```
                                    Pr845
                                                      20                  40                  60
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom GTAGAAACTGGTGTATTGTCCCCTGGTATGATCGTTACATTTGCCCCTGCCAATGTAACC 60
                          350-10_c2 GTAGAAACTGGTGTATTGTCCCCTGGTATGATCGTTACATTTGCCCCTGCCAATGTAACC 60
                          350-10_c3 GTAGAAACTGGTGTATTGTCCCCTGGTATGATCGTTACATTTGCCCCTGCCAATGTAACC 60
                          350-10_c5 GTAGAAACTGGTGTATTGTCCCCTGGTATGATCGTTACATTTGCCCCTGCCAATGTAACC 60
                          355-8_c11 GTAGAAACTGGTGTATTGTCCCCTGGTATGATCGTTACATTTGCCCCTGCCAATGTAACC 60
                          355-8_c13 GTAGAAACTGGTGTATTGTCCCCTGGTATGATCGTTACATTTGCCCCTGCCAATGTAACC 60
                          355-8_c14 GTAGAAACTGGTGTATTGTCCCCTGGTATGATCGTTACATTTGCCCCTGCCAATGTAACC 60
                                                      80                 100                 120
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom ACTGAGGTCAAATCTGTAGAAATGCACCACGAATCCTTAACTGAAGCACATCCAGGTGAT 120
                          350-10_c2 ACTGAGGTCAAATCTGTAGAAATGCACCACGAATCCTTAACTGAAGCACATCCAGGTGAT 120
                          350-10_c3 ACTGAGGTCAAATCTGTAGAAATGCACCACGAATCCTTAACTGAAGCACATCCAGGTGAT 120
                          350-10_c5 ACTGAGGTCAAATCTGTAGAAATGCACCACGAATCCTTAACTGAAGCACATCCAGGTGAT 120
                          355-8_c11 ACTGAGGTCAAATCTGTAGAAATGCACCACGAATCCTTAACTGAAGCACATCCAGGTGAT 120
                          355-8_c13 ACTGAGGTCAAATCTGTAGAAATGCACCACGAATCCTTAACTGAAGCACATCCAGGTGAT 120
                          355-8_c14 ACTGAGGTCAAATCTGTAGAAATGCACCACGAATCCTTAACTGAAGCACATCCAGGTGAT 120
                                                     140                 160                 180
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom AATGTTGGTTTTAATGTCAAAAATGTGTCTATCAAGGATATCAAACGTGGTATGGTTGCG 180
                          350-10_c2 AATGTTGGTTTTAATGTCAAAAATGTGTCTATCAAGGATATCAAACGTGGTATGGTTGCG 180
                          350-10_c3 AATGTTGGTTTTAATGTCAAAAATGTGTCTATCAAGGATATCAAACGTGGTATGGTTGCG 180
                          350-10_c5 AATGTTGGTTTTAATGTCAAAAATGTGTCTATCAAGGATATCAAACGTGGTATGGTTGCG 180
                          355-8_c11 AATGTTGGTTTTAATGTCAAAAATGTGTCTATCAAGGATATCAAACGTGGTATGGTTGCG 180
                          355-8_c13 AATGTTGGTTTTAATGTCAAAAATGTGTCTATCAAGGATATCAAACGTGGTATGGTTGCG 180
                          355-8_c14 AATGTTGGTTTTAATGTCAAAAATGTGTCTATCAAGGATATCAAACGTGGTATGGTTGCG 180
                                                     200                 220                 240
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom TCTGACAGCAAAAATGATCCAGCCAAAGAAGCCAAAACCTTTTATGCACAGGTATTCTTT 240
                          350-10_c2 TCTGACAGCAAAAATGATCCAGCCAAAGAAGCCAAAACCTTTTATGCACAGGTATTCTTT 240
                          350-10_c3 TCTGACAGCAAAAATGATCCAGCCAAAGAAGCCAAAACCTTTTATGCACAGGTATTCTTT 240
                          350-10_c5 TCTGACAGCAAAAATGATCCAGCCAAAGAAGCCAAAACCTTTTATGCACAGGTATTCTTT 240
                          355-8_c11 TCTGACAGCAAAAATGATCCAGCCAAAGAAGCCAAAACCTTTTATGCACAGGTATTCTTT 240
                          355-8_c13 TCTGACAGCAAAAATGATCCAGCCAAAGAAGCCAAAACCTTTTATGCACAGGTATTCTTT 240
                          355-8_c14 TCTGACAGCAAAAATGATCCAGCCAAAGAAGCCAAAACCTTTTATGCACAGGTATTCTTT 240
                                                     260                 280                 300
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom AATTTTTGTACTTAACTTATCAGTTTGTATAAGCGTGTTGGCCGTGGCTTGCCACTTGCT 300
                          350-10_c2 AATTTTTGTACTTAACTTATCAGTTTGTATAAGCGTGTTGGCCGTGGCTTGCCACTTGCT 300
                          350-10_c3 AATTTTTGTACTTAACTTATCAGTTTGTATAAGCGTGTTGGCCGTGGCTTGCCACTTGCT 300
                          350-10_c5 AATTTTTGTACTTAACTTATCAGTTTGTATAAGCGTGTTGGCCGTGGCTTGCCACTTGCT 300
                          355-8_c11 AATTTTTGTACTTAACTTATCAGTTTGTATAAGCGTGTTGGCCGTGGCTTGCCACTTGCT 300
                          355-8_c13 AATTTTTGTACTTAACTTATCAGTTTGTATAAGCGTGTTGGCCGTGGCTTGCCACTTGCT 300
                          355-8_c14 AATTTTTGTACTTAACTTATCAGTTTGTATAAGCGTGTTGGCCGTGGCTTGCCACTTGCT 300
                                                     320                 340                 360
