

A preview of the input text data (3 arrays) in Excel.

Galaxy34 - Microsoft Excel

FileHomeInsertPage LayoutFormulasDataReviewViewAdd-InsTeam

A1tracking_id

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	
1	tracking_id	class_code	nearest_ref_id	gene_id	gene_short_name	tss_id	locus	length	coverage	status	q1_FPKM	q1_conf_lo	q1_conf_hi	q2_FPKM	q2_conf_lo	q2_conf_hi
2	XLOC_000	-	-	XLOC_000	-	-	chr1:4037	-	-	OK	0	0	0	1.44E+06	0	0
3	XLOC_000	-	-	XLOC_000	-	-	chr11:133	-	-	OK	8115.76	0	20476.1	0	0	0
4	XLOC_000	-	-	XLOC_000	-	TSS1	chr14:648	-	-	OK	16.751	0	64.1298	29004.5	0	0
5	XLOC_000	-	-	XLOC_000	-	-	chr14:648	-	-	OK	0	0	0	357634	0	0
6	XLOC_000	-	-	XLOC_000	-	-	chr16:672	-	-	OK	0	0	0	8002.4	0	0
7	XLOC_000	-	-	XLOC_000	NM_00435	TSS2,TSS3	chr19:482	-	-	OK	nan	0	nan	nan	0	0
8	XLOC_000	-	-	XLOC_000	NM_00172	TSS5,TSS6	chr19:523	-	-	OK	nan	0	nan	nan	0	0
9	XLOC_000	-	-	XLOC_000	NM_00115	-	chr19:561	-	-	OK	2071.53	0	4238.87	507.925	0	0
10	XLOC_000	-	-	XLOC_000	NM_00586	-	chr19:632	-	-	OK	612.793	0	1347.53	2611.73	0	0
11	XLOC_000	-	-	XLOC_000	NM_00104	TSS8,TSS9	chr19:678	-	-	OK	3309.7	439.287	6180.12	123.306	0	0
12	XLOC_000	-	-	XLOC_000	-	TSS10	chr19:734	-	-	OK	197.91	0	498.76	0	0	0
13	XLOC_000	-	-	XLOC_000	NM_00281	TSS11,TSS12	chr19:748	-	-	FAIL	0	0	0	nan	0	0
14	XLOC_000	-	-	XLOC_000	NR_03615	-	chr19:764	-	-	OK	6.64598	0	16.7261	0	0	0
15	XLOC_000	-	-	XLOC_000	NM_00192	TSS16	chr19:811	-	-	OK	328.538	0	716.161	270.502	0	0
16	XLOC_000	-	-	XLOC_000	NM_00522	TSS17,TSS18	chr19:923	-	-	OK	nan	0	nan	nan	0	0
17	XLOC_000	-	-	XLOC_000	NM_02410	TSS20	chr19:935	-	-	OK	nan	0	nan	2940.99	121.251	0
18	XLOC_000	-	-	XLOC_000	NM_13865	-	chr19:960	-	-	OK	0	0	0	0	0	0
19	XLOC_000	-	-	XLOC_000	NM_00436	TSS22,TSS23	chr19:977	-	-	OK	nan	0	nan	nan	0	0
20	XLOC_000	-	-	XLOC_000	NM_01911	TSS26,TSS27	chr19:995	-	-	OK	13406.3	5764.07	21048.6	12146.5	5869.09	0
21	XLOC_000	-	-	XLOC_000	NM_01225	TSS38,TSS39	chr19:101	-	-	FAIL	nan	0	nan	nan	0	0
22	XLOC_000	-	-	XLOC_000	NM_00103	TSS46,TSS47	chr19:105	-	-	OK	nan	0	nan	nan	0	0
23	XLOC_000	-	-	XLOC_000	NM_00045	TSS49,TSS50	chr19:115	-	-	OK	nan	0	nan	nan	0	0
24	XLOC_000	-	-	XLOC_000	NM_00100	TSS51	chr19:119	-	-	OK	nan	0	nan	nan	0	0
25	XLOC_000	-	-	XLOC_000	NM_17740	TSS52,TSS53	chr19:120	-	-	OK	nan	0	nan	nan	0	0
26	XLOC_000	-	-	XLOC_000	NM_00128	TSS54,TSS55	chr19:122	-	-	FAIL	19766.9	5080.2	34453.6	42118.2	9062.13	0
27	XLOC_000	-	-	XLOC_000	NM_01791	TSS59,TSS60	chr19:122	-	-	OK	4257.58	274.21	8240.96	13510.9	1436.6	0
28	XLOC_000	-	-	XLOC_000	NM_03285	TSS61,TSS62	chr19:130	-	-	OK	nan	0	nan	nan	0	0
29	XLOC_000	-	-	XLOC_000	NM_02440	TSS69,TSS70	chr19:133	-	-	FAIL	0	0	0	0	0	0
30	XLOC_000	-	-	XLOC_000	NM_01895	TSS71,TSS72	chr19:138	-	-	OK	nan	0	nan	nan	0	0
31	XLOC_000	-	-	XLOC_000	NM_00101	TSS76,TSS77	chr19:139	-	-	OK	57090.5	24057.9	90123.2	236684	56184.4	0
32	XLOC_000	-	-	XLOC_000	NM_00588	TSS78,TSS79	chr19:140	-	-	OK	1491.72	67.421	2916.01	2296.17	0	0
33	XLOC_000	-	-	XLOC_000	NM_13835	TSS80	chr19:144	-	-	OK	2637.83	151.613	5124.04	489.409	0	0

