

RNA-Seq Manuscript Supplementary Material

Table S1. Samples used in this study.

SampleID	Tissue	Genotype	Replicate	TotalReadPair	TrimmedReadPair	MappingRate	UniqueMappingRate
BR001	blade_v12	B73	1	9,456,463	9,367,415	98.4%	92.0%
BR002	blade_v12	B73	2	10,614,657	10,530,486	98.5%	93.3%
BR004	blade_v12	B73	3	10,983,851	10,894,598	98.4%	92.4%
BR003	blade_v12	Mo17	1	9,456,508	9,374,216	92.2%	89.5%
BR005	blade_v12	Mo17	2	9,878,003	9,791,778	92.5%	89.0%
BR007	blade_v12	Mo17	3	10,136,440	10,049,207	94.1%	44.7%
BR006	blade_v12	B73xMo17	1	13,109,236	13,005,210	95.2%	85.3%
BR008	blade_v12	B73xMo17	2	9,958,057	9,762,863	91.7%	83.3%
BR009	blade_v12	B73xMo17	3	10,368,573	10,283,237	95.1%	89.5%
BR010	auricle_v12	B73	1	12,161,908	12,062,687	97.3%	92.6%
BR011	auricle_v12	B73	2	8,756,804	8,681,487	97.7%	92.1%
BR012	auricle_v12	B73	3	9,205,753	9,115,520	98.4%	93.8%
BR013	auricle_v12	Mo17	1	12,629,990	12,534,713	92.3%	70.6%
BR014	auricle_v12	Mo17	2	12,106,840	12,015,331	91.9%	87.9%
BR015	auricle_v12	Mo17	3	12,789,833	12,688,046	91.9%	88.8%
BR016	auricle_v12	B73xMo17	1	13,001,085	12,894,656	95.2%	91.6%
BR017	auricle_v12	B73xMo17	2	10,302,708	10,221,028	95.0%	91.2%
BR018	auricle_v12	B73xMo17	3	10,717,426	10,612,110	93.9%	90.0%
BR019	sheath_v12	B73	1	11,363,325	11,252,448	98.3%	92.9%
BR020	sheath_v12	B73	2	11,653,190	11,560,292	98.5%	92.9%
BR021	sheath_v12	B73	3	10,397,926	10,313,536	98.3%	92.0%
BR022	sheath_v12	Mo17	1	10,300,996	10,223,999	91.0%	87.7%
BR023	sheath_v12	Mo17	2	10,610,559	10,504,881	90.6%	87.7%
BR024	sheath_v12	Mo17	3	10,818,591	10,732,498	91.1%	87.9%
BR025	sheath_v12	B73xMo17	1	10,460,515	10,317,769	89.3%	82.3%
BR026	sheath_v12	B73xMo17	2	13,454,079	13,205,917	90.2%	86.1%
BR027	sheath_v12	B73xMo17	3	10,947,765	10,796,345	93.0%	87.8%
BR028	internode_v12	B73	1	11,704,246	11,566,394	97.2%	92.1%
BR029	internode_v12	B73	2	7,280,863	7,207,320	97.4%	90.3%
BR030	internode_v12	B73	3	11,511,692	11,382,708	98.1%	92.2%
BR031	internode_v12	Mo17	1	11,675,275	11,554,947	90.9%	88.8%
BR032	internode_v12	Mo17	2	18,897,584	18,677,705	90.6%	87.5%
BR033	internode_v12	Mo17	3	11,763,511	11,618,868	90.2%	88.4%
BR034	internode_v12	B73xMo17	1	11,446,013	11,309,805	94.4%	91.1%
BR035	internode_v12	B73xMo17	2	10,813,338	10,680,875	94.0%	89.8%
BR036	internode_v12	B73xMo17	3	12,185,937	12,056,501	94.8%	90.8%
BR037	tassel_v12	B73	1	11,869,598	11,767,998	98.1%	87.1%
BR038	tassel_v12	B73	2	13,057,367	12,963,185	98.1%	80.7%
BR039	tassel_v12	B73	3	11,971,434	11,876,376	98.4%	87.0%
BR040	tassel_v12	Mo17	1	10,198,649	10,119,317	92.7%	81.0%
BR041	tassel_v12	Mo17	2	9,541,534	9,458,818	92.5%	88.7%
BR042	tassel_v12	Mo17	3	12,122,651	12,028,360	92.7%	75.8%
BR043	tassel_v12	B73xMo17	1	11,577,660	11,490,867	94.8%	88.7%
BR044	tassel_v12	B73xMo17	2	9,209,055	9,080,007	94.2%	83.3%
BR045	tassel_v12	B73xMo17	3	11,345,207	11,254,362	94.7%	89.2%
BR046	ear_v14	B73	1	10,279,754	10,201,193	97.0%	76.9%
BR047	ear_v14	B73	2	10,892,889	10,799,410	98.1%	88.5%
BR048	ear_v14	B73	3	10,423,251	10,340,695	98.2%	87.4%
BR049	ear_v14	Mo17	1	11,158,750	11,087,463	93.4%	90.5%
BR050	ear_v14	Mo17	2	10,615,140	10,544,171	92.6%	90.0%
BR051	ear_v14	Mo17	3	10,130,338	10,058,913	93.5%	90.6%
BR052	ear_v14	B73xMo17	1	9,779,316	9,705,723	96.0%	91.8%
BR053	ear_v14	B73xMo17	2	10,765,471	10,691,005	96.1%	91.9%
BR054	ear_v14	B73xMo17	3	10,866,113	10,786,414	96.0%	91.8%

Table S1. Samples used in this study. (continued)

