

**Additional File 6: Repeat-based alignment of the unique gene sequences.** Only the second exon is shown, because the leader and intron alignments are identical to those shown in Additional Files 2 and 3. Element borders are indicated by vertical black lines, and are labeled above the sequence. Repeats are indicated by shaded boxes, which each different color (red = type 1; blue = type 2; green = type 3; yellow = type 4; and purple = type 5).

Er1

Er2

Er3...

10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180

Table of DNA sequences with 180 rows and columns. The first column contains row numbers (2-05 to 2-1544). The table is divided into three vertical sections: Er1 (columns 1-90), Er2 (columns 100-180), and Er3... (columns 170-180). The Er2 and Er3... sections are highlighted with a light red background. The sequences consist of uppercase letters (A, C, G, T) representing nucleotides.

Repeat 1.1

Repeat 1.2...





...Er3 Er4 Er5

190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360

4-1545	CGGAGACAAGATGGTGGACCAATGGGTGGAAGGAGGTTTCGATGGACCTGGATTTGGTGCCCC	285
4-1547	ACAAATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
4-1548	ACATATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
4-1550	ACAAATGGAAGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
4-2410	CGGAGACAAGATGGTGGACCAATGGGTGGAAGGAGGTTTCGATGGACCTGGATTTGGTGCCCC	285
4-2412	CGGAGACAAGATGGTGGACCAATGGGTGGAAGGAGGTTTCGATGGACCTGGATTTGGTGCCCC	285
4-2415	ACATATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
4-2449	CGGAGACAAGATGGTGGACCAATGGGTGGAAGGAGGTTTCGATGGACCTGGATTTGGTGCCCC	285
10-01	ACATATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-02	GCAGATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-03	ACAAATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-04	ACAGATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-06	CGGAGACAAGATGGTGGACCAATGGGTGGAAGGAGGTTTCGATGGACCTGGAATTTGGTGCCCC	285
10-07	ACAGATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-10	CCATAGGCAAAAATGGTGGACCAATGGGTGGAAGGAGGTTTCGATGGACCTAGATTTTGGTGCCCC	360
10-11	ACATATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-13	CCATAGGCAAAAATGGTGGACCAATGGGTGGAAGGAGGTTTCGATGGACCTAGATTTTGGTGCCCC	360
10-14	CGGAGACAAGATGGTGGACCAATGGGTGGAAGGAGGTTTCGATGGACCTGGATTTGGTGCCCC	285
10-15	CGGAGACAAGATGGTGGACCAATGGGTGGAAGGAGGTTTCGATGGACCTGGATTTGGTGCCCC	285
10-17	GCAGATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-18	GCAGATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-19	CGGAGACAAGATGGTGGACCAATGGGTGGAAGGAGGTTTCGATGGACCTGGATTTGGTGCCCC	285
10-20	ACAAATGGAAGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-21	CGGAGACAAGATGGTGGACCAATGGGTGGAAGGAGGTTTCGATGGACCTGGATTTGGTGCCCC	285
10-22	CGGAGACAAGATGGTGGACCAATGGGTGGAAGGAGGTTTCGATGGACCTGGATTTGGTGCCCC	285
10-24	CGGAGACAAGATGGTGGACCAATGGGTGGAAGGAGGTTTCGATGGACCTGGATTTGGTGCCCC	285
10-25	ACAAATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-26	ACAAATGGAAGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-28	ACAAATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-29	ACAAATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-30	ACAAATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-31	GCAGATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-32	ACAAATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-35	GCAGATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-37	ACAAATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-38	ACAAATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-39	ACATATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-40	GCAGATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-42	ACATATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-43	ACATATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-46	ACAAATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-50	GCAGATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-51	GCAGATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-52	GCAGATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-54	ACAGATGGATGGACCGAGACAAAATGGCGGTCCGATGGGTGGT	210
10-55	CGGAGACAAGATGGTGGACCAATGGGTGGAAGGAGGTTTCGATGGACCTGGATTTGGTGCCCC	285

...Repeat 1.2

Repeat 1.3

Repeat 1.4...









