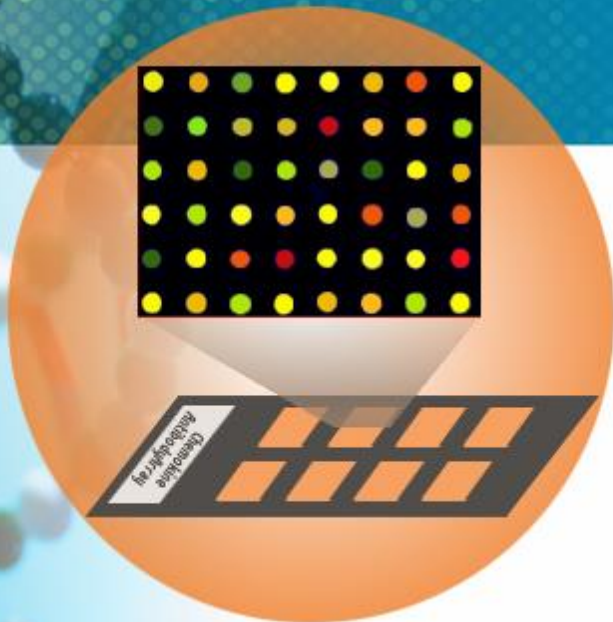


Microarray 기초 및 분석

(주)이바이오젠



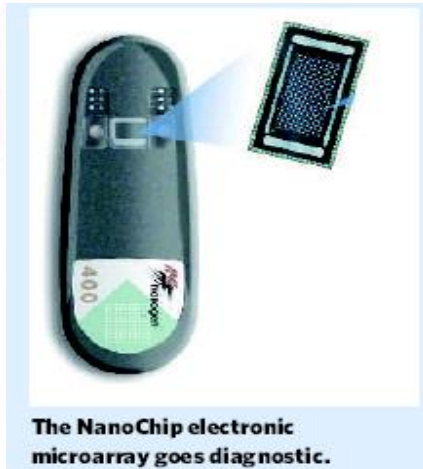
목 차

- 마이크로어레이 기초
 - 정의 / 분류 / 제작기술 / 원리
- Gene Expression 실험분석
 - 시료준비
 - RNA QC
 - 실험분석 과정
 - 데이터분석

바이오칩 & 마이크로어레이 - 정의



Flexibility at low density in CombiMatrix's 4 × 2K CustomArrays.



The NanoChip electronic microarray goes diagnostic.

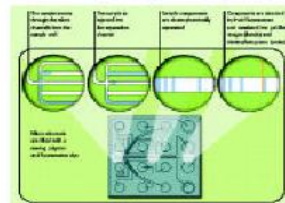
1. 유리, 실리콘, 플라스틱 등의 매체 위에 생체 분자를 집적하여 만든 것
2. 현재 DNA, 단백질, 화학물질, 유기물질 등 바이오 소재를 집적하여 만든 Microarray를 총칭하여 바이오 칩이라 함
3. 유전자 및 단백질 발현연구, 바이오마커 발굴, 진단제품, 바이오센서, 신약개발, 독성물질분석, 환경모니터링, 식품위해성평가 등 광범위하게 응용 할수 있음.



Affymetrix



Nanogen



Caliper

4. BioChip = BT + NT + IT

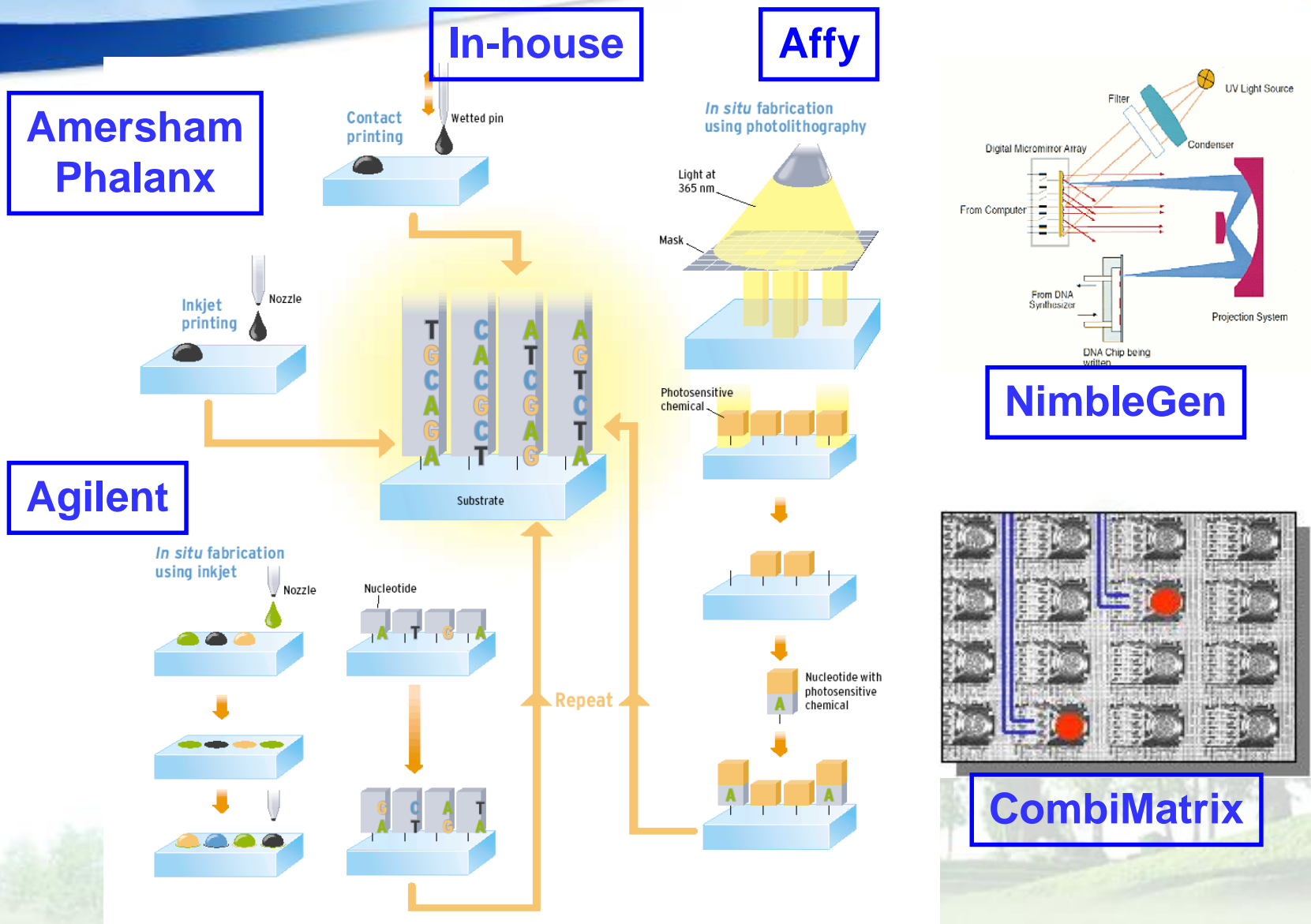
바이오칩 - 분류

| 분류 | 명칭 | 특징 |
|------|-----------------|--|
| 제조형태 | 마이크로어레이 칩 | 수천 혹은 수만 개 이상의 생체물질을 고체기질에 일정한 간격으로 배열. |
| | 마이크로프루딕스 칩 | 마이크로 크기의 3차원 채널을 가공해서 생체물질을 흘러주면서 반응을 봄. |
| 탐지물질 | DNA 마이크로어레이 | 고체기질에 많은 종류의 DNA를 일정하게 배열. |
| | Protein 마이크로어레이 | 고체기질에 많은 종류의 Protein를 일정하게 배열. |
| | Tissue 마이크로어레이 | 고체기질에 많은 종류의 Tissue를 일정하게 배열. |
| | Lab-on-a-chip | 마이크로어레이 칩과 마이크로프루딕스 칩이 혼합되어 일련의 실험과정을 칩상에서 구현. |
| 응용분야 | 연구용 바이오칩 | 바이오 마커발굴 및 질병의 메커니즘을 찾아 질병진단제 개발 및 신약개발에 응용. |
| | 질병진단용 바이오칩 | 자궁경부암 진단용 및 백혈병, 당뇨병, 각종 암 등의 다양한 질병을 진단하는 목적. |
| | 생체삽입용 바이오칩 | 생체내에 마이크로 바이오칩(바이오센서)를 삽입하여 각종 생체내 반응을 모니터링 함. |

DNA 마이크로어레이 - 분류

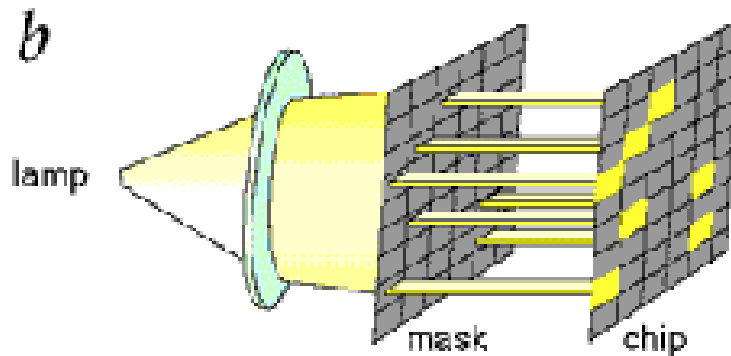
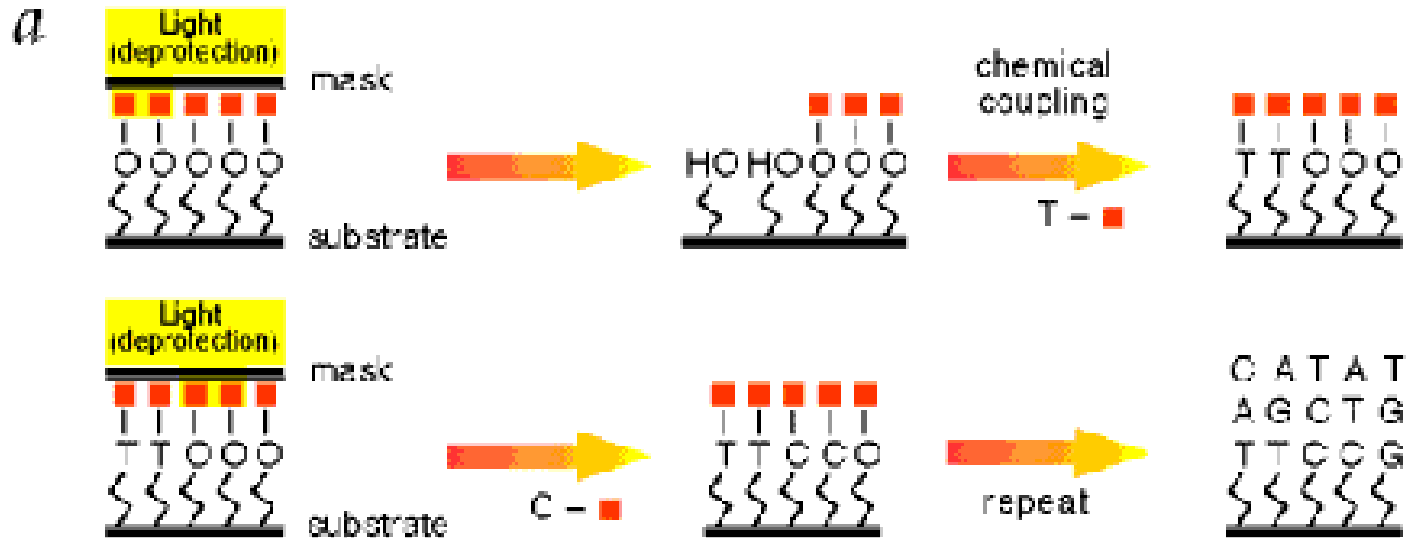
| | cDNA | Short oligo | Long oligo |
|--------------------------------|--|---|-------------------------|
| System | Closed = Out-dated probe | | |
| Probe | cDNA (≥ 200 bp) | Oligo (20~30mer) | Oligo (60~70mer) |
| Probe source | PCR products | Synthesis | |
| Sensitivity | Highest | Same as left or less | |
| Specificity | Low | High? | |
| Chip making | Spotting or inkjet | <i>In situ</i>, spotting or inkjet | |
| Reliability | Less | More? | |
| Detect splicing variant | Not | OK? | |
| Application | Expression Profile, CGH | Expression profile, Genotyping, SNP, Resequencing, CGH, ChIP | |

