

FC 1	Lane 1	B73-1-S-AR001	Mo17-1-S-AR003	BxM-1-S-AR008	MxB-1-S-AR009
	Lane 2	B73-1-MZ-AR001	Mo17-1-MZ-AR003	BxM-1-MZ-AR008	MxB-1-MZ-AR009
	Lane 3	B73-1-C-AR001	Mo17-1-C-AR003	BxM-1-C-AR008	MxB-1-C-AR009
	Lane 4	B73-1-EZ-AR001	Mo17-1-EZ-AR003	BxM-1-EZ-AR008	MxB-1-EZ-AR009
	Lane 5	B73-2-S-AR009	Mo17-2-S-AR001	BxM-2-S-AR003	MxB-2-S-AR008
	Lane 6	B73-2-EZ-AR009	Mo17-2-EZ-AR001	BxM-2-EZ-AR003	MxB-2-EZ-AR008
	Lane 7	B73-2-C-AR009	Mo17-2-C-AR001	BxM-2-C-AR003	MxB-2-C-AR008
	Lane 8	B73-2-MZ-AR009	Mo17-2-MZ-AR001	BxM-2-MZ-AR003	MxB-2-MZ-AR008
FC 2	Lane 1	B73-3-C-AR008	Mo17-3-C-AR009	BxM-3-C-AR001	MxB-3-C-AR003
	Lane 2	B73-3-EZ-AR008	Mo17-3-EZ-AR009	BxM-3-EZ-AR001	MxB-3-EZ-AR003
	Lane 3	B73-3-S-AR008	Mo17-3-S-AR009	BxM-3-S-AR001	MxB-3-S-AR003
	Lane 4	B73-3-MZ-AR008	Mo17-3-MZ-AR009	BxM-3-MZ-AR001	MxB-3-MZ-AR003
	Lane 5	B73-4-C-AR003	Mo17-4-C-AR008	BxM-4-C-AR009	MxB-4-C-AR001
	Lane 6	B73-4-MZ-AR003	Mo17-4-MZ-AR008	BxM-4-MZ-AR009	MxB-4-MZ-AR001
	Lane 7	B73-4-S-AR003	Mo17-4-S-AR008	BxM-4-S-AR009	MxB-4-S-AR001
	Lane 8	B73-4-EZ-AR003	Mo17-4-EZ-AR008	BxM-4-EZ-AR009	MxB-4-EZ-AR001

Figure S1 Distribution of 64 samples across 16 lanes on two flow cells (FC) for RNA-seq. Per lane four samples with different barcodes were pooled. Barcodes: AR001, AR003, AR008, AR009; BxM: B73xMo17, MxB: Mo17xB73; S: stele, C: cortex, MZ: meristematic zone, EZ: elongation zone.

Table S1: Sequencing output (in 100 bp reads) of the 64 primary root tissue samples.

FC1			GENOTYPE					TOTAL
			B73	Mo17	B73 x Mo17	Mo17 x B73	UNKNOWN	
Lane	Rep	Zone	AR001 (ATCAGC)	AR003 (TTAGGC)	AR008 (ACTTGA)	AR009 (GATCAG)	OTHER	TOTAL
1	1	Stele (S)	23,920,572 (45.1%)	8,840,168 (16.7%)	6,875,917 (13.0%)	7,072,858 (13.3%)	6,290,586 (11.9%)	53,000,101
2	1	Cortex (C)	20,316,965 (38.4%)	14,031,056 (26.5%)	7,063,766 (13.4%)	6,557,514 (12.4%)	4,914,880 (9.3%)	52,884,181
3	1	Meristematic (MZ)	21,656,211 (39.3%)	11,965,981 (21.7%)	8,211,436 (14.9%)	7,692,558 (13.9%)	5,635,154 (10.2%)	55,161,340
4	1	Elongation (EZ)	22,407,708 (39.8%)	14,511,782 (25.8%)	5,167,060 (9.2%)	7,640,345 (13.6%)	6,556,154 (11.6%)	56,283,049
5	2	Stele (S)	9,065,418 (21.6%)	9,099,375 (21.7%)	10,048,544 (24.0%)	10,568,360 (25.2%)	3,096,723 (7.4%)	41,878,420
6	2	Cortex (C)	8,035,938 (17.7%)	10,418,576 (23.0%)	12,912,672 (28.5%)	10,241,287 (22.6%)	3,727,355 (8.2%)	45,335,828
7	2	Meristematic (MZ)	10,603,238 (23.4%)	8,915,713 (19.7%)	11,233,768 (24.8%)	10,729,362 (23.7%)	3,765,481 (8.3%)	45,247,562
8	2	Elongation (EZ)	10,153,096 (23.4%)	8,690,910 (20.0%)	10,680,402 (24.6%)	10,137,329 (23.4%)	3,711,650 (8.6%)	43,373,387
TOTAL			126,159,146 (32.1%)	86,473,561 (22.0%)	72,193,565 (18.4%)	70,639,613 (18.0%)	37,697,983 (9.6%)	393,163,868

