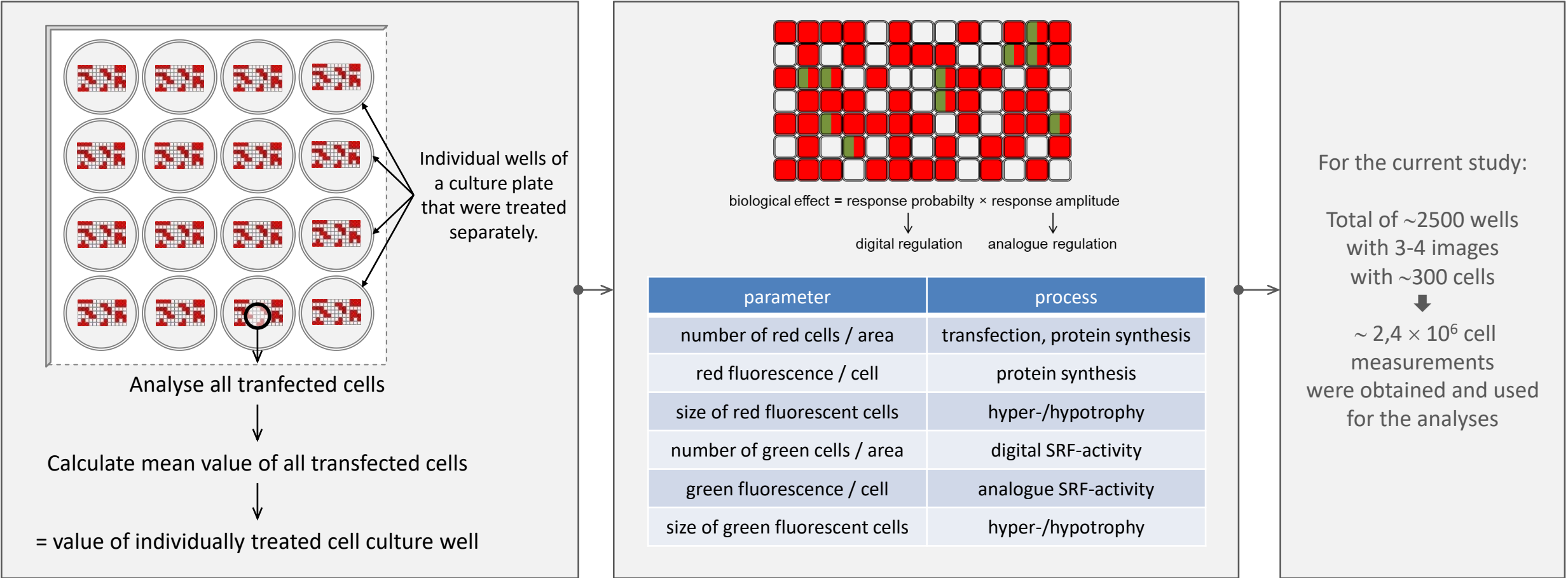
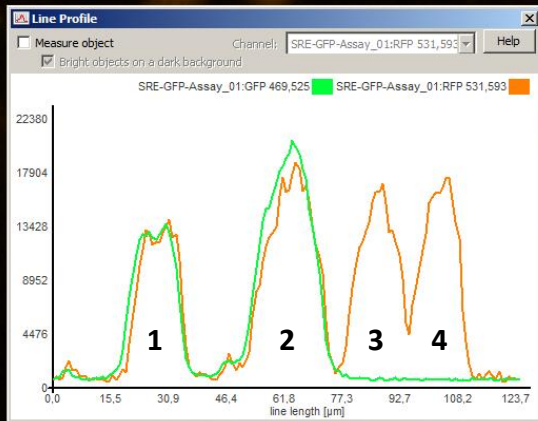


Supplementary methods SM01: Basic workflow of digital microscopy applied in reporter assay or in-cell-ELISA (part 1)

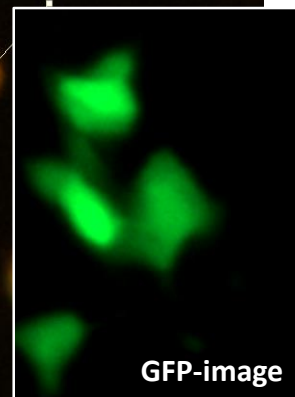


Supplementary methods SM02: Basic workflow of digital microscopy applied in reporter assay or in-cell-ELISA (part 2)

Identify transfected cells (in this image RFP served as transfection control = red cells)



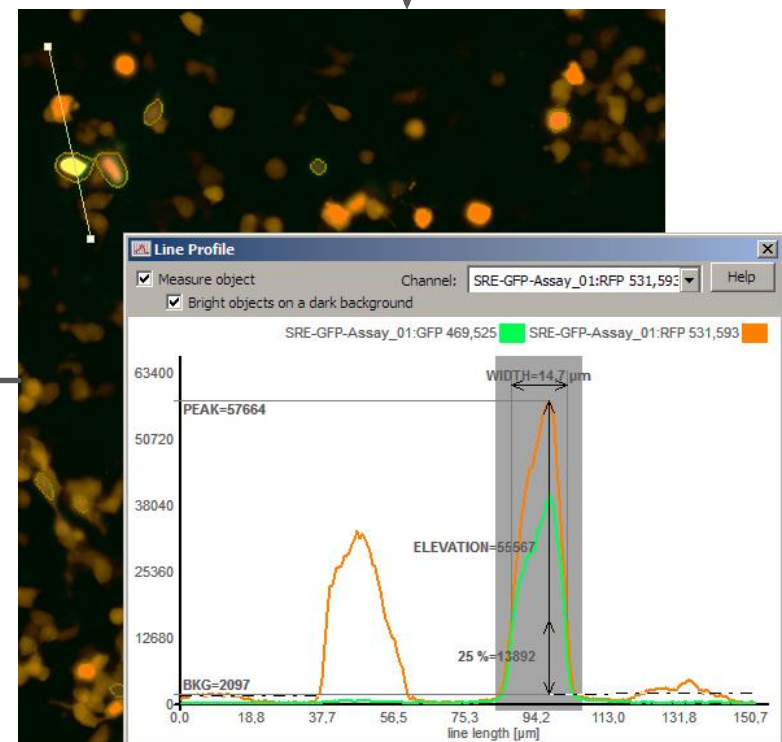
Cells 1, 2, 3 and 4 are transfected.
Cells 1 and 2 are positive for the reporter gene GFP, cells 3 and 4 are GFP-negative)



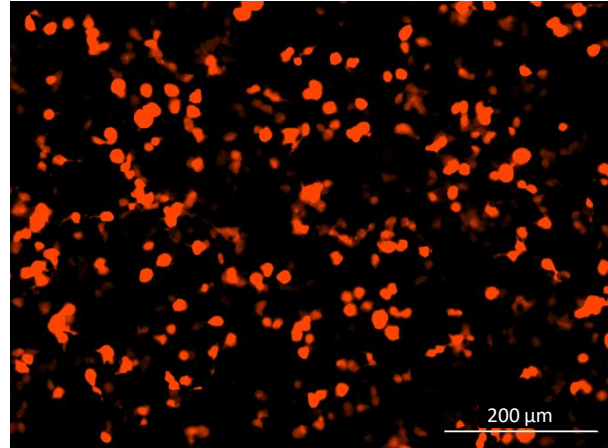
1. Identify transfected cells.
2. Measure signal intensity integral of interest in transfected cells: Either the reporter GFP or an endogenous protein marked by a specific primary and an Alexa Fluor 568 labelled secondary antibody.

Individual values from all analysed cells per well are used to calculate mean per well

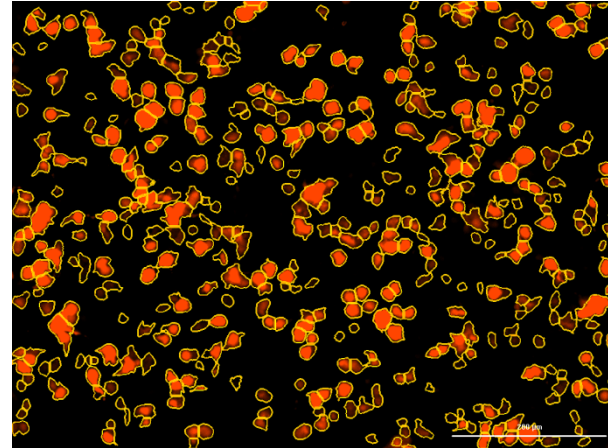
| # | Size | Circularity | Area | Perimeter | Mean [RFP] | StdDev [RFP] |
|----|------|-------------|------|-----------|------------|--------------|
| 1 | 28,4 | 0,297 | 580 | 99,1 | 11738 | 9212 |
| 2 | 17,4 | 0,649 | 236 | 56,6 | 4837 | 2390 |
| 3 | 14,6 | 0,378 | 157 | 49,1 | 2328 | 515 |
| 4 | 33,1 | 0,328 | 797 | 119,0 | 5959 | 3629 |
| 5 | 11,3 | 0,655 | 98,5 | 36,8 | 3266 | 3633 |
| 6 | 13,7 | 0,278 | 133 | 54,0 | 2225 | 1931 |
| 7 | 18,8 | 0,771 | 276 | 61,2 | 3619 | 1850 |
| 8 | 22,5 | 0,4 | 378 | 84,9 | 3430 | 2174 |
| 9 | 23,3 | 0,923 | 424 | 76,0 | 14518 | 18138 |
| 10 | 31,7 | 0,465 | 760 | 118,9 | 3379 | 988 |
| 11 | 35,8 | 0,255 | 895 | 140,7 | 8353 | 8292 |
| 12 | 13,8 | 0,404 | 142 | 45,9 | 3401 | 2868 |
| 13 | 19,2 | 0,567 | 284 | 64,8 | 3633 | 2056 |
| 14 | 19,4 | 0,999 | 287 | 64,5 | 5481 | 4554 |
| 15 | 19,4 | 0,755 | 293 | 70,1 | 3872 | 1909 |
| 16 | 30,5 | 0,261 | 653 | 112,1 | 5295 | 3843 |
| 17 | 19,5 | 0,449 | 286 | 65,5 | 3873 | 2493 |
| 18 | 31,0 | 0,187 | 635 | 111,1 | 7815 | 7507 |
| 19 | 21,3 | 0,35 | 333 | 74,1 | 2870 | 574 |
| 20 | 18,3 | 0,194 | 224 | 60,6 | 2345 | 341 |
| 21 | 14,0 | 0,745 | 153 | 50,6 | 4833 | 2492 |
| 22 | 29,2 | 0,552 | 655 | 103,6 | 5614 | 3918 |
| 23 | 25,6 | 0,429 | 533 | 99,1 | 4831 | 3955 |
| 24 | 33,5 | 0,349 | 821 | 118,7 | 10558 | 10722 |
| 25 | 29,8 | 0,574 | 684 | 110,6 | 3756 | 1243 |
| 26 | 18,3 | 0,853 | 262 | 59,5 | 2693 | 647 |
| 27 | 14,4 | 0,669 | 161 | 46,9 | 2756 | 689 |



