

**Table S1.** The original paired-end reads.

Species	Uncompressed file/kb
<i>L. cassis</i>	10,091,509/10,091,509
<i>N. radula</i>	7,467,310/7,467,310
<i>C. grata</i>	8,553,973/8,553,973
<i>L. goshimai</i>	7,454,544/7,454,544
<i>P. conulus</i>	14,760,357/14,760,357
<i>P. saccharina lanx</i>	14,461,217/14,461,217
<i>P. ryukyuensis</i>	16,165,902/16,165,902
<i>C. nigrolineata</i>	12,972,845/12,972,845
<i>C. toreuma</i> (GD)	14,172,310/14,172,310
<i>C. toreuma</i> (HN)	18,663,524/18,663,524
<i>S. flexuosa</i>	12,406,821/12,406,821

**Table S2.** The parameters of different size of genome skims calculated by Skmer.

0.1G

	Coverage	Genome_length	Error_rate	Read_length
<i>S. flexuosa</i>	NA	NA	NA	229
<i>L. cassis</i>	NA	NA	NA	235
<i>N. radula</i>	NA	NA	NA	234
<i>C. grata</i>	NA	NA	NA	238
<i>L. goshimai</i>	NA	NA	NA	234
<i>P. conulus</i>	NA	NA	NA	233
<i>P. saccharina lanx</i>	NA	NA	NA	232
<i>P. ryukyuensis</i>	NA	NA	NA	234
<i>C. nigrolineata</i>	NA	NA	NA	243
<i>C. toreuma</i> (GD)	NA	NA	NA	237
<i>C. toreuma</i> (HN)	NA	NA	NA	234

0.5G

---

	Coverage	Genome_length	Error_rate	Read_length
<i>S. flexuosa</i>	1.5013287792624153	95750346	0.028200929350726822	229
<i>L. cassis</i>	1.3327740387547855	45463855	0.027914606109592177	234
<i>N. radula</i>	0.9152781068328262	110192677	0.01567515129507513	234
<i>C. grata</i>	0.5036046394650663	174661355	0.008291417727817385	238
<i>L. goshimai</i>	1.6776567653334804	49808401	0.028761549753830717	234
<i>P. conulus</i>	1.314254793107782	102469388	0.02150057228294544	233
<i>P. saccharina lanx</i>	0.9278481344981513	119876574	0.01775294465663002	232
<i>P. ryukyuensis</i>	1.3659537009334826	75619675	0.02491465125299086	234
<i>C. nigrolineata</i>	0.5179819107059459	148918377	0.010116997073165712	243
<i>C. toreuma</i> (GD)	0.7217787063366554	144208905	0.013825683369604325	237
<i>C. toreuma</i> (HN)	0.7051828916055268	144004463	0.01409483746843987	234

---

1G

	Coverage	Genome_length	Error_rate	Read_length
<i>S. flexuosa</i>	1.0029473619968219	280995598	0.016122217186681498	229
<i>L. cassis</i>	0.9050214990722926	129731681	0.015727142054512533	234
<i>N. radula</i>	0.8636988451143478	226908173	0.007429620144492	234
<i>C. grata</i>	0.6852204637580797	251596063	0.0037109939709843998	238
<i>L. goshimai</i>	1.1259212744418114	143346414	0.017574206420095217	234
<i>P. conulus</i>	1.0438850315377552	253264561	0.012019595240989833	233
<i>P. saccharina lanx</i>	0.8560015672871802	253444900	0.008890363121627054	232
<i>P. ryukyuensis</i>	1.0079677742963102	200437899	0.014262985885386215	234
<i>C. nigrolineata</i>	0.6892807532643411	220849531	0.005215118095972748	243
<i>C. toreuma</i> (GD)	0.7659604249090144	268961901	0.006168678299533492	237
<i>C. toreuma</i> (HN)	0.758536873487782	264678395	0.006597347393543118	234

