

METHOD

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# An optimized microarray platform for assaying genomic variation in *Plasmodium falciparum* field populations

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## Abstract

We present an optimized probe design for copy number variation (CNV) and SNP genotyping in the *Plasmodium falciparum* genome. We demonstrate that variable length and isothermal probes are superior to static length probes. We show that sample preparation and hybridization conditions mitigate the effects of host DNA contamination in field samples. The microarray and workflow presented can be used to identify CNVs and SNPs with 95% accuracy in a single hybridization, in field samples containing up to 92% human DNA contamination.

## Background

*Plasmodium falciparum* is the intracellular parasite responsible for the majority of the world's malaria morbidity and mortality burden in humans, causing an estimated 243 million episodes of malaria and 863,000 deaths each year [1]. Efforts to control and eradicate malaria are hampered by the accelerated evolution of drug resistance in the parasite. To date, the parasite has developed resistance to all major antimalarial drugs, raising concerns about the spread of drug-resistant parasites and the ability to effectively treat malaria [2]. The development of new technologies aimed at understanding parasite genome variability provides hope in identifying new drug targets, implementing smarter treatment plans, and ultimately reducing or eliminating the burden of malaria.

Genome variation such as SNPs and copy number variation (CNV) underpins *P. falciparum* drug resistance. The primary determinant of chloroquine resistance is a mutation in the *P. falciparum* chloroquine resistance transporter gene on chromosome (chr) 7 [3,4]. *In vitro* resistance to the antifolate drugs sulfadoxine and pyrimethamine increases in a step-wise manner as mutations accrue in dihydrofolate reductase and dihydropteroate

synthase [5-8]. Varying copy number of the *P. falciparum* multidrug resistance 1 gene on chr 5 influences parasite susceptibility to a range of antimalarial drugs, including mefloquine, lumefantrine, quinine, and artemisinin [9-11]. Amplification on chr 12 of GTP cyclohydrolase 1 of the folate biosynthesis pathway is correlated with antifolate drug resistance [12,13]. These examples emphasize the importance of genomic variation in drug resistance and need to assay both SNPs and CNV genome-wide in the malaria parasite.

Microarrays provide a relatively fast and inexpensive way of examining genomic variation in *P. falciparum* [14]. Array comparative genomic hybridization (CGH) has been successfully used to look at structural variation and CNV in multiple *P. falciparum* strains [12,15-17], while large-scale sequencing efforts identifying SNPs [18-20] have spurred the development of SNP microarrays. Neafsey *et al.* [21] genotyped 1,638 out of 3,000 queried SNPs with 100% accuracy using an Affymetrix 3K SNP assay. Mu *et al.* [22] used Affymetrix molecular inversion probe technology to genotype 2,763 of 3,354 SNPs with >90% call rate. Multiple groups have successfully applied CGH for SNP detection with 80 to 90% sensitivity to approximately 3,000 SNPs [23,24] and identified parameters influencing SNP detection [24,25]. However, the reported detection rates are based on a core subset of SNPs (approximately 3,000) in a genome

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with more than 100,000 cataloged SNPs (PlasmoDB v5.5) [26].

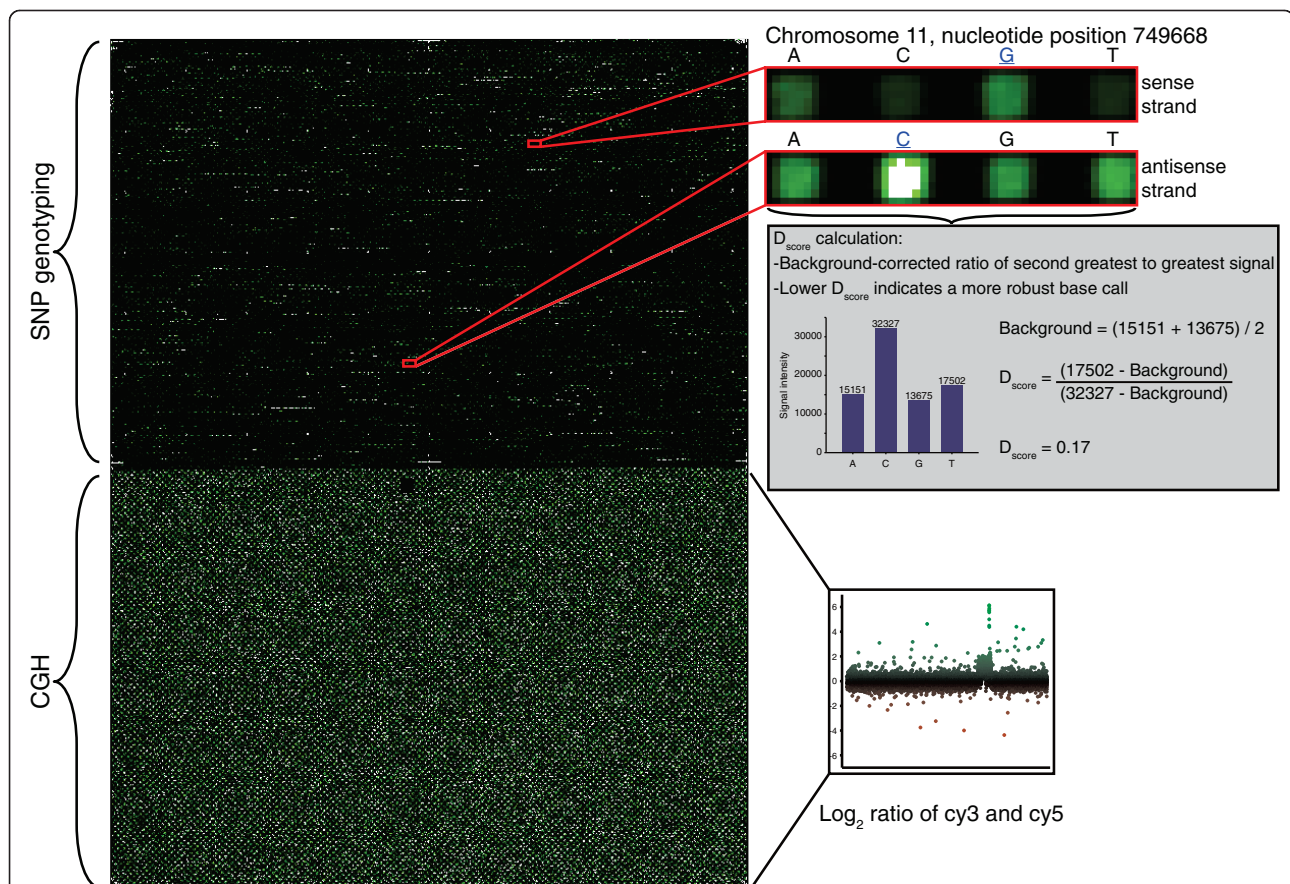
Our central goal was to develop a single microarray platform that can assay CNV and genotype SNPs simultaneously and to optimize this platform for the challenges of monitoring monoclonal patient blood samples from field studies. We first empirically determined the optimum probe lengths and melting temperatures for SNP genotyping in the 81% AT *P. falciparum* genome. This was used to guide the design of a single high-resolution genotyping microarray with variable length probes optimized for high quality SNP genotyping and CNV detection (Figure 1). One half of the microarray interrogates 45,524 SNP loci using optimized resequencing probes 29 to 41 bp in length capable of making a base call at a precise nucleotide position [27]. The second half identifies CNV using tiled CGH probes 50 to 75 bp in length. We determine the reliability and accuracy of the CNV-SNP array using the laboratory lines 3D7, HB3, Dd2, SC05, and 7C126. We then validate the

