

Tutorial 5: Accessing gene expression profiles using BarChart



Overview of BarChart

Why use BarChart:

Displays expression data for a single gene across multiple arrays within the same experiment or across different experiments. It gives the user an overview of the differential expression levels of this gene across different samples.

How to get BarChart:

- <1> From Gene List (the most popular usage)
- <2> From Tool Panel
- <3> From T-test result
- <4> From Library windows, such as ChipLib or other Libs
- <5> Advanced: launch BarChart from data content tree

Functions associated with BarChart:

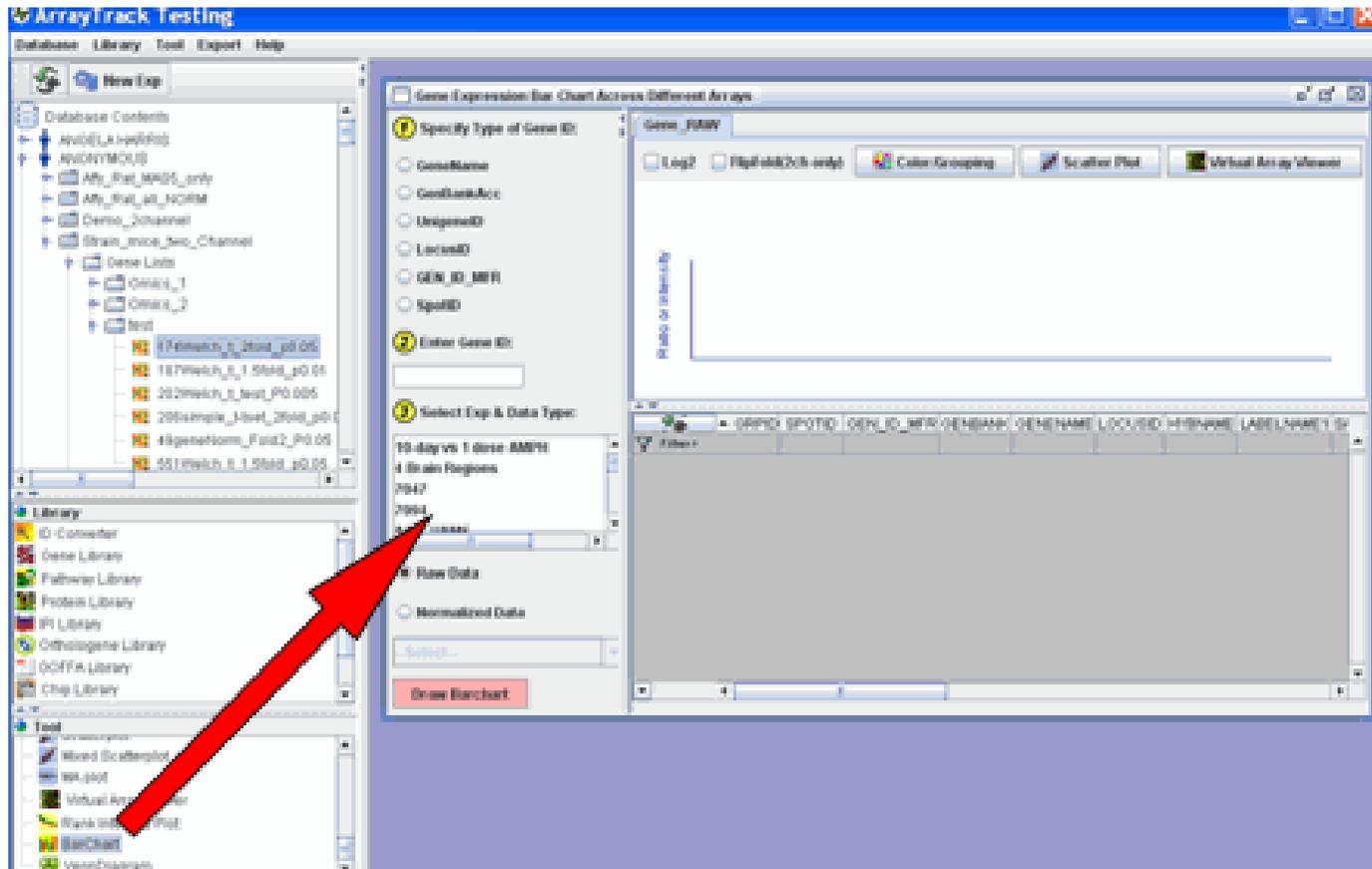
- <1> Query/sort BarChart table
- <2> Grouping bars with color
- <3> View standard deviation
- <4> Others: apply log₂, flip fold, link to Libraries, ScatterPlot, etc.
- <5> Advanced: cross multi-experiment comparison

