



# Исследование функциональных характеристик генома (3-II)

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Кафедра информационной биологии ФЕН НГУ



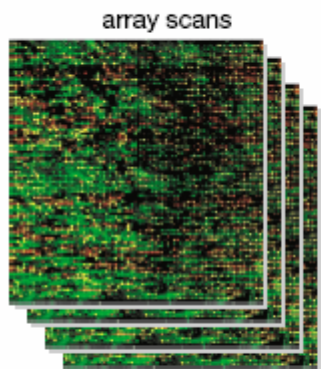
# Исследование функциональных характеристик генома

## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы

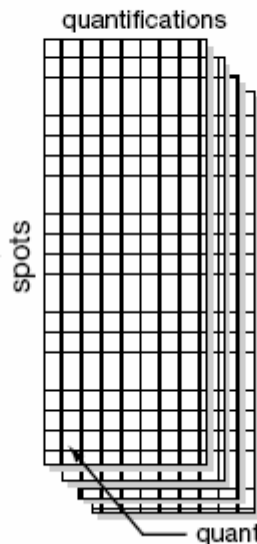


### Интернет-ресурсы для сбора , хранения и распространения биочип-данных

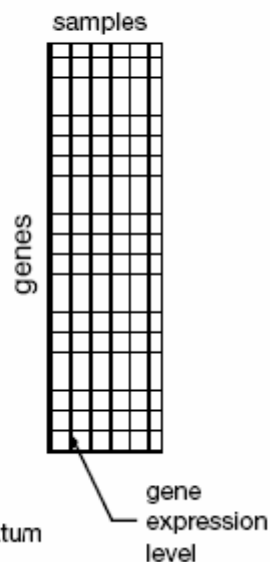
Исходные данные



Матрицы измерений



Матрицы данных по экспрессии генов



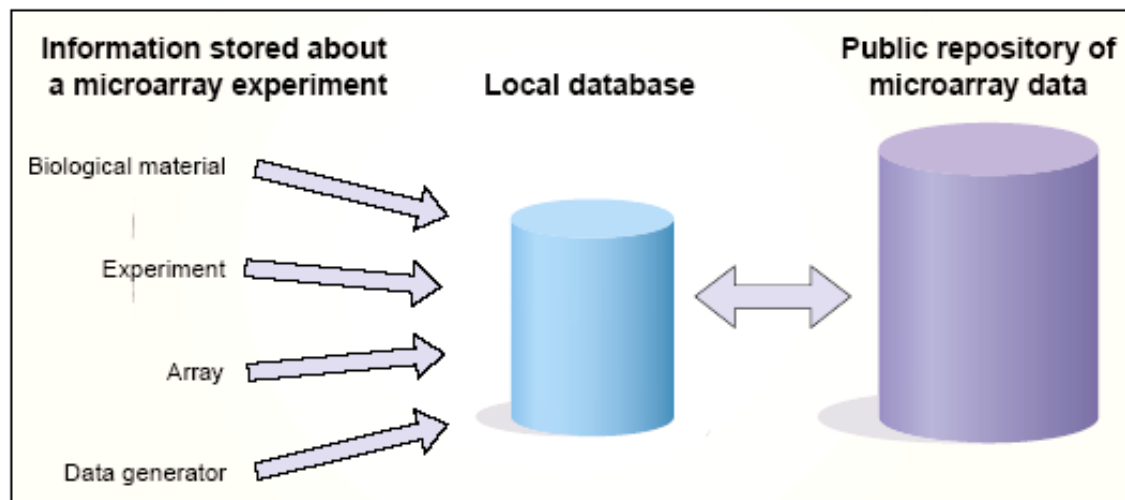


# Исследование функциональных характеристик генома

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### СООБЩЕСТВО MGED



- MicroArray Gene Expression Markup Language (MAGE-ML) - создан для создания общего формата, чтобы достичь сравнимости результатов
- Minimum Information About a Microarray Experiment (MIAME) - создан для определения типа информации и степени подробности, с которой исследователь обязан ее представить;
- MGED Society Ontology Working Group (<http://www.mged.org/ontology>) - создана для формирования набора контролируемых словарей и онтологий, необходимых для описания биологических образцов и экспер. процедур.

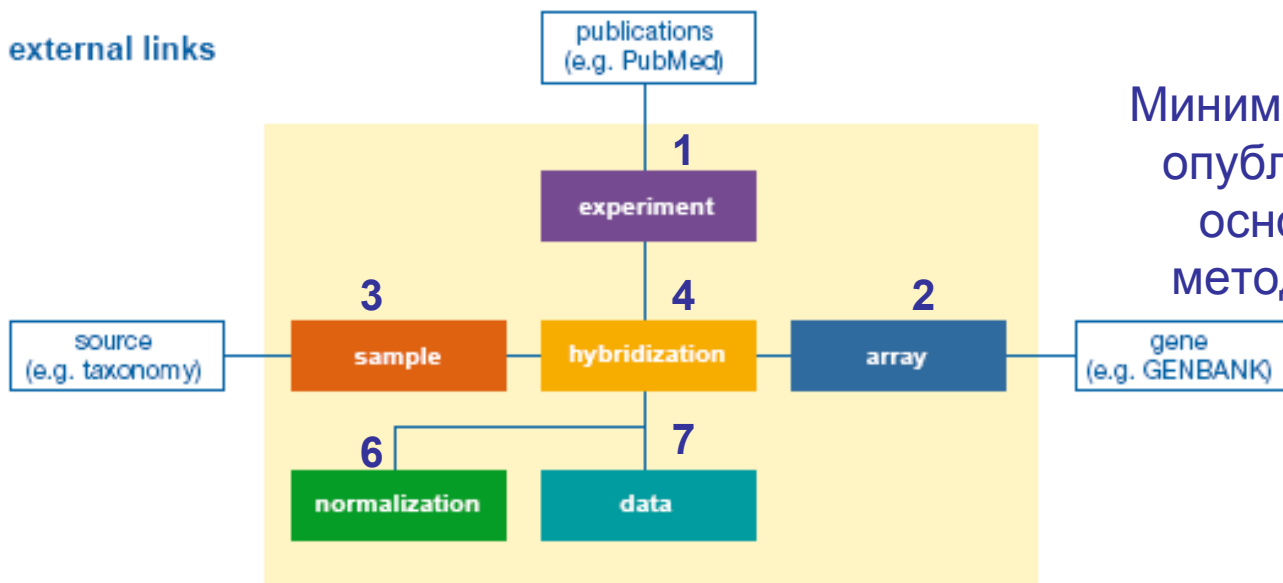


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### MINIMUM INFORMATION ABOUT A MICROARRAY EXPERIMENT (MIAME)



