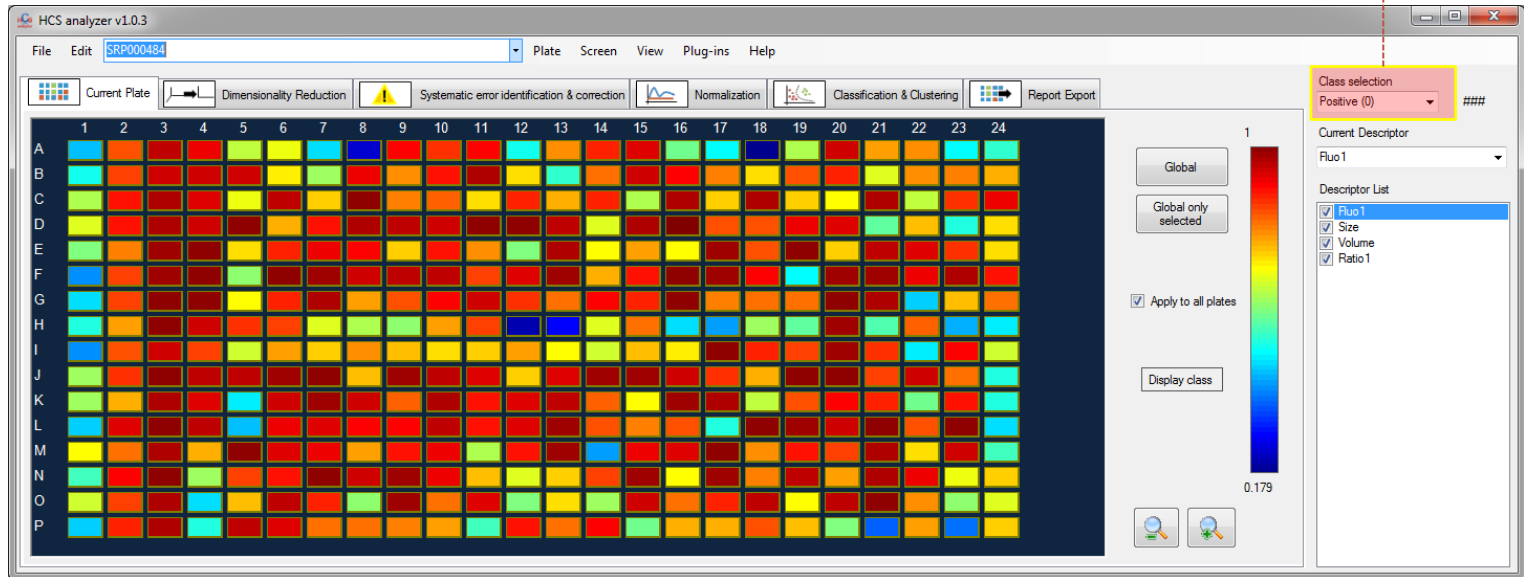




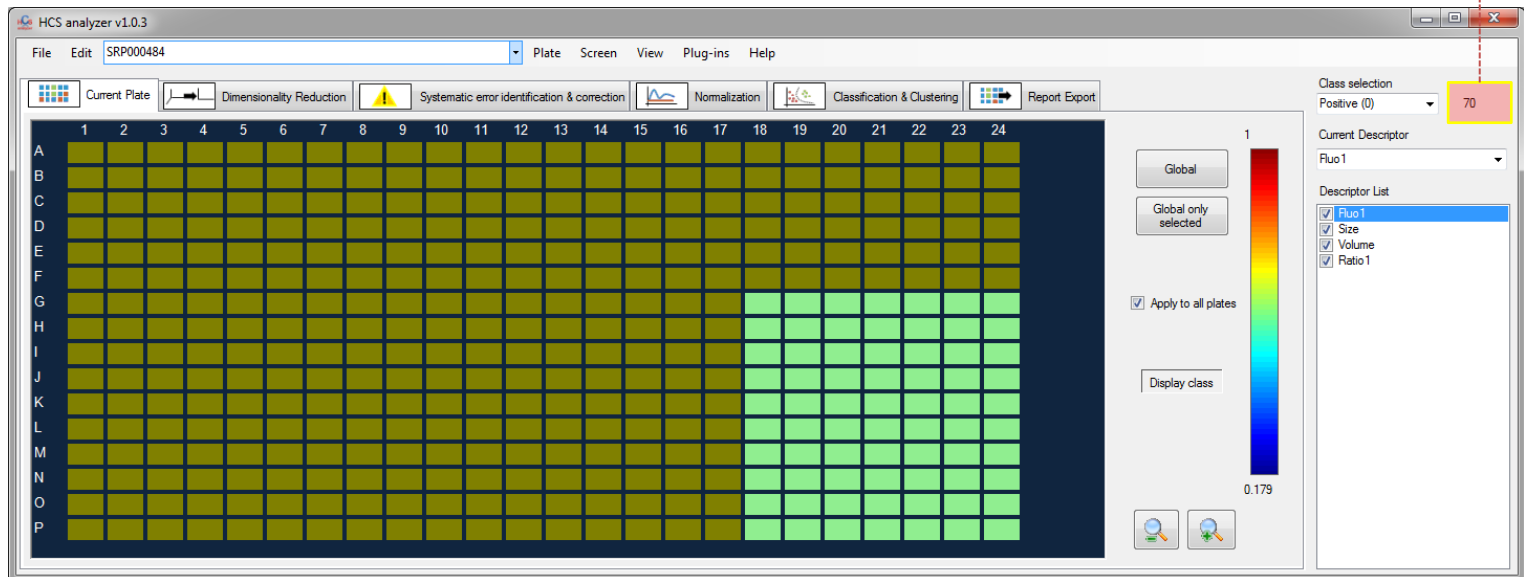
Visual Documentation v1.0.3

User Interface

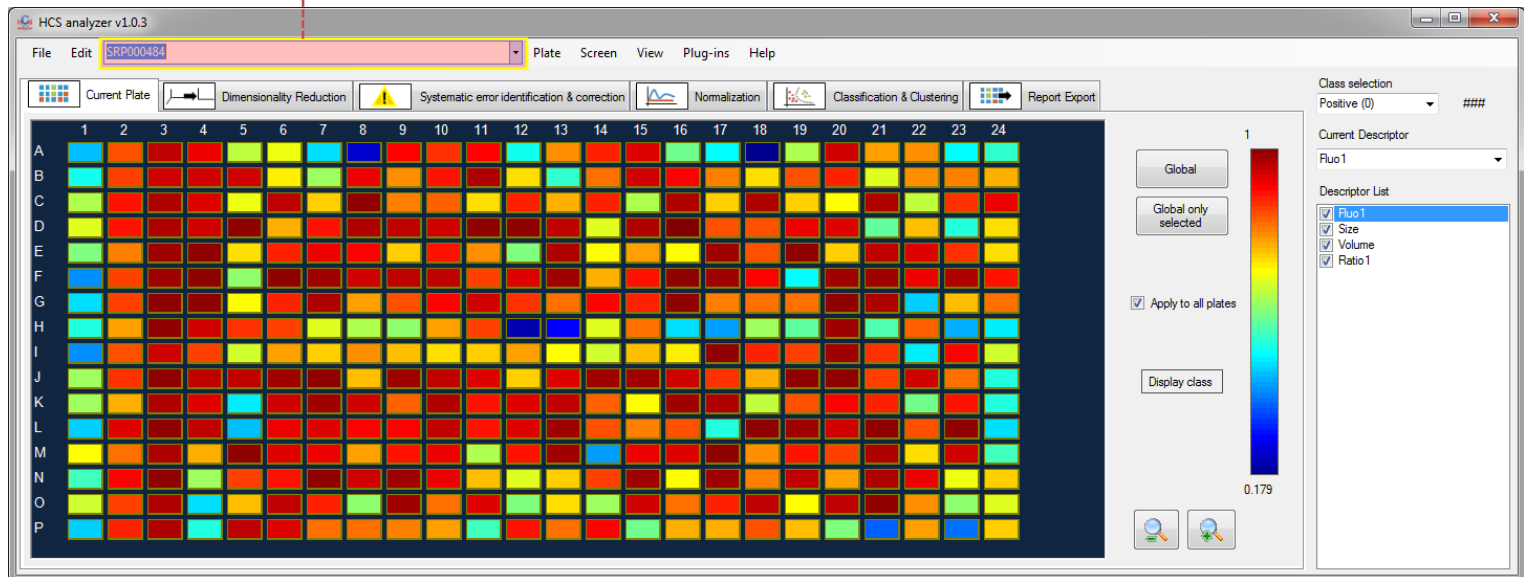
Active class
(for selection and
some processes)



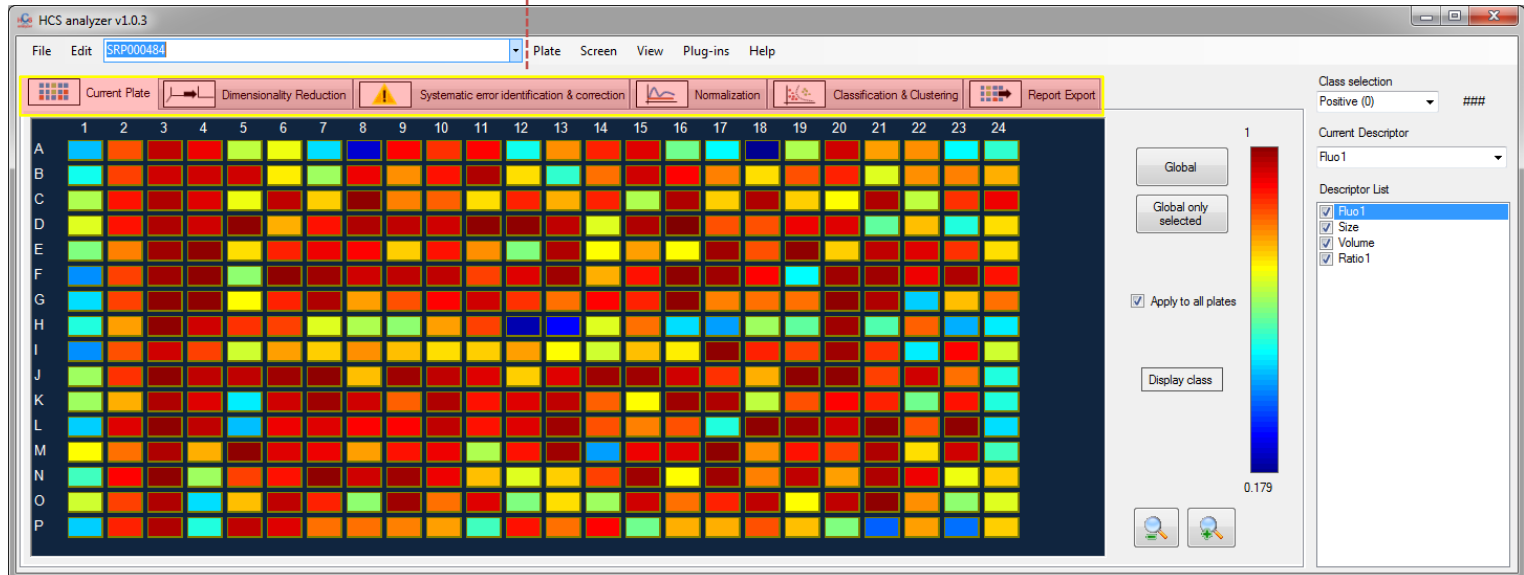
Number of wells associated
with the active class
(current plate only)



Current activated
plate



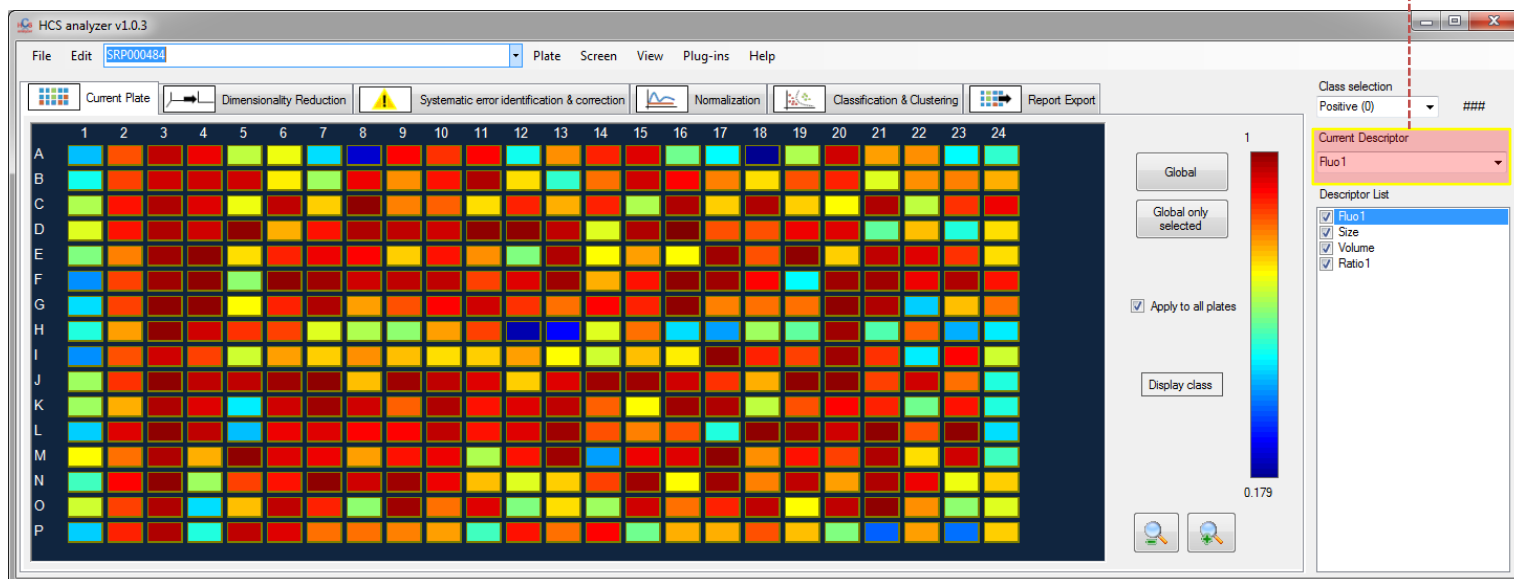
Process pipeline



Wells coordinate



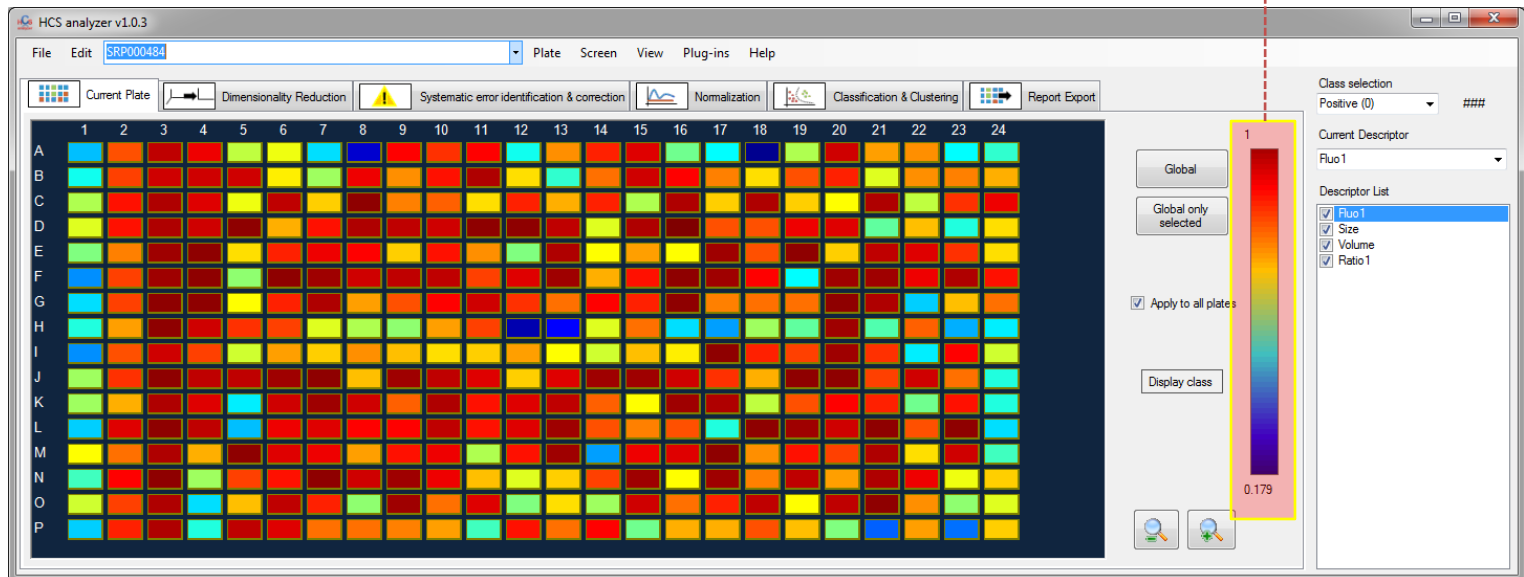
Currently activated
descriptor



Current plate readouts display
corresponding to the selected
descriptor



Look up table
related to the current
plate and the current
descriptor



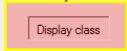
Available and activated descriptors
When inactivated, the descriptors
will not be taken into account
for any process.



Zoom in and Zoom out
(can also be performed with the mouse
wheel)



Global
Global elec
polyto



When checked
class selection is performed on all
the currently activated plates

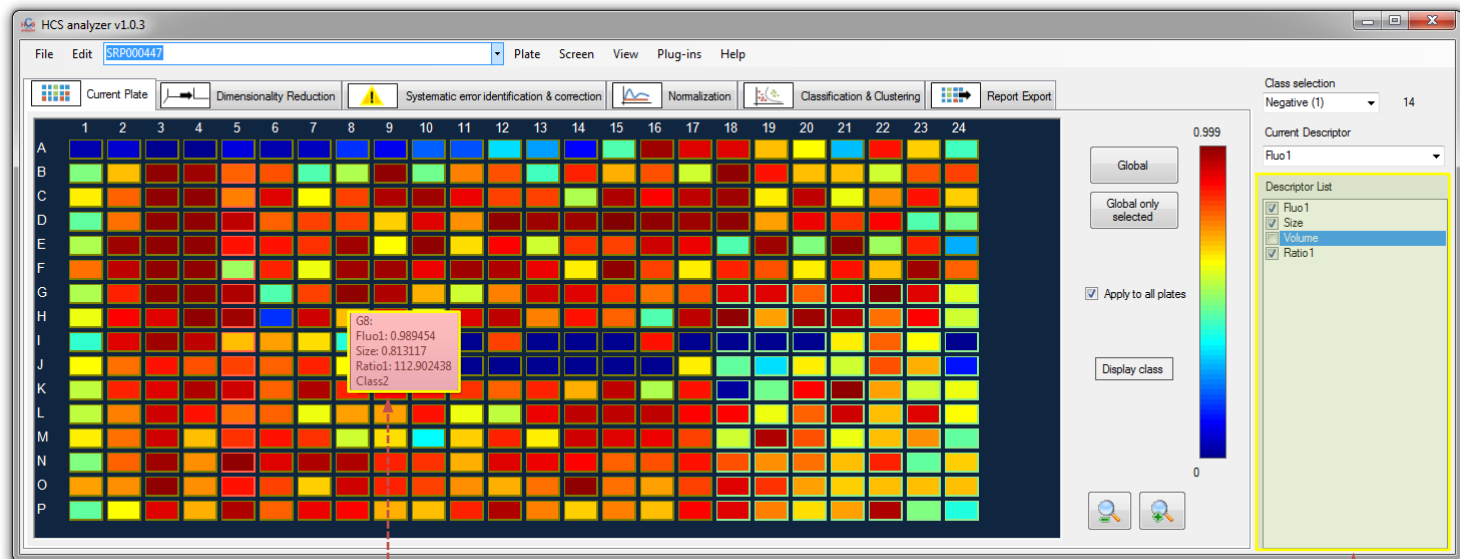


When pressed, all the wells will
turned into the currently selected
class (including non activated wells)

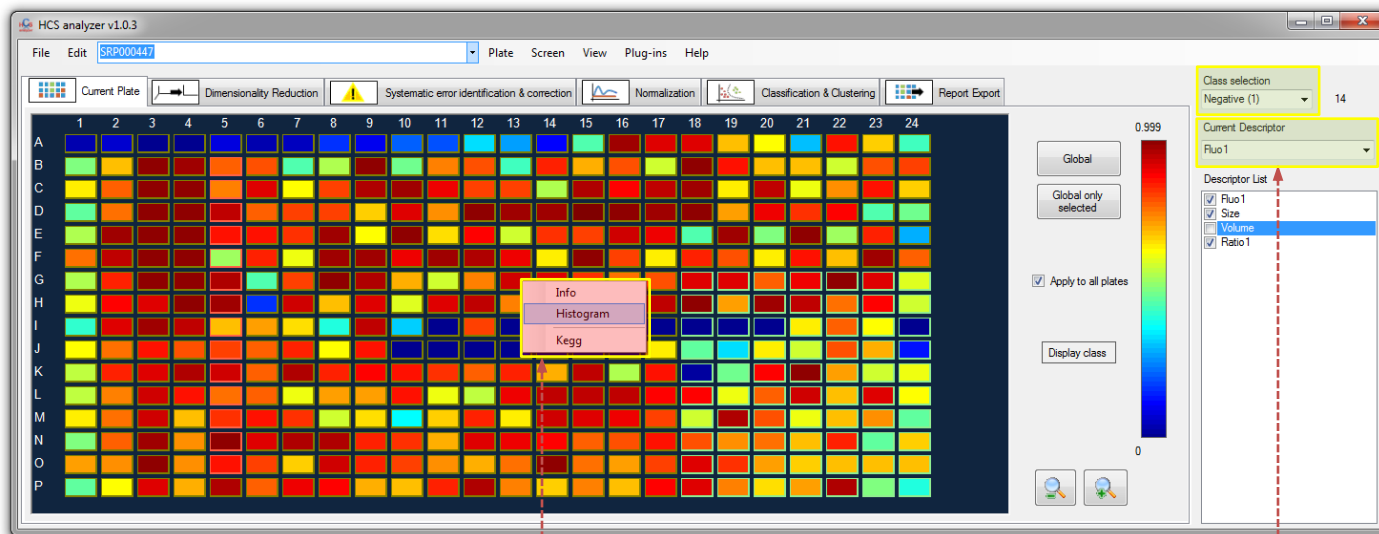


When pressed, the wells will turned
into the currently selected class
(only activated wells are concerned)

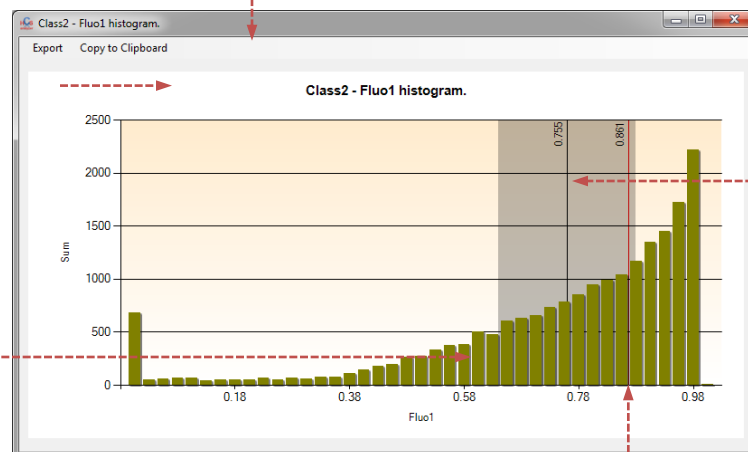




When the mouse cursor is placed over a well, a list of information is displayed. This includes: Well position, name (if so), list of all the activated descriptors with their corresponding values and the class



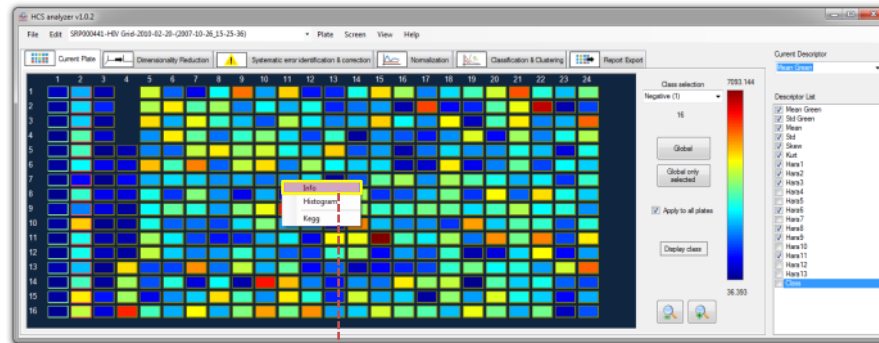
Contextual menu: **Histogram**
(right click on a well)



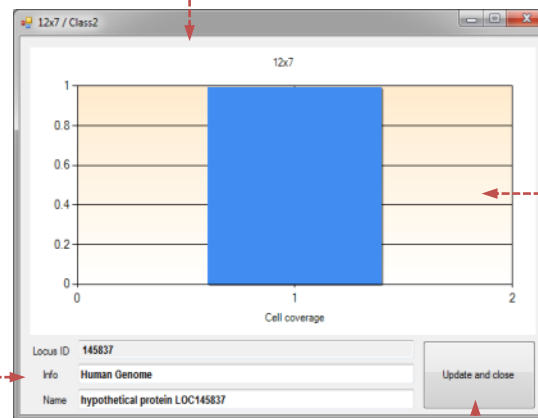
Histogram of the selected histogram within the active class over the entire list of active plates.
(The histogram color is related to the class)

Average and standard deviation of the displayed histogram

Current value of the selected well



Contextual menu: **Info** (right click over a well)



Display (if loaded) locus ID, information and Name associated to the current well (Info and Name are editable)

Representation of the distribution (if available) of the current well selected descriptor

Save new Info and Name

Options

Options

Misc... Syst. Errors Ident.

