

MicroArray Explorer - A Java-based Tool For Data Mining Microarrays

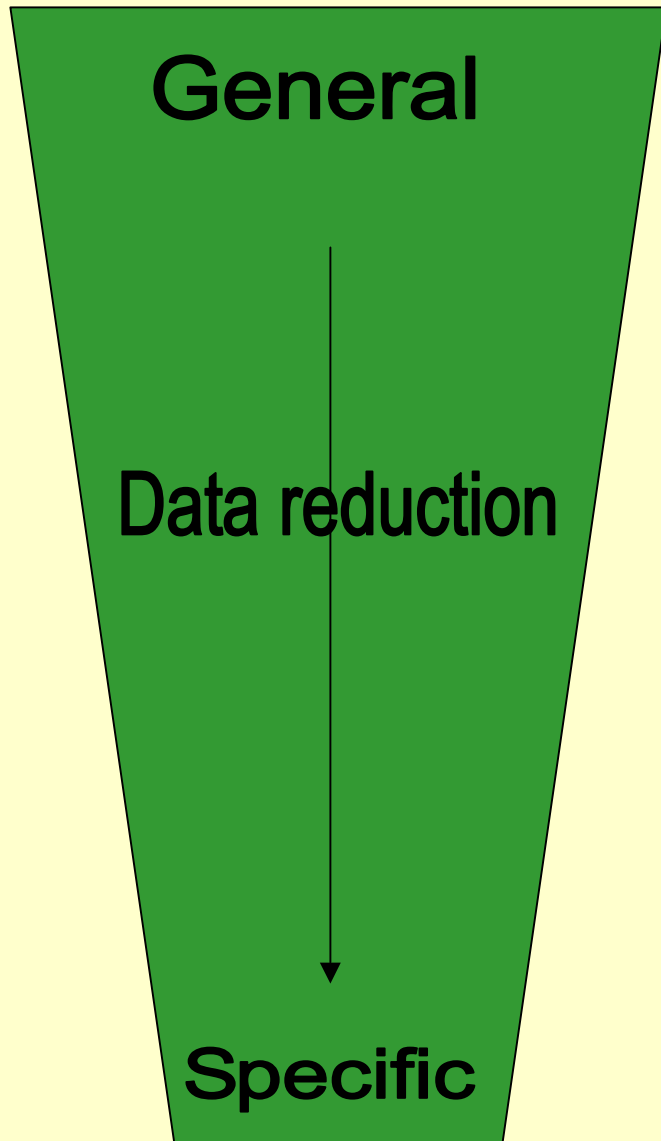
<http://www.lecb.ncifcrf.gov/MAExplorer>

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Data Mining - Finding Putative Relevant Patterns



Quantified array spot data for multiple samples

Organize by sample, gene expr, gene sets

Change views, normalization, data filters

Visualize and query: plots, cluster, reports

Explore external genomic databases

Results

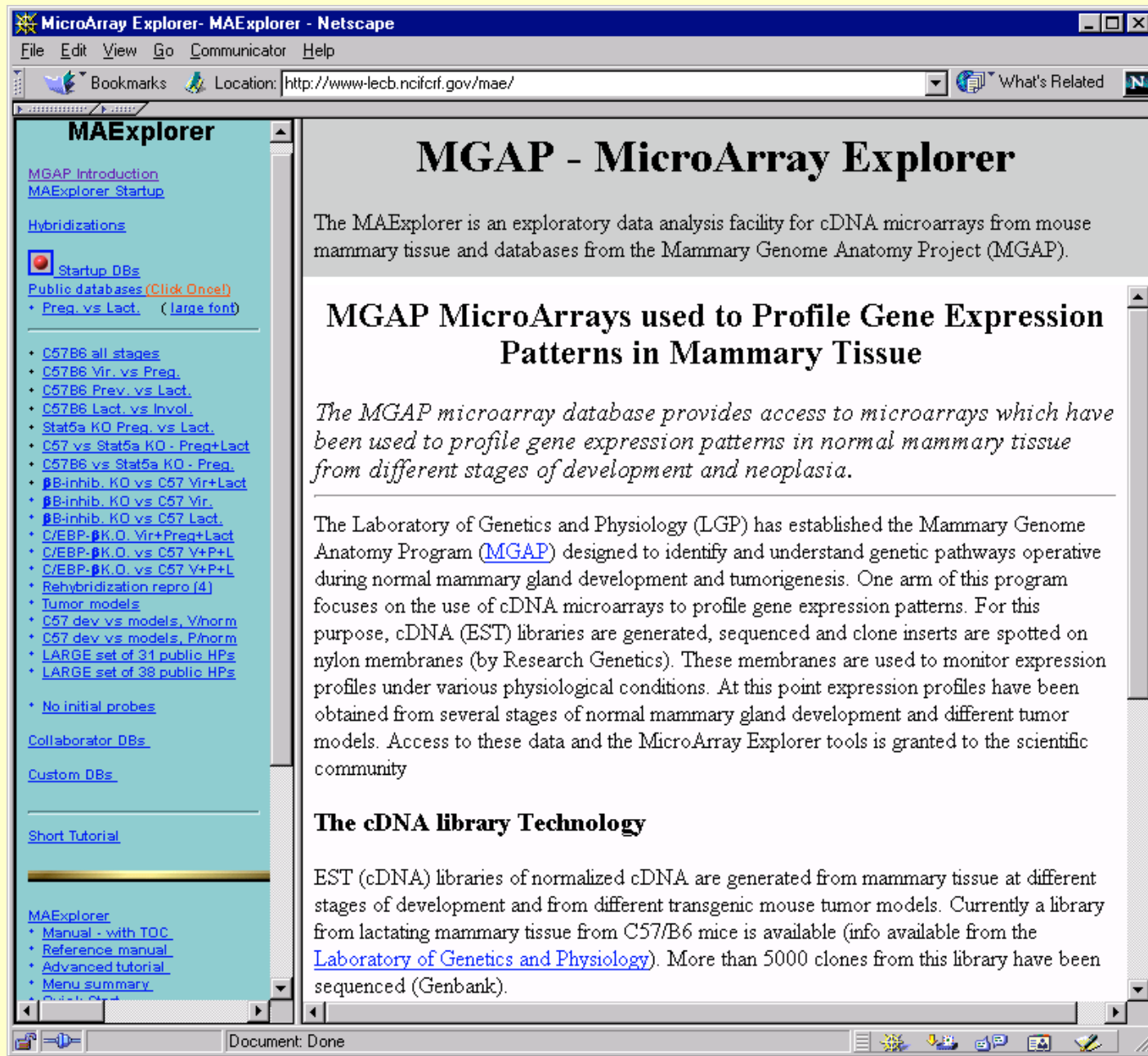
What is the MicroArray Explorer?

- **MAExplorer is a flexible Java stand-alone (off-line) or applet (Web-based) microarray data-mining tool**
- Handles multiple cDNA arrays with replicate spots
- Handles intensity or ratio (Cy3/Cy5) quantified array data
- Analyzes data for 2-conditions and expression profiles
- Data-filters gene sets by statistics, clustering, gene set membership
- Direct data manipulation in graphics, spreadsheets
- Accesses genomic Web servers from plots and reports
- Currently oriented for cDNA, extending to protein arrays

MAExplorer was Developed for the Mammary Genome Anatomy Program

- MGAP models, histology, expression
<http://mammary.nih.gov/>
- Mouse models of
 1. normal mammary development C57B6
 2. Knock-outs: Stat5a (-,-) & (+,-), CEBP null, TGF α etc.
 3. Tumor models: WAP taq, p53 mutant, etc.
 4. Transgenics: WAP Int3, BRCA1, etc.
- Initially, MAExplorer was a Java applet for analyzing MGAP arrays <http://www.lecb.ncifcrf.gov/mae>
- MAExplorer identified genes in preferentially expressed during lactation, ***Nucleic Acids Res.* (2000) 28:4452**

Mammary Genome Anatomy Program MAExplorer <http://www.lecb.ncifcrf.gov/mae>



The screenshot shows a Netscape browser window titled "MicroArray Explorer- MAExplorer - Netscape". The address bar shows the URL "http://www.lecb.ncifcrf.gov/mae/". The main content area features a large heading "MGAP - MicroArray Explorer" and a sub-heading "MGAP MicroArrays used to Profile Gene Expression Patterns in Mammary Tissue". The text describes the MGAP microarray database and its use in profiling gene expression patterns in normal mammary tissue. A sidebar on the left contains a navigation menu with links to "MGAP Introduction", "MAExplorer Startup", "Hybridizations", "Startup DBs", "Public databases (Click Once!)", "C57B6 all stages", "C57B6 Vir. vs Preg.", "C57B6 Prev. vs Lact.", "C57B6 Lact. vs Invol.", "Stat5a KO Preg. vs Lact.", "C57 vs Stat5a KO - Preg+Lact", "C57B6 vs Stat5a KO - Preg.", "BB-inhib. KO vs C57 Vir+Lact", "BB-inhib. KO vs C57 Vir.", "BB-inhib. KO vs C57 Lact.", "C/EBP-βK.O. Vir+Preg+Lact", "C/EBP-βK.O. vs C57 V+P+L", "C/EBP-βK.O. vs C57 V+P+L", "Rehybridization repro (4)", "Tumor models", "C57 dev vs models, V/horm", "C57 dev vs models, P/horm", "LARGE set of 31 public HPs", "LARGE set of 38 public HPs", "No initial probes", "Collaborator DBs", "Custom DBs", "Short Tutorial", "MAExplorer", "Manual - with TOC", "Reference manual", "Advanced tutorial", "Menu summary", and "Quick Start".

MAExplorer

[MGAP Introduction](#)
[MAExplorer Startup](#)

[Hybridizations](#)

[Startup DBs](#)
[Public databases \(Click Once!\)](#)
• [Preg. vs Lact.](#) ([large font](#))

- [C57B6 all stages](#)
- [C57B6 Vir. vs Preg.](#)
- [C57B6 Prev. vs Lact.](#)
- [C57B6 Lact. vs Invol.](#)
- [Stat5a KO Preg. vs Lact.](#)
- [C57 vs Stat5a KO - Preg+Lact](#)
- [C57B6 vs Stat5a KO - Preg.](#)
- [BB-inhib. KO vs C57 Vir+Lact](#)
- [BB-inhib. KO vs C57 Vir.](#)
- [BB-inhib. KO vs C57 Lact.](#)
- [C/EBP-βK.O. Vir+Preg+Lact](#)
- [C/EBP-βK.O. vs C57 V+P+L](#)
- [C/EBP-βK.O. vs C57 V+P+L](#)
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• [No initial probes](#)

[Collaborator DBs](#)

[Custom DBs](#)

[Short Tutorial](#)

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• [Manual - with TOC](#)
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MGAP - MicroArray Explorer

The MAExplorer is an exploratory data analysis facility for cDNA microarrays from mouse mammary tissue and databases from the Mammary Genome Anatomy Project (MGAP).

MGAP MicroArrays used to Profile Gene Expression Patterns in Mammary Tissue

The MGAP microarray database provides access to microarrays which have been used to profile gene expression patterns in normal mammary tissue from different stages of development and neoplasia.

