


MeV Hierarchical Clustering(HCL)

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MeV

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JAVA 설치 <https://www.oracle.com/technetwork/java/javase/downloads/jre8-downloads-2133155.html>

Java SE Runtime Environment 8u201 ← 업데이트되면 여기 있는 숫자는 변경될 수 있고 관계없음. 가입/로그인 필요.

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|----------------------------|-----------|--|
| Linux x86 | 68.1 MB | jre-8u201-linux-i586.rpm |
| Linux x86 | 83.8 MB | jre-8u201-linux-i586.tar.gz |
| Linux x64 | 64.91 MB | jre-8u201-linux-x64.rpm |
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| Windows x86 Online | 1.87 MB | jre-8u201-windows-i586-iftw.exe |
| Windows x86 Offline | 63.53 MB | jre-8u201-windows-i586.exe |
| Windows x86 | 66.51 MB | jre-8u201-windows-i586.tar.gz |
| Windows x64 | 71.44 MB | jre-8u201-windows-x64.exe |
| Windows x64 | 71.29 MB | jre-8u201-windows-x64.tar.gz |

MeV input 파일 만들기

* ExDEGA에서 input파일을 불러오는 방법

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O |
|---|------------------|---------------|-------------|-----------|-------|-------|-----------|-----------|-------|-------|---------------------------------|--------|--------|-------|--------|
| 1 | Filter: 23420 | | Fold change | | | | p-value | | | | Average of Normalized RC (log2) | | | | |
| 2 | ID | Gene Symbol | A/Control | B/Control | B/A | D/C | A/Control | B/Control | B/A | D/C | Control | A | B | C | D |
| 3 | 1 | 0610005C13Rik | 0.836 | 0.822 | 0.983 | 2.133 | 0.041 | 0.888 | 0.039 | 0.144 | 7.925 | 7.666 | 7.642 | 9.418 | 10.511 |
| 4 | 2 | 0610007N19Rik | 0.837 | 0.964 | 1.152 | 4.518 | 0.082 | 0.149 | 0.115 | 0.085 | 10.370 | 10.113 | 10.317 | 4.420 | 6.596 |

Fold change(log2)값으로 자동 output

DEG Analysis

Significant Gene Selection

Analysis Graph

Clustering Heatmap Support

Type

☒ Foldchange
☐ Normalized Data
☐ Z-Score

Export Data Select

☐ Name
☐ A/Control
☐ B/Control
☐ B/A
☐ D/C

Data Export

각 샘플의 발현값을 기반으로
z-score값을 계산하여 자동output

*단 샘플이 2개일 때는 z-score로 표현할 수 없음.

