$ \begin{array}{c c} \mathrm{ID} & \mathrm{Support} \\ & \mathrm{eQTL} \\ & \mathrm{study} \end{array} \\ \mathbf{Zm00001d0} & \mathrm{li2013,li201} \end{array} $	Support GRN fu2013, lei- boff2015, lin2017,	TF Annotation  Auxin response factor 4	Target enrichment  (25) histone H3-K9 methylation; (9) cytokinesis by cell plate formation; (8) cell proliferation
Zm00001d00 <b>\$1261</b> 3,li2013	atlas, leiboff2015,	Zinc finger protein	(57) cysteine biosynthetic process; (45) photosynthesis, light harvesting in photosystem I; (38) photosynthesis
Zm00001d0 li2013	maza- heri2019, huang2018, li2013, krem- ling2018, zhou2018, baute2016, baute2015 tissue	CONSTANS LIKE 5	Slight reactions; (16) rRNA processing; (15) photosystem II assembly; (8) Calvin-Benson-Bassham cycle  (9) rRNA processing; (8)
Zm00001d00 <b>4095</b> g2018	atlas, zhou2018 li2013, baute2016	tolerance- like protein basic helix- loop- helix (bHLH) DNA-	Calvin-Benson-Bassham cycle
Zm00001d0 wang2018 Zm00001d0044492017,wang	wang2018,	binding super-family protein  C2H2-like zinc	(11) pentose-phosphate shunt
Zm00001d0 liu2017,war Zm00001d006FZTN3 Zm00001d0 li2013	baute2015 li2013, baute2015	finger protein WRI1 tran- scription factor1 Transcriptio factor bHLH130 GRAS	(22) glycolysis I (from glucose 6-phosphate)  or(11) L-alanine degradation II (to D-lactate)
Zm00001d00672013 Zm00001d0 liu2017	li2013, baute2015 li2013, baute2015 baute2015, wang2018	tran- scription factor Protein SHORT- ROOT BEL1- like	(6) C4 photosynthetic carbon assimilation cycle, PEPCK type
Zm00001d01 <b>0π83</b> 017	li2013, baute2015	home- odomain protein 9 Putative GATA tran- scription factor family	
Zm00001d0 wang2018 Zm00001d012605g2018 Zm00001d0 li2013	li2013, baute2015 li2013, baute2015 li2013,	protein myb domain protein 81 MRP interact- ing1 BEL1-	(6) glycolysis I (from glucose 6-phosphate)
Zm00001d015 <b>whin</b> g2018	baute2015 li2013, baute2015	like home- odomain protein 3 sequence- specific DNA binding tran-	(10) suberin monomers biosynthesis
Zm00001d0 wang2018 Zm00001d0179900g2018	li2013, baute2016, baute2015 li2013, wang2018	scription factors Dof zinc finger protein DOF 2.1 Dof zinc finger protein	
Zm00001d0 wang2018 Zm00001d018465g2018	li2013, baute2016 li2013, baute2016,	DOF5.4 Homeodom leucine zipper family IV protein	(27) triacylglycerol degradation; (15) phenylpropanoid biosynthesis; (11) very long chain fatty acid biosynthesis I
Zm00001d0 liu2017 Zm00001d0200d2017,wang	baute2015 li2013, baute2016, baute2015 gB0083, baute2016, baute2015	Protein PHR1- LIKE 3 Ethylene- responsive tran- scription	
Zm00001d0 wang2018 Zm00001d02 <b>iv403</b> g2018	li2013, baute2015 li2013, baute2015	factor ERF117 Typical P-type R2R3 Myb protein indetermina domain7	t(9) UDP-sugars interconversion
Zm00001d0 wang2018 Zm00001d021v701g2018 Zm00001d0 liu2017	baute2015 mazaheri20 baute2015 li2013, wang2018 li2013, baute2015	Protein NLP2 Transcriptio factor ILR3 bZIP tran- scription	(6) sucrose degradation II (sucrose synthase)
Zm00001d024230017,wang Zm00001d0 wang2018	gB0083, baute2015 li2013, baute2015	factor 16 Nuclear tran- scription factor Y subunit C-2 NAC domain- containing	
Zm00001d02 <b>4323g</b> 2018	eichten2013, baute2015	containing protein 21/22 Putative WRKY DNA- binding domain super- family protein	(48) flavonoid biosynthesis (in equisetum); (16) anthocyanin biosynthesis
Zm00001d0 wang2018 Zm00001d02625ig2018	eichten2013 li2013, baute2015 li2013, baute2015	plant color compo- nent at R1 Putative AP2/EREB tran- scription factor su-	(14) L-glutamine degradation I; (12) anthocyanin biosynthesis; (11) glycerophosphodiester degradation; (10) flavonoid biosynthesis (in equisetum)
Zm00001d0 wang2018 Zm00001d028007g2018	li2013, baute2015	perfamily protein Floral homeotic protein APETALA 2 Calmodulin-	(11) proanthocyanidins biosynthesis from flavanols  (26) gluconeogenesis I; (7) fatty acid
Zm00001d0 wang2018	li2013, baute2015	binding tran- scription activator 2 Homeobox- leucine zipper protein	biosynthesis initiation I
Zm00001d02 <b>9963</b> g2018  Zm00001d0 li2013,wang	baute2015, wang2018	v	(48) response to wounding; (15) cutin biosynthesis; (10) regulation of
Zm00001d03 <b>%</b> 27g2018	li2013, baute2016, baute2015	scription factor7  Dof zinc finger protein	transcription, DNA-templated; (8) jasmonic acid biosynthesis; (6) regulation of transcription, DNA-templated; (5) response to wounding (11) cell proliferation; (9) regulation of transcription, DNA-templated
