

Theoretical and Applied Genetics

Map-based cloning of *Zmccr3* and its network construction and validation for regulating maize seed germination

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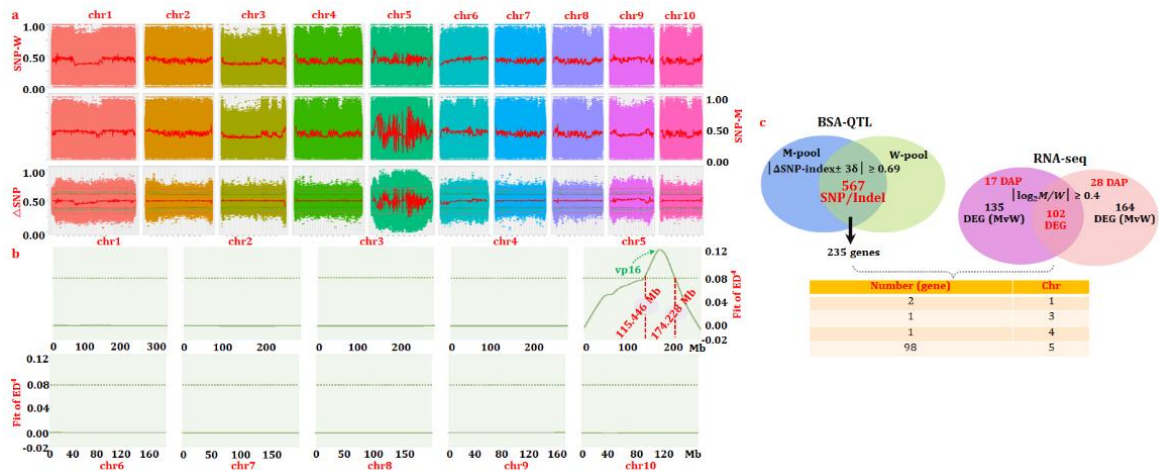


Fig. S1 The QTL mapping and verification of vp16-QTL locus

Notes: ^aLoess plot (with curve fitted by 99% confidence interval with red lines) on the whole genome using a window of 1-Mb and a step size of 1-kb by SNP-index (W-index and M-index) and Δ SNP-index (W-index – M-index) with 40X BSA-QTL resequencing, and a threshold of SNP-index and Δ SNP-index = 0.5. gDNA of the W-pool and M-pool from leaves of individuals with non-isolated (as *AA*) and isolated (as *Aa*) self-pollinated plants (*BC*₄*F*₂), respectively; ^bLoess fit curve calculated by Euclidean distance (ED) on the whole genome. The dotted lines show the 95% confidence interval defined; ^cVerification of the vp16-QTL locus using joint BSA-QTL with a threshold $|(\Delta$ SNP-index) $\pm 3\delta$ = 0.8 and RNA-seq analysis on the whole genome with a threshold $|\log_2(M/W)| = 0.4$. gDNA of the W-pool and M-pool for BSA-QTL resequencing from leaves of individuals with non-isolated (as *AA*) and isolated (as *Aa*) self-pollinated plants (*BC*₄*F*₂), respectively. Δ SNP-index = (W-index – M-index). δ means total standard deviation from SNP-index (W-pool and M-pool). RNA-seq from red kernels (as M) and wild-type kernels (as W) with non-isolated self-pollinated plants (*BC*₄*F*₂). DEG is abbreviation for differentially expressed genes.

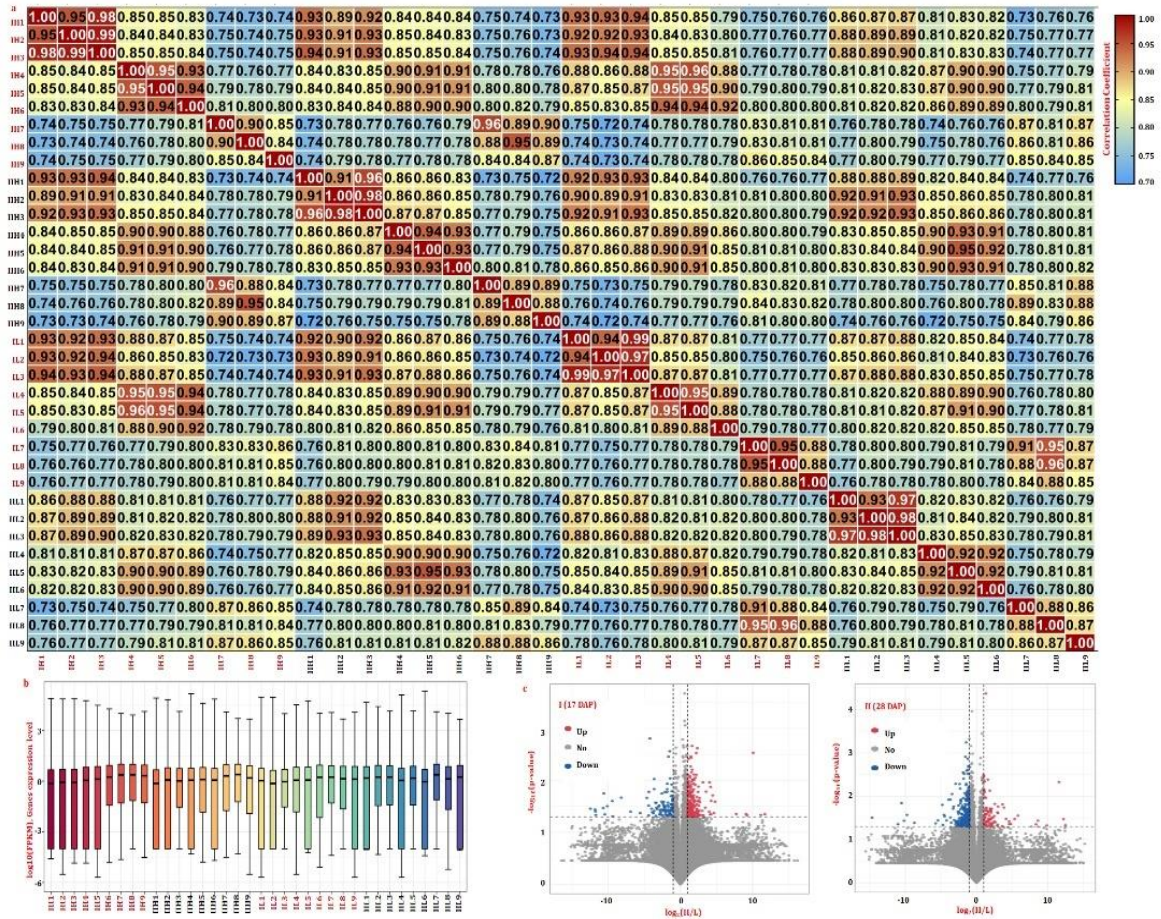


Fig. S2 The evaluation of gene expression levels from RNA-seq

Notes: For RNA-seq of 36 samples (including vp16, MP and IL; M of vp16 and high PHS of MP/IL as H, W of vp16 and low PHS of MP/IL as L). H, L, I, II, 1-9 represent high and low PHS, at 17DAP, 28DAP, and the different samples, respectively. ^aThe correlation analysis of the expression levels between samples; ^bThe variation of expression levels in samples; ^cVolcanic plots of expressed genes with high (H) and low (L) PHS.

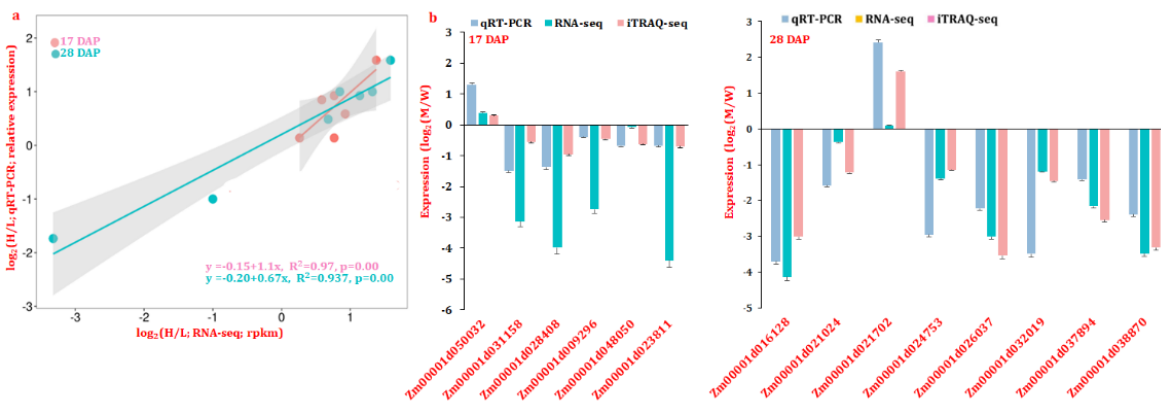


Fig. S3 Comparison of gene expression levels between RNA-seq/iTRAQ and qRT-PCR

Notes: Expression of RNA-seq is standardised with log2(M/W). relative expression level of qRT-PCR with log2(M/W) by calculations $2^{-\Delta\Delta CT}$. Endogenous control is GAPDH (NC_050099), $n = 5$. Randomly select samples from 17 DAP and 28 DAP for qRT-PCR; ^aFor RNA-seq and qRT-PCR from H-PHS and L-PHS; ^bRNA-seq, iTRAQ and qRT-PCR from M and W of vp16. Expression of iTRAQ for M and W of vp16 is standardised with log2(M/W).

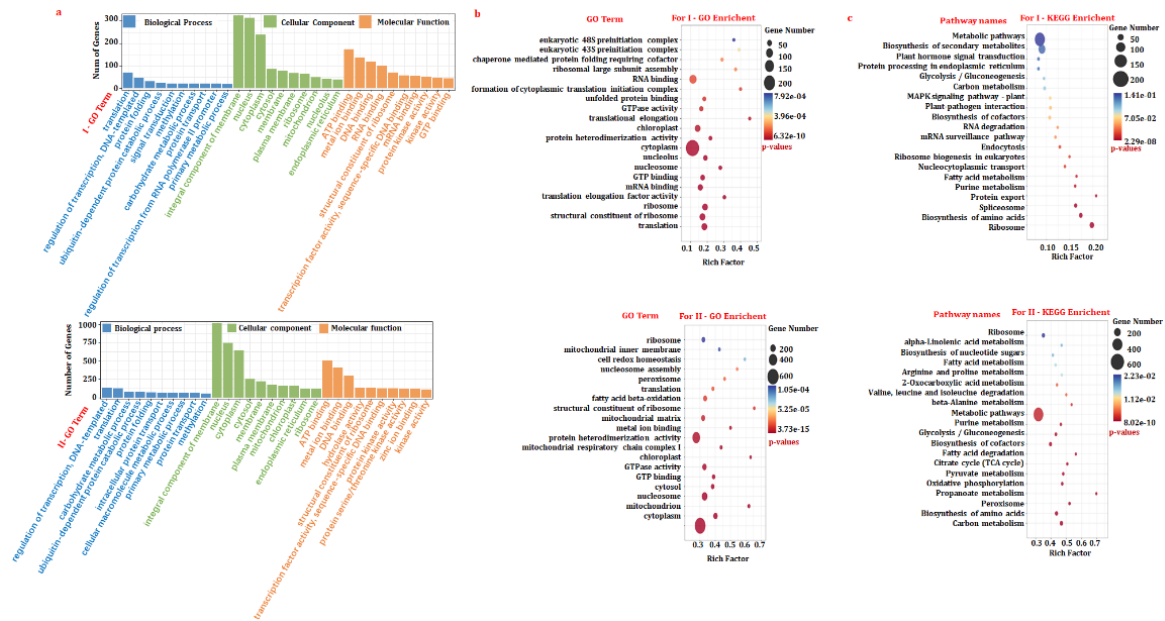


Fig. S4 Enrichment analysis of GO and KEGG for RNA-seq

Notes: For RNA-seq of 36 samples (including vp16, MP and IL; M of vp16 and high PHS of MP/IL as H, W of vp16 and low PHS of MP/IL as L). H, L, I, II represent high and low PHS, at 17DAP, 28DAP, respectively. ^aEnrichment histograms of the top ten GO term with more DEGs in three processes; ^{b,c}Scatter plots of the top twenty GO and KEGG with $p < 0.05$ and more DEGs, where the size and colour of the dots represent the number of enriched DEGs and different p-values in GO and KEGG, respectively.

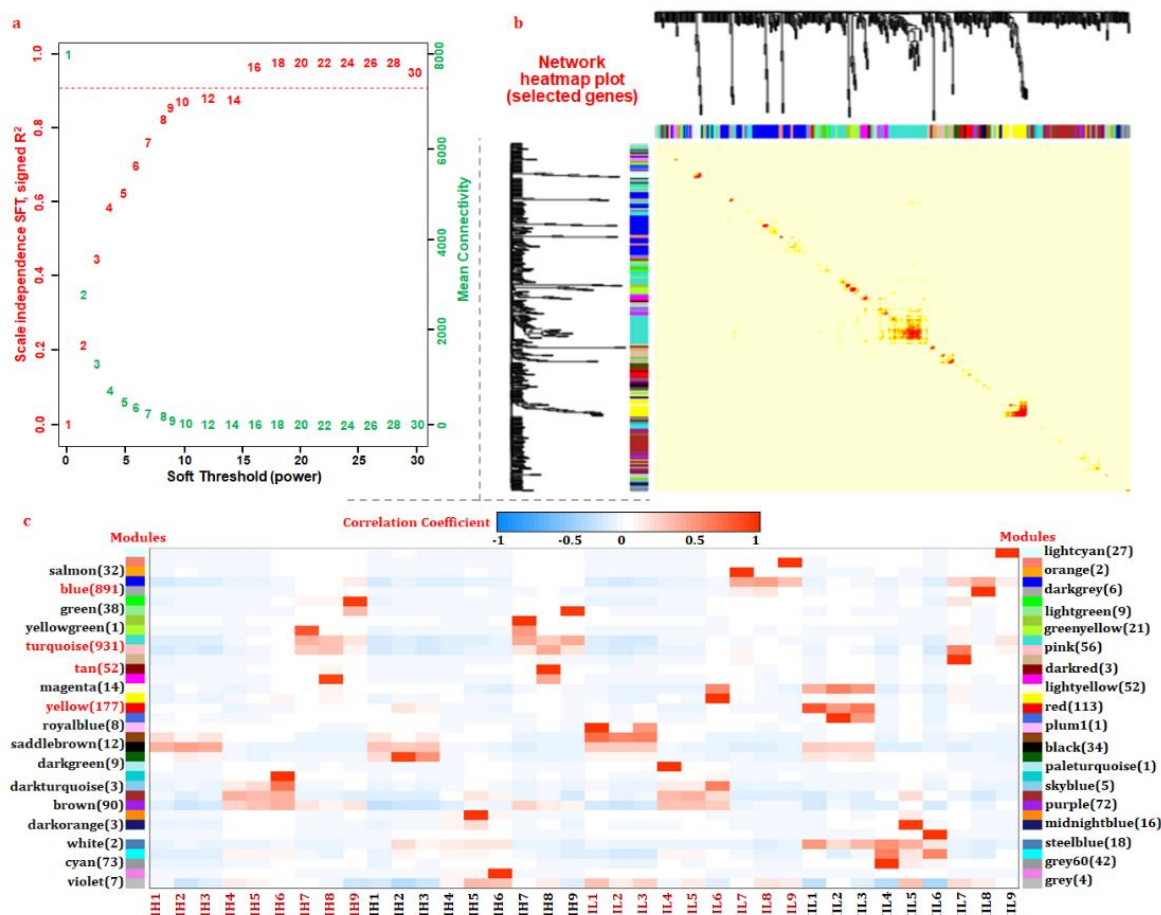


Fig. S5 Identification for modules from WGCNA of RNA-seq

Notes: ^aScale independence and mean connectivity of analysis of the network topology analysis for different soft-threshold powers. X-axis and Y-axis as a function of the soft-thresholding power, and the scale-free fit index (R^2 , threshold value = 0.9, red fonts) or mean connectivity (degree, green fonts); ^bHeatmap plot of modules by co-expression genes. The horizontal and vertical axes represent different modules. The brightness indicates the degree of correlation between modules with the topological overlap matrix (TOM). Light and dark red colours represent low and high overlap between genes, respectively. ^cA heatmap of eigengene adjacency analysis for the expression level in modules between the samples. Red, blue, and colour depth of the color indicate positive, negative, and strong or weak correlations, respectively. The modules and Numbers (red fonts) are the screening modules and their gene numbers. (Numbers), H, L, I, II, 1 – 9 represent gene numbers in modules, from high and low PHS, at 17 DAP, at 28 DAP, and different samples, respectively.

