**Supplementary Table S1.** Target regions for probe design for targeted sequencing. Coordinates were extracted using genome assembly GRCh37/hg19.

Genomic region	Target
chr4:1,790,039-1,820,600	FGFR3 locus
chr8:38,258,656-38,331,352	FGFR1 locus
chr5:1,295,162-1,295,662	TERT promoter (500 bp)
chr13:48,877,883-49,056,026	RB1 exons
chr21:17,911,328-17,911,570	miR-99a locus
chr9:8,314,246-10,612,723	PTPRD exons
chrX:76,937,000-76,940,142	ATRX # exon 8
chrX: 76,763,788-76,891,418	ATRX # exons 16-end
chr8:38,585,704-38,710,546	TACC1 exons
chr4:1,723,217-1,746,905	TACC3 exons
chr9:21,967,751-21,994,490	CDKN2A exons
chr10:89,623,195-89,728,532	PTEN exons
chr3:178,916,614-178,952,152	PIK3CA exons in coding region
chr12:112,856,536-112,947,717	PTPN11 exons
chr4:55,095,264-55,146,925	PDGFRA exons
chr4:55,095,264-55,146,925	MET exons
chr17:7579650-7579750	P53 # exon 3
chr17:7579300-7579600	P53 # exon 4
chr17:7578350-7578570	P53 # exon 5
chr17:7578150-7578300	P53 # exon 6
chr17:7577480-7577630	P53 # exon 7
chr17:7577000-7577180	P53 # exon 8
chr17:7576840-7576940	P53 # exon 9
chr17:7576520-7576680	P53 # exon 10
chr17:7573910-7574050	P53 # exon 11
chr2:209113040-209113190	IDH1 # exon 4
chr15:90631790-90631940	IDH2 # exon 4
chr11:65429530-65431330	RELA # exons 1-3
chr7:140453090-140453190	BRAF # exon 15
chr7:140481400-140494300	BRAF # exons 8-11
chr7:55084974-55275667	EGFR gene
chr5: 60003061 -80002241	CNA negative control region 1 (21 probes)
chr8: 60001061 -80002241	CNA negative control region 2 (21 probes)
chr18: 30000975 -50001334	CNA negative control region 3 (14 probes)
chr11: 70001061-90005243	CNA negative control region 4 (19 probes)

Supplementary Table 2. Overview of targeted sequencing cohort and the obtained results (separate file)

a)
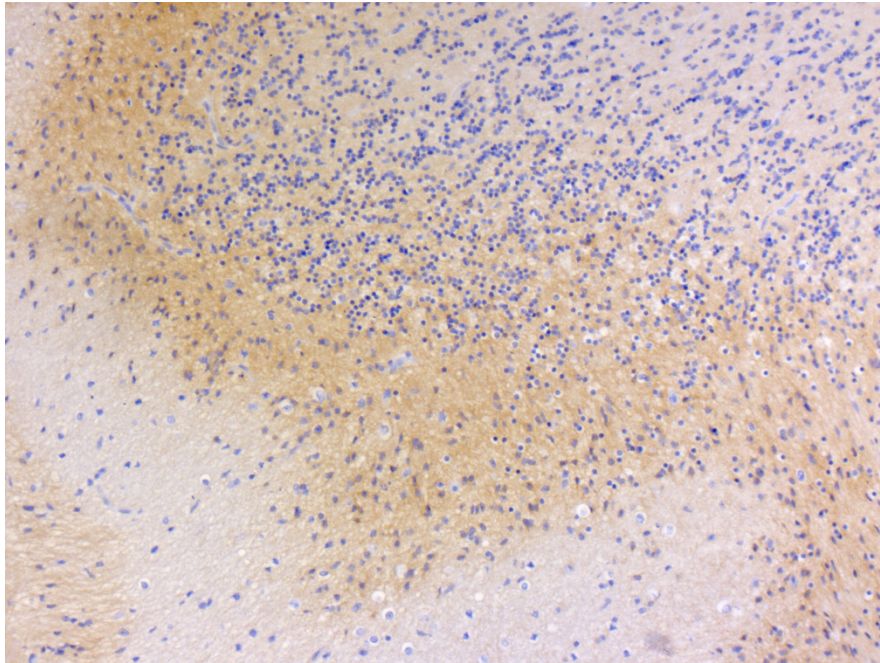
b)
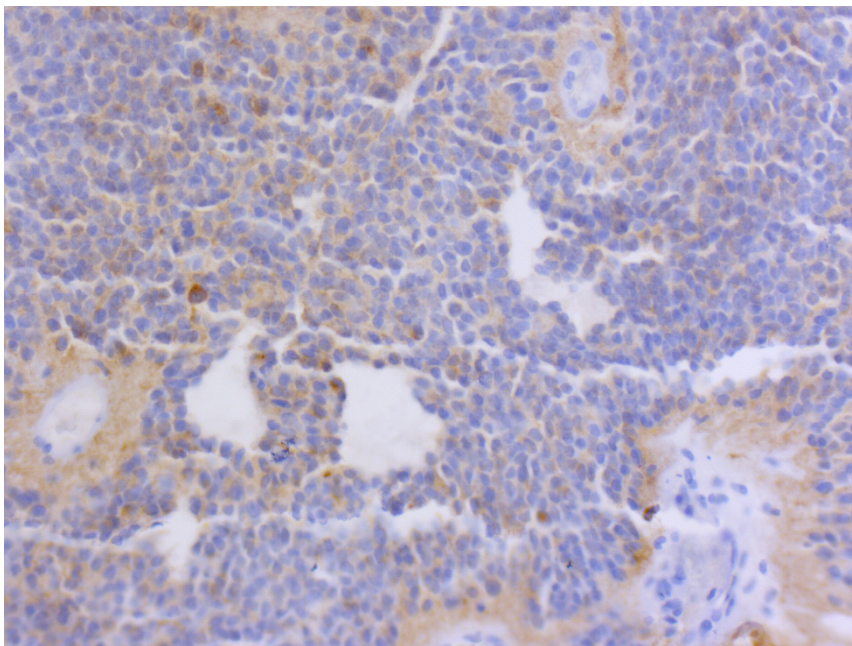
Supplementary Figure S1. a) Weak-to-moderate FGFR3 staining was observed in cerebellar molecular layer (100x magnification). b) FGFR3 staining in pseudorosette structures in ependymoma (200x magnification).