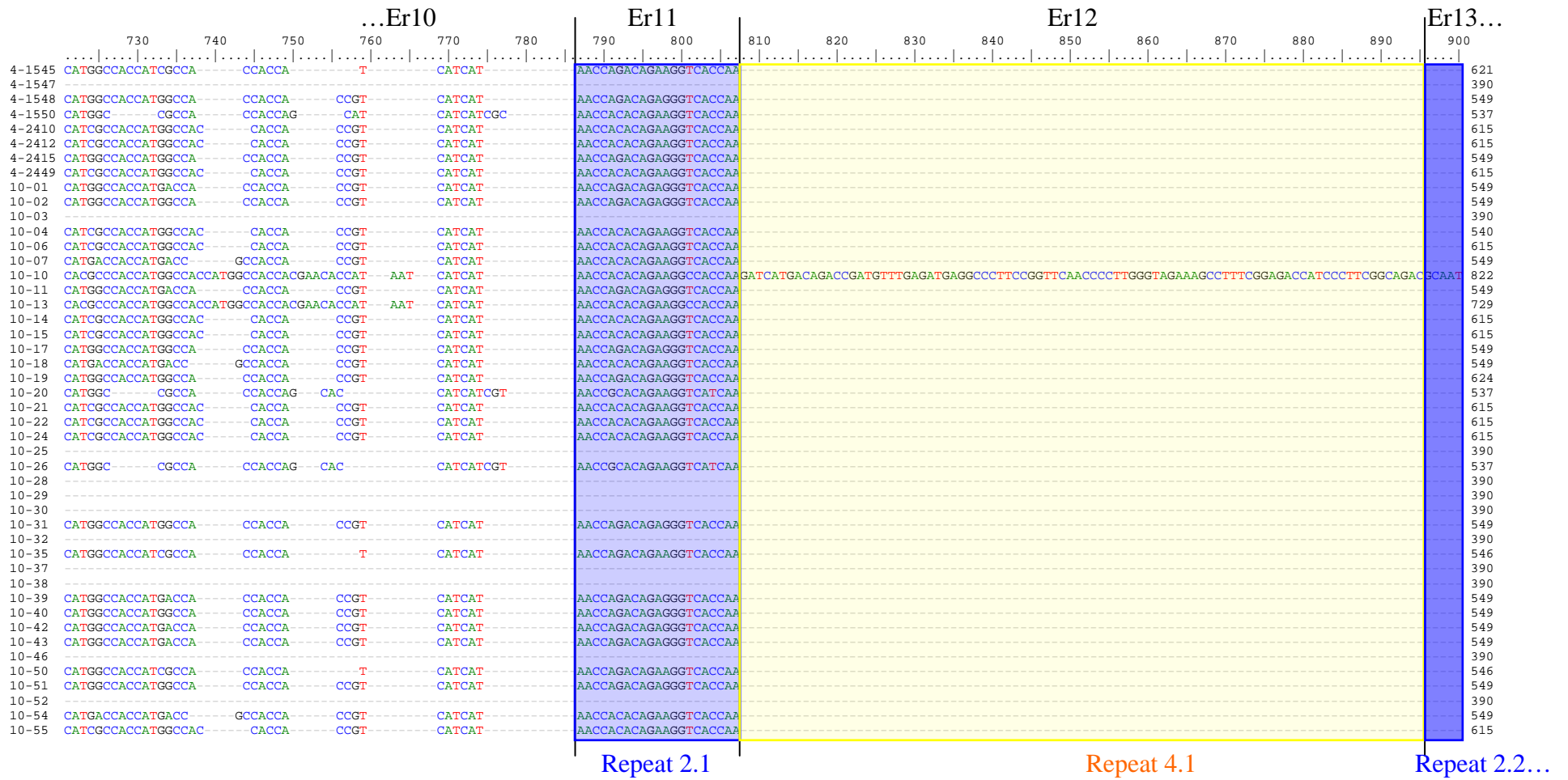
	Er7	Er8	Er9	Er10...
	550 560 570 580 590 600	610 620 630 640 650	660 670 680 690 700	710 720
4-1545		CACCGTCAAGGTCCTCCTCAGGACCGCCAGAGGAACAAACCGTTTCGGTCAG	GCAACTACAGCAGCGAGGAGGATGGCCGACCTCACCCCTCACCAC	CATCGCCAC 570
4-1547				390
4-1548		CACCGTCAAGGTCACCTCAGGACCGACCAGAGGAACAAACCGTTTCGGTCAG	GCAAATGAACGCAACGAGGAGGATGGCCGTCTCACCCCTCACCAC	CATGGCCAC 495
4-1550		CACCGTCAAGGTCCTCCTCAGGACCGACCAGAGGAACAAACCGTTTCGGTCAG	GCAAACGAAAGCAGCGATGAGGATGGCCGTCTCACCCCTCACCAC	486
4-2410		CACCGTCAAGGTCATCCTCAGGACCAAGCAGAGGAACAAACCGTTTAGTCAG	GCAAACGAAAGCAGCGAGGAGGATGGCCGTCTCACCCCTCACCAC	561
4-2412		CACCGTCAAGGTCATCCTCAGGACCAAGCAGAGGAACAAACCGTTTCGGTCAG	GCAAACGAAAGCAGCGAGGAGGATGGCCGTCTCACCCCTCACCAC	561
4-2415		CACCGTCAAGGTCACCTCAGGACCGACCAGAGGAACAAACCGTTTCGGTCAG	GCAAATGAACGCAACGAGGAGGATGGCCGTCTCACCCCTCACCAC	CATGGCCAC 495
4-2449		CACCGTCAAGGTCATCCTCAGGACCAAGCAGAGGAACAAACCGTTTCGGTCAG	GCAAACGAAAGCAGCGAGGAGGATGGCCGTCTCACCCCTCACCAC	561
10-01		CACCGTCAAGGTCACCTCAGGACCGACCAGAGGAACAAACCGTTTCGGTCAG	GCAAATGAACGCAACGAGGAGGATAGCCGTCTCACCCCTCACCAC	CATCGCCAC 495
10-02		CACCGTCAAGGTCACCTCAGGACCGACCAGAGGAACAAACCGTTTCGGTCAG	GCAACTACAGCAGCGAGGAGGATGGCCGTCTCACCCCTCACCAC	CATGGCCAC 495
10-03				390
10-04		CACCGTCGAGGTCATCCTCAGGACCAAGCAGAGGAACAAACCGTTTCGGTCAG	GCAAACGAAAGCAGCGAGGAGGATGGCCGTCTCACCCCTCACCAC	486
10-06		CACCGTCGAGGTCATCCTCAGGACCAAGCAGAGGAACAAACCGTTTCGGTCAG	GCAAACGAAAGCAGCGAGGAGGATGGCCGTCTCACCCCTCACCAC	561
