
R2 Faqs and Workflows

Release 1.0.0.b

The R2 support team

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Contents

1	R2 Frequently Asked Questions (FAQs)	3
1.1	General questions.	3
1.2	Analysis questions.	3
1.3	Adapting visuals.	4
2	Workflows	5
2.1	Workflow: Generate a direct link to a public dataset in R2	5
2.2	Workflow: Marking samples in a YY or XY plot	5
2.3	Workflow: Drawing lines between samples in an XY plot	8
2.4	Workflow: Final Remarks	11

This contains a collection of Frequently Asked Questions and Workflows for R2; a biologist friendly, web based genomics analysis and visualization application developed by Jan Koster at the department of Oncogenomics in the Academic Medical Center (AMC) Amsterdam, the Netherlands. For citations, please include the following website: 'R2: Genomics Analysis and Visualization Platform (<http://r2.amc.nl> <http://r2platform.com>)'

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Table of Contents

R2 Frequently Asked Questions (FAQs)

A collections of questions and answers about the R2 platform

1.1 General questions.

1. Which platforms does R2- support?
2. Can I shield my data up to publication?
3. Which kind of data does R2 support?
4. Which expression data platforms are supported by R2?
5. Can I analyse my date within a collaborative setting?
6. Why can't I see survival data in my dataset of interest?
7. Can I upload my own data?
8. How can I make corrections to data that I already submitted?
9. How can I delete my own dataset or make my dataset public?
10. Is there a list of platforms R2 is currently supporting?
11. If I use the datagrabber I don't get the sample annotation with it?

1.2 Analysis questions.

1. A Gene Ontology analyses results in a category of more then 100 entries how can I identify the individual genes?
2. When I perform a hierarchical clustering how can I cluster for each group separately?
3. When I perform a K-means clustering how can extract the gene order from the program?
4. When I use the GEO analysis tool and compare the resulting gene list I get a different gene list (70% overlap) compared to the result of the "Find differential expression" option of R2. Is there an explanation for this discrepancy?

5. Using the R2 grabber I got different expression levels from the same dataset compared to the TCGA alternative
6. How do I retrieve a list of differentially expressed genes between two or more datasets
7. In a certain article the gene name which was linked to a probe identifier gives a different gene name
8. Why can't I use every dataset in the megasamples analyses.

1.3 Adapting visuals.

1. How can I mark a sample
2. Can I generate a SVG-plot with R2.
3. Is it possible to add an trendline in XY plot

Typical workflows that explore the combinations of analysis possible in R2

2.1 Workflow: Generate a direct link to a public dataset in R2

If you would like to include a direct link to a public dataset in R2, then you can follow the procedure described here.

1. Make sure that you are NOT logged in with your own account. So log off in case that you are logged in.
2. Navigate to the dataset to which you would like to create a link. You can use the 'change dataset' link in 'box 2' for this.
3. Finally, click on the 'goto main' link in the upper left corner of the screen.
4. The web address that will now appear can be copied directly and be provided as a reference to the dataset.

2.2 Workflow: Marking samples in a YY or XY plot

1. Marking a single sample

With the 'samples to mark' option, you can make samples stand out. The easiest is marking a single sample using the R2 default setting. Make sure that you add a samplename (e.g. itcc0288) from the current dataset and press 'redraw'. The indicated sample is now highlighted by an orange line.

