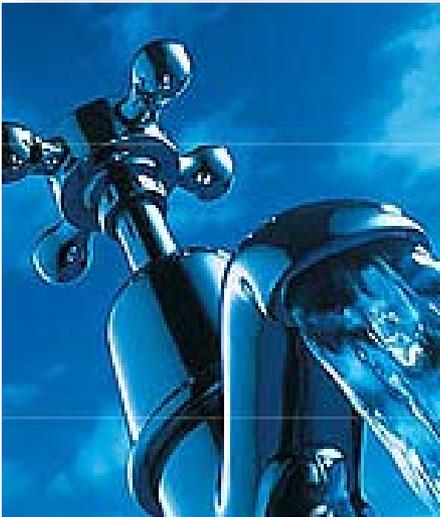


International Symposium for HPTLC
8. July 2011, Basel

Effect-directed analysis of landfill leachate using HPTLC/AMD with bioluminescence detection



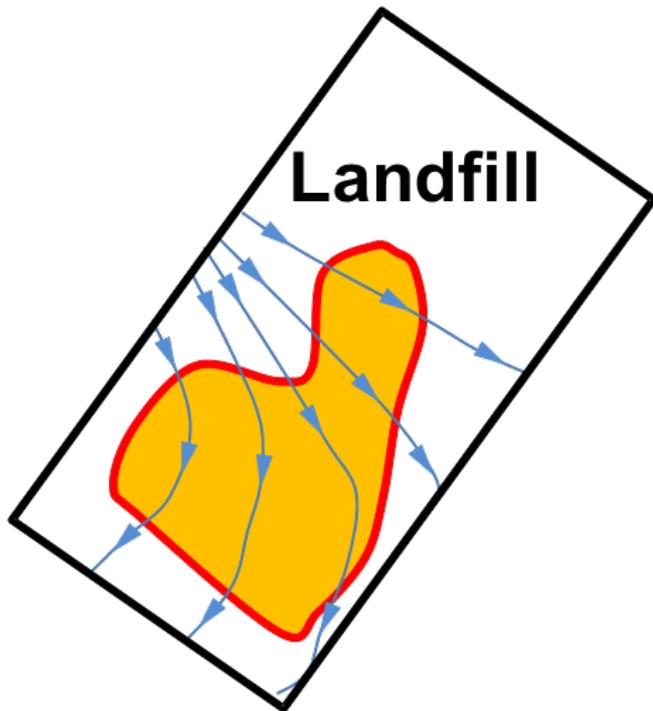
**Stefan C. Weiss^{1,2}, Wolfgang Schulz¹,
Wolfgang K.L. Ruck² and Walter H. Weber¹**

¹Zweckverband Landeswasserversorgung
Laboratory for Operation Control and Research
Langenau, Germany

