

**Table S11. The classification of repeat sequence in *A. montana* genome.**

	RepBase TEs		TE Proteins		<i>De novo</i>		Combined TEs	
	Length (bp)	%in Genome	Length (bp)	% in Genome	Length (bp)	% in Genome	Length (bp)	% in Genome
DNA	4,559,947	0.47	101,110	0.01	30,237,719	3.10	33,342,979	3.42
LINE	5,688,285	0.58	3,119,637	0.32	7,556,530	0.78	10,645,783	1.09
SINE	73,667	0.01	0	0.00	6,083	0.00	79,750	0.01
LTR	138,120,632	14.18	142,973,243	14.67	472,774,582	48.52	482,534,290	49.52
Other	2,599	0.00	222	0.00	0	0.00	2,821	0.00
Unknown	68,553	0.01	0	0.00	61,808,465	6.34	61,874,470	6.35
Total	148,355,745	15.23	146,192,655	15.00	555,911,418	57.05	568,830,198	58.38

\*LINE, long interspersed nuclear element; SINE, short interspersed element; LTR, long terminal repeat;

\*Denovo+Repbse denotes transposable elements identified by RepeatMasker (<http://www.repeatmasker.org>) with default options after RepeatModeler/RepeatScout/Piler/LTR\_finder software uses with RepBase database prediction.

\*TE proteins are transposable elements identified in the genome through the annotation of RepeatProteinMask software using the RepBase database.

\*Combined TEs involved a combination of the above two methods.

\*Unknown repeat sequences could not be clustered using RepeatMasker.