DNA 마이크로어레이 - 제작기술



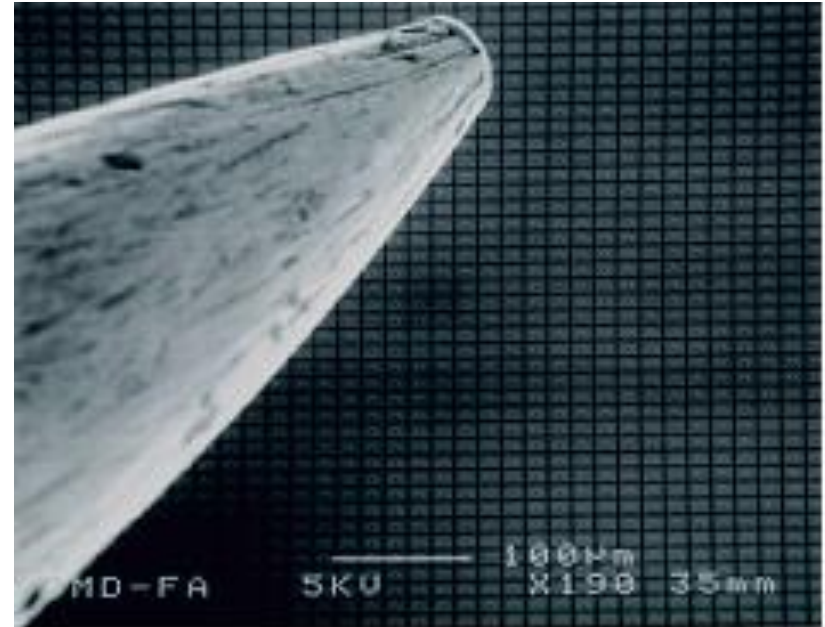
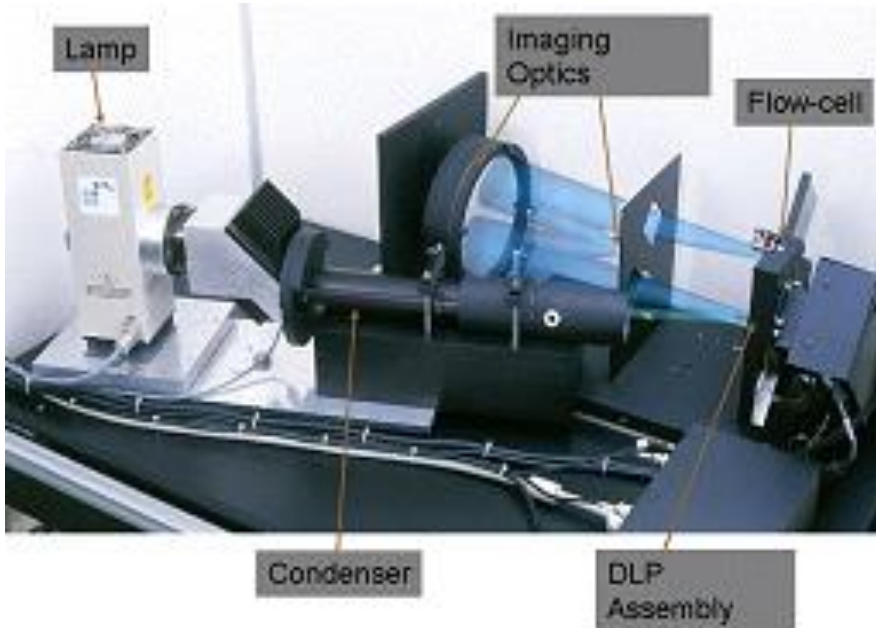
DNA 마이크로어레이 - 제작기술

