

**Table S5. Enrichment analysis based on differentially expressed miRNAs at intermediate time post HHV-6 infection (7 d.p.i.)**

| <b>Pathways</b>                                 | <b><i>p</i> val</b> | <b>adj <i>p</i> val</b> |
|---|---------------------|-------------------------|
| Gene Expression                                 | 1.08E-27            | 1.08E-25                |
| Metabolism of proteins                          | 1.18E-13            | 5.9E-12                 |
| Cell Cycle, Mitotic                             | 1.03E-12            | 3.43E-11                |
| Organelle biogenesis and maintenance            | 5.16E-12            | 1.29E-10                |
| Infectious disease                              | 2.36E-11            | 4.72E-10                |
| Cell Cycle                                      | 4.32E-11            | 6.56E-10                |
| Metabolism                                      | 4.59E-11            | 6.56E-10                |
| DNA Repair                                      | 2.52E-10            | 3.15E-09                |
| HIV Life Cycle                                  | 5.56E-10            | 6.18E-09                |
| HIV Infection                                   | 8.29E-10            | 8.29E-09                |
| Developmental Biology                           | 9.64E-10            | 8.76E-09                |
| Late Phase of HIV Life Cycle                    | 2.71E-09            | 2.26E-08                |
| Membrane Trafficking                            | 2.97E-09            | 2.28E-08                |
| Vesicle-mediated transport                      | 1.26E-08            | 9E-08                   |
| Disease   | 3.15E-08            | 2.1E-07                 |
| Generic Transcription Pathway                   | 4.19E-08            | 2.62E-07                |
| Transcription                                   | 6.24E-08            | 3.67E-07                |
| Post-translational protein modification         | 1.21E-07            | 6.72E-07                |
| Assembly of the primary cilium                  | 2.21E-07            | 1.16E-06                |
| Translation                                     | 3.32E-07            | 1.66E-06                |
| Mitotic G2-G2/M phases                          | 5.78E-07            | 2.75E-06                |
| Mitotic G1-G1/S phases                          | 6.87E-07            | 3.12E-06                |
| Axon guidance                                   | 7.43E-07            | 3.16E-06                |
| G2/M Transition                                 | 7.79E-07            | 3.16E-06                |
| Mitochondrial translation                       | 7.91E-07            | 3.16E-06                |
| Cell Cycle Checkpoints                          | 1.05E-06            | 4.04E-06                |
| Mitotic Metaphase and Anaphase                  | 1.43E-06            | 5.3E-06                 |
| Mitotic Anaphase                                | 1.63E-06            | 5.82E-06                |
| Processing of Capped Intron-Containing Pre-mRNA | 1.86E-06            | 6.34E-06                |
| Mitochondrial translation initiation            | 2.03E-06            | 6.34E-06                |
| Mitochondrial translation elongation            | 2.03E-06            | 6.34E-06                |
| Mitochondrial translation termination           | 2.03E-06            | 6.34E-06                |
| S Phase   | 2.46E-06            | 7.45E-06                |
| mRNA Splicing - Major Pathway                   | 3.27E-06            | 9.34E-06                |
| mRNA Splicing                                   | 3.27E-06            | 9.34E-06                |
| Programmed Cell Death                           | 3.97E-06            | 1.1E-05                 |
| Beta-catenin independent WNT signaling          | 4.33E-06            | 1.16E-05                |
| SUMOylation                                     | 4.46E-06            | 1.16E-05                |
| Separation of Sister Chromatids                 | 4.51E-06            | 1.16E-05                |
| MyD88-independent TLR3/TLR4 cascade             | 5.21E-06            | 1.27E-05                |