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom TAGCATGATAAATCAATCAACTTGACATTCCATCAATTTTGTTCAACAGAAACAGGACCT 360
                          350-10_c2 TAGCATGATAAATCAATCAACTTGACATTCCATCAATTTTGTTCAACAGAAACAGGACCT 360
                          350-10_c3 TAGCATGATAAATCAATCAACTTGACATTCCATCAATTTTGTTCAACAGAAACAGGACCT 360
                          350-10_c5 TAGCATGATAAATCAATCAACTTGACATTCCATCAATTTTGTTCAACAGAAACAGGACCT 360
                          355-8_c11 TAGCATGATAAATCAATCAACTTGACATTCCATCAATTTTGTTCAACAGAAACAGGACCT 360
                          355-8_c13 TAGCATGATAAATCAATCAACTTGACATTCCATCAATTTTGTTCAACAGAAACAGGACCT 360
                          355-8_c14 TAGCATGATAAATCAATCAACTTGACATTCCATCAATTTTGTTCAACAGAAACAGGACCT 360
                                                     380                 400                 420
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom TTAAATAGCAAACAAAATATTGAAATAAAACTGTATGATTTTGTCACTATCGTTTATGTG 420
                          350-10_c2 TTAAATAGCAAACAAAATATTGAAATAAAACTGTATGATTTTGTCACTATCGTTTATGTG 420
                          350-10_c3 TTAAATAGCAAACAAAATATTGAAATAAAACTGTATGATTTTGTCACTATCGTTTATGTG 420
                          350-10_c5 TTAAATAGCAAACAAAATATTGAAATAAAACTGTATGATTTTGTCACTATCGTTTATGTG 420
                          355-8_c11 TTAAATAGCAAACAAAATATTGAAATAAAACTGTATGATTTTGTCACTATCGTTTATGTG 420
                          355-8_c13 TTAAATAGCAAACAAAATATTGAAATAAAACTGTATGATTTTGTCACTATCGTTTATGTG 420
                          355-8_c14 TTAAATAGCAAACAAAATATTGAAATAAAACTGTATGATTTTGTCACTATCGTTTATGTG 420
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                                                       440                 460                 480
                                                        |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom  CCCACCATGAAAATTTTACAAAGAAGTGGAACTGTTTGAAAGTTCATTAGCAAGAACAAA 480
                          350-10_c2  CCCACCATGAAAATTTTACAAAGAAGTGGAACTGTTTGAAAGTTCATTAGCAAGAACAAA 480
                          350-10_c3  CCCACCATGAAAATTTTACAAAGAAGTGGAACTGTTTGAAAGTTCATTAGCAAGAACAAA 480
                          350-10_c5  CCCACCATGAAAATTTTACAAAGAAGTGGAACTGTTTGAAAGTTCATTAGCAAGAACAAA 480
                          355-8_c11  CCCACCATGAAAATTTTACAAAGAAGTGGAACTGTTTGAAAGTTCATTAGCAAGAACAAA 480
                          355-8_c13  CCCACCATGAAAATTTTACAAAGAAGTGGAACTGTTTGAAAGTTCATTAGCAAGAACAAA 480
                          355-8_c14  CCCACCATGAAAATTTTACAAAGAAGTGGAACTGTTTGAAAGTTCATTAGCAAGAACAAA 480
                                                       500                 520                 540
                                                        |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom  TCCTAGAAATGTTAGATTTGTGTCAAGAATTTCAAGATTTTTGTTTCTTGGCAAGTTTTT 540
                          350-10_c2  TCCTAGAAATGTTAGATTTGTGTCAAGAATTTCAAGATTTTTGTTTCTTGGCAAGTTTTT 540
                          350-10_c3  TCCTAGAAATGTTAGATTTGTGTCAAGAATTTCAAGATTTTTGTTTCTTGGCAAGTTTTT 540
                          350-10_c5  TCCTAGAAATGTTAGATTTGTGTCAAGAATTTCAAGATTTTTGTTTCTTGGCAAGTTTTT 540
                          355-8_c11  TCCTAGAAATGTTAGATTTGTGTCAAGAATTTCAAGATTTTTGTTTCTTGGCAAGTTTTT 540
                          355-8_c13  TCCTAGAAATGTTAGATTTGTGTCAAGAATTTCAAGATTTTTGTTTCTTGGCAAGTTTTT 540
                          355-8_c14  TCCTAGAAATGTTAGATTTGTGTCAAGAATTTCAAGATTTTTGTTTCTTGGCAAGTTTTT 540
                                                       560                 580                 600
                                                        |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom  AGCACTTGCTTAGGGAACTATTTAAAATATTAATTTTTATTGAATAAAGAACCAACCTGT 600
                          350-10_c2  AGCACTTGCTTAGGGAACTATTTAAAATATTAATTTTTATTGAATAAAGAACCAACCTGT 600
                          350-10_c3  AGCACTTGCTTAGGGAACTATTTAAAATATTAATTTTTATTGAATAAAGAACCAACCTGT 600
                          350-10_c5  AGCACTTGCTTAGGGAACTATTTAAAATATTAATTTTTATTGAATAAAGAACCAACCTGT 600
                          355-8_c11  AGCACTTGCTTAGGGAACTATTTAAAATATTAATTTTTATTGAATAAAGAACCAACCTGT 600
                          355-8_c13  AGCACTTGCTTAGGGAACTATTTAAAATATTAATTTTTATTGAATAAAGAACCAACCTGT 600
