

NGS TARGET ENRICHMENT

SureSelect^{XT}

Human Methyl-Seq

Uncover Epigenetic Signatures Faster



Benefits

- 84 Mb design covering 3.7 million CpGs
- Probes are not methylation-state dependent
- High sensitivity with single base resolution
- Increased throughput and reduced cost
- Reduce bias compared to existing methylation methods

The First Comprehensive Methylation Discovery System

SureSelect^{XT} 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, CpG island shelves, undermethylated regions, promoters, and differentially methylated regions (DMRs).

SureSelect^{XT} Human Methyl-Seq

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

SureSelect^{XT} Human Methyl-Seq Protocol

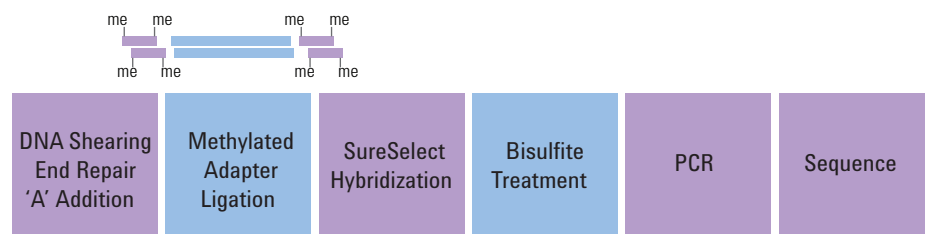


Figure 1. The SureSelect^{XT} Human Methyl-Seq protocol is optimized for DNA methylation analysis using the Agilent SureSelect target enrichment system.



SureSelect^{XT} Human Methyl-Seq Content Types

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

GeneSpring NGS software for DNA Methylation Analysis

- Quickly visualize methylation level, CpG region coverage, read alignment, and base quality
- Gain biological insight by identifying methylation states with single base-pair resolution and by overlaying with specific genes of interest
- Find DMR's & DMC's, their genic & intergenic effects, and correlate to QPCR, ChIP-seq, and RNA-seq results

SureSelect^{XT} Human Methyl-Seq Results

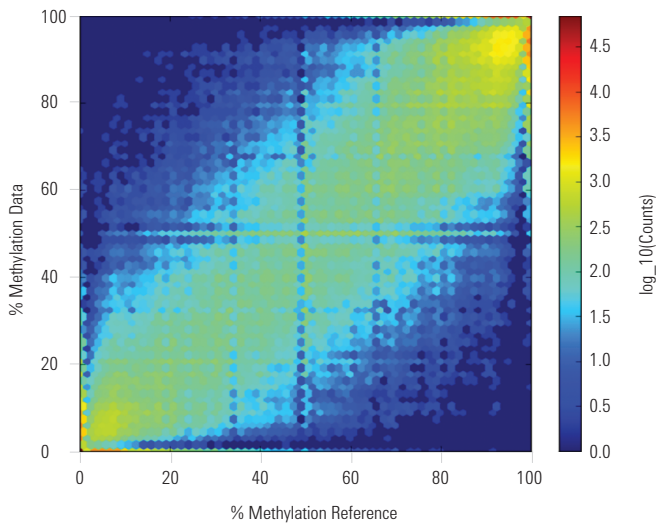


Figure 2. Methyl-Seq achieves excellent correlation with whole genome bisulfite sequencing (WGS) data (R=0.93, Lister R. et al. 2009).

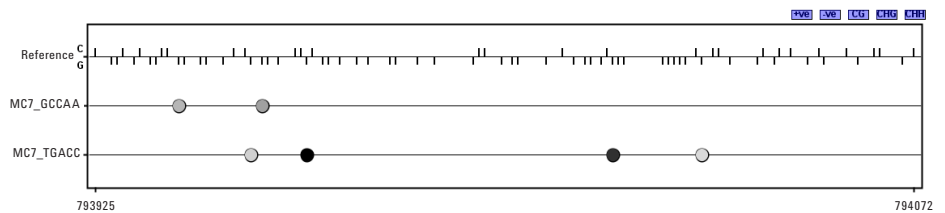


Figure 3. GeneSpring NGS allows you to easily visualize methylation results. Lollipop plot shows methylated C's as circles colored by intensities relative to their methylation level or p-values.

Request more information or buy online: www.agilent.com/genomics/methylseq



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