



Extended Data Figure 1 | DNA fingerprint analysis of ependymoma sequence data. a, b, Unsupervised clustering of ChIP-seq, RNA-seq, WES, WGS, and Illumina DNA methylation profiles with genotypes that have an

average heterozygosity score greater than 0.25 in the Heidelberg ($n = 25$ independent samples) (a) and Toronto cohorts ($n = 18$ independent samples) (b).