

Mitochondrial Genome Sequence of *Salvia officinalis* (Lamiales: Lamiaceae) Suggests Diverse Genome Structures in Cogeneric Species and Finds the Stop Gain of Genes through RNA Editing Events

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Table S1 Statistic summary of the sequencing data generated by Nanopore and Illumina platforms.

Sequencing descriptors	Sequencing platform	
	Nanopore	Illumina
Total number of nucleotides (raw data, bp)	11,326,908,802	16,380,908,800
Total Number of Reads	505,210	163,809,088
Mean Read Length (bp)	22,420	100
Total Number of Mapped Reads	23,959 (MC1), 13,431(MC2)	3,291,507 (MC1), 1,021,009(MC2)
Average Coverage Depth	327.77 (MC1), 396.13 (MC2)	969.556 (MC1), 903.15 (MC2)

Table S2 Results for mapping Nanopore long reads to the four possible conformations associated with three HSPs (r01–r52). “MC1/2”: mitogenome chromosome 1/2. The recombination frequency was calculated as the number of reads mapped to conformations having less number of mapped reads divided by that mapped to all four conformations.

ID of the HSP	Query sequence	Subject sequence	Identity (%)	Alignment Length	Numbers of Mismatches	Numbers of Gap openings	Positions of Repeat Copy 1		Positions of Repeat Copy 2		E-value	Type	Numbers of Long Reads Mapped to Each Conformation				Recombination frequency (%)
							Start	End	Start	End			c1	c2	c3	c4	
r03	MC1	MC1	87.861	173	15	6	190502	190671	94435	94266	1.26E-49	inverted	15	32	0	0	0
r04	MC1	MC1	100	80	0	0	226961	227040	28759	28838	1.28E-34	direct	23	26	0	0	0
r05	MC1	MC1	97.5	80	2	0	166752	166831	29701	29780	2.78E-31	direct	0	7	0	0	0
r06	MC1	MC1	94.937	79	1	1	221621	221696	28709	28631	2.8E-26	inverted	26	26	0	0	0
r07	MC1	MC1	98.507	67	1	0	181259	181325	82141	82075	1.01E-25	inverted	20	13	1	0	0
r08	MC1	MC1	100	61	0	0	253935	253995	237908	237848	4.68E-24	inverted	17	29	1	0	0
r09	MC1	MC1	98.387	62	1	0	222237	222298	183614	183675	6.06E-23	direct	17	19	0	0	0
r10	MC1	MC1	93.243	74	4	1	242683	242756	29375	29303	2.18E-22	inverted	15	26	0	0	0

r11	MC1	MC1	100	53	0	0	5835 2	5840 4	4704 6	4709 8	1.31E-19	direct	20	23	0	0	0
r12	MC1	MC1	100	53	0	0	2308 17	2308 69	5840 4	5835 2	1.31E-19	invert ed	15	20	0	0	0
r13	MC1	MC1	100	52	0	0	8179 4	8184 5	3821 3	3816 2	4.71E-19	invert ed	20	31	0	0	0
r14	MC1	MC1	100	46	0	0	2348 54	2348 99	4594 8	4599 3	1.02E-15	direct	25	37	0	0	0
r15	MC1	MC1	97.95 9	49	0	1	2277 88	2278 35	1603 05	1603 53	3.67E-15	direct	17	20	0	0	0
r16	MC1	MC1	91.37 9	58	5	0	1385 05	1385 62	6555 3	6561 0	4.75E-14	direct	18	28	0	0	0
r17	MC1	MC1	97.72 7	44	1	0	1496 21	1496 64	2616 10	2615 67	6.14E-13	invert ed	25	28	0	0	0
r18	MC1	MC1	100	40	0	0	1710 82	1711 21	1929 6	1933 5	2.21E-12	direct	21	25	0	0	0
r19	MC1	MC1	100	40	0	0	1823 55	1823 94	9107 7	9111 6	2.21E-12	direct	12	22	0	0	0
r20	MC1	MC1	95.34 9	43	2	0	9825 0	9829 2	2739 5	2735 3	1.03E-10	invert ed	18	26	0	0	0
r21	MC1	MC1	100	37	0	0	1288 25	1288 61	1266 75	1267 11	1.03E-10	direct	26	23	0	0	0
r22	MC1	MC1	91.66 7	48	3	1	1799 01	1799 48	6802 0	6797 4	1.33E-09	invert ed	20	13	0	0	0
r23	MC1	MC1	100	35	0	0	8604 8	8608 2	8593 1	8596 5	1.33E-09	direct	3	16	0	0	0

r24	MC1	MC1	100	35	0	0	188677	188711	129203	129237	1.33E-09	direct	12	19	0	0	0
r25	MC1	MC1	90.196	51	4	1	67974	68023	179948	179898	1.33E-09	inverted	16	21	0	0	0
r26	MC1	MC1	100	34	0	0	186062	186095	59133	59100	4.78E-09	inverted	7	24	0	0	0
r27	MC1	MC1	97.222	36	1	0	110507	110542	27781	27746	1.72E-08	inverted	29	36	0	0	0
r28	MC1	MC1	97.222	36	1	0	135779	135814	126679	126644	1.72E-08	inverted	16	27	0	0	0
r29	MC1	MC1	94.872	39	2	0	236663	236701	166693	166731	1.72E-08	direct	26	2	0	0	0
r30	MC1	MC1	100	30	0	0	189917	189946	58633	58604	0.0000008	inverted	11	25	0	0	0
r31	MC1	MC1	100	29	0	0	96839	96867	95259	95287	0.00000288	direct	17	24	0	0	0
r32	MC1	MC2	100	90	0	0	28822	28911	6978	7067	3.54E-40	direct	23	18	0	0	0
r33	MC1	MC2	97.674	86	2	0	26796	26881	12509	12424	1.28E-34	direct	20	14	0	0	0
r34	MC1	MC2	98.611	72	1	0	138426	138497	12641	12570	1.67E-28	direct	20	15	0	0	0
r35	MC1	MC2	95.062	81	0	1	164744	164824	34518	34594	2.16E-27	direct	50	23	0	0	0
r36	MC1	MC2	85.981	107	11	2	26755	26857	7617	7511	1.68E-23	direct	25	19	0	0	0

r37	MC1	MC2	100	46	0	0	1451 08	1451 53	4177	4132	1.02E-15	direct	30	19	0	0	0
r38	MC1	MC2	97.95 9	49	1	0	9674 5	9679 3	5625	5577	1.02E-15	direct	33	7	0	0	0
r39	MC1	MC2	85.89 7	78	7	2	5838 7	5846 0	2643 4	2635 7	4.75E-14	direct	30	12	0	0	0
r40	MC1	MC2	100	40	0	0	1164 73	1165 12	3550 3	3546 4	2.21E-12	direct	28	14	0	0	0
r41	MC1	MC2	100	37	0	0	2307 06	2307 42	2633 0	2636 6	1.03E-10	direct	8	17	0	0	0
r42	MC1	MC2	95.34 9	43	1	1	1430 45	1430 86	8716	8674	3.7E-10	direct	21	17	0	0	0
r43	MC1	MC2	91.48 9	47	2	1	1775 00	1775 44	7245	7199	4.78E-09	direct	17	19	0	0	0
r44	MC1	MC2	100	31	0	0	1070 17	1070 47	3662 3	3665 3	0.000000 222	direct	23	23	0	0	0
r45	MC1	MC2	100	29	0	0	6555 3	6558 1	1251 9	1249 1	0.000002 88	direct	28	16	0	0	0
r46	MC1	MC2	90.24 4	41	4	0	2030 11	2030 51	2032 2	2036 2	0.000002 88	direct	30	18	0	0	0
r48	MC1	MC2	95.83 3	48	2	0	1385 95	1385 48	7487	7534	2.53E-14	direct	11	7	0	0	0
r49	MC1	MC2	94.28 6	35	0	2	6559 2	6555 8	2641 5	2644 7	0.000001 54	direct	14	24	0	0	0
r50	MC1	MC2	96.77 4	31	1	0	1283 21	1282 91	2179 8	2182 8	0.000001 54	direct	20	22	0	0	0

r51	MC1	MC2	100	28	0	0	1385 44	1385 17	2641 5	2644 2	0.000001 54	direct	13	18	0	0	0
r52	MC2	MC2	96.22 6	53	2	0	1244 8	1250 0	7511	7563	4.21E-17	direct	2	24	0	0	0

Table S3 PCR primers used to detect the homologous recombination of the three repeats in the *S. officinalis* mitogenome.

Primer Name	Corresponding DBS ID	Corresponding Repetitive sequence ID	Primer Sequence (5'→3')
saof-r01-F1	DBS01	r01	TGGCAACAACCAGAATGAAA
saof-r01-R1	DBS01	r01	CGCTATTCAGGCCGTTACTC
saof-r01-F2	DBS01	r01	AATCAACCGAAGAGGGGACT
saof-r01-R2	DBS01	r01	CACCTCTTCTTTTGCCTTCG
saof-r02-F1	DBS02	r02	CGCTCTCTCAGACGTTTCCA
saof-r02-R1	DBS02	r02	CGATTTTCGTTCCGCTGCTAC
saof-r02-F2	DBS02	r02	GGTTGGCATTGGGGAAGTCT
saof-r02-R2	DBS02	r02	TTGGGCTTTGCTCTTACCGA
saof-r03-F1	DBS03	r47	AGATACCTTCCCCCGGACTT
saof-r03-R1	DBS03	r47	CAATGGACTATGCCTGCTGC
saof-r03-F2	DBS03	r47	CCCTTAGCTTTTGGCGTTTCG
saof-r03-R2	DBS03	r47	GGAAGAGCGGAGCAGTCAAA

Table S4 Simple sequence repeats in the *S. officinalis* mitogenome. MC1/2: mitogenome chromosome 1/2.

[illegible]

Table S5 Detailed information of the simple sequence repeats in the *S. officinalis* mitogenome. MC1/2: mitogenome chromosome 1/2. The simple sequence repeats in the exonic regions of genes are highlighted with asterisks.

Chromosome	ID	Start	End	Repeat type	Repeat unit
MC1	SSR1	2062	2073	tetra-	(ATTC)3
MC1	SSR2	9248	9259	mono-	(A)12
MC1	SSR3	15954	15965	tetra-	(TTTC)3
MC1	SSR4	22901	22915	penta-	(AAGAG)3
MC1	SSR5	27147	27158	tetra-	(TGCC)3
MC1	SSR6	29637	29648	di-	(CT)6
MC1	SSR7	29887	29896	di-	(CT)5
MC1	SSR8	41762	41773	tetra-	(GGTC)3
MC1	SSR9	43093	43107	tri-	(AAT)5
MC1	SSR10	47505	47516	tetra-	(CTTT)3
MC1	SSR11	49986	49997	tri-	(AGA)4
MC1	SSR12	51577	51588	tetra-	(CCAA)3
MC1	SSR13	53213	53224	tetra-	(AAGA)3
MC1	SSR14	57328	57339	tri-	(GAA)4
MC1	SSR15	60765	60774	di-	(TG)5
MC1	SSR16	63084	63093	di-	(TA)5
MC1	SSR17*	66156	66167	tetra-	(TCTT)3
MC1	SSR18*	72382	72396	penta-	(CTTTT)3
MC1	SSR19	74363	74377	tri-	(TTC)5
MC1	SSR20	81956	81967	tetra-	(GCTA)3
MC1	SSR21	83825	83842	hexa-	(TTAGAG)3
MC1	SSR22	84906	84917	tri-	(GAA)4
MC1	SSR23	91667	91681	penta-	(GAAAG)3
MC1	SSR24	92866	92877	tetra-	(AAGA)3
MC1	SSR25	97264	97281	hexa-	(TTTATA)3
MC1	SSR26	104007	104018	tri-	(TTA)4
MC1	SSR27	105009	105018	di-	(GA)5
MC1	SSR28	113445	113459	penta-	(AGCTA)3
MC1	SSR29	124448	124459	tetra-	(GAAA)3
MC1	SSR30	132713	132724	tetra-	(CCTC)3
MC1	SSR31	135514	135525	tri-	(AGT)4
MC1	SSR32	138876	138893	hexa-	(CTATTA)3
MC1	SSR33	142826	142837	tetra-	(GCTC)3
MC1	SSR34	147535	147546	tri-	(CTT)4
MC1	SSR35	148000	148011	tetra-	(GAAA)3
MC1	SSR36	148634	148645	tetra-	(AAAG)3
MC1	SSR37	152086	152095	di-	(CT)5
MC1	SSR38	153889	153900	tri-	(AGA)4
MC1	SSR39	165316	165327	tetra-	(TTTC)3

MC1	SSR40	172992	173003	tetra-	(CATT)3
MC1	SSR41	178918	178932	tri-	(TAT)5
MC1	SSR42*	184739	184750	tetra-	(CATT)3
MC1	SSR43	194172	194182	mono-	(T)11
MC1	SSR44	202376	202387	di-	(AG)6
MC1	SSR45	204811	204822	tri-	(CTA)4
MC1	SSR46	205986	205997	tetra-	(TTTG)3
MC1	SSR47	209291	209302	tetra-	(TAAA)3
MC1	SSR48	212121	212132	tri-	(ACT)4
MC1	SSR49	214541	214550	di-	(AG)5
MC1	SSR50	215994	216008	penta-	(CAATA)3
MC1	SSR51	216372	216383	tetra-	(TTTC)3
MC1	SSR52	217234	217245	tetra-	(CTGG)3
MC1	SSR53	221348	221357	di-	(AG)5
MC1	SSR54	224542	224553	tetra-	(GCCG)3
MC1	SSR55	236633	236650	hexa-	(TTTACA)3
MC1	SSR56	236833	236842	mono-	(T)10
MC1	SSR57	241691	241700	di-	(CT)5
MC1	SSR58*	242042	242051	mono-	(T)10
MC1	SSR59*	244673	244687	penta-	(CTAGT)3
MC1	SSR60	247011	247022	tri-	(TAA)4
MC1	SSR61	247555	247566	tetra-	(TCTT)3
MC1	SSR62	249767	249778	tetra-	(AGAT)3
MC1	SSR63	252341	252350	di-	(AT)5
MC1	SSR64	255694	255705	tetra-	(AGAA)3
MC1	SSR65	261609	261620	tetra-	(TTCT)3
MC1	SSR66	263325	263336	tetra-	(AAGC)3
MC1	SSR67	265540	265551	tetra-	(AGAA)3
MC2	SSR68	830	839	di-	(TC)5
MC2	SSR69	5103	5112	di-	(AT)5
MC2	SSR70	9766	9775	di-	(TC)5
MC2	SSR71	18627	18641	penta-	(TATAA)3
MC2	SSR72	20392	20403	tetra-	(TCTA)3
MC2	SSR73*	25215	25226	tetra-	(AAGA)3
MC2	SSR74	25703	25714	tetra-	(AATA)3
MC2	SSR75	26570	26581	tetra-	(AGTG)3
MC2	SSR76	37406	37415	mono-	(A)10
MC2	SSR77	37494	37503	mono-	(A)10
MC2	SSR78	38492	38501	mono-	(A)10

Table S6 Long tandem repeats in the mitogenome of *S. officinalis*. The tandem repeats units in the exonic regions of genes were highlighted with the asterisks.

Chromosomes	ID	Indices	Period size(bp)	Copy Number	Consensus Size (bp)	Percent Matches	Percent Indels	Score	Bases number				Entropy (0–2)
									A	G	C	T	
MC1	TR1	34927-35003	18	4.3	18	90	6	102	33	6	25	33	1.82
MC1	TR2	34928-35003	36	2.1	36	90	0	116	34	6	25	34	1.82
MC1	TR3	57560-57594	17	2	18	88	5	54	25	20	31	22	1.98
MC1	TR4	66206-66278	33	2.3	31	84	11	87	28	15	8	47	1.73
MC1	TR5	167466-167500	17	2	18	94	5	63	48	22	0	28	1.51
MC1	TR6	167493-167538	23	2	23	86	0	65	60	6	6	26	1.46
MC1	TR7	190941-190979	20	2	20	84	0	51	69	7	17	5	1.32
MC2	TR8*	25104-25176	33	2.3	31	84	11	87	47	8	15	28	1.73
MC2	TR9	25792-25817	12	2.2	12	100	0	52	19	30	7	42	1.79

Table S7 List of mitochondrial plastid DNA (MTPT) in the *S. officinalis* mitogenome. MC1/2: mitogenomic chromosomes 1/2.

MTPT ID	Chromosome	Identity (%)	Alignment Length (bp)	Number of Mismatches	Number of Gap openings	Positions on the Chloroplast Genome		Positions on the Mitochondrial Genome		Genes Located in the MTPT Fragments	E value	Score
						Start	End	Start	End			
mtpt01	MC1	100	4261	0	0	141708	145968	37176	32916	<i>ycf2</i> fragment, <i>ycf15</i>	0	7869
mtpt02	MC1	100	1447	0	0	149035	150481	55242	56688	<i>rpl23</i> , <i>trnI</i> -CAU	0	2673
mtpt03	MC1	98.582	141	2	0	36259	36399	62423	62283		1.93E-65	250
mtpt04	MC1	98.485	66	1	0	54329	54394	64471	64536		2.04E-25	1.17E+02
mtpt05	MC1	94.118	85	4	1	126934	127017	105341	105425	<i>trnN</i> -GUU	9.42E-29	1.28E+02
mtpt06	MC1	92	50	3	1	134881	134930	130404	130452		5.79E-11	6.94E+01
mtpt07	MC1	93.75	80	5	0	51266	51345	136496	136575	<i>trnM</i> -CAU	1.58E-26	1.21E+02
mtpt08	MC1	100	386	0	0	43011	43396	159908	159523		0	7.13E+02
mtpt09	MC1	75.599	459	100	11	10034	10486	160245	160697		1.95E-55	2.17E+02
mtpt10	MC1	79.705	882	139	31	98634	99497	166520	165661		4.62E-171	6.01E+02
mtpt11	MC1	99.972	3598	1	0	135731	139328	167076	170673	<i>rps7</i>	0	6.64E+03
mtpt12	MC1	100	41	0	0	115938	115978	168353	168393		3.46E-13	7.68E+01
mtpt13	MC1	100	43	0	0	55410	55452	195019	195061		2.67E-14	8.05E+01
mtpt14	MC1	97.531	81	2	0	8	88	200038	200118	<i>trnH</i> -GUG	4.35E-32	1.39E+02
mtpt15	MC1	89.313	131	13	1	29441	29570	218815	218685	<i>trnD</i> -GUC	2.58E-39	1.63E+02
mtpt16	MC1	88.95	181	16	2	44071	44251	219338	219514		1.51E-56	2.20E+02
mtpt17	MC1	78.889	90	16	3	7827	7915	219501	219414	<i>trnS</i> -GGA	1.25E-07	5.84E+01

mtpt18	MC1	87.64	178	11	4	44790	44967	219520	219686		2.55E-49	1.96E+02
mtpt19	MC1	97.561	164	4	0	33546	33709	245207	245044		6.83E-75	2.81E+02
mtpt20	MC1	100	1698	0	0	31491	33188	246897	245200	<i>psbD</i>	0	3.14E+03
mtpt21	MC1	92.661	109	3	2	71222	71329	252451	252347		5.59E-36	1.52E+02
mtpt22	MC2	100	196	0	0	65279	65474	11286	11481	<i>trnP-UGG</i>	2.4E-99	363
mtpt23	MC2	100	128	0	0	65075	65202	11110	11237	<i>trnW-CCA</i>	1.5E-61	237

Table S8 Summary of RNA editing sites detected in the PCGs of the *S. officinalis* mitogenome. “Nt Pos” and “AA Pos” mean the positions of the RNA editing sites in the nucleotide and amino acid sequences of the PCGs. P: the sequence was successfully validated by both PCR amplification and Sanger sequencing experiments. N: the sequence was successfully amplified by PCR but the Sanger sequencing results differed from those expected. NA: the sequence was not validated by PCR and Sanger sequencing experiments. The 193 sites of *S. officinalis* mitogenome homologous to those of the *S. miltiorrhiza* mitogenome are underlined.

Gene	Nt Pos	AA Pos	Reference Nt	Nt coverage	Nt Base Count [A,C,G,T]	Nt allsubs	Nt Frequency	Effect	PCR Success	Codon Position
atp4	59	20	C	4474	[0, 31, 0, 4443]	CT	0.99	TCT (S) => TTT (F)	P	2
atp4	71	24	C	5250	[1, 27, 0, 5222]	CT CA	0.99	TCA (S) => TTA (L)	P	2
atp4	<u>89</u>	30	C	4834	[0, 107, 0, 4727]	CT	0.98	TCA (S) => TTA (L)	P	2
atp4	118	40	C	5023	[0, 18, 0, 5005]	CT	1	CGT (R) => TGT (C)	P	1
atp4	<u>215</u>	72	C	6007	[1, 39, 0, 5967]	CT CA	0.99	TCG (S) => TTG (L)	P	2
atp4	227	76	C	6076	[0, 84, 1, 5991]	CT CG	0.99	CCC (P) => CTC (L)	P	2
atp4	<u>248</u>	83	C	5278	[0, 27, 0, 5251]	CT	0.99	CCT (P) => CTT (L)	P	2
atp4	<u>251</u>	84	C	5577	[0, 37, 1, 5539]	CT CG	0.99	CCG (P) => CTG (L)	P	2
atp4	<u>395</u>	132	C	2771	[0, 9, 0, 2762]	CT	1	TCA (S) => TTA (L)	P	2
atp4	<u>407</u>	136	C	2590	[1, 5, 0, 2584]	CT CA	1	CCA (P) => CTA (L)	P	2
atp4	416	139	C	2323	[0, 23, 0, 2300]	CT	0.99	ACT (T) => ATT (I)	P	2
atp6	<u>26</u>	9	C	9490	[1, 84, 0, 9405]	CT CA	0.99	TCA (S) => TTA (L)	NA	2
atp6	<u>77</u>	26	C	10579	[0, 30, 1, 10548]	CT CG	1	CCG (P) => CTG (L)	NA	2
atp6	<u>146</u>	49	C	8603	[0, 53, 0, 8550]	CT	0.99	TCG (S) => TTG (L)	NA	2
atp6	164	55	C	8739	[0, 78, 1, 8660]	CT CG	0.99	TCG (S) => TTG (L)	NA	2
atp6	172	58	C	7290	[0, 14, 0, 7276]	CT	1	CGT (R) => TGT (C)	NA	1
atp6	<u>311</u>	104	C	10524	[0, 41, 0, 10483]	CT	1	TCA (S) => TTA (L)	NA	2

atp6	370	124	C	9843	[0, 32, 0, 9811]	CT	1	CCT (P) => TCT (S)	NA	1
atp6	<u>373</u>	125	C	9878	[0, 48, 0, 9830]	CT	1	CAT (H) => TAT (Y)	NA	1
atp8	30	16	C	3042	[0, 1434, 0, 1608]	CT	0.53	TCA (S) => TTA (L)	NA	2
atp8	58	20	C	2774	[0, 131, 1, 2642]	CT CG	0.95	CTC (L) => TTC (F)	P	1
atp9	212	71	C	1446	[0, 5, 0, 1441]	CT	1	TCA (S) => TTA (L)	NA	2
ccmB	28	10	C	57	[0, 29, 0, 28]	CT	0.49	CAT (H) => TAT (Y)	NA	1
ccmB	<u>80</u>	27	C	30	[0, 20, 0, 10]	CT	0.33	TCG (S) => TTG (L)	NA	2
ccmB	87	87	C	39	[0, 25, 0, 14]	CT	0.36	ATC (I) => ATT (I)	NA	3
ccmB	<u>128</u>	43	C	34	[4, 0, 30, 0]	CT	0.12	TCA (S) => TTA (L)	NA	2
ccmB	286	96	C	36	[0, 25, 0, 11]	CT	0.31	CGG (R) => TGG (W)	NA	1
ccmB	<u>304</u>	102	C	38	[0, 26, 0, 12]	CT	0.32	CGT (R) => TGT (C)	NA	1
ccmB	313	105	C	40	[0, 25, 0, 15]	CT	0.38	CGT (R) => TGT (C)	NA	1
ccmB	338	113	C	39	[0, 26, 0, 13]	CT	0.33	CCG (P) => CTG (L)	NA	2
ccmB	<u>367</u>	123	C	39	[0, 34, 0, 5]	CT	0.13	CGG (R) => TGG (W)	NA	1
ccmB	380	127	C	37	[0, 29, 0, 8]	CT	0.22	CCA (P) => CTA (L)	NA	2
ccmB	<u>424</u>	142	C	25	[0, 22, 0, 3]	CT	0.12	CGT (R) => TGT (C)	NA	1
ccmB	<u>428</u>	143	C	27	[0, 20, 0, 7]	CT	0.26	TCG (S) => TTG (L)	NA	2
ccmB	<u>551</u>	184	C	7	[1, 0, 6, 0]	CT	0.14	TCA (S) => TTA (L)	NA	2
ccmC	<u>38</u>	13	C	487	[0, 40, 0, 447]	CT	0.92	TCA (S) => TTA (L)	NA	2
ccmC	76	26	C	398	[0, 12, 0, 386]	CT	0.97	CGG (R) => TGG (W)	NA	1
ccmC	<u>103</u>	35	C	347	[0, 5, 0, 342]	CT	0.99	CAT (H) => TAT (Y)	NA	1
ccmC	115	39	C	305	[0, 16, 0, 289]	CT	0.95	CGG (R) => TGG (W)	NA	1
ccmC	133	45	C	310	[0, 23, 0, 287]	CT	0.93	CTT (L) => TTT (F)	NA	1
ccmC	<u>161</u>	54	C	235	[0, 6, 0, 229]	CT	0.97	CCC (P) => CTC (L)	NA	2
ccmC	179	60	C	194	[0, 2, 0, 192]	CT	0.99	GCG (A) => GTG (V)	NA	2
ccmC	184	62	C	195	[0, 4, 0, 191]	CT	0.98	CGG (R) => TGG (W)	NA	1

ccmC	253	85	C	139	[0, 124, 0, 15]	CT	0.11	CTT (L) => TTT (F)	NA	1
ccmC	281	94	C	65	[0, 8, 0, 57]	CT	0.88	ACA (T) => ATA (I)	NA	2
ccmC	<u>299</u>	100	C	41	[0, 21, 0, 20]	CT	0.49	TCT (S) => TTT (F)	NA	2
ccmC	<u>331</u>	111	C	27	[0, 11, 0, 16]	CT	0.59	CGG (R) => TGG (W)	NA	1
ccmC	<u>395</u>	132	C	18	[0, 14, 0, 4]	CT	0.22	TCG (S) => TTG (L)	NA	2
ccmC	399	133	C	18	[0, 10, 0, 8]	CT	0.44	TTC (F) => TTT (F)	NA	3
ccmC	400	134	C	18	[0, 14, 0, 4]	CT	0.22	CTT (L) => TTT (F)	NA	1
ccmC	<u>436</u>	146	C	16	[0, 13, 0, 3]	CT	0.19	CCT (P) => TCT (S)	NA	1
ccmC	446	149	C	15	[0, 13, 0, 2]	CT	0.13	CCG (P) => CTG (L)	NA	2
ccmC	458	153	C	14	[0, 12, 0, 2]	CT	0.14	TCA (S) => TTA (L)	NA	2
ccmC	<u>548</u>	183	C	4	[0, 3, 0, 1]	CT	0.25	TCT (S) => TTT (F)	NA	2
ccmC	<u>568</u>	190	C	4	[0, 3, 0, 1]	CT	0.25	CCT (P) => TCT (S)	NA	1
ccmC	575	192	C	4	[0, 3, 0, 1]	CT	0.25	CCC (P) => CTC (L)	NA	2
ccmC	605	202	C	4	[0, 3, 0, 1]	CT	0.25	TCC (S) => TTC (F)	NA	2
ccmC	<u>608</u>	203	C	4	[0, 0, 0, 4]	CT	1	CCC (P) => CTC (L)	NA	2
ccmC	614	205	C	4	[0, 1, 0, 3]	CT	0.75	TCA (S) => TTA (L)	NA	2
ccmC	<u>650</u>	217	C	4	[0, 0, 0, 4]	CT	1	CCT (P) => CTT (L)	NA	2
ccmC	673	225	C	4	[0, 1, 0, 3]	CT	0.75	CCT (P) => TCT (S)	NA	1
ccmFc	<u>16</u>	6	C	319	[0, 270, 0, 49]	CT	0.15	CAC (H) => TAC (Y)	NA	1
ccmFc	<u>38</u>	13	C	312	[0, 25, 0, 287]	CT	0.92	TCC (S) => TTC (F)	NA	2
ccmFc	50	17	C	247	[0, 15, 0, 232]	CT	0.94	CCT (P) => CTT (L)	NA	2
ccmFc	52	18	C	263	[0, 22, 0, 241]	CT	0.92	CGT (R) => TGT (C)	NA	1
ccmFc	<u>103</u>	35	C	288	[0, 5, 0, 283]	CT	0.98	CCC (P) => TCC (S)	NA	1
ccmFc	122	41	C	360	[0, 13, 0, 347]	CT	0.96	TCC (S) => TTC (F)	NA	2
ccmFc	<u>146</u>	49	C	363	[0, 2, 0, 361]	CT	0.99	CCT (P) => CTT (L)	NA	2
ccmFc	<u>151</u>	51	C	370	[0, 5, 0, 365]	CT	0.99	CCT (P) => TCT (S)	NA	1

ccmFc	<u>155</u>	52	C	370	[0, 15, 0, 355]	CT	0.96	TCA (S) => TTA (L)	NA	2
ccmFc	310	104	C	479	[0, 9, 0, 470]	CT	0.98	CGT (R) => TGT (C)	NA	1
ccmFc	321	107	C	503	[0, 422, 0, 81]	CT	0.16	CCC (P) => CCT (P)	NA	3
ccmFc	334	112	C	455	[0, 175, 0, 280]	CT	0.62	CTT (L) => TTT (F)	NA	1
ccmFc	<u>378</u>	126	C	397	[0, 131, 0, 266]	CT	0.67	TTC (F) => TTT (F)	NA	3
ccmFc	390	130	C	431	[0, 389, 0, 42]	CT	0.1	CTC (L) => CTT (L)	NA	3
ccmFc	406	136	C	437	[0, 15, 0, 422]	CT	0.97	CGT (R) => TGT (C)	NA	1
ccmFc	1228	410	C	64	[0, 2, 0, 62]	CT	0.97	CGG (R) => TGG (W)	NA	1
ccmFc	1233	411	C	61	[0, 55, 0, 6]	CT	0.1	ATC (I) => ATT (I)	NA	3
ccmFn	<u>38</u>	13	C	1934	[0, 8, 0, 1926]	CT	1	CCG (P) => CTG (L)	NA	2
ccmFn	<u>98</u>	33	C	1456	[0, 157, 0, 1299]	CT	0.89	CCT (P) => CTT (L)	NA	2
ccmFn	<u>137</u>	46	C	727	[0, 51, 0, 676]	CT	0.93	TCG (S) => TTG (L)	NA	2
ccmFn	142	48	C	772	[0, 70, 0, 702]	CT	0.91	CGT (R) => TGT (C)	NA	1
ccmFn	<u>151</u>	51	C	763	[0, 100, 0, 663]	CT	0.87	CCT (P) => TCT (S)	NA	1
ccmFn	165	55	C	750	[0, 609, 0, 141]	CT	0.19	TCC (S) => TCT (S)	NA	3
ccmFn	<u>248</u>	83	C	1184	[0, 60, 0, 1124]	CT	0.95	TCA (S) => TTA (L)	NA	2
ccmFn	256	86	C	1305	[0, 52, 0, 1253]	CT	0.96	CGG (R) => TGG (W)	NA	1
ccmFn	283	95	C	1315	[0, 42, 0, 1273]	CT	0.97	CTT (L) => TTT (F)	NA	1
ccmFn	371	124	C	1198	[0, 34, 0, 1164]	CT	0.97	TCG (S) => TTG (L)	NA	2
ccmFn	<u>378</u>	126	C	1173	[1, 179, 0, 993]	CT CA	0.85	TTC (F) => TTT (F)	NA	3
ccmFn	<u>713</u>	238	C	631	[1, 27, 0, 603]	CT CA	0.96	CCT (P) => CTT (L)	NA	2
ccmFn	722	241	C	612	[0, 60, 0, 552]	CT	0.9	TCA (S) => TTA (L)	NA	2
ccmFn	732	244	C	640	[0, 481, 0, 159]	CT	0.25	TCC (S) => TCT (S)	NA	3
ccmFn	760	254	C	761	[1, 25, 0, 735]	CT CA	0.97	CGT (R) => TGT (C)	NA	1
ccmFn	782	261	C	866	[0, 76, 0, 790]	CT	0.91	TCA (S) => TTA (L)	NA	2
ccmFn	794	265	C	983	[0, 45, 0, 938]	CT	0.95	CCA (P) => CTA (L)	NA	2

ccmFn	<u>809</u>	270	C	985	[0, 48, 0, 937]	CT	0.95	TCA (S) => TTA (L)	NA	2
ccmFn	867	289	C	1158	[0, 420, 0, 738]	CT	0.64	GGC (G) => GGT (G)	NA	3
ccmFn	<u>958</u>	320	C	1275	[0, 37, 0, 1238]	CT	0.97	CGC (R) => TGC (C)	NA	1
ccmFn	1276	426	C	886	[0, 62, 0, 824]	CT	0.93	CGG (R) => TGG (W)	NA	1
ccmFn	1304	435	C	892	[0, 56, 0, 836]	CT	0.94	CCA (P) => CTA (L)	NA	2
ccmFn	1321	441	C	970	[0, 60, 0, 910]	CT	0.94	CAT (H) => TAT (Y)	NA	1
ccmFn	1336	446	C	957	[0, 57, 0, 900]	CT	0.94	CGG (R) => TGG (W)	NA	1
ccmFn	1354	452	C	1161	[0, 71, 0, 1090]	CT	0.94	CGG (R) => TGG (W)	NA	1
ccmFn	1387	463	C	1292	[0, 64, 0, 1228]	CT	0.95	CGG (R) => TGG (W)	NA	1
ccmFn	1448	483	C	1704	[0, 19, 0, 1685]	CT	0.99	TCC (S) => TTC (F)	NA	2
ccmFn	1472	491	C	1660	[0, 27, 0, 1633]	CT	0.98	CCA (P) => CTA (L)	NA	2
ccmFn	1484	495	C	1597	[0, 30, 0, 1567]	CT	0.98	TCA (S) => TTA (L)	NA	2
ccmFn	1519	507	C	1212	[0, 28, 0, 1184]	CT	0.98	CCC (P) => TCC (S)	NA	1
cob	114	38	C	4575	[1, 3354, 0, 1220]	CT CA	0.27	TTC (F) => TTT (F)	NA	3
cob	180	60	C	4081	[0, 3256, 0, 825]	CT	0.2	TAC (Y) => TAT (Y)	NA	3
cob	<u>298</u>	100	C	3977	[0, 26, 0, 3951]	CT	0.99	CAC (H) => TAC (Y)	NA	1
cob	325	109	C	3603	[0, 35, 0, 3568]	CT	0.99	CAT (H) => TAT (Y)	NA	1
cob	358	120	C	3628	[0, 49, 1, 3578]	CT CG	0.99	CGG (R) => TGG (W)	NA	1
cob	<u>568</u>	190	C	3727	[0, 32, 0, 3695]	CT	0.99	CAT (H) => TAT (Y)	NA	1
cob	853	285	C	5247	[0, 36, 0, 5211]	CT	0.99	CAT (H) => TAT (Y)	NA	1
cob	908	303	C	4047	[0, 36, 0, 4011]	CT	0.99	TCA (S) => TTA (L)	NA	2
cob	982	328	C	2417	[0, 163, 0, 2254]	CT	0.93	CAC (H) => TAC (Y)	NA	1
cob	1015	339	C	1949	[0, 39, 0, 1910]	CT	0.98	CGC (R) => TGC (C)	NA	1
cob	1084	362	C	1072	[0, 19, 0, 1053]	CT	0.98	CCT (P) => TCT (S)	NA	1
cob	1160	387	C	393	[0, 264, 0, 129]	CT	0.33	ACG (P) => ATG (M)	NA	2
cox1	<u>242</u>	81	C	6994	[0, 27, 0, 6967]	CT	1	TCT (S) => TTT (F)	P	2

cox1	<u>254</u>	85	C	8482	[0, 31, 0, 8451]	CT	1	TCT (S) => TTT (F)	P	2
cox1	<u>452</u>	151	C	3351	[0, 11, 0, 3340]	CT	1	TCT (S) => TTT (F)	P	2
cox1	515	172	C	1820	[0, 5, 0, 1815]	CT	1	TCC (S) => TTC (F)	P	2
cox1	<u>551</u>	184	C	1139	[0, 5, 0, 1134]	CT	1	TCA (S) => TTA (L)	P	2
cox1	590	197	C	578	[0, 3, 0, 575]	CT	0.99	CCA (P) => CTA (L)	P	2
cox1	715	239	C	48	[0, 0, 0, 48]	CT	1	CGG (R) => TGG (W)	P	1
cox1	761	254	C	2262	[0, 48, 0, 2214]	CT	0.98	TCC (S) => TTC (F)	N	2
cox1	1078	360	C	8275	[0, 6261, 0, 2014]	CT	0.24	CTG (L) => TTG (L)	N	1
cox1	1186	396	C	9741	[0, 5, 0, 9736]	CT	1	CAC (H) => TAC (Y)	P	1
cox1	1405	469	C	4684	[0, 30, 0, 4654]	CT	0.99	CGT (R) => TGT (C)	P	1
cox1	1413	471	C	4508	[0, 2153, 0, 2355]	CT	0.52	TTC (F) => TTT (F)	N	3
cox1	1433	478	C	3399	[0, 14, 0, 3385]	CT	1	TCA (S) => TTA (L)	P	2
cox1	1489	497	C	1439	[0, 6, 0, 1433]	CT	1	CCA (P) => TCA (S)	N	1
cox1	1499	500	C	1238	[0, 11, 0, 1227]	CT	0.99	CCA (P) => CTA (L)	P	2
cox2	<u>47</u>	16	C	5613	[0, 63, 0, 5550]	CT	0.99	TCT (S) => TTT (F)	NA	2
cox2	<u>419</u>	140	C	3296	[0, 72, 0, 3224]	CT	0.98	ACG (P) => ATG (M)	NA	2
cox2	437	146	C	2919	[0, 118, 0, 2801]	CT	0.96	CCA (P) => CTA (L)	NA	2
cox2	<u>452</u>	151	C	2567	[0, 131, 0, 2436]	CT	0.95	TCA (S) => TTA (L)	NA	2
cox2	520	174	C	872	[0, 31, 0, 841]	CT	0.96	CCT (P) => TCT (S)	NA	1
cox2	533	178	C	664	[0, 34, 0, 630]	CT	0.95	CCT (P) => CTT (L)	NA	2
cox2	595	199	C	228	[58, 170, 0, 0]	CA	0.25	CAG (Q) => AAG (K)	NA	1
cox2	<u>608</u>	203	C	161	[0, 2, 0, 159]	CT	0.99	TCG (S) => TTG (L)	NA	2
cox2	697	233	C	44	[0, 3, 0, 41]	CT	0.93	CCT (P) => TCT (S)	NA	1
cox2	718	240	C	53	[0, 5, 0, 48]	CT	0.91	CGG (R) => TGG (W)	NA	1
cox3	174	58	C	4400	[0, 3807, 0, 593]	CT	0.13	TTC (F) => TTT (F)	N	3
cox3	245	82	C	3733	[0, 32, 0, 3701]	CT	0.99	CCT (P) => CTT (L)	P	2

cox3	<u>304</u>	102	C	2928	[0, 32, 3, 2893]	CT CG	0.99	CGG (R) => TGG (W)	P	1
cox3	<u>311</u>	104	C	2931	[0, 120, 2, 2809]	CT CG	0.96	TCT (S) => TTT (F)	P	2
cox3	314	105	C	2893	[0, 56, 0, 2837]	CT	0.98	TCT (S) => TTT (F)	P	2
cox3	<u>419</u>	140	C	5644	[0, 50, 0, 5594]	CT	0.99	CCC (P) => CTC (L)	P	2
cox3	422	141	C	5327	[0, 93, 0, 5234]	CT	0.98	CCT (P) => CTT (L)	P	2
cox3	566	189	C	8247	[1, 110, 0, 8136]	CT CA	0.99	TCC (S) => TTC (F)	P	2
cox3	567	189	C	8377	[0, 4704, 0, 3673]	CT	0.44	TCC (S) => TTT (F)	N	3
cox3	754	252	C	697	[0, 7, 0, 690]	CT	0.99	CGG (R) => TGG (W)	P	1
cox3	764	255	C	627	[0, 16, 0, 611]	CT	0.97	CCA (P) => CTA (L)	P	2
matR	32	11	C	1325	[0, 31, 0, 1294]	CT	0.98	TCC (S) => TTC (F)	NA	2
matR	43	15	C	1270	[0, 54, 0, 1216]	CT	0.96	CCC (P) => TCC (S)	NA	1
matR	237	79	C	317	[0, 276, 0, 41]	CT	0.13	TCC (S) => TCT (S)	NA	3
matR	<u>254</u>	85	C	327	[0, 251, 0, 76]	CT	0.23	TCC (S) => TTC (F)	NA	2
matR	258	86	C	341	[0, 261, 0, 80]	CT	0.23	GCC (A) => GCT (A)	NA	3
matR	326	109	C	375	[0, 15, 0, 360]	CT	0.96	CCA (P) => CTA (L)	NA	2
matR	413	138	C	362	[0, 18, 0, 344]	CT	0.95	TCG (S) => TTG (L)	NA	2
matR	<u>1400</u>	467	C	939	[0, 799, 0, 140]	CT	0.15	TCG (S) => TTG (L)	NA	2
matR	1522	508	C	996	[0, 799, 0, 197]	CT	0.2	CCC (P) => TCT (S)	NA	1
matR	1524	508	C	1009	[0, 778, 0, 231]	CT	0.23	CCC (P) => TCT (S)	NA	3
matR	1658	553	C	1363	[0, 37, 0, 1326]	CT	0.97	TCC (S) => TTC (F)	NA	2
matR	1679	560	C	1133	[0, 59, 0, 1074]	CT	0.95	CCT (P) => CTT (L)	NA	2
matR	1699	567	C	1004	[0, 63, 0, 941]	CT	0.94	CGC (R) => TGC (C)	NA	1
matR	1713	571	C	1011	[0, 258, 0, 753]	CT	0.74	TAC (Y) => TAT (Y)	NA	3
matR	1735	579	C	937	[0, 49, 0, 888]	CT	0.95	CAC (H) => TAC (Y)	NA	1
matR	1766	589	C	793	[0, 29, 0, 764]	CT	0.96	CCG (P) => CTG (L)	NA	2
matR	1805	602	C	698	[0, 29, 0, 669]	CT	0.96	CCA (P) => CTA (L)	NA	2

matR	1823	608	C	586	[0, 30, 0, 556]	CT	0.95	TCA (S) => TTA (L)	NA	2
mttB	<u>16</u>	6	C	310	[0, 207, 0, 103]	CT	0.33	CAT (H) => TAT (Y)	P	1
mttB	<u>26</u>	9	C	339	[0, 73, 0, 266]	CT	0.78	CCG (P) => CTG (L)	P	2
mttB	<u>64</u>	22	C	319	[0, 28, 0, 291]	CT	0.91	CGG (R) => TGG (W)	P	1
mttB	<u>100</u>	34	C	176	[0, 75, 0, 101]	CT	0.57	CGT (R) => TGT (C)	P	1
mttB	112	38	C	154	[0, 46, 0, 108]	CT	0.7	CCG (P) => TCG (S)	P	1
mttB	<u>128</u>	43	C	115	[0, 72, 0, 43]	CT	0.37	TCT (S) => TTT (F)	P	2
mttB	131	44	C	108	[0, 50, 0, 58]	CT	0.54	CCA (P) => CTA (L)	P	2
mttB	178	60	C	158	[0, 20, 0, 138]	CT	0.87	CGT (R) => TGT (C)	P	1
mttB	<u>188</u>	63	C	160	[0, 26, 0, 134]	CT	0.84	TCA (S) => TTA (L)	P	2
mttB	201	67	C	173	[0, 150, 0, 23]	CT	0.13	TTC (F) => TTT (F)	N	3
mttB	202	68	C	172	[0, 51, 0, 121]	CT	0.7	CCG (P) => TCG (S)	P	1
mttB	236	79	C	184	[0, 93, 0, 91]	CT	0.49	TCT (S) => TTT (F)	P	2
mttB	262	88	C	192	[0, 16, 0, 176]	CT	0.92	CAT (H) => TAT (Y)	P	1
mttB	<u>328</u>	110	C	112	[0, 49, 0, 63]	CT	0.56	CTC (L) => TTC (F)	P	1
mttB	<u>331</u>	111	C	112	[0, 23, 0, 89]	CT	0.79	CAT (H) => TAT (Y)	P	1
mttB	<u>344</u>	115	C	98	[0, 58, 0, 40]	CT	0.41	TCT (S) => TTT (F)	P	2
mttB	346	116	C	102	[0, 34, 0, 68]	CT	0.67	CGC (R) => TGC (C)	P	1
mttB	<u>373</u>	125	C	80	[0, 56, 0, 24]	CT	0.3	CTT (L) => TTT (F)	P	1
mttB	<u>376</u>	126	C	74	[0, 21, 0, 53]	CT	0.72	CCC (P) => TCC (S)	P	1
mttB	379	127	C	84	[0, 56, 0, 28]	CT	0.33	CGG (R) => TGG (W)	P	1
mttB	<u>407</u>	136	C	347	[0, 10, 0, 337]	CT	0.97	CCA (P) => CTA (L)	P	2
mttB	472	158	C	573	[0, 16, 0, 557]	CT	0.97	CAT (H) => TAT (Y)	P	1
mttB	<u>497</u>	166	C	617	[0, 26, 0, 591]	CT	0.96	TCG (S) => TTG (L)	P	2
mttB	505	169	C	635	[0, 26, 0, 609]	CT	0.96	CCA (P) => TCA (S)	P	1
mttB	541	181	C	517	[0, 46, 0, 471]	CT	0.91	CGT (R) => TGT (C)	P	1

mttB	554	185	C	365	[0, 85, 0, 280]	CT	0.77	CCA (P) => CTA (L)	P	2
mttB	<u>578</u>	193	C	245	[0, 37, 0, 208]	CT	0.85	TCC (S) => TTC (F)	P	2
mttB	610	204	C	152	[0, 6, 0, 146]	CT	0.96	CCG (P) => TCG (S)	P	1
mttB	616	206	C	149	[0, 17, 0, 132]	CT	0.89	CTC (L) => TTC (F)	P	1
mttB	667	223	C	73	[0, 5, 0, 68]	CT	0.93	CGT (R) => TGT (C)	P	1
mttB	672	224	C	128	[0, 19, 0, 109]	CT	0.85	TTC (F) => TTT (F)	N	3
mttB	<u>713</u>	238	C	97	[0, 4, 0, 93]	CT	0.96	TCG (S) => TTG (L)	P	2
nad1	<u>215</u>	72	C	642	[0, 17, 0, 625]	CT	0.97	TCC (S) => TTC (F)	NA	2
nad1	265	89	C	324	[0, 13, 0, 311]	CT	0.96	CGG (R) => TGG (W)	NA	1
nad1	<u>307</u>	103	C	114	[0, 3, 0, 111]	CT	0.97	CCG (P) => TTG (S)	NA	1
nad1	<u>308</u>	103	C	108	[0, 1, 0, 107]	CT	0.99	CCG (P) => TTG (L)	NA	2
nad1	<u>376</u>	126	C	40	[0, 0, 0, 40]	CT	1	CGG (R) => TGG (W)	NA	1
nad1	<u>401</u>	134	C	43	[0, 11, 0, 32]	CT	0.74	TCT (S) => TTT (F)	NA	2
nad1	<u>436</u>	146	C	28	[0, 6, 0, 22]	CT	0.79	CCT (P) => TCT (S)	NA	1
nad1	490	164	C	48	[0, 22, 0, 26]	CT	0.54	CCC (P) => TCT (S)	NA	1
nad1	492	164	C	46	[0, 36, 0, 10]	CT	0.22	CCC (P) => TCT (S)	NA	3
nad1	493	165	C	43	[0, 11, 0, 32]	CT	0.74	CGT (R) => TGT (C)	NA	1
nad1	500	167	C	47	[0, 11, 0, 36]	CT	0.77	TCG (S) => TTG (L)	NA	2
nad1	536	179	C	47	[0, 6, 0, 41]	CT	0.87	TCC (S) => TTC (F)	NA	2
nad1	635	212	C	13	[0, 3, 0, 10]	CT	0.77	TCA (S) => TTA (L)	NA	2
nad1	<u>725</u>	242	C	258	[0, 30, 0, 228]	CT	0.88	CCA (P) => CTA (L)	NA	2
nad1	734	245	C	279	[0, 73, 0, 206]	CT	0.74	TCG (S) => TTG (L)	NA	2
nad1	<u>740</u>	247	C	271	[0, 67, 0, 204]	CT	0.75	TCT (S) => TTT (F)	NA	2
nad1	743	248	C	275	[0, 66, 0, 209]	CT	0.76	CCA (P) => CTA (L)	NA	2
nad1	755	252	C	587	[0, 160, 0, 427]	CT	0.73	CCG (P) => CTG (L)	NA	2
nad1	779	260	C	817	[0, 68, 0, 749]	CT	0.92	TCC (S) => TTC (F)	NA	2

nad1	792	264	C	956	[0, 455, 0, 501]	CT	0.52	CCC (P) => CCT (P)	NA	3
nad1	823	275	C	1072	[0, 18, 0, 1054]	CT	0.98	CTC (L) => TTC (F)	NA	1
nad1	898	300	C	1042	[0, 17, 0, 1025]	CT	0.98	CGG (R) => TGG (W)	NA	1
nad1	909	303	C	832	[0, 395, 0, 437]	CT	0.53	TTC (F) => TTT (F)	NA	3
nad1	<u>928</u>	310	C	613	[0, 12, 0, 601]	CT	0.98	CGG (R) => TGG (W)	NA	1
nad2	<u>26</u>	9	C	147	[0, 6, 0, 141]	CT	0.96	TCC (S) => TTC (F)	NA	2
nad2	223	75	C	550	[0, 14, 0, 536]	CT	0.97	CTT (L) => TTT (F)	NA	1
nad2	252	84	C	541	[0, 159, 0, 382]	CT	0.71	TTC (F) => TTT (F)	NA	3
nad2	303	101	C	301	[0, 117, 0, 184]	CT	0.61	TTC (F) => TTT (F)	NA	3
nad2	<u>308</u>	103	C	266	[0, 24, 0, 242]	CT	0.91	TCT (S) => TTT (F)	NA	2
nad2	<u>311</u>	104	C	265	[0, 38, 0, 227]	CT	0.86	TCC (S) => TTC (F)	NA	2
nad2	356	119	C	136	[0, 15, 0, 121]	CT	0.89	CCA (P) => CTA (L)	NA	2
nad2	361	121	C	130	[0, 15, 0, 115]	CT	0.88	CCT (P) => TCT (S)	NA	1
nad2	<u>367</u>	123	C	125	[0, 19, 0, 106]	CT	0.85	CGC (R) => TGC (C)	NA	1
nad2	<u>401</u>	134	C	105	[0, 19, 0, 86]	CT	0.82	TCA (S) => TTA (L)	NA	2
nad2	<u>428</u>	143	C	92	[0, 16, 0, 76]	CT	0.83	CCT (P) => CTT (L)	NA	2
nad2	<u>497</u>	166	C	39	[0, 6, 0, 33]	CT	0.85	TCG (S) => TTG (L)	NA	2
nad2	788	263	C	1447	[0, 26, 0, 1421]	CT	0.98	TCT (S) => TTT (F)	NA	2
nad2	800	267	C	1565	[0, 29, 0, 1536]	CT	0.98	TCA (S) => TTA (L)	NA	2
nad2	<u>809</u>	270	C	1591	[0, 37, 0, 1554]	CT	0.98	TCT (S) => TTT (F)	NA	2
nad2	<u>928</u>	310	C	1218	[0, 33, 0, 1185]	CT	0.97	CAT (H) => TAT (Y)	NA	1
nad2	<u>958</u>	320	C	1031	[0, 19, 0, 1012]	CT	0.98	CGT (R) => TGT (C)	NA	1
nad2	<u>1028</u>	343	C	498	[0, 9, 0, 489]	CT	0.98	TCA (S) => TTA (L)	NA	2
nad2	1058	353	C	356	[0, 17, 0, 339]	CT	0.95	TCA (S) => TTA (L)	NA	2
nad2	<u>1298</u>	433	C	199	[0, 4, 0, 195]	CT	0.98	GCG (A) => GTG (V)	NA	2
nad2	<u>1400</u>	467	C	320	[0, 7, 0, 313]	CT	0.98	TCA (S) => TTA (L)	NA	2

nad2	<u>1408</u>	470	C	315	[0, 10, 0, 305]	CT	0.97	CCA (P) => TTA (S)	NA	1
nad2	1409	470	C	315	[0, 4, 0, 311]	CT	0.99	CCA (P) => TTA (L)	NA	2
nad2	1416	472	C	315	[0, 21, 0, 294]	CT	0.93	CCC (P) => CCT (P)	NA	3
nad2	1457	486	C	68	[0, 0, 0, 68]	CT	1	TCA (S) => TTA (L)	NA	2
nad3	44	15	C	333	[0, 19, 0, 314]	CT	0.94	TCG (S) => TTG (L)	P	2
nad3	62	21	C	290	[0, 20, 0, 270]	CT	0.93	CCA (P) => CTA (L)	P	2
nad3	79	27	C	220	[0, 49, 0, 171]	CT	0.78	CCA (P) => TTA (S)	P	1
nad3	<u>80</u>	27	C	219	[0, 15, 0, 204]	CT	0.93	CCA (P) => TTA (L)	P	2
nad3	124	42	C	154	[0, 13, 0, 141]	CT	0.92	CAC (H) => TAC (Y)	P	1
nad3	<u>146</u>	49	C	111	[0, 12, 0, 99]	CT	0.89	TCC (S) => TTC (F)	P	2
nad3	208	70	C	22	[0, 5, 0, 17]	CT	0.77	CCT (P) => TTT (F)	P	1
nad3	<u>209</u>	70	C	26	[0, 6, 0, 20]	CT	0.77	CCT (P) => TTT (F)	P	2
nad3	<u>215</u>	72	C	25	[0, 7, 0, 18]	CT	0.72	CCG (P) => CTG (L)	P	2
nad3	230	77	C	18	[0, 5, 0, 13]	CT	0.72	TCC (S) => TTC (F)	P	2
nad3	247	83	C	4	[0, 3, 0, 1]	CT	0.25	CCT (P) => TCT (S)	P	1
nad3	<u>251</u>	84	C	4	[0, 3, 0, 1]	CT	0.25	CCC (P) => CTC (L)	P	2
nad3	266	89	C	10	[0, 3, 0, 7]	CT	0.7	CCC (P) => CTC (L)	P	2
nad3	<u>275</u>	92	C	12	[0, 3, 0, 9]	CT	0.75	TCT (S) => TTT (F)	P	2
nad3	317	106	C	10	[0, 1, 0, 9]	CT	0.9	TCT (S) => TTT (F)	P	2
nad3	<u>344</u>	115	C	7	[0, 0, 0, 7]	CT	1	TCG (S) => TTG (L)	P	2
nad3	349	117	C	9	[0, 0, 0, 9]	CT	1	CGG (R) => TGG (W)	P	1
nad4	<u>65</u>	22	C	1284	[0, 138, 0, 1146]	CT	0.89	ACT (T) => ATT (I)	NA	2
nad4	68	23	C	1305	[0, 8, 0, 1297]	CT	0.99	CCT (P) => CTT (L)	NA	2
nad4	75	25	C	1342	[0, 1031, 0, 311]	CT	0.23	TTC (F) => TTT (F)	NA	3
nad4	<u>98</u>	33	C	1094	[0, 10, 0, 1084]	CT	0.99	CCG (P) => CTG (L)	NA	2
nad4	<u>149</u>	50	C	659	[0, 4, 0, 655]	CT	0.99	CCT (P) => CTT (L)	NA	2

nad4	157	53	C	722	[0, 2, 0, 720]	CT	1	CGG (R) => TGG (W)	NA	1
nad4	<u>188</u>	63	C	516	[0, 37, 0, 479]	CT	0.93	TCT (S) => TTT (F)	NA	2
nad4	353	118	C	51	[0, 0, 0, 51]	CT	1	ACA (T) => ATA (I)	NA	2
nad4	<u>359</u>	120	C	47	[0, 4, 0, 43]	CT	0.91	TCT (S) => TTT (F)	NA	2
nad4	<u>367</u>	123	C	46	[0, 1, 0, 45]	CT	0.98	CGT (R) => TGT (C)	NA	1
nad4	<u>407</u>	136	C	16	[0, 1, 0, 15]	CT	0.94	CCT (P) => CTT (L)	NA	2
nad4	<u>424</u>	142	C	12	[0, 1, 0, 11]	CT	0.92	CTT (L) => TTT (F)	NA	1
nad4	427	143	C	9	[0, 6, 0, 3]	CT	0.33	CCC (P) => TTC (S)	NA	1
nad4	<u>428</u>	143	C	11	[0, 8, 0, 3]	CT	0.27	CCC (P) => TTC (F)	NA	2
nad4	440	147	C	12	[0, 0, 0, 12]	CT	1	CCA (P) => CTA (L)	NA	2
nad4	599	200	C	2433	[1, 4, 0, 2428]	CT CA	1	TCA (S) => TTA (L)	NA	2
nad4	637	213	C	1726	[0, 1435, 0, 291]	CT	0.17	CTA (L) => TTA (L)	NA	1
nad4	<u>650</u>	217	C	1683	[0, 10, 0, 1673]	CT	0.99	TCT (S) => TTT (F)	NA	2
nad4	758	253	C	385	[0, 3, 0, 382]	CT	0.99	CCT (P) => CTT (L)	NA	2
nad4	810	270	C	223	[0, 170, 0, 53]	CT	0.24	CCC (P) => CCT (P)	NA	3
nad4	847	283	C	118	[0, 91, 0, 27]	CT	0.23	CCA (P) => TTA (S)	NA	1
nad4	<u>848</u>	283	C	110	[0, 13, 0, 97]	CT	0.88	CCA (P) => TTA (L)	NA	2
nad4	878	293	C	79	[0, 4, 0, 75]	CT	0.95	TCG (S) => TTG (L)	NA	2
nad4	997	333	C	628	[0, 113, 0, 515]	CT	0.82	CTA (L) => TTA (L)	NA	1
nad4	1001	334	C	585	[0, 47, 0, 538]	CT	0.92	CCG (P) => CTG (L)	NA	2
nad4	1007	336	C	632	[0, 50, 0, 582]	CT	0.92	TCA (S) => TTA (L)	NA	2
nad4	1100	367	C	1068	[0, 19, 0, 1049]	CT	0.98	TCA (S) => TTA (L)	NA	2
nad4	1120	374	C	821	[0, 39, 0, 782]	CT	0.95	CTC (L) => TTC (F)	NA	1
nad4	1123	375	C	842	[0, 46, 0, 796]	CT	0.95	CCT (P) => TCT (S)	NA	1
nad4	1142	381	C	759	[0, 39, 0, 720]	CT	0.95	TCC (S) => TTC (F)	NA	2
nad4	1163	388	C	689	[0, 7, 0, 682]	CT	0.99	TCA (S) => TTA (L)	NA	2

nad4	<u>1298</u>	433	C	103	[0, 7, 0, 96]	CT	0.93	GCG (A) => GTG (V)	NA	2
nad4	1346	449	C	8	[0, 0, 0, 8]	CT	1	CCA (P) => CTA (L)	NA	2
nad4	1364	455	C	3	[0, 0, 0, 3]	CT	1	TCC (S) => TTC (F)	NA	2
nad4	<u>1408</u>	470	C	9	[0, 1, 0, 8]	CT	0.89	CAC (H) => TAC (Y)	NA	1
nad4	1424	475	C	7	[0, 3, 0, 4]	CT	0.57	CCG (P) => CTG (L)	NA	2
nad4L	11	4	C	269	[0, 13, 0, 256]	CT	0.95	TCT (S) => TTT (F)	P	2
nad4L	17	6	C	286	[0, 29, 0, 257]	CT	0.9	TCA (S) => TTA (L)	P	2
nad4L	25	9	C	283	[0, 16, 0, 267]	CT	0.94	CGG (R) => TGG (W)	P	1
nad4L	<u>56</u>	19	C	59	[0, 11, 0, 48]	CT	0.81	CCT (P) => CTT (L)	P	2
nad4L	<u>65</u>	22	C	27	[0, 22, 0, 5]	CT	0.19	TCA (S) => TTA (L)	P	2
nad4L	70	24	C	30	[0, 23, 0, 7]	CT	0.23	CCA (P) => TCA (S)	P	1
nad4L	<u>80</u>	27	C	37	[0, 16, 0, 21]	CT	0.57	TCA (S) => TTA (L)	P	2
nad4L	<u>101</u>	34	C	240	[0, 15, 0, 225]	CT	0.94	TCG (S) => TTG (L)	P	2
nad4L	<u>128</u>	43	C	377	[0, 13, 0, 364]	CT	0.97	TCG (S) => TTG (L)	P	2
nad4L	<u>149</u>	50	C	476	[0, 8, 0, 468]	CT	0.98	TCA (S) => TTA (L)	P	2
nad4L	158	53	C	539	[0, 23, 0, 516]	CT	0.96	TCA (S) => TTA (L)	P	2
nad4L	<u>167</u>	56	C	567	[0, 25, 0, 542]	CT	0.96	TCA (S) => TTA (L)	P	2
nad4L	222	74	C	641	[0, 567, 0, 74]	CT	0.12	TTC (F) => TTT (F)	P	3
nad4L	<u>251</u>	84	C	377	[0, 5, 0, 372]	CT	0.99	TCT (S) => TTT (F)	P	2
nad5	<u>155</u>	52	C	48	[0, 11, 0, 37]	CT	0.77	CCG (P) => CTG (L)	NA	2
nad5	<u>242</u>	81	C	239	[0, 21, 0, 218]	CT	0.91	CCG (P) => CTG (L)	NA	2
nad5	<u>359</u>	120	C	440	[0, 12, 0, 428]	CT	0.97	TCT (S) => TTT (F)	NA	2
nad5	374	125	C	896	[0, 26, 0, 870]	CT	0.97	CCA (P) => CTA (L)	NA	2
nad5	<u>398</u>	133	C	942	[0, 17, 0, 925]	CT	0.98	TCT (S) => TTT (F)	NA	2
nad5	539	180	C	1232	[0, 35, 0, 1197]	CT	0.97	CCT (P) => CTT (L)	NA	2
nad5	<u>548</u>	183	C	1280	[0, 33, 0, 1247]	CT	0.97	TCG (S) => TTG (L)	NA	2

nad5	<u>608</u>	203	C	1179	[0, 32, 0, 1147]	CT	0.97	GCC (A) => GTC (V)	NA	2
nad5	609	203	C	1139	[0, 906, 0, 233]	CT	0.2	GCC (A) => GTT (V)	NA	2
nad5	629	210	C	1189	[0, 27, 0, 1162]	CT	0.98	TCT (S) => TTT (F)	NA	2
nad5	676	226	C	1044	[0, 19, 0, 1025]	CT	0.98	CTT (L) => TTT (F)	NA	1
nad5	<u>713</u>	238	C	1203	[0, 16, 0, 1187]	CT	0.99	TCG (S) => TTG (L)	NA	2
nad5	<u>725</u>	242	C	1279	[0, 16, 0, 1263]	CT	0.99	TCA (S) => TTA (L)	NA	2
nad5	835	279	C	1166	[0, 41, 0, 1125]	CT	0.96	CCG (P) => TCG (S)	NA	1
nad5	1310	437	C	103	[0, 5, 0, 98]	CT	0.95	TCA (S) => TTA (L)	NA	2
nad5	1490	497	C	758	[0, 68, 0, 690]	CT	0.91	CCC (P) => CTC (L)	NA	2
nad5	1550	517	C	1199	[0, 95, 0, 1104]	CT	0.92	ACC (T) => ATC (I)	NA	2
nad5	1568	523	C	1197	[0, 80, 0, 1117]	CT	0.93	CCG (P) => CTG (L)	NA	2
nad5	1580	527	C	1191	[0, 84, 0, 1107]	CT	0.93	TCA (S) => TTA (L)	NA	2
nad5	1589	530	C	1103	[0, 110, 0, 993]	CT	0.9	TCT (S) => TTT (F)	NA	2
nad5	1610	537	C	1351	[0, 223, 0, 1128]	CT	0.83	TCC (S) => TTC (F)	NA	2
nad5	1695	565	C	684	[0, 586, 0, 98]	CT	0.14	TTC (F) => TTT (F)	NA	3
nad5	1895	632	C	78	[0, 14, 0, 64]	CT	0.82	TCA (S) => TTA (L)	NA	2
nad5	1916	639	C	54	[0, 12, 0, 42]	CT	0.78	TCT (S) => TTT (F)	NA	2
nad5	1918	640	C	56	[0, 14, 0, 42]	CT	0.75	CGT (R) => TGT (C)	NA	1
nad5	1958	653	C	33	[0, 4, 0, 29]	CT	0.88	TCG (S) => TTG (L)	NA	2
nad5	1981	661	C	30	[0, 3, 0, 27]	CT	0.9	CGT (R) => TGT (C)	NA	1
nad6	<u>26</u>	9	C	2037	[0, 114, 1, 1922]	CT CG	0.94	CCT (P) => CTT (L)	NA	2
nad6	88	30	C	1440	[0, 25, 0, 1415]	CT	0.98	CCC (P) => TTC (F)	NA	1
nad6	<u>89</u>	30	C	1457	[0, 31, 0, 1426]	CT	0.98	CCC (P) => TTC (F)	NA	2
nad6	95	32	C	1467	[0, 95, 0, 1372]	CT	0.94	CCA (P) => CTA (L)	NA	2
nad6	<u>103</u>	35	C	1668	[0, 32, 0, 1636]	CT	0.98	CGC (R) => TGC (C)	NA	1
nad6	<u>161</u>	54	C	2957	[0, 62, 0, 2895]	CT	0.98	CCA (P) => CTA (L)	NA	2

nad6	169	57	C	3157	[0, 48, 0, 3109]	CT	0.98	CAT (H) => TAT (Y)	NA	1
nad6	191	64	C	3983	[0, 27, 0, 3956]	CT	0.99	TCA (S) => TTA (L)	NA	2
nad6	306	102	C	6191	[1, 4510, 0, 1680]	CT CA	0.27	TTC (F) => TTT (F)	NA	3
nad6	463	155	C	1391	[0, 14, 0, 1377]	CT	0.99	CCT (P) => TCT (S)	NA	1
nad6	569	190	C	101	[0, 2, 0, 99]	CT	0.98	TCT (S) => TTT (F)	NA	2
nad7	45	15	C	147	[0, 115, 0, 32]	CT	0.22	TTC (F) => TTT (F)	NA	3
nad7	<u>77</u>	26	C	70	[0, 13, 0, 57]	CT	0.81	TCA (S) => TTA (L)	NA	2
nad7	<u>137</u>	46	C	18	[0, 5, 0, 13]	CT	0.72	TCA (S) => TTA (L)	NA	2
nad7	200	67	C	17	[0, 3, 0, 14]	CT	0.82	TCT (S) => TTT (F)	NA	2
nad7	<u>209</u>	70	C	17	[0, 9, 0, 8]	CT	0.47	TCA (S) => TTA (L)	NA	2
nad7	244	82	C	1731	[0, 48, 0, 1683]	CT	0.97	CAT (H) => TAT (Y)	NA	1
nad7	<u>251</u>	84	C	1743	[0, 59, 0, 1684]	CT	0.97	TCA (S) => TTA (L)	NA	2
nad7	<u>316</u>	106	C	3061	[0, 28, 0, 3033]	CT	0.99	CGT (R) => TGT (C)	NA	1
nad7	335	112	C	3450	[0, 21, 0, 3429]	CT	0.99	TCA (S) => TTA (L)	NA	2
nad7	<u>344</u>	115	C	3572	[0, 68, 0, 3504]	CT	0.98	TCA (S) => TTA (L)	NA	2
nad7	383	128	C	3372	[0, 34, 0, 3338]	CT	0.99	TCA (S) => TTA (L)	NA	2
nad7	531	177	C	2232	[0, 1905, 0, 327]	CT	0.15	TCC (S) => TCT (S)	NA	3
nad7	534	178	C	2263	[0, 1936, 0, 327]	CT	0.14	TTC (F) => TTT (F)	NA	3
nad7	<u>578</u>	193	C	1586	[0, 17, 0, 1569]	CT	0.99	TCA (S) => TTA (L)	NA	2
nad7	724	242	C	744	[0, 24, 0, 720]	CT	0.97	CAT (H) => TAT (Y)	NA	1
nad7	739	247	C	599	[0, 26, 0, 573]	CT	0.96	CCT (P) => TTT (F)	NA	1
nad7	<u>740</u>	247	C	609	[0, 24, 0, 585]	CT	0.96	CCT (P) => TTT (F)	NA	2
nad7	769	257	C	487	[0, 17, 0, 470]	CT	0.97	CGC (R) => TGC (C)	NA	1
nad7	926	309	C	1810	[0, 1545, 0, 265]	CT	0.15	TCA (S) => TTA (L)	NA	2
nad7	944	315	C	2402	[0, 51, 0, 2351]	CT	0.98	CCT (P) => CTT (L)	NA	2
nad7	1050	350	C	1882	[0, 44, 0, 1838]	CT	0.98	CCC (P) => CCT (P)	NA	3

nad7	1057	353	C	1854	[0, 110, 0, 1744]	CT	0.94	CGT (R) => TGT (C)	NA	1
nad7	1103	368	C	745	[0, 5, 0, 740]	CT	0.99	TCT (S) => TTT (F)	NA	2
nad7	1124	375	C	558	[0, 0, 0, 558]	CT	1	CCA (P) => CTA (L)	NA	2
nad7	1137	379	C	473	[0, 362, 0, 111]	CT	0.23	GTC (V) => GTT (V)	NA	3
nad7	1166	389	C	149	[0, 10, 0, 139]	CT	0.93	TCT (S) => TTT (F)	NA	2
nad9	15	5	C	4345	[0, 95, 0, 4250]	CT	0.98	TTC (F) => TTT (F)	P	3
nad9	<u>92</u>	31	C	4365	[0, 37, 0, 4328]	CT	0.99	TCT (S) => TTT (F)	P	2
nad9	113	38	C	5111	[0, 253, 0, 4858]	CT	0.95	CCA (P) => CTA (L)	P	2
nad9	<u>167</u>	56	C	6302	[0, 63, 0, 6239]	CT	0.99	TCG (S) => TTG (L)	P	2
nad9	<u>298</u>	100	C	9255	[0, 68, 1, 9186]	CT CG	0.99	CCG (P) => TCG (S)	P	1
nad9	<u>328</u>	110	C	7221	[1, 52, 1, 7167]	CT CA CG	0.99	CGG (R) => TGG (W)	P	1
nad9	368	123	C	5797	[0, 28, 0, 5769]	CT	1	TCC (S) => TTC (F)	P	2
nad9	<u>398</u>	133	C	3982	[0, 14, 0, 3968]	CT	1	TCA (S) => TTA (L)	P	2
nad9	439	147	C	2185	[0, 66, 0, 2119]	CT	0.97	CTT (L) => TTT (F)	P	1
rpl5	8	3	C	550	[0, 411, 0, 139]	CT	0.25	CCA (P) => CTA (L)	N	2
rpl5	35	12	C	596	[0, 71, 0, 525]	CT	0.88	TCA (S) => TTA (L)	P	2
rpl5	<u>47</u>	16	C	636	[0, 121, 0, 515]	CT	0.81	CCG (P) => CTG (L)	P	2
rpl5	<u>64</u>	22	C	692	[0, 390, 0, 302]	CT	0.44	CAC (H) => TAC (Y)	N	1
rpl5	160	54	C	769	[0, 90, 0, 679]	CT	0.88	CCG (P) => TTG (L)	P	1
rpl5	<u>161</u>	54	C	795	[0, 658, 0, 137]	CT	0.17	CCG (P) => TTG (L)	N	2
rpl5	441	147	C	549	[0, 178, 0, 371]	CT	0.68	ATC (I) => ATT (I)	N	3
rpl5	509	170	C	396	[0, 31, 0, 365]	CT	0.92	CCA (P) => CTA (L)	P	2
rpl5	<u>512</u>	171	C	382	[0, 27, 0, 355]	CT	0.93	CCG (P) => CTG (L)	P	2
rpl5	529	177	C	398	[0, 29, 0, 369]	CT	0.93	CAA (O) => TAA (*)	P	1
rpl5	666	222	C	195	[0, 159, 0, 36]	CT	0.18	ATC (I) => ATT (I)	N	3

rpl10	<u>101</u>	34	C	361	[0, 64, 0, 297]	CT	0.82	TCA (S) => TTA (L)	NA	2
rpl10	134	45	C	342	[0, 170, 0, 172]	CT	0.5	CCA (P) => CTA (L)	NA	2
rpl16	<u>221</u>	74	C	414	[0, 1, 0, 413]	CT	1	TCG (S) => TTG (L)	P	2
rps3	<u>92</u>	31	C	484	[0, 13, 0, 471]	CT	0.97	TCA (S) => TTA (L)	NA	2
rps3	<u>512</u>	171	C	1912	[0, 89, 0, 1823]	CT	0.95	TCA (S) => TTA (L)	NA	2
rps3	<u>713</u>	238	C	1950	[0, 60, 0, 1890]	CT	0.97	TCG (S) => TTG (L)	NA	2
rps3	986	329	C	1603	[0, 1299, 0, 304]	CT	0.19	TCG (S) => TTG (L)	NA	2
rps3	1022	341	C	1013	[1, 9, 0, 1003]	CT CA	0.99	CCA (P) => CTA (L)	NA	2
rps3	1355	452	C	2246	[0, 18, 0, 2228]	CT	0.99	CCG (P) => CTG (L)	NA	2
rps3	1496	499	C	979	[0, 20, 0, 959]	CT	0.98	TCA (S) => TTA (L)	NA	2
rps3	1582	528	C	584	[0, 9, 0, 575]	CT	0.98	CCT (P) => TCT (S)	NA	1
rps4	176	59	C	882	[0, 37, 0, 845]	CT	0.96	TCA (S) => TTA (L)	NA	2
rps4	205	69	C	745	[0, 30, 0, 715]	CT	0.96	CAT (H) => TAT (Y)	NA	1
rps4	219	73	C	736	[0, 148, 0, 588]	CT	0.8	CCC (P) => CCT (P)	NA	3
rps4	<u>275</u>	92	C	691	[0, 20, 0, 671]	CT	0.97	CCA (P) => CTA (L)	NA	2
rps4	<u>287</u>	96	C	661	[0, 13, 0, 648]	CT	0.98	TCG (S) => TTG (L)	NA	2
rps4	<u>299</u>	100	C	727	[0, 17, 0, 710]	CT	0.98	CCG (P) => CTG (L)	NA	2
rps4	<u>316</u>	106	C	726	[0, 102, 0, 624]	CT	0.86	CGT (R) => TGT (C)	NA	1
rps4	<u>344</u>	115	C	730	[0, 14, 0, 716]	CT	0.98	CCG (P) => CTG (L)	NA	2
rps4	443	148	C	901	[0, 770, 0, 131]	CT	0.15	GCG (A) => GTG (V)	NA	2
rps4	483	161	C	1072	[0, 924, 0, 148]	CT	0.14	ATC (I) => ATT (I)	NA	3
rps4	491	164	C	1038	[1, 37, 0, 1000]	CT CA	0.96	TCA (S) => TTA (L)	NA	2
rps4	592	198	C	1889	[0, 1421, 0, 468]	CT	0.25	CGC (R) => TGC (C)	NA	1
rps4	<u>848</u>	283	C	495	[0, 443, 0, 52]	CT	0.11	TCG (S) => TTG (L)	NA	2
rps4	852	284	C	484	[0, 371, 0, 113]	CT	0.23	ACC (T) => ACT (T)	NA	3
rps4	941	314	C	237	[0, 3, 0, 234]	CT	0.99	TCG (S) => TTG (L)	NA	2

rps4	952	318	C	223	[0, 8, 0, 215]	CT	0.96	CAT (H) => TAT (Y)	NA	1
rps4	962	321	C	182	[0, 15, 0, 167]	CT	0.92	CCA (P) => CTA (L)	NA	2
rps4	977	326	C	165	[0, 8, 0, 157]	CT	0.95	TCT (S) => TTT (F)	NA	2
rps4	<u>1028</u>	343	C	60	[0, 1, 0, 59]	CT	0.98	CCA (P) => CTA (L)	NA	2
rps4	1042	348	C	46	[0, 2, 0, 44]	CT	0.96	CGG (R) => TGG (W)	NA	1
rps10	102	34	C	186	[0, 13, 0, 173]	CT	0.93	GTC (V) => GTT (V)	NA	3
rps10	132	44	C	120	[0, 107, 0, 13]	CT	0.11	TCC (S) => TCT (S)	NA	3
rps10	210	70	C	44	[0, 32, 0, 12]	CT	0.27	TTC (F) => TTT (F)	NA	3
rps10	214	72	C	38	[0, 0, 0, 38]	CT	1	CGG (R) => TGG (W)	NA	1
rps10	278	93	C	19	[0, 0, 0, 19]	CT	1	TCG (S) => TTG (L)	NA	2
rps10	<u>307</u>	103	C	9	[0, 0, 0, 9]	CT	1	CGA (O) => TGA (*)	NA	1
rps12	104	35	C	1162	[0, 20, 0, 1142]	CT	0.98	CCG (P) => CTG (L)	NA	2
rps12	159	53	C	571	[0, 474, 0, 97]	CT	0.17	GCC (A) => GCT (A)	NA	3
rps12	196	66	C	366	[0, 4, 0, 362]	CT	0.99	CAC (H) => TAC (Y)	NA	1
rps12	<u>221</u>	74	C	239	[0, 10, 0, 229]	CT	0.96	TCG (S) => TTG (L)	NA	2
rps12	284	95	C	73	[0, 1, 0, 72]	CT	0.99	TCC (S) => TTC (F)	NA	2
rps13	<u>56</u>	19	C	1136	[0, 41, 0, 1095]	CT	0.96	TCA (S) => TTA (L)	P	2
rps13	<u>100</u>	34	C	901	[0, 34, 0, 867]	CT	0.96	CGT (R) => TGT (C)	P	1
rps13	<u>287</u>	96	C	140	[0, 1, 0, 139]	CT	0.99	TCG (S) => TTG (L)	P	2

Table S9 Summary of single nucleotide polymorphisms (SNPs) detected in the PCGs of *S. officinalis* mitogenome. “Nt Pos” means the nucleotide position of a SNP in a PCG.

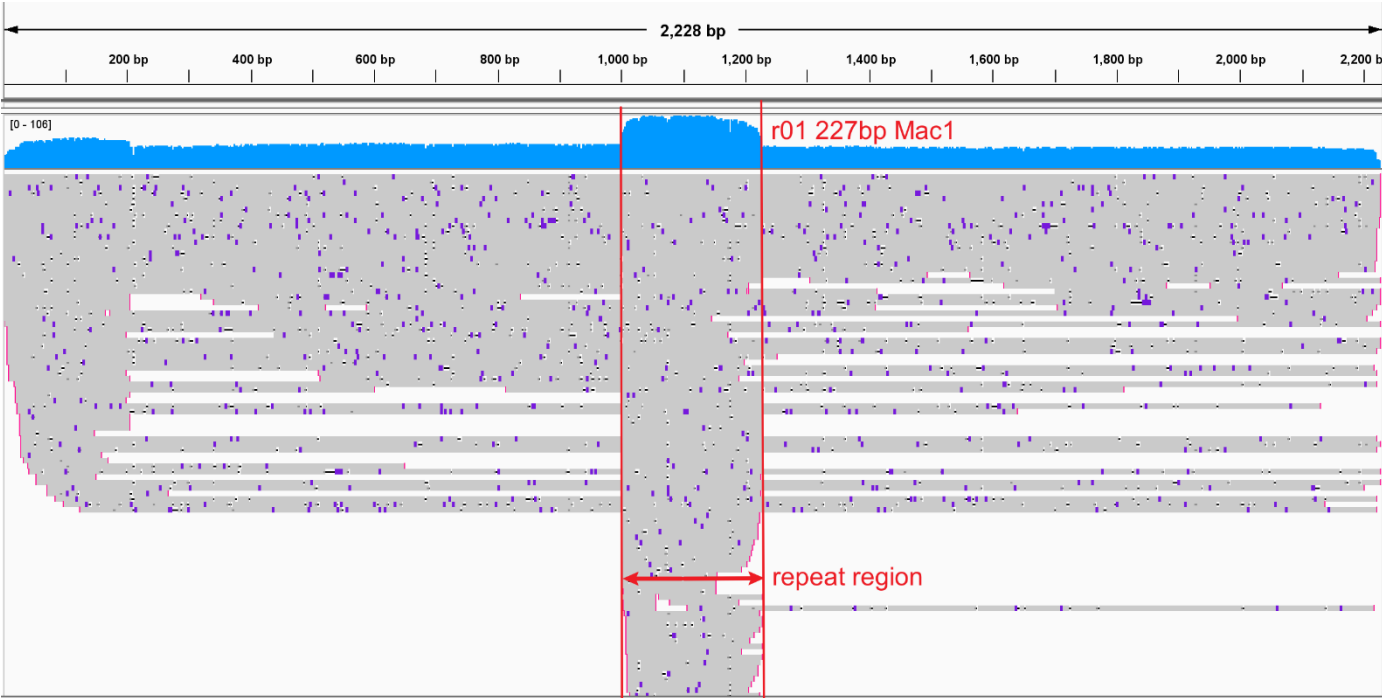
Gene	Nt Pos	Nt reference	Nt coverage	Nt Base Count [A,C,G,T]	Nt allsubs	Nt Frequency
ccmFn	1417	G	152	[15, 0, 137, 0]	GA	0.1
ccmFn	1448	C	161	[0, 131, 0, 30]	CT	0.19
ccmFn	1449	C	157	[10, 126, 21, 0]	CG CA	0.14
ccmFn	1457	A	154	[135, 0, 19, 0]	AG	0.12
ccmFn	1471	C	156	[0, 136, 0, 20]	CT	0.13
ccmFn	1486	G	157	[29, 0, 128, 0]	GA	0.18
ccmFn	1496	C	153	[0, 137, 0, 16]	CT	0.1
ccmFn	1818	G	113	[21, 0, 92, 0]	GA	0.19
ccmc	45	C	122	[0, 110, 0, 12]	CT	0.1
ccmc	179	C	165	[19, 146, 0, 0]	CA	0.12
ccmc	190	A	167	[151, 0, 16, 0]	AG	0.1
rpl5	413	C	279	[0, 251, 0, 28]	CT	0.1
atp9	35	C	132	[13, 119, 0, 0]	CA	0.1
atp9	125	C	145	[0, 128, 0, 17]	CT	0.12
cox2	149	C	56	[0, 49, 0, 7]	CT	0.12
cox2	153	C	49	[0, 43, 0, 6]	CT	0.12
atp1	906	C	739	[0, 188, 0, 551]	CT	0.75
atp1	912	A	712	[191, 0, 521, 0]	AG	0.73
atp1	918	C	719	[533, 186, 0, 0]	CA	0.74
atp1	921	T	715	[0, 537, 0, 178]	TC	0.75
atp1	924	C	614	[0, 186, 0, 428]	CT	0.7
atp1	936	G	666	[0, 480, 186, 0]	GC	0.72
atp1	1002	A	186	[158, 0, 28, 0]	AG	0.15
atp1	1023	T	1096	[0, 919, 0, 177]	TC	0.84
atp1	1590	C	99	[0, 88, 11, 0]	CG	0.11
atp1	1604	T	435	[0, 83, 0, 352]	TC	0.19
rps3	21	A	118	[94, 0, 24, 0]	AG	0.2
rps3	27	G	121	[22, 0, 99, 0]	GA	0.18
rpl16	15	C	149	[0, 133, 0, 16]	CT	0.11
nad3	12	T	184	[0, 43, 0, 141]	TC	0.23
nad3	29	A	137	[123, 14, 0, 0]	AC	0.1
nad3	30	T	142	[14, 0, 0, 128]	TA	0.1
nad3	45	G	144	[0, 14, 130, 0]	GC	0.1
nad3	48	A	137	[123, 0, 14, 0]	AG	0.1
nad3	51	T	139	[0, 0, 14, 125]	TG	0.1
nad3	60	T	172	[0, 40, 0, 132]	TC	0.23
nad3	62	C	170	[0, 131, 0, 39]	CT	0.23
nad3	99	G	183	[46, 0, 137, 0]	GA	0.25
matR	1496	G	164	[16, 0, 148, 0]	GA	0.1
matR	1526	T	129	[0, 17, 0, 112]	TC	0.13
ccmFc	583	A	217	[184, 33, 0, 0]	AC	0.15
ccmFc	620	C	218	[0, 192, 26, 0]	CG	0.12
ccmFc	405	G	163	[19, 0, 144, 0]	GA	0.12

Table S10 PCR primers used to validate the RNA editing sites from eleven PCGs in the *S. officinalis* mitogenome.

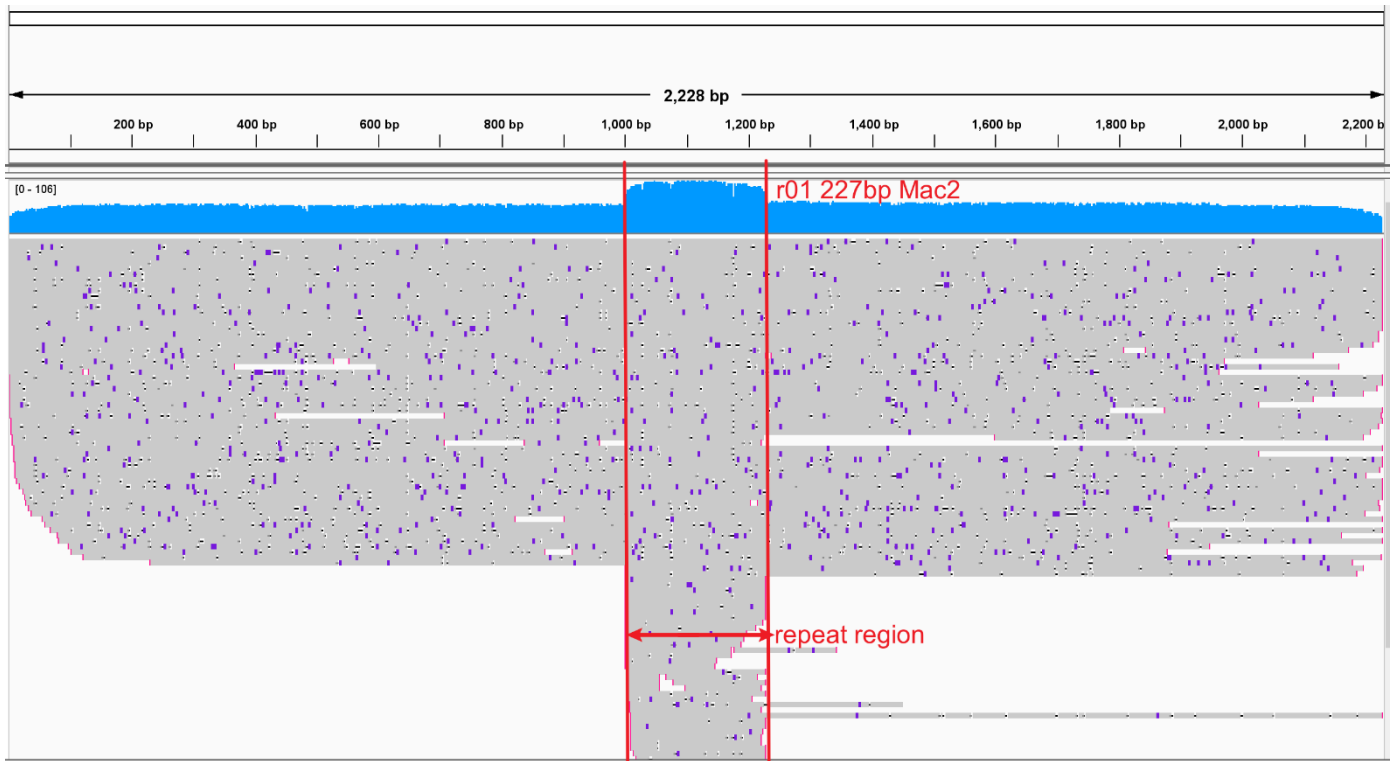
Primer Name	PCG name	Primer Sequence
so-atp4-F1	atp4	CCACTTCCCGTTCAGTTGCT
so-atp4-R1	atp4	TGGATCCGCTCTTCTGTGAAC
so-atp8-F1	atp8	ACACAATTCTTCTGGTCATGCCT
so-atp8-R1	atp8	GCTCTTCCGAACGACCAAGT
so-cox1-F1	cox1	GGGGAGCGGAACCTTTTAC
so-cox1-R1	cox1	ACAGTCCCAGCATATAGCGCA
so-cox1-F2	cox1	AGTAGAAGAGAGAAGCACCCCTG
so-cox1-R2	cox1	AGTAGCAATCGGCGACCTTT
so-cox3-F1	cox3	ACAACCGAGGCAAAGTGGTT
so-cox3-R1	cox3	GGAGTTCTCTTTGTCTTCGAGC
so-mttB-F1	mttB	TAAAGATGCGCCGGTCGTAG
so-mttB-R1	mttB	TGTTGGTTGAGAATTGCTCTGG
so-nad3-F1	nad3	TTTCCGGTATGTAGCTCCGC
so-nad3-R1	nad3	GCATCGCTCTTTCCTTTGTCC
so-nad4L-F1	nad4L	ATTCTACGTTCCCGACACGG
so-nad4L-R1	nad4L	AAGAAAACGAAAGGAGAAATTCGT
so-nad9-F1	nad9	CTTCATTTTTAGAGGAAGAAGCGGA
so-nad9-R1	nad9	TTCTATTGATTTGTCTCCTGGACT
so-rpl5-F1	rpl5	CTTTTTGAAGGCGATAGTTCACAGT
so-rpl5-R1	rpl5	TGGATCAATAGAAAAGGGGCTCT
so-rpl16-F1	rpl16	CTTTCATATCGAGCCATTGAAGCA
so-rpl16-R1	rpl16	TTTTGAATCCCGGTCCGGTT
so-rps13-F1	rps13	ACAGCCCATTCTGATTCCAGC
so-rps13-R1	rps13	TCTTCAGCAGGTAGGCTGCAC

Figure S1 The alignment of the Nanopore reads to the four conformations of the three double bifurcating structures (DBS), named DBS01-DBS03, found in the unitig graph. The unitig graph was generated using Unicycler from Illumina reads that were filtered with GetOrganelle for mitochondrial reads. The major conformations (Mac) refer to the conformations in the DBS structure supported by more long reads. The minor conformations (Mic) refer to the conformations in the DBS structure supported by less long reads. It should be emphasized that the repetitive sequences affiliated with DBS01, DBS02, and DBS03 are identical to the high-scoring pairs (HSPs): r01, r02, and r47, respectively. Each figure can be divided into three parts from top to bottom. The top part shows the reference sequences with their coordinates. The middle part shows the read coverage bar chart in blue. The name and length of the repeat and the name of the conformation are shown above the coverage plot. The bottom part shows the reads' alignment to the reference sequences. The repeat region is shown as a double-headed arrow. The boundaries of the repeat regions of the DBS structure are indicated with red vertical lines.

