.5	0	0.43	61951902	TTAAGAACTCGCCATATAGC	-1	GCTATAGGGGAATCTTAA	6.8	76.9444828	0	
BEST1 Mutation	Location	WT	MT	sgRNA candidates	Position	Strand	Sequence	PAM	Specificity Score	Efficiency Score	Comp eff at WT	ASE score	Position	Guide	Guide Strand	Edited 5'->3' Sequence	Edit Scores	Efficiency Score	scarless repair
L35K		61951909	CATCTACAAGCTGCTATATGGCCAGTTCTTAATCTCTGCTCTG	0	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
BEST1 Mutation	Location	WT	MT	sgRNA candidates	Position	Strand	Sequence	PAM	Specificity Score	Efficiency Score	Comp eff at WT	ASE score	Position	Guide	Guide Strand	Edited 5'->3' Sequence	Edit Scores	Efficiency Score	scarless repair
L41P		61951928	GCGGAGTTCTTAATCTCTGCTCTGCTACTACATCCGCTTT	61951929	-1	GGATGATGATAGTAGCAGG	AGG	59.7	54.9	19.6	0.26	61951933	AAGCGGATGATGATGATAGCA	-1	TGCTACTACATCCACTTT	0.8	78.6157351	0	
				61951933	-1	AAGCGGATGATGATGATAGCA	GgG	78.6	66.0	100	0.00	61951934	AAAGCGGATGATGATGATAGC	-1	GCTACTACATCCACTTT	4.6	82.039877	0	
BEST1 Mutation	Location	WT	MT	sgRNA candidates	Position	Strand	Sequence	PAM	Specificity Score	Efficiency Score	Comp eff at WT	ASE score	Position	Guide	Guide Strand	Edited 5'->3' Sequence	Edit Scores	Efficiency Score	scarless repair
Q58Leu		61955127	aGGCTGGCCCTCACGGAAGAACACAGCTGATGTTGAGAACTG	61955118	-1	CAGCTGATGTTCTCCGTGA	GGG	85.6	67.1	100	0.00	61955118	CAGCTGATGTTCTCCGTGA	-1	TCACGGAAGAACACAACTA	0.8, 4.1	85.6357741	0	
				61955119	-1	TCAGCTGATGTTCTCCGTG	AGG	81.6	69.8	61.1	0.22	61955119	TCAGCTGATGTTCTCCGTG	-1	CACGGAAGAACACAACTA	4.6, 6.4	81.6166894	0	
BEST1 Mutation	Location	WT	MT	sgRNA candidates	Position	Strand	Sequence	PAM	Specificity Score	Efficiency Score	Comp eff at WT	ASE score	Position	Guide	Guide Strand	Edited 5'->3' Sequence	Edit Scores	Efficiency Score	scarless repair
T91I		61955742	TTCTACGTGACGCTGGTGCACCGCTGGTGAACAGTACGAG	61955744	1	TGACGCTGGTCTGTAACCGC	TGG	93.7	53.3	17.2	0.41	61955744	TGACGCTGGTCTGTAACCGC	1	TGATGTTGCTGTAACCGC	11.6, 13.4	93.665206	0	
				61955747	1	CGCTGGTCTGTAACCGCTGG	TGG	91.3	54.5	38.7	0.31	61955747	CGCTGGTCTGTAACCGCTGG	1	TGTTGTTGTAACCGCTGG	0.8, 0.5, 25.4	91.3186015	0	
BEST1 Mutation	Location	WT	MT	sgRNA candidates	Position	Strand	Sequence	PAM	Specificity Score	Efficiency Score	Comp eff at WT	ASE score	Position	Guide	Guide Strand	Edited 5'->3' Sequence	Edit Scores	Efficiency Score	scarless repair
R92G		61955744	CTACGTGACGCTGGTGCACCGCTGGTGAACAGTACGAGAA	61955740	1	TACGTGACGCTGGTGCAGC	CgG	95.3	56.5	0	0.54	61955740	TACGTGACGCTGGTGCAGC	1	TATGTGATGCTGGTGCAGC	5.6, 6.8	95.2968945	0	
				61955744	1	TGACGCTGGTCTGTAACCGC	TGG	90.1	53.1	19.6	0.38	61955744	TGACGCTGGTCTGTAACCGC	1	TGATGTTGCTGTAACCGC	11.6, 13.4	90.0697165	0	