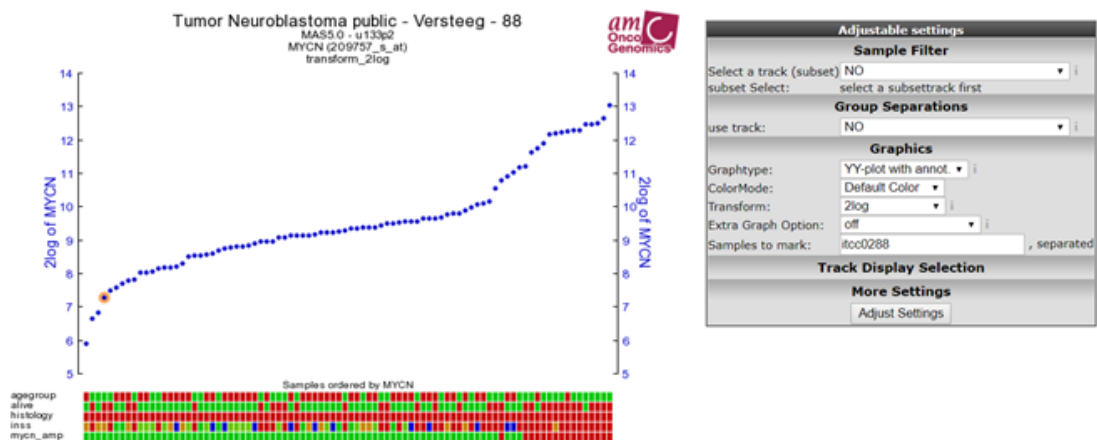


Figure 1: Mark a single sample

1. Types of markings

We can change the type of mark by changing the mark method from ‘dot’, to one of the other methods. ‘circle’ will draw an open circle around the sample; epicenter will draw a range of larger circles around the marked patient; and ‘arrow’ will place an arrow pointing to the sample.

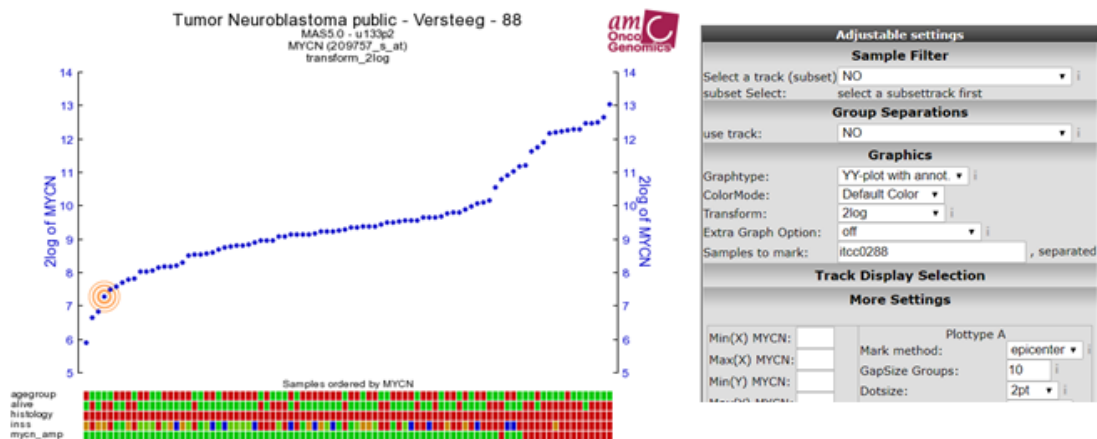


Figure 2: Mark options

1. Coloring and marking multiple samples

Marking more than 1 sample is achieved by ‘,’ separation (e.g. itcc0288,itcc0021,itcc0013,itcc0132). Thus far all have been of the same color. We can also change the color of the marker by adding ‘:’ followed by a hex color (e.g. itcc0288,itcc0021,itcc0013,itcc0132:00ff00).

