Enabling efficient, cost-effective sequencing of the human whole exome.

Key features

- Complete whole exome coverage
- Rapid same-day workow
- Exceptional target capture performance

For research use only. Not for use in diagnostic procedures.

NEXTFLEX human whole exome sequencing panel

NEXTFLEX Human Whole Exome Sequencing (WES) Panel is a comprehensive solution that covers all target regions of major WES panels available in the market. With a target size of 37.1 Mb, the panel does not compromise performance in terms of coverage and uniformity, enabling efficient, cost-effective sequencing of the human whole exome. The panel coverage spans across exon regions from RefSeq, CCDS, and GENCODE.

The NEXTFLEX WES panels perform well against hard-to-capture regions such as GC-rich regions.

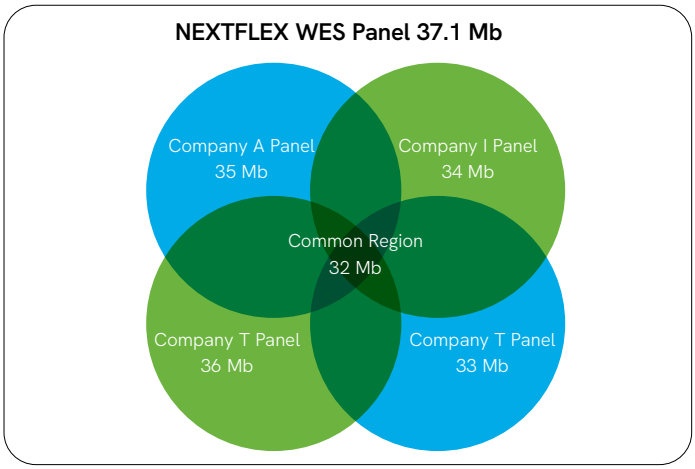

Figure 1. The NEXTFLEX WES Panel covers the target regions of all major whole exome panels in the market, which include WES panels from company A, company I and company T. Among the regions that Company A and T failed to cover from their own target regions, the NEXTFLEX WES panel covers an additional 60 Kb and 306 Kb of Company A and T respectively (data not shown). Most of these regions are challenging to capture due to GC-rich and repeated sequences. Through optimized probe design and panel synthesis technology, the NEXTFLEX Whole Exome Panel successfully covers the challenging regions that other company products struggle with.

