

Pr845

20 40 60

expected sequence of Eef1a-FLAG-2A-eGFP allele GTAGAAACTGGTGTATTGTCCCCCTGGTATGATCGTTACATTTGCCCTGCCAATGTAACC 60

347-10 LHA clone 1 GTAGAAACTGGTGTATTGTCCCCCTGGTATGATCGTTACATTTGCCCTGCCAATGTAACC 60

347-10 LHA clone 2 GTAGAAACTGGTGTATTGTCCCCCTGGTATGATCGTTACATTTGCCCTGCCAATGTAACC 60

347-10 LHA clone3 GTAGAAACTGGTGTATTGTCCCCCTGGTATGATCGTTACATTTGCCCTGCCAATGTAACC 60

354-3 LHA clone 1 GTAGAAACTGGTGTATTGTCCCCCTGGTATGATCGTTACATTTGCCCTGCCAATGTAACC 60

354-3 LHA clone 2 GTAGAAACTGGTGTATTGTCCCCCTGGTATGATCGTTACATTTGCCCTGCCAATGTAACC 60

354-3 LHA clone 3 GTAGAAACTGGTGTATTGTCCCCCTGGTATGATCGTTACATTTGCCCTGCCAATGTAACC 60

354-5_L5 GTAGAAACTGGTGTATTGTCCCCCTGGTATGATCGTTACATTTGCCCTGCCAATGTAACC 60

354-5_L6 GTAGAAACTGGTGTATTGTCCCCCTGGTATGATCGTTACATTTGCCCTGCCAATGTAACC 60

354-5_L8 GTAGAAACTGGTGTATTGTCCCCCTGGTATGATCGTTACATTTGCCCTGCCAATGTAACC 60

347-10_R5 - - - - -

347-10_R6 - - - - -

347-10_R7 - - - - -

354-3_R1 - - - - -

354-3_R2 - - - - -

354-3_R10 - - - - -

354-5_R9 - - - - -

354-5_R11 - - - - -

354-5_R12 - - - - -

80 100 120

expected sequence of Eef1a-FLAG-2A-eGFP allele ACTGAGGTCAAATCTGTAGAAATGCACCACGAATCCTTAACTGAAGCACATCCAGGTGAT 120

347-10 LHA clone 1 ACTGAGGTCAAATCTGTAGAAATGCACCACGAATCCTTAACTGAAGCACATCCAGGTGAT 120

347-10 LHA clone 2 ACTGAGGTCAAATCTGTAGAAATGCACCACGAATCCTTAACTGAAGCACATCCAGGTGAT 120

347-10 LHA clone3 ACTGAGGTCAAATCTGTAGAAATGCACCACGAATCCTTAACTGAAGCACATCCAGGTGAT 120

354-3 LHA clone 1 ACTGAGGTCAAATCTGTAGAAATGCACCACGAATCCTTAACTGAAGCACATCCAGGTGAT 120

354-3 LHA clone 2 ACTGAGGTCAAATCTGTAGAAATGCACCACGAATCCTTAACTGAAGCACATCCAGGTGAT 120

354-3 LHA clone 3 ACTGAGGTCAAATCTGTAGAAATGCACCACGAATCCTTAACTGAAGCACATCCAGGTGAT 120

354-5_L5 ACTGAGGTCAAATCTGTAGAAATGCACCACGAATCCTTAACTGAAGCACATCCAGGTGAT 120

354-5_L6 ACTGAGGTCAAATCTGTAGAAATGCACCACGAATCCTTAACTGAAGCACATCCAGGTGAT 120

354-5_L8 ACTGAGGTCAAATCTGTAGAAATGCACCACGAATCCTTAACTGAAGCACATCCAGGTGAT 120

347-10_R5 - - - - -

347-10_R6 - - - - -

347-10_R7 - - - - -

354-3_R1 - - - - -

354-3_R2 - - - - -

354-3_R10 - - - - -

354-5_R9 - - - - -

354-5_R11 - - - - -

354-5_R12 - - - - -

140 160 180

expected sequence of Eef1a-FLAG-2A-eGFP allele AATGTTGGTTTTAATGTCAAAAATGTGTCTATCAAGGATATCAAACGTGGTATGGTTGCG 180

