Gene Regulation Solutions

Microarrays and Next-Generation Sequencing

Agilent Technologies

The Agilent Microarrays Advantage

Agilent Microarrays Lead the Industry in:

• Up-to-Date Content

SurePrint G3 Human Gene Expression v3 Microarrays feature new content from the recent Ref Seq build, unlike competitors' microarrays. This content includes long non-coding RNA (lncRNA) probes designed in collaboration with Professor Jo Vandesompele to completely cover the LNCipedia 2.1 database.

• Widest Dynamic Range

Sequence fidelity is the key to maximizing dynamic range in gene expression microarray experiments. The Agilent SurePrint inkjet oligonucleotide synthesis process dramatically increases probe sequence fidelity, providing superior dynamic range for Agilent microarrays.

These microarrays capture data across a 5 log dynamic range, while other platforms compress the signal into 2.5 logs, resulting in imperfect data capture.

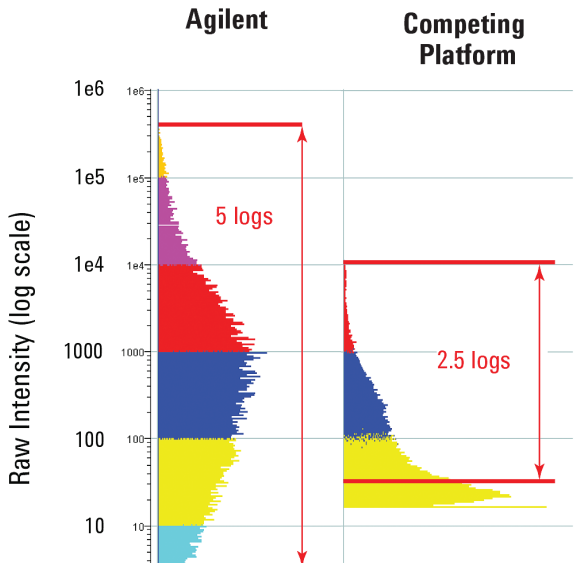


Figure 1. Signal intensity plots across log change. Agilent captures data across five orders of magnitude, while the major competitive array captures just under three.

• Highest Sensitivity

The Agilent microarray platform produces accurate relative quantitation of gene expression at sensitivity levels far exceeding other array platforms.

Figure 2. The Agilent SurePrint G3 Human miRNA Microarray V3 contains eight 60,000 feature arrays printed on a microscope slide. P/N: G4470C.

• Easy Customization

Create your own custom microarray using Agilent's online eArray software. These arrays can be ordered at no additional charge with no minimum order, and often the same turn-around time as competitors' catalog arrays.

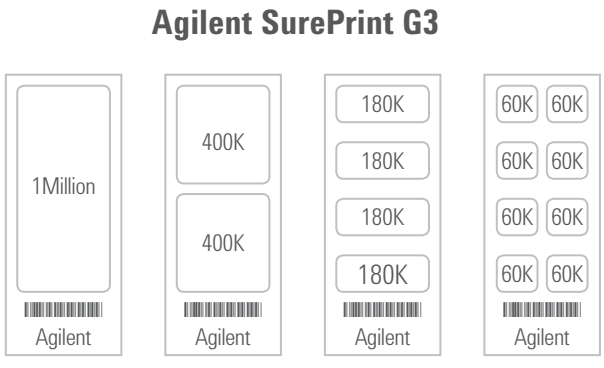


Figure 3. Schematic illustration of all of the Agilent SurePrint.

Are You Capturing All the Data That is Within Your Sample?

Agilent provides a broad portfolio of tools with high sensitivity and specificity to understand the role of gene regulation in cancer, constitutional disease and cell development. Take advantage of industry-leading data reproducibility & concordance between microarray and sequencing platforms to capture all the data from your samples and drive statistical power within your study.

Agilent Gene Regulation Tools		
Microarrays		**Sequencing**
SurePrint G3 Human Gene Expression v3 featuring lncRNA	SurePrint DNA Methylation	SureSelect^{XT} Strand-Specific RNA-Seq
SurePrint miRNA	ChIP-on-chip	SureSelect^{XT} MethylSeq
Custom Design Available Across All Platforms		

Key Products for Gene Expression

Catalog Microarrays:

SurePrint miRNA Microarrays

Agilent's proprietary probe design and unique labeling method provide industry leading sensitivity and specificity.

In the miRQC platform benchmark study, SurePrint miRNA arrays had the most consistent performance in miRNA detection, superior to qPCR, sequencing, and other microarrays[1].

Human miRNA Microarray Kit (V3)
Based on Sanger miRBase.
P/N: G4470C

Mouse miRNA Microarray Kit
Release 21.0
P/N: G4859C

Rat miRNA Microarray Kit
Release 21.0
P/N: G4473C

SurePrint Model Organism Microarrays

Manufacturing flexibility and consistency make Agilent your ideal partner for model organism studies.

