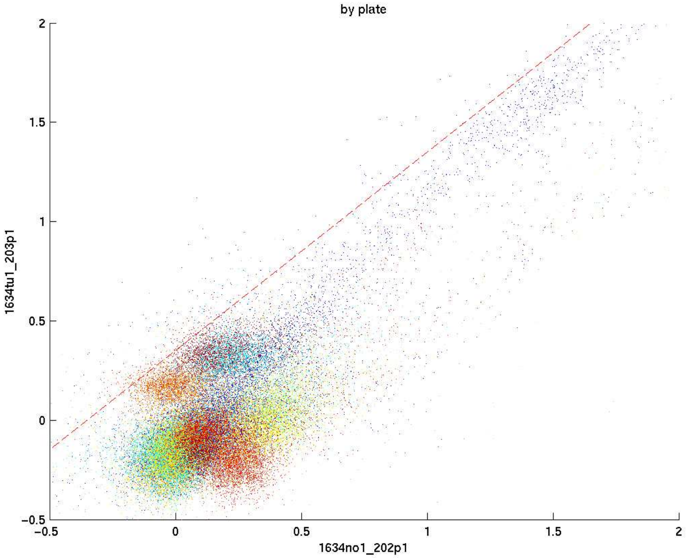
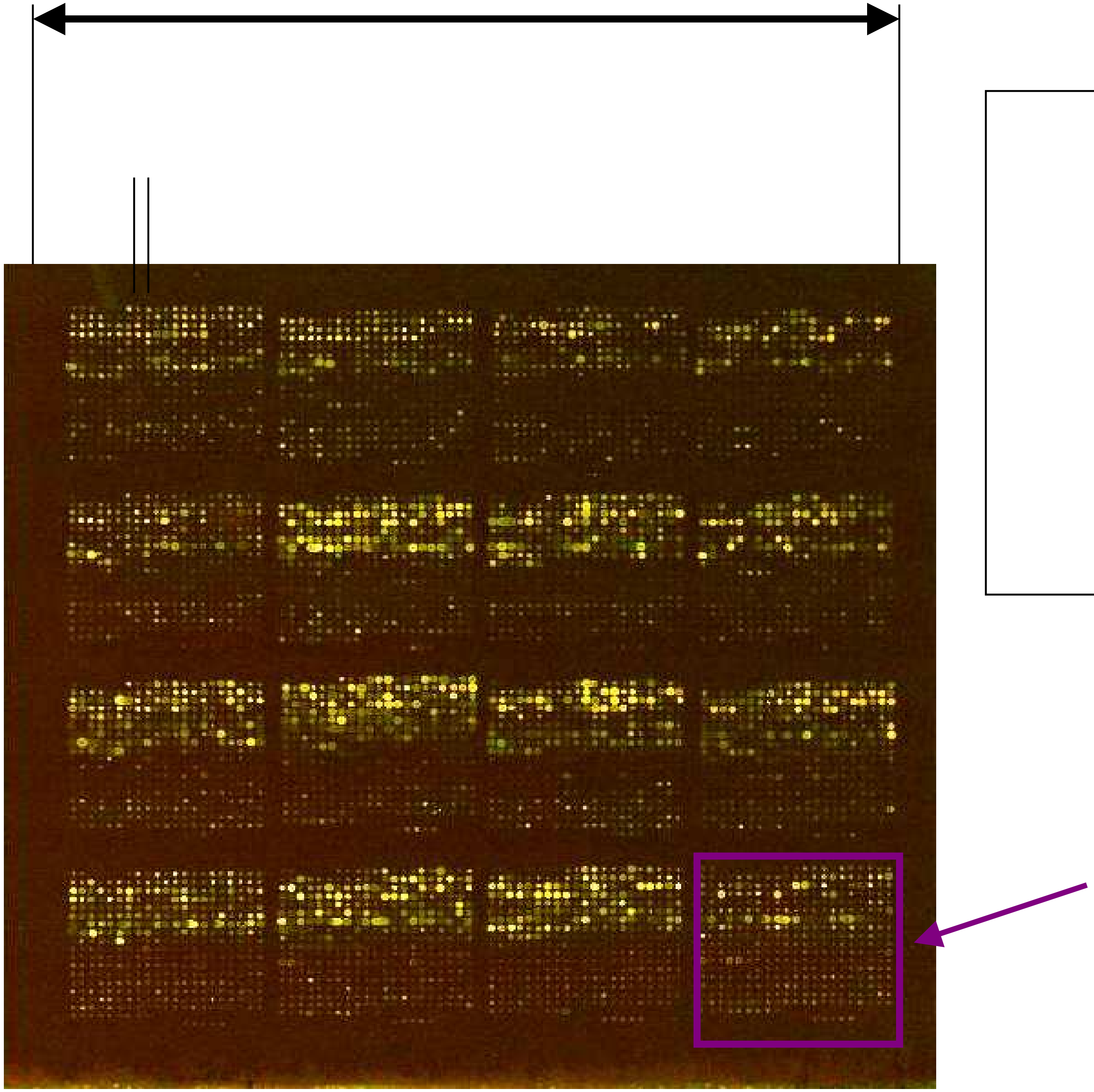
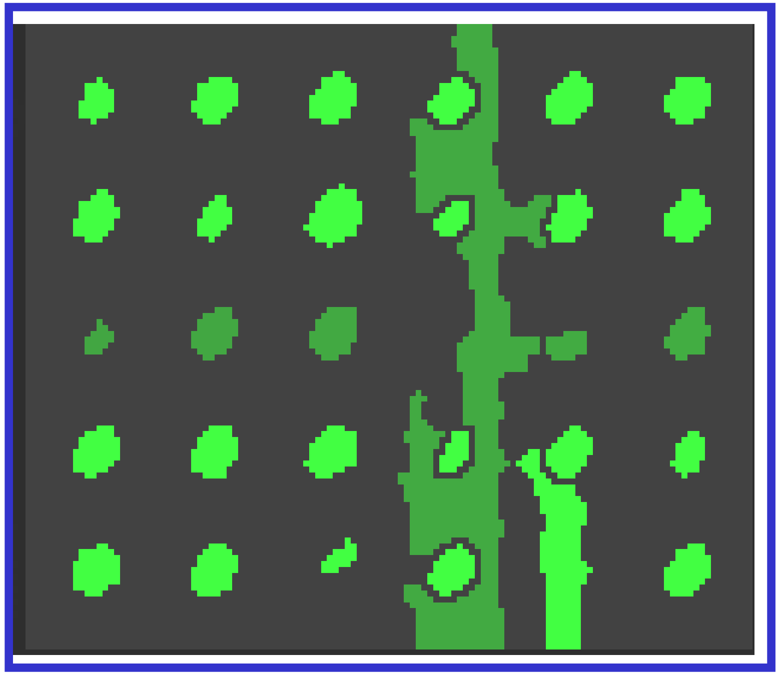
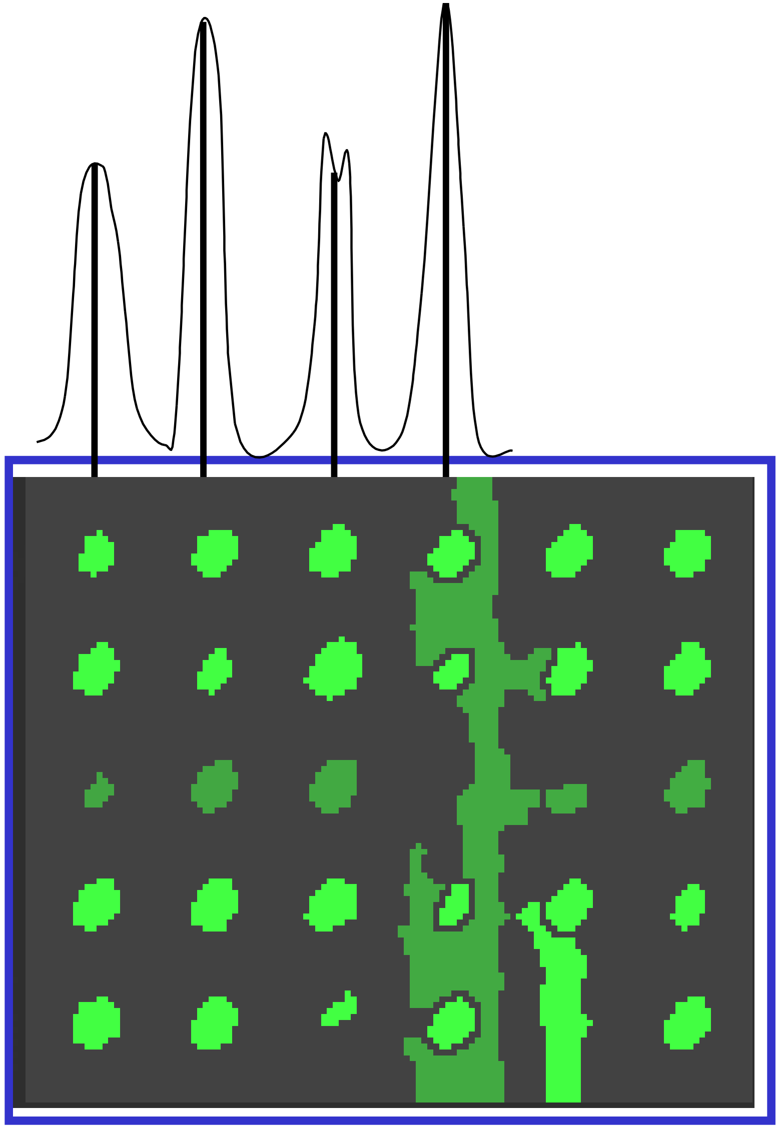
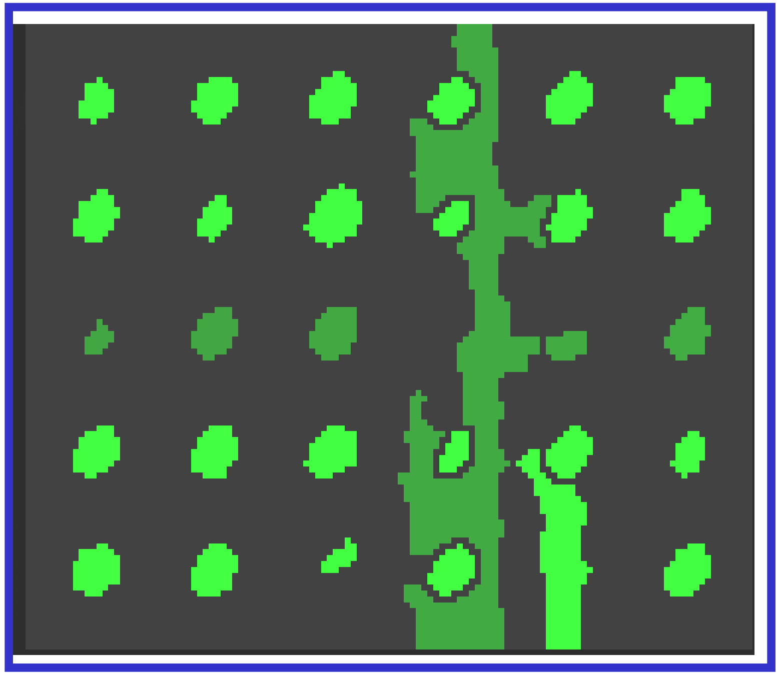
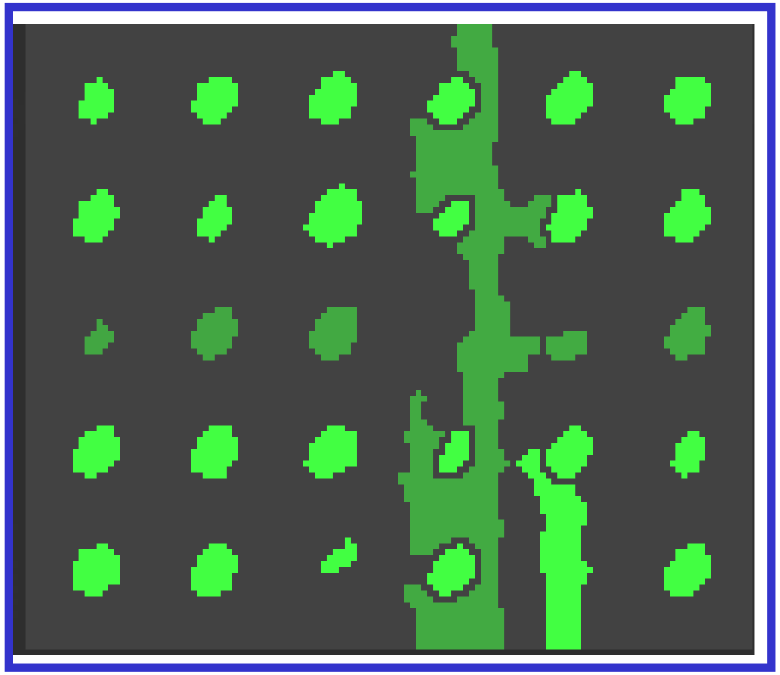

