

Supplemental Table S1. Anatomical characteristics on four maize root types. Transverse sections collected at 3mm from the root tip of the primary root 7 days after germination (DAG), seminal root 9 DAG, crown root 15 DAG, brace root 60 DAG. Different letters indicated significant differences among means ($p \leq 0.05$ by one-way ANOVA analysis). Error bars indicate means \pm SE; n = 4 roots from four individual maize plants.

	Primary root	Seminal root	Crown root	Brace root
Total transversal area, mm ²	0.39±0.04b	0.29±0.03c	0.41±0.08b	2.49±0.13a
Stele transversal area, mm ²	0.06±0.008b	0.042±0.005c	0.07±0.006b	0.6±0.12a
Meta-xylem area total, mm ²	0.014±0.002b	0.0083±0.0011c	0.014±0.002b	0.058±0.011a
Meta-xylem area average, mm ²	0.0028±0.0006ab	0.0017±0.0002b	0.0024±0.0002ab	0.0034±0.0009a
Number of cortical cell layers	7.2±0.8b	6.5±1.2b	7±1.4b	16.8±2.5a
Number of meta-xylem elements	5.4±0.5bc	4.3±0.3c	6.2±1.1b	17.5±3.6a
Phloem pole pericycle length, μ m	14.5±0.5b	15±0.2b	16.1±0.6ab	17.1±0.3a
Phloem pole pericycle width, μ m	11.2±0.4b	11.2±0.2b	12.3±0.7ab	14.2±0.5a
Xylem pole pericycle length, μ m	10.4±0.2b	10.1±0.6b	11.4±0.4ab	13±0.5a
Xylem pole pericycle width, μ m	6.4±0.3b	6.1±0.5b	8.6±0.6ab	10.7±0.6a

Supplemental Table S2. Overview of LCM-RNAseq outputs, mapping results and alignments to the B73 reference genome. The total reads of each sequenced sample have been mapped to the filtered gene set (FGS) of maize. Only uniquely mapping reads have been further considered. PR, primary root; SR, seminal root; CR, crown root; BR, brace root. Homo LN, homogeneous low nitrate; Local HN, local high nitrate.

Sample	Total no. reads	Reads no. after trimming	Reads no. mapped on genome ^a	Reads no. mapped without stacks ^b	Reads no. mapped on FGS ^c
PR-Homo LN-1	22,393,992	22,390,694	15,042,416	13,102,793	11,551,091
PR-Homo LN-2	22,163,124	22,159,902	14,944,871	13,493,180	11,342,952
PR-Homo LN-3	20,593,382	20,590,222	13,941,443	12,172,277	10,588,645
PR-Local HN-1	19,598,452	19,595,478	13,237,168	11,641,917	10,122,269
PR-Local HN-2	21,882,574	21,879,247	14,993,060	13,419,619	12,072,672
PR-Local HN-3	21,798,320	21,795,040	14,828,031	13,213,931	11,830,761
SR-Homo LN-1	22,258,402	22,254,801	15,188,592	13,426,855	11,777,341
SR-Homo LN-2	20,920,568	20,919,535	14,280,656	12,754,274	11,494,099
SR-Homo LN-3	23,430,820	23,427,390	16,016,689	14,136,501	12,478,875
SR-Local HN-1	22,186,730	22,183,345	14,893,348	13,070,550	11,488,660
SR-Local HN-2	21,013,588	21,010,237	14,219,966	12,509,130	10,889,938
SR-Local HN-3	24,297,876	24,294,213	16,494,921	14,451,629	12,777,933
CR-Homo LN-1	20,982,794	20,979,713	14,080,795	12,266,831	10,773,231
CR-Homo LN-2	22,042,874	22,039,704	14,938,136	13,051,240	11,643,063
CR-Homo LN-3	22,221,340	22,218,945	14,954,404	12,991,758	11,528,158
CR-Local HN-1	20,455,568	20,453,287	13,669,473	12,099,367	10,015,618
CR-Local HN-2	26,737,304	26,734,390	18,158,937	15,671,775	13,549,279
CR-Local HN-3	26,759,680	26,756,862	18,134,901	15,748,463	13,855,881
BR-Homo LN-1	26,371,332	26,368,335	18,012,853	15,890,342	13,787,719
BR-Homo LN-2	22,741,034	22,737,431	15,469,224	13,761,059	11,408,106
BR-Homo LN-3	26,777,180	26,772,998	18,557,532	16,180,354	13,660,643

Sample	Total no. reads	Reads no. after trimming	Reads no. mapped on genome^a	Reads no. mapped without stacks^b	Reads no. mapped on FGS^c
BR-Local HN-1	23,385,006	23,381,515	15,593,786	13,966,392	11,969,219
BR-Local HN-2	25,201,686	23,179,892	16,816,139	14,980,484	12,445,158
BR-Local HN-3	26,945,550	26,941,335	18,059,936	16,181,048	13,617,452

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

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

^c Mapped to the 39,656 gene models of the filtered gene set (FGS) of maize (Release 5b.60).

Supplemental Table S3. “Classical” maize genes detected among nitrate responsive genes identified in phloem pole pericycle cells of maize brace roots. The classical genes related to DNA synthesis and cell cycle were highlighted.

