Report

	SRR5759239_assembly.scafSeq	SRR5759239_assembly.scafSeq_broken
# contigs (>= 0 bp)	206180	-
# contigs (>= 1000 bp)	60710	78472
# contigs (>= 5000 bp)	18060	12582
# contigs (>= 10000 bp)	6063	2082
# contigs (>= 25000 bp)	286	13
# contigs (>= 50000 bp)	1	0
Total length (>= 0 bp)	319316154	-
Total length (>= 1000 bp)	276060567	245437426
Total length (>= 5000 bp)	174592094	97683232
Total length (>= 10000 bp)	90616329	26654247
Total length (>= 25000 bp)	8630198	364862
Total length (>= 50000 bp)	58464	0
# contigs	84785	119664
Largest contig	58464	32297
Total length	293096881	274794774
Reference length	322899837	322899837
GC (%)	33.55	33.44
Reference GC (%)	33.73	33.73
N50	6389	3561
NG50	5642	2860
N75	3049	1792
NG75	2193	1061
L50	13105	22031
LG50	15585	29577
L75	29637	49293
LG75	38261	75304
# misassemblies	1243	594
# misassembled contigs	1174	576
Misassembled contigs length	6702382	1879270
# local misassemblies	772	414
# scaffold gap size misassemblies	8	-
# unaligned mis. contigs	215	73
# unaligned contigs	7939 + 2423 part	2745 + 721 part
Unaligned length	10177570	2997190
Genome fraction (%)	86.744	83.783
Duplication ratio	1.010	1.005
# N's per 100 kbp	888.39	36.31
# mismatches per 100 kbp	19.09	13.00
# indels per 100 kbp	40.08	11.35
Largest alignment	58464	32297
Total aligned length	281701047	271244601
NA50	6261	3528
NGA50	5508	2829
NA75	2914	1758
NGA75	2043	1026
LA50	13314	22176
LGA50	15848	29800
LA75	30357	49804
LGA75	39480	76489

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).
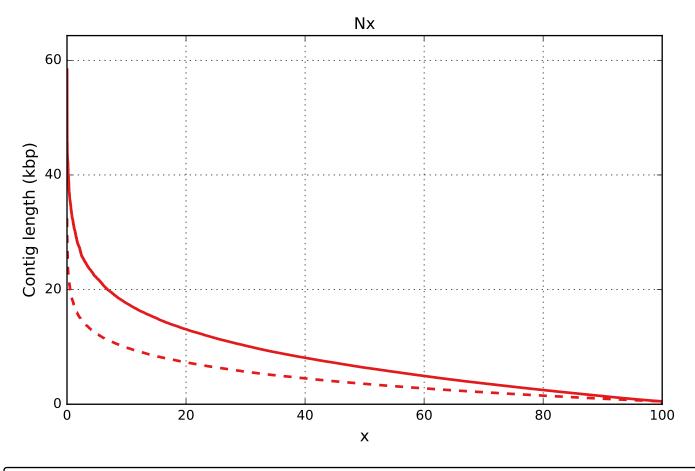
Misassemblies report

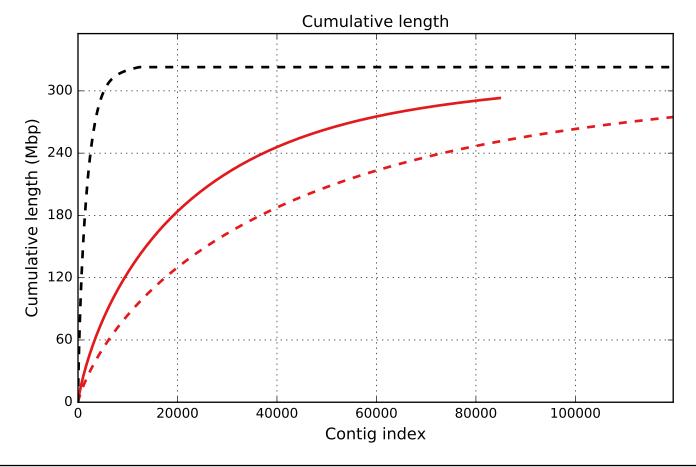|	SRR5759239_assembly.scafSeq	SRR5759239_assembly.scafSeq_broken
# misassemblies	1243	594
# relocations	75	49
# translocations	1152	533
# inversions	16	12
# misassembled contigs	1174	576
Misassembled contigs length	6702382	1879270
# local misassemblies	772	414
# scaffold gap size misassemblies	8	-
# misassemblies caused by fragmented reference	212	119
# unaligned mis. contigs	215	73
# mismatches	53457	35172
# indels	112265	30715
# indels (<= 5 bp)	51446	24515
# indels (> 5 bp)	60819	6200
Indels length	799536	102560