Affymetrix : photolithography



DNA 마이크로어레이 - 제작기술

Nimblegen : photolithography using MAS tech



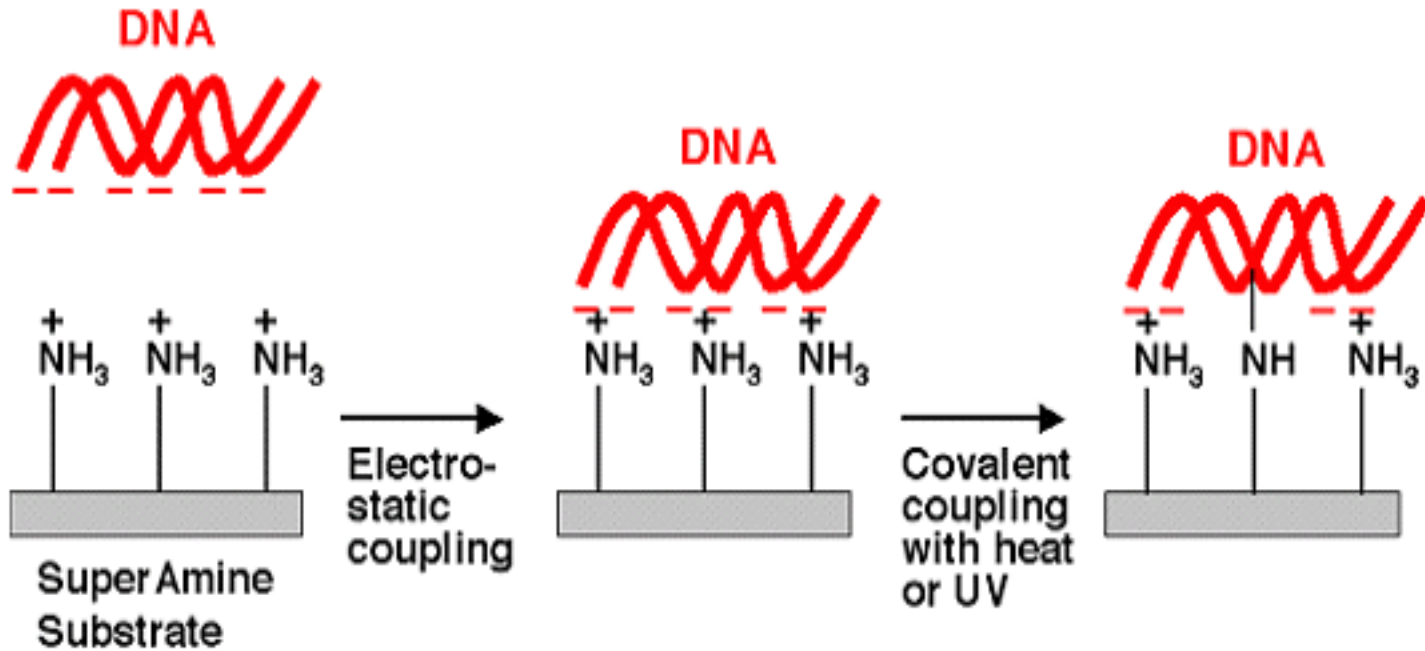
DNA 마이크로어레이 - 제작기술

cDNA microarray 제작 과정



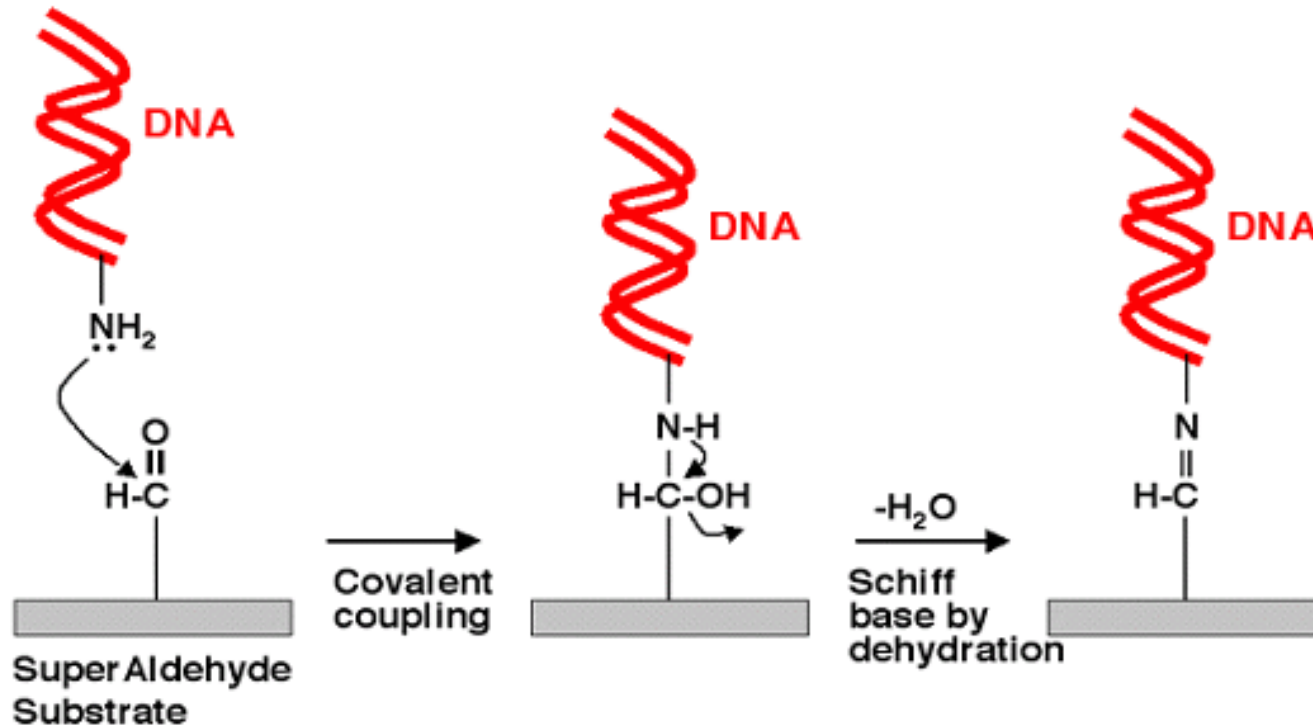
DNA 마이크로어레이 - 제작기술

Glass slide type : Amine coated slide



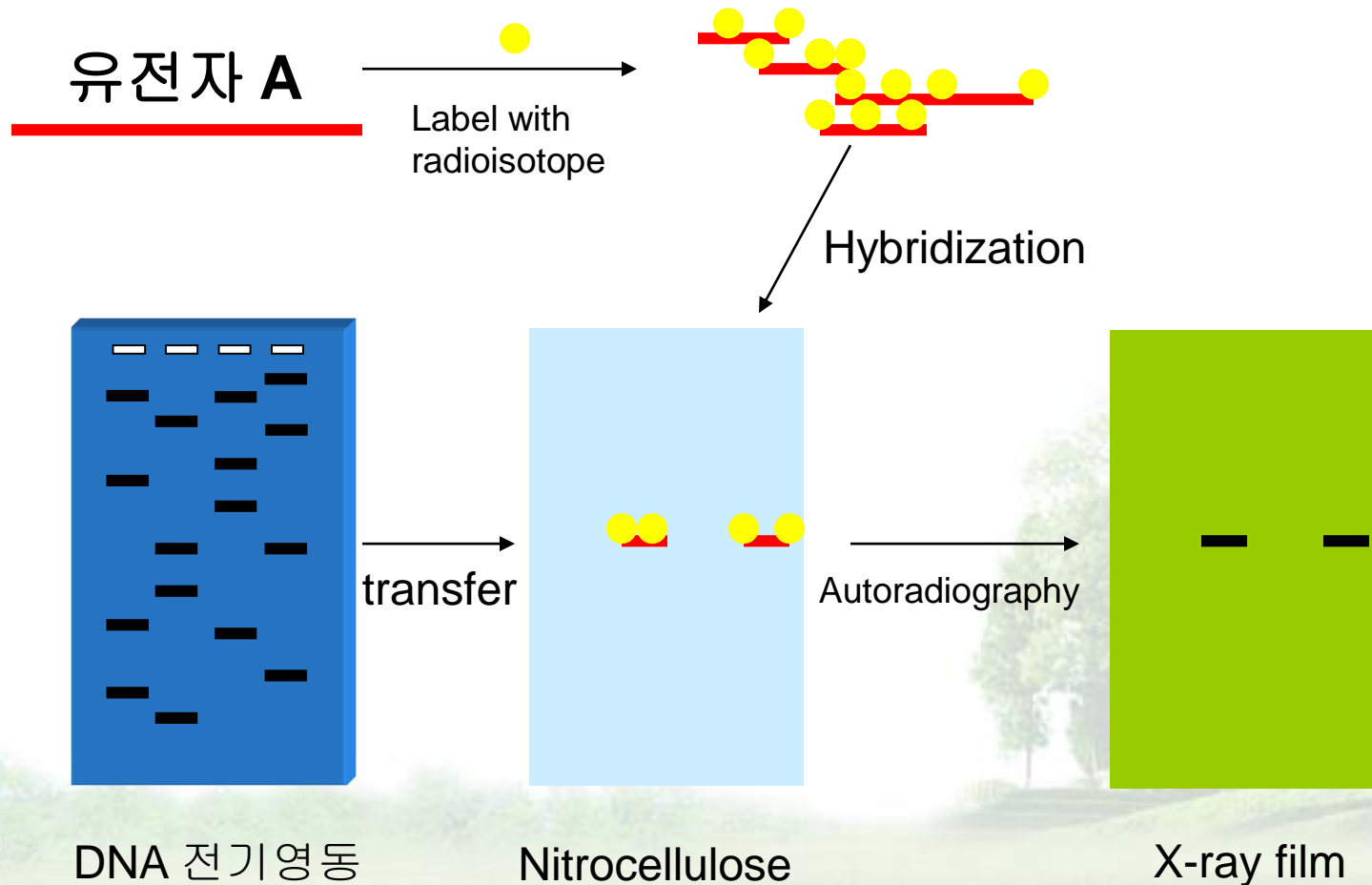
DNA 마이크로어레이 - 제작기술

Glass slide type : Aldehyde coated slide



DNA 마이크로어레이 - 원리

Southern Hybridization (Southern Blot):
Detection of specific sequences among DNA fragments separated by gel electrophoresis. J. Mol. Biol. (1975)



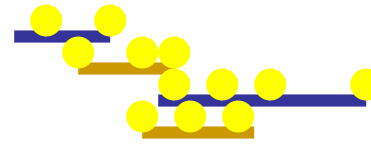
DNA 마이크로어레이 - 원리

Reverse Hybridization Assay Similar to DNA Chip

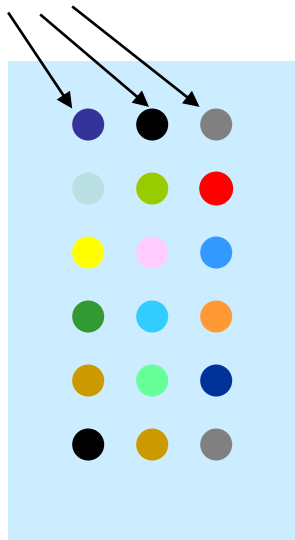
Mixture of different mRNA
(total cellular RNA from sample A)



Label with radioisotope

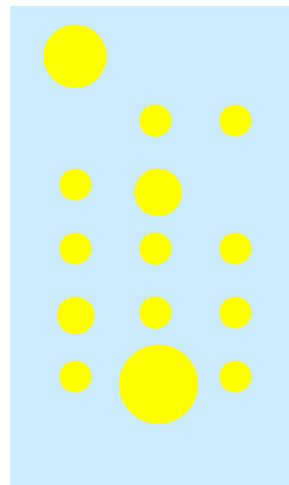


다른 종류의 DNA or genes



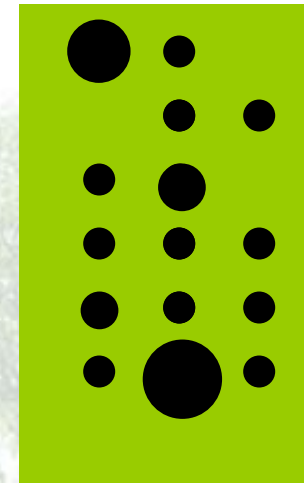
Nitrocellulose Membrane

Hybridization



Nitrocellulose

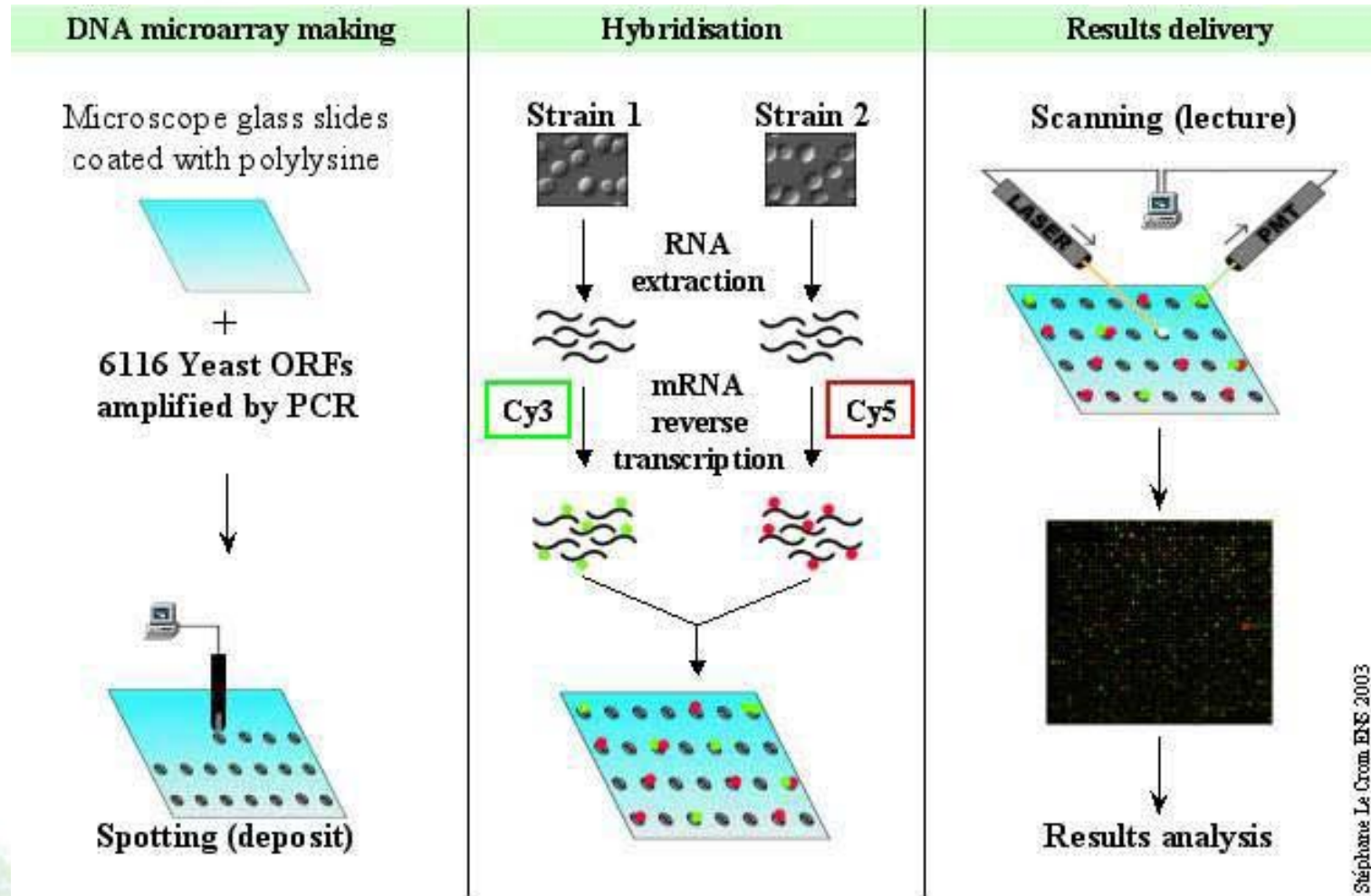
Autoradiography



X-ray film (Autoradiogram)

DNA 마이크로어레이 - 원리

High-Throughput Screening using DNA Chip



Stéphane Le Crom, ENS 2003

DNA 마이크로어레이 - 원리

High-Throughput Screening using DNA Chip

DNA microarray making

Microscope glass slides coated with polylysine

Hybridisation

Strain 1

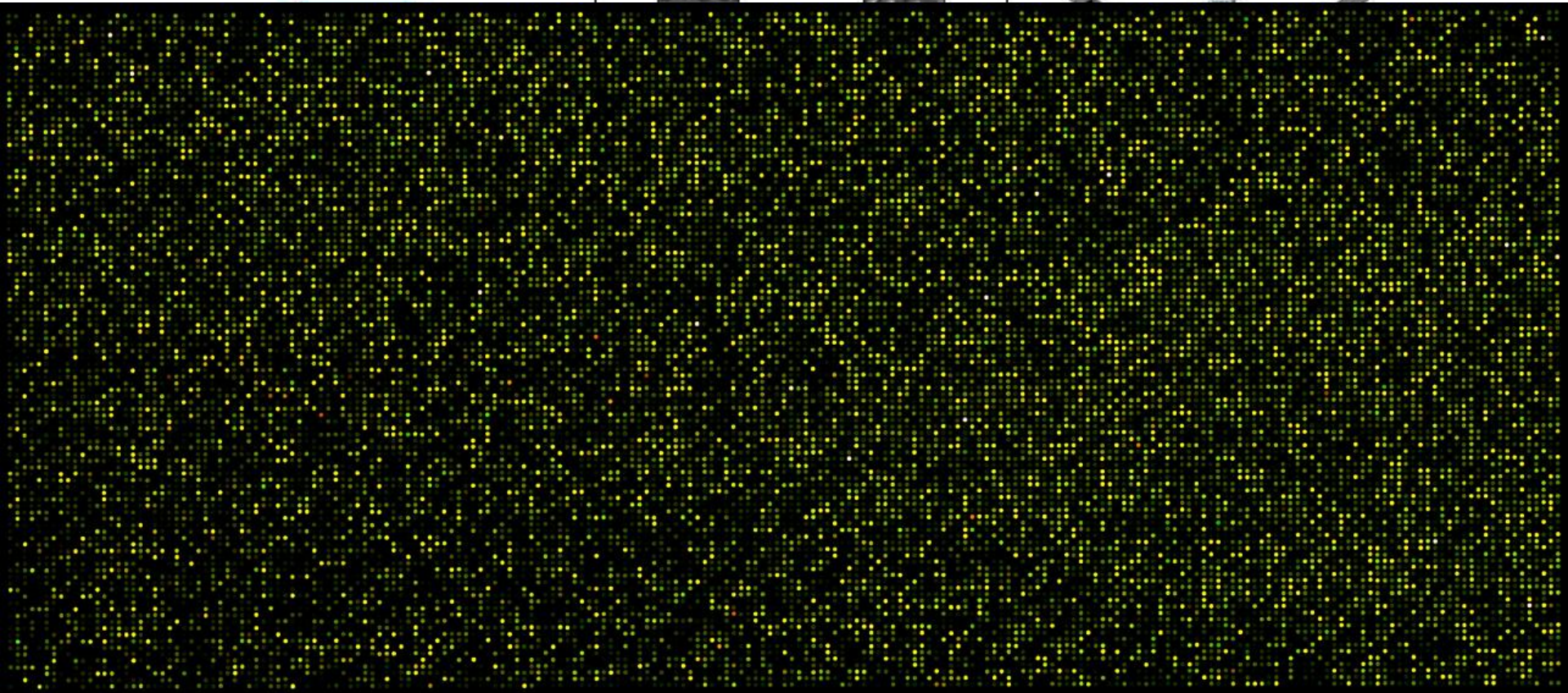
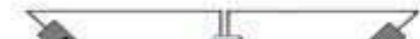