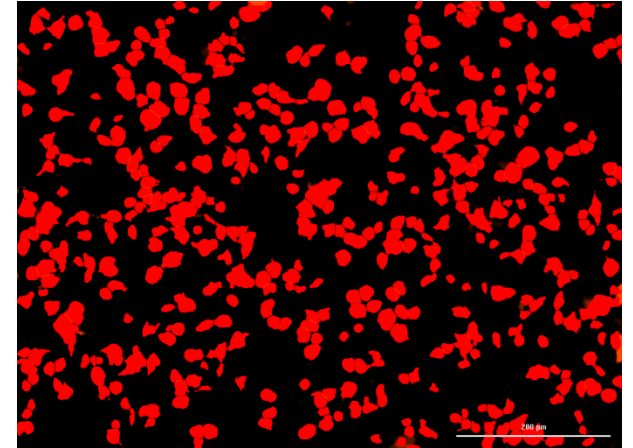
1. Acquire microscope images
(red channel is shown)



2. Identify, count and measure red cells
(number, area, intensity)



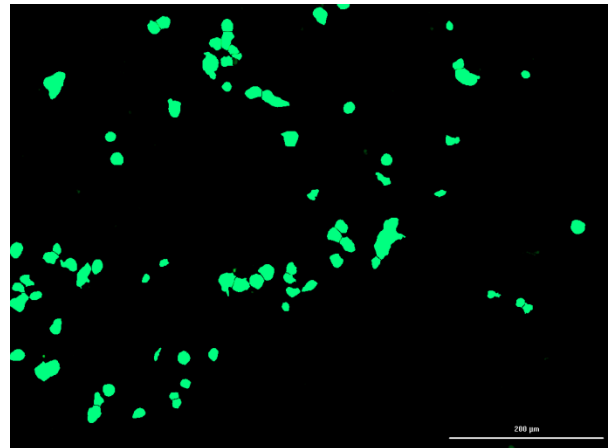
3. Use the areas of red cells to determine the
SRF-reporter activity in the green channel.



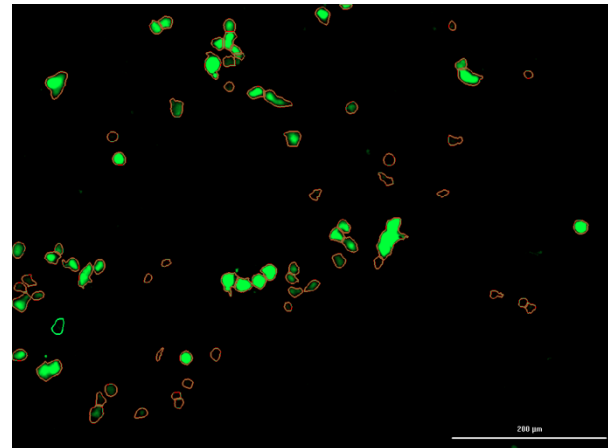
Supplementary methods SM03.

Process of data acquisition for SRF-reporter assay with digital microscopy.

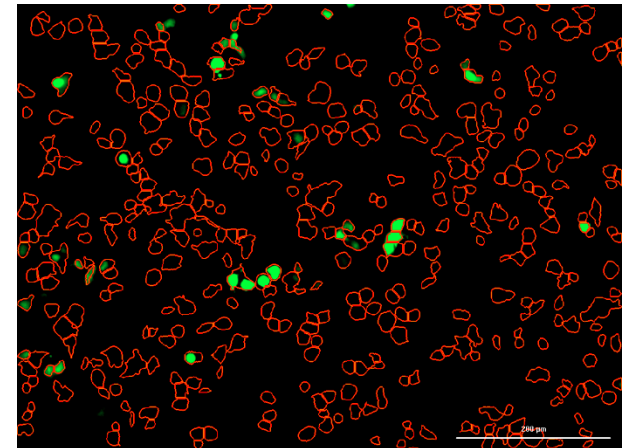
Example 1: Control conditions



6. Count and measure green cells
(number, area, intensity)

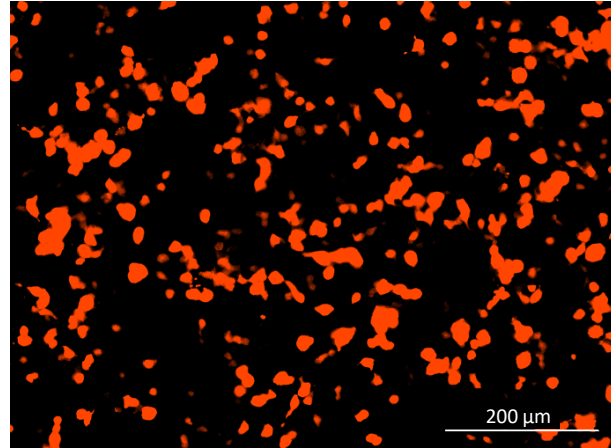


5. Identify green cells in the green channel

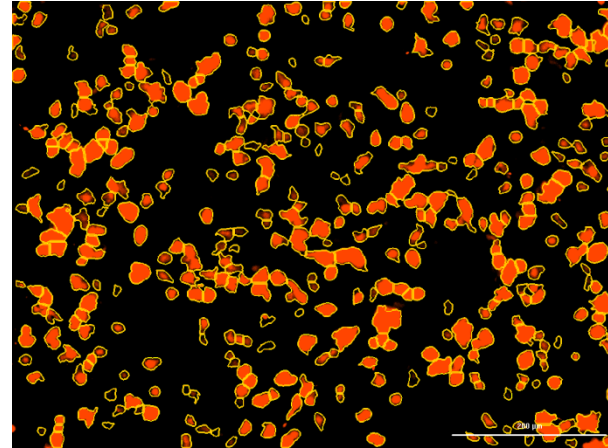


4. Measure green parameters in the
areas of red cells (number, intensity)

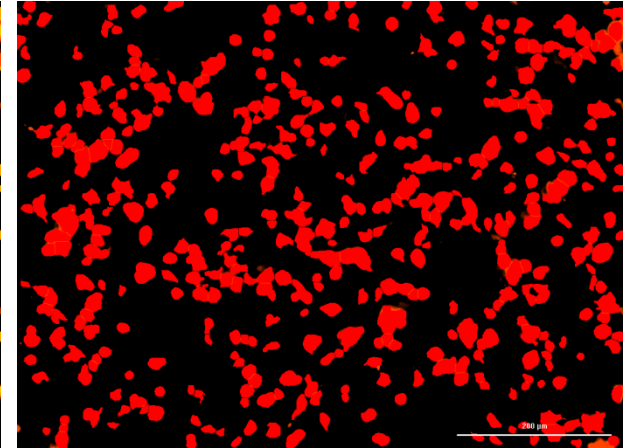
1. Acquire microscope images
(red channel is shown)



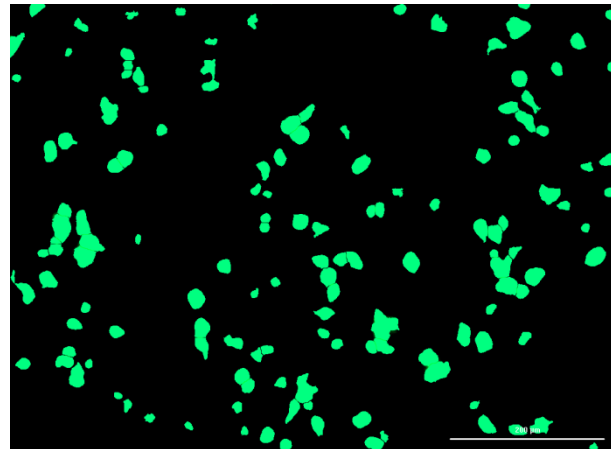
2. Identify, count and measure red cells
(number, area, intensity)



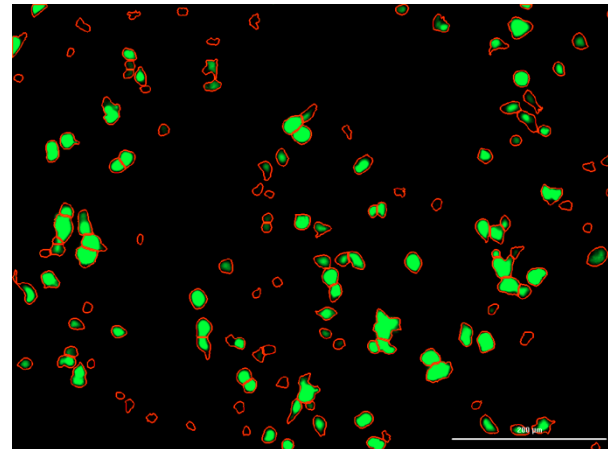
3. Use the areas of red cells to determine the
SRF-reporter activity in the green channel.



