

How to use Affymetrix Expression Console Software to convert .cel files into .txt files and then import .txt files into BRB-ArrayTools?

1. Download and install Affymetrix Expression Console

Here is the link of Affymetrix Expression Console download website.

http://www.affymetrix.com/browse/level_seven_software_products_only.jsp?productId=131414&categoryId=35623#1_1

Here is the link where you could download Affymetrix Expression Console (64bit).

http://www.affymetrix.com/products_services/software/download/expression_console/expression_console_download_terms.affx?v=Release1.2.1.64bit

(You may be asked to register if you don't have an account.)

The screenshot shows the Affymetrix website's Customer Login page. At the top, there is a navigation bar with links: Home, Products, Brands, Community, Support, Partners & Programs, About Affymetrix, Careers, and NetAffx. A search bar is located below the navigation bar. The main content area is titled 'Customer Login' and includes a 'Returning Customer' section with fields for 'Email ID' and 'Password', a 'Submit' button, and a link for 'Need login assistance?'. There is also a 'New Customer' section with a 'Register Now' link and a list of reasons to register. A sidebar on the left contains a 'Customer Login' button and a 'Contact Us' button. At the bottom, there is a footer with sections for 'Highlights', 'Community', 'Company', 'Contact Us', and 'Share your story'.

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Are you a new customer? [Register Now](#) to start enjoying all the benefits of the Affymetrix website.

Why Register?

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- Update your profile information
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By creating an account, you acknowledge and agree to the [Terms of Use](#) concerning your access to and use of the Affymetrix website and the services and content provided on the Affymetrix website, and our [Privacy Policy](#). Read them carefully before you finish creating your account.

Highlights <ul style="list-style-type: none">NetAffx Analysis CenterAffymetrix CommunityAffymetrix ConnectPromotions	Community <ul style="list-style-type: none">Affymetrix CommunityAffymetrix ConnectCytogenetics Research CommunityGene Communities	Company <ul style="list-style-type: none">About AffymetrixContact UsInvestorsCareers	Contact Us <ul style="list-style-type: none">Contact AffymetrixRegional Contact InformationTechnical SupportWebsite Feedback	Share your story <ul style="list-style-type: none">Affymetrix FacebookAffymetrix TwitterAffymetrix YouTubeAffymetrix LinkedIn
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After you logged in, please accept license agreement to start download the software.

Expression Console™ Software Download

☐ I'd like to receive notifications about the Expression Console™ Software.

With what array applications are you planning on using the Expression Console Software?

- ☐ 3' Expression Arrays
☐ Exon Arrays
☐ both
☐ neither

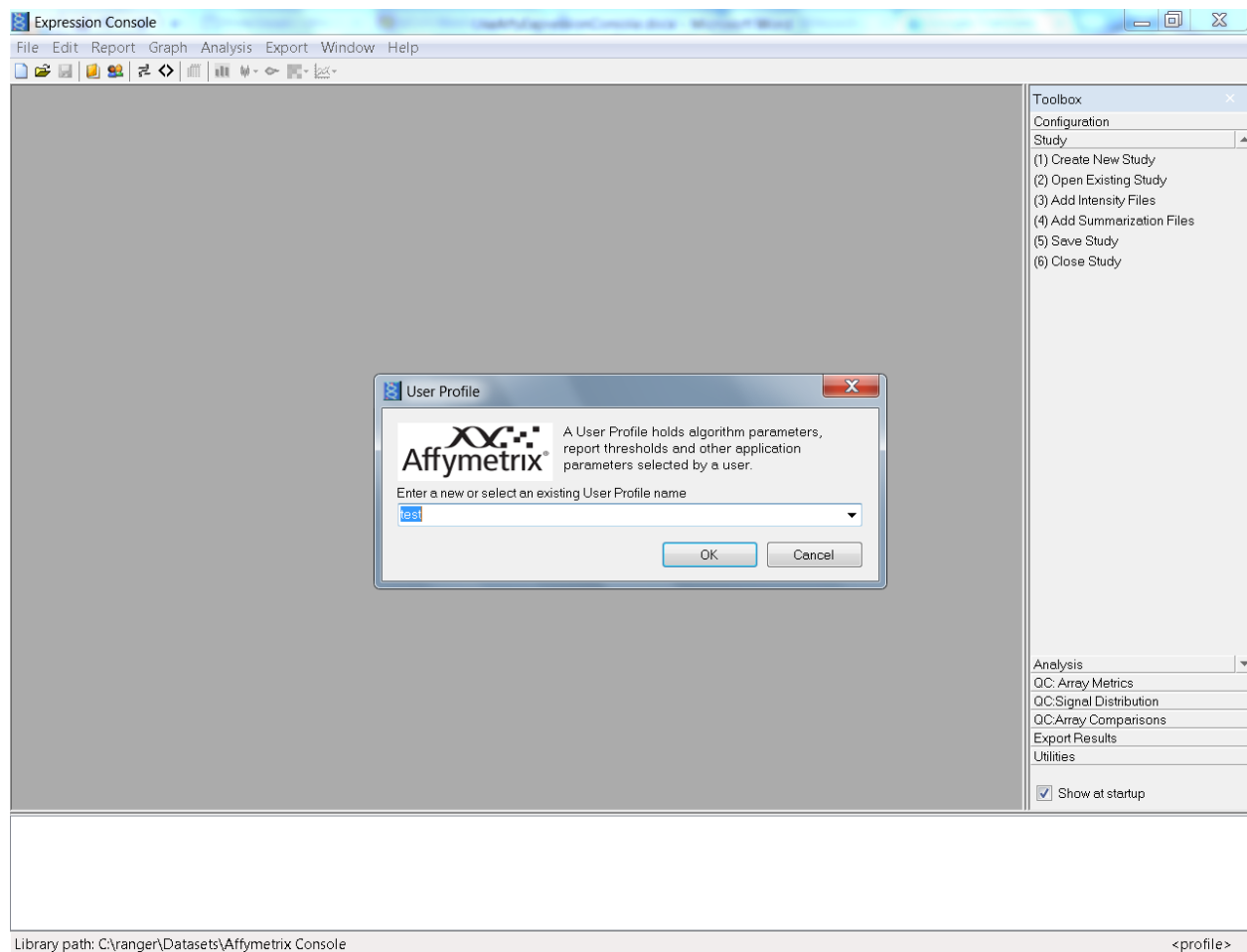
What application are you intending on using Expression Console in conjunction with?

- ☐ GCOS
☐ Affymetrix Genechip Command Console (AGCC)
☐ both
☐ neither

I Accept

I have read and understood, and agree to the User Agreement.

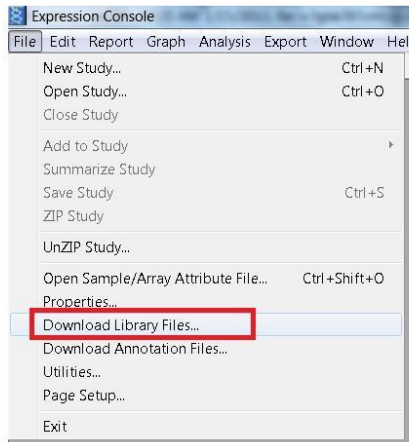
2. After you downloaded software to your local computer and finished installation, please open software and you will see the following screen.



3. Create a new User Profile

4. Download Library file for your array chip type. (The following screen shot show you how to download library file for Mouse Exon 1.0 ST array. The library name is MoEx_1_0-st-v1)

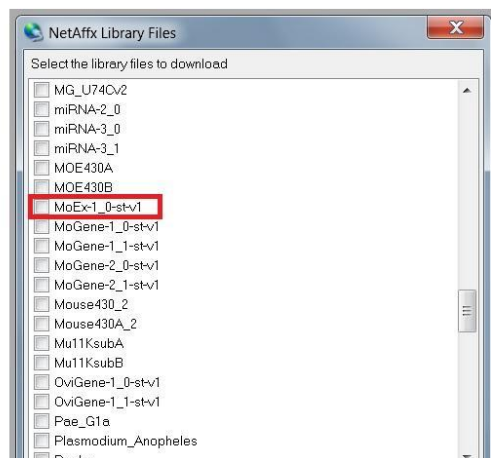
Step 1



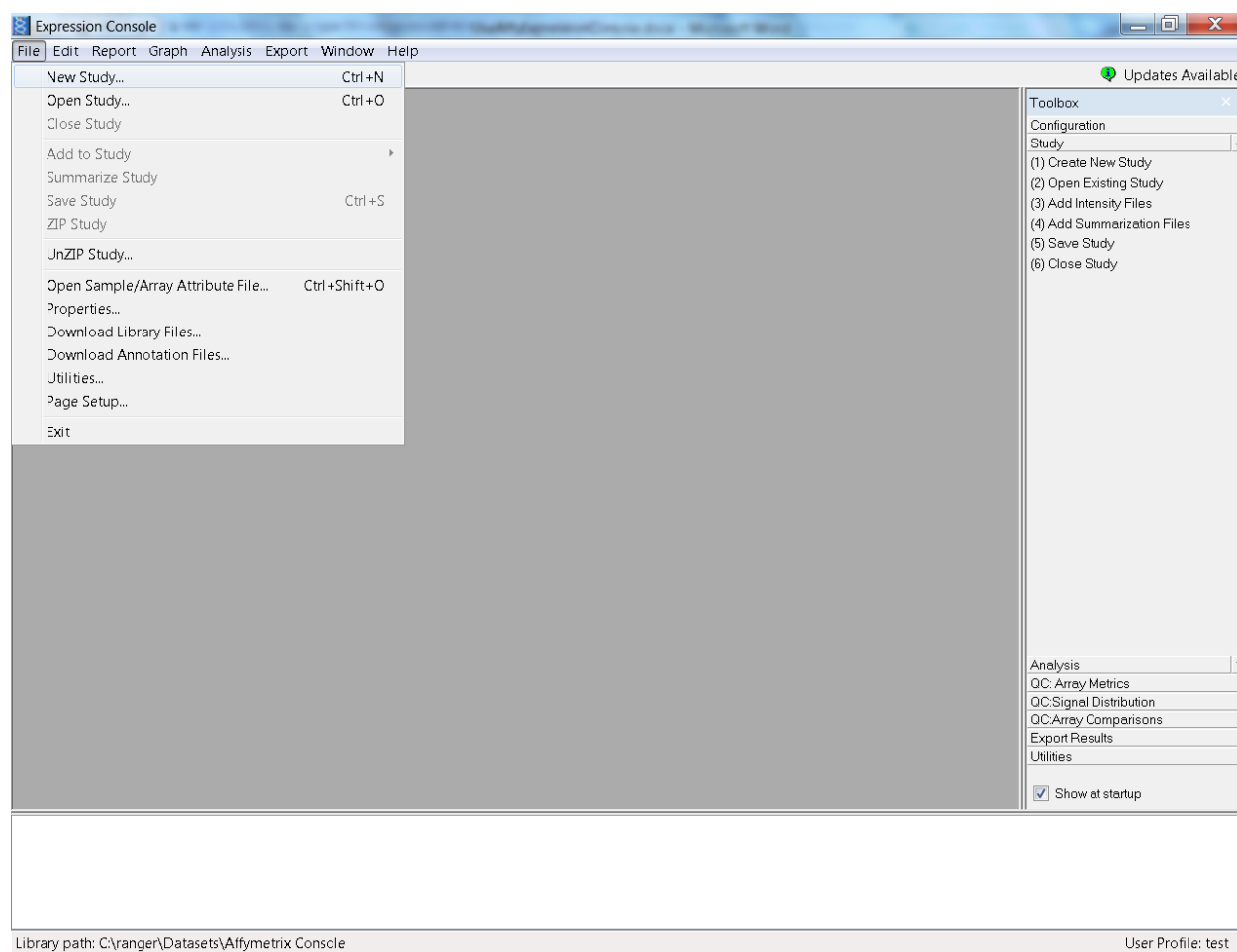
Step 2: log in or register if you do not have an account.



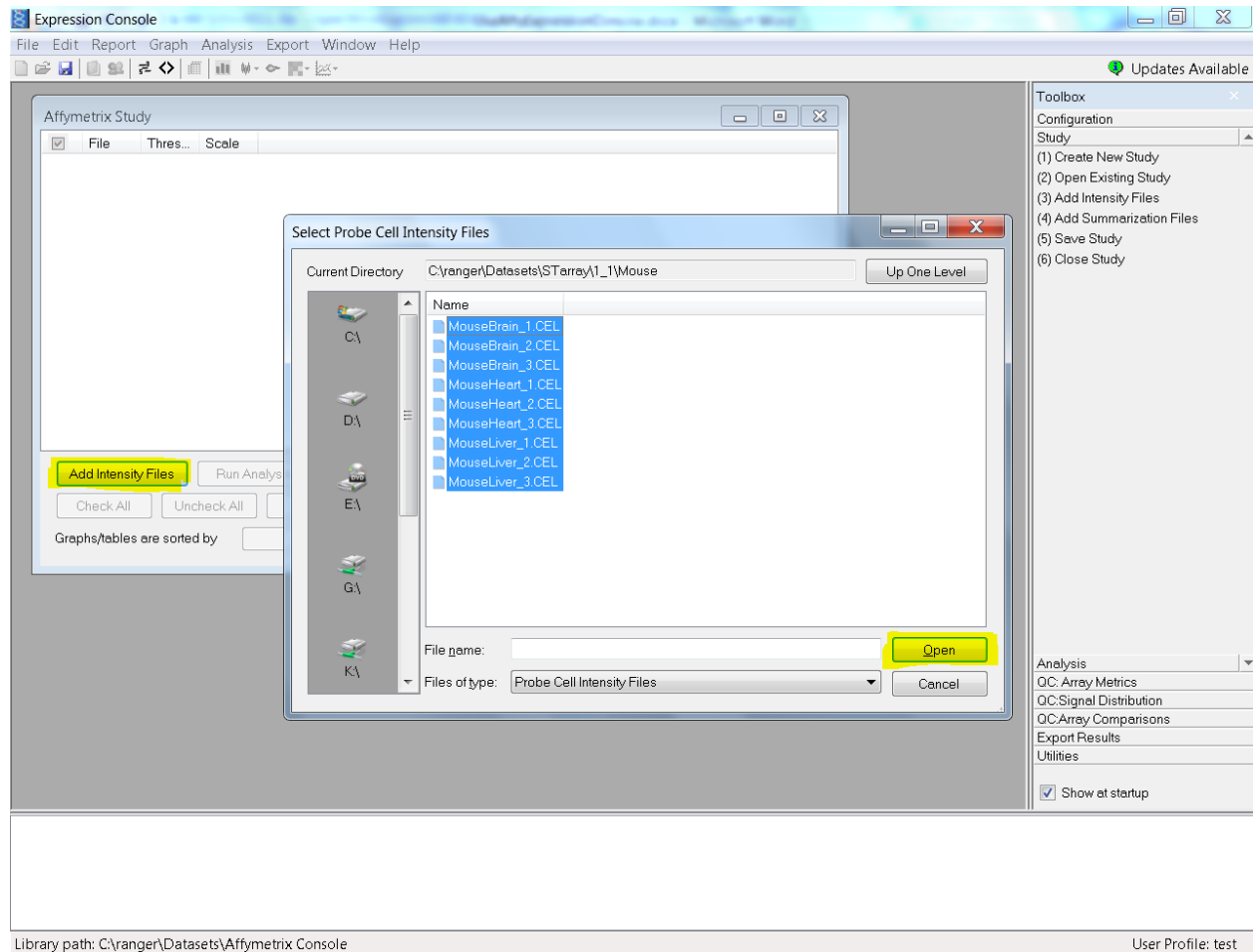
Step 3: look for cdf file for Mouse Exon 1.0 St array and download it.