DEG Analysis

Significant Gene Selection

Analysis Graph

Clustering Heatmap Support

Type

☐ Foldchange
☒ Normalized Data
☐ Z-Score

Export Data Select

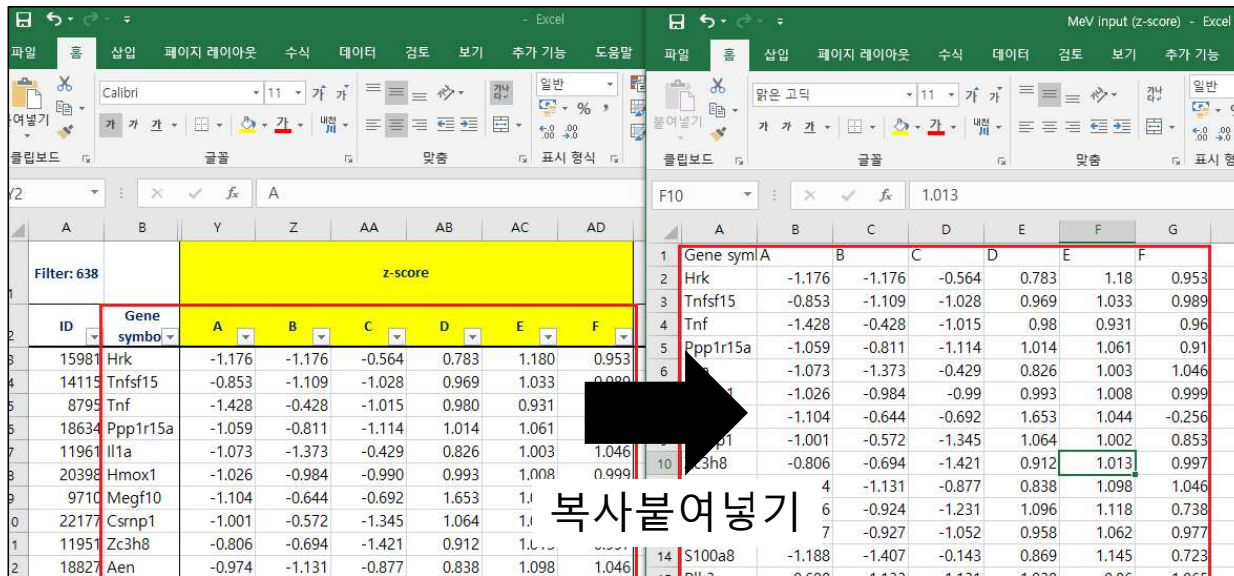
☐ Name
☐ Control
☐ A
☐ B
☐ C
☐ D

Data Export

MeV input 파일 만들기

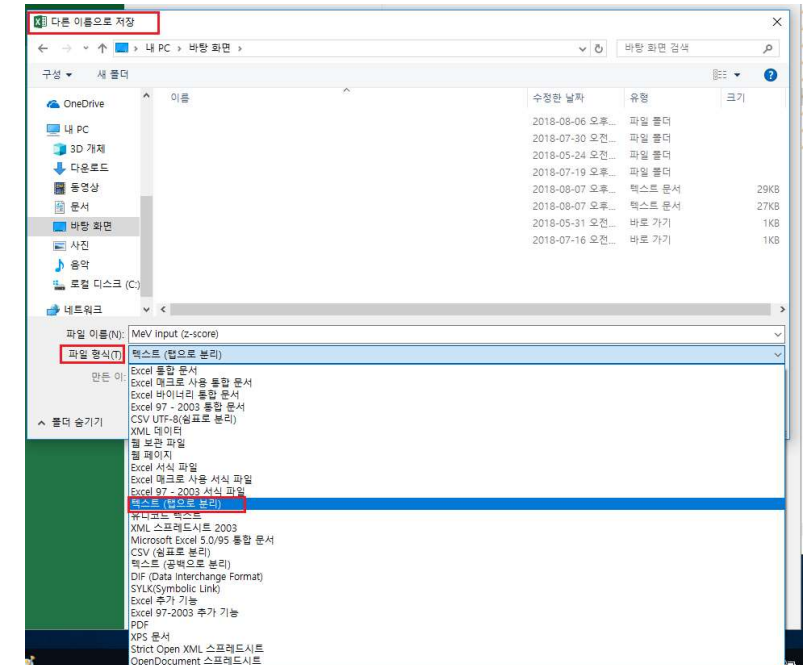
* ExDEGA를 이용하지 않을 때

- (1) Gene symbol과 Fold change값 혹은 Normalized data(log2)을 새로운 엑셀파일에 가져온다.
(z-score 구하기는 별도의 매뉴얼을 참고한다.)
- (2) Fold change의 경우는 log2로 변환한다. (수식 " $=\text{LOG}(\text{셀영역}, 2)$ ")

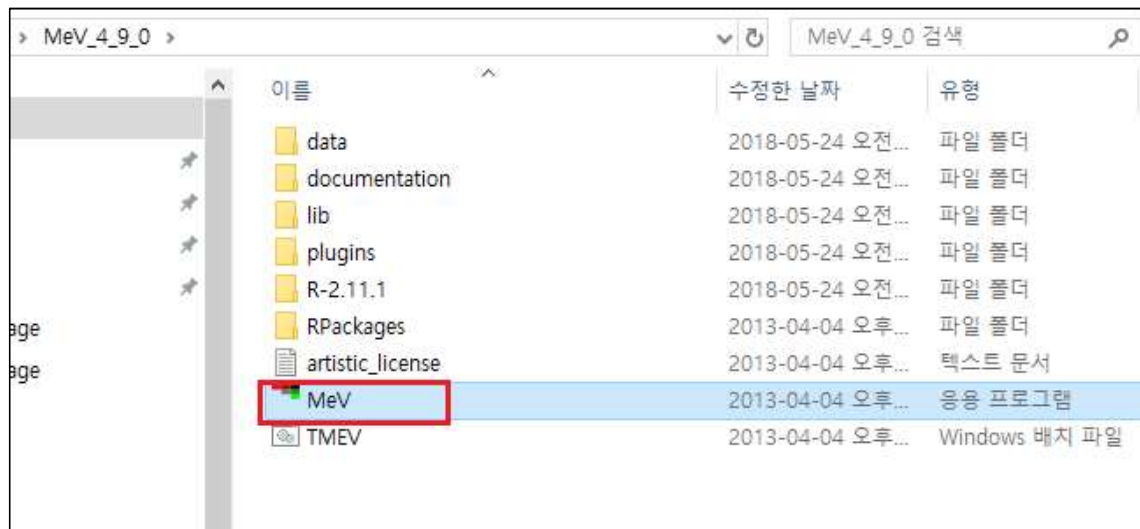


| ID | Gene symbol | A | B | C | D | E | F |
|-------|-------------|--------|--------|--------|-------|-------|-------|
| 15981 | Hrk | -1.176 | -1.176 | -0.564 | 0.783 | 1.180 | 0.953 |
| 14115 | Tnfsf15 | -0.853 | -1.109 | -1.028 | 0.969 | 1.033 | 0.989 |
| 8795 | Tnf | -1.428 | -0.428 | -1.015 | 0.980 | 0.931 | 0.96 |
| 18634 | Ppp1r15a | -1.059 | -0.811 | -1.114 | 1.014 | 1.061 | 0.91 |
| 11961 | Il1a | -1.073 | -1.373 | -0.429 | 0.826 | 1.003 | 1.046 |
| 20398 | Hmox1 | -1.026 | -0.984 | -0.990 | 0.993 | 1.008 | 0.999 |
| 9710 | Megf10 | -1.104 | -0.644 | -0.692 | 1.653 | 1.1 | 1.046 |
| 22177 | Csrnp1 | -1.001 | -0.572 | -1.345 | 1.064 | 1.1 | 1.046 |
| 11951 | Zc3h8 | -0.806 | -0.694 | -1.421 | 0.912 | 1.013 | 0.997 |
| 18827 | Aen | -0.974 | -1.131 | -0.877 | 0.838 | 1.098 | 1.046 |

