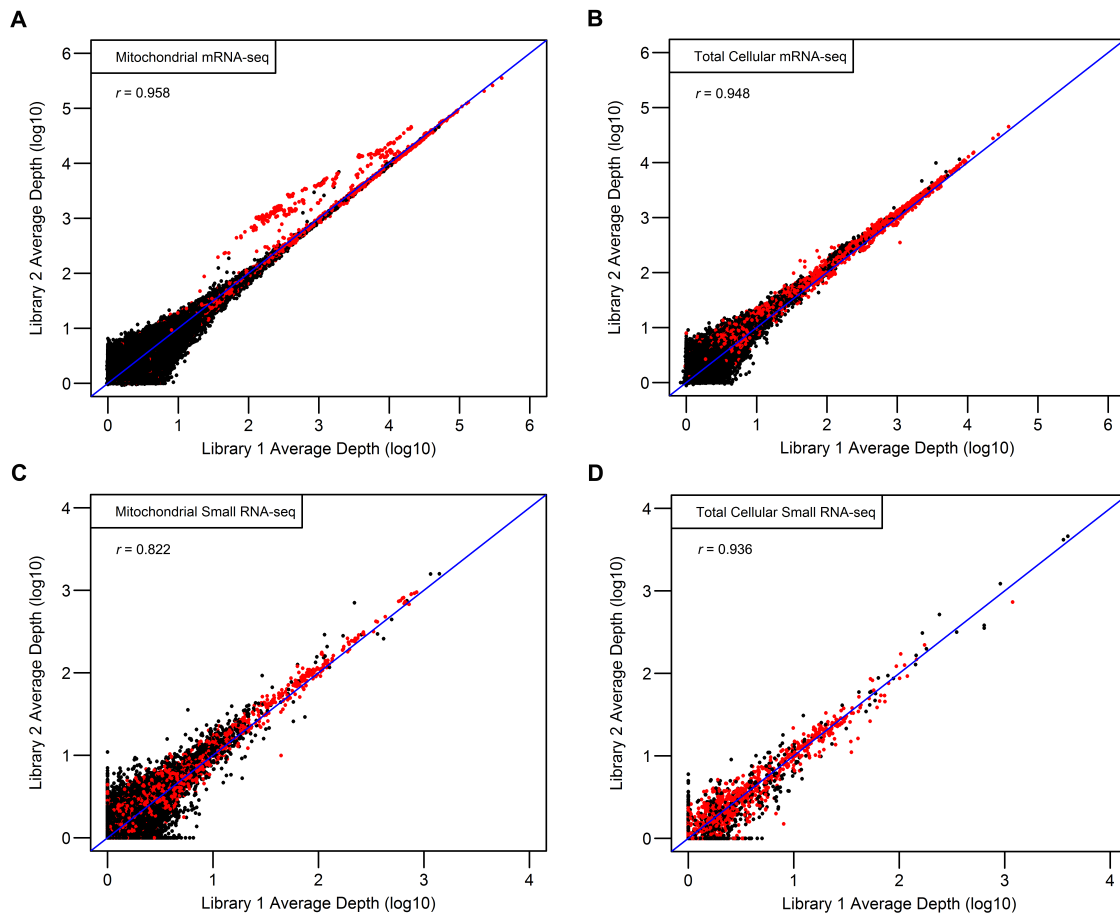


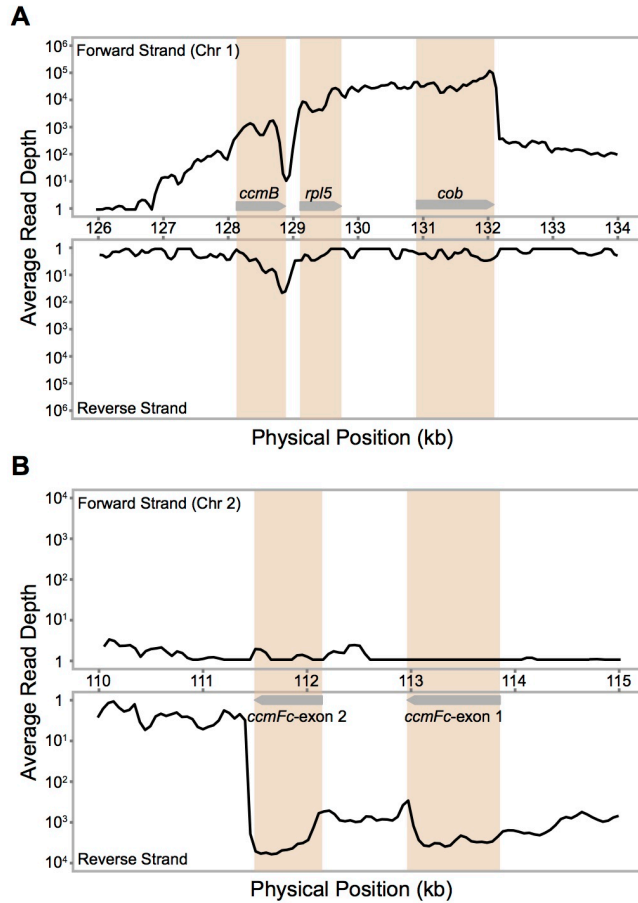
### Figure S1

Correlation between RNA-seq read depths for pairs of biological replicates. Coverage estimates (in terms of average read depth) are based on a sliding window with a window size of 200 bp and a step size of 100 bp. (A) mitochondrial-enriched mRNA-seq libraries; (B) total-cellular mRNA-seq libraries; (C) mitochondrial-enriched small RNA-seq libraries; (D) total-cellular small RNA-seq libraries. The red points represent annotated gene regions, including introns and 2 kb of 5' and 3' flanking sequences. The  $r$ -values represent the Pearson's correlation coefficient as calculated in R. 1:1 lines are shown in blue.



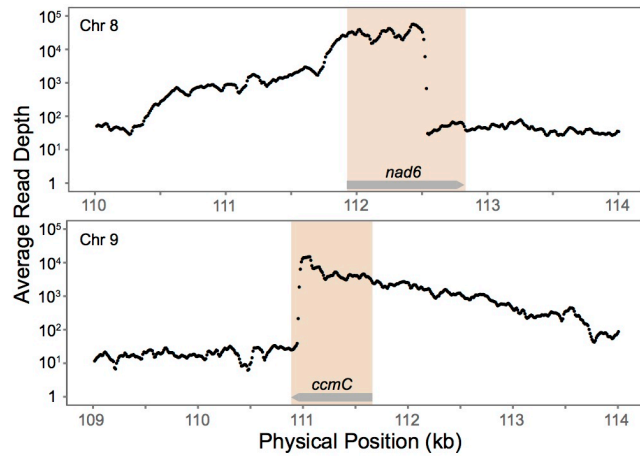
### Figure S2

Illustration of strand specificity in mRNA-seq libraries. Coverage estimates (in terms of average read depth) are based on a sliding window with a window size of 100 bp and a step size 50 bp for the average of two replicates of mitochondrial-enriched libraries. Coverage values for forward and reverse strands were displayed above and below the x-axis, respectively. The pink shading indicates the boundaries of protein-coding genes/exons, and the gray arrows indicate the orientation of the coding strand.



### Figure S3

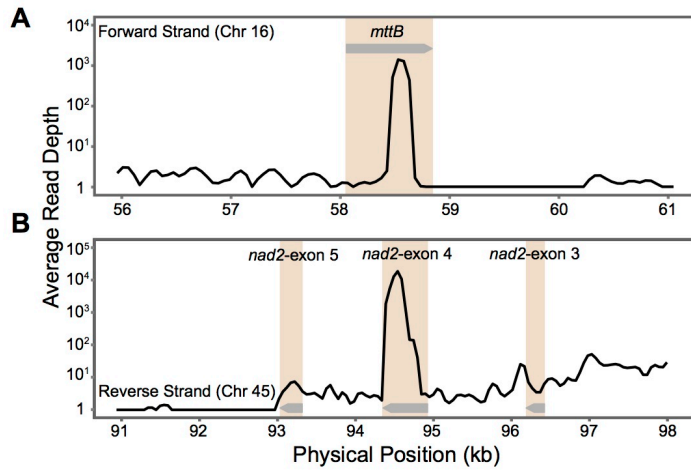
The decline in mRNA-seq coverage prior to the first in-frame stop codon in *nad6* and *ccmC*. Coverage estimates (in terms of average read depth) are based on a sliding window with a window size of 20 bp and a step size of 10 bp for the average of two replicates of mitochondrial-enriched libraries. The pink shading indicates the boundaries of the protein-coding genes, and the gray arrows indicate the orientation of the coding strand.





