**Table S4. Enriched GO categories.**

|  |  |  |
| --- | --- | --- |
| **GO ID** | **Name** | **P-value** |
| GO:0006415  | translational termination  | 5.45E-33  |
| GO:0016032  | **viral reproduction**  | 1.26E-30  |
| GO:0019058  | **viral infectious cycle**  | 1.43E-30  |
| GO:0022415  | **viral reproductive process**  | 2.85E-30  |
| GO:0006414  | translational elongation  | 2.98E-30  |
| GO:0034623  | cellular macromolecular complex disassembly  | 8.34E-30  |
| GO:0019083  | **viral transcription**  | 9.65E-30  |
| GO:0019080  | **viral genome expression**  | 9.65E-30  |
| GO:0032984  | macromolecular complex disassembly  | 2.01E-29  |
| GO:0031018  | endocrine pancreas development  | 7.36E-28  |
| GO:0071845  | cellular component disassembly at cellular level  | 1.56E-27  |
| GO:0022411  | cellular component disassembly  | 2.92E-27  |
| GO:0043624  | cellular protein complex disassembly  | 5.63E-27  |
| GO:0043241  | protein complex disassembly  | 1.35E-26  |
| GO:0006412  | translation  | 2.06E-26  |
| GO:0031016  | pancreas development  | 4.57E-25  |
| GO:0034621  | cellular macromolecular complex subunit organization  | 2.81E-21  |
| GO:0035270  | endocrine system development  | 3.43E-21  |
| GO:0048610  | cellular process involved in reproduction  | 1.10E-18  |
| GO:0071822  | protein complex subunit organization  | 5.58E-16  |
| GO:0043933  | macromolecular complex subunit organization  | 1.50E-15  |
| GO:0022414  | reproductive process  | 3.49E-08  |
| GO:0000003  | reproduction  | 4.03E-08  |
| GO:0006396  | RNA processing  | 3.82E-07  |
| GO:0016071  | mRNA metabolic process  | 5.80E-05  |
| GO:0007093  | mitotic cell cycle checkpoint  | 1.44E-03  |
| GO:0008380  | RNA splicing  | 2.34E-03  |
| GO:0042274  | ribosomal small subunit biogenesis  | 2.93E-03  |
| GO:0012501  | programmed cell death  | 7.88E-03  |
| GO:0006364  | rRNA processing  | 1.01E-02  |
| GO:0006260  | DNA replication  | 1.14E-02  |
| GO:0002576  | platelet degranulation  | 1.25E-02  |
| GO:0016072  | rRNA metabolic process  | 1.39E-02  |
| GO:0031575  | mitotic cell cycle G1/S transition checkpoint  | 1.50E-02  |
| GO:0071779  | G1/S transition checkpoint  | 1.50E-02  |
| GO:0006090  | pyruvate metabolic process  | 1.50E-02  |
| GO:0046034  | ATP metabolic process  | 1.82E-02  |
| GO:2000045  | regulation of G1/S transition of mitotic cell cycle  | 1.97E-02  |
| GO:0042273  | ribosomal large subunit biogenesis  | 2.02E-02  |
| GO:0072431  | signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint  | 2.14E-02  |
| GO:0072395  | signal transduction involved in cell cycle checkpoint  | 2.14E-02  |
| GO:0072413  | signal transduction involved in mitotic cell cycle checkpoint  | 2.14E-02  |
| GO:0072404  | signal transduction involved in G1/S transition checkpoint  | 2.14E-02  |
| GO:0072474  | signal transduction involved in mitotic cell cycle G1/S checkpoint  | 2.14E-02  |
| GO:0006977  | DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest  | 2.14E-02  |
| GO:0072422  | signal transduction involved in DNA damage checkpoint  | 2.14E-02  |
| GO:0072401  | signal transduction involved in DNA integrity checkpoint  | 2.14E-02  |
| GO:0006096  | glycolysis  | 2.38E-02  |
| GO:0000075  | cell cycle checkpoint  | 3.43E-02  |
| GO:0071158  | positive regulation of cell cycle arrest  | 3.59E-02  |
| GO:0006457  | protein folding  | 3.59E-02  |
| GO:0006915  | apoptosis  | 3.77E-02  |
| GO:0006397  | mRNA processing  | 4.25E-02  |
| GO:0031571  | mitotic cell cycle G1/S transition DNA damage checkpoint  | 4.79E-02  |