Access BarChart

<2>From TOOL panel

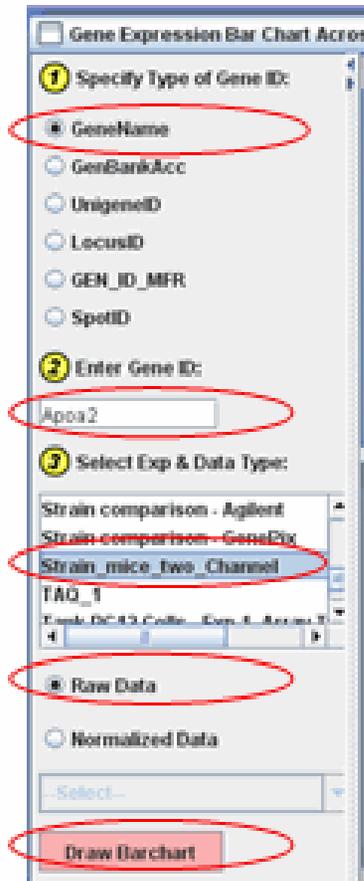
Use it when you know gene id and experiment name

- Double click BarChart node from Tool Panel (the bottom left window)
- A BarChart window is shown.



Access BarChart

<2> From Tool panel (cont.)



1) Specify gene type

2) Specify gene ID

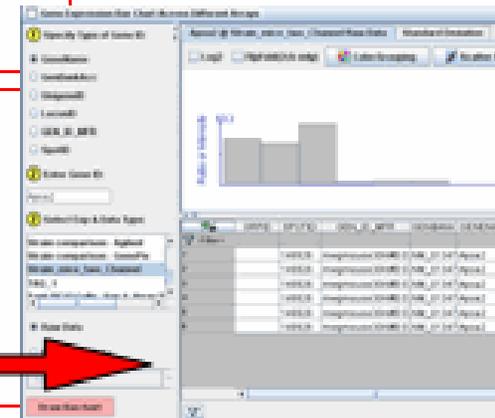
3) Select experiment name

4) Select data type mod

- Raw

- Normalized (select normalization method from drop down list)

5) Click 'Draw Barchart' button



Access BarChart

<3> From T-test Result

Please refer Tutorial 1 for generating T-test result.

Select a gene in the T-test result and choose BarChart from "Selected-Spot" menu.

The screenshot shows a software window titled "T-Test Results" with a table of gene expression data. The table has columns for Gene Mtr ID, LOCUSID, GENENAME, REFSEQ, SPOTID, P, Abs Fold C..., and Fold C... The "Selected-Spot" menu is open, and "Bar Chart" is selected. Below the table, there are filtering options for significance, mean channel intensities, and absolute fold change, along with buttons for "Apply Filters", "Clear Filters", "P-Value Plot", "Create Sig. Gene List", "HCA", "PCA", and "Volcano Plot".

File	Selected-Spot	All-Spots	Advanced	Gene Mtr ID	LOCUSID	GENENAME	REFSEQ	SPOTID	P	Abs Fold C...	Fold C...	
1				...	76894	0610027B...	NM_029790	144114	0.6471	1.1446	1.144	
2				NM_013556	mwgmous...	15452	Hprt	NM_013556	144115	0.494	1.2362	0.808
3				NM_008046	mwgmous...	14313	Fst	NM_008046	144116	0.108	1.5271	1.527
4				NM_008806	mwgmous...	18587	Pde6b	NM_008806	144117	0.2797	1.8196	1.819
5				BCD13794	mwgmous...	76932	Arfp2	144118	0.9868	1.0055	1.005	
6				NM_009335	mwgmous...	21420	Tcfap2c	NM_009335	144119	0.9588	1.0086	0.991
7				AJ246002	mwgmous...	50850	Spg4	144120	0.1451	2.3731	0.421	
8				NM_008262	mwgmous...	15379	Onecut1	NM_008262	144121	0.9914	1.0069	1.006
9				AK020471	mwgmous...	12631	Ctfl	144122	0.9998	1.0001	1.000	
10				NM_019951	mwgmous...	58529	Spe18	NM_019951	144123	0.4685	1.2003	1.200
11				BCD27041	mwgmous...	22758	Zfp96	144124	0.522	1.0826	0.923	
12				AK014702	mwgmous...	74589	4833415F1...	NM_029013	144125	0.415	1.3688	1.368
13				NM_033852	mwgmous...	110648	Lmx1a	NM_033852	144126	0.6949	1.0967	1.096
14				NM_016792	mwgmous...	53382	Txn1	NM_016792	144127	0.9983	1.0006	1.000