Strain 2



Results delivery

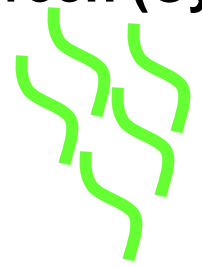
Scanning (lecture)



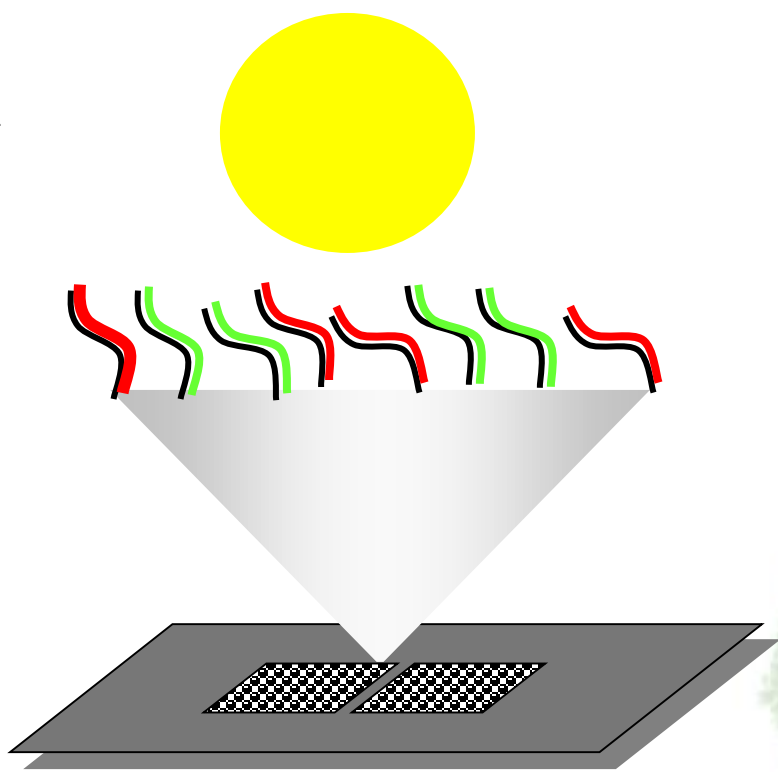
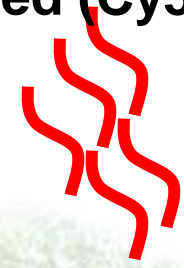
DNA 마이크로어레이 - 원리

Microarray : Competitive Hybridization (I)

Reference RNA
- Green (Cy3)



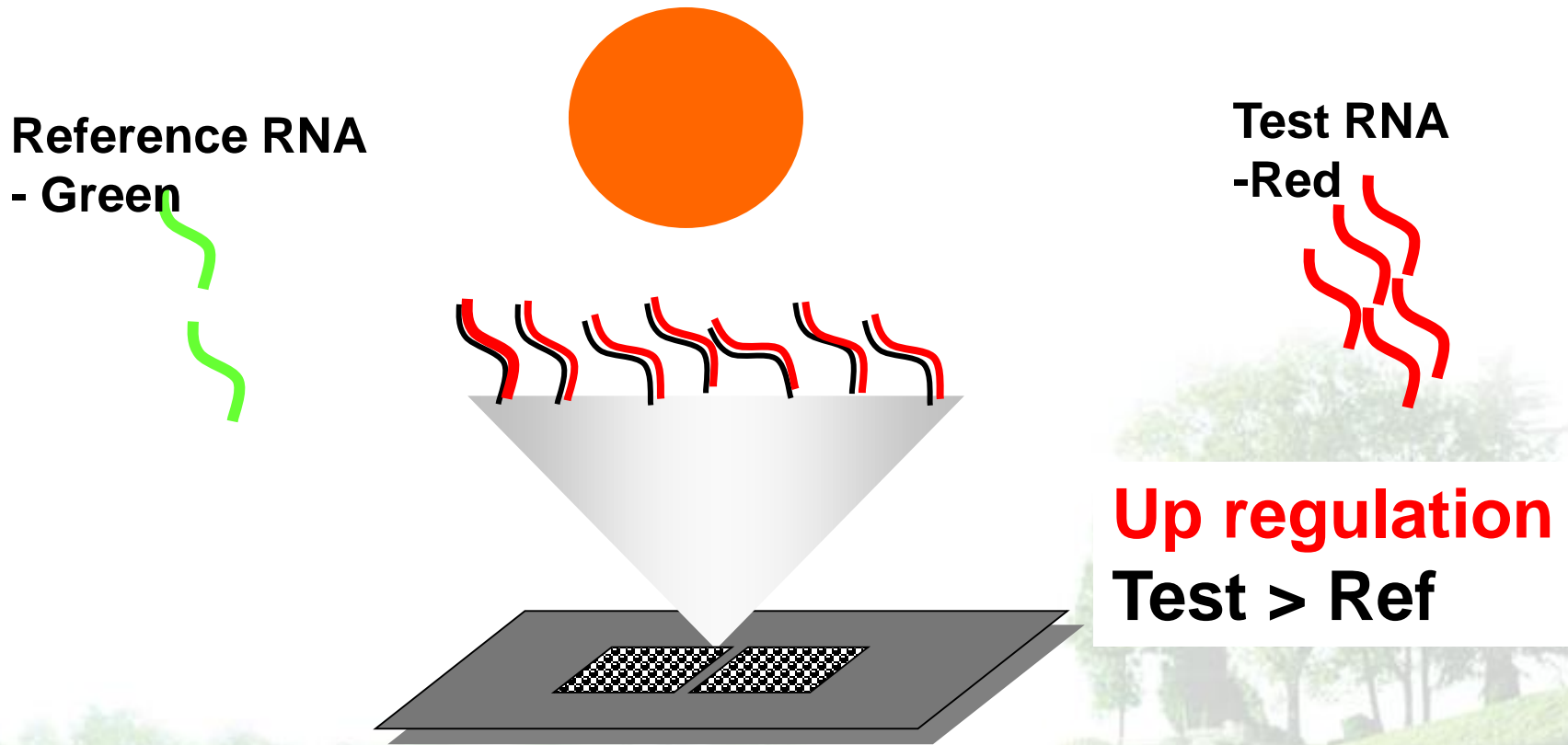
Test RNA
- Red (Cy5)



No Change
Test = Ref

DNA 마이크로어레이 - 원리

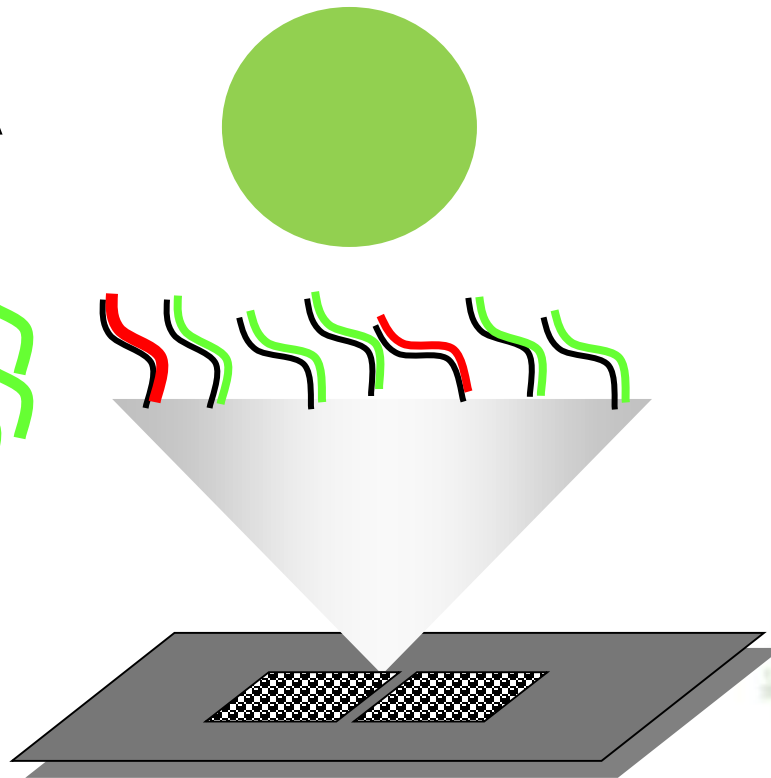
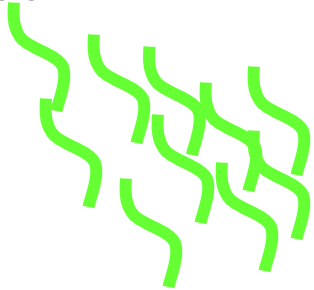
Microarray : Competitive Hybridization (II)



DNA 마이크로어레이 - 원리

Microarray : Competitive Hybridization (III)