10-07		CACCGTCAAGGACCACTCAGGATCGATCAGAGGAACAAACCGTTTCGGTCAG	GCAAATGAAGCAGCGAGGAGGATGGCCGTCTCACCCCTCACCAC	CATCGCCAC 495
10-10	CATCATCAAGGTGCAGGAAGACCTTTCTTCGGCAATCCTCCTCTTTAAACCAGAACAGGAAACCG		GCAAACGAGCAGCGAGGAGGATGGCCGTCTCACCCCTCACCAC	GATCGCCAC 660
10-11		CACCGTCAAGGTCACCTCAGGACCGACCAGAGGAACAAACCGTTTCGGTCAG	GCAAATGAACGCAACGAGGAGGATAGCCGTCTCACCCCTCACCAC	CATCGCCAC 495
10-13	CATCATCAAGGTGCAGGAAGACCTTTCTTCGGCAATCCTCCTCTTTAAACCAGAACAGGAAACCG		GCAAACGAGCAGCGAGGAGGATGGCCGTCTCACCCCTCACCAC	GATCGCCAC 660
10-14		CACCGTCAAGGTCATCCTCAGGACCAAGCAGAGGAACAAACCGTTTCGGTCAG	GCAAACGAAAGCAGCGAGGAGGATGGCCGTCTCACCCCTCACCAC	561
10-15		CACCGTCAAGGTCATCCTCAGGACCAAGCAGAGGAACAAACCGTTTCGGTCAG	GCAAACGAAAGCAGCGAGGAGGATGGCCGTCTCACCCCTCACCAC	561
10-17		CACCGTCAAGGTCACCTCAGGACCGACCAGAGGAACAAACCGTTTCGGTCAG	GCAACTACAGCAACGAGGAGGATGGCCGTCTCACCCCTCACCAC	CATGGCCAC 495
10-18		CACCGTCAAGGACCACTCAGGATCGATCAGAGGAACAAACCGTTTCGGTCAG	GCAAATGAAGCAGCGAGGAGGATGGCCGTCTCACCCCTCACCAC	CATCGCCAC 495
10-19		CACCGTCAAGGTCACCTCAGGACCGACCAGAGGAACAAACCGTTTCGGTCAG	GCAACTACAGCAACGAGGAGGATGGCCGTCTCACCCCTCACCAC	CATGGCCAC 570
10-20		CACCGTCAAGGTCCTCCTCAGGACCGACCAGAGGAACAAACCGTTTCGGTCAG	GCAAACGAAAGCAGCGATGAGGATGGCCGTCTCACCCCTCACCAC	486
10-21		CACCGTCAAGGTCATCCTCAGGACCAAGCAGAGGAACAAACCGTTTCGGTCAG	GCAAACGAAAGCAGCGAGGAGGATGGCCGTCTCACCCCTCACCAC	561
10-22		CACCGTCAAGGTCATCCTCAGGACCAAGCAGAGGAACAAACCGTTTCGGTCAG	GCAAACGAAAGCAGCGAGGAGGATGGCCGTCTCACCCCTCACCAC	561
10-24		CACCGTCAAGGTCATCCTCAGGACCAAGCAGAGGAACAAACCGTTTCGGTCAG	GCAAACGAAAGCAGCGAGGAGGATGGCCGTCTCACCCCTCACCAC	561