FC2			GENOTYPE					TOTAL
			B73	Mo17	B73 x Mo17	Mo17 x B73	UNKNOWN	
Lane	Rep	Zone	AR001 (ATCAGC)	AR003 (TTAGGC)	AR008 (ACTTGA)	AR009 (GATCAG)	OTHER	TOTAL
1	3	Stele (S)	8,315,490 (20.2%)	12,387,951 (30.0%)	7,550,133 (18.3%)	10,581,893 (25.6%)	2,423,775 (5.9%)	41,259,242
2	3	Cortex (C)	9,140,452 (20.1%)	10,004,144 (22.0%)	15,408,287 (33.9%)	8,180,020 (18.0%)	2,735,805 (6.0%)	45,468,708
3	3	Meristematic (MZ)	10,758,794 (25.7%)	9,485,218 (22.7%)	9,884,147 (23.7%)	9,333,688 (22.3%)	2,329,274 (5.6%)	41,791,121
4	3	Elongation (EZ)	9,521,326 (21.2%)	9,830,516 (21.8%)	8,242,965 (18.3%)	14,722,587 (32.7%)	2,690,450 (6.0%)	45,007,844
5	4	Stele (S)	10,991,014 (24.9%)	9,898,573 (22.4%)	8,765,011 (19.9%)	11,720,198 (26.6%)	2,737,049 (6.2%)	44,111,845
6	4	Cortex (C)	10,860,880 (23.5%)	9,498,061 (20.5%)	13,318,940 (28.8%)	9,660,963 (20.9%)	2,885,105 (6.2%)	46,223,949
7	4	Meristematic (MZ)	11,085,115 (26.1%)	10,266,232 (24.2%)	9,873,982 (23.2%)	8,718,446 (20.5%)	2,557,891 (6.0%)	42,501,666
8	4	Elongation (EZ)	9,251,277 (21.1%)	6,093,690 (13.9%)	12,642,411 (28.9%)	10,544,453 (24.1%)	5,248,825 (12.0%)	43,780,656
TOTAL			79,924,348 (22.8%)	77,464,385 (22.1%)	85,685,876 (24.5%)	83,462,248 (23.8%)	23,608,174 (6.7%)	350,145,031

Table S2: Sequencing output after trimming the reads, mapping them to the maize genomic sequence, removal of redundant reads and determination of reads in the gene space of maize.