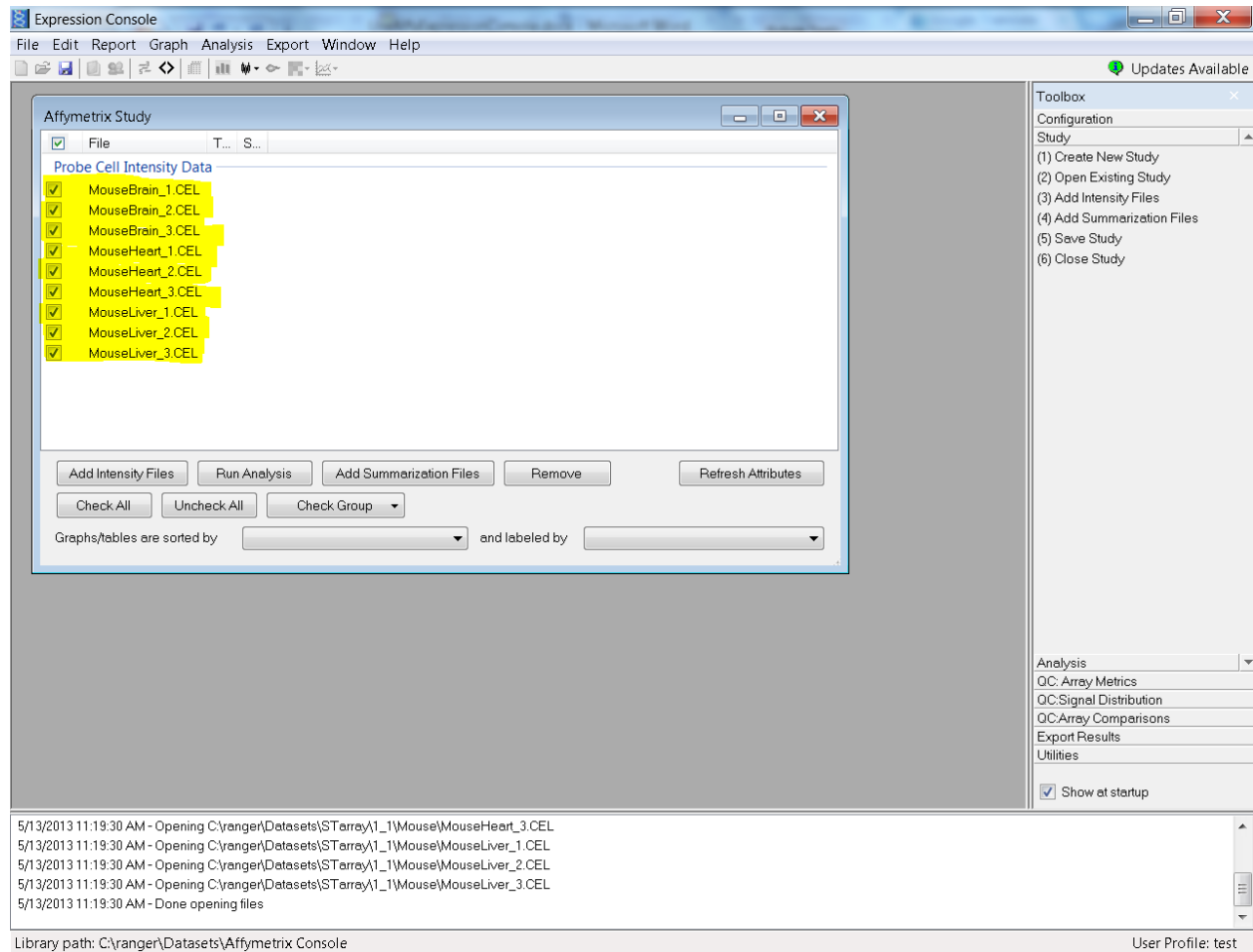
5. Create a new study



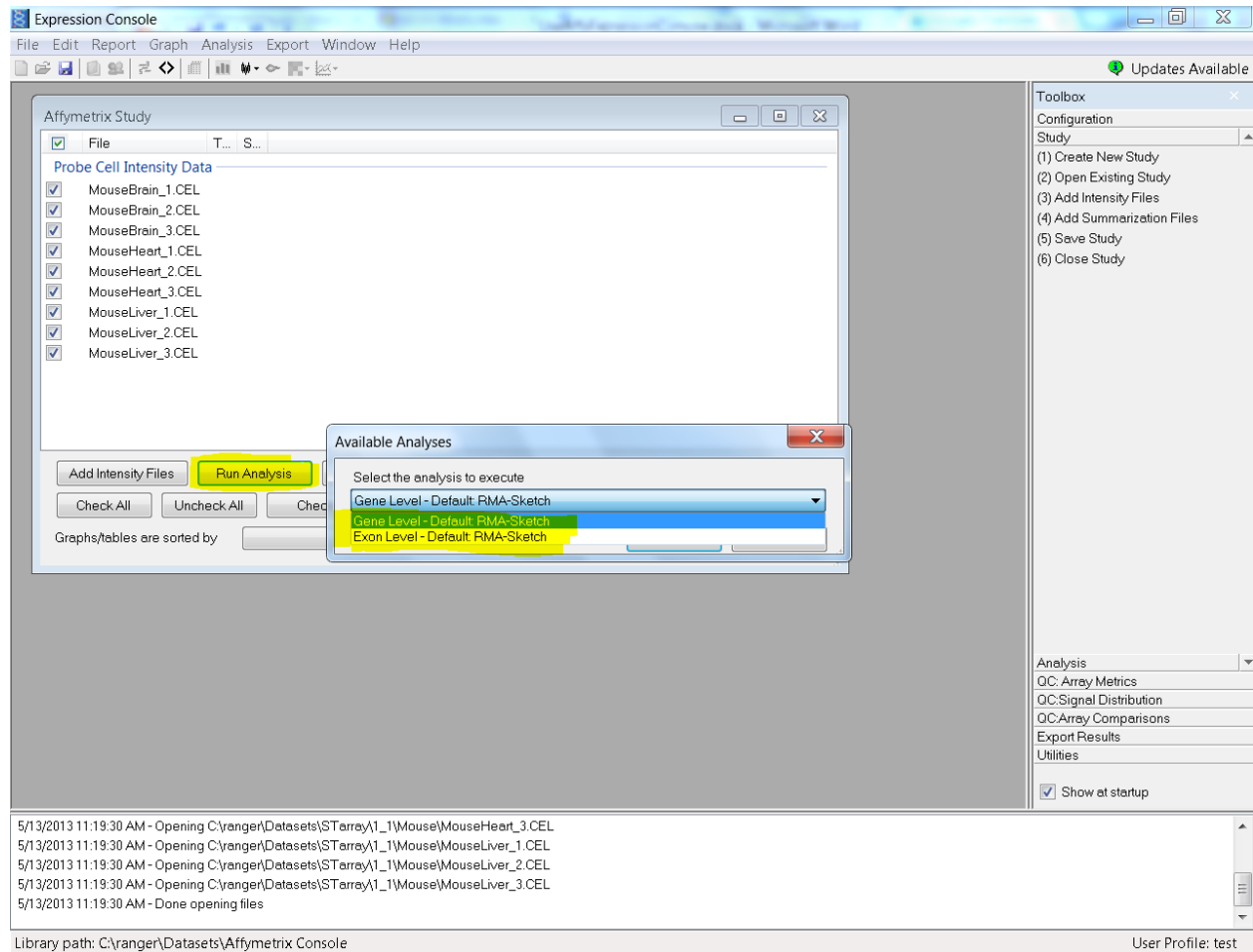
6. Add Intensity files (Browse for your data set .cel files. I used Mouse 1.1 ST array data as an example.)



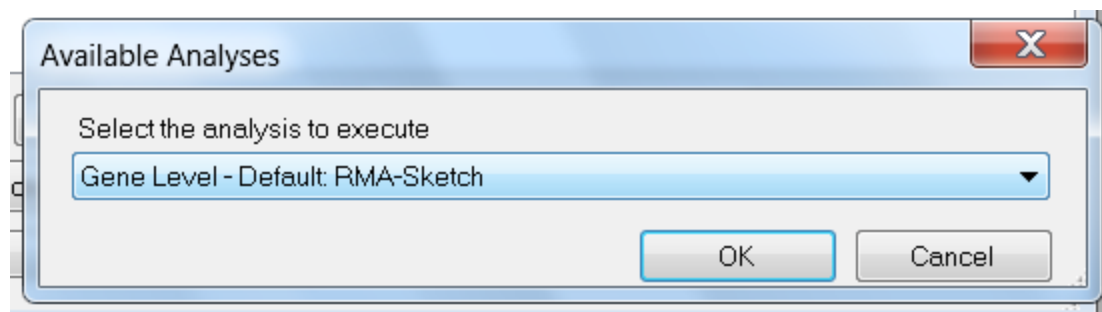
After you clicked open button, you should see all you .cel files were loaded. (I highlight them in yellow.)



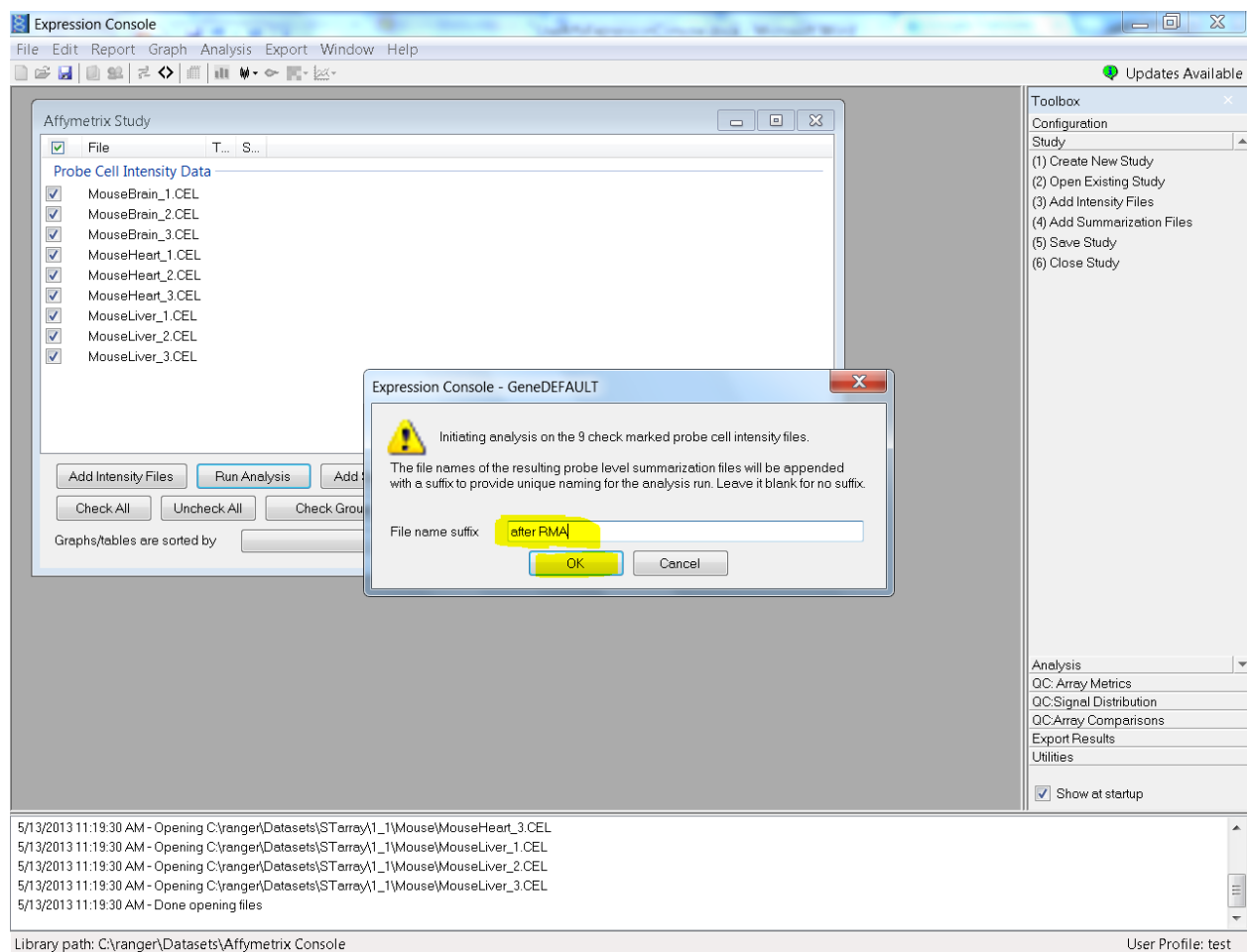
7. Run RMA (Click Run Analysis -> Choose Gene level (if you analyze Affymetrix Gene ST arrays, including 1.0, 1.1, 2.0 and 2.1) OR Exon level (if you analyze Affymetrix Exon arrays))



