

# Twist Exome 2.0 Panel

Thoughtfully curated content, paired with best-in-class performance

## EXOME DEFINITION

- 36.5 Mb targets
- 99% of targets covered  $\geq 20\times$

## KEY HIGHLIGHTS

### Coverage that makes a difference

- Covers 36.5 Mb of human protein-coding and noncoding regions
- Based on recent releases of major gene databases
- Includes carefully curated clinical content

### Best-in-class performance

- Uniform enrichment of target regions
- NGS QC of all probes

### Customizable

- Easily spike-in content into the exome
- Effective across multiplex target enrichment workflows
- Run overnight or same-day workflows

### Save on sequencing costs

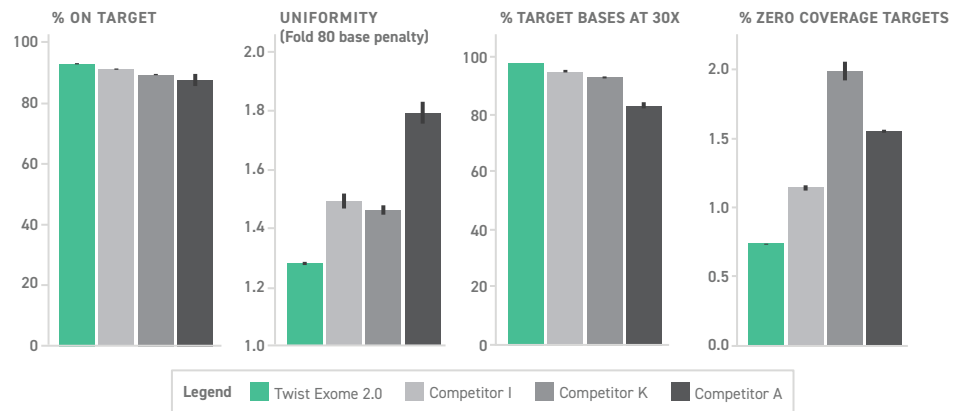
- Increased depth per sample or more samples per run
- Lower sequencing costs

Targeted Sequencing approaches can be an effective way to save on sequencing costs by focusing on specific genes or regions of interest. But even good targeted sequencing panels, specifically those like exomes, often necessitate a compromise between the inclusion of relevant content and panel performance. Compromise no more.

Introducing Twist’s Exome 2.0 — the latest addition to our robust and ever-advancing NGS Target Enrichment portfolio. This new Exome enrichment panel has been carefully designed to help alleviate common sequencing pitfalls and provide researchers with best-in-class uniformity, on-target rate, duplicate rate, and target coverage; all while delivering on the most up-to-date set of protein-coding and clinically relevant content, including noncoding variants.

## Best-in-class performance

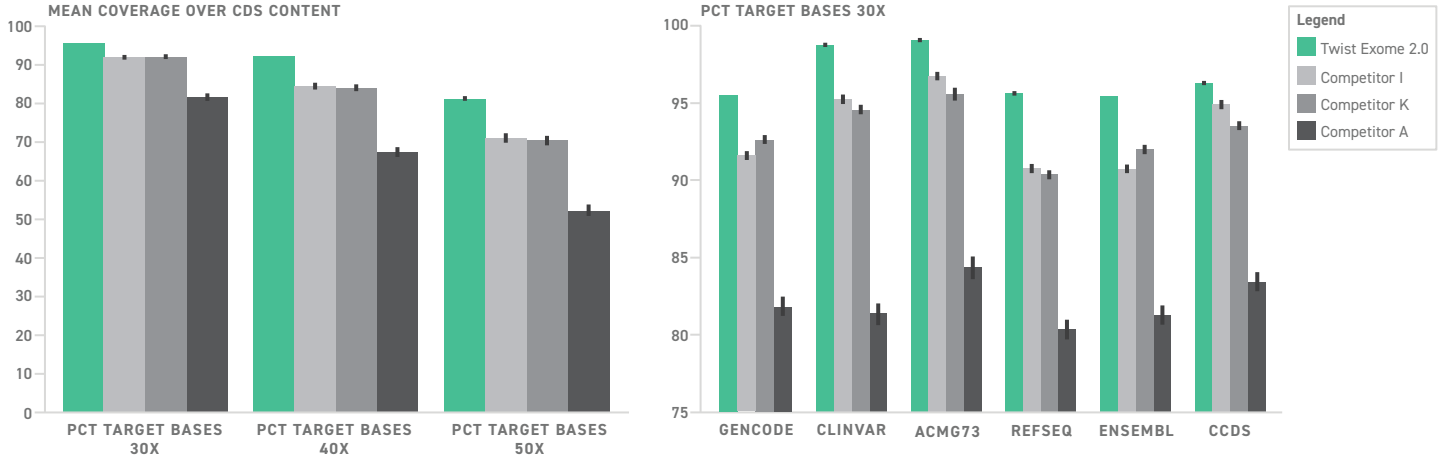
Twist Exome 2.0 earns the title “best-in-class” by outperforming top competitors and enabling the most efficient exome sequencing in the market. Compared to other exome panels, Twist Exome 2.0 delivers higher uniformity and a higher on-target rate as well as lower drop out and duplicate read rates. Together, this equates to fewer wasted reads and maximal coverage of target sequences.