Galaxy34

Ready

100%

The data header looks like

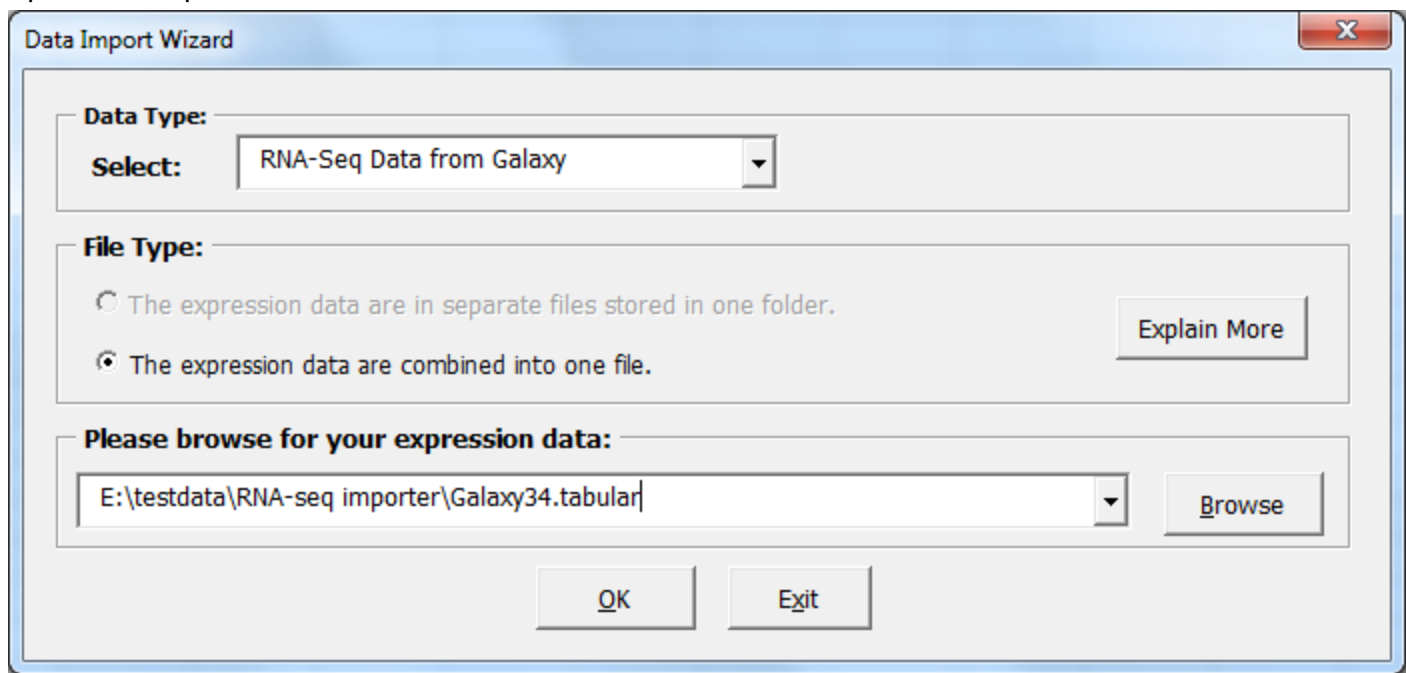
```
> x <- scan("clipboard", "")
Read 19 items
> x
[1] "tracking_id"      "class_code"      "nearest_ref_id"  "gene_id"
[5] "gene_short_name" "tss_id"          "locus"           "length"
[9] "coverage"         "status"          "q1_FPKM"         "q1_conf_lo"
[13] "q1_conf_hi"       "q2_FPKM"         "q2_conf_lo"      "q2_conf_hi"
[17] "q3_FPKM"          "q3_conf_lo"      "q3_conf_hi"
```

Each array occupies 3 columns in the input file although only FPKM column will be used.

A close look at the FPKM columns (Columns K, N and Q)