347-10 LHA clone 1 AATGTTGGTTTTAATGTCAAAAATGTGTCTATCAAGGATATCAAACGTGGTATGGTTGCG 180

347-10 LHA clone 2 AATGTTGGTTTTAATGTCAAAAATGTGTCTATCAAGGATATCAAACGTGGTATGGTTGCG 180

347-10 LHA clone3 AATGTTGGTTTTAATGTCAAAAATGTGTCTATCAAGGATATCAAACGTGGTATGGTTGCG 180

354-3 LHA clone 1 AATGTTGGTTTTAATGTCAAAAATGTGTCTATCAAGGATATCAAACGTGGTATGGTTGCG 180

354-3 LHA clone 2 AATGTTGGTTTTAATGTCAAAAATGTGTCTATCAAGGATATCAAACGTGGTATGGTTGCG 180

354-3 LHA clone 3 AATGTTGGTTTTAATGTCAAAAATGTGTCTATCAAGGATATCAAACGTGGTATGGTTGCG 180

354-5_L5 AATGTTGGTTTTAATGTCAAAAATGTGTCTATCAAGGATATCAAACGTGGTATGGTTGCG 180

354-5_L6 AATGTTGGTTTTAATGTCAAAAATGTGTCTATCAAGGATATCAAACGTGGTATGGTTGCG 180

354-5_L8 AATGTTGGTTTTAATGTCAAAAATGTGTCTATCAAGGATATCAAACGTGGTATGGTTGCG 180

347-10_R5 - - - - -

347-10_R6 - - - - -

347-10_R7 - - - - -

354-3_R1 - - - - -

354-3_R2 - - - - -

354-3_R10 - - - - -

354-5_R9 - - - - -

354-5_R11 - - - - -

354-5_R12 - - - - -

Figure S5 - Page

		200		220		240				
expected sequence of Eef1a-FLAG-2A-eGFP allele	TCTGACAGCAAAAATGATCCAGCCAAAGAAGCCAAAACCTTTTATGCACAGGTATTCTTT					240				
347-10 LHA clone 1	TCTGACAGCAAAAATGATCCAGCCAAAGAAGCCAAAACCTTTTATGCACAGGTATTCTTT					240				
347-10 LHA clone 2	TCTGACAGCAAAAATGATCCAGCCAAAGAAGCCAAAACCTTTTATGCACAGGTATTCTTT					240				
347-10 LHA clone 3	TCTGACAGCAAAAATGATCCAGCCAAAGAAGCCAAAACCTTTTATGCACAGGTATTCTTT					240				
354-3 LHA clone 1	TCTGACAGCAAAAATGATCCAGCCAAAGAAGCCAAAACCTTTTATGCACAGGTATTCTTT					240				
354-3 LHA clone 2	TCTGACAGCAAAAATGATCCAGCCAAAGAAGCCAAAACCTTTTATGCACAGGTATTCTTT					240				
354-3 LHA clone 3	TCTGACAGCAAAAATGATCCAGCCAAAGAAGCCAAAACCTTTTATGCACAGGTATTCTTT					240				
354-5_L5	TCTGACAGCAAAAATGATCCAGCCAAAGAAGCCAAAACCTTTTATGCACAGGTATTCTTT					240				
354-5_L6	TCTGACAGCAAAAATGATCCAGCCAAAGAAGCCAAAACCTTTTATGCACAGGTATTCTTT					240				
354-5_L8	TCTGACAGCAAAAATGATCCAGCCAAAGAAGCCAAAACCTTTTATGCACAGGTATTCTTT					240				
347-10_R5	-					-				
347-10_R6	-					-				
347-10_R7	-					-				
354-3_R1	-					-				
354-3_R2	-					-				
354-3_R10	-					-				
354-5_R9	-					-				
354-5_R11	-					-				
354-5_R12	-					-				
		260		280		300				
expected sequence of Eef1a-FLAG-2A-eGFP allele	AATTTTTGTA	CTTA	AACTT	ATCAGTT	TGATAAGCGT	TGGCCG	TGGCTT	GCCACT	TGCT	300
347-10 LHA clone 1	AATTTTTGTA	CTTA	AACTT	ATCAGTT	TGATAAGCGT	TGGCCG	TGGCTT	GCCACT	TGCT	300
347-10 LHA clone 2	AATTTTTGTA	CTTA	AACTT	ATCAGTT	TGATAAGCGT	TGGCCG	TGGCTT	GCCACT	TGCT	300
347-10 LHA clone 3	AATTTTTGTA	CTTA	AACTT	ATCAGTT	TGATAAGCGT	TGGCCG	TGGCTT	GCCACT	TGCT	300
354-3 LHA clone 1	AATTTTTGTA	CTTA	AACTT	ATCAGTT	TGATAAGCGT	TGGCCG	TGGCTT	GCCACT	TGCT	300
354-3 LHA clone 2	AATTTTTGTA	CTTA	AACTT	ATCAGTT	TGATAAGCGT	TGGCCG	TGGCTT	GCCACT	TGCT	300
354-3 LHA clone 3	AATTTTTGTA	CTTA	AACTT	ATCAGTT	TGATAAGCGT	TGGCCG	TGGCTT	GCCACT	TGCT	300
354-5_L5	AATTTTTGTA	CTTA	AACTT	ATCAGTT	TGATAAGCGT	TGGCCG	TGGCTT	GCCACT	TGCT	300
354-5_L6	AATTTTTGTA	CTTA	AACTT	ATCAGTT	TGATAAGCGT	TGGCCG	TGGCTT	GCCACT	TGCT	300
354-5_L8	AATTTTTGTA	CTTA	AACTT	ATCAGTT	TGATAAGCGT	TGGCCG	TGGCTT	GCCACT	TGCT	300
347-10_R5	-									-
347-10_R6	-									-
347-10_R7	-									-
354-3_R1	-									-
354-3_R2	-									-
354-3_R10	-									-
354-5_R9	-									-
354-5_R11	-									-
354-5_R12	-									-
		320		340		360				
expected sequence of Eef1a-FLAG-2A-eGFP allele	TAGCATGATAAATCAATCAACTTGACATTCCATCAATTTTGTTC AACAGAAACAGGACCT					360				
347-10 LHA clone 1	TAGCATGATAAATCAATCAACTTGACATTCCATCAATTTTGTTC AACAGAAACAGGACCT					360				
347-10 LHA clone 2	TAGCATGATAAATCAATCAACTTGACATTCCATCAATTTTGTTC AACAGAAACAGGACCT					360				
347-10 LHA clone 3	TAGCATGATAAATCAATCAACTTGACATTCCATCAATTTTGTTC AACAGAAACAGGACCT					360				
354-3 LHA clone 1	TAGCATGATAAATCAATCAACTTGACATTCCATCAATTTTGTTC AACAGAAACAGGACCT					360				
354-3 LHA clone 2	TAGCATGATAAATCAATCAACTTGACATTCCATCAATTTTGTTC AACAGAAACAGGACCT					360				
354-3 LHA clone 3	TAGCATGATAAATCAATCAACTTGACATTCCATCAATTTTGTTC AACAGAAACAGGACCT					360				
354-5_L5	TAGCATGATAAATCAATCAACTTGACATTCCATCAATTTTGTTC AACAGAAACAGGACCT					360				
354-5_L6	TAGCATGATAAATCAATCAACTTGACATTCCATCAATTTTGTTC AACAGAAACAGGACCT					360				
354-5_L8	TAGCATGATAAATCAATCAACTTGACATTCCATCAATTTTGTTC AACAGAAACAGGACCT					360				
347-10_R5	-					-				
347-10_R6	-					-				
347-10_R7	-					-				
354-3_R1	-					-				
354-3_R2	-					-				
354-3_R10	-					-				
354-5_R9	-					-				
354-5_R11	-					-				
354-5_R12	-					-				

		560	580	600	
expected sequence of Eef1a-FLAG-2A-eGFP allele	AGCACTTGCTTAGGGA	ACTATTTAAA	ATTAATTTTT	ATTGAATAAAGA	ACCAACCTGT 600
347-10 LHA clone 1	AGCACTTGCTTAGGGA	ACTATTTAAA	ATTAATTTTT	ATTGAATAAAGA	ACCAACCTGT 600
347-10 LHA clone 2	AGCACTTGCTTAGGGA	ACTATTTAAA	ATTAATTTTT	ATTGAATAAAGA	ACCAACCTGT 600
347-10 LHA clone 3	AGCACTTGCTTAGGGA	ACTATTTAAA	ATTAATTTTT	ATTGAATAAAGA	ACCAACCTGT 600
354-3 LHA clone 1	AGCACTTGCTTAGGGA	ACTATTTAAA	ATTAATTTTT	ATTGAATAAAGA	ACCAACCTGT 600
354-3 LHA clone 2	AGCACTTGCTTAGGGA	ACTATTTAAA	ATTAATTTTT	ATTGAATAAAGA	ACCAACCTGT 600
354-3 LHA clone 3	AGCACTTGCTTAGGGA	ACTATTTAAA	ATTAATTTTT	ATTGAATAAAGA	ACCAACCTGT 600
354-5_L5	AGCACTTGCTTAGGGA	ACTATTTAAA	ATTAATTTTT	ATTGAATAAAGA	ACCAACCTGT 600
354-5_L6	AGCACTTGCTTAGGGA	ACTATTTAAA	ATTAATTTTT	ATTGAATAAAGA	ACCAACCTGT 600
354-5_L8	AGCACTTGCTTAGGGA	ACTATTTAAA	ATTAATTTTT	ATTGAATAAAGA	ACCAACCTGT 600
347-10_R5	-				-
347-10_R6	-				-
347-10_R7	-				-
354-3_R1	-				-
354-3_R2	-				-
354-3_R10	-				-
354-5_R9	-				-
354-5_R11	-				-
354-5_R12	-				-
		620	640	660	
expected sequence of Eef1a-FLAG-2A-eGFP allele	TTGACTTTTATTAGTA	AATAAAGCTAAA	ATTATGGCCTAAAT	CATAATTTATTAT	TGTGATT 660
347-10 LHA clone 1	TTGACTTTTATTAGTA	AATAAAGCTAAA	ATTATGGCCTAAAT	CATAATTTATTAT	TGTGATT 660
347-10 LHA clone 2	TTGACTTTTATTAGTA	AATAAAGCTAAA	ATTATGGCCTAAAT	CATAATTTATTAT	TGTGATT 660
347-10 LHA clone 3	TTGACTTTTATTAGTA	AATAAAGCTAAA	ATTATGGCCTAAAT	CATAATTTATTAT	TGTGATT 660
354-3 LHA clone 1	TTGACTTTTATTAGTA	AATAAAGCTAAA	ATTATGGCCTAAAT	CATAATTTATTAT	TGTGATT 660
354-3 LHA clone 2	TTGACTTTTATTAGTA	AATAAAGCTAAA	ATTATGGCCTAAAT	CATAATTTATTAT	TGTGATT 660
354-3 LHA clone 3	TTGACTTTTATTAGTA	AATAAAGCTAAA	ATTATGGCCTAAAT	CATAATTTATTAT	TGTGATT 660
354-5_L5	TTGACTTTTATTAGTA	AATAAAGCTAAA	ATTATGGCCTAAAT	CATAATTTATTAT	TGTGATT 660
354-5_L6	TTGACTTTTATTAGTA	AATAAAGCTAAA	ATTATGGCCTAAAT	CATAATTTATTAT	TGTGATT 660
354-5_L8	TTGACTTTTATTAGTA	AATAAAGCTAAA	ATTATGGCCTAAAT	CATAATTTATTAT	TGTGATT 660
347-10_R5	-				-
347-10_R6	-				-
347-10_R7	-				-
354-3_R1	-				-
354-3_R2	-				-
354-3_R10	-				-
354-5_R9	-				-
354-5_R11	-				-
354-5_R12	-				-
		680	700	720	
expected sequence of Eef1a-FLAG-2A-eGFP allele	TGGGAAAGAAATTTGT	GTTGATTTTTCC	ATTAATTTGTA	AAAAACAAAATCG	AAAGTTAA 720
347-10 LHA clone 1	TGGGAAAGAAATTTGT	GTTGATTTTTCC	ATTAATTTGTA	AAAAACAAAATCG	AAAGTTAA 720
347-10 LHA clone 2	TGGGAAAGAAATTTGT	GTTGATTTTTCC	ATTAATTTGTA	AAAAACAAAATCG	AAAGTTAA 720
347-10 LHA clone 3	TGGGAAAGAAATTTGT	GTTGATTTTTCC	ATTAATTTGTA	AAAAACAAAATCG	AAAGTTAA 720
354-3 LHA clone 1	TGGGAAAGAAATTTGT	GTTGATTTTTCC	ATTAATTTGTA	AAAAACAAAATCG	AAAGTTAA 720
354-3 LHA clone 2	TGGGAAAGAAATTTGT	GTTGATTTTTCC	ATTAATTTGTA	AAAAACAAAATCG	AAAGTTAA 720
354-3 LHA clone 3	TGGGAAAGAAATTTGT	GTTGATTTTTCC	ATTAATTTGTA	AAAAACAAAATCG	AAAGTTAA 720
354-5_L5	TGGGAAAGAAATTTGT	GTTGATTTTTCC	ATTAATTTGTA	AAAAACAAAATCG	AAAGTTAA 720
354-5_L6	TGGGAAAGAAATTTGT	GTTGATTTTTCC	ATTAATTTGTA	AAAAACAAAATCG	AAAGTTAA 720
354-5_L8	TGGGAAAGAAATTTGT	GTTGATTTTTCC	ATTAATTTGTA	AAAAACAAAATCG	AAAGTTAA 720
347-10_R5	-				-
347-10_R6	-				-
347-10_R7	-				-
354-3_R1	-				-
354-3_R2	-				-
354-3_R10	-				-
354-5_R9	-				-
354-5_R11	-				-
354-5_R12	-				-

