RESEARCH NOTE

Long read nanopore sequencing for detection of *HLA* and *CYP2D6* variants and haplotypes [version 1; peer review: 2 approved]

Ron Ammar¹, Tara A. Paton², Dax Torti¹, Adam Shlien³, Gary D. Bader^{id}1,4,5

¹The Donnelly Centre, University of Toronto, Toronto, ON, M5S3E1, Canada

²The Centre for Applied Genomics, The Hospital for Sick Children, Toronto, ON, M5G0A4, Canada

³Department of Laboratory Medicine and Pathobiology, University of Toronto; Program in Genetics and Genome Biology & Department of Paediatric Laboratory Medicine The Hospital for Sick Children, Toronto, ON, M5G1X8, Canada

⁴Department of Computer Science, University of Toronto, Toronto, ON, M5S3G4, Canada

⁵Department of Molecular Genetics, University of Toronto, Toronto, ON, M5S1A8, Canada

V1 First published: 21 Jan 2015, 4:17
<https://doi.org/10.12688/f1000research.6037.1>
 Latest published: 20 May 2015, 4:17
<https://doi.org/10.12688/f1000research.6037.2>

Abstract

Haplotypes are often critical for the interpretation of genetic laboratory observations into medically actionable findings. Current massively parallel DNA sequencing technologies produce short sequence reads that are often unable to resolve haplotype information. Phasing short read data typically requires supplemental statistical phasing based on known haplotype structure in the population or parental genotypic data. Here we demonstrate that the MinION nanopore sequencer is capable of producing very long reads to resolve both variants and haplotypes of *HLA-A*, *HLA-B* and *CYP2D6* genes important in determining patient drug response in sample NA12878 of CEPH/UTAH pedigree 1463, without the need for statistical phasing. Long read data from a single 24-hour nanopore sequencing run was used to reconstruct haplotypes, which were confirmed by HapMap data and statistically phased Complete Genomics and Sequenom genotypes. Our results demonstrate that nanopore sequencing is an emerging standalone technology with potential utility in a clinical environment to aid in medical decision-making.

Keywords

nanopore , DNA , sequencing , haplotype , pharmacogenomics

This article is included in the Nanopore Analysis gateway.

Open Peer Review

Approval Status

	1	2
version 2		
(revision)		
20 May 2015	view	
version 1		
21 Jan 2015	view	view

1. **Martin Kennedy**, University of Otago, Christchurch, New Zealand

2. **Thomas Hoenen**, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Hamilton, USA

Any reports and responses or comments on the article can be found at the end of the article.

This article is included in the **Bioinformatics** gateway.

Corresponding authors: Ron Ammar (ron.ammar@mail.utoronto.ca), Gary D. Bader (gary.bader@utoronto.ca)

Competing interests: R.A. is a member of the Oxford Nanopore Technologies Inc. MinION Access Programme and the MinION instrument and R7.3 flowcells were received free of charge.

Grant information: This study was funded by a Large-scale Applied Project grant from Genome Canada and the Ontario Genomics Institute (grant ID OGI-068). We confirm that the funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Copyright: © 2015 Ammar R *et al.* This is an open access article distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited. Data associated with the article are available under the terms of the [Creative Commons Zero "No rights reserved" data waiver](#) (CC0 1.0 Public domain dedication).

How to cite this article: Ammar R, Paton TA, Torti D *et al.* **Long read nanopore sequencing for detection of *HLA* and *CYP2D6* variants and haplotypes [version 1; peer review: 2 approved]** F1000Research 2015, 4:17 <https://doi.org/10.12688/f1000research.6037.1>

First published: 21 Jan 2015, 4:17 <https://doi.org/10.12688/f1000research.6037.1>

Introduction

An important aspect of precision medicine is the study of how genes influence individual response to drug therapies, known as pharmacogenomics (PGx). PGx genotyping impacts the choice of drug dosing in many medical contexts. As an example, in acute lymphoblastic leukemia patients the metabolizer status of thiopurine methyltransferase (*TPMT*) must be considered when calculating the initial drug dose of mercaptopurine (6-MP) to ensure proper treatment and avoid fatal toxicity^{1,2}.

PGx data are typically collected by sequencing a small panel of known PGx genes via traditional Sanger sequencing, or targeted genotyping technologies³. Diagnostic labs are also exploring the use of whole genome or exome sequencing (WGS, WES) for PGx. However, existing methods have various limitations, which may lead to adverse drug responses. WGS and WES methods may fail to capture or provide adequate sequence coverage for certain PGx loci. Targeted genotyping approaches, such as Taqman (Life Technologies), Luminex (Luminex Corp.) or Sequenom (Agena Bioscience), can fail to detect novel loss-of-function mutations due to their selective interrogation of predefined genomic loci. In a diagnostic clinic, where results are often required within days of administering diagnostic tests, some existing technologies can delay the return of clinical results. Current massively parallel technologies have high capital costs (ranging from \$100,000–\$1,000,000) requiring clinical laboratories to purchase and maintain large instruments to perform in-house genotyping. Alternatively, a laboratory can send these PGx samples to a third party service for a fee, but may wait up to several months for a clinical report.

Clinical haplotypes, tightly-linked collections of inherited alleles, that are responsible for a plethora of medical phenotypes including patient drug response are important in many medical sequencing applications. Information about haplotypes, or genotype phase, can be inferred from parental genotypes or genetic pattern frequency in the human population, however, these predictions can be inaccurate if *de novo* or rare haplotypes are encountered in a patient^{4,5}. Due to the chromosomal distance between alleles, current short read technologies in use for PGx are often unable to resolve haplotype information without supplemental statistical phasing or parental genotypic data.

Recently, Oxford Nanopore Technologies Inc. has developed the MinION, a real time nanopore-based DNA sequencing instrument which is compact, inexpensive and faster than most established DNA sequencing technologies. The time it takes from initiation of library preparation to basecalling the first sequence read is approximately 3 hours and the instrument is capable of detecting long sequence reads in excess of 50kb (according to the manufacturer, ONT). Nanopore-based technology promises major advances in DNA sequencing by offering an inexpensive (e.g. on the order of \$1000) pocket-sized device for clinical diagnostics or field experiments.

Here we report nanopore-based sequencing of three clinically relevant PGx genes to identify medically actionable variants and haplotypes without statistical phasing.

Methods

PCR amplification

Primer sequences for *HLA-A*, *HLA-B* and *CYP2D6* are available in [Table S1](#). For *CYP2D6*, we designed primers to specifically amplify *CYP2D6* while not amplifying the 94% identical *CYP2D7*. PCR primer specificity was verified using UCSC *in silico* PCR. We used the standard protocol (for fragments up to 8 kb) of the KAPA LongRange HotStart PCR system: 5× KAPALongRange Buffer (without Mg²⁺) 1×, MgCl₂ (25 mM) 1.75 mM, dNTPs (10 mM each dNTP) 0.3 mM, Fwd primer (10 μM) 0.5 μM, Rev primer (10 μM) 0.5 μM 50ng of genomic DNA (1ul of a 50ng/ul preparation), KAPA LongRange HotStart DNA Polymerase (2.5 U/μl) 1.25 U/50 μl, PCR grade water up to 50μl. For *HLA-A* and *HLA-B*, genomic sequence was downloaded from UCSC Browser with common SNPs masked. Primers were designed using Primer3 using parameters of 68°C for optimal annealing temp and 26bp minimum primer length⁶.

Oxford Nanopore genomic DNA library preparation

The DNA libraries were prepared using the Oxford Nanopore Genomic DNA Sequencing protocol (SQK-MAP003). 1.5μg of PCR product was used (instead of the suggested 1μg based on improved yield in earlier testing) with equimolar amounts of *CYP2D6*, *HLA-A* and *HLA-B* amplicons in solution. DNA was not fragmented because the PCR amplicons were already at the desired size for sequencing and downstream haplotyping (4–5Kbp; [Table S1](#)). In accordance with the protocol, we end-repaired the DNA with the NEBNext end repair module (New England Biolabs, cat. no. E6050) and subsequently dA-tailed the sample using the NEB-Next dA-tailing module (New England Biolabs cat. no. E6053), prior to ligation of nanopore-specific adapters. All purifications were accomplished with Agencourt AMPure XP beads (Beckman Coulter Inc., cat. no. A63880). Throughout the library preparation, care was taken not to vortex or vigorously pipette/mix the library to avoid shearing the DNA into smaller fragments.

