**Supplementary Material**

**Table S1** Analysis of variance (ANOVA) broad-sense heritability (*hB2*) of the investigated traits

**Table S2** Average phenotypic values for the germination related traits of parents and recombinant inbred lines (RIL) under control and PEG6000-treatment conditions

**Table S3** Correlations among the drought tolerance traits at germination stage

**Table S4** Correlation of drought tolerance coefficients among the drought tolerance traits at germination stage

**Table S5** QTL clusters for drought tolerance related traits at germination stage

**Table S6** High confidence genes annotation in the physical intervals of reference wheat genome corresponding to the QTL for drought tolerance in Berkut/Worrakatta RIL population

**Table S7** Transcriptional patterns of candidate genes under PEG6000 or drought stress

**Table S1** Analysis of variance (ANOVA) broad-sense heritability (*hB2*) of the investigated traits

|  |  |  |
| --- | --- | --- |
| **Trait 1** | **Source of variation** | ***hB2*** |
| **Genotype** | **Treatment** | **G×T 2** | **Replicate** | **Error** |
| GP | 0.148\*\* | 15.166\*\* | 0.024\*\* | 0.004 | 0.003 | 0.86 |
| GR | 0.194\*\* | 28.708\*\* | 0.028\*\* | 0.004 | 0.003 | 0.87 |
| GI | 0.386\*\* | 52.175\*\* | 0.058\*\* | 0.010\*\* | 0.006 | 0.87 |
| RN | 1.478\*\* | 17.938 | 0.701\*\* | 0.072\*\* | 0.132 | 0.66 |
| RL | 15.199\*\* | 19137.180\*\* | 6.373\*\* | 1.443\*\* | 0.710 | 0.69 |
| SH | 4.298\*\* | 10318.262\*\* | 1.786\*\* | 0.009\*\* | 0.274 | 0.69 |
| CL | 0.560\*\* | 15.070\*\* | 0.204\*\* | 0.016 | 0.029 | 0.72 |

1. GP, germination potential; GR, germination rate; GI, germination index; RN, root number; RL, root length; SH, shoot height; CL, coleoptile length. 2. The letters G and T indicate genotypes and treatments, respectively. \*\* Significant at the *P*<0.01 level.

**Table S2** Average phenotypic values for the germination related traits of parents and recombinant inbred lines (RIL) under control and PEG6000-treatment conditions

|  |  |  |  |
| --- | --- | --- | --- |
| **Trait 1** | **Treatment 2** | **Parent** | **RIL** |
| **Berkut** | **Worrakatta**  | **Mean 3** | **Min** | **Max** | **SD** | **CV (%)** | **Skewness** | **Kurtosis** |
| GP | CK | 0.77 | 0.73 | 0.47 | 0.01 | 0.88 | 0.18 | 38.62 | -0.12 | -0.52 |
|  | PEG | 0.34 | 0.49 | 0.28 \*\* | 0.00 | 0.71 | 0.16 | 55.91 | 0.39 | -0.52 |
| GR | CK | 0.88 | 0.95 | 0.65 | 0.05 | 0.98 | 0.21 | 31.72 | -0.55 | -0.42 |
|  | PEG | 0.48 | 0.88 | 0.40 \*\* | 0.01 | 0.87 | 0.18 | 44.30 | 0.29 | -0.55 |
| GI | CK | 0.99 | 0.96 | 0.77 | 0.03 | 1.51 | 0.31 | 39.99 | 0.04 | -0.47 |
|  | PEG | 0.61 | 0.78 | 0.44 \*\* | 0.01 | 1.09 | 0.23 | 52.39 | 0.50 | -0.28 |
| RN | CK | 3.70 | 4.25 | 4.57 | 1.24 | 5.16 | 0.46 | 10.06 | -2.15 | 9.10 |
|  | PEG | 2.90 | 3.95 | 4.37 \*\* | 0.47 | 5.27 | 0.72 | 16.43 | -2.38 | 7.85 |
| RL | CK | 14.14 | 10.44 | 10.83 | 1.77 | 15.96 | 2.24 | 20.70 | -0.68 | 0.47 |
| (cm) | PEG | 6.42 | 5.81 | 4.38 \*\* | 0.22 | 9.26 | 1.47 | 33.60 | -0.09 | 0.15 |
| SH | CK | 8.46 | 6.84 | 7.57 | 0.72 | 10.13 | 0.92 | 12.11 | -1.68 | 10.69 |
| (cm) | PEG | 4.58 | 3.15 | 2.83 \*\* | 0.05 | 6.35 | 1.09 | 38.47 | -0.01 | -0.21 |
| CL | CK | 1.67 | 1.91 | 1.85 | 0.53 | 2.50 | 0.27 | 14.70 | -0.50 | 1.28 |
| (cm) | PEG | 1.70 | 2.08 | 1.67 \*\* | 0.08 | 2.48 | 0.42 | 25.42 | -1.00 | 1.59 |
| DTC\_GP | - | 0.45 | 0.67 | 0.61 | 0.00 | 2.39 | 0.28 | 45.67 | 0.91 | 4.61 |
| DTC\_GR | - | 0.56 | 0.92 | 0.62 | 0.09 | 1.46 | 0.20 | 32.47 | 0.43 | 0.97 |
| DTC\_GI | - | 0.62 | 0.81 | 0.57 | 0.07 | 1.27 | 0.21 | 36.58 | 0.30 | -0.03 |
| DTC\_RN | - | 0.77 | 0.93 | 0.96 | 0.14 | 1.40 | 0.16 | 16.71 | -1.36 | 5.39 |
| DTC\_RL | - | 0.47 | 0.56 | 0.41 | 0.03 | 0.98 | 0.14 | 33.09 | 0.34 | 1.12 |
| DTC\_SH | - | 0.54 | 0.46 | 0.37 | 0.01 | 1.07 | 0.14 | 37.28 | 0.35 | 1.38 |
| DTC\_CL | - | 1.02 | 1.09 | 0.90 | 0.05 | 1.69 | 0.21 | 22.93 | -1.21 | 3.16 |
| D-value | - | 0.17 | 0.57 | 0.42 | 0.05 | 0.67 | 0.11 | 25.53 | -0.48 | 0.35 |