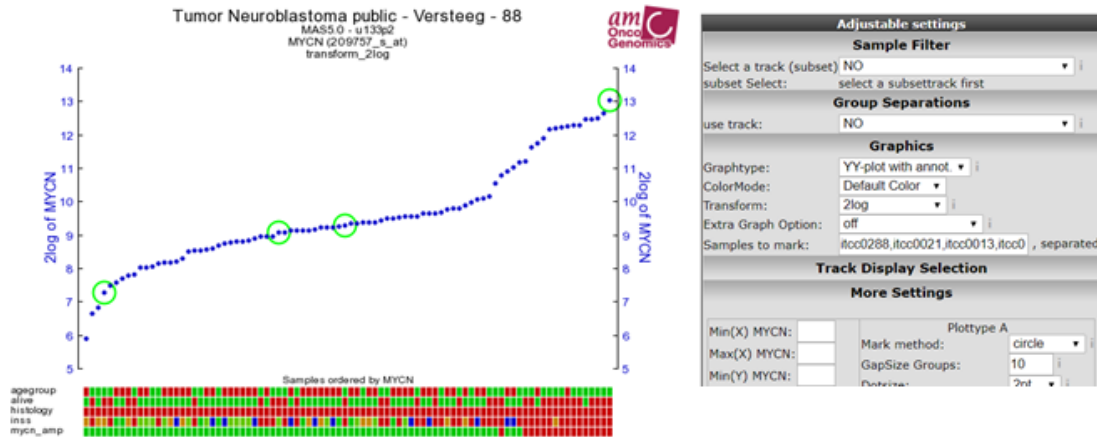


Figure 3: Mark and color multiple samples

1. Defining sample groups

The previous example made all 4 samples green. We can also define groups and define different colors to every group. Groups are separated by ';'. To color our previous example with 2 groups, each having a different color, we define the following: `itcc0288,itcc0021:ff00ff;itcc0013,itcc0132:00ff00`

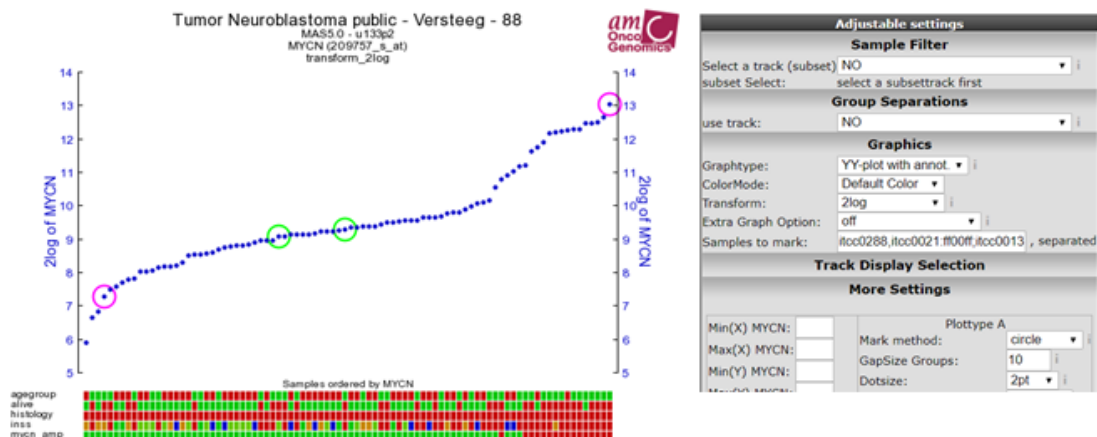


Figure 4: Mark with sample groups

1. Advanced usage

As a default, the mark method will be defined from the dropdown box as we have used in step 2. However, you can also define the method within the 'samples to mark' box by adding another ':' after the color representation. Defining this will overrule the default setting, and

thus also enable the use of different markings within the same figure. So the skeleton for advanced usage is : ‘sample1,sample2:color1:method1;sample3,sample4:color2:method2’. For example: “‘itcc0288:0000ff:dot;itcc0021:ff00ff:arrow;itcc0013,itcc0132:00ff00:epicenter”” creates the markings as shown in the figure.

