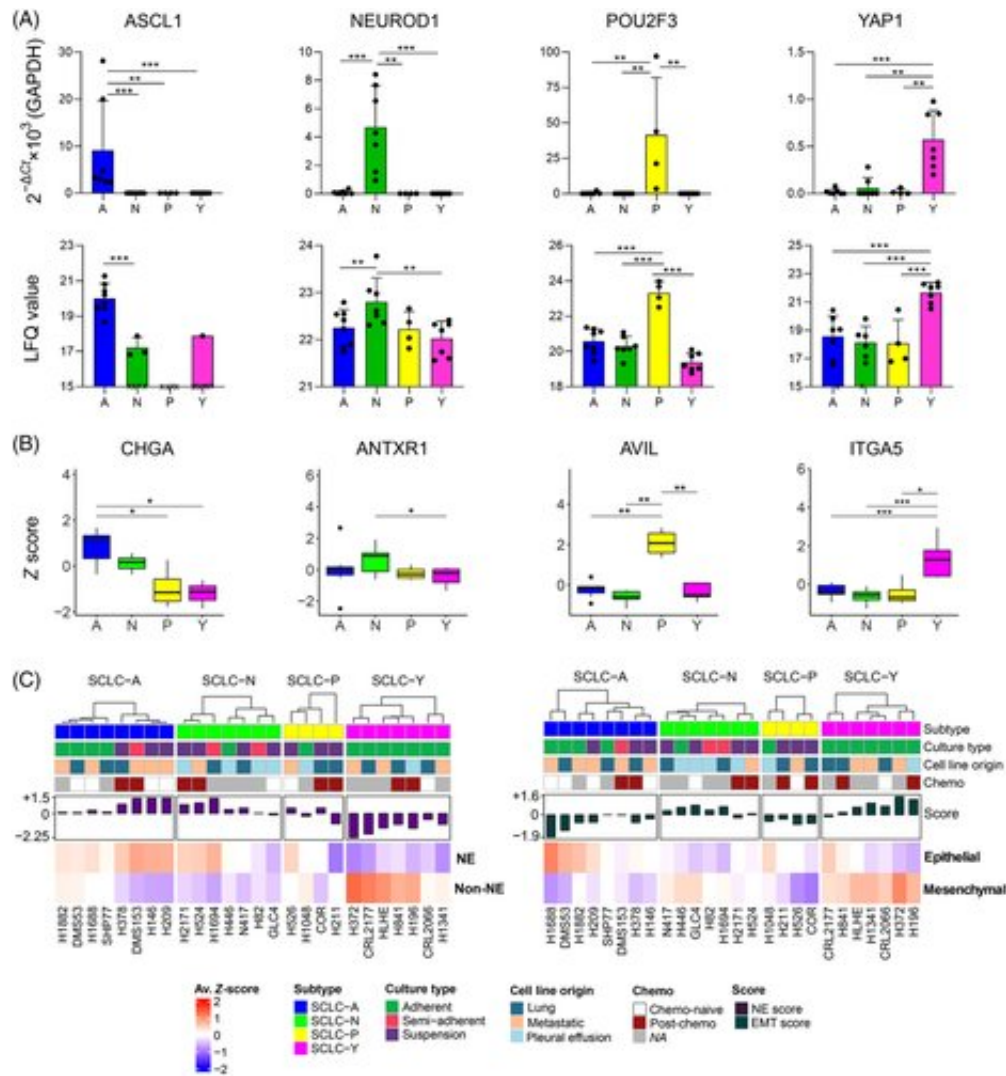# New approaches to personalized treatment for small cell lung cancer

October 6 2022, by Johannes Angerer

Proteomic analysis of small-cell lung cancer (SCLC) cell lines highlights molecular heterogeneity: (A) The mRNA expression of key genes ASCL1, NEUROD1, POU2F3 and YAP1 to determine the molecular subtypes (top). Data is shown as mean ± SD of the $2^{-\Delta Ct} \times 1000$ value, normalized to

glyceraldehyde 3-phosphate dehydrogenase (GAPDH). Each dot represents one cell line and is the mean of two biological replicates performed in triplicates. The significance of Mann–Whitney U tests is indicated above the boxplots (*p