



**Figure Legend. Normalized expression values of genes within gene modules identified by coexpression analysis of 15 combined expression experiments.**

A condition-independent data set was created using expression data from fifteen different rice gene expression experiments. Data were downloaded from NCBI GEO or EBI ArrayExpress (E-MEXP-1766, E-MEXP-2267, E-MEXP-2506, GSE4471, GSE6719, GSE6893, GSE6901, GSE10373, GSE11025, GSE15046, GSE16739, GSE17245, GSE18361, GSE19024, GSE19239). Data were processed using Weighted Gene Coexpression Network Analysis to identify modules of highly correlated genes (Zhang and Horvath, 2005). Sample names are derived from the original treatments: Time course of gene expression values during aerobic germination (M-MEXP-1766); Time course of gene expression values during anaerobic and aerobic germination (M-MEXP-2267);rice seed was germinated anaerobically, anaerobically for 24 hours followed by aerobic conditions or anaerobically for 24 hours followed by aerobic conditions); Time course of gene expression values in rice shoots during photo- and thermo-periods (E-MEXP-2506; shoots of rice plants were harvested every four hours, treatments consisted of photo- and thermo-periods or constant light or temperature conditions: photoperiods (LDHH), 12 hours light (L)/12 hours dark (D) at a constant temperature (31C; HH); photothermocycles (LDHC); 12 hours light (L)/12 hours dark (D) with a high day temperature (31C) and a low night temperature (20C); thermocycles (LLHC); continuous light (LL) with 12 hours high/12 hours low temperature (31C, day, 20C, night), and an initial 48 hours of continuous light followed by cycling photo- and/or thermo-periods (LL LDHC, LL LDHH, LL LLHC)); Gene expression values from Striga hermonthica root infection time course of rice cultivars IAC165 and Nipponbare (GSE10373); Gene expression values after infection with rice stripe virus (RSV) of rice cultivars WuYun3 and KT95 (GSE11025); Gene expression values from shoots from wild type (Taichung 65) and three gibberellin signalling mutants (GSE15046, gid1-3, gid2-1, slr1); Time course of gene expression values after infection with Xanthomonas oryzae pv. oryzae, Xanthomonas oryzae pv. oryzaicola or mock infection (GSE16793); Gene expression values from 10 day old seedlings grown with or without Fe and/or P (GSE17245); Time course of gene expression values after infection with Magnaporthe oryzae strain Guy11 or mock infection (GSE18361); Gene expression values from various tissues (GSE19024, germinating seed harvested 72 hour post imbibition (germinating seed), light and dark grown plumule harvested 48 h after germination (plumule 1, plumule 2); light and dark grown radicles harvested 48 h after germination (radicle 1, radicle 2); 3 day old seedling (seedling 1); tetraol stage seedling (seedling 2); less than 1 mm panicle (panicle 1); 3 to 5 mm panicle (panicle 3); 40 to 50 mm panicle (panicle 4); heading panicle (panicle 5); palealemma 1 day before flowering (palealemma 1); stamen 1 day before flowering (stamen 1); spikelet 3 days post anthesis (spikelet); endosperm 7 days post anthesis (endosperm 1); endosperm 14 days post anthesis (endosperm 2); endosperm 21 days post anthesis (endosperm 3); shoot of seedling with three tillers (shoot); roots of seedling with three tillers (root); sheath tissues from plants with panicles less than 1 mm (sheath 1); sheath tissues from plants with panicles between 40 and 50 mm (sheath 2); leaf tissues from plants with panicles less than 1 mm (leaf 1); leaf tissues from plants with panicles between 40 and 50 mm (leaf 2); leaf tissues from plants with panicles between 40 and 50 mm (leaf 3); stem tissue 5 days before flowering (stem 1); stem tissue 14 days post anthesis (stem 2)); Gene expression values from wild type and transgenic rice containing the maize Rxo1 resistance gene after infection with Xanthomonas oryzae pv. oryzaicola or mock infection (GSE19239); Gene expression values from roots of rice cultivars Azucena and Bala grown in 0 ppm or 1 ppm AsO4 (GSE4471); Gene expression values from roots and leaves 30 and 120 min after zeatin application (GSE6719); Gene expression values from a panicle and seed developmental series (GSE6893, shoot apical meristems (SAM), panicles between 0 and 3 cm long (inflorescence P1), panicles between 3 and 5 cm long (inflorescence P2), panicles between 5 and 10 cm long (inflorescence P3), panicles between 10 and 15 cm long (inflorescence P4), panicles between 15 and 20 cm long (inflorescence P5), between 22 and 30 cm long - mature pollen stage (P6), developing seed 0 to 2 days after pollination (dap); seed S1), developing seed 3 to 4 dap (seed S2), developing seed 5 to 10 dap (seed S3), developing seed 11 to 20 dap (seed S4), developing seed 21 to 29 dap (seed S5)); Gene expression values from seedlings 3 hours after stress treatments (GSE6901, control, drought, salt, cold). Expression data are represented here as normalized values (Z-scores). Module names: black (A), blue (B), brown (C), cyan (D), green (E), green-yellow (F), magenta (G), midnightblue (H), pink (I), purple (J), red (K), salmon (L), tan (M), turquoise (N), yellow (O).