utility and robustness of the microarray using field samples with limited parasite DNA and high human DNA contamination present using blood collected from humans at the Thailand-Burma border.

## Results

### Effects of probe length and probe melting temperature on the robustness of base calls

Using a prototype 5K SNP chip, the performance of static probe lengths was compared to the performance of variable length, isothermal probes on base calling robustness. A base call is considered robust when a probe quartet has a single high nucleotide signal relative to the other three nucleotide signals, and the sense and antisense base calls are complementary. A  $D_{score}$  calculating the background noise relative to the highest signal intensity in a probe quartet (Figure 1, grey inset) was used to compare the performance of static probes and isothermal probes. A  $D_{score}$  close to 1 indicates high background noise and poor discrimination ability



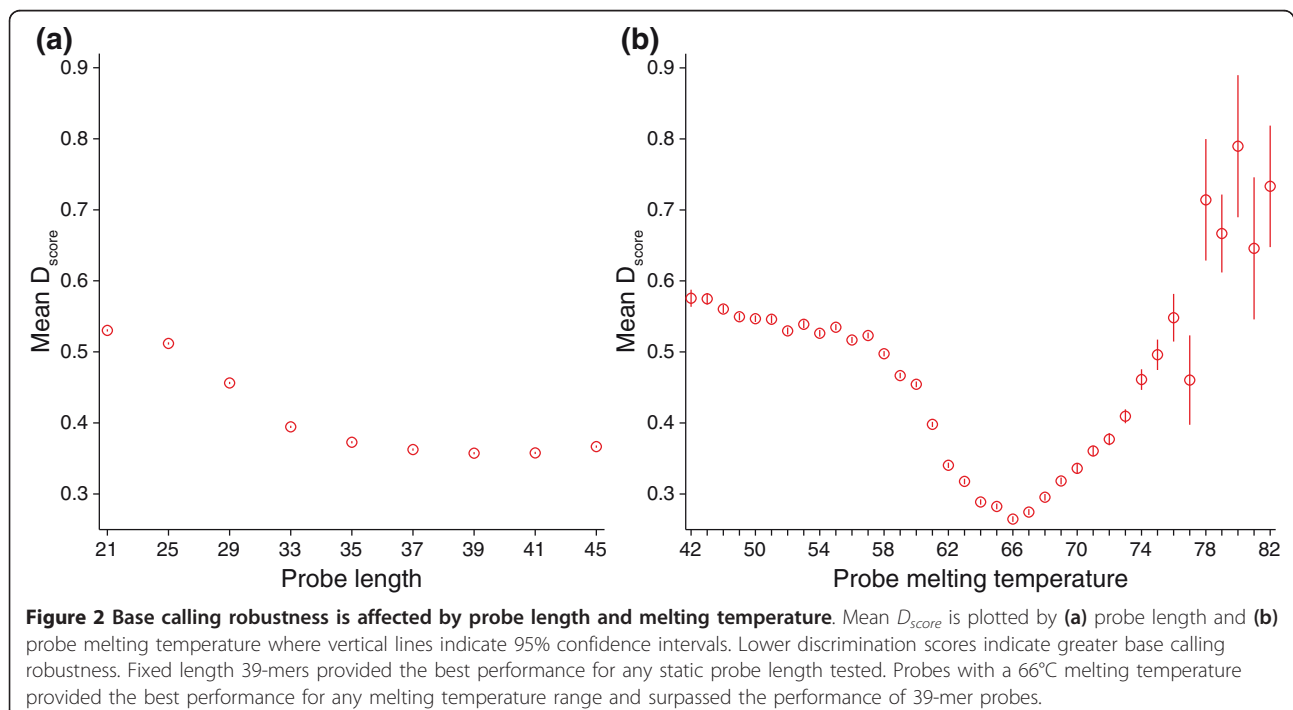
**Figure 1 Microarray layout and design.** The microarray contains blocks of probesets for SNP genotyping and CGH. SNP genotyping probesets are composed of two probe quartets, one for each strand (red blowouts). Probes from one quartet typically have hybridization signals in a similar dynamic range. These signals are used to determine a base call and calculate base calling robustness, which is expressed as a  $D_{score}$  where the two lesser hybridization signals are used to estimate background noise for each probe quartet (grey inset). The CGH probesets record data that are used to generate  $\log_2$  ratios of a test and reference sample.

