Report

	A5-MiSeq	Canu	Falcon	Flye	Hinge	SGA	SOAPdenovo2	SPAdes
# contigs (>= 0 bp)	36	9	2035	1	20	1632	168	79
# contigs (>= 1000 bp)	28	9	2035	1	20	49	37	33
# contigs (>= 5000 bp)	21	9	1934	1	20	40	24	25
# contigs (>= 10000 bp)	21	4	510	1	20	35	22	24
# contigs (>= 25000 bp)	20	1	4	1	18	30	21	21
# contigs (>= 50000 bp)	15	1	0	1	12	18	15	16
Total length (>= 0 bp)	2799146	2996962	17835328	2896520	5944427	3309657	2917604	2797545
Total length (>= 1000 bp)	2793070	2996962	17835328	2896520	5944427	2776426	2894112	2780900
Total length (>= 5000 bp)	2776324	2996962	17451865	2896520	5944427	2752582	2863170	2762168
Total length (>= 10000 bp)	2776324	2948460	6655923	2896520	5944427	2716862	2844483	2754268
Total length (>= 25000 bp)	2759350	2907970	113813	2896520	5905258	2626527	2833517	2697403
Total length (>= 50000 bp)	2571882	2907970	0	2896520	5723931	2183412	2612477	2496997
# contigs	36	9	2035	1	20	81	41	40
Largest contig	450615	2907970	35416	2896520	1311967	346827	424112	406941
Total length	2799146	2996962	17835328	2896520	5944427	2797127	2896877	2784943
Reference length	2821361	2821361	2821361	2821361	2821361	2821361	2821361	2821361
GC (%)	32.69	32.73	33.21	32.74	32.73	32.66	32.69	32.66
Reference GC (%)	32.87	32.87	32.87	32.87	32.87	32.87	32.87	32.87
N50	244991	2907970	9071	2896520	927032	109236	180321	174162
NG50	177125	2907970	15602	2896520	1311923	109236	180321	174162
N75	108646	2907970	7124	2896520	925015	56713	127759	108187
NG75	107881	2907970	14275	2896520	1311923	56713	127759	108187
L50	4	1	746	1	3	8	5	6
LG50	5	1	76	1	2	8	5	6
L75	9	1	1304	1	4	17	10	11
LG75	10	1	124	1	2	17	10	11
# misassemblies	67	59	2112	54	102	47	29	54
# misassembled contigs	19	5	1306	1	13	22	14	16
Misassembled contigs length	2657100	2948842	11291289	2896520	5571626	2178929	2197596	2442882
# local misassemblies	92	30	182	30	97	85	57	87
# scaffold gap ext. mis.	0	0	0	0	0	2	23	0
# scaffold gap loc. mis.	0	0	0	0	0	32	749	4
# unaligned mis. contigs	2	2	97	0	1	1	2	4
# unaligned contigs	2 + 18 part	0 + 5 part	23 + 573 part	0 + 1 part	0 + 19 part	17 + 28 part	5 + 24 part	7 + 22 part
Unaligned length	277097	303026	2227431	274608	634601	279926	315386	277825
Genome fraction (%)	88.836	92.505	89.225	92.502	92.561	88.509	86.544	88.562
Duplication ratio	1.006	1.032	6.200	1.005	2.033	1.008	1.057	1.003
# N's per 100 kbp	1.43	0.00	0.00	0.00	0.00	54.52	4749.56	28.73
# mismatches per 100 kbp	1393.76	204.49	1583.09	192.50	592.39	1392.58	1251.78	1390.06
# indels per 100 kbp	49.19	14.52	867.97	11.57	1126.30	48.29	41.24	48.11
Largest alignment	171163	329791	24089	329938	323857	171354	259183	171154
Total aligned length	2518098	2692695	15571683	2618043	5303669	2509007	2442671	2504468
NA50	72014	92196	4915	92541	91667	54884	91655	72014
NGA50	72014	92541	11704	92541	151987	54884	103869	72014
NA75	23621	42503	2200	54665	42243	22215	29124	23621
NGA75	23441	56976	10376	56975	113990	21757	32466	22340
LA50	13	9	1150	8	20	14	11	13
LGA50	13	8	101	8	6	14	10	13
LA75	30	21	2471	19	44	35	25	30
LGA75	31	18	164	18	11	36	23	31

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	67	59	2112	54	102	47	29	54
# contig misassemblies	67	59	2112	54	102	46	25	54
# c. relocations	67	59	2106	54	102	46	25	54
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	0	6	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	1	4	0
# s. relocations	0	0	0	0	0	1	4	0
# s. translocations	0	0	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0	0	0
# misassembled contigs	19	5	1306	1	13	22	14	16
Misassembled contigs length	2657100	2948842	11291289	2896520	5571626	2178929	2197596	2442882
# local misassemblies	92	30	182	30	97	85	57	87
# scaffold gap ext. mis.	0	0	0	0	0	2	23	0
# scaffold gap loc. mis.	0	0	0	0	0	32	749	4
# unaligned mis. contigs	2	2	97	0	1	1	2	4
# mismatches	34933	5337	39852	5024	15470	34775	30565	34733
# indels	1233	379	21850	302	29413	1206	1007	1202
# indels (<= 5 bp)	1096	320	21370	249	29151	1079	887	1068
# indels (> 5 bp)	137	59	480	53	262	127	120	134
Indels length	6182	2594	38106	2439	39620	5707	6910	5656

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	2	0	23	0	0	17	5	7
Fully unaligned length	3052	0	188293	0	0	24149	9944	7580
# partially unaligned contigs	18	5	573	1	19	28	24	22
Partially unaligned length	274045	303026	2039138	274608	634601	255777	305442	270245
# N's	40	0	0	0	0	1525	137589	800

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).