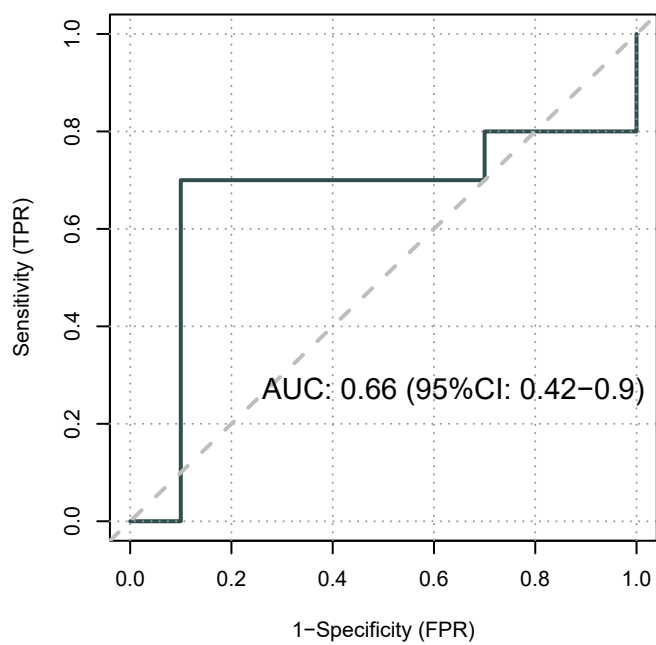


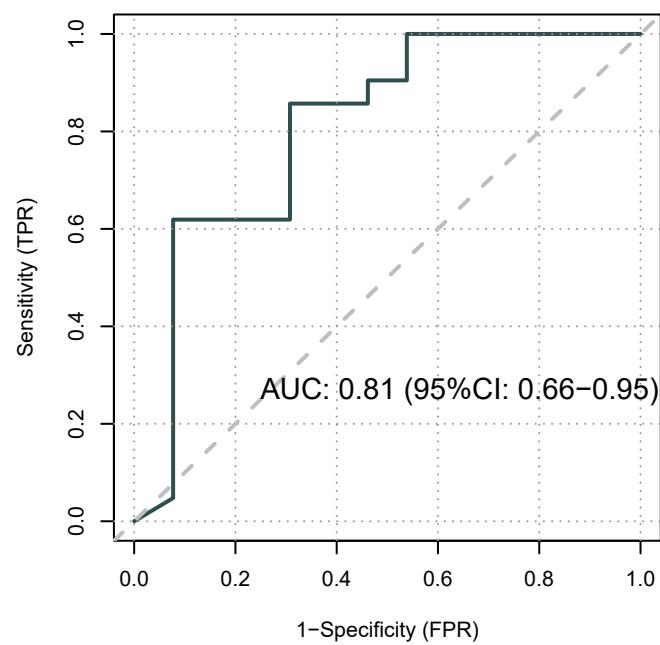
**Figure S1. Boxplots depicting the correlation of immune cells infiltration with Stem.Sig and TMB. (Mann-Whitney U test; ns, not significant; \*P < 0.05, \*\*P < 0.01, \*\*\*P < 0.001, \*\*\*\*P < 0.0001)**