Минимальная информация об опубликованном эксперименте, основанном на ДНК-биочип-методе, включает шесть типов описаний:

1. План эксперимента - набор отдельных гибридизационных экспериментов
2. План биочипа – содержание пятен/ячеек, компоновка по рядам и т.д.
3. Образцы – источник, приготовление экстрактов, способ мечения
4. Гибридизация – процедура и параметры
5. Измерение – характеристики изображений и сканнеров
6. Нормировка – способ, коэффициенты и т.д.



# Исследование функциональных характеристик генома

## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы

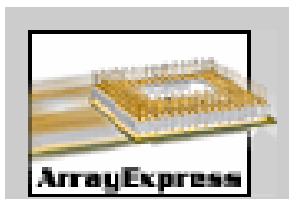


### Основные базы данных по ДНК-биочиповым экспрессионным данным:



Gene Expression Omnibus

NCBI



ArrayExpress

at the EBI



Stanford MicroArray Database

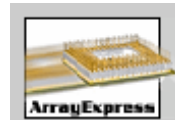


# Исследование функциональных характеристик генома

## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы



### Соотношение между основными объектами





# Исследование функциональных характеристик генома

## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы



### GEO - Gene Expression Omnibus (NCBI)

NCBI > GEO Not logged in | [Login](#)

**Gene Expression Omnibus:** a gene expression/molecular abundance repository supporting [MIAME compliant](#) data submissions, and a curated, online resource for gene expression data browsing, query and retrieval.

**GEO navigation**

- QUERY**
  - DataSets  [GO](#)
  - Gene profiles  [GO](#)
  - GEO accession  [GO](#)
  - GEO BLAST
- BROWSE**
  - DataSets
  - GEO accessions
    - Platforms
    - Samples
    - Series
- SUBMIT**
  - Direct deposit / update
  - Create new account

**Public data**

GPL Platforms	2192
GSM Samples	78979
GSE Series	3467
<i>Total</i>	<i>84638</i>

**Site contents**

**Documentation**

- Overview | [FAQ](#)
- [Web deposit guide](#)
- [Batch deposit guide](#)
- [Linking & citing](#)
- [Journal citations](#)
- [DataSet clusters](#)
- [GEO announce list](#)
- [Data disclaimer](#)
- [GEO staff](#)

**Query & Browse**

- [Repository browser](#)
- [Submitter contacts](#)
- [SAGEmap](#)
- [FTP site](#)
- [GEO Profiles](#)
- [GEO DataSets](#)

**Deposit & Update**

- [Direct deposit](#)



# Исследование функциональных характеристик генома

## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы



### GEO: связь между объектами

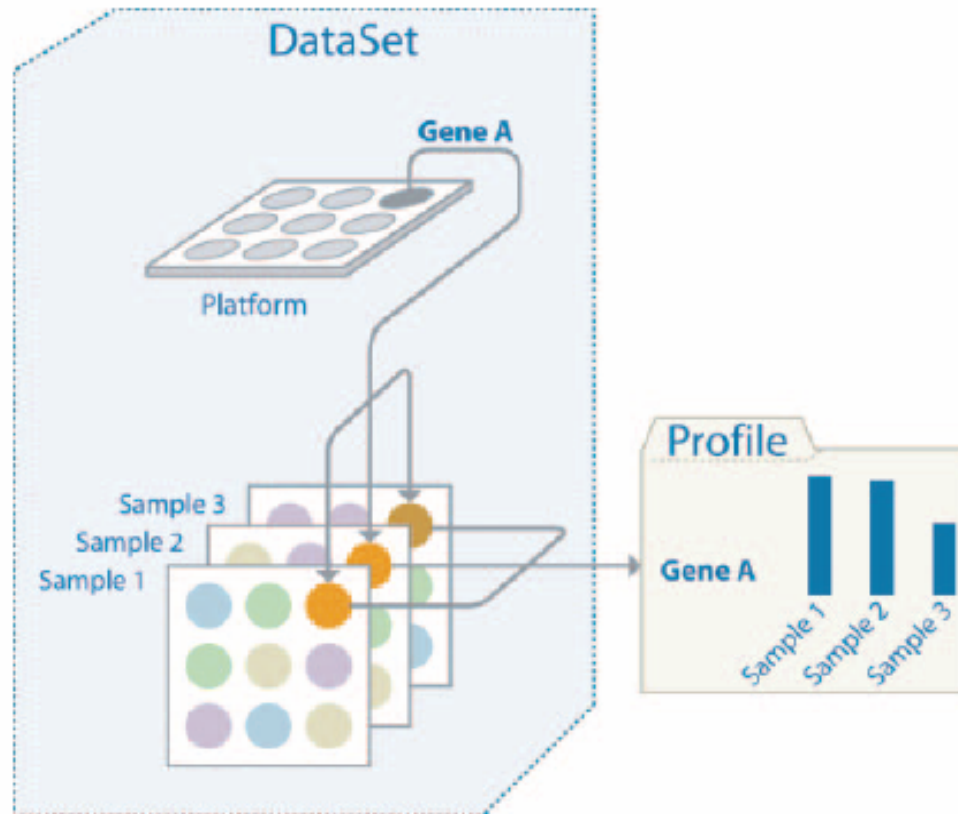


Figure 1. Schematic diagram of the relationships between GEO Platform, Sample, DataSet and Profiles. For each gene on a Platform (e.g. Gene A), multiple Sample measurement values are generated (Sample1–Sample3). Related Samples make up a DataSet, from which multiple, individual gene profile entities are generated.