                          355-8_c14  AGCACTTGCTTAGGGAACTATTTAAAATATTAATTTTTATTGAATAAAGAACCAACCTGT 600
                                                       620                 640                 660
                                                        |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom  TTGACTTTTATTAGTAATAAAGCTAAAATTATGGCCTAAATCATAATTTATTATGTGATT 660
                          350-10_c2  TTGACTTTTATTAGTAATAAAGCTAAAATTATGGCCTAAATCATAATTTATTATGTGATT 660
                          350-10_c3  TTGACTTTTATTAGTAATAAAGCTAAAATTATGGCCTAAATCATAATTTATTATGTGATT 660
                          350-10_c5  TTGACTTTTATTAGTAATAAAGCTAAAATTATGGCCTAAATCATAATTTATTATGTGATT 660
                          355-8_c11  TTGACTTTTATTAGTAATAAAGCTAAAATTATGGCCTAAATCATAATTTATTATGTGATT 660
                          355-8_c13  TTGACTTTTATTAGTAATAAAGCTAAAATTATGGCCTAAATCATAATTTATTATGTGATT 660
                          355-8_c14  TTGACTTTTATTAGTAATAAAGCTAAAATTATGGCCTAAATCATAATTTATTATGTGATT 660
                                                       680                 700                 720
                                                        |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom  TGGGAAAGAAATTTGTGTTGATTTTTCCATTAATATTGTAAAAACAAAATCGAAAGTTAA 720
                          350-10_c2  TGGGAAAGAAATTTGTGTTGATTTTTCCATTAATATTGTAAAAACAAAATCGAAAGTTAA 720
                          350-10_c3  TGGGAAAGAAATTTGTGTTGATTTTTCCATTAATATTGTAAAAACAAAATCGAAAGTTAA 720
                          350-10_c5  TGGGAAAGAAATTTGTGTTGATTTTTCCATTAATATTGTAAAAACAAAATCGAAAGTTAA 720
                          355-8_c11  TGGGAAAGAAATTTGTGTTGATTTTTCCATTAATATTGTAAAAACAAAATCGAAAGTTAA 720
                          355-8_c13  TGGGAAAGAAATTTGTGTTGATTTTTCCATTAATATTGTAAAAACAAAATCGAAAGTTAA 720
                          355-8_c14  TGGGAAAGAAATTTGTGTTGATTTTTCCATTAATATTGTAAAAACAAAATCGAAAGTTAA 720
                                                       740                 760                 780
                                                        |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom  TTTCTTTCAAAAATTACTTTTAGGTCATCATTCTCAATCATCCAGGTGAGATTCATGCTG 780
                          350-10_c2  TTTCTTTCAAAAATTACTTTTAGGTCATCATTCTCAATCATCCAGGTGAGATTCATGCTG 780
                          350-10_c3  TTTCTTTCAAAAATTACTTTTAGGTCATCATTCTCAATCATCCAGGTGAGATTCATGCTG 780
                          350-10_c5  TTTCTTTCAAAAATTACTTTTAGGTCATCATTCTCAATCATCCAGGTGAGATTCATGCTG 780
                          355-8_c11  TTTCTTTCAAAAATTACTTTTAGGTCATCATTCTCAATCATCCAGGTGAGATTCATGCTG 780
                          355-8_c13  TTTCTTTCAAAAATTACTTTTAGGTCATCATTCTCAATCATCCAGGTGAGATTCATGCTG 780
                          355-8_c14  TTTCTTTCAAAAATTACTTTTAGGTCATCATTCTCAATCATCCAGGTGAGATTCATGCTG 780
                                                       800                 820                 840
                                                        |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom  GTTACCAACCTGTTTTGGATTGCCACACTGCTCACGTTGCCTGCAAATTTACAGAATTAA 840
                          350-10_c2  GTTACCAACCTGTTTTGGATTGCCACACTGCTCACGTTGCCTGCAAATTTACAGAATTAA 840
                          350-10_c3  GTTACCAACCTGTTTTGGATTGCCACACTGCTCACGTTGCCTGCAAATTTACAGAATTAA 840
                          350-10_c5  GTTACCAACCTGTTTTGGATTGCCACACTGCTCACGTTGCCTGCAAATTTACAGAATTAA 840
                          355-8_c11  GTTACCAACCTGTTTTGGATTGCCACACTGCTCACGTTGCCTGCAAATTTACAGAATTAA 840
                          355-8_c13  GTTACCAACCTGTTTTGGATTGCCACACTGCTCACGTTGCCTGCAAATTTACAGAATTAA 840
                          355-8_c14  GTTACCAACCTGTTTTGGATTGCCACACTGCTCACGTTGCCTGCAAATTTACAGAATTAA 840
                                                       860                 880                 900
                                                        |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom  AGCAGAAATGTGATAGACGAAGTGGTAAAGTTTTAGAAGAAAATCCCAAAATGGTTAAAT 900
                          350-10_c2  AGCAGAAATGTGATAGACGAAGTGGTAAAGTTTTAGAAGAAAATCCCAAAATGGTTAAAT 900
                          350-10_c3  AGCAGAAATGTGATAGACGAAGTGGTAAAGTTTTAGAAGAAAATCCCAAAATGGTTAAAT 900
                          350-10_c5  AGCAGAAATGTGATAGACGAAGTGGTAAAGTTTTAGAAGAAAATCCCAAAATGGTTAAAT 900