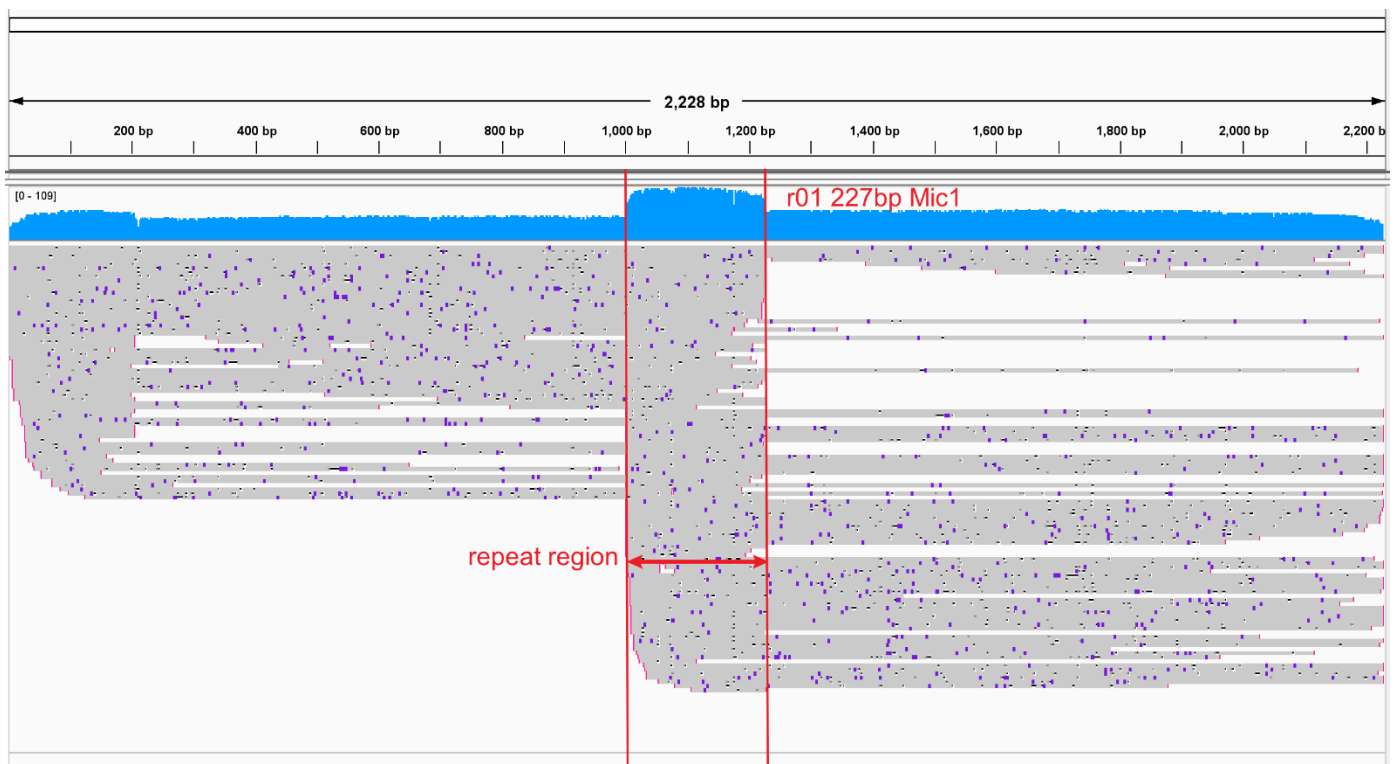
a Mapping of long reads to the major conformation Mac1 of the DBS01/r01.



b Mapping of long reads to the major conformation Mac2 of the DBS01/r01.



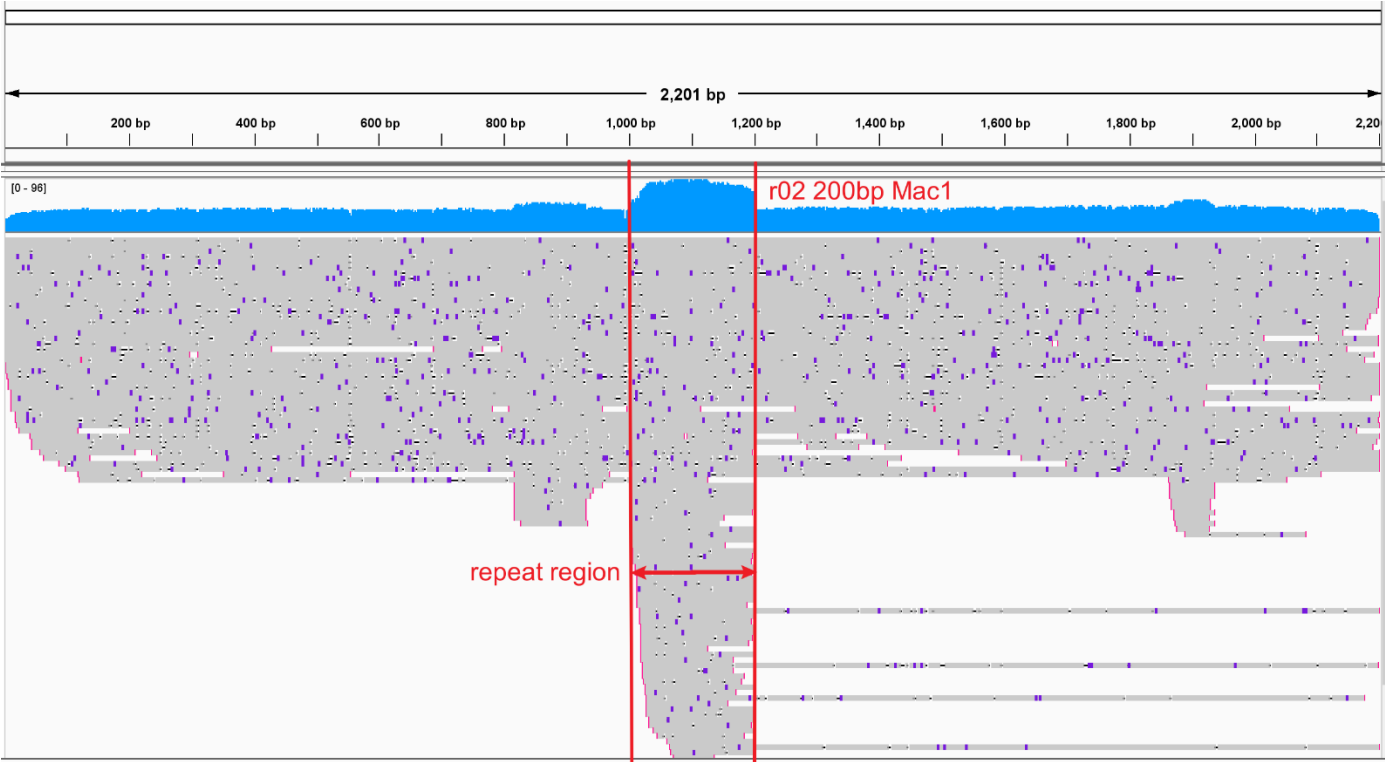
c Mapping of long reads to the minor conformation Mic1 of the DBS01/r01.



d Mapping of long reads to the minor conformation Mic2 of the DBS01/r01.



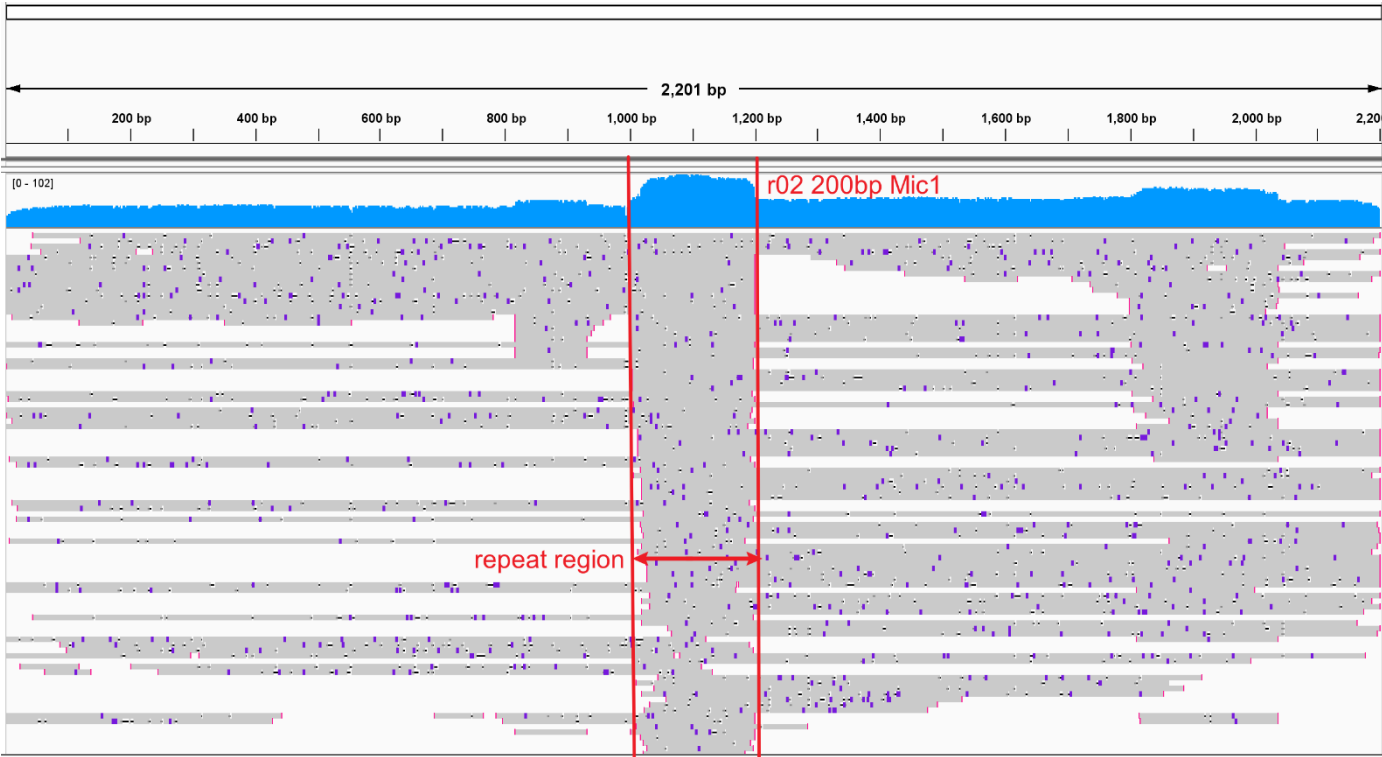
e Mapping of long reads to the major conformation Mac1 of the DBS02/r02.



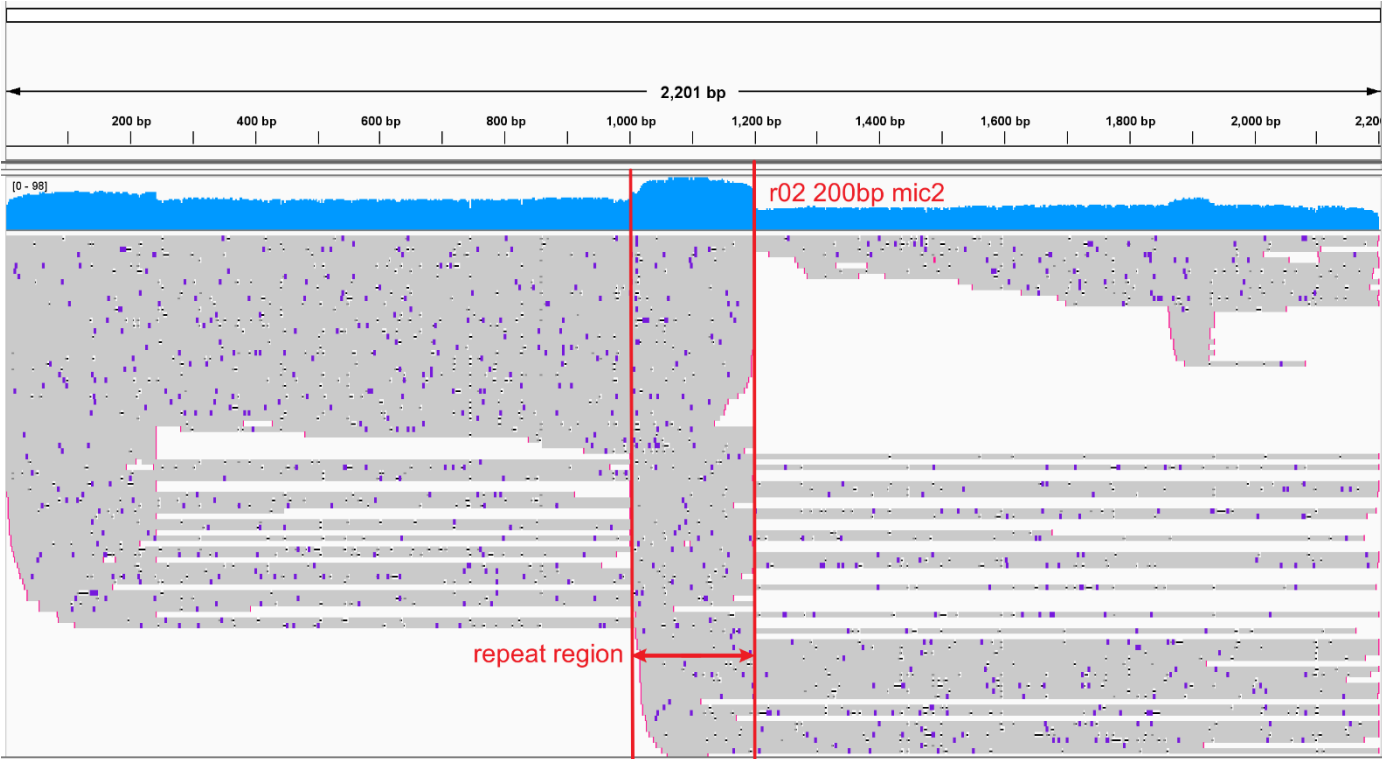
f Mapping of long reads to the major conformation Mac2 of the DBS02/r02.



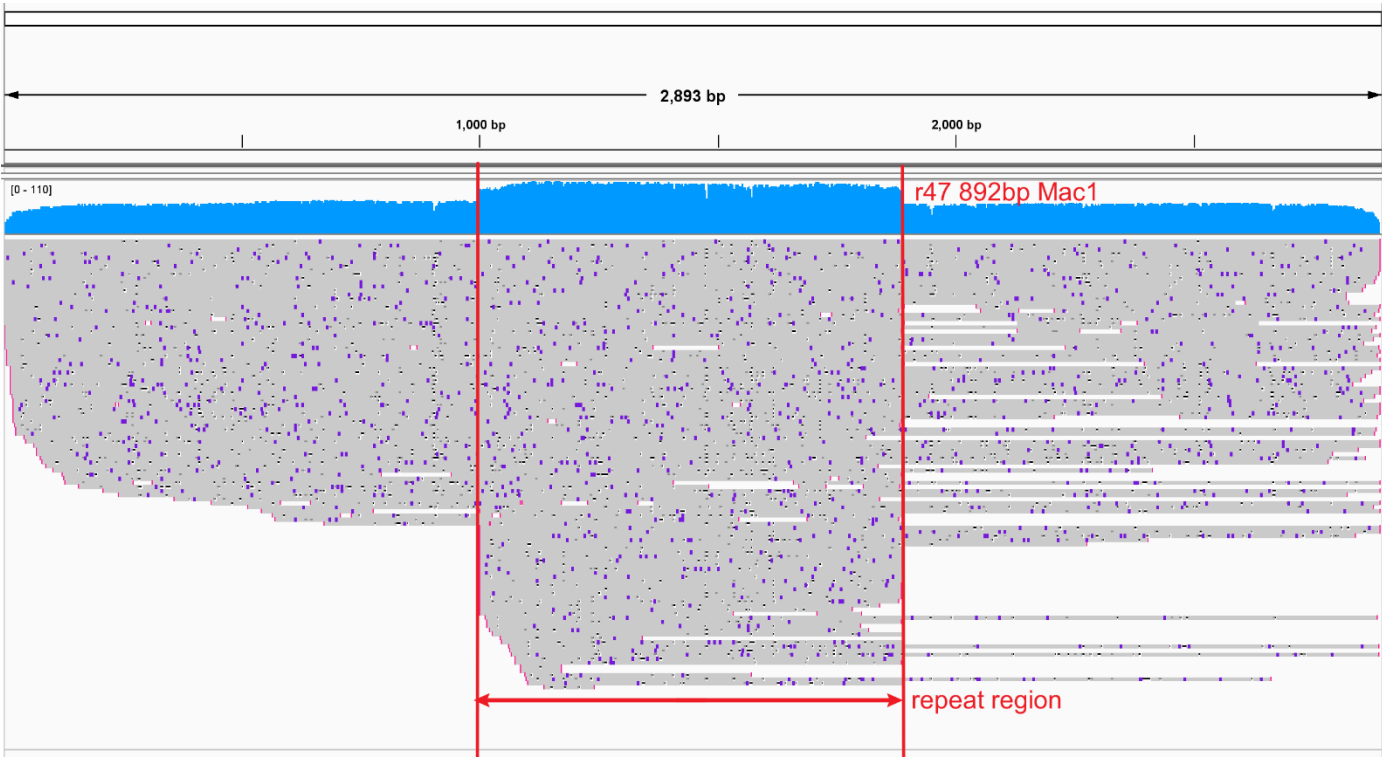
g Mapping of long reads to the minor conformation Mic1 of the DBS02/r02.



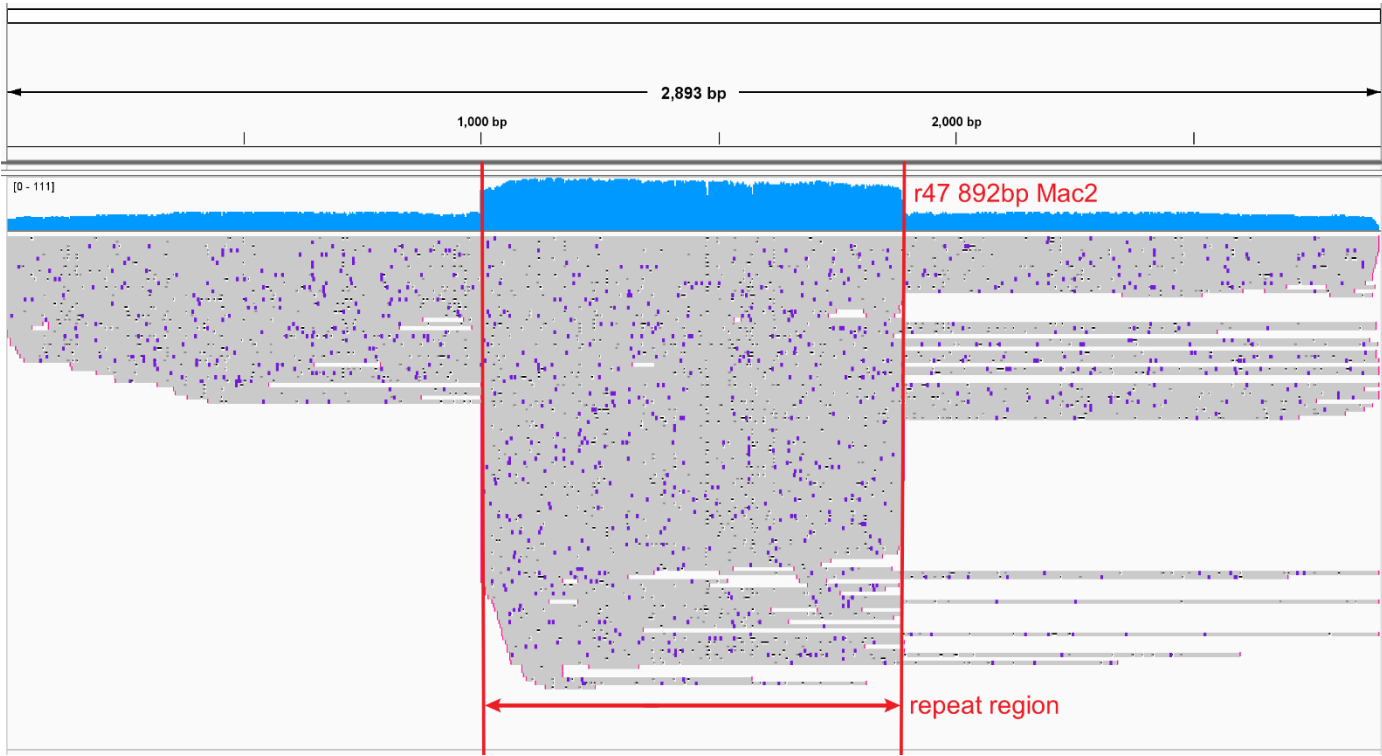
h Mapping of long reads to the minor conformation Mic1 of the DBS02/r02.



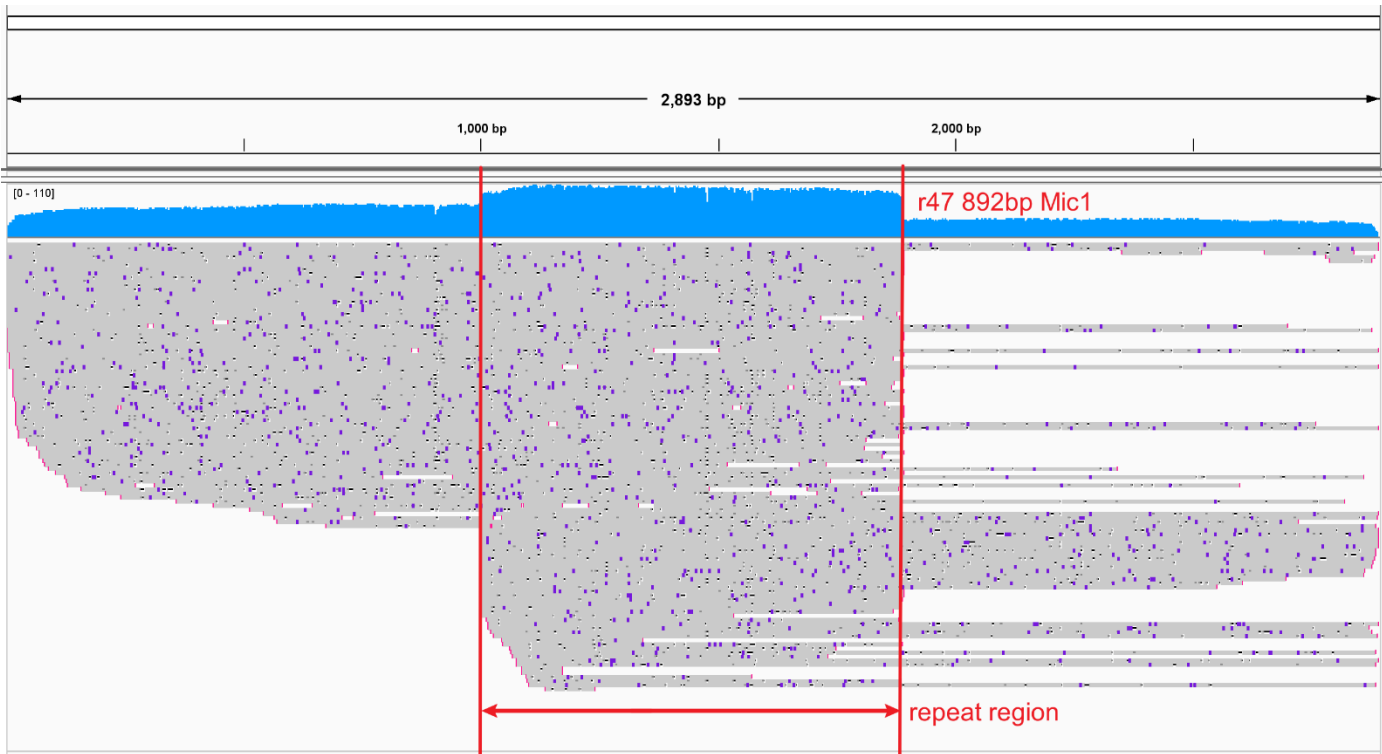
i Mapping of long reads to the major conformation Mac1 of the DBS03/r47.



j Mapping of long reads to the major conformation Mac2 of the DBS03/r47.



k Mapping of long reads to the minor conformation Mic1 of the DBS03//r47.



l Mapping of long reads to the minor conformation Mic1 of the DBS03/r47.

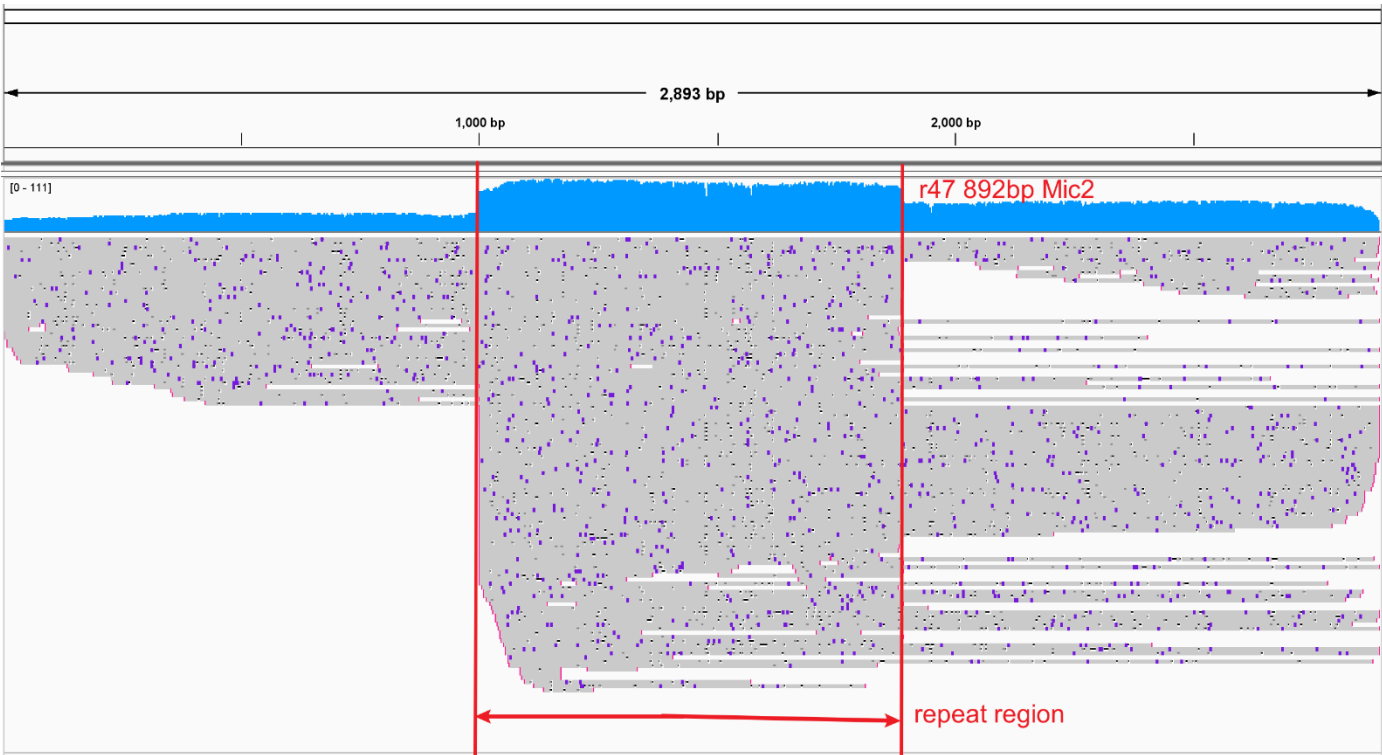


Figure S2 Mapping results of Nanopore and Illumina reads to the mitochondrial chromosomes 1 (MC1) and 2 (MC2) of the *S. officinalis*. Panels a and b show the mapping results of the Nanopore reads to MC1 and MC2, respectively. Panels c and d show the mapping results of all Illumina reads to the MC1 and MC2, respectively. The X-axis shows the nucleotide position, and the Y-axis shows the corresponding coverage depth.

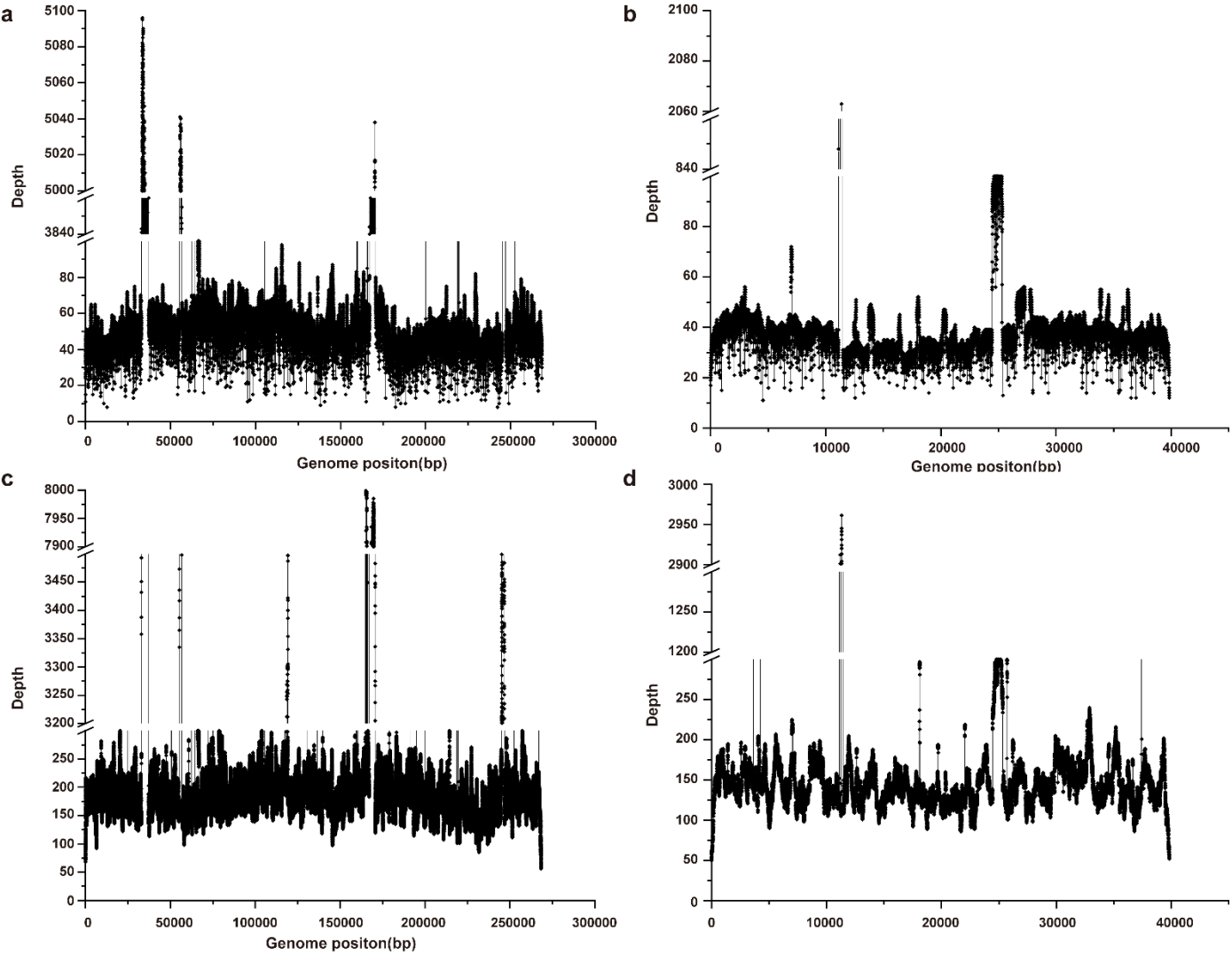
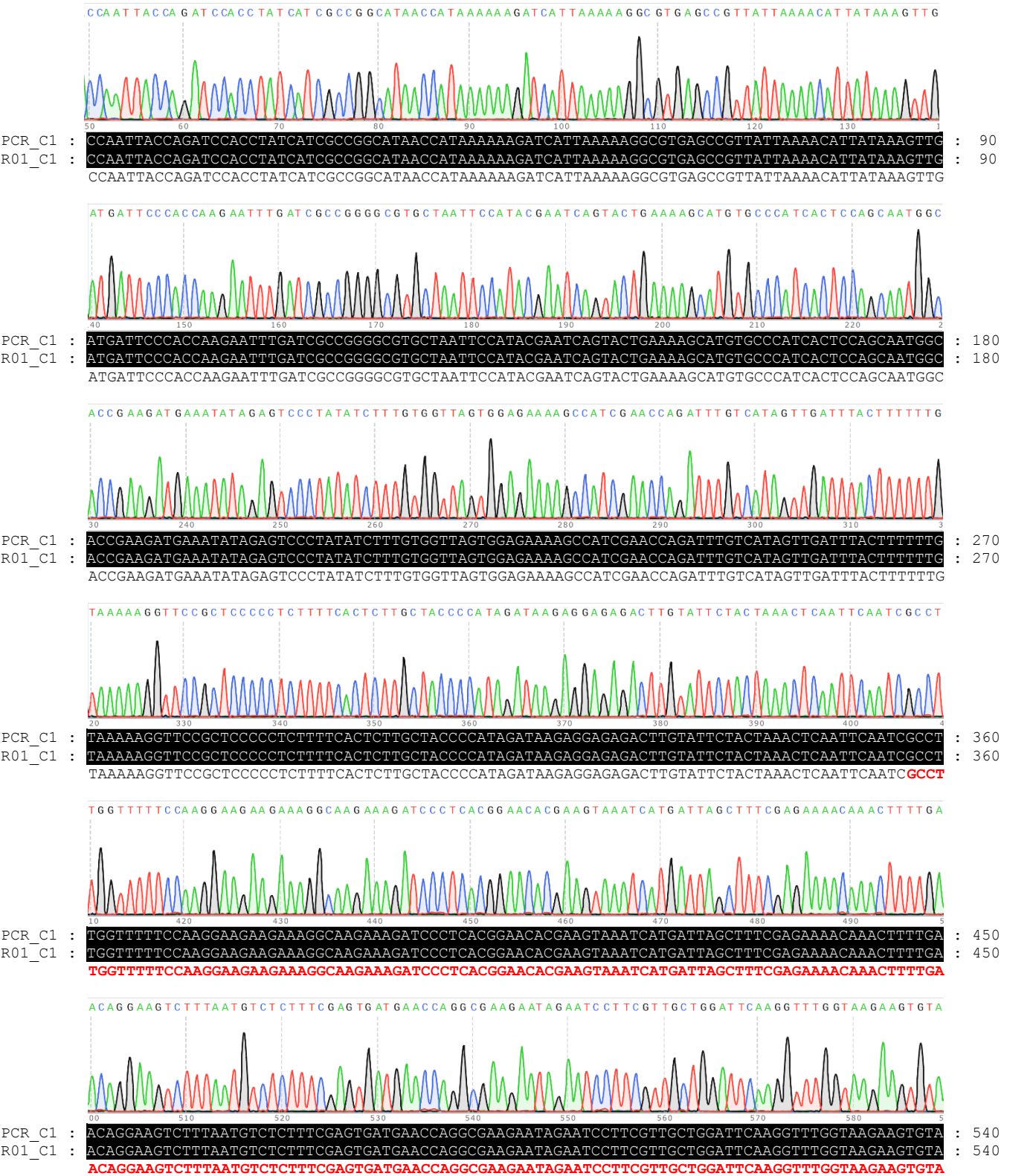
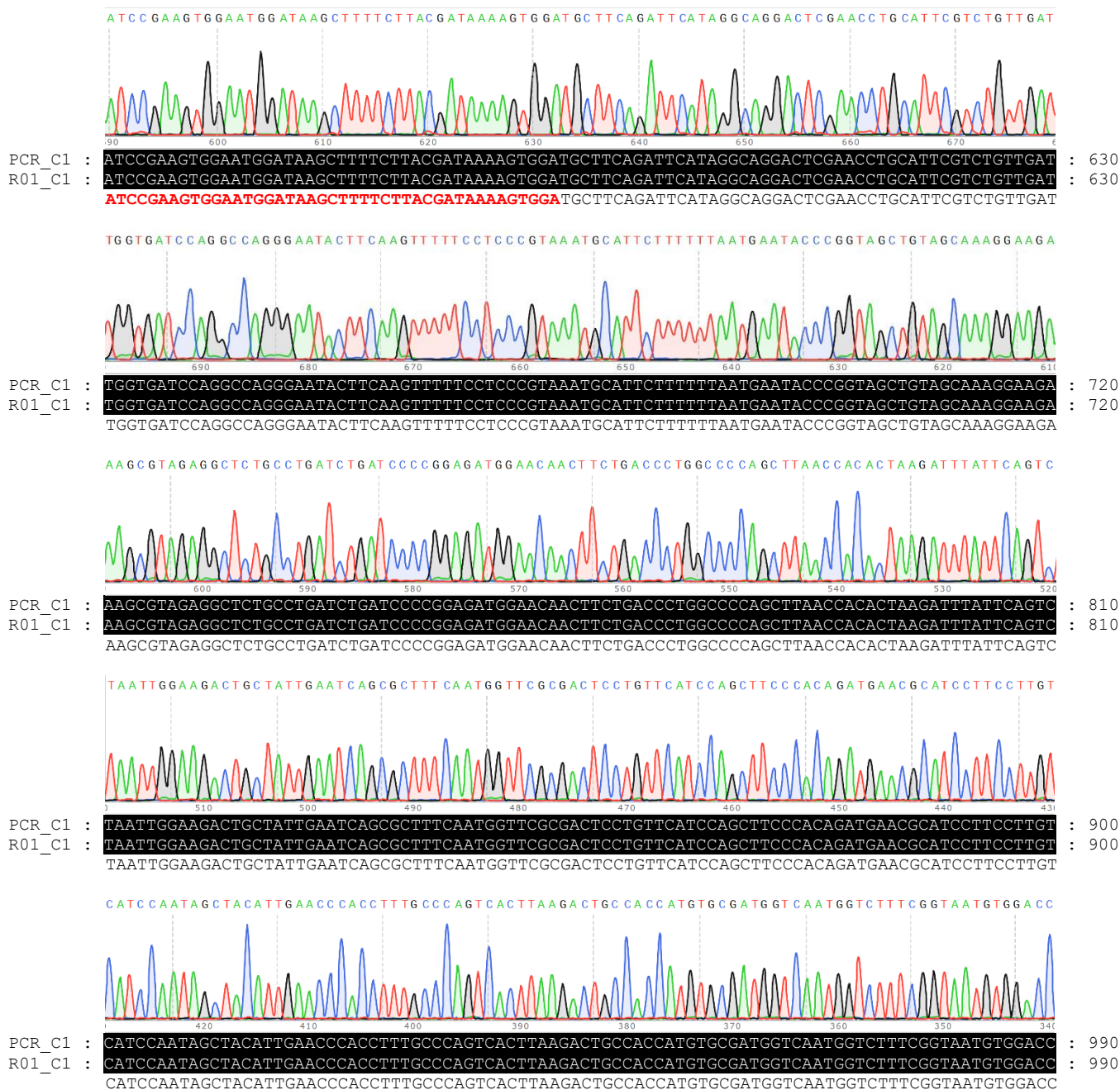


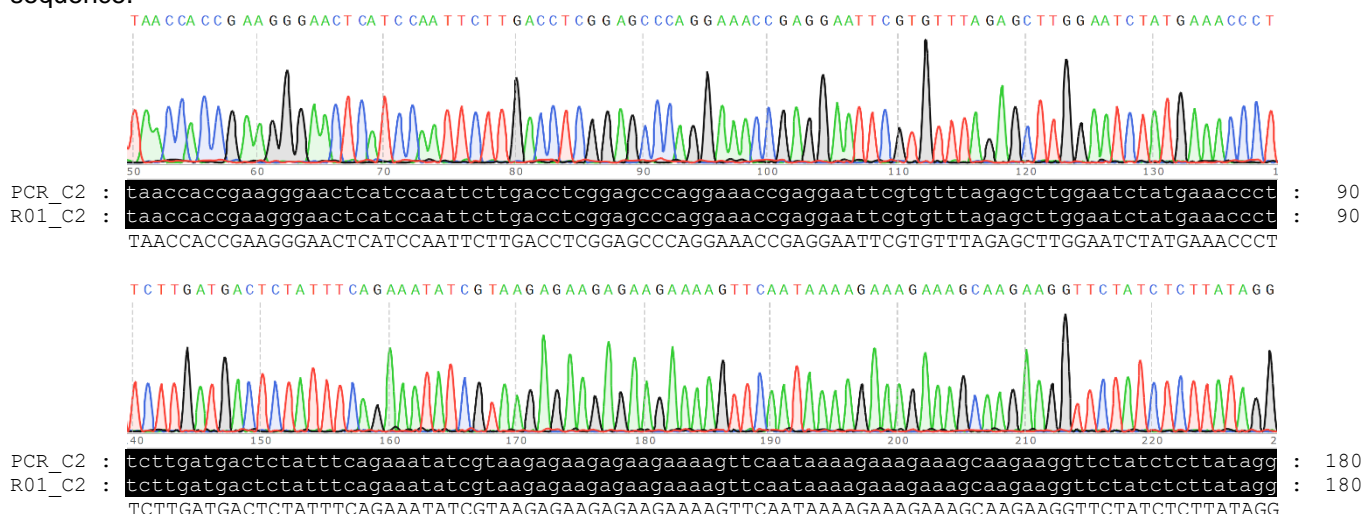
Figure S3 Validation of the presence of the four conformations c1-4 of DBS01, DBS02, and DBS03, corresponding to the recombination products mediated by the three repeats R01, R02, and R47. PCR primers were designed based on the four conformations. The genomic DNA were then amplified by PCR, and the PCR products were subject to Sanger sequencing. The sequencing chromatograms, the Sanger sequencing results (labeled with “PCR” and conformation number), the expected sequences (labeled with repeat id and conformation number), and the consensus sequences are shown at the top of chromatograms and below the chromatograms. Panels a-i correspond to DBS01, DBS02, and DBS03, affiliated with the repetitive sequences r01, r02, and r47. The sequences of r01, r02, and r047 were high-lighted in bold red.

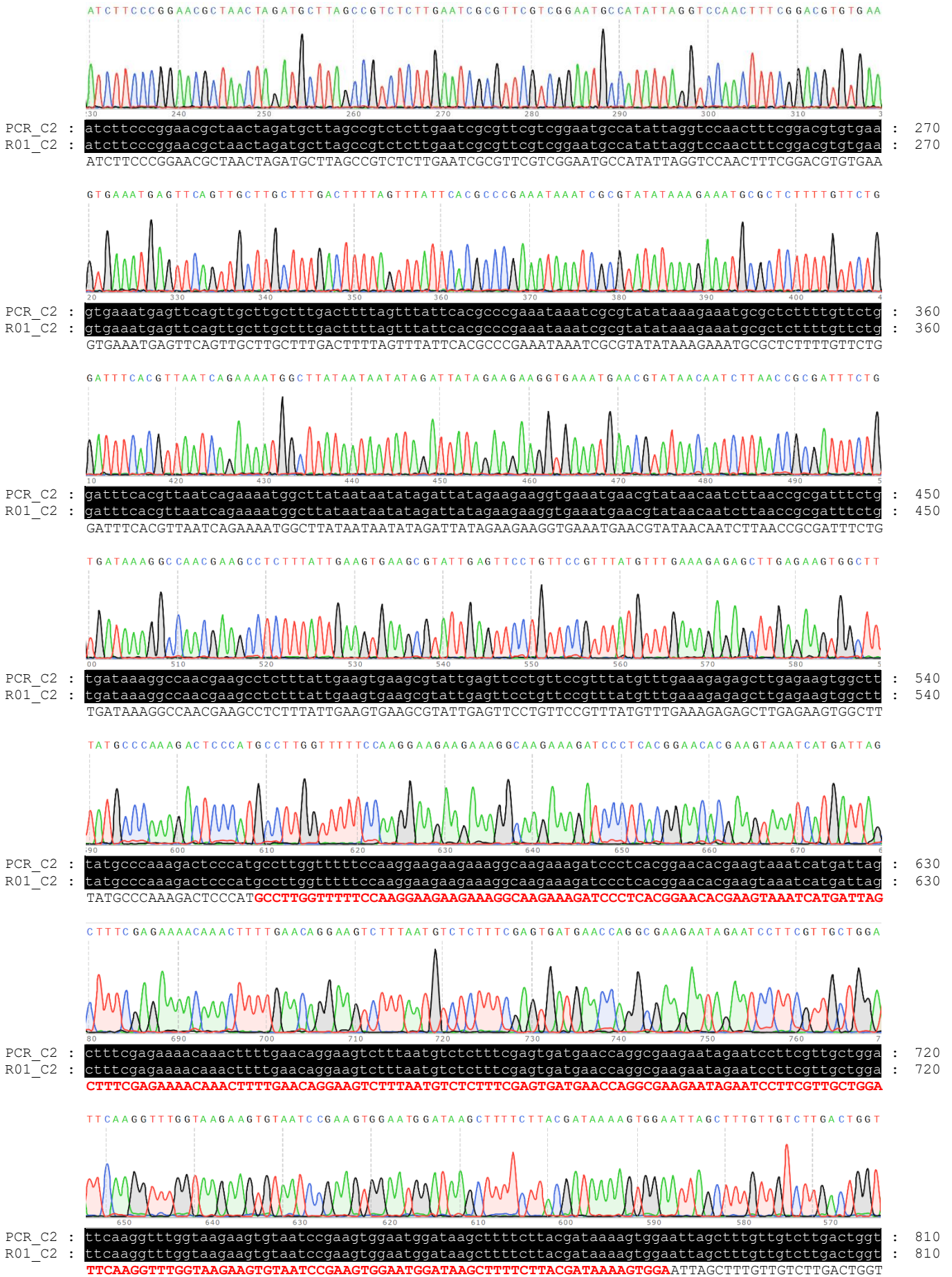
a comparison of the sequence obtained from PCR amplification and Sanger sequencing (R01-C1) and the expected sequence.

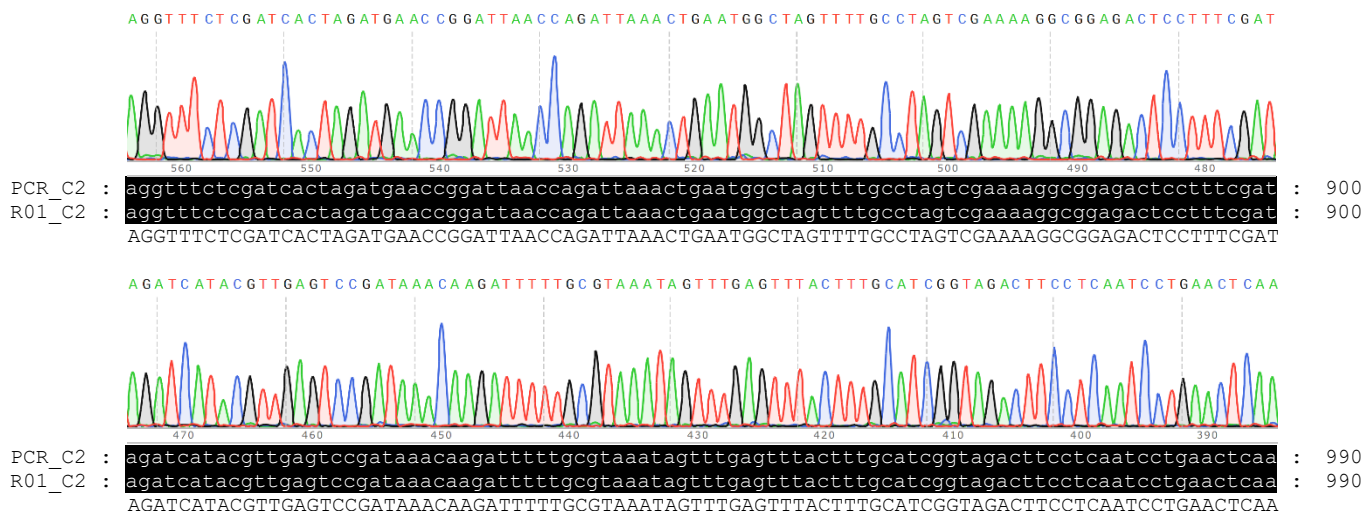




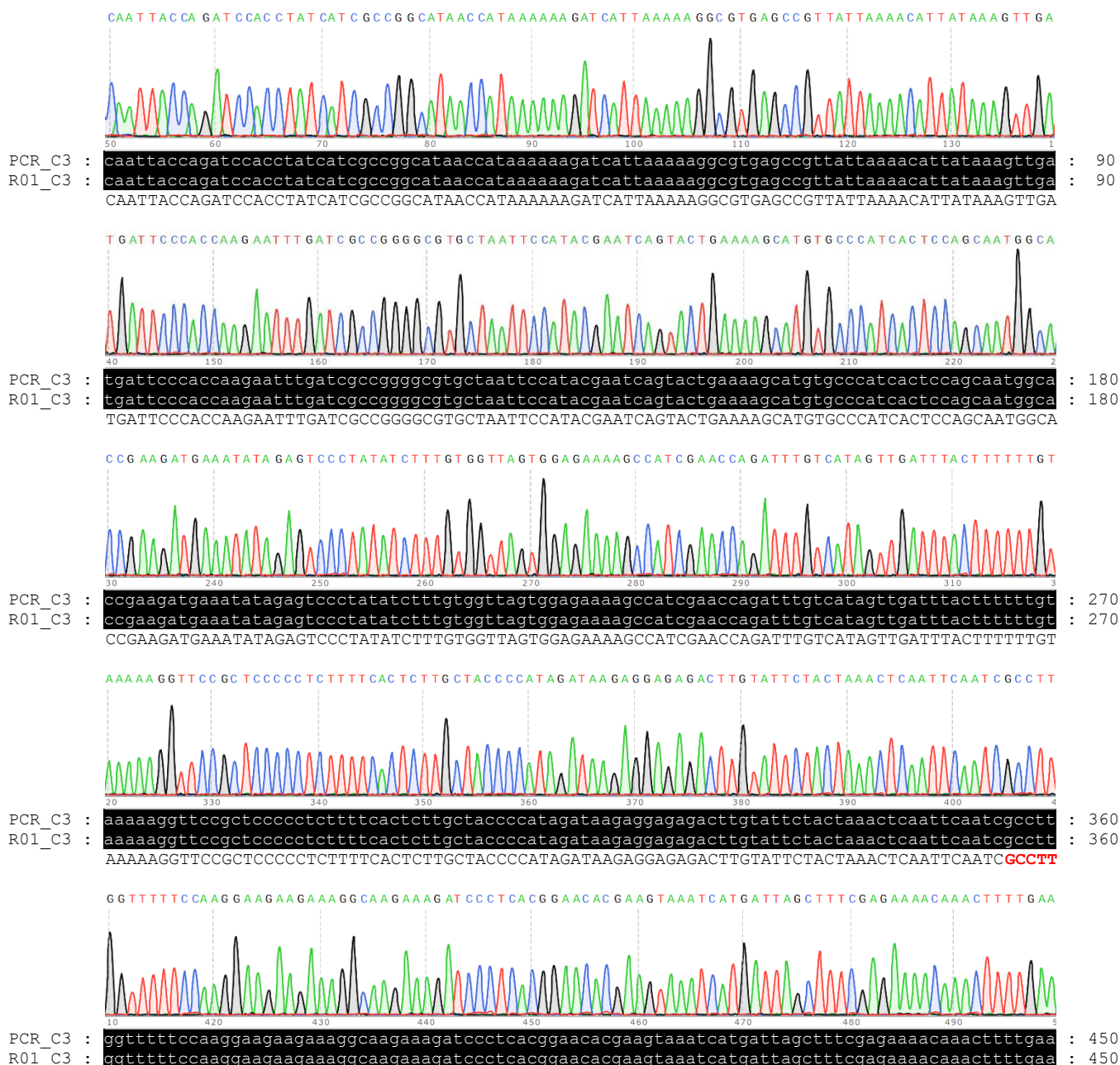
b comparison of the sequence obtained from PCR amplification and Sanger sequencing (R01-C2) and the expected sequence.

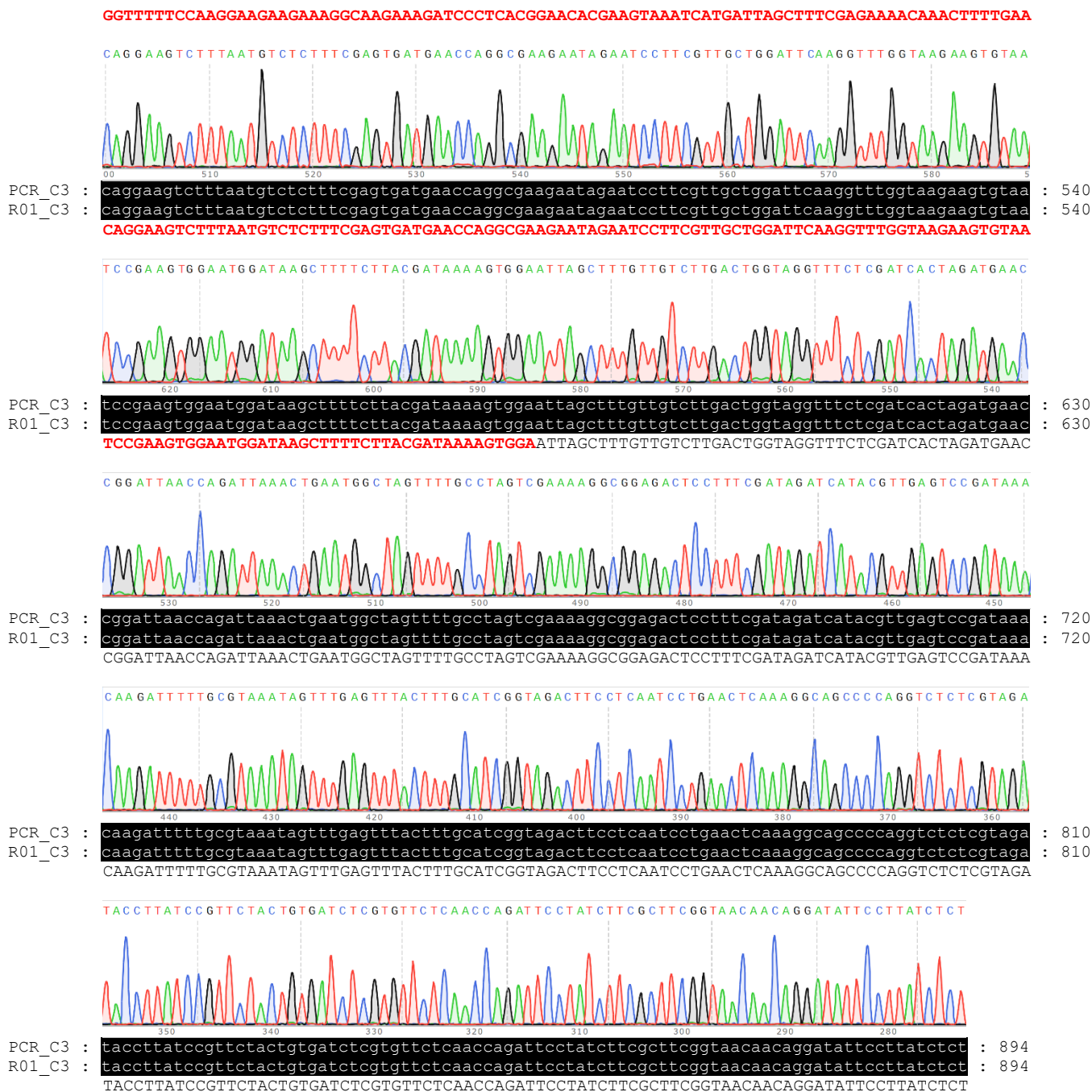




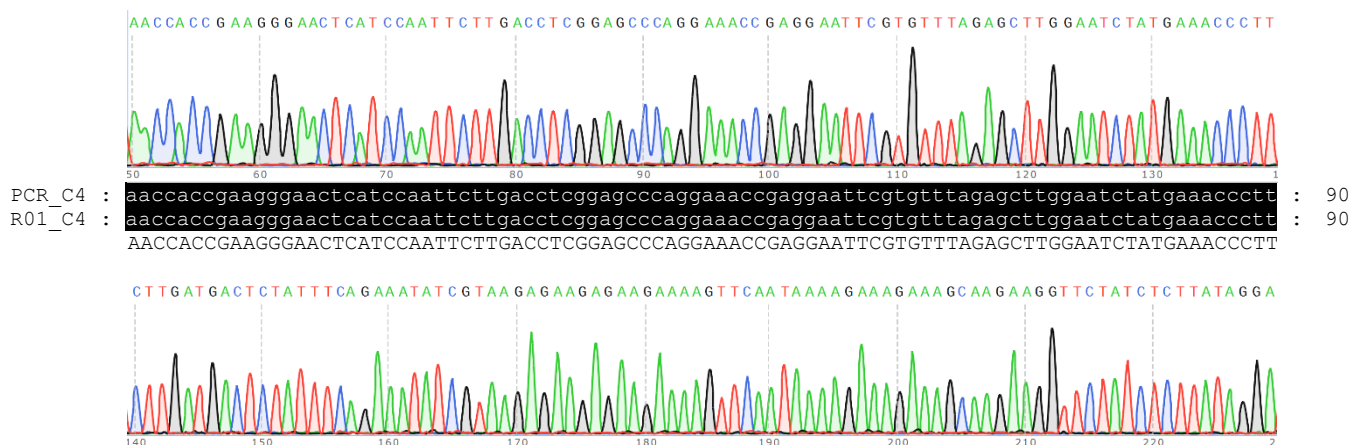


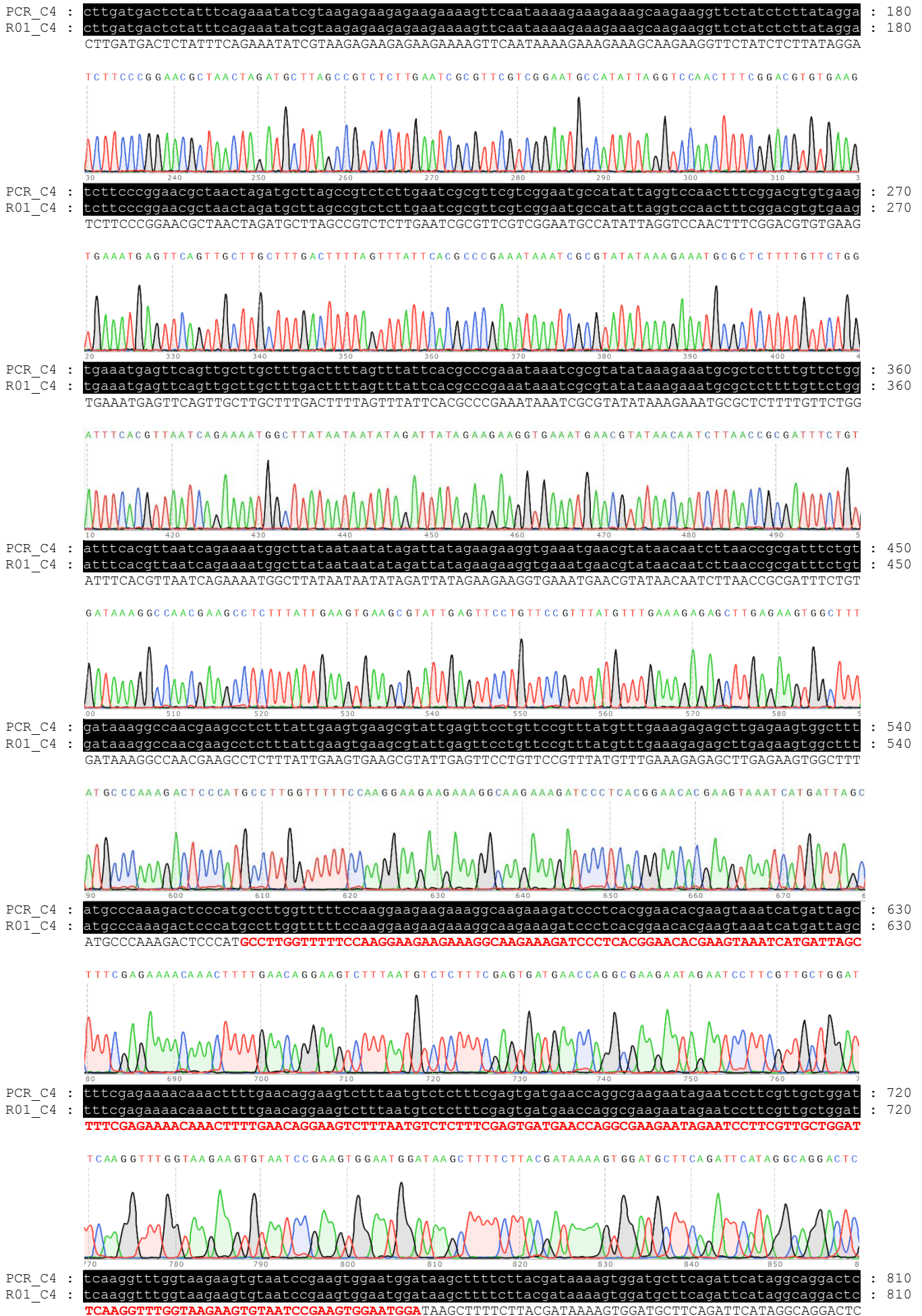
c comparison of the sequence obtained from PCR amplification and Sanger sequencing (R01-C3) and the expected sequence.

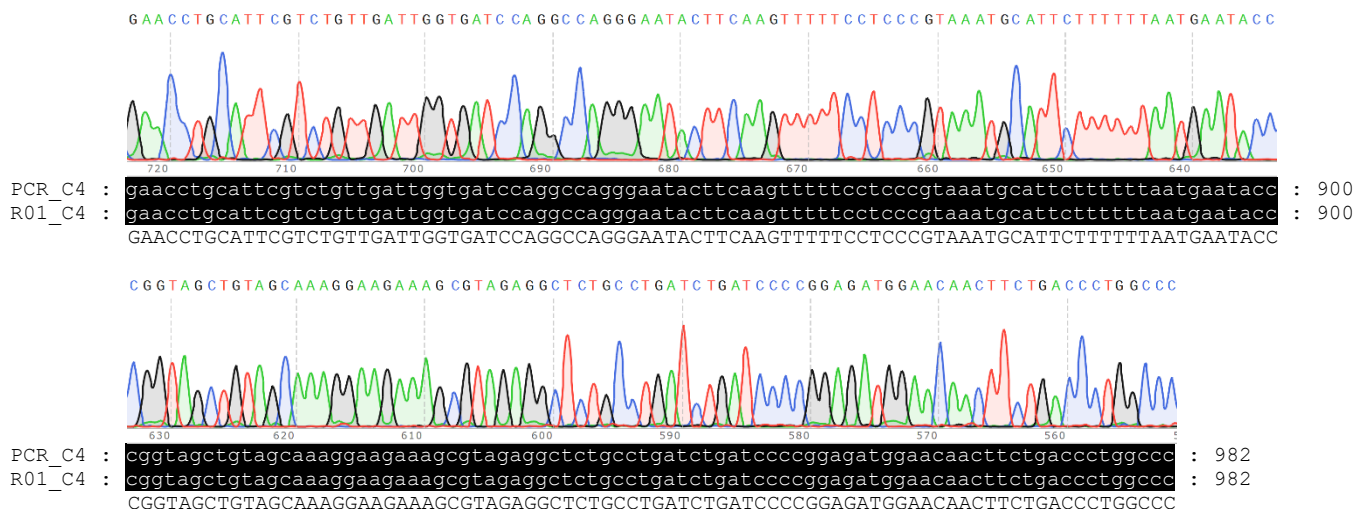




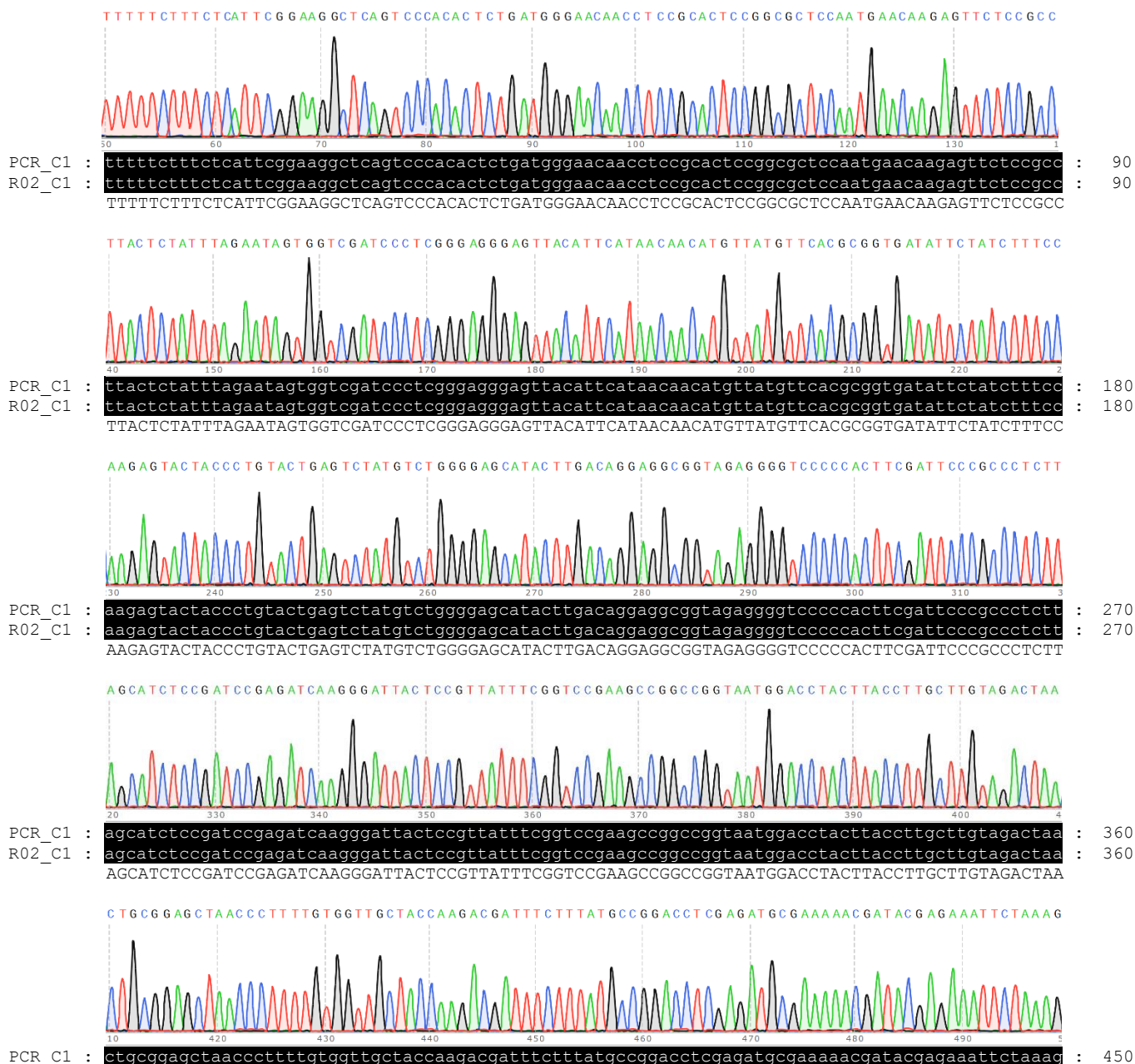
d comparison of the sequence obtained from PCR amplification and Sanger sequencing (R01-C4) and the expected sequence.

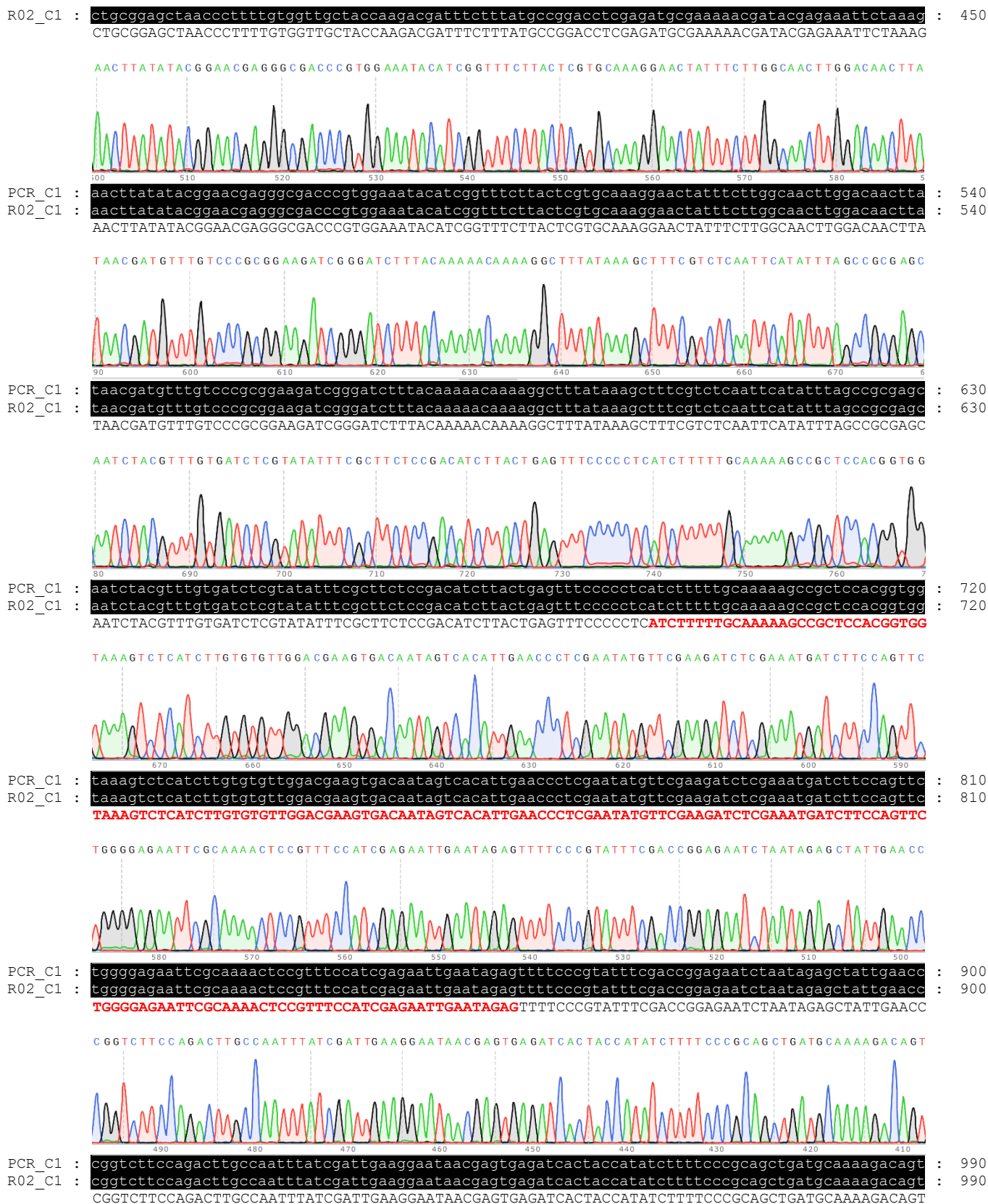




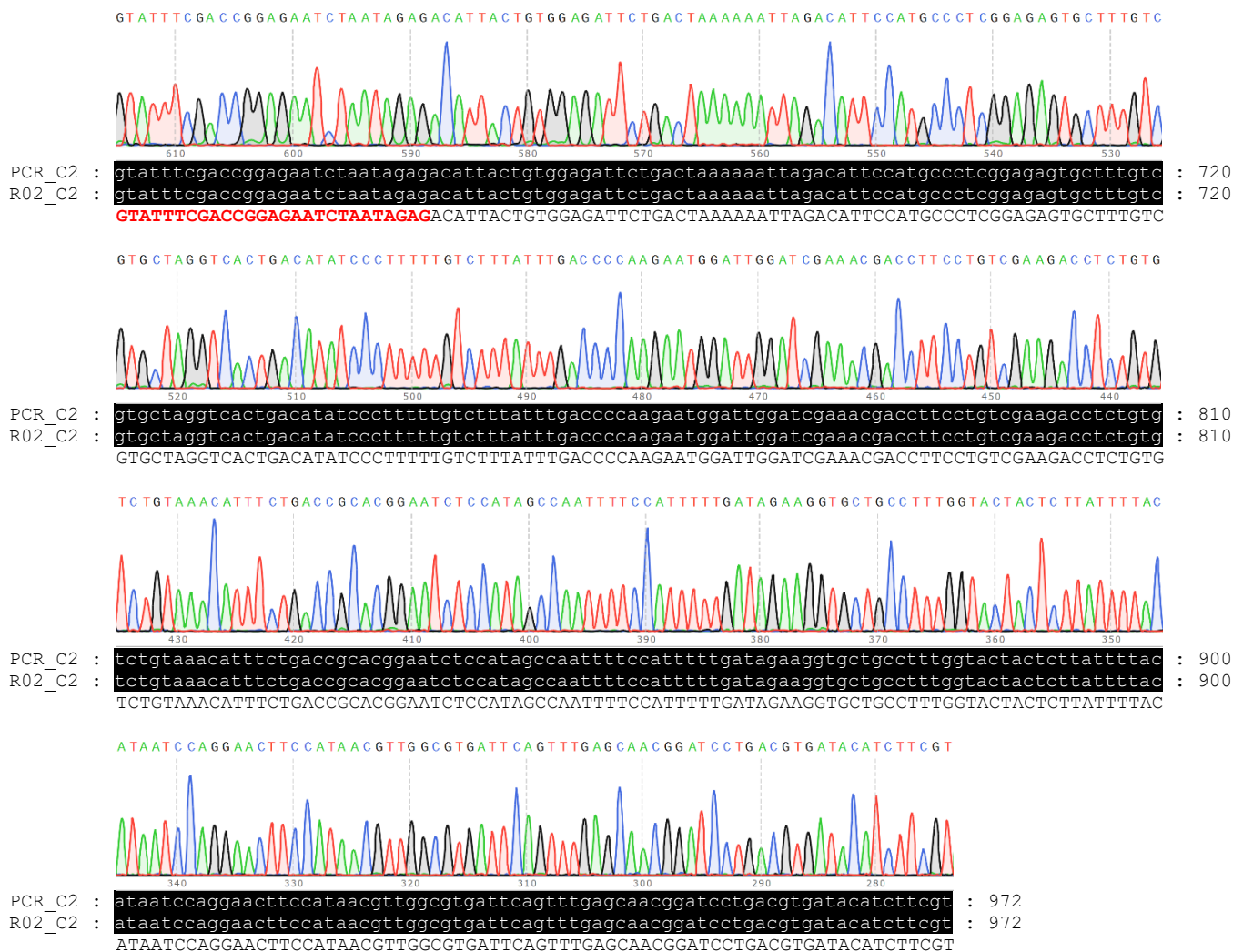


e comparison of the sequence obtained from PCR amplification and Sanger sequencing (R02-C1) and the expected sequence.

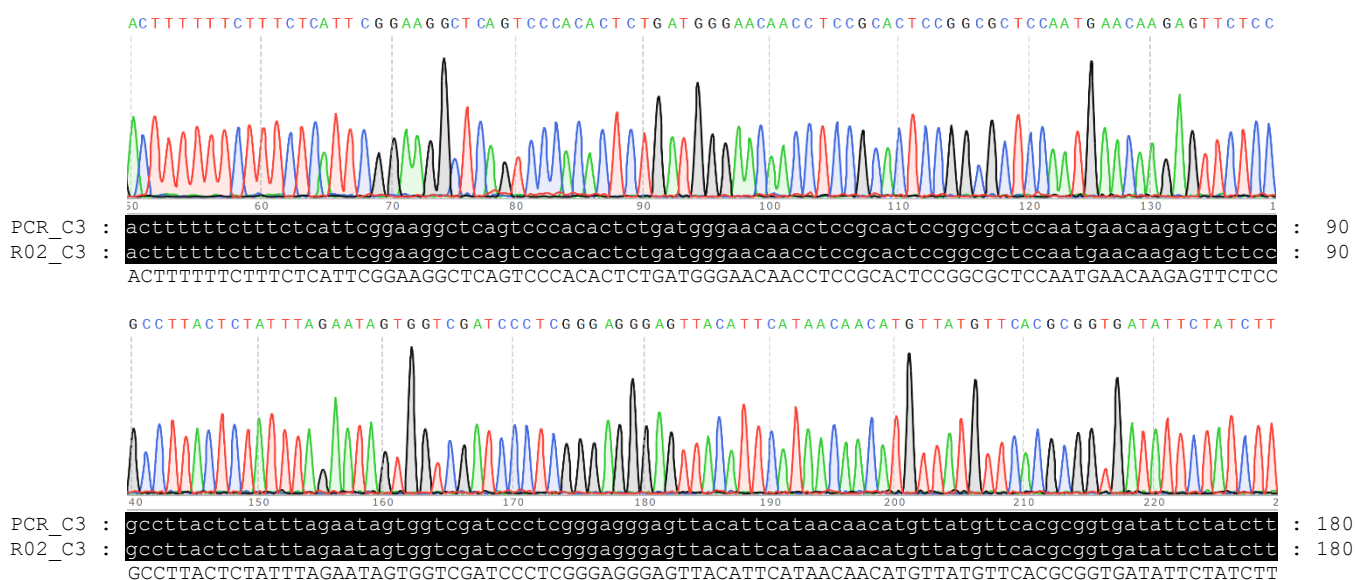


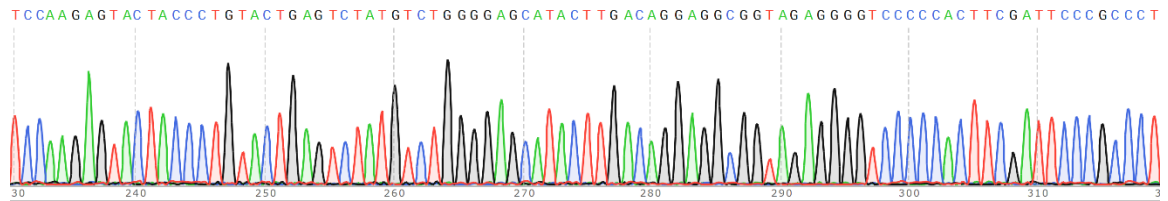


f comparison of the sequence obtained from PCR amplification and Sanger sequencing (R02-C2) and the expected sequence.

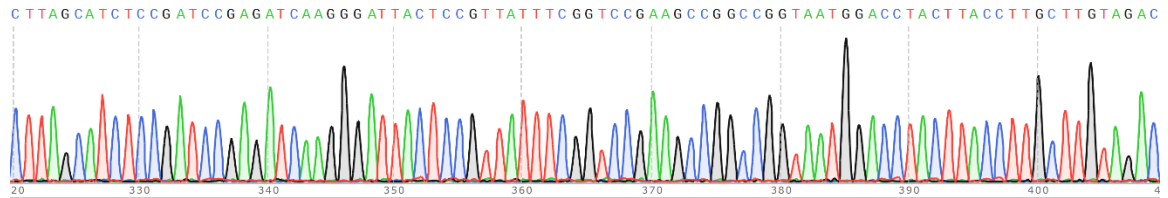


g comparison of the sequence obtained from PCR amplification and Sanger sequencing (R02-C3) and the expected sequence.