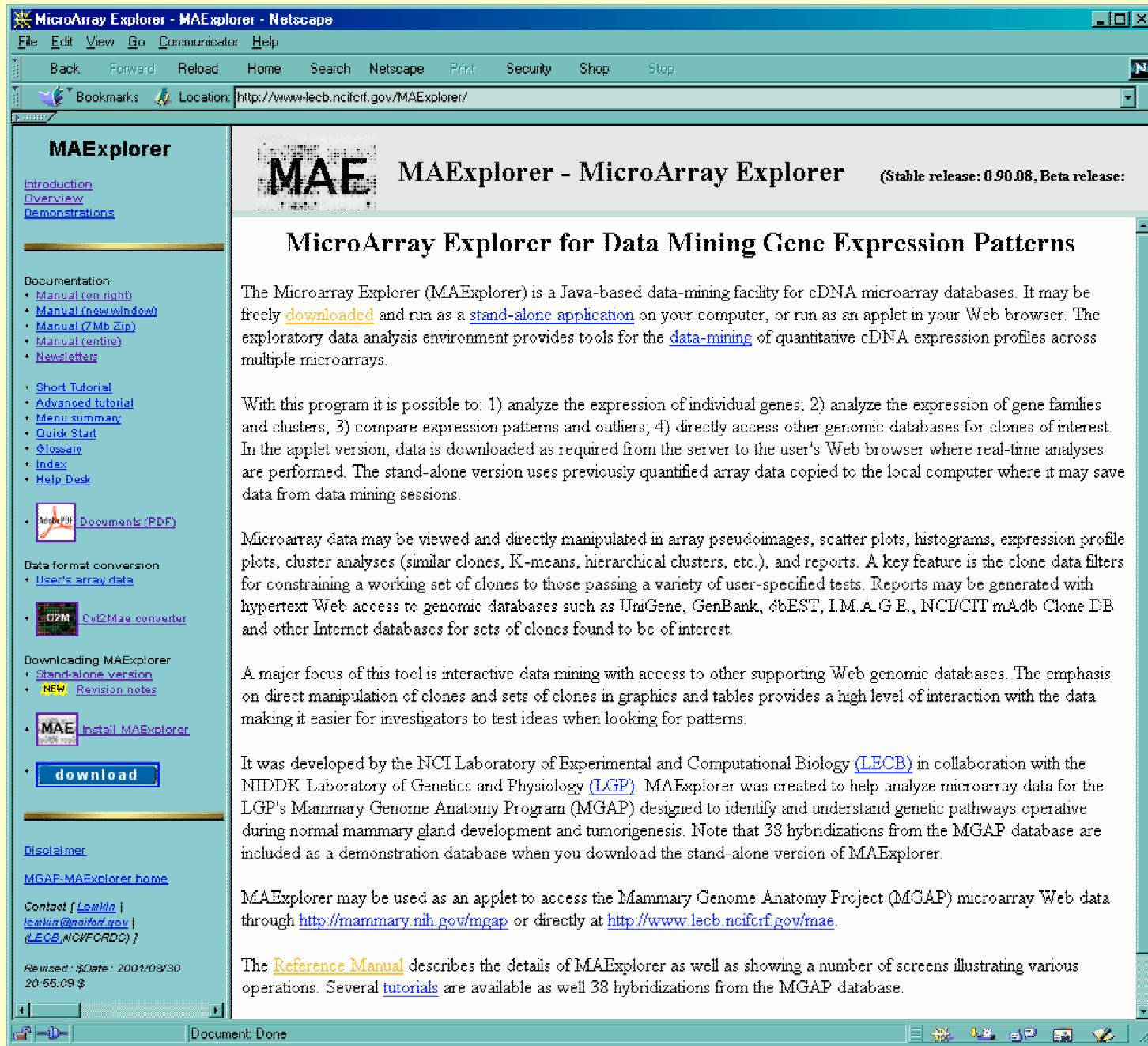
The Laboratory of Genetics and Physiology (LGP) has established the Mammary Genome Anatomy Program ([MGAP](#)) designed to identify and understand genetic pathways operative during normal mammary gland development and tumorigenesis. One arm of this program focuses on the use of cDNA microarrays to profile gene expression patterns. For this purpose, cDNA (EST) libraries are generated, sequenced and clone inserts are spotted on nylon membranes (by Research Genetics). These membranes are used to monitor expression profiles under various physiological conditions. At this point expression profiles have been obtained from several stages of normal mammary gland development and different tumor models. Access to these data and the MicroArray Explorer tools is granted to the scientific community

The cDNA library Technology

EST (cDNA) libraries of normalized cDNA are generated from mammary tissue at different stages of development and from different transgenic mouse tumor models. Currently a library from lactating mammary tissue from C57/B6 mice is available (info available from the [Laboratory of Genetics and Physiology](#)). More than 5000 clones from this library have been sequenced (Genbank).

MAExplorer Home Page

<http://www.lecb.ncifcrf.gov/MAExplorer>



The screenshot shows a Netscape browser window titled "MicroArray Explorer - MAExplorer - Netscape". The address bar shows the URL "http://www.lecb.ncifcrf.gov/MAExplorer/". The page content is organized into a sidebar on the left and a main content area on the right.

MAExplorer

[Introduction](#)
[Overview](#)
[Demonstrations](#)

Documentation

- [Manual \(on right\)](#)
- [Manual \(new window\)](#)
- [Manual \(7 Mb Zip\)](#)
- [Manual \(entire\)](#)
- [Newsletters](#)

• [Short Tutorial](#)

• [Advanced tutorial](#)


• [Menu summary](#)

• [Quick Start](#)

• [Glossary](#)


• [Index](#)

• [Help Desk](#)

•  [Documents \(PDF\)](#)


Data format conversion

- [User's array data](#)

•  [O2M Cvt2Mae converter](#)

Downloading MAExplorer

- [Stand-alone version](#)
- **NEW** [Revision notes](#)

•  [Install MAExplorer](#)

• [download](#)

[Disclaimer](#)

[MGAP-MAExplorer home](#)

Contact ([Leatkin](#) | [leatkin@ncifcrf.gov](#) | [LECB, NCI/FCRF](#))

Revised: \$Date: 2001/08/30 20:55:09 \$

MAExplorer - MicroArray Explorer (Stable release: 0.90.08, Beta release:)

MicroArray Explorer for Data Mining Gene Expression Patterns

The Microarray Explorer (MAExplorer) is a Java-based data-mining facility for cDNA microarray databases. It may be freely [downloaded](#) and run as a [stand-alone application](#) on your computer, or run as an applet in your Web browser. The exploratory data analysis environment provides tools for the [data-mining](#) of quantitative cDNA expression profiles across multiple microarrays.

With this program it is possible to: 1) analyze the expression of individual genes; 2) analyze the expression of gene families and clusters; 3) compare expression patterns and outliers; 4) directly access other genomic databases for clones of interest. In the applet version, data is downloaded as required from the server to the user's Web browser where real-time analyses are performed. The stand-alone version uses previously quantified array data copied to the local computer where it may save data from data mining sessions.

Microarray data may be viewed and directly manipulated in array pseudomages, scatter plots, histograms, expression profile plots, cluster analyses (similar clones, K-means, hierarchical clusters, etc.), and reports. A key feature is the clone data filters for constraining a working set of clones to those passing a variety of user-specified tests. Reports may be generated with hypertext Web access to genomic databases such as UniGene, GenBank, dbEST, I.M.A.G.E., NCI/CIT mAdb Clone DB and other Internet databases for sets of clones found to be of interest.

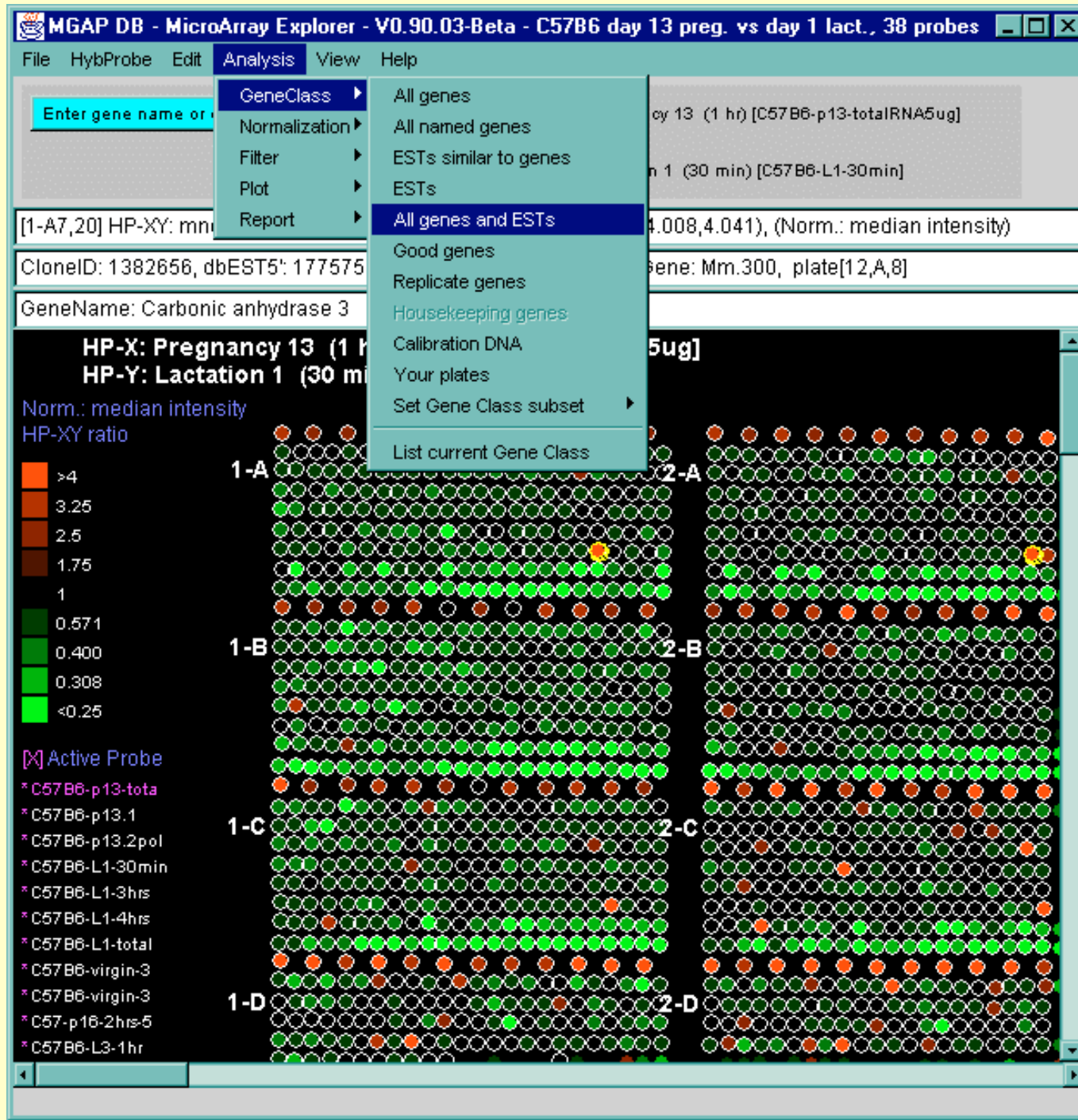
A major focus of this tool is interactive data mining with access to other supporting Web genomic databases. The emphasis on direct manipulation of clones and sets of clones in graphics and tables provides a high level of interaction with the data making it easier for investigators to test ideas when looking for patterns.

It was developed by the NCI Laboratory of Experimental and Computational Biology ([LECB](#)) in collaboration with the NIDDK Laboratory of Genetics and Physiology ([LGP](#)). MAExplorer was created to help analyze microarray data for the LGP's Mammary Genome Anatomy Program (MGAP) designed to identify and understand genetic pathways operative during normal mammary gland development and tumorigenesis. Note that 38 hybridizations from the MGAP database are included as a demonstration database when you download the stand-alone version of MAExplorer.

MAExplorer may be used as an applet to access the Mammary Genome Anatomy Project (MGAP) microarray Web data through <http://mammary.nih.gov/mgap> or directly at <http://www.lecb.ncifcrf.gov/mae>.

The [Reference Manual](#) describes the details of MAExplorer as well as showing a number of screens illustrating various operations. Several [tutorials](#) are available as well 38 hybridizations from the MGAP database.