# Исследование функциональных характеристик генома

## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы



### GEO: пример профиля для гена мыши

NCBI Entrez GEO Profiles

My NCBI [Sign In] [Register]

All Databases | GEO Profiles | for PPARg | Go | Clear | Save Search

Limits | Preview/Index | History | Clipboard | Details

Display Summary | show 100 | Subgroup effect | Send to

All: 13779

Items 1 - 100 of 13779 | Page 1 of 138 Next

1: GDS1616 record | GPL81 97926\_s\_at [Mus musculus] 4 samples Profile Neighbors, Sequence Neighbors, Homologs, Links

Annotation: Pparg: peroxisome proliferator activated receptor gamma Nr1c3, PPAR-gamma, PPAR-gamma2

Reporter: NM\_011146

Experiment: Akt kinase constitutive activation effect on embryonic stem cells, gene expression



90: GDS1272 record | GPL81 97926\_s\_at [Mus musculus] 6 samples Profile Neighbors, Sequence Neighbors, Homologs, Links

Annotation: Pparg: peroxisome proliferator activated receptor gamma Nr1c3, PPAR-gamma, PPAR-gamma2

Reporter: NM\_011146

Experiment: Luteinizing hormone overexpression effect on mammary gland, gene expression array-based count

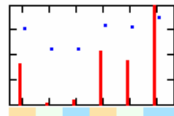


91: GDS559 record | GPL96 208510\_s\_at [Homo sapiens] 6 samples Profile Neighbors, Sequence Neighbors, Homologs, Links

Annotation: PPARG: peroxisome proliferative activated receptor, gamma HUMPPARG, NR1C3, PPARG1, PPARG2

Reporter: NM\_015869

Experiment: Inflammatory bowel disease (HG-U133A), gene expression array-based count

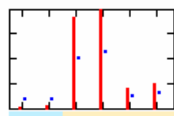


92: GDS817 record | GPL91 37104\_at [Homo sapiens] 6 samples Profile Neighbors, Sequence Neighbors, Homologs, Links

Annotation: PPARG: peroxisome proliferative activated receptor, gamma HUMPPARG, NR1C3, PPARG1, PPARG2

Reporter: NM\_005037 NM\_015869 NM\_138711 NM\_138712

Experiment: Breast cancer cell expression profiles (HG-U95A), gene expression array-based transformed count



Microarray GEO profiles of PPAR $\gamma$ ,



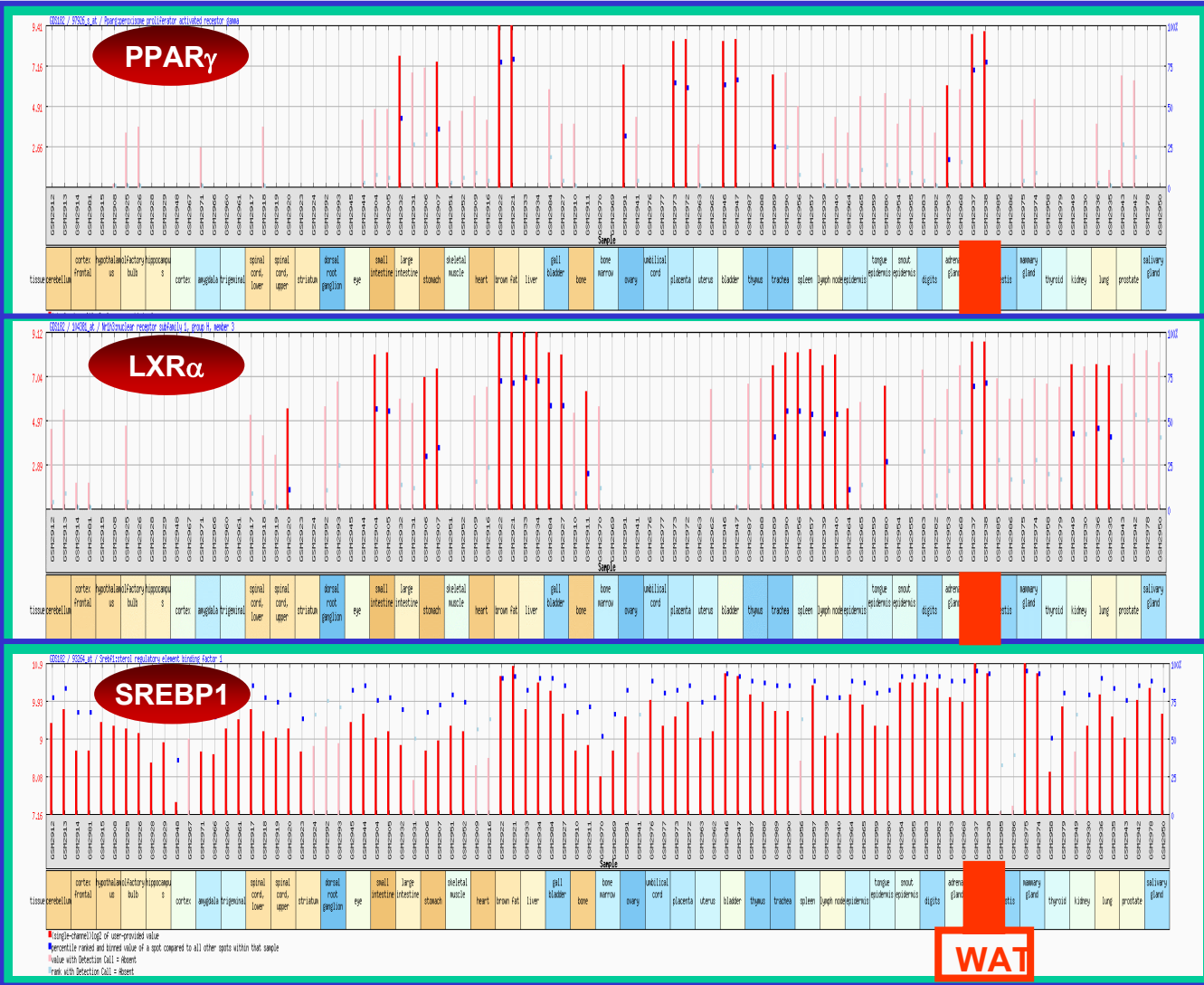
# Исследование функциональных характеристик генома

## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы



### GEO: пример профиля для генов мыши

Microarray GEO profiles of PPAR $\gamma$ , LXR $\alpha$  and SREBP-1c in 45 mouse tissues and organs (MG-U74A)








# Исследование функциональных характеристик генома

## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы







Gene Expression Omnibus

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HOME | SEARCH | SITE MAP
NAR 2006 Paper | NAR 2002 Paper | FAQ | MIAME | Email GEO

NCBI > GEO > GDS

**GDS Summary**

<b>Accession:</b>	GDS1332 <a href="#">View Expression (GEO profiles)</a>		
<b>Title:</b>	Huntington's disease: peripheral blood expression profile (Codelink Uniset 20K)		
<b>DataSet type:</b>	gene expression array-based (RNA / spotted oligonucleotide)		
<b>Summary:</b>	Analysis of blood samples of 5 presymptomatic and 12 symptomatic Huntington's disease (HD) patients. Studies suggest that gene expression may be altered in a variety of tissues in HD, including peripheral blood. Results identify potential markers for HD.		
<b>Platform:</b>	GPL1449: GE Codelink Human Uniset I, II, and 20K		
<b>Sample organism:</b>	Homo sapiens	<b>Platform organism:</b>	Homo sapiens
<b>Feature count:</b>	19881	<b>Value type:</b>	transformed count
<b>Series:</b>	<a href="#">GSE1767</a>	<b>PubMed ID:</b>	<a href="#">16043692</a>
<b>Series published:</b>	07/22/2005	<b>Last GDS update:</b>	12/02/2005

**Subset and Sample Info**

**Sample selection**

check all

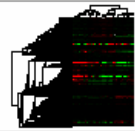
uncheck all  
 uncheck all

toggle

**Data**

download

analysis



**3 assigned subsets**

Samples	Type	Description
<input checked="" type="checkbox"/> (14)	disease state	normal
<input checked="" type="checkbox"/> (5)	disease state	presymptomatic
<input checked="" type="checkbox"/> (12)	disease state	symptomatic

GDS1332 only
  ranks
  values
  subset effects

Two-tailed t-test (A vs B)

A		B
<input type="checkbox"/>	↔	<input type="checkbox"/>
<input type="checkbox"/>	↔	<input type="checkbox"/>
<input type="checkbox"/>	↔	<input type="checkbox"/>

Query A vs. B

31 samples, order: none

GSM30698 : N1 Codelink

GSM30699 : N2 Codelink

GSM30700 : N3 Codelink

GSM30701 : N4 Codelink

Выявление  
достоверной  
разницы в  
экспрессии генов

Иерархическая  
кластеризация  
экспрессии генов



# Исследование функциональных характеристик генома

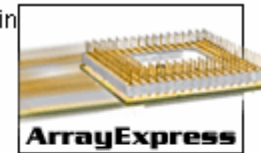
## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы



# ArrayExpress

# at the EBI

ArrayExpress is a public repository for microarray data, which is aimed at storing well annotated data in accordance with [MGED](#) recommendations.



- [Query Database >>](#)
- [Login To Database >>](#)
- [NEW FTP access >>](#)
  
- [Try gene queries in prototype data warehouse >>](#)
  
- [Submissions](#)
- [Help & Documentation](#)
  - [FAQ](#)
  - [Statistics](#)
- [Microarray Standards](#)
- [Software](#)
  - [Database Creation](#)
  - [Query Interface](#)
  
- [Microarray Home >>](#)

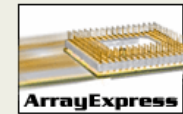
Current Content Overview:		
Experiments:	1797	<a href="#">View</a>
Arrays:	1222	<a href="#">View</a>
Protocols:	8512	<a href="#">View</a>
Hybridizations:	53665	

Please read our [ArrayExpress FAQ](#) before contacting us at [arrayexpress@ebi.ac.uk](mailto:arrayexpress@ebi.ac.uk).



# Исследование функциональных характеристик генома

## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы



You are logged in as *guest* [Login »](#)

ArrayExpress ( 1797 Experiments with 53665 Hybs, 1222 Arrays )

[Help](#)

### Query for Experiments

Give an experiment **accession number**  for example E-MANP-2, or search by **keyword**  [Query »](#)

or fill out some of the following fields to get a list of matching experiments:

**Species**

**Experiment type**

**Experimental Factors**

**Description contains the word**

**Author**

**Laboratory**

**Publication**

**Array accession number**

**Array design name**

**Array provider**

### Query for Arrays

Give an array **accession number**  for example A-TIGR-32, [Query »](#)

or fill out some of the following fields to get a list of matching arrays:

**Array design name**

**Array provider**

### Query for Protocols

Give a protocol **accession number**  for example P-SNGR-8, [Query »](#)

or fill out the following field to get a list of protocols of the given type:

