

**Table S1.** Polymorphic sites localized in *H. argophyllus* and the hybrid (*H. annuus* VIR114A x *H. argophyllus*) mitogenomes while comparing with *H. annuus* fertile line HA89 (MG735191.1 NCBI accession)

HA89 line mitogenome position	HA89 line sequence	<i>H. argophyllus</i> mitogenome position	<i>H. argophyllus</i> sequence	The hybrid mitogenome position	The hybrid sequence	Localization/ mutation
36361	T	36359	T	36360	<b>G</b>	orf259/ Asp251Glu
36540	G	36539	<b>T</b>	36539	G	IGR*
37267	G	37266	<b>A</b>	37266	G	IGR
75333	A	75332	A	75328	<b>C</b>	IGR
116778	G	116762	G	116773	T	IGR
133548	T	133440	<b>A</b>	133543	T	IGR
133550	T	133442	<b>G</b>	133545	T	IGR
133551	A	133443	<b>G</b>	133546	A	IGR
147359	C	147252	<b>A</b>	147354	C	IGR
169030	G	168923	G	169025	<b>T</b>	nad6/ Ser232Tyr
190815	G	190712	G	202153	A	IGR
211811	<b>C</b>	211708	G	216085	G	IGR
230114	A	230011	A	234388	<b>C</b>	rpl16/ Lys32Gln
269064	<b>G</b>	268958	C	273334	C	atp6/ Lys46Asn
293547	T	293441	<b>G</b>	297818	T	IGR

\*IGR – intergenic regions

**Table S2.** Manually revised REDO results (RNA editing sites) revealed by RNA-seq reads mapping. RNA editing sites, the same as obtained by the prediction method, are in bold

Gene name	Gene position	Amino acid position	Position in codon	Substitution type (Ref->Alt)	Substitution in codon (Ref->Alt)	Amino acid substitution (Ref->Alt)
atp1	<b>1490</b>	<b>497</b>	<b>2</b>	C->T	<b>CCA-&gt;CTA</b>	P->L
	<b>1292</b>	<b>431</b>	<b>2</b>	C->T	<b>CCG-&gt;CTG</b>	P->L
	<b>1216</b>	<b>406</b>	<b>1</b>	C->T	<b>CTT-&gt;TTT</b>	L->F
	<b>1178</b>	<b>393</b>	<b>2</b>	C->T	<b>TCA-&gt;TTA</b>	S->L
	<b>1064</b>	<b>355</b>	<b>2</b>	C->T	<b>TCG-&gt;TTG</b>	S->L
	<b>1039</b>	<b>347</b>	<b>1</b>	C->T	<b>CCC-&gt;TCC</b>	P->S
atp4	<b>407</b>	<b>136</b>	<b>2</b>	C->T	<b>CCA-&gt;CTA</b>	P->L
	<b>395</b>	<b>132</b>	<b>2</b>	C->T	<b>TCA-&gt;TTA</b>	S->L
	251	84	2	C->T	CCG->CTG	P->L
	248	83	2	C->T	CCT->CTG	P->L
	<b>215</b>	<b>72</b>	<b>2</b>	C->T	<b>TCA-&gt;TTA</b>	S->L
	<b>138</b>	<b>46</b>	<b>3</b>	C->T	<b>ATC-&gt;ATT</b>	I->I
	<b>118</b>	<b>40</b>	<b>1</b>	C->T	<b>CGT-&gt;TGT</b>	R->C
	<b>89</b>	<b>30</b>	<b>2</b>	C->T	<b>TCA-&gt;TTA</b>	S->L
	<b>71</b>	<b>24</b>	<b>2</b>	C->T	<b>TCA-&gt;TTA</b>	S->L
	<b>59</b>	<b>20</b>	<b>2</b>	C->T	<b>TCT-&gt;TTT</b>	S->F
	<b>atp8</b>	<b>47</b>	<b>2</b>	C->T	<b>TCA-&gt;TTA</b>	S->L
		58	1	C->T	CTC->TTC	L->F
	<b>452</b>	<b>151</b>	<b>2</b>	C->T	<b>CCA-&gt;CTA</b>	P->L

