



Development of a Comprehensive NGS Workflow for the Analysis of Tumor *BRCA1* and *BRCA2* Mutations and Large Rearrangements

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Abstract

Patients with germline or somatic *BRCA1* and *BRCA2* mutations are sensitive to PARP inhibitor treatment. However, current clinical testing of *BRCA1/2* is limited to germline mutations in blood samples. In the present study, we have developed and validated a workflow for *BRCA1/2* mutation test in patient tumor samples, which can identify both germline and somatic mutations. Our approach combined targeted capturing with the BRCA MASTR assay and consequent sequencing using Miseq, a benchtop next-generation sequencing (NGS) platform. The cut-offs for calling substitution mutations and large rearrangements were defined using 45 normal human samples, and then evaluated using 9 human cell lines harboring known *BRCA1/2* mutations, as well as 100 patient tumor tissue samples. At a sensitive mutant allele frequency threshold of 5%, all somatic mutation calls were confirmed using an independent technology. Using amplicon-specific cut-offs for large deletion calls, one out of two large deletion candidates was confirmed by the long-range PCR. In summary, our workflow offers a useful tool for testing tumor *BRCA1/2* mutations including substitutions, small insertions or deletions (indels) and large deletions.

Keywords

NGS, *BRCA1*, *BRCA2*, Mutation, Large rearrangement

Background

The *BRCA1* and *BRCA2* genes are two key components of the homologous recombination repair (HRR) pathway in DNA double-strand breaks (DSBs) repair [1]. Deleterious mutations in the *BRCA1/2* genes lead to an increased risk for breast or ovarian cancer as part of hereditary breast-ovarian cancer syndrome [2]. In many countries, *BRCA1/2* gene testing of blood samples has become routine practice for patients with family history of breast and ovarian cancer. Decision-making for prevention or treatment of these tumor types heavily rely on gene test results. Recently, preclinical and clinical studies have shown that the *BRCA1/2* mutation carriers

are more sensitive to poly adenosine diphosphate (ADP) ribose polymerase (PARP) inhibitors such as Olaparib and Veliparib [3-7]. Clinical benefit of PARP inhibitors has also been validated in ovarian cancer patients with germline and somatic *BRCA1/2* mutations [5]. Therefore, *BRCA1/2* could serve as a critical biomarker for patient selection in PARP inhibitor treatment. However, somatic mutations in tumors are not detected by blood testing, which is currently the mainstream method. Direct testing in tumor samples is in great need to identify additional patients with somatic mutations that may also benefit from PARP inhibitor treatment.

As *BRCA1* and *BRCA2* are very long genes lacking mutation hotspots, direct sequencing of these genes are of great interest. On the technology side, next-generation sequencing (NGS) technologies, based on parallel sequencing of individual DNA fragments, are setting the new standard in speed and cost effectiveness of genome sequence analysis. Benchtop NGS platforms like the Illumina MiSeq are feasible options for routine clinic use with short turnaround time and high cost effectiveness. Current bottleneck for NGS gene testing is in data analysis. Although several mutation calling pipelines have recently been developed for the *BRCA1/2* gene testing by NGS method [8-18], they mostly focused on detection of germline *BRCA1/2* mutations from blood samples. So far, only two pipelines were reported for somatic mutation detection from tumor samples. Frampton et al. [18] developed and validated an NGS panel of 287 cancer related genes from formalin-fixed and paraffin-embedded (FFPE) tumor tissue samples [18]. Pritchard et al. [8] developed the UW-OncoPlex assay for comprehensive analysis of 194 clinically relevant cancer genes [8]. However, these two NGS workflow and mutation calling pipelines were not designed and validated for the extremely complicated patterns of genomic variants in *BRCA1/2* genes. To enhance patient selection for PARP inhibitor therapy, there is an emerging need to develop a comprehensive NGS workflow focusing on tumor *BRCA1/2* mutation testing.

