Table S4. Assessment of assembly quality of (A) lodgepole pine and (B) jack pine transcriptome data for presence of full length (FL) terpenoid pathway genes. Targets that had one contiguous sequence with coverage of at least 95 % length and with at least 99 % nucleotide sequence identity were considered to be full length (FL). Abbreviations: NP – targets not present; PT – prenyltransferases; TPS – terpene synthase; P450 – cytochrome P450.;

(A) Lodgepole pine

Assembly	**PT (7 unique genes)**			**TPS-d (19 unique genes)**			**P450 – CYP720B (8 unique genes)**		
	FL	**Not FL**	**NP**	**FL**	**Not FL**	**NP**	**FL**	**Not FL**	**NP**
Sanger (CAP3)	5	2	-	0	6	13	0	2	6
454 (Newbler)	4	2	1	6	3	10	6	1	1
Illumina (Trinity)	4	3	-	5	7	7	1	7	-
Sanger/454 Hybrid	6	1	-	3	11	5	6	0	2

(B) Jack pine

Assembly	**PT (9 unique genes)**			**TPS-d (21 unique genes)**			**P450 – CYP720B (8 unique genes)**		
	FL	**Not FL**	**NP**	**FL**	**Not FL**	**NP**	**FL**	**Not FL**	**NP**
Sanger (CAP3)	2	3	4	1	4	16	1	5	2
454 (Newbler)	7	1	1	7	4	10	6	1	1
Illumina (Trinity)	5	4	-	7	9	5	3	4	1
Sanger/454 Hybrid	7	2	-	6	6	9	7	1	-