

Tutorial 5: Accessing gene expression profiles using 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, Scatter Plot etc;
- <5> Advanced: cross multi-experiment comparison.

<1> From Gene List

- 1) Double click a genelist node from database content tree in the top left window.
- 2) A genelist table will show up.
- 3) Highlight a record from genelist table, and right-clicking shows a popup menu.
- 4) Select 'Bar Chart' from the popup menu.
- 5) A Bar Chart window is displayed with the selected gene's profile across all normalized data set within the specific experiment that this genelist belongs to.

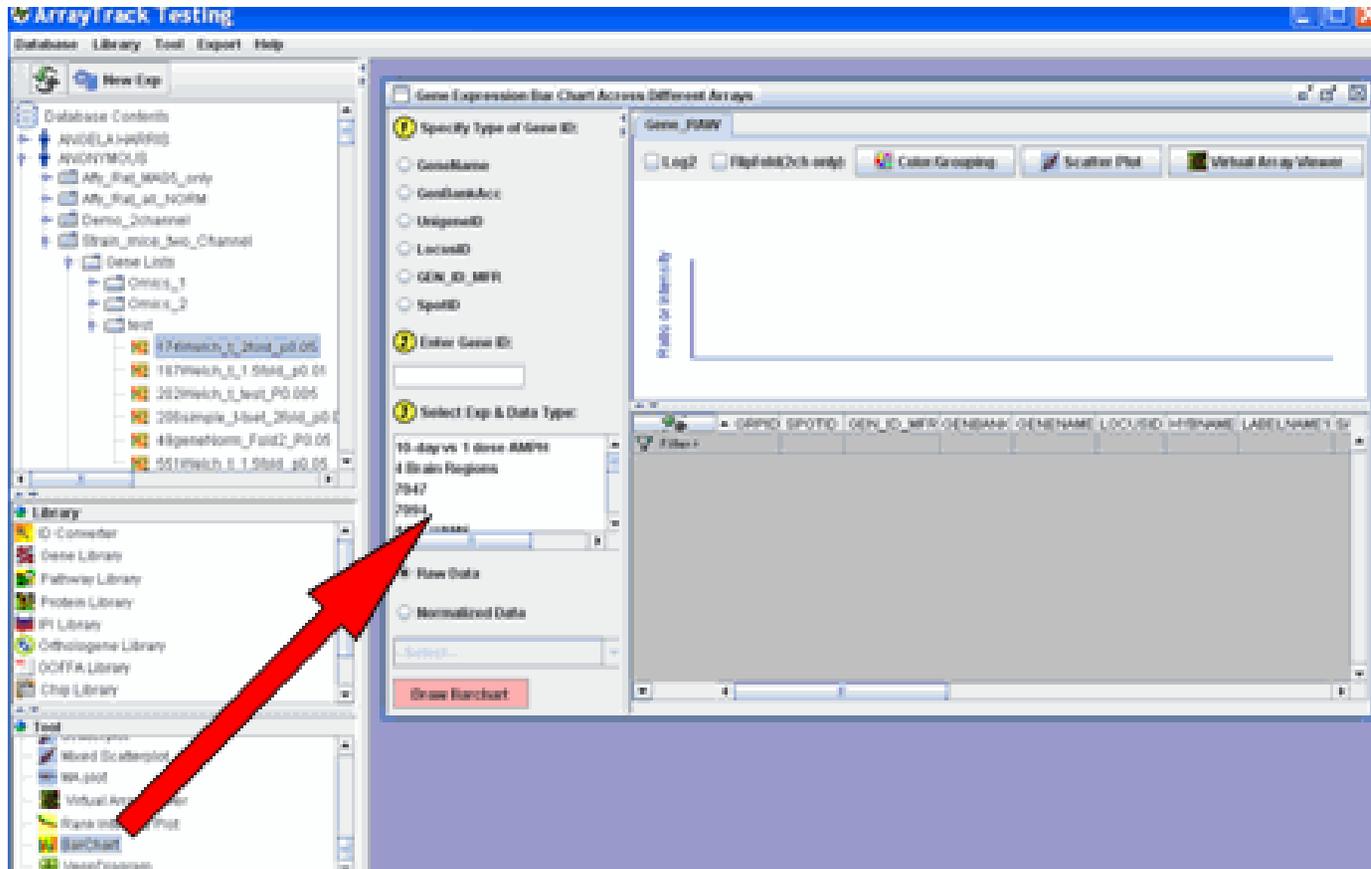
The screenshot illustrates the workflow for generating a bar chart from a gene list. On the left, a 'Database Contents' tree shows the 'Omics_1' folder selected. The main window, titled 'SIGNIFICANT_GENELIST', displays a table with columns: GENELIST_NAME, EXPID, GENEBANKACC, GENENAME, LOCUSID, FOLD, and PVALU. A red arrow points from the tree to the table. A context menu is open over the table, with 'Bar Chart' selected. Another red arrow points from the menu to a 'Gene Expression for Chart Across Different Stages' window, which shows a bar chart and a data table.