In the present study, we have selected the BRCA MASTR assay

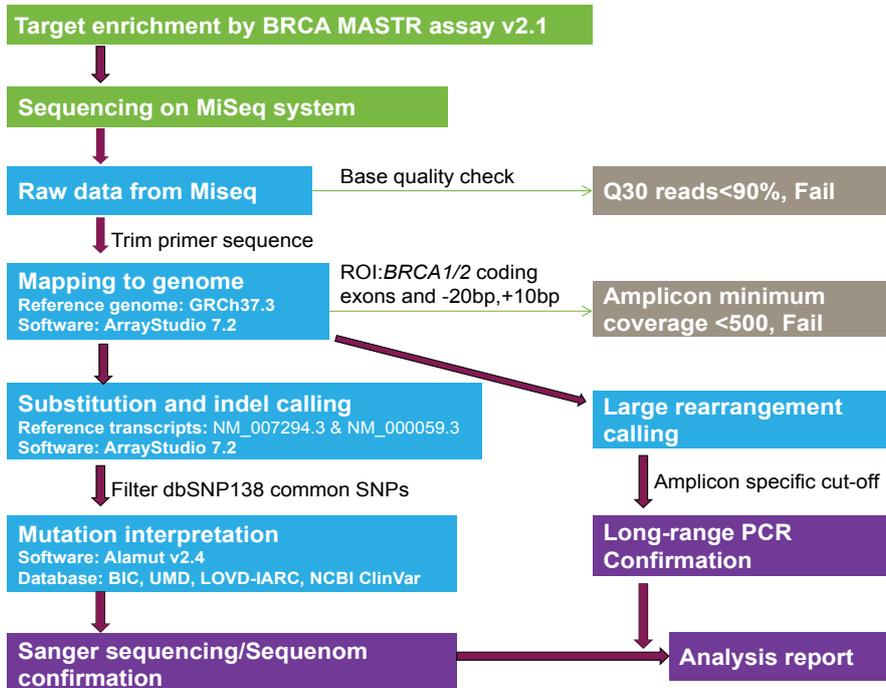


Figure 1: NGS workflow for tumor *BRCA1/2* mutation testing

Experimental process is shown in the green box. Quality control process is shown in gray box. Informatics analysis process is shown in blue box. Wet lab confirmation and analysis report are shown in purple box.

(Multiplicom) coupled with the benchtop MiSeq platform. In addition to the experimental workflow, we have also developed comprehensive bioinformatics pipelines for calling *BRCA1/2* mutations including substitutions, small insertions or deletions (indels) and large rearrangements from freshly frozen human normal tissues. This workflow was then validated using human cell lines with the known *BRCA1/2* mutations, and eventually tested on a cohort of tumor tissue samples from 100 breast cancer patients.

Methods

Patients and samples

Frozen tissues adjacent to tumors from 45 patients were generously provided by Zhongshan hospital and Beijing tumor hospital. These tissues were previously known to have two copies of *BRCA1/2* genes by array CGH analysis (data not shown), and therefore were used in this study as normal control to define biological baseline of the workflow. Nine human cell lines from American Type Culture Collection (ATCC) with known *BRCA1/2* mutations and three commercially available normal human DNA samples (Promega, USA) were used to validate the workflow. Furthermore, 100 patients who were diagnosed with breast cancer from Feb. 2008 to Sep. 2013 at West China Hospital were recruited into this study for *BRCA1/2* mutation testing and validation. All fresh frozen tissues from breast cancer patients were reviewed by the pathologist to ensure a tumor content of more than 50%. The human study was approved by the Ethics Committee of the hospitals, and the written informed consent was provided by the patients.

DNA extraction and quality check

DNA was extracted using Genra Puregene kit (QIAGEN, Germany) following the manufacturer's instructions. DNA concentration and purity were assessed using Nanodrop 2000 (Thermo Fischer Scientific, USA), and all DNA samples had A260/280 nm ratio between 1.8-2.0.

Multiplex PCR based targeted sequencing

The coding exons and flanking regions of *BRCA1* and *BRCA2* genes were enriched using BRCA MASTR assay v2.1 (Multiplicom,

Belgium), which contains 93 primer pairs in five reactions, according to the manufacturer's instructions. Briefly, a target-specific multiplex PCR was performed, followed by a second PCR with universal primers to integrate sequencing adaptors and indexing tags. The universal PCR amplified products were purified with the Agencourt AMPure XP kit (Beckman Coulter Genomics, USA), quantified with the Quant-iT dsDNA BR Assay kit using Qubit[®] 2.0 Fluorometer (Life Technologies, USA), pooled at equal nanomolar and sequenced using MiSeq Reagents v2.0 (2 × 250 bp pair-end sequencing) on MiSeq system (Illumina, USA).

Bioinformatics analysis

The informatics pipeline was shown in figure 1. The region of interest (ROI) was defined as the coding exon sequence plus 20 bp in the preceding intron and 10 bp in the following intron to ensure correct analysis of consensus splicing sites. Primer sequences were trimmed off from raw reads using custom scripts. Mapping, substitution mutation and indel calling are completed in Array Studio v7.2 (OmicSoft, USA), a commercially available software. The raw reads were aligned to reference human genome GRCh37.3, and non-uniquely mapped reads were then removed. The size detection window for small indels was set up to 60 bp, and the minimum amplicon coverage was set to 500×. All variants were called using reference transcripts NM_007294.3 for *BRCA1* and NM_000059.3 for *BRCA2*, respectively. Base quality was set to Q30, and mutant allele frequency cut-off setting was described in details in the Results section. The variants were then filtered by dbSNP138 to remove common SNPs, and all variant nomenclature follows the Human Genome Variation Society (HGVS) guidelines.

Customized scripts were developed to call large rearrangements in *BRCA1/2* genes as shown in the Results section.

Confirmation of substitution mutations and indels

All substitution mutation and indel candidates with mutant allele frequency > 0.2 were confirmed by Sanger sequencing. Briefly, each candidate was amplified using MASTR assay primer pair that covers the specific mutation site. The PCR products were sequenced in both directions on an ABI 3730XL DNA analyzer (Life Technologies, USA).