복사붙여넣기

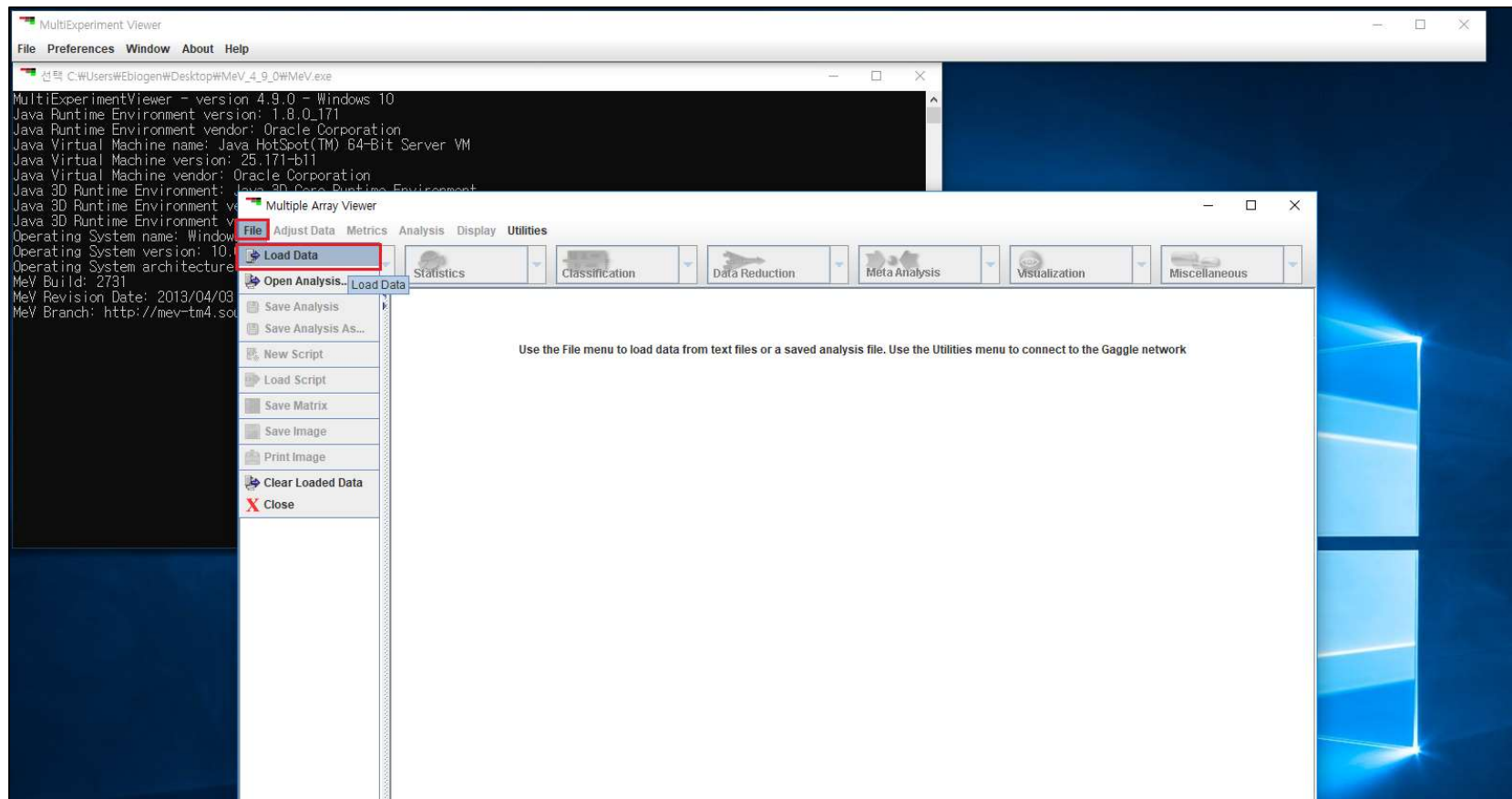


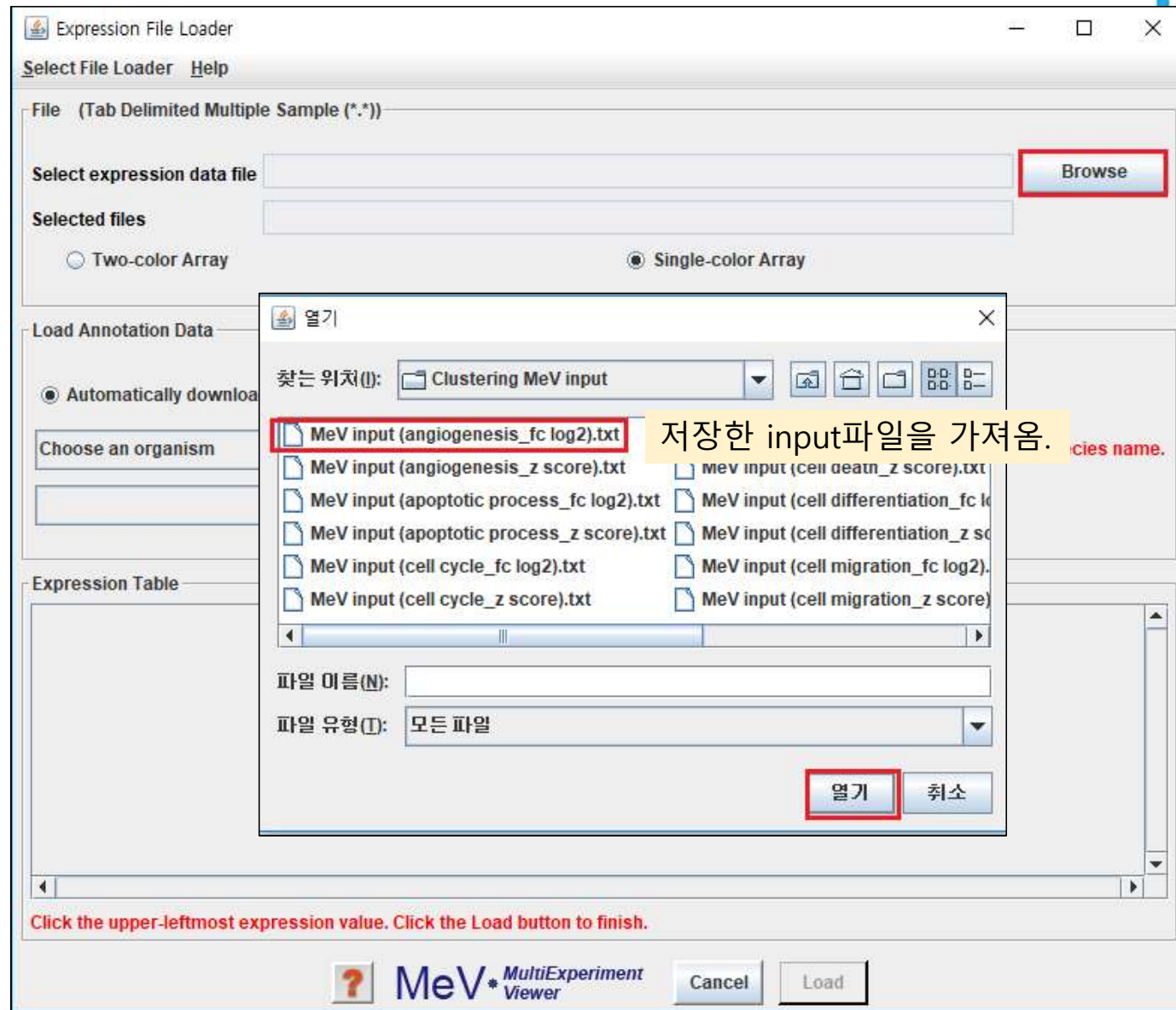
다름이름으로저장 > 텍스트(탭으로분리) 저장



MeV가 작동이 안 될 경우
아래의 TMEV를 이용한다.

File> Load Data





Expression File Loader

Select File Loader Help

File (Tab Delimited Multiple Sample (*.*))

Select expression data file

Selected files

☐ Two-color Array ☒ Single-color Array

Load Annotation Data


☒ Automatically download ☐ Load from local file ☒ Load Annotation

Choose an organism Please choose an array and species name.

