WELGENE 威健生技

全方位基因體及轉錄體分析

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Welgene Biotech. Co. Ltd

http://www.welgene.com.tw

威健生技 高通量服務的領導者

Office Area

Service Lab

Agilent Technologies
Authorized Distributor

Agilent Technologies
Certified Service Provider

Biotech Building, Nan-Kang Business Park

EPIGENTEK
KEEP IT SIMPLE AND SMART

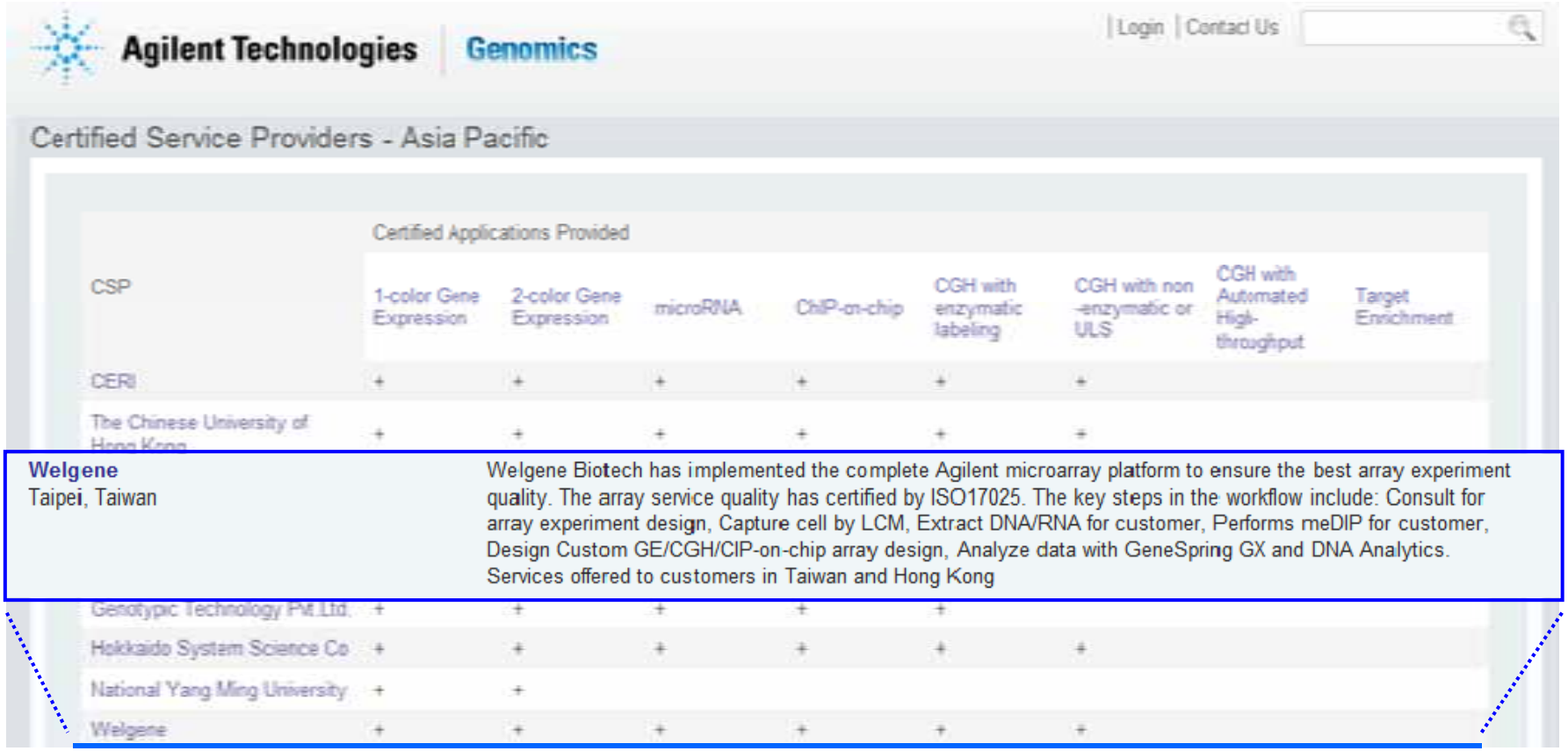
ISO 17025

Quality is Assured

Welgene Biotech. Co. Ltd
http://www.welgene.com.tw

Agilent Certification

- Agilent certified service provider since 2007



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Certified Service Providers - Asia Pacific

CSP	Certified Applications Provided							
	1-color Gene Expression	2-color Gene Expression	microRNA	ChIP-on-chip	CGH with enzymatic labeling	CGH with non-enzymatic or ULS	CGH with Automated High-throughput	Target Enrichment
CERI	+	+	+	+	+	+		
The Chinese University of Hong Kong	+	+	+	+	+	+		
Genotypic Technology Pvt.Ltd.	+	+	+	+	+			
Hokkaido System Science Co	+	+	+	+	+	+		
National Yang Ming University	+	+						
Welgene	+	+	+	+	+	+		

Welgene
Taipei, Taiwan

Welgene Biotech has implemented the complete Agilent microarray platform to ensure the best array experiment quality. The array service quality has certified by ISO17025. The key steps in the workflow include: Consult for array experiment design, Capture cell by LCM, Extract DNA/RNA for customer, Performs meDIP for customer, Design Custom GE/CGH/CIP-on-chip array design, Analyze data with GeneSpring GX and DNA Analytics. Services offered to customers in Taiwan and Hong Kong

ISO17025 Certification

- ISO certification since 2006 (SBIR support)

認證依據： ISO/IEC 17025：2005

初次認證日期： 九十五年八月二十九日

認證範圍： 測試領域，如續頁

實驗室主管：林怡杏

認可事項

14.01 生物科技

核糖核酸,組織,細胞株

B999 基因表現

RNA Isolation (Sr-03-A)

Low RNA Input Fluorescent Linear Amplification & Agilent Oligo Microarray Hybridization Spike-In Control(Sa-03-A)

測試組與對照組做相對量測試

報告簽署人：林怡杏,林燦灄,黃信智

客戶文獻

- **Hepatogastroenterology. 2006 Jul-Aug;53(70):484-90**. Distinct gene expression profiles in gastric epithelial cells induced by different clinical isolates of Helicobacter pylori--implication of bacteria and host interaction in gastric carcinogenesis.
- **Ann Surg Oncol. 2006 Nov;13(11):1474-84.** A gene expression profile for vascular invasion can predict the recurrence after resection of hepatocellular carcinoma: a microarray approach.
- **Fertility and Sterility 2006, Vol. 86(6):1650-1658**, Identification of ten novel genes involved in human spermatogenesis by microarray analysis of testicular tissue.,
- **Oncol Rep. 2006 Apr;15(4):919-26**. A homologue of the Drosophila headcase protein is a novel tumor marker for early-stage colorectal cancer.
- **Oncogene. 2007**. Molecular Signatures of Metaplastic Carcinoma of Breast by Large-Scale Transcriptional Profiling: Identification of Genes Potentially Related to Epithelial-Mesenchymal Transition..
- **BMC Genomics. 2008 Feb 29;9:109** Altered expression patterns of lipid metabolism genes in an animal model of HCV core-related, nonobese, modest hepatic steatosis.
- **Breast Cancer: Basic and Clinical Research. 2008.** Comparison and Identification of Estrogen-Receptor Related Gene Expression Profiles in Breast Cancer of Different Ethnic Origins.

2009 **Labeled microRNA pull-down assay system: an experimental approach for high-throughput identification of microRNA-target mRNAs**
Nucleic Acids Research, 2009, Vol. 37, No. 10 e77

2009 **Statistical identification of gene association by CID in application of constructing ER regulatory network**
BMC Bioinformatics 2009, 10:85 doi:10.1186/1471-2105-10-85

2009 **Interactions between octaarginine and U-937 human macrophages: global gene expression profiling, superoxide anion content, and cytokine production.**
J Control Release. 2009 Nov 3;139(3):197-204. Epub 2009 Jul 18.

2009 **Hepatic inflammation mediated by hepatitis C virus core protein is ameliorated by blocking complement activation.**
BMC Med Genomics. 2009 Aug 8;2:51.

2010 **A time-course study of gene responses of chicken granulosa cells to Salmonella Enteritidis infection.**
Vet Microbiol. 2010 Jan 25. [Epub ahead of print]

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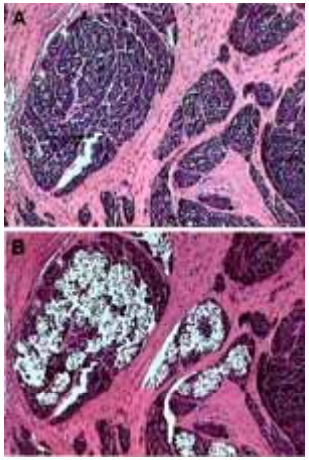
服務內容

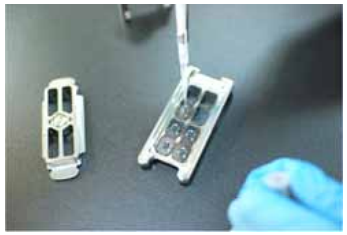
LCM
RNA isolation
Sample preparation

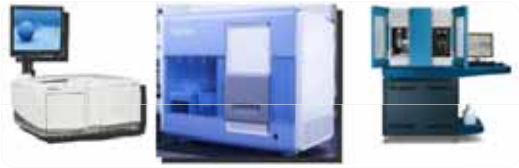
Array / NGS experiment

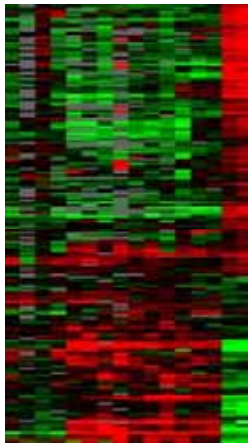
Data analysis (GeneSpring GX)

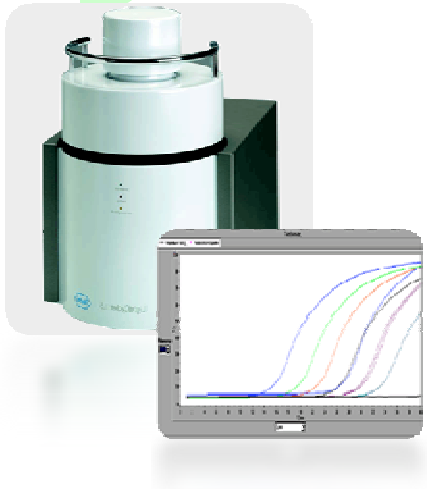
Validation (Q-RT-PCR)











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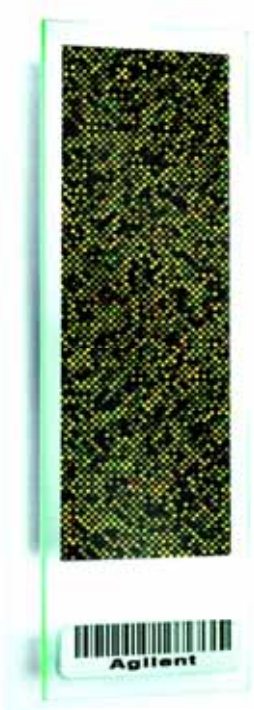
分析技術

Microarray



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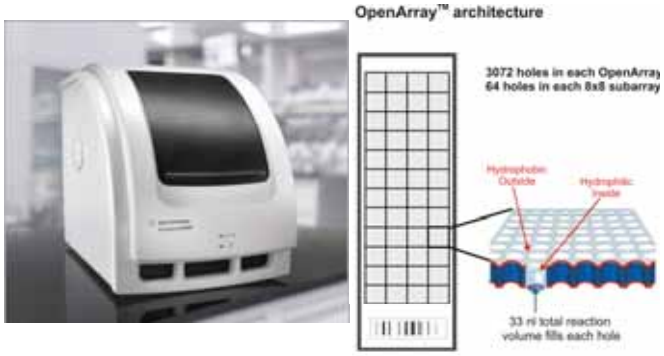
Q-RT-PCR Array



