Genome-wide identification, splicing and expression analysis of the myosin gene family in maize (*Zea mays.*)

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Supplementary Tables

Supplementary Table S1. A list of primers used in this study.

Usage	Primer Name	Sequence (5′--------3′)
Semi-quantitative RT PCR	ZmVIII-1-F	GACGGATGAGGGAGACGAA
	ZmVIII-1-R	CAGGCAGAAAGTAAAGCACAA
	ZmVIII-2-F	CAGCCTAAACCCAGACATG
	ZmVIII-2-R	CAATTCAGTAGTCCTTGACCC
	ZmVIII-3-F	CAACGACACTGGGTCAAGG
	ZmVIII-3-R	ATGCCTTGCACATTTCAACAA
	ZmXI-1-F	TGAGAAAGACAGGGAGGCA
	ZmXI-1-R	ACGCCAGAACTCCACATAACT
	ZmXI-2-F	TTTTGAGGAGGCAGGACAC
	ZmXI-2-R	ATGGATGACTGGTTGAGGC
	ZmXI-3-F	CGGTCAGCAGTTCGTTCC
	ZmXI-3-R	ACGACTCGGTAGATGTGG
	ZmXI-4-F	CAGAACGACGAGACGGGGTAG
	ZmXI-4-R	TGGACAAATTGCAGGAGAAAC
	ZmXI-5-F	CGGACATCATCAGGCTTAG
	ZmXI-5-R	TCCCGACGAAGCAGTAAG
	ZmXI-6-F	AACCGAGGAAATTGCAGAG
	ZmXI-6-R	TGACAGCGACCTACAAAGA
	ZmXI-7-F	ATGCGGGTGCTAATGACA
	ZmXI-7-R	AACTGTAAGGGCGGAATC
	ZmXI-8-F	CTCCTCTTGAGGCGTGAAT
	ZmXI-8-R	ATGTTTGGCATTGACTTCG
	ZmXI-9-F	TGACCAAGGAATCAAGCG
	ZmXI-9-R	TCTAATGCCAACCGAGCC
	ZmXI-10-F	AGGATTATTTCCACCAGCAA
	ZmXI-10-R	CTACCACCAATTAGGAAATCTA
	ZmXI-11-F	AAGTCACGACCTTTGTCCG
	ZmXI-11-R	GATTGTCGCCCAATAACCA
	ZmUBQ-Q-F	CTGGTGCCCTCTCCATATGG
	ZmUBQ-Q-R	CAACACTGACACGACTCATGACA
Putative full length myosins gap covering	ZmXI-2-Gap-F	ATGGGACTACAGGGTTATCAGGG
	ZmXI-2-Gap-R	GCCTCTTTGGCAGTGACATCTT
	ZmXI-6-Gap-F	TCAAAGACGGATTTCACCCTG

	ZmXI-6-Gap-R	AAGGTTCCGCAATGCCCTTT
	ZmXI-7-Gap-F	ACGGAAAGCACCAAGATG
	ZmXI-7-Gap-R	AGGCCTGAAACAAATGCA
	ZmXI-8- Gap-F1	GTGAAAGCGGTGCTGGTAAA
	ZmXI-8- Gap-R1	GCATTGTTTCCACTTGCGATA
	ZmXI-8- Gap-F2	GCCACTCTTCGTGAGATGGA
	ZmXI-8- Gap-R2	CAGTTGCCCTGGTGGCTTTA
	ZmXI-9- Gap-F	AATGGACATTGTGGGCATC
	ZmXI-9- Gap-R	CATTGCTATCGTGTTTCTGC
	ZmXI-10- Gap-F	TTGTATCAGGATTATTTCCACCAG
	ZmXI-10- Gap-R	GACTAGCCACTGCTGATCGTCT
	HDO1-5RACE1	TCATCACTACTTTTGCGAGTCACA
	HDO1-5RACE2	GCATTTCCCCTCGACTTCCTTCA
Vector construction for subcellular localization and GUS activity assay	O1head domain-f	GCGAATTCATGAGCTACCGGAAGGGGTTG
	O1head domain-r	CGGTCGACTCCTCCTCCTCCTCCTCCAGCACGGCGCATATCTAAAAT
	O1 head domain IQ-f	GCGAATTCATGAGCTACCGGAAGGGGTTG
	O1 head domain IQ-r	CGGTCGACTCCTCCTCCTCCTCCTCCTAGCTCCTTTCTTGCAAGCTT
	eYFP-F	GCGAATTCGTCGACATGGTGAGCAAGGGCGAGGAG
	eYFP-R	CGCTCGAGCTTGTACAGCTCGTCCATGCC
	O1-P1-F	CGTCTAGACGGGATAACCACCGTGTCAT
	O1-P1-R	ATCCCGGGCCTGCCGAAACCCTAAGCTC
	O1-P2-F	CGTCTAGACAGAGCAGGCCGCATTGATC
	O1-P2-R	ATCCCGGGGTATGGTCAGAAACCCAACGCA
Alternatively spliced transcripts detection	ZmXI-2-F1	AGGGTTATTTCCACAAGCA
	ZmXI-2-R1	CTCGCCCTGATAACCCTGT
	ZmXI-5-F	CGGACATCATCAGGCTTAG
	ZmXI-5-R	TCCCGACGAAGCAGTAAG
	ZmXI-7-F1	ACGGAAAGCACCAAGATG
	ZmXI-7-R1	GAATAGCCGCAACAACCC
	ZmXI-8-F	CTCCTCTTGAGGCGTGAAT
	ZmXI-8-R	ATGTTTGGCATTGACTTCG
	ZmXI-10-F	AGGATTATTTCCACCAGCAA
	ZmXI-10-R	CTACCACCAATTAGGAAATCTA
	ZmXI-11-F	AAGTCACGACCTTTGTCCG
	ZmXI-11-R	GATTGTCGCCCAATAACCA

Supplementary Table S2. Sequences encoding myosin homologs retrieved from maize genome by BLASTP and TBLASTN searches

No.	**Chromosome**				**BAC Accession No.**	**Length (kb)**	**Exon**	**Gene Accession No.**	**No. of Amino Acid**	**MW (kDa)**	**pI**	**Domains**
	No.	**Position (bp) From**	**to**	**Strand**								
1	1	229190070	229205919	-	AC212453.4	15.850	23	GRMZM2G113202	1191	133.472	8.53	MH, IQ, CC
2	1	279808989	279812370	+	AC186902.4	3.382	11	GRMZM2G174083	576	65.536	9.41	MH, IQ
3	1	300108722	300149560	-	AC194061.3	40.839	38	GRMZM2G471108	1506	170.675	7.70	MH, IQ, DIL
4	2	166318980	166322361	+	AC217911.3	3.382	11	GRMZM2G066638	576	65.536	9.41	MH, IQ
5	3	203463334	203479533	+	AC186669.3	16.200	19	GRMZM2G113319	712	80.298	7.00	MH
6	3	203500963	203507842	+	AC195154.3	6.880	20	AC195154.3_FG004	1181	132.743	5.61	DIL
7	3	220883061	220902116	-	AC155377.1	19.056	39	AC155377.1_FG001	1529	173.465	8.53	MH, IQ, DIL
8	4	176870473	176897290	-	AC186563.4	26.818	38	GRMZM2G449909	1520	173.204	8.85	MH, IQ, CC, DIL
9	5	7359267	7367484	-	AC208084.3	8.218**?**	34	GRMZM2G460396	990	113.532	8.01	MH, IQ
10	5	25983026	25994059	-	AC210058.3	11.034	23	GRMZM2G139583	1194	134.072	8.50	MH, IQ, CC
11	5	36445589	36472676	+	AC211332.4	27.088	19	GRMZM2G478078	561	63.417	6.31	MH
12	5	36513549	36530714	+	AC208533.3	17.166	18	GRMZM2G110976	525	60.762	9.47	DIL
13	5	215701287	215703407	+	AC208470.3	2.121	8	GRMZM2G332687	457	50.738	6.52	MH
14	5	215703639	215714449	+	AC208470.3	10.811	30	GRMZM2G034362	1046	119.027	9.04	MH, IQ, DIL
15	6	161542870	161547726	+	AC203402.3	4.857	15	GRMZM2G476843	625	70.851	6.86	DIL
16	6	161483674	161486706	+	AC217943.4	3.033	7	GRMZM2G445423	266	29.647	7.66	MH
17	7	36208341	36213235	+	AC204070.3	4.895	12	GRMZM2G139712	457	50.738	6.52	MH
18	7	36246283	36261130	+	AC204070.3	14.848	16**?**	GRMZM2G302553	527	59.691	5.31	DIL
19	7	157571319	157580965	-	AC198603.3	9.647	24	GRMZM2G057380	1238	139.825	9.13	MH, IQ, CC
20	8	154746952	154761121	-	AC199632.4	14.170	19	GRMZM2G058155	734	83.113	7.02	MH
21	8	154701271	154704616	-	AC199632.4	3.345	12	GRMZM2G306703	493	55.523	6.44	DIL

22	9	4288567	4298608	-	AC211649.3	10.042	39	GRMZM2G435294	1529	173.418	8.92	MH, IQ, DIL

1, Grey and dark grey shading indicate the incomplete myosin sequences.
2, The paired colored sequences are two separated parts of a putative complete myosin gene.
3, Domains presented in the putative myosin sequences were determined using the PFAM and SMART databases.
4, MH, myosin head; IQ, putative calmdulin-binding motif; CC, coiled-coil; DIL, dilute.

Supplementary Table S3. Major domains presented in maize myosin proteins

No.	**Accession number**	**Domain predicted**									
		Myosin N		**Head**		**IQ**		**CC**		**DIL**	
		Range	**E-value**	**Range**	**E-value**	**Range**	**E-value**	**Range**	**E-value**	**Range**	**E-value**
VIII-1	GRMZM2G113202	---	---	193-849	$9e^{-225}$	867-883	0.073	981-1039	1090	---	---
						885-907	13.6				
						913-932	0.00014				
						936-953	0.025				
VIII-2	GRMZM2G139583	---	---	276-933	$2.8e^{-226}$	951-967	0.078	1065-1123	----	---	---
						969-991	1.28e				
						997-1016	0.00015				
						1020-1037	0.027				
VIII-3	GRMZM2G057380	---	---	219-875	$2.9e^{-218}$	888-910	1.32e	1023-1072	----	----	----
						911-933	1.09e				
						937-959	4.13e				
						965-982	0.0019				
XI-1	GRMZM2G471108	23-60	$2.9e^{-8}$	76-731	$2.4e^{-236}$	749-766	0.0066	888-1062	---	1325-1432	$8e^{-37}$
						711-789	0.0082				
						797-814	0.1				
						816-838	$2.74e^{2}$				
						843-862	$2.8e^{-5}$				
						867-886	0.085				
XI-2	KF493895	11-47	$6.4e^{-9}$	64-719	$7.8e^{-241}$	733-755	16	1424-1612	1610	1924-1993	$1.4e^{-19}$
						781-803	140				
						804-826	70				
						829-851	12.1				
						855-874	0.065				

XI-3	AC155377.1-FG001	11-49	$8.2e^{-13}$	64-719	$5.4e^{-242}$	736-754	0.048	---	---	1347-1453	$2.8e^{-35}$
						759-777	0.00081				
						784-802	0.0037				
						807-826	0.034				
						831-851	0.012				
						856-874	0.13				
XI-4	GRMZM2G449909	9-44	0.02	62-719	$1.8e^{-231}$	758-777	0.001	973-1054	55100	1334-1440	$3e^{-33}$
						783-802	0.0087				
						808-825	0.0004				
						831-844	0.17				
						854-874	0.031				
XI-5	GRMZM2G460396	---	---	1-653	$9e^{-238}$	670-688	0.045				
						690-712	1.9e				
						718-736	0.0023				
						738-760	$1.33e^{2}$				
						763-785	3.91e				
						789-808	0.03				
XI-6	KF493897	7-26	0.079	65-751	$3.1e^{-220}$	769-786	0.4	942-1080	2190	1335-1440	$2.3e^{-32}$
						788-810	191				
						813-835	9.73				
						836-858	61				
						864-876	0.36				
						886-906	0.3				
XI-7	KF493892	51-88	$2.5e^{-9}$	104-760	$1.1e^{-20}$	777-795	0.05	---	---	1375-1482	$8e^{-37}$
						799-819	0.0015				
						825-843	0.0065				
						848-866	0.0083				
						872-891	0.00021				
						896-915	0.00084				

XI-8	KF493894	11-48	$1.7e^{-7}$	65-610	$3.2e^{-202}$	633-652	0.0085	959-1088	2190	1794-1898	$6.9e^{-29}$
						724-742	0.69	1140-1252	1970		
						744-766	4.46	1311-1399	64400		
XI-9	KF493893	11-48	$4.8e^{-6}$	64-718	$2.1e^{-231}$	736-753	0.0011	---	---	1326-1433	$1.3e^{-35}$
						759-776	0.054				
						783-801	0.0024				
						807-825	0.12				
						830-849	$7.8e^{-6}$				
						854-873	0.0021				
XI-10	KF493896	11-46	$1.2e^{-7}$	64-719	$3.2e^{-241}$	736-754	0.9	1199-1285	1570	1698-1803	$8.7e^{-31}$
						808-825	0.95	1315-1390	1520		
						832-845	0.84				
						855-874	0.045				
XI-11	GRMZM2G435294	11-46	$9.2e^{-5}$	64-720	$3.6e^{-241}$	734-756	6.27e	---	---	1347-1453	$7.8e^{-36}$
						759-778	0.029				
						785-804	0.033				
						805-827	8.05e				
						835-852	0.029				
						856-875	0.017				

1, Domains presented in the putative myosin sequences were determined using the PFAM and SMART databases.

