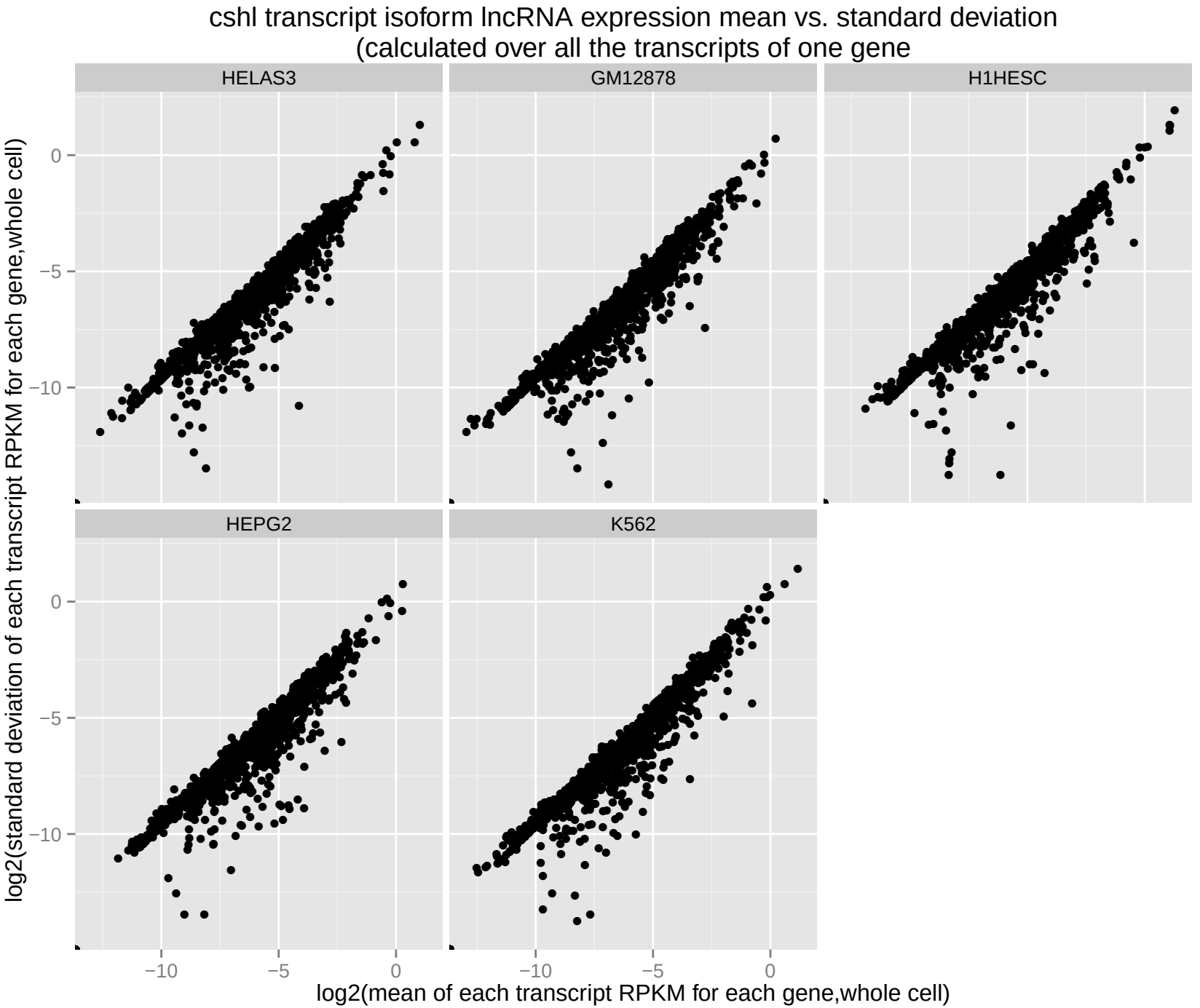
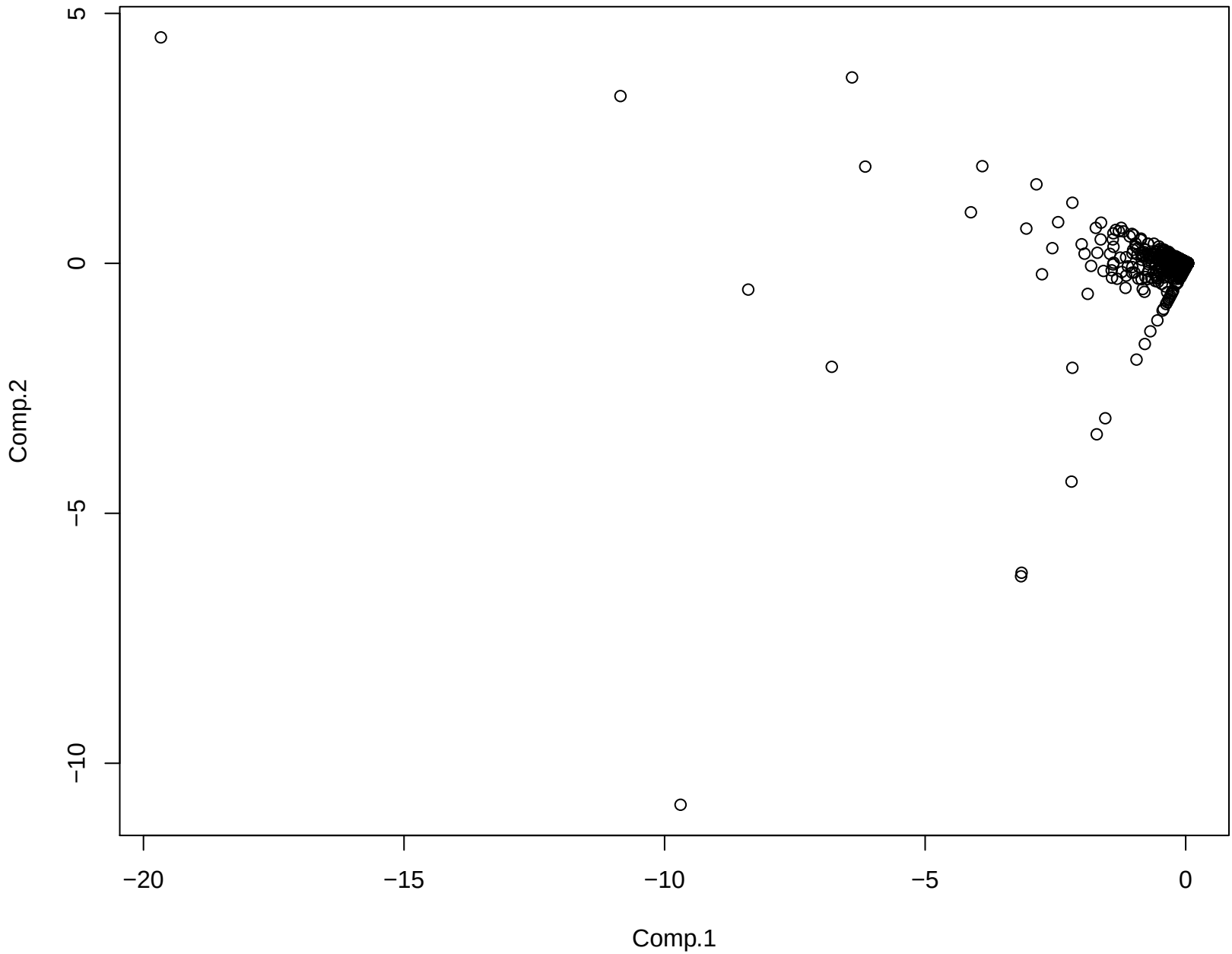
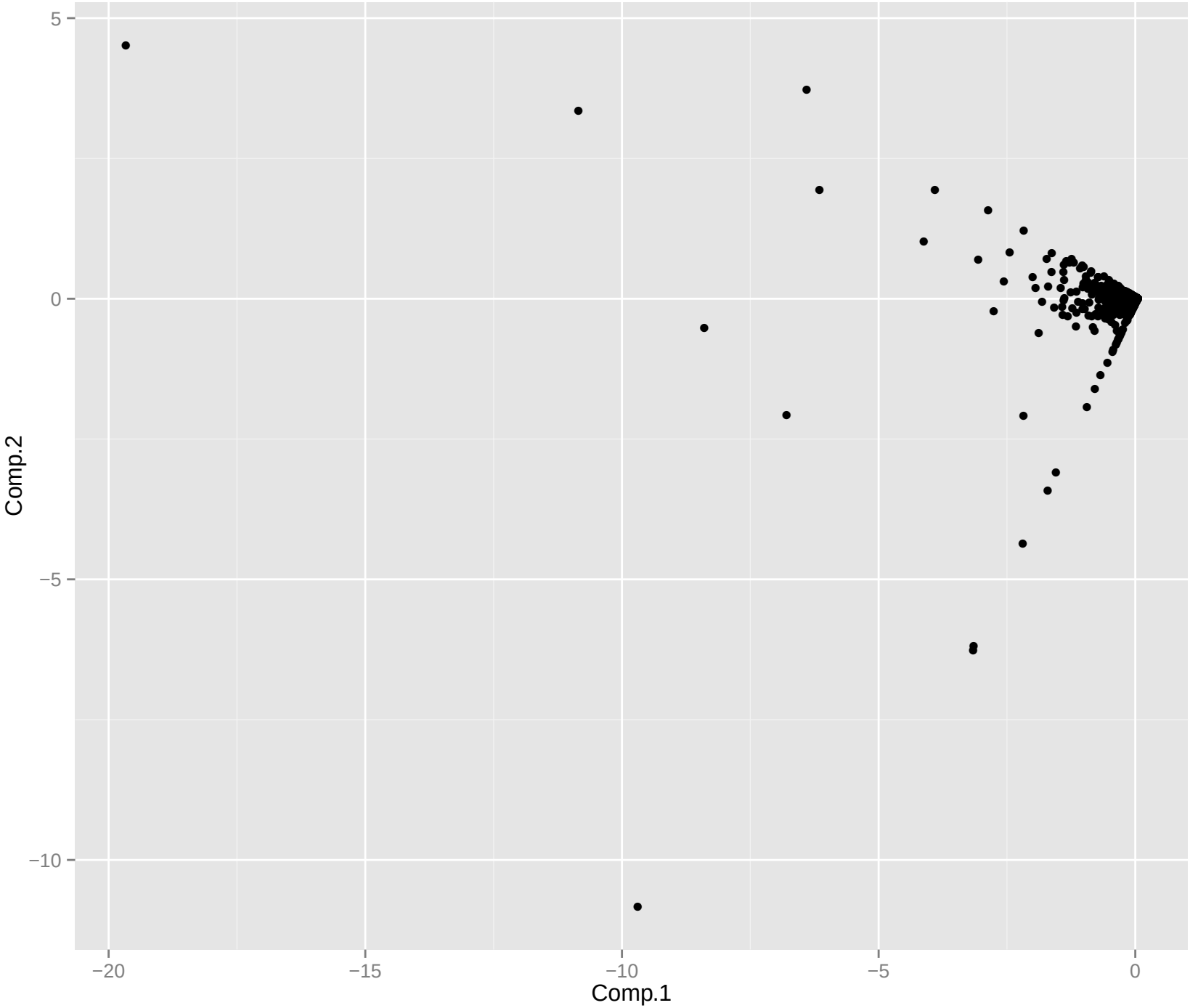
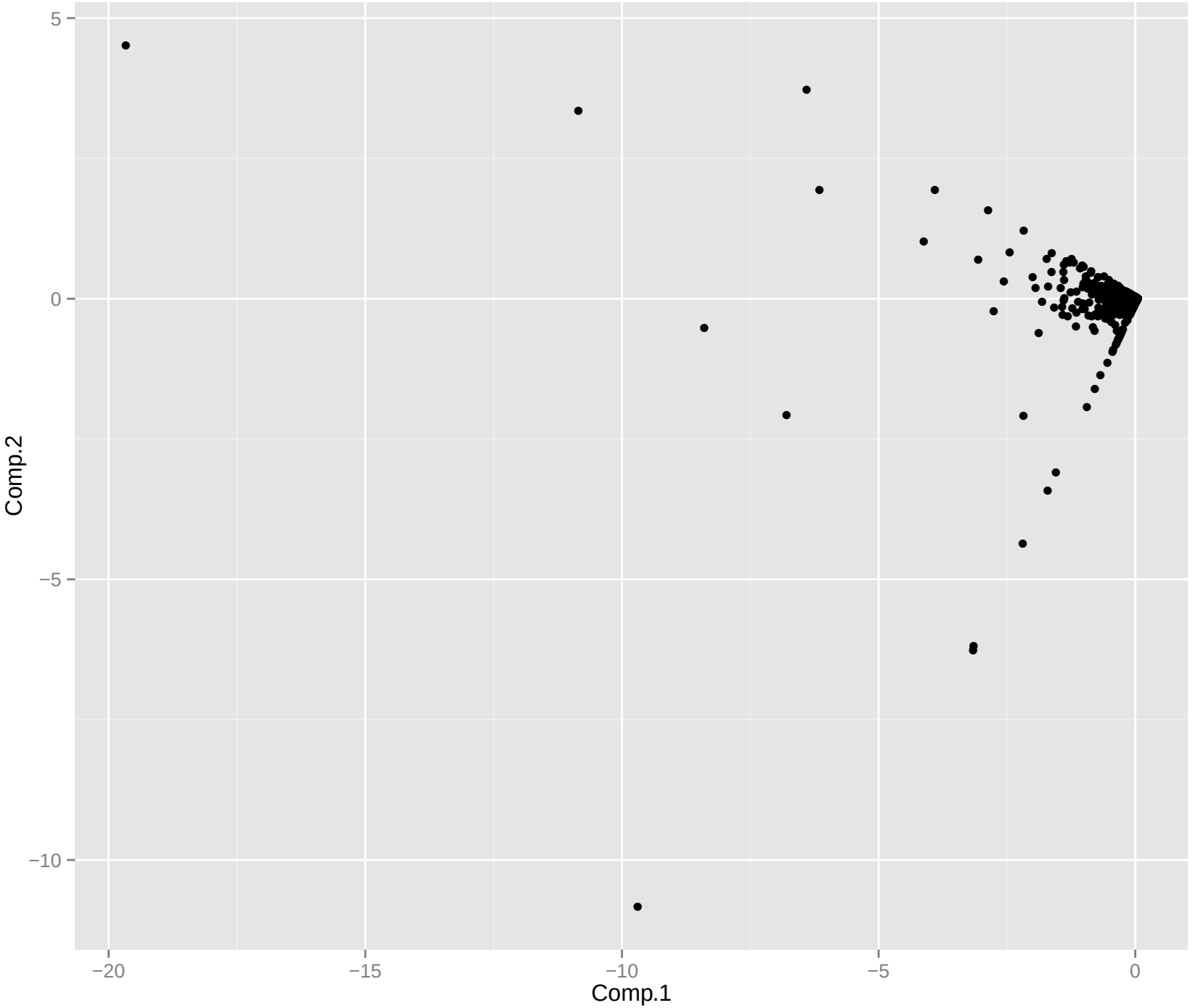
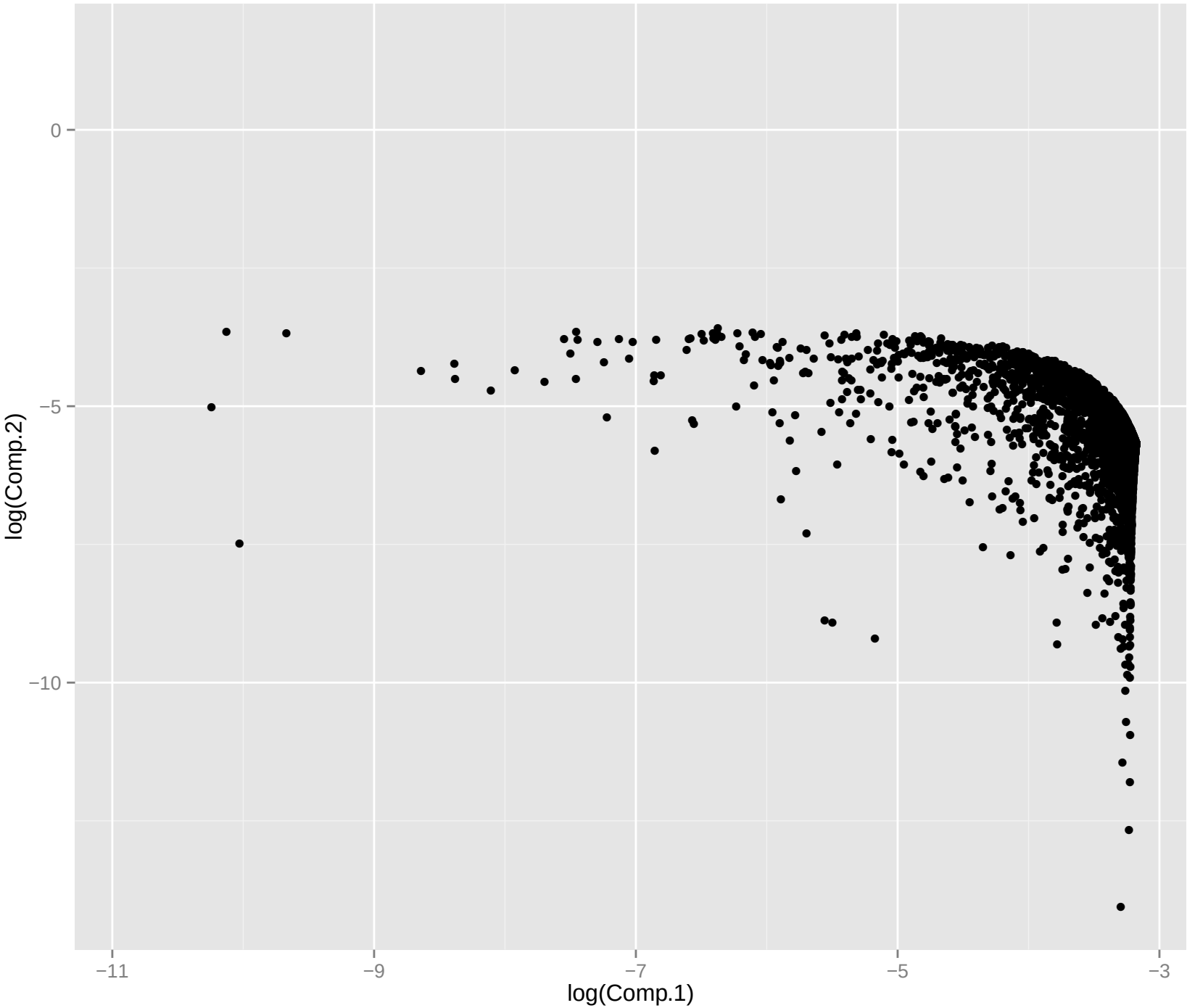
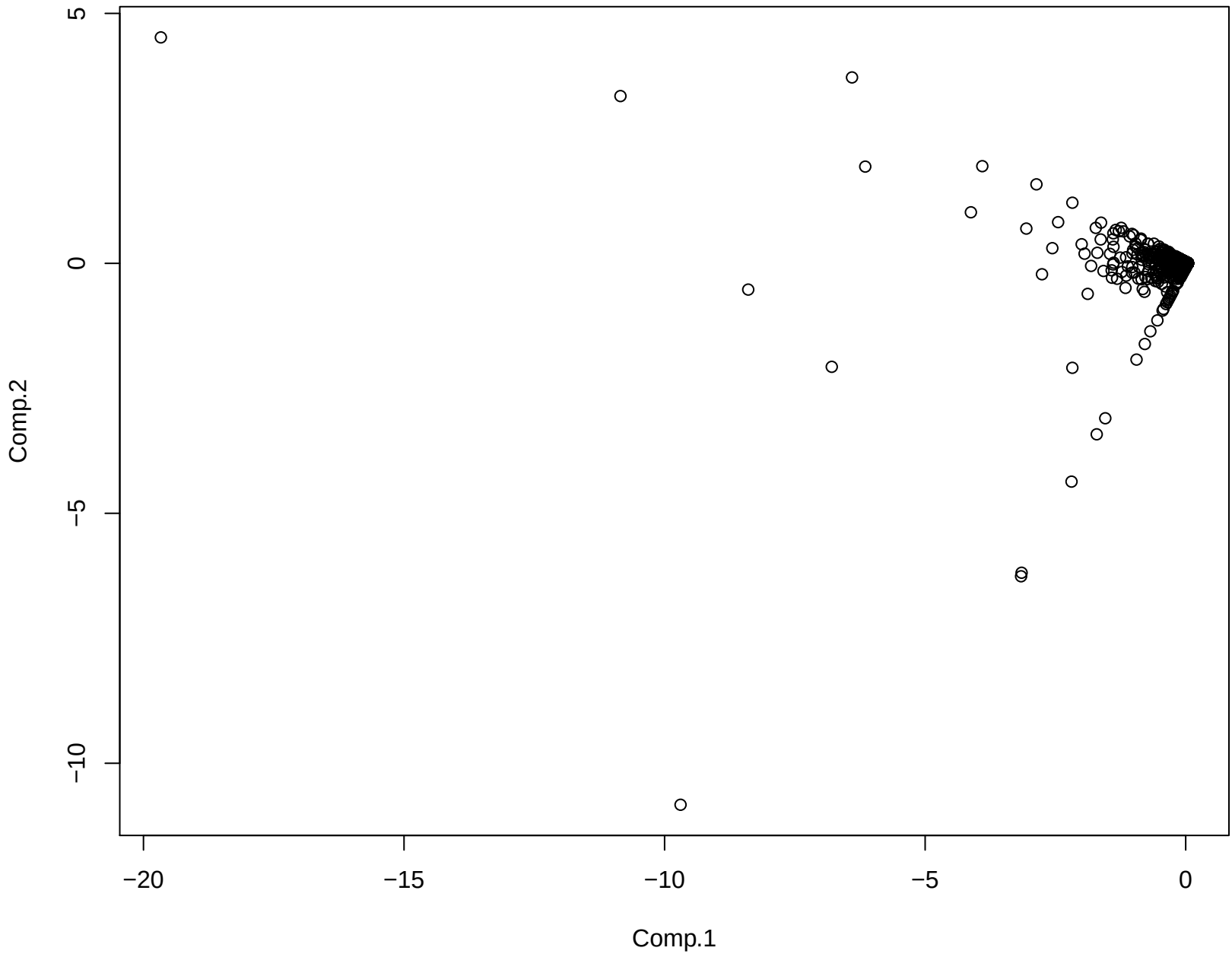

cshl transcript isoform lncRNA expression mean vs. standard deviation
(calculated over all the transcripts of one gene
HELAS3
GM12878
H1HESC
HEPG2
K562
0
−5
−10
log2(standard deviation of each transcript RPKM for each gene,whole cell)
log2(mean of each transcript RPKM for each gene,whole cell)

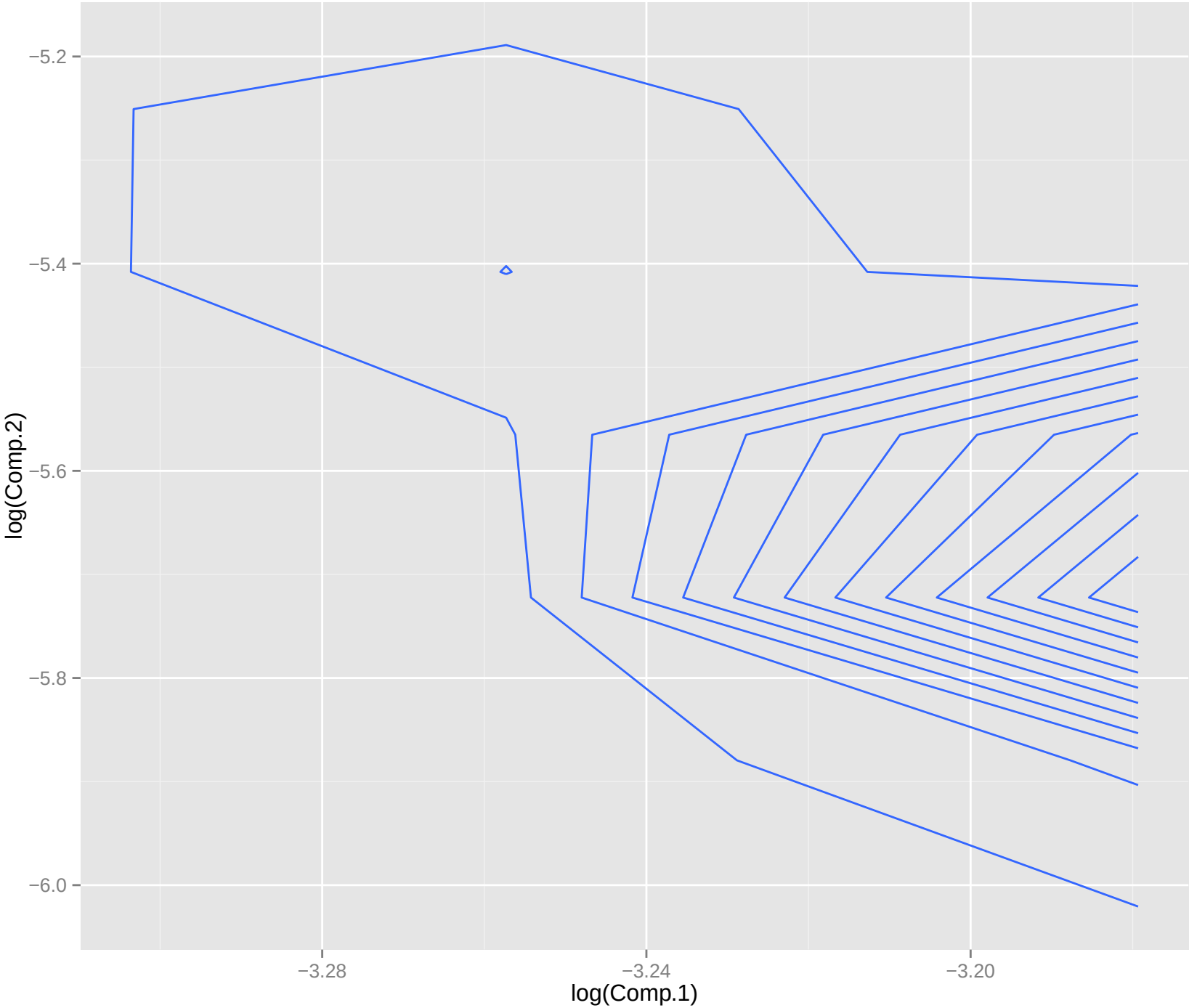

5
0
−5
−10
Comp.2
−20
−15
−10
−5
0
Comp.1

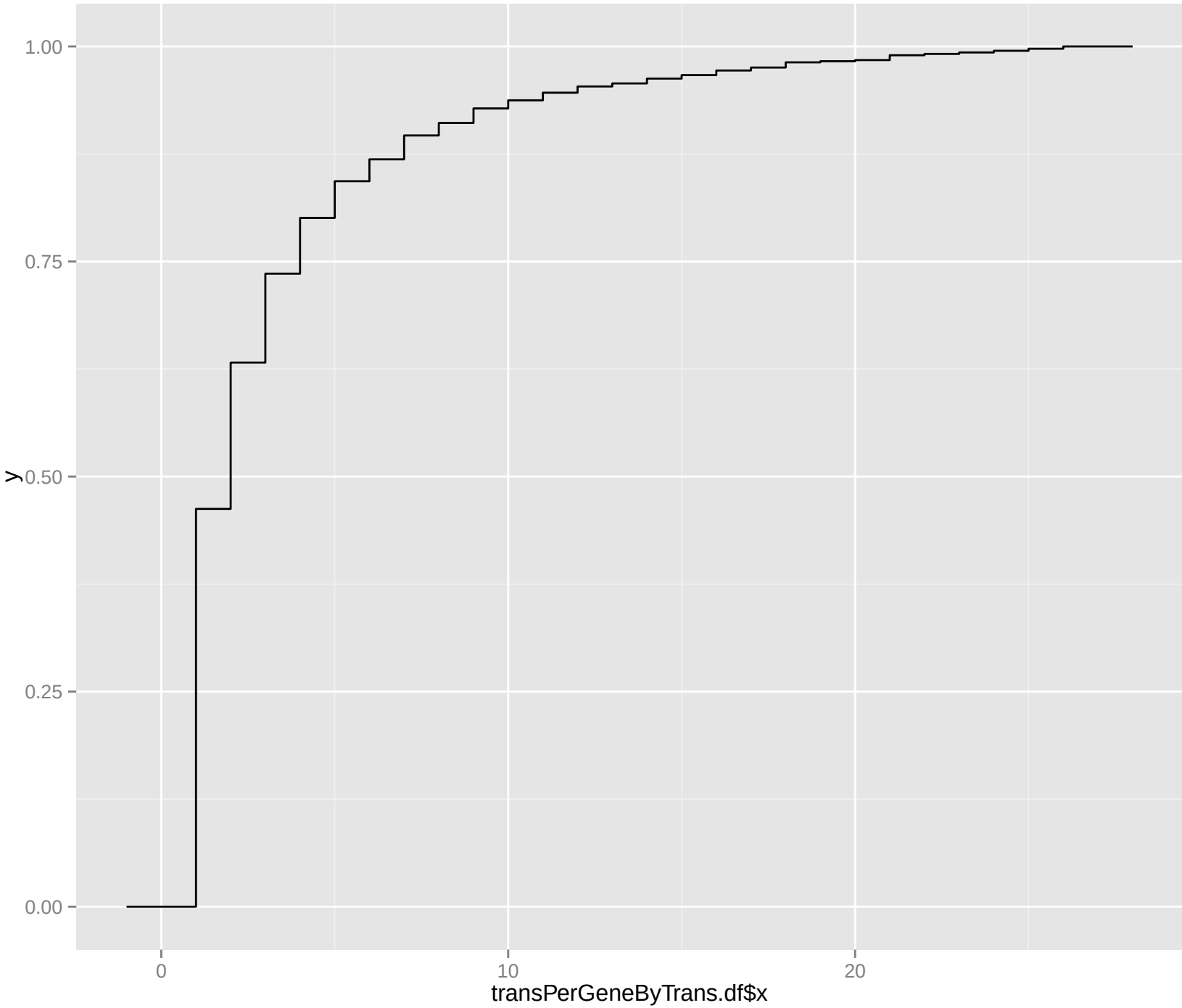

5
0
−5
−10
Comp.2
−20
−15
−10
−5
0
Comp.1

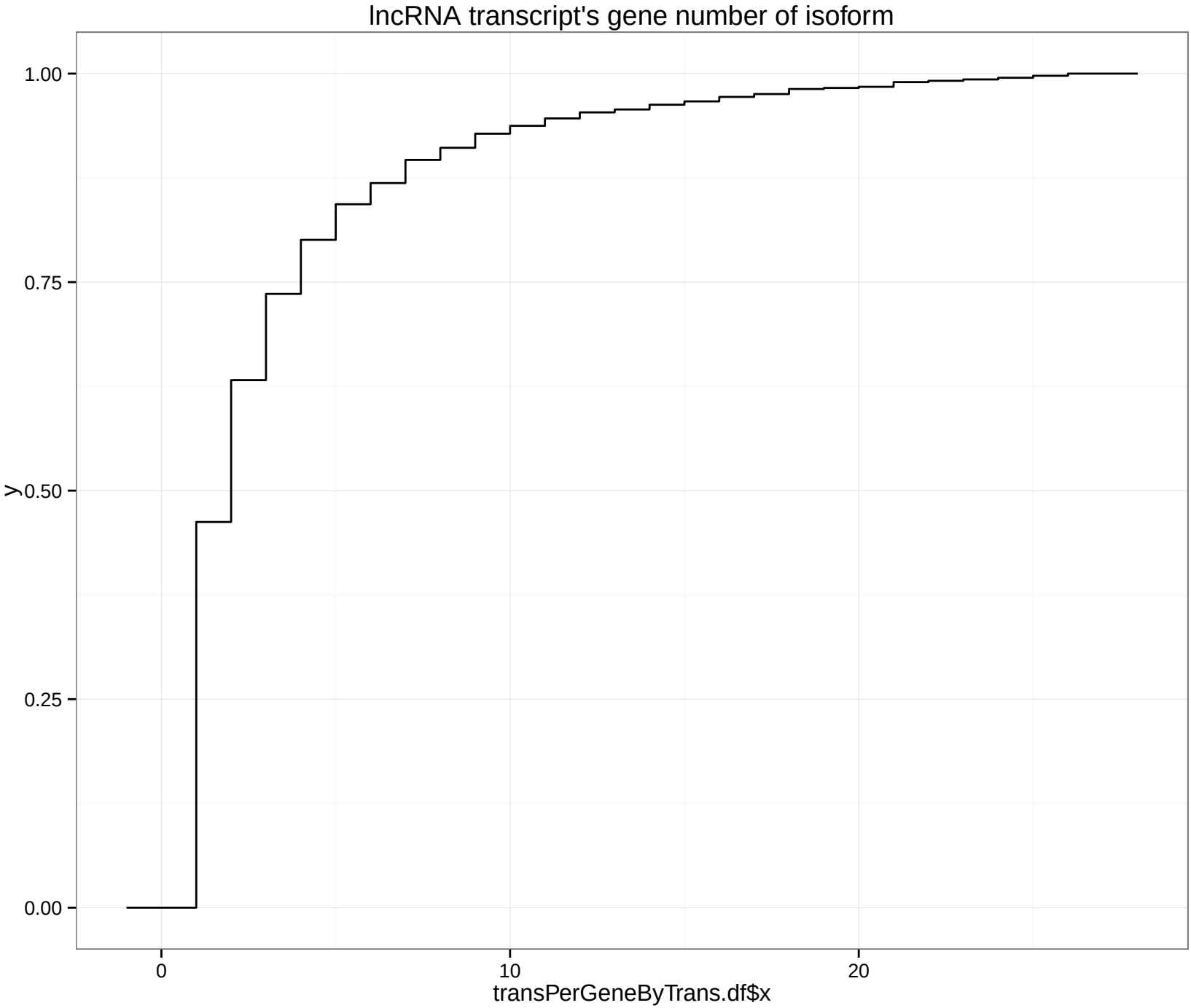

5
0
−5
−10
Comp.2
−20
−15
−10
−5
0
Comp.1

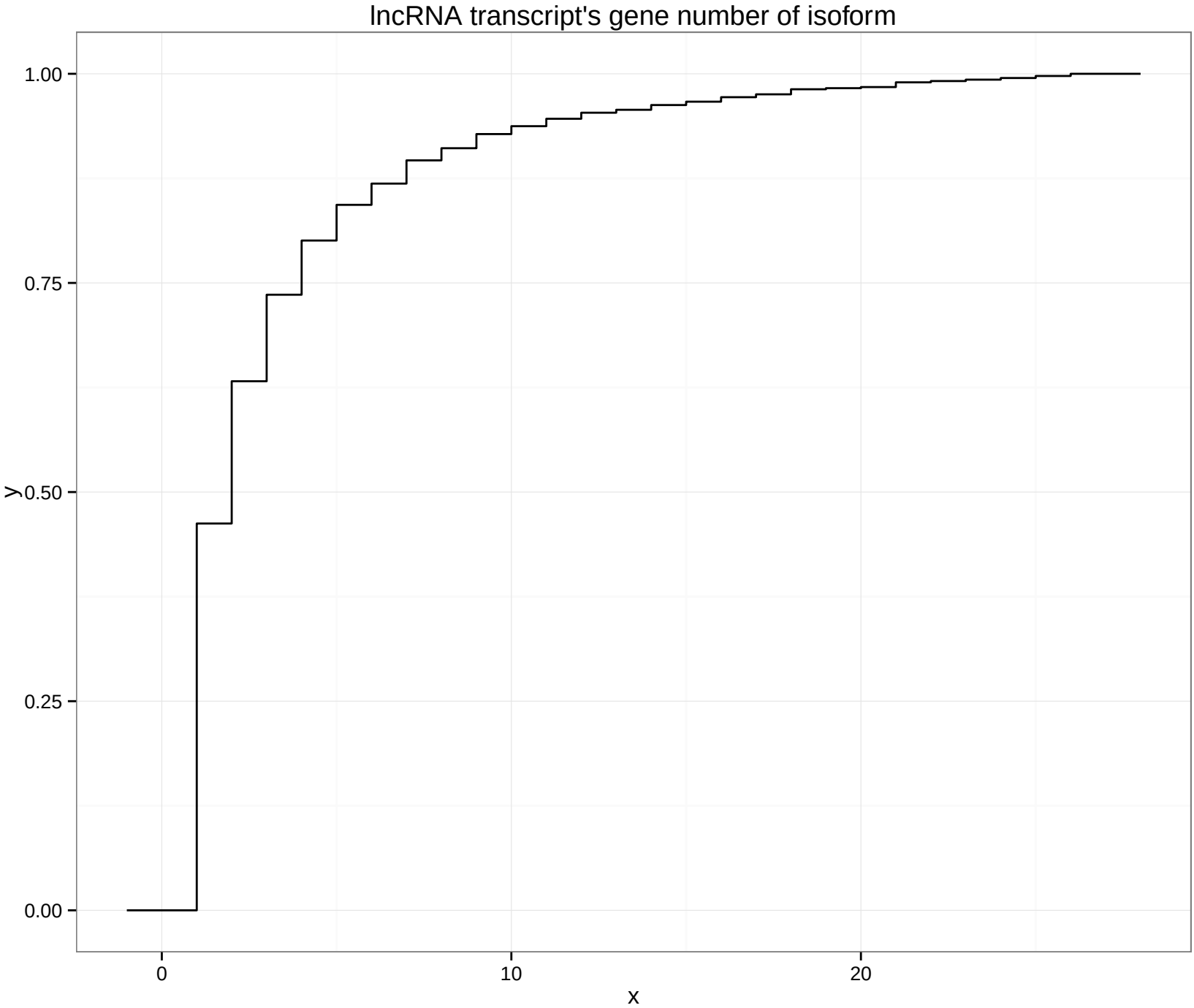

0
−5
−10
log(Comp.2)
−11
−9
−7
−5
−3
log(Comp.1)

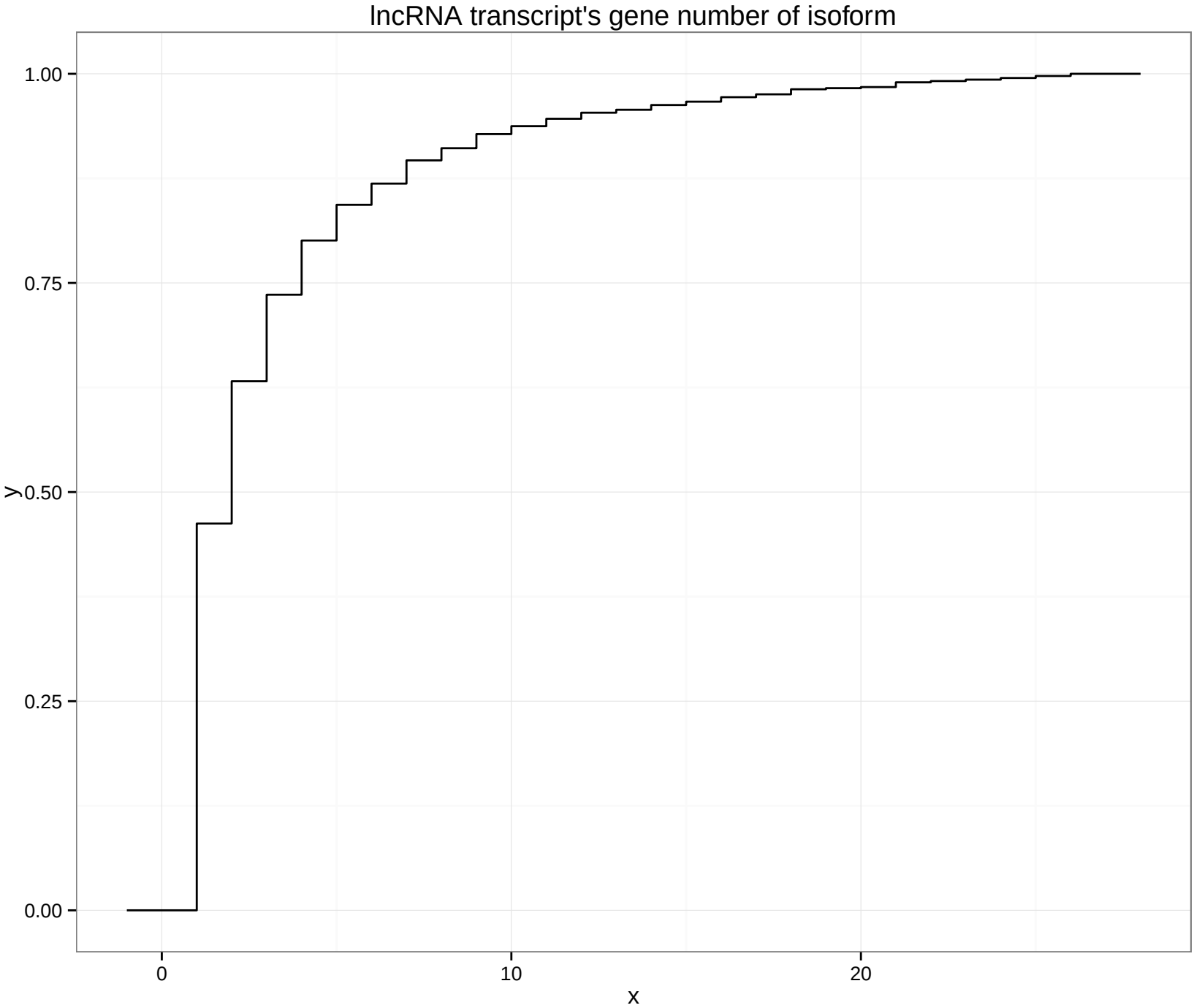

5
0
−5
−10
Comp.2
−20
−15
−10
−5
0
Comp.1

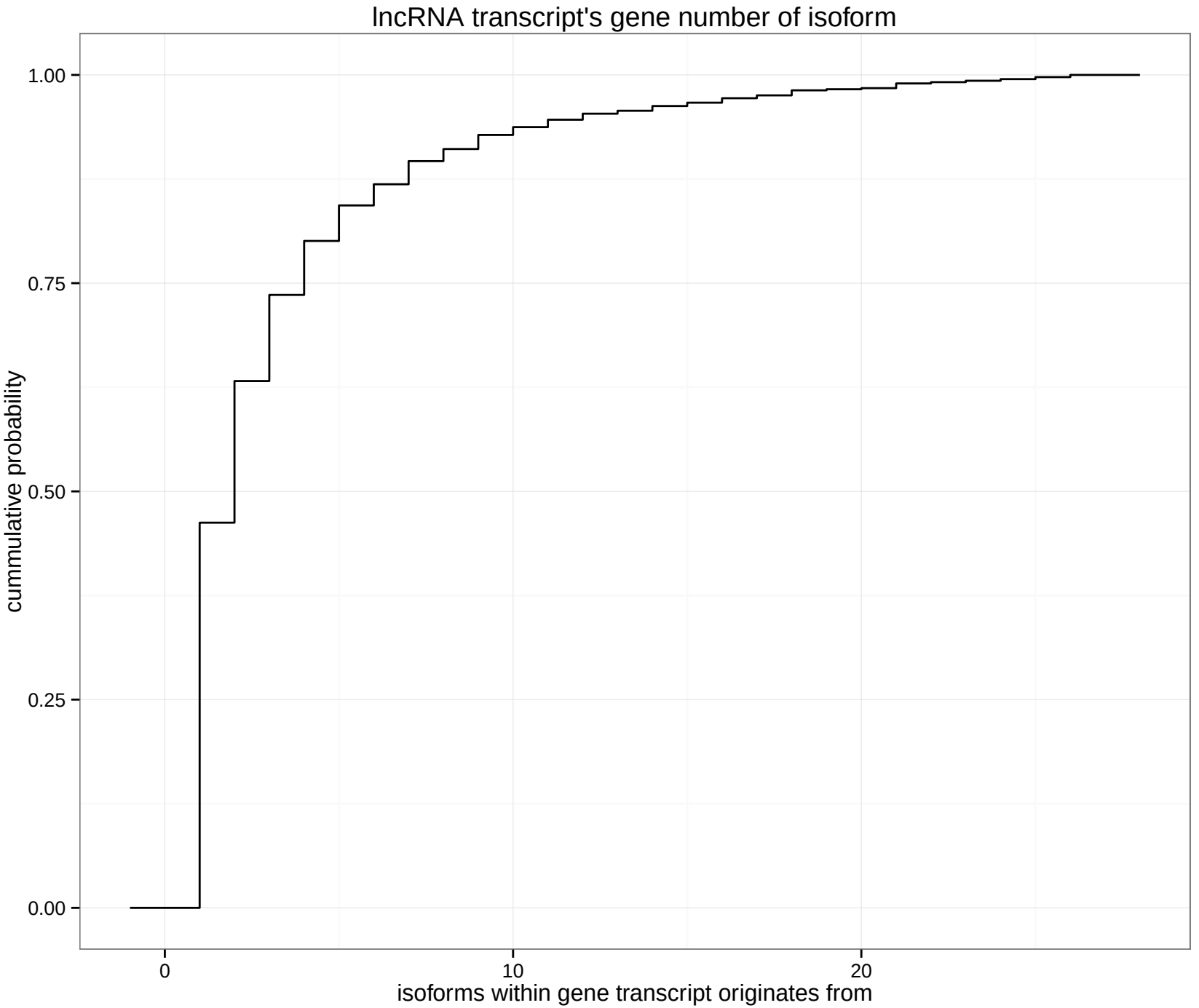

−5.2
−5.4
−5.6
−5.8
−6.0
log(Comp.2)
−3.28
−3.24
−3.20
log(Comp.1)