GENELIST_NAME	EXPID	GENEBANKACC	GENENAME	LOCUSID	FOLD	PVALU
187gene_P0.01_F1	272	NM_010010	Cyp46a1	13116	8.435	0
187gene_P0.01_F1	272	BC003305	Lpl	16956	10.9684	0
187gene_P0.01_F1	272	NM_018789	Dtha5h	54722	1.5268	0
187gene_P0.01_F1	272
187gene_P0.01_F1	272
187gene_P0.01_F1	272
187gene_P0.01_F1	272
187gene_P0.01_F1	272
187gene_P0.01_F1	272
187gene_P0.01_F1	272
187gene_P0.01_F1	272

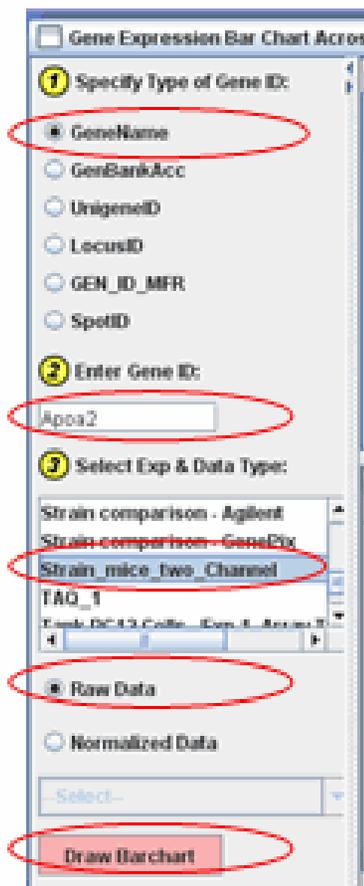
<2> From Tool panel

Use it when you know gene id and experiment name

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



<2> From Tool panel (cont.)



1) Specify gene type

2) Specify gene ID

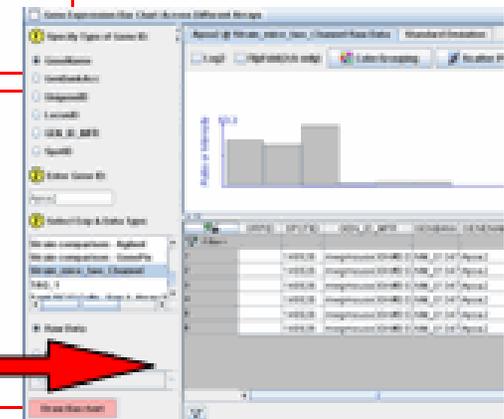
3) Select experiment name

4) Select data type mod

- Raw

- Normalized (select normalization method from drop down list)

5) Click 'Draw Barchart' button



<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.

