



Supplemental Table S2. Frequency distribution of mutations by grade.

Gene	Total (N=101)		Grade III (N=16)		Grade IV (N=85)	
	N	%	N	%	N	%
<b>ABCC9</b>						
Wild-type	98	97.03	16	100	82	96.47
Mutated	3	2.97	0	0.0	3	3.53
<b>ARHGAP5</b>						
Wild-type	100	99.01	16	100	84	98.82
Mutated	1	0.99	0	0.0	1	1.18
<b>ATRX</b>						
Wild-type	95	94.06	15	93.75	80	94.12
Mutated	6	5.94	1	6.25	5	5.88
<b>BRAF</b>						
Wild-type	97	96.04	16	100	81	95.29
Mutated	4	3.96	0	0.0	4	4.71
<b>BRCA1</b>						
Wild-type	97	96.04	16	100	81	95.29
Mutated	4	3.96	0	0.0	4	4.71
<b>CDH18</b>						
Wild-type	100	99.01	16	100	84	98.82
Mutated	1	0.99	0	0.0	1	1.18
<b>CDK4</b>						
Wild-type	100	99.01	16	100	84	98.82
Mutated	1	0.99	0	0.0	1	1.18
<b>CDKN2C</b>						
Wild-type	100	99.01	16	100	84	98.82
Mutated	1	0.99	0	0.0	1	1.18
<b>CIC</b>						
Wild-type	99	98.02	16	100	83	97.65
Mutated	2	1.98	0	0.0	2	2.35
<b>COL1A2</b>						
Wild-type	100	99.01	16	100	84	98.82
Mutated	1	0.99	0	0.0	1	1.18
<b>CREBBP</b>						
Wild-type	99	98.02	16	100	83	97.65
Mutated	2	1.98	0	0.0	2	2.35
<b>CTNND2</b>						
Wild-type	98	97.03	16	100	82	96.47
Mutated	3	2.97	0	0.0	3	3.53
<b>DAXX</b>						
Wild-type	99	98.02	16	100	83	97.65
Mutated	2	1.98	0	0.0	2	2.35
<b>DNAH3</b>						
Wild-type	100	99.01	16	100	84	98.82
Mutated	1	0.99	0	0.0	1	1.18
<b>DSG3</b>						
Wild-type	100	99.01	16	100	84	98.82
Mutated	1	0.99	0	0.0	1	1.18
<b>EGFR</b>						
Wild-type	86	85.15	15	93.75	71	83.53
Mutated	15	14.85	1	6.25	14	16.47
<b>ERBB2</b>						
Wild-type	100	99.01	16	100	84	98.82
Mutated	1	0.99	0	0.0	1	1.18
<b>FGFR3</b>						
Wild-type	100	99.01	16	100	84	98.82
Mutated	1	0.99	0	0.0	1	1.18
<b>IDH1</b>						
Wild-type	88	87.13	6	37.50	82	96.47
Mutated	13	12.87	10	62.50	3	3.53
<b>IDH2</b>						
Wild-type	100	99.01	16	100	84	98.82
Mutated	1	0.99	0	0.0	1	1.18
<b>IDH1/2</b>						
Wild-type	87	86.10	6	37.50	81	95.29
Mutated	14	13.90	10	62.50	4	4.71
<b>KEL</b>						
Wild-type	97	96.04	16	100	81	95.29
Mutated	4	3.96	0	0.0	4	4.71
<b>LZTR1</b>						
Wild-type	97	96.04	16	100	81	95.29
Mutated	4	3.96	0	0.0	4	4.71
<b>MET</b>						
Wild-type	99	98.02	16	100	83	97.65
Mutated	2	1.98	0	0.0	2	2.35
<b>MIL3</b>						
Wild-type	100	99.01	16	100	84	98.82
Mutated	1	0.99	0	0.0	1	1.18
<b>MIL4</b>						
Wild-type	99	98.02	16	100	83	97.65
Mutated	2	1.98	0	0.0	2	2.35
<b>NF1</b>						
Wild-type	94	93.07	16	100	78	91.76
Mutated	7	6.93	0	0.0	7	8.24
<b>NOTCH1</b>						
Wild-type	98	97.03	16	100	82	96.47
Mutated	3	2.97	0	0.0	3	3.53
<b>NOTCH2</b>						
Wild-type	100	99.01	16	100	84	98.82
Mutated	1	0.99	0	0.0	1	1.18
<b>NOTCH4</b>						
Wild-type	99	98.02	16	100	83	97.65
Mutated	2	1.98	0	0.0	2	2.35
<b>PDGFRA</b>						
Wild-type	95	94.06	16	100	79	92.94
Mutated	6	5.94	0	0.0	6	7.06
<b>PHLDB1</b>						
Wild-type	100	99.01	16	100	84	98.82
Mutated	1	0.99	0	0.0	1	1.18
<b>PIK3CA</b>						
Wild-type	99	98.02	16	100	83	97.65
Mutated	2	1.98	0	0.0	2	2.35
<b>PTEN</b>						
Wild-type	95	94.06	16	100	79	92.94
Mutated	6	5.94	0	0.0	6	7.06
<b>RTEL1</b>						
Wild-type	100	99.01	15	93.75	85	100
Mutated	1	0.99	1	6.25	0	0.0
<b>SETD2</b>						
Wild-type	100	99.01	16	100	84	98.82
Mutated	1	0.99	0	0.0	1	1.18
<b>SPTA1</b>						
Wild-type	99	98.02	16	100	83	97.65
Mutated	2	1.98	0	0.0	2	2.35
<b>TP53</b>						
Wild-type	76	75.25	8	50.0	68	80.00
Mutated	25	24.75	8	50.0	17	20.00
<b>TERT</b>						
Mutated	75	74.26	9	56.25	66	77.65
Wild-type	26	25.74	7	43.75	19	22.35
<b>TERT/NF1</b>						
Both wild-type	25	24.75	7	43.75	18	21.18
Both mutated	6	5.94	0	0.0	6	7.06
TERT mutated/NF1 wild-type	69	68.32	9	56.25	60	70.59
TERT wild-type/NF1 mutated	1	0.99	0	0.0	1	1.18
<b>MGMT</b>						
Unknown	24	23.76	5	31.25	19	22.35
Unmethylated	22	21.78	1	6.25	21	24.71
Methylated	55	54.46	10	62.50	45	52.35

