

Supplementary Table 1A. Sequences of inserts used for cloning of fluoPEER plasmids. To clarify the cloning proces, both top and bottom oligos are shown in 5' to 3' orientation including required overlaps for cloning. The nucleotides of the cloning overlaps (in small letters) are not included in the 'insert length'. When the genomic target mutation is no frameshift/nonsense (premature stop codon) mutation, the fluoPEER insert is minimally changed relative to the genomic target to create a frameshift/nonsense mutation.

fluoPEER plasmid insert	Insert sequence with overlaps for cloning	Insert Length (bp)	Type of mutation on genomic DNA	Differences in insert relative to genomic target	In frame?	Contains stop codon?
HEK3_5bp-del-Top	tcgaccTTGGGGCCCGAGACTGAGCACGTGATGGCAGAGGAAAGGAAGCCCTGCTTCCTCCAGAGGg	59	Frameshift	Same as genomic DNA	no	-
HEK3_5bp-del-Bottom	gtaccCCTCTGGAGGAAGCAGGGCTTCCTTTCCCTGCGCATCAGTGCTCAGTCTGGGCCCCAAg	59	Frameshift	Same as genomic DNA	no	-
GFP-BFP-peg1+2-fs-Top	tcgaccggtgaccaccctgaacctacggcggtgcagtgcttcagccggtaccccc	46	SNV	Additional 1bp insert (a) at +7/+8	no	-
GFP-BFP-peg1+2-fs-Bottom	gtaccggggtagctgcggtgaagcaactgcacgcgtaggttcagggttggtcacgg	46	SNV	Additional 1bp insert (a) at +7/+8	no	-
GFP-BFP-peg3-fs-Top	tcgaccggtgaccaccctgaccttacggcggtgcagtgcttcagccggtaccccc	46	SNV	Additional 1bp insert (t) at +8	no	-
GFP-BFP-peg3-fs-Bottom	gtaccggggtagctgcggtgaagcaactgcacgcctgaaggtcagggttggtcacgg	46	SNV	Additional 1bp insert (t) at +8	no	-
CFTR_F508del-fs-Top	tcgaccATTAAAGAAAATACTCATTTGGTGTTCCTATGATGAATATAGATACg	46	3bp deletion	4bp instead of 3bp del	no	-
CFTR_F508del-fs-Bottom	gtaccGTATCTATATTTCATCATAGGAACACCAATGAGTATTTTCTTTAATg	46	3bp deletion	4bp instead of 3bp del	no	-
CFTR_G542X-Top	tcgaccAAAGACAATATAGTCTTTTGAGAAGTGGAATCACACTGAGTGGAg	45	Nonsense	Same as genomic DNA	yes	yes
CFTR_G542X-Bottom	gtaccTCCACTCAGTGTGATTCACCTTCTCAAGAACAATATATTGTCTTTg	45	Nonsense	Same as genomic DNA	yes	yes
ATP8B1-R600Q-fs-Top	tcgaccGCCATTTTGGACTTCAACAGCTGaaCcGaAGCGAATGTCTATCATTGGTAAGg	52	SNV	Additional 1bp insert (a) at +4	no	-
ATP8B1-R600Q-fs-Bottom	gtaccCTTACCAATGATAGACATTCGCTTCTgGtTCACTGTTGAAGTCCAAAATGGCg	52	SNV	Additional 1bp insert (a) at +4	no	-
ABCb4_E1012X-Top	tcgaccCACTTATTTCATGCTGTTTTTAAAGACAACCTCTGATTGACAGCTACAGTGAAg	51	Nonsense	Same as genomic DNA	yes	yes
ABCb4_E1012X-Bottom	gtaccTTCACGTAGCTGTCAATCAGAGGTTGTCTTTAAAACAGCATGAATAAGTGg	51	Nonsense	Same as genomic DNA	yes	yes
MUT-R369H-Top	tcgaccGATCCCTACAATAATATaTGTCCGTACTGAAGAAGCAATGGCAGCag	49	SNV	Additional 1bp insert (a) at +7/+10	yes	