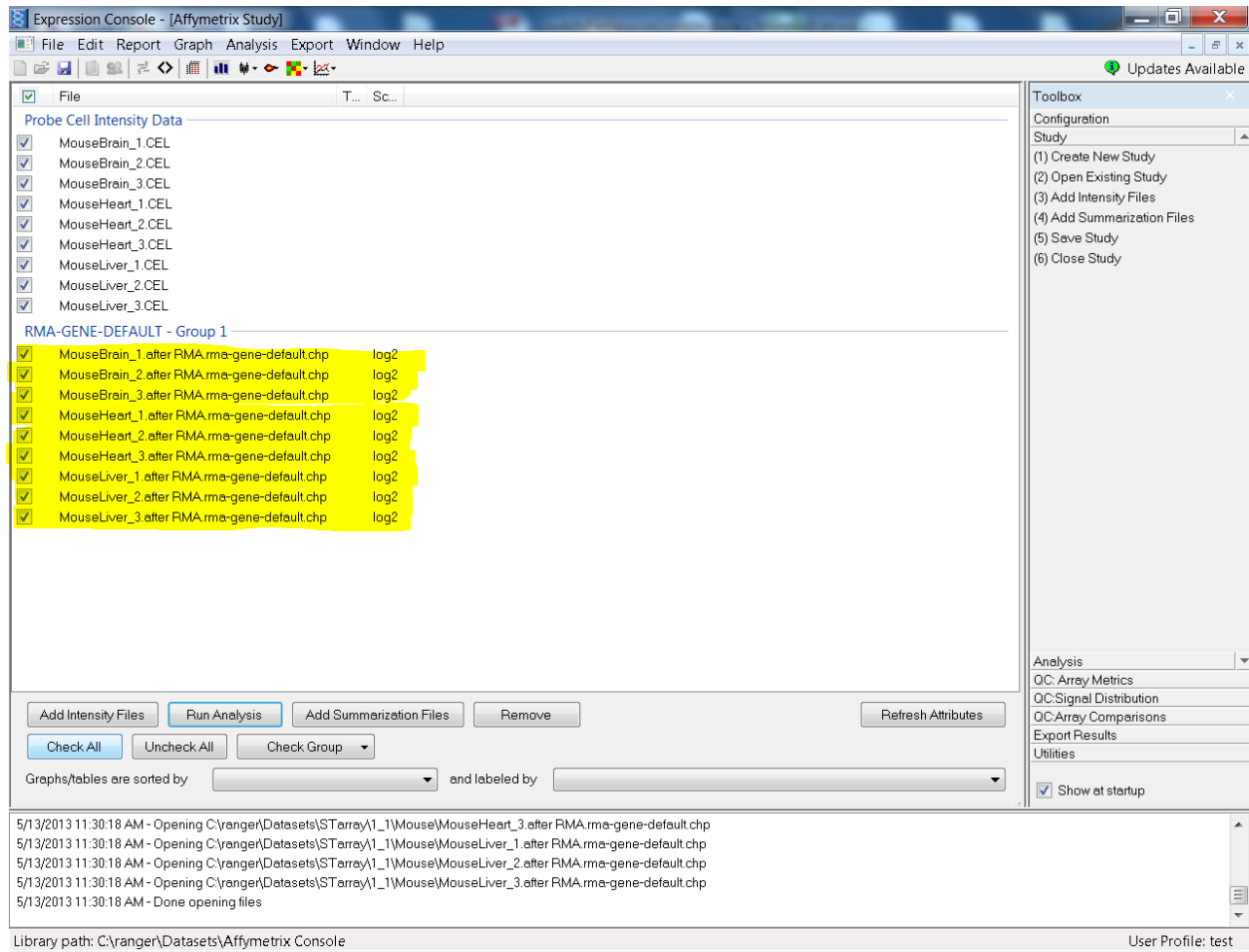
I will use Gene level because the example data set is a Mouse ST 1.1 array data.



Give a file name suffix (after RMA for example) and then click OK to proceed

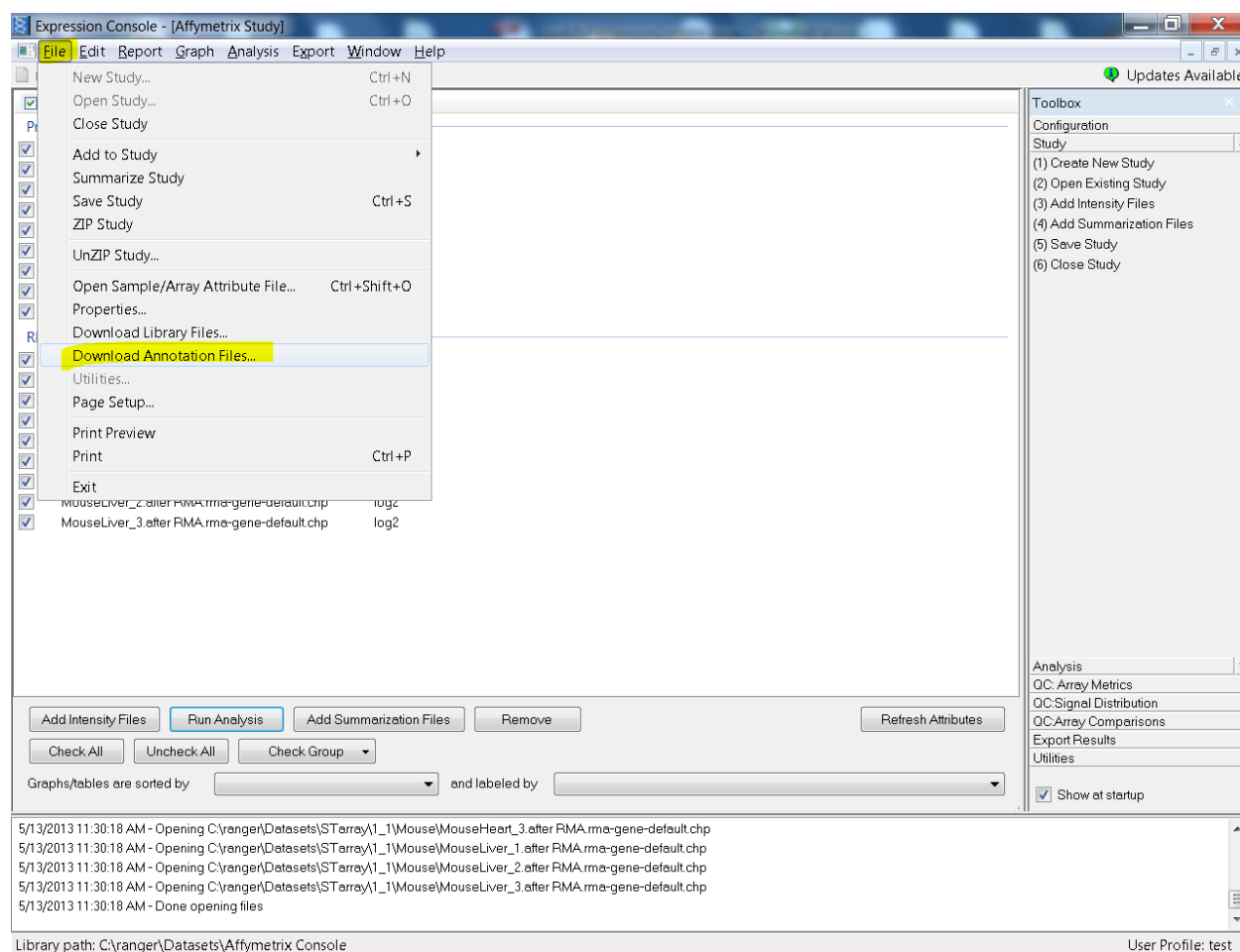


After RMA was finished, you will see more files are loaded in your study.

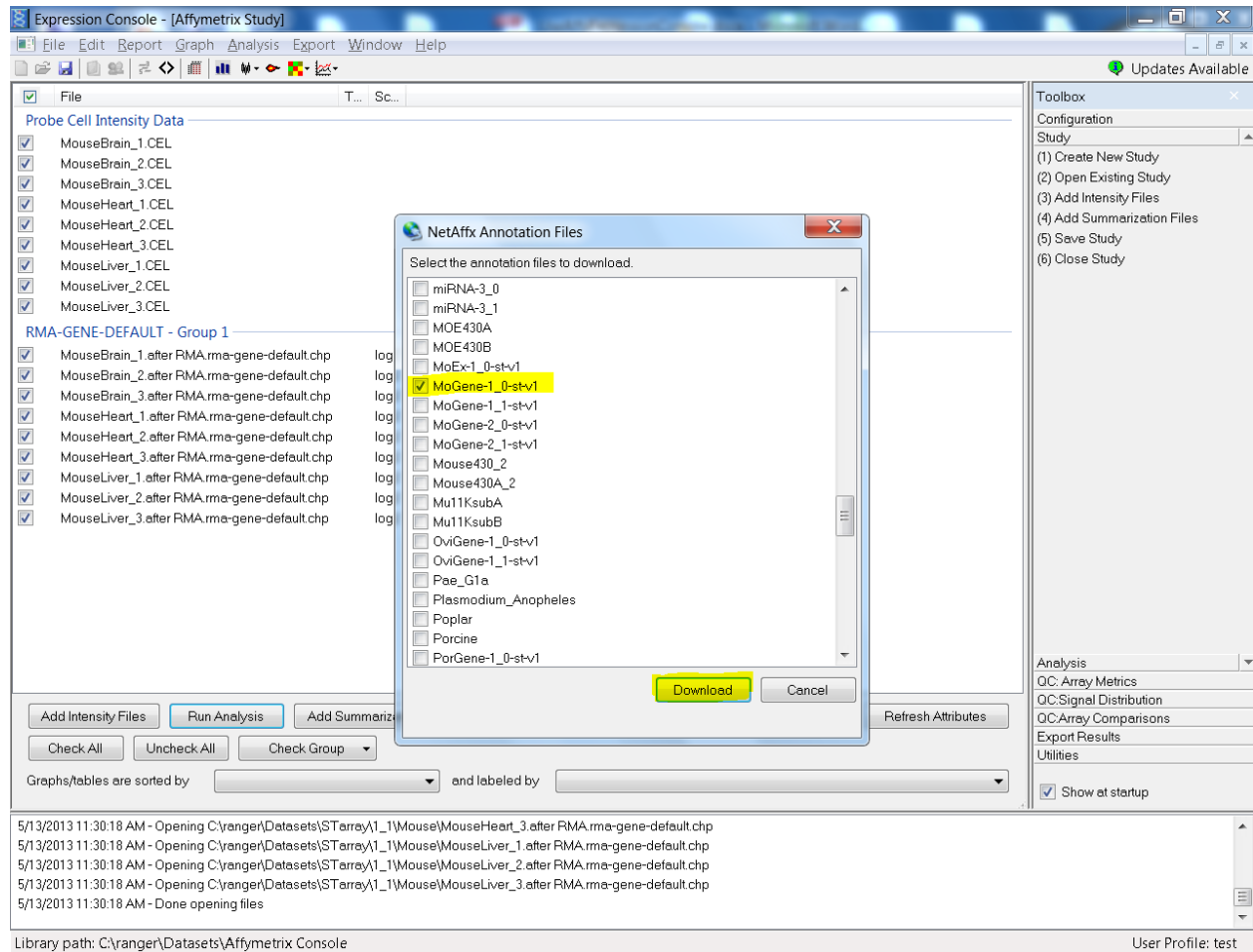


8. Import annotation for your data.

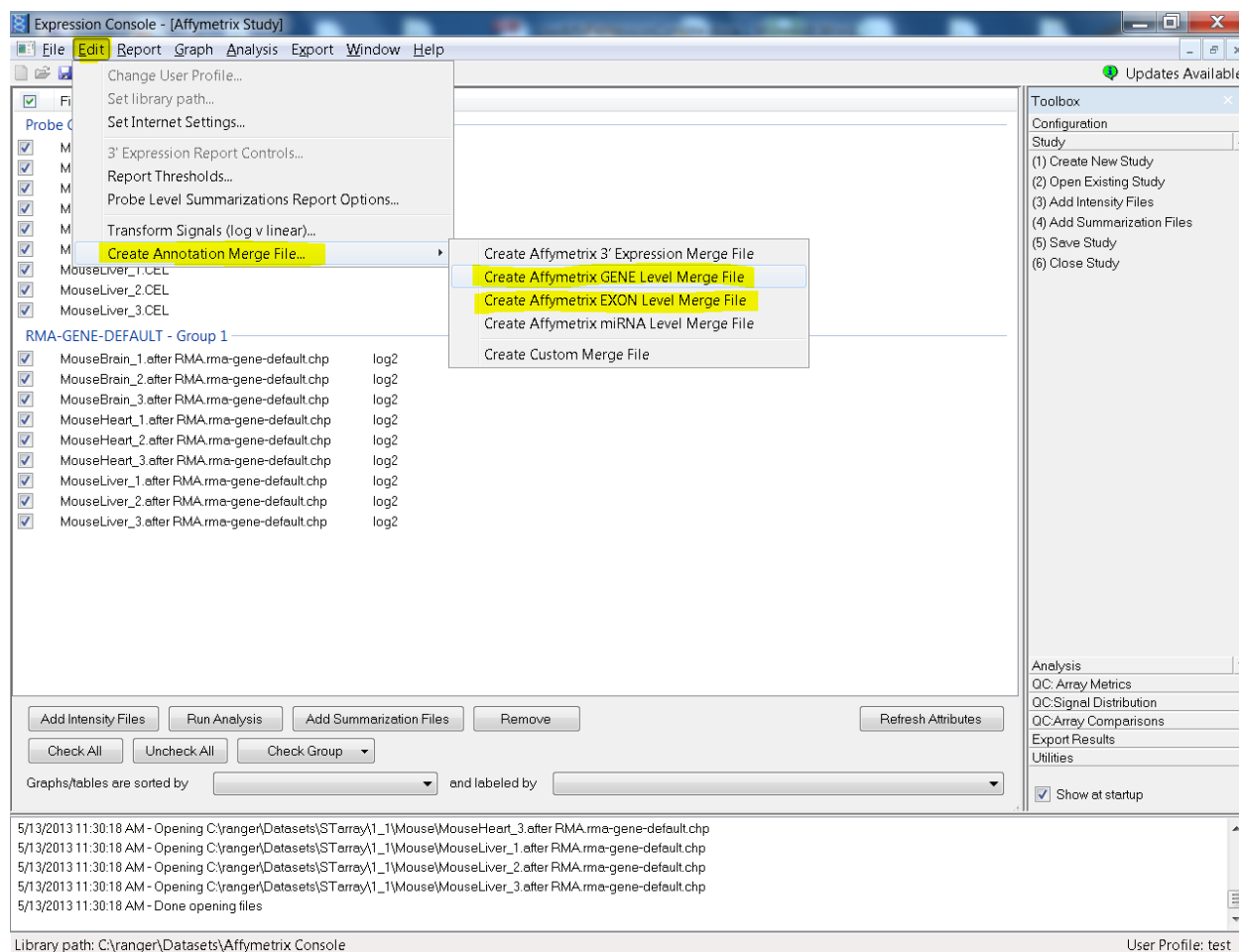
Download Annotation file (Go to File -> Download Annotation Files)



Select the annotation file for your data and Click Download button. (I need to download MoGene-1_0-st-v1 because I use Mouse 1.0 ST Gene array as an example.)

