

Table S23: NHEJ allele sequences in non-overlapping gene-drive cage trials

WT		Frame	Hom	Het
A1-G3	GCGGGCAGCGGATGGTTCGGTCTACGGGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS	1/2	
	GCGGGCAGCGGATGGTTCGGTCTACAGGGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC*	FS		1/2
	GCGGGCAGCGGATGGTTCGGTCTACGGAACAGGGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	IF		1/2
A1-G7	GCGGGCAGCGGATGGTTCGG-----GCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS	5/7	
	GCGGGCAGCGGATGGTTCGGTCTACG (ins473bp) GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC**	FS	2/7	
A1-G10	GCGGGCAGCGGATGAAC-----GCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS	6/8	1/8
	GCGGGCAGCGGATGGTTCGGTTC---GCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	IF	1/8	
A1-G13	GCGGGCAGCGGATGGTTCGGTCTACG (ins473bp) GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC**	FS		6/9
	GCGGGCAGCGGATGAAC-----GCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		5/9
A3-G5	GCGGGCAGCGGATGGTTCGGTCTACAGGAACGTTTAC-GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS	1/4	1/4
	GCGGGCAGCGGATGGTTCGGTCTACCATCATCAGGGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS	2/4	1/4
A3-G6	GCGGGCAGCGGATGGTTCGGTCTGGCCGTGGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		1/1
	GCGGGCAGCGGATGGTTCGGTCTACGAGGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC*	FS		1/1
A3-G7	GCGGGCAGCGGATGGTTCGGTCTACCATCATCAGGGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		1/1
	GCGGGCAGCGGATGGTTCGGTCTACAAGGAACAGGGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		1/1
A3-G7	GCGGGCAGCGGATGGTTCGGTCTACGAGGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		5/5
	GCGGGCAATCATCGGATCATCGGA-----GTAGC	FS		5/5
B1-G4	GCGGGCAGCGGATGGTTCGGTCTACG (ins473bp) GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC**	FS	2/3	
	GCGGGCAGCGGATGGTTCGGTCTACA-----GCATGAACGCGGGCTTTGAAGACTGTAGC	IF	1/3	
B1-G5	GCGGGCAGCGGATGGTTCGGTCTACG (ins473bp) GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS	1/1	
B1-G7	GCGGGCAGCGGATGGTTCGGTCTAC-----AGGGCATGAACGCGGGCTTTGAAGACTGTAGC*	FS		9/9
	GCGGGCAGCGGATGGTTCGGTCTACAGGGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		2/9
	GCGGGCAGCGGATGGTTCGGTCTACGATGAACGATGGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	IF		3/9
	GCGGGCAGCGGATGGTTCGGTCTACGTAACGATGGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		1/9
	GCGGCATGCCCTGC-----GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC*	FS		3/9
B1-G10	GCGGGCAGCGGATGGTTCGGTCTAC-----AGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS	16/16	
B2-G7	GCGGCATGCCCTGC-----GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC*	FS	2/2	
B2-G10	GCGGGCAGCGGATGGTTCGGTTC---GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC*	IF		12/14
	GCGGGCAGCGGATGGTTCGGTCTGTCCGGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		10/14
	GCGGGCAGCGGATGGTTCGGTCTCGGGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		2/14
	GCGGGCAGCGGATGGTTCGGTCTACGAGGGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		2/14
	GCGGGCAGCGGATGGTTCGGTTC-----CGTTCCAGCGGATGAACGCGGGCTTTGAAGACTGTAGC	IF		2/14
B2-G11	GCGGGCAGCGGATGGTTCGGTCTACAGGAACGGAACCC--GCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS	1/2	1/2
	GCGGGCAGCGGATGGTTCGGTCTA--GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		1/2
B3-G4	GCGGGCAGCGGATGGTTCGGTCTAC-----AGGGCATGAACGCGGGCTTTGAAGACTGTAGC*	FS	1/2	
B3-G5	GCGGGCAGCGGATGGTTCGGTCTACAGTACA-GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS	4/4	
B3-G6	GCGGGCAGCGGATGGTTCGGTCTACAGTACA-GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		4/4
	GCGGGCAGCGGATGGTTCGGTCTACGTTCCGGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		4/4
B3-G7	GCGGGCAGCGGATGGTTCGGTCTACAGTACA-GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		10/23
	GCGGGCAGCGGATGGTTCGGTCTATGGCACGCGATGGTTCGAT--GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		9/23
	GCGGGCAGCGGATGGTTCGGTTC---GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC*	IF	2/23	16/23
	GCGGGCAGCGGATGGTTCGGTCTACATGAACGC-GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		2/23
	GCGGGCAGCGGATGGTTCGGTCTACATTCGA-GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		1/23
	GCGGGCAGCGGATGGTTCGGTCTAC-----AGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		3/23
	GCGGGCAGCGGATGGTTCGGTCTATGGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	IF		1/23
B3-G10	GCGGGCAGCGGATGGTTCGGTTC---GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	IF	2/12	3/12
	GCGGGCAGCGGATGGTTCGGTCTAC-----GGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		6/12
	GCGGGCAGCGGATGGTTCGGTCTACATTCGC-GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		6/12
	GCGGGCAGCGGATGAAC-----GCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS	1/12	
	GCGGGCAGCGGATGGTTCGGTCTACGGTTCGC-GCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		3/12
C1-G7	GCGGGCAGCGGATGGTTCGG-----GCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS	1/4	
C1-G11	GCGGGCAGCGGATGGTTCGGTTC---GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS	4/7	
C1-G13	GCGGGCAGCGGATGGTTCGGTCTAC-----AGGGCATGAACGCGGGCTTTGAAGACTGTAGC*	FS		1/3
	GCGGGCAGCGGATGGTTCGGTCTA--GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS	1/3	1/3

