| **Characteristic** | **No**, N = 37*1* | **Yes**, N = 40*1* | **p-value***2* |
| --- | --- | --- | --- |
| glioma\_progression\_overall |  |  | >0.9 |
| N | 4 (27%) | 7 (30%) |  |
| Y | 11 (73%) | 16 (70%) |  |
| Unknown | 22 | 17 |  |
| sex |  |  | 0.8 |
| F | 14 (38%) | 14 (35%) |  |
| M | 23 (62%) | 26 (65%) |  |
| age\_at\_surgery | 53 (42, 63) | 52 (44, 64) | >0.9 |
| race |  |  | >0.9 |
| American Indian/Alaska native | 0 (0%) | 1 (2.5%) |  |
| Asian | 2 (5.4%) | 3 (7.5%) |  |
| Black | 1 (2.7%) | 0 (0%) |  |
| Hispanic | 1 (2.7%) | 2 (5.0%) |  |
| Other | 1 (2.7%) | 1 (2.5%) |  |
| Unknown | 1 (2.7%) | 1 (2.5%) |  |
| White | 31 (84%) | 32 (80%) |  |
| steroids\_at\_surgery |  |  | 0.2 |
| N | 6 (29%) | 10 (36%) |  |
| Unknown | 6 (29%) | 2 (7.1%) |  |
| Y | 9 (43%) | 16 (57%) |  |
| Unknown | 16 | 12 |  |
| grade\_category |  |  | >0.9 |
| High | 28 (76%) | 30 (75%) |  |
| Low | 6 (16%) | 6 (15%) |  |
| Unknown | 3 (8.1%) | 4 (10%) |  |
| x16s\_seq\_batch |  |  | 0.11 |
| Batch 3 | 4 (11%) | 12 (30%) |  |
| Batch 4 | 17 (46%) | 16 (40%) |  |
| Batch 5 | 16 (43%) | 12 (30%) |  |
| glioma\_idh\_mutation |  |  | 0.4 |
| Mutant | 16 (43%) | 14 (35%) |  |
| Unknown | 1 (2.7%) | 0 (0%) |  |
| Wild | 20 (54%) | 26 (65%) |  |
| glioma\_fu\_time | 314 (145, 574) | 465 (220, 661) | 0.3 |
| Unknown | 21 | 14 |  |
| glioma\_recurrent\_status\_at\_surg |  |  | 0.6 |
| N | 20 (54%) | 19 (48%) |  |
| Y | 17 (46%) | 21 (53%) |  |
| *1*n (%); Median (IQR) | | | |
| *2*Fisher's exact test; Pearson's Chi-squared test; Wilcoxon rank sum test | | | |