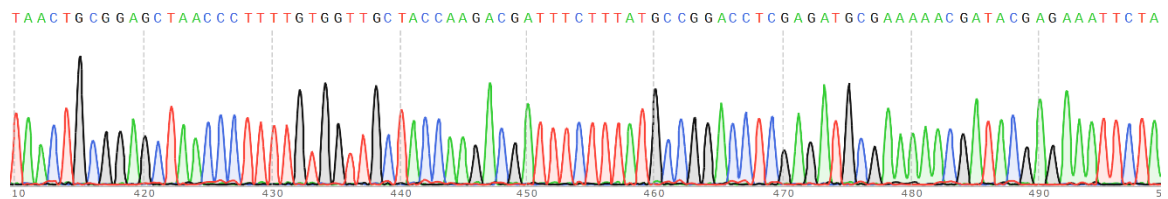




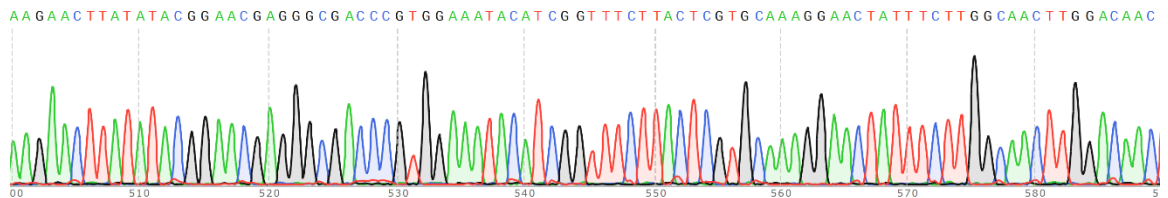
PCR_C3 : tccaagagtactaccctgtactgagctatgtctgtgggagcatacttgacaggaggcggtagaggggtccccacttcgattcccgccct : 270
 R02_C3 : tccaagagtactaccctgtactgagctatgtctgtgggagcatacttgacaggaggcggtagaggggtccccacttcgattcccgccct : 270
 TCCAAGAGTACTACCCCTGACTGAGTCTATGTCTGGGGAGCATACTTGACAGGAGGCGGTAGAGGGTCCCCACTTCGATTCCCGCCCT



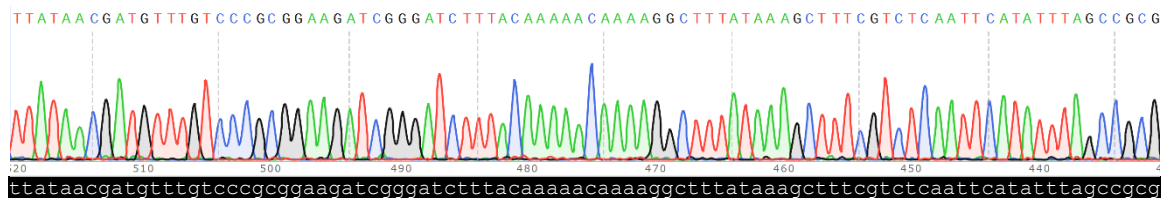
PCR_C3 : cttagcatctccgatccgagatcaagggtactccgttatttcgggtccgaagcggcggtaatggacctacttaccttgcttgtagac : 360
 R02_C3 : cttagcatctccgatccgagatcaagggtactccgttatttcgggtccgaagcggcggtaatggacctacttaccttgcttgtagac : 360
 CTTAGCATCTCCGATCCGAGATCAAGGGATTACTCCGTTATTTTCGGTCCGAAGCGGCGGTAATGGACCTACTTACCTTGCTTGAGAC



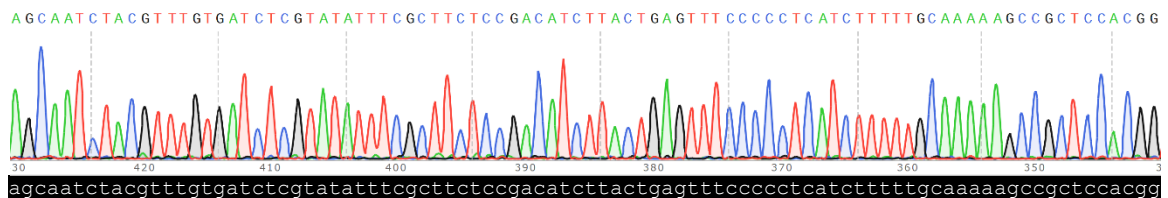
PCR_C3 : taactgcgagctaaccttttgtggtgtctaccaagacgatttcttattgccggacctcgagatgcgaaaaacgatacagagaaattcta : 450
 R02_C3 : taactgcgagctaaccttttgtggtgtctaccaagacgatttcttattgccggacctcgagatgcgaaaaacgatacagagaaattcta : 450
 TAACTGCGGAGCTAACCTTTTGTGGTGTCTACCAAGACGATTCTTTATGCCGGACCTCGAGATGCGAAAAACGATACGAGAAATTCTA



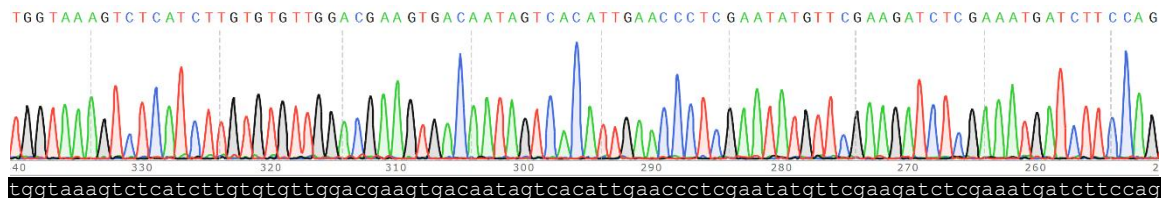
PCR_C3 : aagaacttataatcgggaacgagggcgacccgtggaataacatcggtttcttactcgtgcaaaggaactatttcttggcaacttggacaac : 540
 R02_C3 : aagaacttataatcgggaacgagggcgacccgtggaataacatcggtttcttactcgtgcaaaggaactatttcttggcaacttggacaac : 540
 AAGAACTTATATACGGAACGAGGCGACCCGTGGAATACATCGGTTTCTTACTCGTGCAAAGGAACCTATTCTTGGCAACTTGGACAAC



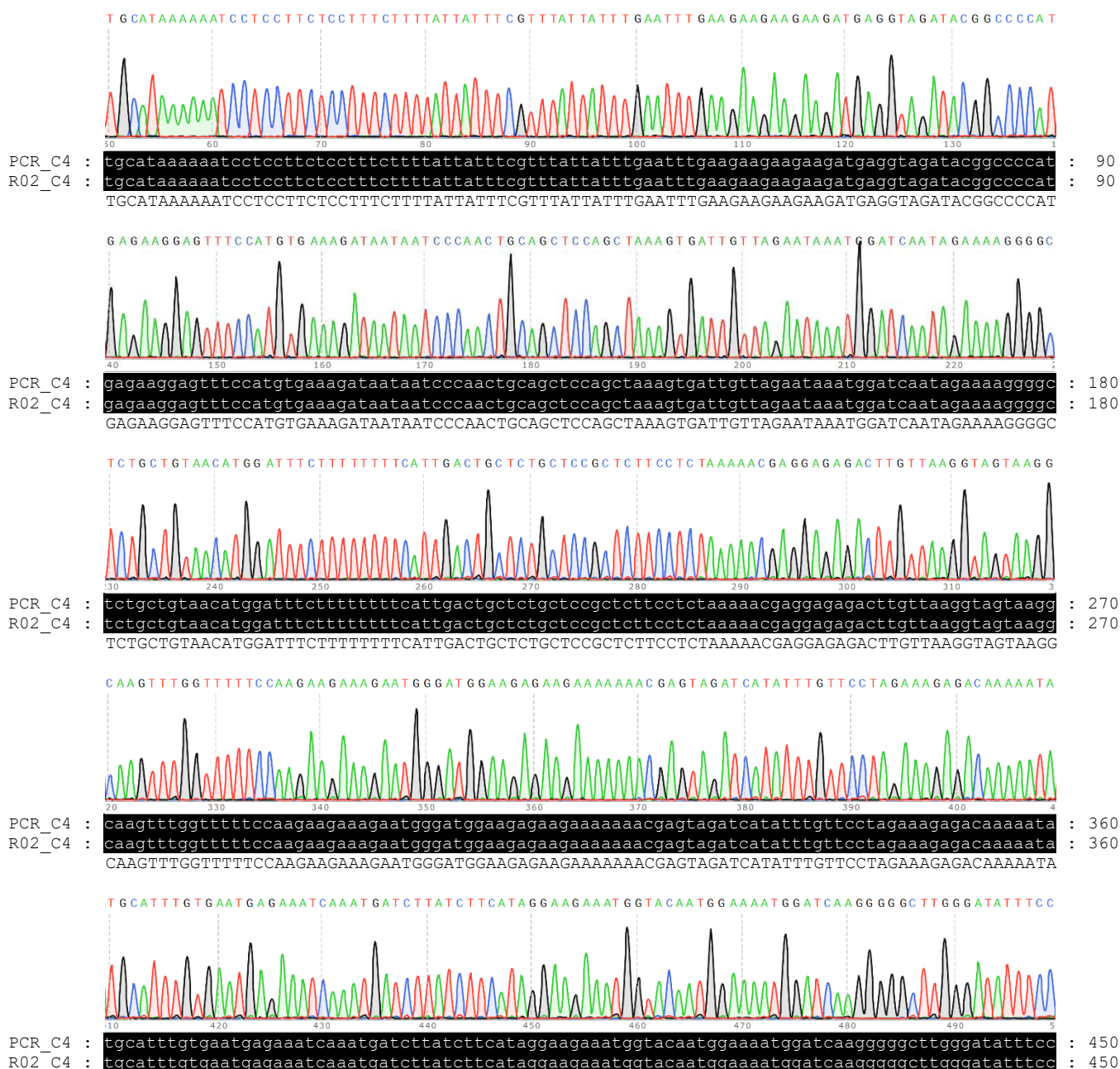
PCR_C3 : ttataacgatgtttgtcccgcggaagatcgggatctttacaaaaacaaaaggctttataaagctttcgtctcaattcatatttagccgcg : 630
 R02_C3 : ttataacgatgtttgtcccgcggaagatcgggatctttacaaaaacaaaaggctttataaagctttcgtctcaattcatatttagccgcg : 630
 TTATAACGATGTTTGTCCCGCGAAGATCGGGATCTTTACAAAAACAAAAGGCTTTATAAAGCTTTCGTCGAATTATTTAGCCGCG

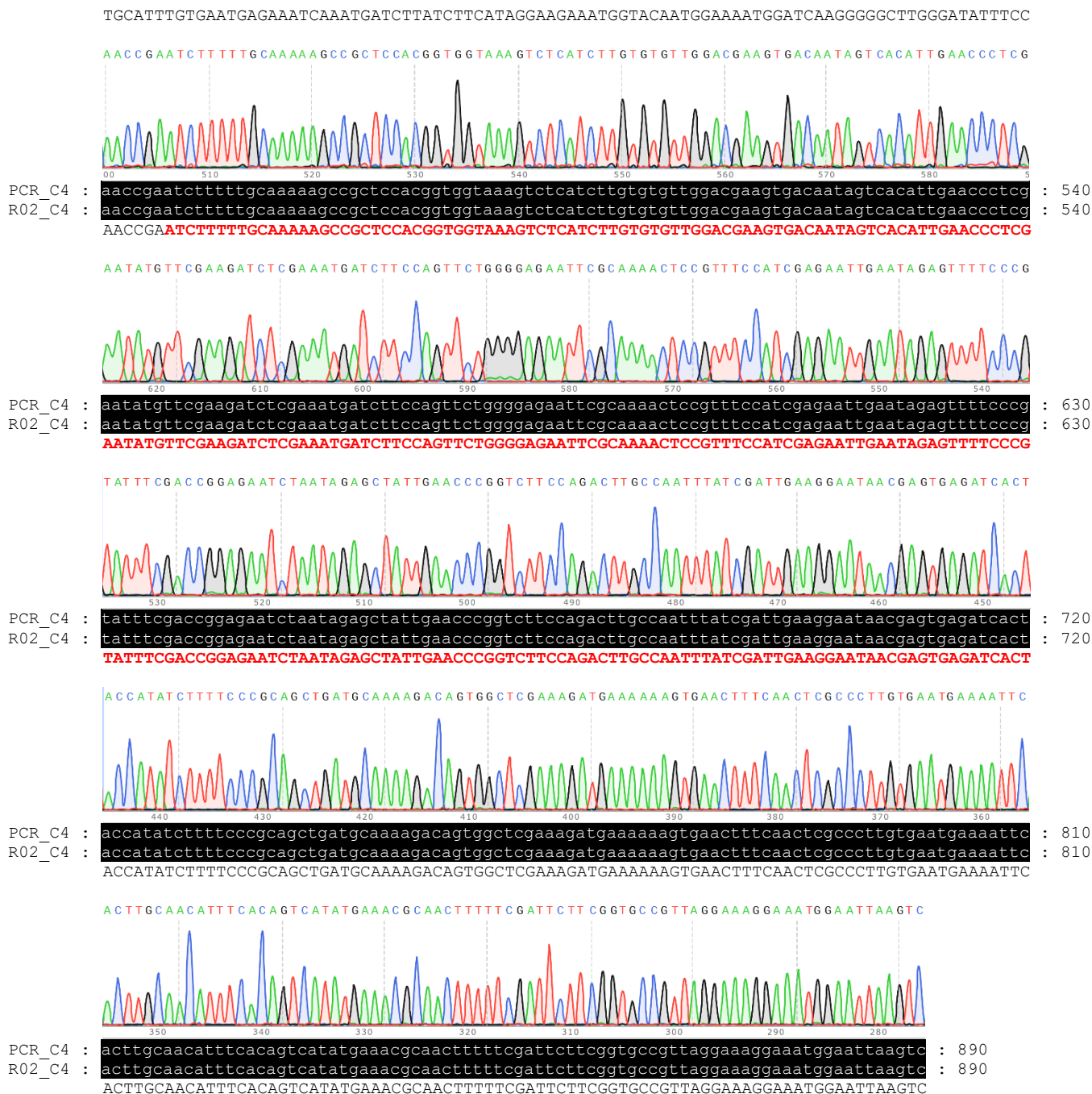


PCR_C3 : agcaatctacgtttgtgatctcgtatatttcgcttctccgacatcttactgagtttccctctcatcttttgcacaaaagcgctccacgg : 720
 R02_C3 : agcaatctacgtttgtgatctcgtatatttcgcttctccgacatcttactgagtttccctctcatcttttgcacaaaagcgctccacgg : 720
 AGCAATCTACGTTTGTGATCTCGTATTTTCGCTTCTCCGACATCTTACTGAGTTTCCCTCTCATTTTTGCAAAAAGCGCTCCACGG

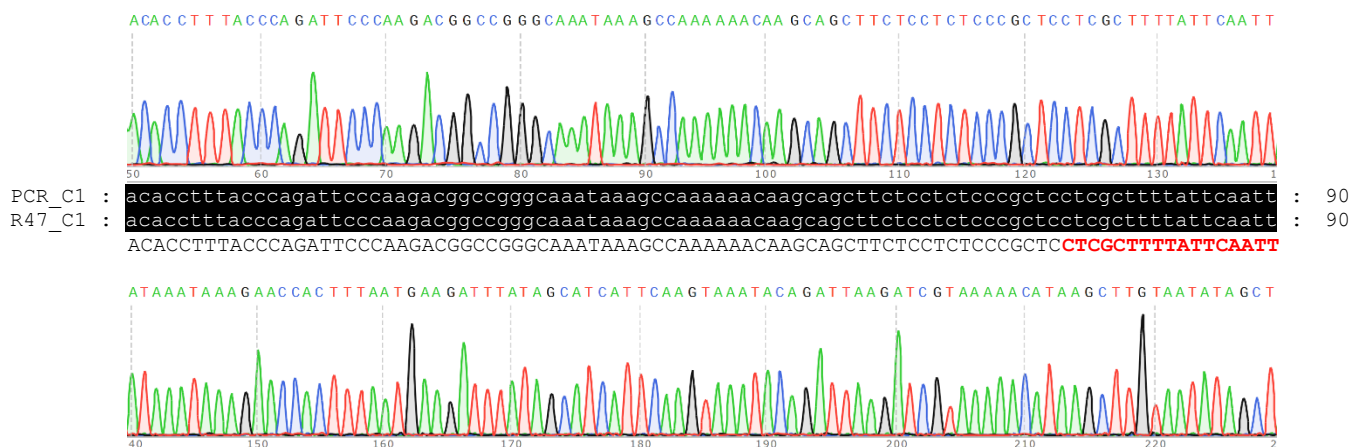


PCR_C3 : tggtaaagtctcatcttgtgtgttggacgaagtgcacattgaacctcgaatatgttcgaagatctcgaaatgatcttccag : 810
 R02_C3 : tggtaaagtctcatcttgtgtgttggacgaagtgcacattgaacctcgaatatgttcgaagatctcgaaatgatcttccag : 810
TGGTAAAGTCTCATCTTGTGTTGGACGAAGTGACAAATAGTCACATTGAACCTCGAATATGTTTGAAGATCTCGAAATGATCTTCCAG



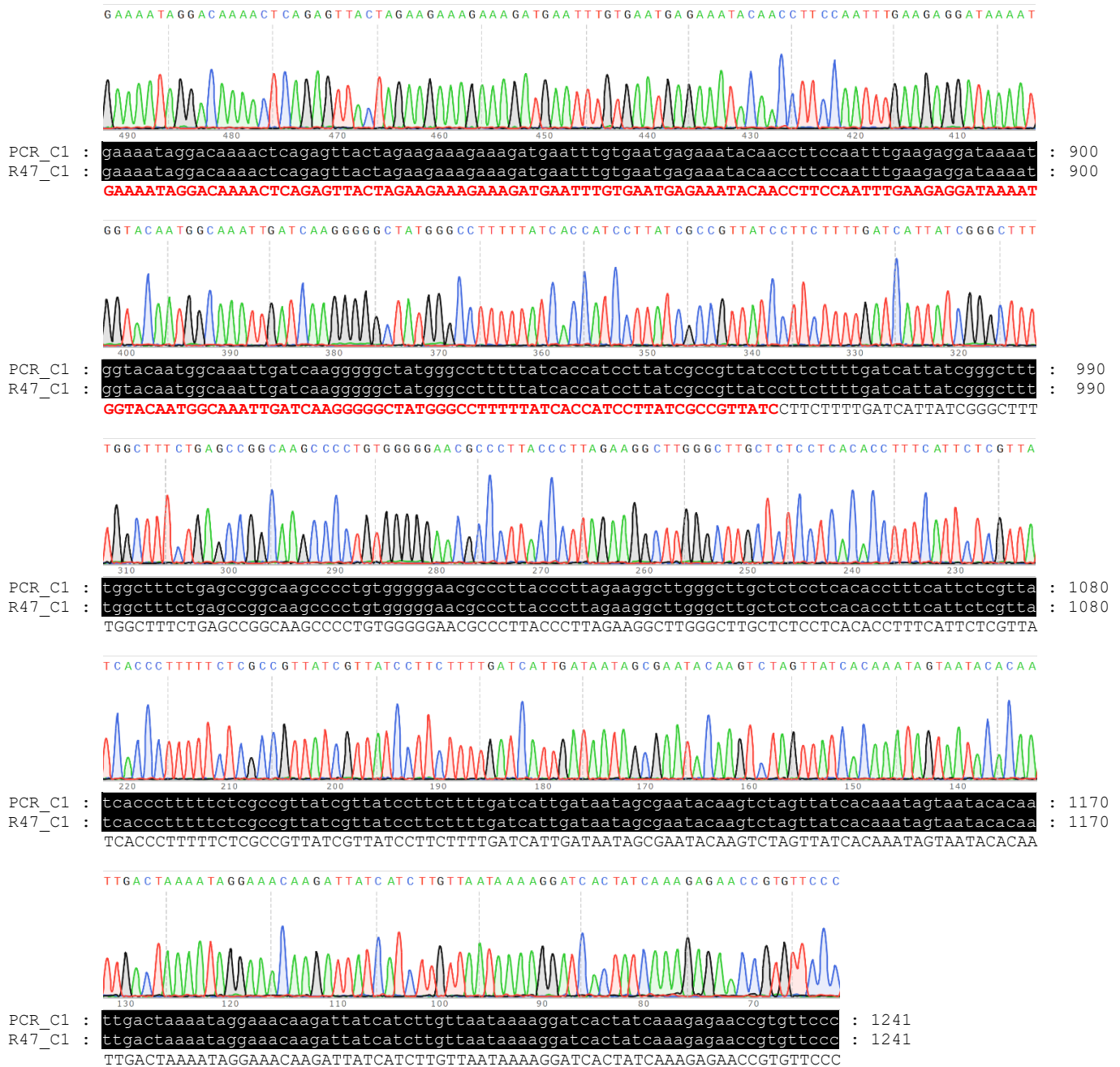


i comparison of the sequence obtained from PCR amplification and Sanger sequencing (R47-C1) and the expected sequence.



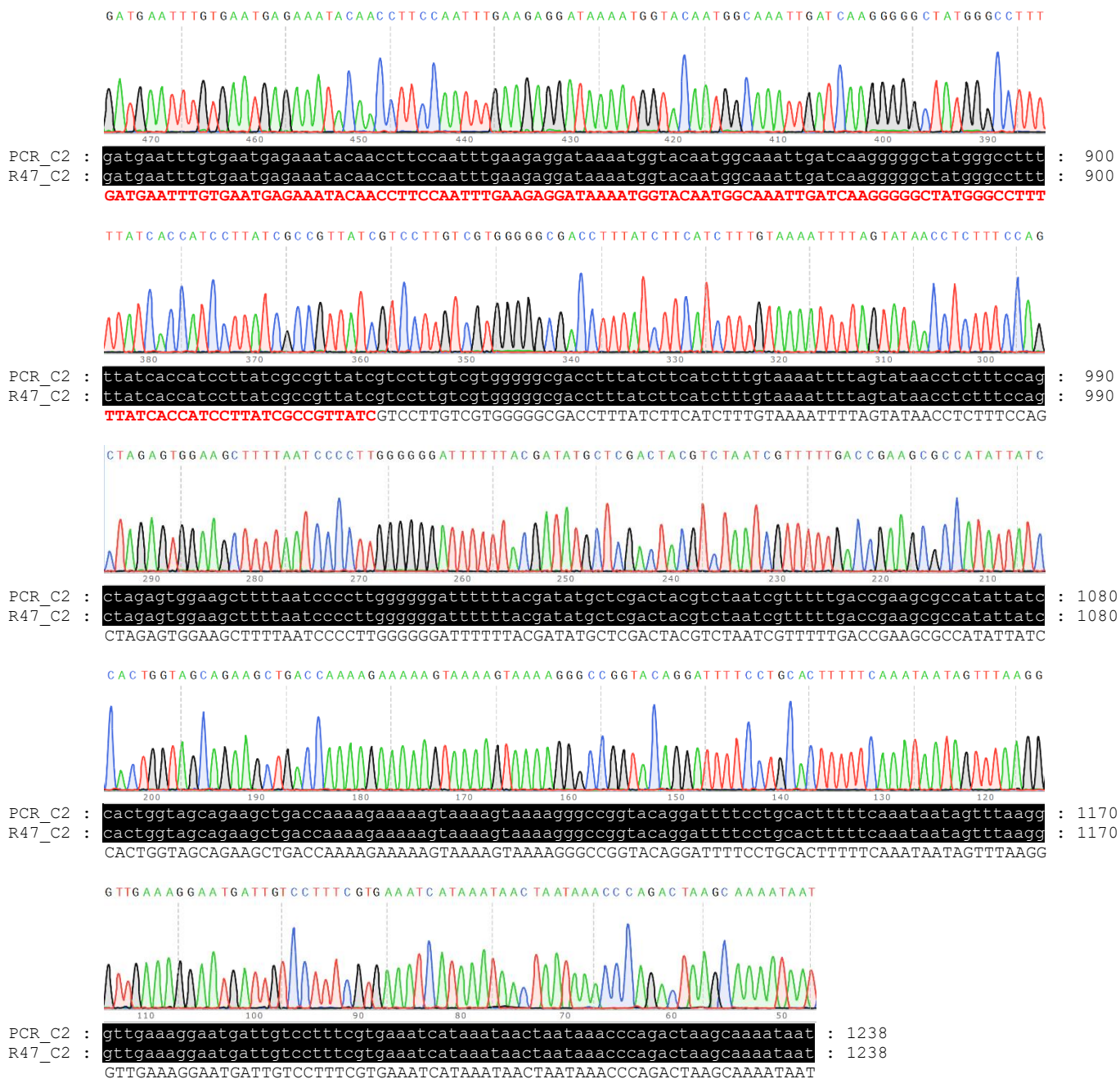
The figure displays 10 Sanger sequencing chromatograms, each representing a specific region of a DNA sequence. Each chromatogram compares two samples: PCR_C1 (top trace) and R47_C1 (bottom trace). The DNA sequence is shown above the traces, with a red highlight indicating a mismatch between the two samples. The chromatograms show peaks for A (green), C (blue), G (black), and T (red). The regions are numbered 1 through 10, corresponding to the sequence positions indicated in the table below.

Region	PCR_C1 Sequence	R47_C1 Sequence	Mismatch
1	ataataaagaacacactttaatgaagatttatagcatcattccaagtaaatacagattaaagatcgtaaaaacataagcttgtaatatagct	ataataaagaacacactttaatgaagatttatagcatcattccaagtaaatacagattaaagatcgtaaaaacataagcttgtaatatagct	ATAAATAAGAACCACCTTTAATGAAGATTTATAGCATCATTC AAGTAAATACAGATTAAAGATCGTAAAAACATAAGCTTGTAATATAGCT
2	acgcctaattccagaccagtttaagtgaagaactataaagaagacgtgtagaccctatgaataaaaaagatcattcatatagcata	acgcctaattccagaccagtttaagtgaagaactataaagaagacgtgtagaccctatgaataaaaaagatcattcatatagcata	ACGCCTAATTCCAGACCAGTTAATGCAAGAACTATAAAGAAAGGACCTGTAGACCCTATGAATAAAAAAGATCATTTCATACATAGCATA
3	gtccaagcgaaccacttaaaatctttactaaactatgacggccatcatattagcaataaacgtattcctaagcttaattgcgcgaaaa	gtccaagcgaaccacttaaaatctttactaaactatgacggccatcatattagcaataaacgtattcctaagcttaattgcgcgaaaa	GTCCAAGCGAACCCACTTAAATCTTTACTAAACTATGACCGGCCATCATATTAGCAAATAAACGTATTCTTAAGCTTAATGCGCGAAAA
4	caatgagggattagctcaaggagtaactaaaaaaggggctaaggggaagtgggactcctgcgggtaatgagaagcttaaaaaatgaagacca	caatgagggattagctcaaggagtaactaaaaaaggggctaaggggaagtgggactcctgcgggtaatgagaagcttaaaaaatgaagacca	CAATGAGGGATTAGCTCAAGGAGTACTAAAAAAGGGGCTAAGGGAAGTGGGACTCCTGCGGGTAATGAGAAGCTTAAAAAATGAAGACCA
5	ttctttacaaatcccactatagtaagtccaataaaaaagagaaaaatgagagacccaagtaacgataaaatgacttggtactgtgaagcta	ttctttacaaatcccactatagtaagtccaataaaaaagagaaaaatgagagacccaagtaacgataaaatgacttggtactgtgaagcta	TTCTTTACAAATCCCACCTATAGTAATGCCAATAAAAAAGAGAAAATGAGAGACCCAAAGTAACGATAAAATGACTTGTTACTGTGAAGCTA
6	taagggatcataccctgcagattacgaaataacgaaaaagtaaaagtaaccgagatgcaagggaaaaacggttggtttcacattgccagaa	taagggatcataccctgcagattacgaaataacgaaaaagtaaaagtaaccgagatgcaagggaaaaacggttggtttcacattgccagaa	TAAGGGATCATACCCTGCAGATTACGAAATAACGAAAAAGTAAAAAGTAACCGAGATGCAAGGGAAAAACGGTTGTTTCACATTGCCAGAA
7	agaccacctaattgttgctttaccagggttcggaacaaaatcataaataaagctctaccagggttgccaagcatttggtactgactttcct	agaccacctaattgttgctttaccagggttcggaacaaaatcataaataaagctctaccagggttgccaagcatttggtactgactttcct	AGACCACCTATTGTTCGTTTACCAGGTTTCGGAACAAAATCATAAATAAGCTCTACCAGGGATTGCCAAGCATTGGTACTGACTTTTCCT
8	cctcccttttttagtaactgtaactgaacgaaaaataaaaaatttagtaactgtaactgaatgaaaagaaatttgagtaactaaatgaaaa	cctcccttttttagtaactgtaactgaacgaaaaataaaaaatttagtaactgtaactgaatgaaaagaaatttgagtaactaaatgaaaa	CCTCCCTTTTTTAGTAACGTGTAACGTAACGAAAAATAAAAAATTTAGTAACGTGAATGAAAAGAAATTTGAGTAACATAATGAAAA
9	ataataaagaacacactttaatgaagatttatagcatcattccaagtaaatacagattaaagatcgtaaaaacataagcttgtaatatagct	ataataaagaacacactttaatgaagatttatagcatcattccaagtaaatacagattaaagatcgtaaaaacataagcttgtaatatagct	ATAAATAAGAACCACCTTTAATGAAGATTTATAGCATCATTC AAGTAAATACAGATTAAAGATCGTAAAAACATAAGCTTGTAATATAGCT
10	acgcctaattccagaccagtttaagtgaagaactataaagaagacgtgtagaccctatgaataaaaaagatcattcatatagcata	acgcctaattccagaccagtttaagtgaagaactataaagaagacgtgtagaccctatgaataaaaaagatcattcatatagcata	ACGCCTAATTCCAGACCAGTTAATGCAAGAACTATAAAGAAAGGACCTGTAGACCCTATGAATAAAAAAGATCATTTCATACATAGCATA

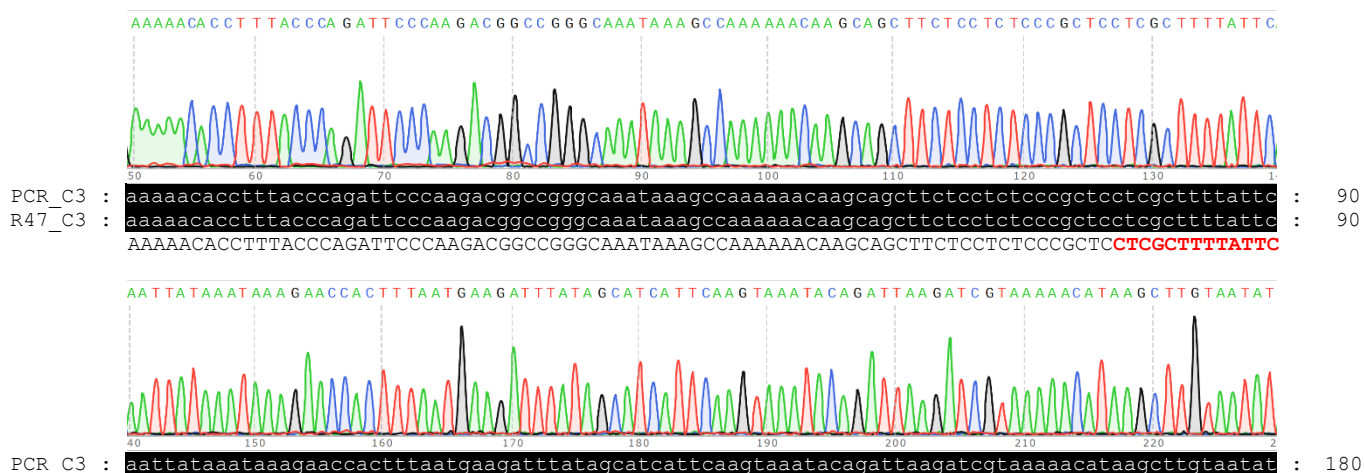


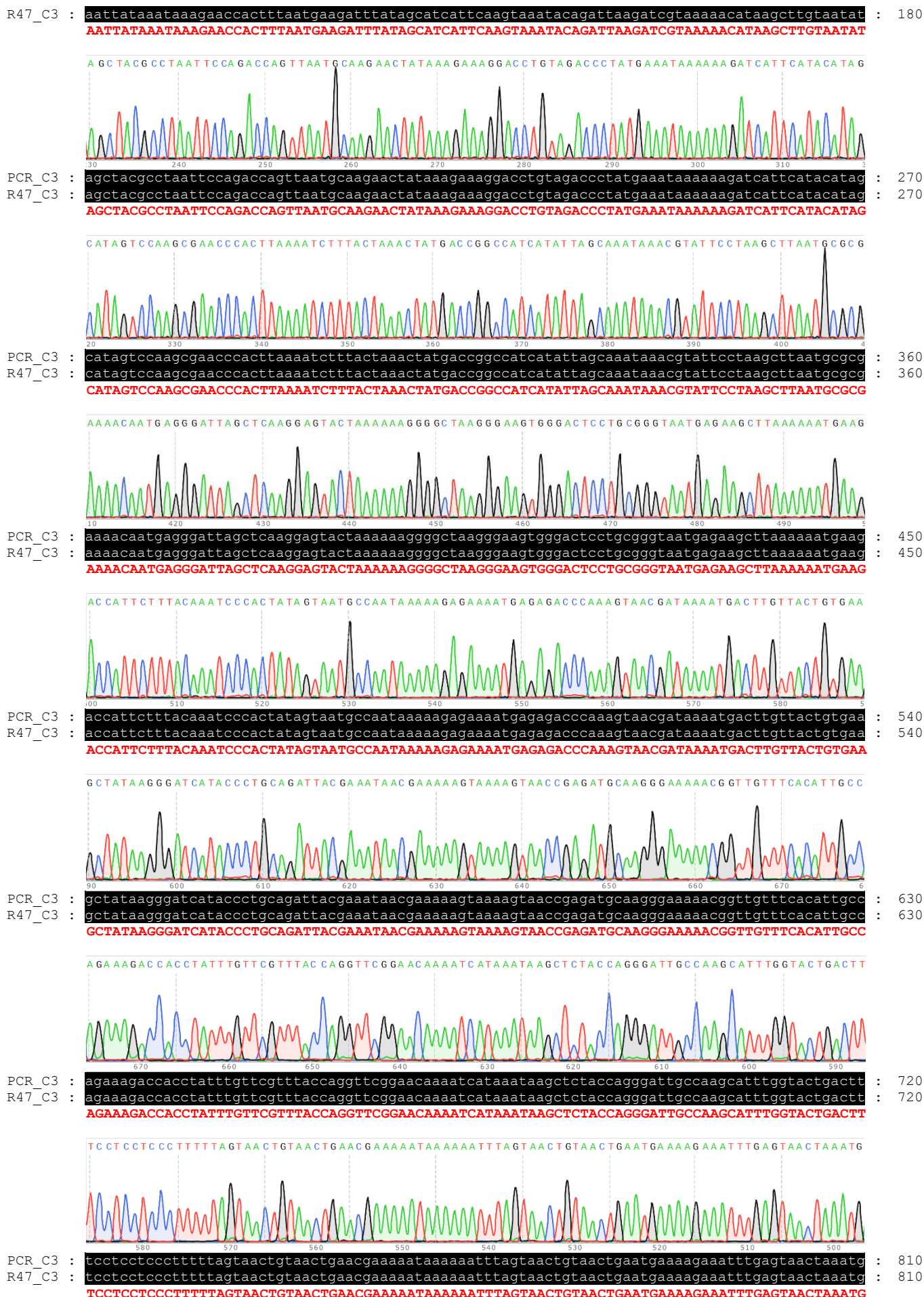
j comparison of the sequence obtained from PCR amplification and Sanger sequencing (R47-C2) and the expected sequence.

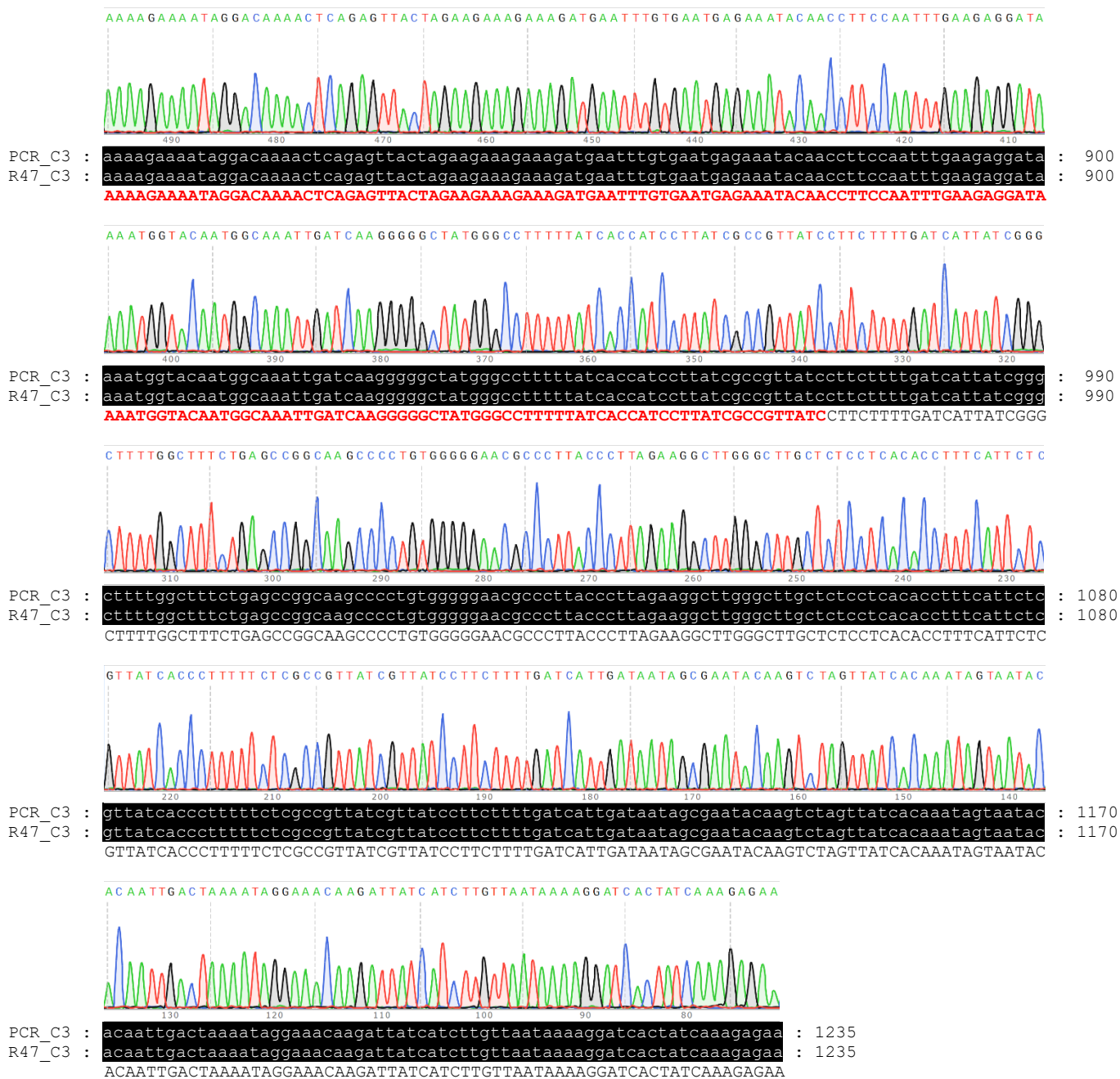




κ comparison of the sequence obtained from PCR amplification and Sanger sequencing (R47-C3) and the expected sequence.

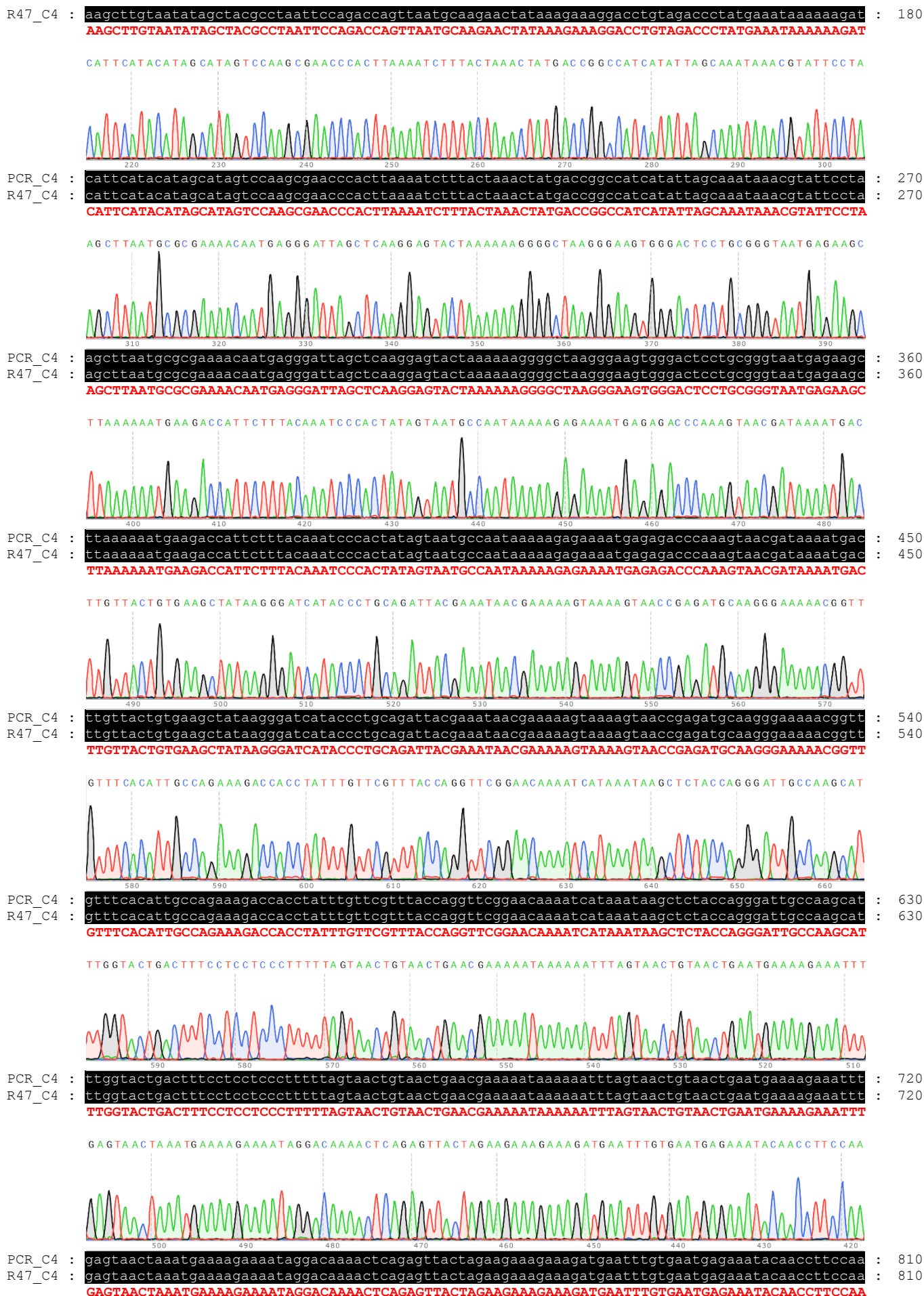


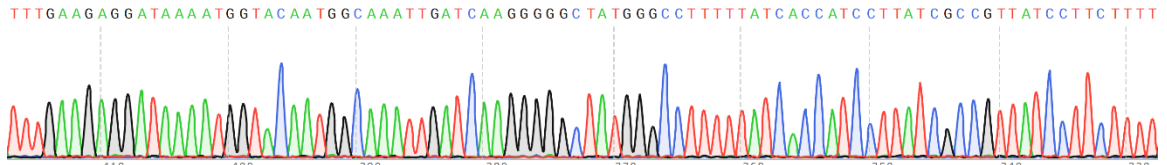




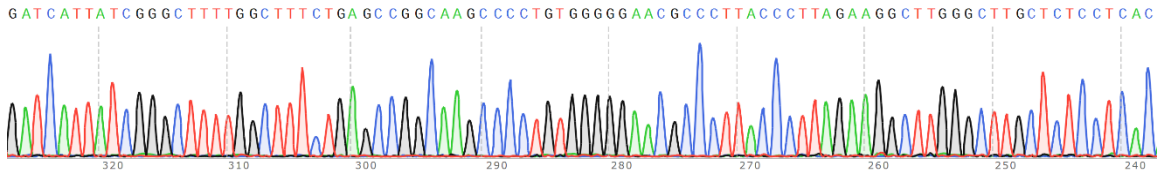
1 comparison of the sequence obtained from PCR amplification and Sanger sequencing (R47-C4) and the expected sequence.



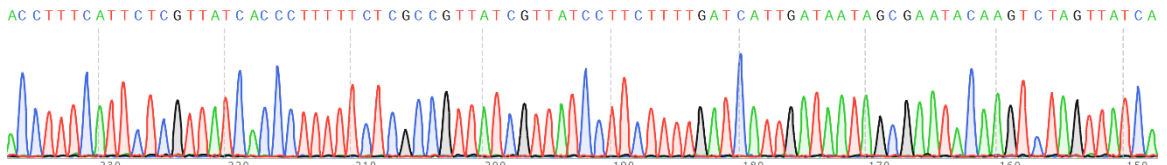




PCR_C4 : tttgaagaggataaaaatggtacaatggcaaattgatcaagggggctatgggacctttttatcaccatccttategccggttatccttctttt : 900
 R47_C4 : tttgaagaggataaaaatggtacaatggcaaattgatcaagggggctatgggacctttttatcaccatccttategccggttatccttctttt : 900
TTTGAAGAGGATAAAATGGTACAAATGGCAAATTGATCAAGGGGGCTATGGGCTTTTTATCACCATCCTTATCGCCGTTATCCTTCTTTT



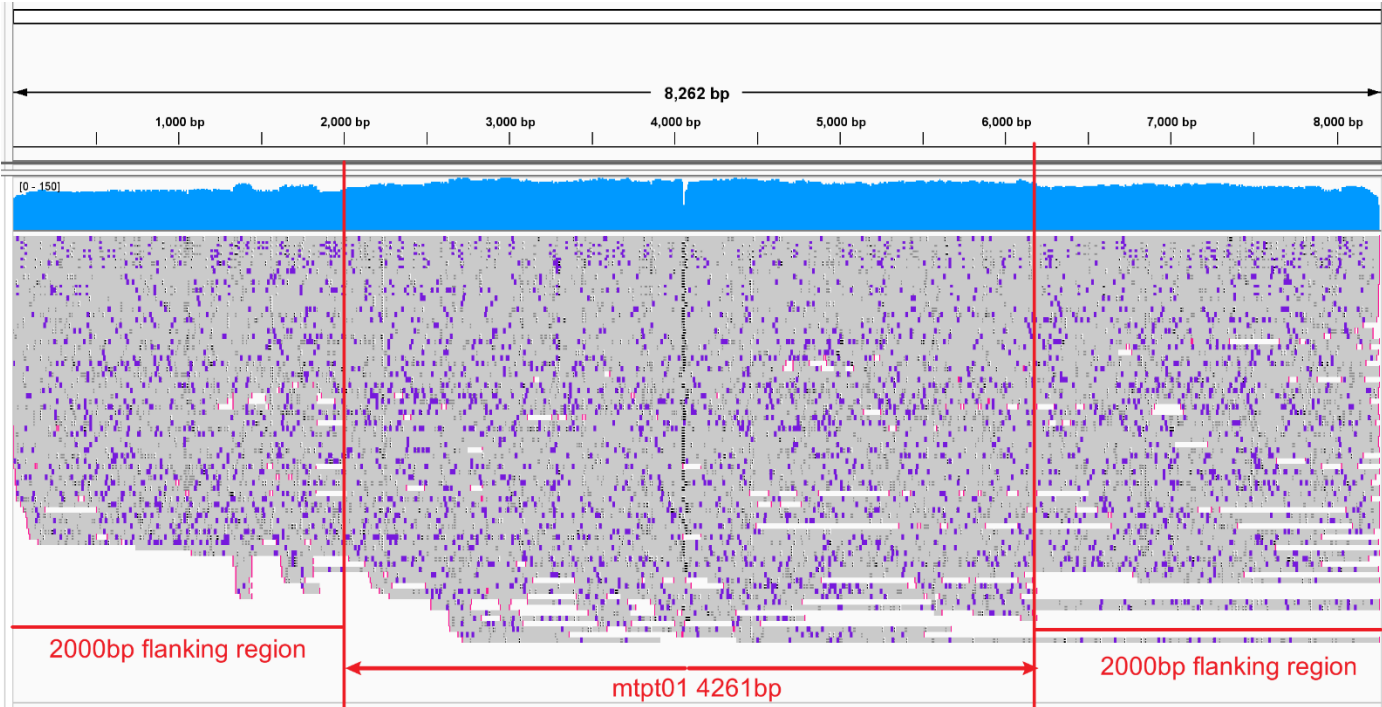
PCR_C4 : gatcattatcgggcttttggctttctgagccggcaagcccctgtgggggaacgcccttacccttagaaggcttgggcttgctctcctcac : 990
 R47_C4 : gatcattatcgggcttttggctttctgagccggcaagcccctgtgggggaacgcccttacccttagaaggcttgggcttgctctcctcac : 990
 GATCATTATCGGGCTTTTGGCTTTCTGAGCCGGCAAGCCCCTGTGGGGGAACGCCCTTACCCTTAGAAGGCTTGGGCTTGCTCTCCTCAC



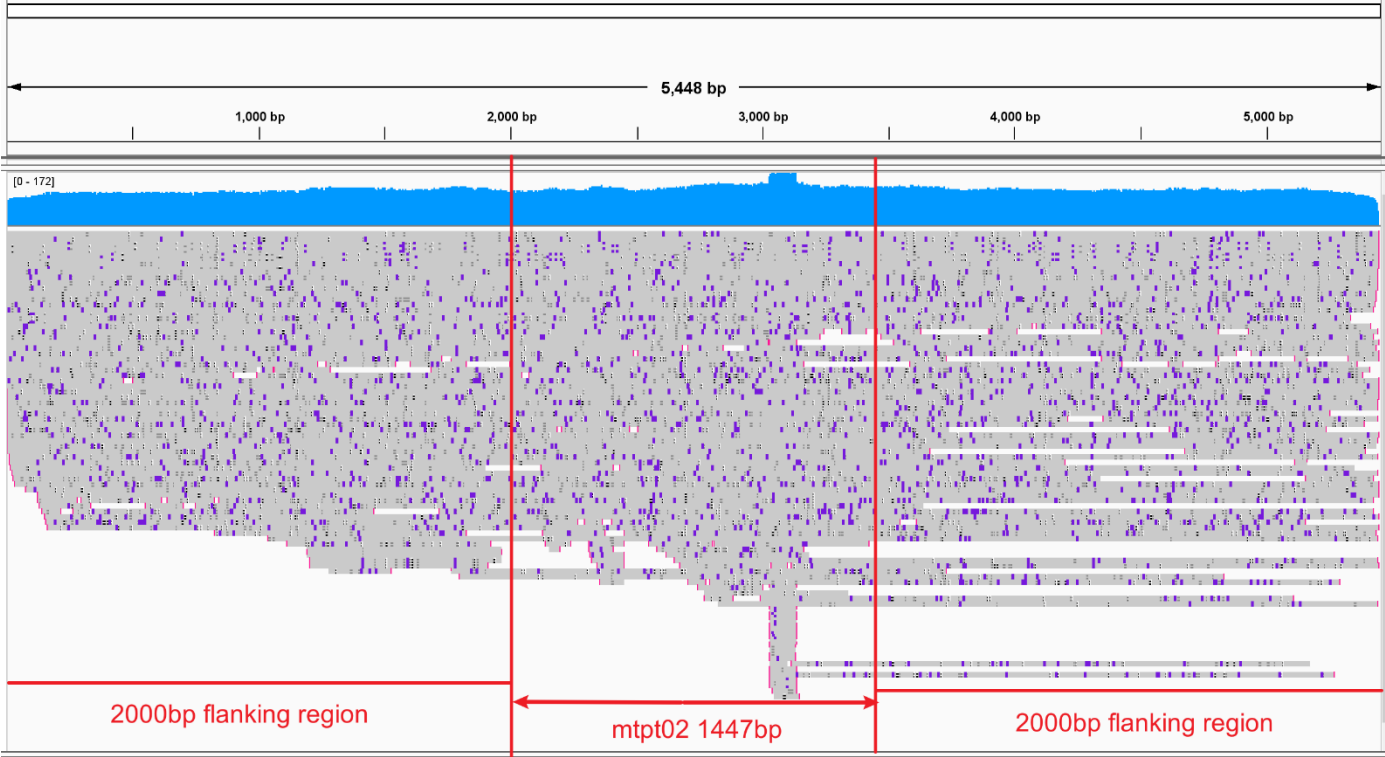
PCR_C4 : acctttcattctcgttatcacctttttctcgccggttatcgttatccttcttttgatcattgataatagcgaataacaagtctagttatca : 1080
 R47_C4 : acctttcattctcgttatcacctttttctcgccggttatcgttatccttcttttgatcattgataatagcgaataacaagtctagttatca : 1080
 ACCTTTCATTCTCGTTATCACCTTTTTCTCGCCGTTATCGTTATCCTTCTTTTGATCATTGATAATAGCGAATACAAGTCTAGTTATCA

Figure S5 Alignment of the Nanopore long reads to the MTPTs and their flanking sequences in the mitogenome of *S. officinalis*. Panels a-w show the alignment of the Nanopore long reads to the 21 MTPT sequences on MC1 (mtpt01 to mtpt21) and 2 MTPT sequences on MC2 (mtpt22 to mtpt23). The figures were generated using IGV. The MTPT sequence was shown on the top of each figure with its coordinates. The coverage depth was shown with a blue bar chart. The reads were represented with gray lines. The regions in gray represent a match. The purple regions represent small indels. Regions shown with other colors represent mismatched bases. The MTPT sequences are indicated with red lines that have arrowheads at each end. The flanking sequences that are 2000 bp long are indicated with red lines without arrowheads.

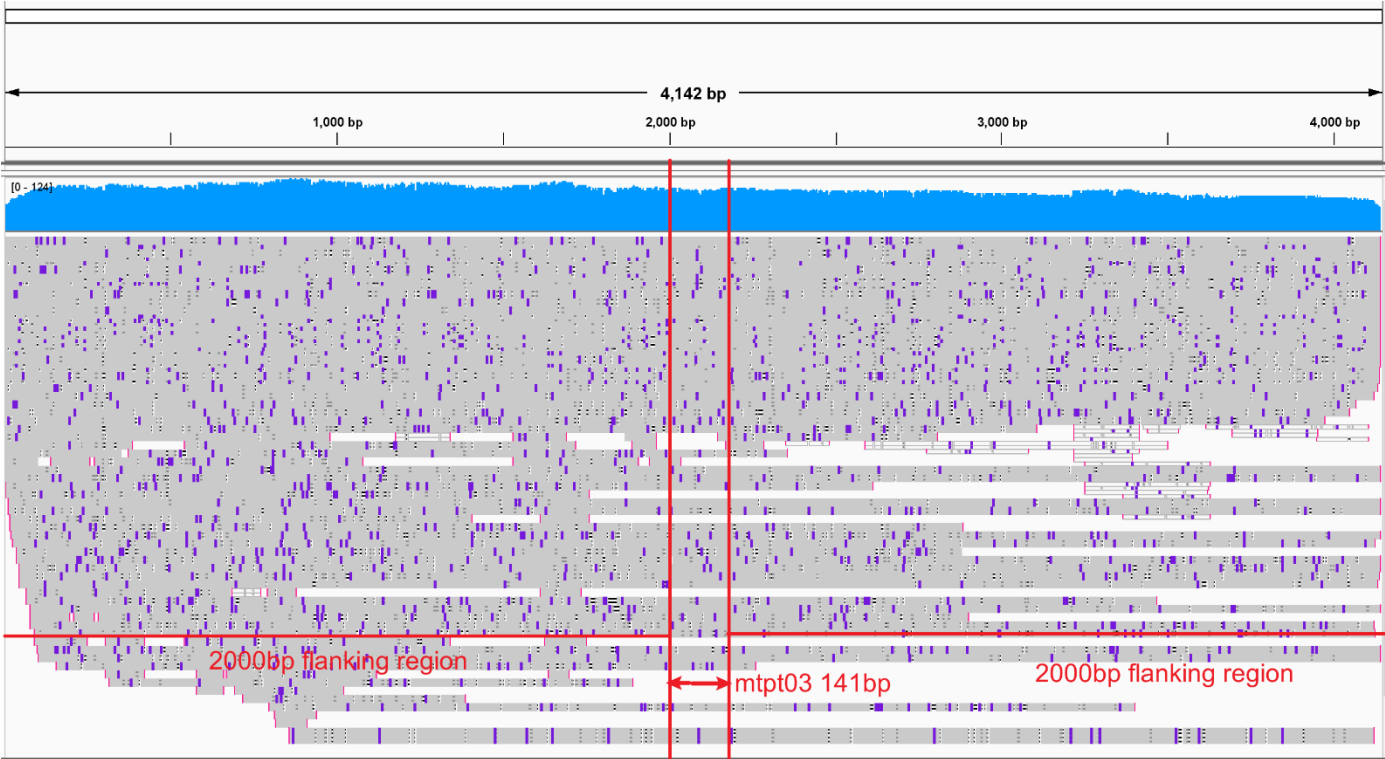
a alignment of Nanopore long reads to mtpt01 and its flanking sequences.



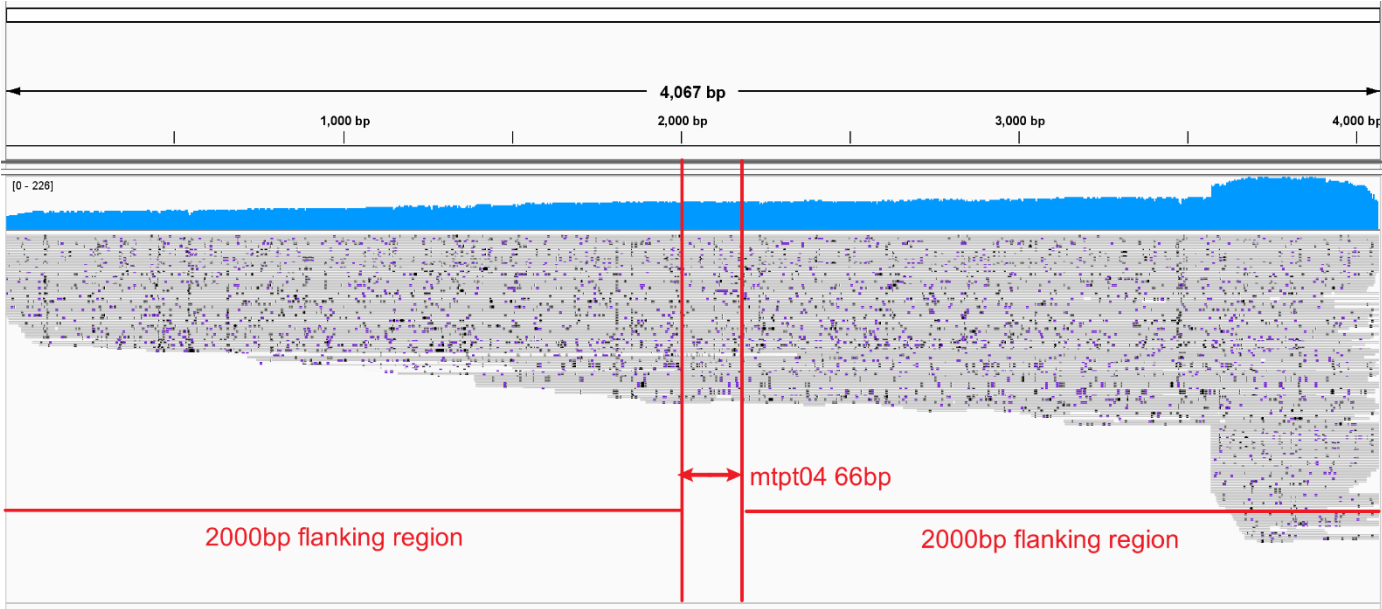
b alignment of Nanopore long reads to mtpt02 and its flanking sequences.



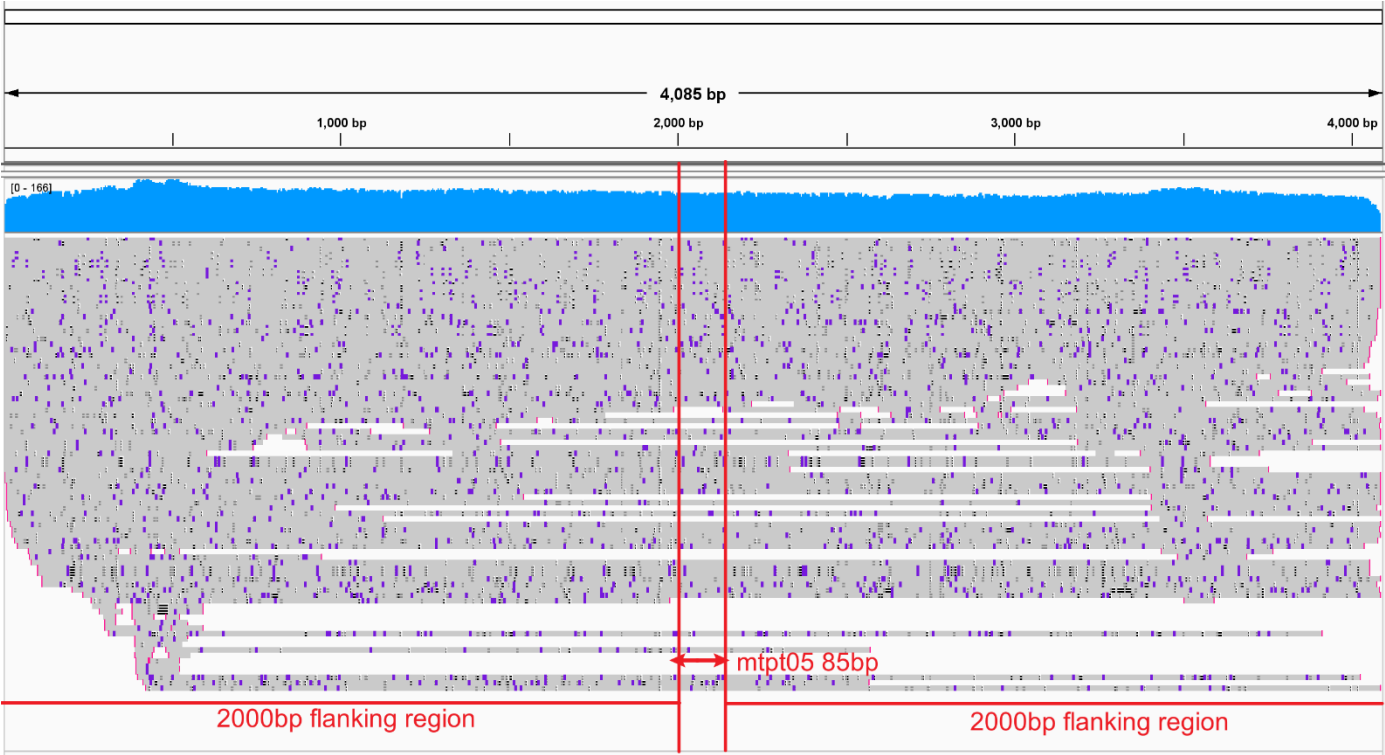
c alignment of Nanopore long reads to mtpt03 and its flanking sequences.



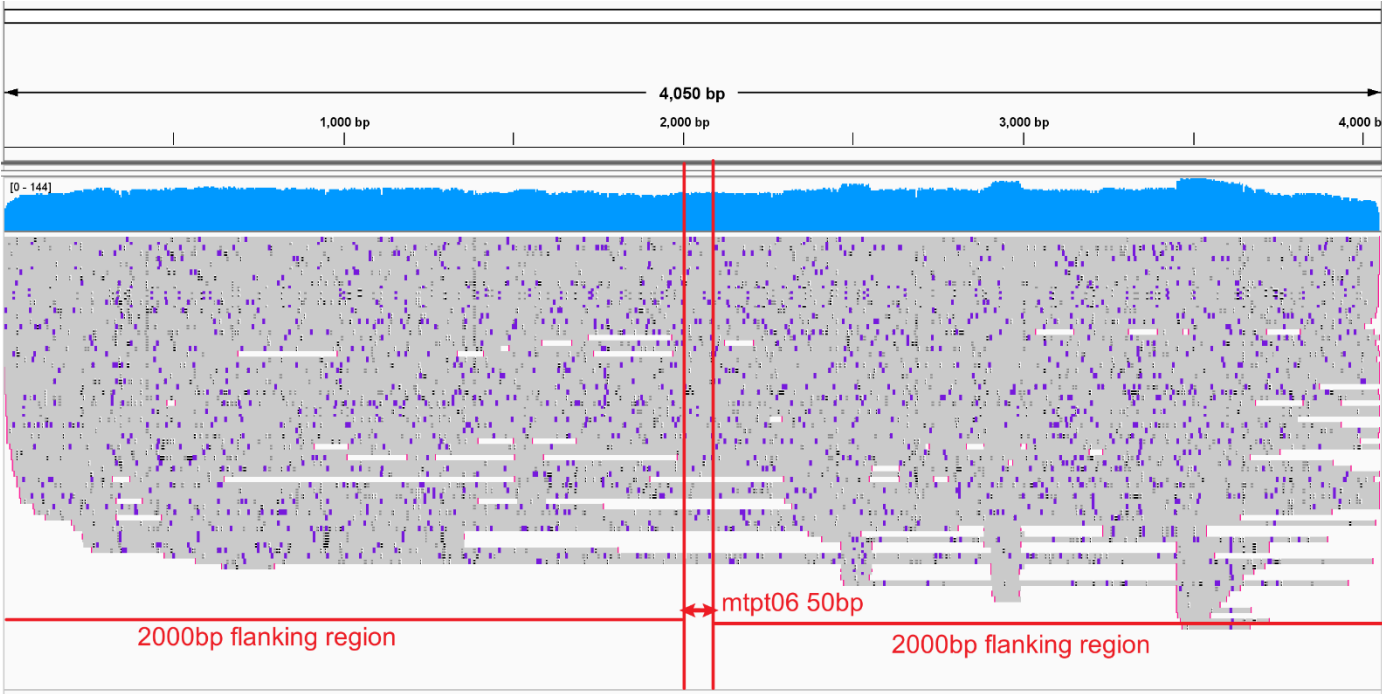
d alignment of Nanopore long reads to mtpt04 and its flanking sequences.



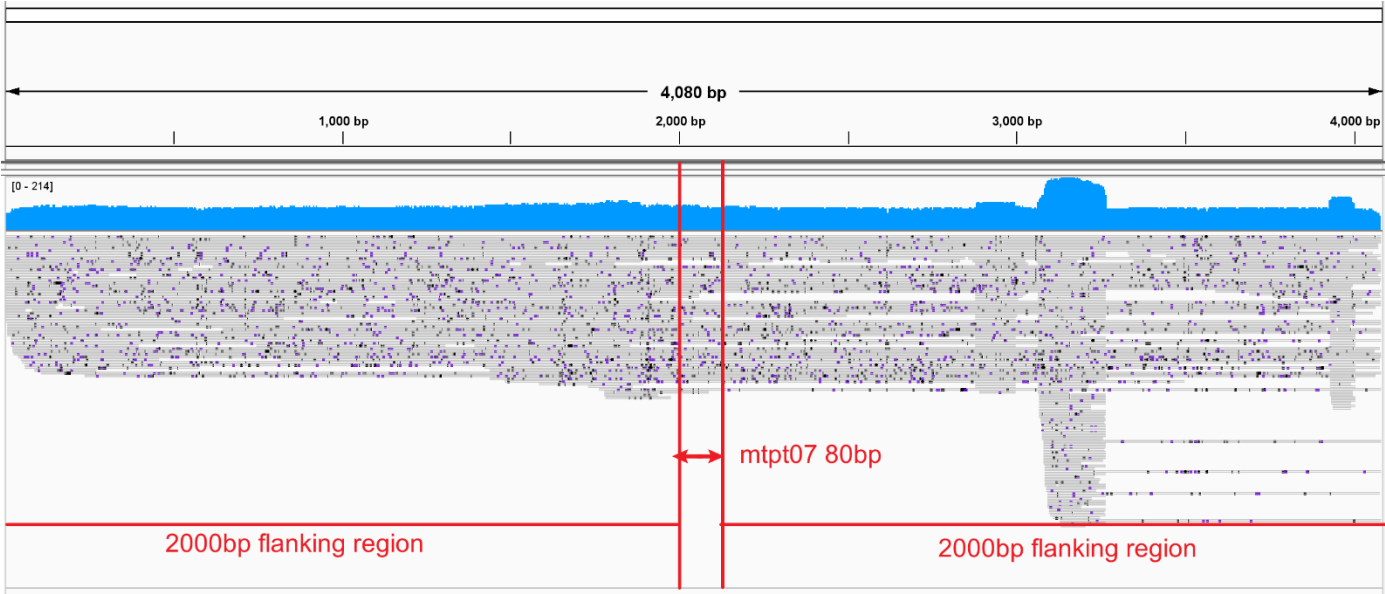
e alignment of Nanopore long reads to mtp05 and its flanking sequences.



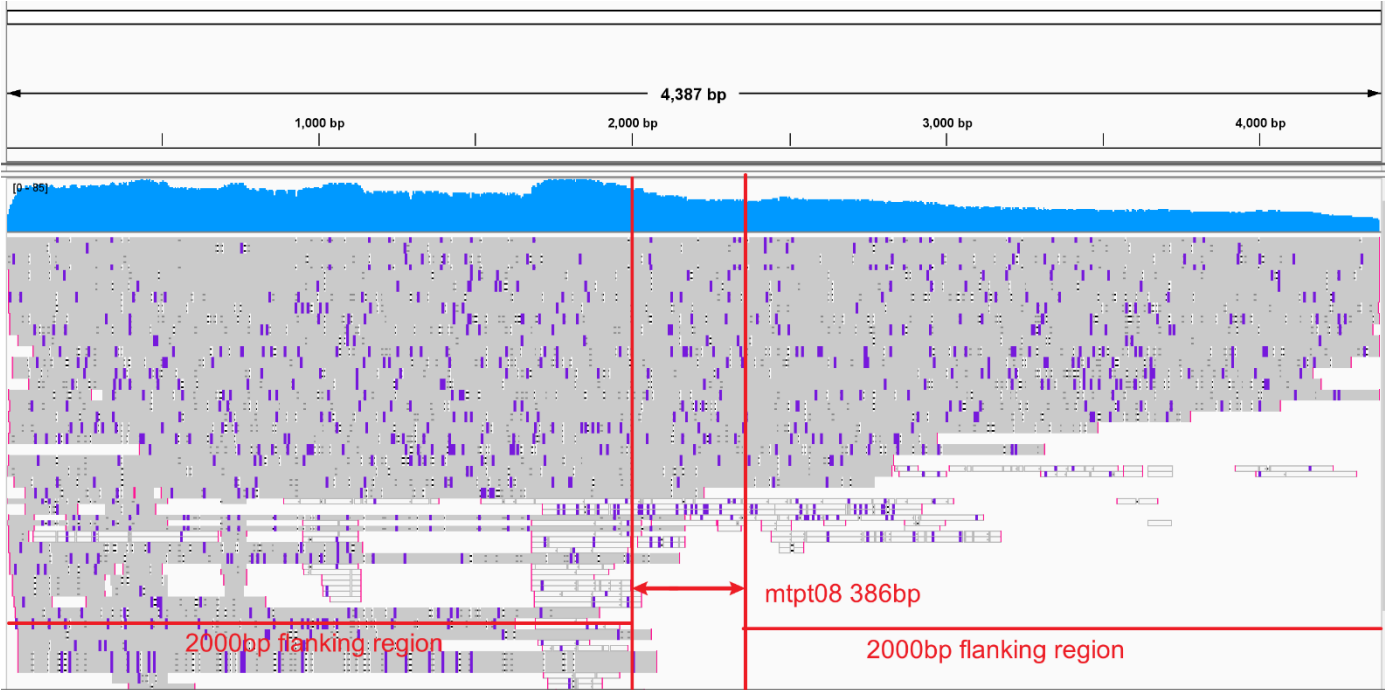
f alignment of Nanopore long reads to mtpt06 and its flanking sequences.



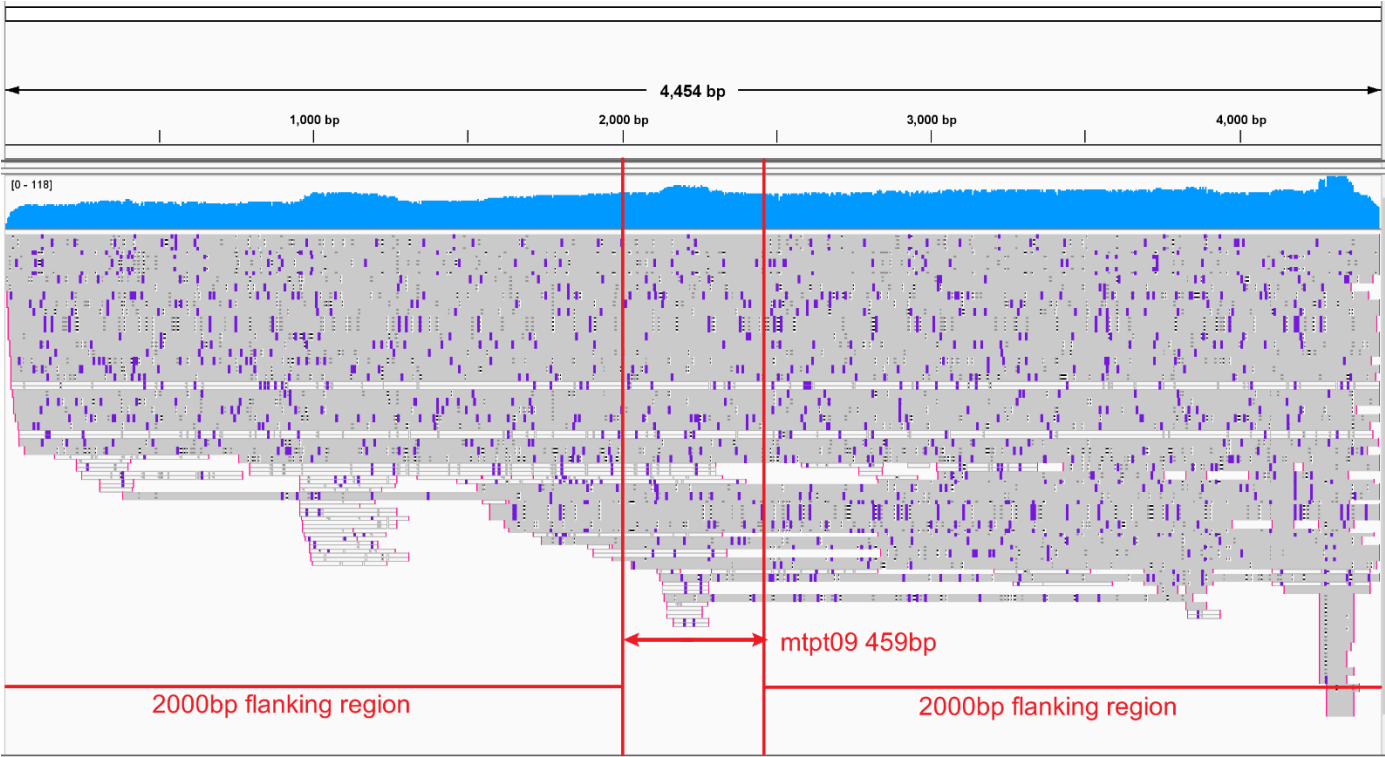
g alignment of Nanopore long reads to mtpt07 and its flanking sequences.



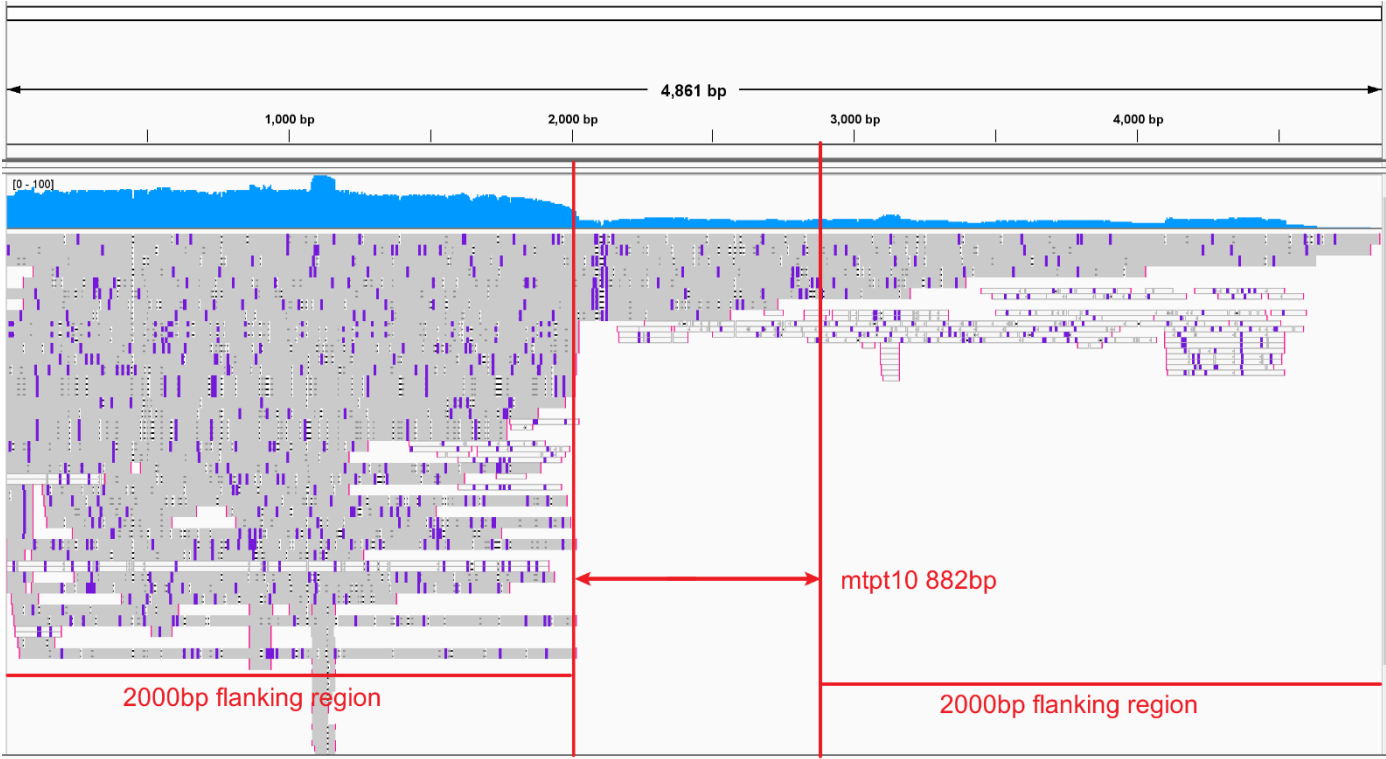
h alignment of Nanopore long reads to mtpt08 and its flanking sequences.



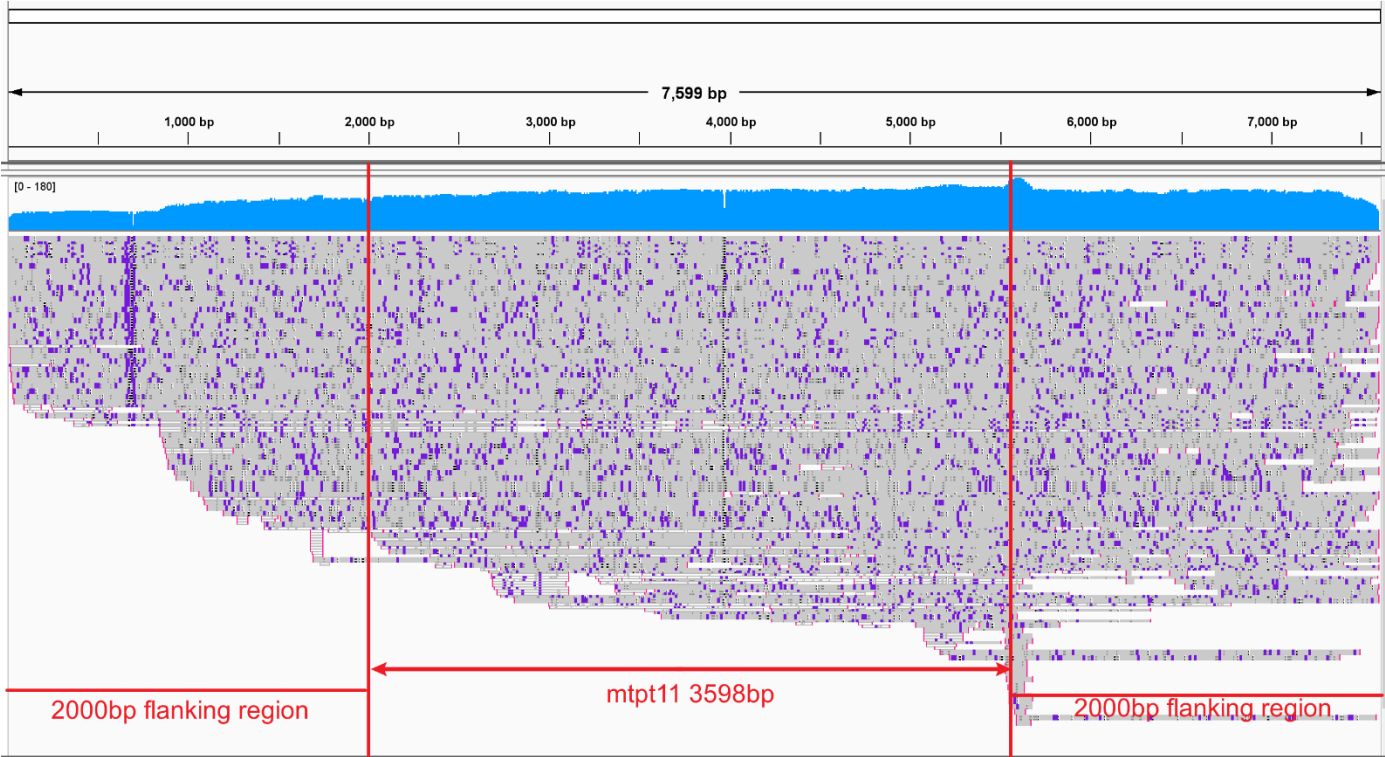
i alignment of Nanopore long reads to mtpt09 and its flanking sequences.



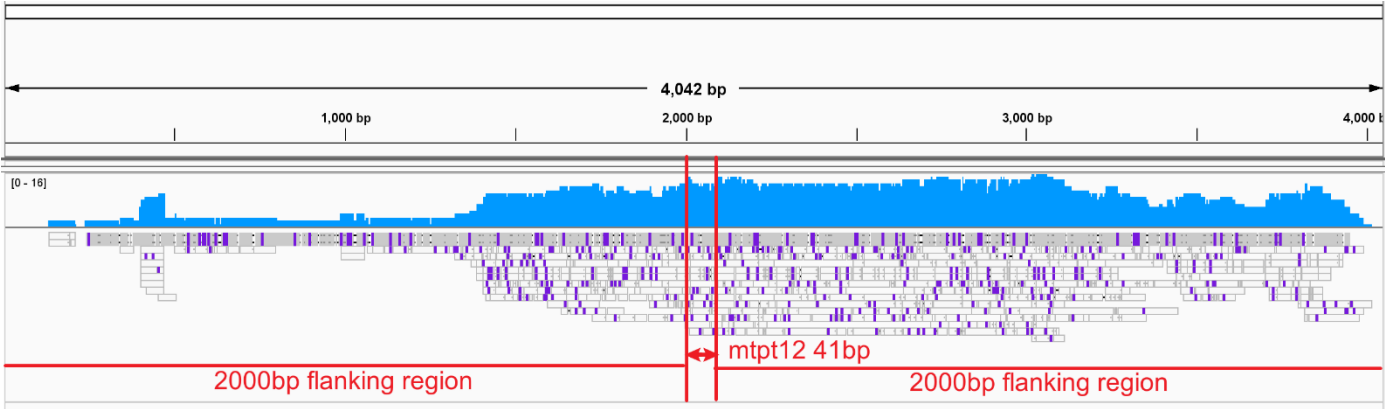
j alignment of Nanopore long reads to mtp10 and its flanking sequences.



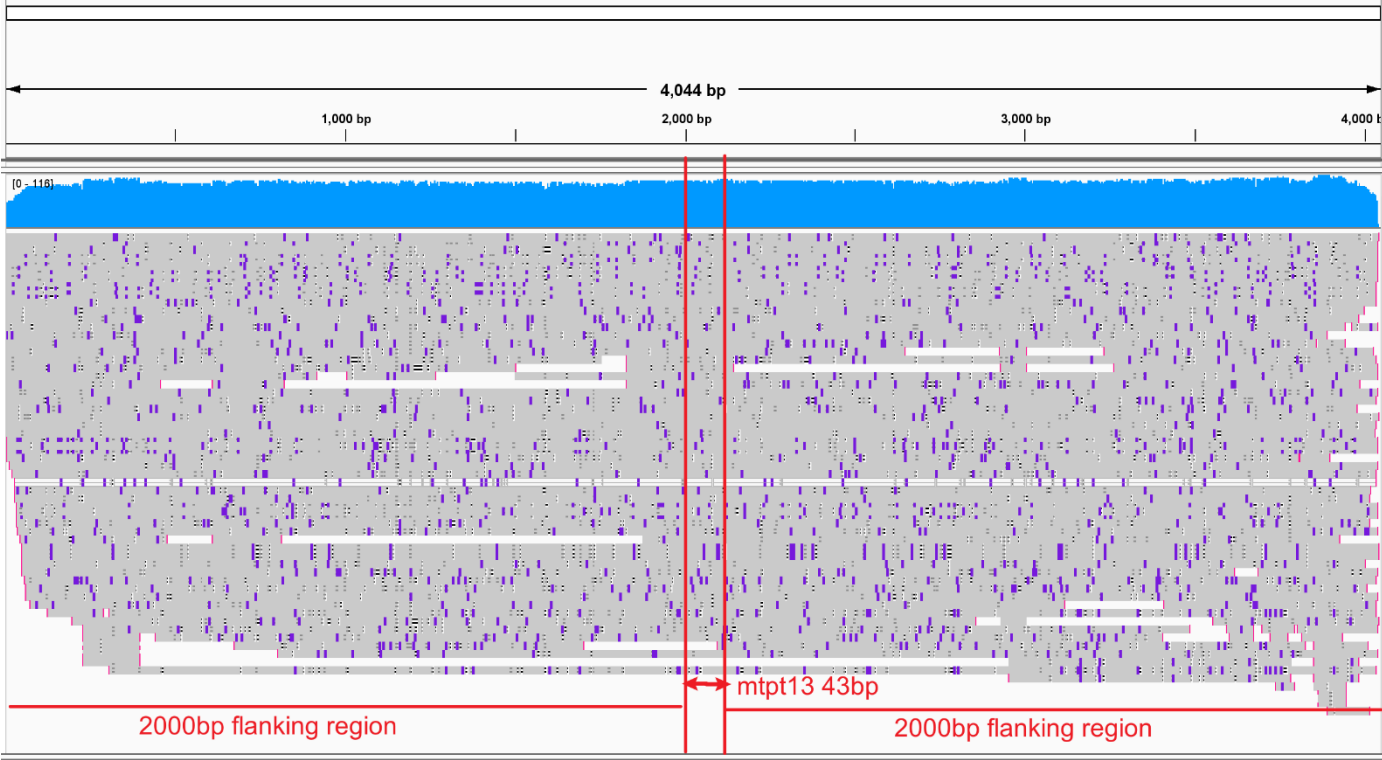
k alignment of Nanopore long reads to mtpt11 and its flanking sequences.



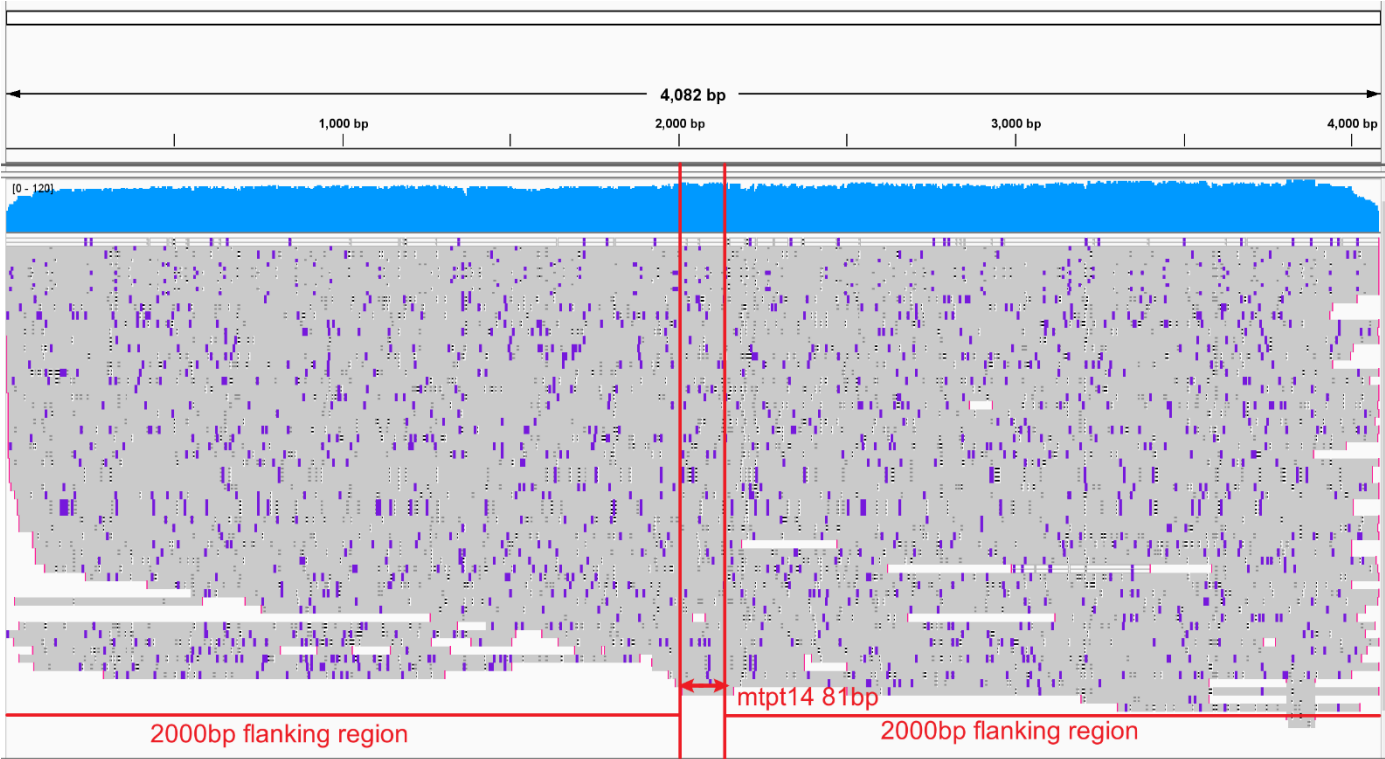
I alignment of Nanopore long reads to mtpt12 and its flanking sequences.



m alignment of Nanopore long reads to mtpt13 and its flanking sequences.



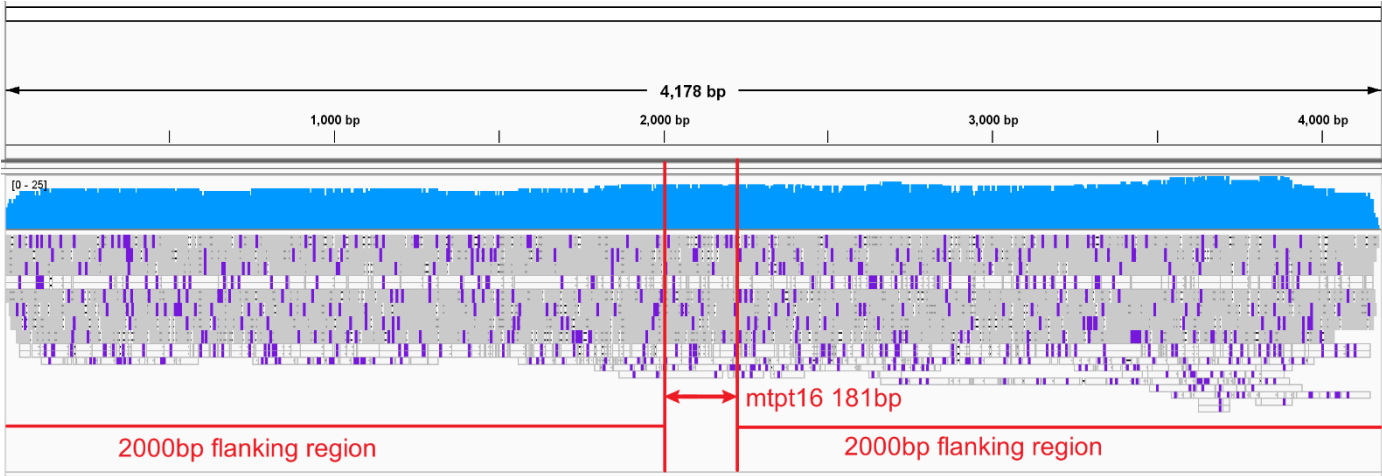
n alignment of Nanopore long reads to mtpt14 and its flanking sequences.



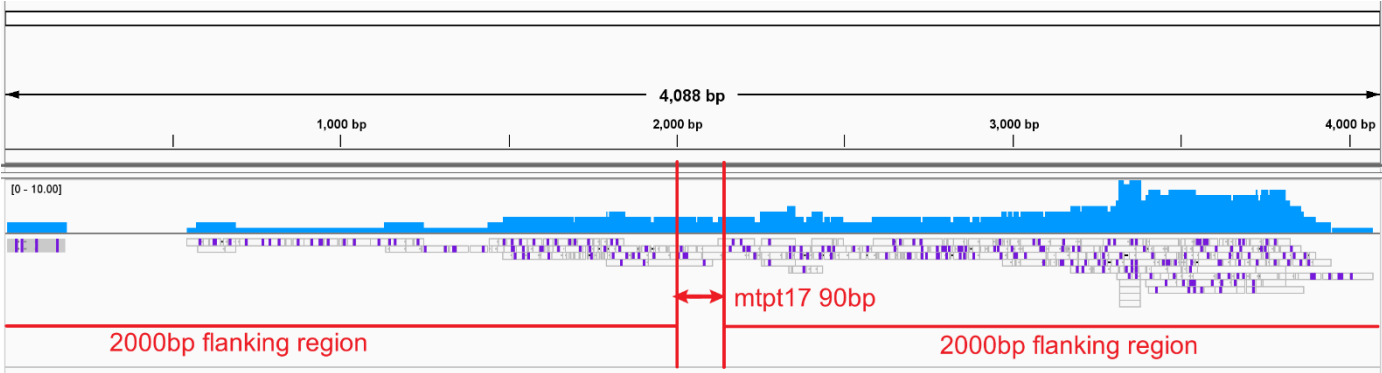
o alignment of Nanopore long reads to mtp15 and its flanking sequences.



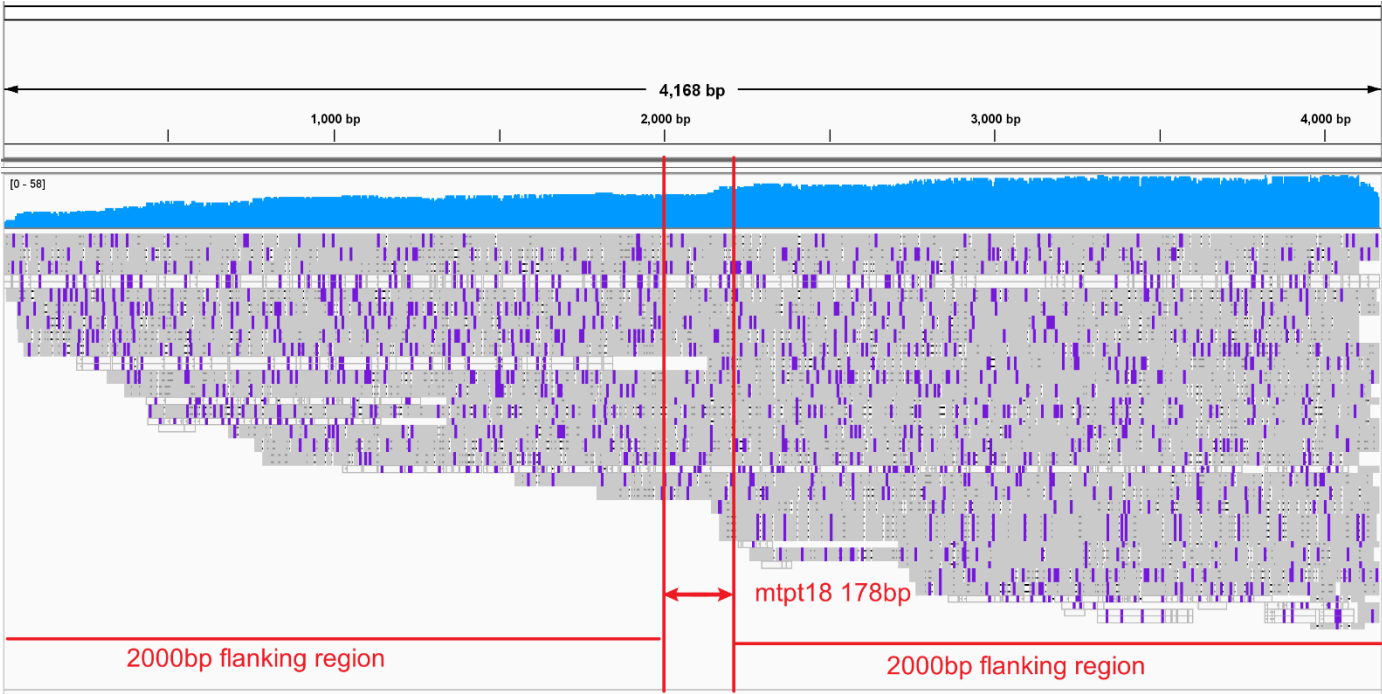
p alignment of Nanopore long reads to mtpt16 and its flanking sequences.