²Leuphana University Lüneburg
Institute for Environmental Chemistry, Germany

weiss.s@lw-online.de

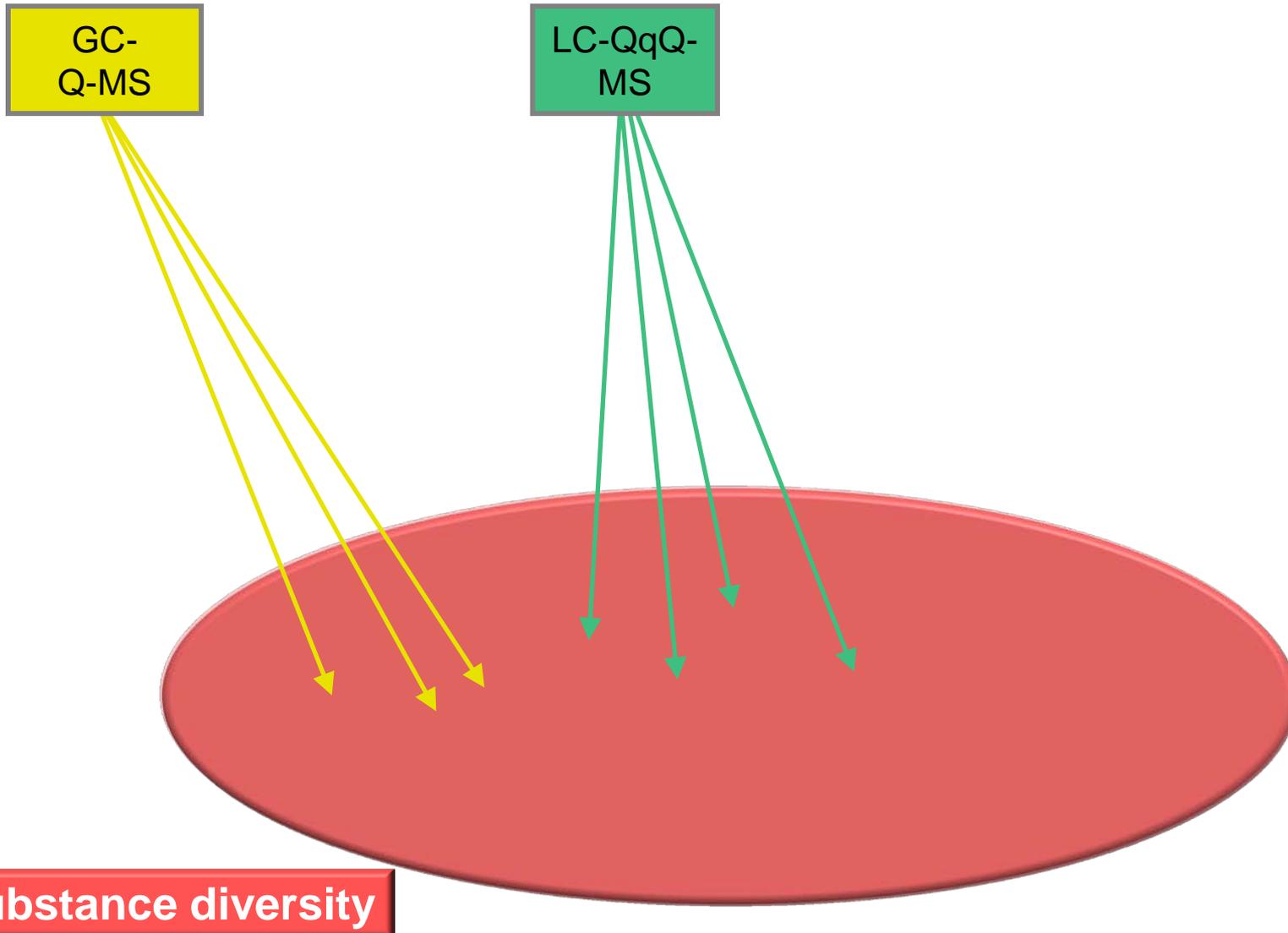
Exploration of contaminated sites



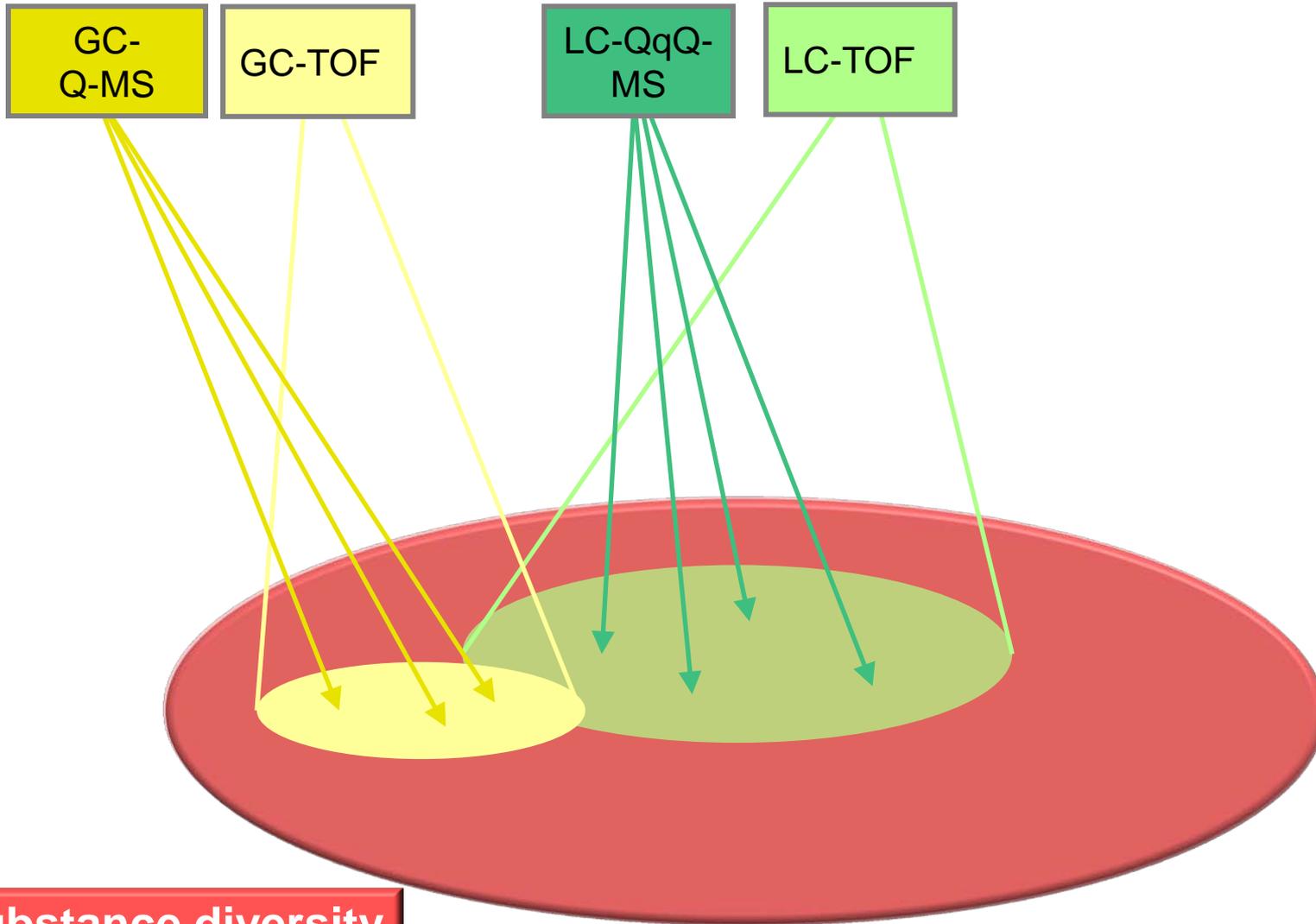
Definition of the problem

- How heavy polluted is this area?
- Which is the method of choice for evaluating the contamination?
- Which substances have a higher priority to be identified?

