### Supplementary Table 1. Association between the clinicopathologic characteristics and patients’ mortality in the CGGA dataset

| Variables          | Group     | Alive | Dead | P value | Non-relapse | Relapse | P value | Statistical method |
|--------------------|-----------|-------|------|---------|-------------|---------|---------|-------------------|
| Age                |           | 39.68 | 40.93| 0.21    | 39.98       | 40.51   | 0.59    | Student t test    |
| Gender             | Female    | 103   | 83   | 0.43    | 124         | 69      | 0.84    | Fisher’s exact test |
|                   | Male      | 123   | 116  |         | 158         | 93      |         |                   |
| Grade              | II        | 122   | 54   | <0.001  | 138         | 50      | <0.001  | Fisher’s exact test |
|                   | III       | 104   | 145  |         | 144         | 111     |         |                   |
| IDH1 mutation      | Wild-type | 34    | 60   | <0.001  | 66          | 30      | 0.15    | Fisher’s exact test |
|                   | Mutant    | 165   | 128  |         | 184         | 123     |         |                   |
| 1p19q codeletion   | Wild-type | 115   | 145  | <0.001  | 166         | 107     | 0.74    | Fisher’s exact test |
|                   | Mutant    | 91    | 36   |         | 83          | 49      |         |                   |
| Radiation therapy  | No        | 60    | 39   | 0.16    | 67          | 35      | 0.91    | Fisher’s exact test |
|                   | Yes       | 163   | 150  |         | 203         | 112     |         |                   |
| Chemotherapy       | No        | 75    | 56   | 0.4     | 95          | 37      | 0.02    | Fisher’s exact test |
|                   | Yes       | 148   | 135  |         | 172         | 113     |         |                   |
Supplementary Table 2. The associations of top ten genes with overall survival of LGG patients in the TCGA dataset

| Gene   | Chisq value | P value | Median | HR   | 2.50%CI | 97.50%CI | P value |
|--------|-------------|---------|--------|------|---------|----------|---------|
| SP1    | 16.39       | <0.001  | 1393.94| 4.99 | 2.66    | 9.35     | <0.001  |
| EYA3   | 19.24       | <0.001  | 72.98  | 5.73 | 2.86    | 11.47    | <0.001  |
| ZSCAN20| 15.26       | <0.001  | 59.06  | 4.77 | 2.45    | 9.29     | <0.001  |
| ITPRIPL1| 40.30      | <0.001  | 30.38  | 5.13 | 2.54    | 10.39    | <0.001  |
| ZNF217 | 31.05       | <0.001  | 227.98 | 4.58 | 2.38    | 8.84     | <0.001  |
| DISP2  | 16.07       | <0.001  | 426.04 | 0.25 | 0.14    | 0.45     | <0.001  |
| CKMT1B | 20.06       | <0.001  | 327.92 | 0.22 | 0.12    | 0.41     | <0.001  |
| AQP7   | 29.22       | <0.001  | 2.09   | 0.23 | 0.12    | 0.43     | <0.001  |
| GPR162 | 9.47        | <0.001  | 1873.33| 0.27 | 0.15    | 0.49     | <0.001  |
| CHGB   | 19.59       | <0.001  | 1871.33| 0.26 | 0.14    | 0.47     | <0.001  |

Supplementary Table 3. The associations of top ten genes with overall survival of LGG patients in the CGGA dataset

| Gene   | Chisq value | P value | Median | HR   | 2.50%CI | 97.50%CI | P value |
|--------|-------------|---------|--------|------|---------|----------|---------|
| SP1    | 14.96       | <0.001  | 4.97   | 1.67 | 1.21    | 2.29     | <0.001  |
| EYA3   | 40.81       | <0.001  | 2.63   | 1.97 | 1.35    | 2.88     | <0.001  |
| ZSCAN20| 22.08       | <0.001  | 0.51   | 1.88 | 1.37    | 2.59     | <0.001  |
| ITPRIPL1| 22.08      | <0.001  | 0.65   | 1.61 | 1.16    | 2.22     | <0.001  |
| ZNF217 | 17.31       | <0.001  | 1.34   | 1.75 | 1.26    | 2.42     | <0.001  |
| DISP2  | 19.83       | <0.001  | 8.32   | 0.48 | 0.35    | 0.67     | <0.001  |
| CKMT1B | 15.40       | <0.001  | 8.48   | 0.72 | 0.52    | 0.99     | 0.04    |
| AQP7   | 18.04       | <0.001  | 0.16   | 0.65 | 0.47    | 0.89     | 0.01    |
| GPR162 | 18.04       | <0.001  | 92.68  | 0.66 | 0.48    | 0.90     | 0.01    |
| CHGB   | 26.40       | <0.001  | 23.15  | 0.65 | 0.45    | 0.92     | 0.02    |
## Supplementary Table 4. GO terms of 183 survival-associated genes

| Gene            | Term ID               | Term name                                                                 | Adjusted p_value | Term size | Query size | Intersection size |
|-----------------|-----------------------|---------------------------------------------------------------------------|------------------|-----------|------------|-------------------|
| Risk gene       | GO:0000278            | mitotic cell cycle                                                        | <0.001           | 1083      | 959        | 154               |
| Risk gene       | GO:1903047            | mitotic cell cycle process                                               | <0.001           | 892       | 959        | 135               |
| Risk gene       | GO:0007049            | cell cycle                                                                | <0.001           | 1902      | 959        | 217               |
| Risk gene       | GO:0022402            | cell cycle process                                                        | <0.001           | 1403      | 959        | 176               |