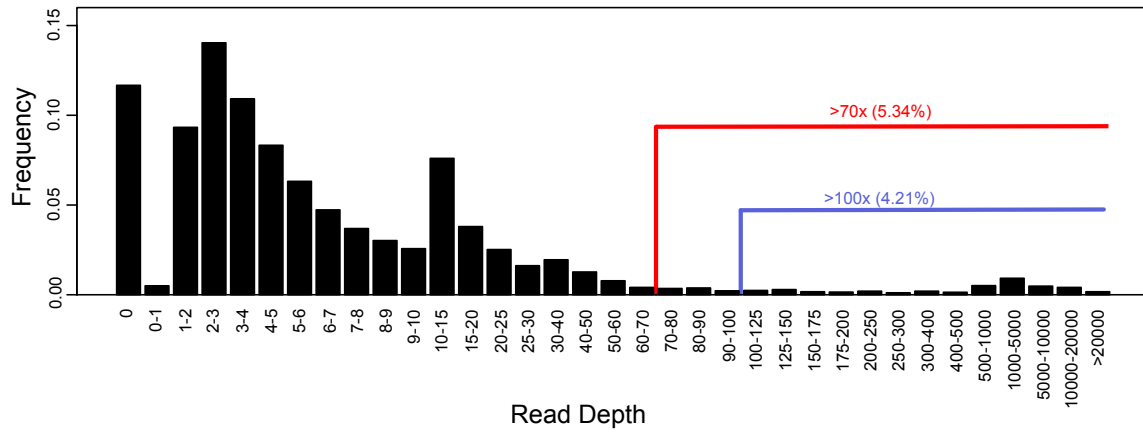
### Figure S5

Examples of pseudogenes containing internal regions that are perfectly identical to the intact copy of the gene and are therefore subject to cross-mapping of reads that originate from the intact gene copy. Coverage estimates (in terms of average read depth) are based on a sliding window with a window size of 100 bp and a step size 50 bp for the average of two replicates of mitochondrial-enriched libraries. The pink shading indicates the boundaries of pseudogenes/exons, and the gray arrows indicate the orientation of the coding strand. Internal regions corresponding to coverage spikes in the (A) *mttB* and (B) *nad2-exon4* pseudogenes are identical to the corresponding functional genes.



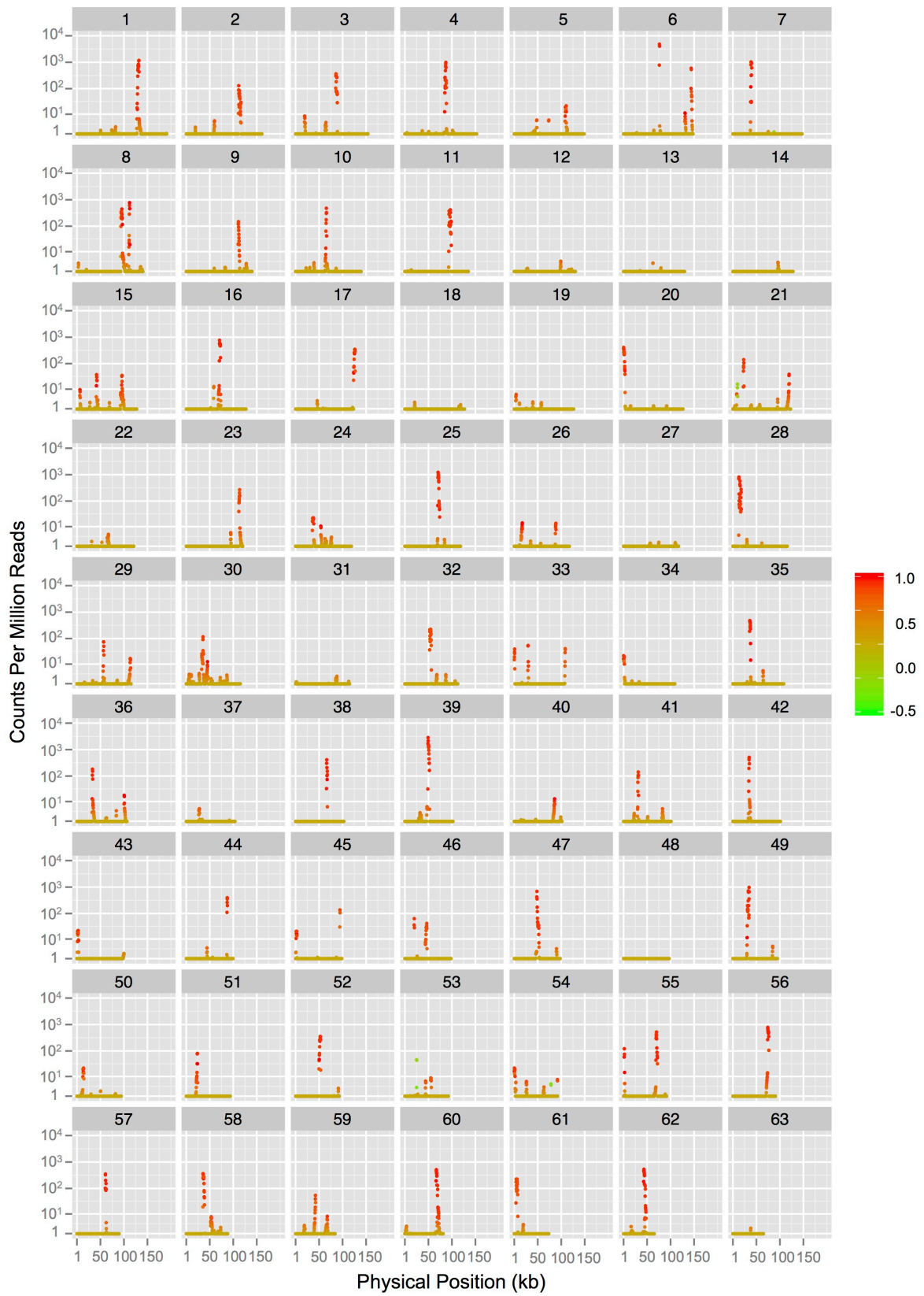
**Figure S6**

The frequency distribution of average mRNA-seq read depth. Read depths are calculated based on 500-bp windows across the entire mitochondrial genome for the average of two replicates of mitochondrial-enriched libraries. The 5% tail of the distribution corresponds to windows with coverage  $>70\times$ . Windows with  $>100\times$  are found in the 4% tail of the distribution.



**Figure S7**

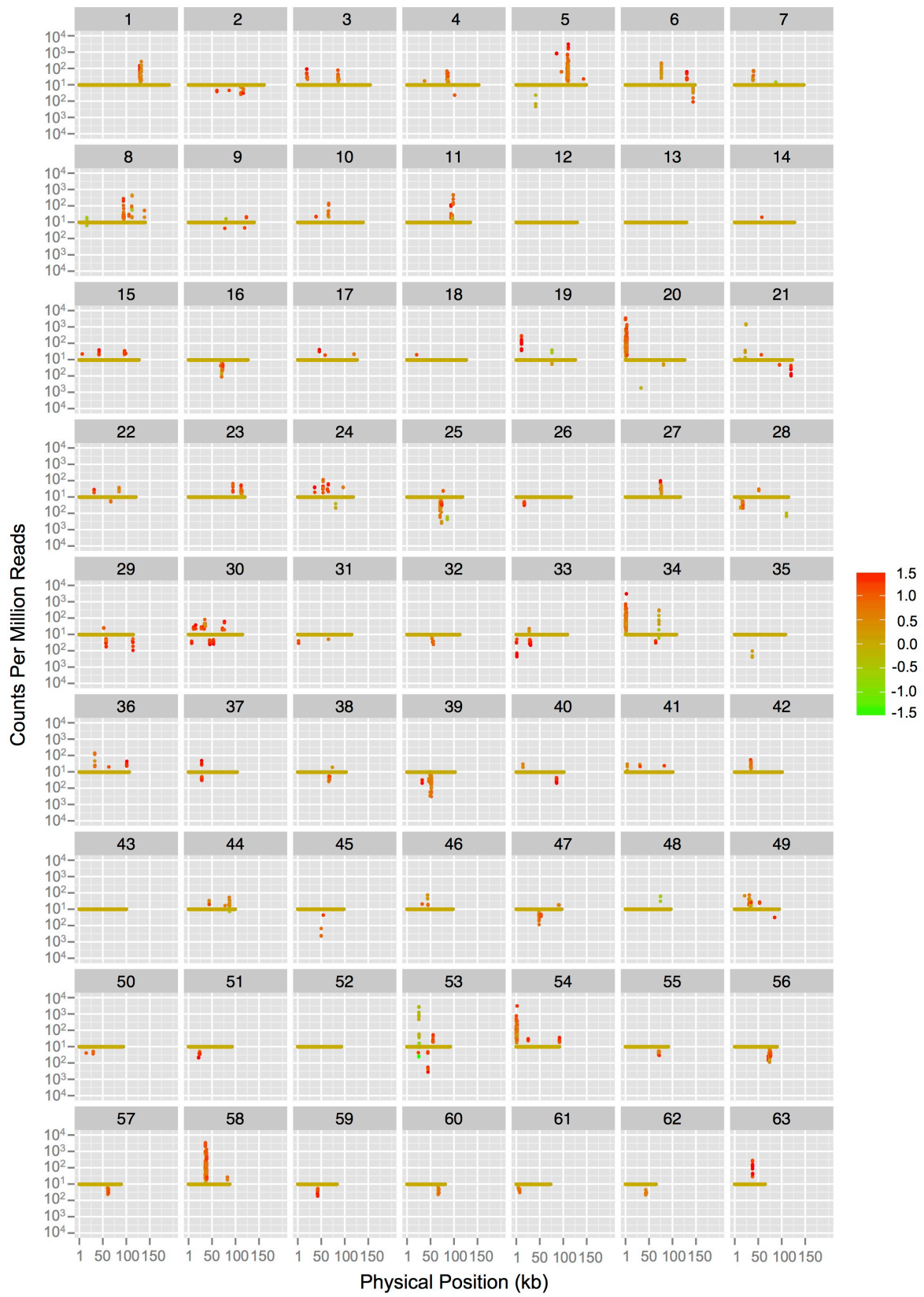
Mitochondrial enrichment for mRNA-seq relative to total-cellular libraries across the 63 chromosomes of the *Silene noctiflora* mitochondrial genome. This plot is a duplicate of Figure 1 except that points are color-coded based on their degree of overrepresentation in the mitochondrial-enriched libraries. Red and green points indicate overrepresentation in the mitochondrial-enriched and total-cellular libraries, respectively. Color scaling is based on the ratio of mitochondrial-enriched to total-cellular read depths (in terms of counts per million) expressed on a  $\log_{10}$  scale. Expression values were set to a minimum of 1 for these calculations.





