Table S3. Quality control results of brain transcriptome sequencing data for the three treatment stages in the HT group of *C. fuscus*.

	C-1	C-2	C-3	T72-1	T72-2	T72-3	R72-1	R72-2	R72-3
Raw reads	44091880	46958978	39275842	46783252	46310654	46155506	55501424	48989730	46407478
Clean reads	42667890	45789006	38316990	45980412	45141474	45074152	53383510	46750246	44329342
Clean bases (G)	6.4G	6.87G	5.75G	6.9G	6.77G	6.76G	8.01G	7.01G	6.65G
Q20（%）	96.52	96.45	96.57	96.67	96.74	96.63	97.56	97.44	97.31
Q30（%）	91.5	91.43	91.71	91.77	91.89	91.72	93.52	93.27	93.02
GC pct（%）	42.49	42.29	42.77	42.86	43.82	43.22	47.19	47.48	47.26
Total Mapped	35290844 (82.71%)	36508012 (79.73%)	29797708 (77.77%)	39566755 (86.05%)	36836515 (81.6%)	36290634 (80.51%)	47602975 (89.17%)	42096822 (90.05%)	39302680 (88.66%)
Uniq Mapped Reads	34822826 (81.61%)	35931720 (78.47%)	29209802 (76.23%)	39038653 (84.9%)	36265195 (80.34%)	35687664 (79.18%)	46608302 (87.31%)	41203890 (88.14%)	38609345 (87.1%)
Multiple Mapped Reads	468018 (1.1%)	576292 (1.26%)	587906 (1.53%)	528102 (1.15%)	571320 (1.27%)	602970 (1.34%)	994673 (1.86%)	892932 (1.91%)	693335 (1.56%)