1. GP, germination potential; GR, germination rate; GI, germination index; RN, root number; RL, root length; SH, shoot height; CL, coleoptile length; DTC\_GP, drought tolerance coefficient of germination potential; DTC\_GR, drought tolerance coefficient of germination rate; DTC\_GI, drought tolerance coefficient of germination index; DTC\_RN, drought tolerance coefficient of root number; DTC\_RL, drought tolerance coefficient of root length; DTC\_SH, drought tolerance coefficient of shoot height; DTC\_CL, drought tolerance coefficient of coleoptile length; D-value, comprehensive drought tolerance evaluation. 2*.* CK, control; PEG, PEG6000 treatments. 3. This column indicates significant differences in the mean values of RILs between CK and PEG treatments; \*\* Significant at the *P* < 0.01 level.

**Table S3** Correlations among the drought tolerance traits at germination stage

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Trait 1** | **GP** | **GR** | **GI** | **RN** | **RL** | **SH** | **CL** |
| GP |  | 0.92\*\* | 0.95\*\* | 0.22\*\* | 0.27\*\* | 0.25\*\* | 0.26\*\* |
| GR | 0.94\*\* |  | 0.93\*\* | 0.27\*\* | 0.40\*\* | 0.33\*\* | 0.36\*\* |
| GI | 0.98\*\* | 0.96\*\* |  | 0.24\*\* | 0.35\*\* | 0.32\*\* | 0.27\*\* |
| RN | 0.44\*\* | 0.44\*\* | 0.44\*\* |  | 0.30\*\* | 0.48\*\* | 0.31\*\* |
| RL | 0.56\*\* | 0.56\*\* | 0.57\*\* | 0.48\*\* |  | 0.46\*\* | 0.27\*\* |
| SH | 0.52\*\* | 0.54\*\* | 0.53\*\* | 0.58\*\* | 0.72\*\* |  | 0.54\*\* |
| CL | 0.49\*\* | 0.54\*\* | 0.49\*\* | 0.58\*\* | 0.61\*\* | 0.74\*\* |  |

1*.* GP, germination potential; GR, germination rate; GI, germination index; RN, root number; RL, root length; SH, shoot height; CL, coleoptile length.The upper right triangle indicates the correlation coefficients under the control condition, whereas the lower left triangle indicates correlation coefficients under the PEG6000 condition. \*\* Significant at the *P*<0.01 level.