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).
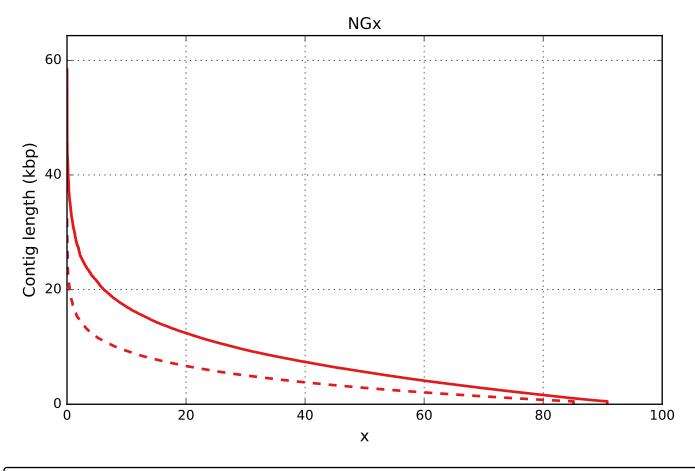
Unaligned report

	SRR5759239_assembly.scafSeq	SRR5759239_assembly.scafSeq_broken
# fully unaligned contigs	7939	2745
Fully unaligned length	7199634	2038200
# partially unaligned contigs	2423	721
Partially unaligned length	2977936	958990
# N's	2603843	99765

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).
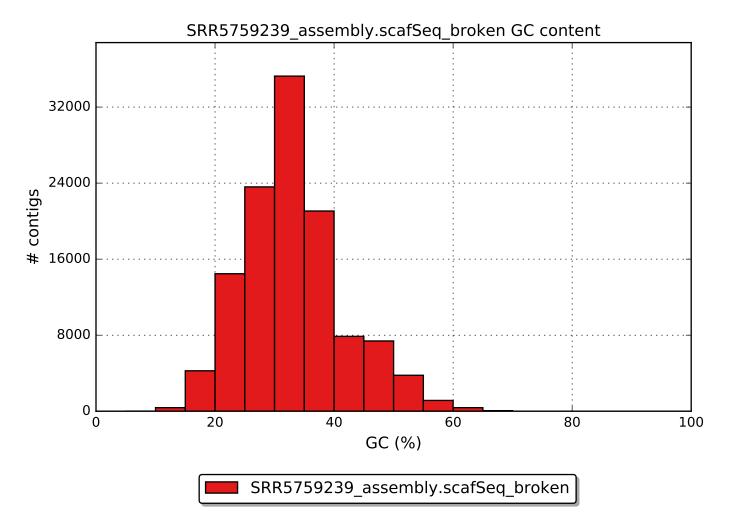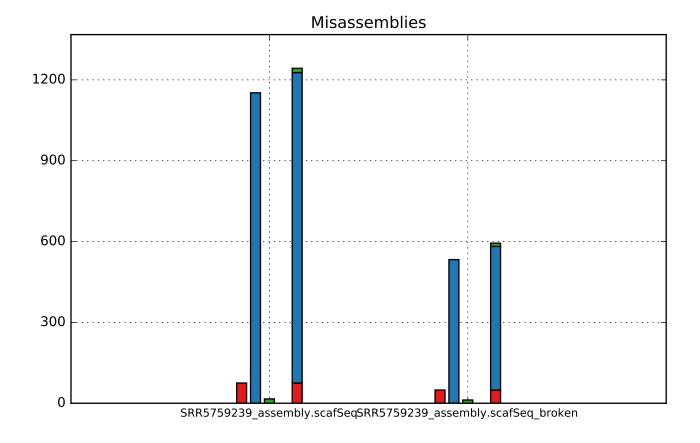
Nx

Cumulative length

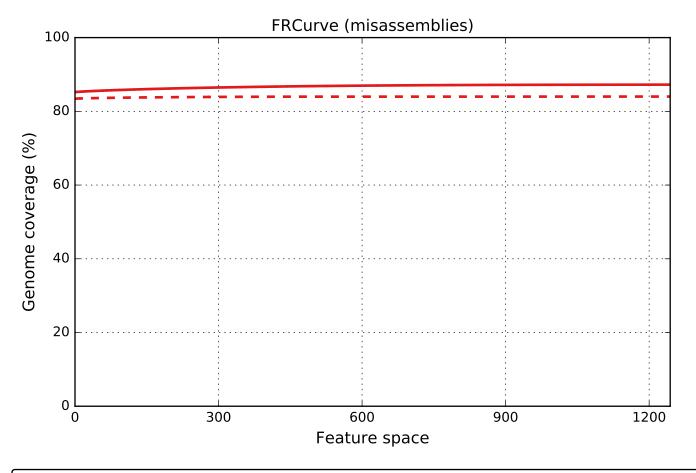SRR5759239_assembly.scafSeq — — — SRR5759239_assembly.scafSeq_broken — — Refe

