

Table S6 The nucleotide and haplotype diversity of flavonoid biosynthesis genes, positively selected genes and the reference loci in *A.squarrosu*m.

Loci	<i>L</i>	<i>N</i>	<i>S</i> (singl.)	<i>R</i> <sub>m</sub>	Total		Haplotype diversity		Nonsynonymous sites		Silent sites	
					$\theta_{wt}$	$\pi_t$	<i>N</i> <sub>h</sub>	<i>H</i> <sub>e</sub>	$\theta_{wa}$	$\pi_a$	$\theta_{ws}$	$\pi_s$
<b>Flavonoid biosynthesis genes</b>												
	575	95	2(2)	0	0.00068	0.00133	2	0.382	0.00048	0.00095	0.00155	0.00304
<i>PAL</i>	High	18	0	n.a.	0	0	1	0	0	0	0	0
	Middle	40	0	n.a.	0	0	1	0	0	0	0	0
	Low	37	2(2)	0	0.00083	0.00163	2	0.468	0.0006	0.00116	0.00191	0.00373
	400	102	1(1)	0	0.00048	0.00125	2	0.502	0	0	0.00214	0.00559
<i>C4H</i>	High	18	1(1)	0	0.00073	0.00106	2	0.425	0	0	0.00324	0.00473
	Middle	40	1(1)	0	0.00059	0.00096	2	0.385	0	0	0.00262	0.00428
	Low	44	1(1)	0	0.00057	0.00042	2	0.169	0	0	0.00256	0.00188
	436	97	2(2)	0	0.00079	0.0014	3	0.553	0.00052	0.00033	0.00161	0.00472
<i>4CL7</i>	High	18	1(1)	0	0.00055	0.00118	2	0.514	0	0	0.00226	0.00483
	Middle	36	2(2)	0	0.00095	0.00167	3	0.602	0.00063	0.00068	0.00194	0.00476
	Low	43	2(2)	0	0.00091	0.00127	3	0.528	0.00061	0.00014	0.00187	0.00475
	962	97	2(2)	0	0.0004	0.00049	3	0.46	0	0	0	0
<i>C3H</i>	High	18	0	n.a.	0	0	1	0	0	0	0	0
	Middle	35	0	n.a.	0	0	1	0	0	0	0	0
	Low	44	2(2)	0	0.00048	0.00045	3	0.418	0	0	0	0
	102	1(1)	0	0.00044	0.00115	2	0.502	0	0	0.00183	0.00476	
<i>FOMT</i>	High	434	18	0	n.a.	0	1	0	0	0	0	0
	Middle	41	1(1)	0	0.00054	0.00081	2	0.351	0	0	0.00222	0.00333
	Low	43	1(1)	0	0.00053	0.00048	2	0.21	0	0	0.00219	0.00200
	291	102	2(2)	0	0.00132	0.0027	2	0.393	0.00172	0.00352	0	0
<i>FNS</i>	High	18	0	n.a.	0	0	1	0	0	0	0	0

	Middle	40	0	n.a.	0	0	1	0	0	0	0	0	
	Low	44	2(2)	0	0.00157	0.00332	2	0.485	0.00203	0.00429	0	0	
		561	101	3(3)	0	0.00103	0.00239	4	0.535	0.00047	0.00115	0.00261	0.00588
<i>F3'H</i>	High	18	1(1)	0	0.00052	0.00052	2	0.294	0	0	0.00197	0.00199	
	Middle	39	3(3)	0	0.00126	0.00236	4	0.565	0.00058	0.00116	0.00320	0.00575	
	Low	44	3(3)	0	0.00123	0.00097	3	0.212	0.00056	0.00051	0.00311	0.00227	
		312	100	2(2)	0	0.00124	0.00199	2	0.311	0.0008	0.00129	0.00289	0.00463
<i>F3H</i>	High	18	0	n.a.	0	0	1	0	0	0	0	0	
	Middle	39	0	n.a.	0	0	1	0	0	0	0	0	
	Low	43	2(2)	0	0.00148	0.00324	2	0.505	0.00096	0.00209	0.00344	0.00752	
		601	100	2(2)	0	0.00064	0.0015	3	0.46	0.00042	0.00097	0.00141	0.00332
<i>CYP75B4</i>	High	18	0	n.a.	0	0	1	0	0	0	0	0	
	Middle	40	0	n.a.	0	0	1	0	0	0	0	0	
	Low	42	2(2)	0	0.00077	0.00110	3	0.354	0.0005	0.00075	0.00170	0.00231	
		703	99	1(1)	0	0.00028	0.00014	2	0.097	0.0036	0.00018	0	0
<i>CHS</i>	High	18	0	n.a.	0	0	1	0	0	0	0	0	
	Middle	37	1(1)	0	0.00034	0.00034	2	0.24	0.0045	0.0045	0	0	
	Low	44	0	n.a.	0	0	1	0	0	0	0	0	
		944	81	9(9)	5	0.00192	0.0028	15	0.817	0	0	0	0
<i>CHI</i>	High	18	3(3)	0	0.00092	0.00055	4	0.471	0	0	0	0	
	Middle	22	5(5)	2	0.00145	0.00176	6	0.823	0	0	0	0	
	Low	41	7(7)	2	0.00173	0.00277	9	0.709	0	0	0	0	
		304	99	3(3)	1	0.00191	0.00398	5	0.623	0.00086	0.00088	0.00498	0.01298
<i>COMT</i>	High	18	3(3)	0	0.00287	0.00499	3	0.601	0.00129	0.00209	0.00749	0.01348	
	Middle	39	3(3)	1	0.00233	0.00251	4	0.317	0.00105	0.00102	0.00608	0.00699	
	Low	42	2(2)	1	0.00153	0.00208	4	0.362	0	0	0.00597	0.00812	