Expression Table

| Gene Symb... | FSA-12h /c... | FSA-24h /c... | PPTP-12h /... | PPTP-24h /... |
|--------------|---------------|---------------|---------------|---------------|
| NDNF | -1.6185757... | -1.1708765... | -1.50459668 | -2.7364020... |
| ROBO4 | -1.0677622... | -1.3681324... | -1.18470494 | -1.0456476... |
| ITGAV | 1.0151485... | 1.2640974... | 1.20830624 | -1.3758047... |
| ATP5B | 1.2507409... | 1.2864618... | 1.1763527... | 1.0808363... |
| ANXA2 | 1.4078095... | 1.3318955 | 1.24765535 | 1.4324511... |
| ITGB1BP1 | 1.5491678... | 1.5381770... | 1.3965519... | 1.81158488 |
| SCG2 | 1.7202259... | 2.2529200... | 2.0598657... | 1.1573677... |
| PDCD6 | 1.9250628... | 1.8325522... | 1.7299594... | 1.6607817... |
| MYDGF | 2.3461087... | 2.2632934... | 1.9876108... | 2.4881931... |
| HTATIP2 | 2.4463033... | 2.7268811... | 2.3226913... | 2.2802166... |

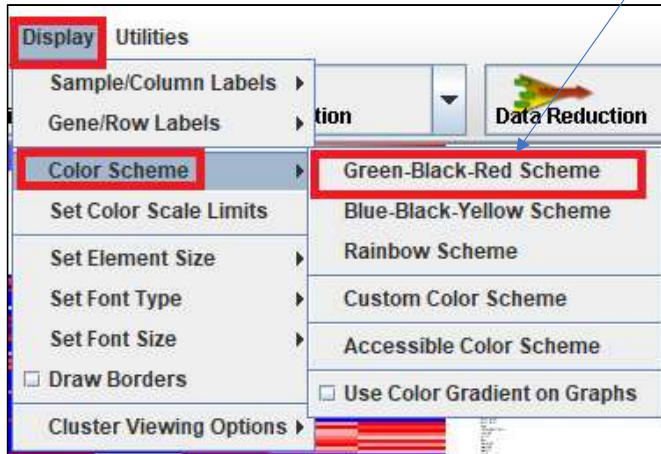
Click the upper-leftmost expression value. Click the Load button to finish.

 MeV MultiExperiment Viewer

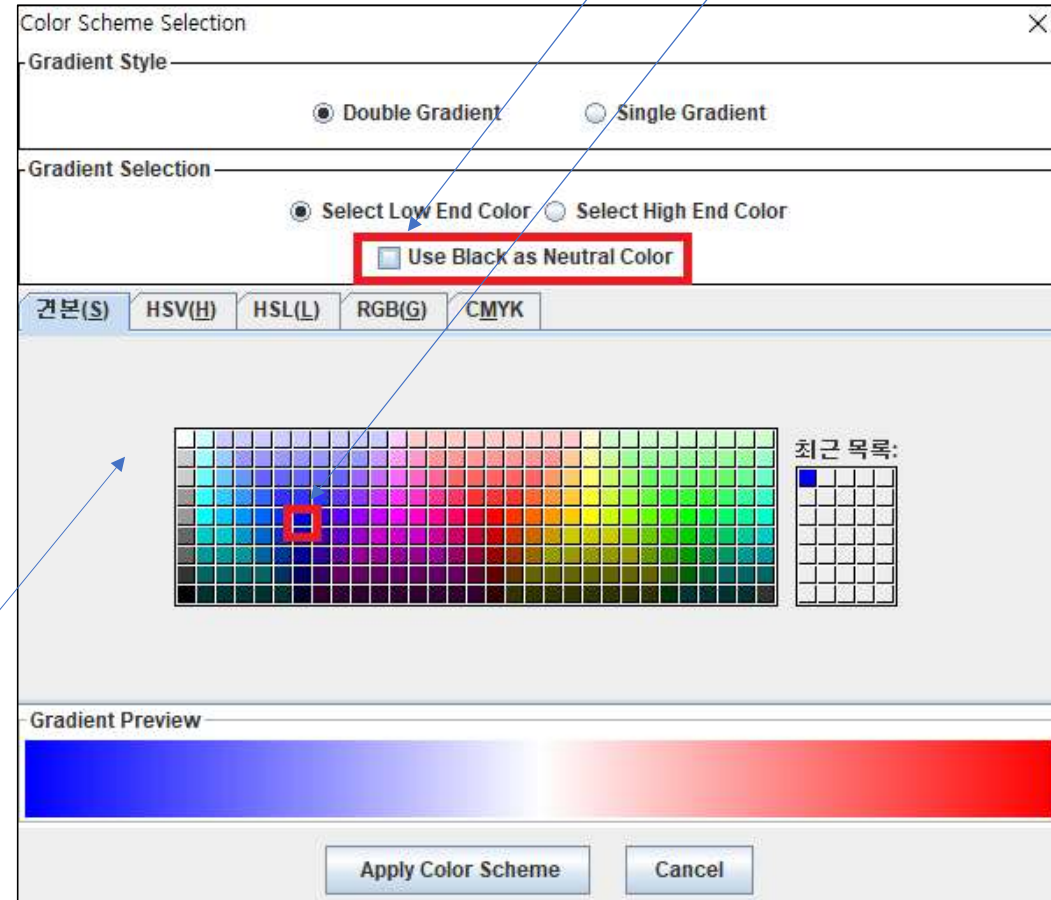
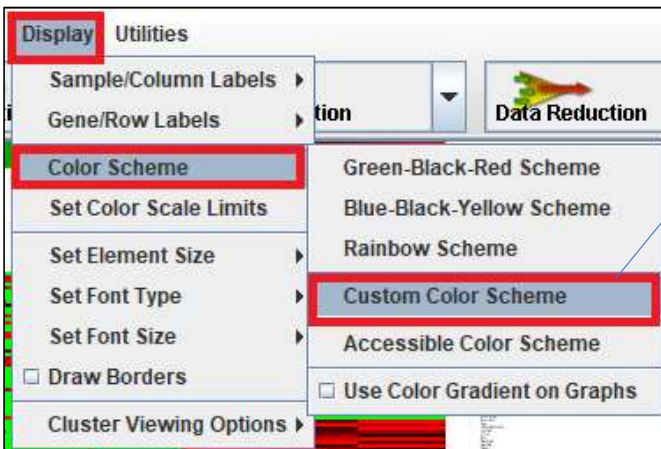
정상적으로 가져와지면 table로 확인할 수 있음.