Strategy Target Analysis

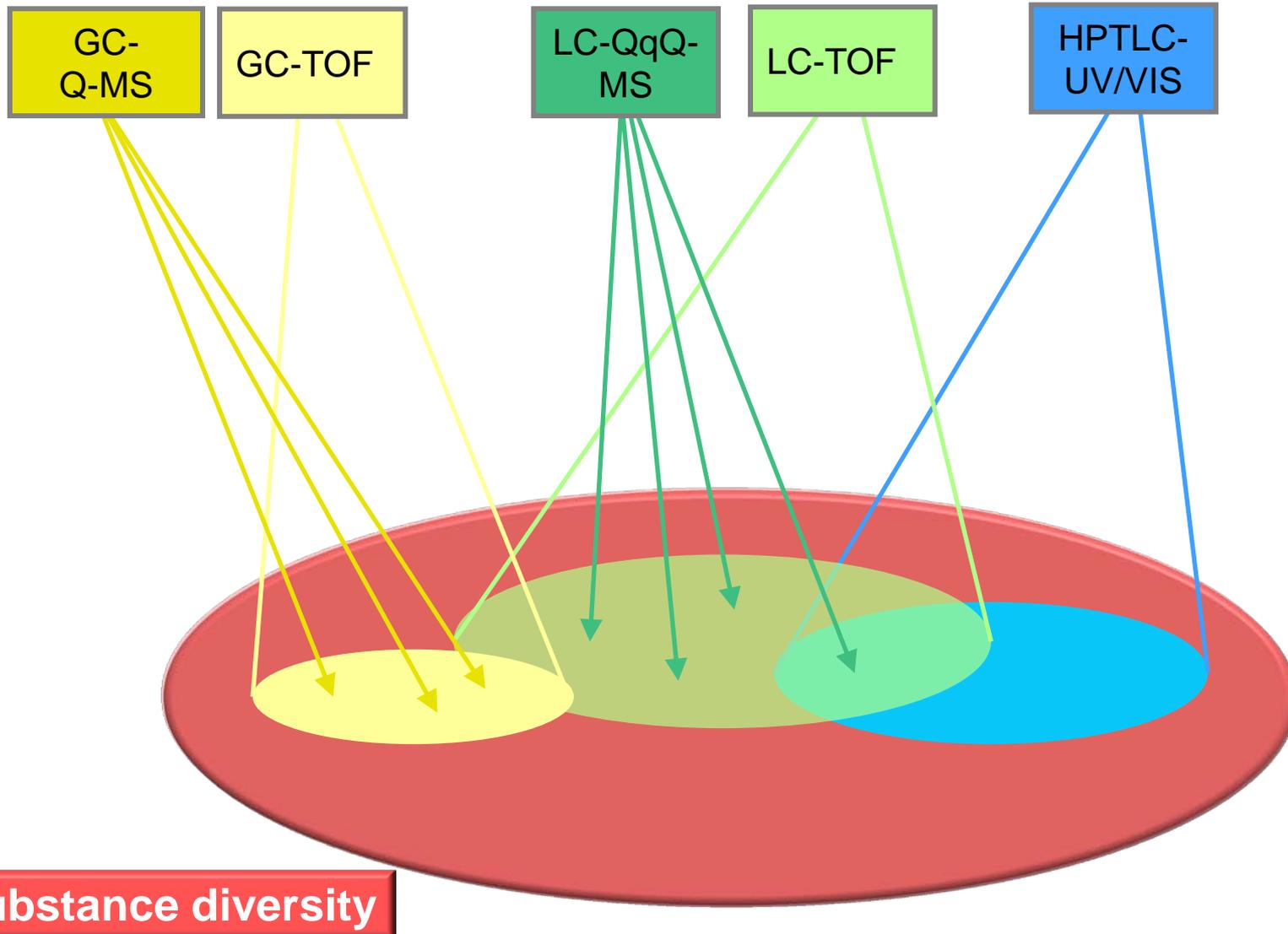


Strategy Non-Target-Screening

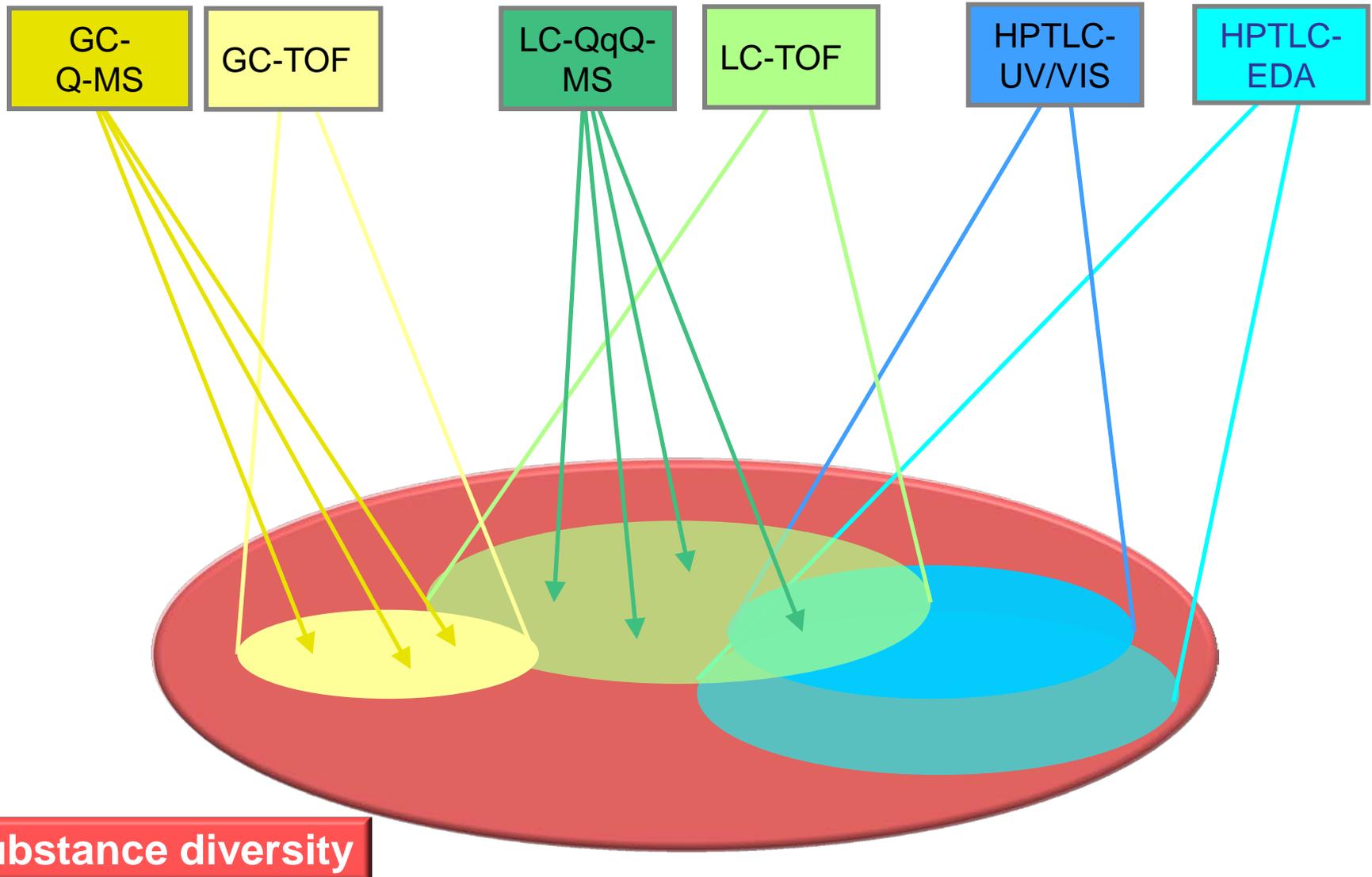


Substance diversity

Strategy Non-Target-Screening



Strategy Non-Target-Screening with effect-directed analysis (EDA)