Oxford Nanopore MinION sequencing and basecalling

The MinION flowcell (R7.3 flowcell chemistry) was run for 24 hours using the MinKNOW software (v47.3) producing 24,859 fast5 files, corresponding to individual reads from base detection events at specific nanopore channels. Online basecalling was performed using the Metrichor software (v2.23). The MinION outputs 3 reads for each dsDNA molecule that passes through a pore. The leading ssDNA is referred to as “1D template” and its complementary ssDNA strand is the “1D complement”. When both 1D template and 1D complement reads are basecalled, a 2D consensus sequence is determined based on complementarity. We observed 19,655 1D template reads, 9,584 1D complement reads and 7,540 2D reads. The mean lengths were 2,693bp for 1D template, 2,706bp for 1D complement and 3,486bp for 2D consensus.

Read alignment

Existing massively parallel sequencing instruments, such as the Illumina HiSeq 2500, produce accurate short reads typically up to ~250bp in length. These sequencers can produce hundreds of millions of reads which need to be rapidly aligned to a reference genome. Current computational methods for accurate alignment

of these reads, including BWA⁷ and Bowtie2⁸ are based on the Burrows-Wheeler Transform FM index, and they are designed to align short reads with minimal variation to a reference assembly. BWT-FM methods are insufficiently sensitive to align much longer reads with higher error rates⁹. These long reads, generated by single molecule sequencers such as the Oxford Nanopore MinION or the Pacific Biosciences RS II, have a significantly higher error rate, enriched for insertions or deletions (indels) rather than substitutions⁹. Mapping of these reads is best suited to aligners that were originally designed for whole genome alignments, such as LAST¹⁰. We chose to use BLASR, originally developed for the Pacific Biosciences system, to align our data, because it was designed to align long error-prone reads rather than genomes⁹.

All reads were aligned to the human genome reference assembly GRCh37.p13 (hg19) using default BLASR parameters (gap open penalty = ten, gap extension penalty = zero, minimum seed length = 12). The use of other parameters, such as a gap-open penalty of zero (with default gap extension penalty = zero) did not alter the results, even though it may be expected to do so given the prevalence of indels expected in single molecule nanopore sequencing. The majority of successfully aligned long read fragments were obtained from 2D basecalls (Table 1), and these were of higher quality because they are consensus reads constructed from corresponding 1D template and complement. For the final alignment data, for each separate read event (1D template, 1D complement and 2D consensus), we selected the 2D if it was available. Since the 1D reads typically had lower mapping accuracy and significantly shorter aligned fragments (Table 1), these were not included in our variant or haplotype calling analysis.

Finally, we performed two separate alignments depending on our desired sequencing application: a) gene targets with highly similar nearby genes; and b) highly polymorphic gene targets. The first analysis only selected the single best alignment for each long read. This was critical for the gene *CYP2D6* because the *CYP2D* locus on chromosome 22 harbors two paralogous pseudogenes *CYP2D7* and *CYP2D8P*¹¹. In particular, *CYP2D6* and *CYP2D7* are highly similar (94% identity, BLAST E-value = 0.0) and are positioned in tandem on the chromosome. By allowing reads to only map to a single best hit, we were able to verify that the PCR selectively amplified *CYP2D6* and not nearby related genes (see coverage in Figure 1). Our second analysis was performed due to the high degree of polymorphism in the MHC locus on chromosome 6. As part of the MHC haplotype project¹², multiple reference contigs for this highly variable region are included in the GRCh37 reference

assembly as indicated in the release notes (http://www.ncbi.nlm.nih.gov/genome/guide/human/release_notes.html). Since long reads from the NA12878 *HLA-A* and *HLA-B* genes mapped to different chromosome 6 reference haplotype contigs, by allowing multiple alignments to the reference (up to 10) for each read, we could gather all reads for a single gene in a single pileup to any of the eight *HLA-A/B* loci to generate a consensus sequence. For this study, we used the reference chromosome 6 contig NC_000006.11 (not the MHC haplotype project contigs).

Variant detection and haplotype identification

Due to the long reads, high error rates and continuously evolving error profile of the MinION basecalls at this early stage of technology roll out, variant callers such as the Genome Analysis Toolkit's UnifiedGenotyper or HaplotypeCaller¹³ were unable to identify variants or haplotypes in the MinION sequence data during our trials. Variant and haplotype level information, however, was readily accessible based on coverage of aligned reads, which we extracted using SAMTools via the Pysam wrapper (<http://github.com/pysam-developers/pysam>)¹⁴.

Mean coverage was 1236.4× for *CYP2D6* (single best hit alignment), 785.5× for *HLA-A* (multi-hit alignment) and 1416.3× for *HLA-B* (multi-hit alignment).

Variants were detected using a naïve threshold requiring 1/3 of reads to contain the variant genotype at that position. While this was effective for substitution detection, we are likely to detect many false positive deletions due to the high deletion error rate (Table 1). Haplotype proportions were identified by interrogating clinical marker positions (Table S2) across all reads aligned to a particular gene to establish the proportion of reads corresponding to each haplotype. Pharmacogenomic haplotypes were verified by comparison to diagnostic data sets (see below) using the MedSavant software (www.medsavant.com; manuscript in review) with the pharmacogenomics app that we developed. The PGx app interprets human pharmacogenomic variants with medically actionable output based on published guidelines established by the Clinical Pharmacogenetics Implementation Consortium (CPIC) and the Pharmacogenomics Knowledgebase (www.pharmgkb.org).

Validation of genotypes by Complete Genomics, and clinical diagnostic Sequenom MassARRAY and qPCR

Complete Genomics WGS data for NA12878 were obtained from the public 69 genomes project (CG analysis pipeline version 2.0.0; <http://www.completegenomics.com/public-data/69-Genomes/>)¹⁵.

Table 1. Basecall and read mapping statistics.

Read Type	Number of reads	Mean Length, unaligned (bp)	Number of reads aligned	% of reads aligned	Mean Length, aligned fragment (bp)	Mean substitution frequency	Mean deletion frequency	Mean insertion frequency	Mean mapping accuracy (for each read [match bp/total bp])
1D template	19655	2693.7	3793	19.3%	872.8	8.9%	13.9%	5.7%	71.5%
1D complement	9584	2705.7	2717	28.3%	292.7	7.3%	15.4%	4.1%	73.2%
2D consensus	7540	3486.3	4761	63.1%	2952.3	7.0%	13.3%	5.3%	74.3%

Figure 1. Integrate Genomics Viewer (IGV) diagram of MinION reads aligned to the *CYP2D* locus on chromosome 22 from 42,521,411 to 42,552,401. The majority of reads aligned across the entire length of *CYP2D6* as was expected by selective PCR amplification. Downstream, an insignificant number of read fragments aligned to *CYP2D7* and *CYP2D8* (*2D8* is located from 42,545,874 to 42,551,097; exon-intron diagram not shown in gene annotation track). Due to the extremely high coverage at *CYP2D6*, not all reads are shown in this pileup diagram.

10ng of genomic DNA from NA12878 was genotyped for 36 SNP, indel and copy number variants for *CYP2D6* using the iPLEX® ADME *CYP2D6* Panel v1.0, developed by Assays by Agena (formerly Sequenom) on the MassARRAY4 System. Haplotype assignment and copy number determination was done using Typer software version 4.0 (Agena Biosciences).

In parallel, copy number estimation of *CYP2D6* was performed using the Taqman copy number assays Hs04502391_cn and Hs04083572_cn (Life Technologies) using the manufacturer's recommended protocol (Figure S1). The assay was performed in quadruplicate on 10ng genomic DNA for each sample in a 96-well plate. The 10μL reaction mix consisted of 5μL 2× Taqman Genotyping Master Mix (Life Technologies), 0.5μL of 20X copy number assay (described above), 0.5μL TaqMan RNase P Copy Number Reference Assay (Life Technologies cat. no. 4403326), 2μL water and 2μL of 5ng/μL genomic DNA. Cycling conditions for the reaction were 95°C for 10 min, followed by 40 cycles of 95°C for 15 sec and 60°C for 1 min. Samples were analyzed using the ViiA™ 7 Real-Time PCR System (Life Technologies) and analyzed using Copy-Caller Software (Life Technologies). The HuRef sample was used as a 2-copy calibrator sample.

Validation of haplotypes by statistical phasing and HapMap Complete Genomics WGS and Sequenom MassARRAY genotypes were statistically phased using the BEAGLE software (v4.0) and

the 1000 Genomes Project phase 3 reference panel (<http://faculty.washington.edu/browning/beagle/beagle.html>)⁴. For the *HLA-A/B* genes, phase information was obtained from the HapMap phase 2 data (<http://hapmap.ncbi.nlm.nih.gov/downloads/index.html.en>)¹⁶. *HLA-A/B* alleles were determined using the GATK HLAcaller software package (<http://gatkforums.broadinstitute.org/discussion/65/hla-caller>).

