

**Table S1.** Content of the 553,721 bp mitochondrial genome of *Liriodendron tulipifera*.

Category	Feature	#	bp (%)†
<b>Genes</b>			
	protein coding	41	34,499 (6.2)
	pseudogenes	2	670 (0.1)
	rRNA	3	5,883 (1.1)
	mt-derived tRNA	13	996 (0.2)
	cp-derived tRNA	7	443 (0.1)
<b>Introns</b>			
	<i>cis</i> -spliced	20	36,353 (6.6)
	<i>trans</i> -spliced	5	n.d.
<b>Intergenic</b>			
	mt-derived*	n.d.	128,887 (23.3)
	cp-derived	25	26,887 (4.9)
	repeats > 500 bp	10	51,615 (9.4)
	repeats < 500 bp	n.d.	29,713 (5.4)
	transposon-like	n.d.	5,940 (1.1)
	unknown	n.d.	254,098 (45.9)

\* includes *trans*-spliced introns

† sum across categories exceeds 100.0% due to overlapping features such as genes in repetitive regions; see Methods.

	<i>atp1</i>	<i>atp4</i>	<i>atp6</i>	<i>atp8</i>	<i>atp9</i>	<i>ccmB</i>	<i>ccmC</i>	<i>ccmFc</i>	<i>ccmFN</i>	<i>cob</i>
<i>Arabidopsis</i>	5	8	1	ND	4	39	28	16	33	7
<i>Brassica</i>	4	8	1	3	4	39	25	ND	24	8
<i>Oenothera</i>	3	ND	22	6	4	46	28	18	44	13
<i>Citrullus</i>	7	13	22	3	7	34	16	11	ND	13
<i>Cucurbita</i>	3	12	20	3	6	33	17	13	ND	13
<i>Beta</i>	3	12	11	2	5	30	28	13	22	13
<i>Silene</i>	3	11	11	2	4	27	23	12	ND	9
<i>Nicotiana</i>	6	10	15	5	10	46	30	18	24	12
<i>Oryza</i>	4	9	15	3	8	35	34	27	ND	19
<i>Vitis</i>	8	5	17	6	4	6	15	6	ND	25
<i>Liriodendron</i>	14	16	29	6	15	49	41	24	34	30
<b>Edit Sites</b>	<b>18</b>	<b>21</b>	<b>35</b>	<b>15</b>	<b>17</b>	<b>71</b>	<b>53</b>	<b>68</b>	<b>51</b>	<b>45</b>

	<i>cox1</i>	<i>cox2</i>	<i>cox3</i>	<i>matR</i>	<i>mttB</i>	<i>nad1</i>	<i>nad2</i>	<i>nad3</i>	<i>nad4</i>	<i>nad4L</i>
<i>Arabidopsis</i>	ND	9	8	9	24	21	31	10	32	9
<i>Brassica</i>	1	8	7	8	27	20	24	8	35	9
<i>Oenothera</i>	ND	14	ND	8	20	24	35	13	ND	ND
<i>Citrullus</i>	18	9	9	4	21	20	26	12	43	13
<i>Cucurbita</i>	18	10	6	4	27	19	25	9	33	13
<i>Beta</i>	ND	8	4	9	19	18	23	10	19	9
<i>Silene</i>	ND	2	1	8	15	17	20	7	16	8
<i>Nicotiana</i>	13	12	8	11	43	22	28	15	37	13
<i>Oryza</i>	4	15	ND	ND	33	19	29	13	20	10
<i>Vitis</i>	22	16	10	11	ND	12	18	3	21	7
<i>Liriodendron</i>	37	14	19	19	58	33	49	21	58	13
<b>Edit Sites</b>	<b>42</b>	<b>23</b>	<b>23</b>	<b>23</b>	<b>72</b>	<b>45</b>	<b>64</b>	<b>32</b>	<b>78</b>	<b>17</b>