MUT-R369H-Bottom	gtaccTGCTGCCATTGCTTCTATTGCAGTACGGACATATATTATTGTAGGGATCg	49	SNV	Additional 1bp insert (a) at +7/+10	yes	
IARS1-I1174N+stop-Top	tcgaccCTTCTTTGTCAGTAACTCAACCTACAGCTCCTGAATGCAAAAGCCACAa	48	SNV	Additional nonsense A>T at +12	yes	yes
IARS1-I1174N+stop-Bottom	gtaccTTGTGGCTTTGCATTACGAGAGCTGTAGGTTGATTACTGACAAAAGAGg	48	SNV	Additional nonsense A>T at +12	yes	yes
CTNNB1-various-TOP	tcgaccCACTGGCAGCAACAGCTCTTACCTGGACTCTGGATCCATTCTGTTGCCACTACCACag	56	3-12bp del	Additional 1bp deletion at +7/+14	no	-
CTNNB1-various-Bottom	gtaccCACTGGCAGCAACAGCTTACCTGGACTCTGGATCCATTCTGTTGCCACTACCACAg	56	3-12bp del	Additional 1bp deletion at +7/+14	no	-
DeepPE-target-1-Top	tcgaccacCCTTTAAGATGCCATGGCTAGTGCAGGgAAGAGATCAATATAGAAGTg	49	SNV	Additional 1bp insert (a) at +7	no	-
DeepPE-target-1-Bottom	gtaccAGCTTCTATAGTTATCTTTTctCCTGGACTAGCCATGGCATCTTAAAGTg	49	SNV	Additional 1bp insert (a) at +7	no	-
DeepPE-target-2-Top	tcgacccaacCTACTGACCAAGCCAACGCTGCTGAGGaTCAAGAGGCTGAAGGAGCTag	52	SNV	Additional 1bp insert (a) at +7	no	-
DeepPE-target-2-Bottom	gtaccTAGCTCCTTCAGCTCTTTGatCCTCAGACGCTTGCGTTGTCAGTAAGttg	52	SNV	Additional 1bp insert (a) at +7	no	-
DeepPE-target-3-Top	tcgaccCCGTGTGCTAGCGCATGACCTCGCGGaAGGCCATCCATGGCCAAAGCTag	49	SNV	Additional 1bp insert (a) at +7	no	-
DeepPE-target-3-Bottom	gtaccTAGCTTTCGCCATGGATGGCCtTCGCGAGGTCATGCCGTACGCACACGGg	49	SNV	Additional 1bp insert (a) at +7	no	-
HEK3-PAM-TGAG-Top	tcgaccTTGGGGCCCGAGACTGAGCACGTGATGAGAGAGGAAGGAAGCCCTGCTg	48	NA	NA	yes	yes
HEK3-PAM-TGAG-Bottom	gtaccAGCAGGGCTTCCTTTCCCTCTCATCAGTGCTCAGTCTGGGCCCCAAg	48	NA	NA	yes	yes
HEK3-PAM-TGCC-Top	tcgaccTTGGGGCCCGAGACTGAGCACGTGATGCCAGAGGAAGGAAGCCCTGCTg	48	NA	NA	yes	yes
HEK3-PAM-TGCC-Bottom	gtaccAGCAGGGCTTCCTTTCCCTCTCGCATCAGTGCTCAGTCTGGGCCCCAAg	48	NA	NA	yes	yes
HEK3-PAM-TGGG-Top	tcgaccTTGGGGCCCGAGACTGAGCACGTGATGGGAGAGGAAGGAAGCCCTGCTg	48	NA	NA	yes	yes
HEK3-PAM-TGGG-Bottom	gtaccAGCAGGGCTTCCTTTCCCTCTCCATCAGTGCTCAGTCTGGGCCCCAAg	48	NA	NA	yes	yes
HEK3-PAM-TGTG-Top	tcgaccTTGGGGCCCGAGACTGAGCACGTGATGTGAGAGGAAGGAAGCCCTGCTg	48	NA	NA	yes	yes
HEK3-PAM-TGTG-Bottom	gtaccAGCAGGGCTTCCTTTCCCTCTCAGTACAGTGCTCAGTCTGGGCCCCAAg	48	NA	NA	yes	yes
HEK3-PAM-TGAC-Top	tcgaccTTGGGGCCCGAGACTGAGCACGTGATGACAGAGGAAGGAAGCCCTGCTg	48	NA	NA	yes	yes
HEK3-PAM-TGAC-Bottom	gtaccAGCAGGGCTTCCTTTCCCTCTGTCATCAGTGCTCAGTCTGGGCCCCAAg	48	NA	NA	yes	yes
HEK3-PAM-TGCC-Top	tcgaccTTGGGGCCCGAGACTGAGCACGTGATGCCAGAGGAAGGAAGCCCTGCTg	48	NA	NA	yes	yes
HEK3-PAM-TGCC-Bottom	gtaccAGCAGGGCTTCCTTTCCCTCTGGCATCAGTGCTCAGTCTGGGCCCCAAg	48	NA	NA	yes	yes
HEK3-PAM-TGGC-Top	tcgaccTTGGGGCCCGAGACTGAGCACGTGATGGCAGAGGAAGGAAGCCCTGCTg	48	NA	NA	yes	yes
