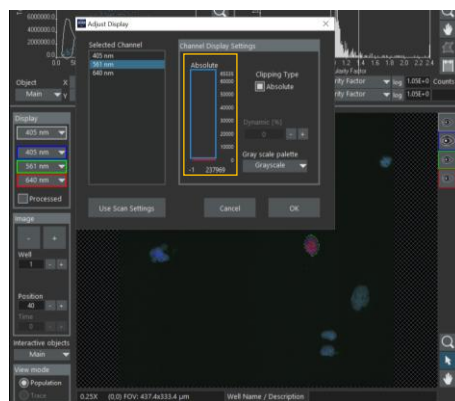
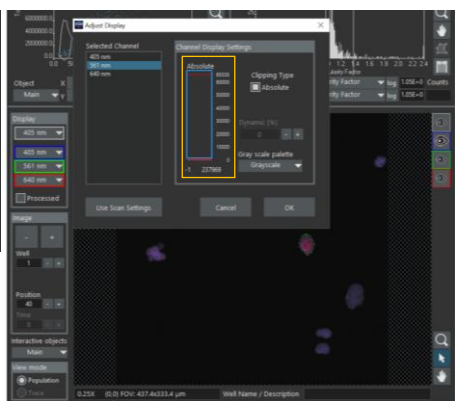
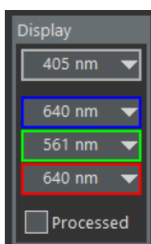
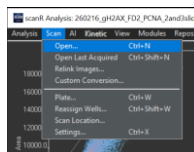


Load data from microscope
Scan → Open ... (Ctrl + N) → find Folder → experiment_descriptor.xml

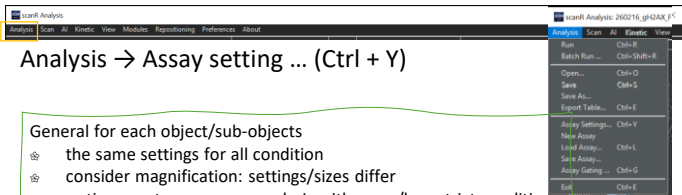
Or open previous analysis (to apply previous settings)
Analysis → Open



Display
 ✪ colors can be combined
 e.g. blue + red = magenta

View → Adjust Display
 ✪ Adjust intensity (usually it is necessary to go very low)
 ✪ it has to be done for each channel separately

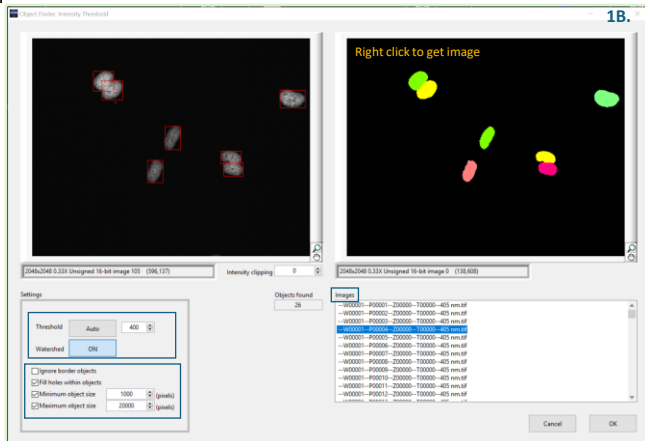
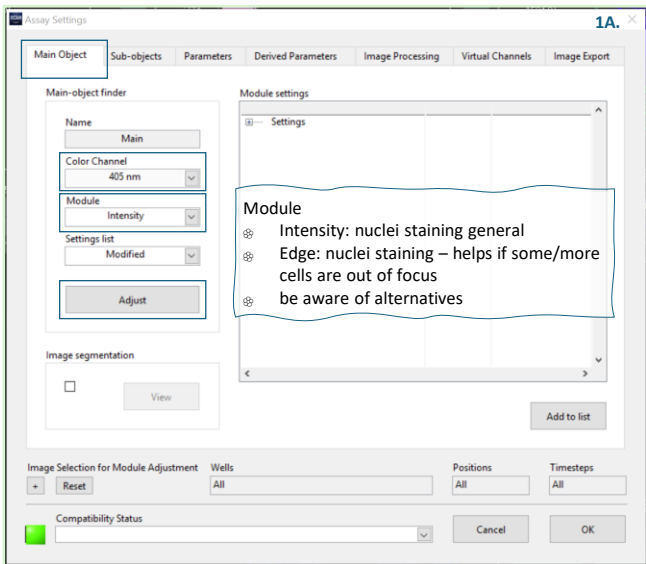
✪ can be done also later (for gating)



