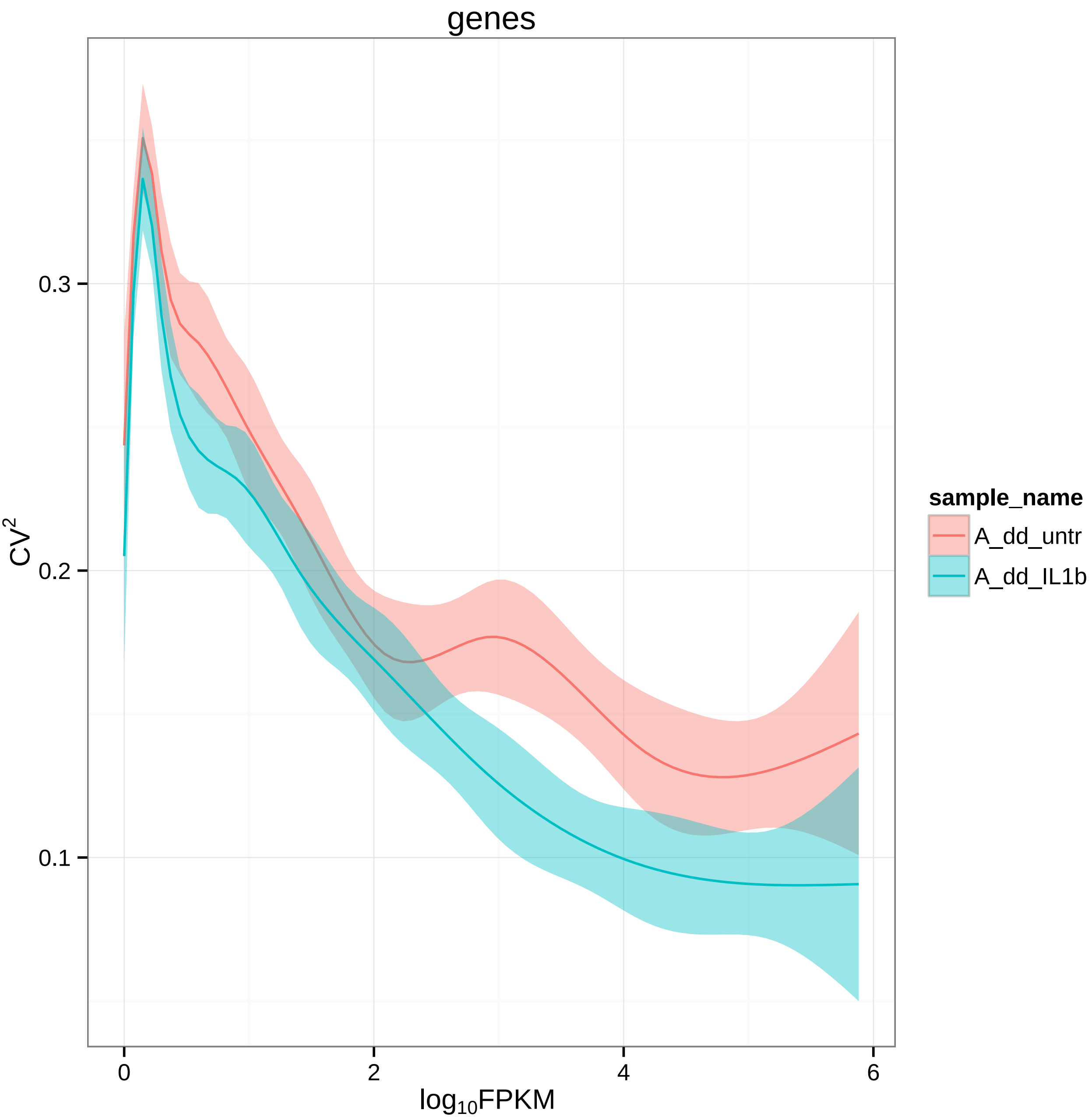
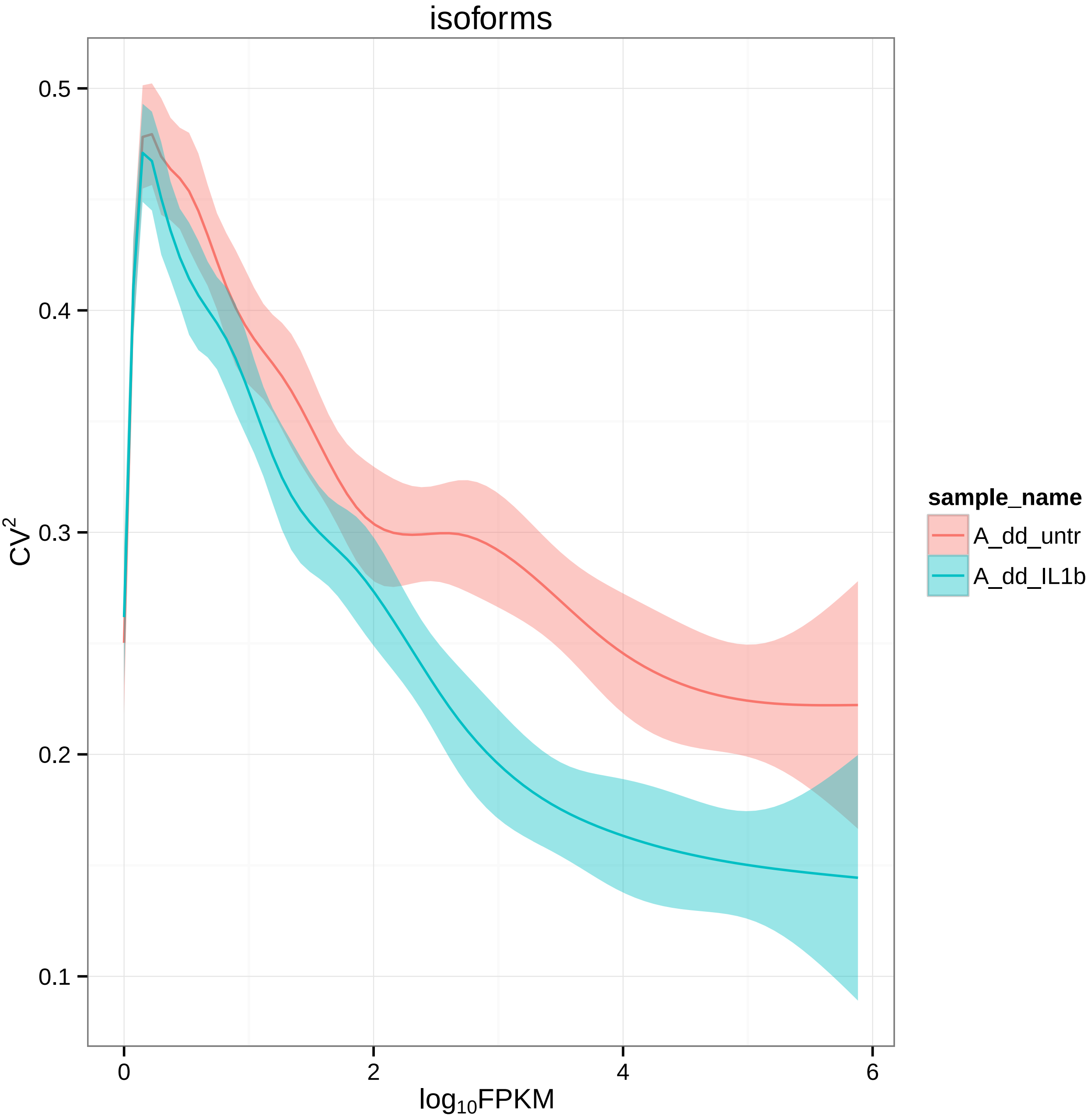
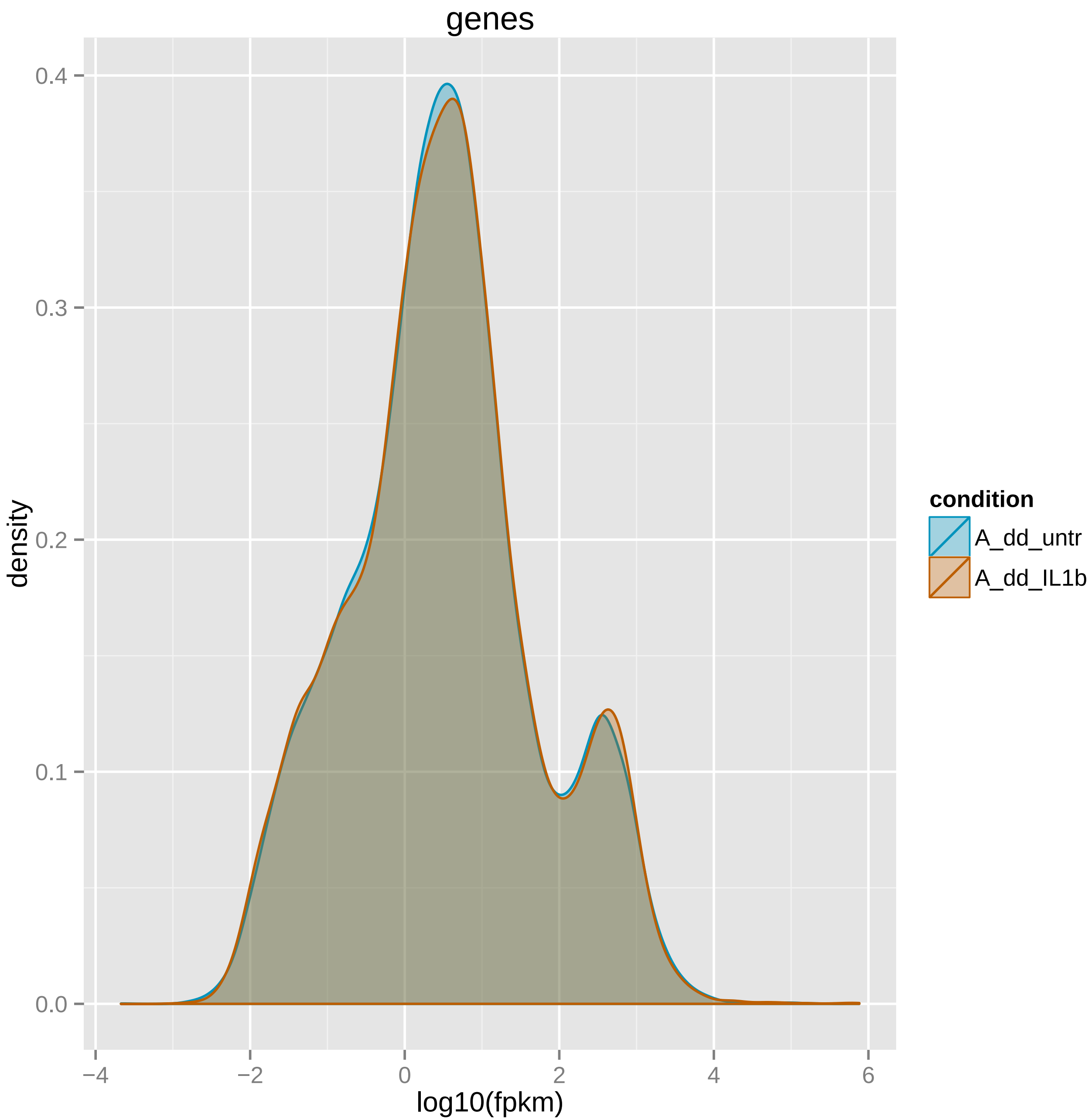
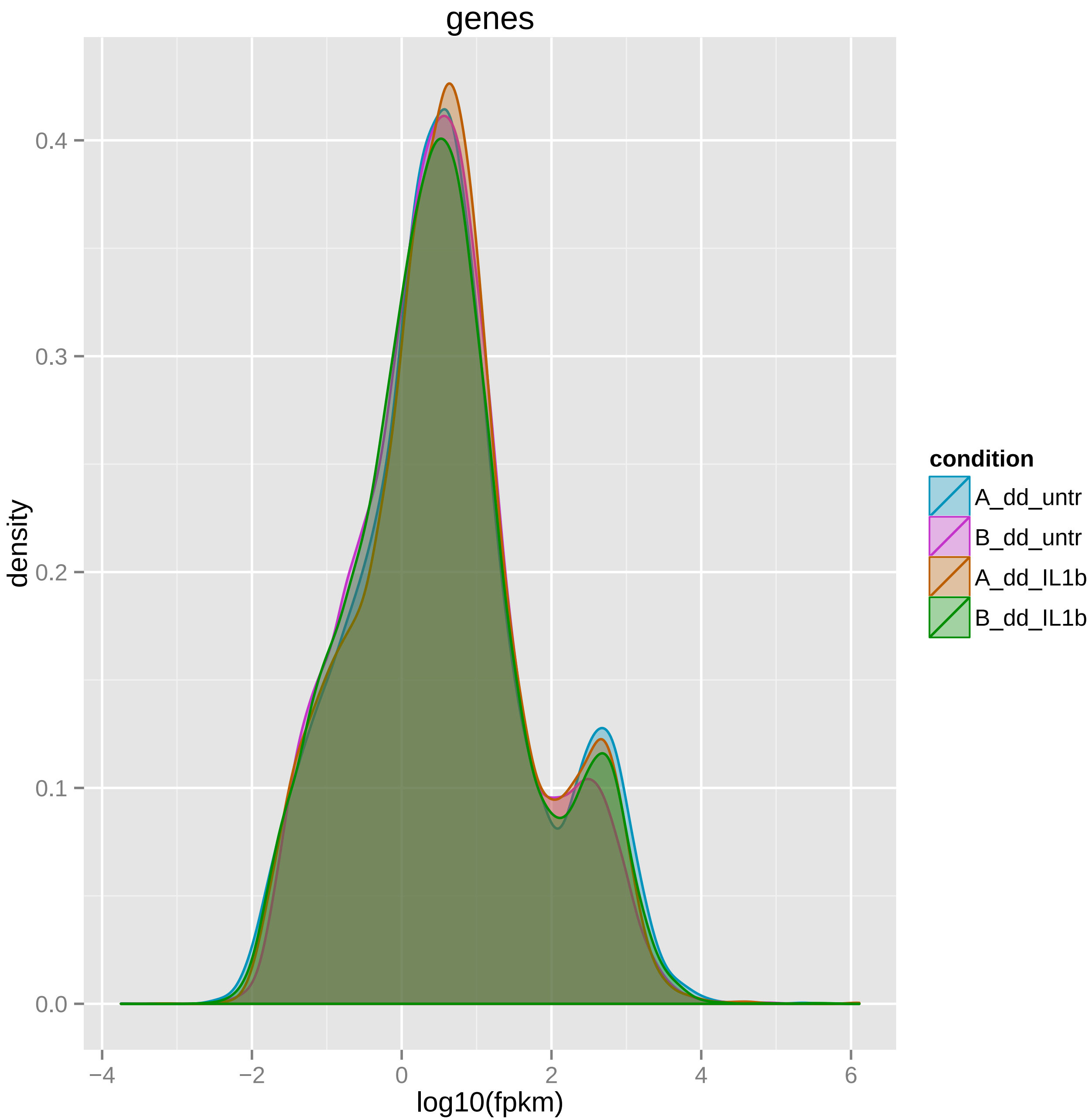
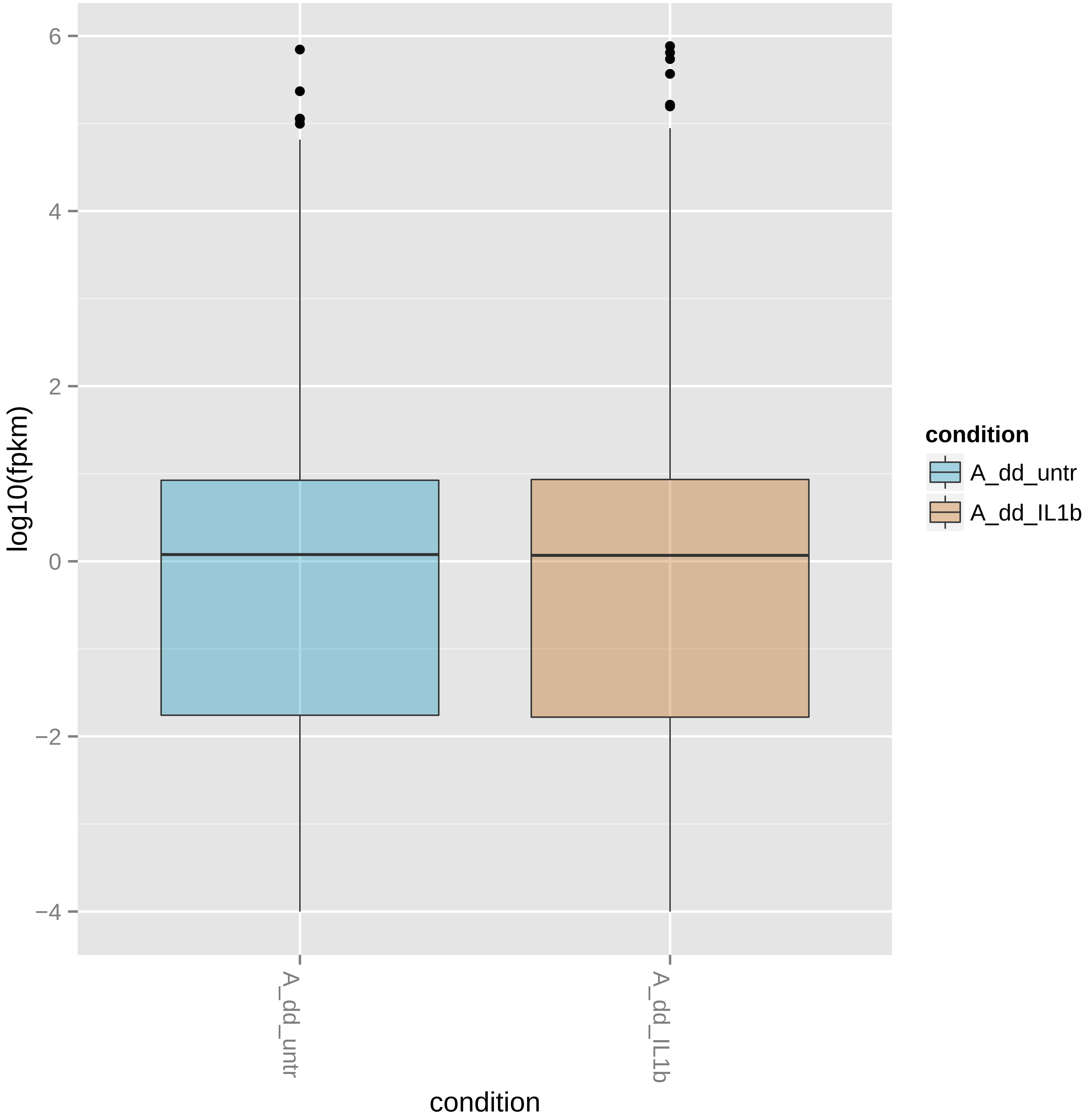
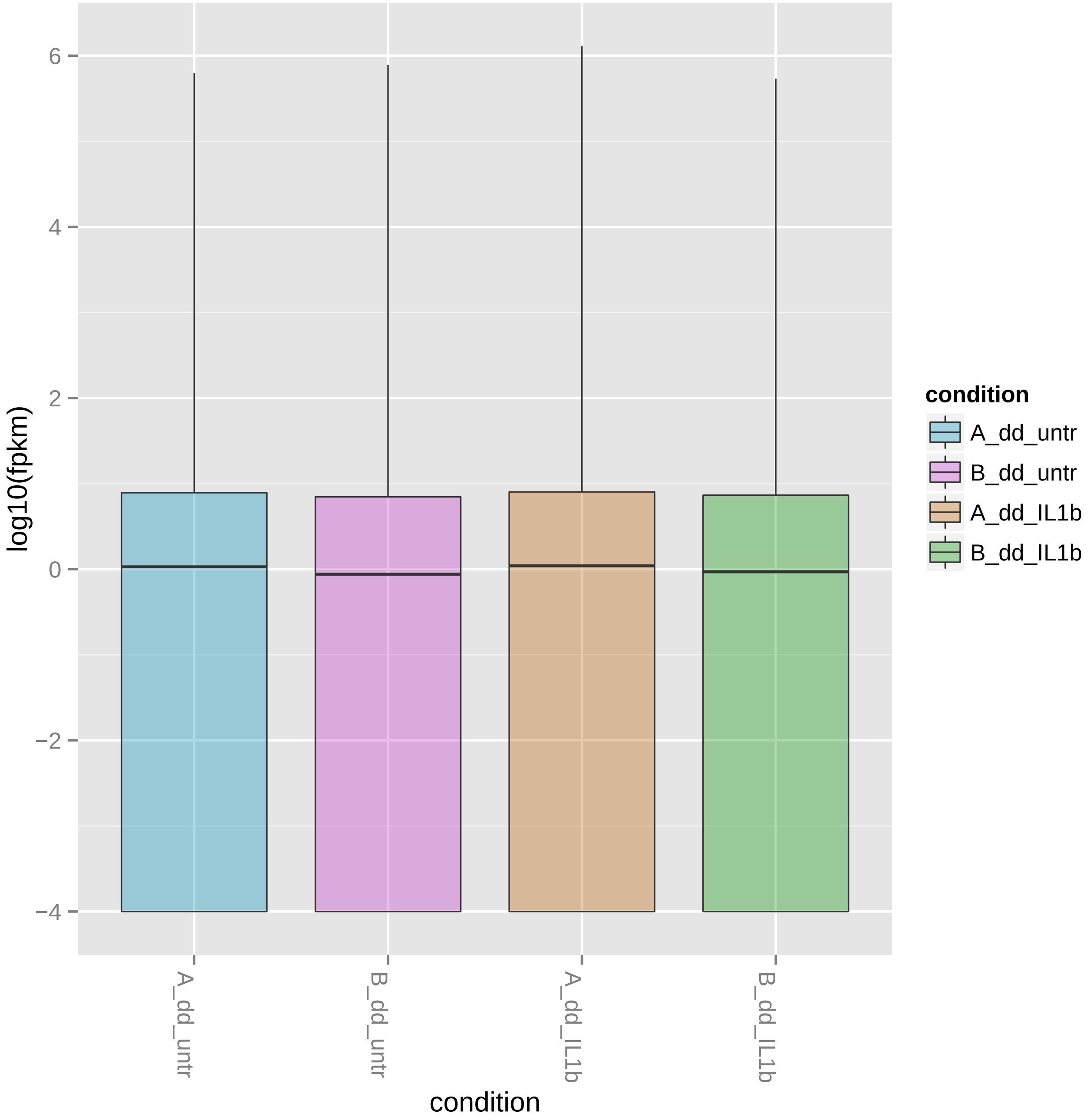