Reference RNA
- Green

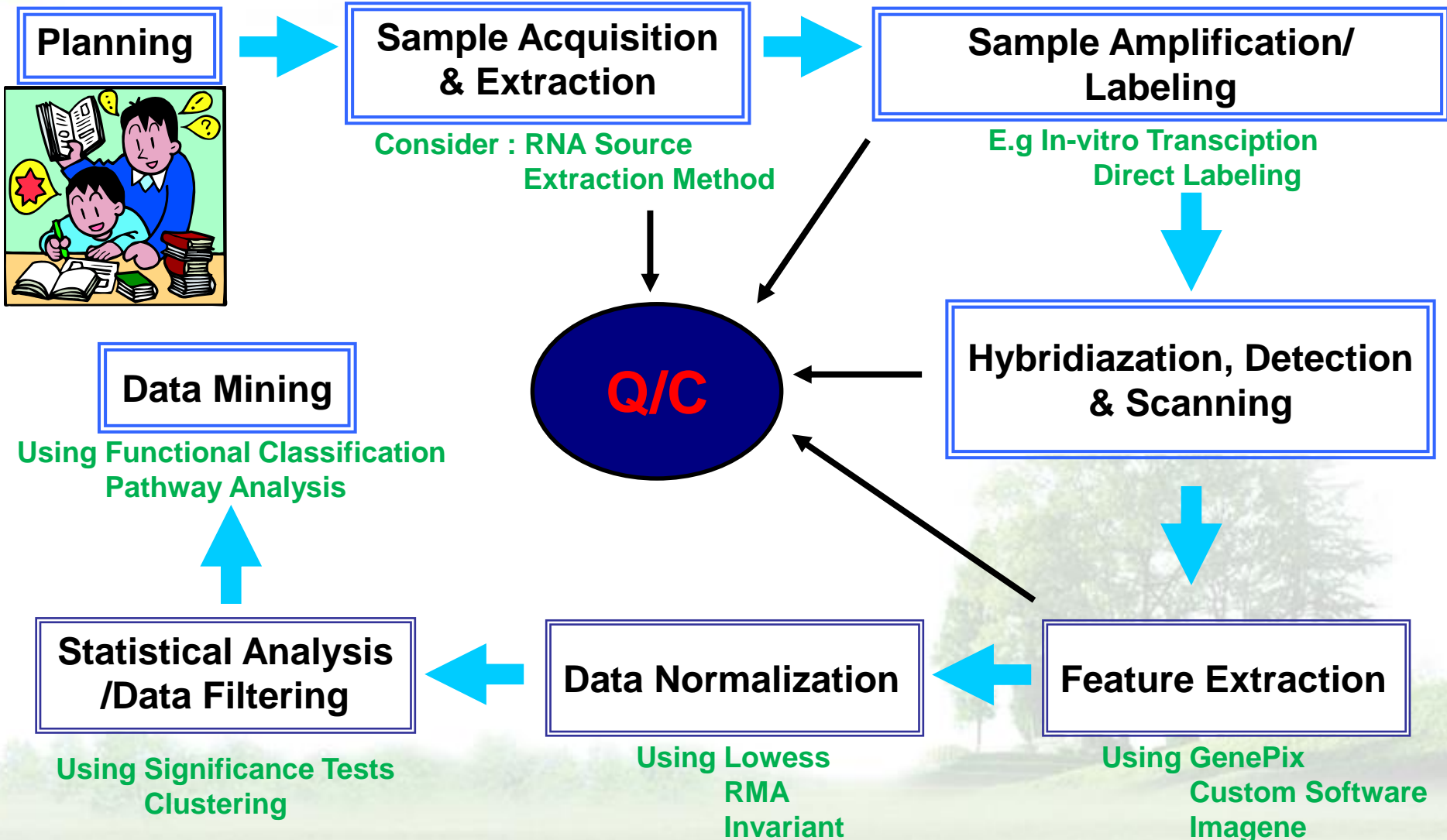


Test RNA
-Red



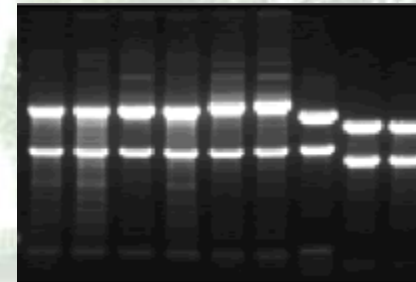
Down regulation
Test < Ref

Microarray Process

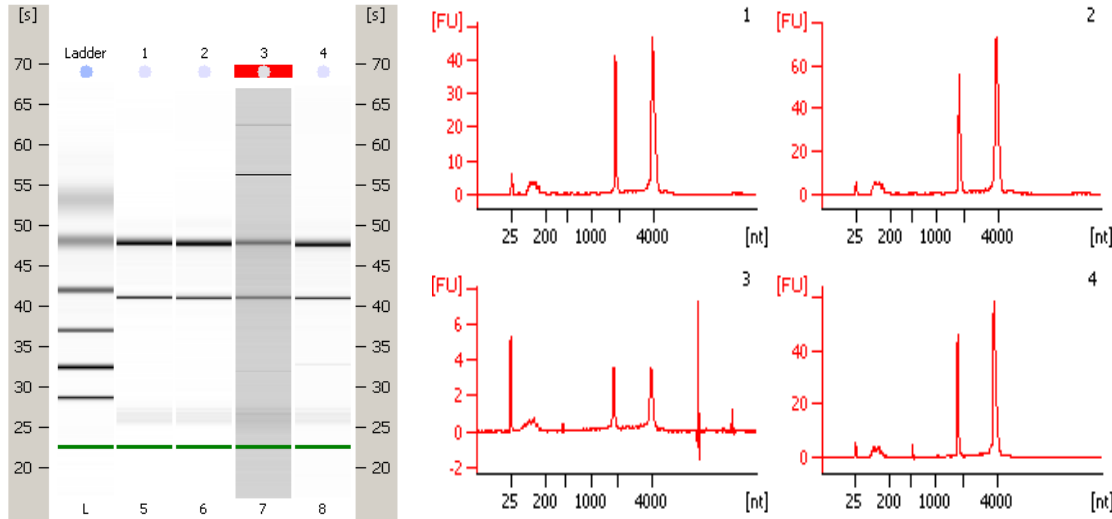


Gene Expression- 시료준비

- Total RNA : ~ 5 μ g
- TriZol 이용 시 예상되는 RNA양 (tissue 1mg, cultured cell 1*10⁶당)
 - Liver and spleen, 6-10 μ g
 - Kidney, 3-4 μ g
 - Skeletal muscles and brain, 1-1.5 μ g
 - Placenta, 1-4 μ g
 - Epithelial cells (1 \times 10⁶ cultured cells), 8-15 μ g
 - Fibroblasts, (1 \times 10⁶ cultured cells) 5-7 μ g
- RNA 분리
 - RNA 분리는 InVitrogen사에서 제공하는 TriZol 시약의 표준 방법으로 수행
 - 분리된 RNA는 RNase free water나 DEPC DW에 녹여 보관
- RNA QC
 - Spectrophotometry : OD260/OD280값
 - Denaturing agarose gel electrophoresis
 - RNA의 양 및 농도
- RNA Delivery : Dry ice packing

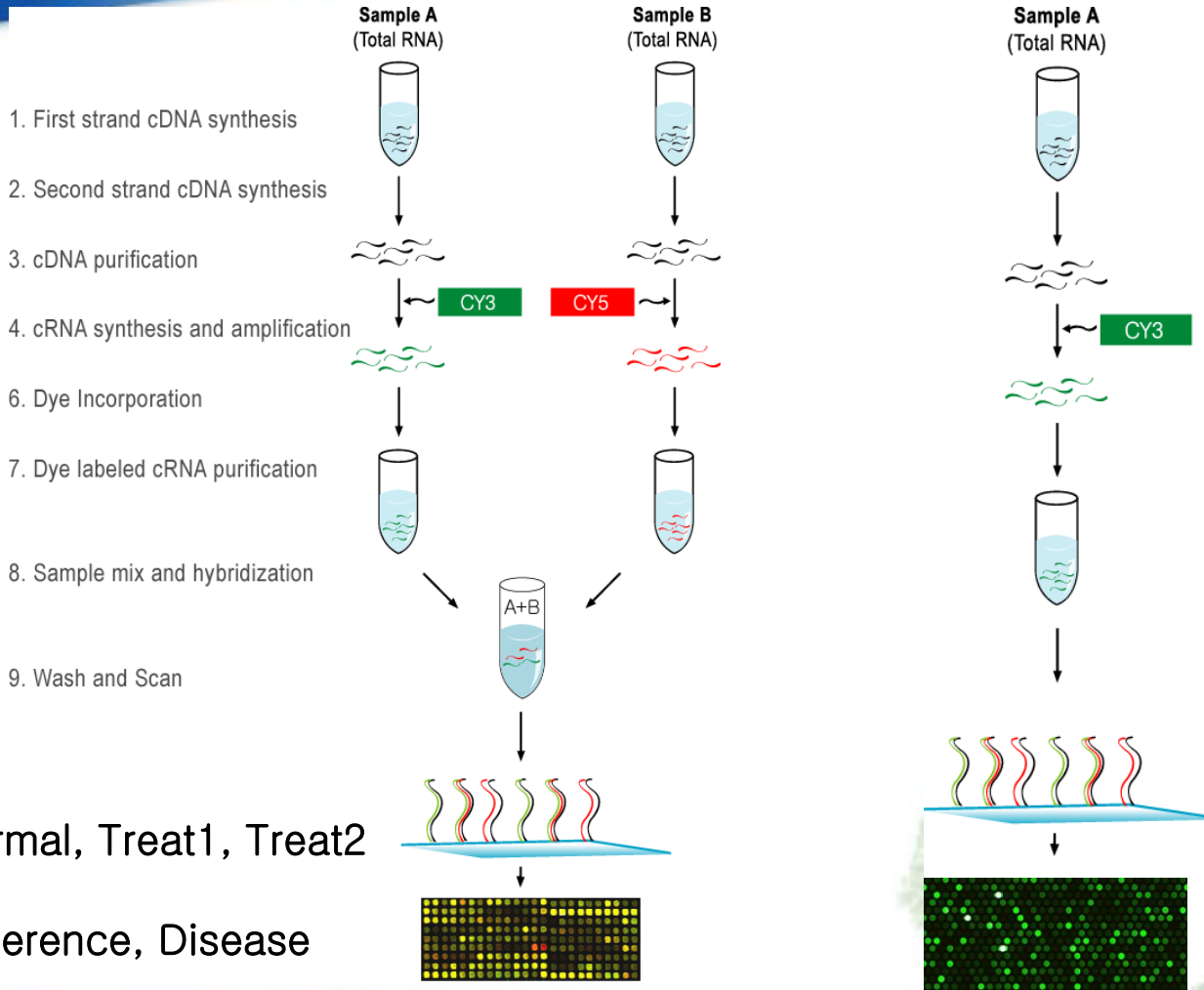


Gene Expression- RNA QC



| Sample | ug/ul | 260/230 | Total (ug) | Ratio(28s/18s) | RIN |
|--------|--------|---------|------------|----------------|------|
| 1 | 1.7616 | 1.86 | 44.040 | 2.1 | 10.0 |
| 2 | 2.1745 | 1.99 | 43.490 | 2.2 | 10.0 |
| 3 | 0.1870 | 1.24 | 3.740 | 1.5 | N/A |
| 4 | 2.0139 | 1.81 | 56.3892 | 2.3 | 10.0 |

Gene Expression- 실험과정



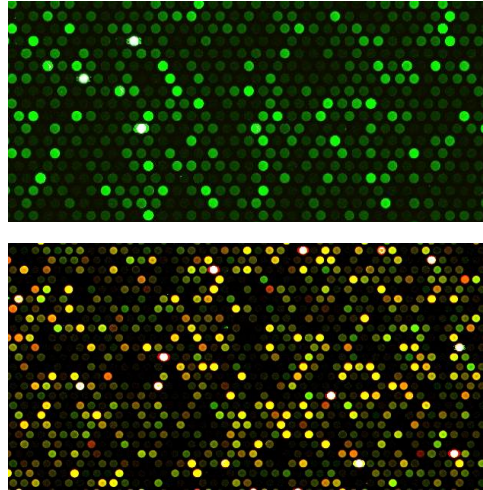
Case 1 : Normal, Treat1, Treat2

Case 2 : Reference, Disease

Case 3 : 그룹A (control, test1, tetst2, ...)
 그룹B(control, test1, tetst2, ...)

Gene Expression- Data Featuring

<Scanning>



<Quantification>

| | A | B | C | D | E | F | G | H |
|----|---------------|--------------|--------------|--------------|-----------|---------------------------------------|-------------|-----------|
| 3 | File Name (*) | Con vs pio 5 | Con vs pio 6 | Con vs pio 9 | Genbank | Description | GO biologic | GO molecu |
| 4 | Systematic | Normalized | Normalized | Normalized | | | | |
| 5 | A_51_P454913 | 0.776195 | 0.8092215 | 0.9232904 | AK085143 | Mus musculus 13 days embryo lung | | |
| 6 | A_52_P311491 | 0.5511575 | 0.6368426 | 0.56348026 | AK077387 | Mus musculus GO:000191; GO:001991 | | |
| 7 | A_51_P323531 | 0.9706048 | 1.05593 | 1.5188317 | AK006229 | Mus musculus adult male testis cDNA | | |
| 8 | A_51_P183025 | 0.87164724 | 0.97410125 | 1.0382049 | NM_133893 | Mus musculus 2'-5' oligoadenylate | | |
| 9 | A_52_P179250 | 0.68676186 | 0.71581167 | 0.58900946 | AK129129 | Mus musculus mRNA for mRNAA0322 | | |
| 10 | A_52_P370935 | 0.5959569 | 0.4959046 | 0.5537083 | NM_178072 | Mus musculus glucocorticoid GO:000302 | | |
| 11 | A_52_P30065 | 1.2210503 | 1.6897353 | 1.5375633 | NM_028950 | Mus musculus NOL1/NOP2/Sun do | | |
| 12 | A_51_P415029 | 0.32358786 | 0.3104921 | 0.33155575 | NM_008715 | Mus musculus DEAD/H 1 GO:00036 | | |
| 13 | A_51_P117881 | 1.3056123 | 1.9919642 | 1.1720015 | NM_153069 | Mus musculus GO:0042742(defense r | | |
| 14 | A_52_P731333 | 0.5113991 | 0.5293184 | 0.7219636 | AK042046 | Mus musculus 3 days neonate thym | | |
| 15 | A_51_P105709 | 0.9239396 | 0.7363092 | 1.0647944 | AK010336 | Mus musculus ES cells GO:00048 | | |
| 16 | A_51_P517672 | 1.1373165 | 1.3780099 | 0.99864537 | NM_178779 | Mus musculus GO:001651 GO:00048 | | |
| 17 | A_51_P517182 | 1.3145977 | 1.3100575 | 1.0146214 | AK052687 | Mus musculus 0 day neonate kidne | | |
| 18 | A_51_P310196 | 0.8029882 | 0.7776163 | 1.1047196 | NM_011616 | Mus musculus GO:000691 GO:00051 | | |
| 19 | A_51_P458924 | 0.8972804 | 1.0500262 | 1.1530378 | NM_026066 | Mus musculus GO:000691 GO:00051 | | |
| 20 | A_51_P126643 | 1.6671212 | 1.1038653 | 1.273038 | NM_018772 | Mus musculus brain protein I3 (Br3) | | |
| 21 | A_52_P368214 | 1.058741 | 1.4626783 | 1.0003675 | NM_194355 | Mus musculus spire homolog 1 (Dro | | |
| 22 | A_52_P5905 | 0.9221169 | 0.7093989 | 0.92920095 | AK016730 | Mus musculus adult male testis cDNA | | |
| 23 | A_51_P126647 | 1.3278081 | 1.3344353 | 1.0538936 | NM_025463 | Mus musculus RIKEN cDNA 181000 | | |
| 24 | A_52_P537887 | 0.8559414 | 0.91282666 | 0.98567035 | | Q923Z3 (Q923Z3) MTO 1, partial (| | |
| 25 | A_52_P468269 | 0.6282661 | 0.6498462 | 0.80612063 | NM_018675 | Mus musculus GO:000633 GO:00036 | | |
| 26 | A_51_P230873 | 0.5750123 | 0.4381685 | 0.3697818 | NM_019499 | Mus musculus GO:000001 GO:00055 | | |
| 27 | A_51_P198335 | 1.508715 | 0.8425273 | 1.0621856 | NM_008068 | Mus musculus GO:00068 GO:00048 | | |