2, Myosin N, N-terminal SH3-like; Head, myosin head; IQ, putative calmdulin-binding motif; CC, coiled-coil; DIL, dilute.

Supplementary Table S4. Analysis of intron and exon sizes and intron phases in maize myosins

Number		**Class VIII**			**Class XI**										
		VIII-1	**VIII-2**	**VIII-3**	**XI-1**	**XI-2**	**XI-3**	**XI-4**	**XI-5**	**XI-6**	**XI-7**	**XI-8**	**XI-9**	**XI-10**	**XI-11**
Exon1	**Size**	417	564	1199	218	282	378	325	135	135	252	438	246	315	45
Intron1-2	**Size**	1918	1676	554	476	687	2965	957	76	158	160	770	1547	712	176
	Phase	0	0	0	0	0	0	0	-	0	0	0	0	0	0
Exon2	**Size**	102	102	102	144	129	129	150	144	144	144	129	129	129	129
Intron2-3	**Size**	85	79	80	756	2363	595	764	98	264	125	499	425	2557	110
	Phase	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Exon3	**Size**	144	144	144	146	144	144	146	146	146	146	144	144	144	144
Intron3-4	**Size**	71	77	268	87	83	88	80	69	85	150	103	224	84	146
	Phase	0	0	0	2	0	0	2	2	2	2	0	0	0	0
Exon4	**Size**	151	151	151	157	146	146	160	157	157	157	146	146	146	146
Intron4-5	**Size**	79	76	79	319	103	108	378	101	108	95	113	79	104	214
	Phase	1	1	1	0	2	2	0	0	0	0	2	2	2	2
Exon5	**Size**	28	28	28	59	157	157	59	59	59	59	157	157	157	157
Intron5-6	**Size**	844	836	90	93	137	114	304	69	318	96	148	203	138	742
	Phase	2	2	2	2	0	0	2	2	2	2	0	0	0	0
Exon6	**Size**	166	166	166	160	59	59	157	160	157	160	59	59	59	59
Intron6-7	**Size**	84	75	88	447	6372	91	1353	88	1439	201	167	128	4646	121
	Phase	0	0	0	0	2	2	0	0	0	0	2	2	2	2
Exon7	**Size**	64	64	64	150	160	160	150	150	150	150	160	160	160	160
Intron7-8	**Size**	107	108	113	84	98	111	134	109	100	89	72	184	98	84
	Phase	1	1	1	0	0	0	0	0	0	0	0	0	0	0
Exon8	**Size**	14	14	14	137	150	150	137	137	137	137	150	150	150	150
Intron8-9	**Size**	91	85	80	86	92	81	491	79	2379	86	84	85	107	98
	Phase	0	0	0	2	0	0	2	2	2	2	0	0	0	0

Exon9	**Size**	85	85	85	147	137	137	147	147	147	147	137	137	137	137
Intron9-10	**Size**	211	213	187	111	95	90	70	119	71	127	149	78	100	92
	Phase	1	1	1	2	2	2	2	2	2	2	2	2	2	2
Exon10	**Size**	104	104	104	102	147	147	102	102	102	102	147	147	147	147
Exon10-11	**Size**	111	109	91	3641	74	89	360	90	868	670	82	99	74	100
	Phase	0	0	0	2	2	2	2	2	2	2	2	2	2	2
Exon11	**Size**	139	139	139	58	102	102	58	58	58	58	102	102	102	102
Intron11-12	**Size**	776	795	106	114	96	89	85	104	81	100	93	4282	95	81
	Phase	1	1	1	0	2	2	0	0	0	0	2	2	2	2
Exon12	**Size**	119	119	119	102	58	58	102	102	102	102	58	58	58	58
Intron12-13	**Size**	5068	97	84	943	83	75	1140	80	17674	402	78	82	83	101
	Phase	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Exon13	**Size**	153	153	153	38	102	102	38	38	38	38	102	102	102	102
Intron13-14	**Size**	79	251	79	90	199	1304	84	134	74	109	111	331	1387	661
	Phase	0	0	0	2	0	0	2	2	2	2	0	0	0	0
Exon14	**Size**	90	90	90	127	38	35	127	127	127	127	38	38	38	38
Intron14-15	**Size**	379	341	882	3111	291	144	89	84	98	76	149	70	105	91
	Phase	0	0	0	0	2	2	0	0	0	0	2	2	2	2
Exon15	**Size**	78	78	78	168	127	127	174	171	174	171	127	127	127	127
Intron15-16	**Size**	1167	1143	583	73	121	88	549	72	429	81	85	8890	118	109
	Phase	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Exon16	**Size**	159	159	159	132	168	171	132	132	132	132	165	165	168	171
Intron16-17	**Size**	112	110	148	755	2618	4508	1384	111	169	82	24525	76	1079	100
	Phase	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Exon17	**Size**	204	204	201	110	132	132	110	107	110	110	277	132	132	132
Intron17-18	**Size**	90	90	363	75	84	70	586	128	148	87	105	847	84	85
	Phase	0	0	0	2	0	0	2	2	2	2	1	0	0	0

Exon18	**Size**	206	206	206	61	110	110	61	61	90	61	89	110	110s	110
Intron18-19	**Size**	72	79	95	285	80	93	6631	114	243	1676	123	82	82	111
	Phase	2	2	2	0	2	2	0	0	2	0	0	2	2	2
Exon19	**Size**	133	136	136	178	61	61	178	178	61	178	120	61	61	61
Intron19-20	**Size**	191	190	153	103	9463	149	1023	100	22499	104	89	583	?	77
	Phase	0	0	0	1	0	0	1	1	0	1	0	0	0	0
Exon20	**Size**	130	139	130	206	178	178	206	206	178	206	99	178	178	178
Intron20-21	**Size**	105	102	136	378	97	148	180	78	18061	598	85	90	?	76
	Phase	1	1	1	0	1	1	0	0	1	0	0	1	1	1
Exon21	**Size**	147	147	147	120	206	206	120	120	206	120	189	206	206	206
Intron21-22	**Size**	99	100	86	257	145	117	210	83	222	117	237	2436	?	132
	Phase	1	1	1	0	0	0	0	0	0	0	0	0	0	0
Exon22	**Size**	80	80	125	99	120	120	99	99	120	99	140	120	120	120
Intron22-23	**Size**	145	139	316	14936	74	89	609	90	2392	652	10185	4129	?	98
	Phase	0	0	0	0	0	0	0	0	0	0	2	0	0	0
Exon23	**Size**	1053	931	207	210	99	99	222	216	99	213	168	99	99	99
Intron23-24	**Size**			83	100	167	94	160	84	266	139	3460	?	?	161
	Phase			0	0	0	0	0	0	0	0	2	0	0	0
Exon24	**Size**			956	140	189	222	140	140	222	140	168	210	189	219
Intron24-25	**Size**				81	229	307	119	87	292	128	4038	?	?	167
	Phase				2	0	0	2	2	0	2	2	0	0	0
Exon25	**Size**				109	140	140	112	53	119	121	168	140	140	140
Intron25-26	**Size**				210	2251	258	268	348	73	88	137	99	?	110
	Phase				0	2	2	0	1	2	0	2	2	2	2
Exon26	**Size**				36	168	115	51	167	91	39	167	109	14	112
Intron26-27	**Size**				75	219	91	91	109	244	89	92	159	5798	97
	Phase				0	2	0	0	0	0	0	1	0	1	0

Exon27	**Size**		57	168	54	90	101	84	84	148	39	148	51
Intron27-28	**Size**		89	176	97	259	188	136	71	93	78	15389	101
	Phase		0	2	0	0	2	0	0	2	0	2	0
Exon28	**Size**		171	168	81	171	181	171	171	168	78	168	81
Intron28-29	**Size**		120	150	126	95	106	76	562	111	99	164	85
	Phase		0	2	0	0	0	0	0	2	0	2	0
Exon29	**Size**		150	168	171	144	156	150	156	168	171	168	171
Intron29-30	**Size**		4893	76	699	1772	312	867	79	7925	234	100	108
	Phase		0	2	0	0	0	0	0	2	0	2	0
Exon30	**Size**		204	168	153	177	207	177	186	136	150	168	156
Intron30-31	**Size**		1280	77	93	76	74	140	137	809	564	239	86
	Phase		0	2	0	0	0	0	0	0	0	2	0
Exon31	**Size**		105	168	207	138	147	138	135	161	174	168	207
Intron31-32	**Size**		83	1301	82	126	85	1042	81	96	1826	91	83
	Phase		0	2	0	0	0	0	0	2	0	2	0
Exon32	**Size**		71	168	141	71	71	71	71	210	153	210	144
Intron32-33	**Size**		77	77	86	321	137	87	78	111	73	107	152
	Phase		2	2	0	2	2	2	2	2	0	2	0
Exon33	**Size**		100	168	71	100	100	97	100	124	71	126	71
Intron33-34	**Size**		480	5244	74	541	216	81	70	76	90	83	100
	Phase		0	2	2	0	0	0	0	0	2	2	2
Exon34	**Size**		57	168	100	57	121	57	57	93	100	91	100
Intron34-35	**Size**		250	155	76	86		8665	196	118	586	10073	117
	Phase		0	2	0	0		0	0	0	0	0	0
Exon35	**Size**		57	189	57	57		57	57	72	57	81	57
Intron35-36	**Size**		75	58	80	90		219	128	89	8200	75	99
	Phase		0	2	0	0		0	0	0	0	0	0

Exon36	**Size**		81	168	57	81		81	81	186	57	195	57
Intron36-37	**Size**		73	579	94	89		75	262	157	297	344	86
	Phase		0	2	0	0		0	0	0	0	0	0
Exon37	**Size**		89	168	81	83		83	83	345	81	339	81
Intron37-38	**Size**		105	423	118	133		119	89	79	337	79	79
	Phase		2	2	0	2		2	2	0	0	0	0
Exon38	**Size**		706	168	83	499		444	20	138	86	132	83
Intron38-39	**Size**			105	85				130	82	79	91	97
	Phase			2	2				1	0	2	0	2
Exon39	**Size**			165	549				95	71	627	71	201
Intron39-40	**Size**			134						92		73	
	Phase			2						2		2	
Exon40	**Size**			168						100		100	
Intron40-41	**Size**			189						1231		73	
	Phase			2						0		0	
Exon41	**Size**			210						57		57	
Intron41-42	**Size**			111						110		235	
	Phase			2						0		0	
Exon42	**Size**			121						57		57	
Intron42-43	**Size**			80						405		82	
	Phase			0						0		0	
Exon43	**Size**			93						81		81	
Intron43-44	**Size**			94						89		100	
	Phase			0						0		0	
Exon44	**Size**			81						83		83	
Intron44-45	**Size**			77						101		99	
	Phase			0						2		2	

Exon45	**Size**		195		115	575
Intron45-46	**Size**		348			
	Phase		0			
Exon46	**Size**		345			
Intron46-47	**Size**		79			
	Phase		0			
Exon47	**Size**		132			
Intron47-48	**Size**		86			
	Phase		0			
Exon48	**Size**		71			
Intron48-49	**Size**		79			
	Phase		2			
Exon49	**Size**		100			
Intron49-50	**Size**		75			
	Phase		0			
Exon50	**Size**		57			
Intron50-51	**Size**		130			
	Phase		0			
Exon51	**Size**		480			
Intron51-52	**Size**		80			
	Phase		0			
Exon52	**Size**		441			

The number colored in red represents the uncertain fragment length because of the loss of the genomic data in current maize genome release.