by plate
1634tu1_203p1
1634no1_202p1
2
1.5
1
0.5
0
−0.5
−0.5
0
0.5
1
1.5
2

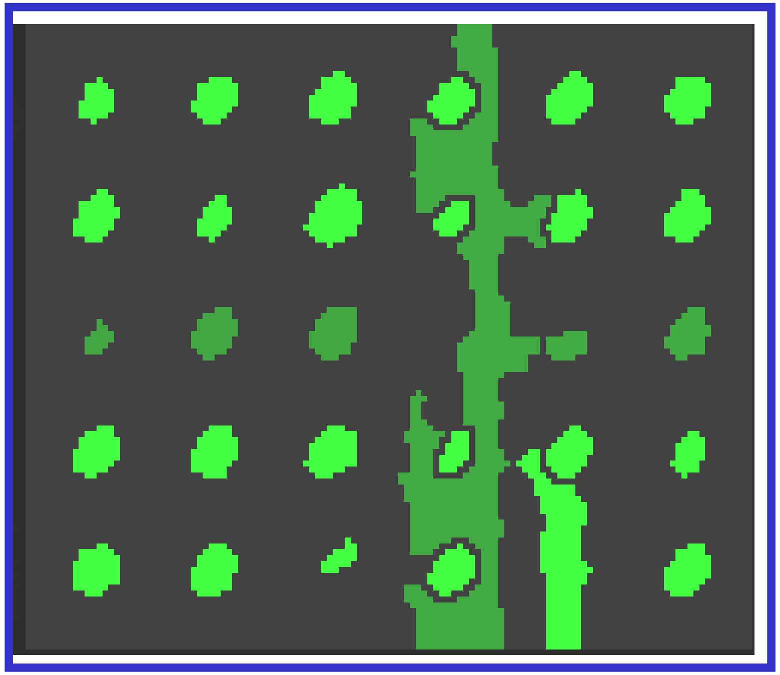


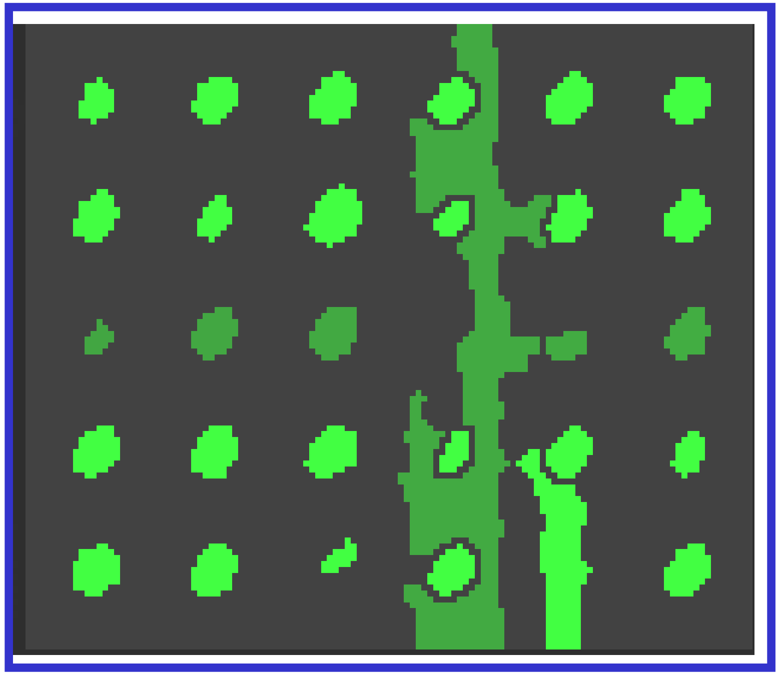


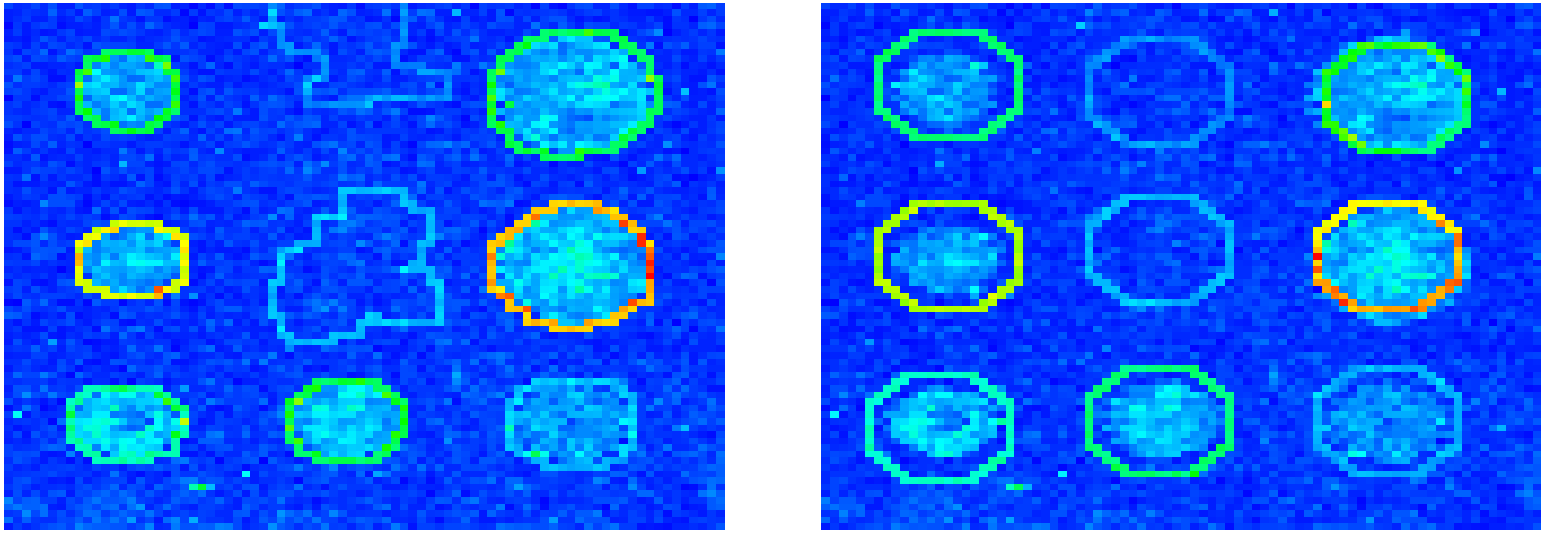


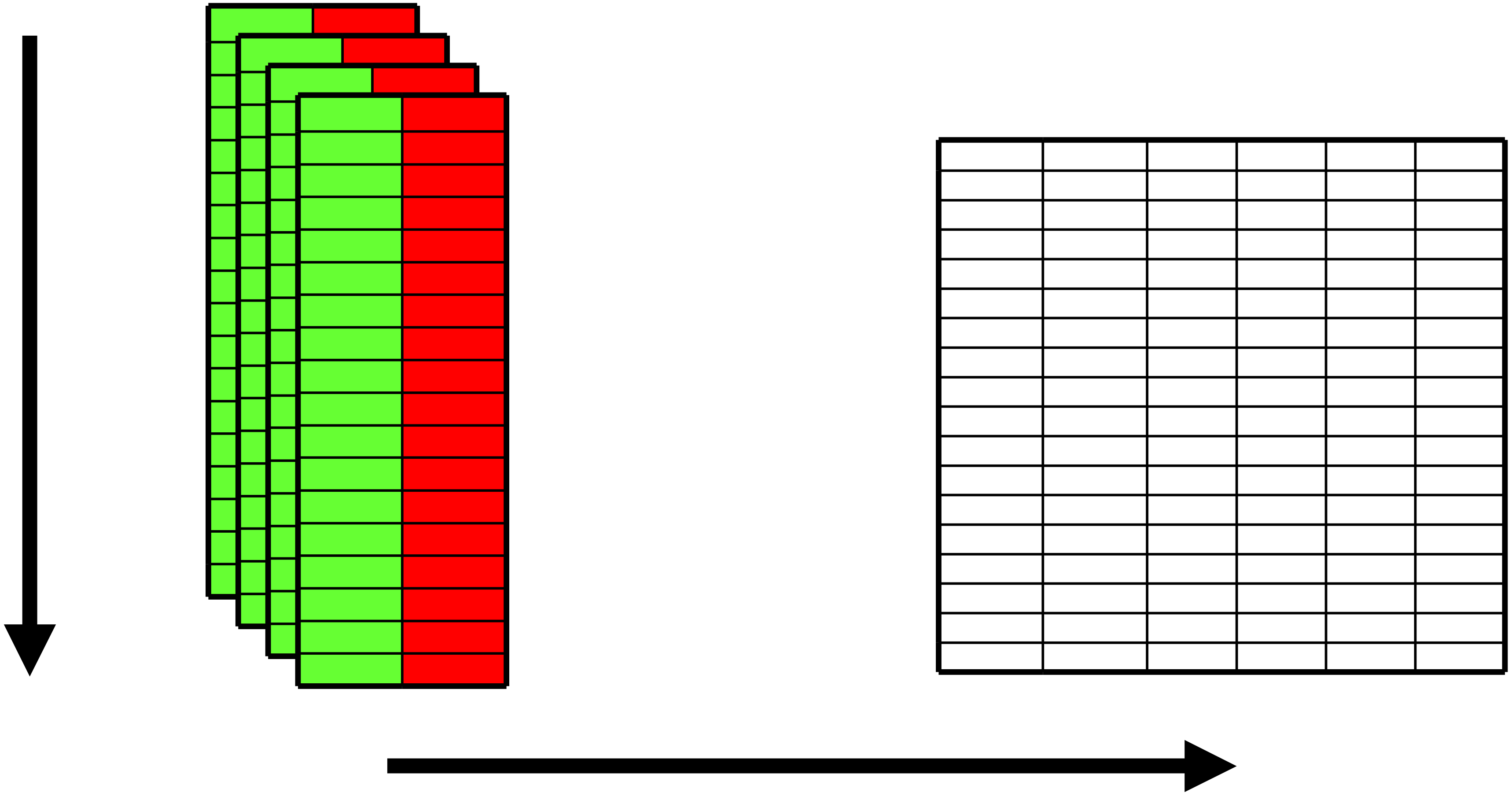


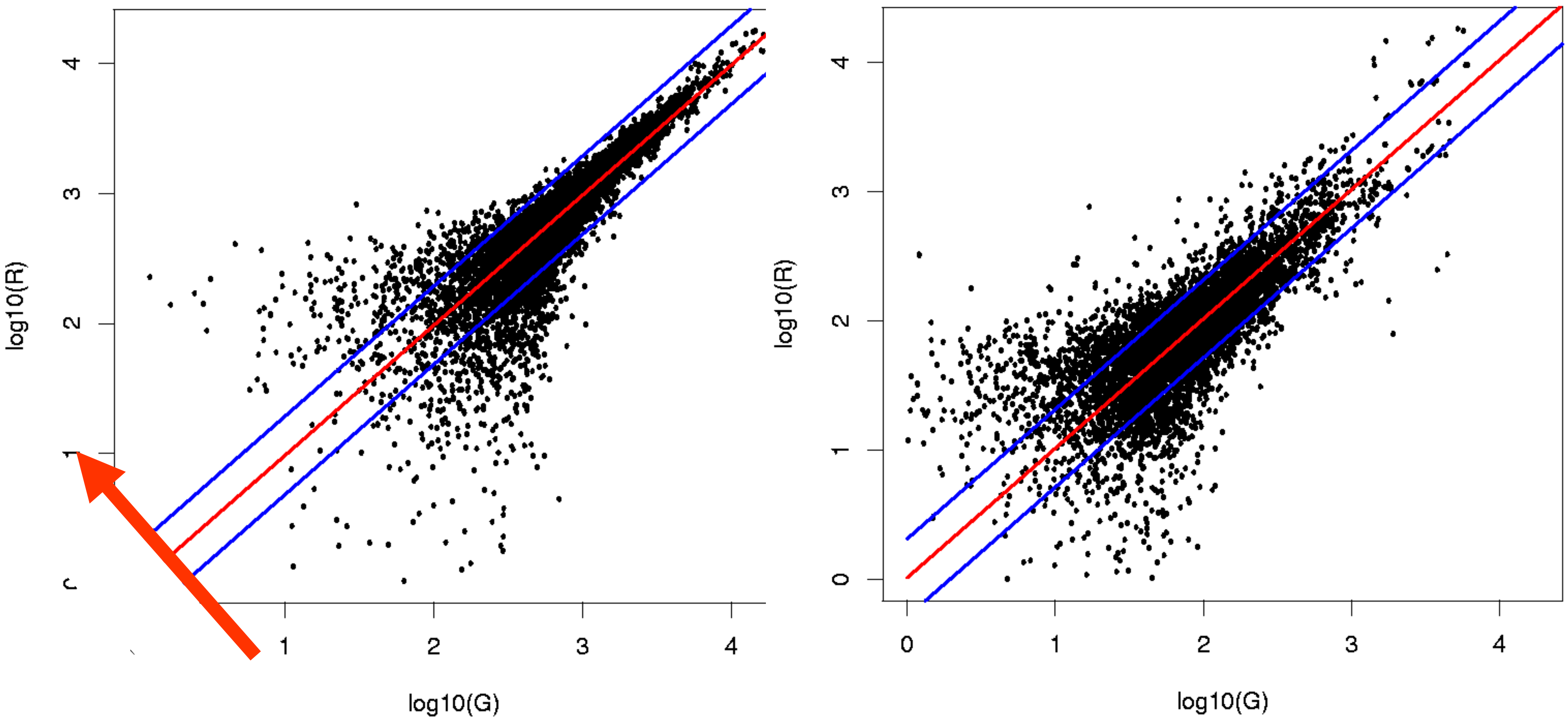