| Risk gene       | GO:0044770            | cell cycle phase transition                                              | <0.001           | 642       | 959        | 99                |
| Risk gene       | GO:0051276            | chromosome organization                                                   | <0.001           | 1247      | 959        | 150               |
| Risk gene       | GO:0044772            | mitotic cell cycle phase transition                                       | <0.001           | 597       | 959        | 94                |
| Risk gene       | GO:0034645            | cellular macromolecule biosynthetic process                              | <0.001           | 4944      | 959        | 393               |
| Risk gene       | GO:0051301            | cell division                                                            | <0.001           | 613       | 959        | 93                |
| Risk gene       | GO:0044260            | cellular macromolecule metabolic process                                  | <0.001           | 8402      | 959        | 587               |
| Risk gene       | GO:0007059            | chromosome segregation                                                    | <0.001           | 328       | 959        | 64                |
| Risk gene       | GO:0009059            | macromolecule biosynthetic process                                        | <0.001           | 5118      | 959        | 401               |
| Risk gene       | GO:0043170            | macromolecule metabolic process                                           | <0.001           | 9774      | 959        | 654               |
| Risk gene       | GO:0051726            | regulation of cell cycle                                                  | <0.001           | 1264      | 959        | 144               |
| Risk gene       | GO:0006996            | organelle organization                                                    | <0.001           | 3988      | 959        | 328               |
| Risk gene       | GO:0090304            | nucleic acid metabolic process                                            | <0.001           | 5153      | 959        | 397               |
| Risk gene       | GO:0007346            | regulation of mitotic cell cycle                                          | <0.001           | 711       | 959        | 96                |
| Risk gene       | GO:0010564            | regulation of cell cycle process                                          | <0.001           | 792       | 959        | 102               |
| Risk gene       | GO:0031323            | regulation of cellular metabolic process                                  | <0.001           | 6386      | 959        | 461               |
| Risk gene       | GO:0019219            | regulation of nucleobase-containing compound metabolic process            | <0.001           | 4062      | 959        | 324               |
| Risk gene       | GO:0051171            | regulation of nitrogen compound metabolic process                         | <0.001           | 5997      | 959        | 437               |
| Risk gene       | GO:2000112            | regulation of cellular macromolecule biosynthetic process                 | <0.001           | 3970      | 959        | 317               |
| Risk gene       | GO:0006139            | nucleobase-containing compound metabolic process                          | <0.001           | 5684      | 959        | 418               |
| Risk gene       | GO:0000070            | mitotic sister chromatid segregation                                      | <0.001           | 157       | 959        | 38                |
| Risk gene       | GO:0140014            | mitotic nuclear division                                                  | <0.001           | 271       | 959        | 51                |
| Risk gene       | GO:0080090            | regulation of primary metabolic process                                   | <0.001           | 6180      | 959        | 445               |
| Risk gene       | GO:0051252            | regulation of RNA metabolic process                                       | <0.001           | 3795      | 959        | 303               |
| Risk gene       | GO:0032774            | RNA biosynthetic process                                                  | <0.001           | 3688      | 959        | 296               |
| Risk gene       | GO:0034654            | nucleobase-containing compound biosynthetic process                       | <0.001           | 4161      | 959        | 325               |
| Risk gene                                                                 | GO:0010556 | p-value | q-value | fold change |
|--------------------------------------------------------------------------|------------|---------|---------|-------------|
| regulation of macromolecule biosynthetic process                         | 0.001      | 4136    | 959     | 323         |
| Risk gene regulation of macromolecule metabolic process                   | 0.006      | 6649    | 959     | 469         |