MeV를 처음 활용하였을 때는 "Green-Black-Red" Scheme인데
색을 변경하고자 한다면, 오른쪽 이미지와 같이 설정할 수 있음. (체크해지, 파란색선택)

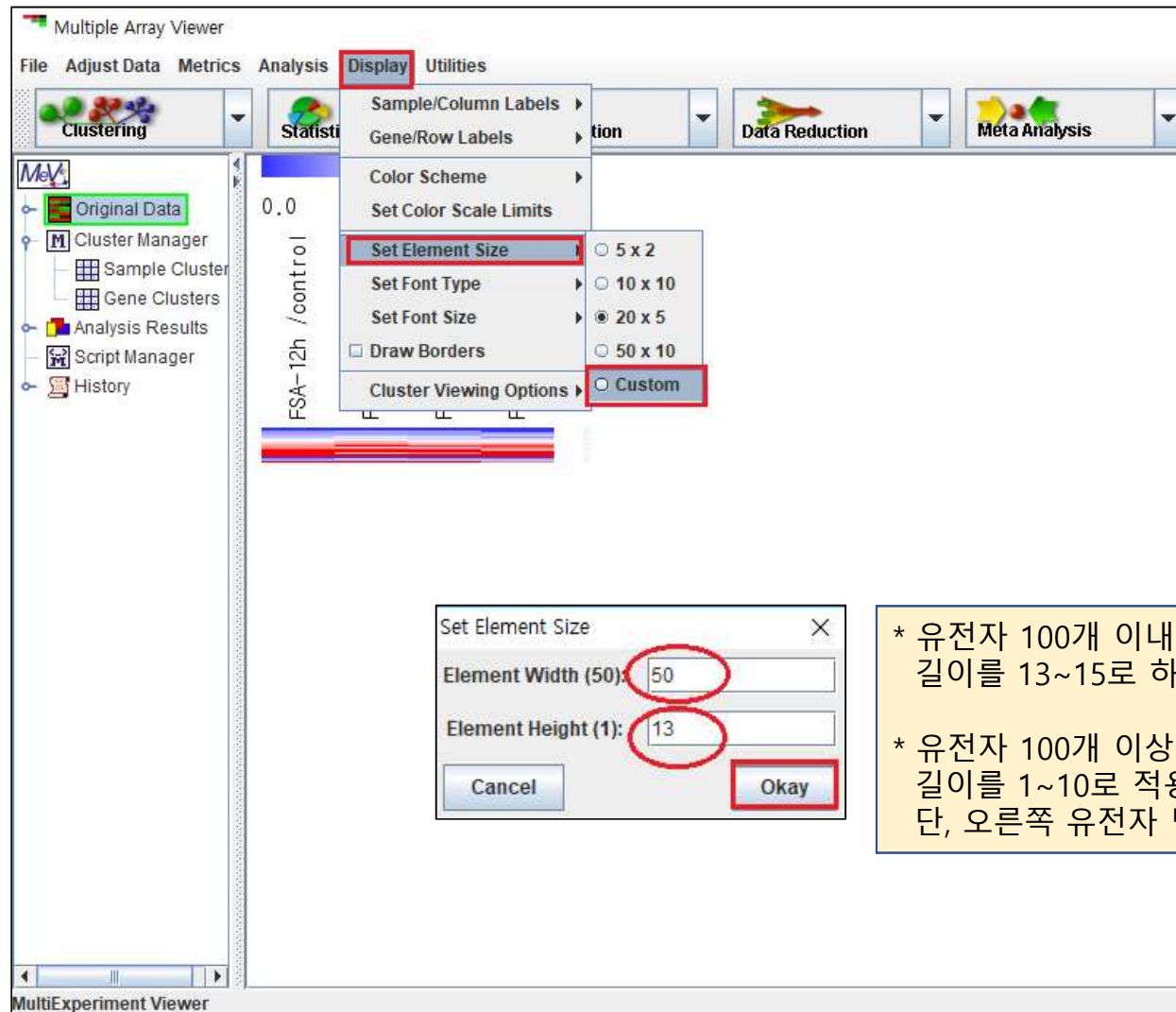
기본



변경할 경우



Input한 샘플수, 유전자수에 맞게 적절한 이미지 크기를 조정할 수 있음.



* 유전자 100개 이내 일 때,
길이를 13~15로 하면 적절

* 유전자 100개 이상 일 때,
길이를 1~10로 적용
단, 오른쪽 유전자 명은 식별 어려움.

Multiple Array Viewer

File Adjust Data Metrics Analysis **Display** Utilities

Clustering Statistical Data Reduction Meta Analysis

Original Data

Cluster Manager

Sample Cluster

Gene Clusters

Analysis Results

Script Manager

History

FSA-12h / control

NDHF
ROB04
ITGAV
ATP5B
ANXA2
ITGB1BP
SCG2
PDCD6
MYDGF
HTATIP2
SAT1
IL18
PECAM1
ACVRL1
KDR
SEMA5A
DLL1
EGR3
FGF2
PGF
RSP03
PDCD10
PDCD3
EMCN

Color Scale Limits

Gradient Style

☒ Double Gradient ☐ Single Gradient

Color Range Selection

Lower Limit (min. data value = -3.77): -3

Midpoint Value (median data value = 2.33): 0

Upper Limit (max. data value = 5.56): 3

Update Limits

Color Saturation Statistics

| | Number | Percent |
|----------------------------|--------|---------|
| Elements Off Color Scale | 32 | 33.3 |
| Elements Below Lower Limit | 13 | 13.5 |
| Elements Above Upper Limit | 19 | 19.8 |

