## 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 ear_v14	Mo17	1	11,158,750	11,087,463	93.4%	90.5%
BR050	ear_v14 ear_v14	Mo17 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 ear_v14	B73xMo17	1	9,779,316	9,705,723	96.0%	91.8%
BR053	ear_v14 ear_v14	B73xMo17	2	10,765,471	10,691,005	96.0% 96.1%	91.8%
			3		10,786,414		91.9% 91.8%
BR054	ear_v14	B73xMo17	3	10,866,113	10,/80,414	96.0%	71.0/0

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		Mo17 Mo17	3	12,363,396	12,261,701	92.5%	89.1%
BR070	spikelets_0DAP spikelets_0DAP	B73xMo17	1	10,329,056	10,246,209	95.4%	90.7%
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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 Mo17	3	11,612,393	11,504,790	94.3%	84.8%
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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%
	_			12,101,000	12,001,704		
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%
	_			7,571,014			
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 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%
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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 endosperm_27DAP	B73xMo17	3	14,883,939	14,783,781	97.7%	69.4%
DIXIOZ	endospenii_2/DAF	D/3XIVIO1/	3	14,000,739	14,/03,/81	<i>31.1</i> /0	UJ.4 /0

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		Mo17		12,018,006	11,651,375	90.6%	76.7%
	embryo_imbibedseed	Mo17 Mo17	1				80.3%
BR188 BR227	embryo_imbibedseed embryo_imbibedseed	Mo17 Mo17	2 3	19,136,137 10,606,785	18,583,167 10,249,652	91.8% 92.1%	64.7%
BR245	·	Mo17		15,060,983		91.8%	80.4%
	embryo_imbibedseed		4		14,635,237		
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%
211210	seeding mension_11DAS	1,101/	3	14,000,012	10,700,241	70.770	, 1.0 /0

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

SampleID	Tissue	Genotype	Replicate	TotalReadPair	Trimmed Read Pair	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. B7	3 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	d 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