| Risk gene regulation of transcription, DNA-templated                     | 0.006      | 3445    | 959     | 280         |
| Risk gene transcription, DNA-templated                                    | 0.006      | 3624    | 959     | 291         |
| Risk gene nucleic acid-templated transcription                            | 0.009      | 3674    | 959     | 294         |
| Risk gene cellular component organization                                 | 0.016      | 6374    | 959     | 453         |
| Risk gene nuclear chromosome segregation                                  | 0.009      | 267     | 959     | 49          |
| Risk gene nitrogen compound metabolic process                             | 0.006      | 10110   | 959     | 652         |
| Risk gene cellular component organization or biogenesis                   | 0.007      | 6559    | 959     | 462         |
| Risk gene regulation of nucleic acid-templated transcription              | 0.019      | 3520    | 959     | 283         |
| Risk gene heterocycle biosynthetic process                                | 0.001      | 4226    | 959     | 326         |
| Risk gene regulation of RNA biosynthetic process                          | 0.001      | 3525    | 959     | 283         |
| Risk gene sister chromatid segregation                                    | 0.000      | 189     | 959     | 40          |
| Risk gene primary metabolic process                                       | 0.004      | 10599   | 959     | 676         |
| Risk gene regulation of cell cycle phase transition                       | 0.019      | 485     | 959     | 69          |
| Risk gene biosynthetic process                                            | 0.009      | 6307    | 959     | 446         |
| Risk gene aromatic compound biosynthetic process                          | 0.001      | 4235    | 959     | 325         |
| Risk gene organic substance biosynthetic process                         | 0.019      | 6225    | 959     | 441         |
| Risk gene heterocycle metabolic process                                   | 0.004      | 5860    | 959     | 420         |
| Risk gene regulation of gene expression                                  | 0.001      | 5035    | 959     | 372         |
| Risk gene cellular biosynthetic process                                   | 0.004      | 6111    | 959     | 434         |
| Risk gene regulation of mitotic cell cycle phase transition               | 0.019      | 446     | 959     | 65          |
| Risk gene regulation of metabolic process                                | 0.001      | 7175    | 959     | 493         |
| Risk gene regulation of biosynthetic process                             | 0.009      | 4373    | 959     | 332         |
| Risk gene regulation of cellular biosynthetic process                    | 0.003      | 4289    | 959     | 326         |
| Risk gene DNA conformation change                                        | 0.007      | 357     | 959     | 56          |
| Risk gene cellular aromatic compound metabolic process                    | 0.006      | 5905    | 959     | 420         |
| Risk gene DNA replication                                                | 0.000      | 279     | 959     | 48          |
| Risk gene nuclear division                                                | 0.000      | 416     | 959     | 61          |
| Risk gene negative regulation of cell cycle                              | 0.004      | 636     | 959     | 80          |
| Risk gene cell cycle G1/S phase transition                               | 0.004      | 301     | 959     | 50          |
| Risk gene organic cyclic compound biosynthetic process                   | 0.019      | 4388    | 959     | 330         |
| Risk gene RNA metabolic process                                          | 0.001      | 4653    | 959     | 345         |
| Risk gene                                                                 | GO:            | p-value | N1 | N2 | p-value | N1 | N2 | p-value |
|-------------------------------------------------------------------------|----------------|---------|----|----|---------|----|----|---------|
| G1/S transition of mitotic cell cycle                                   | 0000082        | <0.001  | 277| 959| 47      | 277| 959| 47      |
| organelle fission                                                       | 0048285        | <0.001  | 464| 959| 64      | 464| 959| 64      |
| DNA-dependent DNA replication                                           | 0006261        | <0.001  | 156| 959| 33      | 156| 959| 33      |
| organic cyclic compound metabolic process                               | 1901360        | <0.001  | 6138| 959| 427     | 6138| 959| 427     |
| cellular nitrogen compound metabolic process                            | 0034641        | <0.001  | 6463| 959| 444     | 6463| 959| 444     |
| DNA metabolic process                                                   | 0006259        | <0.001  | 950 | 959| 101     | 950 | 959| 101     |
| cellular response to DNA damage stimulus                                | 006974         | <0.001  | 876 | 959| 95      | 876 | 959| 95      |