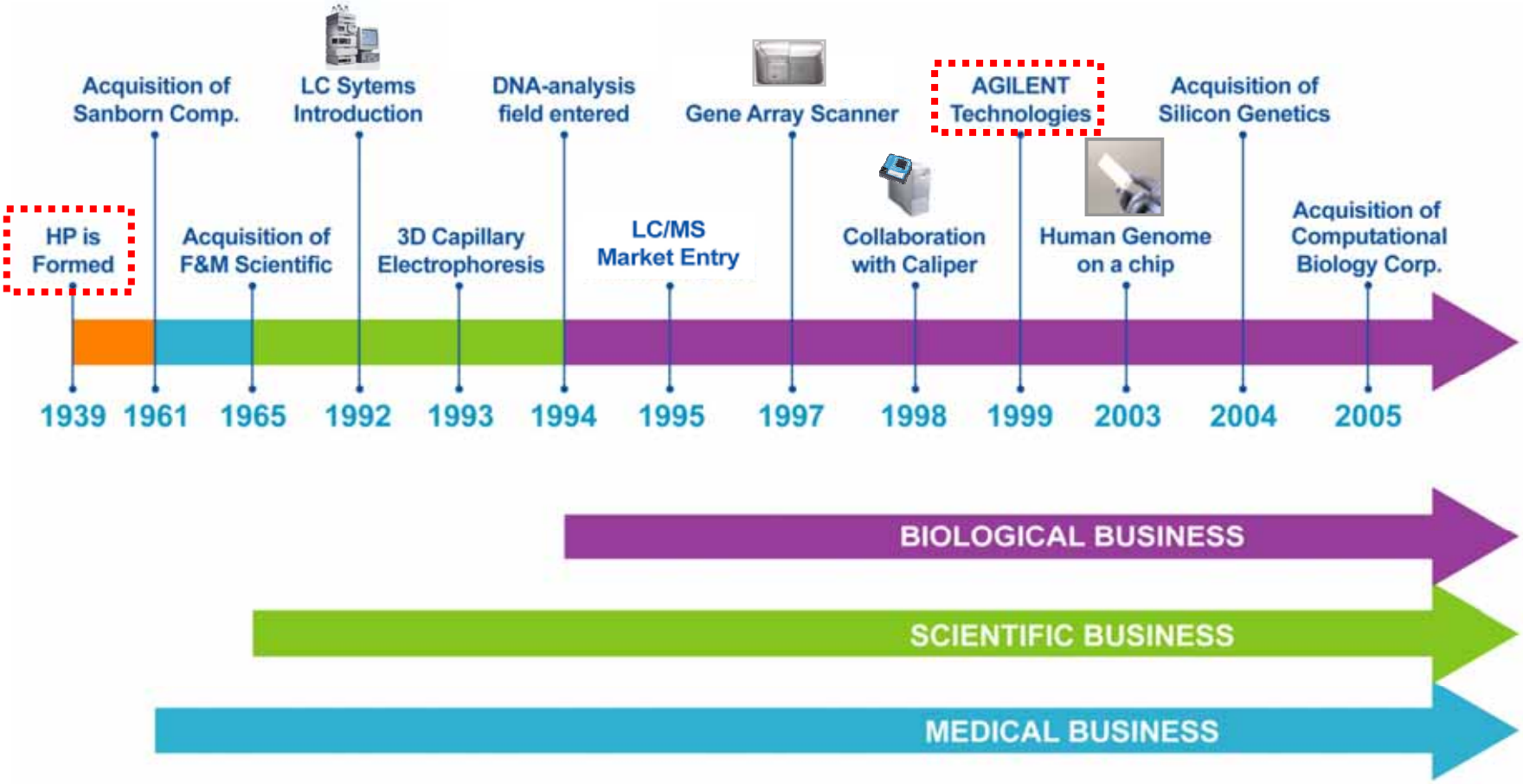
NGS

Illumina Solexa

AB SOLiD

Roche 454

Agilent Technologies

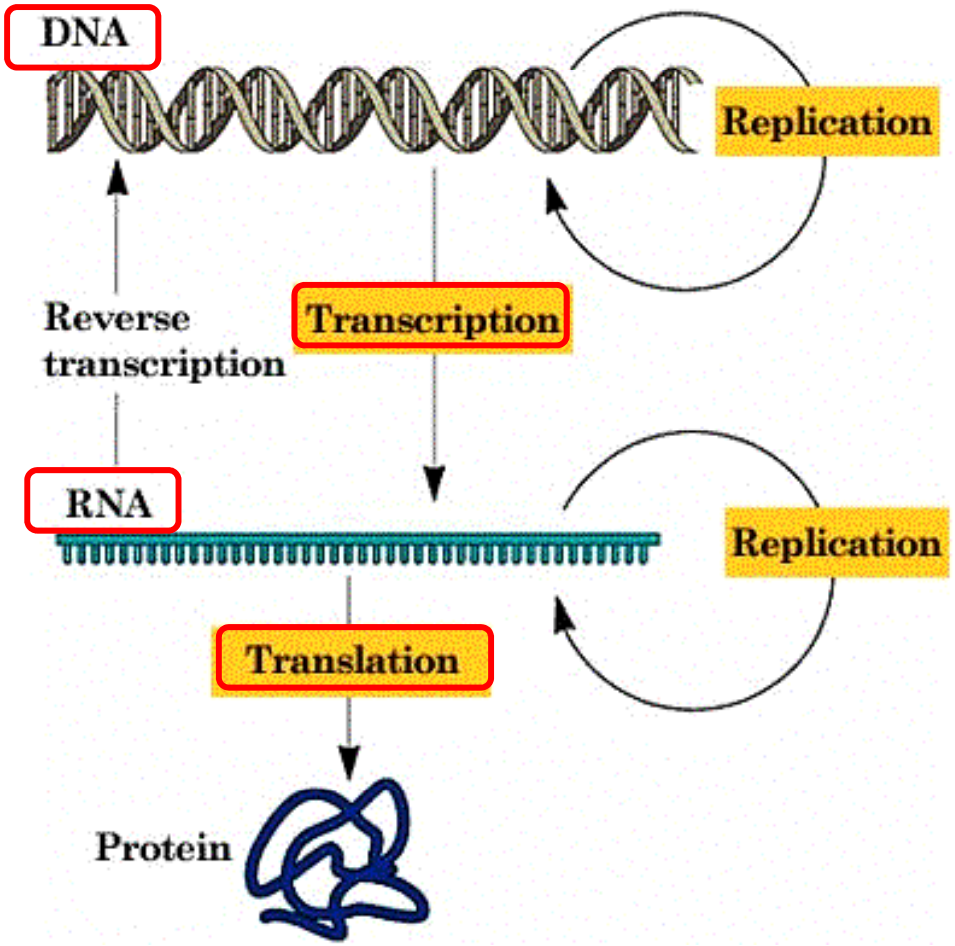


全方位的核酸分析服務

SNP Analysis
(Q-PCR array / Transcriptome-Seq)
aCGH / CNV
(microarray)
DNA Methylation
(microarray / MeDIP-Seq)

Gene Expression
(microarray / DGE / RNA-Seq)
Alternative Splicing
(Transcriptome-Seq / Deep-Seq)
miRNA Expression
(microarray / miRNA-Seq)

Transcription Factor Binding
Histone Modification
(ChIP-on-chip / ChIP-Seq)



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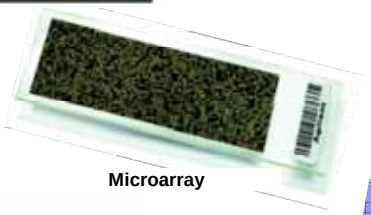
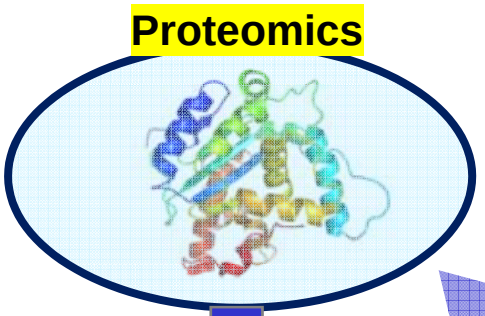
Integration of Multi-omics Research



Microarray

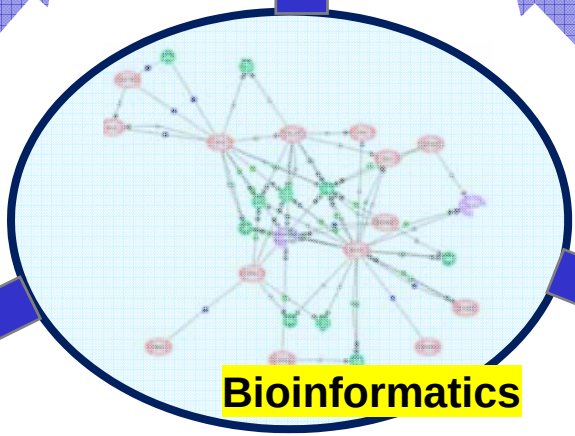
Microarray Scanner



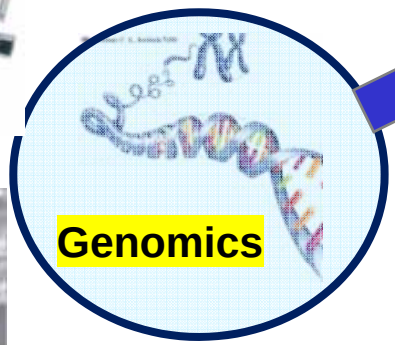
Proteomics

HPLC Systems

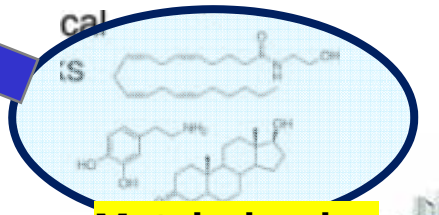
HPLC Chip/MS



Bioinformatics



Genomics



Metabolomics

GC/MS

Genomic Workgroup

Mass Profiler Pro

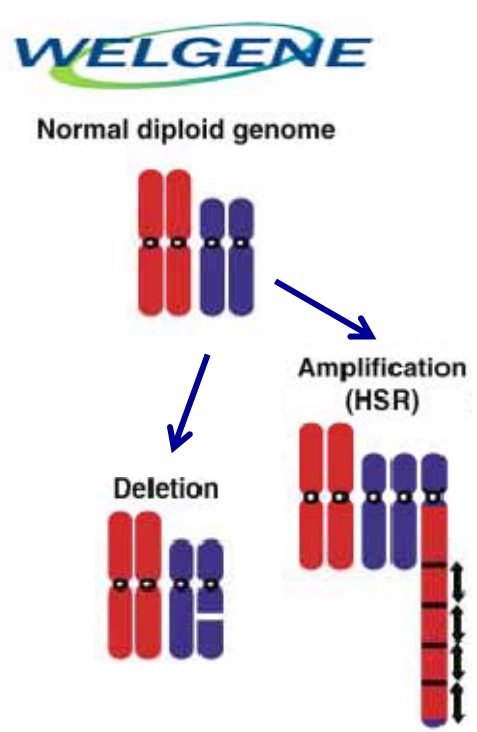
GeneSpring GX

MassHunter Workstation

Applications

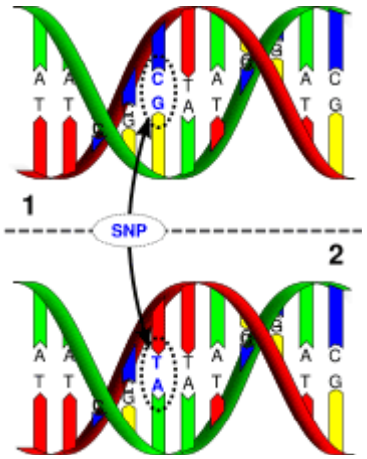
- Genomics Study (SNP, CNV)
- Transcriptomics Study (mRNA / miRNA expression, Alternative Splicing)
- Transcription Factor Binding (ChIP assay)
- Epigenomics Study (Methylation, Histone Modification)

Genomics Study



Copy Number Variation (CNV):

- Copy number variation (CNV):DNA segments in which copy-number varies between two or more genomes
- Ranges from a thousand to millions of DNA bases in size
- CNVs have been associated with susceptibility to disease, complex behavioral traits, and other phenotypic variability
- Identifying statistically significant CNVs is important in understanding the underlying mechanism of disease and disease susceptibility

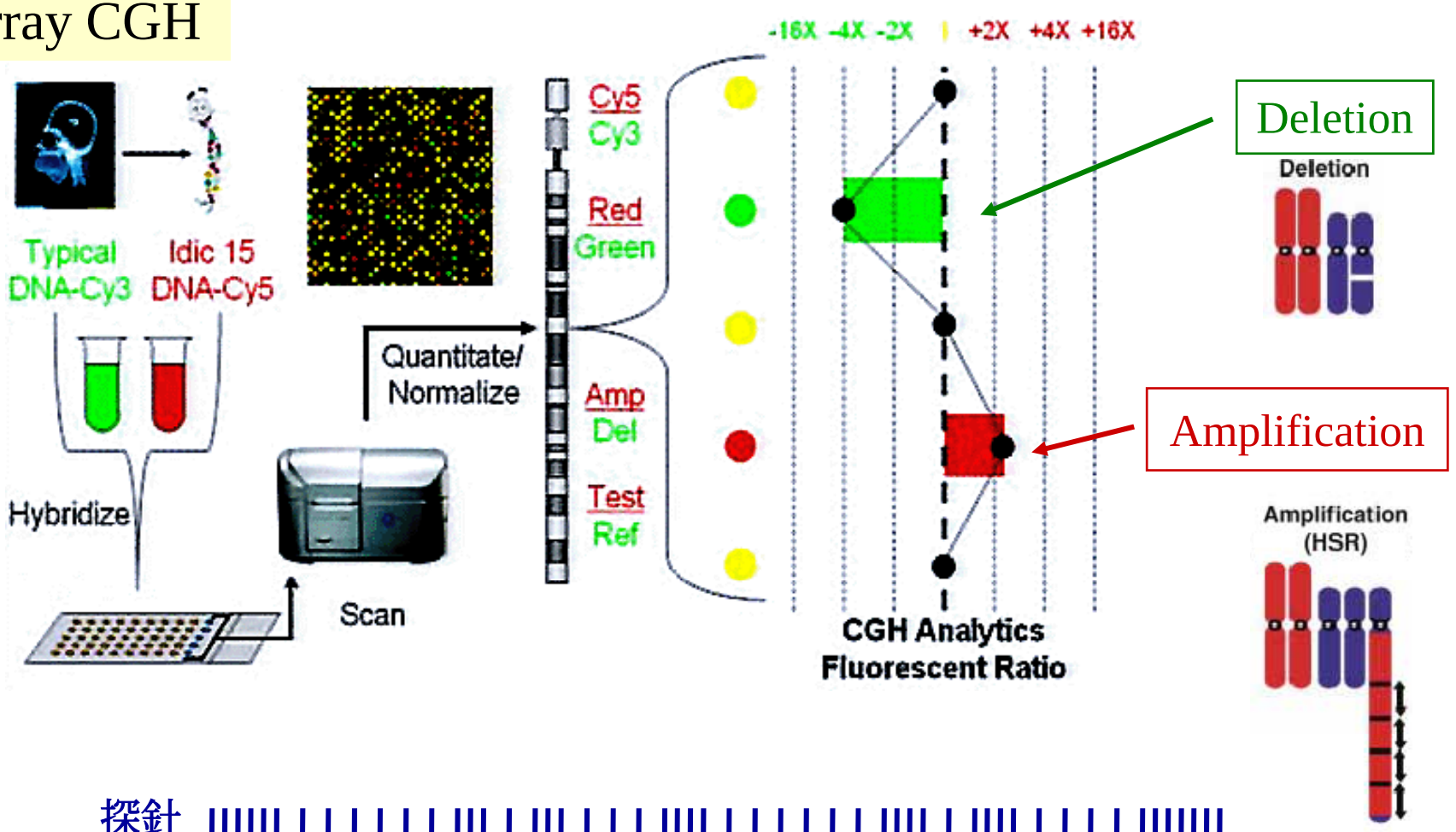


Single Nucleotide Polymorphisms (SNPs):

- DNA sequence variations that occur when a single nucleotide in genome is altered
- Variation must occur in at least 1% of the population to be considered a SNP
- Occur every 100 to 300 bases