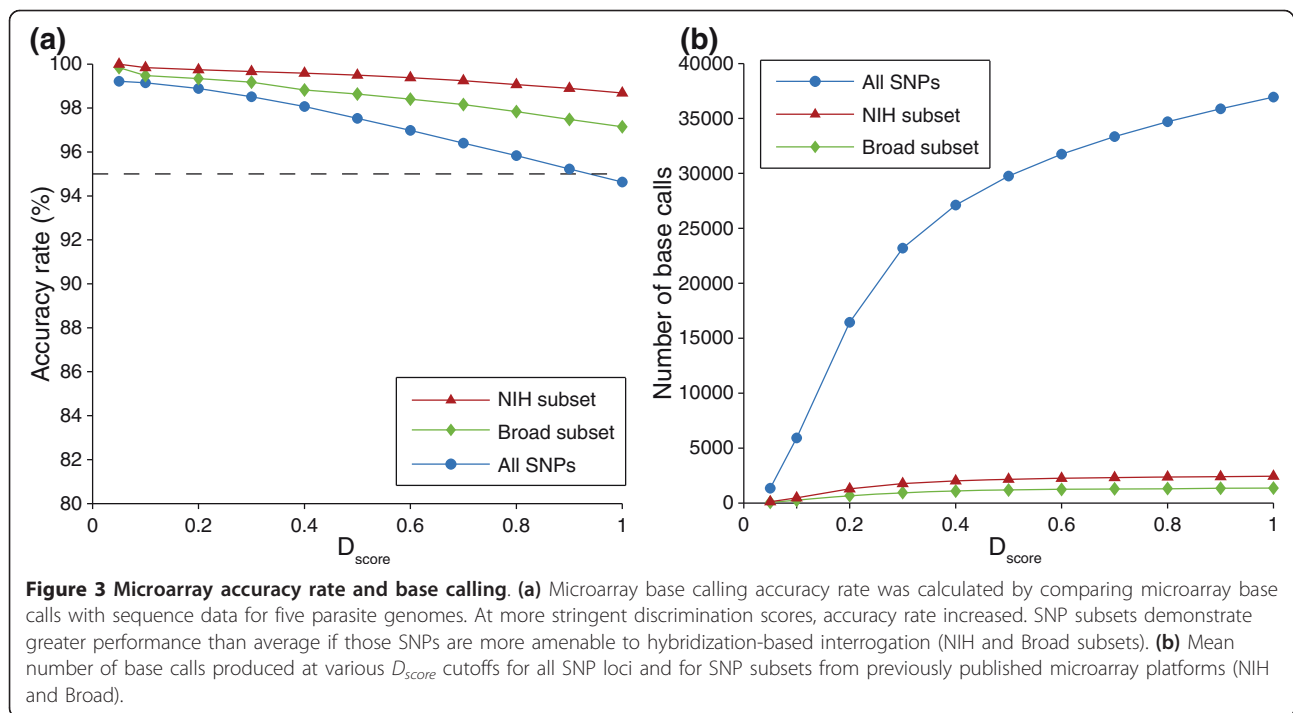
between probe signals, while a score close to 0 indicates low background noise and good discrimination ability. The mean  $D_{score}$  of the 5K SNP chips was plotted for static probe lengths (Figure 2a) and for probe melting temperature (Figure 2b). Statistical analysis with a one-way ANOVA indicates significant differences between mean  $D_{score}$  at various probe lengths ( $P < 0.0001$ ), and a Tukey's multiple comparison test indicates that all probe lengths except 39- and 41-mers have a significantly different mean  $D_{score}$  ( $P < 0.05$ ). Out of the nine tested probe lengths, 39-mer probes generated the lowest mean  $D_{score}$  with the best discrimination ability ( $\bar{x} = 0.3575$ ). A one-way ANOVA analysis indicates probe melting temperature  $D_{score}$  are significantly different from one another ( $P < 0.0001$ ), and a Tukey's multiple comparison test indicates melting temperature in the 66°C range was significantly different from other melting temperatures ( $P < 0.05$ ). The lowest mean  $D_{score}$  with the best discrimination ability for probe melting temperatures was generated at 66°C from the range of 42 to 82°C ( $\bar{x} = 0.2647$ ), and this outperformed any static probe lengths. Similar performance was seen when comparing exons, introns, and intergenic regions (Figure S1 in Additional file 1).