HEK3-PAM-TGGC-Bottom	gtaccAGCAGGGCTTCCTTTCCCTCTGCCATCAGTGCTCAGTCTGGGCCCCAAg	48	NA	NA	yes	yes
HEK3-PAM-TGTC-Top	tcgaccTTGGGGCCCGAGACTGAGCACGTGATGTACAGAGGAAGGAAGCCCTGCTg	48	NA	NA	yes	yes
HEK3-PAM-TGTC-Bottom	gtaccAGCAGGGCTTCCTTTCCCTCTGACATCAGTGCTCAGTCTGGGCCCCAAg	48	NA	NA	yes	yes
HEK3-PAM-TAAG-Top	tcgaccTTGGGGCCCGAGACTGAGCACGTGATAACAGAGGAAGGAAGCCCTGCTg	48	NA	NA	yes	yes
HEK3-PAM-TAAG-Bottom	gtaccAGCAGGGCTTCCTTTCCCTCTTATCAGTGCTCAGTCTGGGCCCCAAg	48	NA	NA	yes	yes
HEK3-PAM-TACG-Top	tcgaccTTGGGGCCCGAGACTGAGCACGTGATACGAGAGGAAGGAAGCCCTGCTg	48	NA	NA	yes	yes
HEK3-PAM-TACG-Bottom	gtaccAGCAGGGCTTCCTTTCCCTCTCGTATCAGTGCTCAGTCTGGGCCCCAAg	48	NA	NA	yes	yes
HEK3-PAM-TAGG-Top	tcgaccTTGGGGCCCGAGACTGAGCACGTGATAGGAGAGGAAGGAAGCCCTGCTg	48	NA	NA	yes	yes
HEK3-PAM-TAGG-Bottom	gtaccAGCAGGGCTTCCTTTCCCTCTCTATCAGTGCTCAGTCTGGGCCCCAAg	48	NA	NA	yes	yes
HEK3-PAM-TATG-Top	tcgaccTTGGGGCCCGAGACTGAGCACGTGATATGAGAGGAAGGAAGCCCTGCTg	48	NA	NA	yes	yes
HEK3-PAM-TATG-Bottom	gtaccAGCAGGGCTTCCTTTCCCTCTCATATCAGTGCTCAGTCTGGGCCCCAAg	48	NA	NA	yes	yes
HEK3-PAM-TAAC-Top	tcgaccTTGGGGCCCGAGACTGAGCACGTGATAACAGAGGAAGGAAGCCCTGCTg	48	NA	NA	yes	yes
HEK3-PAM-TAAC-Bottom	gtaccAGCAGGGCTTCCTTTCCCTCTGTATTACAGTGCTCAGTCTGGGCCCCAAg	48	NA	NA	yes	yes
HEK3-PAM-TACC-Top	tcgaccTTGGGGCCCGAGACTGAGCACGTGATACCAAGAGGAAGGAAGCCCTGCTg	48	NA	NA	yes	yes
HEK3-PAM-TACC-Bottom	gtaccAGCAGGGCTTCCTTTCCCTCTGGTATCAGTGCTCAGTCTGGGCCCCAAg	48	NA	NA	yes	yes
HEK3-PAM-TAGC-Top	tcgaccTTGGGGCCCGAGACTGAGCACGTGATAGCAGAGGAAGGAAGCCCTGCTg	48	NA	NA	yes	yes
HEK3-PAM-TAGC-Bottom	gtaccAGCAGGGCTTCCTTTCCCTCTGCTATCAGTGCTCAGTCTGGGCCCCAAg	48	NA	NA	yes	yes
HEK3-PAM-TATC-Top	tcgaccTTGGGGCCCGAGACTGAGCACGTGATATACAGAGGAAGGAAGCCCTGCTg	48	NA	NA	yes	yes
HEK3-PAM-TATC-Bottom	gtaccAGCAGGGCTTCCTTTCCCTCTGATATCAGTGCTCAGTCTGGGCCCCAAg	48	NA	NA	yes	yes
POLG-base-edit-Top	tcgaccAGAAGTCGTgATGGATCTGaCCAATGATgCCTGCCAGTCTCCTCAGGAGg	51	SNV	Frame +1	yes	yes
POLG-base-edit-Bottom	gtaccCTCTGAGAGCAGCTGGCAGGCATCATTGGtCAGATCCATCcACGACTTCTg	51	SNV	Frame +1	yes	yes
POLG-prime-edit-Top	tcgaccCTGGCTACCTCTCTCTCGAGAGCAGCTGGCAGGCATCATTGGtgAGATCCATCAACGACTTCTTCATCTCCCGCT	81	SNV	Additional C>G at +8	yes	yes
POLG-prime-edit-Bottom	gtaccAGCTCCAGCGGGAGATgAAGAAGTCGTTGATgGATCTcaCCAATGATGCCTGCCAGTCTCTCAGGAGAGGGTA	81	SNV	Additional C>G at +8	yes	yes

Supplementary Table 1B. Sequences of pegRNAs used in prime editing experiments. All sequences are shown in 5' to 3' orientation. pegRNAs are a concatenation of the spacer sequence, the sgRNA scaffold, and the 3' extension (contains PBS and RT template (RTT)).