Zm00001d0 wang2018 Zm00001d030908g2018	li2013, baute2015 li2013, baute2015	DOF2.2 B3 domain- containing protein B3 domain- containing protein	
Zm00001d0 wang2018 Zm00001d03 <b>1665</b> g2018 Zm00001d0 li2013,li201	baute2015, wang2018 baute2016, baute2015 tissue atlas,	factor bHLH62 Transcriptio factor bHLH137 BEL1- like	(24) response to wounding; (7) response to wounding on (12) triacylglycerol degradation  (34) Calvin-Benson-Bassham cycle; (23) photosystem II assembly; (10)
Zm00001d03 <b>49204</b> 3	lin2017, li2019, zhou2018, krem- ling2018, huang2018, baute2016, baute2015	home- odomain protein 4	rRNA processing; (9) isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway; (7) gluconeogenesis I; (7) photosynthesis light reactions; (7) response to cytokinin; (7) positive regulation of transcription, DNA-templated; (6) photosynthetic electron transport in photosystem I; (5) response to salt stress
Zm00001d0 li2013,li201	atlas, zhou2018 shaefer2018 baute2015,	NAC	
Zm00001d03 <b>5i291</b> 3	li2013, baute2016 tissue atlas,	domain tran- scription factor su- perfamily protein Protein LSD1	(6) GDP-mannose biosynthesis
Zm00001d0 liu2017 Zm00001d03 <b>6(204</b> 3 Zm00001d0 wang2018	huang2018 lin2017, zhou2018 li2013, baute2016	protein B-box zinc finger protein 22 NAC	(20) glycolysis I (from glucose 6-phosphate)  (8) glycerophosphodiester degradation
Zm00001d04 <b>18220</b> 17 Zm00001d0 li2013	krem- ling2018, wang2018 baute2016, baute2015 huang2018,	domain contain- ing protein 36 DNA binding protein Two-	
Zm00001d0 li2013 Zm00001d04 <b>3i220</b> 13,li2013	li2013  ,ki20thXing201 baute2016, shae- fer2018,	component response regulator ARR11	(20) homogalacturonan degradation
Zm00001d0 li2013,wang	li2019, tissue atlas, lin2017, zhou2018, li2013 li2013, baute2015	C3H- type tran-	
Zm00001d044355g2018 Zm00001d0 li2013	li2013, baute2015 huang2018, zhou2018	scription factor B3 domain- containing protein	(8) regulation of transcription by RNA polymerase II; (7) cellulose biosynthesis; (7) triacylglycerol
Zm00001d04 <b>55&amp;0</b> 17	li2013, baute2016, baute2015	Putative MYB DNA- binding domain super- family	degradation
Zm00001d0 li2013,liu20	atlas, eichten2013 maza- heri2019, lin2017, krem- ling2018, huang2018, li2019, zhou2018, li2013,	protein Zinc finger	(66) rRNA processing; (21) photosynthesis light reactions; (14) photosynthesis, light harvesting in photosystem I; (12) thylakoid membrane organization; (12) RNA modification; (10) response to cytokinin; (7) Calvin-Benson-Bassham cycle; (6) chloroplast organization
Zm00001d04 <b>63(23)</b> 17 Zm00001d0 li2013,liu20	baute2015 fu2013, li2013, baute2016, baute2015 tissue atlas, eichten2013 lin2017, krem-	tran- scription	4-phosphate pathway; (60) thylakoid membrane organization; (24) 3,8-divinyl-chlorophyllide <i>a</i>
	ling2018, huang2018, li2019, zhou2018, baute2016, wang2018, lei- boff2015, shae- fer2018, li2013,	factor su-	biosynthesis I (aerobic, light-dependent); (18) positive regulation of transcription, DNA-templated; (13) pyrimidine ribonucleotides interconversion; (12) RNA modification; (10) chloroplast organization; (10) palmitate biosynthesis II (bacteria and plants); (6) chloroplast organization; (6) tetrapyrrole biosynthesis I (from glutamate)
Zm00001d04 <b>6442</b> 017 Zm00001d0 li2013,wang	baute2015 li2013, baute2016, baute2015 leiboff2015, shae- fer2018, lin2017,	FAR1- domain family sequence basic leucine- zipper 52	<ul><li>(7) formate oxidation to CO<sub>2</sub></li><li>(15) cell proliferation</li></ul>
Zm00001d0475663g2018 Zm00001d0 wang2018 Zm00001d0476999g2018	li2013, baute2015 li2013, baute2015 li2013, baute2015 li2013,	ethylene insensitive- like1 Zinc finger protein 1 Putative	(6) translation
Zm00001d0 li2013	leiboff2015, lin2017,	HLH DNA- binding domain super- family protein Putative home-	
Zm00001d05 <b>27298</b> 3	zhou2018	home- obox DNA- binding domain super- family protein Homeodoma	nin-
Zm00001d05 <b>2729H</b> 3 Zm00001d0 wang2018	leiboff2015, shae- fer2018, li2013 li2013, baute2016, baute2015	Homeodoma like super- family protein Putative WRKY DNA- binding domain	
Zm00001d05 <b>3i22)4</b> 3	tissue atlas, krem- ling2018, h:2019	domain super- family protein myb domain protein 60	(33) thylakoid membrane organization; (30) isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway; (22) rRNA processing; (17) trioudely cored degradation; (11)
	li2019, zhou2018		response to cold; (9) chloroplast organization; (7) photosystem II assembly; (7) Calvin-Benson-Bassham cycle; (5) photosynthesis light reactions; (5) RNA modification