#### Microarray base calling accuracy

Microarray data for 3D7, HB3, Dd2, SC05, and 7C126 ( $n = 15, 5, 3, 2,$  and  $2$ , respectively) were compared to genome sequence data to ascertain base calling accuracy (Figure 3a). A useable base call was made at a SNP

locus when the sense and antisense probesets indicated complementary bases; otherwise, there would be no base call for that SNP locus. Figure 3a depicts mean microarray accuracy plotted by  $D_{score}$ ; also depicted are CNV-SNP array data for the SNP subsets that are represented on SNP genotyping microarrays developed by the Broad Institute [21] and NIH [22]. The CNV-SNP array genotypes 1,507 of the 1,631 publicly available Broad Institute SNPs and 2,621 of the 2,743 publicly available NIH SNPs. For all SNP sets, a lower  $D_{score}$  is associated with higher accuracy. SNPs from the Broad Institute and NIH maintain >95% accuracy at all  $D_{score}$  cutoffs with 97.1% accuracy and 98.7% accuracy, respectively, at a  $D_{score}$  cutoff of 1. The accuracy of all SNPs assayed on the CNV-SNP array maintain >95% accuracy for  $D_{score} \leq 0.9$  but drops to an average accuracy of 94.6% at a  $D_{score}$  of 1. Figure 3b depicts the mean number of base calls made by the microarray plotted by  $D_{score}$  for all SNPs and for the SNP subsets from the Broad Institute and NIH microarray platforms (Figure 3b). On average, a microarray hybridization yielded 36,948 base calls from the 45,524 assayed SNP loci for a base call rate of 81.2%. The Broad Institute and NIH SNP subsets had an average call rate of 90.7% and 93.0%, respectively. Lower numbers of base calls are made at more stringent  $D_{score}$  cutoffs for all data sets. When comparing accuracy for SNP subsets in exons, introns, and intergenic regions, introns and intergenic regions perform similarly, and exons exhibited the best performance (Table 1).





### Comparative genomic hybridization performance

Segmentation analyses on multiple hybridizations of HB3 and Dd2 against the reference 3D7 detected the same copy number events detected in HB3 and Dd2 hybridizations against 3D7 found previously [25]. Median probe spacing between the 5' end of CGH probes is 52 bp, providing a fine resolution view of CNV that can precisely implicate breakpoints to within 100 bp. The resolution provided by this platform is equivalent to a previous NimbleGen CGH chip [25]. Figure 4 shows CGH scatterplots demonstrating microarray-based CNV breakpoint detection in comparison with the exact breakpoint determined through capillary sequencing.

CNV events are highly reproducible between replicate hybridizations with this microarray platform (Figure S2 in Additional file 1). Features, including a 500 bp CNV event, were recognized and consistent between hybridizations; however, it becomes more difficult to confidently detect small CNV events algorithmically. CNV event detection is still possible with whole genome amplification (WGA) samples (Figure S3 in Additional file 1), although the amplification process introduces noise, confounding CNV detection by any platform, particularly reducing confidence in small events. Degraded samples can not be recovered for effective CGH by WGA.

### Applications to *P. falciparum* field samples

Standard probe labeling protocols utilize random nonamers with balanced base composition. However, *P.*

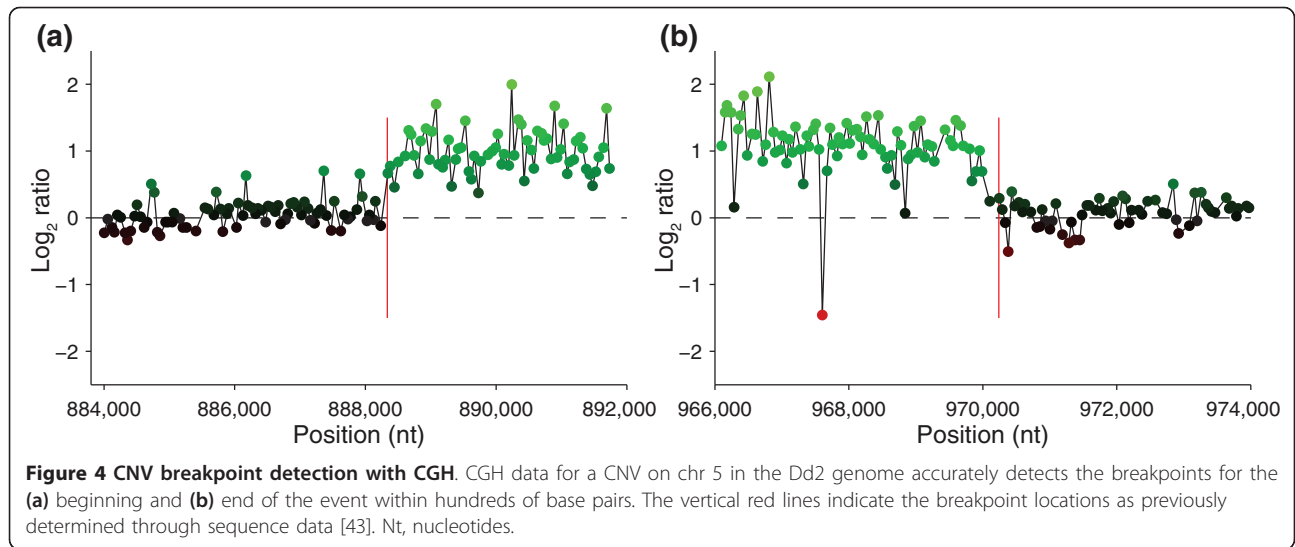
*falciparum* has an extremely high AT content of 81% [28], which reduces the performance of 50% AT random nonamers and may introduce bias during amplification of the parasite genome. To test the effect of random nonamer AT composition on labeling performance and microarray data, labeling yields of 65% AT random nonamers ( $38,357 \pm 3468.1$  ng) were compared with labeling yields of 50% AT random nonamers ( $18,865 \pm 4530.7$  ng). The data pass a D'Agostino-Pearson normality test and a paired *t*-test, indicating that 65% AT random nonamers generate a significantly greater yield of labeled DNA than 50% AT random nonamers ( $P < 0.01$ ). We see no adverse effects on base calling accuracy or CGH performance when using this modified labeling procedure.