**Protocol type**



# Исследование функциональных характеристик генома

## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы



### Описание эксперимента и ресурсы

1 / 1	Experiment : <b>E-AFMX-1</b>	Submitter(s) : <b>Khaïtovich</b>	Lab : <b>Evolutionary Genetics</b>
<b>Experiment Design Type</b> : species			
<b>(Generated description):</b> Experiment with 21 hybridizations, using 21 samples of species [Mus caroli, Mus spretus, Homo sapiens, Pongo pygmaea, Macaca mulatta, Mus musculus, Pan troglodytes], using 21 arrays of array design [Affymetrix Genechip® Murine Genome U74Av2 [MG_U74Av2], Affymetrix Genechip® Human Genome U95Av2 [HG_U95Av2]], producing 21 raw data files and 2 transformed and/or normalized data files.			
<b>(Submitter's description 1):</b> Microarray technologies allow the identification of large numbers of expression differences within and between species. Although environmental and physiological stimuli are clearly responsible for changes in the expression levels of many genes, it is not known whether the majority of changes of gene expression fixed during evolution between species and between various tissues within a species are caused by Darwinian selection or by stochastic processes. We find the following: (1) expression differences between species accumulate approximately linearly with time; (2) gene expression variation among individuals within a species correlates positively with expression divergence between species; (3) rates of expression divergence between species do not differ significantly between intact genes and expressed pseudogenes; (4) expression differences between brain regions within a species have accumulated approximately linearly with time since these regions emerged during evolution. These results suggest that the majority of expression differences observed between species are selectively neutral or nearly neutral and likely to be of little or no functional significance. Therefore, the identification of gene expression differences between species fixed by selection should be based on null hypotheses assuming functional neutrality. Furthermore, it may be possible to apply a molecular clock based on expression differences to infer the evolutionary history of tissues.			
<b>Retrieve data &gt;&gt;</b>	<b>Experimental protocols &gt;&gt;</b>	<b>Get MAGE-OM view &gt;&gt;</b>	
<b>Providers &gt;&gt;</b>	<b>Array design used &gt;&gt;</b>	- <b>Experiment's directory</b> in the FTP >>	
<b>Bibliographic references &gt;&gt;</b>	<b>Samples &gt;&gt;</b>	- <b>MAGE-ML</b> : ( .tgz (63 MB) )	
		- <b>Biosamples</b> : ( .png .svg .xls )	
		- <b>Hybridizations</b> : ( .xls )	



# Исследование функциональных характеристик генома

## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы



### MAGE-TAB

Example 1 - Simple Iterated Design

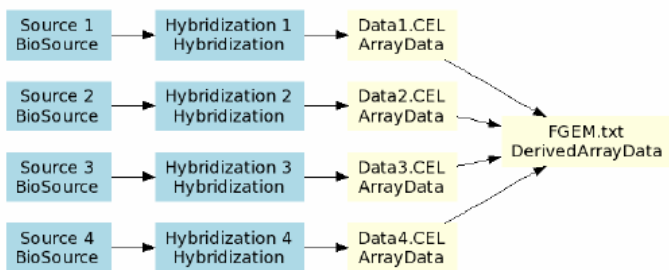


Figure 2.1a: Simple iterated design.

For extremely simple applications such as the example above, a table may be as simple as the following example, in which the protocol referenced by the identifier P-XMPL-10 should include all the processing needed to get from the source sample to the final hybridization:

Source ID	Protocol REF	Hybridization ID	ArrayData URI	DerivedArrayData URI
Source 1	P-XMPL-10	Hybridization 1	Data1.CEL	FGEM.txt
Source 2	P-XMPL-10	Hybridization 2	Data2.CEL	FGEM.txt
Source 3	P-XMPL-10	Hybridization 3	Data3.CEL	FGEM.txt
Source 4	P-XMPL-10	Hybridization 4	Data4.CEL	FGEM.txt

Example 3 - Iterated Design dual channel

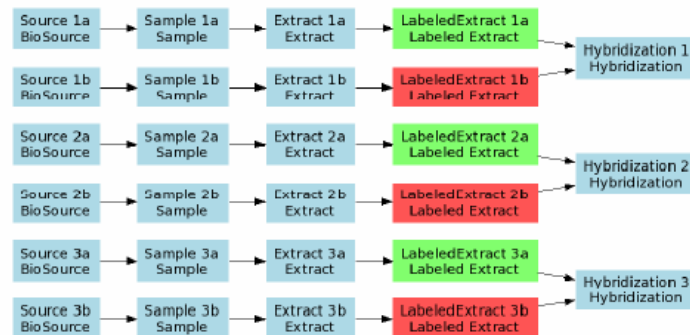


Figure 2.3: Iterated design, dual channel

Source ID	Sample ID	Extract ID	LabeledExtract ID	Label	Hybridization ID
Source 1a	Sample 1a	Extract 1a	LabeledExtract 1a	Cy3	Hybridization 1
Source 1b	Sample 1b	Extract 1b	LabeledExtract 1b	Cy5	Hybridization 1
Source 2a	Sample 2a	Extract 2a	LabeledExtract 2a	Cy3	Hybridization 2
Source 2b	Sample 2b	Extract 2b	LabeledExtract 2b	Cy5	Hybridization 2
Source 3a	Sample 3a	Extract 3a	LabeledExtract 3a	Cy3	Hybridization 3
Source 3b	Sample 3b	Extract 3b	LabeledExtract 3b	Cy5	Hybridization 3



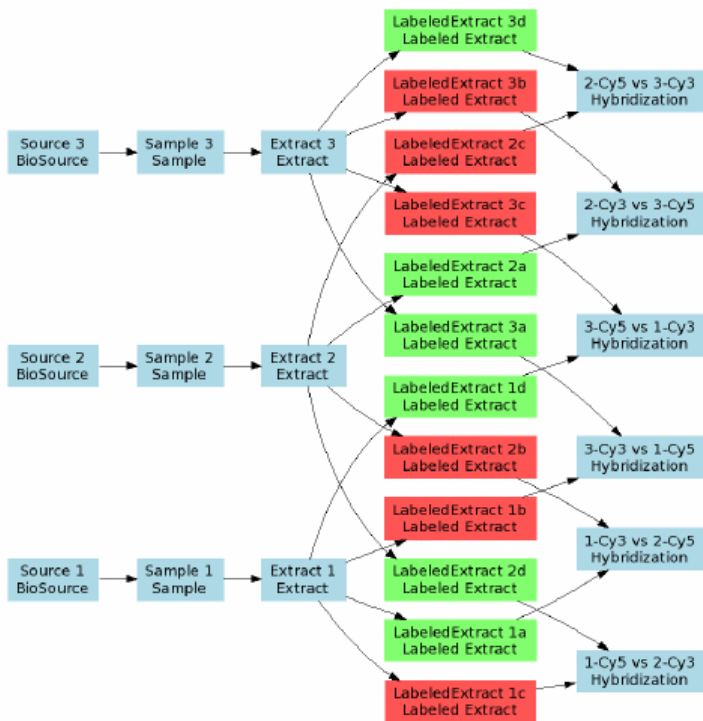
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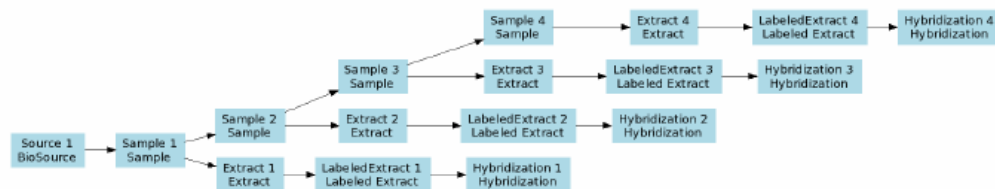