q3_conf_hi														
	F	G	H	I	J	K	L	M	N	O	P	Q	R	S
1	tss_id	locus	length	coverage	status	q1_FPKM	q1_conf_l	q1_conf_h	q2_FPKM	q2_conf_l	q2_conf_h	q3_FPKM	q3_conf_l	q3_conf_hi
2	-	chr1:4037	-	-	OK	0	0	0	1.44E+06	0	3.32E+06	0	0	0
3	-	chr11:133	-	-	OK	8115.76	0	20476.1	0	0	0	8115.76	0	20476.1
4	TSS1	chr14:648	-	-	OK	16.751	0	64.1298	29004.5	0	59161.2	16.751	0	64.1298
5	-	chr14:648	-	-	OK	0	0	0	357634	0	899924	0	0	0
6	-	chr16:672	-	-	OK	0	0	0	8002.4	0	19529.5	0	0	0
7	TSS2,TSS3	chr19:482	-	-	OK	nan	0	nan	nan	0	nan	nan	0	nan
8	TSS5,TSS6	chr19:523	-	-	OK	nan	0	nan	nan	0	nan	nan	0	nan
9	-	chr19:561	-	-	OK	2071.53	0	4238.87	507.925	0	1091.29	2071.53	0	4238.87
10	-	chr19:632	-	-	OK	612.793	0	1347.53	2611.73	0	5418.52	612.793	0	1347.53
11	TSS8,TSS9	chr19:678	-	-	OK	3309.7	439.287	6180.12	123.306	0	369.919	3309.7	439.287	6180.12
12	TSS10	chr19:734	-	-	OK	197.91	0	498.76	0	0	0	197.91	0	498.76
13	TSS11,TSS	chr19:748	-	-	FAIL	0	0	0	nan	0	nan	0	0	0
14	-	chr19:764	-	-	OK	6.64598	0	16.7261	0	0	0	6.64598	0	16.7261
15	TSS16	chr19:811	-	-	OK	328.538	0	716.161	270.502	0	609.001	328.538	0	716.161
16	TSS17,TSS	chr19:923	-	-	OK	nan	0	nan	nan	0	nan	nan	0	nan
17	TSS20	chr19:935	-	-	OK	nan	0	nan	2940.99	121.251	5760.72	nan	0	nan
18	-	chr19:960	-	-	OK	0	0	0	0	0	0	0	0	0
19	TSS22,TSS	chr19:977	-	-	OK	nan	0	nan	nan	0	nan	nan	0	nan
20	TSS26,TSS	chr19:995	-	-	OK	13406.3	5764.07	21048.6	12146.5	5869.09	18424	13406.3	5764.07	21048.6
21	TSS38,TSS	chr19:101	-	-	FAIL	nan	0	nan	nan	0	nan	nan	0	nan
22	TSS46,TSS	chr19:105	-	-	OK	nan	0	nan	nan	0	nan	nan	0	nan
23	TSS49,TSS	chr19:115	-	-	OK	nan	0	nan	nan	0	nan	nan	0	nan
24	TSS51	chr19:119	-	-	OK	nan	0	nan	nan	0	nan	nan	0	nan
25	TSS52,TSS	chr19:120	-	-	OK	nan	0	nan	nan	0	nan	nan	0	nan
26	TSS54,TSS	chr19:122	-	-	FAIL	19766.9	5080.2	34453.6	42118.2	9062.13	75174.2	19766.9	5080.2	34453.6
27	TSS59,TSS	chr19:122	-	-	OK	4257.58	274.21	8240.96	13510.9	1436.6	25585.3	4257.58	274.21	8240.96
28	TSS61,TSS	chr19:130	-	-	OK	nan	0	nan	nan	0	nan	nan	0	nan
29	TSS69,TSS	chr19:133	-	-	FAIL	0	0	0	0	0	0	0	0	0
30	TSS71,TSS	chr19:138	-	-	OK	nan	0	nan	nan	0	nan	nan	0	nan
31	TSS76,TSS	chr19:139	-	-	OK	57090.5	24057.9	90123.2	236684	56184.4	417184	57090.5	24057.9	90123.2
32	TSS78,TSS	chr19:140	-	-	OK	1491.72	67.421	2916.01	2296.17	0	4970.95	1491.72	67.421	2916.01
33	TSS80	chr19:144	-	-	OK	2637.83	151.613	5124.04	489.409	0	1125.29	2637.83	151.613	5124.04

Open data import wizard



The image shows a 'Data Import Wizard' dialog box with a standard Windows-style title bar (blue with a close button). The dialog is divided into three main sections. The first section, 'Data Type:', contains a 'Select:' label and a dropdown menu currently showing 'RNA-Seq Data from Galaxy'. The second section, 'File Type:', contains two radio button options: 'The expression data are in separate files stored in one folder.' (unselected) and 'The expression data are combined into one file.' (selected). An 'Explain More' button is located to the right of these options. The third section, 'Please browse for your expression data:', contains a text input field with the path 'E:\testdata\RNA-seq importer\Galaxy34.tabular' and a 'Browse' button to its right. At the bottom of the dialog are 'OK' and 'Exit' buttons.

Data Import Wizard

Data Type:

Select: RNA-Seq Data from Galaxy

File Type:

☐ The expression data are in separate files stored in one folder.

☒ The expression data are combined into one file.

[Explain More](#)

Please browse for your expression data:

E:\testdata\RNA-seq importer\Galaxy34.tabular

[Browse](#)

[OK](#) [Exit](#)

The wizard will auto fill out the form.

General Format Importer

Please select the header line that identifies the columns:

5 q1_FPKM q1_conf_lo q1_conf_hi q2_FPKM q2_conf_lo q2_conf_hi

First data line:

XLOC_000001 - - XLOC_000001 - - chr1:40371543-40371636

File format: single channel intensity

Unique ID (Probeset, Well, or Spot ID): Col 1: tracking_id

Data for first array begins in column: Col 11: q1_FPKM

Data for second array begins in column: Col 14: q2_FPKM

Data columns for the FIRST array:

Signal intensity: Col 11: q1_FPKM

Spot Flag (optional):

Spot Size (optional):

Explain More

Reset Back Next Exit

Microsoft Excel

Your data set has 3 arrays.

Is this correct?