atp9	262	88	1	C->T	CGA->TGA	R->*
	254	85	2	C->T	TCC->TTC	S->F
	251	84	2	C->T	TCA->TTA	S->L
	230	77	2	C->T	CCA->CTA	P->L
	221	74	2	C->T	TCG->TTG	S->L
	173	58	2	C->T	TCA->TTA	S->L
	131	44	2	C->T	TCG->TTG	S->L
	121	41	2	C->T	CTT->TTT	L->F
	89	30	2	C->T	TCA->TTA	S->L
ccmB	43	15	1	C->T	CCC->TCC	P->S
	68	23	2	C->T	TCT->TTT	S->F
	71	24	2	C->T	CCA->CTA	P->L
	80	27	2	C->T	TCA->TTA	S->L
	128	43	2	C->T	TCA->TTA	S->L
	137	46	2	C->T	TCC->TTC	S->F
	188	63	2	C->T	CCT->CTT	P->L
	193	65	1	C->T	CCT->TCT	P->S
	286	96	1	C->T	CGG->TGG	R->W
	304	102	1	C->T	CGT->TGT	R->C
	313	105	1	C->T	CGT->TGT	R->C
	338	113	2	C->T	CCG->CTG	P->L
	367	123	1	C->T	CGG->TGG	R->W
	380	127	2	C->T	CCG->CTG	P->L
	424	142	1	C->T	CGT->TGT	R->C
	428	143	2	C->T	TCG->TTG	S->L
	467	156	2	C->T	TCG->TTG	S->L
	503	168	2	C->T	CCA->CTA	P->L
	512	171	2	C->T	TCT->TTT	S->F
	514	172	1	C->T	CGT->TGT	R->C
	551	184	2	C->T	TCA->TTA	S->L
	554	185	2	C->T	TCG->TTG	S->L
	572	191	2	C->T	CCG->CTG	P->L
	596	199	2	C->T	TCG->TTG	S->L
	611	204	2	C->T	TCA->TTA	S->L
ccmC	673	225	1	C->T	CCT->TCT	P->S
	656	219	2	C->T	CCA->CTA	P->L
	619	207	1	C->T	CGT->TGT	R->C
	614	205	2	C->T	TCA->TTA	S->L
	608	203	2	C->T	CCC->CTC	P->L
	605	202	2	C->T	TCC->TTC	S->F
	575	192	2	C->T	CCC->CTC	P->L
	568	190	1	C->T	CCT->TCT	P->S
	521	174	2	C->T	TCG->TTG	S->L
	497	166	2	C->T	TCT->TTT	S->F
	436	146	1	C->T	CCT->TCT	P->S
	421	141	1	C->T	CGT->TGT	R->C
	400	134	1	C->T	CTT->TTT	L->F
	395	132	2	C->T	TCG->TTG	S->L
	331	111	1	C->T	CGG->TGG	R->W
	299	100	2	C->T	TCT->TTT	S->F

ccmFC	281	94	2	C->T	ACA->ATA	T->I
	184	62	1	C->T	CGG->TGG	R->W
	179	60	2	C->T	GCG->GTG	A->V
	161	54	2	C->T	CCT->CTT	P->L
	133	45	1	C->T	CTT->TTT	L->F
	115	39	1	C->T	CGG->TGG	R->W
	103	35	1	C->T	CAT->TAT	H->Y
	76	26	1	C->T	CGG->TGG	R->W
	5	2	2	C->T	TCC->TTC	S->F
	1615	539	1	C->T	CGA->TGA	R->*
	1568	523	2	C->T	TCG->TTG	S->L
	1539	513	3	C->T	ATC->ATT	I->I
	1534	512	1	C->T	CGG->TGG	R->W
	1439	487	2	C->T	CCG->CTG	P->L
	1439	480	2	C->T	CCA->CTA	P->L
	1231	411	1	C->T	CGG->TGG	R->W
	1009	337	1	C->T	CCA->TCA	P->S
	406	136	1	C->T	CGT->TGT	R->C
	391	131	1	C->T	CGT->TGT	R->C
	334	112	1	C->T	CTT->TTT	L->F
ccmFN	310	104	1	C->T	CGT->TGT	R->C
	303	101	3	C->T	GCC->GCT	A->A
	155	52	2	C->T	TCA->TTA	S->L
	151	51	1	C->T	CCT->TCT	P->S
	122	41	2	C->T	TCT->TTT	S->F
	119	40	2	C->T	TCT->TTT	S->F
	52	18	1	C->T	CGT->TGT	R->C
	50	17	2	C->T	CCT->CTT	P->L
	38	13	2	C->T	TCC->TTC	S->F
	35	12	2	C->T	ACT->ATT	T->I
	1507	503	1	C->T	CCC->TCC	P->S
	1472	491	2	C->T	TCA->TTA	S->L
	1460	487	2	C->T	CCA->CTA	P->L
	1456	486	1	C->T	CTT->TTT	L->F
	1436	479	2	C->T	TCG->TTG	S->L
	1417	473	1	C->T	CTT->TTT	L->F
	1375	459	1	C->T	CGG->TGG	R->W
	1342	448	1	C->T	CGG->TGG	R->W
	1324	442	1	C->T	CGG->TGG	R->W
	1309	437	1	C->T	CAT->TAT	H->Y
	1292	431	2	C->T	CCA->CTA	P->L
	1264	422	1	C->T	CGG->TGG	R->W
	973	325	1	C->T	CGT->TGT	R->C
	800	267	2	C->T	TCA->TTA	S->L
	785	262	2	C->T	CCA->CTA	P->L
	773	258	2	C->T	TCA->TTA	S->L
	751	251	1	C->T	CGT->TGT	R->C
	713	238	2	C->T	TCG->TTG	S->L
	704	235	2	C->T	CCT->CTT	P->L
	604	202	1	C->T	CAT->TAT	H->Y