**Table S4** Correlation of drought tolerance coefficients among the drought tolerance traits at germination stage

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Trait 1** | **DTC\_GP** | **DTC\_GR** | **DTC\_GI** | **DTC\_RN** | **DTC\_RL** | **DTC\_SH** |
| DTC\_GR | 0.74\*\* |  |  |  |  |  |
| DTC\_GI | 0.91\*\* | 0.89\*\* |  |  |  |  |
| DTC\_RN | 0.35\*\* | 0.39\*\* | 0.37\*\* |  |  |  |
| DTC\_RL | 0.47\*\* | 0.51\*\* | 0.52\*\* | 0.47\*\* |  |  |
| DTC\_SH | 0.39\*\* | 0.42\*\* | 0.39\*\* | 0.49\*\* | 0.64\*\* |  |
| DTC\_CL | 0.37\*\* | 0.47\*\* | 0.41\*\* | 0.55\*\* | 0.51\*\* | 0.74\*\* |

1*.* DTC\_GP, drought tolerance coefficient of germination potential; DTC\_GR, drought tolerance coefficient of germination rate; DTC\_GI, drought tolerance coefficient of germination index; DTC\_RN, drought tolerance coefficient of root number; DTC\_RL, drought tolerance coefficient of root length; DTC\_SH, drought tolerance coefficient of shoot height; DTC\_CL, drought tolerance coefficient of coleoptile length. \*\* Significant at the *P*<0.01 level.

**Table S5** QTL clusters for drought tolerance related traits at germination stage

|  |  |  |  |
| --- | --- | --- | --- |
| **Clusters** | **Physical interval (Mb) 1** | **Marker interval** | **QTL 2** |
| C5A | 11.70-20.61 | *AX-111258240-AX-94458300* | *QGR.xjau-5AS, QCL.xjau-5AS, QD.xjau-5AS* |
| C5D | 560.42-567.39 | *AX-94524442−AX-110998507* | *QGP.xjau-5DL, QSH.xjau-5DL, QD.xjau-5DL* |

1. Physical interval, physical positions of SNP markers based on wheat genome sequences from the International Wheat Genome Sequencing Consortium (IWGSC, <http://www.wheatgenome.org/>). 2*.* GP, germination potential; GR, germination rate; SH, shoot height; CL, coleoptile length; D-value, comprehensive drought tolerance evaluation.

**Table S6** High confidence genes annotation in the physical intervals of reference wheat genome corresponding to the QTL for drought tolerance in Berkut/Worrakatta RIL population

