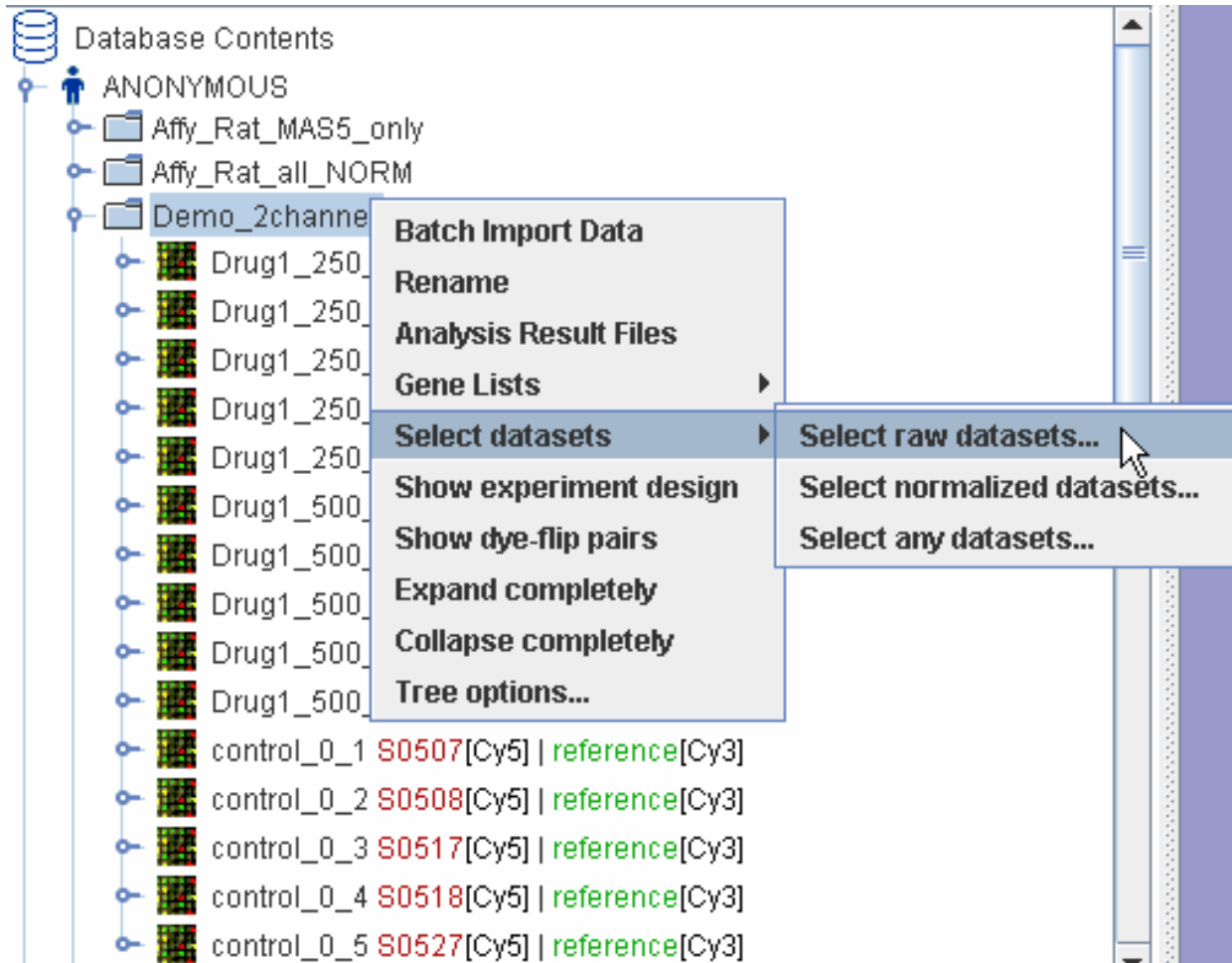


# Tutorial 9B: Data Export



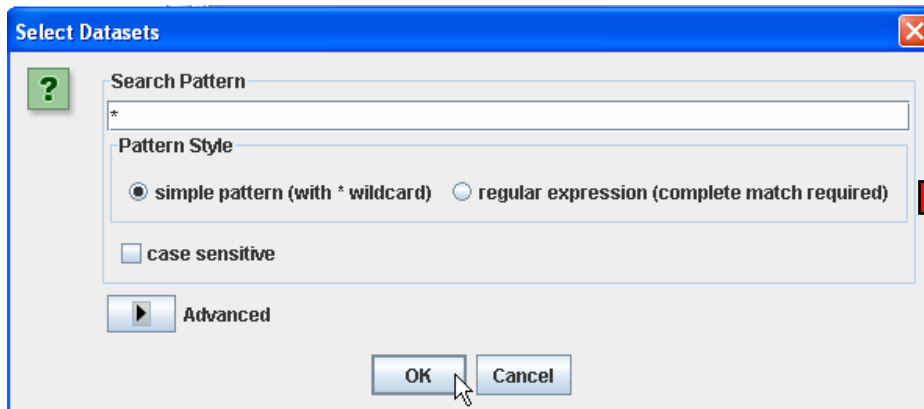
# Data Export



Right-click the experiment, ->select datasets -> select raw datasets...if you want To export raw data.