                          355-8_c11  AGCAGAAATGTGATAGACGAAGTGGTAAAGTTTTAGAAGAAAATCCCAAAATGGTTAAAT 900
                          355-8_c13  AGCAGAAATGTGATAGACGAAGTGGTAAAGTTTTAGAAGAAAATCCCAAAATGGTTAAAT 900
                          355-8_c14  AGCAGAAATGTGATAGACGAAGTGGTAAAGTTTTAGAAGAAAATCCCAAAATGGTTAAAT 900
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                                                      920                 940                 960
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom CTGGTGATGCTGCTATGGTTACTTTGACTCCTTCTAAGCCTATGTGTGTTGAAGCTTTCT 960
                          350-10_c2 CTGGTGATGCTGCTATGGTTACTTTGACTCCTTCTAAGCCTATGTGTGTTGAAGCTTTCT 960
                          350-10_c3 CTGGTGATGCTGCTATGGTTACTTTGACTCCTTCTAAGCCTATGTGTGTTGAAGCTTTCT 960
                          350-10_c5 CTGGTGATGCTGCTATGGTTACTTTGACTCCTTCTAAGCCTATGTGTGTTGAAGCTTTCT 960
                          355-8_c11 CTGGTGATGCTGCTATGGTTACTTTGACTCCTTCTAAGCCTATGTGTGTTGAAGCTTTCT 960
                          355-8_c13 CTGGTGATGCTGCTATGGTTACTTTGACTCCTTCTAAGCCTATGTGTGTTGAAGCTTTCT 960
                          355-8_c14 CTGGTGATGCTGCTATGGTTACTTTGACTCCTTCTAAGCCTATGTGTGTTGAAGCTTTCT 960
                                                      980                1,000               1,020
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom CTGACTACCAGCCATTGGGTCGTTTTGCTGTACGTGACATGAGACAAACTGTTGCTGTTG 1020
                          350-10_c2 CTGACTACCAGCCATTGGGTCGTTTTGCTGTACGTGACATGAGACAAACTGTTGCTGTTG 1020
                          350-10_c3 CTGACTACCAGCCATTGGGTCGTTTTGCTGTACGTGACATGAGACAAACTGTTGCTGTTG 1020
                          350-10_c5 CTGACTACCAGCCATTGGGTCGTTTTGCTGTACGTGACATGAGACAAACTGTTGCTGTTG 1020
                          355-8_c11 CTGACTACCAGCCATTGGGTCGTTTTGCTGTACGTGACATGAGACAAACTGTTGCTGTTG 1020
                          355-8_c13 CTGACTACCAGCCATTGGGTCGTTTTGCTGTACGTGACATGAGACAAACTGTTGCTGTTG 1020
                          355-8_c14 CTGACTACCAGCCATTGGGTCGTTTTGCTGTACGTGACATGAGACAAACTGTTGCTGTTG 1020
                                                     1,040               1,060               1,080
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom GAGTTATCAAGAGTGTTGAAAAGGCCGATGCTACTGGTAAAATGACAAAATCAGCTCAAA 1080
                          350-10_c2 GAGTTATCAAGAGTGTTGAAAAGGCCGATGCTACTGGTAAAATGACAAAATCAGCTCAAA 1080
                          350-10_c3 GAGTTATCAAGAGTGTTGAAAAGGCCGATGCTACTGGTAAAATGACAAAATCAGCTCAAA 1080
                          350-10_c5 GAGTTATCAAGAGTGTTGAAAAGGCCGATGCTACTGGTAAAATGACAAAATCAGCTCAAA 1080
                          355-8_c11 GAGTTATCAAGAGTGTTGAAAAGGCCGATGCTACTGGTAAAATGACAAAATCAGCTCAAA 1080
                          355-8_c13 GAGTTATCAAGAGTGTTGAAAAGGCCGATGCTACTGGTAAAATGACAAAATCAGCTCAAA 1080
                          355-8_c14 GAGTTATCAAGAGTGTTGAAAAGGCCGATGCTACTGGTAAAATGACAAAATCAGCTCAAA 1080
                                                     1,100               1,120               1,140
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom AGGCTACCGGAAAGAAAAAATGGTCACATCCACAATTTGAAAAAGGTGGAGGTTCAGGAG 1140
                          350-10_c2 AGGCTACCGGAAAGAAAAAATGGTCACATCCACAATTTGAAAAAGGTGGAGGTTCAGGAG 1140
                          350-10_c3 AGGCTACCGGAAAGAAAAAATGGTCACATCCACAATTTGAAAAAGGTGGAGGTTCAGGAG 1140
                          350-10_c5 AGGCTACCGGAAAGAAAAAATGGTCACATCCACAATTTGAAAAAGGTGGAGGTTCAGGAG 1140
                          355-8_c11 AGGCTACCGGAAAGAAAAAATGGTCACATCCACAATTTGAAAAAGGTGGAGGTTCAGGAG 1140
                          355-8_c13 AGGCTACCGGAAAGAAAAAATGGTCACATCCACAATTTGAAAAAGGTGGAGGTTCAGGAG 1140
                          355-8_c14 AGGCTACCGGAAAGAAAAAATGGTCACATCCACAATTTGAAAAAGGTGGAGGTTCAGGAG 1140
                                                     1,160               1,180               1,200
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom GTGGATCAGGTGGAGGTTCATGGAGCCATCCACAATTTGAAAAAGGTGCTAGTGGAGAAG 1200
                          350-10_c2 GTGGATCAGGTGGAGGTTCATGGAGCCATCCACAATTTGAAAAAGGTGCTAGTGGAGAAG 1200
                          350-10_c3 GTGGATCAGGTGGAGGTTCATGGAGCCATCCACAATTTGAAAAAGGTGCTAGTGGAGAAG 1200
                          350-10_c5 GTGGATCAGGTGGAGGTTCATGGAGCCATCCACAATTTGAAAAAGGTGCTAGTGGAGAAG 1200