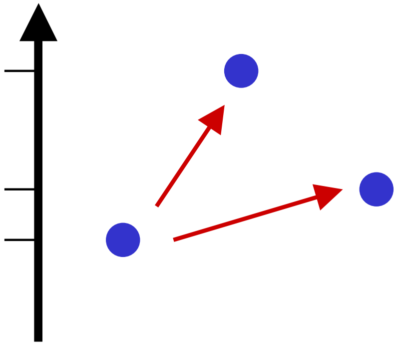


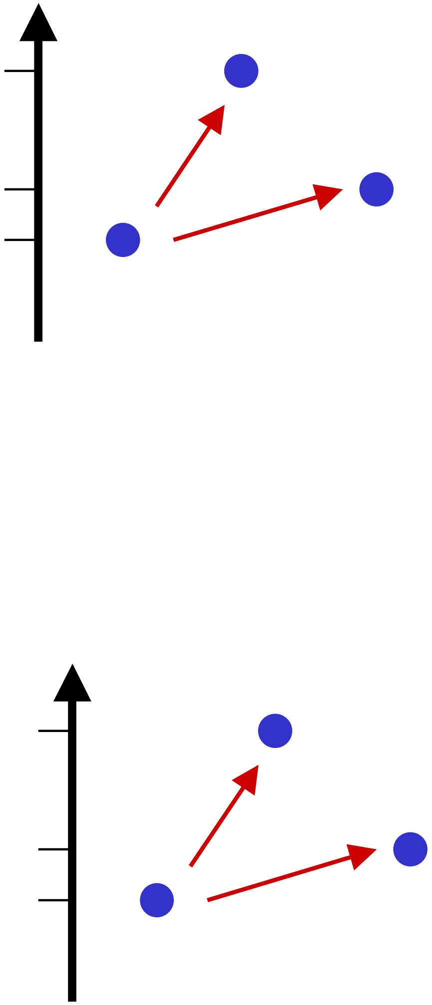


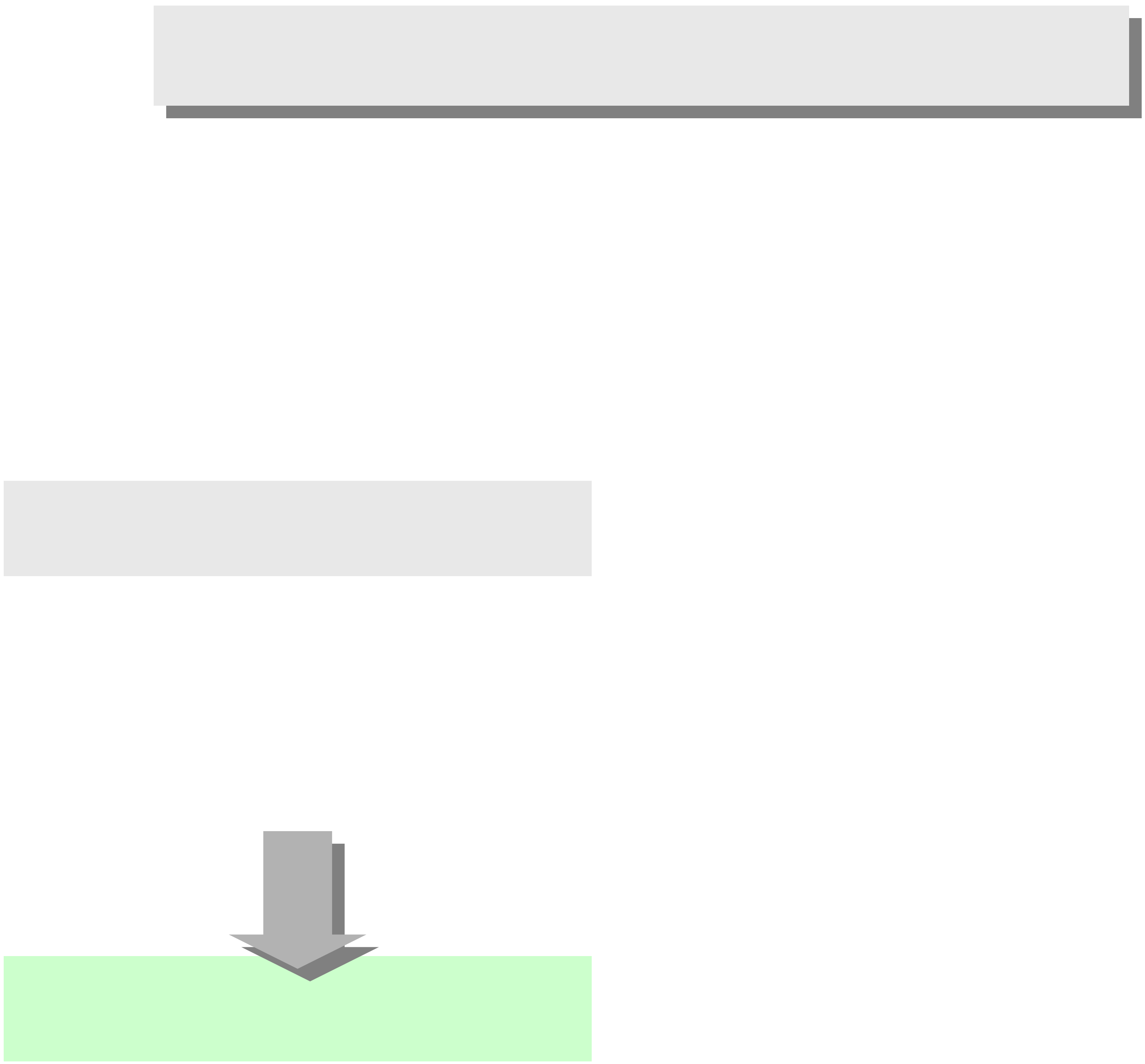


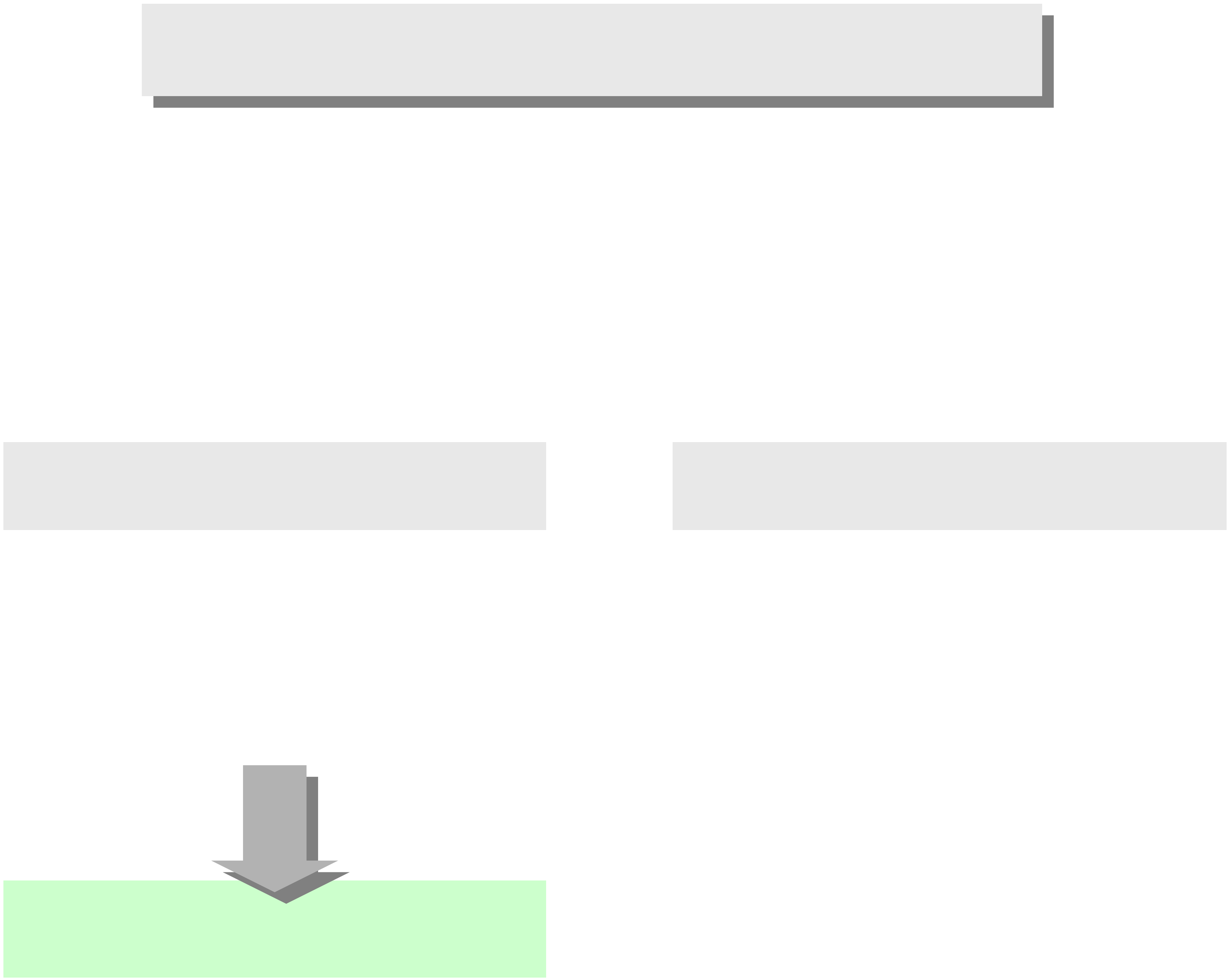


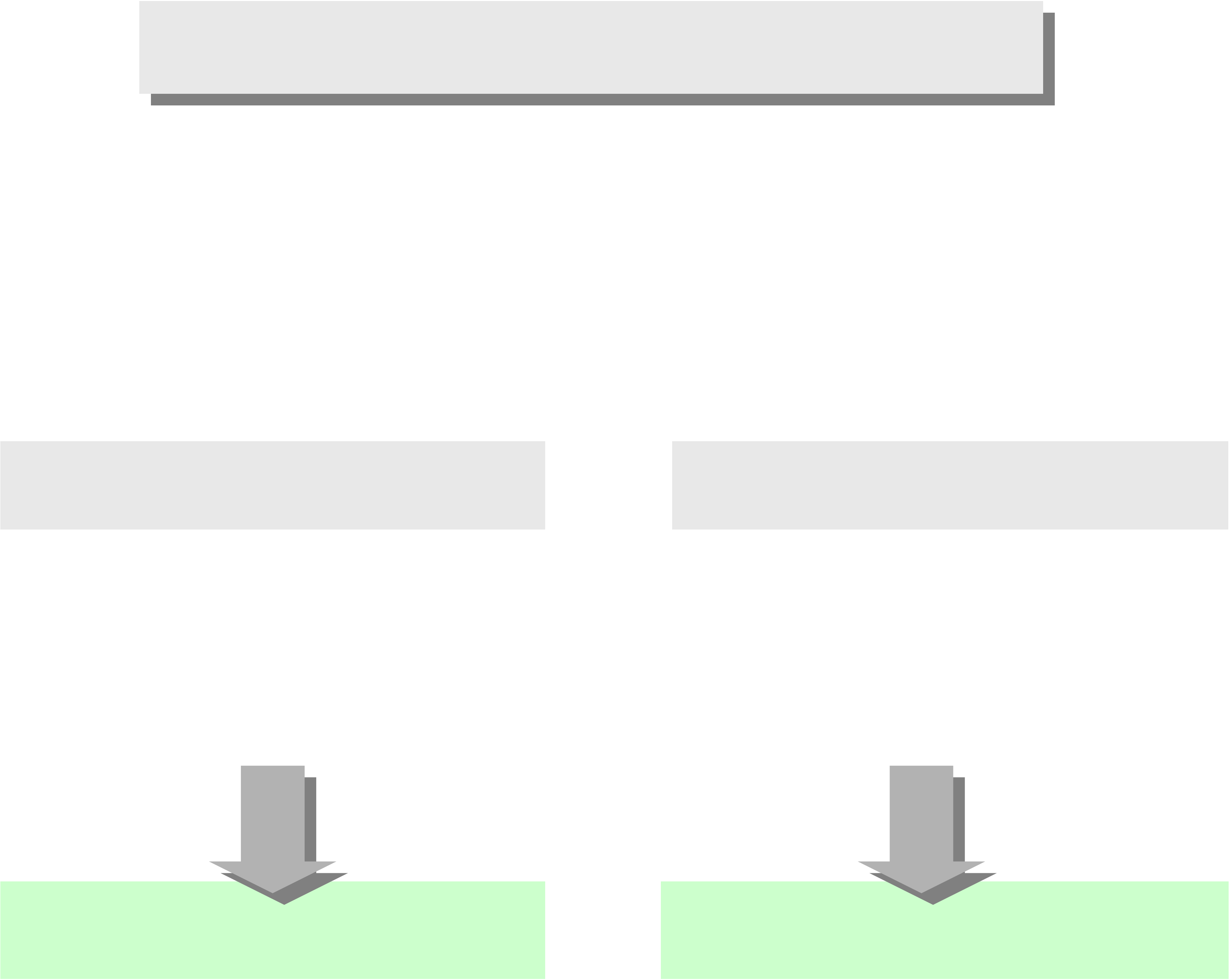

log10(R)
4
3
2
1
1
2
3
4
log10(G)
log10(R)
4
3
2
1
0
0
1
2
3
4
log10(G)