Yes No

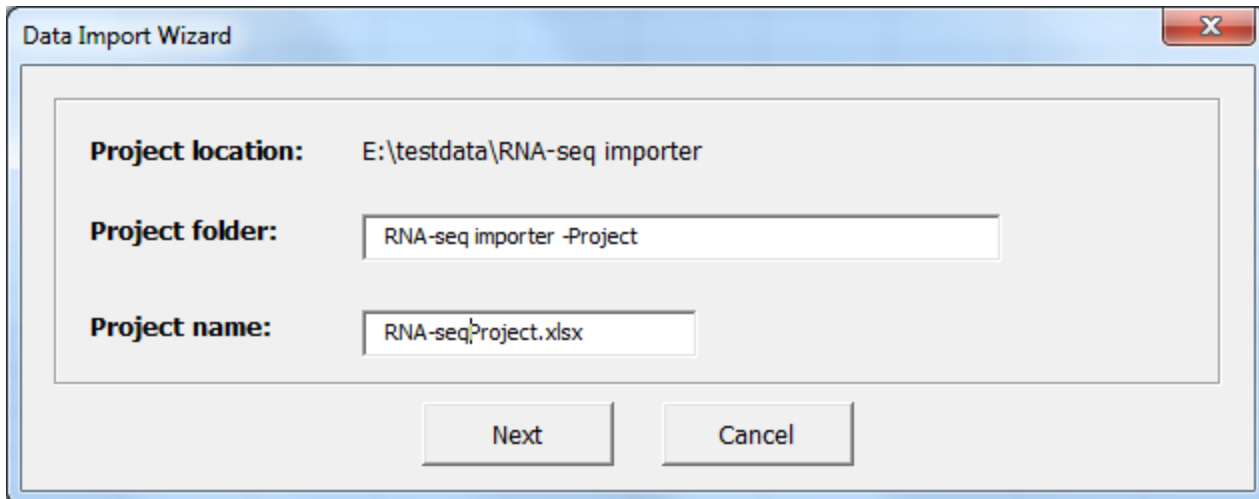
Select 'Col 5: gene_short_name' from the dropdown list of 'GenBank Accession' ([RefSeq Accession](#)) for annotation use (if I did not select any gene identifiers, the dataset will not be able to run annotation though we can still run most of analyses in BRB-ArrayTools).

The screenshot shows the 'Data Import Wizard' window. The first section, 'Please specify the location of your gene identifiers:', has two radio buttons: 'The identifiers are stored alongside the expression data.' (selected) and 'The identifiers are stored in a separate file.' The second section, 'Please select your Gene identifiers file:', has a 'File:' text box, a 'Browse' button, and a 'Header line #' dropdown. The third section, 'Please select the available gene identifiers:', contains several dropdown menus: 'Unique ID (Well or Spot ID, etc.):' (selected 'Col 1: tracking_id'), 'EntrezId:', 'Clone ID (IMAGE or ATCC ID, etc.):', 'Gene Name ,Title or Description:', 'UniGene Cluster ID:', 'GenBank Accession:' (selected 'Col 5: gene_short_name'), 'Gene Symbol:', 'Map Location:', and 'microRNA ID:'. The fourth section has a checkbox 'Annotate the project with these gene ids, instead of using the data from SOURCE database.' and an 'Organisms:' dropdown. At the bottom are buttons for 'Reset', 'Back', 'Next', 'Exit', and 'Explain More'.

In the experiment descriptor input, we can let the software to enter a default one

The screenshot shows the 'Data Import Wizard' window at a later step. The first section has a checked checkbox 'I do not have an experiment descriptor file. Please create a template with just array ids.' The second section, 'Experiment descriptor file:', has a 'File:' text box containing 'E:\testdata\RNA-seq importer\ExpDescFile.xls' and a 'Browse' button. At the bottom are buttons for 'Back', 'Next', 'Exit', and 'Explain More'.

I change the project name from its default although it is not necessary



The 'Data Import Wizard' dialog box is shown. It has a title bar with a close button. The main area contains three labels with corresponding text boxes: 'Project location:' with the value 'E:\testdata\RNA-seq importer', 'Project folder:' with the value 'RNA-seq importer -Project', and 'Project name:' with the value 'RNA-seqProject.xlsx'. At the bottom, there are two buttons: 'Next' and 'Cancel'.