Analysis → Assay setting ... (Ctrl + Y)

General for each object/sub-objects

- the same settings for all condition
- consider magnification: settings/sizes differ
- option: run two or more analysis with more/less strict conditions



Threshold

- intensity of signal against background

Ignore borders

- optional, can be gated out

Watershed ON

- to separate object close or together

Minimum and Maximum object size

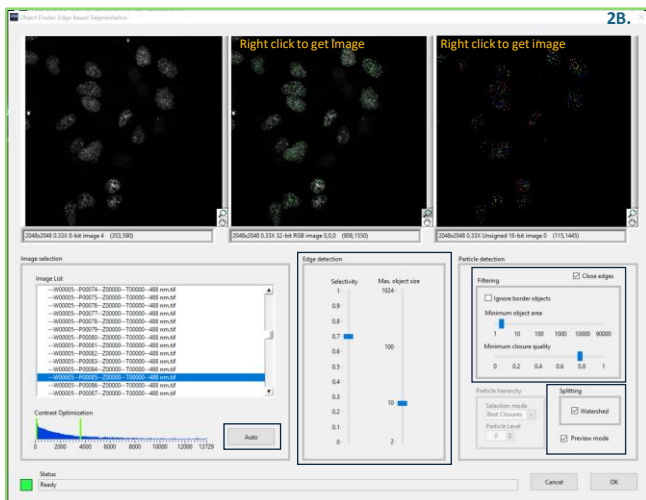
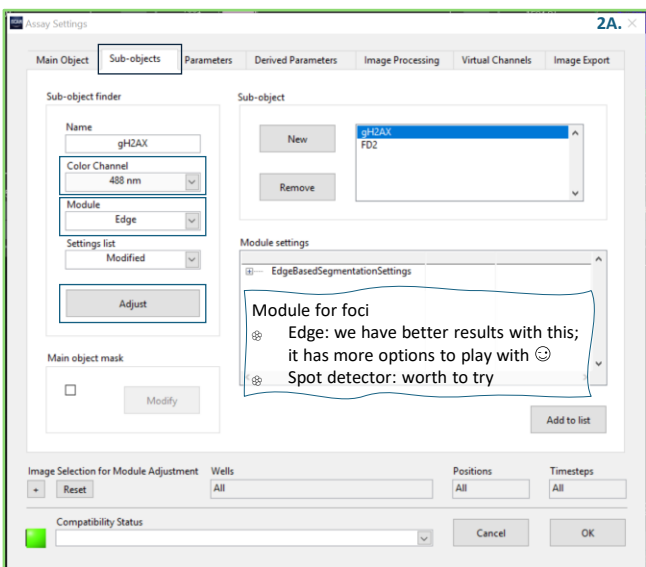
- to find almost all cells – it can be excluded later in gating

Images

W0000X ... X ... individual well/cover slip

P0000X ... image

- go through a few images and different treatments/ctrl to see, if settings are fine for all conditions

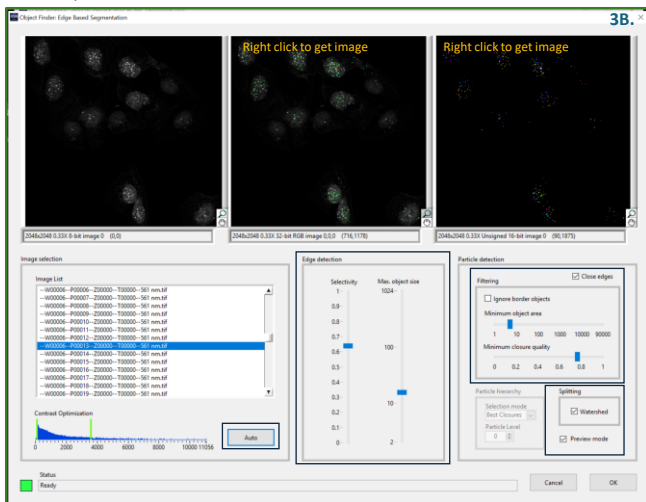
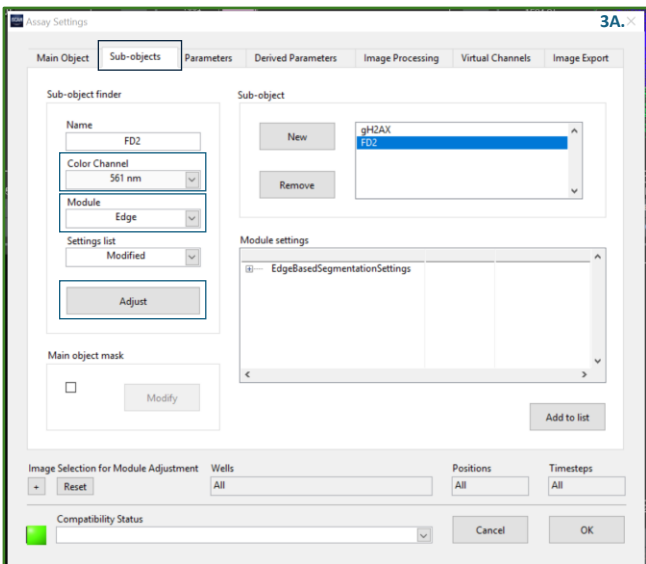


