Table S2. Quality control results of brain transcriptome sequencing data for the three treatment stages in the NT group of *C. fuscus*.

	C-1	C-2	C-3	T72-1	T72-2	T72-3	R72-1	R72-2	R72-3
Raw reads	48877970	46139384	45099818	47022306	46603088	49361708	55974106	46956116	41187130
Clean reads	47417476	44951646	42310080	45982418	45692716	47848808	54391062	45556406	39096830
Clean bases (G)	7.11G	6.74G	6.35G	6.9G	6.85G	7.18G	8.16G	6.83G	5.86G
Q20（%）	96.55	96.93	96.39	96.56	96.68	96.84	97.3	97.22	96.8
Q30（%）	91.71	92.33	91.67	91.7	91.86	92.17	92.94	92.86	91.96
GC pct（%）	41.31	43.56	45.97	43.49	43.24	43.18	45.2	45.9	46.39
Total Mapped	39583492 (83.48%)	38432912 (85.5%)	30689089 (72.53%)	29656259 (64.49%)	37052602 (81.09%)	39802244 (83.18%)	47686785 (87.67%)	40303530 (88.47%)	34645506 (88.61%)
Uniq Mapped Reads	39095739 (82.45%)	37924855 (84.37%)	29979095 (70.86%)	29066135 (63.21%)	36481594 (79.84%)	39245407 (82.02%)	46832887 (86.1%)	39434611 (86.56%)	34076241 (87.16%)
Multiple Mapped Reads	487753 (1.03%)	508057 (1.13%)	709994 (1.68%)	590124 (1.28%)	571008 (1.25%)	556837 (1.16%)	853898 (1.57%)	868919 (1.91%)	569265 (1.46%)