HumanHT-12 v3 Expression BeadChip

Powerful gene expression profiling in a high-throughput format to accelerate whole-genome expression and integrated genotyping and gene expression studies.

HumanHT-12 BeadChip Highlights

- **Broad Content:**
  More than 48,000 probes covering RefSeq and UniGene annotated genes
- **Ideal for eQTL Studies:**
  Consistent content and software tools for integration with Illumina genotyping products
- **High Throughput:**
  Low input requirements and 12 arrays per BeadChip
- **Cost Effective:**
  Inexpensive profiling platform to support large expression studies or combined genotyping/gene expression studies

Introduction

Illumina has created a lower cost high-throughput version of the powerful HumanWG-6 Gene Expression BeadChip. The HumanHT-12 BeadChip supports highly efficient whole-genome expression studies and expression-based quantitative trait loci (eQTL) studies. The HumanHT-12 contains the same panel of probes as the HumanWG-6 BeadChip, but provides higher throughput processing of 12 samples per BeadChip.

High-Throughput Expression Profiling

Illumina provides an industry-leading portfolio of gene expression microarrays for whole-genome profiling. The addition of the HumanHT-12 BeadChip supports the needs of researchers looking for the same high-quality content in a higher throughput format. With this BeadChip, expression information can easily be incorporated in genome-wide association (GWA) studies, and large gene expression studies can be completed more quickly and economically.

eQTL Studies

As GWA studies are used to explore increasingly complex diseases, the use of gene expression signatures for phenotype information is becoming more important1-3. Illumina provides the industry's most powerful DNA Analysis BeadChips in high-throughput multi-sample Infinium® HD formats. The HumanHT-12 BeadChip matches these products with highly efficient expression profiling.

Whole-Genome Expression Analysis

Since the HumanHT-12 BeadChip provides identical content to the proven HumanWG-6 BeadChip4,5, researchers can shift to the higher throughput product with confidence. The 12-sample format facilitates large-scale gene expression applications, such as differential expression analysis, disease classification, and pathway analysis.

Figure 1: HumanHT-12 Expression BeadChip

Content

The high-value content on the HumanHT-12 Expression BeadChips provides genome-wide transcriptional coverage of well-characterized genes, gene candidates, and splice variants, with a significant portion targeting well-established sequences supported by peer-reviewed literature. Like the HumanWG-6 BeadChip, each array on the HumanHT-12 Expression BeadChip targets more than 25,000 annotated genes with more than 48,000 probes. Probes were designed using the RefSeq (Build 36.2, Rel 22) and the UniGene (Build 199) databases (Table 1). Illumina guarantees that > 99.99% of the bead types will be present on any given HumanHT-12 array. This means up to five HumanWG-6 probes may be represented with only 0, 1, or 2 copies on each HumanHT-12 array.

Probe Design

The probe set was optimized bioinformatically with a multi-step algorithm using several parameters:

- **Lack of similarity to other genes**
- **Absence of highly repeated sequence in the genome**
- **Sequence complexity**
- **Self-complementarity for hairpin structure prediction**
- **Melting temperature for hybridization uniformity**
- **Distance from 3' end of the transcript**

High-Quality Data

As with all Illumina products, the HumanHT-12 BeadChip was rigorously tested to ensure robust assays and accurate results. Reproducibility and precision have been demonstrated by high concordance

Table 1: HumanHT-12 BeadChip Content

Probes	Description	Probes*
RefSeq Content (Build 36.2, Release 22)		
NM	Coding transcript, well-established annotation	27,455
XM	Coding transcript, provisional annotation	7,870
NR	Non-coding transcript, well-established annotation	446
XR	Non-coding transcript, provisional annotation	196
Supplementary Content		
UniGene (Build 199)	Experimentally confirmed mRNA sequences that align to EST clusters	12,837
TOTAL		**48,804**

*99.99% coverage specification

between hybridization replicates, ensuring minimal false discovery rates in differential expression analysis. Technical replicates show high reproducibility (Figure 2), similar to that using the HumanWG-6 BeadChip. High sensitivity and precision are driven in part by 50-base probe-to-target complementarity and average 15-fold feature redundancy.

Software

Illumina's BeadStudio Gene Expression Module enables simplified data management for hierarchical organization of samples, groups, groupsets, and associated project analysis. It offers gene-level statistical analysis tools for differential analysis, heat map visualization, and clustering. HumanHT-12 BeadChip output files can also be exported to third-party gene expression analysis software.