20160 genes

Significance Filtering

P Values < without adjustment

Target False Discovery Rate (FDR):

Select # genes by lowest p-values

Mean Channel Intensities > Bad Flags <=

Abs Fold Change > Advanced>>

Apply Filters Clear Filters

P-Value Plot Create Sig. Gene List HCA PCA Volcano Plot

Access BarChart

<4> From ChipLib and other Libs

- Select gene from library table
- Click “BarChart” button on the top of tool bars

The screenshot displays the 'Chip Library' application window. On the left, there are several configuration panels: 'Load Chip Type' (set to 'Atty_HO-U133_Plus_2'), 'Specify ID Type' (with radio buttons for GeneBankAcc, RefSeq, UnigeneID, LocusID, SwissProtAcc, GEN_ID_MIR, SpotID, GeneName), and 'Enter Searching Data'. The main area contains a table with columns: ARRAYTYPE NAME, SPOTID, POS_DESCR_MFR, GEN_ID_MFR, GENE BANK ACC, and GENE NAME. The 'GEN_ID_MFR' column is highlighted in blue. At the top of the table, there are buttons for 'Genes', 'Proteins', 'Pathways', 'Orthologues', 'GO', and 'Bar Chart'. The 'Bar Chart' button is circled in red. A red arrow points from a text box to this button. The text box contains the instruction: 'Select the gene from library table, then click BarChart button'.

ARRAYTYPE NAME	SPOTID	POS_DESCR_MFR	GEN_ID_MFR	GENE BANK ACC	GENE NAME
Atty_HO-U133_Plus_2	173087	1	1552256_at	NM_005505	SCARB1
Atty_HO-U133_Plus_2	173088	2	1552257_at	NM_015140	HAAH153
Atty_HO-U133_Plus_2	173089	3	1552258_at	NM_052871	
Atty_HO-U133_Plus_2	173078	4	1552261_at	NM_088735	YFDC2
Atty_HO-U133_Plus_2	173071	5	1552263_at	NM_138957	MAPK1
Atty_HO-U133_Plus_2	173072	6	1552264_at	NM_138957	MAPK1
Atty_HO-U133_Plus_2	173073	7	1552266_at	NM_145024	ACAM3
Atty_HO-U133_Plus_2	173074	8	1552268_at	NM_138796	LOC138153
Atty_HO-U133_Plus_2	173075	9	1552271_at	NM_153359	MOC24975
Atty_HO-U133_Plus_2	173076	10	1552272_at	NM_153359	MOC24975
Atty_HO-U133_Plus_2	173077	11	1552274_at	BC034479	Pink
Atty_HO-U133_Plus_2	173078	12	1552275_at	U0573647	Pink
Atty_HO-U133_Plus_2	173079	13	1552276_at	NM_084332	VPS18
Atty_HO-U133_Plus_2	173080	14	1552277_at	NM_088955	MOC17337
Atty_HO-U133_Plus_2	173081	15	1552278_at	NM_088959	MOC9564
Atty_HO-U133_Plus_2	173082	16	1552279_at	AK024181	MOC9564
Atty_HO-U133_Plus_2	173083	17	1552280_at	NM_138379	TMD4
Atty_HO-U133_Plus_2	173084	18	1552281_at	NM_173596	SLC39A5
Atty_HO-U133_Plus_2	173085	19	1552283_at	NM_024786	ZHHC11
Atty_HO-U133_Plus_2	173086	20	1552286_at	NM_088953	ATP6V1E2
Atty_HO-U133_Plus_2	173087	21	1552287_at	NM_001132	AFGL1
Atty_HO-U133_Plus_2	173088	22	1552288_at	BC034926	
Atty_HO-U133_Plus_2	173089	23	1552289_at	BC034926	
Atty_HO-U133_Plus_2	173090	24	1552291_at	NM_017881	PINK
Atty_HO-U133_Plus_2	173091	25	1552293_at	NM_152774	MOC42080
Atty_HO-U133_Plus_2	173092	26	1552295_at	NM_152364	SLC39A3
Atty_HO-U133_Plus_2	173093	27	1552296_at	NM_153274	YMOCL2
Atty_HO-U133_Plus_2	173094	28	1552298_at	NM_145025	Cd68