Import / Export Display Clustering Classification Correlation matrix

Well position mode

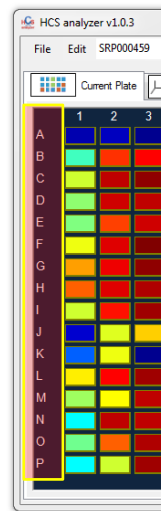
A01 1 1

☒ Single Mode ☐ Double Mode

Import Names

☐ If not named, then inactive

Ok



Import

Plate Dimensions

Columns 24

Rows 16

Data Name	Selection	Type
Plate384	<input checked="" type="checkbox"/>	Plate name
Well 384w	<input checked="" type="checkbox"/>	Column
Cat	<input checked="" type="checkbox"/>	Row
Catalog Number	<input type="checkbox"/>	Descriptor

Options

Misc... Syst. Errors Ident.

Import / Export Display Clustering Classification Correlation matrix

Well position mode

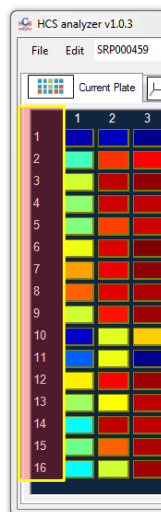
A01 1 1

☐ Single Mode ☒ Double Mode

Import Names

☐ If not named, then inactive

Ok



Import

Plate Dimensions

Columns 24

Rows 16

Data Name	Selection	Type	Readout 0
Plate384	<input checked="" type="checkbox"/>	Plate name	SRP000459
Well 384w	<input checked="" type="checkbox"/>	Well position	D24
Cat	<input type="checkbox"/>	Descriptor	Druggable
Catalog Number	<input type="checkbox"/>	Descriptor	1
Gene Symbol	<input type="checkbox"/>	Descriptor	1

Options

Mac / Syst. Errors Ident. / Import / Export / Display / Clustering / Classification / Correlation matrix

Histogram

☐ Display distribution ☒ Display average value

☒ Display Statistics

☒ Display well information

☒ Name ☐ Info ☐ Locus ID

Plate Design

Gutter: 4

Graph Design

Gradient Color:

Ok



Options

Mac / Syst. Errors Ident. / Import / Export / Display / Clustering / Classification / Correlation matrix

Histogram

☐ Display distribution ☒ Display average value

☒ Display Statistics

☐ Display well information

☐ Name ☐ Info ☐ Locus ID

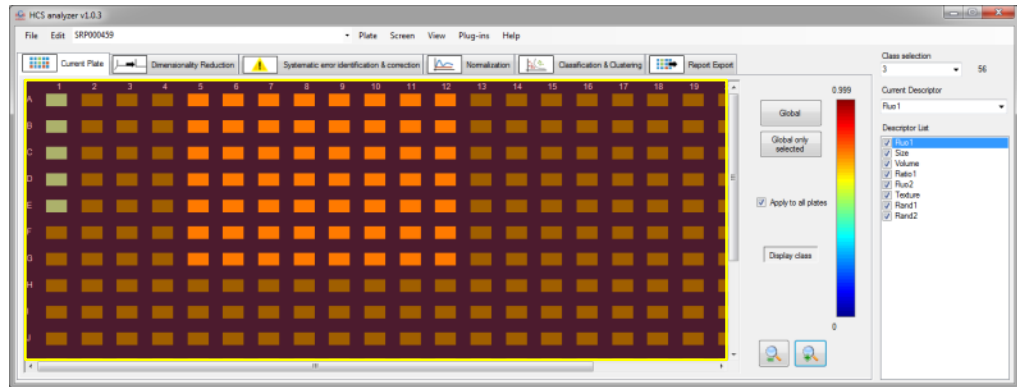
Plate Design

Gutter: 20

Graph Design

Gradient Color:

Ok



Options

Mac / Syst. Errors Ident. / Import / Export / Display / Clustering / Classification / Correlation matrix

Histogram

☐ Display distribution ☒ Display average value

☒ Display Statistics

☒ Display well information

☒ Name ☐ Info ☐ Locus ID

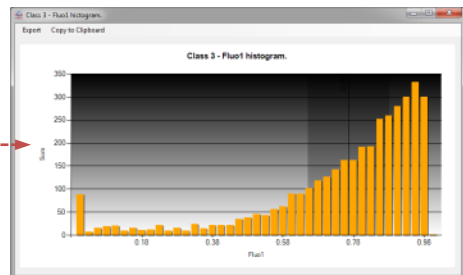
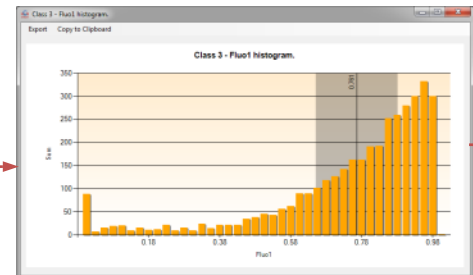
Plate Design

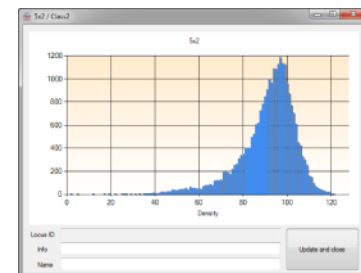
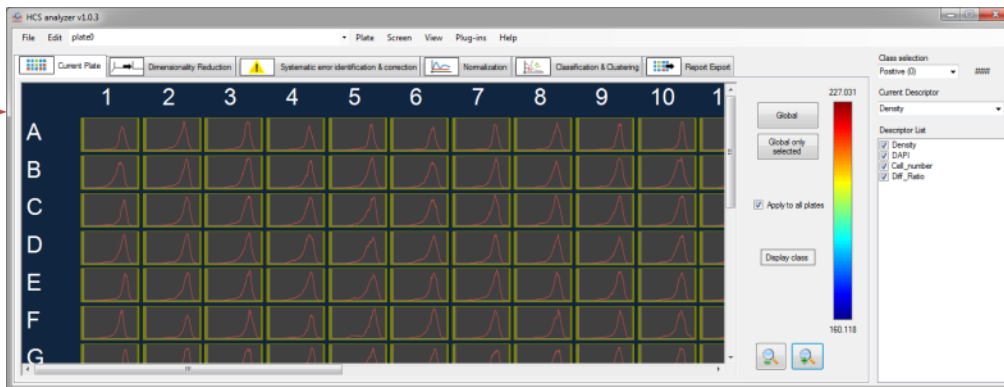
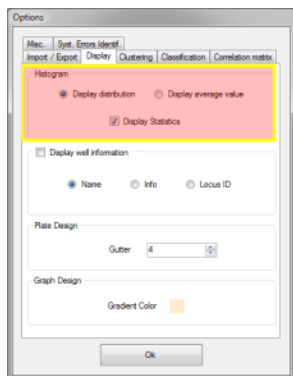
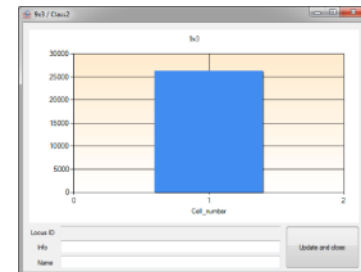
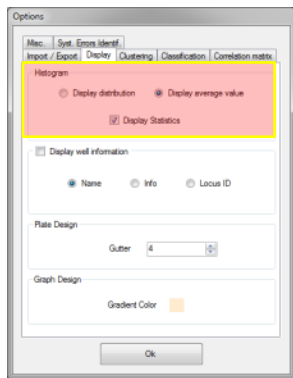
Gutter: 20

Graph Design

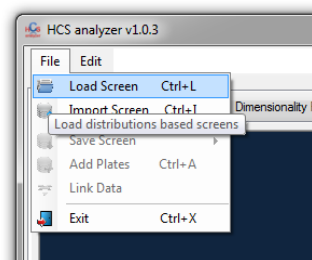
Gradient Color:

Ok





Note: display distribution option requires the have loaded a distributions based screen



Options

Import / Export / Display / Clustering / Classification / Correlation matrix

Mac: ☐ Sys. Errors ident.

Internet Browser

☒ Internet Explorer ☐ Google Chrome

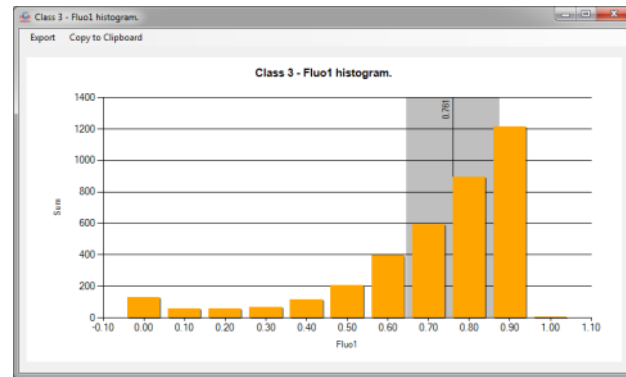
Histogram

Bin Number

Graphics

Maximum Width

OK



Options

Import / Export / Display / Clustering / Classification / Correlation matrix

Mac: ☐ Sys. Errors ident.

Internet Browser

☒ Internet Explorer ☐ Google Chrome

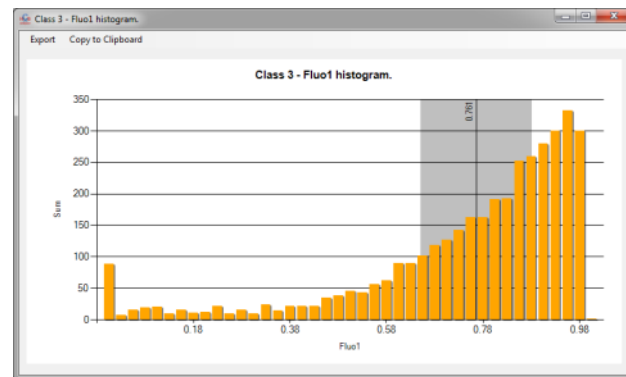
Histogram

Bin Number

Graphics

Maximum Width

OK



Options

Misc. | Errors Ident. & Correct. | Generate Screening | Import / Export | Display | Clustering | Classification | Correlation matrix

Histogram

☐ Display distribution ☒ Display average value

☒ Display Statistics

☐ Display well information

☒ Name ☐ Info ☐ Locus ID

Plate Design

Gutter 4

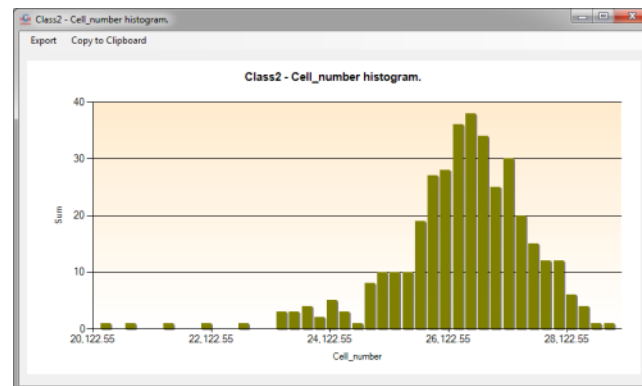
Graph Design

Gradient Color

Chart Performance

☐ Fast Display

Ok



Options

Misc. | Errors Ident. & Correct. | Generate Screening | Import / Export | Display | Clustering | Classification | Correlation matrix

Histogram

☐ Display distribution ☒ Display average value

☒ Display Statistics

☐ Display well information

☒ Name ☐ Info ☐ Locus ID

Plate Design

Gutter 4

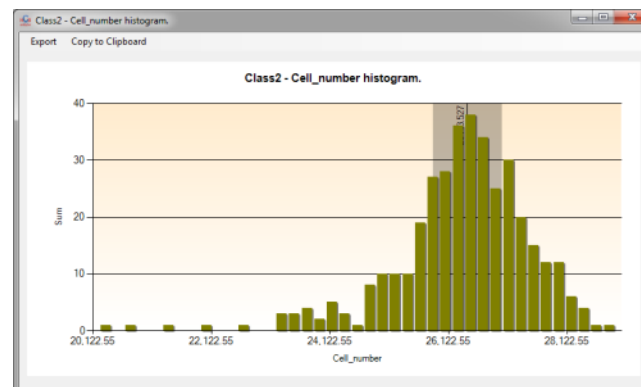
Graph Design

Gradient Color

Chart Performance

☒ Fast Display

Ok



Options

Misc. Errors Identif. & Correct. Generate Screening

Import / Export Display Clustering Classification Correlation matrix

Histogram

☐ Display distribution ☒ Display average value

☒ Display Statistics

☐ Display well information

☒ Name ☐ Info ☐ Locus ID

Plate Design

Gutter 4

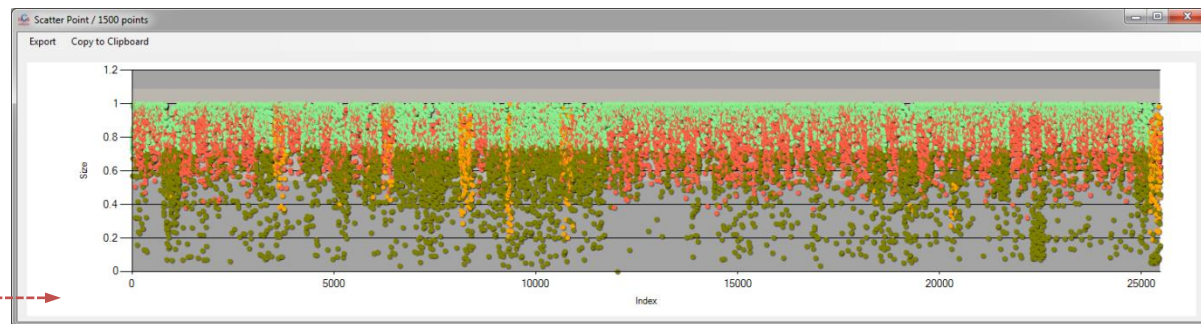
Graph Design

Gradient Color

Chart Performance

☒ Fast Display

Ok



Options

Misc. Errors Identif. & Correct. Generate Screening

Import / Export Display Clustering Classification Correlation matrix

Histogram

☐ Display distribution ☒ Display average value

☒ Display Statistics

☐ Display well information

☒ Name ☐ Info ☐ Locus ID

Plate Design

Gutter 4

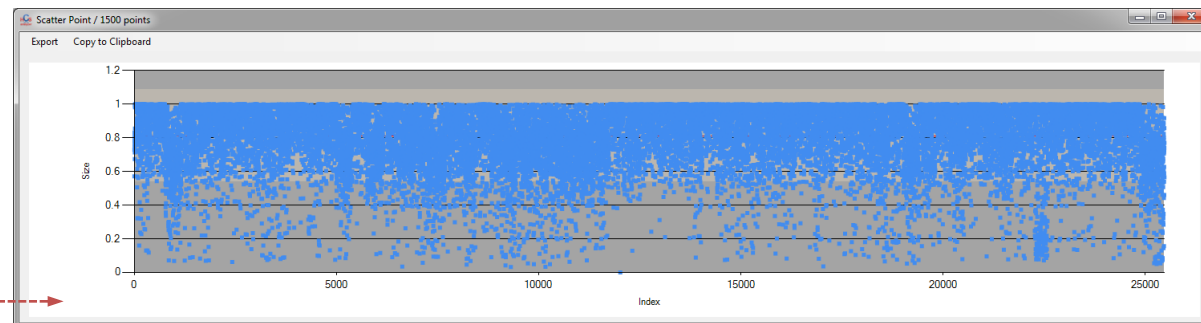
Graph Design

Gradient Color

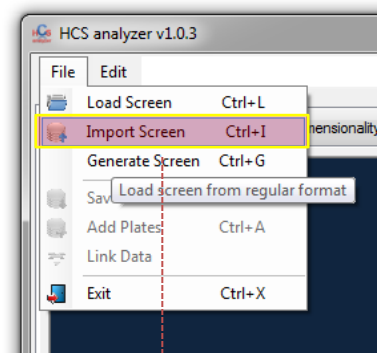
Chart Performance

☒ Fast Display

Ok



Importing Data



Import

Plate Dimensions

Columns 24

Rows 16

	Data Name	Selection	Type	Readout 0	Readout 1	Readout 2
▶	Plate384	<input checked="" type="checkbox"/>	Plate name ▼	SRP000459	SRP000479	SRP000502
	Well 384w	<input checked="" type="checkbox"/>	Well position ▼	D24	P20	G11
	Cat	<input type="checkbox"/>	Descriptor ▼	Druggable	Druggable	Druggable
	Catalog Number	<input type="checkbox"/>	Descriptor ▼	1	2	3
	Gene Symbol	<input type="checkbox"/>	Descriptor ▼	1	2	3
	Description	<input type="checkbox"/>	Descriptor ▼	adrenocortical dy...	deleted in esoph...	hypothetical pr
	Locus ID	<input type="checkbox"/>	Descriptor ▼	65057	115123	57574
	Fluo1	<input type="checkbox"/>	Descriptor ▼	0.8228594	0.7233504	0.9090863
	Size	<input type="checkbox"/>	Descriptor ▼	0.9823682	0.9870385	0.7240621
	Volume	<input type="checkbox"/>	Descriptor ▼	59.26911984	183.9027118	137.0042838
	Ratio1	<input type="checkbox"/>	Descriptor ▼	144.2518279	234.0326818	139.0108669
	Fluo2	<input type="checkbox"/>	Descriptor ▼	90.0408859	176.5919403	74.81596763
	Texture	<input type="checkbox"/>	Descriptor ▼	104.5234322	231.5573299	195.0901458
	Rand1	<input type="checkbox"/>	Descriptor ▼	48.66297765	0.909940097	34.82005831
	Rand2	<input type="checkbox"/>	Descriptor ▼	35.75050135	7.755161101	5.351135178
	Rand3	<input type="checkbox"/>	Descriptor ▼	36.28191786	22.86227618	40.45101283
	Rand4	<input type="checkbox"/>	Descriptor ▼	14.83044153	23.36147298	0.397935311

Ok

Plate dimensions

Import

Plate Dimensions

Columns 24

Rows 16

	Data Name	Selection	Type	Readout 0	Readout 1	Readout 2
▶	Plate384	<input checked="" type="checkbox"/>	Plate name ▼	SRP000459	SRP000479	SRP000502
	Well 384w	<input checked="" type="checkbox"/>	Well position ▼	D24	P20	G11
	Cat	<input type="checkbox"/>	Descriptor ▼	Druggable	Druggable	Druggable
	Catalog Number	<input type="checkbox"/>	Descriptor ▼	1	2	3
	Gene Symbol	<input type="checkbox"/>	Descriptor ▼	1	2	3
	Description	<input type="checkbox"/>	Descriptor ▼	adrenocortical dy...	deleted in esoph...	hypothetical pr
	Locus ID	<input type="checkbox"/>	Descriptor ▼	65057	115123	57574
	Fluo1	<input type="checkbox"/>	Descriptor ▼	0.8228594	0.7233504	0.9090863
	Size	<input type="checkbox"/>	Descriptor ▼	0.9823682	0.9870385	0.7240621
	Volume	<input type="checkbox"/>	Descriptor ▼	59.26911984	183.9027118	137.0042838
	Ratio1	<input type="checkbox"/>	Descriptor ▼	144.2518279	234.0326818	139.0108669
	Fluo2	<input type="checkbox"/>	Descriptor ▼	90.0408859	176.5919403	74.81596763
	Texture	<input type="checkbox"/>	Descriptor ▼	104.5234322	231.5573299	195.0901458
	Rand1	<input type="checkbox"/>	Descriptor ▼	48.66297765	0.909940097	34.82005831
	Rand2	<input type="checkbox"/>	Descriptor ▼	35.75050135	7.755161101	5.351135178
	Rand3	<input type="checkbox"/>	Descriptor ▼	36.28191786	22.86227618	40.45101283
	Rand4	<input type="checkbox"/>	Descriptor ▼	14.83044153	23.36147298	0.397935311

Ok

Import

Plate Dimensions

Columns 24

Rows 16

	Data Name	Selection	Type	Readout 0	Readout 1	Readout 2
▶	Plate384	<input checked="" type="checkbox"/>	Plate name	SRP000459	SRP000479	SRP000502
	Well 384w	<input checked="" type="checkbox"/>	Well position	D24	P20	G11
	Cat	<input type="checkbox"/>	Descriptor	Druggable	Druggable	Druggable
	Catalog Number	<input type="checkbox"/>	Descriptor	1	2	3
	Gene Symbol	<input type="checkbox"/>	Descriptor	1	2	3
	Description	<input type="checkbox"/>	Descriptor	adrenocortical dy...	deleted in esoph...	hypothetical pr
	Locus ID	<input type="checkbox"/>	Descriptor	65057	115123	57574
	Fluo1	<input type="checkbox"/>	Descriptor	0.8228594	0.7233504	0.9090863
	Size	<input type="checkbox"/>	Descriptor	0.9823682	0.9870385	0.7240621
	Volume	<input type="checkbox"/>	Descriptor	59.26911984	183.9027118	137.0042838
	Ratio1	<input type="checkbox"/>	Descriptor	144.2518279	234.0326818	139.0108669
	Fluo2	<input type="checkbox"/>	Descriptor	90.0408859	176.5919403	74.81596763
	Texture	<input type="checkbox"/>	Descriptor	104.5234322	231.5573299	195.0901458
	Rand1	<input type="checkbox"/>	Descriptor	48.66297765	0.909940097	34.82005831
	Rand2	<input type="checkbox"/>	Descriptor	35.75050135	7.755161101	5.351135178
	Rand3	<input type="checkbox"/>	Descriptor	36.28191786	22.86227618	40.45101283
	Rand4	<input type="checkbox"/>	Descriptor	14.83044153	23.36147298	0.397935311

Ok

Readouts preview

Names that be associated
with the data

Import

Plate Dimensions

Columns: 24

Rows: 16

Data Name	Selection	Type	Readout 0	Readout 1	Readout 2
Plate384	<input checked="" type="checkbox"/>	Plate name	SRP000459	SRP000479	SRP000502
Well 384w	<input checked="" type="checkbox"/>	Well position	D24	P20	G11
Cat	<input checked="" type="checkbox"/>	Descriptor	Druggable	Druggable	Druggable
Catalog Number	<input type="checkbox"/>	Descriptor	1	2	3
Gene Symbol	<input type="checkbox"/>	Descriptor	1	2	3
Description	<input checked="" type="checkbox"/>	Descriptor	adrenocortical dy...	deleted in esoph...	hypothetical pr
Locus ID	<input checked="" type="checkbox"/>	Descriptor	65057	115123	57574
Fluo1	<input checked="" type="checkbox"/>	Descriptor	0.8228594	0.7233504	0.9090863
Size	<input checked="" type="checkbox"/>	Descriptor	0.9823682	0.9870385	0.7240621
Volume	<input checked="" type="checkbox"/>	Descriptor	59.26911984	183.9027118	137.0042838
Ratio1	<input checked="" type="checkbox"/>	Descriptor	144.2518279	234.0326818	139.0108669
Fluo2	<input checked="" type="checkbox"/>	Descriptor	90.0408859	176.5919403	74.81596763
Texture	<input checked="" type="checkbox"/>	Descriptor	104.5234322	231.5573299	195.0901458
Rand1	<input type="checkbox"/>	Descriptor	48.66297765	0.909940097	34.82005831
Rand2	<input type="checkbox"/>	Descriptor	35.75050135	7.755161101	5.351135178
Rand3	<input checked="" type="checkbox"/>	Descriptor	36.28191786	22.86227618	40.45101283
Rand4	<input checked="" type="checkbox"/>	Descriptor	14.83044153	23.36147298	0.397935311

