**Table S3.** Transcript classes and sequence search results of clones with significant homologies

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Class†** | **DETDFs‡** | **EST with BLASTn** | **Protein by BLASTx of the EST best match** | **TAIR BLASTx** | **Processes** |
| **ID; Name; e-value** | **ID; Name; e-value** | **ID; GO function; e-value** |
| A | GA1 | FL806617.1; Panicum virgatum late flowering buds + seed development (H) *Panicum virgatum* cDNA clone; 5,6e-02 | XP\_004957139.1; PREDICTED: BURP domain-containing protein 15-like [*Setaria italica*]; 1e-42 | n§ | Unknown |
| A | GA2 | EY274919.1; BG1 MaltedMorex *Hordeum vulgare* subsp. vulgare cDNA; 2e-04 | XP\_013442961.1; hypothetical protein MTR\_0055s0030 [*Medicago truncatula*]; 1e-55 | n | Unknown |
| A | GA7 | GR999328.1; ransId-215195 CACATN1 *Coffea arabica* cDNA clone; 2,3 e-02 | CDP06495.1; unnamed protein product [*Coffea canephora*]; 1e-169 | AT3G08940; chlorophyll binding; e-124 | Metabolism |
| A | GA8 | GE136847.1; 454GmaGlobSeed879495 Soybean Seeds Containing Globular-Stage Embryos *Glycine max* cDNA; 7,9e-01 | KHN36936.1; Putative rhamnose biosynthetic enzyme 1 [*Glycine max*]; 6e-52 | AT1G53500; UDP-4-keto-6-deoxy-glucose-3,5-epimerase activity; 0.0 | Metabolism |
| A | GA9 | AW668101.1; GA\_\_Ea0012L05 *Gossypium arboreum* 7-10 dpa fiber library *Gossypium arboreum* cDNA clone; 6e-05 | XP\_012490289.1; PREDICTED: putative pentatricopeptide repeat-containing protein At1g02420 [*Gossypium raimondii*]; 5e-51 | AT1G02420; Unknown; 0.0 | Unknown |
| A | GA10 | CD447312.1; E04912707F09.g Endosperm\_1 *Zea mays* cDNA; 1e-11 | NP\_001106011.1; Select seq ref|NP\_001106011.1| zein-alpha 19D1 precursor [*Zea mays*]; 1e-12 | n | Unknown |
| A | GC4 | GO244915.1; OEAA-070810\_Plate5o21.b1 cDNA library from Olive leaves y fruits *Olea europaea* cDNA; 1e-04 | XP\_022842474.1 serine/threonine-protein kinase PBL27-like [*Olea europaea* var. sylvestris]; 5e-98 | AT5G18610; Kinase activity; 0.0 | Signal transduction |
| A | GG4 | DR958840.1; ZM\_BFb0063D12.f ZM\_BFb *Zea mays* cDNA; 8e-04 | n | -¶ | Unknown |
| A | GG5 | FL364156.1; 24457224 CERES-505 *Zea mays* cDNA clone 1613391; 6,9e-02 | n | - | Unknown |
| A | GG6 | JG873047.1; UNQ108-P10.x1d-t UNQ (*Panicum virgatum* cv. Alamo-AP13) *Panicum virgatum* cDNA; 2e-03 | NP\_001136479.1; uncharacterized protein LOC100216593 [*Zea mays*]; 8e-26 | AT5G27640; Protein binding; e-150 | Protein destination and storage |
| A | GG7 | JG946532.1; UNQ107-E05.x1d-t UNQ (*Panicum virgatum* cv. Alamo-AP13) Panicum virgatum cDNA; 3e-05 | AQK71444.1; 1,4-alpha-glucan-branching enzyme 2, chloroplastic/amyloplastic [*Zea mays*]; 4e-131 | AT5G03650; 1,4-alpha-glucan branching enzyme activity; 0.0 | Metabolism |
| A | GG8 | HO041044.1; ocpsga0\_0424\_H03.ab1 Soybean immature seed full-length-enriched cDNA library *Glycine max* cDNA; 5,6e-02 | KRH74203.1; hypothetical protein GLYMA\_01G005600 [*Glycine max*]; 8e-52 | AT4G29240; Unknown; e-123 | Unknown |
| B | TA4 | CX108251.1; BI148C22 A normalized whole-life-cycle cDNA library of rice *Oryza sativa* Indica Group cDNA clone; 3e-03 | n | - | Unknown |