Larger yields of labeled DNA are generated by 65% AT random nonamers, allowing the amount of initial starting DNA to be reduced. We evaluated decreasing amounts of starting material that could generate the necessary 10  $\mu$ g of labeled DNA for hybridization. Labeling yields using 250 ng, 375 ng, 500 ng, and 1,000 ng of starting DNA for 3D7, HB3, and Dd2 were

**Table 1 Microarray accuracy in exons, introns, and intergenic regions**

Location	Accuracy, $D_{score} \leq 1.0$	Accuracy, $D_{score} \leq 0.5$
Exon	96.3%	98.5%
Intron	91.2%	95.4%
Intergenic region	90.4%	94.9%

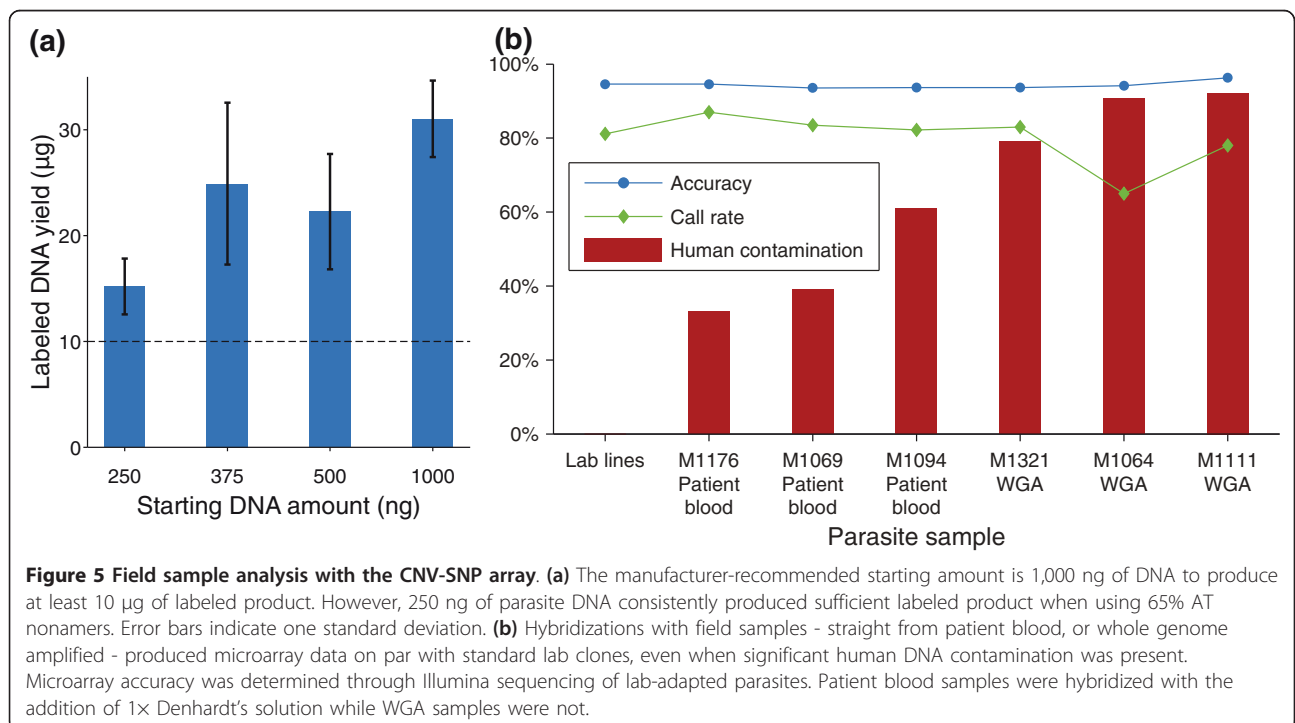




quantified (Figure 5a) and hybridized on the microarray. More than 10  $\mu\text{g}$  of labeled DNA was obtained from all labeling reactions and no base calling or CNV detection differences were seen between the different starting amounts, indicating a starting DNA amount  $\leq 250$  ng is sufficient to generate high quality hybridization data.

Human DNA is invariably present in field-collected samples of parasite DNA and is especially high when leukocyte depletion is not used in the extraction method. In some cases, human DNA may constitute >90% of the total DNA extracted from infected blood

samples and can hinder downstream uses of the parasite DNA for microarray hybridizations or sequencing. Nucleic acid blockers are commonly used in microarray hybridizations to prevent random probe binding to non-target nucleic acids and were tested on our microarray to prevent performance reduction in samples with significant amounts of human DNA contamination. We tested various nucleic acid blockers and found that 1 $\times$  Denhardt's solution provided the greatest number of base calls with no negative impact on CGH data when compared to hybridizations with bovine serum albumin,



dimethyl sulfoxide, human Cot1 DNA, salmon sperm, and yeast tRNA. To test for the effect of human DNA contamination on our microarray, several DNA samples were extracted from Thailand-Burma patient blood samples or were whole genome amplified from patient blood. The amount of human DNA present in each sample was quantified, and 33 to 92% of the total DNA was found to be human, with WGA samples containing the most human DNA. WGA is generally, but not always, helpful as there is some variability in data generated from WGA samples. Using 250 ng of parasite DNA, field samples were hybridized to the microarray and examined for the number and accuracy of base calls (Figure 5b); accuracy was determined using Illumina sequences generated from the same samples (M Manske, unpublished observations). This platform is able to produce high quality data with samples containing extensive host DNA contamination equivalent to data from purified lab line DNA (Figure 5b).