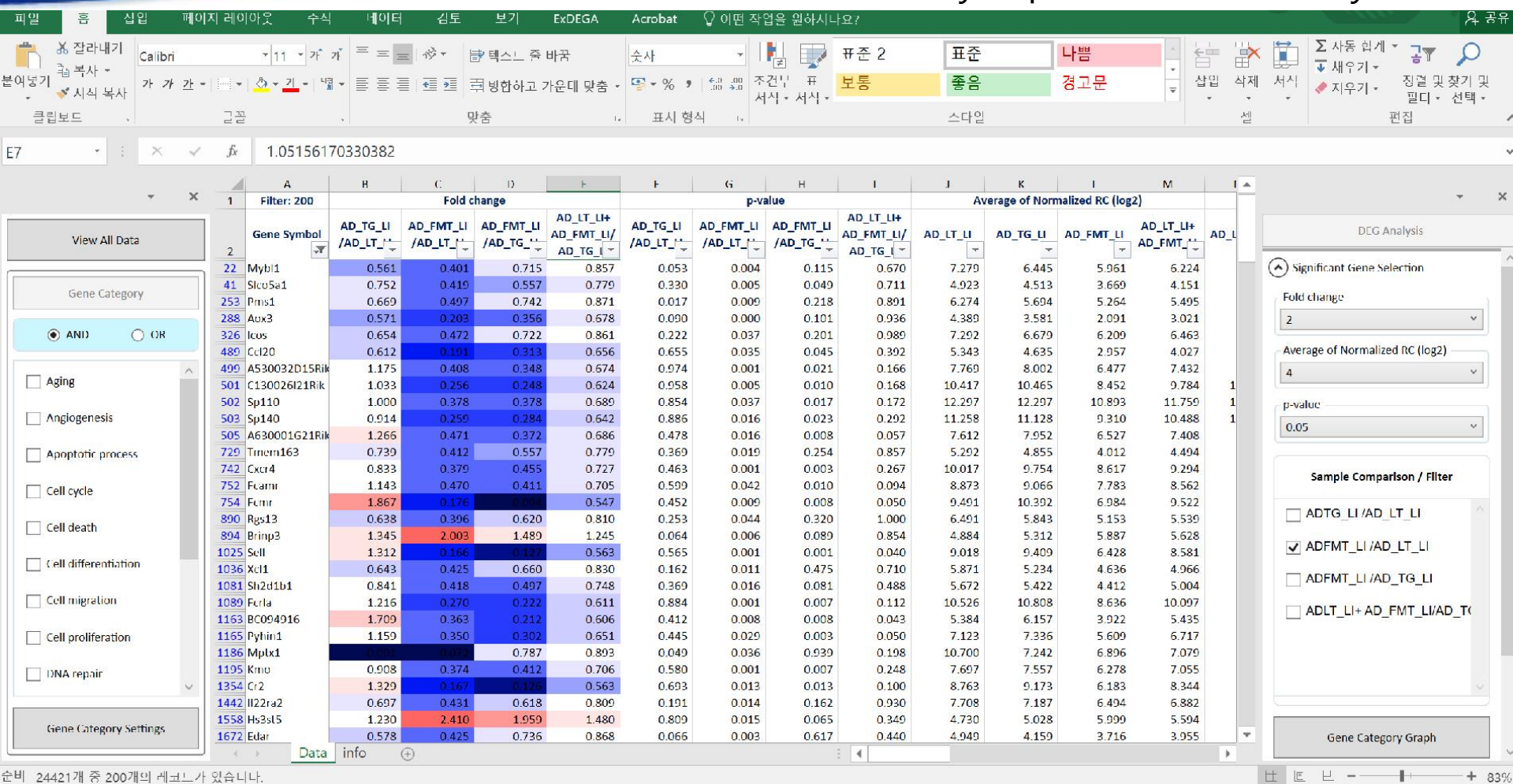
<Normalization>

| | A | B | C | D | E | F | G | H | I | J | K | L | M |
|----|----------|----------------------|-----|------------|------------|------|------|------|------------|-----------|---------|---------|------|
| 31 | Supplier | Agilent Technologies | | | | | | | | | | | |
| 32 | Block | Column | Row | Name | ID | X | Y | Dia. | F635 Media | F635 Mean | F635 SD | F635 CV | B635 |
| 34 | 1 | 1 | 1 | GE_BrightC | GE_BrightC | 865 | 2495 | 55 | 65535 | 59016 | 10812 | 18 | 61 |
| 35 | 1 | 2 | 1 | GE_BrightC | GE_BrightC | 940 | 2495 | 55 | 65017 | 58736 | 10547 | 17 | 68 |
| 37 | 1 | 3 | 1 | DarkCorner | DarkCorner | 1015 | 2495 | 45 | 160 | 166 | 90 | 54 | 47 |
| 38 | 1 | 4 | 1 | DarkCorner | DarkCorner | 1090 | 2500 | 45 | 124 | 144 | 81 | 56 | 43 |
| 39 | 1 | 5 | 1 | DarkCorner | DarkCorner | 1160 | 2495 | 55 | 119 | 142 | 91 | 64 | 38 |
| 40 | 1 | 6 | 1 | DarkCorner | DarkCorner | 1230 | 2495 | 45 | 118 | 148 | 113 | 76 | 40 |
| 41 | 1 | 7 | 1 | DarkCorner | DarkCorner | 1310 | 2500 | 50 | 139 | 137 | 85 | 62 | 47 |
| 42 | 1 | 8 | 1 | DarkCorner | DarkCorner | 1385 | 2500 | 50 | 129 | 135 | 85 | 62 | 42 |
| 43 | 1 | 9 | 1 | DarkCorner | DarkCorner | 1460 | 2495 | 50 | 125 | 135 | 89 | 65 | 41 |
| 44 | 1 | 10 | 1 | DarkCorner | DarkCorner | 1530 | 2495 | 50 | 128 | 146 | 91 | 62 | 41 |
| 45 | 1 | 11 | 1 | DarkCorner | DarkCorner | 1605 | 2495 | 45 | 116 | 131 | 81 | 61 | 43 |
| 46 | 1 | 12 | 1 | DarkCorner | DarkCorner | 1680 | 2495 | 45 | 134 | 149 | 98 | 65 | 38 |
| 47 | 1 | 13 | 1 | DarkCorner | DarkCorner | 1750 | 2495 | 65 | 121 | 2183 | 9354 | 428 | 40 |
| 48 | 1 | 14 | 1 | DarkCorner | DarkCorner | 1825 | 2500 | 50 | 113 | 131 | 88 | 67 | 39 |
| 49 | 1 | 15 | 1 | DarkCorner | DarkCorner | 1895 | 2495 | 55 | 130 | 143 | 86 | 60 | 40 |
| 50 | 1 | 16 | 1 | DarkCorner | DarkCorner | 1970 | 2495 | 45 | 140 | 156 | 101 | 64 | 39 |
| 51 | 1 | 17 | 1 | DarkCorner | DarkCorner | 2045 | 2495 | 50 | 111 | 127 | 74 | 58 | 37 |
| 52 | 1 | 18 | 1 | DarkCorner | DarkCorner | 2120 | 2495 | 45 | 166 | 175 | 82 | 46 | 36 |
| 53 | 1 | 19 | 1 | DarkCorner | DarkCorner | 2190 | 2495 | 55 | 141 | 155 | 97 | 62 | 38 |
| 54 | 1 | 20 | 1 | AK053031 | A_51_P145 | 2265 | 2495 | 55 | 204 | 231 | 137 | 59 | 38 |
| 55 | 1 | 21 | 1 | NM_01982 | A_52_P674 | 2340 | 2495 | 55 | 3415 | 3392 | 1092 | 32 | 40 |

<Significant data>

Data Analysis- ExDEGA

ExDEGA : Excel based Differentially Expressed Gene Analysis tool



The screenshot displays the ExDEGA Excel spreadsheet interface. The main data table is filtered to 200 genes. The columns include Gene Symbol, Fold change (AD_TG_LI/AD_LT_LI, AD_FMT_LI/AD_TG_LI, AD_FMT_LI/AD_FMT_LI, AD_LT_LI+/AD_FMT_LI+/AD_TG_LI+), p-value (AD_TG_LI/AD_LT_LI, AD_FMT_LI/AD_FMT_LI, AD_FMT_LI/AD_TG_LI, AD_LT_LI+/AD_FMT_LI+/AD_TG_LI+), and Average of Normalized RC (log2) (AD_LT_LI, AD_TG_LI, AD_FMT_LI, AD_LT_LI+/AD_FMT_LI+).

On the right side, there is a 'DEG Analysis' sidebar with the following settings:

- Significant Gene Selection:
 - Fold change: 2
 - Average of Normalized RC (log2): 4
 - p-value: 0.05
- Sample Comparison / Filter:
 - ADTG_LI/AD_LT_LI
 - ADFMT_LI/AD_LT_LI
 - ADFMT_LI/AD_TG_LI
 - ADLT_LI+AD_FMT_LI/AD_TG_LI+
- Gene Category Graph: (Visible at the bottom)

At the bottom left, a status bar indicates: "순번 24421개 중 200개의 레코드가 있습니다." (Number 24421 out of 200 records are displayed).

- ❖ Add Another GO 기능을 통해 사용자가 원하는 GO를 자유롭게 구성할수 있습니다.
- ❖ Significant gene을 매우 빠르고 쉽게 데이터를 취할수 있고 그래프로 표현할수 있습니다.

Data Analysis- ExDEGA

Microsoft Word ribbon: 파일, 홈, 삽입, 페이지 레이아웃, 수식, 레퍼터, 검토, 보기, ExDEGA, Acrobat, 이편 작업을 원하시나요?

Word status bar: E7, 1.05156170330382

Excel spreadsheet columns: Filter: 200, Fold change, p-value, Average of Normalized RC (log2)

Gene Ontology Graph

% of Total Significant

Bar Graph

% Up Significant (orange), % Dn Significant (green)

| Biological Process | % Up Significant | % Dn Significant |
|-----------------------|------------------|------------------|
| Aging | 1 | 2 |
| Angiogenesis | 1 | 3 |
| Apoptotic process | 0 | 5 |
| Cell cycle | 1 | 5 |
| Cell death | 0 | 5 |
| Cell differentiation | 4 | 28 |
| Cell migration | 1 | 12 |
| Cell proliferation | 1 | 6 |
| DNA repair | 0 | 2 |
| Extracellular matrix | 2 | 4 |
| Immune response | 1 | 30 |
| Inflammatory response | 1 | 14 |
| Neurogenesis | 1 | 8 |
| RNA splicing | 0 | 0 |
| Secretion | 2 | 2 |

| Gene ID | Gene Name | FC | Log2 FC | p-value | AD | LT | LI+ | Average of Normalized RC (log2) | | | | | |
|---------|-----------|-------|---------|---------|-------|-------|-------|---------------------------------|-------|-------|-------|-------|-------|
| 1195 | Ktno | 0.908 | -0.374 | 0.412 | 0.706 | 0.580 | 0.001 | 0.007 | 0.248 | 7.607 | 7.557 | 6.278 | 7.055 |
| 1354 | Cr2 | 1.329 | 0.167 | 0.136 | 0.563 | 0.693 | 0.013 | 0.013 | 0.100 | 8.763 | 9.173 | 6.183 | 8.344 |
| 1442 | Il22ra2 | 0.697 | -0.431 | 0.618 | 0.809 | 0.191 | 0.014 | 0.162 | 0.930 | 7.708 | 7.187 | 6.494 | 6.882 |
| 1558 | Hs3st5 | 1.230 | 2.410 | 1.959 | 1.480 | 0.809 | 0.015 | 0.065 | 0.349 | 4.730 | 5.028 | 5.999 | 5.594 |
| 1672 | Edar | 0.578 | -0.425 | 0.736 | 0.868 | 0.065 | 0.003 | 0.617 | 0.440 | 4.949 | 4.159 | 3.716 | 3.955 |

DEG Analysis

Significant Gene Selection

Fold change: 2

Average of Normalized RC (log2): 4

p-value: 0.05

Sample Comparison / Filter

- ADTG_LI / AD_LT_LI
- ADFMT_LI / AD_LT_LI
- ADFMT_LI / AD_TG_LI
- ADLT_LI+ AD_FMT_LI / AD_TG_LI

Gene Category Graph

순번 24421개 중 200개의 레코드가 있습니다.