| **QTL 1** | **Gene ID** | **Start/bp** | **End/bp** | **Function description** |
| --- | --- | --- | --- | --- |
| *QD.xjau-5AS* | *TraesCS5A02G016100* | 11907808 | 11909024 | Werner Syndrome-like exonuclease |
|  | *TraesCS5A02G016200* | 11935532 | 11942908 | Pleiotropic drug resistance ABC transporter |
|  | *TraesCS5A02G016300* | 11965278 | 11969496 | Haloacid dehalogenase-like hydrolase domain-containing protein |
|  | *TraesCS5A02G016400* | 12191633 | 12192562 | Serine/threonine-protein kinase |
|  | *TraesCS5A02G016500* | 12192649 | 12194214 | Serine/threonine-protein kinase |
|  | *TraesCS5A02G016600* | 12408198 | 12415458 | Terpene synthase |
|  | *TraesCS5A02G016700* | 12555790 | 12561217 | Terpene synthase |
|  | *TraesCS5A02G016800* | 12578834 | 12579466 | TTF-type zinc finger protein with HAT dimerization domain-containing protein |
|  | *TraesCS5A02G016900* | 12678629 | 12678826 | RING/U-box superfamily protein |
|  | *TraesCS5A02G017000* | 12818891 | 12821550 | ATP synthase subunit epsilon, mitochondrial |
|  | *TraesCS5A02G017100* | 13090834 | 13091370 | hydroxyproline-rich glycoprotein family protein |
|  | *TraesCS5A02G017200* | 13095398 | 13095934 | Protein phosphatase 2C family protein |
|  | *TraesCS5A02G017300* | 13141891 | 13142402 | ArfGap/RecO-like zinc finger domain-containing protein |
|  | *TraesCS5A02G017400* | 13408834 | 13413704 | TIR-NB-LRR type resistance protein RPV1 |
|  | *TraesCS5A02G017500* | 13415677 | 13417357 | Transducin/WD40 repeat-like superfamily protein |
|  | *TraesCS5A02G017600* | 14028116 | 14028935 | Flagellar P-ring protein |
|  | *TraesCS5A02G017700* | 14134454 | 14137315 | myosin XI D |
|  | *TraesCS5A02G017800* | 14185800 | 14186348 | DNA topoisomerase |
|  | *TraesCS5A02G017900* | 14193486 | 14194163 | Thaumatin-like protein |
|  | *TraesCS5A02G018000* | 14227418 | 14228125 | Thaumatin-like protein |
|  | *TraesCS5A02G018100* | 14254486 | 14255163 | Thaumatin-like protein |
|  | *TraesCS5A02G018200* | 14266435 | 14266950 | Thaumatin-like protein |
|  | *TraesCS5A02G018300* | 14299117 | 14299632 | Thaumatin-like protein |
|  | *TraesCS5A02G018400* | 14416683 | 14417358 | Thaumatin-like protein |
|  | *TraesCS5A02G018500* | 14486728 | 14487270 | Pathogenesis-related thaumatin family protein |
|  | *TraesCS5A02G018600* | 14491485 | 14492223 | Thaumatin-like protein |
|  | *TraesCS5A02G018700* | 14497102 | 14498015 | Thaumatin-like protein, putative |
|  | *TraesCS5A02G018800* | 14502697 | 14503438 | Thaumatin-like protein |
|  | *TraesCS5A02G018900* | 14508248 | 14508986 | Thaumatin-like protein |
|  | *TraesCS5A02G019000* | 14511510 | 14514580 | Thaumatin-like protein |
|  | *TraesCS5A02G019100* | 14519439 | 14520162 | Thaumatin-like protein |
|  | *TraesCS5A02G019200* | 14844273 | 14848275 | Fatty acid 2-hydroxylase |
|  | *TraesCS5A02G019300* | 14921945 | 14923291 | Ethylene-responsive nuclear-like protein, putative |
|  | *TraesCS5A02G019400* | 15029344 | 15030813 | 3'-N-debenzoyl-2'-deoxytaxol N-benzoyltransferase |
|  | *TraesCS5A02G019500* | 15038831 | 15039385 | Pathogenesis-related thaumatin family protein |
|  | *TraesCS5A02G019600* | 15844722 | 15850922 | Nucleolar complex protein 2-like protein |
|  | *TraesCS5A02G019700* | 15865175 | 15867507 | PI-PLC X domain-containing protein |
|  | *TraesCS5A02G019800* | 16413639 | 16415639 | F-box family protein |
|  | *TraesCS5A02G019900* | 16543562 | 16545091 | ATP synthase subunit alpha |
|  | *TraesCS5A02G020000* | 16545455 | 16545796 | ATP synthase subunit 9, mitochondrial |
|  | *TraesCS5A02G020100* | 16574345 | 16574815 | ATPase subunit 8 |
|  | *TraesCS5A02G020200* | 16576141 | 16576518 | 30S ribosomal protein S12 |
|  | *TraesCS5A02G020300* | 16576563 | 16576919 | NADH-ubiquinone oxidoreductase chain 3 |
|  | *TraesCS5A02G020400* | 16599705 | 16600427 | Cytochrome c biogenesis C |
|  | *TraesCS5A02G020500* | 16601604 | 16601920 | myo-inositol-1-phosphate synthase 2 |
|  | *TraesCS5A02G020600* | 16621745 | 16622272 | NADH-ubiquinone oxidoreductase chain 4 |
|  | *TraesCS5A02G020700* | 16974437 | 16975461 | BZIP transcription factor |
|  | *TraesCS5A02G020800* | 16980676 | 16987625 | Anaphase-promoting complex subunit 5 |
|  | *TraesCS5A02G020900* | 17221683 | 17224224 | Phytoene synthase |
|  | *TraesCS5A02G021000* | 17281199 | 17283047 | transmembrane protein, putative (DUF594) |
|  | *TraesCS5A02G021100* | 17466195 | 17466857 | Protein FAR1-RELATED SEQUENCE 5 |