10-25				390
10-26		CACCGTCAAGGTCCTCCTCAGGACCGACCAGAGGAACAAACCGTTTCGGTCAG	GCAAACGAAAGCAGCGATGAGGATGGCCGTCTCACCCCTCACCAC	486
10-28				390
10-29				390
10-30				390
10-31		CACCGTCAAGGTCACCTCAGGACCGACCAGAGGAACAAACCGTTTCGGTCAG	GCAACTACAGCAACGAGGAGGATGGCCGTCTCACCCCTCACCAC	CATGGCCAC 495
10-32				390
10-35		CACCGTCAAGGTCCTCCTCAGGACCGCCAGAGGAACAAACCGTTTCGGTCAG	GCAACTACAGCAGCGAGGAGGATGGCCGACCTCACCCCTCACCAC	CATCGCCAC 495
10-37				390
10-38				390
10-39		CACCGTCAAGGTCACCTCAGGACCGACCAGAGGAACAAACCGTTTCGGTCAG	GCAAATGAACGCAACGAGGAGGATAGCCGTCTCACCCCTCACCAC	CATCGCCAC 495
10-40		CACCGTCAAGGTCACCTCAGGACCGACCAGAGGAACAAACCGTTTCGGTCAG	GCAACTACAGCAACGAGGAGGATGGCCGTCTCACCCCTCACCAC	CATGGCCAC 495
10-42		CACCGTCAAGGTCACCTCAGGACCGACCAGAGGAACAAACCGTTTCGGTCAG	GCAAATGAACGCAACGAGGAGGATAGCCGTCTCACCCCTCACCAC	CATCGCCAC 495
10-43		CACCGTCAAGGTCACCTCAGGACCGACCAGAGGAACAAACCGTTTCGGTCAG	GCAAATGAACGCAACGAGGAGGATAGCCGTCTCACCCCTCACCAC	CATCGCCAC 495
10-46				390
10-50		CACCGTCAAGGTCCTCCTCAGGACCGCCAGAGGAACAAACCGTTTCGGTCAG	GCAACTACAGCAGCGAGGAGGATGGCCGACCTCACCCCTCACCAC	CATCGCCAC 495
10-51		CACCGTCAAGGTCACCTCAGGACCGACCAGAGGAACAAACCGTTTCGGTCAG	GCAACTACAGCAACGAGGAGGATGGCCGTCTCACCCCTCACCAC	CATGGCCAC 495
10-52				390
10-54		CACCGTCAAGGTCCTCCTCAGGACCGCCAGAGGAACAAACCGTTTCGGTCAG	GCAAATGAAGCAGCGAGGAGGATGGCCGTCTCACCCCTCACCAC	CATCGCCAC 495
10-55		CACCGTCAAGGTCATCCTCAGGACCAAGCAGAGGAACAAACCGTTTCGGTCAG	GCAAACGAAAGCAGCGAGGAGGATGGCCGTCTCACCCCTCACCAC	561