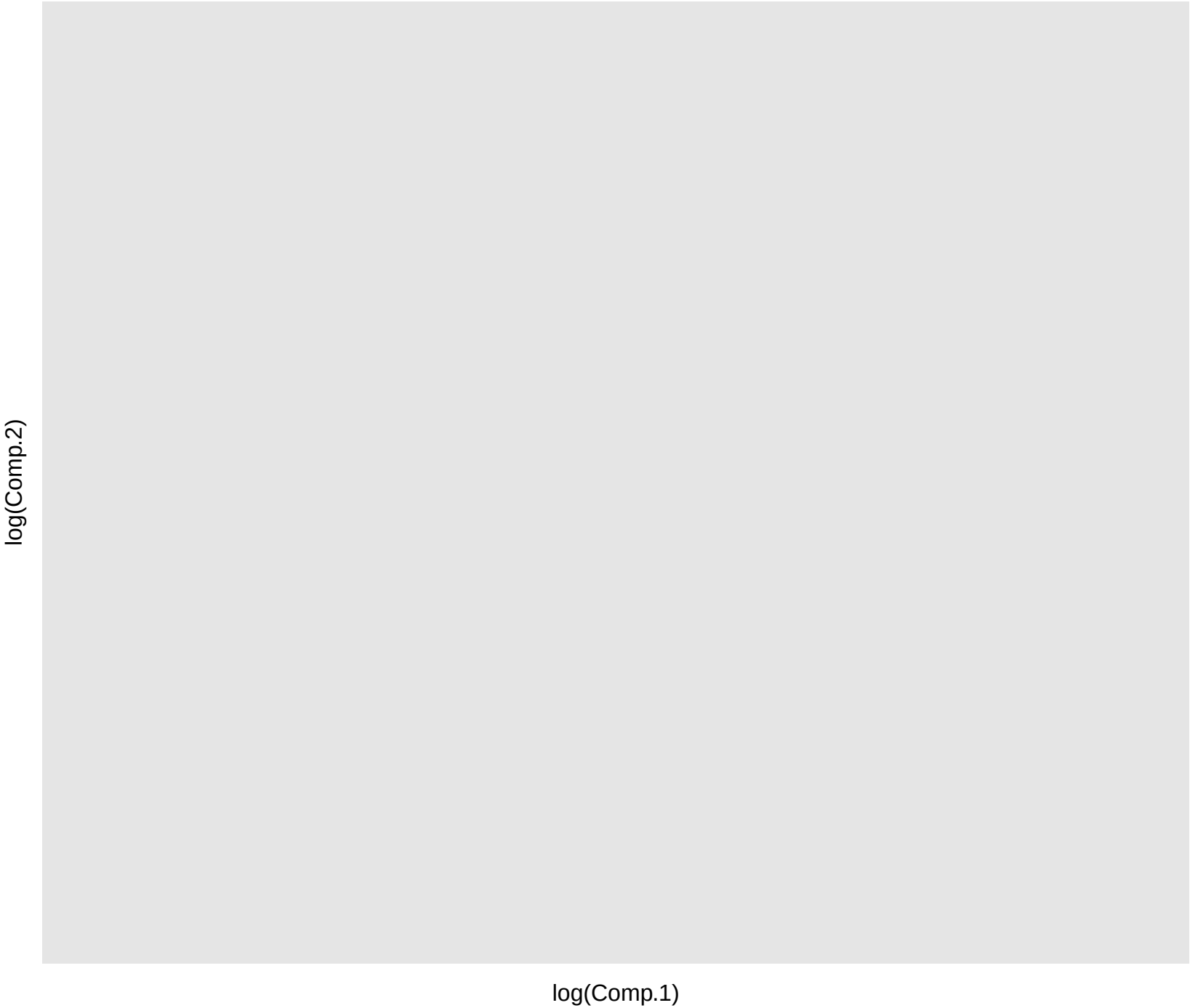

1.00
0.75
0.50
0.25
0.00
y
0
10
20
transPerGeneByTrans.df$x

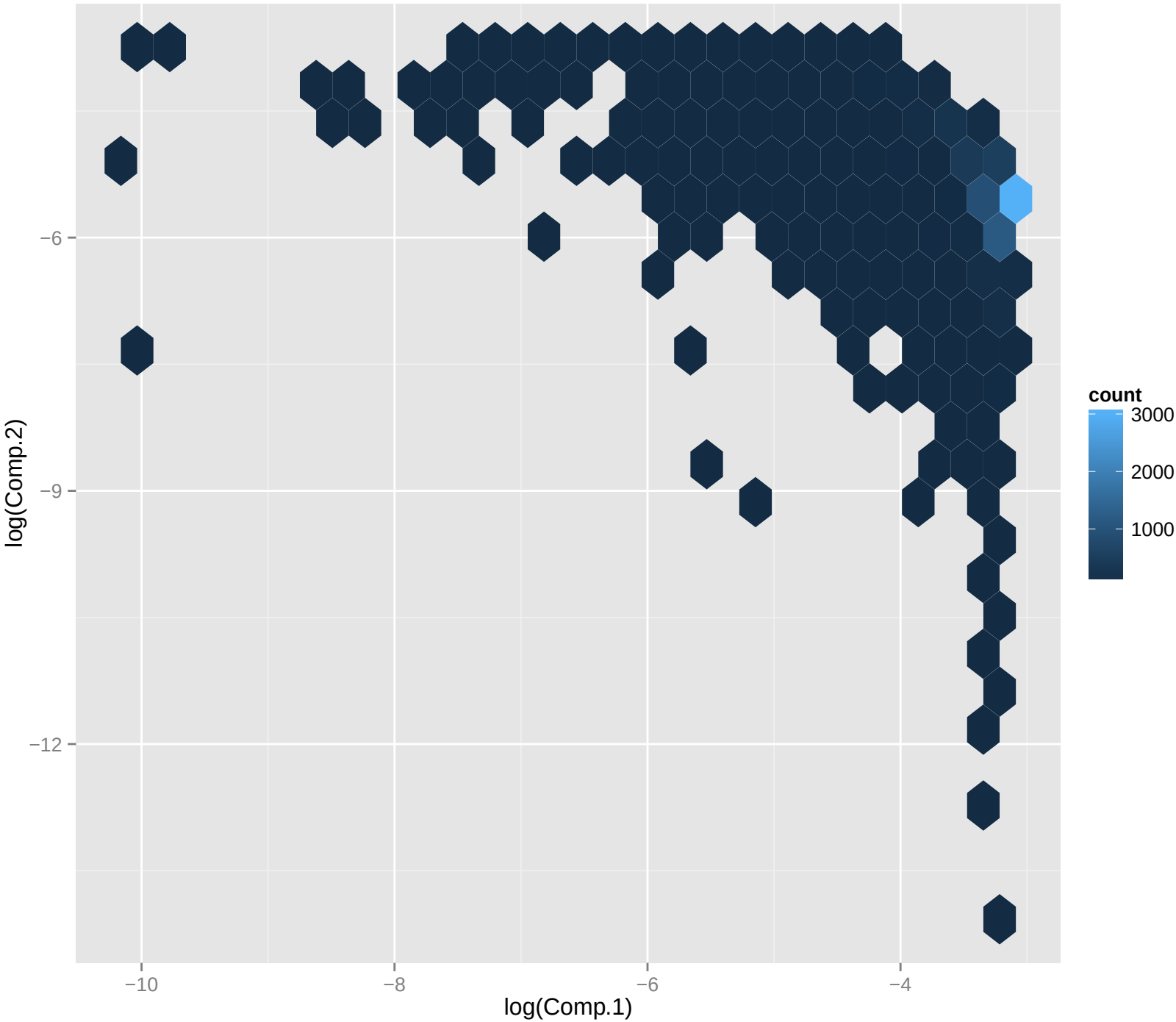

lncRNA transcript's gene number of isoform
1.00
0.75
0.50
0.25
0.00
y
0
10
20
transPerGeneByTrans.df$x

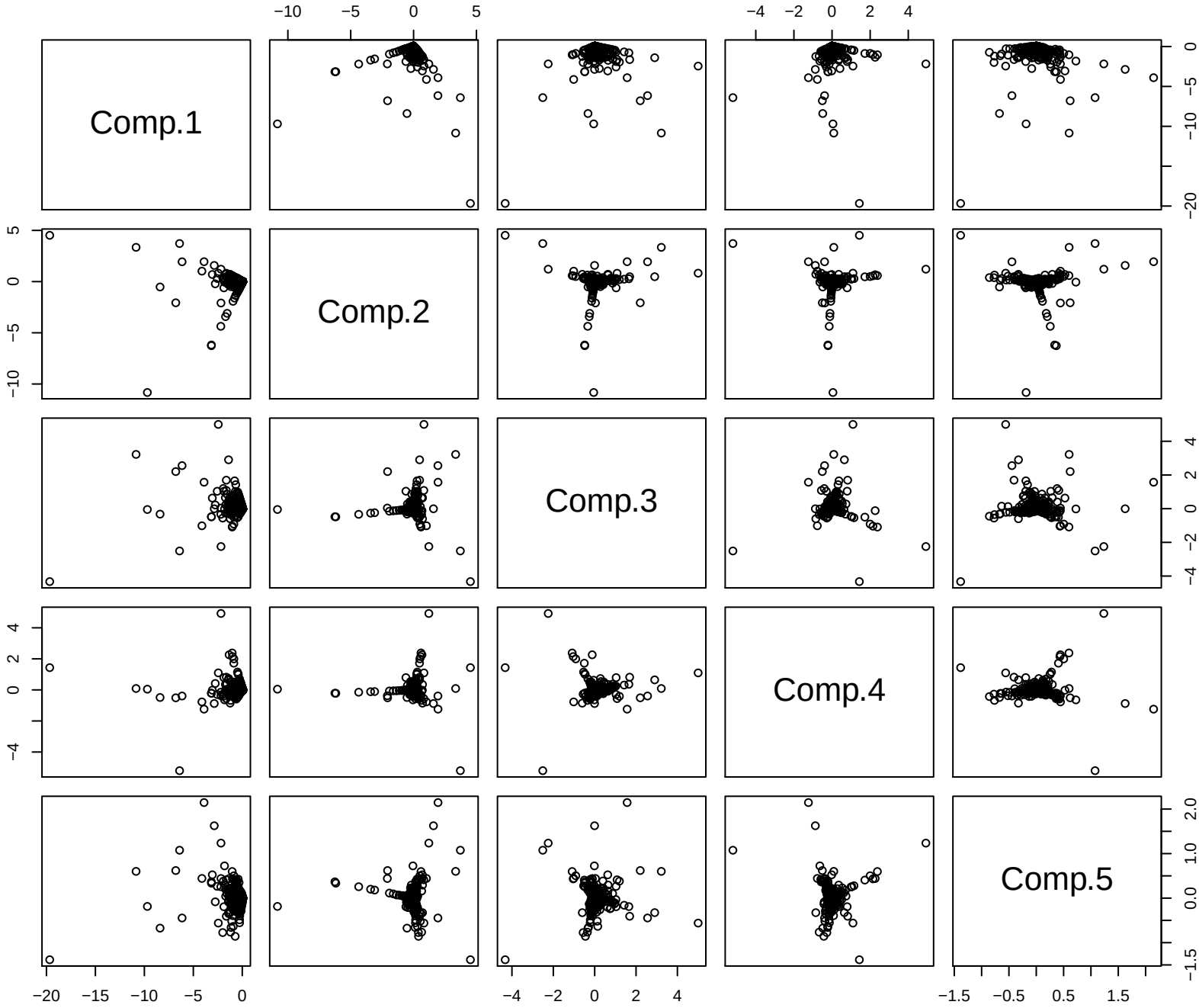

lncRNA transcript's gene number of isoform
1.00
0.75
0.50
0.25
0.00
y
0
10
20
x

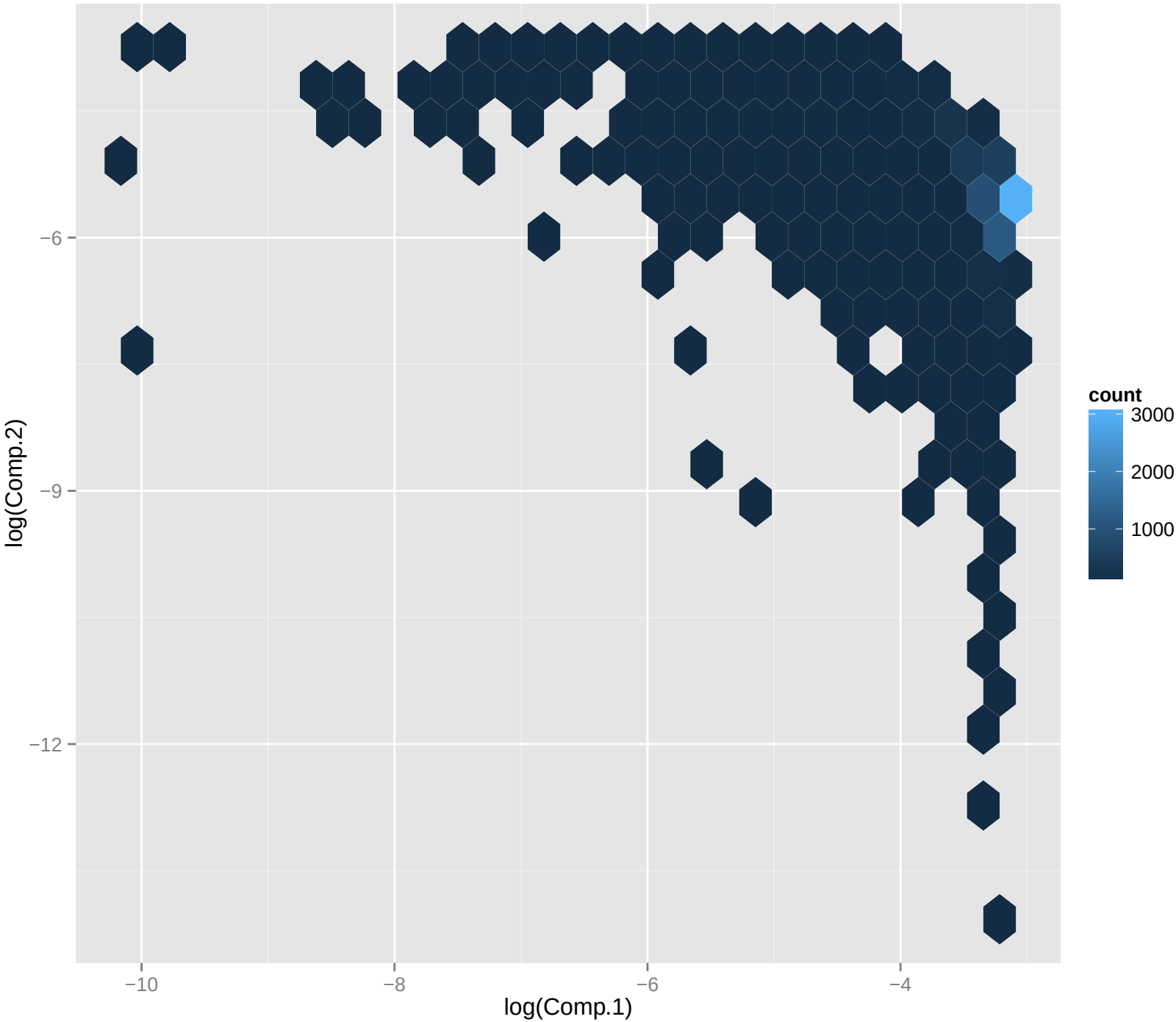

lncRNA transcript's gene number of isoform
1.00
0.75
0.50
0.25
0.00
y
0
10
20
x

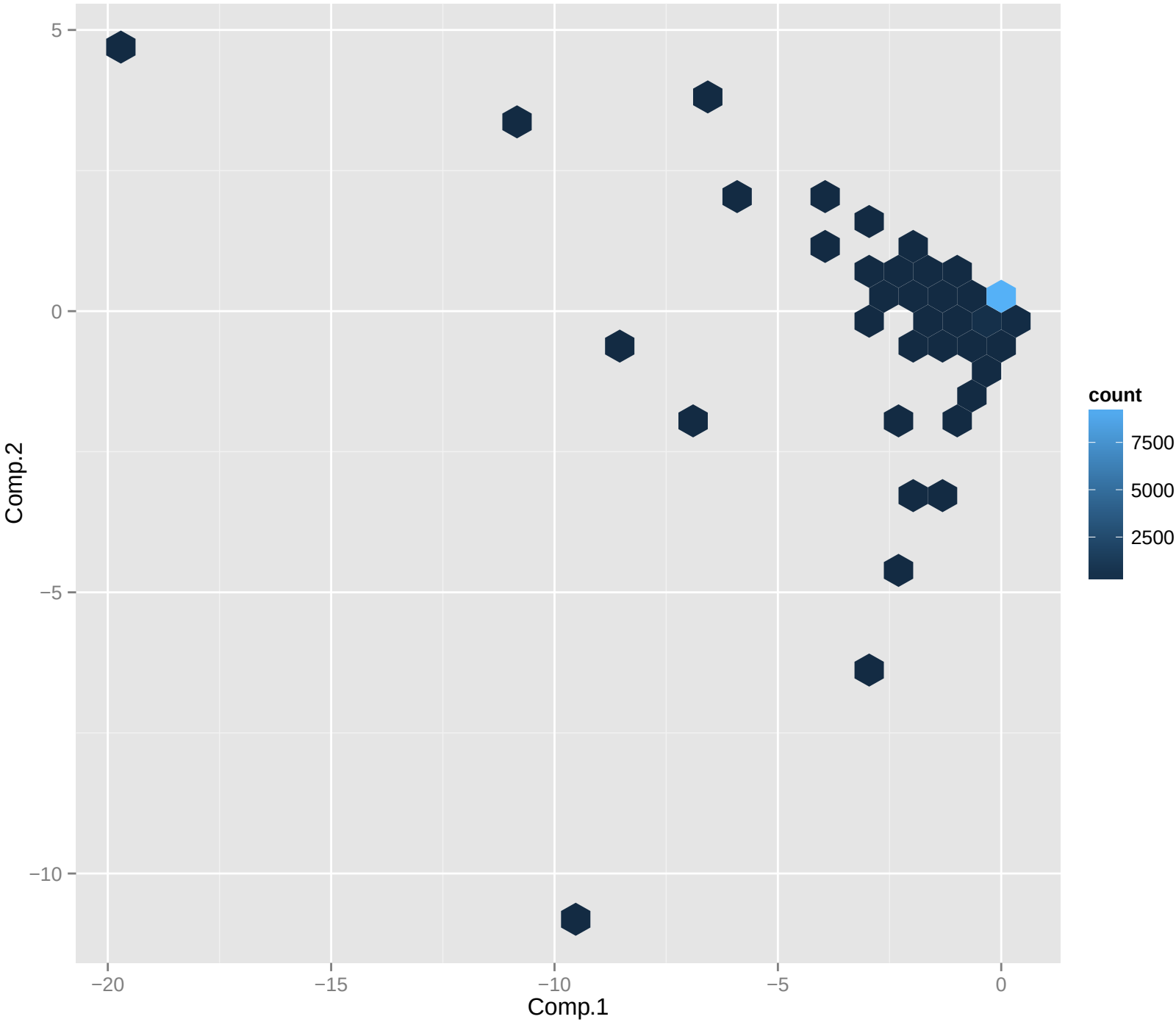

lncRNA transcript's gene number of isoform
1.00
0.75
0.50
0.25
0.00
cummulative probability
0
10
20
isoforms within gene transcript originates from

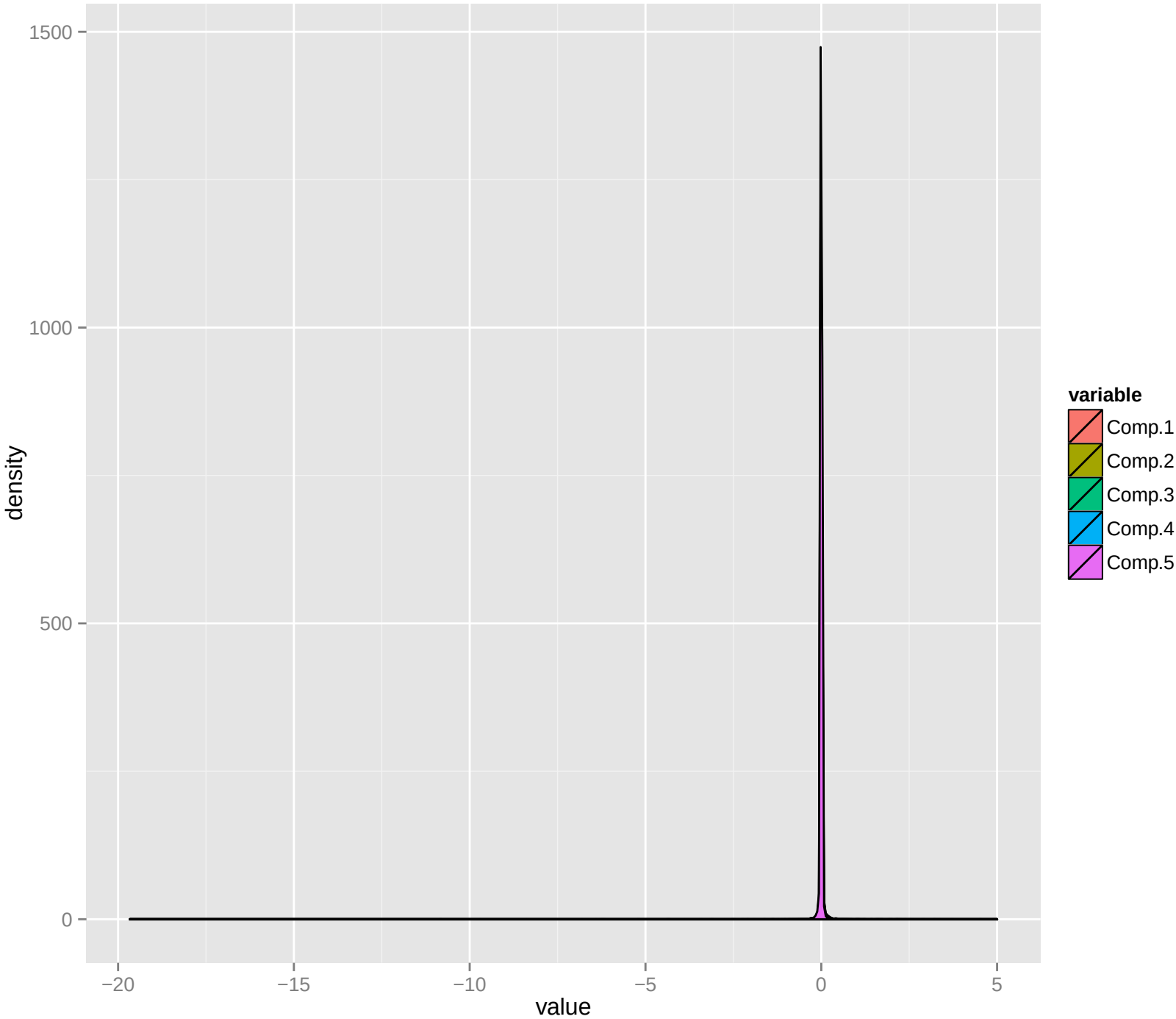

log(Comp.2)
log(Comp.1)

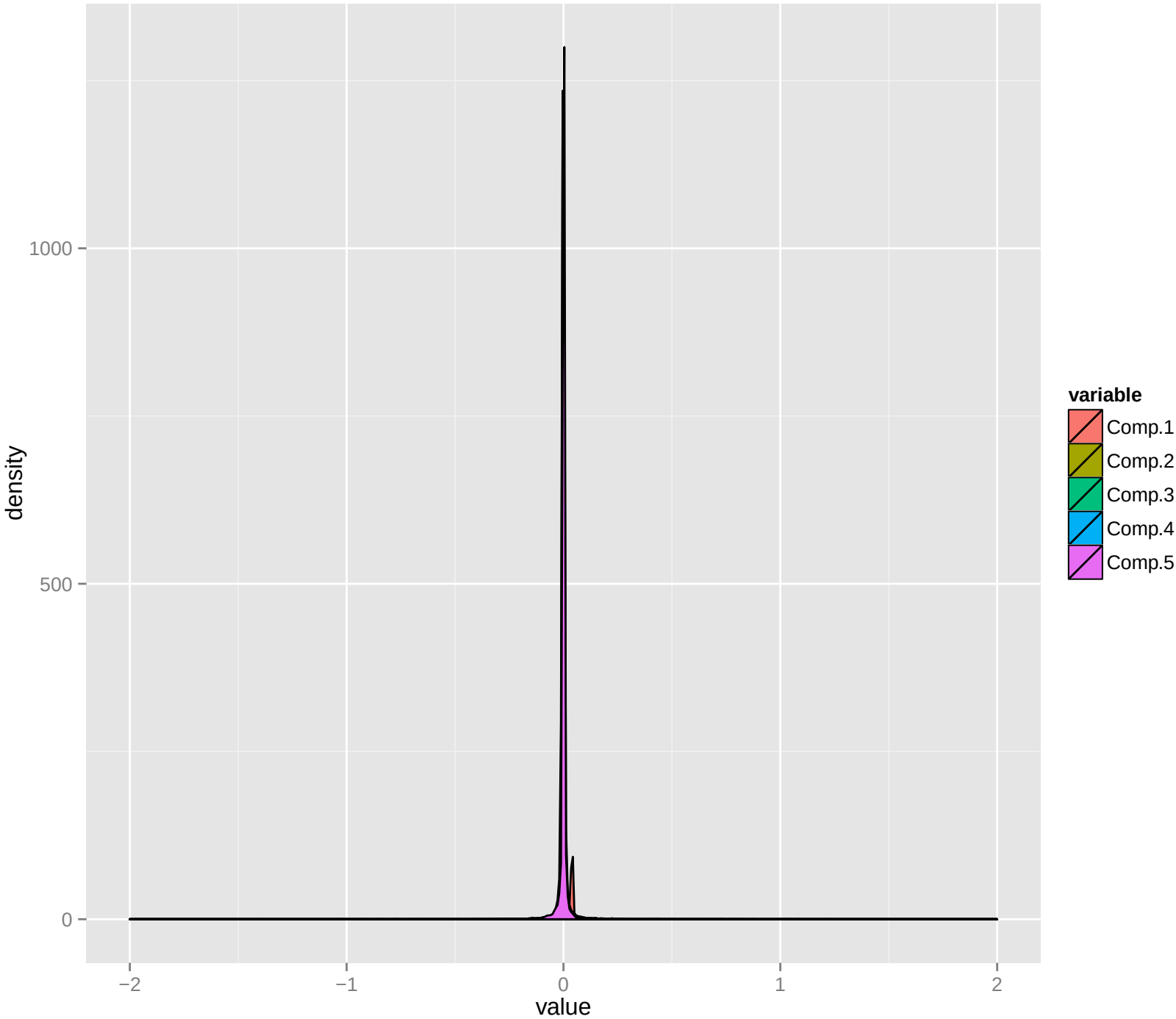

log(Comp.2)
−6
−9
−12
−10
−8
−6
−4
log(Comp.1)
count
3000
2000
1000

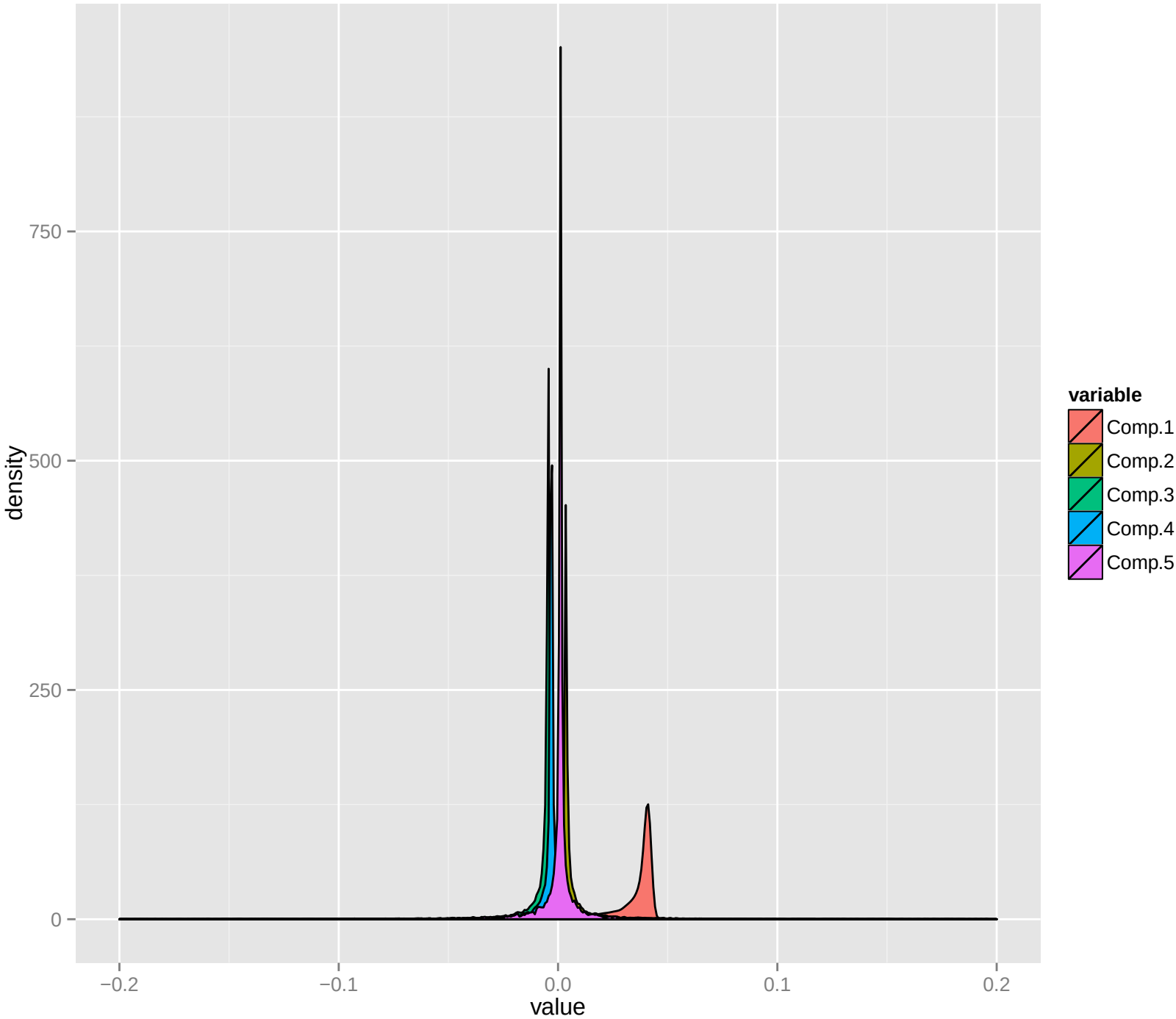

Comp.1
Comp.2
Comp.3
Comp.4
Comp.5
−10 −5 0 5
−4 −2 0 2 4
0 −5 −10 −20
5 0 −5 −10
4 2 0 −2 −4
4 2 0 −4
2.0 1.0 0.0 −1.5
−20 −15 −10 −5 0
−4 −2 0 2 4
−1.5 −0.5 0.5 1.5

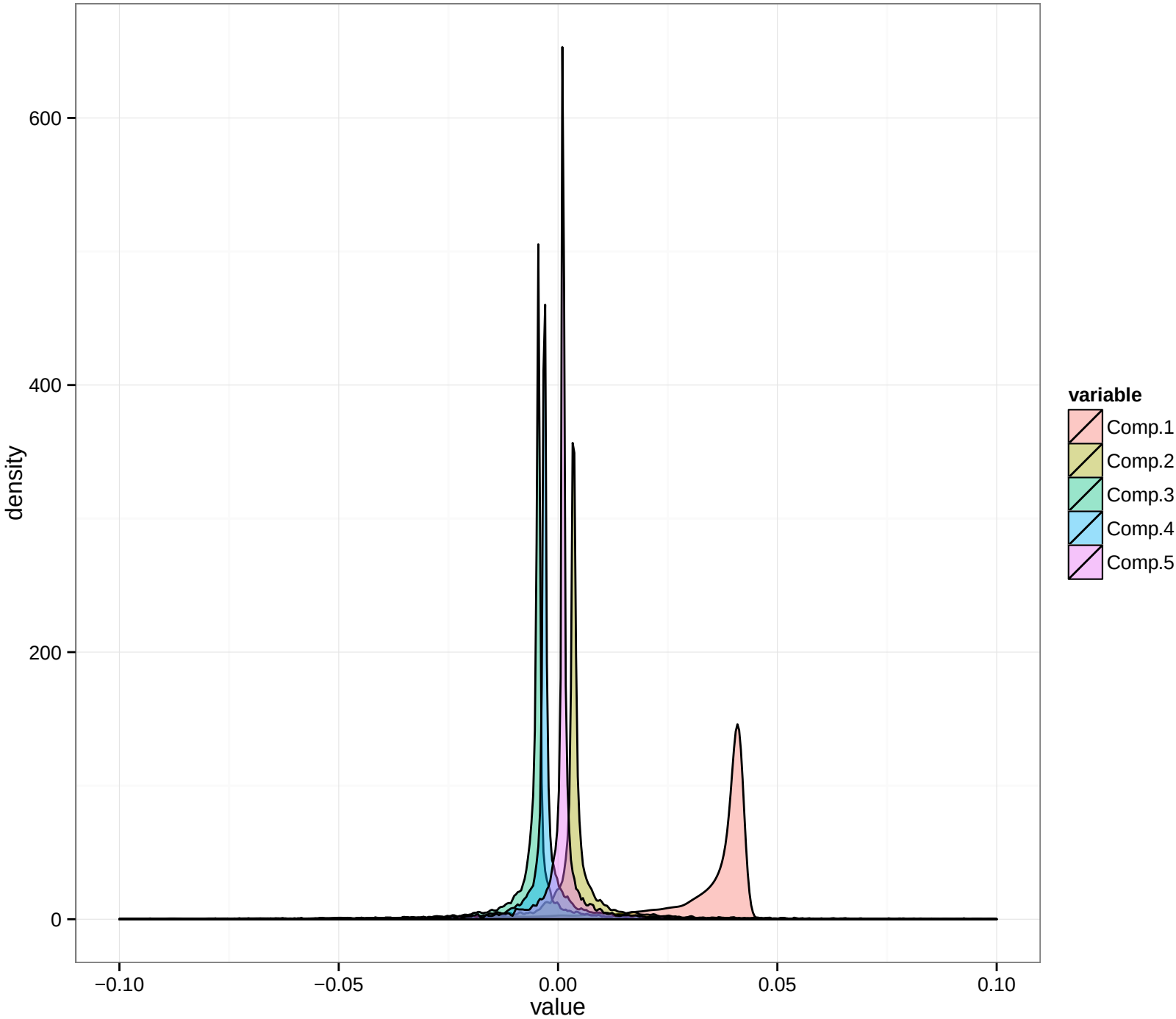

log(Comp.2)
−6
−9
−12
−10
−8
−6
−4
log(Comp.1)
count
3000
2000
1000

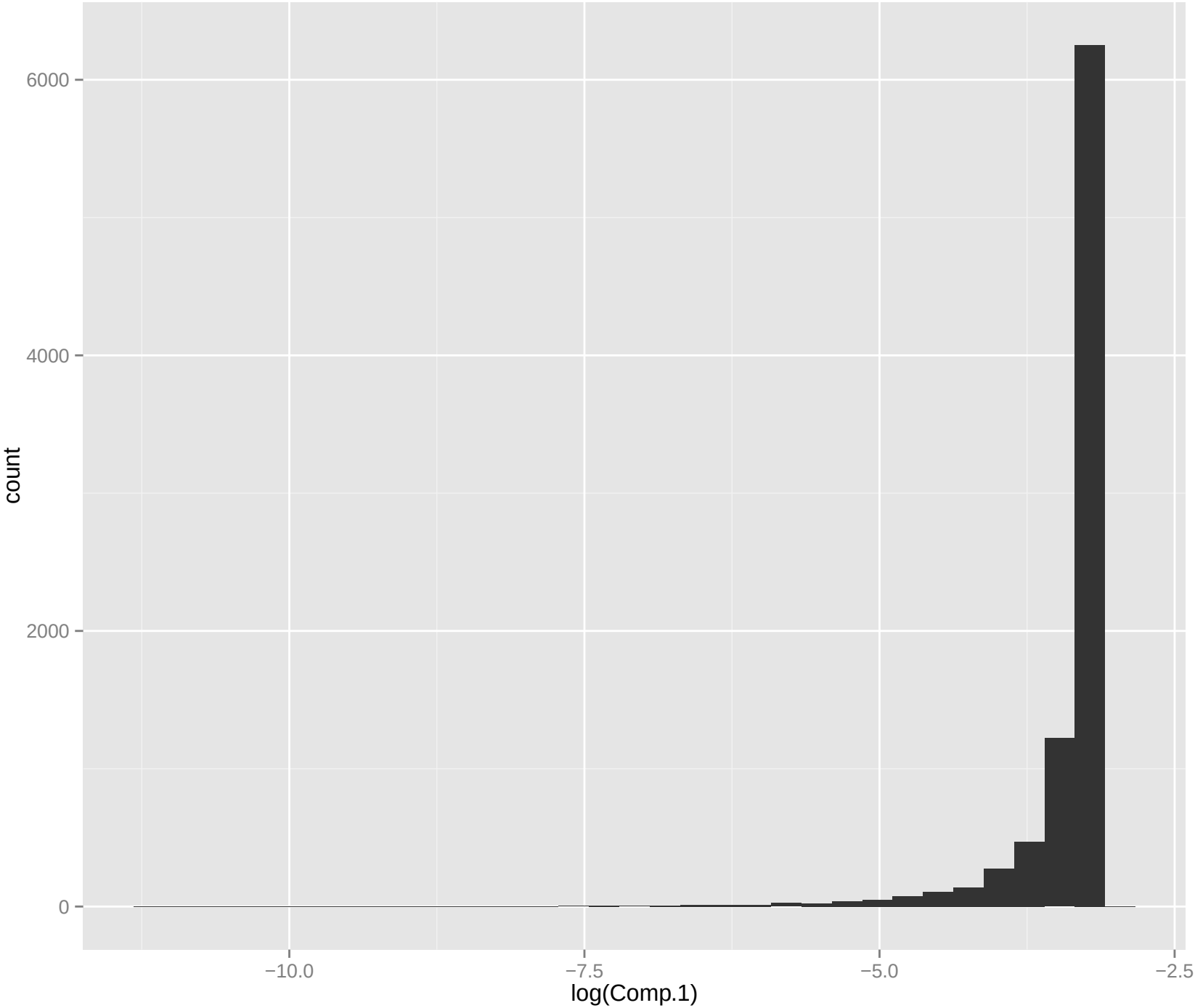

5
0
−5
−10
Comp.2
−20
−15
−10
−5
0
Comp.1
count
7500
5000
2500

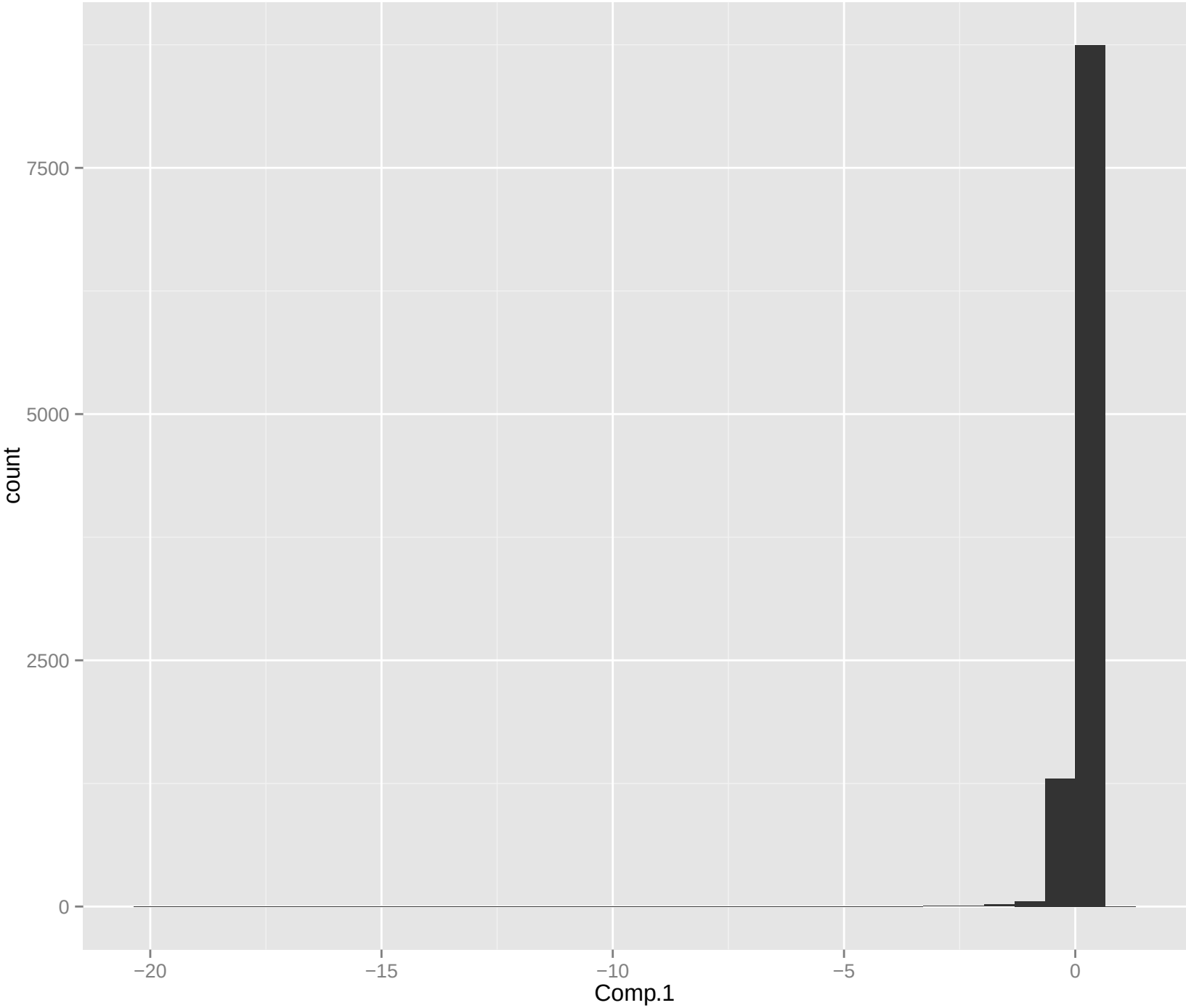

1500
1000
500
0
density
−20
−15
−10
−5
0
5
value
variable
Comp.1
Comp.2
Comp.3
Comp.4
Comp.5

