Report

	assemblies_23_Purge_Scaffold_purged	assemblies_VW4_HiFiasm.asm.15.p_ctg
# contigs (>= 0 bp)	146	155
# contigs (>= 1000 bp)	146	155
# contigs (>= 5000 bp)	146	155
# contigs (>= 10000 bp)	146	155
# contigs (>= 25000 bp)	145	129
# contigs (>= 50000 bp)	137	93
Total length (>= 0 bp)	240460580	189539930
Total length (>= 1000 bp)	240460580	189539930
Total length (>= 5000 bp)	240460580	189539930
Total length (>= 10000 bp)	240460580	189539930
Total length (>= 25000 bp)	240444987	188978472
Total length (>= 50000 bp)	240158381	187681393
# contigs	146	155
Largest contig	11436107	15732951
Total length	240460580	189539930
GC (%)	30.03	30.20
N50	3187088	4330548
N90	972783	1126936
L50	27	13
L90	79	44
# total reads	4553296	5352270
# left	0	(
# right	0	(
Mapped (%)	99.94	99.96
Properly paired (%)	0.0	0.0
Avg. coverage depth	190	236
Coverage >= 1x (%)	99.98	99.98
# N's per 100 kbp	0.00	0.00
# predicted genes (unique)	16075	12133
# predicted genes (>= 0 bp)	18333 + 0 part	14162 + 2 par
# predicted genes (>= 300 bp)	16300 + 0 part	12390 + 2 par
# predicted genes (>= 1500 bp)	8068 + 0 part	5946 + 2 par
# predicted genes (>= 3000 bp)	3701 + 0 part	2780 + 0 pari

All statistics are based on contigs of size >= 3000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Reads report

	assemblies_23_Purge_Scaffold_purged	assemblies_VW4_HiFiasm.asm.15.p_ctg
# total reads	4553296	5352270
# left	0	0
# right	0	0
# mapped	4550725	5350046
Mapped (%)	99.94	99.96
# properly paired	0	0
Properly paired (%)	0.0	0.0
# singletons	0	0
Singletons (%)	0.0	0.0
# misjoint mates	0	0
Misjoint mates (%)	0.0	0.0
Avg. coverage depth	190	236
Coverage >= 1x (%)	99.98	99.98
Coverage >= 5x (%)	99.96	99.96
Coverage >= 10x (%)	99.94	99.94

All statistics are based on contigs of size >= 3000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).









