SureSeq myPanel™

A Sysmex Group Company

SureSeq myPanel™ NGS Custom Prostate Cancer panel

Prostate cancer is now the second leading cause of cancer in men, with recent genome-wide studies helping to clarify the genetic basis of this common but complex disease[1]. Many of these studies have reinforced the importance of homologous end repair genes including: *ATM, BRCA1, BRCA2* and *PALB2*, in the mechanism of prostate cancer development. Mutations in these genes result in cells having to repair lesions through other non-conservative mutagenic mechanisms.

Choose your ideal prostate cancer NGS panel from our range of fully optimised NGS panel content. Simply mix and match the genes or individual exons you require and get the most out of your sequencing runs. Use in conjunction with the SureSeq FFPE DNA Repair Mix* for improved NGS library yields, %OTR (on target rate) and mean target coverage from challenging FFPE derived samples.

SureSeq myPanel offers:

- **Hybridisation-based enrichment delivering unparalleled coverage uniformity**
  Detect low frequency prostate cancer variants consistently with confidence and minimise the requirement for supplementary fill-in with Sanger sequencing
- **Pre-optimised panels that meet your technical requirements and work with your samples**
  No more lengthy in-house optimisation, decreasing assay development time
- **Bespoke panel content**
  Sequence only what's relevant for your cancer research, increase throughput and save on sequencing reagents
- **Panel content designed with experts and from current literature to target all relevant regions including intronic and splice sites**
  Get the most comprehensive insight into disease-driving mutations

Superior Coverage Uniformity

A number of genetic factors have been found that increase prostate cancer risk, including heritable mutations in the genes *BRCA1* and *BRCA2. BRCA1* is a key player in cellular control systems, having been linked to DNA damage response and repair, transcriptional regulation and chromatin modelling[2], while *BRCA*2 function is linked to DNA recombination and repair processes, being of particular importance in the regulation of *RAD51* activity.

Figure 1a, illustrates the superior uniformity of coverage of key exons of *BRCA1*, and Figure 1b, *BRCA2* from an FFPE sample.