Results

To evaluate the MinION for diagnostic PGx sequencing, we selectively amplified and sequenced the genes *CYP2D6*, *HLA-A*, and *HLA-B* from the CEPH/UTAH pedigree 1463 sample NA12878. *CYP2D6* is a pharmacogenetically vital cytochrome P450 gene because it encodes a protein responsible for metabolism of 20% of clinically used drugs¹¹. The diagnostic relevance of *2D6* is derived from its significant polymorphism which contributes to dramatic inter-individual variability in enzyme activity¹¹. Also important are the *HLA* genes which are clinically relevant for solid organ transplantation and accurate dosing of abacavir, allopurinol and carbamazepine, used to treat HIV/AIDS, hyperuricemia and seizure disorders, respectively^{17–19}. The *HLA* genes are among the most polymorphic loci in the human genome, making their sequencing and confident typing difficult with current short read DNA sequencing methods. These three genes were also chosen for sequencing due to their length (4–5Kbp), which did not require long range PCR amplification methods.

PCR amplicons of these three genes from NA12878 (CEPH/Utah Pedigree 1463) were sequenced on the MinION instrument yielding 19655 read events. Each read event could be basecalled in multiple forms, as a template or complement strand (1D) or as a consensus of the two (2D), and we obtained 36779 1D and 2D reads in total. For the purpose of diagnostic evaluation, we chose to align only the consensus 2D reads due to their lower error rate and extended length (Table 1; see Methods). Reads were aligned to the human genome (GRCh37), with an abundance of aligned reads 4–5Kb in length representing full-length PCR amplicons. As well, smaller aligned read fragments were observed, some of which are speculated to be byproducts of shearing during experimental DNA handling (Figure 2A, Table S1).

With depth of coverage of ~1000x for each of the genes, many chromosomal positions were called with 70–90% consensus, demonstrating that as coverage of loci increases on the MinION, confidence improves with regard to specific base calls (Figure 2B). While the MinION basecalls are emitted with a comparatively high error rate (Table 1), the majority of errors appear to be randomly distributed across the length of the reads, which is why increasing coverage can yield a consensus that matches variant calls from existing sequencing and genotyping platforms such as Illumina, Complete Genomes and Sequenom.

MinION-called variants and haplotypes were validated against statistically phased genotypes from multiple platforms including Complete Genomics and Sequenom MassARRAY (see Methods). Based on the statistically phased genotypes, we determined that NA12878 possesses both the *3 and *4 loss-of-function alleles for *CYP2D6*, and this *3/*4 diplotype is interpreted as reduced metabolism of drugs such as codeine (an opiate) and olanzapine (an atypical antipsychotic)^{20–22}.

CYP2D6 haplotype proportions were identified by interrogating clinical marker positions across all aligned reads to establish the proportion of reads corresponding to each PGx haplotype (Table S2). Only reads spanning all clinical markers were included (n = 404), so that haplotypes could be measured by linkage of markers on a single DNA molecule. The MinION data confirmed the statistically-phased haplotypes by direct interrogation of markers from individual reads (Figure 2C). However, we also observed a prominent *2 haplotype, which we could not account for given that our Sequenom MassARRAY and qPCR results indicated that the *CYP2D6* locus was diploid (no copy number variation) and could only correspond to a *3/*4 diplotype. To determine whether the *2 haplotype could arise from mismatched *CYP2D7* DNA, which was not supposed to be PCR amplified (see Methods), we interrogated four positions with different bases between *CYP2D6*

Figure 2. **A.** Length distribution of aligned reads. 4–5Kb reads represent full-length PCR amplicons. Slightly smaller fragments were likely byproducts of shearing during DNA handling in the experimental protocol. **B.** With depth of coverage of ~1000x for each of the genes, many chromosomal positions were called with 70–90% consensus. This is a short window of aligned reads for the *4 locus of *CYP2D6* with over 1200x coverage. The heterozygous *4 allele rs1065852 is indicated with the arrow. **C.** Proportions of haplotypes of *CYP2D6*, *HLA-A* and *HLA-B* when directly measured from individual reads spanning all haplotype markers.

and *CYP2D7* reference sequences and found that all reads corresponded to *CYP2D6* (Supplementary File S1). Finally, we hypothesized that the *2 haplotype might arise due to *3 and *4 duplexes forming during PCR (effectively outcompeting the primer binding during the annealing step), but this was ruled out by identifying the *2 haplotype using only 1D reads. It is possible that this *2 haplotype arose either due to early cycle template switching during PCR or sample contamination²³. Also, the relative proportion of haplotypes was likely skewed by potential biases during PCR amplification.

The *HLA-A* and *HLA-B* haplotypes were determined in the same way as the *CYP2D6* haplotypes, using predefined markers from the HapMap project. In *HLA-A* (only spanning reads, *n* = 203), the most abundant haplotype matched the transmitted haplotypes of the parents NA12891 and NA12892, which both transmitted an identical haplotype (Figure 2C). Accounting for the errors in MinION sequencing, when allowing for a single mismatch in the haplotype, ~85% of reads confirm the NA12878 diplotype. In *HLA-B* (only spanning reads, *n* = 202), the majority of reads corresponded to the transmitted and untransmitted haplotypes of the parent NA12891, with only 8.4% of reads corresponding to the transmitted haplotype of parent NA12892 (Figure 2C). This could be a result of potential contamination suspected earlier in described above with *CYP2D6*. As suggested for *CYP2D6*, the relative proportion of HLA haplotypes was likely also affected by PCR bias during amplification. *HLA* alleles were called with 4-digit resolution using the GATK HLA Caller, but due to the high error rates of nanopore reads, HLA alleles did not match with alleles called using HapMap data (Table S3)²⁴.

Nanopore reads and alignments

Data File

<http://dx.doi.org/10.6084/m9.figshare.1289717>

Conclusions and discussion

Phasing of genotypes is critical to prevent misinterpretation of PGx variants. The importance of correct phasing of PGx genotypes is illustrated with the gene *TPMT*, which plays a critical role in the metabolism of thiopurine, a drug used to treat acute lymphoblastic leukemia. In a recent study²⁵, an individual was reported to have a *TPMT* *3B/*3C diplotype, based on observed heterozygous genotypes for the rs1142345 and rs1800460 variants, but this was a misinterpretation due to faulty haplotyping and *1/*3A is the correct diplotype. The rs1800460 variant is present in both *3A and *3B haplotypes while the rs1142345 variant is present in both *3A and *3C haplotypes. As a result, it was possible for the individual to have a *1/*3A diplotype or a *3B/*3C diplotype. Clinically, a *1/*3A diplotype corresponds to an intermediate metabolizer, requiring a 30–70% reduction in thiopurine dose, while a *3B/*3C diplotype corresponds to a poor metabolizer with a 90% reduction in dose². An individual who receives a standard dose and is a poor metabolizer can experience fatal toxicity, while a low dose for a normal metabolizer can lead to disease progression. Clinical trials have demonstrated the medical importance of *TPMT* haplotyping in treatment of myeloid leukemias and non-malignant immunologic disorders^{2,26}.

Long sequence reads aid haplotype identification by determining which genetic variants are in phase (i.e. on the same DNA strand). If the *TPMT* genotypes from the example above were sequenced using nanopore-based long read technology, the *1/*3A diplotype would likely be called correctly (note that rs1142345 and rs1800460 are only 8,310bp apart).

While nanopore sequencing with the MinION is demonstrably error-prone in its current stage of development, we assert that this technology holds promise for clinical applications because accurate consensus sequences can be built with sufficient coverage given the high number of reads generated. As well, we have been able to successfully call haplotypes from long reads *de novo* in the absence of parental haplotypes or statistical phasing. The MinION device produced sufficiently long mappable reads to phase all variants in the loci examined. As error rates on the MinION decrease, we can expect to deconvolute these data into more accurate diplotypes with less noise and will be able to measure how much multi-sample multiplexing can be supported by a single run.

According to the CPIC, 63 genes and 132 drugs have guidelines for pharmacogenomic status (<http://www.pharmgkb.org/cpic/pairs>), and this list is constantly expanding. With increasing guidelines and demands for PGx in the clinic, affordable and rapid nanopore sequencing may hold great utility.

Data availability

figshare: Nanopore reads and alignments, doi: <http://dx.doi.org/10.6084/m9.figshare.1289717>²⁷

Raw nanopore reads and alignment files are available at the NCBI Sequence Read Archive, accession SRP051851 (<http://www.ncbi.nlm.nih.gov/sra/?term=SRP051851>).

Author contributions

RA, AS and GDB conceived the study. TAP designed and performed the PCR amplification. RA and DT performed the library preparation. RA performed the sequencing and downstream analysis. RA, TAP and GDB drafted the manuscript. All authors were involved in the revision of the draft manuscript and have agreed to the final content.