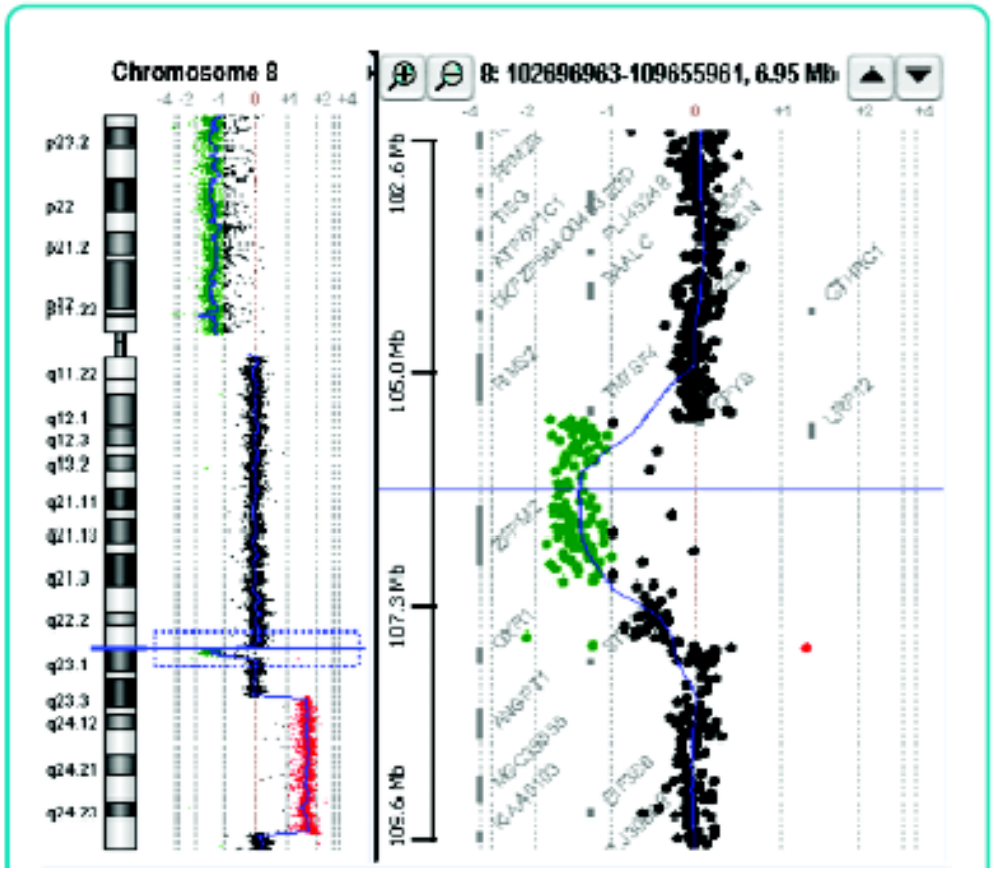
aCGH / CNV Array分析

Array CGH

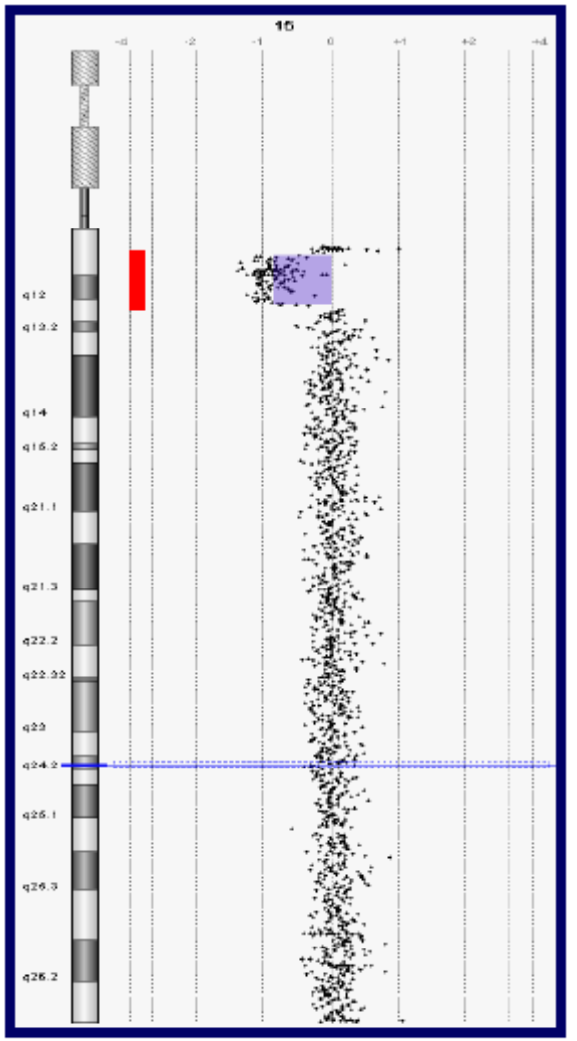


尋找癌症或疾病相關的染色體變異點

Human colon carcinoma cell line HT29



PWS/AS deletion



Database of Genomic Variants

Hosted by: The Centre for

A curated catalogue of structural variation in the human genome

About The Project | Genome Browser | Download | Li

Please select genome assembly: GRCh

View Data by Chromosome

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X

Keyword Search

Search

Exact Match? Yes No

Examples: clone name, accession number, cytoband or gene

Genet Med 2008:10(6):415–429. article

Enhanced detection of clinically relevant genomic imbalances using a targeted plus whole genome oligonucleotide microarray

Erin L. Baldwin, PhD, Ji-Yun Lee, PhD, Douglas M. Blake, BS, Brian P. Bunke, BS, Chad R. Alexander, BS, Amy L. Kogan, BS, David H. Ledbetter, PhD, and Christa L. Martin, PhD

wellcome trust sanger institute

RSS | Human Genetics | Model Organisms | Pathogens | Bioinformatics | Sequencing

Scientific Divisions

Human Genetics

Model Organisms

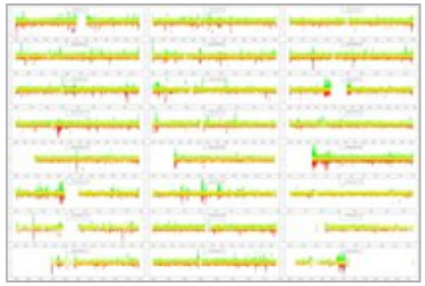
Pathogens

Bioinformatics

Sequencing

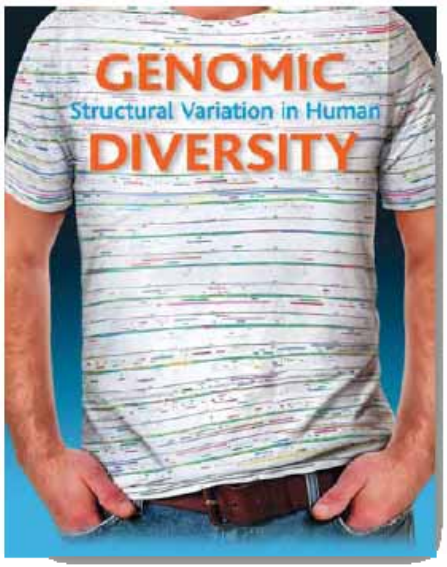
Hide Navigation

The Copy Number Variation (CNV) Project



Genetic diseases are caused by a variety of
of large chunks of DNA sequence consisting
mutation has often been overlooked in previc
disease is caused by copy number variation
occur in families result from these kinds of r
malaria. The contribution of CNV to the com

Mutations (of any type) that increase the ch
developing a common disease are also likel
frequencies in apparently healthy population



High-resolution array CGH analysis of salivary gland tumors reveals fusion and amplification of the FGFR1 and PLAG1 genes in ring chromosomes.

Persson F, Winnes M, Andrén Y, Wedell B, Dahlenfors R, Asp J, Mark J, Enlund F, Stenman G.

Lundberg Laboratory for Cancer Research, Department of Pathology, Sahlgrenska University Hospital, Göteborg University, Göteborg, Sweden.

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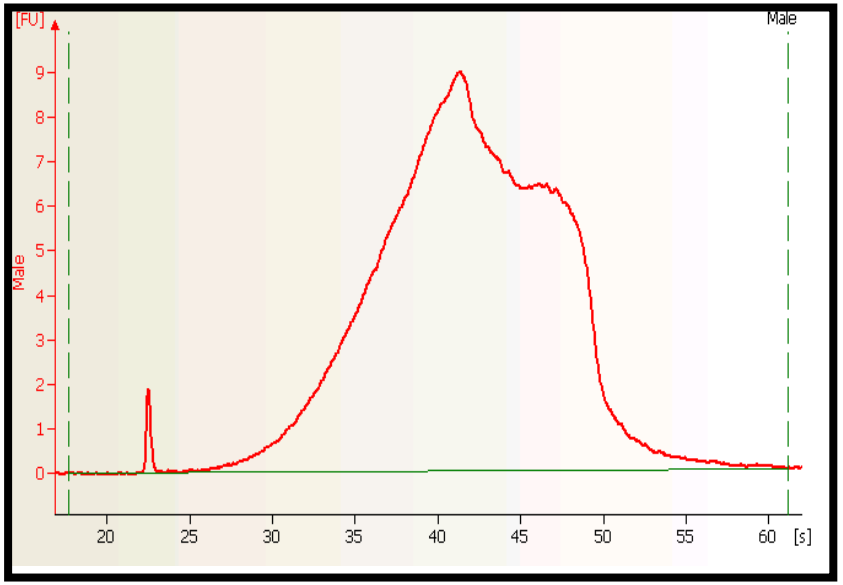
Requirement for Specimens

- DNA
  - Quantity
    - ≥ 4 ug
  - Quality
    - OD260/280 >1.7,
    - size > 4 kb

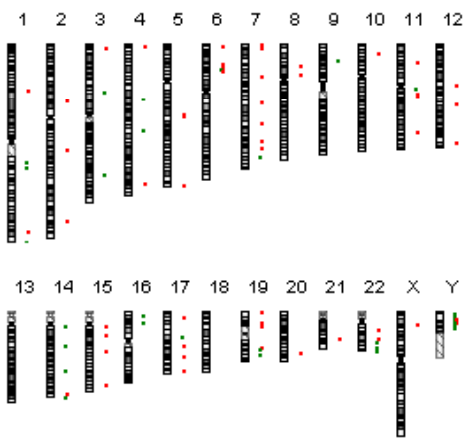


aCGH /CNV Result

Analysis Settings

Aberration Algorithm	: ADM-2
Threshold	: 6.0
Centralization	: ON
Bin Size	: 10
Centralization Threshold	: 6.0
Fuzzy Zero	: ON
Combine Replicates (Intra Array)	: OFF
Genome	: hg18
Aberration Filters	: minProbes = 3 AND minAvgAbsLogRatio = 0.4 AND maxAberrations = 100 AND percentPenetrance = 0
Feature Level Filters	: NONE
Expand Non Unique Probes	: OFF
Genomic Boundaries	: Not Applied

Genome Overview

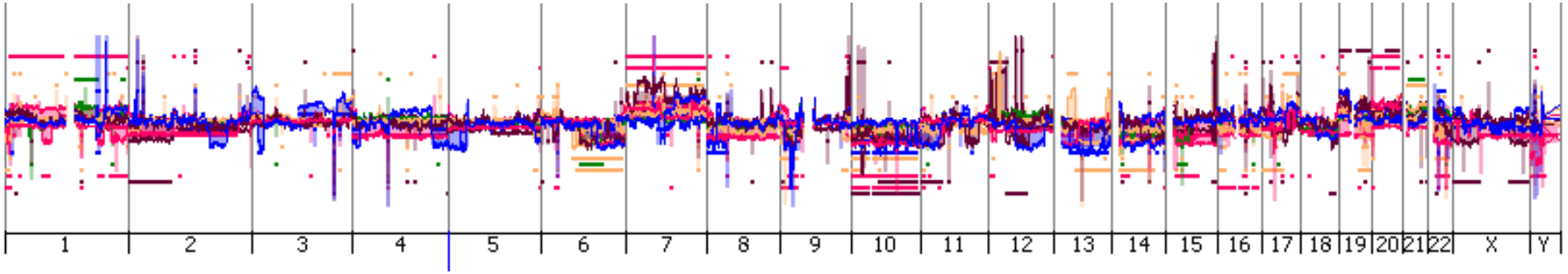


Aberration	CytoBand	ChrName	ProbeName	Start	Stop	Description	Genes	hg18_CNV	Hs_hg18_(	Human hg18 cytoband	Logratio
1.1	p32.1	chr1	A_16_P00	59012360	59012417	Unknown				1p32.1	0.486557
1.2	p32.1	chr1	A_14_P20	59018512	59018571	Unknown				1p32.1	0.647439
1.3	p32.1	chr1	A_14_P12	59019101	59019160	Homo sapi	JUN			1p32.1	0.487863
1.4	p32.1	chr1	A_14_P13	59021301	59021350	Homo sapi	JUN			1p32.1	0.911086
1.5	p32.1	chr1	A_14_P10	59022152	59022210	Homo sapi	JUN			1p32.1	0.757187
1.6	q21.1	chr1	A_16_P00	1.47E+08	1.47E+08	Homo sapiens neurobl		CNV_3313	CNV_8288	1q21.1	-0.50044
1.7	q21.1	chr1	A_16_P00	1.47E+08	1.47E+08	Unknown		CNV_3313	CNV_8288	1q21.1	-0.77127
1.8	q21.1	chr1	A_16_P00	1.47E+08	1.47E+08	Unknown		CNV_3313	CNV_8288	1q21.1	-0.69443
1.9	q21.1	chr1	A_14_P13	1.47E+08	1.47E+08	Unknown		CNV_3313	CNV_8288	1q21.1	-0.32059
1.1	q21.1	chr1	A_16_P35	1.47E+08	1.47E+08	Unknown		CNV_3313	CNV_8288	1q21.1	-1.26298
1.11	q22	chr1	A_16_P00	1.53E+08	1.53E+08	Homo sapiens glucosi		CNV_3315	CNV_3315	1q22	-0.51631
1.12	q22	chr1	A_16_P35	1.53E+08	1.53E+08	Homo sapiens glucosi		CNV_3315	CNV_3315	1q22	-0.12569
1.13	q22	chr1	A_16_P00	1.53E+08	1.53E+08	Homo sapiens glucosi		CNV_3315	CNV_3315	1q22	-0.45874
1.14	q22	chr1	A_16_P00	1.53E+08	1.53E+08	Homo sapiens glucosi		CNV_3315	CNV_3315	1q22	-0.38016
1.15	q22	chr1	A_16_P15	1.53E+08	1.53E+08	Homo sapiens glucosi		CNV_3315	CNV_3315	1q22	-0.80982

Technician: Date:__/__/__ Supervisor Date:__/__/__

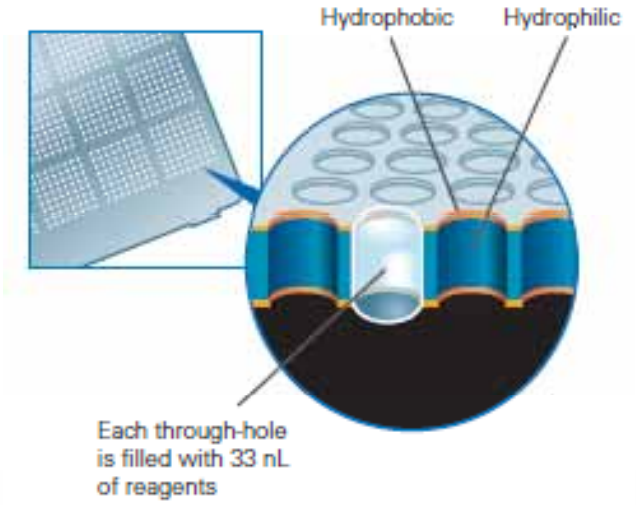
Text Summary Report for Sample GC-05_US85003611_251469359030_S01

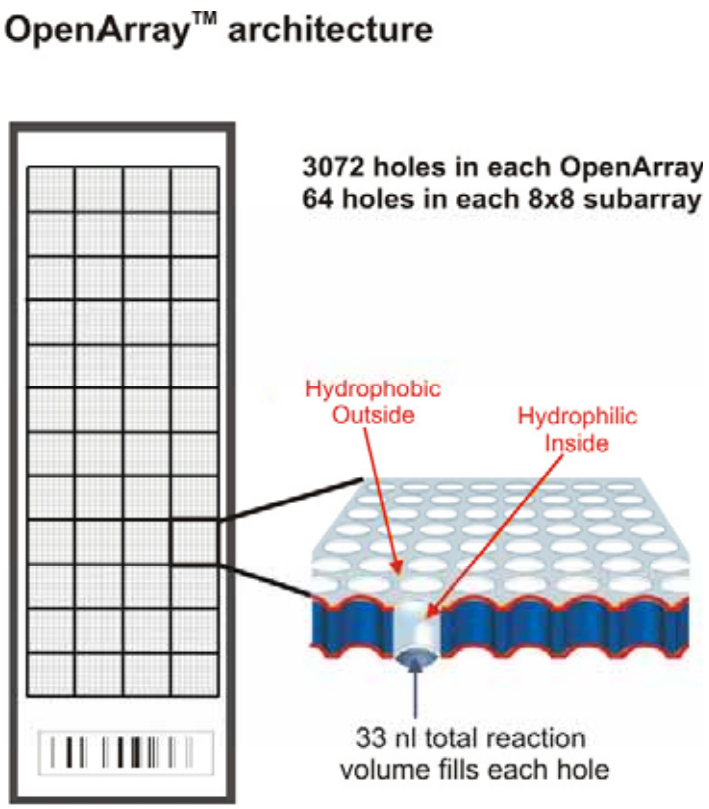
Event No	Chr	Cytoband	#Probes	Amp/Del	P-value	Annotations
1	chr1:59012160-59022352	p32.1	5	0.658026	3.63E-10	JUN, 1p32.1
2	chr1:147386718-147476054	q21.1	5	-0.677868	3.42E-10	CNV_3313, CNV_2326, CNV_1328...
3	chr1:153451703-153463890	q22	5	-0.458142	1.07E-10	CNV_3315, CNV_4257, CNV_3315...



