

The Omni family of microarrays.

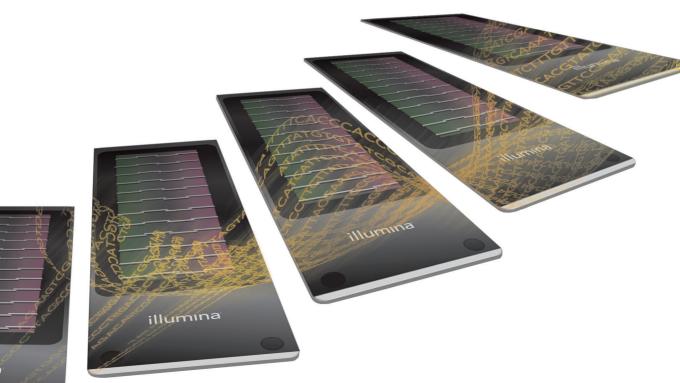
Highest value content. Flexibility to customize.

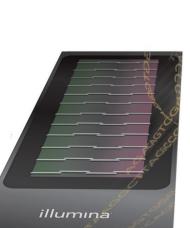


Illumina microarrays.

- Powerful genome-wide genotyping
- Flexibility to tailor studies with custom content
- Maximum coverage for association testing
- Highest resolution for copy number analysis

All backed by the proven Infinium® Assay.





A new era of discovery.

Propelled by over a decade of genomic research, the human genetics community has made a quantum leap in the amount of variation identified across diverse human populations.

Leveraging these results, we've developed a variety of genetic analysis tools to cover the human genome like never before.

Empowering you to dig deeper into human traits and disease, find causes, and unlock answers. Leading to new hypotheses. New discoveries. And a new understanding of human health.



Maximize your opportunity for discovery.

Get powerful genome-wide coverage through intelligent tagSNP selection on each Omni microarray. Common and rare markers from the International HapMap and 1000 Genomes (1kGP) projects were carefully selected to increase your chances of finding meaningful and true associations across the genome, including gene regions and the MHC.

An array for any study. Any budget.

The Omni family gives you the flexibility to study the widest range of genetic variation—no matter your study size, sample population, research focus, or budget. Choose the Omni5 for the most comprehensive coverage, plus the option to add up to 500K custom markers. Or, start with common variants using the OmniExpress.



HumanOmni5-Quad

- ~4.3 million high-value, tag SNP markers delivering coverage down to 1% MAF, including over 2 million genic markers
- Flexibility to add up to 500K custom variants
- Highest density spacing of any whole-genome genotyping array (~1 marker/680 bp)

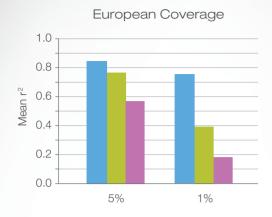
HumanOmni2.5-8*

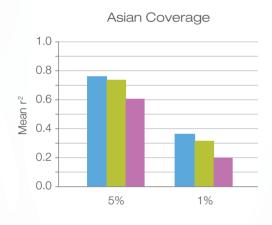
- Coverage of common and rare SNPs down to 2.5% MAF
- Flexibility to add up to 250K custom variants

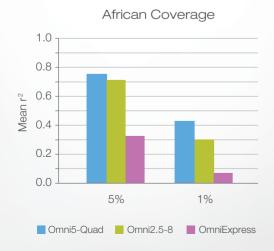
HumanOmniExpress*

- Focused on common variants down to 5% MAF, with the industry's highest throughput
- Flexibility to add up to 200K markers

*Content from the HumanExome BeadChip can be added to each of these arrays.







Highest coverage. Better identification.

Maximum coverage with Omni arrays increases your opportunity to identify associated variants across the genome. These charts show the average coverage at 5% MAF and 1% MAF for the Omni5, Omni2.5 and OmniExpress, as estimated from 1kGP data from three world regions—Europe, East Asia, and Africa.

Designed for the most power, Omni arrays offer the highest coverage—even when the target MAF drops to 1%. You can add 200K markers to the OmniExpress or Omni2.5, or up to 500K custom markers to the Omni5, to increase genome-wide coverage or marker density in regions of interest.



Superior imaging. Easy workflow.

The Omni family of microarrays works with the advanced technology of the Illumina HiScan® and iScan systems. Scalable, streamlined workflows offer simple sample prep, minimal hands-on time, and built-in quality control.

Add the SQ Module to the HiScan system, and harness the combined power of next-generation sequencing and microarrays on one integrated platform: HiScanSQ[™]. Giving you unlimited possibilities for your research.

All systems offer industry-leading accuracy, superior call rates, and high resolution copy number data. Features that have helped generate the data leading to hundreds of peer-reviewed publications, and thousands of associations.

GenomeStudio®

View and analyze data for any Illumina technology with this highly visual, easy-to-use software. Designed for simple project creation for a wide range of microarray and sequencing applications, including genotyping, gene expression, DNA sequencing, and RNA sequencing.

Beeline software

Save time, reduce data size, and generate reports easily. Beeline software parallelizes SNP calculations, and reduces experimental data size with seamless integration to GenomeStudio for data analysis.





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