

**Supplemental Table 4.** Counts of paralogous gene pairs by expression class and duplication type.

Class	alpha	beta	gamma	proximal	tandem	TE<16MYA	TE≥16MYA	Total
0	84 (2.7%)	37 (2.6%)	16 (3.2%)	223 (28.8%)	574 (27.1%)	297 (17.5%)	52 (2.8%)	1,283 (11.2%)
1	397 (12.8%)	219 (15.4%)	90 (17.8%)	223 (28.8%)	530 (25.0%)	601 (35.5%)	363 (19.5%)	2,423 (21.1%)
2	957 (30.9%)	265 (18.7%)	94 (18.6%)	122 (15.8%)	338 (15.9%)	295 (17.4%)	508 (27.3%)	2,579 (22.5%)
3	1570 (50.7%)	814 (57.3%)	283 (56.0%)	192 (24.8%)	641 (30.2%)	473 (27.9%)	860 (46.2%)	4,833 (42.1%)
4	88 (2.8%)	85 (6.0%)	22 (4.4%)	14 (1.8%)	38 (1.8%)	27 (1.6%)	78 (4.2%)	352 (3.1%)
Total	3096	1420	505	774	2121	1693	1861	11470

**Supplemental Table 5.** Counts of scB expression for Class I paralogues. A total of 2,423 pairs were assigned to Class 1 (scA expressed in > 1 cell/cluster in at least one cluster, scB expressed in ≤ 1 cell/cluster in all 36 RCCs).

scA expression cutoff <sup>1</sup>	Class 1 pairs	scB expressed at ≥5 reads in at least one SRA library	
		All SRA libraries	Excluding root libraries <sup>2</sup>
> 1 cell	2,423	2,253 (93.0%)	2,214 (91.4%)
> 1 cell, >1 RCC	2,153	1,998 (92.8%)	1,966 (91.3%)
> 1 cell, >5 RCC	1,734	1,604 (92.5%)	1,574 (90.8%)

<sup>1</sup>Criteria for scA to be considered expressed in the root scRNA-seq libraries.

<sup>2</sup>121 out of 213 SRA libraries whose metadata indicate they were derived from root tissue or included root tissue (e.g., whole seedlings), were excluded from the analysis.

**Supplemental Table 6.**  $K_a/K_s$  by expression Class and duplication type.

Class	Duplication type	Count	Ka/Ks	
			Mean	SD
0	all	1,283	0.79	1.06
	alpha	84	0.30	0.18
	beta	37	0.59	0.69
	gamma	16	0.46	0.26
	proximal	223	1.01	1.39
	tandem	574	0.75	0.61
	TE<16 MYA	297	0.96	1.58
	TE≥16 MYA	52	0.43	0.34
1	all	2,423	0.70	1.19
	alpha	397	0.39	0.45
	beta	219	0.44	0.64
	gamma	90	0.41	0.65
	proximal	223	0.87	0.96
	tandem	530	0.79	1.60
	TE<16 MYA	601	1.00	1.54
	TE≥16 MYA	363	0.52	0.52
2	all	2,577	0.44	0.95
	alpha	957	0.22	0.19
	beta	263	0.30	0.33
	gamma	94	0.45	0.61
	proximal	122	0.96	3.67
	tandem	338	0.52	0.56
	TE<16 MYA	295	0.66	0.82
	TE≥16 MYA	508	0.61	0.59
3	all	4,835	0.41	0.68
	alpha	1,570	0.27	0.32
	beta	816	0.31	0.47
	gamma	283	0.39	0.52
	proximal	192	0.65	0.82
	tandem	641	0.44	0.45
	TE<16 MYA	473	0.79	1.64
	TE≥16 MYA	860	0.50	0.49
4	all	352	0.30	0.23
	alpha	88	0.23	0.16
	beta	85	0.24	0.21
	gamma	22	0.31	0.29
	proximal	14	0.41	0.33
	tandem	38	0.33	0.22
	TE<16 MYA	27	0.29	0.15
	TE≥16 MYA	78	0.40	0.29

**Supplemental Table 8.** Breakdown by expression class and duplication mechanism of 4,599 Wang et al., (2013) parologue pairs ubiquitously expressed in root cell clusters (RCC-u gene pairs).

Duplication type	Class	Count	RCC-u mixed	RCC-u both
alpha	0	0	0	0
	1	94	94	0
	2	590	148	442
	3	970	690	280
	4	31	17	14
beta	0	0	0	0
	1	60	60	0
	2	157	43	114
	3	494	371	123
	4	44	29	15
gamma	0	0	0	0
	1	24	24	0
	2	47	8	39
	3	165	131	34
	4	8	5	3
proximal	0	0	0	0
	1	34	34	0
	2	17	3	14
	3	95	83	12
	4	4	3	1
tandem	0	0	0	0
	1	50	50	0
	2	71	25	46
	3	279	233	46
	4	10	5	5
TE<16MYA	0	0	0	0
	1	140	140	0
	2	85	34	51
	3	249	212	37
	4	11	4	7
TE $\geq$ 16 MYA	0	0	0	0
	1	103	103	0
	2	207	66	141
	3	528	406	122
	4	32	26	6