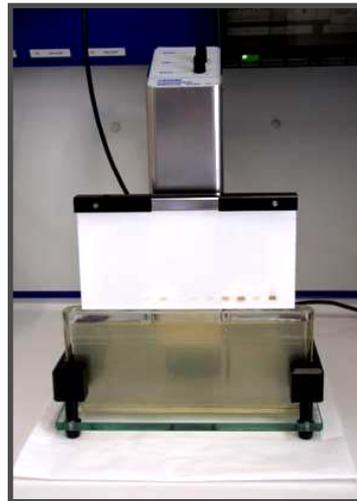


Schematic diagram of the HPTLC-AMD analysis with bioluminescence detection

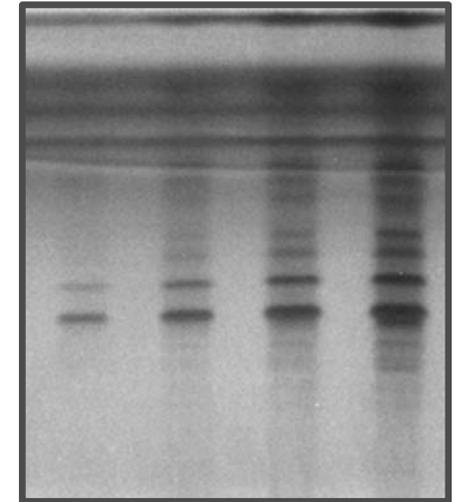
Vibrio fischeri



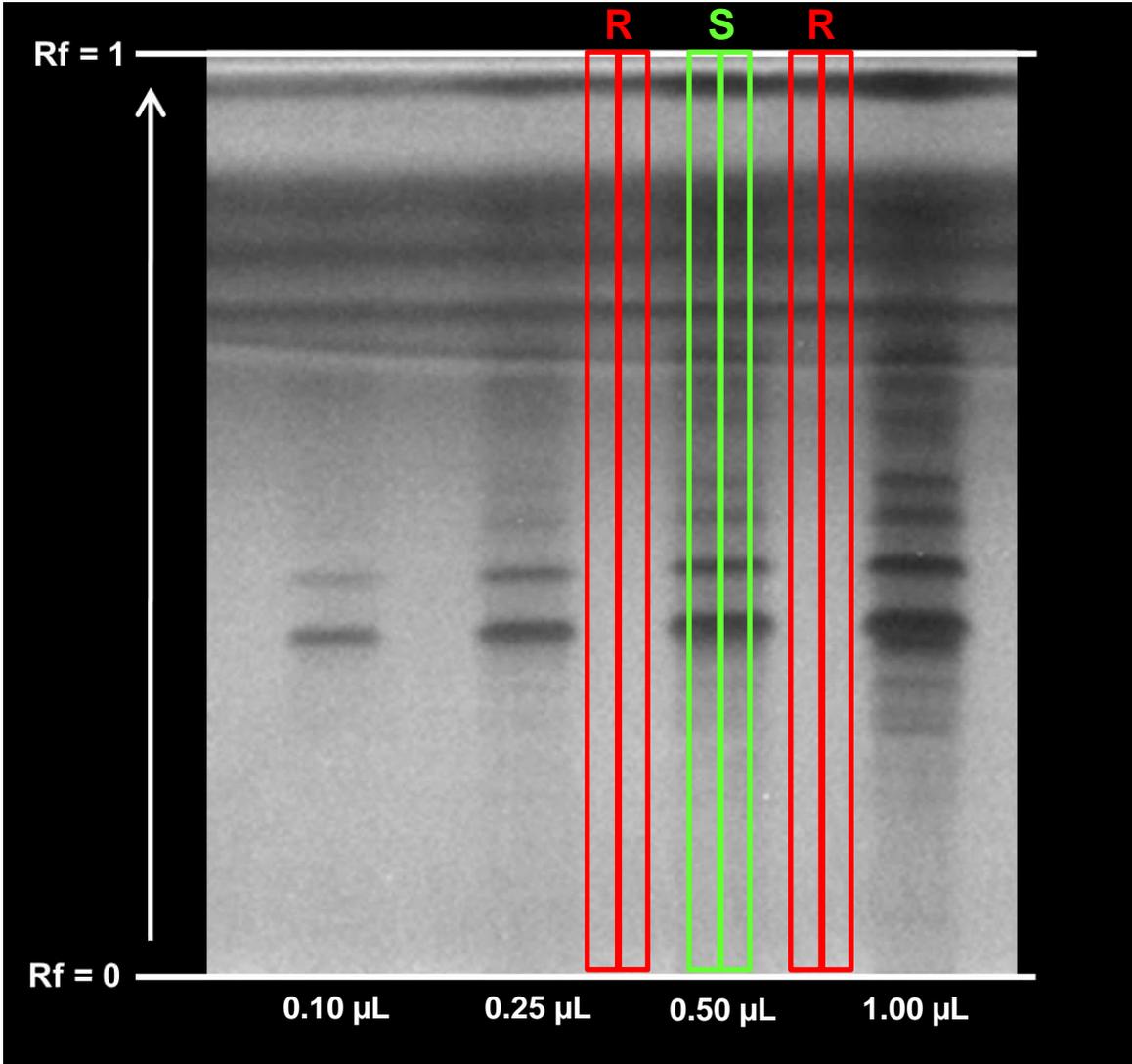
Immersion



Detection



Evaluation of the bioluminescence picture



Calculation of inhibition chromatogram

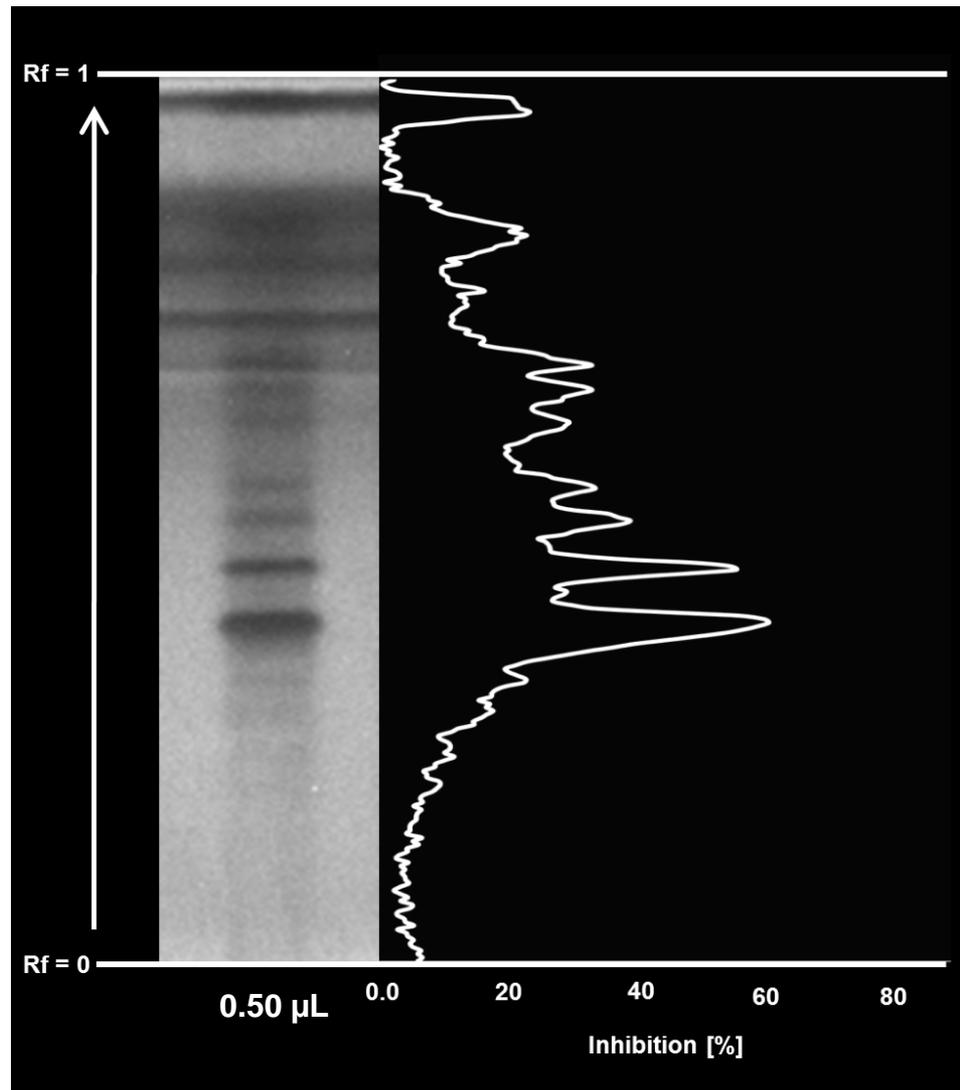
| Pixel row | R left | Track | R right | Average R | Inhibition [%] |
|-----------|--------|--------|---------|-----------|----------------|
| 1 | 192,87 | 191,72 | 187,5 | 190,19 | -0,81 |
| 2 | 193,1 | 191,97 | 188,35 | 190,73 | -0,65 |
| 3 | 192,05 | 191,72 | 188,65 | 190,35 | -0,72 |
| 4 | 195,05 | 192,47 | 190,75 | 192,90 | 0,22 |
| 5 | 196,15 | 192,69 | 192,1 | 194,13 | 0,74 |
| 6 | 197,8 | 189,25 | 193,7 | 195,75 | 3,32 |
| 7 | 197,05 | 184,14 | 193,65 | 195,35 | 5,74 |
| 8 | 198,2 | 177,42 | 193,7 | 195,95 | 9,46 |
| 9 | 199,4 | 171,47 | 195,35 | 197,38 | 13,12 |
| 10 | 199 | 168,53 | 195,95 | 197,48 | 14,66 |
| 11 | 199,25 | 167,58 | 196,65 | 197,95 | 15,34 |
| 12 | 200,25 | 166,64 | 197,6 | 198,93 | 16,23 |
| 13 | 201,75 | 168,14 | 199,35 | 200,55 | 16,16 |
| ⋮ | | | | | |
| 233 | 159,35 | 153,31 | 154,55 | 156,95 | 2,32 |
| 234 | 153,15 | 144,92 | 146,45 | 149,80 | 3,26 |
| 235 | 144,05 | 137,28 | 139,55 | 141,80 | 3,19 |
| 236 | 137,75 | 132,97 | 134,9 | 136,33 | 2,46 |
| 237 | 136,45 | 133,89 | 133,35 | 134,90 | 0,75 |
| 238 | 139,35 | 137,83 | 136,95 | 138,15 | 0,23 |
| 239 | 146,4 | 146,19 | 146,1 | 146,25 | 0,04 |
| 240 | 154,75 | 154,36 | 155,8 | 155,28 | 0,59 |
| 241 | 162,5 | 162,92 | 163,8 | 163,15 | 0,14 |
| 242 | 169,95 | 170,97 | 171,55 | 170,75 | -0,13 |

$$I_{n_k}^S = 1 - \frac{i_{n_k}^S}{i_{n_k}^R}$$

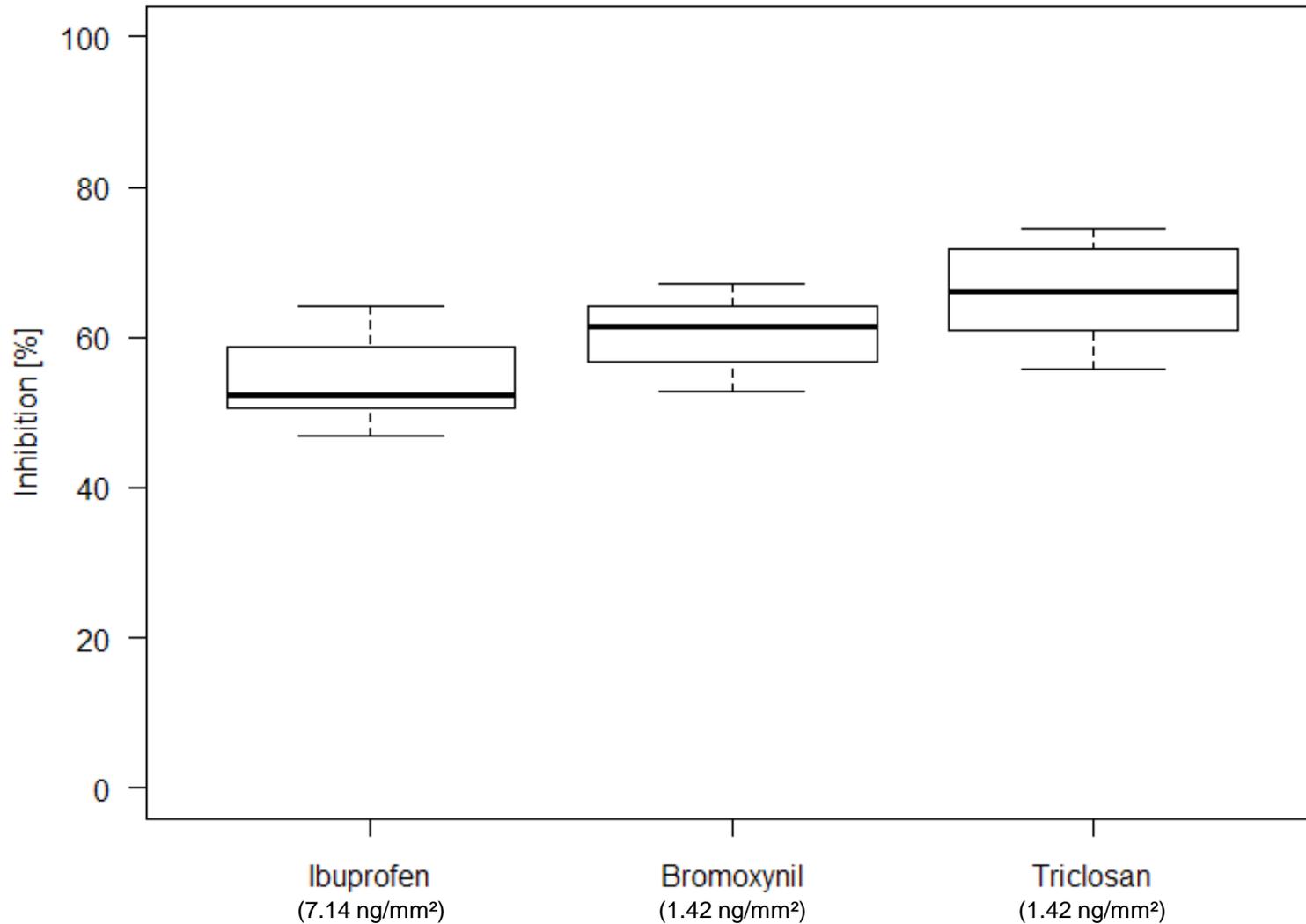
- I = Inhibition
- i = Light intensity
- S = Sample
- R = Reference
- n = Pixel
- k = row

