

Research Core Unit Transcriptomics

# Evaluation of single features' (spots') quality using Agilent's Feature Extraction software

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# Directory

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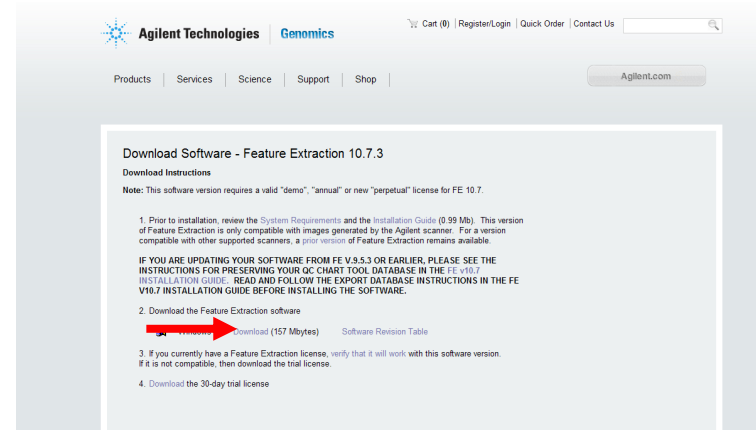
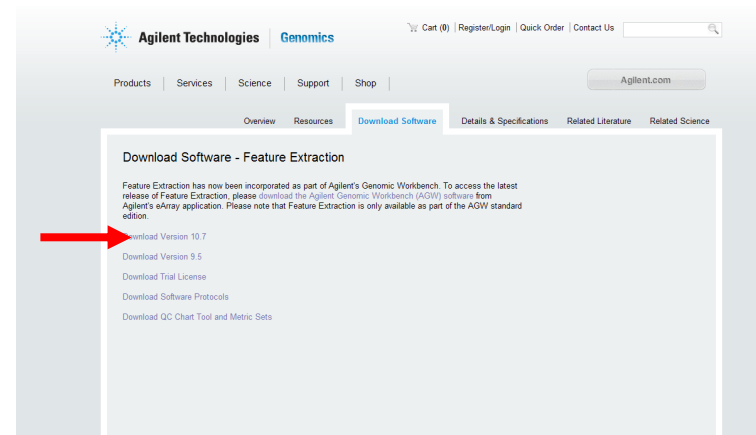
# 1. Author's note

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- Instructions are located on the left side of the slide
- Instruction related visual presentations are located on the right side of the slide
- In these visual presentations, crucial information is highlighted by a red arrow  
(  )
- In case, that more than one arrow is needed, text passages and arrows are numbered, accordingly

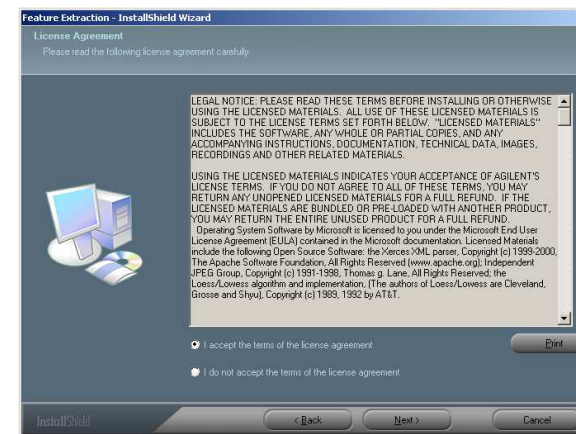
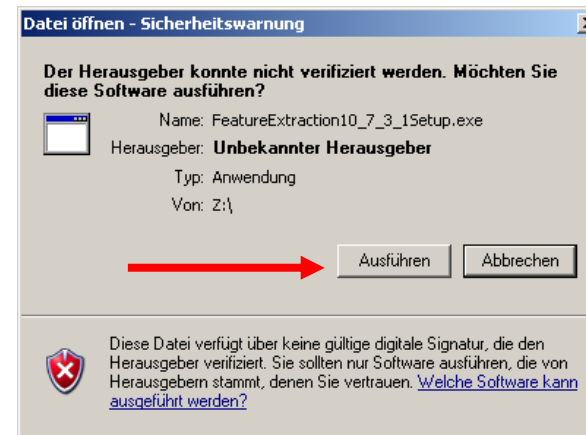
## 2. Download