Supplementary Table S5. Analysis of repetitive sequences presented in the large introns (> 1 kb) in maize myosins using the RepeatMasker program

No. of Genes	No. of Intron	Retroelements			DNA Transposon			Others		
		Length	Percentage	Clade	Length	Percentage	Clade	Length	Percentage	Clade
VIII-1	1-2	-	-	-	296	15.43	-	51	2.66	Low complexity
	12-13	4203	82.93	Ty1/Copia	-	-	-	-	-	-
	15-16	-	-	-	-	-	-	-	-	-
VIII-2	1-2	-	-	-	408(2) 233 178	24.34 13.90 10.62	hobo-Activator Tc1-IS630-Pogo Tourist/Harbinger	-	-	-
	15-16	-	-	-	-	-	-	-	-	-
VIII-3	-	-	-	-	-	-	-	-	-	-
XI-1	10-11	1518(2) 266	41.69 7.31	L1/CIN4 Ty1/Copia	299(2)	8.21	Tourist/Harbinger	-	-	-
	14-15	1068 899	34.33 28.90	L1/CIN4 Ty1/Copia	155	4.98	hobo-Activator	-	-	-
	22-23	146 6883(5) 5257(5)	0.98 46.08 35.20	SINEs L1/CIN4 Ty1/Copia	-	-	-	146 26	0.98 0.17	Small RNA Simple repeats
	29-30	1050 2569	21.46 52.50	L1/CIN4 Ty1/Copia	165	3.37	hobo-Activator	-	-	-
	30-31	125	9.77	L1/CIN4	-	-	-	-	-	-
XI-2	2-3	514	21.75	L1/CIN4	-	-	-	-	-	-

		497(2)	21.03	Ty1/Copia						
	6-7	3593(3)	62.04	Ty1/Copia	655	10.28	hobo-Activator	-	-	-
	16-17	57 1193	2.18 45.57	L1/CIN4 Ty1/Copia	-	-	-	-	-	-
	19-20	6928(4)	73.21	L1/CIN4	88	0.93	hobo-Activator	-	-	-
	25-26	1223 215	54.33 9.55	L1/CIN4 Gypsy/DIRS1						
	29-30	3250(2)	40.54	Ty1/Copia	148(2)	1.85	Tourist/Harbinger	149 133(4)	1.86 1.66	Unclassified Simple repeats
XI-3	1-2	284	9.58	L1/CIN4	212	7.15	-	-	-	-
	13-14	-	-	-	-	-	-	27	2.07	Simple repeats
	16-17	371 1892(3)	8.23 41.97	L1/CIN4 Gypsy/DIRS1	-	-	-	-	-	-
XI-4	6-7	316	23.36	RTE/Bov-B	-	-	-	-	-	-
	12-13	-	-	-	-	-	-	-	-	-
	16-17	-	-	-	84	6.07	Tc1-IS630-Pogo	-	-	-
	18-19	105 4279	1.58 64.53	L1/CIN4 Ty1/Copia	130	1.96	Tourist/Harbinger	-	-	-
	19-20	327	31.96	RTE/Bov-B	-	-	-	-	-	-

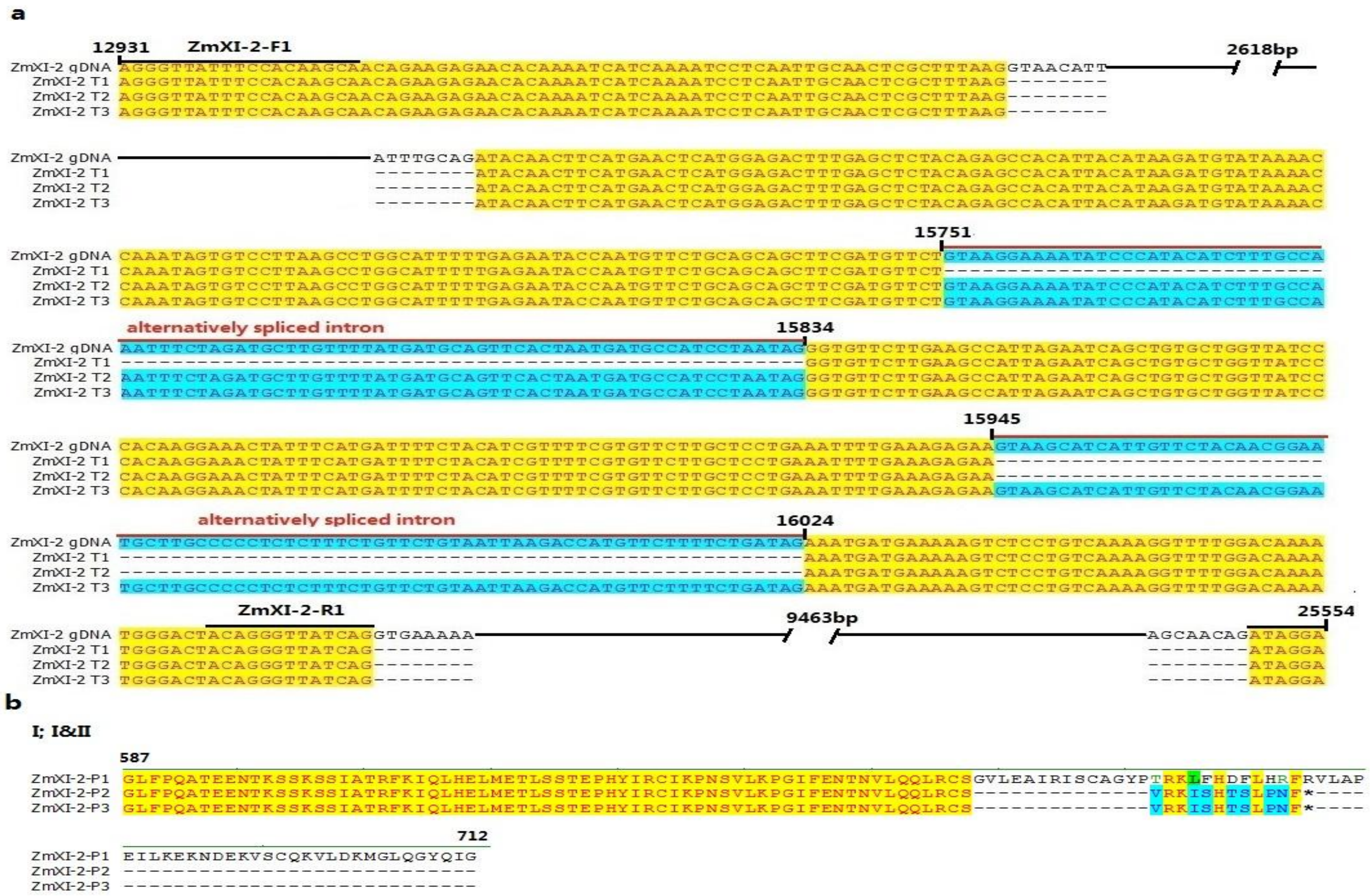
	29-30	767(3) 118	43.28 6.66	L1/CIN4 Ty1/Copia	146	8.24	hobo-Activator	-	-	-
XI-5	-	-	-	-	-	-	-	-	-	-
XI-6	6-7	415	28.84	L1/CIN4	-	-	-	51	3.54	Unclassified
	8-9	1713	72.01	Ty1/Copia	-	-	-	-	-	-
	12-13	2007(2) 7550(3) 5170(3)	11.36 42.72 29.25	RTE/Bov-B L1/CIN4 Ty1/Copia	-	-	-	-	-	-
	19-20	46 7617(9) 4512(6) 4167	0.2 33.85 20.05 18.52	RTE/Bov-B L1/CIN4 Ty1/Copia Gypsy/DIRS1	-	-	-	23	0.1	Simple repeats
	20-21	13171(2) 930	72.93 5.15	Ty1/Copia Gypsy/DIRS1	-	-	-	-	-	-
	22-23	502 54	20.99 2.26	RTE/Bov-B L1/CIN4	127	5.31	Tourist/Harbinger	-	-	-
	31-32	-	-	-	228(2)	21.88	Tourist/Harbinger	-	-	-
	34-35	5443(2) 609(2)	62.82 7.03	L1/CIN4 Ty1/Copia	123	1.42	Tc1-IS630-Pogo	-	-	-
XI-7	18-19	61 223	3.64 13.31	RTE/Bov-B L1/CIN4	166	9.90	Tc1-IS630-Pogo	-	-	-
XI-8	16-17	2620(3) 13201(9) 892(3)	10.68 53.83 3.64	L1/CIN4 Ty1/Copia Gypsy/DIRS1	138	0.56	hobo-Activator	110 157(2)	0.45 0.64	Unclassified Simple repeats

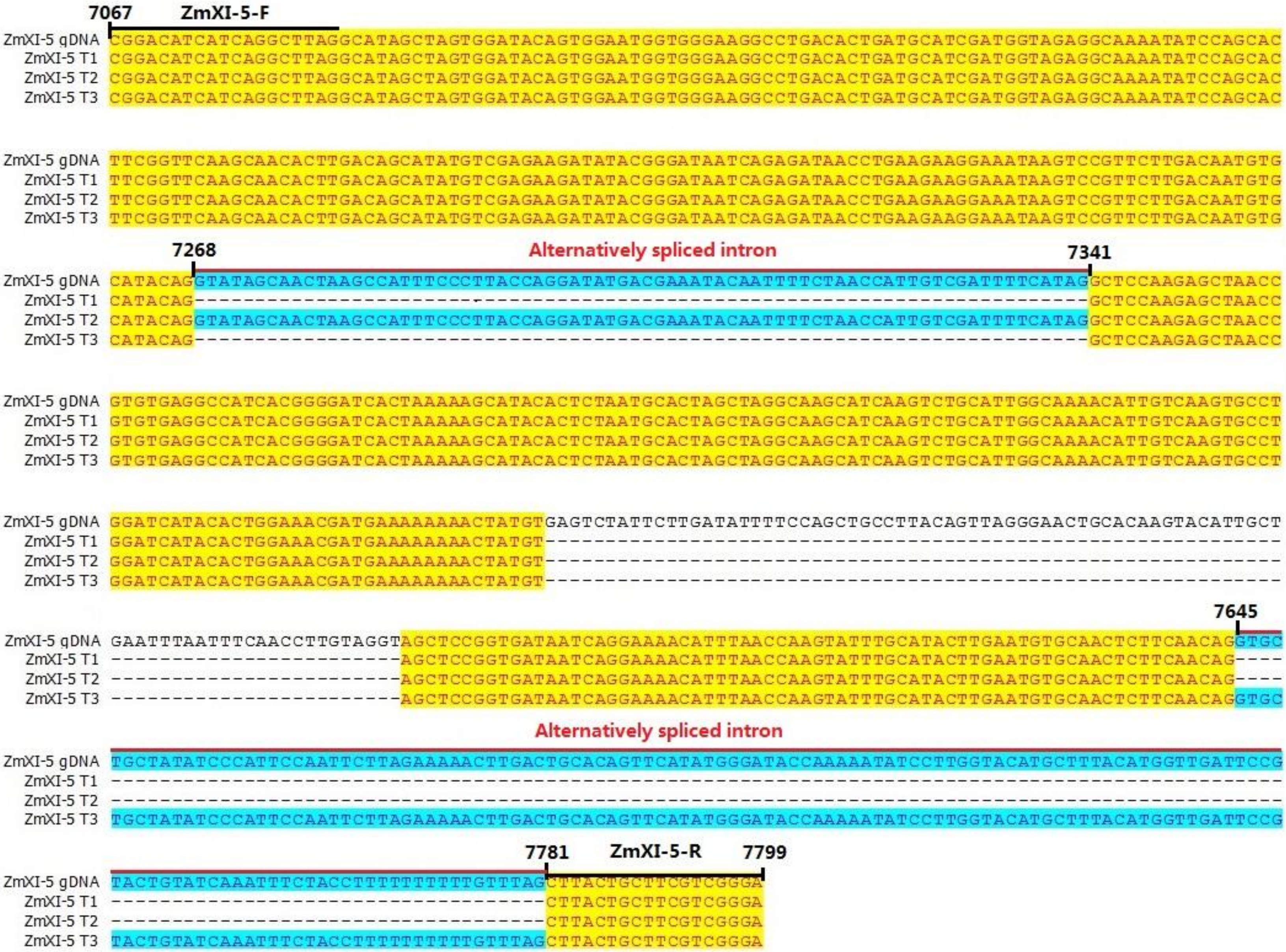
	22-23	7451(3)	73.16	Gypsy/DIRS1	863(3)	8.47	Tourist/Harbinger	-	-	-
					83	0.42	-			
	23-24	1309(6)	37.83	L1/CIN4	-	-	-	149	4.31	Small RNA
		56	1.62	Gypsy/DIRS1						
		149	4.31	SINEs						
	24-25	2300(4)	56.96	L1/CIN4	291	7.21	Tourist/Harbinger	-	-	-
		132	3.27	Ty1/Copia						
		36	0.89	Gypsy/DIRS1						
	29-30	2644	33.36	L1/CIN4	-	-	-	32	0.40	Simple repeats
		3670(5)	46.31	Ty1/Copia						
		301	3.80	-						
	40-41	114	9.26	L1/CIN4	-	-	-	-	-	-
		328	26.65	Gypsy/DIRS1						
XI-9	1-2	-	-	-	382	24.69	hobo-Activator	-	-	-
	11-12	531(2)	12.40	L1/CIN4	-	-	-	-	-	-
		190(2)	4.44	Gypsy/DIRS1						
	15-16	1474	16.58	L1/CIN4	285(2)	3.21	hobo-Activator	62	0.70	Unclassified
		3283(3)	36.93	Ty1/Copia				91	1.02	Simple repeats
	21-22	1888	77.50	RTE/Bov-B	-	-	-	-	-	-
	22-23	1477	35.77	Ty1/Copia	-	-	-	-	-	-
	23-24	189(2)	1.88	L1/CIN4	863	8.58	hobo-Activator	87(3)	0.87	Simple repeats
		4980(2)	49.54	Ty1/Copia						
		1917	19.07	Gypsy/DIRS1						