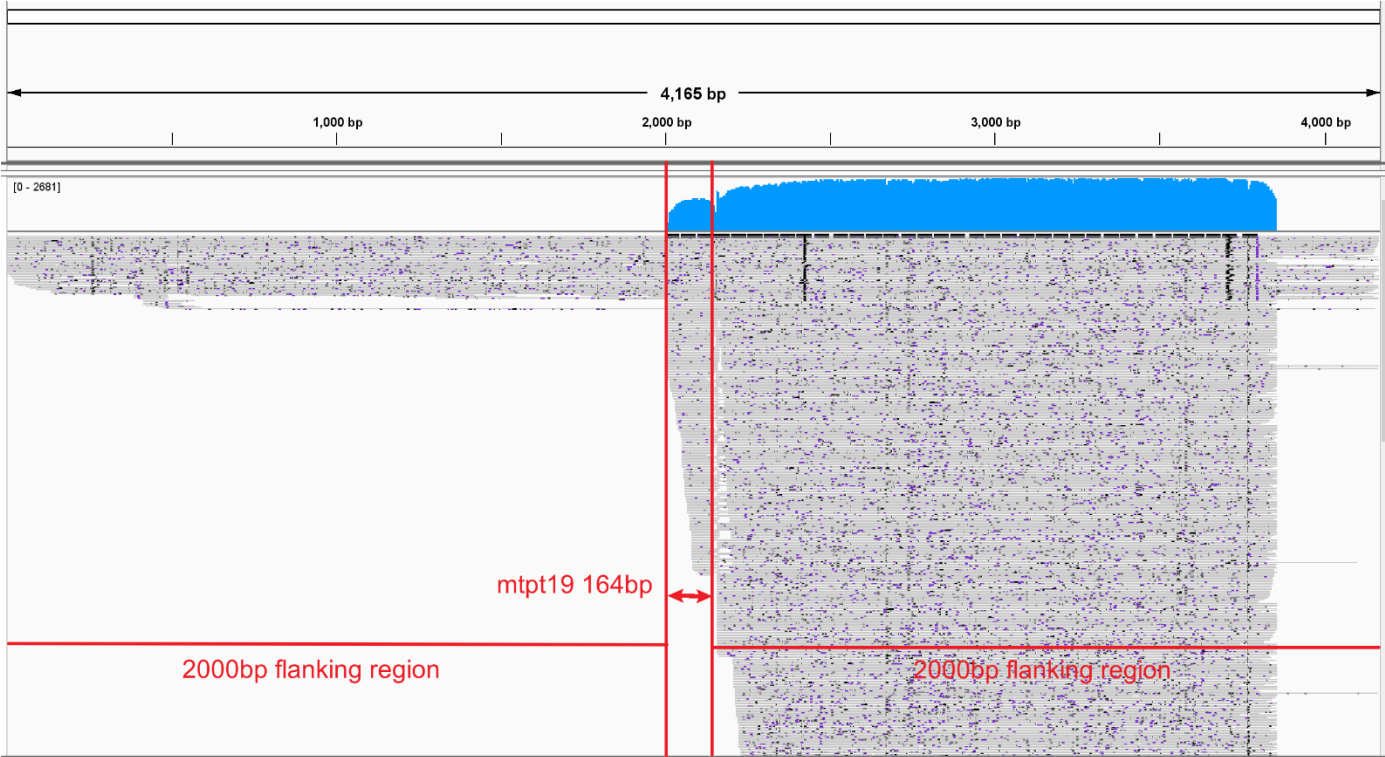
q alignment of Nanopore long reads to mtpt17 and its flanking sequences.



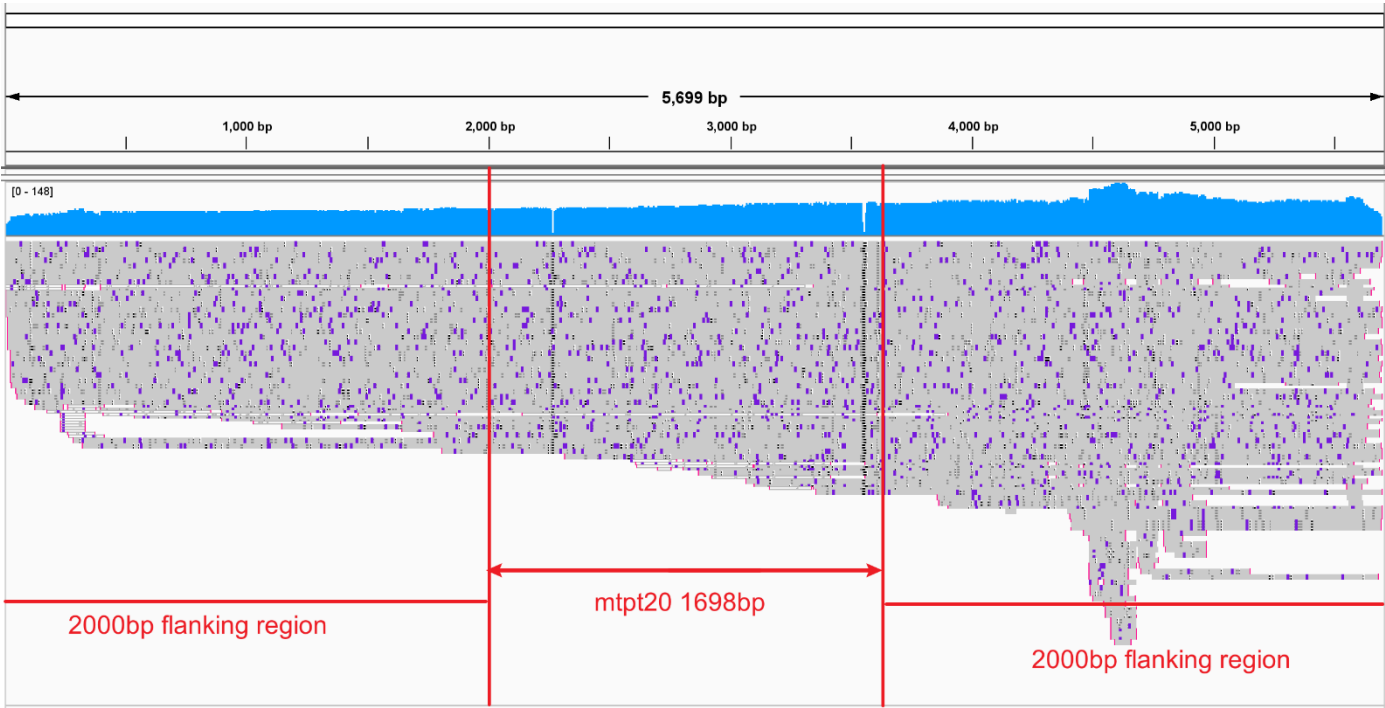
r alignment of Nanopore long reads to mtpt18 and its flanking sequences.



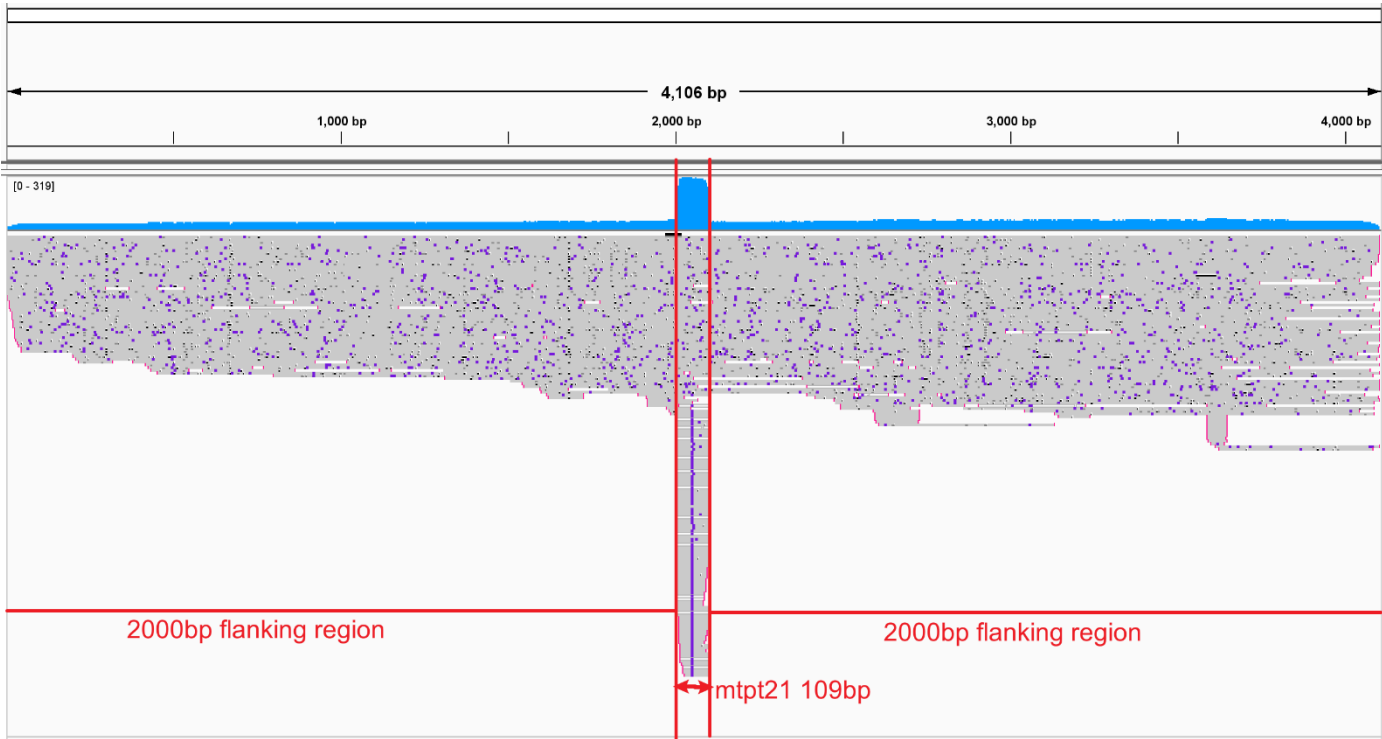
s alignment of Nanopore long reads to mtpt19 and its flanking sequences.



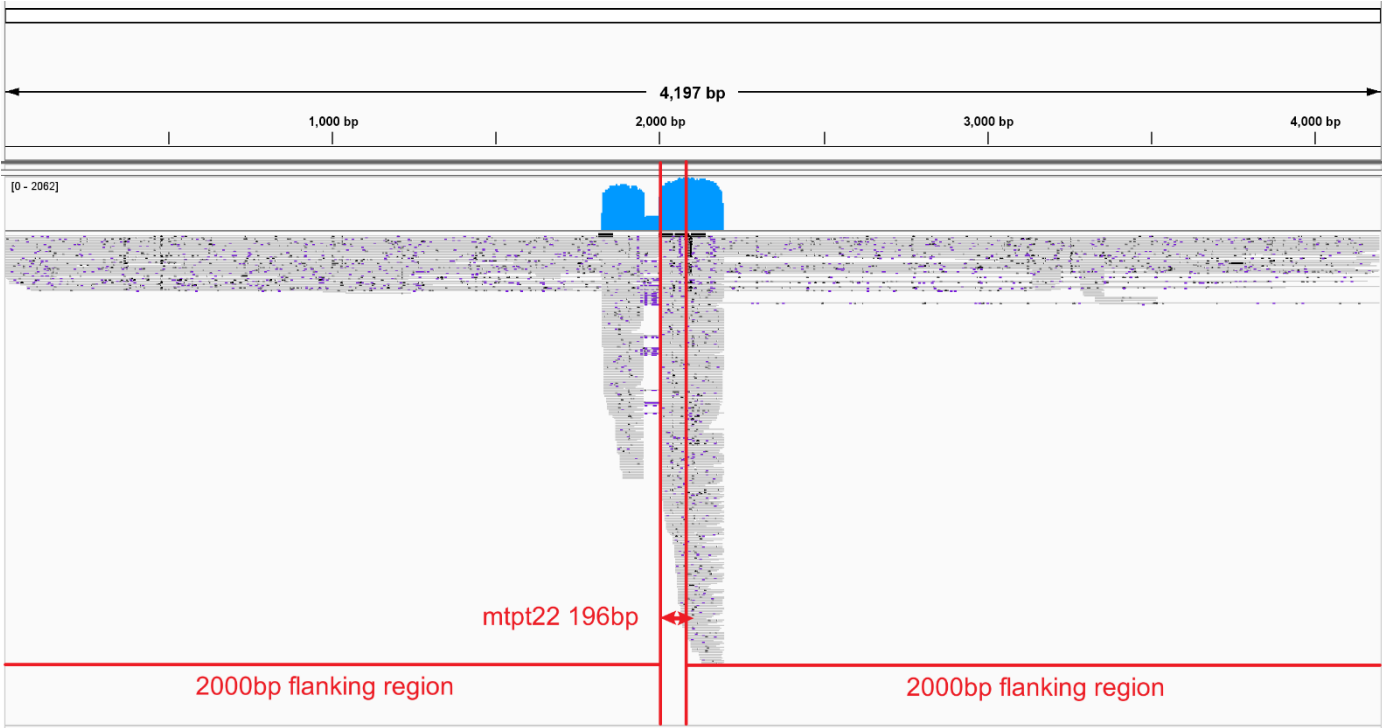
t alignment of Nanopore long reads to mtpt20 and its flanking sequences.



u alignment of Nanopore long reads to mtp21 and its flanking sequences.



v alignment of Nanopore long reads to mtpt22 and its flanking sequences.



w alignment of Nanopore long reads to mtpt23 and its flanking sequences.

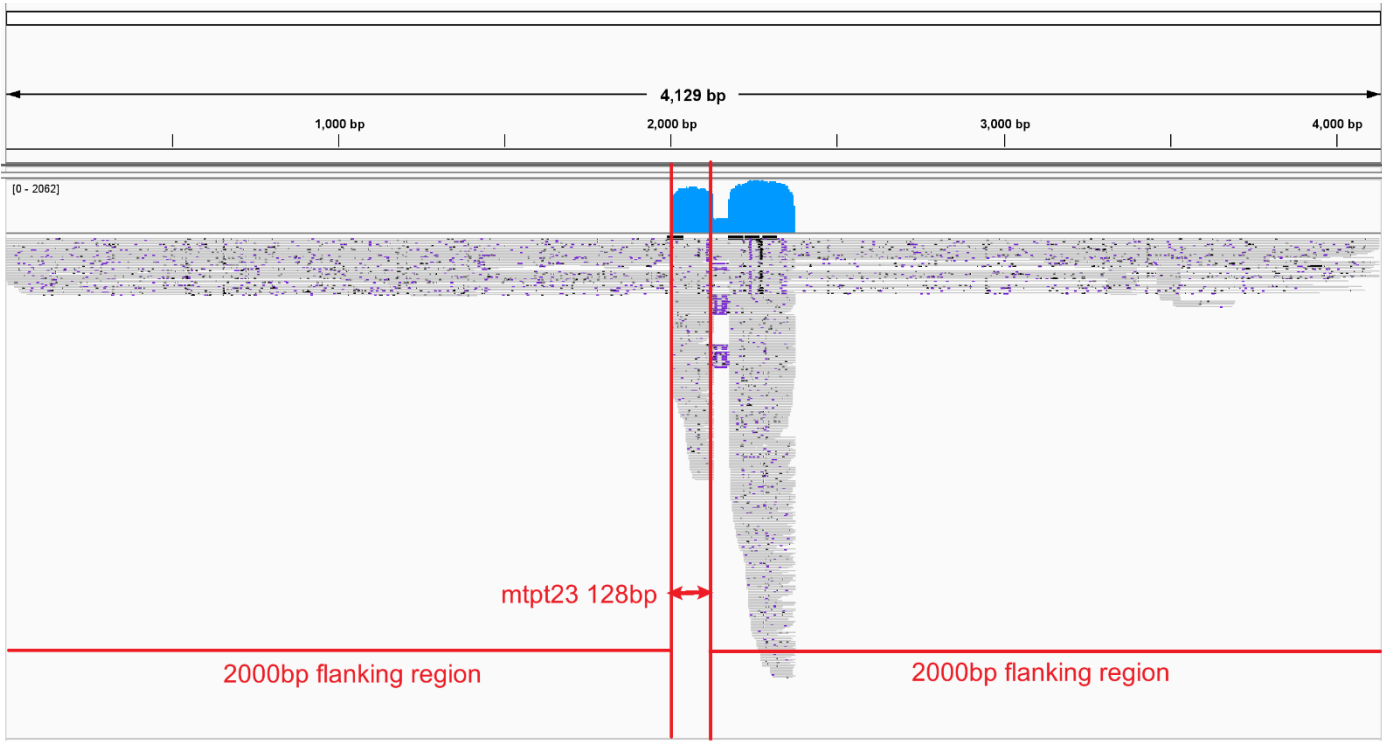
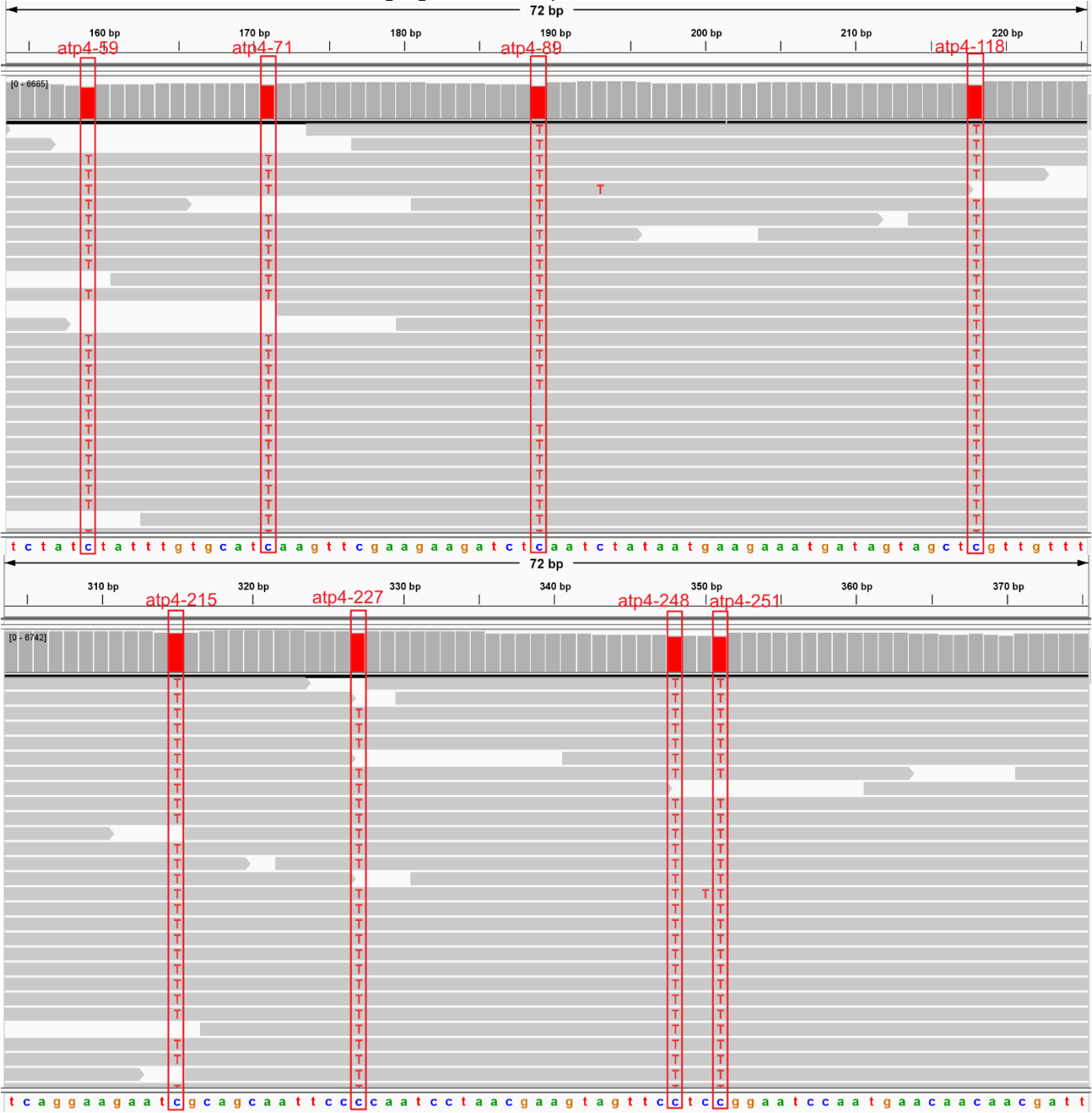
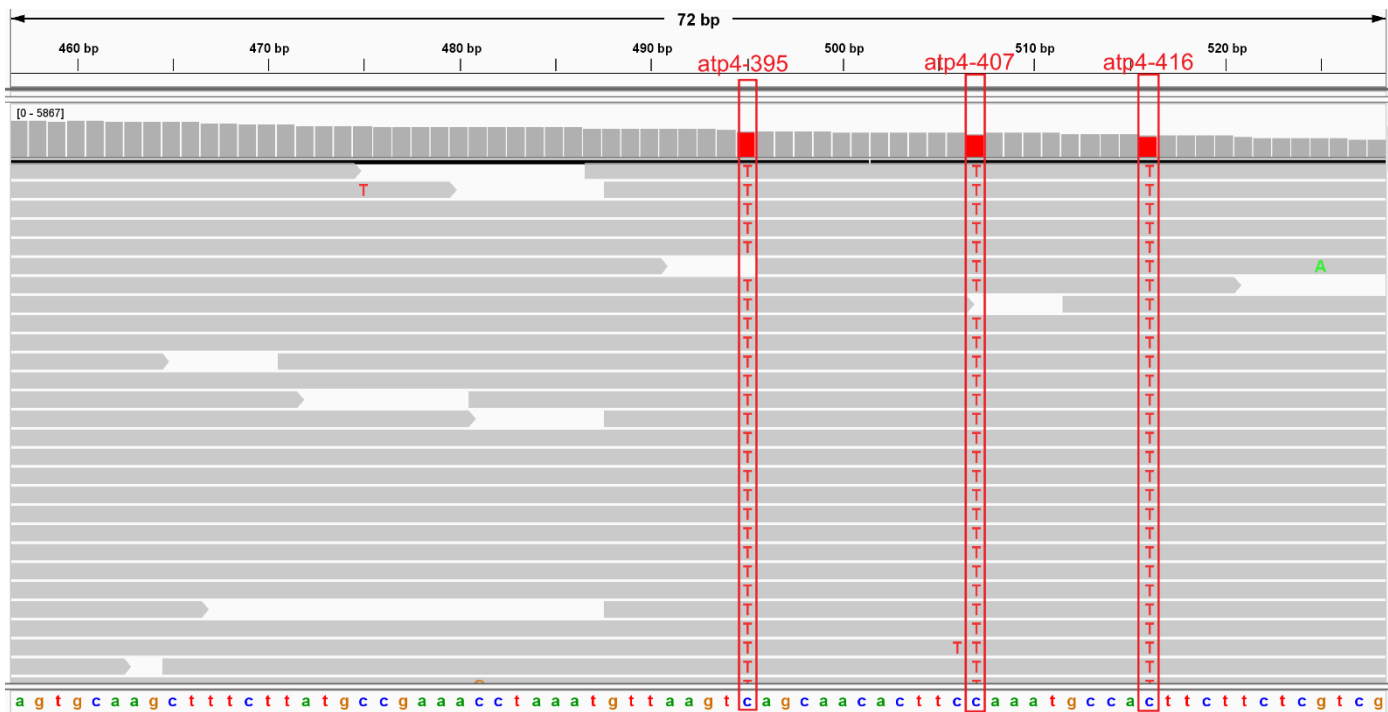


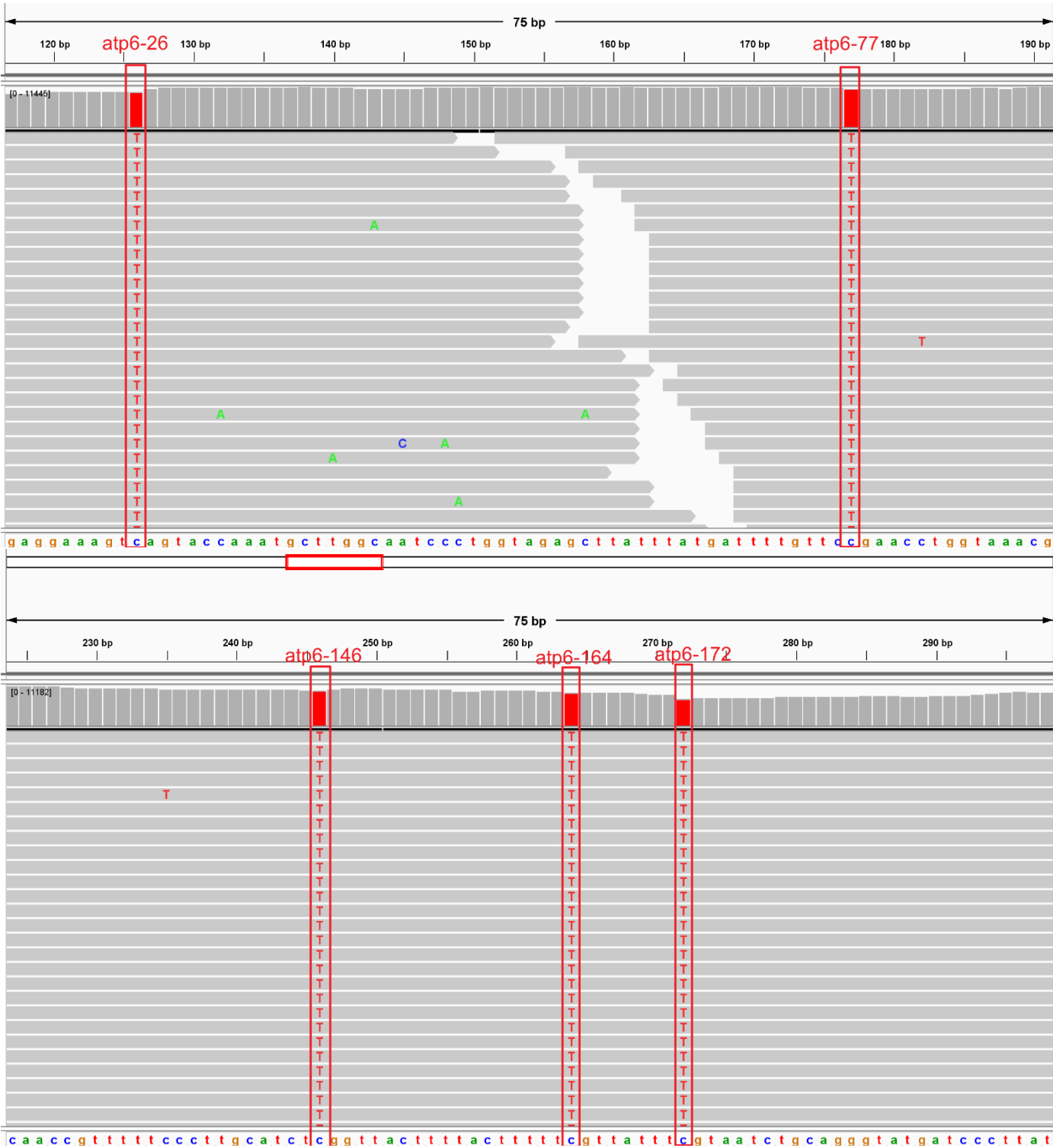
Figure S6 Alignments of the RNA sequencing reads to the coding sequences of twenty PCGs in the mitogenome of *S. officinalis*. The reference sequences are shown at the bottom. The gray lines above represent the reads mapped to the reference sequence. Bases matching those in the reference sequences are shaded in gray. Bases not matching those in the reference sequences are shown in green for “A”, brown for “G”, blue for “C”, and red for “T”. The RNA editing sites are shown in the red squares.

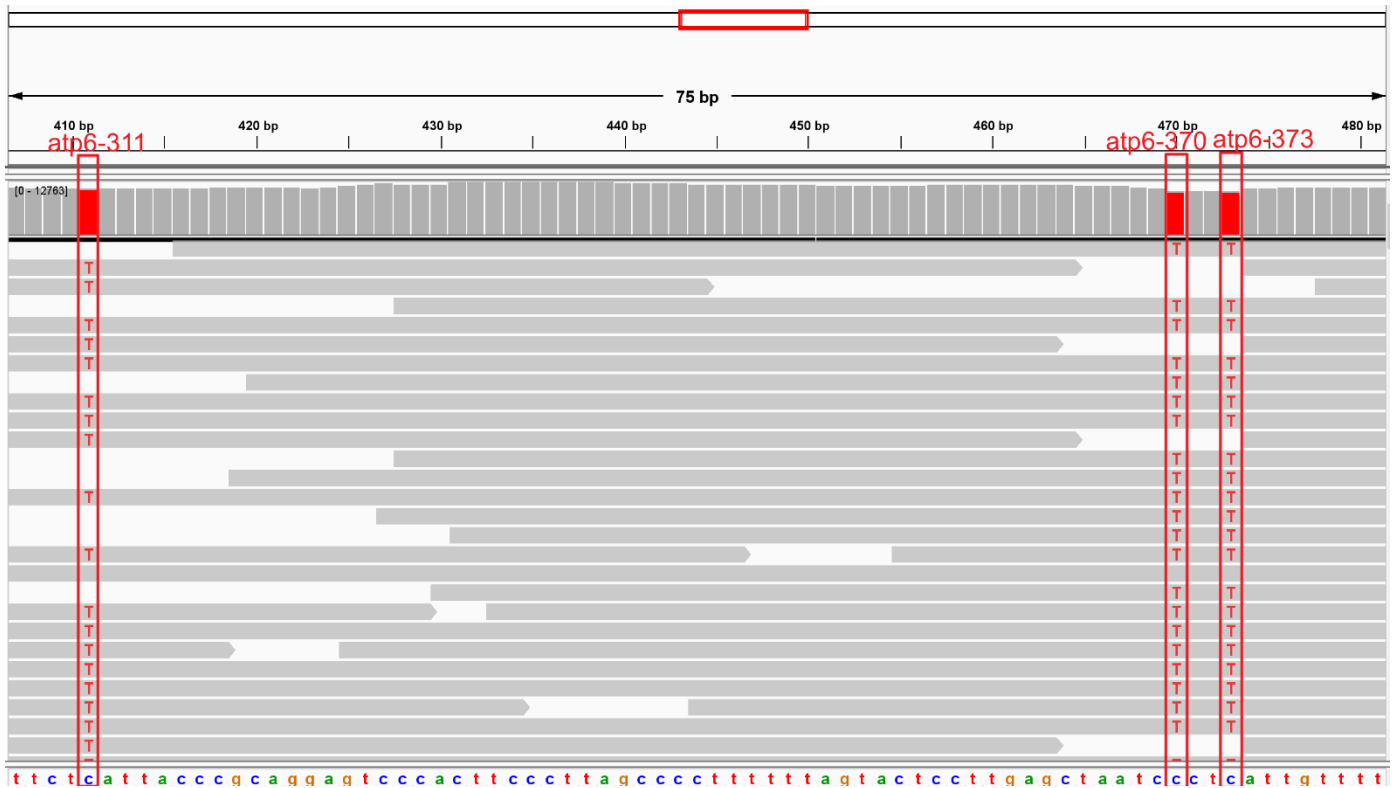
a alignment of RNA-seq reads to the coding sequence of *atp4*. 11 RNA-seq editing sites: atp4-59, 71, 89, 118, 215, 227, 248, 251, 395, 407, and 416 were highlighted in red squares.



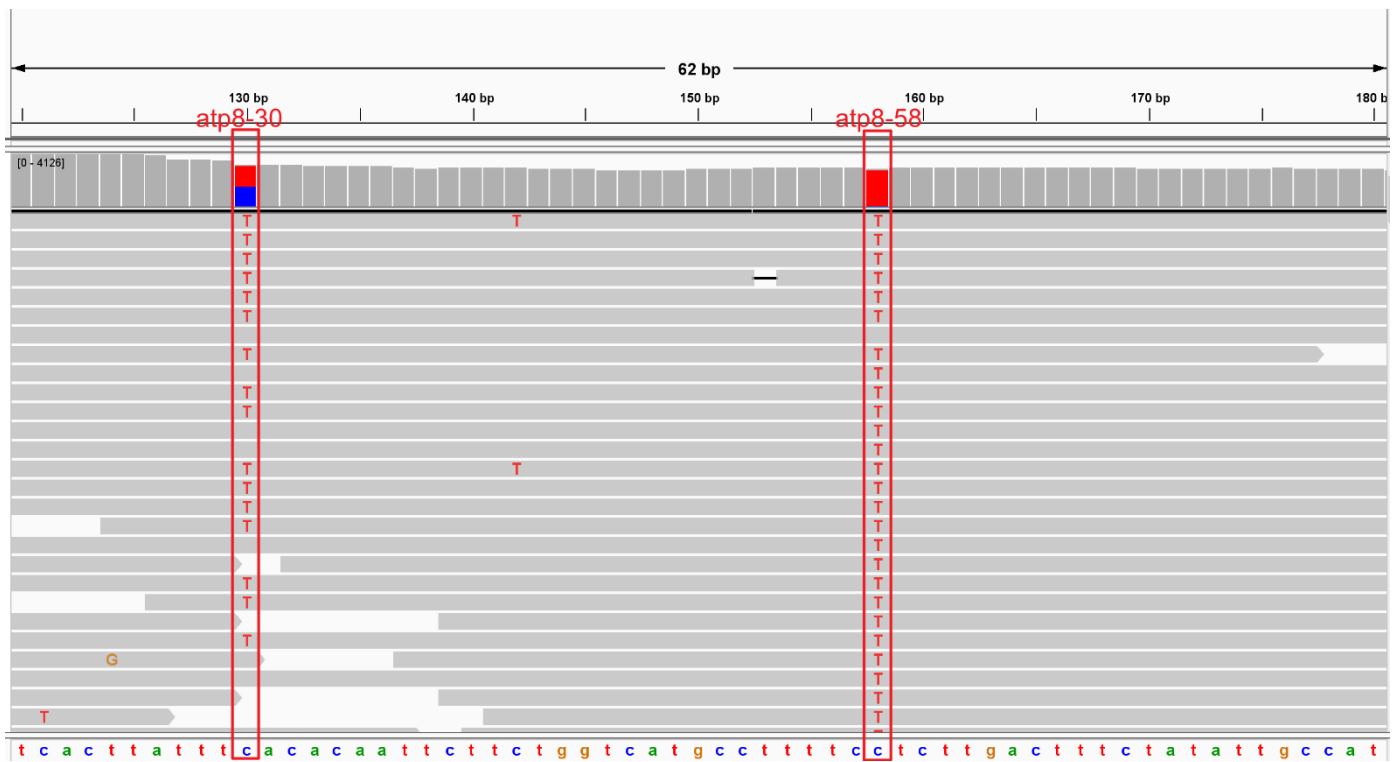


b alignment of RNA-seq reads to the coding sequence of *atp6*. Eight RNA-seq editing sites: *atp6*-26, 77, 146, 164, 172, 311, 370, and 372 were highlighted in red squares.





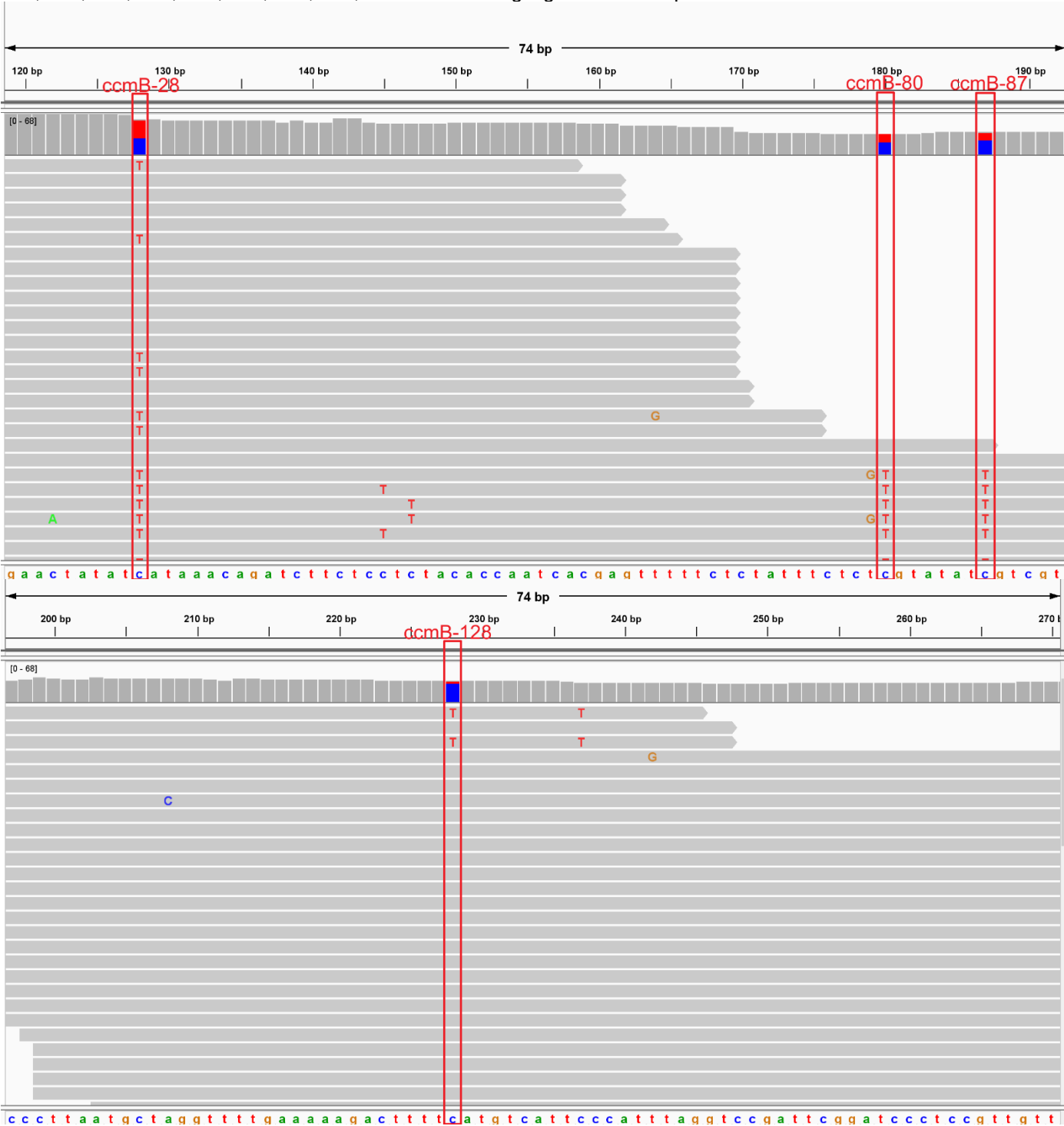
c alignment of RNA-seq reads to the coding sequence of *atp8*. Two RNA-seq editing sites: *atp8*-30 and 58 were highlighted in red squares.

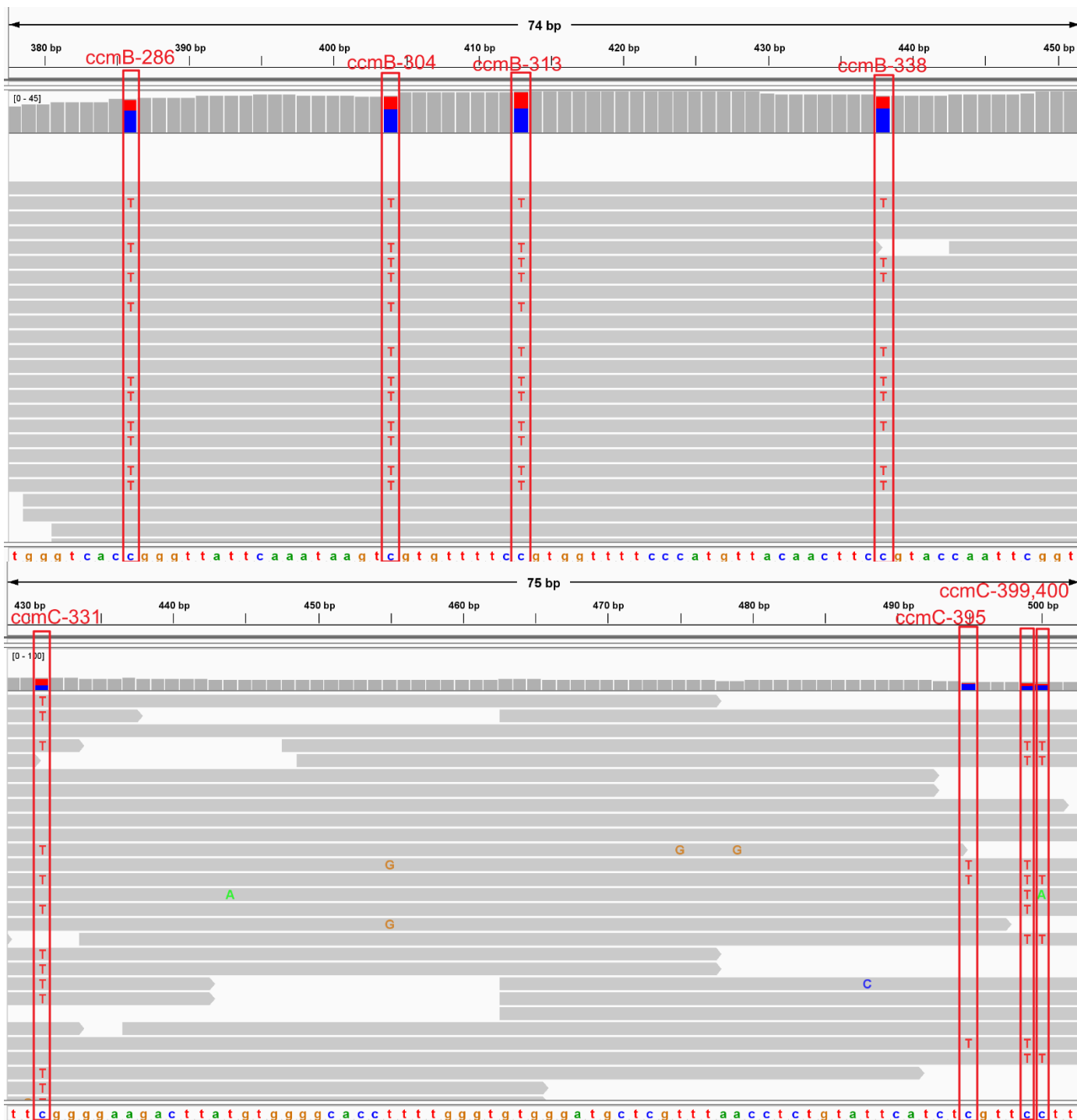


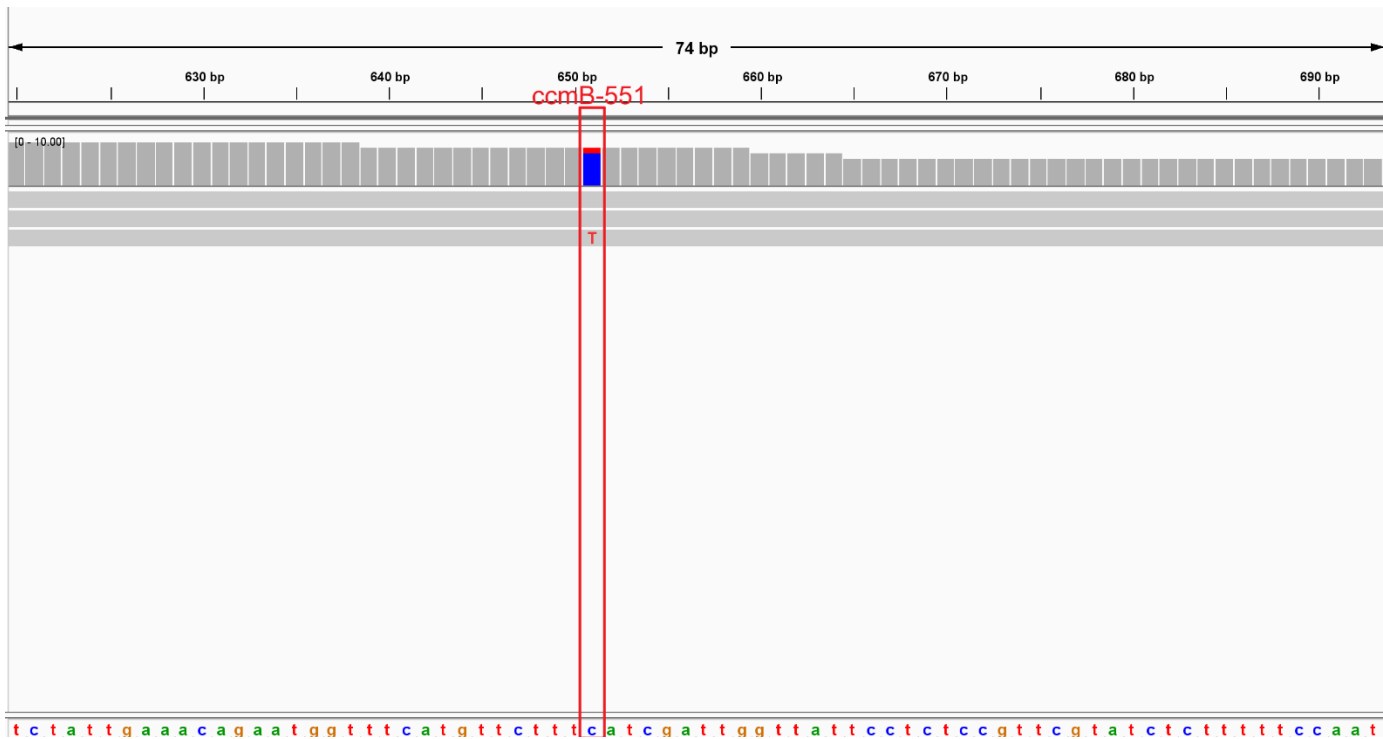
d alignment of RNA-seq reads to the coding sequence of *atp9*. One RNA-seq editing site: atp9-212 was highlighted in red squares.



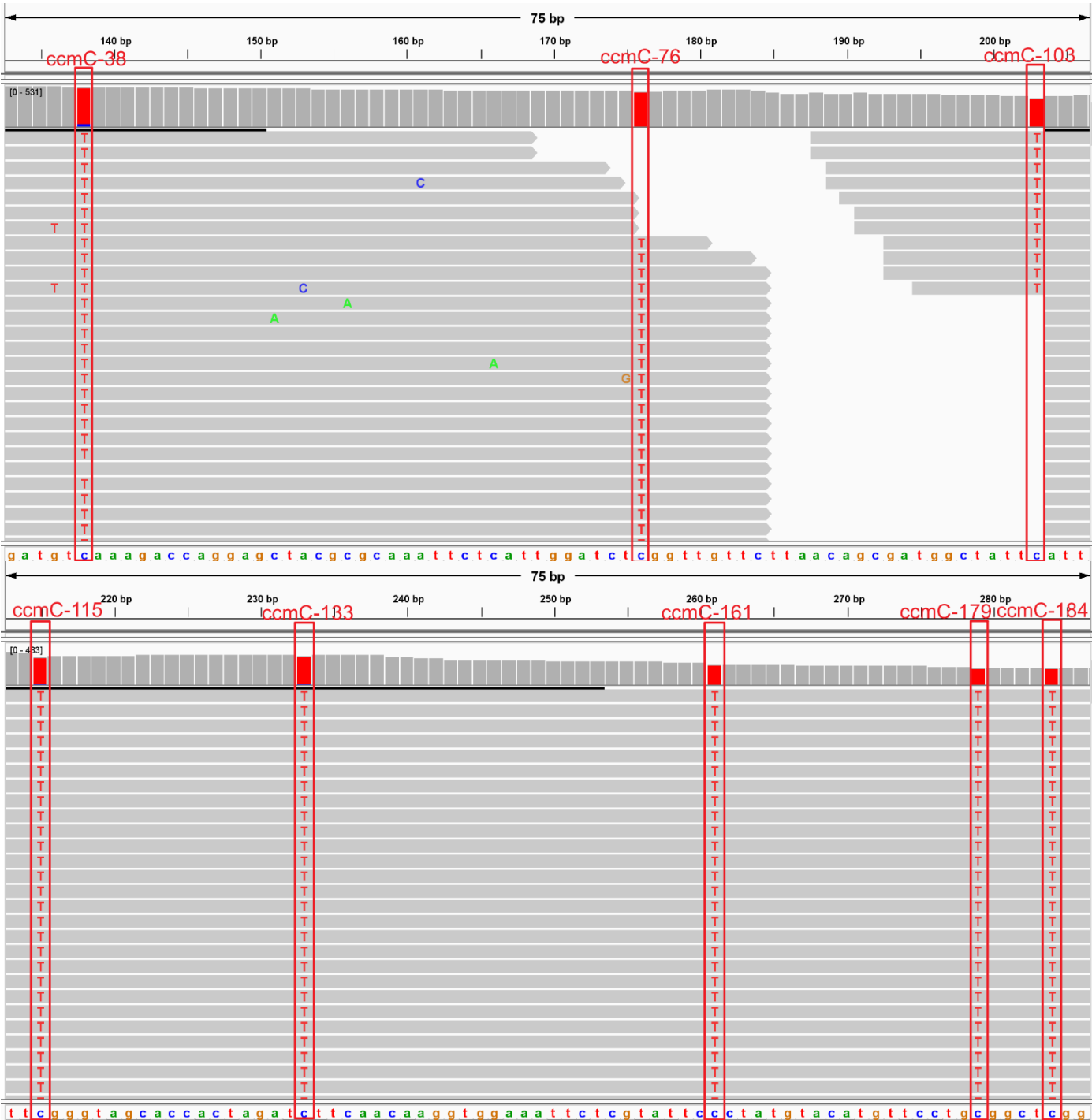
e alignment of RNA-seq reads to the coding sequence of *ccmB*. 13 RNA-seq editing sites: *ccmB*-28, 80, 87, 128, 286, 304, 313, 338, 367, 380, 424, 428, and 551 were highlighted in red squares.

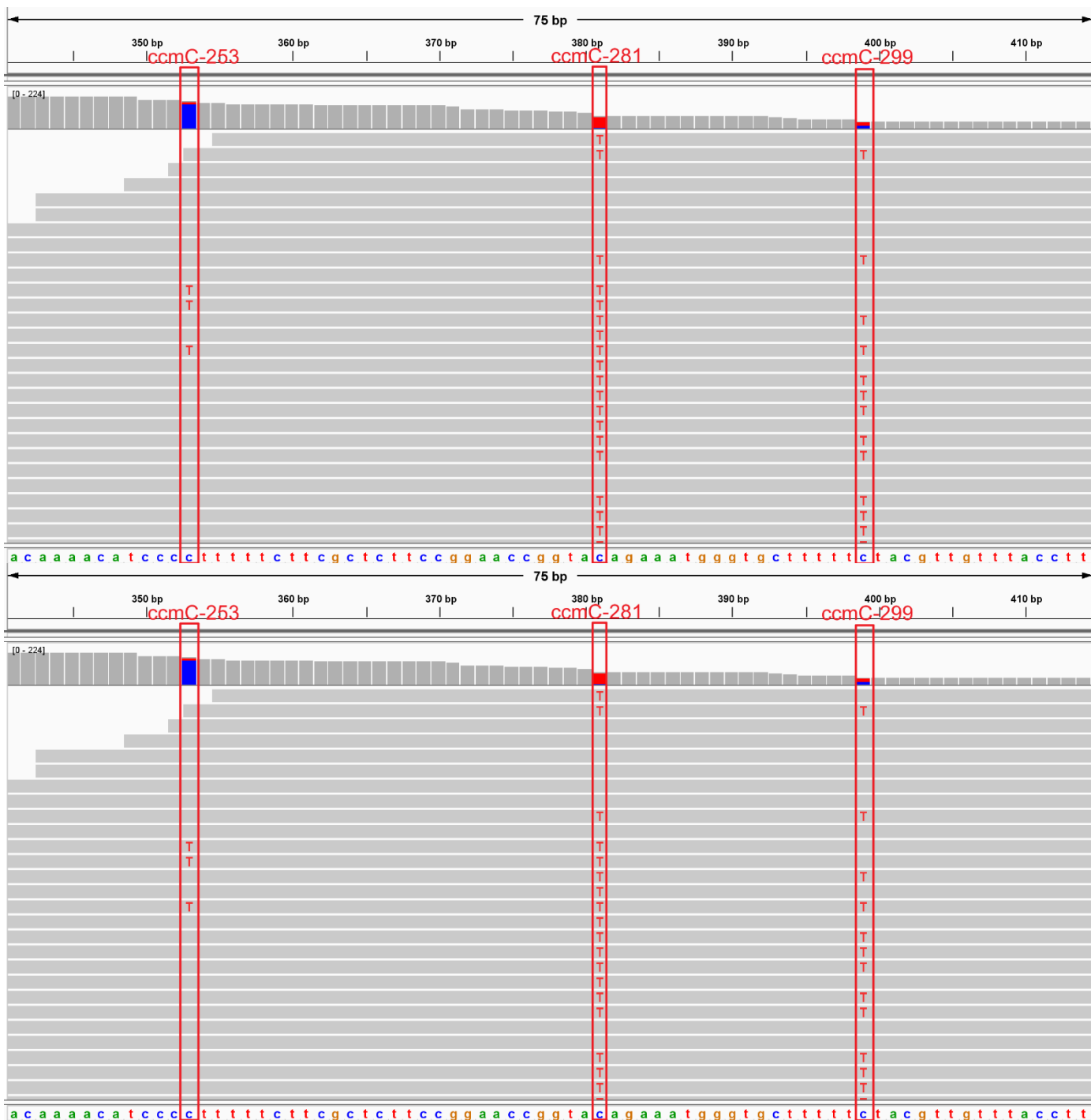


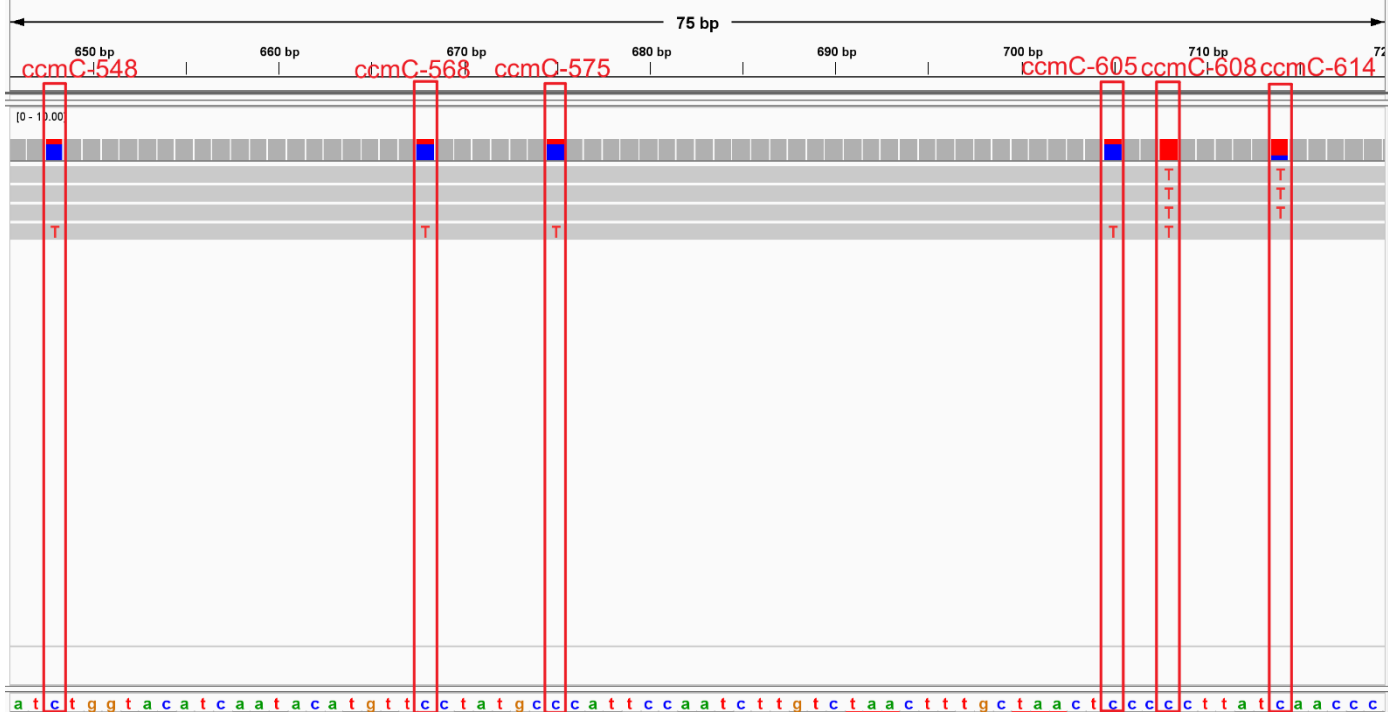
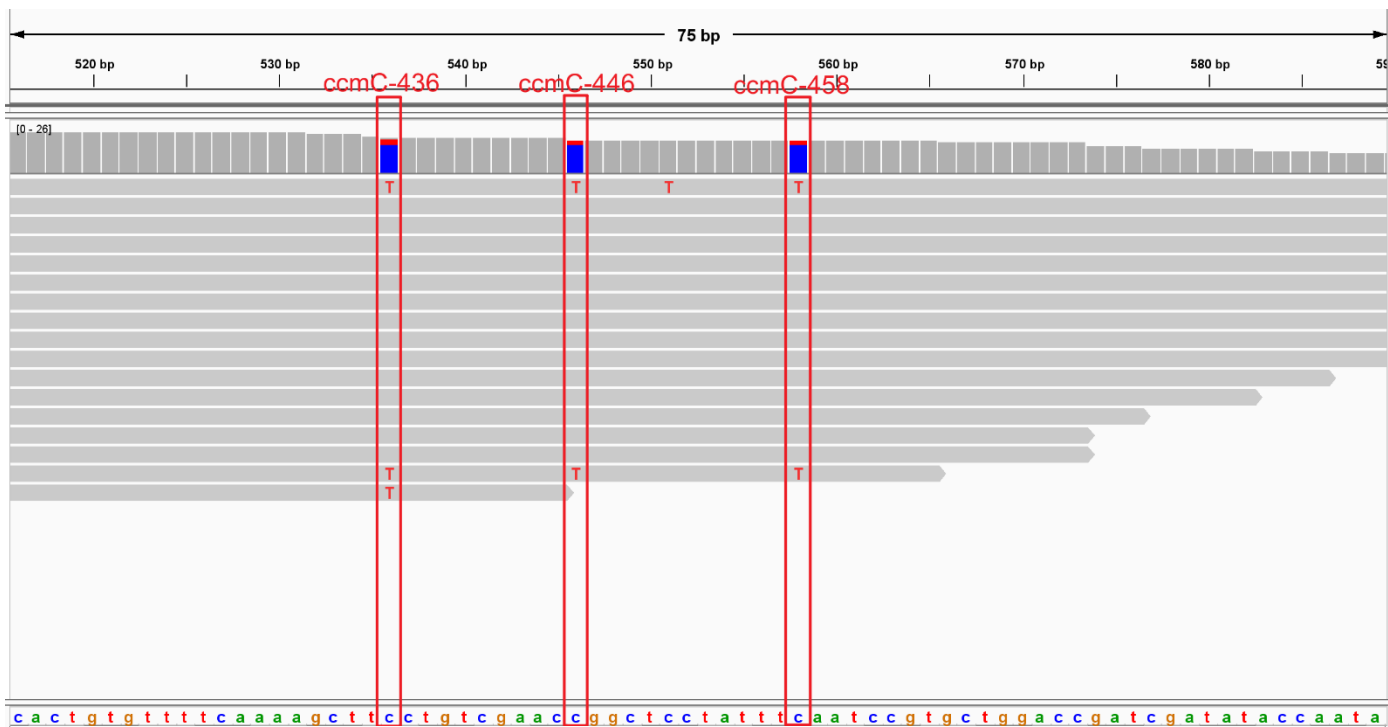


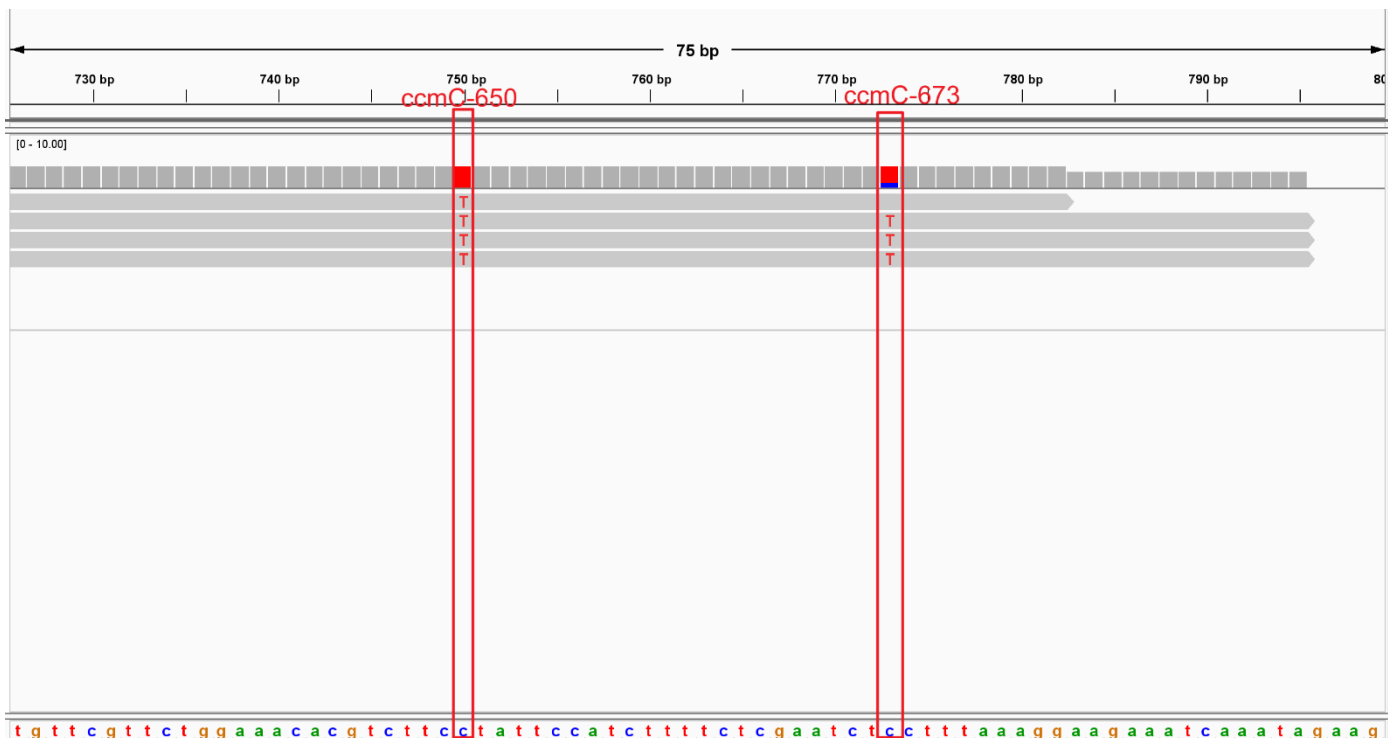


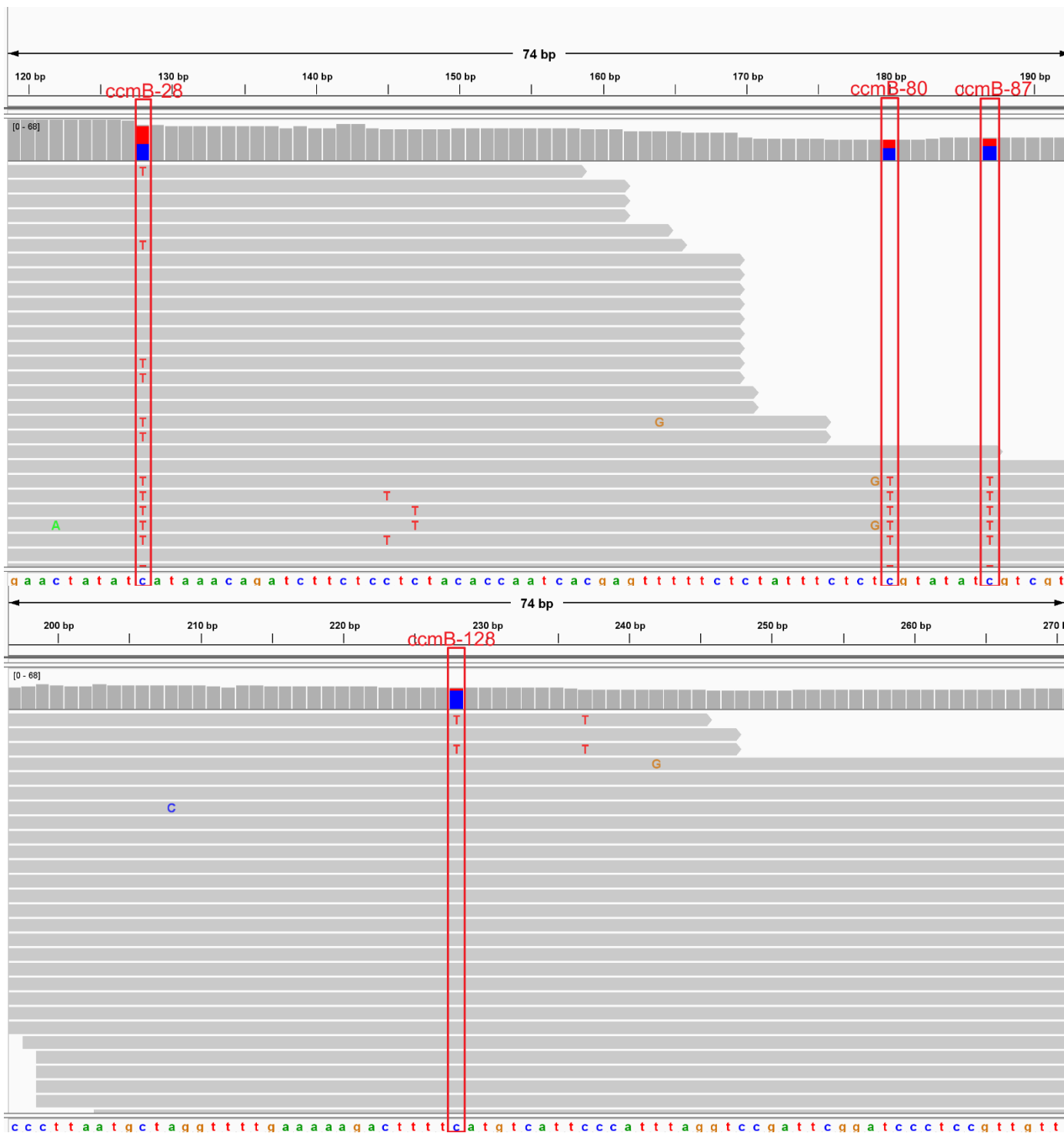
f alignment of RNA-seq reads to the coding sequence of *ccmC*. 26 RNA-seq editing sites: *ccmC*-38, 76, 103, 115, 133, 161, 179, 184, 253, 281, 299, 331, 395, 399, 400, 436, 446, 458, 548, 568, 575, 605, 608, 614, 650, and 673 were highlighted in red squares.

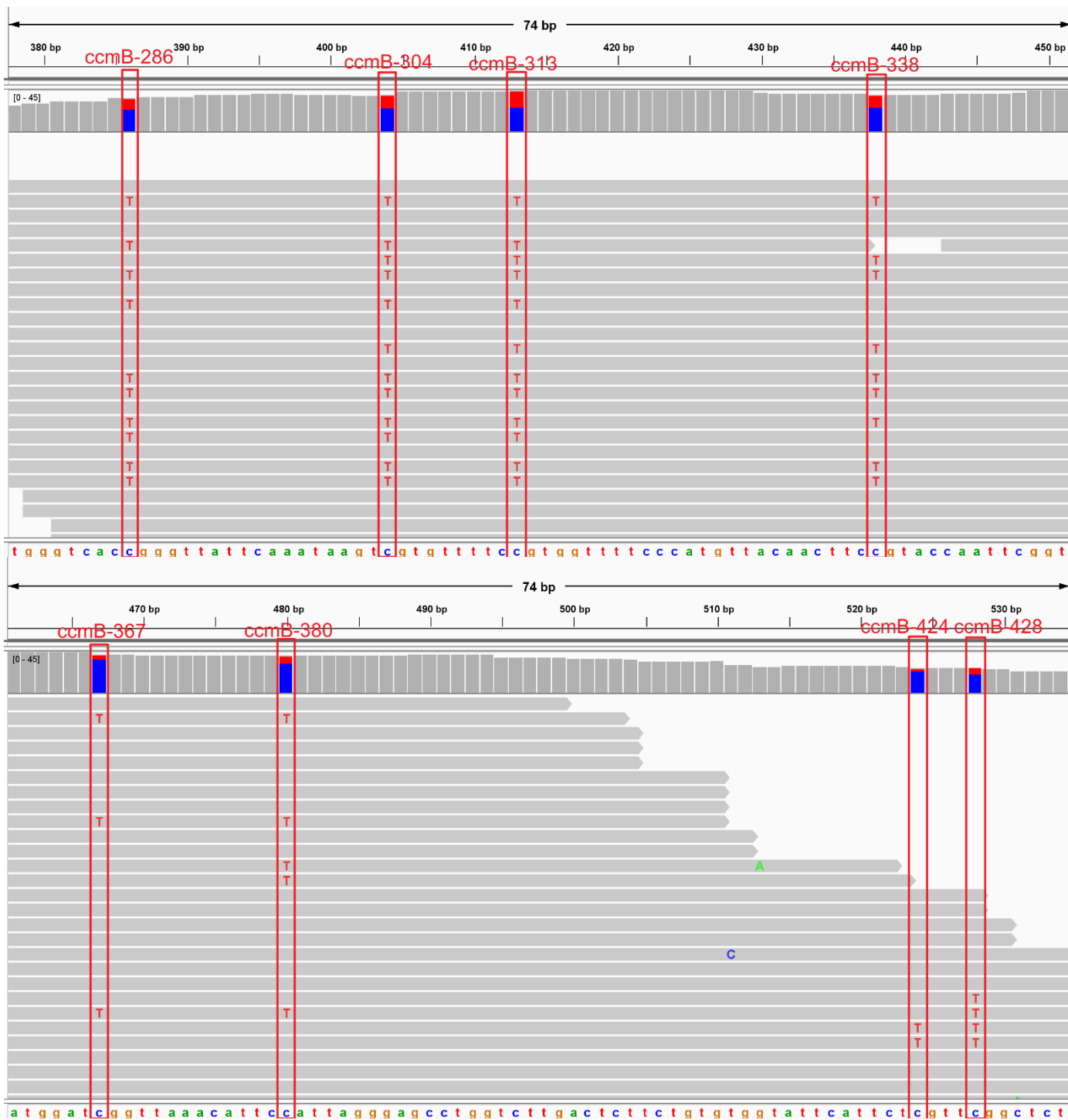


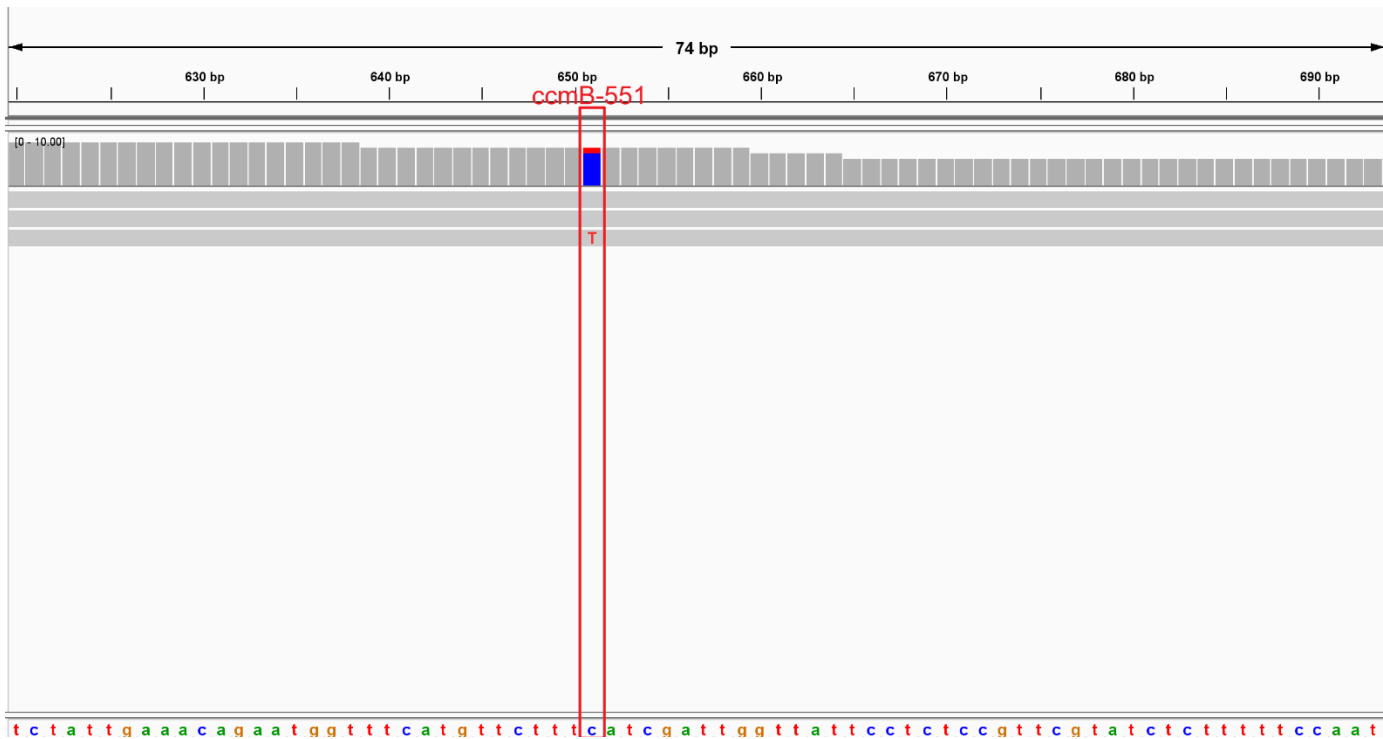




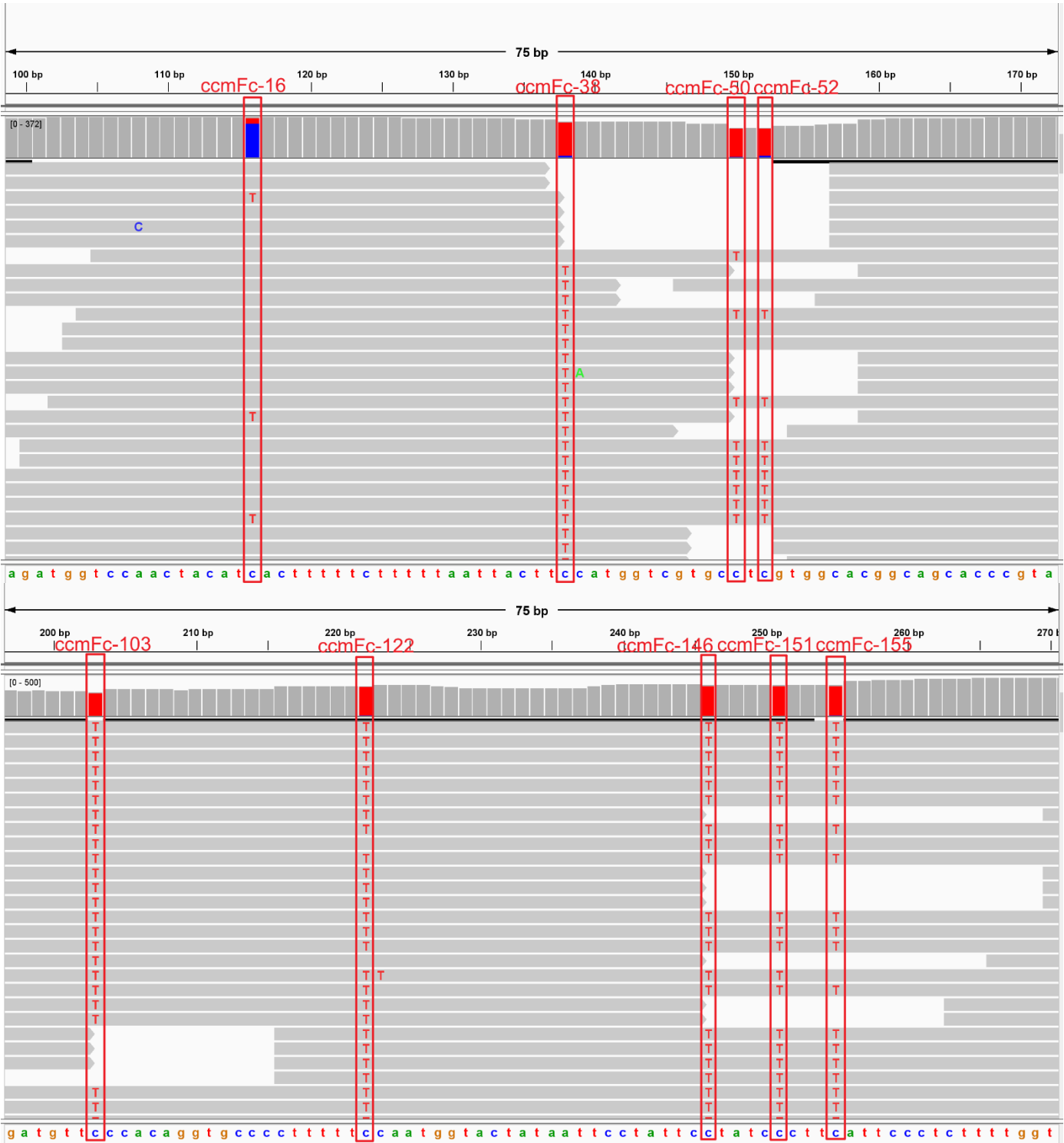


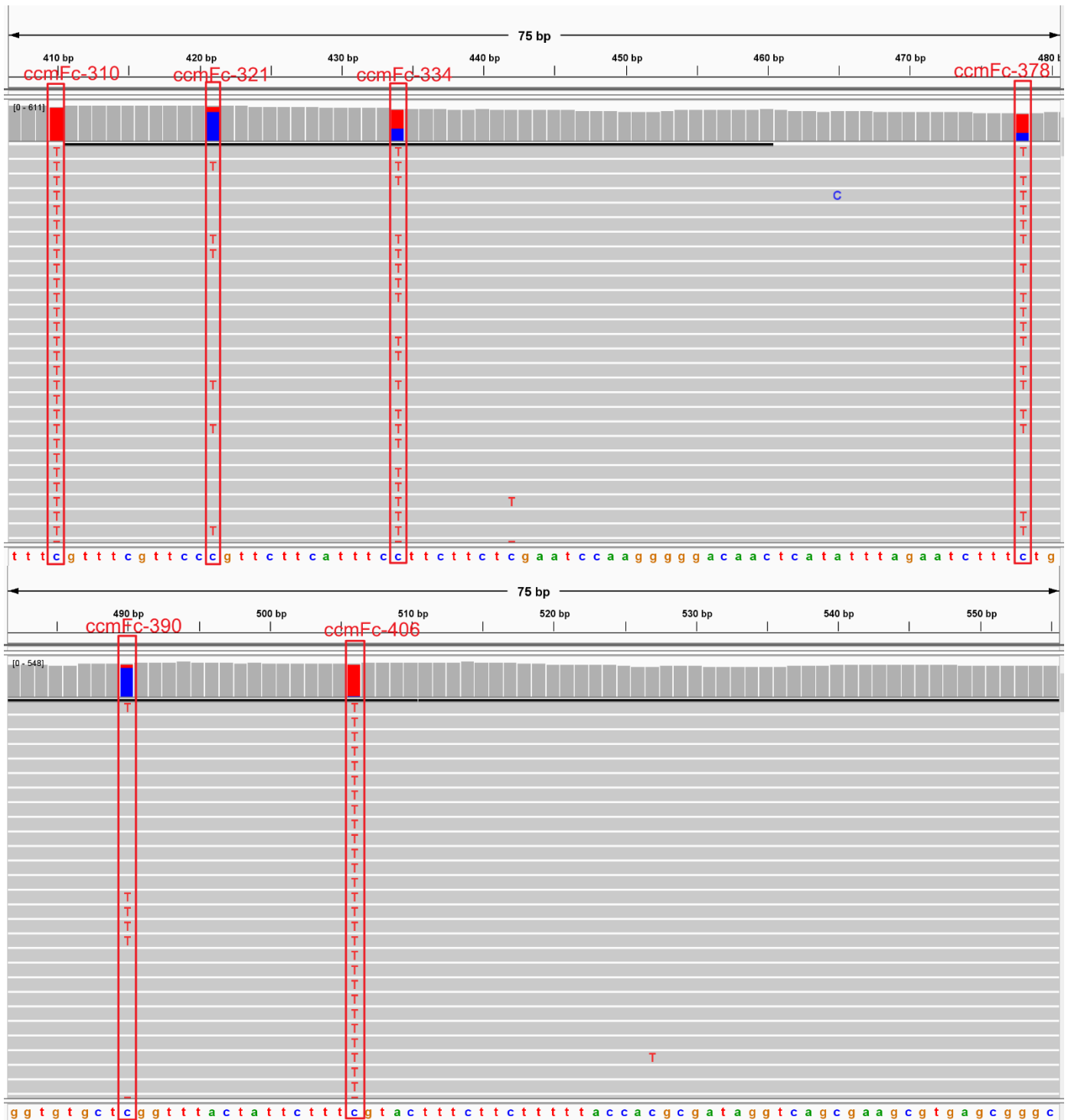


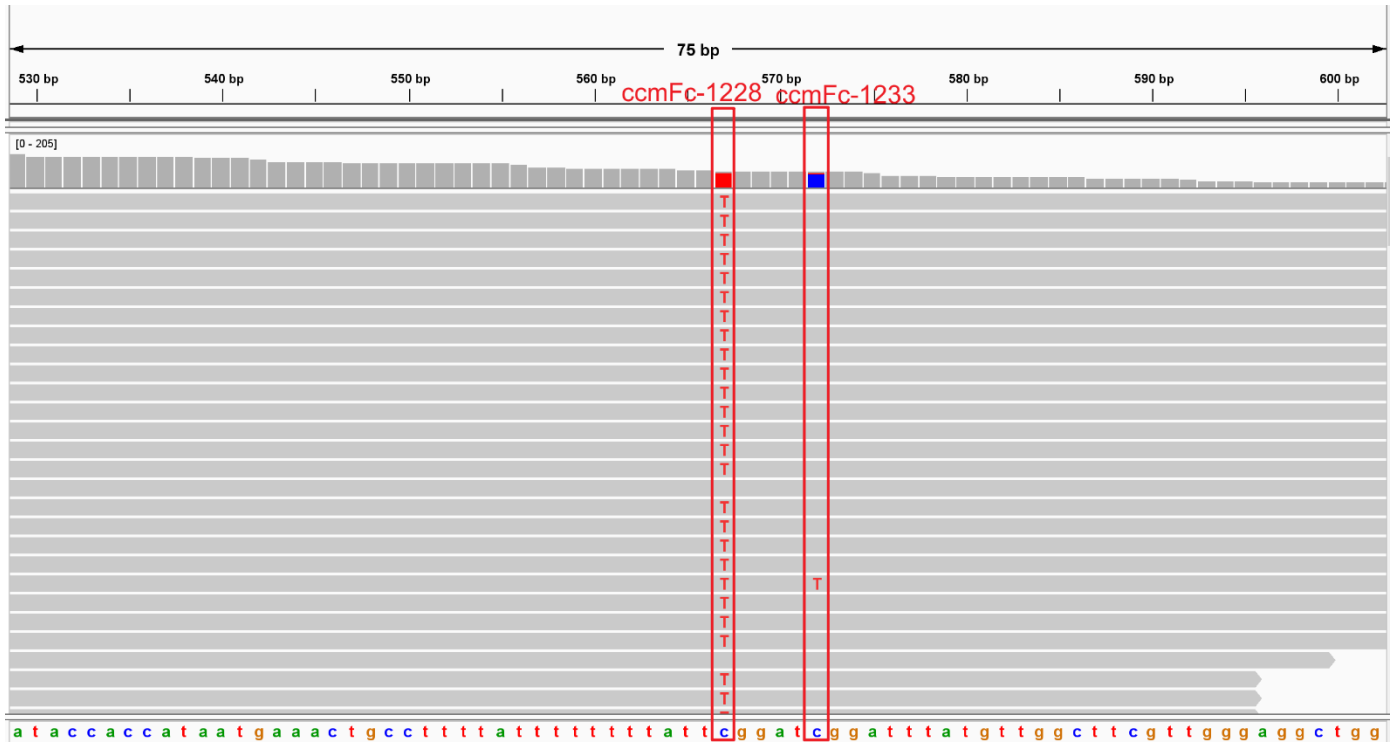




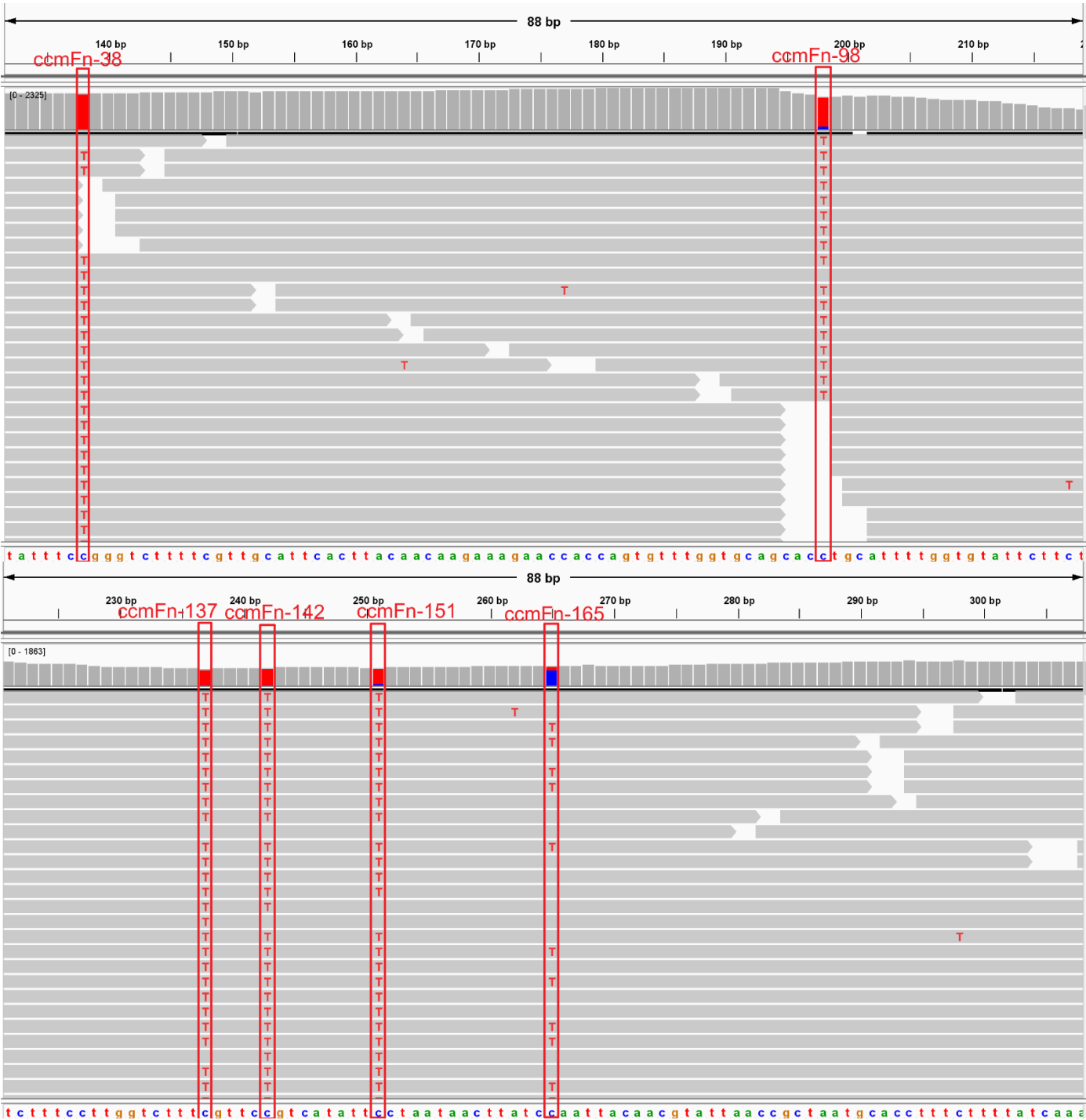
g alignment of RNA-seq reads to the coding sequence of *ccmFc*. 17 RNA-seq editing sites: *ccmFc*-16, 38, 50, 52, 103, 122, 146, 151, 155, 310, 321, 334, 378, 390, 406, 1228, 1233 were highlighted in red squares.

