Supplementary Table 1. Tumor properties from asymptomatic adult Mut3 or Mut4 mice used for MRI

Genotype	ID	Age (weeks)[a]	Tumor volume[b]		Growth per week (%)	Grade	Ki67 density (%)[c]
			1st scan	2nd scan			
Mut3 (n = 3)	8495	26.7	0.051 (1/05)	0.060 (1/13)	15.44	3	21.9
	9042	25.3	0.027 (2/16)	0.029 (2/23)	7.41	3	12.1
	11714	22.7	0.045 (8/10)	0.065 (8/17)	44.44	3	31.4
	mean	24.9		0.051	22.43 ± 11.25[d]		21.8 ± 5.6[d]
	8625	21.6				Excluded; no tumor detection for 3 weeks	
	9044	27.3	0.002 (2/23)	0.0022 (3/2)	10.00	Excluded; too small tumor at 1st scanning[e]	
	11415	26.3				Excluded; no tumor detection for 2 weeks	
	11685	23.4				Excluded; no tumor detection for 2 weeks	
Mut4 (n = 6)	8985	17.9	0.014 (12/12)	0.031 (12/19)	121.43	3	47.5
	9505	13.1	0.023 (12/27)	0.042 (1/5)	42.03	3	30.3
	9660	14.1	0.031 (1/13)	0.058 (1/20)	87.10	3	37.4
	10590	17.1	0.041 (4/13)	0.073 (4/20)	78.05	3	35.7
	10594	14.1	0.012 (3/23)	0.021 (3/30)	75.00	3	39.6
	12130	18.0	0.029 (8/10)	0.085 (8/17)	193.10	3	67.8
	mean	15.7		0.052	99.45 ± 23.46[d]		43.1 ± 5.5[d]
	9075	16.3				Excluded; death during 1st scanning	
	9573	14.1	0.013 (1/5)			Excluded; death during 1st scanning	
	10448	11.4				Excluded; no tumor detection for 6 weeks	
	10592	17.1	0.006 (4/13)	0.032 (4/20)	433.33	Excluded; too small tumor at 1st scanning[e]	
	10589	14.1	0.032 (3/23)			Excluded; death before 2nd scanning	

[a] Age at the first scan

[b] Tumor volume in cm^3 (date of scanning)

[c] Ki67 density = the highest ratio of Ki67-positive cells / total cells (DAPI-positive) in a 0.44 X 0.35 mm^2 field

[d] Mean ± standard error mean

[e] Tumors with volume smaller than 0.01 cm^3 at the 1st scan were excluded to compare tumors at a similar stage and size.

Supplementary Table 2. Sequence of PCR primers used to measure LOH of Nf1 and Pten

PCR for	Name	Sequence	Product size (bp)
Nf1^{f}	g54	5'-AATGT GAAAT TGGTG TCGAG TAAGG TAACC AC-3'	*wt* : 493
	g35	5'-TTAAG AGCAT CTGCT GCTCT TAGAG GGAA-3'	*loxP* : ~600
	g53	5'-TCAGA CTGAT TGTTG TACCT GATGG TTGTA CC-3'	*ΔloxP*: ~300
Pten^{f}	F2	5'-CCATC ACACT AAGGT CTGTG G-3'	*wt* : 135
	R	5'-ACTCC CACCA ATGAA CAAAC-3'	*loxP* : 346
	hD1	5'-CCAGT AGTGA TAGAA CGGAA GTC-3'	*ΔloxP*: 410

Supplementary Table 3. Grade and location of malignant astrocytomas found in symptomatic Mut3, Mut4 or Mut6 mice