Ok

If unchecked,
the corresponding data
will not be loaded

Import

Plate Dimensions

Columns: 24

Rows: 16

	Data Name	Selection	Type	Readout 0	Readout 1	Readout 2
	Plate384	<input checked="" type="checkbox"/>	Plate name	SRP000459	SRP000479	SRP000502
	Well 384w	<input checked="" type="checkbox"/>	Well position	D24	P20	G11
/	Cat	<input type="checkbox"/>	Descriptor	Druggable	Druggable	Druggable
	Catalog Number	<input type="checkbox"/>	Descriptor	1	2	3
	Gene Symbol	<input type="checkbox"/>	Descriptor	1	2	3
	Description	<input checked="" type="checkbox"/>	Descriptor	adrenocortical dy...	deleted in esoph...	hypothetical pr
	Locus ID	<input checked="" type="checkbox"/>	Descriptor	65057	115123	57574
	Fluo1	<input checked="" type="checkbox"/>	Descriptor	0.8228594	0.7233504	0.9090863
	Size	<input checked="" type="checkbox"/>	Descriptor	0.9823682	0.9870385	0.7240621
	Volume	<input checked="" type="checkbox"/>	Descriptor	59.26911984	183.9027118	137.0042838
	Ratio1	<input checked="" type="checkbox"/>	Descriptor	144.2518279	234.0326818	139.0108669
	Fluo2	<input checked="" type="checkbox"/>	Descriptor	90.0408859	176.5919403	74.81596763
	Texture	<input checked="" type="checkbox"/>	Descriptor	104.5234322	231.5573299	195.0901458
	Rand1	<input type="checkbox"/>	Descriptor	48.66297765	0.909940097	34.82005831
	Rand2	<input type="checkbox"/>	Descriptor	35.75050135	7.755161101	5.351135178
	Rand3	<input checked="" type="checkbox"/>	Descriptor	36.28191786	22.86227618	40.45101283
	Rand4	<input checked="" type="checkbox"/>	Descriptor	14.83044153	23.36147298	0.397935311

Ok

Import

Plate Dimensions

Columns: 24

Rows: 16

Data Name	Selection	Type	Readout 0	Readout 1	Readout 2
Plate384	<input checked="" type="checkbox"/>	Plate name	SRP000459	SRP000479	SRP000502
Well 384w	<input checked="" type="checkbox"/>	Well position	D24	P20	G11
Cat	<input checked="" type="checkbox"/>	Name	Druggable	Druggable	Druggable
Catalog Number	<input type="checkbox"/>	Descriptor	1	2	3
Gene Symbol	<input type="checkbox"/>	Descriptor	1	2	3
Description	<input checked="" type="checkbox"/>	Info	adrenocortical dy...	deleted in esoph...	hypothetical pr
Locus ID	<input checked="" type="checkbox"/>	Locus ID	65057	115123	57574
Fluo1	<input checked="" type="checkbox"/>	Descriptor	0.8228594	0.7233504	0.9090863
Size	<input checked="" type="checkbox"/>	Descriptor	0.9823682	0.9870385	0.7240621
Volume	<input checked="" type="checkbox"/>	Plate name	59.26911984	183.9027118	137.0042838
Ratio1	<input checked="" type="checkbox"/>	Well position	144.2518279	234.0326818	139.0108669
Fluo2	<input checked="" type="checkbox"/>	Class	90.0408859	176.5919403	74.81596763
Texture	<input checked="" type="checkbox"/>	Name	104.5234322	231.5573299	195.0901458
Rand1	<input type="checkbox"/>	Locus ID	48.66297765	0.909940097	34.82005831
Rand2	<input type="checkbox"/>	Info	35.75050135	7.755161101	5.351135178
Rand3	<input checked="" type="checkbox"/>	Descriptor	36.28191786	22.86227618	40.45101283
Rand4	<input checked="" type="checkbox"/>	Descriptor	14.83044153	23.36147298	0.397935311

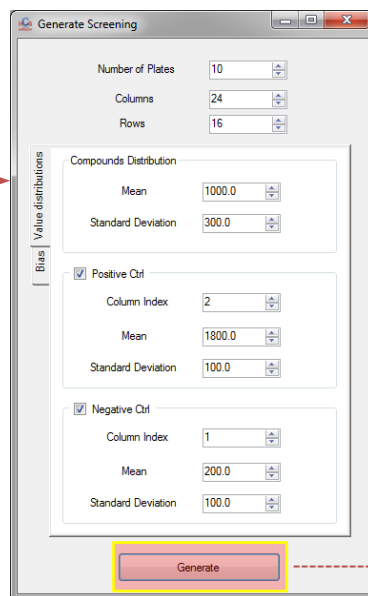
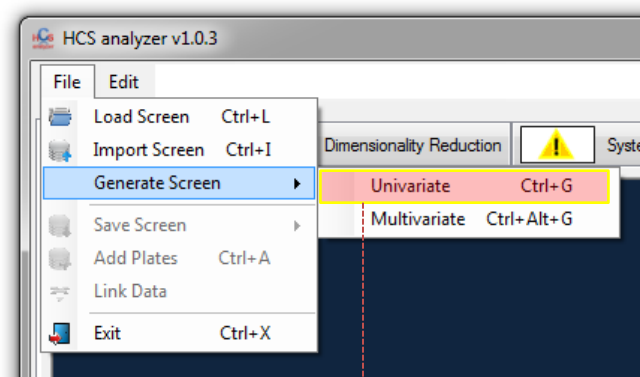
Ok

Data type.

Mandatory: Plate Name, well position and at least one descriptor.

Note: Locus ID should be defined as an integer.

Generating artificial
univariate screening data



Generate Screening

Number of Plates: 10
Columns: 24
Rows: 16

Compounds Distribution

Mean: 1000.0
Standard Deviation: 300.0

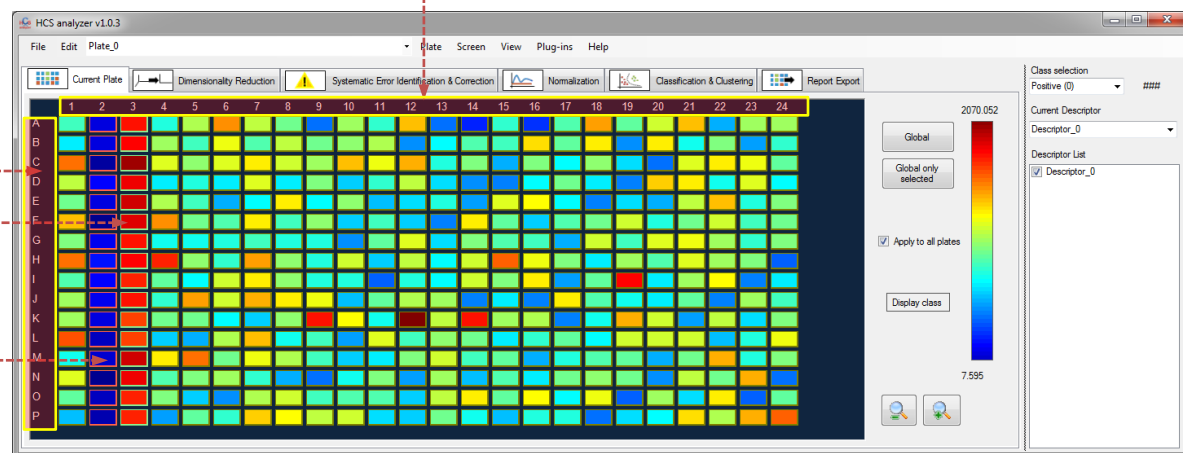
☒ Positive Ctrl

Column Index: 2
Mean: 1800.0
Standard Deviation: 100.0

☒ Negative Ctrl

Column Index: 1
Mean: 200.0
Standard Deviation: 100.0

Generate



Generate Screening

Number of Plates: 10
Columns: 24
Rows: 16

Value distributions

Compounds Distribution

Mean: 1000.0
Standard Deviation: 300.0

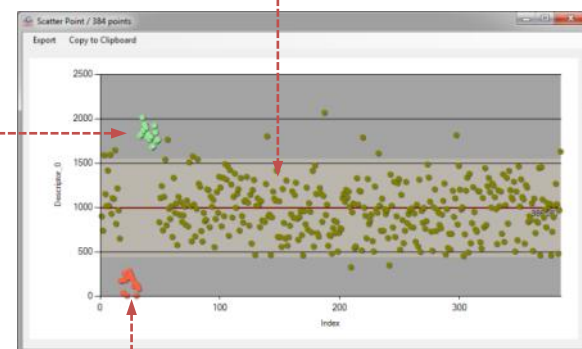
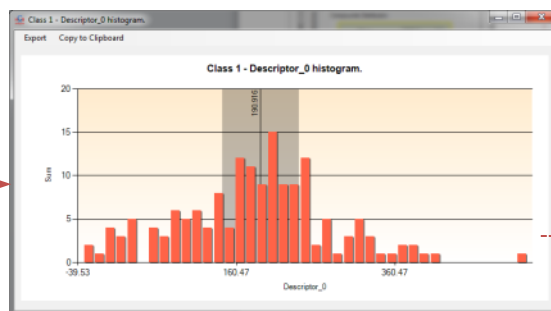
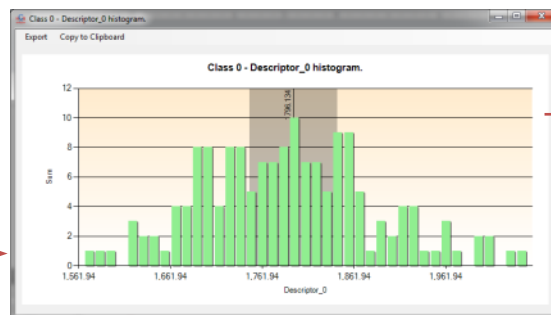
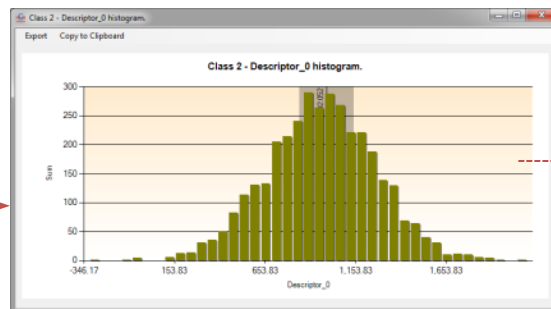
☒ Positive Ctrl

Column Index: 2
Mean: 1800.0
Standard Deviation: 100.0

☒ Negative Ctrl

Column Index: 1
Mean: 200.0
Standard Deviation: 100.0

Generate



Generate Screening

Number of Plates: 10
Columns: 24
Rows: 16

Value distributions

Bias

☒ Row Effect
Shift: 1.0

☒ Column Effect
Shift: 1.0

☒ Edge Effect
Shift: 1.0
Iteration: 8

☒ Bowl Effect
Shift: 1.0
Ratio X/Y: 1.50

Generate

If an effect **X** is selected, it will be combined to original data by the following way:

$$\text{Resulting Data} = \text{Original Data} * (\mathbf{X} + \text{Shift_X})$$

Generate Screening

Number of Plates: 1
Columns: 24
Rows: 16

Bias Value Distributions

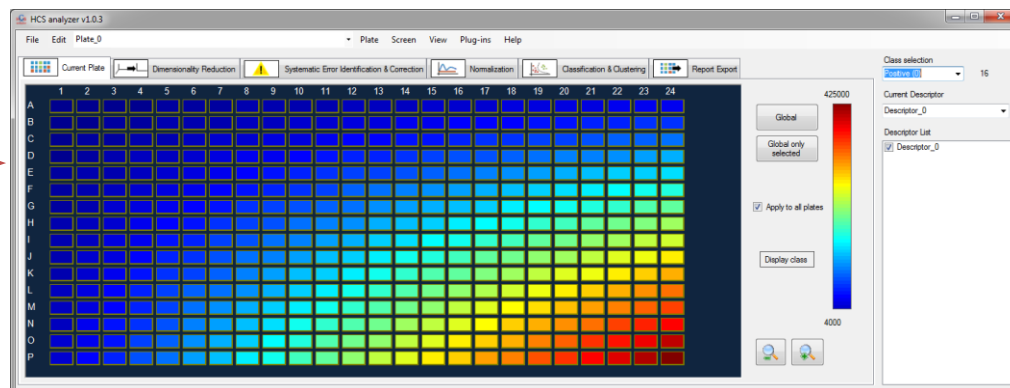
☒ Row Effect
Shift: 1.0

☒ Column Effect
Shift: 1.0

☐ Edge Effect
Shift: 1.0
Iteration: 0

☐ Bowl Effect
Shift: 1.0
Ratio X/Y: 1.50

Generate



Generate Screening

Number of Plates: 1
Columns: 24
Rows: 16

Bias Value Distributions

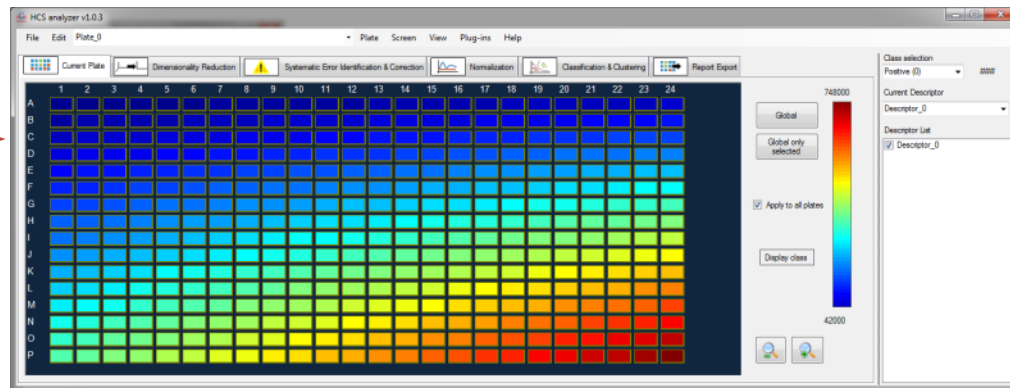
☒ Row Effect
Shift: 1.0

☒ Column Effect
Shift: 20.0

☐ Edge Effect
Shift: 1.0
Iteration: 0

☐ Bowl Effect
Shift: 1.0
Ratio X/Y: 1.50

Generate



The higher **Shift_X** is, the lower **X** contribution to the generated data

Generate Screening

Number of Plates: 1
Columns: 24
Rows: 16

Bias Value distributions

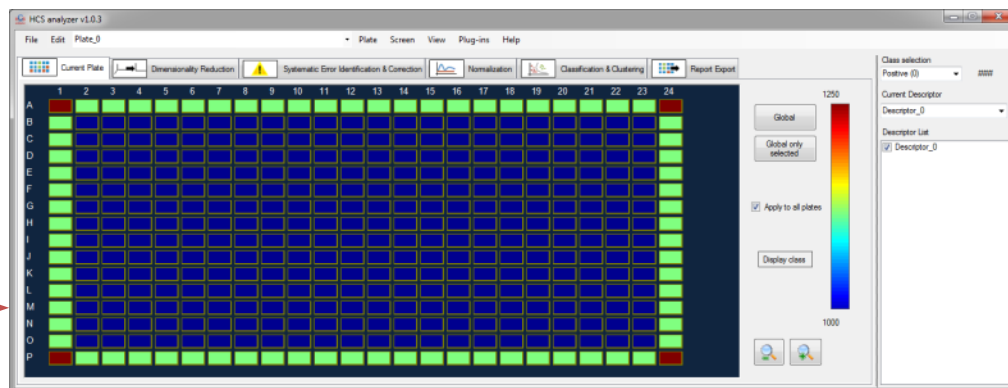
☐ Row Effect
Shift: 1.0

☐ Column Effect
Shift: 1.0

☒ Edge Effect
Shift: 1.0
Iteration: 1

☐ Bias Effect
Shift: 1.0
Ratio X/Y: 1.50

Generate



Generate Screening

Number of Plates: 1
Columns: 24
Rows: 16

Bias Value distributions

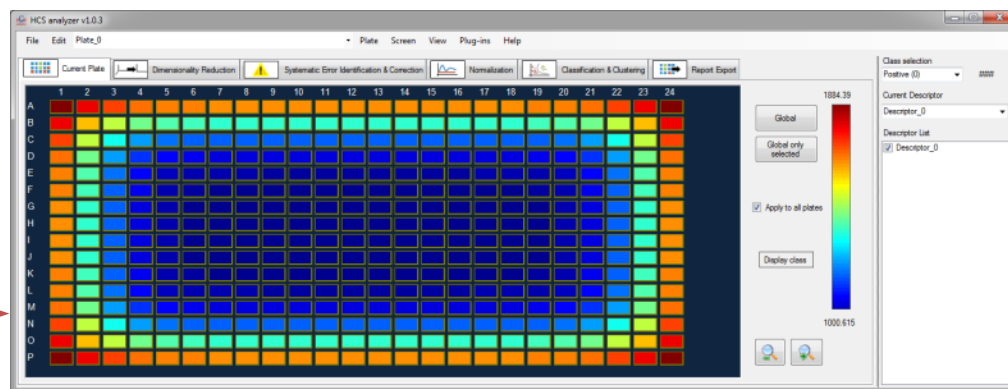
☐ Row Effect
Shift: 1.0

☐ Column Effect
Shift: 1.0

☒ Edge Effect
Shift: 1.0
Iteration: 20

☐ Bias Effect
Shift: 1.0
Ratio X/Y: 1.50

Generate



Generate Screening

Number of Plates: 1
Columns: 24
Rows: 16

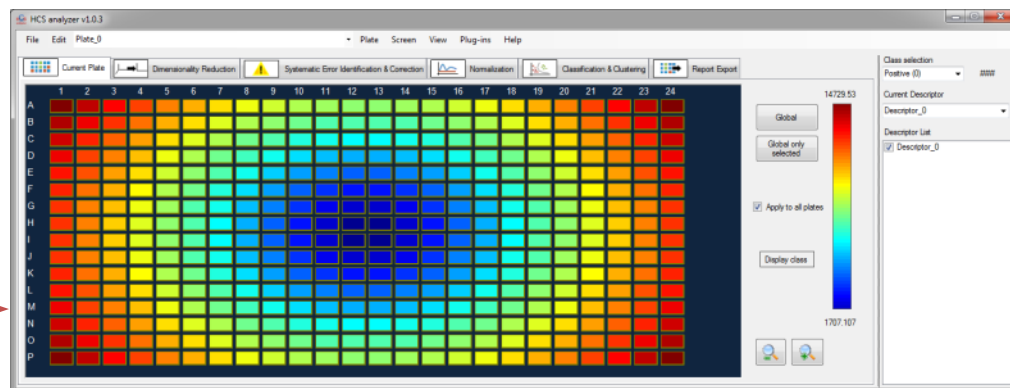
Row Effect
Shift: 1.0

Column Effect
Shift: 1.0

Edge Effect
Shift: 1.0
Iteration: 8

☒ Bowl Effect
Shift: 1.0
Ratio X/Y: 1.00

Generate



Generate Screening

Number of Plates: 1
Columns: 24
Rows: 16

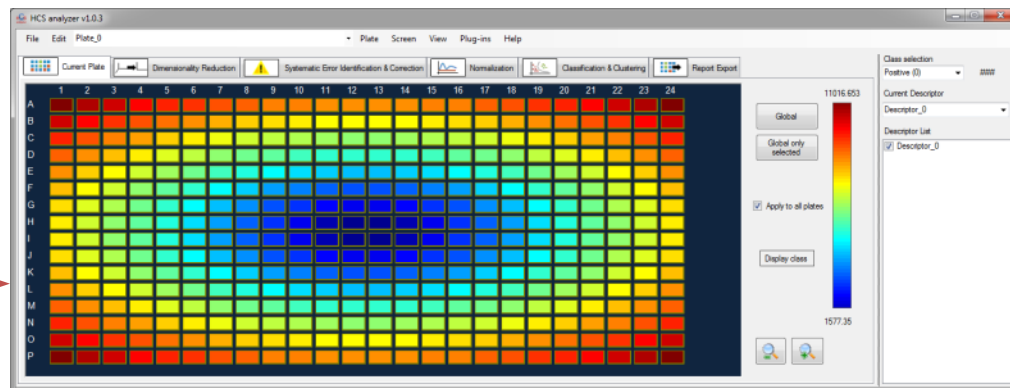
Row Effect
Shift: 1.0

Column Effect
Shift: 1.0

Edge Effect
Shift: 1.0
Iteration: 8

☒ Bowl Effect
Shift: 1.0
Ratio X/Y: 3.00

Generate



If a parameter **X** is checked, its value will vary from, increasing with a step defined in the options window.

Value distributions

Generate Screening

Number of Plates5

Columns16

Rows16

Compounds Distribution

Mean1000.0

Standard Deviation0.0

☒ Positive Ctrl

Column Index2

Mean1000.0

Standard Deviation50.0

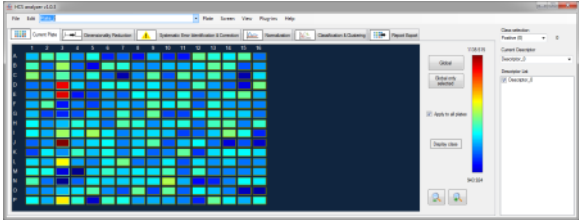
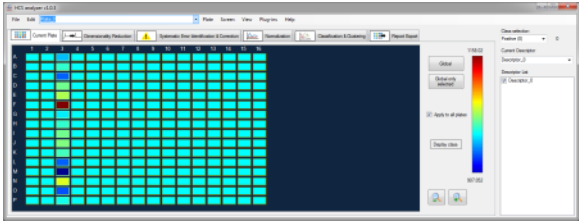
☐ Negative Ctrl

Column Index1

Mean200.0

Standard Deviation100.0

Generate



Options

Import / Export

Display

Clustering

Classification

Correlation matrix

Misc.

Errors Identif. & Correct.