genes
0.3
0.2
0.1
CV²
0
2
4
6
log₁₀FPKM
sample_name
A_dd_untr
A_dd_IL1b

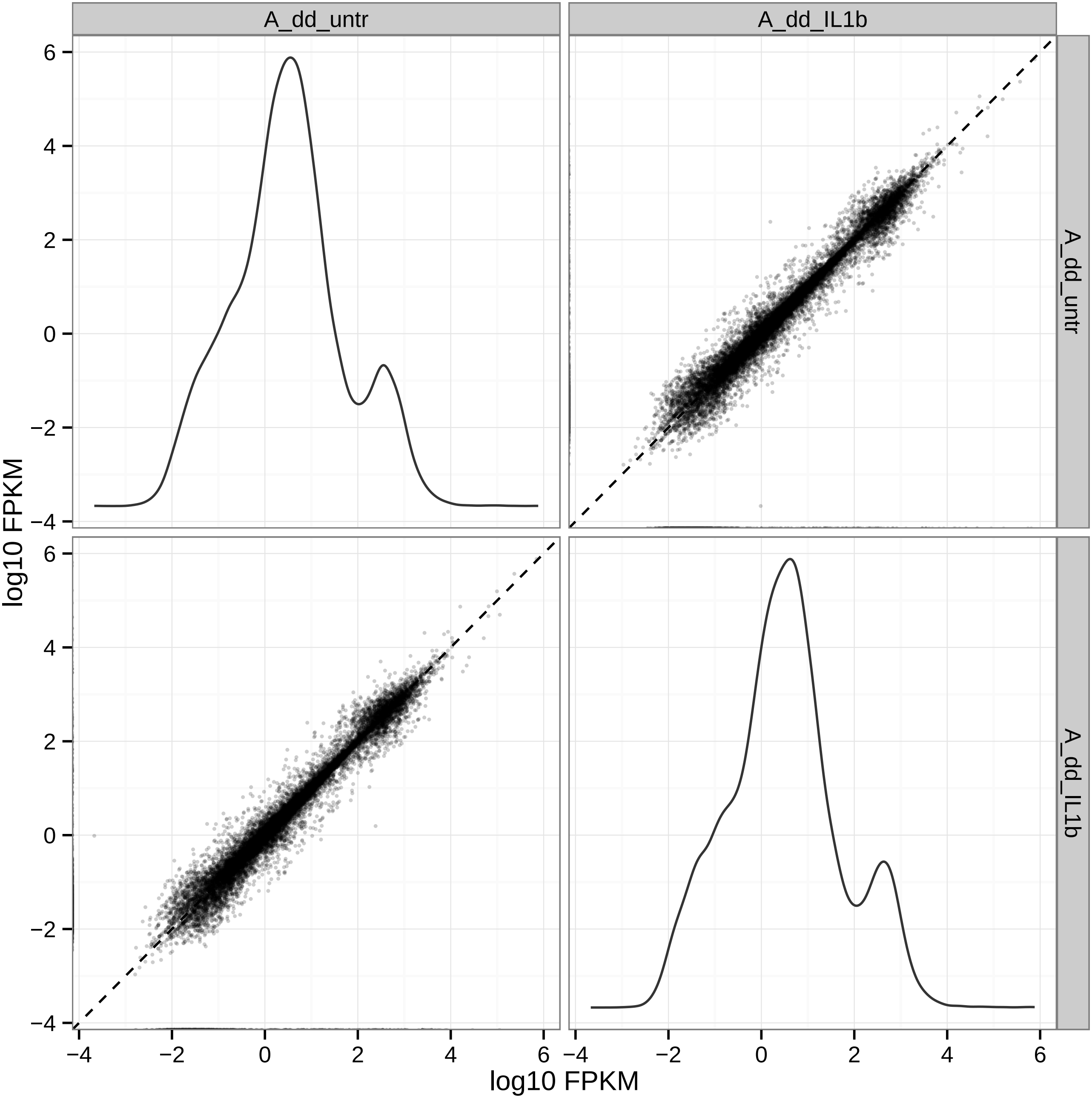

isoforms
0.5
0.4
0.3
0.2
0.1
CV^2
0
2
4
6
log$_{10}$FPKM
sample_name
A_dd_untr
A_dd_IL1b

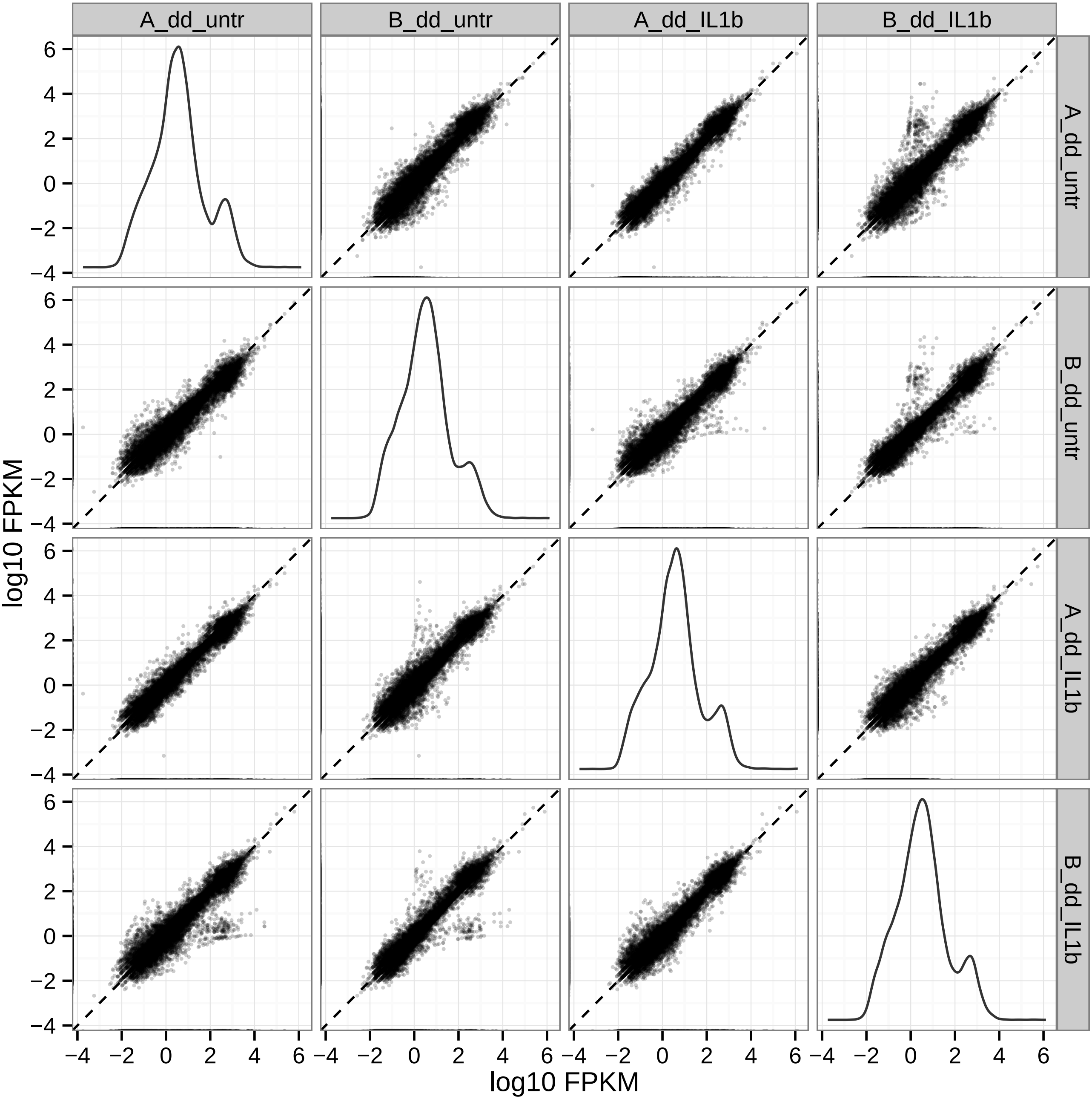

genes
0.4
0.3
0.2
0.1
0.0
density
−4
−2
0
2
4
6
log10(fpkm)
condition
A_dd_untr
A_dd_IL1b

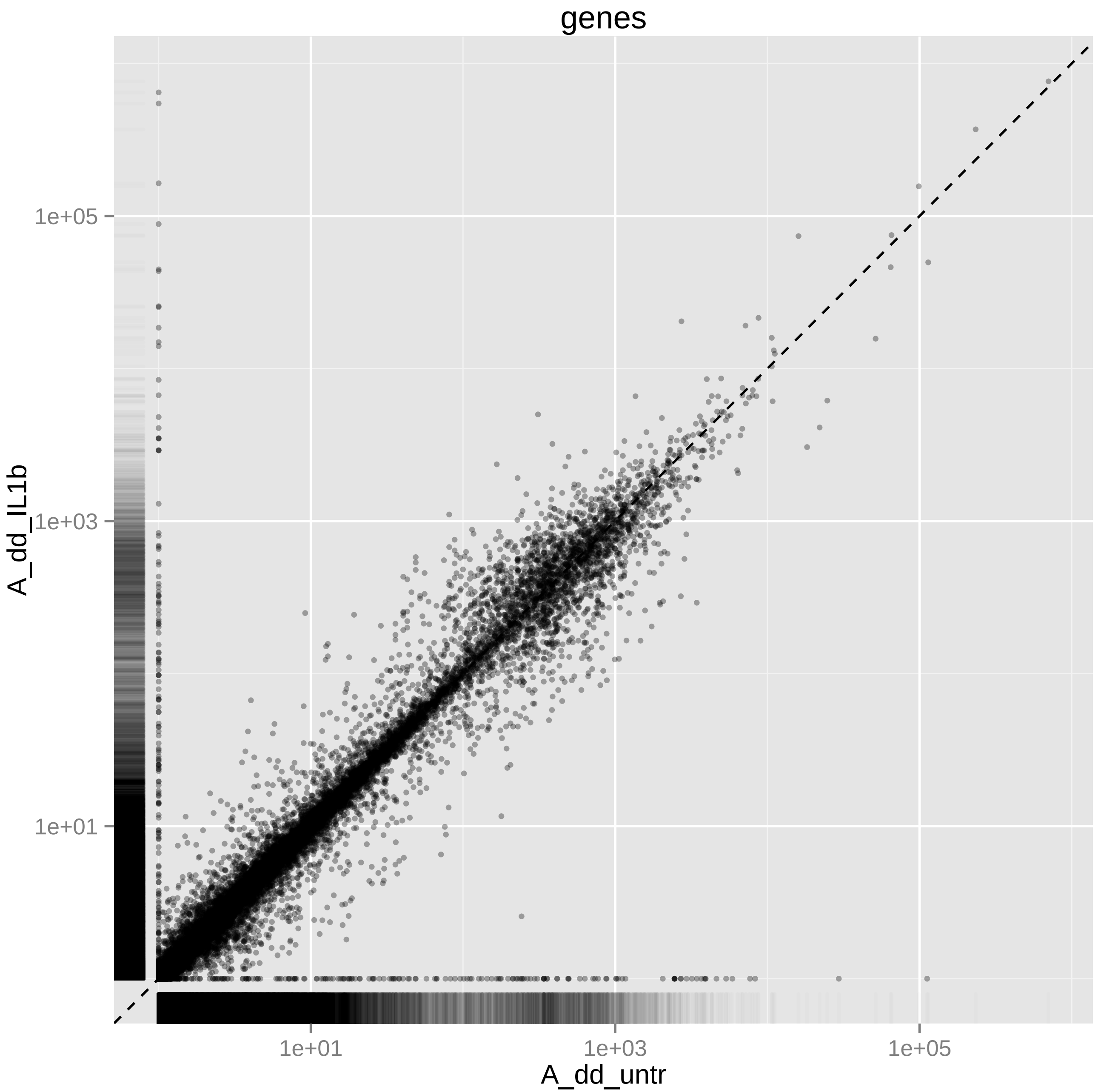

genes
density
0.0
0.1
0.2
0.3
0.4
−4
−2
0
2
4
6
log10(fpkm)
condition
A_dd_untr
B_dd_untr
A_dd_IL1b
B_dd_IL1b

