

**Table S2.** Drought stress and their related candidate genes in model plant. A complement of this table is available from [29].

Gene	Acession number	Plant species	Function	References
<i>IDM1</i>	AT3G14980.1	<i>T. aestivum</i>	Preventing DNA hypermethylation of highly homologous multicopy genes and other repetitive sequences.	[52]
<i>CIPK3</i>	AT2G26980	<i>T. aestivum</i>	Encodes a serine-threonine protein kinase whose expression increases in response to ABA, cold, drought, high salt, and wounding conditions. The gene is expressed in developing seeds and seedlings	[52]
<i>PAL4</i>	AT3G10340	<i>T. aestivum</i>	Controls carbon flux to a variety of bioactive small-molecule aromatic compounds, and lignin	[52]
<i>CYP73A5</i>	AT2G30490	<i>T. aestivum</i>	Catalyzes the first oxidative step of the phenylpropanoid pathway in higher plants by transforming trans-cinnamate into p-coumarate	[52]
<i>ABCG11</i>	AT1G17840	<i>T. aestivum</i>	Essential for synthesis of plant organs like root development	[52]
<i>WAKL21</i>	A4A49_34180	<i>T. aestivum</i>	Signaling receptor of extracellular matrix component	[52]
<i>AMY1</i>	AT4G25000	<i>T. aestivum</i>	Expressed 7 to 9 days after from pollination and during the seed development	[52]
<i>RPS15AE</i>	AT4G29430	<i>T. aestivum</i>	Enables structural constituent of ribosome	[52]
<i>CYP94C1</i>	AT2G27690	<i>T. aestivum</i>	Bioactive phytohormone of the jasmonate hormonal pathway regulating important defensive and developmental processes in plants	[52]
<i>NPY1</i>	YGL067W	<i>T. aestivum</i>	Regulates phototropic responses along with protein kinases	[52]
<i>PSAT2</i>	AT2G17630	<i>T. aestivum</i>	Enables O-phospho-L-serine:2-oxoglutarate aminotransferase activity, pyridoxal phosphate binding	[52]
<i>FH6</i>	AT5G67470	<i>T. aestivum</i>	Enables actin binding	[52]
<i>RXF12</i>	AT1G58370	<i>T. aestivum</i>	Improves the dough's rheological properties, such as softness, ductility, and elasticity, and the bread's specific volume and crumb hardness	[52]
<i>TIN1</i>	AT5G64510	<i>T. aestivum</i>	Acts as transcriptional factor which controls buds outgrowth	[52]
<i>FY</i>	AT5G13480	<i>T. aestivum</i>	Regulation of flowering time	[51]
<i>MAP1A</i>	AT2G45240	<i>T. aestivum</i>	Removes the N-terminal methionine from proteins leading to abnormal development	[51]
<i>LRL2</i>	AT4G30980	<i>T. aestivum</i>	Regulates root hair and sperm cell	[51]

			development	
<i>ERMO2</i>	AT3G07100	<i>T. aestivum</i>	Required for endoplasmic reticulum (ER) morphology	[51]
<i>RGLG2</i>	AT5G14420	<i>T. aestivum</i>	Negatively regulates the drought stress response by mediating the ERF53 transcriptional activity	[51]
<i>RBOHB</i>	AT1G09090	<i>T. aestivum</i>	Plays a role in seed after-ripening	[51]
<i>GNL1</i>	AT5G39500	<i>T. aestivum</i>	Required for endoplasmic reticulum (ER) morphology	[51]
<i>CYP70982</i>	NA	<i>T. aestivum</i>	Not found	[51]
<i>AGO1</i>	AT1G48410	<i>T. aestivum</i>	Regulates genes involved in the cross talk between auxin and light signaling during adventitious root development	[51]
<i>DMP10</i>	OSNPB_010389700	<i>T. aestivum</i>	DOMAIN MEMBRANE PROTEIN 10	[51]
<i>PSKR1</i>	AT2G02220	<i>T. aestivum</i>	Contains dual guanylate cyclase and kinase catalytic activities that operate in vivo	[51]
<i>CSC1</i>	AT4G22120	<i>T. aestivum</i>	Calcium-permeable stretch activated cation channel.	[51]
<i>GME</i>	AT5G28840	<i>T. aestivum</i>	Catalyzes the conversion of GDP-D-mannose to GDP-L-galactose.	[51]
<i>ARR12</i>	HvARR12	<i>H. vulgare</i>	two-component response regulator	[230]
<i>PIP</i>	HvPip	<i>H. vulgare</i>	Proline iminopeptidase	[230]
<i>DI19-2</i>	HvDI19-2	<i>H. vulgare</i>	Dehydration stress-inducible gene	[230]
<i>ADC</i>	HvADC	<i>H. vulgare</i>	Arginine decarboxylase	[230]
<i>HRGP</i>	HvHRGP	<i>H. vulgare</i>	Hydroxyproline-rich glycoprotein	[230]
<i>PRP</i>	HvPRP	<i>H. vulgare</i>	Proline-rich family protein	[230]
<i>C4H</i>	HvC4H	<i>H. vulgare</i>	Cinnamate-4-hydroxylase	[230]
<i>OsALDH2-1</i>	Os01g40860	<i>O. sativa</i>	Expressed in seeds and no essential for seed vigor	[231]
<i>OsALDH2-2</i>	Os01g40870	<i>O. sativa</i>	Expressed in seeds and essential for seed vigor	[231]
<i>OsWRKY45</i>	Os05g25770	<i>O. sativa</i>	Defense ABA signaling pathway	[231]
<i>OsMSOD1</i>	Os05g25850	<i>O. sativa</i>	Limits reactive oxygen species damage during drought stress	[231]
<i>OsRCN1</i>	Os11g05470	<i>O. sativa</i>	Expressed in vein leaf and important for floral transition	[231]
<i>OsZIP79</i>	Os11g05480	<i>O. sativa</i>	Regulation of phytoalexin production	[231]
<i>OsZIP80</i>	Os11g05640	<i>O. sativa</i>	Dehydration stress-inducible gene	[231]
<i>LOC103637669</i>	Zm00001d029938	<i>Z. mays</i>	Protein ARABIDILLO 1	[232]
<i>S1_93277641</i>	Zm00001d029937	<i>Z. mays</i>	Glycoprotein	[232]
<i>PZE-103003226</i>	Zm00001d039319	<i>Z. mays</i>	Tic22-like family protein	[232]
<i>LOC100500952</i>	Zm00001d042997	<i>Z. mays</i>	HIT-type zinc-finger family protein	[232]
<i>LOC100284853</i>	Zm00001d029937	<i>Z. mays</i>	Glycoprotein	[232]
<i>LOC103637669</i>	Zm00001d029938	<i>Z. mays</i>	Protein ARABIDILLO 1	[232]
<i>LOC100272678</i>	Zm00001d020506	<i>Z. mays</i>	26S proteasome non-ATPase regulatory subunit 9	[232]
<i>LOC100283961</i>	Zm00001d013992	<i>Z. mays</i>	Pyridoxal phosphate-dependent transferase family protein	[232]
<i>chr2.S_68691618</i>	Zm00001d003939	<i>Z. mays</i>	11- $\beta$ -hydroxysteroid dehydrogenase	[232]