	30-31	125(2) 123	6.85 6.74	L1/CIN4 Ty1/Copia	-	-	-	-	-	-
	35-36	1052(2) 963(2) 2095	12.83 11.74 20.55	L1/CIN4 Ty1/Copia Gypsy/DIRS1	278(2)	3.39	Tourist/Harbinger	36	0.44	Low complexity
XI-10	2-3	-	-	-	-	-	-	-	-	-
	6-7	2532(3) 609(3)	54.50 13.11	L1/CIN4 Ty1/Copia	35	0.75	hobo-Activator	-	-	-
	13-14	688 60	49.60 4.33	RTE/Bov-B L1/CIN4	-	-	-	51 47	3.68 3.39	Unclassified Simple repeats
	16-17	197(2)	18.26	L1/CIN4	-	-	-	50	4.63	Unclassified
	19-20	3786(6) 3516(4)	40.15 37.29	L1/CIN4 Ty1/Copia	-	-	-	-	-	-
	26-27	1778(2)	30.67	L1/CIN4	70	1.21	Tourist/Harbinger	-	-	-
	27-28	9256(6) 46	60.15 0.30	Ty1/Copia Gypsy/DIRS1	-	-	-	193(3)	1.25	Simple repeats
	34-35	8063(7) 398(2)	80.5 3.95	L1/CIN4 Gypsy/DIRS1	-	-	-	27	0.27	Simple repeats
XI-11	-	-	-	-	-	-	-	-	-	-

Supplementary Figures

Supplementary Figure S1. Sequencing analysis of the alternative splicing events of some maize myosin genes.





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  ZmXI-5 T1 CGGACATCATCAGGCTTAGGCATAGCTAGTGGATACAGTGGAATGGTGGGAAGGCCTGACACTGATGCATCGATGGTAGAGGCAAAATATCCAGCAC
  ZmXI-5 T2 CGGACATCATCAGGCTTAGGCATAGCTAGTGGATACAGTGGAATGGTGGGAAGGCCTGACACTGATGCATCGATGGTAGAGGCAAAATATCCAGCAC
  ZmXI-5 T3 CGGACATCATCAGGCTTAGGCATAGCTAGTGGATACAGTGGAATGGTGGGAAGGCCTGACACTGATGCATCGATGGTAGAGGCAAAATATCCAGCAC

ZmXI-5 gDNA TTCGGTTCAAGCAACACTTGACAGCATATGTCGAGAAGATATACGGGATAATCAGAGATAACCTGAAGAAGGAAATAAGTCCGTTCTTGACAATGTG
  ZmXI-5 T1 TTCGGTTCAAGCAACACTTGACAGCATATGTCGAGAAGATATACGGGATAATCAGAGATAACCTGAAGAAGGAAATAAGTCCGTTCTTGACAATGTG
  ZmXI-5 T2 TTCGGTTCAAGCAACACTTGACAGCATATGTCGAGAAGATATACGGGATAATCAGAGATAACCTGAAGAAGGAAATAAGTCCGTTCTTGACAATGTG
  ZmXI-5 T3 TTCGGTTCAAGCAACACTTGACAGCATATGTCGAGAAGATATACGGGATAATCAGAGATAACCTGAAGAAGGAAATAAGTCCGTTCTTGACAATGTG

ZmXI-5 gDNA CATACAGGTATAGCAACTAAGCCATTTCCCTTACCAGGATATGACGAAATACAATTTTCTAACCATTGTCGATTTTCATAGGCTCCAAGAGCTAACC
  ZmXI-5 T1 CATACAG--------------------------------------------------------------------------GCTCCAAGAGCTAACC
  ZmXI-5 T2 CATACAGGTATAGCAACTAAGCCATTTCCCTTACCAGGATATGACGAAATACAATTTTCTAACCATTGTCGATTTTCATAGGCTCCAAGAGCTAACC
  ZmXI-5 T3 CATACAG--------------------------------------------------------------------------GCTCCAAGAGCTAACC

ZmXI-5 gDNA GTGTGAGGCCATCACGGGGATCACTAAAAAGCATACACTCTAATGCACTAGCTAGGCAAGCATCAAGTCTGCATTGGCAAAACATTGTCAAGTGCCT
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  ZmXI-5 T2 GTGTGAGGCCATCACGGGGATCACTAAAAAGCATACACTCTAATGCACTAGCTAGGCAAGCATCAAGTCTGCATTGGCAAAACATTGTCAAGTGCCT
  ZmXI-5 T3 GTGTGAGGCCATCACGGGGATCACTAAAAAGCATACACTCTAATGCACTAGCTAGGCAAGCATCAAGTCTGCATTGGCAAAACATTGTCAAGTGCCT

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  ZmXI-5 T1 GGATCATACACTGGAAACGATGAAAAAAAACTATGT-------------------------------------------------------------
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  ZmXI-5 T1 ------------------------AGCTCCGGTGATAATCAGGAAAACATTTAACCAAGTATTTGCATACTTGAATGTGCAACTCTTCAACAG----
  ZmXI-5 T2 ------------------------AGCTCCGGTGATAATCAGGAAAACATTTAACCAAGTATTTGCATACTTGAATGTGCAACTCTTCAACAG----
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  ZmXI-5 T2 -------------------------------------------------------------------------------------------------
  ZmXI-5 T3 TGCTATATCCCATTCCAATTCTTAGAAAAACTTGACTGCACAGTTCATATGGGATACCAAAAATATCCTTGGTACATGCTTTACATGGTTGATTCCG