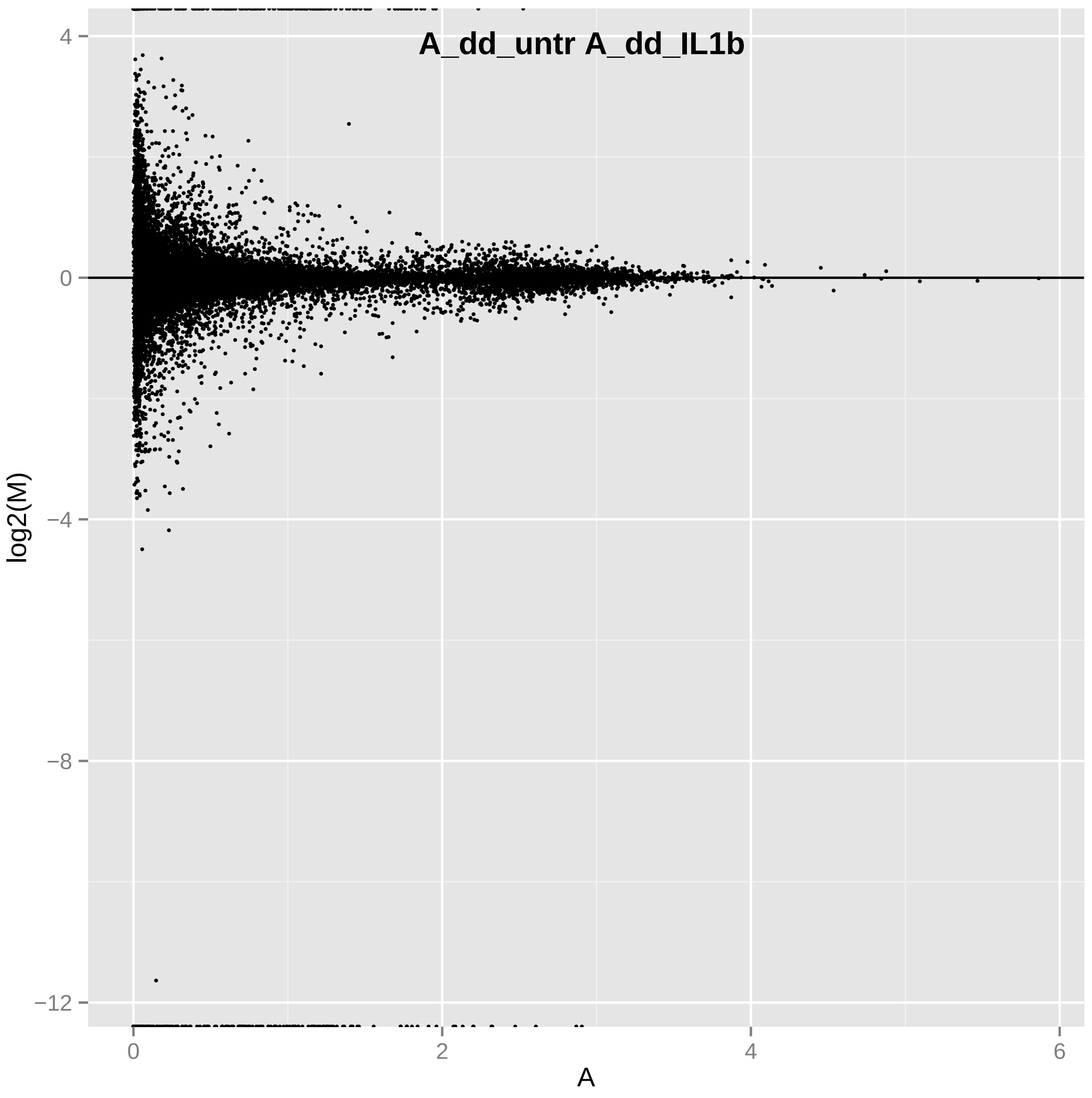

6
4
2
0
−2
−4
log10(fpkm)
A_dd_untr
A_dd_IL1b
condition
condition
A_dd_untr
A_dd_IL1b

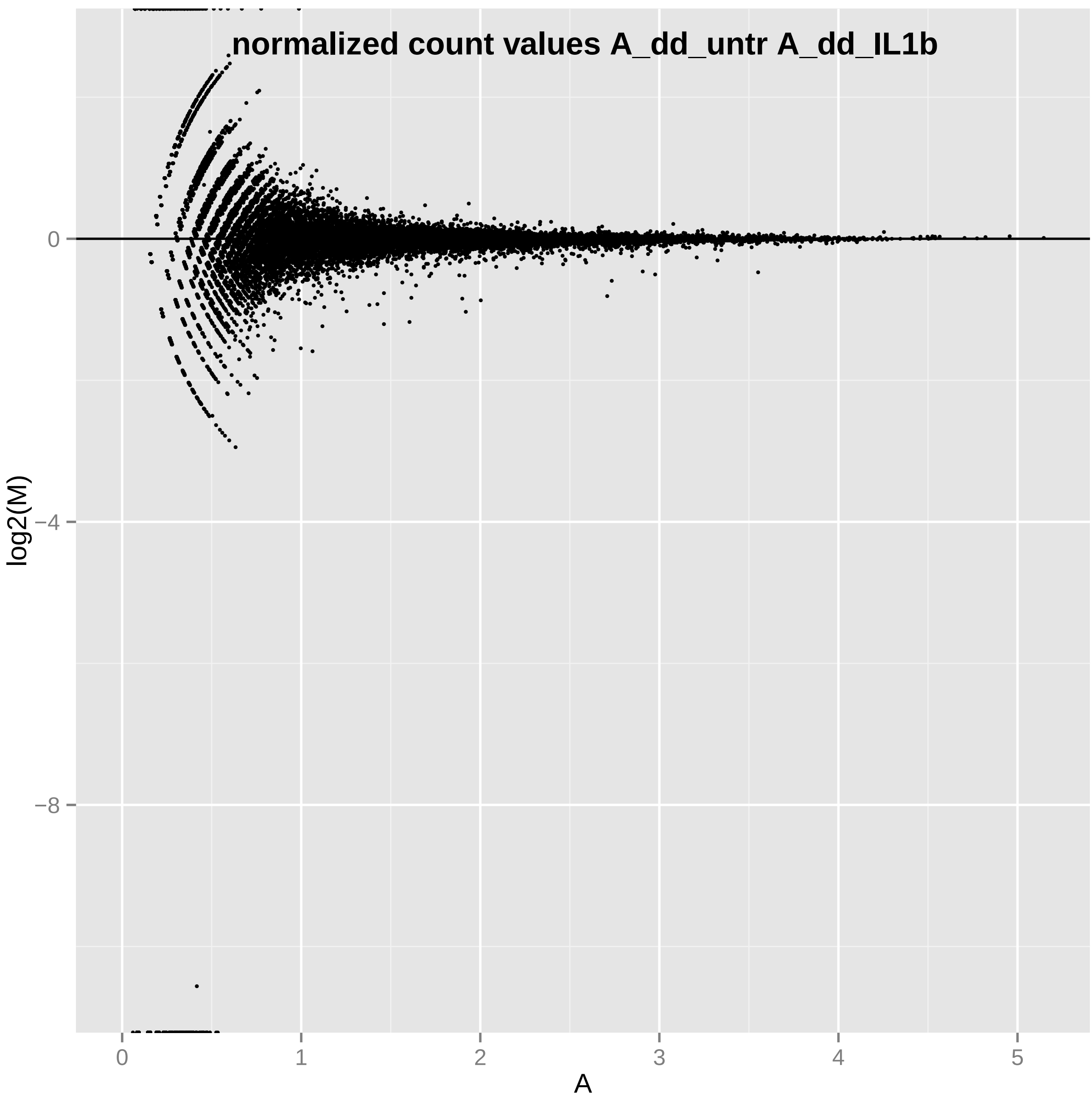

6
4
2
0
−2
−4
log10(fpkm)
A_dd_untr
B_dd_untr
A_dd_IL1b
B_dd_IL1b
condition
condition
A_dd_untr
B_dd_untr
A_dd_IL1b
B_dd_IL1b


A_dd_untr
A_dd_IL1b
A_dd_untr
A_dd_IL1b
log10 FPKM
log10 FPKM
6
4
2
0
−2
−4
6
4
2
0
−2
−4
−4
−2
0
2
4
6
−4
−2
0
2
4
6

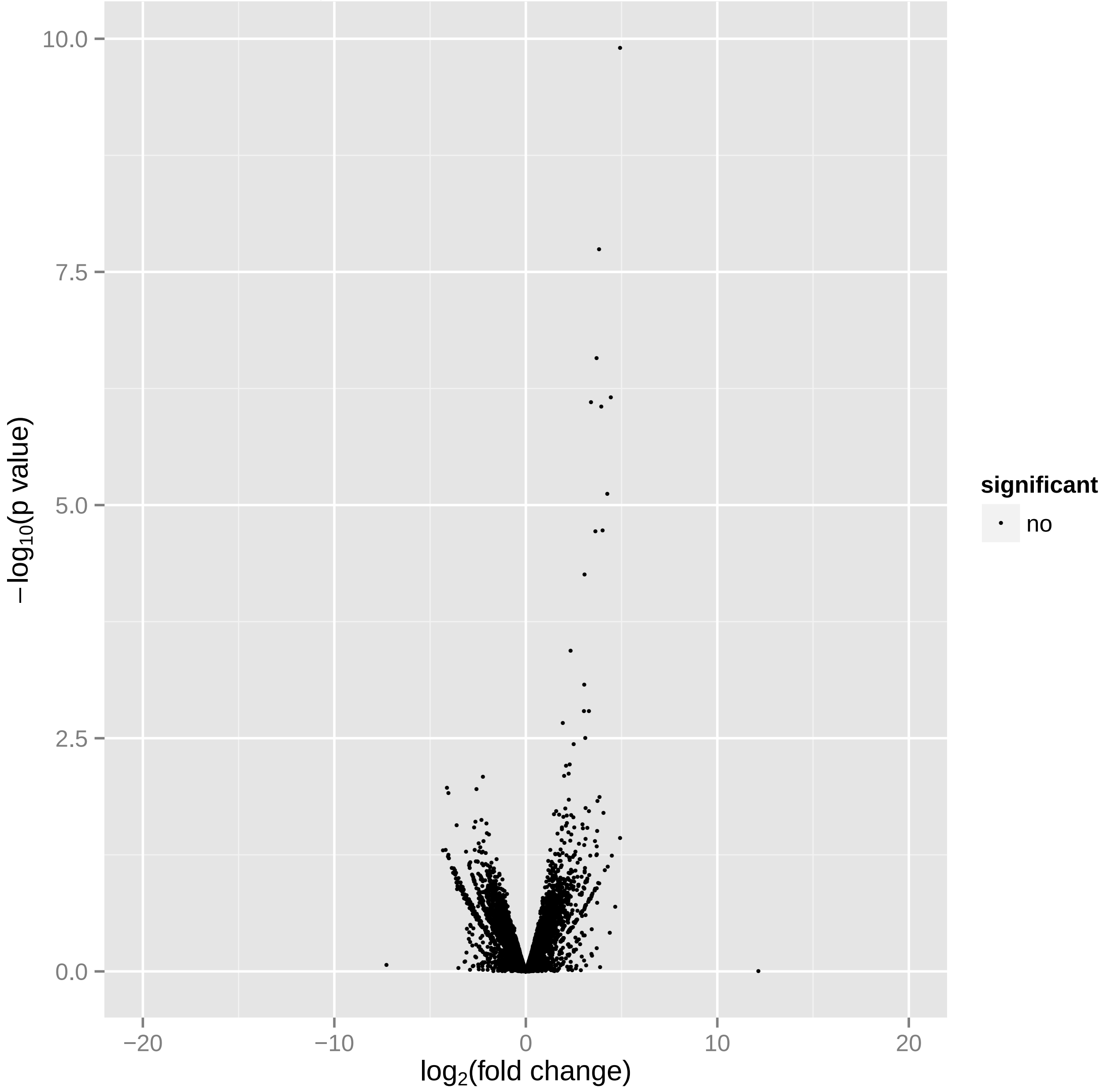

A_dd_untr
B_dd_untr
A_dd_IL1b
B_dd_IL1b
A_dd_untr
B_dd_untr
A_dd_IL1b
B_dd_IL1b
log10 FPKM
log10 FPKM
−4
−2
0
2
4
6