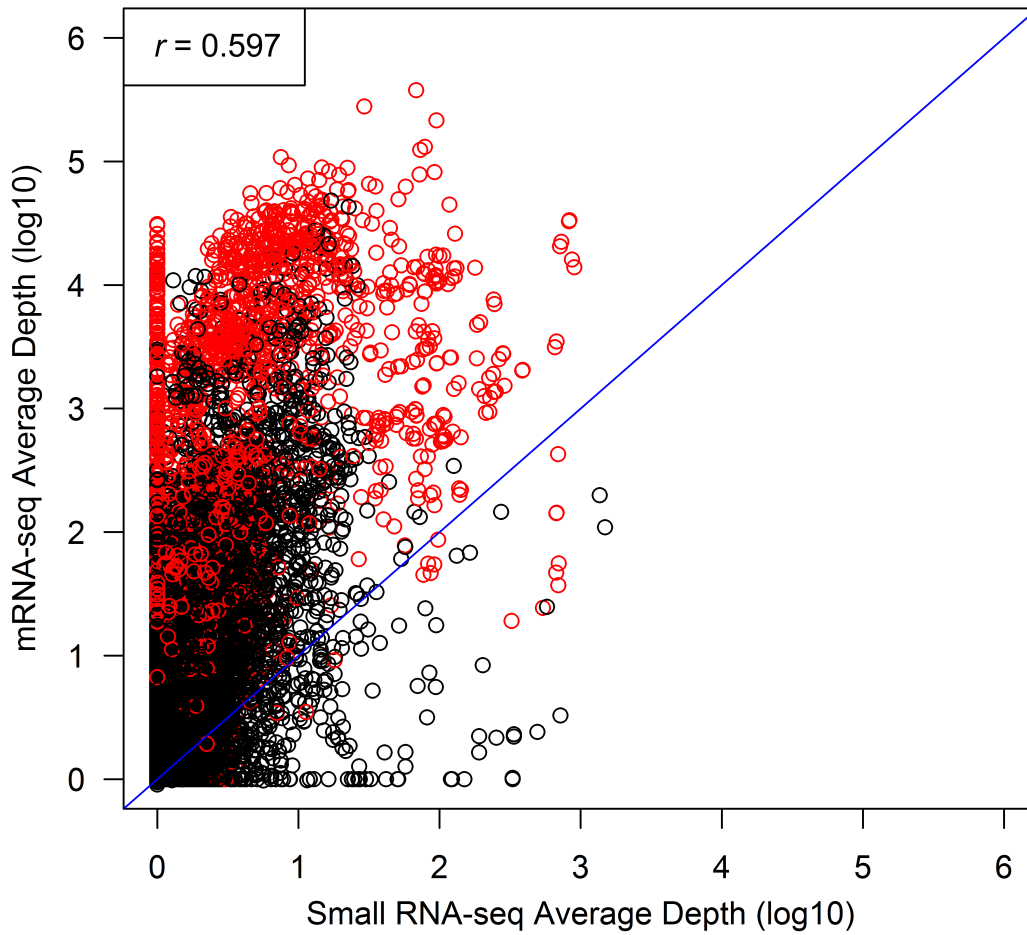
**Figure S8**

Mitochondrial enrichment for small RNA-seq relative to total-cellular libraries across the 63 chromosomes of the *Silene noctiflora* mitochondrial genome. This plot is a duplicate of Figure 3 except that points are color-coded based on their degree of overrepresentation in the mitochondrial-enriched libraries. Red and green points indicate overrepresentation in the mitochondrial-enriched and total-cellular libraries, respectively. Color scaling is based on the ratio of mitochondrial-enriched to total-cellular read depths (in terms of counts per million) expressed on a  $\log_{10}$  scale. Expression values were set to a minimum of 1 for these calculations.



**Figure S9**

Correlation between RNA-seq coverage from mRNA and small-RNA libraries. Coverage estimates (in terms of average read depth) are based on a sliding window with a window size of 200 bp and a step size of 100 bp. Forward and reverse strands within each window were analyzed separately. The red points represent annotated gene regions, including introns and 2 kb of 5' and 3' flanking sequences. The  $r$ -value is the Pearson's correlation coefficient as calculated in R. The 1:1 line is shown in blue.



**Table S1.** Summary of average read depth based on raw read counts for each gene

Chrom	Gene	Start	End	Strand	Length (bp)	Mitochondrial Coverage			Total Cellular Coverage			Ratio
						Lib 1	Lib 2	Mean	Lib 1	Lib 2	Mean	
1	<i>ccmB-a</i>	128198	128818	+	621	1016	980	998	103	124	113	8.80
1	<i>rpl5-1</i>	129131	129712	+	582	11289	10419	10854	1195	1416	1306	8.31
1	<i>cob</i>	130875	132044	+	1170	42423	40005	41214	4449	4800	4624	8.91
2	<i>ccmFc-exon2</i>	111512	112061	-	550	4895	4971	4933	584	615	599	8.23
2	<i>ccmFc-exon1</i>	112986	113752	-	767	3325	3407	3366	456	467	461	7.30
3	<i>nad1-exon2</i>	86375	86456	+	82	9216	7772	8494	1095	1197	1146	7.41
3	<i>nad1-exon3</i>	87835	88026	+	192	25995	23259	24627	2998	3204	3101	7.94
4	<i>nad5-exon1</i>	85304	85533	+	230	14953	13304	14129	1513	1775	1644	8.60
4	<i>nad5-exon2</i>	86399	87614	+	1216	33334	31517	32425	3588	4084	3836	8.45
5	<i>trnM(CAT)</i>	108843	108917	+	75	273	252	263	12	20	16	16.37
5	<i>rrn18-a</i>	109091	110881	+	1791	244	1166	705	80	76	78	9.05
5	<i>rrn5-a</i>	111077	111194	+	118	306	327	316	65	70	67	4.69
6	<i>atp9</i>	76509	76733	+	225	379607	339348	359477	36120	42849	39484	9.10
6	<i>nad1-exon5</i>	144016	144274	-	259	36648	34344	35496	4006	4575	4290	8.27
7	<i>nad5-exon4</i>	38470	38864	+	395	54706	53330	54018	5670	6406	6038	8.95
7	<i>nad5-exon5</i>	39889	40044	+	156	79211	73720	76466	7588	8909	8249	9.27
8	<i>nad2-exon1</i>	94355	94507	+	153	17147	14857	16002	1860	2108	1984	8.07
8	<i>nad2-exon2</i>	95484	95875	+	392	22734	20649	21692	2543	2891	2717	7.98
8	<i>nad6</i>	111927	112811	+	885	21747	20715	21231	2132	2086	2109	10.07
9	<i>ccmC</i>	110920	111654	-	735	5523	5478	5501	724	766	745	7.38
10	<i>nad9</i>	65434	66012	+	579	19091	18461	18776	2119	2410	2264	8.29
11	<i>nad4-exon1</i>	94197	94657	+	461	13852	13346	13599	1577	1793	1685	8.07
11	<i>nad4-exon2</i>	96212	97149	+	938	15458	14569	15014	1698	1935	1817	8.26
11	<i>nad4-exon3</i>	98419	98507	+	89	28525	25300	26912	2644	3137	2891	9.31
16	<i>cox1-a</i>	70929	72512	-	1584	24656	22876	23766	2315	2842	2578	9.22
17	<i>rrn26-a</i>	123577	126684	-	3108	5406	12276	8841	1137	1077	1107	7.99
20	<i>rrn26-b</i>	226	3333	+	3108	5471	12635	9053	1148	1113	1131	8.01
21	<i>nad5-exon3</i>	22965	22986	+	22	3129	3106	3117	429	533	481	6.48
23	<i>mttB-1</i>	113128	113916	+	789	9031	8496	8764	1260	1595	1428	6.14
25	<i>cox3</i>	70464	71261	-	798	49339	44986	47162	4603	5704	5153	9.15
25	<i>atp8</i>	71652	72155	-	504	28094	25678	26886	2906	3573	3239	8.30
28	<i>nad7-exon4</i>	12793	13054	-	262	49837	48556	49196	5213	5844	5528	8.90
28	<i>nad7-exon3</i>	14898	15608	-	711	23235	21765	22500	2331	2660	2496	9.02
28	<i>nad7-exon2</i>	16443	16511	-	69	1976	1755	1866	213	293	253	7.38
28	<i>nad7-exon1</i>	17338	17480	-	143	12140	12220	12180	1377	1502	1440	8.46
32	<i>matR-a</i>	52975	54972	-	1998	6493	6258	6375	897	1017	957	6.66
32	<i>nad1_exon4</i>	56141	56199	-	59	4442	4183	4312	573	999	786	5.49
34	<i>rrn18-b</i>	229	2019	+	1791	241	1165	703	78	75	76	9.21
34	<i>rrn5-b</i>	2215	2332	+	118	314	313	313	61	74	68	4.62
35	<i>nad1-exon1</i>	36866	37251	-	386	12093	11220	11657	1186	1395	1290	9.03
36	<i>nad3-a</i>	33294	33650	+	357	7030	6752	6891	743	740	742	9.29
39	<i>atp6</i>	49368	50297	-	930	75277	74101	74689	7375	8979	8177	9.13
39	<i>atp1</i>	50507	52027	-	1521	29066	31061	30063	3456	4093	3774	7.97
42	<i>rps13</i>	34852	35202	+	351	22480	21292	21886	2383	2622	2503	8.75
43	<i>rrn5-c</i>	968	1085	-	118	316	312	314	65	71	68	4.59
43	<i>rrn18-c</i>	1281	3071	-	1791	242	1154	698	81	76	78	8.90
43	<i>trnM(CAT)</i>	3245	3319	-	75	304	243	273	15	27	21	13.03
44	<i>trnI-CAT</i>	55795	55868	+	74	56	39	48	--	--	--	--
45	<i>rrn5-d</i>	874	991	-	118	333	314	324	57	60	59	5.52
45	<i>rrn18-d</i>	1187	2977	-	1791	241	1152	696	77	75	76	9.16
46	<i>ccmFn</i>	45188	46864	+	1677	1273	1296	1285	188	230	209	6.15
49	<i>trnY-GTA</i>	30558	30639	+	82	213	220	216	11	19	15	14.25
49	<i>nad2-exon3</i>	31145	31305	+	161	19554	17501	18527	2124	2451	2287	8.10
49	<i>nad2-exon4</i>	32891	33463	+	573	29865	29156	29510	3194	3705	3450	8.55