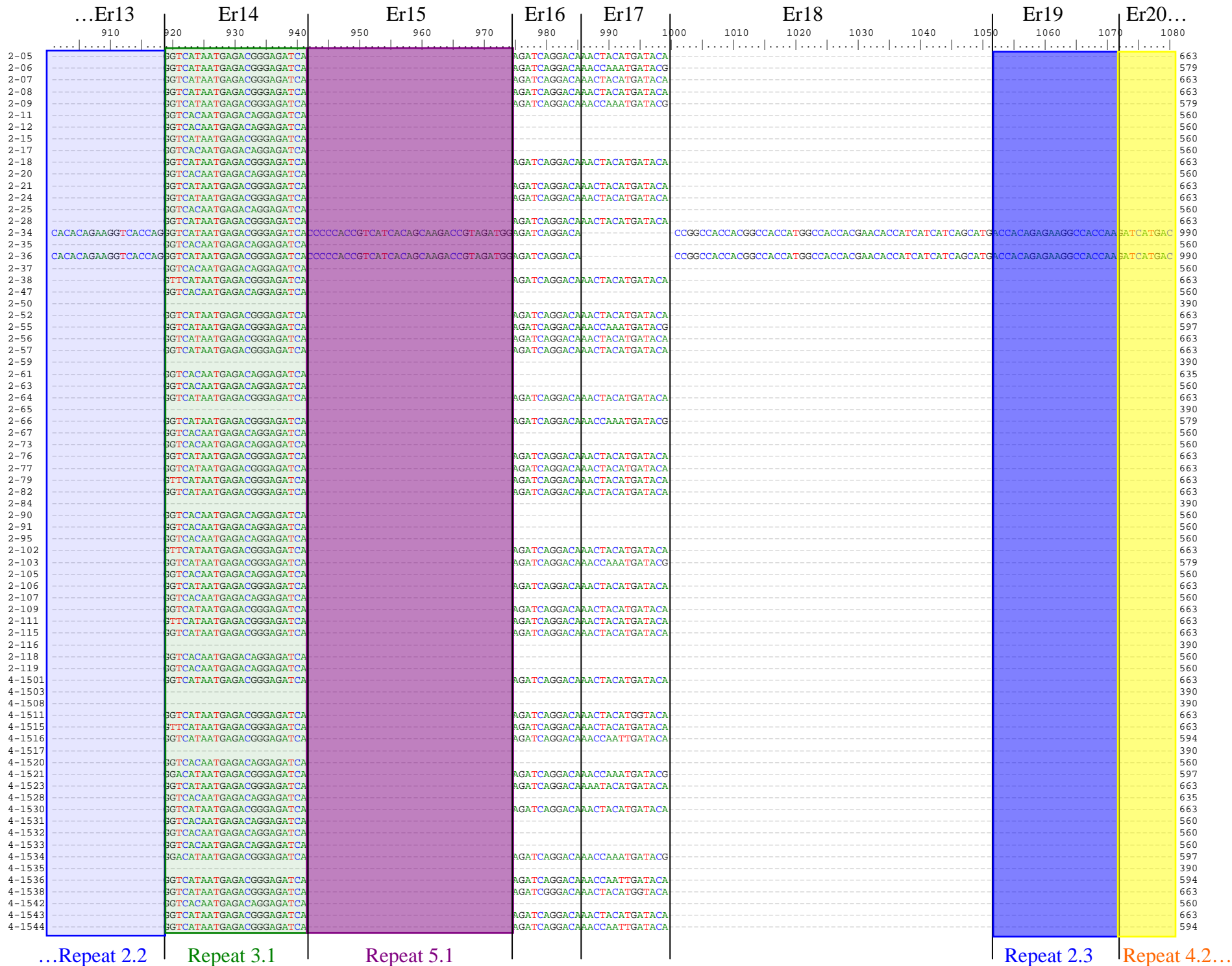
...Er10					Er11		Er12													Er13...																																																																																																																																
730					740		750		760		770		780		790		800		810													820													830													840													850													860													870													880													890													900												
2-05	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
2-06	CATGG	CCA	CCACCA	CCGT	CATCAT	AACCAGACAGAGGGT	CACCAA														531																																																																																																																															
2-07	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
2-08	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
2-09	CATGG	CCA	CCACCA	CCGT	CATCAT	AACCAGACAGAGGGT	CACCAA														531																																																																																																																															
2-11	CATGGC	CGCCA	CCACCAG	CAT	CATCATCGC	AACCACACAGAAGGT	CACCAA														537																																																																																																																															
2-12	CATGGC	CGCCA	CCACCAG	CAT	CATCATCGC	AACCACACAGAAGGT	CACCAA														537																																																																																																																															
2-15	CATGGC	CGCCA	CCACCAG	CAC	CATCATCGT	AACCGCACAGAAGGT	CACCAA														537																																																																																																																															
2-17	CATGGC	CGCCA	CCACCAG	CAT	CATCATCGC	AACCACACAGAAGGT	CACCAA														537																																																																																																																															
2-18	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
2-20	CATGGC	CGCCA	CCACCAG	CAT	CATCATCGC	AACCACACAGAAGGT	CACCAA														537																																																																																																																															
2-21	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
2-24	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
2-25	CATGGC	CGCCA	CCACCAG	CAT	CATCATCGC	AACCACACAGAAGGT	CACCAA														537																																																																																																																															
2-28	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
2-34	CACGCCACC	TGGCCACC	TGGCCACC	GAAACC	CATCATCAA	CATCAT	AACCACACAGAAGGT	CACCAA	GATCATGACAGACC	GATGTTT	GAGATGAGG	CCCTTCCGGTT	CAACCCCTT	GGGTAGAAAGCCTT	TCGGAGACC	TCCCTTC	GGCAGAC	GCAAT	825																																																																																																																																	
2-35	CATGGC	CGCCA	CCACCAG	CAT	CATCATCGC	AACCACACAGAAGGT	CACCAA														537																																																																																																																															
2-36	CACGCCACC	TGGCCACC	TGGCCACC	GAAACC	CATCATCAA	CATCAT	AACCACACAGAAGGT	CACCAA	GATCATGACAGACC	GATGTTT	GAGATGAGG	CCCTTCCGGTT	CAACCCCTT	GGGTAGAAAGCCTT	TCGGAGACC	TCCCTTC	GGCAGAC	GCAAT	825																																																																																																																																	
2-37	CATGGC	CGCCA	CCACCAG	CAT	CATCATCGC	AACCACACAGAAGGT	CACCAA														537																																																																																																																															
2-38	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCAGACAGAAGGT	CACCAA														615																																																																																																																															
2-47	CATGGC	CGCCA	CCACCAG	CAT	CATCATCGC	AACCACACAGAAGGT	CACCAA														537																																																																																																																															
2-50																					390																																																																																																																															
2-52	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
2-55	CATGGCCACC	TGGCCA	CCACCA	CCGT	CATCAT	AACCAGACAGAGGGT	CACCAA														549																																																																																																																															
2-56	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
2-57	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
2-59																					390																																																																																																																															
2-61	CATGGC	CGCCA	CCACCAG	CAT	CATCATCGC	AACCACACAGAAGGT	CACCAA														612																																																																																																																															
2-63	CATGGC	CGCCA	CCACCAG	CAC	CATCATCGT	AACCGCACAGAAGGT	CATCAA														537																																																																																																																															
2-64	CTTCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
2-65																					390																																																																																																																															
2-66	CATGG	CCA	CCACCA	CCGT	CATCAT	AACCAGACAGAGGGT	CACCAA														531																																																																																																																															
2-67	CATGGC	CGCCA	CCACCAG	CAT	CATCATCGC	AACCACACAGAAGGT	CACCAA														537																																																																																																																															
2-73	CATGGC	CGCCA	CCACCAG	CAT	CATCATCGC	AACCACACAGAAGGT	CACCAA														537																																																																																																																															
2-76	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
2-77	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
2-79	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCAGACAGAAGGT	CACCAA														615																																																																																																																															
