**Table S1 The detailed clinical features of LGG patients in TCGA RNA-seq**

|  |  |  |  |
| --- | --- | --- | --- |
| **Covariates** | **Type** | **Total** | **Percentages(%)** |
| Age | <=41 | 260 | 51.69% |
|  | >41 | 243 | 48.31% |
| Gender | Female | 225 | 44.73% |
|  | Male | 278 | 55.27% |
| WHO Grade | II | 243 | 48.31% |
|  | III | 260 | 51.69% |
| Radio status | No | 187 | 37.18% |
|  | Unknown | 72 | 14.31% |
|  | Yes | 244 | 48.51% |
| Chemo status | No | 167 | 33.20% |
|  | Unknown | 66 | 13.12% |
|  | Yes | 270 | 53.68% |
| PRS type | Primary | 489 | 97.22% |
|  | Recurrent | 14 | 2.78% |
| IDH mutation status | No | 34 | 6.76% |
|  | Unknown | 378 | 75.15% |
|  | Yes | 91 | 18.09% |
| expression | High | 251 | 49.90% |
|  | Low | 252 | 50.10% |
| methylation | High | 251 | 49.90% |
|  | Low | 252 | 50.10% |

**Table S2 The detailed clinical features of LGG patients in CGGA microarray**

|  |  |  |  |
| --- | --- | --- | --- |
| **Covariates** | **Type** | **Total** | **Percentages(%)** |
| TCGA subtypes | Classical | 6 | 4.23% |
|  | Mesenchymal | 28 | 19.72% |
|  | Neural | 54 | 38.03% |
|  | Proneural | 54 | 38.03% |
| PRS type | Primary | 127 | 89.44% |
|  | Recurrent | 15 | 10.56% |
| WHO Grade | II | 92 | 64.79% |
|  | III | 50 | 35.21% |
| Gender | Female | 66 | 46.48% |
|  | Male | 76 | 53.52% |
| Age | <=41 | 83 | 58.45% |
|  | >41 | 59 | 41.55% |
| Radio status | No | 18 | 12.68% |
|  | Yes | 124 | 87.32% |
| Chemo status | No | 79 | 55.63% |
|  | Yes | 63 | 44.37% |
| IDH mutation | No | 48 | 33.80% |
|  | Yes | 94 | 66.20% |
| 1p19q codeletion | No | 31 | 21.83% |
|  | Unknown | 97 | 68.31% |
|  | Yes | 14 | 9.86% |
| MGMTp methylation | No | 102 | 71.83% |
|  | Yes | 40 | 28.17% |

**Table S3 The detailed clinical features of LGG patients in CGGA RNA-seq**

|  |  |  |  |
| --- | --- | --- | --- |
| **Covariates** | **Type** | **Total** | **Percentages(%)** |
| PRS type | Primary | 273 | 67.74% |
|  | Recurrent | 130 | 32.26% |
| WHO Grade | II | 177 | 43.92% |
|  | III | 226 | 56.08% |
| Gender | Female | 171 | 42.43% |
|  | Male | 232 | 57.57% |
| Age | <=41 | 222 | 55.09% |
|  | >41 | 181 | 44.91% |
| Radio status | No | 88 | 21.84% |
|  | Yes | 315 | 78.16% |
| Chemo status | No | 134 | 33.25% |
|  | Yes | 269 | 66.75% |
| IDH mutation | No | 100 | 24.81% |
|  | Yes | 303 | 75.19% |
| 1p19q codeletion | No | 280 | 69.48% |
|  | Yes | 123 | 30.52% |
| MGMTp methylation | No | 165 | 40.94% |
|  | Yes | 238 | 59.06% |

**TABLE S4 The gene set enriches the high CCNB1 in TGGA RNA-seq database**

|  |  |  |  |
| --- | --- | --- | --- |
| **NAME** | **NES** | **NOM p-val** | **FDR q-val** |
| KEGG\_CELL\_CYCLE | 2.3947036 | 0 | 0 |
| KEGG\_P53\_SIGNALING\_PATHWAY | 2.2375863 | 0 | 0.001899777 |
| KEGG\_MISMATCH\_REPAIR | 2.0368164 | 0.002053388 | 0.010246888 |
| KEGG\_NUCLEOTIDE\_EXCISION\_REPAIR | 2.034816 | 0 | 0.00893611 |
| KEGG\_HOMOLOGOUS\_RECOMBINATION | 2.024154 | 0 | 0.008971815 |
| KEGG\_DNA\_REPLICATION | 1.9405493 | 0.004132231 | 0.01320121 |
| KEGG\_BASE\_EXCISION\_REPAIR | 1.9381579 | 0.00209205 | 0.012919055 |
| KEGG\_NOTCH\_SIGNALING\_PATHWAY | 1.8296933 | 0.003952569 | 0.027004737 |

**Figure S1 The relationship between somatic copy number alterations for *CCNB1* and infiltration levels of immune cells**

Fig.S1