	sex	p53	spicerbra	spinaivo	prolif_class	age_class	fgfr3_class	fgfr1_class2	fgfr1	fgfr3	grade	oper
oper	N = 112 p= 0.6305	N = 63 p= 0.5432	N = 110 p= 0.1232	N = 110 p= 0.1104	N = 105 p= 0.0076	N = 112 p= 0.3174	N = 108 p= 1	N = 106 p= 0.2558	N = 106 p= 0.2704	N = 108 p= 0.7056	N = 112 p= 0.0256	N = 112
grade	N = 112 p= 0.2543	N = 63 p= 0.0388	N = 110 p= 0	N = 110 p= 0	N = 105 p= 0	N = 112 p= 0.0141	N = 108 p= 0.0125	N = 106 p= 0.0024	N = 106 p= 0.025	N = 108 p= 0.0042	N = 112	
fgfr3	N = 108 p= 0.6757	N = 61 p= 0.3805	N = 106 p= 0	N = 106 p= 0	N = 101 p= 0.2137	N = 108 p= 0.148	N = 108 p= 0	N = 103 p= 0.0126	N = 103 p= 0.0497	N = 108		
fgfr1	N = 106 p= 0.0671	N = 63 p= 0.7447	N = 104 p= 1e−04	N = 104 p= 0.0023	N = 102 p= 0.1452	N = 106 p= 0.4999	N = 103 p= 0.3383	N = 106 p= 0	N = 106			
fgfr1_class2	N = 106 p= 0.0189	N = 63 p= 0.5784	N = 104 p= 1e−04	N = 104 p= 0.0081	N = 102 p= 0.0678	N = 106 p= 0.0925	N = 103 p= 0.1767	N = 106				
fgfr3_class	N = 108 p= 0.6335	N = 61 p= 1	N = 106 p= 2e−04	N = 106 p= 0.0011	N = 101 p= 0.0702	N = 108 p= 0.0801	N = 108					
age_class	N = 112 p= 0.9519	N = 63 p= 0.2855	N = 110 p= 0.0229	N = 110 p= 0.006	N = 105 p= 0.0124	N = 112						
prolif_class	N = 105 p= 0.907	N = 62 p= 0.062	N = 103 p= 0.1132	N = 103 p= 0.0945	N = 105							
spinaivo	N = 110 p= 1	N = 63 p= 0.1099	N = 109 p= 0	N = 110								
spicerbra	N = 110 p= 0.6729	N = 63 p= 0.0059	N = 110									
p53	N = 63 p= 0.7917	N = 63										
sex	N = 112											