- ❑ Visit Agilent's [homepage](#)
- ❑ Download Version 10.7



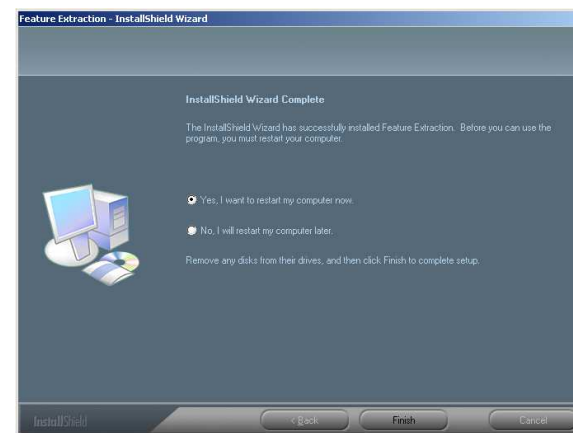
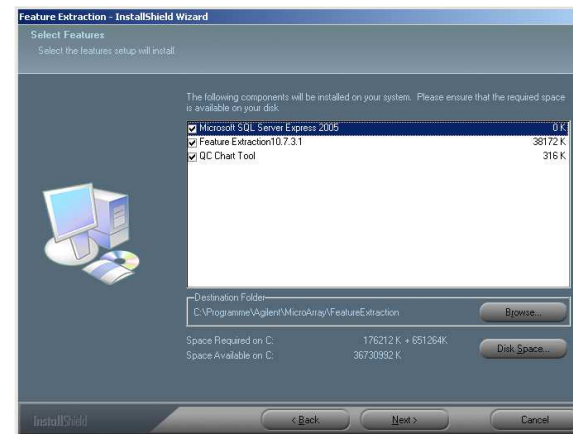
# 3. Installation I

- Double-click the downloaded file
- Click *Next* & decide wether or not to accept the agreement
- At the third party database question just click *Next*



# 3. Installation II

- Select components & destination where it is proposed
- In some cases operating system needs to be updated
- Agree to restart your computer
- Finish installation



# 4. Starting I

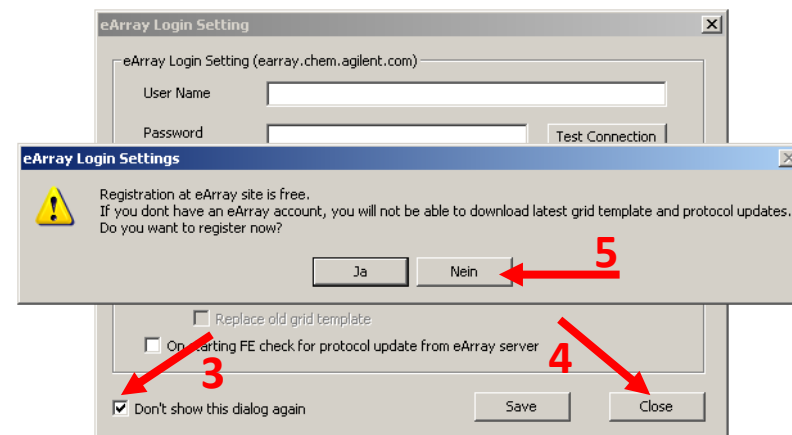
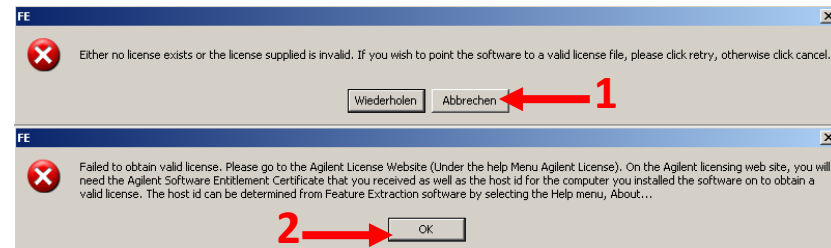
- Next Window click *Abbrechen*(1) & then *OK*(2)