Grayscales

Inhibition chromatogram



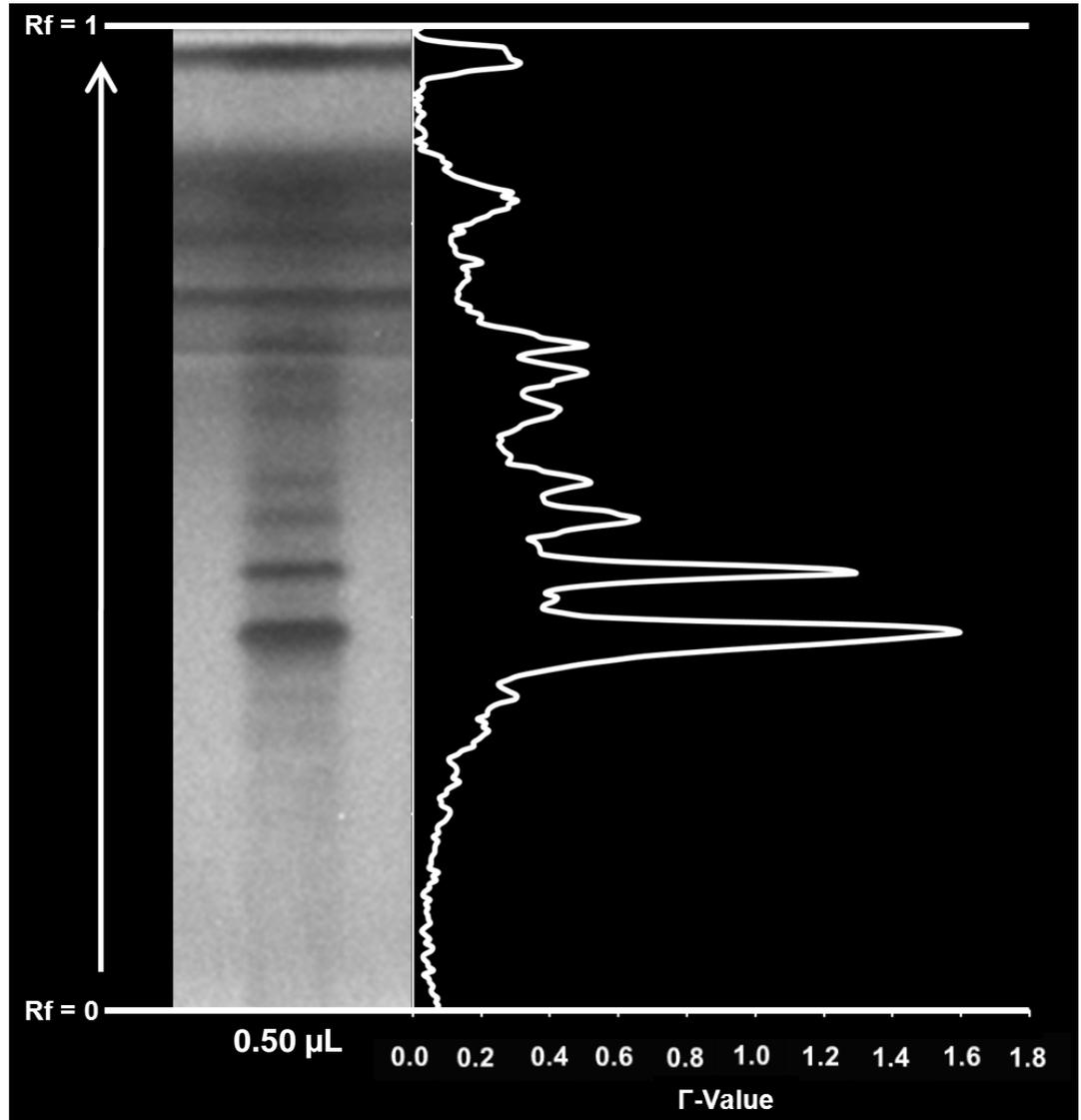
Boxplot for the inhibition of reference substances (N = 54 in a period of 2 months)



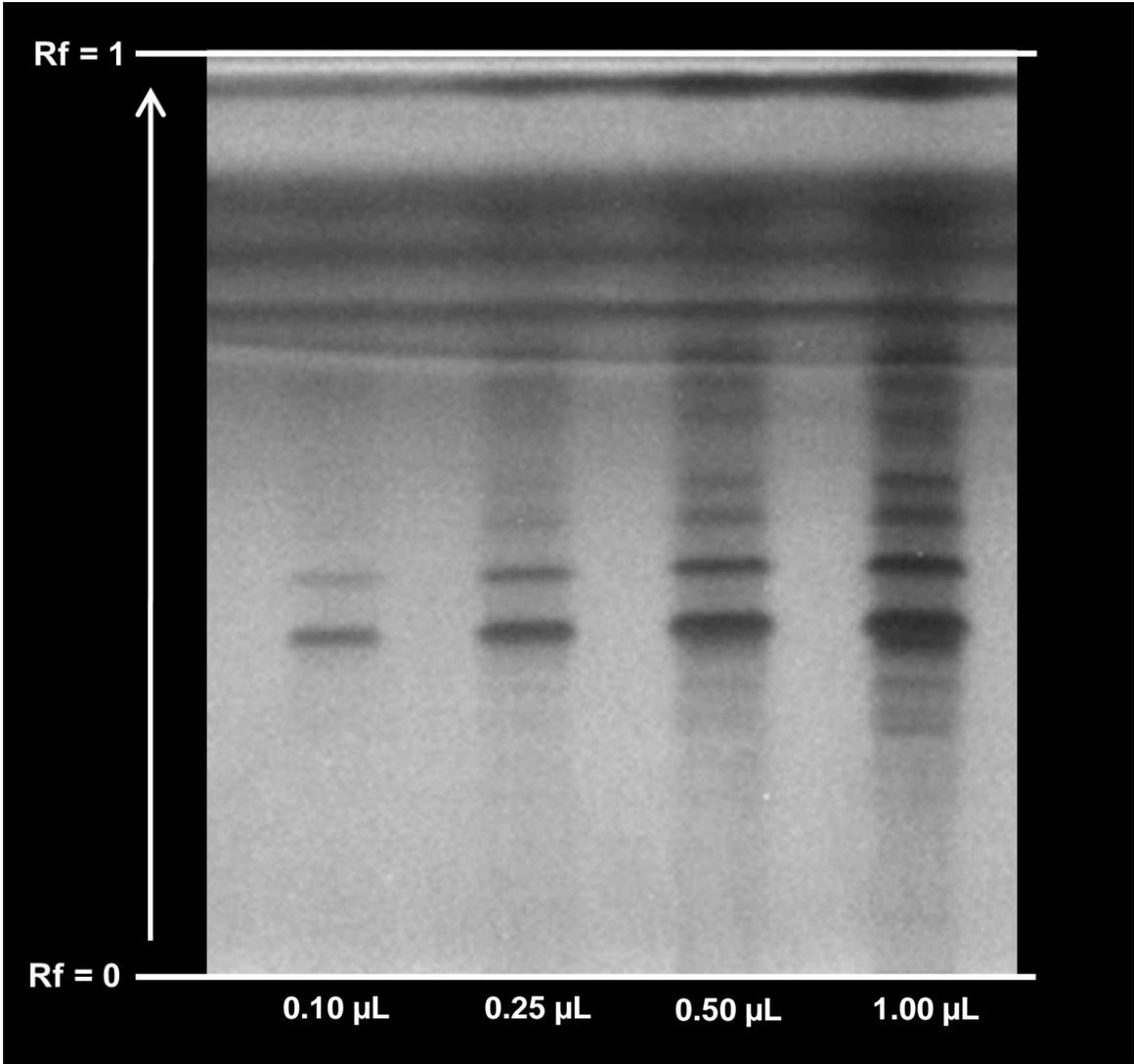
Gamma chromatogram

Gamma-Value:

$$\Gamma = \frac{\text{Inhibition [\%]}}{100 \% - \text{Inhibition [\%]}}$$



Dose-effect relationship



Calculation of the iso-inhibition volume

Gamma value $\Gamma = \frac{I}{100 - I}$ Linearised dose-effect relationship $\lg \Gamma_{i,j} = a_{i,j} + b_{i,j} \cdot \lg V_{i,j}$