Competing interests

R.A. is a member of the Oxford Nanopore Technologies Inc. MinION Access Programme and the MinION instrument and R7.3 flowcells were received free of charge.

Grant information

This study was funded by a Large-scale Applied Project grant from Genome Canada and the Ontario Genomics Institute (grant ID OGI-068).

We confirm that the funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Acknowledgments

The authors thank Stephen Scherer and Peter Ray of the Hospital for Sick Children for contributing diagnostic validation data.

Supplementary material

Applied Biosystems CopyCaller® Software v2.1

1. File: copy_number_Hs04502391_cn_1_data.txt, Target: Hs04502391_cn, Calibrator: 201193 (Venter)
2. File: Hs04083572_copy_number_1_data.txt, Target: Hs04083572, Calibrator: 201193 (Venter)

Figure S1. CopyCaller software analysis of data from Taqman copy number assays Hs04502391_cn and Hs04083572_cn. *CYP2D6* from sample NA12878 was observed to be diploid.

Table S1. Primer sequences and amplicon lengths for *HLA-A*, *HLA-B* and *CYP2D6*.

Oxford Nanopore PGx primer list				
Gene	Primer Name	Primer seq	Chromosomal Coordinates	Amplicon Size
CYP2D6	CYP2D6-2F	TAGCTCCCTGACGCCATGATTTGTCTT	chr22:42,522,077-42,527,144	5,067 bp
CYP2D6	CYP2D6-2R	CCTGGTTATCCCAGAAGGCTTTGCAG		
HLA-A	HLAA-2F	AGAAGAGTCCAGGTGGACAGGTAAGGAGTG	chr6:29,909,854-29,913,805	3,951 bp
HLA-A	HLAA-2R	TTCTACTGAAGGGCCAAGGACAATGGAG		
HLA-B	HLAB-2F	TGGATTCAAGCACCAGATCACTAGAACCCAG	chr6:31,321,279-31,325,303	4,024 bp
HLA-B	HLAB-2R	GTCTCTCCCTGGTTCCACAGACAGATCCT		

Table S2. Haplotype translation table for *CYP2D6*.

Haplotype Id	CYP2D6	rs1065852	rs28371706	rs5030655	rs3892097	rs35742686	rs5030656	rs16947	rs28371725	rs1135840
PA165816576	*1	G	G	A	C	T	CTT	G	C	C
PA165816577	*2	G	G	A	C	T	CTT	A	C	G
PA165816578	*3	G	G	A	C	-	CTT	G	C	C
PA165816579	*4	A	G	A	T	T	CTT	G	C	G
PA165948092	*5	-	-	-	-	-	-	-	-	-
PA165816581	*6	G	G	-	C	T	CTT	G	C	C
PA165948317	*9	G	G	A	C	T	-	G	C	C
PA165816582	*10	A	G	A	C	T	CTT	G	C	G
PA165816583	*17	G	A	A	C	T	CTT	A	C	G
PA165816584	*41	G	G	A	C	T	CTT	A	T	G

Table S3. *HLA* alleles called with 4-digit resolution using the GATK HLACaller.

Locus	HapMap A1	HapMap A2	Nanopore A1	Nanopore A2
HLA-A	0101	1101	0132	0312
HLA-B	0801	5601	0765	5510

Supplementary File S1

BLAST alignment of *CYP2D6* and *CYP2D7*. These genes have 94% identity (E-value = 0.0). To determine if our reads were generated from *CYP2D7* reads, we interrogated reads at the paralogous positions circled in red.

12/2/2014

NCBI Blast:ref|NC_000022.10| (51304566 letters)

BLAST®

Basic Local Alignment Search Tool

[NCBI/ BLAST/ blastn suite-2sequences/ Formatting Results - 7WAFRJZK114](#)
[Formatting options](#)
[Download](#)
[Blast report description](#)

Blast 2 sequences

ref|NC_000022.10| (51304566 letters)

RID	7WAFRJZK114 (Expires on 12-04 04:07 am)	Subject ID	gil224589814 ref NC_000022.10
Query ID	gil224589814 ref NC_000022.10	Description	Homo sapiens chromosome 22, GRCh37.p13 Primary Assembly
Molecule type	dna	Molecule type	dna
Query Length	51304566	Subject Length	51304566
		Program	BLASTN 2.2.30+

Graphic Summary

12/2/2014

NCBI Blast:refNC_000022.10| (51304566 letters)

Dot Matrix View

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Homo sapiens chromosome 22, GRCh37.p13 Primary Assembly	6582	6582	99%	0.0	94%	NC_000022.10

Alignments

Homo sapiens chromosome 22, GRCh37.p13 Primary Assembly
Sequence ID: [refNC_000022.10](#) Length: 51304566 Number of Matches: 1
Range 1: 42522501 to 42526883

Score	Expect	Identities	Gaps	Strand	Frame
6582 bits(3564)	0.0()	4142/4408(94%)	91/4408(2%)	Plus/Plus	

Features:

Query	42536214	TTGGAAC	TACCACATTGCTTTATTGTACATTAGAGCCTCTGGCTAGGGAGCAGGCTGGGG	42536273
Sbjct	42522501	TTGGAAC	TACCACATTGCTTTATTGTACATTAGAGCCTCTGGCTAGGGAGCAGGCTGGGG	42522560
Query	42536274	ACTAGGT	ACCCCATTTCTAGCGGGGCACAGCACAAAGCTCGTAGGGGGATGGGGTCACCAG	42536333
Sbjct	42522561	ACTAGGT	ACCCCATTTCTAGCGGGGCACAGCACAAAGCTCATAGGGGGATGGGGTCACCAG	42522620
Query	42536334	-AAAGCT	GACGACACGAGAGTGGCTGGGCCGGGGCTGTCCGGCGGGCCACGGAGAAGCTGA	42536392
Sbjct	42522621	GAAAGC	-AAAGACACCATGGTGGCTGGGCCGGGGCTGTCCAAGTGGGCACCGAGAAGCTGA	42522679
Query	42536393	AGTGTCT	GCAGCAGGGAGGTGAAGAAGAGGAAGAGCTCCATGCGGGCCAGGGGCTCCCCGA	42536452
Sbjct	42522680	AGTGTCT	GCAGCAGGGAGGTGAAGAAGAGGAAGAGCTCCATGCGGGCCAGGGGCTCCCCGA	42522739
Query	42536453	GGCATGC	CACGGCGGCCCTGTGGGGAGGGAGGGGCGTCAGTGAGCCTGGCTCCTGGGTGAT	42536512
Sbjct	42522740	GGCATGC	CACGGCGGCCCTGTGGGGAGGGAGGGGCGTCAGTGAGCCTGGCTCCTGGGTGAT	42522799
Query	42536513	ACCCCTG	CAAGACTCCACGGAAGGGGACAGGGAGCCGGGCTCCCCACAGGCACCTGCTGA	42536572
Sbjct	42522800	ACCCCTG	CAAGACTCCACGGAAGGGGACAGGGAGCCGGGCTCCCCACAGGCACCTGCTGA	42522859
Query	42536573	GAAAGGC	AGGAAGGCCCTCCGGCTTCACAAAGTGGCCCTGGGCATCCAGGAAGTGTTCGGG	42536632
Sbjct	42522860	GAAAGGC	AGGAAGGCCCTCCGGCTTCACAAAGTGGCCCTGGGCATCCAGGAAGTGTTCGGG	42522919
Query	42536633	GTGGAAG	CGGAAGGGCTTCTTCCAGACGGCCTCATCCTTACGACCCGATGACAGGTGGT	42536692
Sbjct	42522920	GTGGAAG	CGGAAGGGCTTCTTCCAGACGGCCTCATCCTTACGACCCGATGACAGGTGGT	42522979
Query	42536693	GATGAGT	GTCGTTCCCTGGGCAGGAGATGCAGGGTGAGAGTGGGGACTGGACTCTAGGAT	42536752
Sbjct	42522980	GATGAGT	GTCGTTCCCTGGGCAGGAGATGCAGGGTGAGAGTGGGGACTGGACTCTAGGAT	42523039
Query	42536753	GCTGGG	ACCCCTGCCACCAAACACACGGGGGACACACACTGCCTGGCACACAGCTGGACT	42536812
Sbjct	42523040	GCTGGG	ACCCCTGCCACCAAACACACGGGGGACACACACTGCCTGGCACACAGCTGGACT	42523099
Query	42536813	CTGTCA	AACTAGTCTTCCGCCCCGAGAAGCTCCACAGTACCTCTCCGACCCACAGCAGGG	42536872
Sbjct	42523100	CTGTCA	AACTAGTCTTCCGCCCCGAGAAGCTCCACAGTACCTCTCCGACCCACAGCAGGG	42523159
Query	42536873	CGCAGT	CACACCTCTCAGAGGCACCCACACTGCCCCCTCTCCCTGCAGGCGCTGGGTCTCT	42536932
Sbjct	42523160	CGCAGT	CACACCTCTCAGAGGCACCCACACTGCCCCCTCTCCCTGCAGGCGCTGGGTCTCT	42523219
Query	42536933	CCAACAT	TCTGGCAGGTCTGATTGTGCTTCCCCACTAGACGGGGGCTCTGGATGGACAG	42536992
Sbjct	42523220	CCAACAT	TCTGGCAGGTCTGATTGTGCTTCCCCACTAGACGGGGGCTCTGGATGGACAG	42523278
Query	42536993	GCCAGCC	CTGCCTATACTCTGGACCCCCCATCCAAGCGGGGACAGTCAGTGTGGTGGCAT	42537052
Sbjct	42523279	GCCAGCC	CTGCCTATACTCTGGACCCCCCATCCAAGTGGGGACAGTCAGTGTGGTGGCAT	42523338