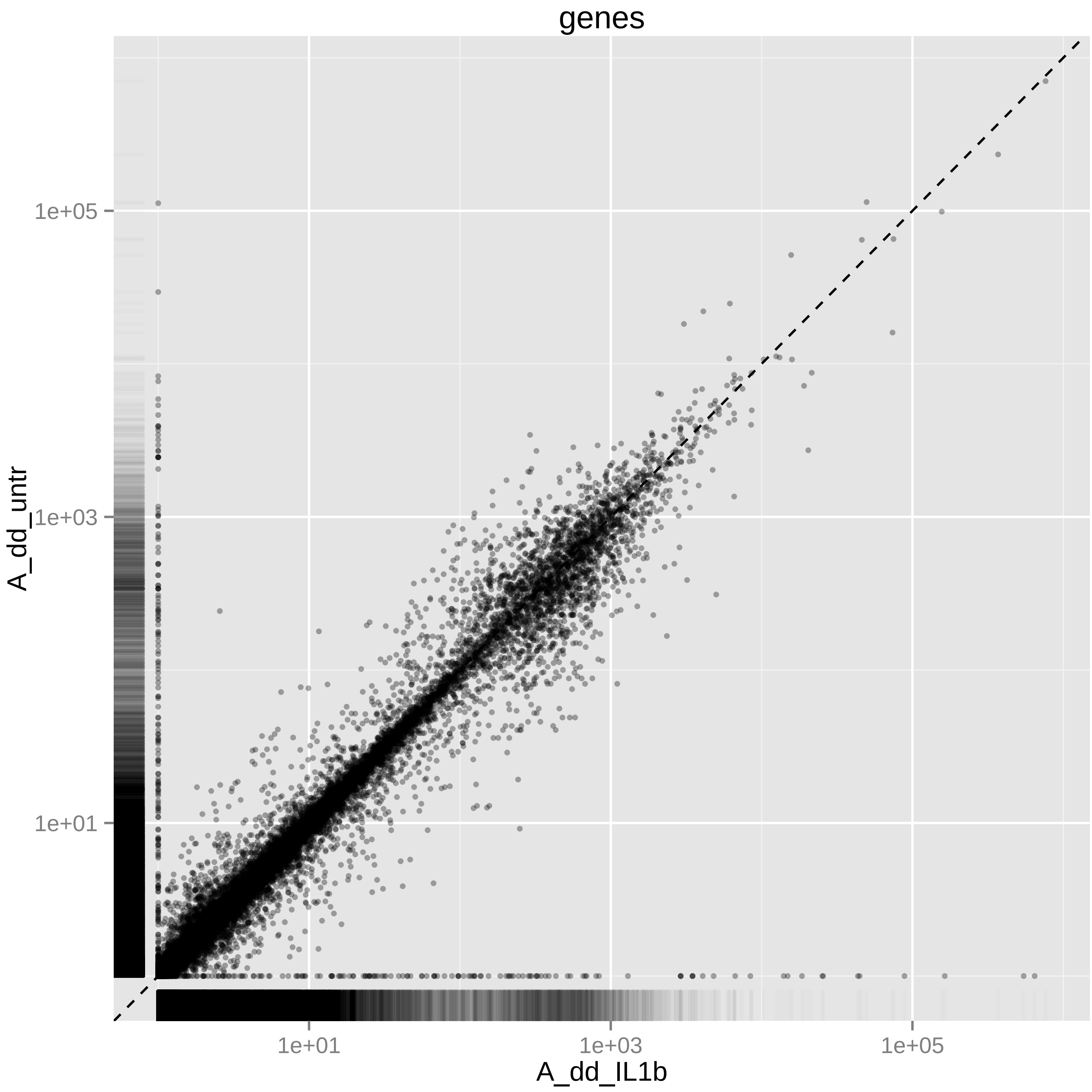

genes
A_dd_IL1b
1e+05
1e+03
1e+01
1e+01
1e+03
1e+05
A_dd_untr

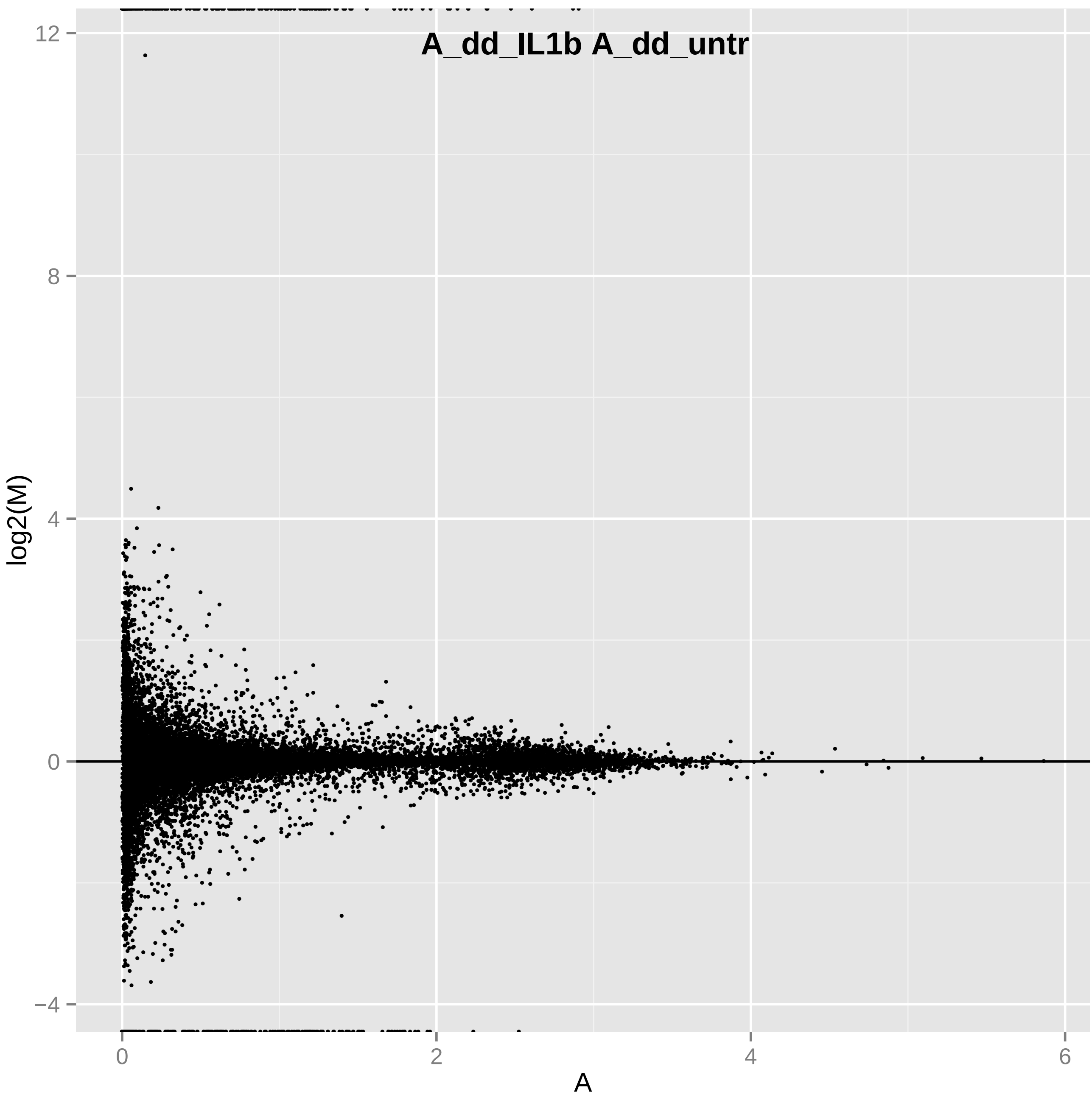

A_dd_untr A_dd_IL1b
log2(M)
4
0
−4
−8
−12
0
2
4
6
A

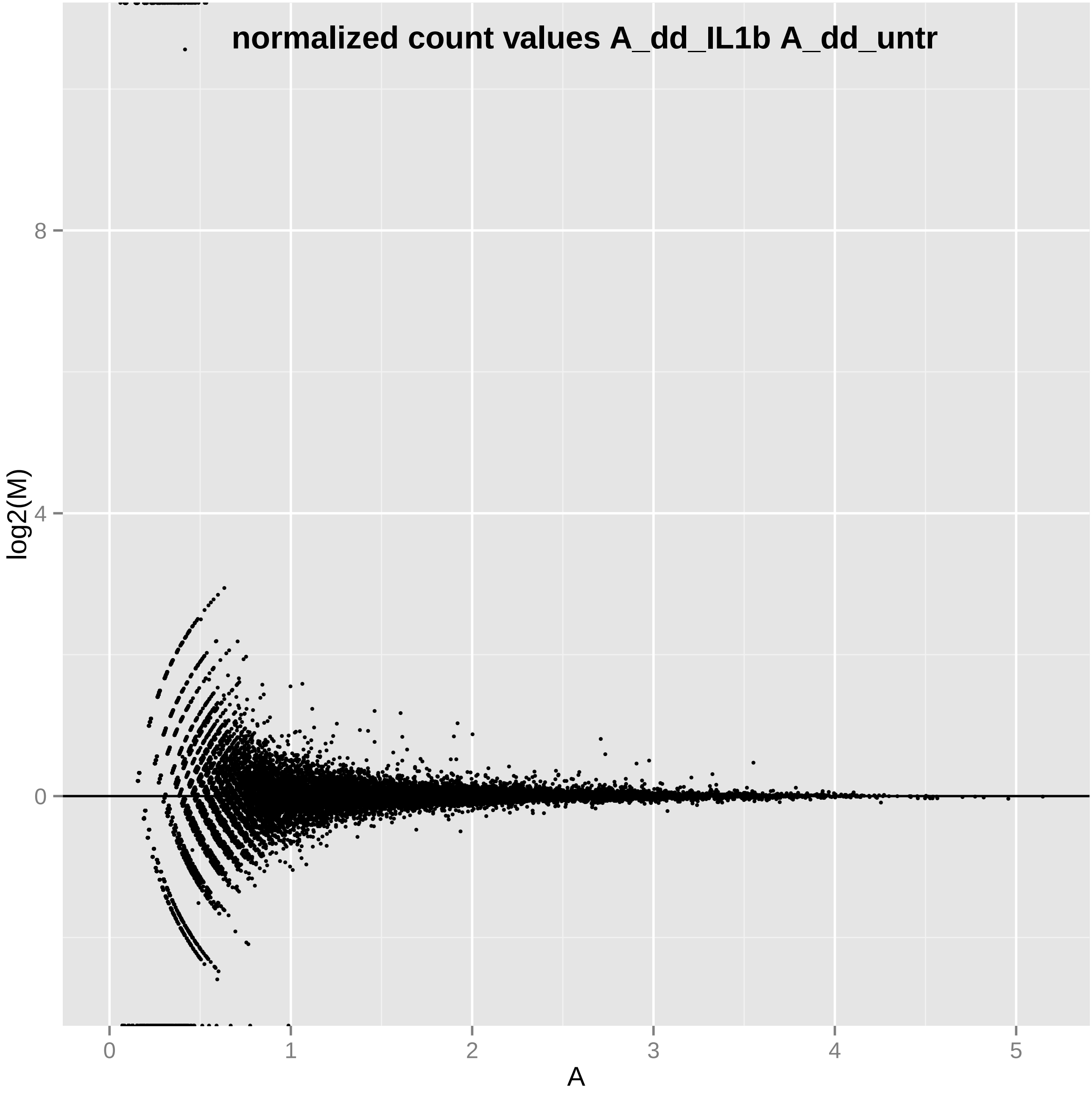

normalized count values A_dd_untr A_dd_IL1b
log2(M)
0
−4
−8
A
0
1
2
3
4
5

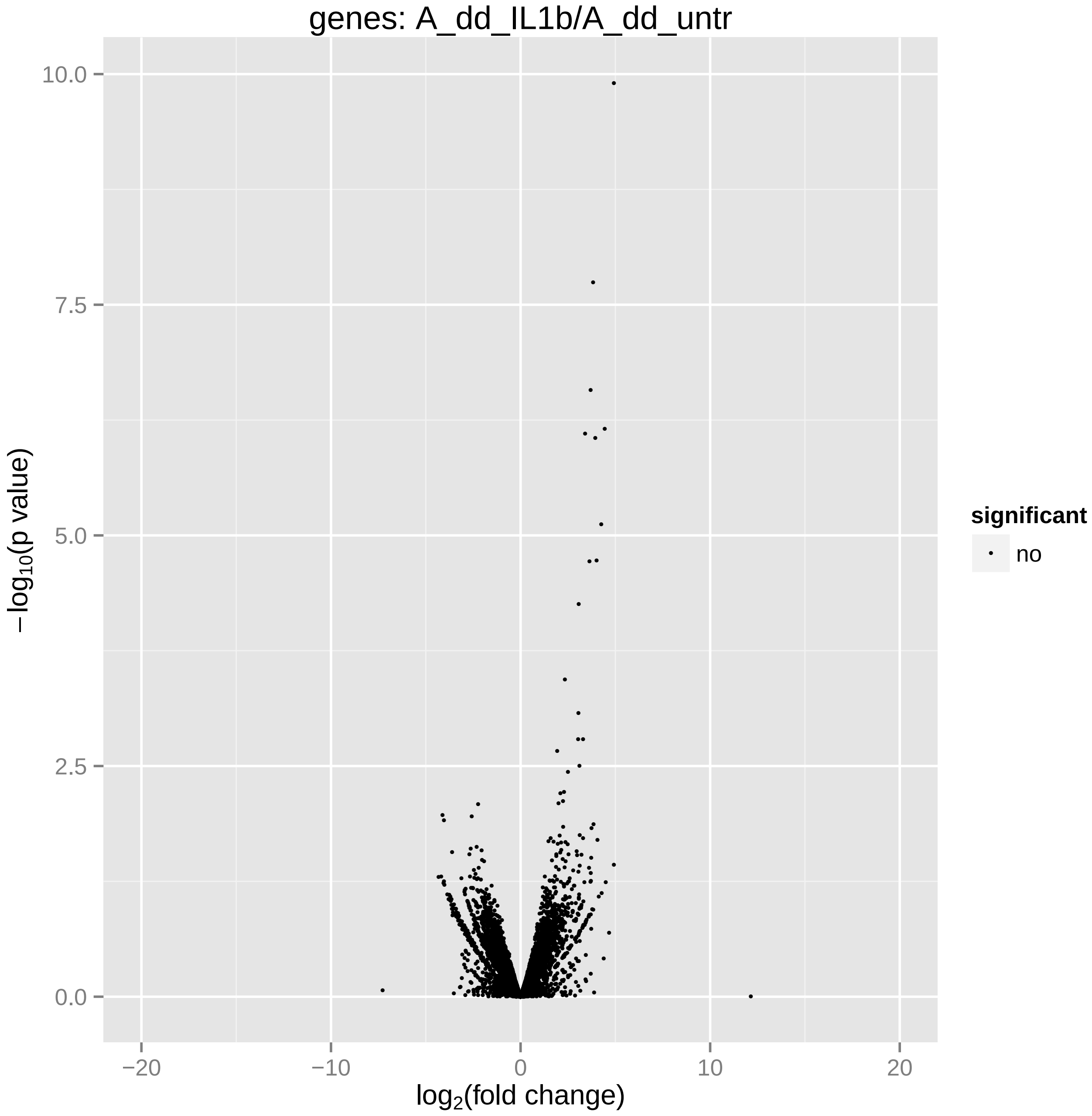
genes: A_dd_IL1b/A_dd_untr

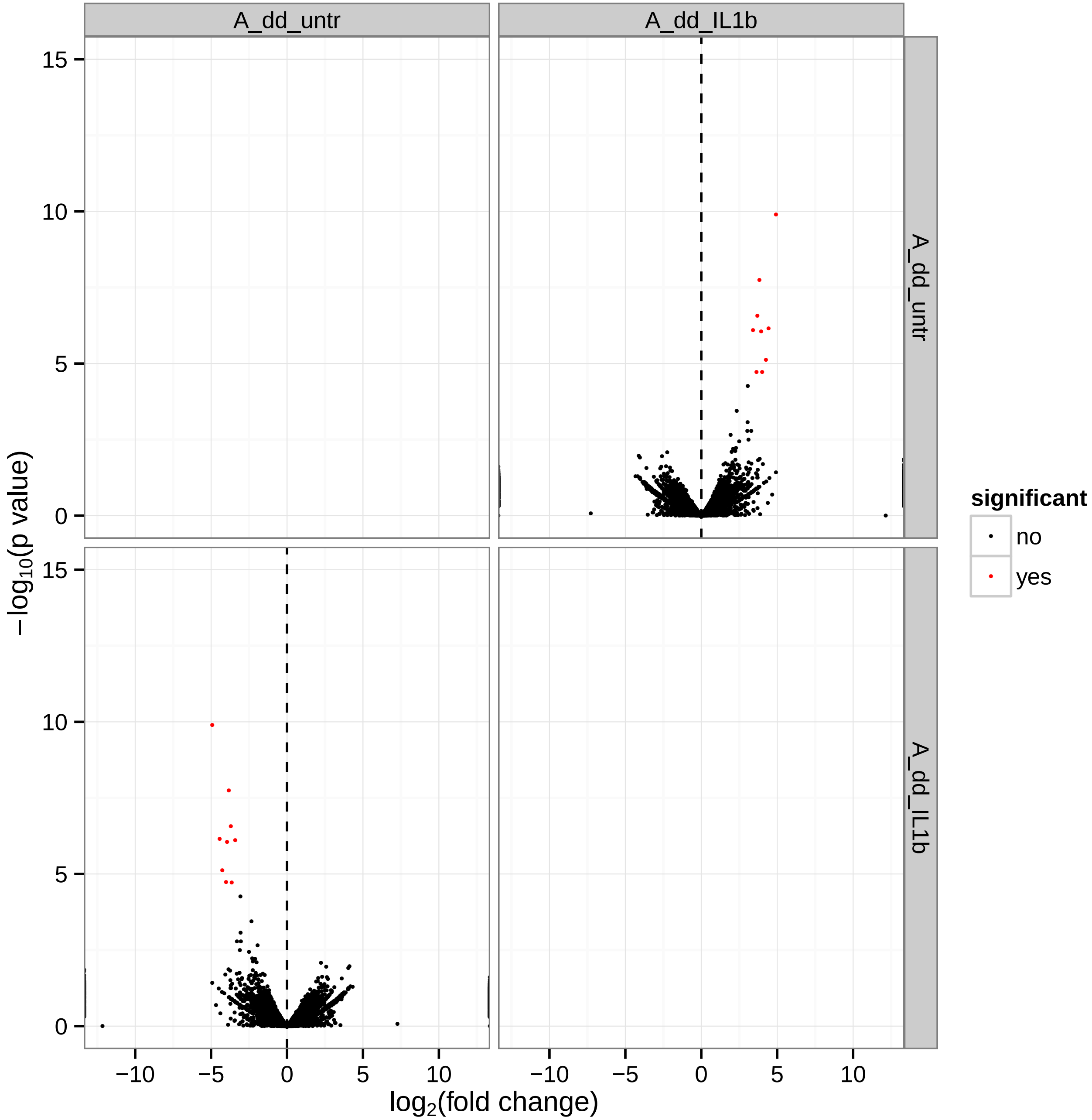


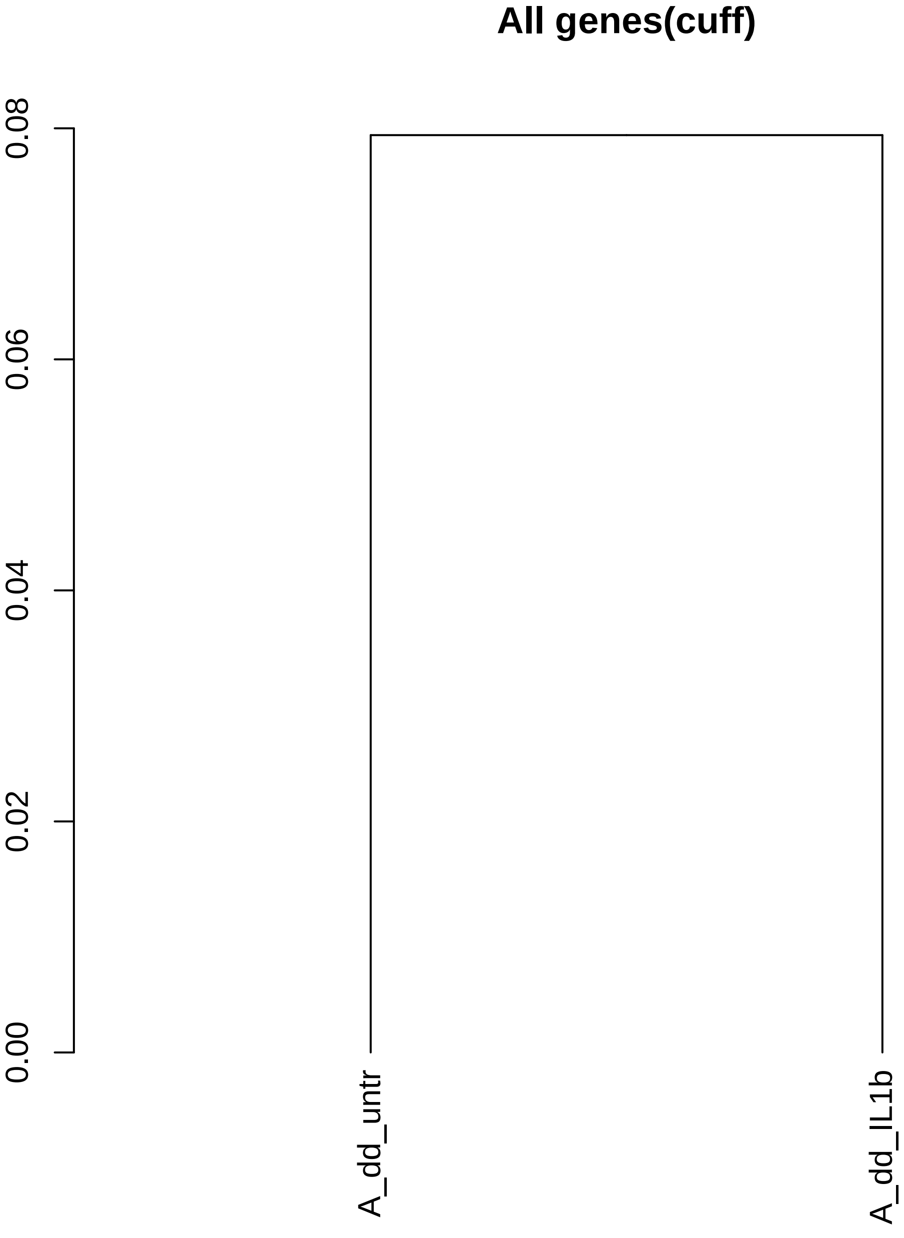

genes
1e+05
1e+03
1e+01
A_dd_untr
1e+01
1e+03
1e+05
A_dd_IL1b


A_dd_IL1b A_dd_untr
log2(M)
12
8
4
0
−4
0
2
4
6
A