ZmXI-5 gDNA TACTGTATCAAATTTCTACCTTTTTTTTTTGTTTAGCTTACTGCTTCGTCGGGA
  ZmXI-5 T1 ------------------------------------CTTACTGCTTCGTCGGGA
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  ZmXI-5 T3 TACTGTATCAAATTTCTACCTTTTTTTTTTGTTTAGCTTACTGCTTCGTCGGGA
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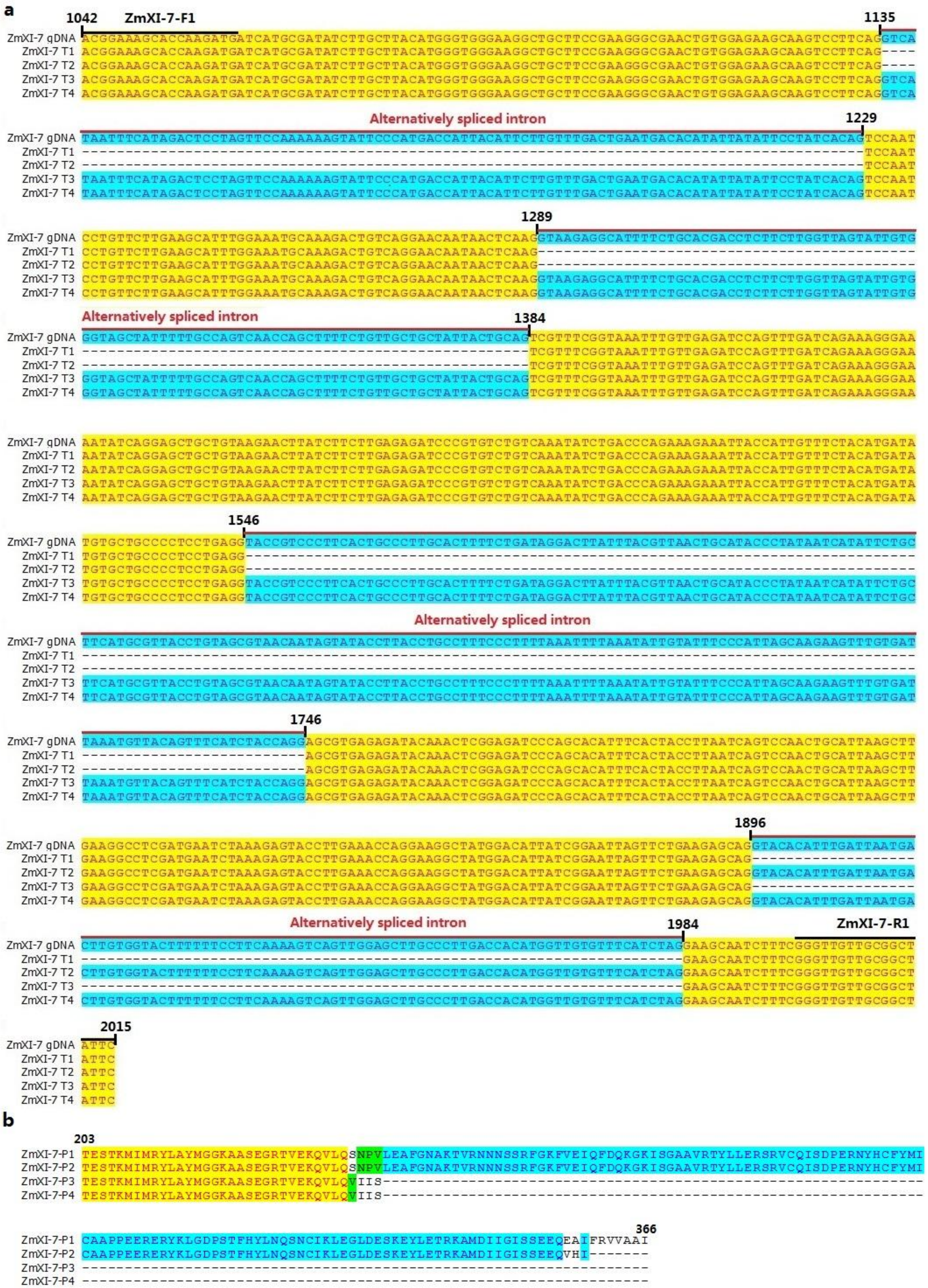
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Alternatively spliced intron
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1546
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1896
1984
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2015
ZmXI-7 gDNA
ZmXI-7 T1
ZmXI-7 T2
ZmXI-7 T3
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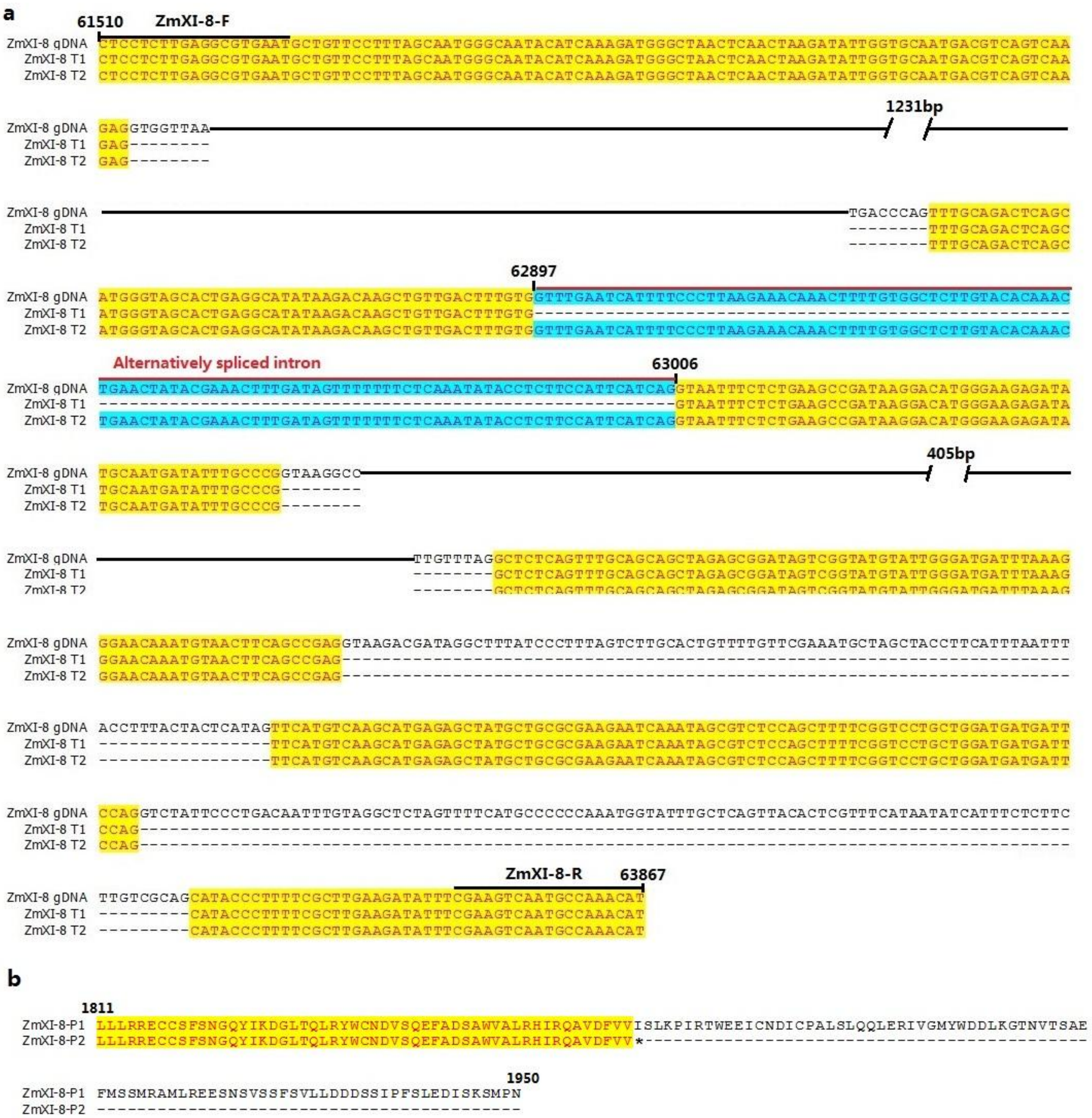
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ZmXI-8 T1 CTCCTCTTGAGGCGTGAATGCTGTTCCTTTAGCAATGGGCAATACATCAAAGATGGGCTAACTCAACTAAGATATTGGTGCAATGACGTCAGTCAA
ZmXI-8 T2 CTCCTCTTGAGGCGTGAATGCTGTTCCTTTAGCAATGGGCAATACATCAAAGATGGGCTAACTCAACTAAGATATTGGTGCAATGACGTCAGTCAA
1231bp
ZmXI-8 gDNA GAGGTGGTTAA
ZmXI-8 T1 GAG--------
ZmXI-8 T2 GAG--------
ZmXI-8 gDNA TGACCCAGTTTGCAGACTCAGC
ZmXI-8 T1 --------TTTGCAGACTCAGC
ZmXI-8 T2 --------TTTGCAGACTCAGC
62897
ZmXI-8 gDNA ATGGGTAGCACTGAGGCATATAAGACAAGCTGTTGACTTTGTGGTTTGAATCATTTTCCCTTAAGAAACAAACTTTTGTGGCTCTTGTACACAAAC
ZmXI-8 T1 ATGGGTAGCACTGAGGCATATAAGACAAGCTGTTGACTTTGTG---
ZmXI-8 T2 ATGGGTAGCACTGAGGCATATAAGACAAGCTGTTGACTTTGTGGTTTGAATCATTTTCCCTTAAGAAACAAACTTTTGTGGCTCTTGTACACAAAC
Alternatively spliced intron
63006
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ZmXI-8 T1 ---GTAATTTCTCTGAAGCCGATAAGGACATGGGAAGAGATA
ZmXI-8 T2 TGAACTATACGAAACTTTGATAGTTTTTTTCTCAAATATACCTCTTCCATTCATCAGGTAATTTCTCTGAAGCCGATAAGGACATGGGAAGAGATA
405bp
ZmXI-8 gDNA TGCAATGATATTTGCCCGGTAAGGCC
ZmXI-8 T1 TGCAATGATATTTGCCCG--------
ZmXI-8 T2 TGCAATGATATTTGCCCG--------
ZmXI-8 gDNA TTGTTTAGGCTCTCAGTTTGCAGCAGCTAGAGCGGATAGTCGGTATGTATTGGGATGATTTAAAG
ZmXI-8 T1 --------GCTCTCAGTTTGCAGCAGCTAGAGCGGATAGTCGGTATGTATTGGGATGATTTAAAG
ZmXI-8 T2 --------GCTCTCAGTTTGCAGCAGCTAGAGCGGATAGTCGGTATGTATTGGGATGATTTAAAG
ZmXI-8 gDNA GGAACAAATGTAACTTCAGCCGAGGTAAGACGATAGGCTTTATCCCTTTAGTCTTGCACTGTTTTGTTCGAAATGCTAGCTACCTTCATTTAATTT
ZmXI-8 T1 GGAACAAATGTAACTTCAGCCGAG--
ZmXI-8 T2 GGAACAAATGTAACTTCAGCCGAG--
ZmXI-8 gDNA ACCTTTACTACTCATAGTTCATGTCAAGCATGAGAGCTATGCTGCGCGAAGAATCAAATAGCGTCTCCAGCTTTTCGGTCCTGCTGGATGATGATT
ZmXI-8 T1 -----------------TTCATGTCAAGCATGAGAGCTATGCTGCGCGAAGAATCAAATAGCGTCTCCAGCTTTTCGGTCCTGCTGGATGATGATT
ZmXI-8 T2 -----------------TTCATGTCAAGCATGAGAGCTATGCTGCGCGAAGAATCAAATAGCGTCTCCAGCTTTTCGGTCCTGCTGGATGATGATT
ZmXI-8 gDNA CCAGGTCTATTCCCTGACAATTTGTAGGCTCTAGTTTTCATGCCCCCCAAATGGTATTTGCTCAGTTACACTCGTTTCATAATATCATTTCTCTTC
ZmXI-8 T1 CCAG--
ZmXI-8 T2 CCAG--
ZmXI-8-R
63867
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ZmXI-8 T2 ---------CATACCCTTTTCGCTTGAAGATATTTCGAAGTCAATGCCAAACAT
b
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ZmXI-8-P2 LLLRRECCSFSNGQYIKDGLTQLRYWCNDVSQEFADSAWVALRHIRQAVDFVV*---
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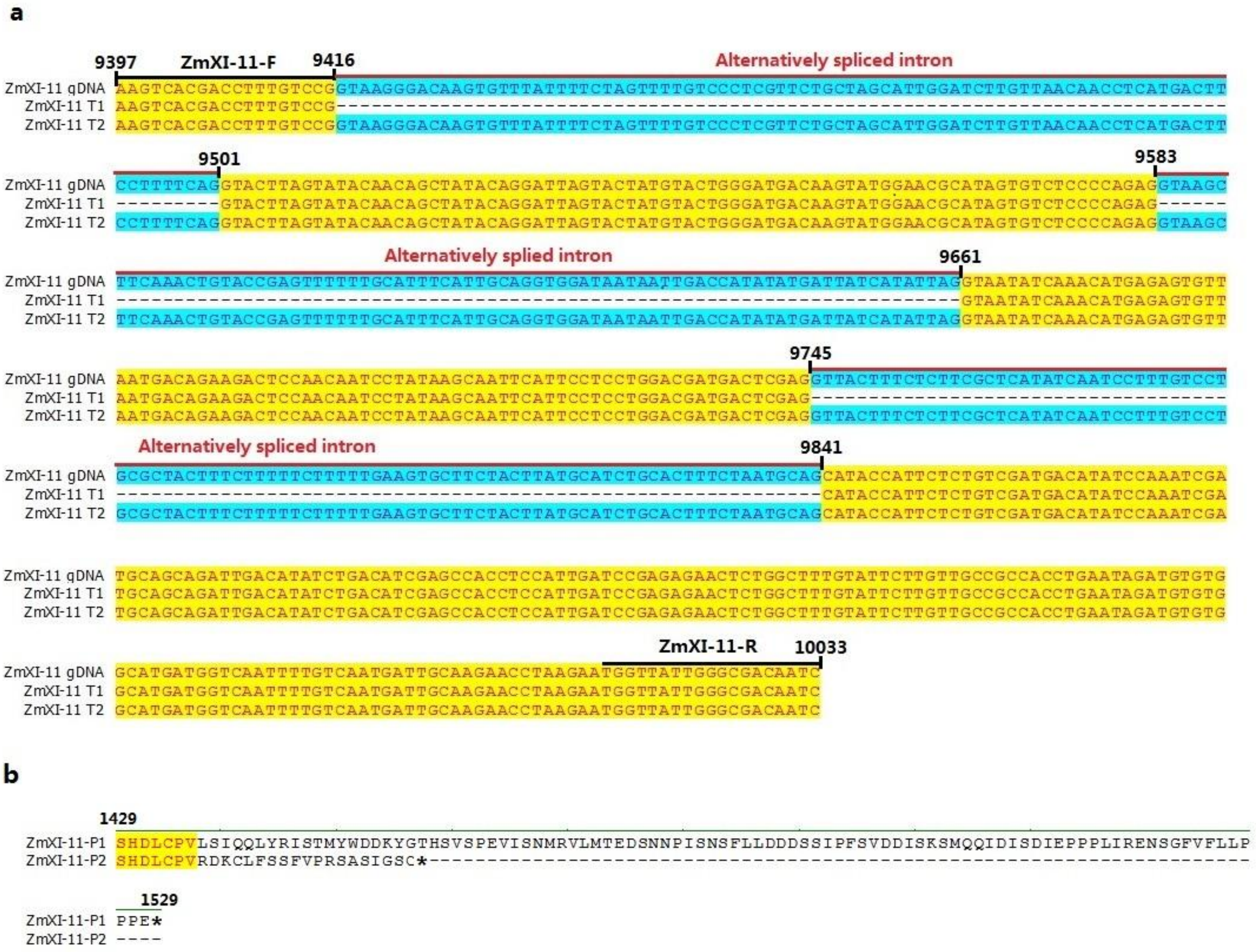
ZmXI-8-P2 --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9416
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ZmXI-11 T1 AAGTCACGACCTTTGTCCG---
ZmXI-11 T2 AAGTCACGACCTTTGTCCGGTAAGGGACAAGTGTTTATTTTCTAGTTTTGTCCCTCGTTCTGCTAGCATTGGATCTTGTTAACAACCTCATGACTT
9501
9583
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ZmXI-11 T2 CCTTTTCAGGTACTTAGTATACAACAGCTATACAGGATTAGTACTATGTACTGGGATGACAAGTATGGAACGCATAGTGTCTCCCCAGAGGTAAGC
Alternatively splied intron
9661
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ZmXI-11 T1 --GTAATATCAAACATGAGAGTGTT
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9745
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Alternatively spliced intron
9841
ZmXI-11 gDNA GCGCTACTTTCTTTTTCTTTTTGAAGTGCTTCTACTTATGCATCTGCACTTTCTAATGCAGCATACCATTCTCTGTCGATGACATATCCAAATCGA
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ZmXI-11-P2 SHDLCPVRDKCLFSSFVPRSASIGSC*---
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Supplementary Figure S2. Transcript evidence and splicing event for maize myosin genes.

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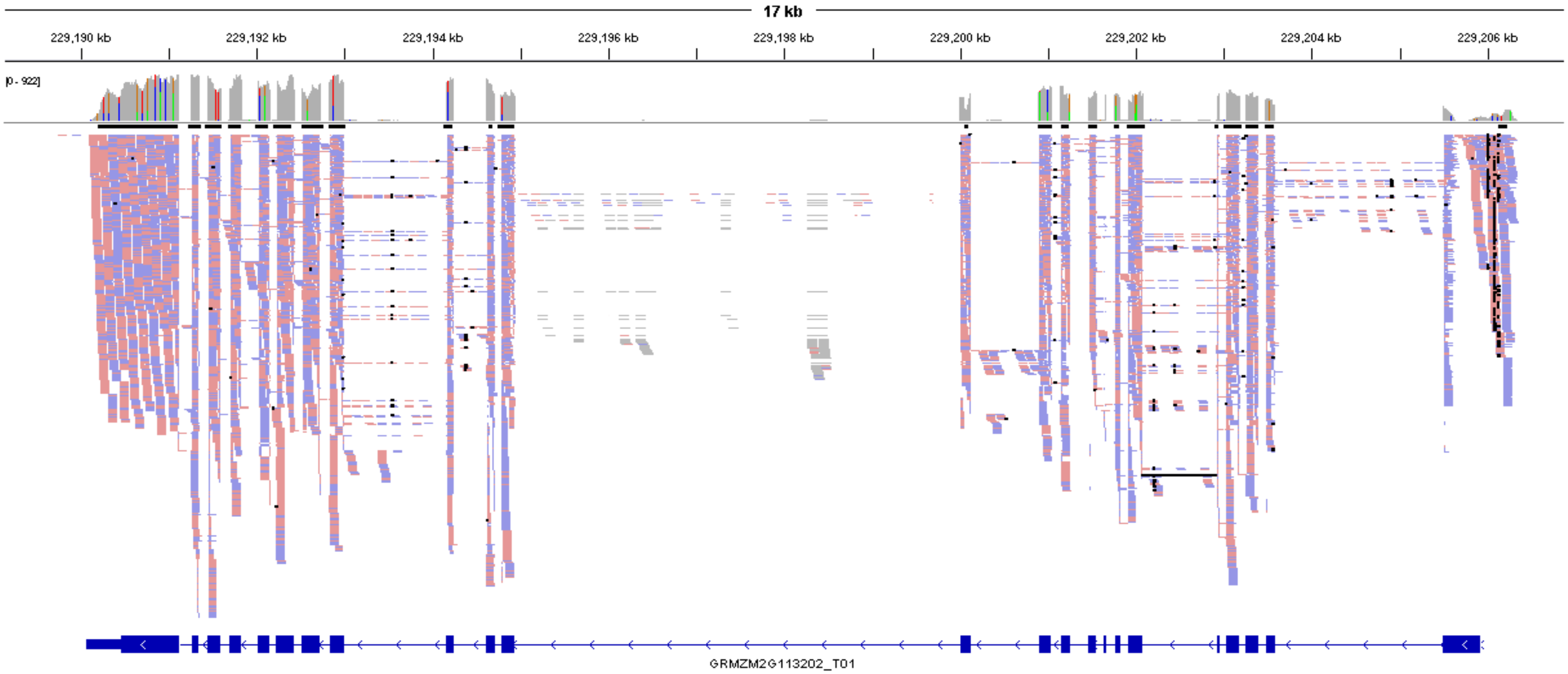

