

T W i S T  
• . . . • BIOSCIENCE

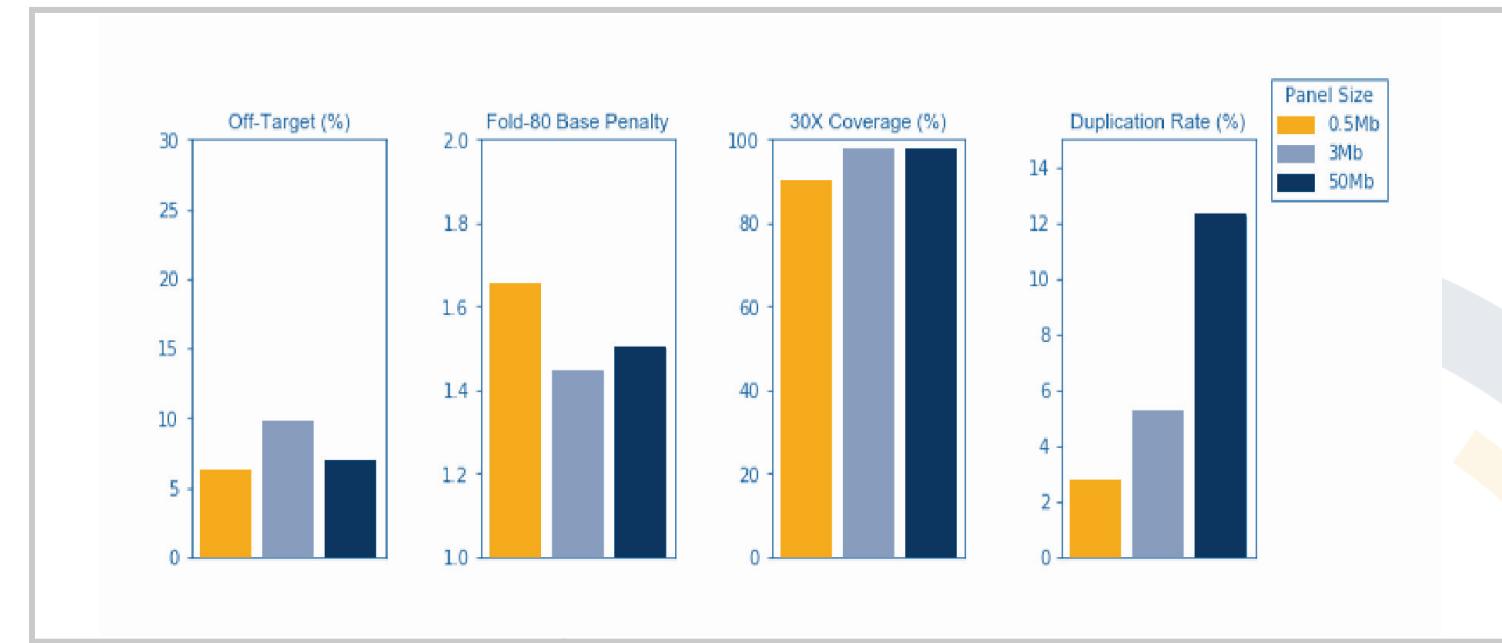
# Methylation sequencing



# TWIST Methylation sequencing workflow

## New Solutions for Methylation Sequencing:

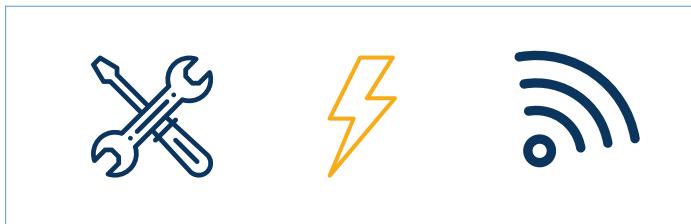
- Exceptional Performance
- Unparalleled Uniformity
- Sensitivity
- Rapid panel iteration
- Design Flexibility
- **Panels compatible with bisulfite and enzymatic conversion methods**



Top Performance for a Broad Range of Panel Sizes

# Pre-capture conversion reduces unique molecule bottleneck

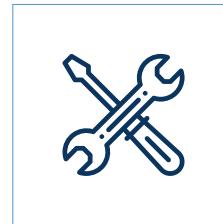
Pre-Capture  
Conversion



- ✓ Greater library complexity
- ✓ Lower input amount



Post-Capture  
Conversion



- ✗ Less library complexity
- ✓ Less complicated probe design



# Complex probe design drives high performance enrichment

## Pre-capture conversion

- ✓ Highly complex design algorithm

## Four Probe Species Synthesized

- ✓ Highly complex design algorithm
- ✓ Fully methylated and unmethylated

## Machine learning strategy

- ✓ Imperial data analysis for adaptive design
- ✓ Integrated stringency filtering