## Discussion

The CNV-SNP array provides robust, accurate data for both laboratory- and field-derived samples. Through optimizations described here, the CNV-SNP array overcomes many hurdles associated with molecular work on *P. falciparum* field samples. Lower starting amounts of DNA are possible when using 65% AT random nonamers that compensate for the extreme AT bias of the genome. This optimization is especially useful for field sample DNA, which is typically scarce and difficult to obtain. It also eliminates the need for *in vitro* culture adaptation of field samples, which is typically used to generate enough DNA for applications like next-generation sequencing and is known to alter CNV and skew results of CNV analyses [29,30]. Using our modified protocol, the CNV-SNP array requires no more than 250 ng of starting parasite DNA with no compromise in data quality. Moreover, the ample yields of labeled DNA from 250 ng of starting parasite DNA indicate that the lower limit has not yet been defined, raising the possibility that finger prick blood samples on filter paper are accessible to this technology. In addition, the CNV-SNP array is robust to samples with high host DNA contamination (>90%) with no drop in data quality, making microarray-based genotyping complementary to higher resolution next-generation sequencing that is sensitive to human DNA contamination in field samples, often requiring sample preprocessing for target DNA enrichment. Notably, high human DNA contamination and low amounts of parasite DNA present serious challenges to genotyping the large number of samples necessary for genome-wide association studies.

Probe design optimizations contribute to the performance of this microarray for the *P. falciparum* genome.

Sense and antisense resequencing probe quartets were used for SNP genotyping on the CNV-SNP array. A SNP call required that sense and antisense probe quartets made complementary calls; furthermore, the robustness of the base call was evaluated using the ratio of background signal versus the probe with the greatest signal intensity. Signal intensities within SNP probe quartets were more similar to each other than to probes in other probe quartets or between sense and antisense probe quartets of the same locus (Figure 1) and indicates the importance of measuring the background signal for each individual SNP quartet - as provided by the resequencing probesets - rather than background noise from the entire array or locus.

Resequencing probes were optimized for SNP genotyping in *P. falciparum* by comparing the performance of probes at static lengths with probes balanced by melting temperature on a prototype 5K SNP array. Probe melting temperature outperformed static probe lengths for optimal SNP detection at a probe melting temperature of 66°C with performance that was reasonably consistent in exons, introns, and intergenic regions (Figure S1 in Additional file 1).

Our results on optimal probe length and melting temperature differ from findings in another study [31]. This is likely due to the use of different methods for calculating probe melting temperature and our optimization to the AT-rich *P. falciparum* genome. However, our broader conclusion that variable length or isothermal probes provide optimal SNP detection is supported across various organisms [31,32], and indicate that longer, isothermal probes increase signal strength while also being short enough to remain sensitive to single base mismatches [32-35].

Resequencing probesets designed for a 66°C melting temperature were generated for 45,524 SNP loci for inclusion on the CNV-SNP array. While longer, isothermal probes improve SNP genotyping, certain loci are more easily genotyped than others, and some remain inaccessible to microarrays and short-read next-generation sequencing technologies. For instance, SNPs in exons have greater genotyping success than SNPs in introns or intergenic regions, likely due to regions of high AT richness or interspersed sequence repetitiveness that hinder probe design and binding specificity in intronic and intergenic regions. Current SNP genotyping microarrays, such as those developed by the NIH and the Broad Institute [21,22], are focused on high quality SNP loci that are easily genotyped across microarray platforms (Figure 3). However, the use of isothermal probes designed at an optimal melting temperature allows us to interrogate more difficult loci and maximize the overall number of SNPs that can be robustly genotyped on the CNV-SNP array (on average, 36,948

useable SNP genotypes with 95% accuracy from a single hybridization).

An interesting debate surrounds the continued value of microarrays with the emergence of next-generation sequencing. As the cost of next-generation sequencing continues to decrease and protocols continue to improve, we will see a realization of the platform providing ultimate resolution and throughput, provoking the prediction that microarrays will soon be rendered obsolete. However, we suggest that the CNV-SNP array will continue to be useful as an 'everylab' tool alongside next-generation sequencing. Whole genome sequencing underpins the SNP discovery needed for chip design; in general, whole genome architecture and ultra-resolution mapping require fully sequenced and assembled genomes. The customizable microarray platform continues to improve in density (4.2 million element custom designs are anticipated in 2011) and offers unique configurations up to 12-plex of 135K probes, leading to a scenario in which a global set of SNPs identified by sequencing can be precisely represented on microarrays for regionally focused or hypothesis-driven designs. To date, microarrays remain cheaper, produce data more quickly, require less computational innovation, and are especially useful for processing large numbers of samples, while producing sufficient resolution and quality for genome-wide association studies and population genomic analysis. Furthermore, although progress is being made in scoring CNV using next-generation sequencing, that technology still lags behind the performance of microarray CGH.