Effect concentration 50

$$I = 50 \longrightarrow \Gamma = 1 \longrightarrow 0 = a_{i,j} + b_{i,j} \cdot \lg V_{i,j} (50)$$

$$\longrightarrow V_{i,j}(50) = 10^{-a_{i,j}/b_{i,j}} \quad \text{Iso-inhibition volume}$$

$$I_i \approx m_i = c_i \cdot V_i \quad \text{Inhibition is proportional to the applied sample volume}$$

$$c_{i,1}(50) \sim \frac{1}{V_{i,1}(50)} \quad \text{Reciprocal iso-inhibition volume}$$

I = Inhibition (%)

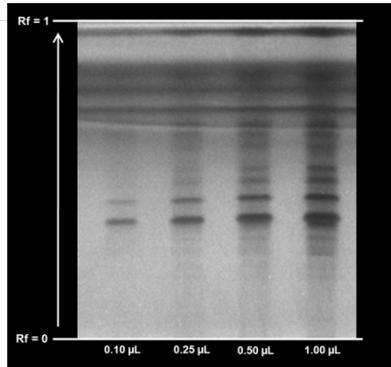
V = Application volume (μl)

$\Gamma_{i,j}$ = Gamma value

i = Substance zone

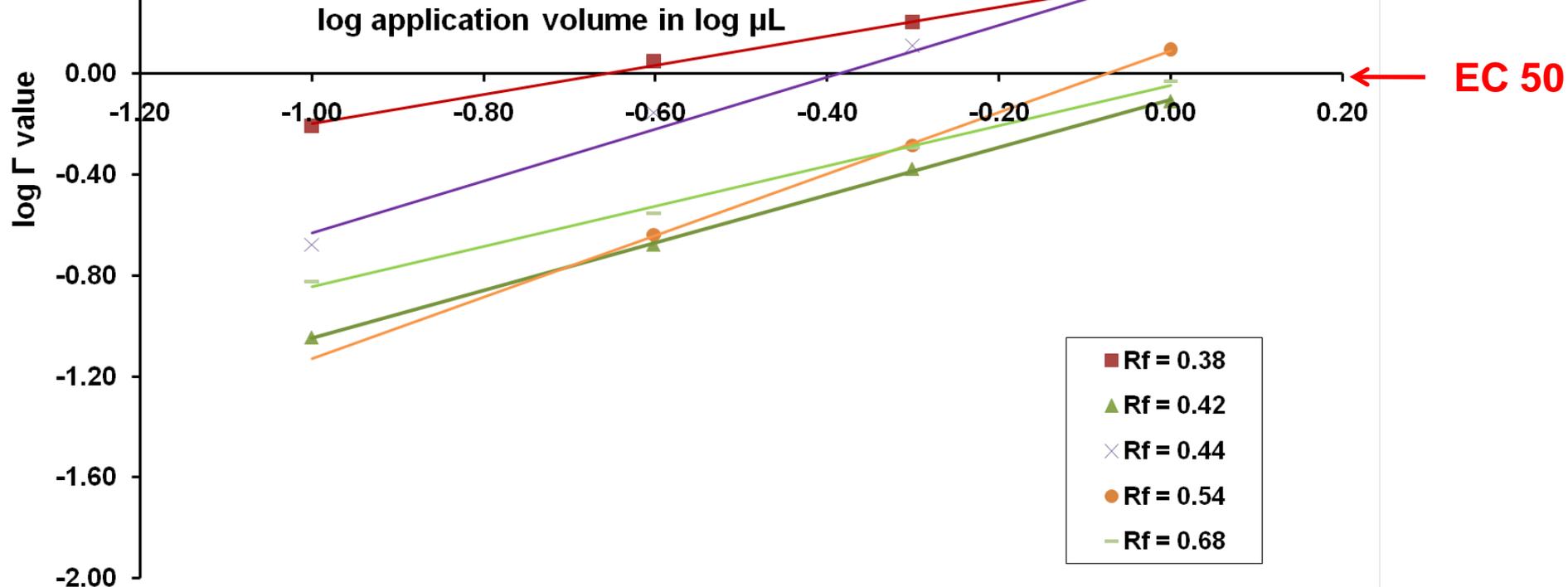
j = Extract (sample)

Linearised dose-effect relationship



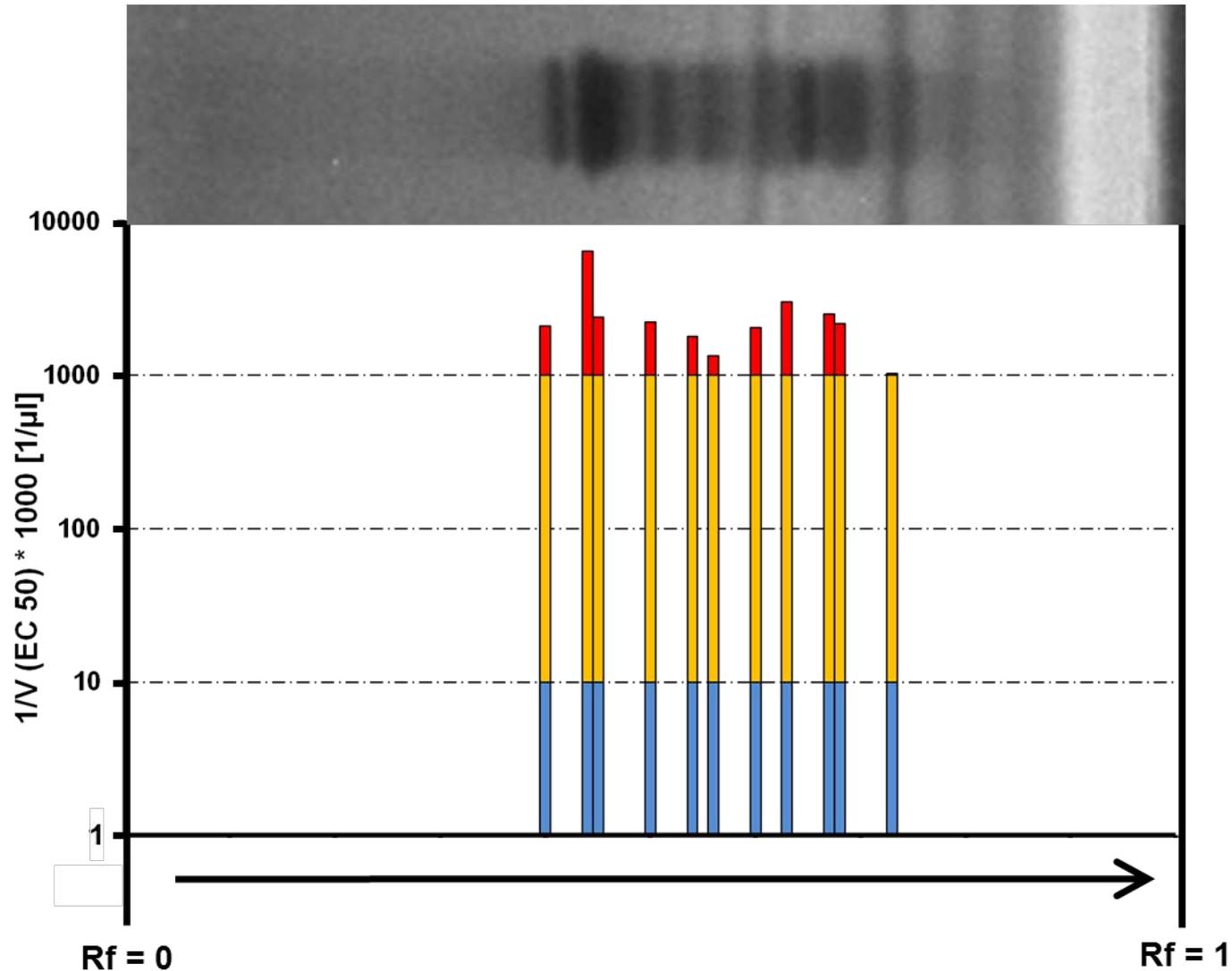
$$\Gamma = \frac{\text{Inhibition [\%]}}{100 \% - \text{Inhibition [\%]}}$$