Genotype	ID	Age (weeks)	Grade	Location of tumor
Mut3	1512	27.0	3	Thalamus/pons/Mb
(n = 11)	2214	32.6	3	Most forebrain including SVZ
	2512	13.0	4	Most forebrain including SVZ
	2897	28.4	3	Most forebrain including SVZ
	2898	26.0	3	Thalamus/pons
	3853	31.0	3	St/SVZ/BS
	5780	44.0	4	St/RMS/OB
	6634	33.6	3	Cx, SVZ, BS
	6953	28.4	3	Most forebrain including SVZ
	8495	27.9	3	St/RMS
	14047	16.7	4	St/RMS/SVZ/Thalamus/Ht
Mut4	652	25.7	3	Pons/Cb
(n = 10)	749	16.7	4	Most forebrain including SVZ
	2244	13.1	3	CC/St
	2247	14.1	3	Cx/CC, thalamus
	2735	14.9	3	Most forebrain including SVZ
	2737	22.3	4	RMS/St/CC/SVZ, Hp, BS
	2901	28.4	3	Most brain, except Cb
	2909	17.4	3	Most forebrain including SVZ
	4025	17.3	3	OB
	5895	20.0	3	St/SVZ/thalamus
Mut5	4567	23.4	4	St, caudal CC, Cb
(n = 6)	11719	20.0	3	OB
	11724	22.7	3	St/SVZ
	11908	22.4	4	CC/SVZ/DG
	11995	26.6	4	St/SVZ/Thalamus
	12365	20.0	4	Thalamus/Ht
Mut6	5142	14.4	4	Caudal CC/Mb/Ht
(n = 8)	5239	14.1	4	CC/Cx, BS
	5245	12.9	4	Pons/Mb
	5586	14.3	4	Most forebrain including SVZ
	8214	18.3	4	St, Caudal CC/Mb/Cb
	8227	16.7	4	Most forebrain including SVZ
	10427	17.9	4	St/SVZ/thalamus
	10897	10.7	3	St, Cb

BS, brain stem; CC, corpus callosum; Cb, cerebellum; Cx, cerebral cortex; DG, dentate gyrus; Hp, hippocampus; Ht, hypothalamus; Mb, midbrain; OB, olfactory bulb; RMS, rostral migratory stream; St, striatum; SVZ, subventricular zone

Supplementary Table 4. BrdU signals detected in the vicinity of the SVZ/RMS of 7-week-old mice one week after labeling

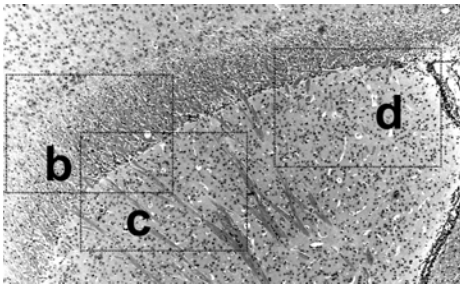
Genotype	Mouse ID	Number of BrdU-positive cells[a]		
		r. CC[b]	r. St[c]	c. St[d]
Control:	12572	27	3	4
$p53^{+/-}$	12574	26	6	7
(n = 6)	12578	10	6	4
	15357	32	5	6
	15360	9	5	5
	15512	21	4	4
	average	20.8 ± 9.5[e]	4.8 ± 1.2	5.0 ± 1.3
cre; $Pten^{f/+}$	9224	22	7	8
(n = 2)	15548	25	6	1
Mut3	15374	25	7	2
(n = 2)	15377	7	8	8
Mut4	15510	24	2	3
(n = 3)	**15511**[f]	**56**	**119**	**38**
	15546	16	6	6
Mut5	12573	32	8	6
(n = 3)	12575	11	8	7
	12579	24	9	8
Mut6	**9219**	**59**	9	**14**
(n = 3)	**9220**	**57**	**30**	9
	9221	37	**32**	**28**

[a] Anatomically matched sections were stained with BrdU antibody and subsequently visualized by Alexa-488-conjugated anti-mouse IgG antibody. BrdU-positive cells in below regions in a 0.87 X 0.69 mm^2 area were counted.

[b] Rostral corpus callosum

[c] Rostral striatum

[d] Caudal striatum



[e] Mean ± standard deviation

[f] Mouse IDs and abnormally increased BrdU counting (more than twice of average of control) were highlighted by a bold font.