49	<i>nad2-exon5</i>	34662	34849	+	188	92370	92099	92235	9733	10912	10323	8.94
50	<i>rm5-e</i>	12422	12539	-	118	308	302	305	75	57	66	4.62
50	<i>rm18-e</i>	12735	14525	-	1791	240	1167	703	78	77	77	9.11
52	<i>rm26-c</i>	50094	53201	-	3108	5364	12381	8872	1128	1070	1099	8.07
54	<i>rm18-f</i>	228	2018	+	1791	242	1162	702	80	77	78	8.96
54	<i>rm5-f</i>	2214	2331	+	118	358	357	357	78	69	73	4.87
54	<i>trnI-CAT</i>	80167	80240	+	74	22	16	19	--	--	--	--
55	<i>nad3-b</i>	1634	1990	-	357	6356	6264	6310	691	671	681	9.27
55	<i>cox2</i>	69579	70355	-	777	18519	17250	17884	1950	2399	2174	8.23
56	<i>cox1-b</i>	74308	75891		1584	24818	22829	23823	2306	2836	2571	9.27
58	<i>rm26-d</i>	35817	38924	+	3108	5484	12531	9008	1159	1110	1134	7.94
59	<i>trnI-CAT</i>	67221	67294	+	74	245	217	231	--	--	--	--
60	<i>atp4-a</i>	67171	67875	-	705	15786	15196	15491	1486	1815	1651	9.38
60	<i>nad4L-a</i>	67923	68225	-	303	12485	11350	11917	1096	1341	1219	9.78
60	<i>ccmB-b</i>	70309	70929	-	621	747	703	725	76	86	81	8.94
61	<i>matR-b</i>	4240	6237	-	1998	6525	6223	6374	912	1003	957	6.66
61	<i>nad1-exon4</i>	6892	6950	-	59	2402	2194	2298	345	448	396	5.80
61	<i>nad5-exon3</i>	39569	39590	-	22	1	1	1	1	1	1	--
62	<i>atp4-b</i>	43681	44268	-	588	16060	15578	15819	1518	1807	1662	9.52
62	<i>nad4L-b</i>	44443	44735	-	293	12298	11409	11853	1114	1375	1245	9.52
62	<i>ccmB-c</i>	46819	47439	-	621	762	692	727	69	86	78	9.37

**Table S2.** Summary of coverage based on RPKM for each gene

Chrom	Gene	Start	End	Strand	Length (bp)	Mitochondrial RPKM		Total Cellular RPKM	
						Lib 1	Lib 2	Lib 1	Lib 2
1	<i>ccmB-a</i>	128198	128818	+	621	1813	1783	1266	1314
1	<i>cob</i>	130875	132044	+	1170	25680	25208	20076	17577
1	<i>rpl5-1</i>	129131	129712	+	582	13045	12692	10258	9763
2	<i>ccmFc</i>	111512	113752	-	2241	1852	2011	1766	1580
3	<i>nad1_exon2-3</i>	86375	88026	+	1652	5181	4949	4824	4406
4	<i>nad5_exon1-2</i>	85304	87614	+	2311	15193	15122	12151	11354
6	<i>atp9</i>	76509	76733	+	225	243232	230507	176175	170519
6	<i>nad1_exon5</i>	144016	144274	-	259	20087	19608	16931	15194
7	<i>nad5_exon4-5</i>	38470	40044	+	1575	16403	16679	12693	11516
8	<i>nad2_exon1-2</i>	94355	95875	+	1521	11265	10770	9425	9530
8	<i>nad6</i>	111927	112811	+	885	15394	15483	11516	9043
9	<i>ccmC</i>	110920	111654	-	735	4004	4166	3933	3395
10	<i>nad9</i>	65434	66012	+	579	12017	12345	10037	9487
11	<i>nad4</i>	94197	98507	+	4311	5369	5354	4441	4362
16	<i>cox1</i>	70929	72512	-	1584	34518	33500	23713	23823
21	<i>nad5_exon3</i>	22965	22986	+	22	0	0	0	0
23	<i>mttB-1</i>	113134	113916	+	783	6062	6017	6325	6635
25	<i>atp8</i>	71652	72155	-	504	17520	17038	14115	13698
25	<i>cox3</i>	70464	71261	-	798	35428	34078	24954	24963
28	<i>nad7</i>	12793	17480	-	4688	6130	6175	4873	4500
32	<i>matR-a</i>	52975	54972	-	1998	8846	8904	9157	8382
32	<i>nad1_exon4</i>	56141	56199	-	59	0	0	0	0
35	<i>nad1_exon1</i>	36866	37251	-	386	7958	7496	5878	5623
36	<i>nad3-a</i>	33294	33650	+	357	6908	6941	5863	4446
39	<i>atp1</i>	50507	52027	-	1521	20089	22890	17674	17172
39	<i>atp6</i>	49368	50297	-	930	57870	60447	42940	41979
42	<i>rps13</i>	34852	35202	+	351	10921	10747	8927	8004
46	<i>ccmFn</i>	45188	46864	+	1677	907	992	958	970
49	<i>nad2_exon3-5</i>	31145	34849	+	3705	9539	9557	7770	7518
55	<i>cox2</i>	69579	70355	-	777	17946	17549	14080	14144
60	<i>atp4-a</i>	67171	67758	-	588	21682	22170	15217	15058
60	<i>nad4L-a</i>	67923	68225	-	303	14629	14154	9709	9343
61	<i>nad1_exon4</i>	6892	6950	-	59	2	7	29	0
61	<i>nad5_exon3</i>	39569	39590	+	22	0	0	0	0

**Table S3.** Summary of ORFs with a minimum length of 201 bp and a minimum average read depth of 100 in the mitochondrial-enriched mRNA-seq libraries.

Chrom	Start	End	Strand	Mean Read Depth		Length (bp)	BlastP
				Library 1	Library 2		
3	20517	21017	+	150	143	501	NADH dehydrogenase subunit 7
5	48135	48359	+	412	403	225	-
5	73579	73800	-	448	402	222	-
6	130396	130677	+	183	169	282	-
6	131782	132084	+	154	138	303	-
8	99294	99596	+	203	170	303	-
15	6443	6715	+	314	290	273	-
15	27836	28039	-	154	173	204	-
15	41526	41759	+	399	377	234	-
15	42451	42810	+	1278	1140	360	NADH dehydrogenase subunit 2
15	93838	94122	+	237	230	285	-
15	94663	94896	+	213	183	234	-
15	95017	95226	+	174	152	210	-
15	96791	97009	+	265	263	219	-
15	98089	98313	+	130	105	225	-
16	58291	58818	+	346	303	528	mttB
19	11206	11457	+	145	166	252	-
21	8198	8425	+	422	398	228	-
21	9977	10207	+	803*	699*	231	photosystem I P700 apoprotein A1
21	119670	119927	-	1710*	1516*	258	-
22	66400	66672	-	109	112	273	-
24	36185	36571	+	898	855	387	ribosomal protein L5
24	54187	54402	+	280	281	216	-
24	54475	54879	+	163	139	405	-
26	88247	88462	+	453	513	216	-
29	55864	56082	-	210*	171*	219	-
29	112522	112725	-	108	103	204	-
29	113026	113256	-	274	245	231	-
29	113833	114057	-	678	627	225	-
29	114123	114335	-	933	862	213	-
30	34569	34913	+	695	584	345	-
30	35484	36026	+	4516	4246	543	NADH dehydrogenase subunit 2
30	43555	43926	-	128	121	372	-
30	44377	44598	-	234	216	222	-
30	45214	45468	-	607	594	255	-
32	87167	87445	+	124	128	279	-
32	107059	107310	-	116	112	252	-
33	358	708	-	835	750	351	-
33	29653	29907	-	1170	986	255	-
33	30251	30451	-	231	195	201	-
36	101925	102140	+	171	159	216	-
37	26965	27177	-	136	129	213	-
38	66657	67385	-	4487	4419	729	ATPase subunit 6
40	84633	84929	-	168	142	297	-
40	85766	85966	-	526	459	201	-