Data Import Wizard

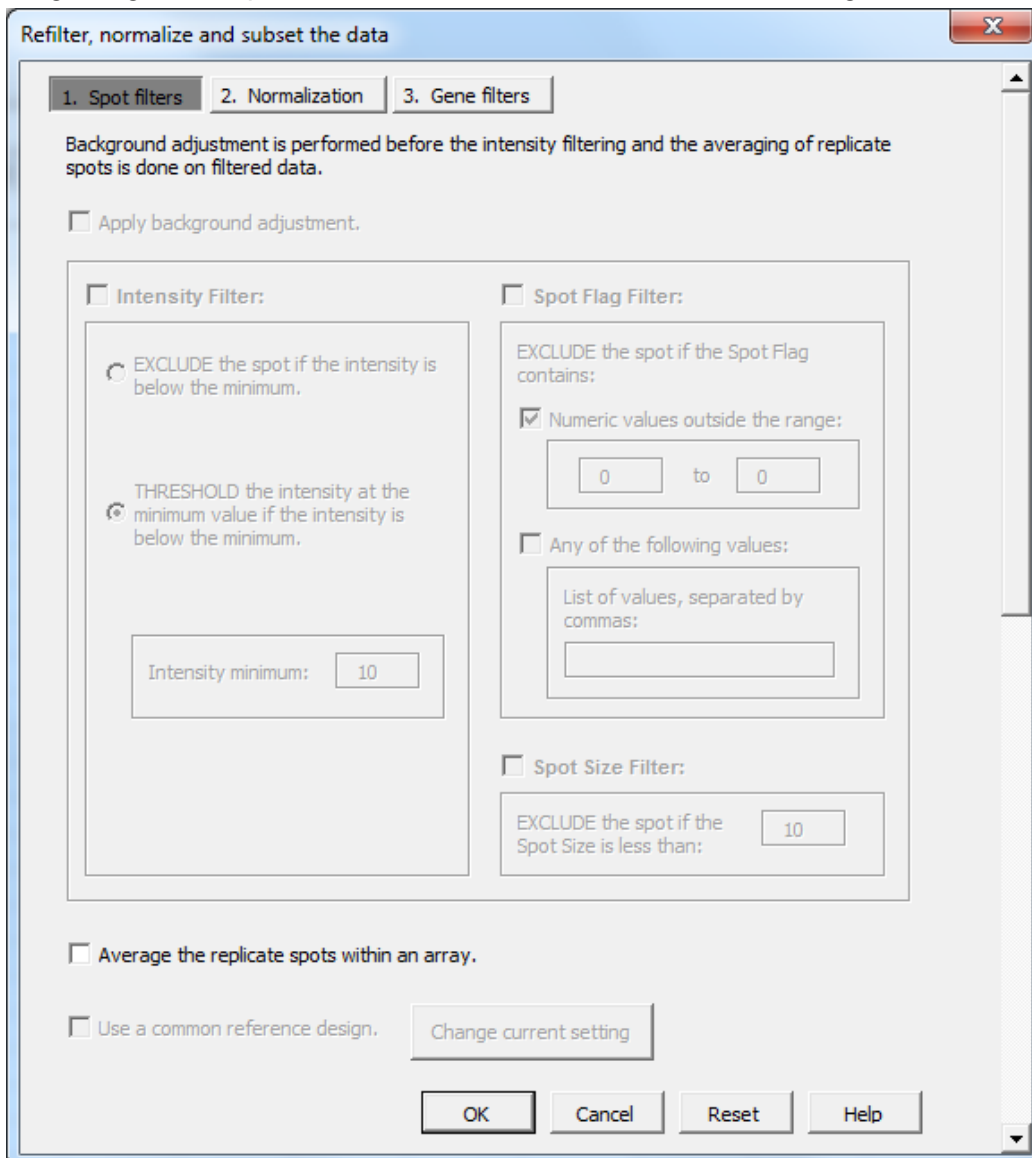
Project location: E:\testdata\RNA-seq importer

Project folder: RNA-seq importer -Project

Project name: RNA-seqProject.xlsx

Next Cancel

Program goes to spot filter, normalization and subset data dialog. Just click 'OK'



The 'Refilter, normalize and subset the data' dialog box is shown. It has a title bar with a close button. The main area has three tabs: '1. Spot filters' (selected), '2. Normalization', and '3. Gene filters'. Below the tabs, there is a paragraph of text: 'Background adjustment is performed before the intensity filtering and the averaging of replicate spots is done on filtered data.' Below this text is a checkbox labeled 'Apply background adjustment.' Below that is a section with two columns. The left column is titled 'Intensity Filter:' and contains two radio buttons: 'EXCLUDE the spot if the intensity is below the minimum.' and 'THRESHOLD the intensity at the minimum value if the intensity is below the minimum.' The right column is titled 'Spot Flag Filter:' and contains a checkbox labeled 'EXCLUDE the spot if the Spot Flag contains:' with a sub-section for 'Numeric values outside the range:' containing two input boxes (both with '0') and a 'to' label. Below this is a checkbox labeled 'Any of the following values:' with a text box for 'List of values, separated by commas:'. At the bottom of the dialog, there are two checkboxes: 'Average the replicate spots within an array.' and 'Use a common reference design.' with a 'Change current setting' button. At the very bottom are four buttons: 'OK', 'Cancel', 'Reset', and 'Help'.

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: 10

☐ Spot Flag Filter:

EXCLUDE the spot if the Spot Flag contains:

☒ Numeric values outside the range:

0 to 0

☐ Any of the following values:

List of values, separated by commas:

☐ Spot Size Filter:

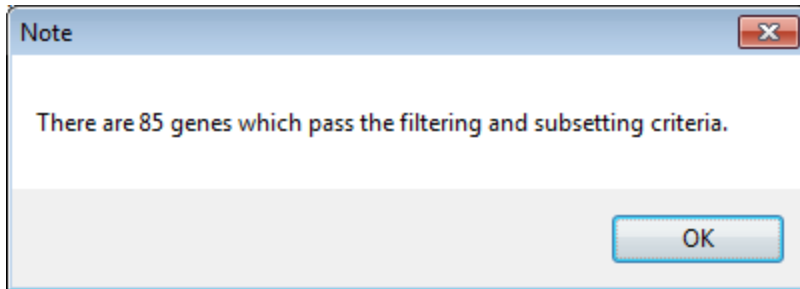
EXCLUDE the spot if the Spot Size is less than: 10

☐ Average the replicate spots within an array.