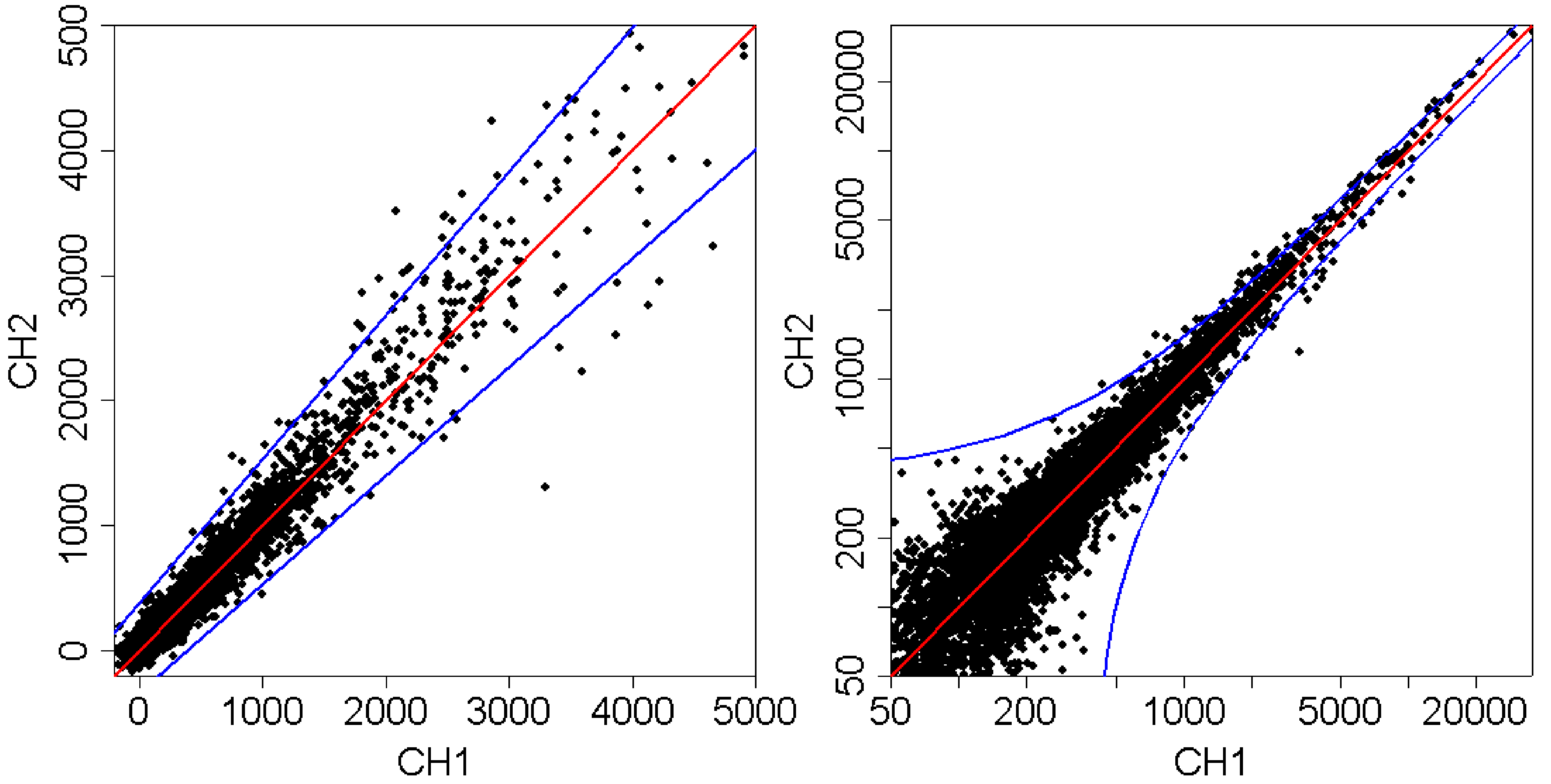


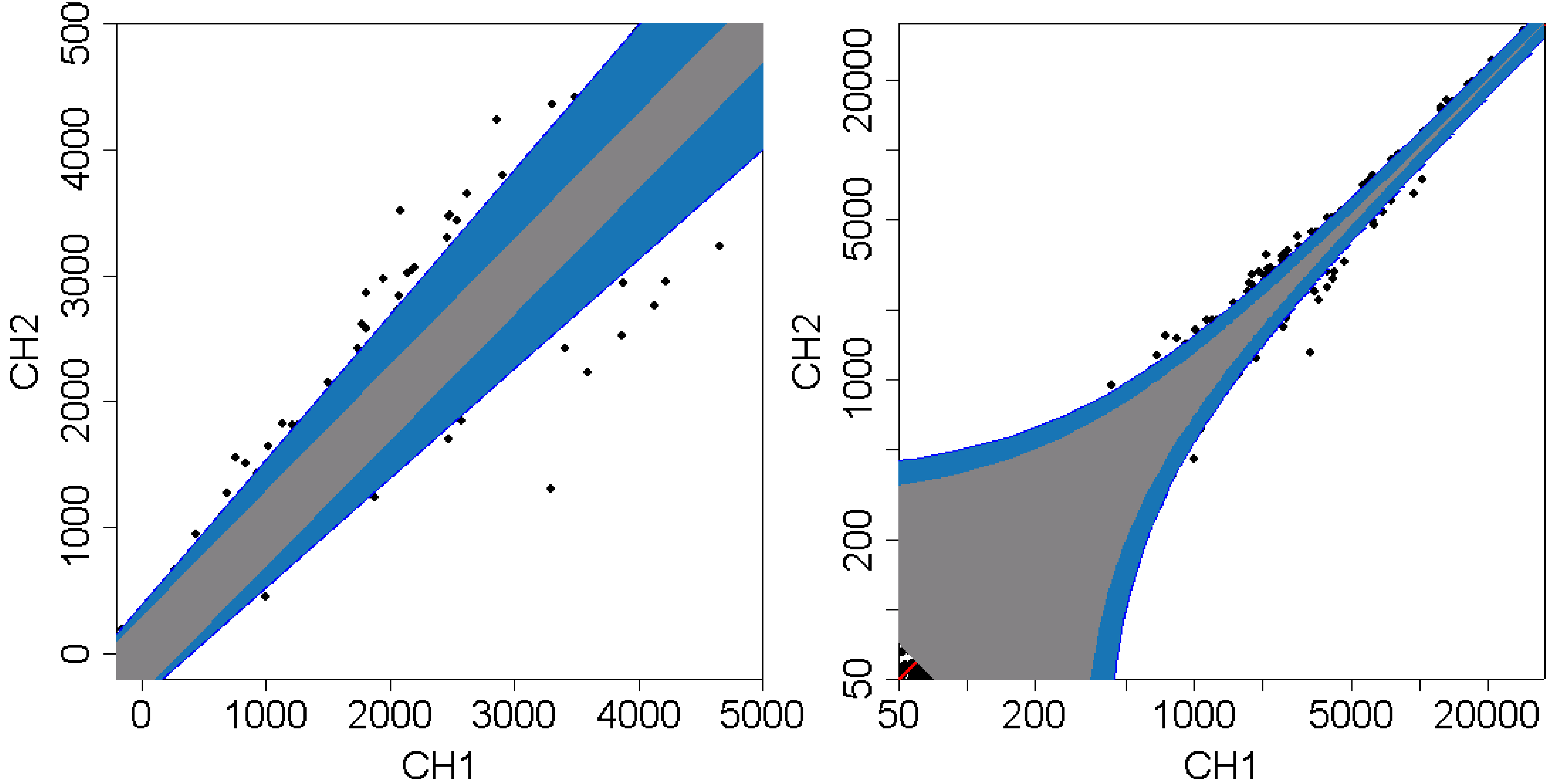


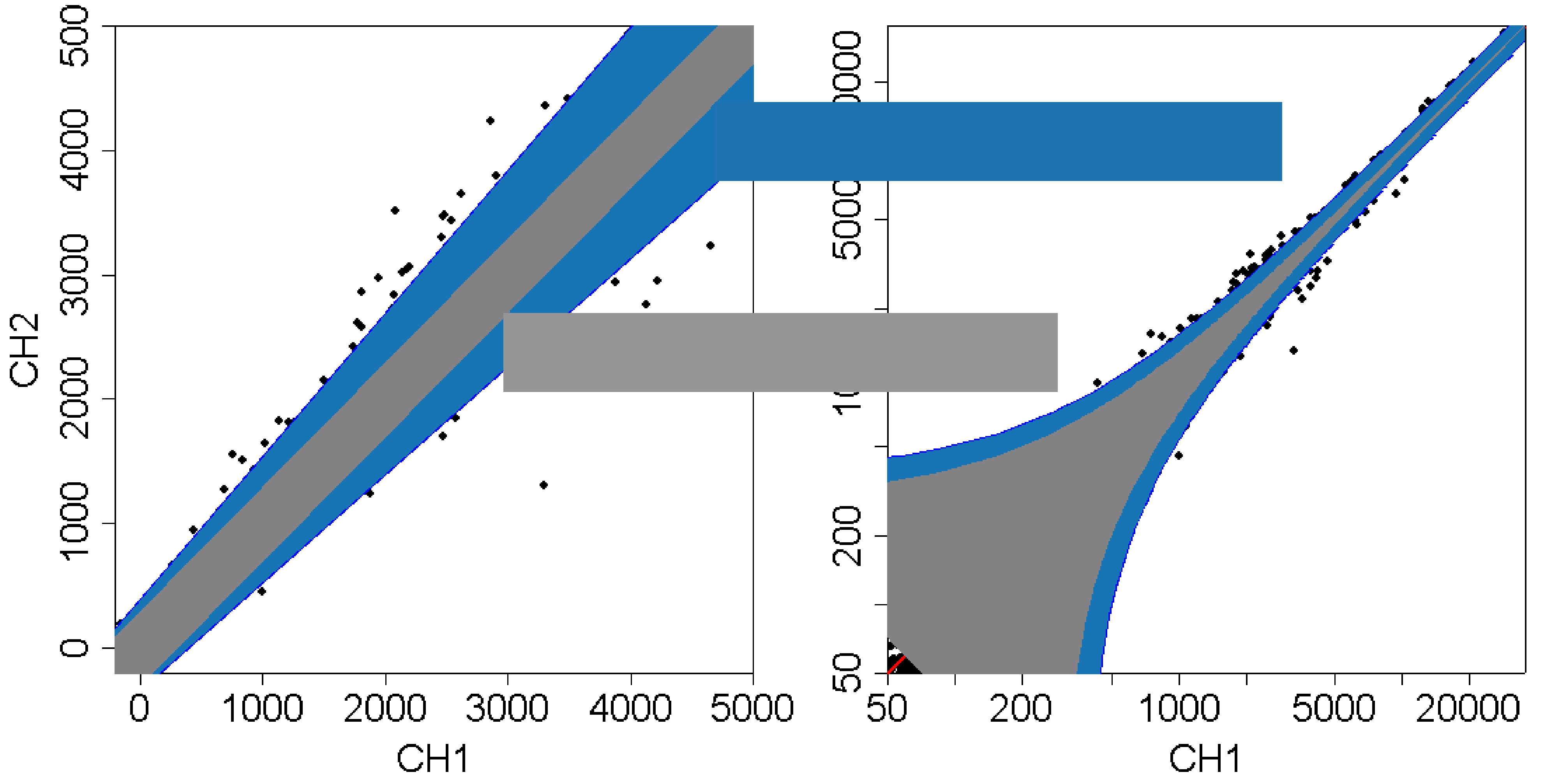




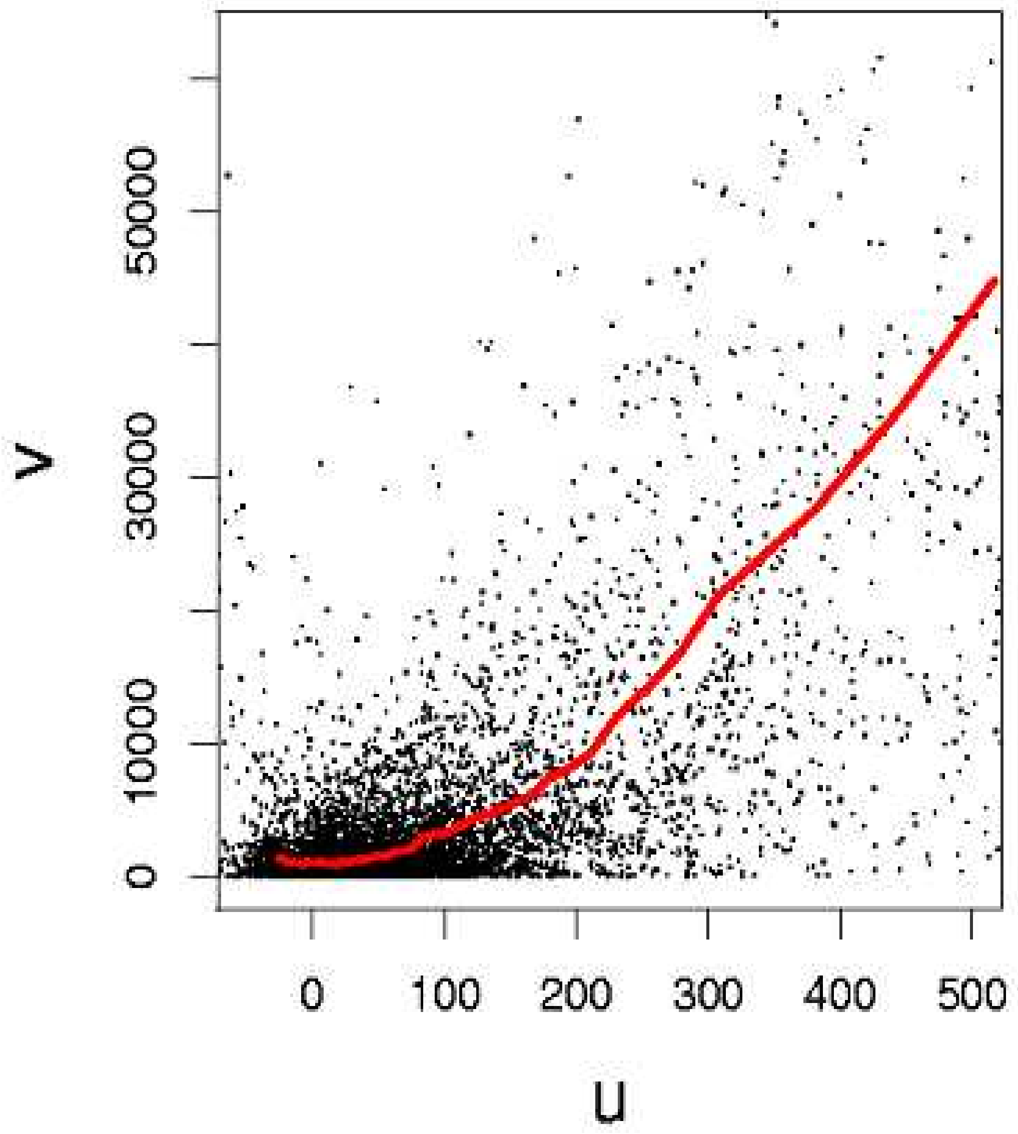



CH2
0
1000
2000
3000
4000
500
0
1000
2000
3000
4000
5000
CH1
CH2
50
200
1000
5000
20000
50
200
1000
5000
20000
CH1

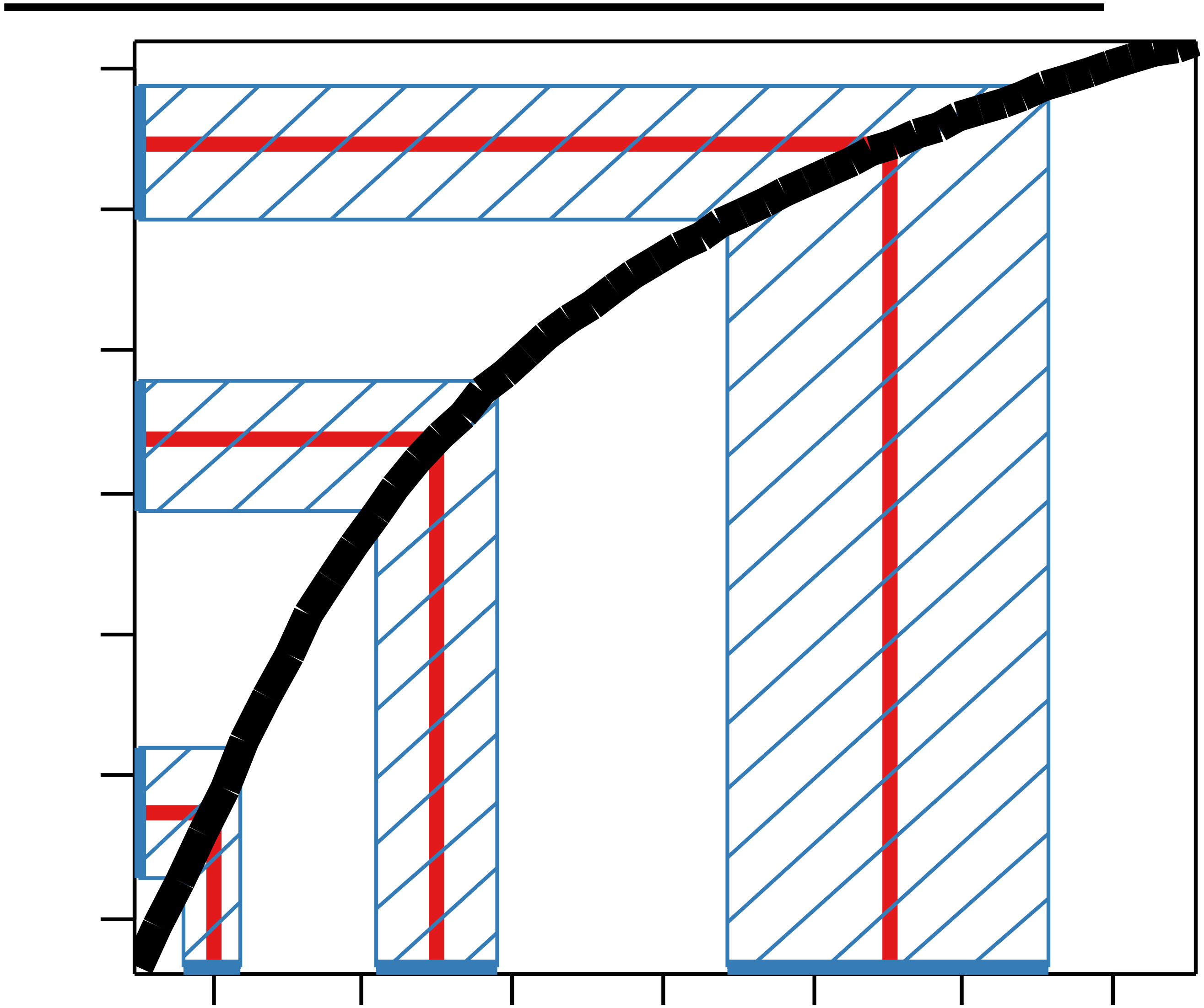

CH2
0
1000
2000
3000
4000
500
CH1
0
1000
2000
3000
4000
5000
CH2
50
200
1000
5000
20000
CH1
50
200
1000
5000
20000



CH2
0
1000
2000
3000
4000
500
0
1000
2000
3000
4000
5000
CH1
50
200
5000
0000
50
200
1000
5000
20000
CH1


v
0
10000
30000
50000
0
100