cob	378	126	3	C->T	TTC->TTT	F->F
	371	124	2	C->T	TCG->TTG	S->L
	289	97	1	C->T	CTT->TTT	L->F
	262	88	1	C->T	CGG->TGG	R->W
	254	85	2	C->T	TCA->TTA	S->L
	200	67	2	C->T	TTC->TTT	P->L
	157	53	1	C->T	CCT->TCT	P->S
	148	50	1	C->T	CGT->TGT	R->C
	143	48	2	C->T	CCG->CTG	P->L
	104	35	2	C->T	CCT->CTT	P->L
	44	15	2	C->T	CCG->CTG	P->L
	229	77	1	C->T	CCG->TCG	P->S
	397	133	1	C->T	CTC->TTC	L->F
	436	146	1	C->T	CAT->TAT	H->Y
	469	157	1	C->T	CGG->TGG	R->W
	530	177	2	C->T	CCA->CTA	P->L
	679	227	1	C->T	CAT->TAT	H->Y
	791	264	2	C->T	TCT->TTT	S->F
	848	283	2	C->T	TCT->TTT	S->F
	919	307	1	C->T	CCC->TCC	P->S
cox1	964	322	1	C->T	CAT->TAT	H->Y
	1019	340	2	C->T	CCA->CTA	P->L
	1093	365	1	C->T	CAC->TAC	H->Y
	1126	376	1	C->T	CGC->TGC	R->C
	1195	399	1	C->T	CCT->TCT	P->S
	122	41	2	C->T	CCG->CTG	P->L
	126	42	3	C->T	GTC->GTT	V->V
	353	118	2	C->T	TCT->TTT	S->F
	365	122	2	C->T	TCT->TTT	S->F
	463	155	1	C->T	CCA->TCA	P->S
	554	185	2	C->T	TCA->TTA	S->L
	563	188	2	C->T	TCT->TTT	S->F
	569	190	2	C->T	CCT->CTT	P->L
	626	209	2	C->T	TCC->TTC	S->F
	662	221	2	C->T	TCA->TTA	S->L
	701	234	2	C->T	CCA->CTA	P->L
	779	260	2	C->T	TCT->TTT	S->F
	826	276	1	C->T	CGG->TGG	R->W
	857	286	2	C->T	CCC->CTC	P->L
	872	291	2	C->T	TCC->TTC	S->F
	965	322	2	C->T	CCT->CTT	P->L
	971	324	2	C->T	TCT->TTT	S->F
	1148	383	2	C->T	TCC->TTC	S->F
	1190	397	2	C->T	CCG->CTG	P->L
	1297	433	1	C->T	CAC->TAC	H->Y
	1385	462	2	C->T	CCG->CTG	P->L
	1398	466	3	C->T	CCC->CCT	P->P
	1516	506	1	C->T	CGT->TGT	R->C
	1544	515	2	C->T	TCA->TTA	S->L
	1600	534	1	C->T	CCA->TCA	P->S

cox2	1610	537	2	C->T	CCG->CTG	P->L
	71	24	2	C->T	TCT->TTT	S->F
	161	54	2	C->T	TCA->TTA	S->L
	163	55	1	C->T	CGG->TGG	R->W
	253	85	1	C->T	CGG->TGG	R->W
	278	93	2	C->T	CCG->CTG	P->L
	379	127	1	C->T	CGG->TGG	R->W
	488	163	2	C->T	ACG->ATG	T->M
	626	209	2	C->T	TCA->TTA	S->L
	668	223	2	C->T	ACC->ATC	T->I
cox3	677	226	2	C->T	TCG->TTG	S->L
	766	256	1	C->T	TCG->TTG	S->L
	781	263	1	C->T	TCG->TTG	S->L
	245	82	2	C->T	CCT->CTT	P->L
	289	97	1	C->T	CTT->TTT	L->F
	298	100	1	C->T	CTT->TTT	L->F
	304	102	1	C->T	CGG->TGG	R->W
	311	104	2	C->T	TCT->TTT	S->F
	314	105	2	C->T	TCT->TTT	S->F
	388	130	1	C->T	CGG->TGG	R->W
matR	419	140	2	C->T	CCC->CTC	P->L
	512	171	2	C->T	TCA->TTA	S->L
	566	189	2	C->T	TCC->TTC	S->F
	653	218	2	C->T	TCG->TTG	S->L
	754	252	1	C->T	CGG->TGG	R->W
	764	255	2	C->T	CCA->CTA	P->L
	1844	615	2	C->T	TCA->TTA	S->L
	1826	609	2	C->T	CCA->CTA	P->L
	1787	596	2	C->T	CCG->CTG	P->L
	1756	586	1	C->T	CAC->TAC	H->Y
mttB	1720	574	1	C->T	CGC->TGC	R->C
	1700	567	2	C->T	CCT->CTT	P->L
	1679	560	2	C->T	TCC->TTC	S->F
	1545	515	3	C->T	CCC->CCT	P->P
	413	138	2	C->T	TCG->TTG	S->L
	326	109	2	C->T	CCA->CTA	P->L
	236	79	2	C->T	TCC->TTC	S->F
	193	65	1	C->T	CCC->TCC	P->S
	147	49	3	C->T	TTC->TTT	F->F
	43	15	1	C->T	CCC->TCC	P->S
	32	11	2	C->T	TCC->TTC	S->F
	23	8	2	C->T	CCG->CTG	P->L
	56	19	2	C->T	TCC->TTC	S->F
	61	21	1	C->T	CGG->TGG	R->W
	97	33	1	C->T	CGT->TGT	R->C
	109	37	1	C->T	CCG->TCG	P->S
	125	42	2	C->T	TCT->TTT	S->F
	128	43	2	C->T	CCA->CTA	P->L
	181	61	1	C->T	CGT->TGT	R->C
	191	64	2	C->T	TCA->TTA	S->L