SNP Q-PCR Array System

基因分型儀器平臺（TaqMan® assay）





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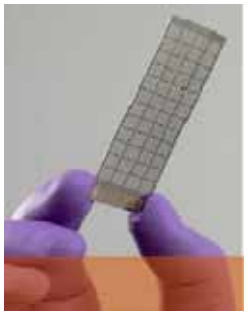
Service Flow

1.Search Taqman assay using SNP ID

2. DNA samples



Order SNP Array assay
Turn around time: 6 weeks

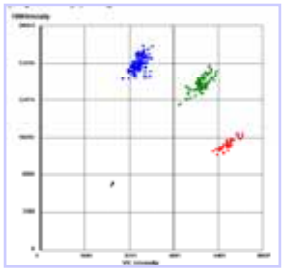
Welgene Service Lac

DNA QC

Samples mixed with Master Mix (containing ROX), and loaded to OpenArray

PCR

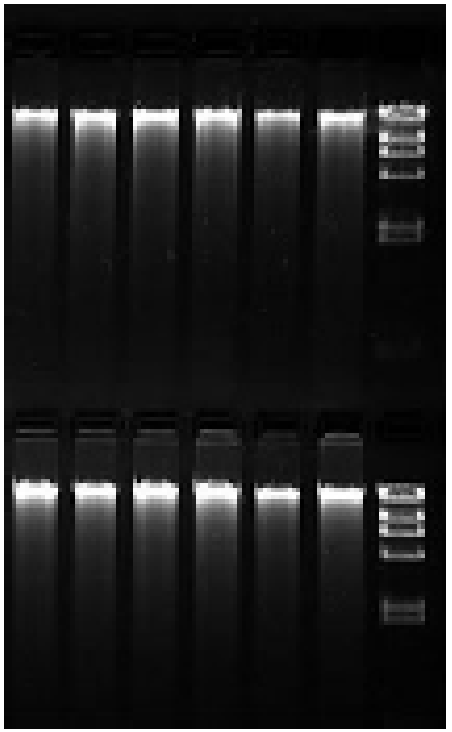
Data readout **Data QC**



Assay Format	Total sample number
16 SNP	1,269
32 SNP	837
64 SNP	874
128 SNP	836

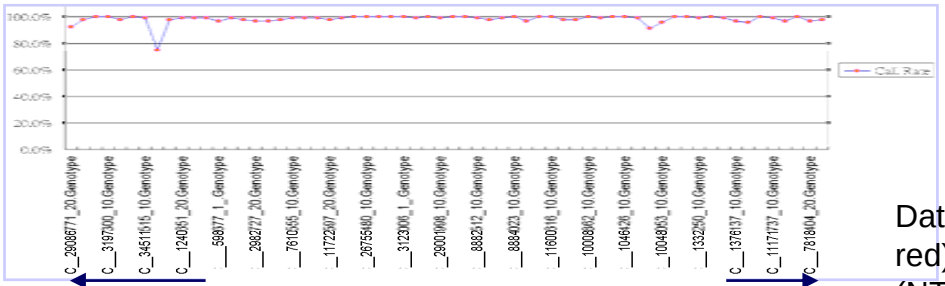
Requirements for input samples

- DNA
  - In nuclease-free water, NOT in T.E
  - Quantity:
    - 400 ng (w/t WGA)
    - Concentration:~50ng/ul
  - Quality:.
    - OD 260/280 >1.7
    - OD 230/280 > 1.7
    - Agarose gel electrophoresis
      - > 10 kb

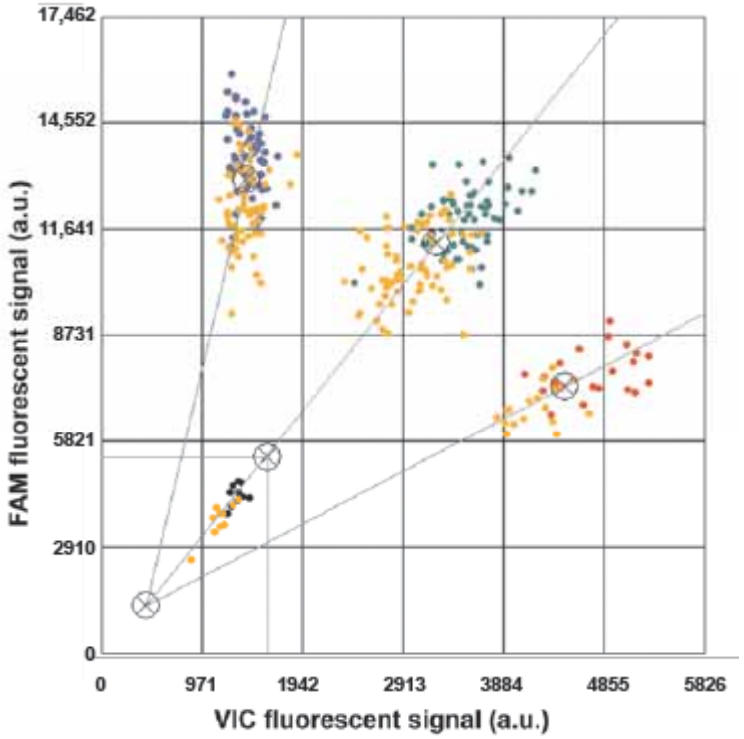


Assay Result

	A	B	C	D	E	F	G
1	OpenArray.SerialNumber	Sample.SampleID	Sample.Description	C__29086771_20.Genotype	C___3168989_10.Genotype	C___8376164_10.Genotype	C___3197300_10.Genotype
2	CAD83	NA17102		No Call	G G	A A	G A
3	CAD83	NA17103		No Call	G A	G A	G G
4	CAD83	NA17104		G G	G G	No Call	A A
5	CAD83	NA17105		G G	G A	A A	G A
6	CAD83	NA17106		No Call	No Call	A A	G A
7	CAD83	NA17107		G A	G A	G A	A A
8	CAD83	NA17108		G G	G A	G A	G A
9	CAD83	NA17109		G A	G G	G A	G A
10	CAD83	NA17111		G A	G A	G A	G A
11	CAD83	NA17115		G G	G A	A A	G A
12	CAD83	NA17117		G A	G G	G A	G A
13	CAD83	NA17125		G G	G A	G G	G A



62 assays, average call = 97.8%



Data points correspond to the two homozygote genotypes (blue, red), the heterozygote genotype (green), the no template control (NTC) (black) for the unamplified DNA samples, and the WGA amplified samples (orange). Samples that fall within the gray box demarcated by the ⊗ symbols are not called. In all cases the call rate was 99% and accuracy was equal to 100%. a.u., arbitrary units.

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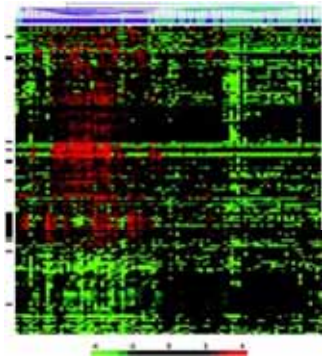
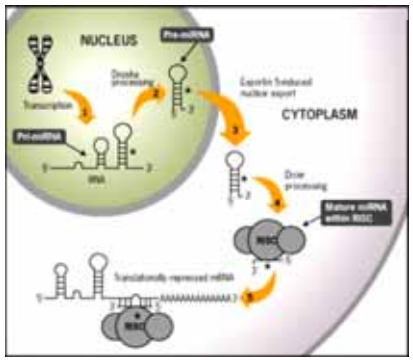
Transcriptomics Study



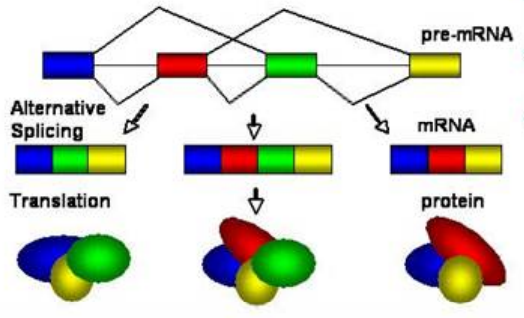
Gene Expression

Gene expression is the process by which information from a gene is used in the synthesis of a functional gene product.



miRNA expression:

- 20~24 nt short single strand RNA molecule
- Endogenous non-coding sequence
- Acting as translation inhibitor by degrading mRNA or blocking protein synthesis



Alternative Splicing:

Alternative splicing occurs as a normal phenomenon in eukaryotes, where it greatly increases the diversity of proteins that can be encoded by the genome; in humans, over 80% of genes are alternatively spliced. There are numerous modes of alternative splicing observed, of which the most common is exon skipping. In this mode, a particular exon may be included in mRNAs under some conditions or in particular tissues, and omitted from the mRNA in others.

Agilent Technologies

60-mer Oligo Expression Array

Human Whole Genome Array 40,000 genes and transcripts

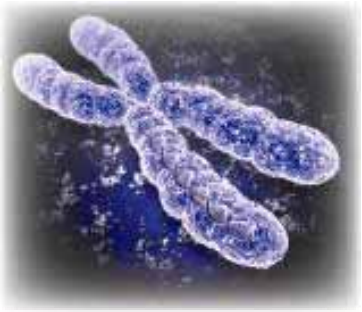
Mouse Whole Genome Array 41,000 genes and transcripts

Rat Whole Genome Array 41,000 genes and transcripts

另有其它物種

Monkey
Pig
Dog
Cat
Arabidopsis
Rice

Yeast
Zebrafish
M. grisea
C. elegans
Xenopus laevis
More…



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http://www.welgene.com.tw

市面最新版的 miRNA array（miRBase V14）

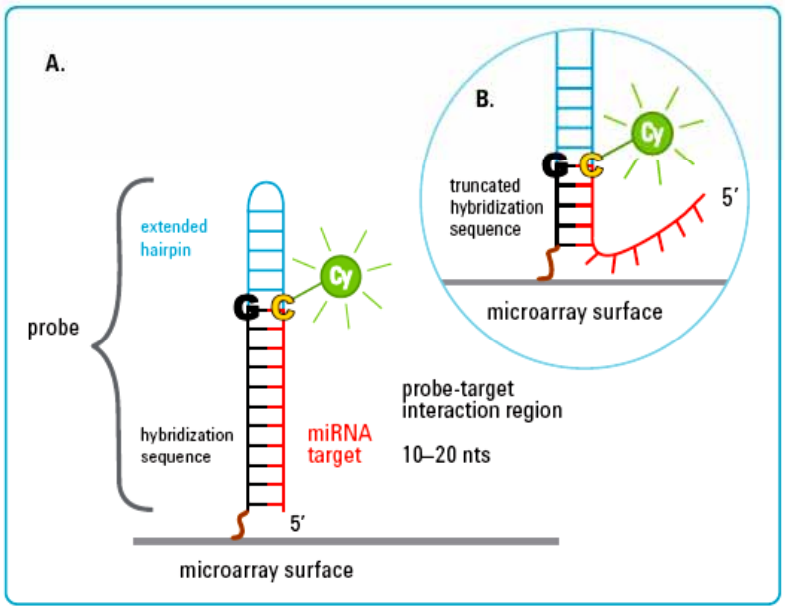


Figure 1. Components of the Agilent miRNA microarray probe design. An unmodified microarray probe (black) is a synthesized sequence that hybridizes to the target miRNA (red). Probes are anchored to the glass slide surface by a stilt (brown). **A.** Inclusion of a G residue (black) to the 5' end of the hybridization sequence complements the 3' end C residue (yellow) introduced in labeling. This additional G-C pair in the probe-target interaction region stabilizes targeted miRNAs relative to homologous RNAs. Additionally, all probes contain a 5' hairpin (blue), abutting the probe-target region, to increase target and size miRNA specificity. **B.** Destabilization of probes that are too stable. For probes requiring it, reduction of probe-target base-pairing is achieved through sequential elimination of base pairing from the 5' end of the miRNA.