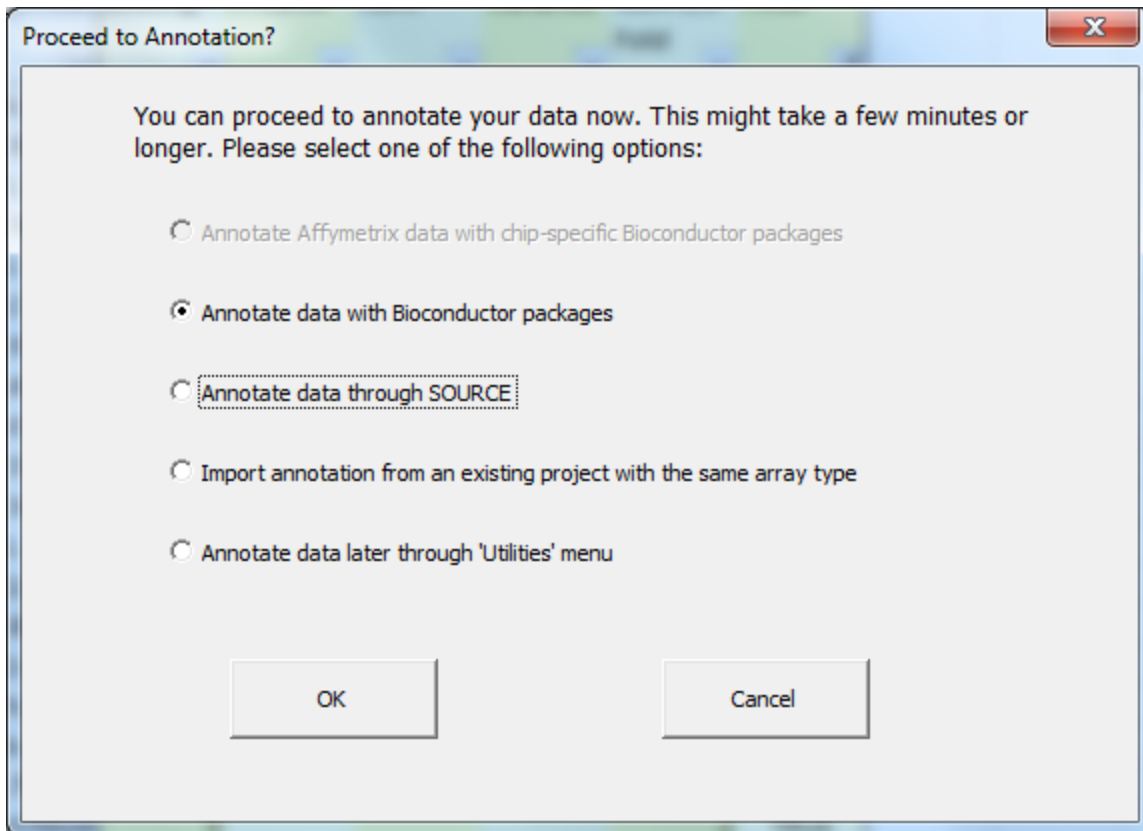
☐ Use a common reference design. Change current setting

OK Cancel Reset Help

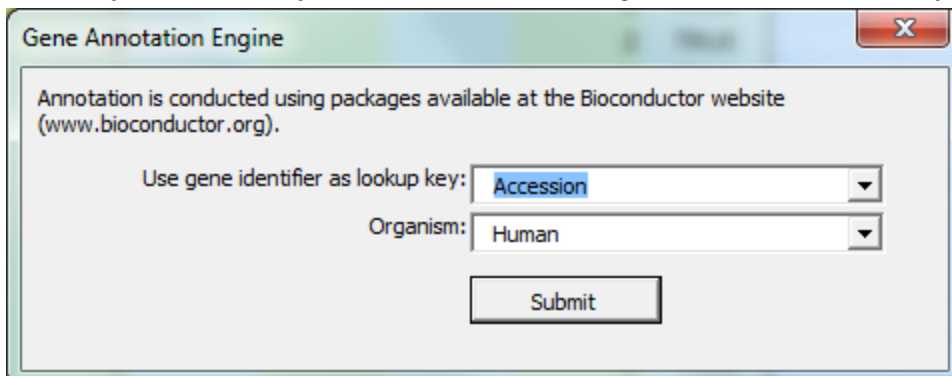
At the end it shows



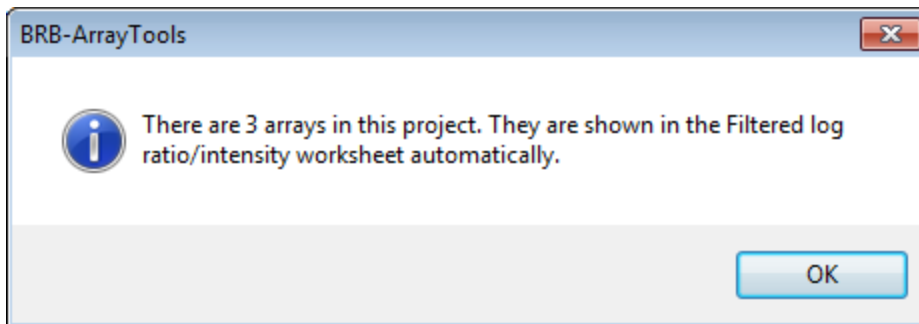
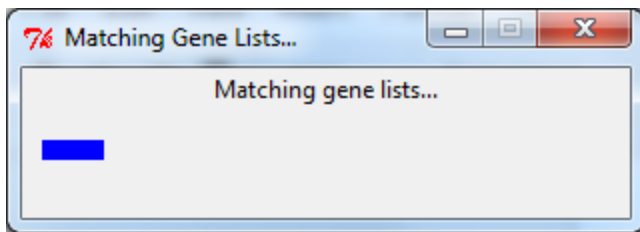
It will prepare to run annotation.



