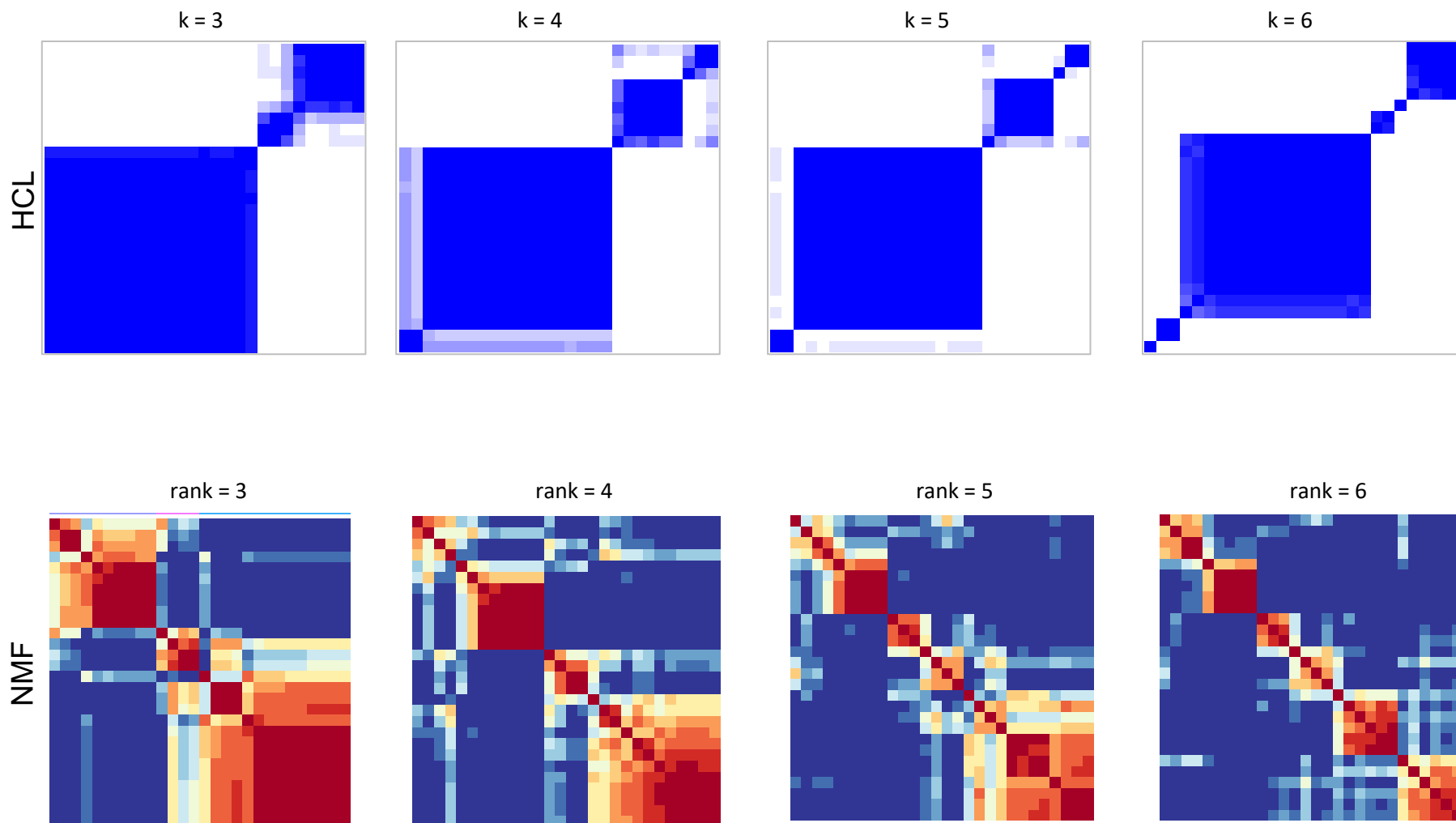


## Supplementary material

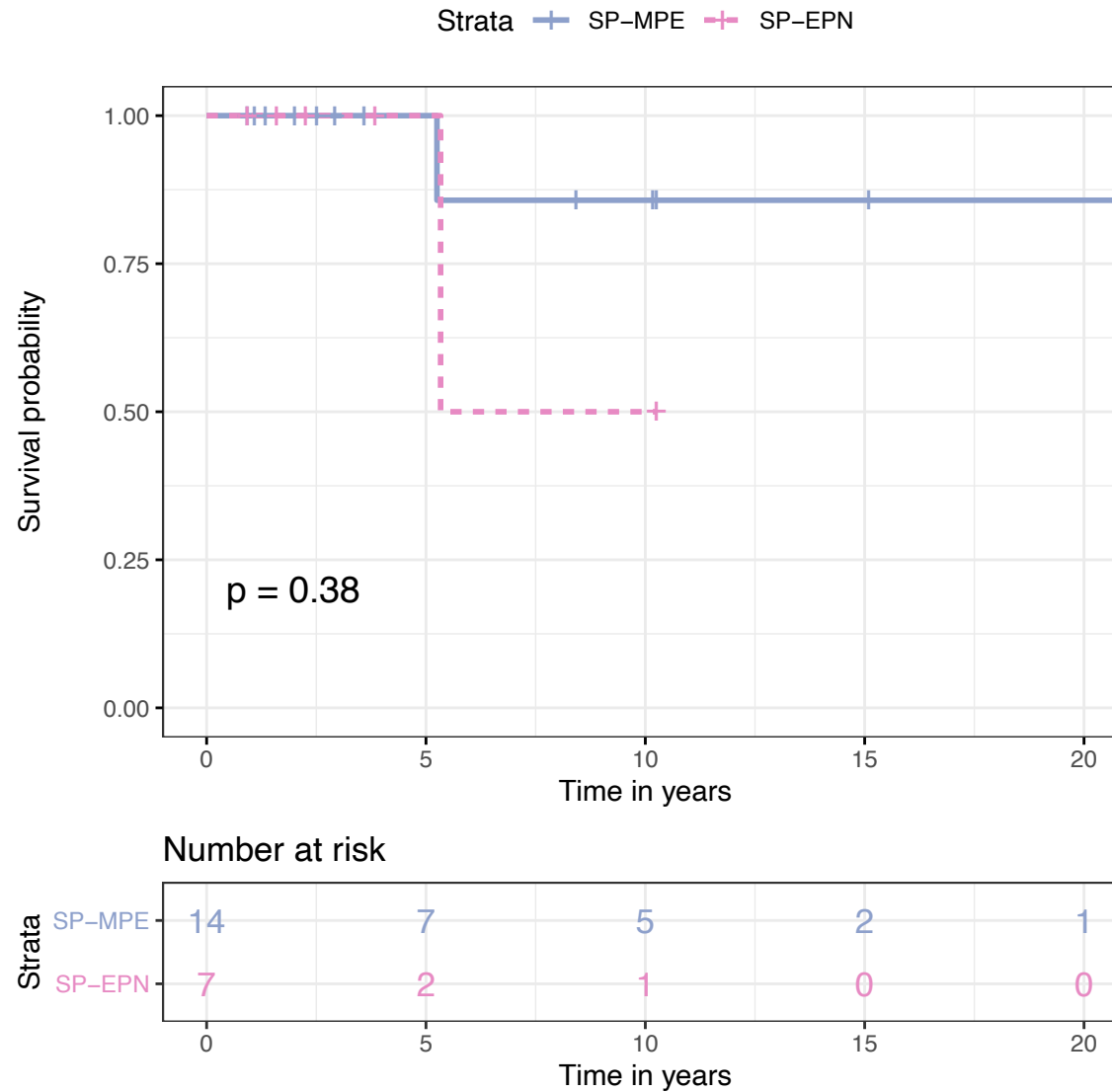
### **Integrative molecular characterization of