nad1	203	68	2	C->T	TCC->TTC	S->F
	205	69	1	C->T	CCG->TCG	P->S
	255	85	3	C->T	CCC->CCT	P->P
	265	89	1	C->T	CAT->TAT	H->Y
	334	112	1	C->T	CAT->TAT	H->Y
	349	117	1	C->T	CGC->TGC	R->C
	356	119	2	C->T	TCC->TTC	S->F
	379	127	1	C->T	CCC->TCC	P->S
	410	137	2	C->T	CCA->CTA	P->L
	450	150	3	C->T	ATC->ATT	I->I
	475	159	1	C->T	CAT->TAT	H->Y
	500	167	2	C->T	TCG->TTG	S->L
	508	170	1	C->T	CCA->TCA	P->S
	544	182	1	C->T	CGT->TGT	R->C
	551	184	2	C->T	CCA->CTA	P->L
	557	186	2	C->T	CCA->CTA	P->L
	613	205	1	C->T	CCG->TCG	P->S
	619	207	1	C->T	CTC->TTC	L->F
	670	224	1	C->T	CCT->TCT	P->S
	707	236	2	C->T	TCT->TTT	S->F
	716	239	2	C->T	TCG->TTG	S->L
	215	72	2	C->T	TCC->TTC	S->F
	265	89	1	C->T	CGG->TGG	R->W
	308	103	2	C->T	CCG->CTG	P->L
	376	126	1	C->T	CGG->TGG	R->W
	436	146	1	C->T	CCT->TCT	P->S
	490	164	1	C->T	CCC->UCC	P->S
	493	165	1	C->T	CGT->TGT	R->C
	500	167	2	C->T	TCG->TTG	S->L
	536	179	2	C->T	TCC->TTC	S->F
	635	212	2	C->T	TCA->TTA	S->L
	937	313	1	C->T	CCC->TCC	P->S
	928	310	1	C->T	CGG->TGG	R->W
	898	300	1	C->T	CGG->TGG	R->W
	802	268	1	C->T	CGG->TGG	R->W
	789	263	3	C->T	ATC->ATT	I->I
	779	260	2	C->T	TCA->TTA	S->L
	755	252	2	C->T	CCG->CTG	P->L
nad2	1285	429	1	C->T	CGT->TGT	R->C
	1255	419	1	C->T	CCA->TCA	P->S
	1136	379	2	C->T	TCG->TTG	S->L
	1067	356	2	C->T	TCA->TTA	S->L
	1037	346	2	C->T	TCA->TTA	S->L
	967	323	1	C->T	CGT->TGT	R->C
	937	313	1	C->T	CAT->TAT	H->Y
	818	273	2	C->T	TCT->TTT	S->F
	809	270	2	C->T	TCA->TTA	S->L
	797	266	2	C->T	TCT->TTT	S->F
	686	229	2	C->T	TCC->TTC	S->F
	671	224	2	C->T	TCT->TTT	S->F