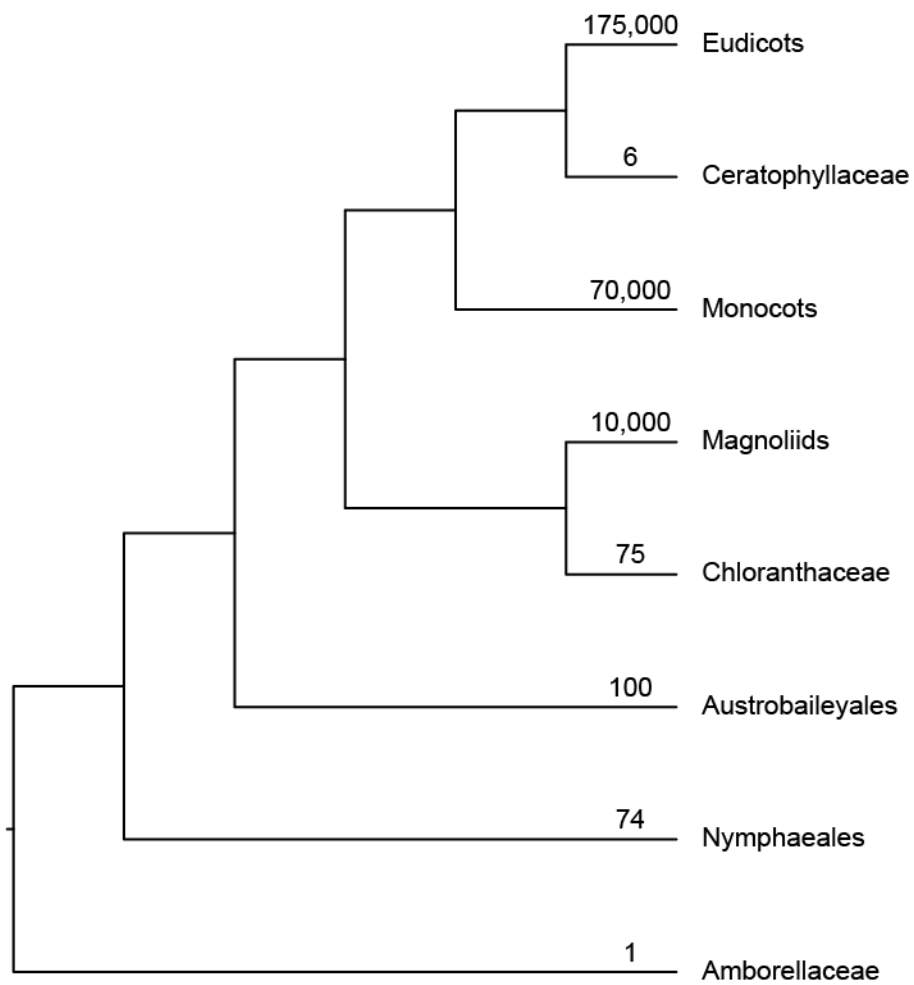
	<i>nad5</i>	<i>nad6</i>	<i>nad7</i>	<i>nad9</i>	<i>rpl2</i>	<i>rpl5</i>	<i>rps10</i>	<i>rps12</i>	<i>rps13</i>	<i>rps14</i>
<i>Arabidopsis</i>	27	10	22	7	1	10	ND	8	ND	ND
<i>Brassica</i>	29	11	23	7	1	9	ND	7	ND	ND
<i>Oenothera</i>	26	ND	ND	ND	4	9	ND	ND	3	2
<i>Citrullus</i>	29	ND	26	7	1	9	5	6	3	ND
<i>Cucurbita</i>	21	ND	25	7	1	8	5	6	3	ND
<i>Beta</i>	17	11	16	5	ND	5	ND	6	2	ND
<i>Silene</i>	18	10	15	5	ND	6	ND	ND	ND	ND
<i>Nicotiana</i>	24	1	23	7	ND	7	ND	4	3	ND
<i>Oryza</i>	11	16	28	11	ND	1	ND	ND	8	ND
<i>Vitis</i>	21	9	19	7	1	13	7	8	6	3
<i>Liriodendron</i>	49	25	39	14	3	12	6	9	7	2
<b>Edit Sites</b>	<b>59</b>	<b>34</b>	<b>45</b>	<b>16</b>	<b>7</b>	<b>16</b>	<b>7</b>	<b>14</b>	<b>11</b>	<b>3</b>