41	81772	82023	-	124	124	252	-
44	86758	87297	+	11959*	11307*	540	cytochrome c oxidase subunit 2
44	87703	87909	+	140*	130*	207	-
45	94347	94790	-	6513	5992	444	NADH dehydrogenase subunit 2
47	47498	47785	-	133	115	288	-
47	48353	49729	-	14286	12960	1377	ribosomal protein S3
47	50250	50528	-	1768	1547	279	-
47	50593	50820	-	1233	1072	228	-
47	52328	52570	-	779	643	243	-
49	84844	85062	-	253	230	219	-
53	55930	56151	+	486	428	222	NADH dehydrogenase subunit 7
54	63317	63526	-	190	175	210	-
57	61121	61849	-	4456	4338	729	ATPase subunit 6
58	53923	54138	+	149	142	216	-
59	41368	41589	-	490	427	222	NADH dehydrogenase subunit 7
59	65656	65946	-	108	112	291	-
60	3277	3486	-	119	126	210	-
63	38053	38304	+	151	165	252	-

\*Coverage values may be inflated because the ORF overlaps with a region that is duplicated or highly similar to another gene.



**Table S4.** Summary of all identified C-to-U RNA editing sites. Sites labeled as intron/IGS were found adjacent to an exon with a *trans*-spliced intron with unknown boundaries, so it is not clear whether they are in the intron or IGS.

Chrom	Position	Strand	Gene/Location	Coverage	Edited (%)	Mean Quality
1	128225	+	ccmB-a	706	99.4	37.5
1	128267	+	ccmB-a	564	96.8	38.2
1	128268	+	ccmB-a	564	96.8	38.2
1	128351	+	ccmB-a	165	97.6	34.5
1	128357	+	ccmB-a	212	88.7	33.6
1	128361	+	ccmB-a	262	95.8	33.5
1	128501	+	ccmB-a	523	99.4	38.0
1	128664	+	ccmB-a	898	97.2	39.0
1	128691	+	ccmB-a	550	97.8	35.7
1	128700	+	ccmB-a	269	82.9	36.8
1	129165	+	rpl5	9124	92.0	37.8
1	129194	+	rpl5	9213	92.8	37.7
1	129474	+	rpl5	3879	94.1	37.5
1	129660	+	rpl5	27632	90.9	37.1
1	131199	+	cob	31293	98.7	38.2
1	131232	+	cob	19165	98.9	35.7
1	131442	+	cob	26100	99.5	39.1
1	131682	+	cob	8374	98.9	34.9
1	131782	+	cob	35816	98.3	37.6
1	132034	+	cob	126110	99.8	39.2
2	111595	-	ccmFc	6047	99.7	38.1
2	111669	-	ccmFc	8243	98.1	37.0
2	113335	-	ccmFc	3976	99.6	36.3
2	113598	-	ccmFc	3832	91.7	37.4
2	113602	-	ccmFc	3745	99.2	37.0
2	113630	-	ccmFc	2659	87.9	38.2
2	113703	-	ccmFc	3529	98.1	35.4
2	113819	-	5UTR-ccmFc	2148	92.5	35.9
2	113910	-	5UTR-ccmFc	1762	20.4	37.3
2	114327	-	5UTR-ccmFc	1495	83.7	37.8
2	115766	-	IGS	502	24.3	36.5
2	115832	-	IGS	527	95.5	36.9
2	115884	-	IGS	230	86.1	36.8
3	19664	+	IGS	336	58.3	39.0
3	19842	+	IGS	428	68.5	38.3
3	87856	+	nad1-3	10633	95.6	36.2
3	87866	+	nad1-3	15401	89.8	36.2
3	87902	+	nad1-3	30676	94.5	36.5

3	88465	+	intron/IGS-nad1-3	2914	88.6	36.6
4	85458	+	nad5-1	10696	97.1	36.6
4	86410	+	nad5-2	19807	98.9	37.3
4	86542	+	nad5-2	24318	99.4	38.3
4	86566	+	nad5-2	33424	99.5	36.6
4	86716	+	nad5-2	21415	97.5	36.8
4	86721	+	nad5-2	23496	96.9	36.6
4	86776	+	nad5-2	26054	99.5	38.2
4	86893	+	nad5-2	30369	98.8	33.8
4	87003	+	nad5-2	37968	99.6	35.6
4	87478	+	nad5-2	65369	99.6	36.2
4	87896	+	intron/IGS-nad5-2	7864	66.7	36.8
5	73794	-	IGS	191	78.0	35.5
6	76528	+	atp9	226140	99.0	35.9
6	144066	-	nad1-5	53836	99.2	36.7
6	144096	-	nad1-5	30260	99.2	37.1
6	144251	-	nad1-5	10431	98.0	34.9
6	144786	-	intron/IGS-nad1-5	2017	90.2	35.5
7	38551	+	nad5-4	54499	97.7	36.8
7	38581	+	nad5-4	92780	99.4	36.2
7	38611	+	nad5-4	71512	99.7	37.7
7	39920	+	nad5-5	41655	98.8	37.0
7	39983	+	nad5-5	69836	99.4	37.2
8	94276	+	5UTR-nad2	18527	34.0	37.0
8	94380	+	nad2-1	29476	93.7	37.9
8	95686	+	nad2-2	8556	98.1	37.5
8	95691	+	nad2-2	8508	98.2	37.1
8	95724	+	nad2-2	9708	96.8	35.6
8	95758	+	nad2-2	22091	98.4	36.3
8	95827	+	nad2-2	23403	97.8	39.0
8	111845	+	5UTR-nad6	20630	94.8	36.2
8	112014	+	nad6	41731	90.9	36.8
8	112015	+	nad6	41731	90.9	36.8
8	112021	+	nad6	40101	85.6	36.4
8	112072	+	nad6	27070	99.6	38.5
8	112117	+	nad6	12981	99.3	37.0
8	112495	+	nad6	38230	99.8	38.6
9	111015	-	ccmC	14144	99.8	39.2
9	111038	-	ccmC	14765	99.4	38.5
9	111074	-	ccmC	8482	97.7	36.5
9	111112	-	ccmC	7311	58.9	39.0
9	111189	-	ccmC	4161	97.4	37.1
9	111214	-	ccmC	3255	28.6	38.0

9	111215	-	ccmC	3255	70.1	37.6
9	111221	-	ccmC	3284	98.3	37.7
9	111225	-	ccmC	3896	98.6	37.5
9	111230	-	ccmC	4074	98.5	37.6
9	111237	-	ccmC	3815	98.3	38.3
9	111242	-	ccmC	3725	99.3	38.5
9	111293	-	ccmC	5003	99.0	37.3
9	111357	-	ccmC	3271	98.1	36.1
9	111504	-	ccmC	3977	98.4	37.3
9	111585	-	ccmC	4296	91.3	38.0
9	111715	-	5UTR-ccmC	2582	40.0	38.0
9	111892	-	5UTR-ccmC	2419	22.8	38.4
9	112186	-	5UTR-ccmC	1751	80.4	36.0
9	112543	-	5UTR-ccmC	838	41.9	37.2
10	65340	+	5UTR-nad9	5769	33.0	37.2
10	65731	+	nad9	21147	99.0	35.6
11	94270	+	nad4-1	11376	96.8	38.3
11	94303	+	nad4-1	16521	95.9	37.2
11	94354	+	nad4-1	17231	96.4	37.6
11	94393	+	nad4-1	15488	98.6	38.1
11	94564	+	nad4-1	11174	98.1	38.2
11	94629	+	nad4-1	6029	87.2	37.8
11	94633	+	nad4-1	5933	97.4	36.6
11	96760	+	nad4-2	16081	98.3	36.6
11	97105	+	nad4-2	5321	98.7	39.1
11	97573	+	intron-nad4	2777	25.7	38.4
11	97708	+	intron-nad4	1918	92.5	37.8
11	98436	+	nad4-3	29316	99.0	37.1
11	98452	+	nad4-3	29492	99.2	39.2
15	42079	+	nad2-pseudo	5715	90.9	34.3
15	42671	+	nad2-pseudo	3822	97.1	38.6
15	42676	+	nad2-pseudo	3816	97.0	39.0
15	42709	+	nad2-pseudo	919	89.9	36.7
16	58517	+	mttb-pseudo	1651	96.9	39.2
16	58525	+	mttb-pseudo	1648	94.8	39.3
19	4132	+	IGS	319	33.2	36.5
19	4323	+	IGS	617	31.3	38.6
21	22674	+	intron/IGS-nad5-3	2032	43.4	37.2
21	22785	+	intron/IGS-nad5-3	1654	81.5	37.1
23	112715	+	5UTR-mttB	3515	47.6	36.7
23	112770	+	5UTR-mttB	4991	25.1	36.9
23	113221	+	mttB	4634	92.4	37.8
23	113257	+	mttB	6540	91.5	38.0

