**Supplementary figure 8. Metabolomic pathways analysis of the differential co-expression networks (modules) based on TSC-LAM samples with and without rapamycin treatment**. For each significant module (empirical p-value < 0.1), metabolomic KEGG pathways detected at 10% Holm–Bonferroni correction are plotted (see supplementary table 6). Modules are identified on the top by a colour bar. Within each metabolomic pathway, red boxes indicate metabolites present in the module and in the KEGG pathway.