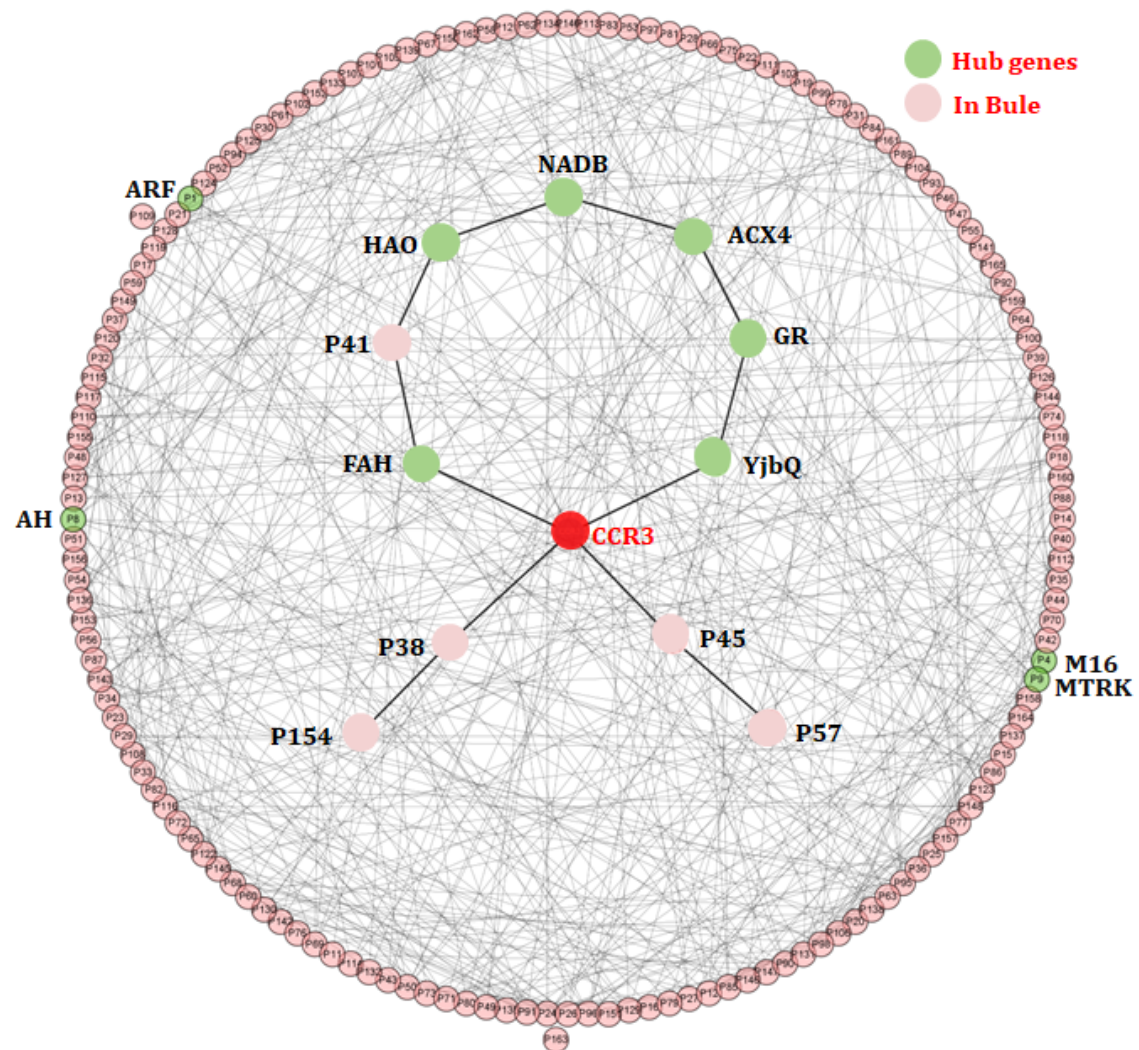


Fig S6 The *ZmCCR3* network of the Blue module with WGCNA

Note: Using [Cytoscape v3.9.0](https://cytoscape.org/) for network drawing. Names other than hub genes are listed in Table S12.

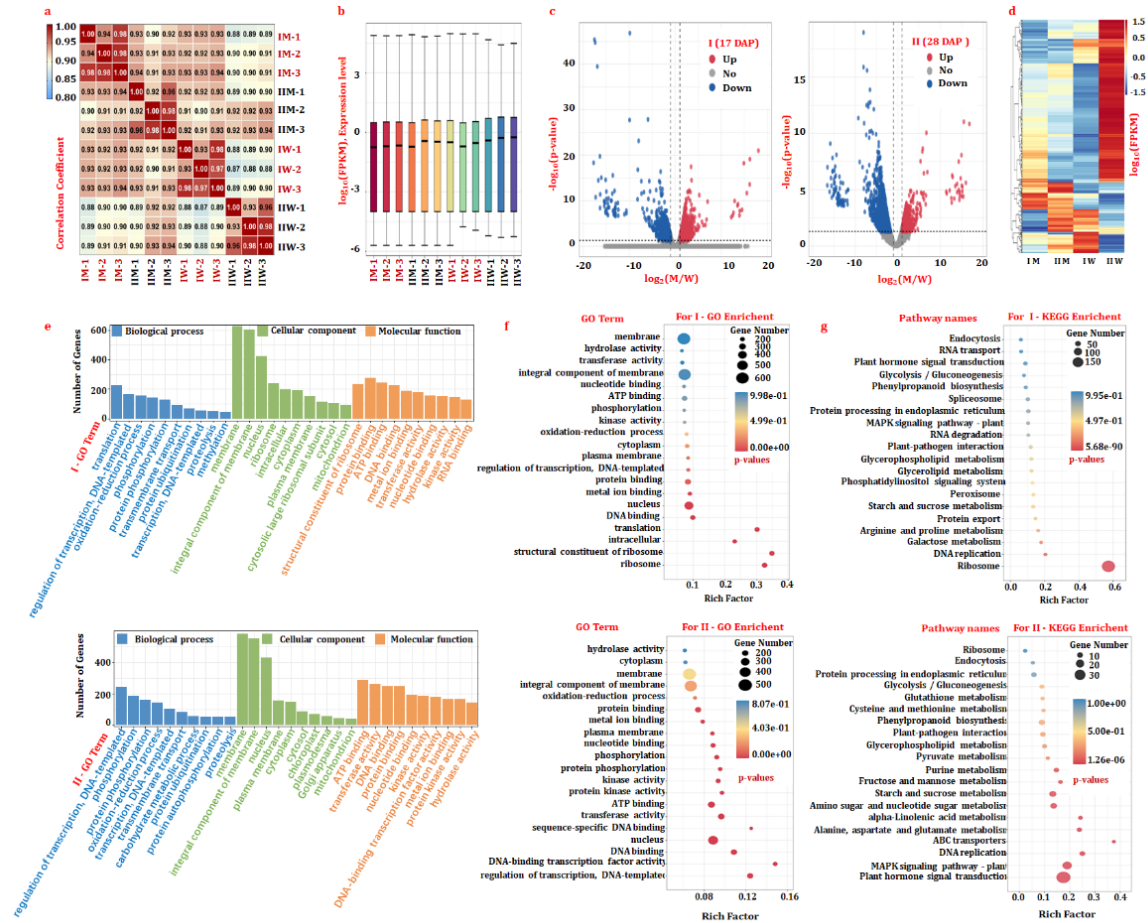


Fig. S7 The evaluation for vp16-RNA-seq and their enrichment analysis of GO and KEGG

Notes: ^aThe correlation analysis of the expression levels between samples; ^bThe variation of expression levels in samples; ^cVolcanic plots of expression levels with high (M) and low (W) PHS. M, W, I, II represent high and low PHS of vp16, at 17DAP, 28DAP, respectively; ^dVolcanic plot for cluster analysis of higher DEG levels ($|\log_2(M/W)| \geq 1$ and $p < 0.05$) in the samples; ^eEnrichment histograms of the top ten GO terms with more DEGs in three processes; ^{f,g}Scatter plots of the top twenty GO and KEGG with $p < 0.05$ and more DEGs, where the size and colour of the dots represent the number of enriched DEGs and different p -values in GO and KEGG, respectively.

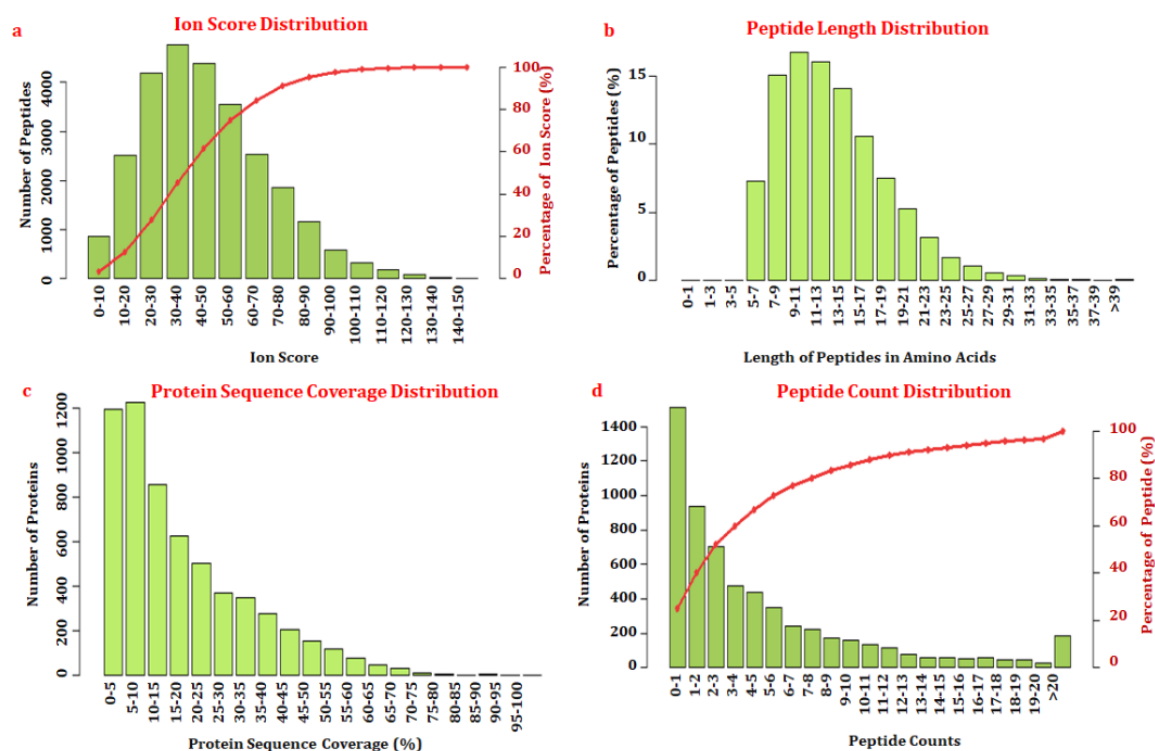


Fig. S8 Quality evaluation of vp16-iTRAQ raw data

Notes: ^aDistribution map of peptide ion scores. The horizontal axis represents the score of the MASCOT peptide segment. The number of peptides on the main vertical axis corresponds to a bar graph in the graph, indicating the number of peptides identified with corresponding ion scores. The cumulative curve on the secondary vertical axis corresponds to the cumulative percentage of peptide segments that are not higher than the corresponding ion score. The MASCOT score of MS2 is relatively ideal, with approximately 70% of peptide segments scoring above 20 and a median peptide segment score of 35; ^bDistribution map of peptide sequence length. The horizontal axis represents the number of amino acids in the identified peptide sequence. The vertical axis represents the number (percentage) of identified peptide segments; ^cDistribution map of protein sequence coverage. The horizontal axis represents the percentage of identified protein sequence coverage. The vertical axis represents the number of identified proteins; ^dDistribution map of the number of identifications per peptide segment. The horizontal axis represents the number of peptide segments used to identify proteins. The number of proteins on the main vertical axis corresponds to a bar in the graph, indicating the number of proteins corresponding to the number of peptide segments identified. The cumulative curve on the secondary vertical axis corresponds to the percentage of protein accumulation where the number of identified peptide segments does not exceed the corresponding value.

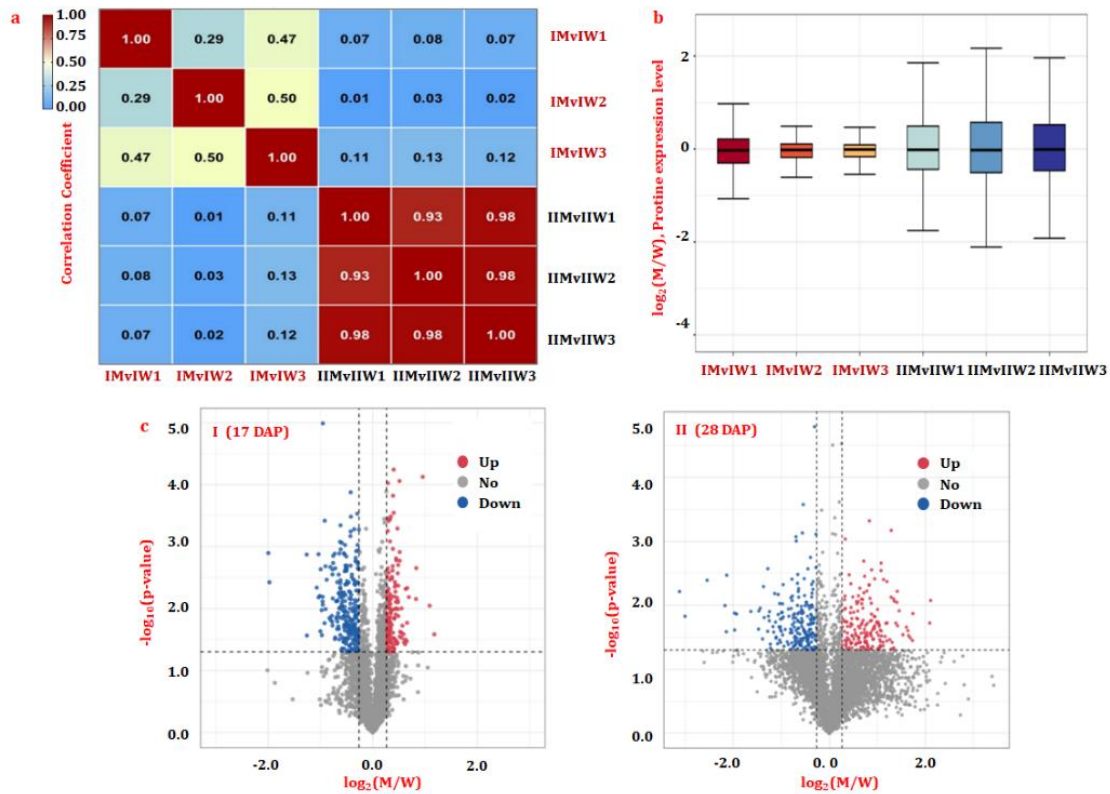


Fig. S9 Quality evaluation of peptide segments for vp16-iTRAQ

Notes: ^{a,b}Heat map for correlation analysis and variation of protein expression levels between samples by ratio as M/W(1–3), respectively. M and W are the mean of protein expression levels from three samples for the mutant and any one sample for the wild-type of vp16. 1–3 means different samples; ^cBox plot of changes in protein expression levels for all samples with ratio as M/W (1–3).

