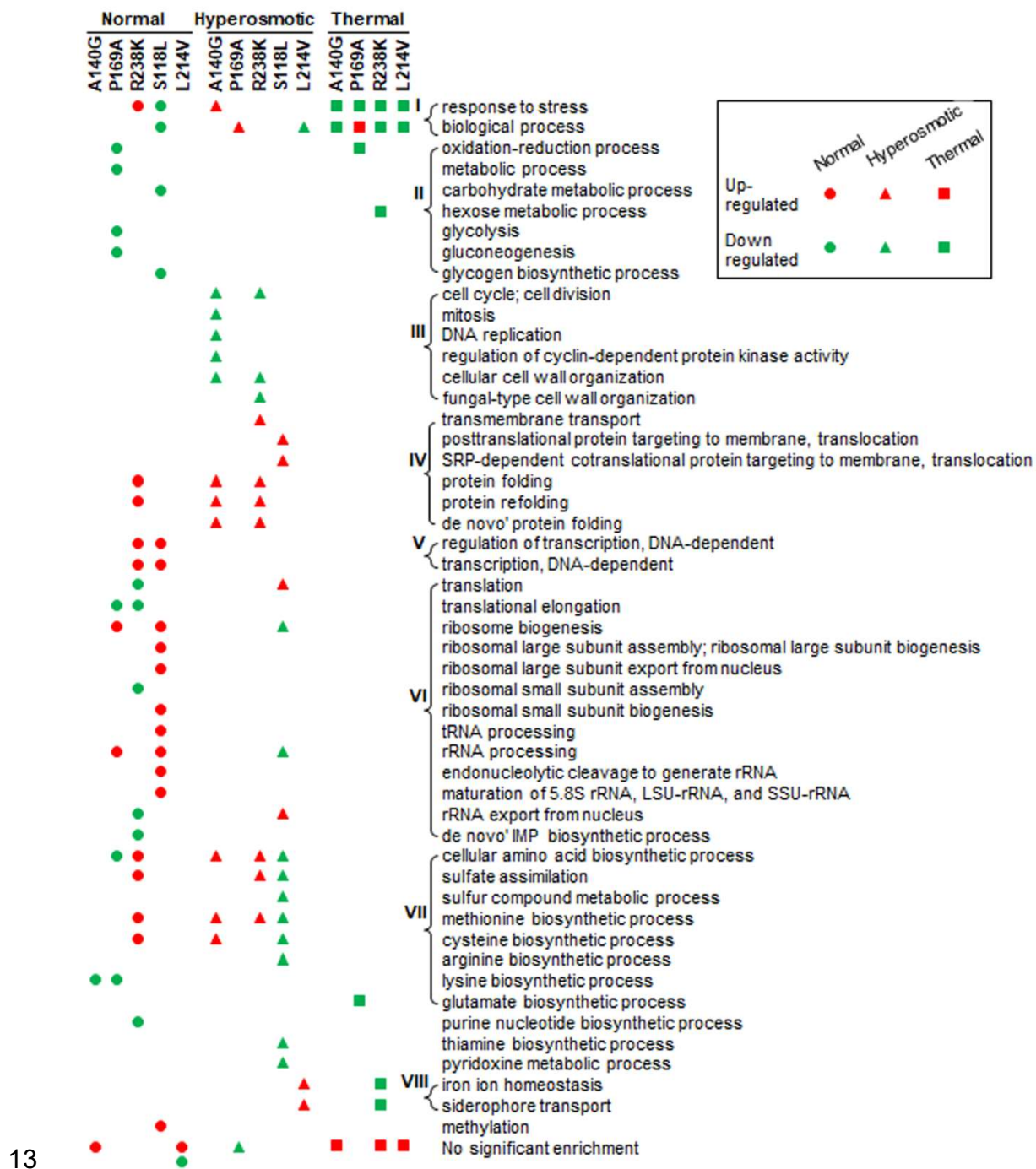


1
 2 **Fig. S1 Principal component analysis of fermentation data at thermal (a) and**
 3 **ethanol (b) stress conditions.**

4 Fermentation data, including cell growth (orange lines), glucose consumption (purple
 5 lines) and ethanol production (turquoise lines) during fermentation (hours 0, 6, 12, 18, 24,
 6 30, 36, 42 and 48), were from all the 36 Spt15 mutant strains and the wild type strain
 7 BY4741 at normal and three stress conditions. Means of biological duplicates are used.
 8 The strains were evaluated in 4 batches, indicated using the circle, triangle, square and
 9 diamond symbols, respectively. Compared to the wild type strain in each batch, mutant
 10 Spt15 strains showing increased or decreased fermentation capacities are indicated by
 11 upward arrow or downward arrow, respectively.

12



13
14 **Fig. S2 Enriched biological processes of SDEGs influenced by key Spt15 mutants.**

15 Significantly differentially expressed genes (SDEGs) were extracted in comparisons of
16 the key Spt15 mutant strains versus the wild type strain BY4741 at each culture condition

17 including normal (circle symbol), hyperosmotic (triangle symbol) and thermal (square
18 symbol) stress conditions. Up-regulated and down-regulated SDEGs were separately
19 subjected to GO enrichment analysis, which are indicated in red and green, respectively.