Supplementary Table 2. Summary of RNA sequencing data information.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Samples** | **Raw reads** | **Clean reads** | **Total genes**  | **Clean read****ratio（%）**  | **Mapped read****ratio （%）** | **Sequenced total genes ratio （%）** |
| tFam1-25-1 | 62589368 | 62420842 | 31753 | 99.73 | 87.26 | 78.57 |
| tFam1-25-2 | 65509400 | 65301248 | 31753 | 99.68 | 88.13 | 66.94 |
| tFam1-25-3 | 68630824 | 68465228 | 31753 | 99.76 | 88.65 | 67.12 |
| tFam2-25-1 | 86571910 | 86354030 | 31753 | 99.75 | 88.14 | 63.41 |
| tFam2-25-2 | 78793712 | 78595476 | 31753 | 99.75 | 88.31 | 65.12 |
| tFam2-25-3 | 79927770 | 79728304 | 31753 | 99.75 | 87.69 | 64.79 |
| sFam1-25-1 | 70313600 | 70117662 | 31753 | 99.72 | 88.08 | 64.52 |
| sFam1-25-2 | 66122446 | 65916006 | 31753 | 99.69 | 88.45 | 66.45 |
| sFam1-25-3 | 53571956 | 53435304 | 31753 | 99.74 | 88.33 | 64.08 |
| sFam2-25-1 | 39071304 | 39013200 | 31753 | 99.85 | 89.70 | 63.98 |
| sFam2-25-2 | 49121972 | 49033582 | 31753 | 99.82 | 88.95 | 62.27 |
| sFam2-25-3 | 47542398 | 47438786 | 31753 | 99.78 | 89.28 | 61.51 |
| tFam1-45-1 | 75580572 | 75399414 | 31753 | 99.76 | 85.82 | 63.87 |
| tFam1-45-2 | 65397450 | 65271578 | 31753 | 99.81 | 87.73 | 66.81 |
| tFam1-45-3 | 68343862 | 68152966 | 31753 | 99.72 | 86.46 | 66.56 |
| tFam2-45-1 | 72511540 | 72360002 | 31753 | 99.79 | 88.11 | 64.26 |
| tFam2-45-2 | 62359500 | 62219256 | 31753 | 99.78 | 87.76 | 63.95 |
| tFam2-45-3 | 67782668 | 67631644 | 31753 | 99.78 | 88.33 | 61.51 |
| sFam1-45-1 | 67807698 | 67654608 | 31753 | 99.77 | 88.56 | 62.42 |
| sFam1-45-2 | 60803442 | 60679300 | 31753 | 99.80 | 87.91 | 65.61 |
| sFam1-45-3 | 78032644 | 77859512 | 31753 | 99.78 | 87.75 | 65.56 |
| sFam2-45-1 | 45190390 | 45090990 | 31753 | 99.78 | 88.48 | 60.74 |
| sFam2-45-2 | 46076252 | 45988338 | 31753 | 99.81 | 88.30 | 61.87 |
| sFam2-45-3 | 48605316 | 48499214 | 31753 | 99.78 | 88.65 | 61.52 |