Supplementary Table 1. Clinical data of adult tumors (n=35).

Variable	WHO°II
Age	
Mean (years)	31
Range (years)	19-67
Gender	
female	14 (40%)
male	21 (60%)
Localization	
infratentorial (cerebellar)	6 (17%)
supratentorial (non-cerebellar)	29 (83%)
Level of resection	
complete	24 (69%)
subtotal	10 (29%)
Biopsy/partial	1 (3%)
Recurrence	
recurrence	9 (26%)
no recurrence	26 (74%)
Follow-up	
median (months)	76
Total	**35**

Supplementary Table 2. Minimally altered regions in low-grade astrocytomas.

Localization	Type of aberration	Count	Start Clone	End Clone	Size (Mb)	Candidate gene(s)
5p15.33-15.1	gain	6	RP1-61C2	RP11-21H5	15.3	TERT, CTNND2
5p13.3-p12	gain	6	RP11-113I22	RP11-28I9	12.5	SKP2, FBXO4
7p22	gain	7	CTB-164D18	RP11-745M18	2.42	PDGFA, EIF3B
7q11.22-q11.23	gain	5	RP11-358M3	RP4-562A11	9.89	BCL7B
7q34	gain	30	RP5-886O8	RP4-726N20	0.97	BRAF
11p15.5	gain	7	RP11-496I9	RP11-113A6	2.4	HRAS, IGF2
14q32.33	gain	4	RP11-73M18	RP11-521B24	1.85	AKT1
19p-p13.11	gain	4	CTD-2108L15	RP11-520G3	19.11	MAP2K2, VAV1

Supplementary Table 3. List of candidate genes on chromosome 7q34 (139186224-140156951).

Symbol	Gene Name	Unigene	Function
TBXAS1	THROMBOXANE A SYNTHASE 1	Hs.520757	hemostasis
PARP12	poly (ADP-ribose) polymerase family, member 12	Hs.602306	unknown
JHDM1D	jumonji C domain containing histone demethylase 1 homolog D	Hs.308710	shromatin reorganisation
SLC37A3	solute carrier family 37 (glycerol-3-phosphate transporter), member 3	Hs.446021	solute carrier
AK131347	FLJ16367		unknown
RAB19B	RAB19, member RAS oncogene family	Hs.583545	signal transduction
MKRN1	makorin, ring finger protein, 1	Hs.490347	transcriptional regulation
DENND2A	DENN/MADD domain containing 2A	Hs.6385	unknown
ADCK2	aarF domain containing kinase 2	Hs.534141	unknown
NDUFB2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2	Hs.655788	respiratory chain
AK098095	FLJ36704		unknown
BRAF	**v-raf murine sarcoma viral oncogene homolog B1**	**Hs.550061**	**proliferation, signal transduction**

Supplementary Table 4. Primer sequences for mutational analysis and genomic sequencing of *BRAF*.

BRAF	Forward Primer	Reverse Primer
Exon 6	*AAACAAGAGAGTAGATACGTCAGTTTC*	AAGTGTAAAATGGTAGGTAGAAAAGAG
Exon 11	*TTCTGTTTGGCTTGACTTGAC*	ACTTGTCACAATGTCACCAC
Exon 12	*AATTAGTGAAAACACCCAAGAATG*	AGTTGCTACCACTGGGAACC
Exon 14	*ACACCCCCAAGTATGTTCTG*	AAATGCAGAAGAAAAAGTCAGG
Exon 15	*CCTAAACTCTTCATAATGCTTGC*	GTAACTCAGCAGCATCTCAGG

Supplementary Table 5. Primer sequences for quantitative real-time PCR.

Gene	Forward Primer	*Reverse Primer*
BRAF	CTCGAGTGATGATTGGGAGATTCCTGATGG	CTGCTGAGGTGTAGGTGCTGTCAC
CCND1	AGCTGCTGCAAATGGAGC	TTCACATCTGTGGCACAG
DCTN2	CGCCATGGCGGACCCTAAAT	TTGTCAGCTCCTCCGCATCGAA
PGK1	AAGTGAAGCTCGGAAAGCTTCTAT	AGGGAAAAGATGCTTCTGGG