

Extended Data Figure 4 | Ependymoma enhancer supporting data.

a, Number of unique H3K27ac peaks detected by MACS1.4 ($P < 1 \times 10^{-9}$ cut-off) with increasing sample number in the Heidelberg cohort ($n = 24$ independent samples). **b**, Box plot of gene expression values comparing typical enhancer ($n = 9,826$ genes) versus super enhancer ($n = 1,682$ genes) associated genes. Statistical analysis was assessed using a two-sided Wilcoxon rank-sum test. Box plots show the centre (median), upper and lower quartile range, and dotted line indicating minima and maxima. **c**, Frequency of enhancer and super enhancer regions as a function of size in base pairs. **d**, Dot plots illustrating the numbers of super enhancers detected in the Heidelberg ($n = 24$ independent samples), Toronto ($n = 18$ independent samples) and normal brain ($n = 7$ independent samples) cohorts. The horizontal bar indicates the mean. **e**, Heatmap illustrating significant gained and lost enhancer loci in both ependymoma cohorts compared to normal brain samples. Comparisons were evaluated using a two-sided Wilcoxon rank-sum test with FDR correction and a cut-off of $FDR < 0.05$. **f**, Example plots of normalized and scaled H3K27ac RPKM profiles at example ependymoma candidate genes in Heidelberg

ependymomas and normal brain (NB) ($n = 32$ independent samples). **g**, Comparison of gene expression of ependymoma super-enhancer-associated genes derived from ref. 11 ($n = 83$ independent samples) with normal brain ($n = 172$ independent samples). Statistical analysis was assessed using a two-sided Wilcoxon rank-sum test. **h**, Table comparing the number and per cent confirmation between the Heidelberg ($n = 24$ independent samples) and Toronto ependymoma cohorts ($n = 18$ independent samples). **i**, G-Profiler pathway-enrichment analysis of ependymoma-specific super-enhancer-associated genes in the Toronto cohort ($n = 18$ independent samples), with statistical significance determined using a hypergeometric test. **j**, Overlap analysis measured by a two-sided binomial test between tumour-specific ependymoma super enhancers and cancer census genes from the Catalogue of Somatic Mutations in Cancer (COSMIC) database. **k**, Classification of tumour-specific ependymoma super enhancer genes also found in the COSMIC database²⁹ as tumour suppressor genes ($n = 12$), oncogenes ($n = 26$), or unknown ($n = 21$).