

Table S2. Mapping statistics of RNA sequencing reads

Sample	Total Raw Reads (M)	Total Clean Reads (M)	Total Mapping(%)	Uniquely Mapping(%)	Clean Reads Ratio (%)	Total Clean Bases (Gb)	Clean Reads Q20 (%)	Clean Reads Q30 (%)	Clean Reads Ratio (%)
dbdb1	114.94	113.79	97.78	90.97	98.99	11.38	98.44	95.31	98.99
dbdb2	112.44	111.56	97.87	90.38	99.22	11.16	98.22	94.66	99.22
dbdb3	114.94	113.97	97.9	90.62	99.16	11.4	98.25	94.7	99.16
dbm1	114.94	113.92	97.83	89.81	99.11	11.39	98.41	95.22	99.11
dbm2	112.44	111.47	97.9	88.88	99.13	11.15	98.38	95.16	99.13
dbm3	114.94	113.86	97.85	89.93	99.06	11.39	98.4	95.19	99.06