File	Selected-Spot	All-Spots	Advanced	Gene Mfr ID	LOCUSID	GENENAME	REFSEQ	SPOTID	P	Abs Fold C...	Fold Chang.
1	U70210	U70210_at	11787	Apbb2	NM_009686	517087	0.4569	1.3753	1.3753		
2	M83649	AFFX-MurF...	14102	Fas	NM_007987	516597	0.3863	1.7525	1.7525		
3	M37897	AFFX-MurL...	16153	Ii10	NM_010548	516598	0.6144	1.3086	0.7642		
4	M16762	AFFX-MurL...	16183	Ii2		516599	0.6289	1.1112	0.8999		
5	M25892	AFFX-MurL...	16189	Ii4	NM_021283	516600	0.8526	1.1082	0.9023		
6	L22190	L22190mR...	20209	Saa2		516814	0.6653	1.1599	0.8622		
7	L42293	L42293mR...	20652	Soat1	NM_009230	516838	0.694	1.2624	0.7921		
8	J02791	J02791_at	24158	Acadm	NM_016986	516751	0.2008	1.1866	1.1866		
9	U20643	U20643m...	24189	Aldoa		517015	0.2536	1.1766	1.1766		
10	M60322	M60322_at	24192	Akr1b4	NM_012498	516918	0.8889	1.0379	0.9635		
11	M60322	M60322_g...	24192	Akr1b4	NM_012498	516919	0.8147	1.1423	0.8754		
12	M28647	M28647_at	24211	Atp1a1		516884	0.3342	1.2638	1.2638		
13	M28647	M28647_g...	24211	Atp1a1		516885	0.8048	1.0432	1.0432		
14	D90049	D90049exo...	24212	Atp1a2		516727	0.3037	1.1818	1.1818		
15	M28648	M28648_s...	24213	Atp1a3		516886	0.0244	2.4225	2.4225		
16	D90048	D90048exo...	24214	Atp1b2		516725	0.939	1.0206	0.9798		
17	D90048	D90048exo...	24214	Atp1b2		516726	0.2906	1.7446	1.7446		

1031 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** **K-Means** **Volcano Plot**

<4> From ChipLib and other Libs

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

The screenshot shows the 'Chip Library' application window. On the left is a sidebar with options for loading and specifying chip types. The main area contains a table with columns: ARRAYTYPE NAME, SPOTID, POS_DESCR_MFR, GENE_ID_MFR, GENE_BARRACC, and GENE_NAME. A red circle highlights the 'BarChart' button in the top toolbar. A red arrow points from this button to a red text box on the right that reads: 'Select the gene from library table, then click BarChart button'.

