**Table S1. Clinical characteristics of GBM populations used in this study.**

|  |  |  |  |
| --- | --- | --- | --- |
| Type | Dataset | Clinical Feature | Cases(n) |
| Training set | TCGA\_GBM(Microarray) | Recurrence |  |  |
|  | Primary | 497 |
|  | Recurrent | 16 |
|  | Secondary | 7 |
|  | NA | 8 |
| Subtype |  |  |
|  | Classical | 198 |
|  | Mesechynal | 165 |
|  | Proneural | 162 |
|  |  |  |
| CIMP\_Status |  |  |
|  | G-CIMP | 46 |
|  | Non G-CIMP | 479 |
| IDH1\_Status |  |  |
|  | Wild | 372 |
|  | Mutant | 30 |
|  | NA | 126 |
| MGMT\_Status |  |  |
|  | Unmethylated | 177 |
|  | Methylated | 170 |
|  | NA | 181 |
| Age |  |  |
|  | >65 | 175 |
|  | ≤65 | 344 |
|  | NA | 9 |
| Gender |  |  |
|  | Male | 314 |
|  | Female | 203 |
|  | NA | 11 |
| Vital |  |  |
|  | Live  | 78 |
|  | Dead | 447 |
|  | NA | 3 |
| Validation set-1 | CGGA\_GBM(Bulk RNA-seq) | Recurrence |  |  |
|  | Primary | 133 |
|  | Recurrent | 104 |
| Subtype |  |  |
|  | Classical | 56 |
|  | Mesechynal | 53 |
|  | Proneural | 73 |
|  | NA | 55 |
| IDH1\_Status |  |  |
|  | Wild | 182 |
|  | Mutant | 45 |
|  | NA | 10 |
| MGMT\_Status |  |  |
|  | Unmethylated | 89 |
|  | Methylated | 104 |
| Age |  |  |
|  | >65 | 26 |
|  | ≤65 | 211 |
| Gender |  |  |
|  | Male | 139 |
|  | Female | 98 |
| Radio\_status |  |  |
|  | Non treated | 24 |
|  | Treated | 192 |
|  | NA | 21 |
| Chemo\_status |  |  |
|  | Non treated | 25 |
|  | Treated | 190 |
|  | NA | 22 |
| Vital |  |  |
|  | Live  | 46 |
|  | Dead | 191 |
| Validation set-2 | LeeY\_GBM(Microarray) | Subtype |  |  |
|  | Classical | 66 |
|  | Mesechynal | 56 |
|  | Proneural | 69 |
| Age |  |  |
|  | >65 | 41 |
|  | ≤65 | 150 |
| Gender |  |  |
|  | Male | 117 |
|  | Female | 74 |
| CIMP\_status |  |  |
|  | G-CIMP | 11 |
|  | Non G-CIMP | 180 |
| Vital |  |  |
|  | Live  | 15 |
|  | Dead | 176 |