



**Table 1: Expression BeadChip Content**

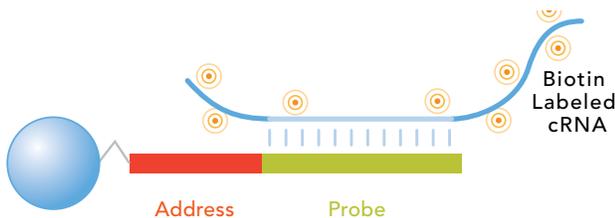
Probes	Description	Human HT-12 v4.0*	Mouse WG-6 v2.0	Mouse Ref-8 v2.0	Rat Ref-12	Human WG DASL HT*
		12-sample	6-sample	8-sample	12-sample	12-sample
<b>RefSeq Content</b>						
NM	Coding transcript, well-established annotation	28,688	26,766	24,854	6,277	27,253
XM	Coding transcript, provisional annotation	11,121	6,856	796	15,983	426
NR	Non-coding transcript, well-established annotation	1,752	56	47	1	1,580
XR	Non-coding transcript, provisional annotation	2,209			12	26
Source	RefSeq source release	Human RefSeq Rel 38	Mouse RefSeq Rel 22		Rat RefSeq Rel 16	Human RefSeq Rel 38
<b>Supplementary Content</b>						
UniGene	Experimentally confirmed mRNA sequences that align to EST clusters	3,461			250	
RIKEN FANTOM2	Exemplar protein-coding sequences from the RIKEN FANTOM2 database		5,659			
RefSeq Release 5	Transcripts with NM and XM annotation in RefSeq Release 5 (Build 33.1)		3,573			
MEEBO	Probes to transcripts that do not align with 100% accuracy to RefSeq, but are confirmed as valid mRNA mapping to clusters in Expressed Sequence Tag databases <sup>9</sup>		2,371			
<b>Total</b>		<b>47,231</b>	<b>45,281</b>	<b>25,697</b>	<b>22,523</b>	<b>29,285</b>

\* > 99.98% of the bead types are present on any HumanHT-12 array

### Direct Hybridization Assay

The Direct Hybridization Whole-Genome Expression assay offers the highest multiplexing capabilities for whole-genome gene expression, simultaneously profiling more than 47,000 transcripts. By combining the most up-to-date genomic content with low-cost, high-throughput array processing, Illumina Expression BeadChips efficiently and economically deliver high-quality data for gene expression studies of any size. They are ideal for applications such as differential expression analysis, disease classification, pathway analysis, and expression-based quantitative trait loci (eQTL) studies.

**Figure 2: Direct Hyb Gene Expression Profiling Bead Design**



Illumina array-based technologies support a broad array of RNA expression profiling products for a variety of applications.

### HumanHT-12 Expression BeadChip

The new HumanHT-12 v4.0 Expression BeadChip supports highly efficient human whole-genome gene expression profiling studies with updated content and industry-leading pricing. Its high-value content 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.

Each array on this BeadChip targets more than 47,000 probes. Illumina guarantees that > 99.98% of the bead types will be present on any given HumanHT-12 array. This means up to five probes may be represented with only 0, 1, or 2 copies on each HumanHT-12 array. Probes were designed to cover content from NCBI RefSeq Release 38 (November 7, 2009), as well as legacy UniGene content.

The 12-sample format facilitates large-scale gene expression applications. With the HumanHT-12 BeadChip, expression information can be easily incorporated into Infinium<sup>®</sup> assay-based genome-wide association studies (GWAS) or methylation studies.

### MouseWG-6 and MouseRef-8 Expression BeadChips

The MouseWG-6 v2.0 and MouseRef-8 v2.0 Expression BeadChips are Illumina's genome-wide gene expression profiling solutions for researchers using the mouse as their model organism. The MouseRef-8 BeadChip features recent content derived from the NCBI RefSeq database. In addition to RefSeq content, the MouseWG-6 BeadChip is supplemented with probes that target the Mouse Exonic Evidence Based Oligonucleotide (MEEBO) set<sup>2</sup>, as well as exemplar protein-coding sequences described in the RIKEN FANTOM24-6 database<sup>3-5</sup>.