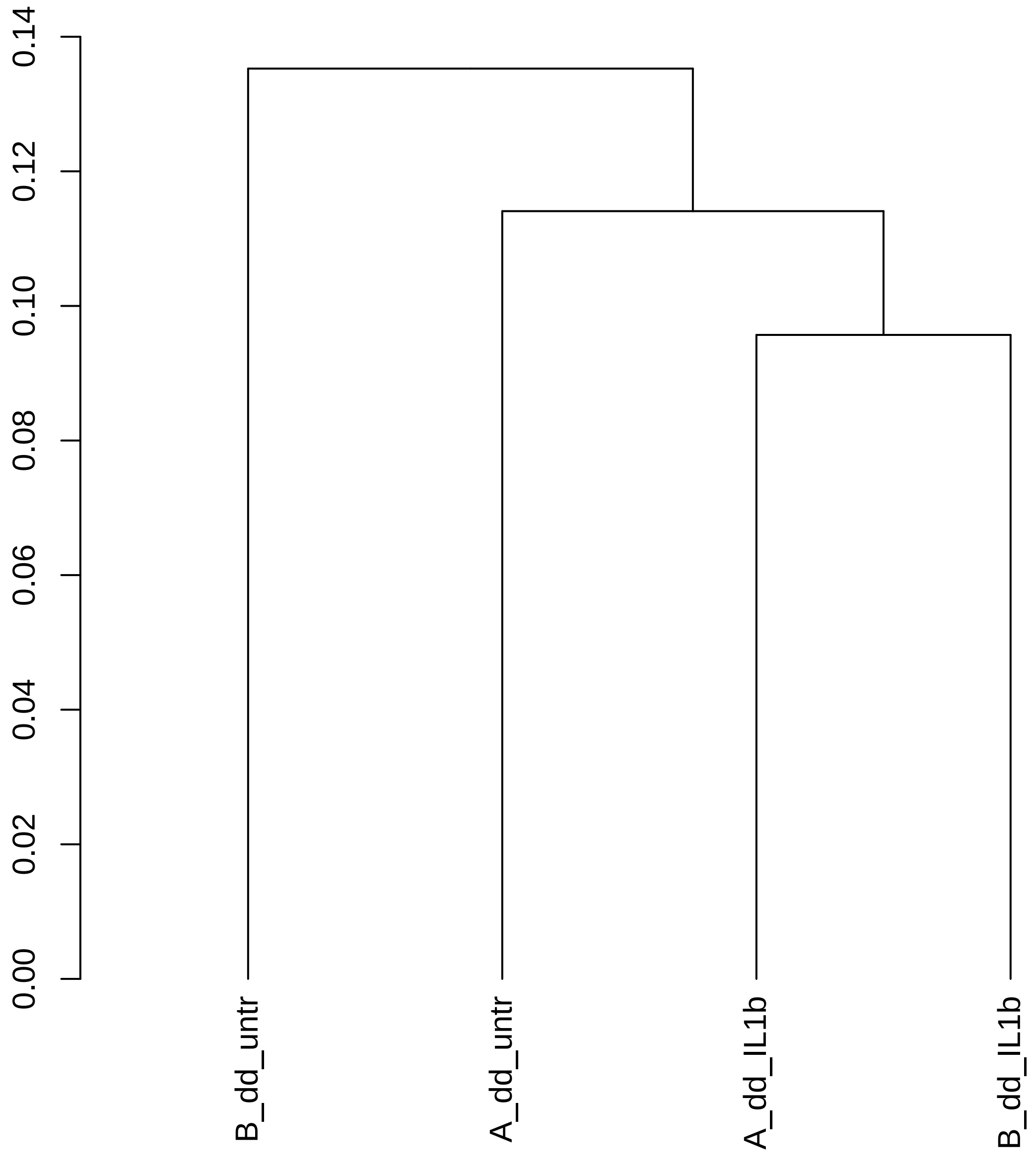

normalized count values A_dd_IL1b A_dd_untr
log2(M)
8
4
0
A
0
1
2
3
4
5

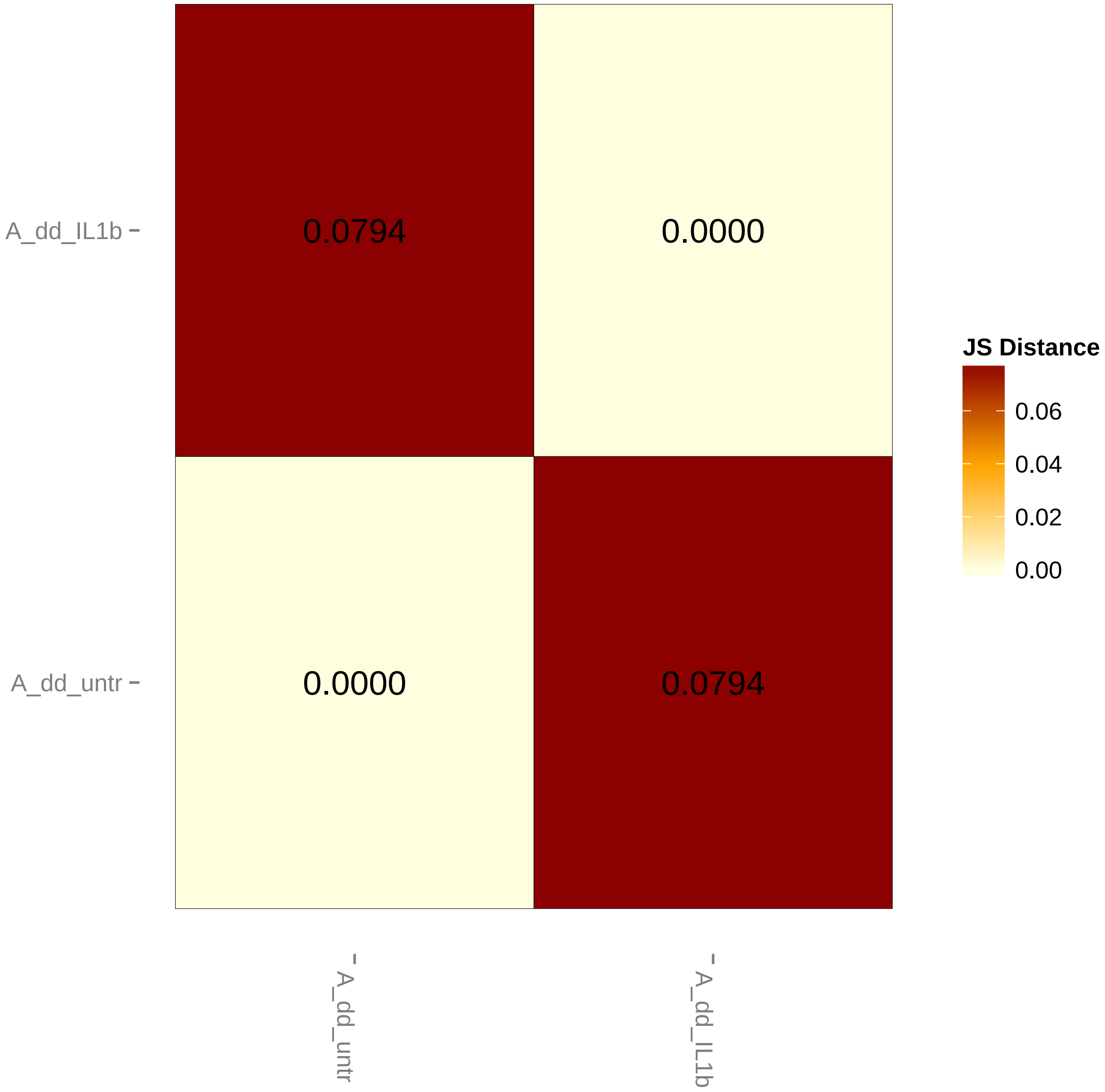

genes: A_dd_IL1b/A_dd_untr
10.0
7.5
5.0
2.5
0.0
$-\log_{10}$(p value)
−20
−10
0
10
20
$\log_2$(fold change)
significant
no

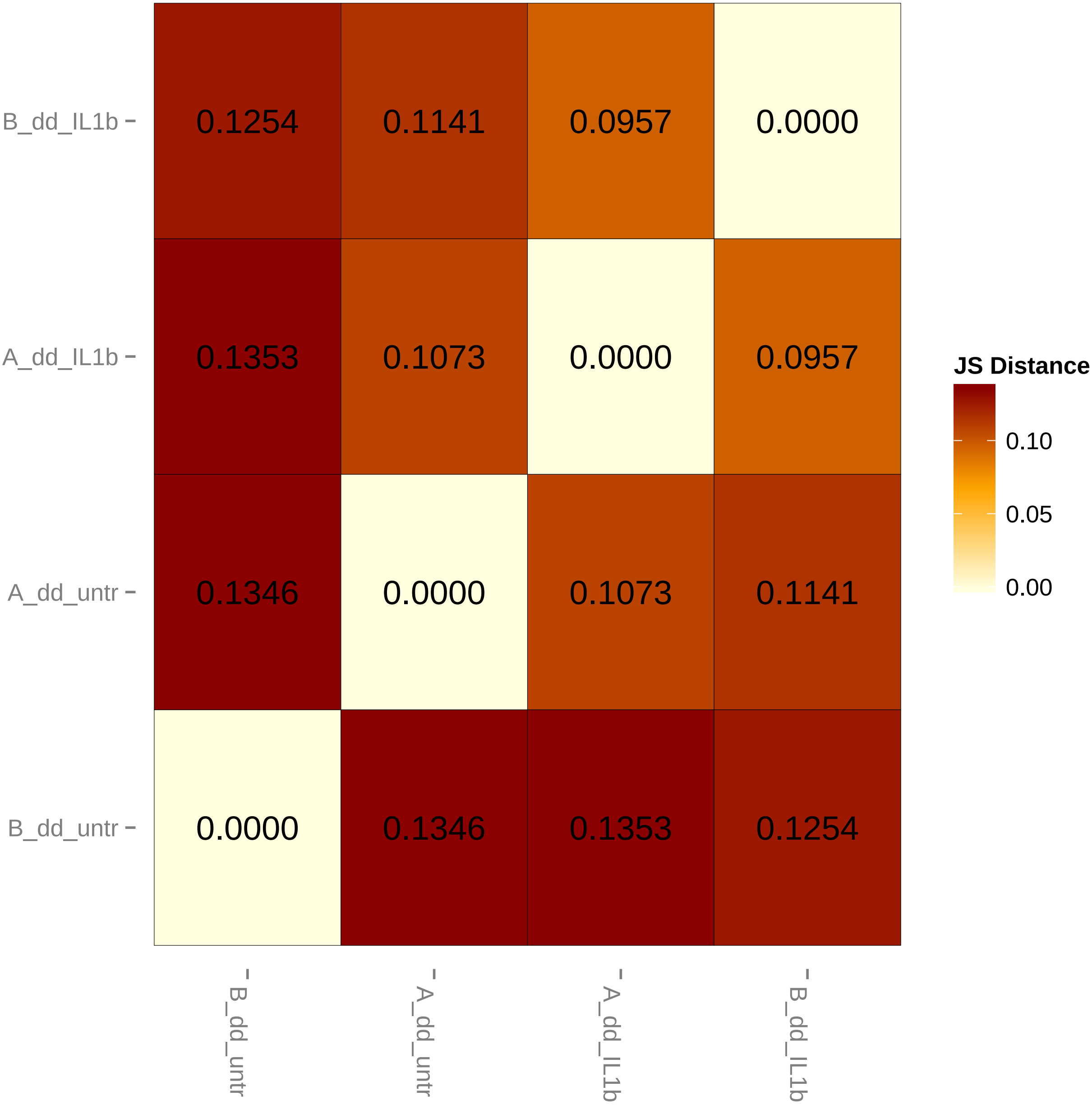

A_dd_untr
A_dd_IL1b
A_dd_untr
A_dd_IL1b
−log10(p value)
log2(fold change)
15
10
5
0
−10
−5
0
5
10
significant
no
yes

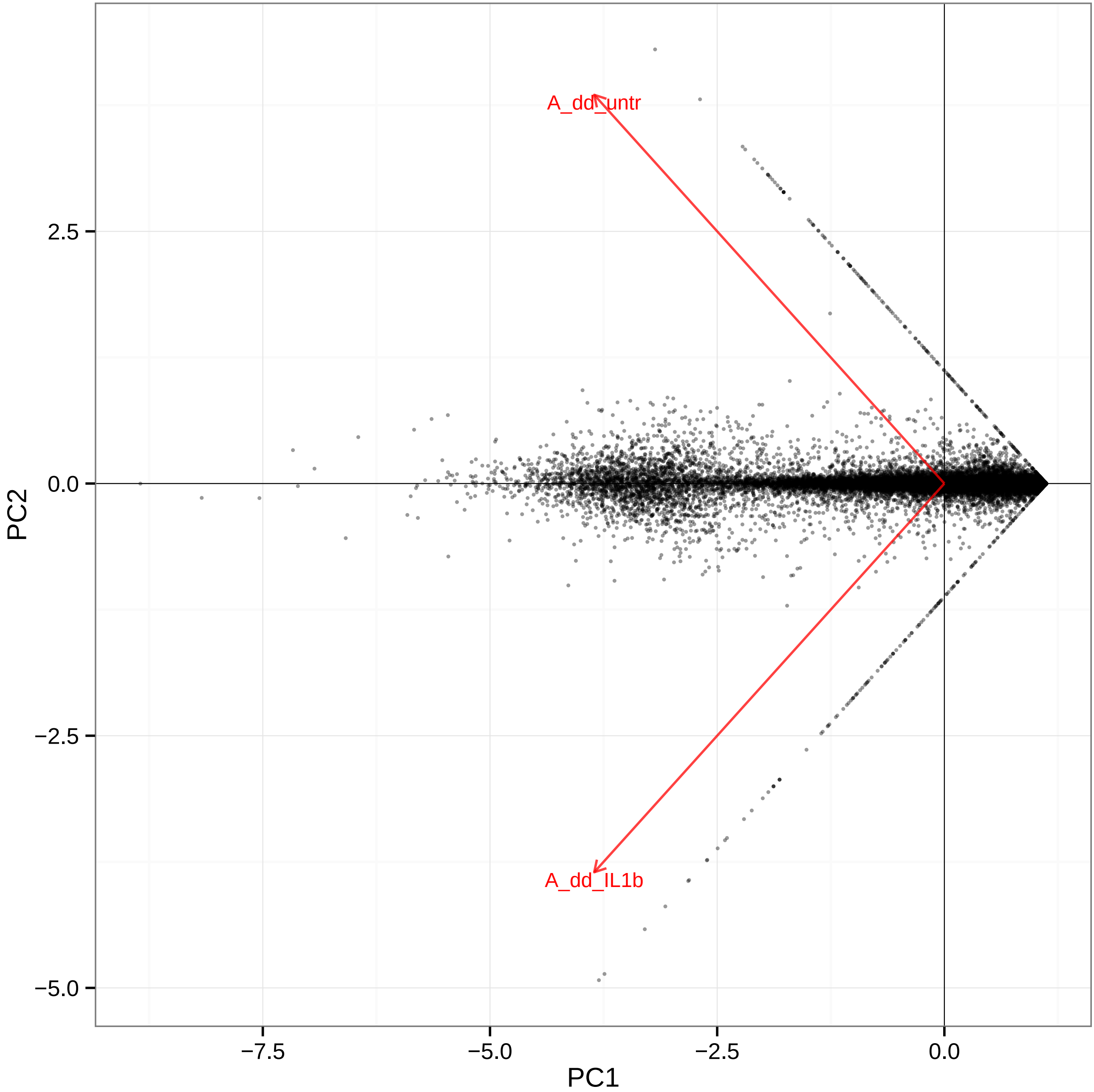

All genes(cuff)
0.00
0.02
0.04
0.06
0.08
A_dd_untr
A_dd_IL1b

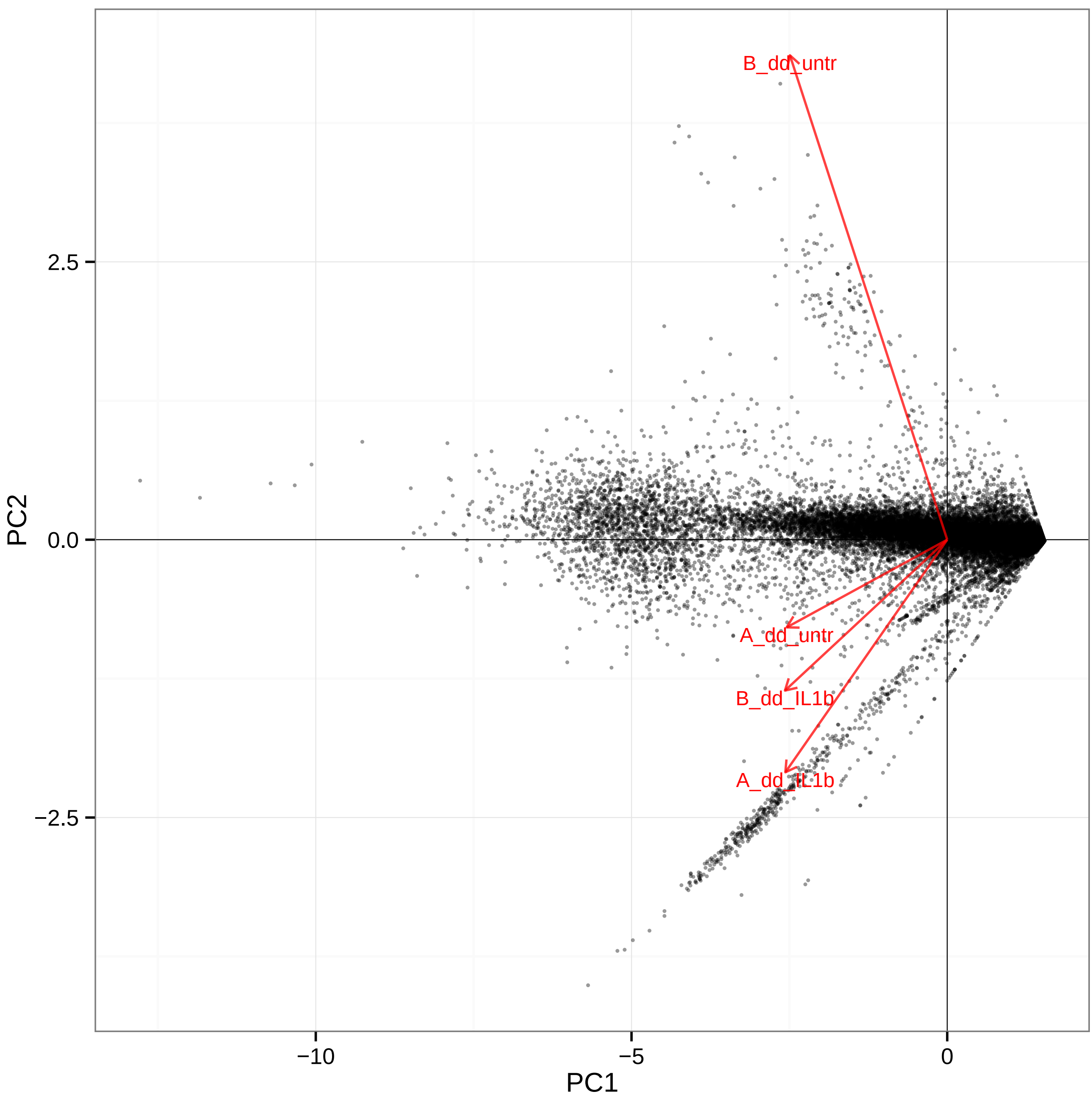
All genes(cuff)