**Positively selected genes**

		754	87	7(7)	0	0.00184	0.00394	6	0.732	0.00385	0.00922	0	0
<i>CCoAOMT</i>	High		18	6(6)	0	0.00231	0.00407	4	0.725	0.00558	0.01002	0	0
	Middle		27	5(5)	0	0.00172	0.00319	3	0.581	0.00502	0.0097	0	0
	Low		42	6(6)	0	0.00185	0.00293	4	0.512	0.00446	0.00661	0	0
		397	94	7(7)	6	0.00303	0.00382	21	0.517	0.00172	0.00242	0.00721	0.00827
<i>HCT</i>	High		18	0	0	0	0	1	0	0	0	0	0
	Middle		40	1(1)	0	0.00051	0.00024	2	0.096	0.00067	0.00032	0	0
	Low		36	7(7)	5	0.00364	0.00715	20	0.903	0.00206	0.00439	0.00865	0.01593
		546	80	6(6)	1	0.00222	0.00356	7	0.637	0.00178	0.00412	0.00294	0.00263
<i>FLS</i>	High		18	0	0	0	0	1	0	0	0	0	0
	Middle		29	6(6)	1	0.0028	0.00246	6	0.594	0.00211	0.00372	0.00349	0.00288
	Low		33	4(4)	0	0.00181	0.00266	5	0.498	0.00234	0.00355	0.00129	0.00185
		326	89	2(2)	0	0.00121	0.00122	3	0.387	0.00646	0.00207	0.01972	0.00275
<i>ANG</i>	High		18	1(1)	0	0.00089	0.00064	2	0.209	0.00118	0.00085	0	0
	Middle		39	2(2)	0	0.00145	0.00101	3	0.316	0.00096	0.00093	0.00295	0.00125
	Low		32	1(1)	0	0.00076	0.00153	2	0.498	0.00102	0.00204	0	0
		607	92	11(11)	4	0.00356	0.0051	14	0.79	0.00144	0.00353	0	0
<i>UNG</i>	High		18	6(6)	0	0.00287	0.0011	2	0.111	0.00213	0.00081	0	0
	Middle		39	9(9)	1	0.00351	0.00582	9	0.814	0.00173	0.00364	0	0
	Low		35	10(10)	3	0.00400	0.00198	8	0.408	0.00178	0.00118	0	0
		866	95	11(11)	1	0.00259	0.0047	6	0.566	n.a.	0.00485	n.a.	0.00441
<i>GPI</i>	High		18	0	n.a.	0	0	1	0	0	0	0	0
	Middle		41	4(4)	1	0.00113	0.00148	3	0.33	0.00117	0.00156	0.00104	0.00129
	Low		36	9(9)	0	0.00262	0.00292	4	0.383	n.a.	0.003	n.a.	0.00275
<i>ELP4</i>		402	90	4(4)	1	0.00196	0.00069	6	0.246	0	0	0	0

	High	18	0	0	0	0	1	0	0	0	0	0	
	Middle	40	3(3)	1	0.00175	0.00104	5	0.355	0	0	0	0	
	Low	32	2(2)	0	0.00124	0.0006	3	0.234	0	0	0	0	
		426	92	11(11)	6	0.00507	0.00625	29	0.872	0.006	0.00596	0.00466	0.00638
<i>CDPK1</i>	High	18	11(11)	5	0.00732	0.00953	13	0.961	0.00888	0.01319	0.00665	0.00796	
	Middle	42	8(8)	4	0.00436	0.00544	15	0.840	0.00532	0.00388	0.01884	0.0357	
	Low	32	4(4)	1	0.00180	0.00227	5	0.581	0	0	0.02013	0.01804	
<b>Reference loci</b>													
		697	91	5(5)	0	0.00141	0.00161	5	0.561	0.00073	0.00024	0.00368	0.0062
<i>Unigene25529</i>	High	18	2(2)	0	0.00083	0.00128	3	0.503	0.00476	0.00068	0.03064	0.00923	
	Middle	37	5(5)	0	0.00172	0.00177	5	0.637	0.00089	0.00030	0.00449	0.0067	
	Low	36	3(3)	0	0.00104	0.00081	3	0.208	0.00054	0.00029	0.00301	0.00254	
		588	94	5(5)	1	0.00166	0.00143	5	0.641	0.0005	0.00005	0.00413	0.00433
<i>Unigene49649</i>	High	18	1(1)	0	0.00049	0.00089	2	0.523	0	0	0.00154	0.00276	
	Middle	41	5(5)	0	0.00119	0.00109	3	0.459	0.00059	0.00012	0.00880	0.00555	
	Low	35	2(2)	1	0.00083	0.00119	4	0.583	0	0	0.00457	0.00662	
		586	83	4(4)	0	0.00137	0.00024	5	0.117	0	0	0	0
<i>Prox3</i>	High	18	1(1)	0	0.0005	0.00019	2	0.111	0	0	0	0	
	Middle	31	2(2)	0	0.00085	0.00042	3	0.185	0	0	0.00318	0.00229	
	Low	34	1(1)	0	0.00042	0.00010	2	0.059	0	0	0	0	
		832	83	1(1)	0	0.00024	0.00003	2	0.025	0	0	0	0
<i>RUS2</i>	High	18	0	0	0	0	1	0	0	0	0	0	
	Middle	25	0	0	0	0	1	0	0	0	0	0	
	Low	37	1(1)	0	0.00029	0.00006	2	0.054	0	0	0	0	

Note: L, length of gene fragments; N, number of samples; S, number of segregating sites; Rm, minimum number of recombination events;  $\theta_w$ , Watterson's parameter;  $\pi$ , nucleotide diversity; Nh, number of haplotypes; He, haplotype diversity; n.a.: not applicable.