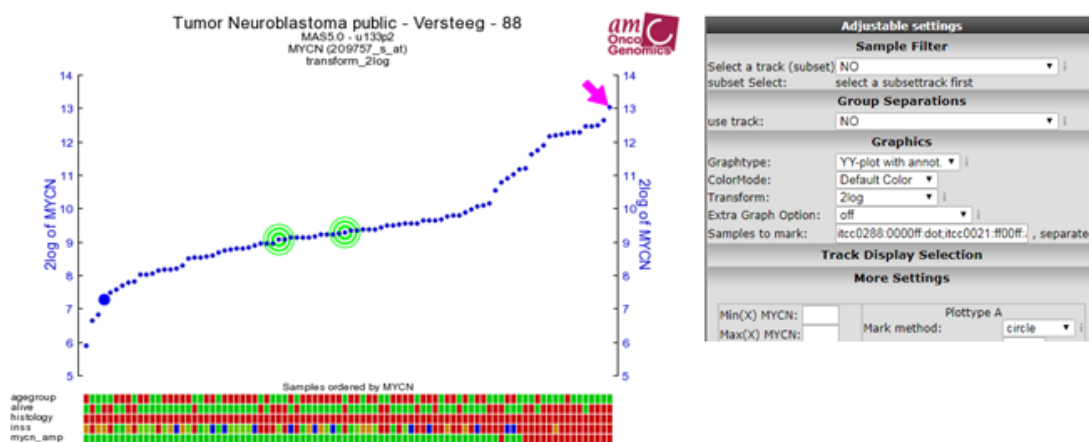


Figure 5: Mark with advanced options



Did you know box

R2 knows a couple of mark options, that you can make use of in the advanced prescriptions:

- ‘dot’: places a thick border around the sample
- ‘circle’: Places a ring around the sample (diameter 9)
- ‘circle_2’: Places a ring around the sample (diameter 4)
- ‘circle_3’: Places a ring around the sample (diameter 1), effectively a thin border
- ‘epicenter’: Places a set of 3 rings descending in width around a sample
- ‘arrow’: Places a block arrow pointing to the sample
- ‘triangle’: Places a filled triangle under the sample

Note: The dotsize does not scale with ‘arrow’ and ‘triangle’ method.

2.3 Workflow: Drawing lines between samples in an XY plot

1. Drawing a line between 2 samples

To indicate a relation between different samples within a dataset it can sometimes be informative to add a line between samples. One can think of a pair for example, or perhaps a temporal relationship such as an on-off state or a time series. Within the XY plot of R2, we have a variable called ‘sample paths’, which can

be used to add a line between samples. The easiest example, is to connect 2 samples within a plot. Using dataset ‘Mixed Neuroblastoma (MES-ADRN-Crest-Exp) - Versteeg - 52 - MAS5.0 - u133p2’, we can add a line between a pair of samples by putting ‘gsm2413241,gsm2413246’ in the sample paths input.

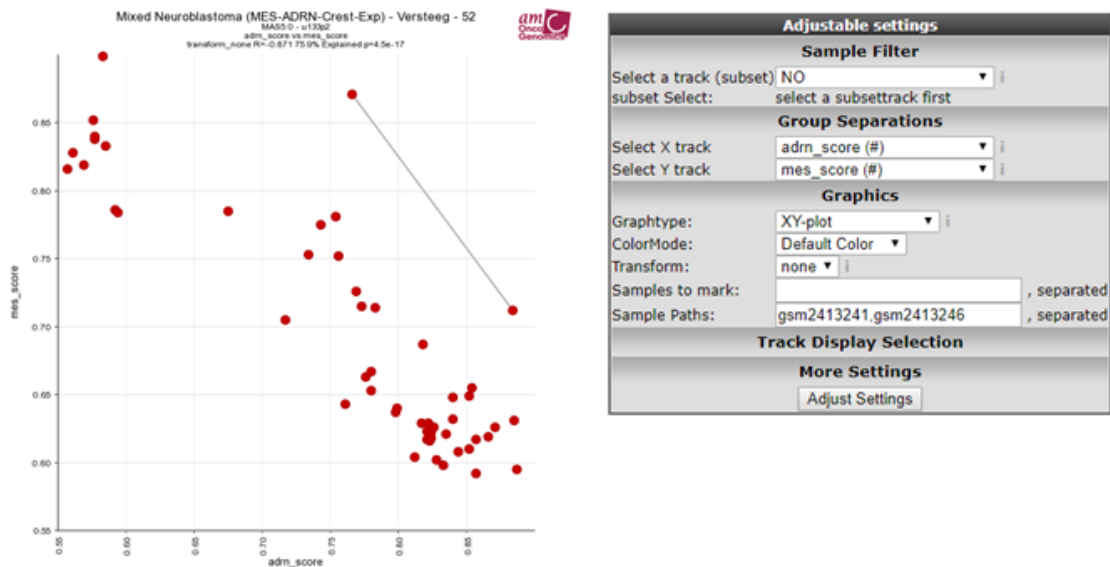


Figure 1: Connect 2 samples

1. Path properties The appearance of the line can also be influenced by providing a color (hex number) and a linewidth. The recipe for these adaptations makes use of ‘:’ and works as follows. sample1,sample2:colorcode:width. Let’s give this a try by making the line red with a thickness of 3. Add ‘gsm2413241,gsm2413246:#ff0000:3’ to the path box.