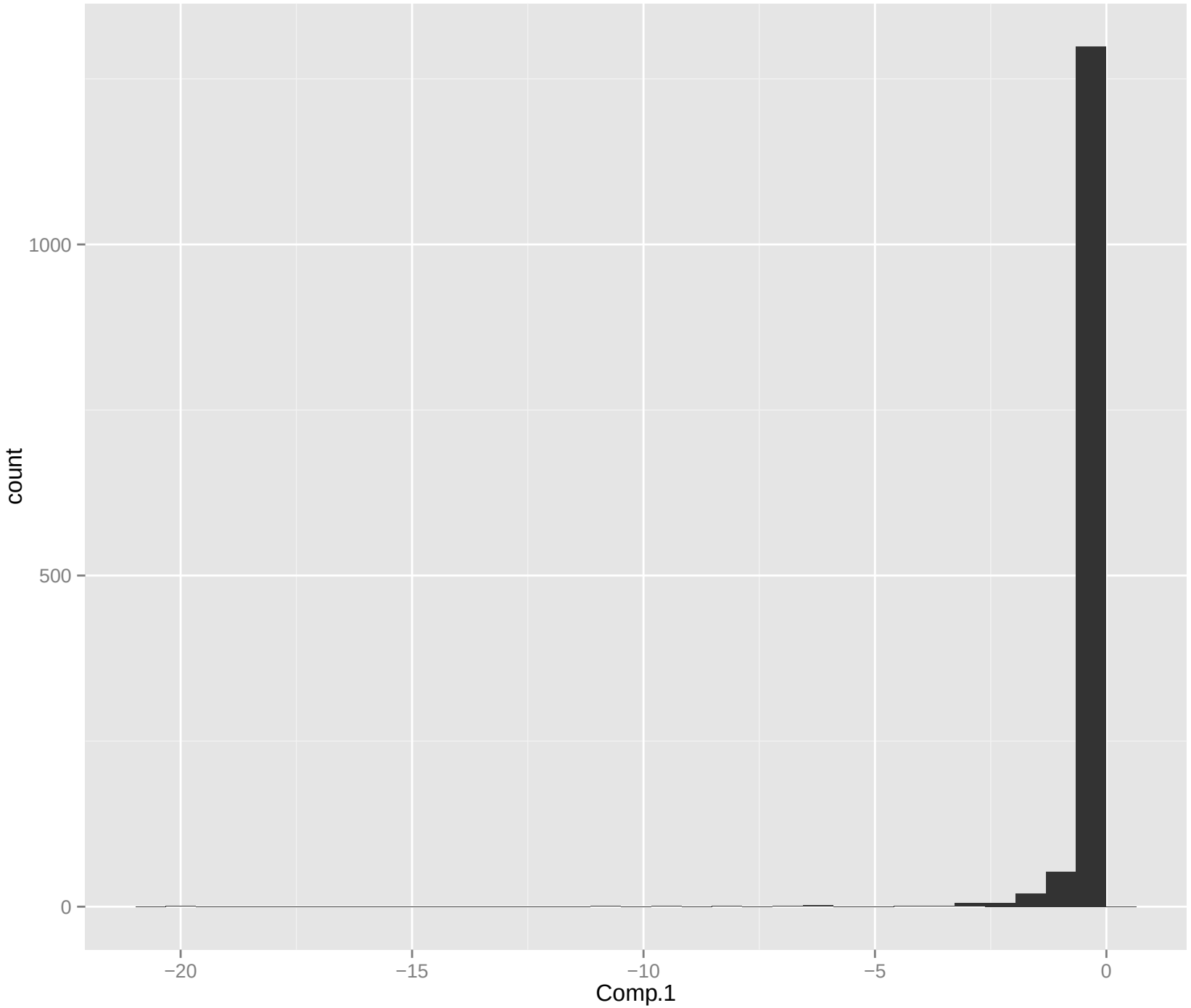

density
1000
500
0
−2
−1
0
1
2
value
variable
Comp.1
Comp.2
Comp.3
Comp.4
Comp.5

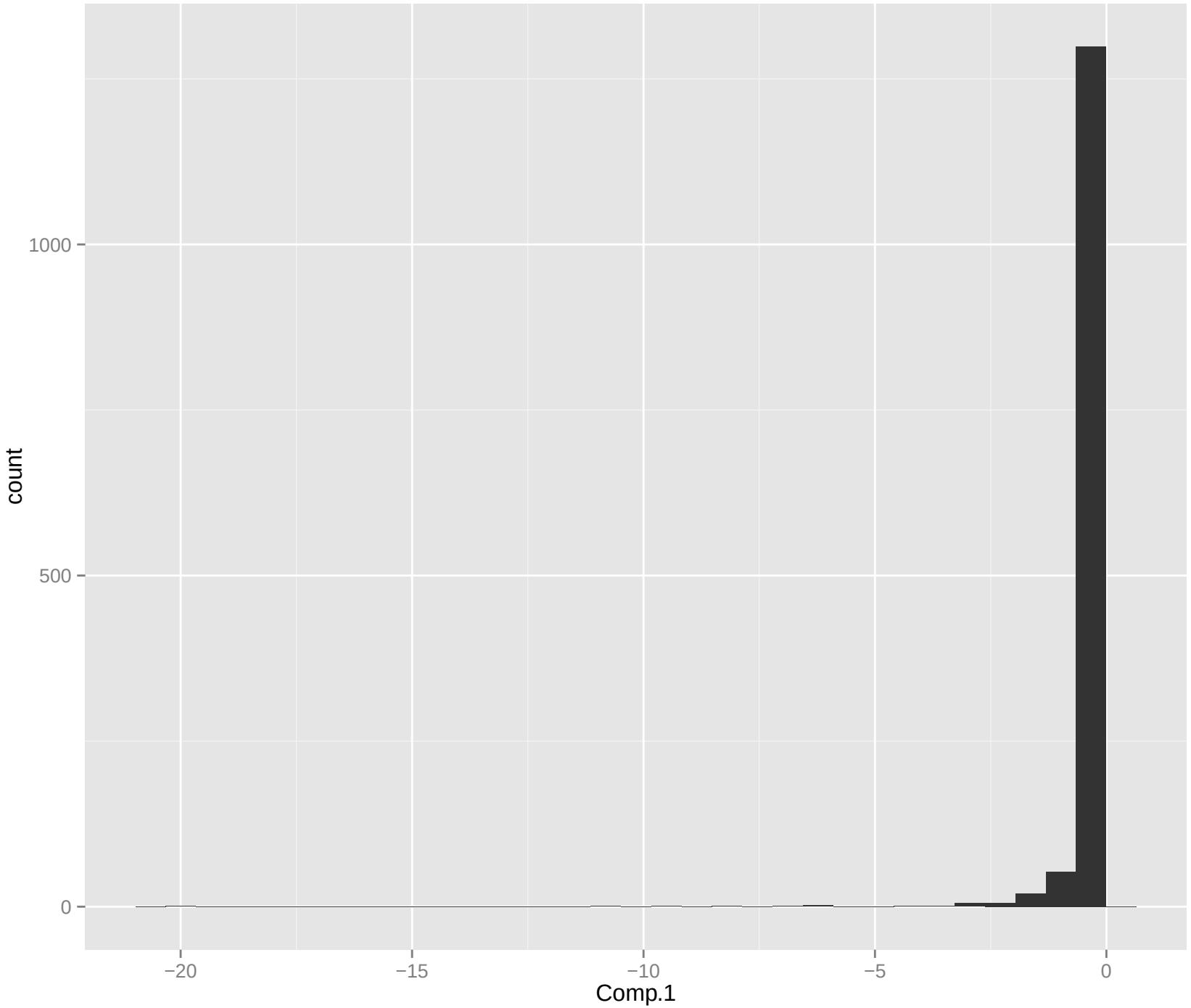

750
500
250
0
density
−0.2
−0.1
0.0
0.1
0.2
value
variable
Comp.1
Comp.2
Comp.3
Comp.4
Comp.5

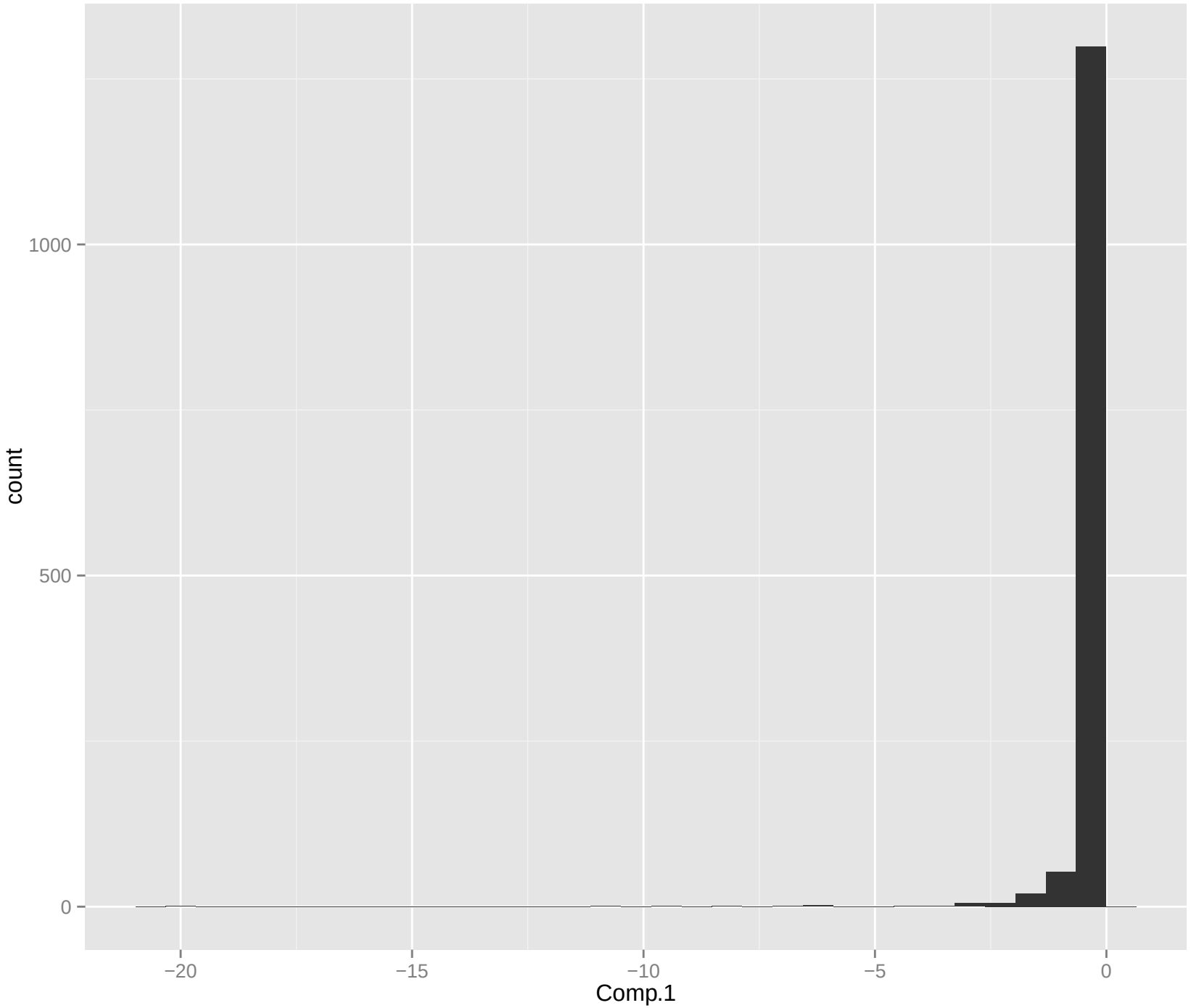

600
400
200
0
density
−0.10
−0.05
0.00
0.05
0.10
value
variable
Comp.1
Comp.2
Comp.3
Comp.4
Comp.5

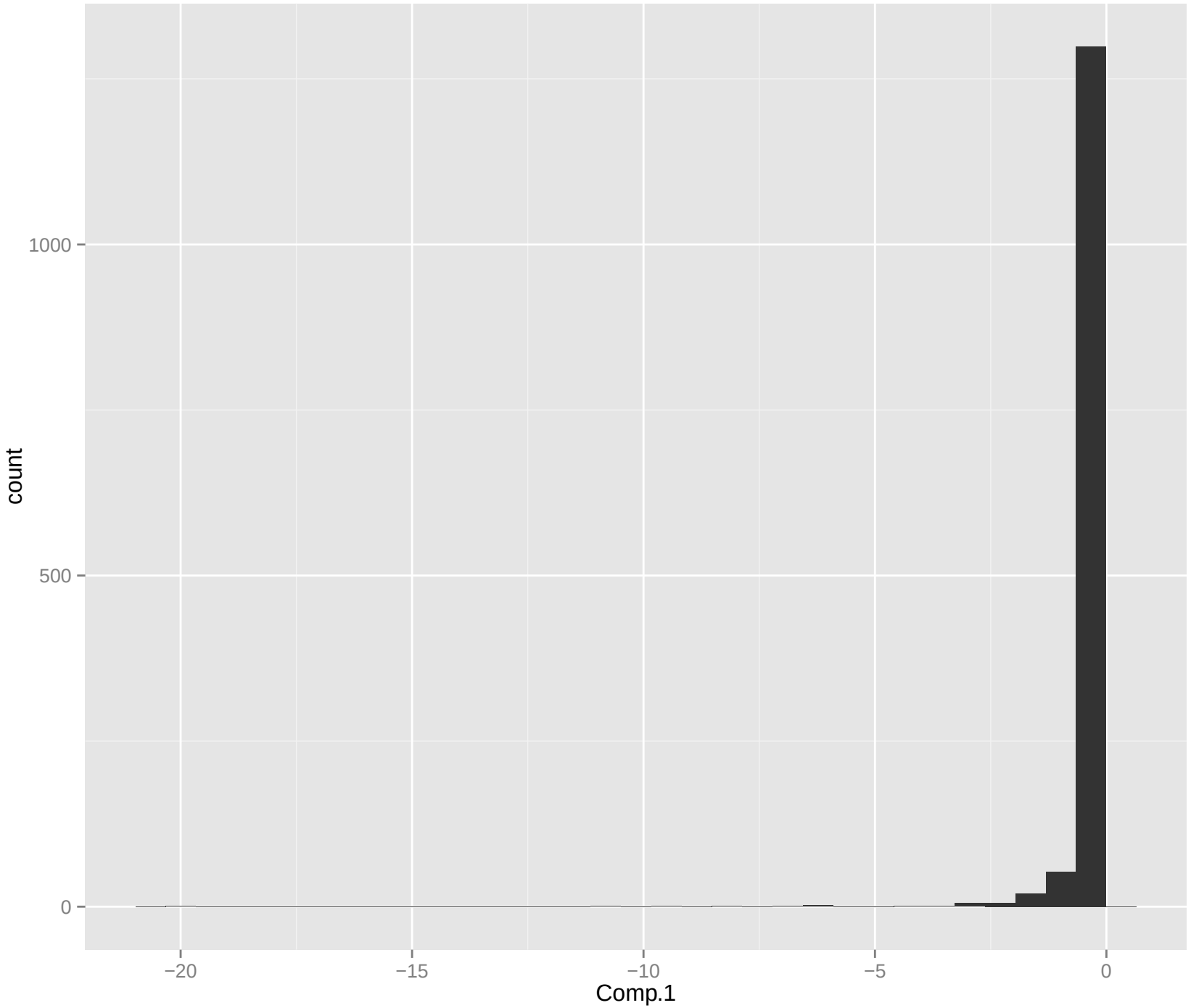

6000
4000
2000
0
count
−10.0
−7.5
−5.0
−2.5
log(Comp.1)

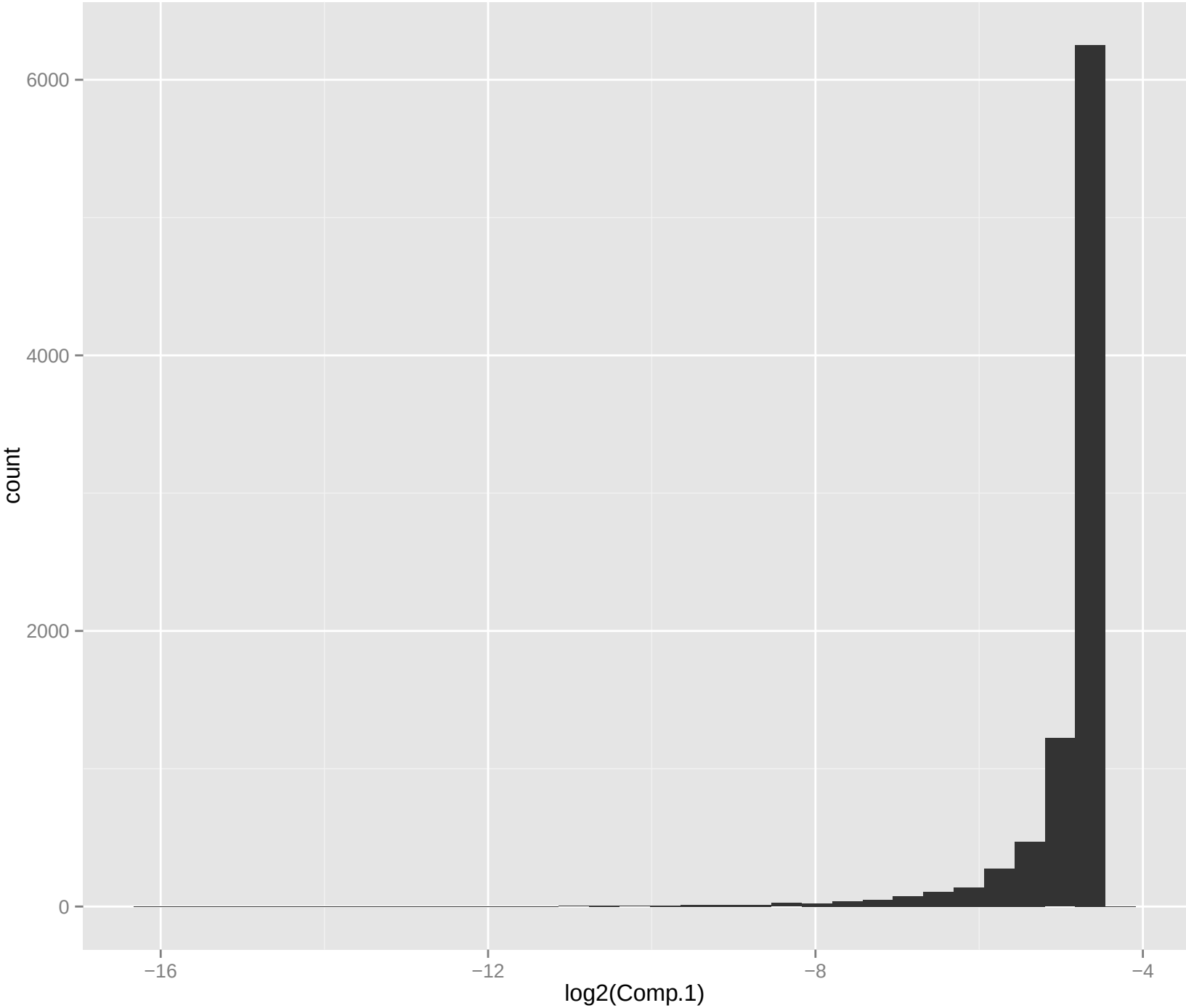

7500
5000
2500
0
count
−20
−15
−10
−5
0
Comp.1

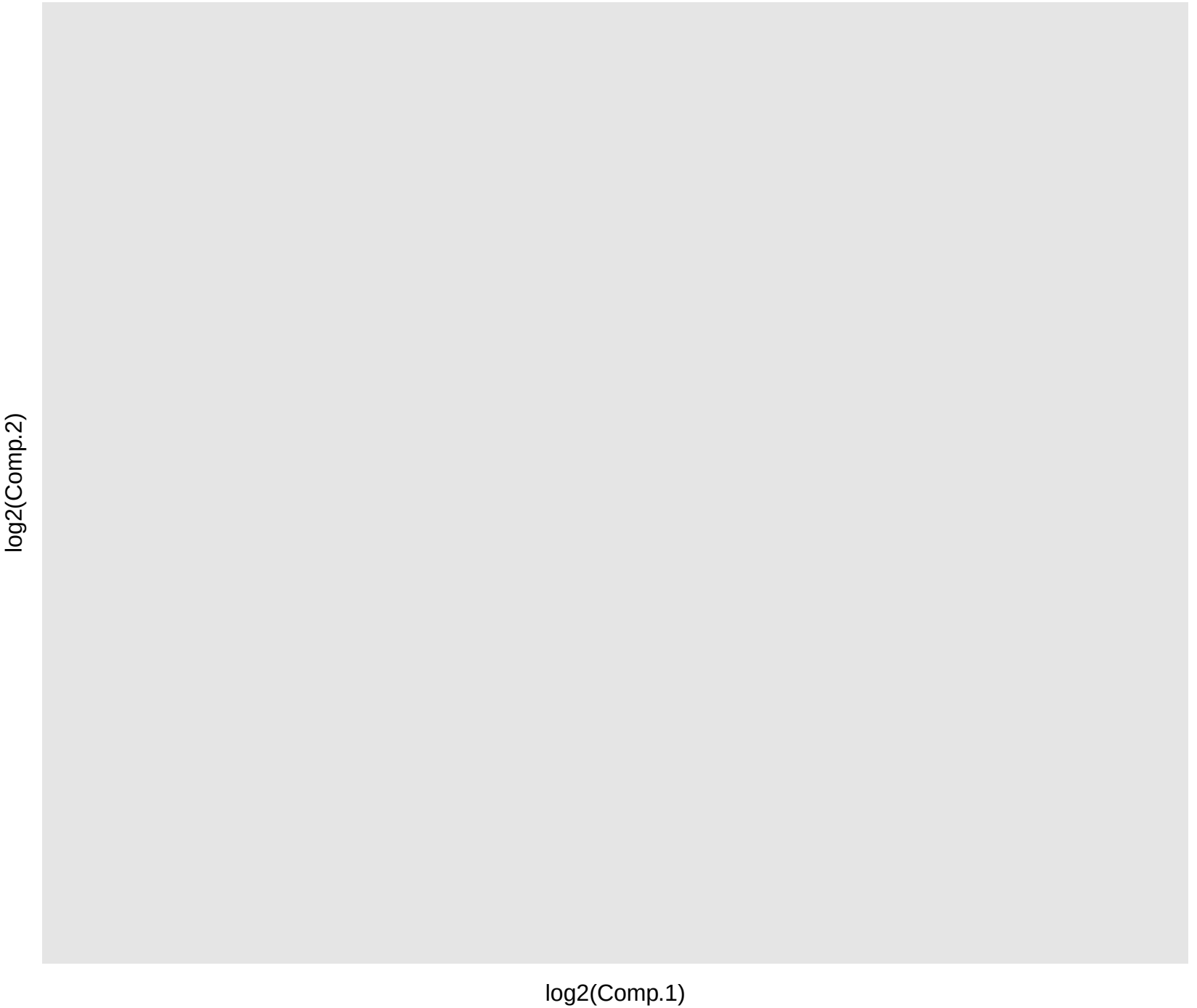

count
1000
500
0
−20
−15
−10
−5
0
Comp.1

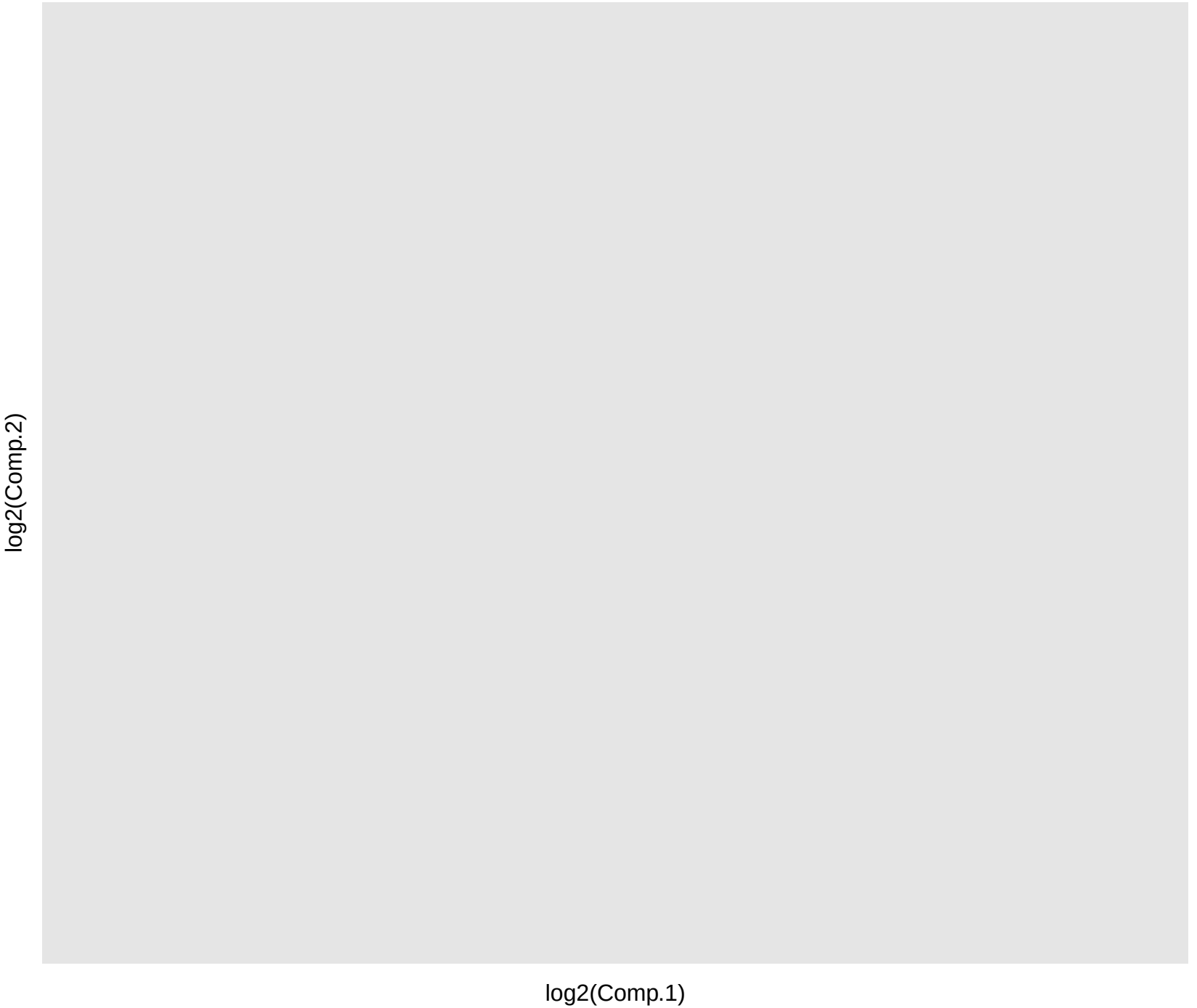

count
1000
500
0
−20
−15
−10
−5
0
Comp.1

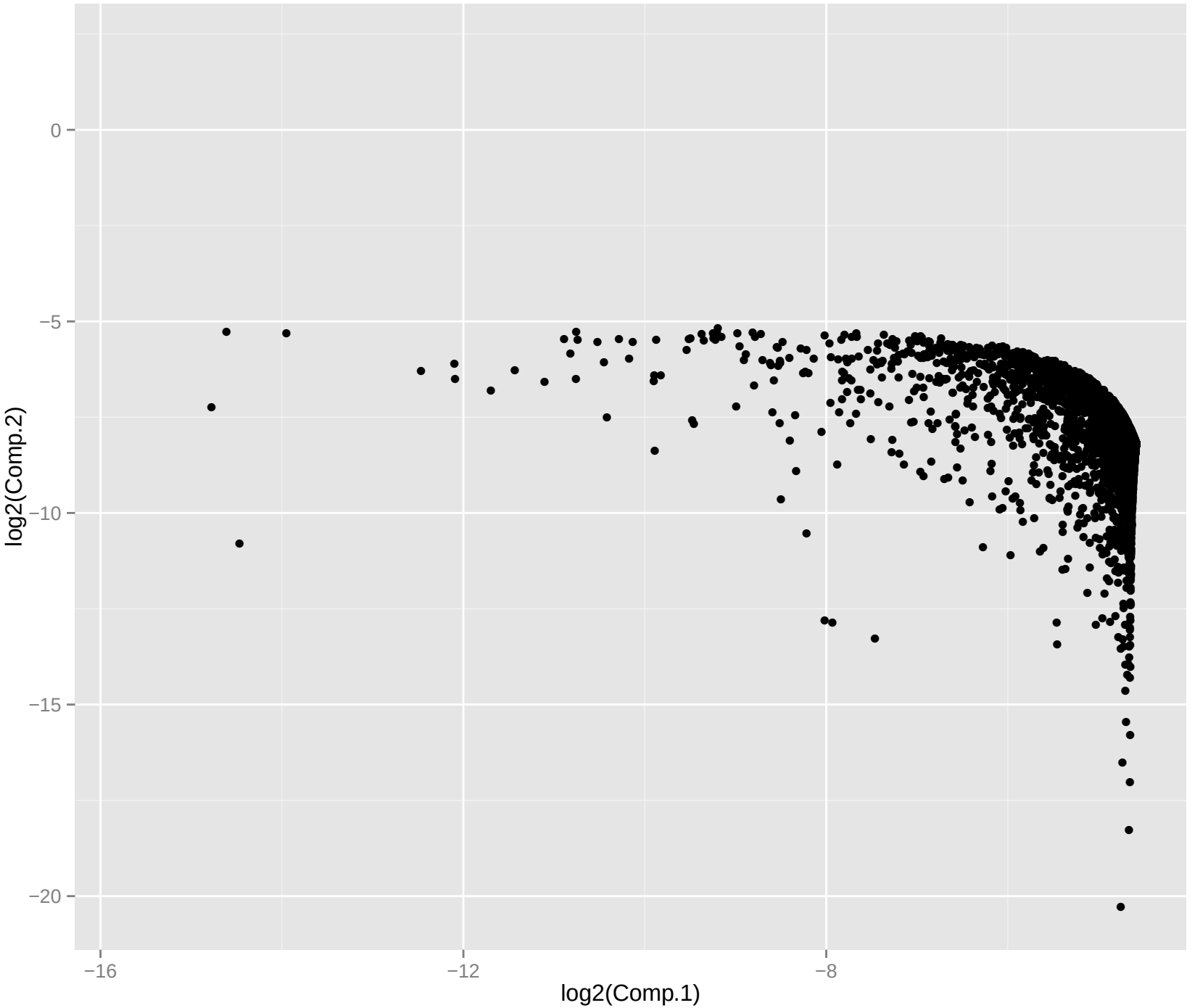

count
1000
500
0
−20
−15
−10
−5
0
Comp.1

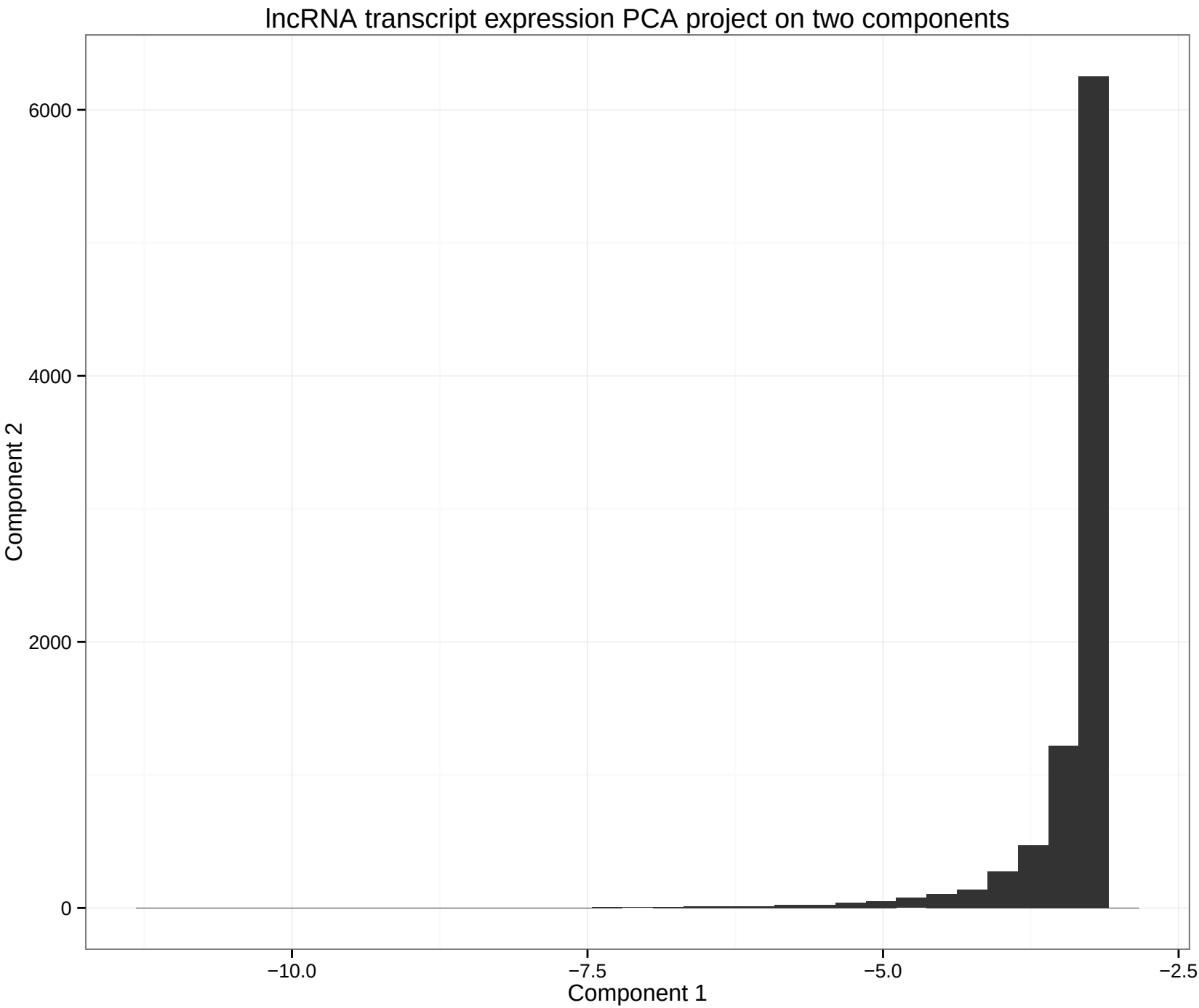

count
1000
500
0
−20
−15
−10
−5
0
Comp.1

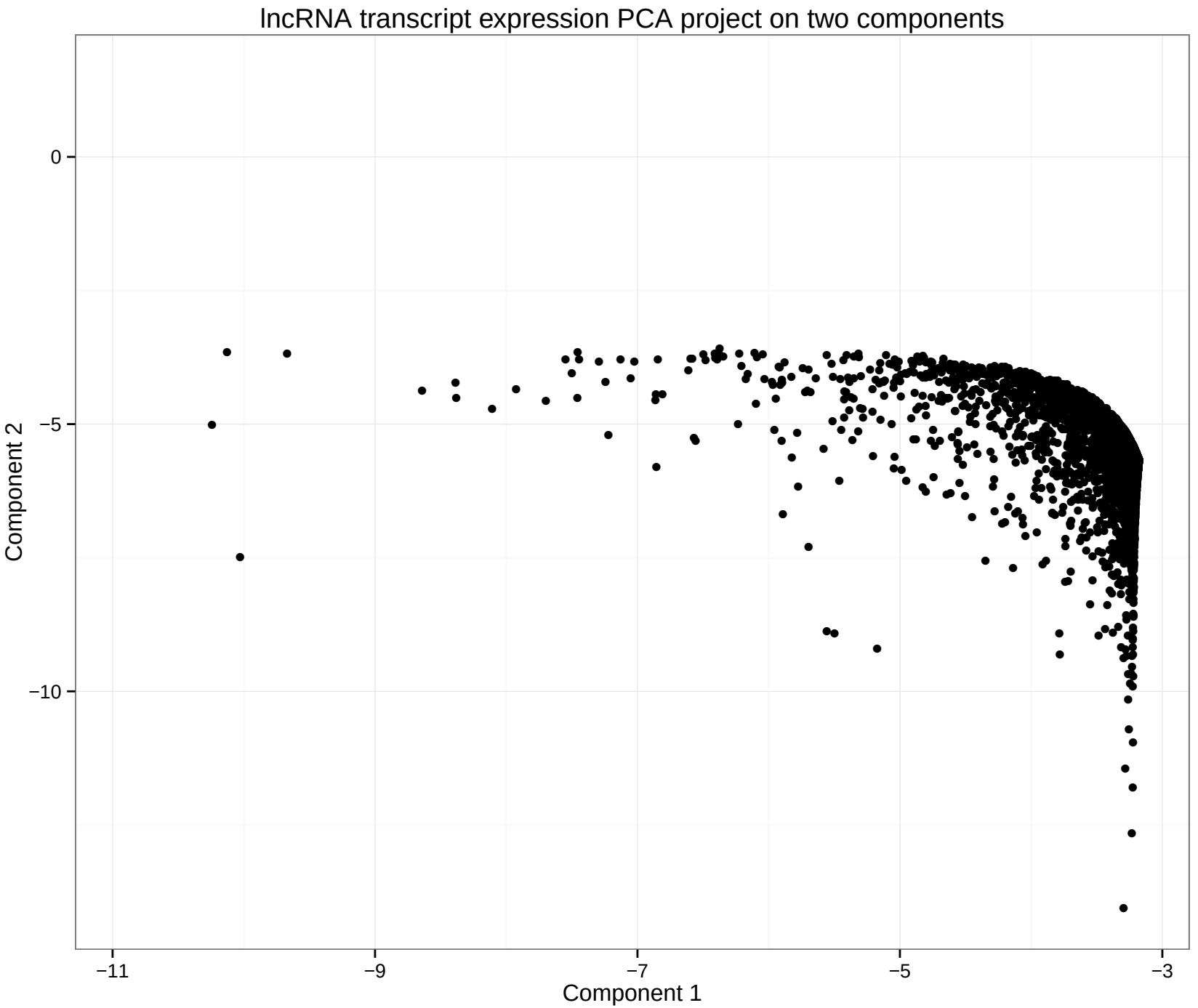

6000
4000
2000
0
count
−16
−12
−8
−4
log2(Comp.1)

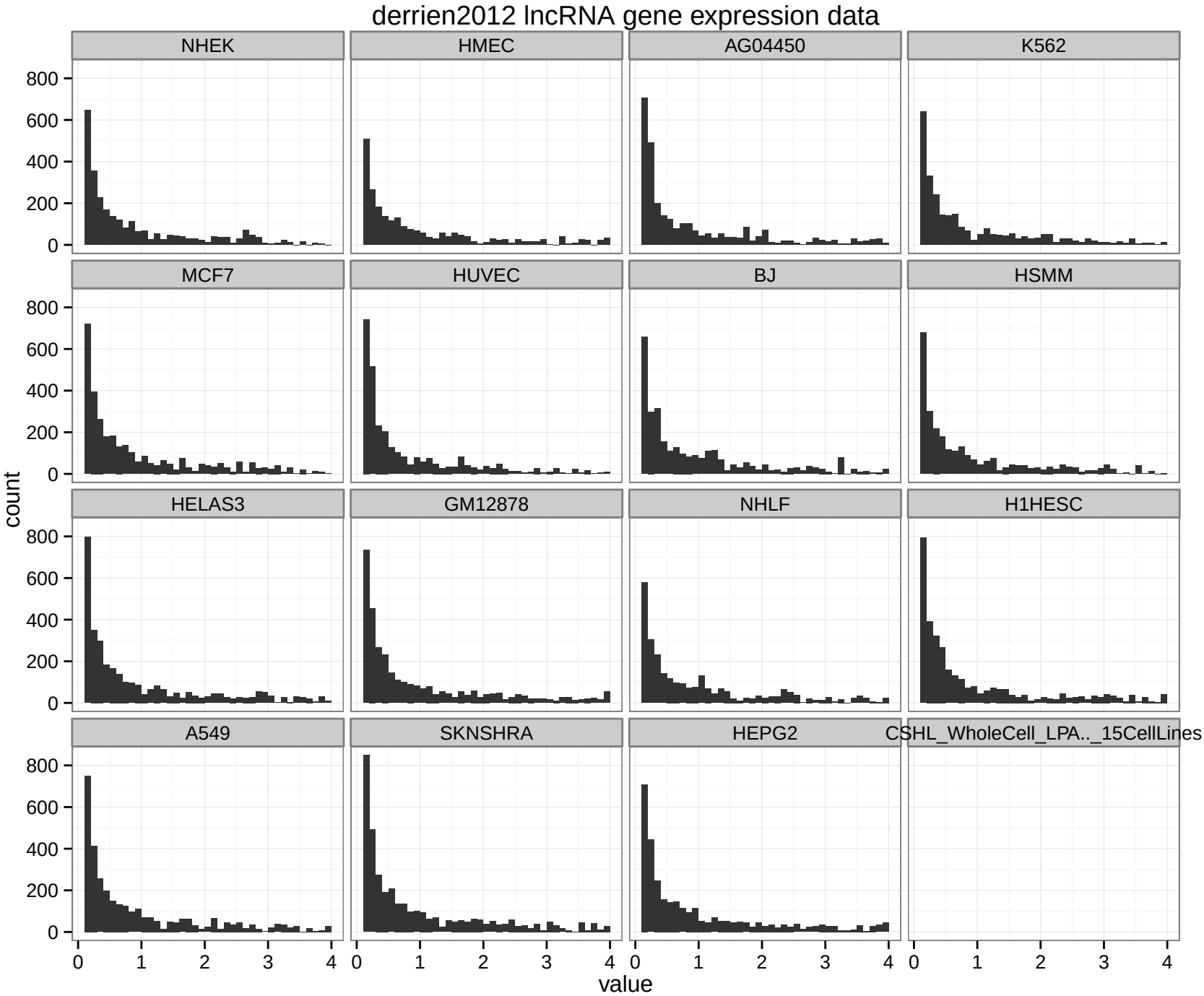

log2(Comp.2)
log2(Comp.1)

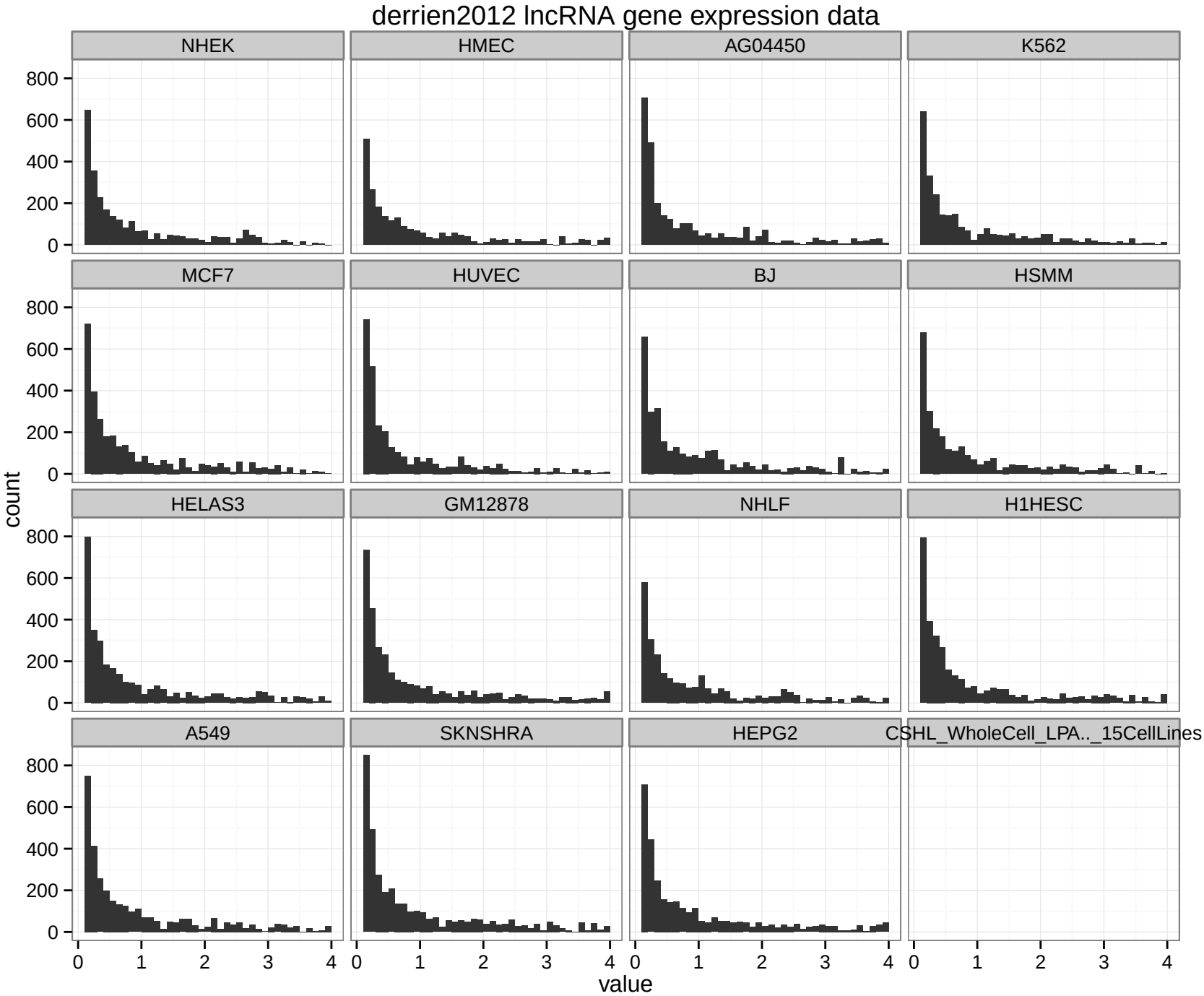

log2(Comp.2)
log2(Comp.1)

