

Alignment-based statistics		Minia_on_data_28
Genome fraction (%)		90.061
Duplication ratio		1.004
Largest alignment		40 450
Total aligned length		4 168 496
NGA50		6536
LGA50		206
Misassemblies		
# misassemblies		2
Misassembled contigs length		19 630
Per base quality		
# mismatches per 100 kbp		16.34
# indels per 100 kbp		2.28
# N's per 100 kbp		0
Statistics without reference		
# contigs		886
Largest contig		40 450
Total length		4 170 116
Total length (>= 1000 bp)		4 081 154
Total length (>= 10000 bp)		1 418 544
Total length (>= 50000 bp)		0