- ❖ Pie chart를 통해 Significant gene 대상으로 BioFunction 분포를 확인하고 영역을 클릭하면 해당 up/down 유전자가 필터링됨.
- ❖ Bar graph를 통해 BioFunction 별로 up/down의 분포를 확인하고 bar를 클릭하면 해당 유전자를 확인할 수 있음.

Data Analysis- ExDEGA

파일 홈 삽입 페이지 레이아웃 수식 데이터 검토 보기 ExDEGA Acrobat 이면 작업을 원하시나요?

Calibri 11 가 가 텍스트 주 바꿈

숫사 표준 나뉨

Venn Diagram Analysis

AD_TG_LI / AD_LT_LI

AD_FMT_LI / AD_LT_LI

AD_FMT_LI / AD_TG_LI

Legend:
 up-regulated
 contra regulated
 down-regulated

Sample Comparison:
 ADTG_LI / AD_LT_LI
 ADFMT_LI / AD_LT_LI
 ADFMT_LI / AD_TG_LI
 ADLT_LI + AD_FMT_LI

Fold change: 1.5
 Average of Normalized RC (log2): 4
 p-value: 0.05

Diagram View
 All
 Save Image

| Gene Symbol | AD_TG_LI / AD_LT_LI | AD_FMT_LI / AD_LT_LI | AD_FMT_LI / AD_TG_LI | AD_LT_LI + AD_FMT_LI / AD_TG_LI |
|----------------|---------------------|----------------------|----------------------|---------------------------------|
| 2761 Gabrg2 | 1.693 | 2.506 | 1.480 | 1.240 |
| 4366 Gm6682 | 1.838 | 1.518 | 0.826 | 0.913 |
| 4728 Arg2 | 1.620 | 1.772 | 1.094 | 1.047 |
| 6797 Pdlim2 | 1.511 | 1.581 | 1.046 | 1.023 |
| 8284 Cudt58 | 1.581 | 1.531 | 0.968 | 0.984 |
| 9538 Ai661453 | 1.501 | 1.516 | 1.010 | 1.005 |
| 11529 Adamts12 | 1.710 | 2.147 | 1.256 | 1.128 |
| 11637 Lcn2 | 1.507 | 1.832 | 1.216 | 1.108 |
| 13673 Fhd1c1 | 1.583 | 1.807 | 1.141 | 1.071 |
| 15946 Abcb4 | 1.573 | 1.535 | 0.976 | 0.988 |
| 18860 Hif3a | 1.585 | 1.618 | 1.021 | 1.010 |
| 19258 Lrn3 | 1.560 | 1.606 | 1.030 | 1.015 |
| 20336 Trnc7 | 1.767 | 2.518 | 1.425 | 1.213 |
| 20734 Mti483 | 1.625 | 1.838 | 1.131 | 1.065 |
| 21806 Osgin1 | 1.547 | 1.585 | 1.024 | 1.012 |
| 24366 Mid1 | 2.092 | 1.641 | 0.784 | 0.892 |

Filter: 16

View All Data

Gene Category

AND OR

Aging

Angiogenesis

Apoptotic process

Cell cycle

Cell death

Cell differentiation

Cell migration

Cell proliferation

DNA repair

Gene Category Settings

Data info

순비 24421개 중 16개의 레코드가 있습니다.

Data Analysis- ExDEGA

Microsoft Word ribbon: 파일, 홈, 삽입, 레이아웃, 수식, 데이터, 검토, 보기, ExDEGA, Acrobat, 이면 작업을 원하시나요?, 공용

Font: Calibri, Size: 11, Bold, Italic, Underline, Paragraph: 들여쓰기, 줄번호, 번호, 글꼴, 맞춤, 표시 형식, 스타일

Language: 표준 2, 표준, 나뭇잎, 보통, 좋음, 경고문

Tools: 사동, 새우기, 지우기, 정렬, 찾기, 필터, 선택, 편집

Worksheet: A11637, Lcn2

| Gene Symbol | AD_TG_LI / AD_LT_LI | AD_FMT_LI / AD_LT_LI | AD_FMT_LI / AD_TG_LI | AD_LT_LI+ / AD_FMT_LI | AD_TG_LI / AD_LT_LI | AD_FMT_LI / AD_LT_LI | AD_FMT_LI / AD_TG_LI | AD_LT_LI+ / AD_FMT_LI | AD_TG_LI / AD_LT_LI | AD_FMT_LI / AD_TG_LI | AD_LT_LI+ / AD_FMT_LI |
|-------------|---------------------|----------------------|----------------------|-----------------------|---------------------|----------------------|----------------------|-----------------------|---------------------|----------------------|-----------------------|
| Lcn2 | ~10.5 | ~11.5 | ~11.5 | ~11.5 | ~10.5 | ~11.5 | ~11.5 | ~11.5 | ~10.5 | ~11.5 | ~11.5 |
| Fhd1 | ~8.5 | ~9.5 | ~9.5 | ~9.5 | ~8.5 | ~9.5 | ~9.5 | ~9.5 | ~8.5 | ~9.5 | ~9.5 |
| Abcb4 | ~7.5 | ~8.5 | ~8.5 | ~8.5 | ~7.5 | ~8.5 | ~8.5 | ~8.5 | ~7.5 | ~8.5 | ~8.5 |
| Hif3a | ~7.5 | ~8.5 | ~8.5 | ~8.5 | ~7.5 | ~8.5 | ~8.5 | ~8.5 | ~7.5 | ~8.5 | ~8.5 |
| Lrnf3 | ~7.5 | ~8.5 | ~8.5 | ~8.5 | ~7.5 | ~8.5 | ~8.5 | ~8.5 | ~7.5 | ~8.5 | ~8.5 |
| Tmc7 | ~8.5 | ~9.5 | ~9.5 | ~9.5 | ~8.5 | ~9.5 | ~9.5 | ~9.5 | ~8.5 | ~9.5 | ~9.5 |
| Mir483 | ~4.5 | ~5.5 | ~5.5 | ~5.5 | ~4.5 | ~5.5 | ~5.5 | ~5.5 | ~4.5 | ~5.5 | ~5.5 |
| Osgin1 | ~10.5 | ~11.5 | ~11.5 | ~11.5 | ~10.5 | ~11.5 | ~11.5 | ~11.5 | ~10.5 | ~11.5 | ~11.5 |

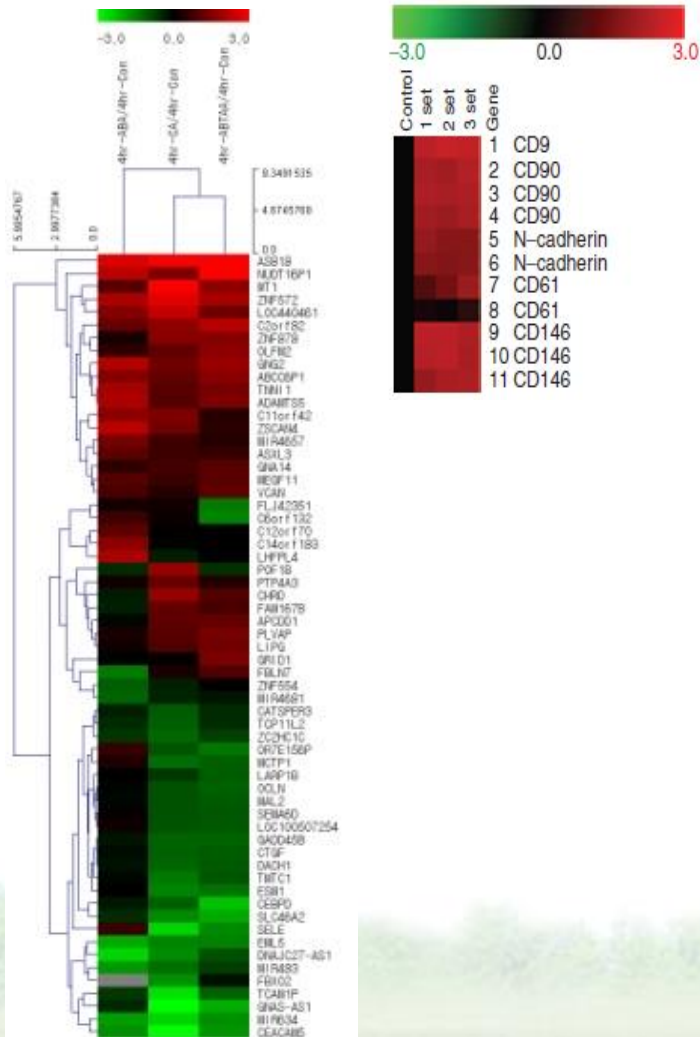
Gene Graph Tool: Average of Normalized RC (log2) vs. Fold Change (log2)

Legend: Lcn2 (blue), Fhd1 (light blue), Abcb4 (purple), Hif3a (dark purple), Lrnf3 (magenta), Tmc7 (red), Mir483 (orange), Osgin1 (yellow)

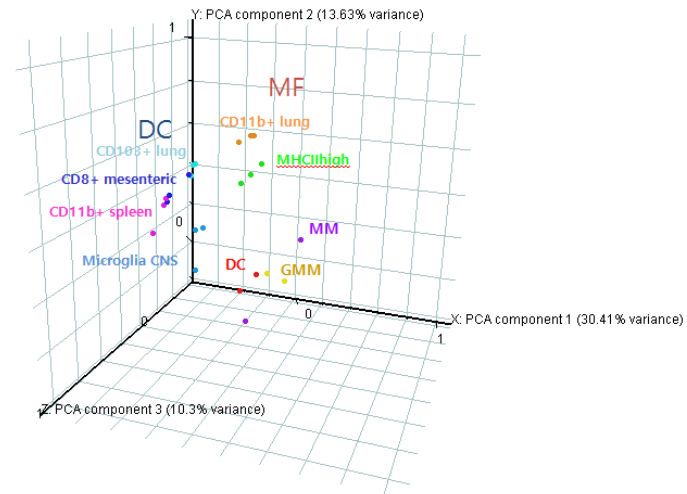
대상을 선택한 다음 <Enter> 키를 누르거나 [붙여넣기]를 선택합니다.