                          355-8_c11 GTGGATCAGGTGGAGGTTCATGGAGCCATCCACAATTTGAAAAAGGTGCTAGTGGAGAAG 1200
                          355-8_c13 GTGGATCAGGTGGAGGTTCATGGAGCCATCCACAATTTGAAAAAGGTGCTAGTGGAGAAG 1200
                          355-8_c14 GTGGATCAGGTGGAGGTTCATGGAGCCATCCACAATTTGAAAAAGGTGCTAGTGGAGAAG 1200
                                                     1,220               1,240               1,260
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom ATTATAAAGATGATGATGATAAAGGTTCAGGTGCTACAAATTTTTCATTATTAAAACAAG 1260
                          350-10_c2 ATTATAAAGATGATGATGATAAAGGTTCAGGTGCTACAAATTTTTCATTATTAAAACAAG 1260
                          350-10_c3 ATTATAAAGATGATGATGATAAAGGTTCAGGTGCTACAAATTTTTCATTATTAAAACAAG 1260
                          350-10_c5 ATTATAAAGATGATGATGATAAAGGTTCAGGTGCTACAAATTTTTCATTATTAAAACAAG 1260
                          355-8_c11 ATTATAAAGATGATGATGATAAAGGTTCAGGTGCTACAAATTTTTCATTATTAAAACAAG 1260
                          355-8_c13 ATTATAAAGATGATGATGATAAAGGTTCAGGTGCTACAAATTTTTCATTATTAAAACAAG 1260
                          355-8_c14 ATTATAAAGATGATGATGATAAAGGTTCAGGTGCTACAAATTTTTCATTATTAAAACAAG 1260
                                                     1,280               1,300               1,320
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom CTGGTGATGTTGAAGAAAATCCAGGTCCAATGACTTCCAAAGGTGAAGAGGTTATCAAAG 1320
                          350-10_c2 CTGGTGATGTTGAAGAAAATCCAGGTCCAATGACTTCCAAAGGTGAAGAGGTTATCAAAG 1320
                          350-10_c3 CTGGTGATGTTGAAGAAAATCCAGGTCCAATGACTTCCAAAGGTGAAGAGGTTATCAAAG 1320
                          350-10_c5 CTGGTGATGTTGAAGAAAATCCAGGTCCAATGACTTCCAAAGGTGAAGAGGTTATCAAAG 1320
                          355-8_c11 CTGGTGATGTTGAAGAAAATCCAGGTCCAATGACTTCCAAAGGTGAAGAGGTTATCAAAG 1320
                          355-8_c13 CTGGTGATGTTGAAGAAAATCCAGGTCCAATGACTTCCAAAGGTGAAGAGGTTATCAAAG 1320
                          355-8_c14 CTGGTGATGTTGAAGAAAATCCAGGTCCAATGACTTCCAAAGGTGAAGAGGTTATCAAAG 1320
                                                     1,340               1,360               1,380
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom AATTTATGCGTTTCAAAGTTCGAATGGAAGGGAGTATGAATGGACATGAGTTTGAGATAG 1380
                          350-10_c2 AATTTATGCGTTTCAAAGTTCGAATGGAAGGGAGTATGAATGGACATGAGTTTGAGATAG 1380
                          350-10_c3 AATTTATGCGTTTCAAAGTTCGAATGGAAGGGAGTATGAATGGACATGAGTTTGAGATAG 1380
                          350-10_c5 AATTTATGCGTTTCAAAGTTCGAATGGAAGGGAGTATGAATGGACATGAGTTTGAGATAG 1380
                          355-8_c11 AATTTATGCGTTTCAAAGTTCGAATGGAAGGGAGTATGAATGGACATGAGTTTGAGATAG 1380
                          355-8_c13 AATTTATGCGTTTCAAAGTTCGAATGGAAGGGAGTATGAATGGACATGAGTTTGAGATAG 1380
                          355-8_c14 AATTTATGCGTTTCAAAGTTCGAATGGAAGGGAGTATGAATGGACATGAGTTTGAGATAG 1380
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                                                     1,400               1,420               1,440
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom AAGGAGAAGGGGAAGGTAGACCCTATGAAGGCACTCAAACGGCTAAGTTAAAAGTTACAA 1440
                          350-10_c2 AAGGAGAAGGGGAAGGTAGACCCTATGAAGGCACTCAAACGGCTAAGTTAAAAGTTACAA 1440
                          350-10_c3 AAGGAGAAGGGGAAGGTAGACCCTATGAAGGCACTCAAACGGCTAAGTTAAAAGTTACAA 1440
                          350-10_c5 AAGGAGAAGGGGAAGGTAGACCCTATGAAGGCACTCAAACGGCTAAGTTAAAAGTTACAA 1440
                          355-8_c11 AAGGAGAAGGGGAAGGTAGACCCTATGAAGGCACTCAAACGGCTAAGTTAAAAGTTACAA 1440
                          355-8_c13 AAGGAGAAGGGGAAGGTAGACCCTATGAAGGCACTCAAACGGCTAAGTTAAAAGTTACAA 1440
                          355-8_c14 AAGGAGAAGGGGAAGGTAGACCCTATGAAGGCACTCAAACGGCTAAGTTAAAAGTTACAA 1440
                                                     1,460               1,480               1,500
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom AGGGAGGTCCACTGCCATTTGCTTGGGATATTTTGTCTCCTCAATTCATGTATGGTTCGA 1500
                          350-10_c2 AGGGAGGTCCACTGCCATTTGCTTGGGATATTTTGTCTCCTCAATTCATGTATGGTTCGA 1500
                          350-10_c3 AGGGAGGTCCACTGCCATTTGCTTGGGATATTTTGTCTCCTCAATTCATGTATGGTTCGA 1500