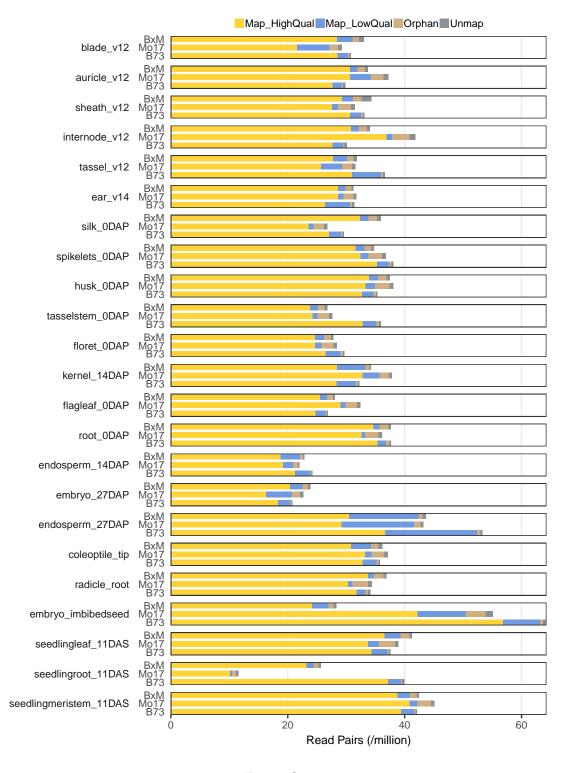


Figure S1

	Pearsor	n (upper right) and	Spearman (lower	r left) Correlation (	Coefficient 0.90	0.95	
blade_v12	blade_v12	blade_v12	auricle_v12	auricle_v12	auricle_v12	sheath_v12	sheath_v12
B73	Mo17	BxM	B73	Mo17	BxM	B73	Mo17
Rep1 BR001 1.00 0.99 Rep2 0.99 BR002 0.99	0.99 BR005 0.99	0.99 BR008 0.99	0.99 BR011 0.97	0.99 BR014 0.96	0.99 BR017 0.93	0.99 0.96 0.99 BR020 0.96	0.99 BR023 0.97
Rep3 0.99 0.99 BR004	0.99 0.99 BR007	0.99 0.99 BR009	0.99 0.98 BR012	0.99 0.98 BR015	0.98 0.97 BR018	0.98 0.98 BR021	0.99 0.99 BR024
sheath v12	internode v12	internode v12	internode v12	tassel v12	tassel v12	tassel v12	ear v14
BxM	B73	Mo17	BxM	B73	Mo17	BxM	B73
Rep1 BR025 0.89 0.96	BR028 0.99 0.95	BR031 0.95 0.97	BR034 <mark>0.99</mark> 0.98	BR037 0.99 0.98	BR040 <b>0.95 0.98</b>	BR043 0.93 0.93	BR046 0.99 0.99
Rep2 0.92 BR026 0.96	0.98 BR029 0.98	0.97 BR032 0.89	0.99 BR035 1.00	0.99 BR038 0.98	0.99 BR041 0.96	0.98 BR044 0.88	0.99 BR047 1.00
Rep3 0.94 0.98 BR027	0.97 0.99 BR030	0.98 0.94 BR033	0.98 0.99 BR036	0.98 0.98 BR039	0.98 BR042	0.96 0.97 BR045	0.99 0.99 BR048
ear_v14	ear_v14	silk_0DAP	silk_0DAP	silk_0DAP	spikelets_0DAP	spikelets_0DAP	spikelets_0DAP
Mo17 Rep1 BR049 0.99 0.99	BxM BR052 1.00 1.00	BR055 0.99 0.99	Mo17 BR058 0.99 0.98	BxM BR061 0.99 0.99	B73	Mo17 BR067 0.97 0.97	BxM
					BR064 0.98 0.98		BR070 0.99 0.99
Rep2 0.99 BR050 0.99	0.99 BR053 1.00	0.99 BR056 1.00	0.99 BR059 0.99	0.99 BR062 0.99	0.99 BR065 0.99	0.98 BR068 0.99	0.99 BR071 0.99
Rep3 0.99 BR051	1.00 0.99 BR054	0.99 0.99 BR057	0.98 0.99 BR060	0.99 0.99 BR063	0.99 0.99 BR066	0.98 0.99 BR069	0.99 0.99 BR072
husk_0DAP B73	husk_0DAP Mo17	husk_0DAP BxM	tasselstem_0DAP B73	tasselstem_0DAP Mo17	tasselstem_0DAP BxM	floret_0DAP B73	floret_0DAP Mo17
Rep1 BR073 0.99 0.98	BR076 0.91 0.92	BR079 0.98 0.98	BR082 <b>0.89 0.97</b>	BR085 0.99 0.98	BR088 <b>0.96 0.96</b>	BR091 0.97 0.99	BR094 0.98 0.98
Rep2 0.99 BR074 0.99	0.95 BR077 0.98	0.99 BR080 0.97	0.97 BR083 0.86	0.99 BR086 0.99	0.99 BR089 0.98	0.99 BR092 0.97	0.97 BR095 0.95
Rep3 0.99 0.99 BR075	0.95 0.98 BR078	0.98 0.98 BR081	0.95 0.92 BR084	0.98 0.97 BR087	0.99 0.99 BR090	0.99 0.98 BR093	0.98 0.97 BR096
		kernel 14DAP					
floret_0DAP BxM	kernel_14DAP B73	Mo17	kernel_14DAP BxM	kernel_14DAP MxB	flagleaf_0DAP B73	flagleaf_0DAP Mo17	flagleaf_0DAP  BxM
Rep1 BR097 1.00 0.99	BR118 1.00 1.00	BR121 1.00 0.99	BR124 1.00 1.00	BR127 1.00 1.00	BR100 1.00 1.00	BR103 1.00 1.00	BR106 1.00 1.00