Please Note:

You will have to do this for every start of the program

- After that check the box at the lower left corner(3)
- Then click *Close*(4)
- After that click *Nein*(5)

Feature Extraction is now ready for use

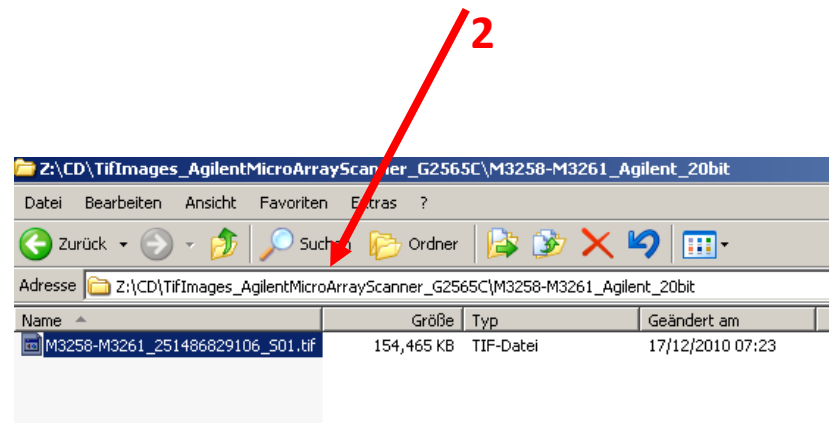
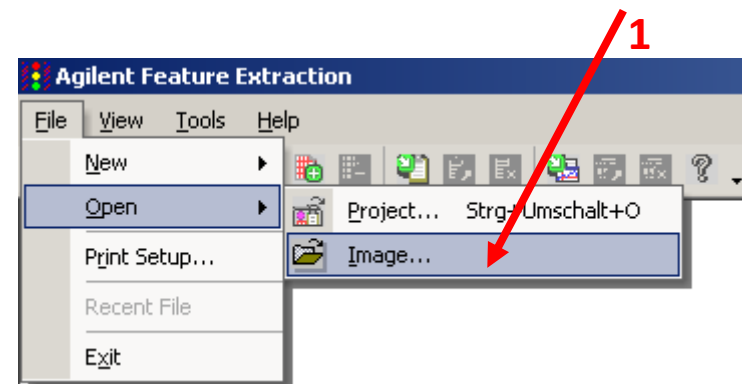






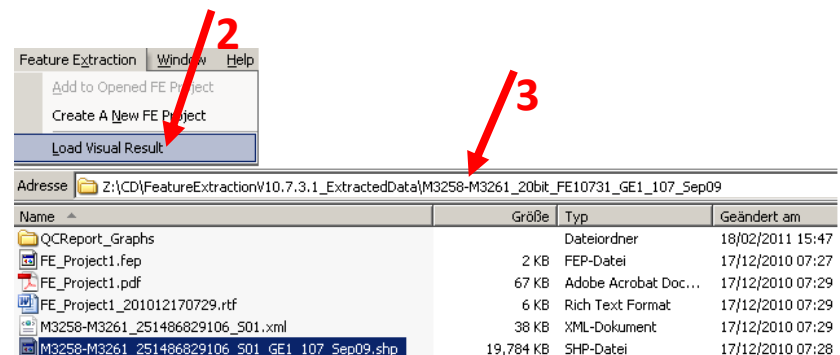
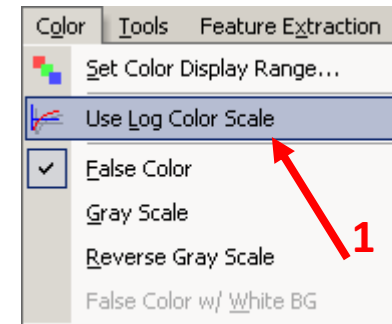
# 6. Usage I