### MAGE-TAB

Example 9. Loop Design with dye swap



Example 10. Complex Time Series







# Исследование функциональных характеристик генома

## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы



**E-AFMX-5** Transcription profiling of human cell lines and tissues (Novartis/GNF) Experiment ranks

Experiment Annotation *Experimental Factors:* organism part, cell type ; *Experiment Type:* organism part comparison design 0.3% 67.18% 77.62%

Gene expression thumbnail. Click for a larger graph and sample annotation.

Individual design element ranks

Gene	Design Elt	Factor	Rank
PPARGC1A	219195_at	devstage	67.56%
PPARGC1A	219195_at	sex	20.38%
PPARGC1A	219195_at	organismpart	29.4%
PPARG	208510_s_at	devstage	96.32%
PPARG	208510_s_at	sex	66.85%
PPARGC1A	219195_at	targetcelltype	59.07%
PPARG	208510_s_at	organismpart	3.01%
PPARG	208510_s_at	targetcelltype	0.3%

LEGEND: Pparg Ppargc1b Ppargc1a PPARGC1A PPARG A830037N07Rik PPARGC1B

**E-MEXP-120** Transcription profiling of bone marrow samples of 31 children with acute lymphoblastic leukemia to identify changes in gene expression that are associated with the current risk assignment, irrespective of the genetic subtype Experiment ranks

Experiment Annotation *Experimental Factors:* sex, age, disease state, clinicalinformation, celltype, individual ; *Experiment Type:* disease state design 1.36% 49.05% 89.48%

Gene expression thumbnail. Click for a larger graph and sample annotation.

Individual design element ranks

Gene	Design Elt	Factor	Rank
PPARGC1A	219195_at	clininfo	82.12%
PPARG	208510_s_at	celltype	65.37%
PPARGC1A	219195_at	sex	1.36%
PPARGC1A	219195_at	celltype	42.55%
PPARG	208510_s_at	age	98.56%
PPARG	208510_s_at	clininfo	79.55%
PPARGC1A	219195_at	age	73.55%
PPARG	208510_s_at	sex	65.06%

LEGEND: Pparg Ppargc1b Ppargc1a PPARGC1A PPARG A830037N07Rik PPARGC1B

**E-AFMX-1** Transcription profiling of human, chimp and mouse brain Experiment ranks

Experiment Annotation *Experimental Factors:* organism ; *Experiment Type:* species design 2.42% 75.44% 3.82%

Gene expression thumbnail. Click for a larger graph and sample annotation.

Individual design element ranks

Gene	Design Elt	Factor	Rank ↓
PPARG	37104_at	organism	2.42%
Ppargc1a	102240_at	organism	24.57%
Pparg	97926_s_at	organism	84.36%

LEGEND: Pparg Ppargc1b Ppargc1a PPARGC1A PPARG A830037N07Rik PPARGC1B



# Исследование функциональных характеристик генома


## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы



### SMD Stanford Microarray Database

<b>SMD</b>	<b>Search</b>	<b>Lists</b>	<b>Links</b>	<b>Help</b>
------------	---------------	--------------	--------------	-------------

<b>SMD Login</b>	<b>Recent Publications</b>
User Name: <input type="text"/> Password: <input type="password"/> <input type="button" value="Login"/>	 <a href="#">Gene expression patterns in human placenta. Sood R, et al. (2006) Proc Natl Acad Sci U S A 103(14):5478-83</a>
<b>Public Data</b>	 <a href="#">Regional activation of chromosomal arm 7q with and without gene amplification in taxane-selected human ovarian cancer cell lines. Wang YC, et al. (2006) Genes Chromosomes Cancer 45(4):365-74</a>
<input type="button" value="Public Login"/> ●	 <a href="#">Genome-wide identification of mRNAs associated with the translational regulator PUMILIO in Drosophila melanogaster. Gerber AP, et al. (2006) Proc Natl Acad Sci U S A 103(12):4487-92</a>
<input type="button" value="Publications"/> ●	 <a href="#">Genetic regulators of large-scale transcriptional signatures in cancer Adler AS, et al. (2006) Nat Genet 38, 421 - 430.</a>
<input type="button" value="S.O.U.R.C.E."/> ●	 <a href="#">Mechanism of the anti-inflammatory effect of colchicine in rheumatic diseases: a possible new outlook through microarray analysis. Ben-Chetrit E, et al. (2006) Rheumatology 45(2):274-82</a>
<input type="button" value="Caryoscope"/> ●	



# Исследование функциональных характеристик генома

## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы



### SMD Stanford Microarray Database

## SMD : View Publication

WORLD

<a href="#">SMD</a>	<a href="#">Search</a>	<a href="#">Lists</a>	<a href="#">Links</a>	<a href="#">Help</a>
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*Bergamaschi A, et al. (2006) Genes Chromosomes Cancer 45(11):1033-40*

**Distinct patterns of DNA copy number alteration are associated with different clinicopathological features and gene-expression subtypes of breast cancer.**

Bergamaschi A, Kim YH, Wang P, Sorlie T, Hernandez-Boussard T, Lonning PE, Tibshirani R, Borresen-Dale AL, Pollack JR

Associated Experiment Sets		Options			
Doxo-Fumi array CGH	Logical Set	<a href="#">View</a>	<input type="button" value="Display Data"/> <input type="button" value="Data Retrieval and Analysis"/>	<a href="#">Meta Data</a> <a href="#">Data</a>	<input type="button" value="Raw Data"/> (672.12 Mbytes)
Doxo-Fumi expression	Logical Set	<a href="#">View</a>	<input type="button" value="Display Data"/> <input type="button" value="Data Retrieval and Analysis"/>	<a href="#">Meta Data</a> <a href="#">Data</a>	<input type="button" value="Raw Data"/> (320.94 Mbytes)