Gene ID	Symbol	Gene Name	Log ₂ FC
AC195340.3_FG001	<i>tua1</i>	<i>alpha tubulin1</i>	1.14
AC209208.3_FG002	<i>pip1b</i>	<i>plasma membrane intrinsic protein1</i>	-2.13
AC235534.1_FG007	<i>ocl2</i>	<i>outer cell layer2</i>	7.77
GRMZM2G003514	<i>zag5</i>	<i>zea agamous5</i>	7.18
GRMZM2G014833	<i>pk4</i>	<i>protein kinase4</i>	2.09
GRMZM2G014914	<i>pip2e</i>	<i>plasma membrane intrinsic protein2</i>	-2.17
GRMZM2G016890	<i>glu1</i>	<i>beta glucosidase1</i>	-3.56
GRMZM2G020187	<i>rgd1</i>	<i>ragged seedling1</i>	1.87
GRMZM2G032003	<i>ugp1</i>	<i>UDP-glucose pyrophosphorylase1</i>	-1.27
GRMZM2G032628	<i>ae1</i>	<i>amylose extender1</i>	5.22
GRMZM2G034647	<i>cyc1</i>	<i>cyclin1</i>	7.49
GRMZM2G036464	<i>gln5</i>	<i>glutamine synthetase5</i>	-1.21
GRMZM2G050514	<i>gln6</i>	<i>glutamine synthetase6</i>	-3.33
GRMZM2G051943	<i>cta1</i>	<i>chitinase A1</i>	-4.66
GRMZM2G056014	<i>cap1</i>	<i>calcium pump1</i>	-1.26
GRMZM2G057823	<i>ald1</i>	<i>aldolase1</i>	-1.53
GRMZM2G059037	<i>afd1</i>	<i>absence of first division1</i>	-1.85
GRMZM2G066191	<i>tub4</i>	<i>beta tubulin4</i>	-3.61
GRMZM2G068506	<i>bt2</i>	<i>brittle endosperm2</i>	1.46
GRMZM2G071959	<i>his2b1</i>	<i>histone2b1</i>	1.77
GRMZM2G073671	<i>cyc3</i>	<i>cyclin3</i>	8.79
GRMZM2G074361	<i>prf1</i>	<i>profilin homolog1</i>	7.72
GRMZM2G081192	<i>pip2c</i>	<i>plasma membrane intrinsic protein2</i>	-7.02
GRMZM2G086971	<i>ypt1</i>	<i>ypt homolog1</i>	1.13
GRMZM2G087741	<i>lg3</i>	<i>liguleless3</i>	-1.53
GRMZM2G088753	<i>sbe1</i>	<i>starch branching enzyme1</i>	2.52

Gene ID	Symbol	Gene Name	Log ₂ FC
GRMZM2G089713	<i>sh1</i>	<i>shrunk1</i>	1.03
GRMZM2G089836	<i>ivr2</i>	<i>invertase2</i>	-4.31
GRMZM2G092125	<i>pip2b</i>	<i>plasma membrane intrinsic protein2</i>	-2.37
GRMZM2G092198	<i>emp4</i>	<i>empty pericarp4</i>	2.25
GRMZM2G096475	<i>mlg3</i>	<i>lea protein group3</i>	-6.69
GRMZM2G097768	<i>stp1</i>	<i>sugar transport1</i>	-1.13
GRMZM2G098346	<i>adh2</i>	<i>alcohol dehydrogenase2</i>	-1.22
GRMZM2G102499	<i>grf1</i>	<i>general regulatory factor1</i>	-1.55
GRMZM2G104546	<i>akh2</i>	<i>aspartate kinase homoserine dehydrogenase2</i>	1.58
GRMZM2G108766	<i>tub3</i>	<i>beta tubulin3</i>	-3.96
GRMZM2G113033	<i>ssu2</i>	<i>ribulose bisphosphate carboxylase small subunit2</i>	-3.82
GRMZM2G113137	<i>cesa6</i>	<i>cellulose synthase6</i>	-1.66
GRMZM2G114642	<i>gl1</i>	<i>glossy1</i>	-3.56
GRMZM2G116273	<i>gst1</i>	<i>glutathione-S-transferase1</i>	-1.20
GRMZM2G119071	<i>his2b2</i>	<i>histone2b2</i>	2.76
GRMZM2G126010	<i>act1</i>	<i>actin1</i>	3.71
GRMZM2G134797	<i>ndk1</i>	<i>nucleotide diphosphate kinase1</i>	-1.99
GRMZM2G136067	<i>hda108</i>	<i>histone deacetylase</i>	1.16
GRMZM2G139300	<i>incw1</i>	<i>cell wall invertase1</i>	-1.78
GRMZM2G147266	<i>fer2</i>	<i>ferritin homolog2</i>	-3.48
GRMZM2G154628	<i>pip2d</i>	<i>plasma membrane intrinsic protein2</i>	-5.66
GRMZM2G156861	<i>lox1</i>	<i>lipoxygenase1</i>	-4.82
GRMZM2G158809	<i>zcn18</i>	<i>phosphatidylethanolamine-binding protein18</i>	2.28
GRMZM2G164696	<i>tub1</i>	<i>beta tubulin1</i>	2.21
GRMZM2G168651	<i>hrg1</i>	<i>hydroxyproline rich glycoprotein1</i>	2.08
GRMZM2G172322	<i>gsr1</i>	<i>glutathione reductase1</i>	-1.99
GRMZM2G178693	<i>pip2a</i>	<i>plasma membrane intrinsic protein2</i>	-2.97