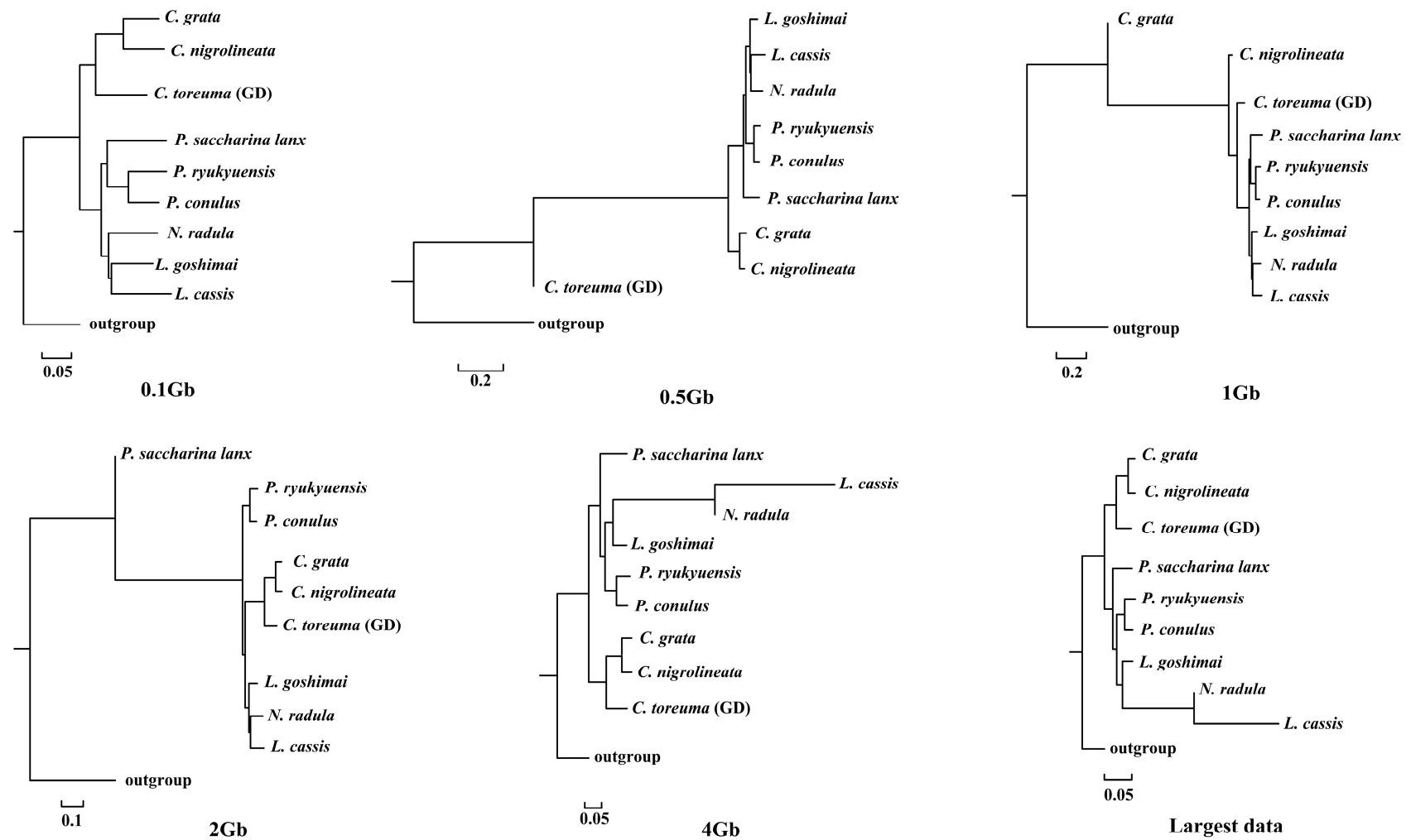
	Coverage	Genome_length	Error_rate	Read_length
<i>S. flexuosa</i>	0.9739603350231031	568184167	0.008350984478455836	229
<i>L. cassis</i>	0.8836878220845178	254302203	0.007915517638578007	234
<i>N. radula</i>	1.1234930557432787	333400647	0.0033993059939037007	234
<i>C. grata</i>	1.1398227918679955	291051615	0.0021502725881005214	238
<i>L. goshimai</i>	1.0073525901651545	308002573	0.009496062842218045	234
<i>P. conulus</i>	1.1328283557791097	460810310	0.006000928817245121	233
<i>P. saccharina lanx</i>	1.1087942016526018	382399050	0.00439628172456763	232
<i>P. ryukyuensis</i>	1.012443020367157	393579569	0.00699520386915653	234
<i>C. nigrolineata</i>	1.105576596622458	272373415	0.0029954150060985674	243
<i>C. toreuma</i> (GD)	1.149406241031329	355042049	0.0032381573580544387	237
<i>C. toreuma</i> (HN)	1.1362944576862781	350783337	0.0035828860869960844	234