$$\lg \Gamma_{i,j} = a_{i,j} + b_{i,j} \cdot \lg V_{i,j}$$

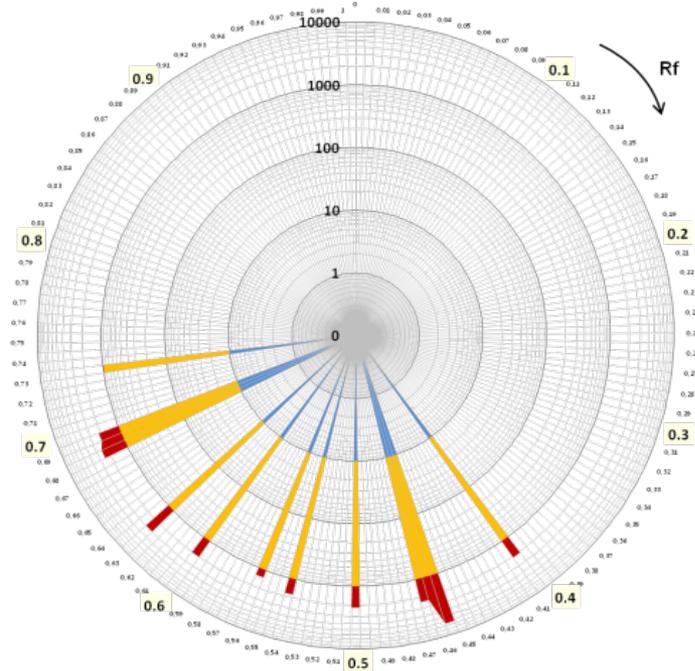
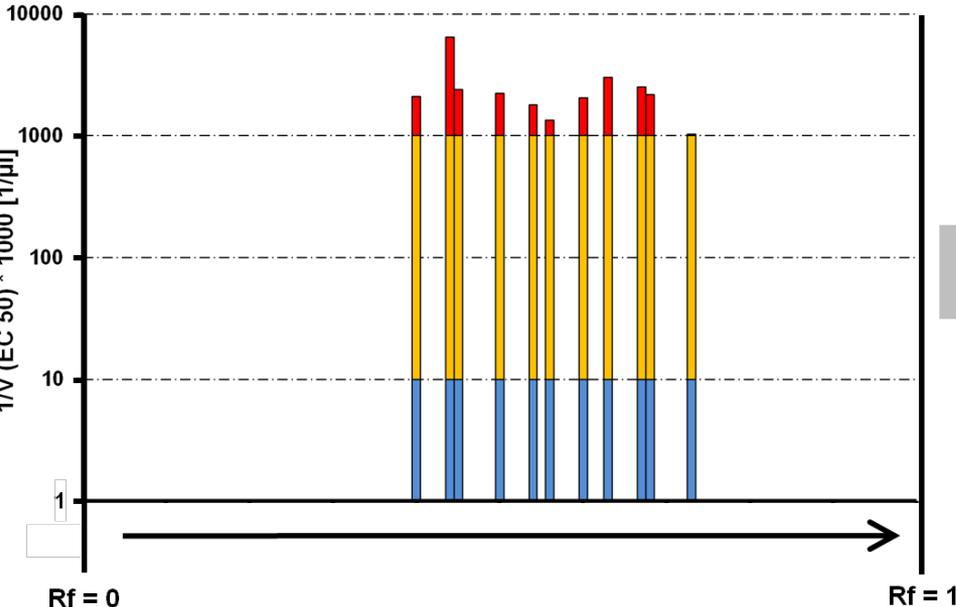


- Rf = 0.38
- ▲ Rf = 0.42
- × Rf = 0.44
- Rf = 0.54
- Rf = 0.68

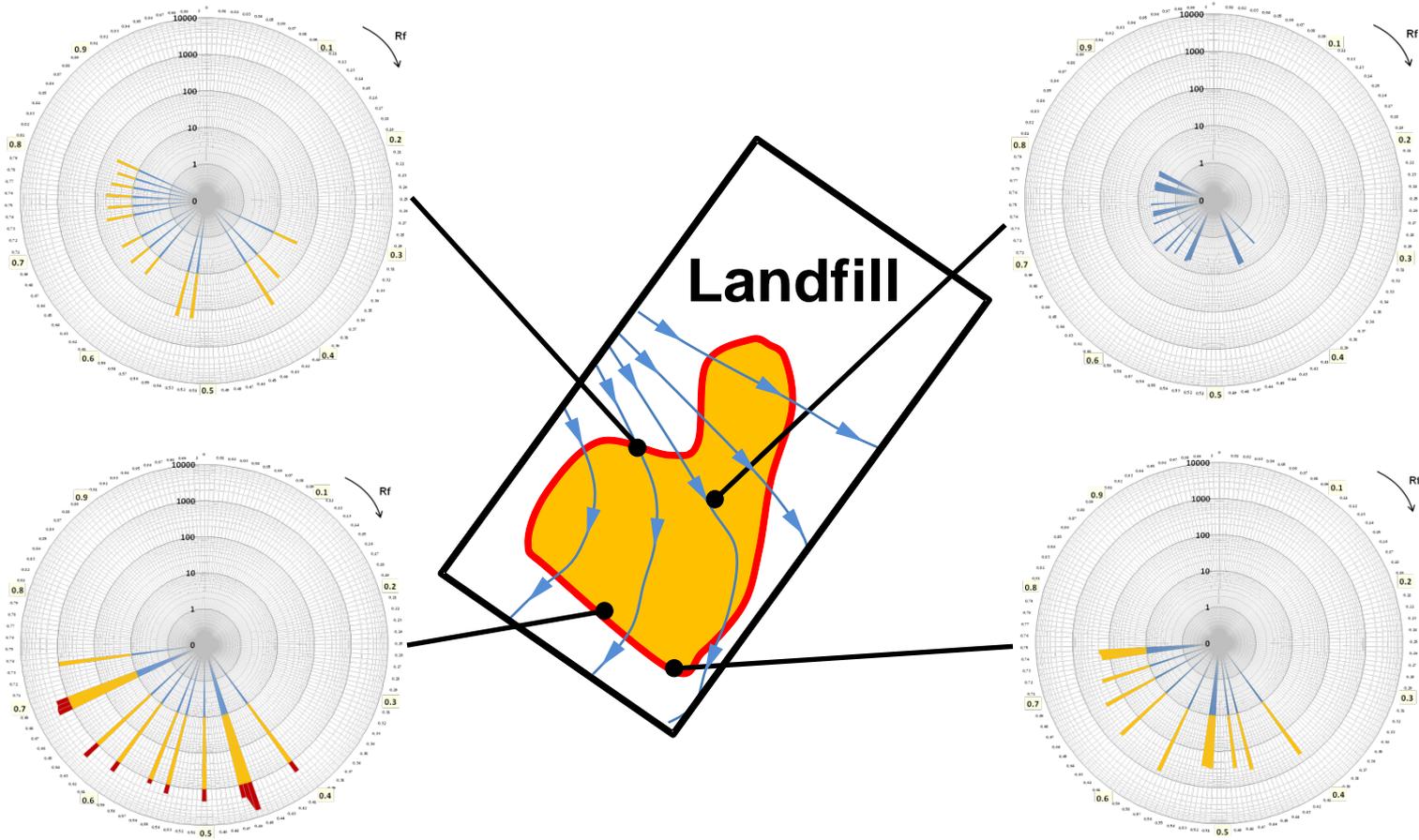
Histogram of the reciprocal iso-inhibition volume (RIV)