Sample	No. Trimmed Reads	No. Aligned Reads (Redundant)	No. Uniquely Aligned Reads	No. Uniquely Aligned Reads in Gene Space
B73-1-C-AR001	16,388,609	14,660,038 (89.5%)	13,648,174 (83.3%)	13,172,135 (96.5%)
B73-1-EZ-AR001	16,745,702	14,945,249 (89.2%)	13,810,778 (82.5%)	13,326,146 (96.5%)
B73-1-MZ-AR001	15,953,658	14,267,806 (89.4%)	12,923,444 (81.0%)	12,428,656 (96.2%)
B73-1-S-AR001	18,533,970	16,579,429 (89.5%)	15,327,648 (82.7%)	14,612,166 (95.3%)
B73-2-C-AR001	8,971,265	7,687,217 (85.7%)	7,115,103 (79.3%)	6,853,468 (96.3%)
B73-2-EZ-AR001	8,567,784	7,457,058 (87.0%)	6,848,279 (79.9%)	6,549,631 (95.6%)
B73-2-MZ-AR001	6,788,030	5,854,237 (86.2%)	5,347,541 (78.8%)	5,153,477 (96.4%)
B73-2-S-AR001	7,789,674	6,739,969 (86.5%)	6,200,219 (79.6%)	5,936,525 (95.7%)
B73-3-C-AR001	9,133,436	7,837,472 (85.8%)	7,248,302 (79.4%)	6,966,514 (96.1%)
B73-3-EZ-AR001	7,970,490	6,793,932 (85.2%)	6,123,962 (76.8%)	5,898,174 (96.3%)
B73-3-MZ-AR001	7,718,082	6,869,088 (89.0%)	5,574,145 (72.2%)	5,344,462 (95.9%)
B73-3-S-AR001	7,124,552	6,195,990 (87.0%)	5,731,598 (80.4%)	5,573,883 (97.2%)
B73-4-C-AR001	9,452,161	8,397,345 (88.8%)	7,710,314 (81.6%)	7,389,321 (95.8%)
B73-4-EZ-AR001	7,347,712	6,515,131 (88.7%)	5,768,250 (78.5%)	5,539,124 (96.0%)
B73-4-MZ-AR001	9,185,126	8,167,311 (88.9%)	7,523,015 (81.9%)	7,195,804 (95.7%)
B73-4-S-AR001	9,324,170	8,218,245 (88.1%)	7,627,840 (81.8%)	7,339,173 (96.2%)
Mo17-1-C-AR003	9,527,953	8,117,089 (85.2%)	7,461,079 (78.3%)	7,146,163 (95.8%)
Mo17-1-EZ-AR003	11,325,634	9,765,747 (86.2%)	8,900,423 (78.6%)	8,560,901 (96.2%)
Mo17-1-MZ-AR003	11,483,966	9,864,430 (85.9%)	9,006,760 (78.4%)	8,629,510 (95.8%)
Mo17-1-S-AR003	7,240,407	6,148,179 (84.9%)	5,659,255 (78.2%)	5,425,456 (95.9%)
Mo17-2-C-AR003	7,620,202	6,665,799 (87.5%)	6,118,610 (80.3%)	5,941,321 (97.1%)
Mo17-2-EZ-AR003	7,332,628	6,331,011 (86.3%)	5,663,282 (77.2%)	5,441,267 (96.1%)
Mo17-2-MZ-AR003	8,799,697	7,674,902 (87.2%)	6,967,846 (79.2%)	6,710,005 (96.3%)
Mo17-2-S-AR003	7,698,343	6,593,702 (85.7%)	5,988,859 (77.8%)	5,779,719 (96.5%)
Mo17-3-C-AR003	8,275,646	7,116,739 (86.0%)	6,215,090 (75.1%)	6,001,696 (96.6%)
Mo17-3-EZ-AR003	8,356,235	7,258,688 (86.9%)	6,640,673 (79.5%)	6,378,837 (96.1%)
Mo17-3-MZ-AR003	8,514,501	7,402,438 (86.9%)	6,790,960 (79.8%)	6,548,750 (96.4%)
Mo17-3-S-AR003	10,766,860	9,321,876 (86.6%)	8,660,103 (80.4%)	8,395,955 (96.9%)
Mo17-4-C-AR003	8,852,880	8,029,115 (90.7%)	7,432,293 (84.0%)	7,181,400 (96.6%)
Mo17-4-EZ-AR003	4,977,253	4,547,423 (91.4%)	4,200,946 (84.4%)	4,056,254 (96.6%)
Mo17-4-MZ-AR003	8,196,806	7,554,971 (92.2%)	6,894,680 (84.1%)	6,626,402 (96.1%)
Mo17-4-S-AR003	8,509,987	7,815,929 (91.8%)	5,935,722 (69.8%)	5,748,829 (96.9%)
BxM-1-C-AR008	6,504,048	5,681,521 (87.4%)	5,281,049 (81.2%)	5,112,251 (96.8%)