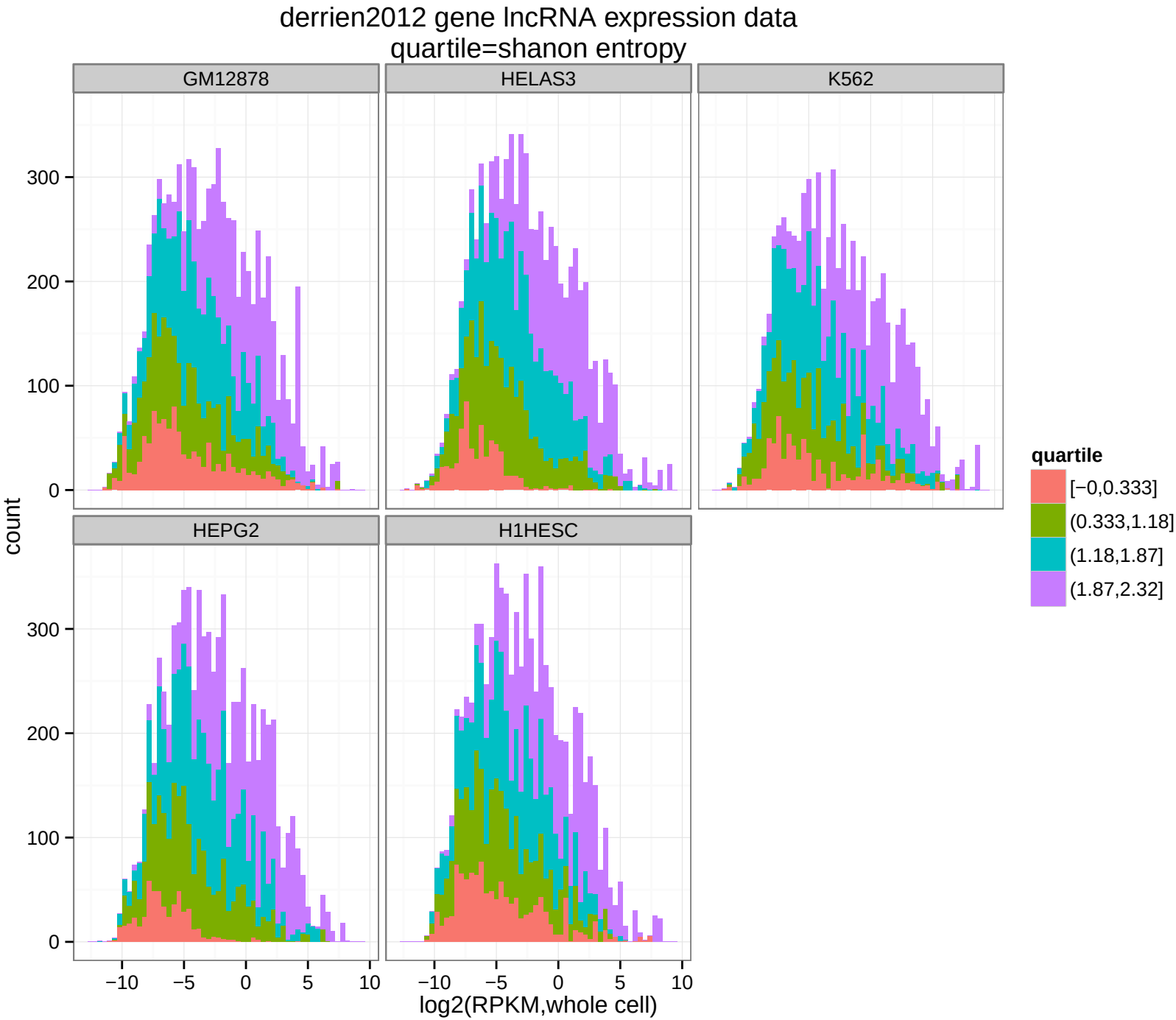

0
−5
−10
−15
−20
log2(Comp.2)
−16
−12
−8
log2(Comp.1)

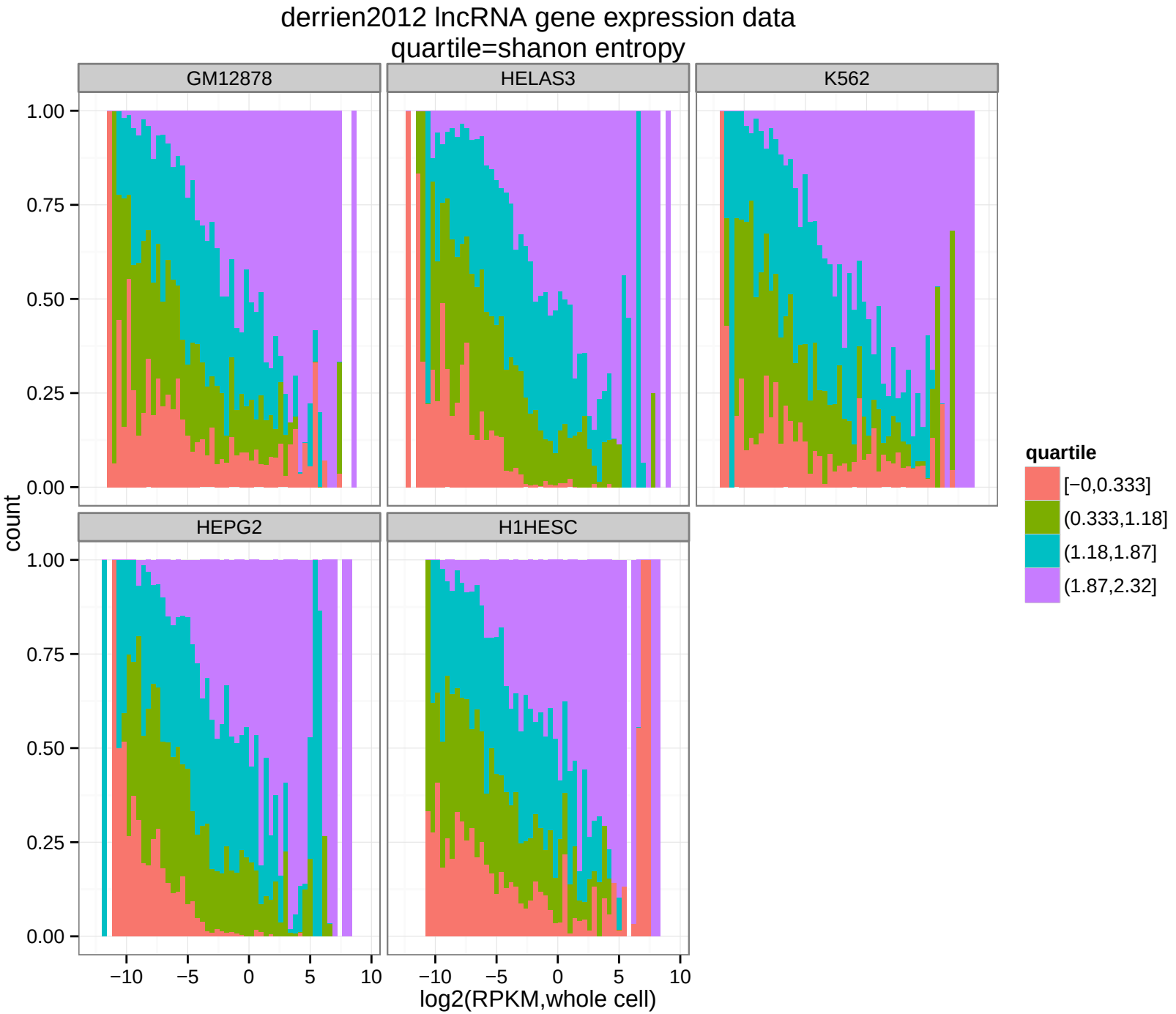

lncRNA transcript expression PCA project on two components
6000
4000
2000
0
Component 2
−10.0
−7.5
−5.0
−2.5
Component 1

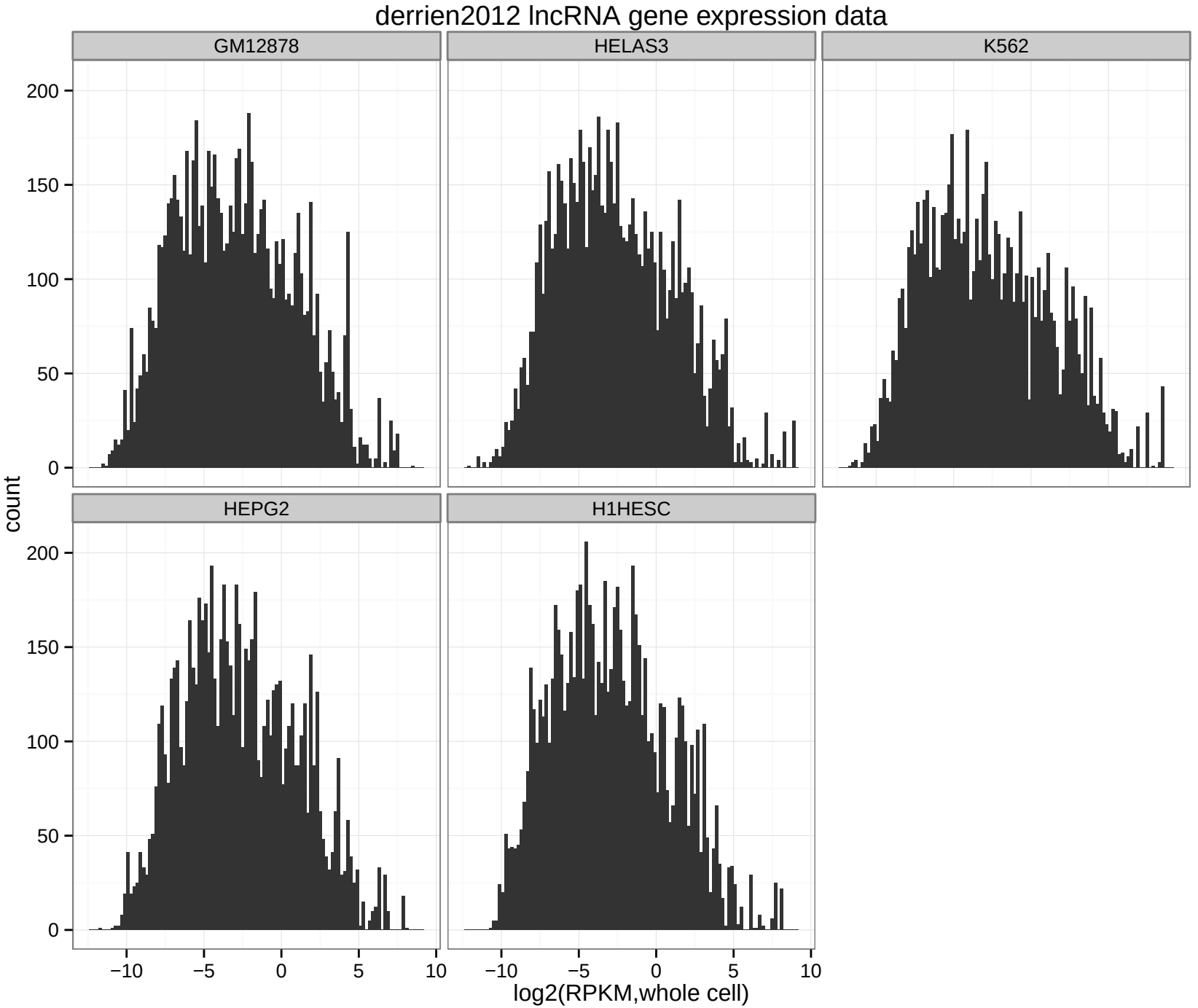

lncRNA transcript expression PCA project on two components
0
−5
−10
Component 2
−11
−9
−7
−5
−3
Component 1

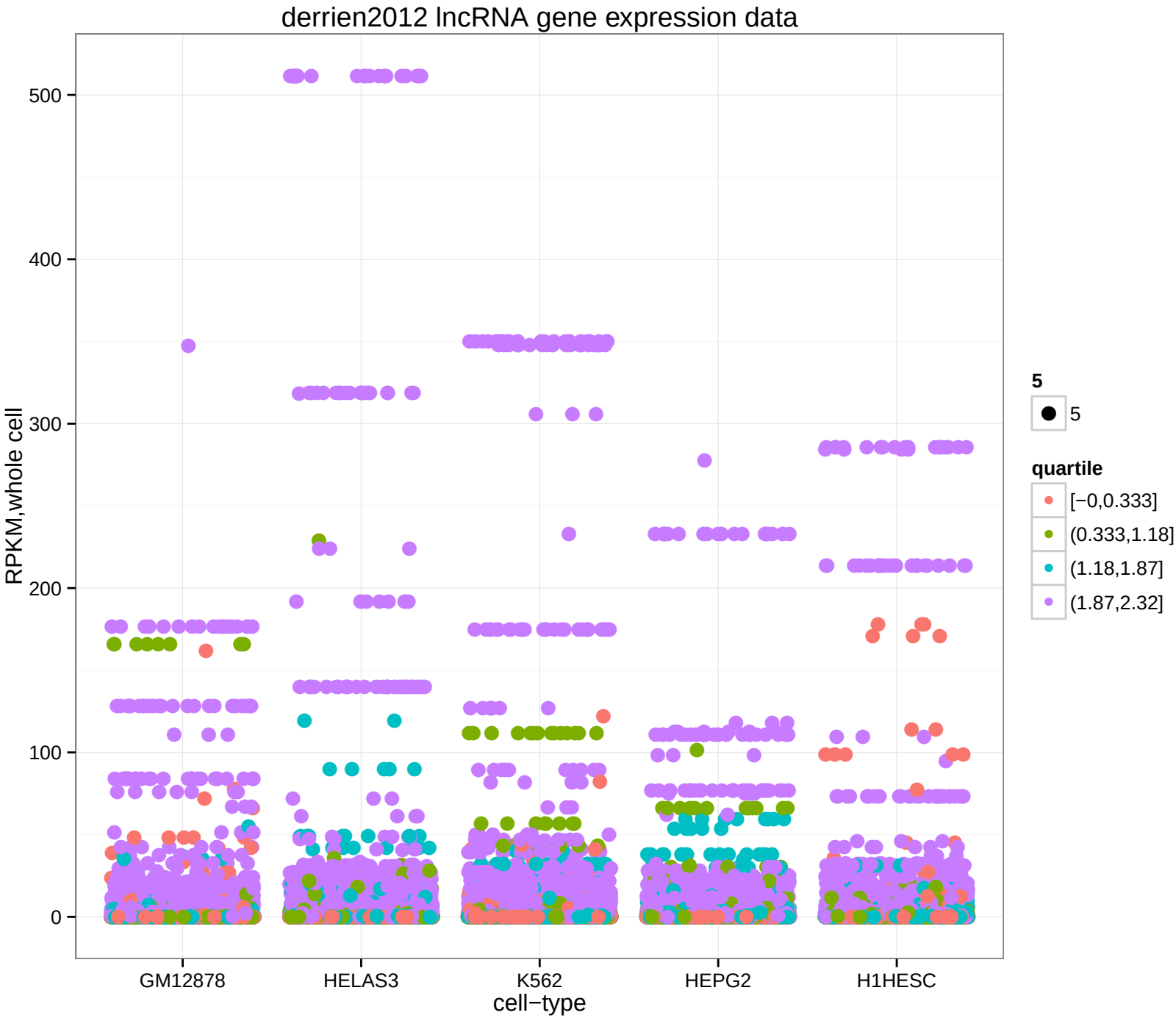

derrien2012 lncRNA gene expression data
NHEK
HMEC
AG04450
K562
MCF7
HUVEC
BJ
HSMM
HELAS3
GM12878
NHLF
H1HESC
A549
SKNSHRA
HEPG2
CSHL_WholeCell_LPA.._15CellLines
count
value
0
200
400
600
800
0
1
2
3
4

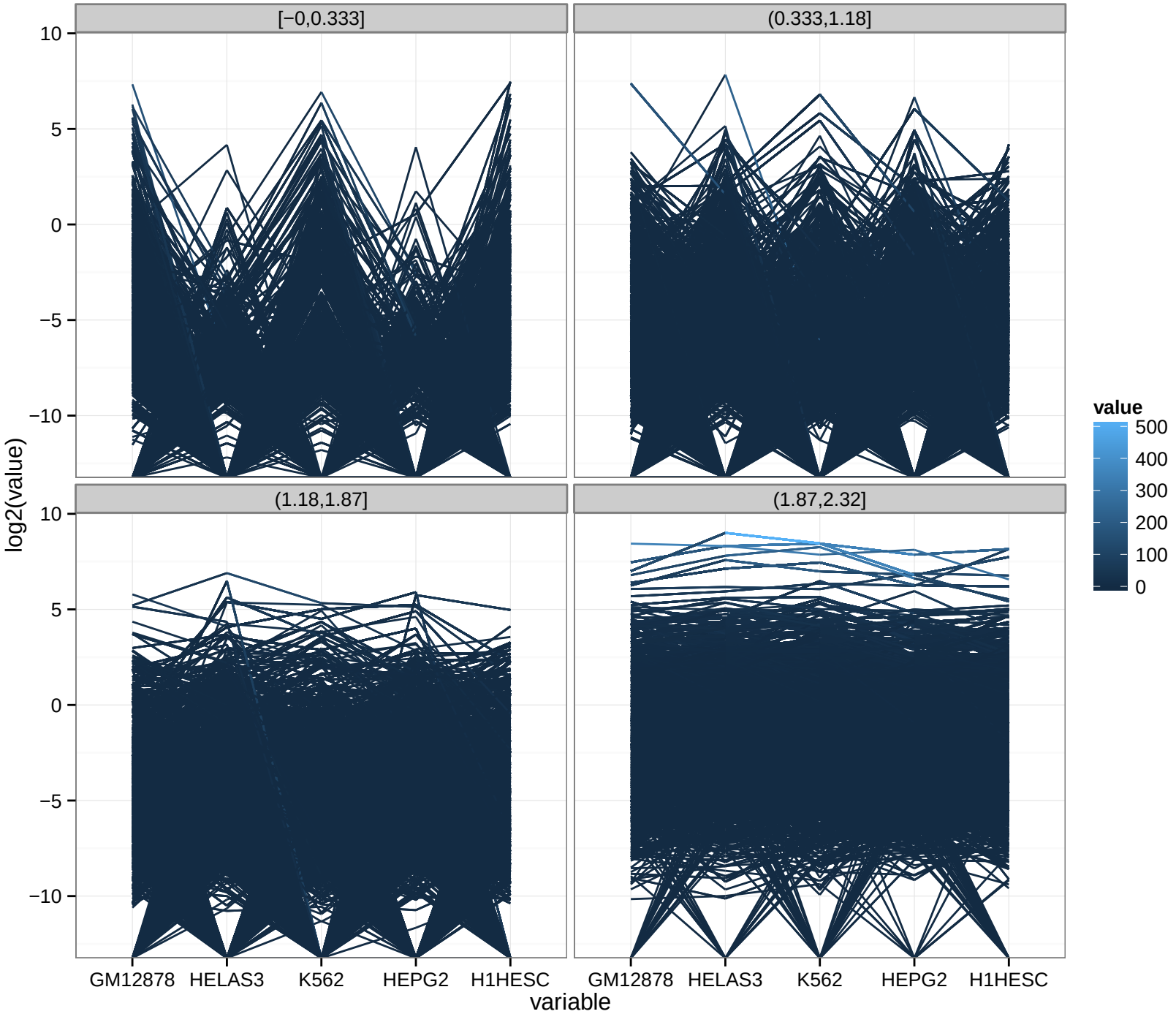

derrien2012 lncRNA gene expression data
NHEK
HMEC
AG04450
K562
MCF7
HUVEC
BJ
HSMM
HELAS3
GM12878
NHLF
H1HESC
A549
SKNSHRA
HEPG2
CSHL_WholeCell_LPA.._15CellLines
count
value
0
200
400
600
800
0
1
2
3
4

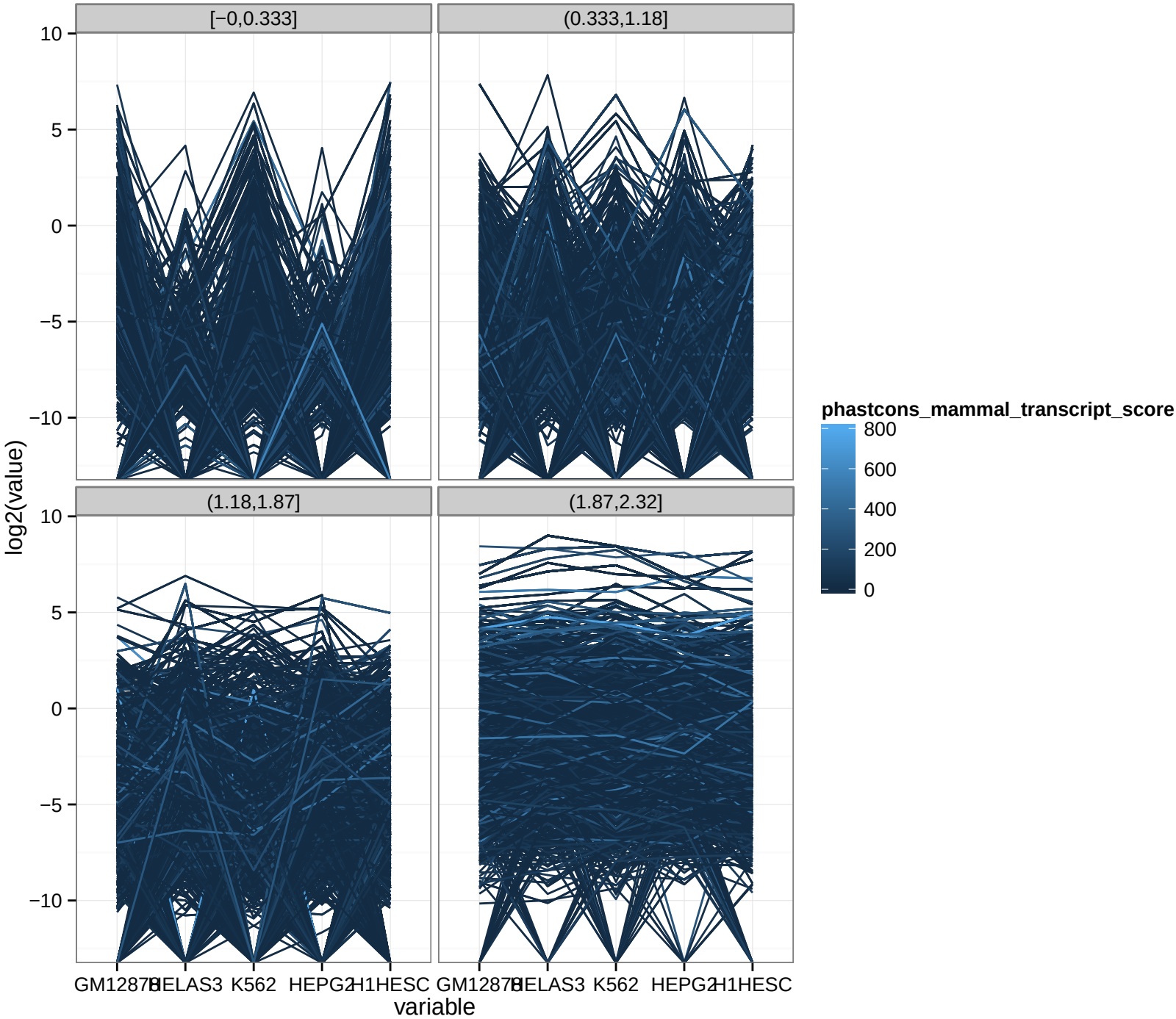

derrien2012 gene lncRNA expression data
quartile=shanon entropy
GM12878
HELAS3
K562
HEPG2
H1HESC
count
300
200
100
0
−10
−5
0
5
10
log2(RPKM,whole cell)
quartile
[−0,0.333]
(0.333,1.18]
(1.18,1.87]
(1.87,2.32]


derrien2012 lncRNA gene expression data
quartile=shanon entropy
GM12878
HELAS3
K562
HEPG2
H1HESC
count
1.00
0.75
0.50
0.25
0.00
−10
−5
0
5
10
log2(RPKM,whole cell)
quartile
[−0,0.333]
(0.333,1.18]
(1.18,1.87]
(1.87,2.32]


derrien2012 lncRNA gene expression data
GM12878
HELAS3
K562
HEPG2
H1HESC
count
200
150
100
50
0
−10
−5
0
5
10
log2(RPKM,whole cell)


derrien2012 lncRNA gene expression data
RPKM,whole cell
500
400
300
200
100
0
GM12878
HELAS3
K562
HEPG2
H1HESC
cell−type
5
5
quartile
[−0,0.333]
(0.333,1.18]
(1.18,1.87]
(1.87,2.32]