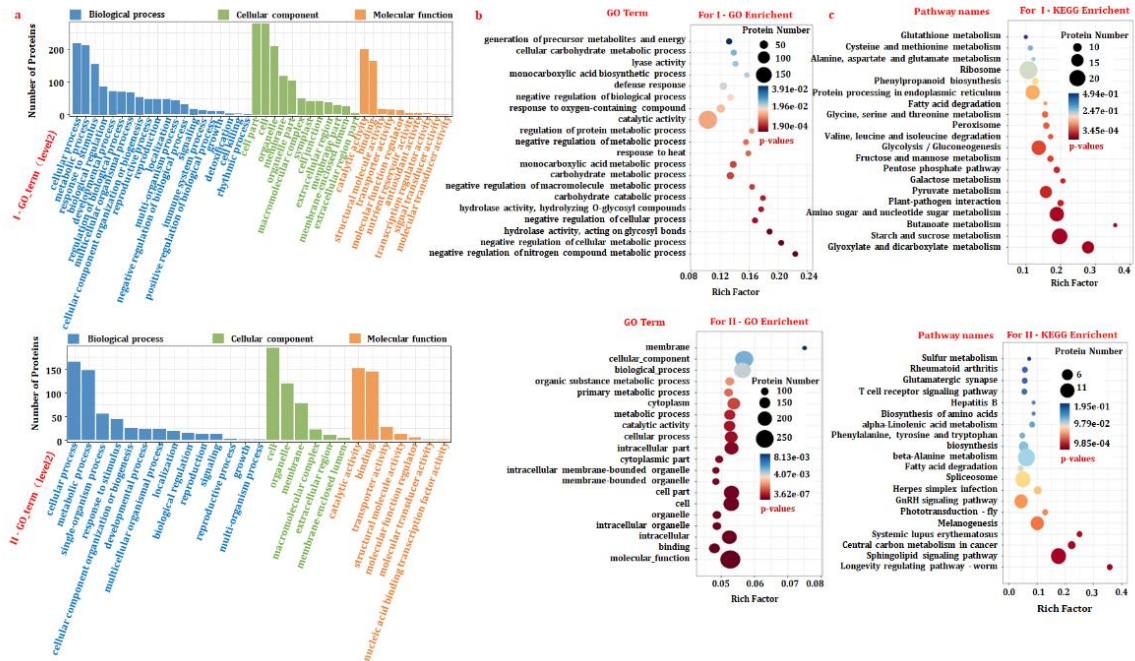


Fig. S10 Enrichment analysis of GO and KEGG for vp16-iTRAQ

1 **Notes:** ^aEnrichment histograms of GO term with more DEPs in three processes; ^{b,c}Scatter plots of the top twenty GO
2 and KEGG with $p < 0.05$ and more DEPs, where the size and colour of the dots represent the number of enriched DEPs
3 and different p-values in GO and KEGG, respectively.

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Table S1 The number of marks or transcripts on the whole genome

Chr	BSA-QTL	RNA-seq	RNA-seq vp16
Chr1	1101456	45549	15183
Chr2	1161715	37964	12655
Chr3	1087585	33131	11044
Chr4	1155286	31010	10337
Chr5	963169	35366	11789
Chr6	514797	25916	8639
Chr7	957399	24539	8180
Chr8	691462	27041	9014
Chr9	712752	22646	7549
Chr10	515754	21193	7064
Total	8861375	304355	101454
Final ^a	4225701	42130	42130

Note:^aFinally applied makers or genes.

2

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Table S2 GWAS using BLUP-PHS and SNP of IL and MP within the QTL-4^a

Locus	Pos/-log ₁₀ p	Locus	Pos/-log ₁₀ p	Locus	Pos/-log ₁₀ p	Locus	Pos/-log ₁₀ p	Locus	Pos/-log ₁₀ p
IL1	132260393/0	IL72	133523983/0.1	IL143	134034950/0.1	MP14	132655924/0.3	MP85	133776621/0
IL2	132299396/0.5	IL73	133524015/0.1	IL144	134034960/0.1	MP15	132656719/0.4	MP86	134015635/0.4
IL3	132308394/0.6	IL74	133524018/0.4	IL145	134041769/0.9	MP16	132712280/0.1	MP87	134016171/0.4
IL4	132311046/0.1	IL75	133524077/0.2	IL146	134041967/0.8	MP17	133332323/0.1	MP88	134062597/0.4
IL5	132311156/0.3	IL76	133524163/0.1	IL147	134044240/0.3	MP18	133333095/0	MP89	134062653/0.4
IL6	132353325/0.2	IL77	133524169/0.1	IL148	134074474/0.3	MP19	133333397/0	MP90	134062726/0.4
IL7	132353368/0.2	IL78	133544651/0.1	IL149	134094443/1.7	MP20	133338535/0.1	MP91	134062747/0.4
IL8	132359867/0.2	IL79	133544718/0.1	IL150	134094503/1.4	MP21	133338697/0	MP92	134062816/0.4
IL9	132362300/0.2	IL80	133566856/0.5	IL151	134094504/1.7	MP22	133338936/0.3	MP93	134062860/0.4
IL10	132362379/0.4	IL81	133571756/0.3	IL152	134094542/0.9	MP23	133501950/0.1	MP94	134079452/0
IL11	132385806/0.1	IL82	133579041/0.1	IL153	134094645/1.3	MP24	133501992/0.1	MP95	134079518/0
IL12	132386002/0	IL83	133579068/0.4	IL154	134095221/0.5	MP25	133501997/0.1	MP96	134079602/0
IL13	132398088/0	IL84	133579120/0.4	IL155	134095372/0.5	MP26	133502032/0.1	MP97	134081697/0
IL14	132446134/0.2	IL85	133582370/0.8	IL156	134095415/0.5	MP27	133502103/0.1	MP98	134081712/0
IL15	132531972/1.6	IL86	133582381/0.8	IL157	134109141/0.4	MP28	133502165/0.1	MP99	134081726/0.1
IL16	132531975/1.6	IL87	133582382/0.8	IL158	134109216/0.4	MP29	133502506/0.4	MP100	134081732/0.1
IL17	132532166/1.4	IL88	133582392/0.8	IL159	134109249/0.4	MP30	133502728/0	MP101	134081749/0
IL18	132532225/1.4	IL89	133582404/0.8	IL160	134109256/0.4	MP31	133502859/0.1	MP102	134081754/0
IL19	132532258/1.3	IL90	133582432/1.3	IL161	134109278/0.4	MP32	133505328/0.1	MP103	134081762/0
IL20	132555911/0.4	IL91	133582438/0.8	IL162	134109843/0.1	MP33	133507380/0.1	MP104	134081769/0.2
IL21	132588900/0.3	IL92	133582537/1.2	IL163	134110043/0.1	MP34	133509365/0.4	MP105	134081776/0
IL22	132639414/0.2	IL93	133582583/0.8	IL164	134110053/0.1	MP35	133509929/0.1	MP106	134081813/0.1
IL23	132639415/0.4	IL94	133582590/0.8	IL165	134119139/0.3	MP36	133510613/0.4	MP107	134191258/0.2
IL24	132639459/0.2	IL95	133584727/0.7	IL166	134138869/0.3	MP37	133512763/0.1	MP108	134191285/0
IL25	132639477/0.2	IL96	133643741/0.1	IL167	134147740/0.4	MP38	133516949/0.1	MP109	134191579/0.2
IL26	132679363/0.1	IL97	133669130/0.2	IL168	134147790/0.4	MP39	133517015/0.1	MP110	134194995/0.4
IL27	132679376/0.1	IL98	133669307/0	IL169	134147859/0.1	MP40	133517771/0.1	MP111	134195301/0.2
IL28	132679431/0.1	IL99	133669354/0.2	IL170	134148259/0.1	MP41	133517882/0.1	MP112	134205227/0.1
IL29	132681779/0.1	IL100	133688131/0.9	IL171	134148376/0.1	MP42	133518202/0.1	MP113	134205299/0
IL30	132906540/0.8	IL101	133688132/0.6	IL172	134148460/0.1	MP43	133518217/0.1	MP114	134205384/0
IL31	132906575/0.8	IL102	133688202/0.9	IL173	134159546/0.1	MP44	133518351/0	MP115	134205391/0.1
IL32	133130035/0.3	IL103	133688333/0.6	IL174	134159664/0.1	MP45	133518384/0	MP116	134205590/0
IL33	133130068/0.3	IL104	133756723/0	IL175	134165367/0.2	MP46	133618277/0	MP117	134206309/0
IL34	133130074/0.3	IL105	133756736/0	IL176	134178438/0.5	MP47	133618308/0	MP118	134206335/0.1
IL35	133160827/0.3	IL106	133756963/0.1	IL177	134178514/0.4	MP48	133618309/0	MP119	134206436/0.1
IL36	133162562/0.2	IL107	133768314/0.3	IL178	134291612/0.3	MP49	133618314/0	MP120	134206470/0.1
IL37	133162585/0.2	IL108	133768354/0.3	IL179	134291745/0.3	MP50	133618344/0	MP121	134470854/0
IL38	133162601/0.2	IL109	133786627/0.1	IL180	134409637/0.3	MP51	133618543/0	MP122	134479062/0.1
IL39	133162619/0.2	IL110	133786696/0.1	IL181	134409661/0.3	MP52	133618555/0	MP123	134484267/0.4
IL40	133273578/0.2	IL111	133786702/0.1	IL182	134409672/0.3	MP53	133618628/0.2	MP124	134485749/0.1
IL41	133273600/0.2	IL112	133786719/0.2	IL183	134487587/0.1	MP54	133618788/0.4	MP125	134485768/0.4
IL42	133283069/0	IL113	133786768/0.3	IL184	134487630/0	MP55	133623869/0	MP126	134487267/0.1
IL43	133298693/0.4	IL114	133786782/0.3	IL185	134487644/0.2	MP56	133624720/0	MP127	134487429/0.1
IL44	133310240/0.6	IL115	133786899/0.7	IL186	134487678/0	MP57	133626092/0	MP128	134487430/0.1
IL45	133316099/0	IL116	133786900/0.1	IL187	134534214/0.1	MP58	133626293/0.1	MP129	134489952/0.4
IL46	133378903/0.4	IL117	133789994/0.4	IL188	134583057/0	MP59	133626299/0.1	MP130	134490984/0.2
IL47	133378931/0.4	IL118	133789996/0.4	IL189	134583079/0	MP60	133626324/0.1	MP131	134506935/0.1

IL48	133379061/0.4	IL119	133819893/0.1	IL190	134583142/0	MP61	133626325/0.1	MP132	134507090/0.1
IL49	133381028/0.3	IL120	133830293/0.3	IL191	134583145/0	MP62	133626327/0.1	MP133	134507109/0.1
IL50	133395206/0.1	IL121	133830298/0.5	IL192	134583206/0	MP63	133719410/0.2	MP134	134581721/0.4
IL51	133395332/0.1	IL122	133834470/0.3	IL193	134583261/0	MP64	133728050/0.4	MP135	134631610/0.2
IL52	133395333/0.1	IL123	133834534/0.3	IL194	134583282/0	MP65	133773755/0.1	MP136	134790772/0.1
IL53	133395360/0.1	IL124	133834547/0.5	IL195	134793725/0.3	MP66	133773780/0.1	MP137	134790773/0.1
IL54	133395374/0.1	IL125	133834614/0.3	IL196	134884164/0.3	MP67	133773783/0	MP138	134790774/0.1
IL55	133395381/0.1	IL126	133846582/0	IL197	134884224/0.3	MP68	133773818/0.1	MP139	134790808/0.3
IL56	133421365/0.1	IL127	133846618/0	IL198	134884349/0.3	MP69	133773828/0.1	MP140	134790833/0.3
IL57	133428071/0	IL128	133846639/0	IL199	134955947/0.1	MP70	133773839/0.1	MP141	134790899/0.3
IL58	133428271/0	IL129	133846673/0	IL200	134956038/0	MP71	133773840/0.1	MP142	134792368/0.1
IL59	133428283/0.2	IL130	133887455/0.1	MP1	132181488/0.8	MP72	133773848/0.1	MP143	134792426/0.1
IL60	133499921/0.1	IL131	133974519/0.3	MP2	132305556/0.3	MP73	133773860/0.1	MP144	134796636/0.1
IL61	133499926/0.1	IL132	133979895/0.1	MP3	132307278/0.2	MP74	133773885/0.1	MP145	134796639/0.1
IL62	133499966/0.1	IL133	133979906/0.1	MP4	132314121/0.3	MP75	133773889/0.1	MP146	134796731/0.1
IL63	133500014/0.1	IL134	133979942/0.1	MP5	132315070/0.3	MP76	133773890/0.1	MP147	134796732/0.1
IL64	133500126/0.1	IL135	133979948/0.1	MP6	132315153/0.3	MP77	133773900/0	MP148	134796733/0.1
IL65	133500133/0.1	IL136	133979972/0.1	MP7	132315187/0.3	MP78	133773998/0.1	MP149	134796734/0.1
IL66	133512209/0.1	IL137	133983348/0	MP8	132315222/0.3	MP79	133774169/0	MP150	134796738/0.1
IL67	133512247/0.1	IL138	133983521/0	MP9	132315285/0.3	MP80	133775378/0.1	MP151	134796830/0.1
IL68	133513985/0.4	IL139	133996810/0.2	MP10	132315298/0.2	MP81	133776117/0	MP152	134796835/0.1
IL69	133514154/0.1	IL140	133996864/0.2	MP11	132505324/0.3	MP82	133776161/0		
IL70	133514224/0.4	IL141	134034930/0.2	MP12	132506791/0.2	MP83	133776225/0		
IL71	133523917/0.3	IL142	134034943/0.1	MP13	132551979/0.2	MP84	133776542/0.1		

Notes: *Significant SNP with threshold $> -\log_{10}p$ with bold red fonts.

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Table S3 Comparison of expression levels of genes from RNA-seq and qRT-PCR

Types	Genes (Zm00001d)	17 DAP			28 DAP		
		H4/L4	H5/L5	Mean (H/L/ $\log_2$ (H/L))	H4/L4	H5/L5	Mean (H/L/ $\log_2$ (H/L))
RNA-seq ^a	028486	3.1/3.4	3.0/10.4	3.1/6.9/-1.2	10.9/75.4	11/104.3	10.9/89.9/-3.0
	028561	7.2/21.4	7.4/24.6	7.3/23/-1.7	9.4/54.4	8.2/45.8	8.8/50.1/-2.5
	029778	24.1/74. 9	29.2/99.9	26.7/87.4/-1.7	70.3/296.4	79.6/424	74.9/360.3/-2.2
	031555	4.7/18.4	5.9/15.4	5.3/16.9/-1.7	3.9/4.1	5.2/4.7	4.6/4.4/0.1
	038810	1.4/13.9	2.8/11.6	2.1/12.8/-2.6	3.8/1.3	4.4/1.4	4.1/1.4/1.6
	047841	4.4/10.1	2.0/14.7	3.2/12.4/-1.9	47.8/118.1	44.8/138	36.2/128.2/-1.8
	048533	2.7/8.3	3.4/9.3	3.1/8.8/-1.5	17.6/11	12.3/10.5	14.9/10.8/0.5
qRT-PCR ^b	028486	1.6/4.7	1.8/2.5	1.7/3.6/-1.1	3.1/31.3	3.3/20.3	3.2/25.8/-3.0
	028561	2.8/10.1	2.9/10.8	2.9/10.5/-1.9	4.8/22.3	5.8/20.5	5.3/21.4/-2.0
	029778	4.6/8.9	4.9/11.7	4.8/10.3/-1.1	9.8/40.1	11/39.2	10.4/39.7/-1.9
	031555	3.3/11.3	3.5/13.7	3.4/12.5/-1.9	2.4/2.0	2.0/1.5	2.2/1.8/0.3
	038810	1.2/9.6	1.3/10.1	1.3/9.9/-3.0	2.5/0.8	2.6/1.2	2.6/1.0/1.4
	047841	3.2/8.7	3.0/8.9	3.1/8.8/-1.5	3.6/15.6	4.9/18.7	4.3/17.2/-2.0
	048533	2.4/9.2	2.9/9.9	2.7/9.6/-1.8	3.9/2.6	3.4/2.7	3.7/2.7/0.5

Notes: ^aThe expression level (rpkm) from high (H4, H5) low PHS (L4, L5) of RNA-seq; ^bStandardization of relative expression level with $\log_2$ (H/L). The endogenous control as GAPDH (NC_050099). $n=5$.

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Table. S4 QTL mapping and information within the QTL by BSA-QTL sequencing

№	Chr	Pos (start/end)	Size (Mb)	Makers (SNP) ^a	Gene/mRNA/ mRNA Anno ^a
QTL-1	5	82,829,049/84,911,624	2.08	10,734	16/39/19
QTL-2	5	89,184,504/91,814,692	2.63	10,914	17/62/40
QTL-3	5	115,198,443/117,727,347	2.53	12,536	6/83/81
QTL-4	5	132,101,517/134,997,331	2.89	20,210	31/39/11
QTL-5	5	135,279,253/138,583,667	3.30	21,845	12/35/29
QTL-6	5	142,619,322/145,036,227	2.42	14,512	19/44/35
QTL-7	5	148,242,481/150,242,481	2.00	10,988	12/24/22

Note:^aNumbers.