Gene ID	Symbol	Gene Name	Log₂ FC
GRMZM2G305046	<i>his2a1</i>	<i>histone2A1</i>	1.83
GRMZM2G307906	<i>ms45</i>	<i>male sterile45</i>	1.60
GRMZM2G316113	<i>rbap1</i>	<i>WD-repeat protein RBAP1</i>	1.11
GRMZM2G333916	<i>dmt101</i>	<i>DNA methyl transferase1</i>	1.82
GRMZM2G392975	<i>pip1c</i>	<i>plasma membrane intrinsic protein1</i>	-1.85
GRMZM2G452178	<i>gn1</i>	<i>gnarley1</i>	-2.14
GRMZM5G846811	<i>rop2</i>	<i>Rho-related protein from plants2</i>	-1.71

Supplemental Table S4. List of 132 transcription factor genes among 2,740 brace root specific nitrate responding genes.

Gene ID	Family	Log ₂ Fc
GRMZM2G139082	AP2	4.71
GRMZM2G416701	AP2	-2.07
GRMZM2G017187	ARF	-1.38
GRMZM2G030710	ARF	1.64
GRMZM2G034840	ARF	5.44
GRMZM2G137413	ARF	1.28
GRMZM2G702026	ARF	1.48
GRMZM2G065478	B3	4.12
GRMZM2G065496	B3	6.26
GRMZM2G109480	B3	5.29
GRMZM2G111123	B3	3.53
GRMZM2G173321	B3	2.13
GRMZM2G313737	B3	1.44
GRMZM2G019806	bHLH	-4.75
GRMZM2G042893	bHLH	-6.36
GRMZM2G057260	bHLH	-4.45
GRMZM2G088443	bHLH	2.12
GRMZM2G101350	bHLH	-4.18
GRMZM2G137426	bHLH	-2.73
GRMZM2G148723	bHLH	1.26
GRMZM2G159456	bHLH	7.42
GRMZM2G171818	bHLH	-1.63
GRMZM2G180452	bHLH	-2.84
GRMZM2G417597	bHLH	3.16
AC203957.3_FG004	bZIP	-2.37
GRMZM2G019106	bZIP	-1.87
GRMZM2G030877	bZIP	-3.06

Gene ID	Family	Log ₂ Fc
GRMZM2G045236	bZIP	1.73
GRMZM2G079365	bZIP	-2.34
GRMZM2G134863	bZIP	-4.57
GRMZM2G448607	bZIP	-2.26
AC233952.1_FG008	C2H2	-4.98
GRMZM2G081782	C2H2	1.21
GRMZM2G159032	C2H2	1.17
GRMZM2G320287	C2H2	5.70
GRMZM2G400714	C2H2	-3.60
GRMZM5G887286	C2H2	2.35
GRMZM5G898314	C2H2	1.14
GRMZM2G068476	C3H	1.20
GRMZM2G151689	C3H	1.08
GRMZM2G171600	CAMTA	-1.43
GRMZM2G060170	CPP	1.38
GRMZM2G153754	CPP	6.58
GRMZM2G322090	CPP	2.09
GRMZM2G098442	DBB	-2.50
GRMZM2G179069	Dof	-3.27
GRMZM2G148506	E2F/DP	3.38
GRMZM2G361659	E2F/DP	6.30
GRMZM2G378665	E2F/DP	4.73
GRMZM2G171179	ERF	-1.50
AC234155.1_FG002	G2-like	-1.62
GRMZM2G009060	G2-like	-1.60
GRMZM2G060485	G2-like	-1.59
GRMZM2G104390	GATA	-3.12
GRMZM2G396451	GATA	1.02
GRMZM2G036966	GeBP	3.17

Gene ID	Family	Log₂ Fc
AC234164.1_FG004	GRAS	4.14
GRMZM2G023872	GRAS	-3.82
GRMZM2G073823	GRAS	-4.05
GRMZM2G179325	GRAS	-2.01
GRMZM2G151266	HB-other	2.27
GRMZM2G154641	HB-other	-2.13
AC235534.1_FG007	HD-ZIP	7.78
GRMZM2G034113	HD-ZIP	-6.15
GRMZM2G041462	HD-ZIP	-4.13
GRMZM2G092517	LBD	-2.77
GRMZM2G055135	LSD	-1.43
GRMZM2G001139	MIKC	4.81
GRMZM2G003514	MIKC	7.18
GRMZM2G005155	MIKC	-2.98
GRMZM2G070034	MIKC	1.23
GRMZM2G105387	MIKC	1.60
GRMZM2G147716	MIKC	-1.12
GRMZM2G099577	M-type	2.61
GRMZM2G000818	MYB	-1.85
GRMZM2G003406	MYB	-2.82
GRMZM2G017520	MYB	-3.06
GRMZM2G052606	MYB	-6.38
GRMZM2G069325	MYB	-2.90
GRMZM2G089686	MYB	-3.92
GRMZM2G119693	MYB	-3.92
GRMZM2G127490	MYB	-3.53
GRMZM2G171781	MYB	-2.02
GRMZM2G096759	MYB_related	1.12
GRMZM2G468479	MYB_related	1.91