		740		760		780	
expected sequence of Eef1a-FLAG-2A-eGFP allele	TTTCTTTCAAAAATTACTTTTAGGTCATCATTCTCAATCATCCAGGTGAGATTCATGCTG						780
347-10 LHA clone 1	TTTCTTTCAAAAATTACTTTTAGGTCATCATTCTCAATCATCCAGGTGAGATTCATGCTG						780
347-10 LHA clone 2	TTTCTTTCAAAAATTACTTTTAGGTCATCATTCTCAATCATCCAGGTGAGATTCATGCTG						780
347-10 LHA clone 3	TTTCTTTCAAAAATTACTTTTAGGTCATCATTCTCAATCATCCAGGTGAGATTCATGCTG						780
354-3 LHA clone 1	TTTCTTTCAAAAATTACTTTTAGGTCATCATTCTCAATCATCCAGGTGAGATTCATGCTG						780
354-3 LHA clone 2	TTTCTTTCAAAAATTACTTTTAGGTCATCATTCTCAATCATCCAGGTGAGATTCATGCTG						780
354-3 LHA clone 3	TTTCTTTCAAAAATTACTTTTAGGTCATCATTCTCAATCATCCAGGTGAGATTCATGCTG						780
354-5_L5	TTTCTTTCAAAAATTACTTTTAGGTCATCATTCTCAATCATCCAGGTGAGATTCATGCTG						780
354-5_L6	TTTCTTTCAAAAATTACTTTTAGGTCATCATTCTCAATCATCCAGGTGAGATTCATGCTG						780
354-5_L8	TTTCTTTCAAAAATTACTTTTAGGTCATCATTCTCAATCATCCAGGTGAGATTCATGCTG						780
347-10_R5	-						-
347-10_R6	-						-
347-10_R7	-						-
354-3_R1	-						-
354-3_R2	-						-
354-3_R10	-						-
354-5_R9	-						-
354-5_R11	-						-
354-5_R12	-						-
		800		820		840	
expected sequence of Eef1a-FLAG-2A-eGFP allele	GTTACCAACCTGTTTTGGATTGCCACACTGCTCACGTTGCCTGCAAAATTTACAGAATTA						840
347-10 LHA clone 1	GTTACCAACCTGTTTTGGATTGCCACACTGCTCACGTTGCCTGCAAAATTTACAGAATTA						840
347-10 LHA clone 2	GTTACCAACCTGTTTTGGATTGCCACACTGCTCACGTTGCCTGCAAAATTTACAGAATTA						840
347-10 LHA clone 3	GTTACCAACCTGTTTTGGATTGCCACACTGCTCACGTTGCCTGCAAAATTTACAGAATTA						840
354-3 LHA clone 1	GTTACCAACCTGTTTTGGATTGCCACACTGCTCACGTTGCCTGCAAAATTTACAGAATTA						840
354-3 LHA clone 2	GTTACCAACCTGTTTTGGATTGCCACACTGCTCACGTTGCCTGCAAAATTTACAGAATTA						840
354-3 LHA clone 3	GTTACCAACCTGTTTTGGATTGCCACACTGCTCACGTTGCCTGCAAAATTTACAGAATTA						840
354-5_L5	GTTACCAACCTGTTTTGGATTGCCACACTGCTCACGTTGCCTGCAAAATTTACAGAATTA						840
354-5_L6	GTTACCAACCTGTTTTGGATTGCCACACTGCTCACGTTGCCTGCAAAATTTACAGAATTA						840
354-5_L8	GTTACCAACCTGTTTTGGATTGCCACACTGCTCACGTTGCCTGCAAAATTTACAGAATTA						840
347-10_R5	-						-
347-10_R6	-						-
347-10_R7	-						-
354-3_R1	-						-
354-3_R2	-						-
354-3_R10	-						-
354-5_R9	-						-
354-5_R11	-						-
354-5_R12	-						-
		860		880		900	
expected sequence of Eef1a-FLAG-2A-eGFP allele	AGCAGAAATGTGATAGACGAAGTGGTAAAGTTTTAGAAGAAAATCCCAAAATGGTTAAAT						900
347-10 LHA clone 1	AGCAGAAATGTGATAGACGAAGTGGTAAAGTTTTAGAAGAAAATCCCAAAATGGTTAAAT						900
347-10 LHA clone 2	AGCAGAAATGTGATAGACGAAGTGGTAAAGTTTTAGAAGAAAATCCCAAAATGGTTAAAT						900
347-10 LHA clone 3	AGCAGAAATGTGATAGACGAAGTGGTAAAGTTTTAGAAGAAAATCCCAAAATGGTTAAAT						900
354-3 LHA clone 1	AGCAGAAATGTGATAGACGAAGTGGTAAAGTTTTAGAAGAAAATCCCAAAATGGTTAAAT						900
354-3 LHA clone 2	AGCAGAAATGTGATAGACGAAGTGGTAAAGTTTTAGAAGAAAATCCCAAAATGGTTAAAT						900
354-3 LHA clone 3	AGCAGAAATGTGATAGACGAAGTGGTAAAGTTTTAGAAGAAAATCCCAAAATGGTTAAAT						900
354-5_L5	AGCAGAAATGTGATAGACGAAGTGGTAAAGTTTTAGAAGAAAATCCCAAAATGGTTAAAT						900
354-5_L6	AGCAGAAATGTGATAGACGAAGTGGTAAAGTTTTAGAAGAAAATCCCAAAATGGTTAAAT						900
354-5_L8	AGCAGAAATGTGATAGACGAAGTGGTAAAGTTTTAGAAGAAAATCCCAAAATGGTTAAAT						900
347-10_R5	-						-
347-10_R6	-						-
347-10_R7	-						-
354-3_R1	-						-
354-3_R2	-						-
354-3_R10	-						-
354-5_R9	-						-
354-5_R11	-						-
354-5_R12	-						-