Since my data has only accession inform, this gene identifier is the only option as lookup key.



2 Tk windows will pop up to show the progress Be patient.



This is the final 'Gene identifiers' worksheet.

Project - Microsoft Excel

	A	B	C	D	E	F	G	H	I	J	K	L	M
	UniqueID	Accession	Name	Symbol	Entrezl	UGClus	Defined_Genelists	Filter					
1	UniqueID												
4	XLOC_000003							TRUE					
9	XLOC_000008	NM_001194	hyperpola	HCN2	610	Hs.124161		TRUE					
10	XLOC_000009	NM_005860	follistatin	FSTL3	10272	Hs.529038		TRUE					
11	XLOC_000010							TRUE					
26	XLOC_000025							TRUE					
27	XLOC_000026	NM_017914	chromoso	C19orf24	55009	Hs.591383		TRUE					
31	XLOC_000030	NM_001018	ribosomal	RPS15	6209	Hs.406683	Ribosome	TRUE					
32	XLOC_000031	NM_005883	adenoma	APC2	10297	Hs.446376	Basal cell carcinoma, Colorec	TRUE					
33	XLOC_000032	NM_138393	receptor	REEP6	92840	Hs.744099		TRUE					
40	XLOC_000039	NM_000479	anti-Mulle	AMH	268	Hs.112432	Cytokine-cytokine receptor i	TRUE					
59	XLOC_000058	NM_001728	basigin	(O BSG	682	Hs.501293		TRUE					
65	XLOC_000064	NM_138690	glutamate	GRIN3B	116444	Hs.660378	Neuroactive ligand-receptor	TRUE					
69	XLOC_000068	NM_152769	chromoso	C19orf26	255057	Hs.346575		TRUE					
70	XLOC_000069	NM_177401	midnolin	MIDN	90007	Hs.465529		TRUE					
72	XLOC_000071	NM_000156	guanidino	GAMT	2593	Hs.81131	Arginine and proline metabo	TRUE					
74	XLOC_000073	NM_017573	proprotei	PCSK4	54760	Hs.46884		TRUE					
79	XLOC_000078	NM_001178002	ATPase, a	ATP8B3	148229	Hs.306212		TRUE					
82	XLOC_000081	NM_001130111	family wit	FAM108A	81926	Hs.465542		TRUE					
104	XLOC_000103							TRUE					
109	XLOC_000108							TRUE					
110	XLOC_000109							TRUE					
111	XLOC_000110	NM_004359	cell divisi	CDC34	997	Hs.514997	Cell Cycle: G2/M Checkpoint,	TRUE					
113	XLOC_000112							TRUE					
114	XLOC_000113	NM_001194	hyperpola	HCN2	610	Hs.124161		TRUE					
115	XLOC_000114	NM_001194	hyperpole	HCN2	610	Hs.124161		TRUE					
117	XLOC_000116							TRUE					
119	XLOC_000118							TRUE					
120	XLOC_000119							TRUE					
121	XLOC_000120							TRUE					
123	XLOC_000122							TRUE					
124	XLOC_000123							TRUE					

Ready 85 of 271 records found

'Gene annotation' worksheet.