Data Analysis- Clustering

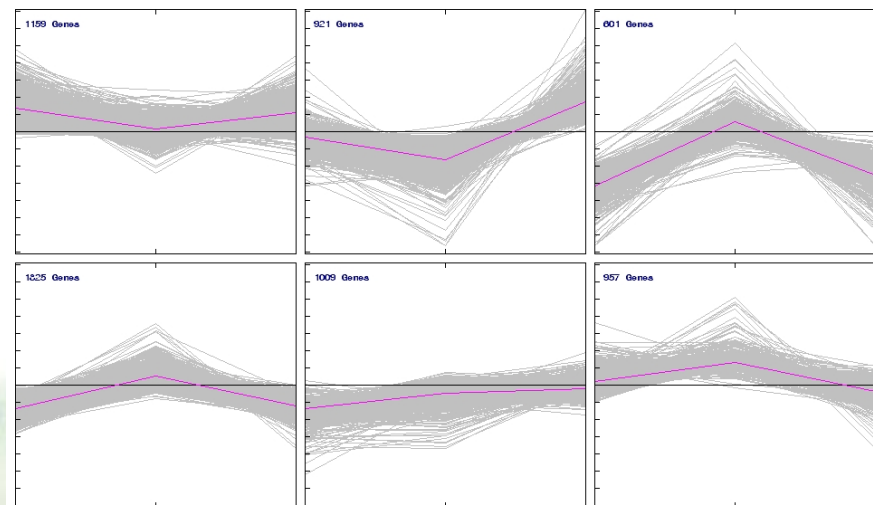
Hierarchical Clustering (HCL)



Principal Component Analysis (PCA)



K-means clustering (KMC)



Data Analysis- Gene Ontology & Pathway

Quick GO DB를 이용한 Gene Ontology 분석

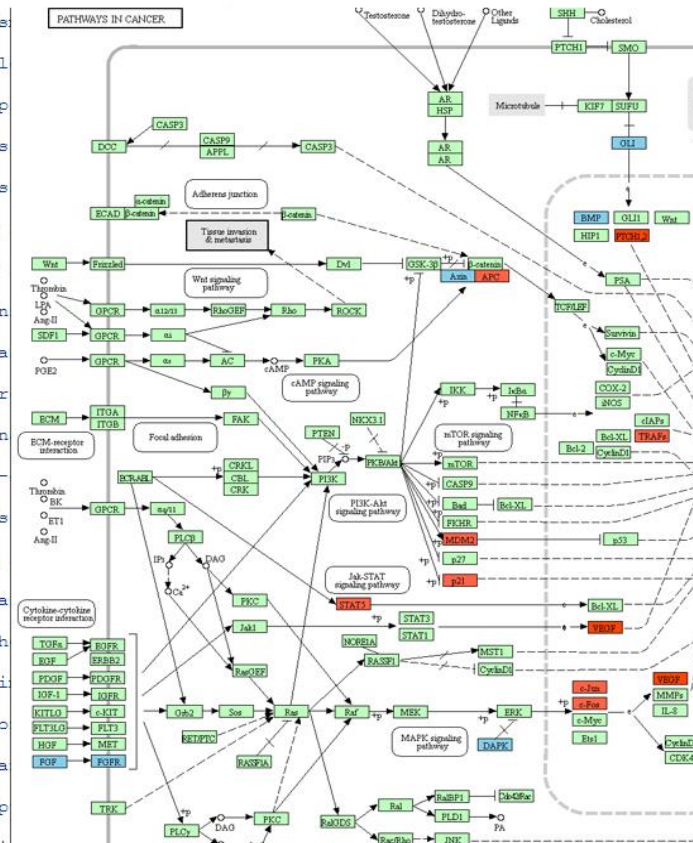
KEGG DB를 이용한 Pathway 분석

Pathway Search Result

Sort by the pathway list

Show all objects

- hsa01100 Metabolic pathways - Homo sapiens (human) (28)
- hsa05200 Pathways in cancer - Homo sapiens (human) (19)
- hsa05034 Alcoholism
- hsa04110 Cell cycle
- hsa05165 Human papillomavirus infection
- hsa05206 MicroRNAs
- hsa04217 Necroptosis
- hsa04151 PI3K-Akt signaling pathway
- hsa05322 Systemic lupus erythematosus
- hsa05166 HTLV-I infection
- hsa04115 p53 signaling pathway
- hsa05203 Viral carcinogenesis
- hsa04010 MAPK signaling pathway
- hsa04060 Cytokine-cytokine receptor interaction
- hsa04210 Apoptosis
- hsa05167 Kaposi's sarcoma-associated herpesvirus infection
- hsa04668 TNF signaling pathway
- hsa04510 Focal adhesion
- hsa05168 Herpes simplex virus infection
- hsa04810 Regulation of lipoprotein metabolism
- hsa05224 Breast cancer
- hsa05202 Transcription
- hsa04080 Neurotrophin signaling pathway



The screenshot shows the QuickGO web interface. The search term 'growth' is entered, and a list of Gene Ontology (GO) terms is displayed. The terms include:

- GO:0009542 granule
- GO:0040007 growth
- GO:0043186 P granule
- GO:0042332 gravitaxis
- GO:0016049 cell growth
- GO:0030426 growth cone
- GO:0044840 gut granule
- GO:0060437 lung growth
- GO:0070088 PHA granule
- GO:0080112 seed growth
- GO:0098868 bone growth
- GO:0009630 gravitropism
- GO:0035265 organ growth
- GO:0042718 yolk granule
- GO:0043036 starch grain
- GO:0060419 heart growth
- GO:0001555 oocyte growth
- GO:0030448 hyphal growth
- GO:0098594 mucin granule
- GO:0033095 aleurone grain
- GO:0040007 growth
- GO:0016049 cell growth
- GO:0030426 growth cone
- GO:0060437 lung growth
- GO:0080112 seed growth
- GO:0098868 bone growth

Data Analysis- Gene Set Enrichment

DAVID tool을 이용한 Functional Annotation 분석

Current Gene List: List_1
Current Background: Homo sapiens

94 DAVID IDs

Check Defaults Clear All

55 short records

| Rank | Category | Term | # | BT | Count |
|------|----------------|--------------------------------------|----|----|-------|
| 1 | GO TERM_BP_FAT | cell-matrix adhesion | 6 | BT | 6 |
| 2 | GO TERM_BP_FAT | cell-substrate adhesion | 6 | BT | 6 |
| 3 | GO TERM_BP_FAT | cell adhesion | 13 | BT | 13 |
| 4 | GO TERM_BP_FAT | biological adhesion | 13 | BT | 13 |
| 5 | GO TERM_BP_FAT | adhesion-mediated signalling pathway | 7 | BT | 7 |
| 6 | GO TERM_BP_FAT | cellular junction homeostasis | 6 | BT | 6 |
| 7 | GO TERM_BP_FAT | cell-cell adhesion | 9 | BT | 9 |
| 8 | GO TERM_BP_FAT | cellular homeostasis | 4 | BT | 4 |
| 9 | GO TERM_BP_FAT | cellular ion homeostasis | 5 | BT | 5 |
| 10 | GO TERM_BP_FAT | cellular system development | 4 | BT | 4 |
| 11 | GO TERM_BP_FAT | cellular tissue development | 7 | BT | 7 |

Gene Report

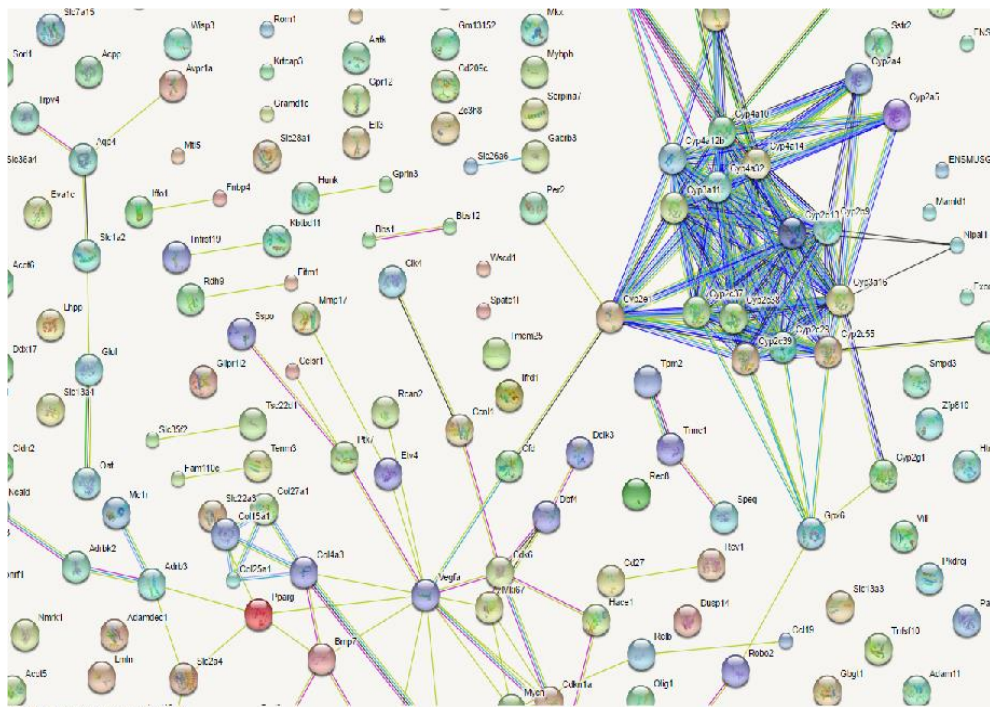
Current Gene List: List_1
Current Background: Homo sapiens
94 DAVID IDs
6 record(s)

| OFFICIAL GENE SYMBOL | GENE NAME | R |
|----------------------|--------------------------------------|----|
| TEK | TEK tyrosine kinase, endothelial | BS |
| ACT | actin filament, form II (beta chain) | BS |
| ITGB1BP1 | integrin beta 1 binding protein 1 | BS |
| ITGA4 | integrin alpha 4 | BS |
| LAMAS | lamins, alpha 5 | BS |
| NID2 | nidogen 2 (osteonidogen) | BS |

MSigDB기반 GSEA 분석

| Gene Set Name [# Genes (K)] | Description | # Genes in overlap (k) | p-value | 1 DR q-value |
|---|---|------------------------|-----------|--------------|
| GO_RR REGULATION_OF_CELL_DIFFERENTIATION [1492] | Any process that modulates the frequency, rate or extent of cell differentiation, the process in which relatively unspecialized cells acquire specialized structural and functional features. | 40 | 1.78 e-10 | 7.41 e-10 |
| GO_RR REGULATION_OF_MORPHOGENESIS_ORGANISMAL_DEVELOPMENT [1672] | Any process that modulates the frequency, rate or extent of multicellular organismal development. | 40 | 9.15 e-10 | 2.01 e-10 |
| GO REGULATION OF NERVOUS SYSTEM DEVELOPMENT [750] | Any process that modulates the frequency, rate or extent of nervous system development, the origin and formation of nervous tissue. | 25 | 1.53 e-14 | 2.26 e-11 |
| GO REGULATION OF CELL DEVELOPMENT [836] | Any process that modulates the rate, frequency or extent of the progression of the cell over time, from its formation to the mature | 26 | 2.2 e-14 | 2.43 e-11 |

String-db tool을 이용한 gene set 분석



| Biological Process (GO) | count in gene set | false discovery rate |
|---|-------------------|----------------------|
| pathway_id: pathway description | | |
| GO:001676: long-chain fatty acid metabolic process | 1 | 2.69e-06 |
| GO:0019573: epoxygenase P450 pathway | 7 | 3.59e-06 |
| GO:0045055: regulation of cell differentiation | 41 | 7.41e-05 |
| GO:004238: oncogenic drug catabolic process | 7 | 0.00116 |
| GO:0030793: regulation of developmental process | 52 | 0.00316 |
| (more...) | | |
| Molecular Function (GO) | count in gene set | false discovery rate |
| pathway_id: pathway description | | |
| GO:0016712: oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen | 1 | 2.3e-09 |
| GO:0070200: aromatase activity | 10 | 1.14e-08 |
| GO:004449: monooxygenase activity | 12 | 1.92e-07 |
| GO:0038292: arachidonic acid epoxidase activity | 8 | 1.59e-07 |
| GO:002057: tetracycline binding | 15 | 1.22e-06 |
| (more...) | | |
| KEGG Pathways | count in gene set | false discovery rate |
| pathway_id: pathway description | | |
| 00170: Pantoic acid metabolism | 10 | 9.07e-10 |
| 00330: Arachidonic acid metabolism | 12 | 3.28e-09 |
| 00140: Steroid hormone biosynthesis | 10 | 3.89e-06 |
| 00511: Linoleic acid metabolism | 8 | 4.72e-06 |
| (more...) | | |

Microarray 전문회사



감사합니다. ^^



(주)이바이오젠

TEL : 02-3141-0791

Email : service@e-biogen.com

<http://www.e-biogen.com>