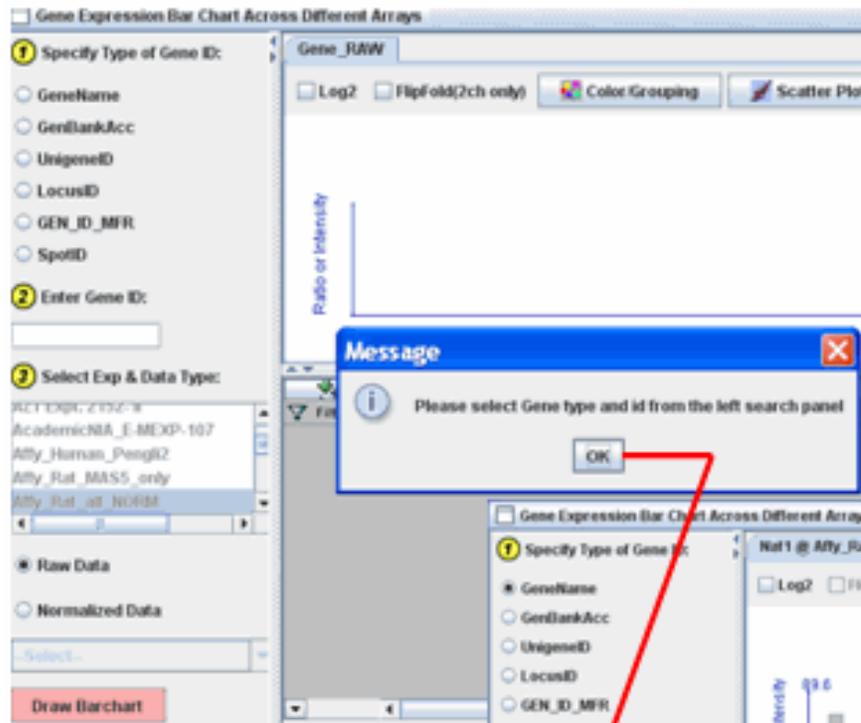
ARRAYTYPE NAME	SPOTID	POS_DESCR_MFR	GENE_ID_MFR	GENE_BARRACC	GENE_NAME	
Atty_HO-U133_Plus_2	173087	1	1552256_a_atNM_005505	SCARB1	gcNM_005505.2 (CG)	
Atty_HO-U133_Plus_2	173088	2	1552257_a_atNM_015140	HAAR153	gcNM_015140.1 (CG)	
Atty_HO-U133_Plus_2	173089	3	1552258_at	NM_052871	LOC101928101 (CG)	
Atty_HO-U133_Plus_2	173079	4	1552261_at	NM_008735	YFDC2	gcNM_008735.1 (CG)
Atty_HO-U133_Plus_2	173071	5	1552263_at	NM_138957	MAPK7	gcNM_138957.1 (CG)
Atty_HO-U133_Plus_2	173072	6	1552264_a_atNM_138957	MAPK7	gcNM_138957.1 (CG)	
Atty_HO-U133_Plus_2	173073	7	1552266_at	NM_145004	ACAM32	gcNM_145004.1 (CG)
Atty_HO-U133_Plus_2	173074	8	1552268_at	NM_138796	LOC128153	gcNM_138796.1 (CG)
Atty_HO-U133_Plus_2	173075	9	1552271_at	NM_153259	MGC24975	gcNM_153259.1 (CG)
Atty_HO-U133_Plus_2	173076	10	1552272_a_atNM_153259	MGC24975	gcNM_153259.1 (CG)	
Atty_HO-U133_Plus_2	173077	11	1552274_at	BC024479	Pvk	gcBC024479.1 (CG)
Atty_HO-U133_Plus_2	173078	12	1552275_a_atBC024479	Pvk	gcBC024479.1 (CG)	
Atty_HO-U133_Plus_2	173079	13	1552276_a_atNM_008432	VP518	gcNM_008432.1 (CG)	
Atty_HO-U133_Plus_2	173080	14	1552277_a_atNM_008655	MGC17337	gcNM_008655.1 (CG)	
Atty_HO-U133_Plus_2	173081	15	1552278_a_atNM_008655	MGC9564	gcNM_008655.1 (CG)	
Atty_HO-U133_Plus_2	173082	16	1552279_a_atAK024181	MGC9564	gcAK024181.1 (CG)	
Atty_HO-U133_Plus_2	173083	17	1552280_at	NM_138379	TMD4	gcNM_138379.1 (CG)
Atty_HO-U133_Plus_2	173084	18	1552281_at	NM_173296	SLC29A5	gcNM_173296.1 (CG)
Atty_HO-U133_Plus_2	173085	19	1552283_a_atNM_024786	ZDHHC11	gcNM_024786.1 (CG)	
Atty_HO-U133_Plus_2	173086	20	1552286_at	NM_008653	ATP11E2	gcNM_008653.1 (CG)
Atty_HO-U133_Plus_2	173087	21	1552287_a_atNM_001132	AF03L1	gcNM_001132.1 (CG)	
Atty_HO-U133_Plus_2	173088	22	1552288_at	BC034926		gcBC034926.1 (CG)
Atty_HO-U133_Plus_2	173089	23	1552289_a_atBC034926		gcBC034926.1 (CG)	
Atty_HO-U133_Plus_2	173090	24	1552291_at	NM_017881	PSXK	gcNM_017881.1 (CG)
Atty_HO-U133_Plus_2	173091	25	1552293_at	NM_152774	MGC42090	gcNM_152774.1 (CG)
Atty_HO-U133_Plus_2	173092	26	1552295_a_atNM_152264	SLC29A13	gcNM_152264.1 (CG)	
Atty_HO-U133_Plus_2	173093	27	1552296_at	NM_152274	YMO3L2	gcNM_152274.1 (CG)
Atty_HO-U133_Plus_2	173094	28	1552298_at	NM_145025	C6orf99	gcNM_145025.1 (CG)