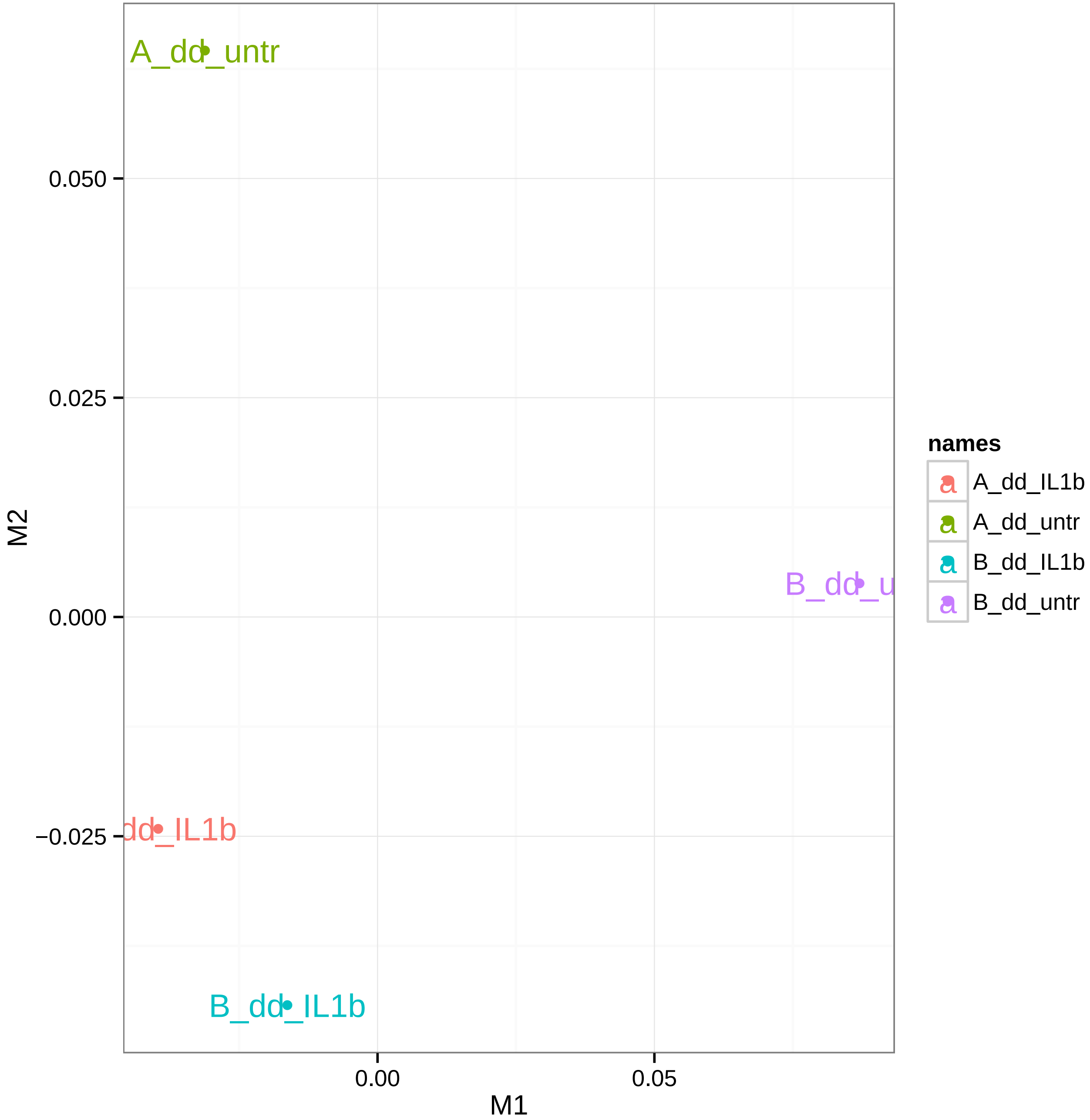


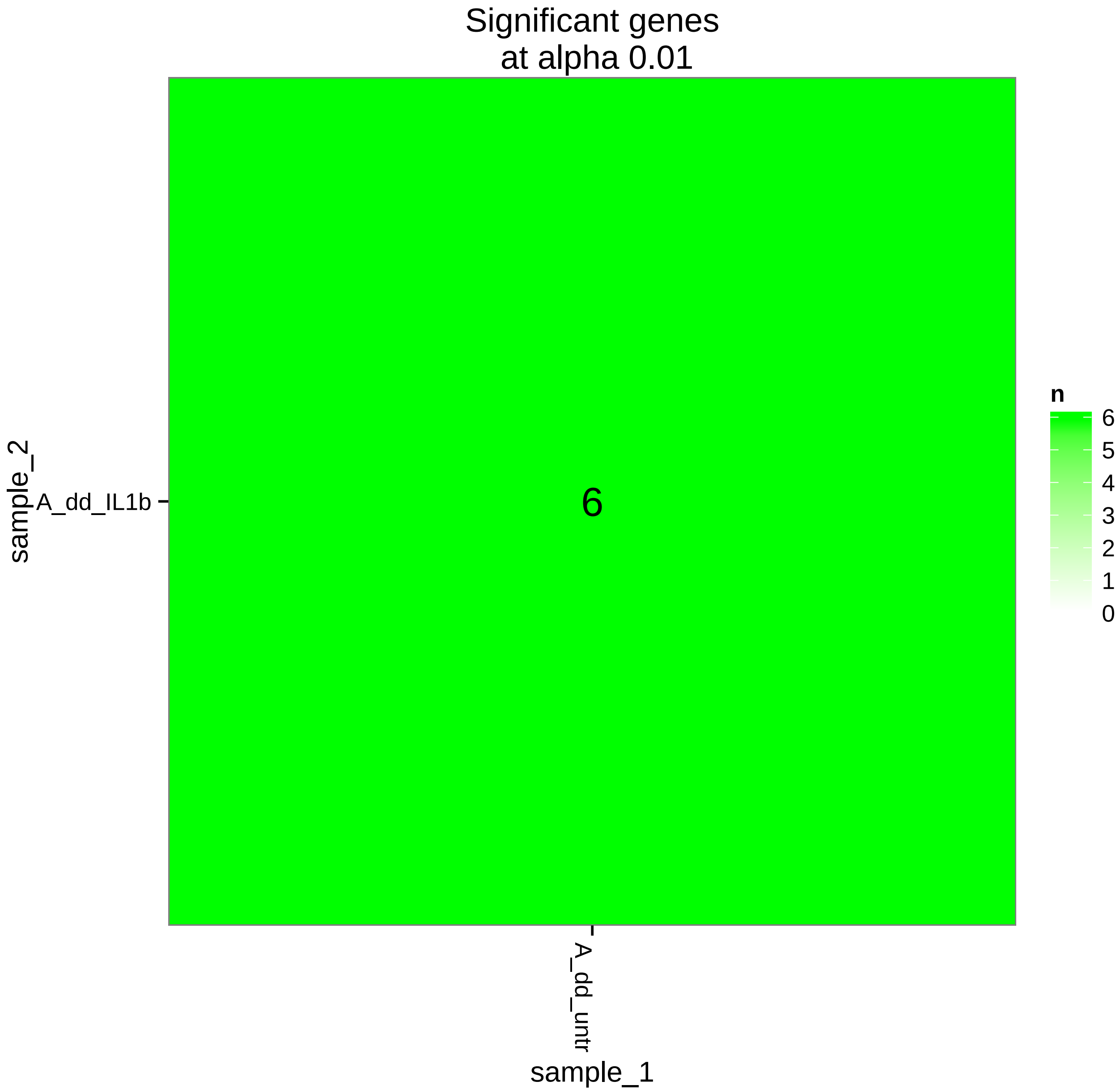

A_dd_IL1b
A_dd_untr
0.0794
0.0000
0.0000
0.0794
A_dd_untr
A_dd_IL1b
JS Distance
0.06
0.04
0.02
0.00

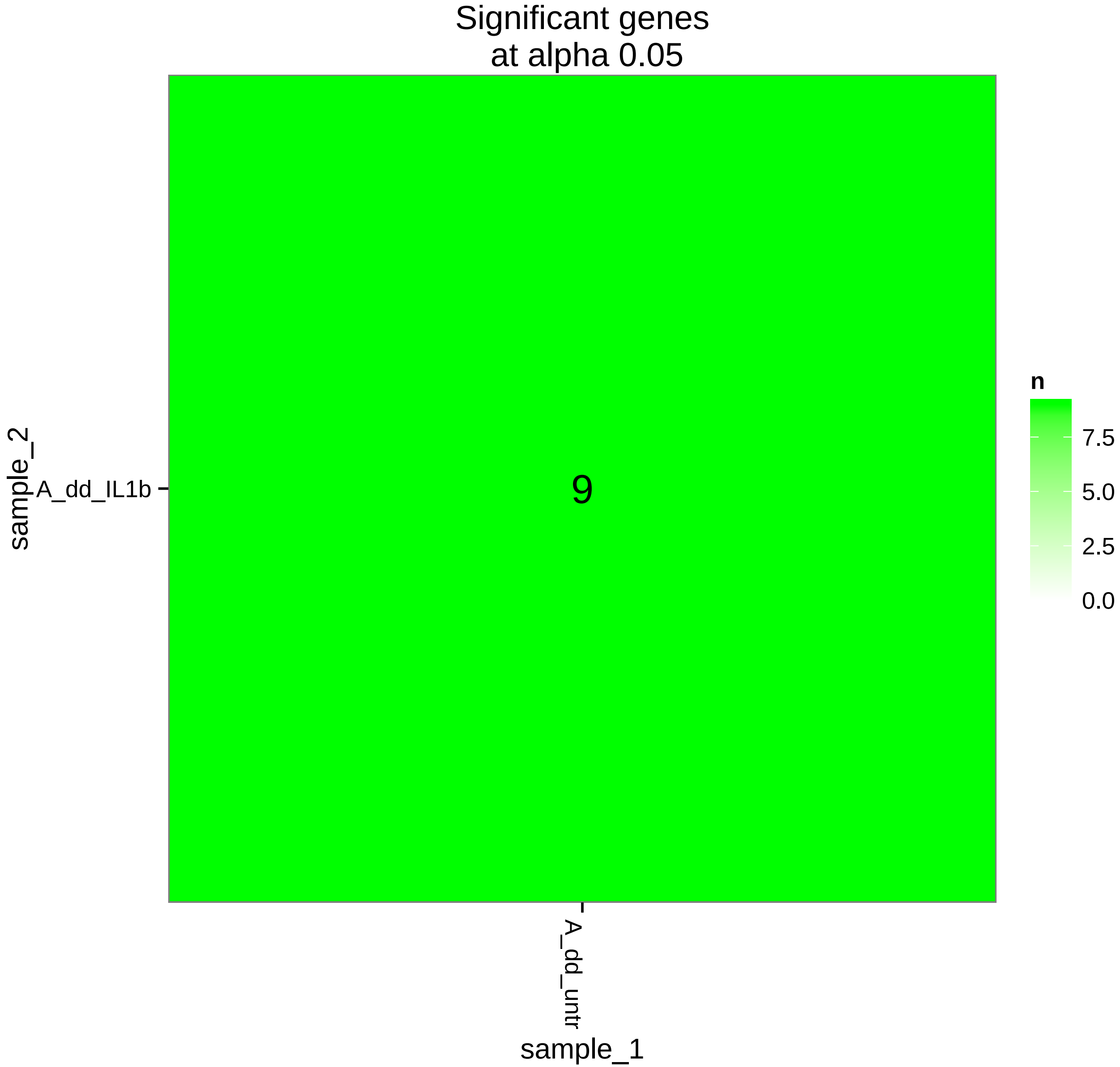

B_dd_IL1b
A_dd_IL1b
A_dd_untr
B_dd_untr
0.1254
0.1141
0.0957
0.0000
0.1353
0.1073
0.0000
0.0957
0.1346
0.0000
0.1073
0.1141
0.0000
0.1346
0.1353
0.1254
B_dd_untr
A_dd_untr
A_dd_IL1b
B_dd_IL1b
JS Distance
0.10
0.05
0.00