pediatric spinal ependymoma: The UK Children's Cancer and Leukaemia Group study**

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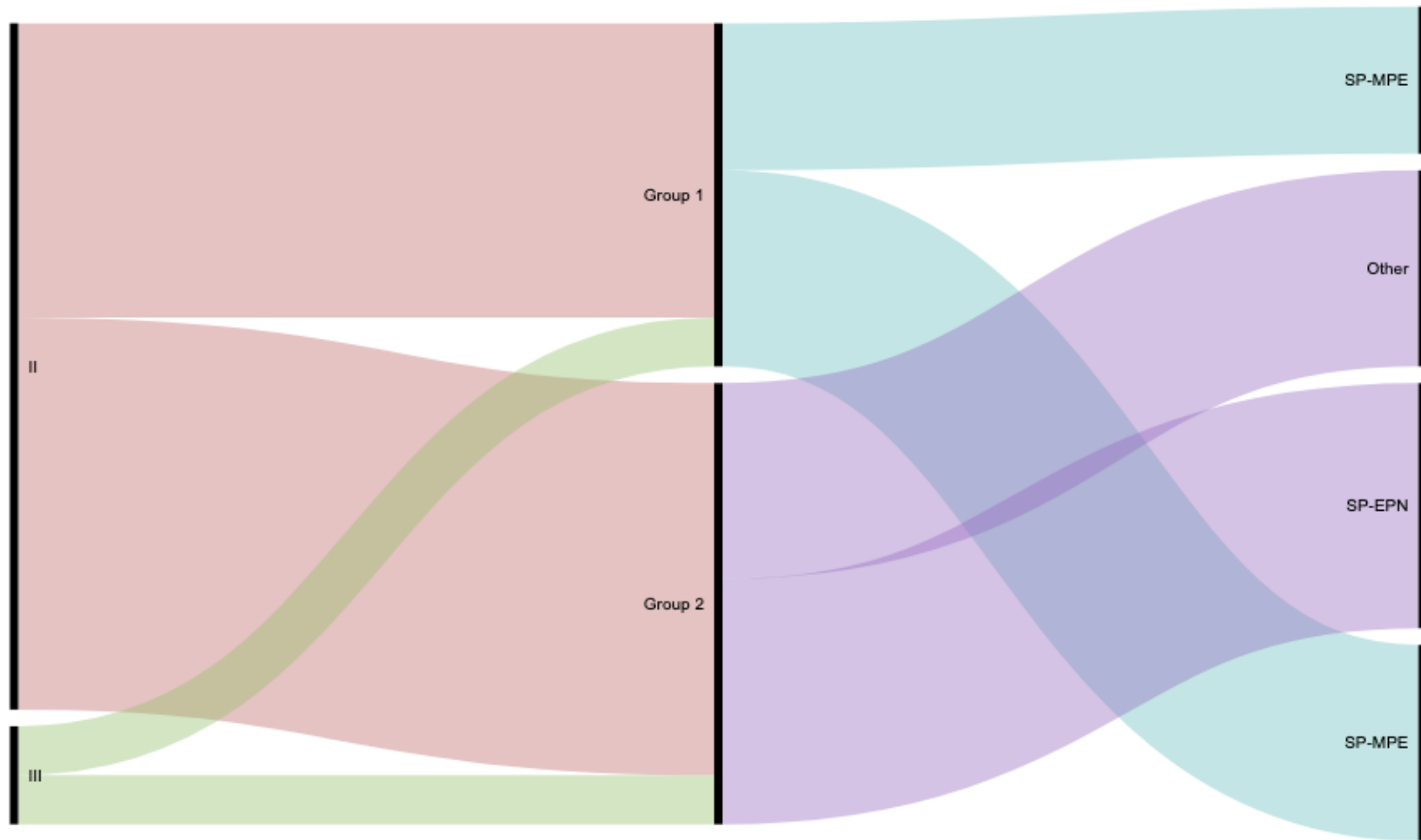