SampleID	Tissue	Genotype	Replicate	TotalReadPair	TrimmedReadPair	MappingRate	UniqueMappingRate
BR055	silk_0DAP	B73	1	10,460,214	10,354,824	98.3%	93.2%
BR056	silk_0DAP	B73	2	10,094,098	10,015,873	98.3%	88.1%
BR057	silk_0DAP	B73	3	9,351,362	9,259,488	98.2%	93.1%
BR058	silk_0DAP	Mo17	1	9,154,814	9,077,113	91.2%	87.0%
BR059	silk_0DAP	Mo17	2	9,271,623	9,184,908	91.2%	88.5%
BR060	silk_0DAP	Mo17	3	8,610,999	8,539,340	91.1%	88.7%
BR061	silk_0DAP	B73xMo17	1	12,378,233	12,274,018	94.4%	90.0%
BR062	silk_0DAP	B73xMo17	2	11,117,019	10,918,321	93.2%	89.5%
BR063	silk_0DAP	B73xMo17	3	12,831,768	12,714,257	95.0%	90.9%
BR064	spikelets_0DAP	B73	1	12,862,409	12,756,383	97.9%	92.4%
BR065	spikelets_0DAP	B73	2	13,140,565	13,016,984	98.4%	93.1%
BR066	spikelets_0DAP	B73	3	12,366,130	12,261,404	98.5%	93.1%
BR067	spikelets_0DAP	Mo17	1	12,302,995	12,214,346	92.0%	88.6%
BR068	spikelets_0DAP	Mo17	2	12,364,997	12,266,006	92.3%	87.6%
BR069	spikelets_0DAP	Mo17	3	12,363,396	12,261,701	92.5%	89.1%
BR070	spikelets_0DAP	B73xMo17	1	10,329,056	10,246,209	95.4%	90.7%
BR071	spikelets_0DAP	B73xMo17	2	12,278,485	12,184,457	95.4%	91.2%
BR072	spikelets_0DAP	B73xMo17	3	12,426,693	12,323,355	95.7%	91.2%
BR073	husk_0DAP	B73	1	12,468,897	12,338,745	98.3%	92.7%
BR074	husk_0DAP	B73	2	11,486,069	11,389,989	98.3%	92.4%
BR075	husk_0DAP	B73	3	11,705,643	11,598,042	98.3%	92.4%
BR076	husk_0DAP	Mo17	1	12,818,182	12,713,872	92.0%	86.0%
BR077	husk_0DAP	Mo17	2	12,761,502	12,635,684	91.4%	88.4%
BR078	husk_0DAP	Mo17	3	12,826,901	12,717,414	91.9%	88.1%
BR079	husk_0DAP	B73xMo17	1	12,503,981	12,395,438	94.7%	90.7%
BR080	husk_0DAP	B73xMo17	2	11,607,643	11,406,667	93.7%	89.8%
BR081	husk_0DAP	B73xMo17	3	13,790,861	13,666,823	95.3%	91.4%
BR082	tasselstem_0DAP	B73	1	12,451,564	12,349,251	97.8%	92.4%
BR083	tasselstem_0DAP	B73	2	12,221,050	12,112,847	98.2%	93.0%
BR084	tasselstem_0DAP	B73	3	11,567,848	11,471,842	98.0%	88.3%
BR085	tasselstem_0DAP	Mo17	1	9,540,165	9,463,815	90.5%	86.0%
BR086	tasselstem_0DAP	Mo17	2	9,089,631	9,011,444	91.1%	88.6%
BR087	tasselstem_0DAP	Mo17	3	9,244,929	9,157,904	91.2%	88.7%
BR088	tasselstem_0DAP	B73xMo17	1	8,876,713	8,797,378	94.5%	89.6%
BR089	tasselstem_0DAP	B73xMo17	2	9,021,520	8,943,627	93.9%	89.6%
BR090	tasselstem_0DAP	B73xMo17	3	9,072,250	8,993,652	94.2%	88.5%
BR091	floret_0DAP	B73	1	10,046,688	9,917,126	98.1%	89.9%
BR092	floret_0DAP	B73	2	10,344,979	10,247,053	98.3%	88.8%
BR093	floret_0DAP	B73	3	9,586,452	9,469,113	98.1%	89.7%
BR094	floret_0DAP	Mo17	1	9,591,540	9,496,979	90.9%	85.9%
BR095	floret_0DAP	Mo17	2	10,171,616	10,050,093	90.1%	86.5%
BR096	floret_0DAP	Mo17	3	8,968,665	8,870,021	91.6%	87.6%
BR097	floret_0DAP	B73xMo17	1	8,971,648	8,871,487	95.1%	90.4%
BR098	floret_0DAP	B73xMo17	2	9,125,085	8,871,603	93.3%	88.3%
BR099	floret_0DAP	B73xMo17	3	10,114,073	10,000,848	95.0%	88.4%
BR118	kernel_14DAP	B73	1	10,936,328	10,843,315	98.3%	87.5%
BR119	kernel_14DAP	B73	2	11,056,044	10,956,542	98.4%	89.4%
BR120	kernel_14DAP	B73	3	10,542,981	10,452,024	98.3%	87.0%
BR121	kernel_14DAP	Mo17	1	13,288,857	13,186,732	94.6%	87.0%
BR122	kernel_14DAP	Mo17	2	13,244,937	13,134,240	94.5%	87.9%
BR123	kernel_14DAP	Mo17	3	11,612,393	11,504,790	94.3%	84.8%
BR124	kernel_14DAP	B73xMo17	1	12,287,598	12,188,660	97.5%	83.1%
BR125	kernel_14DAP	B73xMo17	2	11,390,752	11,303,494	97.4%	82.9%
BR126	kernel_14DAP	B73xMo17	3	10,802,003	10,718,433	97.5%	83.5%

Table S1. Samples used in this study. (continued)

SampleID	Tissue	Genotype	Replicate	TotalReadPair	TrimmedReadPair	MappingRate	UniqueMappingRate
BR127	kernel_14DAP	Mo17xB73	1	11,034,849	10,942,002	95.8%	83.8%
BR128	kernel_14DAP	Mo17xB73	2	12,256,591	12,098,686	95.3%	81.8%
BR129	kernel_14DAP	Mo17xB73	3	12,056,059	11,952,150	95.7%	86.7%
BR100	flagleaf_0DAP	B73	1	8,870,907	8,779,729	98.3%	91.0%
BR101	flagleaf_0DAP	B73	2	8,927,886	8,852,968	98.5%	92.5%
BR102	flagleaf_0DAP	B73	3	9,310,919	9,227,730	98.6%	92.7%
BR103	flagleaf_0DAP	Mo17	1	12,454,393	12,351,934	92.0%	89.9%
BR104	flagleaf_0DAP	Mo17	2	11,124,928	11,016,585	92.4%	89.2%
BR105	flagleaf_0DAP	Mo17	3	9,139,066	9,063,499	92.0%	89.6%
BR106	flagleaf_0DAP	B73xMo17	1	8,237,380	8,161,554	95.1%	90.9%
BR107	flagleaf_0DAP	B73xMo17	2	11,375,396	11,265,249	95.3%	91.5%
BR108	flagleaf_0DAP	B73xMo17	3	8,739,031	8,651,672	95.2%	90.6%
BR109	root_0DAP	B73	1	12,780,458	12,681,574	98.7%	94.4%
BR110	root_0DAP	B73	2	11,071,413	10,726,484	95.8%	92.4%
BR111	root_0DAP	B73	3	14,352,722	14,232,937	98.6%	94.6%
BR112	root_0DAP	Mo17	1	13,432,400	13,337,049	91.9%	90.0%
BR113	root_0DAP	Mo17	2	11,241,291	11,148,033	91.9%	90.5%
BR114	root_0DAP	Mo17	3	11,748,397	11,657,233	91.8%	90.3%
BR115	root_0DAP	B73xMo17	1	12,447,495	12,322,988	94.7%	91.8%
BR116	root_0DAP	B73xMo17	2	13,501,613	13,391,660	95.0%	92.2%
BR117	root_0DAP	B73xMo17	3	12,014,758	11,917,490	95.3%	92.5%
BR130	endosperm_14DAP	B73	1	7,971,614	7,908,501	98.4%	88.1%
BR131	endosperm_14DAP	B73	2	8,354,751	8,297,059	98.6%	87.8%
BR132	endosperm_14DAP	B73	3	8,106,969	8,043,877	98.4%	87.4%
BR133	endosperm_14DAP	Mo17	1	7,996,705	7,944,390	95.1%	87.5%
BR134	endosperm_14DAP	Mo17	2	7,111,069	7,056,236	95.0%	87.7%
BR135	endosperm_14DAP	Mo17	3	7,053,101	7,003,061	94.9%	86.8%
BR136	endosperm_14DAP	B73xMo17	1	7,342,993	7,293,685	97.3%	81.0%
BR137	endosperm_14DAP	B73xMo17	2	7,408,587	7,282,363	95.5%	83.5%
BR138	endosperm_14DAP	B73xMo17	3	8,295,102	8,242,013	97.5%	82.1%
BR139	endosperm_14DAP	Mo17xB73	1	8,353,565	8,292,558	96.2%	83.0%
BR140	endosperm_14DAP	Mo17xB73	2	7,429,170	7,372,156	96.2%	87.1%
BR141	endosperm_14DAP	Mo17xB73	3	8,249,827	8,188,014	96.2%	84.0%
BR142	embryo_27DAP	B73	1	7,372,483	7,316,640	98.5%	87.0%
BR143	embryo_27DAP	B73	2	7,042,198	6,983,724	98.6%	90.4%
BR144	embryo_27DAP	B73	3	6,553,609	6,498,382	98.3%	87.4%
BR145	embryo_27DAP	Mo17	1	7,077,358	7,002,686	91.6%	86.2%
BR146	embryo_27DAP	Mo17	2	7,533,408	7,451,111	91.3%	85.9%
BR147	embryo_27DAP	Mo17	3	8,261,322	8,162,520	92.0%	47.6%
BR148	embryo_27DAP	B73xMo17	1	7,602,835	7,530,655	94.4%	85.5%
BR149	embryo_27DAP	B73xMo17	2	8,456,705	8,336,995	94.2%	87.1%
BR150	embryo_27DAP	B73xMo17	3	8,081,181	7,993,598	94.8%	84.3%
BR151	embryo_27DAP	Mo17xB73	1	8,665,419	8,562,715	94.5%	86.6%
BR152	embryo_27DAP	Mo17xB73	2	8,303,462	8,225,271	94.7%	85.0%
BR153	embryo_27DAP	Mo17xB73	3	7,536,997	7,449,921	94.4%	82.1%
BR154	endosperm_27DAP	B73	1	17,736,115	17,600,317	98.3%	68.5%
BR155	endosperm_27DAP	B73	2	17,169,716	17,057,377	98.3%	68.7%
BR156	endosperm_27DAP	B73	3	18,730,409	18,611,675	98.4%	69.5%
BR157	endosperm_27DAP	Mo17	1	14,649,158	14,549,188	96.2%	67.4%
BR158	endosperm_27DAP	Mo17	2	15,811,476	15,702,263	96.4%	67.2%
BR159	endosperm_27DAP	Mo17	3	13,053,684	12,967,048	96.5%	68.2%
BR160	endosperm_27DAP	B73xMo17	1	14,814,247	14,719,774	97.8%	72.2%
BR161	endosperm_27DAP	B73xMo17	2	14,413,309	14,133,430	95.6%	68.4%
BR162	endosperm_27DAP	B73xMo17	3	14,883,939	14,783,781	97.7%	69.4%

