

Assembly: SpoDel_pri

- db built with kmer size 31 bp

Genome Statistics

ASM_ID	SpoDel_pri
ASM_LEVEL	scaff
Bases	30,870,404
Est_Size	30,589,352
Het_%	1.46926%
GC_%	48.06
Scaff	11
Cont	14
Gaps	3
Longest_Scaff	4,107,596
Scaff_N50	3,054,357
Scaff_NG50	3,054,357
Scaff_N95	1,691,408
Scaff_NG95	2,218,451
Longest_Cont	4,107,596
Cont_N50	2,680,827
Cont_NG50	2,680,827
Cont_N95	1,191,806
Cont_NG95	1,191,806

QV Score

assembly_name	Assembly_Only	Total_Kmers	QV_Score
SpoDel_pri.PRI	207	30869738	66.6492
ALT_missing	0	0	nan
Both	207	30869738	66.6492

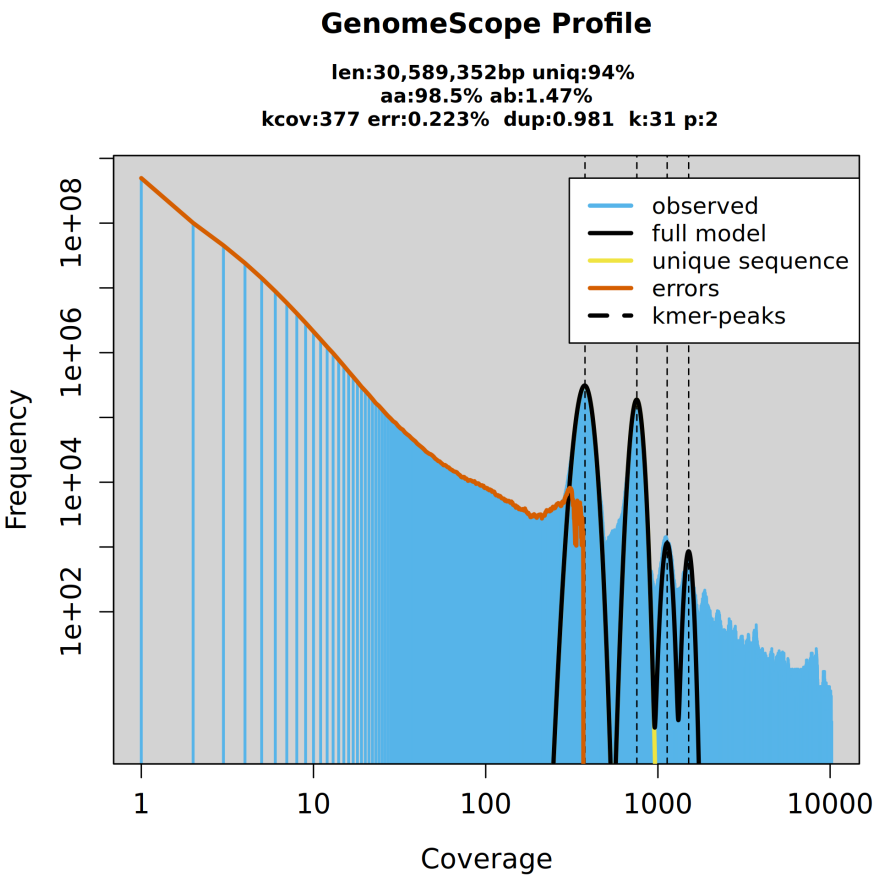
Kmer Completeness

assembly_name	Kmers_Assembly	Kmers_Reads	%
SpoDel_pri.PRI	29725425	42451399	70.0223
ALT_missing	0	42451399	0
both	29725425	42451399	70.0223

