

# UNCOVER EPIGENETIC SIGNATURES FASTER WITH SURESELECT<sup>XT</sup> HUMAN METHYL-SEQ

The First Comprehensive Methylation Discovery System

## Highlights

- 84Mb design
- Covering 3.7 million CpGs
- Comprehensive tool for methylation discovery
- Probes are not methylation-state dependent
- High sensitivity with single base resolution
- Increased throughput and reduced cost
- Increased library complexity
- Reduce bias compared to existing methylation methods

## Summary

SureSelect<sup>XT</sup> Human Methyl-Seq is the first comprehensive target enrichment system to enable researchers to focus on the regions where methylation is known to impact gene regulation: CpG islands, CpG island shores, undermethylated regions, promoters, and differentially methylated regions (DMRs).

## SureSelect<sup>XT</sup> Human Methyl-Seq

- Uniquely delivers more information than methylation microarrays by detecting individual CpGs
- Increases throughput and reduces costs compared to whole genome bisulfite sequencing
- Reveals methylated regions not detected by restriction enzyme and immunoprecipitation or SNP-based assays

## SureSelect<sup>XT</sup> Human Methyl-Seq Protocol



Figure 1. The SureSelect<sup>XT</sup> Human Methyl-Seq protocol is optimized for DNA methylation analysis using the Agilent SureSelect target enrichment system.



## SureSelect<sup>XT</sup> Human Methyl-Seq Results

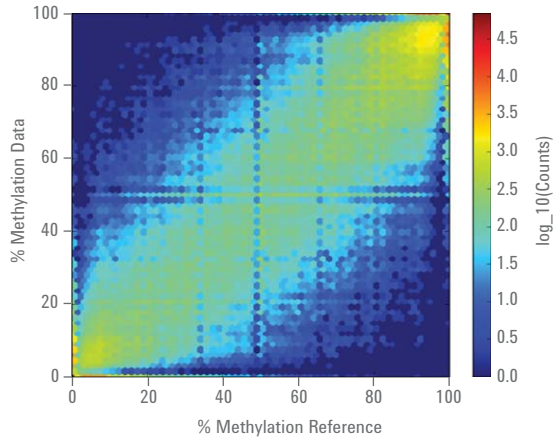


Figure 2. Methyl-Seq achieves excellent correlation with whole genome bisulfite sequencing (WGS) data ( $R=0.93$ , Lister R. *et al.* 2009).

## SureSelect<sup>XT</sup> Human Methyl-Seq Content Types

- CpG islands
- GENCODE promoters
- Cancer, tissue-specific DMRs, or regulatory features in:
  - CpG Islands, shores/shelves ( $\pm 4\text{kb}$ )
  - Enhancers
  - Ensemble regulatory regions
  - DNase I hypersensitive sites

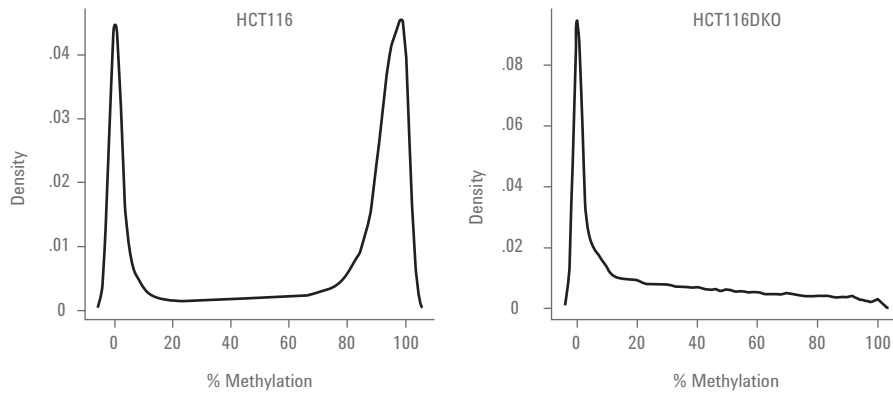


Figure 3. Highly sensitive and accurate methylation detection after SureSelect target enrichment demonstrated DNA methylation differences between HCT116 human colon cancer cells and its methyltransferase double-knockout (DNMT1<sup>-/-</sup> and DNMT3b<sup>-/-</sup>).

[www.agilent.com/genomics/sureselect](http://www.agilent.com/genomics/sureselect)

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