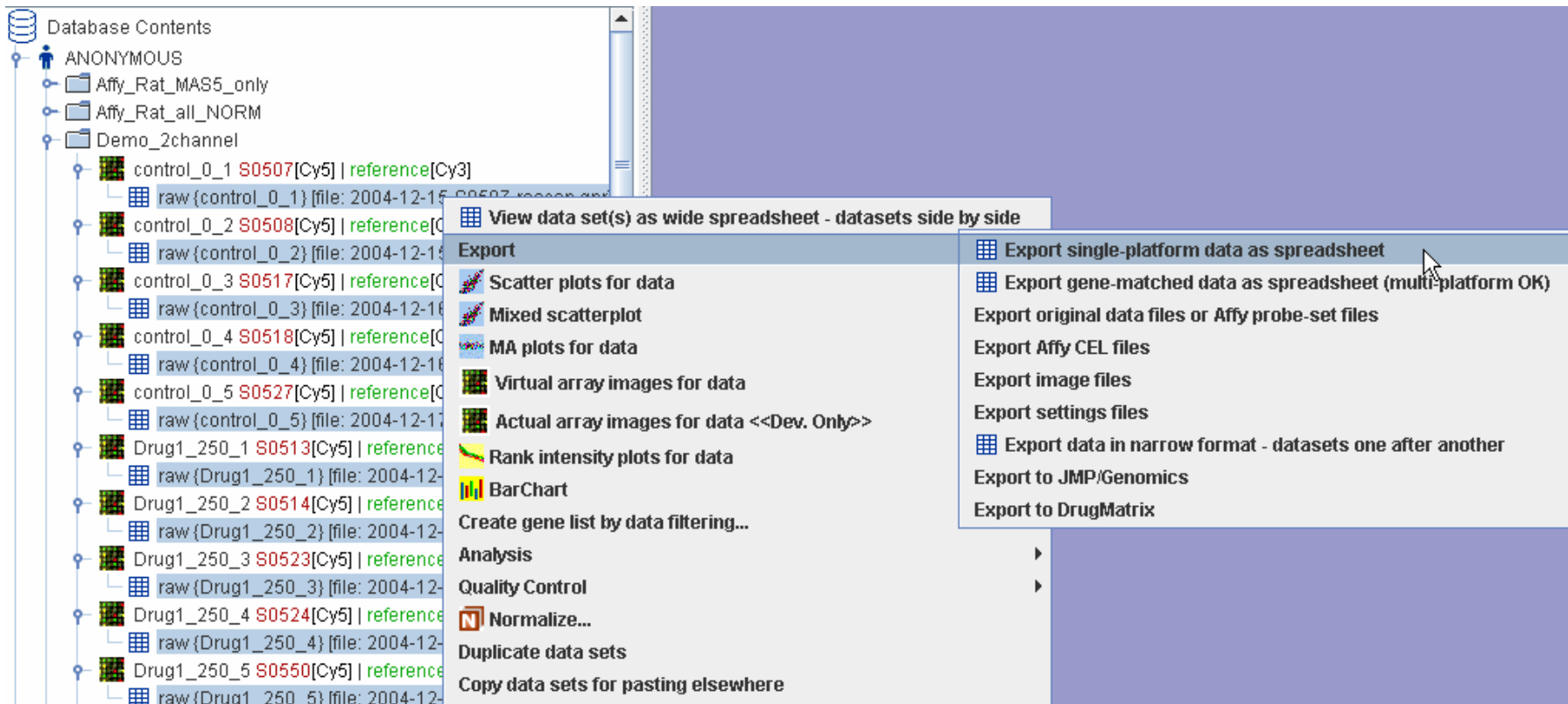
Note: user can also select normalized data to export.

# Data Export



All the selected data will be highlighted.

# Data Export – single-platform data spreadsheet



Right-click the highlighted data, select Export -> Export single-platform data as spreadsheet.

# Data Export – single-platform data spreadsheet

Choose the output options.

Intensity Data Fields

The screenshot shows the 'Export Options' dialog box with the 'Intensity Data Fields' tab selected. The 'Output Options' section is circled in red, and a red arrow points from the text 'Intensity Data Fields' to the 'Intensity Data Fields' tab. The dialog contains the following options:

- include intensities  include spot A-values  subtract backgrounds in intensities
- include separate background columns
- include log intensities  with backgrounds subtracted
- include ratios  with backgrounds subtracted
- include log ratios  with backgrounds subtracted
- ch1/ch2 ratios  ch2/ch1 ratios  both ratios
- Flags**
  - include flag values (as integers)  include original flag values  Exclude spots flagged as bad
  - include spot pixel statistics  include probe p-values
- Log base: 2
- Number of digits to show after decimals: 4
- Group columns by  samples  dyes  datasets

Buttons: OK, Cancel

# Data Export – single-platform data spreadsheet

Dataset Filtering

**Export Options**

Output Options

Intensity Data Fields **Dataset Filtering** Gene Filtering Spot Fields Dataset Naming