	26	9	2	C->T	TCC->TTC	S->F
	232	78	1	C->T	CTT->TTT	L->F
	317	106	2	C->T	TCT->TTT	S->F
	320	107	2	C->T	TCC->TTC	S->F
	344	115	2	C->T	TCT->TTT	S->F
	350	117	2	C->T	TCC->TTC	S->F
	376	126	1	C->T	CGC->TGC	R->C
	410	137	2	C->T	TCA->TTA	S->L
	437	146	2	C->T	CCT->CTT	P->L
	506	169	2	C->T	TCG->TTG	S->L
nad3	5	2	2	C->T	TCA->TTA	S->L
	44	15	2	C->T	CCG->CTG	P->L
	62	21	2	C->T	CCA->CTA	P->L
	80	27	2	C->T	CCA->CTA	P->L
	208	70	1	C->T	CCT->TTT	P->L
	209	70	2	C->T	CCT->TTT	P->L
	215	72	2	C->T	CCG->CTG	P->L
	247	83	1	C->T	CCT->TCT	P->S
	275	92	2	C->T	TCT->TTT	S->F
	317	106	2	C->T	TCT->TTT	S->F
	344	115	2	C->T	TCG->TTG	S->L
	349	117	1	C->T	CGG->TGG	R->W
nad4	1430	477	2	C->T	TCG->TTG	S->L
	433	145	1	C->T	CTT->TTT	L->F
	416	139	2	C->T	CCT->CTT	P->L
	403	135	1	C->T	CGC->TGC	R->C
	376	126	1	C->T	CGT->TGT	R->C
	368	123	2	C->T	TCT->TTT	S->F
	362	121	2	C->T	ACA->ATA	T->I
	261	87	3	C->T	GAC->GAT	D->D
	197	66	2	C->T	TCT->TTT	S->F
	166	56	1	C->T	CGG->TGG	R->W
	158	53	2	C->T	CCT->CTT	P->L
	107	36	2	C->T	CCG->CTG	P->L
	77	26	2	C->T	CCT->CTT	P->L
	74	25	2	C->T	ACT->ATT	T->I
	29	10	2	C->T	TCT->TTT	S->F
nad4L	251	84	2	C->T	TCT->TTT	S->F
	167	56	2	C->T	CCA->CTA	P->L
	158	53	2	C->T	TCA->TTA	S->L
	149	50	2	C->T	TCA->TTA	S->L
	128	43	2	C->T	TCG->TTG	S->L
	101	34	2	C->T	TCG->TTG	S->L
	80	27	2	C->T	TCA->TTA	S->L
	56	19	2	C->T	CCT->CTT	P->L
	25	9	1	C->T	CGG->TGG	R->W
	17	6	2	C->T	TCA->TTA	S->L
	11	4	2	C->T	TCT->TTT	S->F
nad5	1318	440	1	C->T	CTA->TTA	L->L
	1310	437	2	C->T	TCA->TTA	S->L

