Supplementary Figure S1: Spotfire Decision Site® copy number heatmap demonstrating Affymetrix® 500K SNP array results across the genome for 42 primary and six intracranial first recurrent ependymomas. Primary tumors are categorized according to location. Diploid genomic regions are coloured black. Regions exhibiting genomic loss are coloured red, while regions demonstrating gain are coloured green or yellow, depending on whether the gain represents a copy number of three or greater respectively. P = primary, R1 = 1st recurrence.

Supplementary Figure S2: Intracranial ependymoma demonstrating 1q gain on 500K SNP array analysis and 1q25 gain with iFISH. (A) CNAG generated chromosome ideogram of chromosome 1 from the 500K SNP array analysis of ependymoma sample 10P, after normalization with patient matched constitutional DNA. Gain of 1q is evident (arrow demonstrating point of genomic increase to a copy number of three). (B) Copy number gain of the 1q25 sub-region in this tumor was confirmed by iFISH using a 1p36/1q25 dual color probe, demonstrating three green 1q25 signals within each cell nucleus. iFISH verified the copy number status of 1q25 in 18 intracranial ependymomas analyzed on the SNP array (Spearman’s Rank = 0.79; p < 0.0001).

Supplementary Figure S3: Kaplan-Meier progression-free survival (PFS) curves for ependymoma 1q25 gain across individual CNS9204, BBSFOP and CNS9904/RT cohorts. On univariate analysis, 1q25 gain was an adverse marker of PFS in the CNS9204 cohort (Five year PFS of 9 % versus 55 % for tumors without 1q25 gain). A trend towards a worse outcome was seen for 1q25 gain in the BBSFOP cohort (Five year PFS 0 % versus 32 % for tumors without gain), while gain was not associated with a worse PFS in the CNS9904/RT group (Five year PFS 40 % versus 51 % for tumors without 1q25 gain).