Legend:
- p<.0001
- p<.001
- p<.01
- p<.05
- p>=.05

Supplementary Figure ⊂2. Association analyses in the ependymoma cohort including all the cases. p-values were calculated using Fisher's exact test. Cut-off points for patient age classes were 20, 40, 60, and 80 years. In FGFR1 and FGFR3 class, cases were separated into high (moderate or strong staining) and low (negative or weak staining) classes. Oper: primary or recurrent tumor, p53: p53 IHC staining, spicerbra: tumor location (spinal, cerebellum, cerebrum), spinaivo: tumor location (spinal, brain), prolif_class: proliferation index.
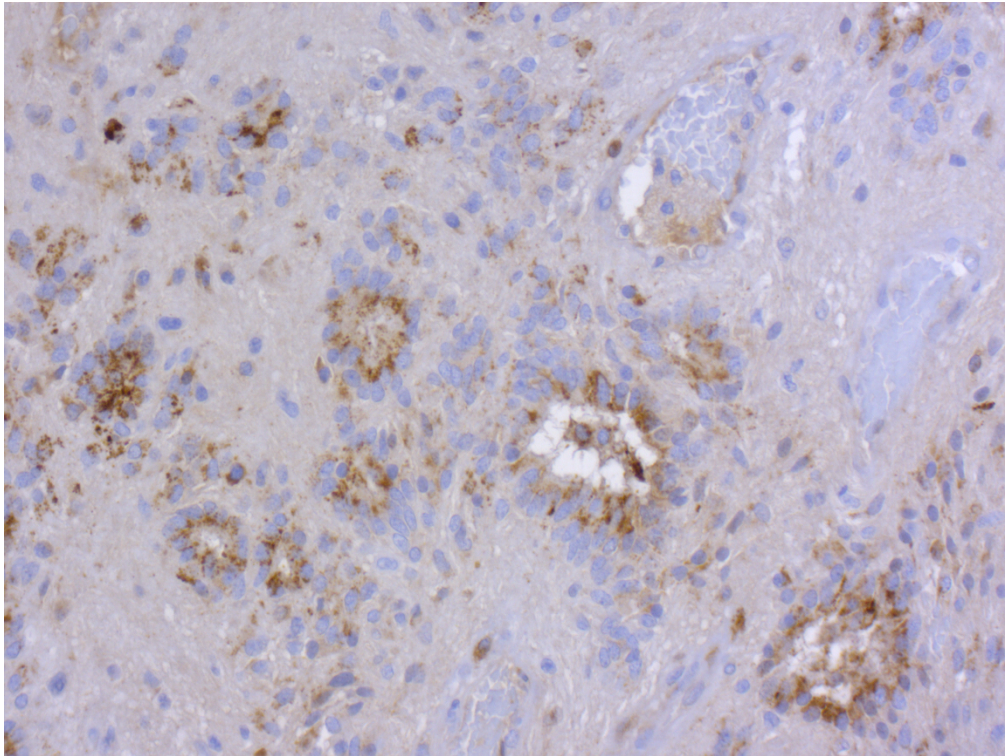
Supplementary Figure S3. Moderate-to-strong FGFR1 staining in ependymal rosettes.
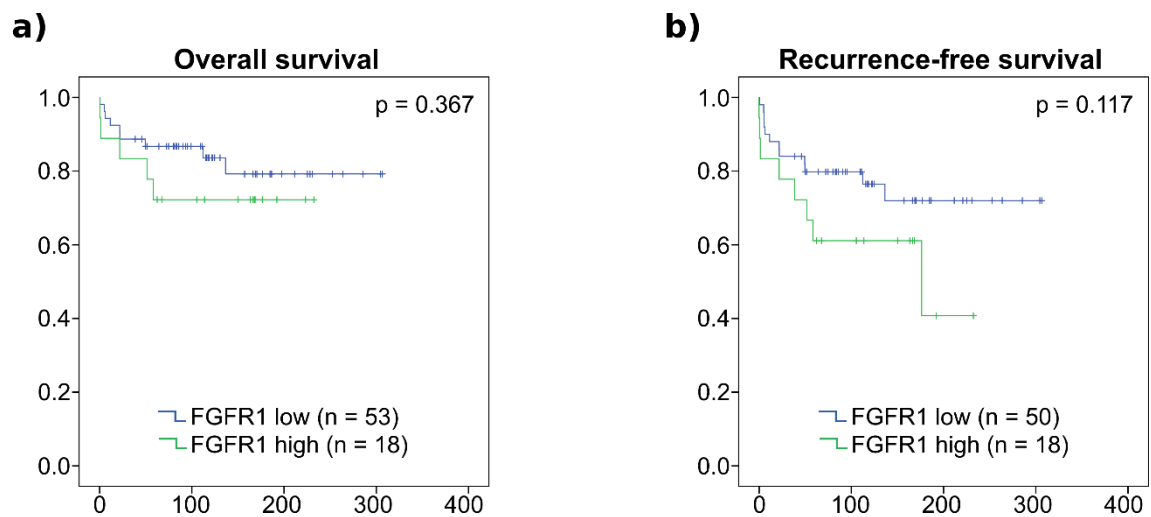

