Supplementary Table 2 Major genes of exon junction complex response drought stress in young tassels

Gene ID	Qi319	X178	Yu12	Chang7-2	Tie7922	Ye478	B73	Dan340	Ji81162	Putative annotation
GRMZM5G801627		3.36	1.58				1.68	1.56	1.96	Zinc finger protein(***c3h39***)
GRMZM2G098813				1.51	-1.46		1.64	1.04	1.73	LFY transcription factor(***zfl1***)
GRMZM2G061292				1.78	-1.45		1.24	1.05	1.30	Zinc finger protein(***dof26***)
GRMZM2G135447		2.18		2.74	2.30	1.90		2.30		Homeobox-transcription factor 8 (***hb8***)
GRMZM5G850129	1.14			1.09	-1.02		1.20	1.50		GRF transcription factor(***grftf11***)
GRMZM2G011357		-7.89			-1.76		-3.95	-1.76	-2.30	Zinc finger protein(***id1***)
GRMZM2G147867	-2.31	-7.61		-2.68		-3.76	-4.03	-2.30	-8.03	NAC transcription factor(***nactf3***)
GRMZM2G111136			-1.18	-1.49	-3.37		-2.10	-1.89	-2.43	SPL transcription factor(***sbp10***)
GRMZM2G044537			1.27		1.72	-2.43	-1.35	1.21	1.97	Zinc finger protein(Os02G45710)
GRMZM2G134687		-2.30	-2.66	-4.05			-1.76	-1.18	-2.22	NAC transcription factor(***nactf88***)
GRMZM2G021276	-2.19	-1.88		-1.79		-1.19	-1.34	-1.58	-3.34	bHLH transcription factor(***bhlh16***)
GRMZM2G042101		-3.19		-1.39	1.32	-1.09			-2.08	bHLH transcription factor(***bhlh155***)
GRMZM2G116491		-2.00	-1.11	-1.41	1.46		-1.27		-2.44	WRKY transcription factor(AT4G31805)
GRMZM2G139372		-2.90	-1.14		-1.30	-1.64			-3.47	bHLH transcription factor(***bhlh51***)

Gene ID	Qi319	X178	Yu12	Chang7-2	Tie7922	Ye478	B73	Dan340	Ji81162	Putative annotation
GRMZM2G162450	-2.19	-7.61		-3.68		-1.23	-10.20	-1.55	-8.35	bHLH transcription factor (***bhlh22***)
GRMZM5G851490		-2.30		-2.09			-2.36	-1.42	-2.59	WRKY transcription factor (Os01G18584)
GRMZM5G813651		-2.02		-1.31			-1.05	-1.04	-3.00	NAC transcription factor(***nactf95***)
GRMZM2G178894		-1.73	-1.21	-1.17	-1.05				-1.49	Zinc finger protein 8 (*ZFP8*, AT2G41940)
GRMZM2G314660		-1.64		-1.03		-1.07	-2.11		-2.16	Trihelix transcription factor18 (***thx18***)
GRMZM2G083850	-8.21			-1.51		-2.88	-1.25	-2.64	-4.13	VIP1 protein (Os05G47470)
GRMZM2G433184		-3.78		-1.36		-1.47	-3.50	-2.83	-4.38	Disease resistance-responsive protein (AT5G42500)
GRMZM2G058394	-1.22	-2.58		-1.29			-1.33		-3.64	Pathogenesis-related thanmatin protein (AT5G02140)
GRMZM2G371167	-1.77	3.35		-2.87		2.22	-1.99	2.07	-4.07	Response to low sulfur 1 (*LSU1*, AT3G49580)
GRMZM2G011006	-2.41	2.07		-1.50		-1.16			-1.41	Oxidative stress 3 (*ATOXS3*,*OXS3*, AT5G56550)
GRMZM2G010909	-1.15		1.45		1.84		1.84	1.30		Wound-induced protein WI12 (Os03G18770), Nuclear transcript factor 2(*NTF2*, AT5G01740)
GRMZM5G854138	-1.84	-1.15	-1.16	-1.87	1.03		-3.70		-2.97	Abscisic stress-ripening (*aasr2*) (***ZmASR2***)
GRMZM2G136910		2.70		-1.20	-1.06	1.59	-3.68			Abscisic stress-ripening (*aasr1*) (***ZmASR1***)
GRMZM2G439951	-1.03	-1.17		-1.19				-1.11	-1.35	Phosphate-responsive 1 protein (*EXO*, AT4G08950)
GRMZM2G008196	-2.10	-9.21		-4.20		-1.72	-4.40	-2.77	-5.46	Phosphate-induced protein 1 (Os06G11650)