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| Toll Like Receptor 3 (TLR3) Cascade                               | 5.21E-06 | 1.27E-05 |
| Apoptosis   | 5.8E-06  | 1.38E-05 |
| TRIF-mediated TLR3/TLR4 signaling                                 | 6.1E-06  | 1.42E-05 |
| Respiratory electron transport                                    | 7.13E-06 | 1.62E-05 |
| Activated TLR4 signalling   | 8.31E-06 | 1.85E-05 |
| RNA Polymerase II Transcription                                   | 8.73E-06 | 1.86E-05 |
| Influenza Infection   | 8.74E-06 | 1.86E-05 |
| SUMOylation of DNA damage response and repair proteins            | 9.76E-06 | 1.99E-05 |
| SUMO E3 ligases SUMOylate target proteins                         | 9.76E-06 | 1.99E-05 |
| M Phase   | 0.000011 | 0.000022 |
| Signaling by TGF-beta Receptor Complex                            | 1.34E-05 | 2.63E-05 |
| Signalling by NGF   | 1.42E-05 | 2.73E-05 |
| Influenza Life Cycle  | 0.000017 | 3.15E-05 |
| Asparagine N-linked glycosylation                                 | 0.000017 | 3.15E-05 |
| G1/S Transition   | 1.75E-05 | 3.18E-05 |
| Eukaryotic Translation Initiation                                 | 1.95E-05 | 3.42E-05 |
| Cap-dependent Translation Initiation                              | 1.95E-05 | 3.42E-05 |
| DNA Replication   | 2.66E-05 | 4.59E-05 |
| Cellular responses to stress                                      | 2.83E-05 | 4.63E-05 |
| Influenza Viral RNA Transcription and Replication                 | 2.89E-05 | 4.63E-05 |
| Toll Like Receptor 10 (TLR10) Cascade                             | 2.92E-05 | 4.63E-05 |
| Toll Like Receptor 5 (TLR5) Cascade                               | 2.92E-05 | 4.63E-05 |
| MyD88 cascade initiated on plasma membrane                        | 2.92E-05 | 4.63E-05 |
| CLEC7A (Dectin-1) signaling                                       | 3.05E-05 | 4.77E-05 |
| Signaling by Wnt  | 3.13E-05 | 4.82E-05 |
| ISG15 antiviral mechanism   | 3.42E-05 | 5.03E-05 |
| Antiviral mechanism by IFN-stimulated genes                       | 3.42E-05 | 5.03E-05 |
| Transcription of the HIV genome                                   | 3.42E-05 | 5.03E-05 |
| Fatty acid, triacylglycerol, and ketone body metabolism           | 4.14E-05 | 5.91E-05 |
| C-type lectin receptors (CLRs)                                    | 4.14E-05 | 5.91E-05 |
| Toll Like Receptor 4 (TLR4) Cascade                               | 4.61E-05 | 6.49E-05 |
| RNA Polymerase II Pre-transcription Events                        | 4.68E-05 | 0.000065 |
| Regulation of PLK1 Activity at G2/M Transition                    | 4.81E-05 | 6.53E-05 |
| SRP-dependent cotranslational protein targeting to membrane       | 0.000049 | 6.53E-05 |
| GTP hydrolysis and joining of the 60S ribosomal subunit           | 0.000049 | 6.53E-05 |
| Synthesis of DNA  | 5.29E-05 | 6.96E-05 |
| L13a-mediated translational silencing of Ceruloplasmin expression | 5.59E-05 | 7.17E-05 |
| 3' -UTR-mediated translational regulation                         | 5.59E-05 | 7.17E-05 |
| Signaling by Interleukins   | 6.36E-05 | 8.05E-05 |
| Cyclin E associated events during G1/S transition                 | 7.48E-05 | 9.35E-05 |
| VEGFA-VEGFR2 Pathway  | 7.97E-05 | 9.84E-05 |
| Autodegradation of Cdh1 by Cdh1:APC/C                             | 8.75E-05 | 0.000107 |
| Cyclin A:Cdk2-associated events at S phase entry                  | 0.000102 | 0.000123 |

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| Anchoring of the basal body to the plasma membrane                  | 0.00012  | 0.000143 |
| Host Interactions of HIV factors                                    | 0.000125 | 0.000147 |
| MyD88:Mal cascade initiated on plasma membrane                      | 0.000132 | 0.000148 |
| Toll Like Receptor TLR1:TLR2 Cascade                                | 0.000132 | 0.000148 |
| Toll Like Receptor TLR6:TLR2 Cascade                                | 0.000132 | 0.000148 |
| Toll Like Receptor 2 (TLR2) Cascade                                 | 0.000132 | 0.000148 |
| Transcriptional regulation of white adipocyte differentiation       | 0.00014  | 0.000156 |
| NGF signalling via TRKA from the plasma membrane                    | 0.000149 | 0.000162 |
| Platelet activation, signaling and aggregation                      | 0.000149 | 0.000162 |
| Signaling by EGFR   | 0.000154 | 0.000165 |
| Regulation of mRNA stability by proteins that bind AU-rich elements | 0.000157 | 0.000165 |
| Signaling by VEGF   | 0.000158 | 0.000165 |
| Mitotic Prometaphase  | 0.000158 | 0.000165 |
| TRAF6 Mediated Induction of proinflammatory cytokines               | 0.000164 | 0.000169 |
| Cellular response to heat stress                                    | 0.000177 | 0.000181 |
| Signaling by NOTCH  | 0.00018  | 0.000182 |
| Toll-Like Receptors Cascades  | 0.000185 | 0.000185 |