MAExplorer GUI-based User Interface



Data Sources

- Schema: tab-delimited experiment data files:
 1. GIPO (array print file)
 2. List of samples in DB
 3. Configuration
 4. Separate spot quantification data files
- Use with any experiment data that uses this schema
- Files are read from:
 1. Local disk for stand-alone application or
 2. Web server for Web-browser applet - optionally cached locally
- Used with data from NCI/CIT-ATC mAdb Web server
- The Cvt2Mae tool is used to convert generic data to this schema

Lists of Hybridized Probe (HP) Samples

- Multiple-sample database may consist of many conditions with replicate samples
- Organize samples as lists of conditions:
 1. X and Y pairs of individual samples
 2. Sets of X and Y replicates (X-set, Y-set)
 3. Ordered expression profile list (E-list)
- Manipulate named lists of sample conditions
- Save and restore named sample lists during analysis and between sessions

Operations on 2- & N-conditions of Samples⁽¹⁾

Set of **HP-X** replicate samples

Set of **HP-Y** replicate samples

Operations on sets of replicate samples- e.g. *t*-test, CV statistical tests

Order list of **HP-E** samples

Operations on order lists of samples: e.g. clustering, Expression Profile plots

(1) “HP” is hybridization probe i.e. the sample hybridized to the chip

Choosing HP-X, HP-Y Sets and HP-E Lists

MGAP DB - MicroArray Explorer

File HybProbe Edit Analysis

Enter gene name or clone ID

HP-X: Pregnancy 13
HP-Y: Lactation 1 (3)

Norm.: median intensity
 HP-XY ratio

>4.0
 3.25
 2.5
 1.75
 1.0
 0.571
 0.4
 0.307
 <0.25

1-A
 1-B
 1-C
 1-D

[X] Active Probe

- * C57B6-virgin-3
- * C57B6-virgin-3
- * C57B6-p13-tota
- * C57B6-p13.1
- * C57B6-p13.2pol
- * C57-p16-2hrs-5
- * C57B6-L1-30min
- * C57B6-L1-3hrs
- * C57B6-L1-4hrs
- * C57B6-L1-total
- * C57B6-L3-1hr

Choose HP-X and HP-Y sets, and HP-E list of hybridization probes

Remaining hybridization sample probes

- C57B6 virgin 3 hours #1 [C57B6-virgin-3]
- C57B6 virgin 3 hours #2 [C57B6-virgin-3]
- C57B6 p16 1hr [C57-p16-2hrs-50]
- C57B6 L3 1hr [C57B6-L3-1hr]
- C57B6 L10 29 hrs #1 [C57B6-L10-29hr]
- C57B6 L10 29 hrs #2 [C57B6-L10-29hr]

HP-X set selected

- C57B6 P13 total RNA 5ug [C57B6-p13.1]
- C57B6 P13.1 poly(A) [C57B6-p13.1]
- C57B6 P13.2 poly(A) [C57B6-p13.2po]

Use above probes

HP-Y set selected

- C57B6 L1 30min [C57B6-L1-30min]
- C57B6 L1 3hrs [C57B6-L1-3hrs]
- C57B6 L1 4hrs [C57B6-L1-4hrs]
- C57B6 L1 total RNA [C57B6-L1-total]

Remaining hybridization sample probes

- C57B6 virgin 3 hours #2 [C57B6-virgin-3]
- C57B6 virgin 3 hours #1 [C57B6-virgin-3]

HP-E ordered list selected

- C57B6 P13 total RNA 5ug [C57B6-p13.1]
- C57B6 P13.1 poly(A) [C57B6-p13.1]
- C57B6 P13.2 poly(A) [C57B6-p13.2po]
- C57B6 p16 1hr [C57-p16-2hrs-50]
- C57B6 L1 30min [C57B6-L1-30min]
- C57B6 L1 3hrs [C57B6-L1-3hrs]

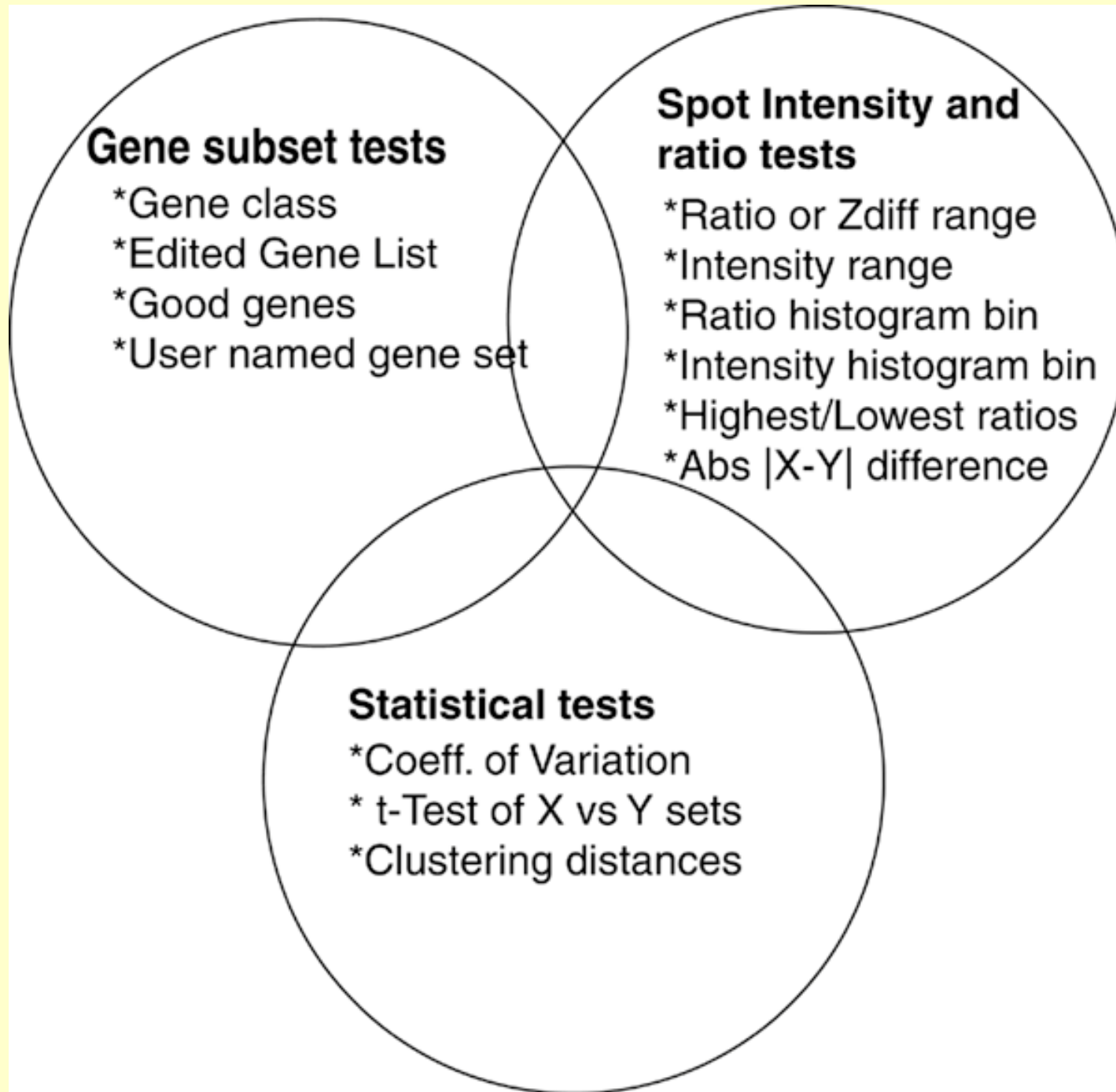
HP: C57B6 virgin 3 hours #1

Project: C57Development

Title: Virgin 10 weeks old (3 hrs) [C57B6-virgin-3hrs-1]

OK Cancel Reset

Gene Data Filter is Intersection of Tests



MAExplorer User Interface - Filter Menu

The screenshot displays the MAExplorer software interface. The main window title is "MGAP DB - MicroArray Explorer - V0.89.12-Beta - Pregnancy day 13: C57BL/6 vs. stat5a (-,-). ...". The "Analysis" menu is open, showing various filtering options. The "Filter by ratio or Zdiff sliders" option is selected, and its sub-menu is also open, showing "Use ratio [R1:R2] or Zdiff [Z1:Z2] sliders" as the active filter. The "Preference sliders" dialog box is also visible, showing the current values for Ratio R1 (0.65), Ratio R2 (1.5), and Spot CV (0.108).

MGAP DB - MicroArray Explorer - V0.89.12-Beta - Pregnancy day 13: C57BL/6 vs. stat5a (-,-). ...

File HybProbe Edit **Analysis** View Help

Enter gene name or

Setting GeneClass t

There are 41 genes passing the Filter

HP-X: C57B6 pregnancy
HP-Y: Stat5a (-,-) pregna

Norm.: median intensity
HP-XY 'set' ratio

1-A
1-B
1-C
1-D
2-C
2-D

Filter menu options:

- GeneClass
- Normalization
- Filter**
 - Filter by GeneClass membership
 - Filter by 'User Filter Gene Set' membership
 - Filter by 'Edited Gene List' membership
 - Filter by 'good genes list' membership
 - Filter by ratio histogram bin
 - Filter by intensity histogram bin
 - Filter by spot intensity [S1:S2] sliders
 - Filter by intensity [I1:I2] sliders
 - Filter by ratio or Zdiff sliders**
 - Use ratio [R1:R2] or Zdiff [Z1:Z2] sliders
 - Inside range
 - Outside range
 - Filter by Spot CV
 - Filter by HP-X,HP-Y t-Test [p-Value] slider
 - Filter by HP-X,HP-Y 'sets' t-Test [p-Value] slider
 - Filter by HP-E clustering [Cluster Dist] slider
 - Filter by Diff(HP-X,HP-Y) [Abs.Diff.] slider
 - Filter genes with highest X/Y ratio or X-Y Zdiff
 - Filter genes with lowest X/Y ratio or X-Y Zdiff
- Plot
- Report

Preference sliders dialog box:

Preference sliders

State scrollers

Ratio R1 0.65

Ratio R2 1.5

Spot CV 0.108

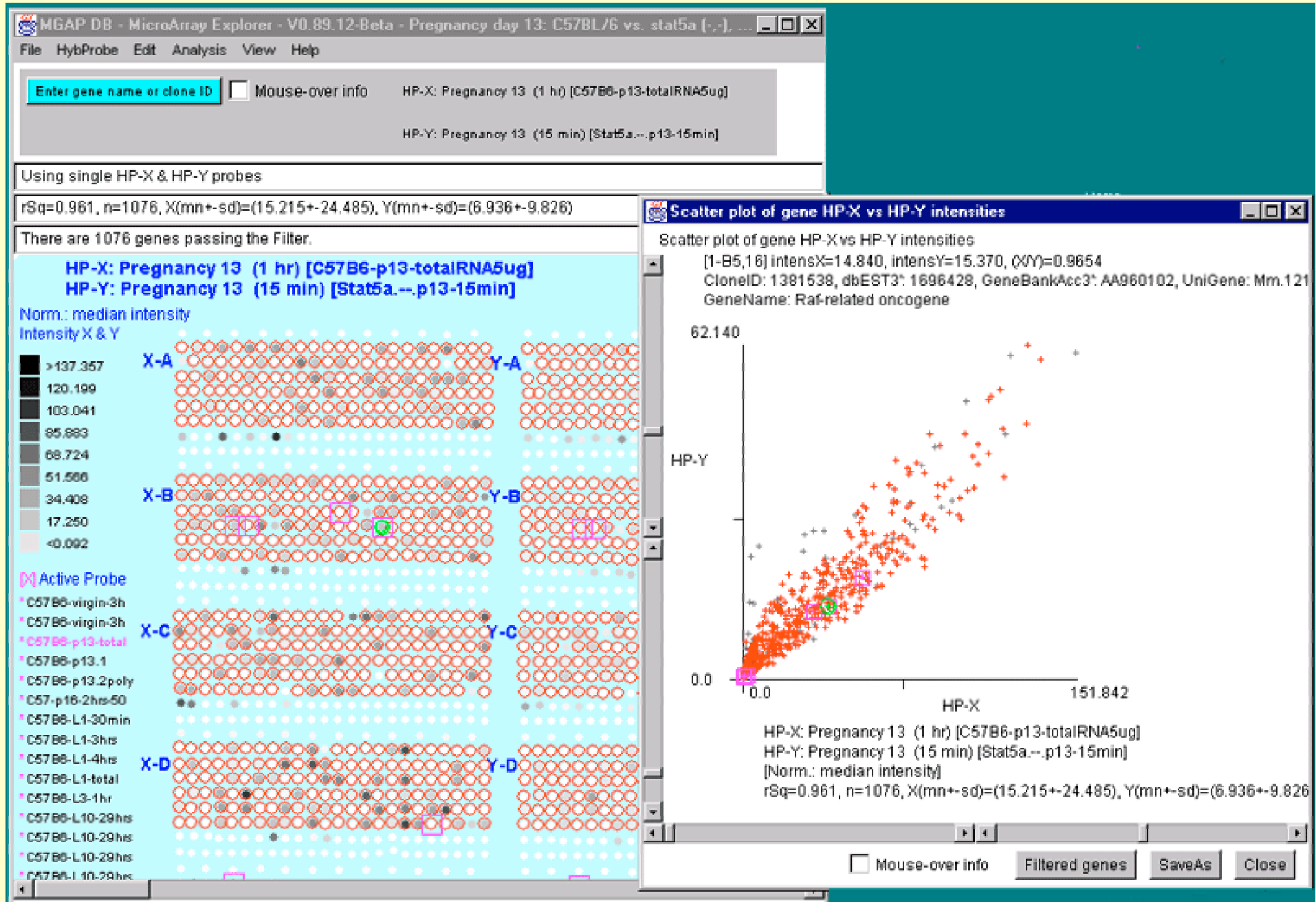
Plots

Plots allow visualization and direct manipulation of gene data

1. Pseudo array image - intensity, ratio (X/Y)
2. Zoomable scatter plots - X vs Y, Cy3 vs Cy5, duplicate spots
3. Histograms - ratio and intensity
4. Expression profiles - individual genes and overlay plots
5. Silhouette plots - similarity clusters, K-means clustering
6. Hierarchical clustering - clustergram, dendrogram

