PRODUCT SHEET

Twist Exome 2.0 & Exome 2.0 plus Comprehensive Spike-in Panels

Thoughtfully curated content, paired with optimized performance

EXOME CONTENT

Exome 2.0

- 36.5 Mb of targets
- 99% of targets covered at >20x

Exome 2.0 plus Comprehensive Spike-in

- 37.6 Mb of targets
- Includes an additional 1.14 Mb of improved coverage of key gene targets

KEY HIGHLIGHTS

Coverage that makes a difference

- Exome 2.0 panel covers essential protein coding regions and noncoding genes
- Addition of the Comprehensive Spike-in adds coverage of key genes and ClinVar content
- Based on major genetic databases
- Includes carefully curated content relevant to human diseases

Robust performance

- Duplexed DNA probes and informed design strategies offer high uniformity of target enrichment
- All Twist TE panels undergo NGS QC for consistent and reliable performance

Adaptable to your needs

- Focused Exome 2.0 base can be customized with additional content
- Effective across multiplex target enrichment workflows
- Run overnight or same-day workflows across multiple sequencing platforms

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

Twist's Exome 2.0 Panel has been carefully designed to help alleviate common sequencing pitfalls and provide researchers with high uniformity, on-target rate, and target coverage; all while delivering on the most updated set of protein-coding and disease relevant content, including noncoding variants. Twist also offers Exome 2.0 plus Comprehensive Spike-in panels for additional content with improved coverage of clinical genomic databases.

Exome 2.0 panel performance

Compared to other leading exome panels, Twist Exome 2.0 delivers higher uniformity and a high 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.

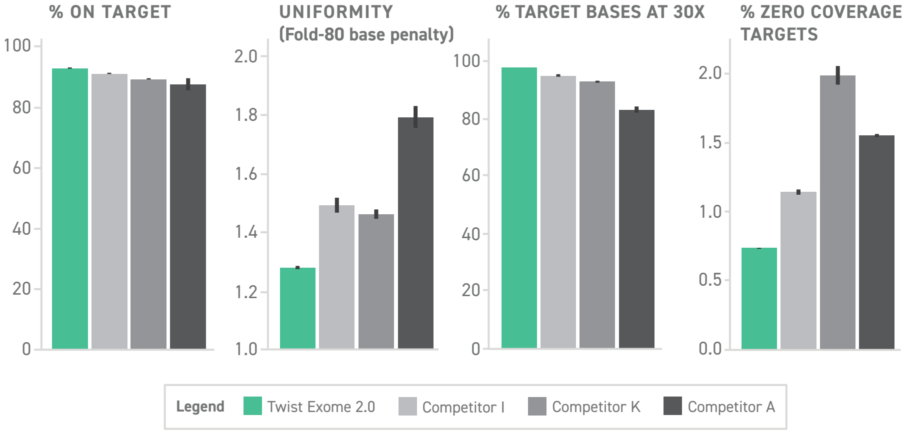

Figure 1. Twist Exome 2.0 demonstrates superior performance over competitors I, K, and A* in (a) on-target rate, calculated as "1-PCT_OFF_BAIT", (b) uniformity, reported as fold-80 base penalty score, (c) % target bases covered at 30X and (d) zero coverage targets or fraction of target bases without any coverage.

Comprehensive coverage of the human exome

Twist Exome 2.0 features an updated design that maximizes coverage of disease 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.