Choose Un-Choose Clear All Groups

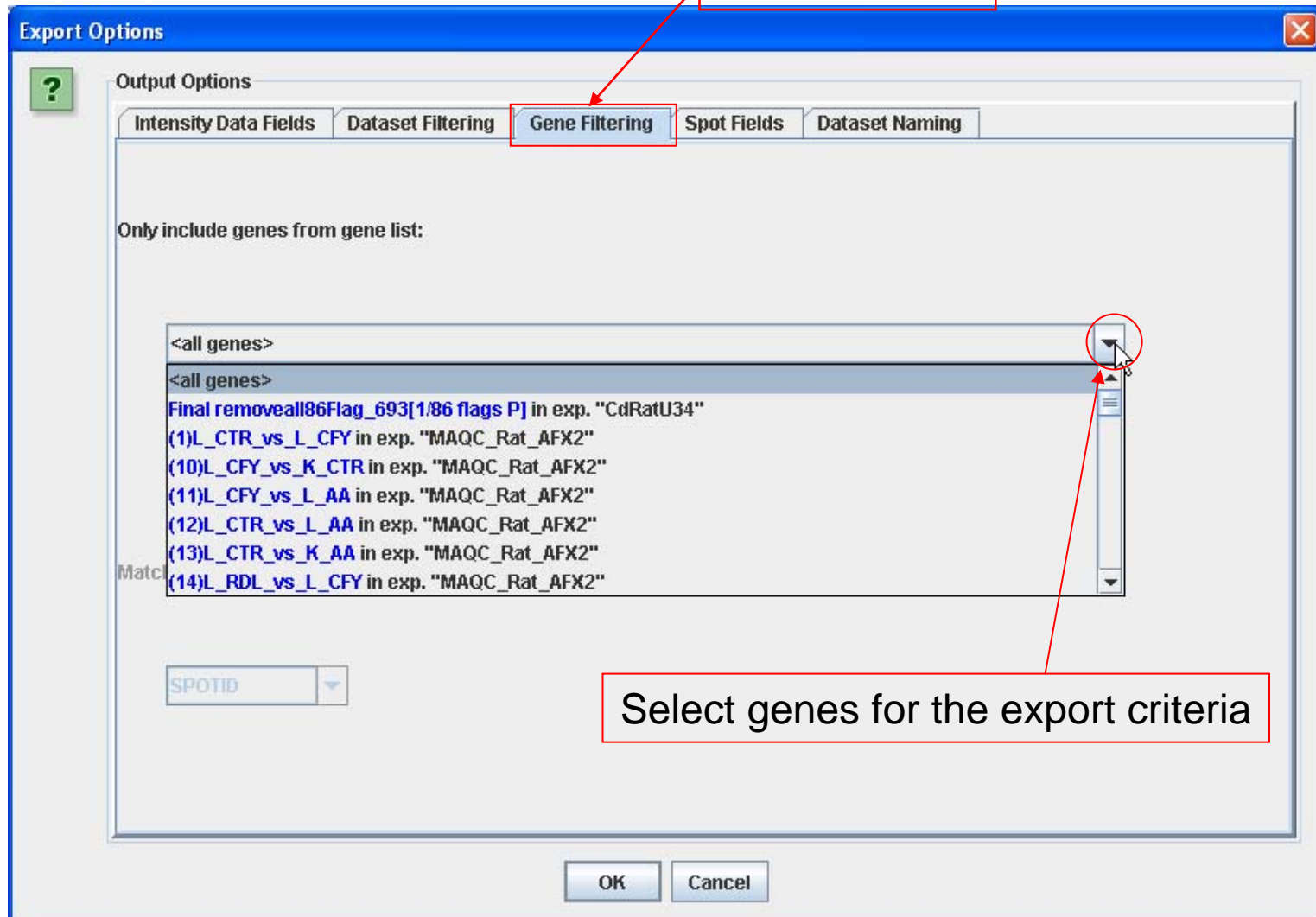
	Hybridization	SAMPLE 1	VIVO DOSING 1	Datafile	LABEL 1	SAMPLE 2	LABEL 2	ARF
1	Drug1_250_1	S0513	Drug1 250 6months	2004-12-15-S0513.gpr	Cy5	reference	Cy3	NCTF
2	Drug1_250_2	S0514	Drug1 250 6months	2004-12-15-S0514.gpr	Cy5	reference	Cy3	NCTF
3	Drug1_250_3	S0523	Drug1 250 6months	2004-12-16-S0523.gpr	Cy5	reference	Cy3	NCTF
4	Drug1_250_4	S0524	Drug1 250 6months	2004-12-16-S0524.gpr	Cy5	reference	Cy3	NCTF
5	Drug1_250_5	S0550	Drug1 250 6months	2004-12-17-S0550.gpr	Cy5	reference	Cy3	NCTF
6	Drug1_500_1	S0515	Drug1 500 6months	2004-12-15-S0515.gpr	Cy5	reference	Cy3	NCTF
7	Drug1_500_2	S0516	Drug1 500 6months	2004-12-15-S0516.gpr	Cy5	reference	Cy3	NCTF
8	Drug1_500_3	S0525	Drug1 500 6months	2004-12-16-S0525.gpr	Cy5	reference	Cy3	NCTF
9	Drug1_500_4	S0526	Drug1 500 6months	2004-12-16-S0526.gpr	Cy5	reference	Cy3	NCTF
10	Drug1_500_5	S0549	Drug1 500 6months	2004-12-17-S0549.gpr	Cy5	reference	Cy3	NCTF
11	control_0_1	S0507	control 0 6months	2004-12-15-S0507-rescan.gpr	Cy5	reference	Cy3	NCTF
12	control_0_2	S0508	control 0 6months	2004-12-15-S0508-rescan.gpr	Cy5	reference	Cy3	NCTF
13	control_0_3	S0517	control 0 6months	2004-12-16-S0517.gpr	Cy5	reference	Cy3	NCTF