12/2/2014

NCBI Blast:reflNC_000022.101 (51304566 letters)

Query	42537053	TGAGGACTAGGTGGCCAGGGTTCCTAGAGTGGGCCACCTGGCAGTAGCCATGCTGGGGC	42537112
Sbjct	42523339	TGAGGACTAGGTGGCCAGGGTTCCTAGAGTGGGCCACCTGGCAGTAGCCATGCTGGGGC	42523398
Query	42537113	TCCACC-GGGGCTGATGCTGAGCTGGGGTGAGGAGGGCGCCAGGCCACCTTAGGGATG	42537171
Sbjct	42523399	TATCACCAGGGGCTGGTGTGAGCTGGGGTGAGGAGGGCGCCAGGCCACCTTAGGGATG	42523458
Query	42537172	CGGAAGCCCTGTACTTCGATGTCATGGGATGTATATGGGTCACACTCAGGGGGATGATG	42537231
Sbjct	42523459	CGGAAGCCCTGTACTTCGATGTCACGGGATGTATATGGGTCACACCCAGGGGGACGATG	42523518
Query	42537232	TCCCCAAAGCGCTGCACCTCGTGAATCACGGCAGTGGTGTAGGGCATGTGAGCCTGGTCA	42537291
Sbjct	42523519	TCCCCAAAGCGCTGCACCTCATGAATCACGGCAGTGGTGTAGGGCATGTGAGCCTGGTCA	42523578
Query	42537292	CCCATCTCTGGTCGCGCACCTGCCCTATCACGTCGTCGATCTCTGTGGACACGGACT	42537351
Sbjct	42523579	CCCATCTCTGGTCGCGCACCTGCCCTATCACGTCGTCGATCTCTGTGGACACGGCCT	42523638
Query	42537352	GGACAGACATGCGTCCCCACAATGGGTGAGCAGCCAGGGGA-CA--C--T--TCCTT	42537402
Sbjct	42523639	GGACAGACATGCGTCCCCACAATGGGTGAGCAGCCAGGGGTCCGGCCCTGACACTCCTT	42523698
Query	42537403	C--G--TCCTGTGTTGGAGGAAGTTAGGCTTACAGGAGCCTGGCCACGCCTGTGCTGGAA	42537458
Sbjct	42523699	CTTGCCCTCCTATGTTGGAGGAGTTCAGGCTTACAGGATCCTGGTCAAGCCTGTGCTTGA	42523758
Query	42537459	GCCCCGGGTGTCCAGCTAAGCCAGGGGCCCCAGCTGTACCCTTCCCTCCCTCAGTCCC	42537518
Sbjct	42523759	GCCCCGGGTGTCCAGCAAAGTTCATGGGCCCCCGCCTGTACCCTTCCCTCCCTCGGCC	42523818
Query	42537519	TGCTTGGGCCCCAGCTGGGCTCAGCTGCACATCCAGGTGTAGGATCATGAGCAGGAGG	42537578
Sbjct	42523819	TGCACTGTTTCCAGATGGGCTCAGCTGCACATCCGGATGTAGGATCATGAGCAGGAGG	42523878
Query	42537579	CCCCAGGCCAGCGTGGTCAAGGTGGTCACCATCCCGCAAGGAACAGGTTACCCACCACT	42537638
Sbjct	42523879	CCCCAGGCCAGCGTGGTCAGGTTGGTCACCATCCCGCAGAGAACAGGTCAGCCACCACT	42523938
Query	42537639	ATGCGCAGGTTCTCATCATGAAGCTGCTCTCAGGGCTCCCTTGGCCTGAGCAGGGCCG	42537698
Sbjct	42523939	ATGCACAGGTTCTCATCATGAAGCTGCTCTCAGGGTTCCCTTGGCCTGAGCAGGGCCG	42523998
Query	42537699	AGAGGATACTCAGGGGATAGAACGGGGTAGCCCCAAATGACCTCCAATTCTGCACCTGT	42537758
Sbjct	42523999	AGAGCATACTC--GGGACAGAACGGGGTAGCCCCAAATGACCTCCAATTCTGCACCTGT	42524056
Query	42537759	CAGCCCAGATGCGGCTCGCCGGGTGATGCACCTGGTCCAACCTTTTGGCCAGCCTCCCTC	42537818
Sbjct	42524057	CAGCCCAGATGCGGCTCGCCGGGTGATGCACCTGGTCCAACCTTTTGGCCAGCCTCCCTC	42524116
Query	42537819	ATTCTCTCTGGGACGTTCAACCCACCACCTTGGCCCCCACCCTGGCAGCCACTCTCACC	42537878
Sbjct	42524117	ATTCTCTCTGGGACGTTCAACCCACCACCTTGGCCCCCACCCTGGCAGCCACTCTCACC	42524176
Query	42537879	TTCTCCTTCTTTGCCAGGAAGGCCTCAGTCAGGTCTCGGGGTGGCTGGGCTGGGTCCCAG	42537938
Sbjct	42524177	TTCTCCTTCTTTGCCAGGAAGGCCTCAGTCAGGTCTCGGGGGGGCTGGGCTGGGTCCCAG	42524236
Query	42537939	GTCATCCTGTGCTCAGTTAGCAGCTCATCCAGCTGGGTGAGGAAAGCCTTTTGGAAAGCGT	42537998
Sbjct	42524237	GTCATCCTGTGCTCAGTTAGCAGCTCATCCAGCTGGGTGAGGAAAGCCTTTTGGAAAGCGT	42524296
Query	42537999	AGGACCTTGCCAGCCAGCGCTGGGATGTCAGGAGGACGGGGACAGCATTCAGCACCTAC	42538058
Sbjct	42524297	AGGACCTTGCCAGCCAGCGCTGGGATATSCAGGAGGACGGGGACAGCATTCAGCACCTAC	42524356
Query	42538059	ACCAGACAGAACGGGGTCTCAATCCCTCCTGTGCTCTGCGTTTCATCTGGACCAGTCTCAG	42538118
Sbjct	42524357	ACCAGACAGAACGGGGTCTCAATCCCTCCTGTGCTCTGCGTTTCACCTGGACAAGTCTCAG	42524416
Query	42538119	GCCCCAGCCATCTCCAGGAAGACCAGGGCTGCCTGTCTTACCCTGACCTCACCAAG	42538178
Sbjct	42524417	GCCCCAGCCATCTCCAGGTAGACCAGGGCTGCCTGTCTTACCCTGACCTCACCAAG	42524476
Query	42538179	TCCCTCCCCAAGTGCCAGCCTCCACCTCTCTCTCTTGGCCAGAGGAGAGACCTAAAAAT	42538238
Sbjct	42524477	TCCCTCCCCAAGTGCCAGCCTCCACC--CTCTCTCTTGGCCAGAGGAGAAACCTAAAAAT	42524534
Query	42538239	CGAAATCTCCAACGTGGACGGG-GGTACAGAGTCTTGGCCTCTCCTGGTGGCCCCCTGAC	42538297
Sbjct	42524535	CGAAATCTCTGACGTGGATAGGAGGTACAGAGTCTTGGCCTCTCCTGGTGGCCCCCTGAC	42524594
Query	42538298	CCGGGCACACCTCTCCACGACCATGTCTGAGATGTCCCCCTCCTCCTCCAGGCCCTTCTT	42538357
Sbjct	42524595	CCGGGCACACCTCTCCACGACCATGTCTGAGATGTCCCCCTCCTCCTCCAGGCCCTTCTT	42524654
Query	42538358	ACAGTGGGGTCTCCTGGAATGTCTTTCCCAAACCATCTACGCAAACTCTGCCCTTCGG	42538417
Sbjct	42524655	ACAGTGGGGTCTCCTGGAATGTCTTTCCCAAACCATCTATGCAAACTCTGCTCTTCGG	42524714
Query	42538418	AGGGCCCACTCCAGCCCCGGCACCTCTCAGGAGCTCGCCCTGCAAGAC-CCT---T---	42538470
Sbjct	42524715	AGGGCCCACTCCAGCCCCGGCACCTCTCGGGAGCTCGCCCTGCAGAGACTCCTCGGTCTC	42524774
Query	42538471	--GCTCCGCACCTCGCGCAGGAAGCCCGACTCCTCCTTCACTCCCTCCTGAGCTAGGTCC	42538528
Sbjct	42524775	TCGCTCCGCACCTCGCGCAGGAAGCCCGACTCCTCCTTCACTCCCTCCTGAGCTAGGTCC	42524834