- To open a TIFF-file(1)
  - Select *File -> Open -> Image*
  - Navigate through the TIFF-folder on your CD(2)
  - Double-click the TIFF-file



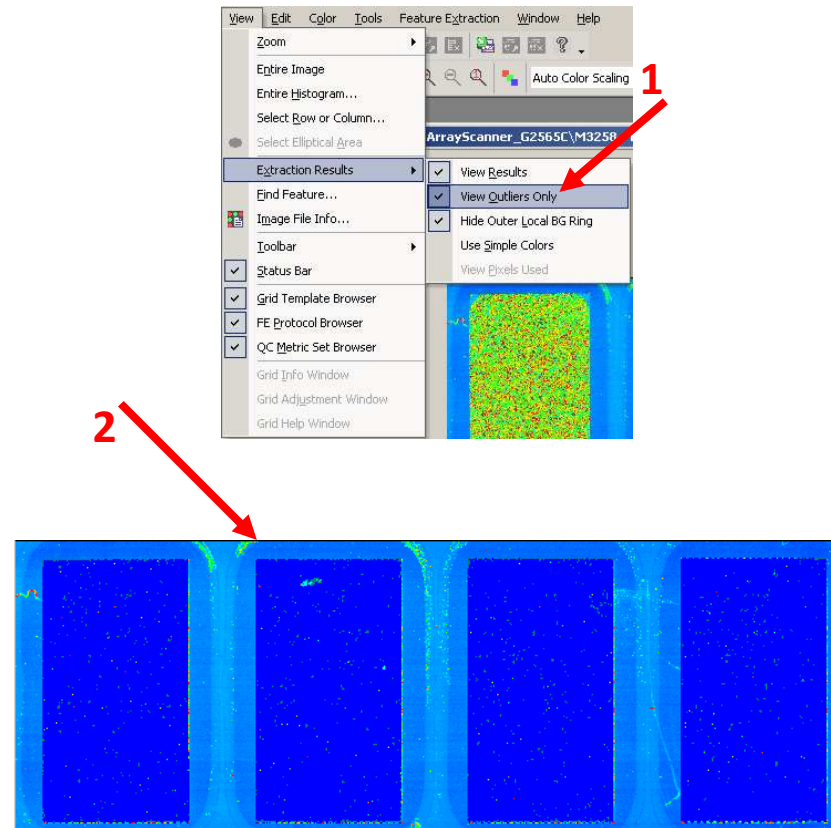
## 6. Usage II

- The TIFF-file will open
  - Select *Color* -> *Use Log Color Scale*(1)
- Then load grid file
  - Select *Feature Extraction* -> *Load Visual Result*(2)
  - Navigate your CD in order to find the grid file(3)
  - Double-click the shp-file



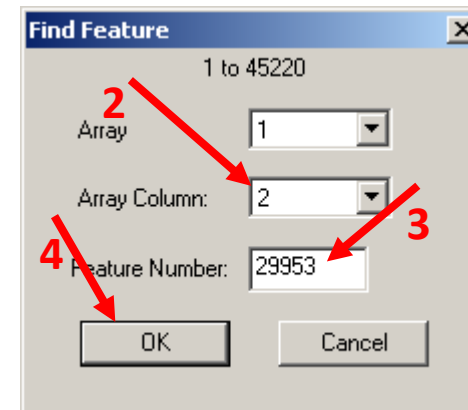
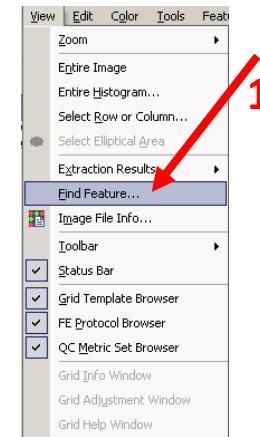
## 6. Usage III