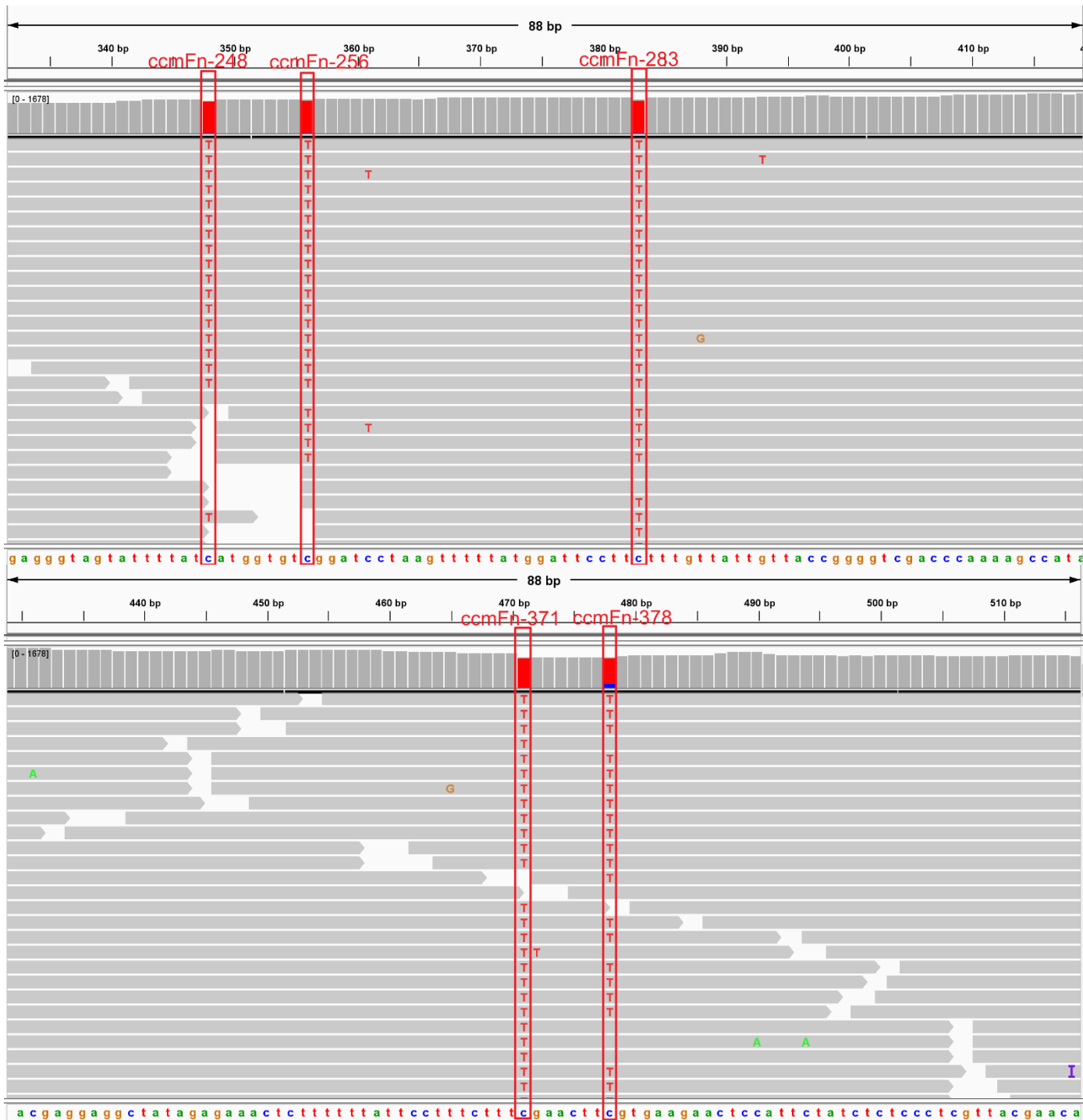


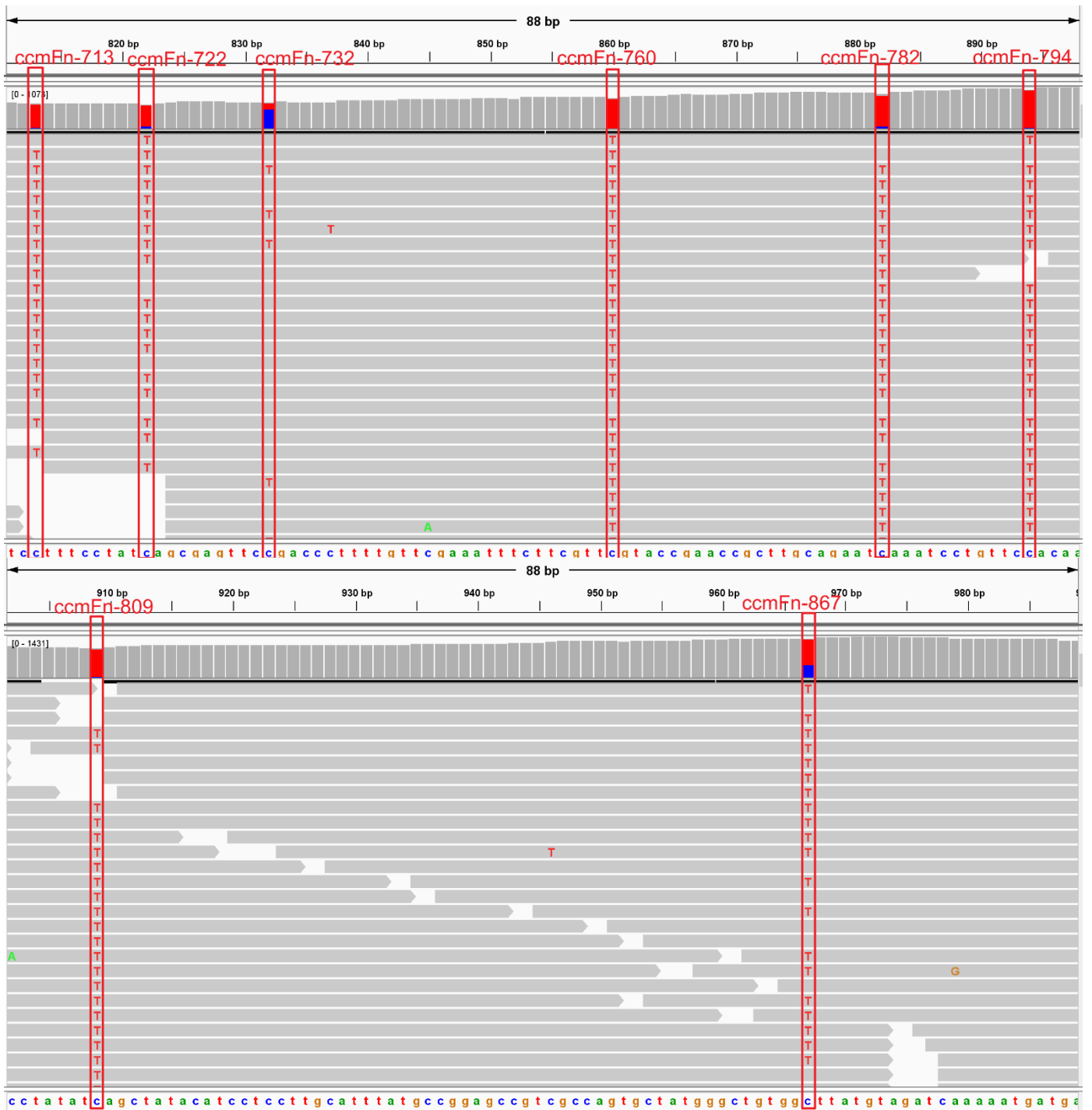


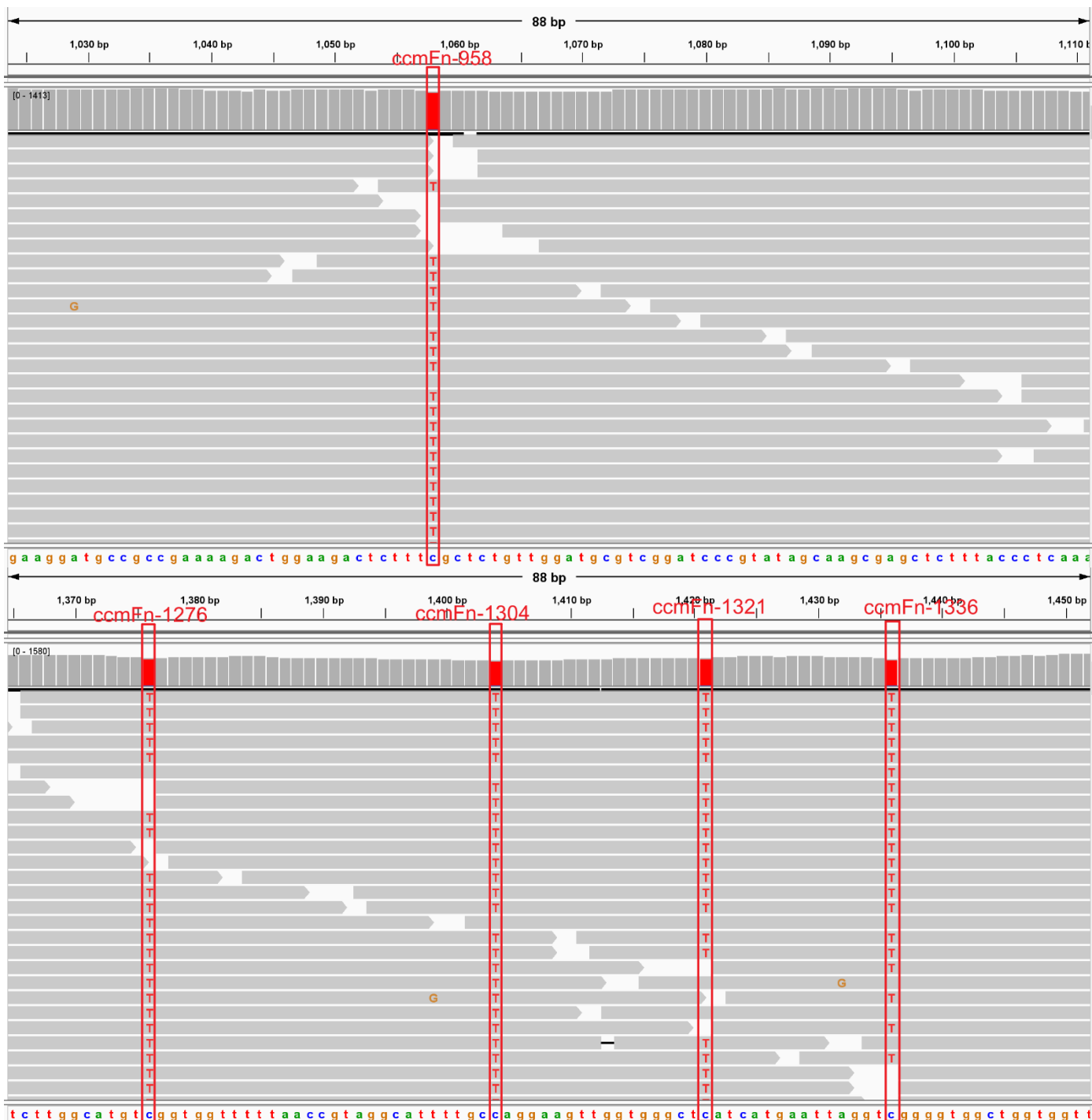


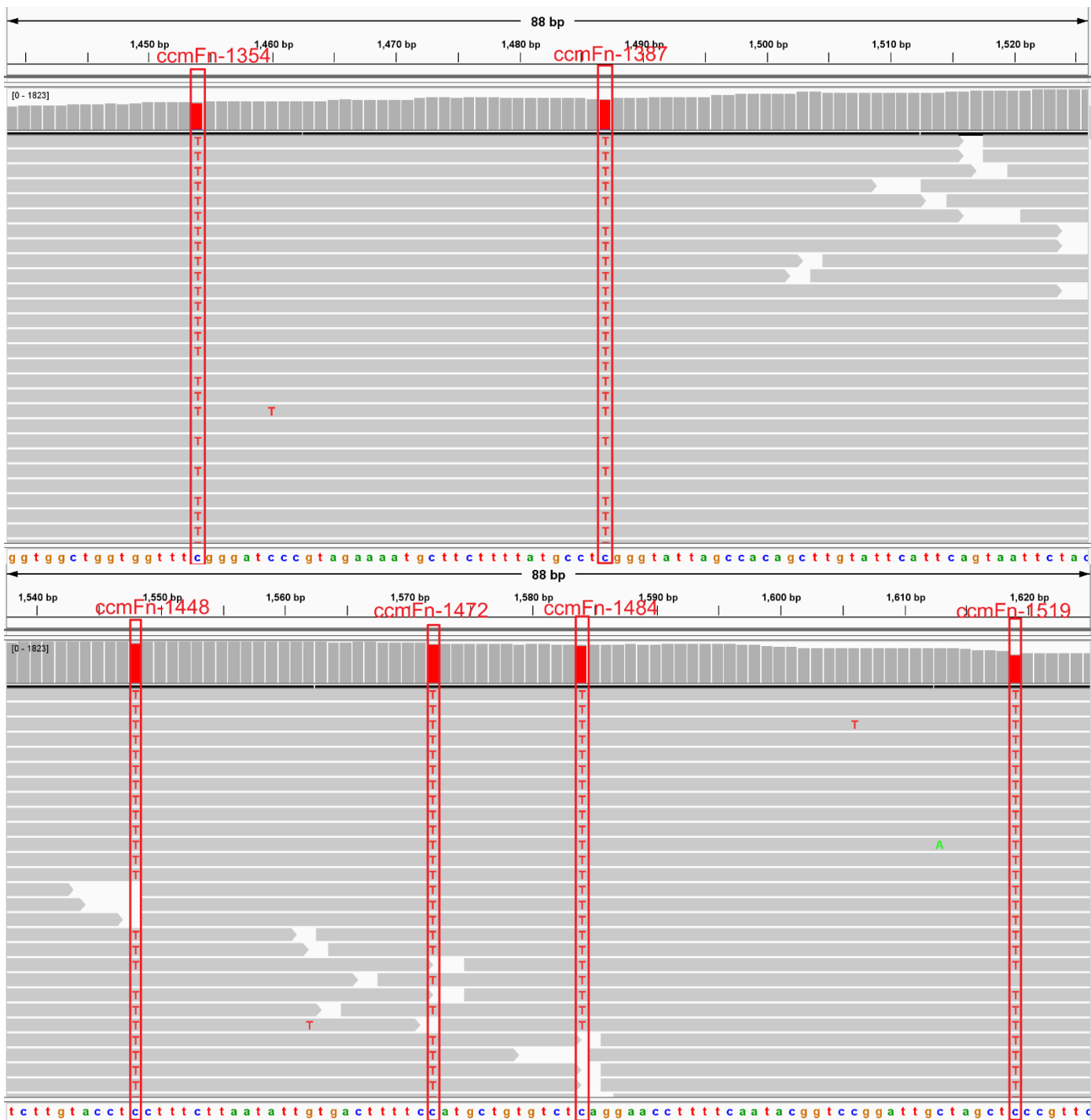
h alignment of RNA-seq reads to the coding sequence of *ccmFn*. 30 RNA-seq editing sites: *ccmFn*-38, 98, 137, 142, 151, 165, 248, 256, 283, 371, 378, 713, 722, 732, 760, 782, 794, 809, 867, 958, 1276, 1304, 1321, 1336, 1354, 1387, 1448, 1472, 1484, 1519 were highlighted in red squares.



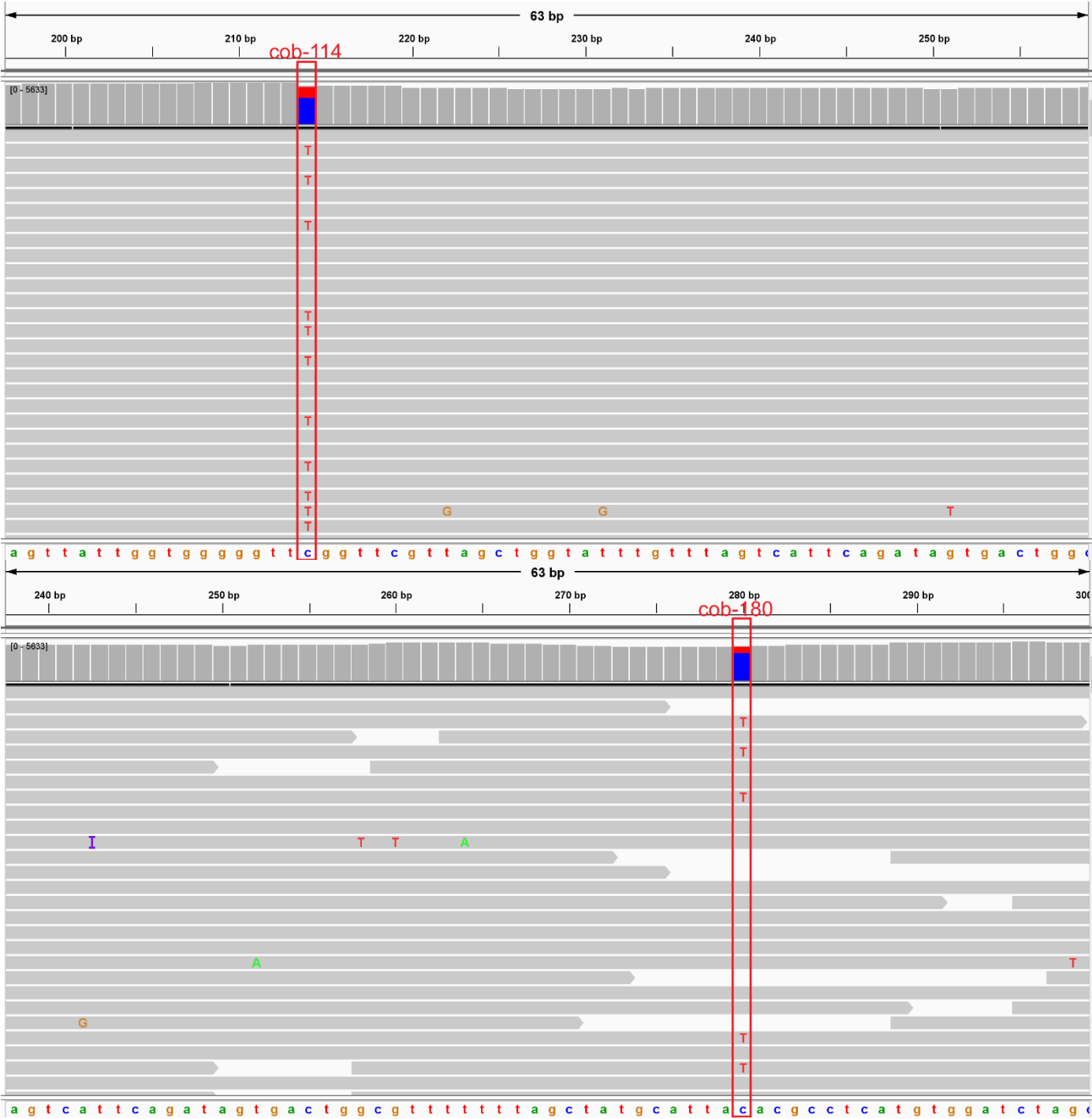


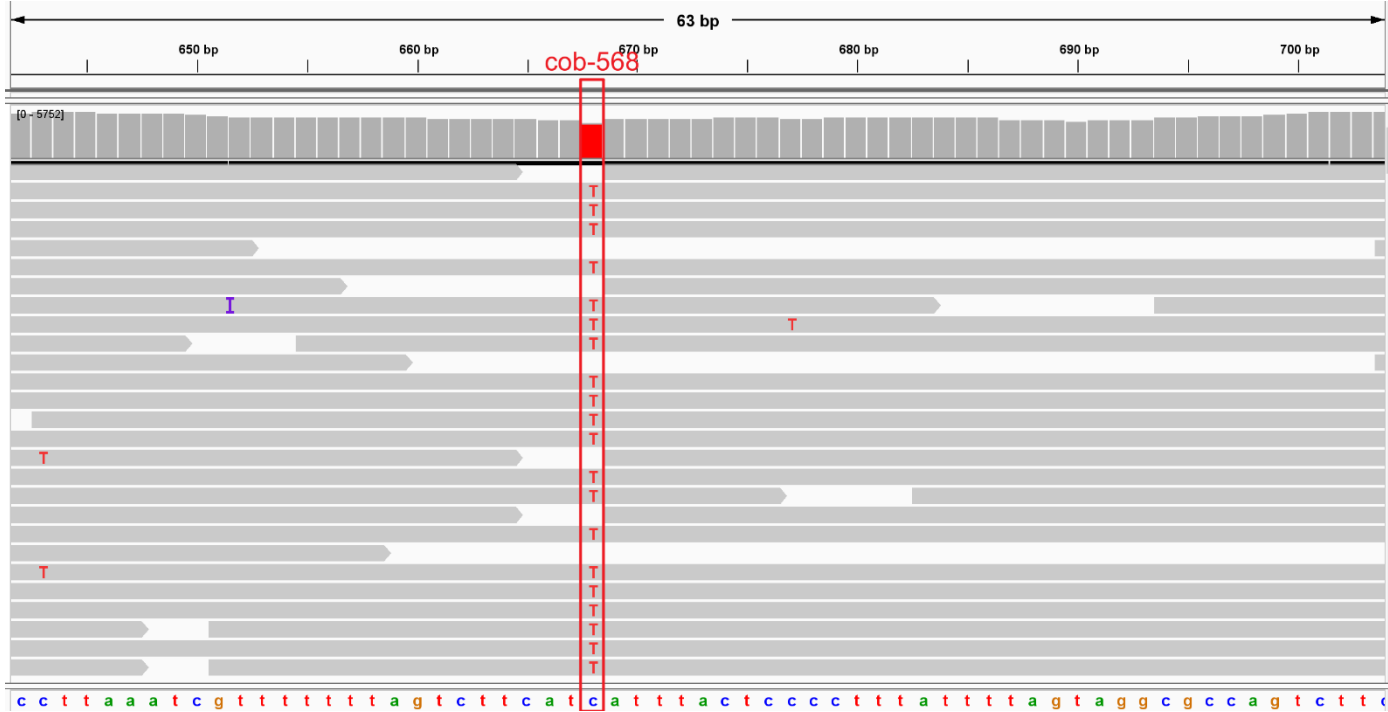
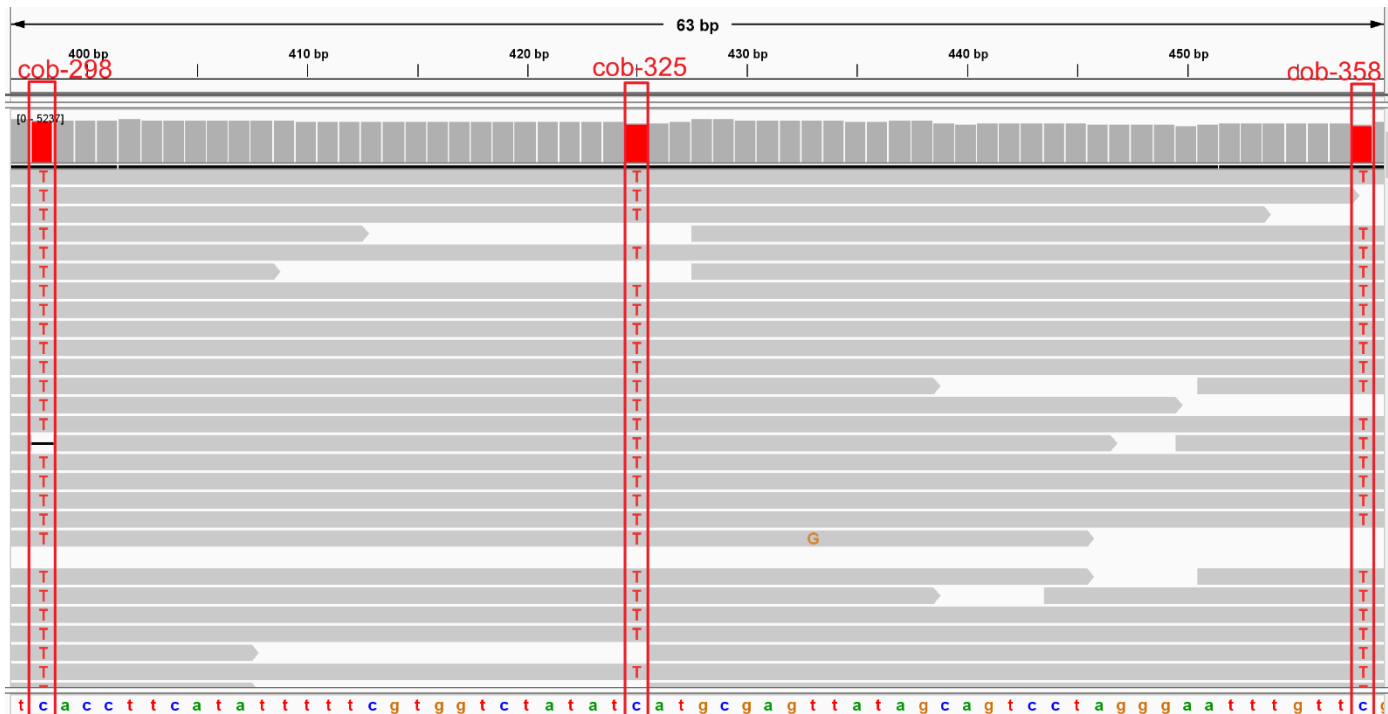


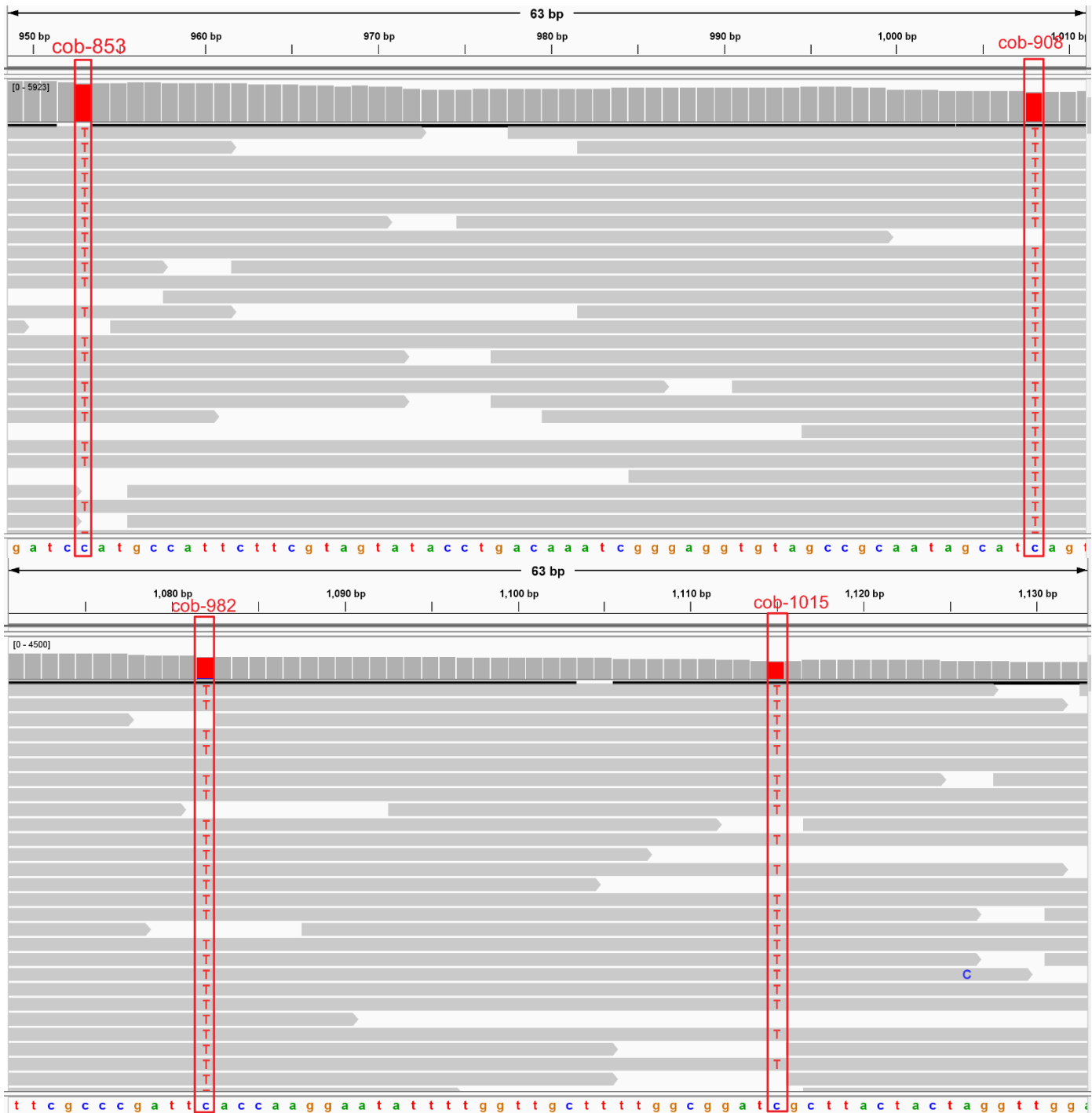


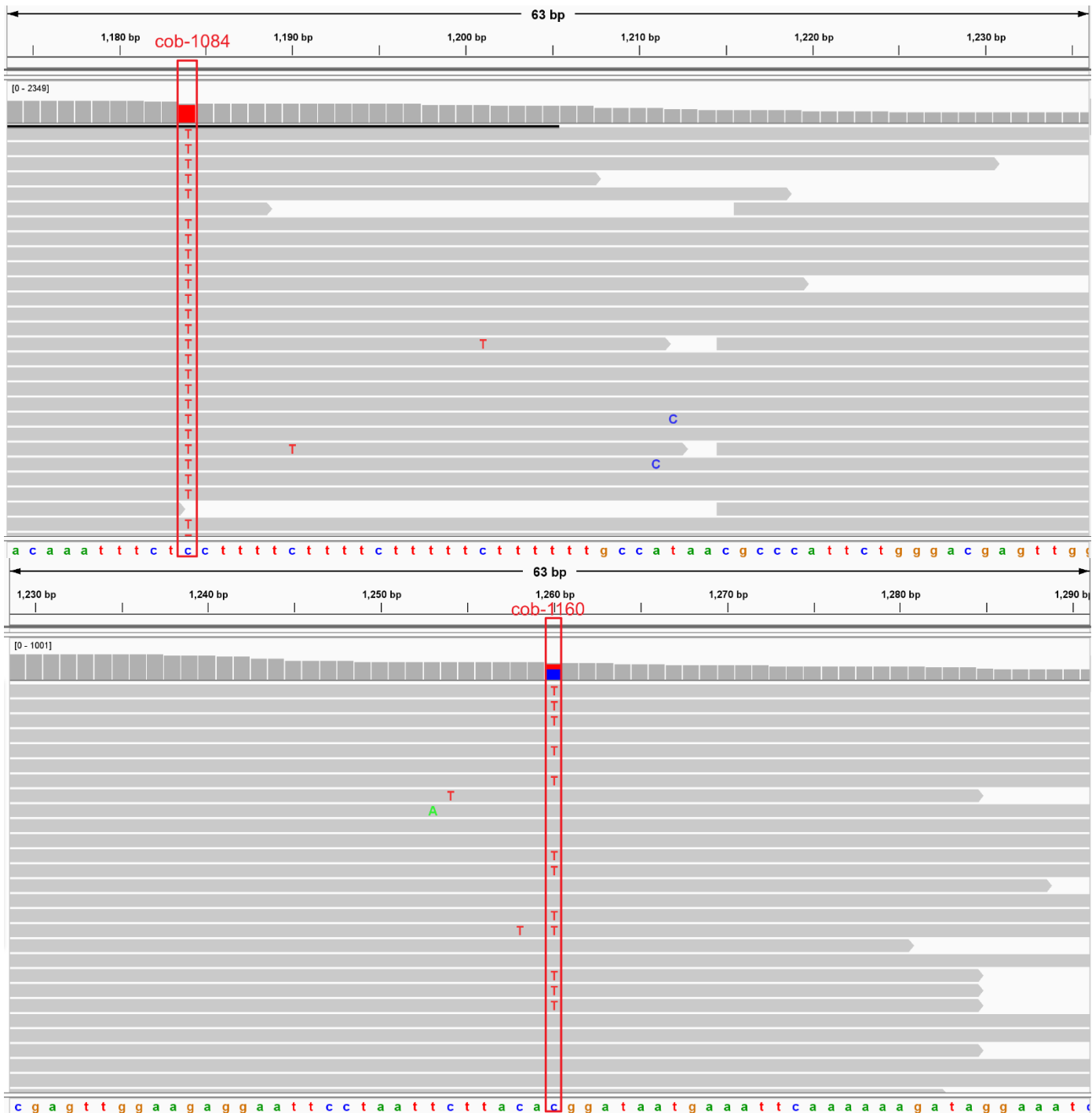


i alignment of RNA-seq reads to the coding sequence of *cob*. 12 RNA-seq editing sites: *cob*-114, 180, 298, 325, 358, 568, 853, 908, 982, 1015, 1084, and 1160 were highlighted in red squares.

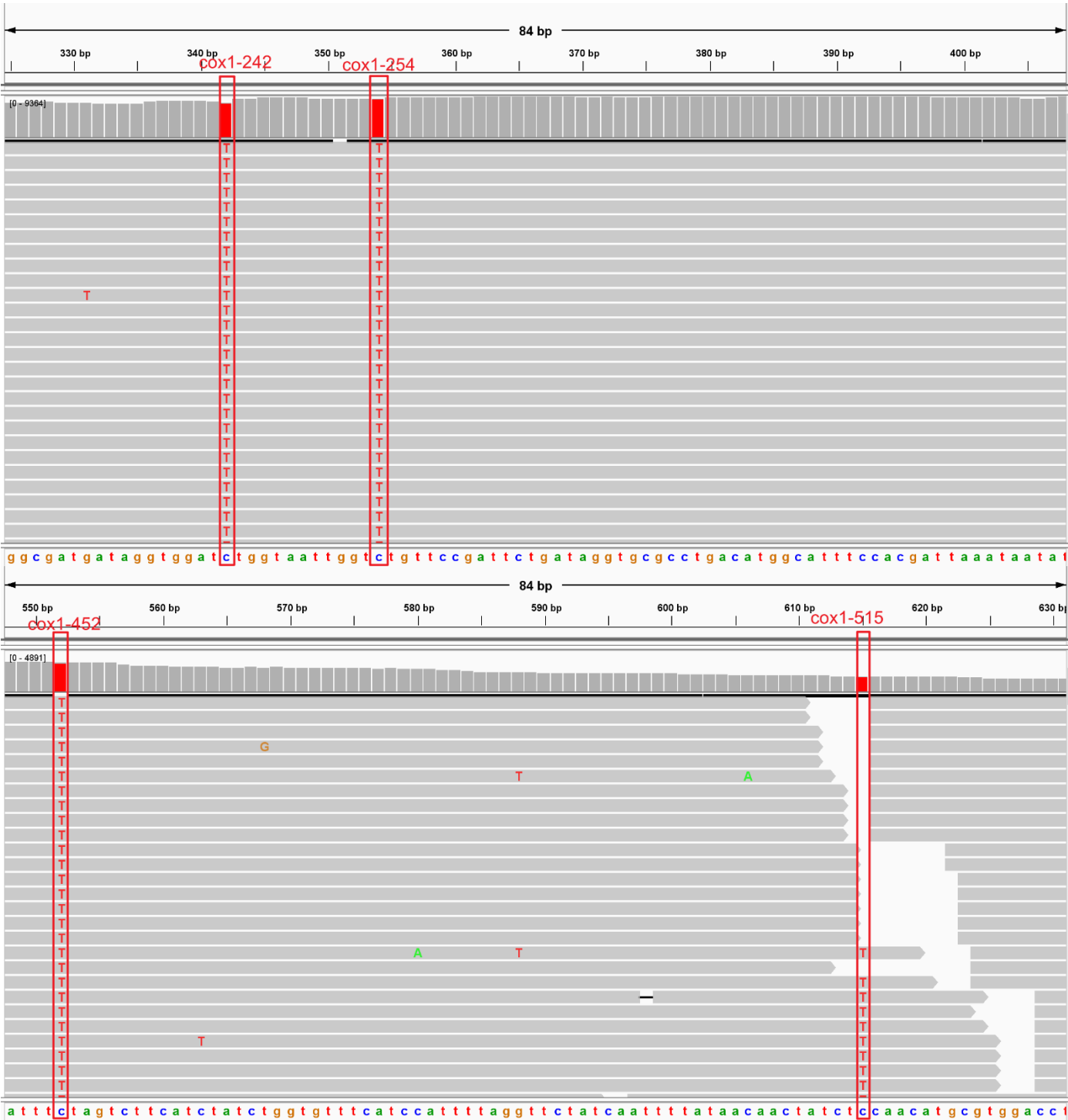


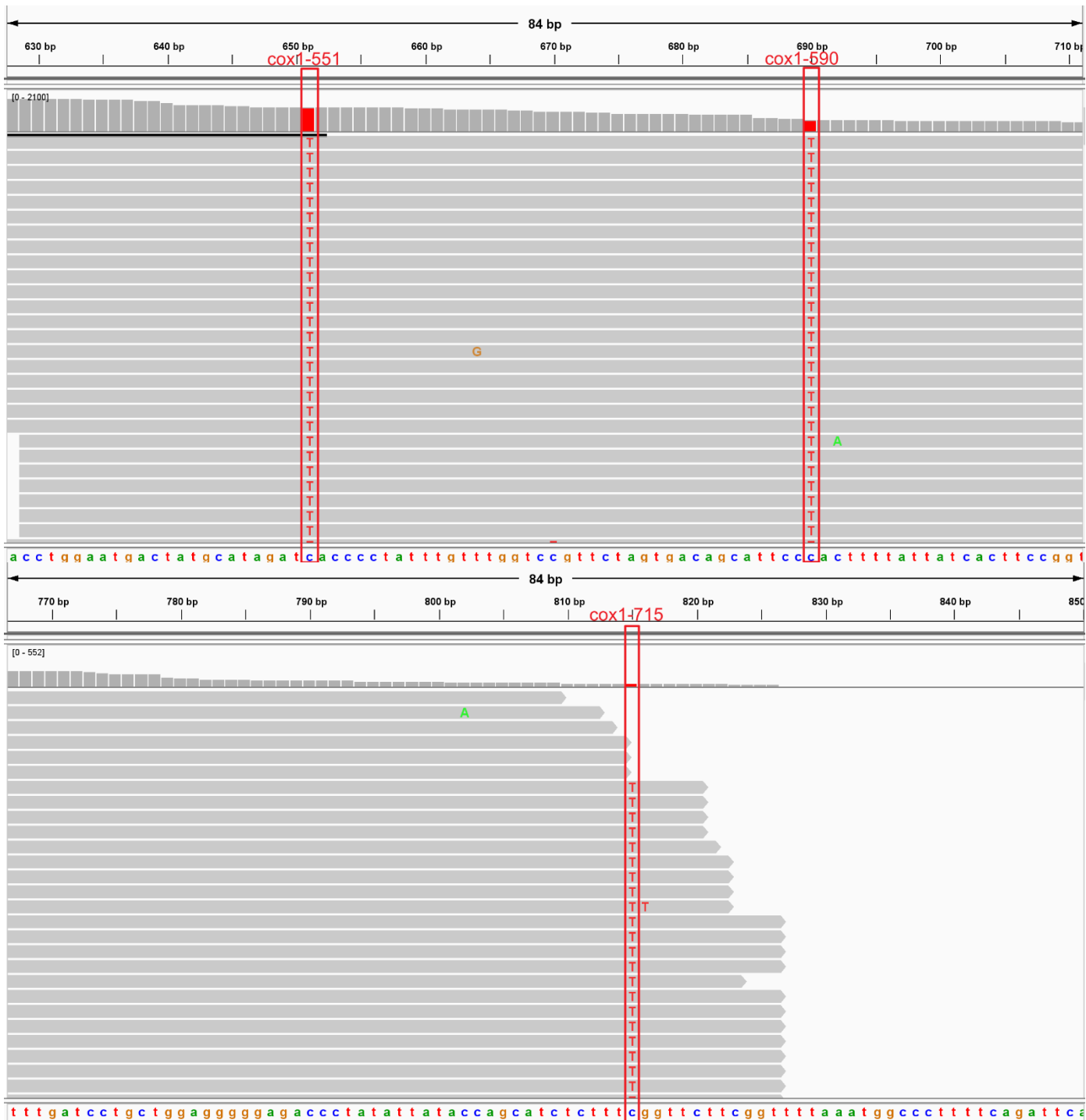


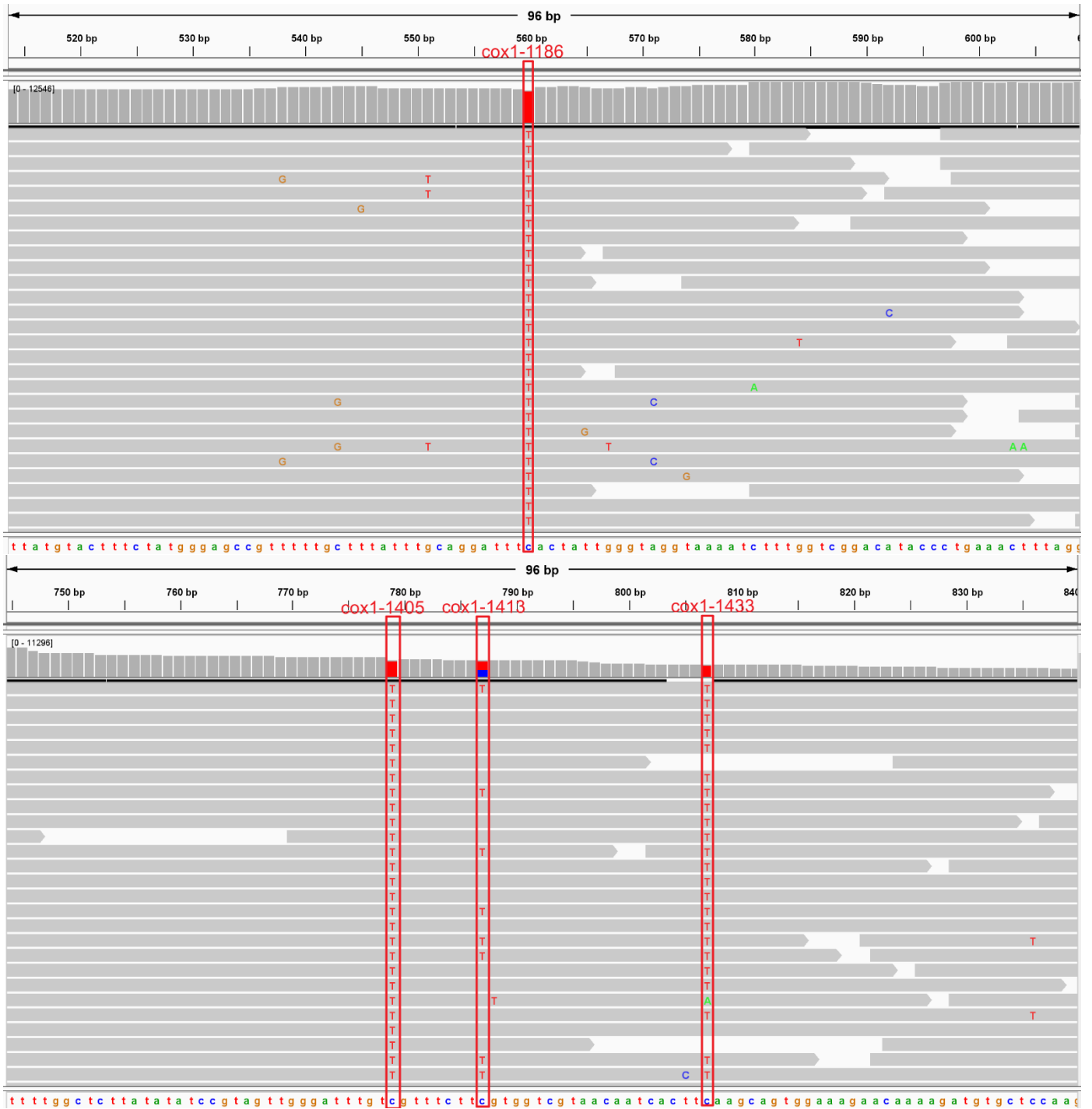


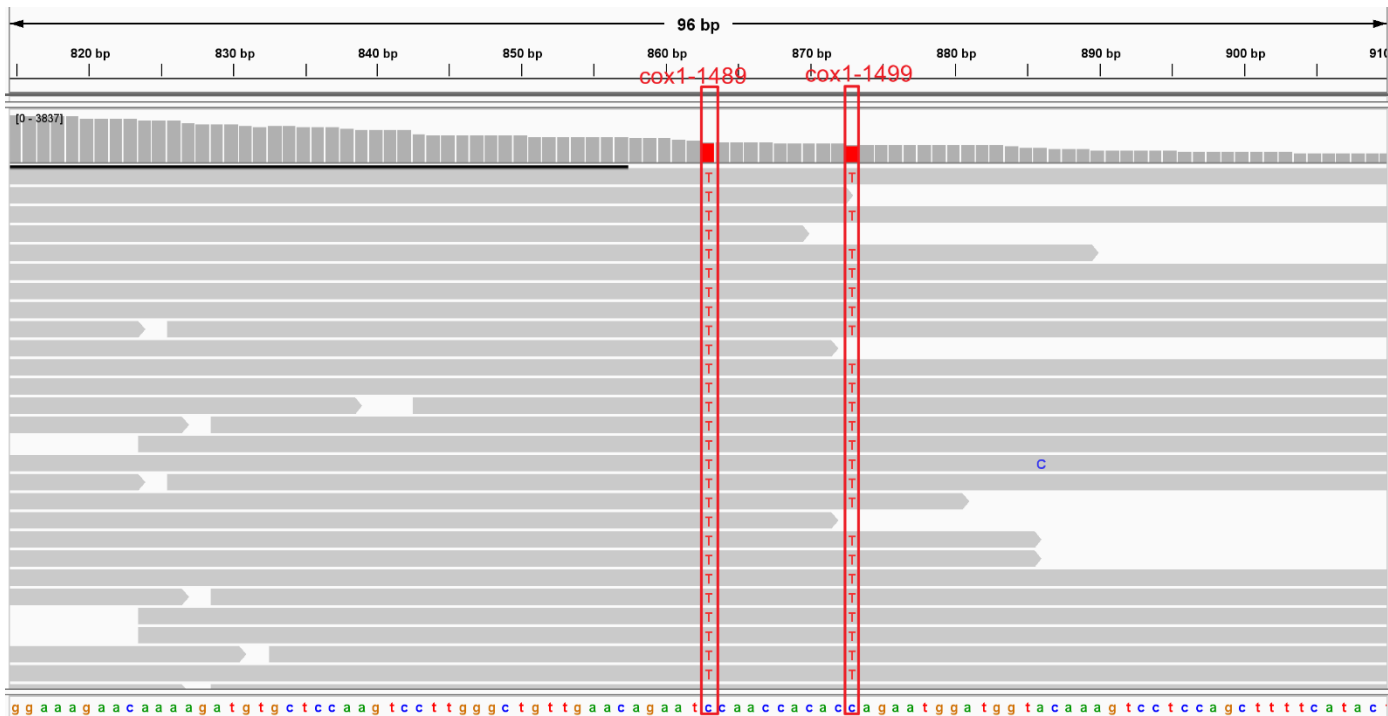


j alignment of RNA-seq reads to the coding sequence of *cox1*. 15 RNA-seq editing sites: *cox1*-242, 254, 452, 515, 551, 590, 715, 761, 1078, 1186, 1405, 1413, 1433, 1489, and 1499 were highlighted in red squares.

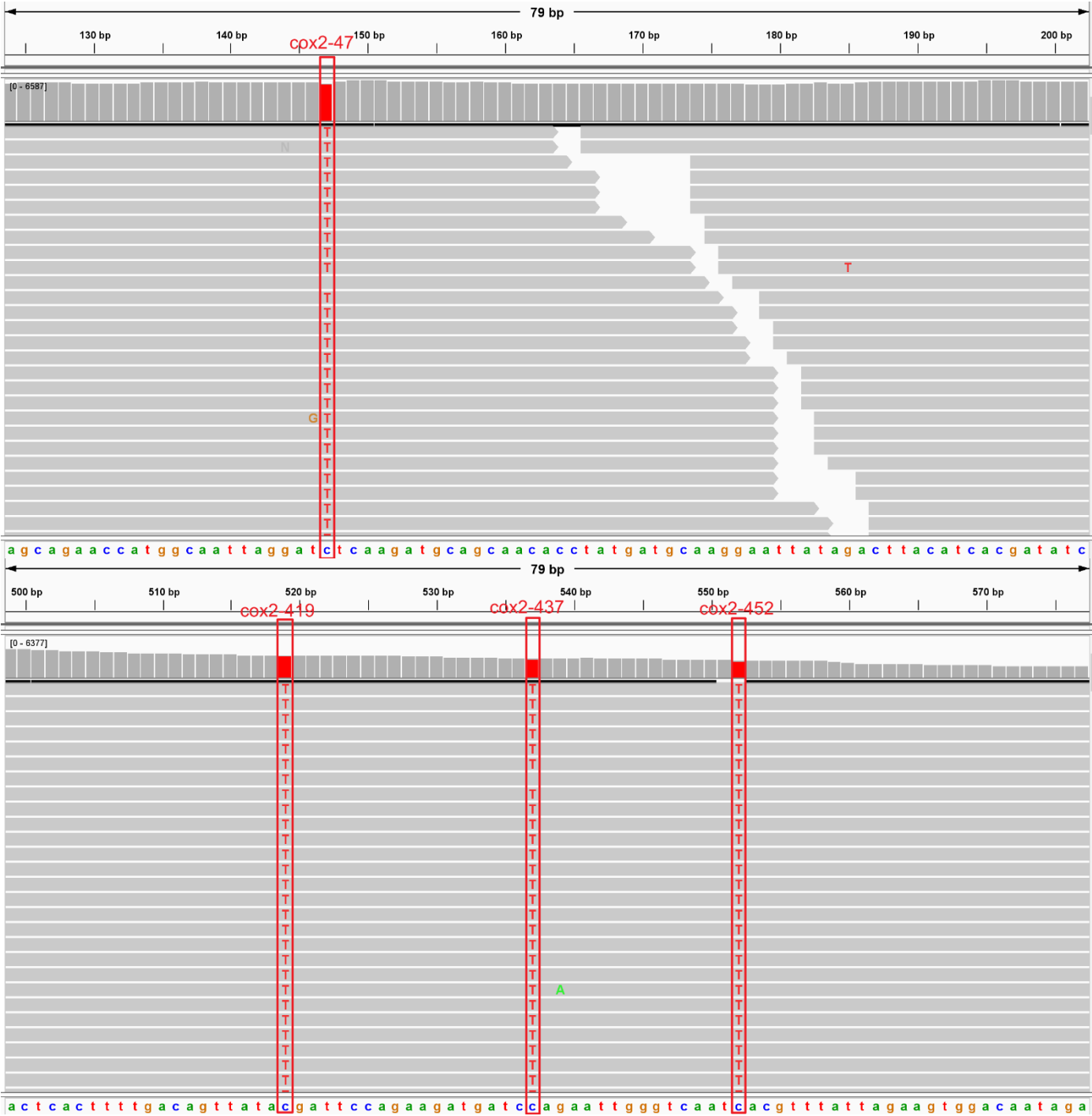




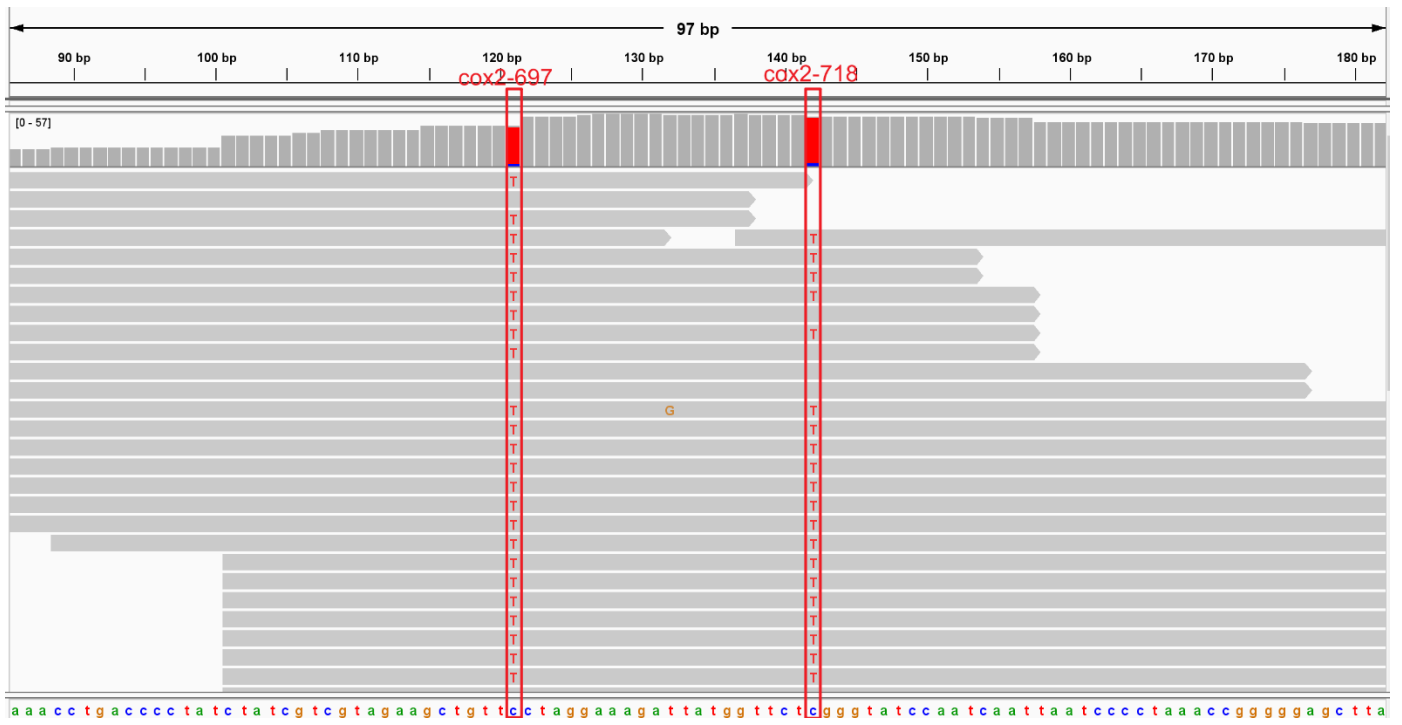




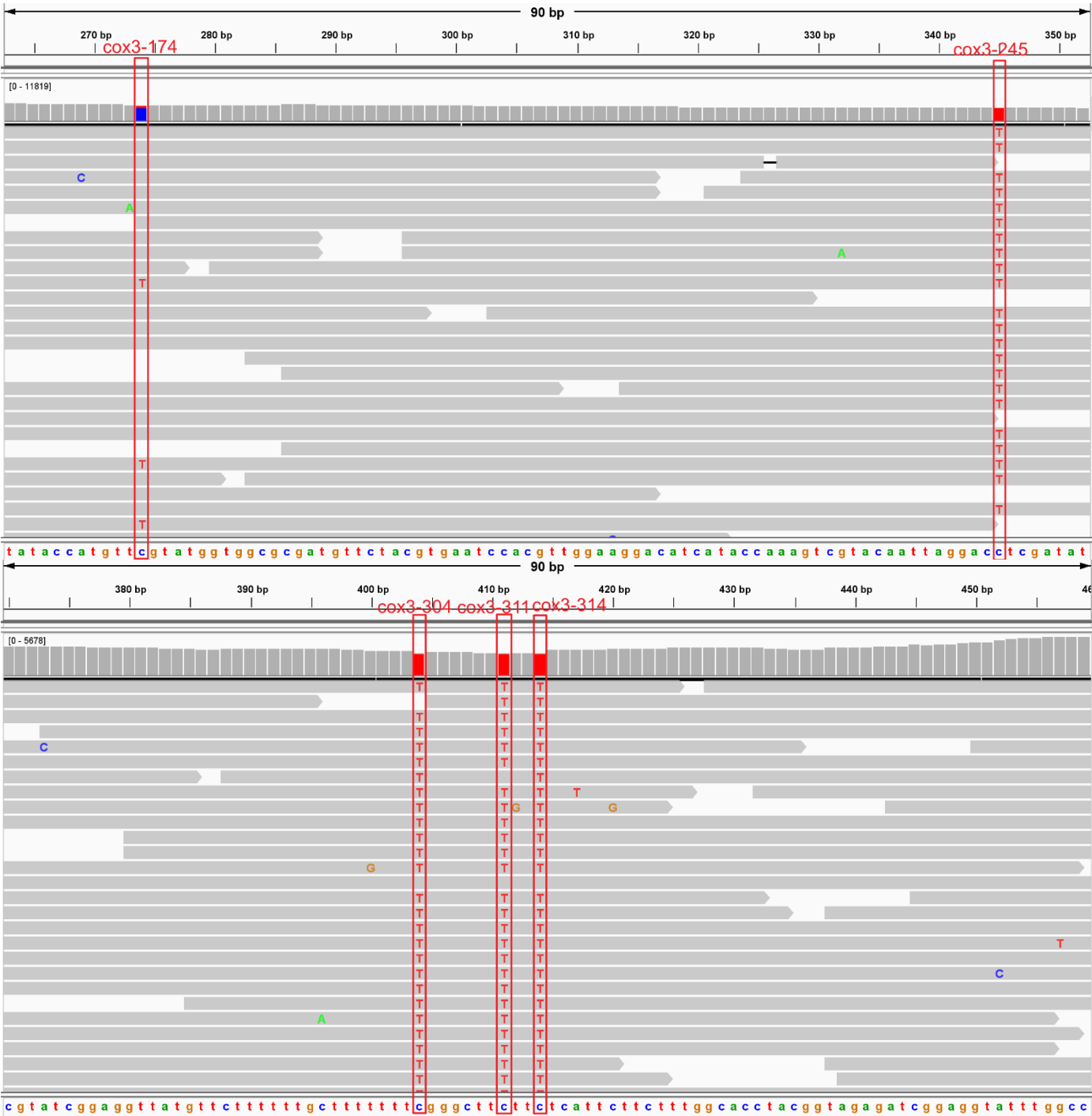
k alignment of RNA-seq reads to the coding sequence of *cox2*. 10 RNA-seq editing sites: *cox2*-47, 419, 437, 452, 520, 533, 595, 608, 697, and 718 were highlighted in red squares.

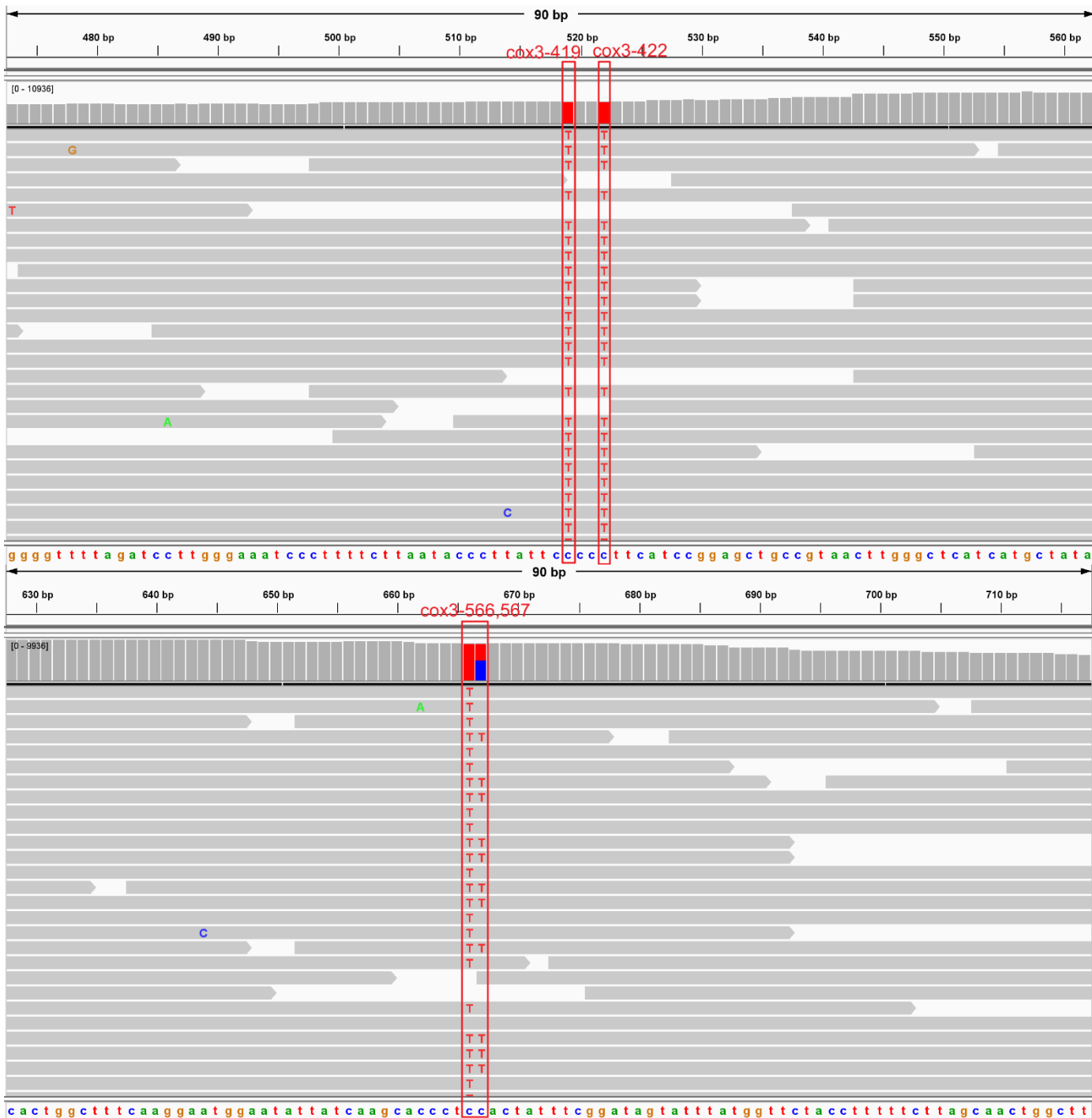


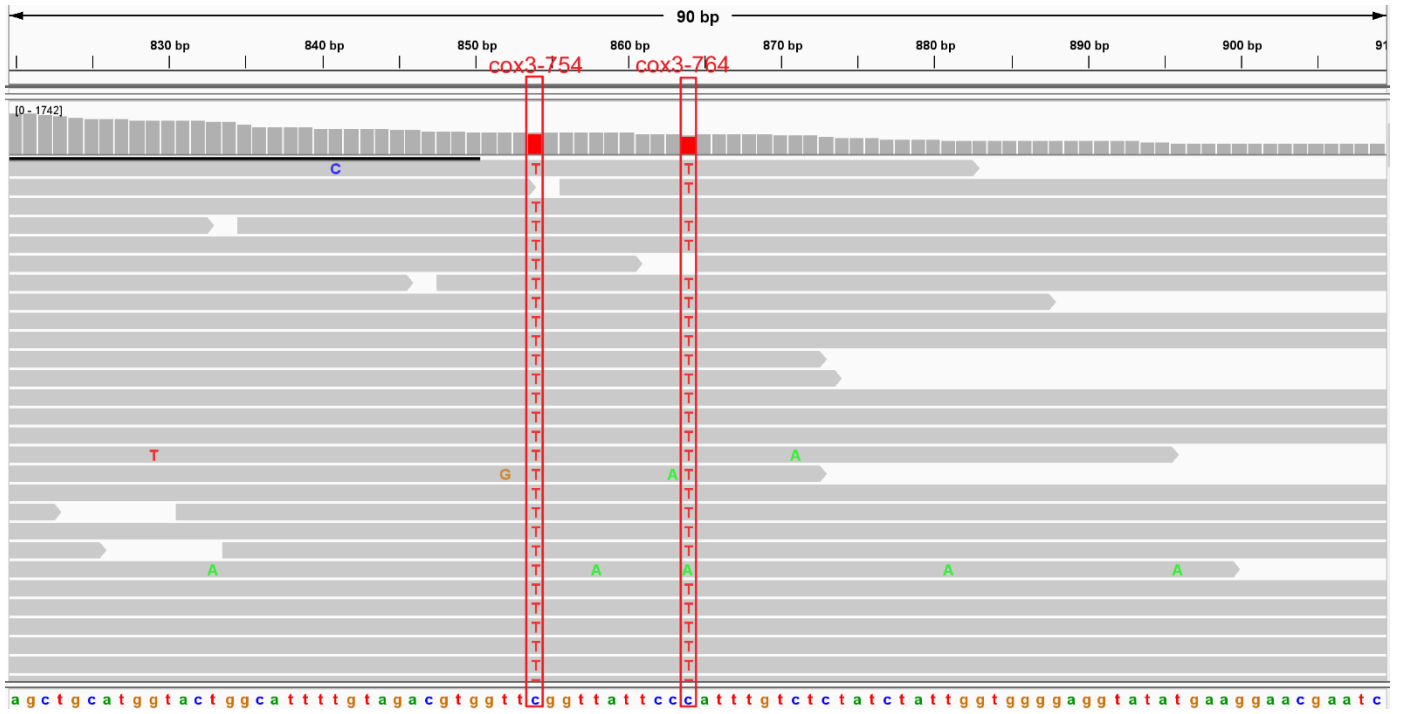




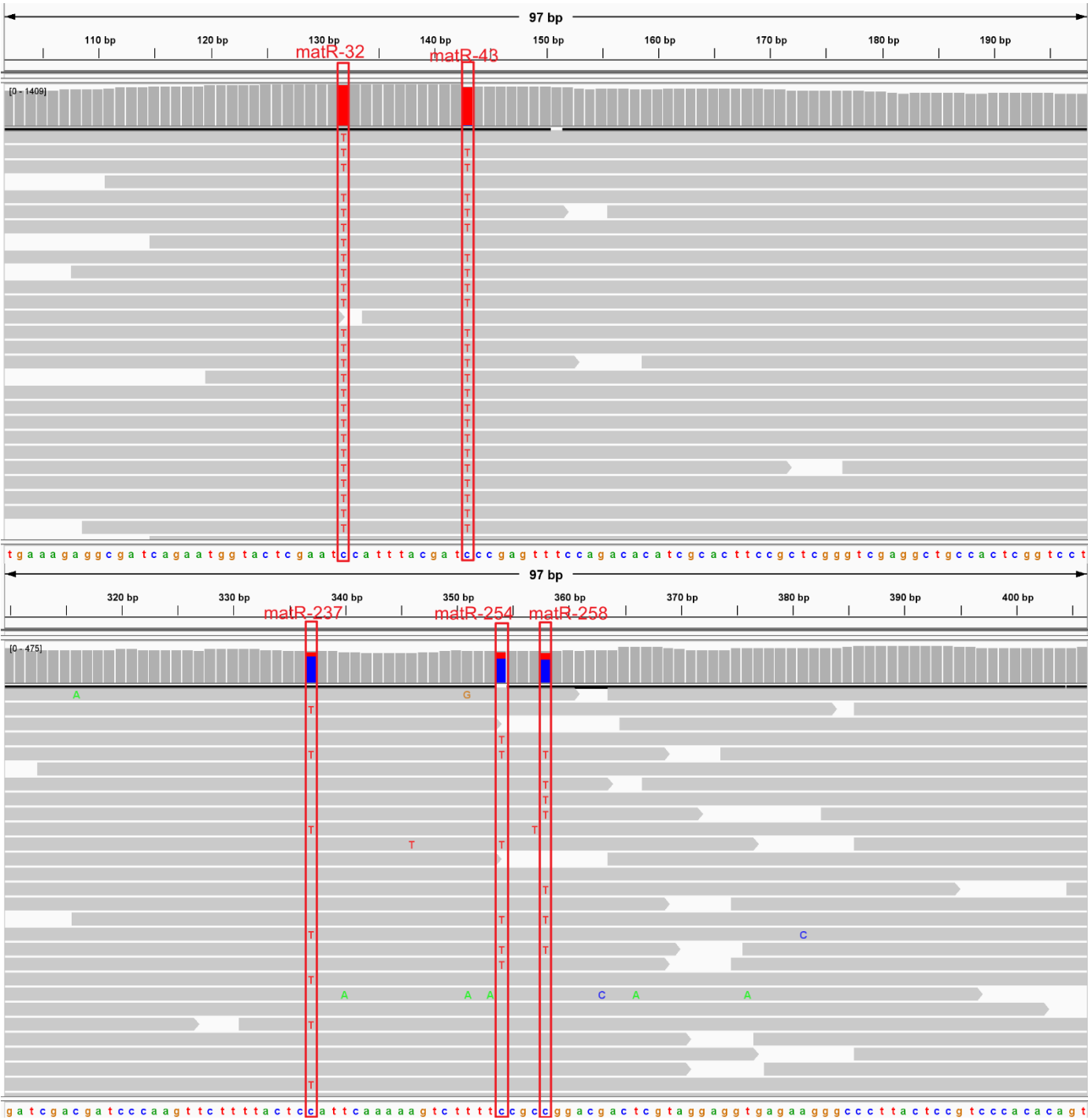
Alignment of RNA-seq reads to the coding sequence of *cox3*. 11 RNA-seq editing sites: *cox3*-174, 245, 304, 311, 314, 419, 422, 566, 567, 754, and 764 were highlighted in red squares.

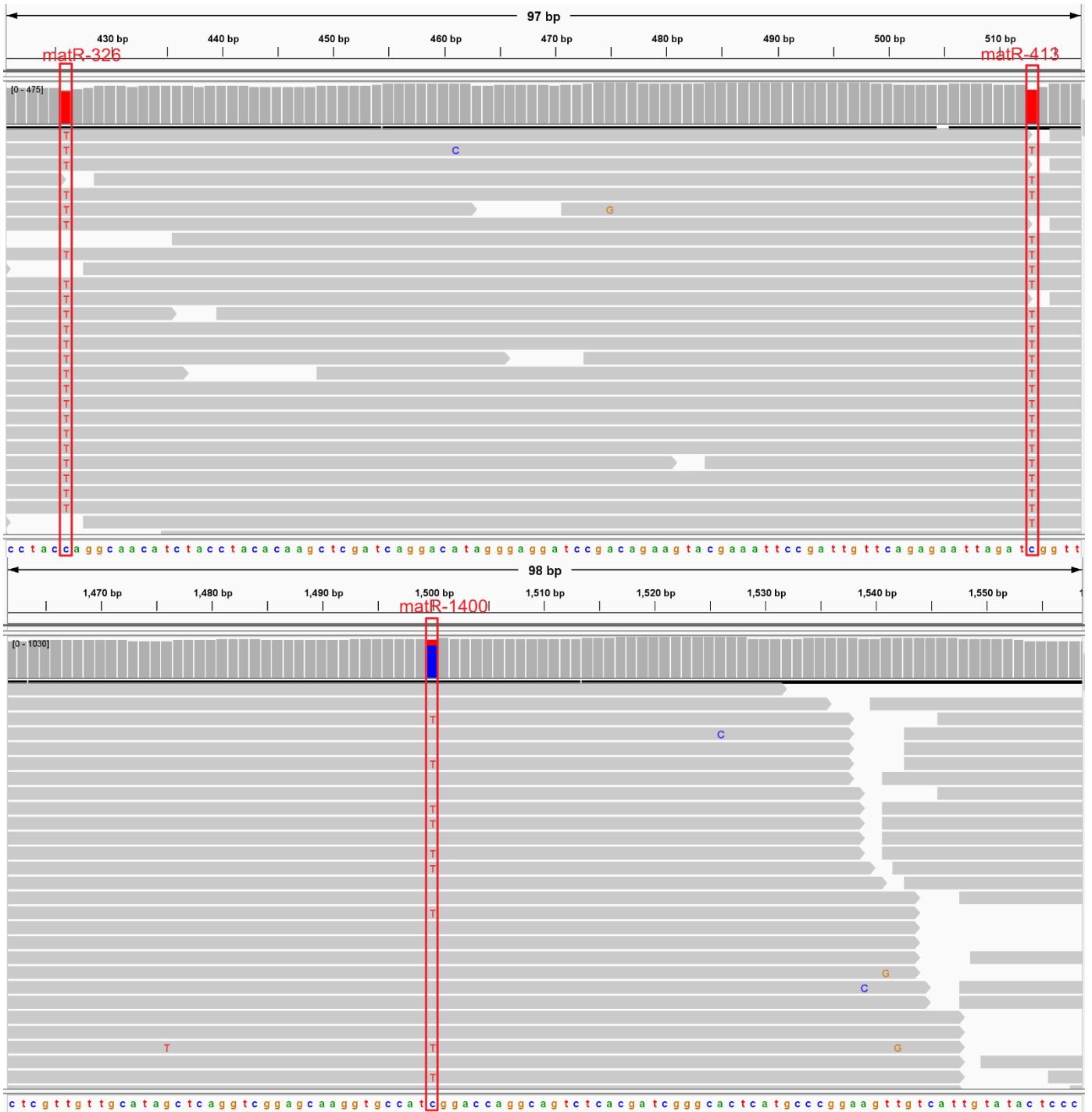




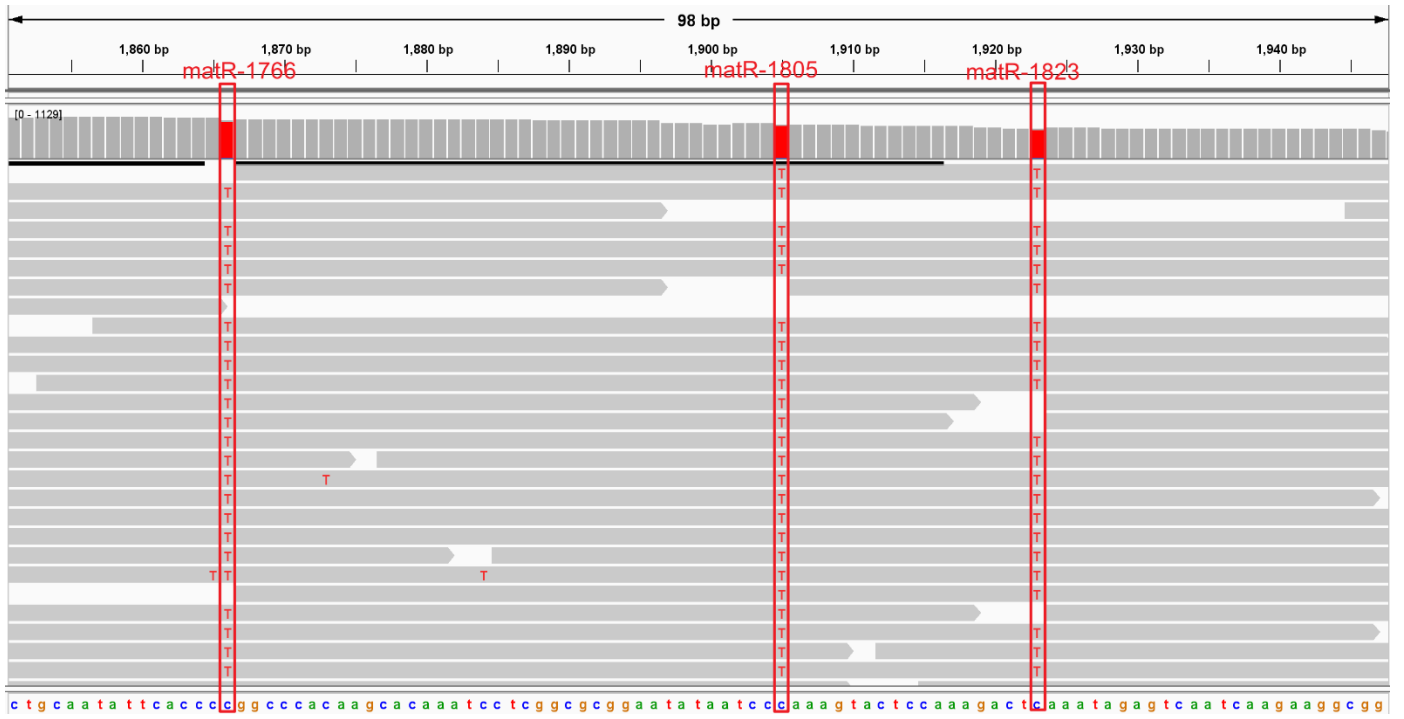


m alignment of RNA-seq reads to the coding sequence of *matR*. 18 RNA-seq editing sites: *matR*-32, 43, 237, 254, 258, 326, 413, 1400, 1522, 1524, 1658, 1679, 1699, 1713, 1735, 1766, 1805, and 1823 were highlighted in red squares.





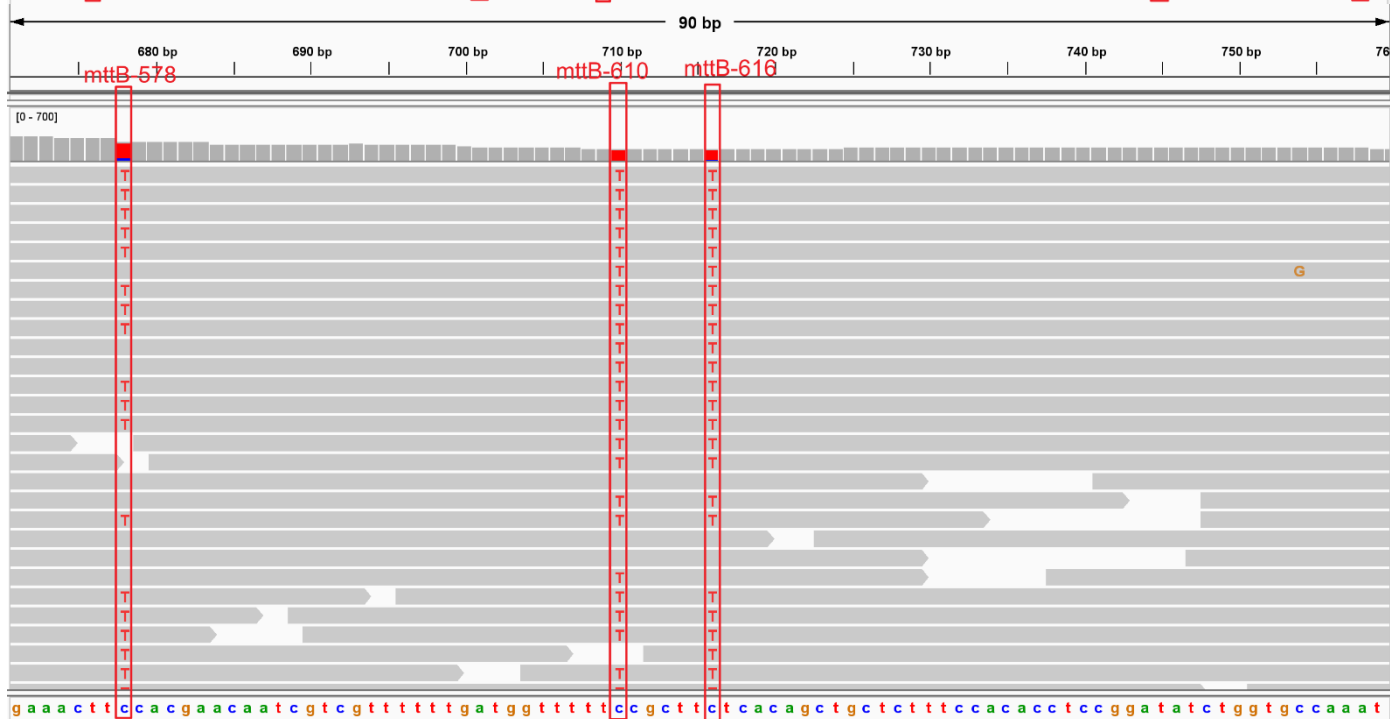
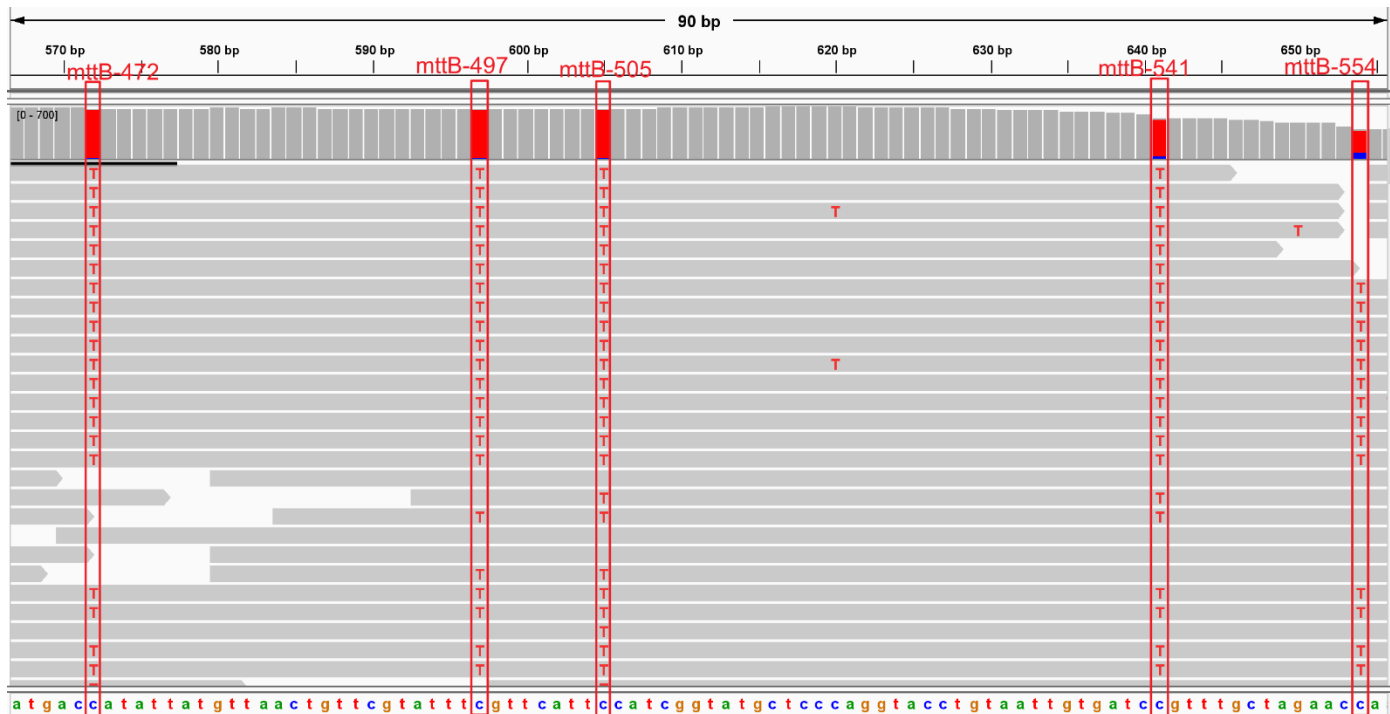


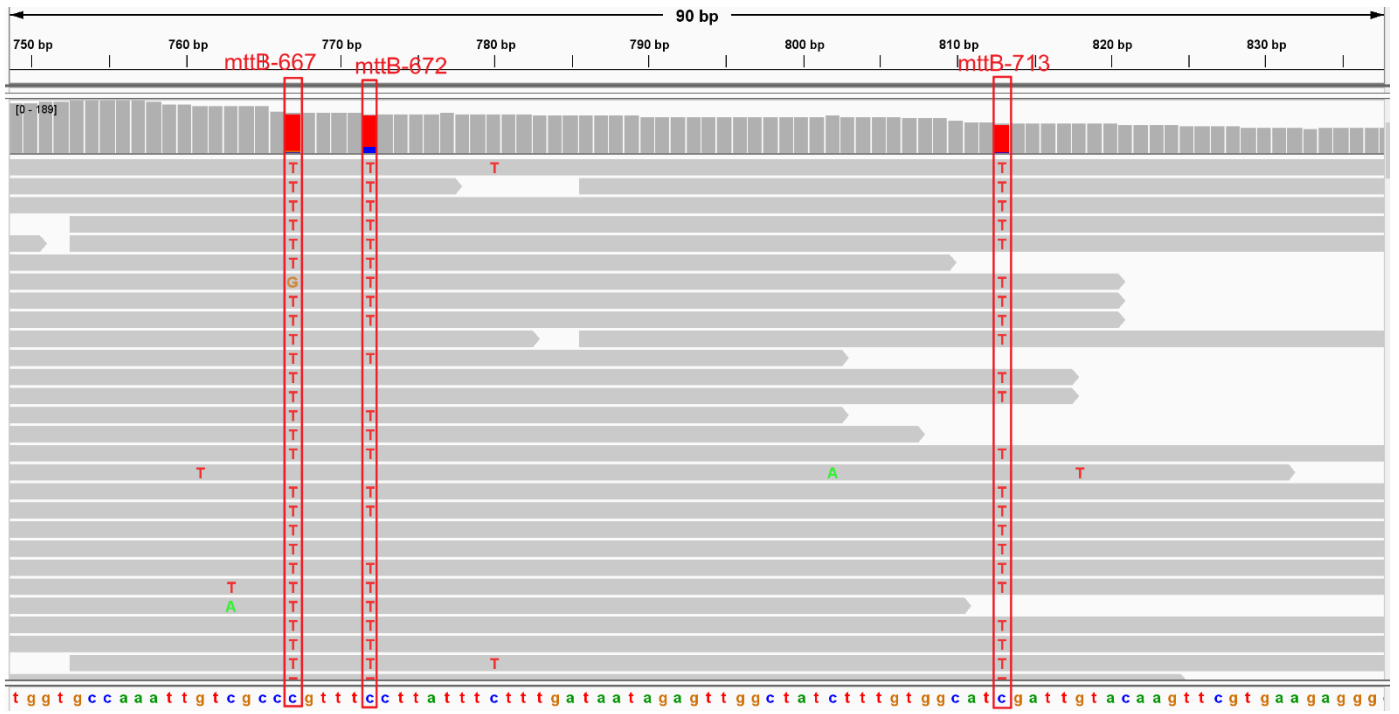


n alignment of RNA-seq reads to the coding sequence of *mttB*. 32 RNA-seq editing sites: *mttB*-16, 26, 64, 100, 112, 128, 131, 178, 188, 201, 202, 236, 262, 328, 331, 344, 346, 373, 376, 379, 407, 472, 497, 505, 541, 554, 578, 610, 616, 667, 672, and 713 were highlighted in red squares.