Generate Screening

Variable parameter steps

Compound noise Std Dev.10.00

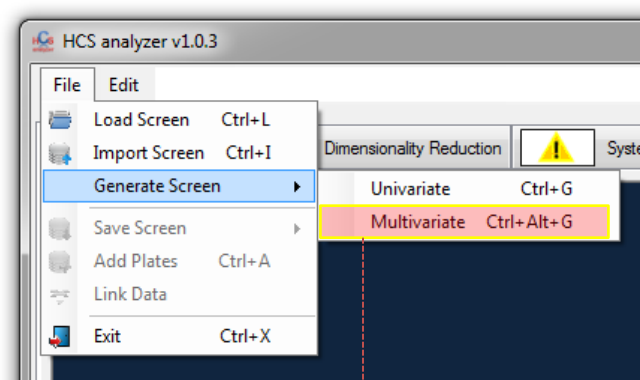
Row effect shift2.00

Ratio X/Y0.10

Diffusion4

Ok

Generating artificial
multivariate screening data



FormForMultivariateScreen

Dimension: 7

Plate Dimension

Number of Plates: 10

Columns: 24

Rows: 16

Name	Column	Selection	Mean0	Stdv0	Mean1	Stdv1	Mean2	Stdv2	Mean3	Stdv3	Mean4	Stdv4	Mean5	Stdv5	Mean6	Stdv6
Phenotype 0	0	<input checked="" type="checkbox"/>	0	20	0	20	0	20	0	20	0	20	0	20	0	20
Phenotype 1	1	<input checked="" type="checkbox"/>	50	20	50	20	50	20	50	20	50	20	50	20	50	20
Phenotype 2	Entire plate	<input checked="" type="checkbox"/>	100	20	100	20	100	20	100	20	100	20	100	20	100	20
Phenotype 3	3	<input type="checkbox"/>	150	20	150	20	150	20	150	20	150	20	150	20	150	20
Phenotype 4	4	<input type="checkbox"/>	200	20	200	20	200	20	200	20	200	20	200	20	200	20
Phenotype 5	5	<input type="checkbox"/>	250	20	250	20	250	20	250	20	250	20	250	20	250	20
Phenotype 6	6	<input type="checkbox"/>	300	20	300	20	300	20	300	20	300	20	300	20	300	20
Phenotype 7	7	<input type="checkbox"/>	350	20	350	20	350	20	350	20	350	20	350	20	350	20
Phenotype 8	8	<input type="checkbox"/>	400	20	400	20	400	20	400	20	400	20	400	20	400	20
Phenotype 9	9	<input type="checkbox"/>	450	20	450	20	450	20	450	20	450	20	450	20	450	20

Generate



FormForMultivariateScreen

Plate Dimension
Number of Plates: 10

Columns: 24
Rows: 16

Dimension: 7

Name	Column	Selection	Mean0	Stdv0	Mean1	Stdv1	Mean2	Stdv2	Mean3	Stdv3	Mean4	Stdv4	Mean5	Stdv5	Mean6	Stdv6
Phenotype 0	0	<input checked="" type="checkbox"/>	0	20	0	20	0	20	0	20	0	20	0	20	0	20
Phenotype 1	1	<input checked="" type="checkbox"/>	50	20	50	20	50	20	50	20	50	20	50	20	50	20
Phenotype 2	Entire plate	<input checked="" type="checkbox"/>	100	20	100	20	100	20	100	20	100	20	100	20	100	20
Phenotype 3	3	<input type="checkbox"/>	150	20	150	20	150	20	150	20	150	20	150	20	150	20
Phenotype 4	4	<input type="checkbox"/>	200	20	200	20	200	20	200	20	200	20	200	20	200	20
Phenotype 5	5	<input type="checkbox"/>	250	20	250	20	250	20	250	20	250	20	250	20	250	20
Phenotype 6	6	<input type="checkbox"/>	300	20	300	20	300	20	300	20	300	20	300	20	300	20
Phenotype 7	7	<input type="checkbox"/>	350	20	350	20	350	20	350	20	350	20	350	20	350	20
Phenotype 8	8	<input type="checkbox"/>	400	20	400	20	400	20	400	20	400	20	400	20	400	20
Phenotype 9	9	<input type="checkbox"/>	450	20	450	20	450	20	450	20	450	20	450	20	450	20

Generate

The dimension corresponds to the number of descriptors



FormForMultivariateScreen

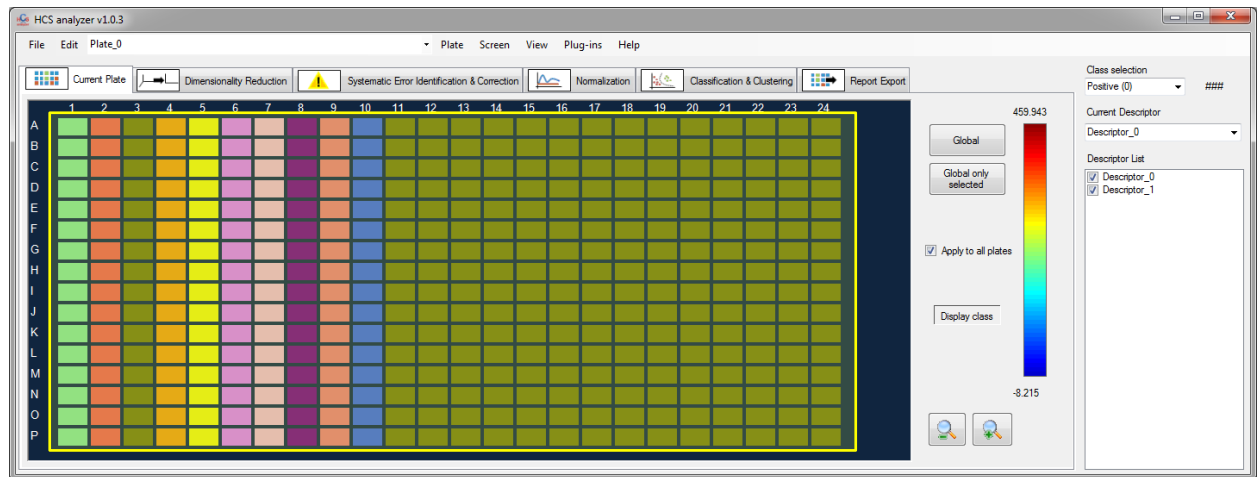
Dimension: 2

Plate Dimension
Number of Plates: 10
Columns: 24
Rows: 16

Name	Column	Selection	Mean0	Stdv0	Mean1	Stdv1
Phenotype 0	0	<input checked="" type="checkbox"/>	0	20	0	20
Phenotype 1	1	<input checked="" type="checkbox"/>	50	20	50	20
Phenotype 2	Entire plate	<input checked="" type="checkbox"/>	100	20	100	20
Phenotype 3	3	<input type="checkbox"/>	150	20	150	20
Phenotype 4	4	<input type="checkbox"/>	200	20	200	20
Phenotype 5	5	<input type="checkbox"/>	250	20	250	20
Phenotype 6	6	<input type="checkbox"/>	300	20	300	20
Phenotype 7	7	<input type="checkbox"/>	350	20	350	20
Phenotype 8	8	<input type="checkbox"/>	400	20	400	20
Phenotype 9	9	<input type="checkbox"/>	450	20	450	20

Generate

Up to 10 different clouds can be generated



FormForMultivariateScreen

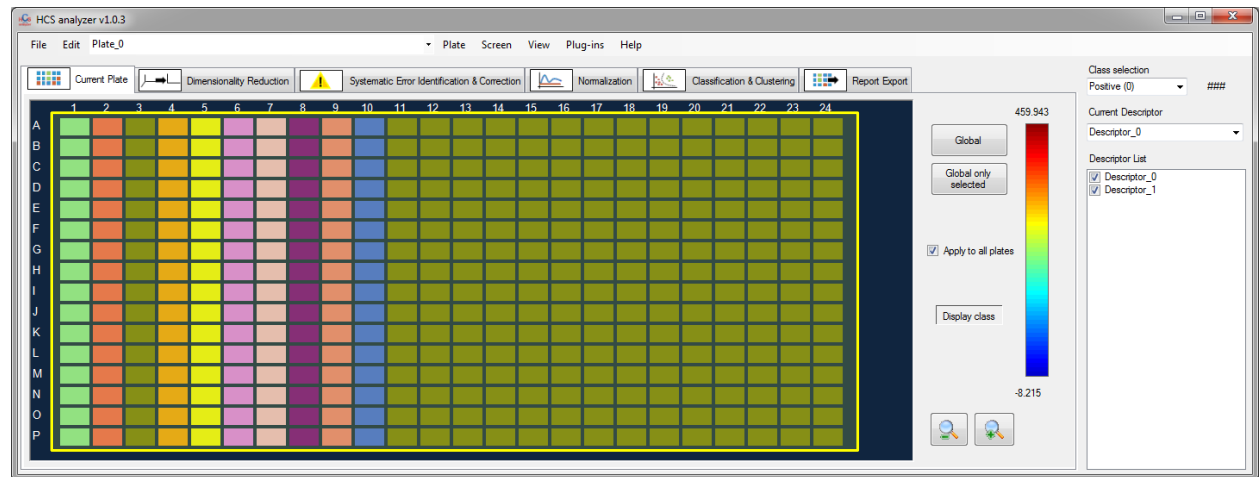
Dimension: 2

Plate Dimension
Number of Plates: 10
Columns: 24
Rows: 16

Name	Column	Selection	Mean0	Stdv0	Mean1	Stdv1
Phenotype 0	0	<input checked="" type="checkbox"/>	0	20	0	20
Phenotype 1	1	<input checked="" type="checkbox"/>	50	20	50	20
Phenotype 2	Entire plate	<input checked="" type="checkbox"/>	100	20	100	20
Phenotype 3	3	<input type="checkbox"/>	150	20	150	20
Phenotype 4	4	<input type="checkbox"/>	200	20	200	20
Phenotype 5	5	<input type="checkbox"/>	250	20	250	20
Phenotype 6	6	<input type="checkbox"/>	300	20	300	20
Phenotype 7	7	<input type="checkbox"/>	350	20	350	20
Phenotype 8	8	<input type="checkbox"/>	400	20	400	20
Phenotype 9	9	<input type="checkbox"/>	450	20	450	20

Generate

Their positions within the plate are defined by column



FormForMultivariateScreen

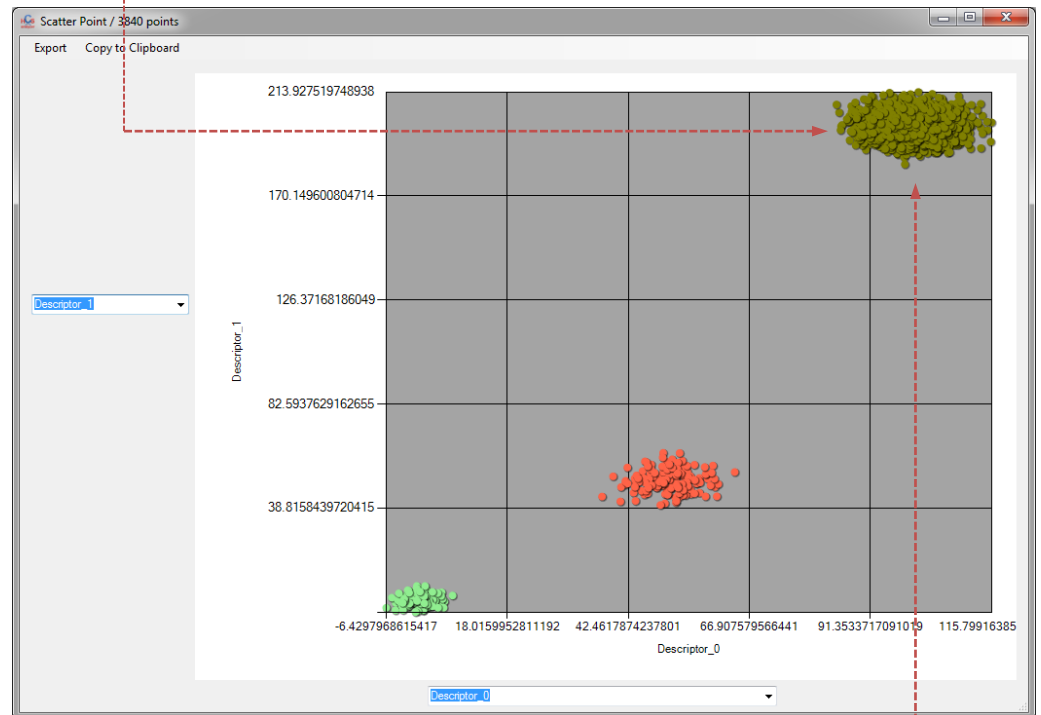
Dimension: 2

Plate Dimension
 Number of Plates: 10
 Columns: 24
 Rows: 16

	Name	Column	Selection	Mean0	Stdv0	Mean1	Stdv1
	Phenotype 0	0	<input checked="" type="checkbox"/>	0	5	0	5
▶	Phenotype 1	1	<input checked="" type="checkbox"/>	50	20	50	20
	Phenotype 2	Entire plate	<input checked="" type="checkbox"/>	100	20	200	20
	Phenotype 3	3	<input type="checkbox"/>	150	20	150	20
	Phenotype 4	4	<input type="checkbox"/>	200	20	200	20
	Phenotype 5	5	<input type="checkbox"/>	250	20	250	20
	Phenotype 6	6	<input type="checkbox"/>	300	20	300	20
	Phenotype 7	7	<input type="checkbox"/>	350	20	350	20
	Phenotype 8	8	<input type="checkbox"/>	400	20	400	20
	Phenotype 9	9	<input type="checkbox"/>	450	20	450	20

Generate

Each cloud (phenotype) is modeled by a Gaussian distribution defined by its means in every dimension



FormForMultivariateScreen

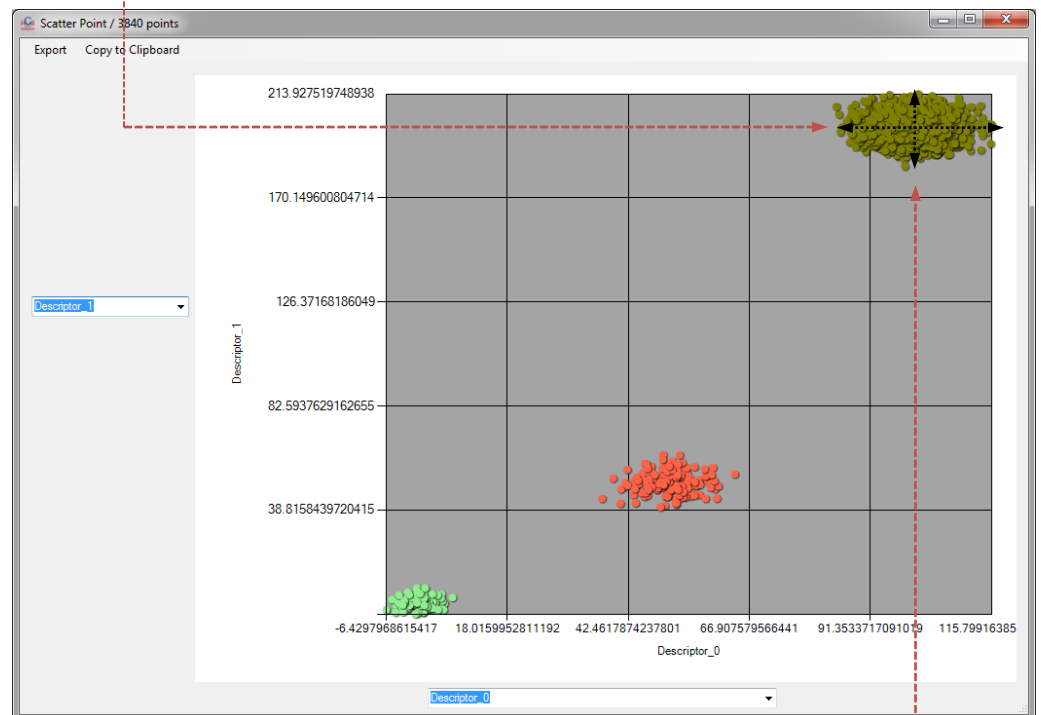
Dimension: 2

Plate Dimension
 Number of Plates: 10
 Columns: 24
 Rows: 16

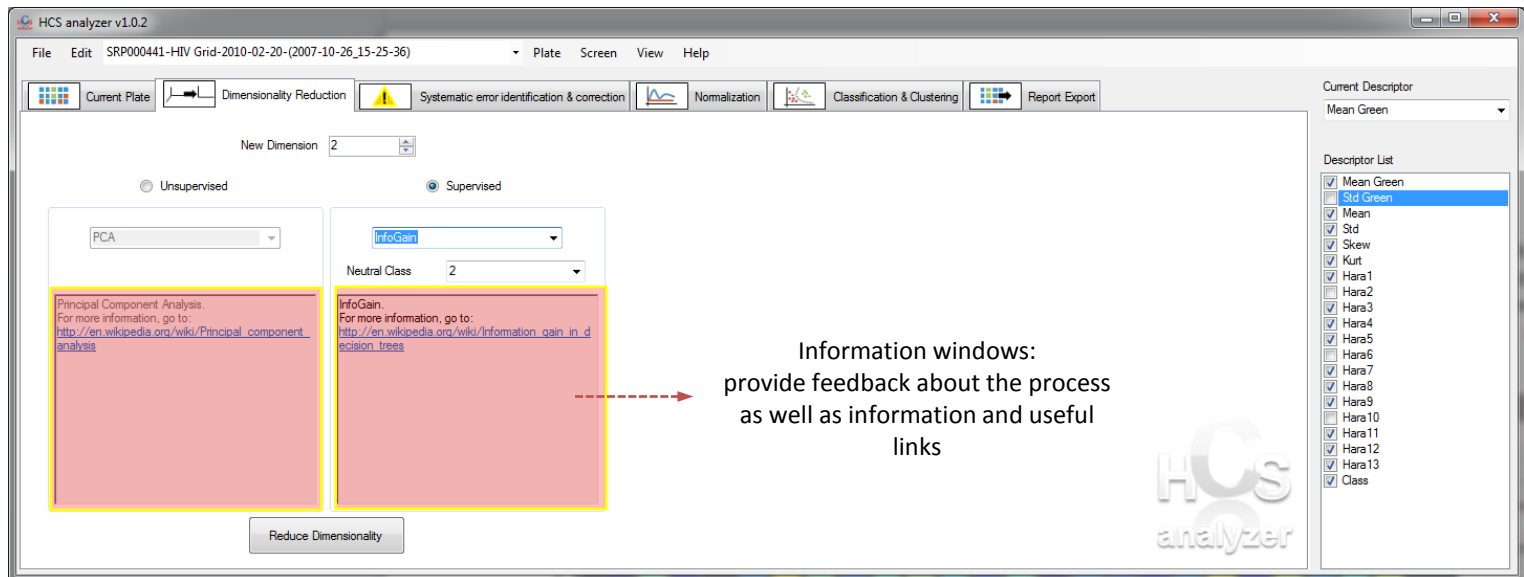
	Name	Column	Selection	Mean0	Stdv0	Mean1	Stdv1
	Phenotype 0	0	<input checked="" type="checkbox"/>	0	5	0	5
▶	Phenotype 1	1	<input checked="" type="checkbox"/>	50	20	50	20
	Phenotype 2	Entire plate	<input checked="" type="checkbox"/>	100	20	200	20
	Phenotype 3	3	<input type="checkbox"/>	150	20	150	20
	Phenotype 4	4	<input type="checkbox"/>	200	20	200	20
	Phenotype 5	5	<input type="checkbox"/>	250	20	250	20
	Phenotype 6	6	<input type="checkbox"/>	300	20	300	20
	Phenotype 7	7	<input type="checkbox"/>	350	20	350	20
	Phenotype 8	8	<input type="checkbox"/>	400	20	400	20
	Phenotype 9	9	<input type="checkbox"/>	450	20	450	20

Generate

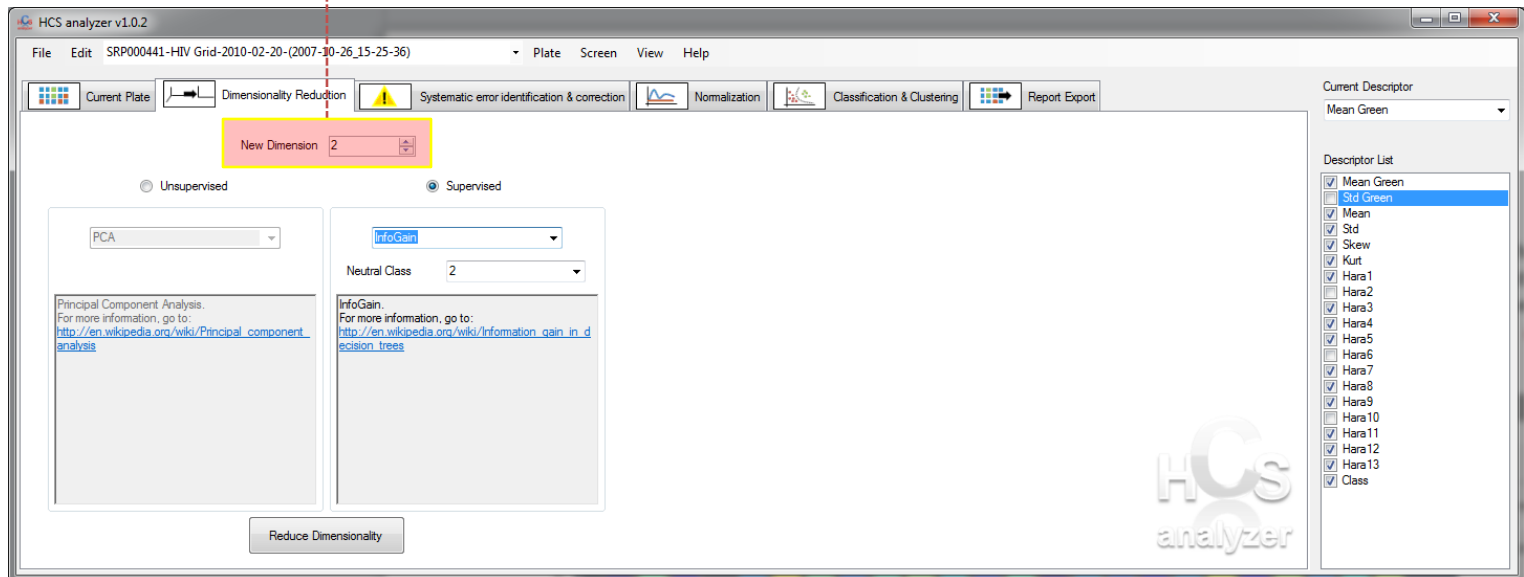
As well as its variances.



Dimensionality reduction



Desired new dimension



HCS analyzer v1.0.2

File Edit SRP000441-HIV Grid-2010-02-20-(2007-10-26_15-25-36) Plate Screen View Help

Current Plate Dimensionality Reduction Systematic error identification & correction Normalization Classification & Clustering Report Export

New Dimension 2

☐ Unsupervised ☒ Supervised

PCA

Principal Component Analysis.
For more information, go to:
http://en.wikipedia.org/wiki/Principal_component_analysis

InfoGain

Neutral Class 2

InfoGain.
For more information, go to:
http://en.wikipedia.org/wiki/Information_gain_in_decision_trees

Reduce Dimensionality

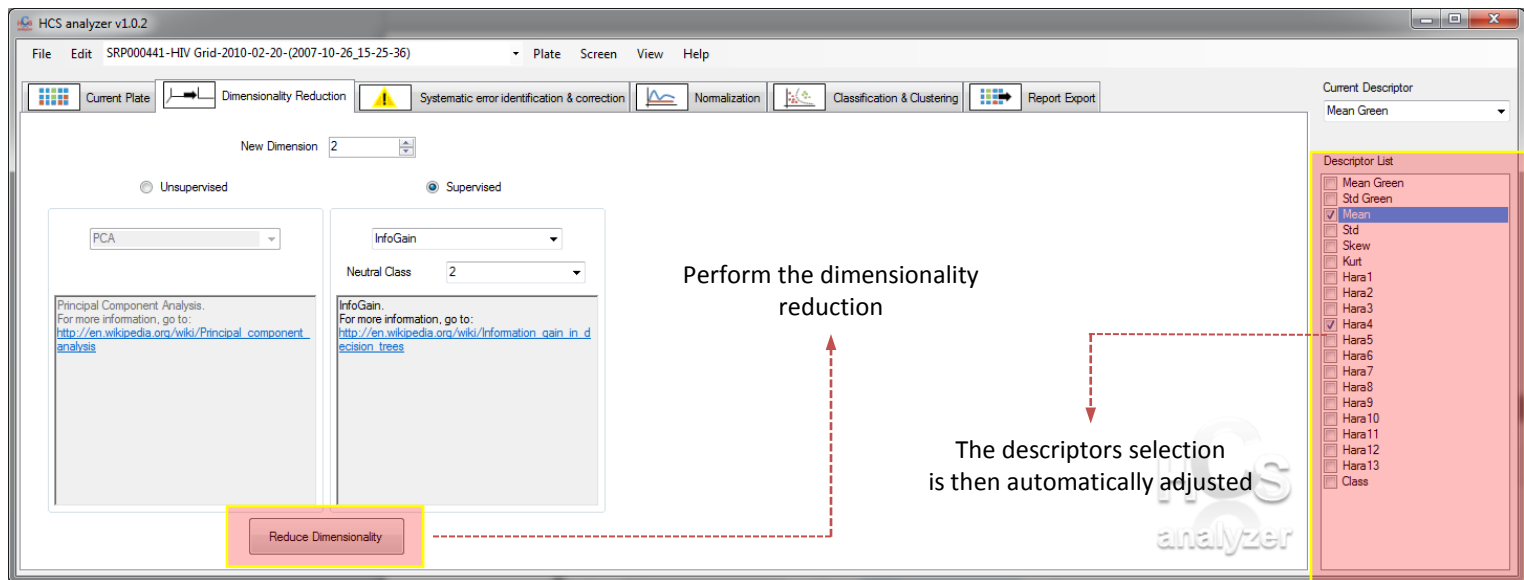
Current Descriptor
Mean Green

Descriptor List

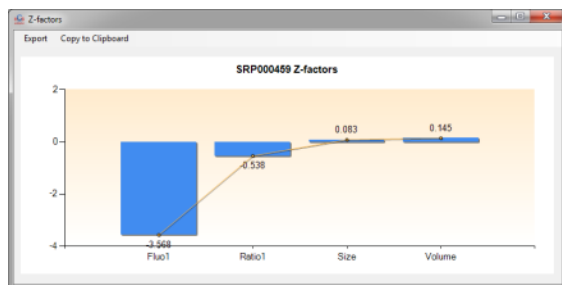
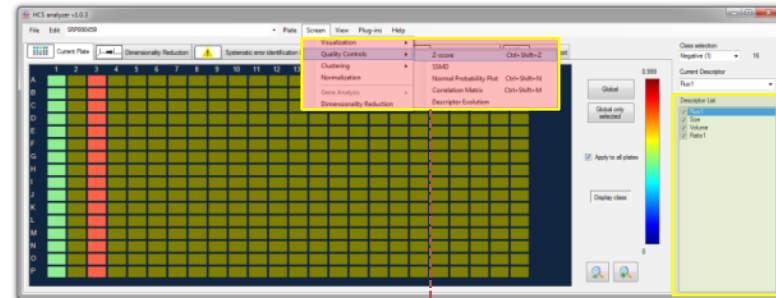
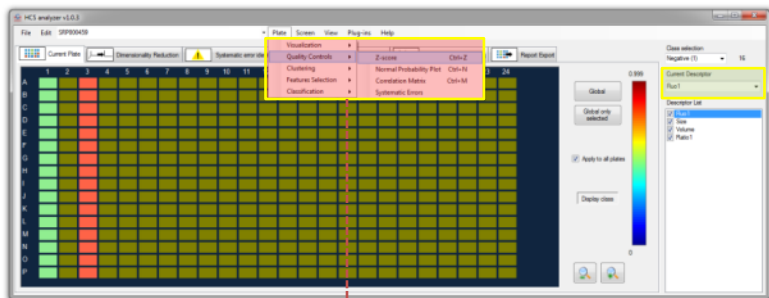
- ☒ Mean Green
- ☒ Std Green
- ☒ Mean
- ☒ Std
- ☒ Skew
- ☒ Kurt
- ☒ Hara1
- ☒ Hara2
- ☒ Hara3
- ☒ Hara4
- ☒ Hara5
- ☐ Hara6
- ☒ Hara7
- ☒ Hara8
- ☒ Hara9
- ☐ Hara10
- ☒ Hara11
- ☒ Hara12
- ☒ Hara13
- ☒ Class