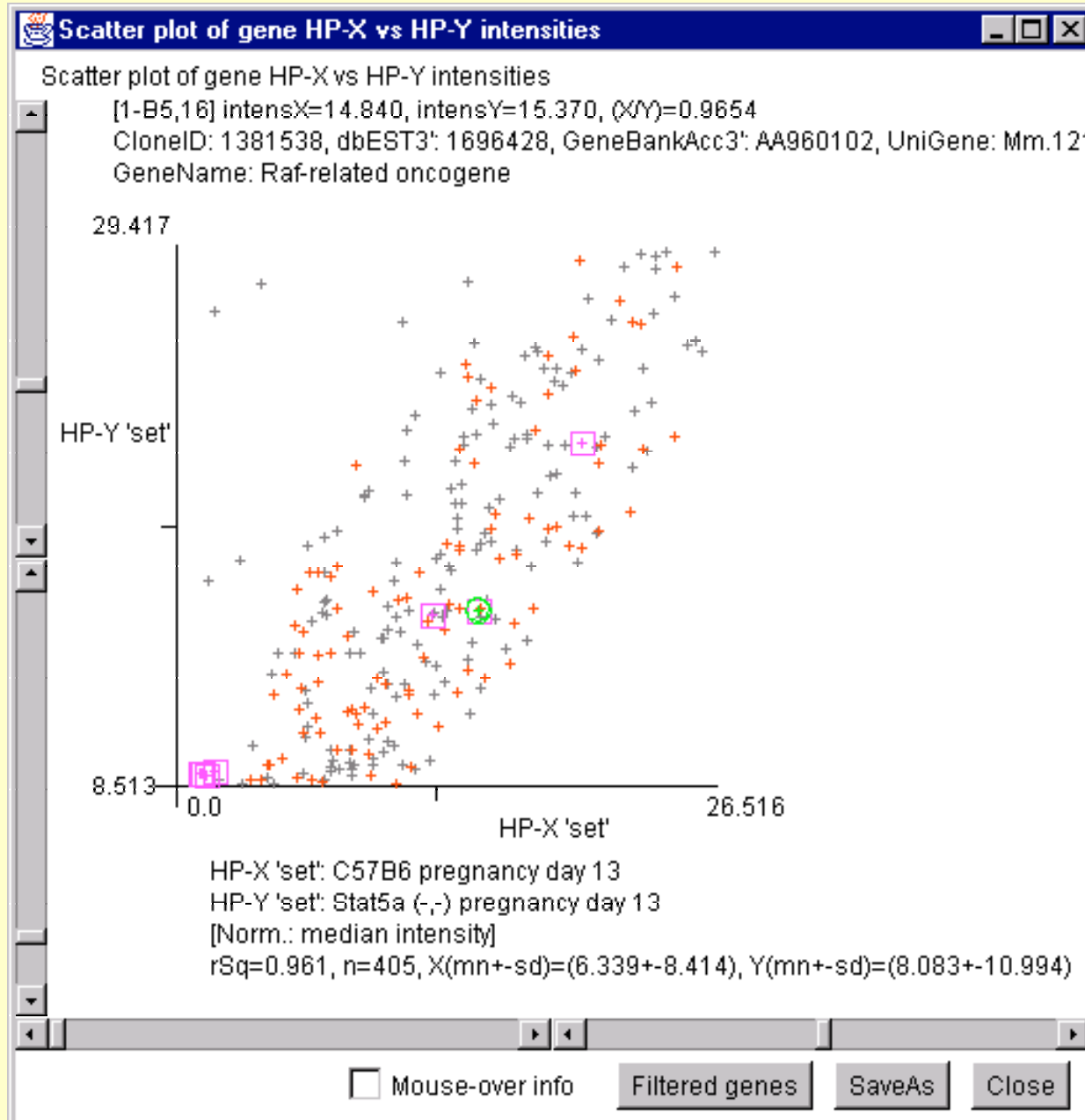
Scatter Plots of Two Conditions

- X-Y scatter plot of two 13-day pregnancy samples: C57B6 vs Stat5a (-,-) [MGAP]

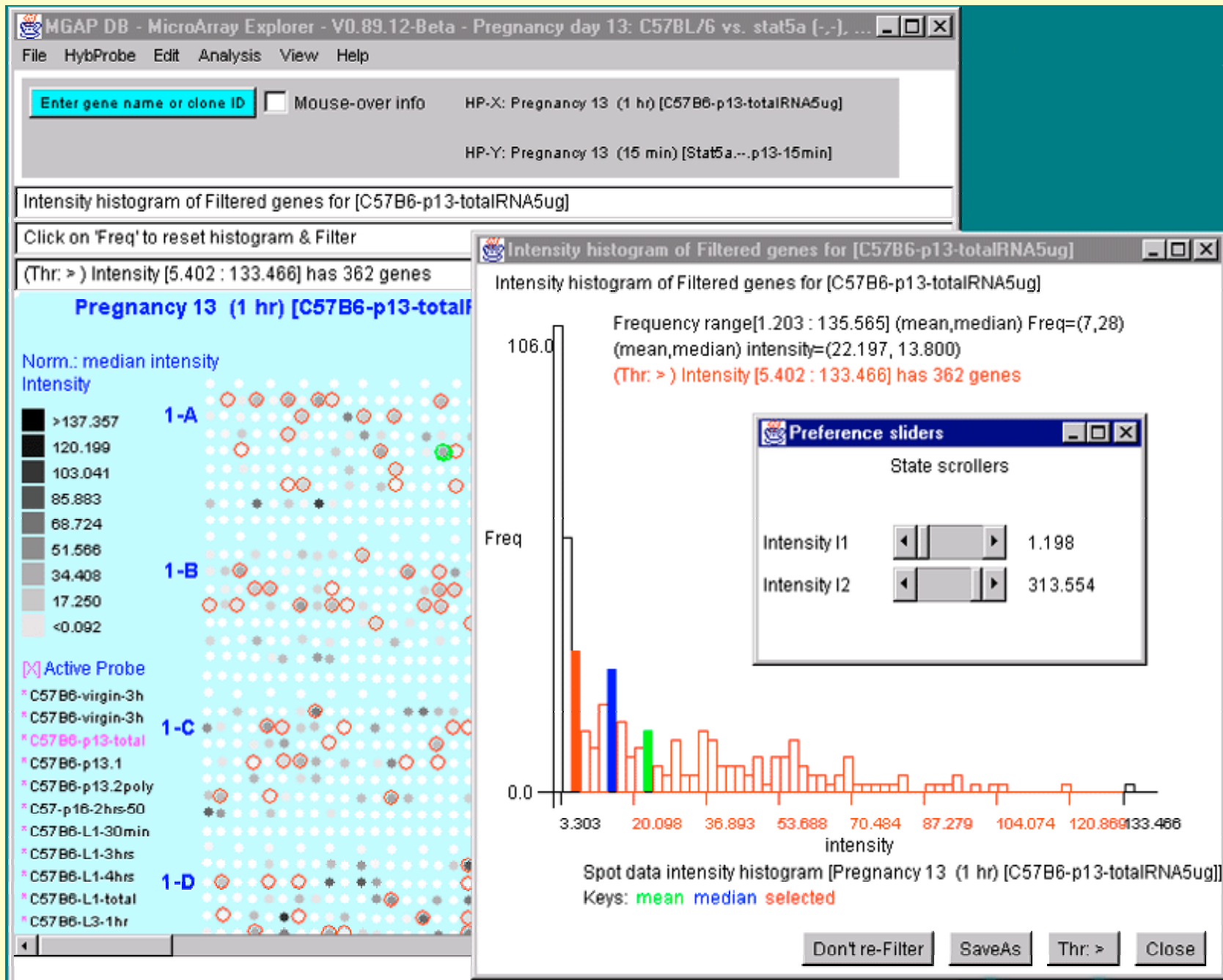


Zoomed X-Y Scatter Plot

- Zoomed-in on Raf-related oncogene (green circle) using scrollbars
- Genes not passing Filter may be grayed out in the plot



Genes Filtered by Intensity-Histogram Bin



Expression Profile Plots of N-conditions

MGAP DB - MicroArray Explorer - V0.89.12-Beta - Pregnancy day 13: C57BL/6 vs. stat5a (-), ...

File HybProbe Edit Analysis View Help

Enter gene name or clone ID MOUSE-OVER info HP-X: Pregnancy 13 (1 hr) [C57B6-p13-totalRNA5ug]
HP-Y: Pregnancy 13 (15 min) [Stat5a...-p13-15min]

[1-A,7] intensity[F1]=31.9504, intensity[F2]=26.4701, F1/F2=1.2070, (Norm.: median intensity)

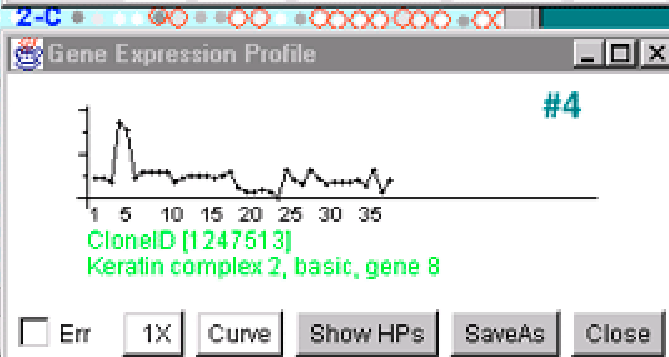
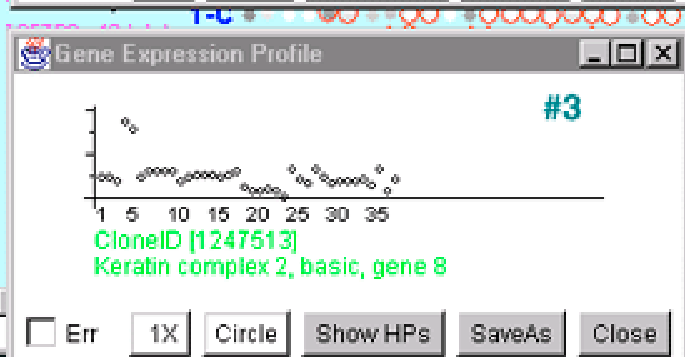
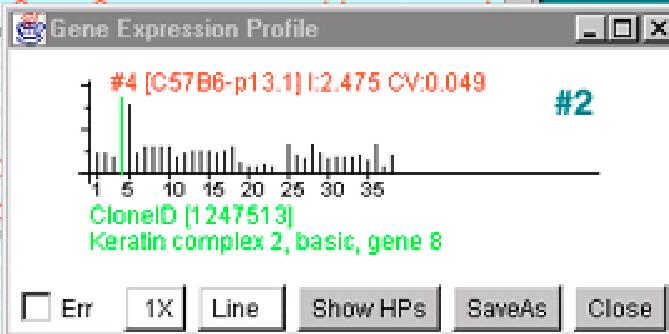
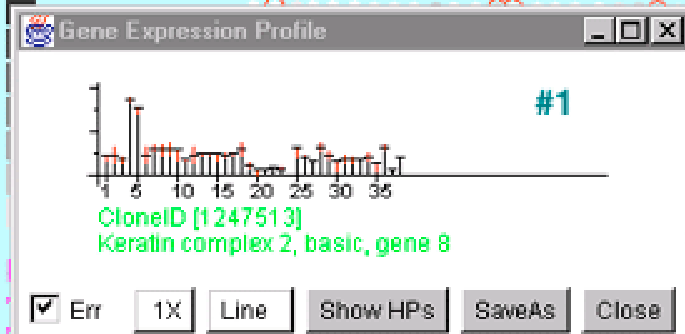
CloneID: 1247513, dbEST3: 1696290, GeneBankAcc3: AA959964, UniGene: Mm.6800, plate[3,A,7]

GeneName: Keratin complex 2, basic, gene 8

Pregnancy 13 (1 hr) [C57B6-p13-totalRNA5ug]

Norm.: median intensity
Intensity

>137.357 1-A 2-A
120.199



Current HP-E expression profile assi...