| B | TA5 | FG177597.1; AGN\_RNC118xl11f1.ab1 AGN\_RNC *Nicotiana tabacum* cDNA; 3e-04 | XP\_022139274.1; alpha-galactosidase-like [*Momordica charantia*]; 2e-59 | AT5G08370; Alpha-galactosidase activity; e-179 | Metabolism |
| C | GA3 | HO776090.1; vsu-ars\_001123\_LI10B00508 VSU-ARS-L10 *Phaseolus acutifolius* cDNA; 1e-09 | KRH17766.1; hypothetical protein; GLYMA\_13G013900 [*Glycine max*]; 5e-50 | AT1G15440; Protein binding; 1,1e-02 | Protein synthesis |
| C | GA4 | BF263146.1; Hordeum vulgare seedling green leaf EST library *Hordeum vulgare* subsp. vulgare cDNA clone; 8e-04 | EMS65358.1; hypothetical protein TRIUR3\_33397 [*Triticum urartu*]; 2e-32 | AT2G15220; Secretory protein; 4e-43 | Protein destination and storage |
| C | GA5 | BF260339.2; HVSMEf0021L19f *Hordeum vulgare* subsp. vulgare cDNA clone; 9e-03 | CAA10664.1; beta-tubulin 2 [*Hordeum vulgare* subsp. vulgare]; 8e-60 | AT5G12250; GTPase activity; e-175 | Cell structure |
| C | GA6 | DB996156.1 Bg05 Burma mangrove cDNA library *Bruguiera gymnorhiza* cDNA clone; 3e-06 | n | - | Unknown |
| C | GC1 | FY257746.1; *Cryptomeria japonica* needle spring growth of a 6-year-old tree *Cryptomeria japonica* cDNA clone; 1,9e-02 | PIA30233.1; hypothetical protein AQUCO\_05700144v1 [*Aquilegia coerulea*]; 2e-66 | AT4G20410; Transporter activity; 6e-72 | Intracellular traffic |
| C | GC3 | CA399431.1; EL01N0319A05.g Endosperm\_3 *Zea mays* cDNA; 3,3e-02 | NP\_001148735.1; uncharacterized protein LOC100282351 [*Zea mays*]; 9e-44 | AT2G37190; Zinc ion binding; 9e-82 | Protein synthesis |
| D | AC1 | JZ515900.1; AC2 ovaries 3 hs after pollination *Paspalum notatum* cDNA; 3e-29 | AAK62411.1; casein kinase II alpha subunit [*Arabidopsis thaliana*]; 7e-19 | AT5G67380; Kinase activity; e-110 | Signal transduction |
| D | AC2 | CB085678.1; hg14c09.g1 Hedyotis centranthoides flower - Stage 2 (NYBG) *Kadua centranthoides* cDNA clone; 3,3e-02 | PIN21347.1; hypothetical protein CDL12\_05951 [*Handroanthus impetiginosus*]; 1e-45 | AT1G74520; Unknown; 8e-35 | Disease/Defense |
| D | AC3 | FD941153.1; RS1GX74TF RS1(AR) *Raphanus sativus* var. oleiformis cDNA 1,1e-02 | XP\_018442344.1; PREDICTED: histone deacetylase HDT2-like [*Raphanus sativus*]; 2e-62 | AT5G22650; Actividad histona desacetilasa; 2e-28 | Transcription |
| D | GG1 | EY658062.1; CS00-C1-100-132-B09-CT.F Sweet orange leaf, greenhouse plant *Citrus sinensis* cDNA; 3e-08 | GAY56740; hypothetical protein CUMW\_174170, partial [*Citrus unshiu*]; 2e-44 | AT2G24260; ADN binding; 2e-57 | Transcription |
| E | AC4 | JZ515900.1; AC2 ovaries 3 hs after pollination *Paspalum notatum* cDNA; 9e-23 | AAK62411.1; casein kinase II alpha subunit [*Arabidopsis thaliana*]; 7e-19 | AT5G67380; Kinase activity; e-110 | Signal transduction |
| E | AC5 | JZ515900.1; AC2 ovaries 3 hs after pollination *Paspalum notatum* cDNA; 6e-219 | AAK62411.1; casein kinase II alpha subunit [*Arabidopsis thaliana*]; 7e-19 | AT5G67380; Kinase activity; e-110 | Signal transduction |
