

Description of Additional Supplementary Files

Supplementary Data 1: Top 80 gene signatures used as reference by Sylogist listed in order of decreasing specificity index S

Supplementary Data 2: Cell type estimation results from the GSE59612 dataset [<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE59612>]. p values determined by 2-tailed, unpaired Student's t -test with correction by the Benjamini-Hochberg procedure

Supplementary Data 3: Cell type estimation results from LGG-GBM dataset. p values determined by 2-tailed, unpaired Student's t -test with correction by the Benjamini-Hochberg procedure

Supplementary Data 4: Information on patients recruited for the study with reference to experiments performed. KPS, Karnofsky Performance Score; *MGMT*, O6-methylguanine-DNA methyltransferase; *ATRX*, ATP-dependent helicase *ATRX*; Wt, wild type; Mut, mutant; Met, methylated; Unmet, unmethylated

Supplementary Data 5: Differentially expressed genes of the scRNA HSC subset. p values determined by 2-tailed, unpaired Student's t -test with Bonferroni correction (Seurat default)

Supplementary Data 6: Differentially expressed genes of the scRNA MPP subset. p values determined by 2-tailed, unpaired Student's t -test with Bonferroni correction (Seurat default)

Supplementary Data 7: Differentially expressed genes of the scRNA GMP subset. p values determined by 2-tailed, unpaired Student's t -test with Bonferroni correction (Seurat default)

Supplementary Data 8: Differentially expressed genes of the scRNA MEP subset. p values determined by 2-tailed, unpaired Student's t -test with Bonferroni correction (Seurat default)

Supplementary Data 9: Univariate Cox regression analysis of selected variables. Two-tailed likelihood ratio test corrected by the Benjamini-Hochberg procedure

Supplementary Data 10: Publicly available datasets analyzed in this study.