Feature selection approaches:
Unsupervised: use all the activated wells of the activated plates to reduce the dimension
Supervised: keep the descriptors required to cluster the classes (but the neutral class)

HCS analyzer

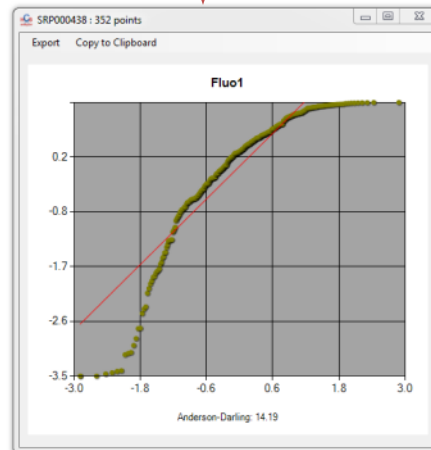
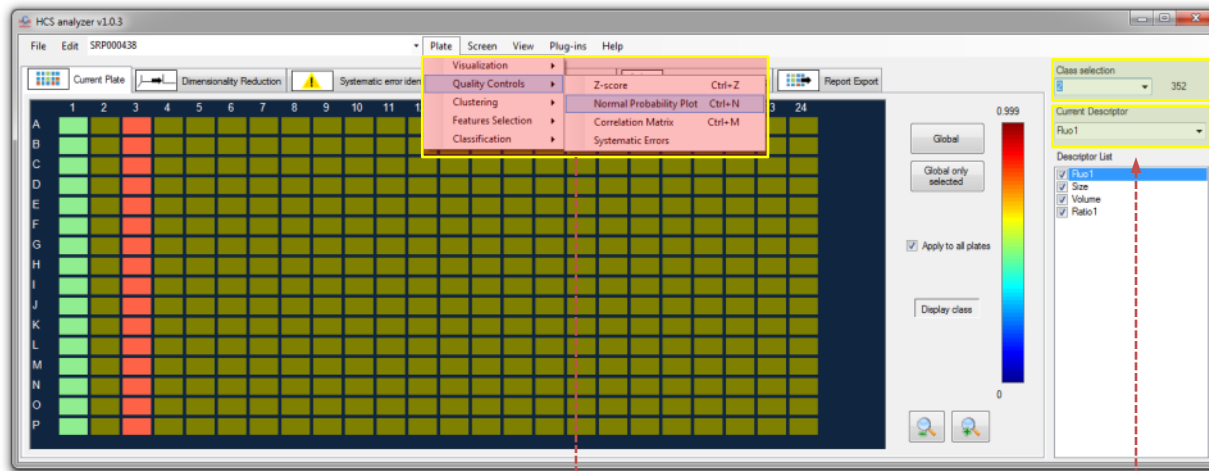


Quality controls



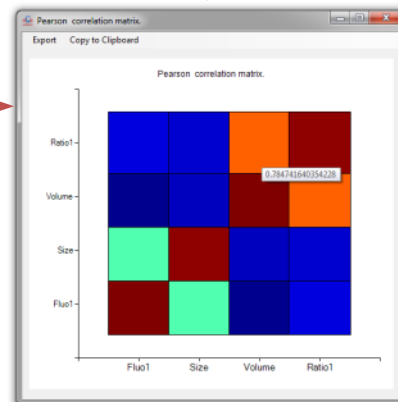
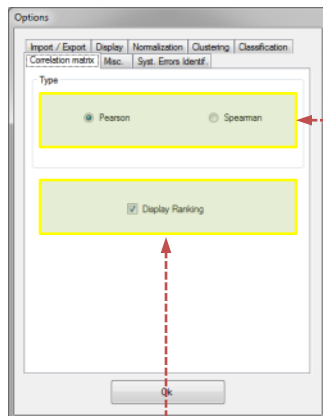
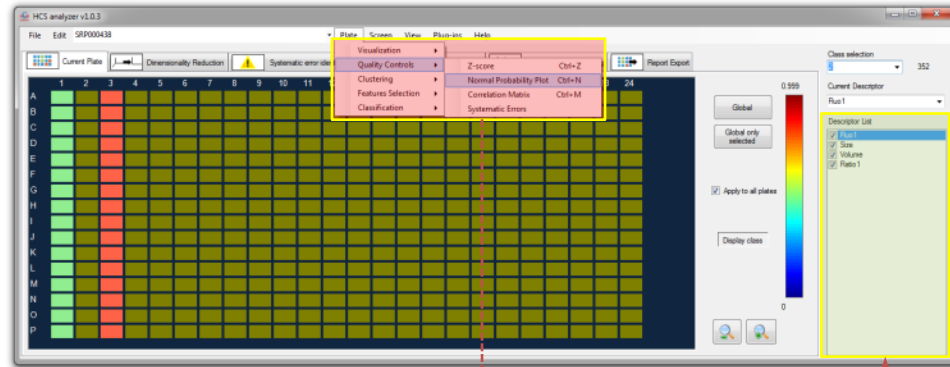
Display the sorted Z-factors of
the current plate for each
selected descriptor

Display the sorted Z-factors of the selected
descriptor for all the active plates

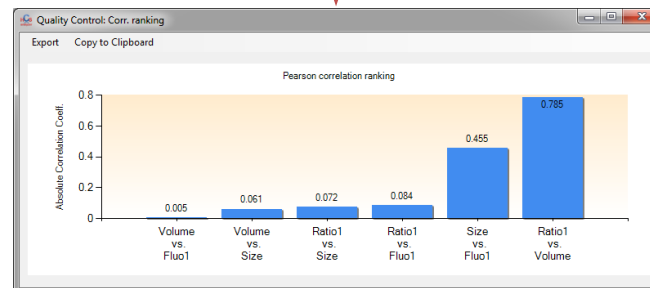


Display the normal probability plot of the current selected descriptor values among the set of points of the selected class.

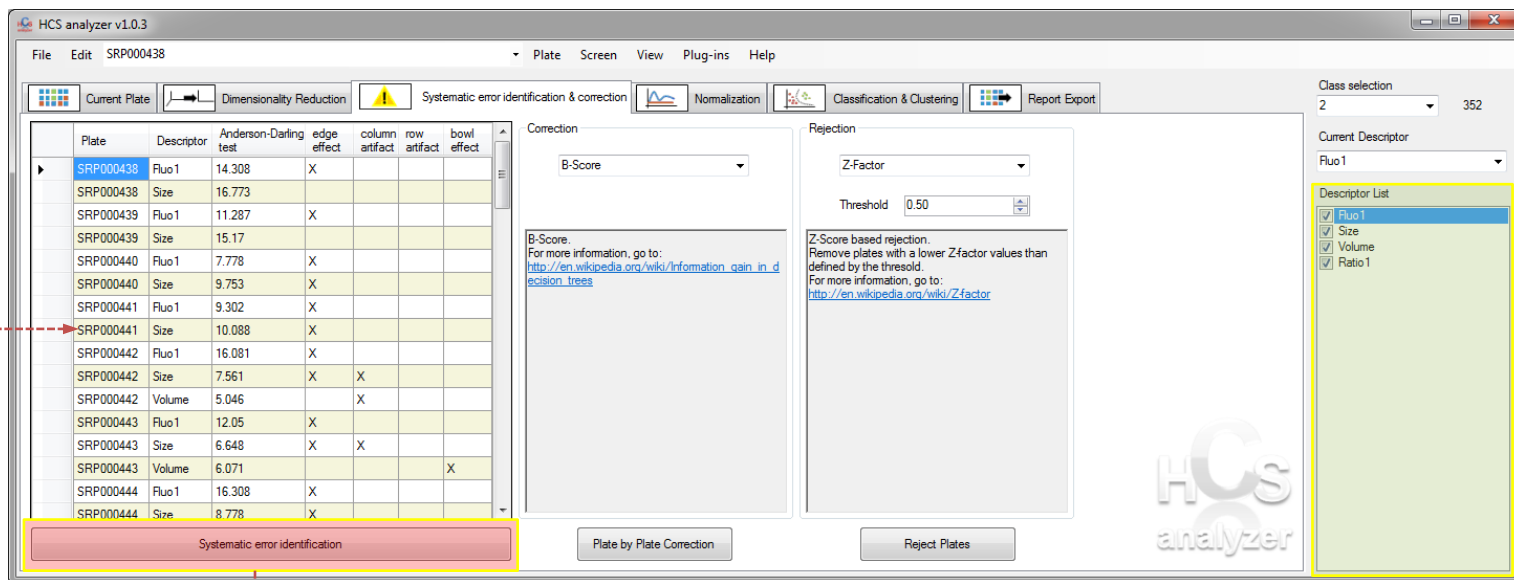
Note: operate the same way for the entire screen.



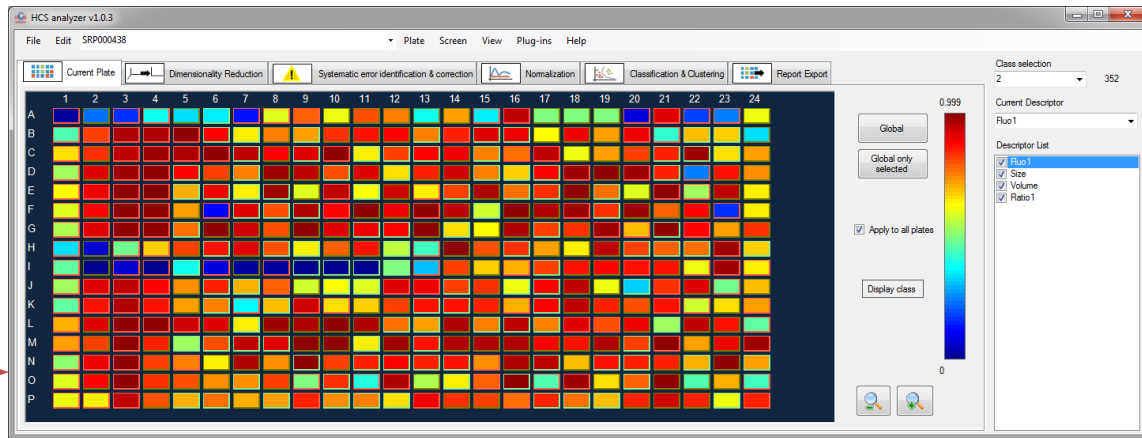
Display the correlation matrix of the active descriptors



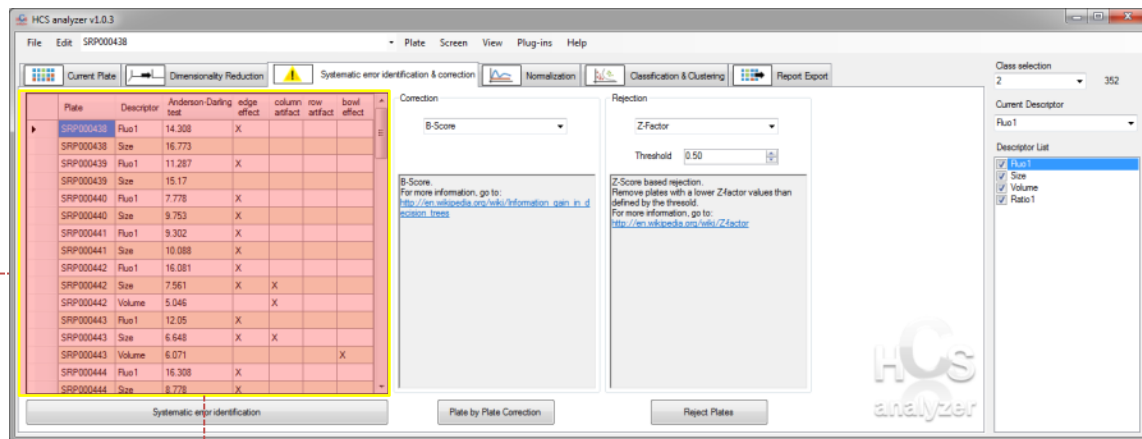
And the ranked corresponding histogram (optional)



Identify the potential systematic errors for each selected plates on each active descriptor



Double click
on a row
display the
corresponding
readouts



Systematic errors identification
parameters can be changed by the
options window

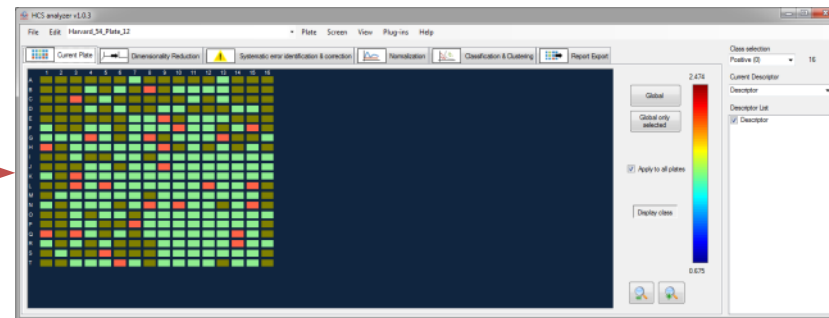
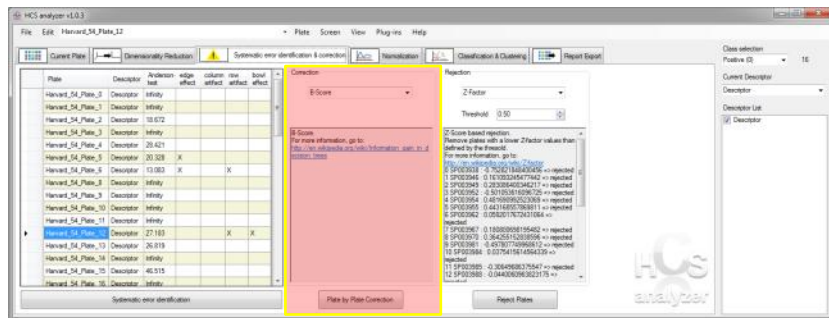
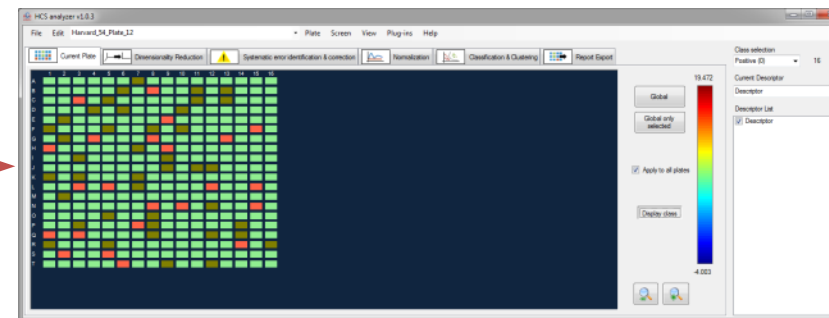
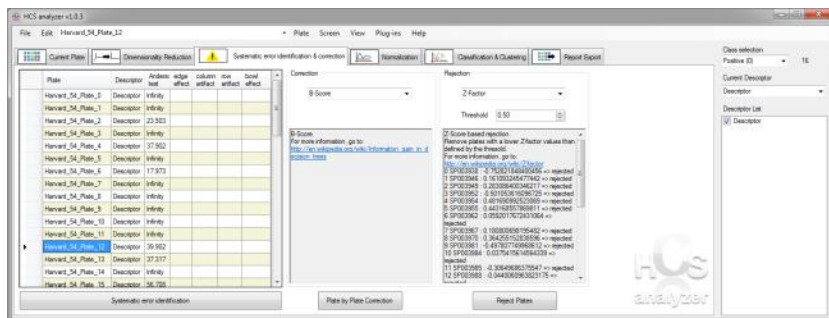
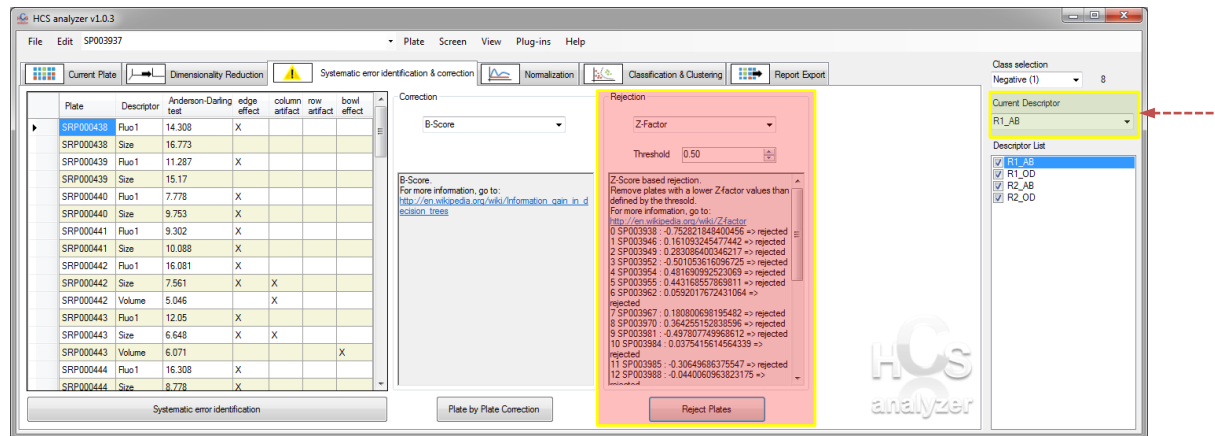


Plate by plate, and descriptor by descriptor, correction procedure can be performed using the dedicated function



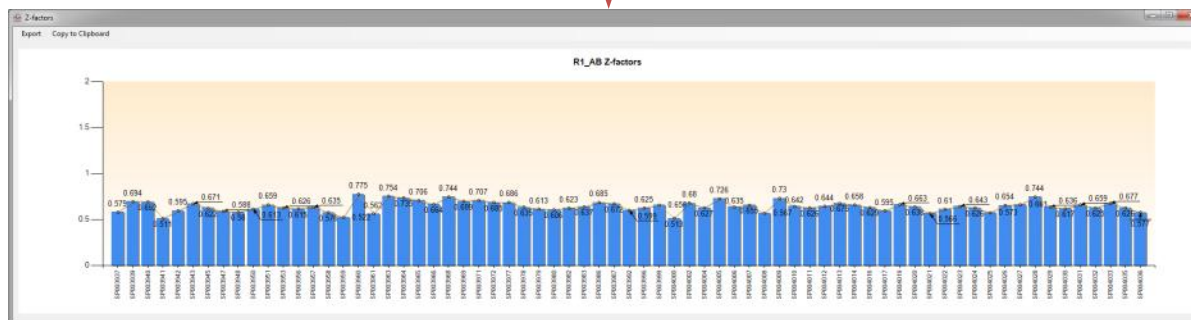


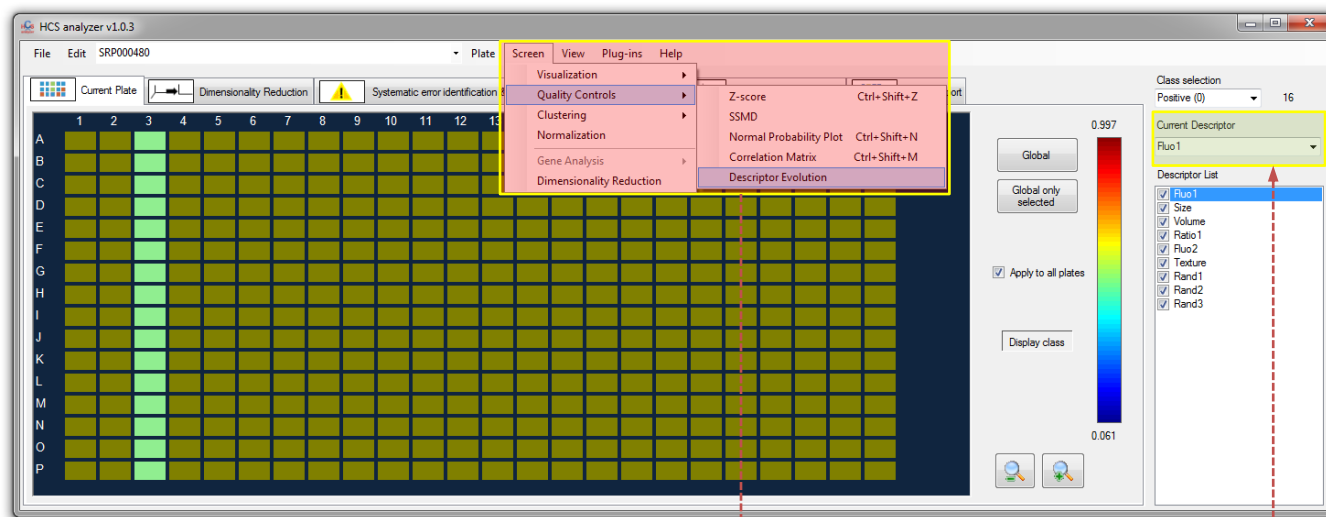
Plates can be rejected
regarding a chosen parameter
(here Z-factor on the current descriptor)

before

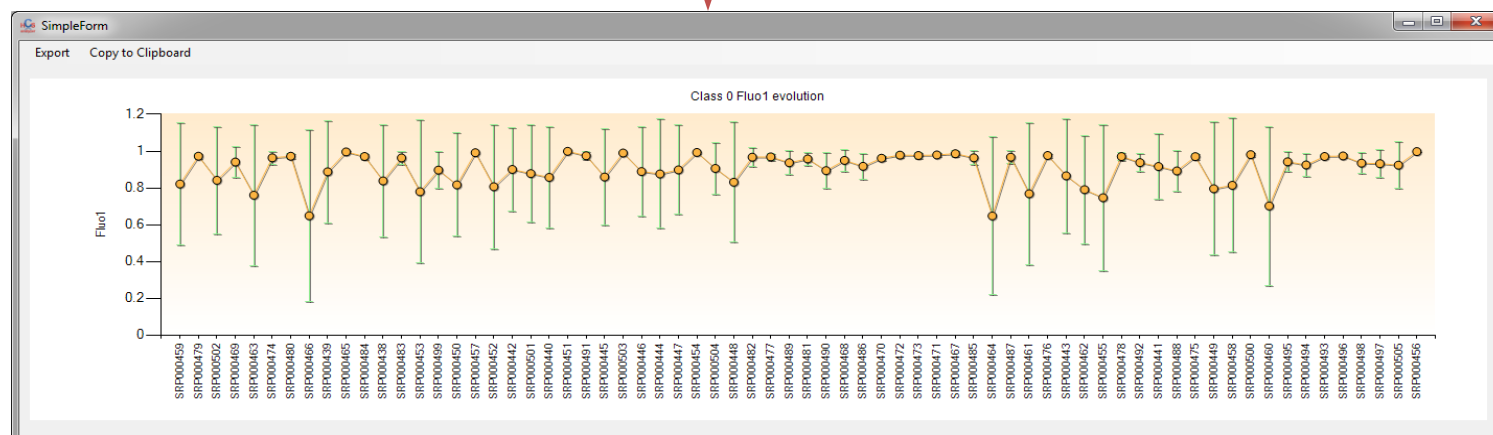


after



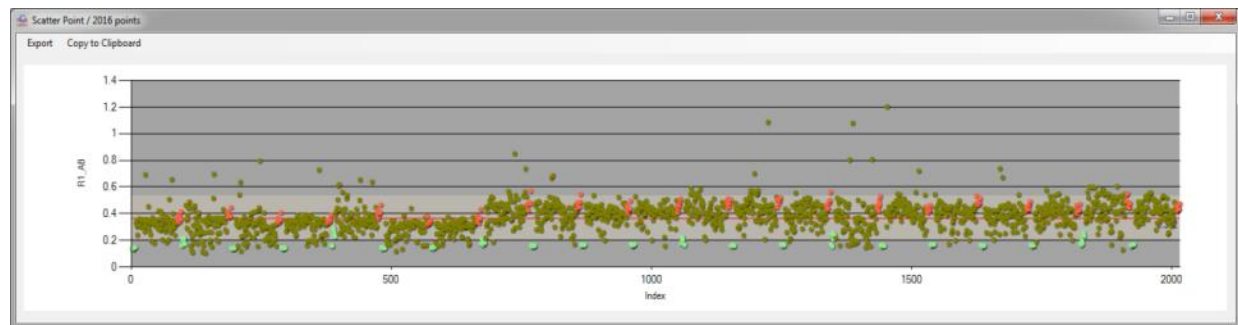
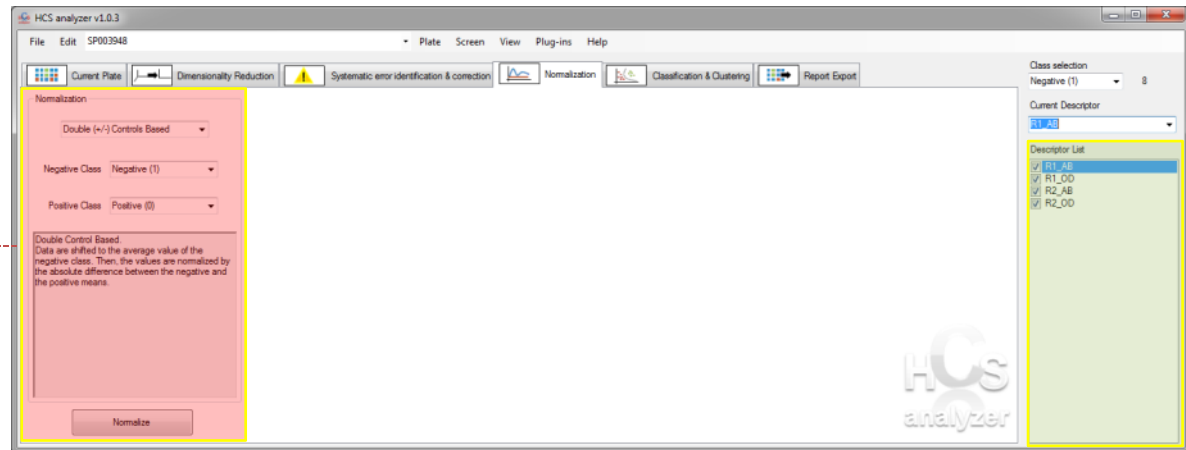