**A**

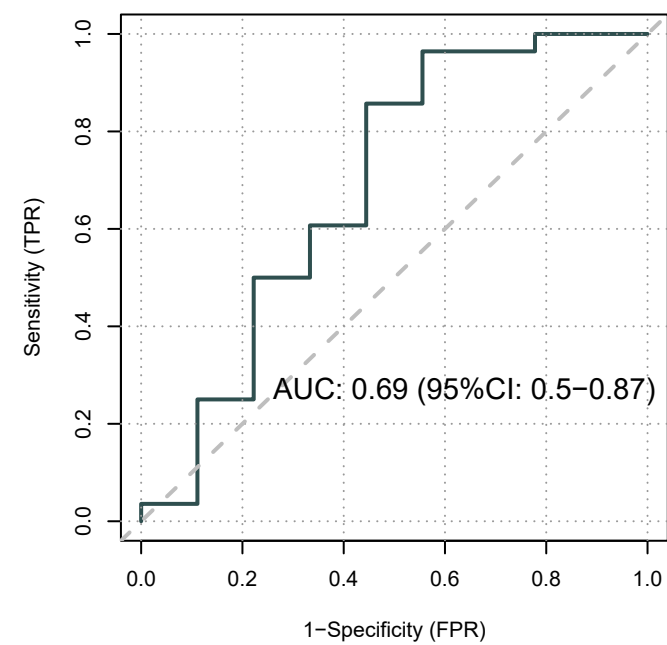
Hugo 2016 SKCM



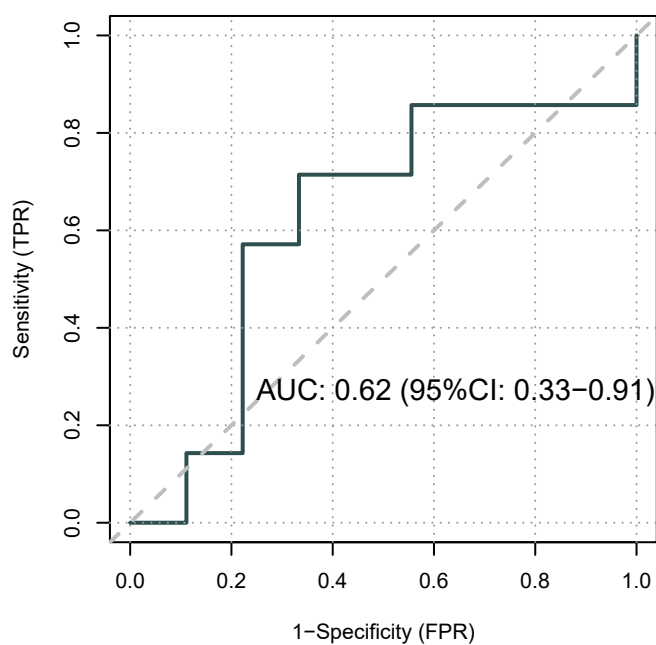