4G

	Coverage	Genome_length	Error_rate	Read_length
<i>S. flexuosa</i>	1.255199716467791	843502458	0.004405105731694392	229
<i>L. cassis</i>	0.8546704594611217	205411753	0.010290676984266778	234
<i>N. radula</i>	1.7091781542083455	400260113	0.001975268301126487	234
<i>C. grata</i>	1.9215991714931617	316407172	0.0015958020516907423	238
<i>L. goshimai</i>	1.1533818579078017	489368197	0.004877242961904393	233
<i>P. conulus</i>	1.5924890918985637	630852603	0.00342944974093351	233
<i>P. saccharina lanx</i>	1.7314412846506766	467909490	0.0027453164655780737	232
<i>P. ryukyuensis</i>	1.353249417848962	566191664	0.003609606512741781	233
<i>C. nigrolineata</i>	1.8734610083546972	309937954	0.002118300972162257	243
<i>C. toreuma</i> (GD)	1.8795930711427973	419087036	0.0020809347574954895	237
<i>C. toreuma</i> (HN)	1.845035501662378	417354301	0.0023113595691213185	234

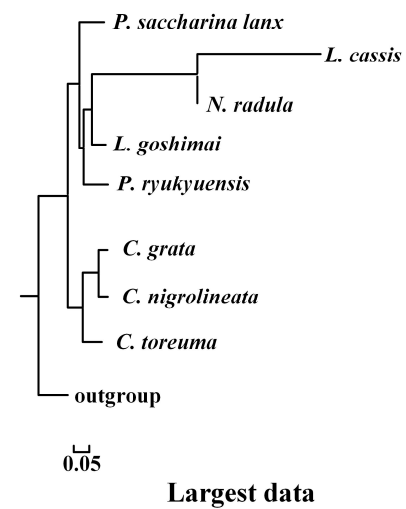
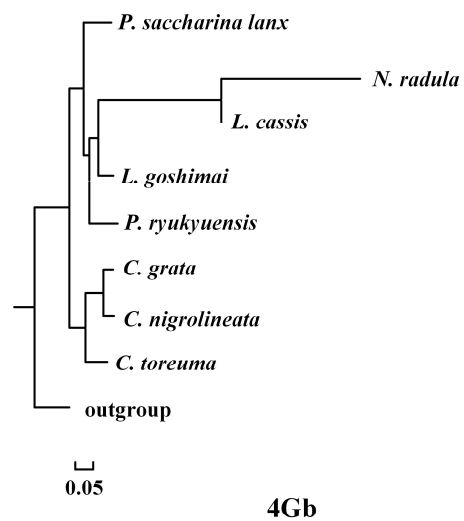
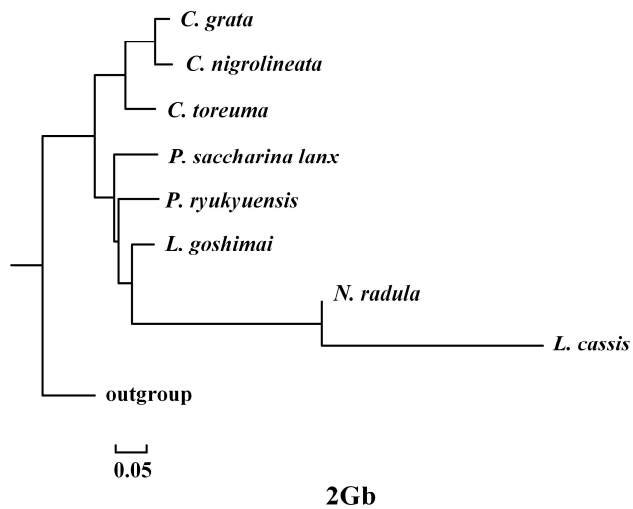
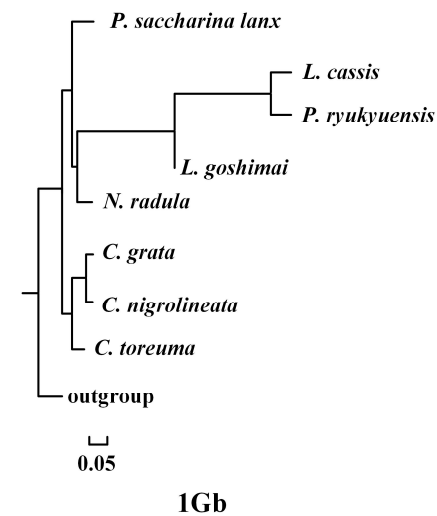
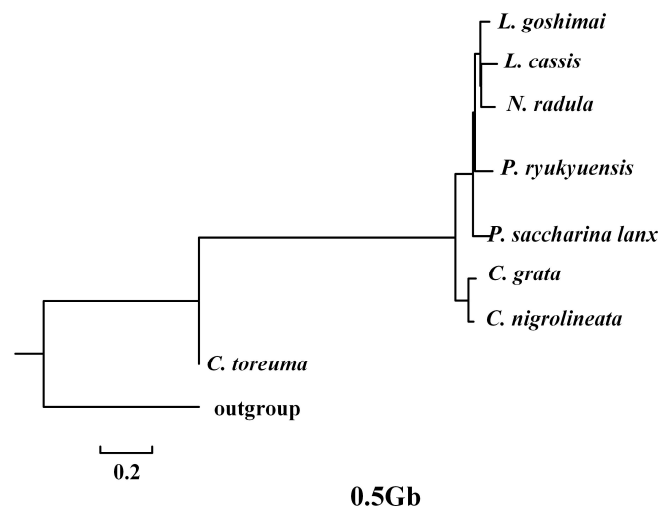
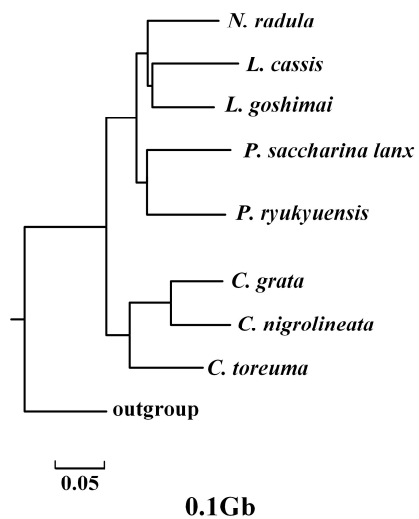
largest data

