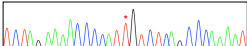
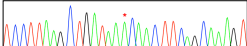
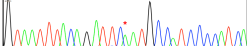
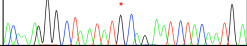
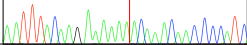
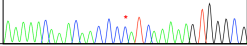
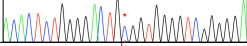
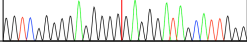
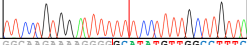
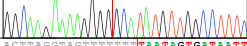
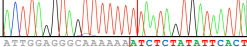
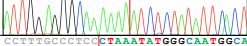
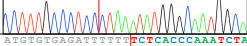
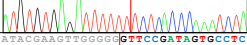
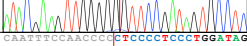
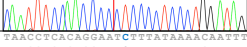
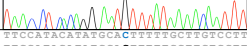
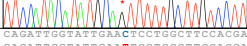
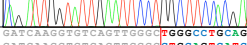
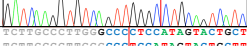
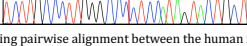


Mismatch location	Mismatch defined following pairwise comparison of Canu assembled reads to the human reference genome (hg19)	Proportion of each nucleotide at SNV sites (determined from aligned nanopore reads)	Sanger sequencing validation	Final result
1	Deletion of 10 "T" nts from a 24 nt poly(T) tract			Sanger sequencing failed; variant unconfirmed
2	SNV	Chr13:49,043,803 T: 1208 (95%) A: 18 (1%) C: 39 (3%) Ref G: 4 (0%) Total: 1269 (100%)	Reference: TCTAGAAAACCCCATCTCTCAGCCCAAAT Assembly: TCTAGAAAACCCCATCTCTCAGCCCAAAT Sanger: TCTAGAAAACCCCATCTCTCAGCCCAAAT 	SNV confirmed
3	SNV	Chr13:49,043,835 T: 6 (0%) A: 1193 (95.0%) C: 4 (0%) G: 54 (4%) Ref Total: 1257 (100%)	Reference: TCCTTAGCTGATTAACCACTTACGCAAAAT Assembly: TCCTTAGCTGATTAACCACTTACGCAAAAT Sanger: TCCTTAGCTGATTAACCACTTACGCAAAAT 	SNV confirmed
4	SNV	Chr13:49,044,143 T: 5 (0%) A: 1211 (97%) C: 8 (1%) G: 23 (2%) Ref Total: 1247 (100%)	Reference: GTAATTTACAGATTGATGCCATCCCCATCA Assembly: GTAATTTACAGATTGATGCCATCCCCATCA Sanger: GTAATTTACAGATTGATGCCATCCCCATCA 	SNV confirmed
5	SNV	Chr13:49,044,819 T: 5 (0%) A: 44 (4%) C: 59 (5%) Ref G: 1081 (91%) Total: 1189 (100%)	Reference: ACAAAAGGCTAATATCCAGAATCTACAATGA Assembly: ACAAAAGGCTAATATCCAGAATCTACAATGA Sanger: ACAAAAGGCTAATATCCAGAATCTACAATGA 	SNV confirmed
6	Insertion of "AAC" into a 7 nt poly(A) tract		Reference: AATTTACAGAAAAACAACCCATCAAAA Assembly: AATTTACAGAAAAACAACCCATCAAAA Sanger: AATTTACAGAAAAACAACCCATCAAAA 	Poly(A) tract length undercalled by a single "A" nucleotide. Inserted non-ref "C" correctly identified.
7	SNV	Chr13:49,044,867 T: 189 (16%) Ref A: 2 (0%) C: 1020 (84%) G: 8 (1%) Total: 1219 (100%)	Reference: AGAAAAACAACCCATCAAAAAGTGGCG Assembly: AAAAAACAACCCATCAAAAAGTGGCG Sanger: AAAAAACAACCCATCAAAAAGTGGCG 	SNV confirmed
8	SNV	Chr13:49,045,543 T: 297 (25%) Ref A: 30 (3%) C: 818 (70%) G: 30 (3%) Total: 1175 (100%)	Reference: ACACCTCTGGGACTGCGGTGGGTGGGGGA Assembly: ACACCTCTGGGACTGCGGTGGGTGGGGGA Sanger: ACACCTCTGGGACTGCGGTGGGTGGGGGA 	SNV confirmed
9	Deletion of a single "G" nt from a 6 nt poly(G) tract		Reference: GGTCTGGGGAGGGGGAGGGATAGCATTGGG Assembly: GGTCTGGGGAGGGGGAGGGATAGCATTGGG Sanger: GGTCTGGGGAGGGGGAGGGATAGCATTGGG 	Poly(G) tract length undercalled by a single "G" nucleotide
10	Insertion of "TAAAAA" into a 14 nt poly(A) tract			Sanger sequencing failed; variant unconfirmed