| gene expression                                                         | 0010467        | <0.001  | 5997| 959| 416     | 5997| 959| 416     |
| positive regulation of nucleobase-containing compound metabolic process | 0045935        | <0.001  | 1905| 959| 167     | 1905| 959| 167     |
| positive regulation of macromolecule biosynthetic process               | 0010557        | <0.001  | 1921| 959| 168     | 1921| 959| 168     |
| negative regulation of mitotic cell cycle                              | 0045930        | <0.001  | 340 | 959| 50      | 340 | 959| 50      |
| organic substance metabolic process                                     | 0071704        | <0.001  | 11268| 959| 695     | 11268| 959| 695     |
| negative regulation of cellular process                                | 0048523        | <0.001  | 5088| 959| 361     | 5088| 959| 361     |
| negative regulation of cell cycle process                              | 0010948        | <0.001  | 359 | 959| 51      | 359 | 959| 51      |
| positive regulation of transcription, DNA-templated                     | 0045893        | <0.001  | 1545| 959| 140     | 1545| 959| 140     |
| negative regulation of biological process                              | 0048519        | <0.001  | 5708| 959| 395     | 5708| 959| 395     |
| positive regulation of RNA metabolic process                            | 0051254        | <0.001  | 1739| 959| 153     | 1739| 959| 153     |
| mitotic cell cycle checkpoint                                           | 0007093        | <0.001  | 168 | 959| 32      | 168 | 959| 32      |
| regulation of chromosome segregation                                    | 0051983        | <0.001  | 107 | 959| 25      | 107 | 959| 25      |
| DNA repair                                                              | 0006281        | <0.001  | 567 | 959| 68      | 567 | 959| 68      |
| cell cycle DNA replication                                              | 0044786        | <0.001  | 63  | 959| 19      | 63  | 959| 19      |
| microtubule cytoskeleton organization                                  | 0000226        | <0.001  | 582 | 959| 69      | 582 | 959| 69      |
| regulation of cellular process                                          | 0050794        | <0.001  | 11382| 959| 697     | 11382| 959| 697     |
| cellular nitrogen compound biosynthetic process                         | 0044271        | <0.001  | 4945| 959| 350     | 4945| 959| 350     |
| cell cycle checkpoint                                                  | 0000075        | <0.001  | 219 | 959| 37      | 219 | 959| 37      |
| positive regulation of nucleic acid-templated transcription             | 1903508        | <0.001  | 1647| 959| 146     | 1647| 959| 146     |
| metabolic process                                                      | 0008152        | <0.001  | 11830| 959| 719     | 11830| 959| 719     |
| negative regulation of cell cycle phase transition                     | 1901988        | <0.001  | 271 | 959| 42      | 271 | 959| 42      |
| positive regulation of RNA biosynthetic process                        | 1902680        | <0.001  | 1648| 959| 146     | 1648| 959| 146     |
| negative regulation of mitotic cell cycle phase transition              | 1901991        | <0.001  | 252 | 959| 40      | 252 | 959| 40      |
| cellular metabolic process                                             | 0044237        | <0.001  | 10857| 959| 669     | 10857| 959| 669     |
| positive regulation of cellular biosynthetic process                   | 0031328        | <0.001  | 2020| 959| 169     | 2020| 959| 169     |
| DNA strand elongation                                                  | 0022616        | <0.001  | 25  | 959| 12      | 25  | 959| 12      |
| Risk gene                                                                 | GO:0009891       | <0.001 | 2054 | 959 | 171 |
|--------------------------------------------------------------------------|------------------|--------|------|-----|-----|
| Risk gene                                                                 | GO:0010717       | <0.001 | 784  | 959 | 83  |
| Risk gene                                                                 | GO:0010628       | <0.001 | 2326 | 959 | 188 |
| Risk gene regulation of mitotic sister chromatid separation              | GO:0010965       | <0.001 | 62   | 959 | 18  |
| Risk gene organelle localization                                         | GO:0051640       | <0.001 | 659  | 959 | 73  |
| Risk gene cell cycle G2/M phase transition                               | GO:0044839       | <0.001 | 276  | 959 | 41  |
| Risk gene chromosome separation                                          | GO:0051304       | <0.001 | 94   | 959 | 22  |
| Risk gene transcription by RNA polymerase II                             | GO:0006366       | <0.001 | 2314 | 959 | 186 |
| Risk gene cellular response to stress                                    | GO:0033554       | <0.001 | 2115 | 959 | 173 |
| Risk gene microtubule cytoskeleton organization involved in mitosis      | GO:1902850       | <0.001 | 139  | 959 | 27  |