[−0,0.333]
(0.333,1.18]
(1.18,1.87]
(1.87,2.32]
log2(value)
10
5
0
−5
−10
GM12878
HELAS3
K562
HEPG2
H1HESC
variable
value
500
400
300
200
100
0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(1.87,2.32]
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log2(value)
GM12878
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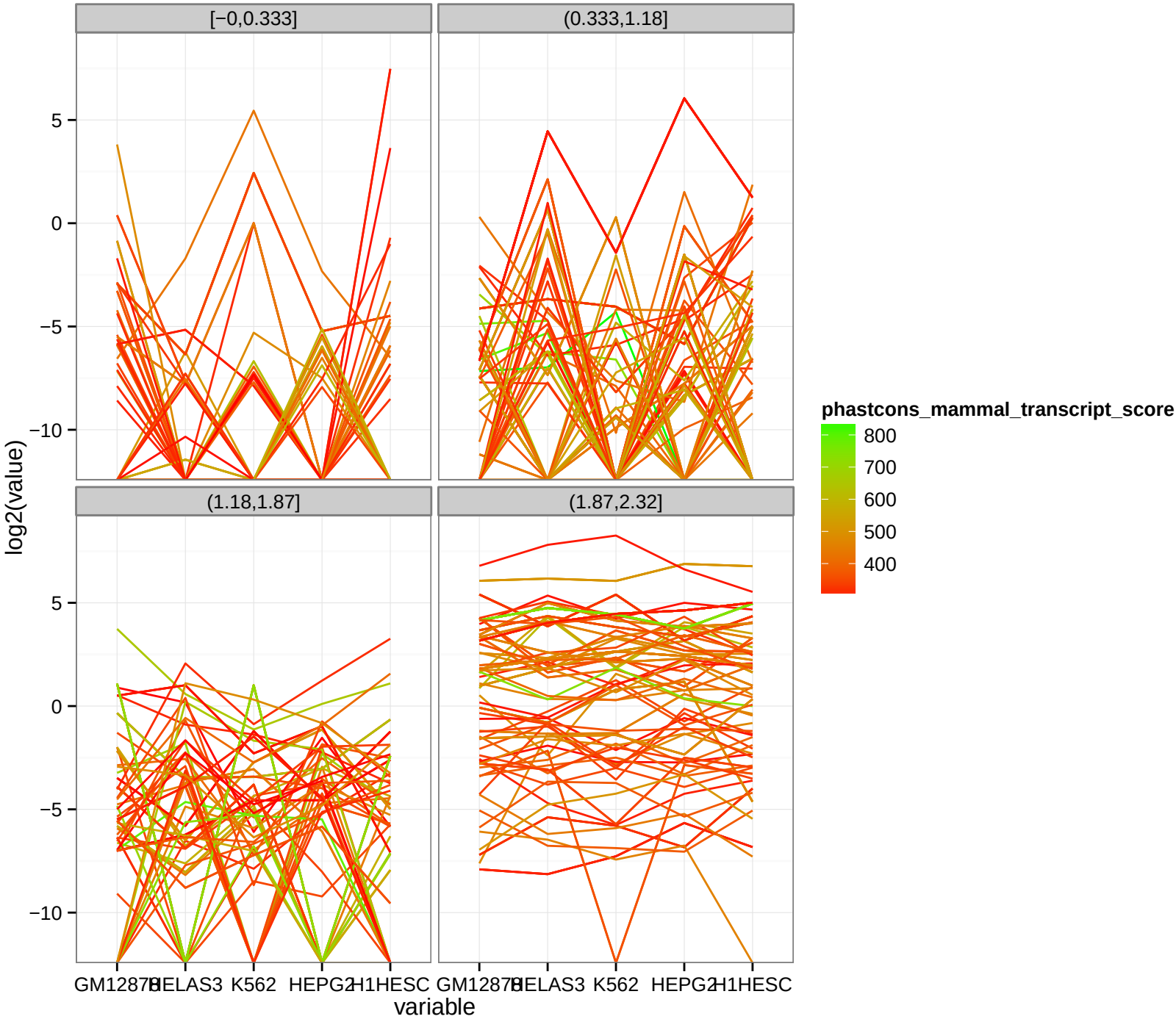
K562
HEPG2
H1HESC
variable
phastcons_mammal_transcript_score
800
600
400
200
0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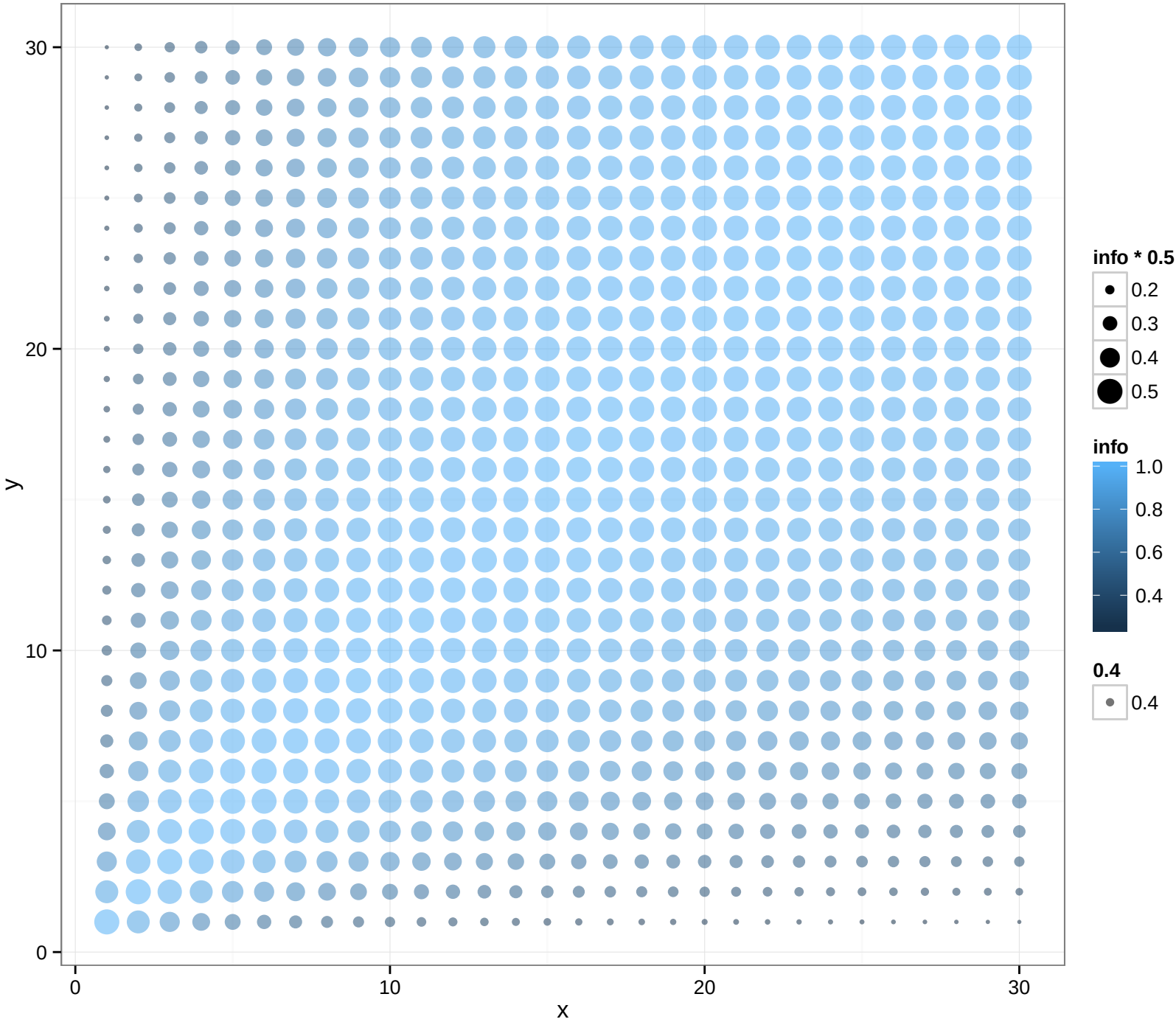
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30
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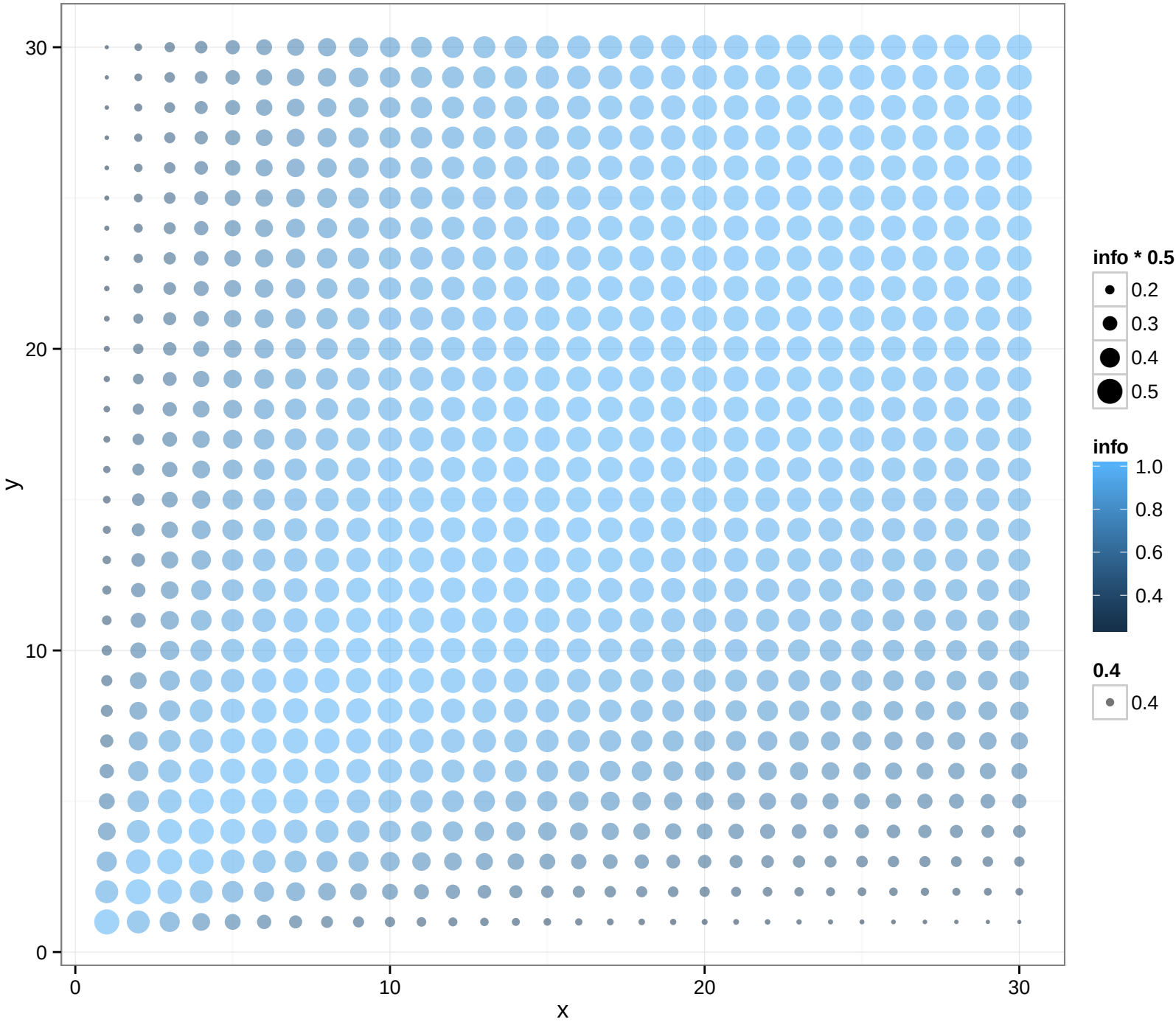
0.4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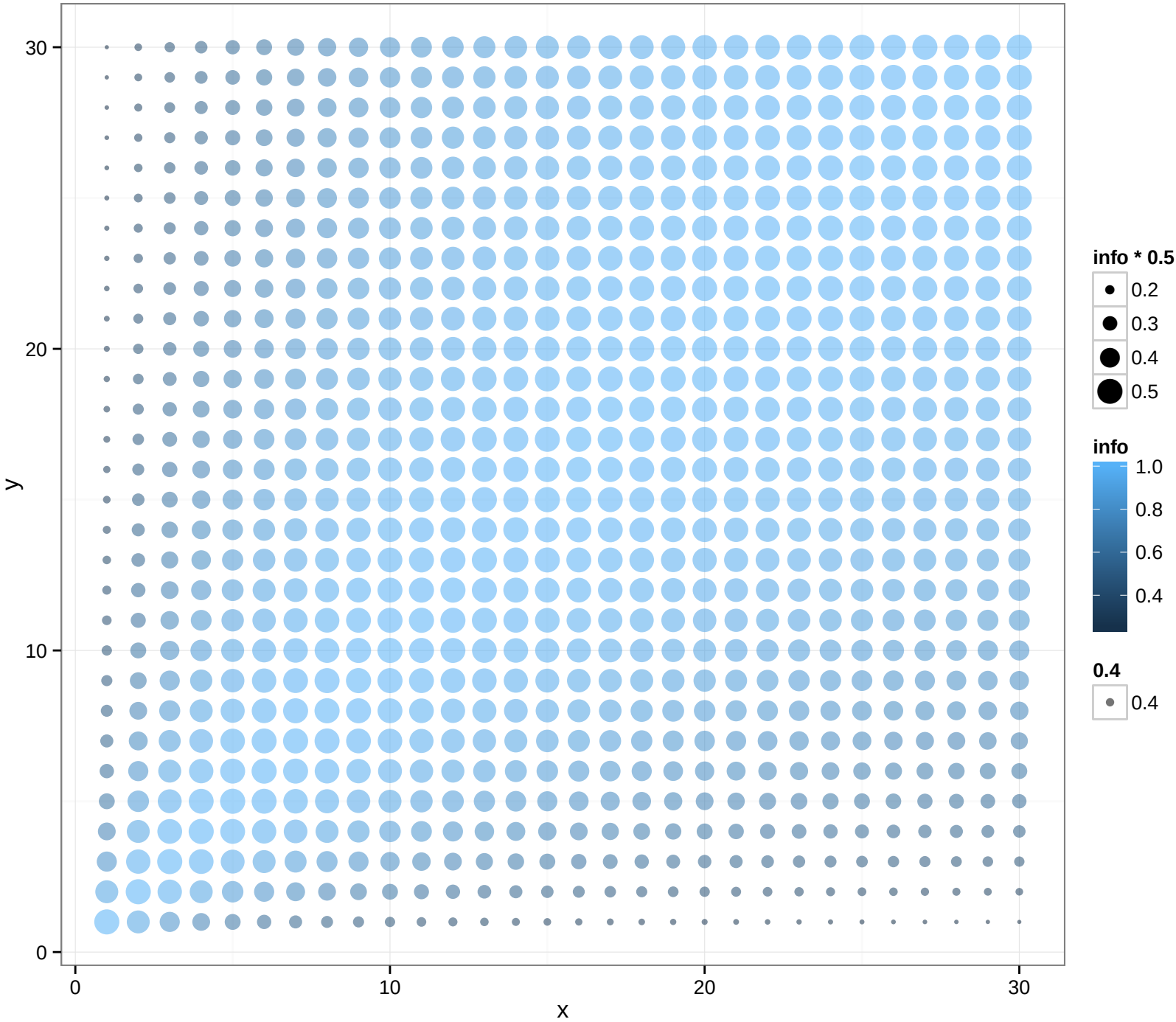
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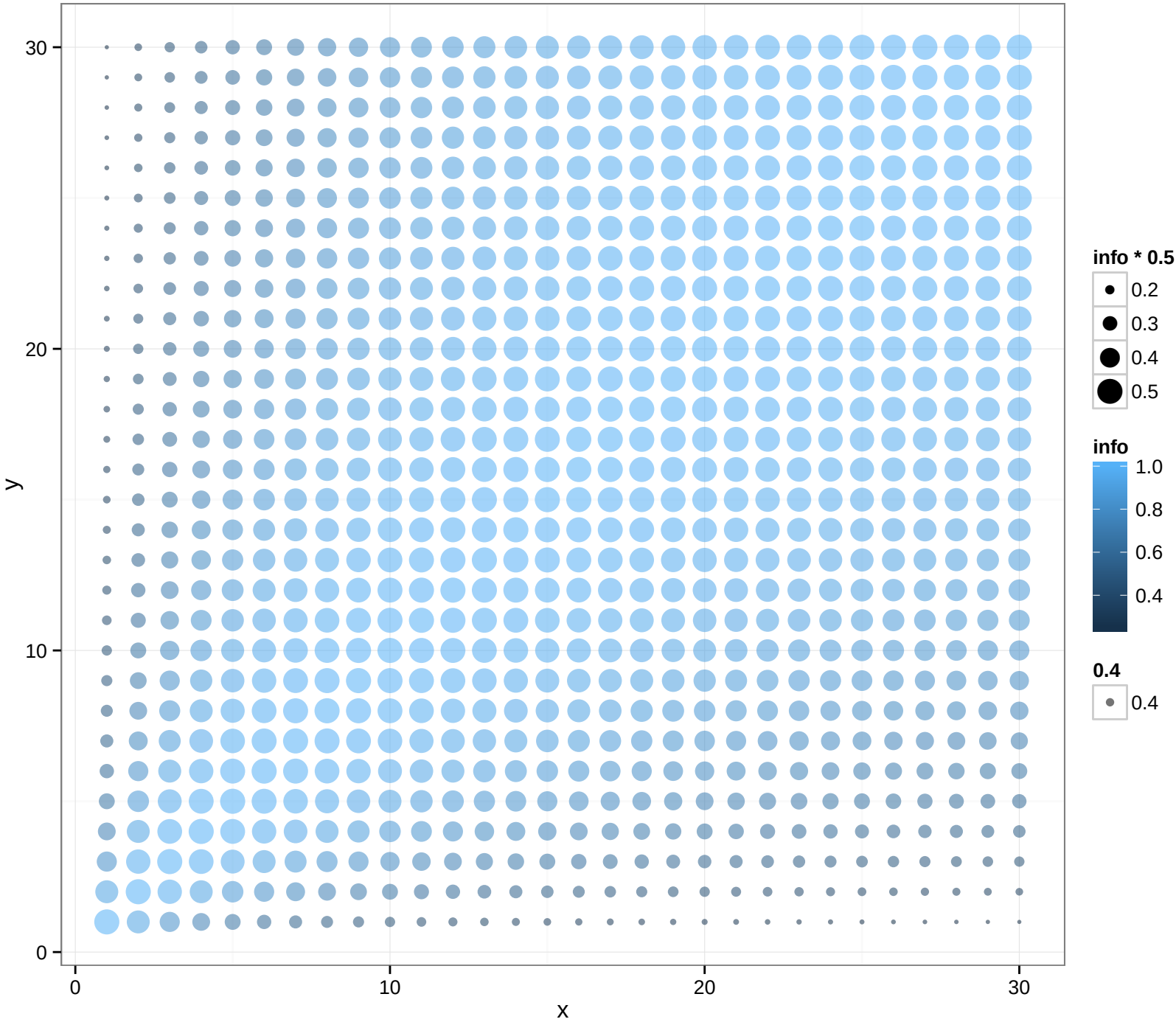
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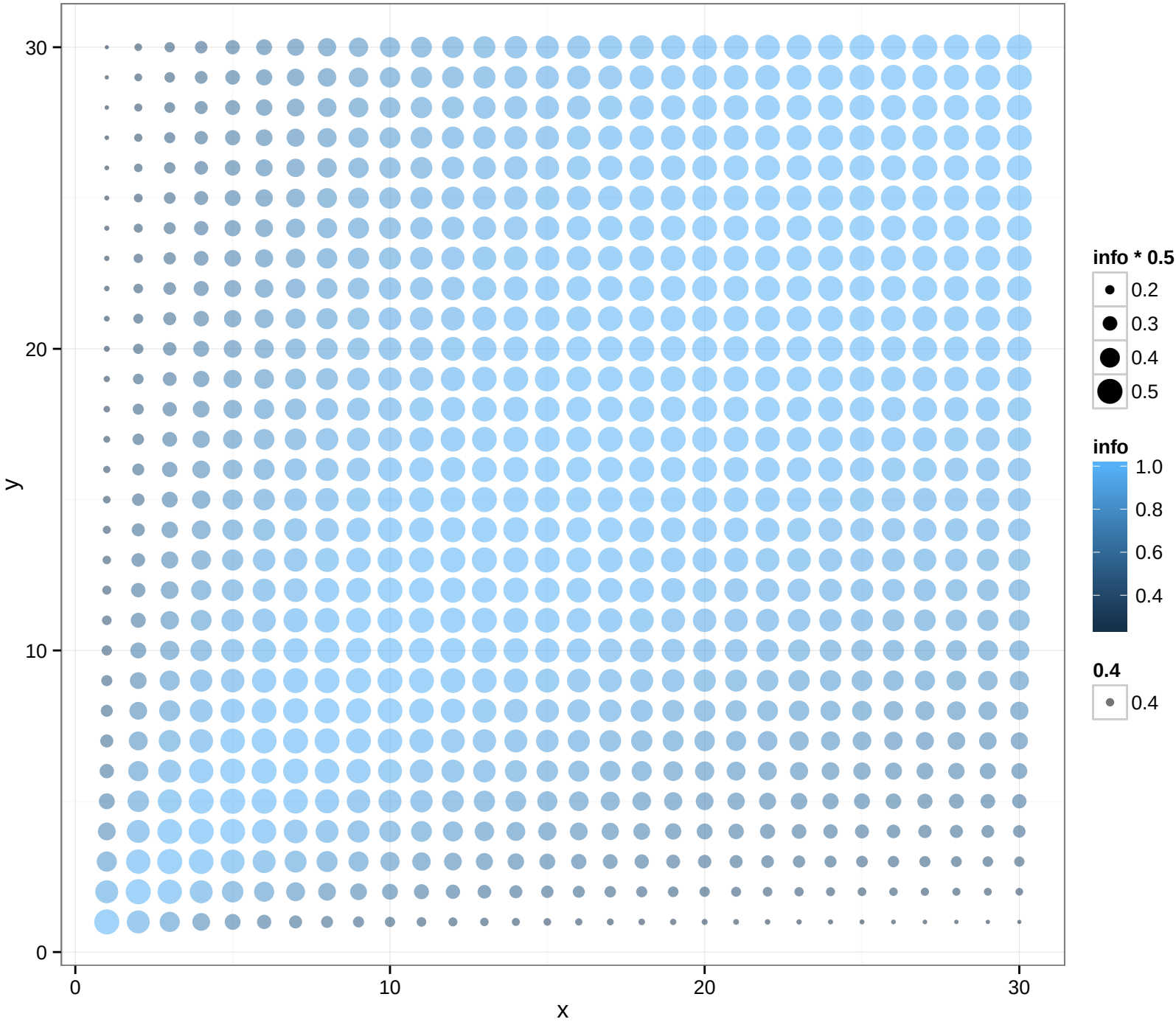
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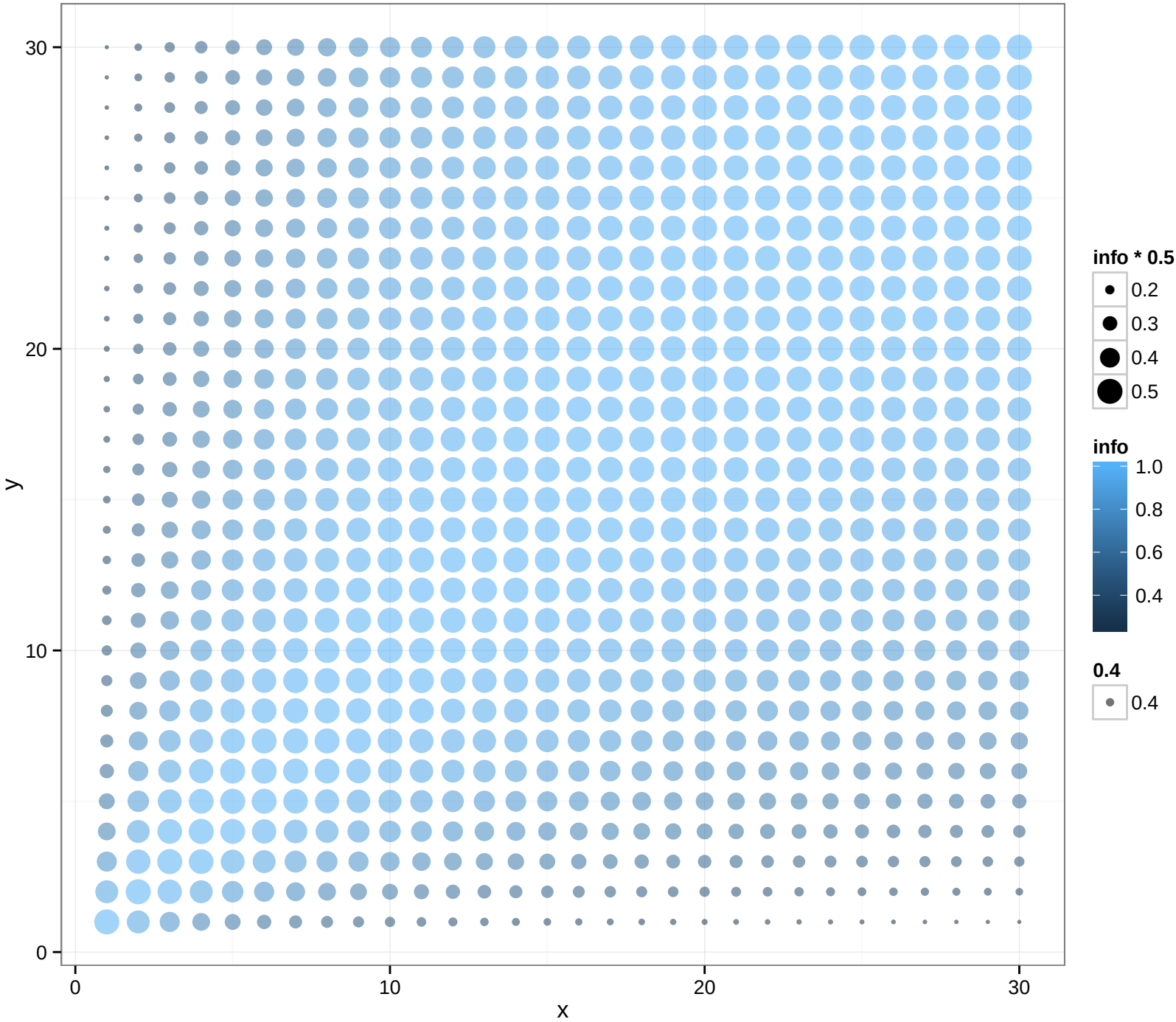
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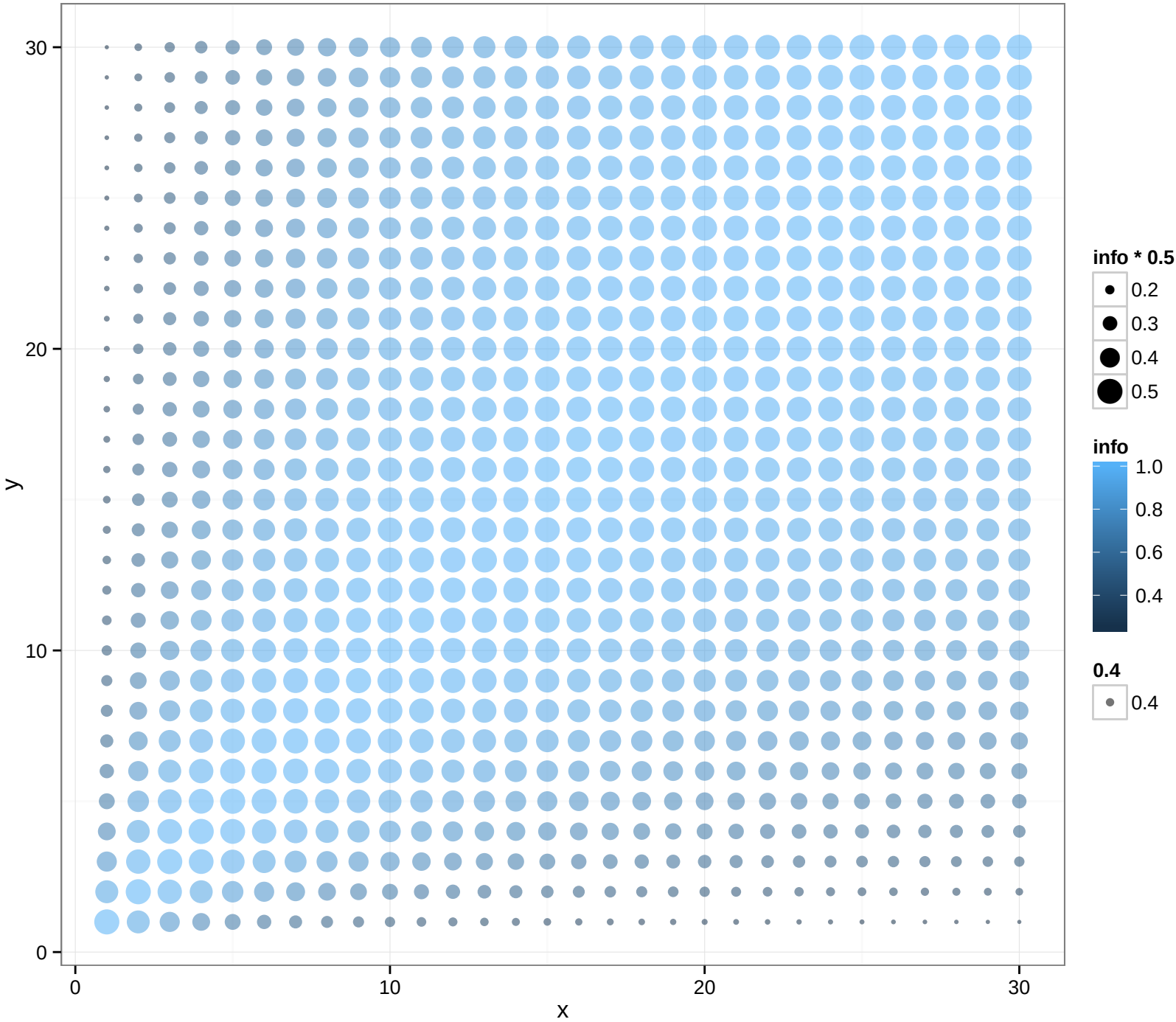
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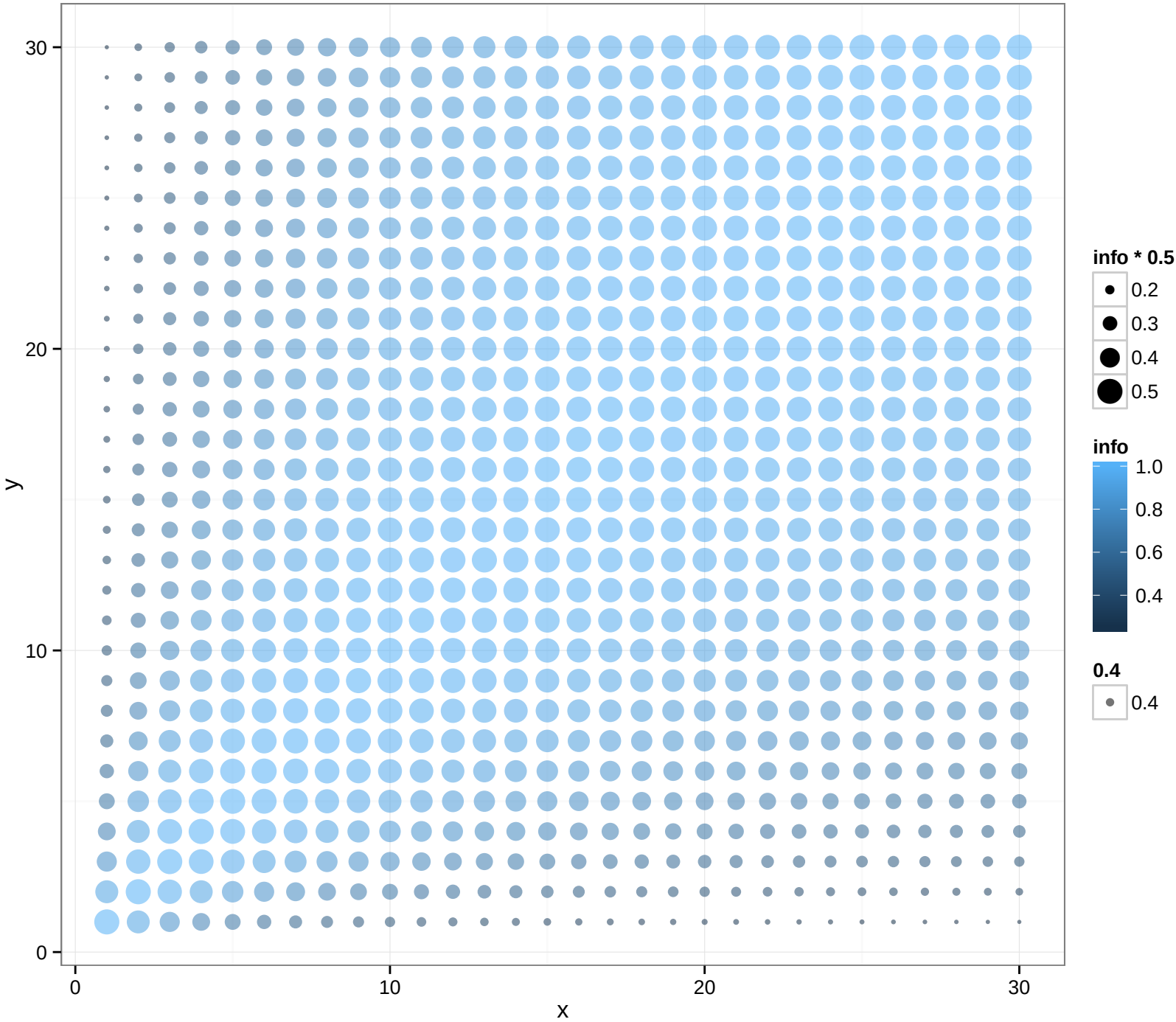
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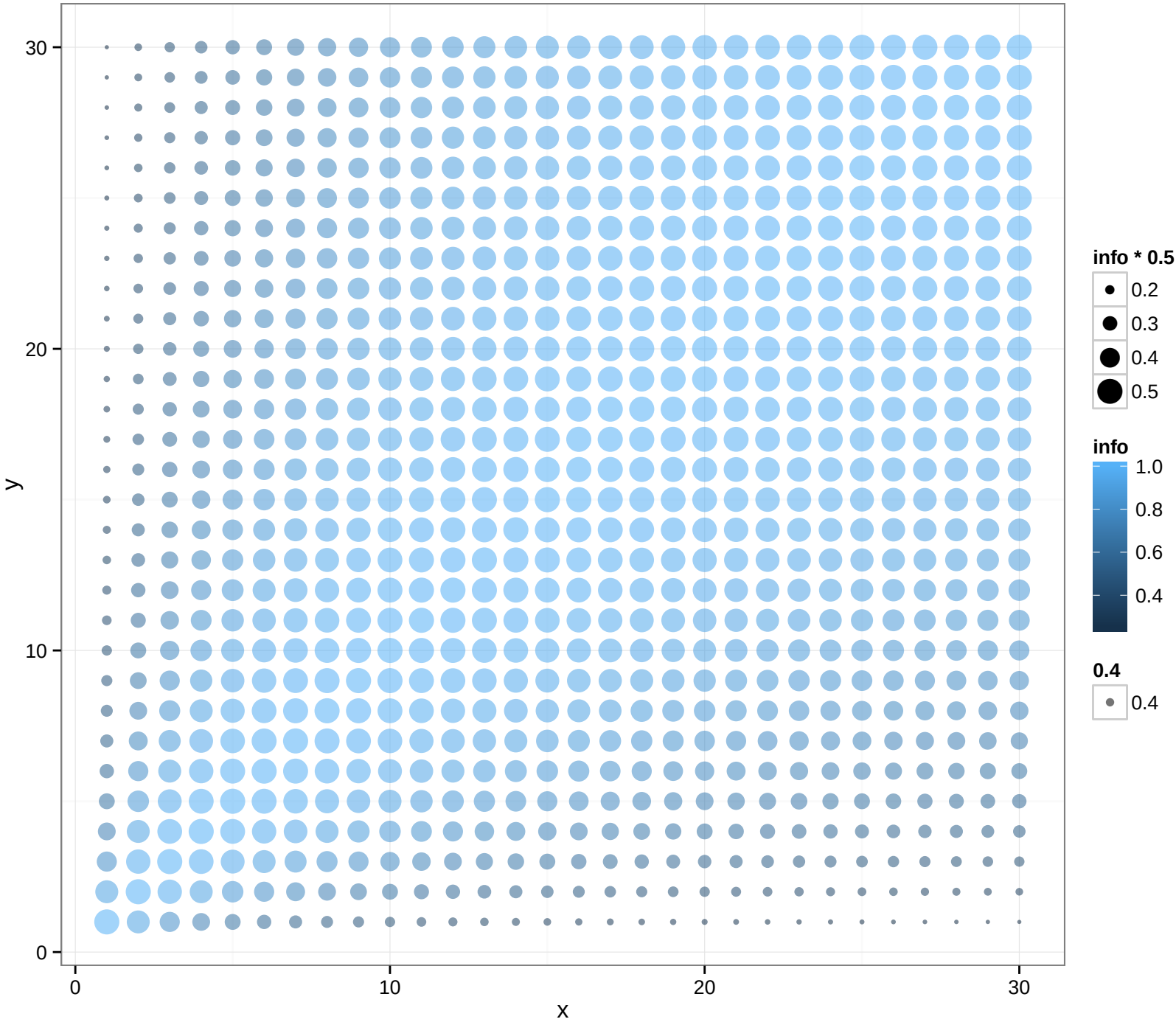
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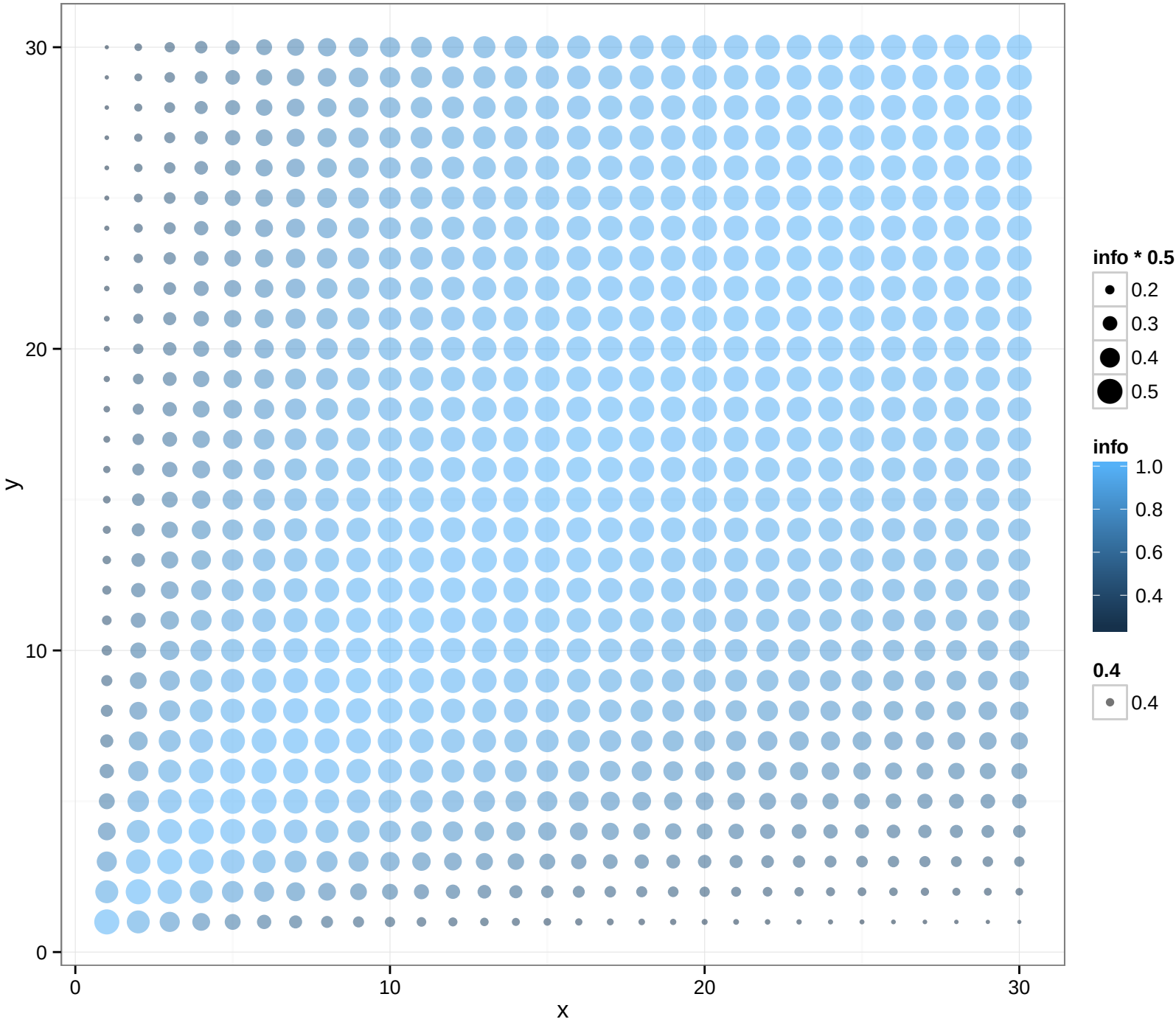
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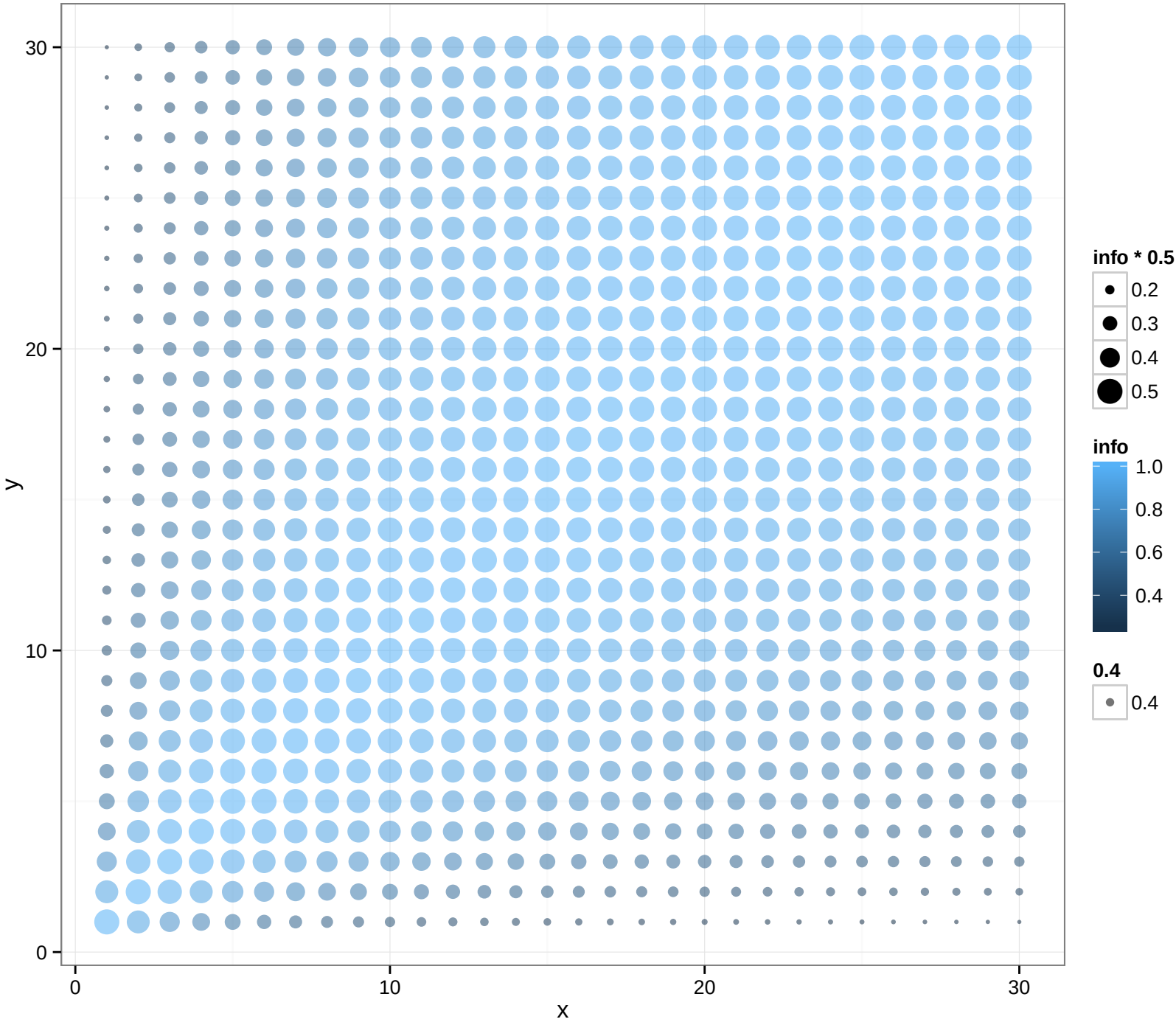
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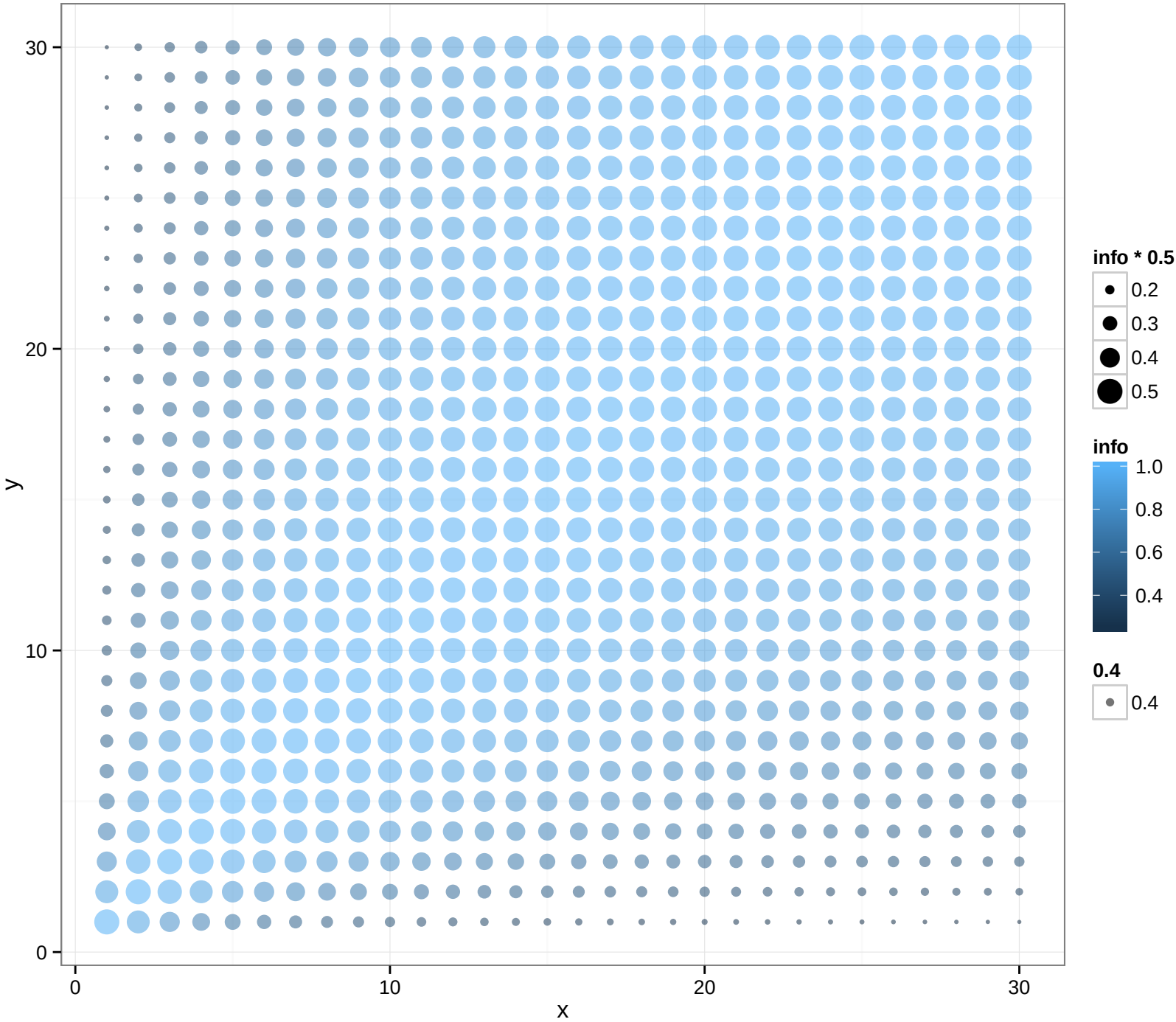
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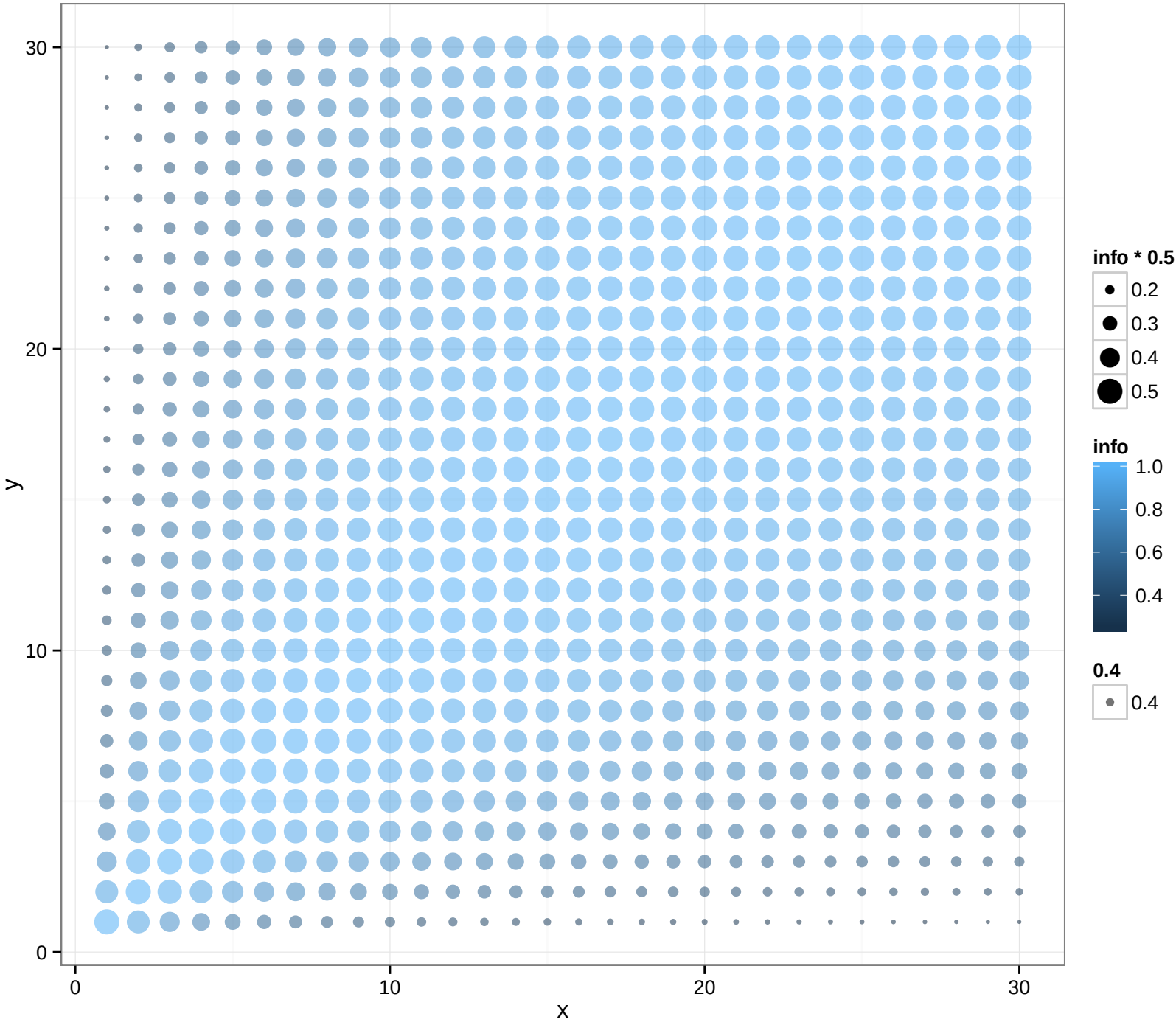
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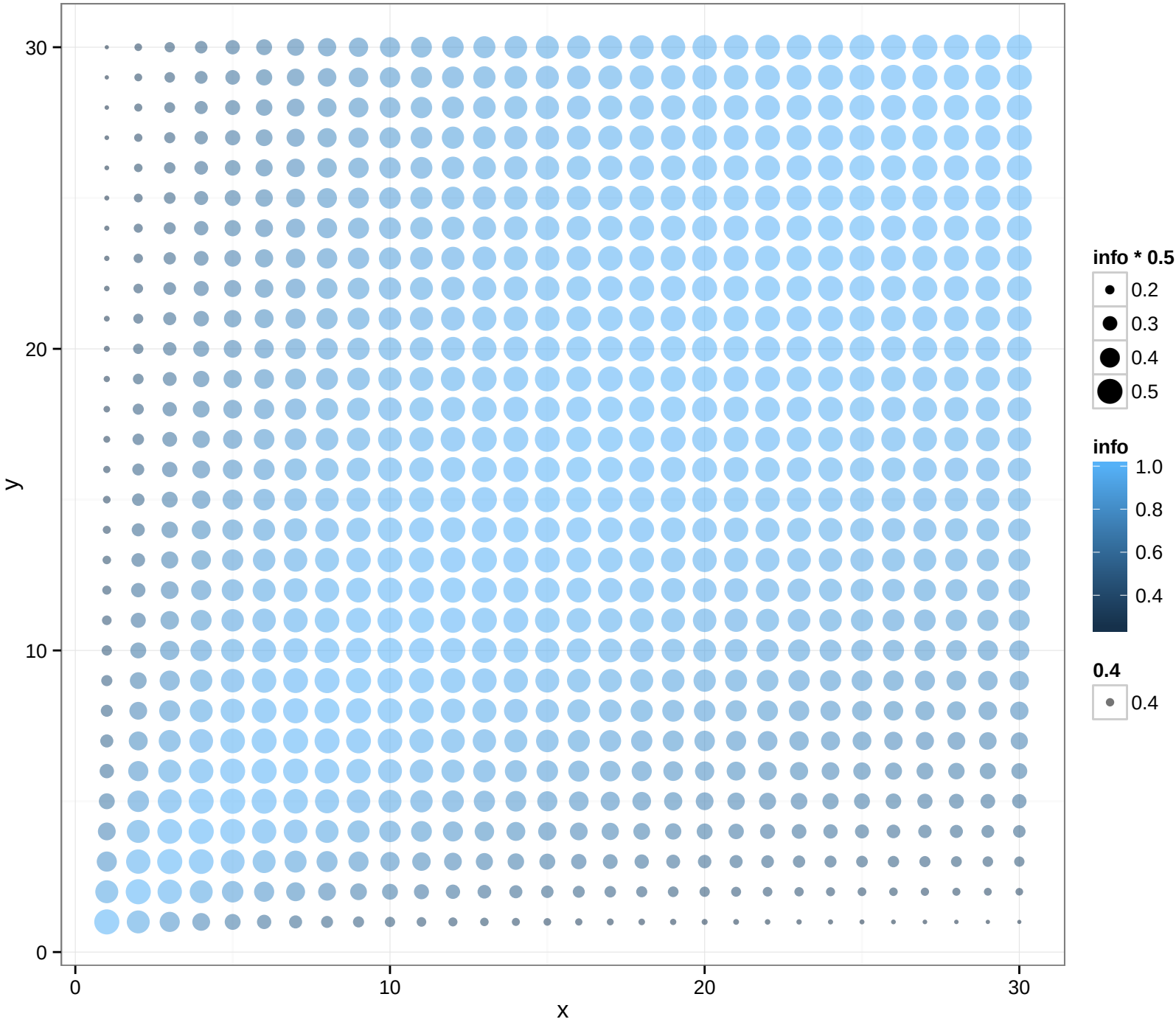
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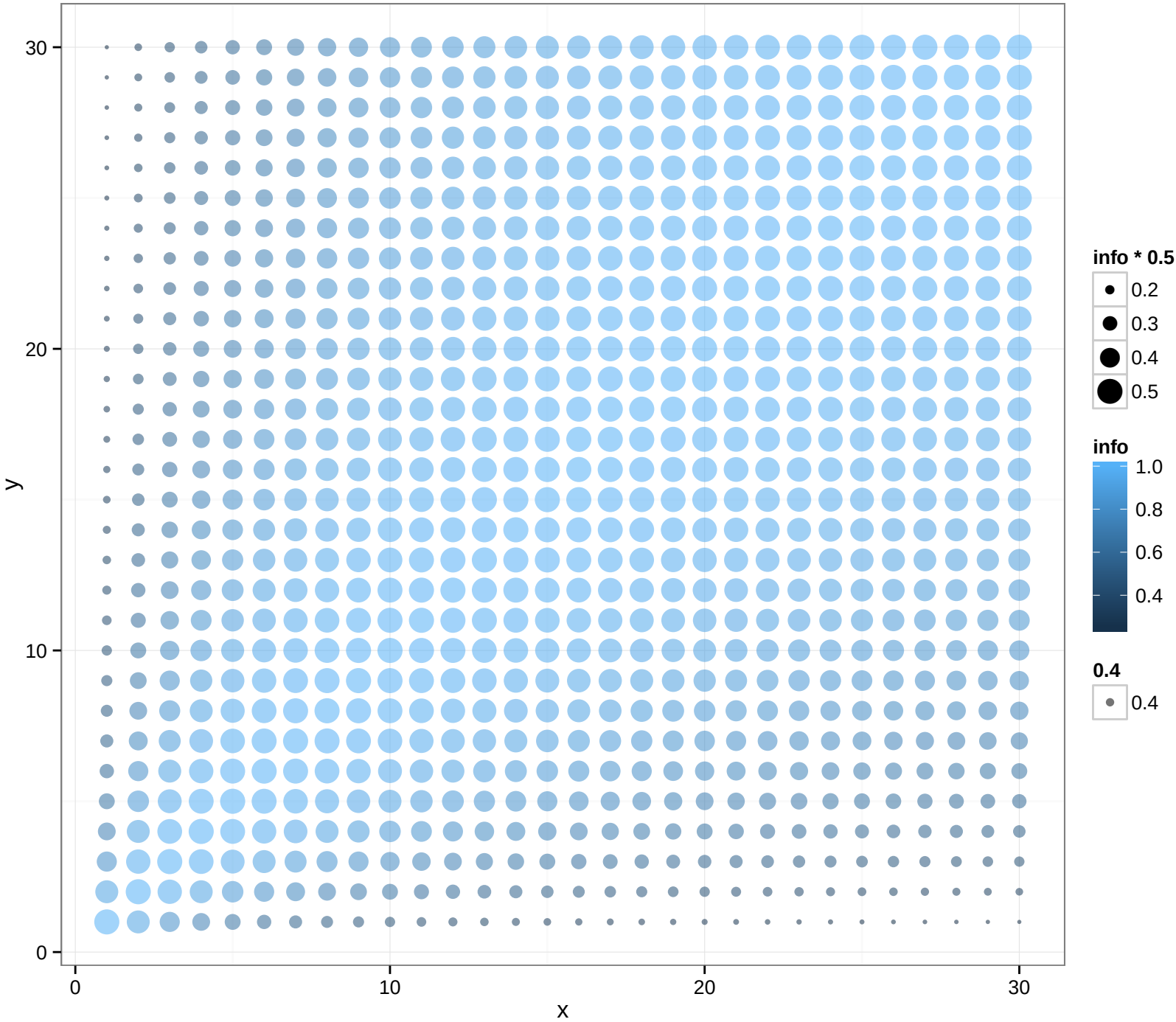
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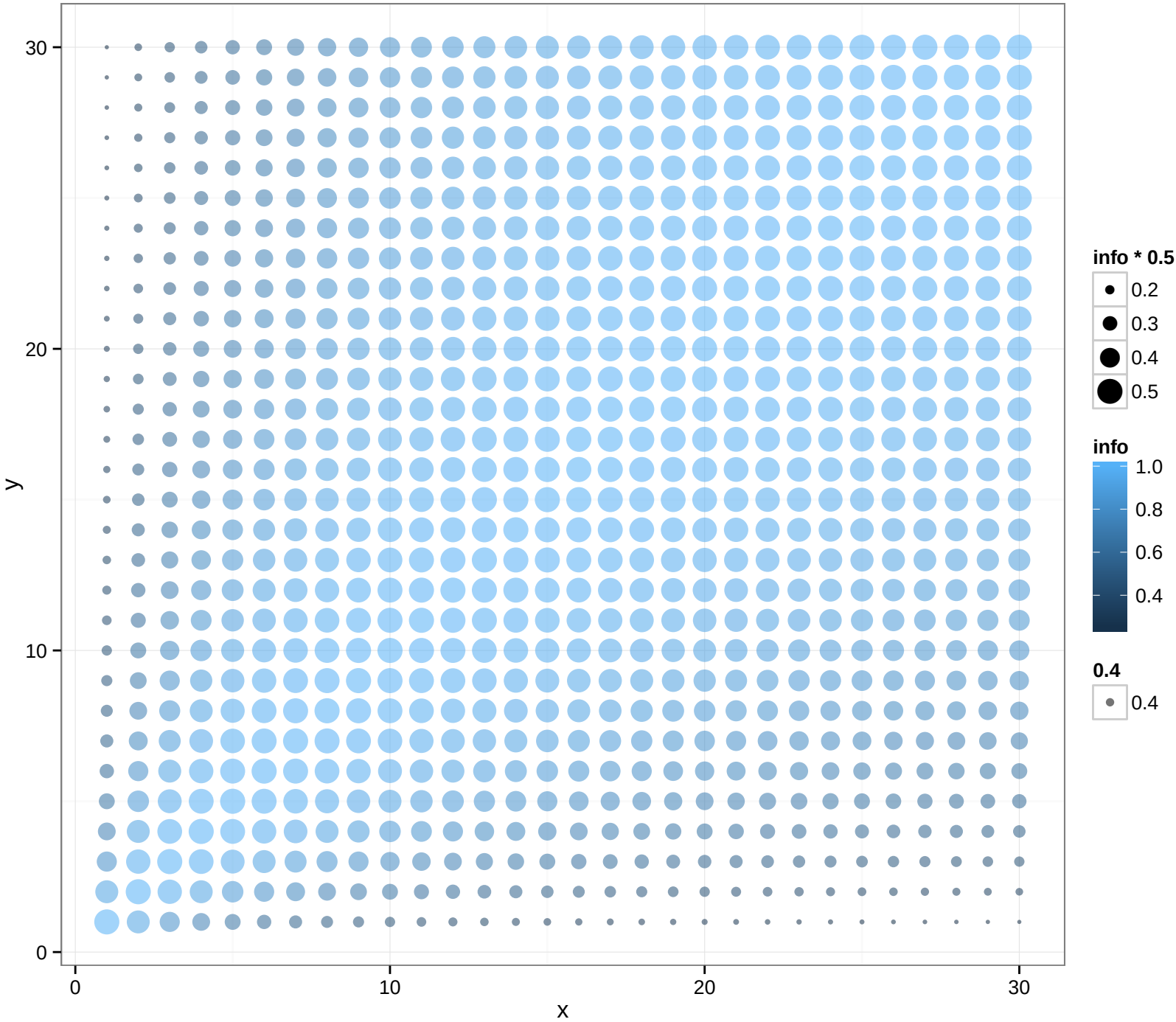
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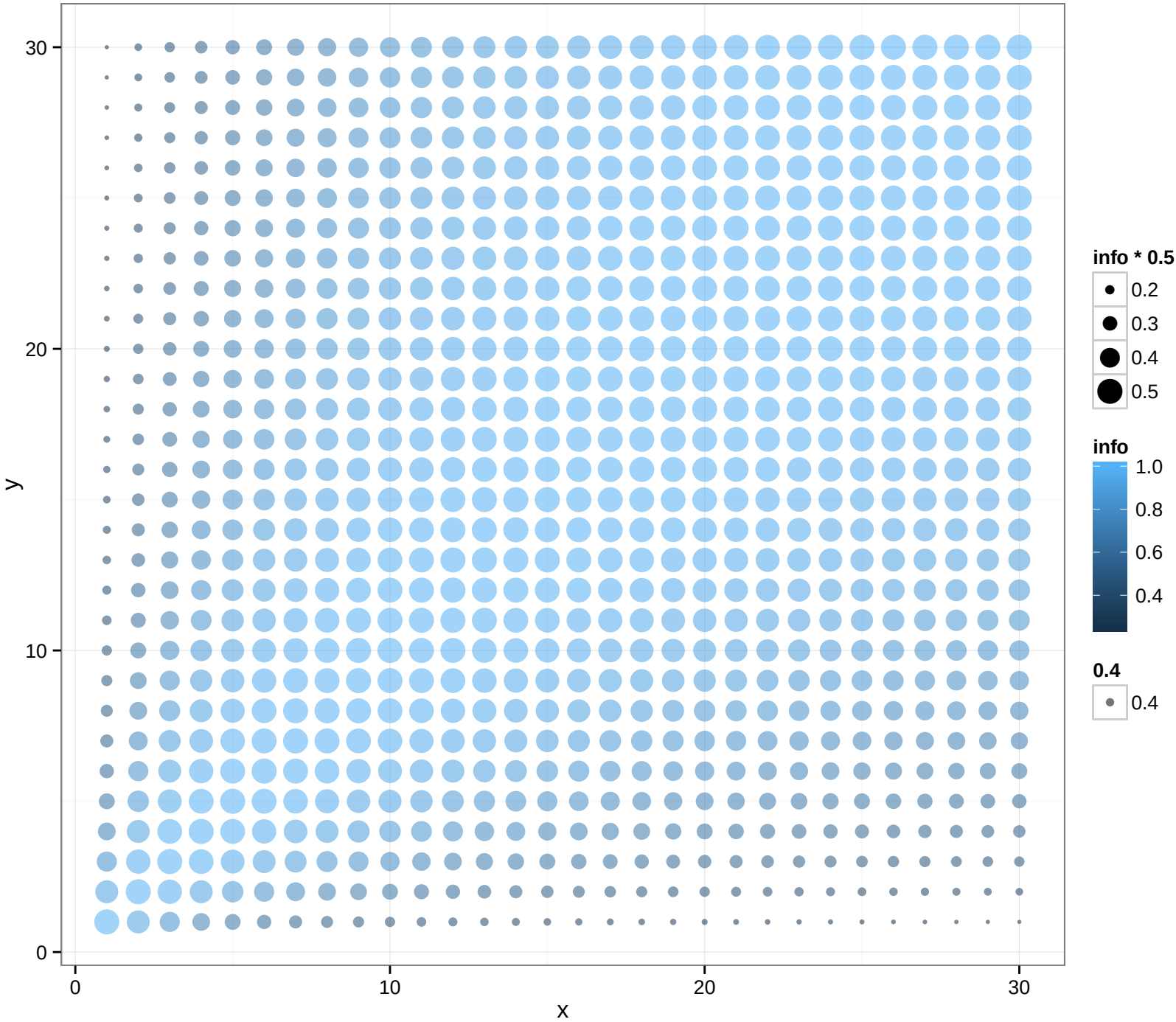
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y
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20
30
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info * 0.5
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info
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0.8
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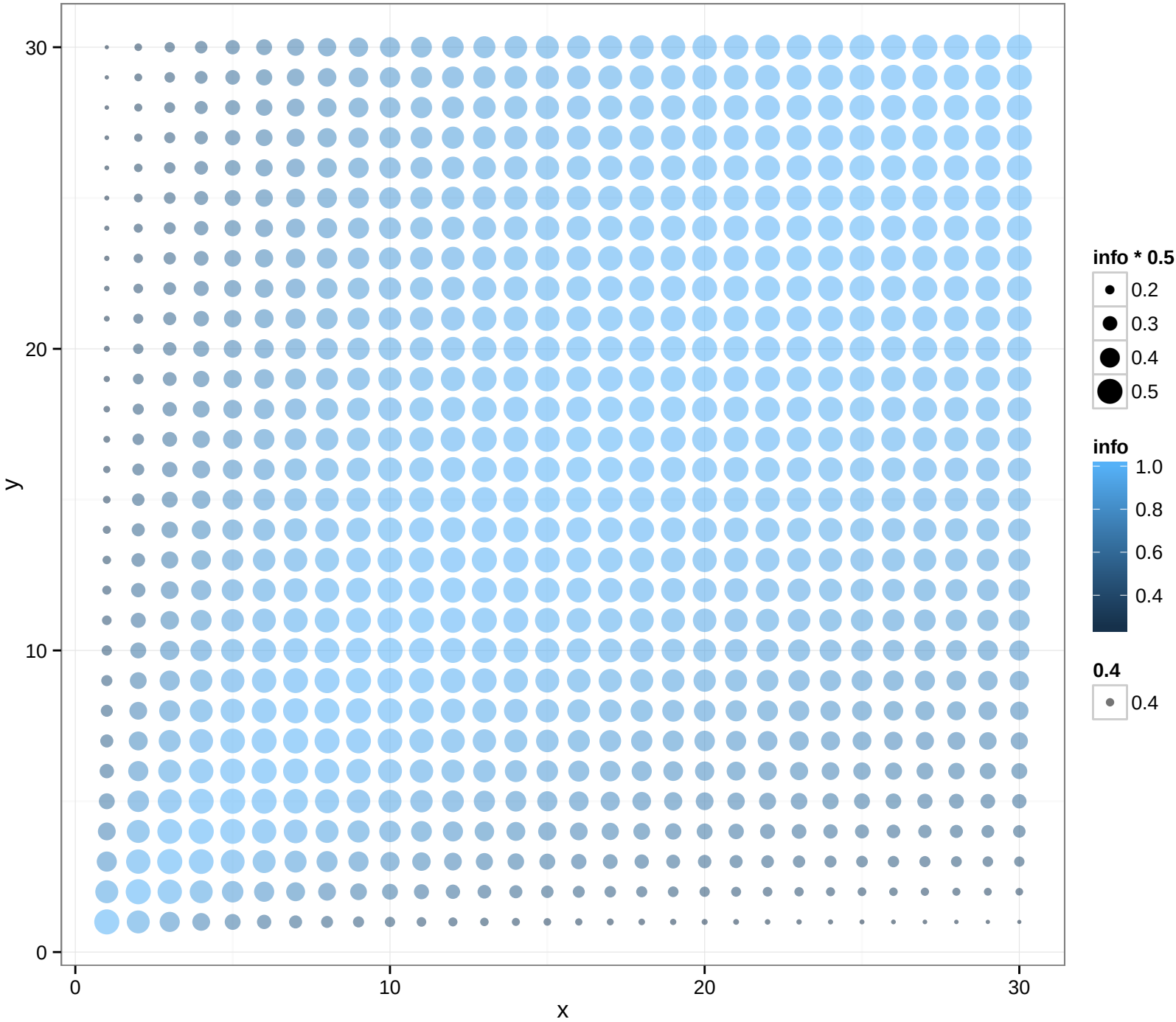
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0
y
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30
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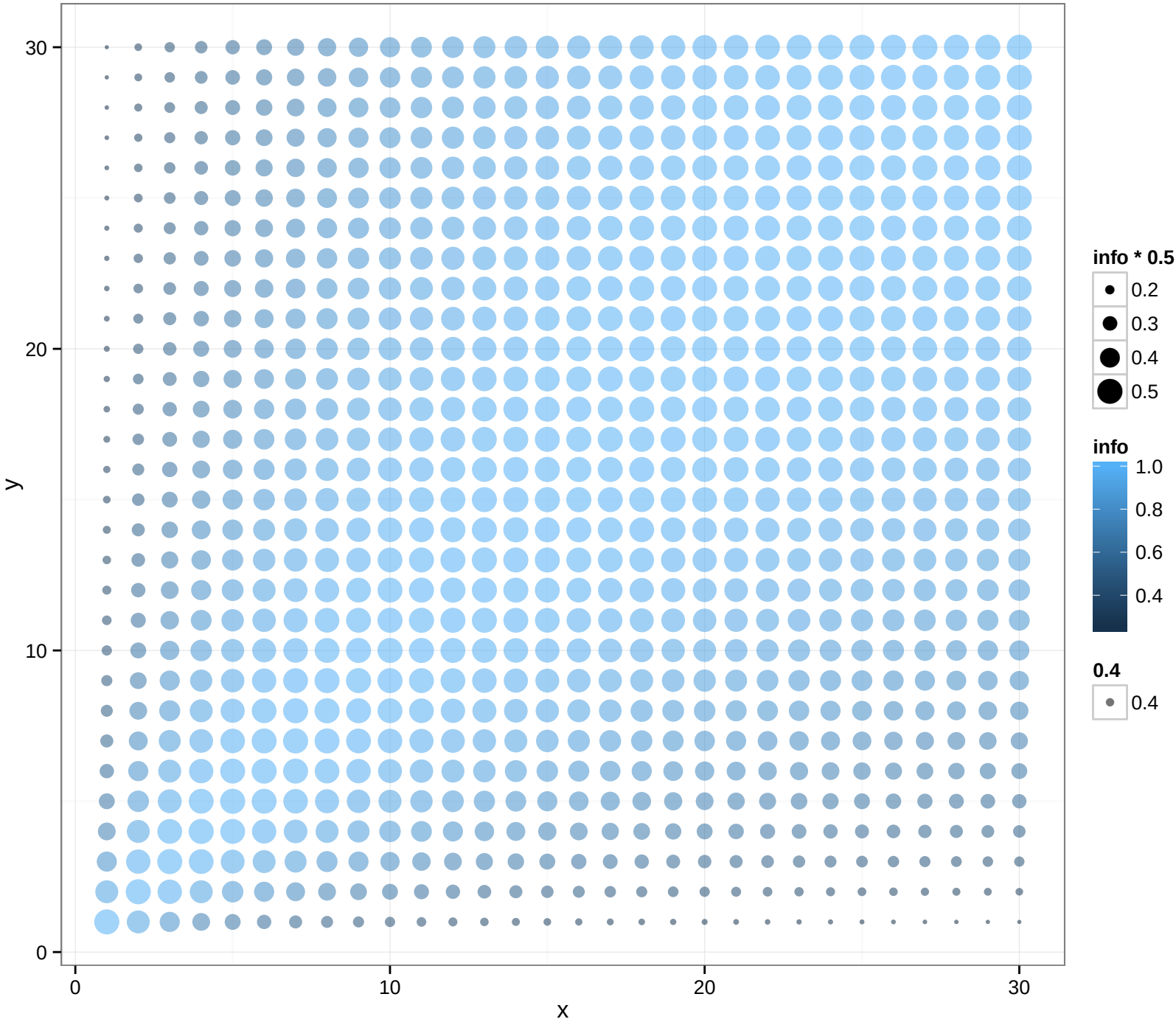
0.4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y
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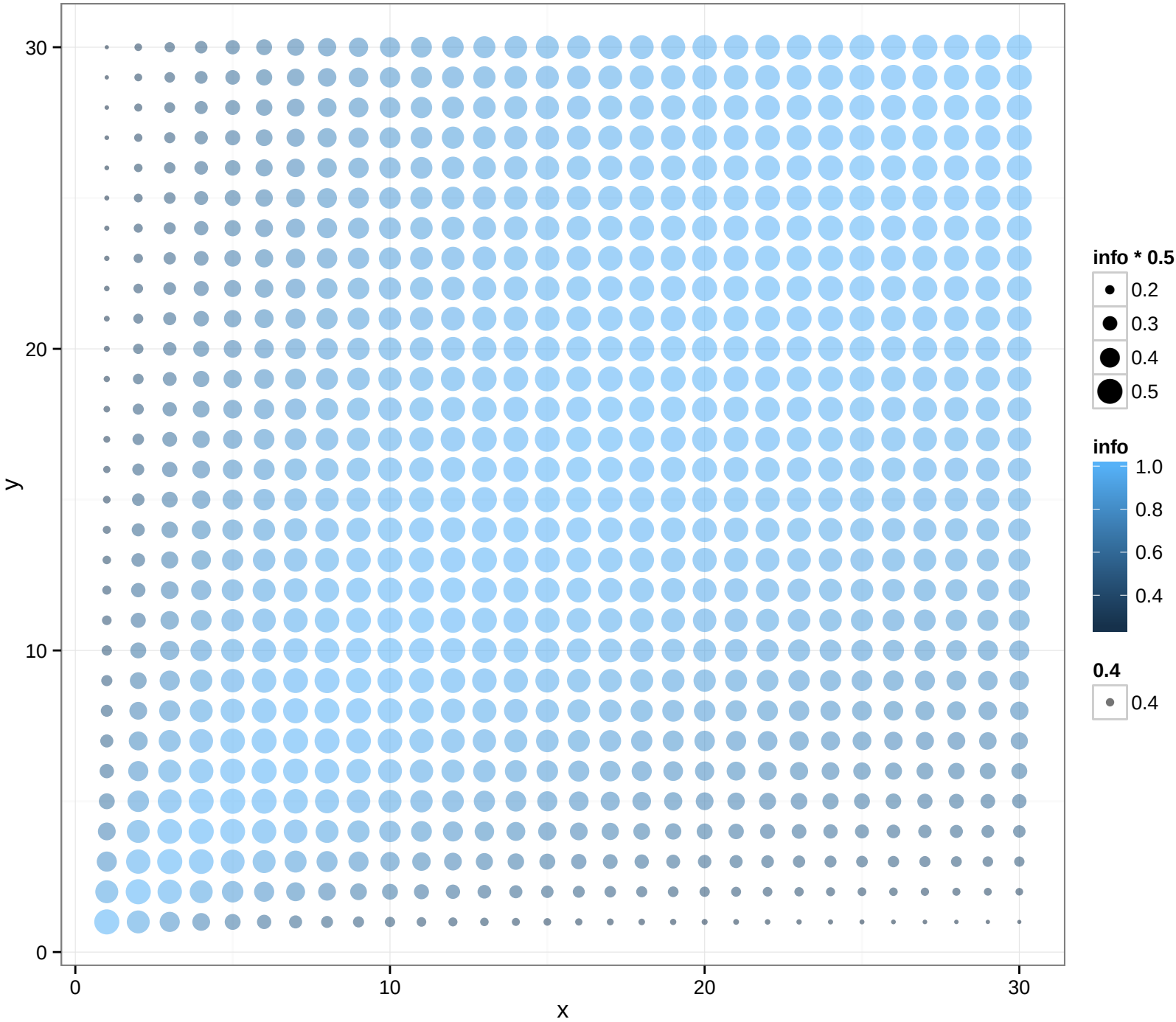
0.4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20
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0
y
0
10
20
30
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0.4
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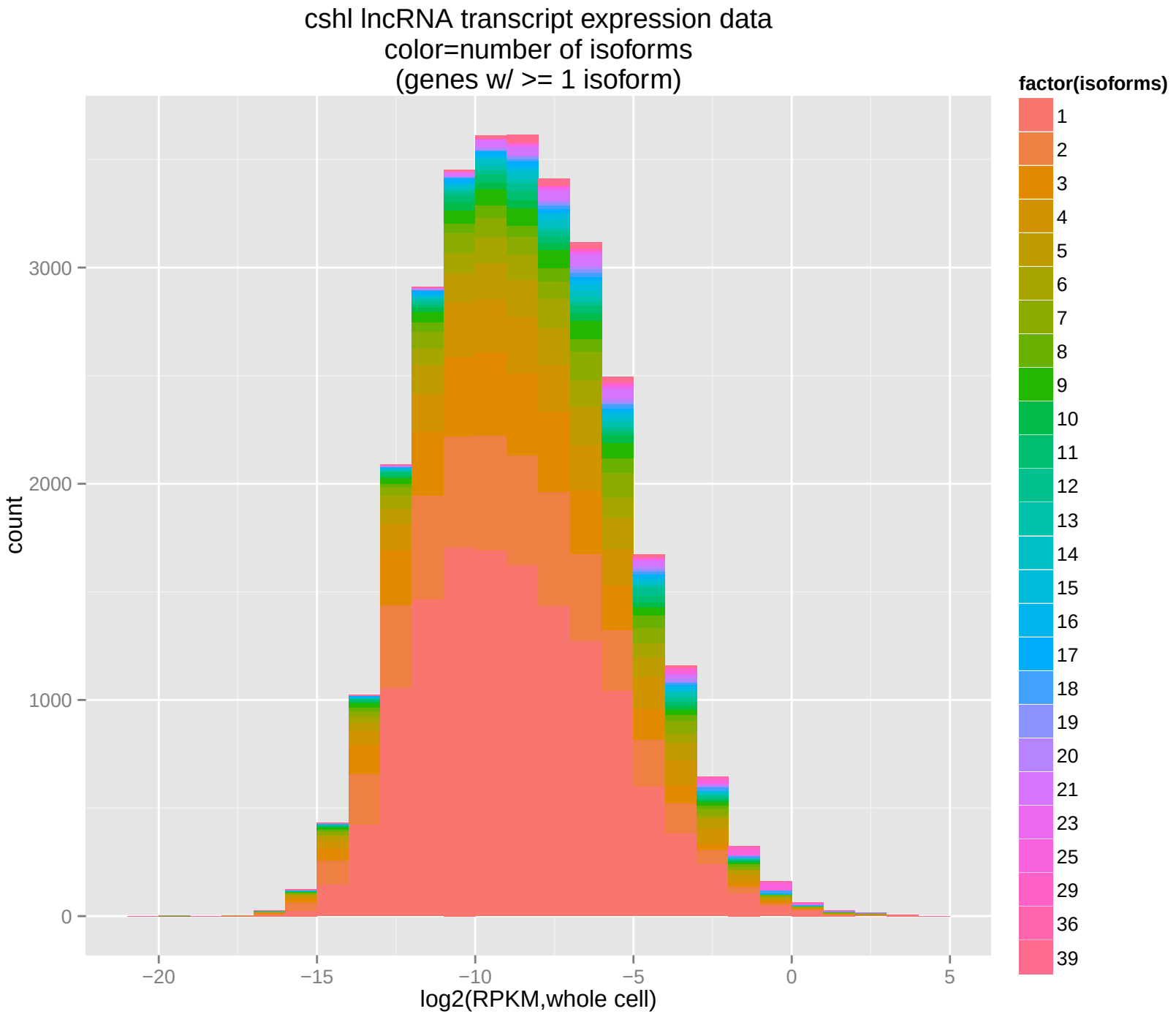
0.4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color=number of isoforms
(genes w/ >= 1 isoform)
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1000
0
−20
−15
−10
−5
0
5
log2(RPKM,whole cell)
factor(isoforms)
1
2
3
4
5
6
7
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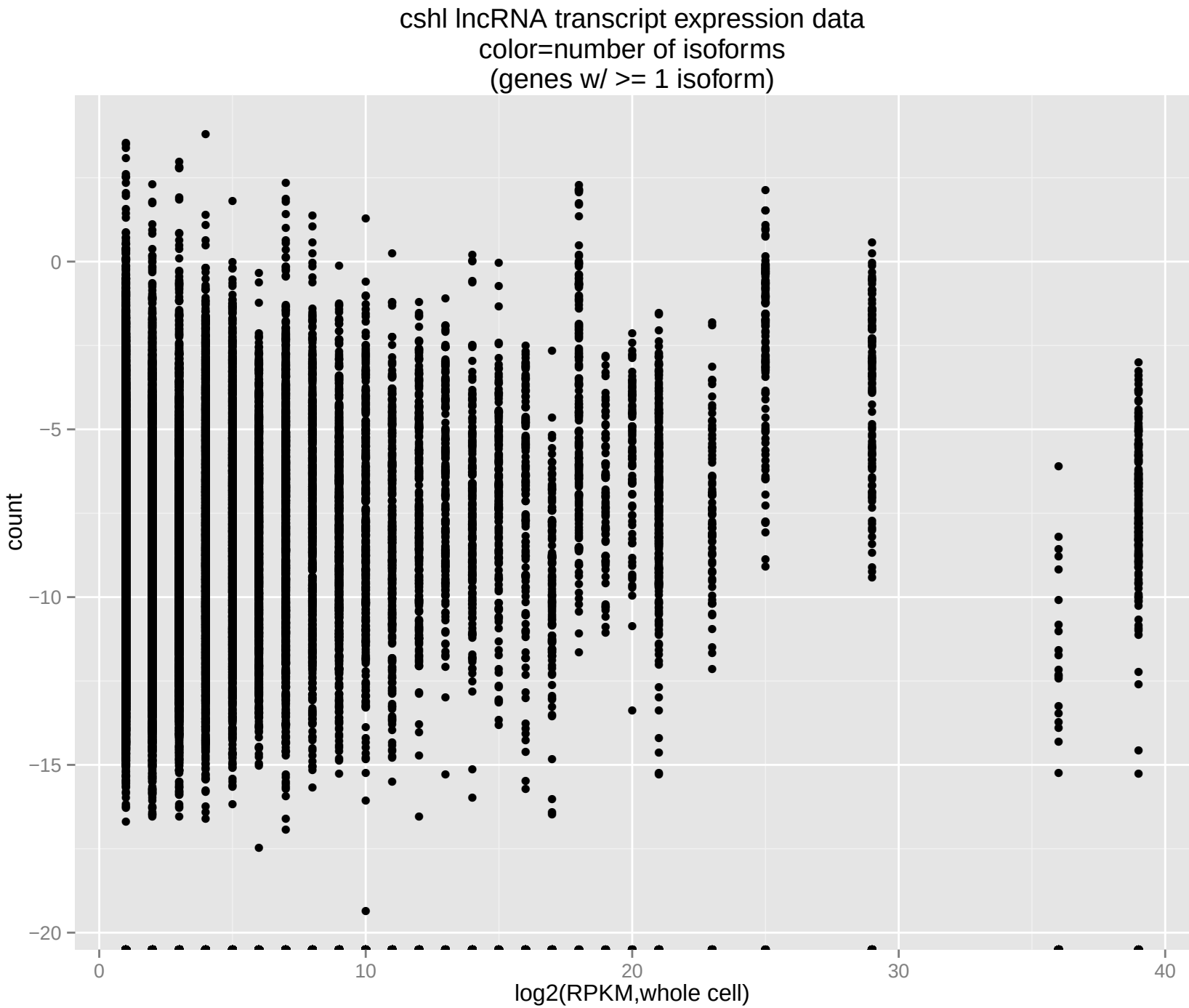
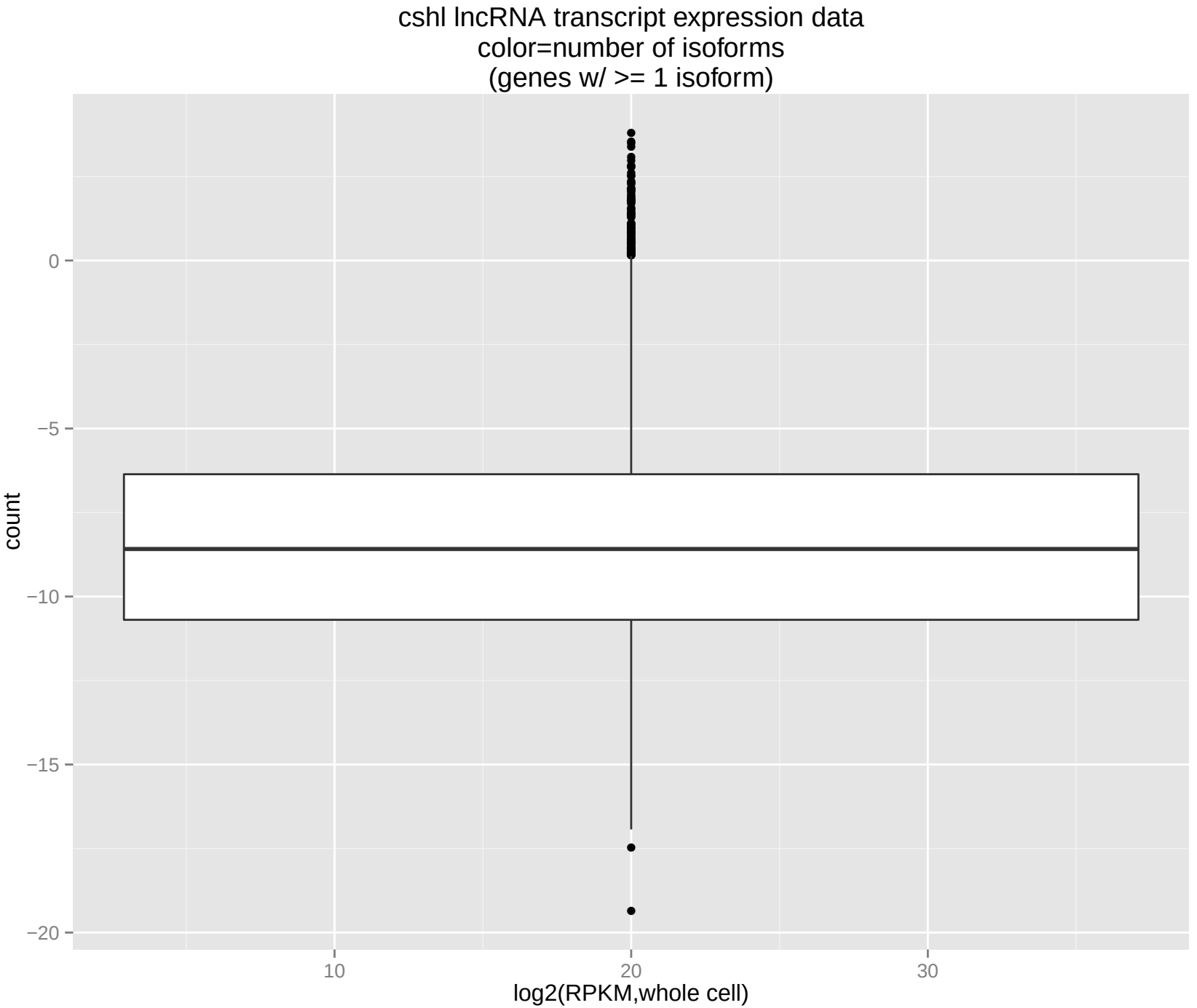