Evolution (average and standard deviation)
of the current descriptor
within a defined class
can be monitored to identify
abnormalities

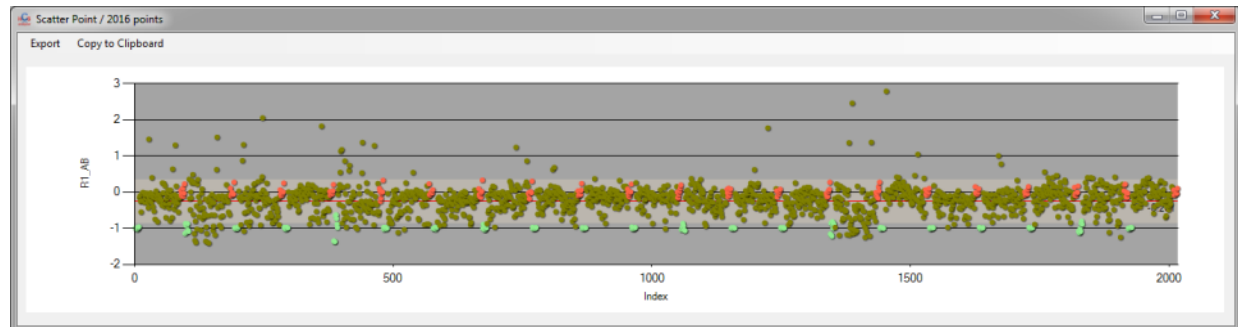


Normalization

Various approaches
for data normalization
of the screening data
are available
(controls based or not)

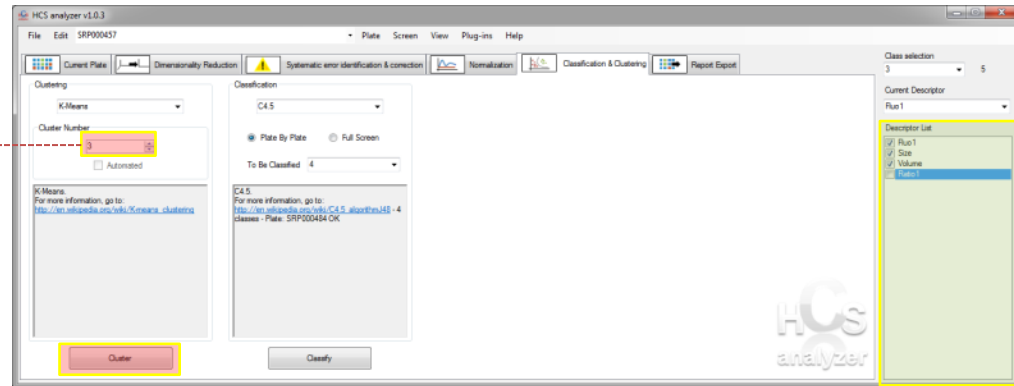


before

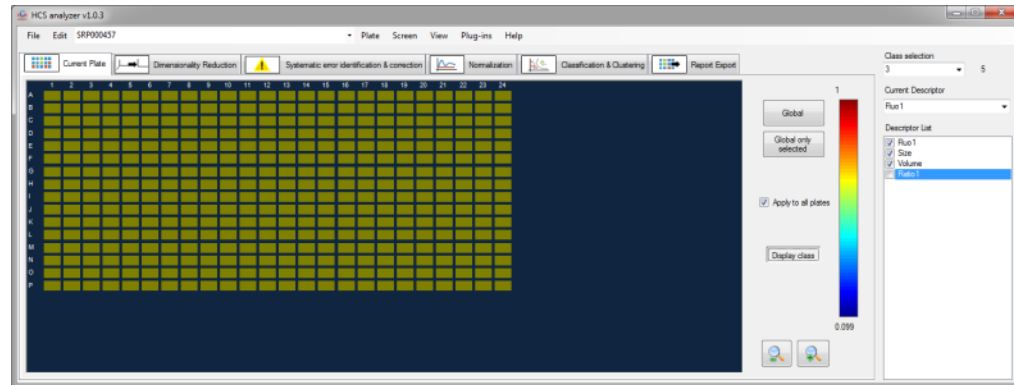


after

Clustering and classification



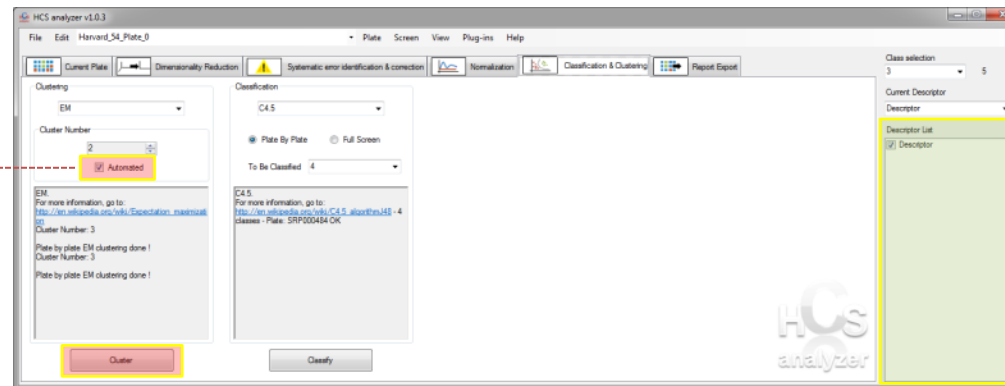
The user has to define the desired cluster number.



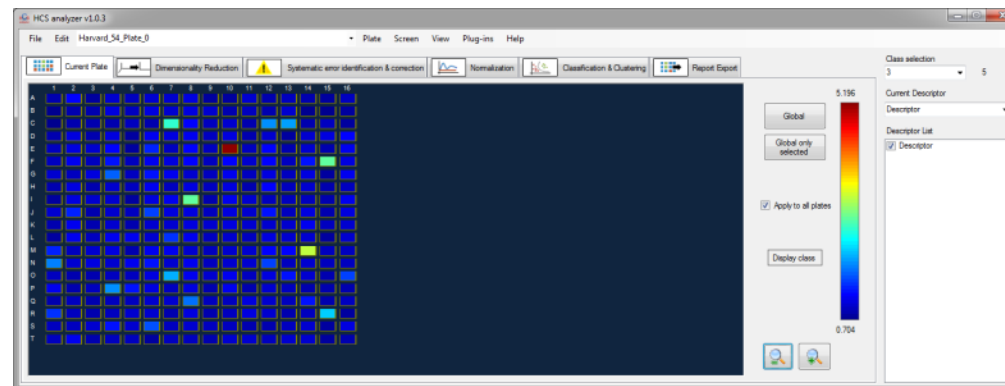
before



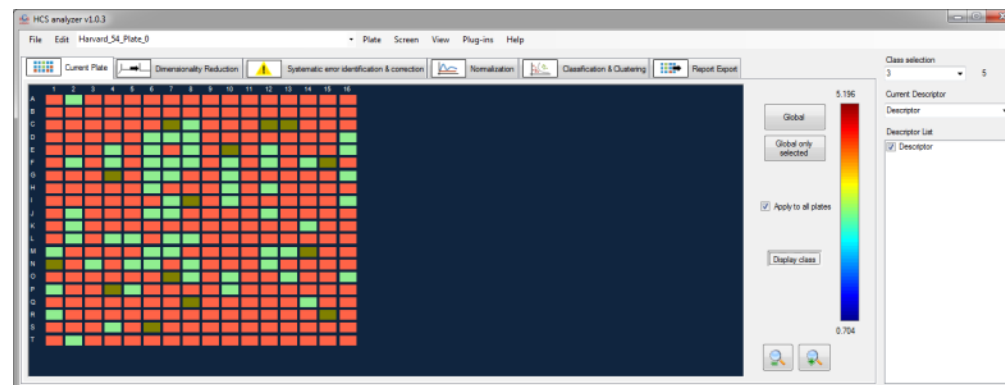
after



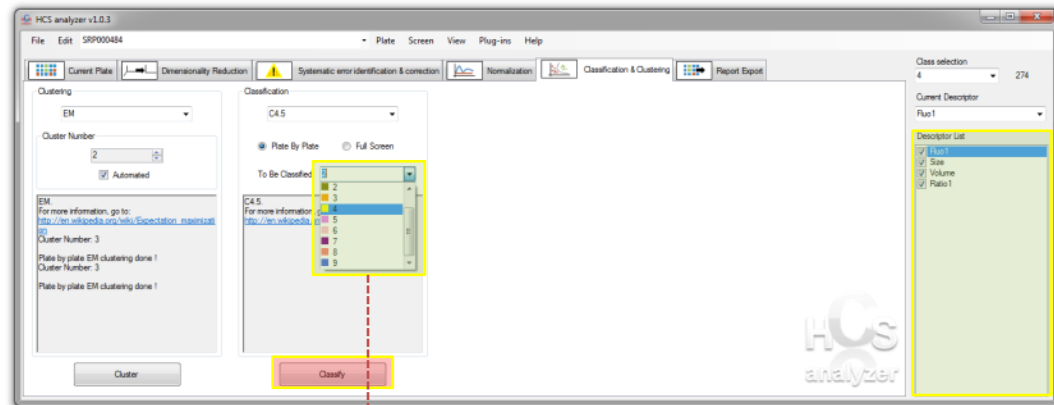
Some clustering methods allow automated evaluation of the optimum number of clusters.
Note: if more than 10 classes are detected, the clustering is not operated.



Original readouts

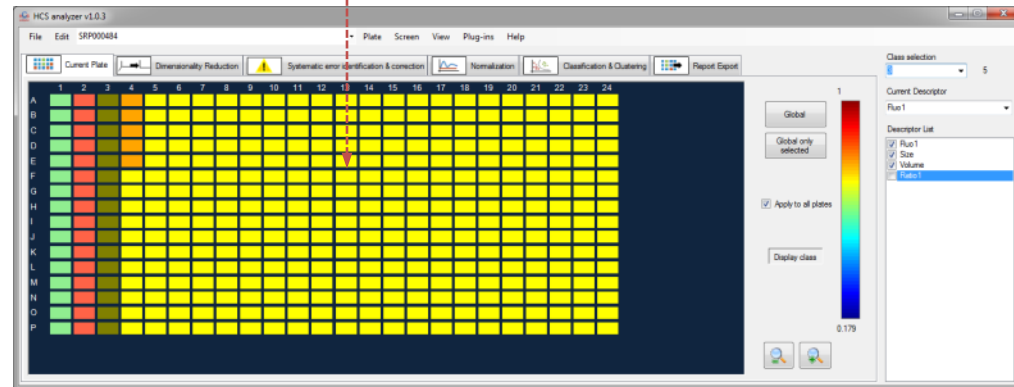


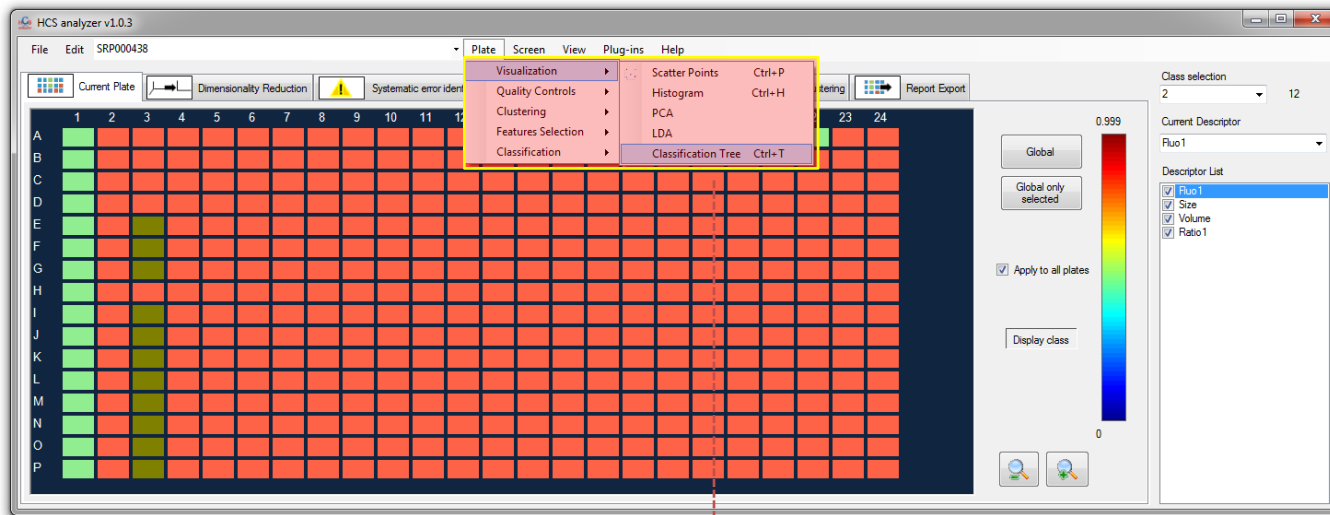
Clustering (here: 3 classes have identified)



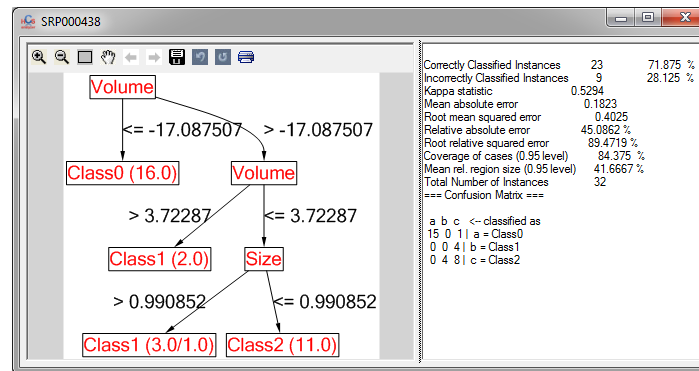
This class will not be used for the learning, but will be classified.

The user has to define the classes for the training.
Plate by plate: the training step is performed on the each plate independently.

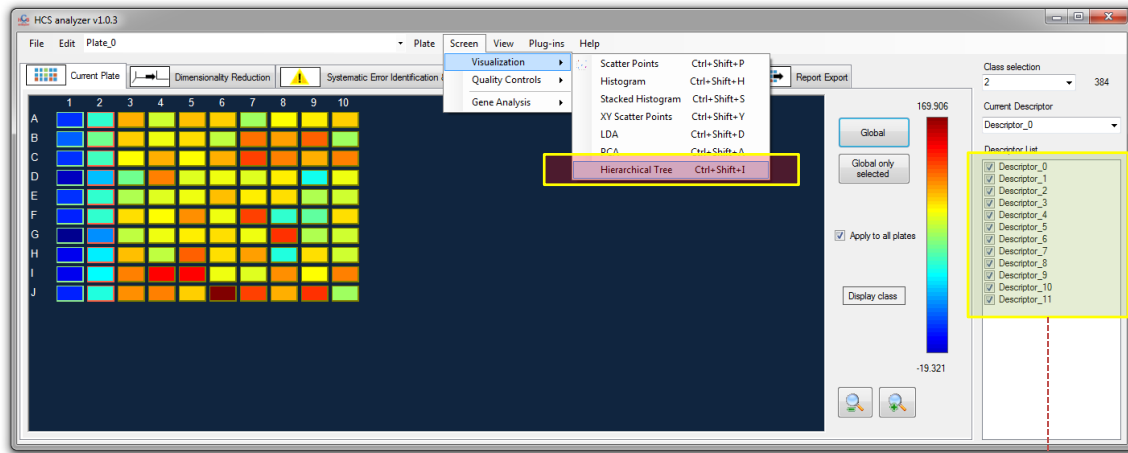




If the classification operated is tree based (C4.5) a tree diagram is affected for each plate.

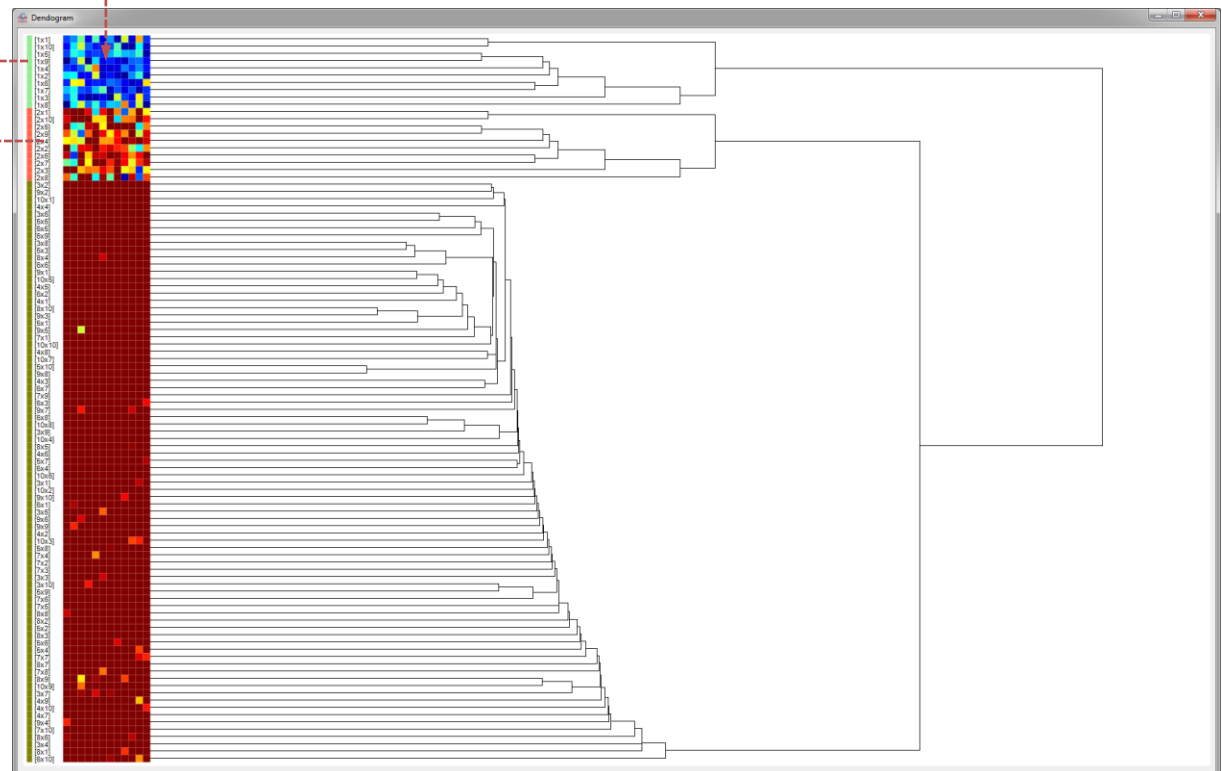


Hierarchical Tree visualization

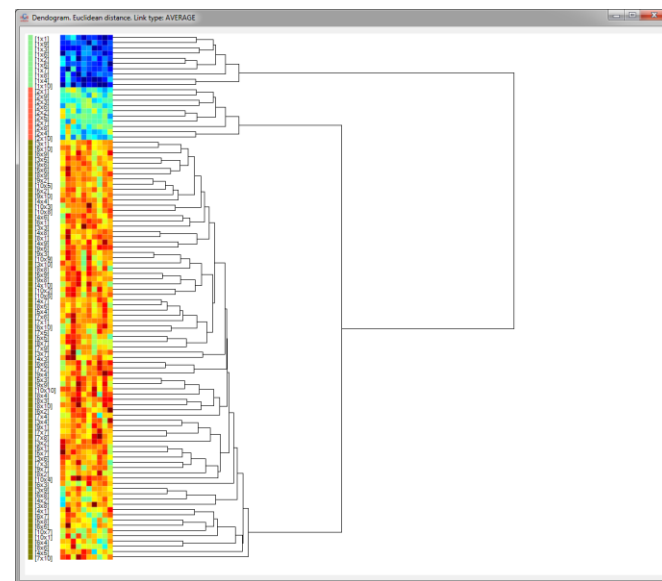
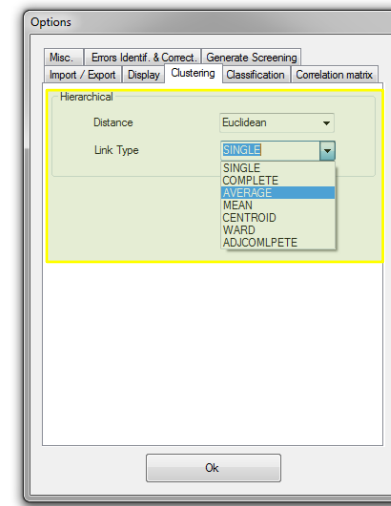
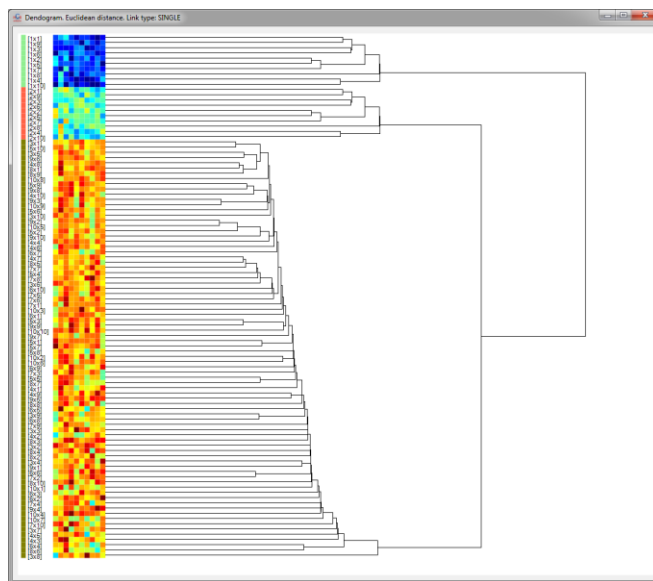
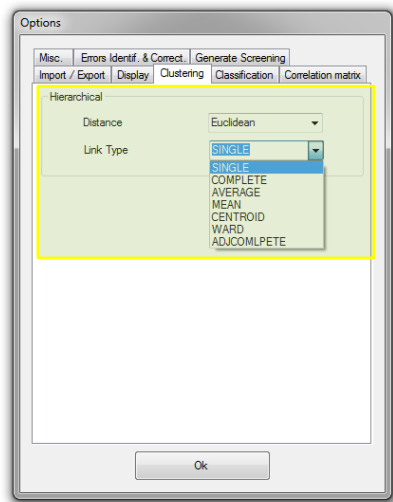