Gradient and Limits Preview

0.00 2.33 3.70

MeV MultiExperiment Viewer

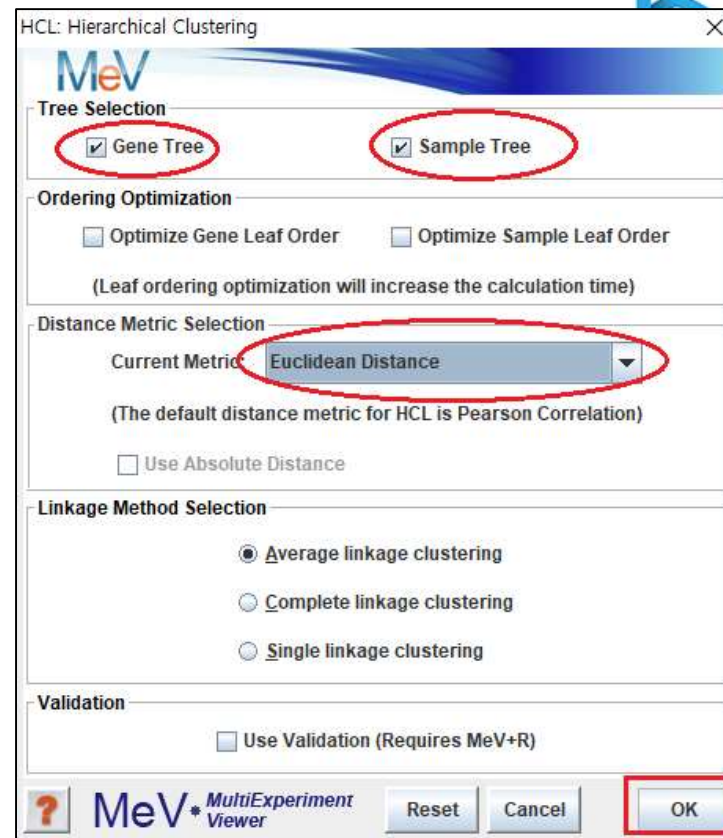
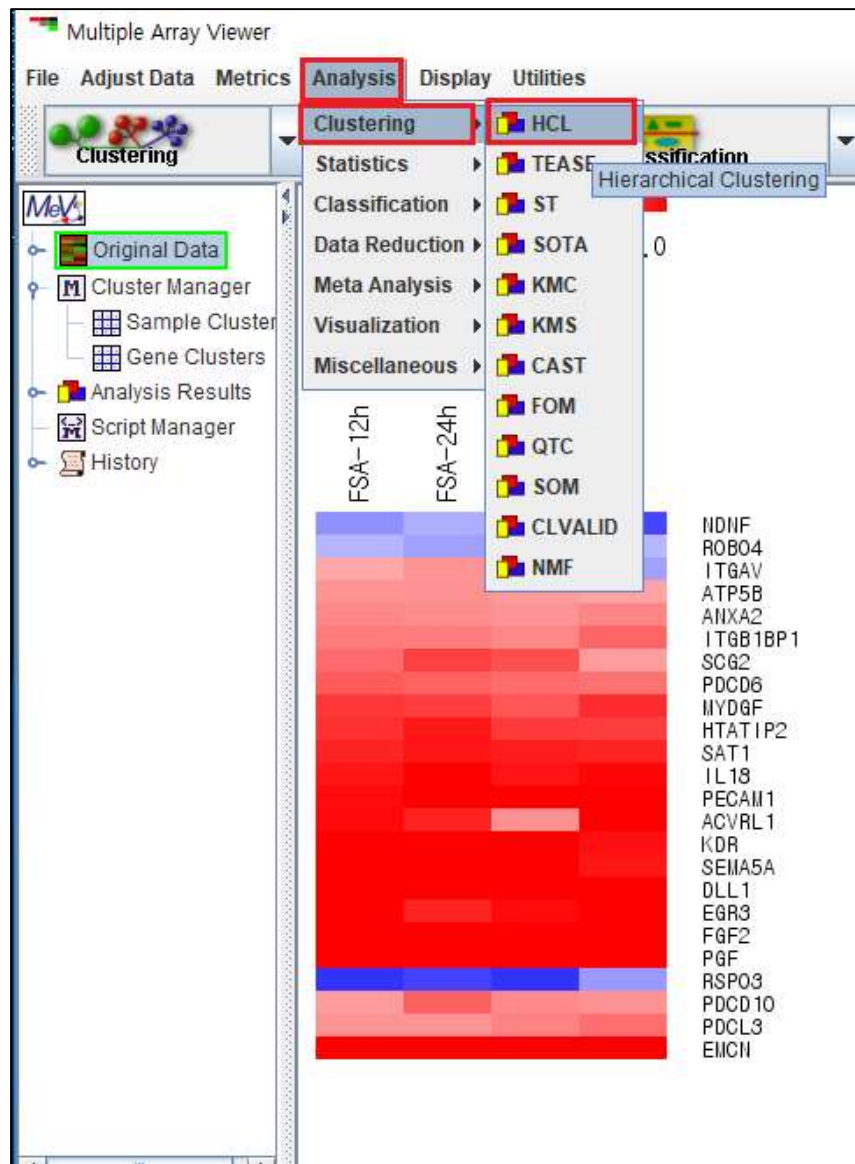
Reset Cancel OK

* Fold change(log2), z-score의 경우,
색의 index는 음수 양수 대칭으로 적절하게 조정

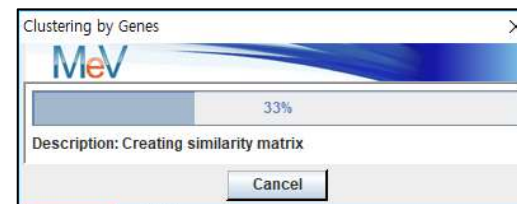
-1 0 1
-2 0 2
-3 0 3
...

