

Report

	A5-MiSeq	Canu	Falcon	Flye	Hinge	SOAPdenovo2	SPAdes
# contigs (>= 0 bp)	670	193	490	26	110	3269	2296
# contigs (>= 1000 bp)	263	193	490	26	108	179	216
# contigs (>= 5000 bp)	194	192	450	25	98	85	158
# contigs (>= 10000 bp)	164	134	395	24	83	79	141
# contigs (>= 25000 bp)	127	24	0	17	56	69	113
# contigs (>= 50000 bp)	86	21	0	16	44	55	82
Total length (>= 0 bp)	11671453	13845950	5954290	11946912	24111267	12274946	11872041
Total length (>= 1000 bp)	11504571	13845950	5954290	11946912	24109373	11681721	11473203
Total length (>= 5000 bp)	11349731	13844168	5803075	11942578	24088124	11502035	11357435
Total length (>= 10000 bp)	11139995	13277307	5371274	11935439	23963787	11458780	11239996
Total length (>= 25000 bp)	10489093	11935367	0	11841555	23569944	11301669	10780243
Total length (>= 50000 bp)	9029598	11829072	0	11814963	23063509	10778353	9602639
# contigs	369	193	490	26	110	293	313
Largest contig	292060	1478515	23227	2780383	1257300	732381	381132
Total length	11574768	13845950	5954290	11946912	24111267	11757938	11537298
Reference length	12157105	12157105	12157105	12157105	12157105	12157105	12157105
GC (%)	38.12	36.20	27.58	38.19	37.98	38.13	38.14
Reference GC (%)	38.15	38.15	38.15	38.15	38.15	38.15	38.15
N50	91325	710827	13483	904913	741619	234358	114579
NG50	87302	789964	-	904738	1015480	234358	109730
N75	55570	306222	10966	582519	448567	127984	71275
NG75	46980	468588	-	581583	873673	118105	60166
L50	39	7	187	4	13	17	35
LG50	42	6	-	5	6	17	38
L75	80	15	309	8	23	33	66
LG75	88	11	-	9	9	35	74
# misassemblies	71	201	258	172	256	55	59
# misassembled contigs	54	56	185	19	38	38	44
Misassembled contigs length	3412296	12310009	2298037	11867823	22128895	5828068	3606168
# local misassemblies	99	1737	2069	266	1375	108	97
# scaffold gap ext. mis.	0	0	0	0	0	19	0
# scaffold gap loc. mis.	7	0	0	0	0	1182	55
# unaligned mis. contigs	14	20	121	0	37	7	3
# unaligned contigs	39 + 29 part	1 + 107 part	3 + 284 part	0 + 22 part	22 + 87 part	9 + 38 part	58 + 23 part
Unaligned length	123547	597175	1791268	227578	2087885	114381	136939
Genome fraction (%)	93.834	95.269	3.176	94.704	93.224	93.195	93.518
Duplication ratio	1.004	1.144	10.781	1.018	1.943	1.028	1.003
# N's per 100 kbp	53.02	0.00	0.00	0.84	0.00	2345.32	67.08
# mismatches per 100 kbp	558.89	1086.87	18909.55	654.21	1705.73	565.56	579.34
# indels per 100 kbp	50.67	140.03	3980.23	97.04	4340.36	53.00	49.20
Largest alignment	238989	546941	17395	546784	532988	538406	328324
Total aligned length	11422884	13088915	4111569	11700248	22012911	11406775	11377122
NA50	77574	160884	3172	230022	195155	149088	102238
NGA50	72006	199769	-	218721	337524	147545	93828
NA75	40615	66277	-	106580	98465	89197	54784
NGA75	36340	102623	-	103353	253095	78368	45331
LA50	48	24	406	18	38	23	41
LGA50	52	19	-	19	15	24	44
LA75	98	56	-	38	83	48	79
LGA75	109	41	-	40	25	52	89

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	SOAPdenovo2	SPAdes
# misassemblies	71	201	258	172	256	55	59
# contig misassemblies	69	201	258	172	256	45	58
# c. relocations	53	84	217	59	110	39	50
# c. translocations	16	115	41	110	144	6	8
# c. inversions	0	2	0	3	2	0	0
# scaffold misassemblies	2	0	0	0	0	10	1
# s. relocations	0	0	0	0	0	0	0
# s. translocations	2	0	0	0	0	10	1
# s. inversions	0	0	0	0	0	0	0
# misassembled contigs	54	56	185	19	38	38	44
Misassembled contigs length	3412296	12310009	2298037	11867823	22128895	5828068	3606168
# local misassemblies	99	1737	2069	266	1375	108	97
# scaffold gap ext. mis.	0	0	0	0	0	19	0
# scaffold gap loc. mis.	7	0	0	0	0	1182	55
# unaligned mis. contigs	14	20	121	0	37	7	3
# mismatches	63755	125881	73016	75321	193317	64077	65866
# indels	5780	16218	15369	11172	491909	6005	5594
# indels (<= 5 bp)	4837	14173	13116	10240	489169	4393	4771
# indels (> 5 bp)	943	2045	2253	932	2740	1612	823
Indels length	26311	66525	55717	33316	643504	68413	22641

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	SOAPdenovo2	SPAdes
# fully unaligned contigs	39	1	3	0	22	9	58
Fully unaligned length	38622	1782	48343	0	150873	10420	48546
# partially unaligned contigs	29	107	284	22	87	38	23
Partially unaligned length	84925	595393	1742925	227578	1937012	103961	88393
# N's	6137	0	0	100	0	275761	7739

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