23	113288	+	mttB	7884	94.9	38.2
23	113419	+	mttB	7037	95.0	35.7
23	113536	+	mttB	10774	77.7	38.1
23	113564	+	mttB	11805	96.3	38.6
23	113654	+	mttB	6393	96.5	37.6
23	113662	+	mttB	5107	94.3	37.2
23	113767	+	mttB	14684	97.5	37.5
23	113870	+	mttB	10718	98.5	37.3
24	36129	+	rpl5-pseudo	756	21.6	37.0
24	36438	+	rpl5-pseudo	554	53.4	37.9
24	36614	+	rpl5-pseudo	1131	52.3	38.0
25	70948	-	cox3	46307	98.4	36.4
25	71370	-	UTR-cox3-atp8	47824	37.2	38.1
25	71684	-	atp8	42085	43.3	37.7
25	72109	-	atp8	15728	96.5	36.7
26	88065	+	IGS	547	78.2	38.9
26	88474	+	IGS	435	33.1	36.7
26	88698	+	IGS	628	67.7	37.1
28	12812	-	nad7-4	82769	99.8	38.5
28	12875	-	nad7-4	44787	99.6	37.3
28	12890	-	nad7-4	42614	99.7	37.8
28	13015	-	nad7-4	24931	97.8	37.2
28	13448	-	intron-nad7	5285	29.8	38.1
28	13533	-	intron-nad7	3941	31.9	35.2
28	14025	-	intron-nad7	3283	84.4	36.9
28	15243	-	nad7-3	22851	98.4	34.8
28	15274	-	nad7-3	16346	99.1	37.3
28	15570	-	nad7-3	22927	98.9	34.5
28	17404	-	nad7-1	11965	93.6	38.3
28	17443	-	nad7-1	18289	92.2	36.2
28	17659	-	5UTR-nad7	16619	51.4	38.9
30	35023	+	nad2-pseudo	529	22.1	39.1
30	35677	+	nad2-pseudo	8419	98.2	37.5
30	35682	+	nad2-pseudo	8373	98.3	37.1
30	35715	+	nad2-pseudo	9679	97.0	35.6
30	35749	+	nad2-pseudo	9024	98.2	38.9
30	35818	+	nad2-pseudo	488	78.7	39.1
32	53108	-	matR-a	11802	87.2	36.8
32	53149	-	matR-a	9387	22.1	37.2
32	53234	-	matR-a	7492	99.1	36.9
32	53755	-	matR-a	4574	60.1	38.0
32	54058	-	matR-a	3155	23.9	36.1
32	54653	-	matR-a	2628	96.0	37.6

32	54786	-	matR-a	13973	99.1	36.5
32	54947	-	matR-a	5453	61.6	36.8
32	55672	-	nad1-4	1957	23.6	34.2
32	56121	-	intron/IGS-nad1-4	2865	30.0	37.8
32	56239	-	intron/IGS-nad1-4	3390	52.1	36.0
33	71	-	IGS	742	39.0	38.2
33	29863	-	IGS	645	40.2	39.7
33	107948	-	IGS	396	25.3	38.3
33	108157	-	IGS	620	20.7	36.8
33	108431	-	IGS	638	24.9	36.4
35	36945	-	nad1-1	16693	85.9	38.0
35	36987	-	nad1-1	14316	98.3	36.8
35	37250	-	nad1-1	14939	66.2	38.3
35	37404	-	5UTR-nad1-1	16994	31.3	36.2
36	33354	+	nad3-a	6388	71.3	37.6
36	33355	+	nad3-a	6388	23.0	37.3
36	33501	+	nad3-a	5325	95.4	38.2
36	33508	+	nad3-a	5207	89.3	38.7
36	33642	+	nad3-a	7891	95.5	39.4
38	66220	-	atp6-pseudo	2038	76.4	38.6
38	66274	-	atp6-pseudo	38730	99.7	39.6
38	66411	-	atp6-pseudo	9151	99.8	36.5
38	66475	-	atp6-pseudo	6720	99.1	37.8
38	66478	-	atp6-pseudo	6746	99.4	38.1
38	66537	-	atp6-pseudo	10741	99.4	37.2
38	66667	-	IGS	12000	99.6	38.6
38	67482	-	IGS	11566	84.3	37.0
38	67559	-	IGS	5923	95.3	38.8
38	67574	-	IGS	5998	95.3	37.1
39	49370	-	atp6	112502	99.8	39.4
39	49424	-	atp6	137427	99.0	36.8
39	49561	-	atp6	54413	99.8	38.3
39	49625	-	atp6	115223	99.5	38.3
39	49628	-	atp6	115192	99.7	38.5
39	49972	-	atp6	95611	99.6	37.9
39	50051	-	atp6	52075	98.9	35.7
39	50849	-	atp1	38708	30.6	36.6
41	30934	+	IGS	5152	56.5	37.1
41	31045	+	IGS	3813	83.8	37.7
42	33886	+	5UTR-rps13	3483	22.5	38.6
42	34519	+	5UTR-rps13	19914	29.7	37.9
42	35465	+	3UTR-rps13	330	39.4	37.8
42	35856	+	3UTR-rps13	474	71.3	38.0

42	35871	+	3UTR-rps13	463	70.0	37.6
42	35934	+	3UTR-rps13	339	54.0	36.3
45	94414	-	nad2-pseudo	836	99.0	33.3
45	94534	-	nad2-pseudo	22249	99.8	39.3
45	94603	-	nad2-pseudo	10371	99.0	34.2
46	19783	-	IGS	1722	33.1	38.7
46	45056	+	5UTR-ccmFn	615	21.5	37.3
46	45240	+	ccmFn	1114	97.3	38.5
46	45285	+	ccmFn	589	91.7	35.4
46	45443	+	ccmFn	951	98.1	37.2
46	45666	+	ccmFn	1626	41.2	36.8
46	45843	+	ccmFn	1677	98.0	36.6
46	45912	+	ccmFn	936	99.4	36.5
46	45939	+	ccmFn	439	99.5	33.4
46	46134	+	ccmFn	1255	21.7	37.5
46	46409	+	ccmFn	780	99.6	38.4
46	46437	+	ccmFn	660	98.8	36.8
46	46454	+	ccmFn	547	98.5	35.7
46	46469	+	ccmFn	679	98.5	35.3
46	46487	+	ccmFn	829	98.9	37.6
46	46520	+	ccmFn	1146	95.2	38.0
46	46531	+	ccmFn	1249	26.3	37.1
46	46538	+	ccmFn	1223	98.5	38.3
46	46712	+	ccmFn	1651	70.6	37.3
47	48627	-	rps3	14592	98.9	38.0
47	48654	-	rps3	9329	98.3	36.6
47	49248	-	rps3	6181	26.8	35.1
47	49296	-	rps3	4139	97.3	36.8
47	51315	-	5UTR-rps3	1236	68.3	38.3
47	52264	-	IGS	1212	39.7	38.4
47	52595	-	IGS	289	39.5	38.0
49	31208	+	nad2-3	24657	31.0	37.6
49	33112	+	nad2-4	42441	99.5	38.7
49	33142	+	nad2-4	45968	99.5	38.7
49	33146	+	nad2-4	50364	98.9	38.1
49	33212	+	nad2-4	28309	90.7	38.4
49	33242	+	nad2-4	34939	99.4	36.1
49	33311	+	nad2-4	24403	99.8	38.9
49	33431	+	nad2-4	3982	82.9	37.0
49	34782	+	nad2-5	154508	98.5	36.2
49	34785	+	nad2-5	160482	99.0	35.2
49	34790	+	nad2-5	155520	96.2	35.5
54	3422	+	UTR-rrn5	202	62.9	37.2

54	3492	+	UTR-rrn5	248	50.8	36.0
55	1642	-	nad3-b	7667	97.3	39.4
55	1776	-	nad3-b	4872	89.3	38.8
55	1783	-	nad3-b	5028	95.5	38.3
55	1929	-	nad3-b	6352	23.7	37.3
55	1930	-	nad3-b	6352	71.0	37.7
55	70100	-	cox2	34143	99.2	37.5
55	70192	-	cox2	27276	98.7	37.0
55	71541	-	5UTR-cox2	4273	79.9	38.2
57	60684	-	atp6-pseudo	1574	98.3	38.6
57	60738	-	atp6-pseudo	38878	99.7	39.6
57	60875	-	atp6-pseudo	9119	99.7	36.5
57	60939	-	atp6-pseudo	6550	99.1	37.7
57	60942	-	atp6-pseudo	6568	99.5	38.1
57	61001	-	atp6-pseudo	10809	99.4	37.3
57	61131	-	IGS	12088	99.6	38.6
57	61946	-	IGS	11426	84.2	37.0
57	62023	-	IGS	5956	95.6	38.7
57	62038	-	IGS	5996	95.6	37.1
60	66673	-	3UTR-atp4-a	30489	50.7	37.8
60	67379	-	atp4	25399	99.4	36.5
60	67535	-	atp4	12301	99.6	37.7
60	67559	-	atp4	15773	99.6	36.7
60	67571	-	atp4	18399	99.7	37.4
60	67697	-	atp4	14692	99.7	38.4
60	67752	-	atp4	11772	81.3	36.8
60	67944	-	nad4L-a	8746	98.9	38.2
60	68095	-	nad4L-a	9427	99.4	38.1
60	68116	-	nad4L-a	8532	98.9	38.0
60	68131	-	nad4L-a	8840	99.5	38.5
60	68179	-	nad4L-a	6910	99.6	39.1
60	68224	-	nad4L-a	3494	89.0	38.2
60	69653	-	UTR-nad4L-a-ccmB-b	4237	89.3	37.5
60	69933	-	UTR-nad4L-a-ccmB-b	6464	81.0	37.2
60	69962	-	UTR-nad4L-a-ccmB-b	6276	79.1	37.8
60	70427	-	ccmB-b	131	84.7	36.8
60	70436	-	ccmB-b	295	96.6	35.7
60	70463	-	ccmB-b	726	96.3	38.9
60	70626	-	ccmB-b	647	98.9	38.2
60	70766	-	ccmB-b	180	88.3	33.6
60	70770	-	ccmB-b	130	83.1	34.0
60	70781	-	ccmB-b	382	100.0	37.4
60	70859	-	ccmB-b	274	92.3	38.8

