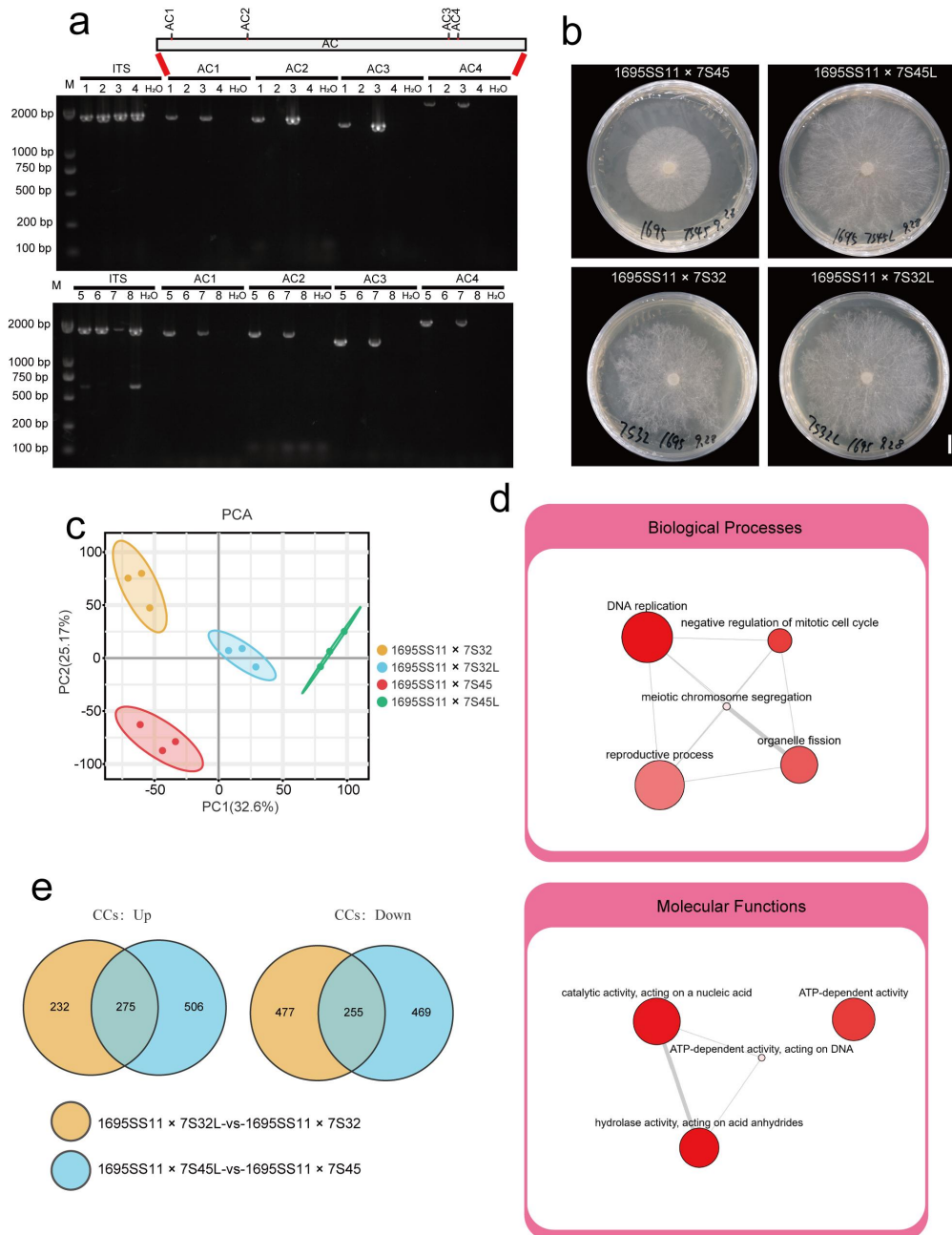




**Figure S11.** RNA-seq analysis of two independent AC-containing and AC-lost strain pairs. (a), PCR confirmation of four constructed matched heterokaryotic strain pairs. AC1–AC4 denote four distinct segments of the AC, with their positions schematically shown above the gel image. Primer sequences are provided in Table. S2. ITS, internal transcribed spacer; M, DNA marker; lane 1, strain 1695SS11 × 7S32; lane 2, strain 1695SS11 × 7S32L; lane 3, strain 1675SS09 × 7S32; lane 4, strain 1675SS09 × 7S32L; lane 5, strain 1695SS11 × 7S45; lane 6, strain 1695SS11 × 7S45L; lane 7, strain 1675SS09 × 7S45; lane 8, strain 1675SS09 × 7S45L; H<sub>2</sub>O, negative control. (b), Phenotypic comparison of AC-containing and AC-lost strains for RNA-seq on PDA. Bar = 1 cm. (c), Principal component analysis of gene expression profiles. Ellipses indicate the 95% confidence intervals. (d), GO enrichment of transcriptionally active AC genes (TPM ≥ 1), with redundant terms summarized using REVIGO. (e), Numbers of differentially expressed genes (DEGs) identified in each AC-containing versus AC-lost comparison.