	<i>rps19</i>	<i>rps3</i>	<i>rps7</i>	<i>sdh3</i>
<i>Arabidopsis</i>	ND	13	ND	ND
<i>Brassica</i>	ND	8	1	ND
<i>Oenothera</i>	7	13	ND	ND
<i>Citrullus</i>	3	7	2	3
<i>Cucurbita</i>	4	10	3	5
<i>Beta</i>	ND	6	2	ND
<i>Silene</i>	ND	4	ND	ND
<i>Nicotiana</i>	5	10	ND	1
<i>Oryza</i>	6	10	2	ND
<i>Vitis</i>	8	9	3	1
<i>Liriodendron</i>	5	17	4	10
<b>Edit Sites</b>	<b>13</b>	<b>31</b>	<b>5</b>	<b>12</b>

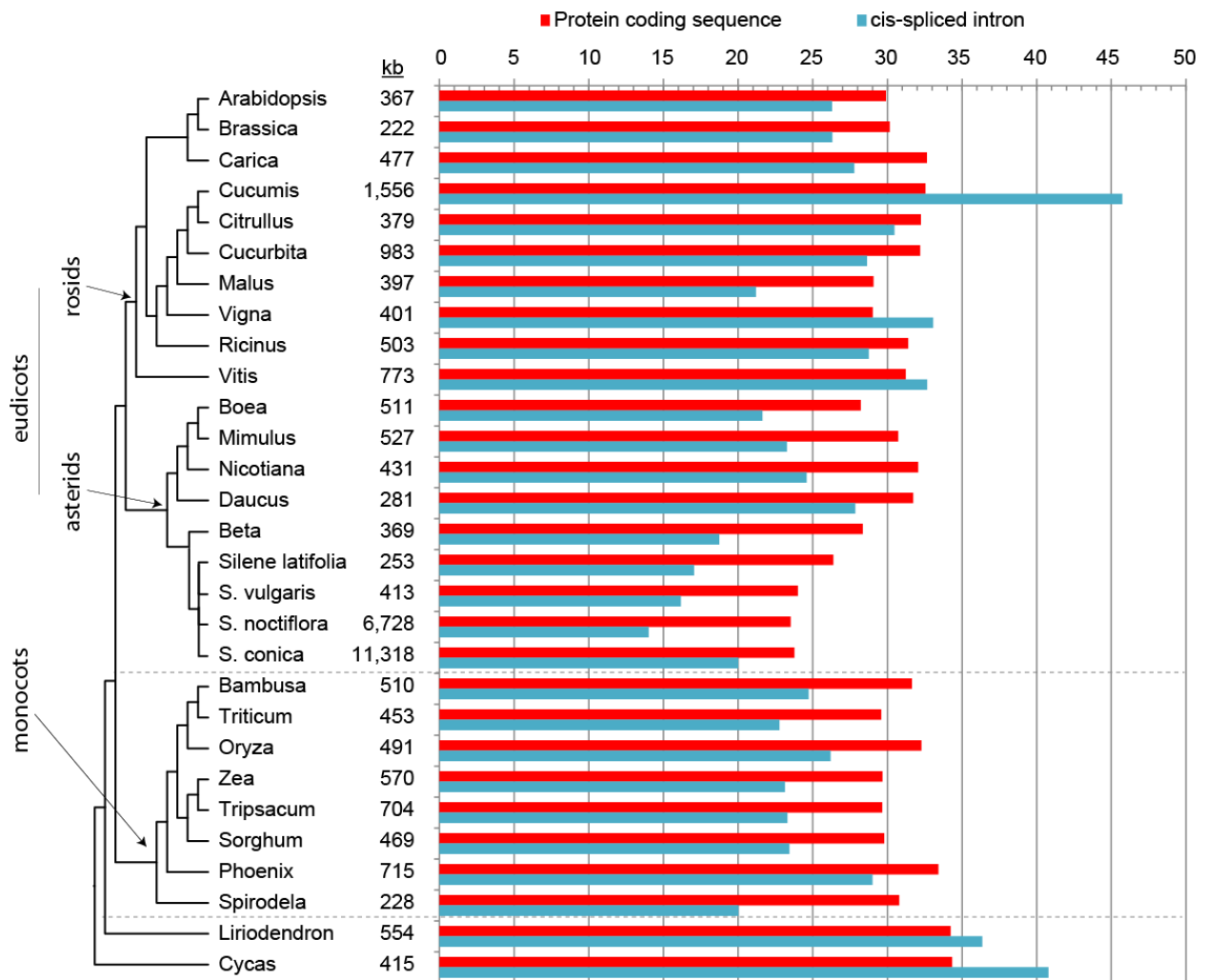
**Table S2.** Empirically determined RNA editing sites in each of the 10 species in the study broken down by gene. ‘ND’ indicates no data available, and the total number of unique edit sites across each gene given at bottom. See Methods for data sources.