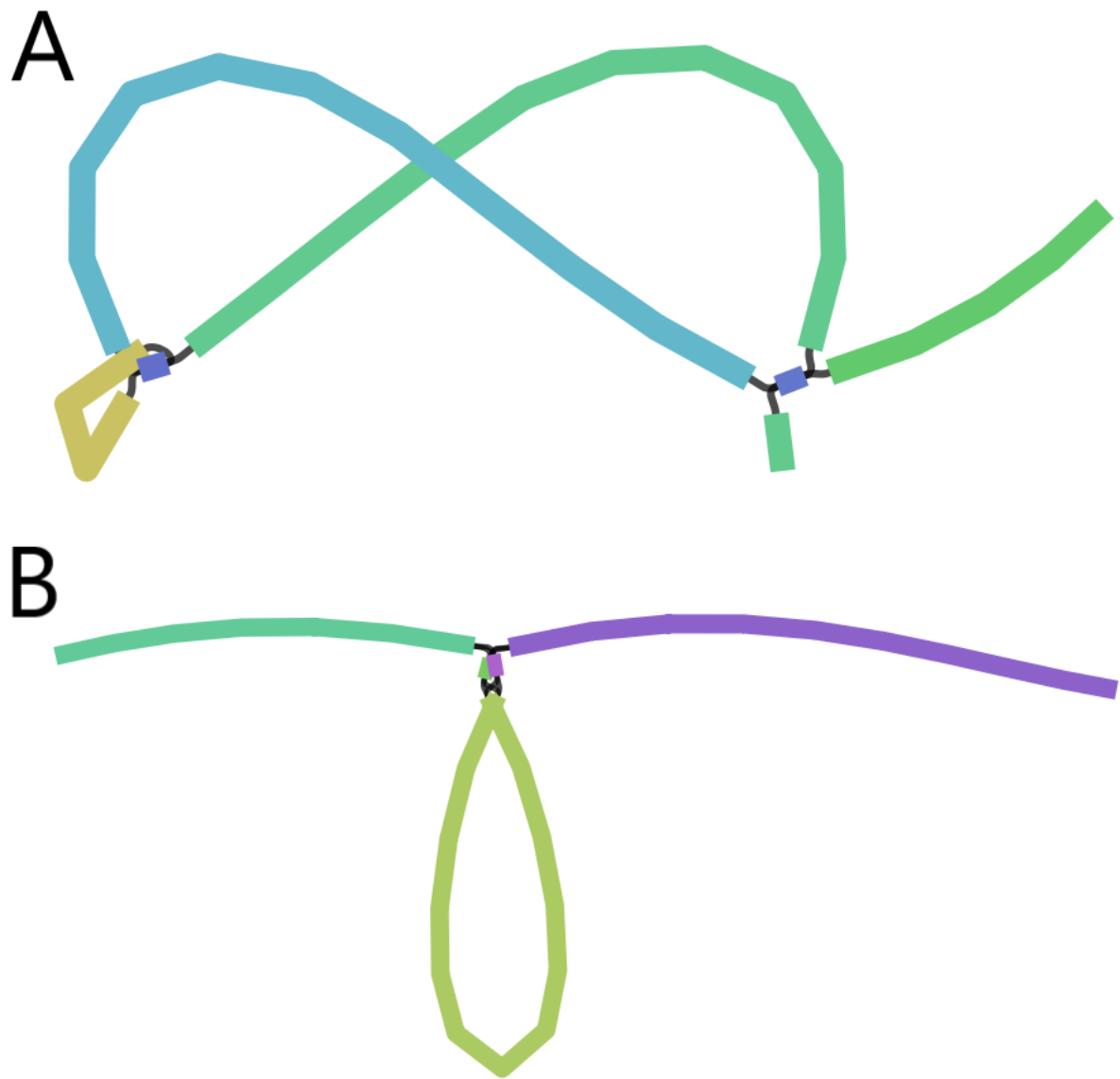
nad6	1184	395	2	C->T	CCA->CTA	P->L
	835	279	1	C->T	CCA->TCA	P->S
	725	242	2	C->T	TCA->TTA	S->L
	713	238	2	C->T	TCG->TTG	S->L
	689	230	2	C->T	GCT->GTT	A->V
	676	226	1	C->T	CTT->TTT	L->F
	631	211	1	C->T	CGC->TGC	R->C
	629	210	2	C->T	TCT->TTT	S->F
	548	183	2	C->T	TCG->TTG	S->L
	539	180	2	C->T	CCT->CTT	P->L
	398	133	2	C->T	TCT->TTT	S->F
	374	125	2	C->T	CCA->CTA	P->L
	359	120	2	C->T	CCT->TTT	P->F
	358	120	1	C->T	CCT->TTT	P->F
	272	91	2	C->T	TCC->TTC	S->F
	242	81	2	C->T	CCG->CTG	P->L
	155	52	2	C->T	CCG->CTG	P->L
	1982	661	2	C->T	TCG->TTG	S->L
	1942	648	2	C->T	CGT->TGT	R->C
	1940	647	1	C->T	TCT->TTT	S->F
	1919	640	2	C->T	TCA->TTA	S->L
	1586	529	2	C->T	CCA->CTA	P->L
	1565	522	2	C->T	TCT->TTT	S->F
	1556	519	2	C->T	TCA->TTA	S->L
	1526	509	2	C->T	ACC->ATC	T->I
	1466	489	2	C->T	CCC->CTC	P->L
	569	190	2	C->T	TCT->TTT	S->F
	463	155	1	C->T	CCT->TCT	P->S
	446	149	2	C->T	TCC->TTC	S->F
	191	64	2	C->T	TCA->TTA	S->L
	169	57	1	C->T	CAT->TAT	H->Y
	161	54	2	C->T	CCA->CTA	P->L
	103	35	1	C->T	CGC->TGC	R->C
	95	32	2	C->T	CCA->CTA	P->L
	89	30	2	C->T	CCC->TTC	P->F
	88	30	1	C->T	CCC->TTC	P->F
nad7	1154	385	2	C->T	TCT->TTT	S->F
	1112	371	2	C->T	CCA->CTA	P->L
	1091	364	2	C->T	TCT->TTT	S->F
	1076	359	2	C->T	TCA->TTA	S->L
	1067	356	2	C->T	TCT->TTT	S->F
	1045	349	1	C->T	CGT->TGT	R->C
	1038	346	3	C->T	CCC->CCT	P->P
	932	311	2	C->T	CCT->CTT	P->L
	764	255	2	C->T	CCT->CTT	P->L
	697	233	1	C->T	CGC->TGC	R->C
	668	223	2	C->T	CCT->TTT	P->F
	667	223	1	C->T	CCT->TTT	P->F
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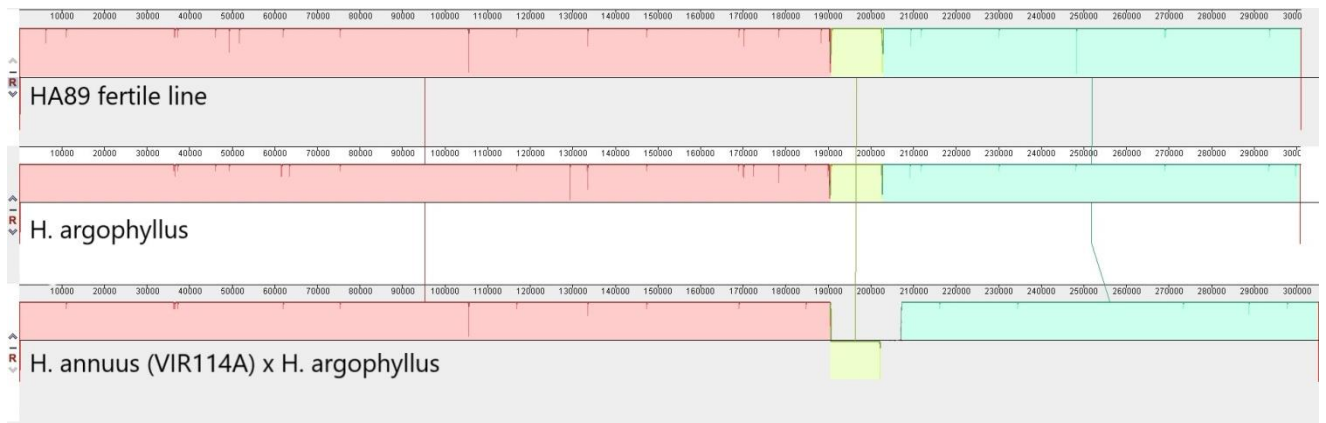
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	278	93	2	C->T	TCA->TTA	S->L
	269	90	2	C->T	TCA->TTA	S->L
	250	84	1	C->T	CGT->TGT	R->C
	185	62	2	C->T	TCA->TTA	S->L
	178	60	1	C->T	CAT->TAT	H->Y
	137	46	2	C->T	TCA->TTA	S->L
	83	28	2	C->T	TCA->TTA	S->L
	77	26	2	C->T	TCA->TTA	S->L
	45	15	3	C->T	TTC->TTT	F->F
	38	13	2	C->T	TCG->TTG	S->L
	92	31	2	C->T	TCT->TTT	S->F
	113	38	2	C->T	CCA->CTA	P->L
	167	56	2	C->T	TCG->TTG	S->L
	190	64	1	C->T	CAT->TAT	H->Y
	298	100	1	C->T	CCG->TCG	P->S
	311	104	2	C->T	CCA->CTA	P->L
	328	110	1	C->T	CGG->TGG	R->W
	368	123	2	C->T	TCC->TTC	S->F
	398	133	2	C->T	TCA->TTA	S->L
	439	147	1	C->T	CTT->TTT	L->F
	539	180	2	C->T	TCT->TTT	S->F
rpl10	239	80	2	C->T	TCG->TTG	S->L
	180	60	3	C->T	ACC->ACT	T->T
	134	45	2	C->T	CCA->CTA	P->L
	101	34	2	C->T	TCA->TTA	S->L
rpl16	83	28	2	C->T	TCA->TTA	S->L
	185	62	2	C->T	ACT->ATT	T->I
	313	105	1	C->T	TCA->TTA	L->F
rpl5	488	163	2	C->T	TCA->TTA	S->L
	521	174	2	C->T	CCG->CTG	P->L
	518	173	2	C->T	CCA->CTA	P->L
	169	57	1	C->T	CCG->TCG	P->S
rps12	92	31	2	C->T	TCG->TTG	S->L
	59	20	2	C->T	CCG->CTG	P->L
	47	16	2	C->T	CCG->CTG	P->L
	35	12	2	C->T	TCA->TTA	S->L
	71	24	2	C->T	TCG->TTG	S->L
	100	34	1	C->T	CGC->TGC	R->C
	104	35	2	C->T	CCG->CTG	P->L
	112	38	1	C->T	CCA->TCA	P->S
	146	49	2	C->T	CCA->CTA	P->L
	196	66	1	C->T	CAC->TAC	H->Y
	221	74	2	C->T	TCG->TTG	S->L
	269	90	2	C->T	TCG->TTG	S->L
rps13	284	95	2	C->T	TCC->TTC	S->F
	26	9	2	C->T	TCA->TTA	S->L

