b

EE5 * EE7 *

EE11

EI1 *

EI4

EI5 * EI6 *

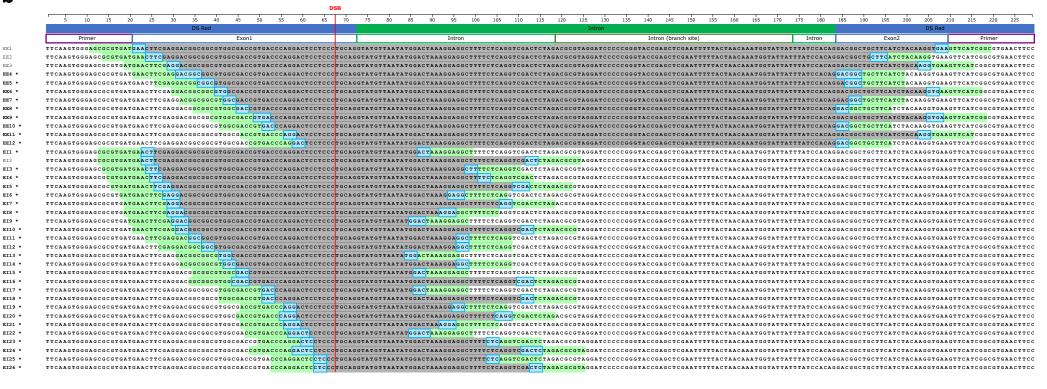
EI7 *

EI10

EI16

EI22

Microhomology scheme: Sense/pCMVΔ, sqRNA A, forward strand

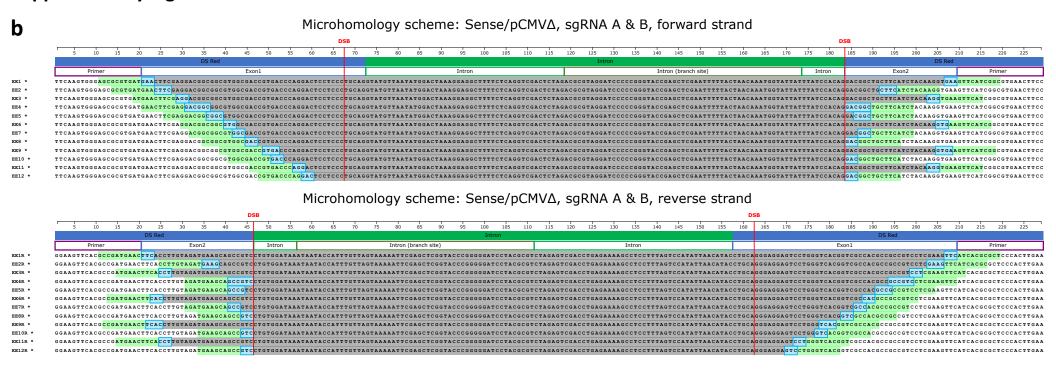


Microhomology scheme: Sense/pCMVΔ, sgRNA B, reverse strand

	5 10 15 2	25 30 35	40 45	50 55	60 65	70 7	5 80	85 90	95 100	105 110	115 120	125 130	135 140	145 150 155	160 165	170 175	180 185	190 195	200 205	210 215	220 225
		DS Red							Intro	n								DS Red			
	Primer Exon2			Intron	Intron (branch site)						Intron				Exon1				Pri	mer	
EE1R *	GGAAGTTCACGCCGATGAAC	TTCACCTTGTAGATG?	CTGTGGATAAATACCATTTGTTAGTAAAAATTCGAGCTCGGTACCCGGGGGATCCTACGC						CTACGCGT	TAGAGTCGA	CCTGAGAAAA	STCCATATTAACATA	CCTGCAGGGAGGAGTCCTGGGTCACGGTCGCCACGCCGTCCTCGAAGTT					TCATCACGCGC	TCCCACTTGAA		
EE2R *	GGAAGTTCACGCCGATGAACTTCACCTTGTAGAT CATGCCGCCCCCCCCCC																				
EE3R *	GGAAGTICACGCCGATGAACTICACCTTTATCATCCAGGGGGGGGATCCATTGATACAATACCATTTGTTAGTAAAAAATTCATACCAGTCGGGGGATCCTACGGGGGATCCTTAGGGCTCGAGAAAAGCCTCCTTTAGTCCATATTAACATACCTGCAGGGAGGG																				
EE4R *	GGAAGTICACGCCGATGAACTICACCTTGTAGATGAAGCA <mark>GCCGTC</mark> TTGGGATAAATAATACCATTTGTTAGTAAAAATTCCAGCGCTCCACGCGGGAGACCTACGCGTCCCACTTGAGCCCTTTAGTCCATATTAACATACCTGCAGGGAGGAGTCCTGGGCACGCCGCCCCCCCC																				
EE5R *	GGAAGTICACGCCGATGAACTTCACCTTGTAGATGAAGCA <mark>CCCTC</mark> TGTGGATAAATAATAACCATTCGTAGTAAAAATATTCGTGCGCGCGC																				
EE6R *	GGAAGTTCACCCCGATGAACTTCACCTTGAGGTGAAGCACCCCCCCGGGTAGAAAAAAAA													TCCCACTTGAA							