Table S1. Samples used in this study. (continued)

SampleID	Tissue	Genotype	Replicate	TotalReadPair	TrimmedReadPair	MappingRate	UniqueMappingRate
BR163	endosperm_27DAP	Mo17xB73	1	14,936,706	14,829,416	97.3%	65.6%
BR164	endosperm_27DAP	Mo17xB73	2	14,553,888	14,434,555	97.1%	65.2%
BR165	endosperm_27DAP	Mo17xB73	3	14,840,064	14,736,047	97.3%	65.0%
BR166	coleoptile_tip	B73	1	12,267,403	12,126,234	98.0%	89.7%
BR167	coleoptile_tip	B73	2	11,485,549	11,384,771	98.4%	93.4%
BR168	coleoptile_tip	B73	3	12,399,486	12,290,630	98.5%	92.0%
BR169	coleoptile_tip	Mo17	1	11,947,303	11,849,179	92.4%	89.8%
BR170	coleoptile_tip	Mo17	2	12,242,354	12,126,048	92.5%	89.9%
BR171	coleoptile_tip	Mo17	3	13,259,951	13,138,932	92.4%	89.1%
BR172	coleoptile_tip	B73xMo17	1	12,391,702	12,284,694	95.2%	91.2%
BR173	coleoptile_tip	B73xMo17	2	12,048,829	11,802,713	93.9%	90.4%
BR174	coleoptile_tip	B73xMo17	3	12,187,226	12,068,545	95.1%	74.0%
BR175	radicle_root	B73	1	12,295,498	12,171,020	97.0%	93.2%
BR176	radicle_root	B73	2	11,534,982	11,416,060	98.1%	93.4%
BR177	radicle_root	B73	3	10,646,209	10,526,034	97.8%	93.2%
BR178	radicle_root	Mo17	1	12,066,875	11,965,649	90.8%	87.2%
BR179	radicle_root	Mo17	2	11,661,817	11,558,386	90.2%	89.2%
BR180	radicle_root	Mo17	3	10,959,894	10,841,662	90.2%	88.7%
BR181	radicle_root	B73xMo17	1	13,122,821	13,004,621	94.2%	91.8%
BR182	radicle_root	B73xMo17	2	12,468,832	12,358,623	94.8%	91.7%
BR183	radicle_root	B73xMo17	3	11,587,217	11,485,773	94.0%	91.5%
BR184	embryo_imbibedseed	B73	1	16,521,544	16,009,522	98.3%	86.8%
BR235	embryo_imbibedseed	B73	2	14,938,224	14,568,853	98.2%	90.7%
BR242	embryo_imbibedseed	B73	3	18,100,445	17,634,613	98.2%	87.9%
BR243	embryo_imbibedseed	B73	4	16,539,617	16,051,406	98.3%	88.9%
BR187	embryo_imbibedseed	Mo17	1	12,018,006	11,651,375	90.6%	76.7%
BR188	embryo_imbibedseed	Mo17	2	19,136,137	18,583,167	91.8%	80.3%
BR227	embryo_imbibedseed	Mo17	3	10,606,785	10,249,652	92.1%	64.7%
BR245	embryo_imbibedseed	Mo17	4	15,060,983	14,635,237	91.8%	80.4%
BR191	embryo_imbibedseed	B73xMo17	1	12,528,211	11,753,391	95.2%	85.1%
BR192	embryo_imbibedseed	B73xMo17	2	16,939,295	16,506,855	95.7%	85.8%
BR230	embryo_imbibedseed	B73xMo17	3	93,569	91,510	5.9%	5.3%
BR193	seedlingleaf_11DAS	B73	1	12,931,365	12,562,955	98.4%	91.0%
BR194	seedlingleaf_11DAS	B73	2	12,993,398	12,476,399	98.7%	91.5%
BR195	seedlingleaf_11DAS	B73	3	12,944,343	12,533,704	98.7%	91.8%
BR196	seedlingleaf_11DAS	Mo17	1	13,154,046	12,759,277	91.3%	86.0%
BR197	seedlingleaf_11DAS	Mo17	2	14,456,660	14,047,653	91.8%	88.5%
BR198	seedlingleaf_11DAS	Mo17	3	12,627,543	12,111,783	91.5%	85.5%
BR199	seedlingleaf_11DAS	B73xMo17	1	13,369,929	12,922,403	95.2%	88.2%
BR200	seedlingleaf_11DAS	B73xMo17	2	12,269,095	11,890,258	94.9%	89.9%
BR201	seedlingleaf_11DAS	B73xMo17	3	16,931,135	16,451,260	95.4%	87.8%
BR202	seedlingroot_11DAS	B73	1	14,286,923	13,837,005	98.2%	92.5%
BR203	seedlingroot_11DAS	B73	2	13,799,806	13,493,069	98.5%	93.3%
BR204	seedlingroot_11DAS	B73	3	12,973,928	12,661,827	98.6%	93.4%
BR206	seedlingroot_11DAS	Mo17	1	11,969,669	11,569,090	90.5%	87.3%
BR207	seedlingroot_11DAS	Mo17	2	18,503	17,654	40.3%	38.8%
BR208	seedlingroot_11DAS	B73xMo17	1	14,247,885	13,919,656	95.2%	90.2%
BR209	seedlingroot_11DAS	B73xMo17	2	12,311,137	11,773,916	95.0%	90.5%
BR211	seedlingmeristem_11DAS	B73	1	15,300,678	14,943,561	98.7%	93.7%
BR212	seedlingmeristem_11DAS	B73	2	13,228,641	12,892,735	98.9%	93.1%
BR213	seedlingmeristem_11DAS	B73	3	14,690,786	14,301,943	98.8%	93.2%
BR214	seedlingmeristem_11DAS	Mo17	1	17,091,762	16,707,591	93.7%	90.3%
BR215	seedlingmeristem_11DAS	Mo17	2	14,961,784	14,610,501	93.7%	90.7%
BR216	seedlingmeristem_11DAS	Mo17	3	14,085,672	13,755,241	93.9%	91.0%

Table S1. Samples used in this study. (*continued*)

SampleID	Tissue	Genotype	Replicate	TotalReadPair	TrimmedReadPair	MappingRate	UniqueMappingRate
BR217	seedlingmeristem_11DAS	B73xMo17	1	15,456,137	15,088,536	96.3%	92.4%
BR218	seedlingmeristem_11DAS	B73xMo17	2	14,791,193	14,459,872	96.5%	90.2%
BR219	seedlingmeristem_11DAS	B73xMo17	3	13,255,400	12,905,133	96.4%	91.7%

Table S2. Enriched Gene Ontology (GO) terms for identified gene sets.