                          350-10_c5 AGGGAGGTCCACTGCCATTTGCTTGGGATATTTTGTCTCCTCAATTCATGTATGGTTCGA 1500
                          355-8_c11 AGGGAGGTCCACTGCCATTTGCTTGGGATATTTTGTCTCCTCAATTCATGTATGGTTCGA 1500
                          355-8_c13 AGGGAGGTCCACTGCCATTTGCTTGGGATATTTTGTCTCCTCAATTCATGTATGGTTCGA 1500
                          355-8_c14 AGGGAGGTCCACTGCCATTTGCTTGGGATATTTTGTCTCCTCAATTCATGTATGGTTCGA 1500
                                                     1,520               1,540               1,560
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom AAGCATACGTTAAACACCCTGCAGATATTCCGGACTATAAGAAGTTATCGTTTCCAGAAG 1560
                          350-10_c2 AAGCATACGTTAAACACCCTGCAGATATTCCGGACTATAAGAAGTTATCGTTTCCAGAAG 1560
                          350-10_c3 AAGCATACGTTAAACACCCTGCAGATATTCCGGACTATAAGAAGTTATCGTTTCCAGAAG 1560
                          350-10_c5 AAGCATACGTTAAACACCCTGCAGATATTCCGGACTATAAGAAGTTATCGTTTCCAGAAG 1560
                          355-8_c11 AAGCATACGTTAAACACCCTGCAGATATTCCGGACTATAAGAAGTTATCGTTTCCAGAAG 1560
                          355-8_c13 AAGCATACGTTAAACACCCTGCAGATATTCCGGACTATAAGAAGTTATCGTTTCCAGAAG 1560
                          355-8_c14 AAGCATACGTTAAACACCCTGCAGATATTCCGGACTATAAGAAGTTATCGTTTCCAGAAG 1560
                                                     1,580               1,600               1,620
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom GTTTTAAATGGGAACGCGTTATGAACTTCGAAGATGGTGGGTTAGTAACAGTAACACAGG 1620
                          350-10_c2 GTTTTAAATGGGAACGCGTTATGAACTTCGAAGATGGTGGGTTAGTAACAGTAACACAGG 1620
                          350-10_c3 GTTTTAAATGGGAACGCGTTATGAACTTCGAAGATGGTGGGTTAGTAACAGTAACACAGG 1620
                          350-10_c5 GTTTTAAATGGGAACGCGTTATGAACTTCGAAGATGGTGGGTTAGTAACAGTAACACAGG 1620
                          355-8_c11 GTTTTAAATGGGAACGCGTTATGAACTTCGAAGATGGTGGGTTAGTAACAGTAACACAGG 1620
                          355-8_c13 GTTTTAAATGGGAACGCGTTATGAACTTCGAAGATGGTGGGTTAGTAACAGTAACACAGG 1620
                          355-8_c14 GTTTTAAATGGGAACGCGTTATGAACTTCGAAGATGGTGGGTTAGTAACAGTAACACAGG 1620
                                                     1,640               1,660               1,680
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom ATAGCAGCTTGCAAGATGGTACGTTAATCTACAAAGTGAAAATGAGAGGCACCAATTTTC 1680
                          350-10_c2 ATAGCAGCTTGCAAGATGGTACGTTAATCTACAAAGTGAAAATGAGAGGCACCAATTTTC 1680
                          350-10_c3 ATAGCAGCTTGCAAGATGGTACGTTAATCTACAAAGTGAAAATGAGAGGCACCAATTTTC 1680
                          350-10_c5 ATAGCAGCTTGCAAGATGGTACGTTAATCTACAAAGTGAAAATGAGAGGCACCAATTTTC 1680
                          355-8_c11 ATAGCAGCTTGCAAGATGGTACGTTAATCTACAAAGTGAAAATGAGAGGCACCAATTTTC 1680
                          355-8_c13 ATAGCAGCTTGCAAGATGGTACGTTAATCTACAAAGTGAAAATGAGAGGCACCAATTTTC 1680
                          355-8_c14 ATAGCAGCTTGCAAGATGGTACGTTAATCTACAAAGTGAAAATGAGAGGCACCAATTTTC 1680
                                                     1,700               1,720               1,740
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom CACCAGATGGACCAGTCATGCAGAAGAAAACTATGGGCTGGGAAGCAAGCACCGAAAGGC 1740
                          350-10_c2 CACCAGATGGACCAGTCATGCAGAAGAAAACTATGGGCTGGGAAGCAAGCACCGAAAGGC 1740
                          350-10_c3 CACCAGATGGACCAGTCATGCAGAAGAAAACTATGGGCTGGGAAGCAAGCACCGAAAGGC 1740
                          350-10_c5 CACCAGATGGACCAGTCATGCAGAAGAAAACTATGGGCTGGGAAGCAAGCACCGAAAGGC 1740
                          355-8_c11 CACCAGATGGACCAGTCATGCAGAAGAAAACTATGGGCTGGGAAGCAAGCACCGAAAGGC 1740
                          355-8_c13 CACCAGATGGACCAGTCATGCAGAAGAAAACTATGGGCTGGGAAGCAAGCACCGAAAGGC 1740
                          355-8_c14 CACCAGATGGACCAGTCATGCAGAAGAAAACTATGGGCTGGGAAGCAAGCACCGAAAGGC 1740
                                                     1,760               1,780               1,800
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom TATATCCTAGGGATGGTGTTTTAAAAGGAGAGATCCATCAAGCTTTGAAACTAAAAGACG 1800
                          350-10_c2 TATATCCTAGGGATGGTGTTTTAAAAGGAGAGATCCATCAAGCTTTGAAACTAAAAGACG 1800
                          350-10_c3 TATATCCTAGGGATGGTGTTTTAAAAGGAGAGATCCATCAAGCTTTGAAACTAAAAGACG 1800
                          350-10_c5 TATATCCTAGGGATGGTGTTTTAAAAGGAGAGATCCATCAAGCTTTGAAACTAAAAGACG 1800