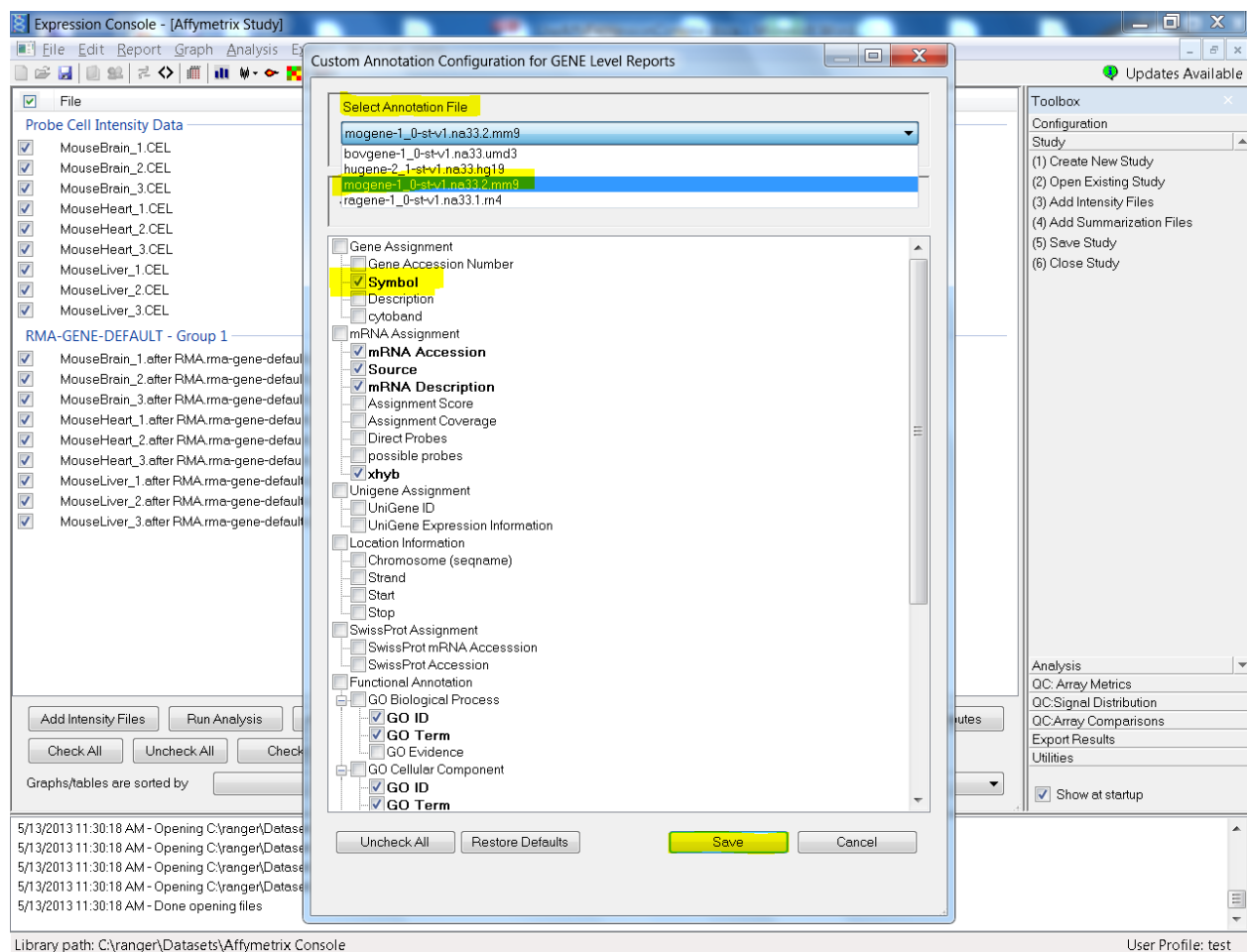


After you finished download, please create Affymetrix Gene OR Exon (Depend on the type of your data) Level Merge File. (I highlight these steps in yellow.)

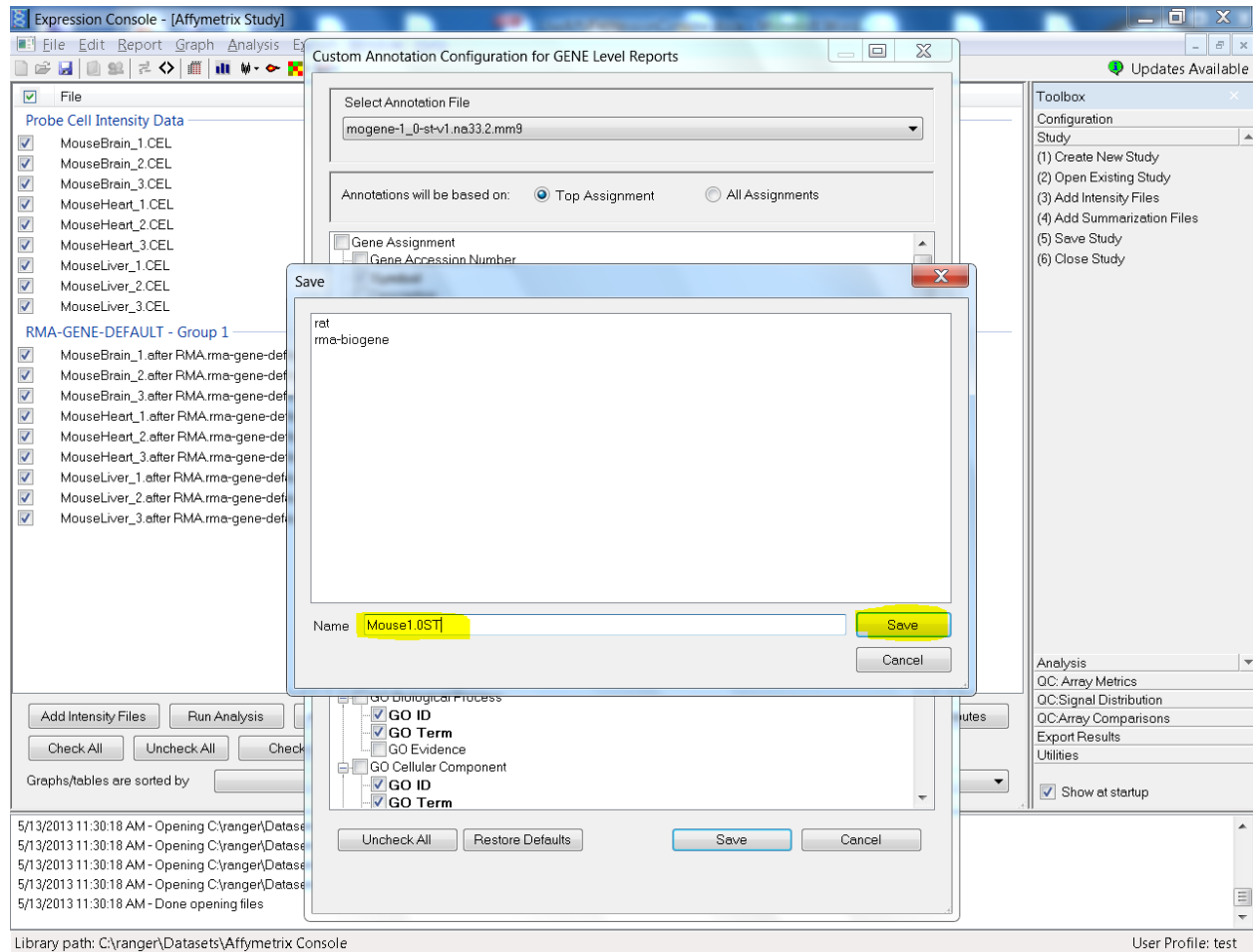


Please select annotation file (I used mogene-1-0-st-v1 as an example here.)

Please make sure you check “**Symbol**”! (It is required by ArrayTools and you must check it.)

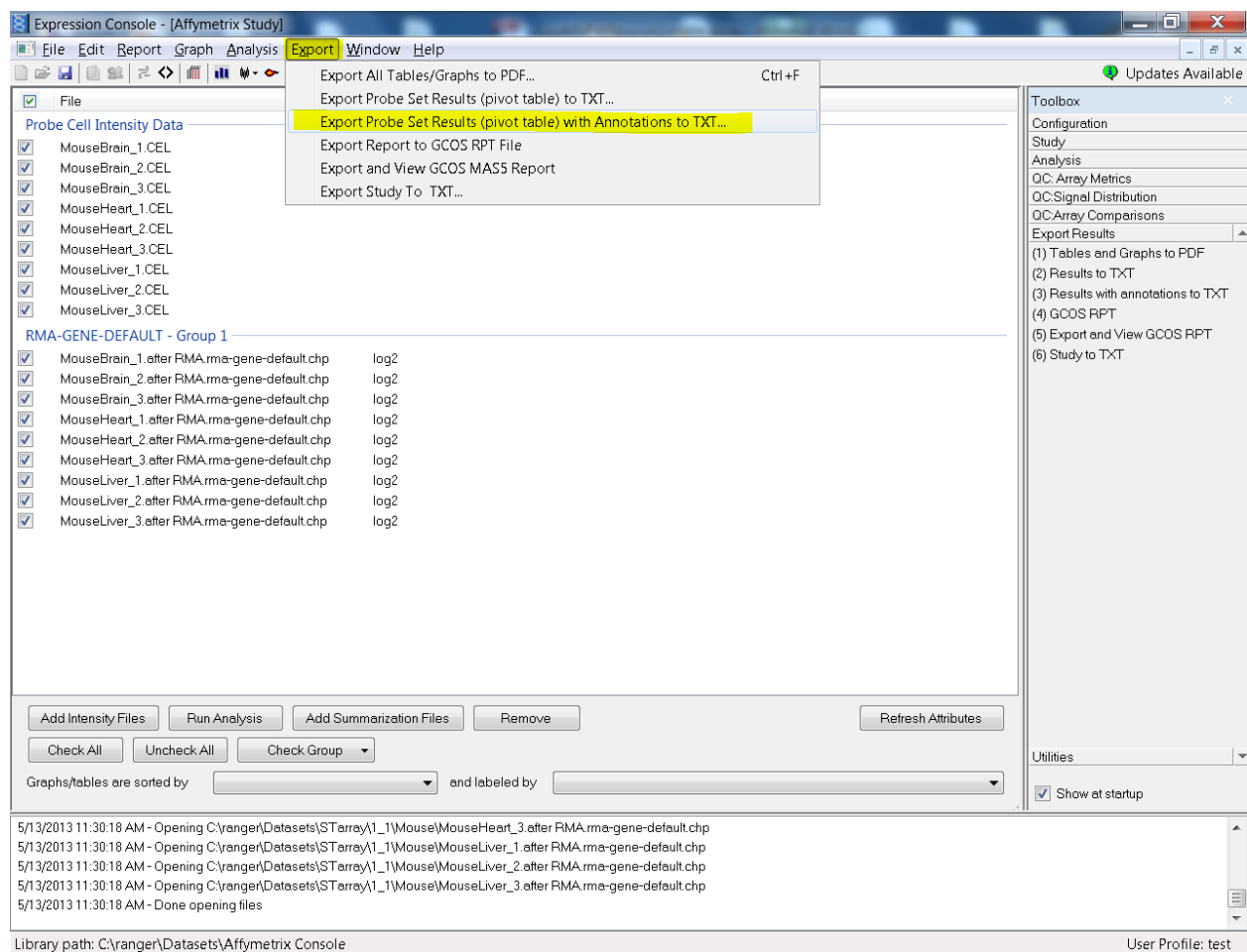


Click Save and give a name for this annotation configuration file (I used Mouse1.0ST.)