Table S5 Verification of the *Zmccr3* locus using joint BSA-QTL and RNA-seq analysis

Nº	Chr	Gene (Zm00001d)	log ₂ (H/L) I/II ^a	ΔSNP ^b	Nº	Chr	Gene (Zm00001d)	log ₂ (H/L) I/II ^a	ΔSNP ^b
1	1	029934	1.1/5.9	0.7	52	5	016076	0.7/1.9	0.7
2	1	031810	0.9/1.2	0.7	53	5	016082	1.1/2.5	0.8
3	3	044674	0.8/0.9	0.7	54	5	016091	0.5/1.4	0.8
4	4	049349	1.5/2.5	0.8	55	5	016103	9.8/3.8	0.8
5	5	016070	1.4/1.5	0.8	56	5	016128	2.4/4.1	0.7
6	5	014084	0.6/0.4	0.7	57	5	016136	0.8/0.9	0.8
7	5	014413	1.0/0.6	0.7	58	5	016142	0.8/3.3	0.8
8	5	014418	1.2/1.8	0.7	59	5	016160	9.8/12.2	0.8
9	5	014455	12.7/9.6	0.7	60	5	016166	0.6/1.1	0.7
10	5	014459	1.4/2.0	0.7	61	5	016181	1.6/1.1	0.7
11	5	014625	1.6/1.7	0.7	62	5	016193	1.0/0.6	0.8
12	5	014967	0.8/0.8	0.7	63	5	016197	0.5/1.8	0.8
13	5	014971	8.5/11.8	0.7	64	5	016198	1.1/1.8	0.8
14	5	015164	1.0/1.4	0.8	65	5	016256	15.5/0.6	0.7
15	5	015196	0.6/1.3	0.7	66	5	016285	9.9/1.5	0.7
16	5	015202	0.9/2.2	0.7	67	5	016365	0.5/1.1	0.8
17	5	015213	0.6/1.7	0.7	68	5	016409	2.7/2.6	0.8
18	5	015229	0.5/1.0	0.7	69	5	016438	0.7/2.1	0.8
19	5	015233	1.8/0.6	0.8	70	5	016459	0.7/0.8	0.8
20	5	015243	1.8/1.7	0.7	71	5	016465	1.0/0.5	0.8
21	5	015272	0.6/1.0	0.8	72	5	016473	1.6/3.4	0.8
22	5	015307	1.2/5.4	0.7	73	5	016479	0.6/0.4	0.8
23	5	015310	1.3/3.7	0.7	74	5	016491	0.8/1.4	0.8
24	5	015313	0.4/0.6	0.7	75	5	016505	0.5/1.9	0.8
25	5	015326	1.2/1.9	0.7	76	5	016529	0.8/0.5	0.7
26	5	015342	1.2/0.7	0.7	77	5	016544	0.8/0.9	0.7
27	5	015344	1.2/1.3	0.7	78	5	016586	1.1/1.3	0.7
28	5	015348	0.6/1.7	0.7	79	5	016588	2.1/0.6	0.7
29	5	015349	12.2/11.9	0.7	80	5	016590	0.5/1.2	0.8
30	5	015362	0.4/1.1	0.8	81	5	016591	0.8/0.7	0.7
31	5	015394	11.6/5.2	0.8	82	5	016648	1.5/1.2	0.8
32	5	015395	1.5/0.9	0.8	83	5	016674	1.5/2.2	0.8
33	5	015401	1.3/0.5	0.8	84	5	016683	2.0/1.2	0.8
34	5	015407	10.2/1.4	0.8	85	5	016692	8.7/9.7	0.7
35	5	015433	0.4/0.9	0.8	86	5	016693	9.7/1.2	0.8
36	5	015446	0.9/0.6	0.8	87	5	016746	0.9/0.5	0.8
37	5	015459	0.4/2.2	0.8	88	5	016766	1.3/0.6	0.8
38	5	015469	1.1/0.7	0.8	89	5	016767	0.9/1.3	0.8
39	5	015520	0.4/0.7	0.8	90	5	016786	1.1/1.4	0.8
40	5	015603	0.8/0.8	0.7	91	5	016806	2.8/1.0	0.7
41	5	015611	3.1/3.3	0.7	92	5	016853	0.7/0.7	0.7
42	5	015618	1.8/0.8	0.7	93	5	016898	1.3/1.0	1.0
43	5	015627	0.7/1.3	0.7	94	5	016941	0.4/0.7	0.7
44	5	015737	4.9/2.6	0.8	95	5	016963	1.8/2.8	0.7
45	5	015746	0.5/0.5	0.8	96	5	017165	0.6/0.6	0.9
46	5	015921	1.1/0.8	0.7	97	5	017202	9.0/0.6	0.9
47	5	015956	0.5/1.1	0.8	98	5	017208	2.0/2.3	0.7
48	5	015964	7.5/2.5	0.8	99	5	017251	2.0/2.0	0.7
49	5	015969	0.8/2.4	0.8	100	5	017280	0.4/1.0	0.7
50	5	015999	0.8/0.5	0.9	101	5	017288	0.9/1.9	0.8
51	5	016001	7.9/1.7	0.9	102	5	017618	1.8/2.3	0.8

Notes: ^aThe threshold is $\text{abs}(\log_2(\text{H/L})) = 0.4$ from RNA-seq of 36 samples with high (H) and low (L) PHS at I (17 DAP) and II (28 DAP); ^bThe threshold is $\text{abs}(\Delta\text{SNP} \pm 3\delta) = 0.7$ from BSA-QTL with ΔSNP = high (H) PHS-index - low (L) PHS-index. δ is total standard error of high (H) PHS-index or low (L) PHS-index.

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Table S6 Genes within the QTL-4 by BSA-QTL

Gene ID (Zm00001d)	Chr: start (B73 RefGen v4)	Description
015929	5: 132179761	GTP-binding protein TypA
015930	5: 132526412	Histone-lysine N-methyltransferase ATXR3
015932	5:132599003	Chromatin modification-related protein EAF3
015934	5:132637131	Pectinesterase
015935	5:132680687	Myb/SANT-like domain-containing protein
015936	5:132744051	Defensin-like protein 6
015939	5:132838540	Pre-mRNA-processing factor 19
015940	5:132980009	GB1/RHD3-type G domain-containing protein
015941	5:132982333	Guanylate-binding family protein
015942	5:132983723	Guanylate-binding family protein
015943	5:132990124	HAT C-terminal dimerisation domain-containing protein
015944	5:133071580	Selenoprotein F/M domain-containing protein
015945	5:133441549	Topless-related protein 2
015947	5:133563180	Craniofacial development protein 2
015948	5:133565009	ATP-dependent Clp protease ATP-binding subunit clpX
015949	5:133613890	ClpA/ClpB AAA lid domain-containing protein
015950	5:133617183	Cytokinin dehydrogenase 6
015951	5:133630615	Serine/threonine-protein kinase Nek1
015952	5:133821714	RING-type E3 ubiquitin transferase
015955	5:133998288	Amelogenin super family
015956	5:134163807	Cinnamoyl-CoA reductase
015957	5:134188430	Acyl-CoA-binding domain-containing protein 3
015960	5:134287992	SGNH hydrolase-type esterase superfamily protein
015961	5:134439009	Mediator of RNA polymerase II transcription subunit 33A
015962	5:134444332	Prolyl oligopeptidase family protein
015963	5:134455335	Protein DETOXIFICATION
015964	5:134537160	Protein DETOXIFICATION
015965	5:134675256	Tyrosine specific protein phosphatase-like
015968	5:134792393	Lysine ketoglutarate reductase trans-splicing protein
015969	5:134894335	IQ-domain 21
015970	5:134952929	Protein kish

Table S7 The primer sequences used in this study

Types	Name	Forward/reverse primers (5'-3')
QTL-makers	C1	CCAAACCCCTACAGAACCGC/CGGCAGCCGTTACATGAGAG
	C13	AGGAGGGAGAGGAAGAGAGGT/TCCCTCTTCACTCTCCTCCCT
	C14	TGTCCCAGTCGAGATGGGTC/CGATGCACAAGGCTCACACT
	C19 ^a	TCTGCGAGTGGGGAAAATGG/ACACTCTAACCTCCGGTCCG
	C23 ^a	GAAACCGAGCGTGGGGATG/GTGCAAGCTCGCTCTCTCTC
	C29	CCATGCCATGGTACGGTGC/CGTCACTTACGCACACGGTA
gDNA (ZmCC R3)	56-1	GCAAAGTCTTCTTCTTCATCC/CCCTGAAGGGCACGTAAGTT
	56-2	GTTCCCGTCTGCTGCTAGAT/TTCGGACCCCATTCCTGTT
	56-3	AGGGAAGACGTGCTGCATAA/ACCACATTTGTAAGCAACGATCA
cDNA (ZmCC R3)	c56-1	AGTAGGTAGATGATGCCGC/AGCCATAGATGATGTTACAACC
	c56-2	ACCCAGATCTTCGTCCTGTC/ACAAACGGCTTGTCATCTGC
	c56-3	ATGTTGCCCTGGCCCATATC/CGTGTCTCAATCCGATCAAAGC
qRT-PCR for validating of RNA-seq (Zm00001d)	028486	CTTTTAGCGGCGAGAGACTG/GATGGGTGGAGAGAACGTGT
	028561	AACAAGGAGCACGAGGAGAA/TGATCTGGACGTTCTTGACG
	029778	CTGTAGACCTTGGGGCTCTG/CGATCGACGCCTCTTAATTT
	031555	ACTCATGGGATCCTGAATGC/ACAGGTTTCCGAGATGGATG
	038810	AACTTCAAGCAGGTCGTCCA/AGGTTGTTCTTGCCGATCC
	047841	AGCAGCCAAGAAAAGCACAT/AAGGGAAATAAGCCCTGGAA
	048533	GAAGCGCCTCTTCCAAGC/AGCTGAGCACCATGTTTCGT
	049641	CGGCATTGTTGAGGGTTTGA/ACAACCGAGACATCCACAGT
qRT-PCR for validating of RNA-seq and iTRAQ (Zm00001d)	009296	CACCCTTCCTACTCTGA/GTTTCTCGTCTACCCAC
	016128	GCAGCAGGCAGCCGTGAAGG/CGCCATGTCGCCGGTGGT
	021024	GGAGCCTCCGAAAGAGGAGCATC/ACGAGTTGGTCCCCTTCAAGAAGTG
	021702	CGTTGTGGACATTGAGGTGGG/TGCTGCTTTGAAGTCTGCTTGC
	023811	CGGCAGCGTTACCACCATG/AGCACCTCCGTCTCACCA
	024753	CGCCTCAATCCTCATCAACT/CACCTCGTCTTGTCTGGAACT
	026037	GTGAAGGAGGGGTCGGCAAAGATG/GCGGCGTCCGCTCGGTG
	028408	CGCAGGAGAACAGGGACAACA/GGCGACATCGGGTCAACTAAT
	031158	GGCAGCCAGGACTTCTAC/GGCAGCCAGGACTTCTAC
	032019	CGAGGAAGGGCAACACATT/TTCAGTATGGTCAGGAAGAGCAA
	037894	CGAGCACACAAGCACGAA/CCGACTGGGTTGCCGTA
	038870	GGCTTCCCACCAGGACAAG/GTGTGCGGACGCCTTCTGCT
	048050	CAAAGCGAGGACGGTGAA/GTCGGGGTGGCTGAAAAC
	050032	TTCCCTCAACCGTCACCTCTC/TGCTCCTCAAACAACCACAAG

^aZmCCR3 in C19 – C23 with ~170 Kb.

Table S8 Candidate mutation locus and genes within vp16-QTL1 – 7 from BSA-QTL

№	Chr	Δ SNP _a	ID ^b	№	Chr	Δ SNP _a	ID ^b	№	Chr	Δ SNP _a	Gene ID ^b
1	1	0.7	029934	190	5	0.7	015603	379	5	0.7	016286
2	1	0.8	030323	191	5	0.7	015611	380	5	0.7	016349
3	1	0.7	031810	192	5	0.8	015611	381	5	0.7	016349
4	3	0.7	044674	193	5	0.8	015618	382	5	0.7	016349
5	4	0.7	049349	194	5	0.7	015627	383	5	0.7	016349
6	4	0.7	049349	195	5	0.9	015638	384	5	0.7	016349
7	4	0.7	049349	196	5	0.7	015638	385	5	0.8	016350
8	4	0.7	049349	197	5	0.7	015685	386	5	0.7	016350
9	5	0.7	013859	198	5	0.8	015733	387	5	0.7	016351
10	5	0.7	014084	199	5	0.9	015737	388	5	0.7	016351
11	5	0.7	014084	200	5	0.8	015746	389	5	0.7	016351
12	5	0.7	014093	201	5	0.7	015754	390	5	0.7	016351
13	5	0.7	014207	202	5	0.8	015770	391	5	0.7	016351
14	5	0.7	014308	203	5	0.8	015814	392	5	0.7	016351
15	5	0.7	014308	204	5	0.7	015901	393	5	0.7	016351
16	5	0.7	014413	205	5	0.8	015905	394	5	0.7	016351
17	5	0.8	014418	206	5	0.8	015921	395	5	0.7	016354
18	5	0.8	014418	207	5	0.8	015921	396	5	0.7	016354
19	5	0.8	014455	208	5	0.7	015921	397	5	0.7	016354
20	5	0.8	014455	209	5	0.8	015921	398	5	0.7	016358
21	5	0.8	014455	210	5	0.7	015921	399	5	0.8	016361
22	5	0.7	014455	211	5	0.7	015943	400	5	0.7	016361
23	5	0.7	014459	212	5	0.7	015948	401	5	0.8	016361
24	5	0.7	014625	213	5	0.8	015948	402	5	0.8	016361
25	5	0.7	014874	214	5	0.7	015948	403	5	0.8	016361
26	5	0.8	014963	215	5	0.8	015956	404	5	0.8	016361
27	5	0.8	014967	216	5	0.8	015956	405	5	0.8	016361
28	5	0.8	014967	217	5	0.9	015956	406	5	0.8	016361

29	5	0.7	01496 7	218	5	0.8	01595 6	407	5	0.7	016361
30	5	0.8	01497 0	219	5	0.8	01595 6	408	5	0.8	016361
31	5	0.7	01497 0	220	5	0.8	01595 6	409	5	0.8	016361
32	5	0.8	01497 1	221	5	0.8	01595 6	410	5	0.8	016361
33	5	0.9	01497 1	222	5	0.8	01595 6	411	5	0.8	016361
34	5	0.7	01497 2	223	5	0.7	01595 6	412	5	0.9	016365
35	5	0.8	01516 4	224	5	0.8	01595 6	413	5	0.8	016365
36	5	0.8	01516 4	225	5	0.7	01595 6	414	5	0.8	016365
37	5	0.8	01516 4	226	5	0.7	01595 6	415	5	0.7	016365
38	5	0.8	01516 4	227	5	0.7	01595 6	416	5	0.8	016365
39	5	0.8	01516 4	228	5	0.8	01595 6	417	5	0.9	016365
40	5	0.8	01516 4	229	5	0.8	01595 6	418	5	0.7	016365
41	5	0.8	01516 4	230	5	0.8	01595 6	419	5	0.7	016365
42	5	0.8	01516 4	231	5	0.9	01595 6	420	5	0.7	016365
43	5	0.8	01516 4	232	5	0.8	01595 6	421	5	0.8	016374
44	5	0.8	01516 4	233	5	0.7	01595 6	422	5	0.9	016374
45	5	0.8	01516 4	234	5	0.7	01595 6	423	5	0.8	016381
46	5	0.7	01517 4	235	5	0.8	01595 6	424	5	0.7	016395
47	5	0.8	01517 4	236	5	0.9	01595 6	425	5	0.7	016395
48	5	0.8	01517 4	237	5	0.9	01595 6	426	5	0.7	016395
49	5	0.8	01517 4	238	5	0.9	01595 6	427	5	0.8	016395
50	5	0.8	01519 6	239	5	0.9	01595 6	428	5	0.8	016395
51	5	0.7	01520 2	240	5	0.9	01595 6	429	5	0.7	016406
52	5	0.7	01521 0	241	5	0.8	01595 6	430	5	0.7	016406
53	5	0.7	01521 0	242	5	0.7	01596 0	431	5	0.8	016407
54	5	0.8	01521 2	243	5	0.8	01596 0	432	5	0.7	016407
55	5	0.7	01521 2	244	5	0.7	01596 3	433	5	0.7	016407
56	5	0.7	01521 2	245	5	0.7	01596 3	434	5	0.8	016407
57	5	0.9	01521 3	246	5	0.7	01596 4	435	5	0.7	016407
58	5	0.8	01521 3	247	5	0.8	01596 9	436	5	0.7	016409