EE7R *	GGAAGTTCACGCCGATGAAC	TTCACCTTGTAGATGA	AGCAGCCGT	CTGTGGATAA	ATAATACCAS	TTTGTTAGT	AAAATTCG	AGCTCGGTA	CCCGGGGGAT	CCTACGCGT	TAGAGTCGA	CCTGAGAAAA	CCTCCTTTAG	STCCATATTAACATA	CCTGCAGGGAGG	AGTCCTGG	GTCACGGTCG	CCACGCCGCCG	TCCTCGAAGT:	TCATCACGCGC	TCCCACTTGAA
EE8R *	GGAAGTTCACGCCGATGAAC	TTCACCTTGTAGATGA	AGCAGCCGT	CTGTGGATAA	ATAATACCAS	TTTGTTAGT	AAAATTCG	AGCTCGGTA	CCCGGGGGAT	CCTACGCGT	TAGAGTCGA	CCTGAGAAAA	CCTCCTTTAG	STCCATATTAACATA	CCTGCAGGGAGG	AGTCCTGG	GTCACGGTCG	CCACGCCGCCG	TCCTCGAAGT:	TCATCACGCGC	TCCCACTTGAA
EE9R *	GGAAGTTCACGCCGATGAAC	TTCACCTTGTAGATGA	AGCAGCCGT	CTGTGGATAA	ATAATACCA	TTTGTTAGT	AAAATTCG	AGCTCGGTA	CCCGGGGGAT	CCTACGCGT	TAGAGTCGA	CCTGAGAAAA	CCTCCTTTAG	STCCATATTAACATA	CCTGCAGGGAGG	AGTCCTGG	GTCACGGTCG	CCACGCCGCCG	TCCTCGAAGT	TCATCACGCGC	TCCCACTTGAA
EE10R *	GGAAGTTCACGCCGATGAAC	TTCACCTTGTAGATGA	AGCAGCCGT	CTGTGGATAA	ATAATACCA	TTTGTTAGT	AAAATTCG	AGCTCGGTA	CCCGGGGGAT	CCTACGCGT	TAGAGTCGA	CCTGAGAAAA	CCTCCTTTAG	STCCATATTAACATA	CCTGCAGGGAGG	AGTCCTGG	GTCACGGTCG	CCACGCCGCCG	TCCTCGAAGT:	TCATCACGCGC	TCCCACTTGAA
EE11R *	GGAAGTTCACGCCGATGAAC	TTCACCTTGTAGATGA	AGCAGCCGT	CTGTGGATAA	ATAATACCAS	TTTGTTAGT	AAAATTCG	AGCTCGGTA	CCCGGGGGAT	CCTACGCGT	TAGAGTCGA	CCTGAGAAAA	CCTCCTTTAG	STCCATATTAACATA	CCTGCAGGGAGG	AGTCCTGG	GTCACGGTCG	CCACGCCGCCG	TCCTCGAAGT:	TCATCACGCGC	TCCCACTTGAA
EE12R *	GGAAGTTCACGCCGATGAAC	TTCACCTTGTAGATGA	AGCAGCCGT	CTGTGGATAA	ATAATACCA	TTTGTTAGT	AAAATTCG	AGCTCGGTA	CCCGGGGGAT	CCTACGCGT	TAGAGTCGA	CCTGAGAAAA	CCTCCTTTAG	STCCATATTAACATA	CCTGCAGGGAGG	AGTCCTGG	GTCACGGTCG	CCACGCCGCCG	TCCTCGAAGT	TCATCACGCGC	TCCCACTTGAA
EE13R *	GGAAGTTCACGCCGATGAAC	TTCACCTTGTAGATGA	AGCAGCCGT	CTGTGGATAA	ATAATACCA	TTTGTTAGT	AAAATTCG	AGCTCGGTA	CCCGGGGGAT	CCTACGCGT	TAGAGTCGA	CCTGAGAAAA	CCTCCTTTAG	STCCATATTAACATA	CCTGCAGGGAGG	AGTCCTGG	GTCACGGTCG	CCACGCCGCCG	TCCTCGAAGT	TCATCACGCGC	TCCCACTTGAA
