

Supplemental Table 1 online. Overview of sample distribution within the flow cell, biological replication, RNA-seq output and mapping results.

Treatment	Genotype	Biological replicate	Illumina indexed adapter	Lane	Total - raw	Uniquely mapped on genome ^a	%	Uniquely mapped on genome without stacks ^b	%	Uniquely mapped without stacks mapped on FGS ^c	%
Control	B73	1	AR001	1	30.180.272	27.200.167	90	15.491.837	57	12.019.096	78
		2	AR008	3	25.459.356	22.726.923	89	15.030.289	66	11.601.942	77
		3	AR010	6	22.252.697	20.084.273	90	12.402.481	62	9.690.231	78
		4	AR011	7	8.085.432	7.213.388	89	5.515.195	76	4.256.678	77
	Mo17	1	AR008	1	25.510.816	22.267.909	87	14.403.243	65	10.925.060	76
		2	AR001	3	47.712.454	41.871.784	88	25.172.752	60	19.173.538	76
		3	AR011	6	21.797.918	18.950.993	87	12.449.894	66	9.561.235	77
		4	AR010	7	16.207.101	14.213.683	88	9.654.736	68	7.395.860	77
	B73xMo17	1	AR010	1	20.020.741	17.757.055	89	12.229.253	69	9.339.808	76
		2	AR011	3	38.101.382	33.972.113	89	21.420.400	63	16.520.899	77
		3	AR001	6	36.301.348	32.263.851	89	19.067.824	59	14.662.376	77
		4	AR008	7	29.114.503	25.687.432	88	16.167.289	63	12.402.023	77
	Mo17xB73	1	AR011	1	24.528.086	21.774.753	89	14.307.676	66	10.561.778	74
		2	AR010	3	23.173.809	20.239.820	87	14.397.859	71	10.892.111	76
		3	AR008	6	36.593.846	32.489.740	89	19.656.741	61	15.029.311	76
		4	AR001	7	16.845.158	14.940.701	89	10.416.766	70	7.967.265	76
Water deficit	B73	1	AR001	2	19.119.496	17.189.324	90	11.533.087	67	8.919.097	77
		2	AR008	4	12.832.759	11.320.171	88	8.361.288	74	6.457.906	77
		3	AR010	5	23.629.579	21.268.876	90	14.562.064	68	11.295.448	78
		4	AR011	8	23.522.007	21.208.212	90	13.080.329	62	10.220.342	78
	Mo17	1	AR008	2	20.519.875	18.026.192	88	11.954.871	66	9.175.607	77
		2	AR001	4	15.943.346	13.950.944	88	9.730.731	70	7.457.661	77
		3	AR011	5	35.003.386	30.656.151	88	20.785.119	68	15.861.972	76
		4	AR010	8	26.595.536	23.221.313	87	15.083.708	65	11.490.660	76
	B73xMo17	1	AR010	2	20.047.868	17.817.017	89	12.413.020	70	9.462.904	76
		2	AR011	4	15.611.343	13.852.834	89	9.988.047	72	7.661.078	77
		3	AR001	5	36.086.599	31.988.517	89	21.743.949	68	16.553.541	76
		4	AR008	8	30.529.098	27.033.306	89	17.207.938	64	13.155.536	76
	Mo17xB73	1	AR011	2	24.501.823	21.735.510	89	14.424.454	66	10.939.414	76
		2	AR010	4	10.448.405	9.299.841	89	6.978.297	75	5.375.433	77
		3	AR008	5	30.966.840	27.504.910	89	19.478.237	71	14.859.292	76
		4	AR001	8	19.716.300	17.515.049	89	11.983.982	68	9.196.910	77
Mean				24.592.474	21.788.836	89	14.284.167	67	10.940.063	77	

^a Mapped to the reference genome (B73 RefGenV2; Schnable et al., 2009)

^b After removal of stacked reads i.e. redundant reads sharing the same start and end coordinate, sequencing direction, an

^c Mapped to the gene models of the "filtered gene set" (FGS_v2) of *Zea mays* (Release 5.b)