- Human rel12 miRNA Array

  955 human-relative miRNA

- Mouse rel14 miRNA Array

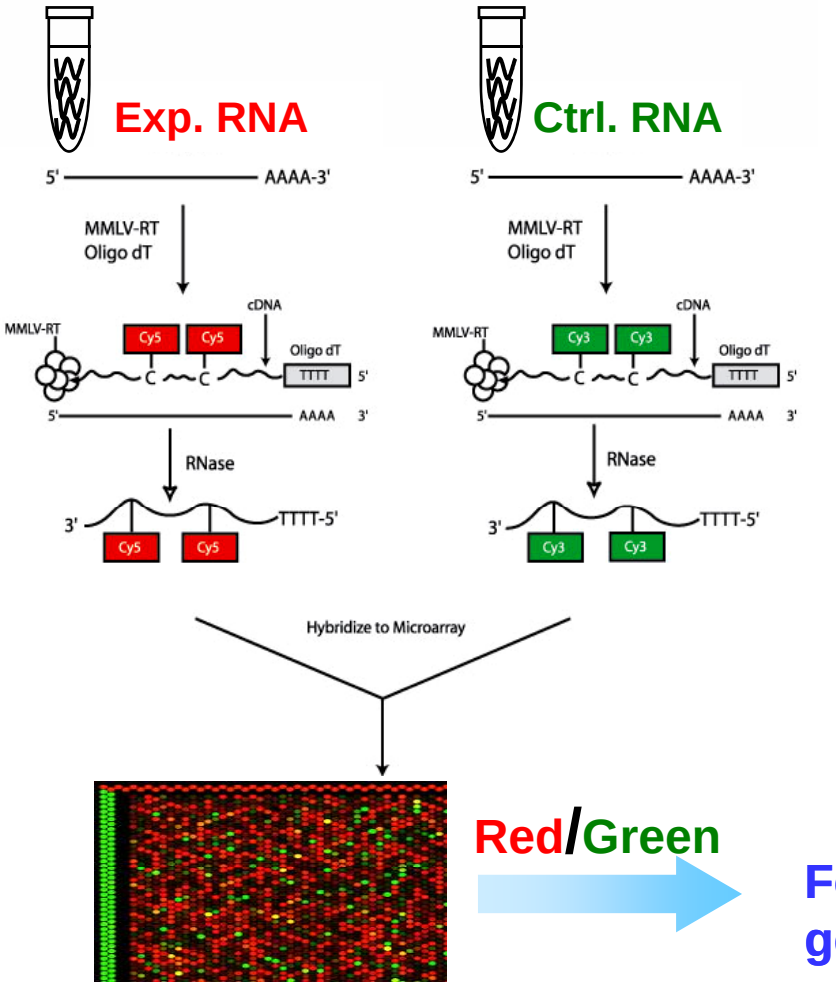
  690 mouse-relative miRNA

- Rat rel14 miRNA Array

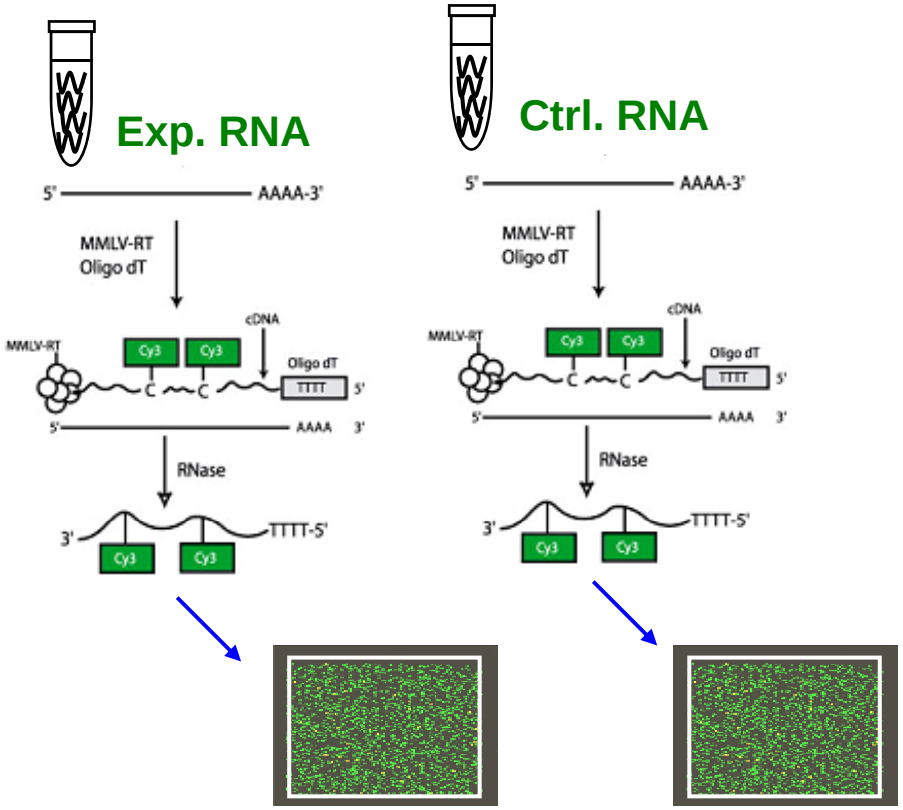
  388 rat-relative miRNA

Dual-Mode Array System

Two color



One color



Fold change of gene expression

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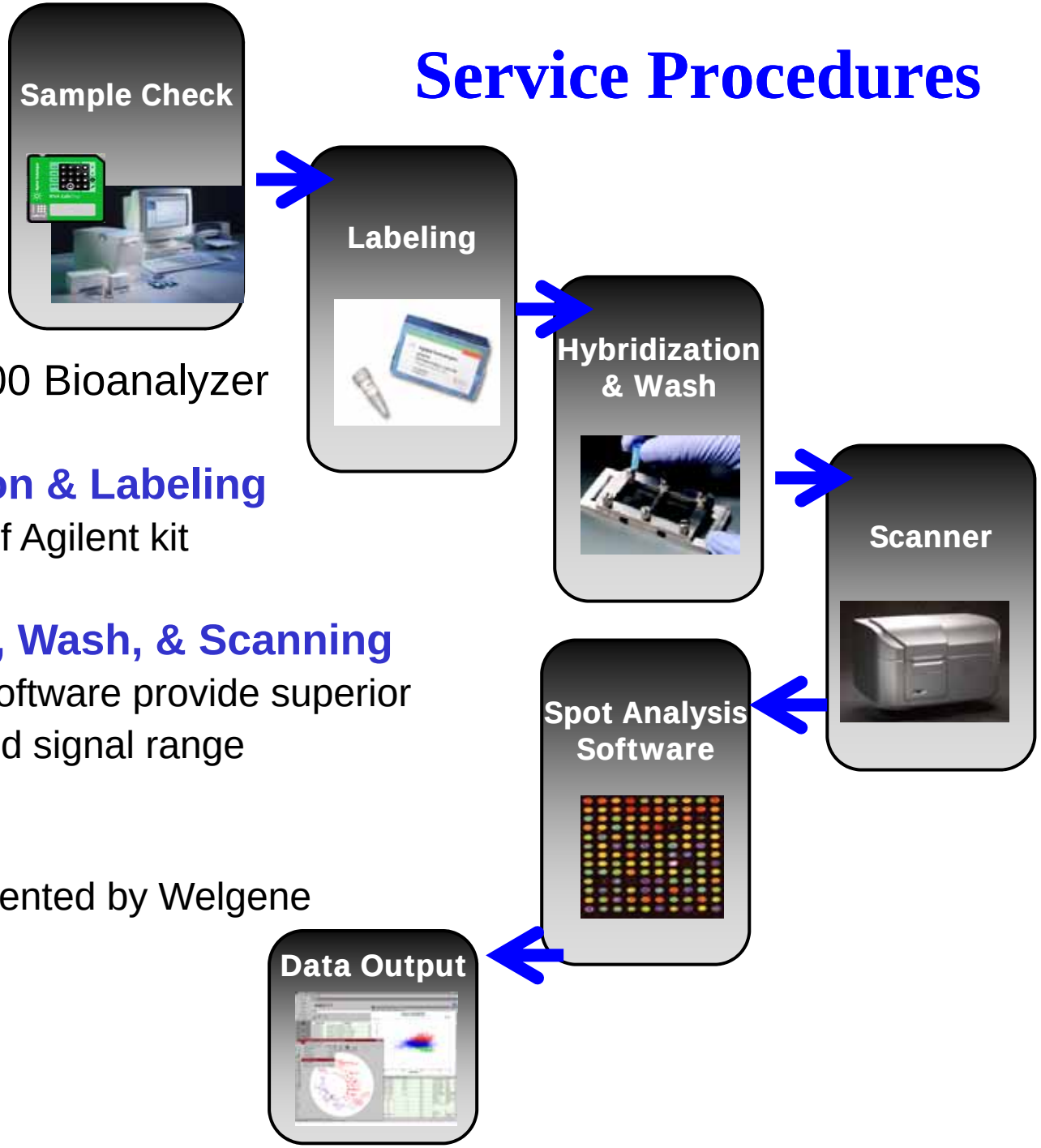
Service Procedures



1. RNA QC Test

-check by Agilent 2100 Bioanalyzer

2. Sample Amplification & Labeling

-process with full sets of Agilent kit

3. Array Hybridization, Wash, & Scanning

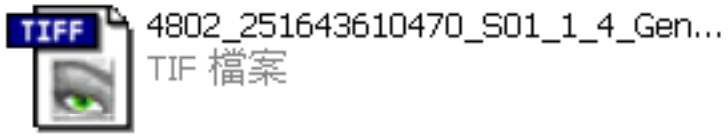
-Agilent scanner and software provide superior resolution and extended signal range

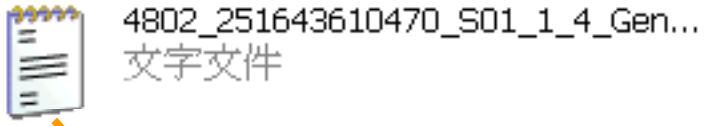
4. Data Output

-easy to use data presented by Welgene

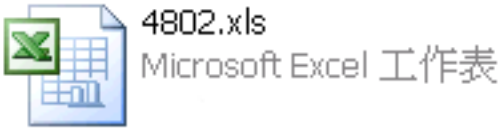
Array Report

1. Array Image





2. Raw Data



3. Excel file

GeneName	SystematicName	Description	PValueLogRatio	Normalized Exprssion Ratio
SPINK1	NM_003122	Homo sapiens serine peptidase inhibitor, Kazal type 1 (SPINK1), mRNA [NM_003122]	0.000	536.450
RAB3B	ENST00000371655	Ras-related protein Rab-3B. [Source:Uniprot/SWISSPROT;Acc:P20337] [ENST00000371655]	0.000	155.765
KCNC2	NM_139136	Homo sapiens potassium voltage-gated channel, Shaw-related subfamily, member 2 (KCNC2), transcript variant 1, mRNA [NM_139136]	0.000	107.736
GUCY2C	NM_004963	Homo sapiens guanylate cyclase 2C (heat stable enterotoxin receptor) (GUCY2C), mRNA [NM_004963]	0.000	75.554
MUC13	NM_033049	Homo sapiens mucin 13, cell surface associated (MUC13), mRNA [NM_033049]	0.000	73.358
LOC344887	BX640843	Homo sapiens mRNA; cDNA DKFZp686B14224 (from clone DKFZp686B14224). [BX640843]	0.000	67.974
REG3A	NM_138938	Homo sapiens regenerating islet-derived 3 alpha (REG3A), transcript variant 2, mRNA [NM_138938]	0.000	67.390

qRT-PCR Service
(for RNA or DNA)

LightCycler

Mx-3000p

TaqMan Assay and SyBR Assay are both available

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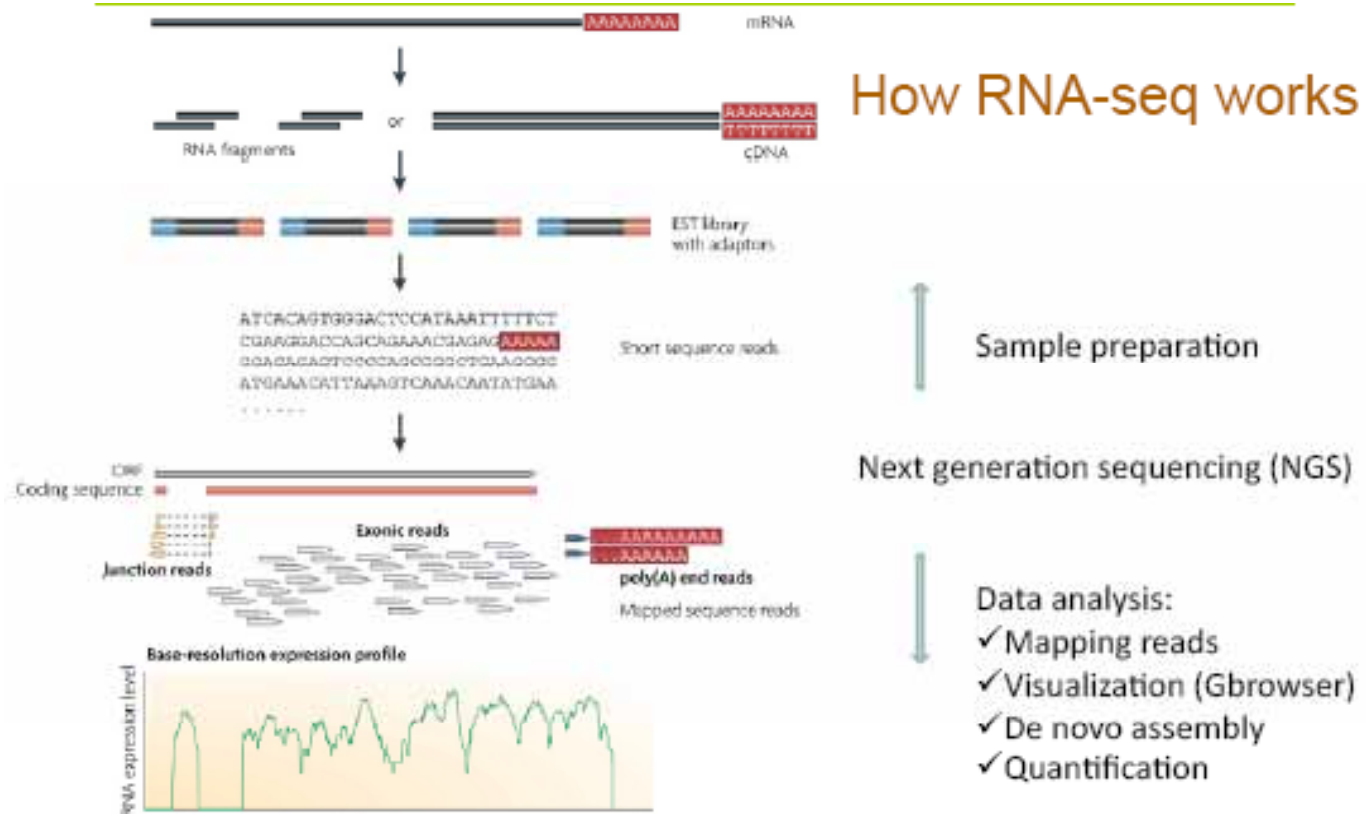
RNA-Seq



How RNA-seq works

Sample preparation

Next generation sequencing (NGS)

Data analysis:
- ✓Mapping reads
- ✓Visualization (Gbrowser)
- ✓De novo assembly
- ✓Quantification

