

Supplemental Table S2. summary of RNA-seq read mapping result

Sample	RawReads(M)	CleanReads(M)	Total reads	Total mapped reads	Uniquely mapped
BP1	47.4	46.42	46420288	45035552(97.02%)	43365982(93.42%)
BP2	39.57	38.71	38706170	37505070(96.90%)	36148522(93.39%)
BP3	47.19	46.26	46261366	45170538(97.64%)	43248064(93.49%)
DR1	47.83	46.99	46989270	46066745(98.04%)	44277335(94.23%)
DR2	48.54	47.48	47478984	46226756(97.36%)	44609320(93.96%)
DR3	46.96	46.1	46103258	45183724(98.01%)	43412367(94.16%)
GrA1	47.85	46.83	46833652	45668759(97.51%)	43534800(92.96%)
GrA2	48.13	47.26	47258052	46153575(97.66%)	43127268(91.26%)
GrA3	48.2	46.95	46945838	45700525(97.35%)	43657373(93.00%)
SE1	49.16	47.83	47832114	46642249(97.51%)	43863620(91.70%)
SE2	48.95	47.22	47221190	46037218(97.49%)	43873970(92.91%)
SE3	48.67	47.48	47478136	46285411(97.49%)	44127690(92.94%)