Table 1: *BRCA1/2* mutations from nine human cell lines.

Sample ID	Gene	Exon/intron	HGVS ID, cDNA	Amino acid change	Allele frequency	Interpretation
HCC1395	BRCA1	ex 20	NM_007294.3:c.5251C > T	R1751*	0.940	5-Pathogenic
HCC1569	BRCA2	ex 11	NM_000059.3:c.5583del	V1862*	0.230	5-Pathogenic
HCC1937	BRCA1	ex 20	NM_007294.3:c.5266dup	E1756fs*74	0.990	5-Pathogenic
MDA-MB-436	BRCA1	in 20	NM_007294.3:c.5277+1G > A	N/A	0.997	5-Pathogenic
BT474	BRCA2	ex 25	NM_000059.3:c.9281C > A	S3094*	0.660	5-Pathogenic
CAL51	BRCA2	ex 11	NM_000059.3:c.2957del	N986 fs*5	0.220	5-Pathogenic
LS180	BRCA2	ex 23	NM_000059.3:c.9097del	T3033fs*29	0.530	5-Pathogenic
HCT116	BRCA2	ex 18	NM_000059.3:c.8021dup	I2675fs*6	0.480	5-Pathogenic
HCT15	BRCA2	ex 11	NM_000059.3:c.3599_3600del & NM_000059.3:c.5351del	C1200* & N1784 fs*7	0.280 0.490	5-Pathogenic 5-Pathogenic

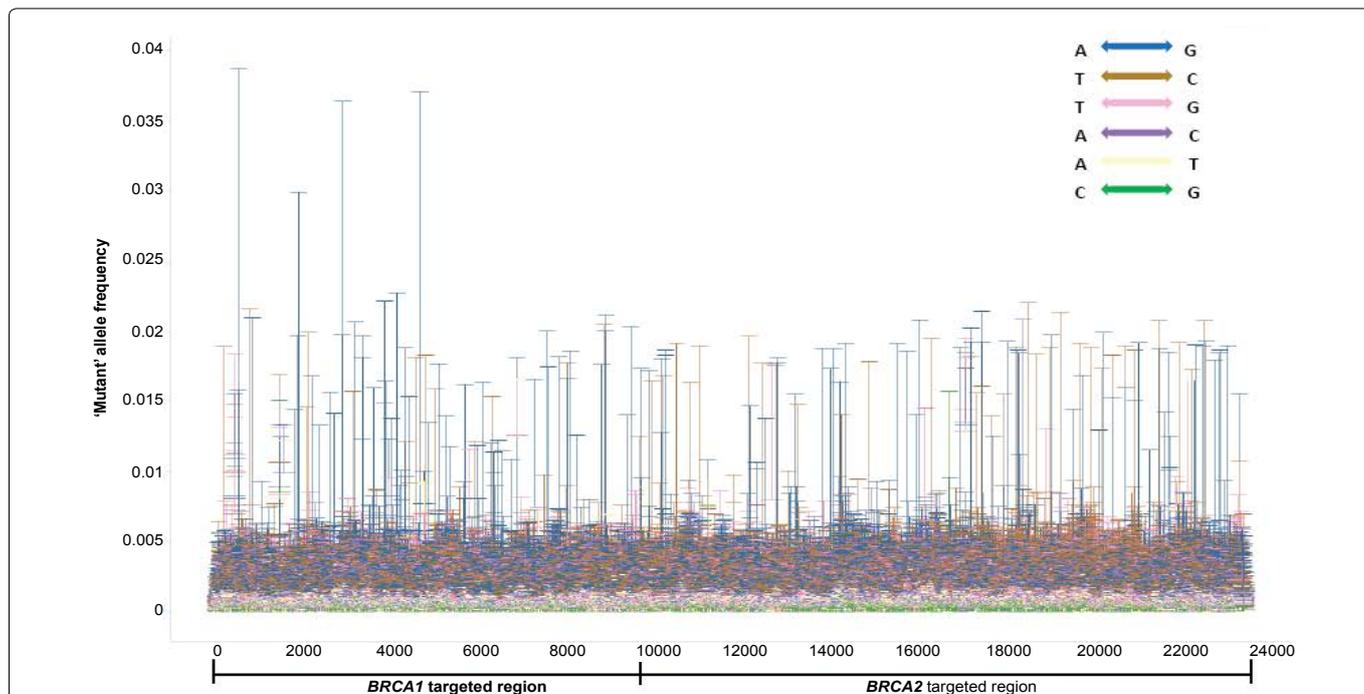


Figure 2: Distribution of locus-specific 'mutant' allele frequency in normal samples

'Mutant' allele frequency distribution in 45 human normal samples were plotted across the *BRCA1/2* targeted region (about 24 Kb) after removal of common SNPs. Maximum allele frequencies, which reflects the error rate of each site, were shown as bars, and each nucleotide type change was shown in a different color.