2-82	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
2-84																					390																																																																																																																															
2-90	CATGGC	CGCCA	CCACCAG	CAC	CATCATCGT	AACCGCACAGAAGGT	CATCAA														537																																																																																																																															
2-91	CATGGC	CGCCA	CCACCAG	CAC	CATCATCGT	AACCGCACAGAAGGT	CATCAA														537																																																																																																																															
2-95	CATGGC	CGCCA	CCACCAG	CAT	CATCATCGC	AACCACACAGAAGGT	CACCAA														537																																																																																																																															
2-102	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCAGACAGAAGGT	CACCAA														615																																																																																																																															
2-103	CATGG	CCA	CCACCA	CCGT	CATCAT	AACCAGACAGAGGGT	CACCAA														531																																																																																																																															
2-105	CATGGC	CGCCA	CCACCAG	CAC	CATCATCGT	AACCGCACAGAAGGT	CATCAA														537																																																																																																																															
2-106	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
2-107	CATGGC	CGCCA	CCACCAG	CAT	CATCATCGC	AACCACACAGAAGGT	CACCAA														537																																																																																																																															
2-109	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
2-111	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCAGACAGAAGGT	CACCAA														615																																																																																																																															
2-115	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
2-116																					390																																																																																																																															
2-118	CATGGC	CGCCA	CCACCAG	CAT	CATCATCGC	AACCACACAGAAGGT	CACCAA														537																																																																																																																															
2-119	CATGGC	CGCCA	CCACCAG	CAT	CATCATCGC	AACCACACAGAAGGT	CACCAA														537																																																																																																																															
4-1501	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
4-1503																					390																																																																																																																															
4-1508																					390																																																																																																																															
4-1511	CATCGCCACC	TGGCCAC	CACCA	CCCT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
4-1515	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
4-1516	CATGGCCACC	TCGCCA	CCACCA	T	CATCAT	AACCAGACAGAAGGT	CACCAA														546																																																																																																																															
4-1517																					390																																																																																																																															
4-1520	CATGGC	CGCCA	CCACCAG	CAT	CATCATCGC	AACCACACAGAAGGT	CACCAA														537																																																																																																																															
4-1521	CATGGCCACC	TGGCCA	CCACCA	CCGT	CATCAT	AACCAGACAGAGGGT	CACCAA														549																																																																																																																															
4-1523	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
4-1528	CATGGC	CGCCA	CCACCAG	CAT	CATCATCGC	AACCACACAGAAGGT	CACCAA														612																																																																																																																															
4-1530	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
4-1531	CATGGC	CGCCA	CCACCAG	CAT	CATCATCGC	AACCACACAGAAGGT	CACCAA														537																																																																																																																															
4-1532	CATGGC	CGCCA	CCACCAG	CAT	CATCATCGC	AACCACACAGAAGGT	CACCAA														537																																																																																																																															
4-1533	CATGGC	CGCCA	CCACCAG	CAT	CATCATCGC	AACCACACAGAAGGT	CACCAA														537																																																																																																																															
4-1534	CATGGCCACC	TGGCCA	CCACCA	CCGT	CATCAT	AACCAGACAGAGGGT	CACCAA														549																																																																																																																															
4-1535																					390																																																																																																																															
4-1536	CATGGCCACC	TCGCCA	CCACCA	T	CATCAT	AACCAGACAGAAGGT	CACCAA														546																																																																																																																															
4-1538	CATCGCCACC	TGGCCAC	CACCA	CCCT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
4-1542	CATGGC	CGCCA	CCACCAG	CAT	CATCATCGC	AACCACACAGAAGGT	CACCAA														537																																																																																																																															
4-1543	CATCGCCACC	TGGCCAC	CACCA	CCGT	CATCAT	AACCACACAGAAGGT	CACCAA														615																																																																																																																															
4-1544	CATGGCCACC	TCGCCA	CCACCA	T	CATCAT	AACCAGACAGAAGGT	CACCAA														546																																																																																																																															