Figure 1a

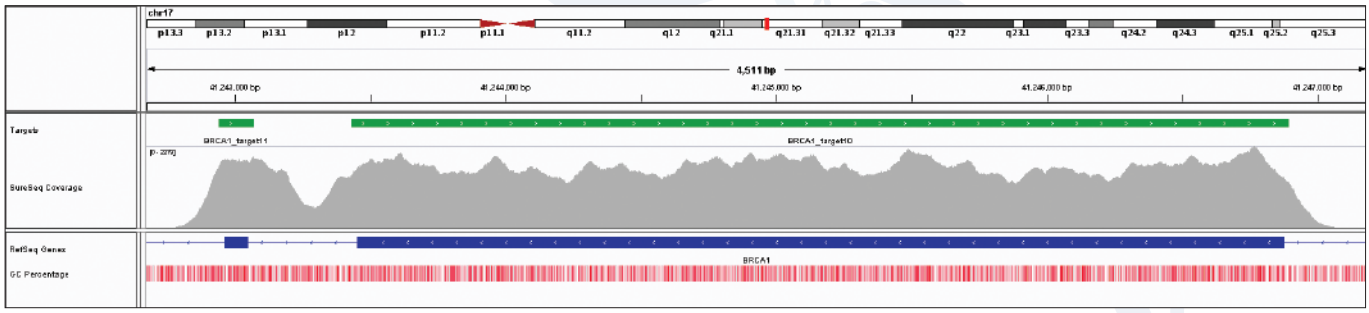


Figure 1b

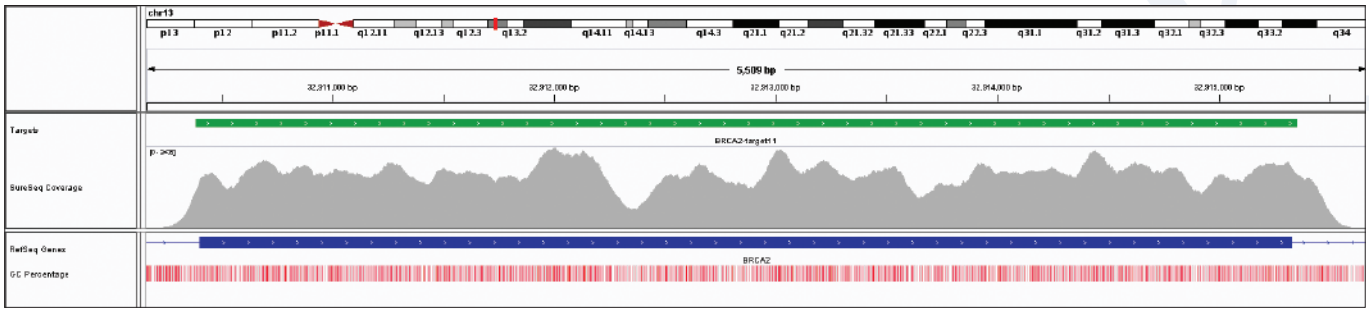


Figure 1a. *BRCA1* exon 9 and 10 coverage, Figure 1b. *BRCA2* exon 11 coverage. Depth of coverage per base (grey). Targeted region (green). Gene coding region as defined by RefSeq (blue). GC percentage (red).

PALB2 is a *BRCA2* binding protein and the *BRCA2-PALB2* interaction is essential for *BRCA2*-mediated DNA repair. Recently it has been shown that correct *PALB2* function is necessary for the homologous recombination repair via interaction with *BRCA1*, revealing that *PALB2* is actually a linker between *BRCA1* and *BRCA2*[3]. The *ATM* gene, located on chromosome 11q 22–23, includes 66 exons with a 9168 base pair coding sequence, and encodes a PI3K-related protein kinase (PIKK) that helps maintain genomic integrity. The PI3K-AKT-mTOR oncogenic pathway is frequently enhanced in prostate cancer playing a vital role in development and maintenance[4].

Figures 2 and 3 illustrate the excellent uniformity of coverage of key exons of *PALB2* and *ATM*, respectively.