Here you can further refine your choice of datasets if necessary, by highlighting datasets and clicking the "Choose" button. If any datasets are chosen (checked icon) when the dialog is dismissed, then only those datasets will be included in the output.

OK Cancel

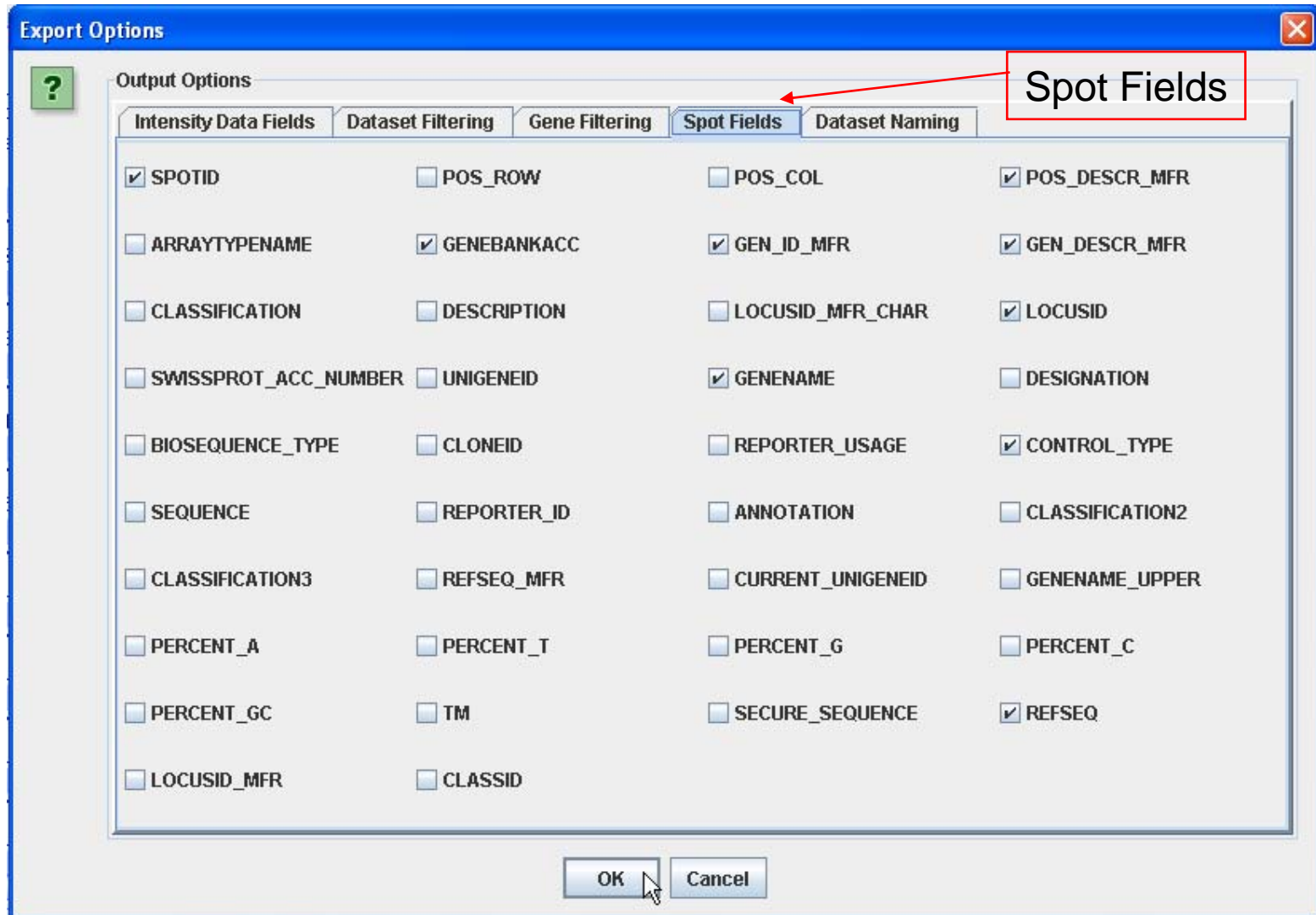
# Data Export – single-platform data spreadsheet

Gene Filtering





# Data Export – single-platform data spreadsheet





# Data Export – single-platform data spreadsheet

**Export Options**

Output Options

Intensity Data Fields   Dataset Filtering   Gene Filtering   Spot Fields   **Dataset Naming**