	Coverage	Genome_length	Error_rate	Read_length
<i>S. flexuosa</i>	1.728193678897708	1019697975	0.0030005034435302003	229
<i>L. cassis</i>	1.4576399556336794	437398847	0.002521865597942541	234
<i>N. radula</i>	2.394840588569781	446504425	0.0015236807962926147	234
<i>C. grata</i>	2.7773452574667132	340994281	0.0014036933986266709	238
<i>L. goshimai</i>	1.4395252523196236	605976119	0.00313680064894728	233
<i>P. conulus</i>	2.2315570578672017	753834277	0.00257679334746419	233
<i>P. saccharina lanx</i>	2.5478325003695264	528630228	0.0022658388657428308	232
<i>P. ryukyuensis</i>	1.8917555040703409	677175949	0.002434969677229337	233
<i>C. nigrolineata</i>	2.7512881584743245	352478197	0.0017901738425651903	243
<i>C. toreuma</i> (GD)	2.709253588460741	486739748	0.0016482778811850451	237
<i>C. toreuma</i> (HN)	2.6691480178728657	484473177	0.0018889276975615488	234

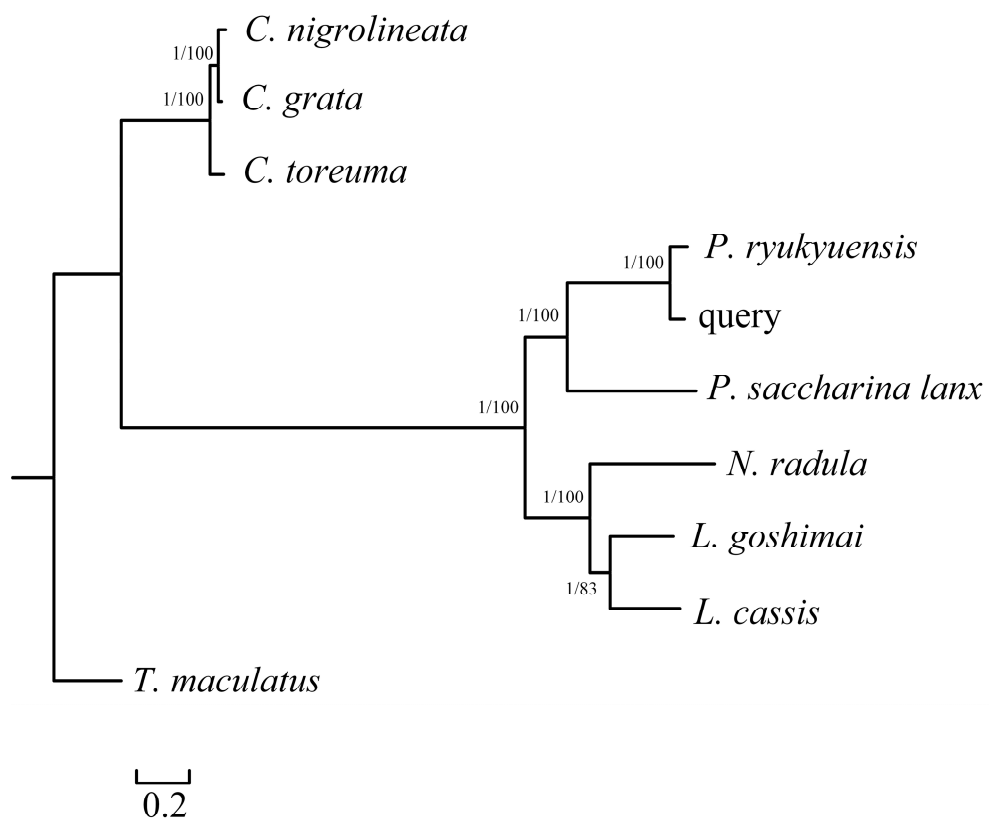


**Figure S1.** The backbone tree of *C. toreuma* (HN) and *S. flexuosa* inferred by FastME under different size of genome skims.

