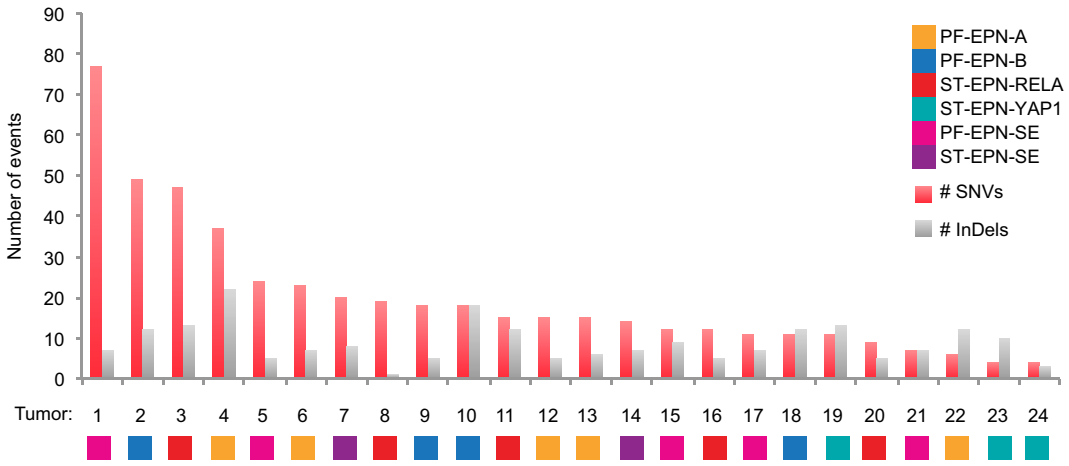
a

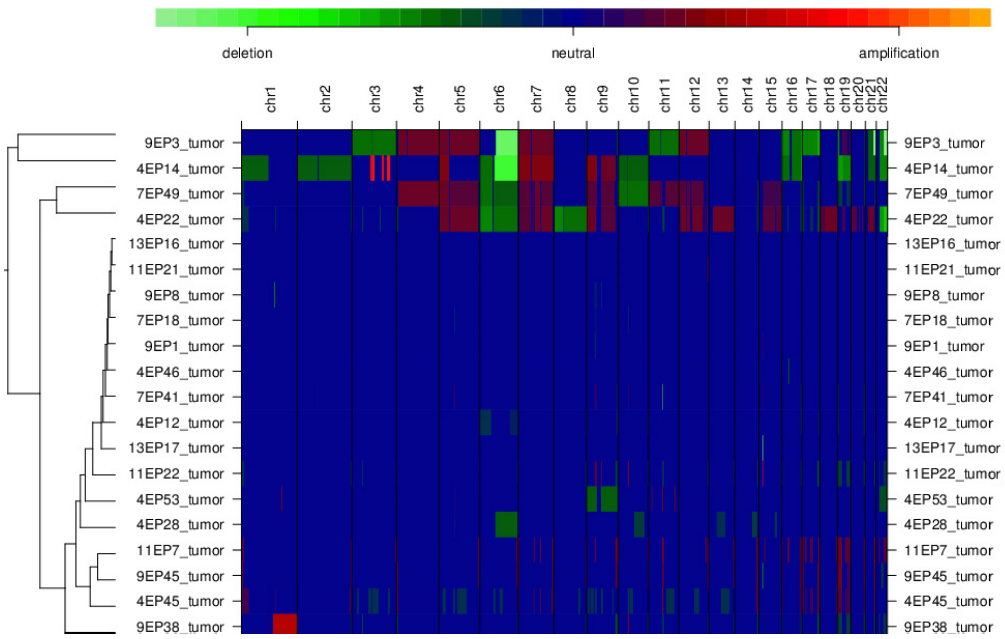


b

Recurrently affected genes (SNVs)	
2/24 (8.33333%)	SHOX
2/24 (8.33333%)	PDE3B
2/24 (8.33333%)	PAK2
2/24 (8.33333%)	MYO15A
2/24 (8.33333%)	ICOSLG
2/24 (8.33333%)	HT T
2/24 (8.33333%)	EPHX4
2/24 (8.33333%)	AGXT2
2/24 (8.33333%)	AC079354.1

Recurrently affected genes (indels)		
2/24	(8.33333%)	WISP1
2/24	(8.33333%)	SORCS1
2/24	(8.33333%)	snoU13
2/24	(8.33333%)	SHCBP1
2/24	(8.33333%)	RP3-470B24.5
2/24	(8.33333%)	PTPRK
2/24	(8.33333%)	NDRG1
2/24	(8.33333%)	FAM169A
2/24	(8.33333%)	DLEU2
2/24	(8.33333%)	CROCCP2

c



Extended Data Figure 2 | Summary of genome sequencing and copy number data. a, Number of somatic single nucleotide variants (SNVs) detected per ependymoma sample. **b**, Frequency of somatic mutations detected across the Heidelberg ependymoma cohort ($n = 24$ independent samples). **c**, Unsupervised hierarchical clustering of copy number alterations detected by WGS in primary ependymoma samples ($n = 24$ independent samples).