Rep2 0.99 BR098 0.99	0.99 BR119 1.00	1.00 BR122 1.00	0.99 BR125 1.00	0.99 BR128 1.00	0.99 BR101 1.00	0.99 BR104 1.00	0.99 BR107 1.00
Rep3 0.99 BR099	0.99 0.99 BR120	0.99 0.99 BR123	0.99 DR126	0.99 BR129	0.99 BR102	0.99 0.99 BR105	0.99 0.99 BR108
root_0DAP B73	root_0DAP Mo17	root_0DAP BxM	endosperm_14DAP B73	endosperm_14DAP Mo17	endosperm_14DAP BxM	endosperm_14DAP MxB	embryo_27DAP B73
Rep1 BR109 0.98 0.99	BR112 1.00 0.99	BR115 0.99 0.97	BR130 1.00 1.00	BR133 1.00 1.00	BR136 1.00 1.00	BR139 0.99 1.00	BR142 1.00 0.99
Rep2 0.99 BR110 0.99	0.99 BR113 0.99	0.99 BR116 0.99	0.99 BR131 1.00	0.99 BR134 1.00	0.98 BR137 0.99	0.99 BR140 1.00	0.99 BR143 0.99
Rep3 0.99 0.99 BR111	0.99 0.99 BR114	0.98 0.99 BR117	0.99 0.99 BR132	0.99 0.99 BR135	0.99 0.98 BR138	0.99 0.99 BR141	0.99 0.99 BR144
embryo_27DAP	embryo_27DAP	embryo_27DAP	endosperm_27DAP	endosperm_27DAP	endosperm_27DAP	endosperm_27DAP	coleoptile_tip
Mo17 Rep1 BR145 1.00 0.99	BxM BR148 1.00 0.99	MxB BR151 1.00 0.99	BR154 0.99 0.99	Mo17 BR157 1.00 1.00	BxM BR160 1.00 1.00	MxB BR163 0.99 0.99	B73 BR166 0.99 0.99
Rep2 0.99 BR146 0.99	0.99 BR149 0.99	0.99 BR152 0.99	0.98 BR155 0.97	0.99 BR158 0.99	0.99 BR161 1.00	0.98 BR164 1.00	0.99 BR167 1.00
Rep3 0.98 0.98 BR147	0.98 0.98 BR150	0.99 0.99 BR153	0.99 0.98 BR156	0.99 0.98 BR159	0.99 0.99 BR162	0.98 0.99 BR165	0.99 0.99 BR168
coleoptile_tip	coleoptile tip	radicle_root	radicle_root	radicle_root	embryo_imbibedseed	embryo_imbibedseed	embryo_imbibedseed
Mo17	BxM	B73	Mo17	BxM	B73	Mo17	BxM
Rep1 BR169 0.99 1.00	BR172 1.00 0.99	BR175 0.99 0.99	BR178 1.00 0.98	BR181 0.97 0.99	BR184 0.93	BR187 0.98 0.96	BR191 0.98
Rep2 0.99 BR170 1.00	0.99 BR173 1.00	0.99 BR176 0.99	0.99 BR179 0.98	0.97 BR182 0.98		0.98 BR188 0.92	0.99 BR192
Rep3 0.99 BR171	0.99 0.99 BR174	0.99 0.99 BR177	0.99 0.98 BR180	0.99 0.98 BR183	0.96 BR242	0.97 0.95 BR227	
seedlingleaf_11DAS B73	seedlingleaf_11DAS Mo17	seedlingleaf_11DAS BxM	seedlingroot_11DAS B73	seedlingroot_11DAS BxM	edlingmeristem_11DA B73	eedlingmeristem_11DA Mo17	eedlingmeristem_11DA BxM
Rep1 BR193 1.00 1.00	BR196 1.00 1.00	BR199 1.00 1.00	BR202 0.99 0.99	BR208 0.99	BR211 0.99 0.97	BR214 0.99 0.99	BR217 1.00 0.99
Rep2 0.99 BR194 1.00	0.99 BR197 1.00	0.99 BR200 1.00	0.99 BR203 0.98	0.99 BR209	0.99 BR212 0.97	0.99 BR215 0.99	0.99 BR218 1.00
Rep3 0.99 0.99 BR195	0.99 0.99 BR198	0.99 0.99 BR201	0.99 0.99 BR204		0.95 0.96 BR213	0.99 0.99 BR216	0.99 0.99 BR219

