

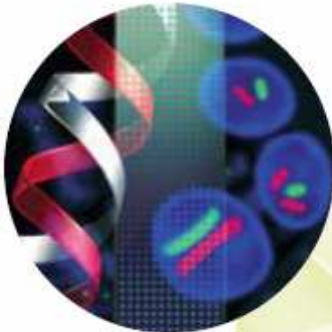
GENOMICS INFORMATICS PROTEOMICS METABOLOMICS
A T C T G A T C C T T C T G A A C G G A A C T A A T T T C A A
G A A T C T G A T C C T T G A A C T A C C T T C C A A G G T G



Agilent High-Definition CGH (HD-CGH) Custom Microarrays

Empowering your Genome Research

Genomic instability is a classic hallmark of cancer and genetic disorders. The Agilent oligo array-based Comparative Genomic Hybridization (aCGH) platform lets you profile DNA copy number variations with superior resolution, on a genome-wide scale and with high-throughput. It delivers unparalleled sensitivity and specificity that you can count on. Agilent High-Definition CGH (HD-CGH) microarrays allow you to create customized aCGH microarrays quickly and easily using an aCGH-optimized database of over 8 million probes. Perform selective and precise mapping of relevant regions-of-interest at the desired resolution, without compromising flexibility and convenience.



The Agilent SurePrint fabrication platform allows quick and easy design iterations tailored to your specific experimental needs. Through Agilent's eArray online application tool and HD-CGH probe library, you design your own HD-CGH microarrays and have total control of your content. Along with this flexibility you still get the reproducibility, dependability, and quality control you expect from Agilent's world-renowned manufacturing processes.

Features and Benefits

Flexibility

- High-resolution tiling in targeted regions-of-interest
- Online design with Agilent eArray application tool
- 60-mer SurePrint *in situ* probe synthesis

- Multiplex arrays for lower cost per experiment
- Scalable, high-throughput platform
- **Sensitivity and Specificity**
- Probe design and validation processes specifically optimized for aCGH
- Total genomic DNA analysis without amplification or complexity reduction
- Dynamic analytical range for challenging and complex, heterogeneous samples
- Low-input sample requirement

Integrated Informatics

- Intuitive GeneSpring CGH visualization and analysis interface
- Integration of aCGH and gene expression data

Quality Support

- QC metrics for quality assessment





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Agilent Technologies

Optimized Probe Design and Selection

Oligonucleotide probes were designed *in silico*, selected, and optimized for sensitivity and specificity in copy number detection by using a multivariate approach. Overall system signal-to-noise ratios were significantly increased by reducing nonspecific noise. First candidate probes representing unique genomic sequences were selected, scored, and filtered using bioinformatics prediction criteria for probe sensitivity, specificity, and responsiveness under appropriate conditions. Selection criteria were based on empirical testing of known genomic aberrations in

comparative model systems, such as XX/XY hybridizations. For human, the resulting candidate probe collection consists of over 8.4 million predesigned aCGH probes with a median probe spacing of 192 bp. The mouse and rat collection contain close to 8 and 7 million probes, with a median probe spacing of 222 bp and 233 bp, respectively. All CGH probes span coding and non-coding regions for comprehensive genome coverage (Tables 1 and 2, rat not shown).

Design What You Want

Agilent customers can create their own custom HD-CGH microarrays using

eArray, Agilent's secure, online array design application tool. eArray gives direct, easy access to Agilent's HD-CGH probe library (including Agilent catalog CGH probes). Search libraries using several parameters (e.g. genome coordinates, cytobands, gene identifiers), select and save probe groups, create custom array layouts based on your format choice, and submit print requests directly to manufacturing. eArray also allows you to work collaboratively with others by sharing custom probe groups and array designs.

<http://earray.chem.agilent.com>

Microarray Specifications

Format	1 x 244K	2 x 105K	4 x 44K	8 x 15K	1 x 44K*	1 x 22K*	2 x 11K*
Microarrays per slide	1	2	4	8	1	1	2
Slide format	1" x 3"	1" x 3"	1" x 3"	1" x 3"	1" x 3"	1" x 3"	1" x 3"
Probe length	60-mer	60-mer	60-mer	60-mer	60-mer	60-mer	60-mer
Feature size	65 µm	65 µm	65 µm	65 µm	115 µm	135 µm	135 µm
Total features	243,504	105,072	45,220	15,744	44,290	22,575	10,807
Available features							
human	238,459	100,446	43,102	14,262	42,920	21,202	10,204
mouse	238,405	100,360	43,020	14,180	43,020	N/A*	N/A*
rat	238,012	100,031	41,242	13,872	N/A*	N/A*	N/A*
Agilent internal quality control features							
human	5,045	4,626	2,118	1,482	1,370	1,373	603
mouse	5,099	4,712	2,200	1,564	1,270	N/A*	N/A*
rat	5,492	5,041	3,978	1,872	N/A*	N/A*	N/A*
Sequence source							
human			UCSC hg17 (NCBI Build 35)				
mouse			UCSC mm7 (NCBI Build 35)				
rat			UCSC rn4 (Baylor HGSC v3.4)				
Hybridization chamber	G2534A	G2534A	G2534A	G2534A	G2534A	G2534A	G2534A
Hybridization gasket slide	G2534-60003	G2534-60002	G2534-60011	G2534-60014	G2534-60003	G2534-60003	G2534-60002
Minimum starting sample input	0.2-0.5 µg genomic DNA (direct labeling)* or 0.05 µg genomic DNA (WGA amplification)						
Labeling type	Random priming using Cyanine 3 and Cyanine 5 nucleotides						
Overall assay time	2-3 days (1-1.5 days actual hands-on time)*						
Storage condition	Room temperature (in the dark)						

