

Table S1: Sequences of primer and other oligonucleotides used in this study

Region	Primer name	Sequence (5' to 3')
Enolase Promoter	EnoP_Bam	AGTGGATCCTGGGGAACTAAATATACTGAAATTC
	EnoP_Nhe	CCATGCTAGCGGCTAAACTTCAATACAAAAATCTC
	EnoP_Avr	CGCACCTAGGTGGGGAACTAAATATACTGAAATTC
	EnoP_Sal	ACGCGTCGACGGCTAAACTTCAATACAAAAATCTC
Aldolase Promoter	AldoP_Bam	TAGTGGATCCAATACTAATTCTTTTGAATTTCCAC
	AldoP_Nhe	CCATGCTAGCTTTTTTCTTTTGAAACAAATAAAATGAG
Tubulin Promoter	TubP_Bam	TCCTGGATCCTAAATAAAATTTAGCCCACTAATTCAACT
	TubP_Nhe	CCATGCTAGCGTTTAACGAATAACTTTAACAAAGAG
Enolase 3'UTR	Eno3'UTRF	TAAGTTCGTGGCGTGTAGGATAGTATCGATTAAGTTTTCTTT TTATCTTAATTA
	Eno3'UTRR	CCGGTAATTAAGATAAAAAGAAAACTTAATCGATACTATCCT ACACGCCACGAACTTAAT
Ribosomal 3'UTR	Ribo3'UTR_Pac	GCCGCTTAATTAAGAAATCTTTTTAGCTGGTTAAGTC
	Ribo3'UTR_Age	TTCGAACCGGTTTAAGCAAAGAACTTATGAAACTG
Tubulin 3' UTR	Tub3'UTR_F	GCCGCTTAATTAATTATCCTTGTTCAATTGAATTCTC
	Tub3'UTR_R	TTCGAACCGGTTAGGGAAAATTCCATAGATTAAGATAC
FRT_Gent_FRT	FRT_Age	GTTTTACCGGTGAAGTTCCTATTCTCTAG
	FRT_Not	TCGAGCGGCCGCGAAGTTCCTATACTTTC
Nluc	Nluc_Nhe	ATTCGCTAGCATGGTCTTCACACTCGAAGATTTC
	Nluc_Pac	GCGCCTTAATTAACACGCCAGAATGCGTTCGCAC
Neo	Neo_NheF	ATTCGCTAGCATGATTGAACAAGATGGTTTACACGCTG
	Neo_Pac	GCGCCTTAATTAATCAGAAGAATTCGTCAAGAAGACGATAG
	Neo_Sal	ACGCGTCGACATGATTGAACAAGATGGTTTACACGCTG
	Neo_NheR	ATTCGCTAGCGAAGAATTCGTCAAGAAGACGATAG
Cas9	Cas9_Nhe	CCATGCTAGCATGGACTATAAGGACCACGACGGAGACTAC
	Cas9_Pac	GCGCCTTAATTAACACTTTTTCTTTTTGCCTGGCCG

TK guide	TKg1_F	GTTGGGCTCAATTTGCTCTAGAAT
	TKg1_R	AAACATTCTAGAGCAAATTGAGCC
Nluc-Stop	Y18StopF	GTAGGAGATTGGAGACAAACTGCAGGAtaaAATTTAGATCAA GTATTAGAGCAAGGTGG
	Y18StopR	CCACCTTGCTCTAATACTTGATCTAAATTttaTCCTGCAGTTTGT CTCCAATCTCCTAC
Nluc G17A	G17A_F	GTAGGAGATTGGAGACAAACTGCAGcaTATAATTTAGATCAA GTATTAGAGCAAGGTGG
	G17A_R	CCACCTTGCTCTAATACTTGATCTAAATTATAtgcTGCAGTTTGT CTCCAATCTCCTAC
Nluc repair	Repair_OligoF	CTAGCATGGTATTTACATTAGAAGATTTTGTAGGAGATTGGA GACAAACTGCAGcaTATAATTTAGATCAAGTATTAGAGCAAGG TGGAGTTTCTTCATTGTTTCAAAATTTAGGCGTTTCAGTG
	Repair_OligoR	CACTGAAACGCCTAAATTTGAAACAATGAAGAACTCCACCT TGCTCTAATACTTGATCTAAATTATAtgcTGCAGTTTGTCTCCAA TCTCCTACAAAATCTTCTAATGTAAATACCATGCTAG
5' TK flank	5'TKUTR_Bam	ATCGGGATCCCATTGTCTAACTTCATCTATGGTC
	5'TKUTR_Nhe	TCGAGCTAGCGTATTTCCAATCTTATTTGCAGTAGG
3' TK flank	3'TKUTR_Pac	TGCATTAATTAAGGCAAAATTTGGCGCAGCTATGG
	3'TKUTR_Age	CGATACCGGTCCTACCATAAGCATCACCAGTAGC
Upstream of 5' TK flank	5'TK_UpsF	ATGAATTCATCGCTTTCAACAATAACTGGTTCAG
Nluc_internal	Nluc_intR	CTTTGGATCGGAGTTACGGACAC
Neo_internal	Neo_intF	CAGACTTAAGGCCCGTATGCCCGACGGTGAAGATCTTGTC
Downstream of 3' TK flank	3'TK_DsR	CAGCTTCTCTCCACCTGATAATATAGTATCTGTACC
TK gene	TKgeneF	ATGGCAAAATTATACTTTTACTATTTCAGCAATGAATGC
	TKgeneR	TTAGAAATTGTATTCTTCACAATTAATTATATGATGTTTTCTGC
Control	cgd4R	TGAGCTCAAAAATATAAGATGGCAC
18S rRNA	18SF	CATGGATAACCGTGGTAAT
	18SR	TACCCTACCGTCTAAAGCTG