Figure 2a

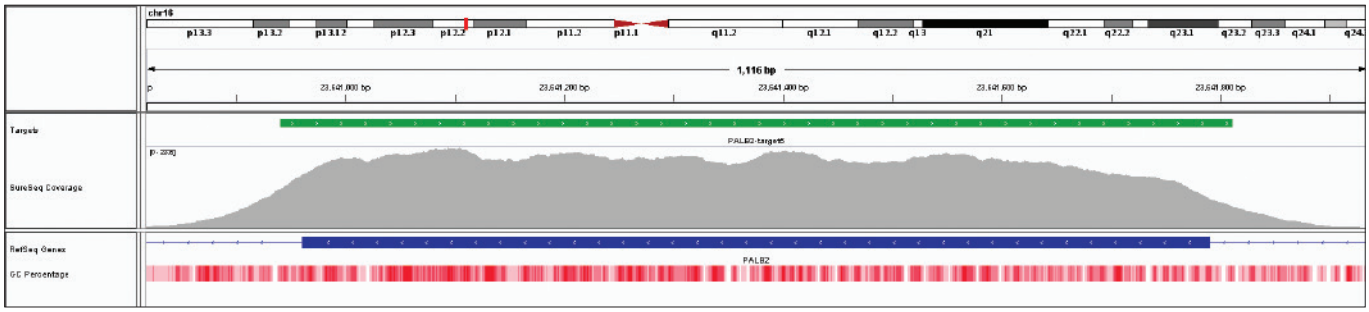


Figure 2b

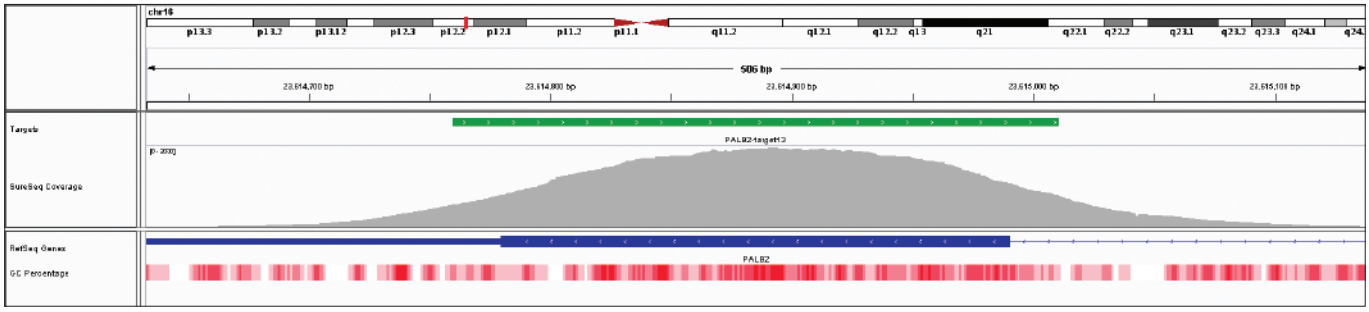


Figure 3a

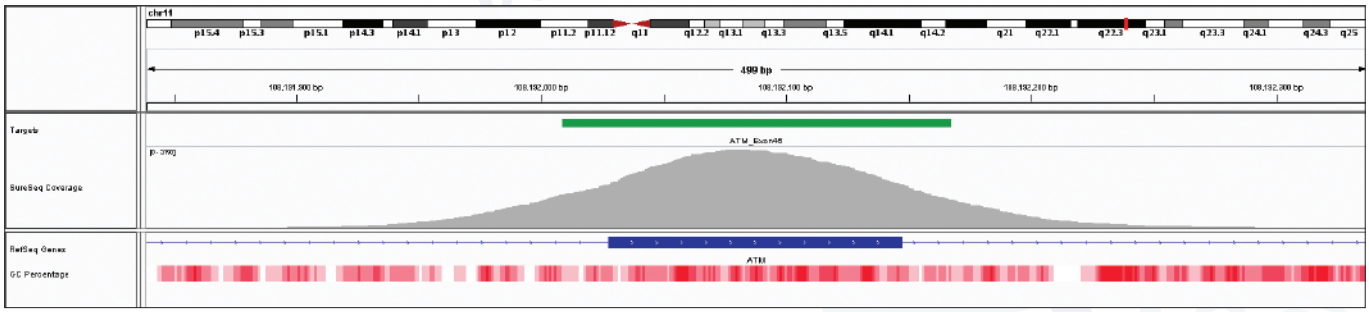
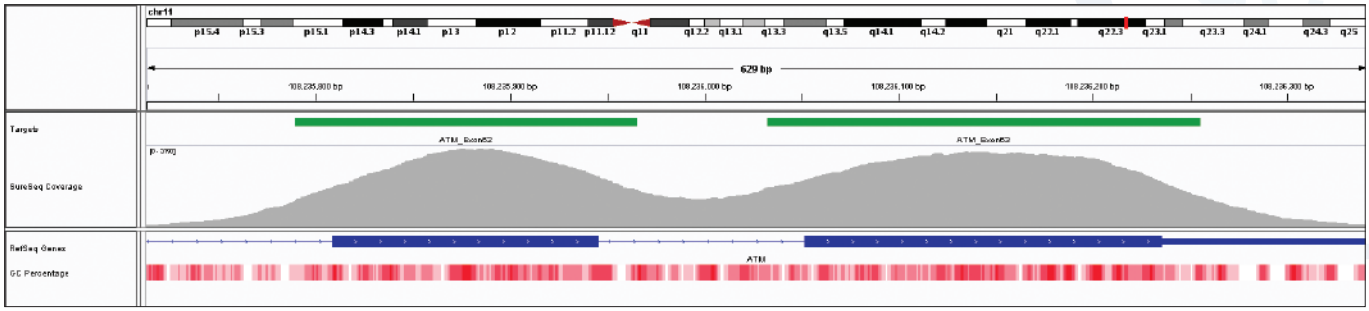