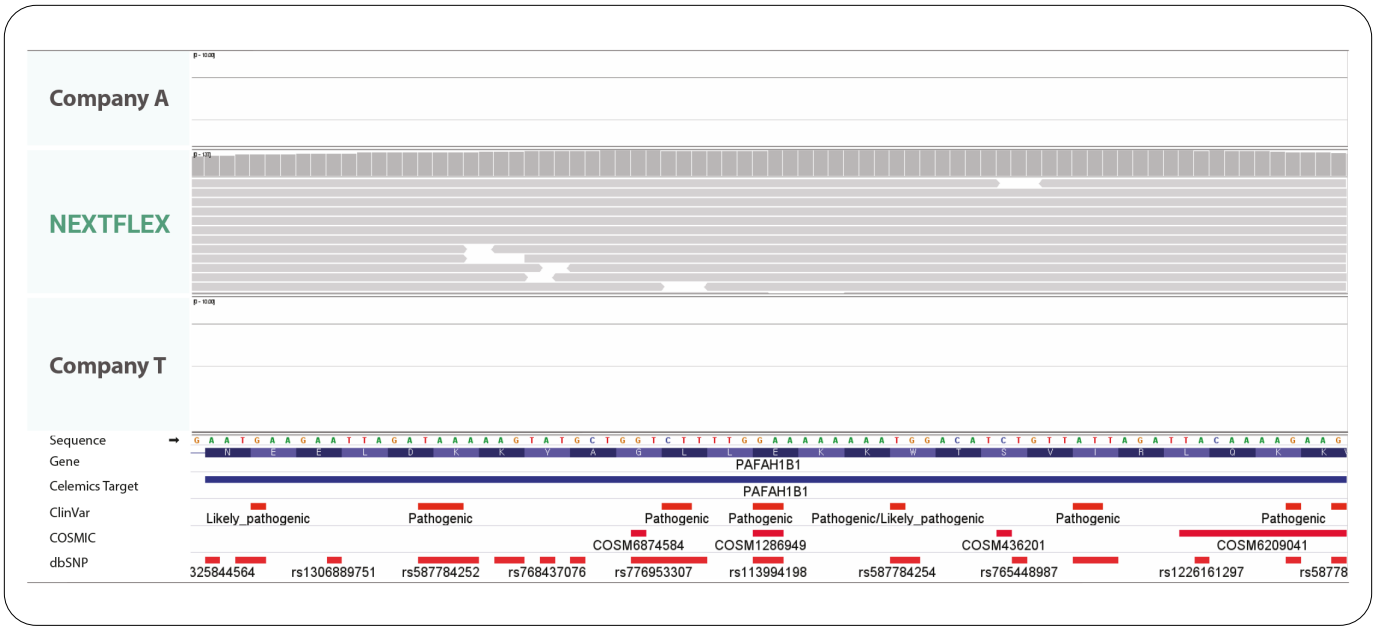

Figure 2. **Superior capture performance and coverage.** While other competitor panels fail to capture the A-T rich regions in a mutation in the PAFAH1B1 gene, the NEXTFLEX WES Panel successfully covers the region.

Figure 3. **Exhaustive coverage for each gene.** The NEXTFLEX WES Panel covers each gene with thorough coverage in comparison to competitor products. The bar graphs indicate the percentage of genes that are covered at **(A)** 20X depth and **(B)** 30X depth. The data from the three panels were downsampled to 5.4 Gb. **(C)** The IGV Figure demonstrates the superior coverage performance of the NEXTFLEX Whole Exome Panel against the TGID1 gene compared to other competitor products.

Exceptional target capture performance

The NEXTFLEX WES Panel provides exceptional target capture performance due to probe design and reagent optimization technology.

Despite some companies who resort to masking the hard-to-capture regions (such as GC- or AT-rich regions and homologous regions) or completely omit the regions from their target in order to enhance the quality of their results, the NEXTFLEX WES Panel provides both high coverage and on-target ratio without reducing the number of target regions. NEXTFLEX WES Panel captures regions that other panels cannot capture with quality coverage and uniformity. The all-around performance of the NEXTFLEX WES panel allows for cost-effective and time-saving sequencing of the whole exome.

Figure 4. **Superior performance in the market.** The NEXTFLEX WES Panel shows exceptional performance compared to other competitor products when measured by **(A)** on-target read ratio, **(B)** 0.2x mean depth coverage uniformity (higher the better), and **(C)** Fold-80 base penalty (lower the better). Third-party laboratories conducted a comparison study between the NEXTFLEX WES Panel, Company A, and Company T panels. The same amount of reference materials NA12878, NA12891, and NA12892 were used. Illumina® instruments were used for the sequencing. The data from the three panels were downsampled to 5.4 Gb.