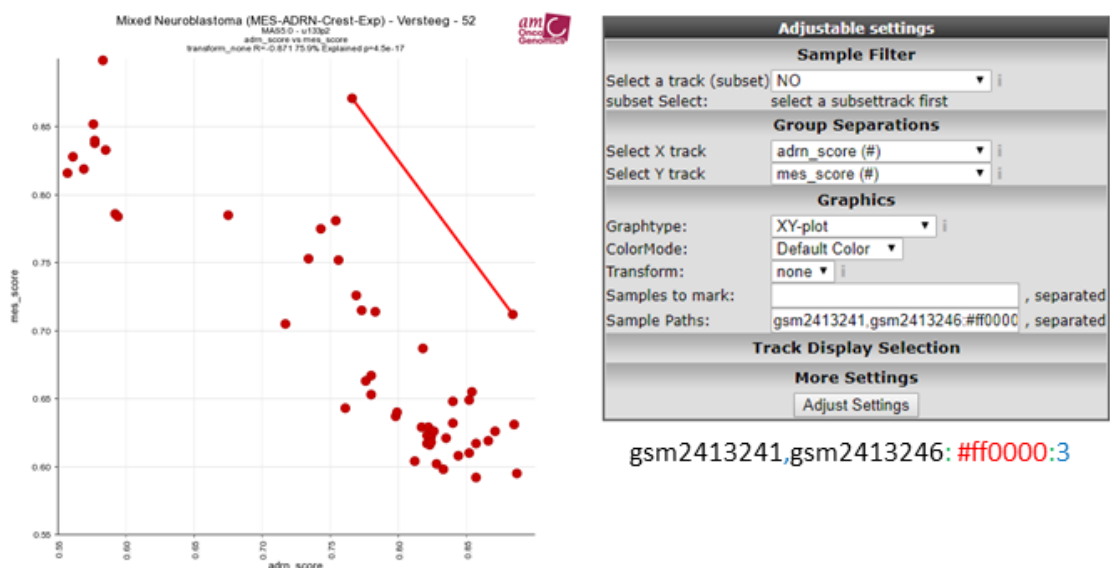
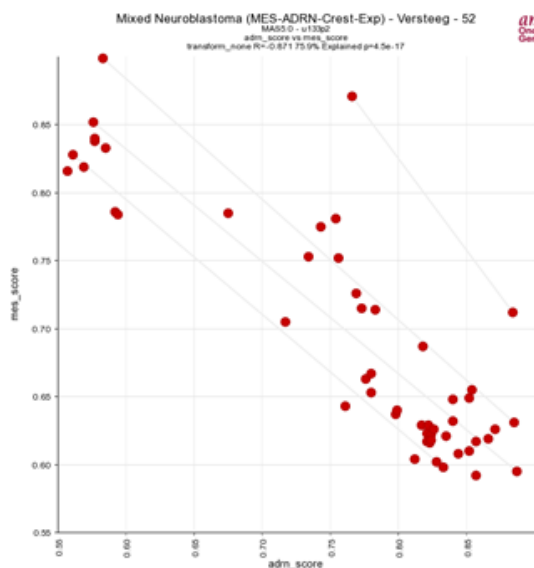


Figure 2: path properties

1. Drawing multiple paths We can draw multiple paths by separating them with ‘;’. Let’s give this a try by drawing a line between 4 pairs of samples in the current dataset in

light grey. Add 'gsm2413241,gsm2413246:#eeeeee; gsm2413239,gsm2413243:#eeeeee; gsm2413242,gsm2413245:#eeeeee; gsm2413240,gsm2413244:#eeeeee' in the sample path box.

