

Figure S1. Distribution of methylation levels and locations of tumor subtype-specific lncRNAs in the genome. Circos plot of the distribution of the top-ranked differential methylated lncRNAs for each chromosome in the genome, the mean methylation values of the lncRNA promoters in the spinal ependymoma group, the mean methylation values of the lncRNA promoters in the spinal myxopapillary group, the mean methylation values of the lncRNA promoters in the spinal subependymoma group. Dot plot of the $-\log_{10}(\text{P-value})$ calculated using ANOVA for each lncRNA ranged between 5.08 and 33.33. lncRNA, long non-coding RNA.