Van 2015 SKCM



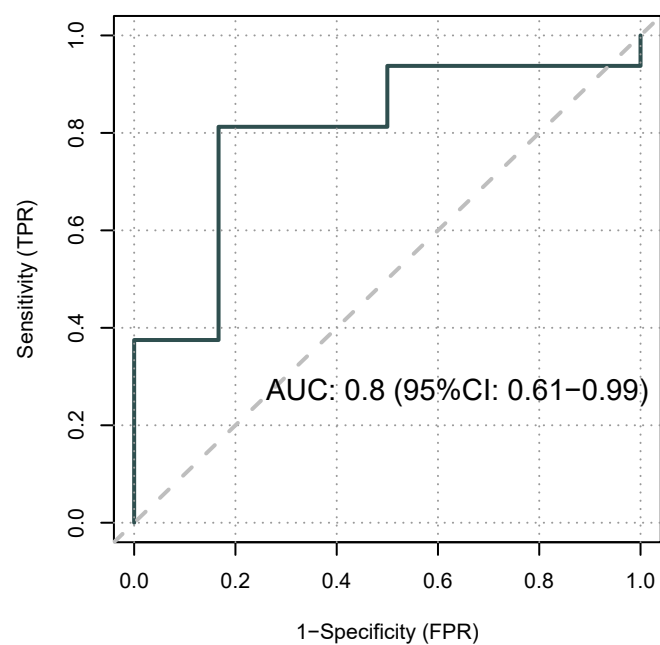
Kim 2018 GC



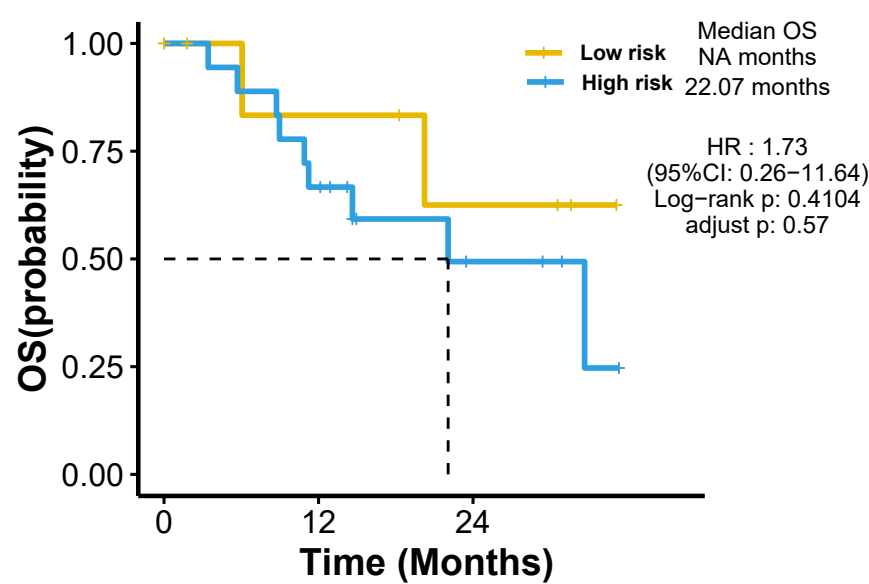