<5> Advanced: From Data Tree

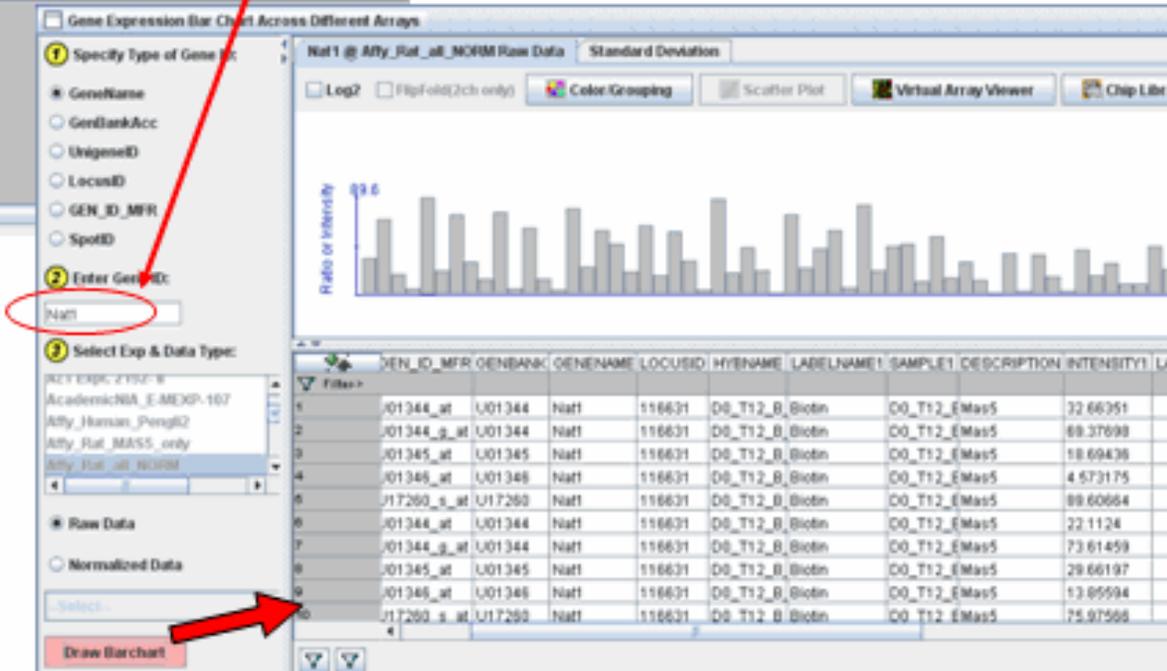
- 1) Select experiment name, then right click to select datasets
- 2) Type in search pattern, matched data will be highlighted in the tree.
- 3) Right click and select "BarChart" to launch. (continue on next page..)

The image illustrates a three-step workflow for selecting datasets from a data tree:

- Right click:** A screenshot of a data tree where a right-click context menu is open over the experiment name 'D0_T12_B_a'. A red box highlights the text 'Right click' and a red arrow points to the menu.
- Select Datasets:** A dialog box titled 'Select Datasets' is shown. The 'Search Pattern' field is highlighted with a red circle. A red arrow points from the 'Select datasets' option in the first screenshot to this dialog box.
- BarChart:** A screenshot of the data tree where the search results are highlighted in blue. A red box highlights the text 'Right click' and a red arrow points to the 'BarChart' option in the context menu. Another red arrow points from the 'BarChart' option to the highlighted search results in the tree.



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



Functions: Query/Sort Barchart Table

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.

