

Table S3. Benchmarking Universal Single-Copy Orthologs (BUSCO) assessment of the *A. montana* assembly genome.

Type	Number	Percent (%)
Complete BUSCOs (C)	1307	90.80
Complete and single-copy BUSCOs (S)	1268	88.10
Complete and duplicated BUSCOs (D)	39	2.70
Fragmented BUSCOs (F)	31	2.20
Missing BUSCOs (M)	102	7.00
Total BUSCO groups searched	1440	100