



Extended Data Figure 3 | Preprocessing and clustering of ependymoma H3K27ac profiles. **a, b**, Box plots of H3K27ac enhancer profiles ($n = 556,676$ enhancer loci evaluated per sample) before quantile normalization for both Heidelberg ($n = 24$ independent samples) (**a**) and Toronto ($n = 18$ independent samples) (**b**) cohorts compared to Roadmap Epigenomics and ENCODE cohorts ($n = 98$ independent samples). Box plots are shown with the centre (median), upper and lower quartile range, and dotted line indicating minima and maxima per sample. **c, d**, Box plots

of H3K27ac enhancers after quantile normalization for both Heidelberg ($n = 24$ independent samples) (**c**) and Toronto ($n = 18$ independent samples) (**d**) cohorts compared to the Roadmap Epigenomics cohort ($n = 98$ independent samples). **e, f**, Unsupervised hierarchical clustering of enhancer profiles as measured using the top 10,000 variant enhancer loci identified in the Roadmap Epigenomics cohort with the Heidelberg ($n = 122$ independent samples) (**e**) and Toronto cohorts ($n = 116$ samples) (**f**) and compared in a pair-wise fashion using a Spearman correlation.