Gene ID	Family	Log ₂ Fc
GRMZM2G531738	MYB_related	1.11
AC212859.3_FG008	NAC	-3.64
AC233865.1_FG003	NAC	-4.90
GRMZM2G027309	NAC	2.16
GRMZM2G031001	NAC	3.24
GRMZM2G048826	NAC	-3.77
GRMZM2G052239	NAC	-4.46
GRMZM2G063522	NAC	-5.20
GRMZM2G100583	NAC	-3.19
GRMZM2G100593	NAC	9.64
GRMZM2G104078	NAC	7.57
GRMZM2G111770	NAC	5.00
GRMZM2G112548	NAC	4.49
GRMZM2G155816	NAC	4.76
GRMZM2G174070	NAC	-1.80
GRMZM2G178998	NAC	-3.01
GRMZM2G181605	NAC	-3.01
GRMZM2G379608	NAC	2.64
GRMZM2G450445	NAC	4.38
GRMZM5G894234	NAC	1.58
GRMZM2G038303	NF-YA	4.48
GRMZM5G853836	NF-YA	-2.05
GRMZM2G083964	NF-YC	1.91
GRMZM2G161680	NF-YC	1.71
GRMZM2G414805	SBP	1.13
GRMZM2G097683	SRS	6.10
GRMZM2G108798	SRS	3.86
GRMZM2G135783	SRS	4.40
GRMZM2G060507	TALE	-6.01

Gene ID	Family	Log₂ Fc
GRMZM2G087741	TALE	-1.53
GRMZM2G099319	TALE	-1.67
GRMZM2G125976	TALE	2.83
GRMZM2G148098	TALE	-2.06
GRMZM2G159431	TALE	-5.90
GRMZM2G452178	TALE	-2.14
GRMZM2G077755	TCP	-4.78
GRMZM2G037823	Trihelix	1.98
GRMZM2G047370	Trihelix	1.36
GRMZM2G169580	Trihelix	-3.41
GRMZM2G314660	Trihelix	-4.50
GRMZM2G469873	Trihelix	1.60
GRMZM2G012262	Whirly	1.47
GRMZM2G052671	WRKY	-1.59
GRMZM2G065290	WRKY	-3.63
GRMZM2G151407	WRKY	1.15
GRMZM2G169564	WRKY	-4.19
GRMZM2G449681	WRKY	-3.29

Supplemental Table S5. List of genes associated with DNA synthesis/chromatin structure. Histones extracted from bin28 of the MapMan analysis. “Classical” maize genes were highlighted in red.

BinCode	BinName	Gene ID	Description	Log ₂ Fc
		AC203761.3_FG002	DNA topoisomerase family protein	1.6
		AC235534.1_FG001	replication factor C 40 kDa	1.77
		GRMZM2G006452	SMC2 (STRUCTURAL MAINTENANCE OF CHROMOSOMES 2)	2.39
		GRMZM2G010105	FAS1 (FASCIATA 1); histone binding	4.22
		GRMZM2G021270	TOPII (TOPOISOMERASE II); ATP binding / DNA binding / DNA topoisomerase (ATP-hydrolyzing)/ DNA topoisomerase/ DNA-dependent ATPase	4.56
		GRMZM2G021674	DNA binding / catalytic/ chromatin binding / nuclease	1.26
28.1	DNA.synthesis/chromatin structure	GRMZM2G030873	ATRH1; ATP-dependent helicase/ DEAD/H-box RNA helicase binding	1.47
		GRMZM2G035168	DEAD/DEAH box helicase	2.58
		GRMZM2G036619	unknown protein	4.99
		GRMZM2G044128	NAP57 (Arabidopsis thaliana homologue of NAP57); pseudouridine synthase	1.68
		GRMZM2G044550	endonuclease/exonuclease/phosphatase family protein	3.23
		GRMZM2G044989	ATP binding / DNA binding / DNA-directed DNA polymerase	3.84
		GRMZM2G059365	ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding	1.15
		GRMZM2G074818	SYN3; protein sister chromatid cohesion 1 protein 3	3

BinCode	BinName	Gene ID	Description	Log ₂ Fc
		GRMZM2G076484	protein ATP-dependent RNA helicase DBP3	1.04
		GRMZM2G086934	replication protein	2.78
		GRMZM2G091006	ARP; DNA-(apurinic or apyrimidinic site) lyase	2.37
		GRMZM2G095865	DNA gyrase subunit A family protein	1.36
		GRMZM2G096184	EMB2656 (EMBRYO DEFECTIVE 2656); binding	2.91
		GRMZM2G096458	FAS1 (FASCIATA 1); histone binding	3.34
		GRMZM2G096759	DNA binding	1.12
		GRMZM2G096920	DNA binding / catalytic/ nuclease	2.67
		GRMZM2G098714	replication protein	3.43
		GRMZM2G101390	unknown protein	5.75
28.1	DNA.synthesis/chromatin structure	GRMZM2G107987	ATP binding / ATP-dependent DNA helicase/ ATP-dependent helicase/ DNA binding / hydrolase, acting on acid anhydrides, in phosphorus- containing anhydrides / nucleic acid binding	1.72
		GRMZM2G113228	ATNTH1 / endonuclease-related	-1.69
		GRMZM2G117028	STI (STICHEL); ATP binding / DNA binding / DNA-directed DNA polymerase	2.05
		GRMZM2G117100	TFL2 (TERMINAL FLOWER 2); DNA binding / methylated histone residue binding	1
		GRMZM2G117238	ORC2 (ORIGIN RECOGNITION COMPLEX SECOND LARGEST SUBUNIT 2); DNA replication origin binding / protein binding	2
		GRMZM2G121210	TOPII (TOPOISOMERASE II); ATP binding / DNA binding / DNA topoisomerase (ATP-hydrolyzing)/ DNA-dependent ATPase	4.95

