Report

	A5-MiSeq	Canu	Falcon	Flye	Hinge	SGA	SOAPdenovo2	SPAdes
# contigs (>= 0 bp)	269	94	1643	24	36	3100	513	4628
# contigs (>= 1000 bp)	95	94	1643	24	36	64	64	116
# contigs (>= 5000 bp)	48	37	570	21	34	45	45	54
# contigs (>= 10000 bp)	44	13	154	19	30	43	42	50
# contigs (>= 25000 bp)	36	7	1	17	24	37	34	39
# contigs (>= 50000 bp)	25	7	0	13	18	25	23	25
Total length (>= 0 bp)	5015104	6490458	8231817	6009857	12075001	5577454	4948352	6372846
Total length (>= 1000 bp)	4924024	6490458	8231817	6009857	12075001	4769496	4867600	4964108
Total length (>= 5000 bp)	4839317	6353252	4882143	6002142	12066081	4730465	4823884	4857263
Total length (>= 10000 bp)	4811851	6123297	1915330	5988393	12034026	4717235	4804789	4824223
Total length (>= 25000 bp)	4669860	6034873	26322	5962021	11955498	4614662	4679427	4636040
Total length (>= 50000 bp)	4294196	6034873	0	5806329	11743430	4204850	4330934	4147535
# contigs	173	94	1643	24	36	114	79	413
Largest contig	860190	4056254	26322	1397046	3358761	921377	1119057	663877
Total length	4976411	6490458	8231817	6009857	12075001	4804081	4877207	5152629
Reference length	4641652	4641652	4641652	4641652	4641652	4641652	4641652	4641652
GC (%)	50.50	50.55	49.78	50.62	50.47	50.64	50.68	50.19
Reference GC (%)	50.79	50.79	50.79	50.79	50.79	50.79	50.79	50.79
N50	197188	4056254	6143	1072054	3356412	196903	216146	196647
NG50	207510	4056254	9582	1349247	3358761	196903	216146	196831
N75	101214	1463536	3589	373741	593881	97720	109091	63517
NG75	104814	4056254	7236	1072054	3356412	102171	118983	104772
L50	8	1	431	3	2	7	6	9
LG50	7	1	196	2	1	7	6	8
L75	17	2	878	5	5	17	15	20
LG75	15	1	336	3	2	16	13	16
# misassemblies	84	196	248	182	382	84	88	81
# misassembled contigs	25	2	213	7	8	29	24	27
Misassembled contigs length	3821080	5519790	1352885	5203316	10800358	3972919	4007224	3892304
# local misassemblies	133	196	212	193	510	127	125	130
# scaffold gap ext. mis.	0	0	0	0	0	3	5	1
# scaffold gap loc. mis.	0	0	0	0	0	20	63	6
# unaligned mis. contigs	8	4	41	6	10	5	3	3
# unaligned contigs	96 + 41 part	82 + 12 part	375 + 333 part	9 + 15 part	18 + 18 part	51 + 40 part	22 + 36 part	350 + 41 part
Unaligned length	725326	2276970	3041859	1805354	3706173	553879	616906	917454
Genome fraction (%)	91.246	89.572	48.749	89.557	89.623	91.188	90.968	91.082
Duplication ratio	1.004	1.013	2.294	1.011	2.012	1.004	1.009	1.002
# N's per 100 kbp	2.35	0.00	0.00	0.00	0.00	60.89	636.51	20.82
# mismatches per 100 kbp	1241.84	2234.66	4872.38	2232.85	4602.26	1241.69	1236.00	1238.66
# indels per 100 kbp	19.17	31.48	160.07	31.92	673.92	20.22	18.80	18.50
Largest alignment	194019	146928	20252	146930	147472	193965	194101	193904
Total aligned length	4238262	4211826	5152719	4201449	8360148	4237989	4227658	4224949
NA50	46684	24795	2499	28464	28410	52805	54887	41435
NGA50	55105	51958	4511	51984	72928	55100	55987	52593
NA75	19789	-	-	-	-	24799	24068	17352
NGA75	25176	18841	3042	18280	64443	26769	26728	25233
LA50	28	58	864	50	102	26	26	31
LGA50	24	31	317	31	25	24	24	25
LA75	69	-	-	-	-	62	63	77
LGA75	58	68	635	70	42	57	56	59

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	84	196	248	182	382	84	88	81
# contig misassemblies	84	196	248	182	382	80	79	81
# c. relocations	84	194	233	180	378	80	79	81
# c. translocations	0	0	0	0	0	0	0	0
# c. inversions	0	2	15	2	4	0	0	0
# scaffold misassemblies	0	0	0	0	0	4	9	0
# s. relocations	0	0	0	0	0	4	9	0
# s. translocations	0	0	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0	0	0
# misassembled contigs	25	2	213	7	8	29	24	27
Misassembled contigs length	3821080	5519790	1352885	5203316	10800358	3972919	4007224	3892304
# local misassemblies	133	196	212	193	510	127	125	130
# scaffold gap ext. mis.	0	0	0	0	0	3	5	1
# scaffold gap loc. mis.	0	0	0	0	0	20	63	6
# unaligned mis. contigs	8	4	41	6	10	5	3	3
# mismatches	52596	92909	110250	92818	191453	52556	52189	52367
# indels	812	1309	3622	1327	28035	856	794	782
# indels (<= 5 bp)	702	1129	3409	1147	27511	691	657	674
# indels (> 5 bp)	110	180	213	180	524	165	137	108
Indels length	3905	7132	9606	7149	44779	7566	5327	3715

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	96	82	375	9	18	51	22	350
Fully unaligned length	236146	451545	1870266	165451	350499	56900	117911	432044
# partially unaligned contigs	41	12	333	15	18	40	36	41
Partially unaligned length	489180	1825425	1171593	1639903	3355674	496979	498995	485410
# N's	117	0	0	0	0	2925	31044	1073

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).