



Figure 4—figure supplement 1. Expression profiles of *TFIIAγ5* and *TFIIAγ1* in 28 tissues covering the entire life cycle of rice varieties Minghui 63 and Zhenshan 97. Data were obtained from a microarray database (<http://www.ncbi.nlm.nih.gov>; accession number GSE19024; Wang et al. Plant J. 61:752-766, 2010). E3, endosperm at 21 days after pollination; E2, endosperm at 14 days after pollination; E1, endosperm at 7 days after heading; Spi, spikelet at 3 days after pollination; Sta, stamen at 1 day before flowering; H, hull at 1 day before flowering; P5, panicle at heading stage; P4, panicle at 4- to 5-cm young panicle stage; P3, panicle at pollen–mother cell formation stage; P2, panicle at pistil and stamen primordium differentiation stage; P1, panicle at secondary branch primordium stage; Ste2, stem at heading stage; Ste1, stem at 5 days before heading; FL2, flag leaf at 14 days after heading; FL1, flag leaf at 5 days before heading; L2, leaf at 4- to 5-cm young panicle stage; L1, leaf at secondary branch primordium stage; She2, sheath at 4- to 5-cm young panicle stage; She1, sheath at secondary branch primordium stage; Sh, shoot of seedling with two tillers; R, root of seedling with two tillers; L & R, leaf and root at three-leaf stage; Em & Ra, embryo and radicle at 3 days after germination; P11, plumule at 48 h after emergence under light; P12, plumule at 48 h after emergence under dark; Ra1, radicle at 48 h after emergence under light; Ra2, radicle at 48 h after emergence under dark; S, germinating seed at 72 h of imbibitions. Expression levels (log₂ transformations of average signal values) are color-coded: yellow and blue denote high and low expression, respectively.