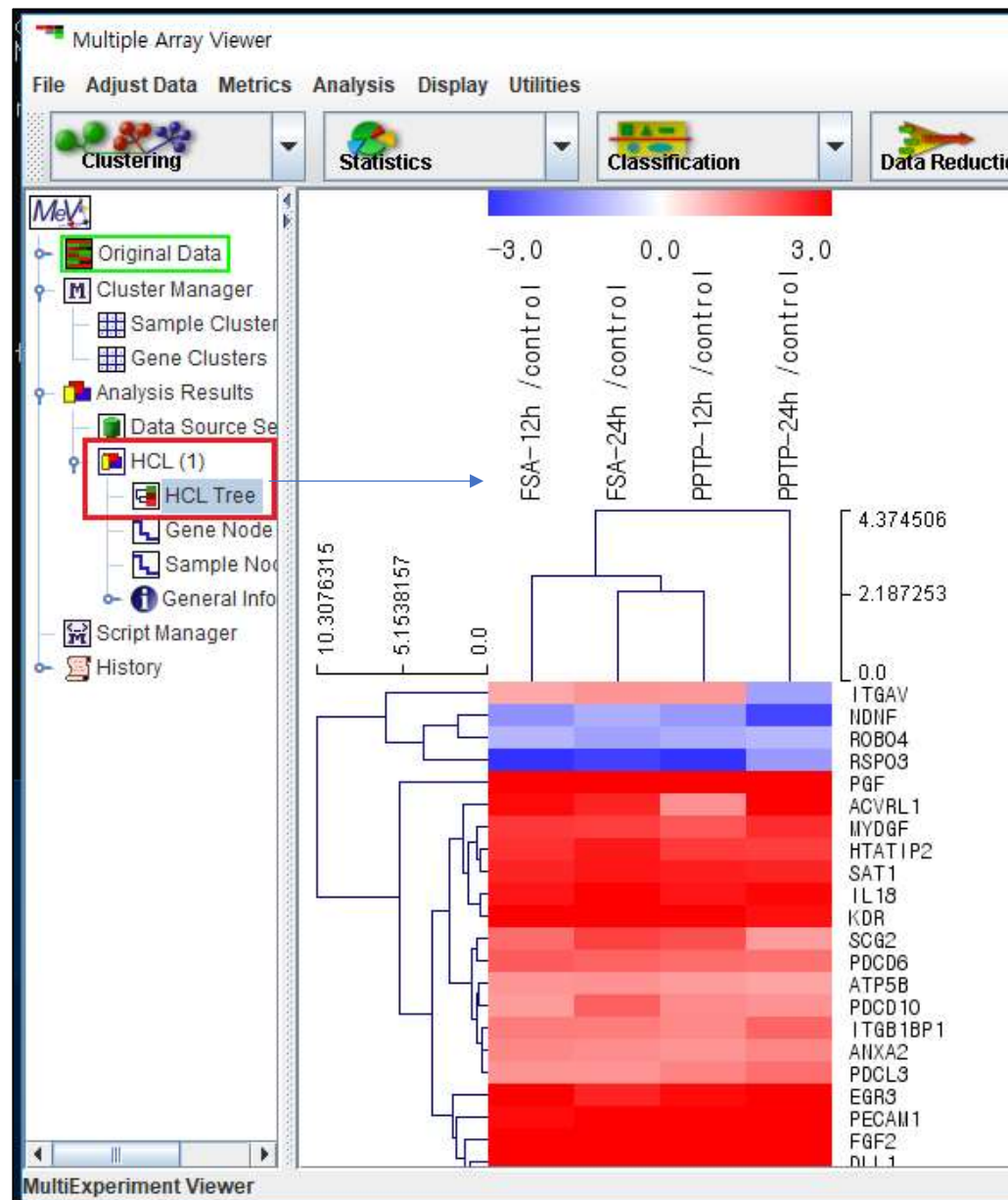
* Normalized data(log2)의 경우,
색의 index는 0부터 시작하여 적절하게 조정

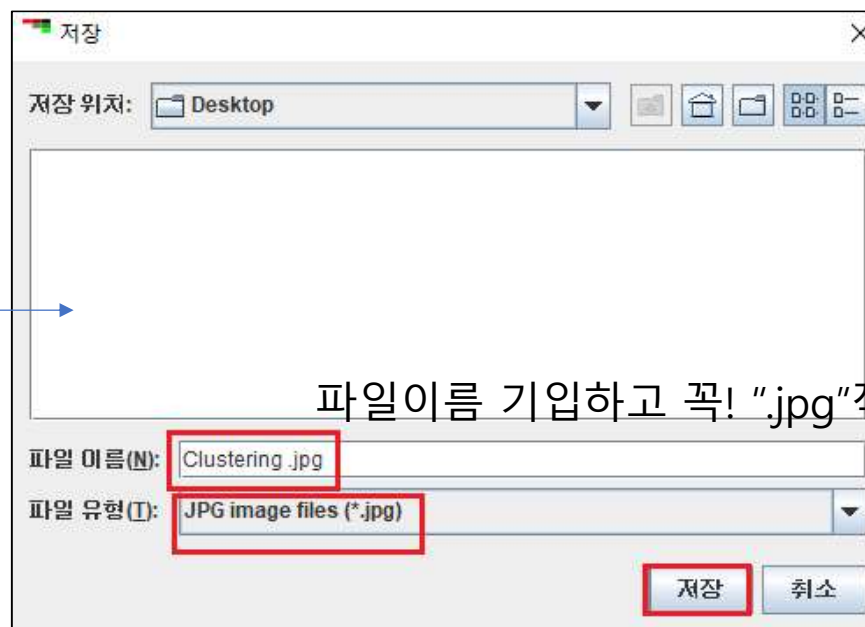
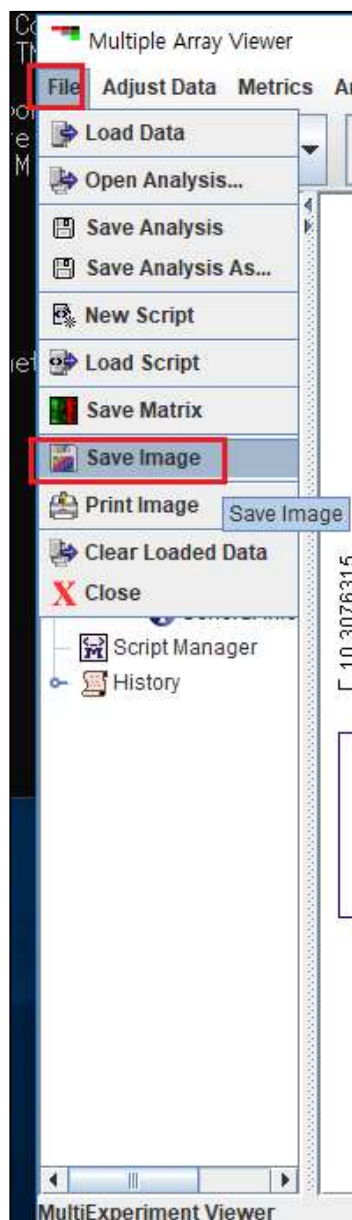
0 7 10
0 5 10
0 6 12
...