- To use the grid file
  - Select *View -> Extraction Results*
  - Deselect *View Outliers Only*(1)
  
- This done, your file should look like this(2)



# 7. Find Feature I

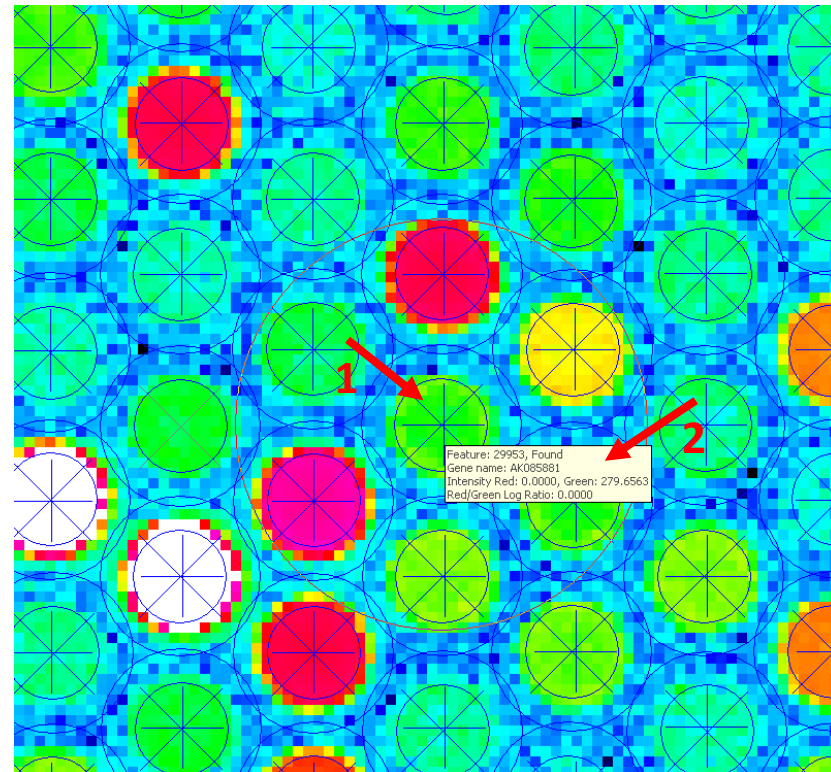
- ❑ To find a specific Feature Number(1)
  - Select *View -> Find Feature*
- ❑ In the next window enter Array Column(2) & Feature Number(3)
- ❑ Click the *OK*-Button(4)



## 7. Find Feature II

- The centered spot(1) is the one you are looking for
- Navigate your mouse cursor over the middle of the centered spot