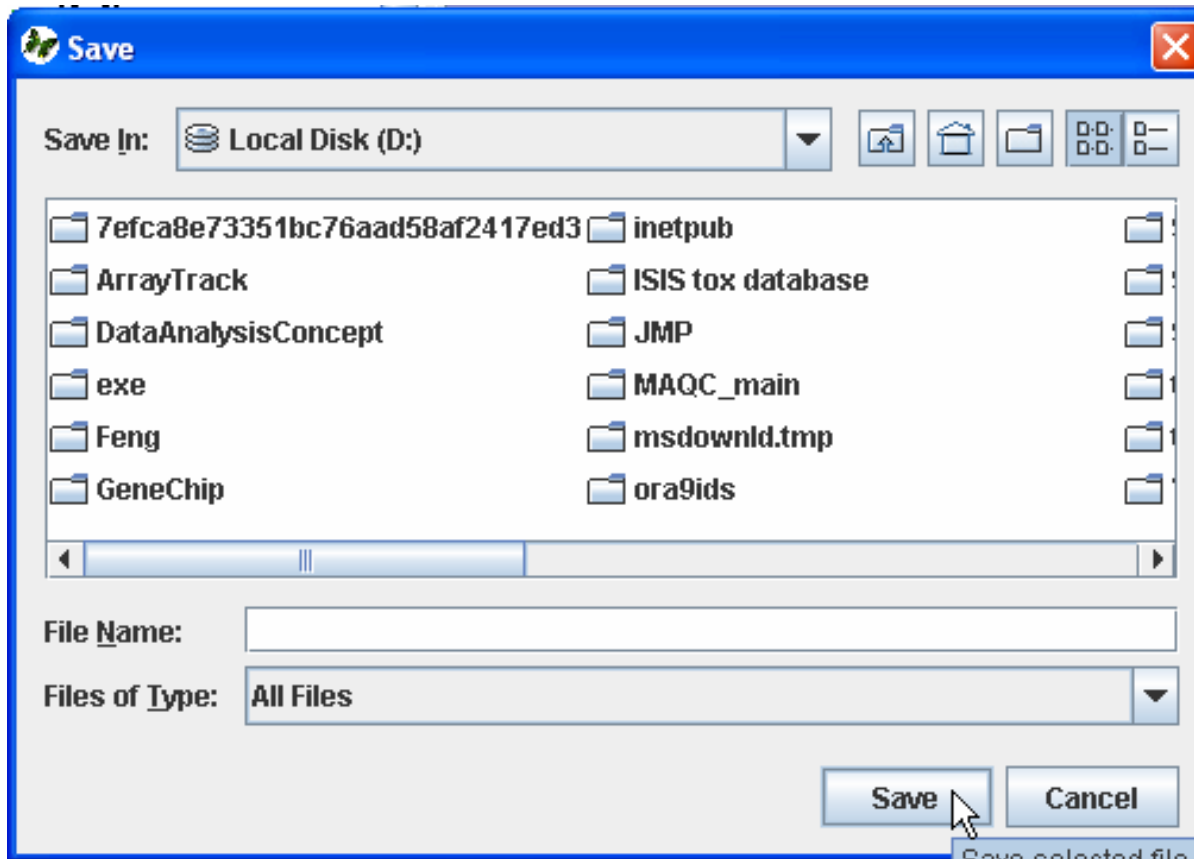
- include hybridization name
- include braces ({} around hybridization name
- include raw dataset description
- include normalization description
- include calculation descriptions in ratio and intensity column names
- include samples in ratio and intensity column names

Dataset Naming

OK   Cancel

This panel controls column naming for dataset columns in the output. Depending on the naming scheme for the datasets, some information may be redundant while necessary information may have been omitted, which can be corrected here.

# Data Export – single-platform data spreadsheet



Save to your folder

# Data Export – Export original files

The screenshot displays a software interface with a tree view on the left and a context menu on the right. The tree view, titled 'Database Contents', shows a hierarchy of folders and files. The 'Export' menu is open, showing various options. The option 'Export original data files or Affy probe-set files' is highlighted with a red box and a mouse cursor.