BinCode	BinName	Gene ID	Description	Log ₂ Fc
28.1	DNA-synthesis/chromatin structure	GRMZM2G121262	endonuclease	1.71
		GRMZM2G121427	ATP binding / ATP-dependent DNA helicase/ DNA binding / hydrolase	2.11
		GRMZM2G129007	DEAD/DEAH box helicase	1.14
		GRMZM2G132704	nucleolar protein gar2-related	-1.38
		GRMZM2G141948	DNA-directed DNA polymerase family protein	1.89
		GRMZM2G143588	POLD2 (DNA POLYMERASE DELTA SMALL SUBUNIT); DNA binding / DNA-directed DNA polymerase	1.35
		GRMZM2G146047	zinc finger (CCCH type) helicase family protein	1.78
		GRMZM2G147390	unknown protein	-2.77
		GRMZM2G151944	DNA-directed DNA polymerase family protein	3.81
		GRMZM2G154267	ATDPB2 (ARABIDOPSIS THALIANA DNA POLYMERASE EPSILON SUBUNIT B2); DNA binding / DNA-directed DNA polymerase/ nucleic acid binding	2.25
		GRMZM2G157267	inositol-1,4,5-trisphosphate 5-phosphatase CVP2	-1.58
		GRMZM2G159008	inositol polyphosphate 5-phosphatase	-9.23
		GRMZM2G162445	MCM3 / DNA replication licensing factor	2.42
		GRMZM2G167338	ATTERT (TELOMERASE REVERSE TRANSCRIPTASE); telomerase/ telomeric template RNA reverse transcriptase	6.6
		GRMZM2G168249	ORC1A (ORIGIN RECOGNITION COMPLEX 1); DNA binding / double-stranded methylated DNA binding	1.58
		GRMZM2G169648	AtPOT1b (protection of telomeres 1b); DNA binding	1.45

BinCode	BinName	Gene ID	Description	Log ₂ Fc
28.1	DNA.synthesis/chromatin structure	GRMZM2G170291	endonuclease/exonuclease/phosphatase family protein	1.85
		GRMZM2G172787	DNA topoisomerase family protein	2.03
		GRMZM2G172956	NAP57 (Arabidopsis thaliana homologue of NAP57); pseudouridine synthase	2.02
		GRMZM2G303752	DEAD/DEAH box helicase	1.47
		GRMZM2G313020	tRNA-splicing endonuclease positive effector	3.04
		GRMZM2G317051	FAS1 (FASCIATA 1); histone binding	2.5
		GRMZM2G322506	tRNA-splicing endonuclease positive effector-related	1.15
		GRMZM2G326328	protein condensin complex subunit 1	2.75
		GRMZM2G328268	unknown protein	2.4
		GRMZM2G342895	unknown protein	9.3
		GRMZM2G346278	RCK (ROCK-N-ROLLERS); ATP binding / ATP-dependent helicase/ DNA helicase	2.95
		GRMZM2G352898	endonuclease/exonuclease/phosphatase family protein	5.51
		GRMZM2G355771	kinase interacting family protein	-1.21
		GRMZM2G361501	MUS81 (MMS AND UV SENSITIVE 81); endonuclease/ nucleic acid binding	6.35
		GRMZM2G398668	endonuclease	1.6
		GRMZM2G420865	DEAD/DEAH box helicase	1.16
		GRMZM2G421655	ATP binding / ATP-dependent DNA helicase/ DNA binding / hydrolase	2.01
		GRMZM2G425986	adenine-DNA glycosylase-related / MYH-related	1.81
		GRMZM5G804064	DEAD/DEAH box helicase	1.56

BinCode	BinName	Gene ID	Description	Log ₂ Fc
28.1	DNA-synthesis/chromatin structure	GRMZM2G455243	ORC1B (ORIGIN OF REPLICATION COMPLEX 1B); DNA binding / double-stranded methylated DNA binding / protein binding	1.44
		GRMZM2G480171	POLGAMMA2 (polymerase gamma 2); DNA binding / DNA-directed DNA polymerase	1.57
		GRMZM5G825512	ORC6 (ORIGIN RECOGNITION COMPLEX PROTEIN 6); DNA binding	3.08
		GRMZM5G857930	POT1a (Protection of Telomeres 1a); telomeric DNA binding	1.18
		GRMZM5G884544	DNA binding	2.37
		GRMZM5G897976	DEAD/DEAH box helicase	1.28
28.1.3	DNA-synthesis/chromatin structure.histone	AC196961.2_FG003	histone H4	2.55
		AC212565.3_FG001	histone H4	2.2
		AC233865.1_FG001	histone H4	2.45
		GRMZM2G003306	histone H2A	1.89
		GRMZM2G016232	histone H4	2.3
		GRMZM2G041381	histone H2A	1.85
		GRMZM2G046841	histone H2B	1.56
		GRMZM2G047813	histone H2A	1.56
		GRMZM2G050833	histone H2A	1.18
		GRMZM2G056231	histone H2A	1.93
		GRMZM2G057852	histone H2B	3.61
		GRMZM2G063896	histone H4	2.96
		GRMZM2G069911	histone H1	2.47
		GRMZM2G071959	histone H2B	1.77
		GRMZM2G072855	histone H4	2.16
GRMZM2G073275	histone H4	2.08		
GRMZM2G078314	histone H3	2.42		