11	Deletion of a single "T" nt from a 7 nt poly(T) tract		Reference: TTCCTGTGGATTTTTTCCTTTGCTGTTA Assembly: TTCCTGTGGATTTTTTCCTTTGCTGTTA Sanger: TTCCTGTGGATTTTTTCCTTTGCTGTTA 	Poly(T) tract length undercalled by a single "T" nucleotide
12	Deletion of a single "G" nt from a 5 nt poly(G) tract		Reference: GGCAAGAAAAGGGGCGATAGTTGGCCTTTC Assembly: GGCAAGAAAAGGGGCGATAGTTGGCCTTTC Sanger: GGCAAGAAAAGGGGCGATAGTTGGCCTTTC 	Poly(G) tract length undercalled by a single "G" nucleotide
13	Deletion of a single "T" nt from an 8 nt poly(T) tract		Reference: ACTTAGGTAGTTTTTAAATAGTATAATT Assembly: ACTTAGGTAGTTTTTAAATAGTATAATT Sanger: ACTTAGGTAGTTTTTAAATAGTATAATT 	Poly(T) tract length undercalled by a single "T" nucleotide
14	Deletion of a single "A" nt from a 7 nt poly(A) tract		Reference: ATTGGAGGGCAAAAATCTCTATATCACT Assembly: ATTGGAGGGCAAAAATCTCTATATCACT Sanger: ATTGGAGGGCAAAAATCTCTATATCACT 	Poly(A) tract length undercalled by a single "A" nucleotide
15	Deletion of a single "C" nt from a 3 nt poly(C) tract		Reference: CCTTTGCCCTCCCTAAATATGGGCAATGGCA Assembly: CCTTTGCCCTCCCTAAATATGGGCAATGGCA Sanger: CCTTTGCCCTCCCTAAATATGGGCAATGGCA 	Poly(C) tract length undercalled by a single "C" nucleotide
16	Deletion of a single "T" nt from a 7 nt poly(T) tract		Reference: ATGTGTGAGATTTTTTCTCACCCAAATCTA Assembly: ATGTGTGAGATTTTTTCTCACCCAAATCTA Sanger: ATGTGTGAGATTTTTTCTCACCCAAATCTA 	Poly(T) tract length undercalled by a single "T" nucleotide
17	Deletion of a single "G" nt from a 6 nt poly(G) tract		Reference: ATACGAATTTGGGGGTTCCGATAGTGCCTC Assembly: ATACGAATTTGGGGGTTCCGATAGTGCCTC Sanger: ATACGAATTTGGGGGTTCCGATAGTGCCTC 	Poly(G) tract length undercalled by a single "G" nucleotide
18	Deletion of a single "C" nt from a 5 nt poly(C) tract		Reference: CAATTTCCAAACCCCTCCCTCCCTGGATAG Assembly: CAATTTCCAAACCCCTCCCTCCCTGGATAG Sanger: CAATTTCCAAACCCCTCCCTCCCTGGATAG 	Poly(C) tract length undercalled by a single "C" nucleotide
19	SNV	Chr13:49,048,628 T: 39 (3%) A: 24 (2%) C: 58 (5%) Ref G: 1146 (90%) Total: 1267 (100%)	Reference: FAACCTCACAGGAATCTTTATAAAACAATTT Assembly: FAACCTCACAGGAATCTTTATAAAACAATTT Sanger: FAACCTCACAGGAATCTTTATAAAACAATTT 	SNV confirmed
20	SNV	Chr13:49,048,757 T: 76 (8%) A: 10 (1%) C: 92 (9%) Ref G: 828 (82%) Total: 1006 (100%)	Reference: TTCATACATATGACATTTTTGCTTGCCTT Assembly: TTCATACATATGACATTTTTGCTTGCCTT Sanger: TTCATACATATGACATTTTTGCTTGCCTT 	SNV confirmed
21	SNV	Chr13:49,049,232 T: 945 (83%) A: 19 (2%) C: 170 (15%) Ref G: 8 (1%) Total: 1142 (100%)	Reference: CAGATTGGTATGAACTCCCTGGCTTCCACGA Assembly: CAGATTGGTATGAACTCCCTGGCTTCCACGA Sanger: CAGATTGGTATGAACTCCCTGGCTTCCACGA 	SNV confirmed
22	Deletion of "TGGGC"; not from within a poly(N) tract	Chr13:49,049,490_49,049,494 Deleted: 916 (71%) Non-deleted: 381 (29%)	Reference: GATCAAGGTGTCAAGTGGGCTGGGCTGCAG Assembly: GATCAAGGTGTCAAGTGGGCTGGGCTGCAG Sanger: GATCAAGGTGTCAAGTGGGCTGGGCTGCAG 	Deletion confirmed
23	Deletion of a single "C" nt from a 4 nt poly(C) tract		Reference: TCTTGCCTTTGGGCCCTCCATAGTACTGCT Assembly: TCTTGCCTTTGGGCCCTCCATAGTACTGCT Sanger: TCTTGCCTTTGGGCCCTCCATAGTACTGCT 	Poly(C) tract length undercalled by a single "C" nucleotide

Supplementary Figure 3: Sanger sequencing validation of mismatched nucleotides identified following pairwise alignment between the human reference sequence and Canu-generated consensus assembly. Mismatch locations correspond to the annotated sites in Supplementary Figure 2.