Access BarChart

<5> Advanced: From Data Tree

- Select experiment name, then right click to select datasets
- Type in search pattern, matched data will be highlighted in the tree.
- Right click and select “BarChart” to launch. (continue on next page..)

The image illustrates the process of accessing the BarChart tool from a data tree through three sequential steps:

- Right click:** A right-click is performed on a node in the data tree, opening a context menu. A red box highlights the text "Right click" and a red arrow points to the menu.
- Select Datasets:** The "Select Datasets" dialog box is shown. The "Search Pattern" field is highlighted with a red circle, and a red arrow points to it from the context menu.
- Right click:** A second right-click is performed on a node in the data tree, opening a context menu. A red box highlights the text "Right click" and a red arrow points to the "BarChart" option in the menu.

Access BarChart

4) Specify gene ID and Type, then click "Draw BarChart" button

The screenshot displays the 'Gene Expression Bar Chart Across Different Arrays' software interface. A message box is overlaid on the interface, stating: 'Please select Gene type and id from the left search panel'. The interface includes a search panel on the left with the following sections:

- 1) Specify Type of Gene ID:** Radio buttons for GeneName, GenBankAcc, UnigeneID, LocusID, GEN_ID_MFR, and SpotID.
- 2) Enter Gene ID:** A text input field containing 'Nat1'.
- 3) Select Exp & Data Type:** A list of data types including 'AcademicNA_E-MEXP-107', 'Atty_Human_Peag12', 'Atty_Rat_MASS_only', and 'Atty_Rat_at_NORM'. The 'Atty_Rat_at_NORM' option is selected.
- Raw Data:** A radio button that is selected.
- Normalized Data:** A radio button that is unselected.
- Draw BarChart:** A red button at the bottom of the search panel.

The main window shows a bar chart titled 'Nat1 @ Atty_Rat_at_NORM Raw Data' with a y-axis labeled 'Ratio or Intensity'. Below the chart is a data table with the following columns: GEN_ID_MFR, GENBANK, GENENAME, LOCUSID, HYENAME, LABELNAME1, SAMPLE1, DESCRIPTION, INTENSITY1, and UNIT. The table contains 10 rows of data for the gene 'Nat1'.

GEN_ID_MFR	GENBANK	GENENAME	LOCUSID	HYENAME	LABELNAME1	SAMPLE1	DESCRIPTION	INTENSITY1	UNIT
01344_at	U01344	Nat1	116631	D8_T12_B_Biotn	CO_T12_EMas5	CO_T12_EMas5		32.66351	
01344_g_at	U01344	Nat1	116631	D8_T12_B_Biotn	CO_T12_EMas5	CO_T12_EMas5		89.37698	
01345_at	U01345	Nat1	116631	D8_T12_B_Biotn	CO_T12_EMas5	CO_T12_EMas5		18.69436	
01346_at	U01346	Nat1	116631	D8_T12_B_Biotn	CO_T12_EMas5	CO_T12_EMas5		4.573175	
117260_s_at	U17260	Nat1	116631	D8_T12_B_Biotn	CO_T12_EMas5	CO_T12_EMas5		89.60664	
01344_at	U01344	Nat1	116631	D8_T12_B_Biotn	CO_T12_EMas5	CO_T12_EMas5		22.1124	
01344_g_at	U01344	Nat1	116631	D8_T12_B_Biotn	CO_T12_EMas5	CO_T12_EMas5		73.61459	
01345_at	U01345	Nat1	116631	D8_T12_B_Biotn	CO_T12_EMas5	CO_T12_EMas5		29.66197	
01346_at	U01346	Nat1	116631	D8_T12_B_Biotn	CO_T12_EMas5	CO_T12_EMas5		13.95594	
117260_s_at	U17260	Nat1	116631	D8_T12_B_Biotn	CO_T12_EMas5	CO_T12_EMas5		75.97566	

BarChart Functions – Query/Sort

Query:

- 1) Type constraint in a particular field on the query row.
- 2) Click query button.
- 3) BarChart will be re-drawn based on the search result.

