

Report

	A5-MiSeq	Canu	Falcon	Flye	Hinge	SGA	SOAPdenovo2	SPAdes
# contigs (>= 0 bp)	180	68	444	16	40	2662	13768	220
# contigs (>= 1000 bp)	165	68	444	16	40	573	458	119
# contigs (>= 5000 bp)	120	68	428	16	40	271	242	99
# contigs (>= 10000 bp)	93	30	265	15	38	140	150	81
# contigs (>= 25000 bp)	54	8	69	5	34	47	52	51
# contigs (>= 50000 bp)	27	8	21	5	28	12	20	34
Total length (>= 0 bp)	5409373	6317921	7517653	5764561	11321918	6001420	6797663	5421489
Total length (>= 1000 bp)	5397449	6317921	7517653	5764561	11321918	5234260	5402442	5384454
Total length (>= 5000 bp)	5281399	6317921	7456192	5764561	11321918	4492149	4845413	5335066
Total length (>= 10000 bp)	5096267	5947838	6215894	5755596	11305156	3550291	4202554	5214318
Total length (>= 25000 bp)	4504837	5681582	3364139	5610886	11241796	2080590	2676630	4747699
Total length (>= 50000 bp)	3569338	5681582	1621691	5610886	10995958	883738	1534944	4132854
# contigs	180	68	444	16	40	765	535	138
Largest contig	421480	1810524	211723	3779838	2012156	139809	124583	421518
Total length	5409373	6317921	7517653	5764561	11321918	5360465	5456872	5396320
Reference length	5427083	5427083	5427083	5427083	5427083	5427083	5427083	5427083
GC (%)	35.37	35.32	35.45	35.28	35.34	35.47	35.39	35.34
Reference GC (%)	35.29	35.29	35.29	35.29	35.29	35.29	35.29	35.29
N50	94223	858185	21016	3779838	821971	18848	24261	94674
NG50	94223	1271827	34235	3779838	2010834	18389	24307	94674
N75	33673	521543	11448	1269366	286971	7445	10869	53460
NG75	33673	765061	18676	1269366	822493	7156	11214	53460
L50	15	3	87	1	4	75	55	14
LG50	15	2	48	1	2	77	54	14
L75	39	5	212	2	11	195	140	33
LG75	39	4	103	2	3	202	138	33
# misassemblies	0	4	15	5	0	1	0	0
# misassembled contigs	0	4	12	1	0	1	0	0
Misassembled contigs length	0	38735	210623	197162	0	502	0	0
# local misassemblies	5	7	59	16	0	5	0	4
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0
# unaligned mis. contigs	46	40	222	6	33	92	85	42
# unaligned contigs	93 + 81 part	9 + 58 part	71 + 355 part	4 + 12 part	5 + 35 part	519 + 202 part	359 + 164 part	66 + 67 part
Unaligned length	5092430	5218627	6100753	4773331	9498606	5029037	4937005	5087952
Genome fraction (%)	5.761	18.489	17.567	17.877	21.753	5.924	5.602	5.632
Duplication ratio	1.014	1.096	1.486	1.022	1.544	1.031	1.710	1.009
# N's per 100 kbp	6.30	0.00	0.00	0.00	0.00	2.33	3920.65	14.82
# mismatches per 100 kbp	3742.19	3769.66	5210.13	3624.57	4393.86	3725.50	3812.37	3765.13
# indels per 100 kbp	37.42	28.10	70.70	26.39	143.41	33.59	32.56	32.06
Largest alignment	31356	15861	30007	63366	10569	31081	13119	31143
Total aligned length	316547	1099326	1415685	991230	1823312	329564	304717	307668
NGA50	-	-	-	-	-	-	-	-

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

	A5-MiSeq	Canu	Falcon	Flye	Hinge	SGA	SOAPdenovo2	SPAdes
# misassemblies	0	4	15	5	0	1	0	0
# contig misassemblies	0	4	15	5	0	1	0	0
# c. relocations	0	4	15	5	0	1	0	0
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0	0	0
# misassembled contigs	0	4	12	1	0	1	0	0
Misassembled contigs length	0	38735	210623	197162	0	502	0	0
# local misassemblies	5	7	59	16	0	5	0	4
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0
# unaligned mis. contigs	46	40	222	6	33	92	85	42
# mismatches	11700	37826	49672	35165	51871	11977	11590	11508
# indels	117	282	674	256	1693	108	99	98
# indels (<= 5 bp)	114	270	638	239	1687	105	96	94
# indels (> 5 bp)	3	12	36	17	6	3	3	4
Indels length	231	559	1484	622	1941	225	351	240

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

	A5-MiSeq	Canu	Falcon	Flye	Hinge	SGA	SOAPdenovo2	SPAdes
# fully unaligned contigs	93	9	71	4	5	519	359	66
Fully unaligned length	751664	146028	820032	93567	161003	1724075	1477993	636544
# partially unaligned contigs	81	58	355	12	35	202	164	67
Partially unaligned length	4340766	5072599	5280721	4679764	9337603	3304962	3459012	4451408
# N's	341	0	0	0	0	125	213945	800

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