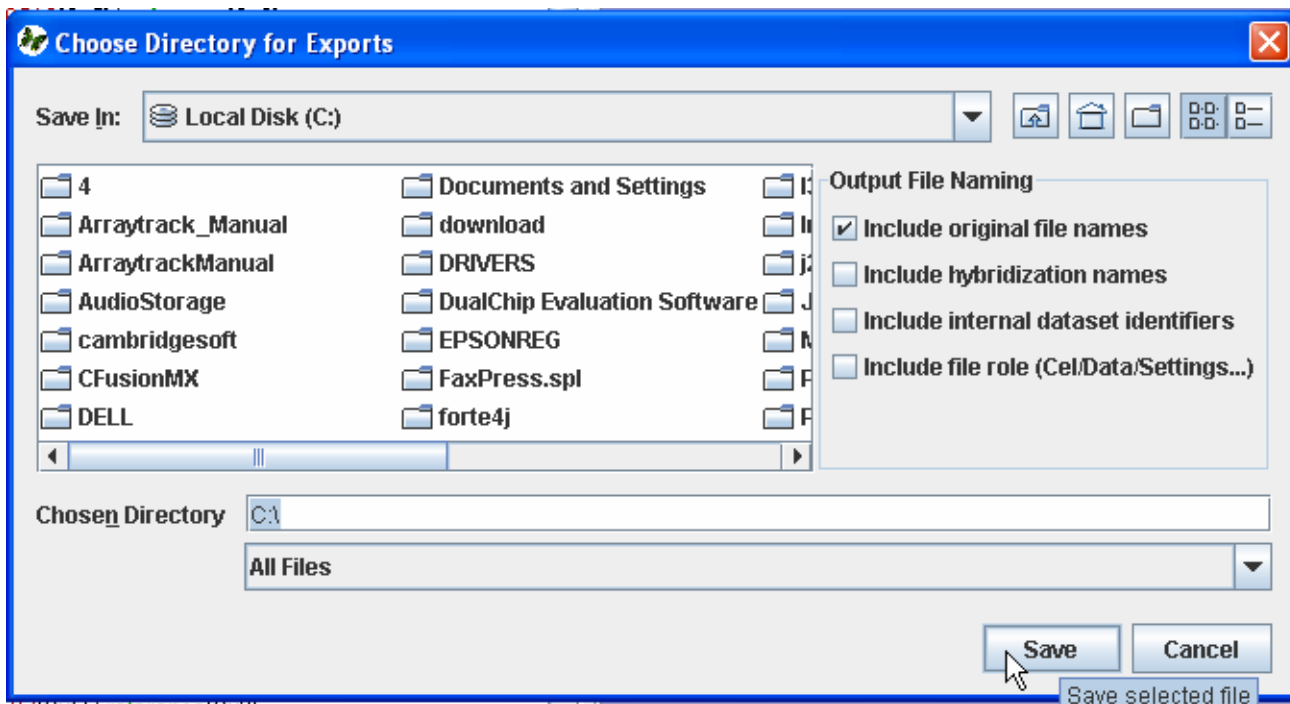
**Database Contents:**

- ANONYMOUS
  - Affy\_Rat\_MAS5\_only
  - Affy\_Rat\_all\_NORM
  - Demo\_2channel
    - Drug1\_250\_1 S0513[Cy5] | reference[Cy3]
      - raw {Drug1\_250\_1} [file: 2004-12-15-S0513.gp...]
    - Drug1\_250\_2 S0514[Cy5] | reference[Cy3]
      - raw {Drug1\_250\_2} [file: 2004-12-15-S0514.gp...]
    - Drug1\_250\_3 S0523[Cy5] | reference[Cy3]
      - raw {Drug1\_250\_3} [file: 2004-12-16-S0523.gp...]
    - Drug1\_250\_4 S0524[Cy5] | reference[Cy3]
      - raw {Drug1\_250\_4} [file: 2004-12-16-S0524.gp...]
    - Drug1\_250\_5 S0550[Cy5] | reference[Cy3]
      - raw {Drug1\_250\_5} [file: 2004-12-17-S0550.gp...]
    - Drug1\_500\_1 S0515[Cy5] | reference[Cy3]
      - raw {Drug1\_500\_1} [file: 2004-12-15-S0515.gp...]
    - Drug1\_500\_2 S0516[Cy5] | reference[Cy3]
      - raw {Drug1\_500\_2} [file: 2004-12-15-S0516.gp...]
    - Drug1\_500\_3 S0525[Cy5] | reference[Cy3]
      - raw {Drug1\_500\_3} [file: 2004-12-16-S0525.gp...]
    - Drug1\_500\_4 S0526[Cy5] | reference[Cy3]
      - raw {Drug1\_500\_4} [file: 2004-12-16-S0526.gp...]
    - Drug1\_500\_5 S0549[Cy5] | reference[Cy3]
      - raw {Drug1\_500\_5} [file: 2004-12-17-S0549.gp...]
    - control\_0\_1 S0507[Cy5] | reference[Cy3]
      - raw {control\_0\_1} [file: 2004-12-15-S0507-resc...]