Class color

Well position



Note: this operation can be time consuming for large number of data



Pathways analysis

Import

Plate Dimensions

Columns: 24

Rows: 16

Data Name	Selection	Type	Readout 0	Readout 1	Readout 2
Plate384	<input checked="" type="checkbox"/>	Plate name	SRP000459	SRP000479	SRP000502
Well 384w	<input checked="" type="checkbox"/>	Well position	D24	P20	G11
Cat	<input type="checkbox"/>	Descriptor	Druggable	Druggable	Druggable
Catalog Number	<input type="checkbox"/>	Descriptor	1	2	3
Gene Symbol	<input type="checkbox"/>	Descriptor	1	2	3
Description	<input type="checkbox"/>	Descriptor	adrenocortical dy	deleted in esoph	hypothetical nm
Locus ID	<input checked="" type="checkbox"/>	Locus ID	65057	115123	57574
Fluo1	<input type="checkbox"/>	Descriptor	0.8228594	0.7233504	0.9090863
Size	<input checked="" type="checkbox"/>	Descriptor	0.9823682	0.9870385	0.7240621
Volume	<input checked="" type="checkbox"/>	Descriptor	59.26911984	183.9027118	137.0042838
Ratio1	<input checked="" type="checkbox"/>	Descriptor	144.2518279	234.0326818	139.0108669
Fluo2	<input checked="" type="checkbox"/>	Descriptor	90.0408859	176.5919403	74.81596763
Tissue	<input type="checkbox"/>	Descriptor	104.6324222	231.6572388	106.0801458

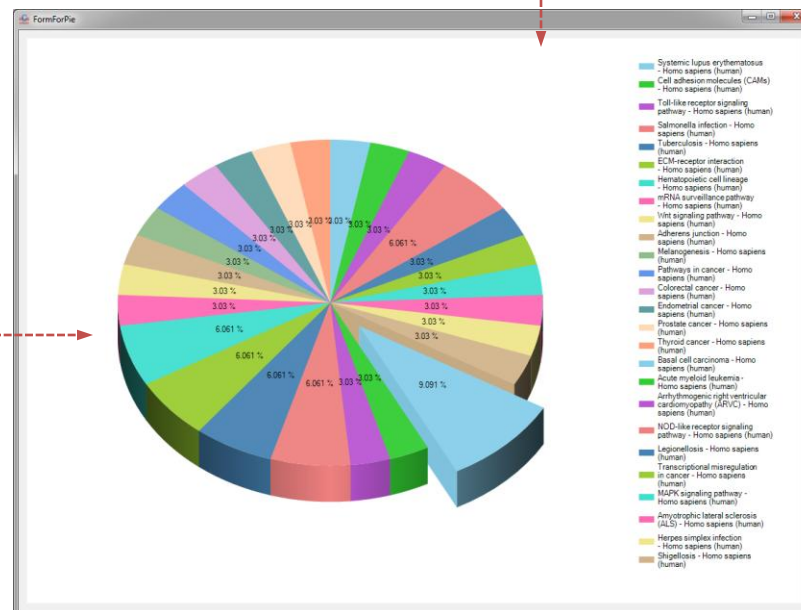
Ok

Locus IDs have to be associated to each well

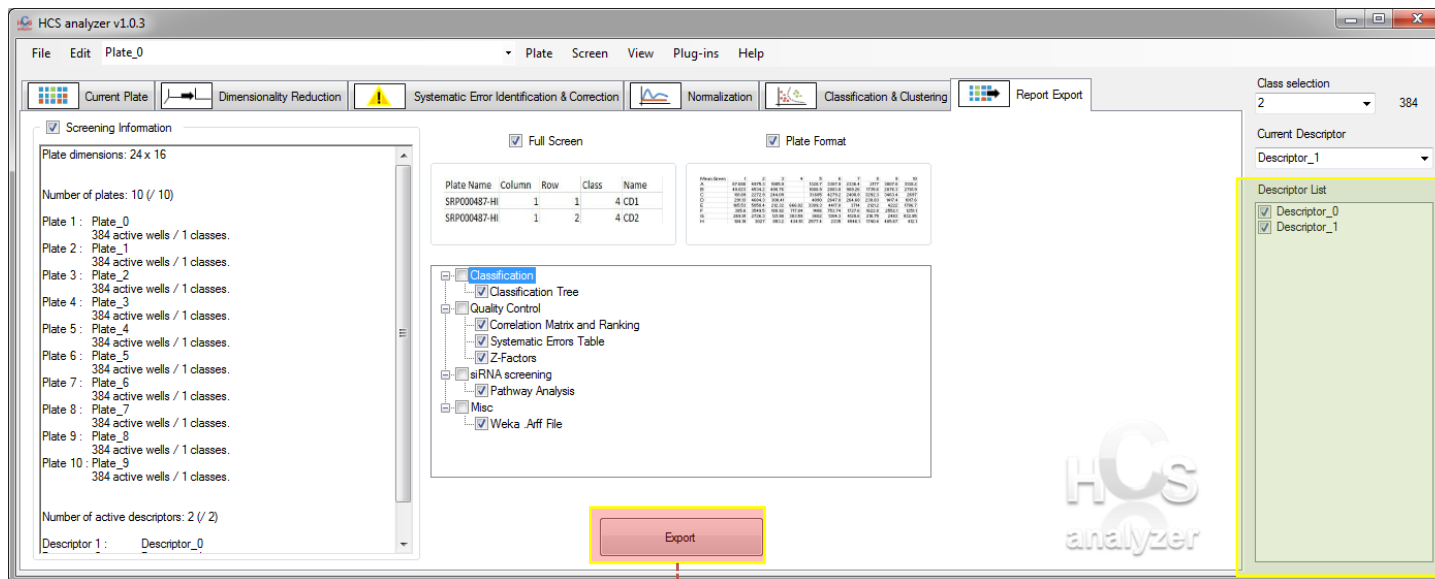


Note: this operation requires internet connection

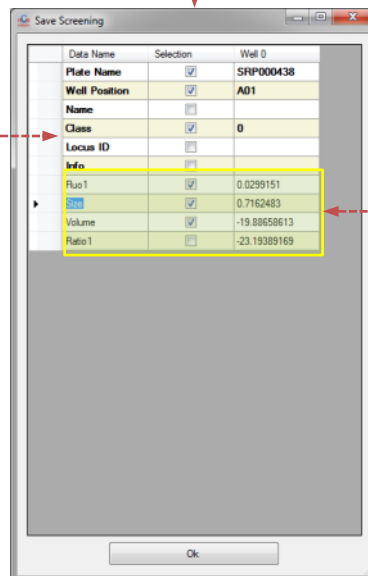
Recurrence of each specific pathway



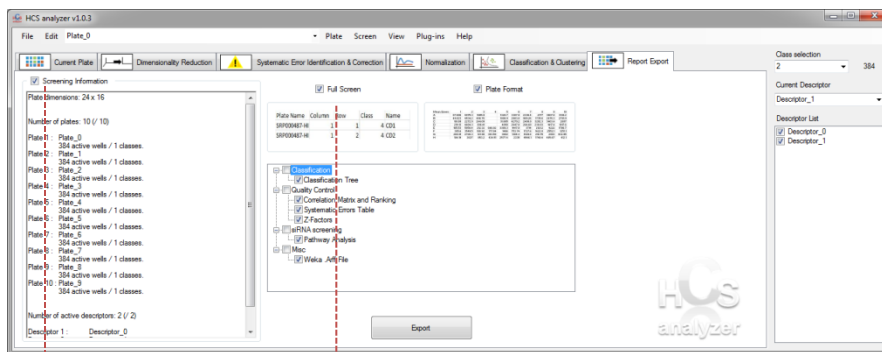
Export



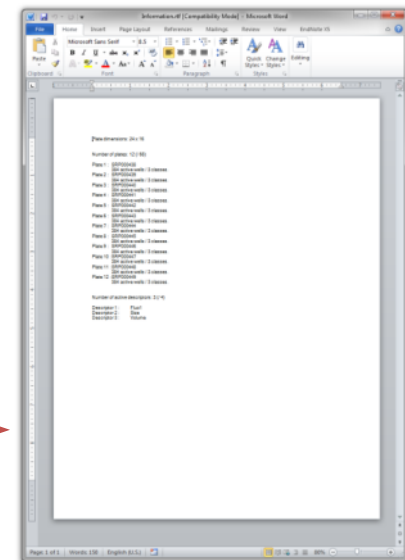
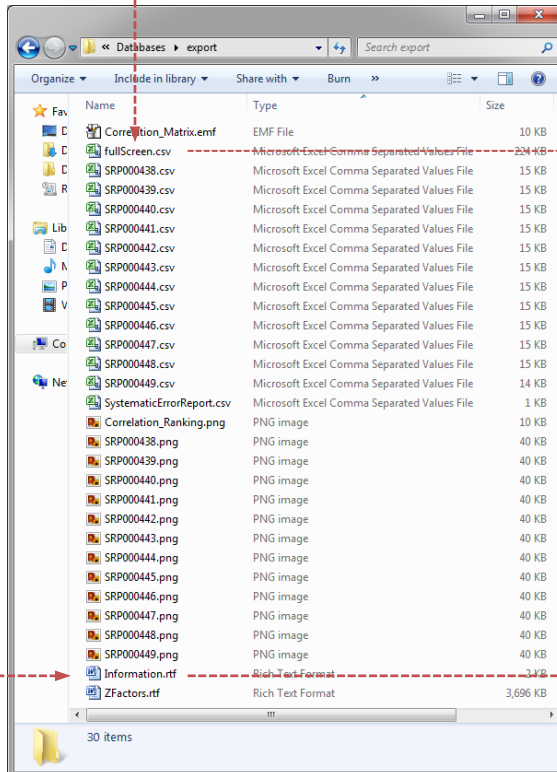
At this stage, names can be modified

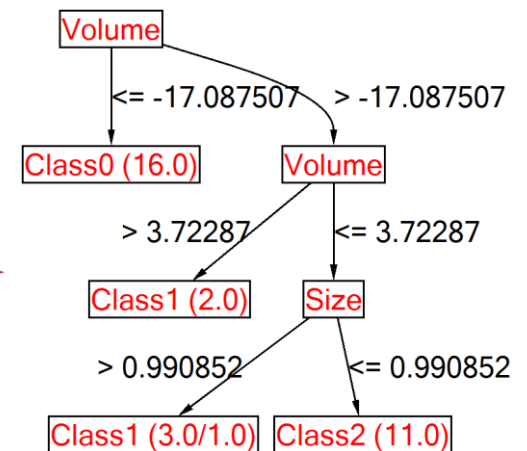
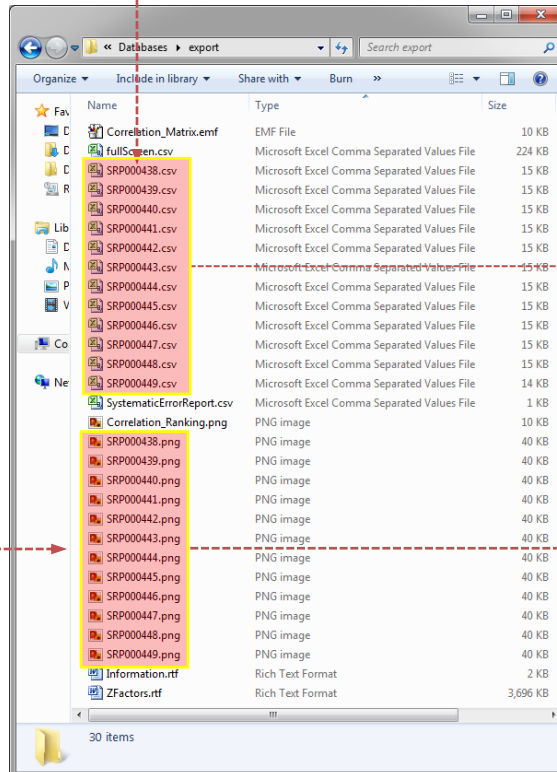
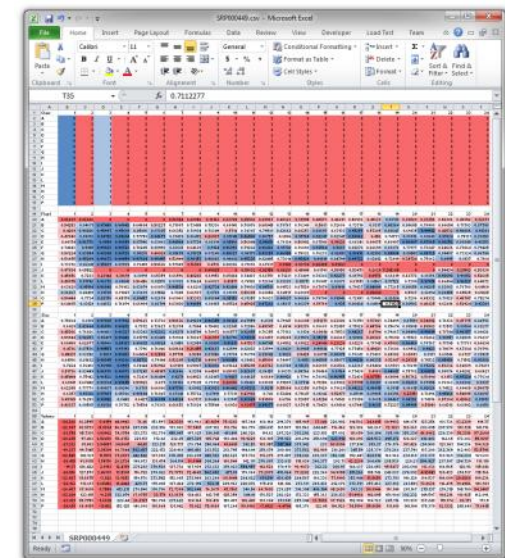
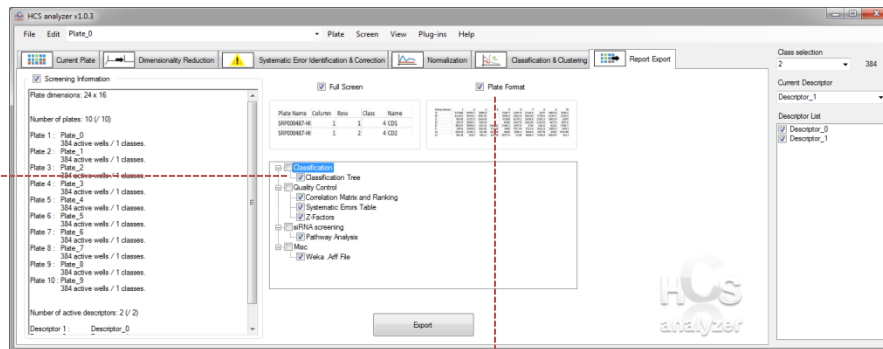


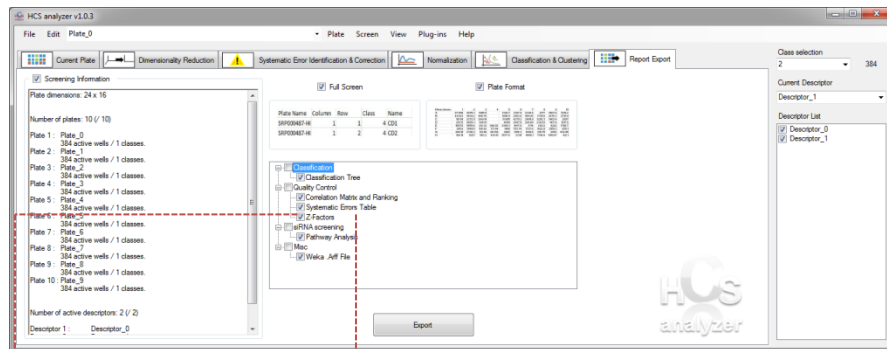
Descriptors are checked regarding the selection but can be modified for the export purpose



Well Position	Class	Pos	Real Size	Volume
A01	0	0.02992	0.71625	-18.8896
B01	0	0.4584	0.92945	-10.5266
C01	0	0.85564	0.67536	-17.365
D01	0	0.58901	0.91971	-17.2936
E01	0	0.85164	0.78725	-13.3757
F01	0	0.58716	0.84613	-18.6867
G01	0	0.54703	0.6222	-18.8075
H01	0	0.33988	0.71788	-19.1103
I01	0	0.46348	0.61562	-17.0875
J01	0	0.53052	0.67328	-18.6184
K01	0	0.47085	0.62584	-17.7694
L01	0	0.706	0.89047	-17.6202
M01	0	0.71305	0.73737	-18.7137
N01	0	0.5127	0.81526	-10.4122
O01	0	0.80041	0.67228	-19.9777
P01	0	0.60873	0.75476	-21.4674
Q01	0	0.22836	0.87776	-19.9178
R01	0	0.81689	0.88013	-18.4175
S01	0	0.62752	0.89013	-103.984
T01	0	0.91343	0.86346	-113.464
U01	0	0.89056	0.89697	-97.7306
V01	0	0.87903	0.91334	-114.419
W01	0	0.91355	0.93167	-94.8381
X01	0	0.07824	0.93157	-87.4028
Y01	0	0.01228	0.91893	-94.4448
Z01	0	0.91486	0.97551	-104.476
A02	2	0.84855	0.87667	-94.6399
B02	2	0.90623	0.80376	-133.265
C02	2	0.83349	0.91278	-101.439
D02	2	0.90568	0.86346	-97.9123
E02	2	0.88106	0.77993	-90.7418
F02	2	0.64688	0.86253	-94.9072
G02	2	0.10884	0.99125	-10.9501
H02	2	0.96458	0.99133	-6.16148
I02	2	0.94487	0.98269	-5.12075
J02	2	0.96033	0.9712	-4.42502
K02	2	0.99751	0.99083	-2.76456
L02	2	0.90342	0.97485	-0.55692







SystematicErrorReport.csv - Microsoft Excel

FileHomeInsertLayoutReferencesFormulasDataReviewViewSendToToolsTeam

Font

Paragraph

References

Formulas

Layout

References

Data

Review

View

SendTo

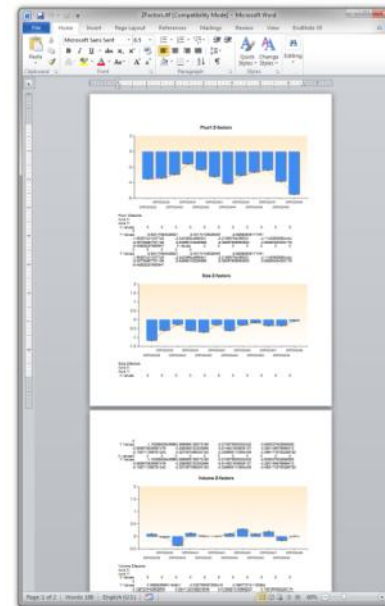
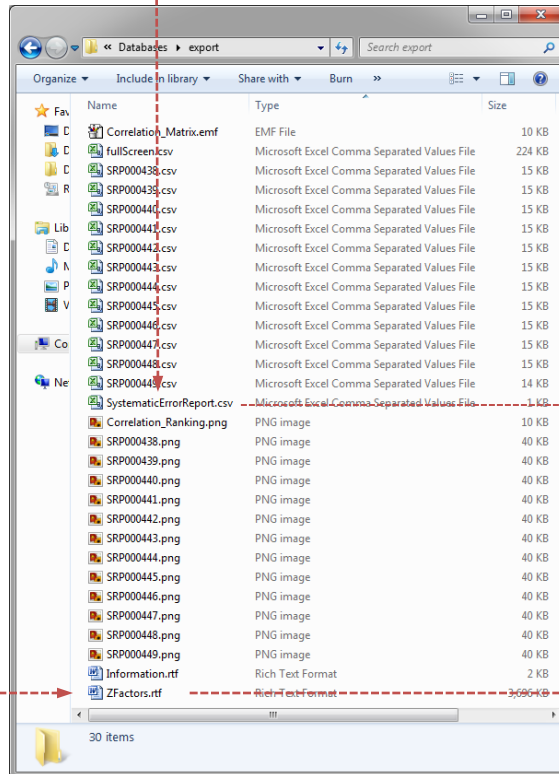
Tools

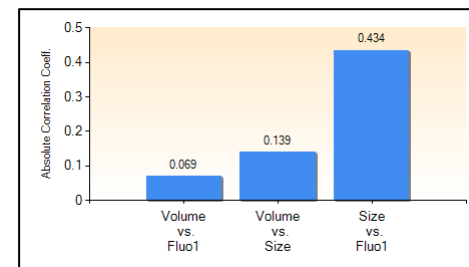
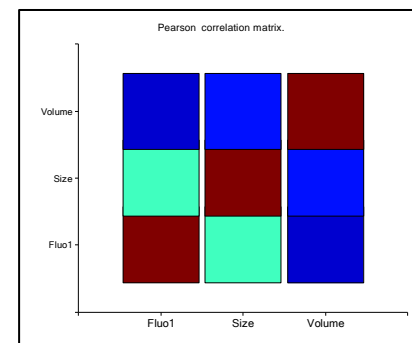
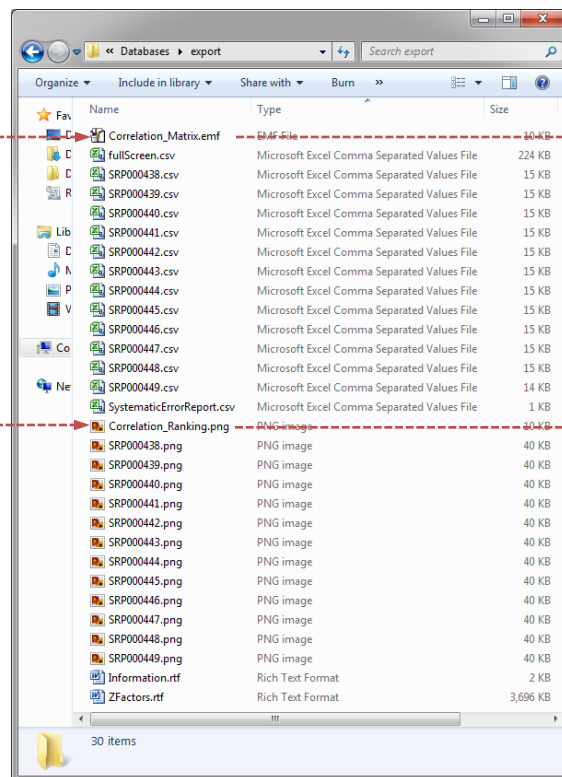
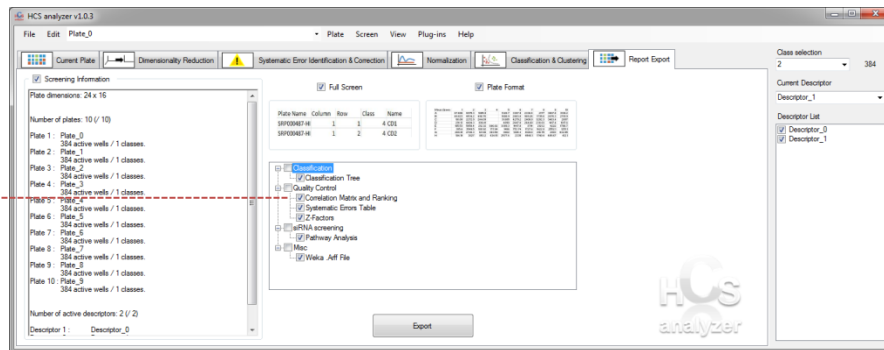
Team

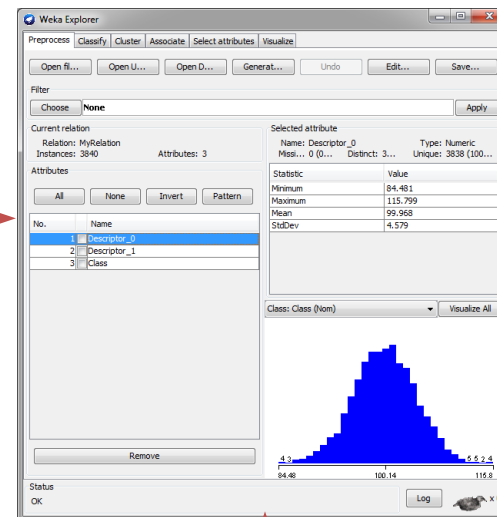
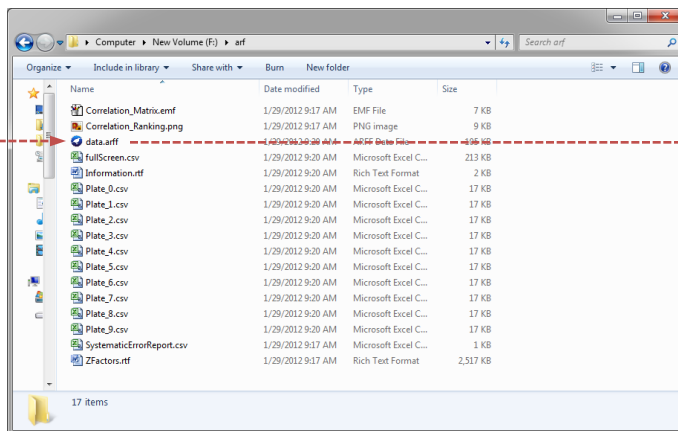
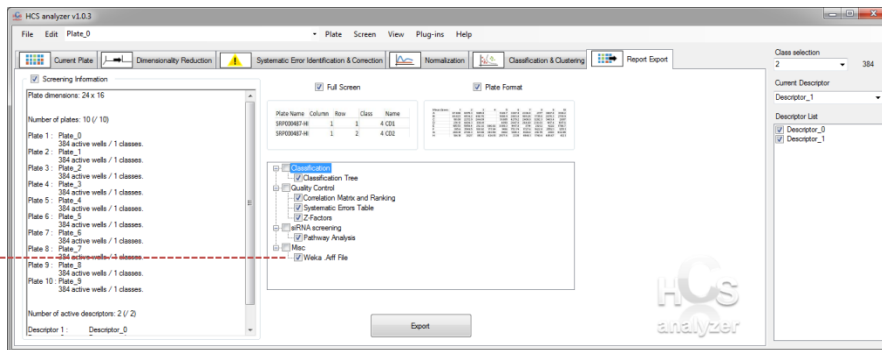
Calibri