rps3	56	19	2	C->T	TCA->TTA	S->L
	100	34	1	C->T	CGT->TGT	R->C
	287	96	2	C->T	TCA->TTA	S->L
	86	29	2	C->T	TCA->TTA	S->L
	120	40	3	C->T	TTC->TTT	F->F
	<b>506</b>	<b>169</b>	<b>2</b>	<b>C-&gt;T</b>	<b>TCA-&gt;TTA</b>	<b>S-&gt;L</b>
	<b>710</b>	<b>237</b>	<b>2</b>	<b>C-&gt;T</b>	<b>TCG-&gt;TTG</b>	<b>S-&gt;L</b>
	<b>1019</b>	<b>340</b>	<b>2</b>	<b>C-&gt;T</b>	<b>CCA-&gt;CTA</b>	<b>P-&gt;L</b>
	<b>1349</b>	<b>450</b>	<b>2</b>	<b>C-&gt;T</b>	<b>CCG-&gt;CTG</b>	<b>P-&gt;L</b>
	<b>1376</b>	<b>459</b>	<b>2</b>	<b>C-&gt;T</b>	<b>CCG-&gt;CTG</b>	<b>P-&gt;L</b>
	1487	496	2	C->T	TCA->TTA	S->L
	1573	525	1	C->T	CCT->TCT	P->S
	<b>1604</b>	<b>535</b>	<b>2</b>	<b>C-&gt;T</b>	<b>TCA-&gt;TTA</b>	<b>S-&gt;L</b>
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	<b>193</b>	<b>65</b>	<b>1</b>	<b>C-&gt;T</b>	<b>CAT-&gt;TAT</b>	<b>H-&gt;Y</b>
	<b>257</b>	<b>86</b>	<b>2</b>	<b>C-&gt;T</b>	<b>CCA-&gt;CTA</b>	<b>P-&gt;L</b>
	<b>266</b>	<b>89</b>	<b>2</b>	<b>C-&gt;T</b>	<b>CCA-&gt;CTA</b>	<b>P-&gt;L</b>
	278	93	2	C->T	TCG->TTG	S->L
	290	97	2	C->T	CCG->CTG	P->L
	<b>335</b>	<b>112</b>	<b>2</b>	<b>C-&gt;T</b>	<b>CCG-&gt;CTG</b>	<b>P-&gt;L</b>
	461	154	2	C->T	TCC->TTC	S->F
	<b>479</b>	<b>160</b>	<b>2</b>	<b>C-&gt;T</b>	<b>TCA-&gt;TTA</b>	<b>S-&gt;L</b>
	<b>905</b>	<b>302</b>	<b>2</b>	<b>C-&gt;T</b>	<b>TCG-&gt;TTG</b>	<b>S-&gt;L</b>
	<b>916</b>	<b>306</b>	<b>1</b>	<b>C-&gt;T</b>	<b>CAT-&gt;TAT</b>	<b>H-&gt;Y</b>
	926	309	2	C->T	CCA->CTA	P->L
	<b>941</b>	<b>314</b>	<b>2</b>	<b>C-&gt;T</b>	<b>TCT-&gt;TTT</b>	<b>S-&gt;F</b>