* N/A = Data currently unavailable * DNA input and processing protocol vary slightly depending on the microarray format * Legacy formats

Table 1. Probe Statistics for the Human HD-CGH Probe Library

Chromosome	Median Probe Spacing	Total	Probe Number			
			Exonic	Intronic	Intergenic	Telomeric-end*
chr1	196 bp	650,560	8,852	368,785	272,923	4,570
chr2	189 bp	744,040	6,972	372,640	364,428	9,431
chr3	186 bp	615,371	5,548	341,766	268,057	10,630
chr4	178 bp	594,597	4,063	264,531	326,003	6,312
chr5	186 bp	549,536	4,407	246,794	298,335	7,972
chr6	186 bp	531,411	4,743	266,394	260,274	9,460
chr7	190 bp	451,565	4,031	253,996	193,538	6,612
chr8	189 bp	442,376	3,175	212,277	226,924	9,165
chr9	196 bp	331,744	3,527	170,535	157,682	9,366
chr10	198 bp	292,123	3,620	219,447	169,056	10,243
chr11	198 bp	282,414	4,726	204,716	172,972	8,054
chr12	190 bp	295,120	5,294	210,931	178,895	10,019
chr13	182 bp	315,908	1,912	131,143	182,853	1,526
chr14	191 bp	270,052	2,798	134,054	133,200	1,011
chr15	200 bp	230,082	3,026	135,709	91,347	2,445
chr16	212 bp	210,380	3,006	113,762	93,612	10,768
chr17	212 bp	213,144	4,499	132,663	75,982	10,692
chr18	188 bp	244,742	1,620	113,437	129,685	13,043
chr19	237 bp	117,160	3,590	77,546	36,024	10,556
chr20	212 bp	172,267	2,189	90,835	79,243	12,188
chr21	190 bp	106,161	989	54,588	50,584	5,533
chr22	234 bp	86,748	1,511	56,331	28,906	5,057
chrX	190 bp	346,546	2,935	150,457	193,154	593
chrY	238 bp	18,148	107	4,293	13,748	599
Total		8,412,195	87,140	4,327,630	3,997,425	175,845
Percentage		100%	1%	51%	48%	2%

*Probes located within 3 MB from either chromosome end.

Table 2. Probe Statistics for the Mouse HD-CGH Probe Library

Chromosome	Median Probe Spacing	Total	Probe Number		
			Exonic	Intronic	Intergenic
chr1	220 bp	581,552	4,675	291,405	285,472
chr2	222 bp	566,091	5,672	313,953	246,466
chr3	214 bp	470,784	3,537	226,115	241,132
chr4	226 bp	442,094	4,117	244,215	194,662
chr5	226 bp	448,647	4,763	257,400	186,484
chr6	222 bp	441,034	3,554	255,390	182,090
chr7	232 bp	269,478	4,615	215,870	148,993
chr8	224 bp	292,340	3,525	199,143	189,672
chr9	226 bp	275,679	4,157	213,586	157,936
chr10	219 bp	296,834	3,363	212,878	180,593
chr11	230 bp	288,339	5,339	223,962	159,038
chr12	222 bp	341,858	2,490	173,295	166,073
chr13	222 bp	342,746	2,487	175,631	164,628
chr14	218 bp	345,342	2,670	187,810	154,862
chr15	221 bp	316,332	2,783	161,573	151,976
chr16	218 bp	299,039	2,211	161,504	135,32
chr17	228 bp	259,577	2,949	147,444	109,184
chr18	220 bp	277,331	1,945	141,993	133,393
chr19	226 bp	183,480	2,317	109,202	71,961
chrX	212 bp	358,809	2,629	165,610	188,570
chrY	384 bp	606	16	295	295
Total		7,596,092	69,814	4,078,274	3,448,004
Percentage		100%	1%	54%	45%

For further information or a quote, please contact m.herman@dnvision.be