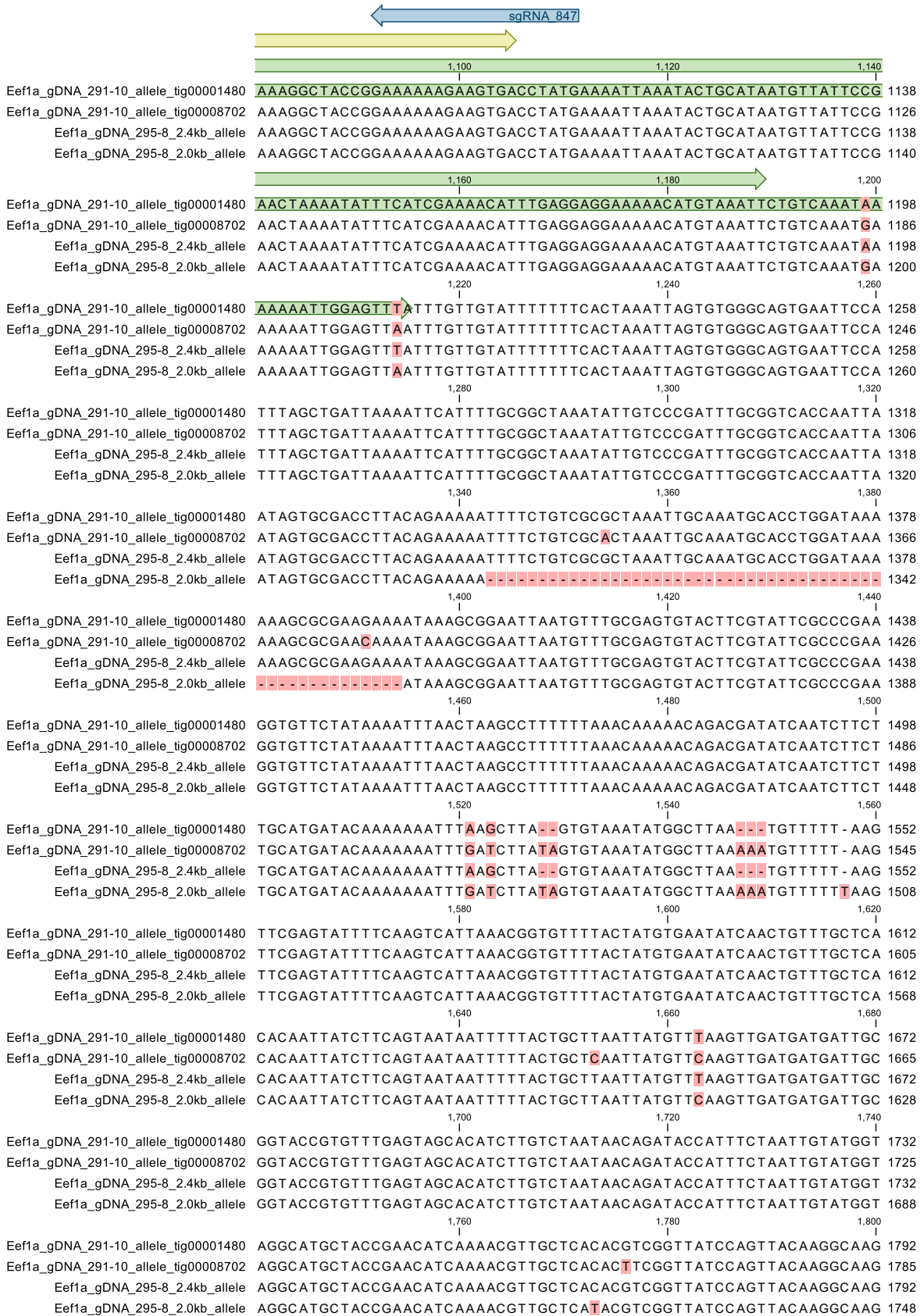
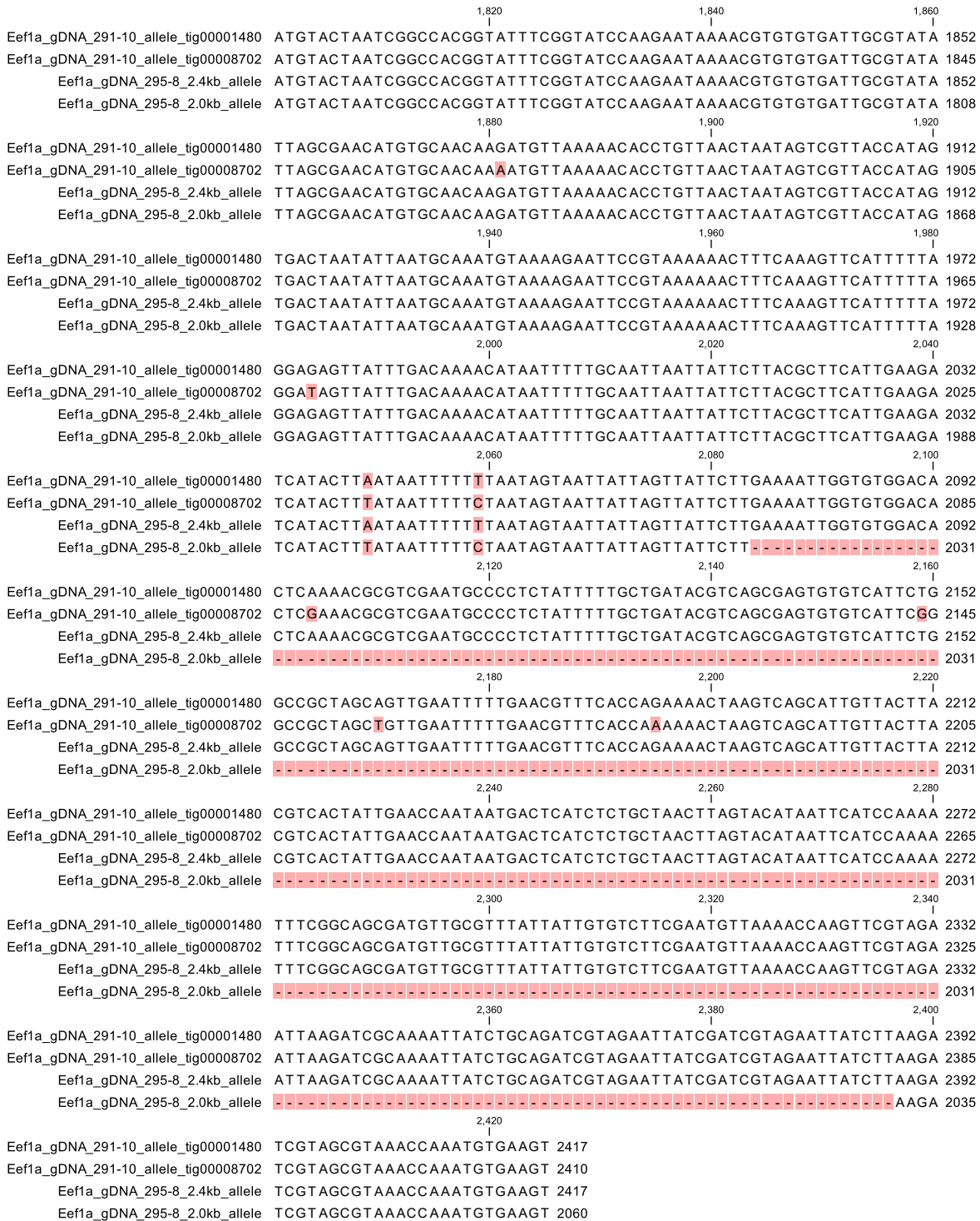


	560	580	600	
Eef1a_gDNA_291-10_allele_tig00001480	TTAGCACTTGCTTAGGGAACATTTTAAATATTAATTTTTATTGAATAAAGAACCAACCT			598
Eef1a_gDNA_291-10_allele_tig00008702	TTAGCACTTGCTTAGGGAACATTTTAAATATTAATTTTTATTGAATAAAGAACCAACCT			596
Eef1a_gDNA_295-8_2.4kb_allele	TTAGCACTTGCTTAGGGAACATTTTAAATATTAATTTTTATTGAATAAAGAACCAACCT			598
Eef1a_gDNA_295-8_2.0kb_allele	TTGGCACTTGCTTAGGGAACATTTTAAATATTAATTTTTATTGAATAAAGAACCAACCT			600
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	620	640	660	
Eef1a_gDNA_291-10_allele_tig00001480	GTTTGACTTTTATTAGTAATAAAGCTAAAATTATGGCCTAAATCATAATTTATTATGTGA			658
Eef1a_gDNA_291-10_allele_tig00008702	GTTTGACTTTTATTAGTAATAAAGCTAAAATTATGGCCTAAATCATAATTTATTATGTGA			646
Eef1a_gDNA_295-8_2.4kb_allele	GTTTGACTTTTATTAGTAATAAAGCTAAAATTATGGCCTAAATCATAATTTATTATGTGA			658
Eef1a_gDNA_295-8_2.0kb_allele	GTTTGACTTTTATTAGTAATAAAGCTAAAATTATGGCCTAAATCATAATTTATTATGTGA			660
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	680	700	720	
Eef1a_gDNA_291-10_allele_tig00001480	TTTGGGAAAGAAATTTGTGTTGATTTTTCCATTAATATTGTA AAAACAAAATCGAAAGTT			718