Current hybridization probe expression profile HP-E 'set a'

- #1 Virgin 10 weeks old (3 hrs) [C57B6-virgin-3hrs-1]
- #2 Virgin 10 weeks old (3 hrs) [C57B6-virgin-3hrs-2]
- #3 Pregnancy 13 (1 hr) [C57B6-p13-totalRNA5ug]
- #4 Pregnancy 13 (1 hr) [C57B6-p13.1]
- #5 Pregnancy 13 (1 hr) [C57B6-p13.2poly-A]
- #6 Pregnancy 16 (1hr) [C57-p16-2hrs-50]
- #7 Lactation 1 (30 min) [C57B6-L1-30min]
- #8 Lactation 1 (3 hrs) [C57B6-L1-3hrs]
- #9 Lactation 1 (4 hrs) [C57B6-L1-4hrs]
- #10 Lactation 1 (30 min) [C57B6-L1-total]
- #11 Lactation 3 (1 hr) [C57B6-L3-1hr]
- #12 Lactation 10 (29 hrs) [C57B6-L10-29hrs-1]
- #13 Lactation 10 (29 hrs) [C57B6-L10-29hrs-2]
- #14 Lactation 10 (29 hrs) [C57B6-L10-29hrs-2nd-1]
- #15 Lactation 10 (29 hrs) [C57B6-L10-29hrs-2nd-2]
- #16 Lactation 10 (6 hrs) [C57B6-L10-6hrs-1]
- #17 Lactation 10 (hrs) [C57B6-L10-6hrs-2]
- #18 Involution 4 (25 hrs) [C57B6-I4-25hrs]
- #19 Pregnancy 13 (15 min) [Stat5a...-p13-15min]
- #20 Pregnancy 13 (15 min) [Stat5a...-p13-15min2]
- #21 Pregnancy 13 (1 hr) [Stat5a...-p13-1hr2]
- #22 Pregnancy 13 (30 min) [Stat5a...-p13-30min]
- #23 Pregnancy 13 (30 min) [Stat5a...-p13-30min2]
- #24 Lactation 1 (30 min) [Stat5a...-L1-30min]
- #25 Virgin (18 hrs) [CEBP-null-virgin-18hrs]
- #26 Pregnancy 13 (18 hrs) [CEBP-null-p13-18hrs]
- #27 Pregnancy 16 (18 hrs) [CEBP-null-p16-18hrs]
- #28 Lactation 1 (1 hr) [CEBP-null-1hr]
- #29 Pregnancy 18 (1 hr) [4A-1hr]
- #30 Pregnancy 18 (5 hrs) [4B-1hr]
- #31 Pregnancy 18 (1 hr) [4C-5hrs]
- #32 * (1 hr) [BA-1hr]
- #33 Virgin (1 hr) [BetaB-Hemo]
- #34 Virgin (1 hr) [BetaB-null-1hr]
- #35 * (1 hr) [HR1-1hr]
- #36 * (5 hrs) [HR2-5hrs]
- #37 Lactation 1 (1 hr) [Inh-31-null-1hr]
- #38 * (1 hr) [WAP-Tag-tumor-1hr]

#5 SaveAs Close

Cluster Genes With Similar Expression

MGAP DB - MicroArray Explorer - V0.89.12-Beta - Pregnancy day 13: C57BL/6 vs. stat5a (-/-) ...

File HybProbe Edit Analysis View Help

Enter gene name or clone ID Mouse-over info HP-X: Pregnancy HP-Y: Pregnancy

[1-B5,16] intensity[F1]=33.0483, intensity[F2]=44.4292, F1/F2=0.7436

CloneID: 1381538, dbEST3: 1696428, GeneBankAcc3: AA960102, U

GeneName: Raf-related oncogene

Pregnancy 13 (1 hr) [C57B6-p13-totalRNA5ug]

Norm.: median intensity
Intensity

- >137.357
- 120.199
- 103.041
- 85.893
- 68.724
- 51.588
- 34.408
- 17.260
- <0.092

Active Probe

- * C57 B6-virgin-3h
- * C57 B6-virgin-3h
- * C57 B6-p13-total
- * C57 B6-p13.1
- * C57 B6-p13.2poly
- * C57-p16-2his-50

Preference sliders

State scrollers

Cluster Distance 10.346

Clusters of specified gene

43 genes in cluster for gene [1381538] Raf-related oncogene

Nbr	CloneID	Similarity	Distance	Gene_Name
#1	1381538	*****	0.0	Raf-related oncogene
#2	1248384	*****	3.3601	Mouse mRNA for 65-kDa macrophage cyt
#3	1248432	*****	3.9787	Prosaposin
#4	1382080	*****	5.5852	ESTs
#5	1248050	*****	5.6164	Mus musculus C57BL/6J ribosomal protein S28 mR
#6	1248601	*****	5.8478	EST
#7	1247522	*****	5.8186	Mus musculus calpain small subunit mRNA, comple
#8	1248181	*****	6.1459	ESTs, Weakly similar to endophilin II [M.musculus]
#9	1248071	*****	6.2855	Histocompatibility 2, class II, locus Ma
#10	1248205	*****	6.4061	Zinc finger protein 147
#11	1248612	*****	6.4636	ESTs, Moderately similar to PIM-1 PROTO-ONCOG
#12	1248061	*****	6.4987	Actin, alpha 1, skeletal muscle
#13	1382182	*****	6.5649	ESTs
#14	1247698	*****	6.5988	Adipocyte protein aP2
#15	1247603	****	7.1112	ESTs
#16	1247827	****	7.3611	ESTs, Highly similar to ATP SYNTHASE LIPID-BIN
#17	1247760	****	7.4661	Protein tyrosine phosphatase, non-receptor type sub
#18	1247612	****	7.5083	ESTs, Weakly similar to GLUTATHIONE S-TRANSFI
#19	1248312	****	7.6253	Protein kinase, mitogen activated kinase 3
#20	1382228	****	7.7015	ESTs, Moderately similar to 60S RIBOSOMAL PRC
#21	1382320	****	7.7464	ESTs, Weakly similar to unknown [S.cerevisiae]
#22	1247687	****	7.8393	ESTs
#23	1382089	****	7.9175	ESTs, Highly similar to EUKARYOTIC INITIATION I
#24	1247513	****	7.9329	Keratin complex 2, basic, gene 8
#25	1382133	****	8.1094	ESTs
#26	1248293	****	8.1281	ESTs
#27	1247621	****	8.1290	Mus musculus Lsc (lsc) oncogene mRNA, complete c
#28	1247553	****	8.2108	Mus musculus bodenin gene
#29	1248599	****	8.2894	ESTs
#30	1248418	****	8.3709	ESTs
#31	1381975	****	8.3764	ESTs
#32	1248239	****	9.1466	ESTs
#33	1381822	****	9.2046	ESTs
#34	1248489	****	9.2580	Preperdin factor, complement
#35	1248025	****	9.3017	ESTs
#36	1248108	****	9.5695	ESTs
#37	1382537	****	9.7768	ESTs
#38	1247609	****	9.9234	ESTs
#39	1247778	****	9.9948	Membrane protein, palmitoylated (55 kDa)
#40	1382220	****	10.0418	ESTs
#41	1382676	****	10.1512	ESTs, Highly similar to MATRIN 3 [Rattus norvegic

Go 'Cluster gene counts' EP plot Cluster-Report SaveAs Close

K-means Clustering of Expression Data

MGAP DB - MicroArray Explorer - V0.89.12-Beta - Pregnancy day 13: C57B1/6 vs. stat5a (-)

Scatter plot of gene HP-X vs HP-Y intensities

Scatter plot of gene HP-X vs HP-Y intensities
 [1-E4,16] intensX=49.203, intensY=17.632, (X/Y)=2.7904
 ClonID: 1246293, dbEST3: 2279221, GeneBankAcc3: AI463151
 GeneName: ESTs

HP-X: Pregnancy 13 (1 hr) [C57B6-p13-totalRNA5ug
 HP-Y: Pregnancy 13 (15 min) [Stat5a.--p13-15min]
 [Norm.: median intensity]
 rSq=0.956, n=73, X(mn+-sd)=(22.965+-26.877), Y(mn+-sd)=(17.632+-26.877)

Mouse-over info

Cluster report for 6 N-Primary Nodes

1247785	****	3	7.204 ESTs
1249521	"	3	8.806 Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds
1381544	"	3	10.895 ESTs, Moderately similar to CALPONIN, ACIDIC ISOFORM [Rattus norvegicus]
1382139	*****	4	NPN [26 genes] in cluster [distNext: 22.580] wiCdist:mn+-sd=11.919+-4.503 CV=0.377 ES*
1247982	*****	4	6.597 ESTs
1248320	*****	4	6.836 ESTs, Weakly similar to HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHRO
1381622	*****	4	7.410 ESTs
1381699	*****	4	7.830 ESTs, Weakly similar to titin [H.sapiens]
1382208	*****	4	8.165 ESTs
1248293	*****	4	8.231 ESTs
1247621	*****	4	8.245 Mus musculus Loo (
1382089	*****	4	8.597 ESTs, Highly simil
1248422	*****	4	9.372 ESTs
1382753	*****	4	9.962 Mus musculus clea
1248152	*****	4	10.085 M. musculus mRN
1248108	*****	4	10.188 ESTs
1247605	*****	4	10.755 ESTs, Weakly simi
1381981	*****	4	11.306 ESTs, Highly simil
1382676	*****	4	11.603 ESTs, Highly simi
1247500	*****	4	11.868 ESTs
1249482	*****	4	12.002 Sterol O-acyltransf
1249488	*****	4	12.164 ESTs, Highly simi
1381940	*****	4	12.613 ESTs, Moderately similar to 6-LIPOXYGENASE ACTIVATING PROTEIN [Ovis an
1247881	***	4	14.789 ESTs
1382201	**	4	17.183 ESTs
1382234	"	4	18.660 CDS antigen, beta chain
1247755	"	4	19.246 ESTs, Highly similar to AUTOANTIGEN PM-SCL [Homo sapiens]
1382281	"	4	21.739 ESTs, Weakly similar to F43C1.3 [C.elegans]
1247935	*****	5	NPN [14 genes] in cluster [distNext: 0.235] wiCdist:mn+-sd=1.686+-2.751 CV=1.631 ES*
1382689	*****	5	0.273 ESTs, Moderately similar to COP1 REGULATORY PROTEIN [Arabidopsis thaliana]
1382585	*****	5	0.387 ESTs, Weakly similar to Zk593.7 [C.elegans]
1248224	*****	5	0.409 ESTs
1381909	*****	5	0.440 ESTs
1248225	*****	5	0.511 Mus musculus heat shock transcription factor 1 (Hsf1) gene, partial cds
1382094	*****	5	0.550 High mobility group protein 1
1382750	*****	5	0.566 Thymoma viral proto-oncogene
1248056	*****	5	0.578 ESTs
1381592	*****	5	1.173 Surflet gene 4
1248054	*****	5	1.173 ESTs, Highly similar to HYPOTHETICAL 34.7 KD PROTEIN IN SPT10-CD14 IN
1382500	*****	5	1.191 ESTs
1248068	*****	5	5.842 ESTs
1248279	*****	5	10.278 ESTs
1247622	*****	6	NPN [13 genes] in cluster [distNext: 0.235] wiCdist:mn+-sd=0.223+-0.081 CV=0.365 ES*
1381603	*****	6	0.183 ESTs, Weakly similar to ubiquitin conjugating enzyme [M.musculus]
1247579	*****	6	0.168 ESTs, Highly similar to SEROTRANSFERRIN PRECURSOR [Homo sapiens]