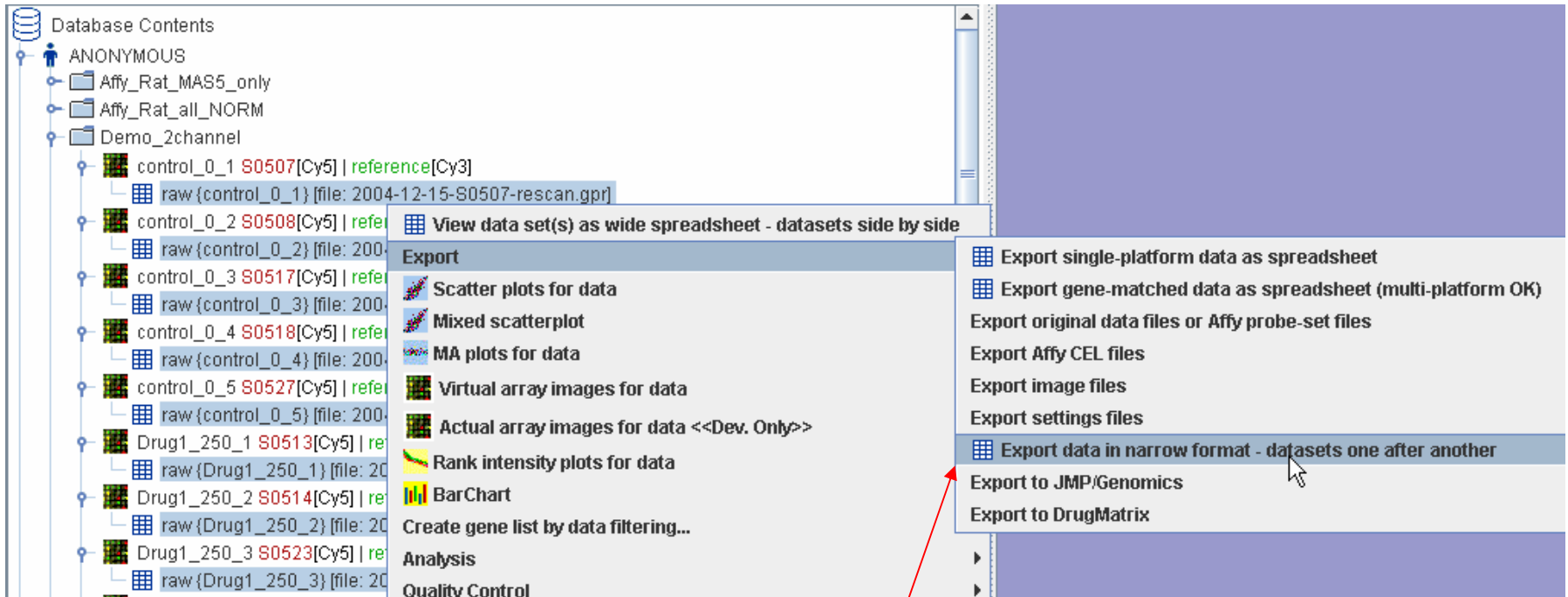
**Export Menu:**

- View data set(s) as wide spreadsheet - datasets side by side
- Export
  - Export single-platform data as spreadsheet
  - Export gene-matched data as spreadsheet (multi-platform OK)
  - Export original data files or Affy probe-set files**
  - Export Affy CEL files
  - Export image files
  - Export settings files
  - Export data in narrow format - datasets one after another
  - Export to JMP/Genomics
  - Export to DrugMatrix
- Scatter plots for data
- Mixed scatterplot
- MA plots for data
- Virtual array images for data
- Actual array images for data <<Dev. Only>>
- Rank intensity plots for data
- BarChart
- Create gene list by data filtering...
- Analysis
- Quality Control
- Normalize...
- Duplicate data sets
- Copy data sets for pasting elsewhere
- Studies
- Tree options...