BxM-1-EZ-AR008	4,067,273	3,613,093 (88.8%)	3,324,277 (81.7%)	3,195,789 (96.1%)
BxM-1-MZ-AR008	5,656,774	4,910,466 (86.8%)	4,503,575 (79.6%)	4,329,550 (96.1%)
BxM-1-S-AR008	5,609,122	4,920,258 (87.7%)	4,559,098 (81.3%)	4,376,685 (96.0%)
BxM-2-C-AR008	9,278,666	7,873,039 (84.9%)	7,221,124 (77.8%)	7,004,000 (97.0%)
BxM-2-EZ-AR008	8,852,122	7,835,252 (88.5%)	7,094,031 (80.1%)	6,795,820 (95.8%)
BxM-2-MZ-AR008	10,830,066	9,501,443 (87.7%)	8,599,988 (79.4%)	8,328,217 (96.8%)
BxM-2-S-AR008	8,512,172	7,483,302 (87.9%)	6,859,233 (80.6%)	6,625,566 (96.6%)
BxM-3-C-AR008	8,620,900	7,792,510 (90.4%)	6,954,354 (80.7%)	6,694,576 (96.3%)
BxM-3-EZ-AR008	7,005,355	6,409,966 (91.5%)	5,845,448 (83.4%)	5,623,613 (96.2%)
BxM-3-MZ-AR008	13,110,359	11,923,294 (90.9%)	11,005,503 (83.9%)	10,635,345 (96.6%)
BxM-3-S-AR008	6,414,730	5,598,017 (87.3%)	5,194,061 (81.0%)	5,057,916 (97.4%)
BxM-4-C-AR008	8,449,833	7,355,783 (87.1%)	6,768,095 (80.1%)	6,549,676 (96.8%)
BxM-4-EZ-AR008	10,095,508	8,750,317 (86.7%)	7,914,440 (78.4%)	7,600,389 (96.0%)
BxM-4-MZ-AR008	11,390,960	9,977,739 (87.6%)	9,039,596 (79.4%)	8,616,116 (95.3%)
BxM-4-S-AR008	7,437,270	6,483,136 (87.2%)	5,475,652 (73.6%)	5,297,083 (96.7%)
MxB-1-C-AR009	5,977,726	5,246,663 (87.8%)	4,858,811 (81.3%)	4,698,735 (96.7%)
MxB-1-EZ-AR009	5,770,141	5,077,870 (88.0%)	4,660,052 (80.8%)	4,472,180 (96.0%)
MxB-1-MZ-AR009	5,330,786	4,753,396 (89.2%)	4,370,514 (82.0%)	4,179,153 (95.6%)
MxB-1-S-AR009	5,697,918	5,073,168 (89.0%)	4,278,989 (75.1%)	4,070,531 (95.1%)
MxB-2-C-AR009	8,926,029	7,926,263 (88.8%)	7,434,847 (83.3%)	7,210,331 (97.0%)
MxB-2-EZ-AR009	8,443,211	7,549,973 (89.4%)	7,013,662 (83.1%)	6,706,902 (95.6%)
MxB-2-MZ-AR009	8,506,466	7,559,208 (88.9%)	7,027,568 (82.6%)	6,788,195 (96.6%)
MxB-2-S-AR009	8,915,967	7,950,087 (89.2%)	7,378,992 (82.8%)	7,089,879 (96.1%)
MxB-3-C-AR009	8,023,533	6,755,575 (84.2%)	6,108,247 (76.1%)	5,891,715 (96.5%)
MxB-3-EZ-AR009	12,698,644	11,102,981 (87.4%)	10,061,320 (79.2%)	9,688,470 (96.3%)
MxB-3-MZ-AR009	6,875,509	5,837,500 (84.9%)	5,297,848 (77.1%)	5,119,062 (96.6%)
MxB-3-S-AR009	9,188,047	7,890,242 (85.9%)	7,278,022 (79.2%)	7,076,217 (97.2%)
MxB-4-C-AR009	7,485,965	6,603,566 (88.2%)	6,121,101 (81.8%)	5,869,737 (95.9%)
MxB-4-EZ-AR009	8,387,389	7,377,150 (88.0%)	6,759,778 (80.6%)	6,514,654 (96.4%)
MxB-4-MZ-AR009	8,261,451	7,297,919 (88.3%)	6,710,921 (81.2%)	6,450,349 (96.1%)
MxB-4-S-AR009	9,993,209	8,817,342 (88.2%)	7,694,526 (77.0%)	7,402,696 (96.2%)
B73 Total	166,994,421	147,185,517 (88.1%)	134,528,612 (80.6%)	129,278,659 (96.1%)
Mo17 Total	137,478,998	120,208,038 (87.4%)	108,536,581 (78.9%)	104,572,465 (96.3%)
BxM Total	131,835,158	116,109,136 (88.1%)	105,639,524 (80.1%)	101,842,592 (96.4%)
MxB Total	128,481,991	112,818,903 (87.8%)	103,055,198 (80.2%)	99,228,806 (96.3%)