Sort: Click header to sort table by columns.

The screenshot shows the 'Gene Expression Bar Chart Across Different Arrays' interface. On the left, under 'Specify Type of Gene ID', 'Raw Data' is selected. Under 'Select Exp & Data Type', 'Atty_Rat_all_NORM' is selected. The main area shows a bar chart at the top and a data table below. A red circle highlights the 'Query' button (a magnifying glass icon) in the top left of the table area. Another red circle highlights the 'DESCRIP1' column header in the table. A red arrow points from the 'Query' button to the 'DESCRIP1' header. A second red arrow points from the 'DESCRIP1' header to the 'DESCRIP1' column in the table, which contains the value 'Max5'. A third red arrow points from the 'Query' button to the bar chart. A red text label '2) Click Query (refresh) button' is positioned above the 'Query' button. A red text label '1) Specify constraint on Query row' is positioned to the right of the 'DESCRIP1' column header. An inset window in the bottom right shows the bar chart after the query is executed, with a significantly lower peak intensity.

SAMPLE2	INTENSITY2	RATIO	FLAG	NOTES	POS_DESCR1	DESCRIP1	ARRAYTYPENAME	ARRAYRAWDATA
1					265	RMA	Atty_RT-U34	15372
2					265	RMA	Atty_RT-U34	15375
3					265	RMA	Atty_RT	
4					265	qPiler16	Atty_RT	
5					265	Pile	Atty_RT	
6					265	Pile	Atty_RT	
7					265	RMA	Atty_RT	
8					265	qPiler16	Atty_RT	
9					265	Pile	Atty_RT	
10					265	Pile	Atty_RT	
11					265	Pile	Atty_RT	
12					265	Pile	Atty_RT	
13					265	Pile	Atty_RT	
14					265	Pile	Atty_RT	
15					265	Pile	Atty_RT	
16					265	Pile	Atty_RT	
17					265	Pile	Atty_RT	
18					265	Pile	Atty_RT	
19					265	Pile	Atty_RT	
20					265	Pile	Atty_RT	