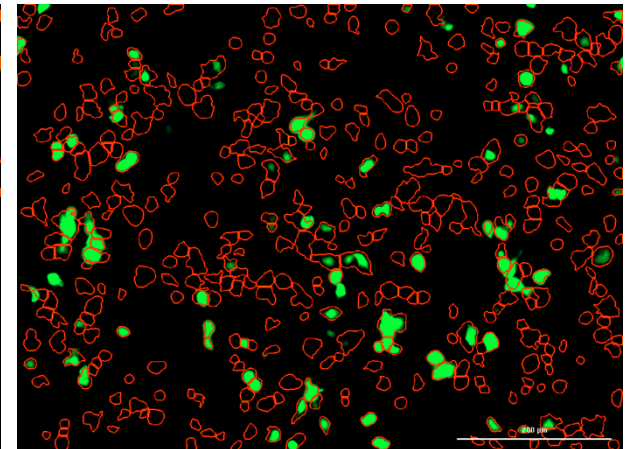
6. Count and measure green cells
(number, area, intensity)



5. Identify green cells in the green channel



4. Measure green parameters in the
areas of red cells (number, intensity)

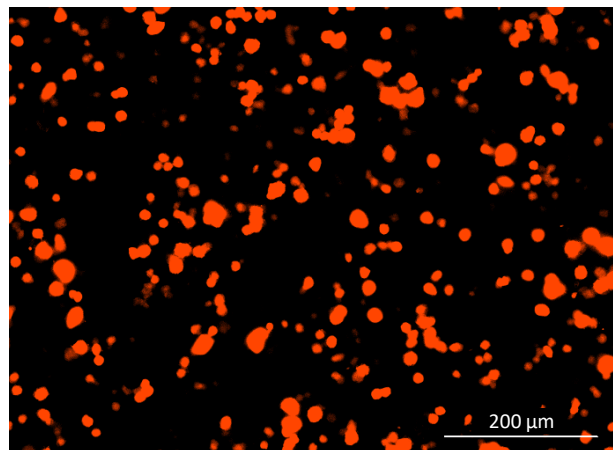


Supplementary methods SM04.

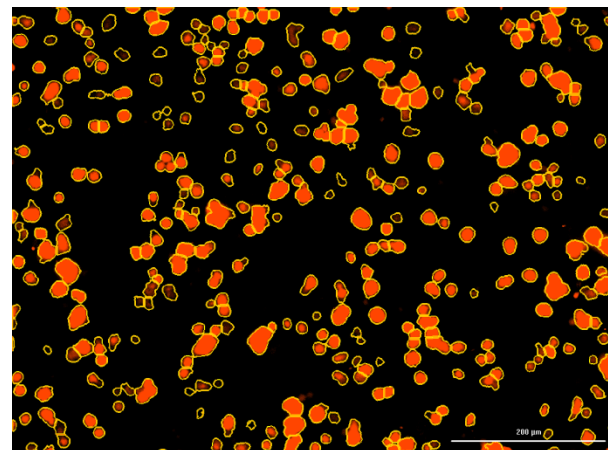
Process of data acquisition for SRF-reporter assay with digital microscopy.

Example 2: 24 h stimulation with 10 μg/l EGF.

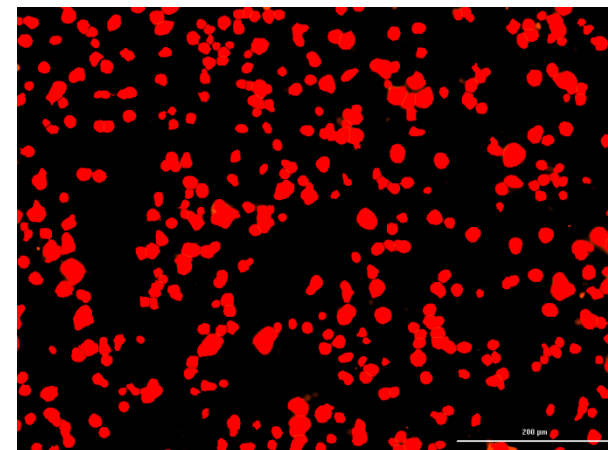
1. Acquire microscope images
(red channel is shown)



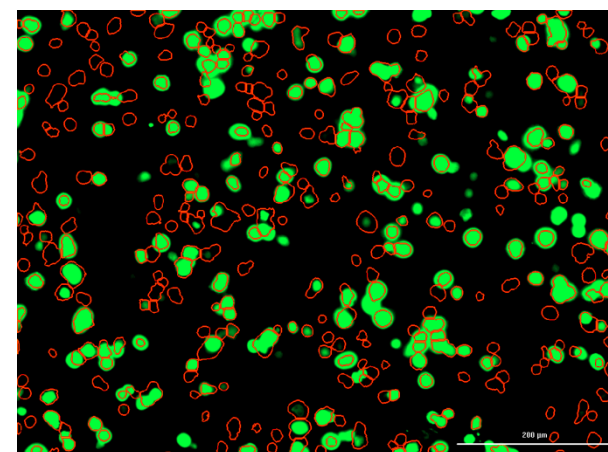
2. Identify, count and measure red cells
(number, area, intensity)



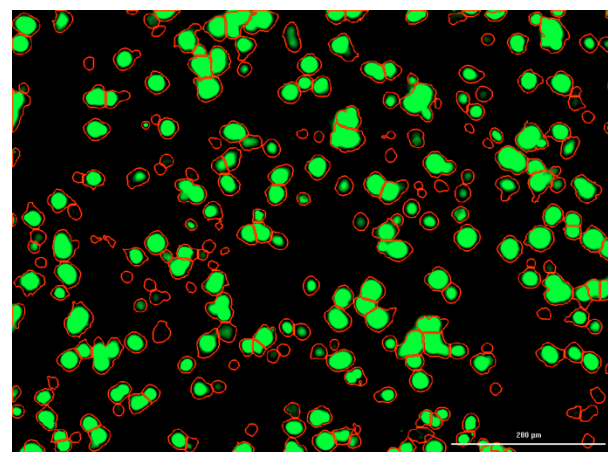
3. Use the areas of red cells to determine the
SRF-reporter activity in the green channel.



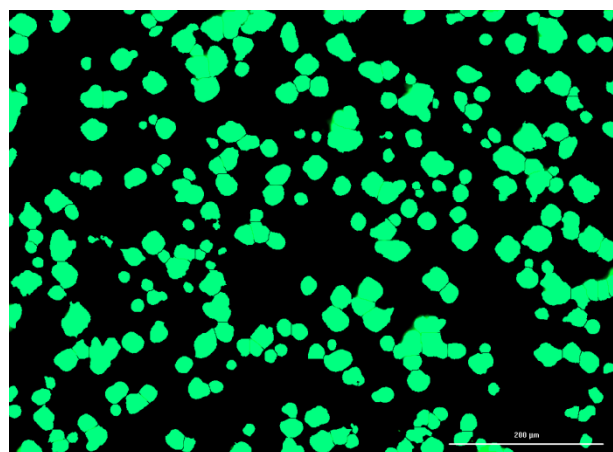
4. Measure green parameters in the
areas of red cells (number, intensity)



5. Identify green cells in the green channel



6. Count and measure green cells
(number, area, intensity)



Supplementary methods SM05.

Process of data acquisition for SRF-reporter assay with digital microscopy.

Example 3: 24 h stimulation with 1 μmol/l PMA.

Supplementary methods SM06.

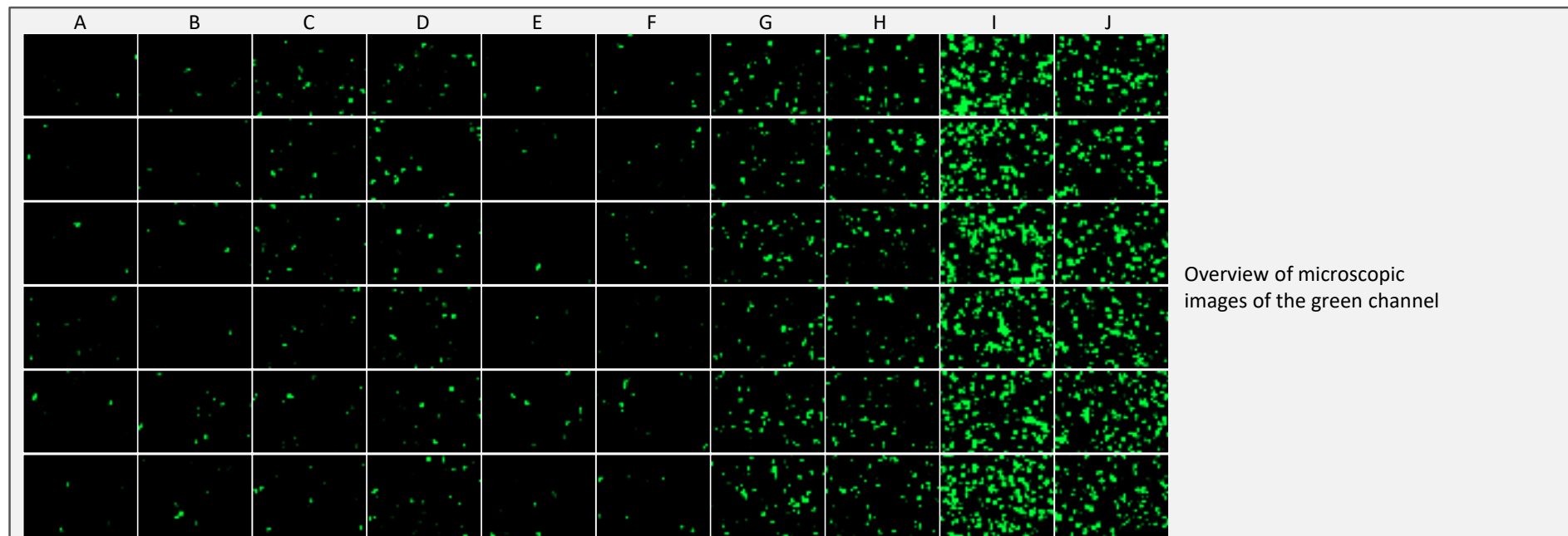
Test comparison of SRF-reporter assay results obtained by single cell digital microscopy or fluorometry.