Supplementary Figure S4. Survival association analysis for FGFR1 staining in the ependymoma cohort was not statistically significant. a) Overall survival, b) Recurrence-free survival. Newly diagnosed cases were divided into two categories: low (negative-to-weak) or high (moderate-to-strong) FGFR1 staining.

	sex	p53	prolif_class	age_class	fgfr3_class	fgfr1_class	fgfr3	fgfr1	oper
oper	N = 115 p= 0.857	N = 77 p= 1	N = 115 p= 0.1887	N = 115 p= 1	N = 79 p= 0.3153	N = 96 p= 0.6959	N = 79 p= 0.2369	N = 96 p= 0.4382	N = 115
fgfr1	N = 96 p= 0.3006	N = 62 p= 0.1312	N = 96 p= 0.4459	N = 96 p= 0.2075	N = 74 p= 0.3375	N = 96 p= 0	N = 74 p= 0.6328	N = 96	
fgfr3	N = 79 p= 0.7323	N = 54 p= 1	N = 79 p= 0.6162	N = 79 p= 0.0104	N = 79 p= 0	N = 74 p= 0.7434	N = 79		
fgfr1_class	N = 96 p= 0.298	N = 62 p= 0.1414	N = 96 p= 0.5643	N = 96 p= 0.3211	N = 74 p= 0.5808	N = 96			
fgfr3_class	N = 79 p= 1	N = 54 p= 1	N = 79 p= 0.182	N = 79 p= 0.0026	N = 79				
age_class	N = 117 p= 0.7691	N = 77 p= 0.0906	N = 117 p= 0.085	N = 117					
prolif_class	N = 117 p= 0.6798	N = 77 p= 0.2294	N = 117						
p53	N = 77 p= 0.6831	N = 77							
sex	N = 117								

Legend:
- p<.0001
- p<.001
- p<.01
- p<.05
- p>=.05

Supplementary Figure S5. Association analyses in the pilocytic astrocytoma cohort including all the cases. p-values were calculated using Fisher's exact test. Cut-off points for patient age classes were 20, 40, 60, and 80 years. In FGFR1 and FGFR3 class, cases were separated into high (moderate or strong staining) and low (negative or weak staining) classes. Oper: primary or recurrent tumor, p53: p53 IHC staining, prolif_class: proliferation index.
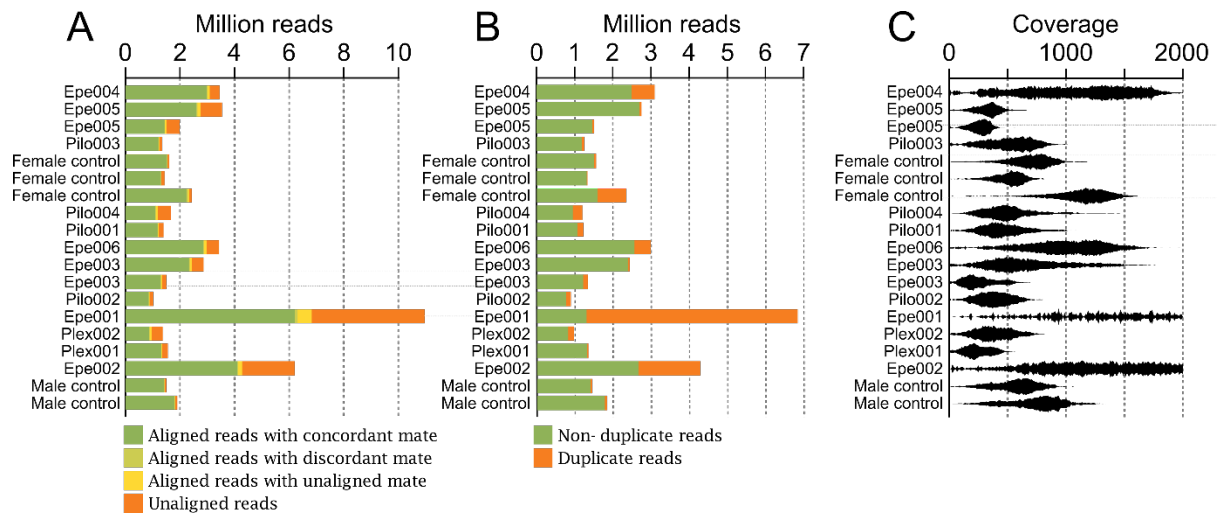
Supplementary Figure S6. Alignment and coverage statistics of the targeted sequencing cohort. (a) Total reads, grouped by alignment result. (b) Number of duplicate reads among all aligned reads. (c) Violin plot showing coverage distribution across all bases in target regions.