200
300
400
500
u

$$\overline{\sqrt{\qquad\qquad}}$$



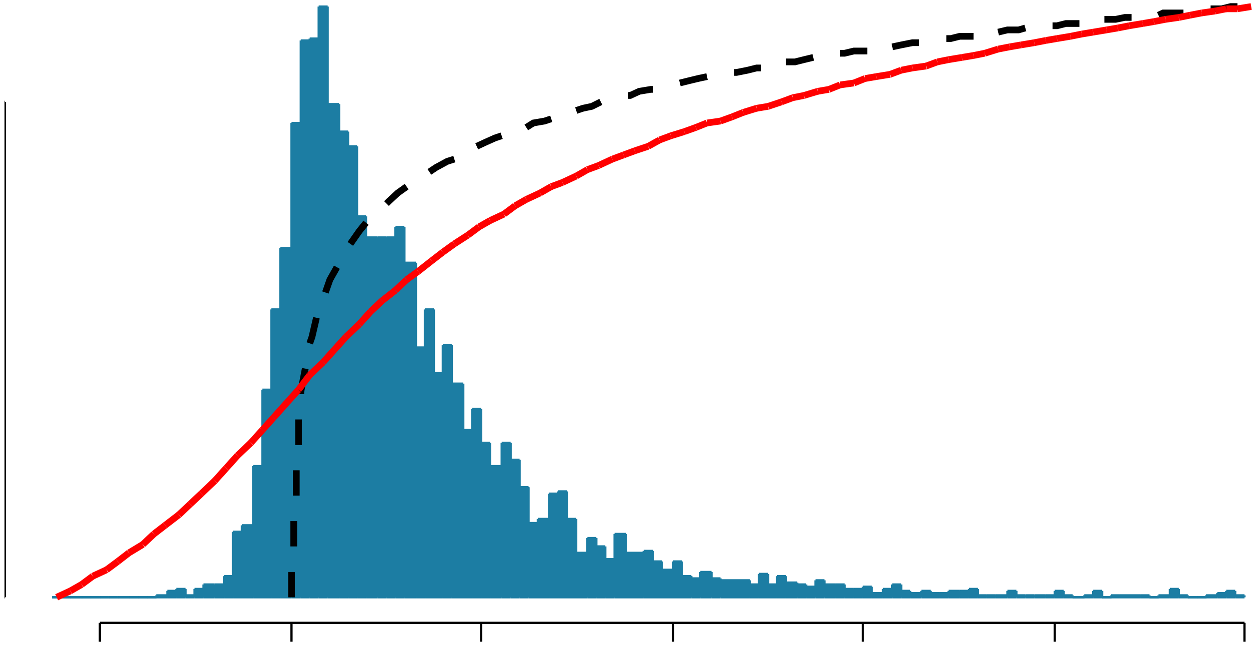
$$\frac{}{\sqrt{}}$$

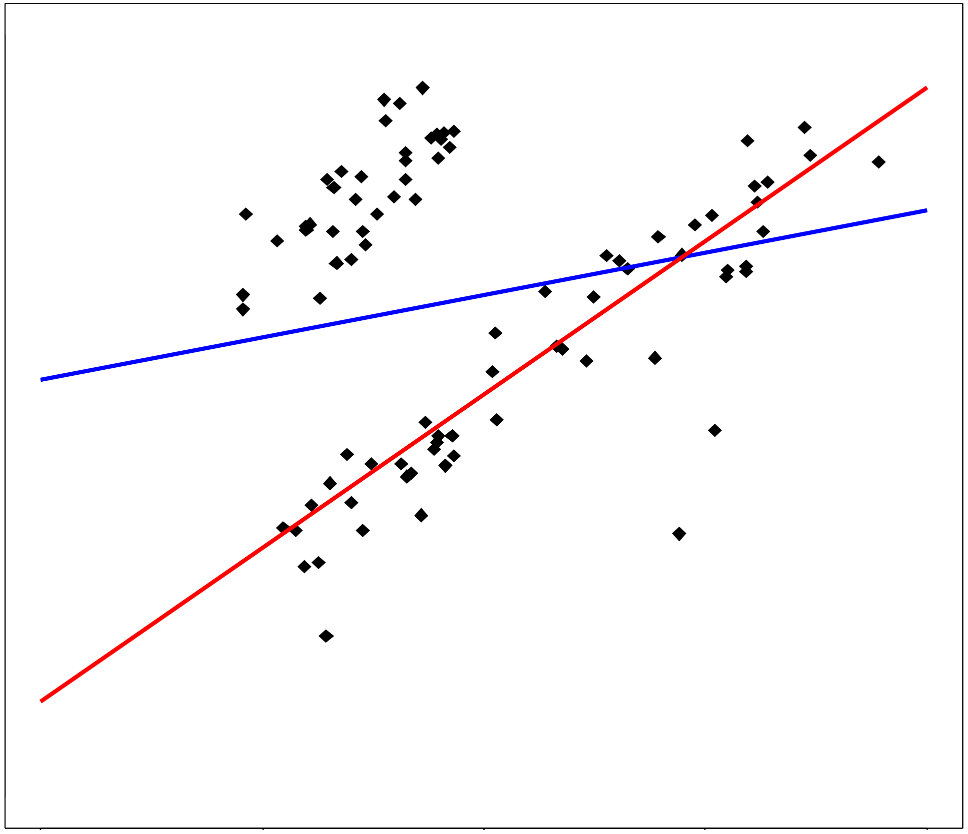
$$\frac{}{\sqrt{\quad}}$$

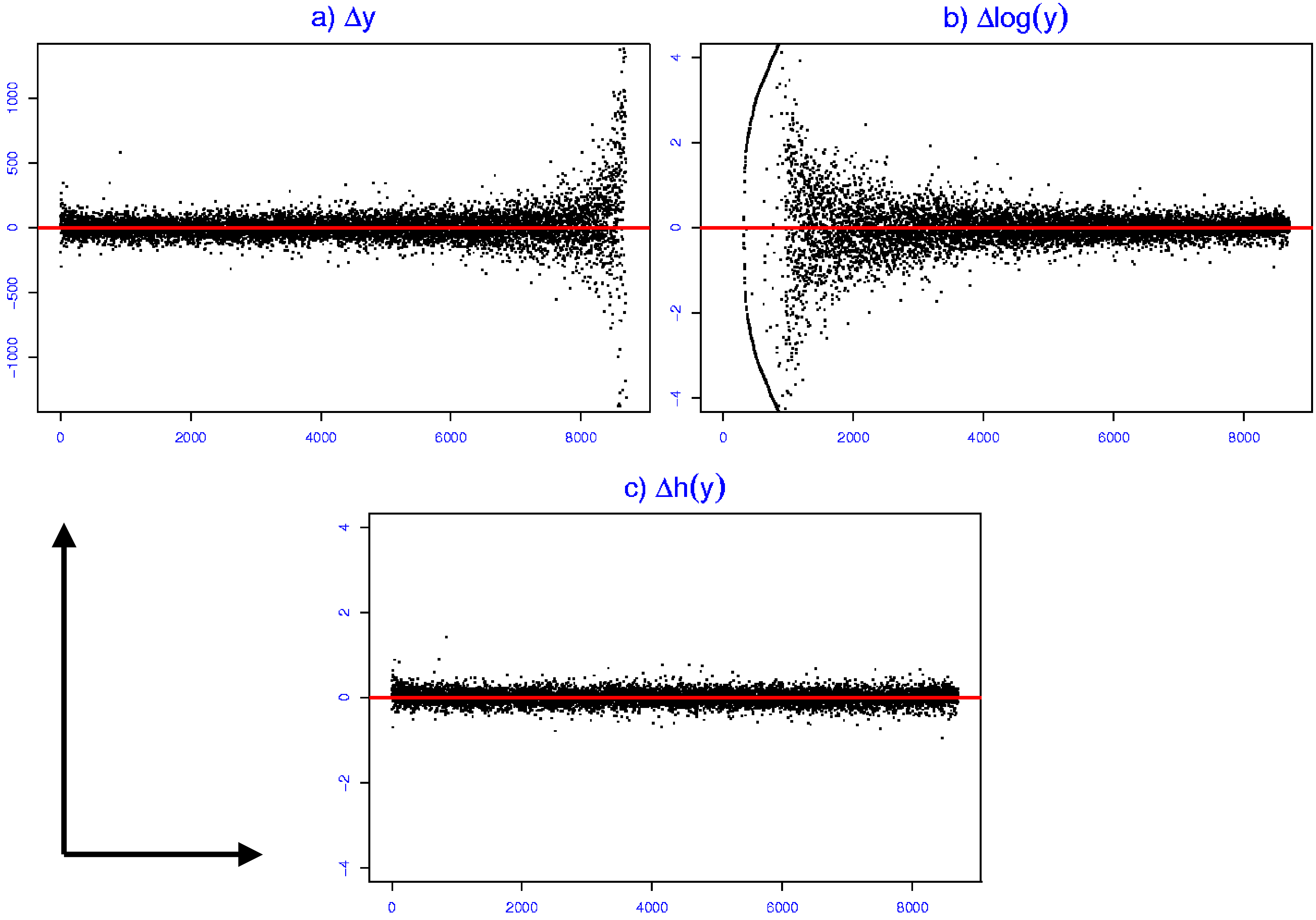
$$\frac{}{\sqrt{}}$$

$$\frac{}{\sqrt{}}$$

$$\frac{\quad}{\sqrt{\quad}}$$






a) Δy
1000
500
0
−500
−1000
0
2000
4000
6000
8000
b) Δlog(y)
4
2
0
−2
−4
0
2000
4000
6000
8000
c) Δh(y)
4
2
0
−2
−4
0
2000
4000
6000
8000

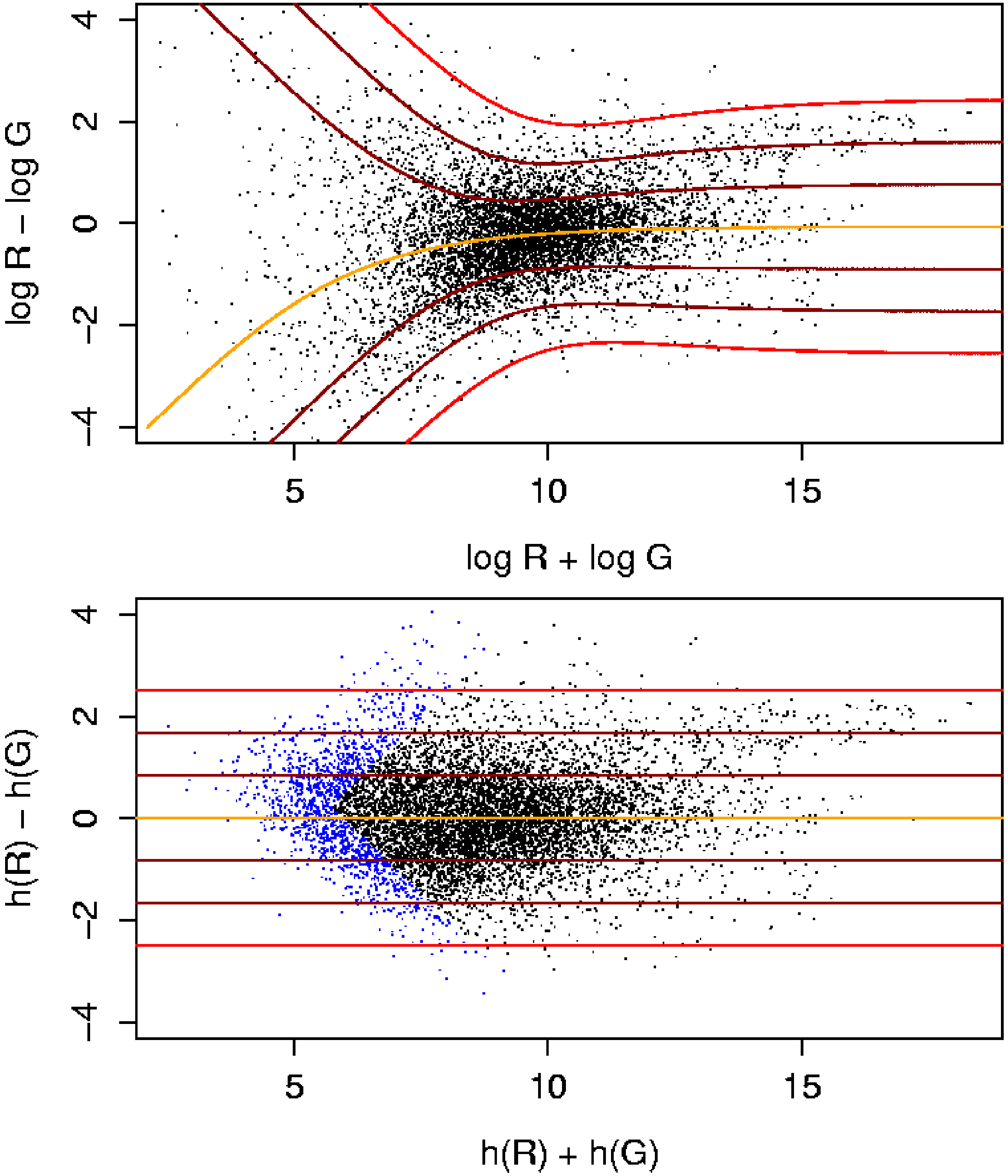

log R – log G
4
2
0
−2
−4
5
10
15
log R + log G
h(R) – h(G)
4
2
0
−2
−4
5
10
15
h(R) + h(G)

