# contigs (>= 0 bp) # contigs (>= 1000 bp) Total length (>= 0 bp) Total length (>= 1000 bp) # contigs Largest contig Total length Reference length GC (%) Reference GC (%) N50 N90 NG50 N90 NG90 auN auNG L50 LG50 L90 LG90 # misassemblies # misassembled contigs	443 71 5601621 5541847 77 467390 5545630 5682322 57.19 57.12 160025 160025 45645 35266 189934.7 185365.7 12 12 34 37	553992; 86 467396 554508; 568232; 57.1; 16002; 16002; 4344; 3130; 185308.; 180832.6
Total length (>= 0 bp) Total length (>= 1000 bp) # contigs Largest contig Total length Reference length GC (%) Reference GC (%) N50 N90 NG90 auN auNG L50 L90 LG90 # misassemblies	5601621 5541847 77 467390 5545630 5682322 57.19 57.12 160025 160025 45645 35266 189934.7 185365.7 12 12 34	553992: 88 467390 554508: 568232: 57.12 16002: 16002: 43442 31309: 185308.: 180832.6
Total length (>= 1000 bp) # contigs Largest contig Total length Reference length GC (%) Reference GC (%) N50 N90 NG90 auN auNG L50 L90 LG90 # misassemblies	5541847 77 467390 5545630 5682322 57.19 57.12 160025 45645 35266 189934.7 185365.7 12 12	86 467390 554508: 568232: 57.1; 57.1; 16002: 4344: 31309: 185308.3
# contigs Largest contig Total length Reference length GC (%) Reference GC (%) N50 NG50 N90 NG90 auN auNG L50 LG90 LG90 # misassemblies	77 467390 5545630 5682322 57.19 57.12 160025 160025 45645 35266 189934.7 185365.7 12 12 34	86 467390 554508: 568232: 57.1; 57.1; 16002: 4344: 31309: 185308.3
Largest contig Total length Reference length GC (%) Reference GC (%) N50 N90 N90 NG90 auN auNG L50 LG50 L90 LG90 # misassemblies	467390 5545630 5682322 57.19 57.12 160025 45645 35266 189934.7 185365.7 12 12 34	467390 554508: 5682322 57.19 57.12 160029 43442 31309 185308.3 180832.6
Total length Reference length GC (%) Reference GC (%) N50 NG50 N90 NG90 auN auNG L50 LG50 L90 LG90 # misassemblies	5545630 5682322 57.19 57.12 160025 160025 45645 35266 189934.7 185365.7 12 12 34	5545083 5682323 57.13 57.13 160023 143443 31303 185308.3 180832.6
Reference length GC (%) Reference GC (%) N50 NG50 N90 NG90 auN auNG L50 LG50 L90 LG90 # misassemblies	5682322 57.19 57.12 160025 160025 45645 35266 189934.7 185365.7 12 12 34	5682327 57.19 57.17 160029 160029 43447 31309 185308.3
GC (%) Reference GC (%) N50 NG50 N90 NG90 auN auNG L50 LG50 LG90 # misassemblies	57.19 57.12 160025 160025 45645 35266 189934.7 185365.7 12 12 34	57.15 57.12 160025 160025 43442 31305 185308.3 180832.6
Reference GC (%) N50 N50 N950 N990 NG90 auN auNG L50 LG50 L90 LG90 # misassemblies	57.12 160025 160025 45645 35266 189934.7 185365.7 12 12	57.12 16002! 16002! 43442 3130! 185308.2
N50 NG50 N90 NG90 auN auNG L50 LG50 LG90 # misassemblies	160025 160025 45645 35266 189934.7 185365.7 12 12	16002! 16002! 4344; 3130! 185308.: 180832.6
NG50 N90 NG90 auN auNG L50 LG50 LG90 # misassemblies	160025 45645 35266 189934.7 185365.7 12 12	16002! 4344; 3130! 185308.; 180832.6
N90 NG90 auN auNG L50 LG50 L90 LG90 # misassemblies	45645 35266 189934.7 185365.7 12 12 34	43447 31309 185308. 180832.6
NG90 auN auNG L50 LG50 L90 LG90 # misassemblies	35266 189934.7 185365.7 12 12 34	31309 185308.3 180832.6
auN auNG L50 LG50 LG90 LG90 # misassemblies	189934.7 185365.7 12 12 34	185308.3 180832.6 12
auNG L50 LG50 L90 LG90 # misassemblies	185365.7 12 12 34	180832.6 12
L50 LG50 L90 LG90 # misassemblies	12 12 34	12
LG50 L90 LG90 # misassemblies	12 34	
L90 LG90 # misassemblies	34	12
L90 LG90 # misassemblies		
LG90 # misassemblies		35
	3/	39
	77	7:
	34	35
Misassembled contigs length	4584292	4544983
# local misassemblies	27	2.
# scaffold gap ext. mis.	0	
# scaffold gap loc. mis.	0	
# unaligned mis. contigs	3	3
# unaligned contigs	14 + 45 part	15 + 46 par
Unaligned length	725787	725892
Genome fraction (%)	84.959	85.279
Duplication ratio	1.007	1.008
# N's per 100 kbp	10.46	0.50
# mismatches per 100 kbp	685.04	686.29
# indels per 100 kbp	20.36	19.5
# genomic features 9	652 + 232 part	9641 + 234 par
Complete BUSCO (%)	97.30	97.30
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	2 + 3 part	2 + 3 par
Largest alignment	313449	313449
Total aligned length	4818722	481795
NA50	65208	65208
NGA50	63744	63744
NA90	-	
NGA90	-	
auNA	82880.8	82701.5
auNGA	80887.1	80704.3
LA50	24	24
LGA50	25	
LA90		

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	microbe-8_fa	microbe-8_fa_broken
# misassemblies	77	77
# contig misassemblies	77	77
# c. relocations	73	73
# c. translocations	4	4
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	34	35
Misassembled contigs length	4584292	4544981
# local misassemblies	27	27
# scaffold gap ext. mis.	0	1
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	3	3
# mismatches	33010	33065
# indels	981	942
# indels (<= 5 bp)	863	837
# indels (> 5 bp)	118	105
Indels length	9573	8906

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	microbe-8_fa	microbe-8_fa_broken
# fully unaligned contigs	14	15
Fully unaligned length	63486	63819
# partially unaligned contigs	45	46
Partially unaligned length	662301	662073
# N's	580	31

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).



