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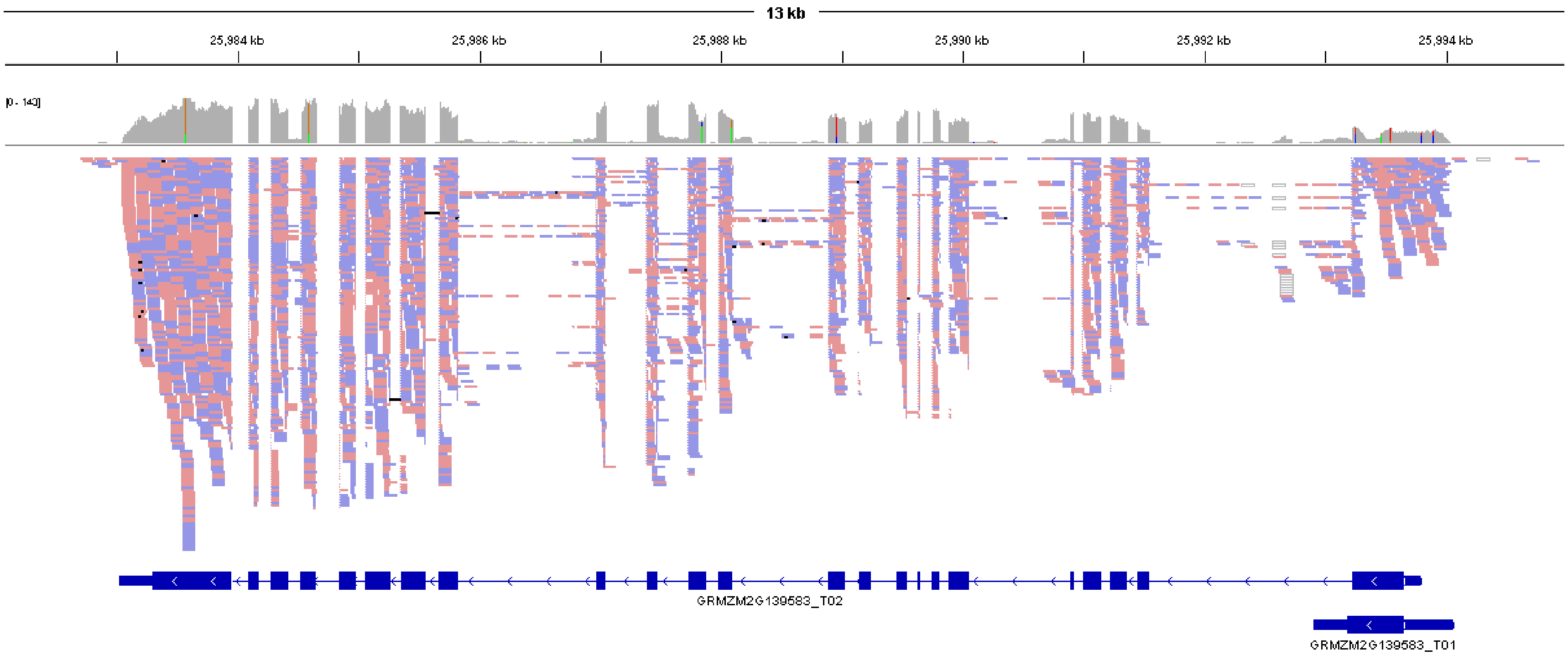
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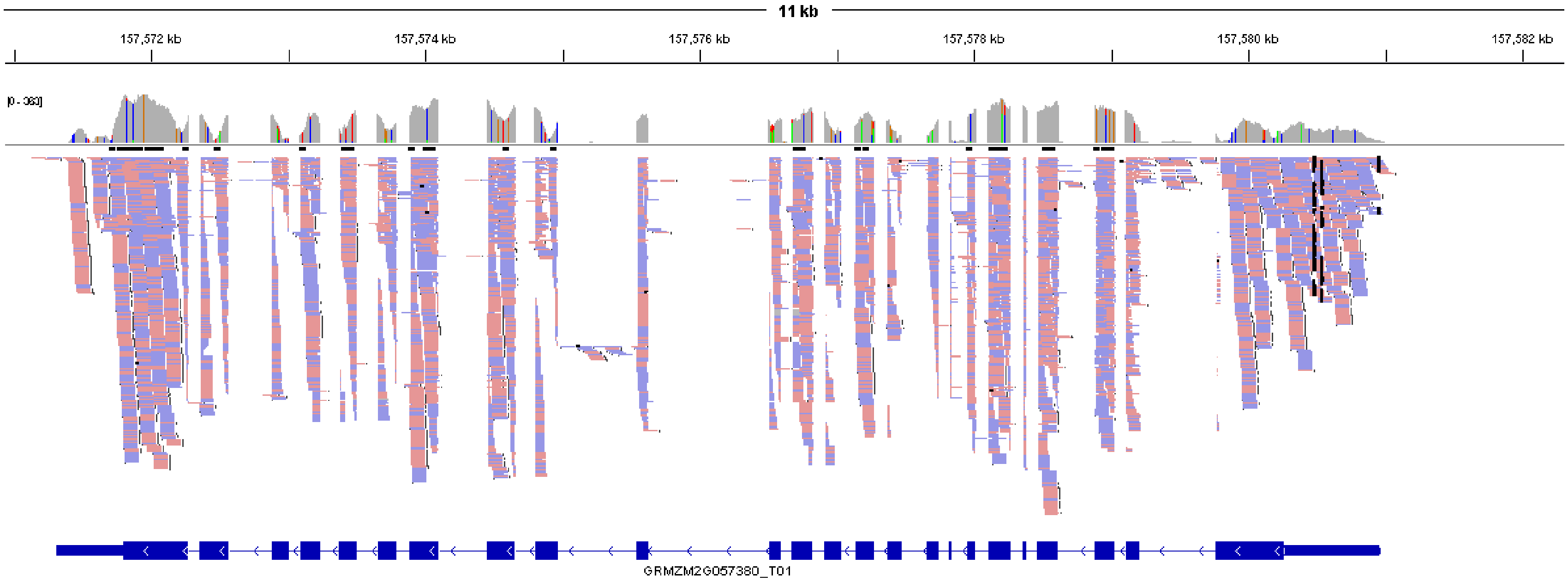
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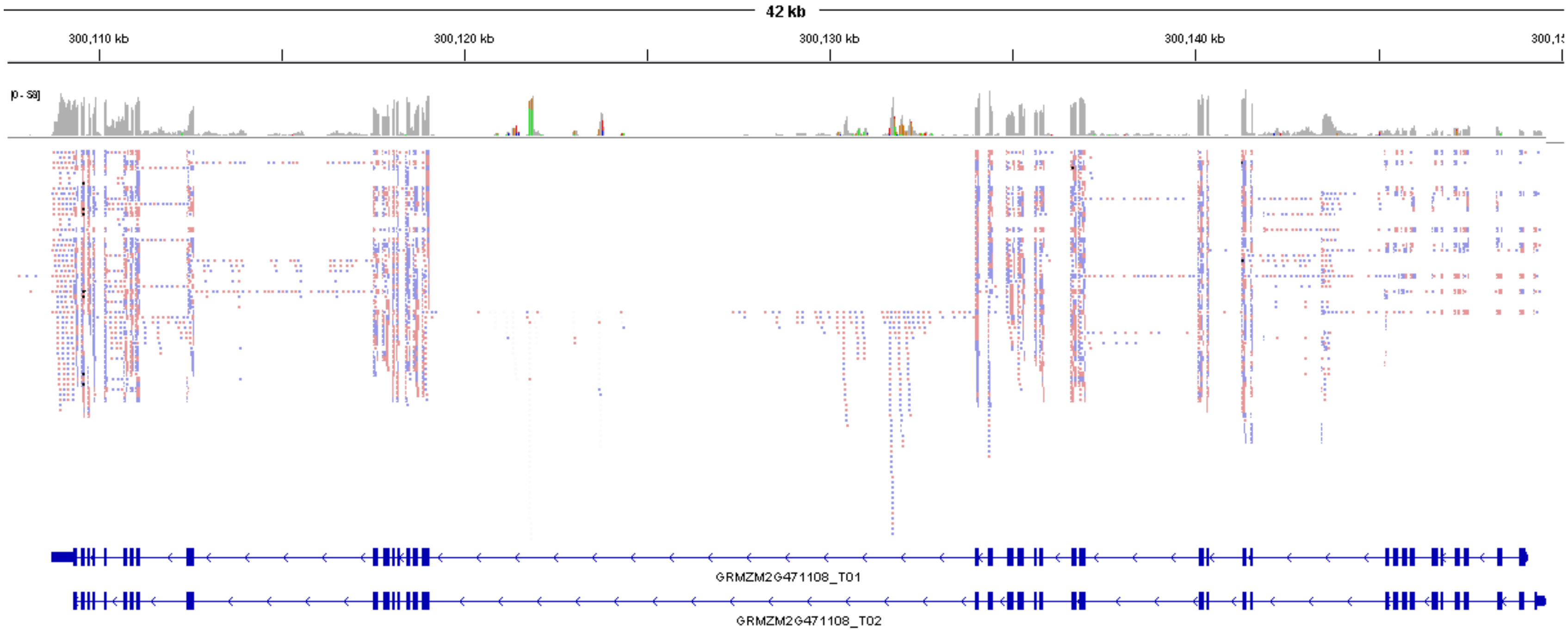
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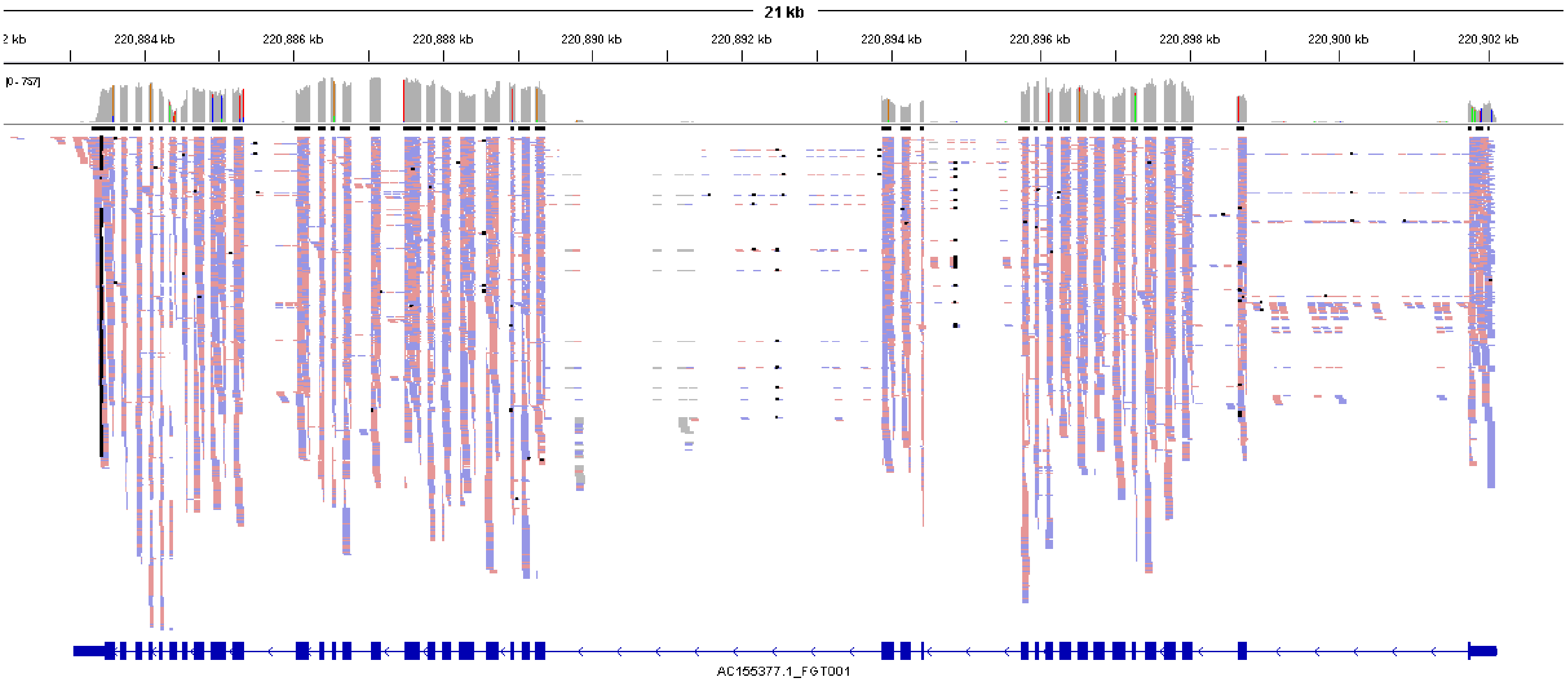
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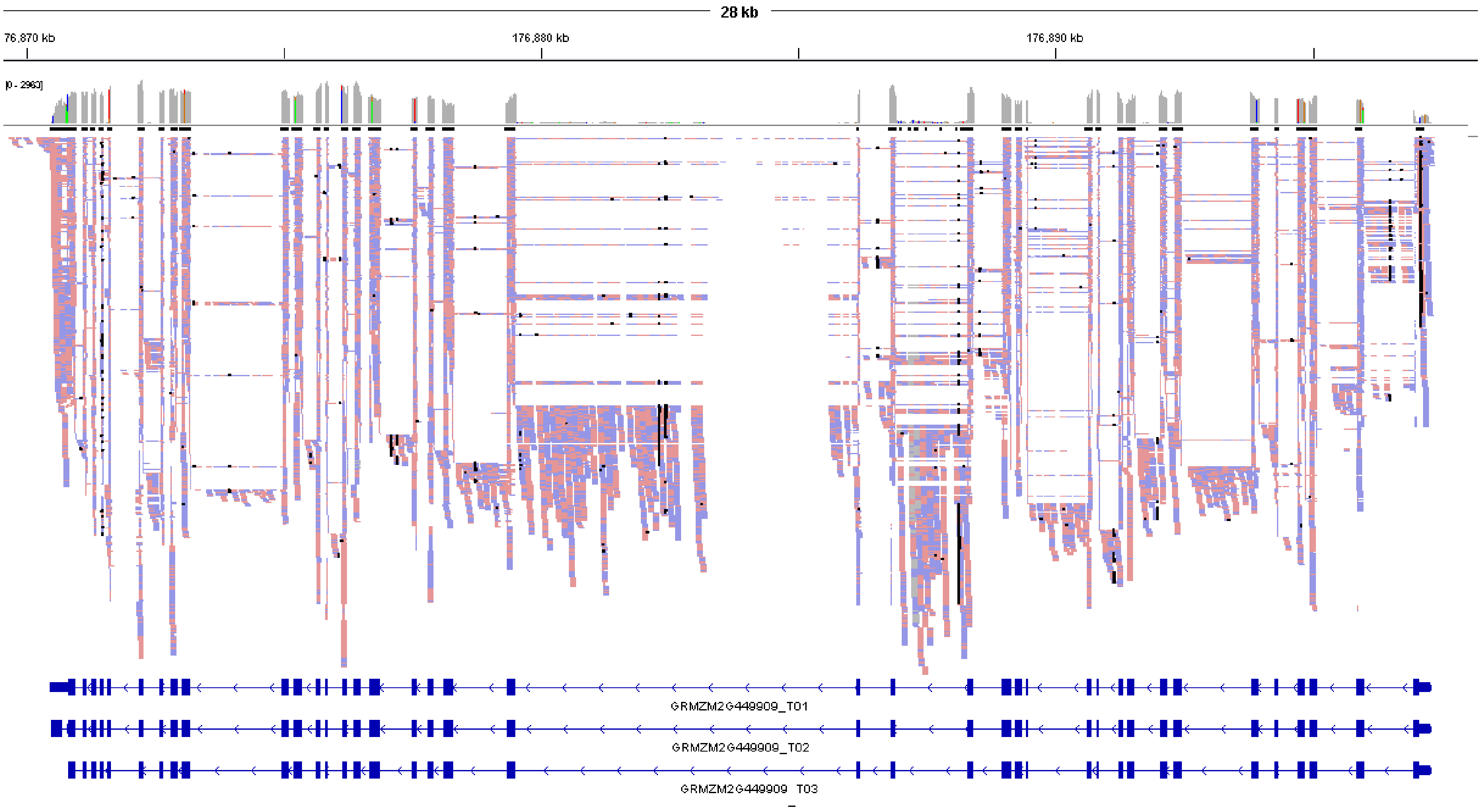
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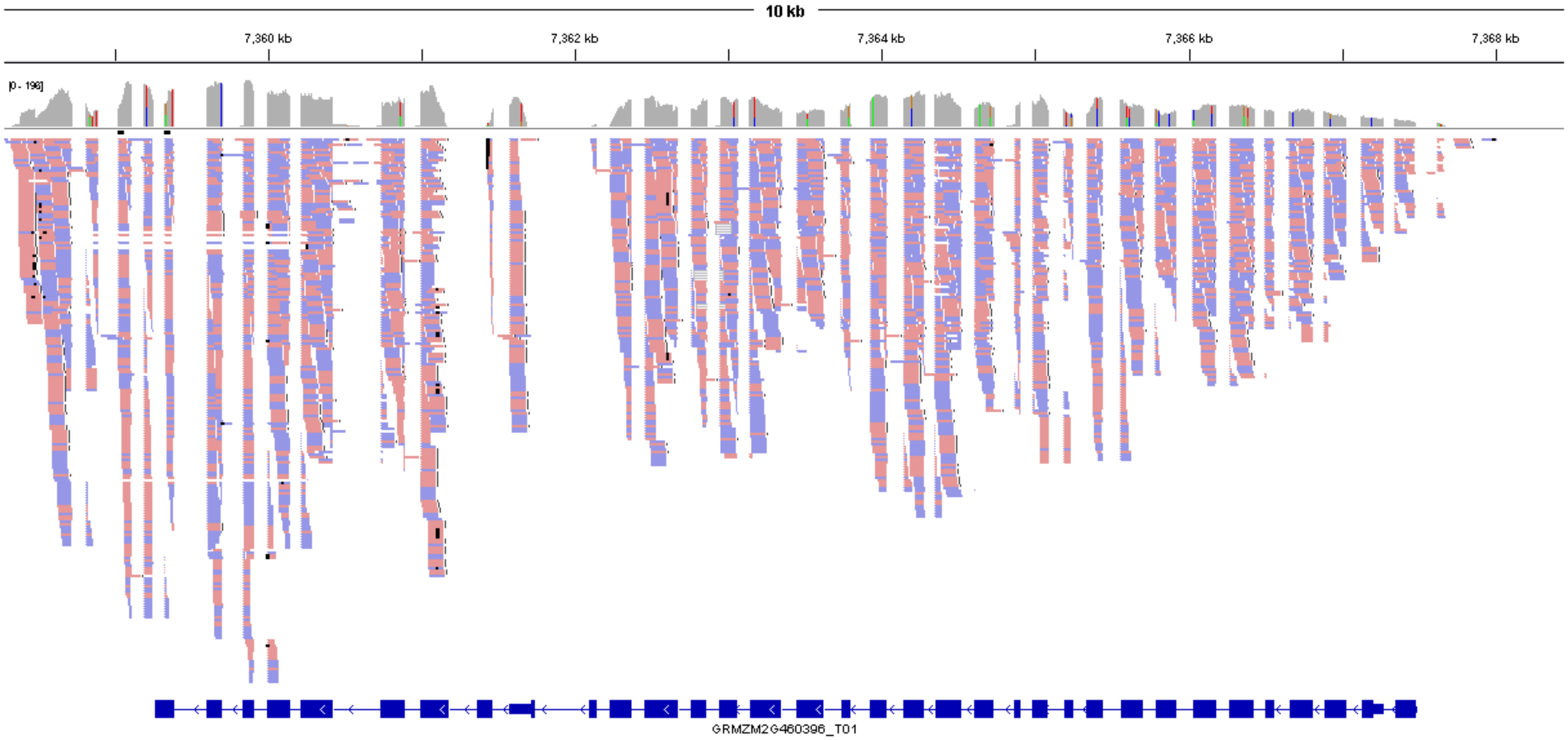
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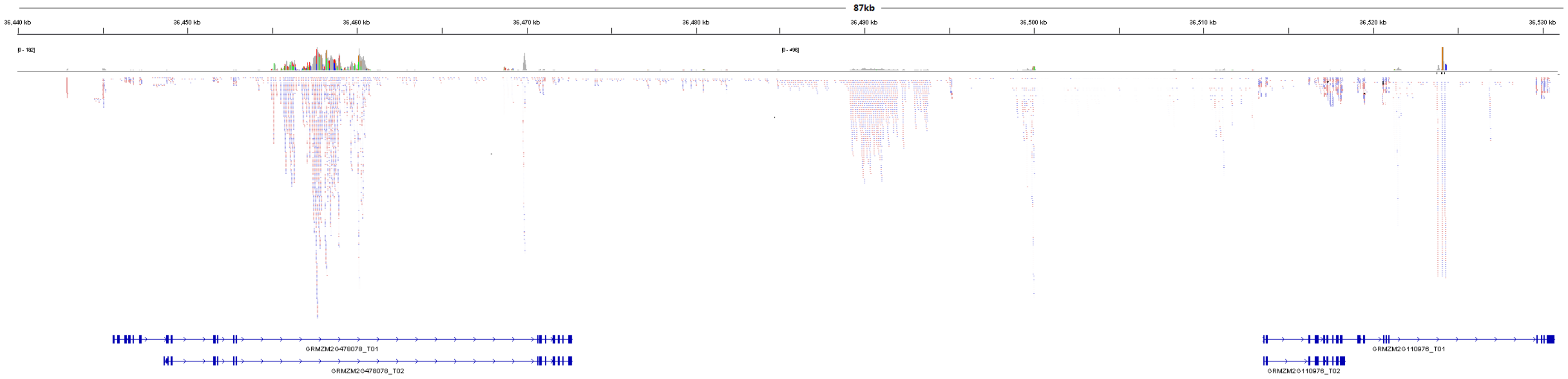