| Risk gene biological regulation                                          | GO:0065007       | <0.001 | 12626| 959 | 753 |
| Risk gene                    mitotic sister chromatid separation            | GO:0051306       | <0.001 | 65   | 959 | 18  |
| Risk gene regulation of transcription by RNA polymerase II               | GO:0006357       | <0.001 | 2159 | 959 | 175 |
| Risk gene nuclear DNA replication                                        | GO:0033260       | <0.001 | 59   | 959 | 17  |
| Risk gene regulation of mitotic nuclear division                         | GO:0007088       | <0.001 | 170  | 959 | 30  |
| Risk gene regulation of chromosome separation                            | GO:1905818       | <0.001 | 67   | 959 | 18  |
| Risk gene metaphase/anaphase transition of mitotic cell cycle            | GO:0007091       | <0.001 | 60   | 959 | 17  |
| Risk gene positive regulation of macromolecule metabolic process         | GO:0010604       | <0.001 | 3620 | 959 | 264 |
| Risk gene G2/M transition of mitotic cell cycle                          | GO:0000086       | <0.001 | 258  | 959 | 38  |
| Risk gene regulation of biological process                               | GO:0050789       | <0.001 | 11969| 959 | 718 |
| Risk gene metaphase/anaphase transition of cell cycle                    | GO:0044784       | <0.001 | 62   | 959 | 17  |
| Risk gene establishment of chromosome localization                       | GO:0051303       | <0.001 | 79   | 959 | 19  |
| Risk gene chromosome localization                                        | GO:0050000       | <0.001 | 80   | 959 | 19  |
| Risk gene DNA packaging                                                  | GO:0006323       | <0.001 | 244  | 959 | 36  |
| Risk gene regulation of organelle organization                           | GO:0033043       | <0.001 | 1321 | 959 | 117 |
| Risk gene DNA geometric change                                           | GO:0032392       | <0.001 | 115  | 959 | 23  |
| Risk gene regulation of mitotic sister chromatid segregation             | GO:0033047       | <0.001 | 73   | 959 | 18  |
| Risk gene cellular localization                                         | GO:0051641       | <0.001 | 3497 | 959 | 254 |
| Risk gene DNA recombination                                              | GO:0006310       | <0.001 | 293  | 959 | 40  |
| Risk gene positive regulation of nitrogen compound metabolic process     | GO:0051173       | <0.001 | 3258 | 959 | 239 |
| Risk gene chordate embryonic development                                 | GO:0043009       | <0.001 | 656  | 959 | 69  |
| Risk gene embryo development                                             | GO:0009790       | <0.001 | 1060 | 959 | 98  |
| Risk gene double-strand break repair                                     | GO:0006302       | <0.001 | 263  | 959 | 37  |
| Gene Name                      | Description                                                                 | GO ID         | P-value | FDR  | FPKM | TPKM |
|-------------------------------|-----------------------------------------------------------------------------|---------------|---------|------|------|------|
| Risk gene                     | embryo development ending in birth or egg hatching                          | GO:0009792    | <0.001  | 674  | 959  | 70   |
| Risk gene                     | positive regulation of cell cycle process                                    | GO:0090068    | <0.001  | 298  | 959  | 40   |
| Risk gene                     | metaphase plate congression                                                  | GO:0051310    | <0.001  | 61   | 959  | 16   |
| Risk gene                     | DNA strand elongation involved in DNA replication                            | GO:006271     | <0.001  | 18   | 959  | 9    |
| Risk gene                     | regulation of nuclear division                                              | GO:0051783    | <0.001  | 194  | 959  | 30   |
| Risk gene                     | positive regulation of cell cycle                                           | GO:0045787    | <0.001  | 391  | 959  | 47   |
| Risk gene                     | centrosome cycle                                                            | GO:0007098    | <0.001  | 125  | 959  | 23   |
| Risk gene                     | positive regulation of metabolic process                                    | GO:009893     | <0.001  | 3911 | 959  | 275  |
| Risk gene                     | DNA duplex unwinding                                                        | GO:0032508    | <0.001  | 107  | 959  | 21   |
| Risk gene                     | chromatin organization                                                      | GO:0006325    | <0.001  | 815  | 959  | 79   |
| Risk gene                     | regulation of cell cycle G2/M phase transition                               | GO:1902749    | <0.001  | 218  | 959  | 32   |
| Risk gene                     | positive regulation of cellular metabolic process                           | GO:0031325    | <0.001  | 3428 | 959  | 246  |