Figure S2

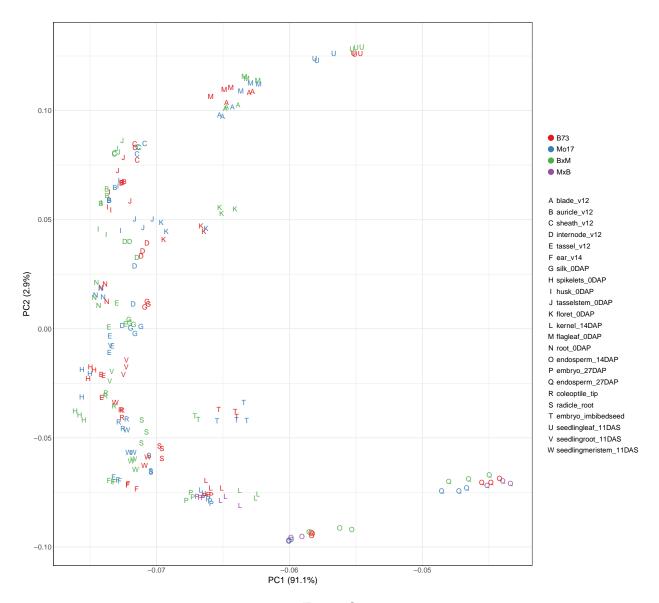


Figure S3

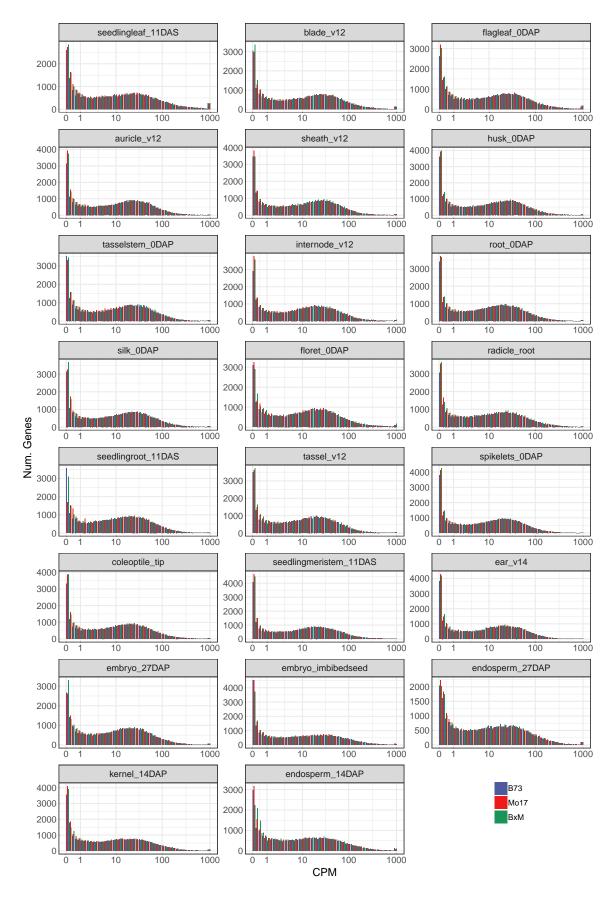


Figure S4

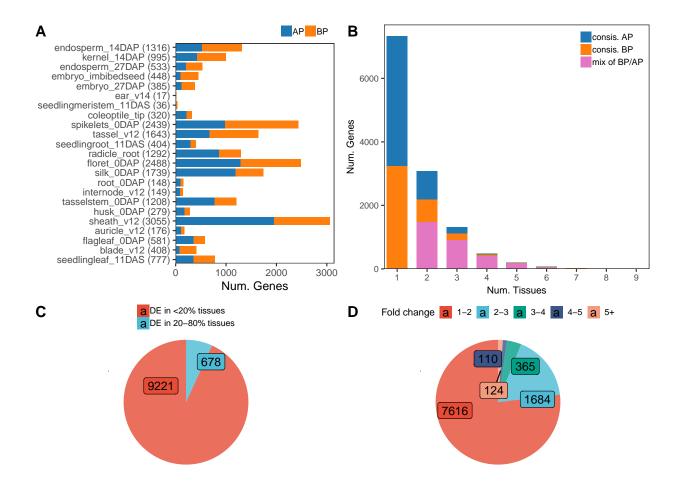


Figure S5

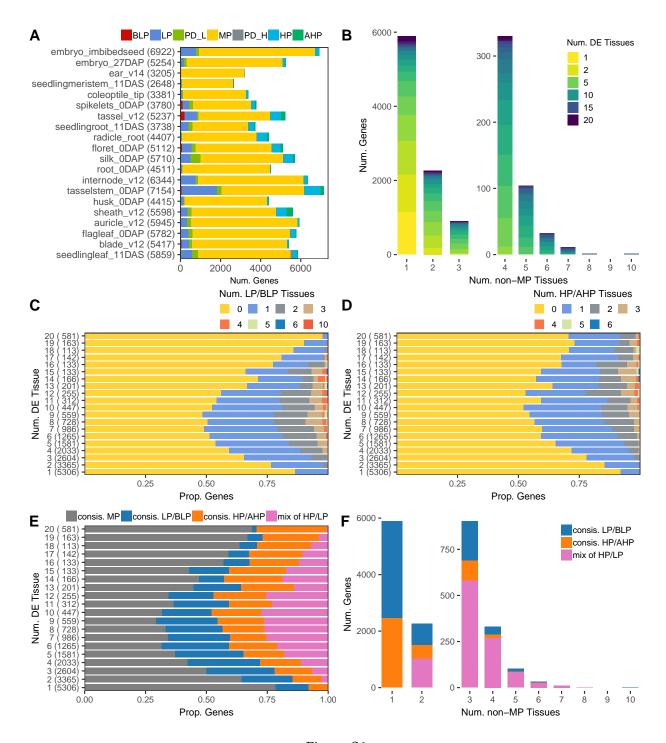


