



Extended Data Figure 6 | Workflow describing the functional validation of ependymoma super enhancer genes. **a**, Workflow of super-enhancer target-gene prioritization for functional evaluation. **b**, Bar chart comparing the top-ranked super-enhancer-associated genes against top-ranked genes detected by RNA-seq defined as significantly increased or overexpressed

compared to normal brain controls across all ependymoma samples ($n = 42$ independent samples). Significant genes were identified by a two-sided Wilcoxon rank-sum test with FDR correction and ranked by FDR corrected P value with a cut-off of less than 0.05.