Preference sliders

State scrollers

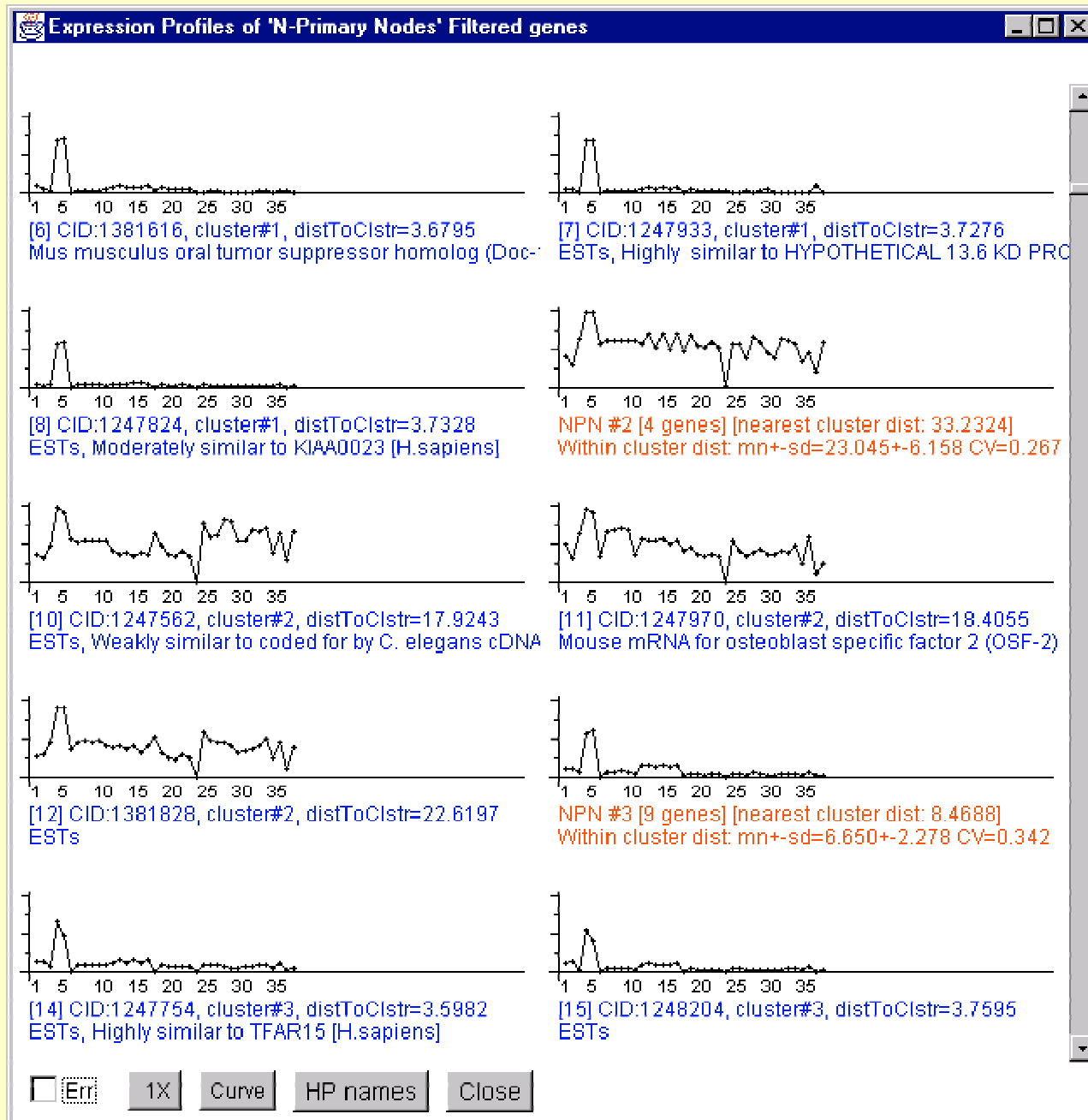
Spot CV

of Clusters

1-D 2-D

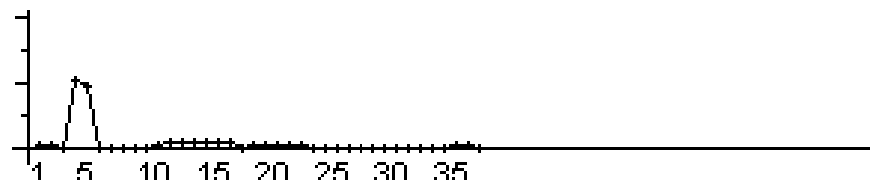
List of Expression Profiles Plots of Clusters

- Scrollable list of EP plots showing genes from clusters #1, #2, #3

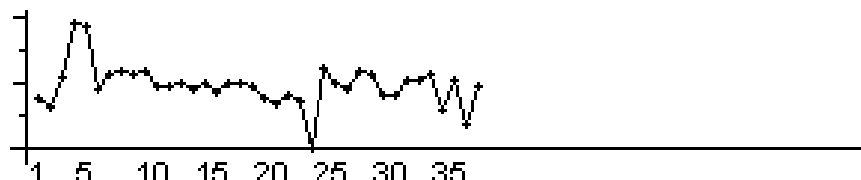


Mean Expression Profiles of K-means Clusters

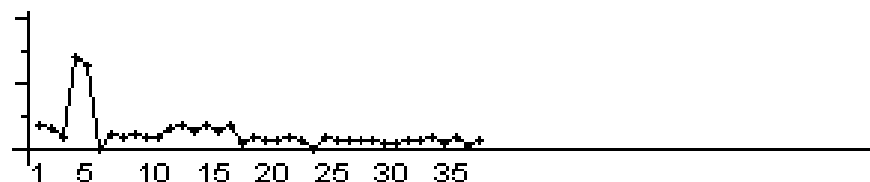
Mean Expression Profiles of 'N-Primary Nodes' clusters



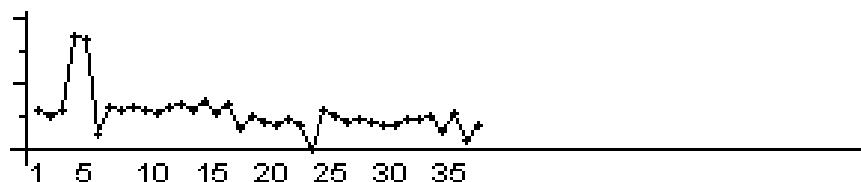
NPN #1 [8 genes] [nearest cluster dist: 1.8891]
Within cluster dist: mn+-sd=2.152+-1.254 CV=0.582



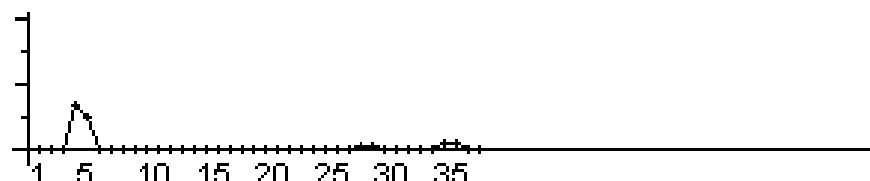
NPN #2 [4 genes] [nearest cluster dist: 33.2324]
Within cluster dist: mn+-sd=23.045+-6.158 CV=0.267



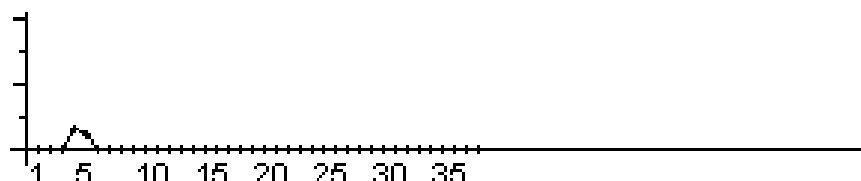
NPN #3 [9 genes] [nearest cluster dist: 8.4688]
Within cluster dist: mn+-sd=6.650+-2.278 CV=0.342



NPN #4 [25 genes] [nearest cluster dist: 22.5600]
Within cluster dist: mn+-sd=11.919+-4.503 CV=0.377



NPN #5 [14 genes] [nearest cluster dist: 0.2357]
Within cluster dist: mn+-sd=1.686+-2.751 CV=1.631



NPN #6 [13 genes] [nearest cluster dist: 0.2357]
Within cluster dist: mn+-sd=0.223+-0.081 CV=0.365

Err

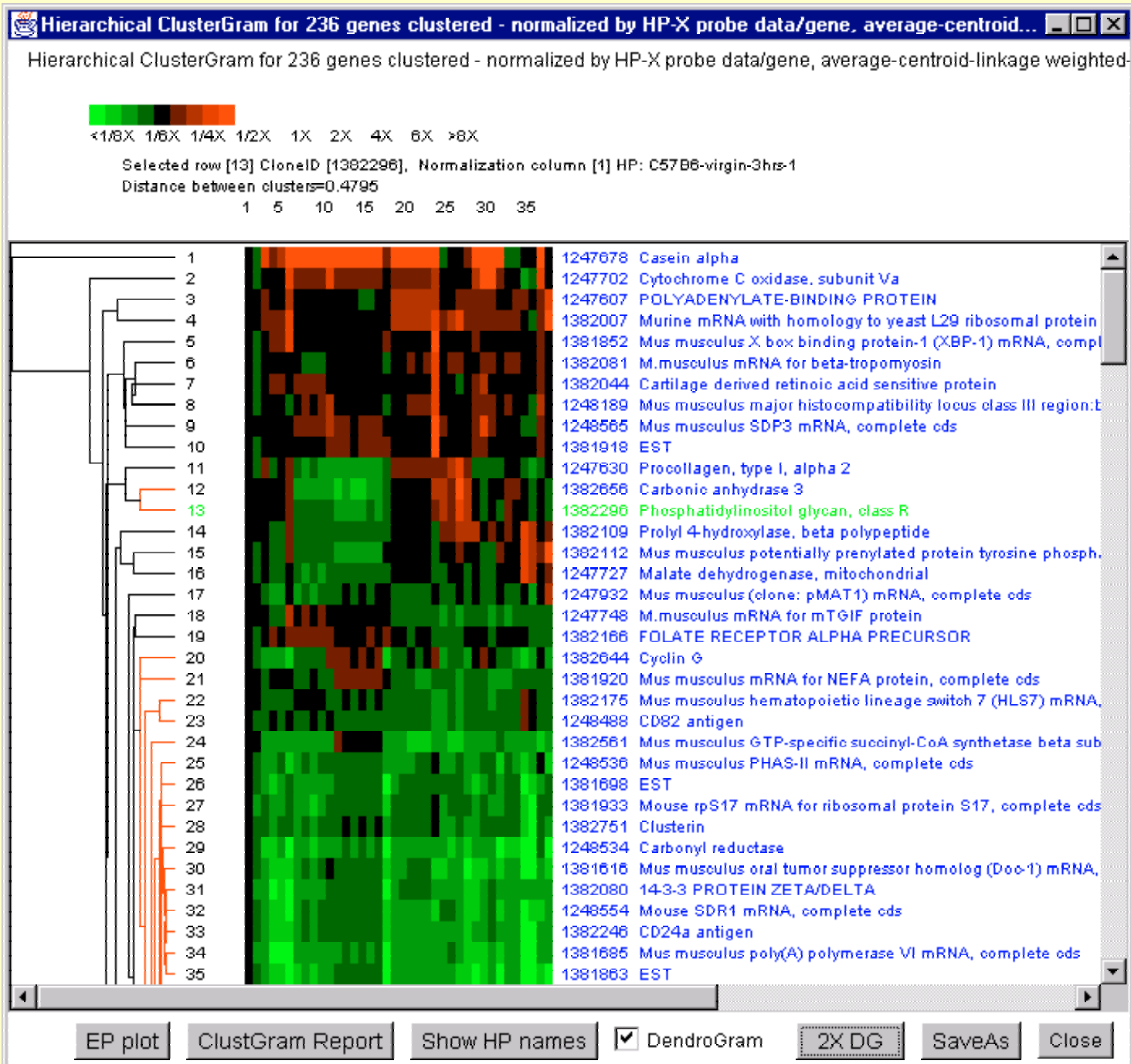
1X

Curve

HP names

Close

Hierarchical Clustering of Expression Data



Reports

- Data reported as:
 1. Web-accessible dynamic spreadsheets or
 2. tab-delimited text exportable to Excel
- Gene set reports - linked to UniGene, GenBank, mAdb, LocusLink, etc.
- Array sample reports - linked to histology and model Web pages
- Pop-up Web browser on specific data from dynamic reports or plots

Gene Set Operations Help Manage Data and Search Results

- All gene sets are named with a directory of existing sets
- Set operations (AND, OR, DIFFERENCE) may be used to create new derived sets
- Special sets:
 1. Filtered genes set holds genes passing the data filter
 2. Edited Gene List holds results of clustering or editing
 3. Normalization set may be used as normalization method
 4. User data filter set may be used as a data filter
- Sets are saved when the session is saved, restored when MAExplorer restarted

Find Gene or Gene Subset by Name Guesser

MGAP DB - MicroArray Explorer - V0.89.12-Beta - Pregnancy day 13: C57BL/6 vs. stat5a (-/-). ...