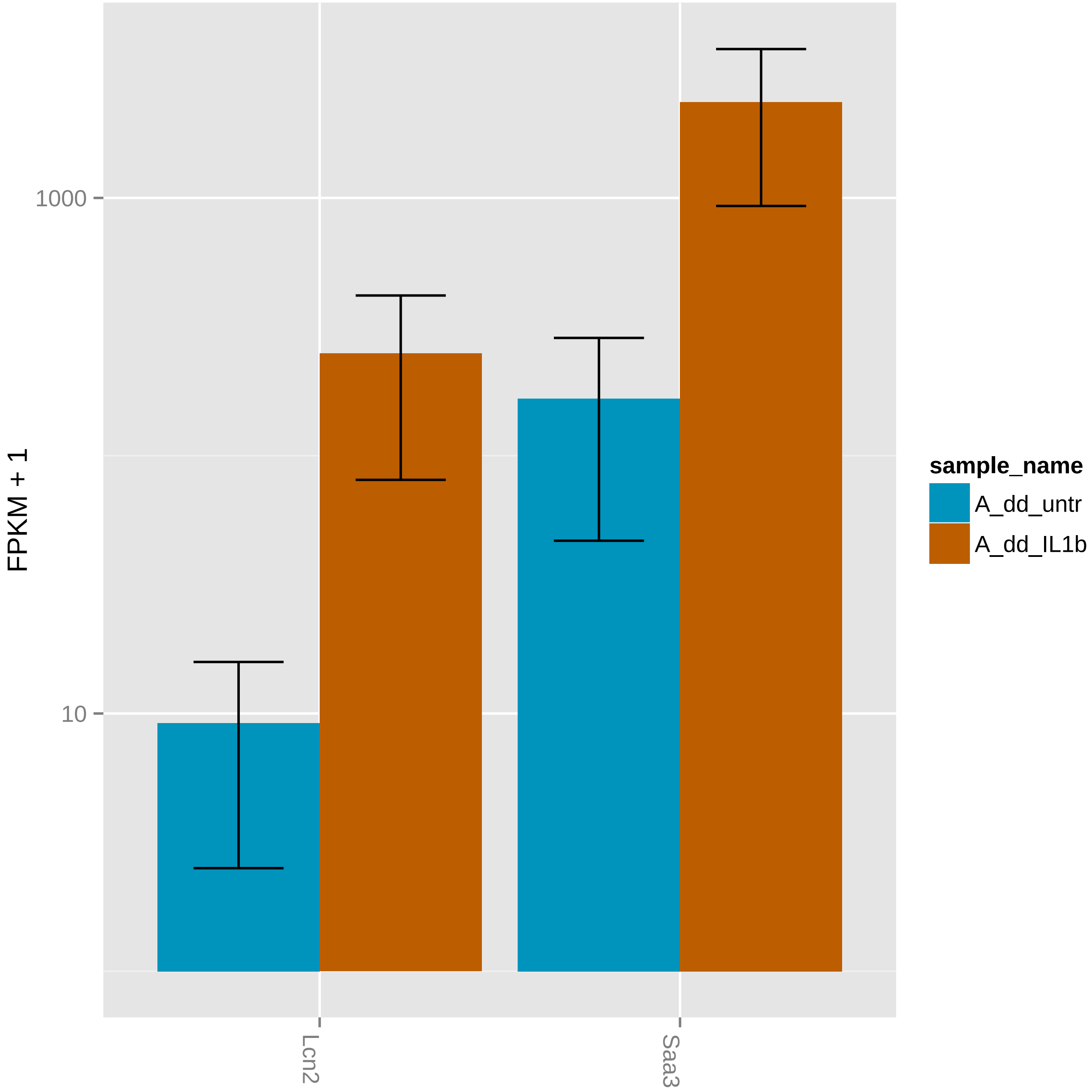

A_dd_untr
A_dd_IL1b
2.5
0.0
−2.5
−5.0
PC2
−7.5
−5.0
−2.5
0.0
PC1

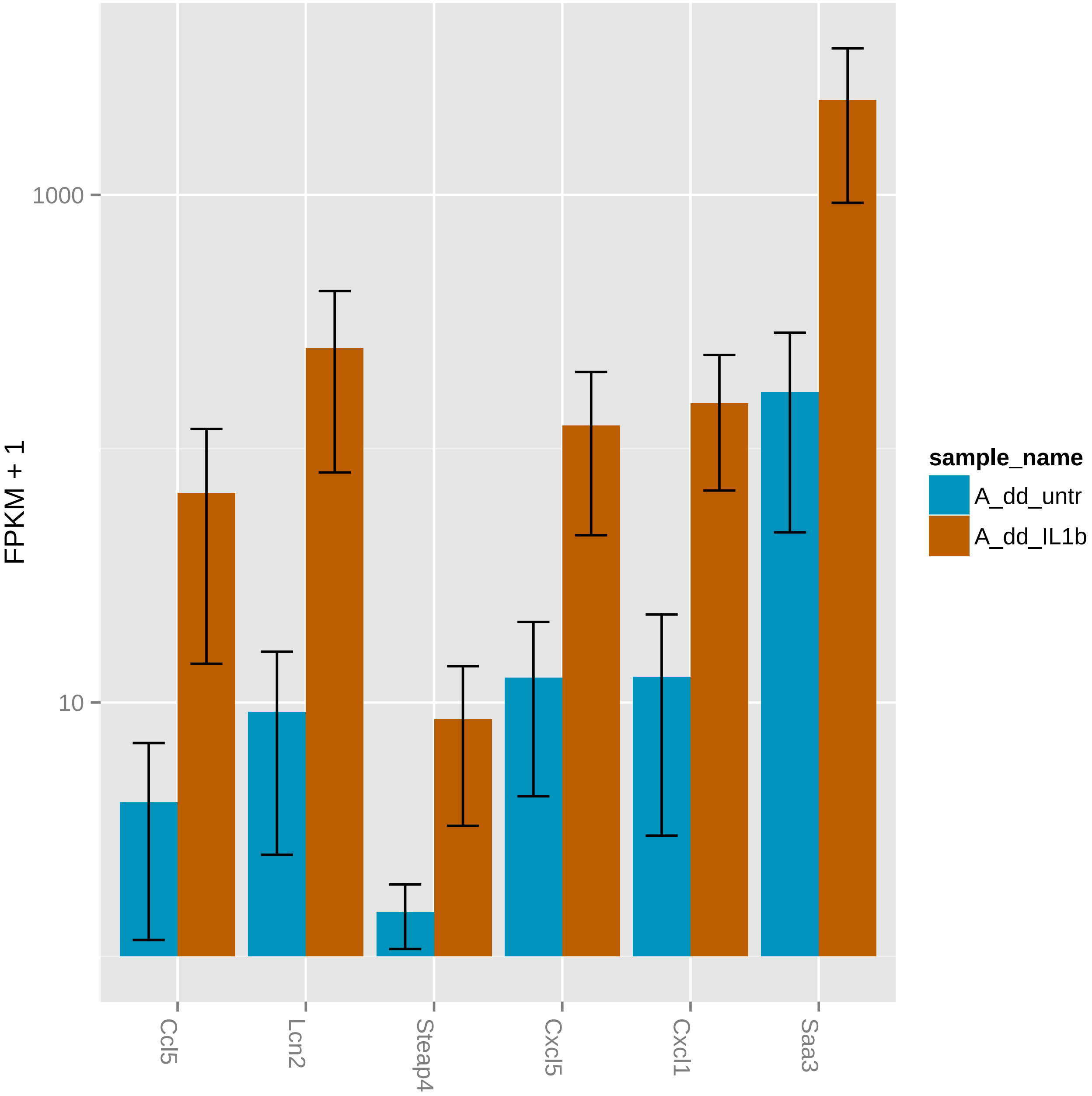

B_dd_untr
A_dd_untr
B_dd_IL1b
A_dd_IL1b
2.5
0.0
−2.5
PC2
−10
−5
0
PC1

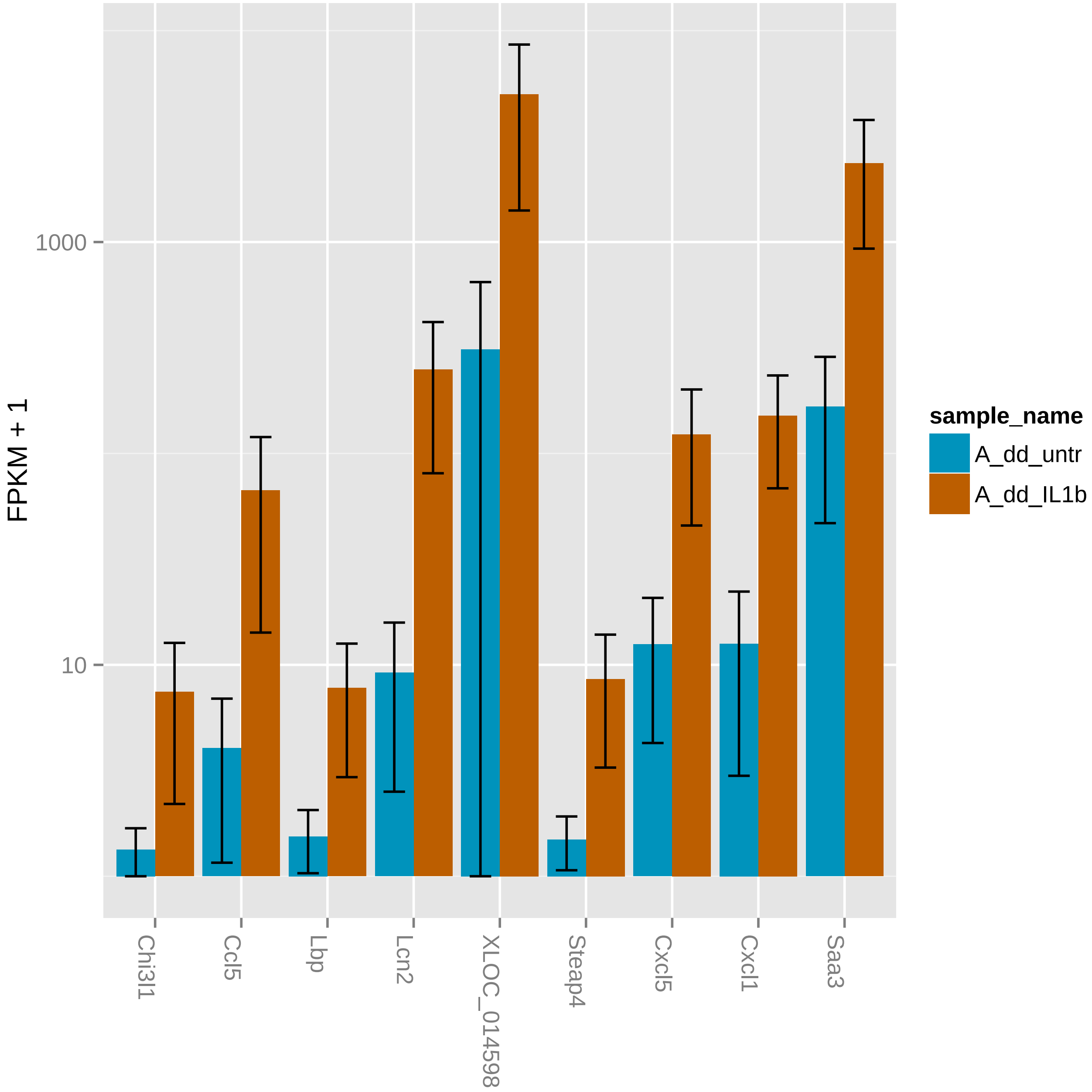

A_dd_untr
dd_IL1b
B_dd_IL1b
B_dd_u
0.050
0.025
0.000
−0.025
M2
0.00
0.05
M1
names
A_dd_IL1b
A_dd_untr
B_dd_IL1b
B_dd_untr

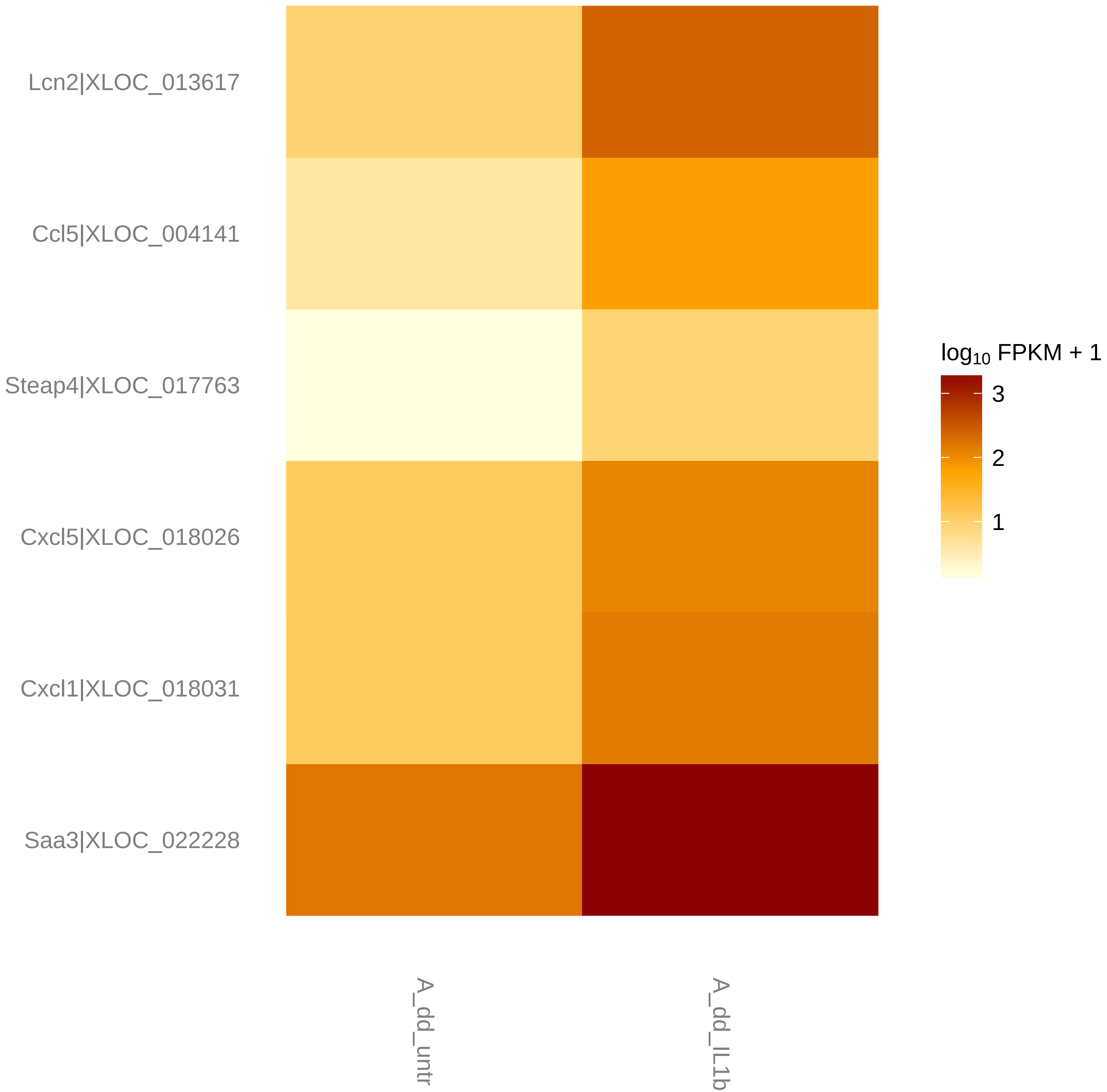

Significant genes
at alpha 0.01
sample_2
A_dd_IL1b
6
A_dd_untr
sample_1
n
6
5
4
3
2
1
0

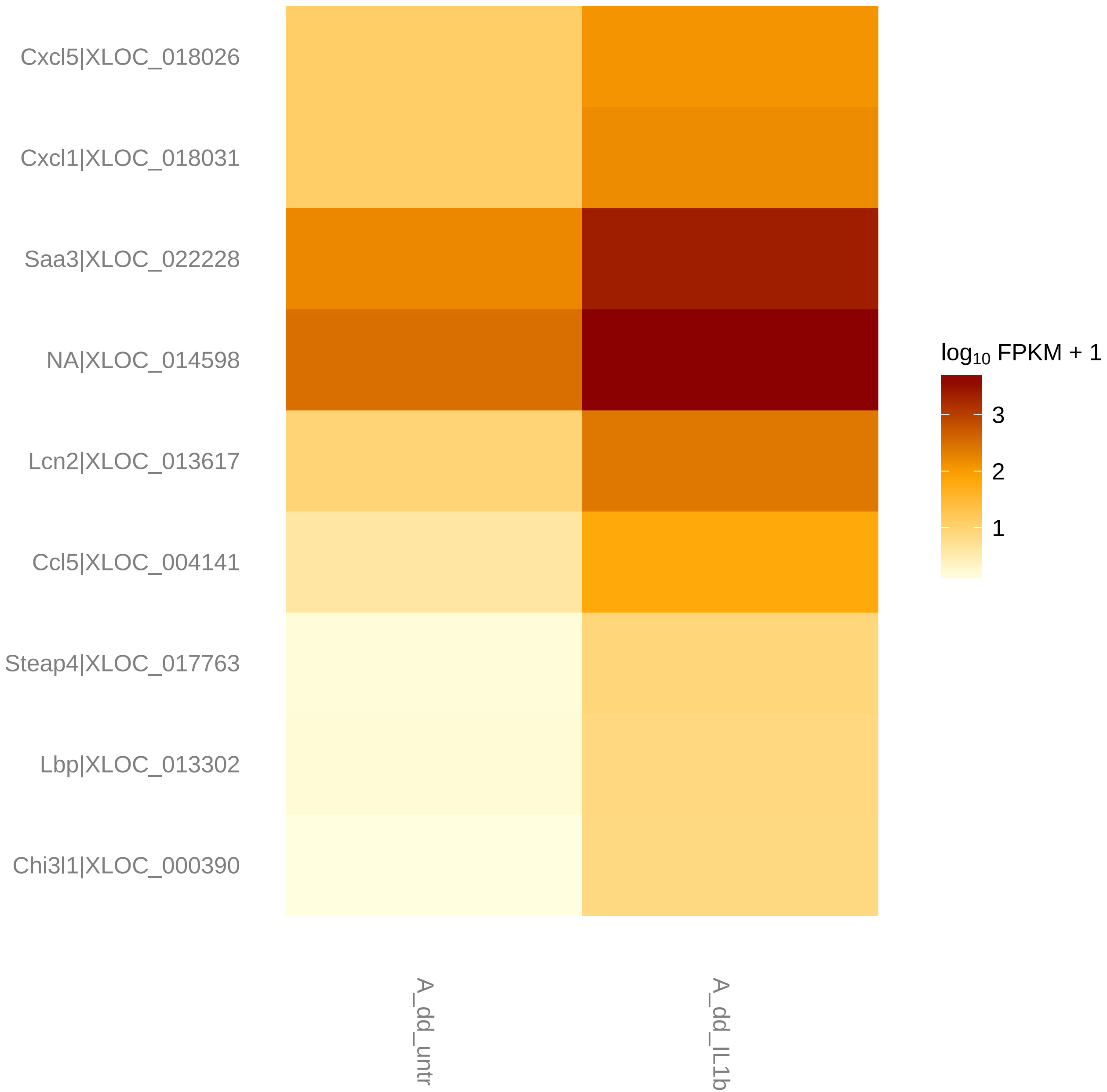

Significant genes
at alpha 0.05
sample_2
A_dd_IL1b
9
A_dd_untr
sample_1
n
7.5
5.0
2.5
0.0

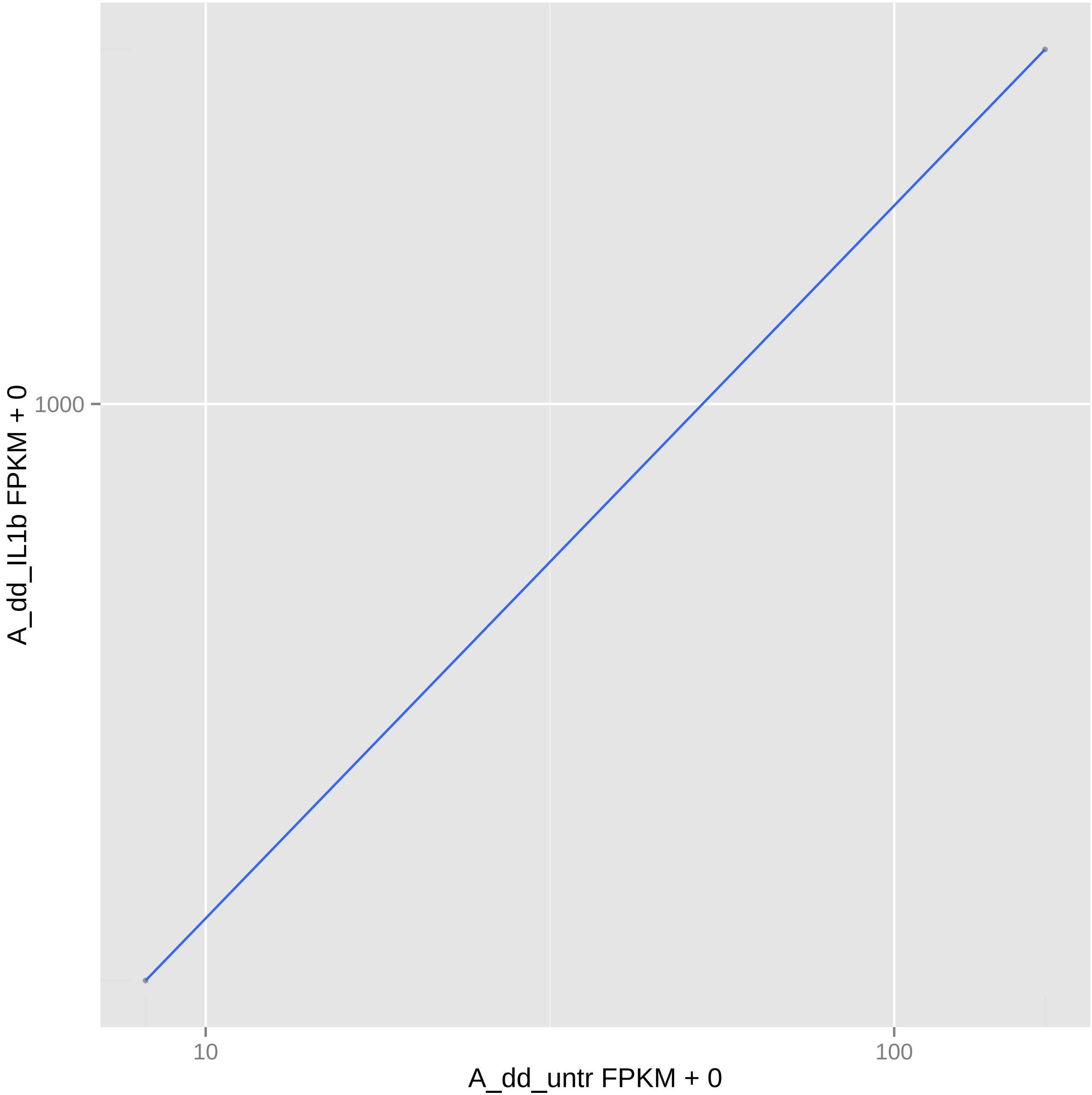

FPKM + 1
1000
10
Lcn2
Saa3
sample_name
A_dd_untr
A_dd_IL1b

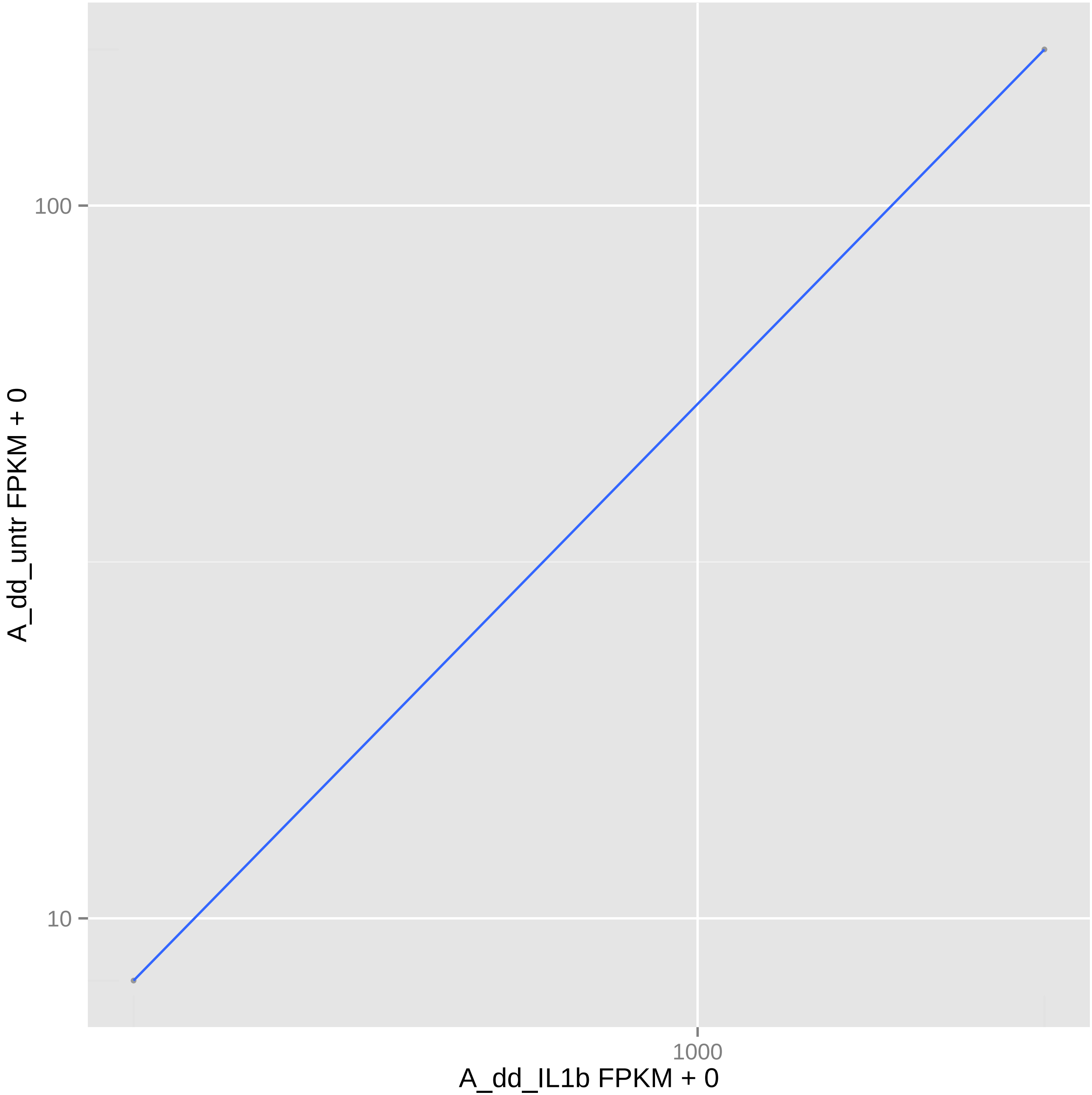

1000
10
FPKM + 1
Ccl5
Lcn2
Steap4
Cxcl5
Cxcl1
Saa3
sample_name
A_dd_untr
A_dd_IL1b