Eef1a_gDNA_291-10_allele_tig00008702	TTTGGGAAAGAAATTTGTGTTGATTTTTCCATTAATATTGTA AAAACAAAATCAAAGTT			706
Eef1a_gDNA_295-8_2.4kb_allele	TTTGGGAAAGAAATTTGTGTTGATTTTTCCATTAATATTGTA AAAACAAAATCGAAAGTT			718
Eef1a_gDNA_295-8_2.0kb_allele	TTTGGGAAAGAAATTTGTGTTGATTTTTCCATTAATATTGTGAAAACAAAATCGAAAGTT			720
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	740	760	780	
Eef1a_gDNA_291-10_allele_tig00001480	AATTTCTTTCAAAAATTA CTTTTAGGTCATCATCTCAATCATCCAGGTGAGATTCATGC			778
Eef1a_gDNA_291-10_allele_tig00008702	AATTTCTTTCAAAAATTA CTTTTAGGTCATCATCTCAATCATCCAGGTGAGATTCATGC			766
Eef1a_gDNA_295-8_2.4kb_allele	AATTTCTTTCAAAAATTA CTTTTAGGTCATCATCTCAATCATCCAGGTGAGATTCATGC			778
Eef1a_gDNA_295-8_2.0kb_allele	AATTTCTTTCAAAAATTA CTTTTAGGTCATCATCTCAATCATCCAGGTGAGATTCATGC			780
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	800	820	840	
Eef1a_gDNA_291-10_allele_tig00001480	TGGTTACCAACCTGTTTTGGATTGCCACACTGCTCACGTTGCCTGCAAAATTTACAGAATT			838
Eef1a_gDNA_291-10_allele_tig00008702	TGGTTACCAACCTGTTTTGGATTGCCACACTGCTCACGTTGCCTGCAAAATTTACAGAATT			826
Eef1a_gDNA_295-8_2.4kb_allele	TGGTTACCAACCTGTTTTGGATTGCCACACTGCTCACGTTGCCTGCAAAATTTACAGAATT			838
Eef1a_gDNA_295-8_2.0kb_allele	TGGTTACCAACCTGTTTTGGATTGCCACACTGCTCACGTTGCCTGCAAAATTTACAGAATT			840