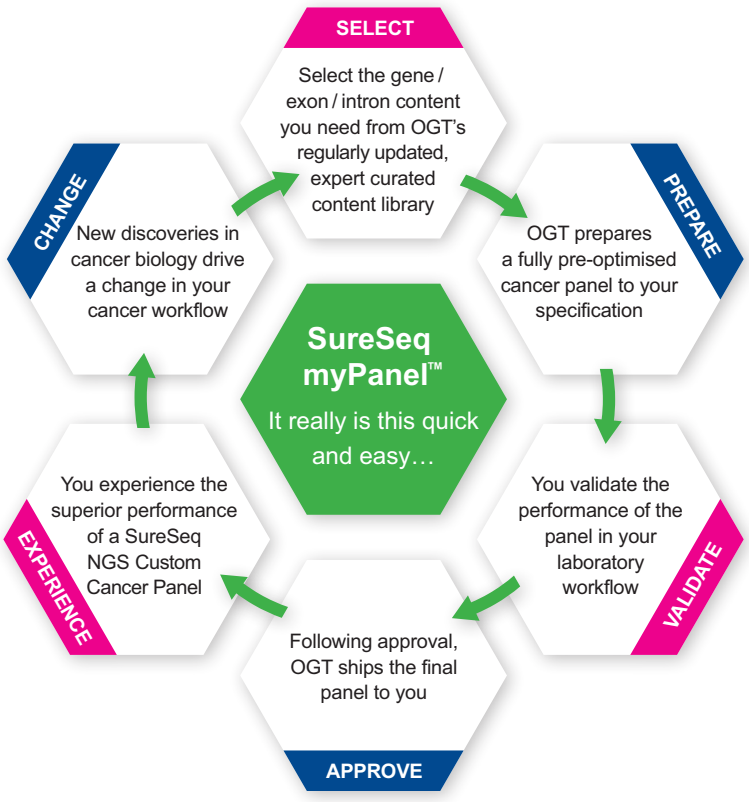
Figure 3b



Figures 3a and 3b. Illustration of the excellent uniformity of coverage of *PALB2* exons 5 (2a) and 13 (2b) and *ATM* exons 45 (3a) and 62 (3b). Depth of coverage per base (grey). Targeted region (green). Gene coding region as defined by RefSeq (blue). GC percentage (red).

Getting started with your next SureSeq myPanel NGS Custom Cancer panel could not be simpler. Select from any of the following myPanel Prostate Cancer whole gene or exonic content below.

ATM	*BRCA1*	*BRCA2*	*PALB2*



For more information about the SureSeq Prostate Cancer NGS panel or any cancer analysis products, visit www.ogt.com or contact us at products@ogt.com.

Ordering information

Product	Contents	Cat. No.
SureSeq myPanel NGS Custom Prostate Cancer Panels	Enrichment baits; SureSeq Interpret Software	Various
SureSeq FFPE DNA Repair Mix*	Enzyme, mix and buffers sufficient for 16 FFPE DNA samples	500079
SureSeq NGS Library Preparation Kit (16)	Bundle of 1 x library preparation kit (16) containing adaptors, PCR primers and enzymes sufficient for 16 samples and 1 x SureSeq NGS Index Kit – Collection A	500070
SureSeq NGS Library Preparation Kit (48)	Bundle of 3 x library preparation kit (16), containing adaptors, PCR primers and enzymes sufficient for 48 samples and 1 x SureSeq NGS Index Kit – Collection B	500073
SureSeq NGS Index Kit - Collection A (16)	16 different indexes, each sufficient for 4 samples (included with SureSeq NGS Library Preparation Kit (16))	500071
SureSeq NGS Index Kit - Collection B (48)	48 different indexes, each sufficient for 4 samples (included with SureSeq NGS Library Preparation Kit (48))	500072

*The SureSeq FFPE DNA Repair Mix can only be purchased in conjunction with SureSeq NGS panels, not as a standalone product.

References

1. Thoma, C, (2015) The complex relationships of malignant cells in lethal metastatic castration-resistant disease, Nature Reviews Urology 12, 237
2. Castro, E. *et al*, (2012) The role of *BRCA1* and *BRCA2* in prostate cancer. Asian Journal of Andrology, 14 (3):409-414.
3. Pakkanen, S. *et al*, (2009) *PALB2* variants in hereditary and unselected Finnish Prostate cancer cases. Journal of Negative Results in BioMedicine, 8 (1).
4. Angèle, S. *et al*, (2004). *ATM* polymorphisms as risk factors for prostate cancer development. British Journal of Cancer, 91(4): 783–787.

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