

Microarray Analysis Section

Once all the raw data files are associated under Microarray Experiment Section of SaDA, the analysis pipeline can be initiated.


User associates all the data together in one section.


The screenshot shows the 'New microarray experiments' form. At the top, there is a header with the SaDA logo, a user profile 'partner1', and navigation links: 'Internal site', 'External site', and 'Reports'. Below this is a secondary navigation bar with links: 'Sampling site', 'Sampling', 'Filter sample', 'Nucleic acid', 'Oligo sequence', and 'Microarray experiments'. A third navigation bar contains links: 'Microarray .GAL', 'Microarray .GPR', 'Microarray Images', 'Microarray Analysis files', and 'Microarray Validations'. The main heading is 'New microarray experiments' with a 'Back' link. A 'Create' button is located above the form. The form is titled 'GENERAL DATA' and contains several fields: 'Associate .gal file' (dropdown menu showing 'GAL-1-UniCam-uAQUA-20150520233214'), 'Associate .gpr file' (dropdown menu showing 'GPR-1-UniCam-uAQUA-'), 'Associate image file' (text input showing 'Image-01-150520-01-/uploads/micro_array_image/image/1/2-A1-01a_R1.jpg'), 'Filter Sample Code' (dropdown menu showing 'P03-110621-01-F01'), 'Person' (dropdown menu showing 'DE SIMONE Simona'), 'Partner' (dropdown menu showing '1 - UniCam'), 'Partner barcode' (text input), and 'Uploaded at' (date and time picker showing '2015 May 20').

The screenshot shows the 'Microarray experiments' table. At the top, there is a header with the SaDA logo, a user profile 'partner1', and navigation links: 'Internal site', 'External site', and 'Reports'. Below this is a secondary navigation bar with links: 'Sampling site', 'Sampling', 'Filter sample', 'Nucleic acid', 'Oligo sequence', and 'Microarray experiments'. A third navigation bar contains links: 'Microarray .GAL', 'Microarray .GPR', 'Microarray Images', 'Microarray Analysis files', and 'Microarray Validations'. The main heading is 'Microarray experiments'. Below the heading are two links: 'New microarray experiment' and 'Analyze Selected Experiment'. The table is titled 'List of Microarray experiments: you can filter (using the lens icon in the bottom of the grid), sort (clicking on the header column), scroll the data in the grid (using the pagination system)'. The table has 10 columns: 'Microarray exp. code', 'Filter sample', 'GAL code', 'Partner', 'GPR code', 'Exp. date', 'Image', 'Select', and 'Edit'. There are three rows of data:

	Microarray exp. code	Filter sample	GAL code	Partner	GPR code	Exp. date	Image	Select	Edit
+ ⓘ	E01-150520-01	P03-110621-01-F01	GAL-1-UniCam-uAQUA-20150520234049	1 - UniCam	GPR-1-UniCam-uAQUA-	2015-05-20		<input type="checkbox"/>	✎
+ ⓘ	E01-150520-02	P03-110621-01-F01	GAL-2-UniCam-20150520234744	1 - UniCam	GPR-2-UniCam-	2015-05-20		<input type="checkbox"/>	✎
+ ⓘ	E01-150520-03	P03-110621-01-F02	GAL-3-UniCam-20150520235020	1 - UniCam	GPR-3-UniCam-uAQUA 3-	2015-05-20		<input type="checkbox"/>	✎

The hybridization experiments that need to be analysed are checked. User can then click the link titled “Analyze Selected Experiment”.



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 Internal site External site Reports







Sampling site Sampling Filter sample Nucleic acid Oligo sequence Microarray experiments

Microarray .GAL Microarray .GPR Microarray Images Microarray Analysis files Microarray Validations


Microarray experiments


[New microarray experiment](#)
[Analyze Selected Experiment](#)

List of Microarray experiments: you can filter (using the lens icon in the bottom of the grid), sort (clicking on the header column), scroll the data in the grid (using the pagination system)

	Microarray exp. code	Filter sample	GAL code	Partner	GPR code	Exp. date	Image	Select	Edit
+ ⓘ	E01-150520-01	P03-110621-01-F01	GAL-1-UniCam-uAQUA-20150520234049	1 - UniCam	GPR-1-UniCam-uAQUA-	2015-05-20		<input checked="" type="checkbox"/>	
+ ⓘ	E01-150520-02	P03-110621-01-F01	GAL-2-UniCam-20150520234744	1 - UniCam	GPR-2-UniCam-	2015-05-20		<input checked="" type="checkbox"/>	
+ ⓘ	E01-150520-03	P03-110621-01-F02	GAL-3-UniCam-20150520235020	1 - UniCam	GPR-3-UniCam-uAQUA 3-	2015-05-20		<input checked="" type="checkbox"/>	

With the click, SaDA sends all the raw data to R programming environment for its further analysis. SaDA calculates signal to noise ratio (SNR) and Total Signal Intensity (TSI) for all the spotted probes. The resulting data is displayed under *Microarray Analysis* section. This analysed secondary data can be exported in CSV and XLS format.



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 Internal site External site Reports

Sampling site Sampling Filter sample Nucleic acid Oligo sequence Microarray experiments

Microarray .GAL Microarray .GPR Microarray Images Microarray Analysis files Microarray Validations

Microarray Analysis

[Export to Excel](#)
[Export to CSV](#)
[Normalize](#)

Select	Analysis ID	Experiment Code	GPR Code	Date	Note
<input type="checkbox"/>	1	E01-150520-01	GPR-1-UniCam-uAQUA-	2015-05-20 22:53:17 UTC	
<input type="checkbox"/>	2	E01-150520-02	GPR-2-UniCam-	2015-05-20 22:53:37 UTC	
<input type="checkbox"/>	3	E01-150520-03	GPR-3-UniCam-uAQUA 3-	2015-05-20 22:54:09 UTC	

Microarray Analysed Data

Analysis ID	Probes	Signal To Noise Ratio	Total Signal Intensity
2	SxtA4813AphAL	0.9354300975414451	-489840
2	gvpC415P	0.8935754471521198	-828960
2	16SRNAOscII522	59.98232570929601	272232556.025
2	AoaC26787AphC	0.8721635969167203	-979680
2	NrlaR58NdNrlaR58N	0.9197380719308355	-628000

In the Microarray Analysis section two data tables are visible. Upper table displays the experiment metadata, like the experiment code, GPR file code, analysis unique ID and date of creation. When user hovers over and clicks on individual rows of table 1, the data in table 2 changes. So for every experiment and generated GPR file there is one analysed data with calculated SNR and TSI for every spotted probe. User can also select on individual row in table 1 and click on Normalize. This action will normalize the SNR and TSI data based on individual control probe intensity. Probe selection menu will appear once the user clicks on Normalize button. SaDA also renders images for normalized

probes hybridization value, generated by the R software and it creates bar charts using jqwidgets charting library.