**Supplementary File 12. GO analysis for MG\_cluster0 top genes only (S≥2)**

|  |  |  |
| --- | --- | --- |
| **GO\_ID** | **GO\_Term** | **S** |
| [GO:0005622](http://amigo.geneontology.org/amigo/term/GO%3A0005622) | intracellular anatomical structure | 12 |
| [GO:0071356](http://amigo.geneontology.org/amigo/term/GO%3A0071356) | cellular response to tumor necrosis factor | 11 |
| [GO:0071347](http://amigo.geneontology.org/amigo/term/GO%3A0071347) | cellular response to interleukin-1 | 8 |
| [GO:0000977](http://amigo.geneontology.org/amigo/term/GO%3A0000977) | RNA polymerase II transcription regulatory region sequence-specific DNA binding | 8 |
| [GO:0043525](http://amigo.geneontology.org/amigo/term/GO%3A0043525) | positive regulation of neuron apoptotic process | 7 |
| [GO:0016607](http://amigo.geneontology.org/amigo/term/GO%3A0016607) | nuclear speck | 7 |
| [GO:0003713](http://amigo.geneontology.org/amigo/term/GO%3A0003713) | transcription coactivator activity | 6 |
| [GO:1900745](http://amigo.geneontology.org/amigo/term/GO%3A1900745) | positive regulation of p38MAPK cascade | 5 |
| [GO:1901653](http://amigo.geneontology.org/amigo/term/GO%3A1901653) | cellular response to peptide | 5 |
| [GO:0000785](http://amigo.geneontology.org/amigo/term/GO%3A0000785) | chromatin | 4 |
| [GO:0071837](http://amigo.geneontology.org/amigo/term/GO%3A0071837) | HMG box domain binding | 4 |
| [GO:0036464](http://amigo.geneontology.org/amigo/term/GO%3A0036464) | cytoplasmic ribonucleoprotein granule | 3 |
| [GO:0036488](http://amigo.geneontology.org/amigo/term/GO%3A0036488) | CHOP-C/EBP complex | 2 |
| [GO:1990617](http://amigo.geneontology.org/amigo/term/GO%3A1990617) | CHOP-ATF4 complex | 2 |
| [GO:1990037](http://amigo.geneontology.org/amigo/term/GO%3A1990037) | Lewy body core | 2 |
| [GO:0030014](http://amigo.geneontology.org/amigo/term/GO%3A0030014) | CCR4-NOT complex | 2 |
| [GO:0000307](http://amigo.geneontology.org/amigo/term/GO%3A0000307) | cyclin-dependent protein kinase holoenzyme complex | 2 |