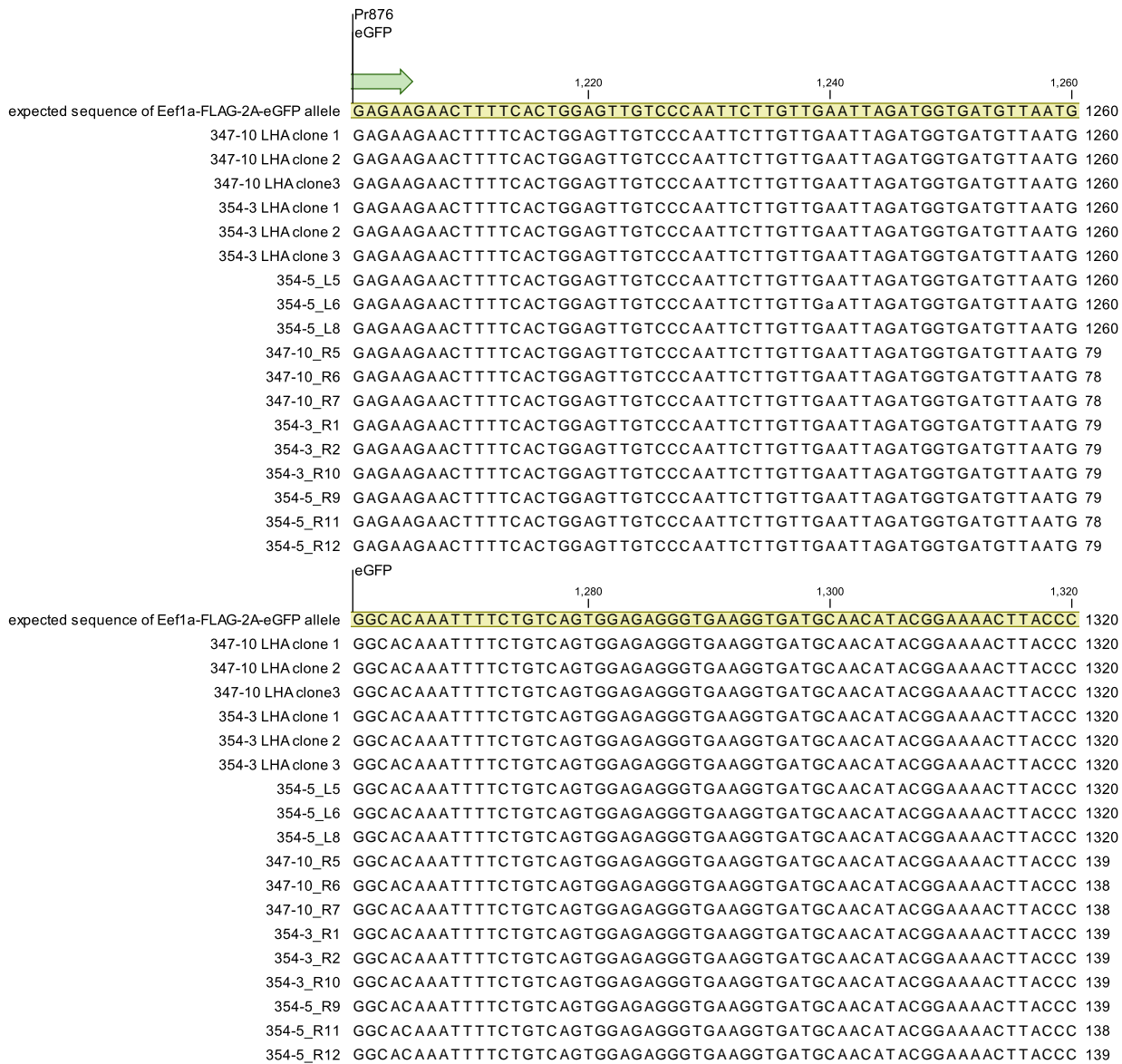
expected sequence of Eef1a-FLAG-2A-eGFP allele CTGGTGATGCTGCTATGGTTACTTTGACTCCTTCTAAGCCTATGTGTGTTGAAGCTTTCT 960
 347-10 LHA clone 1 CTGGTGATGCTGCTATGGTTACTTTGACTCCTTCTAAGCCTATGTGTGTTGAAGCTTTCT 960
 347-10 LHA clone 2 CTGGTGATGCTGCTATGGTTACTTTGACTCCTTCTAAGCCTATGTGTGTTGAAGCTTTCT 960
 347-10 LHA clone 3 CTGGTGATGCTGCTATGGTTACTTTGACTCCTTCTAAGCCTATGTGTGTTGAAGCTTTCT 960
 354-3 LHA clone 1 CTGGTGATGCTGCTATGGTTACTTTGACTCCTTCTAAGCCTATGTGTGTTGAAGCTTTCT 960
 354-3 LHA clone 2 CTGGTGATGCTGCTATGGTTACTTTGACTCCTTCTAAGCCTATGTGTGTTGAAGCTTTCT 960
 354-3 LHA clone 3 CTGGTGATGCTGCTATGGTTACTTTGACTCCTTCTAAGCCTATGTGTGTTGAAGCTTTCT 960
 354-5_L5 CTGGTGATGCTGCTATGGTTACTTTGACTCCTTCTAAGCCTATGTGTGTTGAAGCTTTCT 960
 354-5_L6 CTGGTGATGCTGCTATGGTTACTTTGACTCCTTCTAAGCCTATGTGTGTTGAAGCTTTCT 960
 354-5_L8 CTGGTGATGCTGCTATGGTTACTTTGACTCCTTCTAAGCCTATGTGTGTTGAAGCTTTCT 960
 347-10_R5 - - - - -
 347-10_R6 - - - - -
 347-10_R7 - - - - -
 354-3_R1 - - - - -
 354-3_R2 - - - - -
 354-3_R10 - - - - -
 354-5_R9 - - - - -
 354-5_R11 - - - - -
 354-5_R12 - - - - -

expected sequence of Eef1a-FLAG-2A-eGFP allele CTGACTACCAGCCATTGGGTCGTTTTGCTGTACGTGACATGAGACAAACTGTTGCTGTTG 1020
 347-10 LHA clone 1 CTGACTACCAGCCATTGGGTCGTTTTGCTGTACGTGACATGAGACAAACTGTTGCTGTTG 1020
 347-10 LHA clone 2 CTGACTACCAGCCATTGGGTCGTTTTGCTGTACGTGACATGAGACAAACTGTTGCTGTTG 1020
 347-10 LHA clone 3 CTGACTACCAGCCATTGGGTCGTTTTGCTGTACGTGACATGAGACAAACTGTTGCTGTTG 1020
 354-3 LHA clone 1 CTGACTACCAGCCATTGGGTCGTTTTGCTGTACGTGACATGAGACAAACTGTTGCTGTTG 1020
 354-3 LHA clone 2 CTGACTACCAGCCATTGGGTCGTTTTGCTGTACGTGACATGAGACAAACTGTTGCTGTTG 1020
 354-3 LHA clone 3 CTGACTACCAGCCATTGGGTCGTTTTGCTGTACGTGACATGAGACAAACTGTTGCTGTTG 1020
 354-5_L5 CTGACTACCAGCCATTGGGTCGTTTTGCTGTACGTGACATGAGACAAACTGTTGCTGTTG 1020
 354-5_L6 CTGACTACCAGCCATTGGGTCGTTTTGCTGTACGTGACATGAGACAAACTGTTGCTGTTG 1020
 354-5_L8 CTGACTACCAGCCATTGGGTCGTTTTGCTGTACGTGACATGAGACAAACTGTTGCTGTTG 1020
 347-10_R5 - - - - -
 347-10_R6 - - - - -
 347-10_R7 - - - - -
 354-3_R1 - - - - -
 354-3_R2 - - - - -
 354-3_R10 - - - - -
 354-5_R9 - - - - -
 354-5_R11 - - - - -
 354-5_R12 - - - - -

expected sequence of Eef1a-FLAG-2A-eGFP allele GAGTTATCAAGAGTGTTGAAAAGGCCGATGCTACTGGTAAAATGACAAAATCAGCTCAAA 1080
 347-10 LHA clone 1 GAGTTATCAAGAGTGTTGAAAAGGCCGATGCTACTGGTAAAATGACAAAATCAGCTCAAA 1080
 347-10 LHA clone 2 GAGTTATCAAGAGTGTTGAAAAGGCCGATGCTACTGGTAAAATGACAAAATCAGCTCAAA 1080
 347-10 LHA clone 3 GAGTTATCAAGAGTGTTGAAAAGGCCGATGCTACTGGTAAAATGACAAAATCAGCTCAAA 1080
 354-3 LHA clone 1 GAGTTATCAAGAGTGTTGAAAAGGCCGATGCTACTGGTAAAATGACAAAATCAGCTCAAA 1080
 354-3 LHA clone 2 GAGTTATCAAGAGTGTTGAAAAGGCCGATGCTACTGGTAAAATGACAAAATCAGCTCAAA 1080
 354-3 LHA clone 3 GAGTTATCAAGAGTGTTGAAAAGGCCGATGCTACTGGTAAAATGACAAAATCAGCTCAAA 1080
 354-5_L5 GAGTTATCAAGAGTGTTGAAAAGGCCGATGCTACTGGTAAAATGACAAAATCAGCTCAAA 1080
 354-5_L6 GAGTTATCAAGAGTGTTGAAAAGGCCGATGCTACTGGTAAAATGACAAAATCAGCTCAAA 1080
 354-5_L8 GAGTTATCAAGAGTGTTGAAAAGGCCGATGCTACTGGTAAAATGACAAAATCAGCTCAAA 1080
 347-10_R5 - - - - -
 347-10_R6 - - - - -
 347-10_R7 - - - - -
 354-3_R1 - - - - -
 354-3_R2 - - - - -
 354-3_R10 - - - - -
 354-5_R9 - - - - -
 354-5_R11 - - - - -
 354-5_R12 - - - - -

expected sequence of Eef1a-FLAG-2A-eGFP allele
 347-10 LHA clone 1
 347-10 LHA clone 2
 347-10 LHA clone3
 354-3 LHA clone 1
 354-3 LHA clone 2
 354-3 LHA clone 3
 354-5_L5
 354-5_L6
 354-5_L8
 347-10_R5
 347-10_R6
 347-10_R7
 354-3_R1
 354-3_R2
 354-3_R10
 354-5_R9
 354-5_R11
 354-5_R12

expected sequence of Eef1a-FLAG-2A-eGFP allele
 347-10 LHA clone 1
 347-10 LHA clone 2
 347-10 LHA clone3
 354-3 LHA clone 1
 354-3 LHA clone 2
 354-3 LHA clone 3
 354-5_L5
 354-5_L6
 354-5_L8
 347-10_R5
 347-10_R6
 347-10_R7
 354-3_R1
 354-3_R2
 354-3_R10
 354-5_R9
 354-5_R11
 354-5_R12



eGFP

1,520 1,540 1,560

expected sequence of Eef1a-FLAG-2A-eGFP allele **GGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCG** 1560

