Table S3. Assessment of different sequencing platforms and assembly qualities using Core Eukaryotic Genes Mapping Approaches (CEGMA). Individual and hybrid assemblies were assessed for the presence and full-length cDNA coverage of 458 core eukaryotic proteins using the minimum criteria of at least 90% coverage with a TBLASTN e-value cut-off of 1 x 10^{-20}.

Species	**Assembly**	**# of CEGMA proteins**	
		in assembly	**putatively full length**
Lodgepole pine	Sanger (CAP3)	377	216
	454 (Newbler)	447	330
	Illumina (Trinity)	452	358
	Sanger + 454 (Newbler)	444	325
Jack pine	Sanger (CAP3)	374	211
	454 (Newbler)	446	331
	Illumina (Trinity)	450	362
	Sanger + 454 (Newbler)	445	322