cshl lncRNA transcript expression data
color=number of isoforms
(genes w/ >= 1 isoform)
count
0
−5
−10
−15
−20
0
10
20
30
40
log2(RPKM,whole cell)


cshl lncRNA transcript expression data
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count
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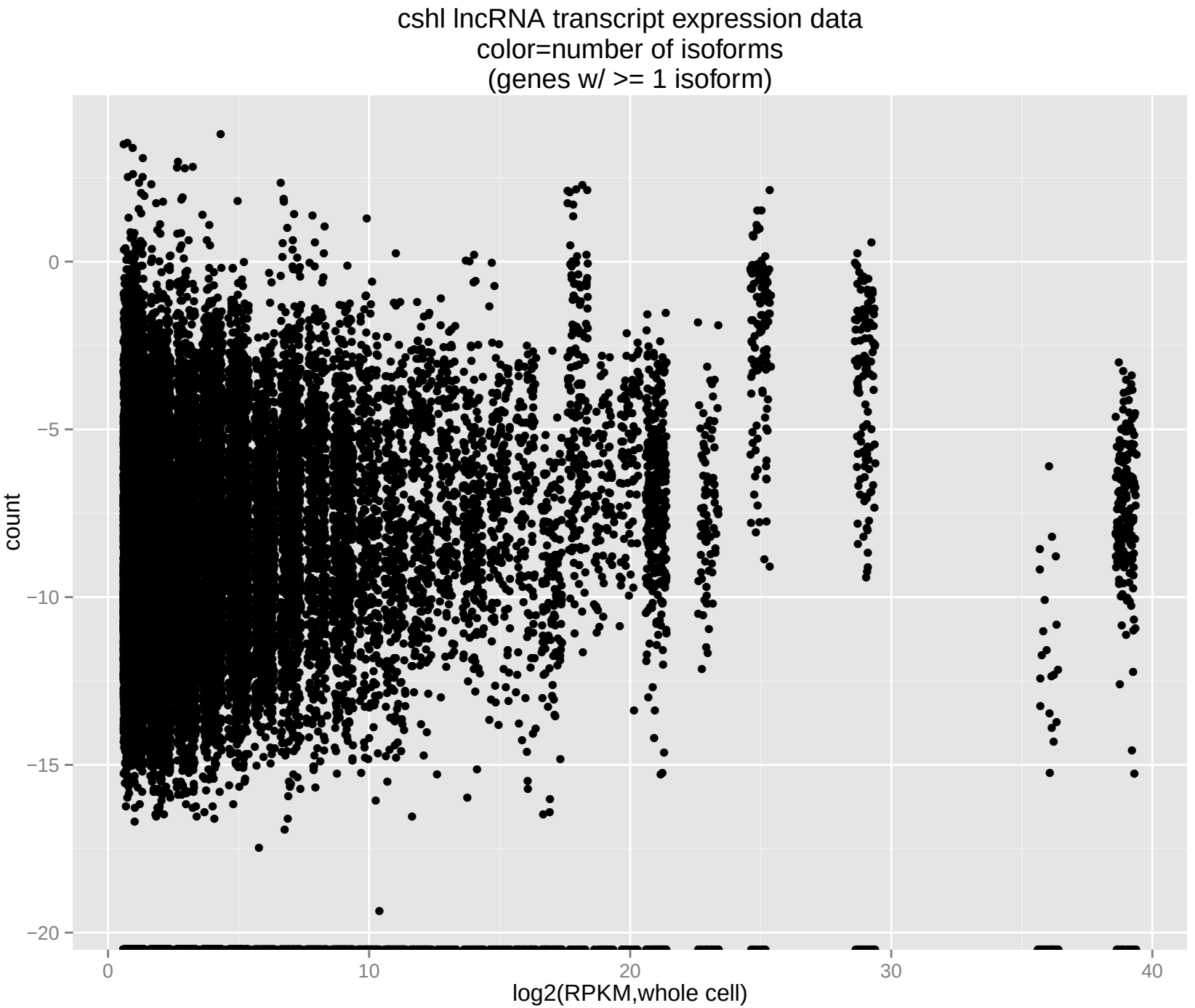
−10
−15
−20
10
20
30
log2(RPKM,whole cell)


cshl lncRNA transcript expression data
color=number of isoforms
(genes w/ >= 1 isoform)
count
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−15
−20
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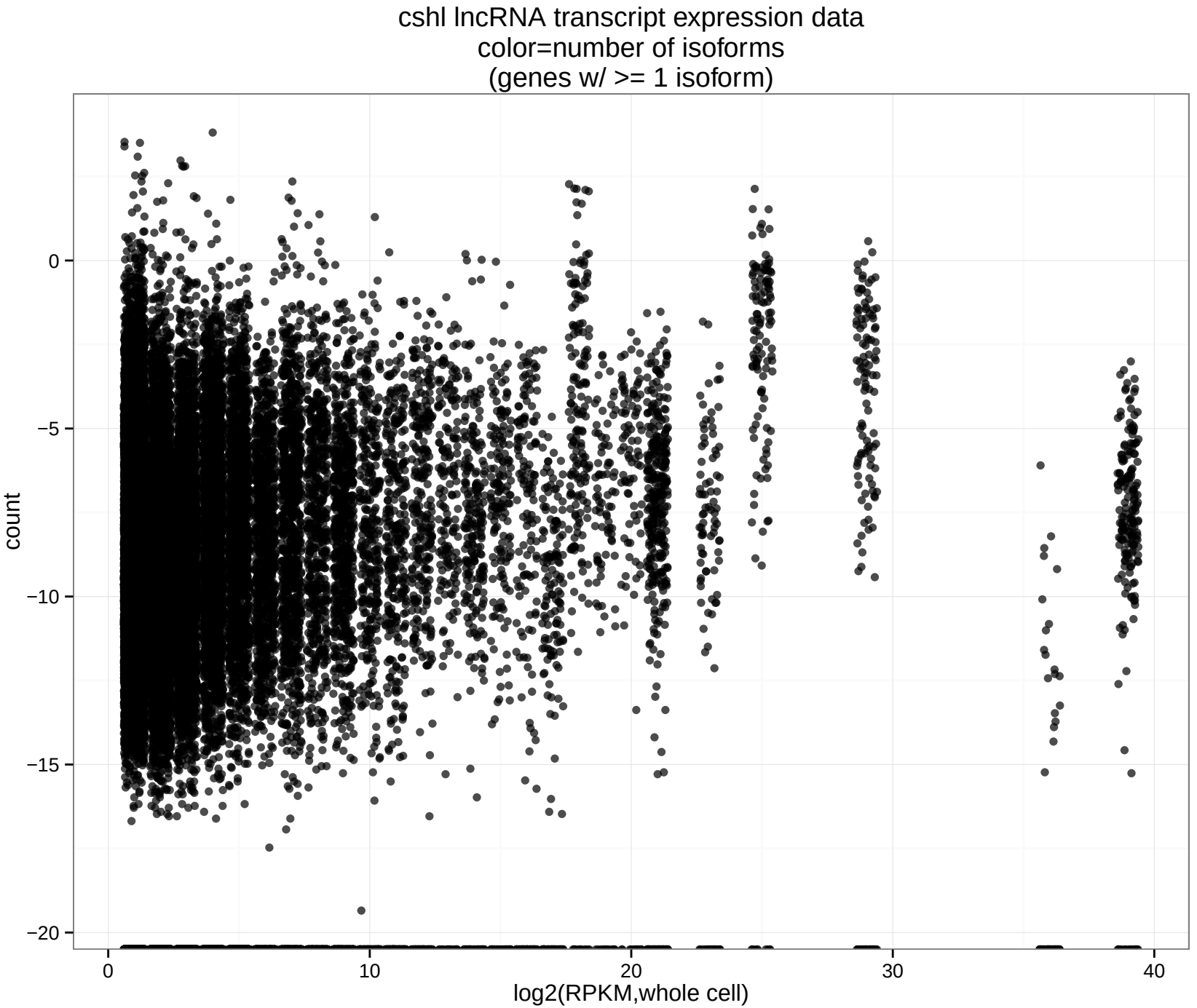
10
20
30
40
log2(RPKM,whole cell)


cshl lncRNA transcript expression data
color=number of isoforms
(genes w/ >= 1 isoform)
count
0
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−10
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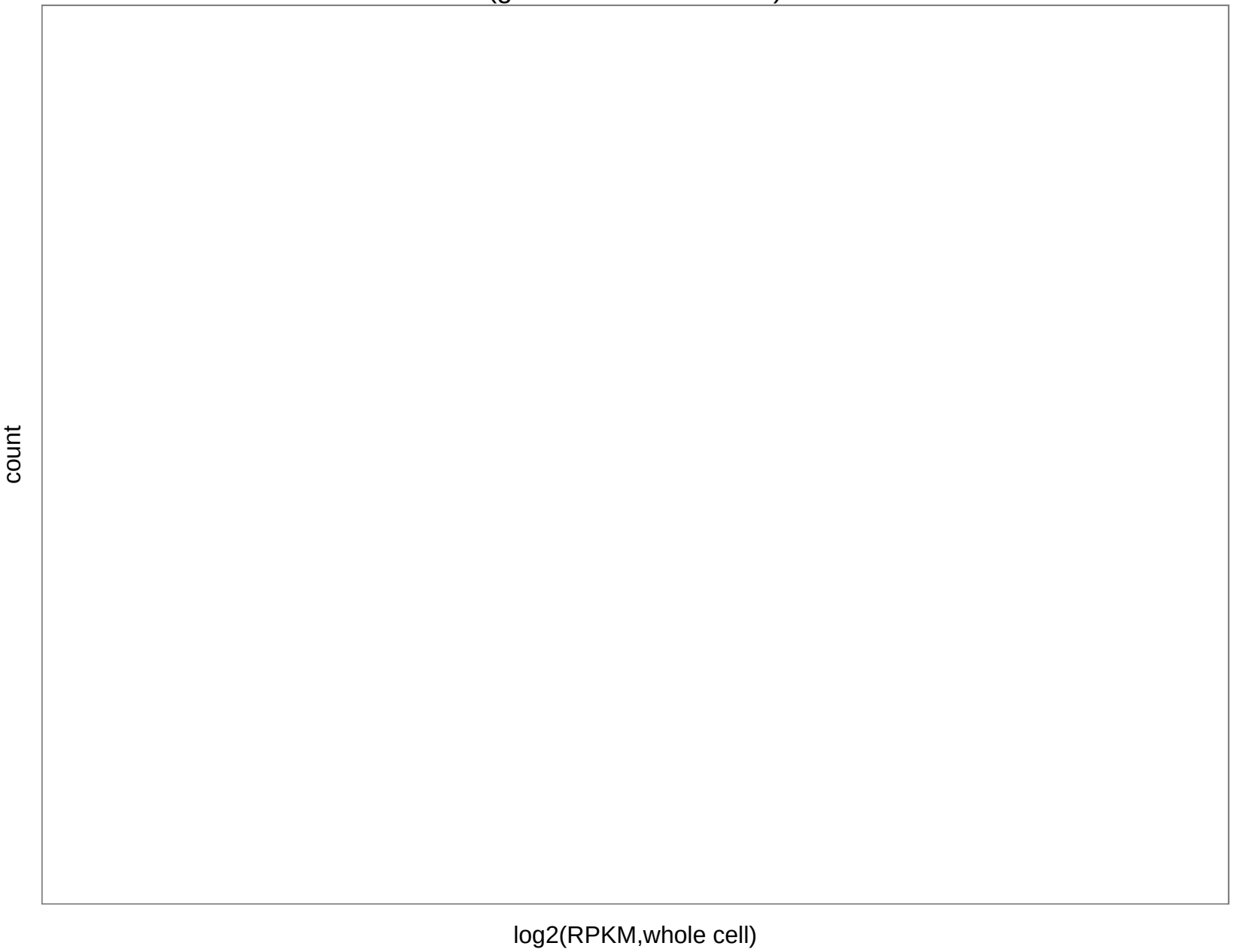
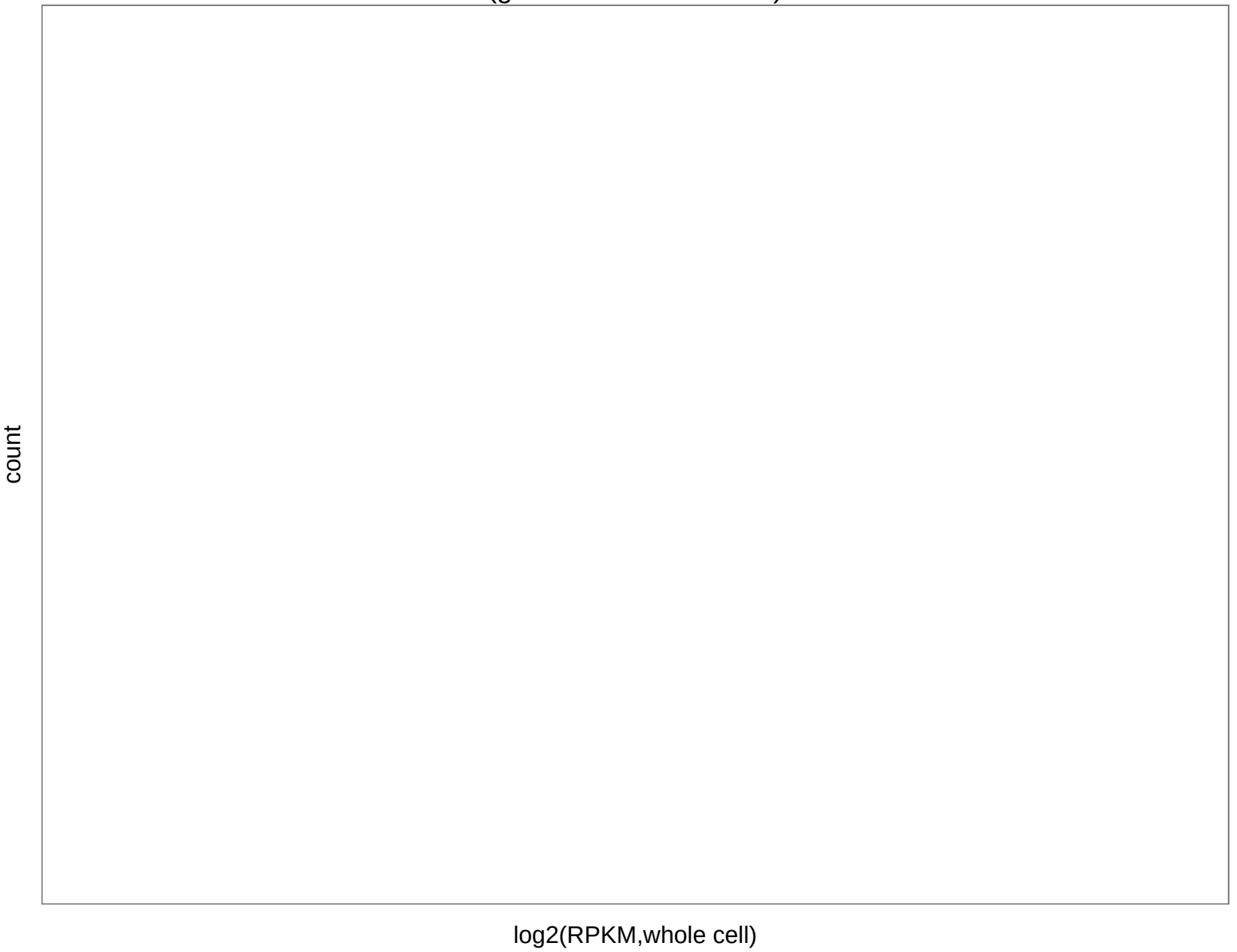
40
log2(RPKM,whole cell)

cshl lncRNA transcript expression data
color=number of isoforms
(genes w/ >= 1 isoform)



cshl lncRNA transcript expression data
color=number of isoforms
(genes w/ >= 1 isoform)



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color=number of isoforms
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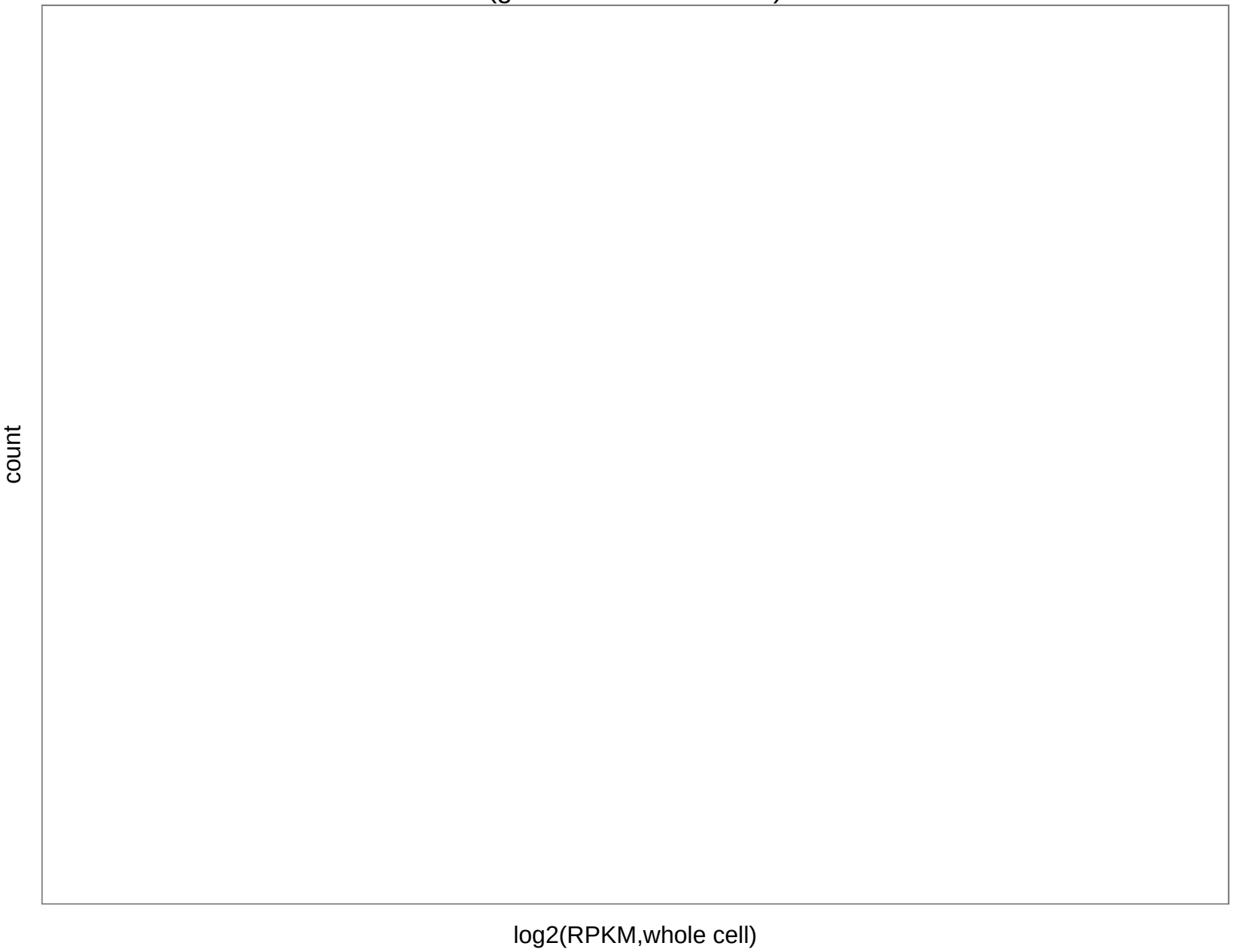

