Data Sheet



GeneChip[®] Drosophila Genome 2.0 Array

The GeneChip® Drosophila Genome 2.0 Array provides comprehensive coverage of the *Drosophila melanogaster* genome for studying the expression of more than 18,500 *D. melanogaster* transcripts. The array was developed based on the content from the release 3.1 of the *D. melanogaster* genome by FlyBase and the Berkeley Drosophila Genome Project (BDGP), funded by the National Human Genome Research Institute, Department of Energy, and Howard Hughes Medical Institute. In addition, other published gene predictions from the Drosophila research community were included on the array.

This Drosophila Genome 2.0 Array includes more than 30 percent more content than the previous generation *D. melanogaster* design.

Applications

The fruit fly *D. melanogaster* is an insect approximately 3 mm in length that is typically found close to decaying fruit. Its short life cycle, easy reproduction in the laboratory, and low cost have contributed to wide use as one of the most valuable model organisms in biological research, particularly in genetics and development.

Besides its use in genetic and developmental studies, *D. melanogaster* is used for studies related to embryology, alcoholism, learning, behavior, ecology, evolution, circadian rhythm, mechanistic pathways, disease, and pharmaceutical development.

D. melanogaster represents one of the most well-understood model organisms. Mutant flies with defects in any of several thousand genes are publicly available, and the entire genome has been sequenced.

The Drosophila Genome 2.0 Array is a valuable tool that enables researchers to quickly and reliably assess the biological effects of small molecules, as well as to investigate the mechanisms of action and signaling pathways responsible for biological processes and developmental changes. Because researchers can interrogate more than 18,500 transcripts in a single experiment, the Drosophila Genome 2.0 Array enables scientists to analyze changes in gene expression at the genome level in order to accelerate ongoing research and facilitate novel discovery.

Array profile

The Drosophila Genome 2.0 Array is a 100-format, 11 µm array design that contains 14 probe pairs per probe set. The design of the new array was largely based on the

Specifications

Number of probe sets	18,880
Number of transcripts	~18,500
Number of arrays in set	One
Array format	100
Feature size	11 µm
Oligonucleotide probe length	25-mer
Probe pairs per sequence	14
Hybridization controls	bioB, bioC, bioD from Escherichia coli and cre from P1 bacteriophage
Poly-A controls	dap, lys, phe, thr, trp from Bacillus subtilis
Housekeeping/control genes	actin (actin 42A), GAPDH (glyceraldehyde-3-phosphate dehydrogenase 2), Eif-4a (eukaryotic initiation factor 4a)
Detection sensitivity	1:100,000*

*As measured by detection in comparative analysis between a complex target containing spiked control transcriptions and a complex target with no spikes.



content from the annotations in release 3.1 of the *Drosophila melanogaster* genome by Flybase and the BDGP. This array design includes more than 30 percent more content than the previous generation *D. melanogaster* design.

In total, the array uses more than 500,000 data points to measure the expression of 18,500 transcripts and variants. Oligonucleotide probes complementary to each

corresponding sequence are synthesized in situ on the arrays. Fourteen pairs of oligonucleotide probes are used to measure the level of transcription of each sequence represented on the Drosophila Genome 2.0 Array.

Instrument/software requirements

- GeneChip[®] Scanner 3000
- Affymetrix[®] GeneChip[®] Command Console[®] Software (AGCC)

Ordering information

Part number	Description	
GeneChip® Drosophila Genome 2.0 Array		
900531	Contains 2 arrays	
900532	Contains 6 arrays	
900533	Contains 30 arrays	

Supporting products

Part number	Description
GeneChip® 3' IVT Express Kit	
901228	10 reactions
901229	30 reactions

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