|  | *TraesCS5A02G021200* | 17468910 | 17470136 | Protein FAR1-RELATED SEQUENCE 5 |
|  | *TraesCS5A02G021300* | 17518462 | 17520358 | Disease resistance protein |
|  | *TraesCS5A02G021400* | 17528356 | 17529306 | Late embryogenesis abundant D-like protein |
|  | *TraesCS5A02G021500* | 17570346 | 17571695 | U3 small nucleolar RNA-associated protein 18-like protein |
|  | *TraesCS5A02G021600* | 17625359 | 17627000 | Threonine dehydratase |
|  | *TraesCS5A02G021700* | 17628643 | 17629426 | Glutathione S-transferase |
|  | *TraesCS5A02G021800* | 17674492 | 17679035 | Threonine dehydratase |
|  | *TraesCS5A02G021900* | 17703779 | 17704144 | Retrotransposon protein, putative, unclassified |
|  | *TraesCS5A02G022000* | 17824573 | 17827737 | TATA-box-binding protein |
|  | *TraesCS5A02G022100* | 17830240 | 17833127 | GATA transcription factor |
|  | *TraesCS5A02G022200* | 17836380 | 17840367 | Cysteine synthase |
|  | *TraesCS5A02G022300* | 18389036 | 18389821 | Zinc finger CCHC domain-containing protein 10 |
|  | *TraesCS5A02G022400* | 18395014 | 18396955 | Mitochondrial metalloendopeptidase OMA1 |
|  | *TraesCS5A02G022500* | 18569781 | 18572691 | Mitochondrial metalloendopeptidase OMA1 |
|  | *TraesCS5A02G022600* | 18576050 | 18578001 | Mitochondrial metalloendopeptidase OMA1 |
|  | *TraesCS5A02G022700* | 18637369 | 18639106 | Amino acid permease family protein, putative, expressed |
|  | *TraesCS5A02G022800* | 18662197 | 18663823 | F-box family protein |
|  | *TraesCS5A02G022900* | 18669662 | 18671875 | ARM repeat superfamily protein |
|  | *TraesCS5A02G023000* | 18673156 | 18676527 | disease resistance protein (TIR-NBS-LRR class) |
|  | *TraesCS5A02G023100* | 18678844 | 18681611 | F-box family protein |
|  | *TraesCS5A02G023200* | 18762793 | 18764187 | Disease resistance protein (NBS-LRR class) family |
|  | *TraesCS5A02G023300* | 18764853 | 18767123 | disease resistance protein (TIR-NBS-LRR class) |
|  | *TraesCS5A02G023400* | 18774453 | 18777439 | Disease resistance protein (TIR-NBS-LRR class) |
|  | *TraesCS5A02G023500* | 18789003 | 18791987 | Leucine-rich repeat receptor-like protein kinase family protein |
|  | *TraesCS5A02G023600* | 18795384 | 18797642 | Glycosyltransferase |
|  | *TraesCS5A02G023700* | 18812811 | 18817203 | Glycosyltransferase |
|  | *TraesCS5A02G023800* | 18857169 | 18858770 | Cysteine protease, putative |
|  | *TraesCS5A02G023900* | 18904814 | 18913230 | Transducin/WD40 repeat-like superfamily protein, putative |
|  | *TraesCS5A02G024000* | 18919216 | 18920536 | Glutathione S-transferase |
|  | *TraesCS5A02G024100* | 18949183 | 18950162 | Glutathione S-transferase |
|  | *TraesCS5A02G024200* | 18950886 | 18951413 | Invertase inhibitor |
|  | *TraesCS5A02G024300* | 19067238 | 19068938 | Cation calcium exchanger |
| *QD.xjau-5BS* | *TraesCS5B02G014000* | 13485208 | 13491566 | Disease resistance protein RPM1 |
|  | *TraesCS5B02G014100* | 13496896 | 13498292 | WAT1-related protein |
|  | *TraesCS5B02G014200* | 13699906 | 13702365 | RING/U-box superfamily protein |
|  | *TraesCS5B02G014300* | 13703223 | 13705574 | Rf2 protein |
|  | *TraesCS5B02G014400* | 13713598 | 13716733 | Ras family protein |
|  | *TraesCS5B02G014500* | 13721857 | 13725934 | Haloacid dehalogenase-like hydrolase domain-containing protein |
| *QD.xjau-5DL* | *TraesCS5D02G559000* | 560477617 | 560479275 | Tubulin binding cofactor C domain-containing protein |
|  | *TraesCS5D02G559100* | 560495049 | 560503654 | Disease resistance protein (NBS-LRR class) family |
|  | *TraesCS5D02G559200* | 560533744 | 560539016 | Disease resistance protein (NBS-LRR class) family |
|  | *TraesCS5D02G559300* | 560789939 | 560791866 | Cytochrome P450 |
|  | *TraesCS5D02G559400* | 560872747 | 560873199 | Photosystem II CP47 reaction center protein |
|  | *TraesCS5D02G559500* | 560873363 | 560873479 | Photosystem II reaction center protein T |
|  | *TraesCS5D02G559600* | 560873528 | 560873659 | Protein PsbN |
|  | *TraesCS5D02G559700* | 560873763 | 560873984 | Photosystem II reaction center protein H |
|  | *TraesCS5D02G559800* | 560876404 | 560876928 | Cytochrome b6-f complex subunit 4 |
|  | *TraesCS5D02G559900* | 560879479 | 560879889 | 30S ribosomal protein S8 |
|  | *TraesCS5D02G560000* | 560880028 | 560880399 | 50S ribosomal protein L14 |
|  | *TraesCS5D02G560100* | 560883540 | 560885373 | Cytochrome P450 |