pegRNA name	pegRNA#	spacer sequence	3' extension sequence	exten. length (nt)	PBS length (nt)	RTT length (nt)	Figure
HEK3_del1-5-NGG		GGCCCAGACTGAGCACGTGA	TGGAGGAAGCAGGGCTTCCTTTCTCTGCCGTGCTCAGTC	42	13	29	1b,c;2c;3a,d,e;S8
GFP-BFP-AGG	GFP-peg1	GCTGAAGCACTGCACGCCG	CTGACCCATGGCGTGCAGTGCG	21	11	10	1d;2c;S4;S8
GFP-BFP-TAG	GFP-peg2	GGCTGAAGCACTGCACGCCG	TGACCCATGGCGTGCAGTGCT	21	11	10	1d;2c;S4;S8
GFP-BFP-CGT	GFP-peg3	GCGGCTGAAGCACTGCACGC	ACCCATGGCGTGCAGTGCTTC	21	11	10	1d;2c;S4;S8
CFTR_508_CAA	peg1	ATATTCATCATAGGAAACAC	ATATCATCTTTGGTGTTTCCTATGATGA	28	13	15	1e
CFTR_508_AAT	peg2	TATTTCATCATAGGAAACACC	AATATCATCTTTGGTGTTTCCTATGATG	28	13	15	1e; S8
CFTR_508_TGA	peg3	TTCATCATAGGAAACACCA	AAAATATCATCTTTGGTGTTTCCTATGA	28	13	15	1e,1f;2c;3a;S8
CFTR_542_AGA-1	peg4	GTGTGATTCCACCTTCTCA	TAGTTTTAGGAGAAGGTGGA	20	10	10	1e;2d
CFTR_542_AGA-2	peg5	GTGTGATTCCACCTTCTCA	ACAATATAGTTTTAGGAGAAGGTGGA	26	10	16	1e;2c,d;S8
CFTR_542_AGA-3	peg6	GTGTGATTCCACCTTCTCA	TAGTTTTAGGAGAAGGTGGAATCAC	25	15	10	1e;2d
ABCB4_1012_AGA	peg7	ACTTATTTCATGCTGTTTTA	TCAGAGGTTGTCTTTCAAACAGCATGAAT	29	13	16	1e
ABCB4_1012_AAA-1	peg8	GTCAATCAGAGGTTGTCTT	CTGTTTGAAAGACAACCTC	19	9	10	1e,f;2c;3a;S8
ABCB4_1012_AAA-2	peg9	GTCAATCAGAGGTTGTCTT	TTCATGCTGTTTGAAAGACAACCTCTGAT	29	13	16	1e
ABCB4_1012_AGG-1	peg10	TCACTGTAGCTGTCAATCA	TTTGAAAGACAACCTCTGATTGACAGCTACA	31	13	18	1e
ABCB4_1012_AGG-2	peg11	TCACTGTAGCTGTCAATCA	TTTGAAAGACAACCTCTGATTGACAGCTACAGT	33	15	18	1e
ATP8B1_600_TGG-1	peg12	CAATGATAGACATTGCGTTC	AGTGATCGGAAGCGAATGTCTATC	24	13	11	1e,1f;2d
ATP8B1_600_TGG-2	peg13	CAATGATAGACATTGCGTTC	TTCAACAGTGATCGGAAGCGAATGTCTAT	29	12	17	1e;2d
IARS1-1174-AGG-1	peg14	GCTTTGCATTTCAGGAGCTG	GTATAACAATCTACAGCTCCTGAATGC	27	12	15	1e,f; 3a,c,e; S7a,b