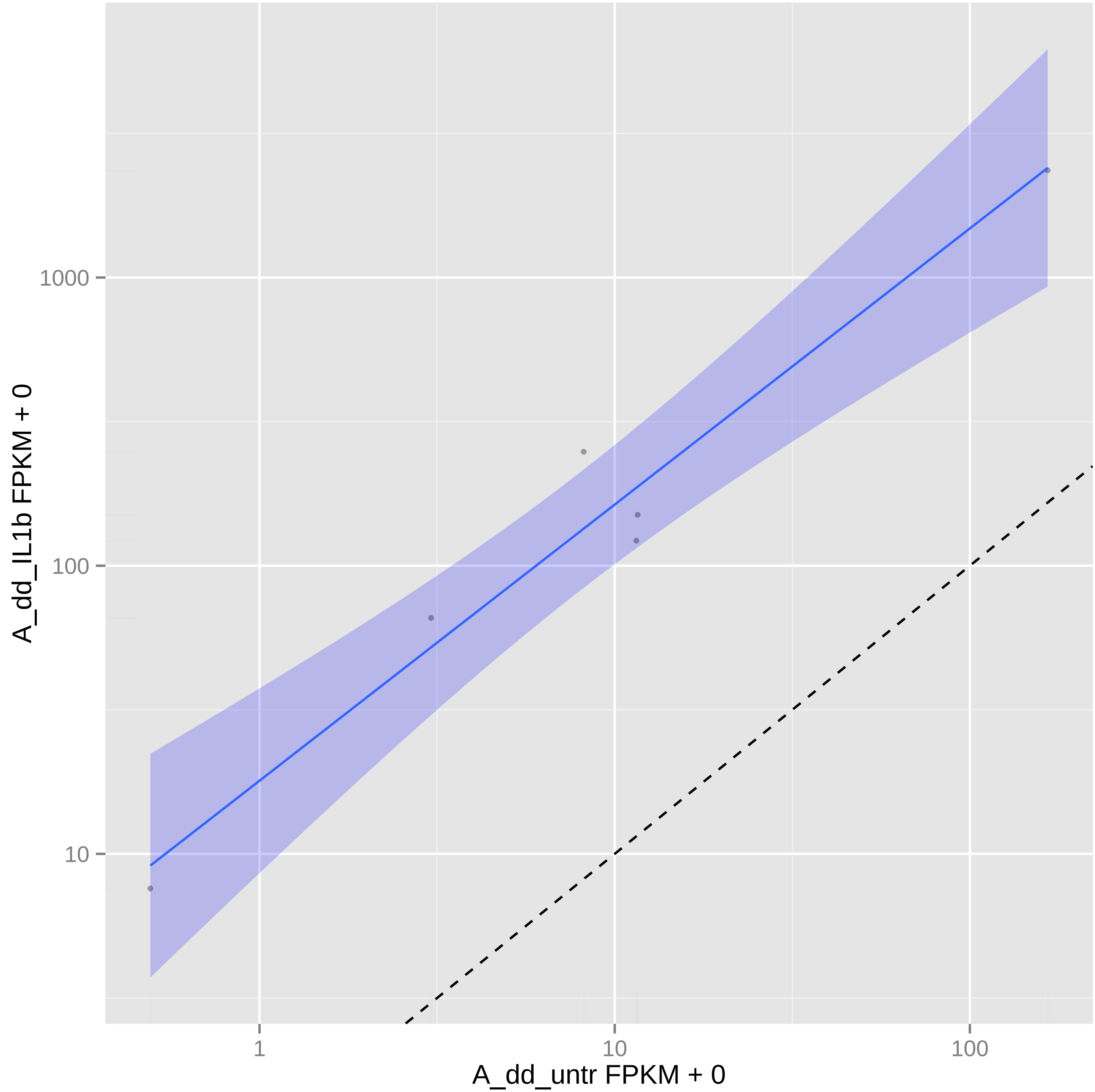

FPKM + 1
1000
10
Chi3l1
Ccl5
Lbp
Lcn2
XLOC_014598
Steap4
Cxcl5
Cxcl1
Saa3
sample_name
A_dd_untr
A_dd_IL1b

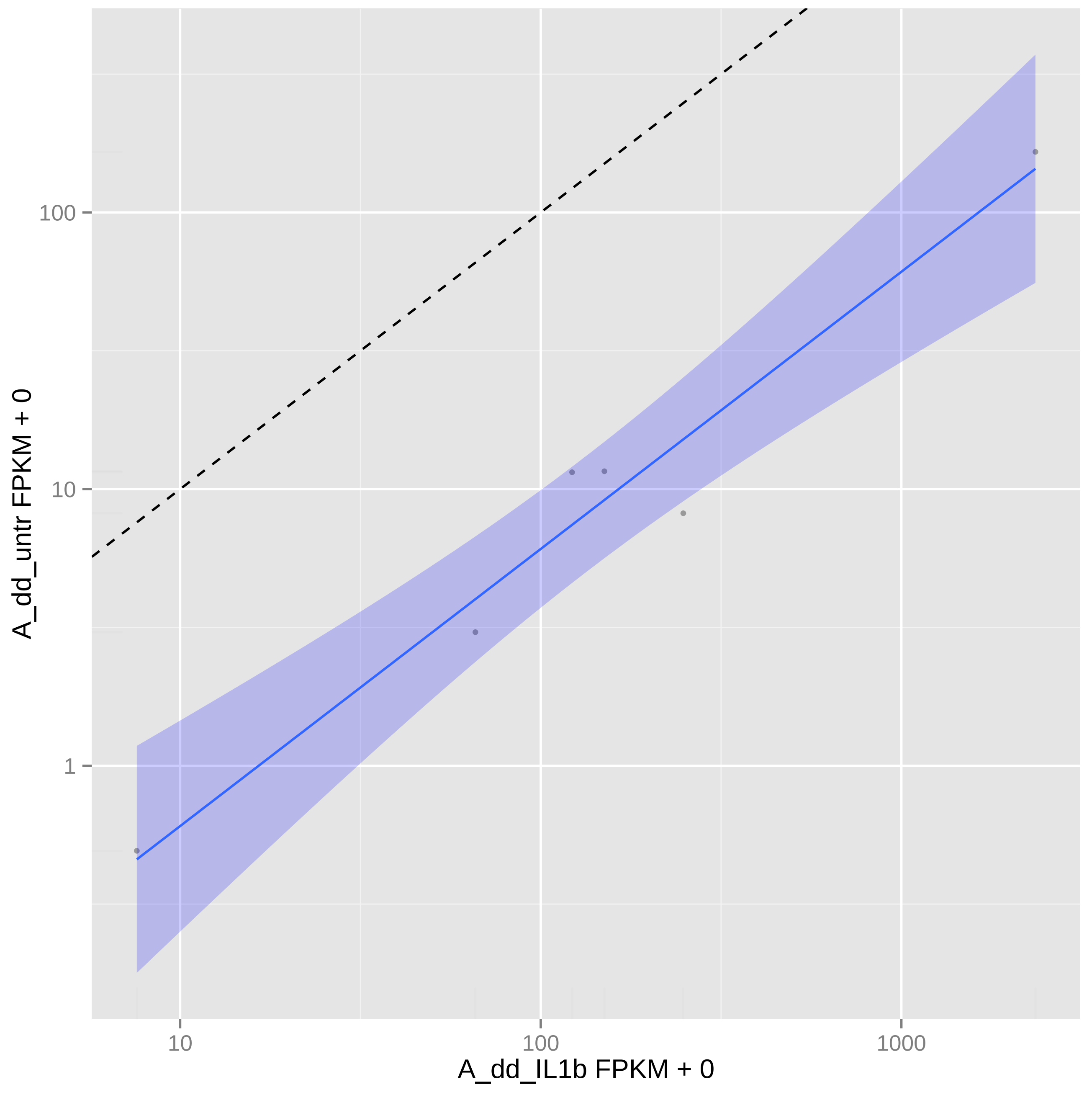

Lcn2|XLOC_013617
Ccl5|XLOC_004141
Steap4|XLOC_017763
Cxcl5|XLOC_018026
Cxcl1|XLOC_018031
Saa3|XLOC_022228
A_dd_untr
A_dd_IL1b
$\log_{10}$ FPKM + 1
3
2
1

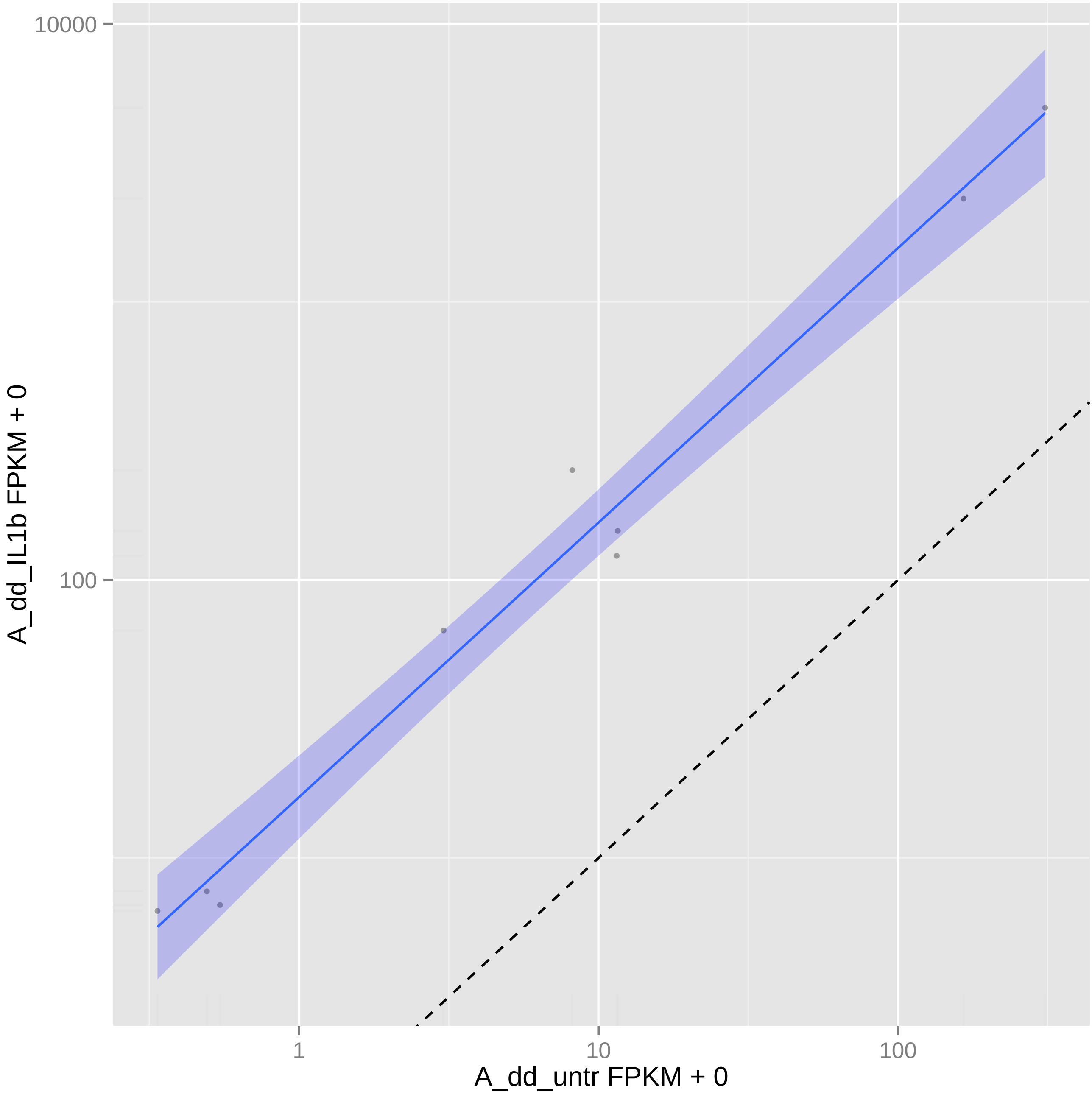

Cxcl5|XLOC_018026
Cxcl1|XLOC_018031
Saa3|XLOC_022228
NA|XLOC_014598
Lcn2|XLOC_013617
Ccl5|XLOC_004141
Steap4|XLOC_017763
Lbp|XLOC_013302
Chi3l1|XLOC_000390
A_dd_untr
A_dd_IL1b
log10 FPKM + 1
3
2
1

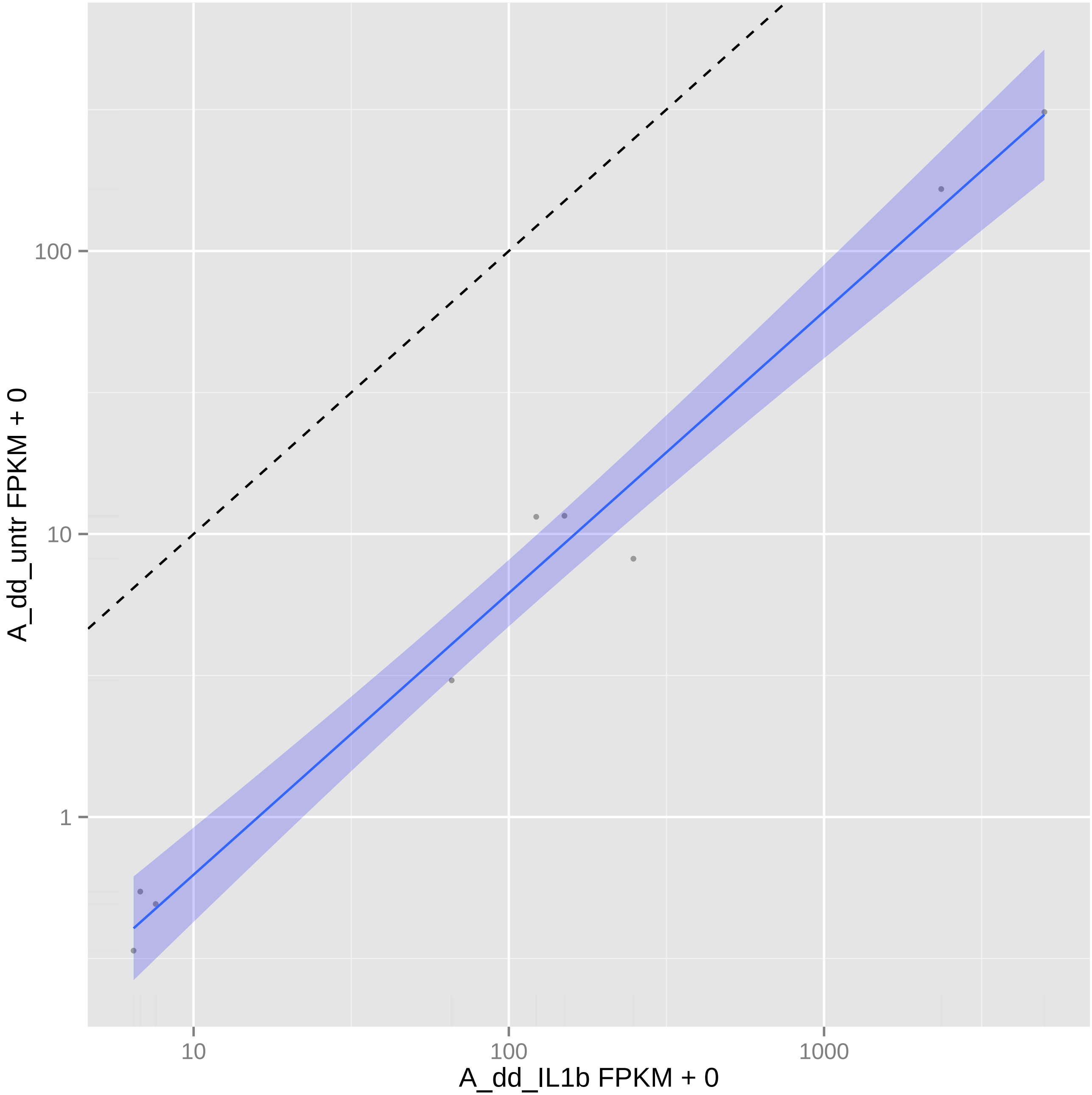

A_dd_IL1b FPKM + 0
1000
10
100
A_dd_untr FPKM + 0


100
10
A_dd_untr FPKM + 0
1000
A_dd_IL1b FPKM + 0


1000
100
10
1
10
100
A_dd_IL1b FPKM + 0
A_dd_untr FPKM + 0


100
10
1
10
100
1000
A_dd_IL1b FPKM + 0
A_dd_untr FPKM + 0


10000
100
1
10
100
A_dd_IL1b FPKM + 0
A_dd_untr FPKM + 0


A_dd_untr FPKM + 0
100
10
1
10
100
1000
A_dd_IL1b FPKM + 0