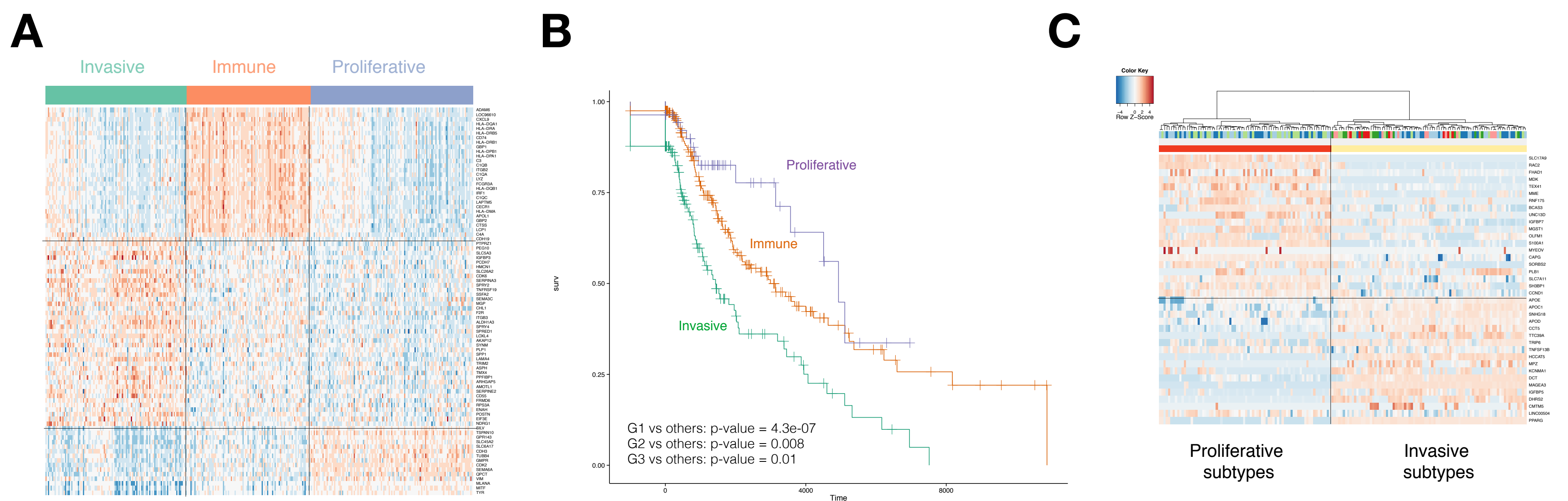




Supplemental Fig. S3 | SAKE identified patient groups with distinct survival outcome. A) SAKE was used to run gene expression clustering on melanoma patient gene expression data from the TCGA consortium. Three major clusters were identified that correspond to invasive, immune, and proliferative subtypes, which reproduces the clusters derived by the TCGA consortium results. A heat map of these results show that the SAKE-identified marker genes clearly separate the samples into three melanoma expression subtypes. **B)** Kaplan-Meier plots indicate a significant difference in overall patient survival rates across the three SAKE groups. A log-rank test was used to test for significance. **C)** Gene signatures for the proliferative and invasive melanoma subtypes were used to run clustering for all melanoma cell lines in the Cancer Cell Line Encyclopedia (CCLE). Melanoma cell lines clearly separate into these two subtypes with 451Lu cells representing the proliferative subtype and A375 cells falling into the invasive subtype.