| Risk gene                     | regulation of mitotic metaphase/anaphase transition                          | GO:0030071    | <0.001  | 58   | 959  | 15   |
| Risk gene                     | mitotic DNA replication                                                     | GO:1902969    | <0.001  | 15   | 959  | 8    |
| Risk gene                     | establishment of organelle localization                                      | GO:0051656    | <0.001  | 436  | 959  | 50   |
| Risk gene                     | mitotic spindle organization                                                 | GO:0007052    | <0.001  | 110  | 959  | 21   |
| Risk gene                     | regulation of cellular component organization                               | GO:0051128    | <0.001  | 2442 | 959  | 185  |
| Risk gene                     | viral process                                                               | GO:0016032    | <0.001  | 910  | 959  | 85   |
| Risk gene                     | double-strand break repair via homologous recombination                      | GO:0000724    | <0.001  | 139  | 959  | 24   |
| Risk gene                     | signal transduction by p53 class mediator                                    | GO:0072331    | <0.001  | 268  | 959  | 36   |
| Risk gene                     | negative regulation of cell cycle G1/S phase transition                      | GO:1902807    | <0.001  | 130  | 959  | 23   |
| Risk gene                     | recombinational repair                                                       | GO:0000725    | <0.001  | 140  | 959  | 24   |
| Risk gene                     | cytoskeleton organization                                                    | GO:0007010    | <0.001  | 1385 | 959  | 117  |
| Risk gene                     | regulation of metaphase/anaphase transition of cell cycle                    | GO:1902099    | <0.001  | 60   | 959  | 15   |
| Risk gene                     | regulation of sister chromatid segregation                                   | GO:0033045    | <0.001  | 85   | 959  | 18   |
| Risk gene                     | protein localization to chromosome                                          | GO:0034502    | <0.001  | 85   | 959  | 18   |
| Risk gene                     | positive regulation of transcription by RNA polymerase II                    | GO:0045944    | <0.001  | 1211 | 959  | 105  |
| Risk gene                     | mitotic metaphase plate congression                                          | GO:0007080    | <0.001  | 46   | 959  | 13   |
| Risk gene                     | small GTPase mediated signal transduction                                   | GO:0007264    | <0.001  | 561  | 959  | 59   |
| Risk gene                     | protein-DNA complex subunit organization                                     | GO:0071824    | <0.001  | 298  | 959  | 38   |
| Risk gene                     | negative regulation of G1/S transition of mitotic cell cycle                | GO:2000134    | <0.001  | 124  | 959  | 22   |
| Risk gene                     | microtubule organizing center organization                                  | GO:0031023    | <0.001  | 134  | 959  | 23   |
| Risk gene                     | anatomical structure morphogenesis                                          | GO:0009653    | <0.001  | 2827 | 959  | 207  |
| Risk gene | GO:0065004 | <0.001 | 254 | 959 | 34 |
|---|---|---|---|---|---|
| protein-DNA complex assembly | | | | | |
| Risk gene | GO:0008608 | <0.001 | 34 | 959 | 11 |
| attachment of spindle microtubules to kinetochore | | | | | |
| Risk gene | GO:0010389 | <0.001 | 201 | 959 | 29 |
| regulation of G2/M transition of mitotic cell cycle | | | | | |
| Risk gene | GO:001501 | <0.001 | 534 | 959 | 56 |
| skeletal system development | | | | | |
| Risk gene | GO:200045 | <0.001 | 180 | 959 | 27 |
| regulation of G1/S transition of mitotic cell cycle | | | | | |
| Risk gene | GO:1902806 | <0.001 | 202 | 959 | 29 |
| regulation of cell cycle G1/S phase transition | | | | | |
| Risk gene | GO:0022607 | <0.001 | 2952 | 959 | 213 |
| cellular component assembly | | | | | |
| Risk gene | GO:0031570 | <0.001 | 160 | 959 | 25 |
| DNA integrity checkpoint | | | | | |
| Risk gene | GO:0048522 | <0.001 | 5798 | 959 | 378 |
| positive regulation of cellular process | | | | | |
| Risk gene | GO:0051298 | <0.001 | 66 | 959 | 15 |
| centrosome duplication | | | | | |
| Risk gene | GO:0006950 | <0.001 | 4112 | 959 | 281 |
| response to stress | | | | | |
| Risk gene | GO:0006338 | <0.001 | 228 | 959 | 31 |
| DNA integrity checkpoint | | | | | |
| Risk gene | GO:006464 | <0.001 | 4216 | 959 | 287 |
| cellular protein modification process | | | | | |
| Risk gene | GO:0036211 | <0.001 | 4216 | 959 | 287 |
| protein modification process | | | | | |
| Risk gene | GO:0070925 | <0.001 | 863 | 959 | 79 |
| organelle assembly | | | | | |
| Risk gene | GO:0033044 | <0.01 | 362 | 959 | 42 |
| regulation of chromosome organization | | | | | |
| Risk gene | GO:0044085 | 0.01 | 3190 | 959 | 226 |
| cellular component biogenesis | | | | | |
| Risk gene | GO:0044403 | 0.01 | 968 | 959 | 86 |
| symbiotic process | | | | | |