BinCode	BinName	Gene ID	Description	Log ₂ Fc
		GRMZM2G079089	histone H2B	1.92
		GRMZM2G080274	histone H1	2.3
		GRMZM2G084195	histone H4	2.68
		GRMZM2G107540	histone H2A	2.81
		GRMZM2G109448	histone H2A	2.86
		GRMZM2G112912	histone H2B	2.33
		GRMZM2G119071	histone H2B	2.76
		GRMZM2G121221	histone H1	2.93
		GRMZM2G141432	histone H2B	1.24
		GRMZM2G143780	histone H4	2.34
		GRMZM2G149178	histone H4	3.48
		GRMZM2G151826	histone H2A	1.64
		GRMZM2G158526	histone H3	2.9
		GRMZM2G163939	histone H2B	1.89
28.1.3	DNA.synthesis/chromatin structure.histone	GRMZM2G179005	histone H3	2.22
		GRMZM2G181153	histone H4	2.55
		GRMZM2G304575	histone H2B	1.35
		GRMZM2G305046	histone H2A	1.83
		GRMZM2G332838	histone H4	1.93
		GRMZM2G342515	histone H2B	2.92
		GRMZM2G349651	histone H4	2.07
		GRMZM2G355773	histone H3	2.43
		GRMZM2G376957	histone H3	4.16
		GRMZM2G387076	histone H3	1.7
		GRMZM2G401147	histone H2B	1.97
		GRMZM2G418258	histone H3	3.12
		GRMZM2G421279	histone H4	2.85
		GRMZM2G448458	histone H2A	2.83
		GRMZM2G451254	histone H3	2.71

BinCode	BinName	Gene ID	Description	Log ₂ Fc
28.1.3	DNA.synthesis/chromatin structure.histone	GRMZM2G472696	histone H2B	2.67
		GRMZM2G475899	histone H3	2.96
		GRMZM2G479684	histone H4	2.82
		GRMZM5G864735	histone H3	3.3
		GRMZM5G873455	histone H1	2.36
		GRMZM5G883764	histone H2A	3.01

Supplemental Table S6. List of genes associated with cell cycle, cell division and cell organization extracted from bin31 of the MapMan analysis. “Classical” maize genes were highlighted in red.

BinCode	BinName	Gene ID	Description	Log ₂ Fc
		AC195154.3_FG004	XIE; motor/ protein binding	-1.35
		AC195340.3_FG001	TUA6; structural constituent of cytoskeleton	1.14
		GRMZM2G001639	PP2-A13 (Arabidopsis thaliana phloem protein 2-A13); carbohydrate binding	-2.55
		GRMZM2G002825	ADF4 (ACTIN DEPOLYMERIZING FACTOR 4); actin binding	-1.15
		GRMZM2G006765	ACT7 (ACTIN 7); structural constituent of cytoskeleton	-4.05
		GRMZM2G007514	SCAR2 (SCAR HOMOLOG 2)	-3.24
		GRMZM2G015127	ADF7 (actin depolymerizing factor 7); actin binding	4.33
31.1	cell.organisation	GRMZM2G016668	ankyrin repeat family protein	-3.52
		GRMZM2G018951	ATP binding / microtubule motor	-2.74
		GRMZM2G023279	myosin heavy chain-related	-2.35
		GRMZM2G026560	chromosome-associated kinesin	5.06
		GRMZM2G029223	kinesin motor protein-related	2.31
		GRMZM2G030169	ACT7 (ACTIN 7); structural constituent of cytoskeleton	-3.47
		GRMZM2G030284	MAP65-3 PLE (PLEIADE); microtubule binding	8.98
		GRMZM2G033785	ZCF125; ATP binding / microtubule motor	4.69
		GRMZM2G034828	kinesin motor family protein	4.64
		GRMZM2G037472	kinesin motor protein-related	-3.04
		GRMZM2G039855	chromosome-associated kinesin	3.42

BinCode	BinName	Gene ID	Description	Log ₂ Fc
		GRMZM2G043346	plectin-related	-1.29
		GRMZM2G045808	ATEB1C (microtubule end binding protein 1); microtubule binding	5.56
		GRMZM2G051782	TUA5; structural constituent of cytoskeleton	3.19
		GRMZM2G056826	protein cadmium tolerance factor	-4.26
		GRMZM2G060702	ADF11 (ACTIN DEPOLYMERIZING FACTOR 11); actin binding	-1.35
		GRMZM2G062084	phragmoplast-associated kinesin-related protein 2 (PAKRP2)	6.13
		GRMZM2G064875	ADF6 (ACTIN DEPOLYMERIZING FACTOR 6); actin binding	3.38
31.1	cell.organisation	GRMZM2G066191	TUB8; structural constituent of cytoskeleton	-3.61
		GRMZM2G069687	SCAR2 (SCAR HOMOLOG 2)	-1.57
		GRMZM2G074361	PRF4 (PROFILIN 4); actin binding	7.72
		GRMZM2G077842	POK2 (PHRAGMOPLAST ORIENTING KINESIN 2); ATP binding / microtubule motor	4.36
		GRMZM2G081322	VLN3 (VILLIN 3); actin binding	1.56
		GRMZM2G082384	kinesin motor protein-related	4.15
		GRMZM2G083475	kinesin motor protein-related	4.51
		GRMZM2G088482	AtPP2-A11 (Phloem protein 2-A11); carbohydrate binding	-2.71
		GRMZM2G092232	kinesin motor protein-related	4
		GRMZM2G099944	TUB8; structural constituent of cytoskeleton	-2.4
		GRMZM2G100714	MAP65-6; microtubule binding	-2.46