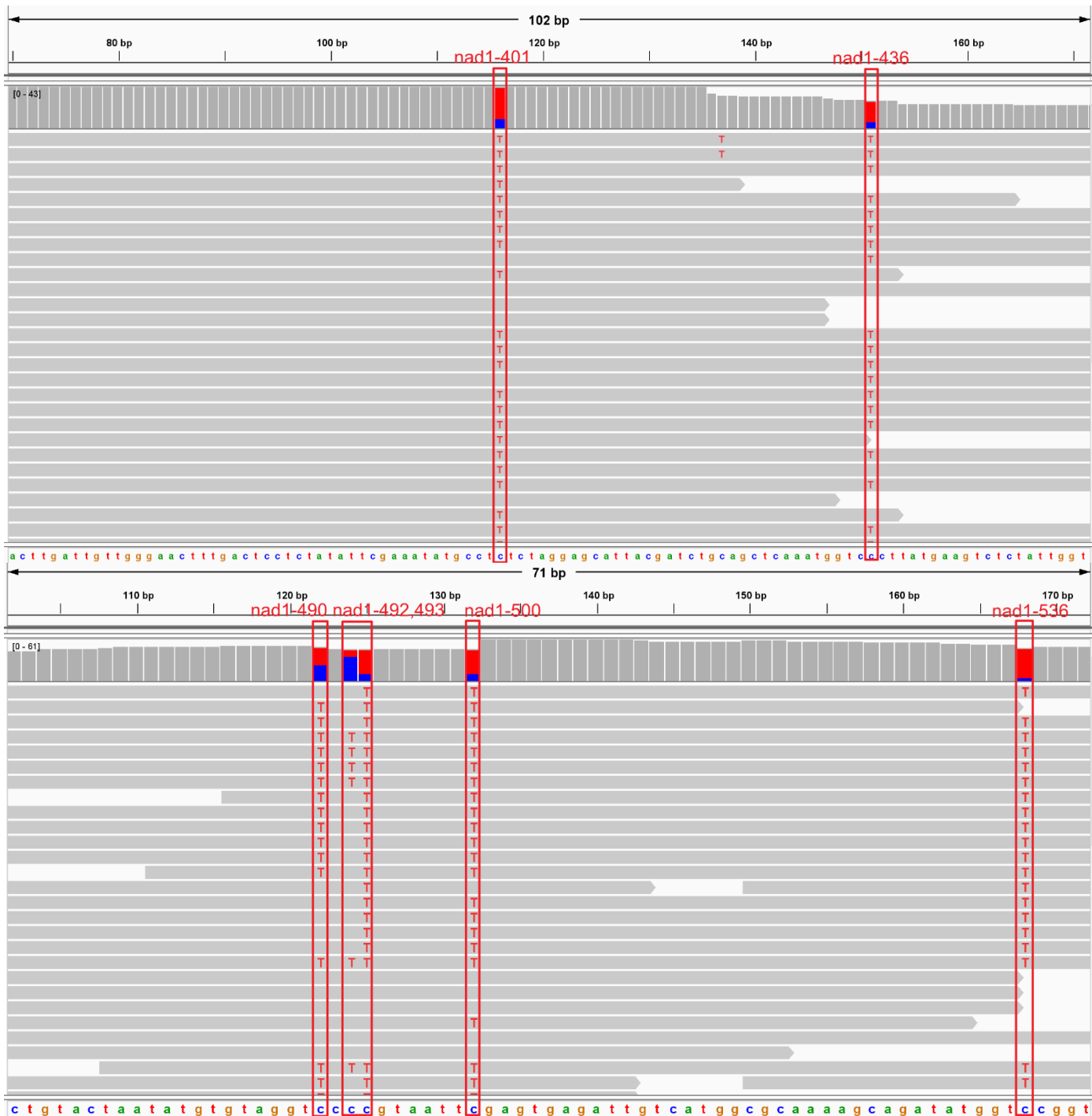


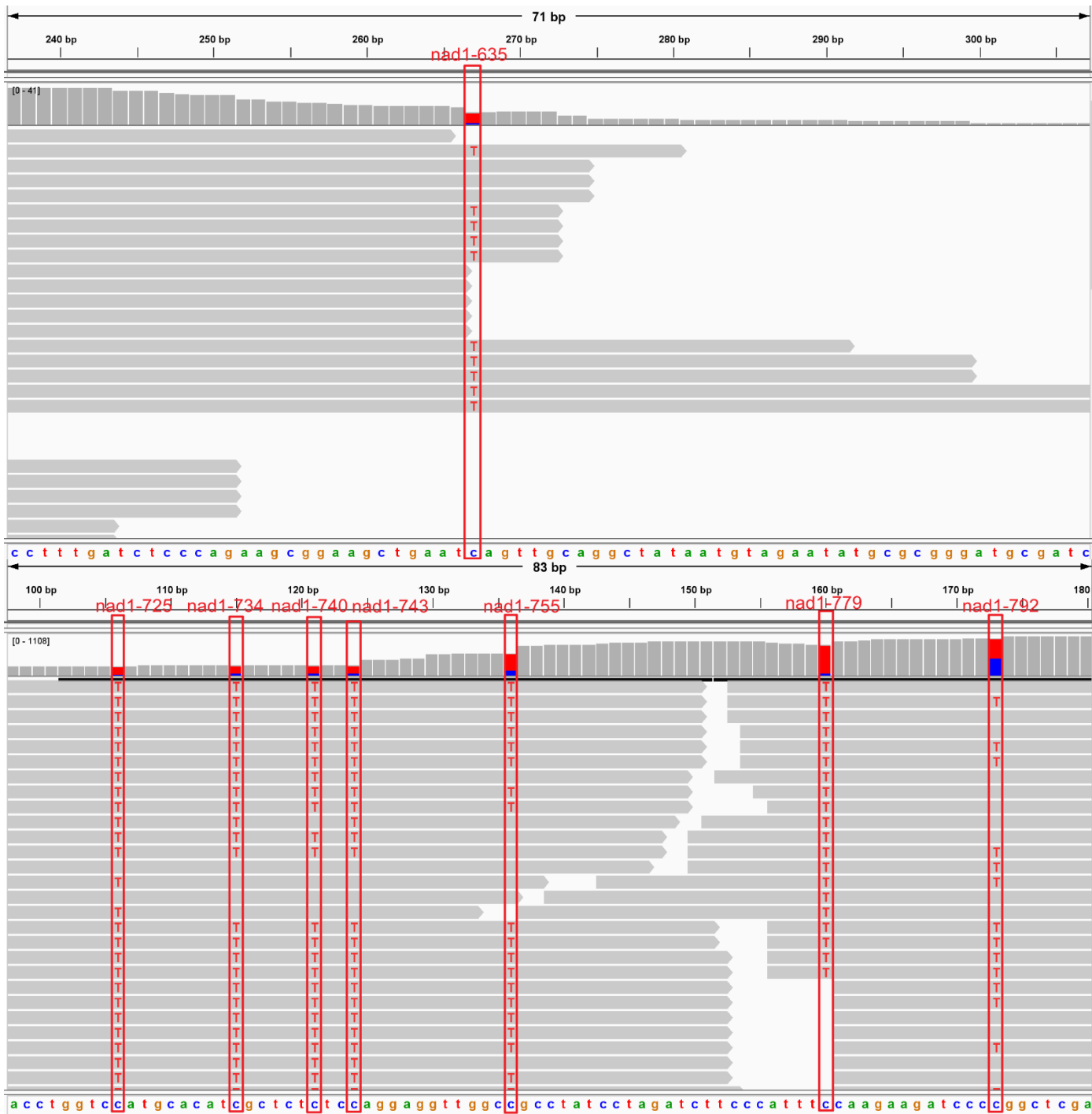


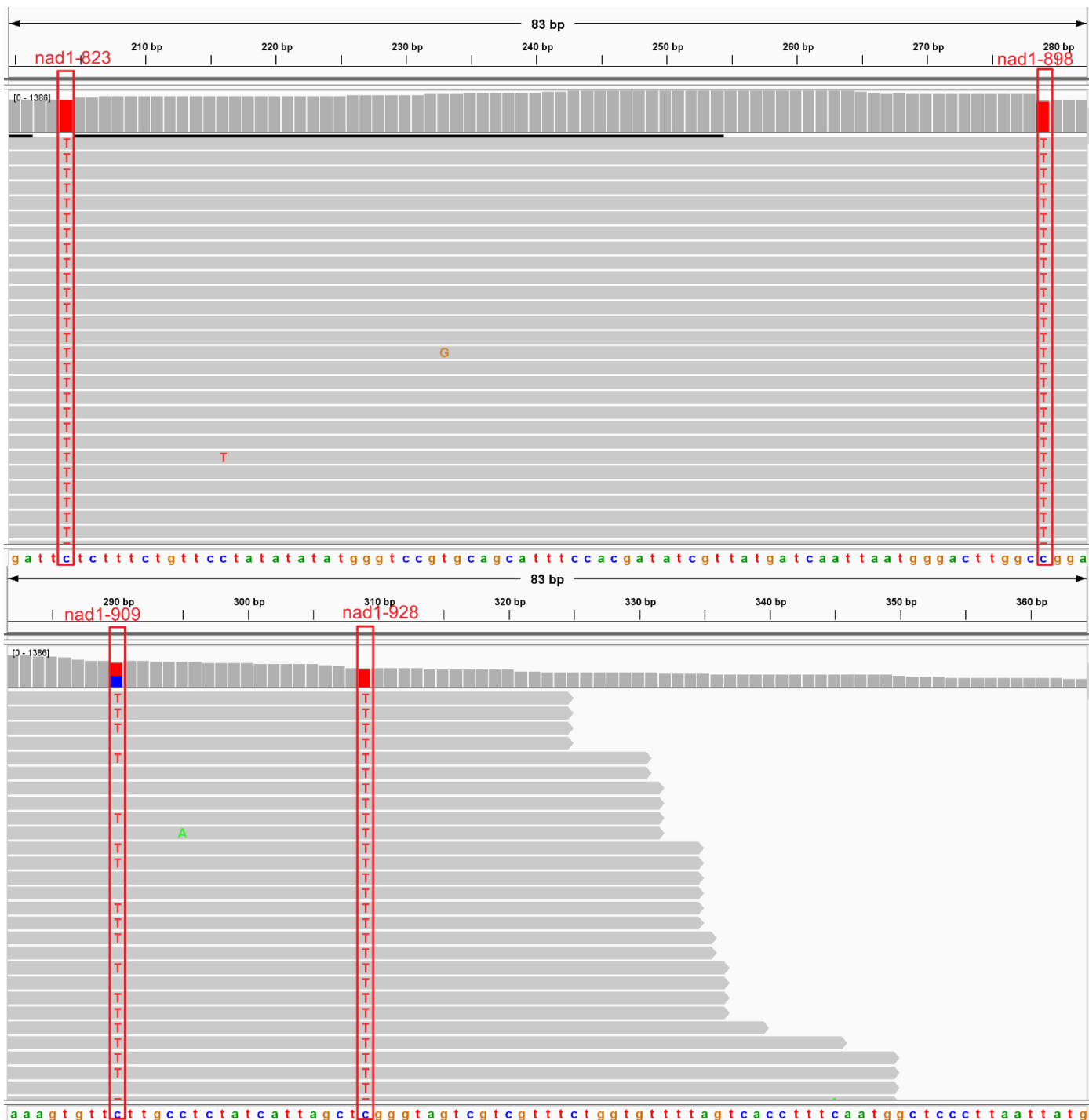


o alignment of RNA-seq reads to the coding sequence of *nad1*. 24 RNA-seq editing sites: *nad1*-215, 265, 307, 308, 376, 401, 436, 490, 492, 493, 500, 536, 635, 725, 734, 740, 743, 755, 779, 792, 823, 898, 909, 928 were highlighted in red squares.

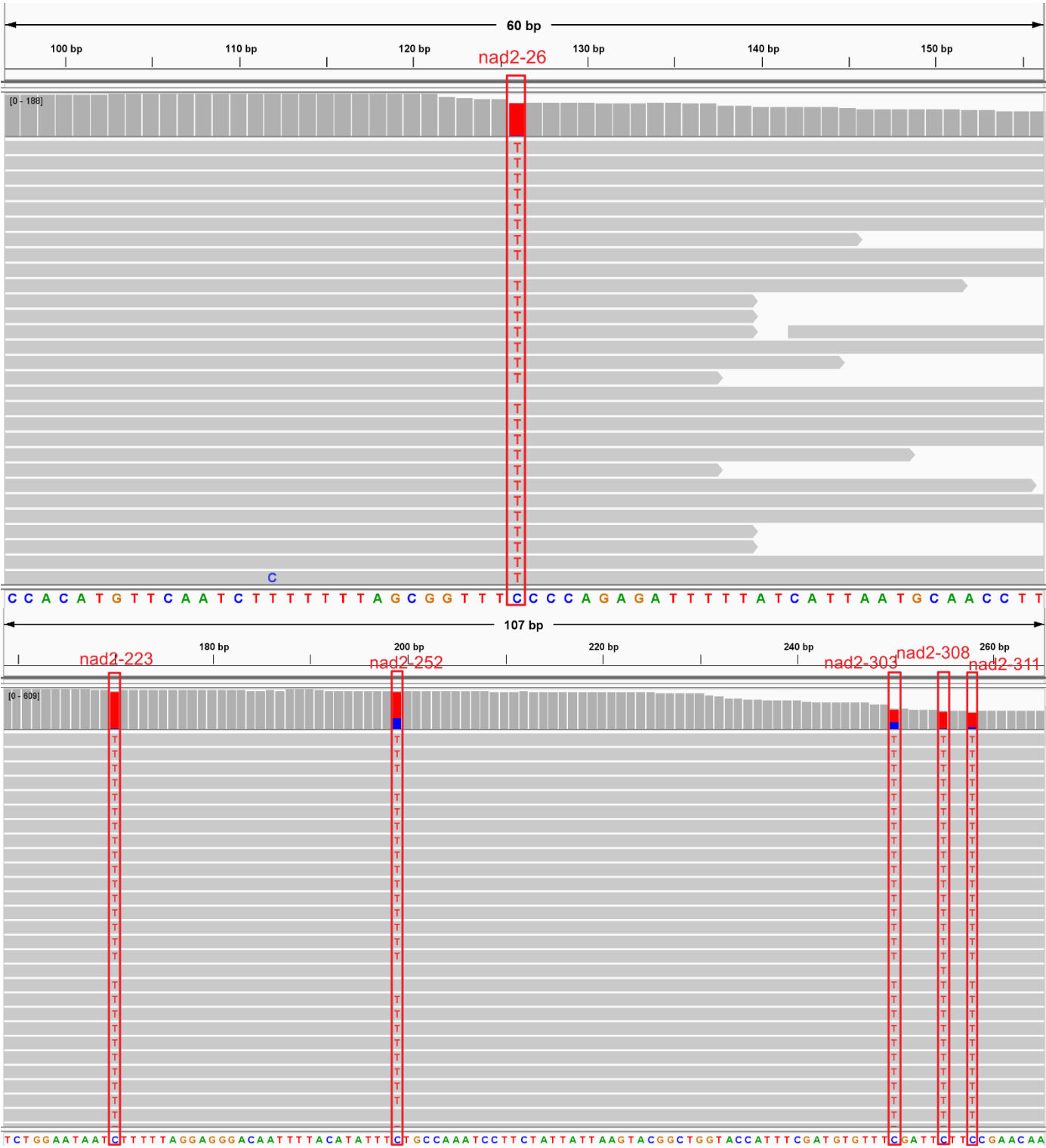


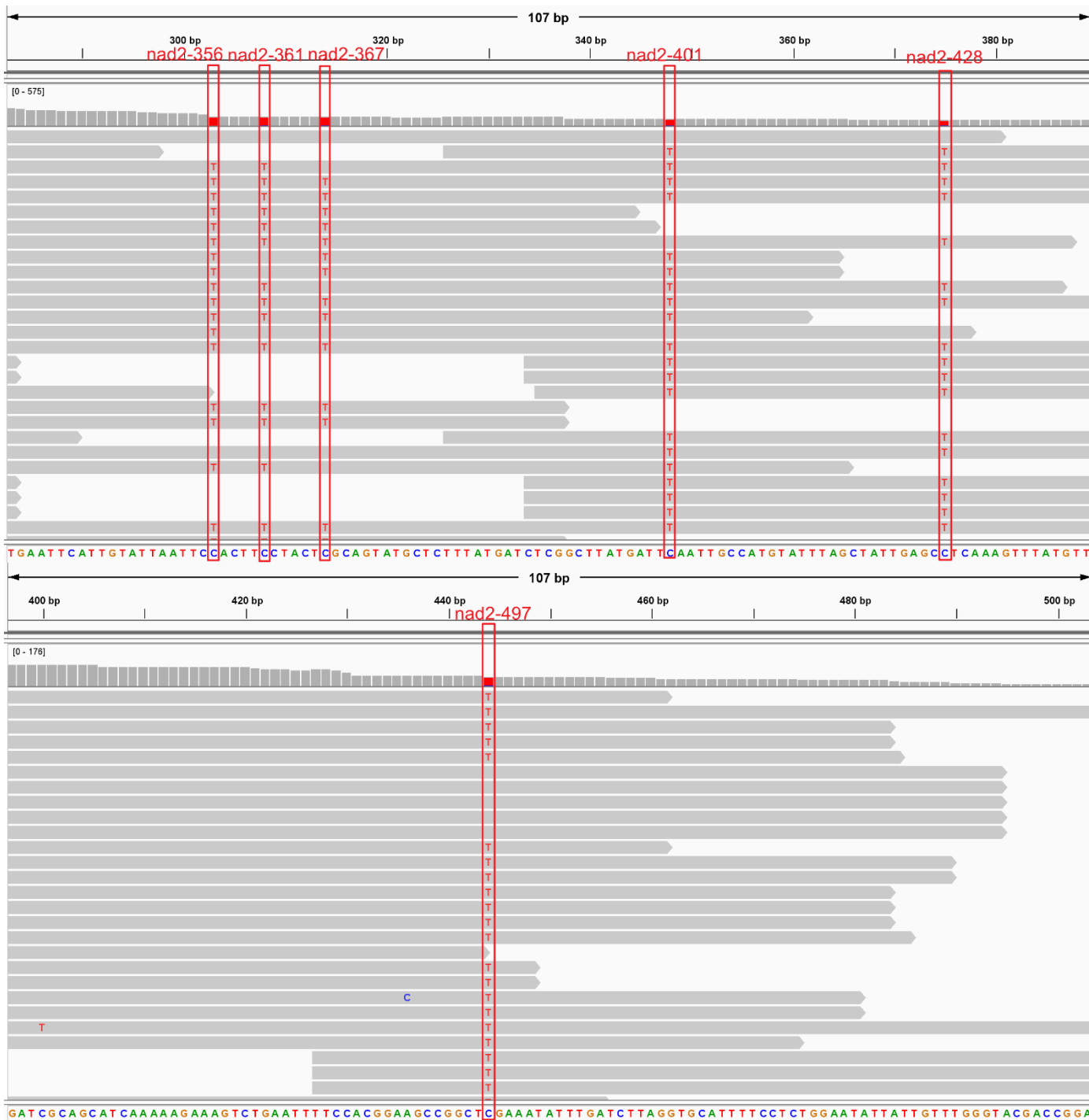


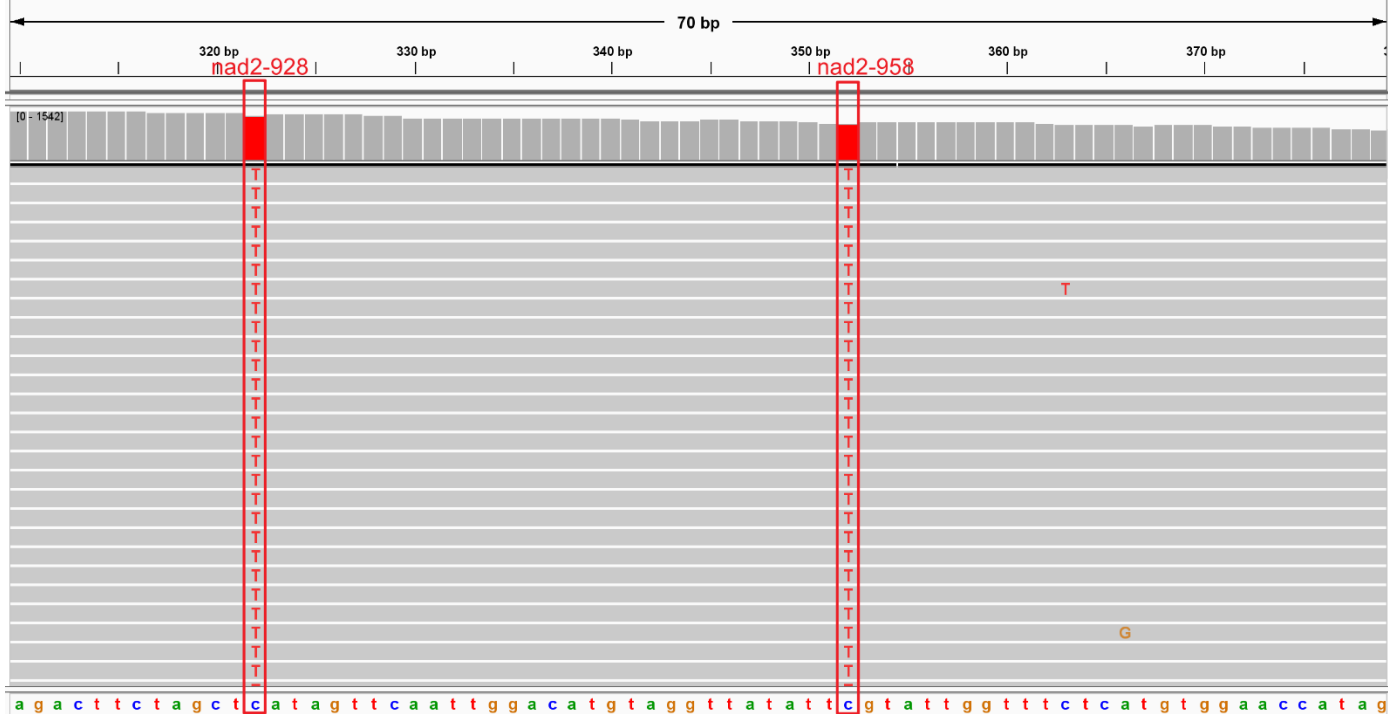
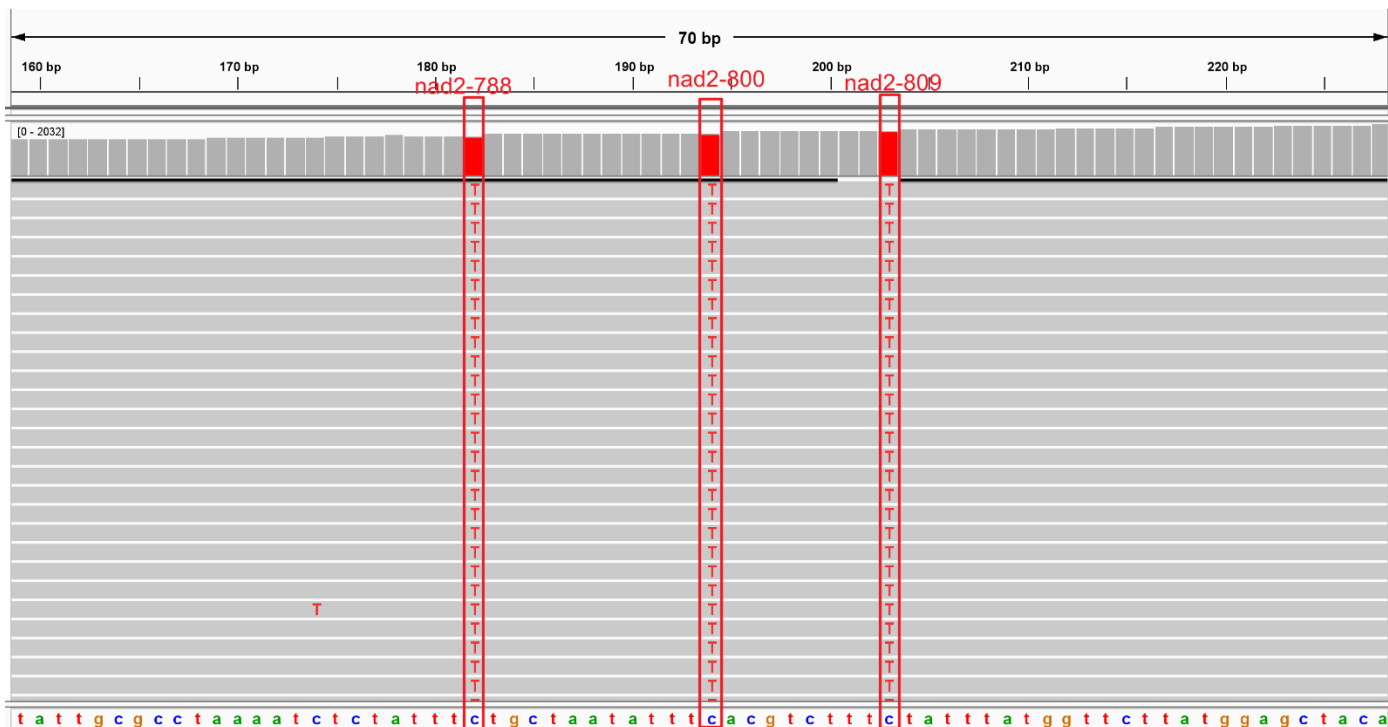


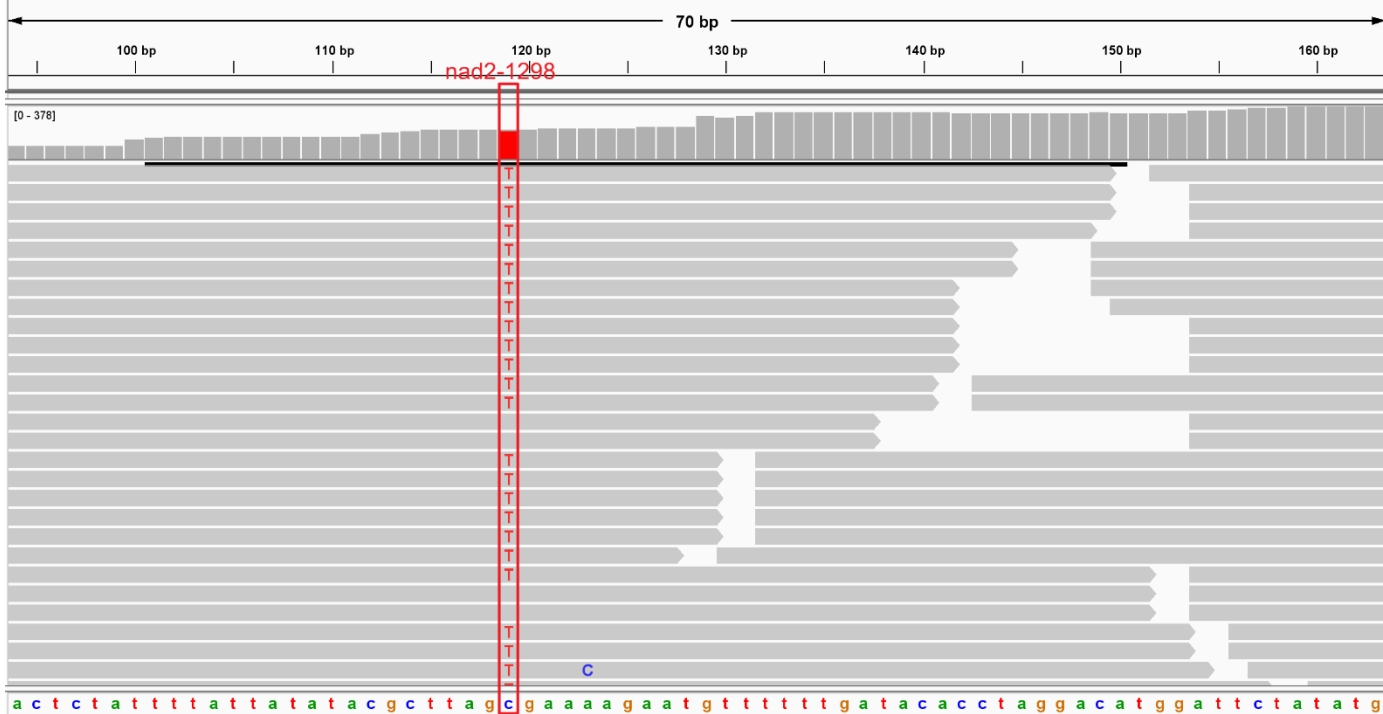
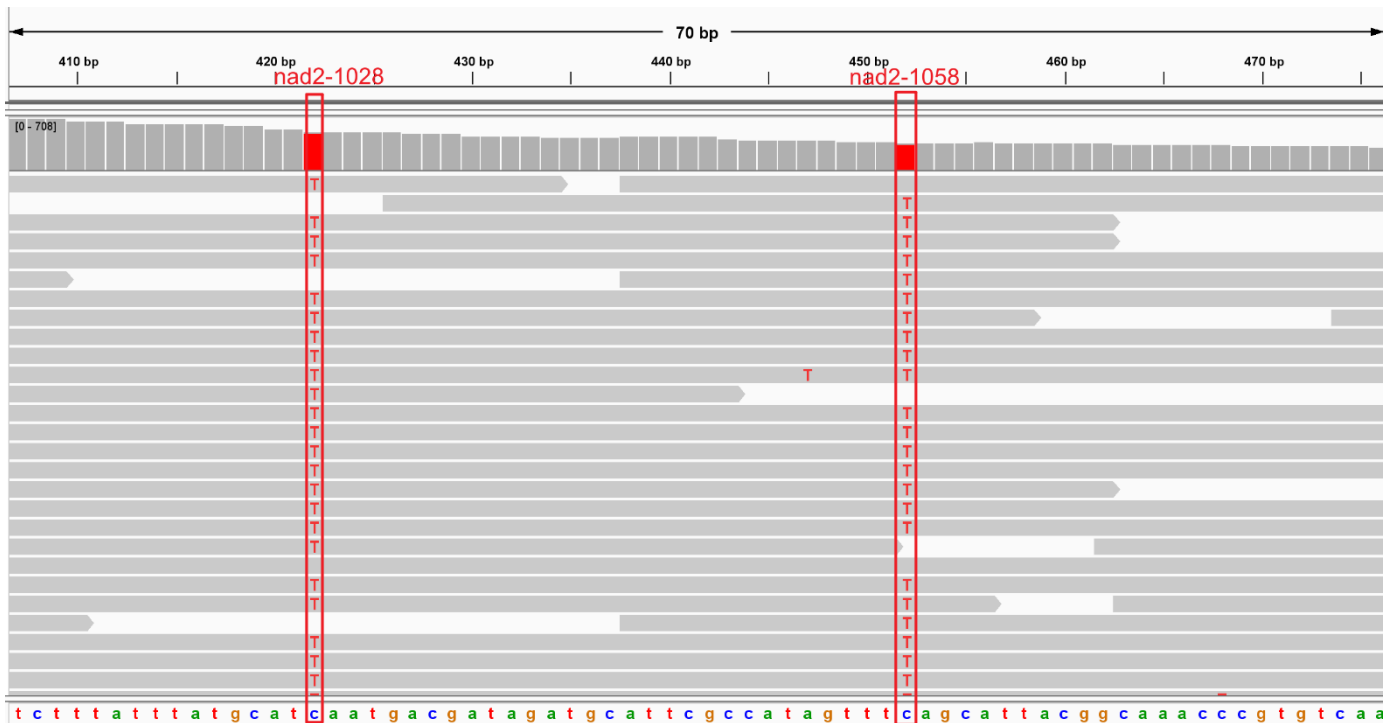


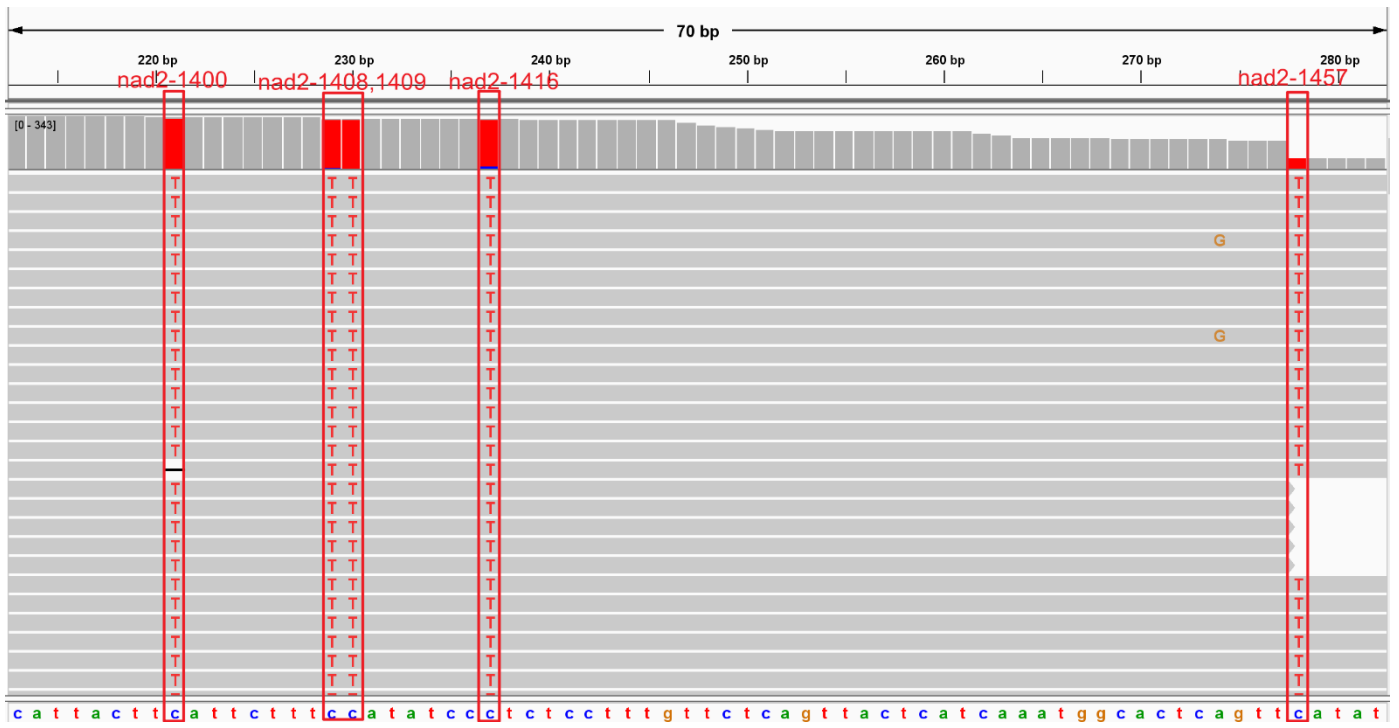
p alignment of RNA-seq reads to the coding sequence of *nad2*. 25 RNA-seq editing sites: *nad2*-26, 223, 252, 303, 308, 311, 356, 361, 367, 401, 428, 497, 788, 800, 809, 928, 958, 1028, 1058, 1298, 1400, 1408, 1409, 1416, 1457 were highlighted in red squares.





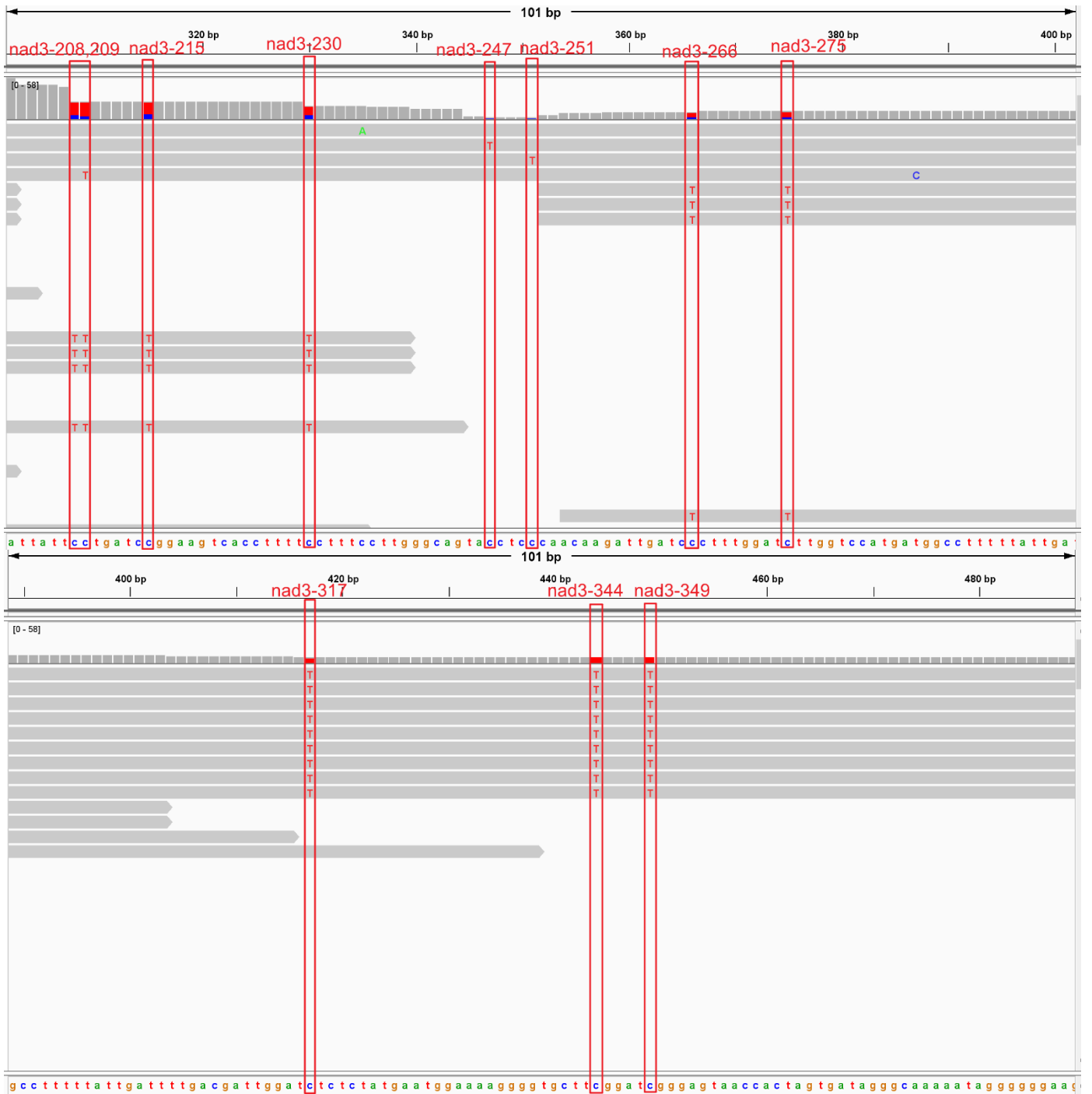




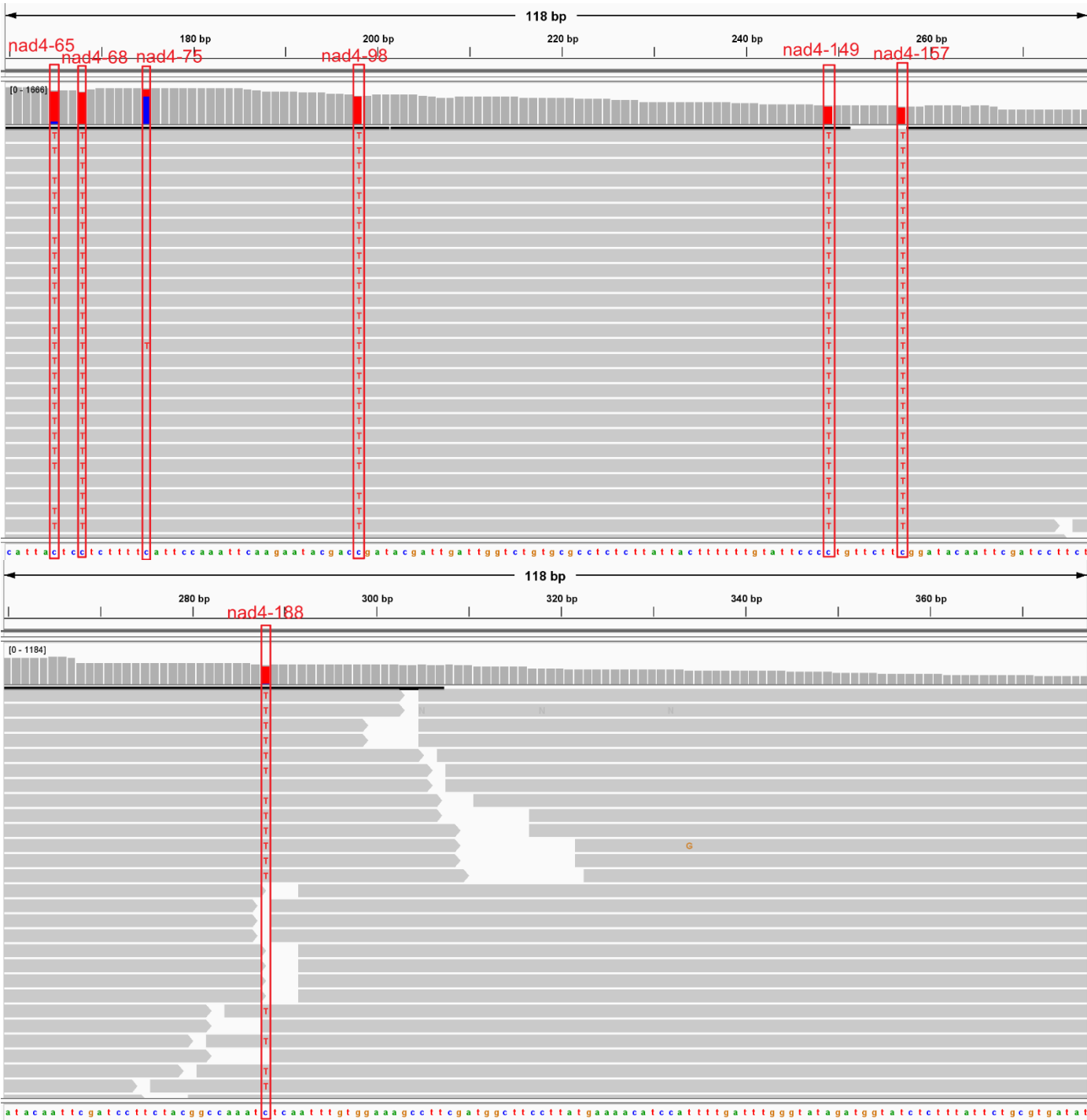


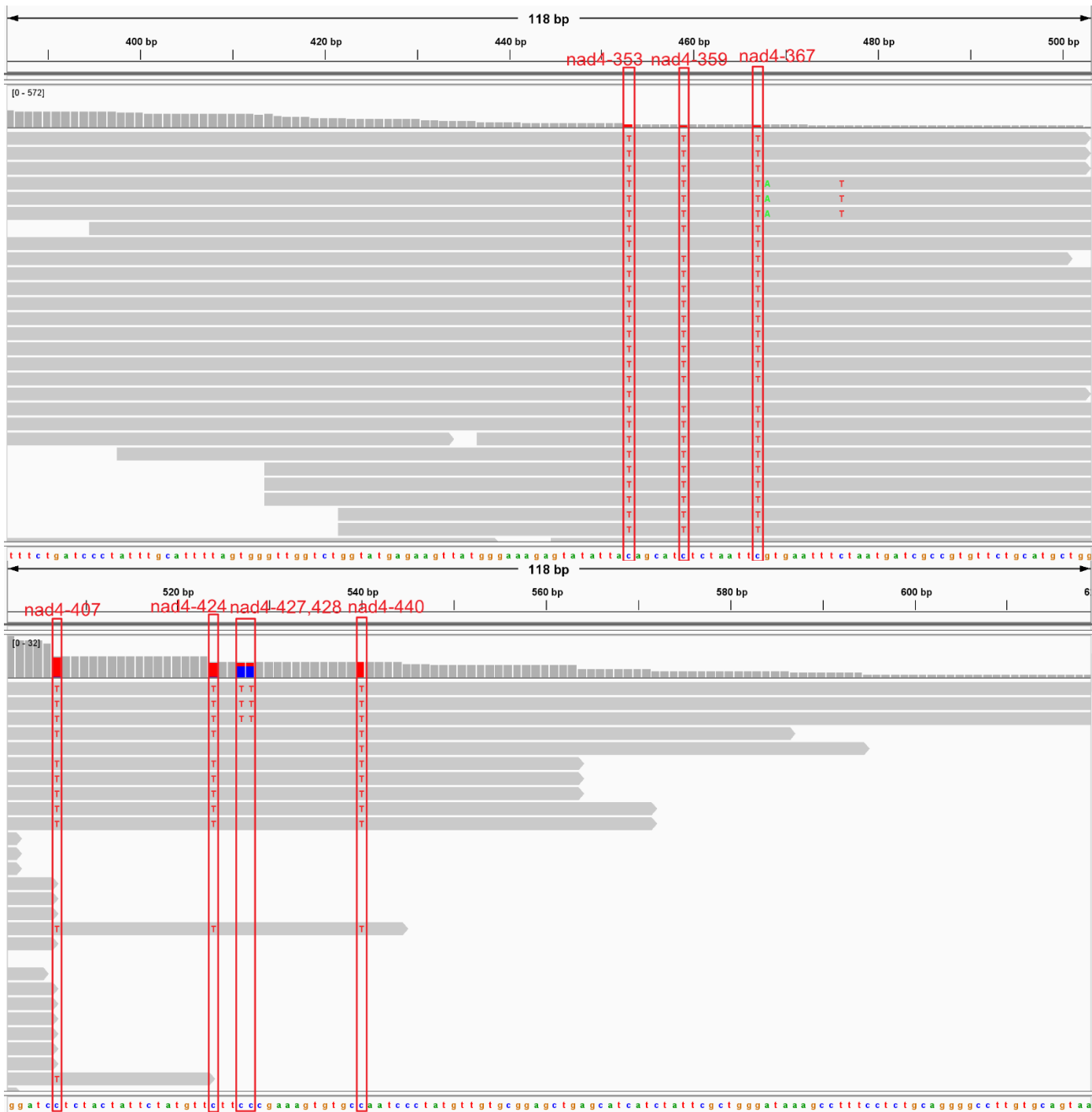
q alignment of RNA-seq reads to the coding sequence of *nad3*. 17 RNA-seq editing sites: *nad3*-44, 62, 79, 80, 124, 146, 208, 209, 215, 230, 247, 251, 266, 275, 317, 344, 349 were highlighted in red squares.

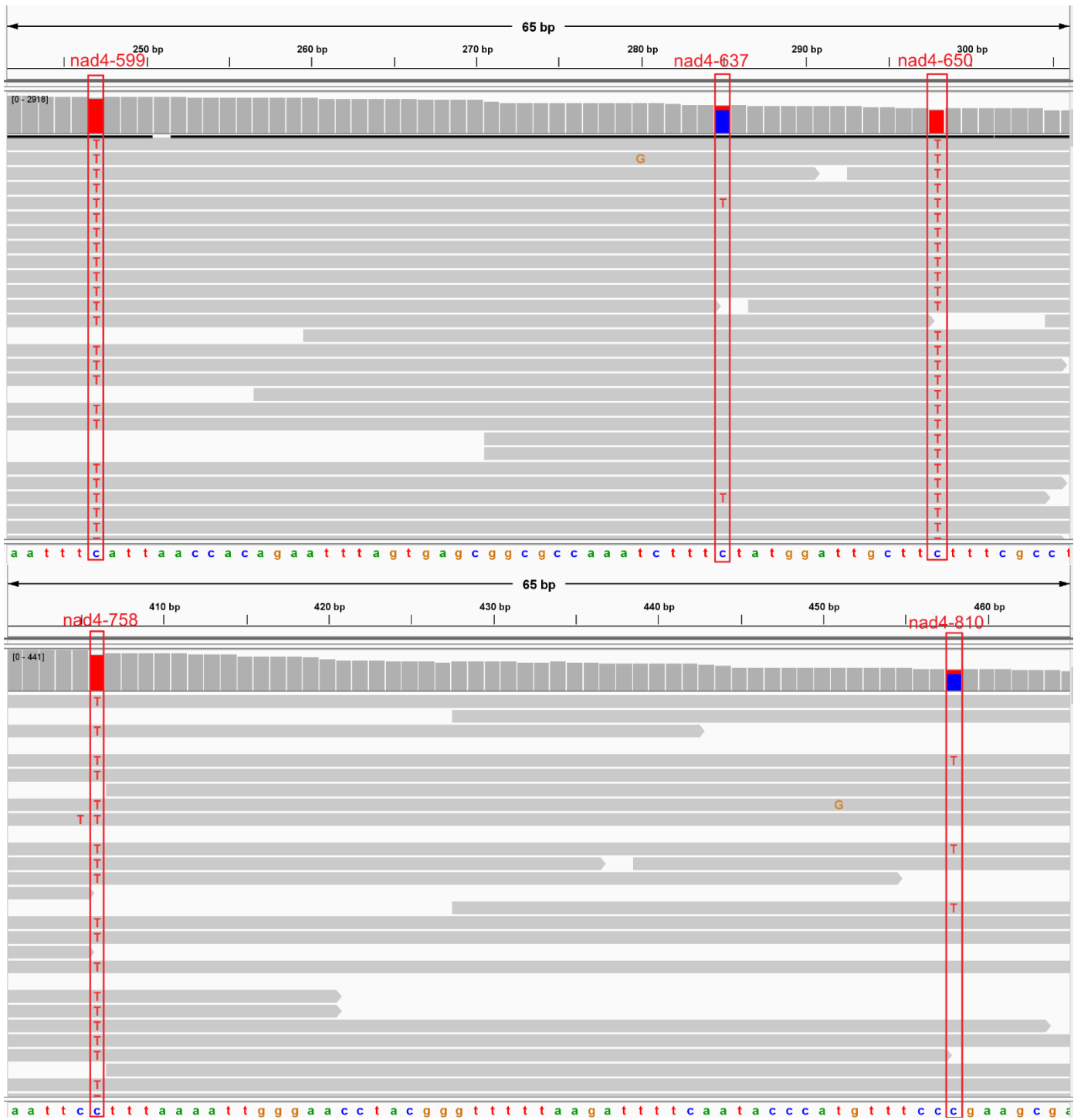


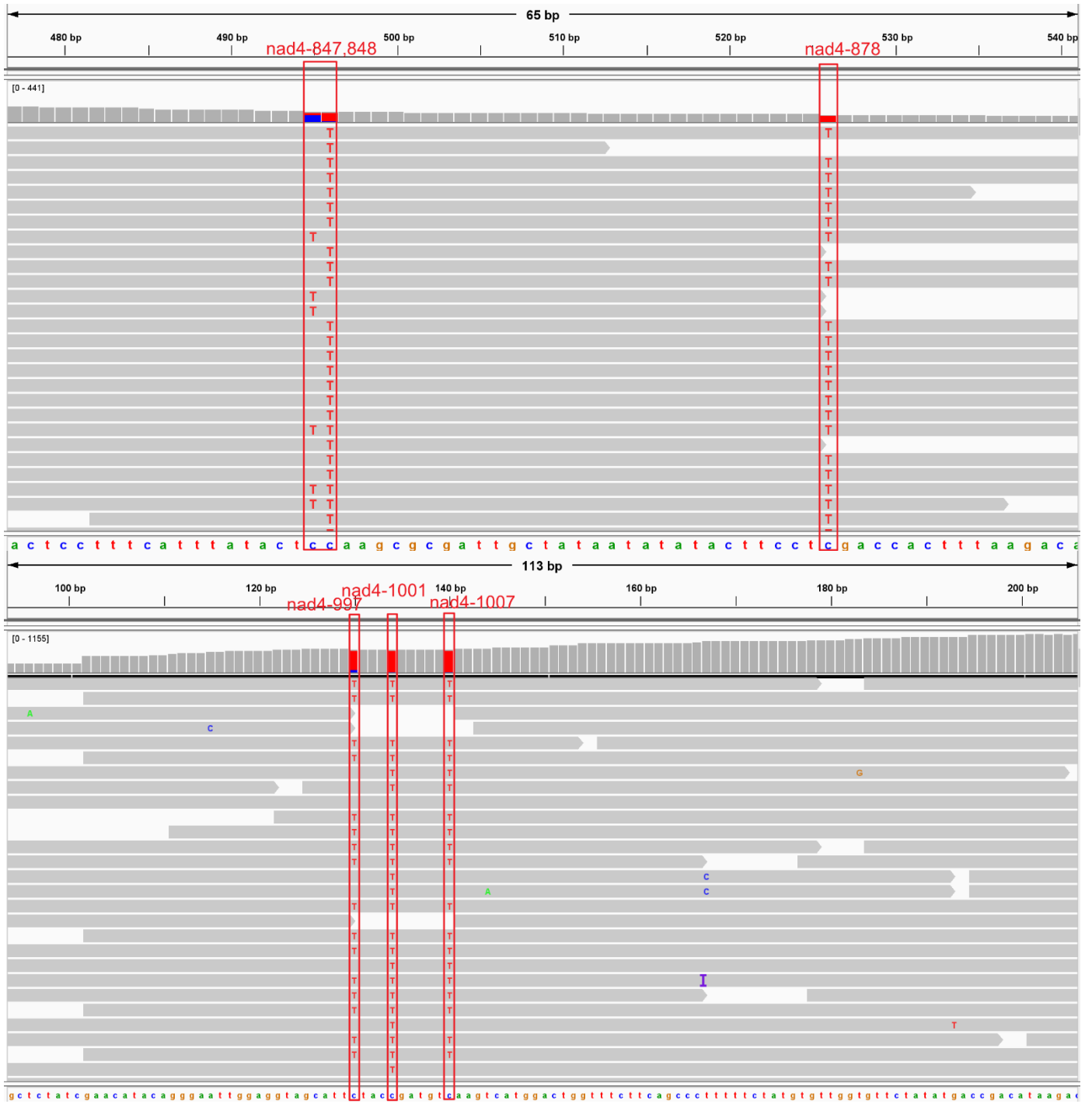


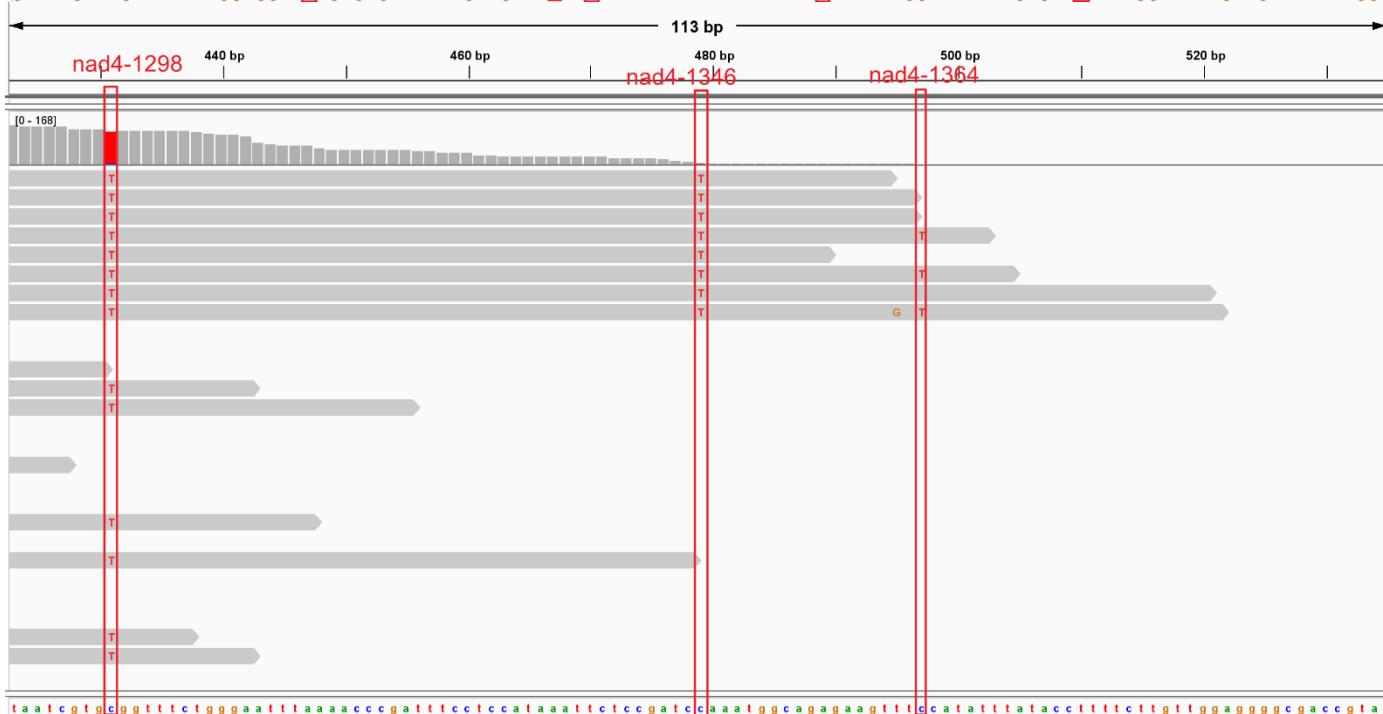
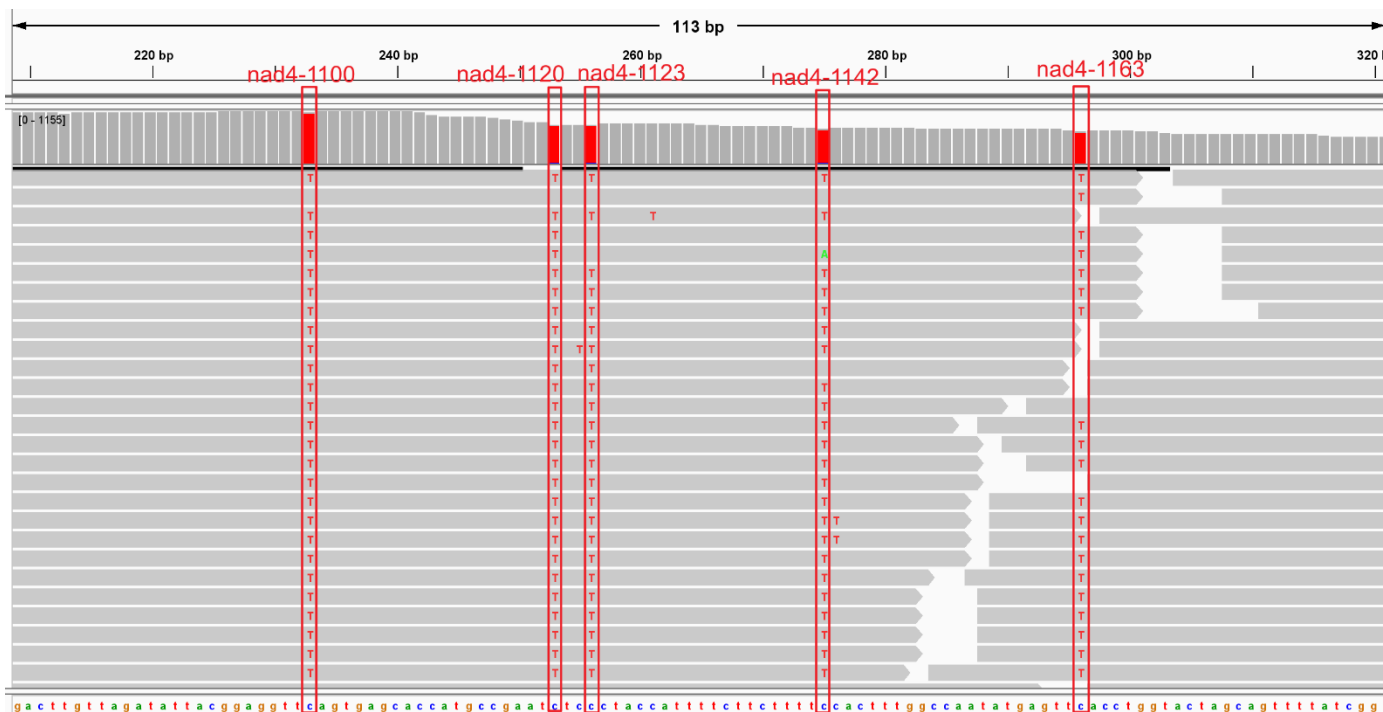
r alignment of RNA-seq reads to the coding sequence of *nad4*. 36 RNA-seq editing sites: *nad4*-65, 68, 75, 98, 149, 157, 188, 353, 359, 367, 407, 424, 427, 428, 440, 599, 637, 650, 758, 810, 847, 848, 878, 997, 1001, 1007, 1100, 1120, 1123, 1142, 1163, 1298, 1346, 1364, 1408, 1424 were highlighted in red squares.

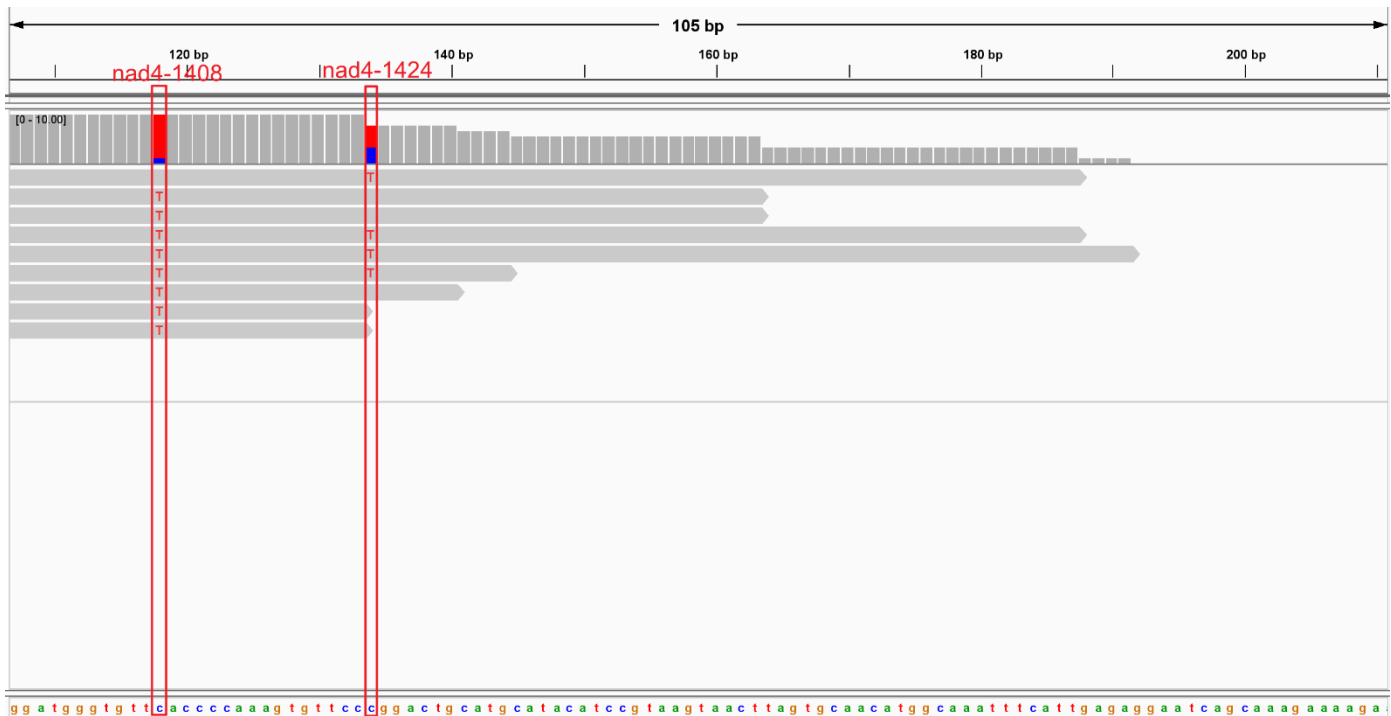




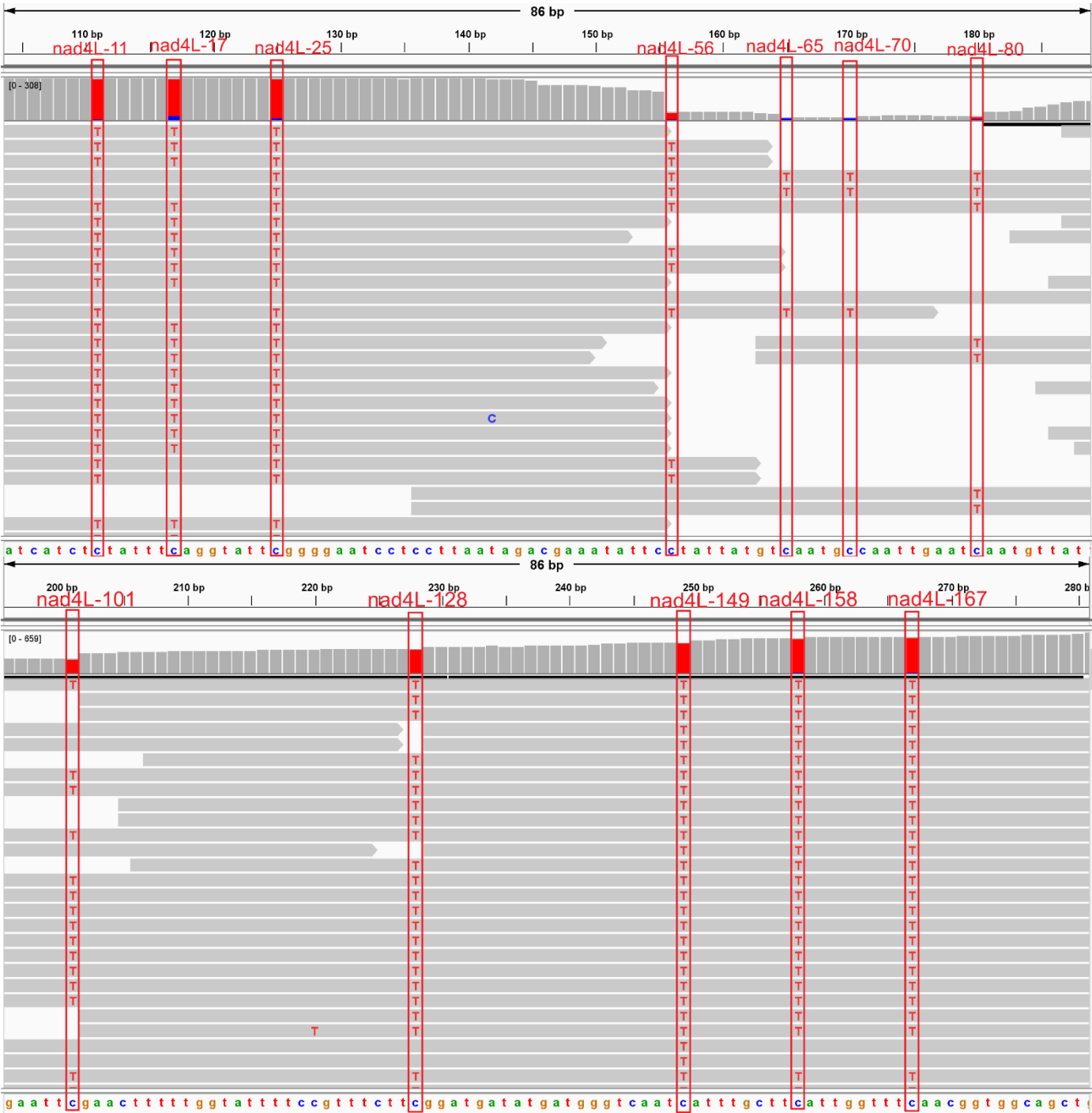


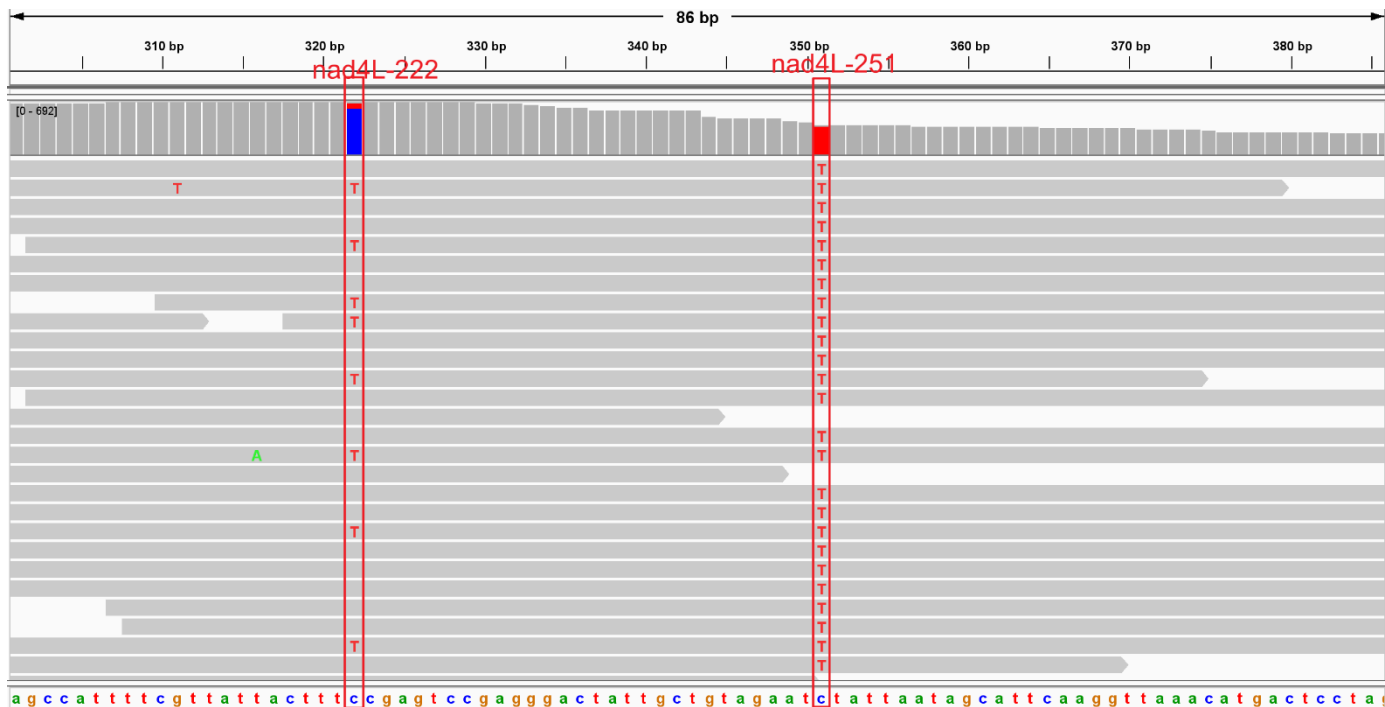




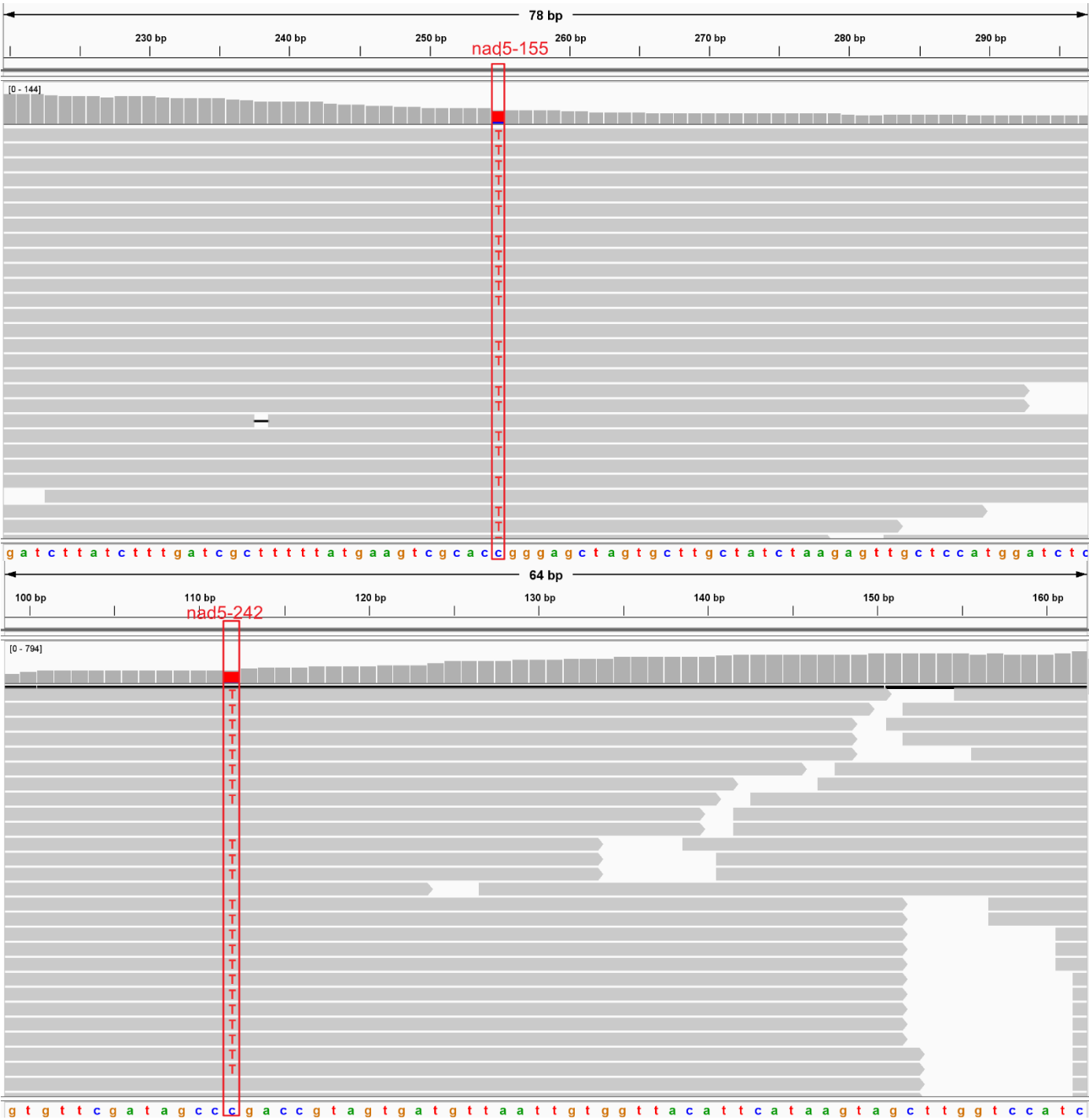


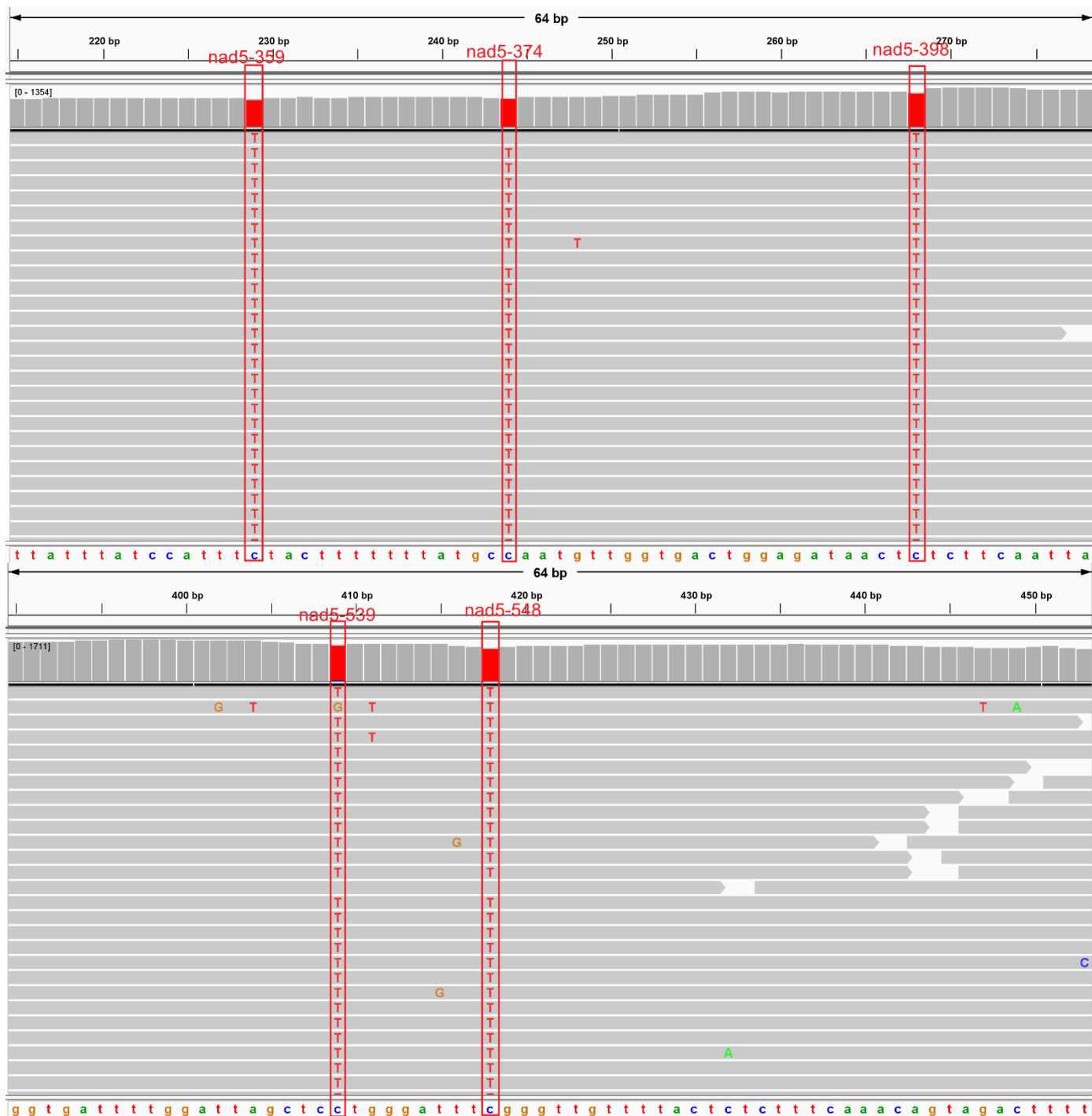
s alignment of RNA-seq reads to the coding sequence of *nad4L*. 14 RNA-seq editing sites: *nad4L*-11, 17, 25, 56, 65, 70, 80, 101, 128, 149, 158, 167, 222, 251 were highlighted in red squares.

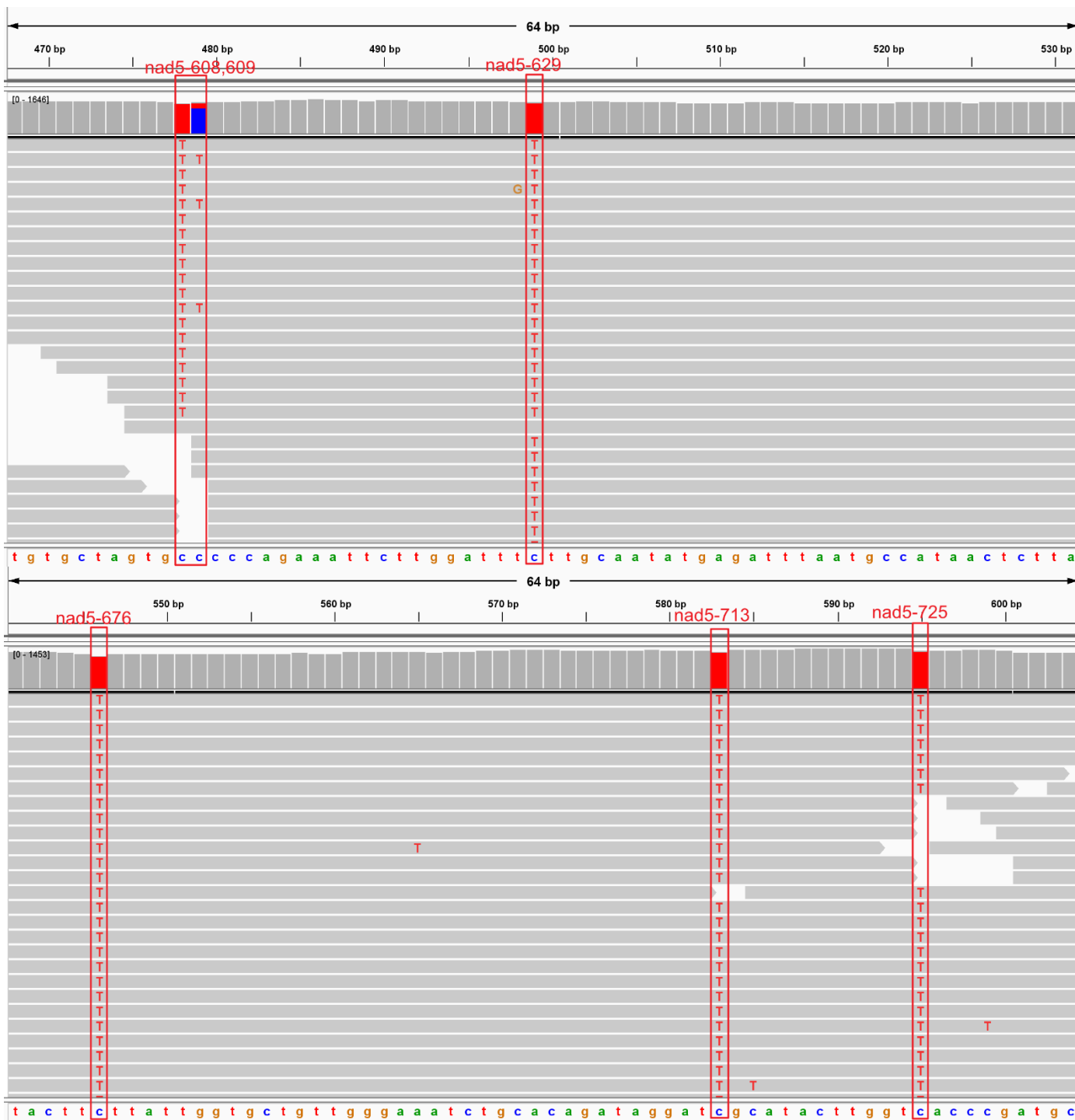


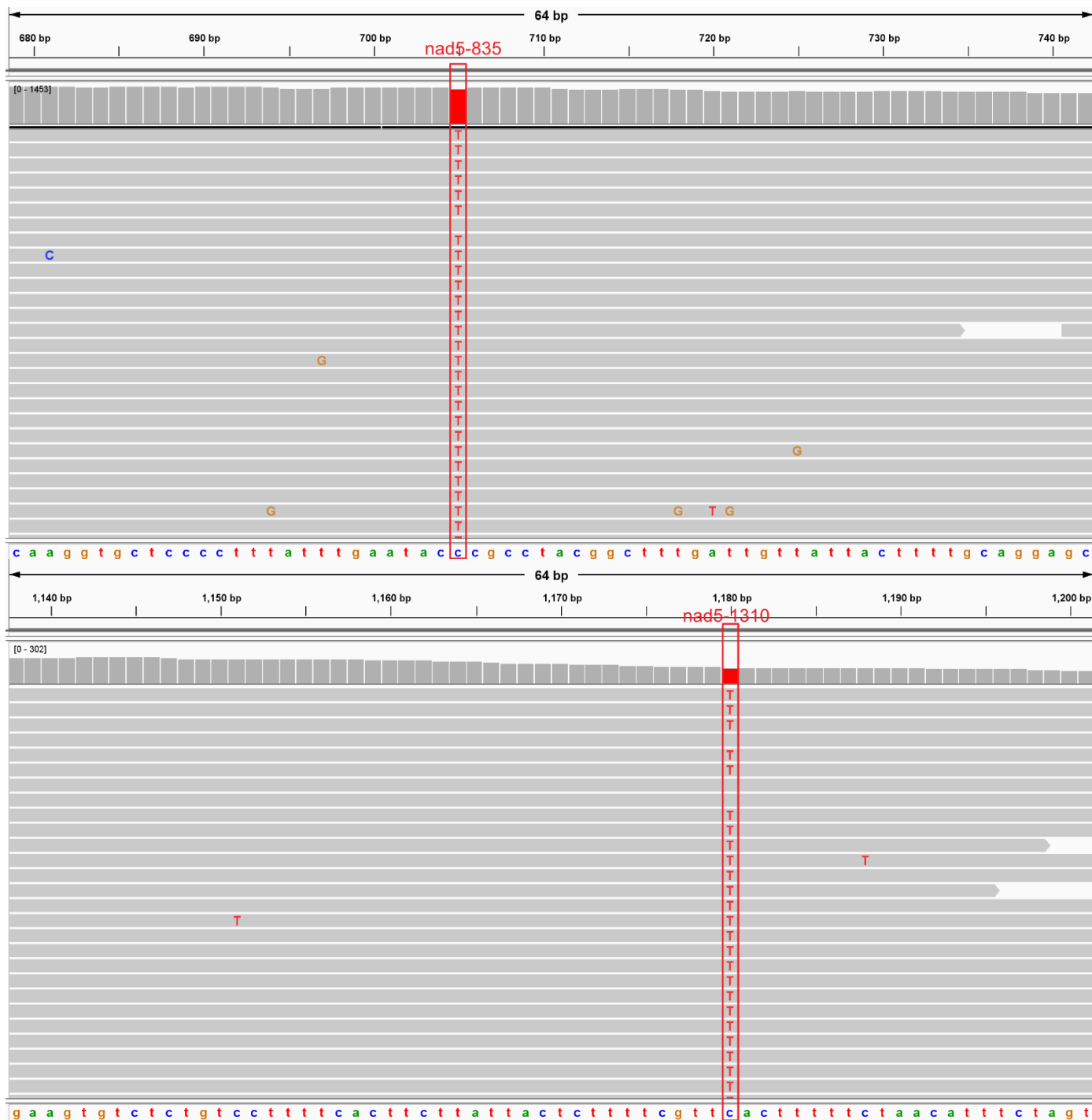


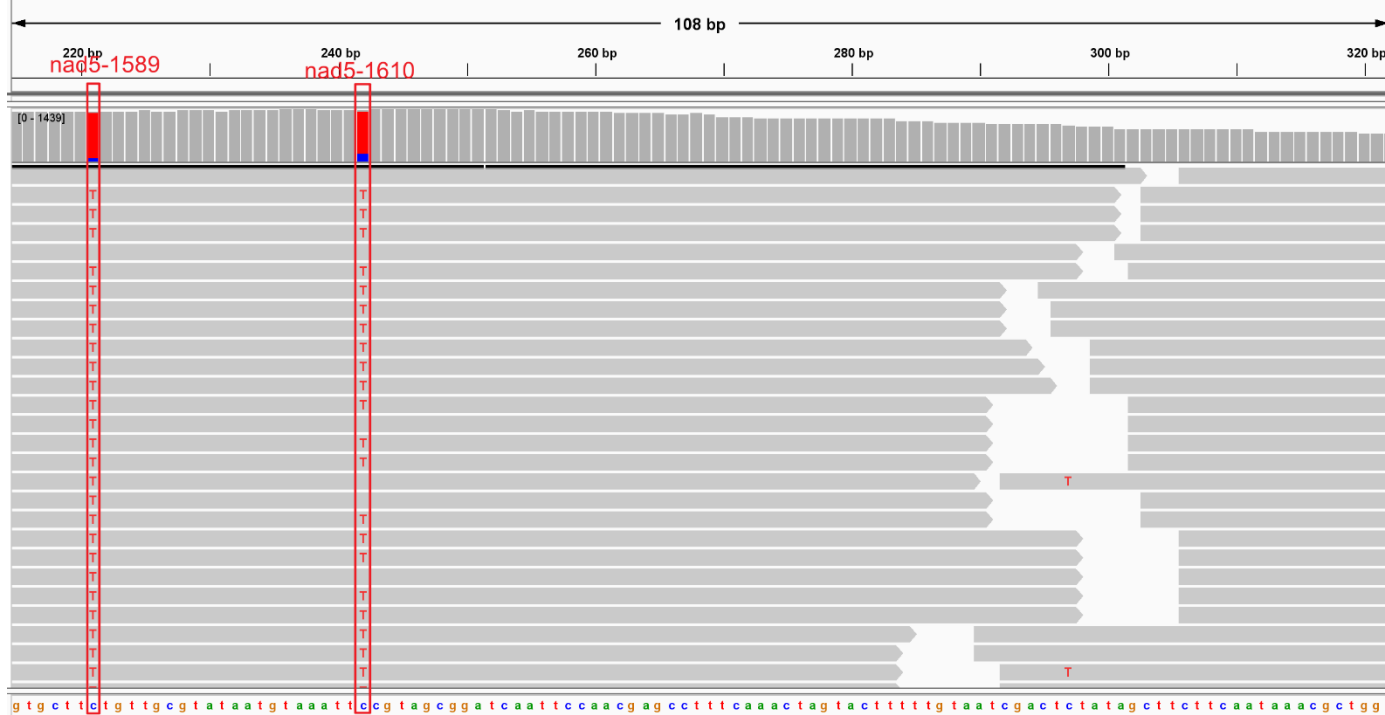
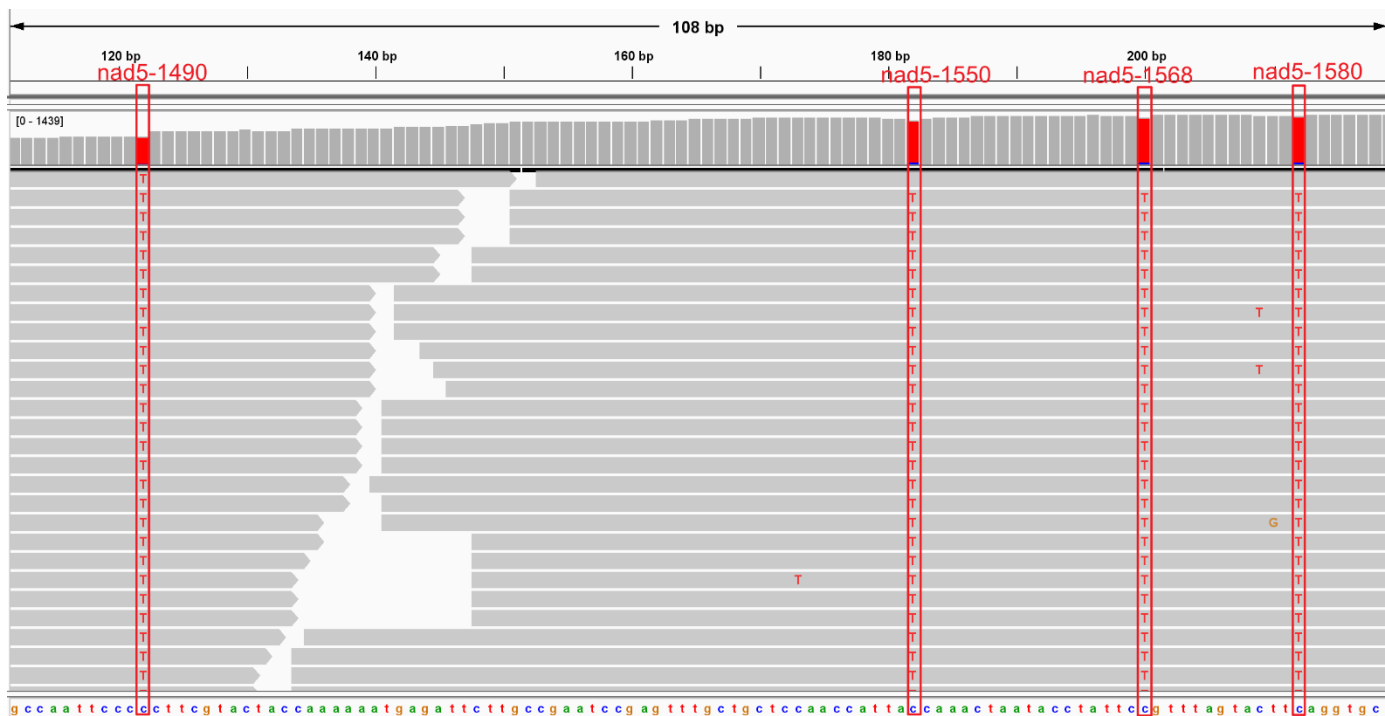
t alignment of RNA-seq reads to the coding sequence of *nad5*. 27 RNA-seq editing sites: *nad5*-155, 242, 359, 374, 398, 539, 548, 608, 609, 629, 676, 713, 725, 835, 1310, 1490, 1550, 1568, 1580, 1589, 1610, 1695, 1895, 1916, 1918, 1958, 1981 were highlighted in red squares.