	mt ssb	95% CI lower	95% CI upper	cp ssb	95% CI lower	95% CI upper
<i>Arabidopsis</i>	0.980	0.825	1.155	4.739	3.966	5.616
<i>Carica</i>	0.257	0.180	0.352	1.552	1.122	2.072
<i>Vigna</i>	0.775	0.642	0.924	6.931	5.929	8.057
<i>Cucurbita</i>	1.219	1.050	1.407	3.215	2.573	3.950
<i>Vitis</i>	0.178	0.123	0.249	0.918	0.695	1.182
<i>Beta</i>	0.964	0.837	1.102	3.406	2.872	4.011
<i>Nicotiana</i>	0.489	0.402	0.589	2.497	2.048	3.011
<i>Zea</i>	0.335	0.241	0.451	2.304	1.681	3.036
<i>Oryza</i>	0.290	0.202	0.399	2.283	1.660	3.016
<i>Liriodendron</i>	0.035	0.015	0.065	0.175	0.085	0.310
<i>Magnolia</i>	0.013	0.003	0.034	0.198	0.103	0.337
<i>Calycanthus</i>	0.120	0.084	0.167	1.091	0.841	1.384

**Table S3.** Estimated silent substitutions per site per billion years (ssb) and associated 95% confidence interval (CI) lower and upper bounds for the taxa in Figure 4 (other than the *Silene* species) for both the concatenated mitochondrial (mt) and plastid (cp) gene alignments.



**Figure S1.** Current consensus cladogram of relationships among the eight major lineages of angiosperms [1]. Numbers above branches are estimates of the number of extant species in each group as reported by APG III [2].



**Figure S2.** Genome content across seed plants. The cladogram at left is based on current phylogenetic consensus [1, 2] and the scale at right is in kb. Genome size, in kb, for each sample is given in the middle column.

1. Soltis DE, Smith SA, Cellinese N, Wurdack KJ, Tank DC, Brockington SF, Refulio-Rodriguez NF, Walker JB, Moore MJ, Carlsward BS *et al*: **Angiosperm phylogeny: 17 genes, 640 taxa.** *Am J Bot* 2011, **98**(4):704-730.
2. **APG3: An update of the Angiosperm Phylogeny Group classification for the orders and families of flowering plants: APG III.** *Bot J Linn Soc* 2009, **161**(2):105-121.