59	5	0.7	01521 3	248	5	0.7	01596 9	437	5	0.7	016438
60	5	0.8	01522 3	249	5	0.8	01596 9	438	5	0.7	016438
61	5	0.7	01522 3	250	5	0.7	01597 7	439	5	0.7	016438
62	5	0.8	01522 3	251	5	0.7	01597 7	440	5	0.9	016438
63	5	0.7	01522 5	252	5	0.8	01597 7	441	5	0.7	016438
64	5	0.7	01522 9	253	5	0.8	01597 7	442	5	0.8	016438
65	5	0.8	01523 3	254	5	0.7	01598 2	443	5	0.7	016438
66	5	0.8	01523 3	255	5	0.7	01598 4	444	5	0.7	016439
67	5	0.8	01523 3	256	5	0.7	01598 9	445	5	0.7	016439
68	5	0.8	01523 3	257	5	0.7	01599 0	446	5	0.7	016439
69	5	0.8	01523 3	258	5	0.8	01599 9	447	5	0.7	016459
70	5	0.8	01523 3	259	5	0.7	01600 1	448	5	0.7	016463
71	5	0.8	01523 3	260	5	0.8	01600 8	449	5	0.7	016463
72	5	0.8	01524 3	261	5	0.8	01600 8	450	5	0.7	016465
73	5	0.7	01524 3	262	5	0.8	01600 8	451	5	0.9	016472
74	5	0.7	01524 3	263	5	0.8	01600 8	452	5	0.8	016472
75	5	0.7	01524 3	264	5	0.7	01600 8	453	5	0.7	016473
76	5	0.8	01525 2	265	5	0.8	01600 9	454	5	0.7	016473
77	5	0.9	01525 8	266	5	0.7	01600 9	455	5	0.8	016475
78	5	1	01525 8	267	5	0.8	01600 9	456	5	0.7	016476
79	5	1	01525 8	268	5	0.7	01601 3	457	5	0.8	016479
80	5	1	01525 8	269	5	0.7	01601 3	458	5	0.7	016479
81	5	0.7	01525 8	270	5	0.8	01601 3	459	5	0.7	016479
82	5	0.7	01526 9	271	5	0.8	01601 3	460	5	0.8	016483
83	5	0.9	01527 2	272	5	0.8	01601 3	461	5	0.9	016483
84	5	0.7	01527 2	273	5	0.8	01601 3	462	5	0.8	016483
85	5	0.7	01527 2	274	5	0.7	01601 3	463	5	0.7	016483
86	5	0.7	01527 2	275	5	0.7	01601 3	464	5	0.7	016483
87	5	0.8	01527 2	276	5	0.7	01601 3	465	5	0.7	016483
88	5	0.8	01527 9	277	5	0.8	01601 3	466	5	0.8	016486

89	5	0.8	01530 7	278	5	0.8	01601 3	467	5	0.7	016486
90	5	0.7	01530 7	279	5	0.7	01601 3	468	5	0.7	016486
91	5	0.7	01531 0	280	5	0.7	01601 4	469	5	0.7	016491
92	5	0.7	01531 0	281	5	0.7	01601 9	470	5	0.7	016505
93	5	0.7	01531 3	282	5	0.9	01601 9	471	5	0.9	016520
94	5	0.7	01531 3	283	5	0.8	01601 9	472	5	0.7	016528
95	5	0.7	01531 4	284	5	0.8	01601 9	473	5	0.7	016528
96	5	0.7	01531 4	285	5	0.7	01603 1	474	5	0.9	016528
97	5	0.7	01531 9	286	5	0.8	01605 6	475	5	0.8	016529
98	5	0.7	01532 5	287	5	0.8	01605 6	476	5	0.7	016542
99	5	0.8	01532 6	288	5	0.8	01605 6	477	5	0.7	016544
100	5	0.8	01532 6	289	5	0.7	01605 6	478	5	0.8	016557
101	5	0.7	01532 6	290	5	0.8	01607 0	479	5	0.8	016557
102	5	0.7	01532 6	291	5	0.7	01607 0	480	5	0.7	016557
103	5	0.7	01532 7	292	5	0.8	01607 0	481	5	0.7	016559
104	5	0.8	01532 8	293	5	0.8	01607 6	482	5	0.7	016565
105	5	0.8	01532 8	294	5	0.7	01608 1	483	5	0.8	016586
106	5	0.8	01534 2	295	5	0.8	01608 1	484	5	0.7	016586
107	5	0.8	01534 4	296	5	0.7	01608 1	485	5	0.7	016586
108	5	0.8	01534 4	297	5	0.7	01608 1	486	5	0.7	016587
109	5	0.7	01534 4	298	5	0.7	01608 2	487	5	0.7	016587
110	5	0.8	01534 7	299	5	0.8	01608 2	488	5	0.8	016588
111	5	0.8	01534 7	300	5	0.8	01608 2	489	5	0.7	016590
112	5	0.7	01534 7	301	5	0.7	01608 2	490	5	0.7	016591
113	5	0.7	01534 8	302	5	0.7	01608 2	491	5	0.8	016595
114	5	0.8	01534 9	303	5	0.7	01608 2	492	5	0.8	016611
115	5	0.7	01534 9	304	5	0.7	01608 2	493	5	0.7	016611
116	5	0.7	01535 5	305	5	0.7	01608 2	494	5	0.7	016611
117	5	0.7	01535 5	306	5	0.7	01608 2	495	5	0.7	016619
118	5	0.7	01535 6	307	5	0.8	01608 5	496	5	0.7	016619

119	5	0.7	01536 1	308	5	0.7	01609 1	497	5	0.7	016619
120	5	0.7	01536 1	309	5	0.7	01609 5	498	5	0.7	016634
121	5	0.7	01536 2	310	5	0.8	01609 5	499	5	0.7	016648
122	5	0.7	01536 2	311	5	0.8	01609 5	500	5	0.8	016648
123	5	0.7	01539 4	312	5	0.8	01609 5	501	5	0.7	016648
124	5	0.7	01539 5	313	5	0.8	01609 5	502	5	0.8	016653
125	5	0.7	01539 5	314	5	0.7	01610 3	503	5	0.8	016653
126	5	0.7	01539 9	315	5	0.7	01610 3	504	5	0.8	016653
127	5	0.7	01540 1	316	5	0.7	01610 6	505	5	0.7	016659
128	5	0.9	01540 7	317	5	0.8	01610 6	506	5	0.7	016674
129	5	0.8	01541 5	318	5	0.7	016119	507	5	0.7	016675
130	5	0.8	01543 3	319	5	0.8	016119	508	5	0.7	016683
131	5	0.7	01543 3	320	5	0.8	016119	509	5	0.7	016686
132	5	0.7	01543 3	321	5	0.7	01612 8	510	5	0.7	016686
133	5	0.7	01544 0	322	5	0.7	01612 8	511	5	0.7	016687
134	5	0.7	01544 0	323	5	0.7	01612 8	512	5	0.8	016687
135	5	0.7	01544 0	324	5	0.7	01612 8	513	5	0.7	016692
136	5	0.7	01544 0	325	5	0.7	01612 8	514	5	0.7	016693
137	5	0.7	01544 0	326	5	0.7	01612 8	515	5	0.7	016694
138	5	0.8	01544 6	327	5	0.7	01613 1	516	5	0.7	016695
139	5	0.8	01544 6	328	5	0.7	01613 1	517	5	0.7	016695
140	5	0.8	01544 6	329	5	0.8	01613 1	518	5	0.7	016695
141	5	0.8	01544 6	330	5	0.8	01613 1	519	5	0.7	016695
142	5	0.7	01544 6	331	5	0.9	01613 6	520	5	0.7	016735
143	5	0.8	01544 6	332	5	0.8	01613 6	521	5	0.8	016735
144	5	0.8	01544 6	333	5	0.7	01613 9	522	5	0.8	016746
145	5	0.8	01544 6	334	5	0.7	01613 9	523	5	0.7	016746
146	5	0.8	01544 6	335	5	0.7	01613 9	524	5	0.7	016746
147	5	0.7	01544 6	336	5	0.8	01614 2	525	5	0.7	016766
148	5	0.8	01544 6	337	5	0.9	01614 2	526	5	0.7	016766

149	5	0.7	01544 6	338	5	0.7	01615 4	527	5	0.8	016767
150	5	0.7	01544 8	339	5	0.7	01616 0	528	5	0.7	016786
151	5	0.8	01545 9	340	5	0.7	01616 0	529	5	0.7	016788
152	5	0.9	01545 9	341	5	0.8	01616 0	530	5	0.7	016788
153	5	0.8	01545 9	342	5	0.7	01616 0	531	5	0.7	016791
154	5	0.7	01545 9	343	5	0.7	01616 6	532	5	0.8	016791
155	5	0.7	01545 9	344	5	0.8	01618 1	533	5	0.7	016793
156	5	0.7	01546 0	345	5	0.9	01618 1	534	5	0.7	016806
157	5	0.7	01546 0	346	5	0.9	01618 1	535	5	0.7	016838
158	5	0.7	01546 0	347	5	0.7	01618 1	536	5	0.7	016853
159	5	0.7	01546 0	348	5	0.7	01618 1	537	5	0.8	016860
160	5	0.8	01546 1	349	5	0.8	01619 3	538	5	0.8	016866
161	5	0.7	01546 1	350	5	0.8	01619 3	539	5	0.7	016874
162	5	0.8	01546 1	351	5	0.7	01619 3	540	5	0.7	016898
163	5	0.8	01546 1	352	5	0.8	01619 7	541	5	0.7	016898
164	5	0.7	01546 4	353	5	0.8	01619 8	542	5	0.7	016898
165	5	0.7	01546 4	354	5	0.7	01619 8	543	5	0.7	016898
166	5	0.7	01546 4	355	5	0.7	01619 8	544	5	0.7	016934
167	5	0.7	01546 4	356	5	0.7	01622 3	545	5	0.7	016941
168	5	0.7	01546 4	357	5	0.7	01622 3	546	5	0.8	016963
169	5	0.8	01546 9	358	5	0.7	01622 3	547	5	0.8	016979
170	5	0.8	01546 9	359	5	0.7	01622 5	548	5	0.8	016980
171	5	0.8	01546 9	360	5	0.7	01623 2	549	5	0.7	017030
172	5	0.8	01546 9	361	5	0.7	01623 2	550	5	0.7	017110
173	5	0.8	01546 9	362	5	0.8	01623 2	551	5	0.7	017165
174	5	0.8	01546 9	363	5	0.8	01623 2	552	5	0.8	017165
175	5	0.7	01547 7	364	5	0.8	01623 2	553	5	0.7	017202
176	5	0.8	01549 5	365	5	0.9	01624 2	554	5	0.7	017202
177	5	0.7	01549 5	366	5	0.7	01624 2	555	5	0.7	017208
178	5	0.8	01549 5	367	5	0.8	01625 6	556	5	0.7	017208

179	5	0.7	01550 5	368	5	0.7	01625 9	557	5	0.8	017208
180	5	0.8	01551 5	369	5	0.8	01626 8	558	5	0.7	017208
181	5	0.9	01551 5	370	5	0.8	01626 8	559	5	0.7	017212
182	5	0.8	01552 0	371	5	0.8	01626 8	560	5	0.7	017212
183	5	0.7	01552 1	372	5	0.8	01626 8	561	5	0.7	017249
184	5	0.7	01552 1	373	5	0.7	01627 4	562	5	0.7	017251
185	5	0.8	01559 5	374	5	0.7	01627 4	563	5	0.7	017280
186	5	0.8	01560 2	375	5	0.8	01628 5	564	5	0.7	017280
187	5	0.7	01560 2	376	5	0.8	01628 5	565	5	0.7	017288
188	5	0.7	01560 2	377	5	0.7	01628 6	566	5	0.8	017618
189	5	0.7	01560 2	378	5	0.7	01628 6	567	9	0.7	046700

Notes: ^aThe threshold is $\text{abs}(\Delta\text{SNP} \pm 3\delta) = 0.7$ from BSA-QTL with ΔSNP = high (H) PHS-index - low (L) PHS-index. δ is total standard error of high (H) PHS-index or low (L) PHS-index; ^bAdd Zm00001d before numbers.

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Table S9 Gene expression using RNA-seq of vp16 within the QTL-4^a

№	Gene ID (Zm00001d)	Chr:start	M (rpkm)/W (rpkm)/log ₂ (M/W)	
			17 DAP	28 DAP
1	015929	5:132179761	1.6/1.8/-0.2	2/3.8/-0.9
2	015930	5:132526412	0/0/0	0/0/0
3	015932	5:132599003	13.7/14/0	20.4/20.7/0
4	015934	5:132637131	0.4/0.2/1.4	0.5/1.4/-1.6
5	015935	5:132680687	0/0/0	0/0/0
6	015936	5:132744051	0/0/0	0/0/0
7	015939	5:132838540	0/0/0	0/0/0
8	015940	5:132980009	0/0.5/-12.3	0/0/0
9	015941	5:132982333	0/0/0	0/0/0
10	015942	5:132983723	0/0/0	0/0/0
11	015943	5:132990124	0/0/0	0/0/0
12	015944	5:133071580	0.1/0.3/-2	0.1/1.8/-4.1
13	015945	5:133441549	5.5/9.3/-0.7	6.7/8/-0.3
14	015947	5:133563180	0/0/0	0/0/0
15	015948	5:133565009	4.2/4.1/0	4.2/3.9/0.1
16	015949	5:133613890	0/0/0	0/0/-8.7
17	015950	5:133617183	0/0/0	0/0/0
18	015951	5:133630615	0.3/0.3/0.1	0/0.3/-11.7
19	015952	5:133821714	3/3.7/-0.3	6.8/16.1/-1.2
20	015955	5:133998288	3/4.8/-0.7	2.7/3.6/-0.4
21	015956	5:134163807	3.2/4.5/-0.5	11.9/26.1/-1.1
22	015957	5:134188430	0/0/0	0/0/0
23	015960	5:134287992	0.5/0.6/-0.3	1/1.5/-0.6
24	015961	5:134439009	2.6/6.7/-1.4	2.4/0.6/1.9
25	015962	5:134444332	9.4/8/0.2	10.2/12.4/-0.3
26	015963	5:134455335	5.1/5.5/-0.1	5.6/4.9/0.2
27	015964	5:134537160	0/0/-7.5	0.9/4.8/-2.5
28	015965	5:134675256	10.5/10.7/0	6.7/11.7/-0.8
29	015968	5:134792393	3.9/3.6/0.1	4.7/8.7/-0.9
30	015969	5:134894335	0.1/0.1/0.8	0.1/0.7/-2.4
31	015970	5:134952929	7/4.5/0.6	5.7/7.2/-0.3

Note: ^aWithin the fine mapping for QTL-4.1
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Table S10 The numbers, type, and expression level of genes alternative splicing^a

Gene ID	Type	Chr:Start	Numbers (I/II)	M/W/abs(log ₂ (M/W)) (rpkm)	
				17DAP (I)	28DAP (II)
Zm000001d015955	AE	5:134000834	2/3	1.4/8.4/-2.6	0.0/3.6/-11.8
	MIR	5:133999464	2/2	2.8/4.9/-0.8	2.8/2.9/-0.1
	TSS	5:133998359	2/3	3.1/3.4/-0.1	1.8/1.1/0.8
	TTS	5:134001588	1/3	1.0/0.0/4.9	2.8/0.4/2.8
	XAE	5:133999310	1/2	0.8/5.0/-2.7	0.0/2.9/-11.5
	XIR	5:134000365	2/1	3.1/3.4/-0.1	1.8/0.7/1.3
	XMIR	5:133999402	1/1	1.1/0.1/3.9	0.0/0.1/-6.0
	Total		11/15	13.1/25.2/-0.9	9.2/11.8/-0.4
Zm000001d015956	IR	5:134164961	2/2	3.9/5.2/-0.4	15.4/16.4/-0.1
	MIR	5:134165047	2/0	0.2/0.0/10.6	0.0/0.0/0.0
	TSS	5:134163807	1/1	7.7/9.7/-0.3	30.8/67.6/-1.1
	TTS	6:134171904	1/1	7.7/9.7/-0.3	30.8/67.6/-1.1
	XSKIP	5:134166568	2/1	3.9/0.0/15.3	0.0/17.5/-17.4
	Total		8/5	31.4/29.9/0.1	92.4/202.9/-1.1

Note: ^aWithin the fine mapping for QTL-4.