11

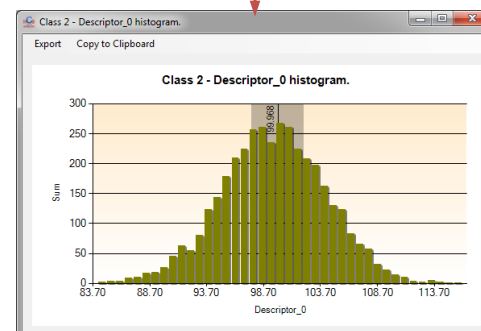
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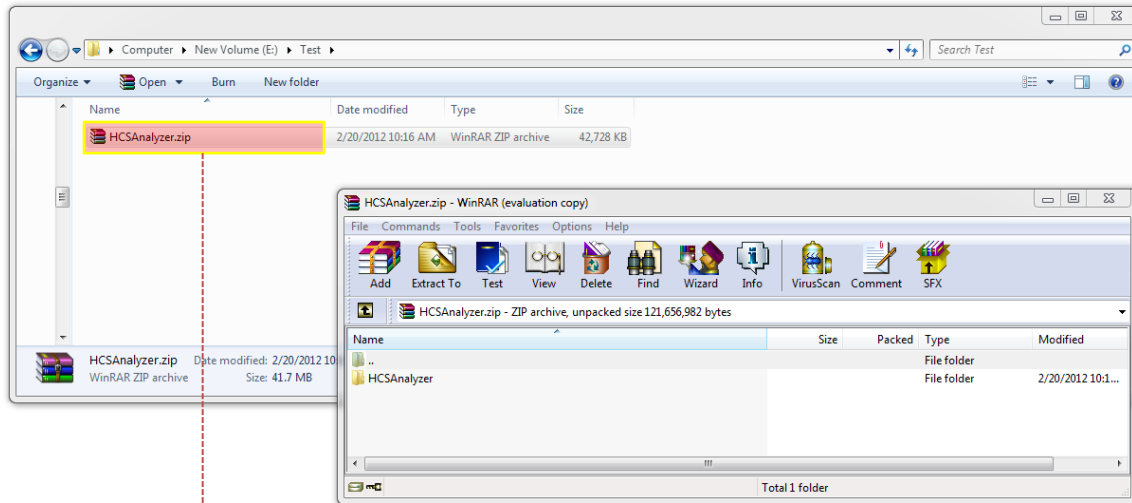


Weka

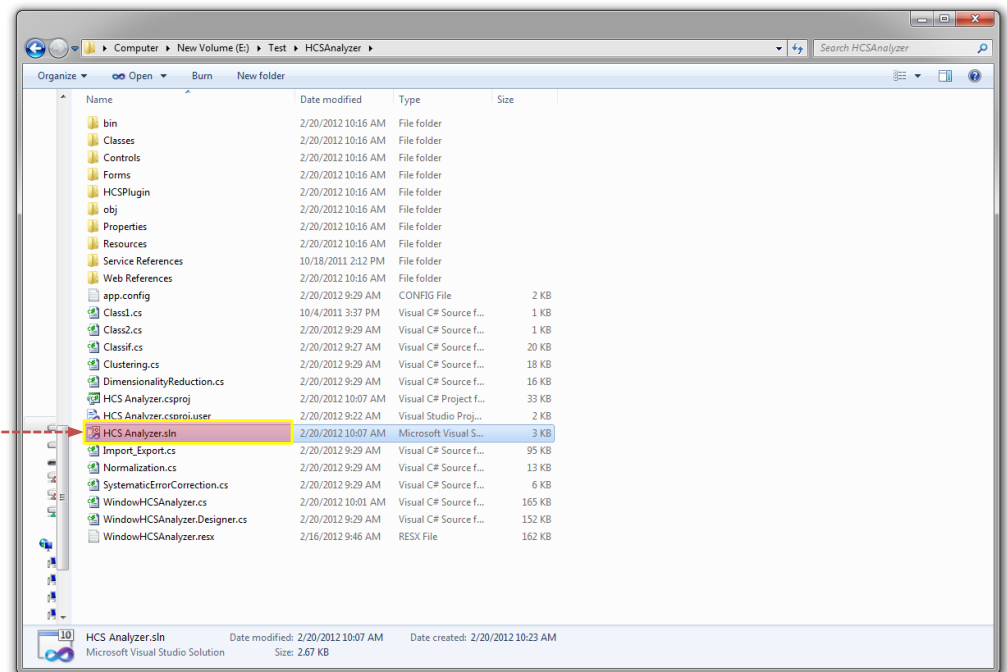


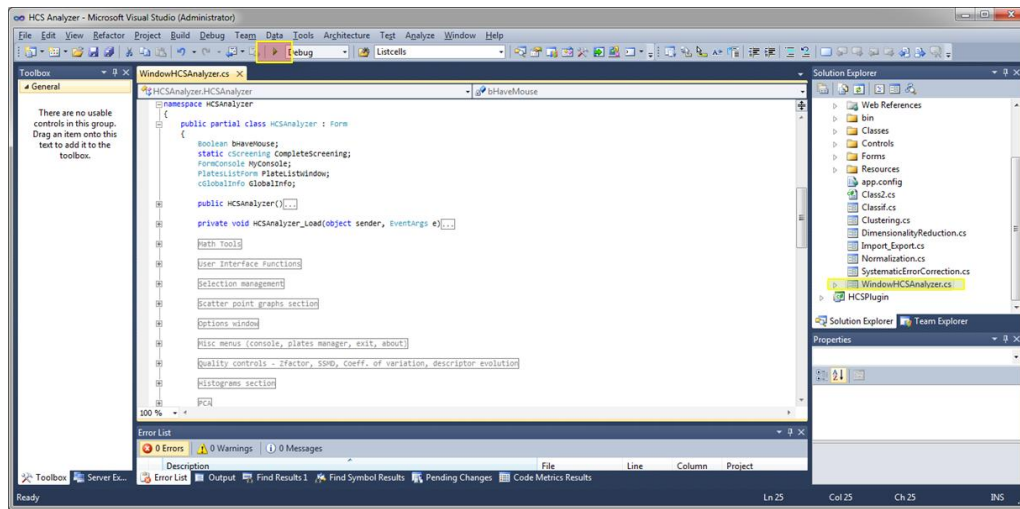
HCS Analyzer

Core Development



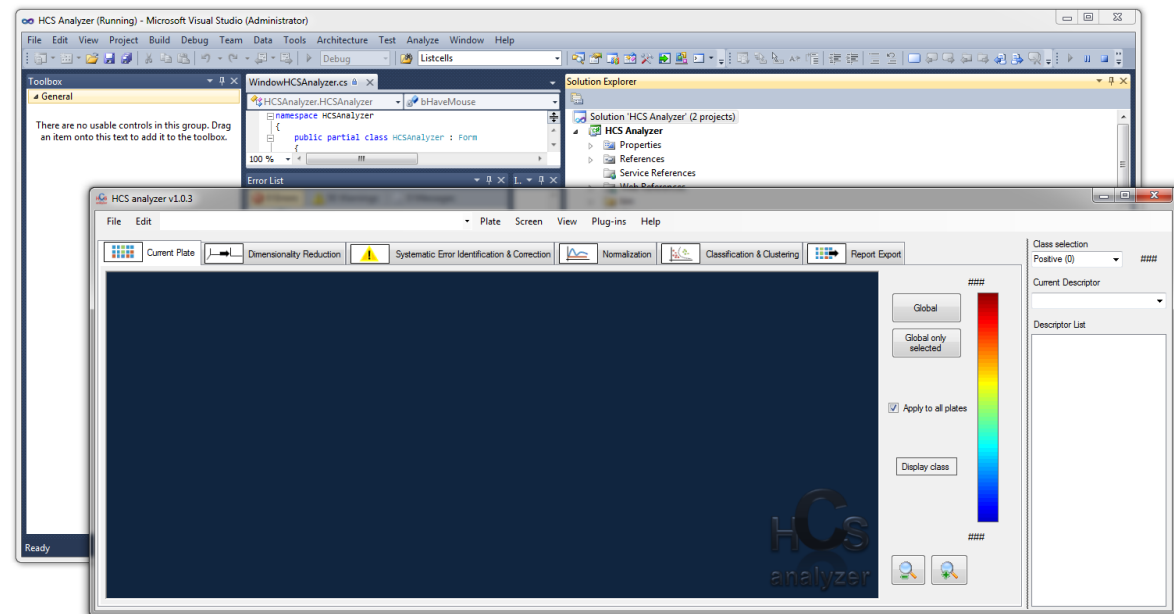
Unpack and launch the solution



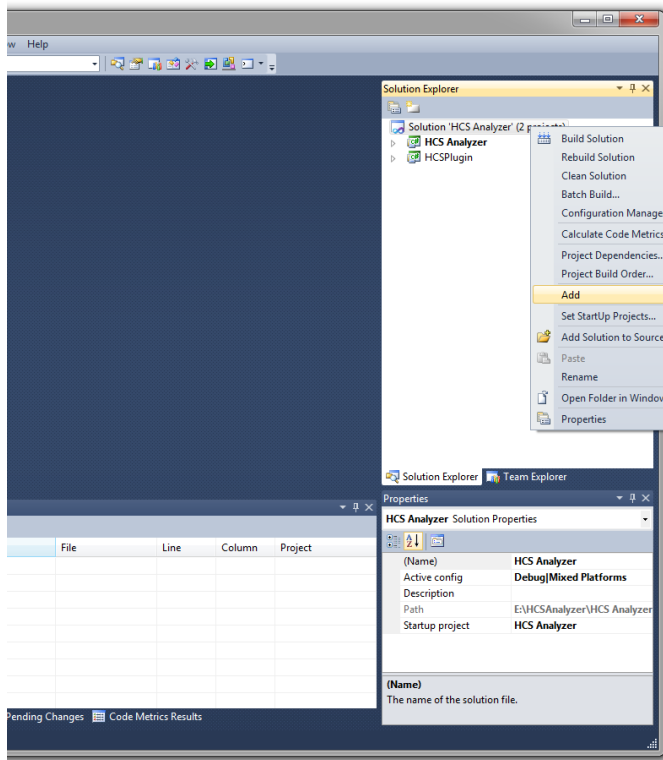


Look, develop, modify, debug, test

Launch and have fun

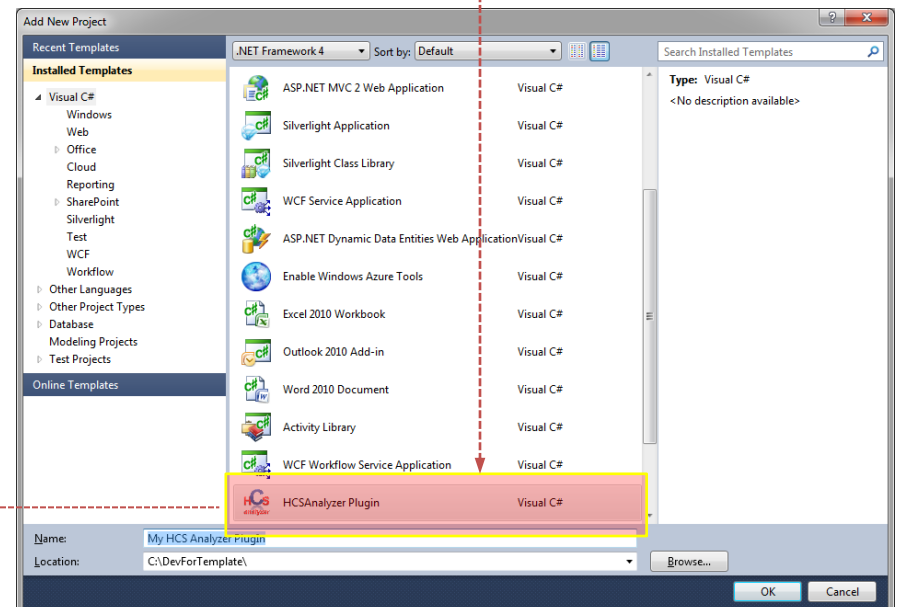


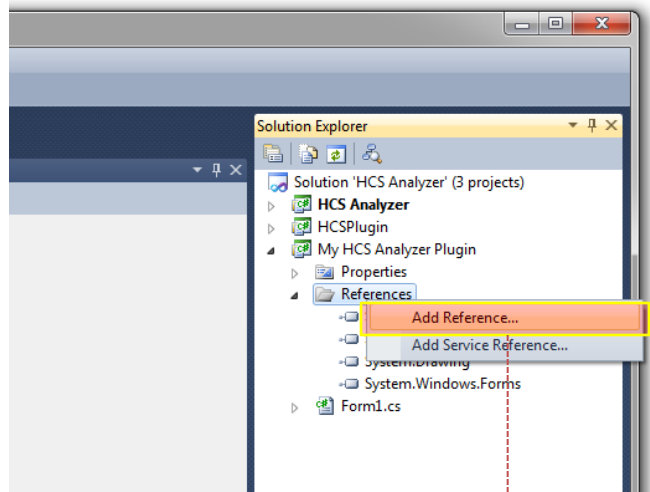
Plugins Development



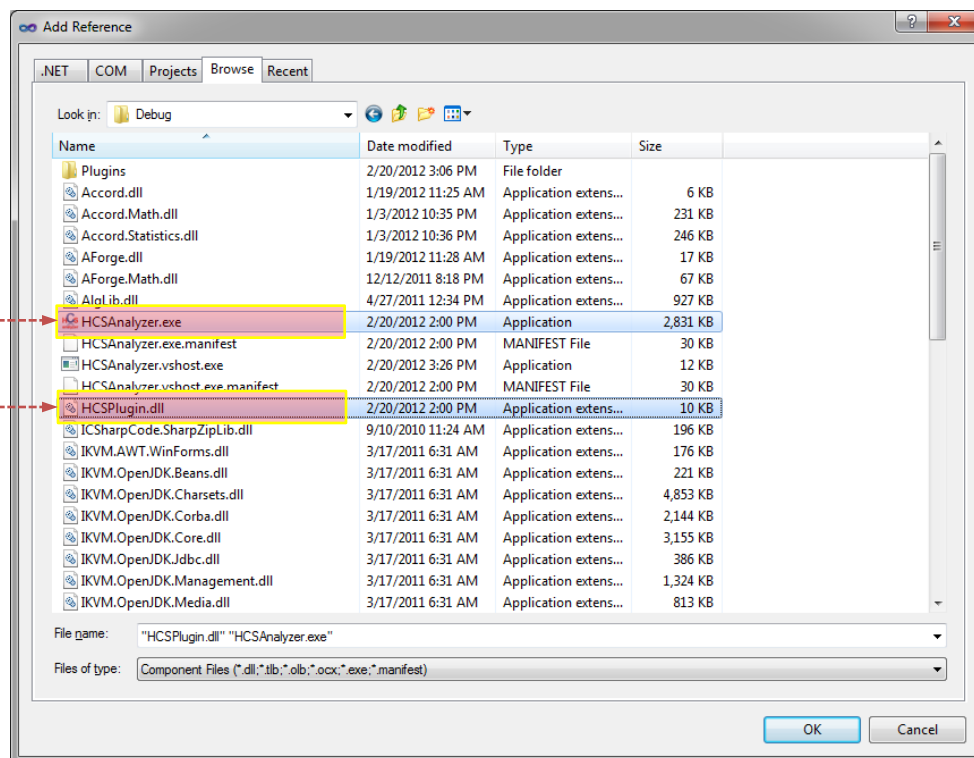
Add a new HCSAnalyzer Plugin project within the global solution

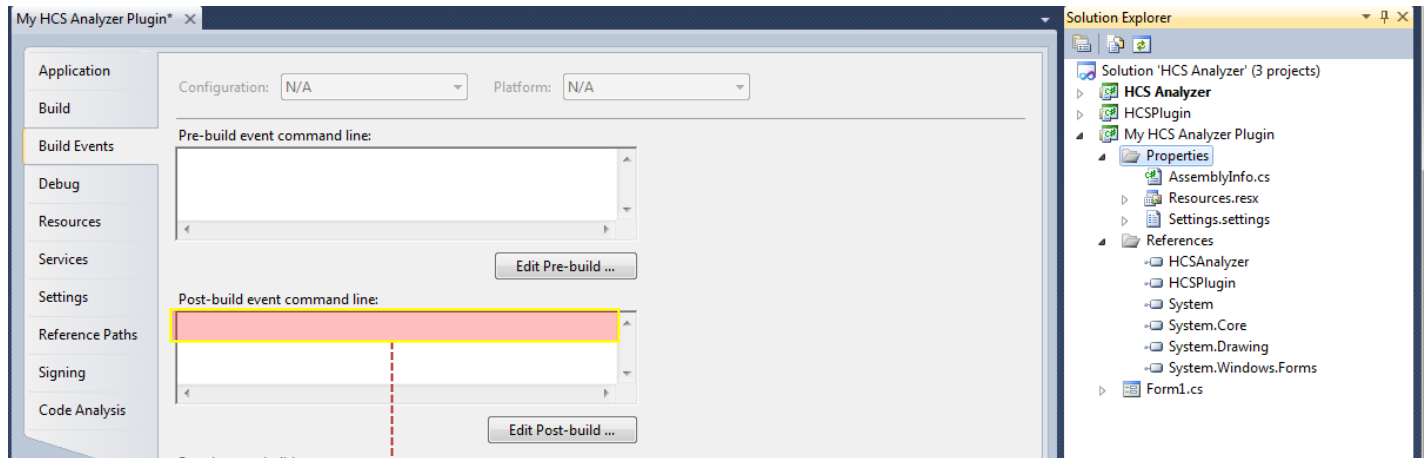
Note: this template is available on our website, and has to be copied in your dedicated visual studio directory



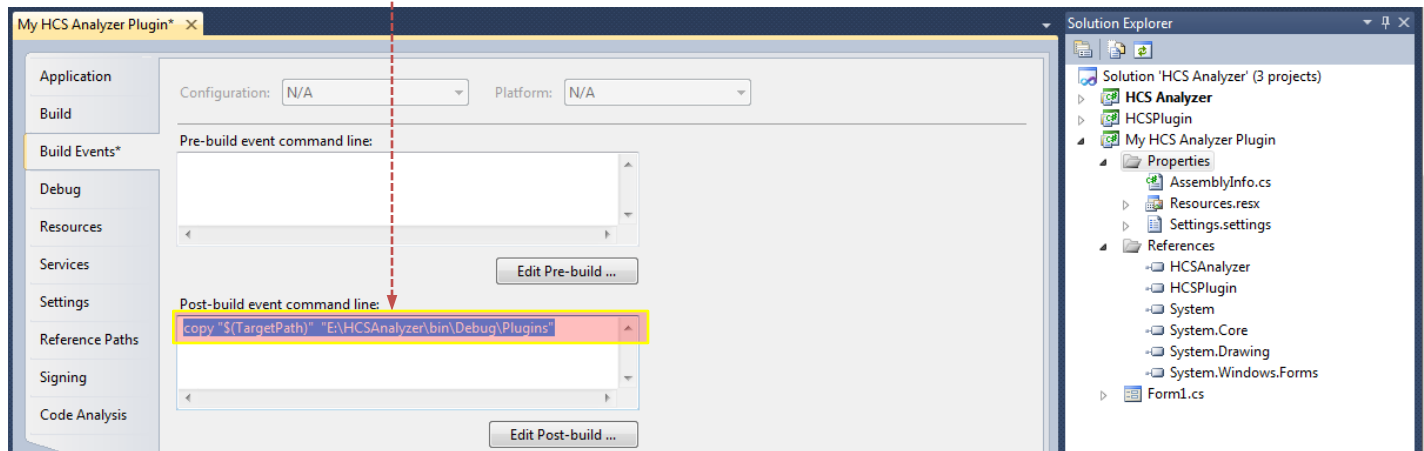


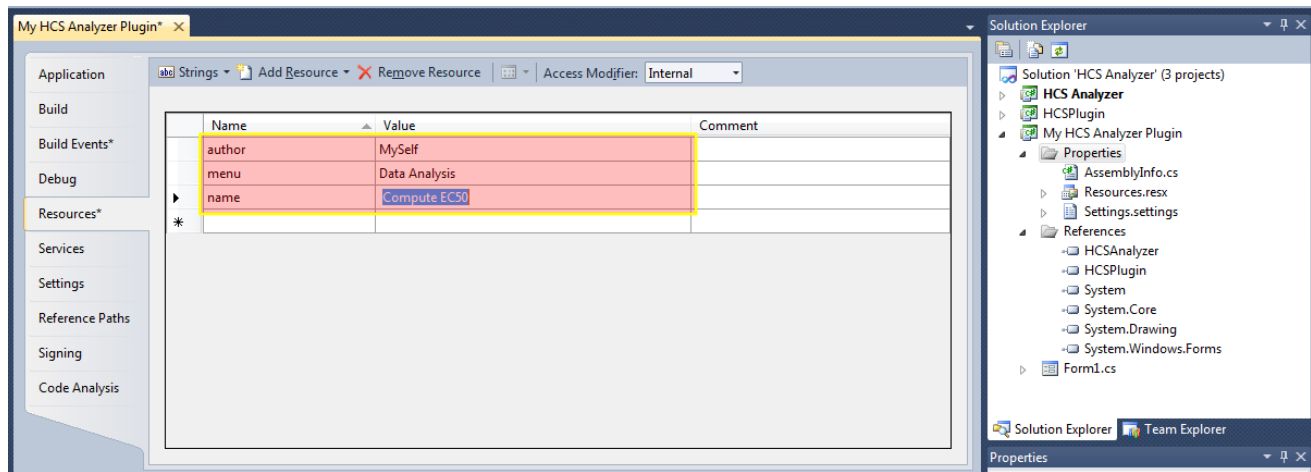
Add the two following references to your project



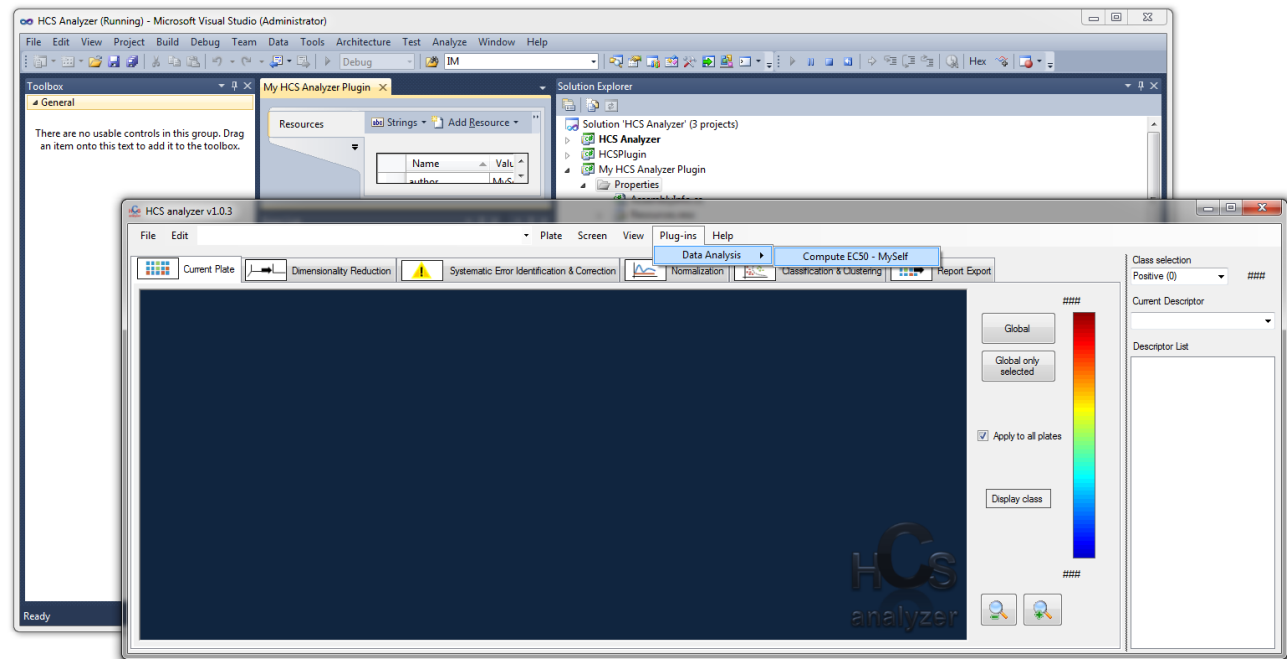


Add your HCS Analyzer plugins directory in the
Post-build event command line





Add information about your plugin (menu, etc.)



Develop your plugin and do not forget to share it