Candidates with allele frequencies between 0.05-0.2 were confirmed by the Mass ARRAY system (Sequenom, USA). Briefly, genomic DNA amplification and single base pair extension were conducted using specific primers that were designed by Sequenom Assay Designer v3.1 software. The allele-specific single base extension products were then quantitatively analyzed using matrix-assisted laser desorption/ionization-time of flight/mass spectrometry (MALDI-TOF/MS) on the Sequenom Mass Array Spectrometer.

Large rearrangement confirmation

The confirmation of large rearrangement candidates from NGS analysis were performed by long-range PCR, followed by Sanger sequencing and primer walking. Specific primers were designed to span the target exons and flanking introns (Supplementary Table 1). The templates were amplified using LA PCR Kit (TaKaRa, Japan). The PCR products were sequenced by a step-by-step primer walking approach to sequence the long DNA templates from end to end on an ABI 3730XL DNA analyzer.

Mutations interpretation

All confirmed variants were interpreted following guidelines from both the American College of Medical Genetics and Genomics (ACMG) and International Agency for Research on Cancer (IARC) guidelines [19,20]. We collected the evidences for interpretation by the Alamut software (Interactive biosoftware, France) in combination with databases including BIC (<http://research.nhgri.nih.gov/bic/>), UMD (<http://www.umd.be/>), NCBI ClinVar database (<http://www.ncbi.nlm.nih.gov/clinvar/>) and LOVD-IARC (<http://brca.iarc.fr/LOVD/home.php>). All variants were classified into 5 classes, and the pathogenic and likely pathogenic mutations were considered as deleterious mutations.

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Results

Experimental design

This study aims to establish a comprehensive NGS workflow for analyzing tumor *BRCA1/2* substitution mutation, indel and large rearrangement as shown in figure 1. For the targeted sequencing of *BRCA1/2* genes, we have selected the BRCA MASTR assay coupled with an Illumina MiSeq sequencing platform, after evaluating various assays and sequencing platforms.

One main goal of this workflow is to enable the calling of somatic mutations with low allele frequencies in human tumor samples using NGS. In addition, we aim to develop a large rearrangement calling pipeline using NGS data. We used the *BRCA1/2* gene sequencing data from 45 human normal tissues to define the cut-offs for mutation and large rearrangement calling. Then, we validated our workflow using 9 human cell lines with known *BRCA1/2* mutations and 100 primary human tumor samples.

Substitution mutation and small indel calling pipeline

To define the mutant allele frequency cut-off, all nucleotides different from the reference allele on human genome GRCh37.3 were called from the 45 human normal tissues. Common polymorphisms