347-10 LHA clone 1 GGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCG 1560

347-10 LHA clone 2 GGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCG 1560

347-10 LHA clone3 GGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCG 1560

354-3 LHA clone 1 GGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCG 1560

354-3 LHA clone 2 GGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCG 1560

354-3 LHA clone 3 GGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCG 1560

354-5_L5 GGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCG 1560

354-5_L6 GGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCG 1560

354-5_L8 GGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCG 1560

347-10_R5 GGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCG 379

347-10_R6 GGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCG 378

347-10_R7 GGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCG 378

354-3_R1 GGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCG 379

354-3_R2 GGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCG 379

354-3_R10 GGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCG 379

354-5_R9 GGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCG 379

354-5_R11 GGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCG 378

354-5_R12 GGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCG 379

eGFP

1,580 1,600 1,620

expected sequence of Eef1a-FLAG-2A-eGFP allele **AGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACA** 1620

347-10 LHA clone 1 AGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACA 1620

347-10 LHA clone 2 AGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACA 1620

347-10 LHA clone3 AGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACA 1620

354-3 LHA clone 1 AGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACA 1620

354-3 LHA clone 2 AGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACA 1620

354-3 LHA clone 3 AGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACA 1620

354-5_L5 AGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACA 1620

354-5_L6 AGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACA 1620

354-5_L8 AGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACA 1620

347-10_R5 AGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACA 439

347-10_R6 AGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACA 438

347-10_R7 AGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACA 438

354-3_R1 AGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACA 439

354-3_R2 AGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACA 439

354-3_R10 AGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACA 439

354-5_R9 AGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACA 439

354-5_R11 AGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACA 438

354-5_R12 AGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACA 439

eGFP

1,640 1,660 1,680

expected sequence of Eef1a-FLAG-2A-eGFP allele **ACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGAATGGAATCAAAGTTA** 1680

347-10 LHA clone 1 ACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGAATGGAATCAAAGTTA 1680

347-10 LHA clone 2 ACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGAATGGAATCAAAGTTA 1680

347-10 LHA clone3 ACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGAATGGAATCAAAGTTA 1680

354-3 LHA clone 1 ACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGAATGGAATCAAAGTTA 1680

354-3 LHA clone 2 ACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGAATGGAATCAAAGTTA 1680

354-3 LHA clone 3 ACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGAATGGAATCAAAGTTA 1680

354-5_L5 ACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGAATGGAATCAAAGTTA 1680

354-5_L6 ACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGAATGGAATCAAAGTTA 1680

354-5_L8 ACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGAATGGAATCAAAGTTA 1680

347-10_R5 ACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGAATGGAATCAAAGTTA 499

347-10_R6 ACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGAATGGAATCAAAGTTA 498

347-10_R7 ACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGAATGGAATCAAAGTTA 498

354-3_R1 ACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGAATGGAATCAAAGTTA 499

354-3_R2 ACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGAATGGAATCAAAGTTA 499

354-3_R10 ACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGAATGGAATCAAAGTTA 499

354-5_R9 ACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGAATGGAATCAAAGTTA 499

354-5_R11 ACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGAATGGAATCAAAGTTA 498

354-5_R12 ACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGAATGGAATCAAAGTTA 499

eGFP

1,700 1,720 1,740

expected sequence of Eef1a-FLAG-2A-eGFP allele **ACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAAC** 1740

347-10 LHA clone 1 ACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAAC 1740

347-10 LHA clone 2 ACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAAC 1740

347-10 LHA clone3 ACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAAC 1740

354-3 LHA clone 1 ACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAAC 1740

354-3 LHA clone 2 ACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAAC 1740

354-3 LHA clone 3 ACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAAC 1740

354-5_L5 ACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAAC 1740

354-5_L6 ACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAAC 1740

354-5_L8 ACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAAC 1740

347-10_R5 ACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAAC 559

347-10_R6 ACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAAC 558

347-10_R7 ACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAAC 558

354-3_R1 ACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAAC 559

354-3_R2 ACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAAC 559

354-3_R10 ACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAAC 559

354-5_R9 ACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAAC 559

354-5_R11 ACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAAC 558

354-5_R12 ACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAAC 559

eGFP

1,760 1,780 1,800

expected sequence of Eef1a-FLAG-2A-eGFP allele **AAAATCTCCAATTGGCGATGGCCCTGTCTTTTACCAGACAACCATTACCTGTCCACAC** 1800

347-10 LHA clone 1 AAAATCTCCAATTGGCGATGGCCCTGTCTTTTACCAGACAACCATTACCTGTCCACAC 1800

347-10 LHA clone 2 AAAATCTCCAATTGGCGATGGCCCTGTCTTTTACCAGACAACCATTACCTGTCCACAC 1800

347-10 LHA clone3 AAAATCTCCAATTGGCGATGGCCCTGTCTTTTACCAGACAACCATTACCTGTCCACAC 1800

354-3 LHA clone 1 AAAATCTCCAATTGGCGATGGCCCTGTCTTTTACCAGACAACCATTACCTGTCCACAC 1800

354-3 LHA clone 2 AAAATCTCCAATTGGCGATGGCCCTGTCTTTTACCAGACAACCATTACCTGTCCACAC 1800

354-3 LHA clone 3 AAAATCTCCAATTGGCGATGGCCCTGTCTTTTACCAGACAACCATTACCTGTCCACAC 1800

354-5_L5 AAAATCTCCAATTGGCGATGGCCCTGTCTTTTACCAGACAACCATTACCTGTCCACAC 1800

354-5_L6 AAAATCTCCAATTGGCGATGGCCCTGTCTTTTACCAGACAACCATTACCTGTCCACAC 1800

354-5_L8 AAAATCTCCAATTGGCGATGGCCCTGTCTTTTACCAGACAACCATTACCTGTCCACAC 1800

347-10_R5 AAAATCTCCAATTGGCGATGGCCCTGTCTTTTACCAGACAACCATTACCTGTCCACAC 619

347-10_R6 AAAATCTCCAATTGGCGATGGCCCTGTCTTTTACCAGACAACCATTACCTGTCCACAC 618

347-10_R7 AAAATCTCCAATTGGCGATGGCCCTGTCTTTTACCAGACAACCATTACCTGTCCACAC 618

354-3_R1 AAAATCTCCAATTGGCGATGGCCCTGTCTTTTACCAGACAACCATTACCTGTCCACAC 619

354-3_R2 AAAATCTCCAATTGGCGATGGCCCTGTCTTTTACCAGACAACCATTACCTGTCCACAC 619

354-3_R10 AAAATCTCCAATTGGCGATGGCCCTGTCTTTTACCAGACAACCATTACCTGTCCACAC 619

354-5_R9 AAAATCTCCAATTGGCGATGGCCCTGTCTTTTACCAGACAACCATTACCTGTCCACAC 619

354-5_R11 AAAATCTCCAATTGGCGATGGCCCTGTCTTTTACCAGACAACCATTACCTGTCCACAC 618

354-5_R12 AAAATCTCCAATTGGCGATGGCCCTGTCTTTTACCAGACAACCATTACCTGTCCACAC 619

eGFP Pr875

1,820 1,840 1,860

expected sequence of Eef1a-FLAG-2A-eGFP allele **AATCTGCCCTTTCGAAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTG** 1860

347-10 LHA clone 1 AATCTGCCCTTTCGAAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTG 1831

