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| --- | --- | --- | --- | --- |
| **Domains related with abiotic streesess** | **InterproScan** | **p value** | **Analysis** | **Function** |
| SNF1-related protein kinase regulatory subunit beta-2 | IPR030070 | 4.740E-06 | FQ | Drought, carbohydrate metabolism, glucose limitation, assimilation of nitrogen |
| Association with the SNF1 complex (ASC) domain | IPR006828 | 2.360E-05 | FQ | Glucose limitation, nutritional stress |
| ASC domain superfamily | IPR037256 | 2.360E-05 | FQ | Glucose limitation |
| Zinc/iron permease | IPR003689 | 8.146E-04 | FQ | Symbiotic nitrogen fixation, acquisition, distribution, homeostasis, and signaling of Zn |
| Zinc/iron permease, fungal/plant | IPR003689 | 8.146E-04 | FQ | Mycorrhizal interaction |
| Molybdopterin dehydrogenase, FAD-binding | IPR016166 | 1.854E-04 | FQ | Purine degradation and stress response |
| 2Fe-2S ferredoxin, iron-sulphur binding site | IPR006058 | 2.983E-04 | FQ | Photosynthesis, biosynthesis of chlorophyll, phytochrome and fatty acids, assimilation of sulphur and nitrogen |
| 2Fe-2S ferredoxin-like superfamily | IPR036010 | 5.300E-06 | FQ | Photosynthesis, biosynthesis of chlorophyll, phytochrome and fatty acids, assimilation of sulphur and nitrogen |
| CO dehydrogenase flavoprotein, C-terminal | IPR005107 | 1.640E-08 | FQ | Blue light, seedling establishment, phototropism and circadian clock regulation |
| CO dehydrogenase flavoprotein, C-terminal domain superfamily | IPR036683 | 1.640E-08 | FQ | Blue light, seedling establishment, phototropism and circadian clock regulation |
| Aldehyde oxidase/xanthine dehydrogenase, molybdopterin binding | IPR008274 | 1.640E-08 | FQ | Biosynthesis of abscisic acid and indole-3-acetic acid, freezing, drought and salinity, purine metabolism |
| NADH:ubiquinone oxidoreductase | IPR003918 | 7.056E-03 | FQ | Reducing nitrate to nitrite |
| NADH-quinone oxidoreductase, subunit D superfamily | IPR038290 | 1.571E-04 | FQ | Reducing nitrate to nitrite |
| NADH-quinone oxidoreductase, subunit D | IPR001135 | 8.570E-05 | FQ | Reducing nitrate to nitrite |
| NADH-quinone oxidoreductase chain 4 | IPR022997 | 8.806E-03 | FQ | Reducing nitrate to nitrite |
| DNA-binding pseudobarrel domain superfamily | IPR015300 | 2.277E-03/1.646E-05 | E, PS | Plant growth and development, modeling of root architecture, and development of seeds |
| Isoprenoid synthase domain superfamily | IPR008949 | 1.909E-04/1.646E-05 | E, PS | Carbon Partitioning Within the Cytoplasmic Pathway |
| Photosystem I PsaA/PsaB superfamily | IPR036408 | 3.878E-04 | E | Uses light energy to mediate electron transfer from plastocyanin to ferredoxin |
| Photosystem I PsaA/PsaB | IPR001280 | 1.190E-05 | E | Uses light energy to mediate electron transfer from plastocyanin to ferredoxin |
| Photosystem I PsaA | IPR006243 | 3.070E-05 | E | Uses light energy to mediate electron transfer from plastocyanin to ferredoxin |
| Photosystem I PsaA/PsaB, conserved site | IPR020586 | 8.806E-03 | E | Uses light energy to mediate electron transfer from plastocyanin to ferredoxin |
| F-box domain | IPR001810 | 1.048E-07/1.155E-07 | E, PS | Floral transition as well as panicle and seed development and floral transition as well as panicle and seed development |
| F-box-like domain superfamily | IPR036047 | 1.114E-09/2.094E-12 | E, PS | Floral transition as well as panicle and seed development and floral transition as well as panicle and seed development |
| F-box associated interaction domain | IPR017451 | 1.032E-21/1.788E-28 | E, PS | Floral transition as well as panicle and seed development and floral transition as well as panicle and seed development |
| Transcription factor, MADS-box superfamily | IPR036879 | 1.212E-35/4.235E-25 | E, PS | Floral development |
| Transcription factor, MADS-box | IPR002100 | 3.387E-35/4.235E-25 | E, PS | Floral development |
| F-box associated domain, type 1 | IPR006527 | 1.075E-05/1.109E-05 | E, PS | Floral development |
| ALOG domain | IPR006936 | 1.949E-03 | E | Key developmental regulators |
| ALOG family | IPR040222 | 5.408E-03 | E | Key developmental regulators |
| START-like domain superfamily | IPR023393 | 3.878E-04 | E | Response to drought, salt, wound and heat stress, stress response |
| Galactose oxidase/kelch, beta-propeller | IPR011043 | 9.958E-03/2.340E-03 | E, PS | Stress responses induced under Fe deficiency in the roots |
| HAT, C-terminal dimerisation domain | IPR008906 | 3.960E-05 | E | Abiotic and biotic stress |
| Protein EMBRYONIC FLOWER 1 | IPR034583 | 2.271E-03 | E | Controls leaves development, shoot architecture and flowering by delaying both the vegetative to reproductive transition and flower initiation |
| Protein NUCLEAR FUSION DEFECTIVE 6 | IPR033251 | 3.534E-04 | E | Nuclear fusion in sexual reproduction |
| Double-stranded RNA-binding protein | IPR031147 | 7.056E-03 | E | Plant hormone signaling |
| Ulp1 protease family, C-terminal catalytic domain | IPR003653 | 2.290E-07 | E | Salt stress signaling |
| Domain of unknown function DUF4283 | IPR025558 | 1.559E-34/2.967E-14 | E, PS | Cell wall biology, vasculature patterning and abiotic/biotic stress response |
| Chlorophyll a/b binding domain superfamily | IPR023329 | 6.638E-03 | PS | Light receptor that captures and delivers excitation energy to photosystems I and II |
| Chlorophyll A-B binding protein, plant | IPR001344 | 6.638E-03 | PS | Light receptor that captures and delivers excitation energy to photosystems I and II |
| Reverse transcriptase zinc-binding domain | IPR026960 | 4.860E-05 | PS | Leaf senescence |

**Additional file 11.** Classifications of domains related with abiotic stresses subject to expansion, positive selection or physicochemical divergence. Some domains were detected to be expanded and positively selected. Ex = expanded, PS = positive selected, FQ = physicochemical divergence. P value is showed for each analysis. The entire list for each analysis is showed in additional files 8, 9 and 10.