ID Support eQTL study	Support GRN	TF Annotation	Target enrichment
Zm00001d0 li2013	li2013, baute2015	Floral homeotic protein APETALA	
Zm00001d00 3D62 3	tissue atlas, huang2018,	2 Zinc finger protein	(28) rRNA processing; (16) photosystem II assembly; (16) photosynthesis light reactions; (6)
Zm00001d0 wang2018	baute2015, wang2018	LIKE 5 C2H2- like zinc	Sphenylpropanoid biosynthesis; (5) chloroplast organization
Zm00001d00 \$0i20 17,wang	g b@ii\$ e2016, baute2015, baute2016,	finger protein WRI1 tran- scription	
$\rm Zm00001d0\ li2013$	baute2015 li2013, baute2015	factor1 Transcription factor bHLH130	(24) L-alanine degradation II (to D-lactate)
Zm00001d00 6/207 3	huang2018, li2013	BRASSINAZ RESISTANT 1	
Zm00001d0 li2013 Zm00001d01 00020 17	li2013, baute2015	GRAS tran- scription factor BEL1-	
	wang2018	like home- odomain protein 9	
Zm00001d0 liu2017	li2013, baute2015	Putative GATA tran- scription factor	
Zm00001d01 2605 g2018	li2013, baute2015	family protein MRP interact-	
Zm00001d0 wang2018	li2013, baute2015	ing1 sequence- specific DNA binding tran-	(18) suberin monomers biosynthesis; (13) L-glutamate degradation IV
Zm00001d0157at3g2018	tissue atlas, zhou2018	scription factors Transcriptio factor HY5	n(73) thylakoid membrane organization; (10) transmembrane transport; (9) positive regulation of
Zm00001d0 wang2018	li2013, baute2015	Dof zinc finger	transcription, DNA-templated; (8) chloroplast organization
Zm00001d01 %465 g2018 Zm00001d0 wang2018	li2013, baute2015 baute2016,	protein DOF2.1 sister of	
Ü	baute2015	indeter- minate spikelet1	
Zm00001d02 00i20 17,wanş	baute2016, baute2015, li2013,	Protein PHR1- LIKE 3	
Zm00001d0 liu2017	baute2015 li2013, baute2015	Ethylene- responsive tran- scription factor	
Zm00001d02 0408 g2018	li2013, baute2015	ERF117 Typical P-type R2R3 Myb protein	(9) gnoveneller :
Zm00001d0 wang2018 Zm00001d0240a2017,wang		domain7 bZIP	(9) sporopollenin precursors biosynthesis; (8) sucrose degradation II (sucrose synthase)
700005	baute2016, baute2015, li2013, baute2015	tran- scription factor 16	
Zm00001d0 liu2017,war	li2013, baute2015, li2013, baute2015	Nuclear tran- scription factor Y subunit C-2	
Zm00001d02 42363 3,liu201	7i2013, baute2015, li2013, baute2015	C-2 NAC domain- containing protein	
$\rm Zm00001d0~wang2018$	li2013, baute2015	21/22 plant color compo-	(57) anthocyanin biosynthesis; (19) flavonoid biosynthesis (in equisetum)
Zm00001d02 9963 g2018	baute2015, wang2018	nent at R1 myb-like tran- scription factor family	
Zm00001d0 wang2018	li2013, baute2016	family protein myc tran- scription factor7	(28) regulation of transcription, DNA-templated; (20) cutin biosynthesis; (14) regulation of transcription, DNA-templated; (13) response to wounding; (9) jasmonic acid biosynthesis; (8) response to wounding; (7) phospholipases
Zm00001d03 %72/ 7g2018	li2013, baute2015	Dof zinc finger protein	wounding; (7) phospholipases (11) microtubule cytoskeleton organization
Zm00001d0 wang2018	li2013, baute2015	DOF2.2 B3 domain- containing protein	(7) xylose degradation I
Zm00001d03 i56i g2018 Zm00001d0 wang2018	baute2015, wang2018 baute2016,	factor bHLH62 Transcripti	n(31) response to wounding; (12) pyrimidine ribonucleosides salvage II; (8) protein targeting to membrane (20) triacylglycerol degradation
Zm00001d03 38938 g2018	tissue atlas, baute2015	factor bHLH137 BEL1- like home-	(34) Calvin-Benson-Bassham cycle; (24) rRNA processing; (7) photosynthesis light reactions; (6)
Zm00001d0 li2013	baute2016, baute2015	odomain protein 4 Putative NAC domain tran- scription factor su- perfamily	photosystem II assembly (6) cellulose biosynthesis
Zm00001d03 51291 3	tissue atlas, huang2018	protein Protein LSD1	(10)
Zm00001d0 li2013	li2013, baute2016	B-box zinc finger protein 22	(19) glycolysis I (from glucose 6-phosphate)
Zm00001d04 1272 017	li2013, baute2016	Putative axial regulator YABBY	
${ m Zm}00001{ m d}0$ li 2013	li2013, baute2015	2 Heat stress tran- scription factor	
Zm00001d04 42260 3	li2013, baute2015	C-1 C3H- type tran- scription	
Zm00001d0 li2013,wang	huang2018, li2013, baute2015, wang2018, li2013,	scription factor B3 domain- containing protein	(5) triacylglycerol degradation
Zm00001d04 47331 3	baute2015 zhou2018, huang2018		(18) triacylglycerol degradation; (8) regulation of transcription by RNA polymerase II
Zm00001d0 liu2017	li2013, baute2016, baute2015	Putative MYB DNA- binding domain super- family	
Zm00001d04 5620 17	li2013, baute2015	family protein Zinc finger protein CONSTANS LIKE	(46) photosynthesis, light harvesting in photosystem I; (19) photosynthesis light reactions; (17) rRNA processing; (7) response to cold; (6) photosynthesis
Zm00001d0 liu2017 Zm00001d04 6402 017	li2013, baute2015 baute2016,	16 Putative	(66) isopentenyl diphosphate
	baute2015	homeodoma like tran- scription factor su- perfamily protein	ibiosynthetic process, methylerythritol 4-phosphate pathway; (59) thylakoid membrane organization; (21) positive regulation of transcription, DNA-templated; (14) tetrapyrrole biosynthesis I (from glutamate); (12) RNA modification; (12) 3,8-divinyl-chlorophyllide <i>a</i> biosynthesis I (aerobic, light-dependent); (8) photosynthesis light reactions
Zm00001d0 liu2017	li2013, baute2016, baute2015	FAR1- domain family sequence	
Zm00001d0476ah9g2018 Zm00001d0_wang2018	li2013, baute2015	basic leucine- zipper 52	(6) translation
Zm00001d0 wang2018 Zm00001d04 7963 g2018	li2013, baute2015 li2013,	ethylene insensitive- like1 Zinc	(6) translation (20) gluconeogenesis I
Zm00001d0 wang2018	baute2015 li2013, baute2015	finger protein 1 Auxin response	
Zm00001d05 384f g2018	li2013, baute2016	factor 1 Putative WRKY DNA- binding domain super-	
Zm00001d0 li2013	tissue atlas, zhou2018, li2019, huang2018	super- family protein myb domain protein 60	(36) thylakoid membrane organization; (27) isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway; (15) chloroplast organization; (12) photosynthesis, light harvesting in photosystem I; (11) Calvin-Benson-Bassham cycle:
			(11) Calvin-Benson-Bassham cycle; (6) response to cytokinin