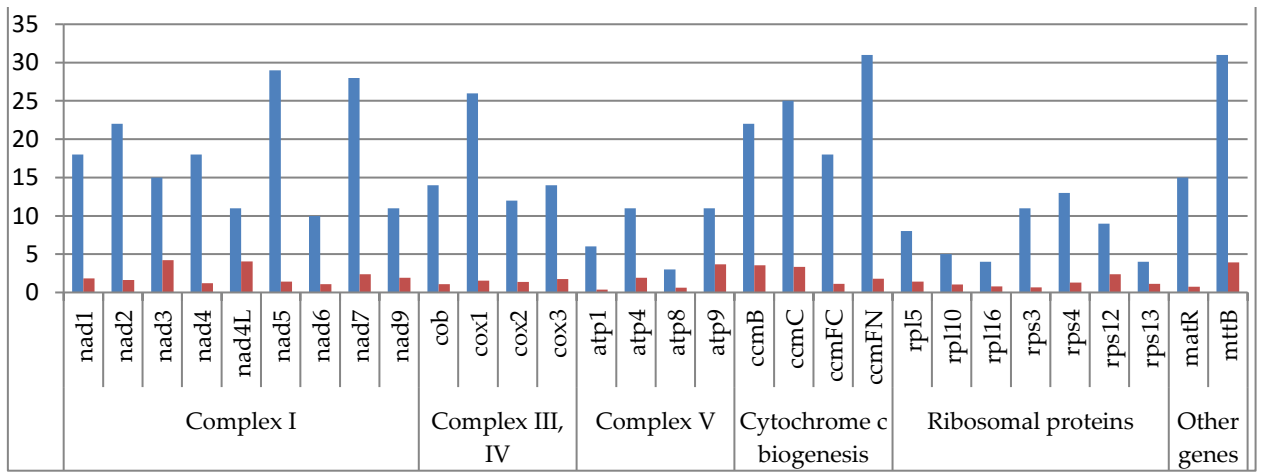
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**Figure S1.** Manually curated final assembly graphs of A) *H. argophyllus* and B) *H. annuus* VIR114A x *H. argophyllus* hybrid visualized using Bandage software. All the contigs displayed are part of the mitochondrial master circle, but the links between some contigs are absent in the graphs (low-coverage regions, which were checked by PCR and reads remapping). The displayed circles are the sub-circle structures. Such sub-circle structures can be resolved in the final graph, which will look like one straight line.



**Figure S2.** The progressive MAUVE alignment of complete mitogenomes: *H. annuus* fertile line HA89 (MG735191.1 NCBI accession), *H. argophyllus* and the hybrid (*H. annuus* VIR114A x *H. argophyllus*)



**Figure S3.** The absolute number of RNA editing substitutions per gene (blue bars) and the relative number of RNA editing substitutions by gene length normalized to 100 bp (red bars) revealed by RNAseq reads mapping