Figure 5a

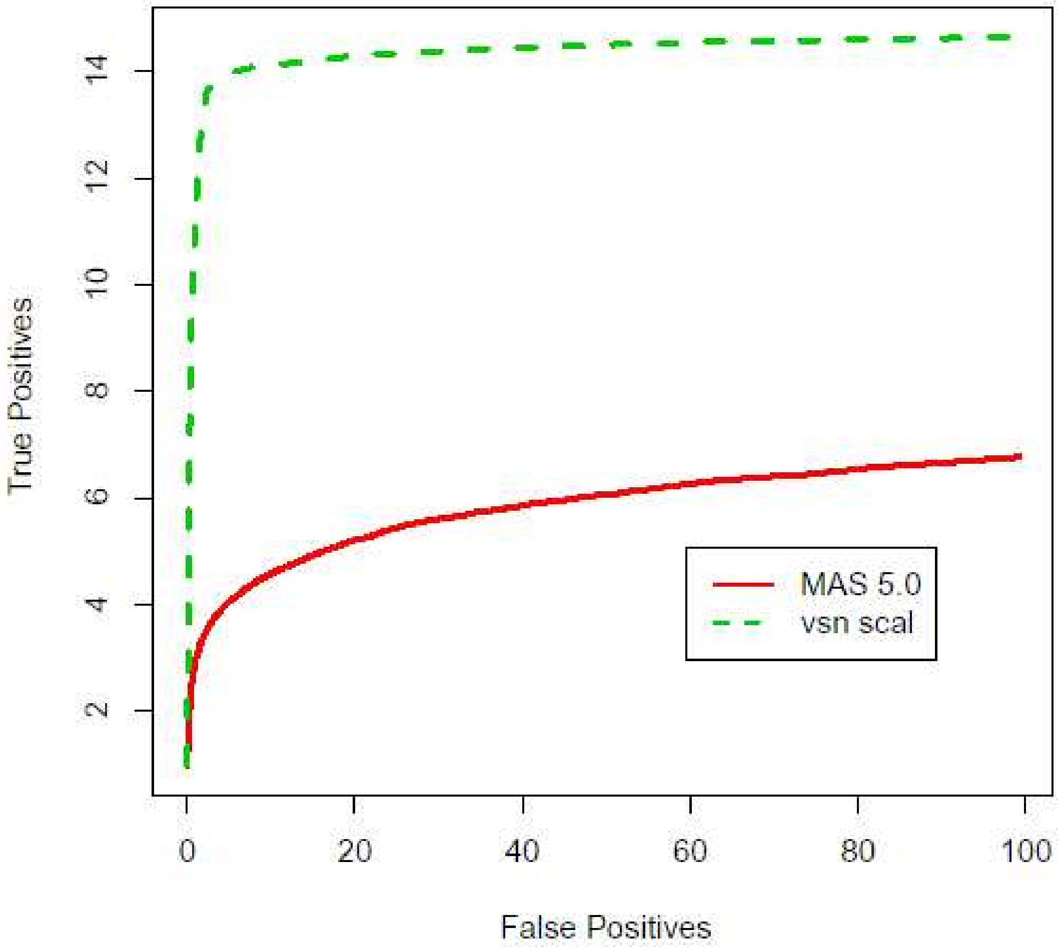
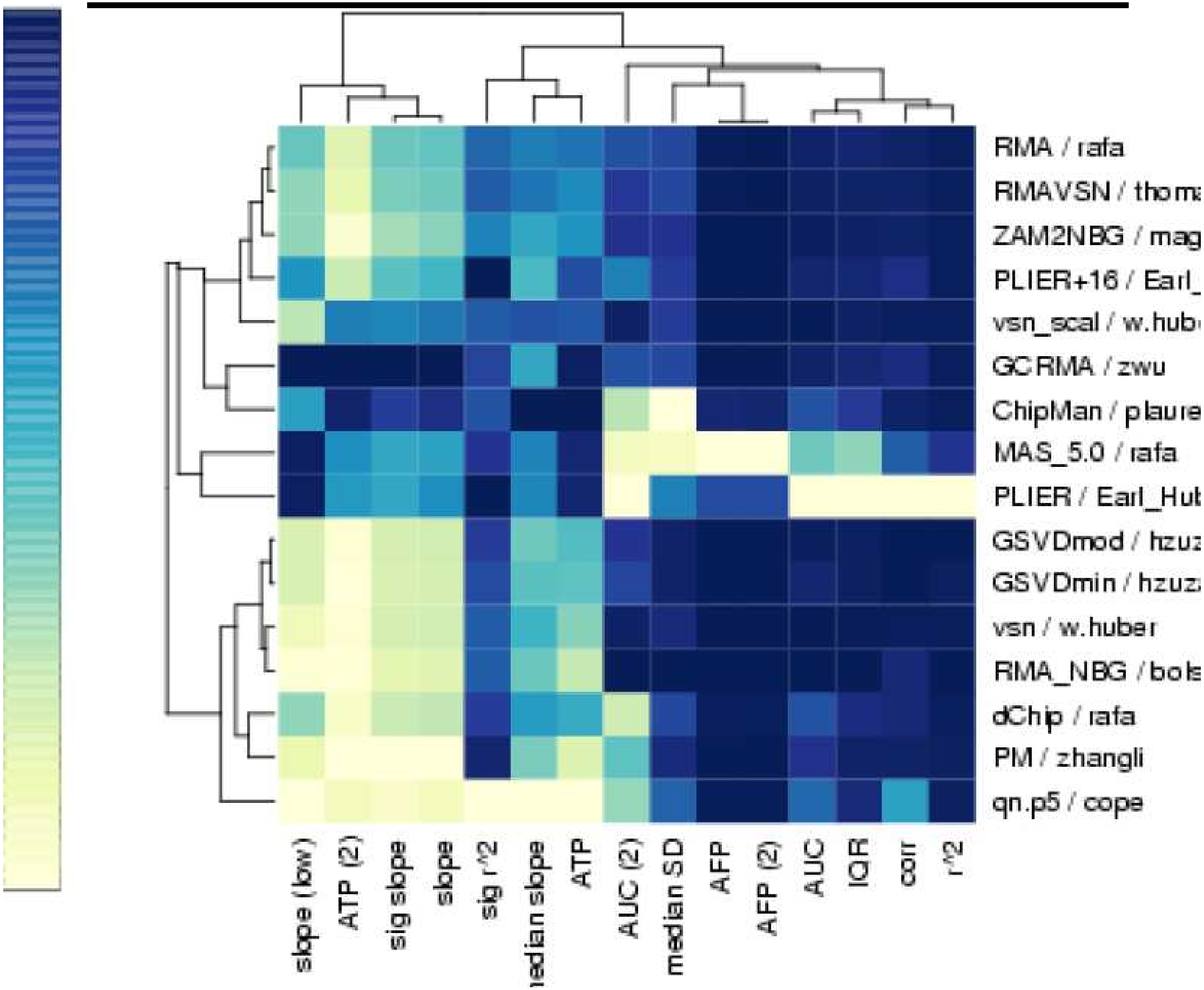
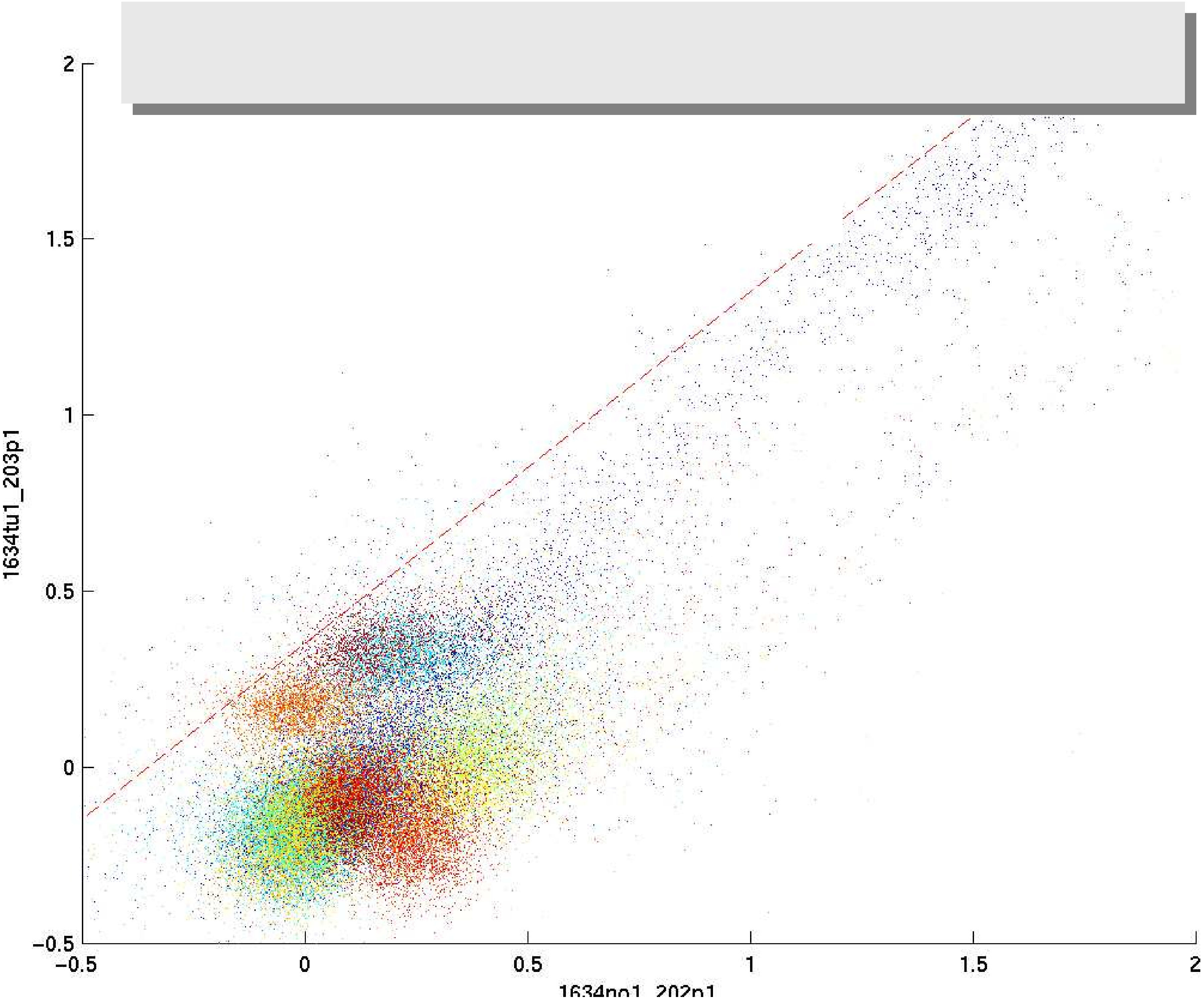


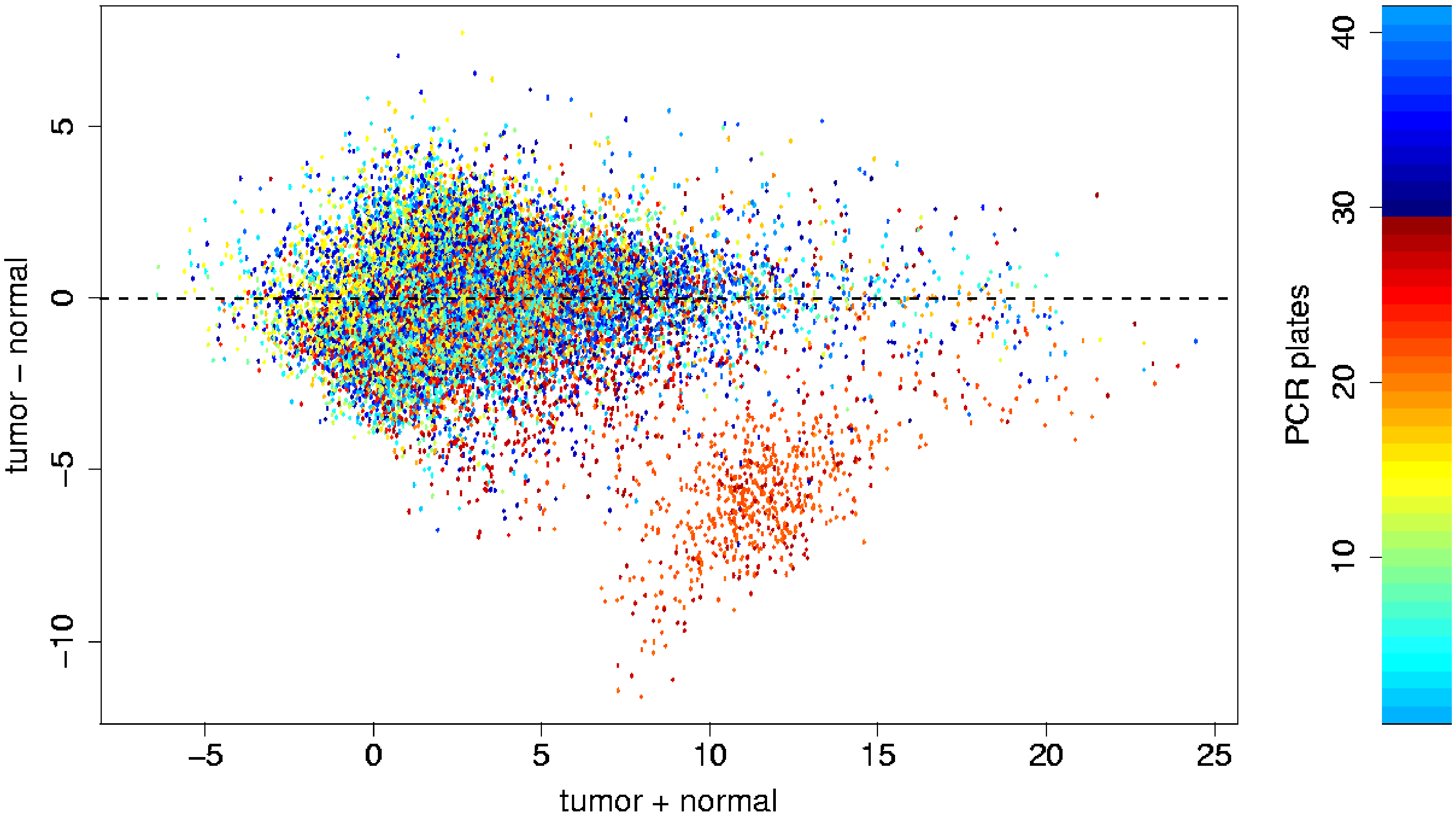
Figure 5a): A typical identification rule for differential expression filters genes with fold change exceeding a given threshold. This figure shows average ROC curves which offer a graphical representation of both specificity and sensitivity for such a detection rule.Average ROC curves based on comparisons with nominal fold changes ranging from 2 to 4096. b) As a) but with nominal fold changes equal to 2.

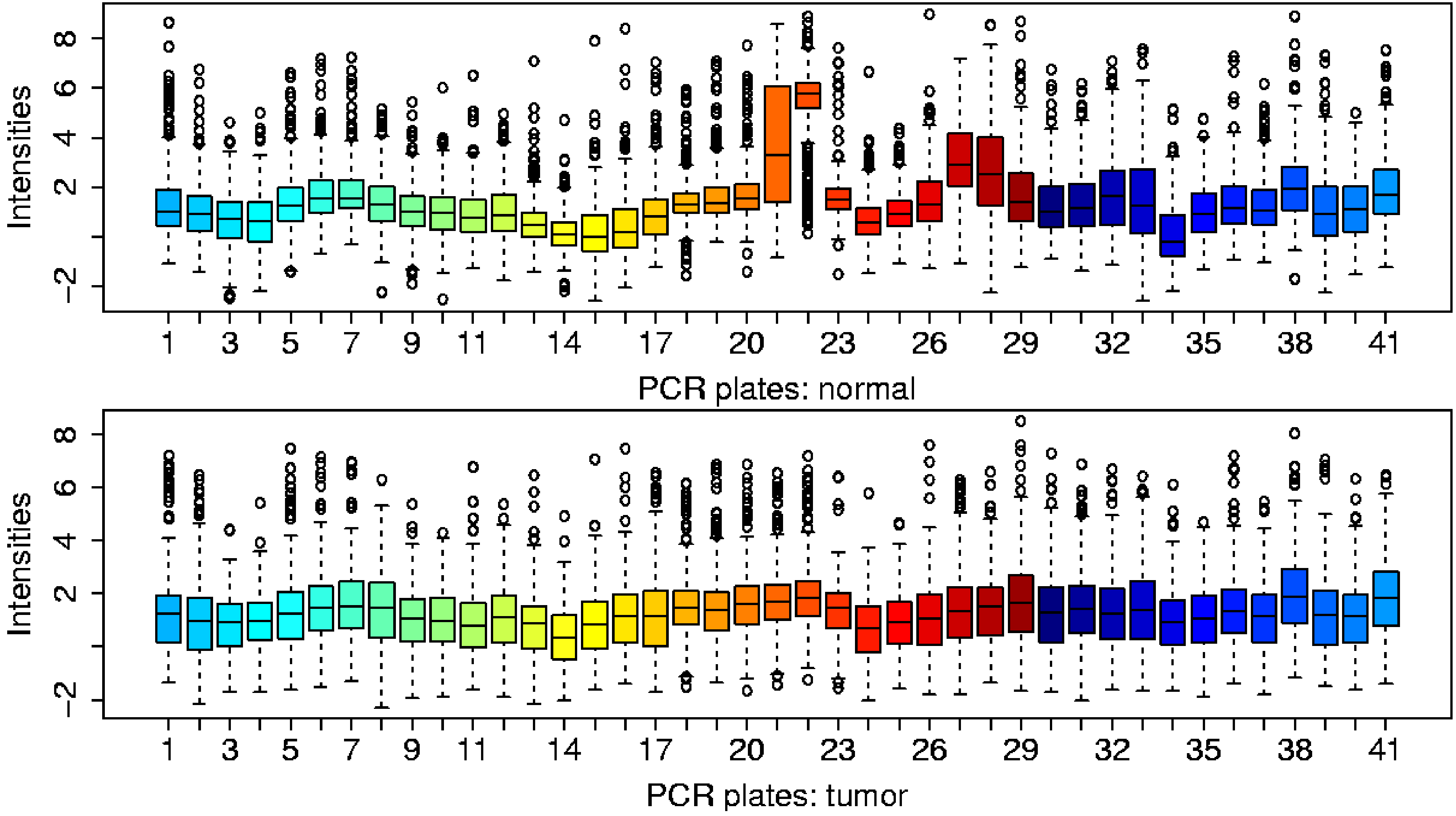

RMA / rafa
RMAVSN / thoma
ZAM2NBG / mag
PLIER+16 / Earl_
vsn_scal / w.hub
GCRMA / zwu
ChipMan / plaure
MAS_5.0 / rafa
PLIER / Earl_Hu
GSVDmod / hzuz
GSVDmin / hzuz
vsn / w.huber
RMA_NBG / bols
dChip / rafa
PM / zhangli
qn.p5 / cope
slope (low)
ATP (2)
sig slope
slope
sig r^2
edian slope
ATP
AUC (2)
median SD
AFP
AFP (2)
AUC
IQR
corr
r^2