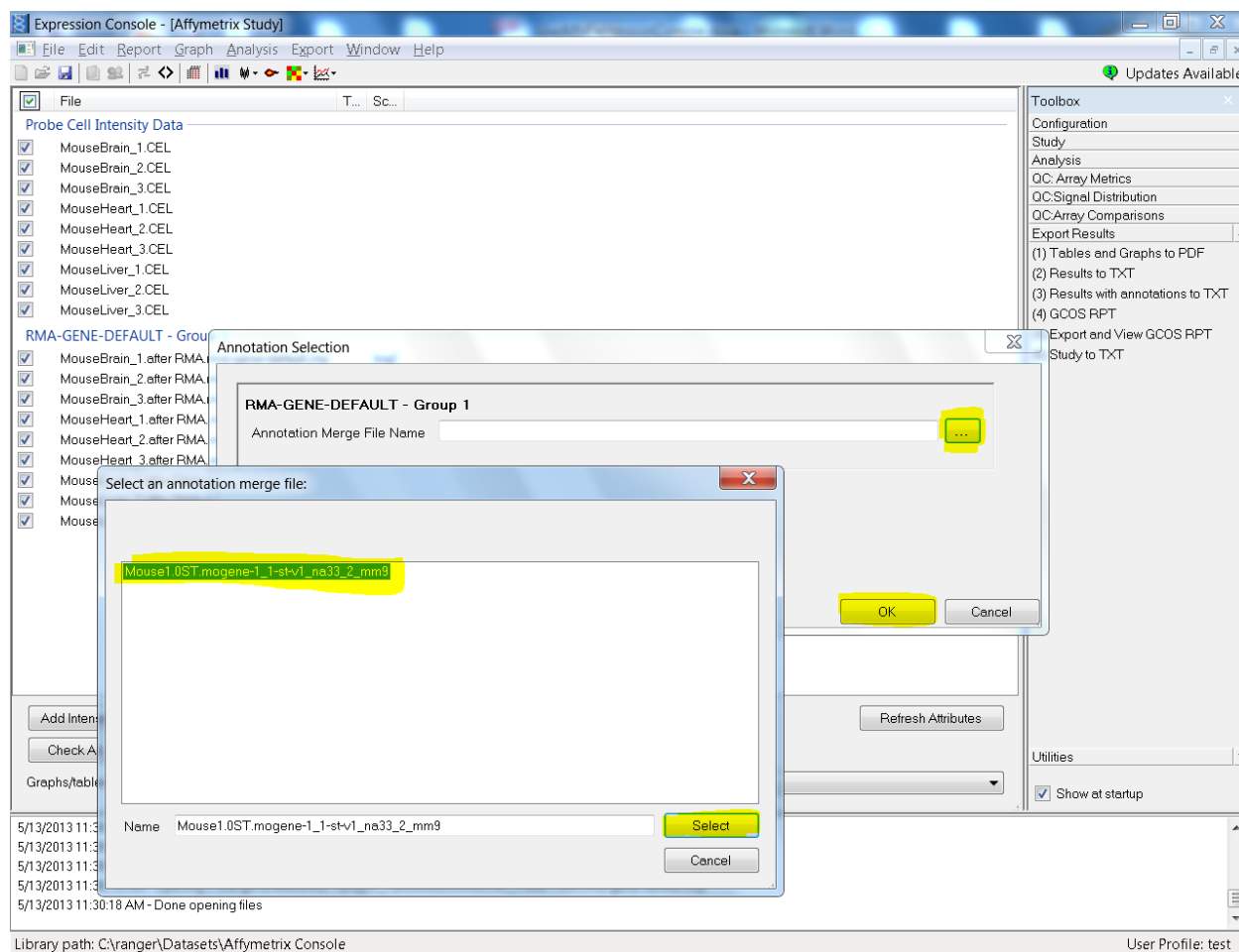


9. Export data into BRB-ArrayTools

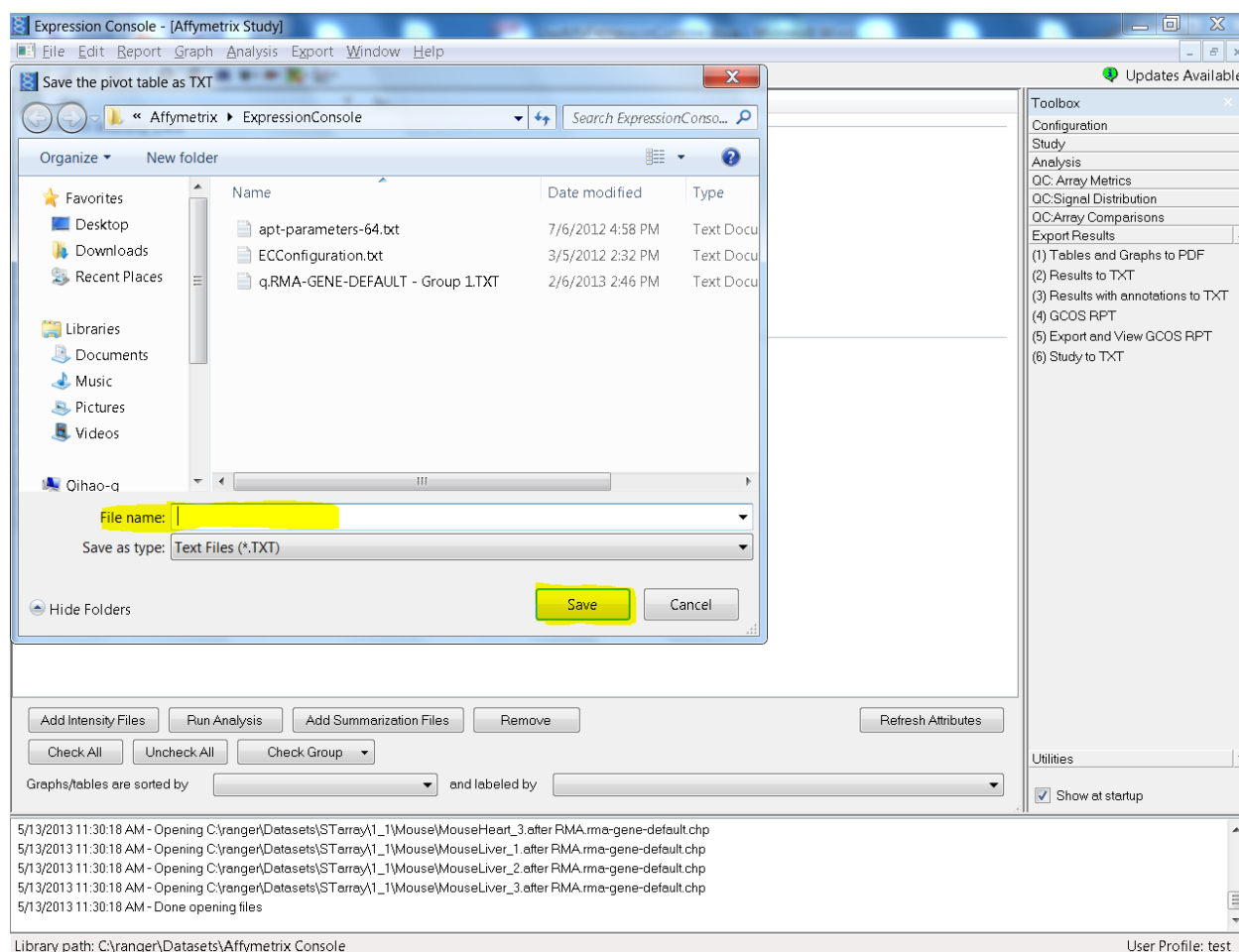
Go to Export -> Export Probe Set Results with Annotations to TXT



Browse for the annotation configuration file that we created and click OK.



Save the output TXT file to your local computer. Please remember the location and name of this file. We are going to import it into ArrayTools in the next step.



10. Modify the TXT file.

Please use Excel to open the TXT file.

Look for “Gene Symbol” column in the first row. Select all the columns that are behind “Gene Symbol” column. Cut and then insert all selected columns to the first column.

After modification, please save all you changes and close the modified TXT file.

(Look for Gene Symbol column. It locates at column K in the example.)

mouse1-1.RMA-GENE-DEFAULT - Group 1.txt - Microsoft Excel									
<div> <div>HomeInsertPage LayoutFormulasDataReviewViewAdd-InsAcrobatTeam</div> <div> ArrayTools - CGHTools - VBAObjectManager - Menu Commands </div> </div>									
	Gene Symbol								
	F	G	H	I	J	K	L	M	
1	MouseHeart	MouseHeart	MouseLiver_	MouseLiver_2.af	MouseLiver_3.af	Gene Symbol	mRNA Accession	mRNA Source	mRNA
2	5.517071	5.517071	5.369722	5.779377	5.517071	---	ENSMUST00000160944	ENSEMBL	cdna
3	3.110623	2.766459	2.932216	2.8609	2.901245	---	ENSMUST00000082908	ENSEMBL	ncrna
4	3.762158	3.618421	3.762158	3.762158	3.762158	Gm10568	AK140060	GenBank HTC	Mouse
5	7.04355	7.059543	4.928565	4.93256	4.890944	---	GENSCAN00000010937	ENSEMBL	cdna
6	10.33312	10.33312	10.76462	10.72258	10.71951	Lypla1	NM_008866	RefSeq	Mouse
7	8.080625	8.593908	8.129901	7.964911	8.286824	Tcea1	NM_011541	RefSeq	Mouse
8	8.008241	8.000153	8.601927	8.581544	8.557664	Atp6v1h	NM_133826	RefSeq	Mouse
9	3.902677	3.566233	3.760245	3.512277	3.820952	Oprk1	ENSMUST00000160339	ENSEMBL	cdna
10	8.767645	8.808738	7.603659	7.61202	7.563105	Rb1cc1	NM_009826	RefSeq	Mouse
11	3.162485	3.19173	3.19173	3.19173	3.393797	Fam150a	NM_001195732	RefSeq	Mouse
12	4.167152	4.004704	4.089813	4.152523	4.016504	Stt18	NR_045188	RefSeq	Mouse
13	8.935433	8.954233	12.61699	12.65603	12.67309	Ahcy	NM_016661	RefSeq	Mouse
14	4.028601	3.685119	3.737784	3.685119	3.685119	---	AK036865	GenBank HTC	Mouse
15	3.409683	3.146556	4.146104	3.708302	3.728558	---	ENSMUST00000102181	ENSEMBL	ncrna
16	4.165266	4.248438	4.207086	4.190471	4.21926	---	ENSMUST00000151704	ENSEMBL	cdna
17	2.958143	2.820468	2.718699	2.786308	2.752583	---	ENSMUST00000083691	ENSEMBL	ncrna
18	6.706551	7.115632	6.297236	6.137553	6.50129	Rrs1	NM_021511	RefSeq	Mouse
19	10.97053	10.88261	10.20984	10.20026	10.23443	Adhfe1	NM_175236	RefSeq	Mouse
20	10.18982	10.16242	9.848963	9.80684	9.745042	Hnrnpa3	NM_053263	RefSeq	Mouse
21	4.290163	4.278069	3.989648	4.16529	3.929659	3110035E14Rik	BC066997	GenBank	Mouse
22	8.607161	8.667062	9.066814	9.038614	9.10573	Sgk3	NM_133220	RefSeq	Mouse
23	3.510679	3.507887	3.482549	3.743876	3.4855	6030422M02Rik	NM_177722	RefSeq	Mouse
24	6.243113	6.298391	7.197338	7.162573	7.169445	Cspp1	NM_026493	RefSeq	Mouse
25	6.382625	6.653358	6.545119	6.604075	6.476193	Cspp1	ENSMUST00000163561	ENSEMBL	cdna
26	7.117793	6.775442	8.098651	7.694497	7.785056	Cspp1	NM_026493	RefSeq	Mouse
27	5.835615	5.935685	6.906957	6.735025	6.926428	Cspp1	NM_026493	RefSeq	Mouse
28	5.779346	5.700308	6.772875	6.58217	7.134377	Cspp1	NM_026493	RefSeq	Mouse
29	5.721189	5.399211	6.511962	6.743135	6.682587	Cspp1	NM_026493	RefSeq	Mouse

(Insert selected columns to the beginning of this file.)

mouse1-1.RMA-GENE-DEFAULT - Group 1.txt - Microsoft Excel

Home Insert Page Layout Formulas Data Review View Add-Ins Acrobat Team

ArrayTools -
CGHTools -
VBAObjectManager -

Menu Calibri 11 A A \$ %

	A	B	C	D	E	F	G	H	I	J	K
1	Probe			Brain_3	MouseHea	MouseHeart	MouseHeart	MouseLiver	MouseLiver_2.af	MouseLiver_3.af	Gene Symbol
2	10			.614699	5.357918	5.517071	5.517071	5.369722	5.779377	5.517071	---
3	10			.719206	2.999887	3.110623	2.766459	2.932216	2.8609	2.901245	---
4	10			.762158	3.762158	3.762158	3.618421	3.762158	3.762158	3.762158	Gm10568
5	10			.992226	7.250093	7.043355	7.059543	4.928565	4.93256	4.890944	---
6	10			.860452	10.33312	10.33312	10.33312	10.76462	10.72258	10.71951	Lypla1
7	10			.377266	8.195377	8.080625	8.593908	8.129901	7.964911	8.286824	Tcea1
8	10			.600511	8.2458	8.008241	8.000153	8.601927	8.581544	8.557664	Atp6v1h
9	10			.800404	3.969083	3.902677	3.566233	3.760245	3.512277	3.820952	Oprk1
10	10			.523182	8.727416	8.767645	8.808738	7.603659	7.61202	7.563105	Rb1cc1
11	10			3.0314	3.19173	3.162485	3.19173	3.19173	3.19173	3.393797	Fam150a
12	10			.583933	3.918948	4.167152	4.004704	4.089813	4.152523	4.016504	Stt18
13	10344713	8.682555	8.72555	8.641001	8.777375	8.935433	8.954233	12.61699	12.65603	12.67309	Ahcy
14	10344715	3.685119	3.57751	3.531521	3.685119	4.028601	3.685119	3.737784	3.685119	3.685119	---
15	10344717	3.371538	3.35603	3.32831	3.333031	3.409683	3.146556	4.146104	3.708302	3.728558	---
16	10344719	4.071959	4.0138	4.080553	4.259968	4.165266	4.248438	4.207086	4.190471	4.21926	---
17	10344721	2.758443	2.75844	2.725845	2.749604	2.958143	2.820468	2.718699	2.786308	2.752583	---
18	10344723	6.311529	6.50129	6.415226	7.179382	6.706551	7.115632	6.297236	6.137553	6.50129	Rrs1
19	10344725	8.065968	7.8425	8.056316	10.9987	10.97053	10.88261	10.20984	10.20026	10.23443	Adhfe1
20	10344741	9.800841	9.73611	9.728243	10.14724	10.18982	10.16242	9.848963	9.80684	9.745042	Hnmpa3
21	10344743	9.852383	9.64986	9.568007	4.57559	4.290163	4.278069	3.989648	4.16529	3.929659	3110035E14Rik
22	10344750	7.444149	7.54611	7.670773	8.700147	8.607161	8.667062	9.066814	9.038614	9.10573	Sgk3
23	10344772	3.404044	3.4855	3.46787	3.4855	3.510679	3.507887	3.482549	3.743876	3.4855	6030422M02Rik
24	10344789	6.817889	6.79305	6.6731	6.152075	6.243113	6.298391	7.197338	7.162573	7.169445	Cspp1
25	10344797	6.246945	6.34798	6.237431	6.485107	6.382625	6.653358	6.545119	6.604075	6.476193	Cspp1
26	10344799	6.881629	6.81414	6.795227	6.892868	7.117793	6.775442	8.098651	7.694497	7.785056	Cspp1
27	10344801	5.884839	6.21394	6.252625	6.013629	5.835615	5.935685	6.906957	6.735025	6.926428	Cspp1
28	10344803	5.974789	5.93843	6.091453	5.703004	5.779346	5.700308	6.772875	6.58217	7.134377	Cspp1
29	10344805	5.773999	5.7296	5.761842	5.301344	5.721189	5.399211	6.511962	6.743135	6.682587	Cspp1

mouse1-1.RMA-GENE-DEFAULT - Gro

Select destination and press ENTER or choose Paste

Average: 10454205.55 Count: 35557 Sum: 3.7171E+11 100%

(After modification, the first column header should be Gene Symbol.)

