

**Table S9. Core Eukaryotic Genes Mapping Approach (CEGMA) and Benchmarking Universal Single-Copy Orthologs (BUSCO) assessment of the *A. montana* annotated genome.**

	Type	Proteins	%Completeness
CEGMA	Complete	226	91.13
	Group 1	61	92.42
	Group 2	52	92.86
	Group 3	54	88.52
	Group 4	59	90.77
	Partial	233	93.95
	Group 1	63	95.45
	Group 2	53	94.64
	Group 3	56	91.8
	Group 4	61	93.85
BUSCO	Complete BUSCOs	1328	96.59
	Complete Single-Copy BUSCOs	1300	94.55
	Complete Duplicated BUSCOs	28	2.04
	Fragmented BUSCOs	17	1.24
	Missing BUSCOs	30	2.18
	Total BUSCO groups searched	1375	100