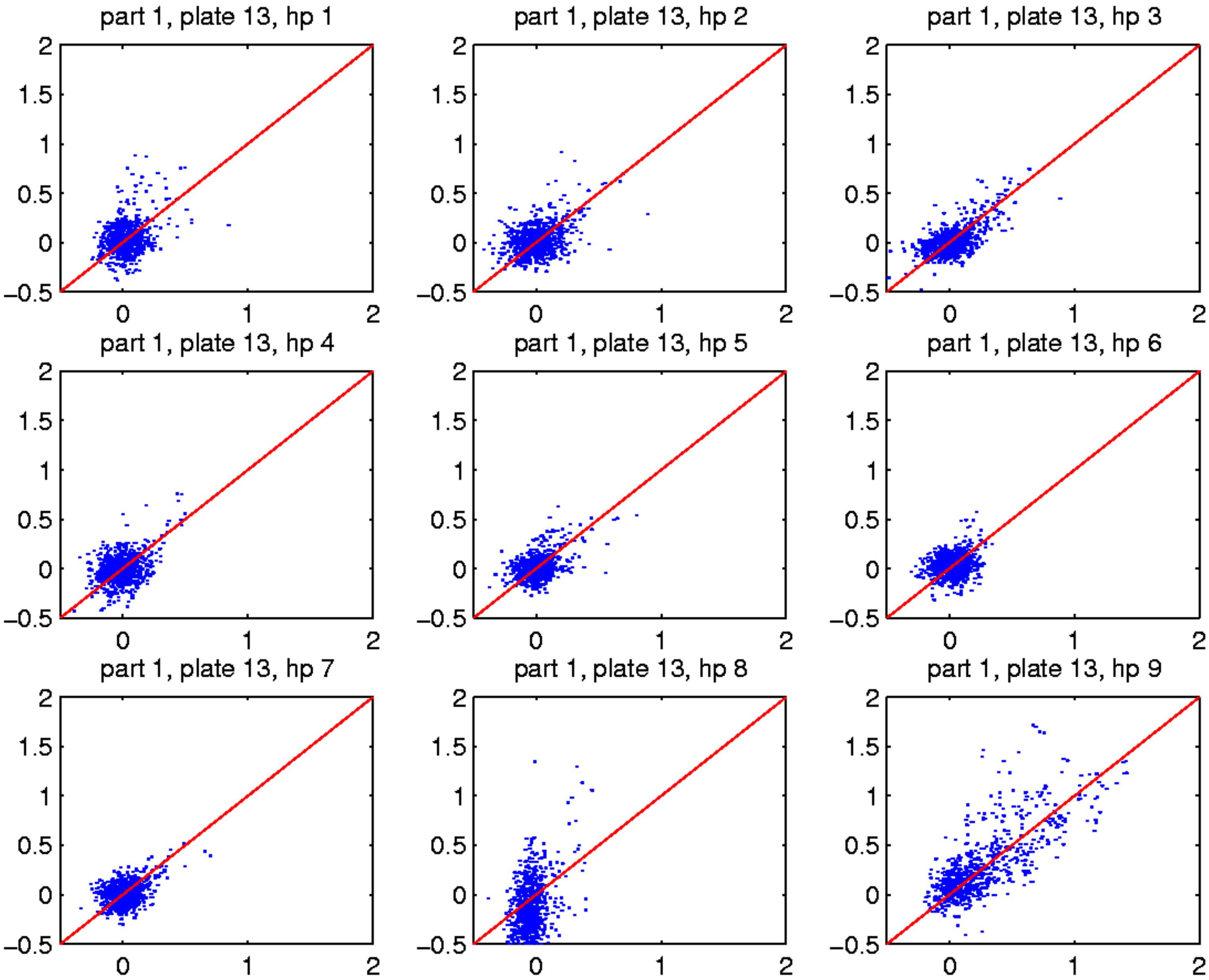
$$\frac{\quad}{\quad}$$

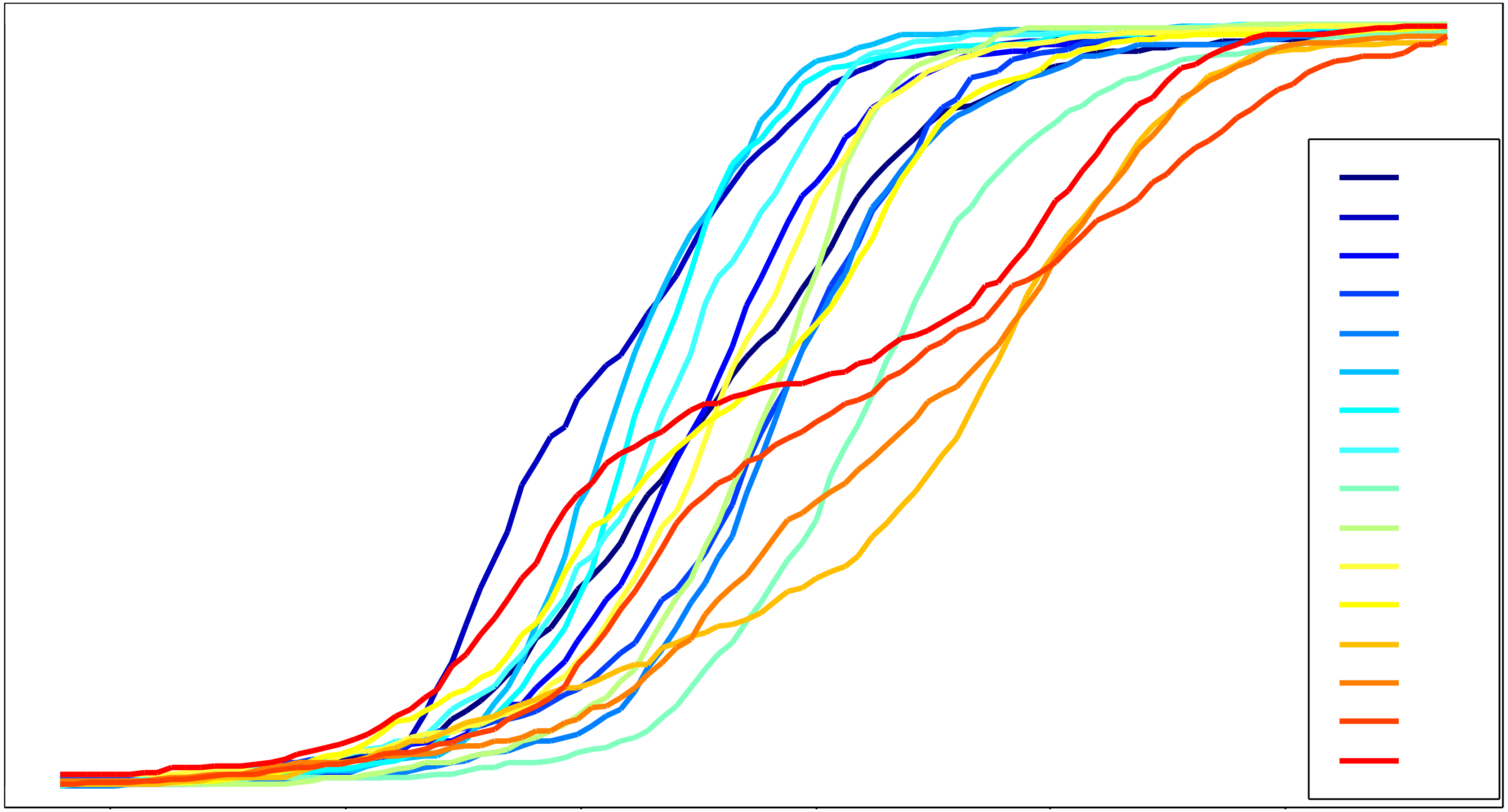
$$\frac{\sqrt{\qquad\qquad}}{\sqrt{\qquad\qquad}}$$

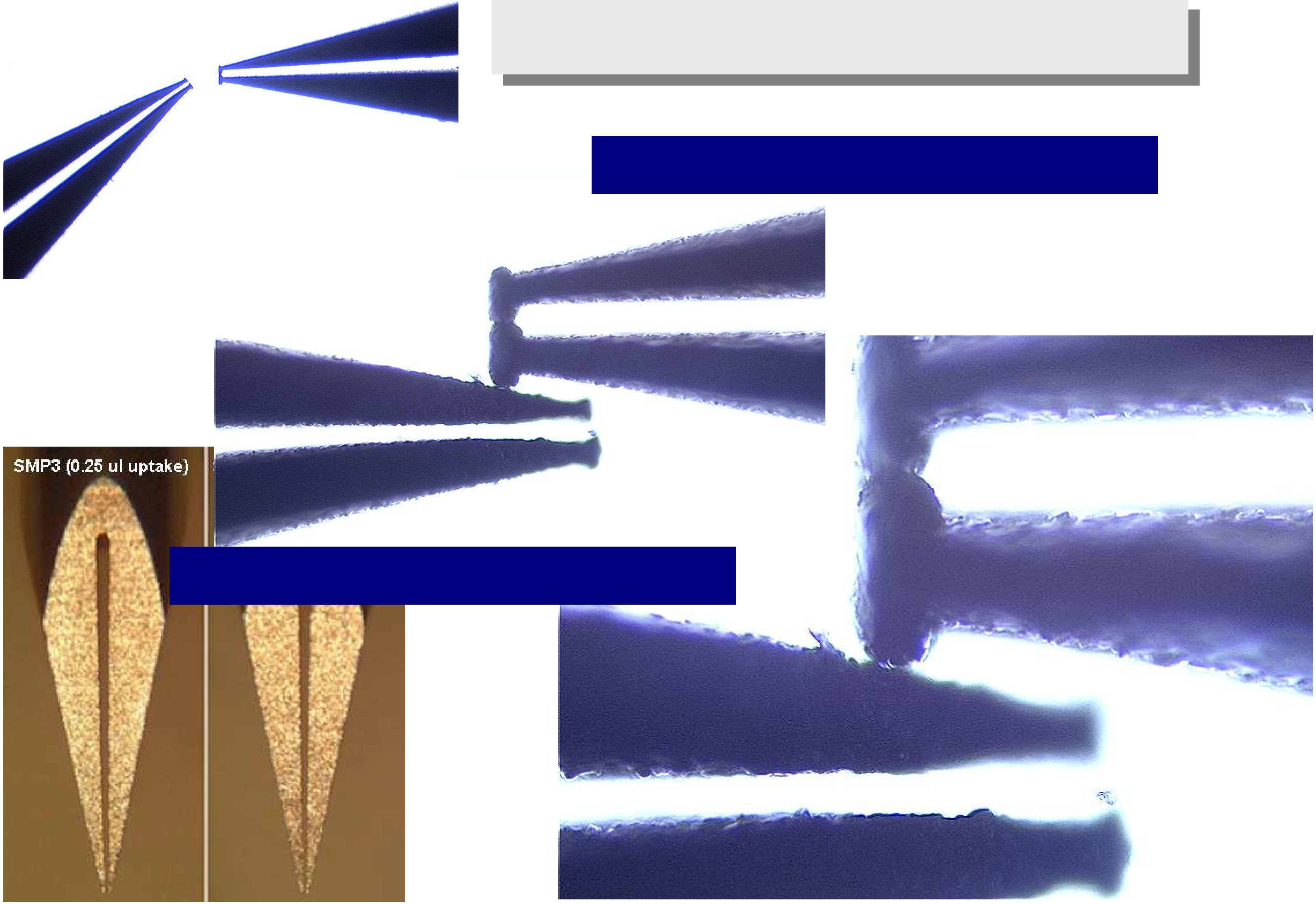

2
1.5
1
0.5
0
−0.5
−0.5
0
0.5
1
1.5
2
1634tu1_203p1
1634no1_202p1

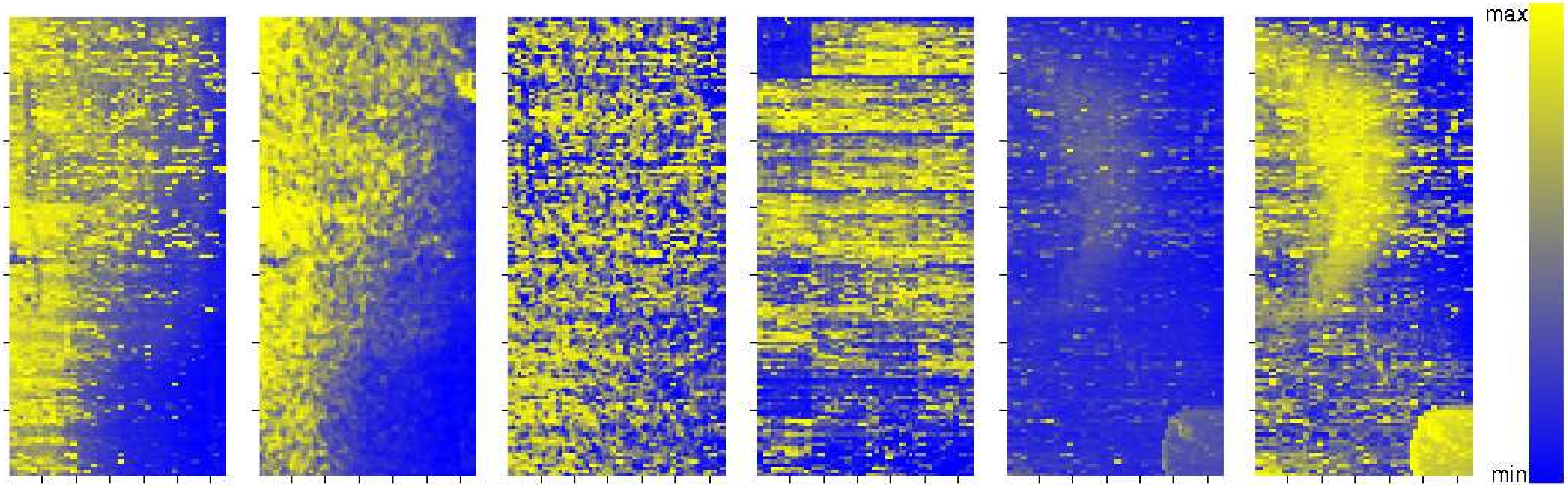

tumor – normal
5
0
–5
–10
–5
0
5
10
15
20
25
tumor + normal
PCR plates
10
20
30
40

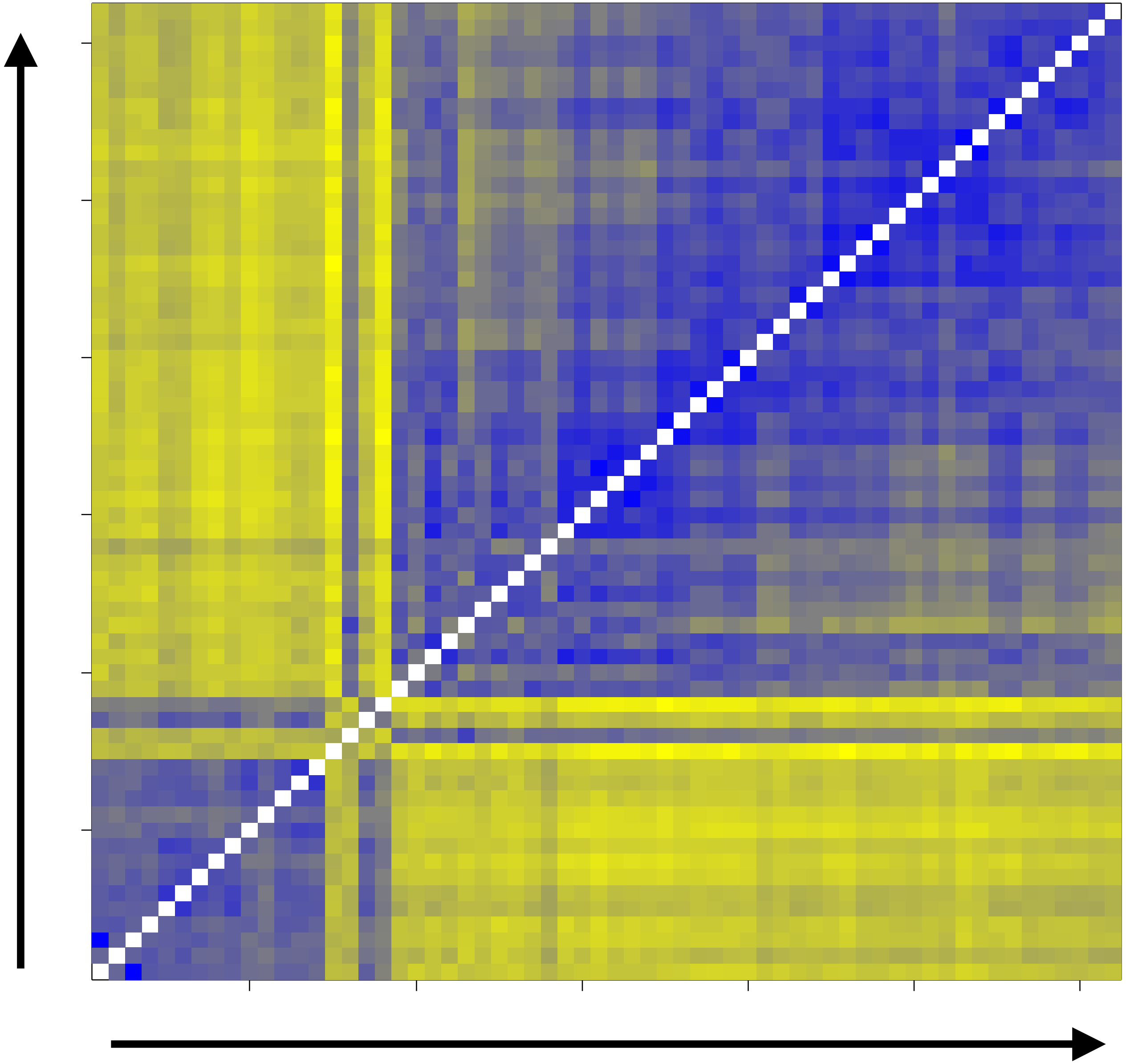

Intensities
8
6
4
2
−2
1
3
5
7
9
11
14
17
20
23
26
29
32
35
38
41
PCR plates: normal
Intensities
8
6
4
2
−2
1
3
5
7
9
11
14
17
20
23
26
29
32
35
38
41
PCR plates: tumor