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	860	880	900	
Eef1a_gDNA_291-10_allele_tig00001480	AAAGCAGAAATGTGATAGACGAAGTGGTAAAGTTTTAGAAGAAAAATCCCAAAATGGTTAA			898
Eef1a_gDNA_291-10_allele_tig00008702	AAAGCAGAAATGTGATAGACGAAGTGGTAAAGTTTTAGAAGAAAAATCCCAAAATGGTTAA			886
Eef1a_gDNA_295-8_2.4kb_allele	AAAGCAGAAATGTGATAGACGAAGTGGTAAAGTTTTAGAAGAAAAATCCCAAAATGGTTAA			898
Eef1a_gDNA_295-8_2.0kb_allele	AAAGCAGAAATGTGATAGACGAAGTGGTAAAGTTTTAGAAGAAAAATCCCAAAATGGTTAA			900
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	920	940	960	
Eef1a_gDNA_291-10_allele_tig00001480	ATCTGGTGATGCTGCTATGGTTACTTTGACTCCTTCTAAGCCTATGTGTGTTGAAGCTTT			958
Eef1a_gDNA_291-10_allele_tig00008702	ATCTGGTGATGCTGCTATGGTTACTTTGACTCCTTCTAAGCCTATGTGTGTTGAAGCTTT			946
Eef1a_gDNA_295-8_2.4kb_allele	ATCTGGTGATGCTGCTATGGTTACTTTGACTCCTTCTAAGCCTATGTGTGTTGAAGCTTT			958
Eef1a_gDNA_295-8_2.0kb_allele	ATCTGGTGATGCTGCTATGGTTACTTTGACTCCTTCTAAGCCTATGTGTGTTGAAGCTTT			960
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	980	1,000	1,020	
Eef1a_gDNA_291-10_allele_tig00001480	CTCTGACTACCAGCCATTGGGTCGTTTTGCTGTACGTGACATGAGACAAACTGTTGCTGT			1018
