**Supplementary Table 1** **Statistical summary of the data that were generated by high-throughput small-RNA sequencing in *Felis catus* microRNAs.**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Sample | Total raw reads | High quality reads | Low quality reads | N% > 10% | 5' adapter contaminants | 3' adapter null | PolyA/T/G/C |
| Control 01 | 25,230,038(100.00%) | 24,891,422(98.66%) | 100,575(0.40%) | 0(0.00%) | 3,776 (0.01%) | 181,678 (0.72%) | 52,587(0.21%) |
| Control 02 | 25,410,594(100.00%) | 24,923,852(98.08%) | 100,174(0.39%) | 0(0.00%) | 4,707 (0.02%) | 298,854 (1.18%) | 83,007(0.33%) |
| CPV 01 | 23,466,804(100.00%) | 22,909,717(97.63%) | 81,129(0.35%) | 0(0.00%) | 3,228 (0.01%) | 431,286 (1.84%) | 41,444(0.18%) |
| CPV 02 | 26,337,331(100.00%) | 25,935,795(98.48%) | 113,187(0.43%) | 53(0.00%) | 3,876 (0.01%) | 253,129 (0.96%) | 31,291(0.12%) |

N%, undetectable gaps at base calling