

Preprocess
OK

Assemble
OK

MapReads
OK

Validate
OK

FindORFS
OK

FindRepeats
SKIPPED

Scaffold
SKIPPED

FindScaffoldORFS
OK

Abundance
OK

Annotate
OK

FunctionalAnnotation
OK

Propagate
SKIPPED

Classify
OK

Browse Results
OK

Selected assembler: spades.47
Selected reference: Mycobacterium_tuberculosis_EAI5_NITR206_uid202218
Sample may have contaminants, only 97.57% contigs/reads >100bp assigned to Mycobacterium. Check Annotate output.

Assembly	Lap	Ale	Cgal	Snp	Frcbam	Orf	N50	Reapr
SPADES.47	-8.528025	-172424658.572994	-1205000000.000000	797	N/A	5109	38,016	N/A
VELVET.47	-8.768155	-226035245.216896	-1050360000.000000	217	N/A	4471	6,610	N/A
MASURCA.47	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

QUAST report

12 November 2013, Tuesday, 17:20:46

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.)

Short report worst.....best

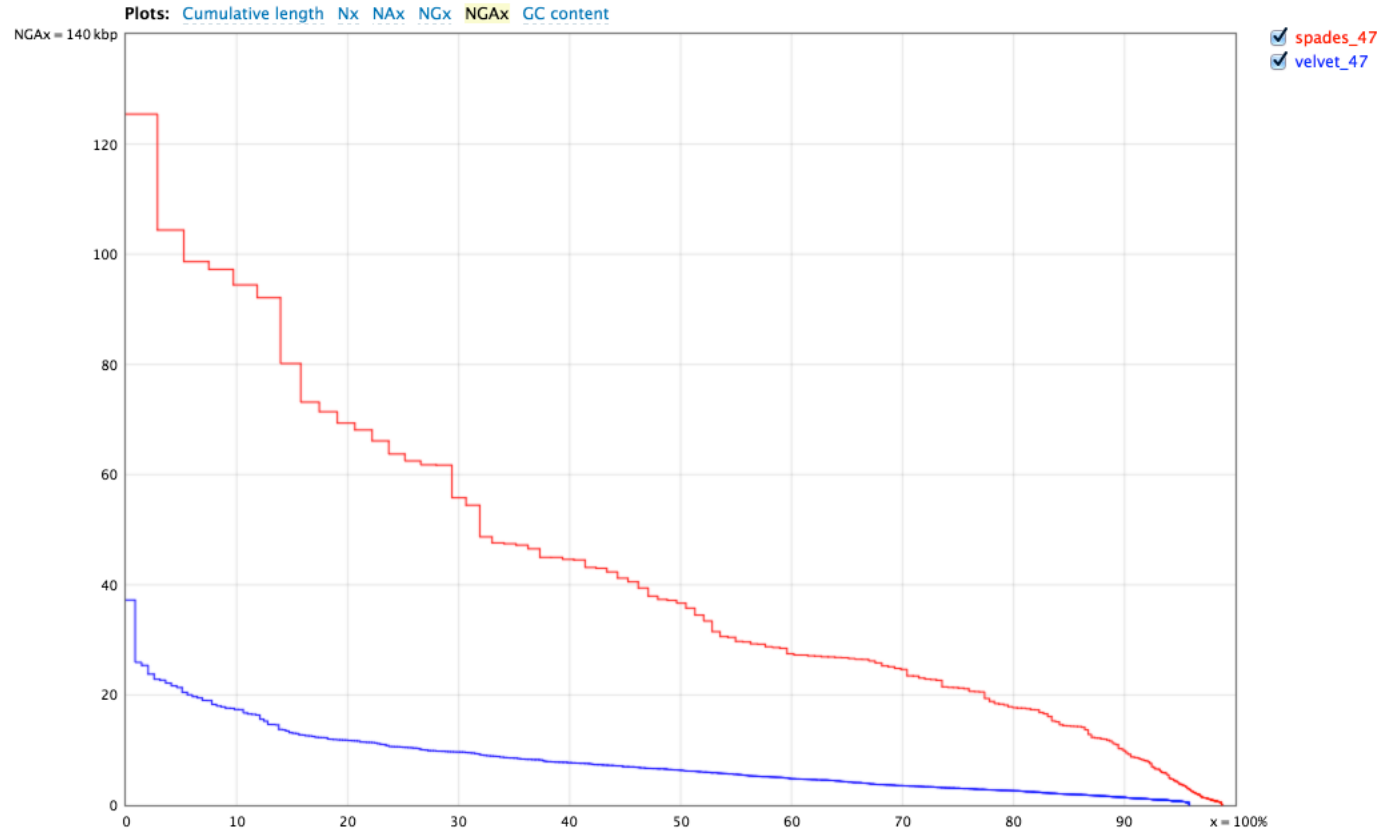
Statistics without reference	spades_47	velvet_47
# contigs	1627	1045
# contigs (>= 0 bp)	1627	1045
# contigs (>= 1000 bp)	531	874
Largest contig	125 443	37 235
Total length	5 541 211	4 248 713
Total length (>= 0 bp)	5 541 211	4 248 713
Total length (>= 1000 bp)	4 792 027	4 120 067
N50	27 266	6656
N75	5902	3379
L50	52	195
L75	137	418
GC (%)	58.52	65.27

Misassemblies		
# misassemblies	16	8
# relocations	16	8
# translocations	0	0
# inversions	0	0
# misassembled contigs	13	7
Misassembled contigs length	475 706	65 772
# local misassemblies	31	19

Unaligned		
# fully unaligned contigs	1359	9
Fully unaligned length	1 173 848	15 804
# partially unaligned contigs	12	16
# with misassembly	1	0
# both parts are significant	3	6
Partially unaligned length	15 870	16 039

Mismatches		
# mismatches	2509	2407
# indels	1303	1058
Indels length	1979	1581
# mismatches per 100 kbp	58.81	57.57
# indels per 100 kbp	30.54	25.31
# short indels (<= 5 bp)	1276	1033
# long indels (> 5 bp)	27	25
# N's	0	0
# N's per 100 kbp	0	0

Genome statistics		
Genome fraction (%)	97.292	95.23
Duplication ratio	1.022	1.009
Largest alignment	125 443	37 235
NG50	37 942	6526
NG75	23 073	3136



14,627,217	Reads
3,916	Contigs
3,916	Scaffolds
5,109	ORFs
0	Motifs