Gene set	GO	P-value	GO name
All genes			
Constitutive	GO:0005739	1.52e-21	mitochondrion
	GO:0022625	3.79e-11	cytosolic large ribosomal subunit
	GO:0006412	1.09e-10	translation
	GO:0046686	2.65e-06	response to cadmium ion
	GO:0006281	5.97e-05	DNA repair
	GO:0005802	5.97e-05	trans-Golgi network
	GO:0005743	6.37e-05	mitochondrial inner membrane
non-DEGs btw. B73 and Mo17			
Above-Parent	GO:0009941	4.52e-14	chloroplast envelope
	GO:0009535	7.25e-12	chloroplast thylakoid membrane
	GO:0022625	6.43e-09	cytosolic large ribosomal subunit
	GO:0010287	1.33e-06	plastoglobule
	GO:0042256	1.43e-06	mature ribosome assembly
	GO:0009570	6.41e-06	chloroplast stroma
Below-Parent	GO:0022625	6.29e-23	cytosolic large ribosomal subunit
	GO:0042256	3.68e-21	mature ribosome assembly
	GO:0006412	1.50e-17	translation
	GO:0005794	1.38e-12	Golgi apparatus
	GO:0022627	1.47e-12	cytosolic small ribosomal subunit
	GO:0048046	1.36e-11	apoplast
	GO:0042788	5.42e-11	polysomal ribosome
	GO:0002181	1.38e-10	cytoplasmic translation
	GO:0005774	6.10e-10	vacuolar membrane
	GO:0005829	2.65e-09	cytosol
	GO:0005618	2.31e-06	cell wall
	GO:0005886	2.31e-06	plasma membrane
	GO:0046686	1.42e-05	response to cadmium ion
	GO:0006096	3.80e-05	glycolytic process
DEGs btw. B73 and Mo17			
HP/AHP	GO:0009535	2.75e-18	chloroplast thylakoid membrane
	GO:0009941	3.86e-16	chloroplast envelope
	GO:0009570	6.31e-09	chloroplast stroma
	GO:0009768	2.19e-08	photosynthesis, light harvesting in photosystem I
	GO:0010287	2.57e-07	plastoglobule
	GO:0009773	7.84e-06	photosynthetic electron transport in photosystem I
LP/BLP	GO:0046658	8.67e-06	anchored component of plasma membrane
	GO:0005886	1.48e-05	plasma membrane

