

Table 1 Summary of GBS clean reads per sample and percentage of alignment to reference genome sequence

Dendrobium species abbreviation	Clean reads pairs per sample	Clean reads per per (bp)	base sample	The proportion of clean reads mapped to the reference genome to the total clean reads (%)	The proportion of clean reads pairs mapped to the reference genome to the total clean reads (%)	The proportion of clean reads singletons mapped to the reference genome to the total clean reads (%)
HS	1 390 262	395 557 949		96.45	80.15	0.72
TP	1 286 162	366 277 414		99.08	91.01	0.27
XJ	1 380 009	391 592 914		96.98	80.08	0.82
FJS	1 170 337	333 221 985		96.91	79.21	0.85