Supplemental Table S3. Results of the Cox univariate regression with respect to OS.

Parameter	Categories	N of patients	N of events	HR	95% CI	P-value
ATRX	Mutated vs. Wild-type	6 vs. 95	6 vs.81	1.54	0.67-3.54	0.313
EGFR	Mutated vs. Wild-type	15 vs. 86	14 vs.73	1.39	0.78-2.47	0.262
IDH1/2	Mutated vs. Wild-type	14 vs. 87	8 vs.79	0.24	0.11-0.52	<b>&lt;0.001</b>
NF1	Mutated vs. Wild-type	7 vs. 94	7 vs.80	3.19	1.44-7.06	<b>0.004</b>
PDGFRA	Mutated vs. Wild-type	6 vs. 95	6 vs.81	1.73	0.75-3.98	0.201
PTEN	Mutated vs. Wild-type	6 vs. 95	6 vs.81	1.37	0.60-3.16	0.455
TP53	Mutated vs. Wild-type	25 vs. 76	22 vs.65	0.88	0.54-1.44	0.619
TERT	Mutated vs. Wild-type	75 vs. 26	68 vs.19	2.28	1.36-3.83	<b>0.002</b>
MGMT	Methylated vs. Unmethylated	55 vs. 22	44 vs. 21	0.47	0.28-0.80	<b>0.006</b>
N mutations per tumor				1.02	0.99-1.05	0.213
N mutated genes per tumor				1.04	0.97-1.10	0.269
Age				1.05	1.03-1.07	<b>&lt;0.001</b>
Ki67				0.99	0.98-1.00	0.177

N, number; HR, hazard ratio; CI, confidence interval

Supplemental Table S4. Results of the Cox univariate regression with respect to OS in patients with wild-type IDH1/2 tumors.

Parameter	Categories	N of patients	N of events	HR	95% CI	P-value
EGFR	Mutated vs. Wild-type	14 vs. 73	13 vs.66	1.20	0.66-2.18	0.560
NF1	Mutated vs. Wild-type	7 vs. 80	7 vs.72	2.70	1.22-5.97	<b>0.014</b>
TP53	Mutated vs. Wild-type	16 vs. 71	16 vs.63	1.63	0.94-2.85	0.085
TERT	Mutated vs. Wild-type	68 vs. 19	63 vs. 16	1.99	1.14-3.47	<b>0.015</b>
MGMT	Methylated vs. Unmethylated	45 vs. 22	39 vs. 21	0.62	0.36-1.05	0.076
N mutations per tumor				1.04	1.01-1.07	<b>0.021</b>
N mutated genes per tumor				1.09	1.02-1.16	<b>0.009</b>
Age				1.05	1.02-1.07	<b>&lt;0.001</b>
Ki67				0.99	0.98-1.01	0.314

N, number; HR, hazard ratio; CI, confidence interval