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Table S11 The selected modules and their hub genes by WGCNA of RNA-seq

Mod ^a	N _o	Gene ID ^b	Chr	Connectivity	log ₂ (H/L), I/II ^c	Description
turquoise	1	053177	4	1171.1	1.1/0.5	Actin-7 (Act7)
	2	032385	1	1104.5	1.7/0.9	Glucose-1-phosphate adenylyltransferase (GPPAT)
	3	043534	3	1097.4	0.9/0.8	Nucleoside triphosphate hydrolases with p-loop (NTPH)
	4	035304	6	1089.2	1.2/0.8	LIM domain-containing protein WLIM1 (WLIM1)
	5	032896	1	1077.4	3.0/1.7	50S ribosomal protein L28 (RP28)
	6	030109	1	1069.2	1.6/1.2	Shikimate kinase (SK)
	7	039167	6	1061.8	1.4/1.2	ClpP family protease (clpP)
	8	027442	1	1060.5	2.9/1.9	50S ribosomal protein L5 (RP5)
	9	027542	1	1050.1	2.5/1.7	Glutathione transferase (GST)
	10	015366	5	1047.0	2.3/2.0	Hydroxymethylbilane synthase (HMBS)
blue	1	031522	1	776.7	-0.7/-1.0	Auxin response factor (ARF)
	2	033555	1	771.2	-0.9/-0.6	Fumarylacetoacetate hydrolase (FAH)
	3	018454	5	759.1	-1.0/-0.9	Glutathione reductase (GR)
	4	021846	7	758.6	-0.9/-0.8	Metalloproteinase M16 (M16)
	5	039768	3	746.5	-0.7/-0.7	Peroxisomal Acyl-CoA Oxidase4 (ACX4)
	6	002261	2	734.5	-1.0/-0.8	(S)-2-hydroxy-acid oxidase (HAO)
	7	004616	2	714.1	-0.4/-0.4	Rossmann-fold NAD(P)-binding domain-containing protein (NADB)
	8	027558	1	712.7	-1.2/-1.0	Aconitate hydratase (AH)
	9	026573	10	710.3	-1.4/-1.2	Methylthioribose kinase (MTRK)
	10	015612	5	706.7	-0.7/-0.6	YibO family protein (YibO)
yellow	1	020339	7	685.9	-2.4/-1.3	Glycosyl hydrolase 81 (GH81)
	2	031555	1	682.8	-1.7/-0.6	Cytochrome b561/DOMON domain protein (CRR)
	3	015100	5	682.0	-1.6/-0.4	Calcium-dependent protein kinase 28 (CDPK28)
	4	007915	2	676.5	-2.2/-0.6	E3 ubiquitin-protein ligase RHF2A (RHF2A)
	5	003533	2	672.5	-2.3/-1.1	Lipoxygenase (LOX)
	6	025166	10	671.2	-3.2/-0.7	NAD(P)-dependent alcohol dehydrogenase (NADADH)
	7	006551	2	668.2	-1.9/-1.0	GRAS domain family (GRAS)
	8	013109	5	656.2	-1.4/-0.5	Calcium-dependent protein kinase 10 (CDPK10)
	9	052653	4	655.7	-2.7/-1.4	Respiratory burst oxidase4 (RBOH)
	10	006621	2	653.5	-1.4/-0.5	Calcium-dependent protein kinase 7 (CDPK7)

tan	1	021385	7	377.1	-0.3/-1.5	NADPH-cytochrome P450 reductase (CPR)
	2	038167	6	277.5	-0.4/-1.5	Lipase (LIP)
	3	016070	5	248.1	1.2/-1.4	Phosphate regulatory homolog1 (PRH1)
	4	012159	8	239.8	-0.4/-1.3	Beta-glucosidase (β -Glu)
	5	016855	5	239.0	-0.5/-0.7	Chloride channel protein (CLCP)
	6	051420	4	227.9	-1.0/-1.8	Dehydrin3 (DHN3)
	7	048344	9	217.4	0.7/-1.3	Expansin-like A2 (EXLA2)
	8	008727	8	166.9	-0.7/-0.9	Phospholipase D (PLD)
	9	022264	7	165.3	0.7/-1.5	Hydrophobic protein LTI6A (LTI6A)
	10	016255	5	163.0	1.5/-1.5	Heat stress transcription factor C-1 (HSEC1)

Notes: ^amean values; ^bAdd Zm00001d before numbers; ^cH/L, I and II represent ratios of average genes expression with high (H) and low (L) PHS, in 17 DAP (I) and 28 DAP (II), respectively.

Table S12 Genes used to construct the *Zmccr3* network from the Blue module

Names ^a	Gene (Zm00001d)	Conne ctivity	log ₂ (H/L); I/II ^b	Description
Zmccr 3	015956	539.2	-0.4/-0.5	Cinnamoyl-CoA reductase 3 (CCR3)
P1	031522	776.7	-0.7/-1.0	Auxin response factor (ARF)
P2	033555	771.2	-0.9/-0.6	Fumarvlacetoacetate hvdrolase (FAH)
P3	018454	759.1	-1.1/-0.9	Glutathione reductase (GR)
P4	021846	758.6	-0.9/-0.8	Metallopeptidase M16 (M16)
P5	039768	746.5	-0.7/-0.7	Peroxisomal Acvl-CoA Oxidase4 (ACX4)
P6	002261	734.5	-1.0/-0.8	(S)-2-hydroxyv-acid oxidase (HAO)
P7	004616	714.1	-0.5/-0.4	Rossmann-fold NAD (P)-binding domain-containing protein (NADB)
P8	027558	712.7	-1.2/-1.0	Aconitate hvdratase (AH)
P9	026573	710.3	-1.4/-1.2	Methylthioribose kinase (MTRK)
P10	015612	706.7	-0.7/-0.6	YibO family protein (YibO)
P11	003166	704.5	-0.7/-0.6	LETM1-like protein (LETM1)
P12	040302	699.1	-0.6/-0.4	Zinc finger CCCH type domain-containing protein ZFN-like 1 (CCCH)
P13	021297	697.3	-0.5/-0.3	Pantothenate kinase 2 (PK2)
P14	034591	692.6	-1.0/-0.8	Triacylglycerol lipase SDP1 (SDP1)
P15	045394	688.8	-0.7/-0.9	NAD (+) diphosphatase (NADD)
P16	007892	686.1	-0.9/-0.7	2-oxoisovalerate dehydrogenase subunit beta 1 mit. (ODSB)
P17	021301	685.7	-1.0/-0.8	LON peptidase1 (LON)
P18	024967	685.2	-1.0/-0.8	Glycerol-3-phosphate dehydrogenase SDP6 mitochondrial (SDP6)
P19	016170	684.9	-1.0/-0.8	Peroxisome biogenesis protein 7 (PBP7)
P20	046593	683.9	-0.9/-0.6	Acid phosphatase1 (AP1)
P21	034886	683.3	-0.5/-0.6	Heat stress transcription factor A-1a (HSTFA-1a)
P22	039904	679.9	-0.4/-0.5	Protein SUPPRESSOR OF K (+) TRANSPORT GROWTH DEFECT 1 (SKD1)
P23	005489	679.9	-0.8/-0.6	D-isomer specific 2-hydroxyacid dehydrogenase family protein (HD)
P24	040084	679.8	-0.6/-0.6	Fructose-bisphosphate aldolase (FBA)
P25	031621	679.0	-1.1/-0.9	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 2 (MTA/SAH)
P26	012559	678.7	-0.6/-0.6	Stomatal closure-related actin-binding protein 1 (SCAB1)
P27	014203	677.3	-0.5/-0.5	F-box/kelch-repeat protein (SKIP11)
P28	015856	675.3	-1.1/-1.0	Citrate synthase1 (CS)
P29	002184	672.6	-0.6/-0.8	Peroxisome biogenesis protein 22 (PB22)
P30	023238	672.0	-0.9/-0.7	Long chain acvl-CoA synthetase 6 peroxisomal (LACS6)
P31	022302	670.8	-0.8/-0.9	Peptidase C15 pyroglutamyl peptidase I-like (PPIK)
P32	035772	669.3	-0.7/-0.6	Peroxisomal membrane protein PEX14 (PEX14)
P33	024333	669.0	-0.9/-1.2	Mitochondrial pyruvate carrier (MPC)

P34	002065	666.7	-1.1/-0.6	Insect resistance3 (IR3)
P35	015905	665.4	-1.6/-1.9	Bidirectional sugar transporter SWEET (SWEET)
P36	051879	664.0	-0.4/-0.5	NAC domain-containing protein 71 (NAC71)
P37	034866	661.5	-0.8/-1.1	Pantoate--beta-alanine ligase (PBAL)
P38	037760	660.1	-0.8/-0.7	O-acetyltransferase (OAT)
P39	052785	657.8	-0.4/-0.8	Plant UBX domain-containing protein 11 (UBXN11)
P40	017119	654.7	-0.8/-0.6	Glucose-6-phosphate 1-dehydrogenase (G6PD)
P41	049734	652.9	-0.6/-0.5	1-phosphatidylinositol-3-phosphate 5-kinase (PI3P5K)
P42	053223	650.4	-1.2/-0.9	L-ascorbate peroxidase 3 peroxisomal (APX3)
P43	047757	650.2	-1.4/-1.4	Ascorbate peroxidase homolog (APX)
P44	038891	650.0	-3.4/-3.9	Phosphoethanolamine N-methyltransferase 3 (PEXMT)
P45	002105	649.6	-0.8/-0.5	V-type proton ATPase subunit D (V-ATPD)
P46	005344	649.5	-0.8/-0.9	Histidine-containing phosphotransfer protein2 (HCP)
P47	003947	648.6	-1.0/-0.7	2-oxoglutarate dehydrogenase, mit. (OGD)
P48	018598	648.2	-1.3/-0.8	Proline transporter 2 (PT2)
P49	008739	646.0	-0.8/-1.0	2-hydroxyacyl-CoA lyase (HACL)
P50	051193	645.8	-1.2/-0.9	Metal-nicotianamine transporter YSL7 (YSL7)
P51	017448	645.3	-1.3/-0.9	Vesicle-associated protein 2-1 (VAP)
P52	045251	643.8	-0.6/-0.4	Acyl-coenzyme A oxidase (ACOX)
P53	050310	642.0	-1.3/-0.8	Homeobox-leucine zipper protein (HLZ)
P54	018555	640.7	-1.1/-1.0	Homoserine kinase (HK)
P55	009182	640.1	-2.4/-1.5	Enoyl-CoA hydratase1 (ECH1)
P56	036440	639.8	-0.9/-0.7	WAT1-related protein (WAT1)
P57	047218	639.8	-0.4/-0.7	Cytochrome c oxidase subunit 6b-1 (COX6B)
P58	013041	639.2	-1.1/-0.9	Cytochrome b-c1 complex subunit 7 (CCS7)
P59	036475	638.2	-1.3/-0.9	ABC1 family protein (ABC1)
P60	052050	635.1	-1.0/-0.5	Nudix hydrolase 3 (NH)
P61	002006	632.8	-0.9/-1.1	Plasma membrane ATPase (ATPase)
P62	040118	632.7	-0.8/-1.0	Sarcoplasmic reticulum histidine-rich calcium-binding protein (SRHRCB)
P63	042282	632.7	-0.8/-0.6	Aldolase-type TIM barrel family protein (TIM)
P64	008432	632.4	-2.4/-1.7	acetyl-CoA acetyltransferase, cytosolic 2 (ACAT)
P65	053308	632.3	-0.9/-0.9	DUF3741 domain-containing protein (DUF3741)
P66	035032	630.4	-0.5/-0.4	GroES-like zinc-binding alcohol dehydrogenase family protein (GroES)
P67	042842	628.3	-1.6/-1.3	Alpha-1,4 glucan phosphorylase (AGP)
P68	021132	624.1	-0.4/-0.5	3-hydroxyisobutyryl-CoA hydrolase 1 (HIBCH)
P69	010227	623.3	-0.7/-0.6	NAC transcription factor (NACTF)
P70	048021	623.0	-1.5/-0.8	Allene oxide synthase1 AOS1)
P71	012765	622.0	-0.6/-0.8	Peptidase M28 family protein (M28)
P72	037521	621.9	-0.4/-0.6	Acyl-coenzyme A oxidase 4 peroxisomal (ACAOX4)
P73	035475	621.0	-2.1/-1.6	Isovaleryl-CoA dehydrogenase mitochondrial (IVD)
P74	049019	620.6	-1.2/-0.7	Ankyrin repeat protein SKIP35 (SKIP35)
P75	030694	620.0	-0.4/-0.4	Thaumatococcus-like protein (TLP)

P76	039422	619.9	-0.8/-0.7	Phosphoribosylaminoimidazole carboxylase (PAICS)
P77	011696	618.8	-0.4/-0.4	Casein kinase family protein (CK)
P78	051362	617.6	-1.4/-1.0	Tonoplast intrinsic protein2 (TI2)
P79	045216	617.3	-1.1/-0.9	alpha/beta-Hydrolases superfamily protein (ABH)
P80	038218	616.1	-1.0/-1.3	Cytochrome c-2 (CytC2)
P81	024393	614.7	-2.0/-1.8	Indole-3-glycerol phosphate synthase chloroplastic (IGPS)
P82	031854	614.7	-0.9/-0.4	Thiaminase2 (Thi2)
P83	008244	614.2	-0.9/-0.9	3-isopropylmalate dehydrogenase (IPMDH)
P84	039893	614.2	-0.8/-0.5	Duplicated homeodomain-like superfamily protein (DHLSP)
P85	037109	613.4	-0.3/-0.4	Smr domain-containing protein (Smr)
P86	027510	613.4	-1.1/-0.7	Protein NLP2 (NLP2)
P87	016902	612.9	-1.0/-1.1	Bifunctional riboflavin biosynthesis protein RIBA 1 chl.(RIBA1)
P88	014344	611.3	-0.8/-0.6	P-loop containing nucleoside triphosphate hydrolases protein (NTH)
P89	028380	610.4	-0.5/-0.5	TSL-kinase interacting protein 1 (TSLIP1)
P90	042884	610.0	-1.8/-1.2	Acyl-coenzyme A oxidase (CAO)
P91	011958	604.2	-1.0/-1.1	Glutathione S-transferase family protein (CST)
P92	008271	602.9	-1.6/-1.0	Hydroxymethylglutaryl-CoA lyase mitochondrial (HMGCL)
P93	016553	602.3	-0.9/-1.1	F-box/kelch-repeat protein (F-box/KR)
P94	006176	601.6	-0.7/-0.4	Plant UBX domain-containing protein 8 (UBX8)
P95	021180	601.4	-0.8/-0.8	BAG-associated GRAM protein 1 (BAG1)
P96	011119	600.0	-1.0/-0.7	Peroxisomal membrane protein PEX14 (PEX14)
P97	020636	597.6	-1.0/-0.7	Cysteine proteinase 2 (CP2)
P98	042494	595.1	-1.4/-1.2	Pentatricopeptide repeat (PPR) superfamily protein (PPR)
P99	017833	594.9	-1.1/-0.5	Ribose-phosphate pyrophosphokinase 4 (RBP4)
P100	051138	594.1	-1.0/-1.0	Glycolipid transfer protein 1 (GLTP)
P101	030526	593.7	-0.5/-0.7	Outer arm dynein light chain 1 protein (OADLC1)
P102	029750	593.4	-0.6/-0.8	DUF3741 domain-containing protein (DUF3741)
P103	033028	593.3	-0.4/-0.5	Colon cancer-associated protein Mic1-like protein expressed (Mic1)
P104	018487	592.4	-2.1/-1.3	Acetyl-CoA C-acyltransferase (ACAT)
P105	003247	592.1	-3.0/-2.6	Malate synthase1 (MS1)
P106	045326	591.8	-1.3/-0.9	6-phosphofructokinase (PFK)
P107	038594	590.3	-1.0/-1.3	Protein translation factor SUI1 homolog 2 (SUI1)
P108	002275	589.6	-0.8/-0.6	ABC transporter C family member 2 (ABCC2)
P109	038227	589.1	-0.3/-0.5	NAC domain transcription factor superfamily protein isoform 1 (PNAC)
P110	025626	587.9	-0.9/-0.9	Betaine aldehyde dehydrogenase 2 mitochondrial (BADH2)
P111	030859	587.3	-0.8/-0.6	Serine hydroxymethyltransferase (SHMT)
P112	038267	585.5	-0.9/-1.2	Maternal effect embryo arrest 59 (MEA59)
P113	035136	585.3	-0.4/-0.4	Succinate dehydrogenase7 (SDH7)
P114	025023	585.2	-1.4/-2.1	2-oxoacid dependent dioxygenase (2-OGDD)
P115	015570	585.1	-1.0/-0.5	Sucrose-phosphate synthase 1 (SPS1)