347-10 LHA clone 2 AATCTGCCCTTTCGAAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTG 1831

347-10 LHA clone3 AATCTGCCCTTTCGAAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTG 1831

354-3 LHA clone 1 AATCTGCCCTTTCGAAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTG 1831

354-3 LHA clone 2 AATCTGCCCTTTCGAAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTG 1831

354-3 LHA clone 3 AATCTGCCCTTTCGAAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTG 1831

354-5_L5 AATCTGCCCTTTCGAAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTG 1831

354-5_L6 AATCTGCCCTTTCGAAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTG 1831

354-5_L8 AATCTGCCCTTTCGAAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTG 1831

347-10_R5 AATCTGCCCTTTCGAAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTG 679

347-10_R6 AATCTGCCCTTTCGAAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTG 678

347-10_R7 AATCTGCCCTTTCGAAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTG 678

354-3_R1 AATCTGCCCTTTCGAAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTG 679

354-3_R2 AATCTGCCCTTTCGAAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTG 679

354-3_R10 AATCTGCCCTTTCGAAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTG 679

354-5_R9 AATCTGCCCTTTCGAAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTG 679

354-5_R11 AATCTGCCCTTTCGAAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTG 678

354-5_R12 AATCTGCCCTTTCGAAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTG 679

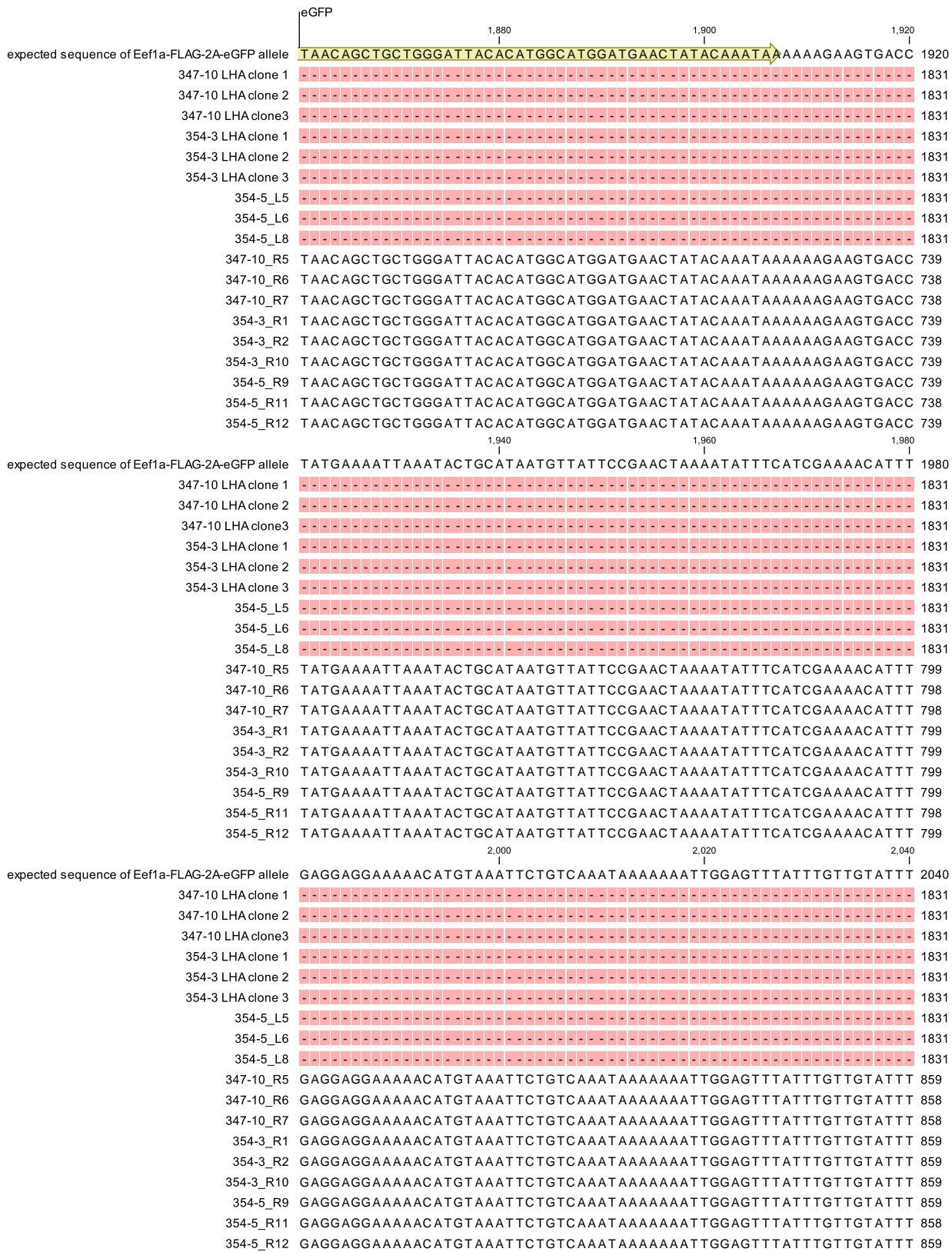


Figure S5 - Page
 12

expected sequence of Eef1a-FLAG-2A-eGFP allele TTTTCACTAAATTAGTGTGGGCAGTGAATTCCATTTAGCTGATTAATAATTCATTTTGCGG 2100
 347-10 LHA clone 1 [redacted] 1831
 347-10 LHA clone 2 [redacted] 1831
 347-10 LHA clone3 [redacted] 1831
 354-3 LHA clone 1 [redacted] 1831
 354-3 LHA clone 2 [redacted] 1831
 354-3 LHA clone 3 [redacted] 1831
 354-5_L5 [redacted] 1831
 354-5_L6 [redacted] 1831
 354-5_L8 [redacted] 1831
 347-10_R5 TTTTCACTAAATTAGTGTGGGCAGTGAATTCCATTTAGCTGATTAATAATTCATTTTGCGG 919
 347-10_R6 TTTTCACTAAATTAGTGTGGGCAGTGAATTCCATTTAGCTGATTAATAATTCATTTTGCGG 918
 347-10_R7 TTTTCACTAAATTAGTGTGGGCAGTGAATTCCATTTAGCTGATTAATAATTCATTTTGCGG 918
 354-3_R1 TTTTCACTAAATTAGTGTGGGCAGTGAATTCCATTTAGCTGATTAATAATTCATTTTGCGG 919
 354-3_R2 TTTTCACTAAATTAGTGTGGGCAGTGAATTCCATTTAGCTGATTAATAATTCATTTTGCGG 919
 354-3_R10 TTTTCACTAAATTAGTGTGGGCAGTGAATTCCATTTAGCTGATTAATAATTCATTTTGCGG 919
 354-5_R9 TTTTCACTAAATTAGTGTGGGCAGTGAATTCCATTTAGCTGATTAATAATTCATTTTGCGG 919
 354-5_R11 TTTTCACTAAATTAGTGTGGGCAGTGAATTCCATTTAGCTGATTAATAATTCATTTTGCGG 918
 354-5_R12 TTTTCACTAAATTAGTGTGGGCAGTGAATTCCATTTAGCTGATTAATAATTCATTTTGCGG 919

expected sequence of Eef1a-FLAG-2A-eGFP allele C TAAATATTGTCCCGATTTGCGGTCACCAATTAATAGTGCGACCTTACAGAAAAATTTTC 2160
 347-10 LHA clone 1 [redacted] 1831
 347-10 LHA clone 2 [redacted] 1831
 347-10 LHA clone3 [redacted] 1831
 354-3 LHA clone 1 [redacted] 1831
 354-3 LHA clone 2 [redacted] 1831
 354-3 LHA clone 3 [redacted] 1831
 354-5_L5 [redacted] 1831
 354-5_L6 [redacted] 1831
 354-5_L8 [redacted] 1831
 347-10_R5 C TAAATATTGTCCCGATTTGCGGTCACCAATTAATAGTGCGACCTTACAGAAAAATTTTC 979
 347-10_R6 C TAAATATTGTCCCGATTTGCGGTCACCAATTAATAGTGCGACCTTACAGAAAAATTTTC 978
 347-10_R7 C TAAATATTGTCCCGATTTGCGGTCACCAATTAATAGTGCGACCTTACAGAAAAATTTTC 978
 354-3_R1 C TAAATATTGTCCCGATTTGCGGTCACCAATTAATAGTGCGACCTTACAGAAAAATTTTC 979
 354-3_R2 C TAAATATTGTCCCGATTTGCGGTCACCAATTAATAGTGCGACCTTACAGAAAAATTTTC 979
 354-3_R10 C TAAATATTGTCCCGATTTGCGGTCACCAATTAATAGTGCGACCTTACAGAAAAATTTTC 979
 354-5_R9 C TAAATATTGTCCCGATTTGCGGTCACCAATTAATAGTGCGACCTTACAGAAAAATTTTC 979
 354-5_R11 C TAAATATTGTCCCGATTTGCGGTCACCAATTAATAGTGCGACCTTACAGAAAAATTTTC 978
 354-5_R12 C TAAATATTGTCCCGATTTGCGGTCACCAATTAATAGTGCGACCTTACAGAAAAATTTTC 979