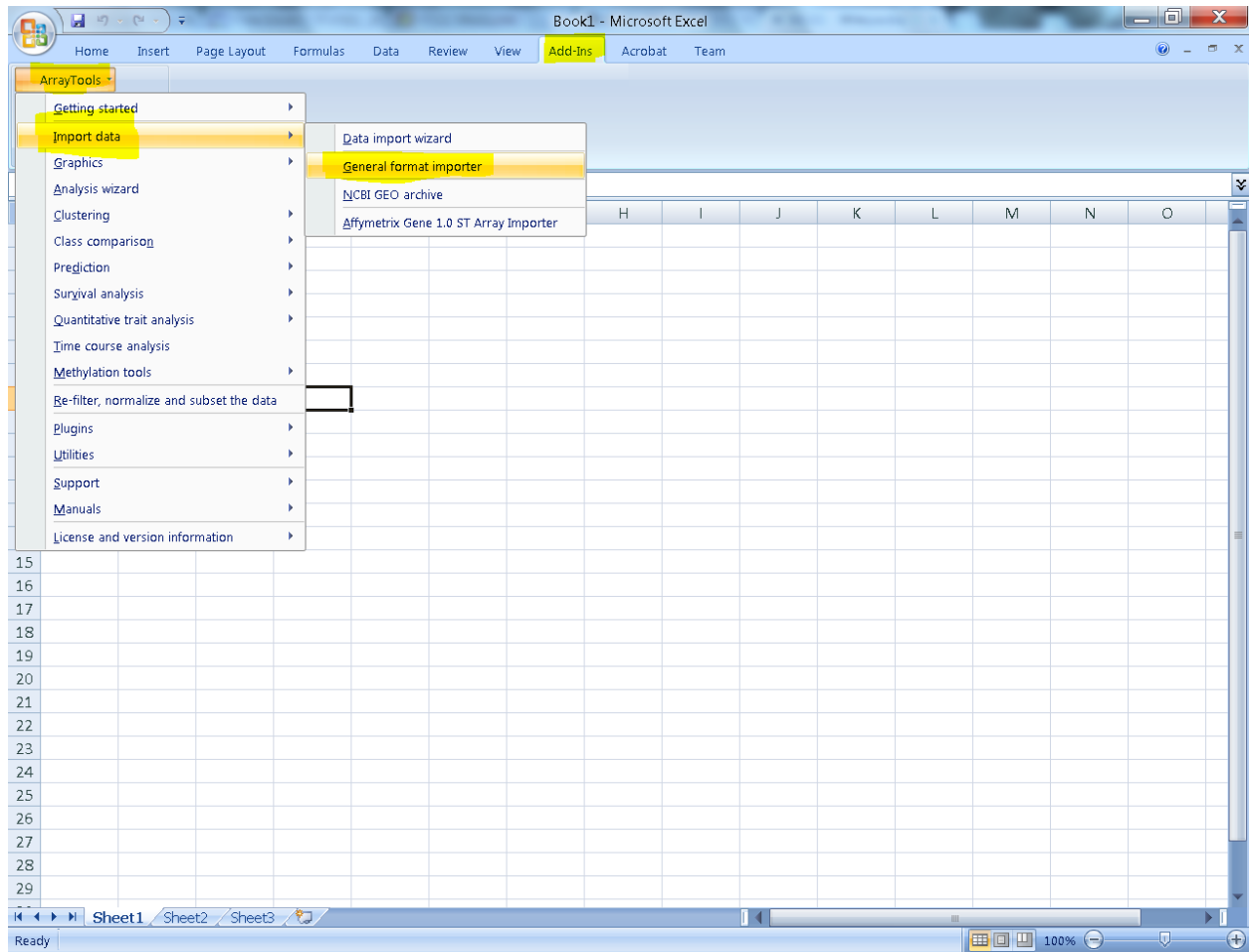
mouse1-1.RMA-GENE-DEFAULT - Group 1.txt - Microsoft Excel				
<div> <div>ArrayTools</div> <div>CGHTools</div> <div>VBAObjectManager</div> <div>Menu Commands</div> </div>				
A1	Gene Symbol			
	A	B	C	
1	Gene Symbol	mRNA Accession	mRNA Source	mRNA - Description
2	---	ENSMUST00000160944	ENSEMBL	cdna:pseudogene chromosome:NCBIM37:1:3044314:3044814:1 gene:ENSMUSC
3	---	ENSMUST00000082908	ENSEMBL	ncrna:snRNA chromosome:NCBIM37:1:3092097:3092206:1 gene:ENSMUSG0000
4	Gm10568	AK140060	GenBank HTC	Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enrich
5	---	GENSCAN00000010937	ENSEMBL	cdna:genscan chromosome:NCBIM37:1:4761212:4762280:1 transcript_biotype:
6	Lypla1	NM_008866	RefSeq	Mus musculus lysophospholipase 1 (Lypla1), mRNA.
7	Tcea1	NM_011541	RefSeq	Mus musculus transcription elongation factor A (SII) 1 (Tcea1), transcript variant
8	Atp6v1h	NM_133826	RefSeq	Mus musculus ATPase, H+ transporting, lysosomal V1 subunit H (Atp6v1h), mRNA
9	Oprk1	ENSMUST00000160339	ENSEMBL	cdna:known chromosome:NCBIM37:1:5579022:5594095:1 gene:ENSMUSG0000
10	Rb1cc1	NM_009826	RefSeq	Mus musculus RB1-inducible coiled-coil 1 (Rb1cc1), mRNA.
11	Fam150a	NM_001195732	RefSeq	Mus musculus family with sequence similarity 150, member A (Fam150a), mRNA.
12	St18	NR_045188	RefSeq	Mus musculus suppression of tumorigenicity 18 (St18), transcript variant 4, non-c
13	Ahcy	NM_016661	RefSeq	Mus musculus S-adenosylhomocysteine hydrolase (Ahcy), mRNA.
14	---	AK036865	GenBank HTC	Mus musculus adult female vagina cDNA, RIKEN full-length enriched library, clon
15	---	ENSMUST00000102181	ENSEMBL	ncrna:miRNA chromosome:NCBIM37:1:8806219:8806328:1 gene:ENSMUSG0000
16	---	ENSMUST00000151704	ENSEMBL	cdna:pseudogene chromosome:NCBIM37:1:8846009:8846348:-1 gene:ENSMUS
17	---	ENSMUST00000083691	ENSEMBL	ncrna:snRNA chromosome:NCBIM37:1:9448751:9448853:1 gene:ENSMUSG0000
18	Rrs1	NM_021511	RefSeq	Mus musculus RRS1 ribosome biogenesis regulator homolog (S. cerevisiae) (Rrs1
19	Adhfe1	NM_175236	RefSeq	Mus musculus alcohol dehydrogenase, iron containing, 1 (Adhfe1), nuclear gene
20	Hnmpa3	NM_053263	RefSeq	Mus musculus heterogeneous nuclear ribonucleoprotein A3 (Hnmpa3), transcrip
21	3110035E14Rik	BC066997	GenBank	Mus musculus RIKEN cDNA 3110035E14 gene, mRNA (cDNA clone MGC:91354 IP
22	Sgk3	NM_133220	RefSeq	Mus musculus serum/glucocorticoid regulated kinase 3 (Sgk3), transcript variant
23	6030422M02Rik	NM_177722	RefSeq	Mus musculus RIKEN cDNA 6030422M02 gene (6030422M02Rik), mRNA.
24	Cspp1	NM_026493	RefSeq	Mus musculus centrosome and spindle pole associated protein 1 (Cspp1), mRNA
25	Cspp1	ENSMUST00000163561	ENSEMBL	cdna:known chromosome:NCBIM37:1:10029866:10057183:1 gene:ENSMUSG0000
26	Cspp1	NM_026493	RefSeq	Mus musculus centrosome and spindle pole associated protein 1 (Cspp1), mRNA
27	Cspp1	NM_026493	RefSeq	Mus musculus centrosome and spindle pole associated protein 1 (Cspp1), mRNA
28	Cspp1	NM_026493	RefSeq	Mus musculus centrosome and spindle pole associated protein 1 (Cspp1), mRNA
29	Cspp1	NM_026493	RefSeq	Mus musculus centrosome and spindle pole associated protein 1 (Cspp1), mRNA

(Save and answer yes if Excel asks you whether you want to keep the format.)

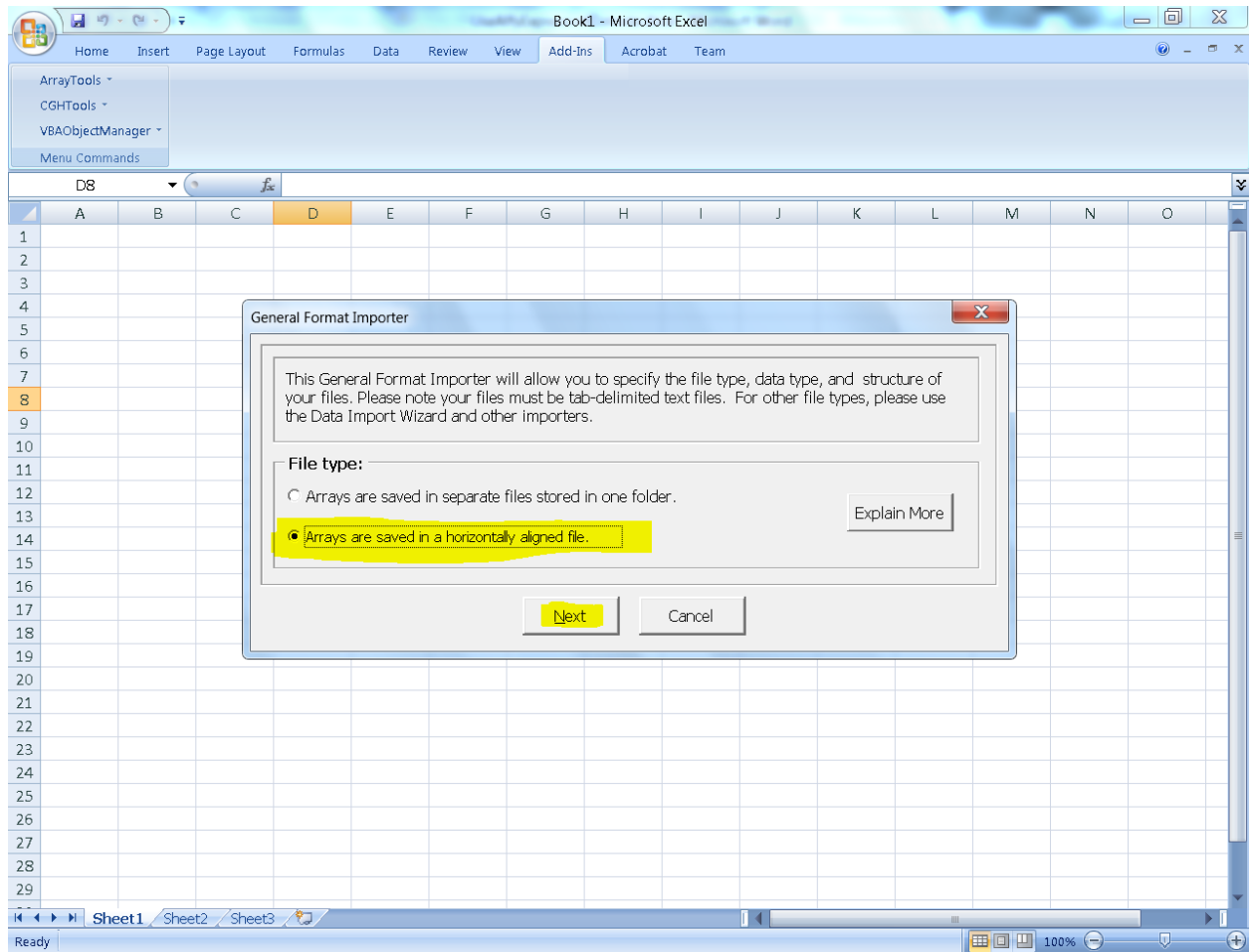
	A	B	C	D
15	---	ENSMUST00000102181	ENSEMBL	ncrna:miRNA chromosome:NCBIM37:1:8806219:8806328:1 gene:ENSMUSG000
16	---	ENSMUST00000151704	ENSEMBL	cdna:pseudogene chromosome:NCBIM37:1:8846009:8846348:-1 gene:ENSMUS
17	---	ENSMUST00000083691	ENSEMBL	ncrna:snRNA chromosome:NCBIM37:1:9448751:9448853:1 gene:ENSMUSG000
18	Rrs1	NM_021511	RefSeq	Mus musculus RRS1 ribosome biogenesis regulator homolog (S. cerevisiae) (Rrs1
19	Adhfe1	NM_175236	RefSeq	Mus musculus alcohol dehydrogenase, iron containing, 1 (Adhfe1), nuclear gene
20	Hnmpa3	NM_053263	RefSeq	Mus musculus heterogeneous nuclear ribonucleoprotein A3 (Hnmpa3), transcrip
21	3110035E14Rik	BC066997	GenBank	Mus musculus RIKEN cDNA 3110035E14 gene, mRNA (cDNA clone MGC:91354 IN
22	Sgk3	NM_133220	RefSeq	Mus musculus serum/glucocorticoid regulated kinase 3 (Sgk3), transcript variant
23	6030422M02Rik	NM_177722	RefSeq	Mus musculus RIKEN cDNA 6030422M02 gene (6030422M02Rik), mRNA.
24	Cspp1	NM_026493	RefSeq	Mus musculus centrosome and spindle pole associated protein 1 (Cspp1), mRNA
25	Cspp1	ENSMUST00000163561	ENSEMBL	cdna:known chromosome:NCBIM37:1:10029866:10057183:1 gene:ENSMUSG00
26	Cspp1	NM_026493	RefSeq	Mus musculus centrosome and spindle pole associated protein 1 (Cspp1), mRNA
27	Cspp1	NM_026493	RefSeq	Mus musculus centrosome and spindle pole associated protein 1 (Cspp1), mRNA
28	Cspp1	NM_026493	RefSeq	Mus musculus centrosome and spindle pole associated protein 1 (Cspp1), mRNA
29	Cspp1	NM_026493	RefSeq	Mus musculus centrosome and spindle pole associated protein 1 (Cspp1), mRNA

11. Use “General Format Importer” in ArrayTools to import the TXT file that was exported from Affymetrix Expression Console.