2) Click Query (refresh) button

1) Specify constraint on Query row

SAMPLE2	INTENSITY2	RATIO	FLAG	NOTES	POS_DESCR_MER	DESCRIPTION	ARRAYTYPE	ARRAYTYPE	ARRAYTYPE
1			0		265	RMA	ABY_RT-U34	15372	
2			0		265	RMA	ABY_RT-U34	15375	
3			0		265	RMA	ABY_RT		
4			0		265	gPiler16	ABY_RT		
5			0		265	Piler	ABY_RT		
6			0		265	Piler	ABY_RT		
7			0		265	RMA	ABY_RT		
8			0		265	gPiler16	ABY_RT		
9			0		265	Piler	ABY_RT		
10			0		265	Piler	ABY_RT		

Functions: Grouping Bars

- 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 bars. The main window displays a bar chart with a y-axis labeled 'Ratio of Intensity' ranging from 0 to 0.7. The chart shows six bars: three red bars followed by three grey bars. Below the chart is a data table with columns: DRPID, SPOTID, ID, HYBNAME, and NORM. The table lists six rows of data for Strain A and Strain B. A 'Color Chooser' dialog box is open, showing a color palette and a 'Percent' field. The 'Color/Grouping' menu is open, with 'Assign Group by Color' and 'Save Group by Color' options highlighted. A red arrow points from the 'Assign Group by Color' option to the 'Color Chooser' dialog box.

The 'Color Chooser' dialog box shows a color palette with a 'Percent' field set to 100%. Below the palette are several color swatches and a 'Print' button.

The 'Color/Grouping' menu is open, showing the following options:

- Assign Group by Color
- Save Group by Color
- Clear Color & Group

The data table below the chart shows the following data:

DRPID	SPOTID	ID	HYBNAME	NORM
1	14440	Strain A Q380	Lowest	
2	14440	Strain A Q381	Lowest	
3	14440	Strain A Q382	Lowest	
4	14440	Strain B Q385	Lowest	
5	14440	Strain B Q386	Lowest	
6	14440	Strain B Q387	Lowest	

The 'Color Chooser' dialog box shows a color palette with a 'Percent' field set to 100%. Below the palette are several color swatches and a 'Print' button.

The 'Color/Grouping' menu is open, showing the following options:

- Assign Group by Color
- Save Group by Color
- Clear Color & Group

The data table below the chart shows the following data:

DRPID	SPOTID	GEN_ID_MFR	GENBANK	GENENAME	LOCUSID	HYB
1	14440	mmwgmouse30K#B.0:NM_02319	Acin1	56215	Strain A	
2	14440	mmwgmouse30K#B.0:NM_02319	Acin1	56215	Strain A	
3	14440	mmwgmouse30K#B.0:NM_02319	Acin1	56215	Strain A	
4	14440	mmwgmouse30K#B.0:NM_02319	Acin1	56215	Strain E	
5	14440	mmwgmouse30K#B.0:NM_02319	Acin1	56215	Strain E	

Functions: Standard Deviation

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

The screenshot shows a software window titled "Gene Expression Bar Chart Across Different Arrays". The interface includes a sidebar with controls for gene selection and data type, a main chart area, and a data table below.

Standard Deviation Chart: The chart displays two bars representing the ratio of intensity for gene Spg4. The left bar is red and the right bar is green. Both bars include error bars representing standard deviation. A red arrow points to the error bars with the text "standard deviation chart after grouping."

Data Table:

	GRPID	SPOTID	GEN_ID_MFR	GENBANK	GENENAME	LOCUSID	HYBNAME	LABELNAME1	SA
1	1	144120	mwgmouse30KFA.0C	AJ246002	Spg4	50850	Strain A Q380	Cy5	Strain /
2	1	144120	mwgmouse30KFA.0C	AJ246002	Spg4	50850	Strain A Q381	Cy5	Strain /
3	1	144120	mwgmouse30KFA.0C	AJ246002	Spg4	50850	Strain A Q382	Cy5	Strain /
4	2	144120	mwgmouse30KFA.0C	AJ246002	Spg4	50850	Strain B Q385	Cy5	Strain t
5	2	144120	mwgmouse30KFA.0C	AJ246002	Spg4	50850	Strain B Q386	Cy5	Strain t
6	2	144120	mwgmouse30KFA.0C	AJ246002	Spg4	50850	Strain B Q387	Cy5	Strain t