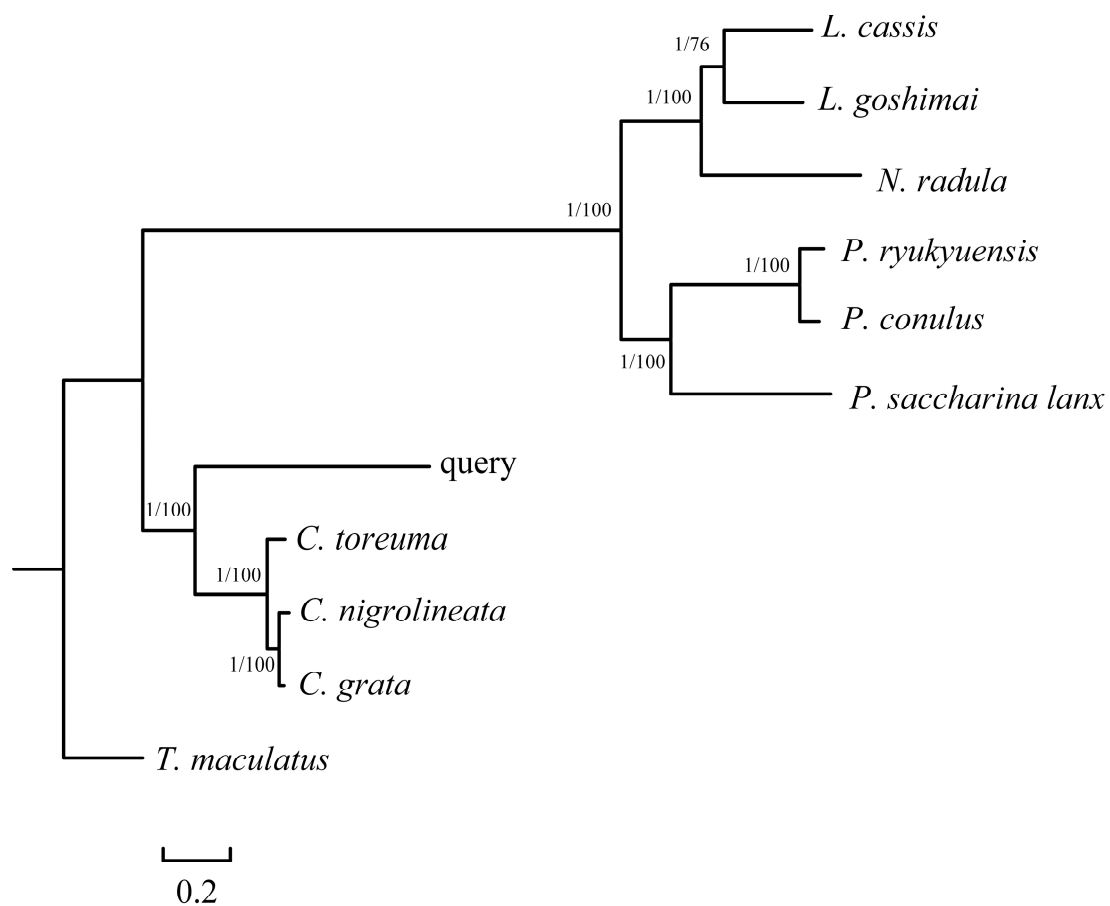




**Figure S2.** The backbone tree of *P. conulus* inferred by FastME under different size of genome skims.



**Figure S3.** Phylogenetic relationships of *P. conulus* (query species) inferred based on concatenated amino acids of 13 mitochondrial protein-coding genes. Numbers at nodes are statistical support values for BI (posterior probabilities)/ML (bootstrap proportions in percentage).



**Figure S4.** Phylogenetic relationships of *S. flexuosa* (query species) inferred based on concatenated amino acids of 13 mitochondrial protein-coding genes. Numbers at nodes are statistical support values for BI (posterior probabilities)/ML (bootstrap proportions in percentage).