We specialize in the major models of mouse and rat, as well as 24 additional catalog or consortium designs, from bovine to equine and cotton.

Mouse Microarray Kit
Release 21.0
P/N: G4852B

Rat Microarray Kit
Release 21.0
P/N: G4473C

Made-to-Order Microarrays

SurePrint DNA Methylation

Microarrays include promoter regions and CpG islands to provide a clear picture of DNA methylation and gene expression.

ChIP-on-Chip Microarrays

Agilent's Human Promoter Microarrays are optimized using probes validated for ChIP-on-chip technology, and are specifically designed for location analysis of human DNA-binding proteins.

(1) McCall, M. N. *et al.*, BMC Bioinformatics, 17:138.

Key Products for Sequencing by Hybrid-Capture

SureSelect^{XT} Strand-Specific RNA-Seq

Targeted RNA Sequencing using hybrid capture reveals the complexity of the human transcriptome more efficiently than WGS alone. Transient or unannotated transcripts that are below the detection limits of conventional sequencing approaches can be found. It is estimated that there is a three-fold increase in isoform detection amongst well-annotated proteins, using SureSelect^{XT}. Data that would be thrown away as noise in conventional assays reveals valuable unassembled transcripts – a clear advantage of hybrid-capture.

Agilent's RNA capture assay for the Illumina sequencing platform leads the industry in workflow ease, strand specificity, less bias and best uniformity of coverage.

SureSelect^{XT} RNA-Seq Products

Agilent offers one total transcriptome sequencing library preparation method and two targeted methods.

SureSelect Strand-Specific RNA Library

Total transcriptome RNA-Seq Library Preparation Kit for the Illumina platform.

16 Rxns: *P/N G9691A*
96 Rxns: *P/N G9691B*

SureSelect^{XT} RNA Reagent Kit

Targeted library preparation using RNA Kinome, Exome V6 + UTR, or custom-designed baits.

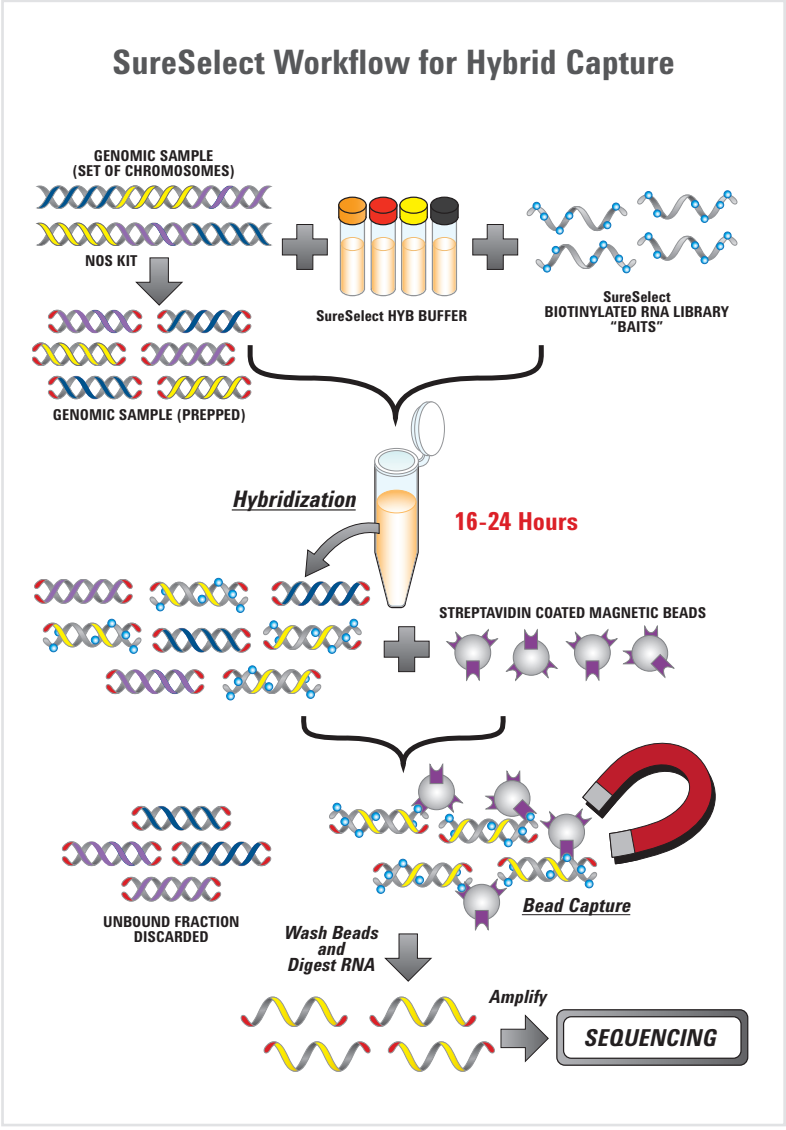
16 Rxns: *P/N G9692A*
96 Rxns: *P/N G9692B*

SureSelect^{XT} RNA Direct to Capture Kit

Targeted library preparation using RNA Kinome, Exome V6 + UTR, or custom-designed baits.