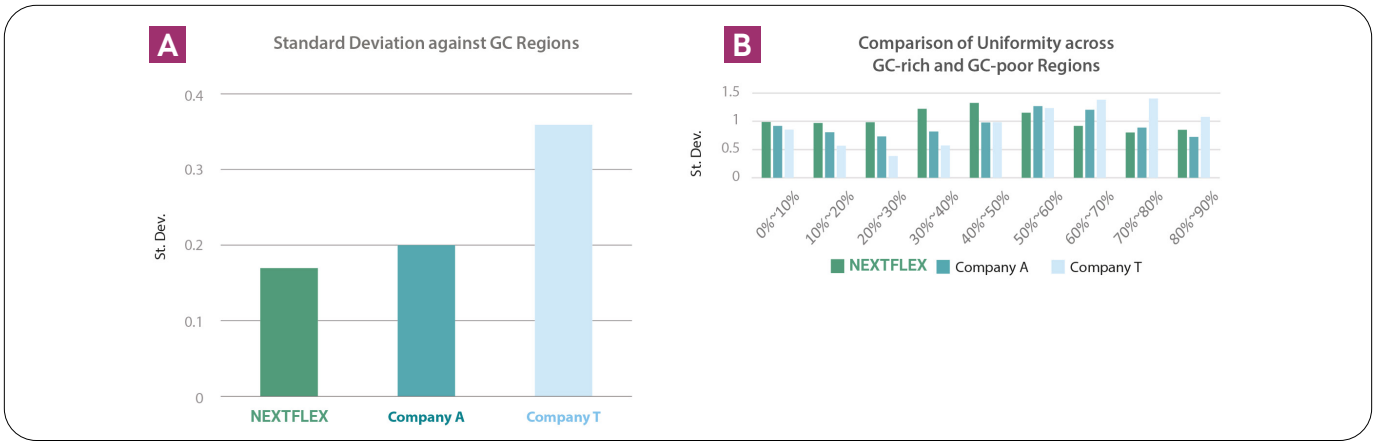

Figure 5. **Exceptional uniformity across low and high GC regions. (A)** The NEXTFLEX WES Panel demonstrates minimal deviation, yielding 0.166 standard deviations (lower the better) across GC-rich and AT-rich regions in comparison to competitor products yielding 0.199 and 0.356 standard deviations. **(B)** The bar graphs shown in different GC ratios also illustrate the consistent uniformity of the NEXTFLEX WES Panel in comparison to the competitor products.

Rapid same-day workflow

Although hybridization capture has great advantages including minimized bias, stable and reliable data results from a variety of sample types, the complexity of the workflow and the long prep time have been obstacles to the users. The NEXTFLEX WES Panel workflow significantly simplifies the process and reduces experiment time. Conventional WES takes 2-3 days to complete one sequencing experiment. With NEXTFLEX WES Panel workflow, the entire experiment can be completed and the NGS run can be started on the same day.

Full bioinformatics capability

Analysis service workflow powered by NEXTFLEX WES panel

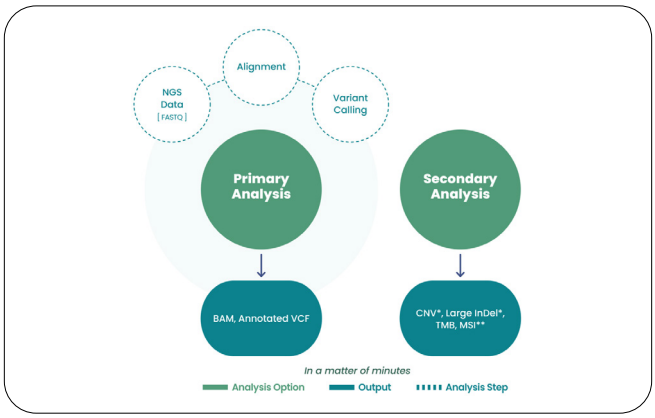

Figure 6. **Bioinformatics support**. Analysis Service powered by Celemics provides easy data transmission by single-click and automated uploads. It also supports real-time troubleshooting throughout primary and secondary analysis and client-specific customization.

Streamlined workflow reduces costs and experiment time

Instruments such as vacuum concentrators, sonicators, and devices to characterize libraries are barriers against complete automation of WES. The NEXTFLEX WES panel does not require this instrumentation and alternatively uses enzymes and beads. The incorporation of normalization beads reduces turn-around time by up to three hours mostly due to eliminating the need for individual library quantification prior to the pooling step. This workflow was optimized to enable a complete walkaway solution with reliable performance. The NEXTFLEX WES Panel incorporates enzymatic fragmentation, bead-based concentration, and a normalization process, eliminating the need for mechanical fragmentation vacuum concentrator, devices to characterize final libraries.

References

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