BinCode	BinName	Gene ID	Description	Log ₂ Fc
		GRMZM2G106028	MAP65-3; microtubule binding	1.97
		GRMZM2G108766	TUB8; structural constituent of cytoskeleton	-3.96
		GRMZM2G108780	PRF4 (PROFILIN 4); actin binding	-1.07
		GRMZM2G109842	PRF4 (PROFILIN 4); actin binding	3.17
		GRMZM2G112337	chloroplast nucleoid DNA-binding protein; MAP65-1 (MICROTUBULE-ASSOCIATED PROTEINS 65-1); microtubule binding	2.12
		GRMZM2G113652	ATP binding / microtubule motor	4.46
		GRMZM2G114841	MAP65-8 (MICROTUBULE-ASSOCIATED PROTEIN 65-8)	-3.22
31.1	cell.organisation	GRMZM2G120244	ATP binding / microtubule motor	5.1
		GRMZM2G126010	ACT7 (ACTIN 7); structural constituent of cytoskeleton	3.71
		GRMZM2G126190	ACT7 (ACTIN 7); structural constituent of cytoskeleton	-1.33
		GRMZM2G127115	VLN1 (VILLIN-LIKE 1); actin binding / actin filament binding	1.14
		GRMZM2G128426	myosin heavy chain-related	2.44
		GRMZM2G132371	kinesin motor protein-related	4.09
		GRMZM2G136219	kinesin motor protein-related	5.34
		GRMZM2G136838	NACK1 HIK (HINKEL); ATP binding / microtubule motor	7.93
		GRMZM2G141208	MAP65-1 (MICROTUBULE-ASSOCIATED PROTEINS 65-1); microtubule binding	3.59
		GRMZM2G142019	myosin heavy chain-related	2.09
		GRMZM2G144415	kinesin-like protein	4.67

BinCode	BinName	Gene ID	Description	Log ₂ Fc
		GRMZM2G150984	phragmoplast-associated kinesin-related protein 2 (PAKRP2)	4.59
		GRMZM2G152328	ACT11 (actin-11); structural constituent of cytoskeleton	-1.79
		GRMZM2G157616	ATP binding / microtubule motor	8.24
		GRMZM2G164696	TUB8; structural constituent of cytoskeleton	2.21
		GRMZM2G173700	kinesin motor protein-related	1.1
		GRMZM2G176047	kinesin motor protein-related	5.54
		GRMZM2G177867	kinesin motor protein-related	4.05
		GRMZM2G178650	pectin-related	-2.32
		GRMZM2G301194	kinesin motor protein-related	5.29
31.1	cell.organisation	GRMZM2G308203	ankyrin repeat family protein	-2.93
		GRMZM2G315594	ATP binding / microtubule motor	4.46
		GRMZM2G320689	kinesin motor protein-related	3.48
		GRMZM2G324467	myosin-related	4.52
		GRMZM2G359566	VLN3 (VILLIN 3); actin binding	2.99
		GRMZM2G363813	catalytic	3.39
		GRMZM2G375593	VLN4 (VILLIN 4); actin binding	-1.38
		GRMZM2G400223	kinesin motor protein-related	8.04
		GRMZM2G409343	XIC; motor/ protein binding	-2.37
		GRMZM2G423861	ZWI (ZWICHEL); calmodulin binding / microtubule motor	-1.05
		GRMZM2G436981	ATK1 (ARABIDOPSIS THALIANA KINESIN 1); microtubule motor	3.15
		GRMZM2G443903	alpha-N-acetylglucosaminidase family / NAGLU family	-1.33
		GRMZM2G449909	XI-I; motor/ protein binding	2.21

BinCode	BinName	Gene ID	Description	Log ₂ Fc
		GRMZM2G451231	ATP binding / microtubule motor	4.14
		GRMZM2G471186	KINESIN-12B; microtubule motor/ plus-end-directed microtubule motor	7.28
		GRMZM2G471904	PPL2 (PsbP-like protein 2); calcium ion binding	2.3
		GRMZM5G817395	kinesin-4; ATP binding / microtubule motor	6.96
		GRMZM5G820912	kinesin-4	7.35
		GRMZM5G824964	EB1C (microtubule end binding protein 1); microtubule binding	2.44
31.1	cell.organisation	GRMZM5G832989	MAP70-2 (microtubule- associated proteins 70-2); microtubule binding	2.93
		GRMZM5G836827	VLN4 (ARABIDOPSIS THALIANA VILLIN 4); actin binding	-1.22
		GRMZM5G853513	TUB8; structural constituent of cytoskeleton	-1.15
		GRMZM5G856071	TUB7; structural constituent of cytoskeleton	2.05
		GRMZM5G877336	POK2 (PHRAGMOPLAST ORIENTING KINESIN 2); ATP binding / microtubule motor	2.69
		GRMZM5G877388	PRF5 (PROFILIN5); actin binding / actin monomer binding	-1.44
		GRMZM5G887077	ATP binding / microtubule motor	7.98
		AC197146.3_FG001	CDC45 (cell division cycle protein 45)	2.3
31.2	cell.division	GRMZM2G003565	UVR8 (UVB-RESISTANCE 8); chromatin binding / guanyl- nucleotide exchange factor	-1.13
		GRMZM2G018689	ribosome recycling factor family protein / ribosome releasing factor family protein	1.64

