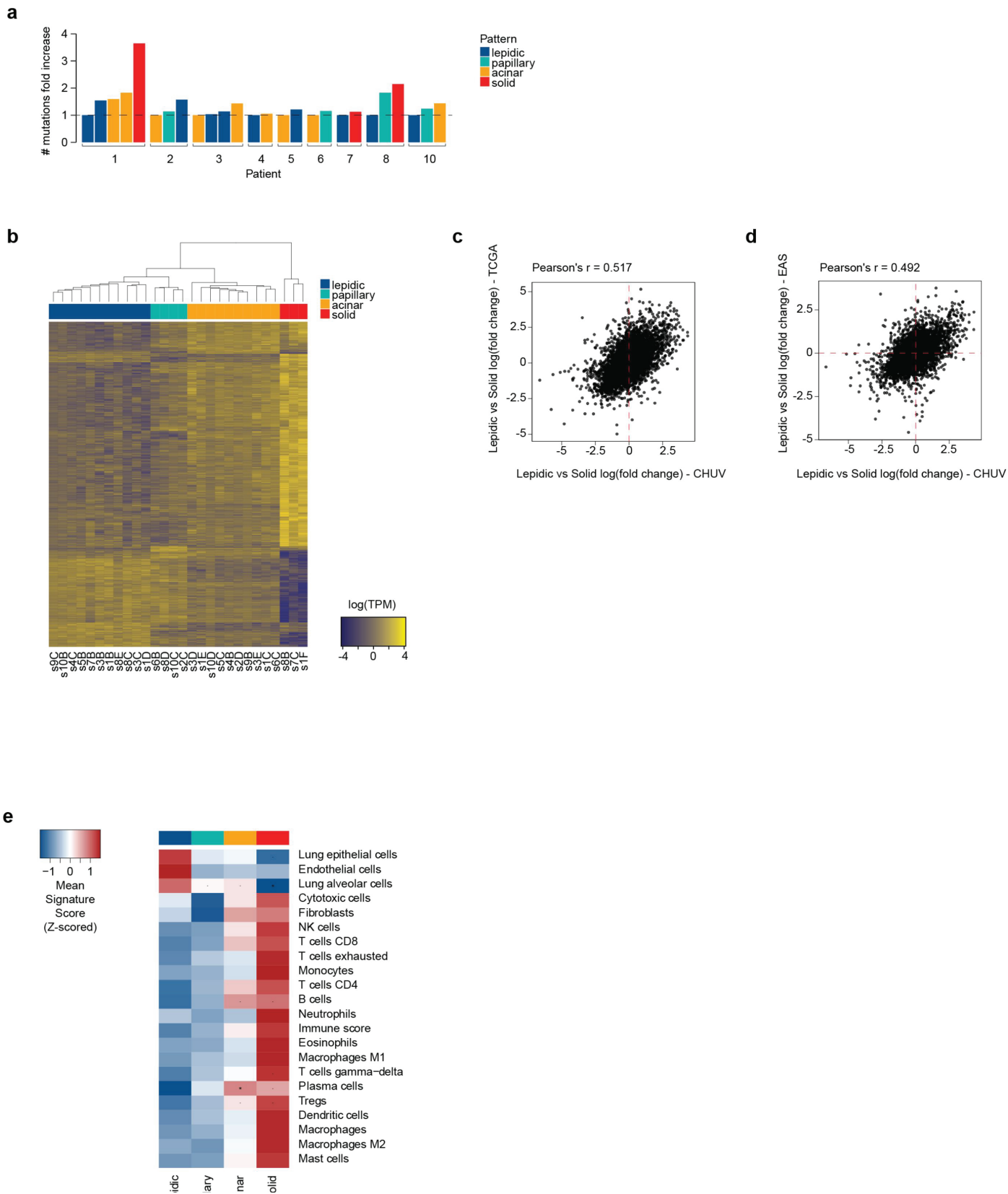


Supplementary Fig. S2



Supplementary Fig. S2

a) Number of mutations across CHUV samples re-scaled dividing by the minimum within each patient samples. Bars are color-coded by pattern.

b) Heatmap representation of differentially methylated loci among patterns (rows, adjusted p-value < 0.1). Samples (columns) are identified by patient number followed by a letter corresponding to individual tumor regions. Heatmap entries show beta values z-scaled after patient effect removal (see Materials and Methods). Histologic patterns are color coded.

c,d) Scatter plots showing gene expression log₂-fold changes for all genes between lepidic and solid patterns in CHUV dataset (X-axis) and TCGA (**c**) and EAS (**d**) datasets (Y-axis).

e) Mean mRNA signature scores for multiple cell types (rows) within each histologic pattern subtype (columns) in CHUV dataset. Values are normalized by rows (Z-scores). Cell types are sorted by descending lepidic-solid difference.