File HybProbe Edit Analysis View Help

Enter gene name or clone ID Mouse-over info HP-X: Pregnancy 13 (1 hr) [C57B6-p13-totalRNA5ug]
HP-Y: Pregnancy 13 (15 min) [Stat5a...p13-15min]

Showing Edited Gene List

$rSq=0.953, n=405, X(mn+-sd)=(15.416+-23.958), Y(mn+-sd)=(7.098+-9.443)$

There are 405 genes passing the Filter.

Pregnancy 13 (1 hr) [C57B6-p13-totalRNA5ug]

Norm.: median intensity
Intensity

- >137.357
- 120.199
- 103.041
- 85.883
- 68.724
- 51.566
- 34.408
- 17.250
- <0.092

Active Probe

- * C57B6-virgin-3h
- * C57B6-virgin-3h
- * C57B6-p13-total
- * C57B6-p13.1
- * C57B6-p13.2poly
- * C57-p16-2hrs-50
- * C57B6-L1-30min
- * C57B6-L1-3hrs
- * C57B6-L1-4hrs
- * C57B6-L1-total
- * C57B6-L3-1hr
- * C57B6-L10-29hrs
- * C57B6-L10-29hrs
- * C57B6-L10-29hrs
- * C57B6-L10-29hrs

Gene Guesser

Enter gene name or clone ID

ONCO

- ESTs, Highly similar to A-RAF PROTO-ONCOGENE SERINI
- ESTs, Moderately similar to FIM-1 PROTO-ONCOGENE SE
- ESTs, Moderately similar to PKS PROTO-ONCOGENE SER
- Jun-B oncogene
- Mus musculus Lsc (lsc) oncogene mRNA, complete cds
- Raf-related oncogene
- Thymoma viral proto-oncogene

Set E.G.L. Done Gene Name Cancel Clear

Gene Set Operations - e.g. 'AND' of Two Sets

The screenshot displays the MGAP DB - MicroArray Explorer interface. The main window shows a heatmap of gene expression data with a color scale from red (>4) to green (<0.25). The heatmap is divided into four quadrants labeled 1-A, 1-B, 1-C, and 1-D. A legend on the left indicates the color scale and lists active probes. An 'Operation dialog - (1st AND 2nd)' window is open, showing the process of combining two gene sets. The dialog has fields for 'Enter 1st gene set name or #' and 'Enter 2nd gene set name or #'. Both fields contain '60 genes closest to Carbonic Anhydrase-III'. Below these are dropdown menus for selecting the operation, both set to 'ALL NAMED GENES'. The 'Enter new gene set name of result' field contains 'named genes in 60 closest to CA-III'. The dialog also has 'Ok' and 'Cancel' buttons. In the background, the 'User Gene Sets' window is visible, listing various gene sets such as '#1 [1727] ALL GENES', '#2 [405] ALL NAMED GENES', and '#11 [32] User Filter Gene Set [assigned: named genes in 60 closest to Carbonic Anhydrase-III]'. The 'MGAP DB - MicroArray Explorer' window title bar shows 'MGAP DB - MicroArray Explorer - V0.90.03-Beta - C57B6...'. The menu bar includes 'File', 'HybProbe', 'Edit', 'Analysis', 'View', and 'Help'. The main window has a search bar 'Enter gene name or clone ID' and a 'Mouse-over info' checkbox. The main window also shows 'HP-X: Pregnancy 13 (1)' and 'HP-Y: Lactation 1 (30 m'.

MGAP DB - MicroArray Explorer - V0.90.03-Beta - C57B6...

User Gene Sets

User Gene Sets
Set# |#genes| title

#1 [1727] ALL GENES
#2 [405] ALL NAMED GENES
#3 [244] ESTs similar to genes
#4 [427] ESTs
#5 [1076] All genes and ESTs
#6 [1727] Good genes
#7 [259] Replicate genes
#8 [0] HousekeepingGenes
#9 [96] Calibration DNA
#10 [77] Your plates
----- User Assignable -----
#11 [32] User Filter Gene Set [assigned: named genes in 60 closest to
#12 [60] Edited Gene List
#13 [0] Normalization Gene Set
----- User definable-----
#14 [1727] ALL CLONES
#15 [1727] Good clones
#16 [60] 60 genes closest to Carbonic Anhydrase-III
#17 [3] subset of replicate genes in 60 genes closet to CA-III
#18 [2] named genes in 60 closest to CA-III

Operation dialog - (1st AND 2nd)

Enter 1st gene set name or #
60 genes closest to Carbonic Anhydrase-III

Enter 2nd gene set name or #
ALL NAMED GENES

Enter new gene set name of result
named genes in 60 closest to CA-III

SaveAs Close

Ok Cancel

Norm.: median intensity
HP-XY ratio

>4
3.25
2.5
1.75
1
0.571
0.400
0.308
<0.25

1-A 2-
1-B 2-
1-C
1-D

[X] Active Probe
* C57B6-p13-tota
* C57B6-p13.1
* C57B6-p13.2pol
* C57B6-L1-30min
* C57B6-L1-3hrs
* C57B6-L1-4hrs
* C57B6-L1-total
* C57B6-virgin-3
* C57B6-virgin-3
* C57-p16-2hrs-5
* C57B6-L3-1hr
* C57B6-L10-29hr
* C57B6-L10-29hr
* C57B6-L10-29hr

File HybProbe Edit Analysis View Help

Enter gene name or clone ID Mouse-over info HP-X: Pregnancy 13 (1)
HP-Y: Lactation 1 (30 m

Scrollable Dynamic Gene Reports

MicroArray Explorer - V0.90.05-Beta - DAC071601Xu74a (PFL edited DC)

File HybProbe Edit Analysis View H

Enter gene name or clone ID Mouse

GENE REPORT - Filtered genes with 100 Highest ratios HP-X[A0111] / HP-Y[A0114 vs A0111]

GENE REPORT - Filtered genes with 100 Highest ratios HP-X[A0111] / HP-Y[A0114 vs A0111]

F1 M34381

	Grid-Coord	Ratio HP-X/HP-Y	GenBank ID	Gene-Name	mAdb CloneDB	LocusLink(GBID)
1	[1-B23,29]	8	M34381	Cluster Incl M34381:P	-	M34381
2	[1-G11,27]	8	A1173996	Cluster Incl A1173996:	-	A1173996
3	[1-I17,20]	8	Y10725	Cluster Incl Y10725:M	-	Y10725
4	[1-G28,34]					
5	[1-G32,15]					
6	[1-C9,10]					
7	[1-D6,4]					
8	[1-G11,32]					
9	[1-E20,39]					

Close Web Access

HP-X: A0111
HP-Y: A0114 vs A0111

Norm.: median intensity
HP-XY ratio

1-A

Legend:

- >4
- 3.25
- 2.5
- 1.75
- 1
- 0.571
- 0.400
- 0.308
- <0.25

Active Probe

- * A0111
- * A0112
- * A0113
- * A0114 vs A0111
- * A0115 vs A0112
- * A0116 vs A0113

Active Filters

Gene Class

LocusLink - Netscape

File Edit View Go Communicator Help

Back Forward Reload Home Search Netscape Print Security Shop Stop

Bookmarks Location: <http://www.ncbi.nlm.nih.gov/LocusLink/list.cgi?ORG=&V=0&Q=+M34381>

NCBI LocusLink

PubMed Entrez BLAST OMIM Taxonomy Structure

Search: LocusLink Display: Brief Organism: All

Query: M34381 Go Clear

View Loci Save Loci

A B C D E F G H I J K L M N O P Q R S T U V W X Y Z

Help

LocusID	Org	Symbol	Description	Position	Links
18999	Mm	Pou5f1	POU domain, class 5, transcription factor 1	17 19.23 cM	P R G P H U

Document: Done

Scrollable Dynamic Gene Reports

MGAP DB - MicroArray Explorer - V0.89.12-Beta - Pregnancy day 13: C57BL/6 vs. stat5a (-,-) ...

File HybProbe Edit Analysis

Enter gene name or clone ID

GENE REPORT - Filtered genes with 50 Highest ratios HP-X[C57B6 pregnancy day 13] / HP-Y[Stat5a (-,-) pregnancy day 13]

F1 1382272

	Grid-Coord	Ratio HP-X/HP-Y	Clone-ID	Gene-Name	Plate-G,R,C	mAdd CloneDB
1	[1-G6,21]	1.9088	1382272	Mus musculus Msx-int	plate[10,G,9]	1382272
2	[1-B4,14]	1.8634	1248264	S100 calcium-binding	plate[6,B,2]	1248264
3						
4						
5						
6						
7						
8						
9						

Genes with highest HP-X/HP-Y

There are 405 genes passing t

HP-X: C57B6 pregna
HP-Y: Stat5a (-,-) pr

Norm.: median intensity
HP-XY 'set' ratio

>4.0
3.25
2.5
1.75
1.0
0.571
0.4
0.307
<0.25

1-A
1-B
1-C
1-D

Active Probe

- * C57B6-p13-total
- * C57B6-p13.1
- * C57B6-p13.2poly
- * Stat5a--p13-1
- * Stat5a--p13-1
- * Stat5a--p13-1
- * Stat5a--p13-3
- * Stat5a--p13-3
- * C57B6-virgin-3h
- * C57B6-virgin-3h
- * C57-p16-2hrs-60

Clone Report - Netscape

File Edit View Go Communicator Help

Bookmarks Location: http://nciarray.nci.nih.gov/cgi-bin/clone_report.cgi?CRITERIA=clone&PARAMETER=IMAGE:1382272

Back Forward Reload Home Search Netscape Print Security Shop Stop

Division of Clinical Sciences NCI
CIT Center for Information Technology

NCI *mAdd* Clone Report

Clone [IMAGE:1382272](#)

Library Source Soares_mammary_gland_NMLMG

Sequence Verification Unknown

3' Sequence [AI462206](#) BLAST Results: [NT](#) [NR](#)

5' Sequence [AA798388](#) BLAST Results: [NT](#) [NR](#)

3' & 5' UG Title Msx-interacting-zinc finger

3' & 5' UG Cluster [tp Mm.6370](#) NCBI's [LocusLink](#) Stanford's [S.O.U.R.C.E.](#)

3' & 5' UG Gene Miz1

3' & 5' UG RefSeq [NM_008602](#)

Document: Done

Correlation Report of all Samples

- Sample vs Sample correlation coefficient report for current set of Filtered genes

HP vs. HP correlation coefficients table, Pregnancy 13 days: C57BL/6 vs. stat5a (-,-), 8 probes

HP vs. HP correlation coefficients table, Pregnancy 13 days: C57BL/6 vs. stat5a (-,-), 8 probes

D2 rSq=0.982, n=405, HP:2(mn+-sd)=(1+-0), HP:3(mn+-sd)=(1+-1)

		C57B6-p13-totalRNAf	C57B6-p13.1	C57B6-p13.2poly-A	Stat5a--.p13-15min	Stat5a--.p13-15min2
1	C57B6-p13-totalRNAf	-	rSq=0.715, n=405, Hf	rSq=0.729, n=405, Hf	rSq=0.953, n=405, Hf	rSq=0.958, n=405, Hf
2	C57B6-p13.1	-	-	rSq=0.982, n=405, Hf	rSq=0.756, n=405, Hf	rSq=0.757, n=405, Hf
3	C57B6-p13.2poly-A	-	-	-	rSq=0.772, n=405, Hf	rSq=0.773, n=405, Hf
4	Stat5a--.p13-15min	-	-	-	-	rSq=0.997, n=405, Hf
5	Stat5a--.p13-15min2	-	-	-	-	-
6	Stat5a--.p13-1hr2	-	-	-	-	-
7	Stat5a--.p13-30min	-	-	-	-	-
8	Stat5a--.p13-30min2	-	-	-	-	-
9	-	-	-	-	-	-

Close

Tab-Delimited Reports Exportable to Excel

MGAP DB - MicroArray Explorer - V0.89.12-Beta - Pregnancy day 13: C57BL/6 vs. stat5a (-,-), ...