|  | *TraesCS5D02G560200* | 560925051 | 560926508 | Jasmonate O-methyltransferase |
|  | *TraesCS5D02G560300* | 561422607 | 561428223 | Terpene synthase |
|  | *TraesCS5D02G560400* | 561572197 | 561573072 | Aquaporin-like protein |
|  | *TraesCS5D02G560500* | 561637590 | 561645324 | NBS-LRR disease resistance protein-like protein |
|  | *TraesCS5D02G560600* | 561673605 | 561678505 | Kinase family protein |
|  | *TraesCS5D02G560700* | 561683302 | 561690143 | Transcriptional corepressor LEUNIG |
|  | *TraesCS5D02G560800* | 561690154 | 561690755 | Flagellar motor switch protein FliM |
|  | *TraesCS5D02G560900* | 561700775 | 561707677 | COP1-interacting-like protein |
|  | *TraesCS5D02G561000* | 561792930 | 561798533 | COP1-interacting-like protein |
|  | *TraesCS5D02G561100* | 561803024 | 561804151 | Leucine-rich repeat receptor-like protein kinase |
|  | *TraesCS5D02G561200* | 561895926 | 561898878 | Disease resistance protein (NBS-LRR class) family |
|  | *TraesCS5D02G561300* | 561923075 | 561927513 | NBS-LRR disease resistance protein-like protein |
|  | *TraesCS5D02G561400* | 561949925 | 561957704 | Disease resistance protein (NBS-LRR class) family |
|  | *TraesCS5D02G561500* | 562003449 | 562006595 | 4-coumarate--CoA ligase like |
|  | *TraesCS5D02G561600* | 562017283 | 562018464 | Protein MIZU-KUSSEI 1 |
|  | *TraesCS5D02G561700* | 562029013 | 562029867 | Aquaporin |
|  | *TraesCS5D02G561800* | 562039310 | 562039927 | Invertase inhibitor |
|  | *TraesCS5D02G561900* | 562052724 | 562053335 | Pectinesterase inhibitor |
|  | *TraesCS5D02G562000* | 562062860 | 562064211 | Heavy metal-associated protein |
|  | *TraesCS5D02G562100* | 562085993 | 562090186 | UPF0176 protein |
|  | *TraesCS5D02G562200* | 562093043 | 562097230 | RNA binding protein, putative |
|  | *TraesCS5D02G562300* | 562100772 | 562102427 | LUC7-like protein |
|  | *TraesCS5D02G562400* | 562121301 | 562126864 | Nuclear factor related to kappa-B-binding protein |
|  | *TraesCS5D02G562500* | 562336860 | 562338975 | F-box protein |
|  | *TraesCS5D02G562600* | 562339610 | 562341715 | Pentatricopeptide repeat-containing protein |
|  | *TraesCS5D02G562700* | 562342621 | 562344051 | Nuclear transport factor 2 (NTF2) family protein |
|  | *TraesCS5D02G562800* | 562345338 | 562346798 | Nuclear transport factor 2 (NTF2) family protein |
|  | *TraesCS5D02G562900* | 562347786 | 562349174 | Nuclear transport factor 2 (NTF2) family protein |
|  | *TraesCS5D02G563000* | 562349452 | 562351653 | dentin sialophosphoprotein |
|  | *TraesCS5D02G563100* | 562410585 | 562410917 | Polynucleotidyl transferase, ribonuclease H-like superfamily protein |
|  | *TraesCS5D02G563200* | 562412366 | 562413034 | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family |
|  | *TraesCS5D02G563300* | 562413634 | 562415047 | Receptor-like protein 2 |
|  | *TraesCS5D02G563400* | 562430669 | 562431781 | Leucine-rich repeat receptor-like protein kinase |
|  | *TraesCS5D02G563500* | 562486969 | 562488335 | Leucine-rich repeat receptor-like protein kinase |
|  | *TraesCS5D02G563600* | 562529984 | 562531111 | Leucine-rich repeat receptor-like protein kinase |
|  | *TraesCS5D02G563700* | 562532624 | 562533742 | Leucine-rich repeat receptor-like protein kinase |
|  | *TraesCS5D02G563800* | 562648050 | 562652469 | Oxidoreductase/transition metal ion-binding protein, putative |
|  | *TraesCS5D02G563900* | 562652985 | 562654854 | Glutathione S-transferase |
|  | *TraesCS5D02G564000* | 562719951 | 562726673 | Pleiotropic drug resistance ABC transporter |
|  | *TraesCS5D02G564100* | 562831922 | 562834971 | TBC1 domain family member |
|  | *TraesCS5D02G564200* | 562926174 | 562927566 | Cytochrome b559 subunit alpha |
|  | *TraesCS5D02G564300* | 563121042 | 563122028 | Protein YIPF |
|  | *TraesCS5D02G564400* | 563339909 | 563340670 | RING/U-box superfamily protein |
|  | *TraesCS5D02G564500* | 563398668 | 563403143 | WRKY transcription factor |
|  | *TraesCS5D02G564600* | 563600094 | 563600381 | RADIALIS-like transcription factor |
|  | *TraesCS5D02G564700* | 563602438 | 563606639 | Outer envelope pore protein 24B, chloroplastic |
|  | *TraesCS5D02G564800* | 563638549 | 563640014 | 30S ribosomal protein 1, chloroplastic |
|  | *TraesCS5D02G564900* | 563714751 | 563715165 | Transposase |
|  | *TraesCS5D02G565000* | 563725855 | 563727293 | Ribosome hibernation promotion factor |
|  | *TraesCS5D02G565100* | 563750290 | 563752014 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein |