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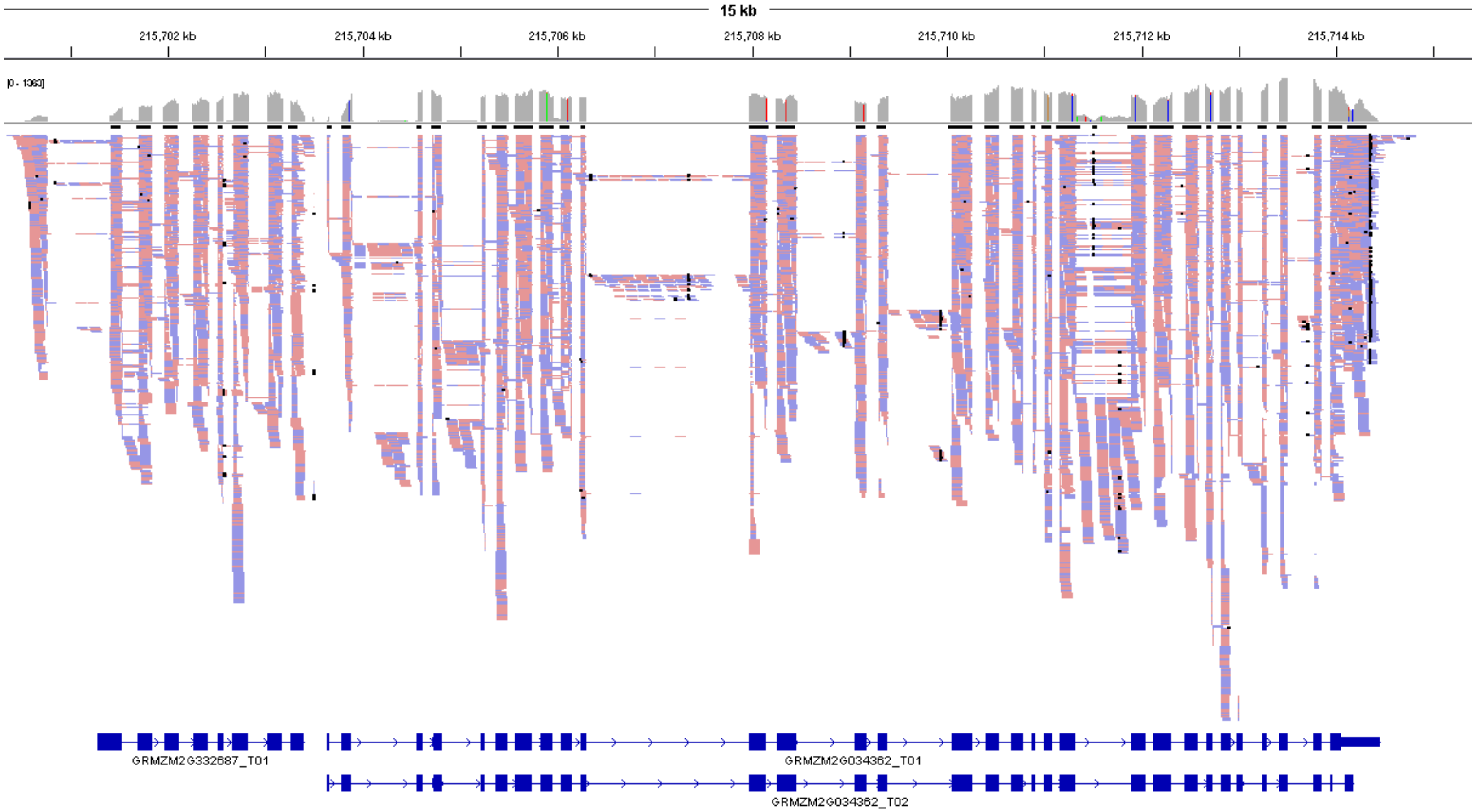
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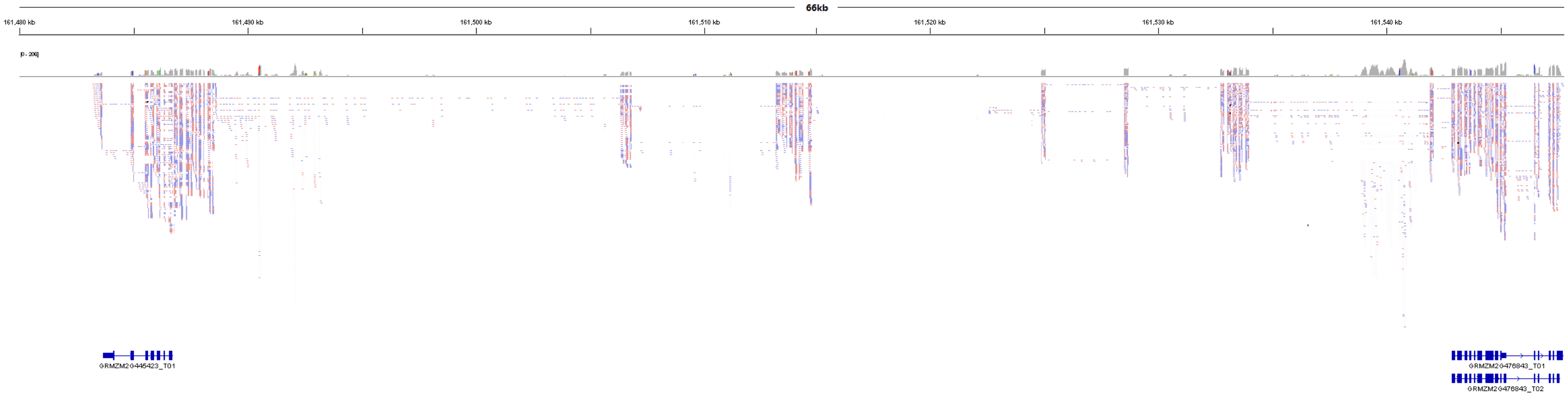
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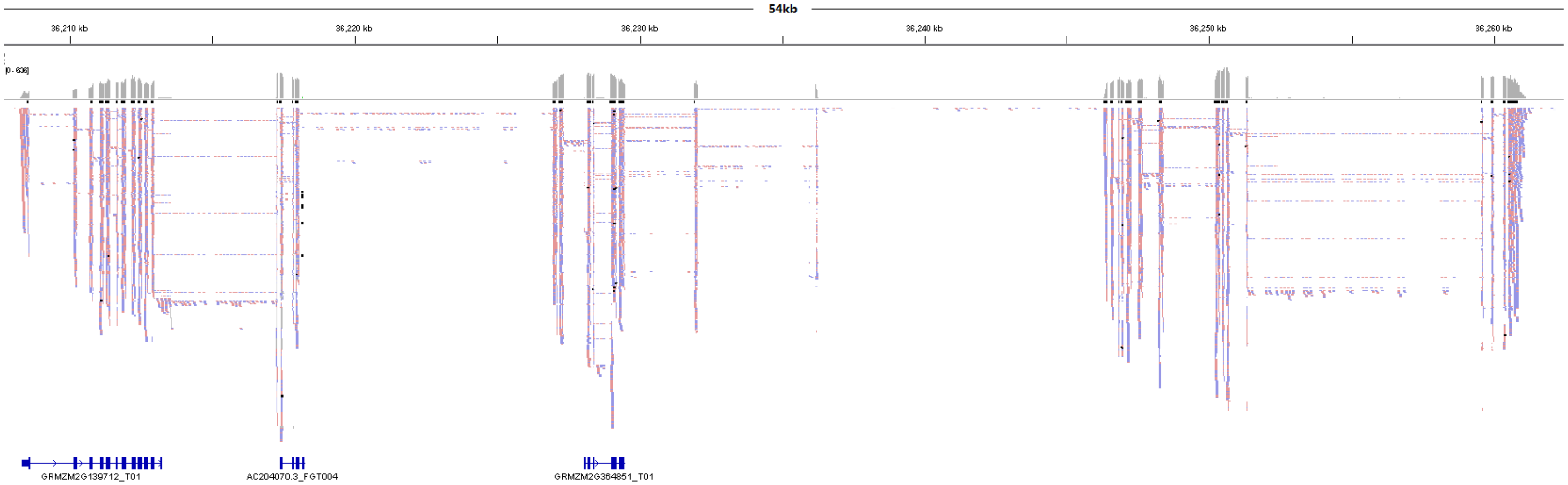
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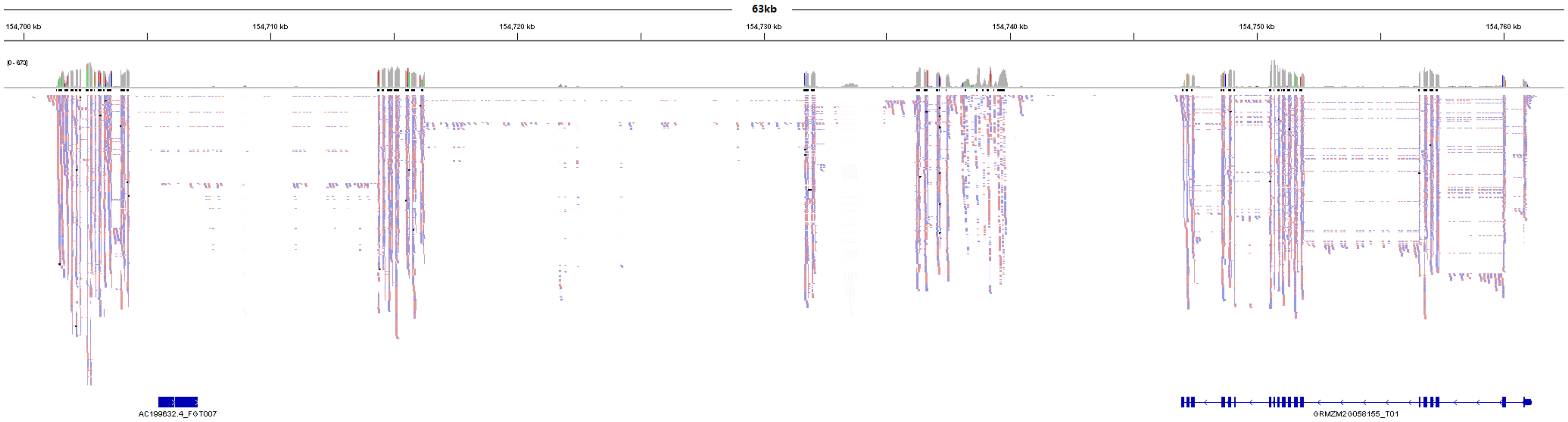
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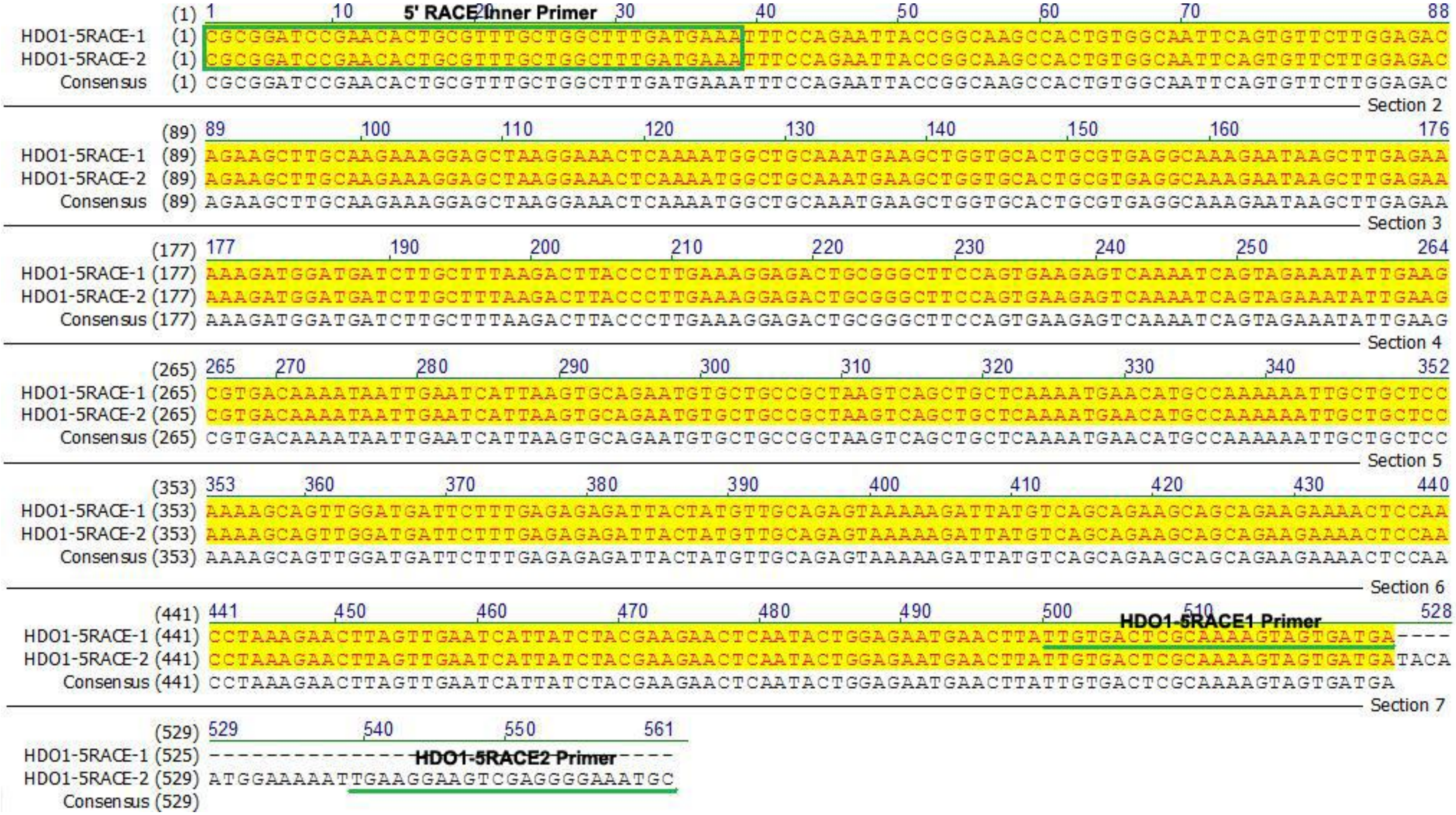
Supplementary Figure S3. The determination of the headless derivative of *O1* using two independent 5′ RACE experiments.



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Consensus       (1) CGCGGATCCGAACACTGCGTTTGCTGGCTTTGATGAAATTTCCAGAATTACCGGCAAGCCACTGTGGCAATTCAGTGTTCTTGGAGAC

               (89) 89
HDO1-5RACE-1   (89) AGAAGCTTGCAAGAAAGGAGCTAAGGAAACTCAAAATGGCTGCAAATGAAGCTGGTGCACTGCGTGAGGCAAAGAATAAGCTTGAGAA
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Consensus      (89) AGAAGCTTGCAAGAAAGGAGCTAAGGAAACTCAAAATGGCTGCAAATGAAGCTGGTGCACTGCGTGAGGCAAAGAATAAGCTTGAGAA

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Consensus     (529)
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