## Conclusions

As *P. falciparum* continues to evolve and evade control and eradication efforts, high-throughput, cost-effective methods of monitoring genomic variation are critical to understanding parasite adaptation. The high AT content of the *P. falciparum* genome is technically challenging for most molecular methods; however, the flexibility of the microarray platform described here allows users to customize and optimize microarrays to individual genomes through alterations of probe lengths, types, and numbers and adjustment of hybridization strategy. This process is applicable to population genomic studies in a wide range of organisms. Utilizing this flexibility, we created a custom high-density CNV-SNP array containing both resequencing probes capable of SNP genotyping and CGH probes for CNV detection. The CNV-SNP array is a reliable, accurate platform that allows simultaneous investigation of CNV and SNPs in a single hybridization. Its low cost, quick turn-around time, low DNA requirements, and resilience to human DNA contamination make it a valuable tool for population genomic studies.

## Materials and methods

### Microarray design

#### Probe length optimization

As an initial step in SNP genotyping optimization, a NimbleGen resequencing microarray consisting of variable length resequencing probesets was developed to assay 5,347 SNP loci. A NimbleGen resequencing probeset is composed of eight probes per SNP locus: four probes each for interrogation of sense and antisense strands. Each probe quartet is identical except for the central nucleotide that assays the nucleotide variant [27]. We downloaded 101,581 candidate SNP loci from PlasmoDB v5.5 [26] for parasite isolates HB3, Dd2, V1/S, 7G8, D10, FCC-2, K1, RO-33, D6, GHANA1, FCB, and IT. Common SNPs (SNPs identified in at least two parasite isolates) were blasted against the 3D7 genome to verify a unique 21-mer SNP typing probe sequence. Probesets with more than one exact match in the genome were discarded. Of the remaining candidate probesets, 5,347 SNP loci were randomly chosen for inclusion on the 5K SNP chip at nine different probe lengths: 21, 25, 29, 33, 35, 37, 39, 41, and 45-mers. Hybridizations following NimbleGen standard CGH procedures [36] were performed using DNA from laboratory clones 3D7, HB3, Dd2, 7G8, and D10.

#### CNV-SNP array

Using NimbleGen's 3-plex custom chip layout, each plex in our 3-plex 720K NimbleGen microarray contains resequencing probes for SNP genotyping and CGH probes for CNV detection (Figure 1). Probes were synthesized using maskless photolithography [37,38] with CGH probes attached by 5T linkers and resequencing probes attached with 15T linkers. Of the 101,581 candidate SNP loci downloaded from PlasmoDB and BLASTed for uniqueness, probesets for all SNPs reported in at least two parasites lines were included in the microarray. Some SNPs represented by a single isolate were included on the array and prioritized by mutation types sensitive to array detection [25]. In total, 45,524 SNP loci queried by 364,192 probes balanced to 66°C melting temperature were included on the microarray. CGH microarray probes were designed using standard NimbleGen CGH protocol [36] modified for the *P. falciparum* genome. Briefly, probes were tiled through the genome at 4-bp interval spacing and filtered for 60 to 80°C melting temperature and 50 to 75 bp length. The resulting probes were clustered with nearest neighbors and sorted to remove probes with extensive sequence identity to any other probe. Probes with more than one 50-mer exact match in the genome or located in hypervariable *var/rif/stevor* genes were discarded. The median spacing between the start of the 355,803 CGH probes is 52 bp.

### Parasite samples

Fresh cultures of cloned 3D7, HB3, Dd2, SC05, and 7C126 lines derived from genotype-confirmed stock material were grown under standard cultivation conditions [39,40]. Parasite DNA was extracted using standard phenol/chloroform extraction and concentrated by salt precipitation [39]. Parasite DNA from the Thailand-Burma border was collected from 5 ml whole blood of symptomatic patients visiting malaria clinics. Buffy coats from the blood samples were removed and infected red blood cells cultured for 24 h to allow ring stage parasites to mature to schizonts to provide more DNA. DNA was extracted using a standard phenol/chloroform protocol. Parasite isolates were screened for multiple infections and identical clones using seven polymorphic microsatellite markers: *ARA2* (chr 11), *POLY $\alpha$*  (chr 4), *TA1* (chr 6), *C2M1* (chr 2), *C3M54* (chr 3), *TA60* (chr 13), and *C4M30* (chr 4). These markers were amplified using fluorescent end-labeled oligos and run on an ABI 3100 capillary sequencer (Applied Biosystems Inc., Foster City, CA, USA) and alleles scored using GeneScan (Applied Biosystems Inc.) and Genotyper (Applied Biosystems Inc.) software. Samples were considered multiple clone infections if one or more of the seven microsatellite loci showed multiple alleles. Only unique genotypes were included in the study. Thailand-Burma samples with an inadequate amount of DNA were whole genome amplified using phi29 DNA polymerase (Fidelity Systems, Gaithersburg, MD, USA). WGA samples were cleaned using a standard phenol/chloroform protocol. Parasite DNA concentrations in the Thailand-Burma samples were measured using quantitative PCR. Patient samples were amplified using SYBRgreen (Applied Biosystems Inc.) with primers specific to the *P. falciparum ama1* gene. Reactions were run on an ABI PRISM 7900HT realtime PCR machine and DNA amounts calculated by comparison with a dilution series of pure DNA from parasite line 3D7. DNA from lab-adapted samples was submitted to the Wellcome Trust Sanger Institute (Hinxton, UK) for Illumina sequencing using 76-bp paired-end reads.

