

Table S11: Comparison of the performances of the RepeatModeler and TEdenovo databanks

Genome	Pipeline	Consensus	S_n^*	S_p^*	R_{CC}
<i>D. mel.</i>	RepeatModeler	141	77.78%	75.89%	19.11%
	TEdenovo	593	92.31%	75.72%	77.94%
<i>A. tha.</i>	RepeatModeler	177	45.90%	57.63%	5.19%
	TEdenovo	1351	74.43%	66.75%	49.35%

S_n^* : percentage of “knowledge-based” consensus sequences matching a *de novo* consensus

S_p^* : percentage of *de novo* consensus sequences matching a “knowledge-based” consensus

R_{CC} : percentage of fully recovered “knowledge-based” consensus sequences