

gRNA name	target gene	GenomeDB ID	gRNA sequence	position in gene of target seq.	Cas9 used	repair template	use notes
eGFP-9	eGFP		GCAAGGGCGAGAGCTGTTAC/CGGGGT	9	SaCas9	n/a	knockout eGFP
eGFP-99	eGFP		GTAAGTTCGGCTCAGCTCGAC/CAGGAT	69	SaCas9	n/a	knockout eGFP
eGFP-156	eGFP		GCCGGTGGTCAGATGAACTT/CAGGGT	156	SaCas9	GATGCCACTACGGCAGCTGACCCCTGAAGTAGATAGATAGTTCATCTGCACCACCGCAAGCTGCCCGTG	knockout eGFP
tdTomato-5	tdTomato		GCAAGGGCGAGAGCTGTTAC/AGGAGT	5	SaCas9	n/a	knockout tdTomato
eGFP-153	eGFP		GGTGGTCAGATGAATCTCA/GGG	153	SpCas9	n/a	knockout eGFP using SpCas9
mCherry-20	mCherry		GAGGATAAATGGCCATCATCA/AGGAGT	20	SaCas9	n/a	knockout mCherry
Faz1-3139	Faz1	TcCLB.509631.140	GAGCTTGAGCAGAGAGCCAGCG/GAGGAT	3139	SaCas9	AGGCTGGCCGATGAGCTTGAACGAAAGCCATAGATAGATACGGCCGAAATGAGAGGCTGGCCGATGAGCTT	knockout Faz1
KMP-13-36	KMP-11	TcCLB.510755.89	GAGCTTGGGGAGATTCTCT/AAAGAT	36	SaCas9	TCTAAGTGAAAATGGCCACCTCTTGAGTAGATAGATAGGATTCGGCAAGCTTGACCCCTGGAT	knockout KMP-11
TcGalF-162	GalF, putative	TcCLB.511353.30 and TcCLB.511301.50	GCCAGGAACTCTAATACAAA/ATGAAT	162	SaCas9	GCCAGCAGCCCTCATTTGATCAATTTTAGATAGATAGTGTAAAACGACGGCCAGTGTAAAGCAGCTCTGGCCCTGTTTTTTG	knockout GalF
NTR-568	nitroreductase	TcCLB.510611.60 and TcCLB.506791.70	GCAGATAGCGCTGCCATAA/ATGAAT	568	SaCas9	CTGGAGATGGGTACTACCACTCAATTTTAGATAGATAGTGTAAAACGACGGCCAGTGGCCAGCTCTCTGGCAGATCGTACTAC	knockout NTR
NTR-348	nitroreductase	TcCLB.510611.60 and TcCLB.506791.70	GTACCGCCTGAATACAGCC/GTGGGT	348	SaCas9	GTACGGGCTCCTACCGCCTGAATACAGTAGATAGATAGTGTAAAACGACGGCCAGTCCGTTGGTGGCTGTTGTCATACAGAGGAG	knockout NTR
NTR-509	nitroreductase	TcCLB.510611.60 and TcCLB.506791.70	GCDCCTGAGATGGGGCTGGAGA/GTGGGT	509	SaCas9	GCCCGCCCGCGCTGGATGGGGCTGGAGTAGATAGTGTAAAACGACGGCCAGTGGTGGTACTACCACTCAATTTAGTGGCA	knockout NTR
CYP51-374	CYP51	TcCLB.506297.260 and TcCLB.510101.50	GAGAGCTGAACTCTTGCGG/AGGAGT	374	SaCas9	AGGATGGGGAGAGCTGAACTCTTGCGTAGATAGTGTAAAACGACGGCCAGTGGAGAGTGGACCAATTCGAGATTTGAGAAC	knockout CYP51
CYP51-137	CYP51	TcCLB.506297.260 and TcCLB.510101.50	GTGCAGTTGGCAGAACCCG/TTGAGT	137	SaCas9	GGACACATTTGGAGTTGGCAGAACCCG TAGATAGATAGTGTAAAACGACGGCCAGTCTTGAGTTATGGAGGATGCAACGCTGAT	knockout CYP51
CYP51-178	CYP51	TcCLB.506297.260 and TcCLB.510101.50	GTGCATCGCTGAACTCA/CGGGGT	178	SaCas9	ATTGTGAGTTGGCAGAACCCGTTGAGTAGATAGTGTAAAACGACGGCCAGTCTTGAGTTATGGAGGATGCAACGCTGATCTCAAG	knockout CYP51
GP72-925	GP72	TcCLB.509561.20	GCATGGGCCATTTGTTGGT/GTGAAT	925	SaCas9	CACATGGGCCATTTGTTGGTACCCATACGAGCTCCAGACTACGCTTACCCATACGAGCTCCAGACTACGCTCTTGTGAATATAACAACA	tag GP72 with HA tag
GP72-1138	GP72	TcCLB.509561.20	GAGCCCLACATCAATCCAG/CGGGGT	1138	SaCas9	CGAGCCCLACATCAATCTACCCATACGAGCTCCAGACTACGCTTACCCATACGAGCTCCAGACTACGCTCACCGGGGTTTTGCTGTGG	tag GP72 with HA tag
GP72-1234	GP72	TcCLB.509561.20	GAAAGGATTCATGATAGCC/CCGGGT	1234	SaCas9	CAATCGAGACCCCGGTTACCCATACGAGCTCCAGACTACGCTTACCCATACGAGCTCCAGACTACGCTATGATGAACTGCTTTCTTG	tag GP72 with HA tag
GP72-1428	GP72	TcCLB.509561.20	GCTCTCTGAGATGCCCT/TTGAGT	1428	SaCas9	CGGAATTTTACCCAGAGTACCCATACGAGCTCCAGACTACGCTTACCCATACGAGCTCCAGACTACGCTGGCATGCTTCAGAGGAGGG	tag GP72 with HA tag
eGFP-435	eGFP		GTTTACTCAGCTTGTGCC/CAGGAT	435	SaCas9	GACTTCAGGAGGAGCGCAACATCTGGGGTAGATAGATAGCACAAAGCTGAGTACAACTACACAGCCAC	knockout eGFP
eGFP-381	eGFP		CTTCAAGCTGATGCGGTCAC/CAGGGT	381	SaCas9	GAGGTGAAGTTGAGGGGCGACCCCTGGTGTAGATAGATAGACCCGATCGAGCTGAAGGGGATCGACTTC	knockout eGFP
LPG(-16)	LPG2	Umpf_34_3120	AATCTTTCGGTGGTTCG/ACGGGT	-16	SaCas9	TTTCAACAAGGCGAATACCCGATGACAAATAGATAGATAGCCCAACCGAAAGATTGCATCGCAACTGT	knockout LPG2
TCRT-181	CRT	TcCLB.509011.40 and TcCLB.510685.10	GAGCAAGGTTCTCGTTCG/CGGGGT	181	SaCas9	GATCGGAGAGAGCAAGGTTCTCGTCTGTAGATAGATAGTGTAAAACGACGGCCAGTACGGAGGATGCGCGGTTTTACGCTTGTCT	knockout CRT

Column D: Red, PAM sequences
Column G: Blue, 3 frame stop codons
Purple, M13 sequence
Green, G manually added
Black, homology arms
Orange, 2xHA sequence