

Report

	A5-MiSeq	Canu	Falcon	Flye	Hinge	SGA	SOAPdenovo2	SPAdes
# contigs (>= 0 bp)	33789	162	735	1827	524	465	1186	117131
# contigs (>= 1000 bp)	570	162	735	1794	512	15	10	3126
# contigs (>= 5000 bp)	33	159	586	1759	493	10	4	51
# contigs (>= 10000 bp)	13	87	235	1669	441	7	3	20
# contigs (>= 25000 bp)	3	4	9	1424	230	0	1	1
# contigs (>= 50000 bp)	1	2	2	844	26	0	1	0
Total length (>= 0 bp)	17250530	2176818	6632654	105594286	13164684	295779	332892	49355010
Total length (>= 1000 bp)	1146514	2176818	6632654	105572503	13156661	130190	139914	4700924
Total length (>= 5000 bp)	372626	2167209	6057449	105452054	13102933	120325	125140	531059
Total length (>= 10000 bp)	236906	1493337	3417479	104762790	12699783	97360	118896	318959
Total length (>= 25000 bp)	110774	525186	525853	100566467	8887158	0	89813	31938
Total length (>= 50000 bp)	55783	463046	296701	78410300	2163351	0	89813	0
# contigs	11739	162	735	1826	522	98	31	26758
Largest contig	55783	359892	191120	404821	196810	17368	89813	31938
Total length	8114295	2176818	6632654	105593896	13164381	181086	155107	20220146
Reference length	119668634	119668634	119668634	119668634	119668634	119668634	119668634	119668634
GC (%)	36.65	43.03	40.95	37.24	41.20	38.14	35.94	36.48
Reference GC (%)	36.06	36.06	36.06	36.06	36.06	36.06	36.06	36.06
N50	637	10862	10115	77106	29795	10612	89813	722
NG50	-	-	-	68321	-	-	-	-
N75	555	9909	7389	49368	22259	792	10266	590
NG75	-	-	-	39432	-	-	-	-
L50	4451	48	225	433	146	7	1	9633
LG50	-	-	-	529	-	-	-	-
L75	7876	101	412	860	272	22	3	17420
LG75	-	-	-	1097	-	-	-	-
# misassemblies	358	90	182	2569	18	0	1	7939
# misassembled contigs	351	73	120	872	4	0	1	6763
Misassembled contigs length	320794	1173616	1704418	65846606	697789	0	730	5978612
# local misassemblies	135	1458	615	17780	34	0	13	547
# scaffold gap ext. mis.	0	0	0	0	0	0	2	0
# scaffold gap loc. mis.	0	0	0	2	0	0	32	3
# unaligned mis. contigs	30	0	82	231	355	0	0	98
# unaligned contigs	188 + 30 part	0 + 7 part	1 + 167 part	1 + 1485 part	95 + 426 part	0 + 0 part	0 + 0 part	232 + 178 part
Unaligned length	145655	10361	798781	17669276	12077820	0	0	312901
Genome fraction (%)	6.496	0.500	2.785	71.501	0.520	0.151	0.119	15.989
Duplication ratio	1.027	3.624	1.753	1.029	1.748	1.005	1.093	1.042
# N's per 100 kbp	783.94	0.00	0.00	0.28	0.00	0.00	6171.22	1.58
# mismatches per 100 kbp	430.18	8266.97	1371.11	1580.49	1506.19	4.44	114.89	823.49
# indels per 100 kbp	58.28	1404.67	2084.29	1683.41	3327.83	1.11	8.46	66.97
Largest alignment	55632	103154	52449	323229	72349	17368	84661	31938
Total aligned length	7821611	1957236	5753720	87783639	1082572	181086	143517	19105410
NA50	618	8557	7414	37683	-	10612	84661	606
NGA50	-	-	-	31223	-	-	-	-
NA75	538	6056	3805	9966	-	792	6244	501
LA50	4631	70	306	791	-	7	1	11859
LGA50	-	-	-	995	-	-	-	-
LA75	8163	145	605	2014	-	22	4	21082

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	358	90	182	2569	18	0	1	7939
# contig misassemblies	358	90	182	2568	18	0	1	7939
# c. relocations	129	60	78	1460	13	0	0	2246
# c. translocations	187	30	104	1100	5	0	1	5613
# c. inversions	42	0	0	8	0	0	0	80
# scaffold misassemblies	0	0	0	1	0	0	0	0
# s. relocations	0	0	0	1	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	351	73	120	872	4	0	1	6763
Misassembled contigs length	320794	1173616	1704418	65846606	697789	0	730	5978612
# local misassemblies	135	1458	615	17780	34	0	13	547
# scaffold gap ext. mis.	0	0	0	0	0	0	2	0
# scaffold gap loc. mis.	0	0	0	2	0	0	32	3
# unaligned mis. contigs	30	0	82	231	355	0	0	98
# mismatches	33388	49425	45626	1350240	9363	8	163	157325
# indels	4523	8398	69358	1438162	20687	2	12	12794
# indels (<= 5 bp)	3831	7902	68542	1419254	20616	1	12	10828
# indels (> 5 bp)	692	496	816	18908	71	1	0	1966
Indels length	17704	20815	108603	1902449	26763	12	15	51996

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	188	0	1	1	95	0	0	232
Fully unaligned length	120181	0	4663	4544	1145948	0	0	162162
# partially unaligned contigs	30	7	167	1485	426	0	0	178
Partially unaligned length	25474	10361	794118	17664732	10931872	0	0	150739
# N's	63611	0	0	300	0	0	9572	320

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).