Auto

- set it to see, but also adjust brightness manually – same range for all condition

Edge & particle detection

- Adjust based on desired objects
- tip : zoom in: to be sure, which foci are masked

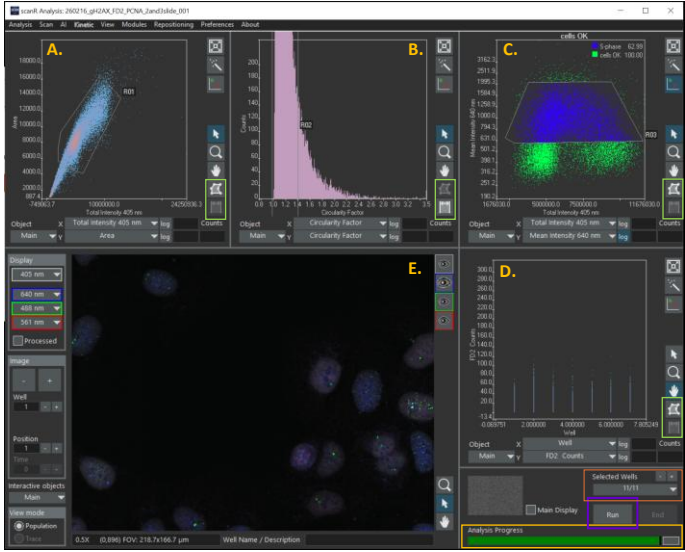


Foci

ID	Measurement	Channel	Object
p1	Well	Main	Main
p2	Position	Main	Main
p3	Area	Main	Main
p4	Area	gH2AX	Main
p5	Area	FD2	Main
p6	Circularity Factor	Main	Main
p7	Total Intensity	405 nm	Main
p8	Mean Intensity	405 nm	Main
p9	Max Intensity	405 nm	Main
p10	Total Intensity	488 nm	Main
p11	Mean Intensity	488 nm	Main
p12	Max Intensity	488 nm	Main
p13	Total Intensity	561 nm	Main
p14	Mean Intensity	561 nm	Main
p15	Max Intensity	561 nm	Main
p16	Total Intensity	640 nm	Main
p17	Mean Intensity	640 nm	Main
p18	Max Intensity	640 nm	Main
p19	gH2AX Counts	Main	Main
p20	FD2 Counts	Main	Main

Example of PLA/SIRF assay

ID	Measurement	Channel	Object
p1	Area	Main	Main
p2	Area	SIRF	Main
p3	Mean Intensity	405 nm	Main
p4	Total Intensity	405 nm	Main
p5	Mean Intensity	561 nm	Main
p6	Total Intensity	561 nm	Main
p7	Mean Intensity	640 nm	Main
p8	Total Intensity	640 nm	Main
p9	Circularity Factor	Main	Main
p10	Well	Main	Main
p11	Position	Main	Main
p12	SIRF Counts	Main	Main



once Parameters set → OK → Run analysis

Gates drawing

- double click by mouse to close gate ("circular" ones)

Gating

- A:** selection of cells
 - ☞ exclude debris (down) or doublets (up) etc.
- B:** selection of circular cells (base on circularity factor)
- C:** Cell cycle (X: Total intensity DAPI / Y: Mean intensity PCNA/Edu)
- D:** Results: condition (Y axis) / well (X axis)
 - ☞ Selected wells – enables to see individual conditions
 - ☞ clicking on the individual points in each plots show the image of object in the view window (E)

Analysis → Assay Gating ...