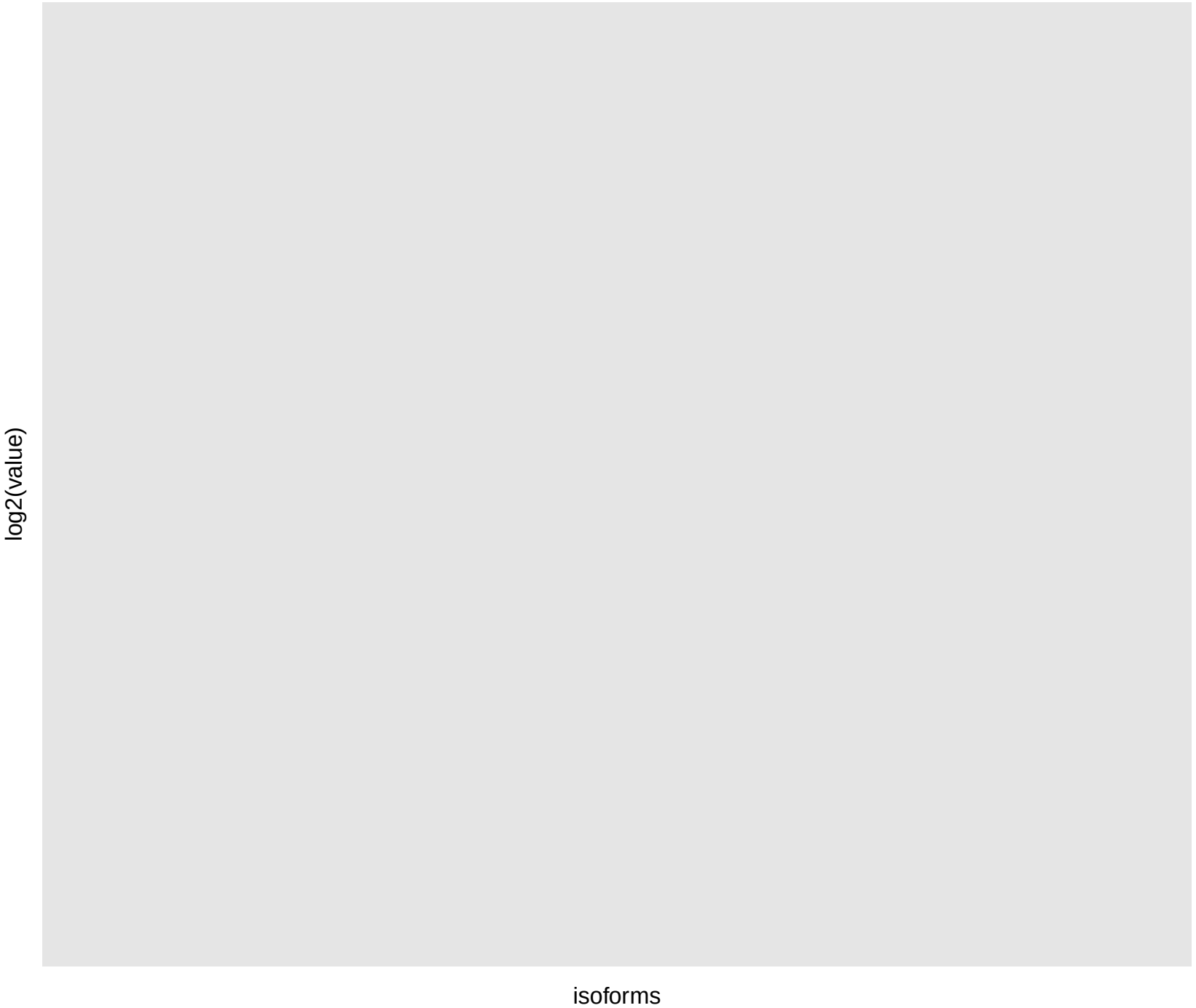
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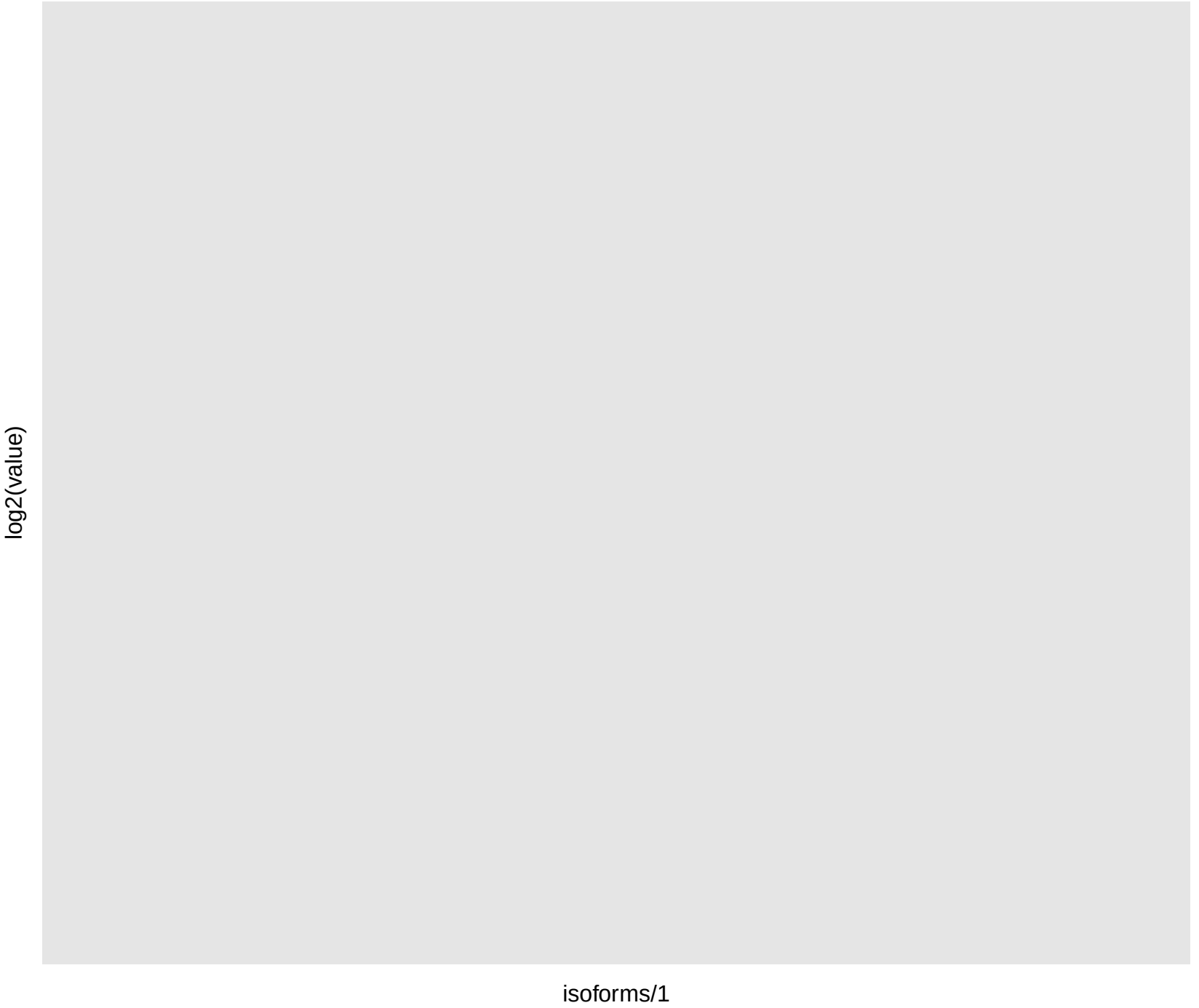
isoforms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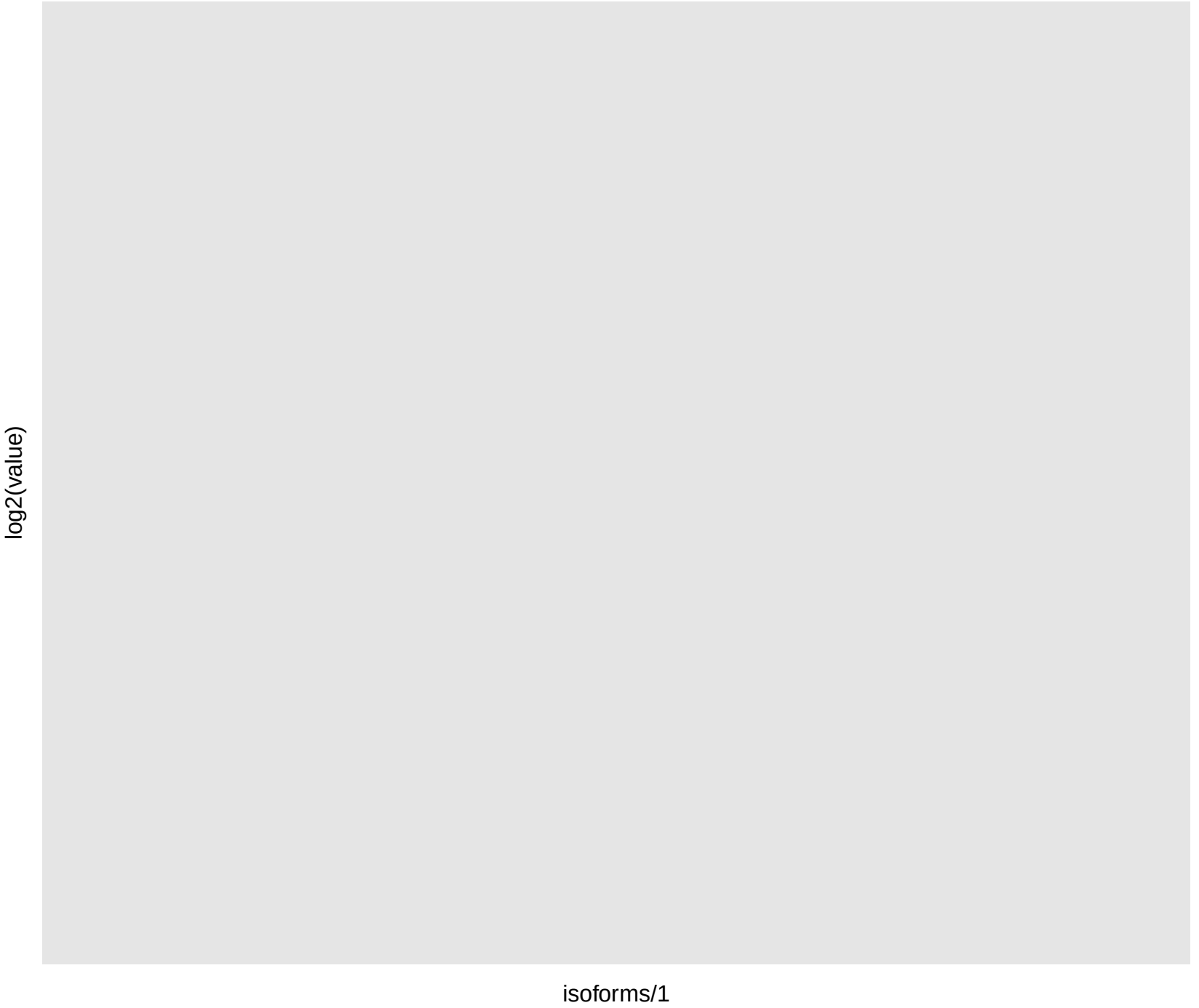
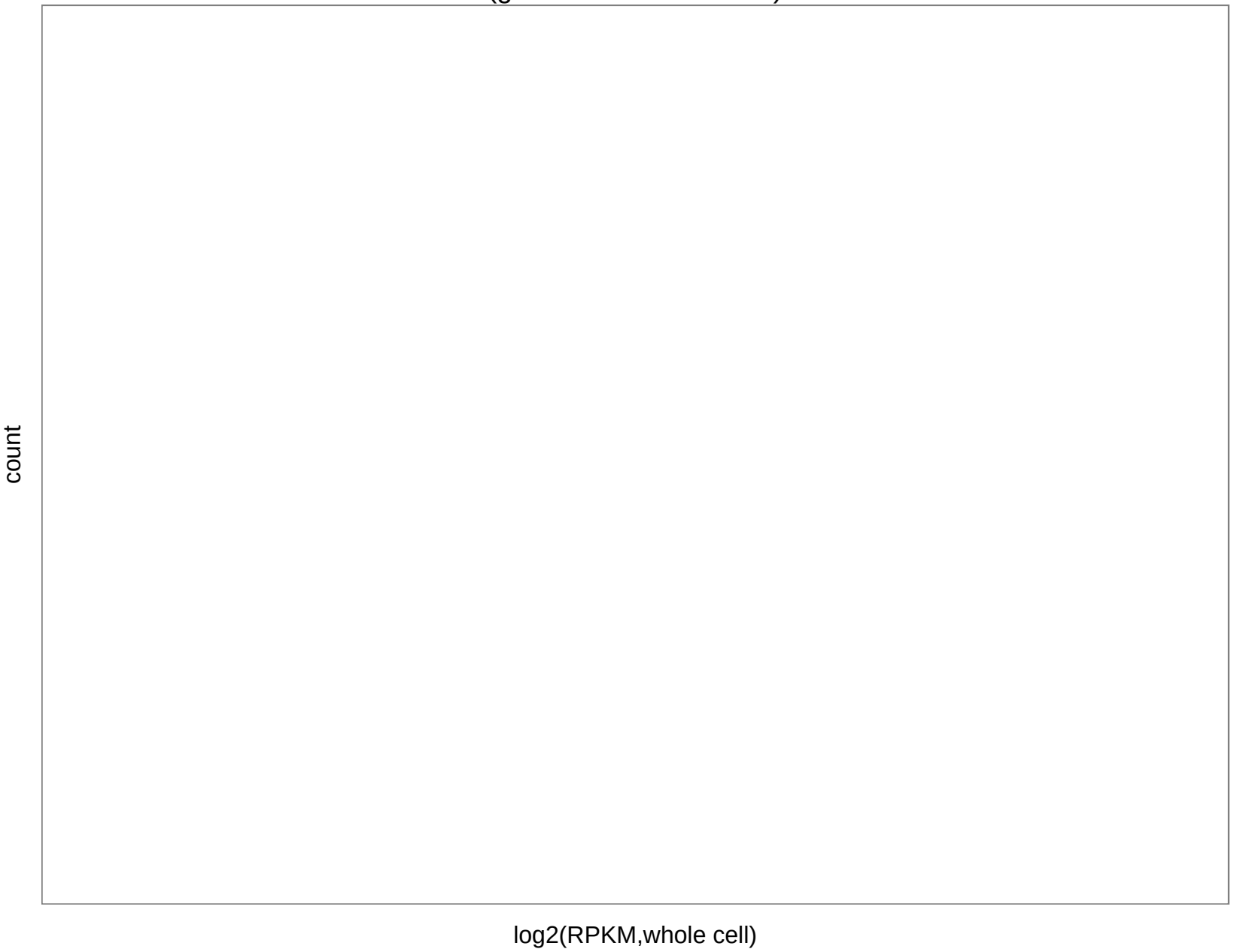
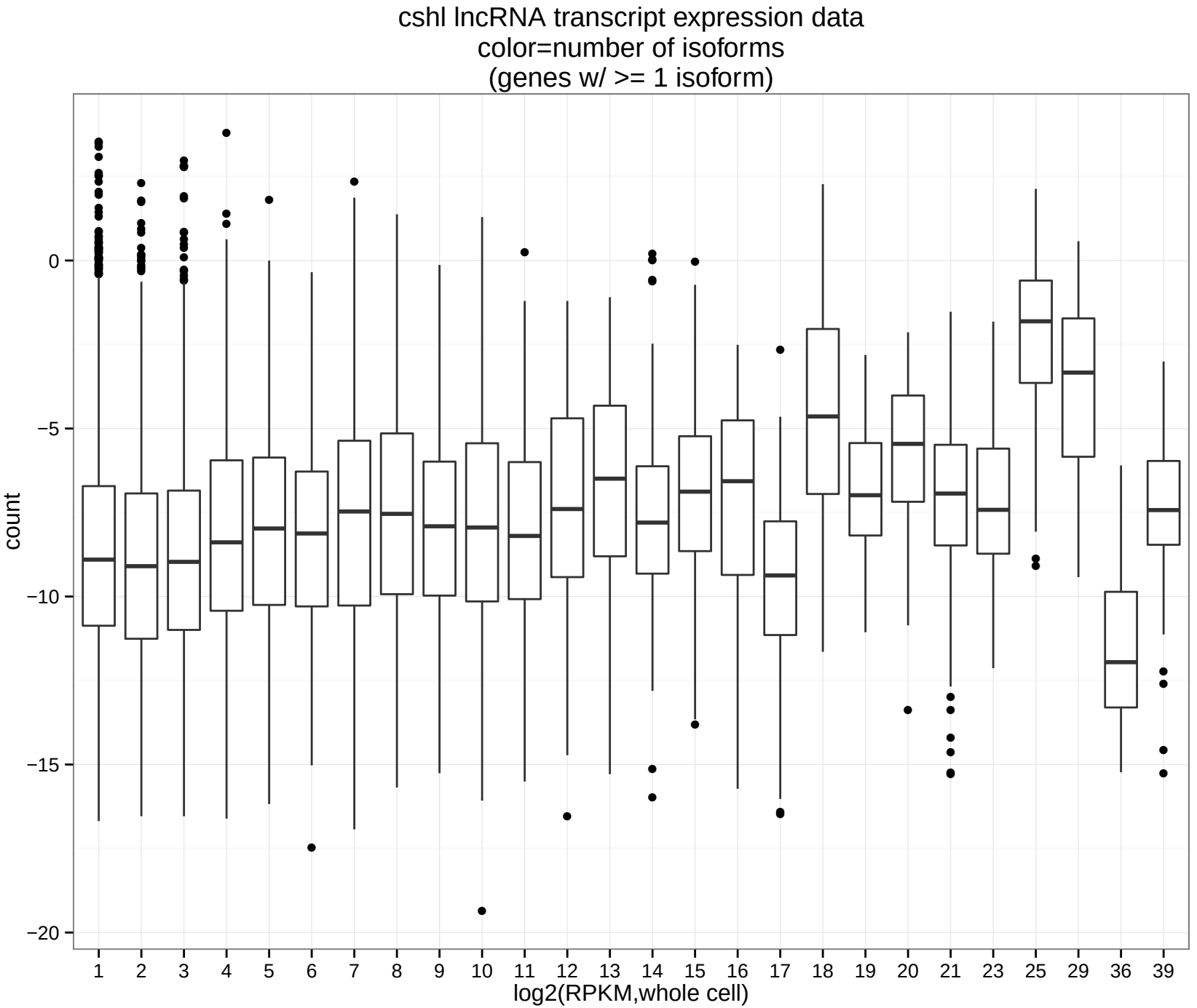

log2(value)
isoforms/1

cshl lncRNA transcript expression data
color=number of isoforms
(genes w/ >= 1 isoform)




cshl lncRNA transcript expression data
color=number of isoforms
(genes w/ >= 1 isoform)
count
0
−5
−10
−15
−20
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
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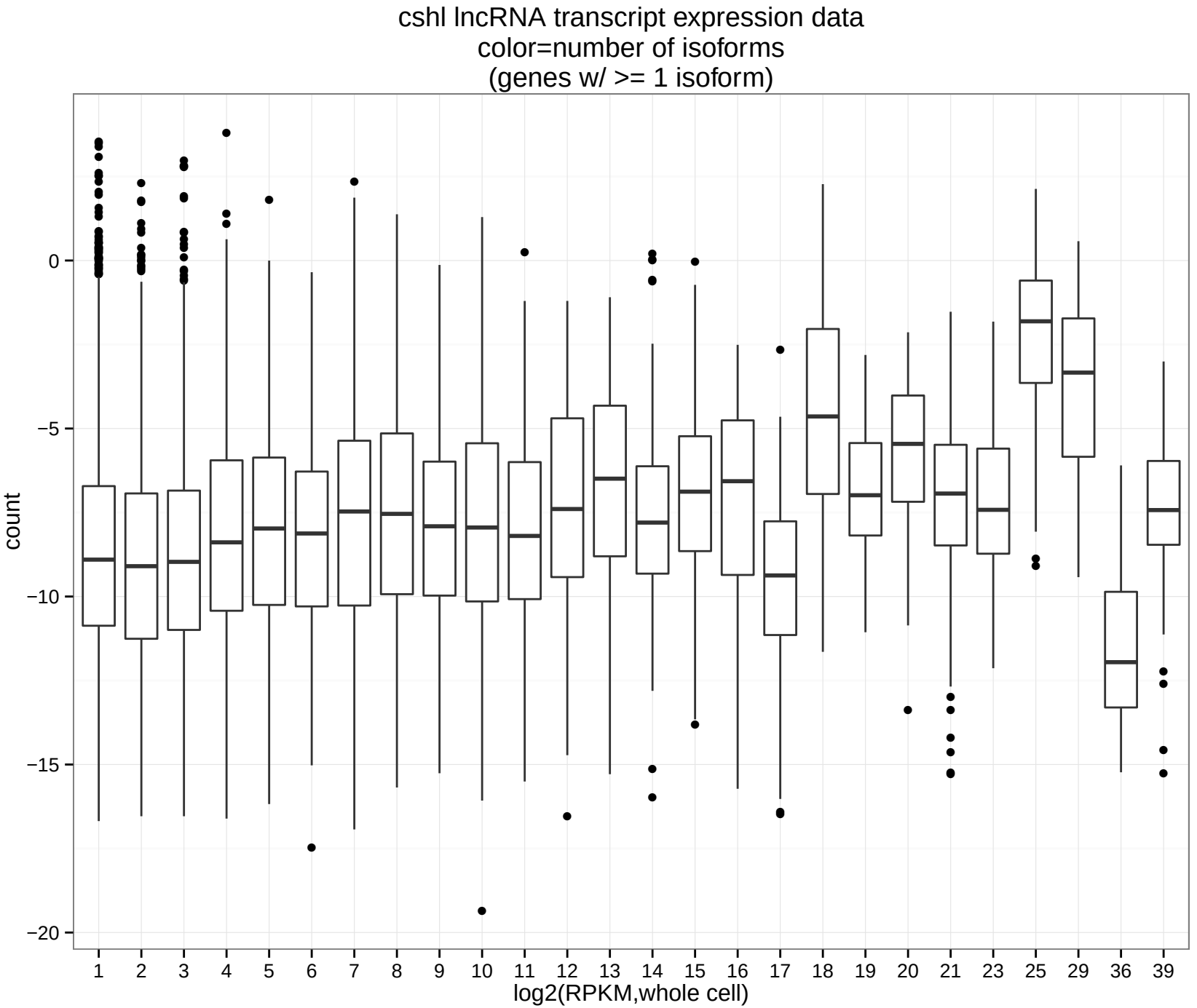
18
19
20
21
23
25
29
36
39
log2(RPKM,whole cell)


cshl lncRNA transcript expression data
color=number of isoforms
(genes w/ >= 1 isoform)
count
0
−5
−10
−15
−20
1
2
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5
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25
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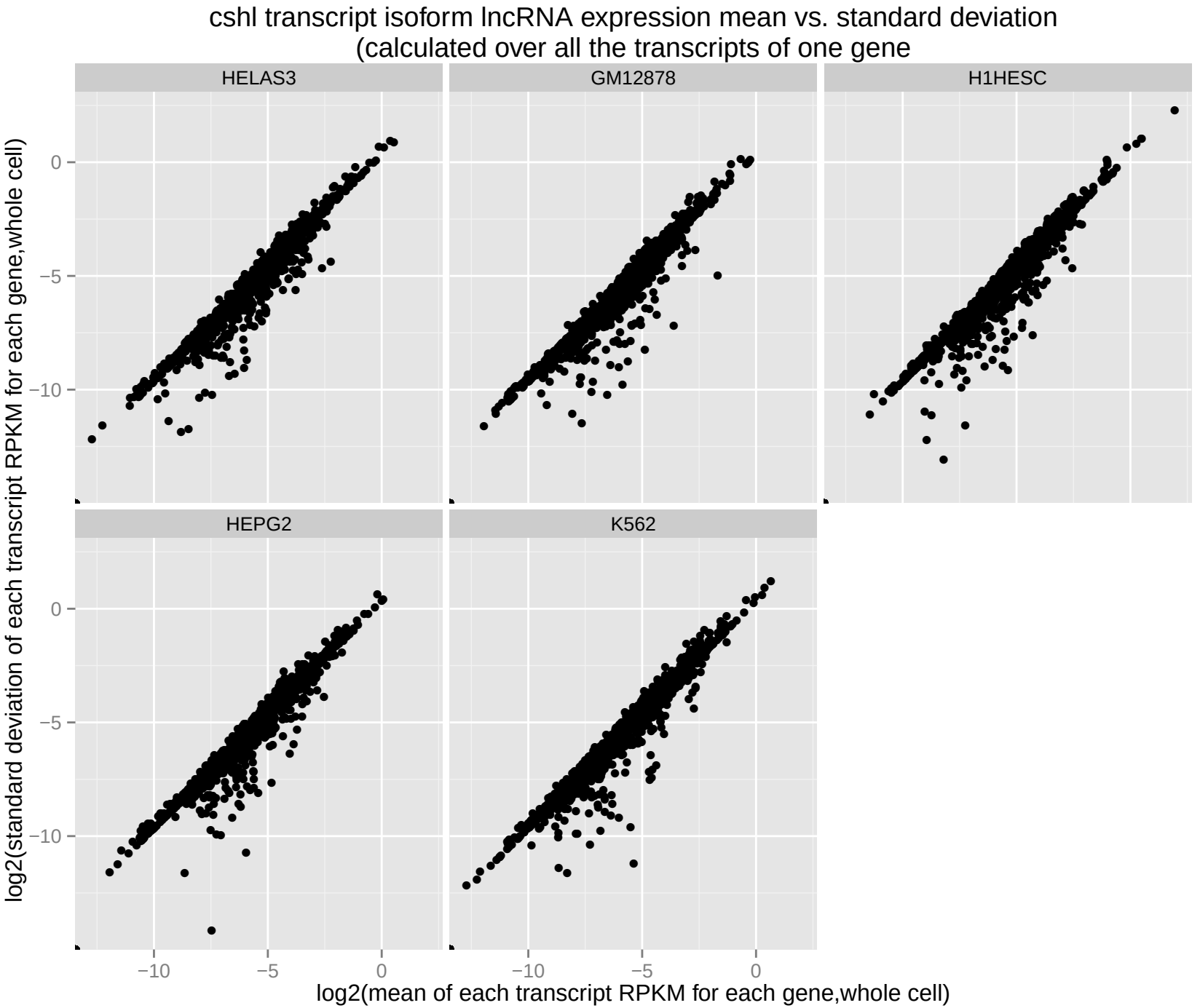
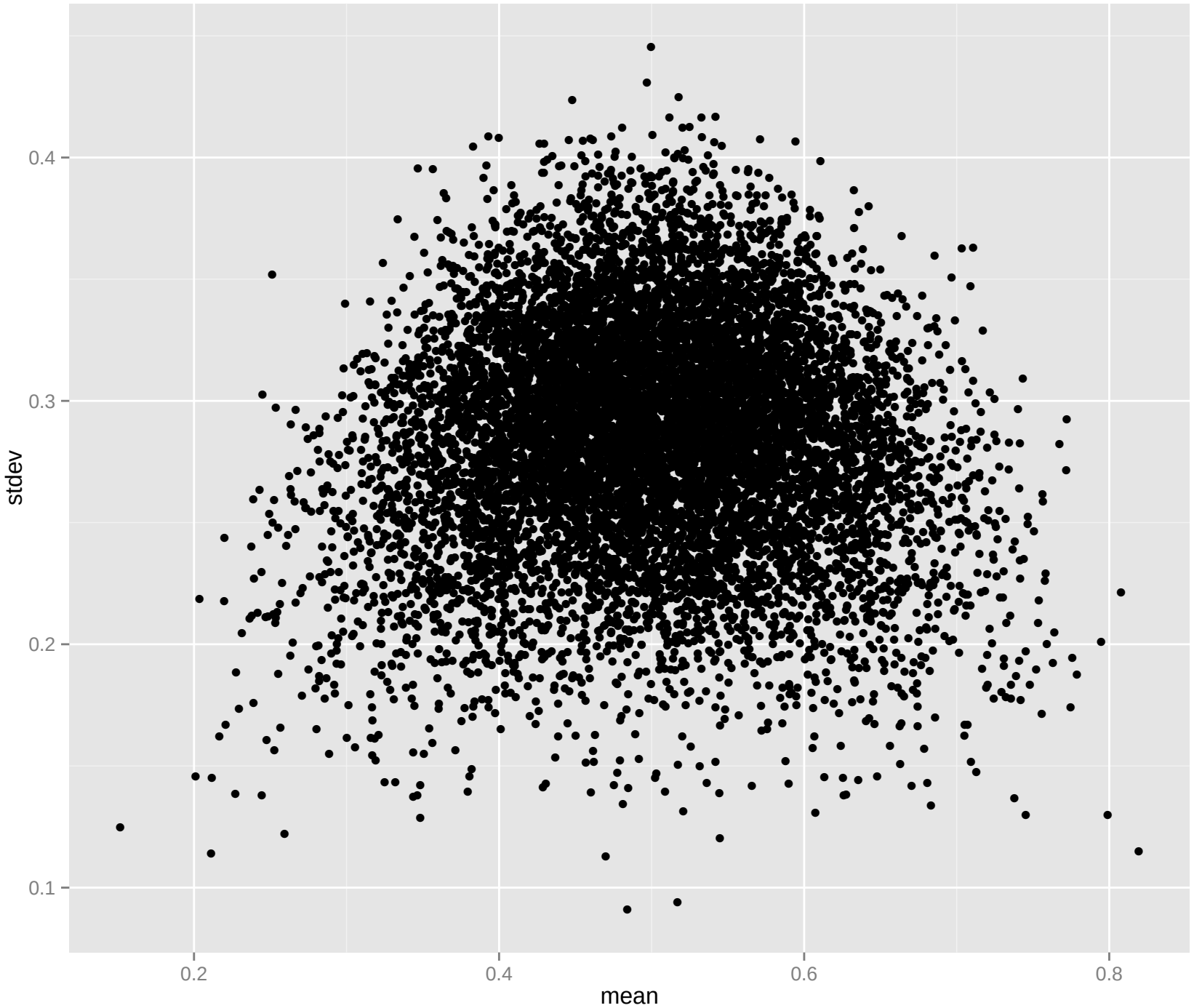
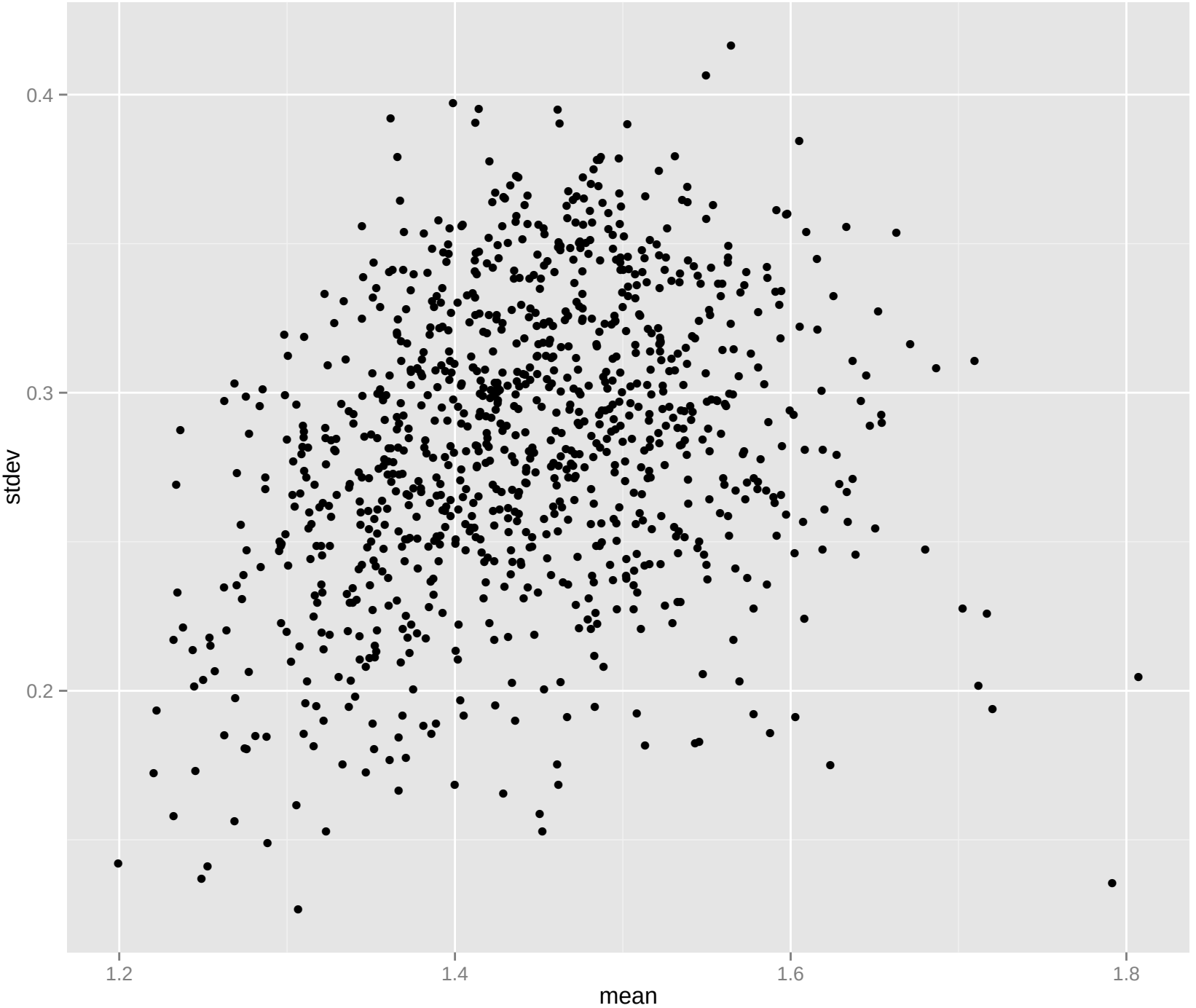
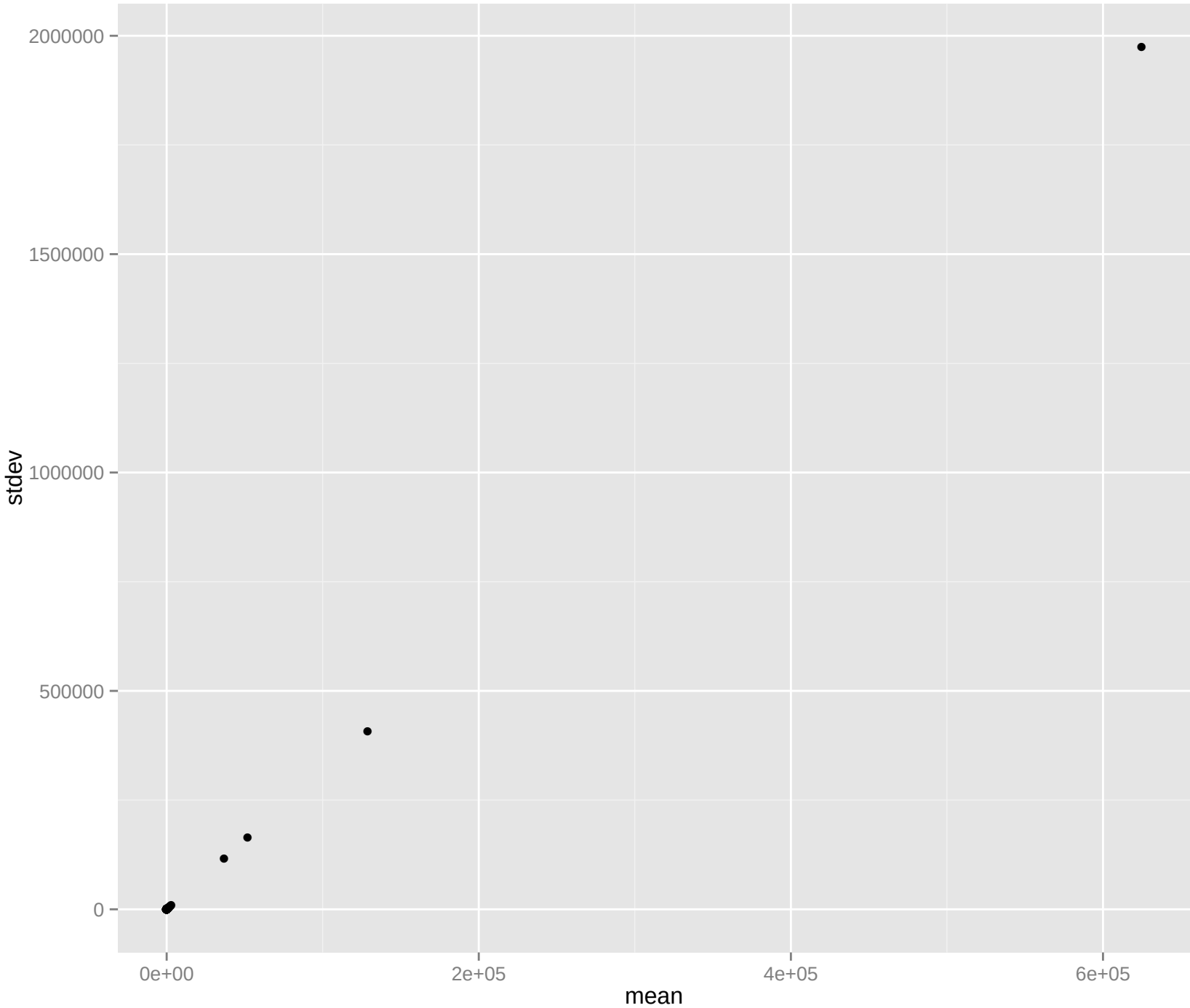
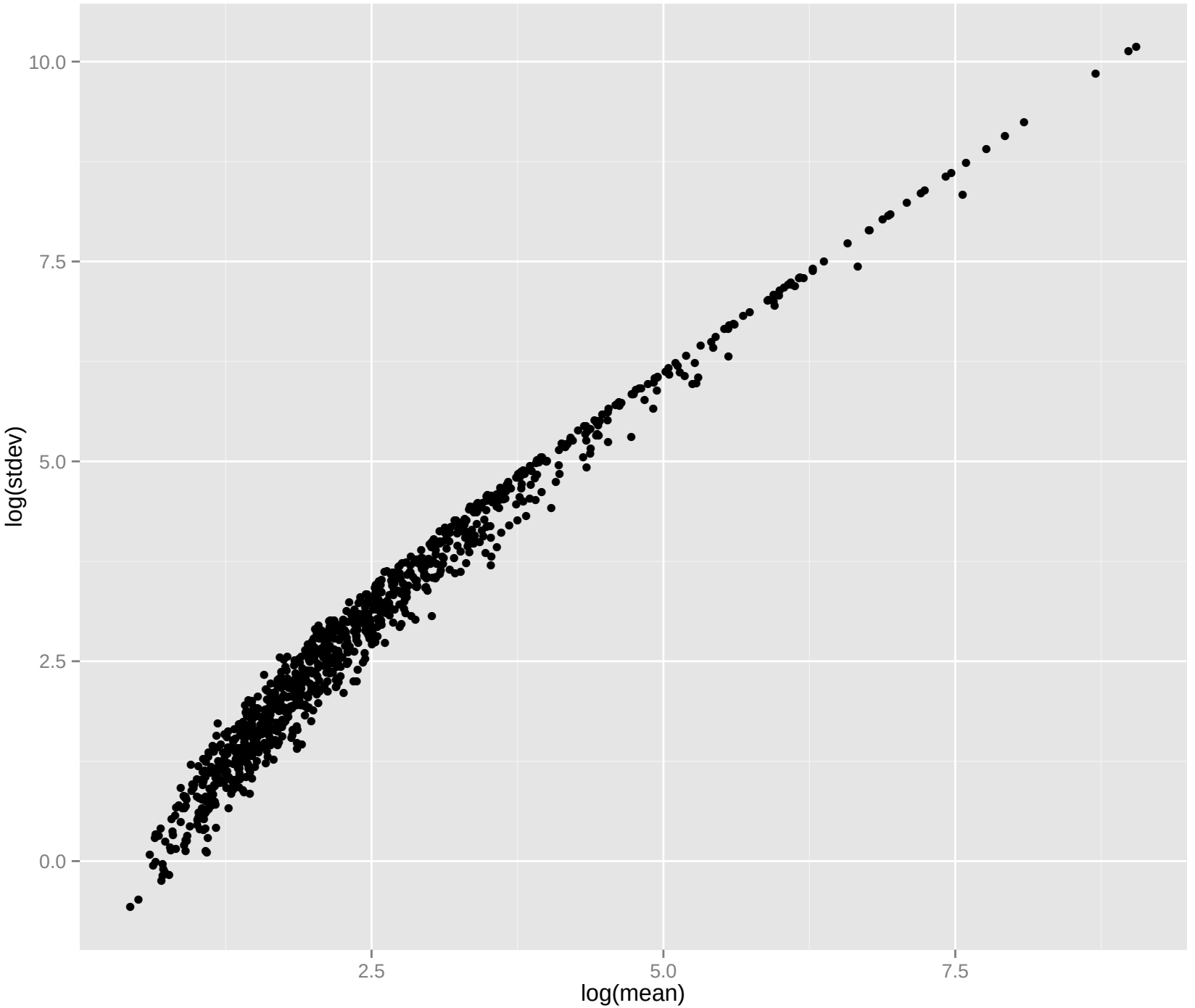
36
39
log2(RPKM,whole cell)