16 Rxns: *P/N 931226*

- No PolyA isolation step required
- Increased specificity
- Much better sensitivity to low expressers
- Robust differential expression analysis
- Higher dynamic range
- Capture of lncRNAs
- Can tolerate lower RNA quality, e.g., FFPE



SureSelect^{XT} Methyl-Seq Products

The first comprehensive target enrichment system to enable researchers to study regions where methylation is known to impact gene regulation: CpG islands, CpG island shores, under-methylated regions, promoters and differentially methylated regions (DMRs).

- Delivers more information than methylation microarrays
- Increases throughput and reduces costs compared to whole genome bisulfite sequencing
- Designs available for human, mouse and rat

SureSelect^{XT} Methyl-Seq Reagent Kit

16 Rxns: *P/N G9651A*
96 Rxns: *P/N G9651B*

SureSelect^{XT} Mouse Methyl-Seq Reagent Kit

16 Rxns: *P/N 931052*

SureSelect^{XT} Rat Methyl-Seq Reagent Kit

16 Rxns: *P/N 931143*
96 Rxns: *P/N 931144*

Concordance Matters

Gene Expression Through the Lens of Arrays & RNA-Seq

Agilent Arrays: Sensitivity, Customization and Concordance
Agilent RNA-Seq: Discovery and Specificity

Data concordance between arrays and RNA-Seq is crucial, as they are often used orthogonally for discovery and verification. Using both methods assures sensitive and accurate determination of differentially expressed transcripts. Array signals that are not compressed are imperative in order for methods to be correlated with each other. Compression will erase subtle differences that are needed to reliably distinguish signal background from true biological signal. Don't get lost in the noise – find signals and confirm signals in high resolution datasets.

Benefits of a Dedicated Agilent Workflow

Choosing an all-Agilent workflow ensures that you are using tools derived from the highest fidelity oligonucleotides and precision chemistry – ensuring your data has the highest resolution.

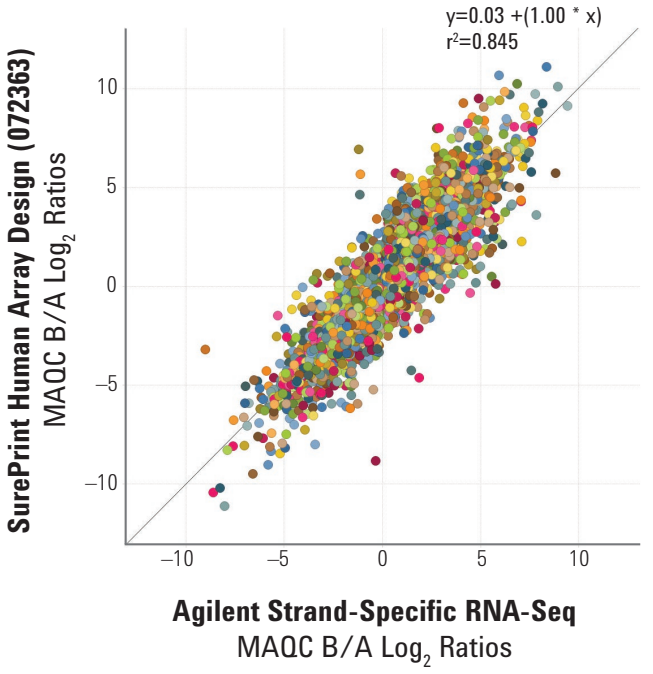
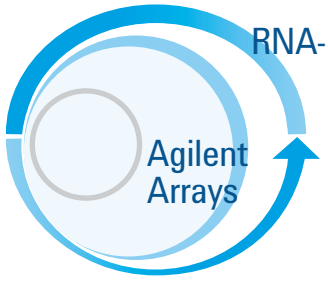


Figure 4. A pairwise scatter plot of SurePrint G3 Human v3 vs the Agilent Strand-Specific RNA-Seq library prep, demonstrating excellent correlation between microarray expression ratios and RNA-Seq ratios for 12,383 different Entrez genes.