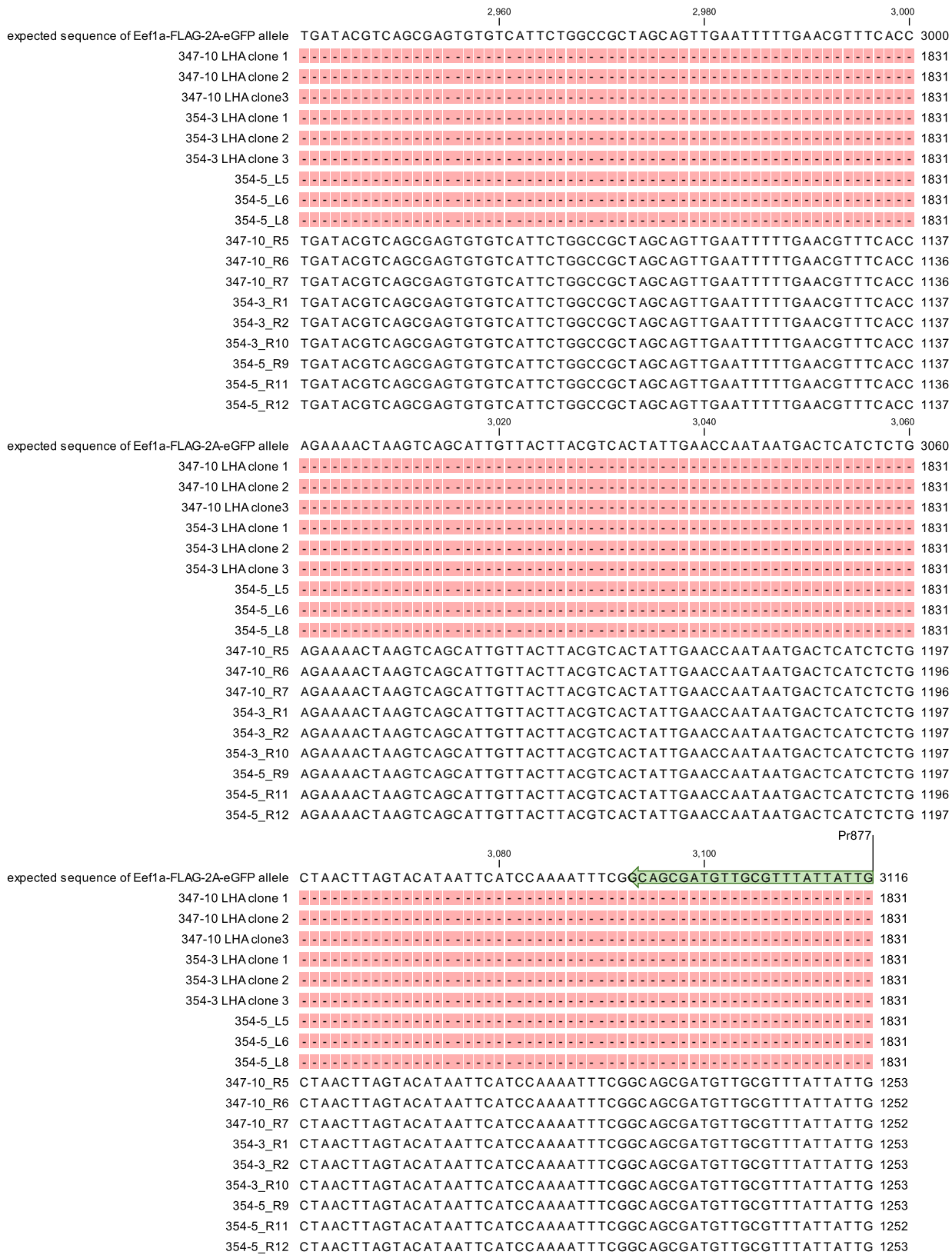
expected sequence of Eef1a-FLAG-2A-eGFP allele TGTCGCGCTAAATTGCAAAATGCACCTGGATAAAAAAGCGCGAAGAAAATAAAGCGG AATT 2220
 347-10 LHA clone 1 [redacted] 1831
 347-10 LHA clone 2 [redacted] 1831
 347-10 LHA clone3 [redacted] 1831
 354-3 LHA clone 1 [redacted] 1831
 354-3 LHA clone 2 [redacted] 1831
 354-3 LHA clone 3 [redacted] 1831
 354-5_L5 [redacted] 1831
 354-5_L6 [redacted] 1831
 354-5_L8 [redacted] 1831
 347-10_R5 TGTCGCGCTAAATTGCAAAATGCACCTGGATAAAAAAGCGCGAAGAAAATAAAGCGG - - - 1035
 347-10_R6 TGTCGCGCTAAATTGCAAAATGCACCTGGATAAAAAAGCGCGAAGAAAATAAAGCGG - - - 1034
 347-10_R7 TGTCGCGCTAAATTGCAAAATGCACCTGGATAAAAAAGCGCGAAGAAAATAAAGCGG - - - 1034
 354-3_R1 TGTCGCGCTAAATTGCAAAATGCACCTGGATAAAAAAGCGCGAAGAAAATAAAGCGG - - - 1035
 354-3_R2 TGTCGCGCTAAATTGCAAAATGCACCTGGATAAAAAAGCGCGAAGAAAATAAAGCGG - - - 1035
 354-3_R10 TGTCGCGCTAAATTGCAAAATGCACCTGGATAAAAAAGCGCGAAGAAAATAAAGCGG - - - 1035
 354-5_R9 TGTCGCGCTAAATTGCAAAATGCACCTGGATAAAAAAGCGCGAAGAAAATAAAGCGG - - - 1035
 354-5_R11 TGTCGCGCTAAATTGCAAAATGCACCTGGATAAAAAAGCGCGAAGAAAATAAAGCGG - - - 1034
 354-5_R12 TGTCGCGCTAAATTGCAAAATGCACCTGGATAAAAAAGCGCGAAGAAAATAAAGCGG - - - 1035

	2,240	2,260	2,280	
expected sequence of Eef1a-FLAG-2A-eGFP allele	AATGTTT GCGAGTGTACTTTCGTATTCGCCCGAAGGTGTTCTATAAAATTTAACTAAGCCT			2280
347-10 LHA clone 1			1831
347-10 LHA clone 2			1831
347-10 LHA clone3			1831
354-3 LHA clone 1			1831
354-3 LHA clone 2			1831
354-3 LHA clone 3			1831
354-5_L5			1831
354-5_L6			1831
354-5_L8			1831
347-10_R5			1035
347-10_R6			1034
347-10_R7			1034
354-3_R1			1035
354-3_R2			1035
354-3_R10			1035
354-5_R9			1035
354-5_R11			1034
354-5_R12			1035
	2,300	2,320	2,340	
expected sequence of Eef1a-FLAG-2A-eGFP allele	TTTTTAAACAAAAACAGACGATATCAATCTTCTTGCATGATACAAAAAATTTAAGCTTA			2340
347-10 LHA clone 1			1831
347-10 LHA clone 2			1831
347-10 LHA clone3			1831
354-3 LHA clone 1			1831
354-3 LHA clone 2			1831
354-3 LHA clone 3			1831
354-5_L5			1831
354-5_L6			1831
354-5_L8			1831
347-10_R5			1035
347-10_R6			1034
347-10_R7			1034
354-3_R1			1035
354-3_R2			1035
354-3_R10			1035
354-5_R9			1035
354-5_R11			1034
354-5_R12			1035
	2,360	2,380	2,400	
expected sequence of Eef1a-FLAG-2A-eGFP allele	GTGTAAATATGGCTTAATGTTTTTAAGTTCGAGTATTTTCAAGTCATTAACGGTGTTTT			2400
347-10 LHA clone 1			1831
347-10 LHA clone 2			1831
347-10 LHA clone3			1831
354-3 LHA clone 1			1831
354-3 LHA clone 2			1831
354-3 LHA clone 3			1831
354-5_L5			1831
354-5_L6			1831
354-5_L8			1831
347-10_R5			1035
347-10_R6			1034
347-10_R7			1034
354-3_R1			1035
354-3_R2			1035
354-3_R10			1035
354-5_R9			1035
354-5_R11			1034
354-5_R12			1035