12/2/2014

NCBI Blast:reflNC_000022.101 (51304566 letters)

Query	42538529	AGCAGCCTGAGGAAGCGAGGGTTCGTCTGCTACTCGAAGCGGGCGCCCGCAGGTGAGGGAGGCG	42538588
Sbjct	42524835	AGCAGCCTGAGGAAGCGAGGGTTCGTCTGCTACTCGAAGCGGGCGCCCGCAGGTGAGGGAGGCG	42524894
Query	42538589	ATCACGTTGCTCACGGCTTTGTCCAAGAGACCGTTGGGGCGAAAGGGGCGTCCCTGGGGGT	42538648
Sbjct	42524895	ATCACGTTGCTCACGGCTTTGTCCAAGAGACCGTTGGGGCGAAAGGGGCGTCCCTGGGGGT	42524954
Query	42538649	GGGAGATGCGGGTAAGGGGTGCGCTTCTCCGTCCTCCCGCCTTCCAGTTCCCGCTGTGTG	42538708
Sbjct	42524955	GGGAGATGCGGGTAAGGGGTGCGCTTCCCGTCCTCCCGCCTTCCAGTTCCCGCTTTGTG	42525014
Query	42538709	CCCTTCTGCCCATCACCCACCGGCTTGGTCGGCGAAGGCGGCACAAAGGCAGGCGGCTC	42538768
Sbjct	42525015	CCCTTCTGCCCATCACCCACCGGAGTGGTTGGCGAAGGCGGCACAAAGGCAGGCGGCTC	42525074
Query	42538769	CTCGGTACCCACTGCTCCAGCGACTTCTTGGCCAGGCCCAAGTTGCGCAAGGTGGAGAC	42538828
Sbjct	42525075	CTCGGTACCCACTGCTCCAGCGACTTCTTGGCCAGGCCCAAGTTGCGCAAGGTGGAGAC	42525134
Query	42538829	GGAGAAGCGCCTCTGCTCGCGCCACGCGGGCCCATAGCGCGACAGGAACACCCCTGGGGG	42538888
Sbjct	42525135	GGAGAAGCGCCTCTGCTCGCGCCACGCGGGCCCATAGCGCGCCAGGAACACCCCTGGGGG	42525194
Query	42538889	CGGGACGGACACGTGGGCGTTGCCATGAAGGCTTGGCCCCACCTCCCGCACCCACTCC	42538948
Sbjct	42525195	TGGGACGGGACACGTGCGCGTGCCATGAAGGCATTAGCCCCACCATCCACCACCCACTCC	42525254
Query	42538949	AACCTTGGCGCTCCACAAGGTCTCCCGCAGTCCCTAGCCCGTCCAGCTGGGCACAGGGC	42539008
Sbjct	42525255	AACCTTAT-GCTCCCCCTGGTCTCCCGCAGTCCCTGGCTCTGTCCAGTGGTCACAGGGC	42525313
Query	42539009	CCACTCTTTGCTCACCCACATTGCTCCCTGCGTGGGGCGGGGTTTGGCCCCACCTCGTC	42539068
Sbjct	42525314	CCACTCTTTGCTCATCCACTTGTCTCCCTGGGCTGGGGCAGGGCTTGGCCCCACCTCGTC	42525373
Query	42539069	TCTGCCCCACCTGACCACCTTTCCTACTCAAGGAAGATCCCGCCCGTCCCG-----CCCAC	42539123
Sbjct	42525374	TCTGCCCCACCTGACCACCTTTCCTACTCAGGAAGACCCCGCGGGCCCGCGCCACCAC	42525433
Query	42539124	ACTGAGCCCGCAGCATAGGCGCGGTCCCGCCGACCGCCACTTCGACGC---AT-C-AGCC	42539178
Sbjct	42525434	ACTGAGCTTACAGCACAGGTGCGGTCCCGCC-CC-CCACTTCGACACCGGATTCCAGCT	42525491
Query	42539179	-----T-CGCC--C---ACC-----GGGCTTCTGGCGGGTCTGGGCAGTAGCCCCGCC	42539222
Sbjct	42525492	GGGAAATGCGCCAGCCTCACCCATTGGGCTCCTGCCAGGTCTCGGCAGTGGCCCCGCCA	42525551
Query	42539223	CTC--C-CA-GCCCA-CA---G-----A-CTCGCACCTCCCCGTGCAGGTGGTTTCTT	42539267
Sbjct	42525552	CTCGTCACAAGCCCGCCCTCGTCCCATGCTCACACTCCCTAGTGCAGGTGGTTTCTT	42525611
Query	42539268	GGCCCACTGTCTCAGCCCACTCGCTGGCCTTTATCTCTGTTTACGTCAGGACCCAC	42539327
Sbjct	42525612	GGCCCGCTGTC-----CCCACTCGCTGGC-----CTGTTTCATGTCCACGACCCCGC	42525658
Query	42539328	GCCCTGTTCGCGCTGCTTGGGCTACGGTACTGTCCACCCGGGGCCACGGAACGCGGT	42539387
Sbjct	42525659	GCCCTCTCTGCCAGCTCGGACTACGGTATCACCCACCCGGGTCCACGGAAT-CTGT	42525717
Query	42539388	CTCTGTCCCCACCGCGCTTGCCTTGGGAACGCGGGCCGAAGCCAGGACCTGGTAGAT	42539447
Sbjct	42525718	CTCTGT-CCCCACCGCTGCTTGCCTTGGGAACGCGGGCCGAACCCAGGATCTGGGTGAT	42525776
Query	42539448	GGCGCAGGCGGGCGGTGCGCGGTGTCCTCGCGCGGGTCACCATCGCTCGCGCACGGC	42539507
Sbjct	42525777	GGCGCAGGCGGGCGGTGCGCGGTGTCCTCGCGCGGGTCACCATCGCTCGCGCACGGC	42525836
Query	42539508	CGCCAGCCCATTTAGCACGACACCGGCTTCAGGCCAGTGCAGGCTGAACACGTCCCC	42539567
Sbjct	42525837	CGCCAGCCCATTTAGCACGACACCGGCTTCAGGCCAGTGCAGGCTGAACACGTCCCC	42525896
Query	42539568	GAAGCGGCGCCGAACATGCAGAGGGAGGGTCAGGGCTCTTGTCAAGCCAGGATCCCCC	42539627
Sbjct	42525897	GAAGCGGCGCCGAACATGCAGAGGGAGGGTCAGGGCTCTTGTCAAGCCAGGATCCCCC	42525956
Query	42539628	AGACTACAGGTCTTAGTCTTATTTGAACCTTGGACGACCCCGGGGCTACCAGGAGTGAG	42539687
Sbjct	42525957	AGACTACAGGTCTTAGTCTTATTTGAACCTTGGACGACCCCGGGGCTACCAGGAGTGAG	42526016
Query	42539688	CAGGTGGAAGGAGGAGACCCAGCCTCCTGATCCTggggcgggggtgggggTCACACCTTC	42539747
Sbjct	42526017	CAGGTGGAAGGAGGAGACCCAGCCTCCTGATCCTGGGGCGGGGGTGGGGGTACACCTTC	42526076
Query	42539748	TGTGATGGAGGAACCTCAGTTTGGATGCGTACCCAGGTATGACCTTGCAAGAGTCACCAA	42539807
Sbjct	42526077	TGTGATGGAGGAACCTCAGTTTGGATGCGTACCCAGGTATGACCTTGCAAGAGTCACCAA	42526136
Query	42539808	AATTGCCGAGAGGCCCACTTAGCATCCCATCCAGATGATGGTCCATGCCGGTGAGCA	42539867
Sbjct	42526137	AATTGCCGAGAGGCCCACTTAGCATCCCATCCAGATGATGGTCCATGCCGGTGAGCA	42526196
Query	42539868	GTGAGGCCCGAGGACCCACAGTGCAAAAGGTTTGAACCGGGTCACTGCACCCCTTCATC	42539927
Sbjct	42526197	GTGAGGCCCGAGGACCCACAGTGCAAAAGGTTTGAACCGGGTCACTGCACCCCTTCATC	42526256
Query	42539928	CTCGATTTCTGTGATTTAAACGGCACTCAGGACTAACTCATCTTCCATTCCCAAGGCCTTT	42539987
Sbjct	42526257	CTCGATTTCTGTGATTTAAACGGCACTCAGGACTAACTCATCTTCCATTCCCAAGGCCTTT	42526316
Query	42539988	CCTTCTGGTGTACGAGAAGGGACTTTGTACTCCATAACATATGTTGCCCAATGGGCTTG	42540047