Gene ID	Qi319	X178	Yu12	Chang7-2	Tie7922	Ye478	B73	Dan340	Ji81162	Putative annotation
GRMZM2G052100	-1.22	-2.15		-1.04			-1.39	-1.64	-1.68	Abscisic stress-ripening (*aasr5*) (***ZmASR5***)
GRMZM2G083599	-2.09	-1.27	-1.32		-1.30		-2.64	-1.86	-2.87	O-Glycosyl hydrolases family 17 protein (AT1G64760)
GRMZM2G476699		-1.86		-1.11	-1.69		-1.33		-2.06	Glycosyltransferase family 61 protein (AT3G18180)
GRMZM2G025783	-1.51	1.31				-1.16		-1.04	-1.37	Galactose oxidase/kelch protein (AT2G44130), F-box domain protein (*OsFBK25*, Os11G14140)
GRMZM2G059693	-2.17	1.37				-1.38	-3.38	-1.23		Lipase (Os05G06140), alpha/beta-hydrolases (AT3G14360)
GRMZM2G315767		-1.28	-1.18	-1.57		-1.35	-1.39		-2.81	Acyl-transferase family protein (Os04G52164)
GRMZM2G018105	-1.68	-2.33		-1.13		-1.34	-1.35		-1.31	Lipase/Acylhydrolase protein (Os02G09620)
GRMZM2G141607	-1.19				-1.47	-1.13		-1.11	-1.33	Oxidoreductase short chain dehydrogenase/reductase (Os08G37130)
GRMZM2G031624	-2.69	-3.97		-1.14	1.46				-2.38	Plant U-box 23 (*PUB23*, AT2G35930)
GRMZM2G135713	-1.93	-1.91	-1.74	-1.16			-1.24			Plant U-box 23 (*PUB23*, AT2G35930)
GRMZM2G122715	-1.17		-1.40	-3.14				-1.04	-2.07	Calcium sensing receptor (*CaS*, AT5G23060)
GRMZM2G088613		2.79	1.20	-1.38			1.49	2.49	2.75	Transducin/WD40 repeat-like protein (AT3G18950)
GRMZM2G118507		-2.26		-1.42		-1.33	-1.01	-2.25		Aluminium activated malate transporter (Os06G22600)
GRMZM2G019974	-1.04			-2.92	-1.96		-1.03		-3.68	Organic cation/carnitine transporter 2 (*OCT2*, AT1G79360)

Gene ID	Qi319	X178	Yu12	Chang7-2	Tie7922	Ye478	B73	Dan340	Ji81162	Putative annotation
GRMZM2G088053	-1.12	-1.75					-1.33	-1.44	-1.96	Nodulin MtN21 /EamA-like transporter (AT1G21890)
GRMZM2G090563		-1.82	-1.45	-2.44			-2.21	-1.16		Lung seven transmembrane receptor (Os05G38720)
GRMZM5G800014	-1.15			-1.89	-2.25		-2.59	-1.13		Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein (AT3G44220)
GRMZM2G017991	-1.20	-2.68	-1.14	-2.38			-2.61	-1.90	-2.52	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein (AT3G44220)
GRMZM2G061910		-1.64			-1.69	-1.21		-1.41	-2.15	Late embryogenesis abundant (LEA) Bydroxyproline-rich glycoprotein (AT5G22870)
AC194158.3_FG005		-1.34	2.45			-2.89	-3.27		1.95	Patatin-like protein 6 (*PLP6*, AT2G39220)
GRMZM2G414047			1.59		1.09		-1.00	2.28	1.40	Patatin-like protein 6 (*PLP7*, AT3G54950)
GRMZM2G330159		1.04		1.10	-2.16		1.86		1.29	Ovate family protein (***ofp16***)
GRMZM2G026927		-3.26		-1.96			-2.07	-1.21	-2.16	Ovate family protein (***ofp28***)
GRMZM2G131421		-1.29	1.28	1.63			3.90	-3.06	3.06	Early nodulin-related protein (AT5G25940)
GRMZM2G085392	-1.05	-2.48	-1.26	-1.61	-1.12		-1.58		-2.33	Early nodulin-like protein 9 (*ENODL9*, AT3G20570)
GRMZM2G072274		1.06		1.49	-3.00		2.79	1.73	1.64	AT-hook motif nuclear-localized protein 22 (***baf1***)
GRMZM2G103512	-1.35			-1.90			-3.56	-1.44	-2.85	Germin-like protein 5 (*GLP5*, AT1G09560)