Columns A-J were incubated with different stimuli for 24 h. Column A = Control.

The upper panel shows an overview of microscopic images of the green channel (= SRF-reporter activity)

The middle panel shows the results of the single cell digital microscopy analysis of the parameters „number of green cells per area“ and mean green fluorescence of transfected cells (=red cells).

The lower panel shows the results of the fluorometry analysis of the parameter „green fluorescence intensity per well“.

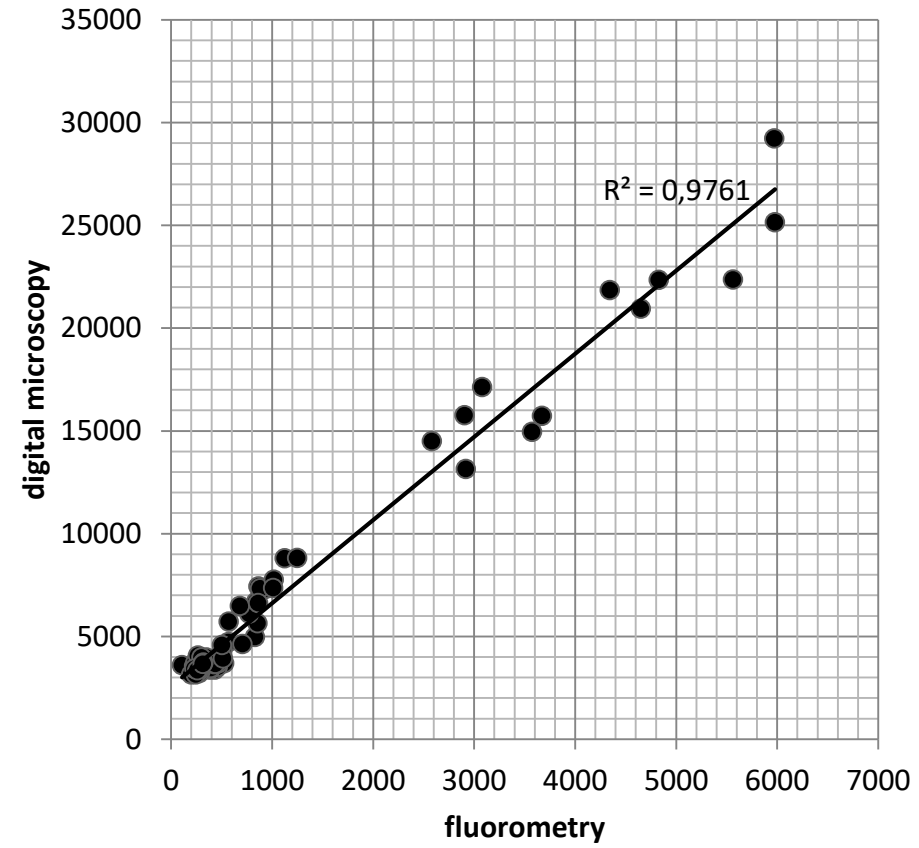


Overview of microscopic images of the green channel

| | | | | | | | | | | |
|-----|------|------|------|------|------|------|------|-------|-------|--|
| 42 | 39 | 82 | 62 | 43 | 38 | 110 | 102 | 211 | 178 | single cell digital microscopy Number of green cells per area |
| 25 | 25 | 40 | 73 | 41 | 36 | 91 | 110 | 217 | 158 | |
| 31 | 37 | 60 | 60 | 21 | 35 | 132 | 112 | 221 | 166 | |
| 48 | 25 | 61 | 76 | 18 | 43 | 83 | 102 | 210 | 157 | |
| 19 | 35 | 48 | 45 | 40 | 46 | 108 | 103 | 207 | 209 | |
| 27 | 43 | 38 | 80 | 23 | 38 | 117 | 133 | 245 | 189 | |
| 982 | 681 | 2271 | 2008 | 818 | 795 | 3977 | 4606 | 26529 | 14429 | mean green fluorescence of transfected cells (=red cells) |
| 818 | 672 | 978 | 2937 | 627 | 898 | 3009 | 6097 | 19635 | 11789 | |
| 749 | 697 | 1270 | 1689 | 633 | 843 | 4720 | 4631 | 19654 | 12237 | |
| 945 | 444 | 1044 | 1921 | 510 | 587 | 3394 | 3774 | 19149 | 13061 | |
| 963 | 1064 | 764 | 1222 | 1354 | 1272 | 5047 | 3920 | 18232 | 13029 | |
| 449 | 716 | 1012 | 1875 | 639 | 949 | 6115 | 4646 | 22437 | 10444 | |
| 525 | 434 | 828 | 567 | 235 | 348 | 842 | 932 | 5969 | 3077 | fluorometry green fluorescence intensity per well |
| 460 | 384 | 461 | 853 | 208 | 107 | 568 | 1122 | 4828 | 2580 | |
| 393 | 285 | 347 | 508 | 294 | 228 | 865 | 880 | 5563 | 3571 | |
| 428 | 198 | 400 | 704 | 279 | 267 | 773 | 680 | 4341 | 2904 | |
| 437 | 243 | 280 | 512 | 266 | 301 | 1017 | 860 | 4650 | 3672 | |
| 243 | 231 | 320 | 501 | 260 | 312 | 1246 | 1010 | 5978 | 2916 | |

Supplementary methods SM07.

Correlation of the SRF-reporter assay results obtained by single cell digital microscopy or fluorometry from **Supplementary methods SM06.**



Supplementary methods SM08.

Examples of microscopy images and process of data acquisition for phospho-pERK1/2 in-cell-ELISA.

Cells were transfected with AT1R.

EGFP served as transfection control (green channel).

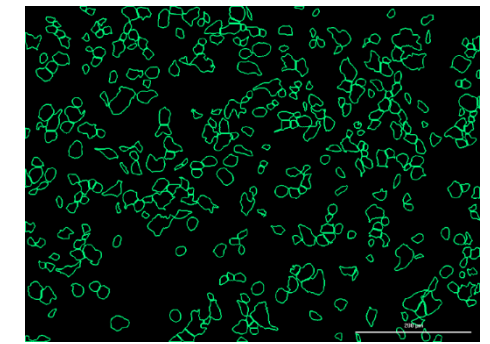
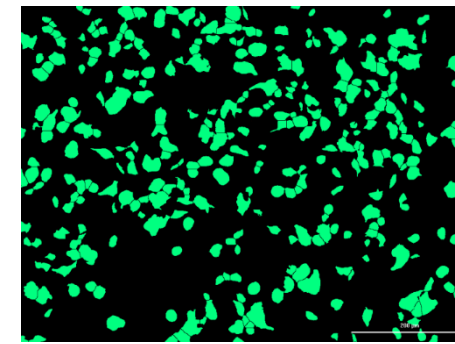
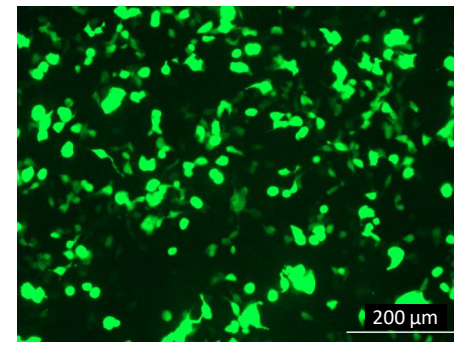
Phospho-pERK1/2 was detected with a rabbit primary antibody and an AlexaFluor568 labeled secondary antibody (red channel).

1. Acquire microscope images in green channel

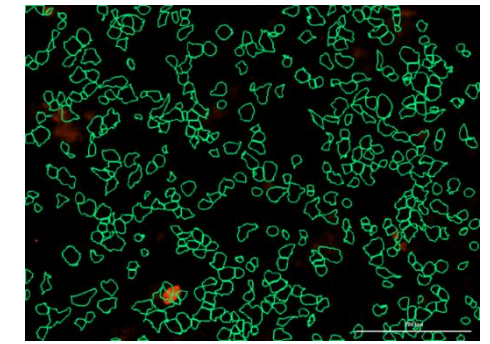
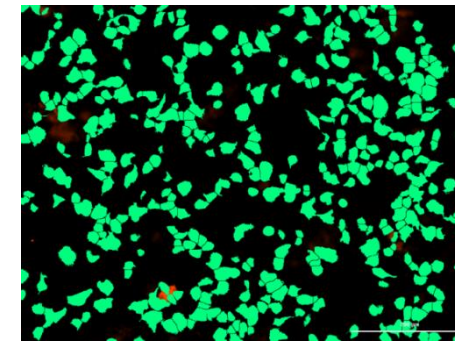
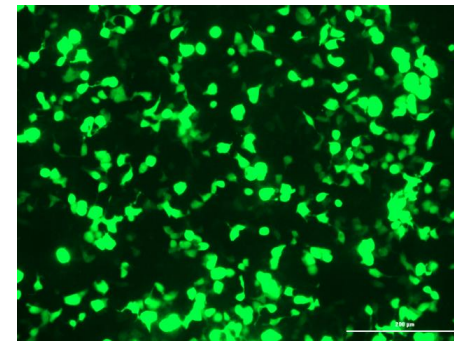
2. Identify & mark transfected (green) cells

