**Table S1. Statistics of RNA-seq data in six human tissues**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Tissue | Total read bases (bp) | # of raw reads | Read length (bp) | GC(%) | AT(%) | Q20(%) | Q30(%) | # of cleaned reads | % | Accession |
| Brain | 6,164,292,398  | 61,032,598  | 101  | 43.87% | 56.13% | 95.94% | 90.53% | 57,430,764  | 94.10% | SRX1830410 |
| Colon | 5,754,163,112  | 56,971,912  | 101  | 43.86% | 56.14% | 96.89% | 92.32% | 53,711,156  | 94.28% | SRX1830402 |
| Heart | 6,711,926,114  | 66,454,714  | 101  | 41.40% | 58.60% | 96.23% | 91.12% | 61,160,848  | 92.03% | SRX1830412 |
| Liver | 5,266,202,620  | 52,140,620  | 101  | 40.21% | 59.79% | 97.02% | 92.63% | 48,074,128  | 92.20% | SRX1830413 |
| Ovary | 6,499,700,470  | 64,353,470  | 101  | 40.88% | 59.12% | 96.04% | 90.81% | 59,294,700  | 92.14% | SRX1830414 |
| Testis | 5,900,540,594  | 58,421,194  | 101  | 42.14% | 57.86% | 96.66% | 92.31% | 54,664,904  | 93.57% | SRX1830405 |