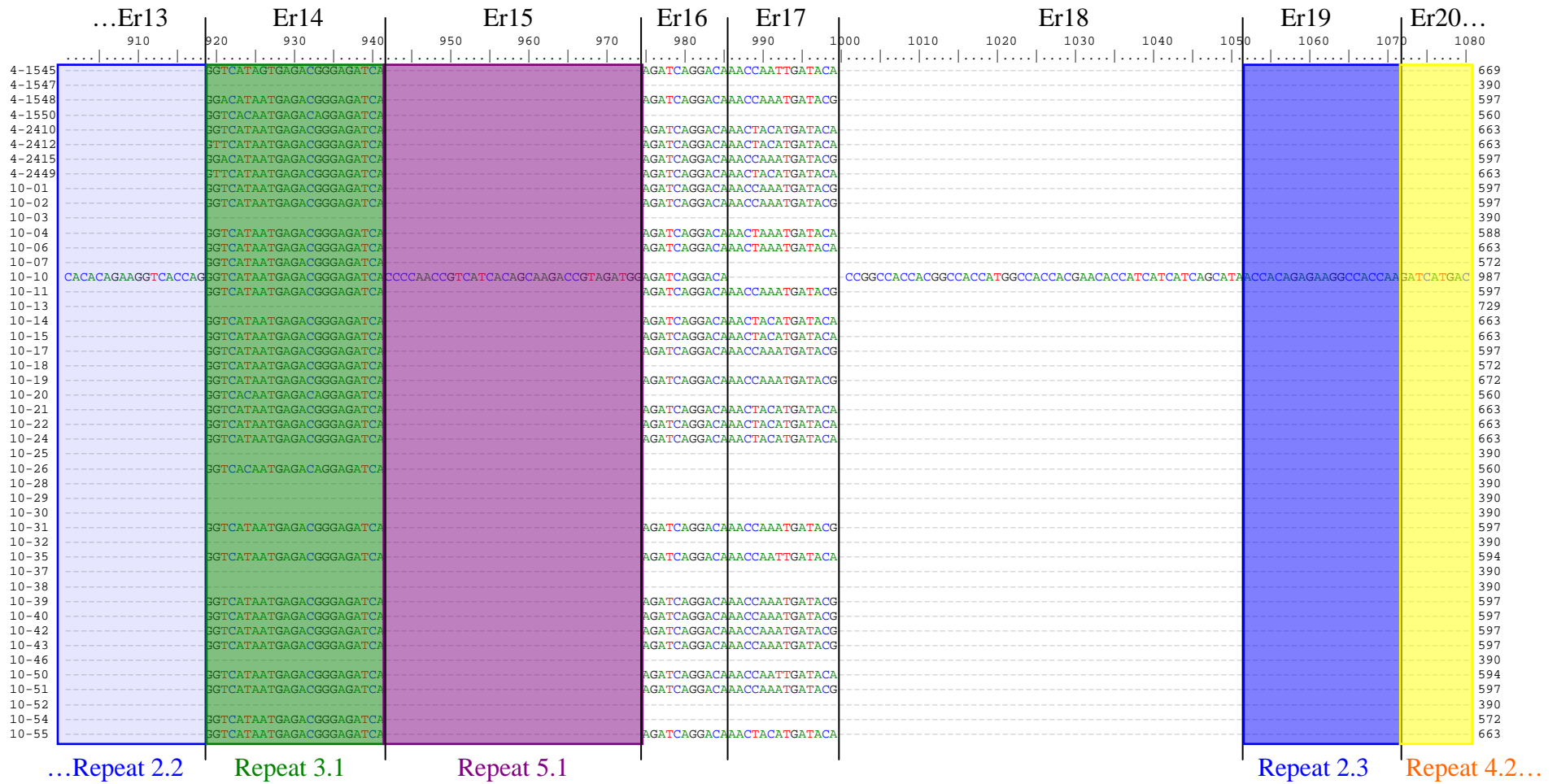
Repeat 2.1

Repeat 4.1

Repeat 2.2...



















