Characteristic	IRR[1]	95% CI[1]	p-value
molecular_subtype			
LGG, wildtype	—	—	
GNG, KIAA1549-BRAF	0.14	0.08, 0.22	<0.001
GNG, wildtype	0.62	0.55, 0.70	<0.001
LGG_CDKN2A/B	0.10	0.05, 0.19	<0.001
LGG_IDH	0.17	0.11, 0.25	<0.001
LGG_NF1	0.17	0.11, 0.25	<0.001
LGG_RTK	0.62	0.55, 0.70	<0.001
LGG, BRAF V600E	0.59	0.51, 0.67	<0.001
LGG, KIAA1549-BRAF	0.69	0.61, 0.78	<0.001
LGG, MYB/MYBL1	0.10	0.05, 0.19	<0.001
LGG, other MAPK	0.28	0.21, 0.35	<0.001
SEGA, wildtype	0.34	0.28, 0.42	<0.001
cluster_assigned			
3	—	—	
1	0.28	0.21, 0.35	<0.001
2	1.48	1.37, 1.61	<0.001
molecular_subtype * cluster_assigned			
GNG, KIAA1549-BRAF * 1	1.81	0.51, 5.12	0.3
GNG, wildtype * 1	0.60	0.28, 1.17	0.2
LGG_CDKN2A/B * 1	14.5	7.44, 31.9	<0.001
LGG_IDH * 1	3.63	1.97, 6.70	<0.001
LGG_NF1 * 1	7.25	4.44, 12.3	<0.001
LGG_RTK * 1	4.23	3.18, 5.71	<0.001

[1] IRR = Incidence Rate Ratio, CI = Confidence Interval

Characteristic	IRR[1]	95% CI[1]	p-value
LGG, BRAF V600E * 1	5.33	4.02, 7.18	<0.001
LGG, KIAA1549-BRAF * 1	18.5	14.2, 24.5	<0.001
LGG, MYB/MYBL1 * 1			
LGG, other MAPK * 1	4.98	3.38, 7.45	<0.001
SEGA, wildtype * 1	2.18	1.37, 3.42	<0.001
GNG, KIAA1549-BRAF * 2	0.51	0.21, 1.13	0.10
GNG, wildtype * 2	0.11	0.05, 0.21	<0.001
LGG_CDKN2A/B * 2	0.90	0.40, 2.13	0.8
LGG_IDH * 2	0.13	0.01, 0.64	0.050
LGG_NF1 * 2	0.94	0.59, 1.56	0.8
LGG_RTK * 2	0.75	0.63, 0.89	<0.001
LGG, BRAF V600E * 2	0.71	0.60, 0.85	<0.001
LGG, KIAA1549-BRAF * 2	2.06	1.80, 2.35	<0.001
LGG, MYB/MYBL1 * 2	0.45	0.12, 1.38	0.2
LGG, other MAPK * 2	0.76	0.54, 1.07	0.11
SEGA, wildtype * 2			

[1] IRR = Incidence Rate Ratio, CI = Confidence Interval