| F | AA17 | DY763058.1; 7S2 Transcript-derived fragments specifically found in SS2-2 *Glycine max* cDNA; 3,3e-02 | KHN15783.1; Protein TIME FOR COFFEE [*Glycine max*]; 3e-10 | AT3G22380; Unknown; 4e-97 | Metabolism |
| G | GG2 | EY747771.1; CS00-C5-003-048-G05-CT.F Sweet orange flower, greenhouse plant *Citrus sinensis* cDNA; 3,2e-02 | AFK47985.1; unknown [*Lotus japonicus*]; 1e-11 | AT2G37470; ADN binding; 8e-48 | Transcription |
| G | GG3 | CO441708.1; MZCCL10035C10.g Maize Endosperm cDNA *Library Zea mays* cDNA; 3,1e-02 | ACG31522.1; Select seq gb|ACG31522.1| 17.5 kDa class II heat shock protein [*Zea mays*]; 3e-73 | AT5G12020; Protein folding; 1e-35 | Protein synthesis |
| H | AC8 | FL220928.1; 2016995 CERES-196 *Zea mays* cDNA clone 419368; 7,3e-01 | ACF81437.1; unknown [*Zea mays*]; 1e-76 | AT3G51030; Protein binding; 2e-33 | Metabolism |
| H | AA2 | CJ949480; Y. *Ogihara* unpublished cDNA library; 6,2e-01 | EMS63026.1: Select seq EMS63026.1 hypothetical protein TRIUR3\_12257 [*Triticum urartu*]; 2e-101 | n | Unknown |
| H | AA3 | CJ963282.1; Y. *Ogihara* unpublished cDNA library; 1,9e-01 | XP\_020177071.1; uncharacterized protein LOC109762608 [*Aegilops tauschii* subsp. tauschii]; 7e-100 | AT1G10585; DNA binding transcription factor activity; 2e-09 | Transcription |
| H | AA4 | JZ515893.1; AA6 ovaries 3 hs after pollination *Paspalum notatum* cDNA; 1,1e-02 | PAN07877.1; hypothetical protein PAHAL\_A03141 [*Panicum hallii*]; 1e-12 | AT5G55830; ATP binding; 4e-98 | Disease/Defense |
| H | AA6 | FK978195.1; 2758608 CERES-227 *Zea mays* cDNA clone; 3,7e-01 | AQK38824.1; Protein DETOXIFICATION 21 [*Zea mays*]; 1e-30 | AT1G33110; Antiporter activity; e-128 | Intracellular traffic |
| H | AA7 | JZ515891.1; AA1 ovaries 3 hs after pollination *Paspalum notatum* cDNA; 2e-02 | ACG35856.1; CER1 [*Zea mays*] 4e-29 | AT1G02205; Aldehyde decarbonylase activity ; 0.0 | Metabolism |
| H | AA8 | GR316807.1; CCOO3260.g1 CCOO *Avena barbata* leaf, grown under ambient rainfall (H) *Avena barbata* cDNA clone; 3,9 e-01 | XP\_020177938.1; cytochrome P450 81D11-like [*Aegilops tauschii* subsp. Tauschii]; 4e-139 | AT4G37340; Oxygen binding; 1e-98 | Metabolism |
| H | AA11 | GW883551.1; Ti\_Con\_121 Timothy drought stress Library *Phleum pratense* cDNA; 2e-06 | n | - | Unknown |
| I | GA11 | FD493788.1; Ltu01b\_111\_B01\_C012.g2 Liriodendron Flower Bud Library *Liriodendron tulipifera* cDNA clone; 8,8e-02 | OVA16281.1; Select seq OVA16281.1 YjeF C-terminal domain [*Macleaya cordata*]; 7e-120 | AT5G19150; ADP-dependent NAD(P)H-hydrate dehydratase activity; e-129 | Metabolism |
| J | TC2 | FL922341.1; CCGO14217.g1 CCGO *Panicum virgatum* root (H) *Panicum virgatum* cDNA clone; 3e-04 | PAN12062.1; hypothetical protein PAHAL\_B02400 [*Panicum hallii*]; 5e-100 | AT5G15080; Kinase activity; 0.0 | Signal transduction |

† Grouping of DETDFs based on the comparative gene expression patterns (as shown table 3).

‡ AA, AC, CC, CG, GA, GC, GG, TA and TC were indicated selective primer combinations.

§ n, similarity below the threshold used (e-value greater than 1).

¶ \_, no hit.