# Data Export – original data files

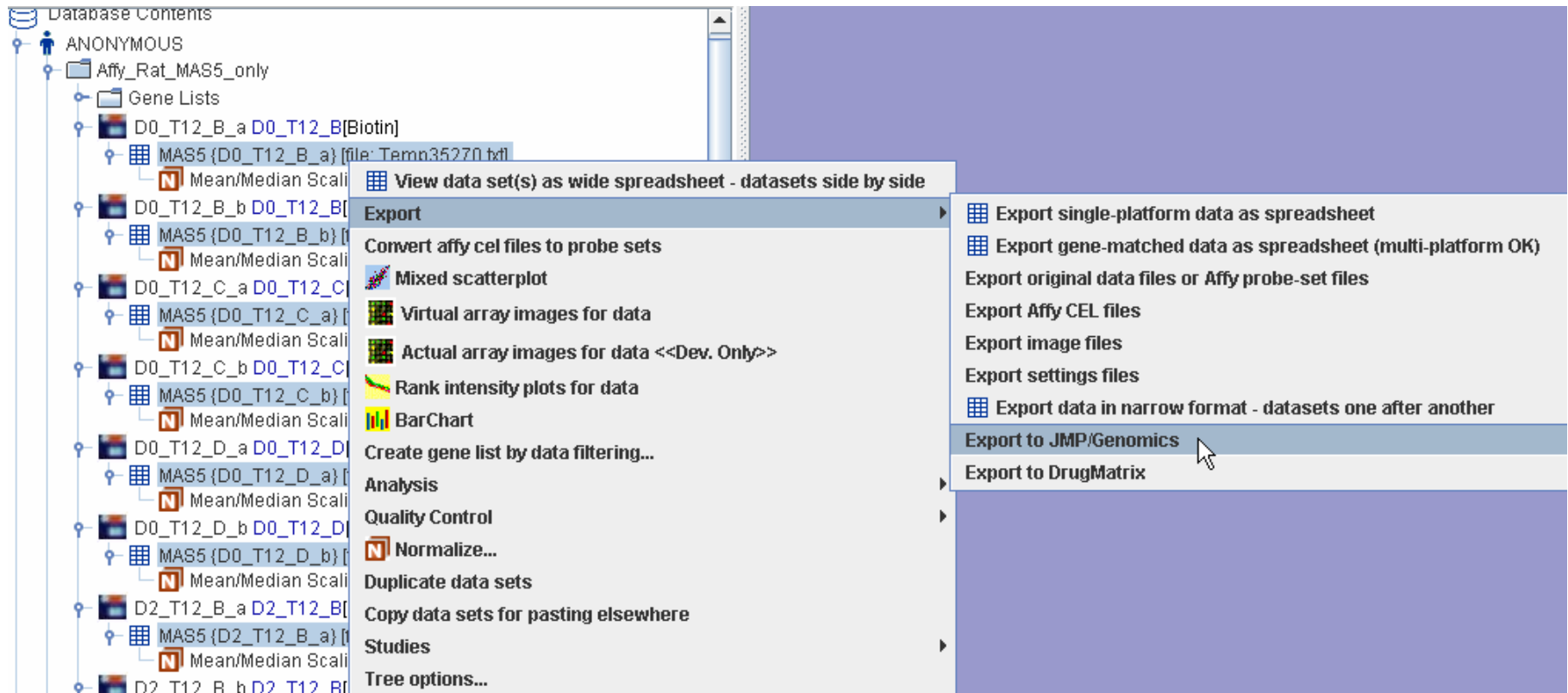


# Data Export- in narrow format



Choosing this option, you will save all the exported data in one file.

# Export Data – to JMP/Genomics



The user need JMP v6.0 or higher to open the exported files.

# Export data – to DrugMatrix

Database Contents

- ANONYMOUS
  - Affy\_Rat\_MAS5\_only
    - Gene Lists
      - D0\_T12\_B\_a D0\_T12\_B[Biotin]
        - MAS5 {D...} Mear
          - Export**
            - View data set(s) as wide spreadsheet - datasets side by side
            - Export
              - Export single-platform data as spreadsheet
              - Export gene-matched data as spreadsheet (multi-platform OK)
              - Export original data files or Affy probe-set files
              - Export Affy CEL files
              - Export image files
              - Export settings files
              - Export data in narrow format - datasets one after another
              - Export to JMP/Genomics
              - Export to DrugMatrix**
          - Convert affy cel files to probe sets
          - Mixed scatterplot
          - Virtual array images for data
          - Actual array images for data <<Dev. Only>>
          - Rank intensity plots for data
          - BarChart
          - Create gene list by data filtering...
          - Analysis
          - Quality Control
            - Normalize...
          - Duplicate data sets
          - Copy data sets for pasting elsewhere
          - Studies
          - Tree options...

This function is only for the data of a few array type

**Unsatisfied Array Type**

Only AFFY\_RAE230A, AFFY\_RG230\_2 and GEHC\_RAT\_WHOLEGENOME300031 array can have this function now .

OK



# Mixed Platform Exporting

When datasets from multiple platforms are exported together, a gene identifier type must be chosen to serve as a “match field” (e.g. “REFSEQ”). Filtering based on a gene identifier may also be done.

For single-platform datasets the single-platform export should be used, as it supports more output options.

# Mixed Platform Exporting

The image shows a software interface with a file tree on the left and a menu system on the right. The file tree includes folders like 'D2\_T12\_D\_a', 'D2\_T12\_D\_b', and 'Strain\_mice\_two\_Channel'. The menu system has an 'Export' option selected, which opens a sub-menu with the following items:

- View data set(s) as wide spreadsheet - datasets side by side
- Export** (highlighted)
  - Export gene-matched data as spreadsheet (multi-platform OK)** (highlighted)
  - Export original data files or Affy probe-set files
  - Export Affy CEL files
  - Export image files
  - Export settings files
  - Export data in narrow format - datasets one after another
  - Export to JMP/Genomics
  - Export to DrugMetrix
- Mixed scatterplot
- Virtual array images for data
- Actual array images for data <<Dev. Only>>
- Rank intensity plots for data
- BarChart
- Create gene list by data filtering...
- Analysis
- Quality Control
- Normalize...
- Duplicate data sets
- Copy data sets for pasting
- View/Edit Referenced Tox. S...
- Tree options...

A red arrow points from the 'Export gene-matched data as spreadsheet (multi-platform OK)' option to a 'Save' dialog box. The 'Save' dialog box has the following details:

- Save In: Fqian.FDA
- Match spots by: REFSEQ
- case sensitive
- Exclude spots flagged as bad
- Only include genes from gene list:
  - 174Welch\_t\_2fold\_p0.05 in exp. "Strain\_mice\_two\_Channel"
  - <all genes>
  - 46 ints >= 10 in exp. "Strain\_mice\_two\_Channel"
  - 123geneMAS5\_Fold1.5\_P0.05 in exp. "Affy\_Rat\_Other"
  - 123geneMAS5\_Fold1.5\_P0.05 in exp. "Strain\_mice\_two\_Channel"
  - 135gene\_PermutationP0.05Fold1.5 in exp. "Affy\_Rat\_Other"
  - 174Welch\_t\_2fold\_p0.05 in exp. "Strain\_mice\_two\_Channel"
  - 187Welch\_t\_1.5fold\_p0.01 in exp. "Strain\_mice\_two\_Channel"
  - Apply 202Welch\_t\_test\_P0.005 in exp. "Strain\_mice\_two\_Channel"
- Subtract backgrounds if available
- Include individual channel values for 2-channel data
- File Name: [empty]
- Files of Type: All Files
- Buttons: Save, Cancel