DataSheet

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Biology for a better world

GeneChip® Gene 1.0 ST Arrays for whole-transcriptome analysis of model and applied research organisms with the GeneChip® Scanner 3000 7G series

Get the most complete and accurate picture of gene expression with whole-transcript resolution

Affymetrix understands the importance of selecting a model organism best suited to answer the biological question being studied. In order to meet your research goals, Affymetrix offers a broad catalog of Gene 1.0 ST Arrays for studying whole-genome expression profiles of many organisms commonly used in research today. This growing catalog of arrays includes organisms commonly used as models for deciphering the molecular mechanisms underlying human disease and agriculture crop improvements.

These model and applied research arrays are the latest addition to the growing family of Affymetrix gene expression microarrays offering whole-transcript coverage. Every design is based on the most recent genome information available and offers the highest probe coverage (a median of up to 25 probes across the full length of the gene). This yields accurate detection for genome-wide transcript expression changes and provides higher resolution and accuracy than other classical 3'-biased microarray solutions on the market. The whole-transcriptome analysis approach enables researchers to detect multiple transcript isoforms from a given gene, including those that could be missed using a 3'-biased expression design, such as splice variants, non-polyadenylated transcripts, transcripts with alternative polyadenylation sites, and truncated transcripts. *For more information on the the GeneChip Scanner 3000 7G series, please visit* www.affymetrix.com.

Benefits of GeneChip Gene 1.0 ST Arrays:

- **Highest transcript coverage** – Get confident expression measurements of well-annotated content with a median of up to 25 probes per gene

- **Whole-transcriptome analysis** – Capture the transcript isoforms you may miss with 3'-biased expression designs

- **High data reproducibility** – Achieve high inter- and intra-array signal correlation (R >0.99)

Design strategy and coverage

GeneChip Gene 1.0 ST Expression Array designs provide the highest coverage of the transcribed genome. We use a comprehensive collection of information sources to design probes that interrogate a median of up to 25 unique sequences of each gene. This design strategy provides

you with the ability to evaluate whole-transcriptome gene expression at the gene and exon levels, which allows the study of transcript variants and alternative splicing events.
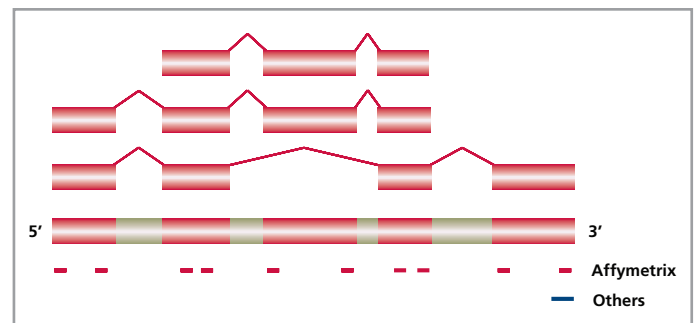
The high number of unique 25-mer probes interrogate a median of up to 625 bases per gene. This high coverage across the entire transcript results in superior performance and data confidence as well as the ability to update your experimental data as the understanding of each genome and transcriptome grows.

For the Gene 1.0 ST Arrays, probes are selected across the entire gene, enabling evaluations at both the gene (transcript) and exon levels, which allows the study of transcript variants and alternative splicing events.

Platform specification	Value
Sensitivity[1]	≥1:100,000 (≥1.5 pM)
Signal correlation coefficient	>0.99
Dynamic range[1]	~3 logs
Total RNA input required	50–500 ng
Probe feature size	5 µm
Background probes	Antigenomic set
Poly-A controls	*dap, lys, phe, thr*
Hybridization controls	*bioB, bioc, bioD, creX*

[1] Sensitivity and dynamic range were determined using a Latin square experimental design with 61 *in vitro* transcribed (IVT), full-length transcripts added to HeLa total RNA. For this experiment, 12 spike pools with different relative abundances were tested. Spike concentration differences were defined as significant if the t-statistic results were greater than a threshold set based on three replicates and 95% confidence.

Ordering information

Part number		Description	Genome build	Probes	Median probes/gene	Gene-level Probe Sets
6 pack of arrays	30 pack of arrays					
901916	901915	Arabidopsis Gene 1.0 ST Array	TAIR10	600,941	22	28,501
901921	901920	Bovine Gene 1.0 ST Array	UMD3.0	526,810	23	24,341
902160	902161	*C. elegans* Gene 1.0 ST Array	WS231	638,442	24	28,305
901926	901925	Canine Gene 1.0 ST Array	canFam2	590,097	24	27,681
901931	901930	Chicken Gene 1.0 ST Array	galGal3	439,582	24	18,214
901942	901941	Cyno-Rhes Gene 1.0 ST Array	RefSeq (Cynomolgus) rheMac2 (Rhesus)	116,050 716,101	24 23	5,319 37,292
901937	901936	Cynomolgus Gene 1.0 ST Array	RefSeq	684,229	20	40,096
902155	902156	Drosophila Gene 1.0 ST Array[1]	r5.45	362,078	25	15,309
901947	901946	Equine Gene 1.0 ST Array	equCab2	504,603	21	25,923
901952	901951	Feline Gene 1.0 ST Array	felCat3	792,191	24	34,942
902243	902244	Guinea Pig Gene 1.0 ST Array	cavPor3	518,682	22	24,974
901962	901961	Marmoset Gene 1.0 ST Array	WUGSC 3.2/calJac3	656,668	21	33,971
901967	901966	Medicago Gene 1.0 ST Array	Mt2.0	654,305	22	38,144
901972	901971	Ovine Gene 1.0 ST Array	oarV2.0	508,538	23	22,047
901977	901976	Porcine Gene 1.0 ST Array	Sscrofa9 (susScr2)	394,580	22	19,212
902238	902239	Rabbit Gene 1.0 ST Array	oryCun2	496,321	22	23,282
901987	901986	Rhesus Gene 1.0 ST Array	rheMac2	716,101	23	37,292
901982	901981	Rice (Cn) Gene 1.0 ST Array (ssp. Indica)	BGI	610,417	15	40,987
901997	901996	Rice (Jp) Gene 1.0 ST Array (ssp. Japonica)	RAP2	521,299	17	29,664
901992	901991	Rice (US) Gene 1.0 ST Array (ssp. Japonica)	osa1r6	816,815	19	45,207
902299	902300	Tomato Gene 1.0 ST Array	SL 2.40	715,135	20	37,815
902002	902001	Soy Bean Gene 1.0 ST Array (includes Bradyrhizobium japonicum)	Glyma1 GeneBank®	1,210,950 123,710	19 16	66,473 8,250
901957	901956	Zebra Finch Gene 1.0 ST Array	TaeGut1	381,165	22	18,595
902007	902006	Zebrafish Gene 1.0 ST Array	danRer6 & Zv9	1,255,682	22	59,302

[1] Supports analysis of *D. melanogaster, D. yakuba,* and *D. simulans* via user configurable setting in Expression Console™ (EC) Software