				61955747	1	CGCTGGTCTGTAACCGCTGG	TGG	85.2	52.7	26.8	0.33	61955747	CGCTGGTCTGTAACCGCTGG	1	TGTTGTTGTAACCGCTGG	0.8, 0.5, 25.4	85.1688349	0	
				61955748	-1	CTCGTACTGTTCCACCAGC	cGG	75.2	55.3	100	0.00	61955748	CTCGTACTGTTCCACCAGC	-1	GCTGGTGAACCAATACAAA	19.0, 16.0, 4.1	75.1890487	0	
BEST1 Mutation	Location	WT	MT	sgRNA candidates	Position	Strand	Sequence	PAM	Specificity Score	Efficiency Score	Comp eff at WT	ASE score	Position	Guide	Guide Strand	Edited 5'->3' Sequence	Edit Scores	Efficiency Score	scarless repair
R92C		61955744	CTACGTGACGCTGGTGCACCGCTGGTGAACAGTACGAGAA	61955744	1	TGACGCTGGTCTGTAACCGC	TGG	81.2	54.2	19.6	0.35	61955744	TGACGCTGGTCTGTAACCGC	1	TGATGTTGCTGTAACCGC	11.6, 13.4	81.1858422	0	
				61955747	1	CGCTGGTCTGTAACCGCTGG	TGG	71.1	53.7	26.8	0.28	61955747	CGCTGGTCTGTAACCGCTGG	1	TGTTGTTGTAACCGCTGG	0.8, 0.5, 25.4	71.0970537	0	
				61955748	-1	CTCGTACTGTTCCACCAGC	aGG	75.2	53.5	100	0.00	61955748	CTCGTACTGTTCCACCAGC	-1	GCTGGTGAACCAATACAAA	19.0, 16.0, 4.1	75.1890487	0	
BEST1 Mutation	Location	WT	MT	sgRNA candidates	Position	Strand	Sequence	PAM	Specificity Score	Efficiency Score	Comp eff at WT	ASE score	Position	Guide	Guide Strand	Edited 5'->3' Sequence	Edit Scores	Efficiency Score	scarless repair
R92S		61955744	CTACGTGACGCTGGTGCACCGCTGGTGAACAGTACGAGAA	61955744	1	TGACGCTGGTCTGTAACCGC	TGG	79.5	54.7	19.6	0.35	61955744	TGACGCTGGTCTGTAACCGC	1	TGATGTTGCTGTAACCGC	11.6, 13.4	79.4690404	0	
				61955747	1	CGCTGGTCTGTAACCGCTGG	TGG	75.5	56.2	26.8	0.31	61955747	CGCTGGTCTGTAACCGCTGG	1	TGTTGTTGTAACCGCTGG	0.8, 0.5, 25.4	75.495335	0	
				61955748	-1	CTCGTACTGTTCCACCAGC	tGG	75.2	47.5	100	0.00	61955748	CTCGTACTGTTCCACCAGC	-1	GCTGGTGAACCAATACAAA	19.0, 16.0, 4.1	75.1890487	0	
BEST1 Mutation	Location	WT	MT	sgRNA candidates	Position	Strand	Sequence	PAM	Specificity Score	Efficiency Score	Comp eff at WT	ASE score	Position	Guide	Guide Strand	Edited 5'->3' Sequence	Edit Scores	Efficiency Score	scarless repair
R92H		61955745	TACGTGACGCTGGTGCACCGCTGGTGAACAGTACGAGAA	61955744	1	TGACGCTGGTCTGTAACCGC	TGG	87.8	55.0	31.5	0.33	61955744	TGACGCTGGTCTGTAACCGC	1	TGATGTTGCTGTAACCGC	11.6, 13.4	87.8034991	0	
				61955747	1	CGCTGGTCTGTAACCGCTGG	TGG	78.3	57.9	17.2	0.38	61955747	CGCTGGTCTGTAACCGCTGG	1	TGTTGTTGTAACCGCTGG	0.8, 0.5, 25.4	78.2885309	0	
				61955748	-1	CTCGTACTGTTCCACCAGt	GGG	82.7	58.4	41.7	0.28	61955748	CTCGTACTGTTCCACCAGt	-1	aCTGGTGAACCAATACAAA	19.0, 16.0, 4.1	82.693454	0	
				61955749	-1	TCTGTACTGTTCCACCAG	tGG	76.3	63.5	100	0.00	61955749	TCTGTACTGTTCCACCAG	-1	CTGGTGAACCAATACAAA	6.8, 21.7, 6.4	76.2936189	0	