

**Supplement Table 1.** Summary of RNA sequencing and mapping using the human genome as the reference.

Sample name	Raw reads	Clean reads	clean bases (G)	Error rate (%)	Q20 (%)	Q30 (%)	GC content (%)
C_1	99748474	96664918	14.50	0.01	97.43	93.53	47.49
C_2	87971062	85654450	12.85	0.01	97.54	93.79	46.97
C_3	96250922	92233510	13.84	0.01	97.66	94.02	47.52
M_1	97517412	94017030	14.10	0.01	97.62	93.93	47.51
M_2	88530574	84432966	12.66	0.01	97.87	94.36	47.32
M_3	96093458	93303762	14.00	0.02	96.20	91.17	47.46

Raw reads: number of raw sequencing reads; Clean reads: filtered sequencing data; Clean bases: the number of branches of clean reads multiplied by the length and converted into the units of G; Error rate: error rate of the sequencing; Q20: the percentage of filtered bases was greater than 20% of the total bases; Q30: the percentage of filtered bases was greater than 30% of the total bases; GC content: the percentage of the total number of G and C bases out of the total number of bases (clean data)