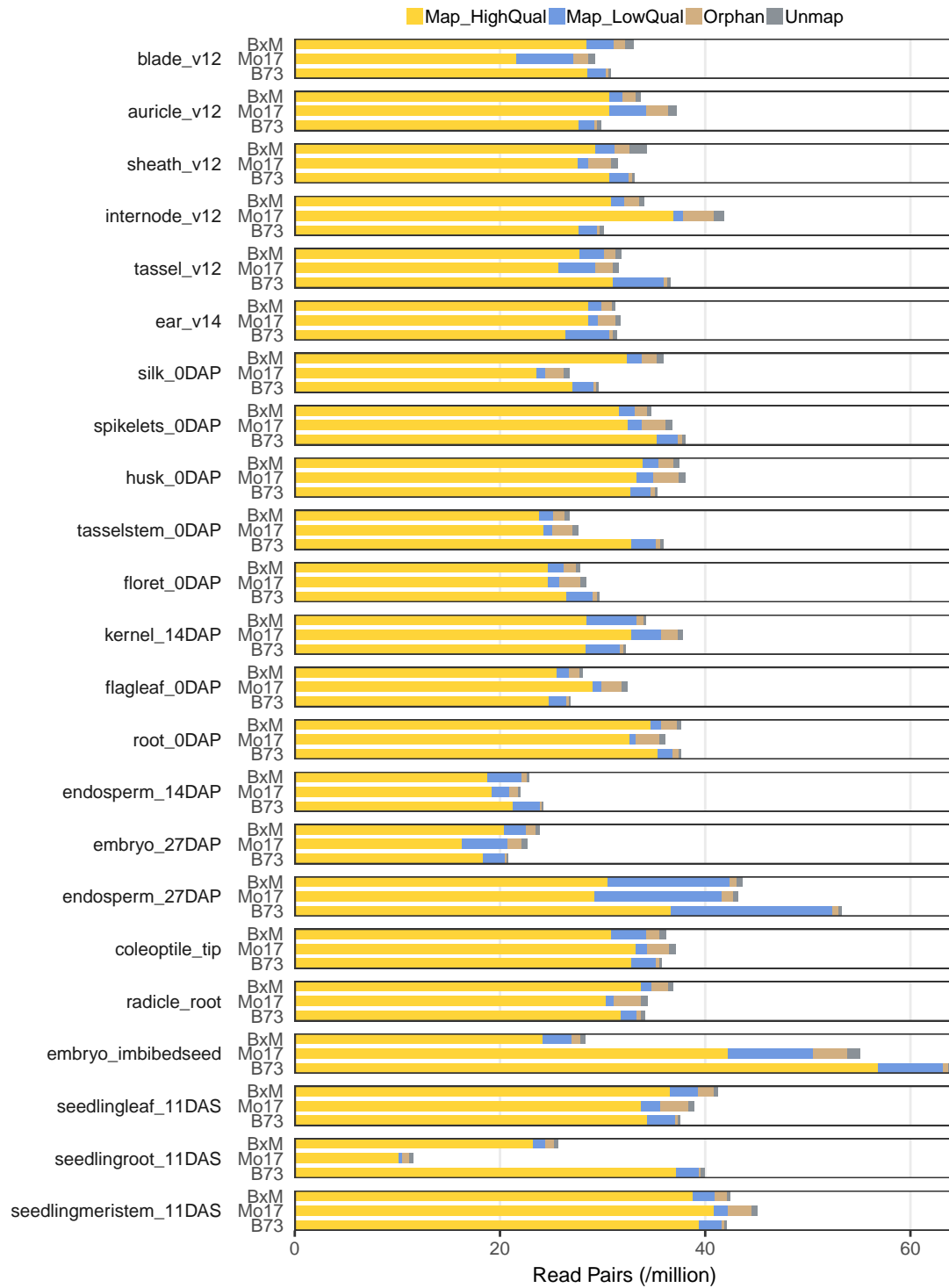


Figure S1

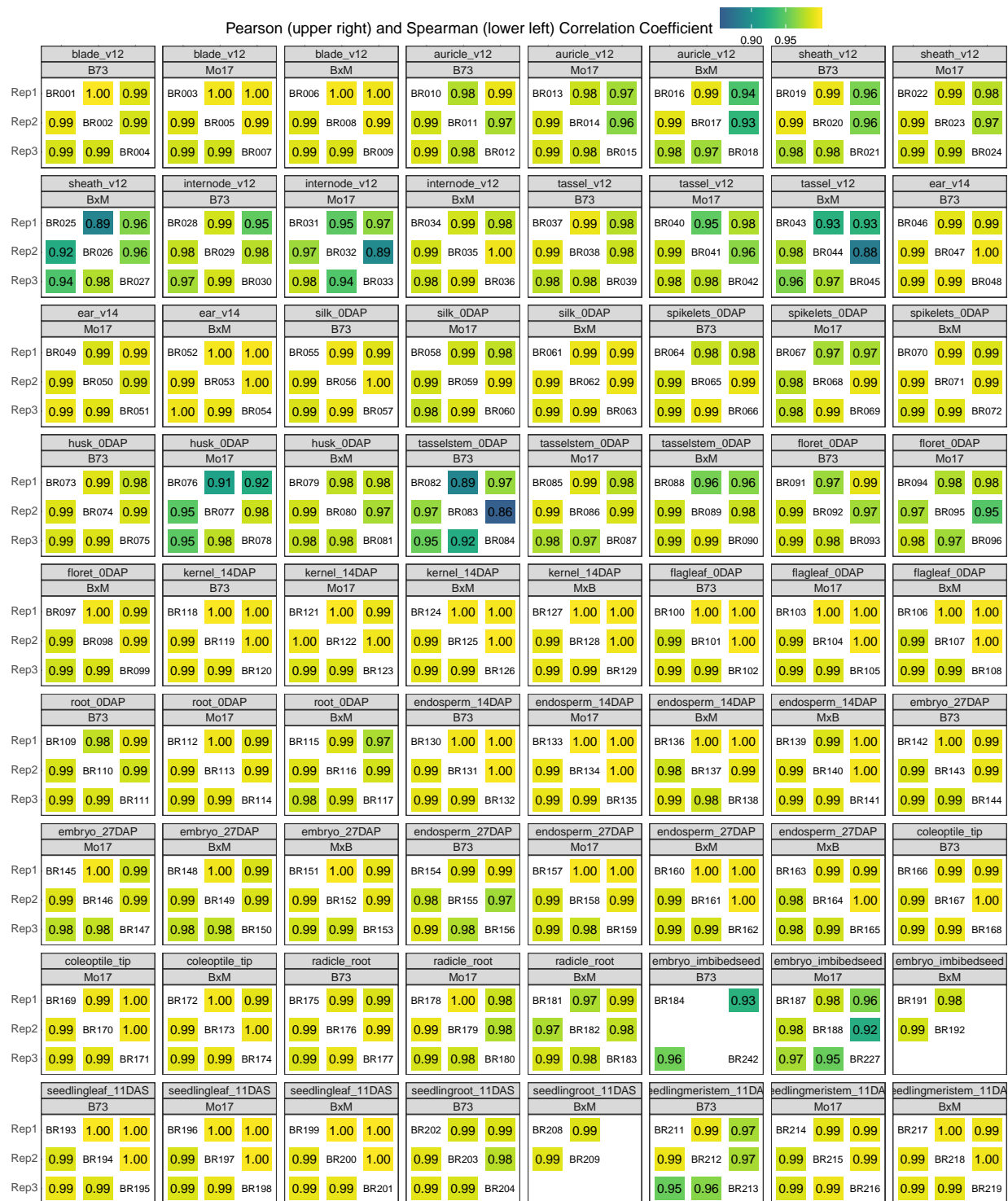


Figure S2

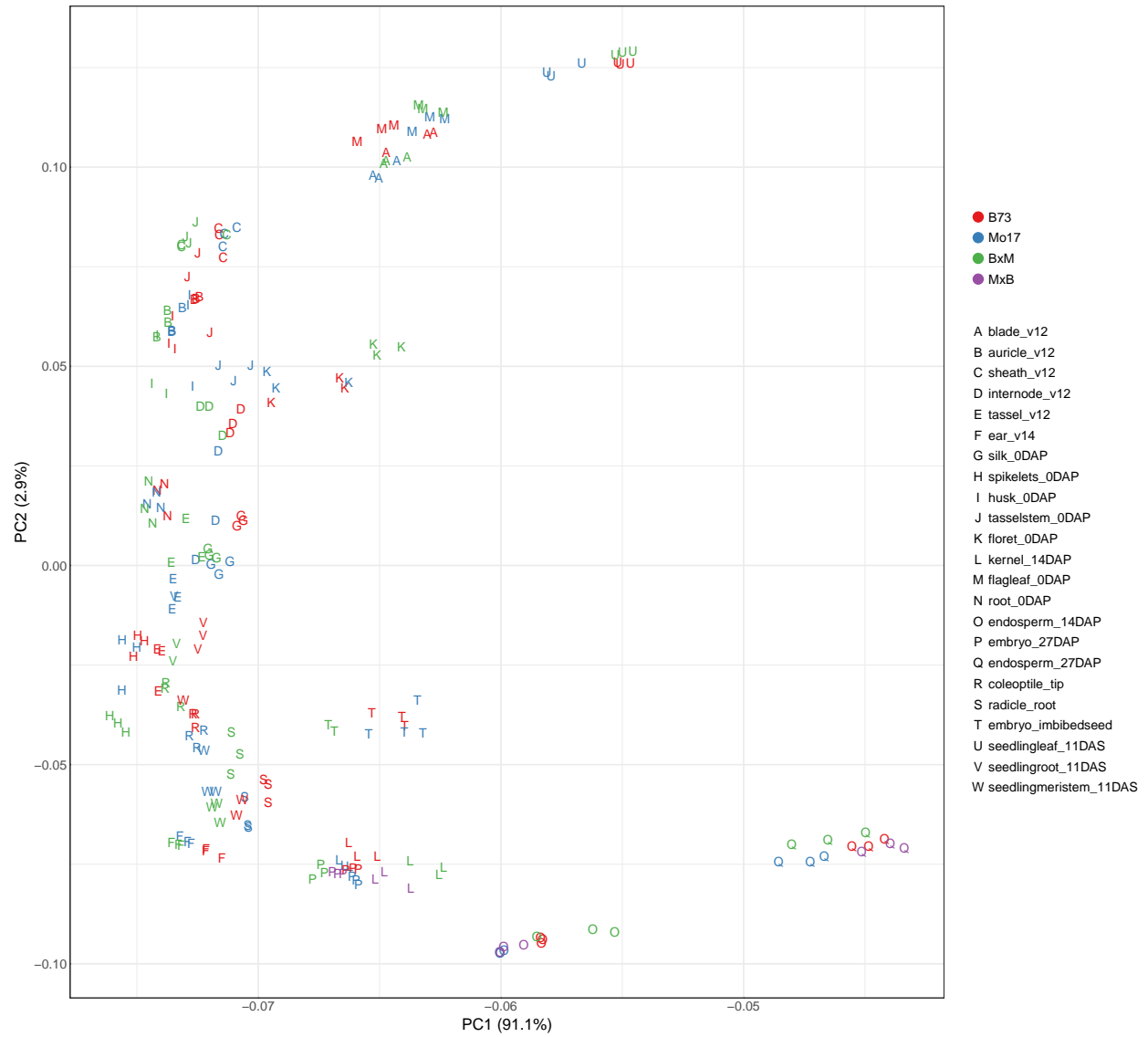