Project - Microsoft Excel																
File Home Insert Page Layout Formulas Data Review View Add-Ins Team																
B2																
	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P
	UniqueID (Double- click)	Name	Accessi	UGClus	Symbol	Entrezl	Chrom	Cytoba	GO	Filter						
1																
4	XLOC_000003									TRUE						
9	XLOC_000	hyperpola	NM_0011	Hs.124161	HCN2	610	19	19p13.3	Biological	TRUE						
10	XLOC_000	follistatin	NM_0058	Hs.529038	FSTL3	10272	19	19p13	Biological	TRUE						
11	XLOC_000010									TRUE						
26	XLOC_000025									TRUE						
27	XLOC_000	chromoso	NM_0179	Hs.591383	C19orf24	55009	19	19p13.3	Cellular C	TRUE						
31	XLOC_000	ribosomal	NM_0010	Hs.406683	RPS15	6209	19	19p13.3	Biological	TRUE						
32	XLOC_000	adenomat	NM_0058	Hs.446376	APC2	10297	19	19p13.3	Biological	TRUE						
33	XLOC_000	receptor a	NM_1383	Hs.744099	REEP6	92840	19	19p13.3	Cellular C	TRUE						
40	XLOC_000	anti-Mulle	NM_0004	Hs.112432	AMH	268	19	19p13.3	Biological	TRUE						
59	XLOC_000	basigin (O	NM_0017	Hs.501293	BSG	682	19	19p13.3	Biological	TRUE						
65	XLOC_000	glutamate	NM_1386	Hs.660378	GRIN3B	116444	19	19p13.3	Biological	TRUE						
69	XLOC_000	chromoso	NM_1527	Hs.346575	C19orf26	255057	19	19p13.3	Cellular C	TRUE						
70	XLOC_000	midnolin	NM_1774	Hs.465529	MIDN	90007	19	19p13.3	Cellular C	TRUE						
72	XLOC_000	guanidino	NM_0001	Hs.81131	GAMT	2593	19	19p13.3	Biological	TRUE						
74	XLOC_000	proprotei	NM_0175	Hs.46884	PCSK4	54760	19	19p13.3	Biological	TRUE						
79	XLOC_000	ATPase, ai	NM_0011	Hs.306212	ATP8B3	148229	19	19p13.3	Biological	TRUE						
82	XLOC_000	family wit	NM_0011	Hs.465542	FAM108A	81926	19	19p13.3	Cellular C	TRUE						
104	XLOC_0000103									TRUE						
109	XLOC_0000108									TRUE						
110	XLOC_0000109									TRUE						
111	XLOC_000	cell divisi	NM_0043	Hs.514997	CDC34	997	19	19p13.3	Biological	TRUE						
113	XLOC_0000112									TRUE						
114	XLOC_000	hyperpola	NM_0011	Hs.124161	HCN2	610	19	19p13.3	Biological	TRUE						
115	XLOC_000	hyperpola	NM_0011	Hs.124161	HCN2	610	19	19p13.3	Biological	TRUE						
117	XLOC_0000116									TRUE						
119	XLOC_0000118									TRUE						
120	XLOC_0000119									TRUE						
121	XLOC_0000120									TRUE						
123	XLOC_0000123									TRUE						
Experiment descriptors Gene annotations Filtered log intensity Gene identifiers																
Ready Filter Mode																

'Experiment descriptors' worksheet

Experiment Names																
1	Experiment Names															
2	q1_FPKM															
3	q2_FPKM															
4	q3_FPKM															
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'Filtered log intensity' worksheet

Project - Microsoft Excel

FileHomeInsertPage LayoutFormulasDataReviewViewAdd-InsTeam

B2

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P
	Display the data	q1_FPKM	q2_FPKM	q3_FPKM	Missing	P-Value	Rank	Variance	Num 1.5-Fold	Filter						
1	UniqueID															
4	XLOC_000003	4.066175	14.82399	4.066175	0				1	TRUE						
9	XLOC_000008	11.01648	8.988472	11.01648	0				1	TRUE						
10	XLOC_000009	9.259256	11.35079	9.259256	0				1	TRUE						
11	XLOC_000010	11.69248	6.946099	11.69248	0				1	TRUE						
26	XLOC_000025	14.2708	15.36216	14.2708	0				1	TRUE						
27	XLOC_000026	12.05582	13.72184	12.05582	0				1	TRUE						
31	XLOC_000030	15.80096	17.8526	15.80096	0				1	TRUE						
32	XLOC_000031	10.54276	11.16501	10.54276	0				1	TRUE						
33	XLOC_000032	11.36514	8.934896	11.36514	0				1	TRUE						
40	XLOC_000039	11.12285	6.682405	11.12285	0				1	TRUE						
59	XLOC_000058	10.34937	9.019938	10.34937	0				1	TRUE						
65	XLOC_000064	8.811506	7.554358	8.811506	0				1	TRUE						
69	XLOC_000068	8.586641	6.541777	8.586641	0				1	TRUE						
70	XLOC_000069	12.68445	11.17491	12.68445	0				1	TRUE						
72	XLOC_000071	10.99743	12.3243	10.99743	0				1	TRUE						
74	XLOC_000073	8.703461	7.84436	8.703461	0				1	TRUE						
79	XLOC_000078	10.70211	7.885653	10.70211	0				1	TRUE						
82	XLOC_000081	11.07658	12.61368	11.07658	0				1	TRUE						
104	XLOC_000103	9.85177	8.70976	9.85177	0				1	TRUE						
109	XLOC_000108	11.44793	9.65308	11.44793	0				1	TRUE						
110	XLOC_000109	11.51841	14.44588	11.51841	0				1	TRUE						
111	XLOC_000110	13.98643	13.1691	13.98643	0				1	TRUE						
113	XLOC_000112	9.236693	5.791277	9.236693	0				1	TRUE						
114	XLOC_000113	10.54008	9.070024	10.54008	0				1	TRUE						
115	XLOC_000114	11.83151	10.75917	11.83151	0				1	TRUE						
117	XLOC_000116	14.40173	11.20518	14.40173	0				1	TRUE						
119	XLOC_000118	11.95098	10.84581	11.95098	0				1	TRUE						
120	XLOC_000119	11.60039	8.213858	11.60039	0				1	TRUE						
121	XLOC_000120	12.37258	13.08388	12.37258	0				1	TRUE						
123	XLOC_000122	15.74619	11.32454	15.74619	0				1	TRUE						

Experiment descriptorsGene annotationsFiltered log intensityGene identifiers

ReadyFilter Mode

100%

DONE!

We can double check the log intensity value. For example, UniqueID=XLOC_000003 shall have $\log_2(16.751)=4.066175$.