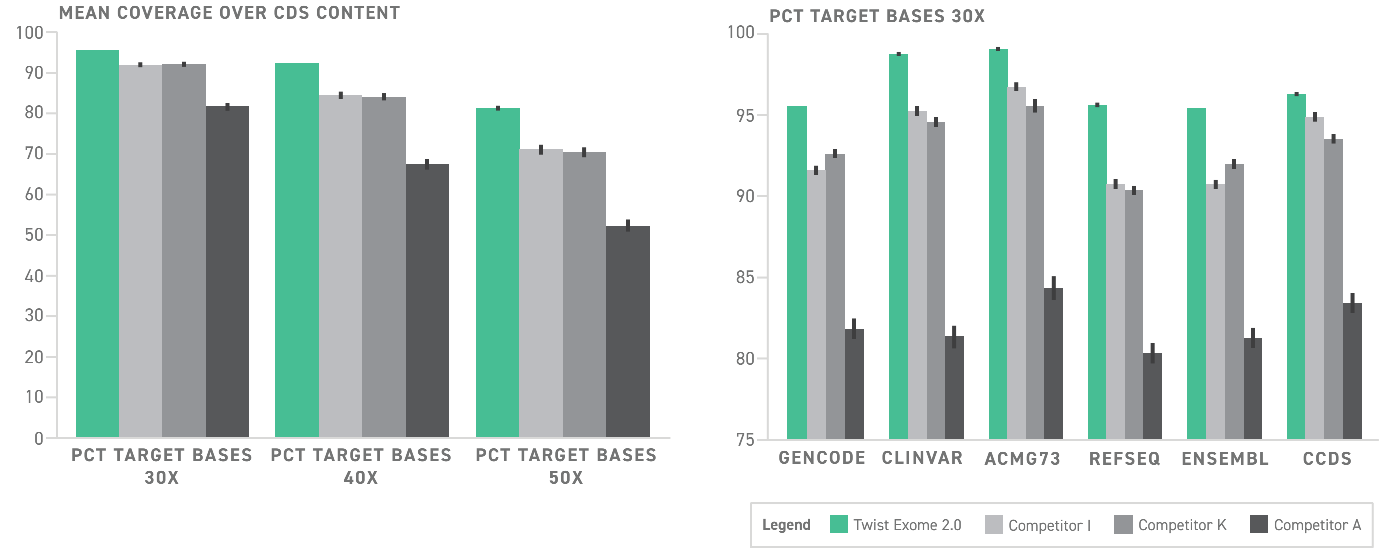

Figure 2. Relative to competitors A, I, K, Twist Exome 2.0 provides the most comprehensive coding content coverage of target regions within the human exome and beyond. Twist Exome 2.0 demonstrated superior mean coverage of (a) protein-coding regions at depths of 30X, 40X & 50X; as well as superior coverage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

Efficient whole exome sequencing

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

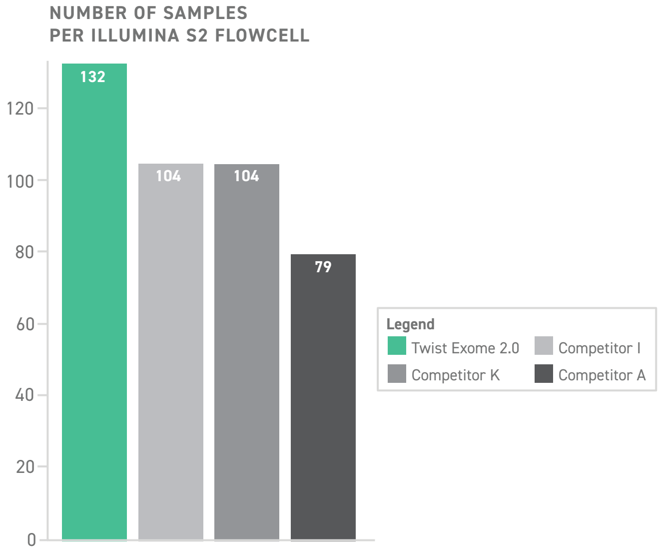

Figure 3. Twist Exome 2.0 provides superior sequencing cost savings compared to competitors I, K, and A*. To demonstrate this, the amount of samples that could fit on an Illumina NovaSeq Instrument S2 flow cell while still achieving 50x coverage over >80% of target bases was calculated for each exome 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 Illumina sequencing data run on the S2 flow cell.*

Options for additional content coverage

The Comprehensive Exome Spike-in offers additional coverage of clinical databases such as ACMG, CCDS, and ClinVar pre-blended with Exome 2.0 and ready for use. This additional 1.14 Mb of target region improves the coverage of these databases for a total target region of 37.6 Mb. As with any Twist target enrichment panel, there is also the option to use Twist's off-the-shelf exome spike-in panels or create custom content to add to Exome 2.0.

EXOME 2.0 PLUS COMPREHENSIVE SPIKE-IN	
SPECIFICITY (1 - % OFF BAIT) :	87.11
UNIFORMITY (FOLD-80 BASE PENALTY) :	1.39
% TARGET BASES AT 30X :	94%
DUPLICATION RATE :	4%

Table 1. Sequencing metrics following target capture with the Exome 2.0 plus Comprehensive Spike-in Panel.

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
Panel for 2 enrichment reactions targeting 36.5 Mb of human protein coding and non-coding regions

104134: Twist Exome 2.0, 12 Reactions
Panel for 12 enrichment reactions targeting 36.5 Mb of human protein coding and non-coding regions

104136: Twist Exome 2.0, 96 Reactions
Panel for 96 enrichment reactions targeting 36.5 Mb of human protein coding and non-coding regions

105034: Twist Exome 2.0 plus Comprehensive Exome Spike-in, 2 Reactions
Panel for 2 enrichment reactions targeting 37.6 Mb of human protein coding and non-coding regions

105035: Twist Exome 2.0 plus Comprehensive Exome Spike-in, 12 Reactions
Panel for 12 enrichment reactions targeting 37.6 Mb of human protein coding and non-coding regions

105036: Twist Exome 2.0 plus Comprehensive Exome Spike-in, 96 Reactions
Panel for 96 enrichment reactions targeting 37.6 Mb of human protein coding and non-coding regions

Twist Bioscience's quality management system governing the design and manufacture of NGS Target Enrichment Panels is ISO 13485:2016 certified (San Francisco, CA).
These products are for research purposes only. Not for diagnostic purposes.