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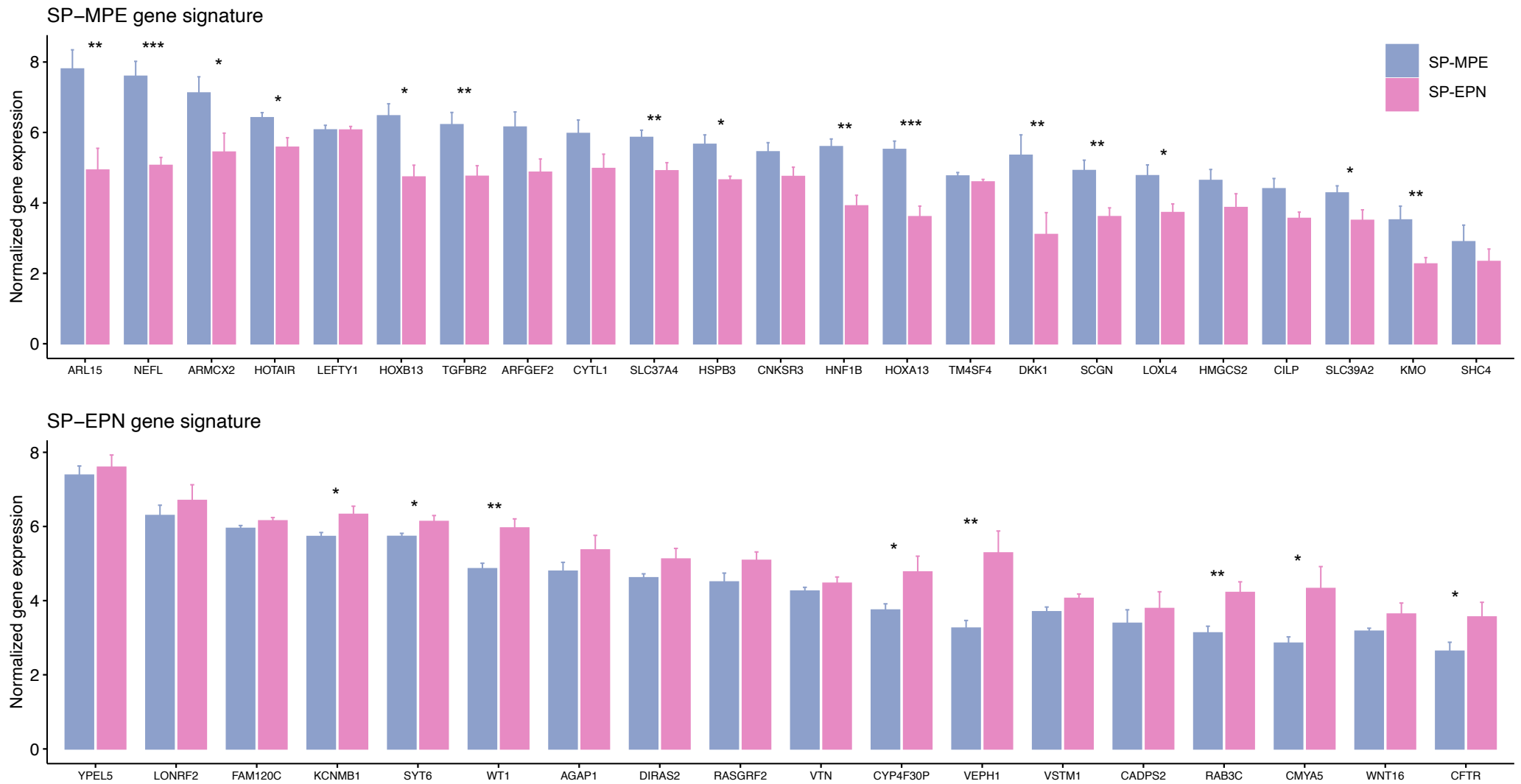
**Supplementary figure S1.** Unsupervised consensus hierarchical clustering (HCL) and non-negative matrix factorization (NMF) of 27 pediatric spinal ependymoma DNA methylation from a rank 2 to 6 classification.