EI27R *	GGAAGTTCACGCCGATGAAC	TTCACCTTGTAGATGA	AGCAGCCGT	CTGTGGATAA	ATAATACCA	TTTGTTAGT	AAAATTCG	AGCTCGGTA	CCCGGGGGAT	CCTACGCGT	TAGAGTCGA	CCTGAGAAAA	CCTCCTTTA	STC CATATTAACATA	CCTGCAGGGAGG	AGTCCTGG	GTCACGGTCG	CCACGCCGCCG	TCCTCGAAGT:	TCATCACGCGC	TCCCACTTGAA
EI28R	GGAAGTTCACGCCGATGAAC	TTCACCTTG TAGATGR	AGCAGCCGT	CTGTGGATAA	ATAATACCA	TTTGTTAGT	AAAATTCG	AGCTCGGTA	CCCGGGGGAT	CCTACGCGT	TAGAGTCGA	CCTGAGAAAA	CCTCCTTTAG	TCCATATTAACATA	CCTGCAGGGAGG	AGTCCTGG	GTCACGGTCG	CCACGCCGCCG	TCCTCGAAGT	TCATCACGCGC	TCCCACTTGAA
EI29R *	GGAAGTTCACGCCGATGAAC	TTCACCTTGTAGATGA	AGCAGCCGT	CTGTGGATAA	ATAATACCA	TTTGTTAGT#	AAAATTCG	AGCTCGGTA	CCCGGGGGAT	CCTACGCGT	TAGAGTCGA	CCTGAGAAAA	CCTCCTTTAG	TCCATAT TAACATA	CCTGCAGGGAGG	AGTCCTGG	GTCACGGTCG	CCACGCCGCCG	TCCTCGAAGT	TCATCACGCGC	TCCCACTTGAA
EI30R *	GGAAGTTCACGCCGATGAAC	TTCACCTTGTAGATGA	AGCAGCCGT	CTGTGGATAA	ATAATACCA	TTTGTTAGT	AAAATTCG	AGCTCGGTA	CCCGGGGGAT	CCTACGCGT	TAGAGTCGA	CCTGAGAAAA	CCTCCTTTAG	STCCATATTAACATA	CCTGCAGGGAGG	AGTCCTGG	GTCACGGTCG	CCACGCCGCCG	TCCTCGAAGT	TCATCACGCGC	TCCCACTTGAA
EI31R *	GGAAGTTCACGCCGATGAAC	TTCACCTTGTAGATGA	AGCAGCCGT	CTGTGGATAA	ATAATACCA	TTTGTTAGT	AAAATTCG	AGCTCGGTA	CCCGGGGGAT	CCTACGCGT	TAGAGTCGA	CCTGAGAAAA	CCTCCTTTAG	TC CATATTAACATA	CCTGCAGGGAGG	AGTCCTGG	GTCACGGTCG	CCACGCCGCCG	TCCTCGAAGT	TCATCACGCGC	TCCCACTTGAA
EI32R *	GGAAGTTCACGCCGATGAAC	TTCACCTTGTAGATGA	AGCAGCCGT	CTGTGGATAA	ATAATACCA	TTTGTTAGT	AAAATTCG	AGCTCGGTA	CCCGGGGGAT	CCTACGCGT	TAGAGTCGA	.CCTGAGAAAAA	CCTCCTTTAG	TCCATATTAACATA	CCTGCAGGGAGG	AGTCCTGG	GTCACGGTCG	CCACGCCGCCG	TCCTCGAAGT	TCATCACGCGC	TCCCACTTGAA