Integrated Analysis

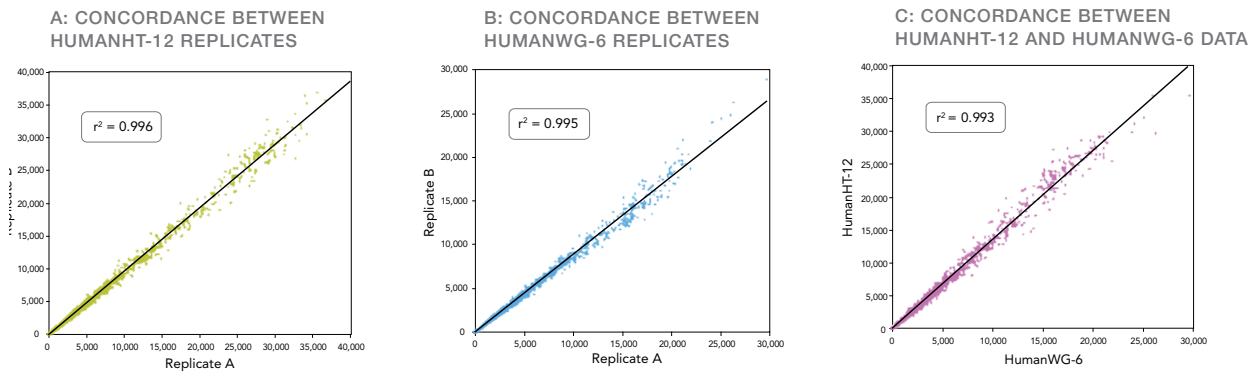
Researchers can easily combine Human Expression BeadChip data with either methylation or miRNA profiling data in a single BeadStudio gene expression project. This enables powerful integrated approaches to studying epigenetic impacts on gene expression. Important for eQTL studies, the flexible data management architecture of BeadStudio supports integrating gene expression probe annotation information with SNP location coordinates. Also, the open API allows for flexible data export and the addition of new features as plug-ins become available.

RNA Analysis Solutions

Illumina provides a broad range of other RNA analysis solutions, including miRNA profiling panels, custom DASL® gene expression panels, and sequencing-based methods for mRNA profiling and miRNA discovery.

The HumanHT-12 represents the fastest and most economical solution for high-quality whole-genome human gene expression profiling. Large-scale expression analysis and eQTL studies benefit greatly from this high-throughput BeadChip. For experiments that require 100% coverage every time, researchers can continue to rely on the HumanWG-6 BeadChip to provide unparalleled data quality for whole-genome expression analysis.

Figure 2: High Reproducibility



Data from the HumanHT-12 exhibit high reproducibility, shown as concordance of technical replicates (A). The HumanHT-12 reproducibility is nearly as high as that of the HumanWG-6 BeadChip (B), and data derived from these two BeadChips are highly concordant (C).

Ordering Information

Catalog No.	Product	Description
BD-103-0603	HumanHT-12 v3 Expression BeadChip Kit (6-pack)	Each BeadChip contains 12 microarrays, allowing for the parallel processing of 12 samples. Includes six BeadChips, hybridization and wash buffers, and wash trays.
BD-103-0203	HumanHT-12 v3 Expression BeadChip Kit (2-pack)	Each BeadChip contains 12 microarrays, allowing for the parallel processing of 12 samples. Includes two BeadChips, hybridization and wash buffers, and wash trays.
Related Products		
IL1791	Illumina TotalPrep RNA Amplification Kit (24 samples)	Ambion (www.ambion.com) offers kit options for processing 24 or 96 samples. Telephone (U.S.A.): 1-800-888-8804
4393543	Illumina TotalPrep-96 RNA Amplification Kit (96 samples)	
TAN07924-142	TargetAmp Nano-g Biotin-aRNA Labeling Kit	Available from Epicentre Biotechnologies (www.epibio.com). Telephone (U.S.A.): 1-800-284-8474

References

1. Goring HH, Curran JE, Johnson MP, Dyer TD, Charlesworth J, et al. (2007) Discovery of Expression Qtls Using Large-Scale Transcriptional Profiling in Human Lymphocytes. Nat Genet 39: 1208-1216.
2. Stranger BE, Forrest MS, Dunning M, Ingle CE, Beazley C, et al. (2007) Relative Impact of Nucleotide and Copy Number Variation on Gene Expression Phenotypes. Science 315: 848-853.
3. Weinsheimer S, Lenk GM, van der Voet M, Land S, Ronkainen A, et al. (2007) Integration of Expression Profiles and Genetic Mapping Data to Identify Candidate Genes in Intracranial Aneurysm. Physiol Genomics 32: 45-57.
4. Idaghdour Y, Storey JD, Jadallah SJ, Gibson G (2008) A Genome-Wide Gene Expression Signature of Environmental Geography in Leukocytes of Moroccan Amazighs. 4: e1000052.
5. Mutarelli M, Cicatiello L, Ferraro L, Grober OM, Ravo M, et al. (2008) Time-Course Analysis of Genome-Wide Gene Expression Data from Hormone-Responsive Human Breast Cancer Cells. 9 Suppl 2: S12.

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