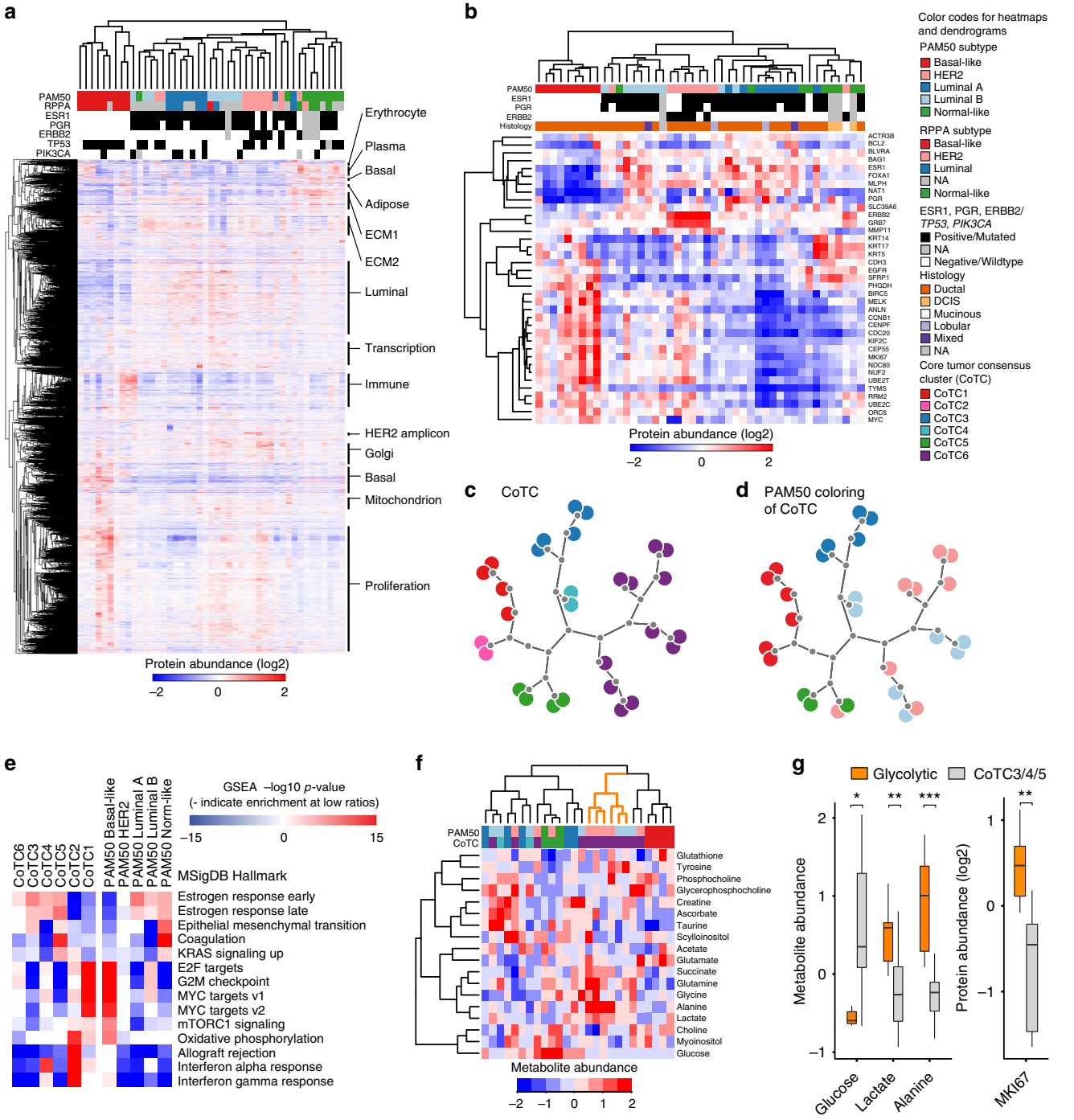

Fig. 2 Proteome clustering, relation to PAM50 subtypes and metabolites. **a** Proteome-driven clustering of proteins mapping to 9995 gene symbols with overlapping quantification in all 45 tumors. Protein cluster characteristics, by GO enrichment analysis, are highlighted to the right (see Supplementary Fig. 2 for details). **b** Clustering of identified and quantified proteins from the PAM50 panel ($n = 37$). **c** Dendrogram visualization of core tumor consensus clusters (CoTC) into six clusters. For details, see Supplementary Methods and Supplementary Fig. 4. **d** PAM50 subtype assignments for the CoTCs in **c**. **e** Ranked gene set enrichment analysis (GSEA) of CoTC and PAM50 subtypes. **f** Clustering of HR-MAS measured metabolite levels and relation to CoTCs and PAM50 subtypes. Tumors with glycolytic characteristics are indicated in orange. HR-MAS data are not available for CoTC2 tumors. **g** Levels of glucose and its conversion product lactate and alanine, as well as MKI67 protein abundance in glycolytic tumors compared to other luminal tumors. T-test, $*p < 0.05$, $**p < 0.01$, $***p < 0.001$. In box plots, center line represents median and the boxed region represents the first to third quartile, whiskers according to Tukey

Correlation also appears to be indicative of co-function, as mapping associations (defined by Pearson correlation > 0.5) of proteins marked by high variance across the Oslo2 Landscape cohort in a manner that minimizes edge length (protein nodes are in proximity to groups of nodes with which they share multiple edges, Supplementary Methods) illustrates that proteins functioning as components of similar biological processes are highly connected (Fig. 3c, Supplementary Fig. 7D, E); a feature also present in the CPTAC dataset (Supplementary Fig. 7F). Considering each CoTC and PAM50 group individually and