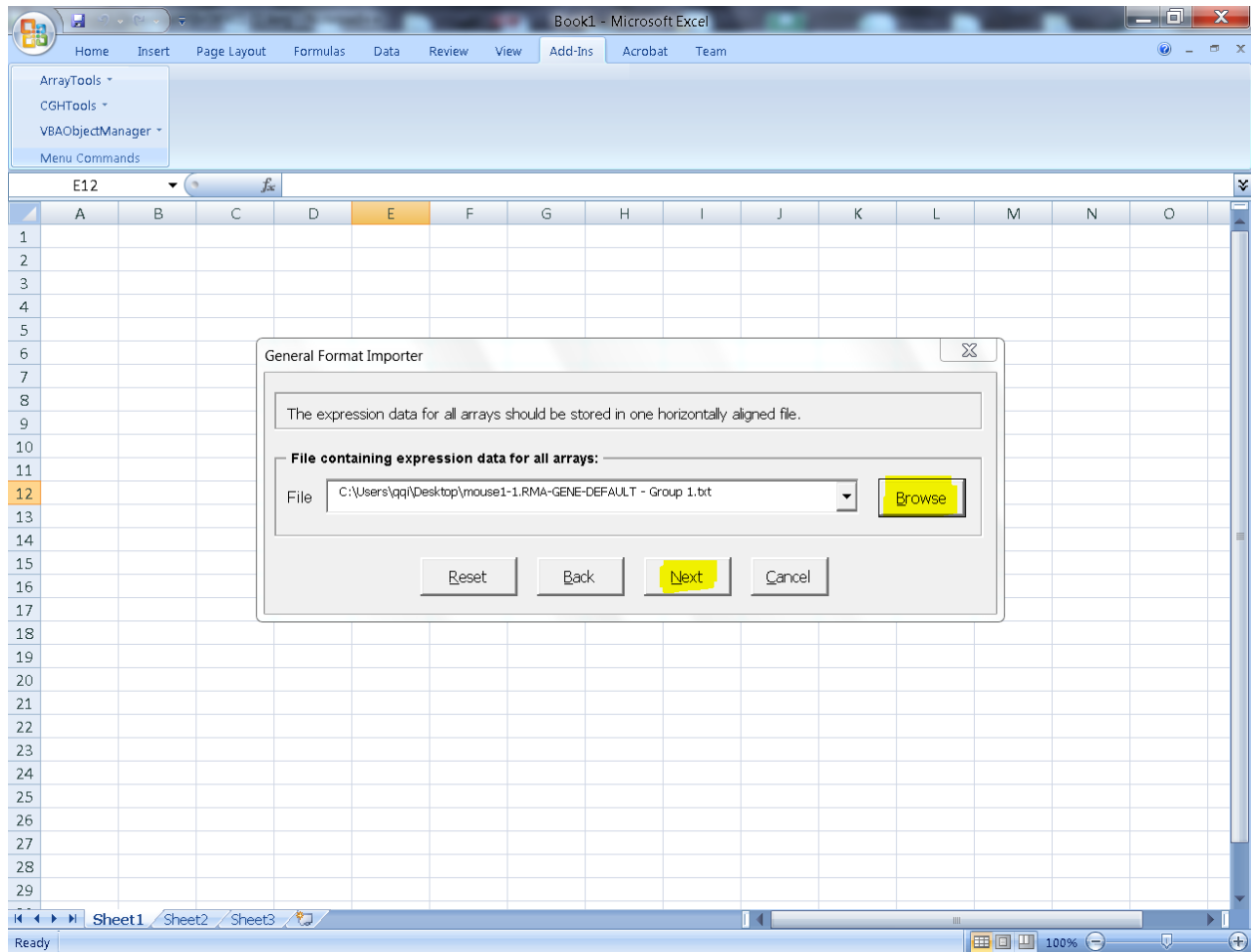
From now on, you will start use ArrayTools. Please open Excel and open General Format Importer in ArrayTools.



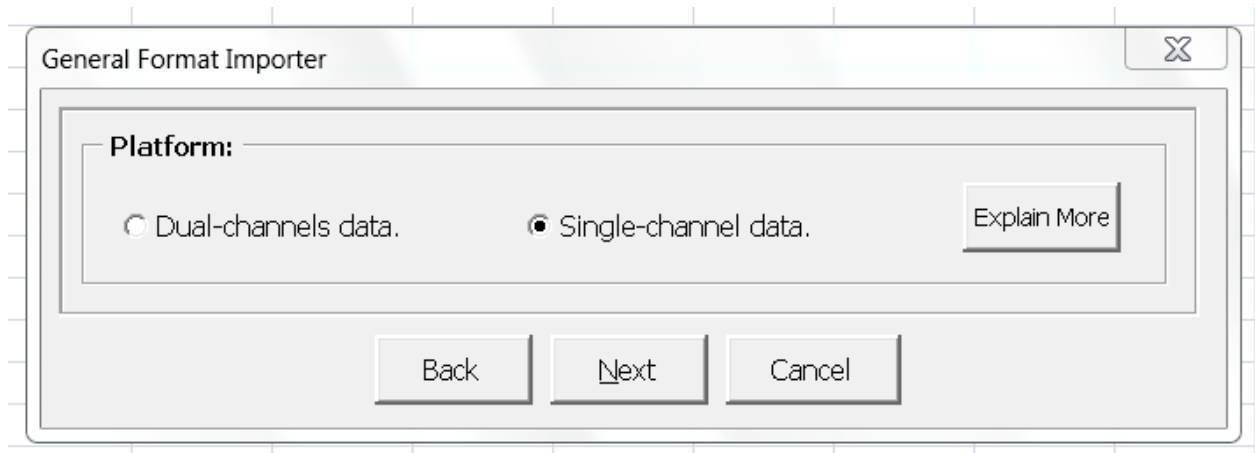
Choose "Arrays are saved in a horizontally aligned file."



Browse for the TXT file.

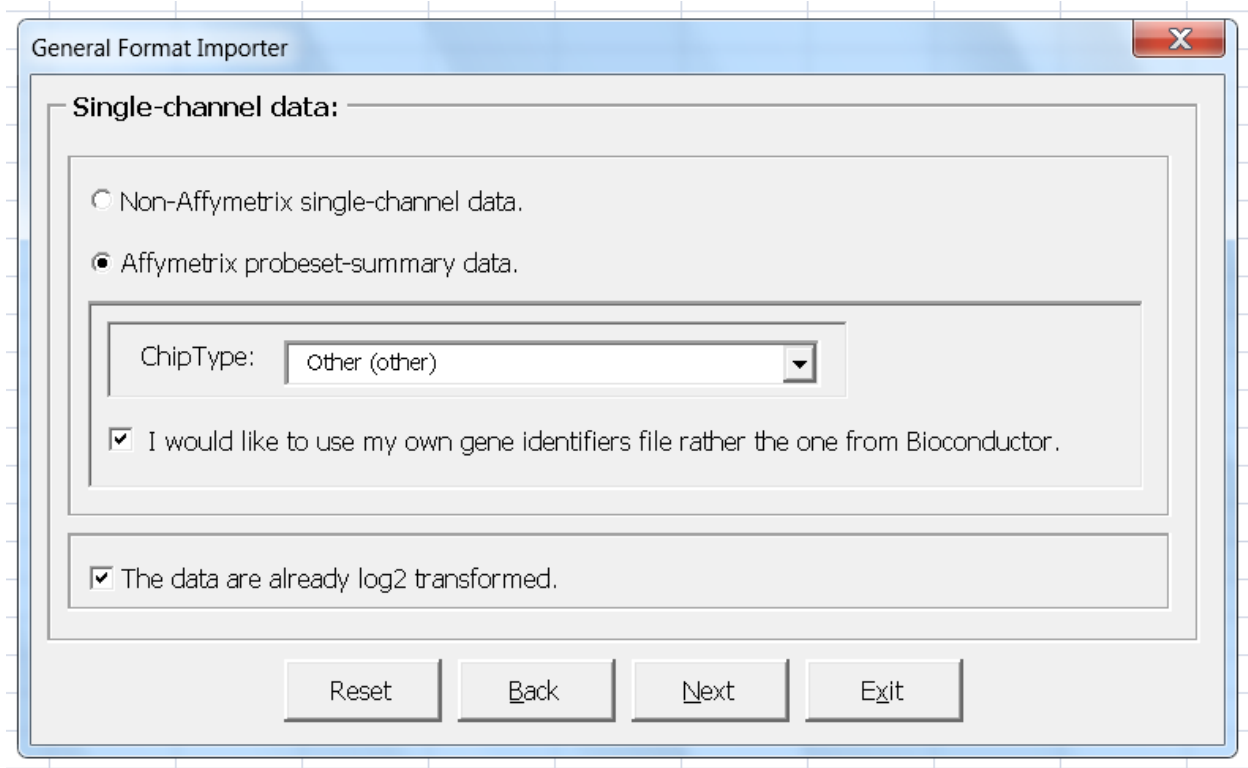


Select "Single-channel data"



Select "Affymetrix probe set-summary data" Chiptype is Other.

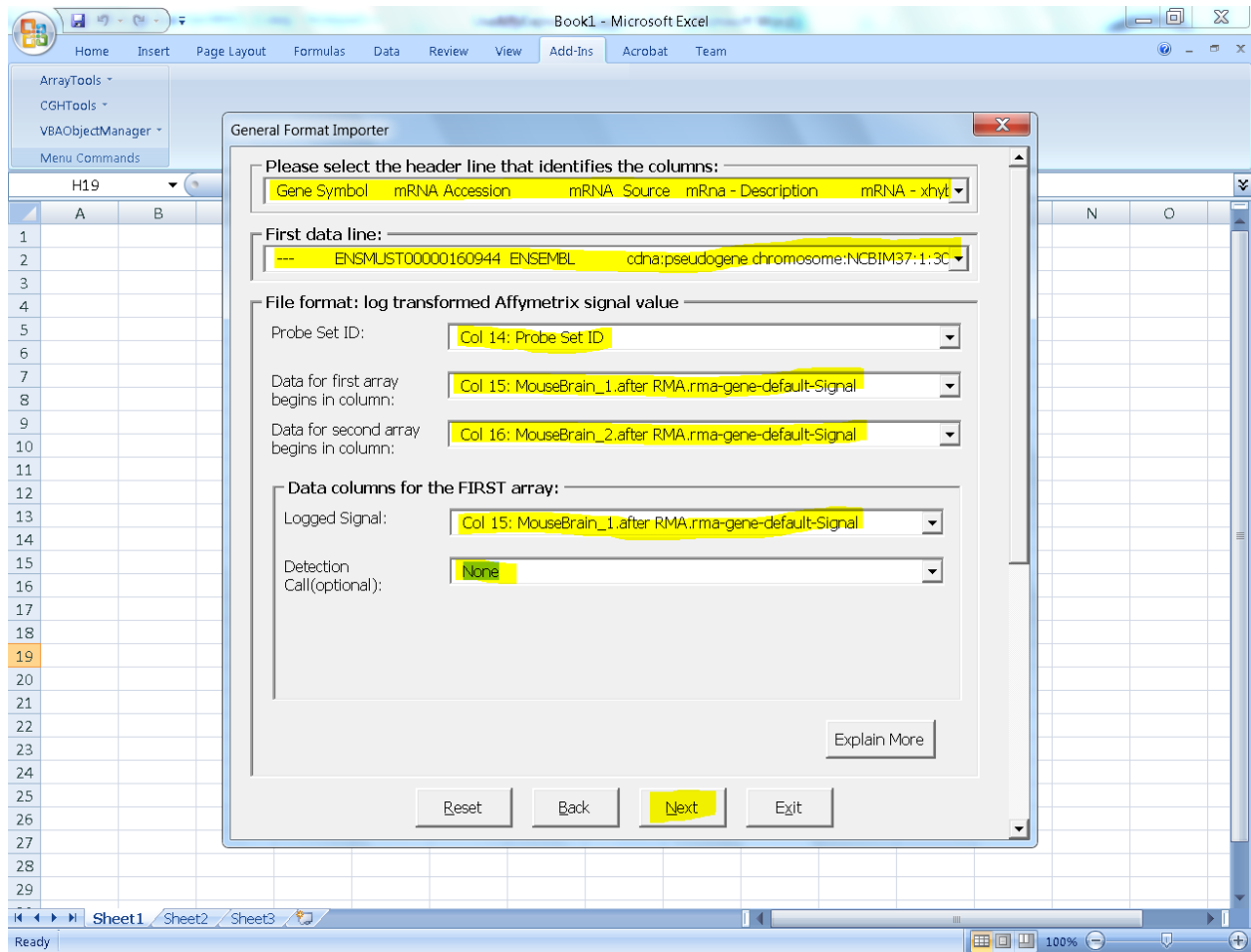
Check “I would like to use my own gene identifiers file rather the one from Bioconductor.” And “The data are already log2 transformed”.