BinCode	BinName	Gene ID	Description	Log ₂ Fc
		GRMZM2G029536	transducin family protein / WD-40 repeat family protein	4.47
		GRMZM2G033828	RBR1 (RETINOBLASTOMA-RELATED 1); transcription factor binding	2.53
		GRMZM2G047143	mitotic spindle checkpoint protein, putative (MAD2)	4.41
		GRMZM2G059037	SYN1 (SYNAPTIC 1); protein sister chromatid cohesion 1 protein 1	-1.85
		GRMZM2G068193	CDKB2;1 (cyclin-dependent kinase B2;1); cyclin-dependent protein kinase	4.55
		GRMZM2G070115	CDKB2;2 (cyclin-dependent kinase B2;2); cyclin-dependent protein kinase	7.43
		GRMZM2G112072	mitotic spindle checkpoint protein, putative (MAD2)	8.09
31.2	cell.division	GRMZM2G121724	FTSZ2-1; protein binding / structural molecule	3.59
		GRMZM2G129444	mitotic checkpoint family protein	1.12
		GRMZM2G131324	ATP-binding family protein	1.1
		GRMZM2G143590	ZYP1b	2.42
		GRMZM2G145879	CDKD1;1 (cyclin-dependent kinase D1;2); cyclin-dependent protein kinase	4.89
		GRMZM2G147603	APC6 / cell division cycle family protein	1.34
		GRMZM2G162546	CDKB2;2 (cyclin-dependent kinase B2;2); cyclin-dependent protein kinase	6.09
		GRMZM2G166684	APC6 / cell division cycle family protein	1.98
		GRMZM2G170591	CDC23 (cell division cycle protein 23) / APC8 (ANAPHASE-PROMOTING COMPLEX SUBUNIT 8)	1.27
		GRMZM2G177070	cell division protein ftsH	2.61

BinCode	BinName	Gene ID	Description	Log ₂ Fc
31.2	cell.division	GRMZM2G315264	CIP111 (CAM INTERACTING PROTEIN 111); ATPase / calmodulin binding	1.73
		GRMZM2G383623	SMC3 (ARABIDOPSIS THALIANA STRUCTURAL MAINTENANCE OF CHROMOSOME 3); ATP binding / transporter	1.87
		GRMZM2G392710	HBT, CDC27b (cell division cycle protein 23) / HBT (HOBBIT); binding	1.41
		GRMZM2G440916	structural maintenance of chromosomes (SMC) family protein (MSS2)	1.43
		GRMZM2G451716	AML4 (ARABIDOPSIS MEI2-LIKE 4); RNA binding / nucleic acid binding / nucleotide binding	2.72
		GRMZM2G467695	cell division cycle protein 16	6.07
		GRMZM2G495626	CDKB1;1 (cyclin-dependent kinase B1;1); cyclin-dependent protein kinase	1.69
		GRMZM2G703490	cell division cycle protein 48, putative / CDC48	1.24
		GRMZM5G814700	AML1 (ARABIDOPSIS MEI2-LIKE PROTEIN 1); RNA binding / protein binding	-1.1
GRMZM5G866734	regulator of chromosome condensation (RCC1) family protein	2.85		
31.3	cell.cycle	GRMZM2G005619	CYCB1;2 / CYC1BAT; cyclin-dependent protein kinase regulator	6.04
		GRMZM2G017081	CYCB3B / cyclin-dependent protein kinase regulator	2.82
		GRMZM2G026346	CYCA3;4 / cyclin-dependent protein kinase regulator	3.69
		GRMZM2G034647	CYCB1;4 / cyclin-dependent protein kinase regulator	7.49
		GRMZM2G061287	CYCB2;4 / cyclin-dependent protein kinase regulator	9.27
		GRMZM2G064005	FZR2 (FIZZY-RELATED 2); signal transducer	-1.93

BinCode	BinName	Gene ID	Description	Log ₂ Fc
		GRMZM2G073003	CYCB1;2 / cyclin-dependent protein kinase regulator	8.46
		GRMZM2G073671	CYCB2;3 / cyclin-dependent protein kinase regulator	8.79
		GRMZM2G115670	CYCT1;4; cyclin-dependent protein kinase	1.24
		GRMZM2G138886	CYCB2;4 / cyclin-dependent protein kinase regulator	5.62
31.3	cell.cycle	GRMZM2G160563	CYCP4;3; cyclin-dependent protein kinase regulator	-2.47
		GRMZM2G178215	CYCA3;1 / cyclin-dependent protein kinase regulator	3.72
		GRMZM2G303157	Unknown function	2.35
		GRMZM2G363437	CYCA3;4 / cyclin-dependent protein kinase regulator	5.6
		GRMZM5G813206	binding	-1.64
		GRMZM5G879536	CYCA2;1 / cyclin-dependent protein kinase regulator	2.15