P116	047461	584.5	-2.0/-1.5	Mitochondria fission 1 protein (MF1)
P117	029860	584.0	-0.9/-0.9	3-hydroxyisobutyryl-CoA hydrolase-like protein 2 mitochondrial (HCHL)
P118	019439	583.4	-0.5/-0.5	Dehydrogenase/reductase SDR family member 2 (sdr2)
P119	019467	583.2	-0.6/-0.5	Spermidine synthase 2 (SPDS2)
P120	010128	582.8	-1.2/-0.9	Acidic ribosomal protein P2b (RPP2b)
P121	020669	580.6	-1.0/-1.0	Formate tetrahydrofolate ligase (FTL)
P122	045728	580.1	-1.1/-0.6	Protein NSP-INTERACTING KINASE 1 (NSP-IK)
P123	012929	579.3	-0.8/-0.9	Receptor protein kinase TMK1 (TMK1)
P124	028267	578.9	-0.7/-0.9	Trehalose-6-phosphate synthase2 (TPS2)
P125	037684	577.9	-1.6/-1.8	Hyaluronan/mRNA-binding protein domain-containing protein (HBP)
P126	036484	577.3	-2.8/-1.9	Aminodeoxychorismate synthase chloroplastic (ADCS)
P127	026445	577.2	-0.7/-0.5	E3 ubiquitin-protein ligase MBR2 (MBR2)
P128	041710	575.8	-1.0/-1.1	Glutathione synthetase chloroplastic
P129	002967	574.7	-0.8/-0.9	AFG1-like ATPase family protein (AFG1)
P130	052776	574.5	-0.9/-0.8	VAMP protein SEC22 (SEC22)
P131	029084	570.5	-1.0/-1.0	Fumarate hydratase 1 mitochondrial (FHM)
P132	033645	569.8	-0.5/-0.7	Phosphatidylinositol 4-phosphate 5-kinase 8 (PI4P5K8)
P133	051392	569.0	-0.4/-0.6	Glutathione peroxidase (GP)
P134	047166	568.9	-0.9/-0.7	Cystathionine gamma-synthase 1 chloroplastic (CGS1)
P135	038755	568.8	-0.8/-0.9	Carnitine racemase/ catalytic (CR/C)
P136	027523	568.2	-1.2/-1.1	Serine/threonine-protein kinase (S/TPK)
P137	028909	566.5	-1.6/-1.2	Enoyl-CoA hydratase 1, peroxisomal (ECH1)
P138	026490	563.3	-1.0/-0.8	Proton-exporting ATPase4 (PEATPase4)
P139	030471	560.4	-0.8/-0.6	Alpha-L-fucosidase 2 (FUCA2)
P140	011526	560.0	-0.6/-0.4	PfkB-like carbohydrate kinase family protein (PfkB)
P141	019656	559.2	-0.3/-0.4	Manganese-dependent ADP-ribose/CDP-alcohol diphosphatase (ADPR/CDPAD)
P142	013173	557.5	-1.3/-0.9	Protein PHLOEM PROTEIN 2-LIKE A10 (PP2)
P143	039263	555.6	-0.3/-0.5	OB-fold nucleic acid binding domain-containing protein (OB)
P144	016918	555.0	-0.8/-0.7	Ubiquitin carboxyl-terminal hydrolase (UCTH)
P145	050051	552.3	-0.3/-0.5	Calcineurin subunit B (CSB)
P146	040850	552.2	-1.4/-0.8	Shikimate biosynthesis protein aroDE (aroDE)
P147	043620	551.9	-0.8/-0.6	NADH dehydrogenase iron-sulfur protein 7 mitochondrial (NADHD)
P148	045311	551.0	-1.9/-1.9	Hydrolase-like protein family (HDL)
P149	020910	550.6	-1.0/-1.3	Induced stolen tip protein TUB8 (TUB8)
P150	044814	549.6	-0.6/-0.3	Protein kinase domain superfamily protein (PKDP)
P151	041982	548.4	-0.8/-0.8	Isopentenyl transferase1 (ITF1)
P152	026476	548.0	-0.5/-0.4	6,7-dimethyl-8-ribityllumazine synthase (DRS)
P153	029238	547.8	-0.8/-0.6	Peptide methionine sulfoxide reductase B5 (PMSR)
P154	010478	547.7	-1.5/-1.1	Peroxisomal carrier protein (PC)
P155	018370	547.1	-1.5/-1.0	Leucine aminopeptidase 2 chloroplastic (LAP2)

P156	034531	547.0	-0.5/-0.5	Acetyltransferase component of pyruvate dehydrogenase (ACOPDC)
P157	048358	546.8	-0.5/-0.7	Aconitate hydratase (AH)
P158	016365	545.4	-0.8/-0.6	Dihydrolipoamide S-acetyltransferase1 (DA)
P159	020365	543.5	-0.3/-0.5	Zinc finger MYND domain-containing protein 15 (MYND)
P160	003159	542.4	-0.6/-1.0	ATP synthase E chain (ATPS)
P161	028905	541.6	-0.3/-0.4	Phytochrome B (PhvB)
P162	030685	539.8	-1.8/-1.8	L-ascorbate peroxidase 2 cytosolic (APX2)
P163	046378	539.4	-0.7/-0.6	PGG domain-containing protein (PGG)
P164	049042	539.3	-1.0/-0.9	Methylthioribose-1-phosphate isomerase (MPI)
P165	044648	539.3	-0.8/-0.8	Alpha-L-arabinofuranosidase 1 (ARAF1)

Notes: Red font in ccr3 pathway; ^a Names in the drawn network; ^b H/L, I and II represent ratios of average genes expression with high (H) and low (L) PHS, in 17 DAP (I) and 28 DAP (II), respectively.

1
2

1 **Table S13** Screening of GO and KEGG by conjoint analysis for RNA-seq and iTRAQ (**p <0.05**)

№ GO or KEGG ^a	Term	p; RNA-seq/ iTRAQ; I II ^b	№	Gene (Zm00001d)	Accessions (protein)	log ₂ (M/W)	
						RNA-seq/iTRAQ/Reg 17 DAP	28 DAP
GO:0000166	nucleotide binding	0.88 /0.68 0.00 /0.00	1	006308	B4G1A4	0.1 /—/—	-2.5 /1.4 /—
			2	009146	B6T681	0.2 /—/—	-1.7 /1.7 /—
			3	035037	B6TB29	0.8 /-0.1 /—	-5.1 /1.5 /—
			4	039654	C0HF52	1.1 /—/up	-2.6 /-1.3 /down
			5	023344	B6THL4	1.6 /0.5 /up	-0.6 /-1.1 /down
			6	024903	C0P4Q3	-1.8 /-0.5 /down	-0.7 /0.2 /—
			7	025659	B4FAW1	1.4 /-0.3 /—	-4.4 /-0.7 /down
			8	031013	B6SKB7	1.2 /-0.4 /—	0.0 /1.0 /—
			9	034501	A0A1D6L840	1.2 /0.4 /up	-2.2 /0.8 /—
			10	041119	A0A1D6MUF1	1.0 /0.3 /up	0.8 /-0.4 /—
			11	042416	A0A804N8X8	-1.0 /0.3 /—	0.3 /0.4 /—
			12	047799	K7VJF3	-1.5 /-0.4 /down	-1.0 /-0.3 /down
			13	048073	B6SXY0	-3.2 /-0.5 /down	-1.4 /-0.6 /down
GO:0003677	DNA binding	0.00 /0.70 0.00 /0.06	1	027760	B4FXB2	2.8 /-0.3 /—	-1.2 /— /down
			2	005322	B6SGC3	2.9 /—/up	-7.9 /-1.9 /down
			3	037988	B6SI37	0.7 /-0.2 /—	-3.5 /-2.5 /down
			4	043277	A0A3L6FE62	-0.6 /—/—	-2.6 /1.5 /—
GO:0003723	chromatin binding	0.00 /0.97 1.00 /0.09	1	005023	B6TG61	1.0 /-0.4 /—	-0.8 /0.1 /—
			2	007810	B6SII7	1.3 /-0.3 /—	-1.1 /-0.3 /down
			3	024511	B6TB97	1.4 /-0.3 /—	-0.8 /1.1 /—
			4	031957	B6SIS5	1.7 /-0.4 /—	-1.7 /-0.7 /down
			5	033147	A0A1D6KWK0	1.7 /-0.4 /—	-0.8 /—/—
			6	034422	B4G286	1.5 /-0.6 /—	-0.6 /-0.5 /—
			7	034550	C0PCQ6	1.5 /-1.0 /—	-0.6 /-0.4 /—
			8	042416	A0A804N8X8	-1.0 /0.3 /—	0.3 /0.4 /—
			9	050920	B4F9G6	1.6 /-0.3 /—	-0.7 /2.0 /—
			10	022630	A0A3L6TAT5	-2.1 /-0.5 /down	-3.9 /2.3 /—
GO:0003824	DNA binding transcription factor activity	0.83 /0.01 0.00 /0.00	1	003247	A0A1D6E7V9	1.4 /-0.5 /—	-0.5 /1.2 /—
			2	011710	A0A1D6G380	1.3 /0.5 /up	0.1 /0.3 /—
			3	016198	B8A0T6	1.1 /1.0 /up	1.8 /0.6 /up
			4	018159	B4FYM6	-2.4 /-0.9 /down	1.0 /1.4 /up
			5	021249	B4FU63	-2.1 /-0.5 /down	0.8 /0.2 /—
			6	021666	B4FTF9	1.1 /-0.5 /—	-0.7 /2.7 /—
			7	025659	B4FAW1	1.4 /-0.3 /—	-4.4 /-0.7 /down
			8	028963	B6SJF7	1.2 /0.3 /up	-0.2 /-0.5 /—
			9	008727	K7VQG5	-1.0 /-0.1 /down	-1.9 /1.5 /—
			10	039670	B8A0J4	-0.5 /0.0 /—	-2.0 /1.5 /—
			11	044906	K7V5I3	1.3 /-0.3 /—	-2.4 /2.0 /—
GO:0005515	RNA binding	0.09 /0.95 0.02 /0.00	1	017401	B6U6S4	-1.1 /-0.3 /down	-0.3 /-0.4 /—
			2	027511	A0A1D6JMR5	1.3 /-0.5 /—	-0.2 /0.9 /—
			3	034356	B6TJ22	1.2 /-0.6 /—	-0.7 /-0.1 /—
			4	051306	C4J4W3	-1.1 /-0.5 /down	-0.4 /-0.3 /—
			5	007862	A0A804MWT6	-1.3 /—/down	-2.7 /-1.5 /down
			6	015127	B6SI51	1.4 /—/up	-1.8 /-1.9 /down
			7	028796	A0A1D6JZP5	1.8 /—/up	-5.9 /-1.2 /down
			8	030086	A0A804LNU1	0.0 /—/—	-2.5 /-1.2 /down
			9	042541	B6U297	-1.3 /-0.6 /down	-1.9 /1.9 /—
			10	045436	K7VSJ5	0.4 /-0.3 /—	-2.0 /-1.2 /down

GO:0005576	catalytic activity	0.32 /0.25 0.70 /0.04	11	052323	B6SV61	1.1 /-0.1 /—	-3.7 /-1.1 /down
			1	053785	B4FVX5	-2.8 /0.4 /—	-0.1 /— /—
			2	022630	A0A3L6TAT5	-2.1 /-0.5 /down	-3.9 /2.3 /—
			3	040026	B6TPF0	1.7 /-0.8 /—	-3.9 /-1.4 /down
			4	043047	Q94KT3	1.7 /0.1 /up	2.1 /2.8 /up
GO:0005577	cellular	0.97 /0.01 0.93 /0.29	5	043988	P93518	-2.7 /-0.5 /down	2.2 /1.5 /up
			1	013737	B4G1Q6	-1.2 /-0.8 /down	-0.5 /-0.7 /—
			2	012120	K7W288	-8.7 /-0.2 /down	2.9 /1.4 /up
			1	024511	B6TB97	1.4 /-0.3 /—	-0.8 /1.1 /—
			2	027760	B4FXB2	2.8 /-0.3 /—	-1.2 /— /down
GO:0005634	extracellular region	0.01 /1.00 0.00 /0.00	3	005322	B6SGC3	2.9 /— /up	-7.9 /-1.9 /down
			4	039654	C0HF52	1.1 /— /up	-2.6 /-1.3 /down
			5	043277	A0A3L6FE62	-0.6 /— /—	-2.6 /1.5 /—
			6	047567	A0A804R5B8	1.4 /-0.7 /—	-3.0 /-2.3 /down
GO:0005737	extracellular space	0.26 /0.93 0.77 /0.00	1	003247	A0A1D6E7V9	1.4 /-0.5 /—	-0.5 /1.2 /—
			2	020898	A0A1D6I6T8	-1.8 /-0.3 /down	0.2 /0.7 /—
			3	024903	C0P4Q3	-1.8 /-0.5 /down	-0.7 /0.2 /—
			4	025659	B4FAW1	1.4 /-0.3 /—	-4.4 /-0.7 /down
			5	027511	A0A1D6JMR5	1.3 /-0.5 /—	-0.2 /0.9 /—
			6	034356	B6TJ22	1.2 /-0.6 /—	-0.7 /-0.1 /—
			7	041119	A0A1D6MUF1	1.0 /0.3 /up	0.8 /-0.4 /—
			8	047799	K7VJF3	-1.5 /-0.4 /down	-1.0 /-0.3 /down
			9	048073	B6SXY0	-3.2 /-0.5 /down	-1.4 /-0.6 /down
			10	050428	B4FR32	-1.4 /-0.5 /down	-1.3 /0.1 /—
			11	052101	A0A1D6QDB3	1.3 /0.6 /up	-0.4 /0.3 /—
			12	039654	C0HF52	1.1 /— /up	-2.6 /-1.3 /down
			13	042541	B6U297	-1.3 /-0.6 /down	-1.9 /1.9 /—
GO:0005739	cell wall	0.28 /0.99 1.00 /0.04	1	008610	B6T540	1.1 /0.3 /up	0.2 /— /—
			2	016198	B8A0T6	1.1 /1.0 /up	1.8 /0.6 /up
			3	051062	K7UWX4	0.7 /0.2 /—	1.0 /-1.4 /—
GO:0005829	cytoplasm	0.43 /0.70 0.60 /0.00	1	003524	B4FQR3	1.5 /-0.5 /—	-1.3 /-0.7 /down
			2	011710	A0A1D6G380	1.3 /0.5 /up	0.1 /0.3 /—
			3	020898	A0A1D6I6T8	-1.8 /-0.3 /down	0.2 /0.7 /—
			4	021249	B4FU63	-2.1 /-0.5 /down	0.8 /0.2 /—
			5	024903	C0P4Q3	-1.8 /-0.5 /down	-0.7 /0.2 /—
			6	034422	B4G286	1.5 /-0.6 /—	-0.6 /-0.5 /—
			7	043730	B6UGS5	2.7 /-1.3 /—	-4.0 /-1.7 /down
			8	009146	B6T681	0.2 /— /—	-1.7 /1.7 /—
			9	009382	B6UH99	0.7 /0.2 /—	-2.4 /-2.2 /down
			10	035037	B6TB29	0.8 /-0.1 /—	-5.1 /1.5 /—
			11	037894	A3KLI0	2.5 /-0.2 /—	-2.2 /-2.5 /down
			12	037985	B6T8E4	2.4 /0.1 /up	-4.1 /-2.7 /down
			13	037988	B6SI37	0.7 /-0.2 /—	-3.5 /-2.5 /down
			14	044211	A0A804NGW1	-0.3 /— /—	-2.1 /-1.2 /down
GO:0005886	endosome	0.15 /0.71 0.00 /0.11	1	020898	A0A1D6I6T8	-1.8 /-0.3 /down	0.2 /0.7 /—
			2	023859	A0A1D6IWH8	-2.8 /-0.8 /down	-2.6 /— /down
			3	024903	C0P4Q3	-1.8 /-0.5 /down	-0.7 /0.2 /—
			4	027511	A0A1D6JMR5	1.3 /-0.5 /—	-0.2 /0.9 /—
			5	030133	A0A1D6KA81	-1.1 /0.4 /—	0.0 /— /—
			6	043128	A0A1D6N948	-1.2 /-0.6 /down	0.4 /— /—

