**Table S1. Enriched GO terms and Pfam domains associated with the duplicates of conserved or divergent expression at each WGD event**

|  |  |  |
| --- | --- | --- |
| WGD event | GO terms | Pfam domains |
| Conserved expression | Divergent expression | Conserved expression | Divergent expression |
| Arabidopsis |  |  |  |  |
| α | GO:0003735, structural constituent of ribosome (F);GO:0006412, protein biosynthesis (P);GO:0005840, ribosome (C);GO:0005730, nucleolus (C);GO:0042254, ribosome biogenesis and assembly (P);GO:0009507, chloroplast (C); GO:0009570, chloroplast stroma (C);GO:0009579, thylakoid (C);GO:0005634, nucleus(C);GO:0003700, transcription factor activity (F);GO:0009535, thylakoid membrane (sensu Viridiplantae) (C);GO:0003677, DNA binding (F); GO:0015934, large ribosomal subunit (C);GO:0005839 ,proteasome core complex (sensu Eukaryota) (C); GO:0010200, response to chitin (P);GO:0015979, photosynthesis (P);GO:0005618, cell wall (C); GO:0006334, nucleosome assembly (P);GO:0045449, regulation of transcription (P) | GO:0003824, catalytic activity (F);GO:0016491, oxidoreductase activity (F);GO:0012505, endomembrane system (C); GO:0006952, defense response (P); GO:0008152, metabolism(P);GO:0016787, hydrolase activity (F);GO:0004126, cytidine deaminase activity (F);GO:0005351, sugar porter activity (F);GO:0005576, extracellular region (C);GO:0016788, hydrolase activity, acting on ester bonds (F) | PF00227, proteasome;PF01423, Sm | PF00450, serine\_carbpept; PF01657,DUF26 |
| β | GO:0006412, protein biosynthesis (P);GO:0003735, structural constituent of ribosome (F);GO:0005840 , ribosome(C); GO:0042254 , ribosome biogenesis and assembly (P); GO:0005730, nucleolus(C)  | - | PF02309, AUX\_IAA; PF02365, NAM; PF00394, Cu-oxidase | PF00702, Hydrolase |
| γ | GO:0003677, DNA binding(F) ;GO:0003700, transcription factor activity (F) | GO:0015144, carbohydrate transporter activity(F) | - | - |
| Rice |  |  |  |  |
| ρ | GO:0005840, ribosome (C); GO:0003700, transcription factor activity (F); GO:0006350, transcription (P); GO:0005198, structural molecule activity (F); GO:0006412 , protein biosynthesis (P); GO:0007275, development (P); GO:0005634, nucleus (C); GO:0003677 , DNA binding (F); GO:0016043, cell organization and biogenesis (P); GO:0005829, cytosol (C)  | GO:0005215, transporter activity (F);GO:0005783, endoplasmic reticulum (C);GO:0005773, vacuole(C);GO:0005739, mitochondrion (C) ;GO:0006810, transport (P); GO:0006519, amino acid and derivative metabolism (P); GO:0016020 , membrane (C);GO:0009058 , biosynthesis (P) | PF02365, NAM; PF00249, Myb\_DNA-binding; PF01095, Pectinesterase PF00319 SRF-TF | PF00450, Peptidase\_S10; PF00635, Motile\_Sperm; PF00005, ABC\_tran  |
| σ | GO:0009653, morphogenesis (P); GO:0030528 , transcription regulator activity (F) | - | PF04690, YABBY; PF00010, HLH  | - |