Gate Name	Count	Tot. %	σMean	σ1DV	σCV %	μMean	μ1DV	μCV %	
H1	None	28790	100.0	5.9E+6	2.3E+6	44.3	0.4E+3	3.1E+3	374
H2	None	28790	100.0	1.2E+0	2.5E-1	19.9	0.0E+0	0.0E+0	NaN
H3	cells OK	19945	74.4	6.3E+6	1.0E+6	30.0	8.5E+2	4.2E+2	49.0
H4	None	28790	100.0	3.8E+0	1.0E+0	30.3	9.8E+0	1.2E+1	127.4

Applying gating

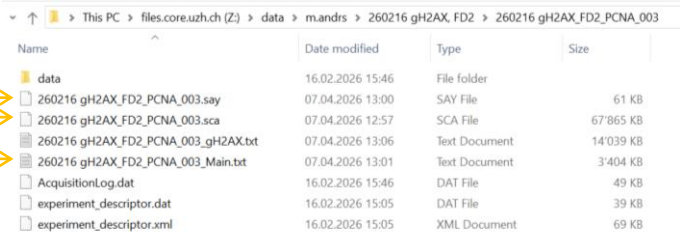
- Analysis → Assay Gating ...
 - ☞ define gates; it has to be written properly (capital letters)
 - ☞ apply gating: right click on plot (A – C) → select desired gate

Export Gallery

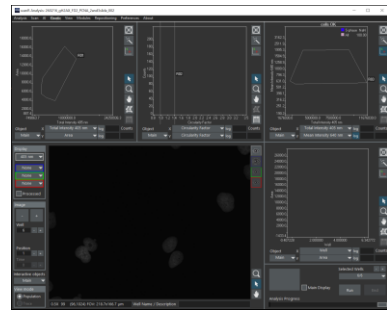
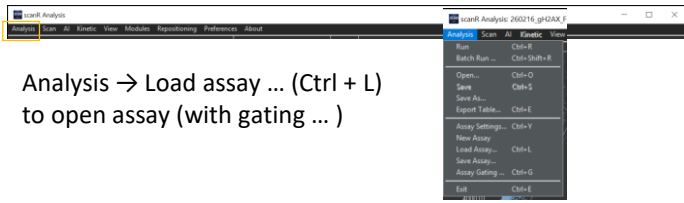
- ☞ according active widow/field
- option: right click on well in plot D.

Finish analysis

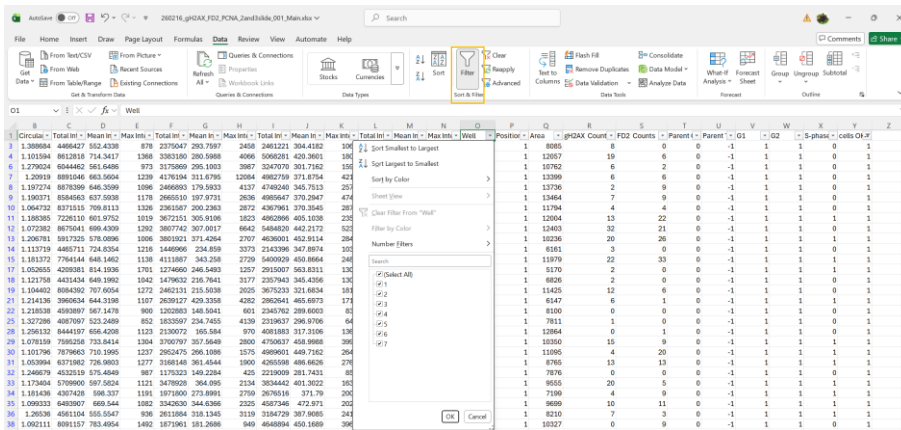
- ☼ save assay: .say
- ☼ save analysis: .sca
- ☼ export analysis (data): _Main.txt
 - ☼ before export be sure everything is saved !!!
 - ☼ it will export all, once _Main is exported close ScanR analysis software from Task manager (it can take long time)



Note: Loading saved assay (.say)



Note: Example of further data processing (.txt)



Open _Main.txt file in Excel

Apply filters
Well ... condition

Tip: Freeze top row (view)

Copy individual values for each condition to a new sheet

	A	B	C	D	E	F	G	H	I
1	260216 gH2AX_FD2_PCNA_003								
2	NT		CPT		CDDP		MMC		
3	well 1		well 2		well 3		well 5		
4									
5									
6		17.59587		52.93338		23.65166		43.20109	
7		3677		5284		4042		3655	
8		647		2797		956		1579	
9	7.994017	16.48001	43.71631	33.64269	30.52251	19.30529	39.67469	27.43256	
10	H2AX foci	FD2 foci	CH2AX foci	FD2 foci	CH2AX foci	FD2 foci	CH2AX foci	FD2 foci	Counts
11	15	26	35	28	29	14	79	38	
12	26	21	46	69	6	17	41	45	
13	9	20	0	1	7	11	26	26	

Example
count FD2 foci >30

=D8/D7*100
=COUNT(D11:D140002)
=COUNTIF(D11:D19002,">30")

Important !!!
Save as excel file, otherwise _Main.txt will be overwritten