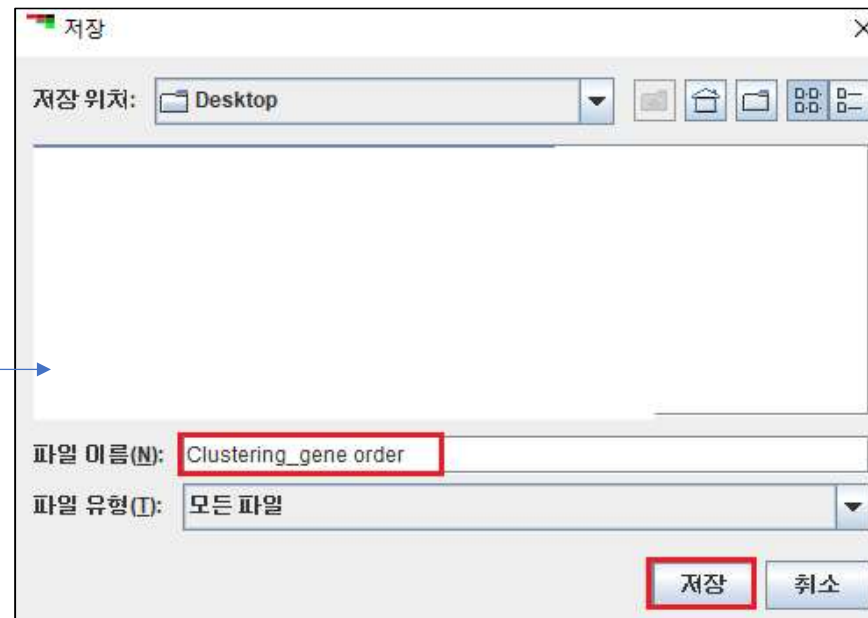
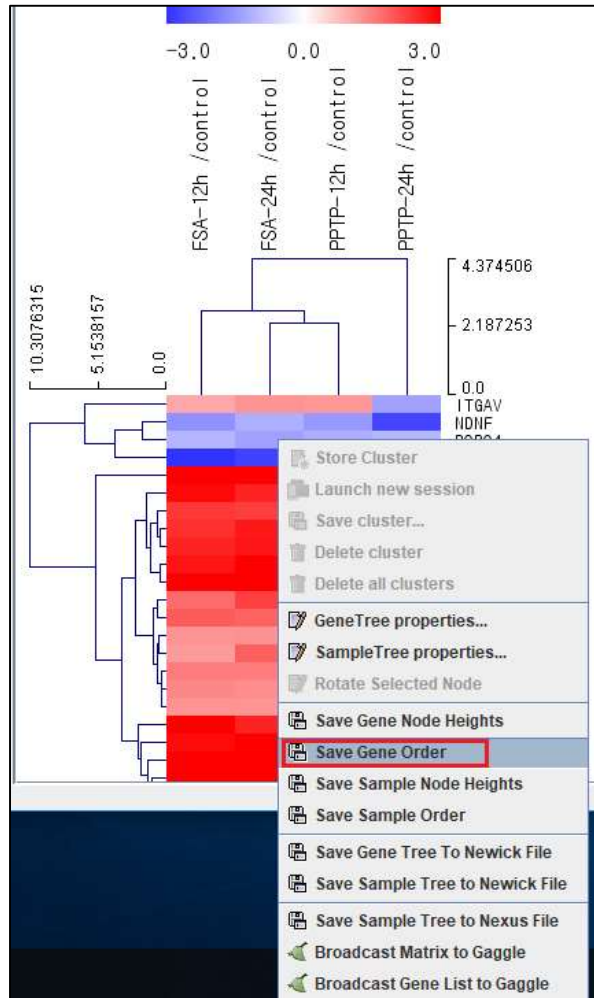
Metric은 Euclidean Distance/ linkage method는 Average linkage clustering 선택!
 * distance를 계산하는 방법이 여러 가지 있는데 그 중에 위 방법을 택한 것이다.







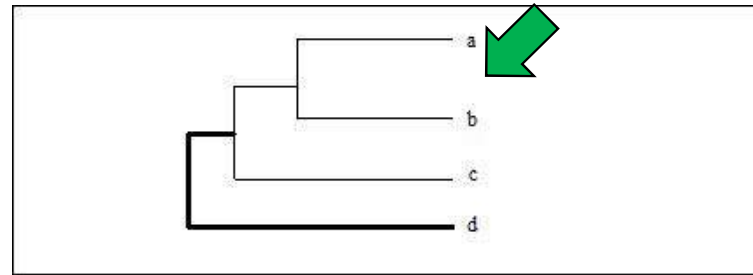
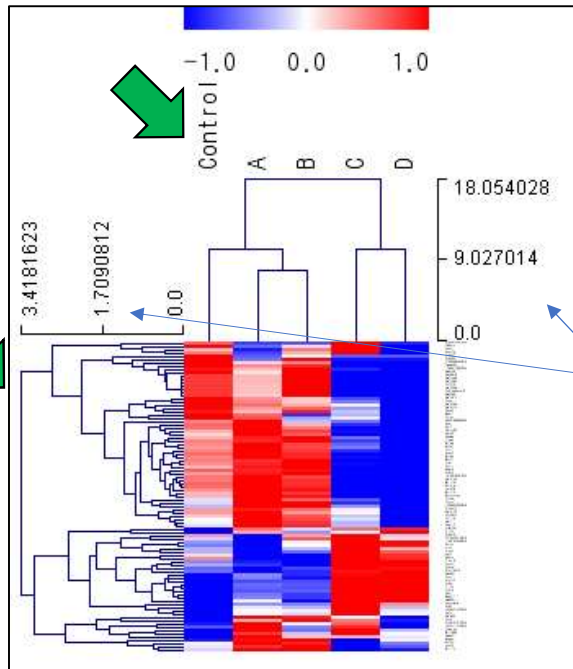
이미지의 RawData 저장. 이미지 위에서 마우스 오른쪽 클릭



※ 결과해석

Clustering 결과에서 상단에 그려지는 tree는 발현이 유사한 샘플들을 grouping하는 것이고 좌측에 그려지는 tree는 발현이 유사한 유전자들을 grouping하는 것이다.

예를 들어, 아래와 같이 clustering 결과가 나왔다면 a, b의 발현이 가장 유사하고 d가 가장 상이한 것입니다.



Clustering 결과에서 gene tree(좌측)위, sample tree(우측)오른쪽에 있는 scale bar를 distance scale bar라고 한다. 유전자 간의 샘플 간의 tree distance가 짧을수록 발현이 유사한 것. 길수록 발현이 상이한 것으로 scale bar를 보고 그 길이를 가늠할 수 있다.