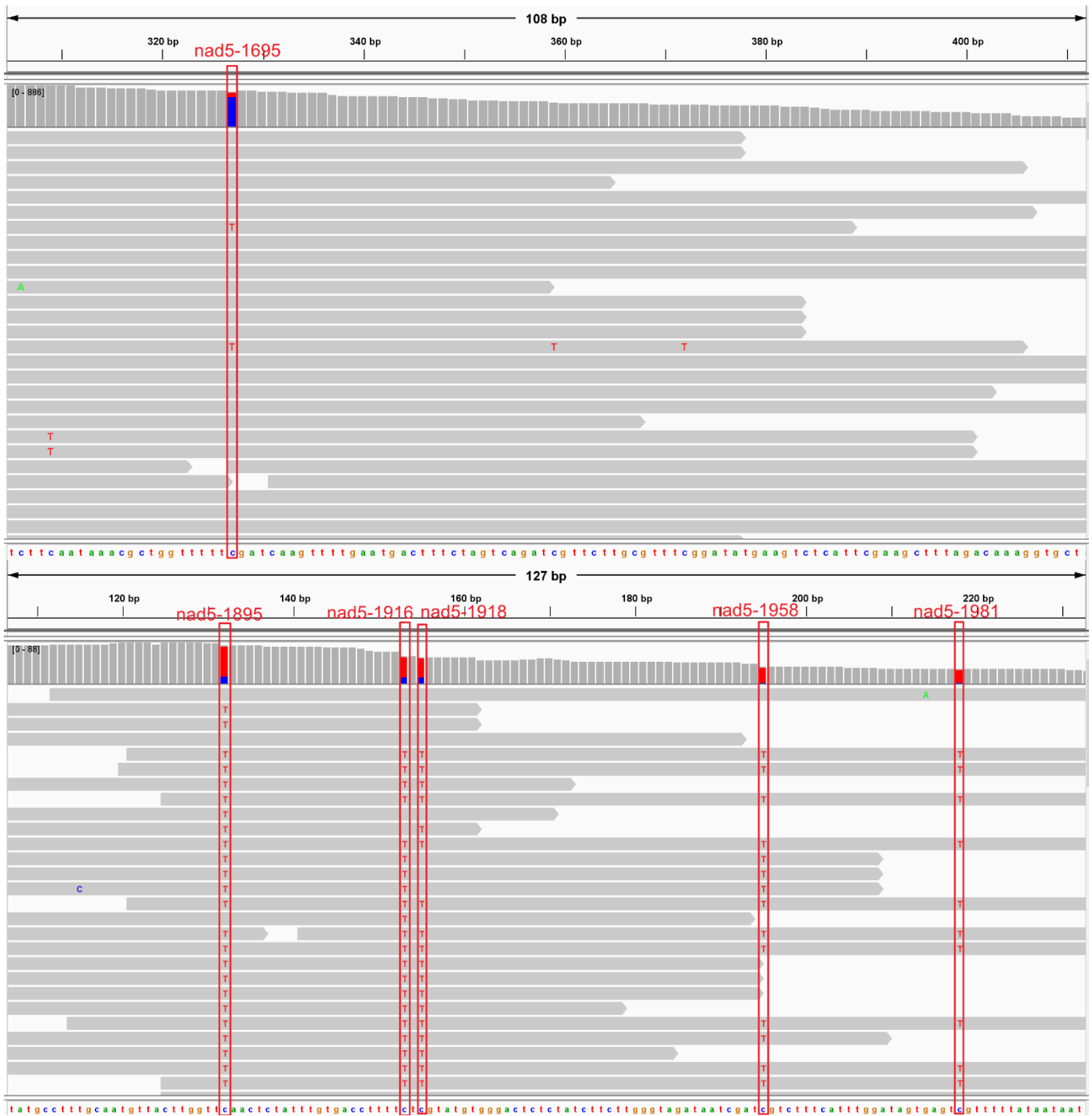




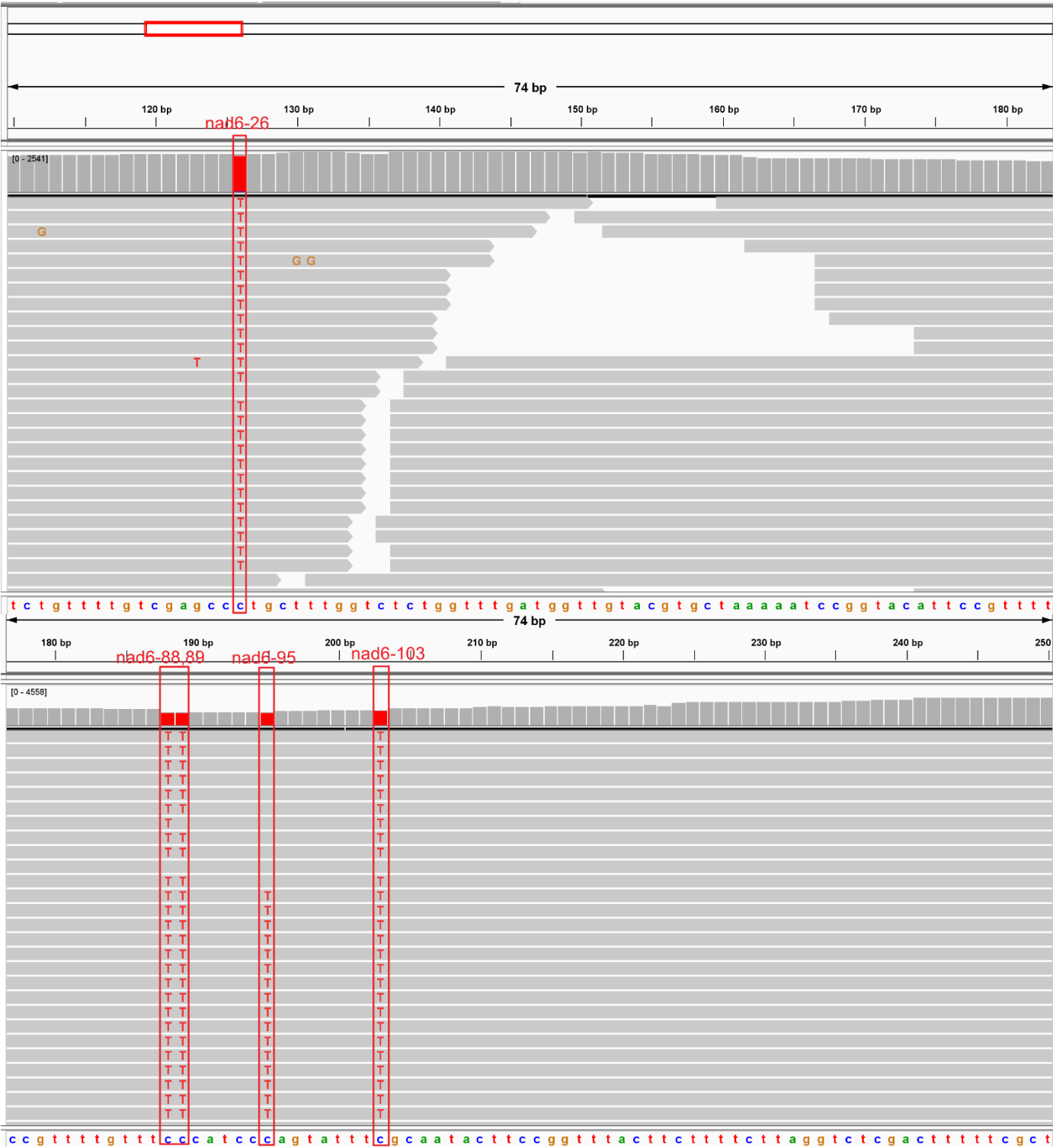


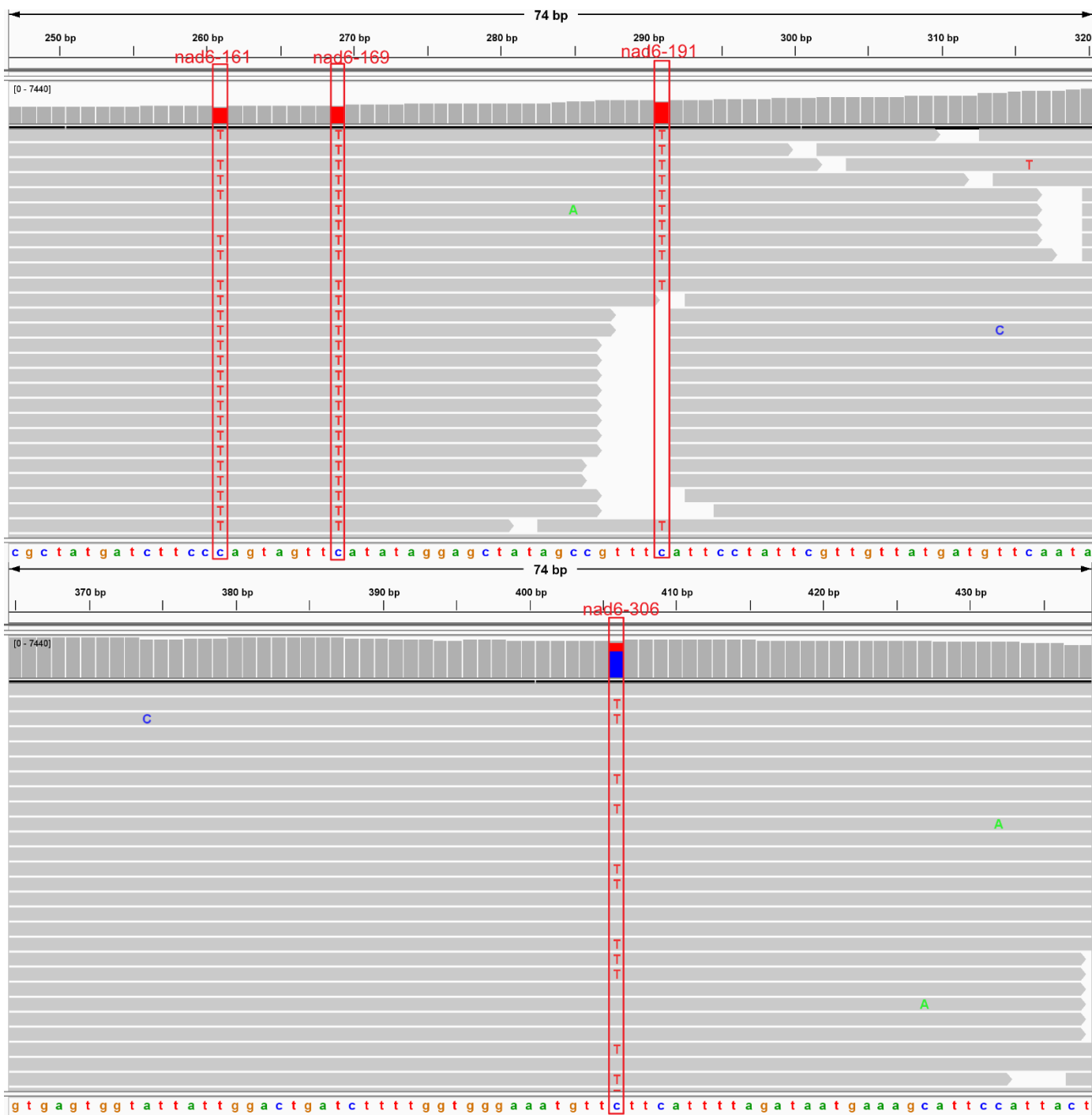


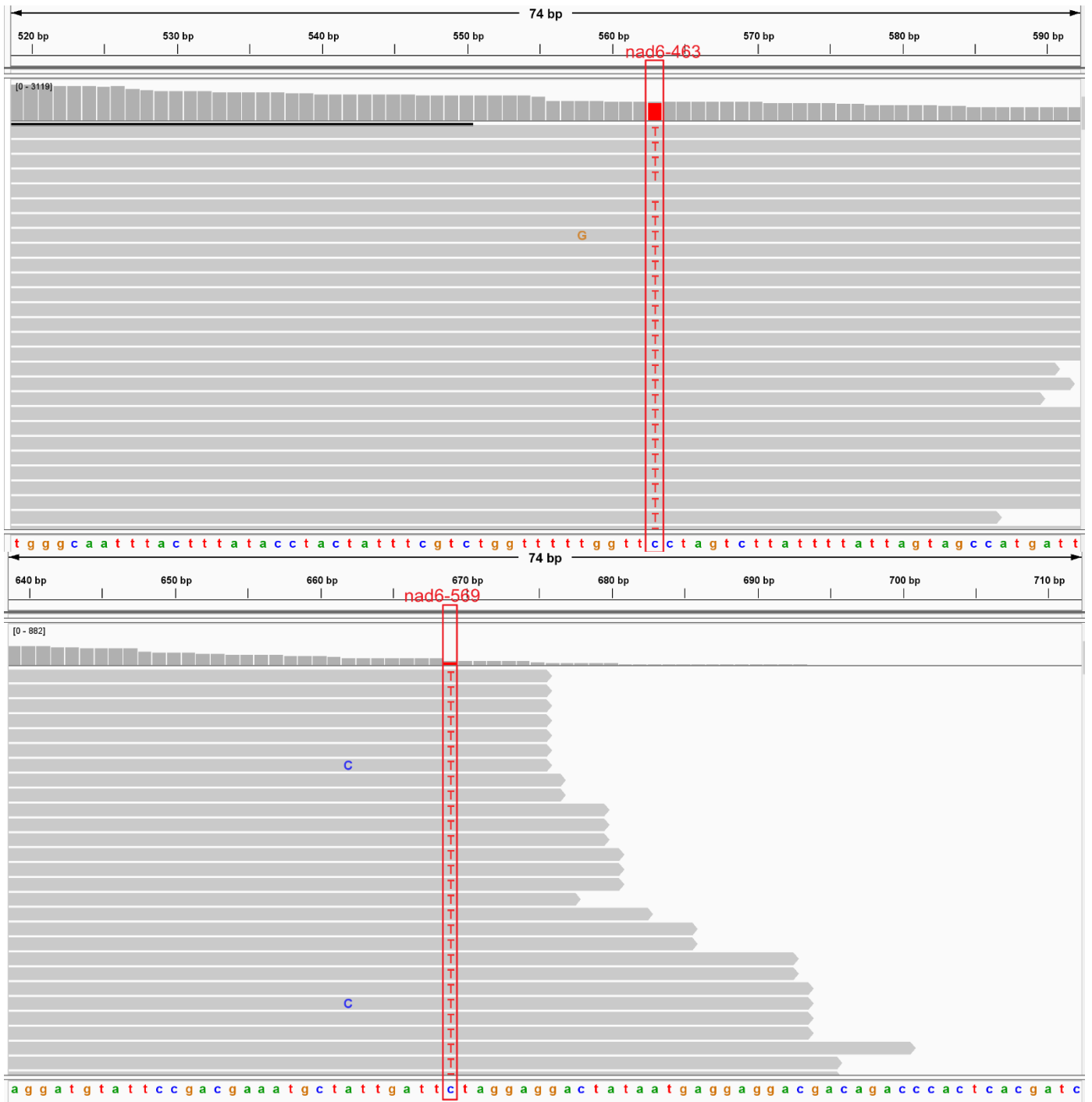




u alignment of RNA-seq reads to the coding sequence of *nad6*. 11 RNA-seq editing sites: *nad6*-26, 88, 89, 95, 103, 161, 169, 191, 306, 463, 569 were highlighted in red squares.

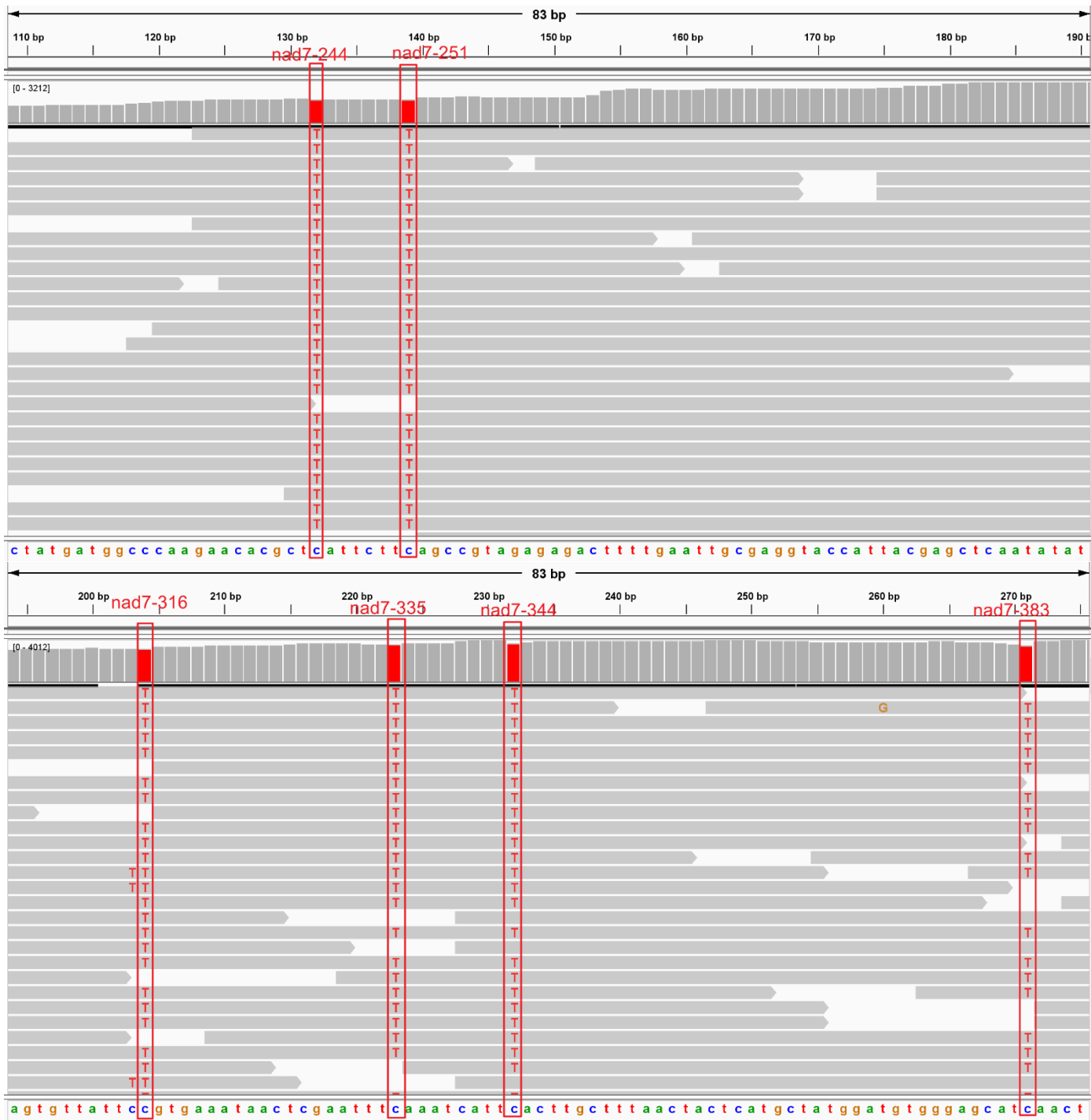


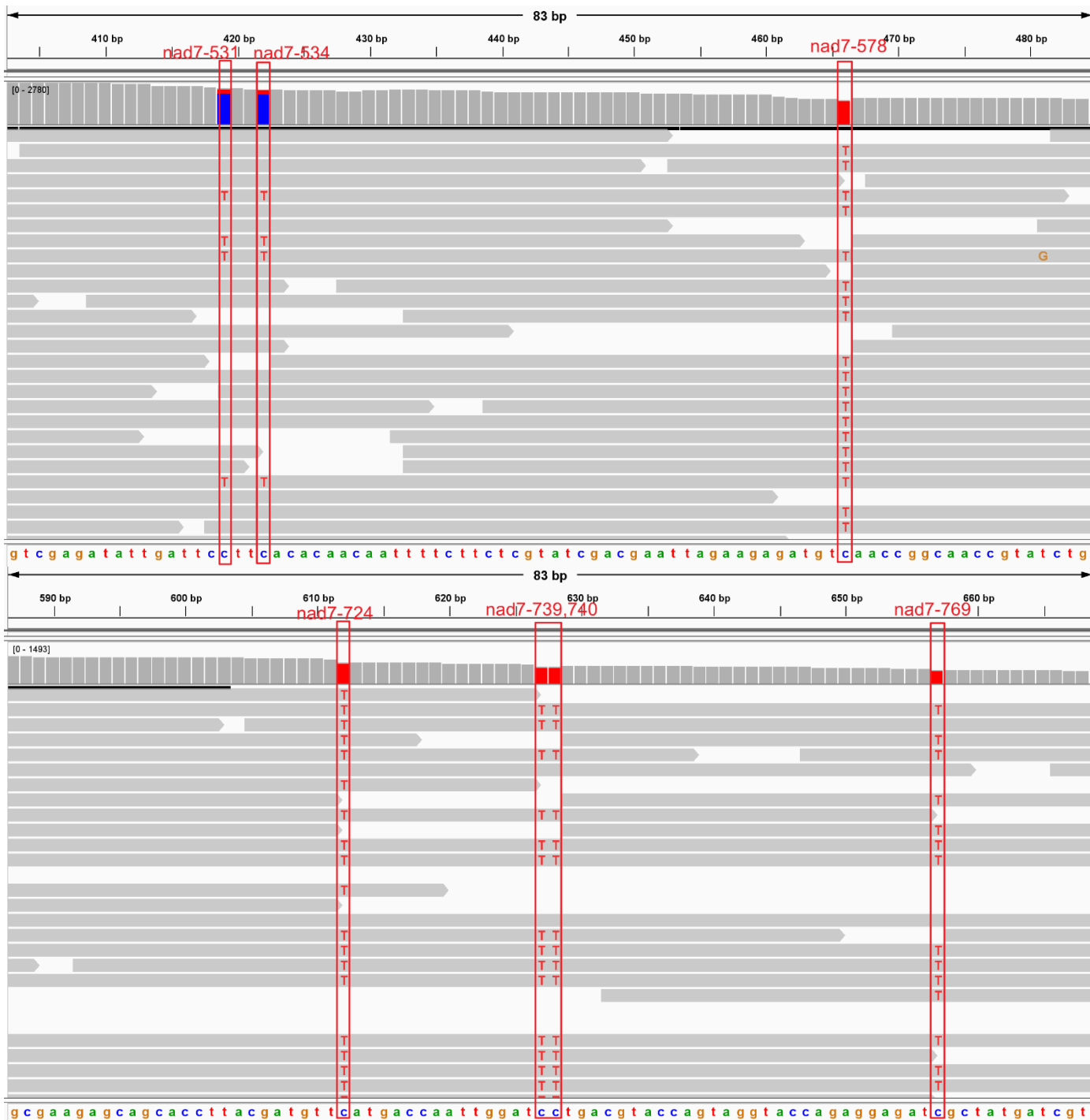


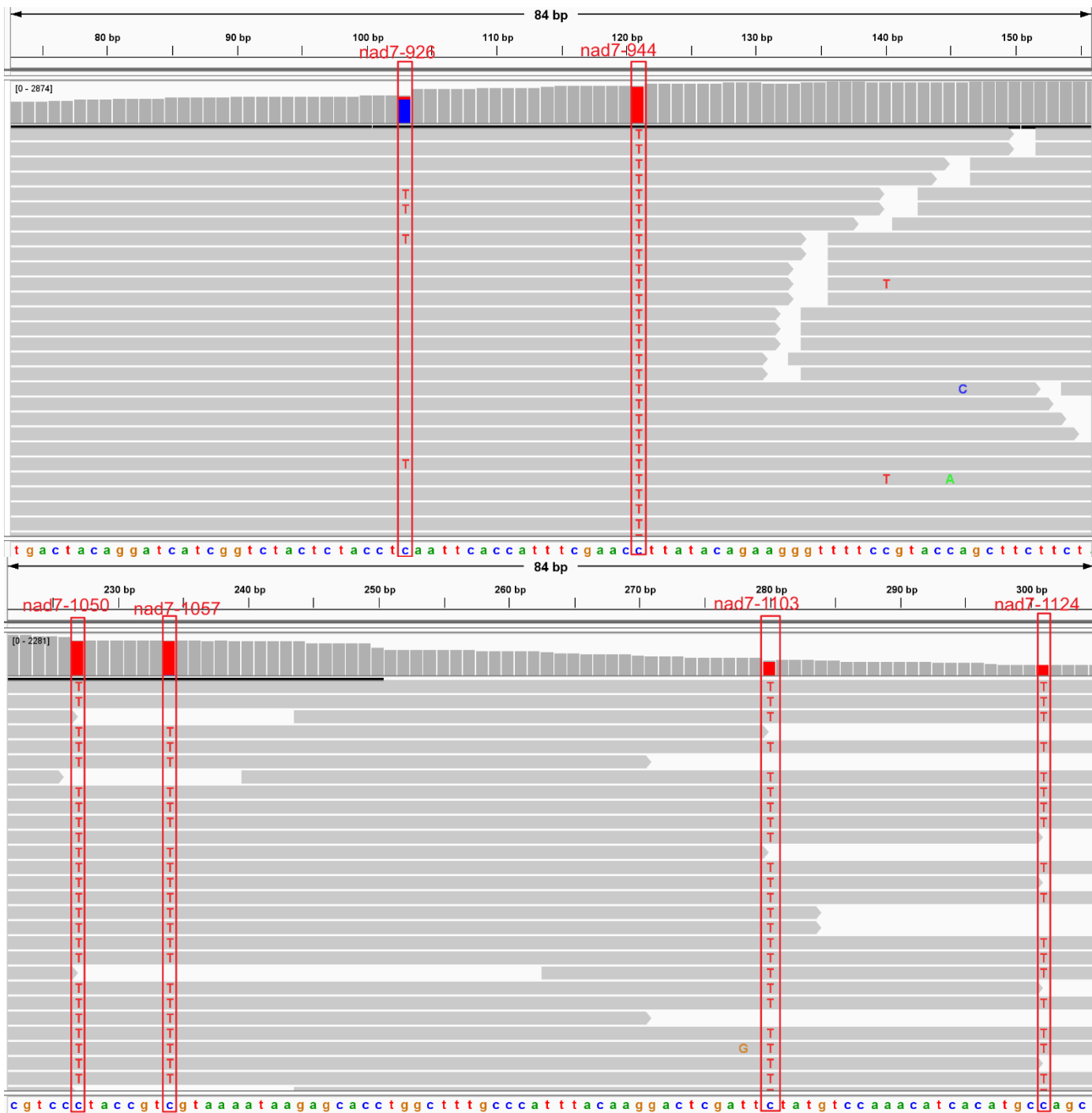


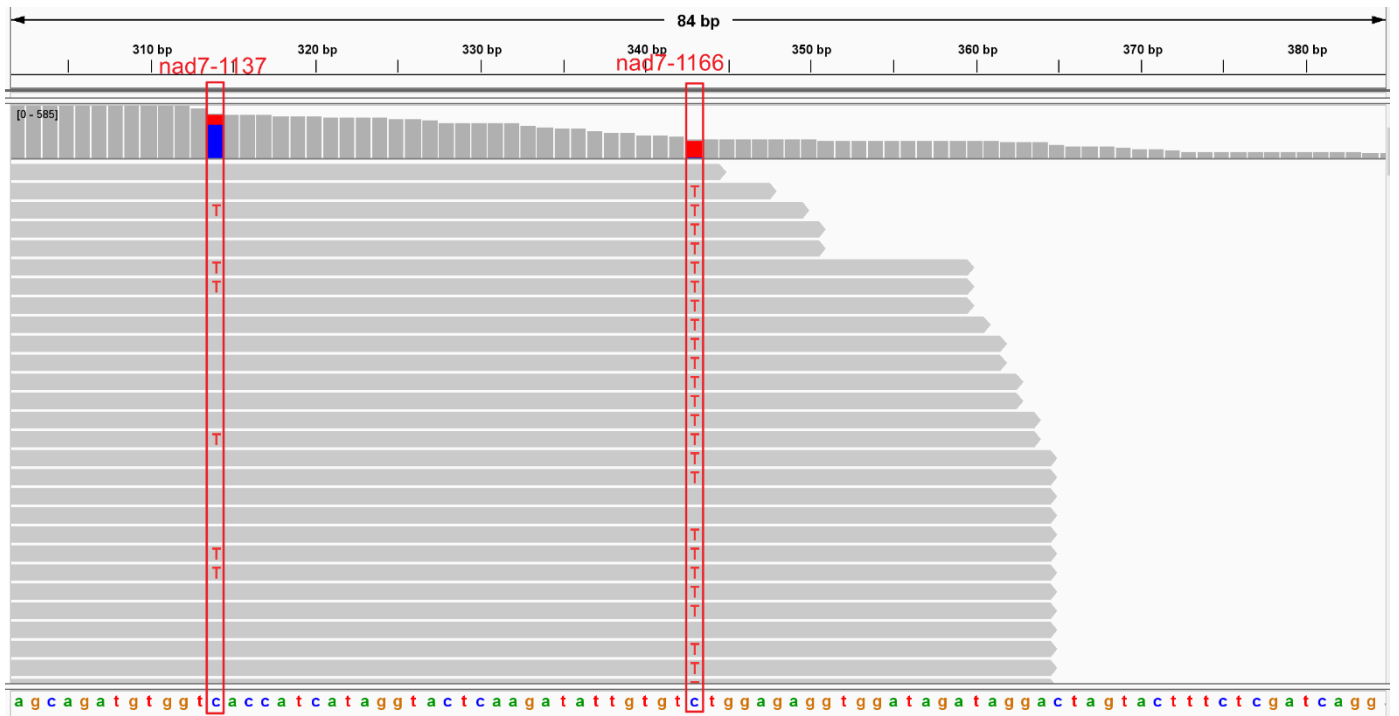
v alignment of RNA-seq reads to the coding sequence of *nad7*. 26 RNA-seq editing sites: *nad7*-45, 77, 137, 200, 209, 244, 251, 316, 335, 344, 383, 531, 534, 578, 724, 739, 740, 769, 926, 944, 1050, 1057, 1103, 1124, 1137, 1166 were highlighted in red squares.



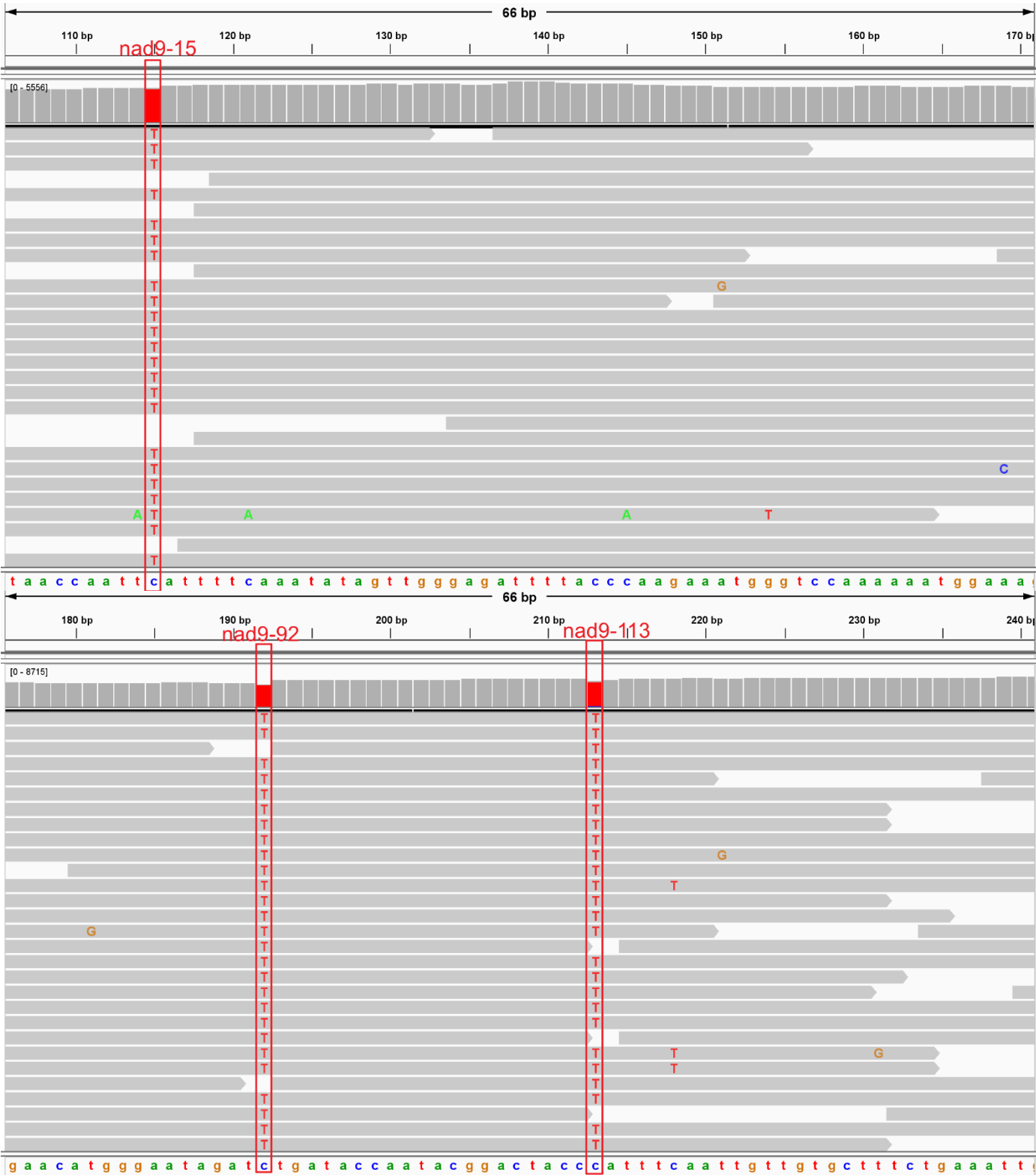


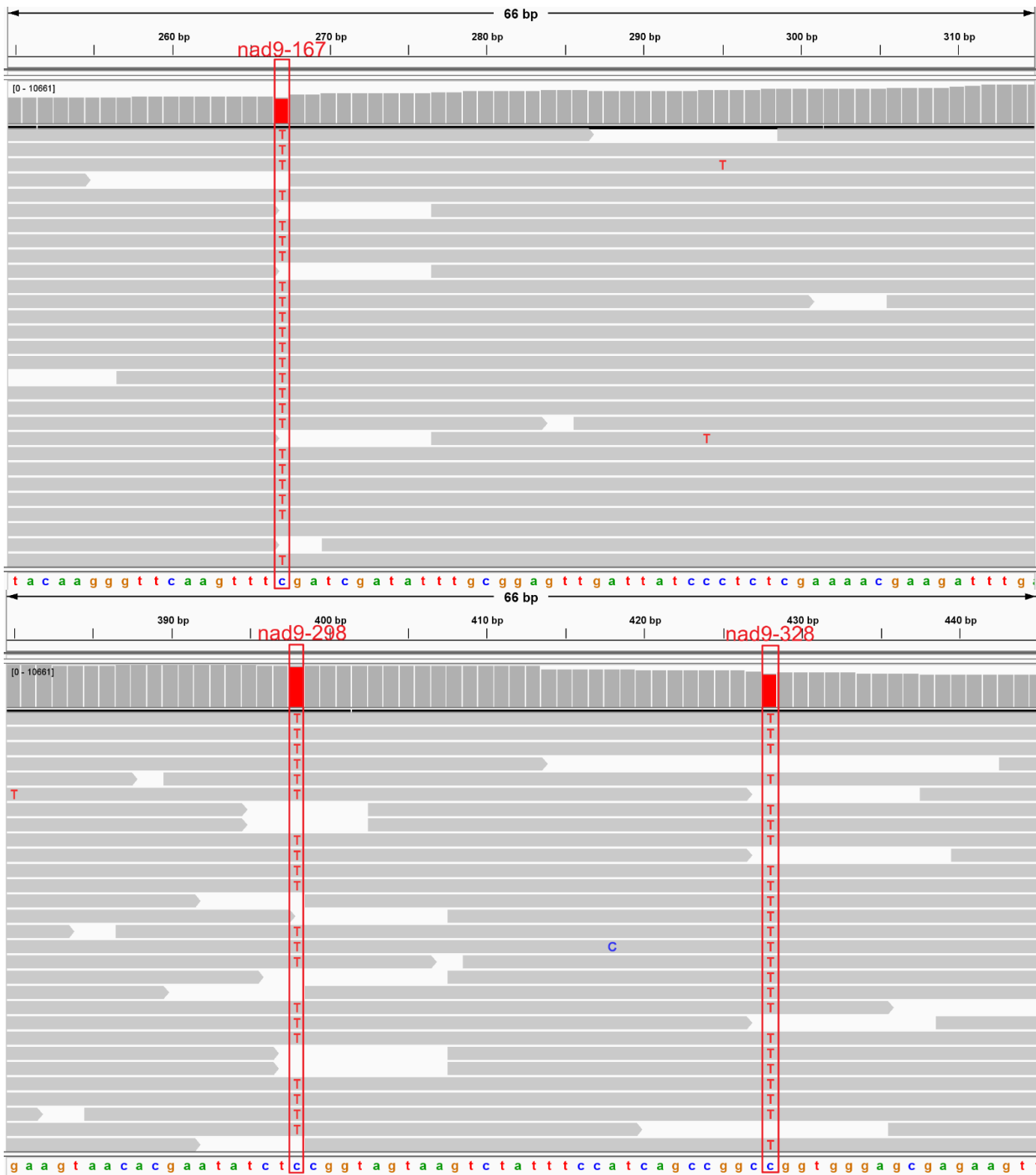


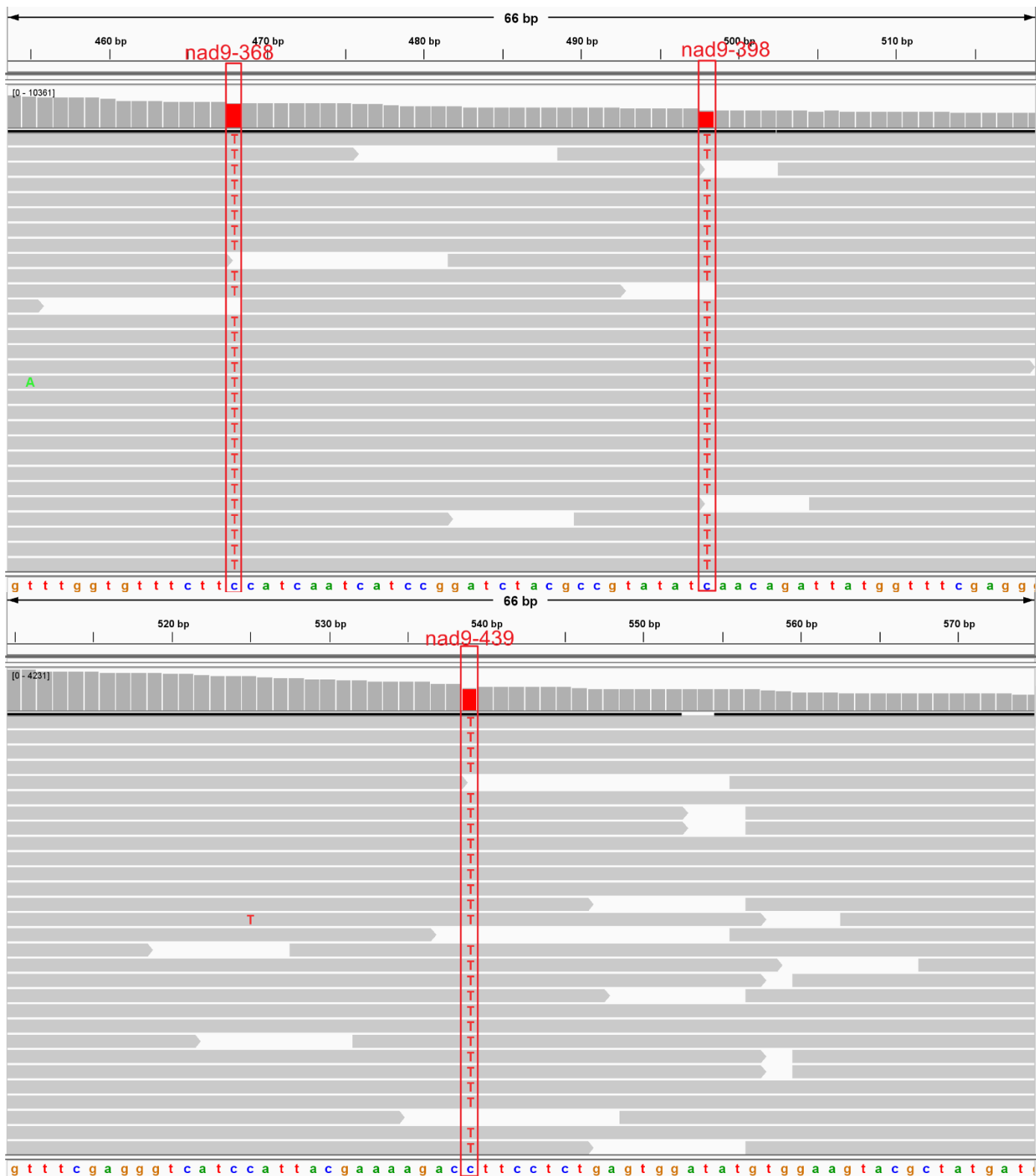




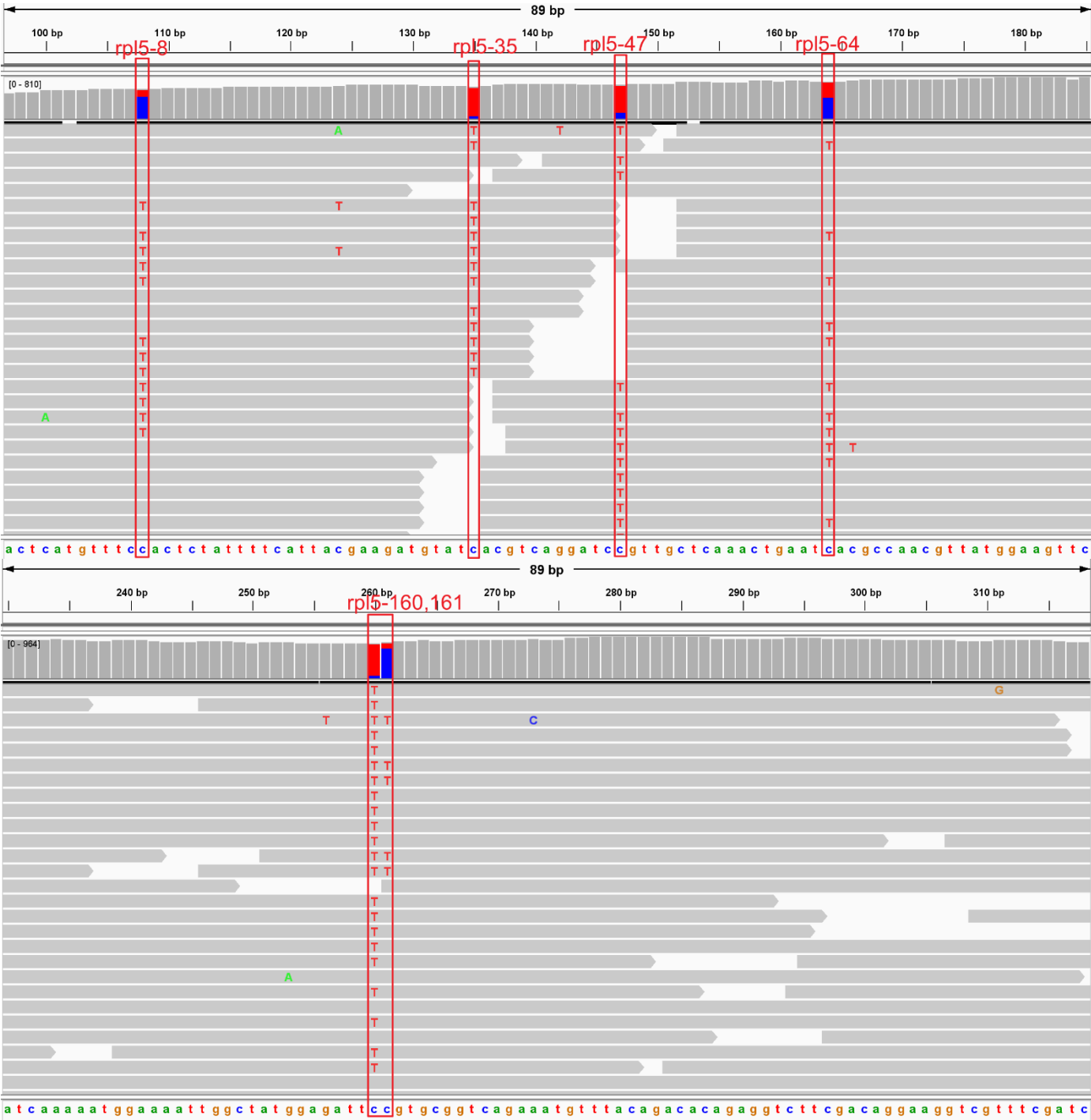
w alignment of RNA-seq reads to the coding sequence of *nad9*. 9 RNA-seq editing sites: *nad9*-15, 92, 113, 167, 298, 328, 368, 398, 439 were highlighted in red squares.

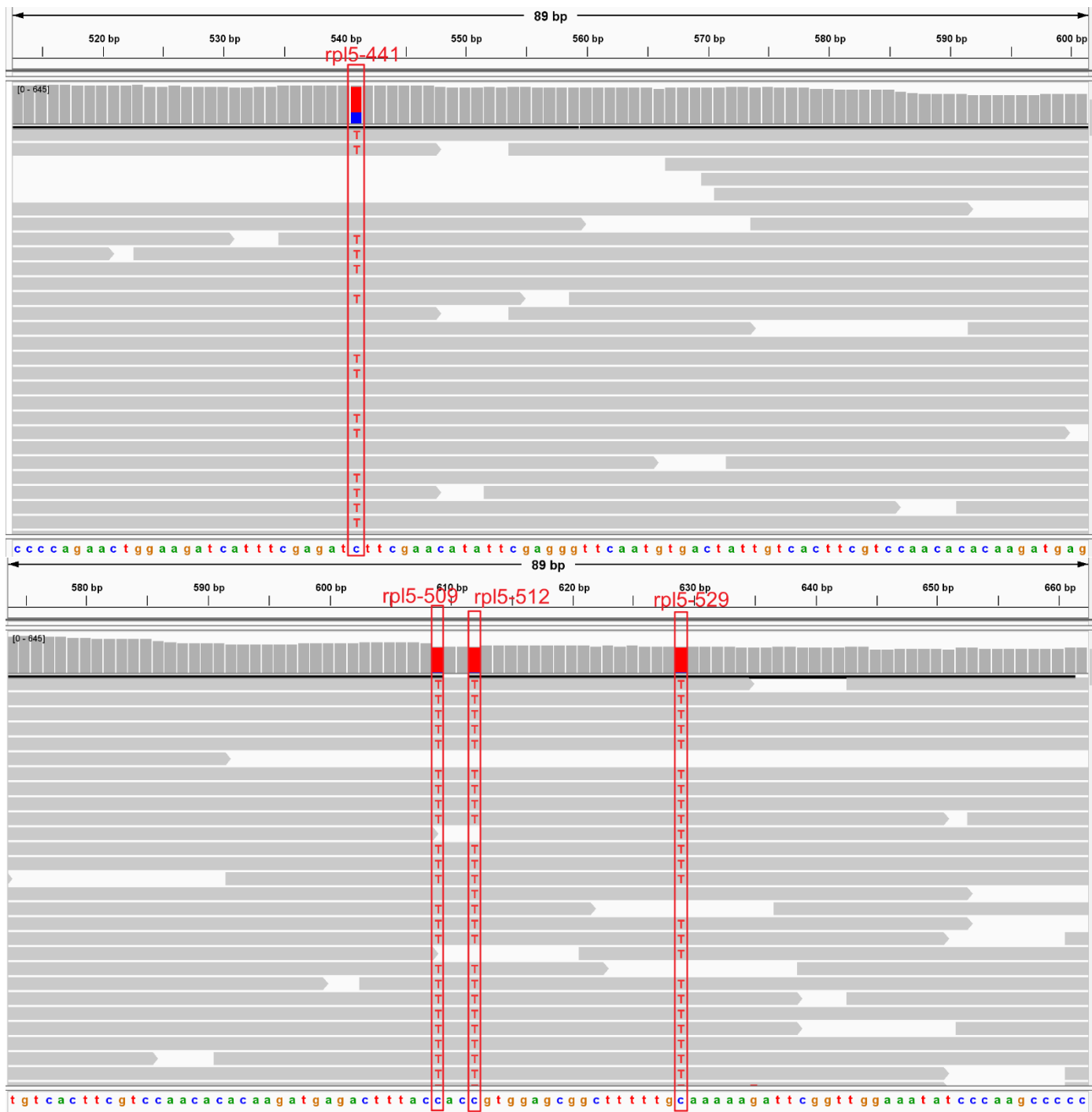


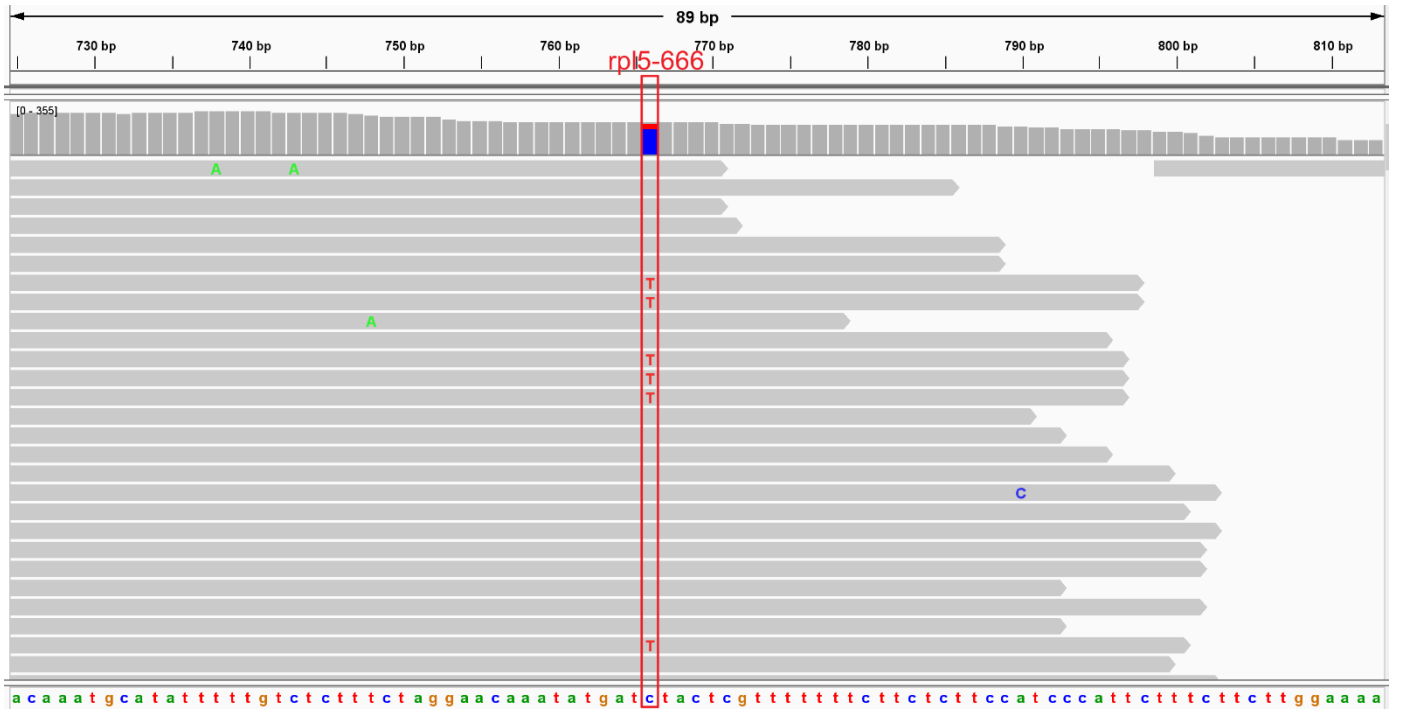




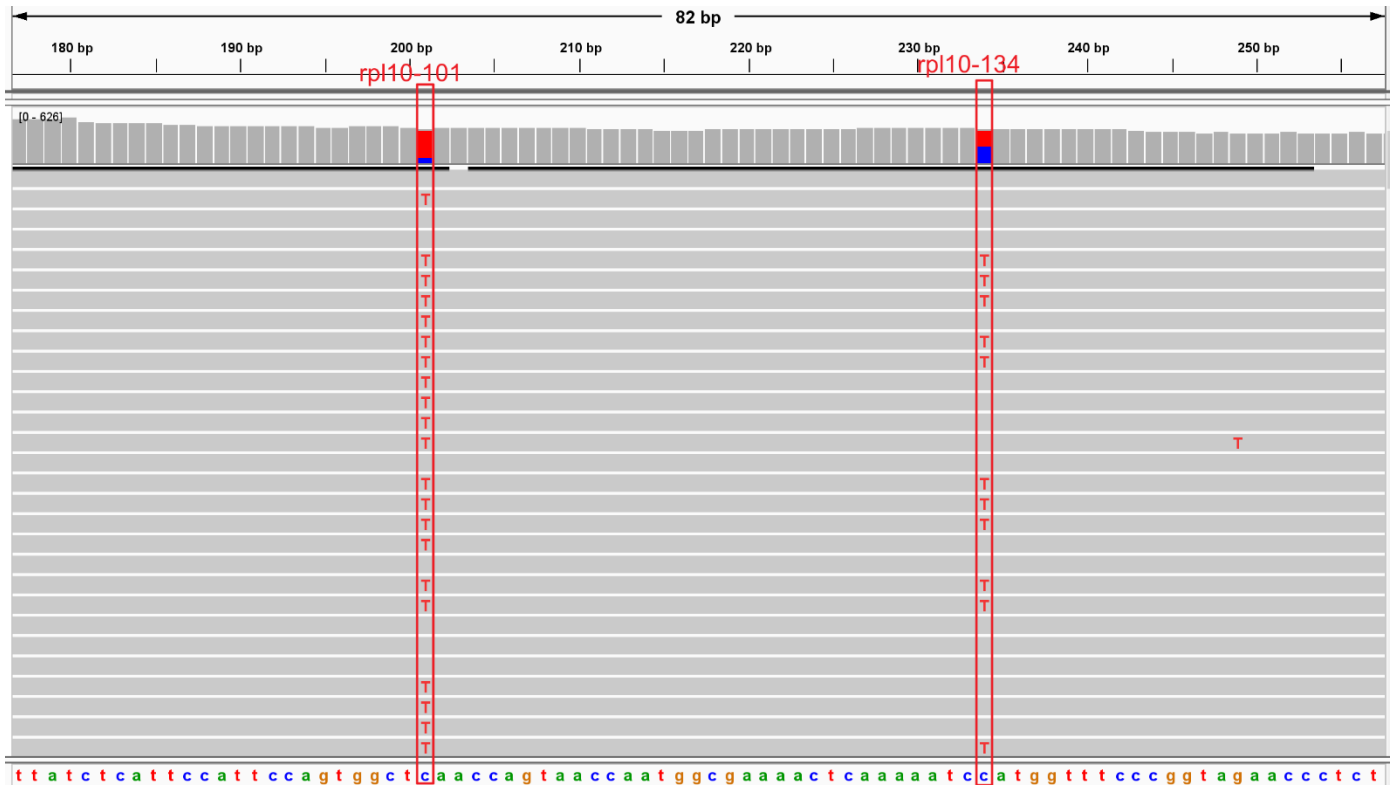
x alignment of RNA-seq reads to the coding sequence of *rp15*. 11 RNA-seq editing sites: *rp15*-8, 35, 47, 64, 160, 161, 441, 509, 512, 529, 666 were highlighted in red squares.



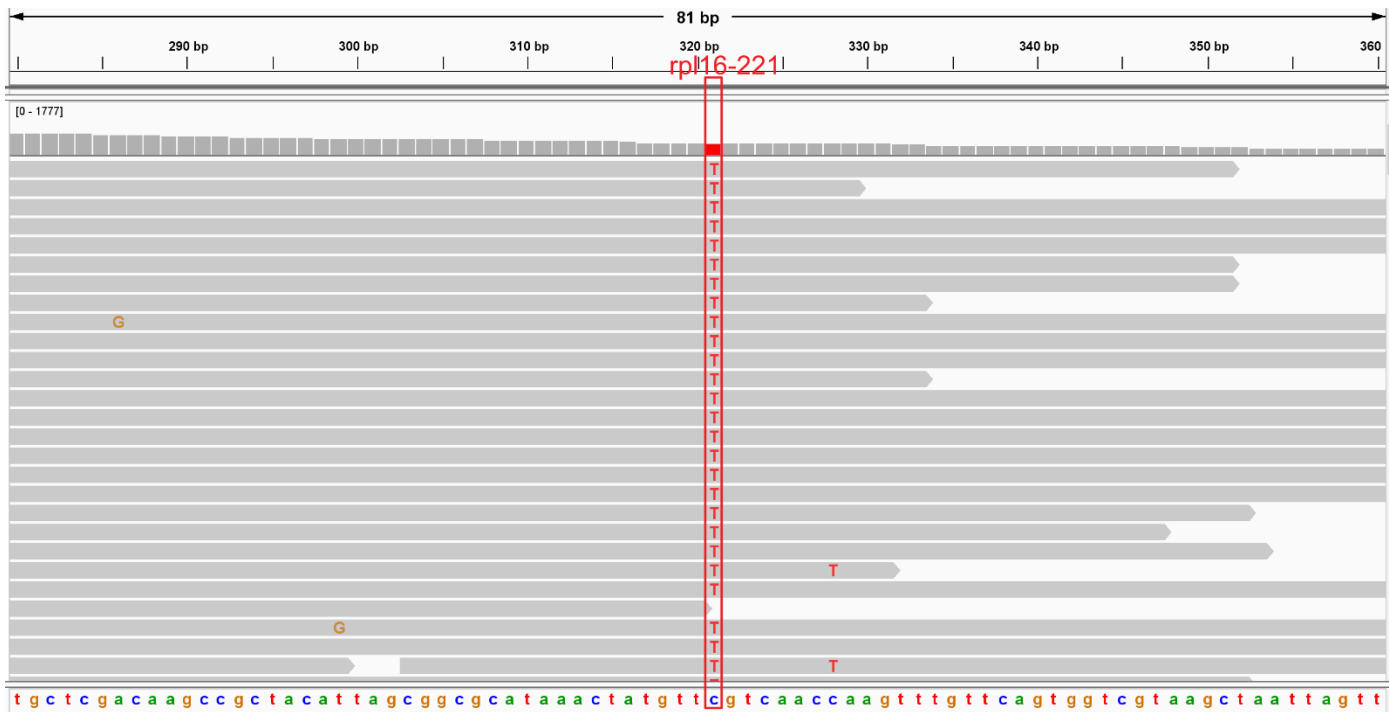




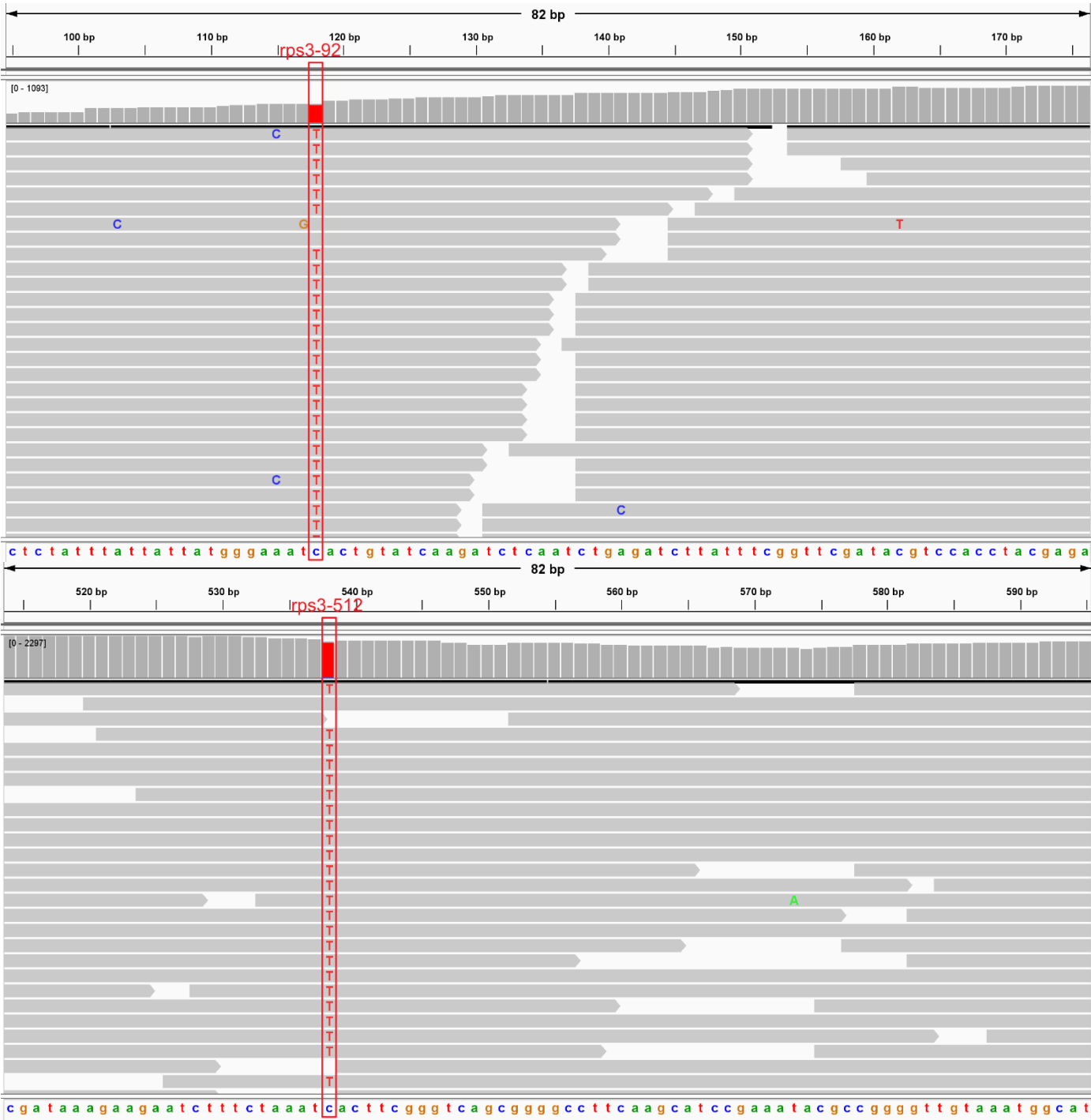
y alignment of RNA-seq reads to the coding sequence of *rpl10*. Two RNA-seq editing sites: *rpl10*-101 and 134 were highlighted in red squares.

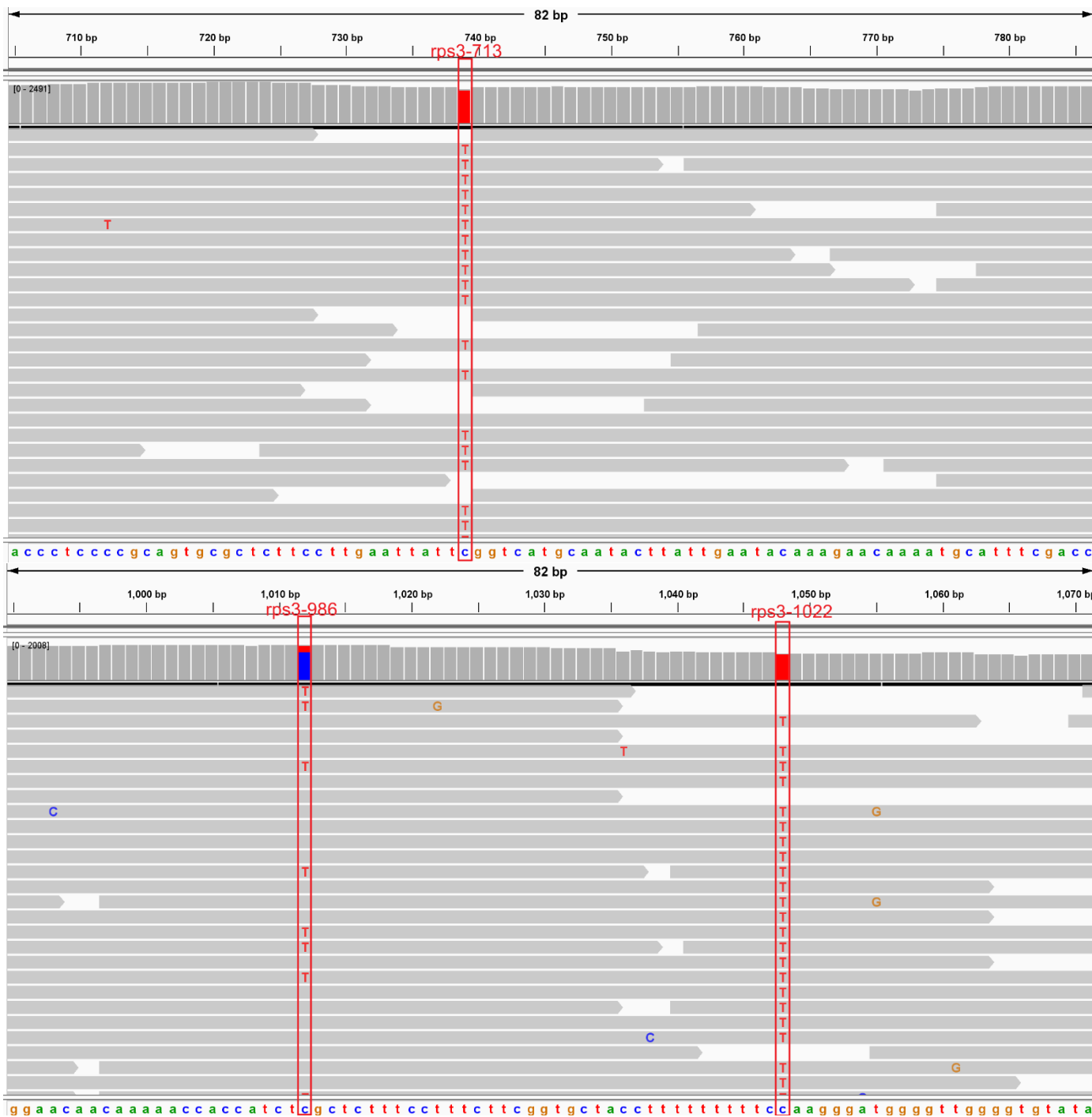


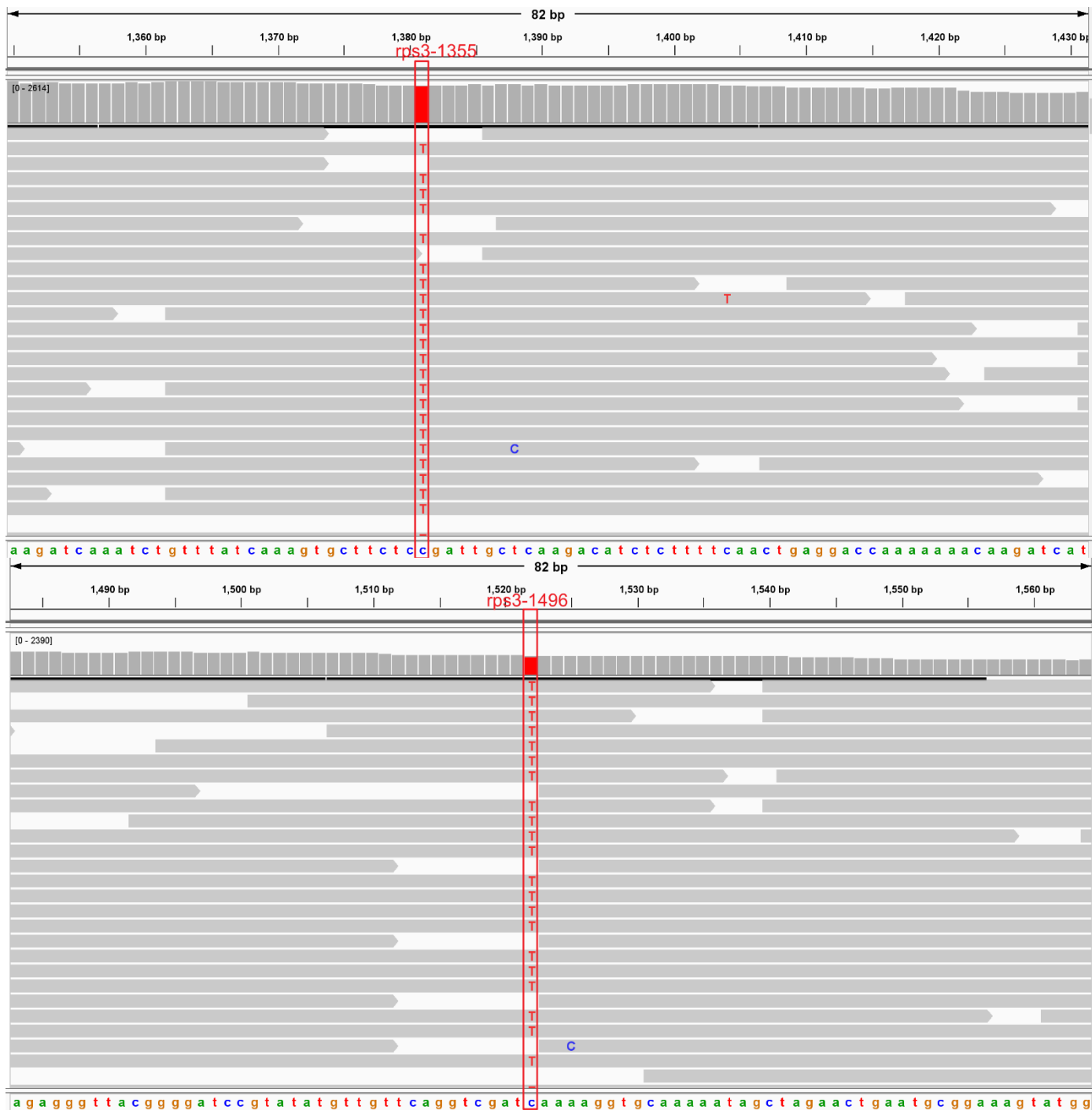
z alignment of RNA-seq reads to the coding sequence of *rp16*. One RNA-seq editing sites: *rp16*-221 was highlighted in red squares.

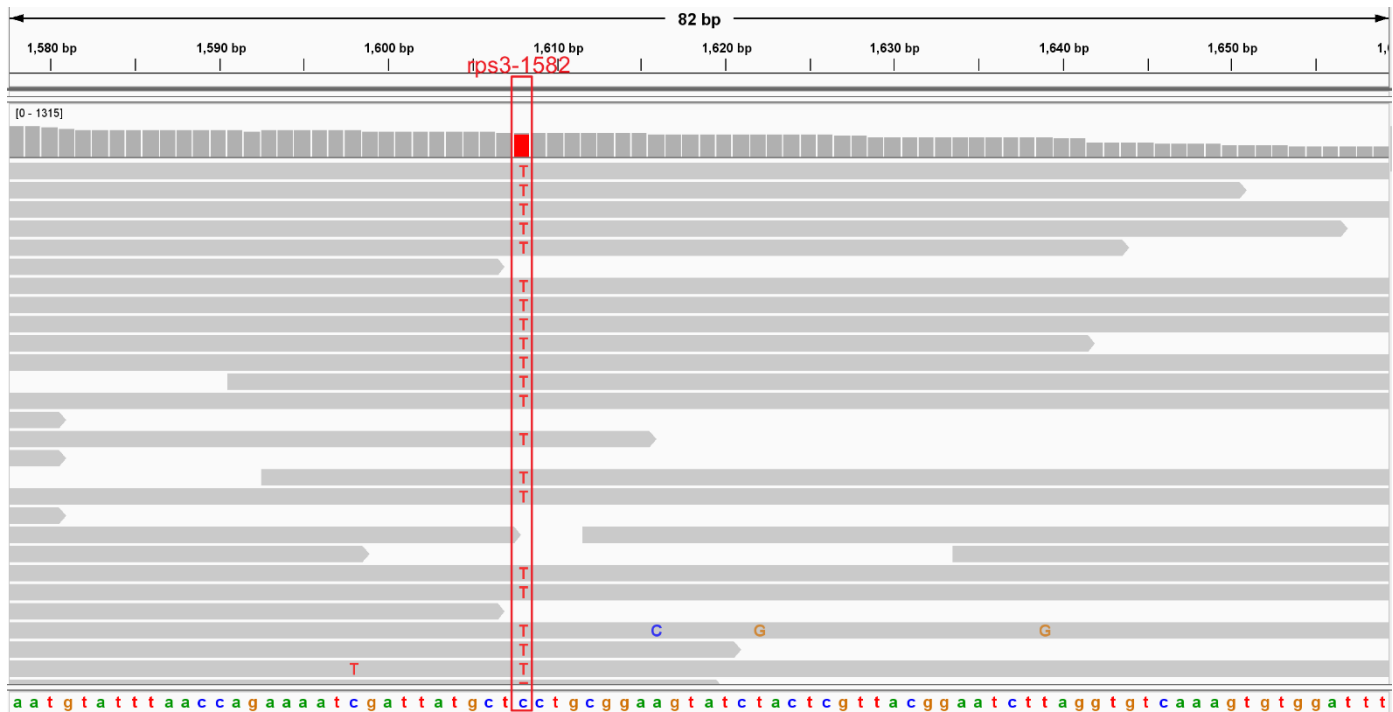


A alignment of RNA-seq reads to the coding sequence of *rps3*. Eight RNA-seq editing sites: *rps3*-92, 512, 713, 986, 1022, 1355, 1496, and 1582 were highlighted in red squares.

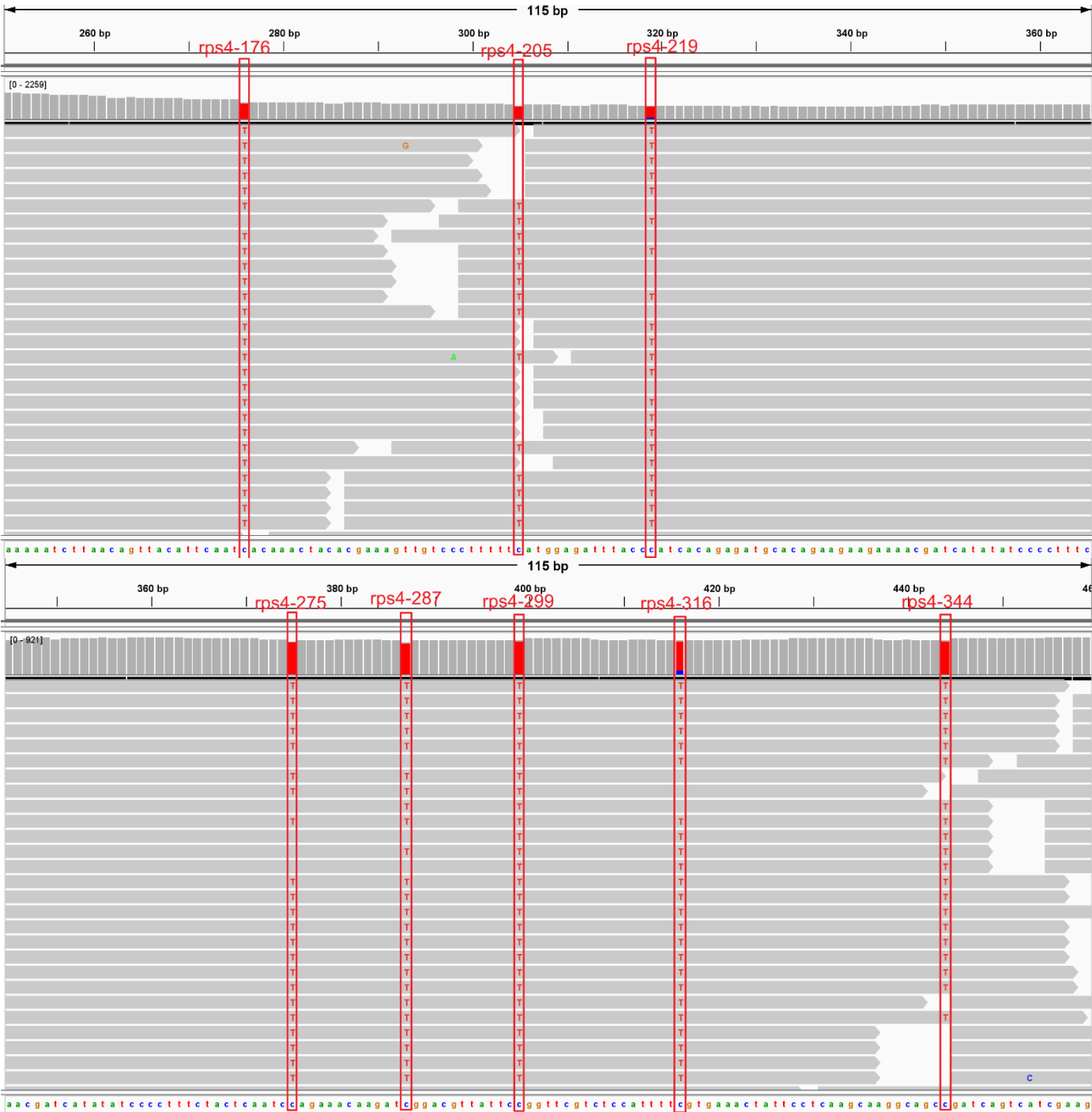


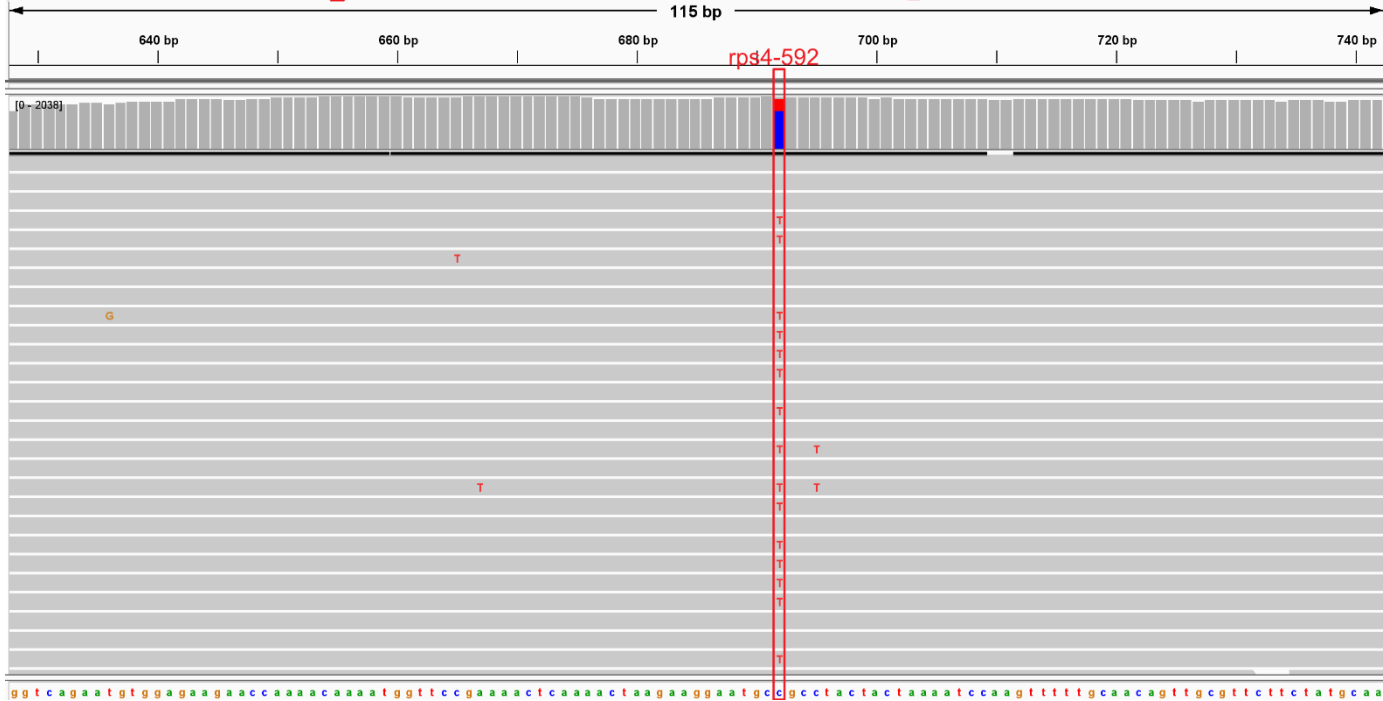
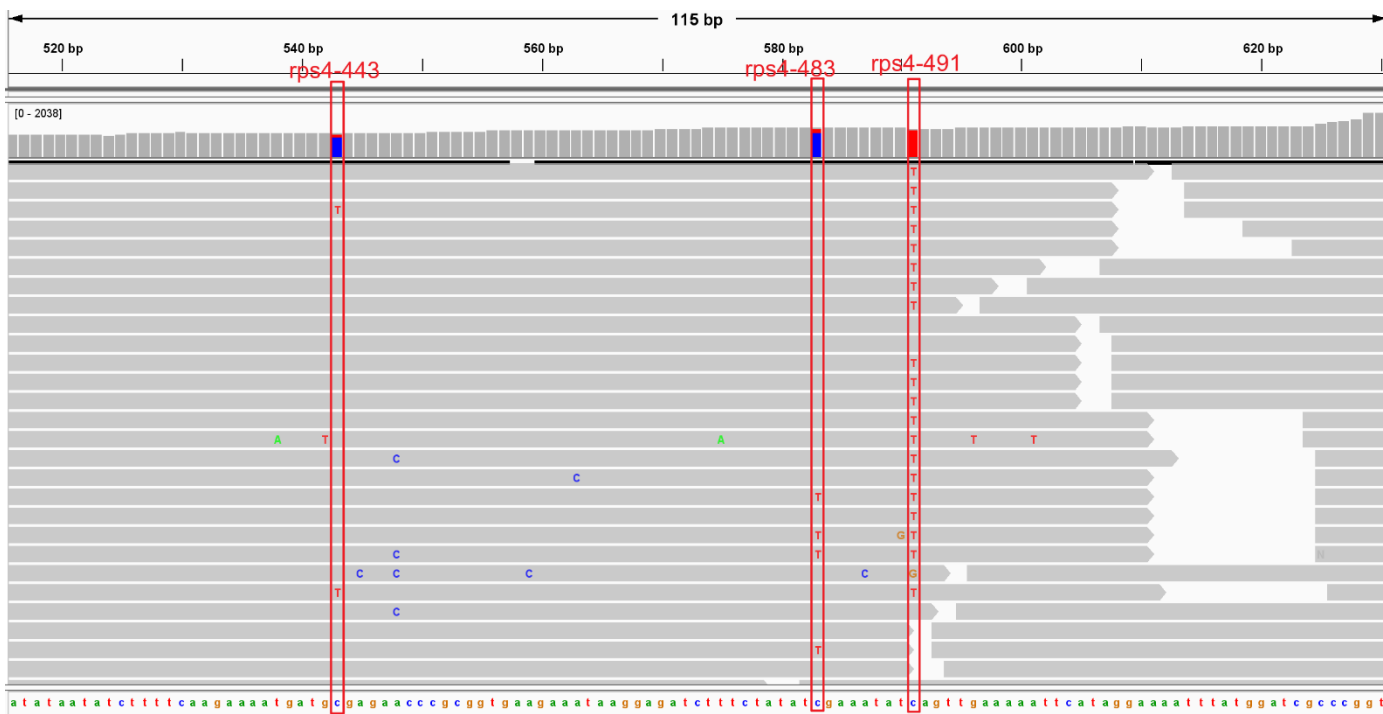


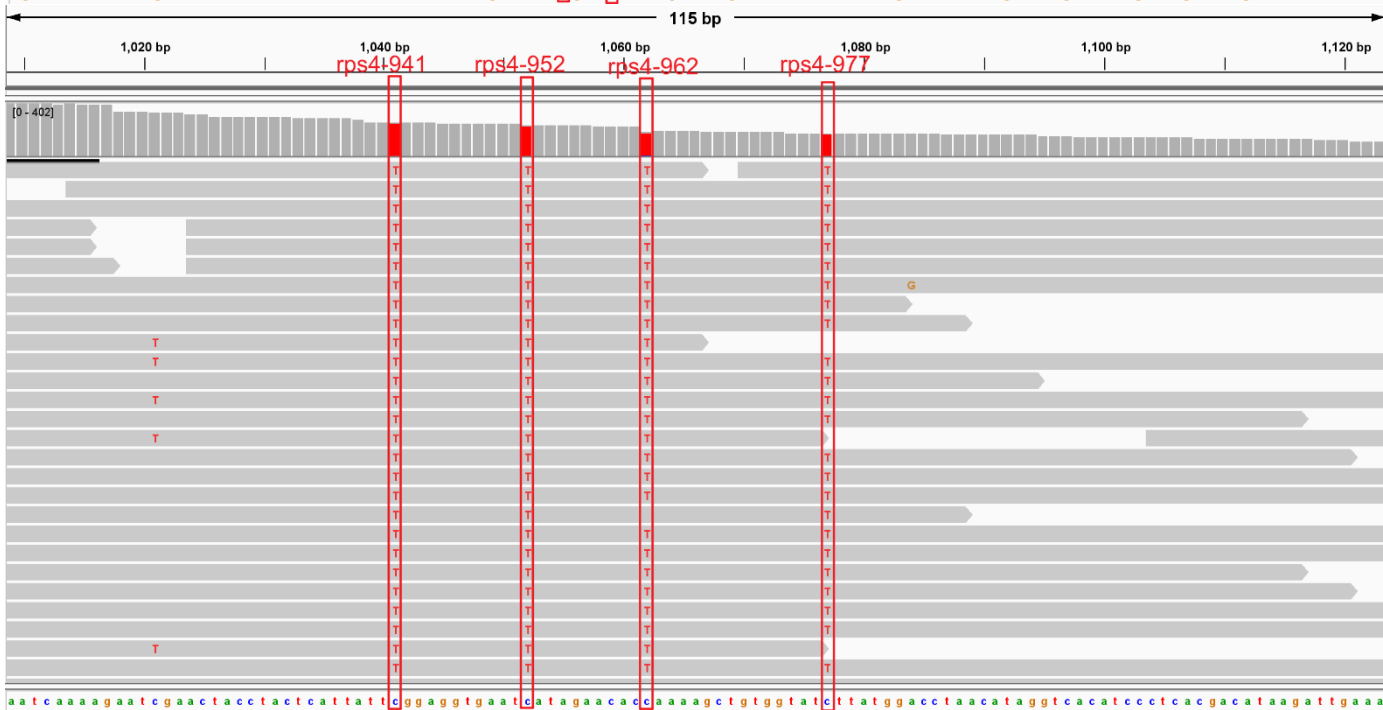
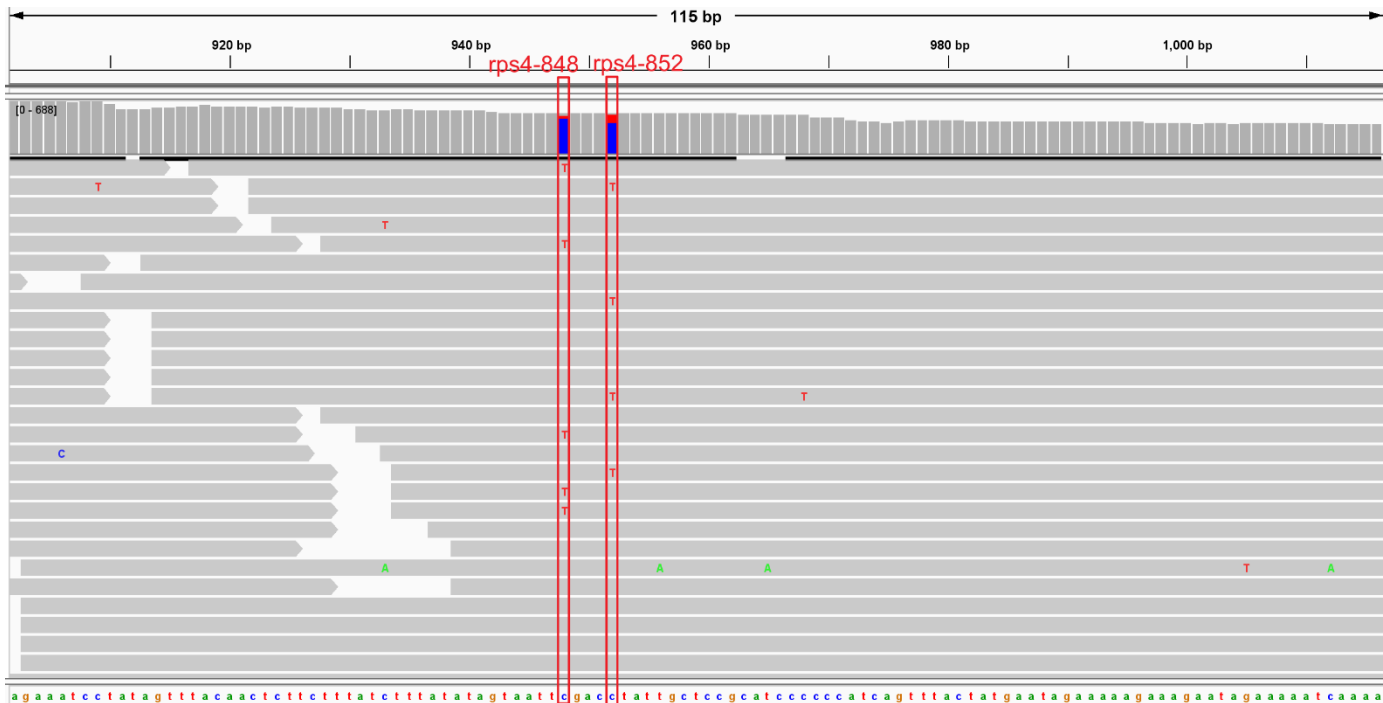


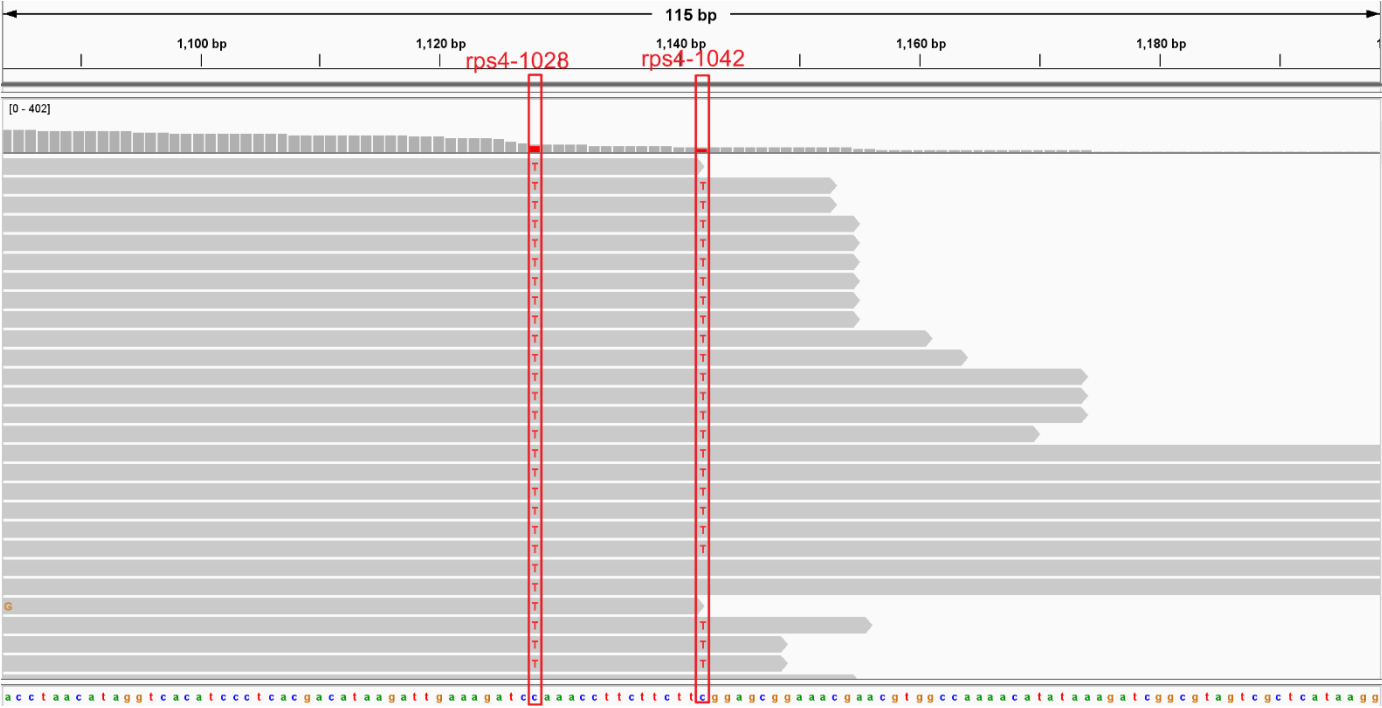


B alignment of RNA-seq reads to the coding sequence of *rps4*. 20 RNA-seq editing sites: *rps4*-176, 205, 219, 275, 287, 299, 316, 344, 443, 483, 491, 592, 848, 852, 941, 952, 962, 977, 1028, 1042 were highlighted in red squares.