The image shows a screenshot of a software window titled "General Format Importer". The window has a standard Windows-style title bar with a close button (X) in the top right corner. The main content area is titled "Single-channel data:" and contains two radio buttons: "Non-Affymetrix single-channel data." (unselected) and "Affymetrix probeset-summary data." (selected). Below the radio buttons is a group box containing a "ChipType:" label and a dropdown menu showing "other (other)". Below the group box is a checkbox labeled "I would like to use my own gene identifiers file rather the one from Bioconductor." which is checked. Below this checkbox is another checkbox labeled "The data are already log2 transformed." which is also checked. At the bottom of the window are four buttons: "Reset", "Back", "Next", and "Exit".

Select the first row as header line, the second row as First data line.

Select “Probe Set ID” column (No.14 in the example) as the Probe Set ID column. (No.15 and No.16 as the first and second array) Then, click Next.



By default, the gene symbol column should be automatically loaded. You could leave the rest gene identifiers as blank. Please do remember to turn on “Annotate the project with these gene ids, instead of using the data from SOURCE database” checkbox and select an organism based on your data. (I used Mouse here as an example.)

Data Import Wizard

Please specify the location of your gene identifiers: —

☒ The identifiers are stored alongside the expression data. ☐ The identifiers are stored in a separate file.

Please select your Gene identifiers file: —

File: Header line #:

Please select the available gene identifiers: —

Unique ID (Well or Spot ID, etc.): EntrezId:

Clone ID (IMAGE or ATCC ID, etc.): Gene Name ,Title or Description:

UniGene Cluster ID: GenBank Accession:

Gene Symbol: Map Location:

microRNA ID:

☒ Annotate the project with these gene ids, instead of using the data from SOURCE database. ☐ Organisms:

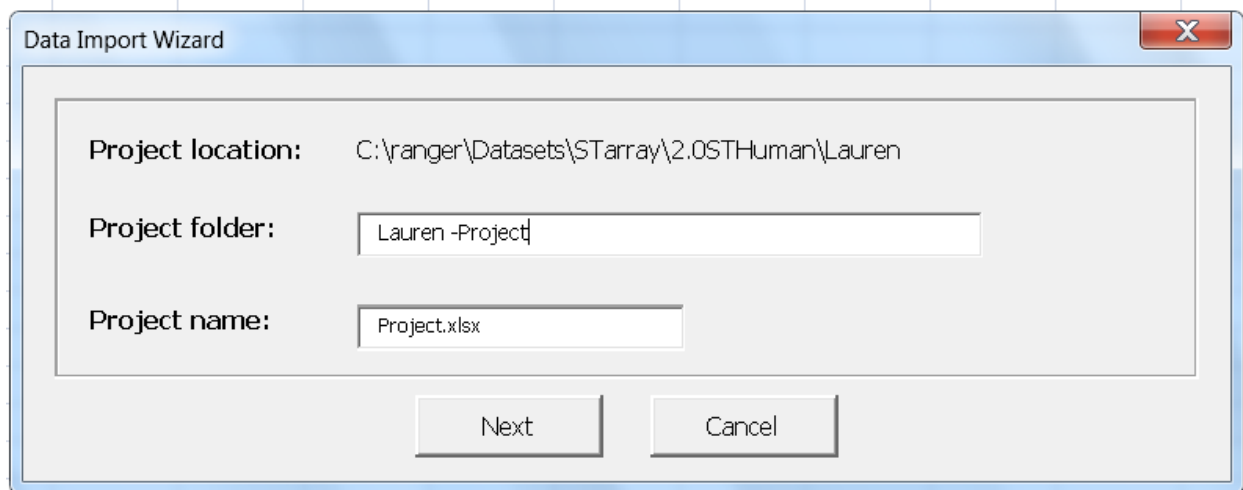
Please verify the number of imported arrays is correct and accept the default setting to create an experiment descriptor file and assign a project folder name.

Data Import Wizard

☒ I do not have an experiment descriptor file. Please create a template with just array ids.

Experiment descriptor file: —

File:



The image shows a 'Data Import Wizard' dialog box with a blue title bar and a red close button. It contains three input fields: 'Project location' with the text 'C:\ranger\Datasets\STarray\2.0STHuman\Lauren', 'Project folder' with 'Lauren -Project', and 'Project name' with 'Project.xlsx'. At the bottom are 'Next' and 'Cancel' buttons.

Data Import Wizard

Project location: C:\ranger\Datasets\STarray\2.0STHuman\Lauren

Project folder: Lauren -Project

Project name: Project.xlsx

Next Cancel

Please do turn off all the Spot filters because RMA was done in Affymetrix expression console.

Refilter, normalize and subset the data

1. Spot filters 2. Normalization 3. Gene filters

Background adjustment is performed before the intensity filtering and the averaging of replicate spots is done on filtered data.

☐ Apply background adjustment.

☐ **Intensity Filter:**

☐ EXCLUDE the spot if the intensity is below the minimum.

☒ THRESHOLD the intensity at the minimum value if the intensity is below the minimum.

Intensity minimum:

☐ **Detection Call**

EXCLUDE the probeset if the Detection Call contains:

Any one of the following values (comma-separated): A,M,P,No Ca

Please turn off all the Normalization options because RMA was done in Affymetrix expression console.

Refilter, normalize and subset the data

1. Spot filters 2. Normalization 3. Gene filters

A log base 2 transformation is applied to the data before the arrays are normalized.

☐ **Normalization method:**

☐ Quantile normalization

☐ Specify Target Percentile

☒ Relative to reference array

☐ Relative to reference array groups

Select Reference Array:

☒ Use median array as reference.

Select:

☐ **Use housekeeping genes only**

☐ HG-U133 (Affy) ☐ HG-U95 (Affy) ☐ HG-Focus (Affy)

☒ Specify a set of housekeeping genes:

☐ **Truncate large intensities:**

Truncate intensities greater than:

You could change the setting of gene filters as you need.

Refilter, normalize and subset the data

1. Spot filters 2. Normalization 3. Gene filters

Gene filters are used to exclude probesets from all experiments.

EXCLUDE a gene under any of the following conditions:

☒ **Minimum Fold-Change:**

Less than % of expression data values have at least a -fold change in either direction from the gene's median value.

☐ **Log Intensity Variation:**

☒ whose variance is in the bottom th percentile

☐ P-value >

☒ **Percent Missing:** exceeds: %

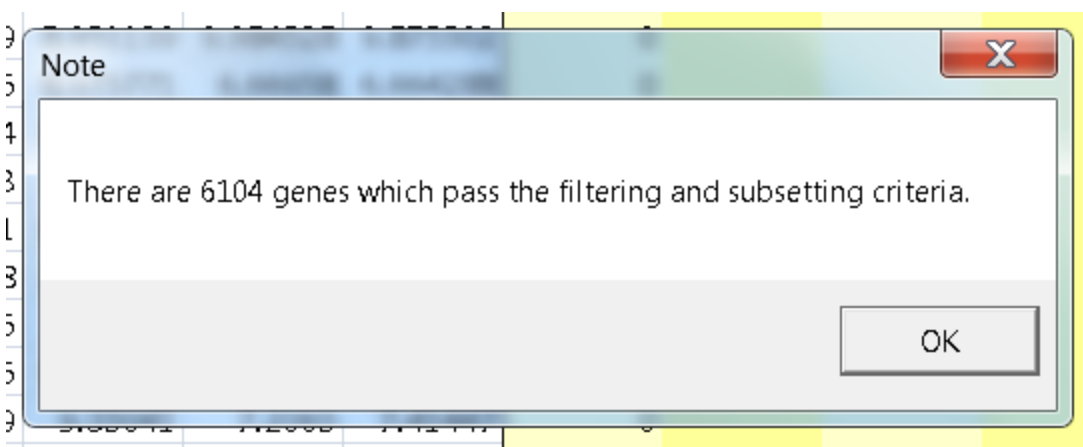
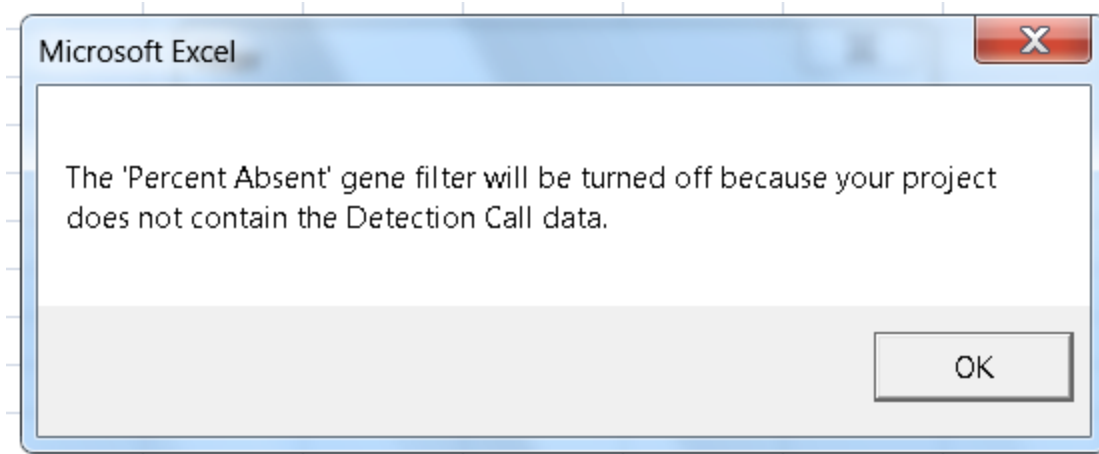
☐ **Minimum Intensity:**

th percentile of intensities is less than

☒ **Percent Absent: (Affymetrix data only)** exceeds: %

OK Cancel Reset Help

Click OK to continue.



It may take as long as five minutes to let ArrayTools process your data. After importing and annotation were finished, you should be able to find the "Gene annotation" worksheet in your project Excel workbook. (I highlight it in yellow in the following screen shot.)

Project.xlsx - Microsoft Excel

Home Insert Page Layout Formulas Data Review View Add-Ins Acrobat Team

ArrayTools -
CGHTools -
VBAObjectManager -
Menu Commands

C17 2.75844311714172

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
	Display the data	MouseBrain_1.aft	MouseBrain_2.aft	MouseBrain_3.aft	MouseHeart_1.aft	MouseHeart_2.aft	Missing	P-Value	Rank	Variance	Num 1.5-Fold	Filter		
1	ProbeSet													
2	10344614	5.517071	5.517071	5.614699	5.357918	5.517071	0					TRUE		
3	10344616	2.826056	2.722072	2.719206	2.999887	3.110623	0					TRUE		
4	10344620	3.806746	3.762158	3.762158	3.762158	3.762158	0					TRUE		
5	10344622	4.898145	4.861268	4.992226	7.250093	7.04355	0					TRUE		
6	10344624	8.873336	8.825998	8.860452	10.33312	10.33312	0					TRUE		
7	10344633	8.327178	8.255224	8.377266	8.195377	8.080625	0					TRUE		
8	10344637	9.66029	9.62784	9.600511	8.2458	8.008241	0					TRUE		
9	10344653	5.889437	6.015046	5.800404	3.969083	3.902677	0					TRUE		
10	10344658	8.524875	8.458801	8.523182	8.727416	8.767645	0					TRUE		
11	10344674	3.19173	2.989047	3.0314	3.19173	3.162485	0					TRUE		
12	10344679	7.610572	7.330499	7.583933	3.918948	4.167152	0					TRUE		
13	10344713	8.682555	8.725549	8.641001	8.777375	8.935433	0					TRUE		
14	10344715	3.685119	3.57751	3.531521	3.685119	4.028601	0					TRUE		
15	10344717	3.371538	3.356029	3.32831	3.333031	3.409683	0					TRUE		
16	10344719	4.071959	4.013802	4.080553	4.259968	4.165266	0					TRUE		
17	10344721	2.758443	2.758443	2.725845	2.749604	2.958143	0					TRUE		
18	10344723	6.311529	6.50129	6.415226	7.179382	6.706551	0					TRUE		
19	10344725	8.065968	7.8425	8.056316	10.9987	10.97053	0					TRUE		
20	10344741	9.800841	9.736105	9.728243	10.14724	10.18982	0					TRUE		
21	10344743	9.852383	9.649856	9.568007	4.57559	4.290163	0					TRUE		
22	10344750	7.444149	7.546112	7.670773	8.700147	8.607161	0					TRUE		
23	10344772	3.404044	3.4855	3.46787	3.4855	3.510679	0					TRUE		
24	10344789	6.817889	6.793054	6.6731	6.152075	6.243113	0					TRUE		
25	10344797	6.246945	6.347981	6.237431	6.485107	6.382625	0					TRUE		
26	10344799	6.881629	6.814136	6.795227	6.892868	7.117793	0					TRUE		
27	10344801	5.884839	6.213937	6.252625	6.013629	5.835615	0					TRUE		
28	10344803	5.674780	5.928434	6.091453	5.703004	5.770346	0					TRUE		

Ready

Experiment descriptors Gene annotations Filtered log intensity Gene identifiers

100%

Congratulation! You successfully imported your data into ArrayTools and could start use all the analysis tools in ArrayTools.

If you have any problems in following this instruction to import your data, please feel free to contact BRB-ArrayTools Supporting Team at arraytools@emmes.com

Thank you so much for using BRB-ArrayTools!