

PacBio Metrics	PkNOH_pre_Hi-C
SMRT cell Number	6
Mapped Subread Bases	3,724,074,640
Average Coverage	144
Mapped Subreads	436,541
Mapped Subreads N50	13,220
Polished Contigs	56
Contigs Coverage >50	35
Max Contig Length	2,476,829
N50 Contig Length	1,207,278
Sum of Contig Length	24,938,209

Supplementary Table 1 - Statistics of HGAP3 assembly output. Note: these data still contain host and organellar DNA contaminants.

PacBio Unitig	Length	Scaffold Assignment
unitig_18_chr1	914,168	scf1
unitig56	14,772	scf2
unitig_23_chr3	719,235	
unitig_30_chr3	345,602	
unitig_0_chr6	489,988	scf3
unitig_3_chr6	606,307	
unitig_12_chr5_13	1,360,573	scf4
unitig_10_chr13	1,435,464	scf5
unitig_15_chr7	1,207,278	scf6
unitig_31_chr7	323,894	
unitig_96_chr11	13,068	scf7
unitig_7_chr10	1,543,775	
unitig_25_chr13	593,400	scf8
unitig45	2,418	
unitig_36_chr4	292,580	
unitig_20_chr4	832,288	
unitig_22_chr2	669,228	scf9
unitig_39_chr2	146,901	
unitig_16_chr12	1,016,298	
unitig_13_chr8	226,016	scf10
unitig_0_chr8	1,066,829	
unitig_35_chr8	268,932	
unitig_34_chr8	9,837	
unitig_32_chr8	410,932	
unitig_2_chr12	1,267,252	scf11
unitig_0_chr12	889,998	
unitig52	21,891	
unitig_1_chr9	2,187,873	scf12
unitig_17_chr11	980,536	scf13
unitig_9_chr11	422,355	
unitig_37_chr11	207,973	
unitig_105_chr11	5,212	
unitig_21_chr11	612,914	
unitig_38_chr11	170,838	
unitig_26_chr14	586,198	scf14
unitig_43_chr14	17,326	
unitig_4_chr14	1,880,748	
unitig_33_chr14	298,116	
unitig_28_chr14	532,183	

Supplementary Table 2 – Contig to scaffold mapping after the addition of Hi-C. PacBio HGAP unitig names are followed by *P. knowlesi* published (PKNH) reference chromosome to which the unitig sequence shares the greatest similarity, e.g. “chr14”.

Scaffold	Consensus Sequence 5' -> 3'	Copy Number
1 (L)	CCCTAAA	345.4
1 (R)	TTCTTTCTTCATTCTTCCTTCCTTAAACC	142.9
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	AAGGA	---
		106.2
2 (L)	GGGGAAGGAAAGAAGGAAGGTTGAG	40.5
2 (L)	GGGTTTA	106.3
3 (L)	AAACCCT	390.9
4 (R)	GGTTTAG	102.4
6 (L)	CCCTAAA	155.0
6 (R)	GGGTTTA	251.4
7 (L)	AGAAAAGA	34.4
7 (R)	CTTTCCTTACCCCTAAGTAGT	33.8
8 (L)	AAACCCT	359.9
8 (R)	TTACTCTTCCTTCTT	59.9
9 (L)	AGGAAAGACTACTTAGGGGTA	72.9
10 (R)	CTTTTTCTTCCTTCCTTAAACCATT	65.8
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	CTTCTTTACTCTTC	---
		60.6
11 (L)	AGACTACTTAGGGGTAAGGAA	31.7
11 (R)	AAGGTTGTAAGGGTGTTAGAAT	165.3
12 (L)	CCCTAAA	563.1
13 (R)	GGGTTTA	107.3
14 (L)	AAAGG	111.2
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	GGGGTAAGGAAAGACTACTTA	---
		125.9

Supplementary Table 3. Sub-telomere Tandem Repeats Analysis. (L) and (R) indicate left and right sub-telomeres of scaffolds as ordered in the assembly. Typical *Plasmodium* telomere repeats were identified on nine scaffolds (bold).