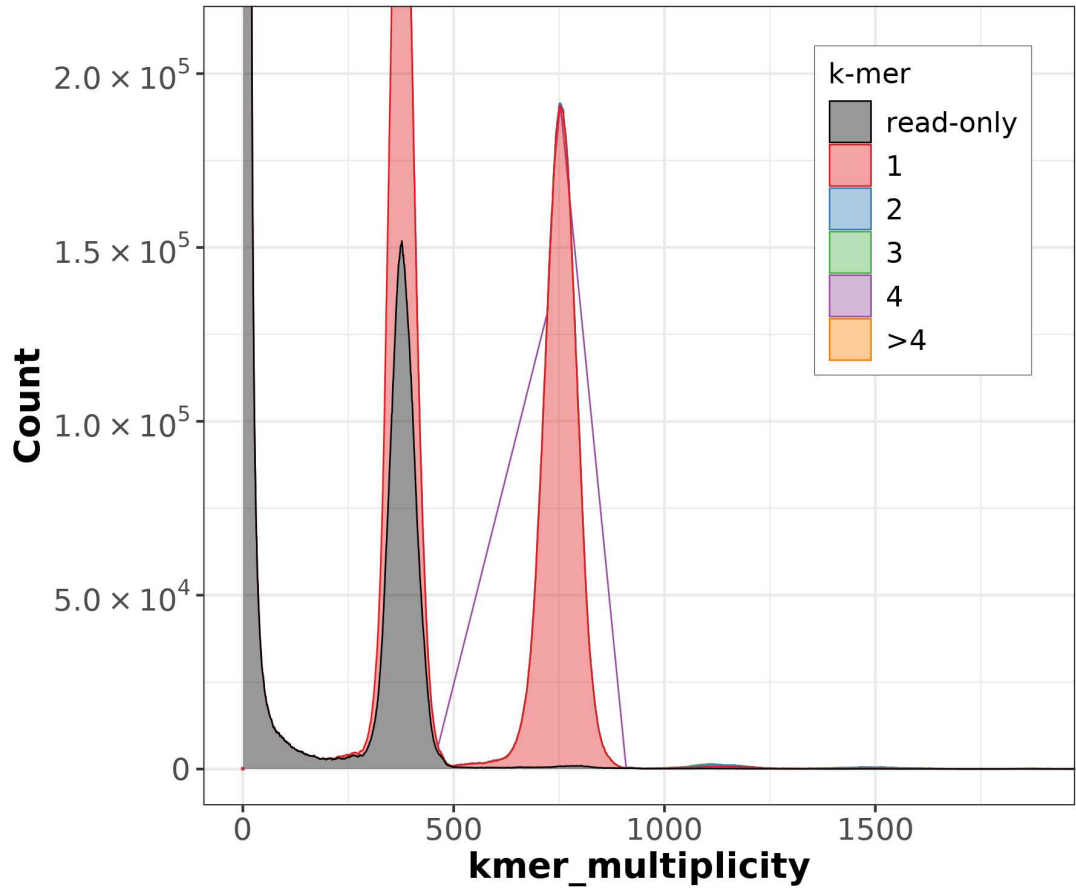
BUSCOv5 (database: polyporales)

C:94.2%[S:93.6%,D:0.6%],F:1.0%,M:4.8%,n:4464
4208 Complete BUSCOs (C)
4179 Complete and single-copy BUSCOs (S)
29 Complete and duplicated BUSCOs (D)
45 Fragmented BUSCOs (F)
211 Missing BUSCOs (M)
4464 Total BUSCO groups searched

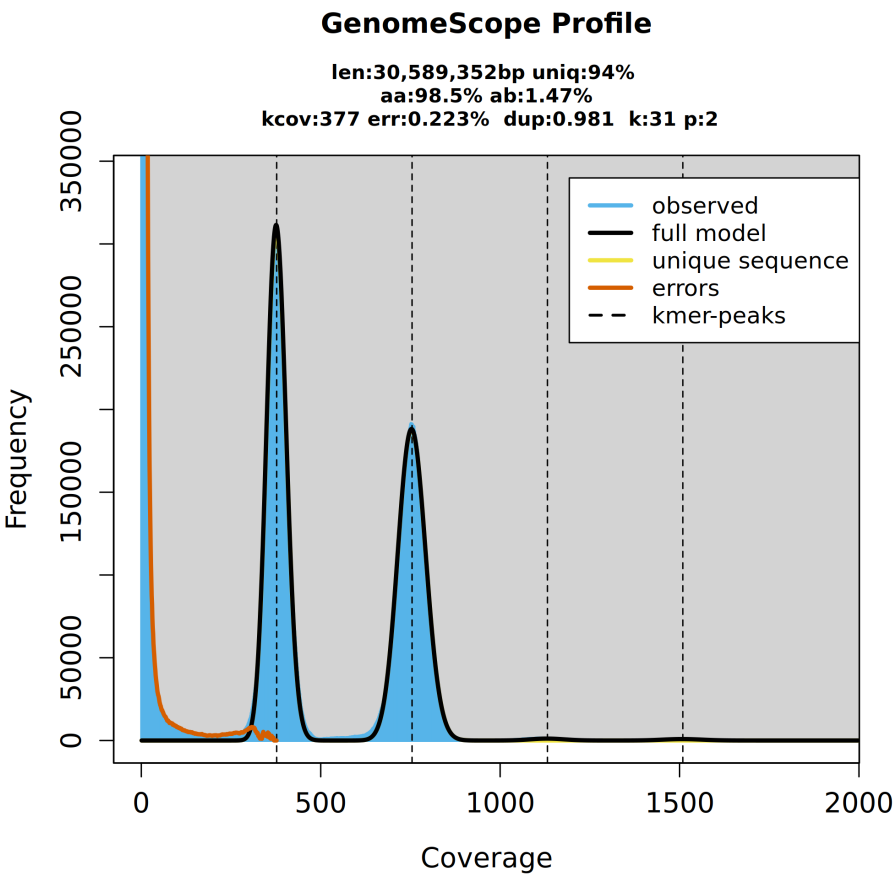
Genomescope2 Profile (Linear)



