

Table S3 Statistics of quality control for offspring reduced-representation genome sequencing data

Sample	Clean_Data(Gb)	HQ_Clean_Data(Gb)	HQ_Q20(%)	HQ_Q30(%)	HQ_GC(%)	Total Read	Total Mapped
D1-1	4.97	4.93	4769041079(96.68%)	4491532495(91.05%)	1972872376(39.97%)	33836130.00	33412534-98.75%
D1-2	3.55	3.53	3435786176(97.47%)	3274002845(92.88%)	1416701685(40.17%)	24182112.00	23965960-99.11%
D2-1	3.63	3.60	3501460874(97.32%)	3331548041(92.6%)	1449619157(40.27%)	24693822.00	24437696-98.96%
D2-2	3.86	3.79	3660313366(96.47%)	3451669226(90.97%)	1522434855(40.11%)	23441912.00	23108729-98.58%
D3-1	4.00	3.97	3867054502(97.36%)	3687125090(92.83%)	1583319949(39.84%)	27259516.00	26949280-98.86%
D3-2	2.97	2.95	2862406056(97.11%)	2717555131(92.2%)	1175865693(39.88%)	20232032.00	20031471-99.01%
D4-1	3.60	3.57	3470912073(97.18%)	3298966331(92.37%)	1428342735(39.97%)	24520352.00	24237167-98.85%
D4-2	3.77	3.75	3653933504(97.54%)	3489631972(93.15%)	1492886908(39.83%)	25713800.00	25473637-99.07%
D5-1	3.50	3.48	3376871875(97.15%)	3208264133(92.3%)	1386106644(39.86%)	23853648.00	23594088-98.91%
D5-2	3.90	3.87	3769851319(97.46%)	3592005306(92.86%)	1537623298(39.73%)	26554154.00	26343160-99.21%