BarChart Functions - Grouping

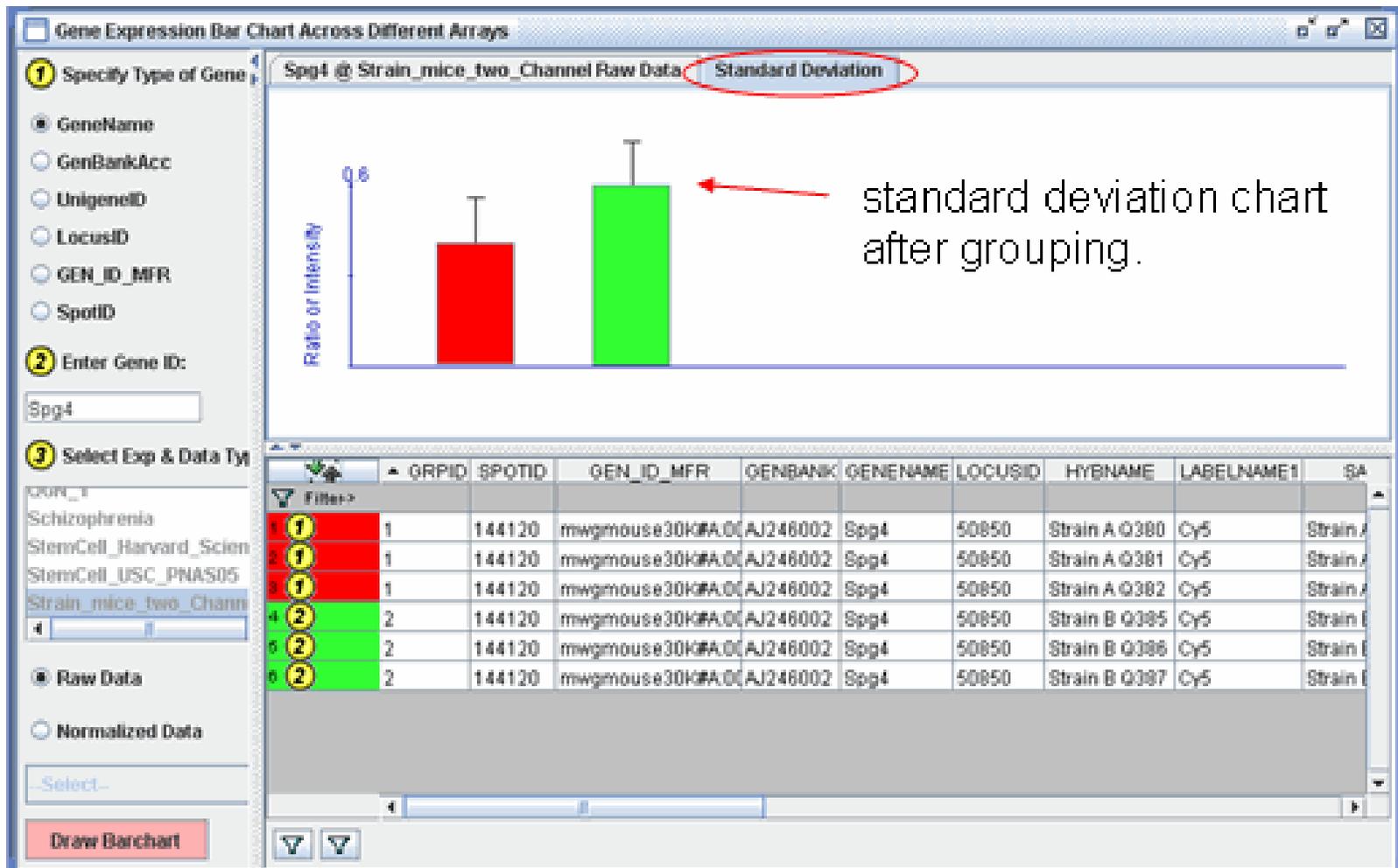
- 1) Select group of records from table or highlight bars from bar chart panel
- 2) Click “Color/Grouping” button and select “Assign Group by Color”
- 3) Once grouping is done, Click “Color/Grouping” button again and select “Save Group by Color”. (the grouping info will be saved for that particular experiment, so when you view other genes within the same experiment, the color of grouping will automatically be applied).

The screenshot illustrates the software interface for grouping data in a bar chart. The main window shows a bar chart with a y-axis labeled 'Ratio of Intensity' ranging from 0 to 7. The chart displays six bars, with the first three being red and the last three being green. A menu is open, showing options: 'Assign Group by Color', 'Save Group by Color', and 'Clear Color & Group'. A red arrow points from the 'Assign Group by Color' option to a 'Color Chooser' dialog box. The 'Color Chooser' dialog box features a color palette and a 'Recent' list. Below the dialog box, a data table is visible with columns: DRPID, SPOTID, GEN_ID, MFR, GENBANK, GENENAME, LOCUSID, and HYBR. The table shows six rows of data, with the first three rows highlighted in red and the last three rows highlighted in green, corresponding to the bars in the chart.

DRPID	SPOTID	GEN_ID	MFR	GENBANK	GENENAME	LOCUSID	HYBR
1	14440	mmwgmouse30kFB.0	NM_02319	Acin1	56215	Strain A	
2	14440	mmwgmouse30kFB.0	NM_02319	Acin1	56215	Strain A	
3	14440	mmwgmouse30kFB.0	NM_02319	Acin1	56215	Strain A	
4	14440	mmwgmouse30kFB.0	NM_02319	Acin1	56215	Strain E	
5	14440	mmwgmouse30kFB.0	NM_02319	Acin1	56215	Strain E	
6	14440	mmwgmouse30kFB.0	NM_02319	Acin1	56215	Strain E	

BarChart Functions - Standard Deviation

- 1) Click "Standard Deviation" tab on the top of barchart panel (the standard deviation chart makes more sense after grouping.)



BarChart Functions - Others

1) "Log2" apply to fold for 2 channels data

2) "Flip Fold" applies to 2 channels data.

3) Link to ScatterPlot

4) Link to ChipLibrary

ARRAYTYPE	SPOTID	POS_DESCR_MFR	GEN_ID_MFR	GENE
NCTR_MWG_Mouse	149926	Block:14-Col:13-Row:18	rnwgmouse30KPB.0	NM_01

Advanced Function: cross-experiment comparison

Specify the type of gene ID

Enter the gene ID

Select more than one exp