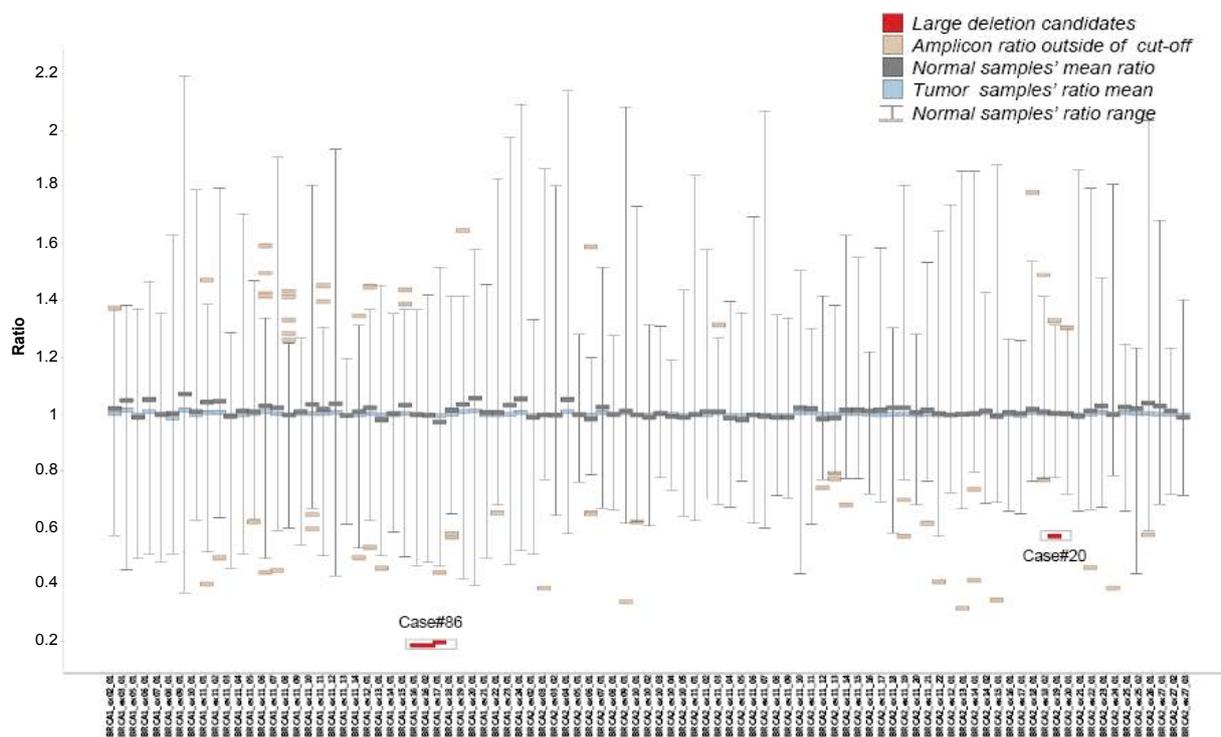


Figure 3: Amplicon-specific ratio distribution in 100 tumor samples

Amplicon ratios were calculated from 45 human normal samples and 100 tumor samples. Mean, minimum and maximum ratios for each amplicon in normal samples were shown as the gray bars. Mean amplicon ratio in 100 tumor samples were shown as the cyan bars. Amplicon ratios outside of the normal range but filtered against the two exclusion criteria were shown as the light brown bars. The remaining candidates were shown as the red bars.

were then filtered out against the dbSNP138 database. Rare variants which are in the dbSNP138 database were also removed. The remaining variants were considered as sequencing errors. The highest error rates of each site in the *BRCA1/2* region of interest (ROI) among 45 samples were shown in figure 2. We found that sequencing error rates were locus-specific and nucleotide-specific. A-G and T-C changes have the highest error rate, while the G-C and A-T changes were the lowest. Across about 24K target regions, the error rates for each position vary from 0.01% to 3.9%. Considering the sensitivity limit of currently available confirmation technologies such as Sequenom mass array used in this study, we set the allele frequency cut-off at 5% for substitution mutation calling in the whole ROI.

For small indel calling, the background error rate was higher than the substitution mutation. For example, the long homopolymers in *BRCA1/2* coding regions and intron-exon boundaries led to a false 1 bp deletion. Therefore, we manually visualized the variants in Array Studio genome browser to remove some such sequencing artifacts and software mapping artifacts. For the remaining indel variants, we also set the allele frequency cut-off at 5% and then confirmed them by Sanger Sequencing or Mass ARRAY system.

Large rearrangement calling pipeline

For *BRCA1/2* gene large rearrangement calling, we used 45 human normal tissue samples to determine the normal range of copy number variation of *BRCA1/2* gene exons. These 45 samples were previously known to have two copies of the *BRCA1/2* genes by array CGH analysis (data not shown). We calculated the ratio of each of the 93 amplicons in each sample based on normalized amplicon coverage.

For sample i , Amplicon j , Sample size N

$$Ratio[i, j] = \frac{AmpliconCoverage[i, j]}{Total\ Reads[i]} / \frac{\sum_{i=1}^N AmpliconCoverage[i, j]}{\sum_{i=1}^N Total\ Reads[i]}$$

For each amplicon, the mean value and range of the ratios in normal samples were summarized in figure 3. The mean values for all amplicons are close to 1, consistent with previous array CGH data. However, the range of ratios varies across amplicons, and the distributions were not always normal. Therefore, we set amplicon specific cut-offs for the ratios by random sampling and permutation. For each amplicon, the 99% confidence interval was taken as the minimum and maximum of acceptable amplicon ratios.

In addition, as reported large rearrangements in *BRCA1/2* genes primarily consist of the deletions of one or more consecutive exons [21], we have also excluded: 1) Samples with multiple inconsecutive amplicons with ratios beyond cut-offs. 2) Samples with a single amplicon beyond cut-offs, covering only part of one exon. The remaining candidates were selected for long-range PCR confirmation.

Cell line validation

Due to the absence of patient tumor samples with known *BRCA1/2* mutations, we used nine cell lines with known *BRCA1/2* mutations to validate the *BRCA1/2* mutation testing workflow described above, including targeted sequencing and mutation calling. Three commercially available normal human DNA samples were used as the negative control. As shown in table 1, our workflow detected all known substitution mutations and indels accurately in these cell lines. Because there are no commercial available cell lines with known *BRCA1/2* large rearrangements, we did not validate the large rearrangement calling pipeline through this approach.

Tumor sample testing

Next we tested our workflow with tumor samples from 100 breast cancer patients. Using 5% mutant allele frequency cut-off, we called a total of 33 *BRCA1/2* substitution mutations and indels (Table 2). Among them, 8 mutations are classified as pathogenic. All of the 33 mutations were fully confirmed by a second platform such as Sanger sequencing or Sequenom mass array (Supplementary Figure 1).

For large rearrangement calling, the amplicon ratios from these 100 tumor samples were shown in figure 3. In total, 64 amplicons in

Table 2: *BRCA1/2* mutations from 100 breast cancer patients.