IARS1-1174-AGG-2	peg15	GCTTTGCATTTCAGGAGCTG	GTATAACAATCTACAGCTCCTGAA	24	9	15	1e
IARS1-1174-AGG-3	peg16	GCTTTGCATTTCAGGAGCTG	TGTCAGTATAACAATCTACAGCTCCTGAATGC	32	12	20	1e
MUT-369-ACA	peg17	TTGCTTCTATTGCAGTATG	ATATTGTTCTGACTGCAATAGAAGC	25	15	10	1e, S7c
MUT-369-TGG	peg18	CCATTGCTTCTATTGCAGT	TTGTTCTGACTGCAATAGAAGCA	23	13	10	1e, S7c
CTNNB1_S1E1_del1-6	peg19	CAACAGTCTTACCTGGACTC	TGGCACCAGAATGGATTTCACAGTAAAGAC	29	12	17	1e;3 a,c,e;S7d
CTNNB1_S1E2_del3-5	peg20	CAACAGTCTTACCTGGACTC	ACCAGAATGGATTGAGTCCAGGTAAGACTGT	31	15	16	1e, S7d
CTNNB1_S2E1_del4-12	peg21	CTGGCAGCAACAGTCTTACC	TGGTAGTGGCACCAGAATGGTAAGACTGTTGCTGCC	36	15	21	1e, S7d
CTNNB1_S2E2_del4-18	peg22	CTGGCAGCAACAGTCTTACC	TGGCACCAGAATGGATTGCGTAAGACTGTTGCT	33	12	21	1e, S7d
HEK3_XtoR	no #	GGCCCAGACTGAGCACGTGA	TCCTCTGCCATCTCGTGCTCAGTCTG	26	13	13	2b
DeepPE-1-1	DP-1-1	AAGATGCCATGGCTAGTCC	TCTTTCCGTGGACTAGCCATGGCATCT	27	15	12	S5
DeepPE-1-2	DP-1-2	AAGATGCCATGGCTAGTCC	TTATCTTTCCGTGGACTAGCCATGGC	26	11	15	S5
DeepPE-1-3	DP-1-3	AAGATGCCATGGCTAGTCC	TTATCTTTCCGTGGACTAGCCATG	24	9	15	S5
DeepPE-2-1	DP-2-1	GACCAAGCCAACGCTGCTG	TTGACGTGAGCAGCGTTGGCTTGGT	25	15	10	S5
DeepPE-2-2	DP-2-2	GACCAAGCCAACGCTGCTG	CTTTGACGTGAGCAGCGTT	19	7	12	S5
DeepPE-2-3	DP-2-3	GACCAAGCCAACGCTGCTG	CTTTGACGTGAGCAGCGTTGGCTTGGT	27	15	12	S5
DeepPE-3-1	DP-3-1	TGCGTACGGCATGACCTCG	TGGCCTCGGCGAGGTGATGCCGTACGC	27	15	12	S5
DeepPE-3-2	DP-3-2	TGCGTACGGCATGACCTCG	GGATGGCCTCGGCGAGGTGATGCCGTACGC	30	15	15	S5
DeepPE-3-3	DP-3-3	TGCGTACGGCATGACCTCG	GCCTCGGCGAGGTGATGCC	19	9	10	S5
POLG-peg1	POLG-1	GAGCAGCTGGCAGGCATCA	ATCTGGCGAATGATGCCTGCC	21	9	12	S9

Supplementary Table 1C. Sequences of nicking sgRNAs used in prime editing (PE3 and PE3b), or sgRNAs used for base editing (ABE).