# Исследование функциональных характеристик генома

## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы




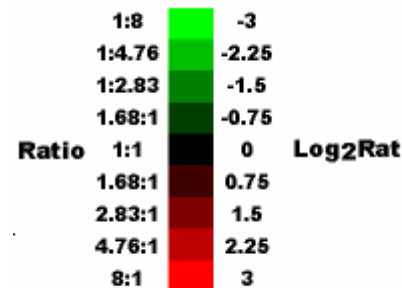
### SMD: SOURCE: генные профили

S.O.U.R.C.E.  
Search

View Clones  
for this Gene

Help

 <b>SOURCE</b> GeneReport <i>M. musculus</i>		Pparg	
<b>Peroxisome proliferator activated receptor gamma</b> <a href="#">UniGene</a> , <a href="#">LocusLink</a>			
<b>Aliases</b>			
<ul style="list-style-type: none"> <li>Nr1c3; Ppar-gamma2</li> </ul>			
<b>Chromosomal Location</b>			
<b>Chromosome/Cytoband</b>		6 E3-F1 6 52.7 cM	
<b>Microarray Gene Expression Data</b>			
<b>Data available</b>		<a href="#">Show Gene Expression Data</a>	



Pparg [Peroxisome proliferator](#)

trigeminal  
 trigeminal  
 DRG  
 DRG  
 spinal\_cord\_lower  
 spinal\_cord\_upper  
 spinal\_cord\_upper  
 spinal\_cord\_lower  
 olfactory\_bulb  
 hypothalamus  
 hypothalamus  
 frontal\_cortex  
 hippocampus  
 hippocampus  
 hippocampus  
 amygdala  
 frontal\_cortex  
 amygdala  
 striatum  
 striatum  
 cortex  
 cortex  
 cerebellum  
 cerebellum  
 eye  
 eye  
 testis  
 testis  
 skeletal\_muscle  
 skeletal\_muscle  
 heart  
 heart  
 brown\_fat  
 brown\_fat  
 adrenal\_gland  
 adrenal\_gland  
 mammary\_gland  
 mammary\_gland  
 prostate  
 prostate  
 thyroid  
 thyroid  
 salivary\_gland  
 salivary\_gland  
 liver  
 liver  
 gall\_bladder  
 gall\_bladder  
 kidney  
 kidney  
 kidney  
 kidney  
 large\_intestine  
 large\_intestine  
 large\_intestine  
 small\_intestine  
 small\_intestine  
 stomach  
 stomach  
 stomach  
 lung  
 lung  
 lung  
 adipose\_tissue  
 adipose\_tissue  
 adipose\_tissue  
 trachea  
 trachea  
 thymus  
 thymus  
 thymus  
 lymph\_node  
 lymph\_node  
 lymph\_node  
 spleen  
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 spleen  
 bone\_narrow  
 bone\_narrow  
 bone  
 bone  
 bone  
 tongue  
 tongue  
 tongue  
 epidermis  
 epidermis  
 epidermis  
 snout\_epidermis  
 snout\_epidermis  
 snout\_epidermis  
 digits  
 digits  
 digits  
 ovary  
 ovary  
 bladder  
 bladder  
 bladder  
 uterus  
 uterus  
 uterus  
 umbilical\_cord  
 umbilical\_cord  
 umbilical\_cord  
 placenta  
 placenta  
 placenta







# Исследование функциональных характеристик генома

## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы



















### SMD:

Анализ качества данных, выявление достоверной дифференциальной разницы в экспрессии генов, картирование на хромосомы

-  = View and Sort Array Data
-  = Download Raw Data
-  = Download Original Data Files
-  = View Array Details
-  = View Array Image and Grids
-  = Clickable Image
-  = Plot Array Data
-  = Align Data to Chromosomes

Your query returned **89** result sets.

Re-sort by:

ExptID	Experiment	Category	Subcategory	SlideName	Result Set	Options	Experimenter	Exp
38940	shdi204 BC/FUMI01-BE	<a href="#">Breast</a>	<a href="#">aCGH tumor tissue</a>	shdi204	default	       	<a href="#">YHKIM</a>	2002
38941	shdi205 BC/FUMI02-BE	<a href="#">Breast</a>	<a href="#">aCGH tumor tissue</a>	shdi205	default	       	<a href="#">YHKIM</a>	2002



# Исследование функциональных характеристик генома

## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы

### Пакеты программ для обработки и анализа биочип-



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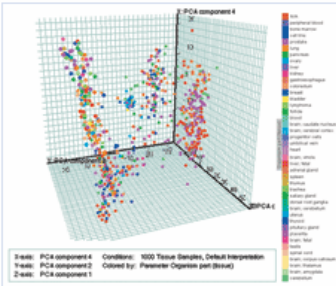
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#### GeneSpring GX



#### Bring your expression data to life

GeneSpring GX is a powerful visualization and analysis solution designed for use with expression data. Regarded as the gold standard in desktop expression analysis, GeneSpring GX allows researchers to identify targets quickly and reliably. By providing statistically meaningful results, GeneSpring GX enables prediction of clinical outcomes and characterization of novel expression patterns. GeneSpring GX is part of an integrated analysis suite that enables visual and analytical comparisons between expression, genotyping, protein, metabolite, and other data types to answer complex biological questions.

<http://www.chem.agilent.com/scripts/pd.s.asp?lpage=27881>

<http://www.bioconductor.org/>

**BIOCONDUCTOR**  
open source software for bioinformatics

Bioconductor is an open source and open development software project for the analysis and comprehension of genomic data.

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**project news**

- ▶ [2006-12-07](#)  
Changes in BioC Devel, November 2006
- ▶ [2006-10-11](#)  
Changes in BioC Devel, October 2006

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**QUICK LINKS**

- ▶ [What is it?](#)

**BioC Release 1.9**

Bioconductor 1.9 was released 4 October, 2006. This release is designed for R 2.4.0. View the packages [here](#).



