



Figure S1. In-depth expression stratification of the validated m6A-driven target genes of the hyper-up and hypo-down clusters. Visualisation of binarised expression differences were based on 72 corresponding samples within the KIRC cohort. Samples with a fold change for the respective genes >1.5 were assigned as 1 (black) and samples with a fold change <0.66 were assigned as -1 (grey). Corresponding samples with neutral expression differences (fold change 0.66-1.5) are shown in white. All samples were homogenised into two groups based on the binarised results. Group 1 shows no expression mismatch according to the Chen et al. report (21) in any of the 7 identified m6A-driven target genes (left side). Group 2 comprises all corresponding samples in which at least one expression mismatch occurred in the TCGA expression stratification (right side). The visualisation shows a homogeneous and consistent expression pattern (expression deviation $<10\%$) only for NDUFA4L2, NXPH4, and UMOD.