Zhao 2019 GBM



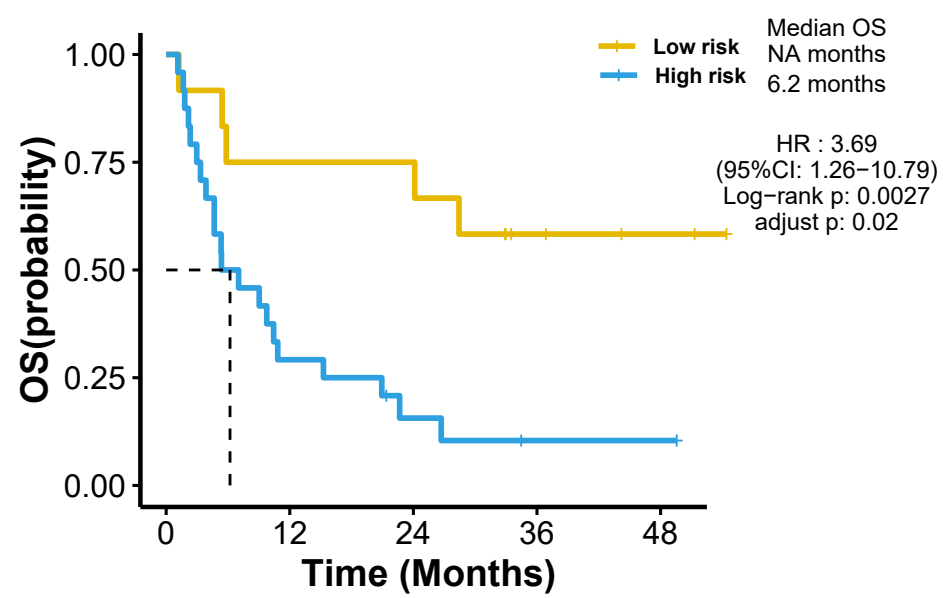
Snyder 2017 UC

**B**