                          355-8_c11 TATATCCTAGGGATGGTGTTTTAAAAGGAGAGATCCATCAAGCTTTGAAACTAAAAGACG 1800
                          355-8_c13 TATATCCTAGGGATGGTGTTTTAAAAGGAGAGATCCATCAAGCTTTGAAACTAAAAGACG 1800
                          355-8_c14 TATATCCTAGGGATGGTGTTTTAAAAGGAGAGATCCATCAAGCTTTGAAACTAAAAGACG 1800
                                                     1,820               1,840               1,860
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom GTGGCCACTATTTGGTGGAATTTAAGACCATATACATGGCTAAGAAACCGGTACAGTTAC 1860
                          350-10_c2 GTGGCCACTATTTGGTGGAATTTAAGACCATATACATGGCTAAGAAACCGGTACAGTTAC 1860
                          350-10_c3 GTGGCCACTATTTGGTGGAATTTAAGACCATATACATGGCTAAGAAACCGGTACAGTTAC 1860
                          350-10_c5 GTGGCCACTATTTGGTGGAATTTAAGACCATATACATGGCTAAGAAACCGGTACAGTTAC 1860
                          355-8_c11 GTGGCCACTATTTGGTGGAATTTAAGACCATATACATGGCTAAGAAACCGGTACAGTTAC 1860
                          355-8_c13 GTGGCCACTATTTGGTGGAATTTAAGACCATATACATGGCTAAGAAACCGGTACAGTTAC 1860
                          355-8_c14 GTGGCCACTATTTGGTGGAATTTAAGACCATATACATGGCTAAGAAACCGGTACAGTTAC 1860
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                                                     1,880               1,900               1,920
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom CGGGATATTATTACGTGGATACTAAGCTAGATATAACATCTCACAACGAGGACTACACAA 1920
                          350-10_c2 CGGGATATTATTACGTGGATACTAAGCTAGATATAACATCTCACAACGAGGACTACACAA 1920
                          350-10_c3 CGGGATATTATTACGTGGATACTAAGCTAGATATAACATCTCACAACGAGGACTACACAA 1920
                          350-10_c5 CGGGATATTATTACGTGGATACTAAGCTAGATATAACATCTCACAACGAGGACTACACAA 1920
                          355-8_c11 CGGGATATTATTACGTGGATACTAAGCTAGATATAACATCTCACAACGAGGACTACACAA 1920
                          355-8_c13 CGGGATATTATTACGTGGATACTAAGCTAGATATAACATCTCACAACGAGGACTACACAA 1920
                          355-8_c14 CGGGATATTATTACGTGGATACTAAGCTAGATATAACATCTCACAACGAGGACTACACAA 1920
                                                     1,940               1,960               1,980
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom TTGTGGAACAATATGAAAGATCAGAAGGCCGTCATCATTTGTTTCTTGGCCATGGCACTG 1980
                          350-10_c2 TTGTGGAACAATATGAAAGATCAGAAGGCCGTCATCATTTGTTTCTTGGCCATGGCACTG 1980
                          350-10_c3 TTGTGGAACAATATGAAAGATCAGAAGGCCGTCATCATTTGTTTCTTGGCCATGGCACTG 1980
                          350-10_c5 TTGTGGAACAATATGAAAGATCAGAAGGCCGTCATCATTTGTTTCTTGGCCATGGCACTG 1980
                          355-8_c11 TTGTGGAACAATATGAAAGATCAGAAGGCCGTCATCATTTGTTTCTTGGCCATGGCACTG 1980
                          355-8_c13 TTGTGGAACAATATGAAAGATCAGAAGGCCGTCATCATTTGTTTCTTGGCCATGGCACTG 1980
                          355-8_c14 TTGTGGAACAATATGAAAGATCAGAAGGCCGTCATCATTTGTTTCTTGGCCATGGCACTG 1980
                                                     2,000               2,020               2,040
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom GTTCCACCGGTAGTGGATCATCAGGTACTGCTTCAAGTGAGGACAACAACATGGCGGTGA 2040
                          350-10_c2 GTTCCACCGGTAGTGGATCATCAGGTACTGCTTCAAGTGAGGACAACAACATGGCGGTGA 2040
                          350-10_c3 GTTCCACCGGTAGTGGATCATCAGGTACTGCTTCAAGTGAGGACAACAACATGGCGGTGA 2040
                          350-10_c5 GTTCCACCGGTAGTGGATCATCAGGTACTGCTTCAAGTGAGGACAACAACATGGCGGTGA 2040
                          355-8_c11 GTTCCACCGGTAGTGGATCATCAGGTACTGCTTCAAGTGAGGACAACAACATGGCGGTGA 2040
                          355-8_c13 GTTCCACCGGTAGTGGATCATCAGGTACTGCTTCAAGTGAGGACAACAACATGGCGGTGA 2040
                          355-8_c14 GTTCCACCGGTAGTGGATCATCAGGTACTGCTTCAAGTGAGGACAACAACATGGCGGTGA 2040
                                                     2,060               2,080               2,100
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom TAAAAGAGTTCATGAGATTTAAAGTGCGAATGGAGGGCTCAATGAATGGACACGAATTTG 2100
                          350-10_c2 TAAAAGAGTTCATGAGATTTAAAGTGCGAATGGAGGGCTCAATGAATGGACACGAATTTG 2100
                          350-10_c3 TAAAAGAGTTCATGAGATTTAAAGTGCGAATGGAGGGCTCAATGAATGGACACGAATTTG 2100
                          350-10_c5 TAAAAGAGTTCATGAGATTTAAAGTGCGAATGGAGGGCTCAATGAATGGACACGAATTTG 2100