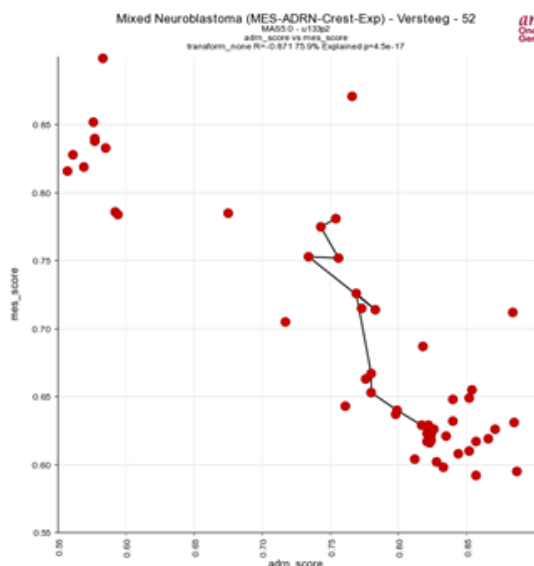


```
gsm2413241,gsm2413246:#eeeeee;
gsm2413239,gsm2413243:#eeeeee;
gsm2413242,gsm2413245:#eeeeee;
gsm2413240,gsm2413244:#eeeeee
```

Figure 3: Connect 2 samples

1. Drawing multisample paths

If the width and color of multiple samples can be the same, then you can also define longer paths by adding more samples in a row, by adding more samples, divided by a ','. Lets give this a try by defining a time series within this dataset. Add 'gsm2413257, gsm2413247, gsm2413248, gsm2413249, gsm2413250, gsm2413251, gsm2413252, gsm2413253, gsm2413254, gsm2413255, gsm2413256:#222222' to the box.

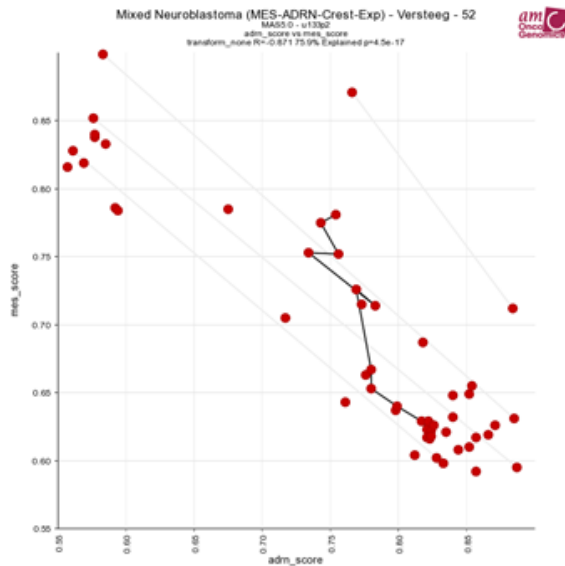


```
gsm2413257,gsm2413247,gsm2413248,
gsm2413249,gsm2413250,gsm2413251,
gsm2413252,gsm2413253,gsm2413254,
gsm2413255,gsm2413256:#222222
```

Figure 4: Connect 2 samples

1. Drawing multisample paths We can also combine the 2 previ-

ous ones into 1 picture by adding ‘gsm2413241,gsm2413246:#eeeeee;gsm2413239,gsm2413243:#eeeeee;gsm2413242,gsm2413245:#eeeeee;gsm2413240,gsm2413244:#eeeeee;gsm2413257,gsm2413247,gsm2413248,gsm2413249,gsm2413250,gsm2413251,gsm2413252,gsm2413253,gsm2413254,gsm2413255,gsm2413256:#222222’ in the sample path box.



```
gsm2413241,gsm2413246:#eeeeee;gsm2413239,gsm2413243:#eeeeee;gsm2413242,gsm2413245:#eeeeee;gsm2413240,gsm2413244:#eeeeee;gsm2413257,gsm2413247,gsm2413248,gsm2413249,gsm2413250,gsm2413251,gsm2413252,gsm2413253,gsm2413254,gsm2413255,gsm2413256:#222222
```

Figure 5: Connect 2 samples

2.4 Workflow: Final Remarks

For description of many functions in R2, we have assembled a tutorial book, which can be found at [r2-tutorials](http://r2-tutorials.com).