	Discovery	Verification	**Sensitivity**	**Specificity**	Ultra Rare or Novel	Sample Input	FFPE Samples	**Concordance** (Technology)	Concordance (Batch)	Throughput	**Easy Customization**
Agilent RNA-Seq	●	●	●	●	●	●	●	●	●	●	●
Agilent Microarrays	●	●	●	●	●	●	●	●	●	●	●
Other Microarrays	●	●	●	●	●	●	●	●	●	●	●

Figure 5. The benefits of an all-Agilent workflow across various attributes, illustrating Agilent's relative strengths in sensitivity, specificity, concordance and easy custom design. Green: outperforms competitors for this attribute; Yellow: comparable to competitors; Red: inferior to competitors.

Integrated Platform: Data Analysis and Contextualization

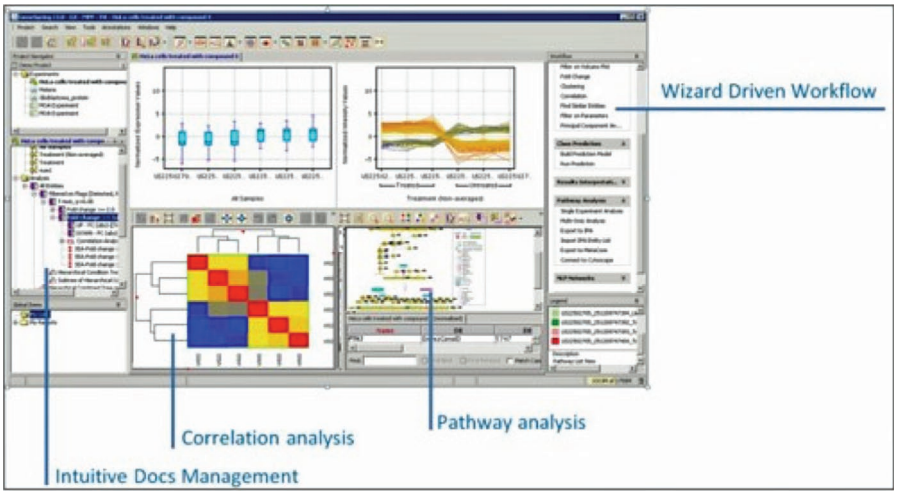
The GeneSpring Suite for Integrated Biology

GeneSpring is designed specifically for the needs of biologists studying gene regulation using microarrays and sequencing technologies. GeneSpring helps investigators in taking an integrated multi-omics approach including data from transcriptomics, genomics, proteomics and metabolomics.

Within GeneSpring's interactive environment, the user can pull disparate information sets together to discern various levels of regulation from their diverse datasets.

Key Functions for Genomics Investigators Include:

- Metadata-analysis for quality control and visualization based on sample parameters including time-course analysis
- Pathway visualization from both sequencing and microarray studies
- Correlation analysis between sequencing and microarray data



Data Import from Strand NGS to GeneSpring

Strand NGS provides dedicated workflows for DNA-Seq, RNA-Seq, Methyl-Seq, Small RNA-Seq, ChIP-Seq and MeDIP-Seq. Strand NGS processed data from DNA-Seq, RNA-Seq and Methyl-Seq analysis can be imported into GeneSpring (see Figure 6 with available datatypes) for further downstream analysis.

The upstream analysis of NGS data is performed in Strand NGS including alignment, quantification & normalization, differential expression, splicing analysis and SNP detection for RNA-Seq. Methyl-Seq analysis tools in Strand NGS include data quality assessment and lollipop plots to show methylated regions within a sample.

Icon	Object	DNA-Seq	RNA-Seq	ChIP-Seq	Methyl-Seq	Small RNA-Seq
	Samples	☑	☑	☑	☑	☑
	Interpretations	☑	☑	■	☑	☑
	Read lists	☑	☑	☑	☑	☑
	Entity lists	☑	☑	☑	☑	☑
	Region lists	☑	☑	☑	☑	☑
	Cluster tree	☐	☐	☐	☐	☐
	Pathway list	☐	☐	☐	☐	☐
	SNP report node	☐	☐	■	■	■
	SNP reports	☑	☑	■	■	■
	SV node	☐	■	■	■	■
	SV region list	☑	■	■	■	■
	Copy number node	☐	■	■	■	■
	CNV pair node	☐	■	■	■	■
	Continuous data	☐	■	■	■	■
	CNV regions	☑	■	■	■	■
	Novel detection report	■	☑	■	■	☑
	Quantification node	■	☐	■	■	☐
	Gene fusion node	■	☐	■	■	■
	Gene fusion report	■	☑	■	■	■
	Motif node	■	■	☑	■	■
	Methylation node	■	■	■	☑	■
	DMC node	■	■	■	☑	■
	Active regions	■	■	■	■	☑

☑ Exported by default ☐ Cannot be exported
☑ Can be chosen for export ■ N/A

Figure 6. This table includes the analysis workflow that was imported into GeneSpring using the NGS experiment import option, and the functionalities available.

Trusted Answers. Together.

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