Eef1a_gDNA_291-10_allele_tig00008702	CTCTGACTACCAGCCATTGGGTCGTTTTGCTGTACGTGACATGAGACAAACTGTTGCTGT			1006
Eef1a_gDNA_295-8_2.4kb_allele	CTCTGACTACCAGCCATTGGGTCGTTTTGCTGTACGTGACATGAGACAAACTGTTGCTGT			1018
Eef1a_gDNA_295-8_2.0kb_allele	CTCTGACTACCAGCCATTGGGTCGTTTTGCTGTACGTGACATGAGACAAACTGTTGCTGT			1020
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	1,040	1,060	1,080	
Eef1a_gDNA_291-10_allele_tig00001480	TGGAGTTATCAAGAGTGTGAAAAGGCCGATGCTACTGGTAAAATGACAAAAATCAGCTCA			1078
Eef1a_gDNA_291-10_allele_tig00008702	TGGAGTTATCAAGAGTGTGAAAAGGCCGATGCTACTGGTAAAATGACAAAAATCAGCTCA			1066
Eef1a_gDNA_295-8_2.4kb_allele	TGGAGTTATCAAGAGTGTGAAAAGGCCGATGCTACTGGTAAAATGACAAAAATCAGCTCA			1078
Eef1a_gDNA_295-8_2.0kb_allele	TGGAGTTATCAAGAGTGTGAAAAGGCCGATGCTACTGGTAAAATGACAAAAATCAGCTCA			1080





S3 Fig. Alignment of *Eef1a* alleles from colonies 291-10 and 295-8. Nucleotide alignment of the region encoding exons 3 and 4 of *Eef1a* from the four alleles in 291-10 and 295-8. Differences are highlighted in red boxes. Sequence features are shown on and above the top sequence of the alignment. Green, mRNA as determined by alignments to 291-10 transcripts. Yellow, coding sequence. Blue, gRNA_847 binding site.