| Risk gene | GO:002252 | 0.01 | 1281 | 959 | 107 |
| immune effector process | | | | | |
| Risk gene | GO:0033365 | 0.01 | 969 | 959 | 86 |
| protein localization to organelle | | | | | |
| Risk gene | GO:0002376 | 0.01 | 3199 | 959 | 226 |
| immune system process | | | | | |
| Risk gene | GO:0007050 | 0.01 | 235 | 959 | 31 |
| cell cycle arrest | | | | | |
| Risk gene | GO:0009888 | 0.01 | 2124 | 959 | 160 |
| tissue development | | | | | |
| Risk gene | GO:0071900 | 0.01 | 527 | 959 | 54 |
| regulation of protein serine/threonine kinase activity | | | | | |
| Risk gene | GO:0033046 | 0.01 | 46 | 959 | 12 |
| negative regulation of sister chromatid segregation | | | | | |
| Risk gene | GO:0000122 | 0.01 | 878 | 959 | 79 |
| negative regulation of transcription by RNA polymerase II | | | | | |
| Risk gene | GO:0009666 | 0.01 | 3232 | 959 | 227 |
| regulation of signal transduction | | | | | |
| Risk gene | GO:0043412 | 0.01 | 4429 | 959 | 297 |
| macromolecule modification | | | | | |
| Risk gene | GO:0044774 | 0.01 | 108 | 959 | 19 |
| mitotic DNA integrity checkpoint | | | | | |
| Risk gene | GO:2000736 | 0.01 | 118 | 959 | 20 |
| regulation of stem cell differentiation | | | | | |
| Risk gene | GO:0000077 | 0.01 | 149 | 959 | 23 |
| DNA damage checkpoint | | | | | |
| Risk gene | GO:0051321 | 0.01 | 251 | 959 | 32 |
| meiotic cell cycle | | | | | |
| Risk gene | GO:0051985 | 0.01 | 47 | 959 | 12 |
| negative regulation of chromosome segregation | | | | | |
| Risk gene | GO:0034508 | 0.01 | 55  | 959  | 13  |
| Risk gene | GO:0051716 | 0.01 | 7761| 959  | 482 |
| Risk gene | GO:0044773 | 0.01 | 100 | 959  | 18  |
| Risk gene | GO:0034728 | 0.01 | 184 | 959  | 26  |
| Risk gene | GO:0063344 | 0.01 | 141 | 959  | 22  |
| Risk gene | GO:0050790 | 0.01 | 2406| 959  | 176 |
| Risk gene | GO:0019882 | 0.02 | 231 | 959  | 30  |
| Risk gene | GO:0019882 | 0.02 | 3680| 959  | 252 |
| Risk gene | GO:0048598 | 0.02 | 197 | 959  | 27  |
| Risk gene | GO:0001701 | 0.02 | 27  | 959  | 9   |
| Risk gene | GO:0001701 | 0.02 | 393 | 959  | 43  |
| Risk gene | GO:2000816 | 0.02 | 41  | 959  | 11  |
| Risk gene | GO:0071459 | 0.02 | 21  | 959  | 8   |
| Risk gene | GO:0000727 | 0.02 | 11  | 959  | 6   |
| Risk gene | GO:0007051 | 0.02 | 177 | 959  | 25  |
| Risk gene | GO:0006333 | 0.02 | 233 | 959  | 29  |
| Risk gene | GO:1905819 | 0.02 | 42  | 959  | 11  |
| Risk gene | GO:0051253 | 0.02 | 1414| 959  | 113 |
| Risk gene | GO:0035556 | 0.02 | 2886| 959  | 204 |
| Risk gene | GO:2001236 | 0.02 | 156 | 959  | 23  |
| Risk gene | GO:0051383 | 0.03 | 22  | 959  | 8   |
| Risk gene | GO:1903046 | 0.03 | 192 | 959  | 26  |
| Risk gene | GO:1902041 | 0.03 | 60  | 959  | 13  |
| Risk gene | GO:0002446 | 0.03 | 497 | 959  | 50  |
| Risk gene | GO:0033048 | 0.03 | 44  | 959  | 11  |
| Risk gene | GO:0031324 | 0.04 | 2740| 959  | 194 |
| Risk gene | GO:0051649 | 0.04 | 2810| 959  | 198 |
| Risk gene | GO:0071897 | 0.04 | 195 | 959  | 26  |
| Risk gene | GO:0007094 | 0.04 | 37  | 959  | 10  |
| Risk gene | GO:0071173 | 0.04 | 37  | 959  | 10  |
| Risk gene | GO:0031577 | 0.04 | 37  | 959  | 10  |
| Gene Type  | Gene Function                                                                 | GO ID       | FDR   | Count | Total | Score |
|-----------|-------------------------------------------------------------------------------|-------------|-------|-------|-------|-------|
| Risk gene | negative regulation of macromolecule metabolic process                        | GO:0010605  | 0.04  | 3200  | 959   | 221   |
| Risk gene | extrinsic apoptotic signaling pathway via death domain receptors               | GO:0008625  | 0.04  | 89    | 959   | 16    |
| Risk gene | DNA replication-independent nucleosome assembly                                | GO:0006336  | 0.04  | 53    | 959   | 12    |
| Risk gene | regulation of cyclin-dependent protein serine/threonine kinase activity        | GO:000079   | 0.04  | 99    | 959   | 17    |
| Risk gene | negative regulation of cellular macromolecule biosynthetic process            | GO:2000113  | 0.04  | 1546  | 959   | 120   |
| Risk gene | negative regulation of transcription, DNA-templated                           | GO:0045892  | 0.05  | 1268  | 959   | 102   |
| Risk gene | regulation of response to stimulus                                            | GO:0048583  | 0.05  | 4359  | 959   | 288   |
| Risk gene | morphogenesis of an epithelium                                                | GO:0002009  | 0.05  | 560   | 959   | 54    |
| Risk gene | integrin-mediated signaling pathway                                           | GO:0007229  | 0.05  | 110   | 959   | 18    |
| Protective gene | anterograde trans-synaptic signaling                                     | GO:0098916  | <0.001 | 718   | 350   | 39    |
| Protective gene | chemical synaptic transmission                                              | GO:0007268  | <0.001 | 718   | 350   | 39    |
| Protective gene | trans-synaptic signaling                                                     | GO:0099537  | <0.001 | 727   | 350   | 39    |
