Assembly: SpoDel_pri

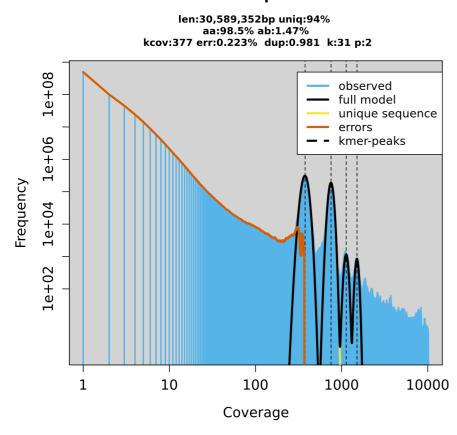
• db built with kmer size 31 bp

Genome Statistics

SpoDel_pri
scaff
30,870,404
30,589,352
1.46926%
48.06
11
14
3
4,107,596
3,054,357
3,054,357
1,691,408
2,218,451
4,107,596
2,680,827
2,680,827
1,191,806
1,191,806

Genomescope2 Profile (Linear)

GenomeScope Profile



Genomescope2 Profile (Log)

GenomeScope Profile len:30,589,352bp uniq:94% aa:98.5% ab:1.47% kcov:377 err:0.223% dup:0.981 k:31 p:2 350000 observed full model unique sequence 250000 errors **–** – kmer-peaks Frequency 150000 50000 0 0 500 1000 1500 2000 Coverage

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)

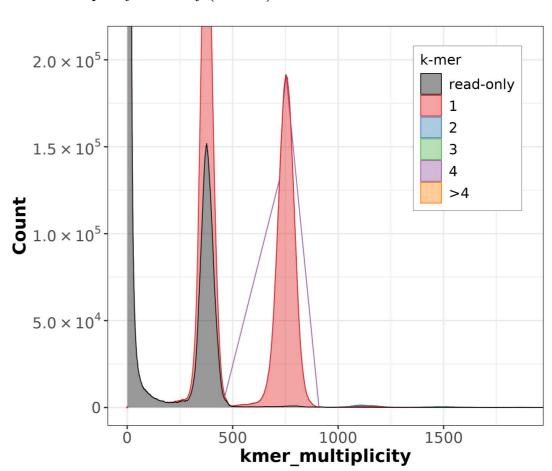
29 Complete and duplicated BUSCOs (D)

45 Fragmented BUSCOs (F)

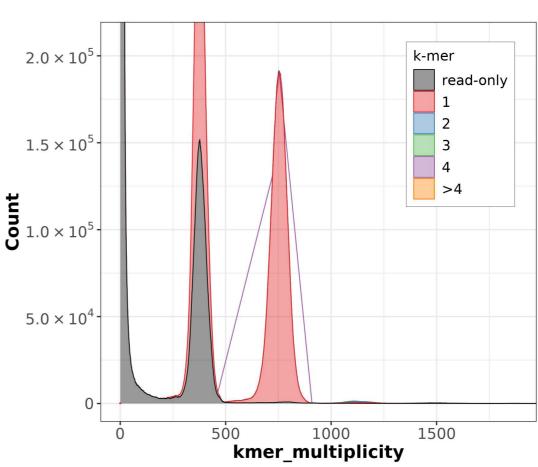
211 Missing BUSCOs (M)

4464 Total BUSCO groups searched

K-mer Multiplicity PRI Only (Stacked)



K-mer Multiplicity PRI + ALT (Stacked)



ASM_ID ASM_LEVEL Bases_Mb Het_% GC_% Gaps_per_Gb Scaff Cont Longest_Scaff_Mb Scaff_NG50_Mb Scaff_NG95_Mb Longest_Cont_Mb Cont_NG50_Mb Cont_NG95_Mb QV Completeness Comp_BUSCOs_% Comp_Single_BUSCOs_% SpoDel_pri scaff 30.87 1.47 48.06 0 11 14 4.11 3.05 2.22 4.11 2.68 1.19 66.65 70.02 94.2 93.6

Bases_Mb Het_% GC_% Gaps_per_Gb Scaff Cont Longest_Scaff_Mb Scaff_NG50_Mb Scaff_NG95_Mb Longest_Cont_Mb Cont_NG50_Mb Cont_NG95_Mb QV Completeness Comp_BUSCOs_% Comp_Single_BUSCOs_%

| Max | Max Max | Max | Max Max | Max |
|-----|---------|-----|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Min | Min Min | Min | Min Min | Min |

 $ASM_ID \quad ASM_LEVEL\ Gaps_per_Gb\ Scaff_NG50_Mb\ Cont_NG50_Mb\quad QV\quad Completeness\ Comp_Single_BUSCOs_\%$

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%		