	GCGGCGCACGCGATGGTTCGGTTC-----AGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		1/3
	GCGGCGCACGCGATGGTTCGGTTCCTACCAT-----ACGCGGGCTTTGAAGACTGTAGC	FS		1/3
C2-G7	GCGGCGCACGCGATGGTTCGGTTCCTACCTTCGGGCGAGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS	1/1	
C2-G10	GCGGCGCACGCGATGGTTCGGTTCCTA--GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS	4/4	
C2-G13	GCGGCGCACGCGATGGTTCGGTTCCTAC-----AGGGCATGAACGCGGGCTTTGAAGACTGTAGC*	FS	1/9	1/9
	GCGGCGCACGCGATGGTTCGGTTCCTACG-CATGCGAGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS	2/9	6/9
	GCGGCGCACGCGATGGTTCGGTTCCTACCAT-----ACGCGGGCTTTGAAGACTGTAGC	FS		1/9
	GCGGCGCACGCGATGGTTCGGTTCCTACGGGCA--GCATGAACGCGGGCTTTGAAGACTGTAGC	FS		1/9
	GCGGCGCACGCGATGGTTCGGTTCCTACGCAACAGGCAGGCATGAACGCGGGCTTTGAAGACTGTAGC	IF		
C3-G4	GCGGCGCACGCGATG-----GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		1/1
	GCGGCGCACGCGATGGTTCGGTTCCTACAGGAACGGAAACC--GCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		1/1
C3-G6	GCGGCGCACGCGATGGTTCGGTTCCTAC-----AGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		1/1
	GCGGCGCACGCGATGGTTCGGTTCCTAC-TCAGGGGCGAAGCGGCAGGCATGAACGCGG	IF		1/1
C3-G7	GCGGCGCACGCGATGGTTCGGTTCCTAC-GGCAGGGCATGAACGCGG	FS		1/1
	GCGGCGCACGCGATGGTTCGGTTCCTA-----GGGCATGAACGCGG	IF		1/1
C3-G10	GCGGCGCACGCGATGGTTCGGTTCCTACGAGGCAGGCATGAACGCGGGCTTTGAAGACTGTAGC*	FS		
	GCGGCGCACGCGATGGTTCGGTTCCTAC-----AGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		1/1
C3-G13	GCGGCGCACGCGATGGTTCGGTTCCTAC-----CAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	IF	4/12	
	GCGGCGCACGCGATGGTTCGGTTCCTA--GCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	IF		2/12
	GCGGCGCACGCGATGGTTCGGTTCCTC-----GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC*	IF		2/12
C3-G13	GCGGCGCACGCGATGGTTCGGTTCCTACGAGGCAGGCATGAACGCGGGCTTTGAAGACTGTAGC*	FS		2/12
C3-G16	GCGGCGCACGCGATGGTTCGGTTCCTAC-----CAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	IF	1/12	4/12
	GCGGCGCACGCGATGGTTCGGTTCCT-----GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	IF		5/12
	GCGGCGCACGCGATGGTTCGGTTCCTC-GGCAGGGCATGAACGCGGGCTTTGAAGACTGTAGC	FS		4/12
	GCGGCGCACGCGATGGGCAGAC-----CATGAACGCGGGCTTTGAAGACTGTAGC	FS		5/12

gRNA target site; PAM; insertion; substitution; deletion; *mutation appeared in multiple cages

++ : insertion sequence is from gRNA scaffold-U6-3'UTR

GGCGCACGCGATGGTTCGGTTCCTACGGGCGTTTGTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAGTGGCACCGAGTCGGTGCTTTTTT
TGTGAAAATTTGATTCACCTTGTGTTTAGGAAAATAATACCTTCCTTTGAAACAGGTATTTACAATGATGGACGATAGAAAAAGACCACCTTAAAATGCTTTATTCAAGCT
ATTGCTTCGATTCCTCATTGAGATCTAATCTCAAATTTGTGATTTAGAAAAACAGCGAATATTGTACTATAATAATTCCTTTGGTAATCTCAGGCTTTCAGTAATGAT
AGAATCCTTAAGACTGTAAGAAATATAAAGTTTAAAAAAGGAAAACAGGTATATCAAATCAGAAAACAACAACAGCTCTTTTCCGTTGAATTCACCTGTACGATGGC
TTAAGGATGAGCTGTAACGAAACCTTACAACAGCCACGCAGAACGGGATCCGGCAGGCATGAACGCG