Supplementary Table S2: Differentially expressed target genes under drought stress.

Turfgrass species	Accession/unigene number	Responsive gene/signal compound	Downstream genes	Related function	Up/down regulation	Tissue	Study	Reference
Festuca arundinacea (Schreb.)	CL5735.Contig4_All	*GolS1*	*Rafs*	Galactinol synthase 1	Up	Rhizome/Rhizome node	RNA-seq	[32]
	CL2933.Contig6_All	*Rafs*	*STS*	Raffinose synthase				
	CL22635.Contig3_All	*PGM*	*SerA, GlyA*	Phosphoglycerate mutases are involved in amino acid synthesis				
	CL241.Contig4_All	*PYL*	*ABF, SnRK2*	ABA sensing				
	CL10647.Contig2_All	*PP2C*	*SnRK2.4, SnRK2.6*	ABA signaling pathway regulation				
	CL11423.Contig1_All	*B-ARR*	*CKX*	CK response regulators				
	CL16538.Contig1_All	*GID1*	*SCFSLY1*	GA signaling regulator				
	CL3797.Contig2_All	*SnRK2*	*RD29B, ABF2*	Sucrose non-fermenting 1–related protein kinase 2				
	*	*NCED*	*AAO3, MCSU*	ABA-responsive element binding factors involved in ABA biosynthesis and signaling pathway				
	CL3512.Contig4_All	*SAURs*	*EXPANSIN, XTH*	SMALL AUXIN UP RNAs				
Festuca arundinacea (Schreb.)	–	*NCED*	*RD29A*	ABA-responsive element binding factors involved in ABA biosynthesis and signaling pathway	Up	Leaf, pseudostem, root, Crown	RNA-seq	[76]
	–	*CYP70A*	*CYP707A*	ABA 8'-hydroxylase				
	–	*LOG*	*ARR5*	CK synthesis				
	–	*CKX*	*ARR12*	CK degradation				
	–	*GA2 oxidase*	*GAMYB/GA20ox*	Gibberellin synthesis degradation gene				
	–	*SWEET/MtN3-like genes*	*SUT1/bZIP53*	Plant growth and development, Sugar transport, Environmental adaptation				
	–	*ACC oxidase*	*ERF1/CTR1*	1-Aminocyclopropane-1-carboxylate oxidase				
	–	*ACC synthase*	*ERF1/VSP*	1-Aminocyclopropane-1-carboxylate synthase				
	–	*12-Oxo PDA reductase*	*JAZ1/VSP*	Jasmonic acid biosynthesis from linolenic acid	Up	Leaf		
	–	*PHOR1*	*GID1*	GA signaling	Up	Leaf, pseudostem, root, Crown		
	–	*SGT*	*PR1*	SA glucosyltransferase, ether and ester forming				
Lolium arundinaceum (Schreb.) Darbysh.	PF00069.20 and PF07714.12	*MAPK/ CDK/ AKT*	*WRKY53/RB1*	Protein kinase	Up	A pool of leaf, shoot, root, and inflorescence	RNA-seq	[77]
	PF00067.17	*CYP family genes*	*GSTU7/ABCC3*	P450				
	PF13041.1	*PPR2*	*Mitochondrial nad4*	RNA-binding proteins/Electron transport chain complex I subunit (RNA-editing target)				
	PF00076.17	*RRM1*	*PCNA*	Ribonucleotide reductase catalytic subunit M1				
	PF13639.1	*zf-RING2*	*CYCD3*	Cell division, Ubiquitin chain assembly, Protein-protein interactions				
	PF00201.13	*UDP-glycosyl transferase*	*UGT78D2*	Secondary metabolite synthesis				
	PF00931.17	*NP-ARC*	*NIR1*	Plant development				
Lolium arundinaceum / Festuca arundinacea (Schreb.)	–	*SOS1*	–	Ion homeostasis	Up	Leaf	qPCR	[1]
	–	*ADC1*	–	Cytosolic polyamine synthetase				
Axonopus compressus L.	–	*MAP kinase1*	–	Triggering a signal transduction pathway	Up	Leaf	RNA-seq	[72]
	–	*PIP2*	–	Facilitating H_2O_2 transport, linking oxidative signaling to stress responses				
Agrostis stolonifera	GR281936.1	*CDPK26*	–	Abiotic stress-responsive TFs	Up	Leaf	qPCR	[10]
	DV866362.1	*MAPK1*	–	Abiotic stress-responsive TFs				
	DV866921.1	*14-3-3*	–	Abiotic stress-responsive TFs				
	DV862003.1	*ABF3*	–	Abiotic stress-responsive TFs				
Lollium perenne L.	JF747479	*HSP70*	*HSFA2, HSP17.6, HSP101*	Heat shock protein 70	Up	Leaf	qPCR	[66]
	XM_047189720	*HSP26.2*	–	Mitochondrial small heat shock protein				
	XM_047191399	*HSP90.6*	–	Heat shock protein 90-6				
	JF747449	*APX*	*GST, GPX, PRX Q, RBOHD, FOX1*	Ascorbate peroxidase, scavenging H_2O_2				
	JF747451	*MDHAR*	–	Monodehydroascorbate reductase, Ascorbic acid-mediated redox regulation-related gene				
	JF747452	*DHAR*	–	Dehydroascorbate reductase is involved in ascorbate recycling				
	XM_047233600	*GR*	*GST, GPX, GSH1, RBOHD*	Glutathione reductase				
	JF747381	*CAT*	*FOX1*	Catalase, scavenging H_2O_2				
	XM_047215214	*POD*	*RBOHD*	Peroxidases involved in stress responses				
	XP_047061758	*Cu/ZnSOD*	*FOX1*	Involved in Antioxidant Defense				
	EL664102	*Trx*	*NTRC, TRXR*	Thioredoxin, plant development, photosynthesis, and metabolism, and stress response				
	XM_047225703	*2-Cys Prx*	*TRXR, PRX Q*	Peroxide, ROS scavenging				
	XM_047224812	*FTR*	–	Involved in antioxidant defense				
	XM_047229918	*sHSP*	–	Chloroplastic small heat shock protein				

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