Figure S6

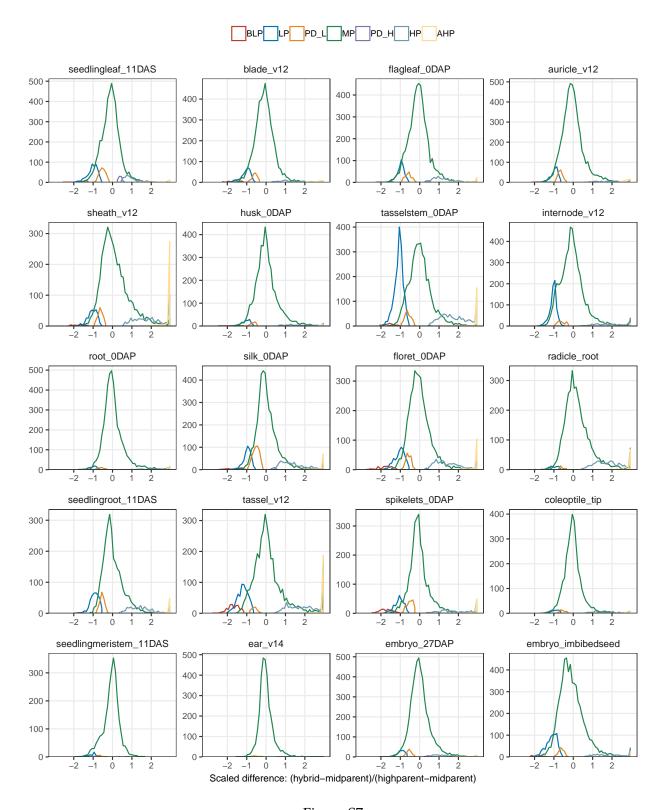


Figure S7

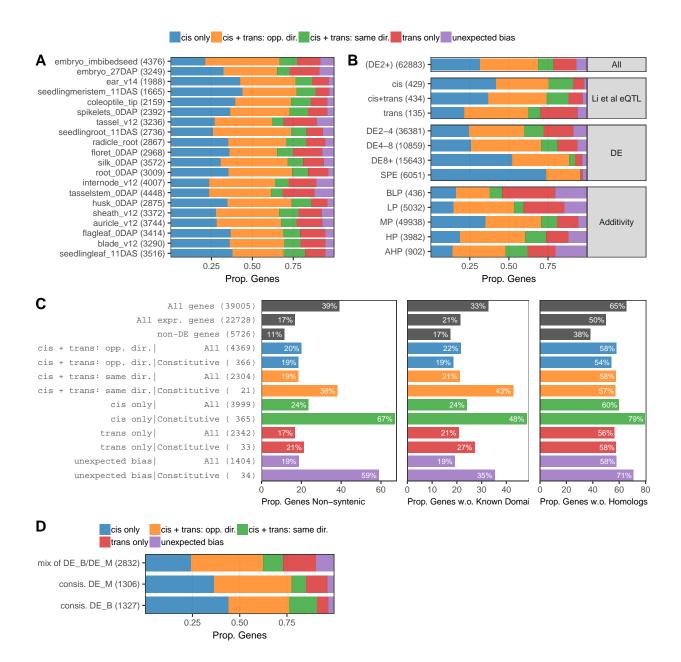


Figure S8

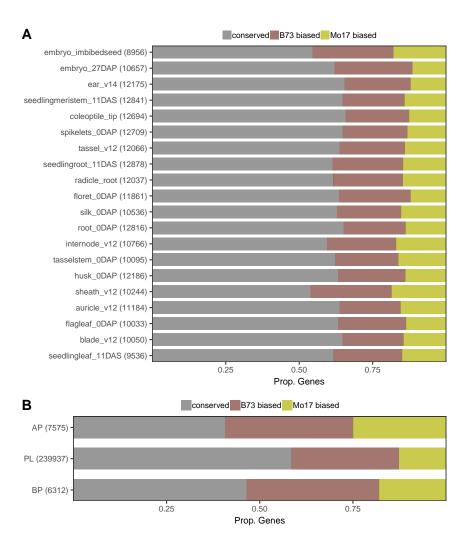


Figure S9

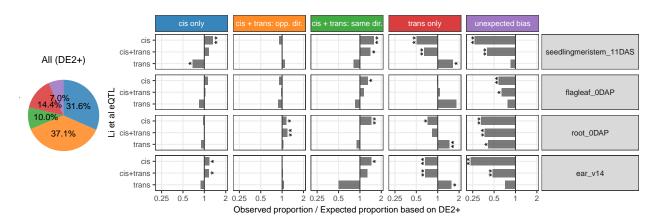


Figure S10