Sample ID	Gene	Exon/intron	HGVS ID, cDNA	Amino acid change	Allele frequency	Interpretation
Case#01	BRCA2	ex16	NM_000059.3:c.7672G > C	E2558Q	0.051	3-VUS
Case#02	BRCA1	ex11	NM_007294.3:c.2566T > C	Y856H	0.487	1-non-pathogenic
	BRCA2	ex10	NM_000059.3:c.1362A > G	K454K	0.405	1-non-pathogenic
Case#03	BRCA1	ex11	NM_007294.3:c.2566T > C	Y856H	0.577	1-non-pathogenic
Case#05	BRCA1	ex11	NM_007294.3:c.2566T > C	Y856H	0.503	1-non-pathogenic
		ex9	NM_007294.3:c.571G > A	V191I	0.514	1-non-pathogenic
Case#07	BRCA2	ex11	NM_000059.3:c.5785A > G	I1929V	0.472	1-non-pathogenic
			NM_000059.3:c.6148G > A	V2050I	0.511	1-non-pathogenic
Case#10	BRCA2	ex18	NM_000059.3:c.8187G > T	K2729N	0.448	1-non-pathogenic
Case#16	BRCA2	ex11	NM_000059.3:c.4148_4149del	D1383 fs*19	0.334	5-Pathogenic
			NM_007294.3:c.2566T > C	Y856H	0.495	1-non-pathogenic
Case#25	BRCA2	ex11	NM_000059.3:c.3473A > G	E1158G	0.463	3-VUS
			NM_000059.3:c.5590G > A	D1864N	0.465	3-VUS
Case#26	BRCA1	ex16	NM_007294.3:c.4883T > C	M1628T	0.500	1-non-pathogenic
Case#28	BRCA1	ex11	NM_007294.3:c.3739G > A	V1247I	0.536	1-non-pathogenic
Case#31	BRCA2	ex11	NM_000059.3:c.3420T > C	S1140S	0.378	1-non-pathogenic
Case#33	BRCA2	ex11	NM_000059.3:c.6402_6406del	N2134fs*3	0.331	5-Pathogenic
Case#34	BRCA2	ex11	NM_000059.3:c.5345A > G	Q1782R	0.506	3-VUS
Case#36	BRCA2	ex25	NM_000059.3:c.9382C > T	R3128*	0.601	5-Pathogenic
Case#39	BRCA2	ex11	NM_000059.3:c.6598T > C	F2200L	0.488	3-VUS
Case#43	BRCA1	ex11	NM_007294.3:c.2566T > C	Y856H	0.737	1-non-pathogenic
Case#47	BRCA2	ex11	NM_000059.3:c.4151del	D1384fs*4	0.327	5-Pathogenic
Case#96	BRCA1	ex08	NM_007294.3:c.446A > C	E149A	0.491	3-VUS
Case#53	BRCA2	ex18	NM_000059.3:c.8187G > T	K2729N	0.401	1-non-pathogenic
Case#59	BRCA1	ex11	NM_007294.3:c.2566T > C	Y856H	0.411	1-non-pathogenic
			NM_000059.3:c.5199C > T	S1733S	0.605	1-non-pathogenic
Case#61	BRCA1	ex16	NM_007294.3:c.4787C > T	S1596L	0.414	3-VUS
Case#62	BRCA2	ex10	NM_000059.3:c.1399A > T	K467*	0.488	5-Pathogenic
		ex11	NM_000059.3:c.6382A > G	K2128E	0.510	2-likely-non-pathogenic
Case#65	BRCA2	ex18	NM_000059.3:c.8187G > T	K2729N	0.353	1-non-pathogenic
Case#67	BRCA2	ex20	NM_000059.3:c.8500A > G	T2834A	0.658	3-VUS
Case#70	BRCA2	ex11	NM_000059.3:c.2175dup	K726 fs*25	0.200	5-Pathogenic
		ex10	NM_000059.3:c.1568A > G	H523R	0.494	3-VUS
Case#74	BRCA1	ex11	NM_007294.3:c.2566T > C	Y856H	0.265	1-non-pathogenic
Case#78	BRCA1	ex11	NM_007294.3:c.2566T > C	Y856H	0.494	1-non-pathogenic
Case#80	BRCA2	ex11	NM_000059.3:c.2806_2809del	D938 fs*21	0.765	5-Pathogenic
			NM_000059.3:c.5785A > G	I1929V	0.236	1-non-pathogenic
Case#82	BRCA2	ex08	NM_000059.3:c.644_646del	E215del	0.558	3-VUS
Case#84	BRCA2	ex18	NM_000059.3:c.8187G > T	K2729N	0.485	1-non-pathogenic
Case#86	BRCA1	ex16-17	NM_007294.3:c.4676_5074del	E1559_T1691del	0.800	5-Pathogenic
Case#95	BRCA2	ex18	NM_000059.3:c.8329A > G	K2777E	0.498	3-VUS
	BRCA1	ex11	NM_007294.3:c.837T > C	H279H	0.495	3-VUS
Case#98	BRCA2	ex10	NM_000059.3:c.1211A > G	N404S	0.436	3-VUS
Case#100	BRCA2	ex13	NM_000059.3:c.6952C > T	R2318*	0.085	5-Pathogenic
	BRCA1	ex11	NM_007294.3:c.3739G > A	V1247I	0.607	1-non-pathogenic

VUS: variants of unknown significance

17 samples were found with ratios outside of the pre-defined normal ranges. After further filtering against the two exclusion criteria set above, only 4 amplicons in 2 samples were called. The 2 candidates include Case #86 with a deletion of 3 consecutive amplicons deletion and Case #20 with a single amplicon deletion. Among these two, only the deletion of 3 consecutive amplicons over exons 16 and 17 of (c.4676_5074del) *BRCA1* (Figure 4A and Figure 4B) in case #86 was confirmed by the long range PCR (Figure 4C). The breakpoint junction sequences of this large deletion were also shown in figure 4D. *BRCA1* exon 16-17 deletion has been reported [21,22] and classified as pathogenic in the UMD database [23], and our long range PCR further defined the exact breakpoints of the deletion, which were never reported before.