Figure S3

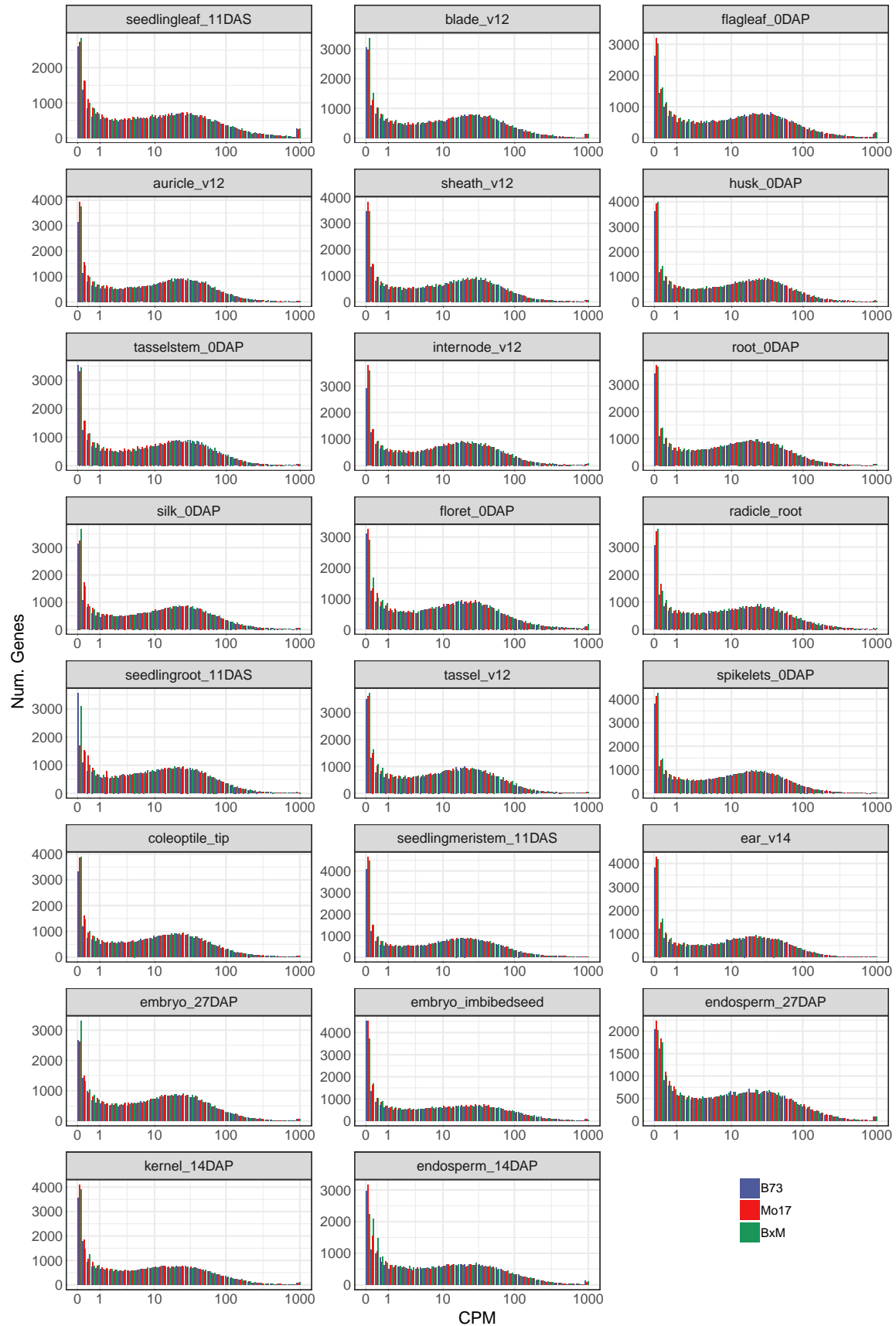


Figure S4

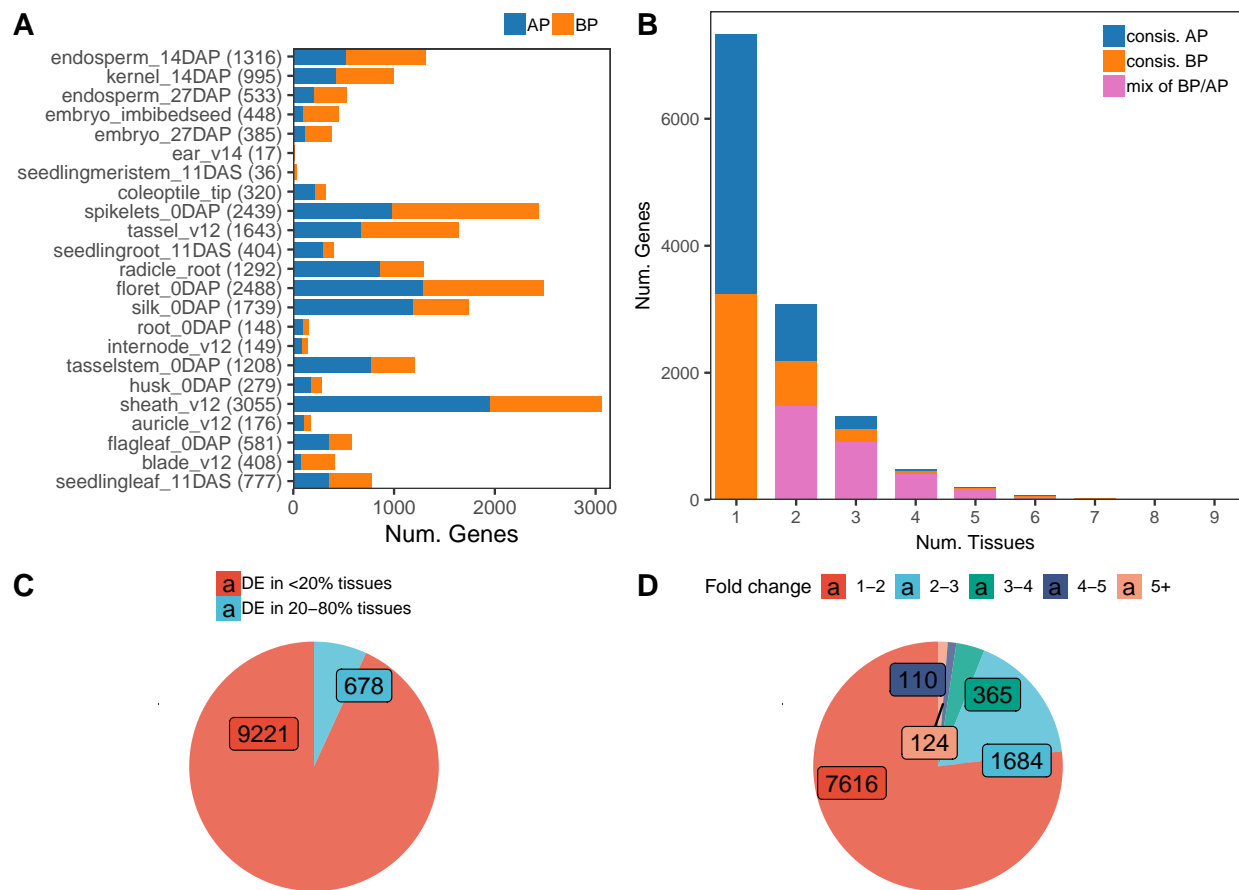


Figure S5

