

Extended Data Figure 5 | Subgroup-specific enhancers of ependymoma.

a, b, Heatmap of all subgroup-specific active enhancers detected in ependymomas in independent samples in the Heidelberg ($n = 24$ independent samples) (**a**) and Toronto ($n = 18$ independent samples) (**b**) cohorts. **c**, Box plot of gene expression for ependymoma SE-SSEA-associated genes in the Heidelberg cohort ($n = 24$ independent samples). Comparisons were made using a two-sided Wilcoxon rank-sum test. Box plots show the centre (median), upper and lower quartile range, and dotted lines indicate minima and maxima. **d–f**, Venn diagrams of the number and percentage of subgroup-specific super-enhancer-associated loci validated between the Heidelberg and Toronto cohorts. **g, h**, Non-negative factorization of ependymoma super enhancer profiles in the Heidelberg ($n = 24$ independent samples) and Toronto ($n = 18$ independent samples) cohorts. **i**, Normalized H3K27ac profiles for

subgroup-specific genomic example loci in the Heidelberg cohort with at least three biological replicates per subgroup, with the exception of ST-EPN-SE, shown as a biological duplicate. **j**, G-Profiler pathway-enrichment analysis of ependymoma subgroup-specific super-enhancer-associated genes in the Heidelberg cohort ($n = 24$ independent samples) with statistical significance determined using a hypergeometric test. **k–n**, H3K27ac profiles surrounding the *EPHB2* (**k**) and *CCND1* (**m**) loci in the Heidelberg cohort with at least three biological replicates per subgroup, with the exception of ST-EPN-SE, shown as a biological duplicate. *EPHB2* (**l**) and *CCND1* (**n**) expression by RNA-seq across ependymoma subgroups in the Heidelberg cohort with horizontal bars indicating the median value and each dot representing an independent ependymoma sample ($n = 24$ independent samples).