GENE EXPRESSION ANALYSIS

SurePrint G3 Gene Expression Microarrays

Find Clarity in Your Expression

Benefits

- **Superior Content**
  Expert-defined, up-to-date, and fully customizable
- **Better Sensitivity**
  >5 logs dynamic range and detect down to 22 fmol
- **Powerful Performance**
  High linearity and concordance with RNA-Seq and ERCC controls

Agilent SurePrint G3 Gene Expression Microarrays for Human (v3), Mouse (v2) and Rat (v2) models incorporate the latest content, and are also a scaffold for researchers to customize content freely via the web-tool eArray. One of the core benefits of the SurePrint technology is that it allows probe updates without cost to manufacturing scalability, enabling Agilent's unparalleled customizability in products to deliver the latest content developments to researchers.

As seen in Table 1, the latest updates to SurePrint G3 Gene Expression Microarrays feature:

- **Human v3:** Updated and expanded coverage of human coding content; new lncRNA content covering all of LNCipedia 2.1, designed in collaboration with Ghent University.
- **Mouse v2**: Complete coverage of known RefSeq coding transcripts; a re-design of lncRNA content for improved probe performance and annotation.
- **Rat v2**: Complete coverage of known and model RefSeq coding and non-coding content.

Microarrays remain a key tool available to researchers among the host of well-known expression modalities, including RNA-Seq and qRT-PCR technologies. Agilent's catalog SurePrint G3 Gene Expression Microarrays are 8x60k density designs that provide a balance of comprehensive data with a fast sample-to-data processing time. These attributes have enabled Agilent Gene Expression Microarrays to become established tools for screening applications to quickly identify individual targets for validation, or to profile multi-target signatures for clinical development.

> *"... Measuring both types of RNA in a single assay provides insight into the biological association between mRNA and lncRNA from relative expression levels," said Professor Jo Vandesompele, Ghent University. "The key is having a good balance of coding and long non-coding features, and LNCipedia 2.1 is an optimal source to pair with Agilent's gene expression content."*

Table 1: Content Comparison between Agilent Microarrays and a leading competitor product

Transcript coverage	Agilent v3 Human	Comp. A	Agilent v2 Mouse	Comp. A	Agilent v2 Rat	Comp. A
RefSeq (Entrez) gene count	**26,083**	24,838	**27,122**	26,515	**30,584**	23,586
NM - RefSeq coding transcript, known	**37,756**	30,654	**29,116**	26,191	**17,619**	16,771
NR - RefSeq non-coding transcript, known	**8,339**	5,638	**3,316**	3,391	**156**	442
XM - RefSeq coding transcript, model	**28,768**	996	**44,306**	1,946	**42,424**	10,376
XR - RefSeq non-coding transcript, model	**8,943**	3,428	**13,129**	3,712	**18,128**	818
lncRNA transcripts	**30,606**	11,086	**4,578**	~2,000		

High Sensitivity & Wide Dynamic Range

Agilent Gene Expression Microarrays feature an industry leading >5 log of dynamic range to linearly capture high and low expressors, as compared to competing systems with only 3 log of dynamic range commonly resulting in signal truncation and compression. Agilent microarrays have been shown to detect as low as 22 fmol (Figure 1) with minimal compression.

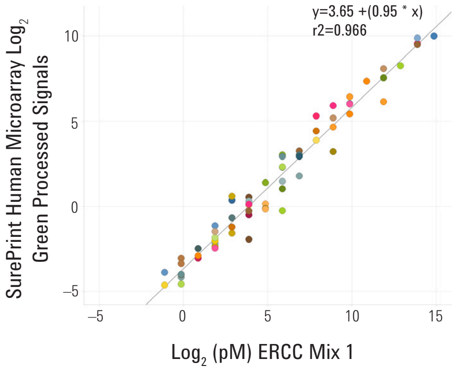

Figure 1. 65 ERCC spike-in probes are shown in a pairwise scatter between expected and SurePrint G3 Human v3 Gene Expression Microarray results. ERCC Mix 1 was diluted 1:1,000 and 2 µl was spiked into 100 ng total RNA. Cy3-labeled cRNA prepared from this sample was run on the SurePrint G3 Human v3 Gene Expression Microarray and probes with green processed signals that were flagged as "well above background" on a majority of the 4 replicate MAQC A microarrays were 75th percentile normalized and the average log$_2$ signals for the ERCC control probes were plotted as a function of the known ERCC transcript molar concentrations in Spike-In Mix 1. Using this filtering criteria, 65 ERCC transcripts were detected in the MAQC A sample containing ERCC Spike-In Mix 1. After adjusting for the volume of Spike-In Mix added to the sample, the sensitivity of this assay was determined to be ~22 fmol and the dynamic range was determined to be 16 log$_2$, or 5 log$_{10}$ orders of magnitude. Very little compression of signals is observed (slope = 0.95) and there is very good correlation between the known concentrations and the microarray signals ($r^2 = 0.966$).

Excellent Concordance

Good concordance with NGS or qPCR platforms is essential to corroborate and validate results. As seen in Figure 2, SurePrint G3 Human Gene Expression Microarray v3 shows a correlation of $r^2>0.85$, and a slope of m=1.00, demonstrating excellent correlation between microarray to NGS results with minimal data compression.

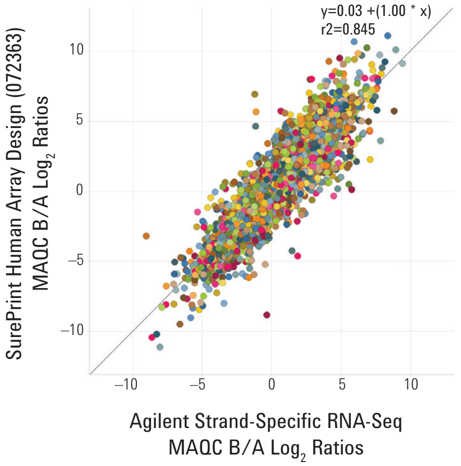

Figure 2. A pairwise scatter of SurePrint G3 Human v3 Gene Expression Microarray (n=4) and Agilent Strand-specific RNA-Seq Library prep (n=3) log$_2$ differential gene expression ratios of the MAQC B/A samples is shown. High confidence gene expression data was generated by filtering for features that were flagged as "well above background" on a majority of the replicate microarrays and NGS having a minimum of 20 mapped reads. The data was further filtered for significant ($p<0.05$) differences in gene expression between the MAQC B and MAQC A samples in each dataset. We observed very high correlation of microarray ratios as compared to RNA-Seq ratios ($r^2 = 0.845$) with very little compression of microarray ratios as compared to RNA-Seq ratios (slope = 1.00) for 12,383 different Entrez genes.

Ordering Information:

Species	Name	Product Number	Kit Size	Format
Catalog Kits				
Human	SurePrint G3 Human Gene Expression v3 Microarray Kit	G4851C	3 slides	8 x 60K
Mouse	SurePrint G3 Mouse Gene Expression v2 Microarray Kit	G4852B	3 slides	8 x 60K
Rat	SurePrint G3 Rat Gene Expression v2 Microarray Kit	G4853B	3 slides	8 x 60K

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