Illumina Solexa

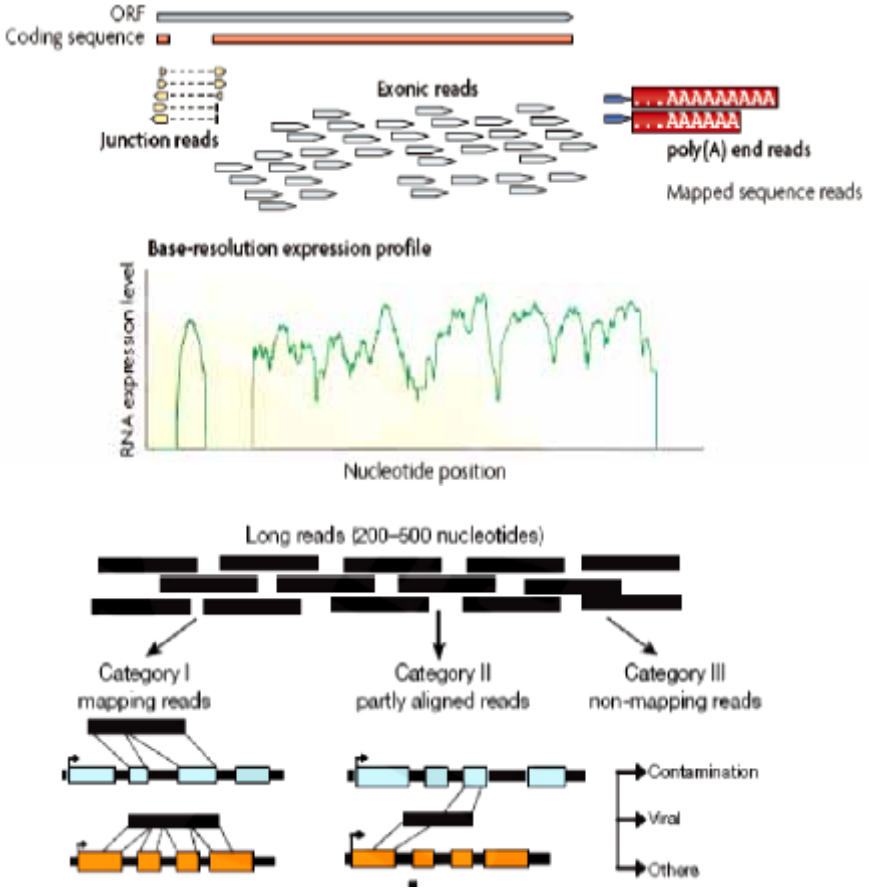
AB SOLiD

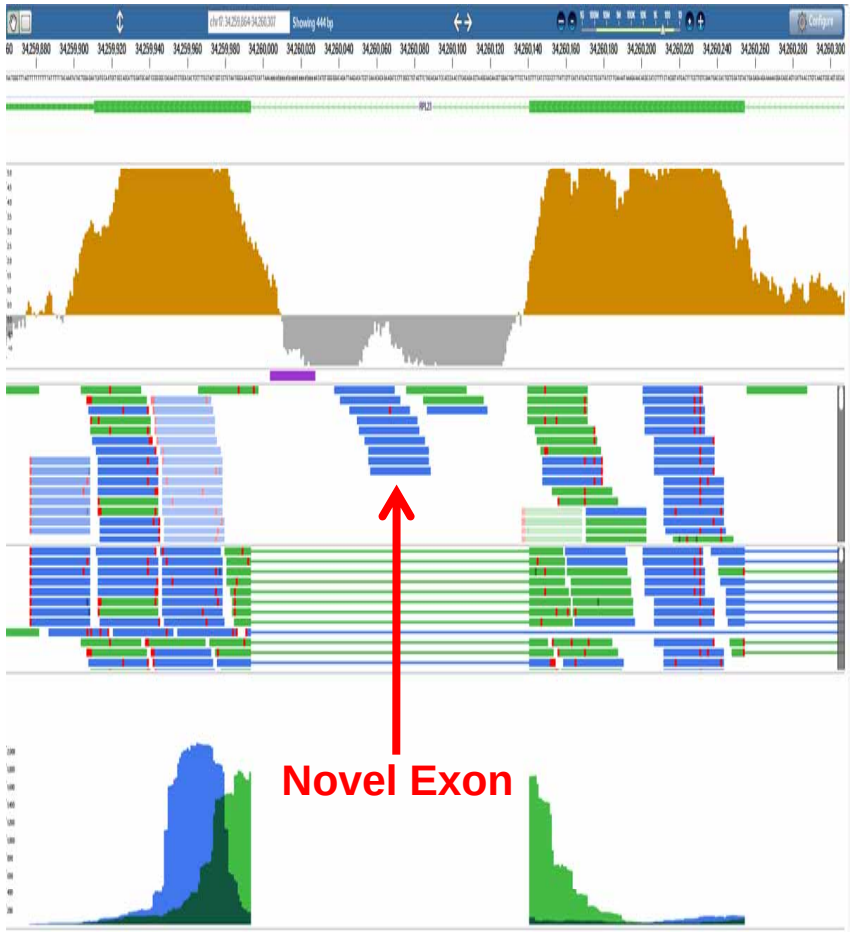
Roche 454

Welgene Biotech. Co. Ltd
http://www.welgene.com.tw

Alternative Splicing / Point Mutation Analysis

每個 RNA 樣品需要準備 20 ug, RNA品質需 RIN >7
進行1-2 G bases的定序量
分析方式需特別討論





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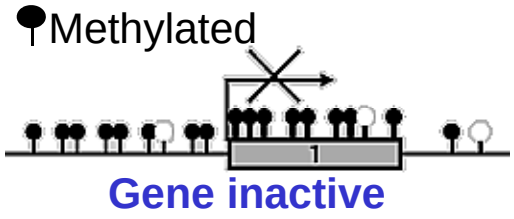
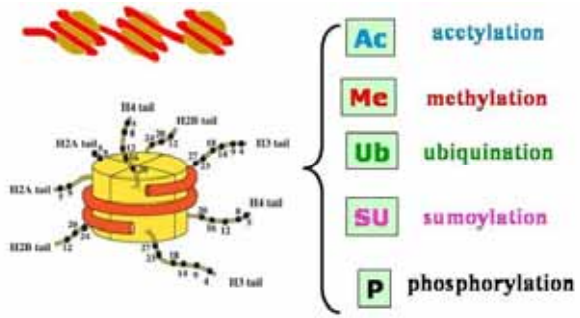
Epigenomics Study



DNA Methylation:

- The CG island is a short stretch of DNA in which the frequency of the CG sequence is higher than other regions. It is also called the CpG island, where "p" simply indicates that "C" and "G" are connected by a phosphodiester bond.
- CpG islands are often located around the promoters of housekeeping genes (which are essential for general cell functions) or other genes frequently expressed in a cell. At these locations, the CG sequence is not methylated. By contrast, the CG sequences in inactive genes are usually methylated to suppress their expression.



Histone Modification:

Histones are subject to a wide variety of posttranslational modifications including but not limited to, lysine acetylation, lysine and arginine methylation, serine and threonine phosphorylation, and lysine ubiquitination and sumoylation (Vasquero 2003). The existence of these modifications and recognition modules led to a well established “histone code” hypothesis proposed by Strahl and Allis (2000). Overall, posttranslational modifications of histones create an epigenetic mechanism for the regulation of a variety of normal and disease-related processes.

Chromatin ImmunoPrecipitation

Genome wide location analysis to examine three different types of targets:

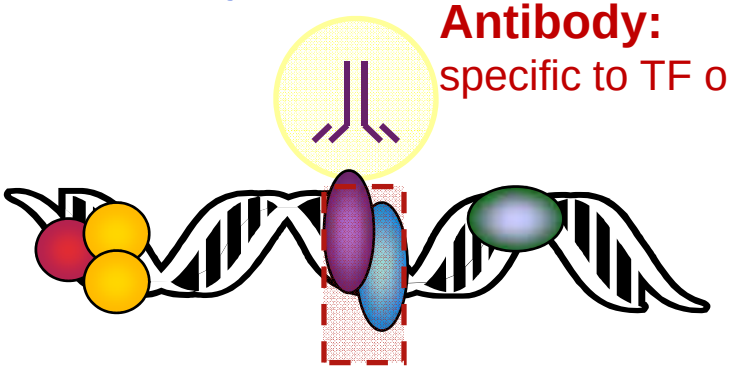
i) Transcription factors

ii) Cofactors

iii) Histone modifiers

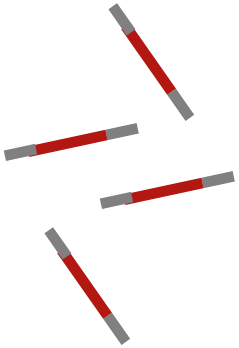
iv) DNA methylation

Antibody:
specific to TF or methylated DNA



***In vivo* protein-DNA complexes**

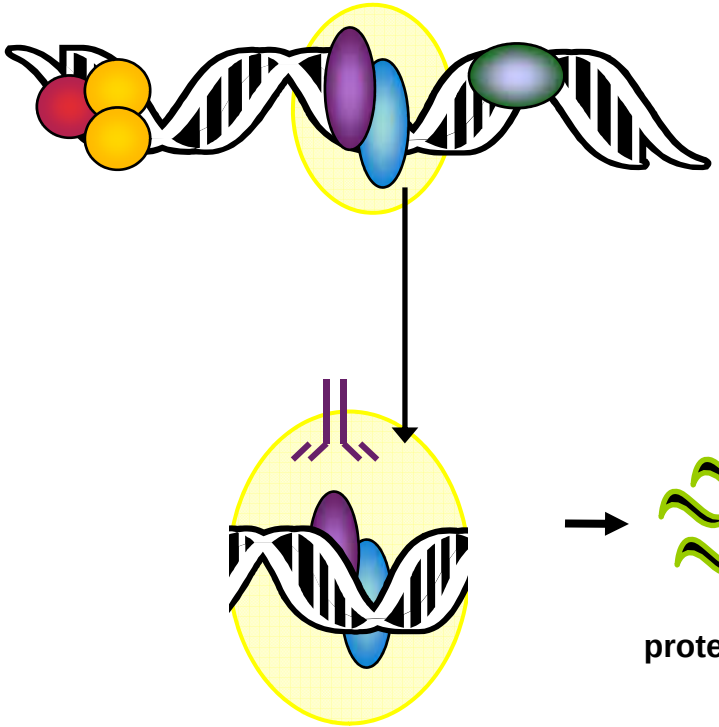
IP chromatin to capture crosslinked protein-DNA complexes
Sonicate complexes to fragment DNA
Reverse and remove crosslinks



Purify and amplify DNA fragments
=
ENRICHED POOL of protein-bound DNA

ChIP-on-chip /ChIP-Seq Concept

Regulatory proteins bind to promoter DNA regions *in vivo*

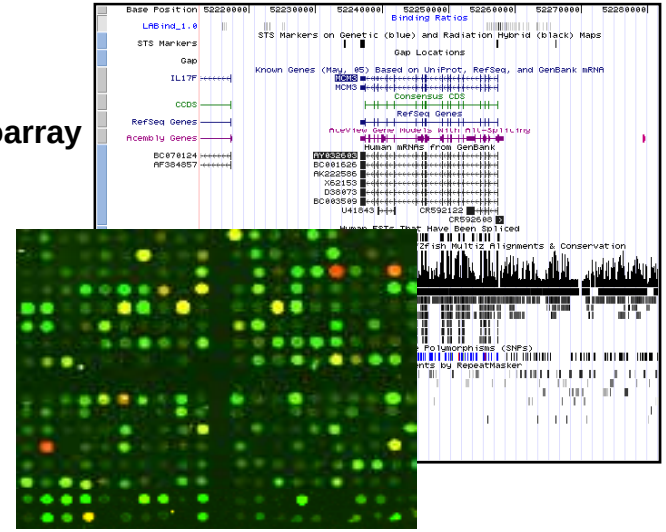


1. **Cross-link protein-DNA complexes**
2. **Lyse cells and sonicate DNA**
3. **IP chromatin to capture and purify bound DNA**
4. **Release and amplify DNA fragments**

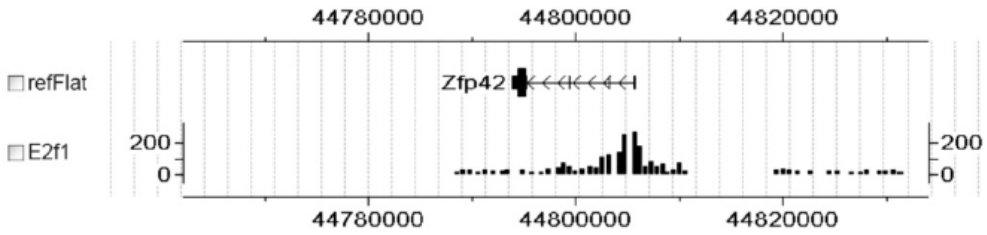
protein-bound DNA fragments

Hybridize to microarray for detection

ChIP Analytics output in UCSC browser view



Sequencing IP-DNA with NGS



Promoter Array Design

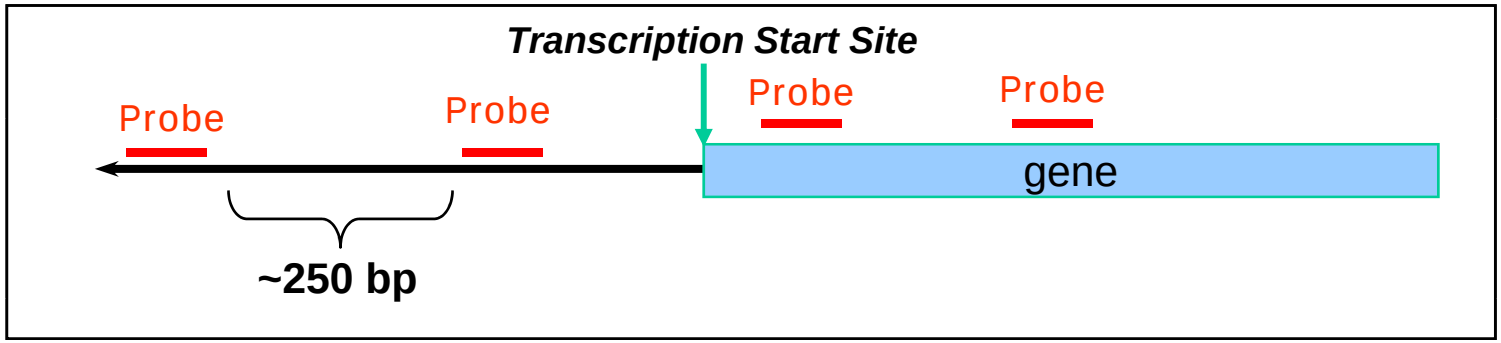
Goals:

- Construct a database of high-quality probes spanning the genome.
- Provide tools to select probes onto arrays for particular applications.

Probe optimization criteria:

- **Uniqueness (low homology)**
- **T_m**
- **Self-structure**
- **Balances spacing with performance**

7.5 kb promoter region— 5.5 kb upstream, 2 kb downstream

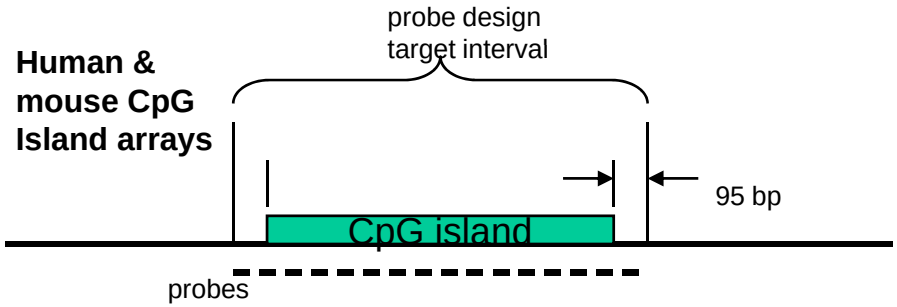


60-mer oligonucleotide probes—critical for the sensitivity and specificity

Average probe spacing parameters have been specifically optimized

Repeat regions are masked to significantly reduce non-specific noise.