GO:0005975	vacuole	0.76 /0.01 0.01 /0.05	7	007862	A0A804MWT6	-1.3 /—/down	-2.7 /-1.5 /down
			8	018399	C5XV18	-0.4 /—/—	-2.1 /-1.2 /down
			9	039654	C0HF52	1.1 /—/up	-2.6 /-1.3 /down
			10	042809	A0A0B4J395	0.0 /—/—	-1.8 /1.5 /—
			1	003776	O81189	-1.5 /0.5 /—	0.3 /0.6 /—
			2	018159	B4FYM6	-2.4 /-0.9 /down	1.0 /1.4 /up
			3	013097	A0A804P7D9	1.2 /—/up	-2.4 /-1.2 /down
GO:0006629	endoplasmic reticulum	0.02 /0.17 0.00 /0.09	4	035037	B6TB29	0.8 /-0.1 /—	-5.1 /1.5 /—
			5	043988	P93518	-2.7 /-0.5 /down	2.2 /1.5 /up
			6	044211	A0A804NGW1	-0.3 /—/—	-2.1 /-1.2 /down
			7	048055	B6TLN1	-2.0 /—/down	-2.7 /-1.2 /down
GO:0008152	Golgi apparatus	0.87 /0.25 0.01 /0.00	1	003776	O81189	-1.5 /0.5 /—	0.3 /0.6 /—
			2	018159	B4FYM6	-2.4 /-0.9 /down	1.0 /1.4 /up
			3	025659	B4FAW1	1.4 /-0.3 /—	-4.4 /-0.7 /down
			4	013097	A0A804P7D9	1.2 /—/up	-2.4 /-1.2 /down
			5	043988	P93518	-2.7 /-0.5 /down	2.2 /1.5 /up
GO:0009536	plasma membrane	0.99 /0.56 0.32 /0.00	1	052101	A0A1D6QDB3	1.3 /0.6 /up	-0.4 /0.3 /—
			2	012293	C0P8C8	2.6 /-0.8 /—	-3.1 /-1.6 /down
GO:0016020	carbohydrate metabolic process	1.00 /0.98 0.43 /0.01	1	005284	B6UA28	1.7 /—/up	-2.5 /-1.9 /down
			2	017786	A0A1D6HHN4	13.5 /0.3 /up	1.3 /0.9 /up
			3	022303	B6UHC9	1.9 /-0.6 /—	-2.7 /-0.8 /down
			4	023859	A0A1D6IWH8	-2.8 /-0.8 /down	-2.6 /— /down
			5	025229	B6SI10	1.4 /-0.7 /—	-2.7 /— /down
			6	025434	K7UIK0	2.6 /-0.5 /—	-4.6 /-1.5 /down
			7	026295	A0A1D6JE74	-8.0 /0.3 /—	7.2 /-0.5 /—
			8	029062	B6SK46	-9.9 /-2.0 /down	4.0 /-1.2 /—
			9	030133	A0A1D6KA81	-1.1 /0.4 /—	0.0 /—/—
			10	031773	A0A1D6KL85	2.1 /-0.5 /—	-2.6 /-1.4 /down
			11	037915	A0A1D6M1S3	1.8 /-0.7 /—	-0.6 /-1.4 /down
			12	043128	A0A1D6N948	-1.2 /-0.6 /down	0.4 /—/—
			13	047638	A0A1D6PC23	1.0 /-0.4 /—	-0.9 /0.0 /—
			14	007862	A0A804MWT6	-1.3 /—/down	-2.7 /-1.5 /down
			15	008727	K7VQG5	-1.0 /-0.1 /down	-1.9 /1.5 /—
			16	012562	B6SS02	-0.2 /—/—	-2.4 /1.6 /—
			17	013494	B6SIZ2	0.3 /-0.7 /—	-2.6 /-1.8 /down
			18	018399	C5XV18	-0.4 /—/—	-2.1 /-1.2 /down
			19	028796	A0A1D6JZP5	1.8 /—/up	-5.9 /-1.2 /down
			20	029349	A0A5J9WEU6	1.9 /-0.6 /—	-2.3 /-1.3 /down
			21	037492	C0PDM0	0.7 /—/—	-2.5 /1.7 /—
			22	039670	B8A0J4	-0.5 /0.0 /—	-2.0 /1.5 /—
			23	042809	A0A0B4J395	0.0 /—/—	-1.8 /1.5 /—
			24	043047	Q94KT3	1.7 /0.1 /up	2.1 /2.8 /up

GO:0016301	nucleobase-containing compound metabolic process	0.80 /0.77 0.00 /0.03	25	043059	B8A3B7	0.3 /-0.4 /—	1.1 /-1.3 /—
			26	048421	A0A811M629	-0.4 /-0.1 /—	-2.4 /1.6 /—
			27	051362	B6TNY0	1.6 /—/up	1.5 /1.5 /up
			28	052323	B6SV61	1.1 /-0.1 /—	-3.7 /-1.1 /down
			29	052407	B6UE73	-0.7 /—/—	1.6 /-1.1 /—
			1	025659	B4FAW1	1.4 /-0.3 /—	-4.4 /-0.7 /down
GO:0016740	DNA metabolic process	0.99 /0.08 0.00 /0.00	2	006308	B4G1A4	0.1 /—/—	-2.5 /1.4 /—
			3	028796	A0A1D6JZP5	1.8 /—/up	-5.9 /-1.2 /down
			4	035037	B6TB29	0.8 /-0.1 /—	-5.1 /1.5 /—
			5	039654	C0HF52	1.1 /—/up	-2.6 /-1.3 /down
			6	052323	B6SV61	1.1 /-0.1 /—	-3.7 /-1.1 /down
			1	003247	A0A1D6E7V9	1.4 /-0.5 /—	-0.5 /1.2 /—
			2	012036	A0A1D6G664	-3.3 /0.4 /—	0.4 /0.9 /—
			3	016198	B8A0T6	1.1 /1.0 /up	1.8 /0.6 /up
			4	019265	C0LNQ9	1.1 /0.4 /up	1.5 /-0.1 /—
			5	025659	B4FAW1	1.4 /-0.3 /—	-4.4 /-0.7 /down
ko0051	Fructose and	0.88 /0.03 0.08 /0.18	6	034356	B6TJ22	1.2 /-0.6 /—	-0.7 /-0.1 /—
			7	009146	B6T681	0.2 /—/—	-1.7 /1.7 /—
ko00500	Starch and sucrose	0.44 /0.02 0.00 /0.22	8	035037	B6TB29	0.8 /-0.1 /—	-5.1 /1.5 /—
			9	039654	C0HF52	1.1 /—/up	-2.6 /-1.3 /down
			10	045436	K7VSJ5	0.4 /-0.3 /—	-2.0 /-1.2 /down
			1	025659	B4FAW1	1.4 /-0.3 /—	-4.4 /-0.7 /down
ko0520	Amino sugar	0.99 /0.02 0.01 /0.27	2	035037	B6TB29	0.8 /-0.1 /—	-5.1 /1.5 /—
			3	043988	P93518	-2.7 /-0.5 /down	2.2 /1.5 /up
			1	021249	B4FU63	-2.1 /-0.5 /down	0.8 /0.2 /—
			2	035037	B6TB29	0.8 /-0.1 /—	-5.1 /1.5 /—
ko00505	Aliphatic	0.39 /0.00 0.36 /0.14	3	043988	P93518	-2.7 /-0.5 /down	2.2 /1.5 /up
			1	028282	C0P4G2	2.1 /-0.3 /—	-3.2 /1.0 /—
ko04626	Plant-pathogen	0.62 /0.29 0.04 /0.16	2	044906	K7V5I3	1.3 /-0.3 /—	-2.4 /2.0 /—
			1	020898	A0A1D6I6T8	-1.8 /-0.3 /down	0.2 /0.7 /—
			2	024903	C0P4Q3	-1.8 /-0.5 /down	-0.7 /0.2 /—
ko04626	Plant-pathogen	0.62 /0.29 0.04 /0.16	3	039944	K7UU06	1.7 /0.6 /up	-2.4 /-1.6 /down

Notes: *Any one of $p < 0.05$ with comparison of expression levels between M and W from iTRAQ or RNA-seq; [†]p-values between M and W at the same stage from RNA-seq or iTRAQ.

Table S14 DEGs or DEPs with the same trend from GO and KEGG

Gene ID (Zm000001d)	Accessions (protein)	Description	log ₂ (M/W); RNA-seq/iTRAQ/Reg ^a	
			17DAP	28DAP
022303	B6UHC9	11-β-hydroxysteroid dehydrogenase 1A	1.9 /-0.6 /—	-2.7 /-0.8 /down
007810	B6SII7	40S ribosomal protein S15-4	1.3 /-0.3 /—	-1.1 /-0.3 /down
034501	A0A1D6L840	AAA-ATPase ASD mit.	1.2 /0.4 /up	-2.2 /0.8 /—
018159	B4FYM6	α-amylase	-2.4 /-0.9 /down	1.0 /1.4 /up
045436	K7VSJ5	Aminomethyltransferase	0.4 /-0.3 /—	-2.0 /-1.2 /down
051362	B6TNY0	Aquaporin TIP2.1	1.6 /—/up	1.5 /1.5 /up
016198	B8A0T6	Aspartate aminotransferase	1.1 /1.0 /up	1.8 /0.6 /up
025659	B4FAW1	ATP-dependent 6-phosphofructokinase	1.4 /-0.3 /—	-4.4 /-0.7 /down
040026	B6TPF0	Bowman-Birk serine protease inhibitors family domain protein	1.7 /-0.8 /—	-3.9 /-1.4 /down
052323	B6SV61	Brassinosteroid LRR receptor kinase	1.1 /-0.1 /—	-3.7 /-1.1 /down

039944	K7UU06	Calmodulin protein 2, touch-induced	1.7 /0.6 /up	-2.4 /-1.6 /down
052101	A0A1D6QDB3	Chaperonin10	1.3 /0.6 /up	-0.4 /0.3 /—
043988	P93518	Chitinase	-2.7 /-0.5 /down	2.2 /1.5 /up
011710	A0A1D6G380	Cytidine deaminase	1.3 /0.5 /up	0.1 /0.3 /—
037894	A3KLI0	Dehydrin DHN1	2.5 /-0.2 /—	-2.2 /-2.5 /down
043730	B6UGS5	Dehydrin Xero 1	2.7 /-1.3 /—	-4.0 /-1.7 /down
003524	B4FQR3	Deoxymugineic acid synthase 1	1.5 /-0.5 /—	-1.3 /-0.7 /down
037988	B6SI37	Embryo specific protein1	0.7 /-0.2 /—	-3.5 /-2.5 /down
037985	B6T8E4	Embryo specific protein5	2.4 /0.1 /up	-4.1 /-2.7 /down
047567	A0A804R5B8	Embryonic protein DC-8	1.4 /-0.7 /—	-3.0 /-2.3 /down
043047	Q94KT3	Expansin	1.7 /0.1 /up	2.1 /2.8 /up
005284	B6UA28	F8M12.18 protein	1.7 /—/up	-2.5 /-1.9 /down
012293	C0P8C8	Ferredoxin	2.6 /-0.8 /—	-3.1 /-1.6 /down
048055	B6TLN1	Glucan endo-13-β-glucosidase 3	-2.0 /—/down	-2.7 /-1.2 /down
047799	K7VJF3	Heat shock 70 kDa 5	-1.5 /-0.4 /down	-1.0 /-0.3 /down
041119	A0A1D6MUF1	Heat shock 70 kDa 6 chl.	1.0 /0.3 /up	0.8 /-0.4 /—
048073	B6SXY0	Heat shock 70 kDa 8	-3.2 /-0.5 /down	-1.4 /-0.6 /down
024903	C0P4Q3	Heat shock protein 90 kDa	-1.8 /-0.5 /down	-0.7 /0.2 /—
020898	A0A1D6I6T8	Heat shock 90-2	-1.8 /-0.3 /down	0.2 /0.7 /—
017401	B6U6S4	Heat shock protein STI	-1.1 /-0.3 /down	-0.3 /-0.4 /—
027760	B4FXB2	Histone H2A	2.8 /-0.3 /—	-1.2 /—/down
005322	B6SGC3	Histone H2B	2.9 /—/up	-7.9 /-1.9 /down
051306	C4J4W3	Hsp70-Hsp90 organizing protein 3	-1.1 /-0.5 /down	-0.4 /-0.3 /—
031773	A0A1D6KL85	HVA22-like protein	2.1 /-0.5 /—	-2.6 /-1.4 /down
012120	K7W288	KDEL-tailed cysteine endopeptidase CEP1	-8.7 /-0.2 /down	2.9 /1.4 /up
009382	B6UH99	LEA protein Lea14-A	0.7 /0.2 /—	-2.4 /-2.2 /down
037915	A0A1D6M1S3	LEA hydroxyproline-rich glycoprotein family	1.8 /-0.7 /—	-0.6 /-1.4 /down
025434	K7UIK0	LEA domain protein	2.6 /-0.5 /—	-4.6 /-1.5 /down
042541	B6U297	Lipoxygenase	-1.3 /-0.6 /down	-1.9 /1.9 /—
028796	A0A1D6JZP5	Meristematic receptor-like kinase	1.8 /—/up	-5.9 /-1.2 /down
008610	B6T540	mit. glycoprotein	1.1 /0.3 /up	0.2 /—/—
017786	A0A1D6HHN4	Monodehydroascorbate reductase (NADH)	13.5 /0.3 /up	1.3 /0.9 /up
050428	B4FR32	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	-1.4 /-0.5 /down	-1.3 /0.1 /—
043128	A0A1D6N948	NHL25	-1.2 /-0.6 /down	0.4 /—/—
023344	B6THL4	Non-specific lipid-transfer protein	1.6 /0.5 /up	-0.6 /-1.1 /down
039654	C0HF52	Non-specific serine/threonine-protein kinase	1.1 /—/up	-2.6 /-1.3 /down
013097	A0A804P7D9	O-Glycosyl hydrolase family 17	1.2 /—/up	-2.4 /-1.2 /down
013494	B6SIZ2	Oleosin	0.3 /-0.7 /—	-2.6 /-1.8 /down
007862	A0A804MWT6	Pangloss2	-1.3 /—/down	-2.7 /-1.5 /down
044211	A0A804NGW1	Phosphoglucomutase	-0.3 /—/—	-2.1 /-1.2 /down
039088	B6TYC3	Phospholipase A1	-1.5 /-0.5 /down	-0.1 /—/—
008727	K7VQG5	Phospholipase D	-1.0 /-0.1 /down	-1.9 /1.5 /—
023859	A0A1D6IWH8	Respiratory burst oxidase homolog protein B	-2.8 /-0.8 /down	-2.6 /—/down
031957	B6SIS5	Ribosomal protein	1.7 /-0.4 /—	-1.7 /-0.7 /down
013737	B4G1Q6	Serpin domain protein	-1.2 /-0.8 /down	-0.5 /-0.7 /—
022630	A0A3L6TAT5	S-like RNase	-2.1 /-0.5 /down	-3.9 /2.3 /—
029349	A0A5J9WEU6	SMP domain protein	1.9 /-0.6 /—	-2.3 /-1.3 /down
015127	B6SI51	SWIb domain protein	1.4 /—/up	-1.8 /-1.9 /down
030086	A0A804LNU1	TPR-like protein	0.0 /—/—	-2.5 /-1.2 /down
018399	C5XV18	Transmembrane protein	-0.4 /—/—	-2.1 /-1.2 /down
025229	B6SI10	Transmembrane protein	1.4 /-0.7 /—	-2.7 /—/down
021249	B4FU63	UDP-glucose 4-epimerase	-2.1 /-0.5 /down	0.8 /0.2 /—
019265	C0LNU9	UDP-glucosyltransferase	1.1 /0.4 /up	1.5 /-0.1 /—
029062	B6SK46	Vicilin-like seed storage protein	-9.9 /-2.0 /down	4.0 /-1.2 /—
028963	B6SJF7	Zinc-binding protein	1.2 /0.3 /up	-0.2 /-0.5 /—

Note: ^a— is not a common trend.

Table S15 Expression levels of WGCNA hub genes and *Zmccr3* pathway genes for correlation analysis

Protein	Type ^a	RNA-seq		iTRAQ	
		Gene ID (Zm00001d)	log ₂ (M/W); I/II ^b	Accessions (Protein)	log ₂ (M/W); I/II ^b
Zmccr3	Zmccr3	015956	-0.5 /-1.1	B4G1Y5	-0.3/-0.1
ACX4	Zmccr3	039768	0.6 /-1.0	A0A1D6ML13	0.0/0.9
ARAF1	other	044648	-0.1/-0.8	C0P4P5	-0.4/0.7
Cox6B	Zmccr3	047218	0.5 /-0.5	B4FNN1	0.0/0.0
FUCA2	other	030471	-1.1/-1.7	A0A096Q2H8	0.0/-0.1
GH81	WGCNA	020339	-0.3 /-3.1	B4F8U2	-0.4/1.2
GR	Zmccr3, other	018454	-0.4/-1.1	B4FWU6	-0.3/1.1
GST	WGCNA	027542	1.1 /-1.0	Q9FQC9	-0.2/0.0
LIP	WGCNA	038167	-0.6 /-2.1	A0A1D6M455	0.0/0.0
LOX	WGCNA	003533	0.8 /-2.5	A0A1D6E9P9	0.0/0.0
NADB	Zmccr3, other	004616	0.2/-0.4	A0A1D6EGI9	0.0/0.0
OAT	Zmccr3	037760	-0.5 /-1.3	A0A1D6M099	0.0/0.0
PLD	WGCNA	008727	-1.0 /-1.9	K7VQG5	-0.1/1.5
RBOH	WGCNA	052653	0.4 /-3.2	K7U7A2	0.0/1.0
YjbQ	Zmccr3	015612	0.6 /-0.5	B6TGW1	0.0/-0.4
β-Glu	WGCNA	012159	-1.4 /-0.7	K7W2F0	0.0/0.0
Act7	WGCNA	053177	0.2/-1.3	B4FRH8	0.0/0.3

Notes: ^aWGCNA, *Zmccr3* and other from WGCNA hub genes, *Zmccr3* pathway genes and their reported related genes, separately; ^bI and II means at 17DAP and 28 DAP.