60	70860	-	ccmB-b	274	92.3	38.8
60	70902	-	ccmB-b	482	97.7	38.0
60	71821	-	5UTR-ccmB-b	310	94.2	37.3
60	72095	-	5UTR-ccmB-b	295	50.2	37.5
61	4373	-	matR-b	11881	86.8	36.8
61	4414	-	matR-b	9532	22.1	37.4
61	4499	-	matR-b	7509	98.9	36.9
61	5020	-	matR-b	4464	60.9	37.8
61	5323	-	matR-b	3161	23.0	36.2
61	5918	-	matR-b	2719	96.1	37.8
61	6051	-	matR-b	13778	99.2	36.4
61	6212	-	matR-b	5399	63.6	36.6
61	6937	-	nad1-4	1887	24.5	34.5
61	7386	-	intron/IGS-nad1-4	2917	30.6	37.5
61	7504	-	intron/IGS-nad1-4	3348	52.2	36.1
62	43183	-	3UTR-atp4-b	30577	50.6	37.8
62	43889	-	atp4-b	25461	99.3	36.5
62	44045	-	atp4-b	12091	99.6	37.7
62	44069	-	atp4-b	15741	99.7	36.7
62	44081	-	atp4-b	18443	99.8	37.4
62	44207	-	atp4-b	14643	99.8	38.4
62	44262	-	atp4-b	11757	80.6	36.8
62	44454	-	nad4L-b	8678	98.9	38.1
62	44605	-	nad4L-b	9326	99.3	38.1
62	44626	-	nad4L-b	8478	99.2	38.0
62	44641	-	nad4L-b	8794	99.6	38.5
62	44689	-	nad4L-b	6912	99.6	39.2
62	44734	-	nad4L-b	3544	88.3	38.2
62	46163	-	UTR-nad4L-b-ccmB-c	4431	89.4	37.5
62	46443	-	UTR-nad4L-b-ccmB-c	6381	80.2	37.1
62	46472	-	UTR-nad4L-b-ccmB-c	6127	78.4	37.8
62	46937	-	ccmB-c	147	73.5	37.0
62	46946	-	ccmB-c	308	95.5	35.6
62	46973	-	ccmB-c	751	95.1	38.8
62	47136	-	ccmB-c	579	98.6	38.3
62	47276	-	ccmB-c	202	92.6	33.7
62	47280	-	ccmB-c	151	88.1	33.7
62	47286	-	ccmB-c	119	91.6	34.6
62	47369	-	ccmB-c	283	90.1	38.5
62	47370	-	ccmB-c	283	90.1	38.5
62	47412	-	ccmB-c	500	98.2	37.9

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**Table S5.** Summary of non-canonical (i.e., other C-to-U) editing sites identified by the CLC algorithm. Sites labeled as Intron/IGS were found adjacent to an exon with a *trans*-spliced intron with unknown boundaries, so it is not clear whether they are in the intron or IGS. UTRs and IGSs were defined/distinguished based on an arbitrary cutoff of 2 kb from annotated coding sequences.

Chrom	Position	Strand	Gene/Location	Reference	Alternative	Coverage	Edited (%)	Mean Quality
1	132088	+	3UTR-cob	T	A	4327	27.34	32.01
8	93669	+	5UTR-nad2	A	C	252	41.67	32.77
11	95250	+	Intron-nad4	G	C	1137	55.50	11.70
21	23158	+	Intron/IGS-nad5-exon3	T	C	4171	59.89	38.43
21	23177	+	Intron/IGS-nad5-exon3	G	A	3791	56.98	38.97
21	23220	+	Intron/IGS-nad5-exon3	A	T	3896	53.85	36.18
33	29936	-	IGS	A	G	599	31.89	34.12
33	29937	-	IGS	T	C	599	31.89	34.12
36	33691	+	3UTR-nad3	T	A	652	20.09	31.76
41	31418	+	IGS	T	C	4137	59.71	38.39
41	31437	+	IGS	G	A	3766	56.72	38.73
41	31480	+	IGS	A	T	3808	52.76	35.93
47	48342	-	3UTR-rps3	A	T	1393	36.47	32.29
55	1593	-	3UTR-nad3	A	T	308	37.66	31.22

**Table S6.** Comparison of identified RNA editing sites in protein-coding genes to previous analysis of RNA editing in another *Silene noctiflora* population by Sloan et al. (2010)

Chrom	Position	Strand	Gene <sup>a</sup>	Coverage	Edited (%)	Mean Quality	2010 Study
1	128225	+	ccmB	706	99.43	37.47	Y
1	128267	+	ccmB	564	96.81	38.22	Y
1	128268	+	ccmB	564	96.81	38.22	Y
1	128351	+	ccmB	165	97.58	34.52	Y
1	128357	+	ccmB	212	88.68	33.59	Y
1	128361	+	ccmB	262	95.80	33.51	Y
1	128501	+	ccmB	523	99.43	38.01	Y
1	128664	+	ccmB	898	97.22	39.00	Y
1	128691	+	ccmB	550	97.82	35.72	Y
1	128700	+	ccmB	269	82.90	36.77	Y
1	129165	+	rpl5	9124	91.98	37.80	Y
1	129194	+	rpl5	9213	92.79	37.72	Y
1	129474	+	rpl5	3879	94.10	37.45	Y
1	129660	+	rpl5	27632	90.88	37.09	Y
1	131199	+	cob	31293	98.68	38.23	Y
1	131232	+	cob	19165	98.89	35.69	Y
1	131442	+	cob	26100	99.49	39.05	Y
1	131682	+	cob	8374	98.88	34.89	Y
1	131782	+	cob	35816	98.30	37.57	Y
1	132034	+	cob	126110	99.76	39.22	Y
2	111595	-	ccmFc	6047	99.67	38.14	Y
2	111669	-	ccmFc	8243	98.11	36.99	Y
2	113335	-	ccmFc	3976	99.57	36.29	Y
2	113598	-	ccmFc	3832	91.73	37.40	Y
2	113602	-	ccmFc	3745	99.23	36.97	Y
2	113630	-	ccmFc	2659	87.89	38.15	Y
2	113703	-	ccmFc	3529	98.07	35.43	Y
3	87856	+	nad1-3	10633	95.60	36.20	Y
3	87866	+	nad1-3	15401	89.76	36.19	Y
3	87902	+	nad1-3	30676	94.51	36.47	Y
4	85458	+	nad5-1	10696	97.09	36.64	Y
4	86410	+	nad5-2	19807	98.91	37.30	Y
4	86542	+	nad5-2	24318	99.41	38.29	Y
4	86566	+	nad5-2	33424	99.48	36.64	Y
4	86716	+	nad5-2	21415	97.48	36.83	Y
4	86721	+	nad5-2	23496	96.87	36.55	Y
4	86776	+	nad5-2	26054	99.52	38.23	Y
4	86893	+	nad5-2	30369	98.75	33.81	Y
4	87003	+	nad5-2	37968	99.59	35.59	Y
4	87478	+	nad5-2	65369	99.62	36.17	Y
6	76528	+	atp9	226140	99.00	35.90	Y
6	144066	-	nad1-5	53836	99.24	36.74	Y

