**Table S6. PBMC transcriptome sequencing data before and after quality control.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Sample** | **Total Raw Reads (Mb)** | **Total Clean Reads (Mb)** | **Total Clean Bases (Gb)** | **Clean Reads Ratio (%)** | **Total Mapping Ratio (%)** | **Uniquely Mapping Ratio (%)** |
| M1\_P-3 | 47.85 | 46.53 | 2.33 | 97.24 | 68.28% | 57.46% |
| M1\_H+25 | 45.41 | 44.09 | 2.2 | 97.1 | 68.70% | 58.24% |
| M1\_H+40 | 44.47 | 43.19 | 2.16 | 97.13 | 68.58% | 57.19% |
| M1\_R+12 | 45.85 | 44.57 | 2.23 | 97.21 | 68.58% | 57.89% |
| M1\_R+24 | 51.14 | 49.66 | 2.48 | 97.11 | 67.12% | 56.21% |
| M1\_R+32 | 38.16 | 37.04 | 1.85 | 97.07 | 67.11% | 55.77% |
| M2\_ P-3 | 35.97 | 34.88 | 1.74 | 96.98 | 66.29% | 54.62% |
| M2\_H+25 | 37.86 | 36.67 | 1.83 | 96.85 | 68.67% | 57.89% |
| M2\_H+40 | 34.62 | 33.6 | 1.68 | 97.05 | 68.14% | 56.31% |
| M2\_R+12 | 39.37 | 38.28 | 1.91 | 97.22 | 69.25% | 54.36% |
| M2\_R+24 | 40.95 | 39.77 | 1.99 | 97.12 | 70.53% | 58.94% |
| M2\_R+32 | 40.51 | 39.27 | 1.96 | 96.95 | 64.59% | 51.65% |
| M3\_H+25 | 20.29 | 18.53 | 0.93 | 91.31 | 69.90% | 59.15% |
| M3\_H+40 | 10.54 | 9.61 | 0.48 | 91.23 | 64.84% | 51.30% |
| M3\_R+24 | 22.35 | 20.43 | 1.02 | 91.39 | 69.94% | 58.91% |
| M3\_R+32 | 20.54 | 18.71 | 0.94 | 91.11 | 68.11% | 56.62% |
| M4\_H+25 | 17.85 | 16.17 | 0.81 | 90.63 | 69.41% | 58.59% |
| M4\_R+12 | 17.14 | 15.7 | 0.78 | 91.58 | 67.69% | 52.26% |
| M4\_R+24 | 20.17 | 18.38 | 0.92 | 91.11 | 68.16% | 57.36% |
| M4\_R+32 | 24.02 | 21.94 | 1.1 | 91.33 | 67.99% | 56.41% |
| M5\_P-3 | 17 | 15.58 | 0.78 | 91.64 | 67.03% | 54.35% |
| M5\_H+25 | 19.94 | 18.17 | 0.91 | 91.15 | 69.98% | 59.06% |
| M5\_R+12 | 29.58 | 28.53 | 1.43 | 96.44 | 62.58% | 51.88% |
| M5\_R+24 | 31.76 | 30.65 | 1.53 | 96.49 | 66.06% | 56.16% |
| M5\_R+32 | 25.75 | 24.83 | 1.24 | 96.43 | 62.01% | 52.32% |