Discussion

In current clinical practice, *BRCA1* and *BRCA2* testing has

been mainly focused on germline mutations in blood samples. The mutant allele frequency cut-off at 15%-20% is sufficient to capture all heterozygous germline mutations [13-15]. This is relatively easier as compared to detection of low frequency somatic mutations in tumor tissues due to tumor heterogeneity. Recent studies showed that patients with somatic *BRCA1/2* mutations are equivalently sensitive to PARP inhibitor treatment as patients with germline *BRCA1/2* mutations [5]. Thus, *BRCA1/2* mutation testing with tumor samples, including both germline and somatic mutations, could help more patients who would benefit from PARP inhibitor therapy. In this study, we developed a comprehensive NGS workflow for detection and analysis of tumor *BRCA1/2* mutations including substitutions, indels and large deletions, using a multiplex PCR technology coupled with a benchtop NGS platform and a customized bioinformatics pipeline. Our results indicate that this workflow achieves a good performance for tumor *BRCA1/2* mutation testing at 5% mutant allele frequency cut-off.

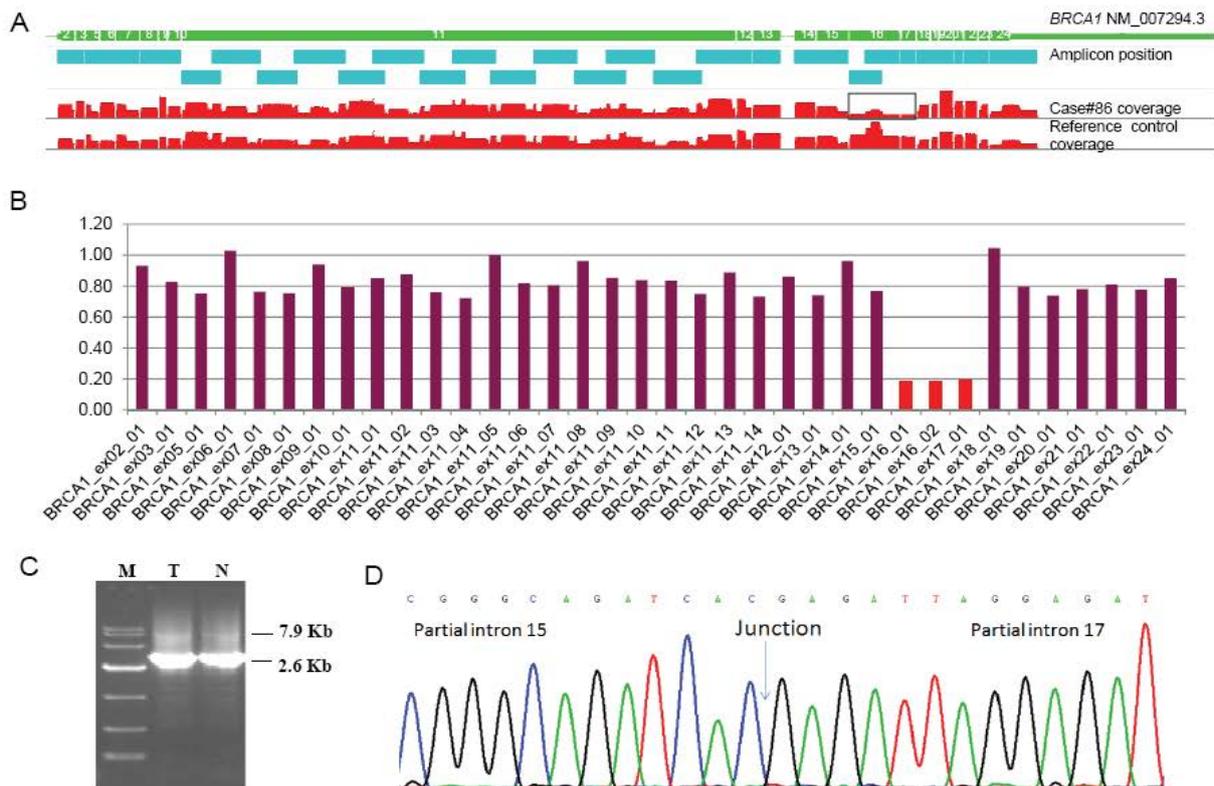


Figure 4: *BRCA1* exon16-17 deletion (c.4676_5074del) calling and confirmation in the Case #86

(A) *BRCA1* exon coverage plot. Case #86 showed much less coverage in the exons 16 and 17 than reference control sample.