File HybProbe Edit Analysis View Help

Enter gene name or clone ID Mouse-over info HP-X: C57B6 pregnancy day 13
HP-Y: Stat5a (-,-) pregnancy day 13

Genes with highest HP-X/HP-Y ratios

There are 405 genes passing the Filter.

HP-X: C57B6 pregnancy day 13
HP-Y: Stat5a (-,-) pregnancy day 13

Norm.: median intensity
HP-XY 'set' ratio

>4.0
 3.25
 2.5
 1.75
 1.0
 0.571
 0.4
 0.307
 <0.25

Active Probe
 * C57B6-p13-total
 * C57B6-p13.1
 * C57B6-p13.2poly
 * Stat5a.-.-p13-1
 * Stat5a.-.-p13-1
 * Stat5a.-.-p13-1
 * Stat5a.-.-p13-3
 * Stat5a.-.-p13-3
 * C57B6-virgin-3h
 * C57B6-virgin-3h
 * C57-p16-2hrs-60

1-A
1-B
1-C
1-D

GENE REPORT - Filtered genes with 50 Highest ratios HP-X[C57B6 preg...]

GENE REPORT - Filtered genes with 50 Highest ratios HP-X[C57B6 pregnancy day 13] / HP-Y[Stat5a

Grid-Coord	Ratio HP-X/HP-Y	Clone-ID	Gene-Name	Plate-G,R,C	mAdd	CI
[1-G6,21]	1.9088	1382272	Mus musculus Msx-interacting-zinc finger protein 1 (Miz1) mRNA, comp			
[1-B4,14]	1.8634	1248264	S100 calcium-binding protein A4	plate[6,B,2]		1248264
[1-A3,17]	1.8456	1248170	Mouse mRNA for SDF2, complete cds	plate[4,A,5]		1248170
[1-H4,15]	1.8449	1248272	ADRENODOXIN PRECURSOR	plate[6,H,3]	1248272	1248272
[1-D5,3]	1.8256	1248351	Abl-interactor 1	plate[7,D,3]	1248351	1248351 AI46337
[1-F7,7]	1.8118	1382525	Acetyl coenzyme A dehydrogenase, medium chain	plate[11,F,7]		
[1-C2,19]	1.7997	1247627	Mus musculus mRNA for osteomodulin, complete cds			plate[2,C,2]
[1-A3,6]	1.7677	1247777	Mus musculus metalloprotease/disintegrin/cysteine rich protein precurs			
[1-B6,7]	1.7562	1381654	TROPOMYOSIN 5, CYTOSKELETAL TYPE	plate[9,B,7]		
[1-B6,9]	1.7499	1381703	B-cell translocation gene 2, anti-proliferative	plate[9,B,9]		
[1-A5,23]	1.7377	1248527	Mus musculus ubiquitin-conjugating enzyme HR6A mRNA, complete c			
[1-C3,10]	1.7316	1247708	Ephrin A1	plate[3,C,10]	1247708	1247708 AA959770
[1-D3,5]	1.7249	1247564	Erythrocyte protein band 7.2	plate[3,D,5]		1247564
[1-C6,2]	1.7190	1381920	Mus musculus mRNA for NEFA protein, complete cds			plate[9,C,2]
[1-D7,16]	1.7081	1382671	Mouse MA-3 (apoptosis-related gene) mRNA, complete cds			plate[12,7,16]
[1-H3,12]	1.7073	1248169	Histocompatibility 2, T region locus 22	plate[3,H,12]		1248169
[1-H4,20]	1.7039	1248345	Mus musculus alpha-methylacetyl-CoA racemase mRNA, complete cds			
[1-D2,14]	1.6611	1247820	Tight junction protein 1	plate[2,D,2]	1247820	1247820
[1-A2,22]	1.6598	1247817	Mus musculus ras-related protein (rab18) mRNA, complete cds			
[1-D4,6]	1.6528	1248184	Mus musculus bromodomain-containing protein BP75 mRNA, complet			
[1-C5,5]	1.6274	1248278	HISTONE H3.3	plate[7,C,5]	1248278	1248278 AI46330

SaveAs Close

Plug-in Extensions to MAExplorer



- Plug-ins will allow investigators to extend capabilities of core MAExplorer program to other analysis methods
- Open Java API, Java examples, donated plug-ins & links to Plugins will be published on our Web site
- Typical plug-ins: normalization, Filters, PCA, clustering, Web-server functional analysis of cluster results, etc.
- Plug-ins will have three types of implementations:
 1. Using 100% Java code
 2. Accessing local programs written in any language
 3. Web-CGI or client-server to specialized genomic DBs

Data Format Conversion for MAExplorer

- Cvt2Mae reads a variety of array data - for both one-of-a kind academic and commercial arrays (eg. Affymetrix, Incyte, etc).
- Users can create an Array Layout description that may be used in subsequent conversions
- Will add generic “MAML” (now “MGED”) standard compatibility (MicroArray XML) for data portability
- Cvt2Mae is undergoing *Beta*-testing

Select a Chip Array-Layout

Cvt2Mae: convert array data to MAExplorer files - Version: 08-21-2001 (Beta) - _ □ ×

Enter data for steps 1, 2, and 3. Then press 'Run' to convert your data to MAExplorer format.

1. Select Chipset:

1.1 (opt.) Select Quant. software used:

2. Select Input Data Files:

2.1 Samples to use '<<file>> sample name'.

Vendor	<input type="text"/>
Layout name	<input type="text"/>
Species	<input type="text"/>
Spots/microarray	<input type="text"/>

3. Select Project Output Folder:

Project output folder:

MAExplorer startup File:

4. Edit and Run

 Expert assign-mode

Status:

Dropdown menu options: -- select a chip layout --, -- select a chip layout --, <User-defined>, Incyte - Mouse, Incyte - Human, Affymetrix - Mouse, Affymetrix - Human

Converted Affymetrix files for Analysis

Cvt2Mae: convert array data to MAExplorer files - Version: 08-21-2001 (Beta) [min] [max] [close]

Enter data for steps 1, 2, and 3. Then press 'Run' to convert your data to MAExplorer format.

1. Select Chipset: Affymetrix - Human

1.1 (opt.) Select Quant. software used: [NONE] pick array data ()

2. Select Input Data Files: Browse file name Browse folder

U937-Affymetrix-2subclones.txt

2.1 Samples to use '<<file>> sample name'. Remove sample Rename sample

<<C:\Temp\AffyData\U937-Affymetrix-2subclones.txt>> [DSD-1-Tel10A-1-U95A]
<<C:\Temp\AffyData\U937-Affymetrix-2subclones.txt>> [DSD-1-Tel10B-1-U95A]
<<C:\Temp\AffyData\U937-Affymetrix-2subclones.txt>> [DSD-1-Tel17A-1-U95A]
<<C:\Temp\AffyData\U937-Affymetrix-2subclones.txt>> [DSD-1-Tel17B-1-U95A]

Vendor	Affymetrix
Layout name	Affymetrix - Human
Species	Human
Spots/microarray	12630

3. Select Project Output Folder: Create New project folder

Project output folder: C:\Temp\junk\

MAExplorer startup File: C:\Temp\junk\MAE\Start.mae

4. Edit and Run Run Edit Layout Assign GIPO fields Assign Quant fields Done

Save Layout Expert assign-mode Reset

Status: ===> Finished writing out data files. Press 'Done' to exit

To start MAExplorer, go to project folder & click on Start.mae.

Affymetrix Data from Cvt2Mae Conversion

The screenshot displays the MicroArray Explorer interface. The title bar reads "C:\Temp\AffyData\ DB - MicroArray Explorer - V0.90.05-Beta - 10A&B vs 17A&B". The menu bar includes "File", "HybProbe", "Edit", "Analysis", "View", and "Help". The "Analysis" menu is open, showing options like "GeneClass", "Normalization", "Filter", "Plot", and "Report". The "Filter" sub-menu is expanded, listing various filtering criteria such as "Filter by GeneClass membership", "Filter by 'User Filter Gene Set' membership", "Filter by 'Edited Gene List' membership", "Filter by 'good genes list' membership", "Filter by genes with replicates", "Filter by ratio histogram bin", "Filter by intensity histogram bin", "Filter by positive intensity data", "Filter by Good Spot data", "Filter by spot intensity [SI1:SI2] sliders", "Filter by intensity [I1:I2] sliders", "Filter by ratio or Zdiff sliders", "Filter by Spot CV", "Filter by HP-X,HP-Y 'sets' t-Test [p-Value] slider", "Filter by HP-E clustering [Cluster Dist] slider", "Filter by Diff(HP-X,HP-Y) [Abs.Diff.] slider", "Filter genes with highest X/Y ratio or X-Y Zdiff", and "Filter genes with lowest X/Y ratio or X-Y Zdiff".

The main window shows a heatmap with a color scale on the left. The scale ranges from red (>4) to green (<0.25). The heatmap is labeled "HP-X: DSD-1-Tel10A-1-US" and "HP-Y: DSD-1-Tel10B-1-US". The legend includes "Norm.: median intensity" and "HP-XY ratio". The legend items are: >4, 3.25, 2.5, 1.75, 1, 0.571, 0.400, 0.308, and <0.25. The legend also includes "Active Probe" (checked), "DSD-1-Tel10A-1", "DSD-1-Tel10B-1", "DSD-1-Tel17A-1", and "DSD-1-Tel17B-1". The legend also includes "Active Filters", "Gene Class", "Active GeneClass", and "ALL GENES".

The heatmap shows a grid of spots, with a yellow circle highlighting a specific spot in the top-left corner. The spots are colored according to the legend, with a mix of red, orange, and green spots.

Converted Incyte files Ready to Analyze

Cvt2Mae: convert array data to MAExplorer files - Version: 08-21-2001 (Beta) [min] [max] [close]

Enter data for steps 1, 2, and 3. Then press 'Run' to convert your data to MAExplorer format.

1. Select Chipset: Affymetrix - Human

1.1 (opt.) Select Quant. software used: [NONE] pick array data ()

2. Select Input Data Files: Browse file name Browse folder

U937-Affymetrix-2subclones.txt

2.1 Samples to use '<<file>> sample name': Remove sample Rename sample

<<C:\Temp\AffyData\U937-Affymetrix-2subclones.txt>>	[DSD-1-Tel10A-1-U95A]
<<C:\Temp\AffyData\U937-Affymetrix-2subclones.txt>>	[DSD-1-Tel10B-1-U95A]
<<C:\Temp\AffyData\U937-Affymetrix-2subclones.txt>>	[DSD-1-Tel17A-1-U95A]
<<C:\Temp\AffyData\U937-Affymetrix-2subclones.txt>>	[DSD-1-Tel17B-1-U95A]

Vendor	Affymetrix
Layout name	Affymetrix - Human
Species	Human
Spots/microarray	12630

3. Select Project Output Folder: Create New project folder

Project output folder: C:\Temp\junk\

MAExplorer startup File: C:\Temp\junk\MAE\Start.mae

4. Edit and Run Run Edit Layout Save Layout Assign GIPO fields Assign Quant fields Done Reset

Expert assign-mode

Status: ===> Finished writing out data files. Press 'Done' to exit

To start MAExplorer, go to project folder & click on Start.mae.

Summary

- MAExplorer is a flexible microarray data-mining tool running on the user's computer
- Uses direct-manipulation, data filtering, built-in graphics, statistics, clustering, gene and sample set operations
- Manages multiple samples, replicates, sets, expression profile lists where the session state may be saved on the disk for later use
- The Cvt2Mae data conversion tools allows use with common chips
- Plug-ins will allow extension with new analytic methods by users
- MAExplorer identified genes in preferentially expressed during lactation, *Nucleic Acids Res.* (2000) **28**:4452
- Freely available for download with documentation on Web site