GC content
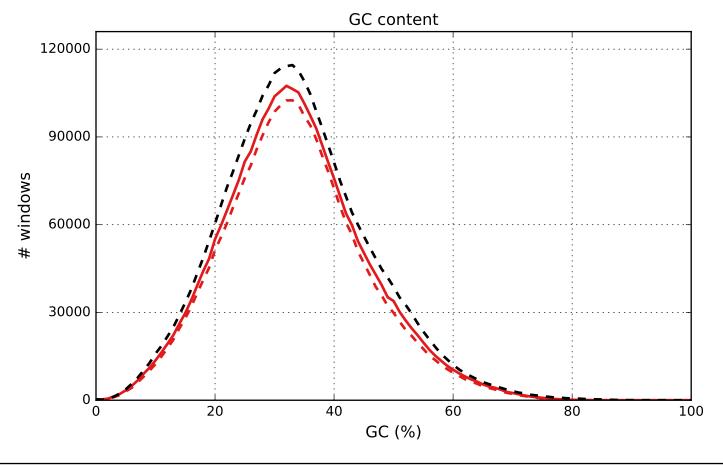
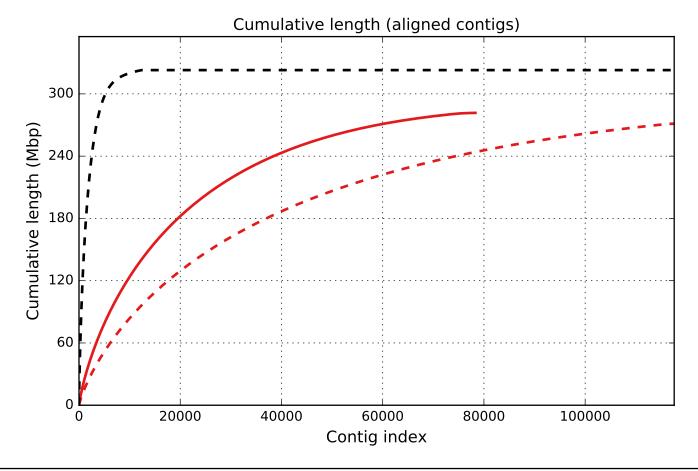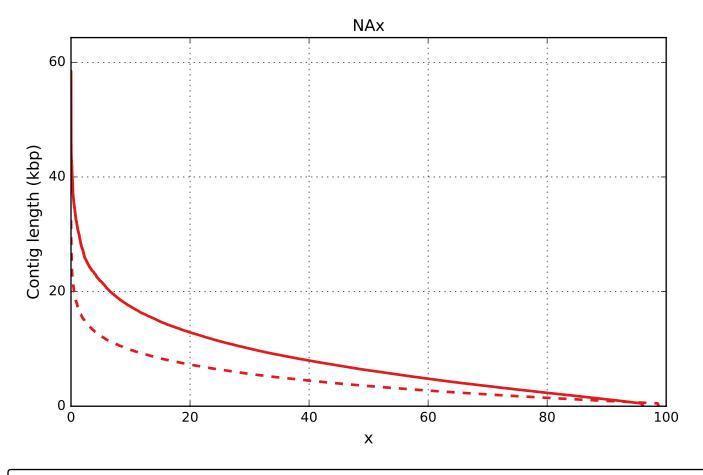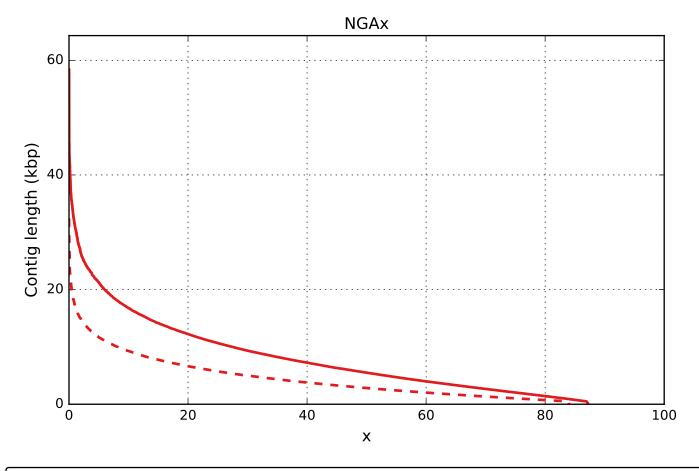SRR5759239_assembly.scafSeq   - - - SRR5759239_assembly.scafSeq_broken   - - - Refe

SRR5759239_assembly.scafSeq_broken GC content

Misassemblies

# relocations	# translocations	# inversions

SRR5759239_assembly.scafSeq SRR5759239_assembly.scafSeq_broken

FRCurve (misassemblies)

Genome coverage (%)

Feature space

SRR5759239_assembly.scafSeq

SRR5759239_assembly.scafSeq_broken

Cumulative length (aligned contigs)

| SRR5759239_assembly.scafSeq | SRR5759239_assembly.scafSeq_broken | Refe |

NAx

Genome fraction, %

SRR5759239_assembly.scafSeq   SRR5759239_assembly.scafSeq_broken