                          355-8_c11 TAAAAGAGTTCATGAGATTTAAAGTGCGAATGGAGGGCTCAATGAATGGACACGAATTTG 2100
                          355-8_c13 TAAAAGAGTTCATGAGATTTAAAGTGCGAATGGAGGGCTCAATGAATGGACACGAATTTG 2100
                          355-8_c14 TAAAAGAGTTCATGAGATTTAAAGTGCGAATGGAGGGCTCAATGAATGGACACGAATTTG 2100
                                                     2,120               2,140               2,160
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom AAATTGAAGGGGAGGGTGAAGGACGACCGTACGAAGGAACACAAACAGCCAAATTGAAAG 2160
                          350-10_c2 AAATTGAAGGGGAGGGTGAAGGACGACCGTACGAAGGAACACAAACAGCCAAATTGAAAG 2160
                          350-10_c3 AAATTGAAGGGGAGGGTGAAGGACGACCGTACGAAGGAACACAAACAGCCAAATTGAAAG 2160
                          350-10_c5 AAATTGAAGGGGAGGGTGAAGGACGACCGTACGAAGGAACACAAACAGCCAAATTGAAAG 2160
                          355-8_c11 AAATTGAAGGGGAGGGTGAAGGACGACCGTACGAAGGAACACAAACAGCCAAATTGAAAG 2160
                          355-8_c13 AAATTGAAGGGGAGGGTGAAGGACGACCGTACGAAGGAACACAAACAGCCAAATTGAAAG 2160
                          355-8_c14 AAATTGAAGGGGAGGGTGAAGGACGACCGTACGAAGGAACACAAACAGCCAAATTGAAAG 2160
                                                     2,180               2,200               2,220
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom TAACTAAGGGAGGTCCTCTTCCTTTTGCATGGGACATCTTATCTCCACAATTTATGTACG 2220
                          350-10_c2 TAACTAAGGGAGGTCCTCTTCCTTTTGCATGGGACATCTTATCTCCACAATTTATGTACG 2220
                          350-10_c3 TAACTAAGGGAGGTCCTCTTCCTTTTGCATGGGACATCTTATCTCCACAATTTATGTACG 2220
                          350-10_c5 TAACTAAGGGAGGTCCTCTTCCTTTTGCATGGGACATCTTATCTCCACAATTTATGTACG 2220
                          355-8_c11 TAACTAAGGGAGGTCCTCTTCCTTTTGCATGGGACATCTTATCTCCACAATTTATGTACG 2220
                          355-8_c13 TAACTAAGGGAGGTCCTCTTCCTTTTGCATGGGACATCTTATCTCCACAATTTATGTACG 2220
                          355-8_c14 TAACTAAGGGAGGTCCTCTTCCTTTTGCATGGGACATCTTATCTCCACAATTTATGTACG 2220
                                                     2,240               2,260               2,280
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom GATCTAAAGCCTATGTCAAACATCCAGCTGATATTCCCGATTACAAGAAACTTAGCTTTC 2280
                          350-10_c2 GATCTAAAGCCTATGTCAAACATCCAGCTGATATTCCCGATTACAAGAAACTTAGCTTTC 2280
                          350-10_c3 GATCTAAAGCCTATGTCAAACATCCAGCTGATATTCCCGATTACAAGAAACTTAGCTTTC 2280
                          350-10_c5 GATCTAAAGCCTATGTCAAACATCCAGCTGATATTCCCGATTACAAGAAACTTAGCTTTC 2280
                          355-8_c11 GATCTAAAGCCTATGTCAAACATCCAGCTGATATTCCCGATTACAAGAAACTTAGCTTTC 2280
                          355-8_c13 GATCTAAAGCCTATGTCAAACATCCAGCTGATATTCCCGATTACAAGAAACTTAGCTTTC 2280
                          355-8_c14 GATCTAAAGCCTATGTCAAACATCCAGCTGATATTCCCGATTACAAGAAACTTAGCTTTC 2280
                                                     2,300               2,320               2,340
                                                       |                   |                   |
expected_sequence_EF1a-SF-P2A-tdTom CAGAGGGATTCAAATGGGAACGTGTGATGAATTTCGAAGATGGAGGTTTAGTTACAGTAA 2340
                          350-10_c2 CAGAGGGATTCAAATGGGAACGTGTGATGAATTTCGAAGATGGAGGTTTAGTTACAGTAA 2340
                          350-10_c3 CAGAGGGATTCAAATGGGAACGTGTGATGAATTTCGAAGATGGAGGTTTAGTTACAGTAA 2340
                          350-10_c5 CAGAGGGATTCAAATGGGAACGTGTGATGAATTTCGAAGATGGAGGTTTAGTTACAGTAA 2340
                          355-8_c11 CAGAGGGATTCAAATGGGAACGTGTGATGAATTTCGAAGATGGAGGTTTAGTTACAGTAA 2340
                          355-8_c13 CAGAGGGATTCAAATGGGAACGTGTGATGAATTTCGAAGATGGAGGTTTAGTTACAGTAA 2340
                          355-8_c14 CAGAGGGATTCAAATGGGAACGTGTGATGAATTTCGAAGATGGAGGTTTAGTTACAGTAA 2340
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Supporting Figure S7

Fig S6. Alignment of upstream and downstream integration sites from *Eef1a*$^{SF\text{-}P2A\text{-}tdTom}$ colonies.
Nucleotide alignment of the region encoding the upstream integration site from the founder colony, 350-10, and one transgenic offspring, 355-8. Three cloned amplicons were sequenced for each animal at each site. Primer binding sites are indicated in green on the expected sequence.