|  | *TraesCS5D02G565200* | 563754730 | 563761374 | Sucrose nonfermenting 4-like protein |
|  | *TraesCS5D02G565300* | 563852369 | 563853283 | Acyl carrier protein |
|  | *TraesCS5D02G565400* | 563854058 | 563860012 | ATP-dependent DNA helicase 2 subunit ku80 |
|  | *TraesCS5D02G565500* | 563903418 | 563903813 | Uracil-DNA glycosylase |
|  | *TraesCS5D02G565600* | 563965630 | 563967393 | Dehydrogenase/reductase SDR family protein |
|  | *TraesCS5D02G565700* | 563967812 | 563970474 | Coatomer subunit zeta |
|  | *TraesCS5D02G565800* | 563972520 | 563974745 | Pentatricopeptide repeat-containing protein |
|  | *TraesCS5D02G565900* | 563976197 | 563979736 | Disease resistance protein (NBS-LRR class) family |
|  | *TraesCS5D02G566000* | 564121997 | 564124216 | F-box protein PP2 |
|  | *TraesCS5D02G566100* | 564226841 | 564230961 | Disease resistance protein (NBS-LRR class) family |
|  | *TraesCS5D02G566200* | 564586950 | 564588126 | Gibberellin 20 oxidase |
|  | *TraesCS5D02G566300* | 564671386 | 564671712 | Retrotransposon protein, putative, unclassified |
|  | *TraesCS5D02G566400* | 564747515 | 564752249 | F-box family protein |
|  | *TraesCS5D02G566500* | 564834402 | 564835825 | Heavy metal-associated protein |
|  | *TraesCS5D02G566600* | 564844410 | 564848900 | La-related protein |
|  | *TraesCS5D02G566700* | 564929124 | 564932658 | GDSL esterase/lipase |
|  | *TraesCS5D02G566800* | 564944243 | 564949917 | GDSL esterase/lipase |
|  | *TraesCS5D02G566900* | 564976204 | 564977775 | Protein DETOXIFICATION |
|  | *TraesCS5D02G567000* | 565041940 | 565044233 | DUF1499 family protein |
|  | *TraesCS5D02G567100* | 565050241 | 565051869 | Avr9/Cf-9 rapidly elicited protein |
|  | *TraesCS5D02G567200* | 565098748 | 565100506 | rRNA N-glycosidase |
|  | *TraesCS5D02G567300* | 565137329 | 565141884 | WD40 repeat-containing protein |
|  | *TraesCS5D02G567400* | 565181431 | 565182199 | NACHT, LRR and PYD domains-containing protein 4F |
|  | *TraesCS5D02G567500* | 565187040 | 565187654 | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family |
|  | *TraesCS5D02G567600* | 565196005 | 565196556 | Harpin-induced protein 1 (Hin1), putative |
|  | *TraesCS5D02G567700* | 565200023 | 565202398 | Ubiquitin carboxyl-terminal hydrolase 2 |
|  | *TraesCS5D02G567800* | 565238589 | 565239026 | 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (flavodoxin) |
|  | *TraesCS5D02G567900* | 565257975 | 565258412 | ARM repeat superfamily protein isoform 1 |
|  | *TraesCS5D02G568000* | 565275556 | 565275990 | mRNA export factor |
|  | *TraesCS5D02G568100* | 565306932 | 565308363 | Protein kinase |
|  | *TraesCS5D02G568200* | 565349244 | 565349842 | Oxidoreductase/transition metal ion-binding protein |
|  | *TraesCS5D02G568300* | 565495068 | 565504151 | Exportin-1 |
|  | *TraesCS5D02G568400* | 565658903 | 565659737 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase |
|  | *TraesCS5D02G568500* | 565702365 | 565703111 | Cytokinin riboside 5'-monophosphate phosphoribohydrolase |
|  | *TraesCS5D02G568600* | 565709852 | 565710215 | Polycomb group RING finger protein 3 |
|  | *TraesCS5D02G568700* | 565712200 | 565713957 | Leucine-rich repeat receptor-like protein kinase family protein |
|  | *TraesCS5D02G568800* | 565717755 | 565719344 | Leucine-rich repeat receptor-like protein kinase family protein |
|  | *TraesCS5D02G568900* | 565727253 | 565728080 | Leucine-rich repeat receptor-like protein kinase family protein |
|  | *TraesCS5D02G569000* | 565731220 | 565732044 | Leucine-rich repeat receptor-like protein kinase family protein |
|  | *TraesCS5D02G569100* | 565733586 | 565734992 | Leucine-rich repeat receptor-like protein kinase family protein |
|  | *TraesCS5D02G569200* | 565744102 | 565748742 | Ripening related protein family |
|  | *TraesCS5D02G569300* | 565785329 | 565786714 | ATP-dependent zinc metalloprotease FtsH |
|  | *TraesCS5D02G569400* | 565816527 | 565817617 | ATP-dependent Clp protease ATP-binding subunit ClpL |
|  | *TraesCS5D02G569500* | 565829963 | 565831564 | Leucine-rich repeat receptor-like protein kinase family protein |
|  | *TraesCS5D02G569600* | 565908933 | 565909823 | carbohydrate esterase, putative (DUF303) |
|  | *TraesCS5D02G569700* | 565950793 | 565953361 | carbohydrate esterase, putative (DUF303) |
|  | *TraesCS5D02G569800* | 565975092 | 565977278 | PGR5-like protein 1A, chloroplastic |