**Figure 1:** Twist Exome 2.0 demonstrates superior performance over competitors I, K, and A\* in (a) On-target rate, calculated as “1-PCT\_OFF\_BAIT”, (b) Uniformity, reported as fold 80 base penalty score, (c) % target bases covered at 30X and (d) zero coverage targets or fraction of target bases without any coverage.

## Most complete coverage of the human exome plus more

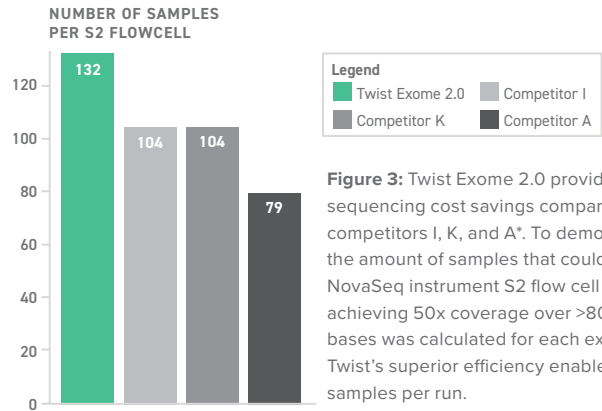
Twist Exome 2.0 features a complete new design that maximizes coverage of clinically relevant regions from the ClinVar database while including updated coverage of protein-coding regions from CCDS, GenCode, RefSeq, Ensembl and ClinVar. In addition, the new design also includes pharmacogenomic SNPs, extended Tert promoter coverage, and 41 Sample ID SNPs for resolving contamination issues (Eurogentest, Pengelly et al.).



**Figure 2:** Relative to competitors A, I, K, Twist Exome 2.0 provides the most comprehensive coding content coverage of target regions within the human exome and beyond. Twist Exome 2.0 demonstrated superior mean coverage of (a) protein-coding regions at depths of 30X, 40X & 50X; as well as superior coverage at 30x across (b) various important databases & gene lists.\*

## Most efficient exome panel

The Twist Exome 2.0 superior uniformity, on-target rate, duplicate rate, and overall coverage translates into a highly efficient, cost-saving exome panel. This efficiency enables you to sequence more samples per run, or else to achieve deeper sequencing over desired targets.



**Figure 3:** Twist Exome 2.0 provides superior sequencing cost savings compared to competitors I, K, and A\*. To demonstrate this, the amount of samples that could fit on a NovaSeq instrument S2 flow cell while still achieving 50x coverage over >80% of target bases was calculated for each exome panel. Twist's superior efficiency enables more samples per run.

\*Two third-party laboratories were hired to conduct an exome comparison between Twist Exome 2.0, Competitor I, Competitor K, and Competitor A, in an attempt to present an unbiased dataset. Libraries were prepared with vendor-specific enzymatic fragmentation methods. Input was at 50 ng gDNA, except for Competitor K that requires 100 ng. All procedures were followed according to vendor protocol. Twist Exome 2.0 was run with the Standard Hybridization v2 & Enzymatic Fragmentation Kit 2.0. Results shown are based on 6 GB of NovaSeq sequencing data run on the S2 flow cell.

Twist Exome 2.0 is part of the Twist Bioscience portfolio of products for NGS Target Enrichment.

### LEARN MORE

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### ORDERING INFORMATION

- 104132:** Twist Exome 2.0, 2 Reactions, Kit  
Panel for 2 enrichment reactions targeting 36.5 Mb of human protein coding and non-coding regions
- 104134:** Twist Exome 2.0, 12 Reactions, Kit  
Panel for 12 enrichment reactions targeting 36.5 Mb of human protein coding and non-coding regions
- 104136:** Twist Exome 2.0, 96 Reactions, Kit  
Panel for 96 enrichment reactions targeting 36.5 Mb of human protein coding and non-coding regions