3. Measure red fluorescence in green cells

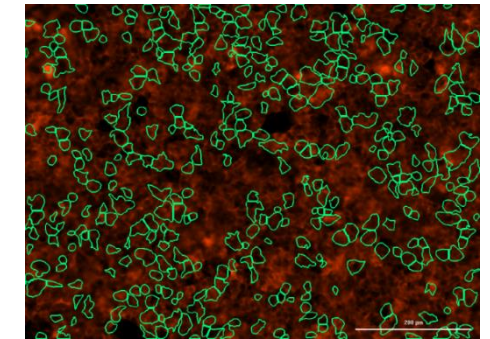
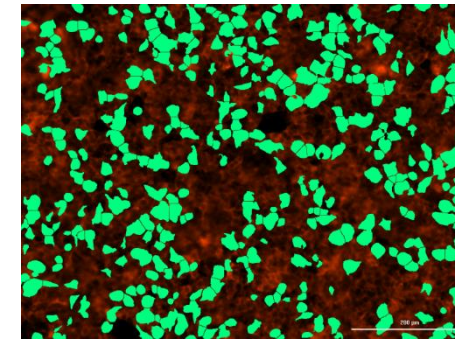
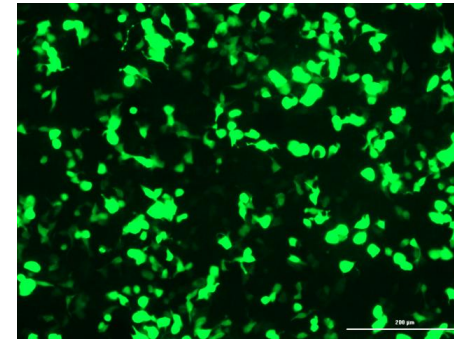
Blank
(without primary antibody)



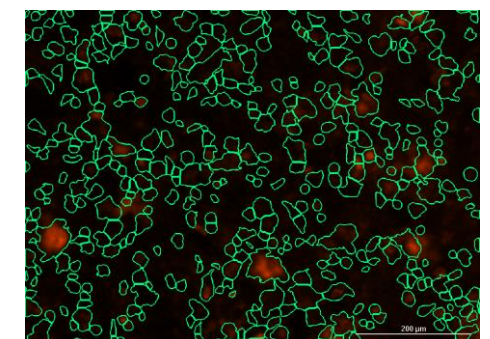
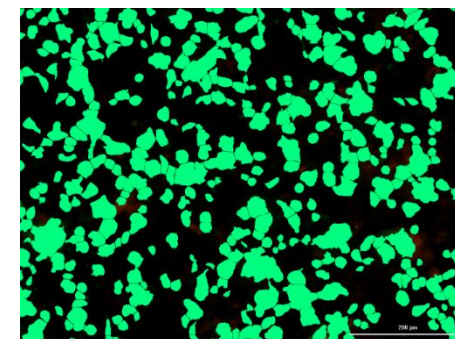
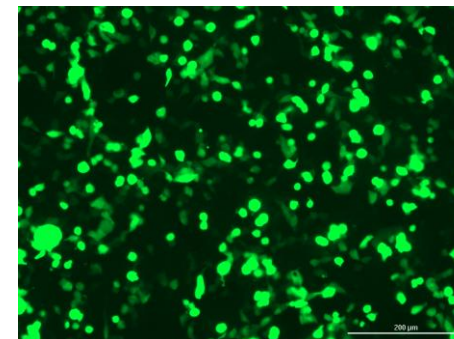
control
(with primary antibody)



10 μg/l EGF for 30 minutes
(with primary antibody)



10 nmol/l angiotensin II
for 30 minutes
(with primary antibody)

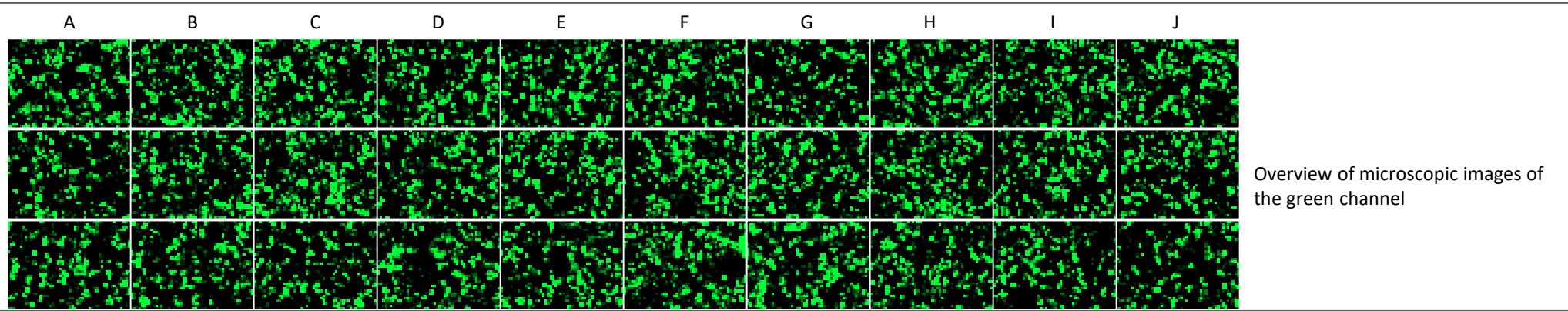


Supplementary methods SM09.

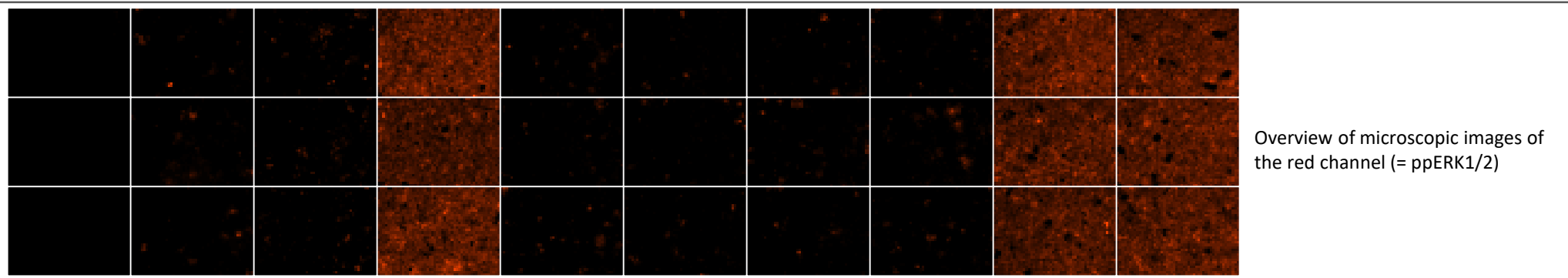
Test comparison of in-cell-ELISA results for ppERK1/2 obtained by single cell digital microscopy or fluorometry.

Columns A-J were incubated with different stimuli for 30 minutes.

Column A = Blank. Column B = control.



Overview of microscopic images of the green channel

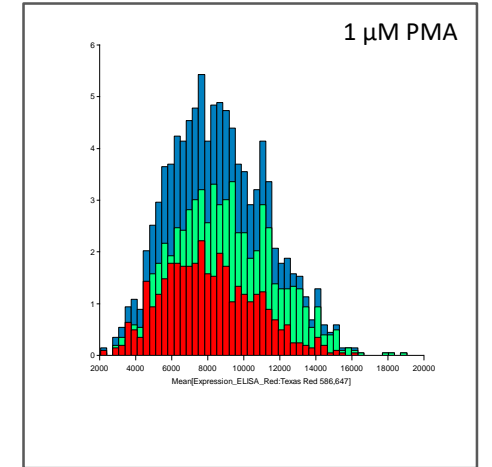
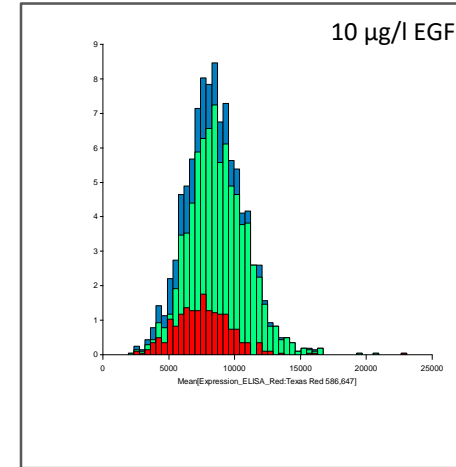
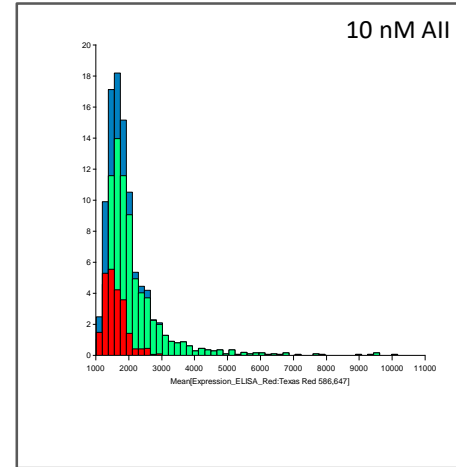
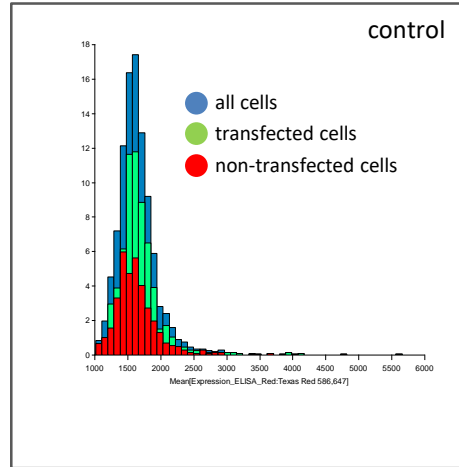
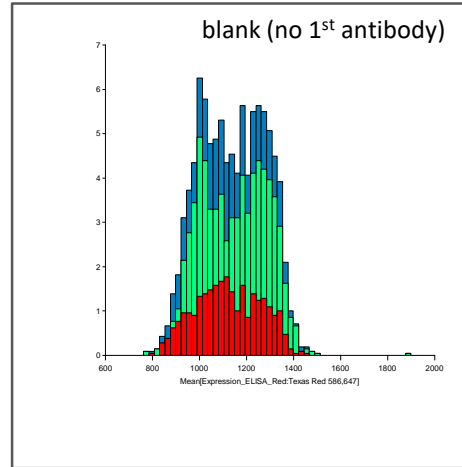