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

ARRAYTYPENAME	SPOTID	POS_DESCR_MFR	GEN_ID_MFR	GENE
NCTR_MWG_Mouse	149926	Block:14-Col:13-Row:18	mwgmouse30K#B.0	NM_01

Gene is highlighted

Advanced Function: How to use BarChart for cross-experiment comparison

Specify the type of gene ID

Enter the gene ID

Select more than one exp

The screenshot shows the 'Gene Expression Bar Chart Across Different Arrays' software interface. The left sidebar contains configuration options: 'Specify Type of Gene ID' (with radio buttons for GeneName, GenBankAcc, UnigeneID, LocusID, GEN_ID_MFR, and SpotID), 'Enter Gene ID' (with a text box containing 'mak'), and 'Select Exp & Data Type' (with a list of experiments including 'ABI_1', 'ABI_1_Ori', 'ABI_2', and 'ABI_2_Ori'). The 'Raw Data' radio button is selected. A 'Draw BarChart' button is at the bottom left. The main window displays a bar chart titled 'mak @ ABI_1; ABI_2 Raw Data' with a 'Standard Deviation' tab. The chart shows two groups of bars: a pink group for experiment 1 and a blue group for experiment 2. A context menu is open over the chart with options: 'Assign Group by Color', 'Save Group by Color', and 'Clear Color & Group'. A red text annotation points to the chart: 'The bar chart for the two experiments grouped in two colors'. Below the chart is a data table with columns: 'gpId', 'SPOTID', 'GEN_ID_MFR', 'GENBANK', 'genename', 'locusId', 'HYBNNAME', 'labelname1', 'SAMPLE1', 'INTENSITY1', and 'labelname2'. The table lists 27 rows of data for the gene 'mak' across two experiments (1 and 2).

	gpId	SPOTID	GEN_ID_MFR	GENBANK	genename	locusId	HYBNNAME	labelname1	SAMPLE1	INTENSITY1	labelname2
13	1	1741687	228830	NM_00590	MAK	4117	ABI_1_C3	ChemiLu	C	154.283	
14	1	1741687	228830	NM_00590	MAK	4117	ABI_1_C4	ChemiLu	C	211.89	
15	1	1741687	228830	NM_00590	MAK	4117	ABI_1_C5	ChemiLu	C	147.237	
16	1	1741687	228830	NM_00590	MAK	4117	ABI_1_D1	ChemiLu	D	144.607	
17	1	1741687	228830	NM_00590	MAK	4117	ABI_1_D2	ChemiLu	D	111.453	
18	1	1741687	228830	NM_00590	MAK	4117	ABI_1_D3	ChemiLu	D	204.938	
19	1	1741687	228830	NM_00590	MAK	4117	ABI_1_D4	ChemiLu	D	180.933	
20	1	1741687	228830	NM_00590	MAK	4117	ABI_1_D5	ChemiLu	D	391.277	
21	2	1741687	228830	NM_00590	MAK	4117	ABI_2_A1	ChemiLu	A	119.667	
22	2	1741687	228830	NM_00590	MAK	4117	ABI_2_A2	ChemiLu	A	127.280	
23	2	1741687	228830	NM_00590	MAK	4117	ABI_2_A3	ChemiLu	A	333.186	
24	2	1741687	228830	NM_00590	MAK	4117	ABI_2_A4	ChemiLu	A	150.67	
25	2	1741687	228830	NM_00590	MAK	4117	ABI_2_A5	ChemiLu	A	160.6	
26	2	1741687	228830	NM_00590	MAK	4117	ABI_2_B1	ChemiLu	B	44.707	
27	2	1741687	228830	NM_00590	MAK	4117	ABI_2_B2	ChemiLu	B	224.193	