<i>S2_226449870</i>	GRMZM2G070937	<i>Z. mays</i>	Leu-rich repeat protein kinase family	[232]
<i>LOC100286093</i>	Zm00001d012167	<i>Z. mays</i>	Silk fibroin (SF16) protein	[232]
<i>SbZfl1</i>	NA	<i>S. bicolor</i>	SET binding factor 1	[67]
<i>SbCN12</i>	NA	<i>S. bicolor</i>	Ortholog of ZCN12 that have been proposed to encode florigens	[67]
<i>BADH</i>	I8G32_RS03395	<i>S. bicolor</i>	2-hydroxycyclohexanecarboxyl-CoA dehydrogenase	[77]
<i>RuBisCO</i>	Csa_5G609710	<i>S. bicolor</i>	Ribulose biphosphate carboxylase small chain, chloroplastic-like	[77]
<i>PEPC</i>	AT3G14940	<i>S. bicolor</i>	Phosphoenolpyruvate carboxylase	[77]
<i>DHN</i>	SORBI_3009G11670 0	<i>S. bicolor</i>	Dehydrin DHN1	[77]
<i>PTKs</i>	NA	<i>S. bicolor</i>		[77]
<i>BADH</i>	NA	<i>Brassica napus</i>	Betaine aldehyde dehydrogenase	[233]
<i>P5CS2</i>	AT3G55610	<i>B. napus</i>	Delta 1-pyrroline-5-carboxylate synthetase	[233]
<i>ADC2</i>	AT4G34710	<i>B. napus</i>	Arginine decarboxylase	[233]
<i>btg-26</i>	HID58_028326	<i>B. napus</i>	Aldehyde dehydrogenase family 7 member A1- Brassica turgor gene 26	[233]
<i>MDA</i>	GRMZM2G081380	<i>Maize</i>	Ca <sup>2+</sup> binding actin bunding protein	[234]
<i>REC</i>	GRMZM2G171179	<i>Maize</i>	AP2/EREB160 transcription factor	[234]
<i>SOD</i>	GRMZM2G152278	<i>Maize</i>	Calcium-dependent lipid binding protein	[234]
<i>BART1_0-P29927</i>	HORVU4Hr1G0603 70	<i>Barley</i>	Protein phosphatase 2C family protein	[235]
<i>BART1_0-P34164</i>	HORVU5Hr1G0279 10	<i>Barley</i>	Chaperone protein htpG family protein	[235]
<i>BART1_0-p07678</i>	HORVU2Hr1G0109 90	<i>Barley</i>	Aquaporin-like superfamily protein	[235]
<i>BART1_0-P51213</i>	HORVU7Hr1G0370 80	<i>Barley</i>	Low quality protein: annexin D2	[235]
<i>BART1_0-P29181</i>	HORVU4Hr1G0495 00	<i>Barley</i>	Sucrose synthase 3	[235]
<i>BART1_0-P15058</i>	HORVU2Hr1G1068 80	<i>Barley</i>	Putative zeaxanthin epoxidase	[235]
<i>BART1_0-P37103</i>	HORVU5Hr1G0707 20	<i>Barley</i>	Molecular chaperone HtpG	[235]
<i>GhHUB2</i>	GhHUB2-A (XM_016856414), GhHUB2-D (XM_016843047)	<i>Cotton</i>	Histone H2B monoubiquitinatin E3 ligase encoding gene	[236]
<i>GhMKK3</i>	HQ828070	<i>Cotton</i>	Enhanced drought tolerance	[237]
<i>GhMAP3K40</i>	LOC107939304	<i>Cotton</i>	Salt and drought stress tolerance at the germination stage	[238]
<i>GhMPK4</i>	CotAD_19088	<i>Cotton</i>	Increased sensitivity to ABA, salt, and drought	[239]
<i>GhMPK17</i>	NM001035863	<i>Cotton</i>	Osmotic and salt stress tolerance	[240]
<i>GbMPK3</i>	NP_190150	<i>Cotton</i>	Enhanced oxidative and drought stress tolerance	[241]