EI33R *	GGAAGTTCACGCCGATGAAC	TTCACCTTGTAGAT GA	AGCAGCCGT	CTGTGGATAA	ATAATACCA:	TTTGTTAGT	AAAATTCG	AGCTCGGTA	CCCGGGGGAT	CCTACGCGT	TAGAGTCGA	.CCTGAGAAAA	CCTCCTTTAG	STCCATATTAACATA	CCTGCAGGGAGG	AGTCCTGG	GTCACGGTCG	CCACGCCGCCG	TCCTCGAAGT:	TCATCACGCGC	TCCCACTTGAA
EI34R *	GGAAGTTCACGCCGATGAAC	TTCACCTTGT <mark>AGA</mark> TGA	AGCAGCCGT	CTGTGGATAA	ATAATACCA	TTTGTTAGT	AAAATTCG	AGCTCGGTA	CCCGGGGGAT	CCTACGCGT	TAGAGTCGA	.CCTGAGAAAAG	CCTCCTTTAG	STCCATATTAACATA	CCTGCAGGGAGG	AGTCCTGG	GTCACGGTCG	CCACGCCGCCG	TCCTCGAAGT	TCATCACGCGC	TCCCACTTGAA
EI35R *	GGAAGTTCACGCCGATGAAC	TTCACCTTGTAGA TGA	AGCAGCCGT	CTGTGGATAA	ATAATACCA	TTTGTTAGT	AAAATTCG	AGCTCGGTA	CCCGGGGGAT	CCTACGCGT	TAGAGTCGA	CCTGAGAAAAG	CCTCCTTTAG	STCCATATTAACATA	CCTGCAGGGAGG	AGTCCTGG	GTCACGGTCG	CCACGCCGCCG	TCCTCGAAGT	TCATCACGCGC	TCCCACTTGAA
EI36R *	GGAAGTTCACGCCGATGAAC	TTCACCTTGTAGATGA	AGCAGCCGT	CTGTGGATAA	ATAATACCA	TTTGTTAGT#	AAAATTCG	AGCTCGGTA	CCCGGGGGAT	CCTACGCGT	TAGAGTCGA	CCTGAGAAAAG	CCTCCTTTAG	STCCATATTAACATA	CCTGCAGGGAGG	AGTCCTGG	GTCACGGTCG	CCACGCCGCCG	TCCTCGAAGT	TCATCACGCGC	TCCCACTTGAA
EI37R *	GGAAGTTCACGCCGATGAAC	TTCACCTTGTAGATGR	AGCAGCCGT	CTGTGGATAA	ATAATACCAS	TTTGTTAGT	AAAATTCG	AGCTCGGTA	CCCGGGGGAT	CCTACGCGT	TAGAGTCGA	CCTGAGAAAA	CCTCCTTTAG	STCCATATTAACATA	CCTGCAGGGAGG	AGTCCTGG	GTCACGGTCG	CCACGCCGCCG	TCCTCGAAGT	TCATCACGCGC	TCCCACTTGAA
EI38R *	GGAAGTTCACGCCGATGAA	TTCACCTTG <mark>TAGA</mark> TGA	AGCAGCCGT	CTGTGGATAA	ATAATACCA	TTTGTTAGT	AAAATTCG	AGCTCGGTA	CCCGGGGGAT	CTACGCGT	TAGA <mark>GTCGA</mark>	CCTGAGAAAA	CCTCCTTTAG	STCCATATTAACATA	CCTGCAGGGAGG	AGTCCTGG	GTCACGGTCG	CCACGCCGCCG	TCCTCGAAGT	TCATCACGCGC	TCCCACTTGAA