	2,420	2,440	2,460	
expected sequence of Eef1a-FLAG-2A-eGFP allele	ACTATGTGAATATCAACTGTTTGGCTCACACAATTATCTTCAGTAATAATTTTTACTGCTT			2460
347-10 LHA clone 1	-----			1831
347-10 LHA clone 2	-----			1831
347-10 LHA clone3	-----			1831
354-3 LHA clone 1	-----			1831
354-3 LHA clone 2	-----			1831
354-3 LHA clone 3	-----			1831
354-5_L5	-----			1831
354-5_L6	-----			1831
354-5_L8	-----			1831
347-10_R5	-----			1035
347-10_R6	-----			1034
347-10_R7	-----			1034
354-3_R1	-----			1035
354-3_R2	-----			1035
354-3_R10	-----			1035
354-5_R9	-----			1035
354-5_R11	-----			1034
354-5_R12	-----			1035
	2,480	2,500	2,520	
expected sequence of Eef1a-FLAG-2A-eGFP allele	AATTATGTTTAAAGTTGATGATGATTGCGGTACCGTGTTTGAGTAGCACATCTTGTCTAAT			2520
347-10 LHA clone 1	-----			1831
347-10 LHA clone 2	-----			1831
347-10 LHA clone3	-----			1831
354-3 LHA clone 1	-----			1831
354-3 LHA clone 2	-----			1831
354-3 LHA clone 3	-----			1831
354-5_L5	-----			1831
354-5_L6	-----			1831
354-5_L8	-----			1831
347-10_R5	-----			1035
347-10_R6	-----			1034
347-10_R7	-----			1034
354-3_R1	-----			1035
354-3_R2	-----			1035
354-3_R10	-----			1035
354-5_R9	-----			1035
354-5_R11	-----			1034
354-5_R12	-----			1035
	2,540	2,560	2,580	
expected sequence of Eef1a-FLAG-2A-eGFP allele	AACAGATACCATTTCCTAATTGATGGTAGGCATGCTACCGAACATCAAAACGTTGCTCAC			2580
347-10 LHA clone 1	-----			1831
347-10 LHA clone 2	-----			1831
347-10 LHA clone3	-----			1831
354-3 LHA clone 1	-----			1831
354-3 LHA clone 2	-----			1831
354-3 LHA clone 3	-----			1831
354-5_L5	-----			1831
354-5_L6	-----			1831
354-5_L8	-----			1831
347-10_R5	-----			1035
347-10_R6	-----			1034
347-10_R7	-----			1034
354-3_R1	-----			1035
354-3_R2	-----			1035
354-3_R10	-----			1035
354-5_R9	-----			1035
354-5_R11	-----			1034
354-5_R12	-----			1035

	2,600	2,620	2,640	
expected sequence of Eef1a-FLAG-2A-eGFP allele	ACGTCGGTTATCCAGTTACAAGGCAAGATGTAATAATCGGCCACGGTATTTTCGGTATCCA			2640
347-10 LHA clone 1	-----			1831
347-10 LHA clone 2	-----			1831
347-10 LHA clone3	-----			1831
354-3 LHA clone 1	-----			1831
354-3 LHA clone 2	-----			1831
354-3 LHA clone 3	-----			1831
354-5_L5	-----			1831
354-5_L6	-----			1831
354-5_L8	-----			1831
347-10_R5	-----			1035
347-10_R6	-----			1034
347-10_R7	-----			1034
354-3_R1	-----			1035
354-3_R2	-----			1035
354-3_R10	-----			1035
354-5_R9	-----			1035
354-5_R11	-----			1034
354-5_R12	-----			1035
	2,660	2,680	2,700	
expected sequence of Eef1a-FLAG-2A-eGFP allele	AGAATAAAACGTTGTGTGATTGCGTATATTAGCGAACATGTGCAACAAGATGTTAAAAACA			2700
347-10 LHA clone 1	-----			1831
347-10 LHA clone 2	-----			1831
347-10 LHA clone3	-----			1831
354-3 LHA clone 1	-----			1831
354-3 LHA clone 2	-----			1831
354-3 LHA clone 3	-----			1831
354-5_L5	-----			1831
354-5_L6	-----			1831
354-5_L8	-----			1831
347-10_R5	-----			1035
347-10_R6	-----			1034
347-10_R7	-----			1034
354-3_R1	-----			1035
354-3_R2	-----			1035
354-3_R10	-----			1035
354-5_R9	-----			1035
354-5_R11	-----			1034
354-5_R12	-----			1035
	2,720	2,740	2,760	
expected sequence of Eef1a-FLAG-2A-eGFP allele	CCTGTTAACTAATAGTCGTTACCATAGTGACTAATATTAATGCAAAATGTAAAAGAATTCC			2760
347-10 LHA clone 1	-----			1831
347-10 LHA clone 2	-----			1831
347-10 LHA clone3	-----			1831
354-3 LHA clone 1	-----			1831
354-3 LHA clone 2	-----			1831
354-3 LHA clone 3	-----			1831
354-5_L5	-----			1831
354-5_L6	-----			1831
354-5_L8	-----			1831
347-10_R5	-----			1035
347-10_R6	-----			1034
347-10_R7	-----			1034
354-3_R1	-----			1035
354-3_R2	-----			1035
354-3_R10	-----			1035
354-5_R9	-----			1035
354-5_R11	-----			1034
354-5_R12	-----			1035

		2,780		2,800		2,820	
expected sequence of Eef1a-FLAG-2A-eGFP allele	GTAAAAAACTTTCAAAGTTCATTTTTAGGAGAGTTATTTGACAAAAACATAATTTTTGCAA						2820
347-10 LHA clone 1						1831
347-10 LHA clone 2						1831
347-10 LHA clone3						1831
354-3 LHA clone 1						1831
354-3 LHA clone 2						1831
354-3 LHA clone 3						1831
354-5_L5						1831
354-5_L6						1831
354-5_L8						1831
347-10_R5						1035
347-10_R6						1034
347-10_R7						1034
354-3_R1						1035
354-3_R2						1035
354-3_R10						1035
354-5_R9						1035
354-5_R11						1034
354-5_R12						1035
		2,840		2,860		2,880	
expected sequence of Eef1a-FLAG-2A-eGFP allele	TTAATTATTCTTACGCTTCATTGAAGATCATACTTAATAATTTTTTTAATAGTAATTATT						2880
347-10 LHA clone 1						1831
347-10 LHA clone 2						1831
347-10 LHA clone3						1831
354-3 LHA clone 1						1831
354-3 LHA clone 2						1831
354-3 LHA clone 3						1831
354-5_L5						1831
354-5_L6						1831
354-5_L8						1831
347-10_R5						1035
347-10_R6						1034
347-10_R7						1034
354-3_R1						1035
354-3_R2						1035
354-3_R10						1035
354-5_R9						1035
354-5_R11						1034
354-5_R12						1035
		2,900		2,920		2,940	
expected sequence of Eef1a-FLAG-2A-eGFP allele	AGTTATTCTTGAAAATTGGTGTGGACACTCAAACGCGTGAATGCCCTCTATTTTTGC						2940
347-10 LHA clone 1						1831
347-10 LHA clone 2						1831
347-10 LHA clone3						1831
354-3 LHA clone 1						1831
354-3 LHA clone 2						1831
354-3 LHA clone 3						1831
354-5_L5						1831
354-5_L6						1831
354-5_L8						1831
347-10_R5						1077
347-10_R6						1076
347-10_R7						1076
354-3_R1						1077
354-3_R2						1077
354-3_R10						1077
354-5_R9						1077
354-5_R11						1076
354-5_R12						1077



S5 Fig. Alignment of upstream and downstream integration sites from *Eef1a*^{FLAG-P2A-eGFP} colonies.

Nucleotide alignment of the regions encoding the up- and downstream integration sites from the founder colony, 347-10, and two transgenic offspring, 354-3 and 354-5. Three cloned amplicons were sequenced for each animal at each site. Primer binding sites are indicated in green on the expected sequence. Differences are highlighted in red boxes. Note that the regions that do not overlap between the upstream and downstream sequences are shown as gaps at the beginning and end of the alignment.