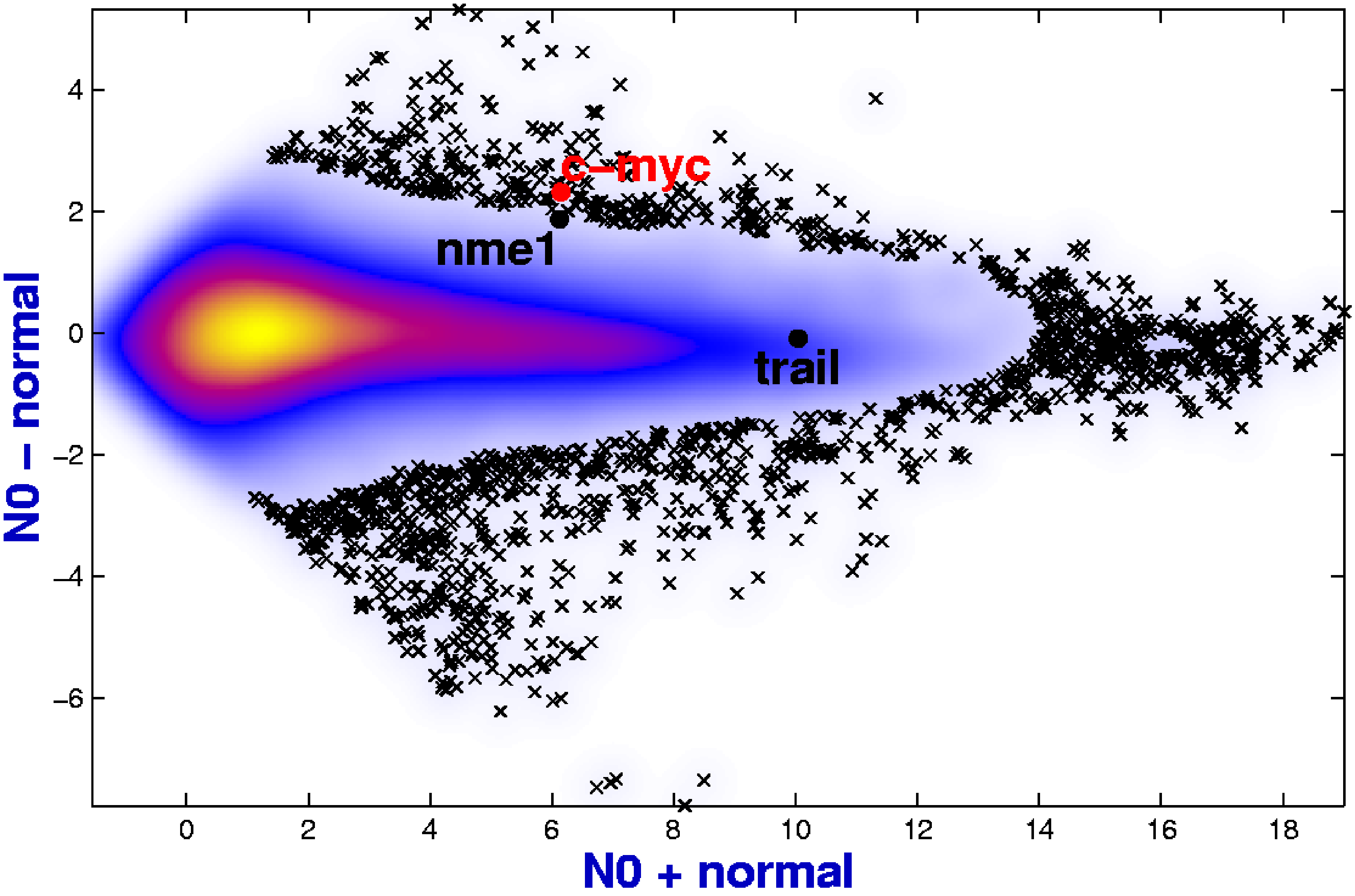

part 1, plate 13, hp 1
part 1, plate 13, hp 2
part 1, plate 13, hp 3
part 1, plate 13, hp 4
part 1, plate 13, hp 5
part 1, plate 13, hp 6
part 1, plate 13, hp 7
part 1, plate 13, hp 8
part 1, plate 13, hp 9
2
1.5
1
0.5
0
−0.5
0
1
2

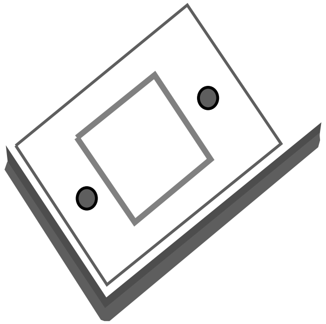


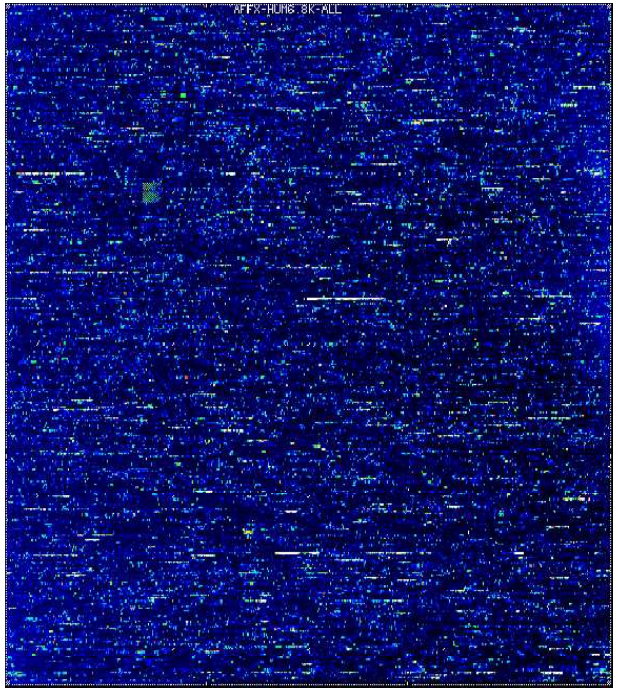

SMP3 (0.25 ul uptake)

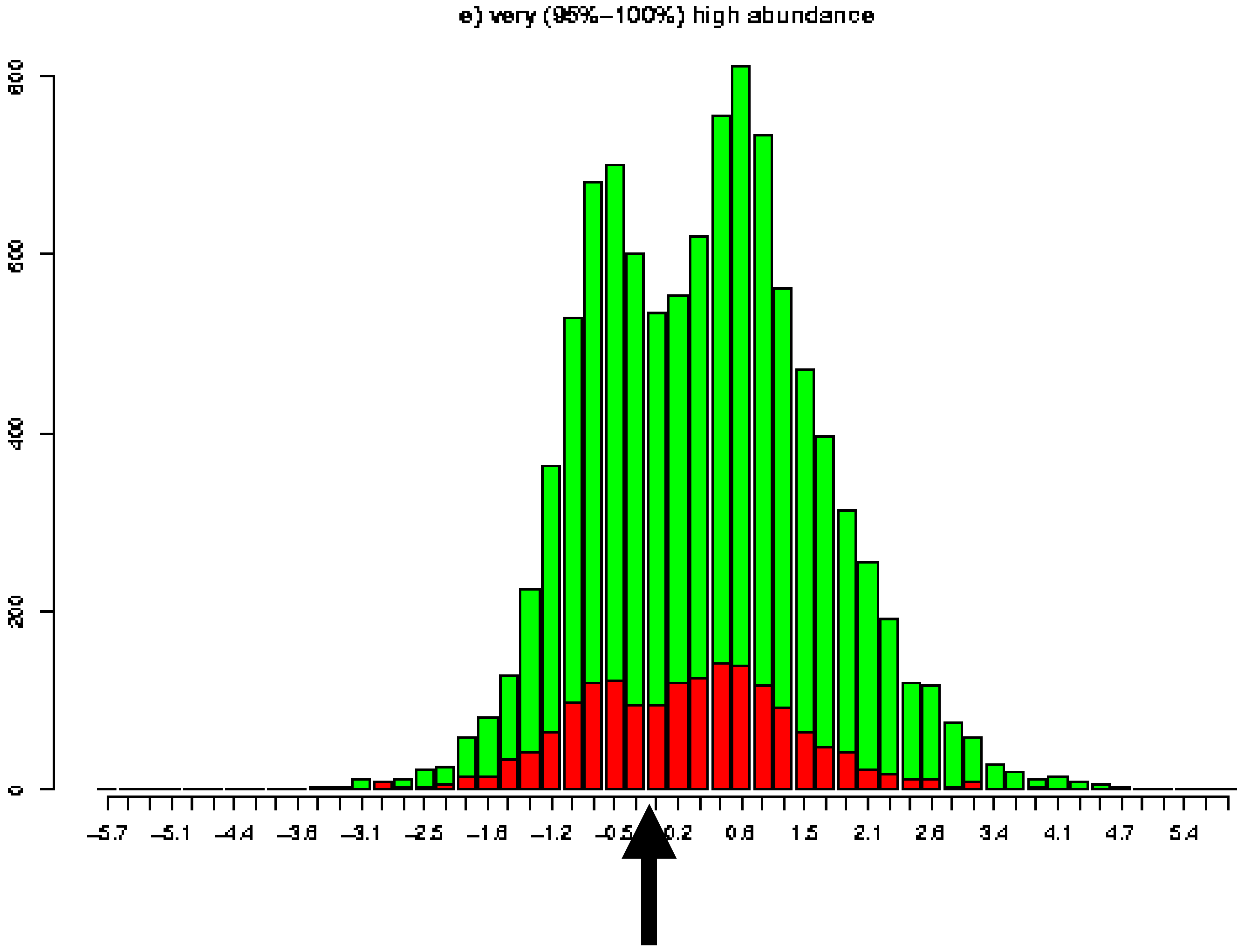

max
min

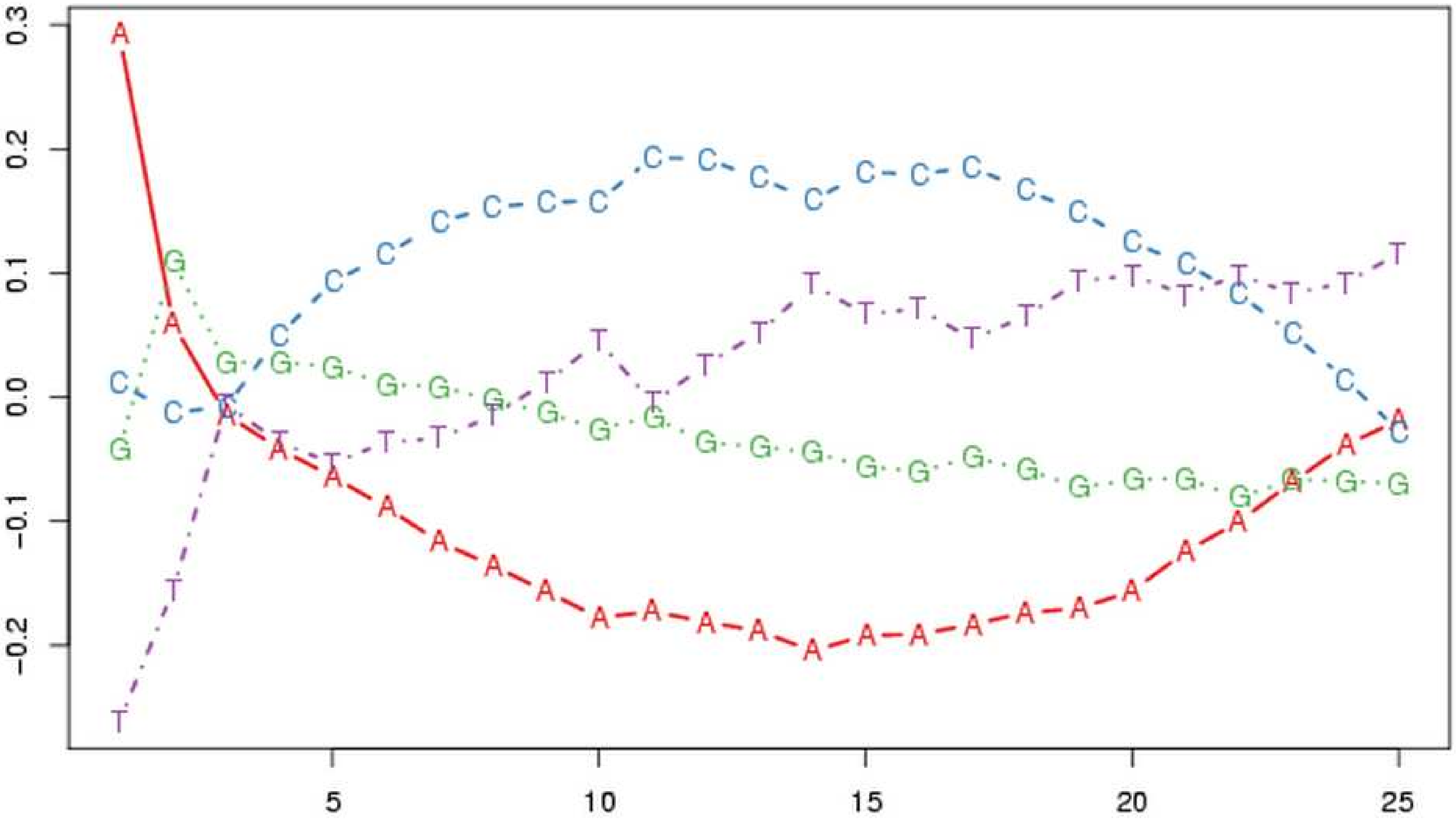



c−myc
nme1
trail
N0 − normal
N0 + normal
4
2
0
−2
−4
−6
0
2
4
6
8
10
12
14
16
18




AFFX-HUM6.8K-ALL


e) very (95%–100%) high abundance
0
200
400
600
800
–5.7
–5.1
–4.4
–3.8
–3.1
–2.5
–1.8
–1.2
–0.5
0.2
0.8
1.5
2.1
2.8
3.4
4.1
4.7
5.4


0.3
0.2
0.1
0.0
−0.1
−0.2
5
10
15
20
25
A
C
G
T