nickng sgRNA (PE3)	spacer sequence	Figure
HEK3-PE3	GTCAACCAGTATCCCGGTGC	3a
CTNNB1-PE3	CCACTCATACAGGACTTGGG	3a,c,d; S7; S10
CFTR_508_nPE3_NGG1	GAGGGTAAAAATTAAGCACAG	1f, 3a
CFTR_508_nPE3_NGG2	GGAGAACTGGAGCCTTCAGA	not shown
CFTR-G542X-pe-PE3b-n-t	AATATAGTTTTAGGAGAAGG	2d
ATP8B1-600-PE3b	TTTTGGACTTCAACAGTGAT	2d
ATP8B1-600-PE3	TCAGTGAACTGGGCACTGAA	1f
MUT-R369H-PE3	TCGTA CTGCAATAGAAGCAA	1f
IARS1_1174-PE3-1	ACTTTGTGTGACTGCAGGAT	not shown
IARS1_1174-PE3-2	CCCACAGCAGGCAGACTGTG	1f; 3a,c,d; S7; S11
ABCB4-1012-PE3b	TATTCATGCTGTTTGAAAGA	2d
ABCB4-1012-PE3	GTATTTGGTGCAGTGGCTCT	1f,3a
POLG-ABE-sgRNA	ATCTGACCAATGATGCCTGC	2f; S9
POLG-PE3	GCACTTATGAGGAGCTCCAG	S9

Supplementary Table 1D. Sequences of PCR and sequencing primers used for amplification and sequencing of target regions. All sequences are shown in 5' to 3' orientation.

PCR and Seq primers	primer sequence	Figure
CFTR_Exon11(508)-PCR-Fw	CAAGTGAATCCTGAGCGTGA	1f, 3a
CFTR_Exon11(508)-PCR-Rv	TCTTCTAGTTGGCATGCTTTGA	1f, 3a
CFTR_Exon11(508)-Seq-Fw	TGAATCCTGAGCGTGATTTG	1f, 3a
CFTR_Exon12(542)-PCR-Fw	TGGAGATGCAATGTTCAAAA	data not shown
CFTR_Exon12(542)-PCR-Rv	CCAAGATACGGGCACAGATT	data not shown
CFTR_Exon12(542)-Seq-Fw	GCCTTTCAAATTCAGATTGAGC	data not shown
ATP8B1_Exon16(600)-PCR-Fw	GTTTTCTCGGGATGTTTTGG	1f
ATP8B1_Exon16(600)-PCR-Rv	cacgcccagccAACAATACC	1f
ATP8B1_Exon16(600)-Seq-Fw	GCAGAGGCCTCAACAATGAGC	1f
IARS1_Exon32(1174)-PCR-Fw	GCTGGTTTTATAGAAAAGGCAATG	1f, 3a,c,e; S7a
IARS1_Exon32(1174)-PCR-Rv	CCAGATGGATGAGGGTCTCT	1f, 3a,c,e; S7a
IARS1_Exon32(1174)-Seq-Fw	GTGGAAAGCATTATCGTAAAAAGA	1f, 3a,c,e; S7a
CTNNB1_Exon3-PCR-Fw	AGCAGGAATCTAGTCTGGATGA	3a,c,d,e
CTNNB1_Exon3-PCR-Rv	ACTCACTATCCACAGTTCAGCA	3a,c,d,e
CTNNB1_Exon3-Seq-Fw	GGATGCAGTACCATTCTTCCAC	3a,c,d,e
HEK3_PCR-Fw	ATGTGGGCTGCCTAGAAAGG	3a,d,e
HEK3_PCR-Rv	GGTGCTGAAAGCCACTGGGC	3a,d,e
HEK3_Seq-Fw	ATGTGGGCTGCCTAGAAAGG	3a,d,e
ABCB4_Exon24(1012)-PCR-Fw	GGATCTTGCCCTCTCCTAG	1f,3a
ABCB4_Exon24(1012)-PCR-Rv	TGTCAGTCAAGTTGCCCAAATAT	1f,3a
ABCB4_Exon24(1012)-Seq-Fw	TGTATGTCGGGAGAAAGGG	1f,3a
MUT-exon6(369)-PCR-Fw	GGCACTAAACACTGAACTCTGA	S7c
MUT-exon6(369)-PCR-Rv	TGAAAACAAAGTTGCAAAGTGGA	S7c
MUT-exon6(369)-Seq-Fw	TGCTGTTTAATCATGTTGCTGT	S7c
GFP-BFP-PCR-Fw	CACCATGGTGAGCAAGGGCGAG	S4
GFP-BFP-PCR-Rv	GATGCGGTTACCAGGGTGTCG	S4
GFP-BFP-Seq-Fw	AACGGCCACAAGTTCAGCGTGT	S4
POLG_A467T-PCR-Fw	GGAGATGGGTGTCTCCTACCTG	2f, S9
POLG_A467T-PCR-Rv	CCAGGGGTCTTCTTTGTACCTCTC	2f, S9
POLG_A467T-Seq-Fw	GGAGATGGGTGTCTCCTACCTG	2f, S9