...Er27a

Er27b

1450 1460 1470 1480 1490 1500 1510 1520

4-1545 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTGAGATCGCAGTCAATGAAGAAGACGTC AATGTGGTCGCCGAGGTGTAG 1092

4-1547 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTCGAGATCGCGATCAATGA ----- TGTCCGCCGAGGTGTAG 771

4-1548 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTGAGATCGCAGTCAATGAAGAAGACGTC AATGTGGTCGCCGAGGTGTAG 990

4-1550 GAAAGCGTAAACGACATCTTCCACCCTTAAATGGTCGAGATCGCAGTCAATGAAGAAGACATCA AATGTGGTCGCCGAGGTGTAG 876

4-2410 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTC ----- GCAATCAATGAAGAAGACATCA AATGTGGTCGCCGAGGTGTAG 1080

4-2412 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTC ----- GCAATCAATGAAGAAGACATCA AATGTGGTCGCCGAGGTGTAG 1080

4-2415 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTGAGATCGCAGTCAATGAAGAAGACGTC AATGTGGTCGCCGAGGTGTAA 990

4-2449 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTC ----- GCAATCAATGAAGAAGACATCA AATGTGGTCGCCGAGGTGTAG 1080

10-01 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTGAGATCGCAGTCAATGAAGAAGACGTC AATGTGGTCGCCGAGGTGTAG 990

10-02 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTGAGATCGCAGTCAATGAAGAAGACGTC AATGTGGTCGCCGAGGTGTAG 990

10-03 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTCGAGATCGCGATCAATGA ----- TGTCCGCCGAGGTGTAG 771

10-04 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTC ----- GCAATCAATGAAGAAGACATCA AATGTGGTCGCCGAGGTGTAG 1005

10-06 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTC ----- GCAATCAATGAAGAAGACATCA AATGTGGTCGCCGAGGTGTAG 1080

10-07 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTGAGATCGCATTC AATGAAGAAGACGTC AATGTGGTCGCCGAGGTGTAG 888

10-10 GAAAGCGTAAACGACATCTTCCACCCTTAAATGTATCGAGATCGCAATCAATGAAGTAGACACCAATGTGGTCGCCGAGGTGTAG 1428

10-11 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTC ----- GCAATCAATGAAGAAGACATCA AATGTGGTCGCCGAGGTGTAG 984

10-13 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTGAGATCGCAGTCAATGAAGAAGACGTC AATGTGGTCGCCGAGGTGTAG 1011

10-14 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTC ----- GCAATCAATGAAGAAGACATCA AATGTGGTCGCCGAGGTGTAG 1080

10-15 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTC ----- GCAATCAATGAAGAAGACATCA AATGTGGTCGCCGAGGTGTAG 1080

10-17 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTGAGATCGCAGTCAATGAAGAAGACGTC AATGTGGTCGCCGAGGTGTAG 990

10-18 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTGAGATCGCATTC AATGAAGAAGACGTC AATGTGGTCGCCGAGGTGTAG 888

10-19 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTC ----- GCAATCAATGAAGAAGACATCA AATGTGGTCGCCGAGGTGTAG 1059

10-20 GAAAGCGTAAACGACATCTTCCACCCTTAAATGGTCGAGATCGCAGTCAATGAAGAAGACATCA AATGGGTCGCCGAGGTGTAG 876

10-21 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTC ----- GCAATCAATGAAGAAGACATCA AATGTGGTCGCCGAGGTGTAG 1080

10-22 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTC ----- GCAATCAATGAAGAAGACATCA AATGTGGTCGCCGAGGTGTAG 1080

10-24 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTGAGATCGCAGTCAATGAAGAAGACGTC AATGTGGTCGCCGAGGTGTAG 1086

10-25 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTCGAGATCGCGATCAATGA ----- TGTCCGCCGAGGTGTAG 771

10-26 GAAAGCGTAAACGACATCTTCCACCCTTAAATGGTCGAGATCGCAGTCAATGAAGAAGACATCA AATGGGTCGCCGAGGTGTAG 876

10-28 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTCGAGATCGCGATCAATGA ----- TGTCCGCCGAGGTGTAG 771

10-29 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTCGAGATCGCGATCAATGA ----- TGTCCGCCGAGGTGTAG 771

10-30 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTCGAGATCGCGATCAATGA ----- TGTCCGCCGAGGTGTAG 771

10-31 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTGAGATCGCAGTCAATGAAGAAGACGTC AATGTGGTCGCCGAGGTGTAG 990

10-32 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTCGAGATCGCGATCAATGA ----- TGTCCGCCGAGGTGTAG 771

10-35 GAAAGCGTAAACGACATCTCCACCAGTGAATGGTTGAGATCGCATTC AATGAAGAAGACGTC AATGTGGTCGCCGAGGTGTAG 1017

10-37 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTCGAGATCGCGATCAATGA ----- TGTCCGCCGAGGTGTAG 771

10-38 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTCGAGATCGCGATCAATGA ----- TGTCCGCCGAGGTGTAG 771

10-39 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTGAGATCGCAGTCAATGAAGAAGACGTC AATGTGGTCGCCGAGGTGTAG 990

10-40 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTCGAGATCGCGATCAATGA ----- TGTCCGCCGAGGTGTAG 975

10-42 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTGAGATCGCAGTCAATGAAGAAGACGTC AATGTGGTCGCCGAGGTGTTA 990

10-43 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTGAGATCGCAGTCAATGAAGAAGACGTC AATGTGGTCGCCGAGGTGTTA 990

10-46 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTCGAGATCGCGATCAATGA ----- TGTGGCCGAGGTGTAG 771

10-50 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTGAGATCGCATTC AATGAAGAAGACGTC AATGTGGTCGCCGAGGTGTAG 1017

10-51 GAAAGCGTAAACGACATCTCCACCCTGAAATGGTCGAGATCGCAGTCAATGAAGAAGACGTC AATGTGGTCGCCGAGGTGTAG 990

10-52 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTCGAGATCGCGATCAATGA ----- TGTCCGCCGAGGTGTAG 771

10-54 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTGAGATCGCATTC AATGAAGAAGACGTC AATGTGGTCGCCGAGGTGTAG 888

10-55 GAAAGCGTAAACGACATCTTCCACCCTGAAATGGTTGAGATCGCAGTCAATGAAGAAGACGTC AATGTGGTCGCCGAGGTGTAG 1086