Microhomology scheme: Sense/pCMVΔ/BranchΔ, sgRNA E, forward strand

80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 225 240 245 250 CTICANGGIGG CATGRAGGG CACGIGAN COGC CACGAGTICAGGG CACGAGGT CAAGGG CACGAGGAC CACGAGAC CTTCAAGGTGCGCATCGTGAAGGTCCCTGAAGTTCGAGGTCGAGGTCGAGGGCGAGGGCGAGGGCGAGGGCGAGGCCCAAGAGCCGTCAAGAGCCGTCAAGAGTGAAGCGCCCGAGTTCCAGTACGGCTCCAAGTGTAAGCAGCCGACAACTCCCGACAACACCGCCAACATCCCCGACATCCCCGACATCCCCGACATCCAGAGAGCTTCAAGAGAGCTGAAGAGCGCTGAA CTICANGGIGG CRATGROUGG CACCIONAL COCCACGACATCONG CONCECUTACION CONCECUTA EE13 CTICAROGIC COLTICA OCCACOTOR ACCOUNTICA OCCACOTOR ACCOUNTICARO ACCOUNT EE18 EE20 * EE21 CTTCAAGGTGCGCATGGAGGGCACGTGAACGTCACAGGTGTACGGCCAGGGCGAAGGGCGAAGGGCGAAGGGCGAAGGGCCAAGAGCCGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGGCCCAAGTGCACAAGAGGGCGAAGAGCCCGAAGGGCTTCAAGTAGAAGAAGTGCCCGAAGGGCTTCAAGTGGGAAGGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGGAGGCTTCAAGTGGAAGGCGAAGAGGCTTCAAGTAGAAGTAGAAGTG EE24 CTICARGET COCCATEGORGE COTTON ACCOUNT CONTROL OF COLOR OF EE26 CTICANGGIGG CRATGINGGIGG CACGIGAN CONCEPTANCE CONTROL OF THE CONTR CTICALOGICCCCATGRAGG CACCOTORAC COCCA GASTICOAD TICALOGIC CACCACO CONTROL CONT EE28 * EE29 EE32 EE34 EE36 * EE38 EE40 * EE42 EE44 * EE45 * EE47 * CTTCAAGGTGCGCATGGAGGGCACGGTGAAGGGCACGGAGGGCGAGGGGGAGGGGGAGGGCGAGGGCGAGGGCGAGGGCAACACCGCGAAACACCGTGAAGGAGGCGAACACCGCGAAACAAGGAGGGGAGGGCTTCAAGGAGGCGTGAACACCGGAGGATCCCCGACATACCAAGAAGAAGAACACCCGACATACAAGAAGAAGTGCCTTCAAGGAGGCTTCAAGTAGGAGGCGCGTGAA EE48 EE53 EE55 * EE57 * EE58 * EE65 * EE68 * EE71 * EE73 * EE74 * EE76 * EE78 * EE79 * EE80 * EER1 * EE82 * EE84 CTTCAAGGTGCGCATGGAGGGCACGTGAACGGCCACGAGTTCGAGGGCGAGGGCGAGGGCGAGGGCCGAGGGCCTCAAGGTGCAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGTGAAGGGCGTGAA EE87 * EE89 * EE90 * EE91 * EE92 * CTTCAAGGTGCCCATGGAGGGCCACGGTGTAACGGCCACGAGTTCCAAGGTCCACGACTTCCAAGGTGCCACGACTTCCAAGGAGCCACCACTACAAGAAGCAGCCCCCAACATCCCCAACTACAAGAAGCAGCTCCAACAAGAACCATCCCGACTTCAAGGAGCCACTTCAAGGAGCACCCCGACTTCAAGGAGCACCTCCAACTACAAGAAGCAGCTCCAAGTACAAGAACCATCCAAGTACAAGAACCATCCAAGTACAAGAACCATCCAAGTACAAGAACCATCCAAGTACAAGAACCATCCAAGTACAAGAACCATCCAAGTACAAGAACCATCCAAGTACAAGAACCATCCAAGTACAAGAACCATCCAAGTACAAGAACCATCCAAGTACAAGAACCATCCAAGTACAAGAACCATCCAAGTACAAGAACCATCCAAGTACAAGAACCATCCAAGTACAAGAACCATCCAAGTACAAGAACCATCCAAGTA CTTCAAGGTGCGCATGGAGGGCACGTGAACGGCCACGAGTTCOAGGTCGAGGGCGAGGGCCGACATCCCCGACGTACAAGAGGCCGCCGAAAGACCGTGAAGGTCAAAGAGAGCCGCGACATCCCCGACATCCCCGACATCCCCGACATCCCCGACATCCCCGACATCCCGACATCCCGACATCCCCGACATCCCCGACATCCCCGACATCCCCGACATCCCCGACATCCCCGACATCCCCGACATCCCCGACATCCCCGACATCCCCGACATCCCCGACATCCCCGACATCCCCGACATCCCCGACATCCCGACATCCCCGACATCCCGACATCCCGACATCCACATCCCGACATCCACATCCCGACATCCACATCCCGACATCCCGACATCCACATCCACATCCACATCCACATCCACATCCACATCCCGACATCCACATCACATCCACATCACATCACATCCACATCAATCACATCACATCACATCAATCACATCAATCACATCAATCACATCAATCACATCAATC EE94 * EE95 * EE97 * EE100 :





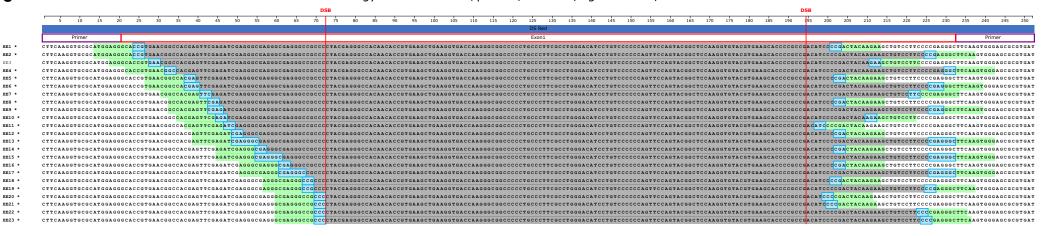
EE9 *

EE13

EE14

EE15

Microhomology scheme: Sense/pCMVΔ/BranchΔ, sqRNA E & J, forward strand



Microhomology scheme: Sense/pCMVΔ/BranchΔ, sgRNA E & J, reverse strand