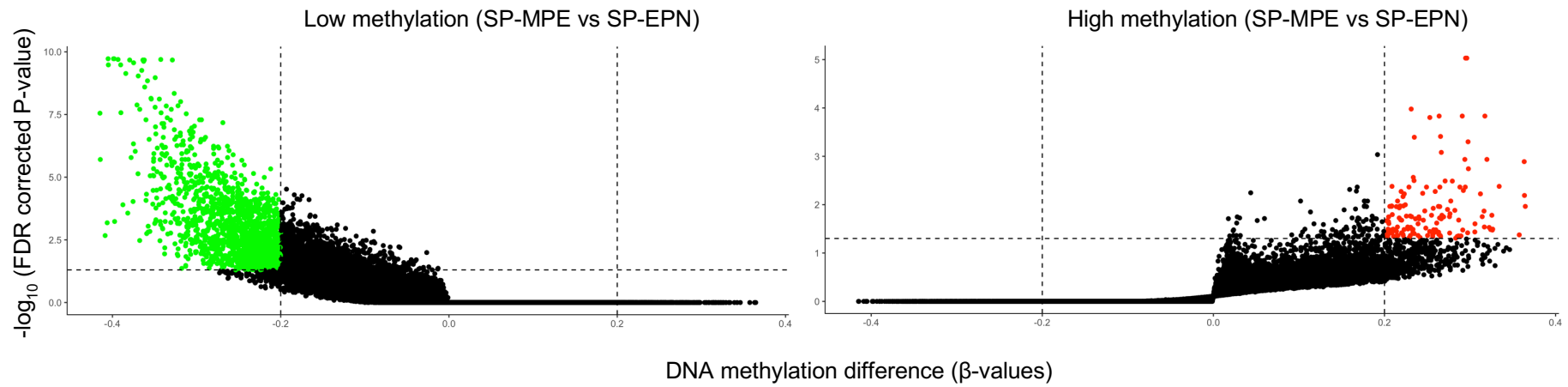
**Supplementary figure S2.** Kaplan-Meier curves of overall survival for our cohort when the patients are stratified by molecular subgroups, SP-MPE and SP-EPN. The median overall survival for the SP-EPN was 5.33 and was not reached for the SP-MPE. Significance levels were determined by log-rank test.



**Supplementary figure S3.** Assignment of grade II and III to molecular ependymoma subgroups based on DAN methylation profiles in our pediatric spinal ependymoma cohort.

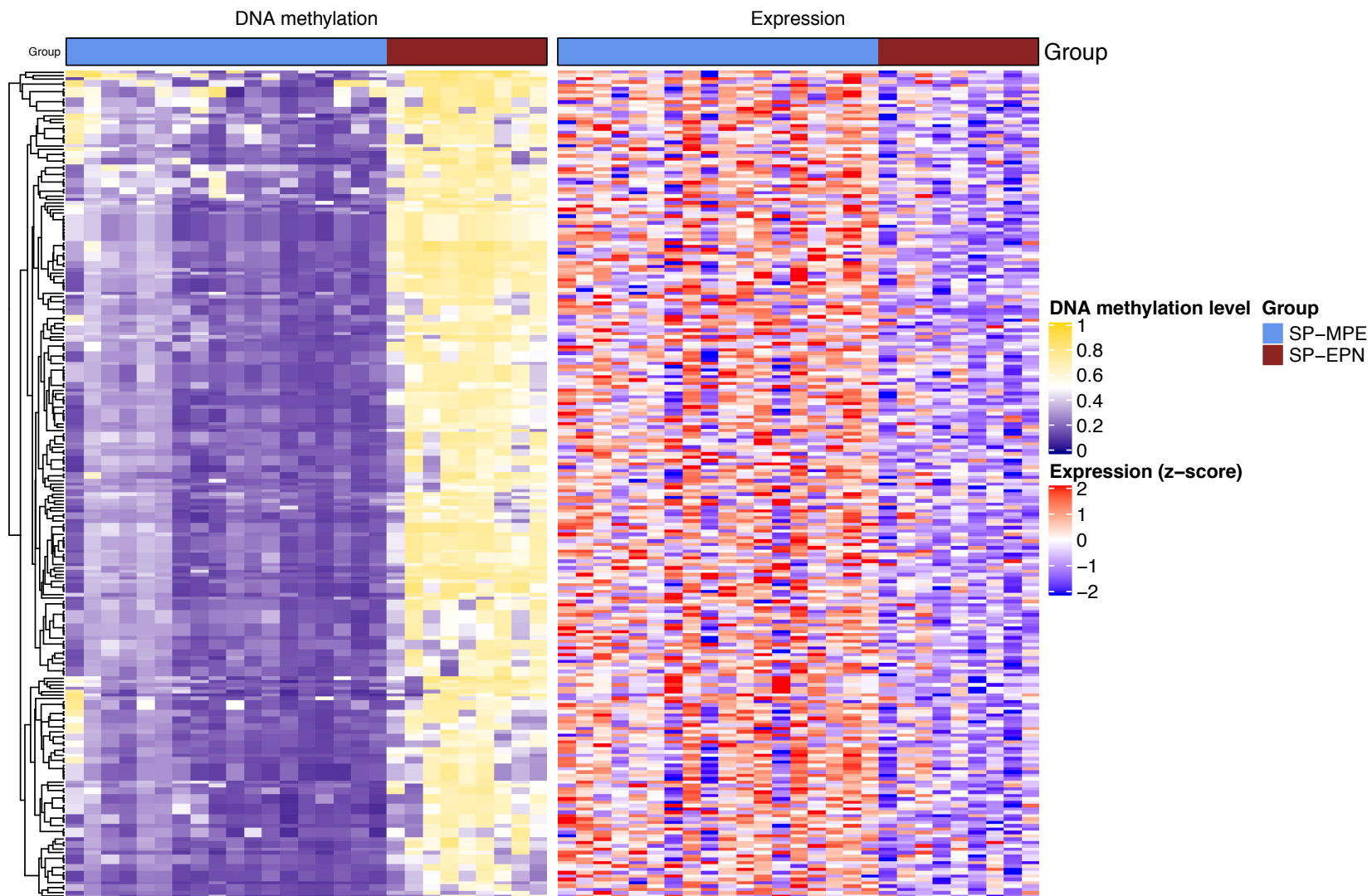


**Supplementary figure S4.** Subgroup-associated gene signature. Bar plot shows the expression levels of signature genes for SP-MPE (top) and SP-EPN subgroups (bottom). The subgroup-specific gene signatures were obtained from the previously published study by Pajtler et.al (2015). The Wilcoxon signed-rank test was used and p values (\*:  $p < 0.05$ ; \*\*:  $p < 0.01$ ; \*\*\*:  $p < 0.001$ ) on the top indicate whether there was a significant difference in the distribution of expression values across the two subgroups, SP-MPE and SP-EPN. The p values for all SP-MPE signature genes remain significant after adjusting for multiple comparisons (false discovery rate, FDR) using the Benjamini-Hochberg adjustment whereas only three genes: *RAB3C*, *VEPH1* and *WT1* remain significant for the SP-EPN gene signature at the  $FDR < 0.05$ .



**Supplementary figure S5.** Differential methylated distal probes. Volcano plots showing DNA methylation differences (x-axis) and their statistical significance (y-axis) between SP-MPE and SP-EPN subgroups. Probes with low (left) and high (right) methylation levels in SP-MPE when compared to the SP-EPN subgroup are shown.

### Correspondence between probe DNA methylation and distal gene expression



**Supplementary figure S6.** Probe-gene pairs showing inverse correlation between methylation and gene expression. Shown are the heatmaps for the significant DNA methylation probes (left) and gene expression (right) pairs at FDR < 0.05.