# Исследование функциональных характеристик генома

## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы

# Пакеты программ для обработки и анализа биочип-данных

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Software > Acuity

### Software

- Microplate Data**
  - SoftMax Pro
  - Softmax Pro Validation Package
- High-Content Imaging**
  - MetaXpress
  - AcuityXpress
- Research Imaging**
  - MetaMorph
  - MetaFluor
  - MetaVue
- Microarray Data**
  - Acuity
  - GenePix Pro
- Electrophysiology Data**

### Acuity 4.0 Enterprise Microarray Informatics

#### Why Upgrade To Acuity 4.0?

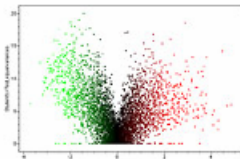
In developing Acuity® 4.0 we have concentrated on cross-platform support, data warehousing, and new enabling analysis and visualization tools:

#### Cross-platform Functionality

- Acuity now supports Oracle as well Microsoft SQL Server databases.
- Full import of Affymetrix CEL, CHP, CDF and DAT files, of all versions.
- Robust Multichip Analysis (RMA) of Affymetrix probe-level data, using quantile or cyclic loess normalization, and summarization by robust linear models or median polish.

#### Data Warehousing

Click on thumbnails below



A volcano plot is a scatter plot of  $-\log(p\text{-value})$  from a t-test or one-way ANOVA, versus log ratio. It allows you to visualize fold-change and statistical significance at the same time, so that one can find genes that are significant and have large fold change, or genes that are significant but have small fold change.

### Acuity

- Literature & Downloads
- Acuity FAQ

### Acuity Support

- Acuity Support

### GenePix Scanners

- GenePix Autoloader 4200AL
- GenePix Professional 4200A
- GenePix 4000B
- GenePix Personal 4100A

[http://www.moleculardevices.com/pages/software/gn\\_acuity.html](http://www.moleculardevices.com/pages/software/gn_acuity.html)



# Исследование функциональных характеристик генома

## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы



## Интернет-ресурсы для обработки и анализа биочип-данных



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### GETTING STARTED

→ Wizard

### QUERY

#### Exon Array

→ Quick Query

Standard Query

→ Probesets

→ Exon Clusters

→ Transcript

Clusters

Batch Query

→ Probesets

→ Exon Clusters

→ Transcript

Clusters

→ Probe Match

#### Expression

→ Quick Query

→ Standard Query

→ Batch Query

→ BLAST

→ Probe Match

→ UCSC Query

#### Genotyping

→ Quick Query

→ Standard Query



### QUERY

#### Getting Started

#### Exon Array

- Search all available information in the database for a particular term or identifier.
- Search for *Probesets* using specific fields in the database for a term or identifier [Standard Query]
- Search for *Exon Clusters* using specific fields in the database for a term or identifier [Standard Query]
- Search for *Transcript Clusters* using specific fields in the database for a term or identifier [Standard Query]
- Retrieve annotations for a probe list [Batch Query]
- Find probes that identically match your sequence(s) [Probe Match]

#### Expression

- Search all available information in the database for a particular term or identifier. This is recommended as a starting point for your searches. [Quick Query]
- Search specific fields in the database for a term or identifier [Standard Query]
- Retrieve annotations for a probe list [Batch Query]

<https://www.affymetrix.com/analysis/netaffx/index.affx>





# Исследование функциональных характеристик генома

## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы



## Интернет-ресурсы для обработки и анализа биочип-данных

The screenshot shows the GeneSifter Data Center website. At the top, there is a navigation bar with 'Home', 'Data Center', and 'Company' links. Below this is a large banner with the GeneSifter logo and the tagline 'Understand the Biology.' The main content area is titled 'Data Center' and features a search bar with the text 'data center'. On the left side, there is a vertical menu with categories: Cardiovascular, Cancer, Immunology, Neuroscience, Endocrinology, Oral Biology, and Hematology. The main text area contains the following information:

### The GeneSifter Data Center

The GeneSifter Data Center provides the research community access to microarray datasets from various fields through the GeneSifter microarray data analysis system. The Data Center includes selected public datasets as well as datasets submitted by current GeneSifter customers.

**Training Resource** Whether you have run the microarrays and have started analyzing the data or you are getting ready to run the experiments or even if you just want to learn more about this powerful, but sometimes intimidating technology, the Data Center can help you develop your analysis skills. GeneSifter provides an accessible set of microarray analysis tools to explore these datasets. Tutorials are provided that will assist in reproducing published results, serve as a guide in looking for noteworthy results and prepare you to examine the data on your own.

<http://www.genesifter.net/web/dataCenter.html>



# Исследование функциональных характеристик генома

## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы



## Интернет-ресурсы для обработки и анализа биочип-данных

### Microarray

Here i will provide the information and links I used during my research. Please [give your comments/s](#)

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[Microarray slide \(pre-spotted\)](#)

[Accessories](#)

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[Alternative array technologies](#)

[Software](#)

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[Protocols](#)

[Trouble Shooting](#)

[Protein Chip/ SELDI-TOF-MS](#)

[Tissue Microarray \(TMA\)](#)

[Hardware](#)

[Software](#)

[TMA slides \(pre-made\)](#)

[Biochip/ Lab-on-a-chip/ Micro Total Analysis System \(uTAS\)](#)

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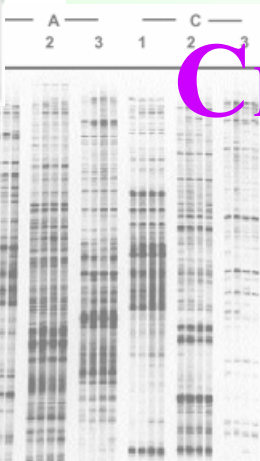
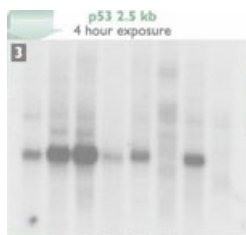
[Other microarray portals](#)

<http://ihome.cuhk.edu.hk/~b400559/array.html>



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## Исследование качественных и количественных характеристик транскриптома: ДНК-биочипы



Спасибо за внимание