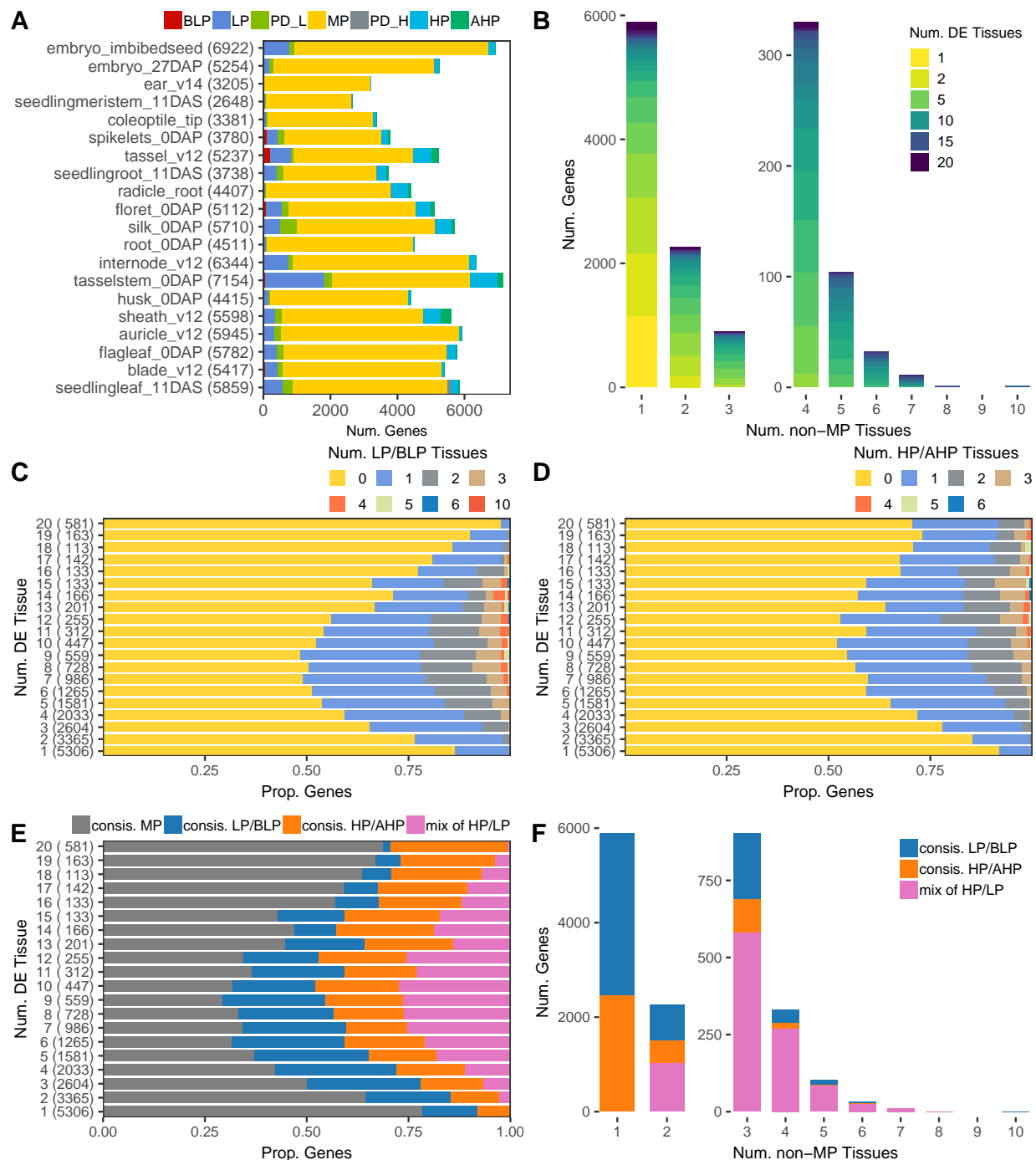


Figure S6

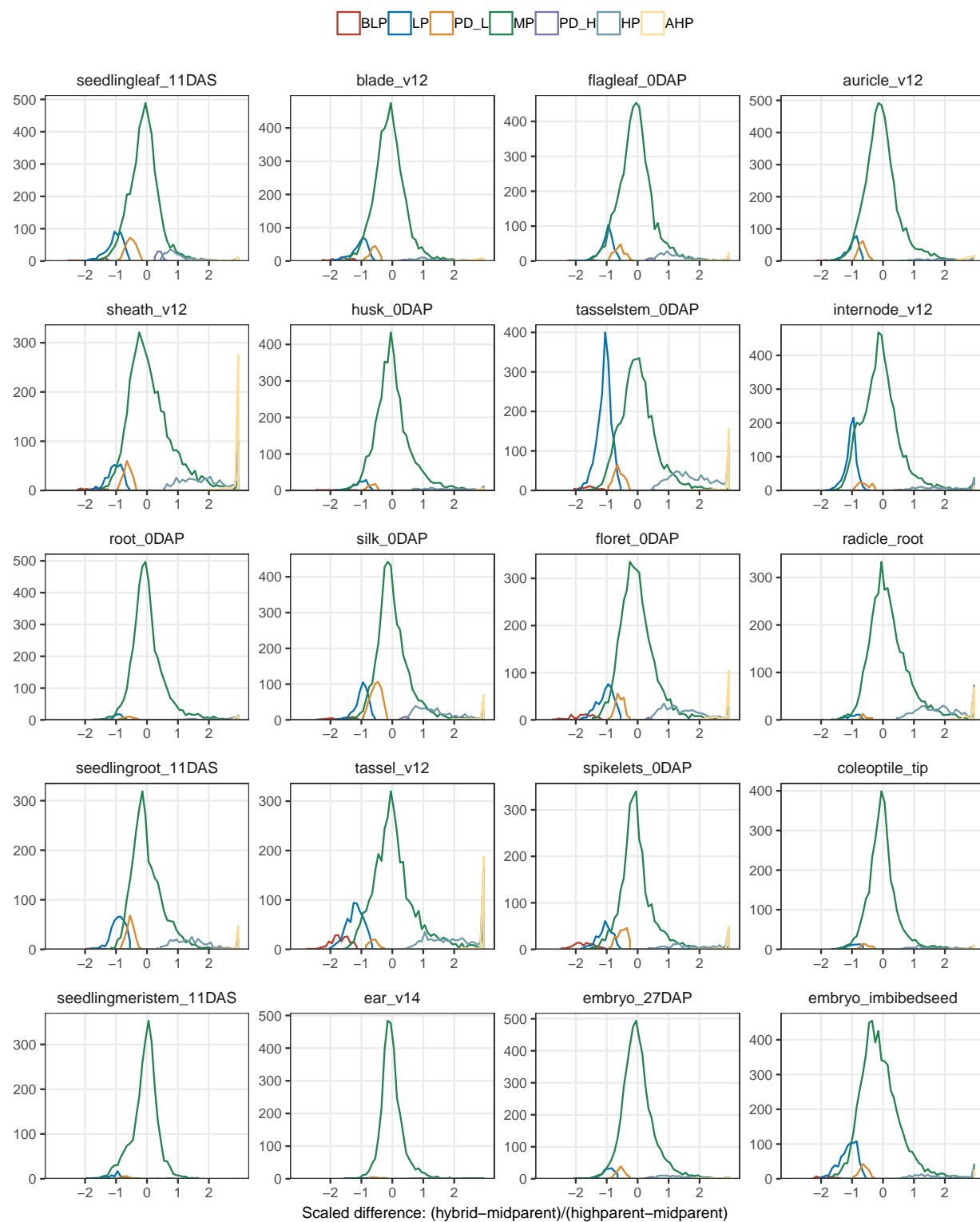


Figure S7

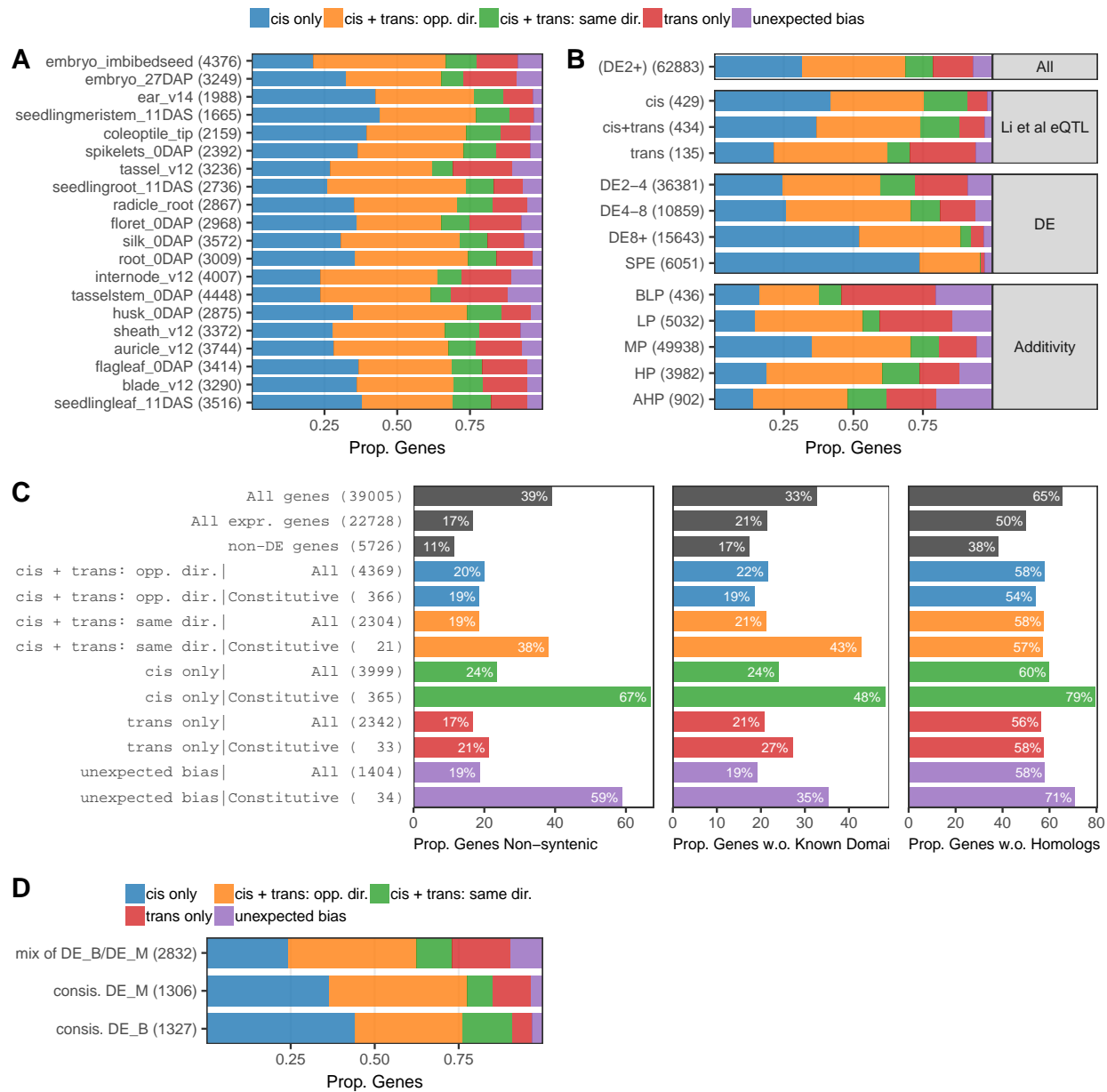


