

Antibody screening by microarray technology – direct identification of selective high-affinity clones

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Description of the semi-automated data evaluation

The data evaluation with Python 3.7 was performed with the development environment Spyder 3.2.2 in the Anaconda environment. The script supplied by us is intended to be used with the very application. After the files have been stored in a separate folder, the correct path needs to be copied into the script (Fig. S1)

```
57
58 #####
59 # 0. Set dir and import Data
60 #####
61
62
63 # sets the source directory, files will be imported and exported in this dir, it must cont
64 source_dir = "C:\\Users\\mpaul\\Desktop\\devel\\chip_paper\\"
65
```

Fig. S1: The correct path needs to be pasted between the “ ” at line 64: Please add double \\ like shown in this example.

The folder should contain the script and the competitive and non-competitive scans as .tif files. Finally, all results are exported as a .txt file in this folder. In Fig. S2 an example is shown with the path.

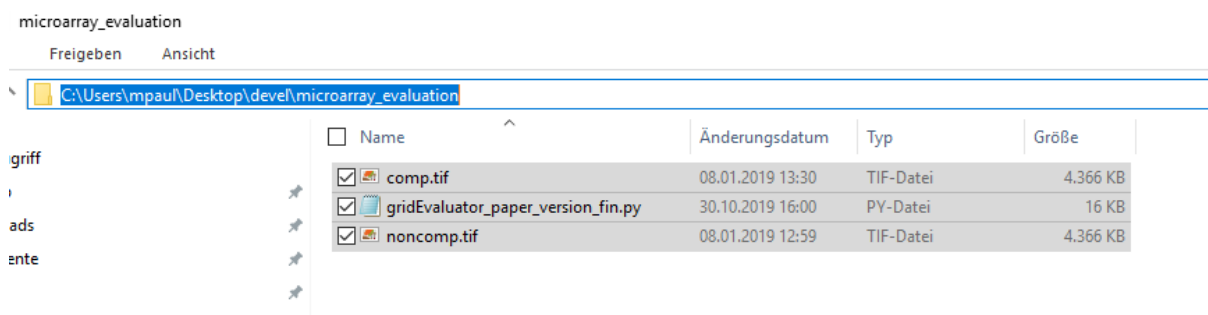


Fig. S2 Example for a folder and the path.

The program requires manual user-input, the parameters needed to evaluate the given sample data of the experiment are supplied by the program as suggestions. To evaluate new scans, the central x- and y-pixel of the first upper left spot are required (Fig. S3), also the grid must be aligned with the x- and the y-axis.

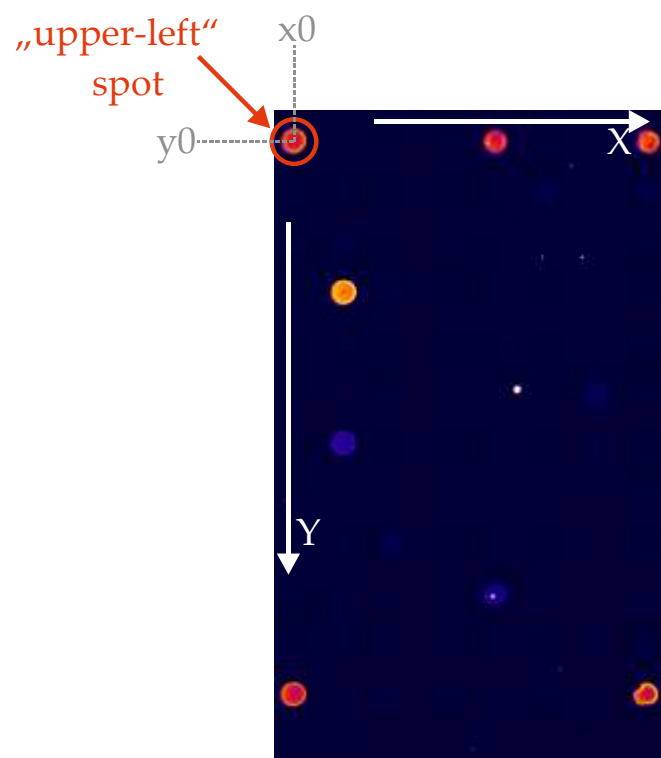


Fig. S3 Determination of the upper-left spot as origin of the coordinates.

When the script was executed successfully, the results will be exported as three .txt files. The quotient to compare the spots along with the spot number and its coordinates on the scan are exported in the results_and_position.txt file.