Overview of microscopic images of the red channel (= ppERK1/2)

| | | | | | | | | | | |
|--------------------------------|------|------|------|------|------|------|------|------|------|---|
| single cell digital microscopy | | | | | | | | | | |
| 1195 | 1643 | 1734 | 6363 | 1763 | 1699 | 1678 | 1746 | 6356 | 5894 | mean red fluorescense (= ppERK1/2) of transfected cells |
| 1167 | 1832 | 1794 | 5089 | 1689 | 1764 | 1846 | 1912 | 5667 | 6030 | |
| 1174 | 1669 | 1690 | 6284 | 1792 | 1664 | 1706 | 1742 | 5439 | 5990 | |

| | | | | | | | | | | |
|-------------|------|------|------|------|------|------|------|------|------|-------------------------------------|
| fluorometry | | | | | | | | | | |
| 1216 | 1715 | 1877 | 6414 | 1828 | 1781 | 1762 | 1772 | 6611 | 5952 | red fluorescence intensity per well |
| 1173 | 1873 | 1928 | 5167 | 1744 | 1850 | 1925 | 1974 | 5889 | 6160 | |
| 1182 | 1679 | 1918 | 6563 | 1835 | 1733 | 1751 | 1716 | 5637 | 6118 | |

Supplementary methods SM10. Comparison of pERK1/2-phosphorylation by in-cell-ELISA and single cell digital microscopy in AT1R-WT-transfected and non-transfected cells of one population. Cells were incubated 30 minutes. Histograms for the distribution of the ppERK1/2-signal (red fluorescence) at the single cell level are shown. The range of the x-axis varies. Quantification see next figure.



Supplementary methods SM11.

Quantification of pERK1/2-phosphorylation by in-cell-ELISA and single cell digital microscopy in AT1R-WT-transfected and non-transfected cells out of one mixed population.

Cells were incubated for 30 minutes.

The upper tables shows the results for transfected cells (identified by green fluorescence).

The lower tables shows the results for non-transfected cells (identified by the lack of green fluorescence).

The show that only cells transfected with AT1R respond to angiotensin II, whereas all cells respond to EGF and PMA that served as positive controls.

| blank | control | 0.1 nM All | 1 nM All | 10 nM All | 10 µg/l EGF | 1 µM PMA | single cell digital microscopy |
|-------------|------------|------------|------------|------------|-------------|-------------|---|
| 1165 | 1655 | 1730 | 1994 | 3014 | 7848 | 8712 | mean red fluorescene (= ppERK1/2) of transfected cells |
| 1143 | 1640 | 1777 | 1971 | 2339 | 8984 | 8828 | |
| 1326 | 1660 | 1742 | 1998 | 2328 | 8699 | 9828 | |
| mean | 100 | 122 | 176 | 306 | 1658 | 1797 | % of control |
| sd | 2 | 5 | 3 | 73 | 110 | 114 | |

| blank | control | 0.1 nM All | 1 nM All | 10 nM All | 10 µg/l EGF | 1 µM PMA | single cell digital microscopy |
|-------------|------------|------------|------------|------------|-------------|-------------|---|
| 1166 | 1454 | 1568 | 1613 | 1689 | 6924 | 8754 | mean red fluorescene (= ppERK1/2) of non-transfected cells |
| 1189 | 1644 | 1491 | 1580 | 1600 | 6849 | 8218 | |
| 1221 | 1604 | 1582 | 1636 | 1654 | 7419 | 8488 | |
| mean | 100 | 95 | 111 | 121 | 1564 | 1944 | % of control |
| sd | 22 | 11 | 6 | 10 | 67 | 58 | |

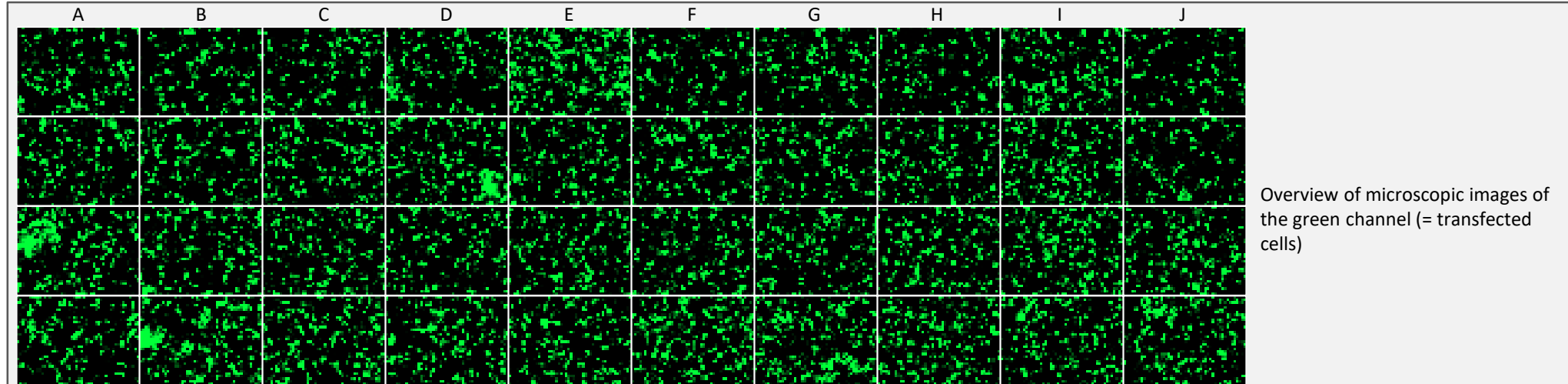
Supplementary methods SM12.

Example of in-cell-ELISA for ppERK1/2 in cells transfected with AT1R-WT, obtained by single cell digital microscopy.

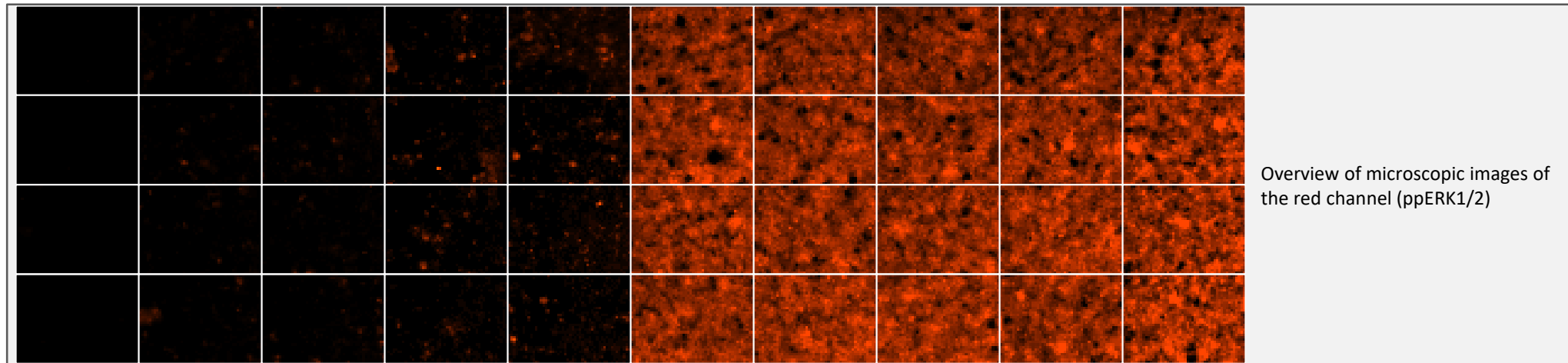
Columns A-J were incubated with different stimuli for 30 minutes.

- A = blank
- B = control
- C = 0.1 nM All
- D = 1 nM All
- E = 10 nM All
- F = 10 $\mu\text{g/l}$ EGF
- G = EGF + 0.1 All
- H = EGF + 1 All
- I = EGF + 10 All
- J = 1 μM PMA

The data show that EGF, PMA as well as All induced pERK1/2-phosphorylation and that the effects of All and EGF are not additive.



Overview of microscopic images of the green channel (= transfected cells)



Overview of microscopic images of the red channel (ppERK1/2)

| | | | | | | | | | | |
|-------------|------------|------------|------------|------------|-------------|-------------|-------------|-------------|-------------|--|
| 1171 | 1689 | 1721 | 2028 | 2977 | 8056 | 8260 | 8057 | 8106 | 8736 | single cell digital microscopy mean red fluorescence (= ppERK1/2) of transfected cells |
| 1147 | 1683 | 1785 | 2094 | 2332 | 9189 | 9004 | 9188 | 9712 | 9478 | |
| 1345 | 1692 | 1761 | 1994 | 2349 | 8923 | 9204 | 9408 | 10319 | 9725 | |
| 1184 | 1754 | 1803 | 1910 | 2228 | 8826 | 9799 | 10044 | 9673 | 10529 | |
| mean | 100 | 111 | 159 | 263 | 1578 | 1628 | 1608 | 1721 | 1644 | |
| sd | 2 | 8 | 22 | 92 | 81 | 105 | 172 | 189 | 136 | % of control |

Supplementary methods figure SM13.

Example of in-cell-ELISA for cFOS in cells transfected with AT1R, obtained by single cell digital microscopy.

Cells were transfected with AT1R-WT.

Columns A-G were incubated with different stimuli for 6 h.