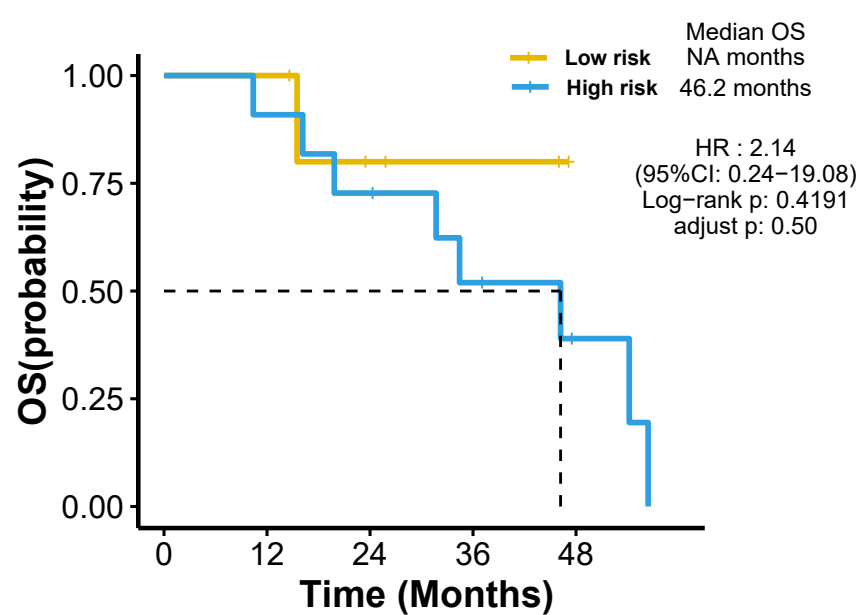
Hugo 2016 SKCM



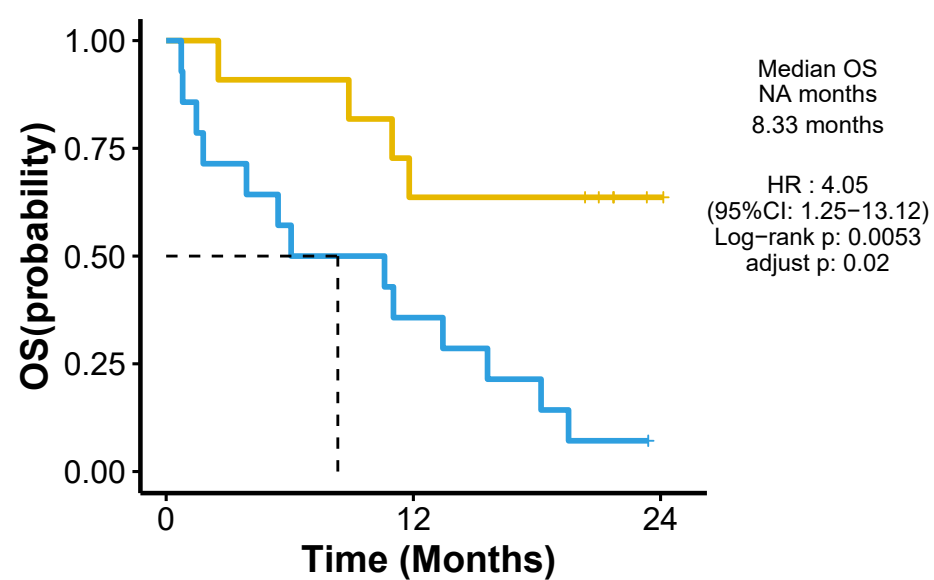
Van 2015 SKCM