### Microarray hybridizations

Labeling and hybridization were conducted using standard NimbleGen CGH procedures [36]. gDNA (250 ng to 1  $\mu$ g) was denatured at 98°C for 10 minutes in the presence of 1 OD of cy3 or cy5-labeled random nonamers at 50% AT richness or 65% AT richness (TriLink Biotechnologies, San Diego, CA, USA). The denatured sample was quick chilled on ice and incubated with 50 units of Klenow fragment (New England Biolabs, Ipswich, MA, USA) and dNTP mix (6 mM each in TE (Sigma Aldrich, St Louis, MO, USA)) for 2 h at 37°C. Reactions were terminated with 0.5 M EDTA and

precipitated with 5 M NaCl in isopropanol. Labeled product was resuspended in water, and 10  $\mu$ g of test and reference samples combined (6  $\mu$ g for 5K SNP chip samples), dried down, and resuspended in hybridization buffer (Roche NimbleGen, Inc., Madison, WI, USA); hybridizations for patient blood samples included 1 $\times$  Denhardt's solution (Sigma Aldrich) in the hybridization buffer. The combined sample was denatured at 95°C for 5 minutes and allowed to hybridize on the array for 24 h (16 h for 5K SNP chip samples) at 42°C in a NimbleGen hybridization system (Roche NimbleGen, Inc.). Microarrays were washed sequentially in Wash Buffer I (2 minutes at room temperature), Wash Buffer II (1 minutes at room temperature), and Wash Buffer III (15 s at room temperature; Roche NimbleGen, Inc.) and dried for 1 minute in a Microarray High-Speed Centrifuge (Arrayit Corp., Sunnyvale, CA, USA). CNV-SNP arrays were scanned at 2  $\mu$ m resolution using a NimbleGen MS 200 Microarray Scanner (Roche NimbleGen, Inc.). 5K SNP chips were scanned at 5  $\mu$ m resolution using a GenePix Pro 4200A Scanner (Molecular Devices, Inc., Sunnyvale, CA, USA). Microarray data are deposited at Gene Expression Omnibus, accession number [GEO:GSE28287].

### Microarray data analysis

#### SNP analysis

Data for 3D7, HB3, Dd2, SC05, and 7C126 were extracted from scanned images and resequencing base reports generated using NimbleScan v2.5 (Roche NimbleGen, Inc.). Base calls were made on resequencing probesets when the sense and antisense probes made complementary base calls. The discrimination score ( $D_{score}$ ) for each probe quartet was calculated as a background corrected ratio of the signal from the second greatest intensity probe from a probe quartet divided by the greatest intensity probe using custom perl scripts (Figure 1, grey insert): (Second highest signal intensity - Background)/(Highest signal intensity - Background). Background for each probe quartet was calculated as the average of the third and fourth highest signal intensities [32]. There is some noise inherent in this base calling method, which can be mitigated by performing technical replicates or incorporating probe replicates into the chip design. For SNP genotyping probes, probeset melting temperature was calculated as previously described [36] where mean melting temperature was calculated from all probes in each probe quartet. The accuracy of the base calls made by the resequencing probes was calculated as the percentage of base calls that matched the reference genome for 3D7 or draft genome assemblies for HB3, Dd2, SC05, and 7C126 [20,28,41]. To ascertain the base called at a SNP locus in the genome assembly, resequencing probes were mapped to draft genome



assemblies using blastall, requiring at least 95% of the probe length with less than four mismatched/indel positions excluding the central nucleotide. Illumina sequence data were aligned to the 3D7 reference genome with SNP-o-matic software [42] to identify SNP locations for comparison to microarray data.

#### Copy number variation analysis

Data for HB3 and Dd2 (n = 6 and n = 4, respectively) hybridized against 3D7 were extracted from scanned images and normalized using NimbleScan v2.5 (Roche NimbleGen, Inc.). Copy number events from the segmentation analysis in HB3 and Dd2 against the reference 3D7 were compared to known CNV in the published literature [25].

#### Additional material

**Additional file 1: Supplementary Figures S1 to S3.** Figure S1: poptimal probe melting temperature is consistent in exons, introns, and intergenic regions. Mean  $D_{score}$  is plotted by probe melting temperature in exons, introns, and intergenic regions; vertical lines indicate 95% confidence intervals. Probes with approximately 66°C melting temperature consistently provided the best performance. Figure S2: CGH data reproducibility. CGH scatterplots for individual CNV events are displayed for replicate hybridizations from independent labeling reactions demonstrating data reproducibility. CNV events from three separate parasite clones are displayed: (a) Dd2; (b) HB3; (c) SC05. The CNV breakpoints are precisely identified between hybridizations. Figure S3: CNV detection in a WGA field sample. CGH scatterplot for a CNV event detected in a WGA field sample, M1064. Four genes (PFE1150w, PFE1155c, PFE1160w, and PFE1165c) are affected by this CNV, including the *P. falciparum* multidrug resistance gene, *pfmdr1*.

#### Abbreviations

Bp: base pair; CGH: comparative genomic hybridization; chr: chromosome; CNV: copy number variation; SNP: single nucleotide polymorphism; WGA: whole genome amplification.

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#### Authors' contributions

JCT conceived of the study, participated in its design and coordination, and drafted the manuscript. BAM participated in study design and coordination, performed microarray hybridizations, and drafted the manuscript. AT participated in microarray design and performed statistical analysis. IHC and TJA participated in study design and assisted with field samples. MM, GM,

and DPK provided Illumina sequencing and data analysis. MTF conceived of the study, participated in its design and coordination, and helped to draft the manuscript.

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