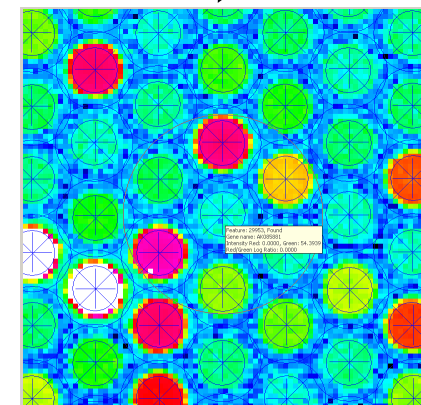
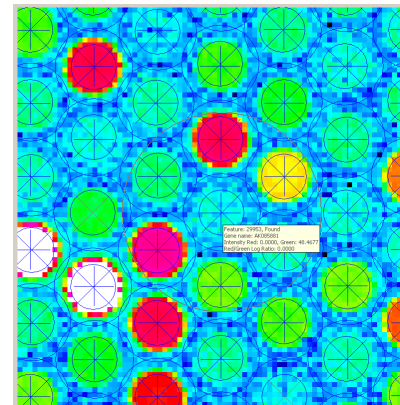
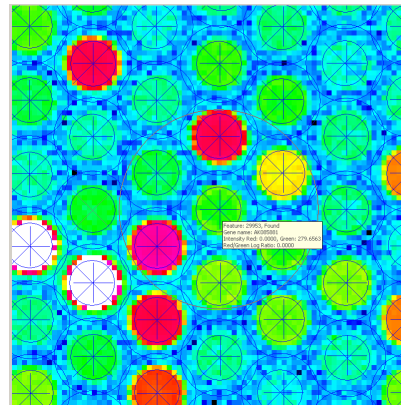
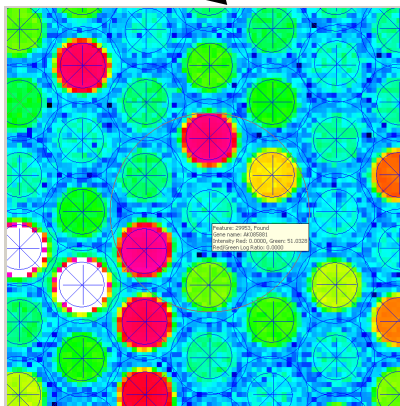
Additional information will appear (2)  
It can be used, verifying, whether having the right spot or not



# 7. Find Feature III

- In order to compare the quality of one spot across all 4 Arrays
  - Repeat the *Find Feature I-II Procedures* by iteratively selecting all 4 arrays columns

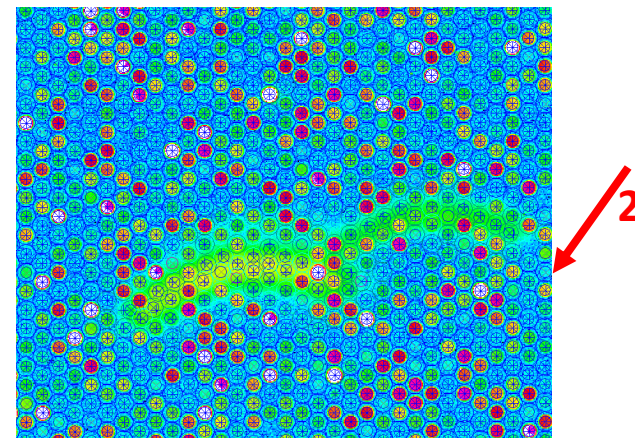
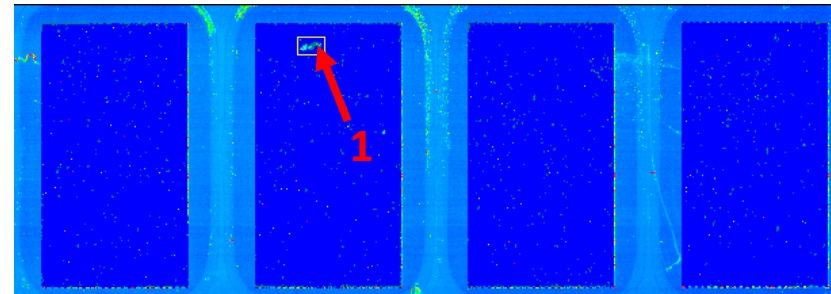
29953																										
K	L	M	N	C	P	G	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AI	AJ	
S	S	S	Fe	F	r	r	d	g	n	u		GeneName	D	g	M3258	g	g	M3259	g	g	M3260	g	g	M3261	g	g
B	#	#	A	A	re	2	1	AK085881	M	0	15	0	1	229	0	0	15	0	0	15	0	0	15	0	0	



## 8. Find Feature Manually

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- To take a closer look manually
- Mark the area concerned with your mouse (1)
- Now the area concerned will be displayed (2)



# Contact

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