6	144096	-	nad1-5	30260	99.22	37.14	Y
6	144251	-	nad1-5	10431	97.95	34.86	Y
7	38551	+	nad5-4	54499	97.68	36.78	Y
7	38581	+	nad5-4	92780	99.44	36.18	Y
7	38611	+	nad5-4	71512	99.68	37.71	Y
7	39920	+	nad5-5	41655	98.84	37.03	Y
7	39983	+	nad5-5	69836	99.41	37.24	Y
8	94380	+	nad2-1	29476	93.73	37.92	Y
8	95686	+	nad2-2	8556	98.14	37.51	Y
8	95691	+	nad2-2	8508	98.19	37.12	Y
8	95724	+	nad2-2	9708	96.82	35.61	Y
8	95758	+	nad2-2	22091	98.37	36.32	Y
8	95827	+	nad2-2	23403	97.83	39.04	Y
8	112014	+	nad6	41731	90.94	36.82	Y
8	112015	+	nad6	41731	90.94	36.82	Y
8	112021	+	nad6	40101	85.62	36.44	Y
8	112072	+	nad6	27070	99.60	38.48	Y
8	112117	+	nad6	12981	99.32	36.95	Y
8	112495	+	nad6	38230	99.81	38.61	Y
9	111015	-	ccmC	14144	99.77	39.24	Y
9	111038	-	ccmC	14765	99.35	38.50	Y
9	111074	-	ccmC	8482	97.74	36.52	Y
9	111112	-	ccmC	7311	58.92	39.03	Y
9	111189	-	ccmC	4161	97.38	37.07	Y
9	111214	-	ccmC	3255	28.60	37.95	N
9	111215	-	ccmC	3255	70.08	37.56	Y
9	111221	-	ccmC	3284	98.29	37.71	Y
9	111225	-	ccmC	3896	98.64	37.48	Y
9	111230	-	ccmC	4074	98.50	37.64	Y
9	111237	-	ccmC	3815	98.32	38.26	Y
9	111242	-	ccmC	3725	99.25	38.49	Y
9	111293	-	ccmC	5003	98.96	37.34	Y
9	111357	-	ccmC	3271	98.14	36.05	Y
9	111504	-	ccmC	3977	98.42	37.34	Y
9	111585	-	ccmC	4296	91.29	38.00	Y
10	65731	+	nad9	21147	98.95	35.61	Y
11	94270	+	nad4-1	11376	96.83	38.28	Y
11	94303	+	nad4-1	16521	95.87	37.15	Y
11	94354	+	nad4-1	17231	96.36	37.61	Y
11	94393	+	nad4-1	15488	98.55	38.11	Y
11	94564	+	nad4-1	11174	98.06	38.21	Y
11	94629	+	nad4-1	6029	87.23	37.76	Y
11	94633	+	nad4-1	5933	97.39	36.59	Y
11	96760	+	nad4-2	16081	98.25	36.57	Y
11	97105	+	nad4-2	5321	98.74	39.10	Y
11	98436	+	nad4-3	29316	98.96	37.12	Y

11	98452	+	nad4-3	29492	99.22	39.18	Y
23	113221	+	mttB	4634	92.43	37.82	Y
23	113257	+	mttB	6540	91.45	38.01	Y
23	113288	+	mttB	7884	94.91	38.24	Y
23	113419	+	mttB	7037	95.01	35.73	Y
23	113536	+	mttB	10774	77.70	38.06	Y
23	113564	+	mttB	11805	96.31	38.55	Y
23	113654	+	mttB	6393	96.45	37.60	Y
23	113662	+	mttB	5107	94.34	37.18	Y
23	113767	+	mttB	14684	97.49	37.50	Y
23	113870	+	mttB	10718	98.49	37.32	Y
25	70948	-	cox3	46307	98.40	36.40	Y
25	71684	-	atp8	42085	43.32	37.69	Y
25	72109	-	atp8	15728	96.52	36.72	Y
28	12812	-	nad7-4	82769	99.83	38.53	Y
28	12875	-	nad7-4	44787	99.56	37.33	Y
28	12890	-	nad7-4	42614	99.69	37.78	Y
28	13015	-	nad7-4	24931	97.83	37.18	Y
28	15243	-	nad7-3	22851	98.38	34.82	Y
28	15274	-	nad7-3	16346	99.06	37.27	Y
28	15570	-	nad7-3	22927	98.92	34.49	Y
28	17404	-	nad7-1	11965	93.64	38.32	Y
28	17443	-	nad7-1	18289	92.21	36.20	Y
32	53108	-	matR-a	11802	87.17	36.84	Y
32	53149	-	matR-a	9387	22.13	37.23	N
32	53234	-	matR-a	7492	99.05	36.89	Y
32	53755	-	matR-a	4574	60.14	38.04	Y
32	54058	-	matR-a	3155	23.87	36.12	N
32	54653	-	matR-a	2628	96.00	37.55	Y
32	54786	-	matR-a	13973	99.11	36.49	Y
32	54947	-	matR-a	5453	61.64	36.78	Y
35	36945	-	nad1-1	16693	85.86	38.00	Y
35	36987	-	nad1-1	14316	98.29	36.77	Y
35	37250	-	nad1-1	14939	66.19	38.33	Y
36	33354	+	nad3-a	6388	71.29	37.61	Y
36	33355	+	nad3-a	6388	22.95	37.34	Y
36	33501	+	nad3-a	5325	95.38	38.19	Y
36	33508	+	nad3-a	5207	89.32	38.71	Y
36	33642	+	nad3-a	7891	95.46	39.37	Y
39	49370	-	atp6	112502	99.83	39.42	Y
39	49424	-	atp6	137427	99.00	36.83	Y
39	49561	-	atp6	54413	99.77	38.34	Y
39	49625	-	atp6	115223	99.52	38.26	Y
39	49628	-	atp6	115192	99.69	38.54	Y
39	49972	-	atp6	95611	99.62	37.93	Y
39	50051	-	atp6	52075	98.85	35.73	Y

39	50849	-	atp1	38708	30.59	36.55	N
46	45240	+	ccmFn	1114	97.31	38.45	Y
46	45285	+	ccmFn	589	91.68	35.43	Y
46	45443	+	ccmFn	951	98.11	37.23	Y
46	45666	+	ccmFn	1626	41.21	36.84	N
46	45843	+	ccmFn	1677	98.03	36.64	Y
46	45912	+	ccmFn	936	99.36	36.50	Y
46	45939	+	ccmFn	439	99.54	33.42	Y
46	46134	+	ccmFn	1255	21.67	37.45	N
46	46409	+	ccmFn	780	99.62	38.37	Y
46	46437	+	ccmFn	660	98.79	36.80	Y
46	46454	+	ccmFn	547	98.54	35.70	Y
46	46469	+	ccmFn	679	98.53	35.29	Y
46	46487	+	ccmFn	829	98.91	37.59	Y
46	46520	+	ccmFn	1146	95.20	37.95	Y
46	46531	+	ccmFn	1249	26.26	37.11	Y
46	46538	+	ccmFn	1223	98.45	38.29	Y
46	46712	+	ccmFn	1651	70.62	37.31	Y
47	48627	-	rps3	14592	98.94	37.98	Y
47	48654	-	rps3	9329	98.33	36.55	Y
47	49248	-	rps3	6181	26.84	35.14	N
47	49296	-	rps3	4139	97.32	36.82	Y
49	31208	+	nad2-3	24657	30.99	37.59	Y
49	33112	+	nad2-4	42441	99.53	38.69	Y
49	33142	+	nad2-4	45968	99.50	38.66	Y
49	33146	+	nad2-4	50364	98.86	38.12	Y
49	33212	+	nad2-4	28309	90.66	38.43	Y
49	33242	+	nad2-4	34939	99.40	36.06	Y
49	33311	+	nad2-4	24403	99.82	38.86	Y
49	33431	+	nad2-4	3982	82.92	37.04	Y
49	34782	+	nad2-5	154508	98.54	36.19	Y
49	34785	+	nad2-5	160482	99.02	35.19	Y
49	34790	+	nad2-5	155520	96.19	35.51	Y
55	70100	-	cox2	34143	99.22	37.52	Y
55	70192	-	cox2	27276	98.65	37.04	Y
60	67379	-	atp4-a	25399	99.41	36.51	Y
60	67535	-	atp4-a	12301	99.57	37.72	Y
60	67559	-	atp4-a	15773	99.61	36.72	Y
60	67571	-	atp4-a	18399	99.70	37.43	Y
60	67697	-	atp4-a	14692	99.72	38.35	Y
60	67752	-	atp4-a	11772	81.30	36.81	Y
60	67944	-	nad4L-a	8746	98.94	38.17	Y
60	68095	-	nad4L-a	9427	99.41	38.12	Y
60	68116	-	nad4L-a	8532	98.85	37.96	Y
60	68131	-	nad4L-a	8840	99.50	38.45	Y
60	68179	-	nad4L-a	6910	99.57	39.14	Y

60	68224	-	nad4L-a	3494	88.95	38.21	Y
61	6937	-	nad1-4	1887	24.54	34.45	Y

<sup>a</sup>Only a single representative is shown for genes with multiple copies in the genome.

**Table S7.** Summary of RNA editing sites that were previously reported in another *Silene noctiflora* population by Sloan et al. (2010) but not identified by the CLC algorithm at a cutoff of 20% editing frequency

<b>Chrom</b>	<b>Position</b>	<b>Strand</b>	<b>Gene</b>	<b>Manual Inspection<sup>a</sup></b>
1	128208	+	ccmB	Not Edited
1	128325	+	ccmB	Highly Edited
1	128345	+	ccmB	Highly Edited
1	128346	+	ccmB	Highly Edited
1	128711	+	ccmB	Highly Edited
1	128748	+	ccmB	Highly Edited
1	128751	+	ccmB	Highly Edited
1	128769	+	ccmB	Highly Edited
1	128793	+	ccmB	Highly Edited
2	113631	-	ccmFc	Highly Edited
23	131163	+	mttB	Partially Edited
35	36944	-	nad1-1	Highly Edited
46	46583	+	ccmFn	Not Edited
49	33396	+	nad2-4	Partially Edited

<sup>a</sup>Manual inspection of all mapped RNA-seq reads was used to classify each site: “Highly Edited” indicates >80%; “Partially Edited” indicates <20%; and “Not Edited” indicates no evidence of editing.