Figure S8

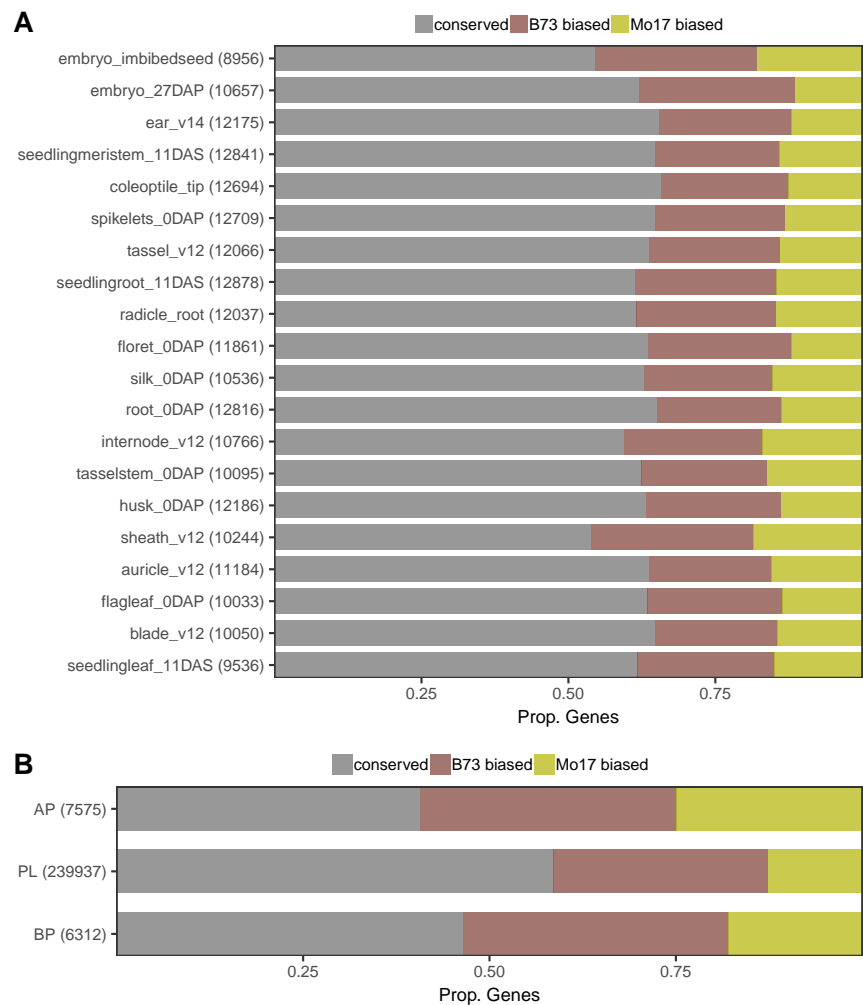


Figure S9

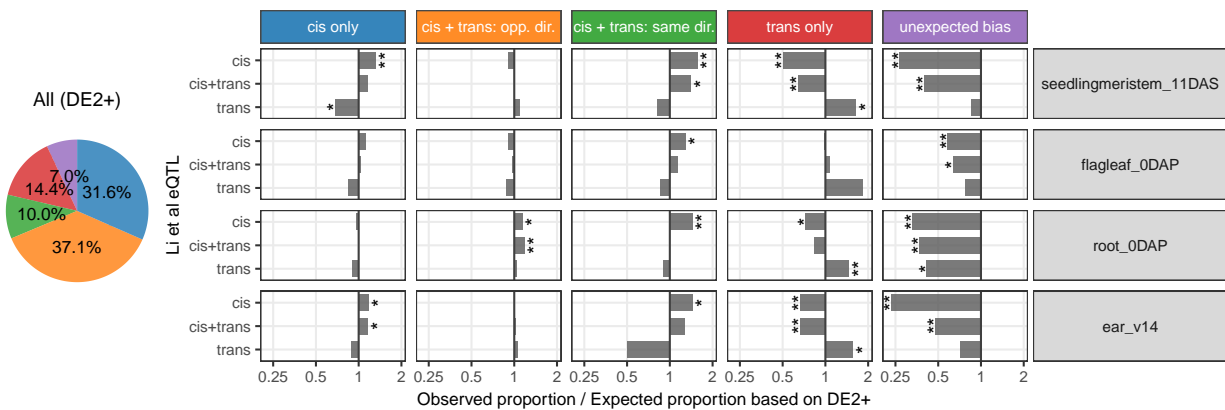


Figure S10