

**Supplementary figure 7. Co-expression network analysis performed separately on TSC-LAM samples treated and not treated with rapamycin.** Dendrogram showing clustering of co-expressed metabolites (modules) for TSC-LAM samples not treated with rapamycin (n = 5) (for group definitions, see supplementary table 3). Top colour bar: colours identify 12 modules generated by unsupervised hierarchical clustering based on untreated TSC-LAM samples; middle colour bar: colours identify 16 modules generated by unsupervised hierarchical clustering based on TSC-LAM samples with rapamycin treatment (n = 7) and rearranged based on untreated TSC-LAM modules ordering; bottom colour bar: colours identify 11 modules generated by differential co-expression analysis and rearranged based on untreated TSC-LAM modules ordering.