Gene ID	Qi319	X178	Yu12	Chang7-2	Tie7922	Ye478	B73	Dan340	Ji81162	Putative annotation
GRMZM2G104616	-1.23	-5.42	-1.06	-2.24		-1.74	-7.00	-1.86	-3.23	Proline-rich protein 2 (*PRP2*, AT2G21140)
AC225718.2_FG006			1.07		1.43	-1.72	-2.40	1.52		Calcium-binding EF-hand protein (AT2G46600)
GRMZM2G010912		-3.43	-1.25	-1.07	1.72		-1.79	-2.33	-2.69	Myosin heavy chain-related protein (AT5G10890)
GRMZM2G320206	-1.32	-2.52		-1.36		-1.32	-1.24		-2.17	Metacaspase 1 (*AtMAC1*, AT1G02170)
GRMZM2G073324		2.22	1.48	2.10	2.07			1.14	1.80	EID1-like 3 (EDL3, AT3G63060)
GRMZM2G141353	-2.91			-5.79	-9.14			-1.64	-4.68	Plant basic secretory protein (AT2G42900)
GRMZM2G053779			-1.94		-1.28	-1.48	-3.52	-2.32		Cupredoxin protein (AT1G72230)
GRMZM2G047319				-1.72	-1.78	-2.63	-2.40		-1.24	Subtilase family protein (AT3G14067)
GRMZM2G107686		-2.98				-1.17	-1.28	-1.27	-2.07	Subtilase family protein (*SDD1*, AT1G04110)
GRMZM2G036980	-1.39	-1.68	-2.39	-2.08	-1.30	-2.28	-1.15	-1.12		VQ domain containing protein (Os05g41250)
GRMZM2G170766		-2.37		-1.07		-1.15	-1.11		-1.25	IQ-domain 26 (*IQD26*, AT3G16490)
GRMZM2G306643	-2.39	2.55	1.04			-1.36	2.14			Protein of unknown function (DUF584）
GRMZM2G142721		1.12		1.26	-1.04		1.16		1.28	Protein of unknown function (DUF640）
GRMZM2G374074			2.88		2.08	-2.41	-2.43	1.05	1.92	Protein of unknown function (DUF1645)
GRMZM2G105522			2.49	-2.57		3.98	-1.23		-10.08	Protein of unknown function (DUF506)
GRMZM2G008622			-1.08			-1.72	-1.08	-1.15	-1.70	protein of unknown function (DUF639)

Gene ID	Qi319	X178	Yu12	Chang7-2	Tie7922	Ye478	B73	Dan340	Ji81162	Putative annotation
GRMZM2G366142	-1.13	-1.51		-1.39	-1.86		-2.07		-1.30	protein of unknown function (DUF868)
GRMZM2G336456			-1.02	-1.11	-1.24		-1.17	-1.04	-1.00	Protein of unknown function (DUF1666)
GRMZM2G084005	-1.33	3.79	1.29		1.39		1.20	1.41	1.85	NO FOUND
GRMZM2G084445	-1.20	-2.01	-1.52			-1.39	-2.19	-1.36	-1.89	NO FOUND
GRMZM2G312146	-1.43	-1.52			-1.16		-1.66		-1.67	NO FOUND
GRMZM2G331766		-1.83	-1.19	-1.44			-1.59		-2.04	NO FOUND
GRMZM2G401883		-1.39		-1.40	-1.81		-1.07		-2.06	NO FOUND
GRMZM2G405017			1.53	1.21	1.39	-1.99		2.07		NO FOUND
GRMZM2G542227		-2.74		-1.53	-1.08	-1.24			-2.77	NO FOUND
GRMZM2G165836	-1.18	-1.50		-1.02	1.09				-2.40	NO FOUND
GRMZM2G454056			2.96		1.88	-1.28		1.19	1.45	NO FOUND
GRMZM2G446363			-2.84		-1.34	-2.39	-13.01	-11.13		NO FOUND
AC210193.4_FG002	-1.00	-1.88	-1.32		-1.01		-1.78	-1.62	-1.83	NO FOUND
GRMZM2G037015			1.98		1.32	-2.61	-1.70		1.42	NO FOUND
GRMZM2G144051		-2.07		-2.09	-1.02			-1.03	-1.65	NO FOUND

Note: Five or more than five inbred lines common genes of EJC in significantly “RNA transcription” pathway were shown ($P<0.05$), and the $\log_2$ values of DEGs were showed by positive or negative numbers to reflect up-regulated or down-regulated expression change, respectively. The putative annotation were shown using maize database (www. maizeGDB.org), the gene ID and

names of homologous genes in rice or Arabidopsis were showed in parentheses and bold gene names showed maize genes.