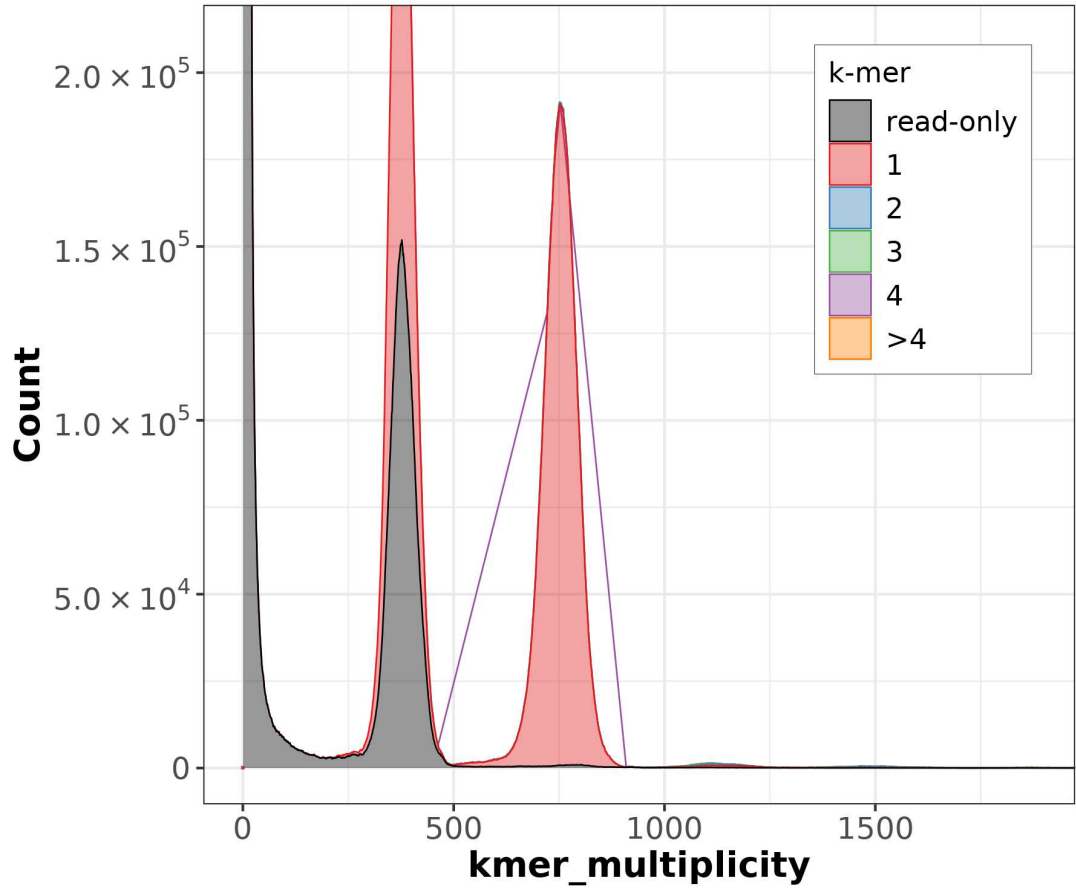
K-mer Multiplicity PRI Only (Stacked)



Genomescope2 Profile (Log)



K-mer Multiplicity PRI + ALT (Stacked)



ASM_ID	ASM_LEVEL	Gaps_per_Gb	Scaff_NG50_Mb	Cont_NG50_Mb	QV	Completeness	Comp_Single_BUSCOs_%
SpoDel_pri	scaff	0	3.05	2.68	66.65	70.02	93.6

Gaps_per_Gb	Scaff_NG50_Mb	Cont_NG50_Mb	QV	Completeness	Comp_Single_BUSCOs_%
< 200	> 100Mbp	> 10Mbp	> 50	> 95%	> 95%
200 - 1000	10Mbp - 100Mbp	1Mbp - 10Mbp	40 - 50	90% - 95%	90% - 95%
1000 - 10000	0.1Mbp - 10Mbp	0.01Mbp - 1Mbp	35 - 40	80% - 90%	80% - 90%
> 10000	< 0.1Mbp	< 0.01Mbp	< 35	< 80%	< 80%