A = Blank

B = control

C = 1 nM All

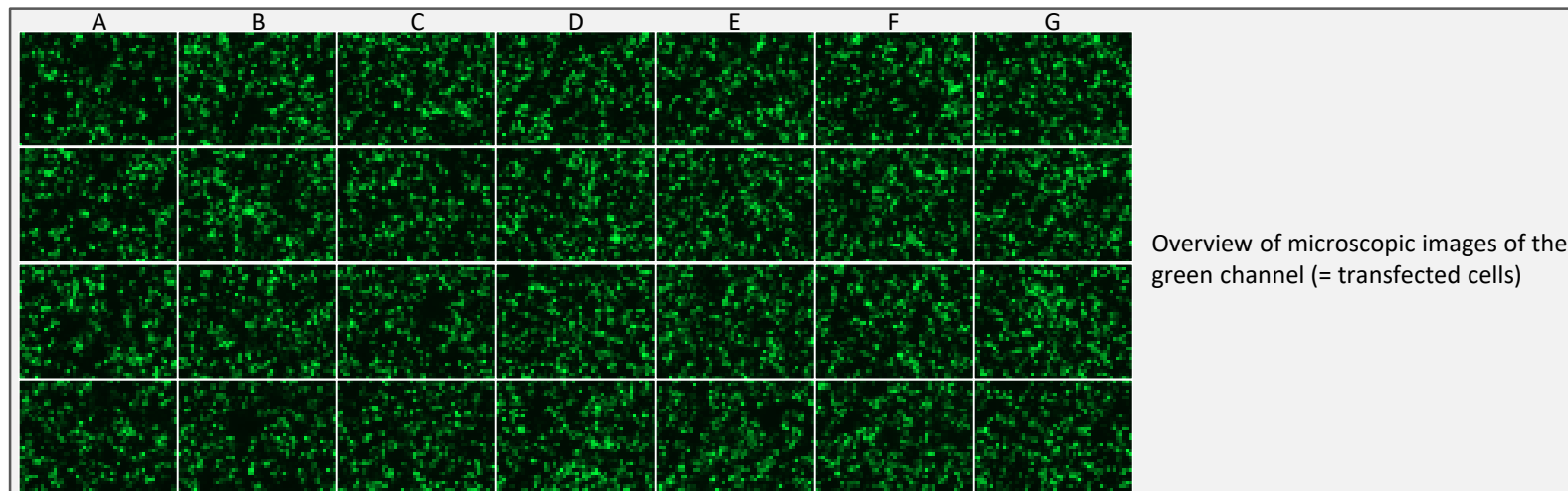
D = 10 nM All

E = 10 µg/l EGF

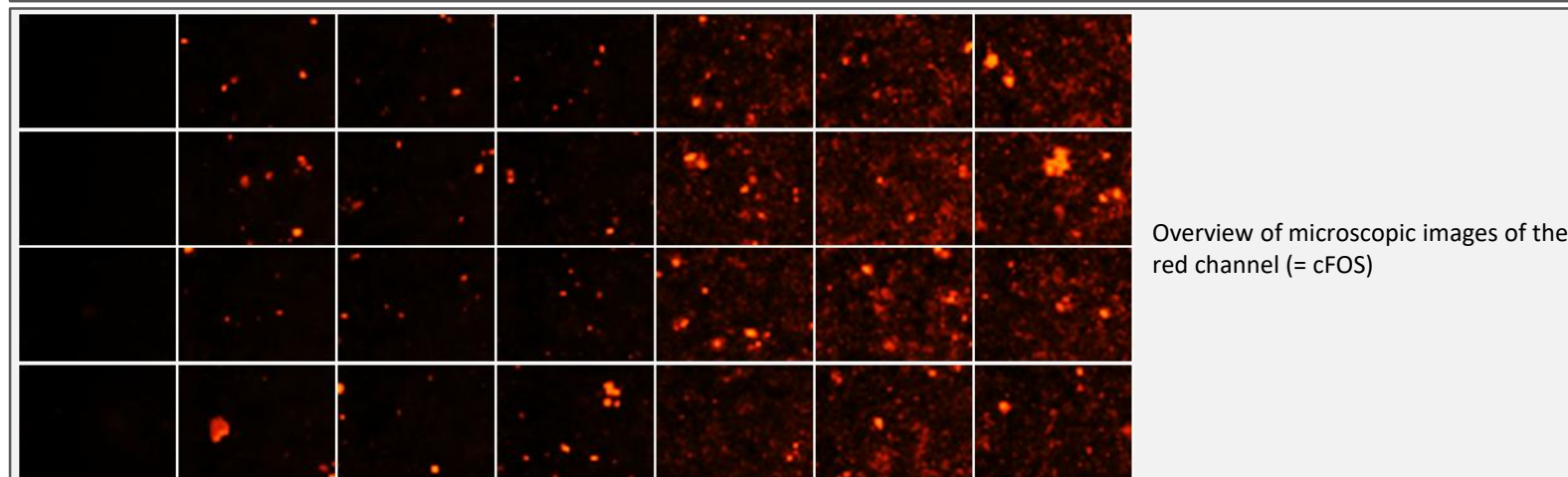
F = EGF + 1 nM All

G = EGF + 10 nM All.

The data show (i) that EGF induces cFOS-expression independently of AT1R expression, whereas All exerts no effect in transfected or non-transfected cells. Furthermore, the data show (ii) a synergistic effect of EGF and All on cFOS-expression in AT1R-transfected cells (compare column E with columns F and G in the upper table) but not in non-transfected cells (lower table).



Overview of microscopic images of the green channel (= transfected cells)



Overview of microscopic images of the red channel (= cFOS)

| | | | | | | | | |
|-------------|------------|------------|------------|------------|------------|------------|---|--------------|
| 1123 | 1373 | 1661 | 1636 | 2762 | 3195 | 3419 | single cell digital microscopy mean red fluorescence (= cFOS) of transfected cells | |
| 1084 | 1567 | 1666 | 1792 | 2575 | 3250 | 3635 | | |
| 1103 | 1689 | 1609 | 1736 | 2395 | 3112 | 3355 | | |
| 1123 | 1538 | 1713 | 1855 | 2421 | 2937 | 3255 | | |
| mean | 100 | 128 | 149 | 330 | 465 | 532 | | % of control |
| sd | 26 | 8 | 19 | 34 | 27 | 32 | | |
| | | | | | | | | |

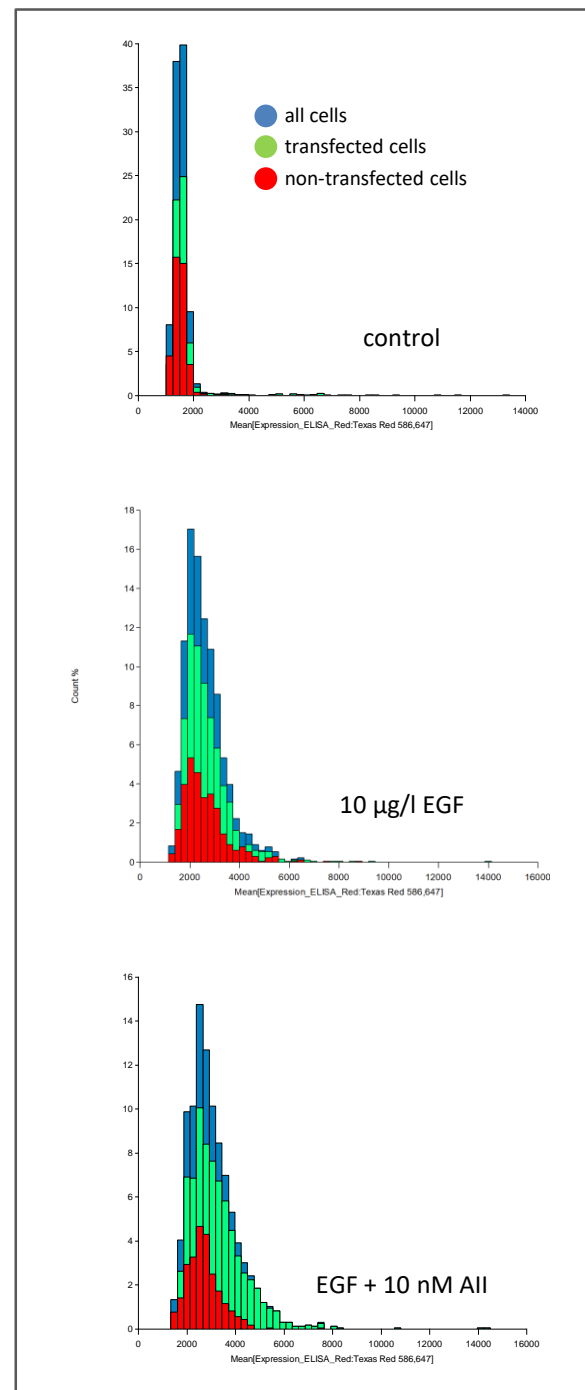
| | | | | | | | | |
|-------------|------------|-----------|-----------|------------|------------|------------|---|--------------|
| 1014 | 1527 | 1425 | 1488 | 2592 | 2463 | 2594 | single cell digital microscopy mean red fluorescence (= cFOS) of non-transfected cells | |
| 1051 | 1540 | 1545 | 1425 | 2550 | 2636 | 2548 | | |
| 1062 | 1463 | 1464 | 1420 | 2581 | 2690 | 2573 | | |
| 1062 | 1480 | 1457 | 1467 | 2426 | 2657 | 2424 | | |
| mean | 100 | 93 | 88 | 327 | 344 | 327 | | % of control |
| sd | 7 | 10 | 6 | 15 | 19 | 14 | | |
| | | | | | | | | |

Supplementary methods SM14.