(B) Amplicon ratios of Case #86. Three amplicons covering the *BRCA1* exons 16 and 17 (NM_007294.3) showed ratios close to 0.2.

(C) Gel image of long-range PCR products. The expected band size of normal allele is 7.9 Kb. The band size of allele with exon16-17 deletion is 2.6 Kb. M, marker DL10000; T, tumor DNA sample; N, paired normal sample.

(D) Sanger sequencing image of the breakpoint flanking sequences with exons 16 and 17 deletion. The sequence before the breakpoint is on *BRCA1* intron 15, and the sequence after the breakpoint is on *BRCA1* intron 17.

For tumor *BRCA1/2* mutation screening, the first essential step is to select an efficient assay and a sequencing platform. We have evaluated both Miseq and PGM platforms, as well as three different assays including BRCA MASTR assay, AmpliSeq BRCA panel and a customized Haloplex BRCA panel (data not shown). We found that MASTR BRCA assay coupled with MiSeq sequencing platform had the best performance in terms of data quality and cost effectiveness. We have also compared different variant callers including GATK [24], Varscan [25], Freebayes [26] and Array Studio for the deep coverage of *BRCA1/2* targeted sequencing datasets. We got identical calling results except for minor differences on mutant allele frequencies and nomenclature (data not shown). We chose Array Studio pipeline for its accuracy in mapping and variant calling, and user-friendly interface.

After a systematic evaluation of error rates of all amplicons, we set the cut-off of mutant allele frequency at $\geq 5\%$ for substitution mutation and indel calling, which had 100% confirmation rate, suggesting superior specificity. The pipeline developed by Pritchard et al. [8] focusing on 194 clinically relevant genes including *BRCA1/2* had 99.2% sensitivity on mutant allele frequency $\geq 10\%$ and 67% sensitivity on mutant allele frequency $< 10\%$ [8]. Frampton et al. [18] also designed a panel of 287 cancer related genes including *BRCA1/2* and showed 100% sensitivity on mutant allele frequency $\geq 10\%$ and 99% sensitivity on mutant allele frequency $< 10\%$ [18]. Our workflow demonstrated the capability to detect *BRCA1/2* mutations in frozen tumor sample with mutant allele frequency $\geq 5\%$. For mutations with allele frequencies $< 5\%$, further studies are warranted for validation using more sensitive confirmation technologies.

A minority of *BRCA1/2* mutations are large rearrangements of DNA segments that disrupt gene function [21]. Traditionally,

Multiplex ligation-dependent probe amplification (MLPA) or qPCR assay was used to detect exonic copy number changes in blood, saliva or FFPE samples. More recent studies use NGS workflow to detect gene copy number variations (CNVs) or large rearrangements [27,28]. Usually, a unified cut-off was set for all amplicons, for example, < 0.6 for deletions and > 1.4 for duplications [10,14,15,29]. However, for multiplex PCR methods, due to different PCR amplification efficiency of each primer pair, the amplicon coverage and their corresponding variance are different. Therefore, we defined amplicon specific cut-offs based on amplicon specific ratio ranges derived from human normal samples. In this study, the candidate with a deletion of three consecutive amplicon (ratio around 0.2) was confirmed by long range PCR, while the candidate with a single amplicon 'deletion' (ratio around 0.5) was not. Taken together, our NGS workflow could serve as a screening method for large rearrangement calling from tumor tissues, which may need further confirmation by a second technology like long-range PCR or MLPA.

In terms of assay robustness, our workflow could load maximum 48 samples in a single run, and complete the experiment process, informatics analysis and mutation interpretation within two weeks. This meets most of *BRCA1/2* mutation testing needs in clinical practice.

Our NGS workflow here offers a useful tool for testing germline and somatic *BRCA1/2* mutations including substitutions, small indels and large deletions in freshly frozen tumor tissues. It combines a benchtop MiSeq NGS platform and improved calling sensitivity. We have developed a bioinformatics pipeline customized for the *BRCA1* and *BRCA2* genes from QC to mapping, substitution/ indel calling and large rearrangement detection. In addition, the workflow has the potential to be applied to other tumor suppressor genes like *TP53* that does not have mutation hotspots.

Competing Interests

Zhengwei Dong, Hua Dong, Xuehua Zhu, Yun Sun, Yunqin Chen, Changting Liu, Xiaolu Yin and Yi Gu are employees of AstraZeneca during this study. No other conflicts of interests to declare.

Authors' Contributions

ZD and HD were responsible for generating and analyzing the data, and drafting the manuscript; XRZ, ZP and HZ for patient sample collection; XHZ, YS and YC for related data confirmation and interpretation. CL and XY for pathology review of the patient tissues, GZ for study design and technical discussion, and YG for overall study design, drafting and finalizing the manuscript. All authors have read and approved the final version.

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