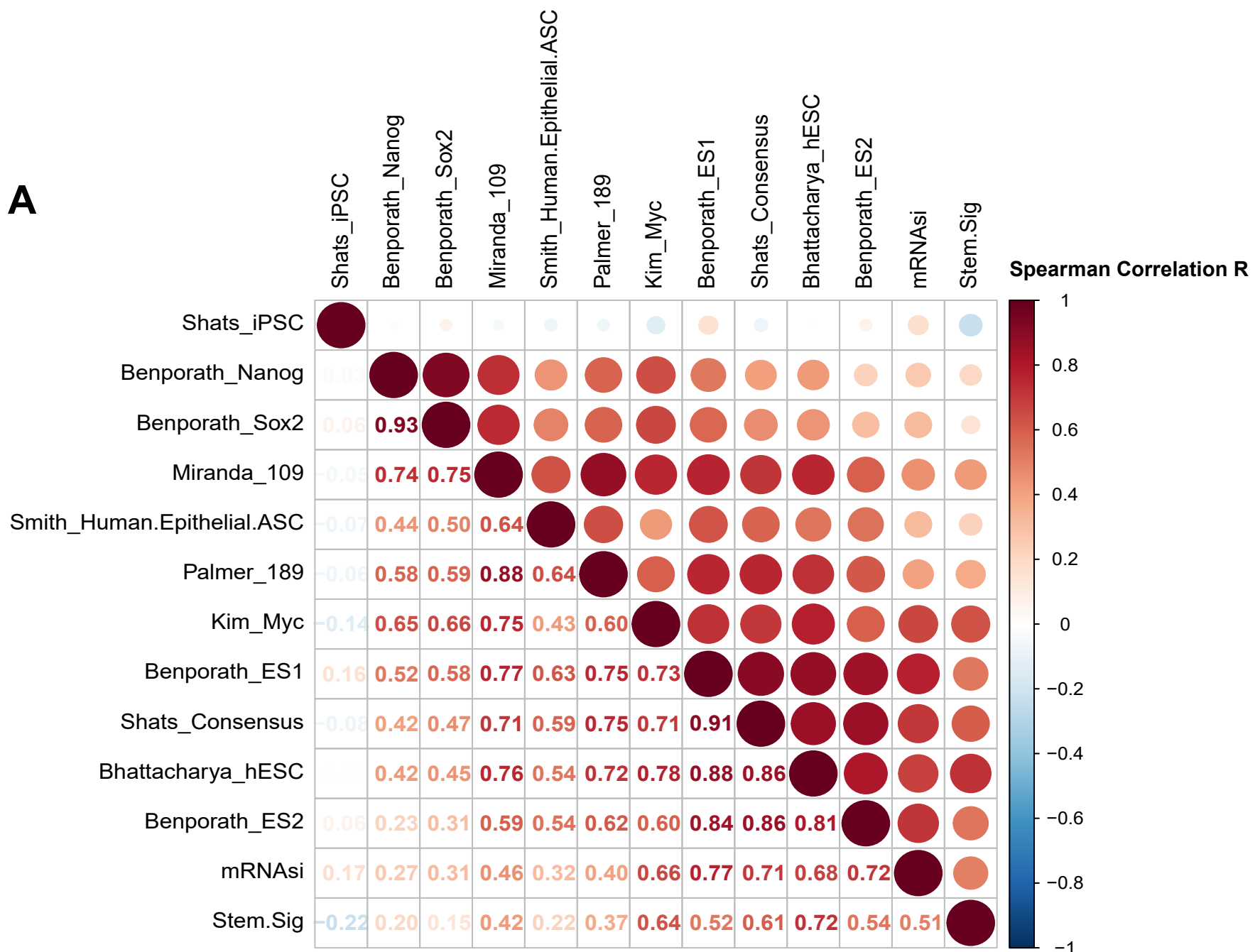
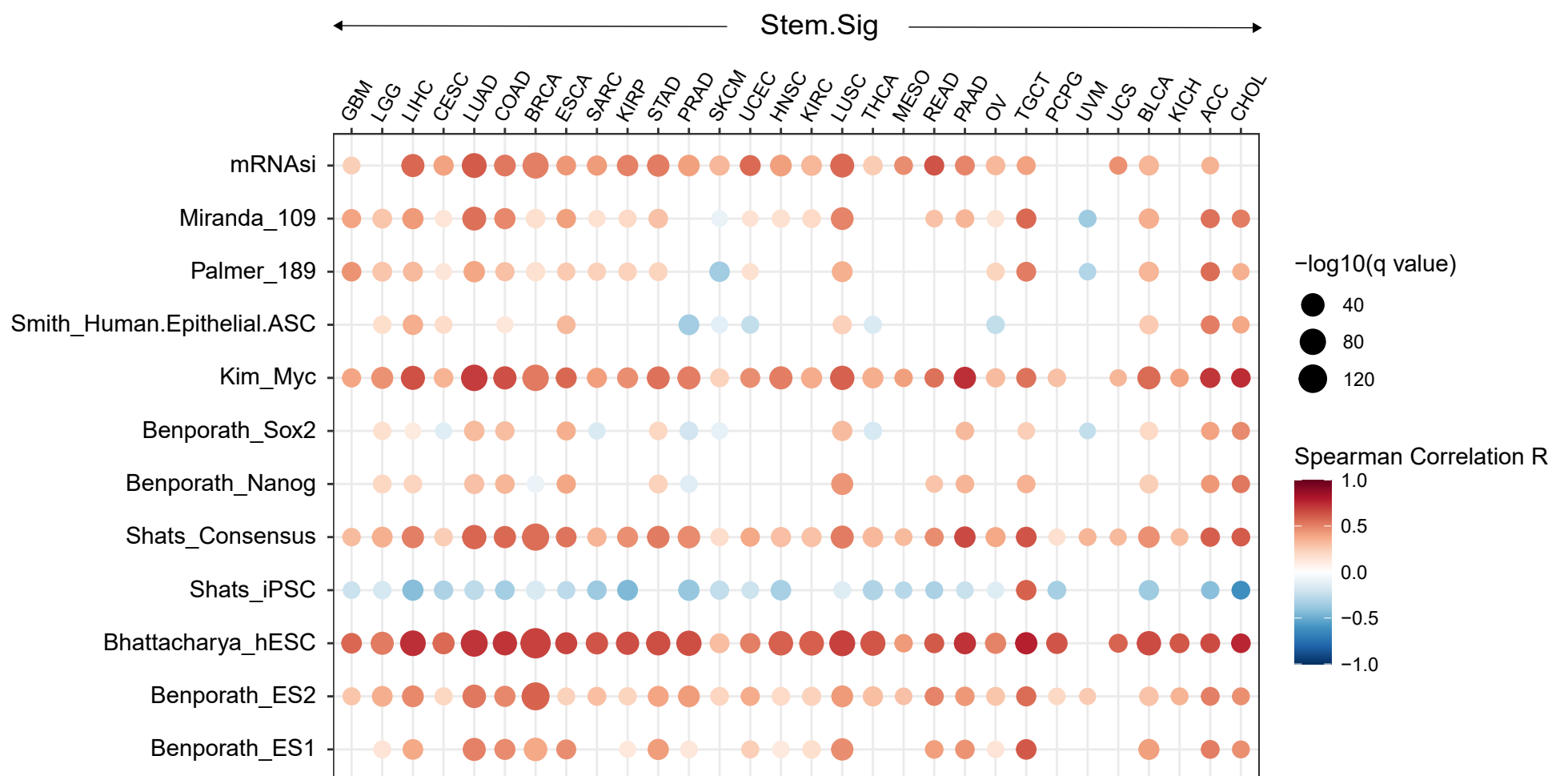
Zhao 2019 GBM