Table S3: Gene Ids of SPE genes assigned to the GO term "apoptosis". The 'X' indicates in which tissue the considered gene showed single parent expression. For each of the four SPE-classes, the GO term apoptosis was significantly overrepresented (q value > 0.00068).

SPE gene ID	GO term	SPE_MZ	SPE_EZ	SPE_C	SPE_S
GRMZM2G450496	GO:0006952 defense response	X	X		X
	GO:0006915 apoptosis				
	GO:0005524 ATP binding				
GRMZM2G306727	GO:0006952 defense response				X
	GO:0006915 apoptosis				
	GO:0005524 ATP binding				
	GO:0005515 protein binding				
GRMZM2G005134	GO:0006952 defense response	X	X	X	X
	GO:0006915 apoptosis				
	GO:0005524 ATP binding				
	GO:0005515 protein binding				
GRMZM2G013170	GO:0006952 defense response				X
	GO:0006915 apoptosis				
	GO:0017111 nucleoside-triphosphatase activity				
	GO:0005524 ATP binding				
GRMZM2G038388	GO:0006952 defense response	X	X	X	X
	GO:0007229 integrin-mediated signaling pathway				
	GO:0006915 apoptosis				
	GO:0008305 integrin complex				
	GO:0007160 cell-matrix adhesion				
	GO:0023052 signaling				
	GO:0004872 receptor activity				
	GO:0023034 intracellular signaling pathway				
	GO:0005524 ATP binding				
	GO:0023033 signaling pathway				
GRMZM5G837251	GO:0006952 defense response				X
	GO:0006915 apoptosis				
	GO:0017111 nucleoside-triphosphatase activity				
	GO:0005524 ATP binding				
GRMZM2G083258	GO:0006952 defense response			X	X
	GO:0006915 apoptosis				
	GO:0005524 ATP binding				
GRMZM2G110894	GO:0006915 apoptosis			X	
	GO:0005515 protein binding				
GRMZM2G141256	GO:0006633 fatty acid biosynthetic process		X		
	GO:0006915 apoptosis				
	GO:0015935 small ribosomal subunit				
	GO:0048871 multicellular organismal homeostasis				
	GO:0009239 enterobactin biosynthetic process				
	GO:0051287 NAD or NADH binding				
	GO:0050826 response to freezing				
	GO:0008667 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase activity				
	GO:0004022 alcohol dehydrogenase (NAD) activity				
	GO:0004316 3-oxoacyl-[acyl-carrier-protein] reductase activity				
	GO:0044281 small molecule metabolic process				
	GO:0042309 homiothermy				
	GO:0044283 small molecule biosynthetic process				
	GO:0050825 ice binding				
	GO:0055114 oxidation reduction				
	GO:0005761 mitochondrial ribosome				
GO:0006952 defense response					