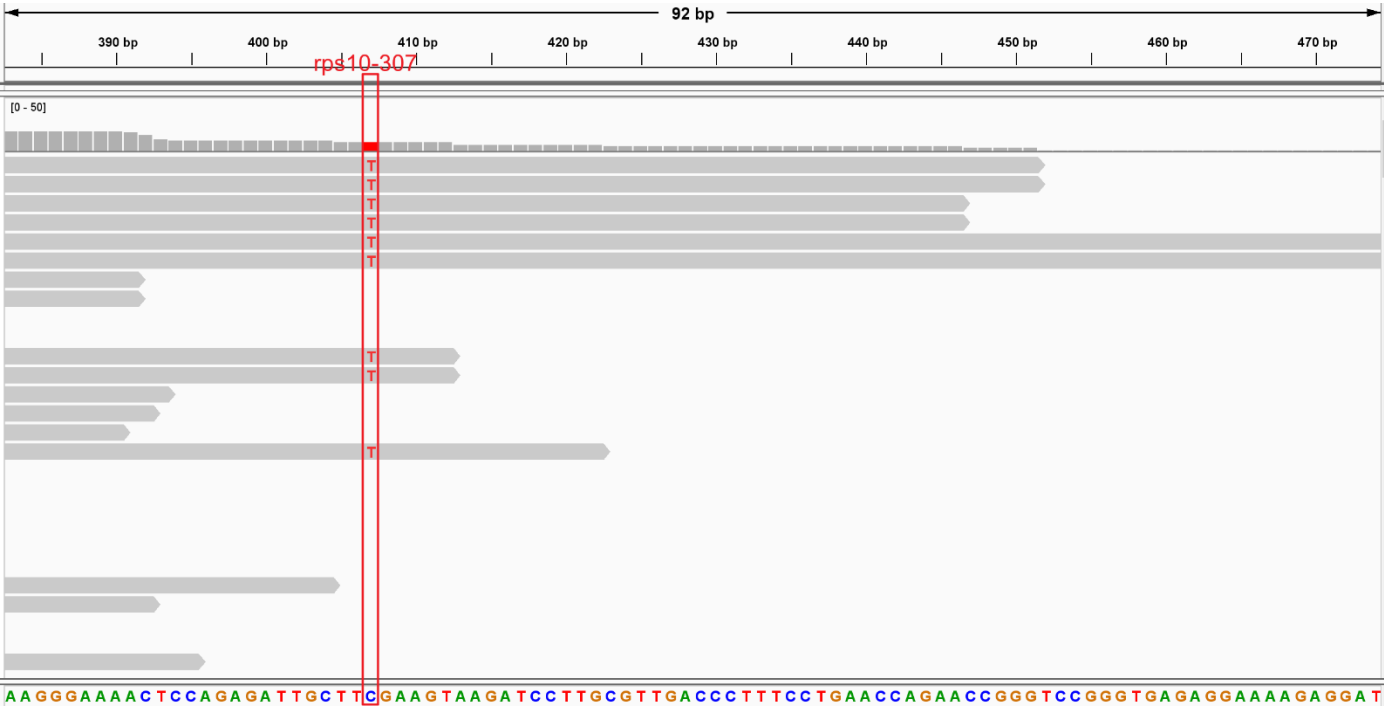




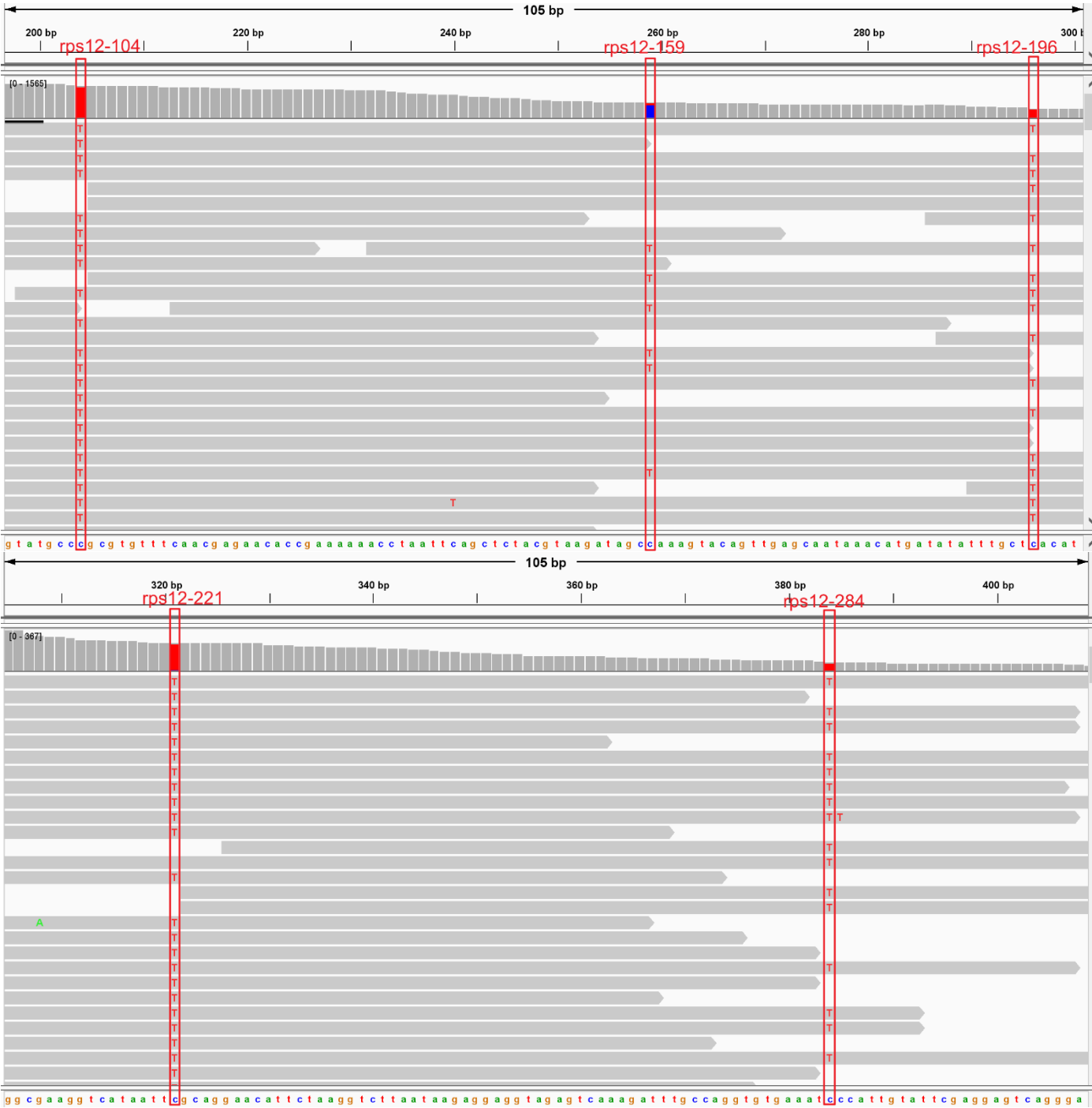


C alignment of RNA-seq reads to the coding sequence of *rps10*. Six RNA-seq editing sites: *rps10*-102, 132, 210, 214, 278, 307 were highlighted in red squares.





D alignment of RNA-seq reads to the coding sequence of *rps12*. Five RNA-seq editing sites: *rps12*-104, 159, 196, 221, 284 were highlighted in red squares.



E alignment of RNA-seq reads to the coding sequence of *rps13*. Three RNA-seq editing sites: *rps13*-56, 100, 287 were highlighted in red squares.

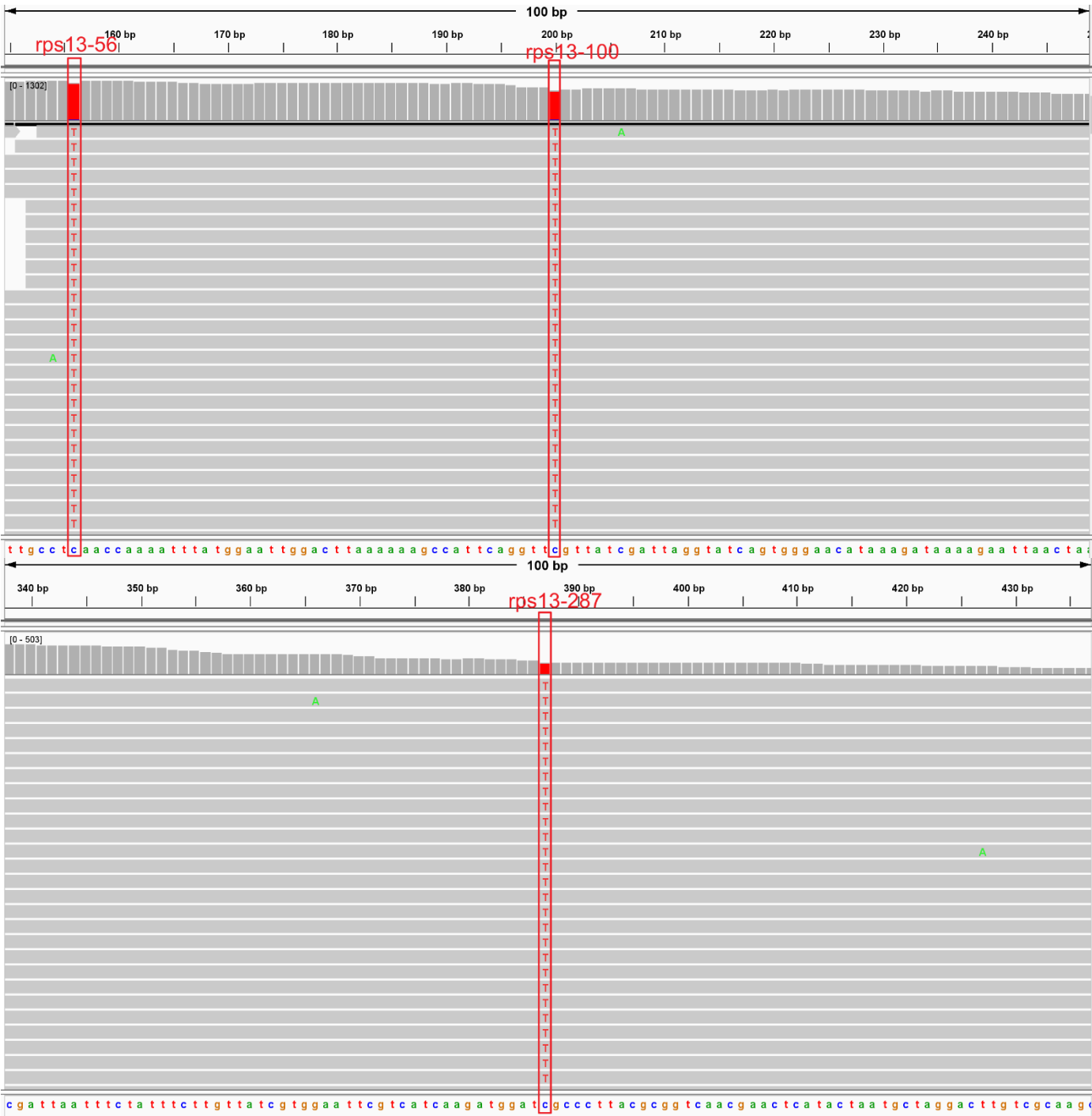
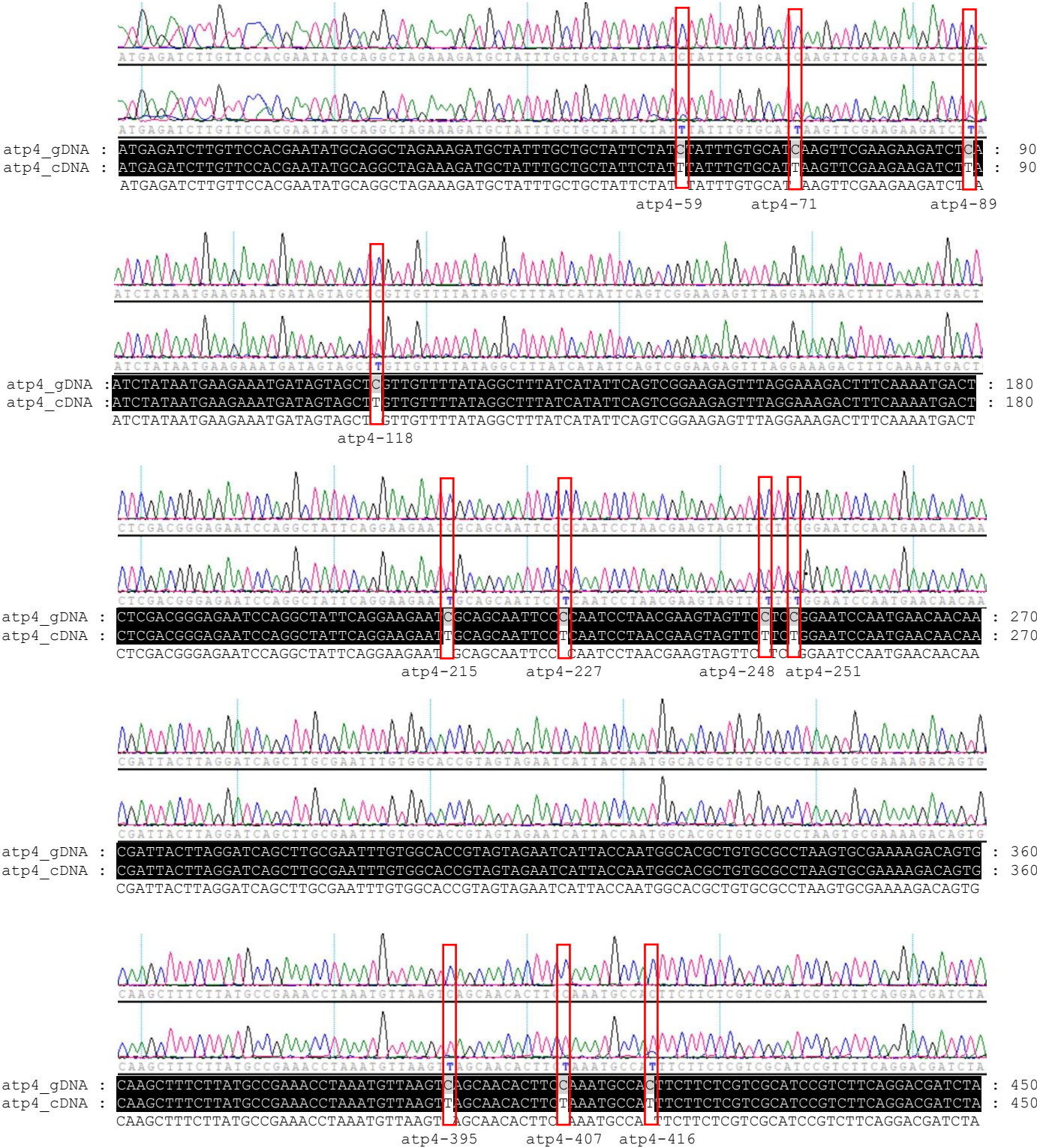
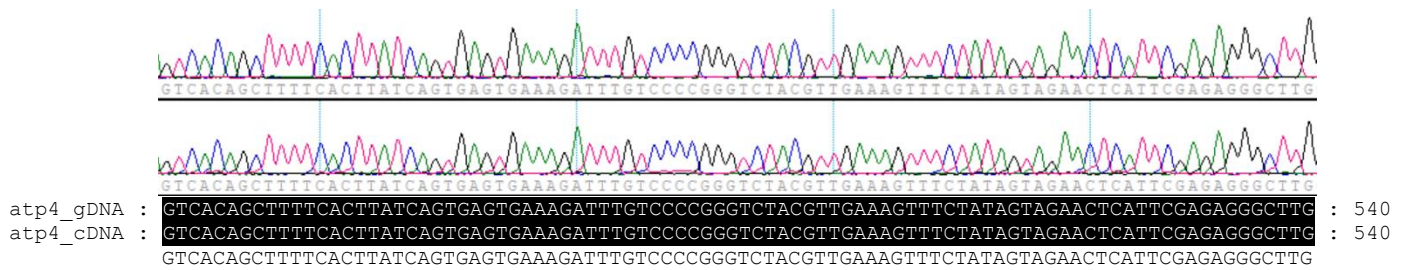


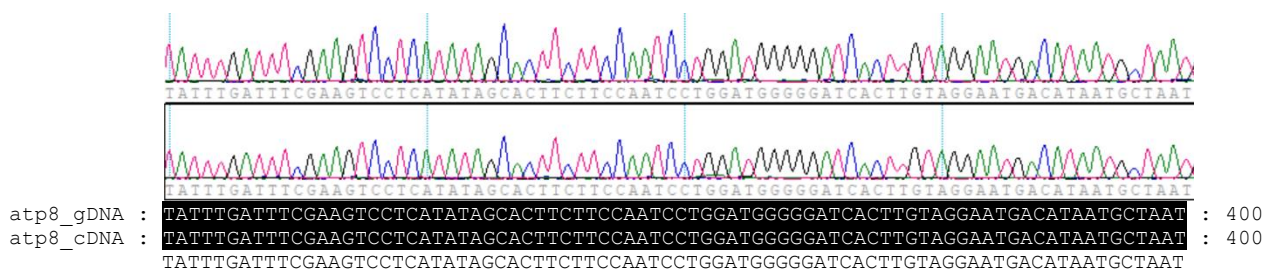
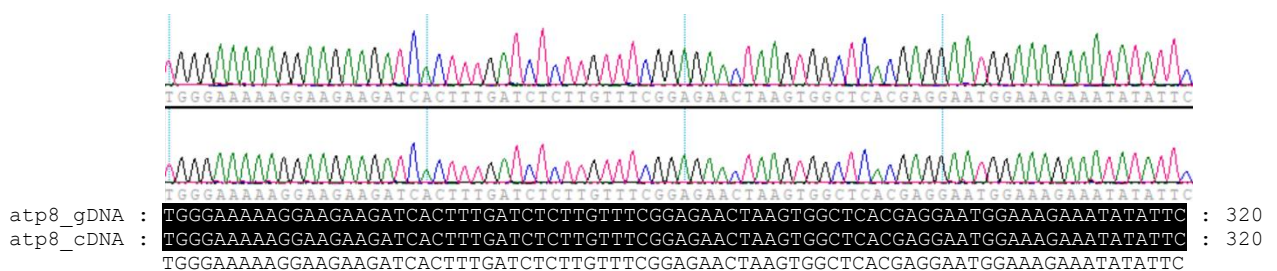
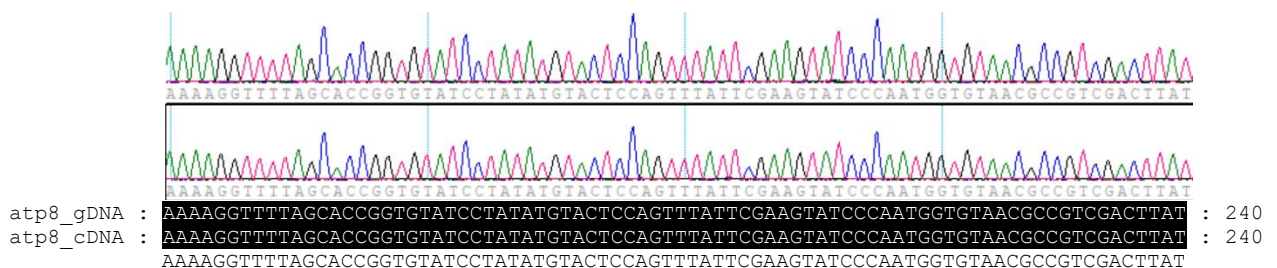
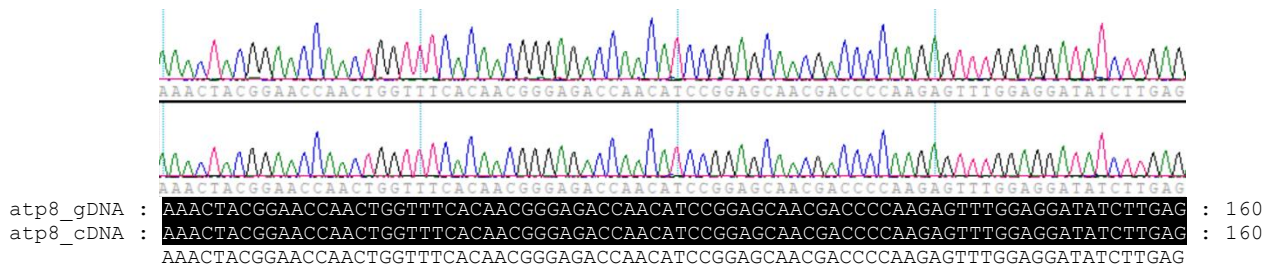
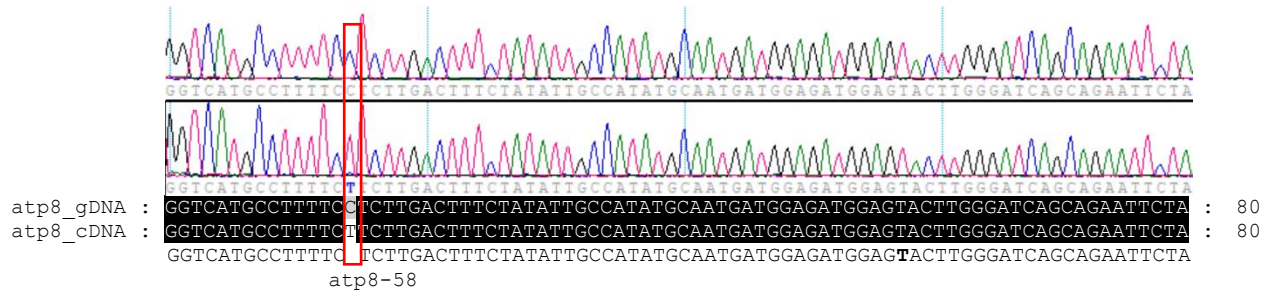
Figure S7 Validation of the RNA editing sites within eleven PCGs using PCR and Sanger sequencing. The top panel shows the sequences and chromatographs from the PCR products amplified using the genomic DNA (gDNA) and complementary DNA (cDNA) as templates. The bottom panel shows the sequences from the PCR products amplified using the gDNA and cDNA. The gene names and the RNA editing sites' positions on the CDs are shown at the bottom of the figure, separated with "-". The red squares highlight the focal RNA editing site.

a validation of the *atp4-59*, *atp4-71*, *atp4-89*, *atp4-118*, *atp4-215*, *atp4-227*, *atp4-248*, *atp4-251*, *atp4-395*, *atp4-407*, and *atp4-416* using PCR amplification and Sanger sequencing experiments.

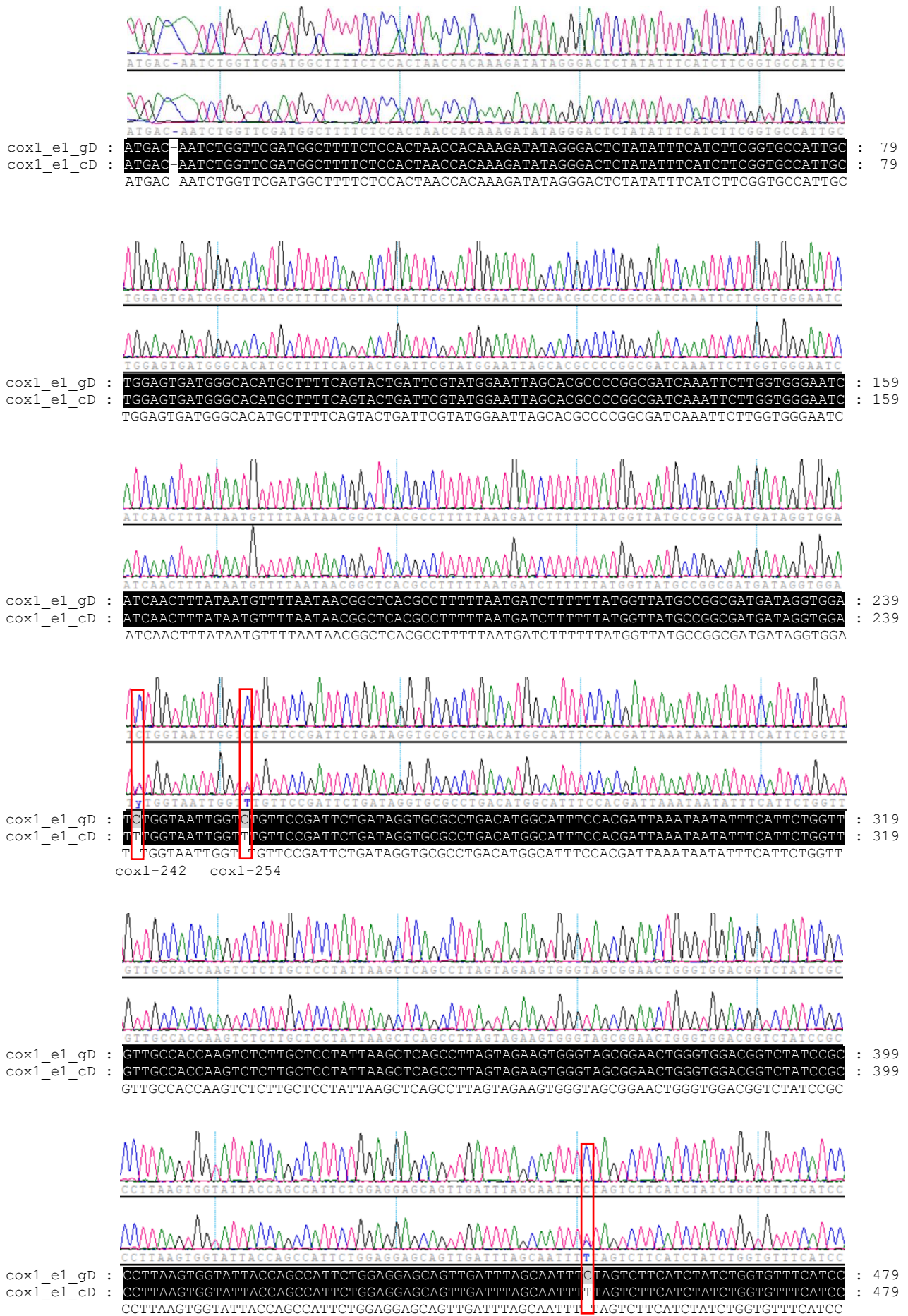


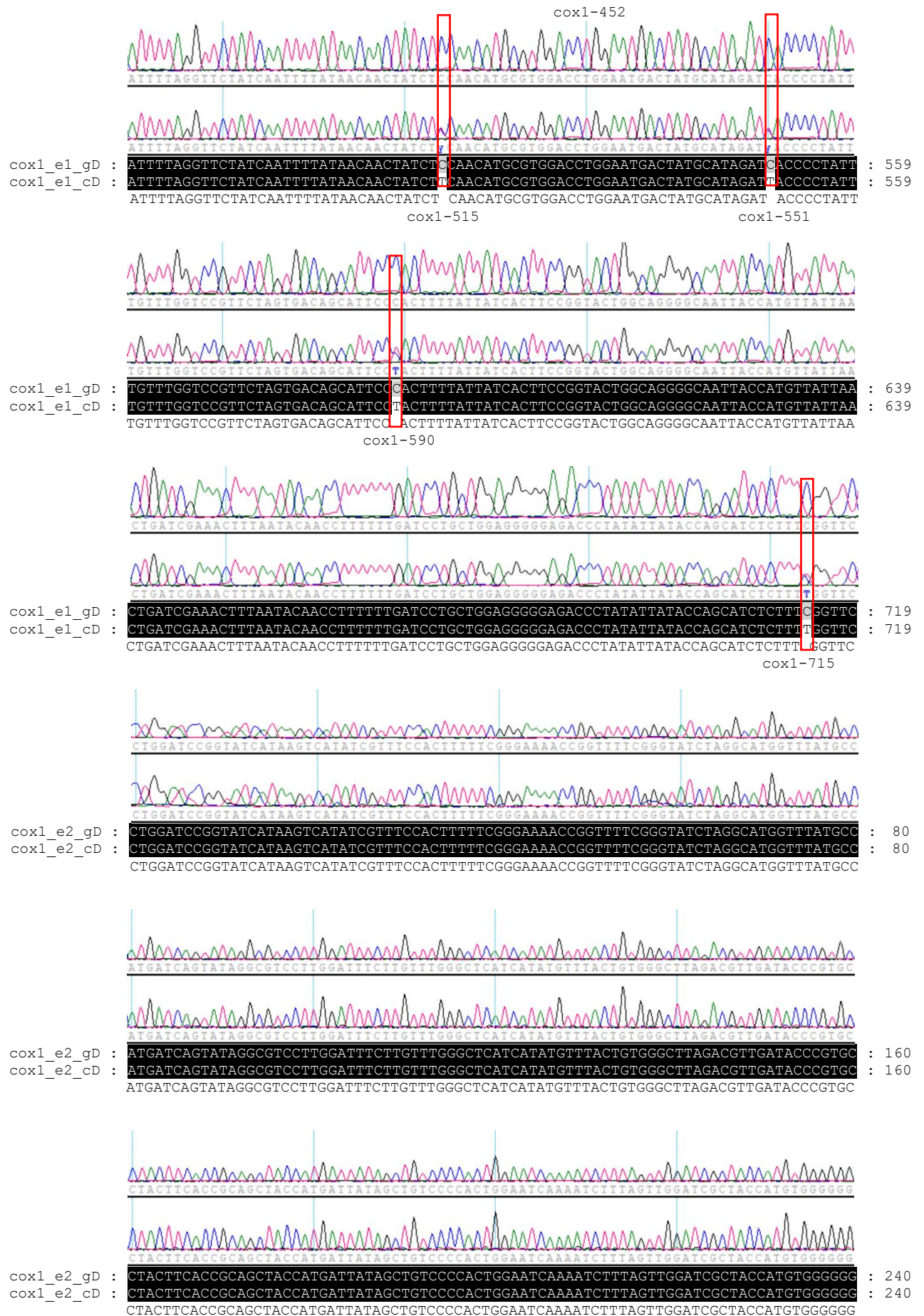


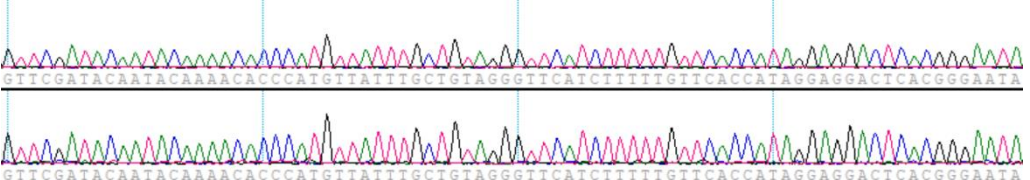
b validation of the *atp8-58* using PCR amplification and Sanger sequencing experiments.



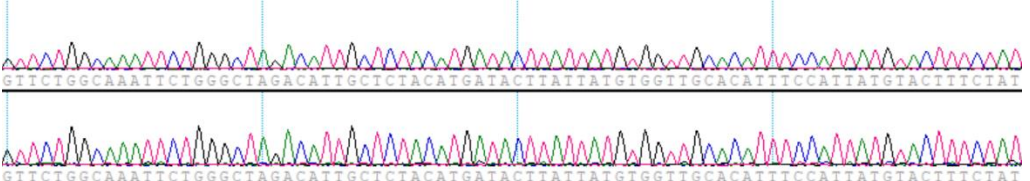
c validation of the *cox1*-242, *cox1*-254, *cox1*-452, *cox1*-515, *cox1*-551, *cox1*-590, *cox1*-715, *cox1*-1186, *cox1*-1405, *cox1*-1433, and *cox1*-1499 using PCR amplification and Sanger sequencing experiments.







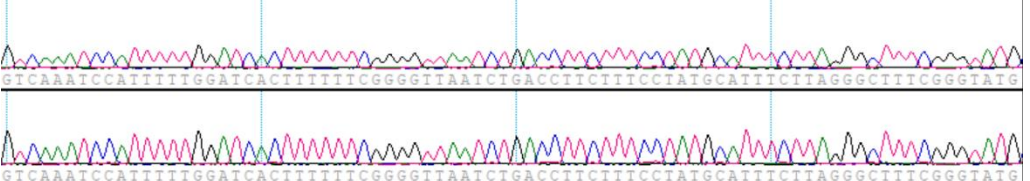
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 cox1_e2_cD : GTTCGATACAATACAAAACACCCATGTTATTTGCTGTAGGGTTCATCTTTTGTTCACCATAGGAGGACTCACGGGAATA : 320
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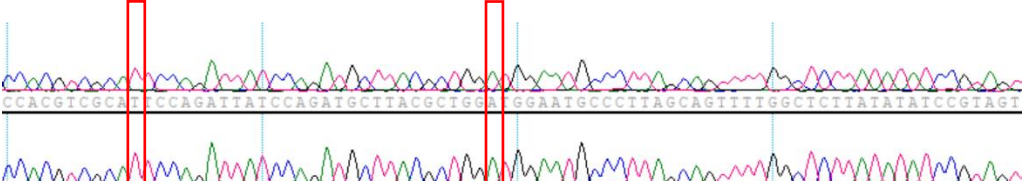
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 cox1_e2_cD : GTTCTGGCAAATCTCTGGGCTAGACATTGCTCTACATGATACTTATTATGTGGTTGCACATTTCCATTATGTACTTTCTAT : 400
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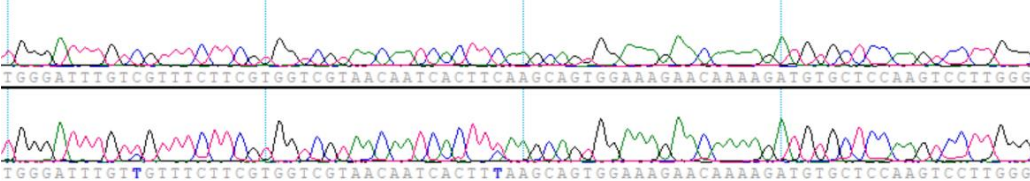
cox1_e2_gD : GGGAGCCGTTTTTGCTTTATTTGCAGGATTTTACTATTGGGTAGGTAAAATCTTTGGTTCGGACATACCCTGAAACTTTAG : 480
 cox1_e2_cD : GGGAGCCGTTTTTGCTTTATTTGCAGGATTTTACTATTGGGTAGGTAAAATCTTTGGTTCGGACATACCCTGAAACTTTAG : 480
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 cox1-1186



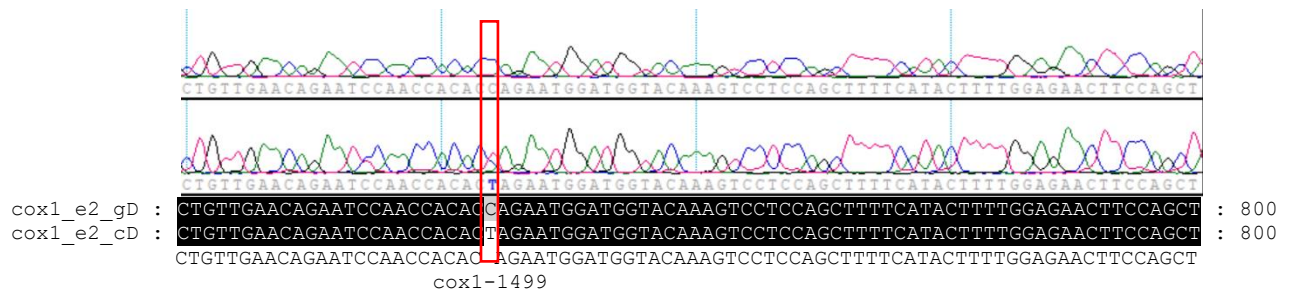
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 cox1_e2_cD : GTCAAATCCATTTTGGATCACTTTTTTCGGGGTTAATCTGACCTTCTTTCCATATGCATTTCTAGGGCTTTTCGGGTATG : 560
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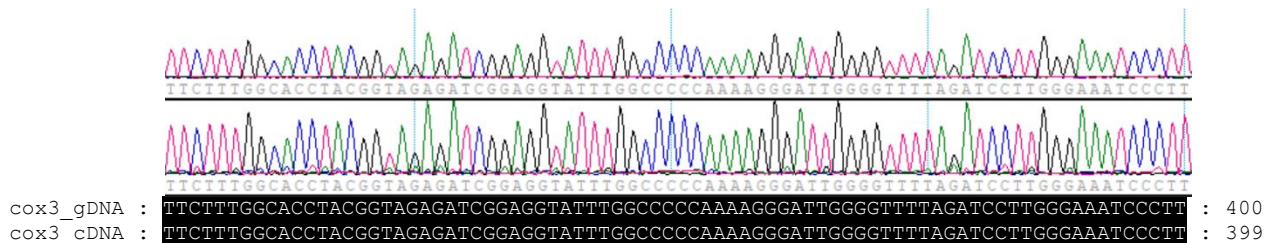
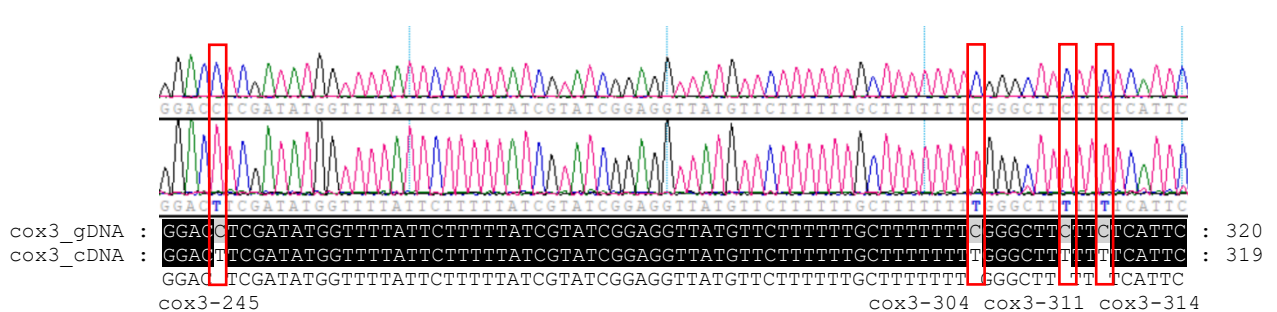
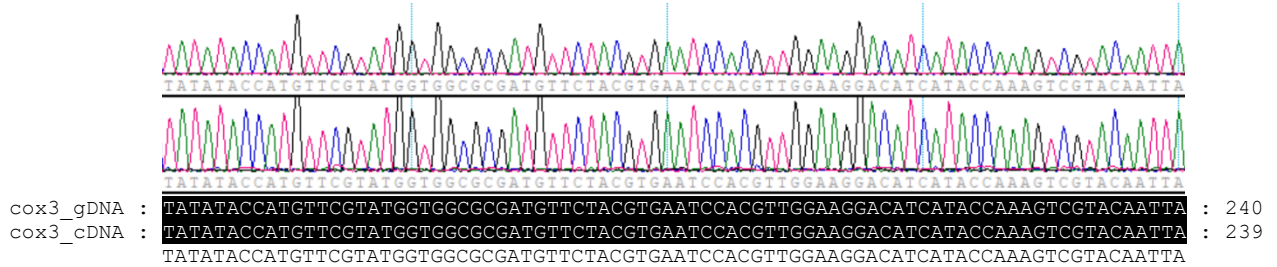
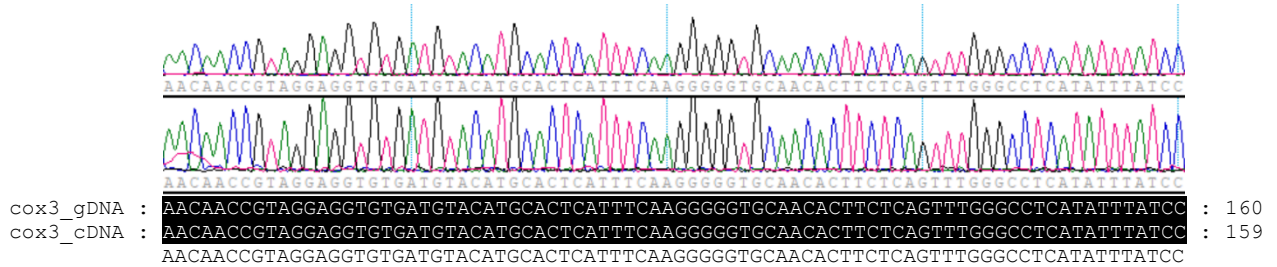
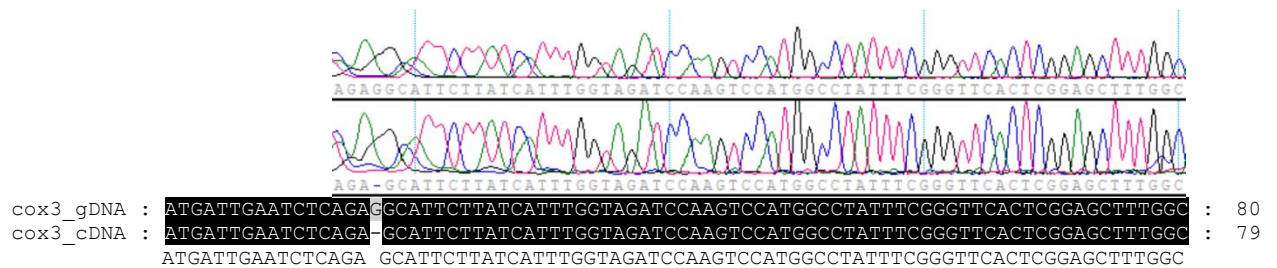
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 cox1_e2_cD : CCACGTCGCATTCCAGATTATCCAGATGCTTACGCTGGATGGAATGCCCTTAGCAGTTTGGCTCTTATATATCCGTAGT : 640
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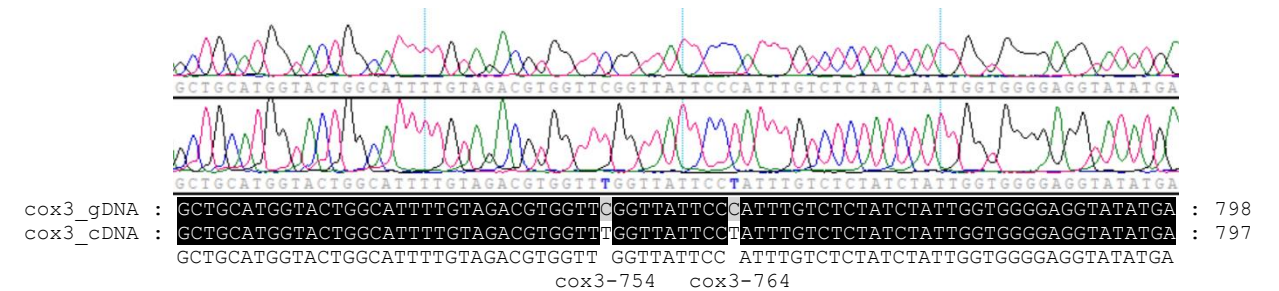
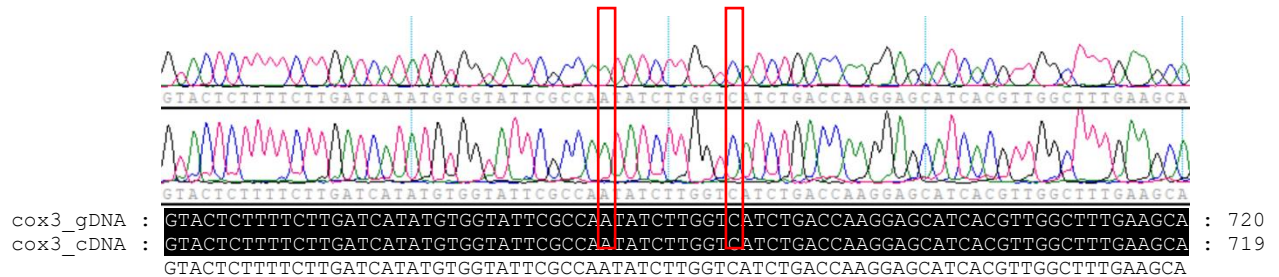
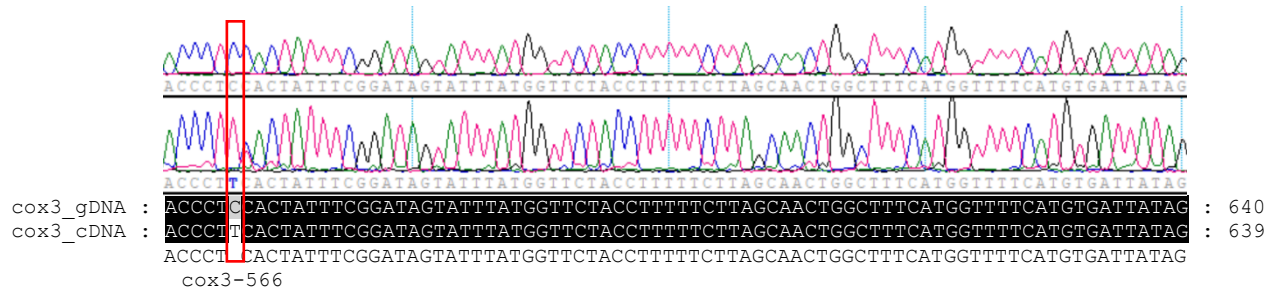
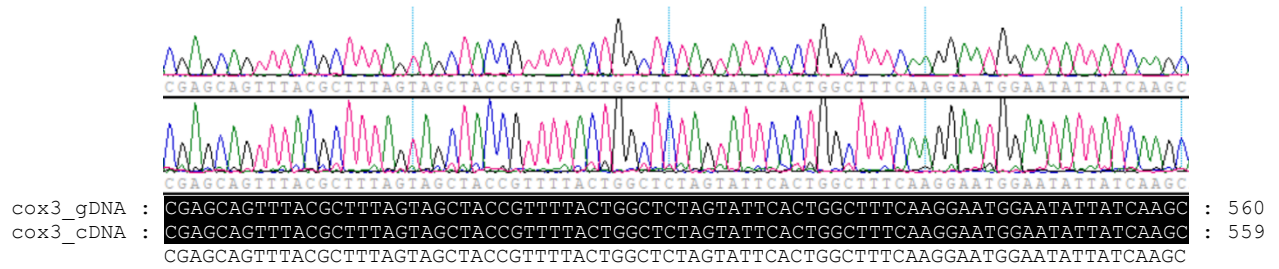
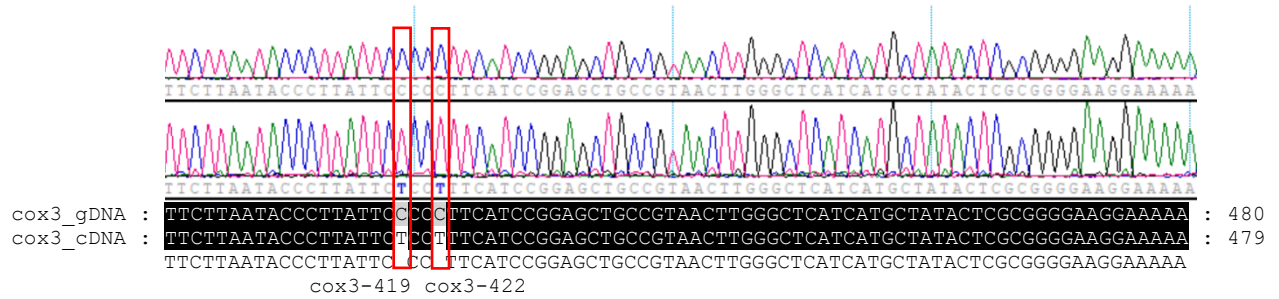
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 cox1-1405 cox1-1433



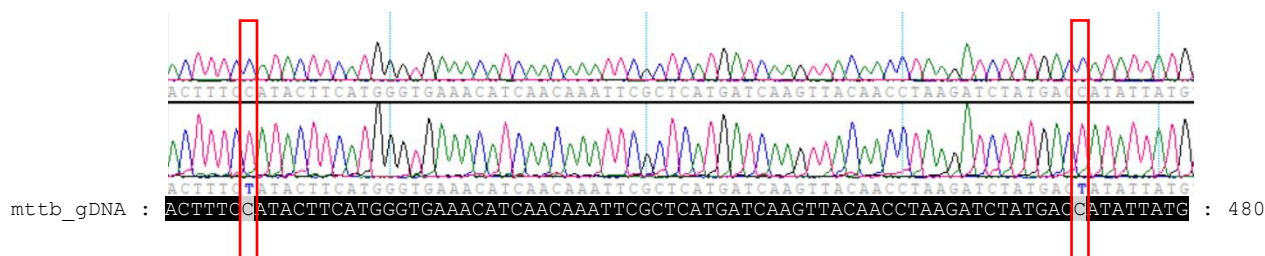
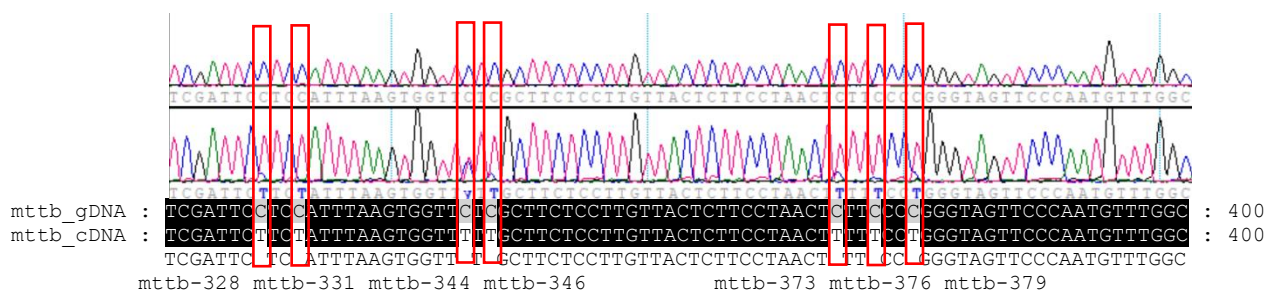
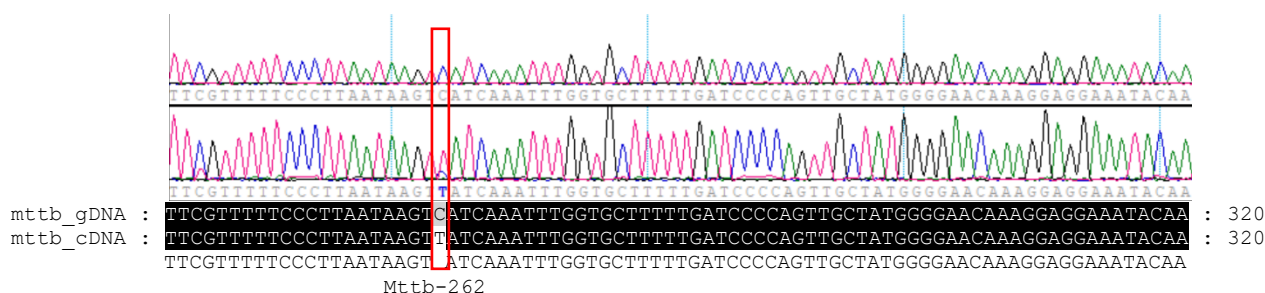
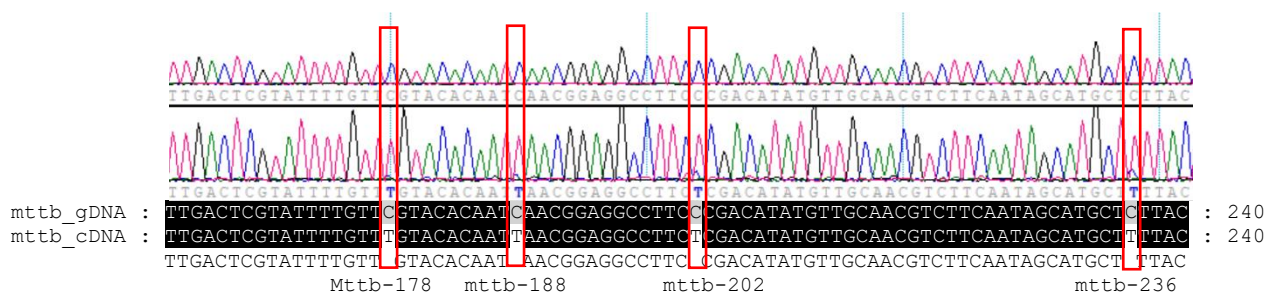
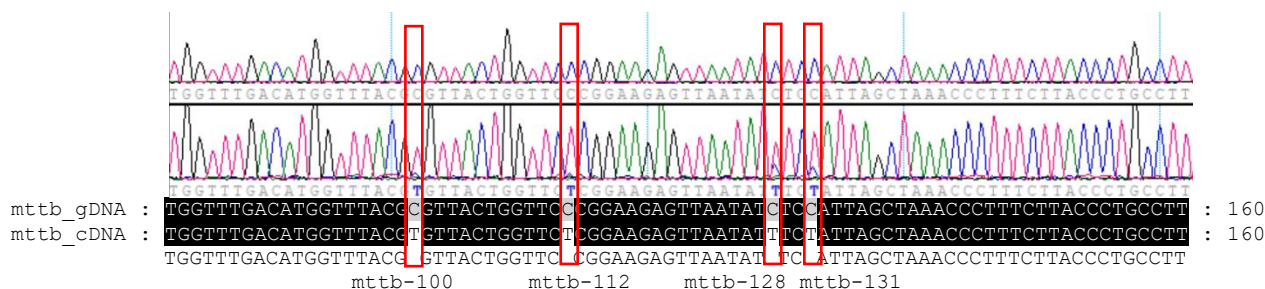
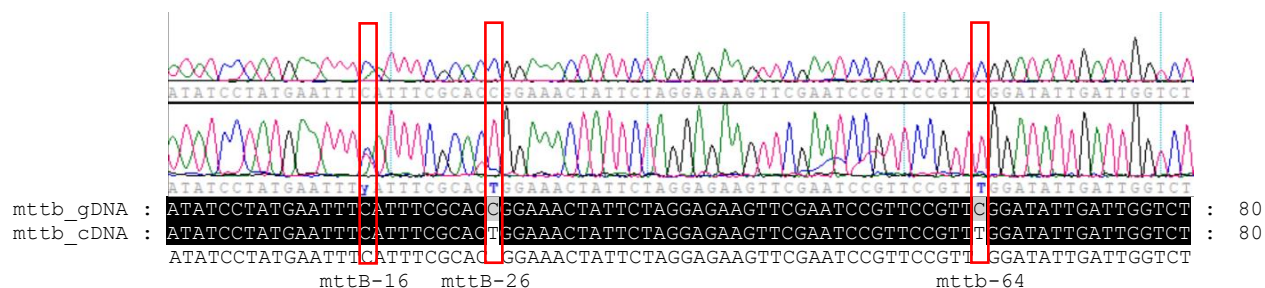
d validation of the *cox3*-245, *cox3*-304, *cox3*-311, *cox3*-314, *cox3*-419, *cox3*-422, *cox3*-566, *cox3*-754, and *cox3*-764 using PCR amplification and Sanger sequencing experiments.



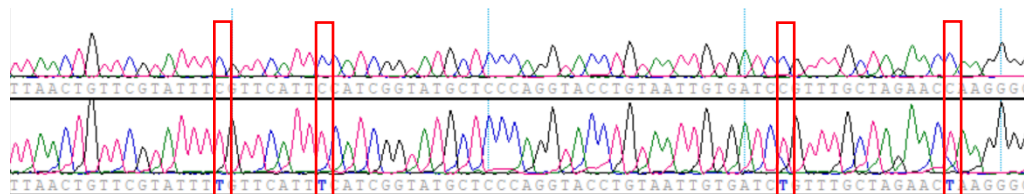
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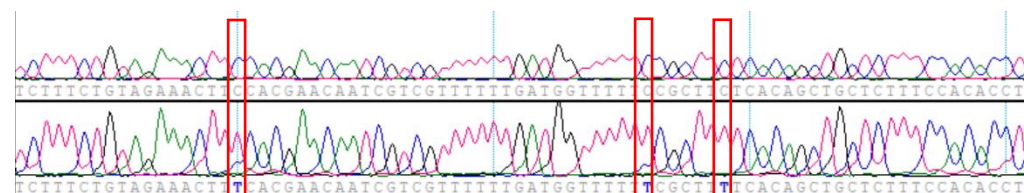
e validation of the *mttB*-16, *mttB*-26, *mttB*-64, *mttB*-100, *mttB*-112, *mttB*-128, *mttB*-131, *mttB*-178, *mttB*-188, *mttB*-202, *mttB*-236, *mttB*-262, *mttB*-328, *mttB*-331, *mttB*-344, *mttB*-346, *mttB*-373, *mttB*-376, *mttB*-379, *mttB*-407, *mttB*-472, *mttB*-497, *mttB*-505, *mttB*-541, *mttB*-554, *mttB*-578, *mttB*-610, *mttB*-616, *mttB*-667, and *mttB*-713 using PCR amplification and Sanger sequencing experiments.



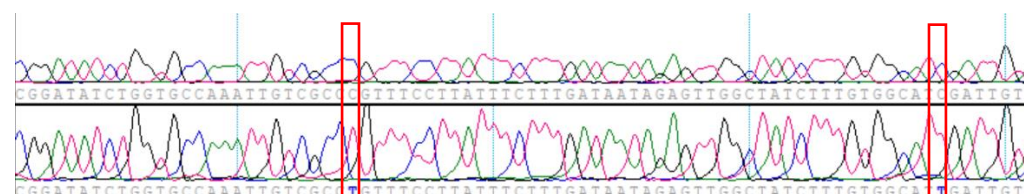
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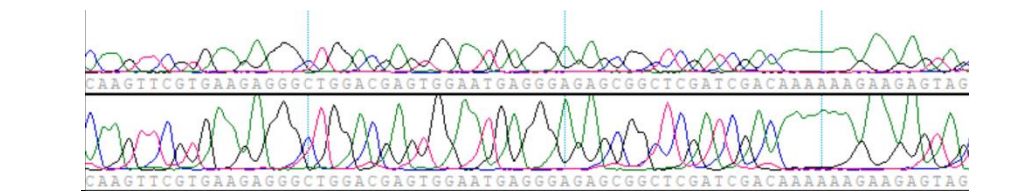
mttb_gDNA : TTAACGTTCGTATTTCTTCATTTCATCGGTATGCTCCAGGTACCTGTAATTGTGATCTTTTGCTAGAACCAAGGGG : 560
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mttb_gDNA : TCTTTCTGTAGAACTTCACGAACAATCGTCGTTTTTGTGGTTTTTCGCTTCACAGCTGCTCTTTCCACACCTC : 640
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 mttb-578 mttb-610 mttb-616

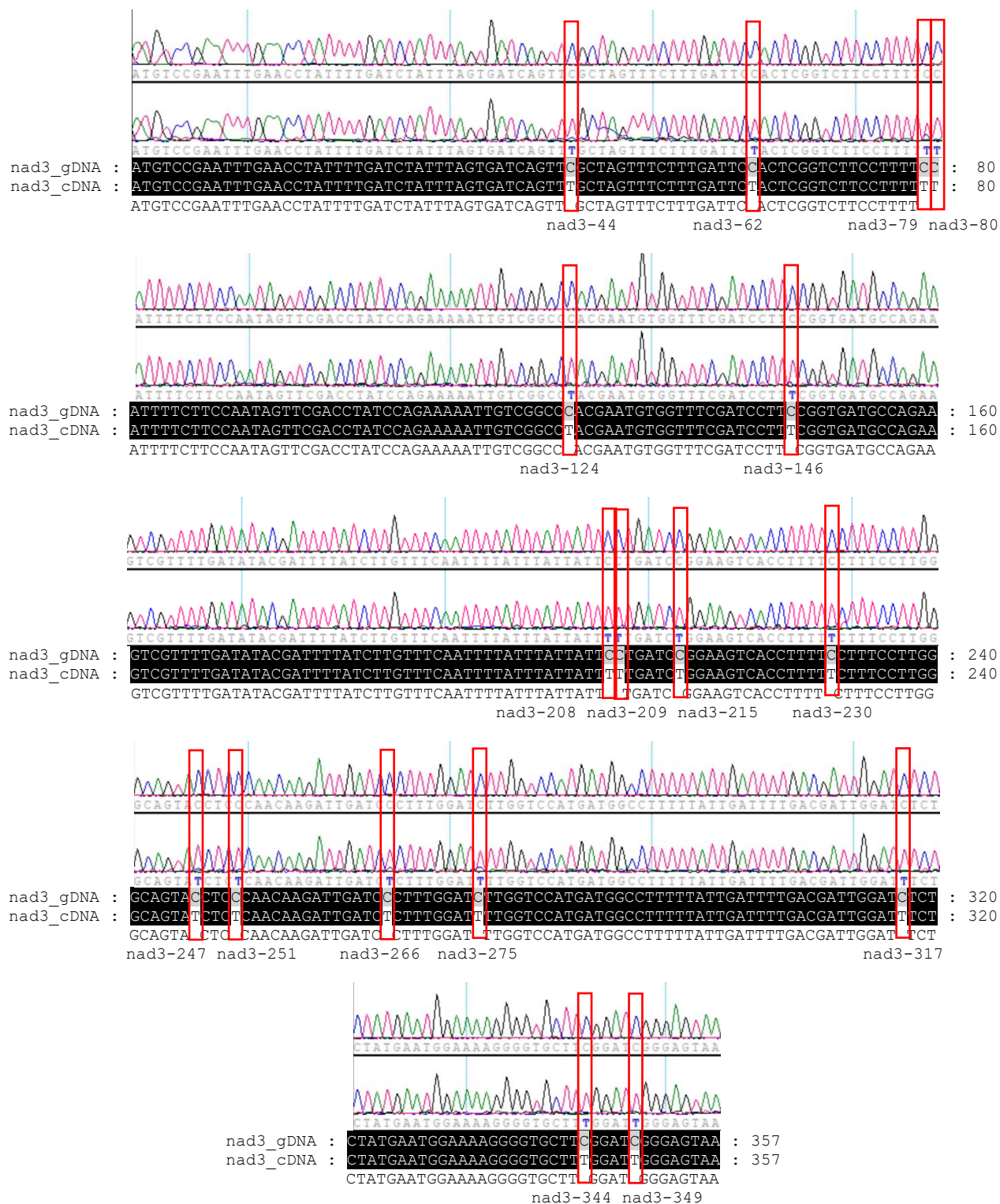


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 mttb-667 mttb-713

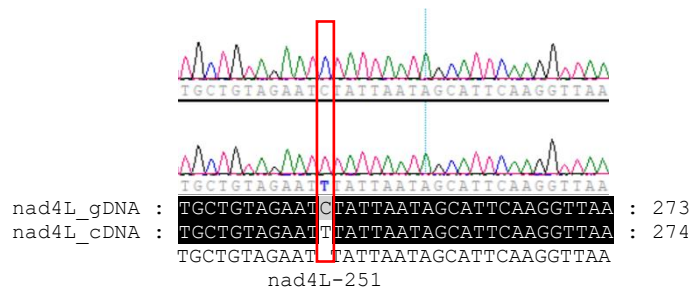
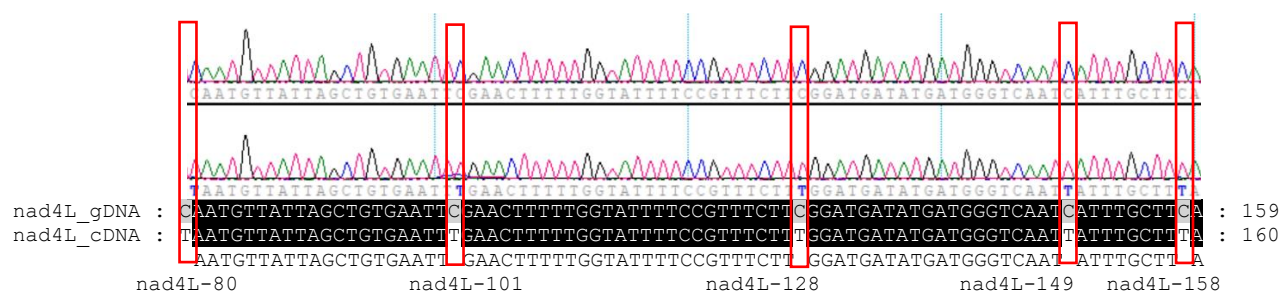


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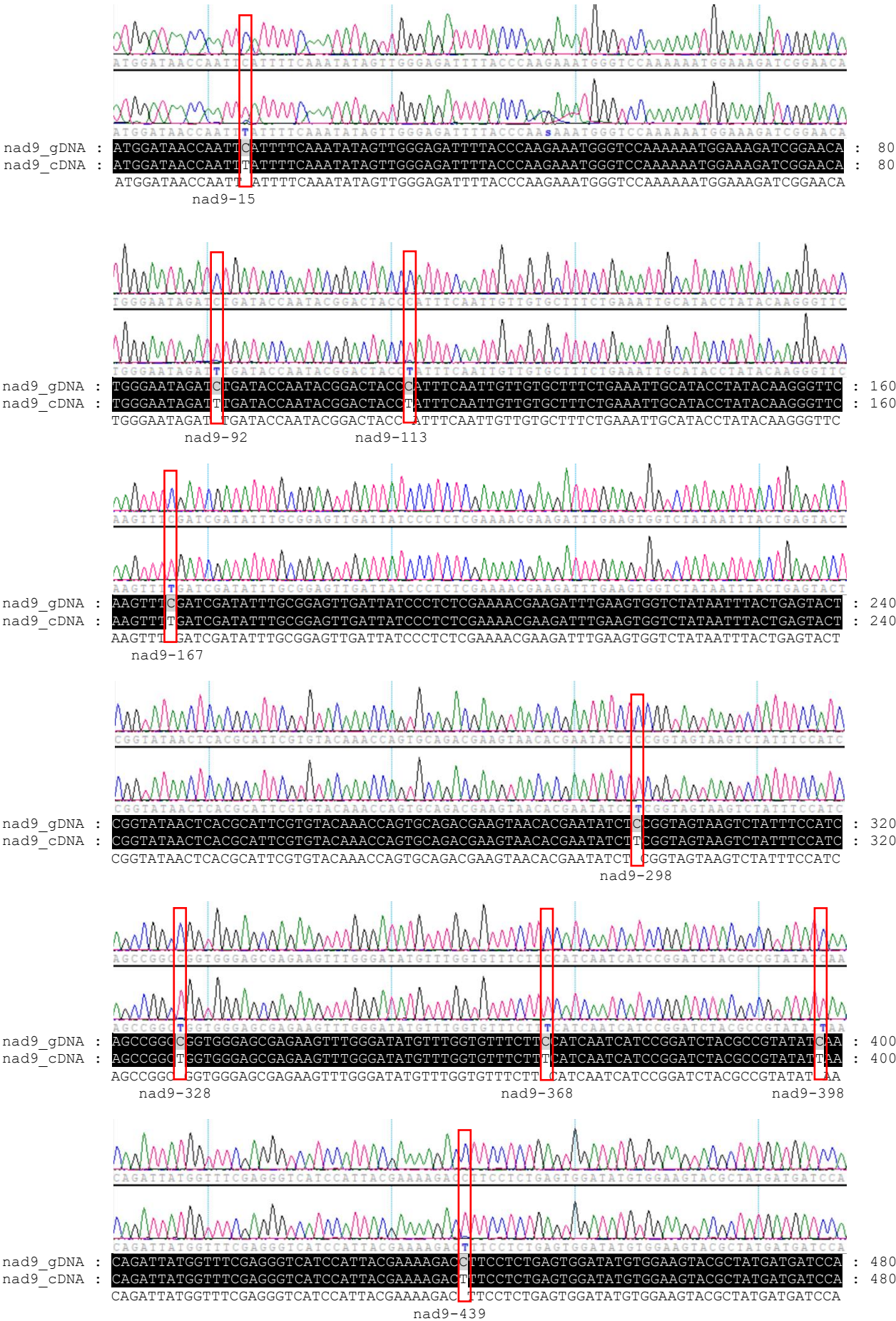
f validation of the *nad3-44*, *nad3-62*, *nad3-79*, *nad3-80*, *nad3-124*, *nad3-146*, *nad3-208*, *nad3-209*, *nad3-215*, *nad3-230*, *nad3-247*, *nad3-251*, *nad3-266*, *nad3-275*, *nad3-317*, *nad3-344*, and *nad3-349* using PCR amplification and Sanger sequencing experiments.

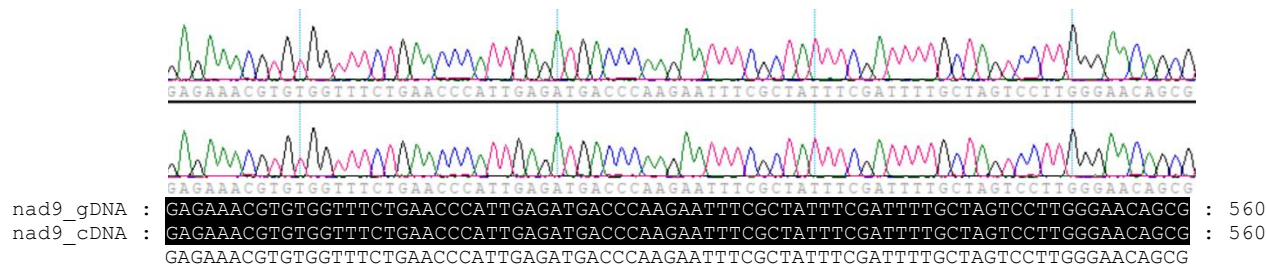


g validation of the *nad4L*-11, *nad4L*-17, *nad4L*-25, *nad4L*-56, *nad4L*-65, *nad4L*-70, *nad4L*-80, *nad4L*-101, *nad4L*-128, *nad4L*-149, *nad4L*-158, *nad4L*-167, *nad4L*-222, and *nad4L*-251 using PCR amplification and Sanger sequencing experiments.

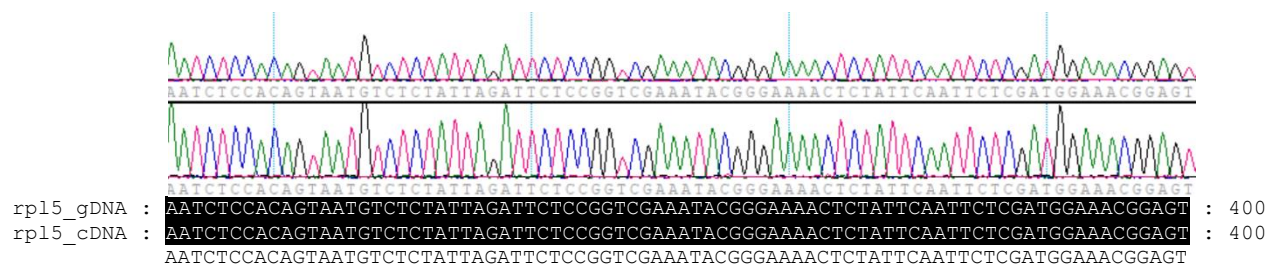
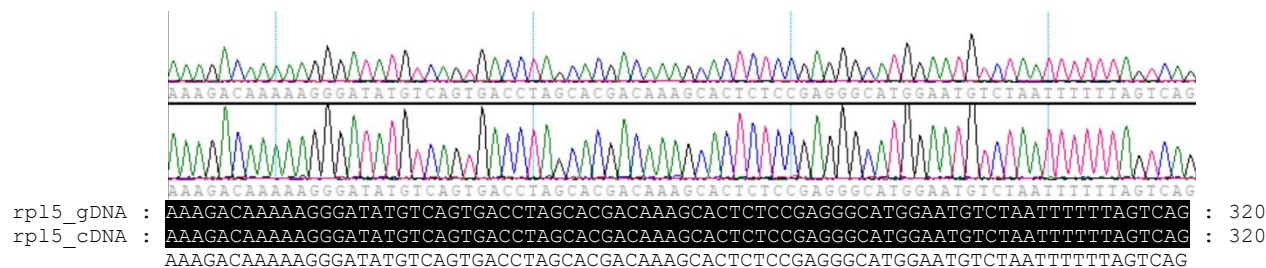
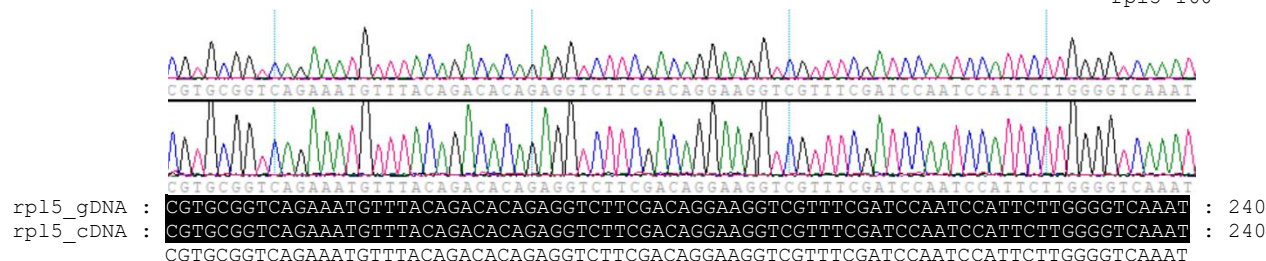
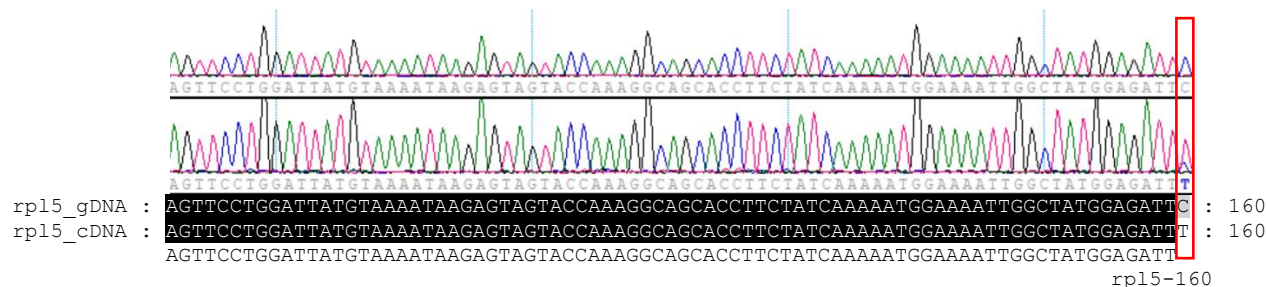
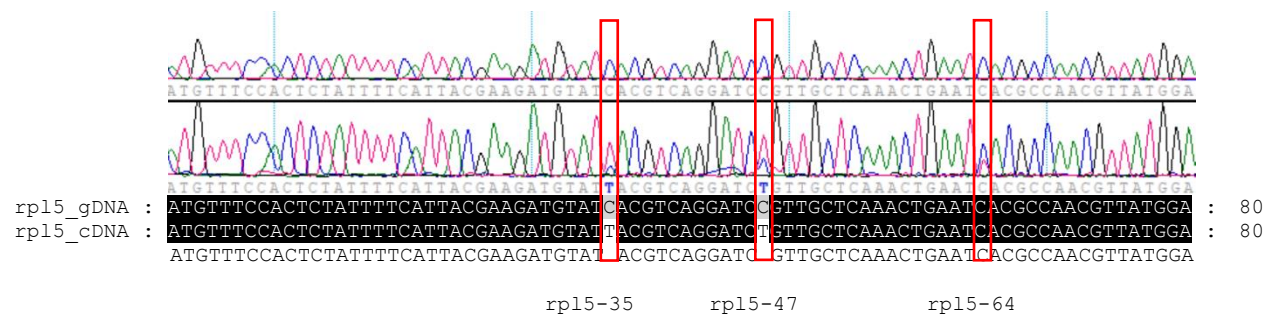


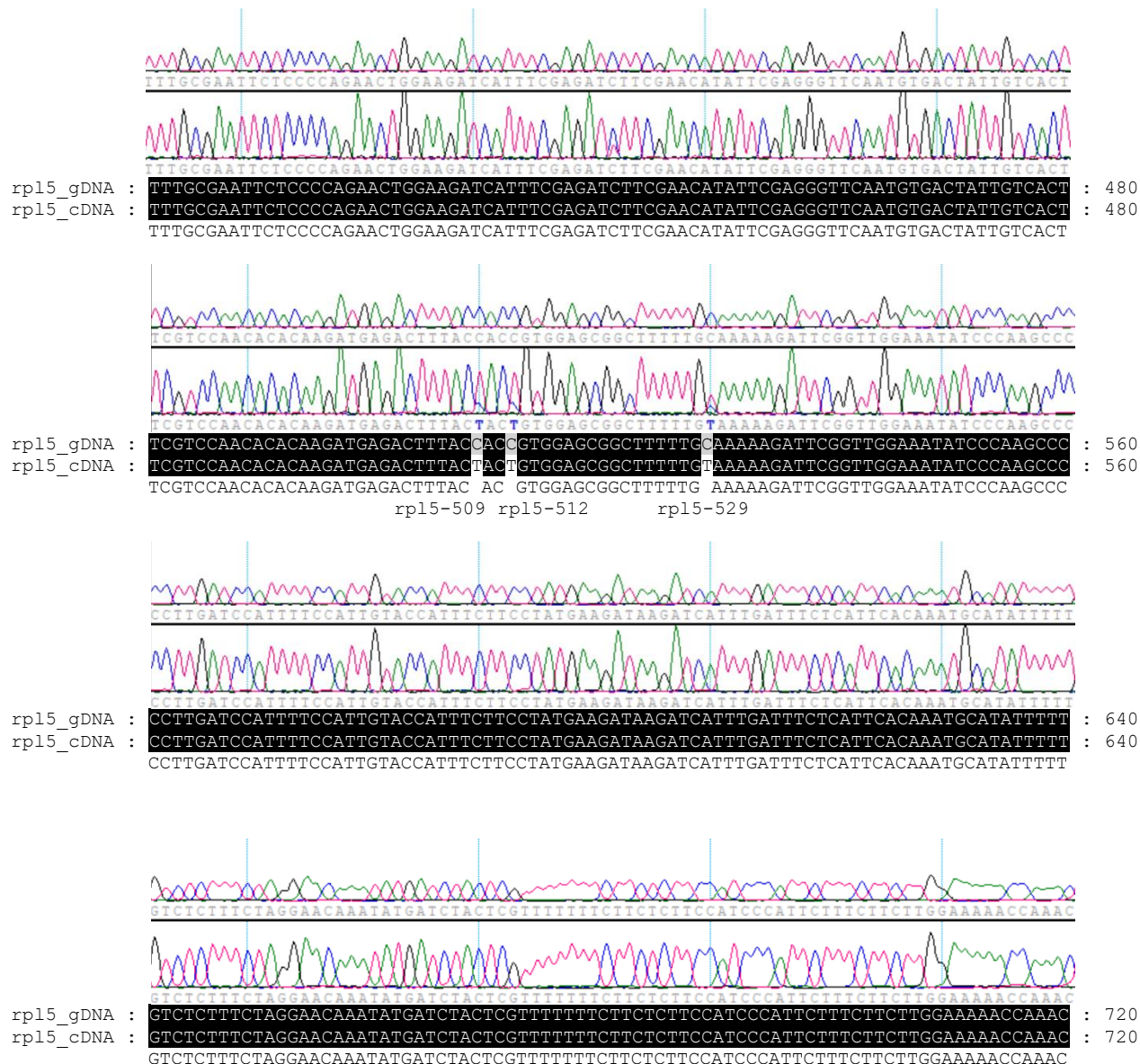
h validation of the *nad9-15*, *nad9-92*, *nad9-113*, *nad9-167*, *nad9-298*, *nad9-328*, *nad9-368*, *nad9-398*, and *nad9-439* using PCR amplification and Sanger sequencing experiments.



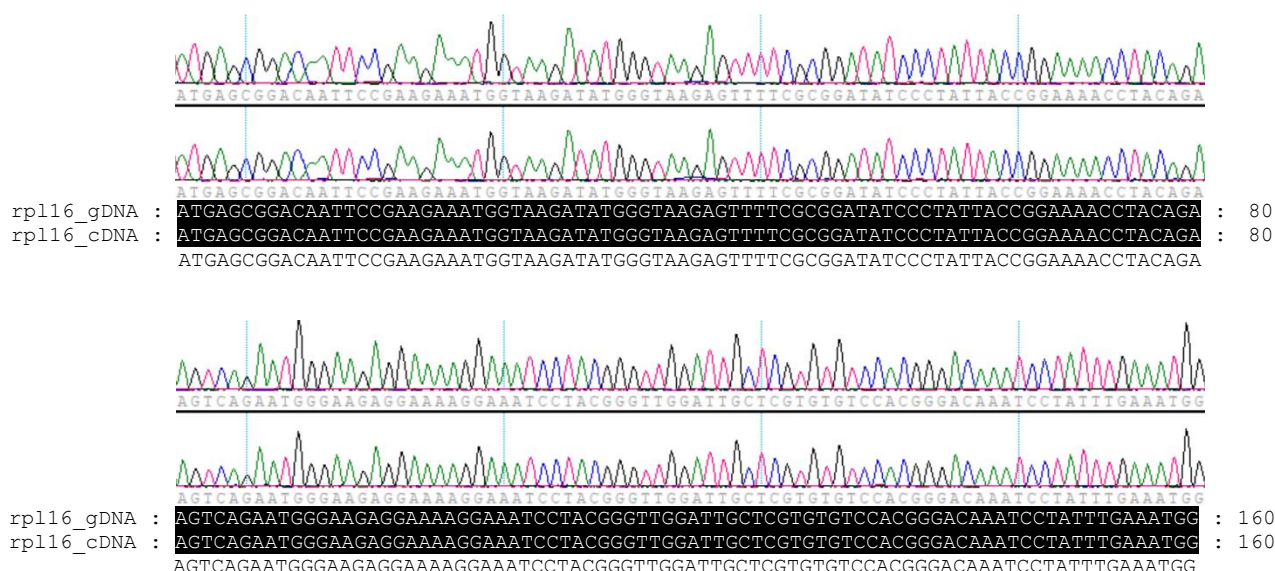


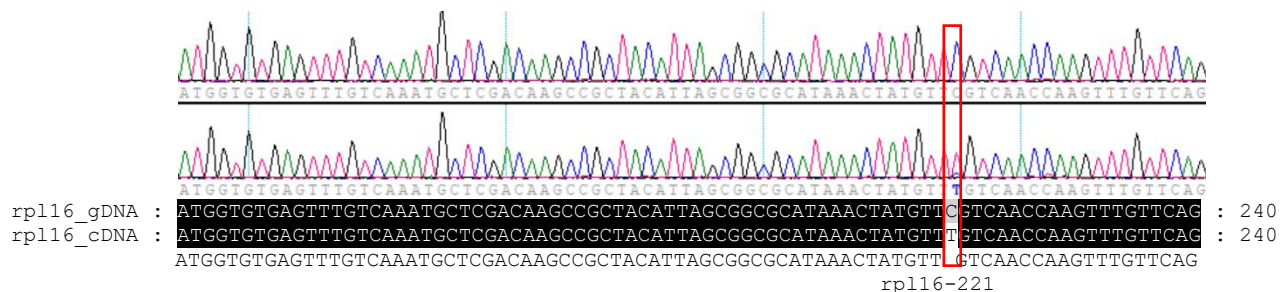
i validation of the *rp15-35*, *rp15-47*, *rp15-160*, *rp15-509*, *rp15-512*, and *rp15-529* using PCR amplification and Sanger sequencing experiments.





j validation of the *rpl16*-221 using PCR amplification and Sanger sequencing experiments.





k validation of the *rps13-56*, *rps13-100*, *rps13-287* using PCR amplification and Sanger sequencing experiments.