Methylation (CpG Island) Array Design



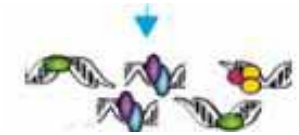
- Tiled arrays with 60-oligomer probes spaced ~100 bp apart for 28,500 islands in human and 16,030 in mouse
- Uses the CpG island probes defined by Gardiner-Garden and Frommer from UCSC Hg18
- Compatible with methylated DNA immunoprecipation method (Keshet et. al, 2006) and possibly other methods

實驗流程	流程說明 詳細 SOP 請下載 Agilent 建議

客戶端製備 chromatin-immunoprecipitation-DNA

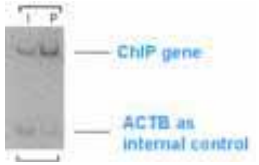
需準備 5x10^7 至 1x10^8 細胞，以 formaldehyde 處理細胞以 cross-link 蛋白質及核酸

磁珠與 ChIP 抗體結合



溶解細胞，並以超音波將 chromatin 片段化至長度 100bp-500bp

進行 chromatin-immunoprecipitation 實驗，解除 cross-link ，並純化 DNA



以基因特異引子確認 ChIP 實驗成功

DNA 樣品需求

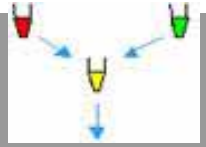
- ChIP DNA , ~500 ng, 長度分布在 100~500 bp
- Input DNA, ~ 8 µg, 長度分布在 100~500 bp
- ChIP 基因特異引子 , 5 µm, 20 µl

ChIP-DNA 、 Input-DNA 及基因特異引子送交威健實驗室

確認 DNA 長度分布

以基因特異引子進行定量 PCR 確認 ChIP 實驗成功

補平 DNA 兩端，並連接上 linker，進行 LM-PCR 以增幅 ChIP- 及 Input-DNA 量



反應，螢光標幟 ChIP- 及 Input-DNA

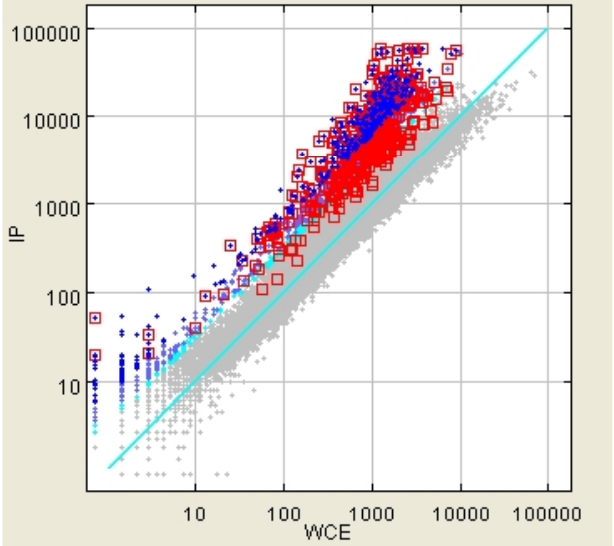
進行 hybridization 及 wash 步驟

輸出，並分析 binding element

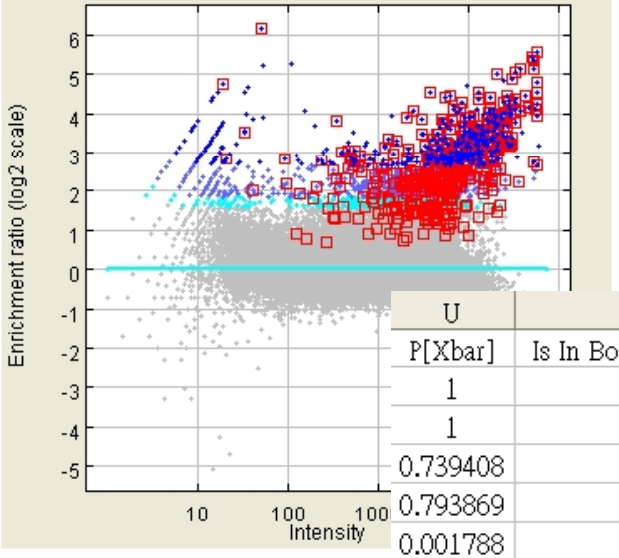
Slide Name: US22502707_251390210429_S01

Number of Probes	44290
Significant Probes	426
Bound Probes	440
Derivative Log ratio spread	0.2474
Normalized Red/Green Correlation (R^2)	0.4031

IP vs WCE

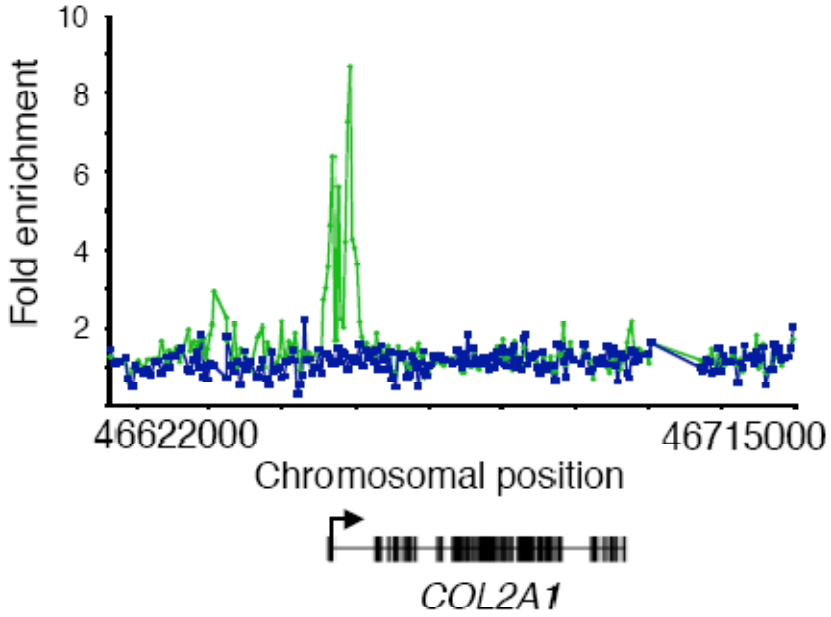


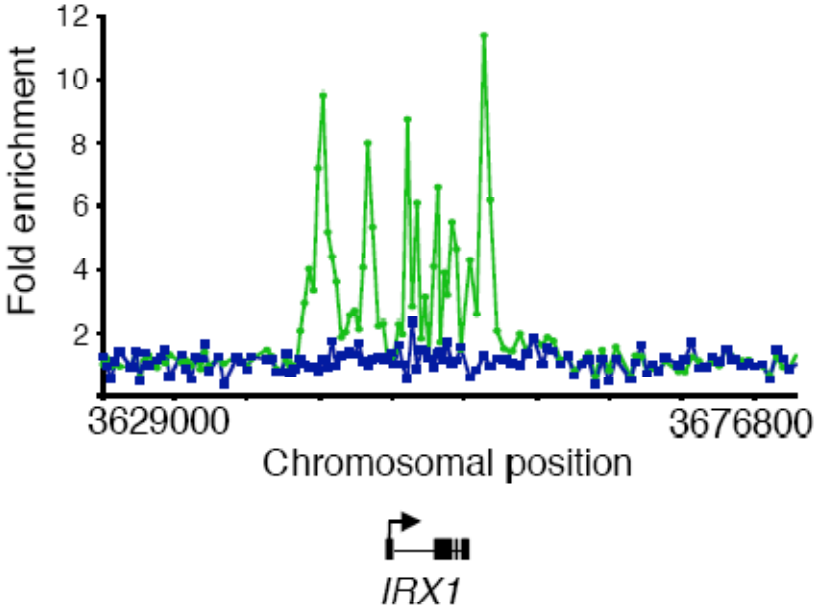
Enrichment ratio (logscale) vs Intensity



U	V	W	X	Y
P[Xbar]	Is In BoundRegion	Exclude	Primary Ar	Secondary
1	0	0	HsCGHBri	NONE
1	0	0	NegativeC	NONE
0.739408	0	0	FAM79A	ref:FAM79
0.793869	0	0	DENND1E	ref:DENNI
0.001788	0	0	TOR1AIP2	ref:TOR1A
0.880848	0	0	PDE6B	ref:PDE6B:
0.363265	0	0	DKFZP434	ref:DKFZP
1	0	0	LACC:GD2	NONE
0.759735	0	0	MTCH1	ref:MTCH1
0.565234	0	0	ESR1	ref:ESR1:-7
0.085293	0	0	MRPS24	ref:MRPS2
0.706946	0	0	FLJ35779	ref:FLJ357
0.133019	0	0	FRS3-C6or	ref:FRS3:-1
0.356215	0	0	DHFRL1	ref:DHFRL
0.089522	0	0	RQCD1	ref:RQCD1
0.017177	0	0	PTGS2	ref:PTGS2:

ChIP-on-chip Result





Polycomb (Suz12) Covers Promoters and Genes

Pol II
Suz12

Methylation Array Result

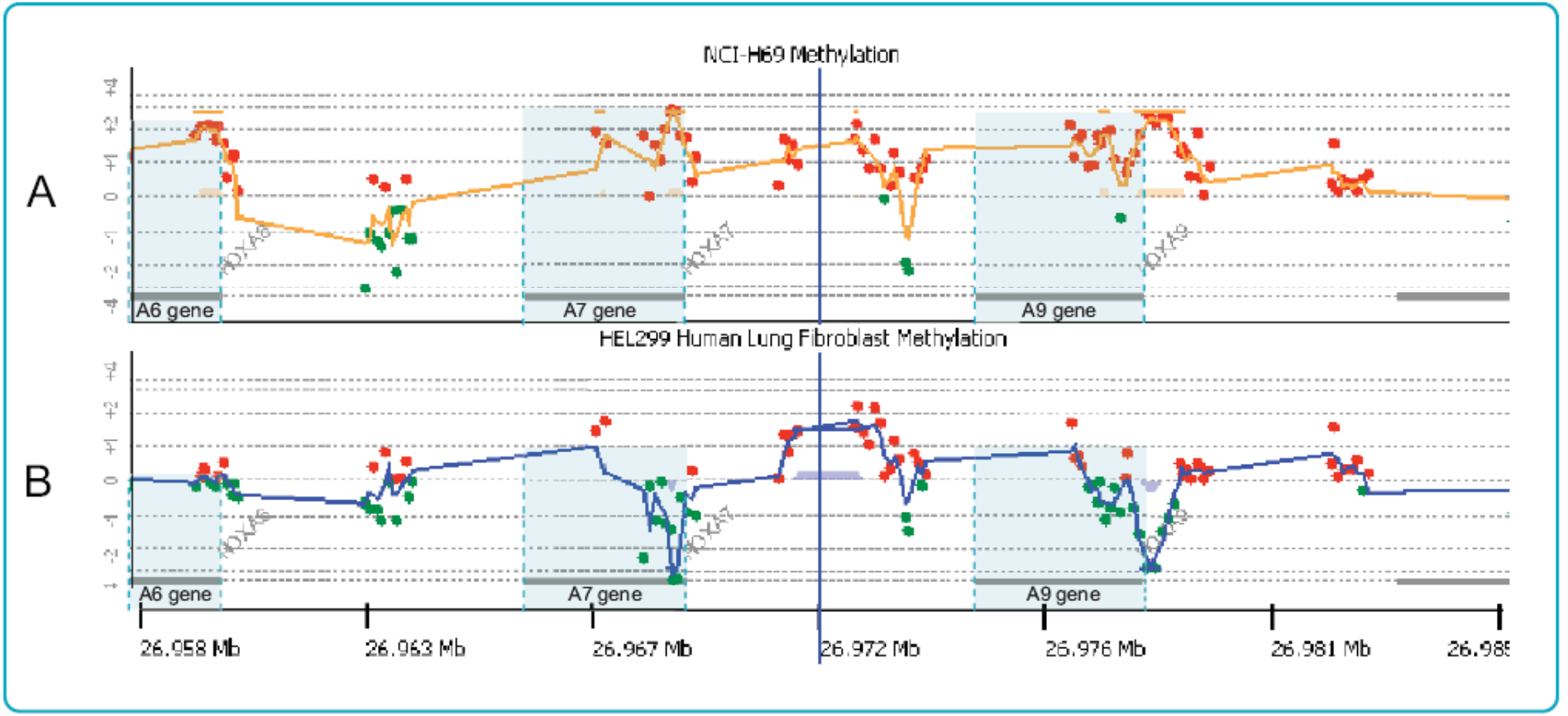
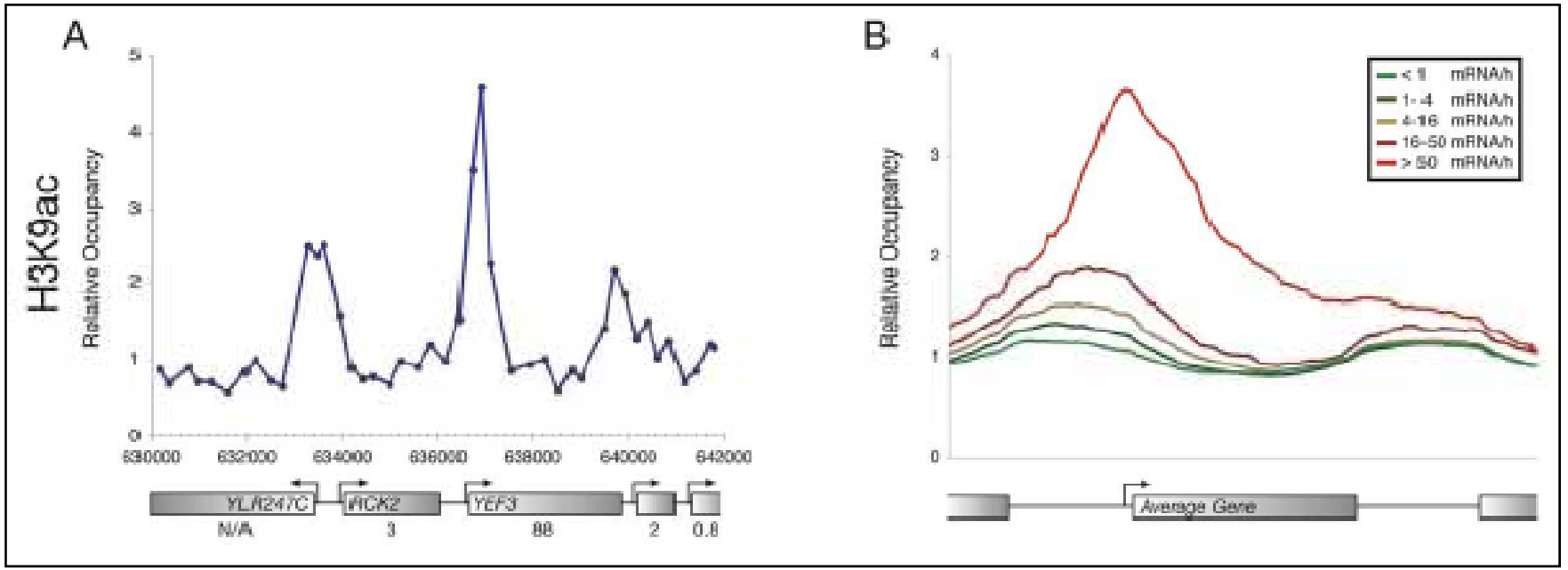


Figure 3. Methylation comparison of the HoxA gene cluster between tumor and normal lung cell lines. Methylated DNA was immunoprecipitated and labeled from genomic DNA (as previously described) from the small cell lung carcinoma NCI-H69 cell line (**Figure 3A**) and the normal embryonic lung fibroblast HEL299 cell line (**Figure 3B**). For each line, samples of both Cy5-labeled mDIP-enriched DNA and Cy3-labeled input genomic DNA were competitively hybridized to an Agilent Human CpG Island Microarray (P/N G4492A). Microarrays were processed, scanned on an Agilent Scanner (P/N G2565BA), and data normalized to a median $\log_2$ ratio of zero. The methylation profile for a portion of the Hox locus on Chromosome 7 is shown. Every point represents an individual CpG island microarray probe. Each colored line (orange for tumor, blue for normal) represents a three-point moving average of the $\log_2$ ratio. Regions of more methylation (red) and less methylation (green) are indicated. Highly methylated regions have $\log_2$ ratios significantly above zero while less methylated regions have log ratios significantly below zero. Profiles clearly show significant differences between the normal and cancer samples at HoxA6, HoxA7, and HoxA9 promoter regions.