AC152495.1_FG017	GO:0006915 apoptosis		X		X
	GO:0005524 ATP binding				
GRMZM2G403407	GO:0043234 protein complex				
	GO:0051258 protein polymerization				
	GO:0006915 apoptosis				X
	GO:0003924 GTPase activity				
	GO:0005524 ATP binding				
GRMZM2G410975	GO:0005525 GTP binding				
	GO:0006915 apoptosis			X	
GRMZM2G302279	GO:0005515 protein binding				
	GO:0006952 defense response				
	GO:0006915 apoptosis				X
GRMZM2G064015	GO:0017111 nucleoside-triphosphatase activity				
	GO:0005524 ATP binding				
	GO:0006952 defense response	X			
GRMZM2G382273	GO:0006915 apoptosis	X	X	X	X
	GO:0005524 ATP binding				
	GO:0006952 defense response				
	GO:0005515 protein binding				
GRMZM5G880361	GO:0006915 apoptosis				X
	GO:0017111 nucleoside-triphosphatase activity				
	GO:0005524 ATP binding				
	GO:0006952 defense response				
GRMZM5G898898	GO:0006915 apoptosis	X	X		
	GO:0017111 nucleoside-triphosphatase activity				
	GO:0005524 ATP binding				
	GO:0005515 protein binding				
GRMZM5G819919	GO:0006952 defense response	X	X	X	X
	GO:0006915 apoptosis				
	GO:0017111 nucleoside-triphosphatase activity				
	GO:0005524 ATP binding				
GRMZM2G061742	GO:0006952 defense response			X	
	GO:0006915 apoptosis				
	GO:0005524 ATP binding				
GRMZM2G136513	GO:0006952 defense response				
	GO:0006915 apoptosis				
	GO:0017111 nucleoside-triphosphatase activity			X	
	GO:0005524 ATP binding				
	GO:0005515 protein binding				
GRMZM2G097135	GO:0006915 apoptosis		X		
	GO:0005515 protein binding				
GRMZM2G452954	GO:0006952 defense response	X	X	X	X
	GO:0006915 apoptosis				
	GO:0005524 ATP binding				
GRMZM2G069382	GO:0003676 nucleic acid binding				
	GO:0006915 apoptosis				
	GO:0006952 defense response			X	X
	GO:0008270 zinc ion binding				
	GO:0005515 protein binding				
GRMZM2G396357	GO:0005524 ATP binding				
	GO:0006952 defense response	X	X	X	X
	GO:0006915 apoptosis				
	GO:0017111 nucleoside-triphosphatase activity				
GRMZM2G000376	GO:0005524 ATP binding				
	GO:0016021 integral to membrane		X	X	
	GO:0008219 cell death				

GRMZM2G065692	GO:0005634 nucleus				
	GO:0006915 apoptosis				
	GO:0006952 defense response		X	X	
	GO:0006355 regulation of transcription, DNA-dependent				
	GO:0034645 cellular macromolecule biosynthetic process				
GRMZM2G030051	GO:0005524 ATP binding				
	GO:0006952 defense response				
	GO:0006915 apoptosis	X		X	
	GO:0017111 nucleoside-triphosphatase activity				
GRMZM2G397785	GO:0005524 ATP binding				
	GO:0006952 defense response				
	GO:0006915 apoptosis	X	X	X	X
	GO:0017111 nucleoside-triphosphatase activity				
GRMZM2G074496	GO:0005524 ATP binding				
	GO:0006952 defense response				
	GO:0006915 apoptosis				X