1. D-value, comprehensive drought tolerance evaluation.

**Table S7** Transcriptional patterns of candidate genes under PEG6000 or drought stress

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene ID** | **Temporary name** | **PEG6000 1** | **Drought 2** |
| **Giza 168** | **Gemmiza 10** |
| **0h** | **2h** | **12h** | **0h** | **2h** | **12h** | **0h** | **1h** | **6h** |
| *TraesCS5A02G022100* | *TaGATAs-5A* | 3.2 | 1.9 | 1.3 | 1.2 | 1.0 | 1.2 | 1.3 | 0.7 | 0.5 |
| *TraesCS5B02G014200* | *TaUbox-5B* | 6.4 | 7.2 | 4.9 | 5.3 | 7.2 | 8.7 | 3.2 | 3.4 | 6.2 |
| *TraesCS5D02G563900* | *TaGSTP-5D* | 36.5 | 49.2 | 17.2 | 39.6 | 22.7 | 39.7 | 8.7 | 8.0 | 9.9 |

The data are retrieved from WheatOmics (http://202.194.139.32/expression/wheat.html)

1 Giza 168 and Gemmiza 10 are tolerant and sensitive cultivars, respectively, subjected to PEG6000 stress before (0 h) and after stress (2 h or 12 h). 2 1-week old wheat seedling leaves subjected to drought stress before (0 h) and after stress (1 h or 6 h) using the Illumina sequencing platform.