| Protective gene | synaptic signaling                                                          | GO:0099536  | <0.001 | 746   | 350   | 39    |
| Protective gene | nervous system development                                                   | GO:0007399  | 0.01  | 2448  | 350   | 78    |
| Protective gene | regulation of postsynaptic membrane potential                                | GO:0060078  | 0.02  | 149   | 350   | 13    |
| Protective gene | vesicle-mediated transport in synapse                                         | GO:0099003  | 0.02  | 223   | 350   | 16    |
| Protective gene | signal release from synapse                                                    | GO:0099643  | 0.02  | 176   | 350   | 14    |
| Protective gene | neurotransmitter secretion                                                    | GO:0007269  | 0.02  | 176   | 350   | 14    |
| Protective gene | synaptic vesicle cycle                                                        | GO:0099504  | 0.02  | 202   | 350   | 15    |
| Protective gene | neurotransmitter transport                                                     | GO:0006836  | 0.03  | 231   | 350   | 16    |
### Supplementary Table 5. KEGG pathways of survival-associated genes

| Gene                     | Term ID             | Term name                                      | Adjusted P value | Term size | Query size | Intersection size |
|-------------------------|---------------------|-----------------------------------------------|------------------|-----------|------------|------------------|
| Protective gene         | Nicotine addiction  | KEGG:05033                                    | 0.01             | 40        | 143        | 6                |
| Protective gene         | Synaptic vesicle cycle | KEGG:04721                                 | 0.01             | 78        | 143        | 8                |
| Protective gene         | Neuroactive ligand-receptor interaction | KEGG:04080                              | 0.04             | 338       | 143        | 16               |
| Risk gene               | Cell cycle          | KEGG:04110                                    | <0.001           | 124       | 470        | 29               |
| Risk gene               | DNA replication     | KEGG:03030                                    | <0.001           | 36        | 470        | 12               |
| Risk gene               | Herpes simplex virus 1 infection | KEGG:05168                           | <0.001           | 487       | 470        | 55               |
| Risk gene               | Homologous recombination | KEGG:03440                             | <0.001           | 41        | 470        | 11               |

### Supplementary Table 6. Multivariate analyses between RFS and the risk score in the TCGA and CGGA cohorts

| Clinical feature | HR      | 95%CI     | P value | Clinical feature | HR      | 95%CI     | P value |
|------------------|---------|-----------|---------|------------------|---------|-----------|---------|
| IDH1             | 0.3     | 0.2-0.44  | <0.001  | Histologic grade | 2.96    | 1.98-4.42 | <0.001  |
| Risk score       | 1.86    | 1.3-2.67  | <0.001  | Chemotherapy     | 1.13    | 0.77-1.68 | 0.53    |
| Risk score       | 1.57    | 1.13-2.18 | <0.001  | Risk score       | 1.57    | 1.13-2.18 | <0.001  |

Notably, HR and CI refer to hazard ratio and confidence interval respectively.

### Supplementary Table 7. The associations of top ten genes with overall survival in the validation dataset

| Gene         | Chisq value | P value | Median | HR  | 2.50%CI | 97.50%CI | P value |
|--------------|-------------|---------|--------|-----|---------|---------|---------|
| DISP2        | 36.95       | <0.001  | 5.06   | 0.47| 0.29    | 0.75    | 0.002   |
| CKMT1B       | 29.64       | <0.001  | 7.02   | 0.53| 0.33    | 0.83    | 0.006   |
| AQP7         | 12.37       | <0.001  | 0.15   | 0.60| 0.39    | 0.92    | 0.02    |
| GPR162       | 9.60        | 0.002   | 41.12  | 0.71| 0.46    | 1.09    | 0.12    |
| CHGB         | 44.65       | <0.001  | 30.93  | 0.45| 0.27    | 0.76    | 0.003   |
| SP1          | 9.40        | 0.002   | 11.23  | 2.03| 1.32    | 3.14    | 0.001   |
| EYA3         | 48.56       | <0.001  | 4.37   | 2.00| 1.16    | 3.45    | 0.01    |
| ZSCAN20      | 20.09       | <0.001  | 1.05   | 1.43| 0.90    | 2.27    | 0.13    |
| ITPRIPL1     | 18.90       | <0.001  | 1.40   | 1.11| 0.70    | 1.77    | 0.65    |
| Clinical feature            | OS       | RFS     |
|----------------------------|----------|---------|
|                            | HR       | 95%CI   | P value | HR       | 95%CI   | P value |
| Histologic grade           | 3.27     | 2.06-5.18 | <0.001  | Histologic grade | 6.4     | 2.53-16.22 | <0.001  |
| IDH1                       | 0.91     | 0.57-1.44 | 0.67    | Chemotherapy   | 0.73    | 0.32-1.67 | 0.46    |
| 1p-19q codeletion           | 0.2      | 0.1-0.39  | <0.001  | Risk score     | 3.23    | 1.44-7.23 | 0.004   |
| Risk score                 | 1.64     | 1-2.67   | 0.047   |           |         |         |         |

Notably, HR and CI refer to hazard ratio and confidence interval respectively.