RIV Polar diagram

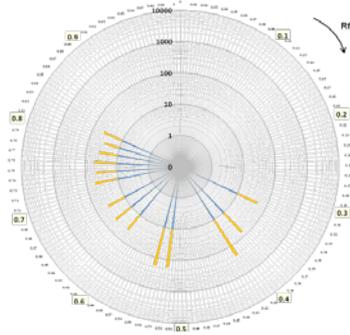


Comparison between the sampling points



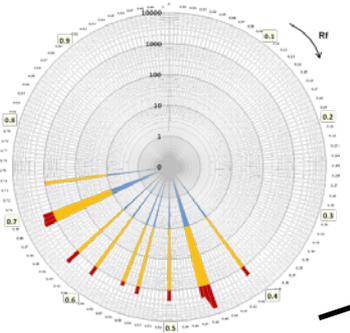
➔ Goundwater flow

Comparison with other analysis data



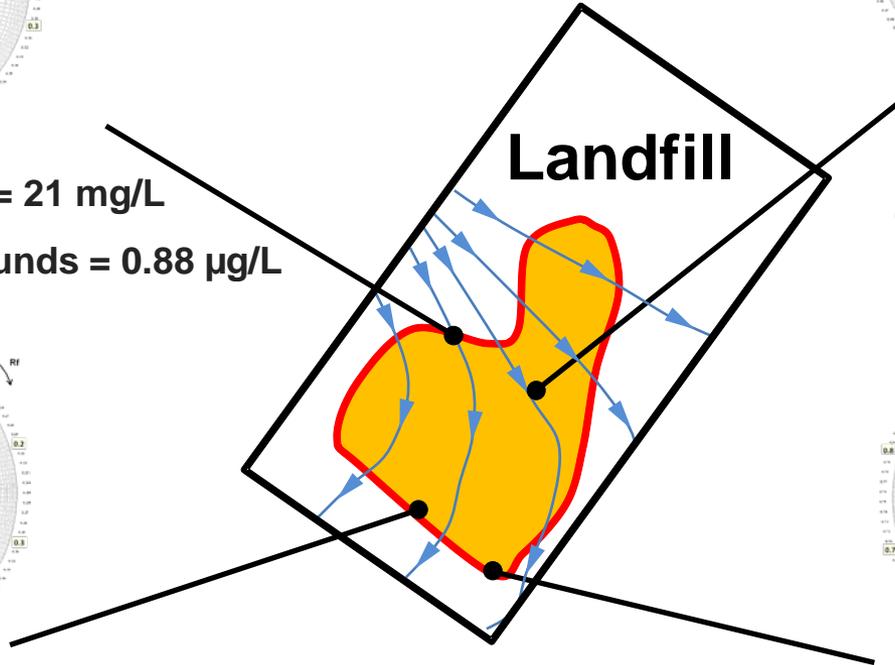
● DOC = 21 mg/L

Σ Target compounds = 0.88 µg/L

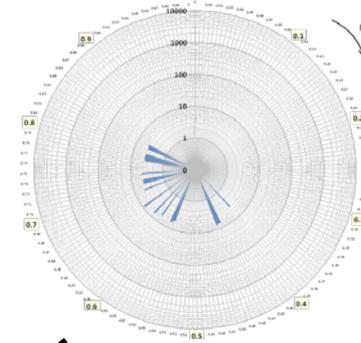


● DOC = 290 mg/L

Σ Target compounds = 41,5 µg/L

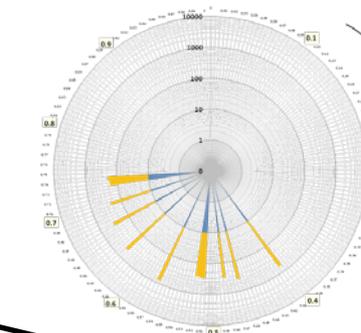


➔ Goundwater flow



● DOC = 2,3 mg/L

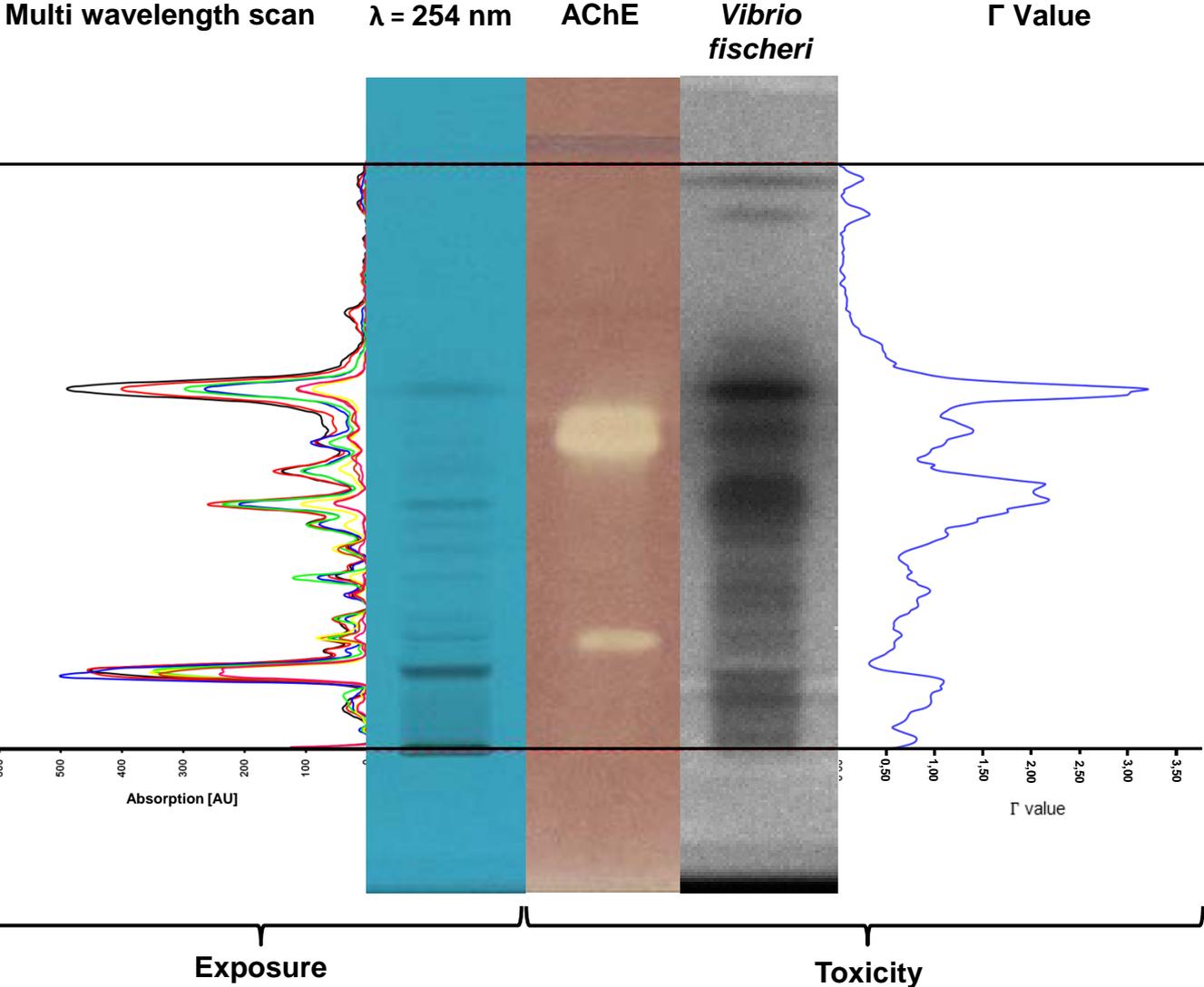
Σ Target compounds = 1,01 µg/L



● DOC = 25 mg/L

Σ Target compounds = 4,11 µg/L

Comparison of the exposure with biological effects



Acknowledgments

Camag

Sarah Künzel

Nicole Jung



the member of staff at
the Laboratory for Operation Control and Research

Thank you very much for your attention!



Introduction of the reciprocal iso-inhibition volume (RIV)

$$m_{i,1}(50) = c_{i,1} \cdot V_{i,1}(50)$$

$$m_{i,2}(50) = c_{i,2} \cdot V_{i,2}(50)$$

$$m_{i,1}(50) = m_{i,2}(50)$$

The same mass for the same substance and the same inhibition

Comparison of substance i in two samples

$$c_{i,1} \cdot V_{i,1}(50) = c_{i,2} \cdot V_{i,2}(50)$$

c = Concentration (ng/ μ l)

V = Application volume (μ l)

i = Substance zone

$$\frac{c_{i,1}}{c_{i,2}} = \frac{\frac{1}{V_{i,1}(50)}}{\frac{1}{V_{i,2}(50)}}$$

Reciprocal
iso-inhibition volume