

**Table S6. The prediction of gene structures of *A. montana* genome.**

Gene set	Protein coding gene number	Average gene length (bp)	Average CDS length (bp)	Average exon per gene	Average exon length (bp)	Average intron length (bp)	
	AUGUSTUS	47,313	2,409.13	1,009.51	4.56	221.26	392.86
De novo	GlimmerHMM	57,812	1,370.87	634.49	2.38	266.12	531.99
	Genscan	51,364	10,601.91	996.00	5.25	189.79	2,261.30
	<i>A. thaliana</i>	28,905	3,839.72	851.53	3.66	232.93	1,125.20
	<i>E. grandis</i>	29,687	4,368.80	885.54	3.64	243.14	1,318.35
Homolog	<i>L. chinense</i>	35,244	5,401.08	864.87	3.31	261.06	1,961.28
	<i>A. chinensis</i>	30,157	4,140.84	890.00	3.67	242.58	1,218.03
	<i>P. trichocarpa</i>	30,464	4,053.64	867.50	3.62	239.82	1,217.36
	RNA-seq	23,094	7,193.20	1,269.19	4.89	259.29	962.80
	CEGMA	427	7,065.37	1,221.17	8.36	146.14	794.48
	MAKER	28,502	5,055.08	1,146.01	4.84	236.91	812.68
	Final set	26,399	5,630.77	1,201.92	4.95	242.87	890.22