12/2/2014

NCBI Blast:reflNC_000022.101 (51304566 letters)

Sbjct	42526317	CTGGTGTTCAGCAGAAGGGAC TTGTACTCCATAACATATGTTGCCCAATGGGCTTG	42526376
Query	42540048	CATGCCCACTGCCAAGTCCAGCTCCACCTCCAGGCCCTTGCCCTACTCTTCCTTGGCCTT	42540107
Sbjct	42526377	CATGCCCACTGCCAAGTCCAGCTCCACCTCCAGGCCCTTGCCCTACTCTTCCTTGGCCTT	42526436
Query	42540108	TGGAAAATCCAGTCCTTCATGCCATGTATAAATGTCCTTCCCCAGGACGTCCCCAAACC	42540167
Sbjct	42526437	TGGAAAATCCAGTCCTTCATGCCATGTATAAATGCCCTTCCTCAGGAAGTCCCCAAACC	42526496
Query	42540168	TGCTTCCCCTTCTCAGCCTGGCTTCTGATCCAGCCTGTGGTTTAACCCACCACCCATGTT	42540227
Sbjct	42526497	TGCTTCCCCTTCTCAGCCTGGCTTCTGGTCCAGCCTGTGGTTTCACCCACCACCCATGTT	42526556
Query	42540228	TGCTGGTGGTGGGGCATCCTCAGGACCTCTGCCGCCCTCCAGGACCTCCTCCCTCACCTG	42540287
Sbjct	42526557	TGCTGGTGGTGGGGCATCCTCAGGACCTCTGCCGCCCTCCAGGACCTCCTCCCTCACCTG	42526616
Query	42540288	GTCGAAGCAGTATGGTGTGTCTGGAAGTCCACATGCAGCAAGGTTGCCCAGCCCGGGCA	42540347
Sbjct	42526617	GTCGAAGCAGTATGGTGTGTCTGGAAGTCCACATGCAGC-AGGTTGCCCAGCCCGGGCA	42526675
Query	42540348	GTGGCAGGGGACCTGCGGGTAGCGTGCAGCCAGCGTTGGTGCCGGTGCATCAGGTCCA	42540407
Sbjct	42526676	GTGGCAGGGGACCTGCGGGTAGCGTGCAGCCAGCGTTGGTGCCGGTGCATCAGGTCCA	42526735
Query	42540408	CCAGGAGCAGGAAGATGGCCACTATCATGCCAGGGGCACCAGTGCTTCTAGCCCCATGG	42540467
Sbjct	42526736	CCAGGAGCAGGAAGATGGCCACTATCACGGCCAGGGGCACCAGTGCTTCTAGCCCCATAC	42526795
Query	42540468	CTGCCTCACTACCAACTGGGCTCCTCTGGACACACCTGGCACCCCCACCCACACAGGCAC	42540527
Sbjct	42526796	CTGCCTCACTACCAAAATGGGCTCCTCTGGACACACCTGGCACCCCCACCCACACAGGCAC	42526855
Query	42540528	AGAGGACCAGGCAGGACACTCTCAGCAC	42540555
Sbjct	42526856	AGAGGACCAGGCAGGACACTCTCAGCAC	42526883

References

1. Evans WE, Hon YY, Bomgaars L, *et al.*: **Preponderance of thiopurine S-methyltransferase deficiency and heterozygosity among patients intolerant to mercaptopurine or azathioprine.** *J Clin Oncol.* 2001; **19**(8): 2293–2301.
[PubMed Abstract](#)
2. Relling MV, Gardner EE, Sandborn WJ, *et al.*: **Clinical Pharmacogenetics Implementation Consortium guidelines for thiopurine methyltransferase genotype and thiopurine dosing.** *Clin Pharmacol Ther.* 2011; **89**(3): 387–391.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
3. Mizzi C, Peters B, Mitropoulou C, *et al.*: **Personalized pharmacogenomics profiling using whole-genome sequencing.** *Pharmacogenomics.* 2014; **15**(9): 1223–1234.
[PubMed Abstract](#) | [Publisher Full Text](#)
4. Browning SR, Browning BL: **Rapid and accurate haplotype phasing and missing-data inference for whole-genome association studies by use of localized haplotype clustering.** *Am J Hum Genet.* 2007; **81**(5): 1084–1097.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
5. Browning SR, Browning BL: **Haplotype phasing: existing methods and new developments.** *Nat Rev Genet.* 2011; **12**(10): 703–714.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
6. Untergasser A, Cutcutache I, Koressaar T, *et al.*: **Primer3—new capabilities and interfaces.** *Nucleic Acids Res.* 2012; **40**(15): e115.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
7. Li H, Durbin R: **Fast and accurate short read alignment with Burrows-Wheeler transform.** *Bioinformatics.* 2009; **25**(14): 1754–1760.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
8. Langmead B, Salzberg SL: **Fast gapped-read alignment with Bowtie 2.** *Nat Methods.* 2012; **9**(4): 357–359.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
9. Chaisson MJ, Tesler G: **Mapping single molecule sequencing reads using basic local alignment with successive refinement (BLASR): application and theory.** *BMC Bioinformatics.* 2012; **13**: 238.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
10. Kielbasa SM, Wan R, Sato K, *et al.*: **Adaptive seeds tame genomic sequence comparison.** *Genome Res.* 2011; **21**(3): 487–493.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
11. Zanger UM, Schwab M: **Cytochrome P450 enzymes in drug metabolism: regulation of gene expression, enzyme activities, and impact of genetic variation.** *Pharmacol Ther.* 2013; **138**(1): 103–41.
[PubMed Abstract](#) | [Publisher Full Text](#)
12. Horton R, Gibson R, Coggill P, *et al.*: **Variation analysis and gene annotation of eight MHC haplotypes: The MHC Haplotype Project.** *Immunogenetics.* 2008; **60**(1): 1–18.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
13. Van der Auwera GA, Carneiro MO, Hartl C, *et al.*: **From fastQ data to high confidence variant calls: The genome analysis toolkit best practices pipeline.** *Curr Protoc Bioinforma.* 2013; **11**(1110): 11.10.1–11.10.33.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
14. Li H, Handsaker B, Wysoker A, *et al.*: **The Sequence Alignment/Map format and SAMtools.** *Bioinformatics.* 2009; **25**(16): 2078–2079.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
15. Drmanac R, Sparks AB, Callow MJ, *et al.*: **Human genome sequencing using unchained base reads on self-assembling DNA nanoarrays.** *Science.* 2010; **327**(5961): 78–81.
[PubMed Abstract](#) | [Publisher Full Text](#)
16. Frazer KA, Ballinger DG, Cox DR, *et al.*: **A second generation human haplotype map of over 3.1 million SNPs.** *Nature.* 2007; **449**(7164): 851–861.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
17. Leckband SG, Kelsoe JR, Dunnenberger HM, *et al.*: **Clinical Pharmacogenetics Implementation Consortium guidelines for HLA-B genotype and carbamazepine dosing.** *Clin Pharmacol Ther.* 2013; **94**(3): 324–8.
[PubMed Abstract](#) | [Free Full Text](#)
18. Martin MA, Hoffman JM, Freimuth RR, *et al.*: **Clinical Pharmacogenetics Implementation Consortium Guidelines for HLA-B Genotype and Abacavir Dosing: 2014 update.** *Clin Pharmacol Ther.* 2014; **95**(5): 499–500.
[PubMed Abstract](#) | [Free Full Text](#)
19. Hershfield MS, Callaghan JT, Tassaneeyakul W, *et al.*: **Clinical Pharmacogenetics Implementation Consortium guidelines for human leukocyte antigen-B genotype and allopurinol dosing.** *Clin Pharmacol Ther.* 2013; **93**(2): 153–8.
[PubMed Abstract](#) | [Free Full Text](#)
20. Zhou, SF: **Polymorphism of human cytochrome P450 2D6 and its clinical significance: part II.** *Clin Pharmacokinet.* 2009; **48**(12): 761–804.
[PubMed Abstract](#) | [Publisher Full Text](#)
21. Crews KR, Gaedigk A, Dunnenberger HM, *et al.*: **Clinical Pharmacogenetics Implementation Consortium guidelines for cytochrome P450 2D6 genotype and codeine therapy: 2014 update.** *Clin Pharmacol Ther.* 2014; **95**(4): 376–82.
[PubMed Abstract](#) | [Free Full Text](#)
22. Hicks JK, Swen JJ, Thorn CF, *et al.*: **Clinical Pharmacogenetics Implementation Consortium guideline for CYP2D6 and CYP2C19 genotypes and dosing of tricyclic antidepressants.** *Clin Pharmacol Ther.* 2013; **93**(5): 402–8.
[PubMed Abstract](#) | [Free Full Text](#)
23. Odelberg SJ, Weiss RB, Hata A, *et al.*: **Template-switching during DNA synthesis by *Thermus aquaticus* DNA polymerase I.** *Nucleic Acids Res.* 1995; **23**(11): 2049–2057.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
24. Listgarten J, Brumme Z, Kadie C, *et al.*: **Statistical resolution of ambiguous HLA typing data.** *PLoS Comput Biol.* 2008; **4**(2): e1000016.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
25. Brownstein CA, Margulies DM, Manzi SF: **Misinterpretation of TPMT by a DTC Genetic Testing Company.** *Clin Pharmacol Ther.* 2014; **95**(6): 598–600.
[PubMed Abstract](#)
26. Stanulla M, Schaeffeler E, Flohr T, *et al.*: **Thiopurine methyltransferase (TPMT) genotype and early treatment response to mercaptopurine in childhood acute lymphoblastic leukemia.** *JAMA.* 2005; **293**(12): 1485–1489.
[PubMed Abstract](#) | [Publisher Full Text](#)
27. Ammar R, Paton TA, Torti D, *et al.*: **Nanopore reads and alignments.** *figshare.* 2015.
[Data Source](#)