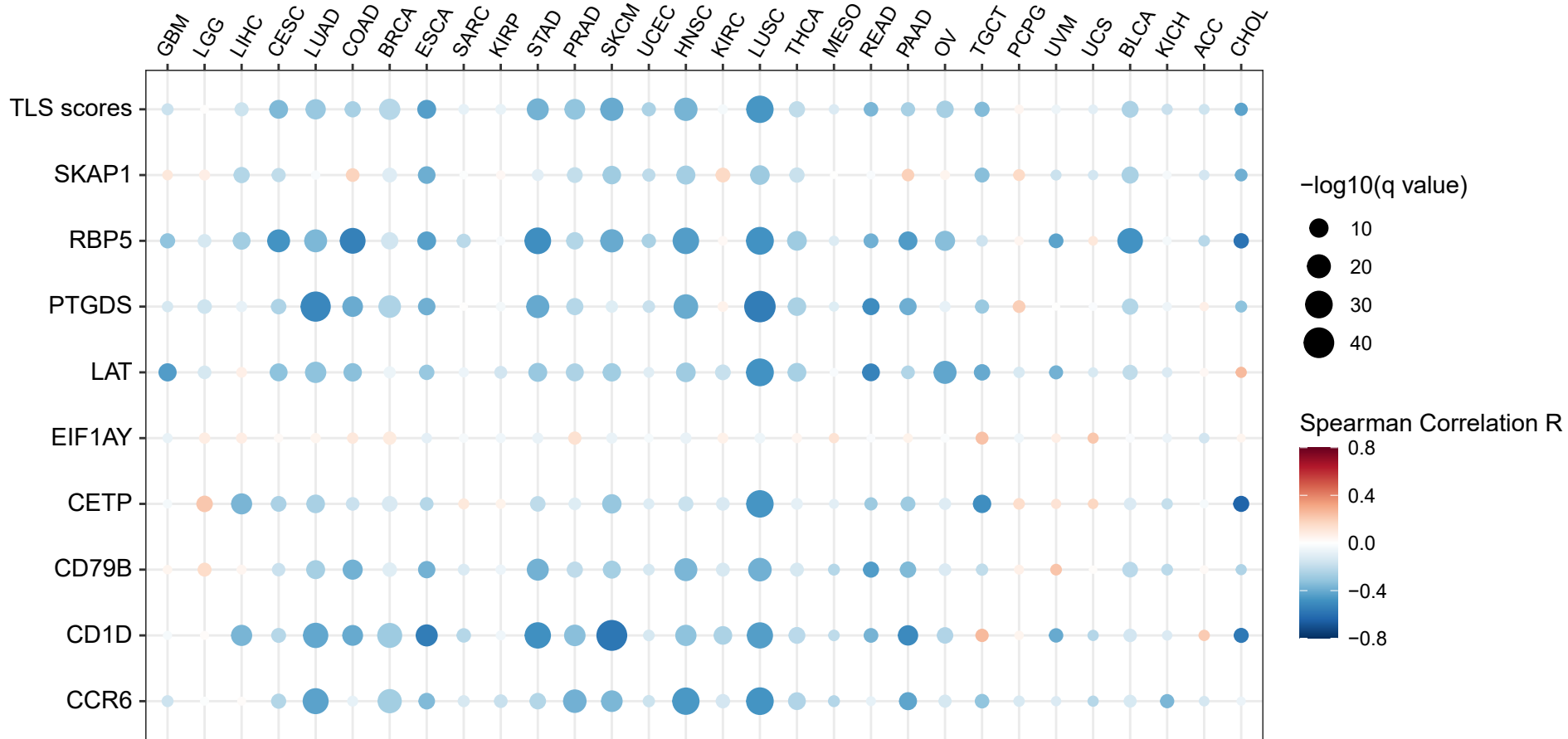
Snyder 2017 UC



**Figure S2. Subgroup analysis of testing set. A. ROC depicting the performance of Stem.Sig individual testing cohort. B. Kaplan-Meier survival plots of individual testing cohort.**

**A****B**

**Figure S3. Correlation plot of Stem.Sig and other stemness signatures.** Stem.Sig positively associated with all stemness signatures except Shats\_iPSC, which does not show significantly positive correlation with any other stemness signature[1–6].



**Figure S4. Association Stem.Sig and expression level of TLS-related genes.** TLS score was calculated as the mean gene expression of TLS-related genes.

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