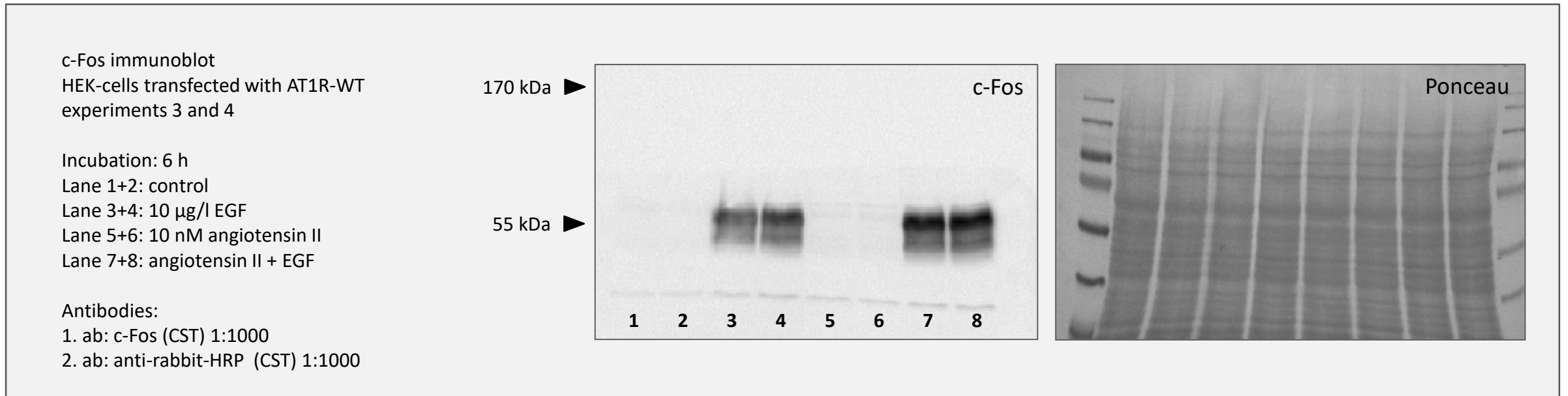
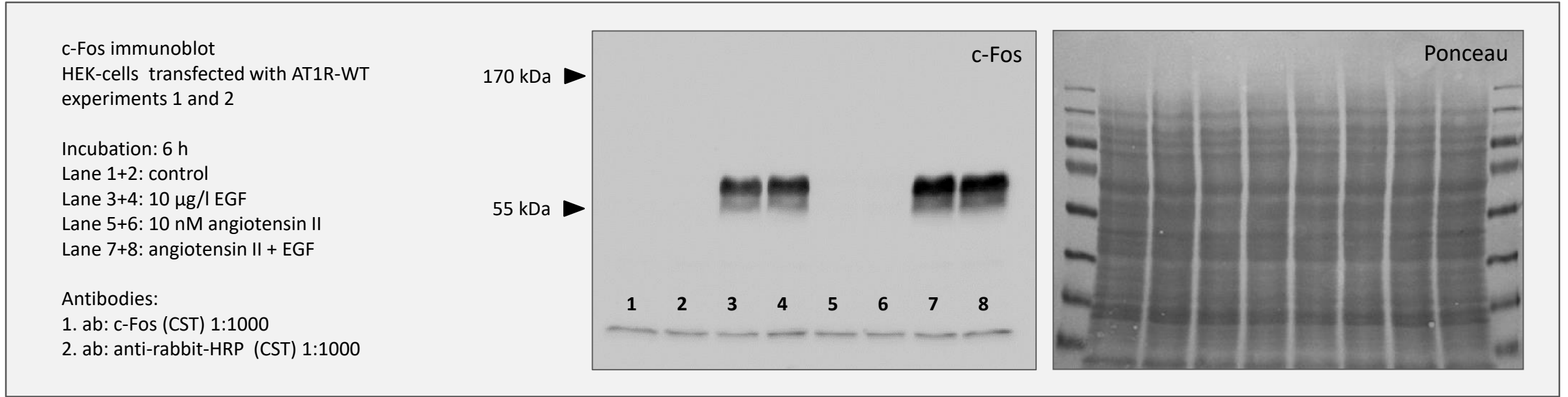
Comparison of cFOS-expression by in-cell-ELISA and single cell digital microscopy in AT1R-WT-transfected and non-transfected cells out of one mixed population, at the individual cell level. Histogramms for the distribution of the cFOS-signal for transfected and non-transfected cells at the single cell level are shown. For quantification see **supplementary methods SM13**.

Cells were incubated for 6 h.

EGF leads to an increased cFOS expression of transfected and non-transfected cells with a similar intensity profile (see middle panel). The addition of angiotensin II (All) leads to an additional increase of cFOS-expression only in transfected (= AT1R expressing) cells (see the different expression profile of transfected and non-transfected cells in the lower panel).



Supplementary methods SM15. Confirmation immunoblots of EGF-All-synergism concerning cFOS-expression in cells expressing AT1R-WT. The four experiments presented here confirm the data obtained by in-cell-ELISA.



Supplementary methods SM16. Confirmation immunoblots for EGF-All-synergism concerning cFOS-expression in cells expressing AT1R-MUT1. The four experiments presented here confirm the data obtained by in-cell-ELISA.

c-Fos immunoblot
HEK-cells transfected with AT1R-MUT
experiments 1 and 2

Inkubation: 6 h

Lane 1+2: control

Lane 3+4: 10 μ g/l EGF

Lane 5+6: 10 nM angiotensin II

Lane 7+8: angiotensin II + EGF

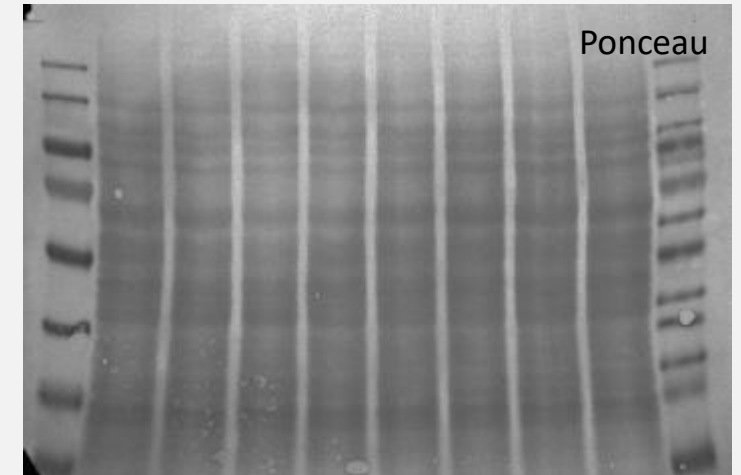
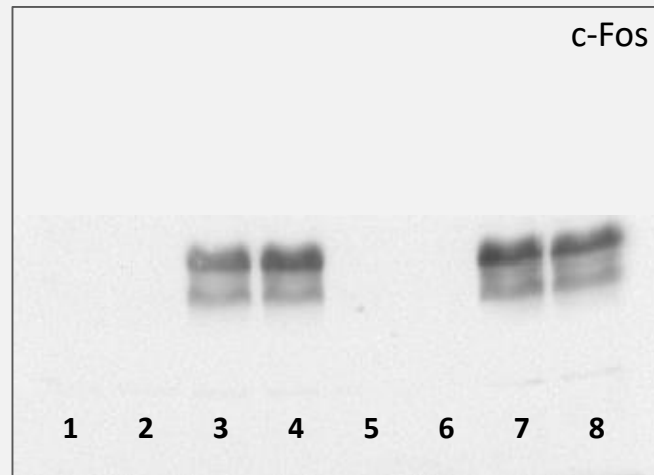
Antibodies:

1. ab: c-Fos (CST) 1:1000

2. ab: anti-rabbit-HRP (CST) 1:1000

170 kDa \blacktriangleright

55 kDa \blacktriangleright



c-Fos immunoblot
HEK-cells transfected with AT1R-MUT
experiments 1 and 2

Inkubation: 6 h

Lane 1+2: control

Lane 3+4: 10 μ g/l EGF

Lane 5+6: angiotensin II + EGF

Lane 7+8: 10 nM angiotensin II

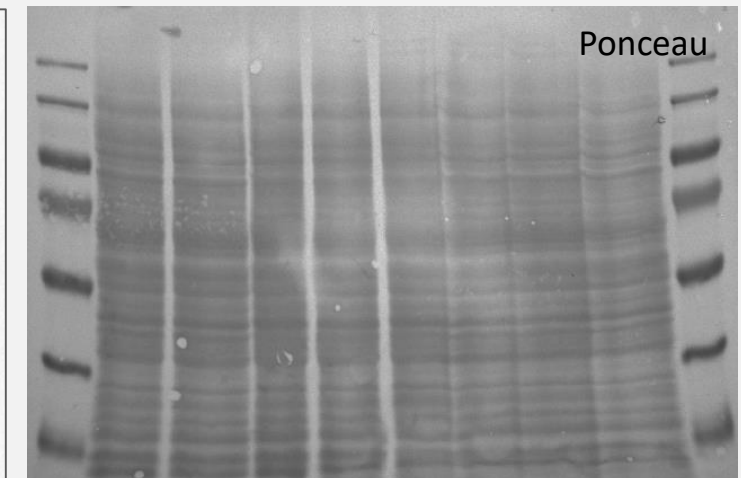
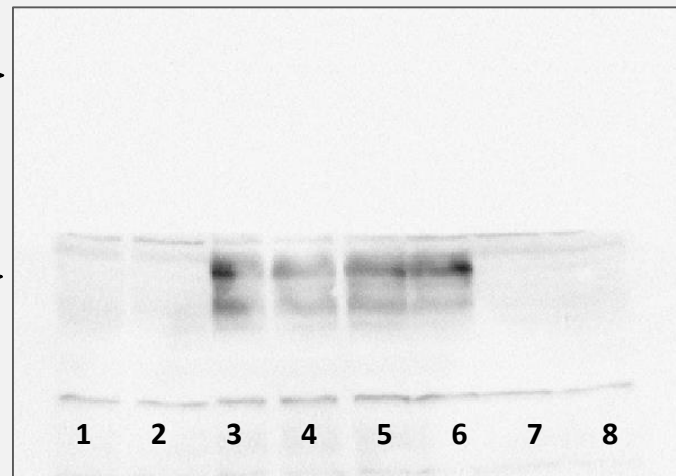
Antibodies:

1. ab: c-Fos (CST) 1:1000

2. ab: anti-rabbit-HRP (CST) 1:1000

170 kDa \blacktriangleright

55 kDa \blacktriangleright



Supplementary methods SM17. Analysis of the immunoblot results for EGF-All-synergism concerning cFOS-expression in cells expressing AT1R-WT or AT1R-MUT1. The data here confirm the data obtained by in-cell-ELISA. Statistical analysis was performed by ANOVA. (N/n = 4/4).