Open Peer Review

Current Peer Review Status:

Version 1

Reviewer Report 30 March 2015

<https://doi.org/10.5256/f1000research.6463.r7919>

© 2015 Hoenen T. This is an open access peer review report distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Thomas Hoenen

Laboratory of Virology, Division of Intramural Research, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Hamilton, MT, USA

This manuscript describes the analysis of three PCR-fragments generated from a human reference sample using a MinION sequencing device. Despite the preliminary nature of the data, and the fact that the paper is based on a single run of a single sample, it will nevertheless be of significant interest, and publication as a research note is in my view justified. In fact, given the broad interest in this emerging new technology, and its applicability to all life sciences (not just human (pharmaco-)genetics), the readership might be much wider than anticipated by the authors. This constitutes at the same time the biggest weakness of the paper, since it is in parts rather inaccessible for readers from fields other than human genetics (e.g. virology or microbiology), for whom this paper might nevertheless be highly relevant.

In order to address the concern that the manuscript is based on a single MinION run, and given the nature of the MAP program, it should be no problem for the authors to repeat the experiment with another sample, and while doing so specifically address the concerns of Dr. Kennedy. In addition, the authors should strive to improve accessibility to a wider audience wherever possible. Finally, it would be helpful to include additional experimental details that are currently missing.

Specific comments:

- PCR cycling conditions should be provided.
- The authors refer to the SQK-MAP003 sequencing protocol. As far as I am aware, Oxford Nanotechnologies does not make the detailed protocol available to people outside the MAP program, although there have been indications that a non-technical version of the protocol will be made available for publication purposes. The authors should reference such a protocol (including a link) as soon as possible, and approach ONT about making it available to the general public, if this hasn't happened already.
- Did the authors perform a PCR purification prior to the library preparation? If so, what was the volume/ratio of Agencourt beads to sample?
- How did the authors extract reads from the fast5 files? Did they use poretools, or another

- tool (which should be referenced)?
- In general, providing more details about the exact bioinformatics workflow would be helpful.
 - What was the rationale for the cut-off of 1/3 of reads for variant calling?
 - It seems odd that the length of the aligned fragments from the 1D reads is so much shorter than the read length. In our hands (using a similar approach on ~2 kB PCR products amplified from virus genomes, albeit with a later chemistry/protocol version (SQK-MAP004) and using LAST for the alignment) we get much longer average alignments (92% for 2D reads, 82% for template reads, and 85% for complement reads, vs. 85%, 23% and 11% reported by the authors). This could either indicate significant advances in base-calling accuracy since the authors performed their experiments, or that their alignment is suboptimal. It might be very interesting to see whether the authors can get longer alignments using LAST or other alignment softwares in their workflow.
 - It would be very helpful if the authors could repeat the experiment using the newest chemistry/protocol/software versions, which have changed considerably over the last months. At the same time this would allow them to address many of the concerns of Dr. Kennedy.

Competing Interests: I am a participant in the MinION access program. Other than that, I have no connections to the authors, and I do not know them. I do not have any competing interests.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 06 February 2015

<https://doi.org/10.5256/f1000research.6463.r7404>

© 2015 Kennedy M. This is an open access peer review report distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Martin Kennedy

Gene Structure and Function Laboratory, Department of Pathology, University of Otago, Christchurch, New Zealand

General comments:

This research note describes preliminary results from the application of a new nanopore sequencing device (the MinIon), under development by Oxford Nanopore Technologies, to the analysis of three amplicons of pharmacogenetic interest.

The paper is suitable for a research note. Although the findings are very preliminary, this is a new technology and there is a lot of interest in understanding its current capabilities, longer-term potential and limitations.

Positive aspects of the report are description of long-read nanopore sequencing on long

amplicons (4-5kb), and description of data handling and bioinformatics approaches this team is using, which may aid others working with the MinIon device. Negative aspects of the report are that all the data are from only one reference sample, and one run on the device; rather than being utterly convincing, the data suggests haplotyping on unknown samples may be possible only once error rates on the MinIon reduce; and there is an unresolved question about the CYP2D6 CNV or haplotype analyses, potentially due to sample contamination.

Despite these issues, the report is still of merit and will be of interest to many in the field.

Specific comments:

Methods

Long PCR has been widely used for specific amplification of CYP2D6, with reaction conditions and primer sequences well established. It is not clear why the authors designed their own primers for this task, or how these novel primers were validated. This should be spelt out more clearly.

It would have been useful to have non-diploid control samples for the CYP2D6 CNV assay – for example a haploid (CYP2D6*5) case or multicopy case, to provide confidence that the assay was working as expected. This is relevant because of the question raised by the *2 haplotype which shows up in the MinIon analysis of NA12878.

Results

Page 6, first para: This description of the possible origins of the mystery CYP2D6*2 haplotype needs some editing for improved clarity. Not clear what is meant by “*3 and *4 duplexes forming”. Also not clear what would cause PCR biases alluded to in the last sentence of this paragraph (and of the following paragraph).

Typos/suggested edits:

Abstract

MinION > MinIon

Should refer to NA12878 as “reference sample” rather than just “sample”

Suggest sentence be modified thus for clarity: “...statistically phased genotype data from Complete Genomics and Sequenom.”

Suggest delete “Standalone” in penultimate line.

Introduction

Suggest this sentence be changed: However, existing methods have various limitations, which may lead to adverse drug responses. > However, existing methods have various limitations, which may lead to failure to detect variants of pharmacogenetic significance.

Methods

Page 3, 2nd para: indels expects > indels expected

Page 4 para 2 – clarify “The HuRef sample...”

Figure 1 title: Integrate > Integrative

Results

Page 5, para 4. First sentence should read thus, for improved clarity: “CYP2D6 haplotype

proportions in MinIon data were identified by interrogating clinical marker positions..."

Supp File S1

It would be helpful to indicate which of the sequences is CYP2D6 and which is CYP2D7.

Competing Interests: I am also a participant in the MinIon Access Programme, and my laboratory is working with the device. I met Dr Ammar at a meeting organised by ONT, and we have a shared interest in use of this technology for pharmacogenetic analysis. However, I have not been involved in the work described here.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

The benefits of publishing with F1000Research:

- Your article is published within days, with no editorial bias
- You can publish traditional articles, null/negative results, case reports, data notes and more
- The peer review process is transparent and collaborative
- Your article is indexed in PubMed after passing peer review
- Dedicated customer support at every stage

For pre-submission enquiries, contact research@f1000.com

F1000Research