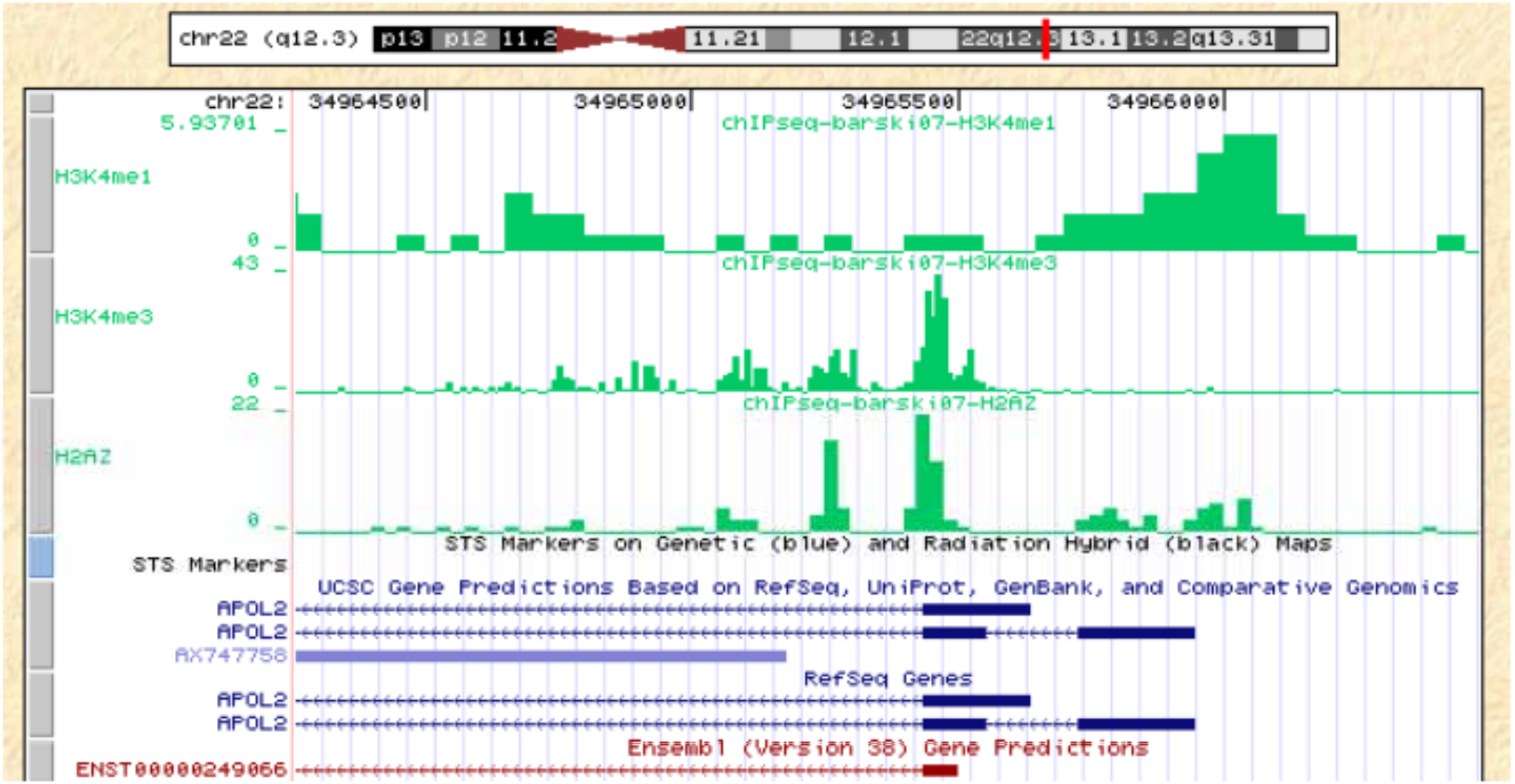
Histone Modification Result



- Histone acetylation enriched at promoter regions and transcriptional start sites of active genes.
  - Acetylation at Gcn5 targets H3K9 and H3K14 and Esa1 targets H4 at Lys 5,8,12 and16.

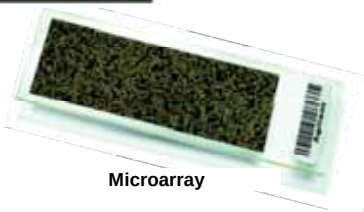
  → Model: transcriptional activators recruit Gcn5 and Esa1 to promoters of genes upon their Activation (Robert et al., 2004) .

ChIP-Seq



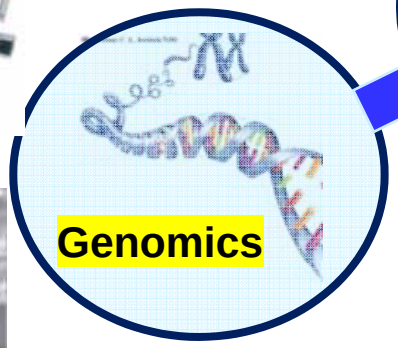
Based on data: from Barski et al. 2007, Cell 129, 823-837.

Integration of Multi-omics Research



Microarray

Microarray Scanner

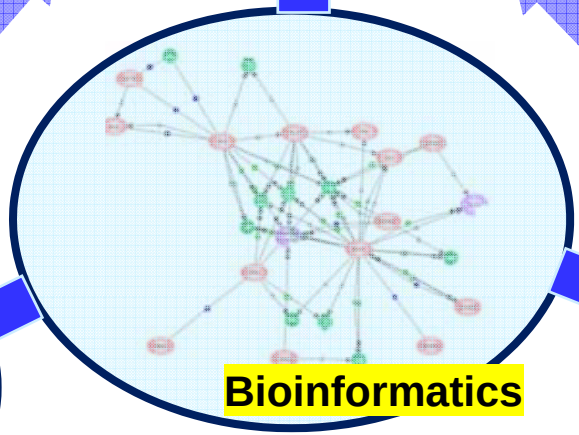


Genomics

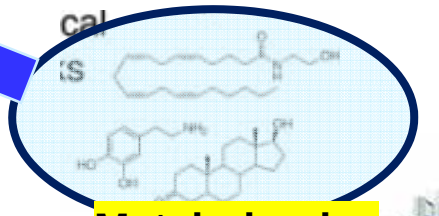
Proteomics

HPLC Systems

HPLC Chip/MS



Bioinformatics



Metabolomics

GC/MS

Genomic Workgroup

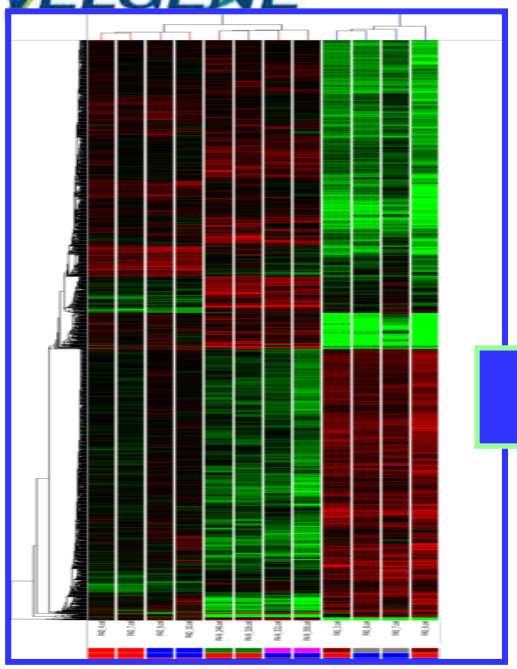
Mass Profiler Pro

GeneSpring GX

MassHunter Workstation

WELGENE

進階數據分析服務

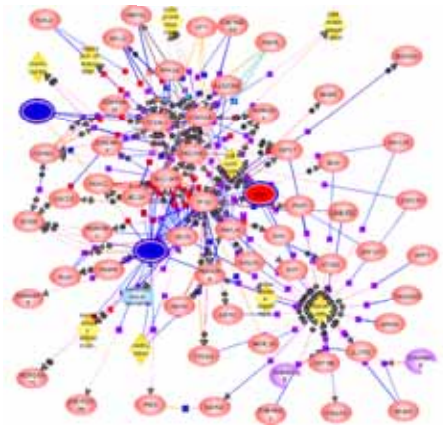


Find Significantly Expressed Genes

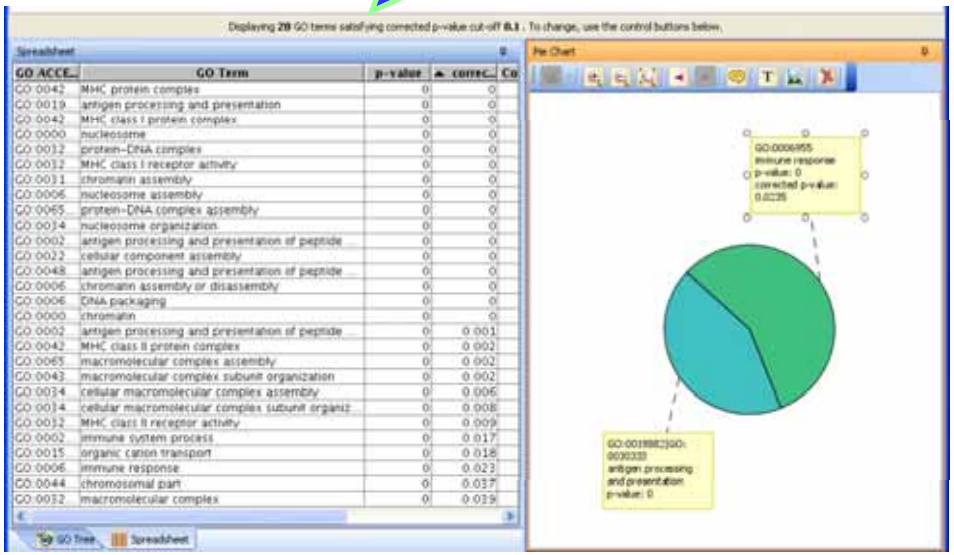
ProbeName	GeneSymbol	Common name	Description
A_23_P64873	DCN	NM_001920	Homo sapiens decorin (DCN), transcript variant A1, mRNA [NM_001920]
A_23_P421401	PDGFRB	NM_002609	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB), mRNA [NM
A_23_P209625	CYP1B1	NM_000104	Homo sapiens cytochrome P450, family 1, subfamily B, polypeptide 1 (CYP1B1), mRNA [NM_
A_23_P211233	COL6A2	NM_001849	Homo sapiens collagen, type VI, alpha 2 (COL6A2), transcript variant 2C2, mRNA [NM_0018
A_23_P164057	MFAP4	NM_002404	Homo sapiens microfibrillar-associated protein 4 (MFAP4), mRNA [NM_002404]
A_23_P142533	COL3A1	NM_000090	Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominan
A_23_P2063	LUM	NM_002345	Homo sapiens lumican (LUM), mRNA [NM_002345]
[illegible]168	CPM	NM_001874	Homo sapiens carboxypeptidase M (CPM), transcript variant 1, mRNA [NM_001874]
[illegible]	SPON2	NM_012445	Homo sapiens spondin 2, extracellular matrix protein (SPON2), mRNA [NM_012445]
[illegible]	PRRX2	NM_016307	Homo sapiens paired related homeobox 2 (PRRX2), mRNA [NM_016307]
[illegible]	COL3A1	NM_000090	Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominan
[illegible]16	GPM6B	NM_001001996	Homo sapiens glycoprotein M6B (GPM6B), transcript variant 2, mRNA [NM_001001996]
A_23_[illegible]0033	PDGFRA	NM_006206	Homo sapiens platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), mRNA [N

Network Analysis

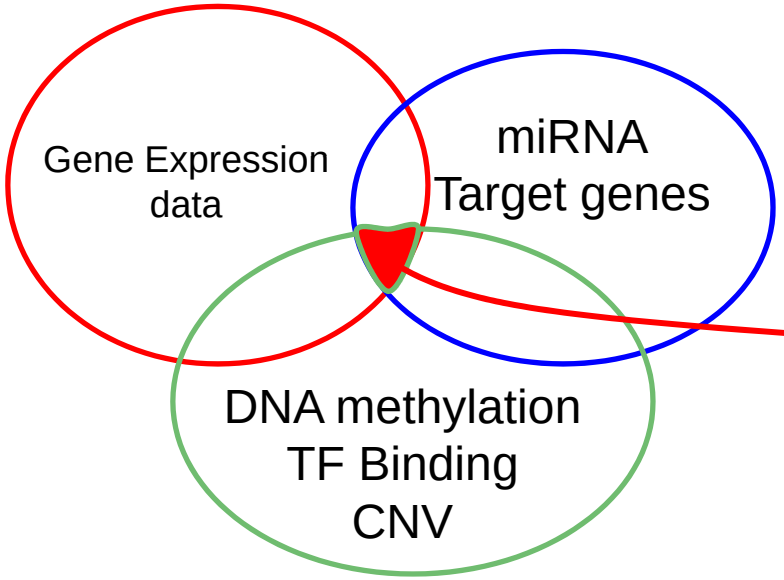
GO Analysis

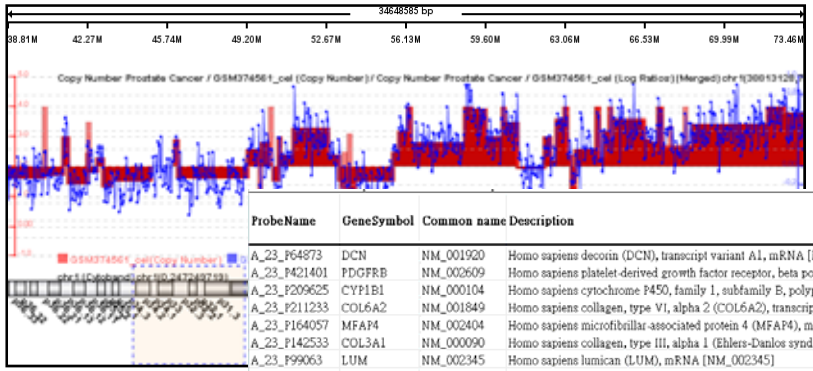


BioPax, NLP, MeSH



整合性數據分析





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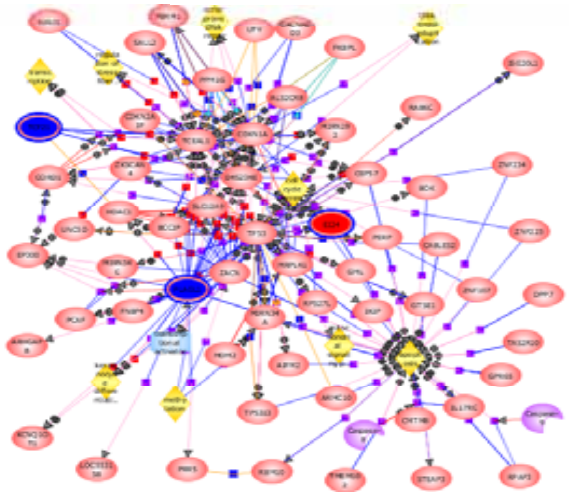
A_23_P99063	LUM	NM_002345	Homo sapiens lumican (LUM), mRNA [NM_002345]
A_23_P162668	CPM	NM_001874	Homo sapiens carboxypeptidase M (CPM), transcript variant 1, mRNA [NM_001874]
A_23_P121533	SPON2	NM_012445	Homo sapiens spondin 2, extracellular matrix protein (SPON2), mRNA [NM_012445]
A_23_P83298	PRRX2	NM_016307	Homo sapiens paired related homeobox 2 (PRRX2), mRNA [NM_016307]
A_24_P935491	COL3A1	NM_000090	Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominan
A_23_P378416	GPM6B	NM_001001996	Homo sapiens glycoprotein M6B (GPM6B), transcript variant 2, mRNA [NM_001001996]
A_23_P300033	PDGFRA	NM_006206	Homo sapiens platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), mRNA [N

Find overlapped genes



Build possible gene interaction network

Thank you for your attending
Wish you have a day

Welgene Biotech Co., Ltd.

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