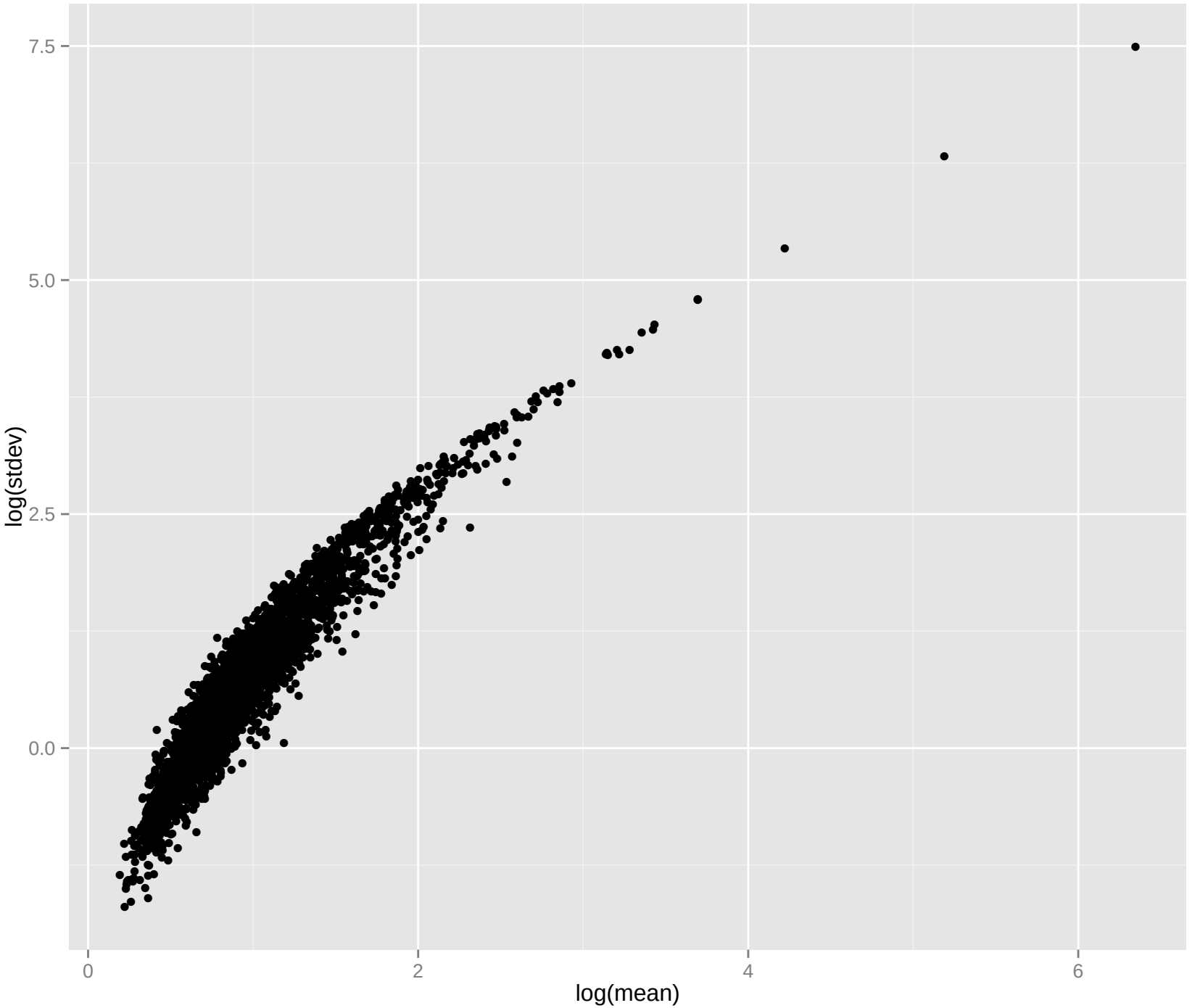

cshl transcript isoform lncRNA expression mean vs. standard deviation
(calculated over all the transcripts of one gene
HELAS3
GM12878
H1HESC
HEPG2
K562
0
−5
−10
log2(standard deviation of each transcript RPKM for each gene,whole cell)
log2(mean of each transcript RPKM for each gene,whole cell)

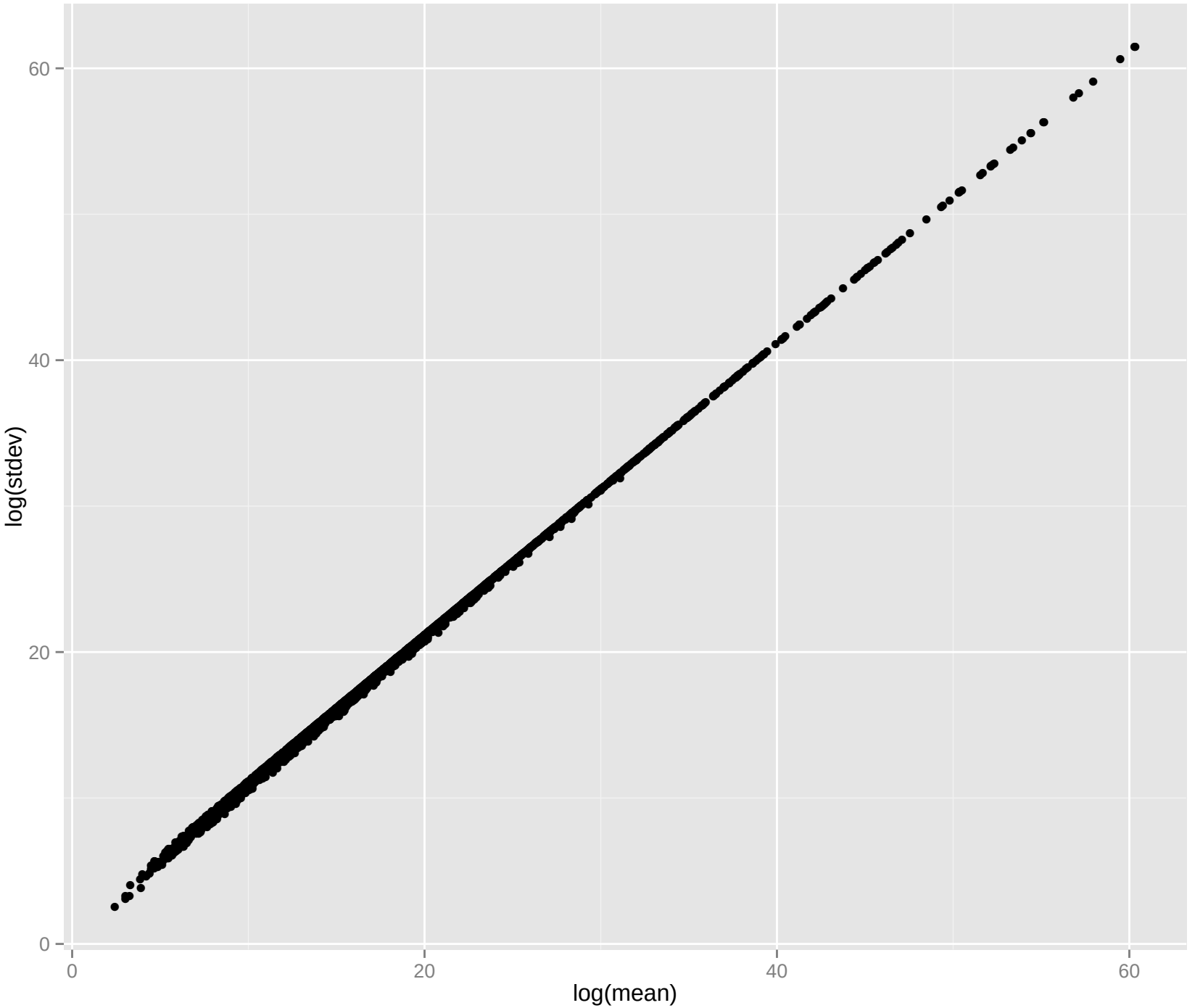

0.4
0.3
0.2
0.1
stdev
0.2
0.4
0.6
0.8
mean

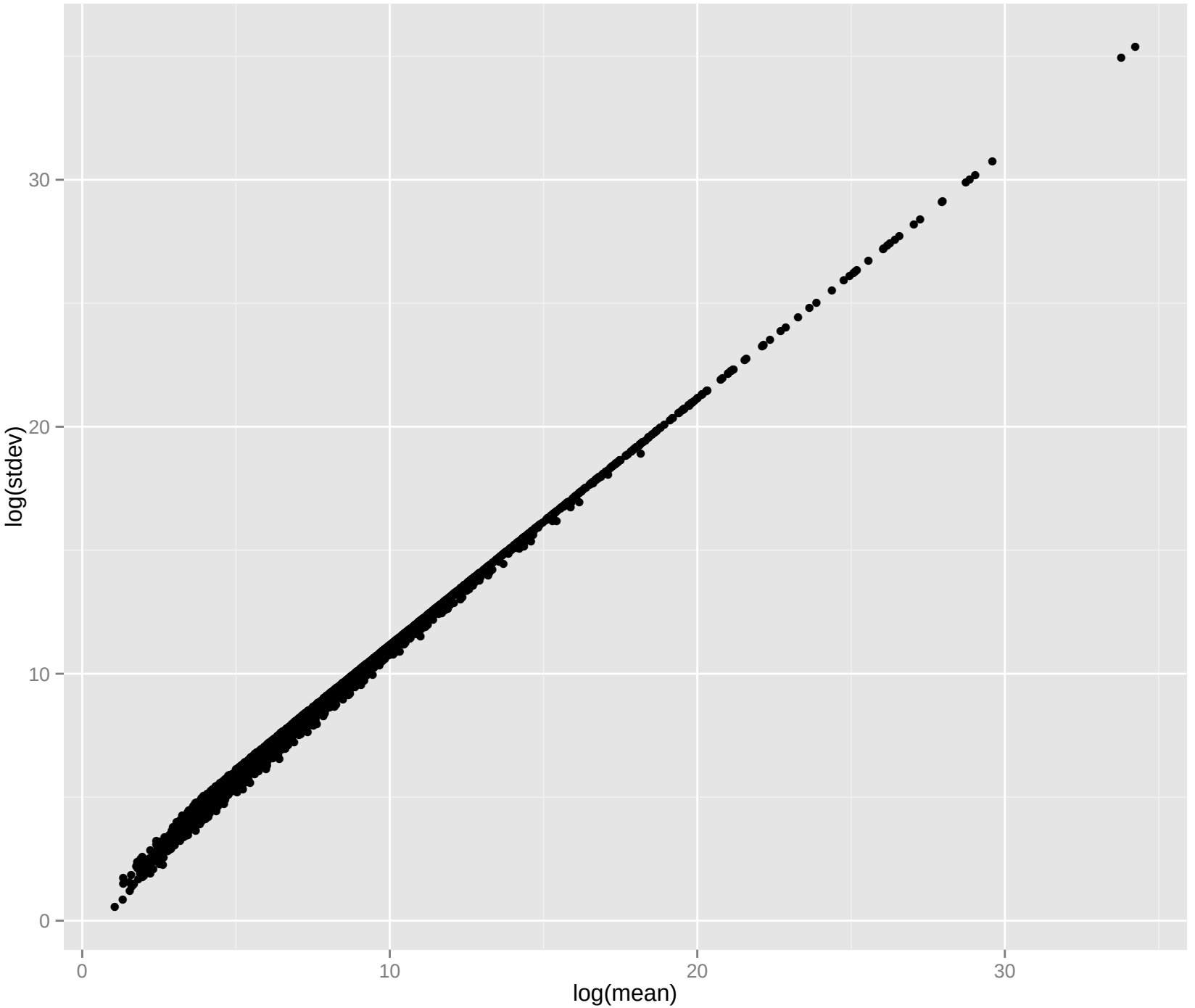

0.4
0.3
0.2
stdev
1.2
1.4
1.6
1.8
mean

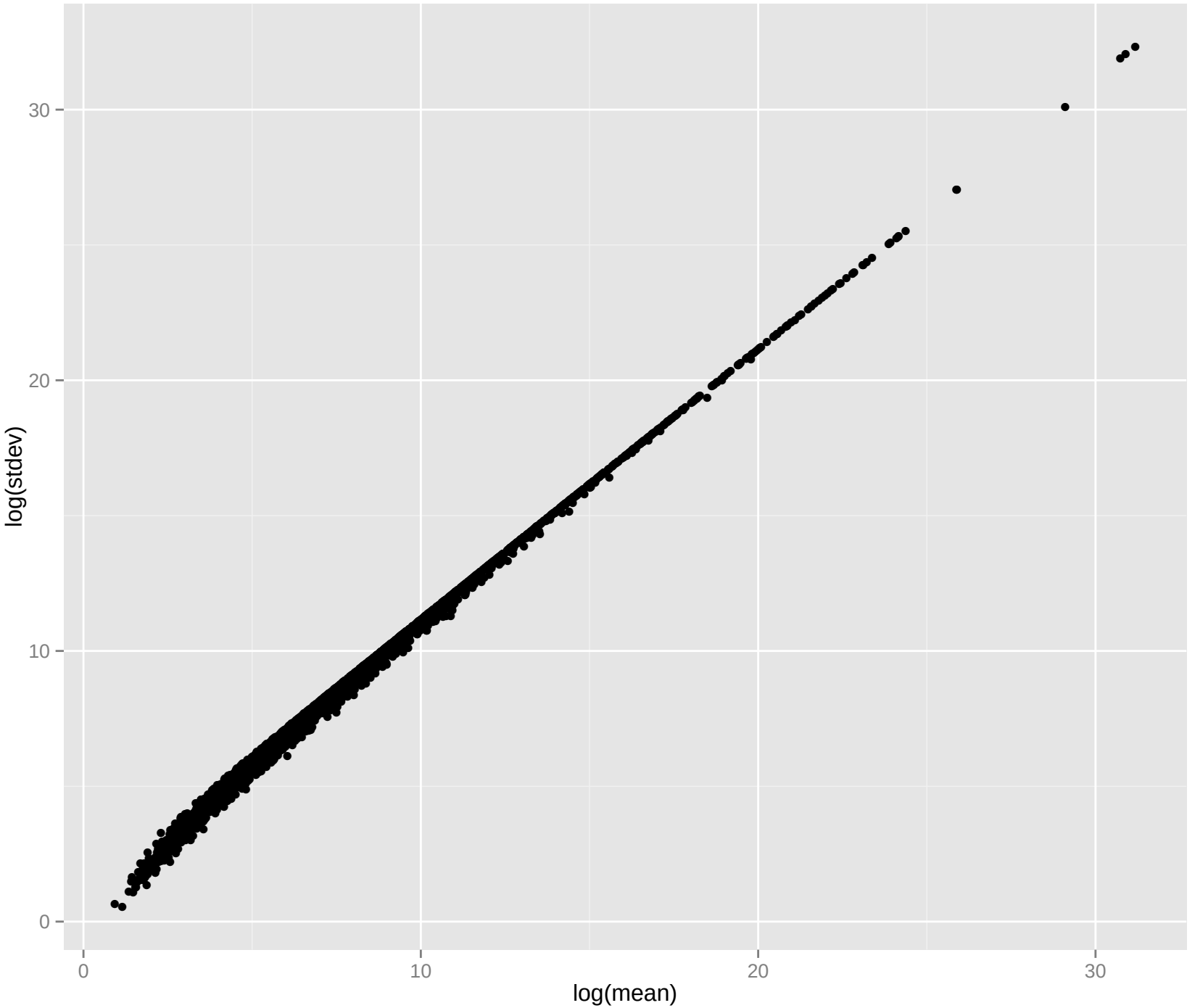

2000000
1500000
1000000
500000
0
stdev
0e+00
2e+05
4e+05
6e+05
mean

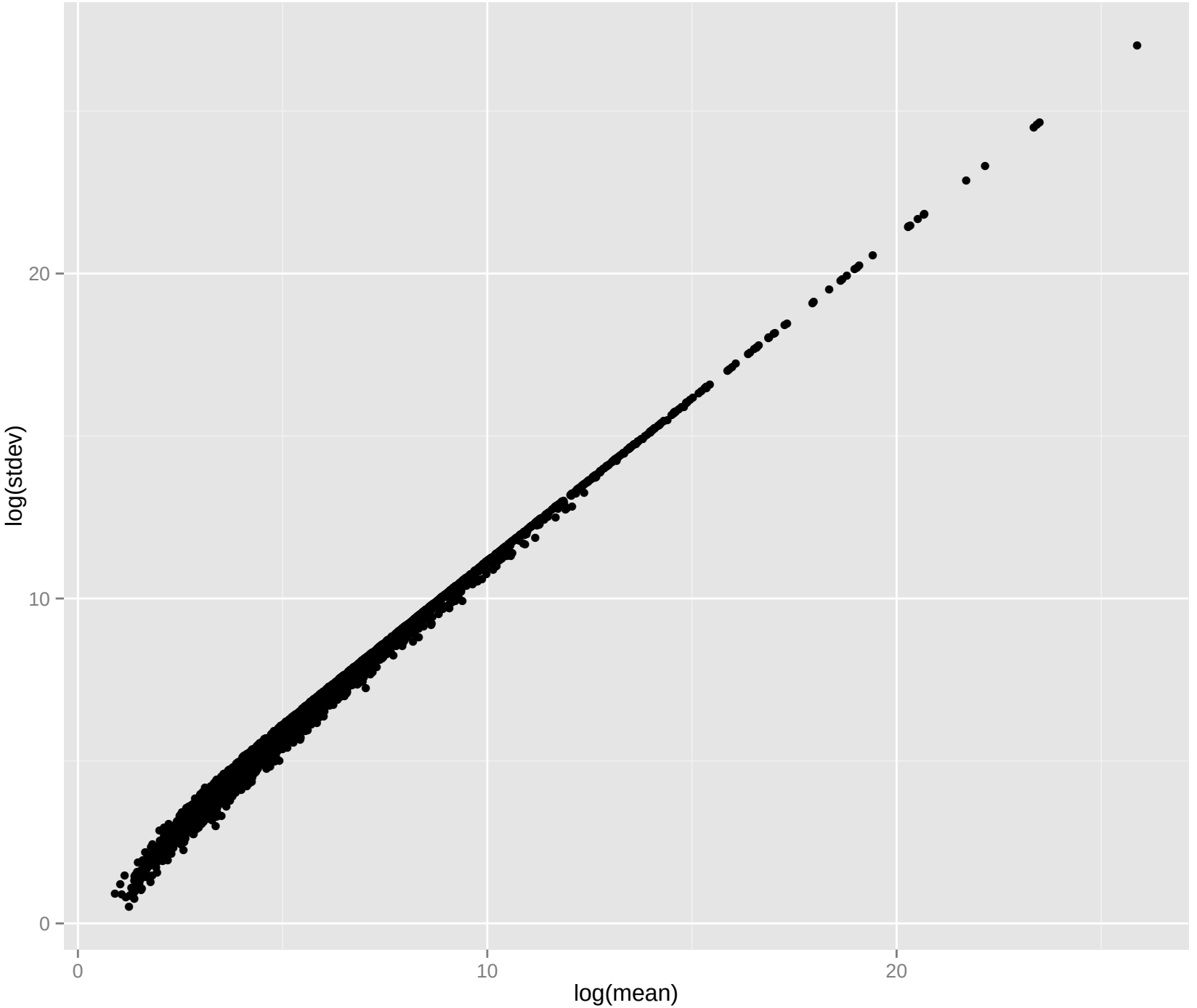

10.0
7.5
5.0
2.5
0.0
log(stdev)
2.5
5.0
7.5
log(mean)

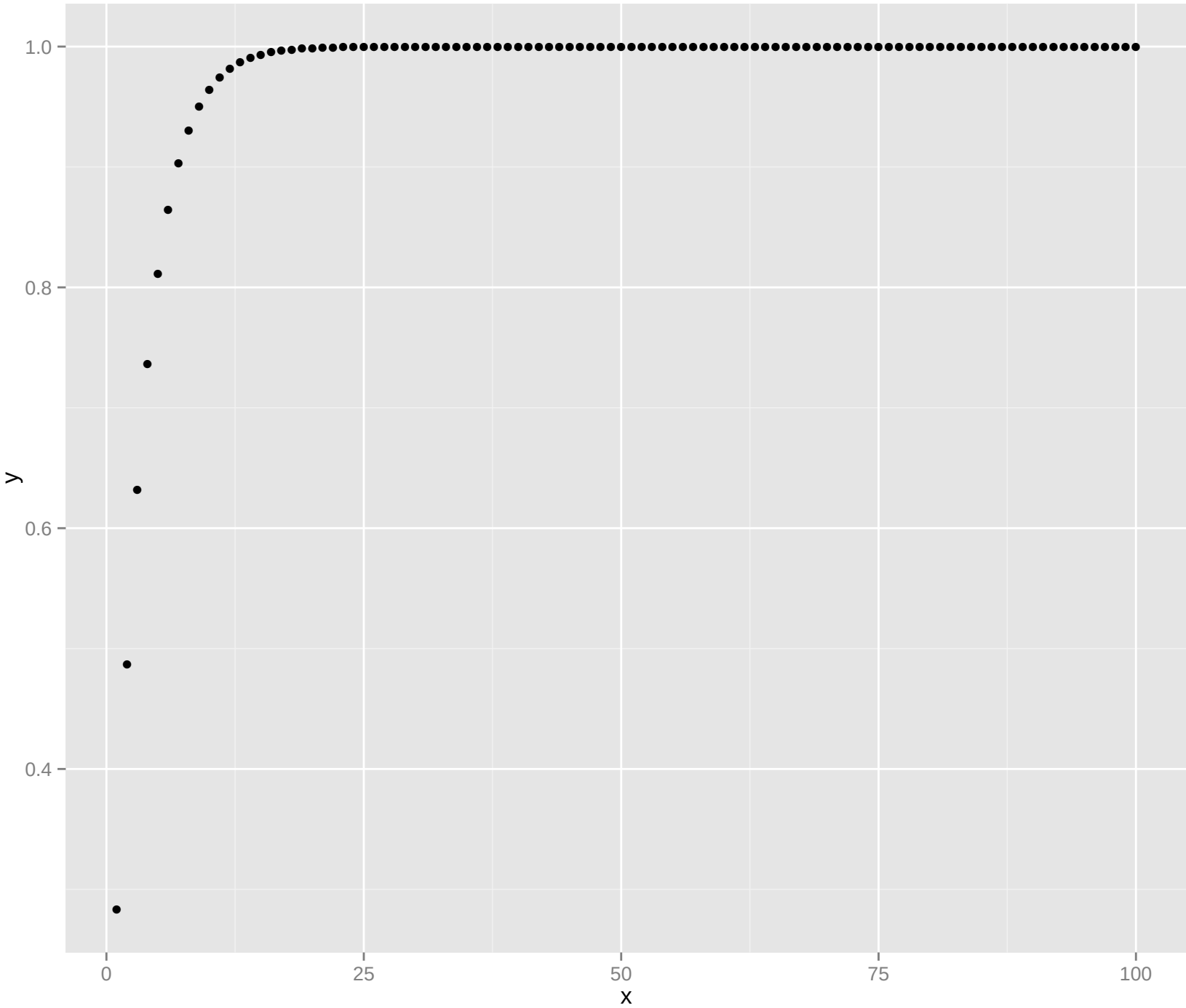

7.5
5.0
2.5
0.0
log(stdev)
0
2
4
6
log(mean)

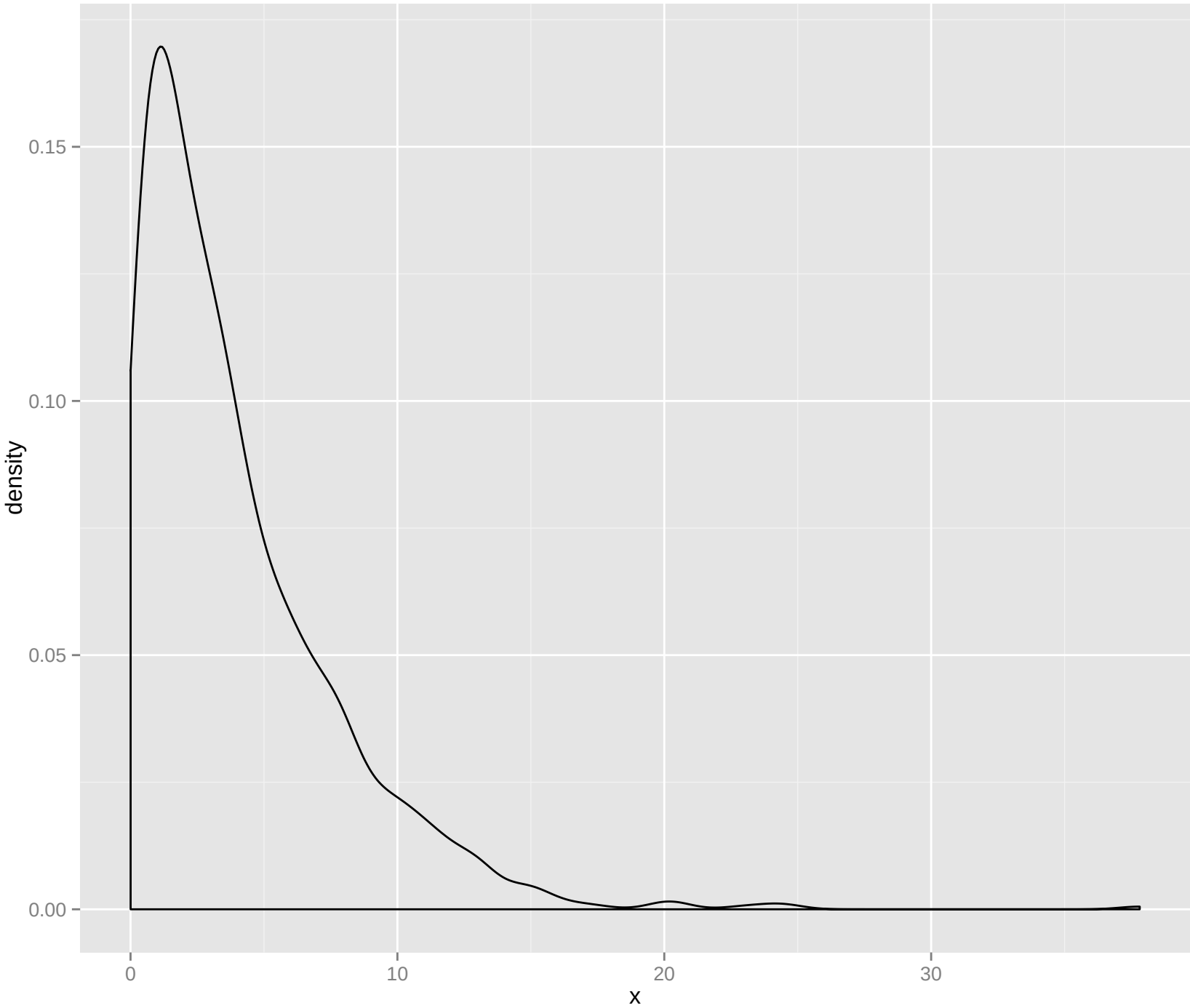

60
40
20
0
log(stdev)
0
20
40
60
log(mean)

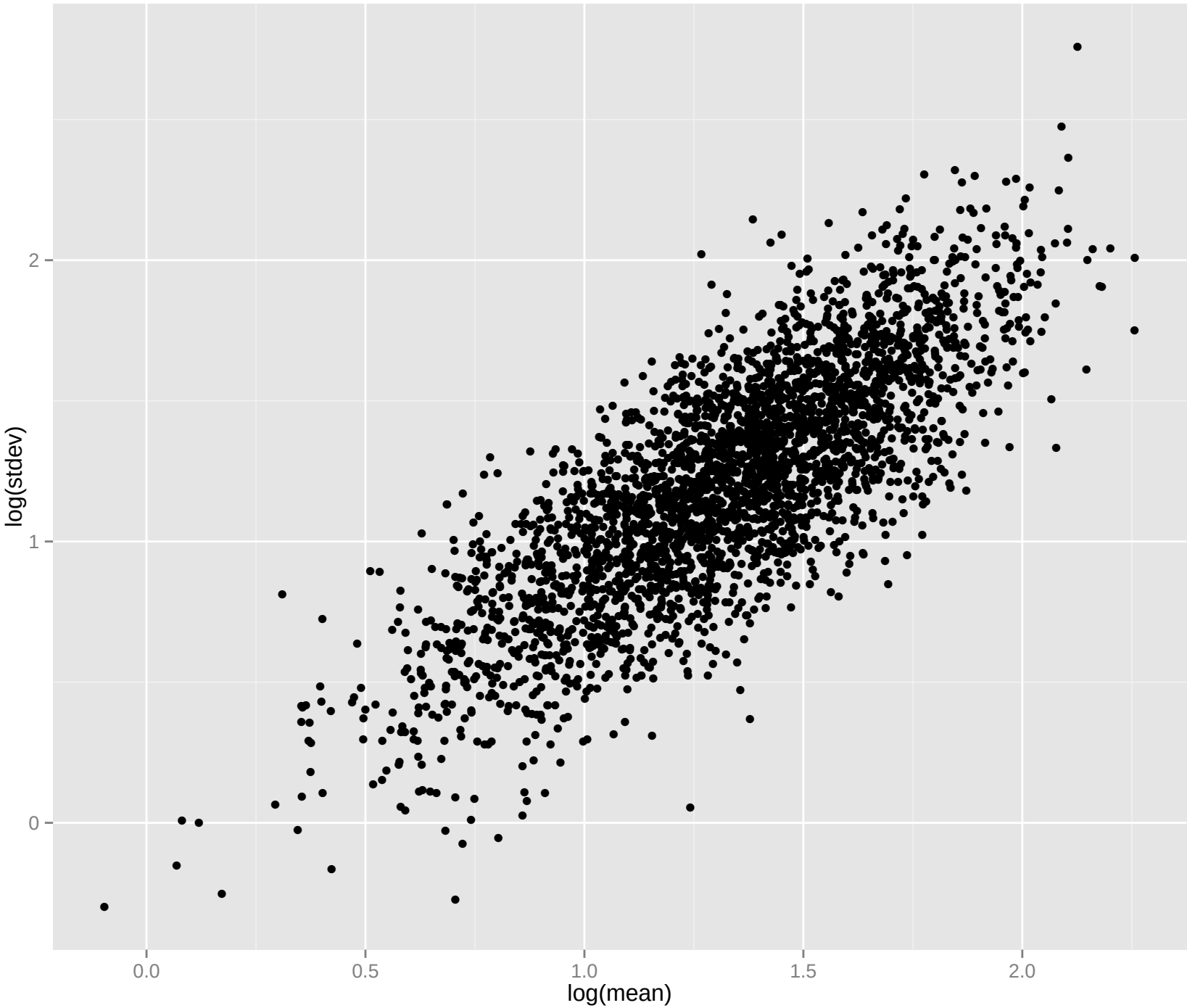

30
20
10
0
log(stdev)
0
10
20
30
log(mean)

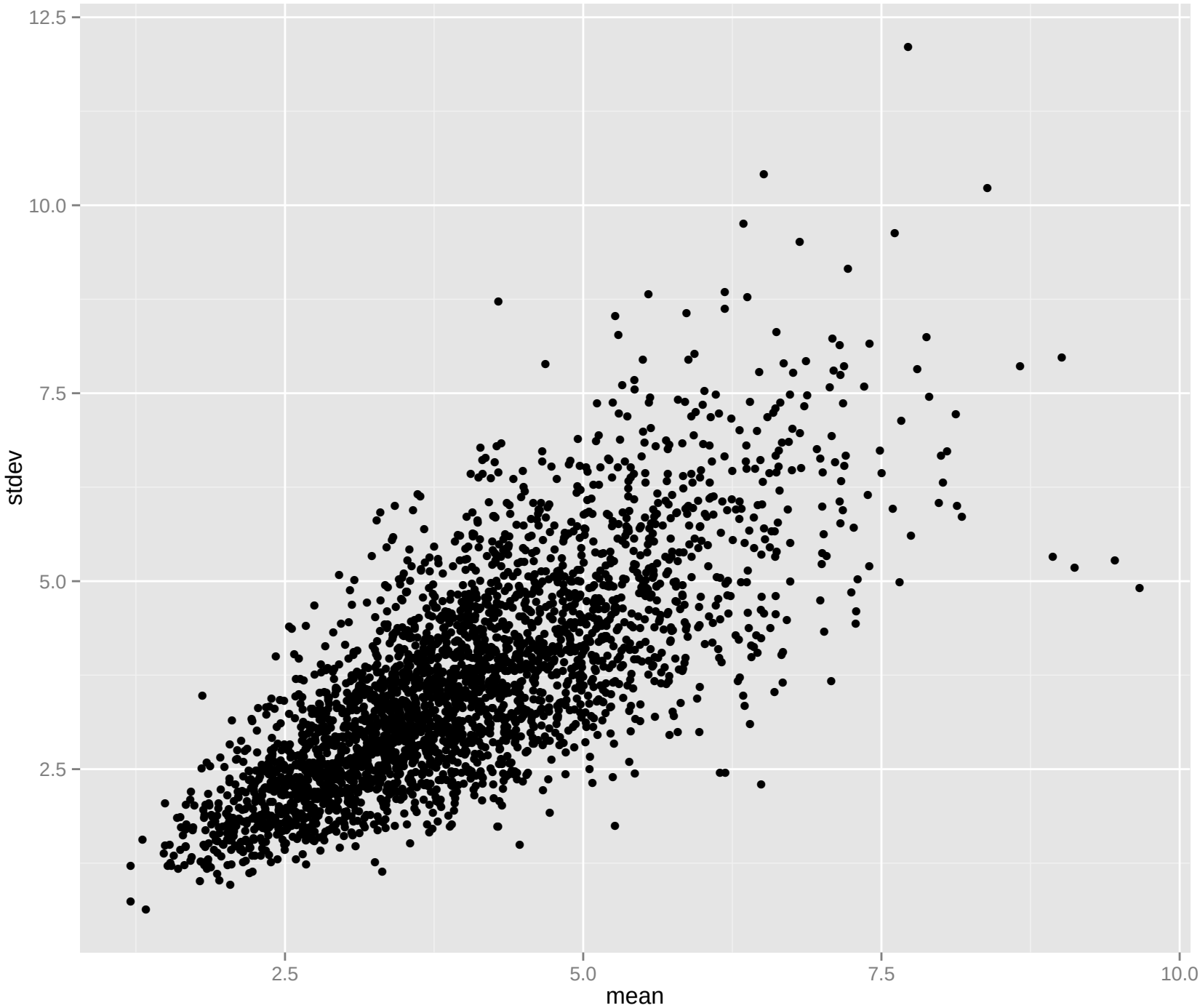

30
20
10
0
log(stdev)
0
10
20
30
log(mean)

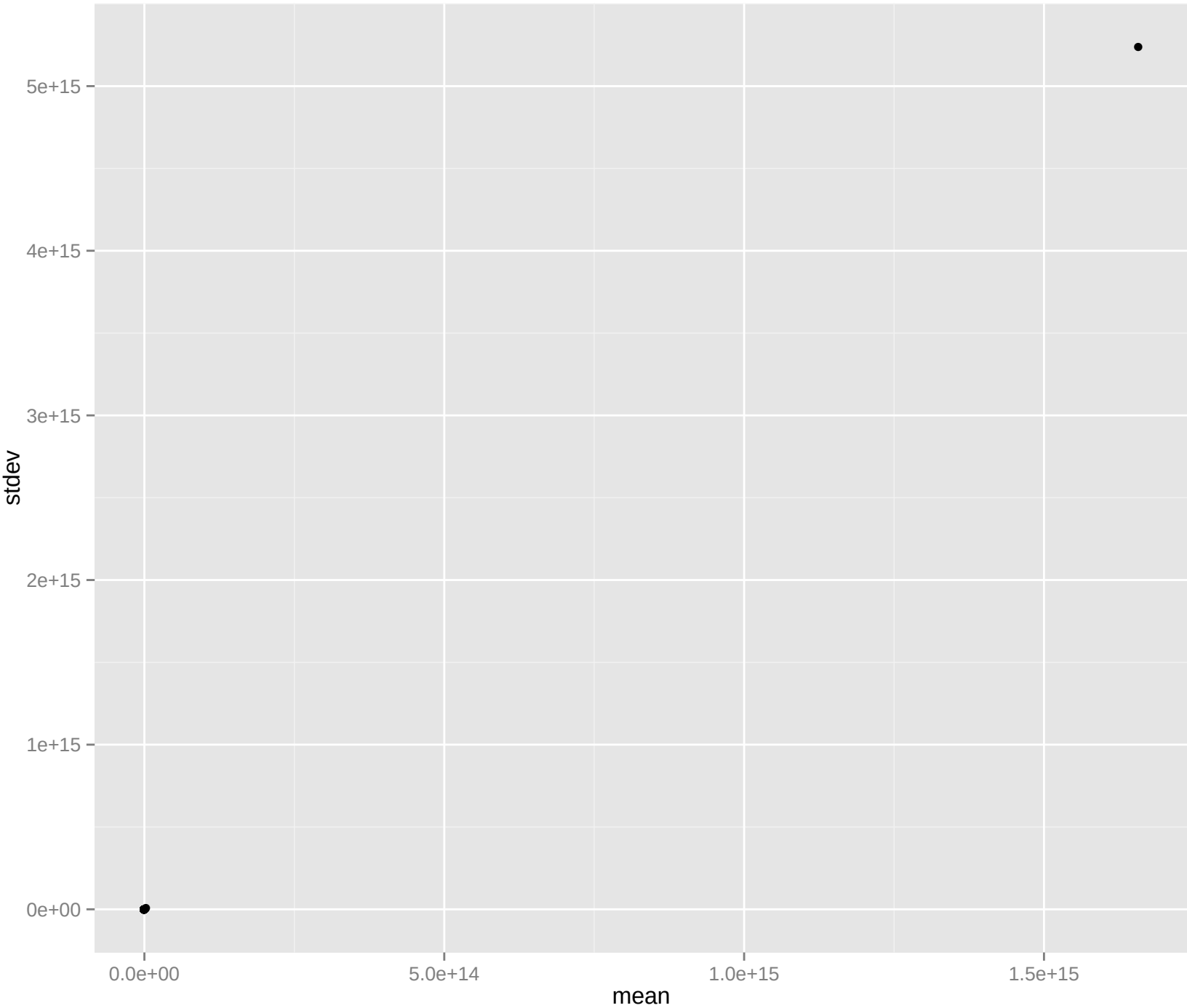

log(stdev)
20
10
0
0
10
20
log(mean)

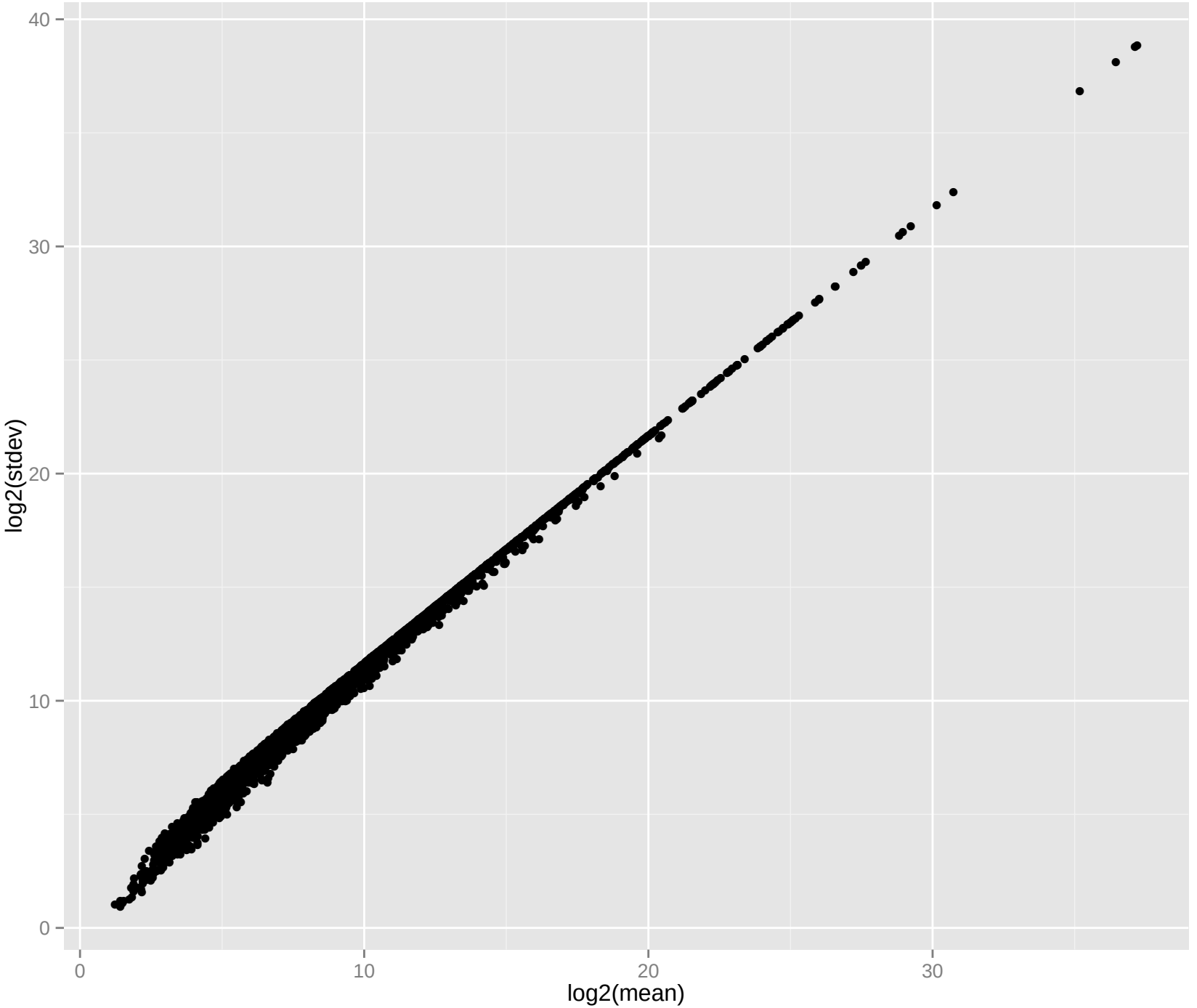

1.0
0.8
0.6
0.4
y
0
25
50
75
100
x

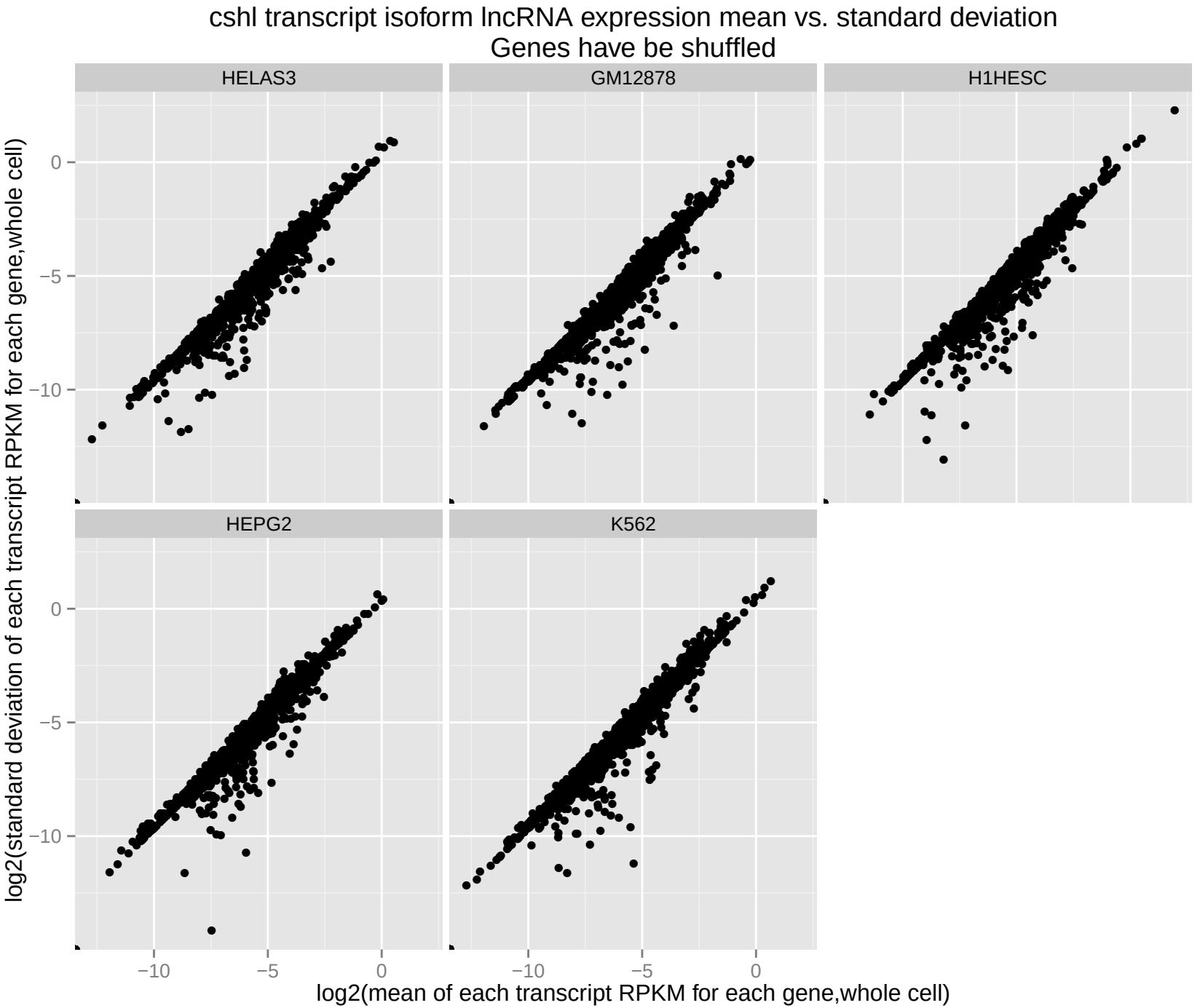

0.15
0.10
0.05
0.00
density
0
10
20
30
x

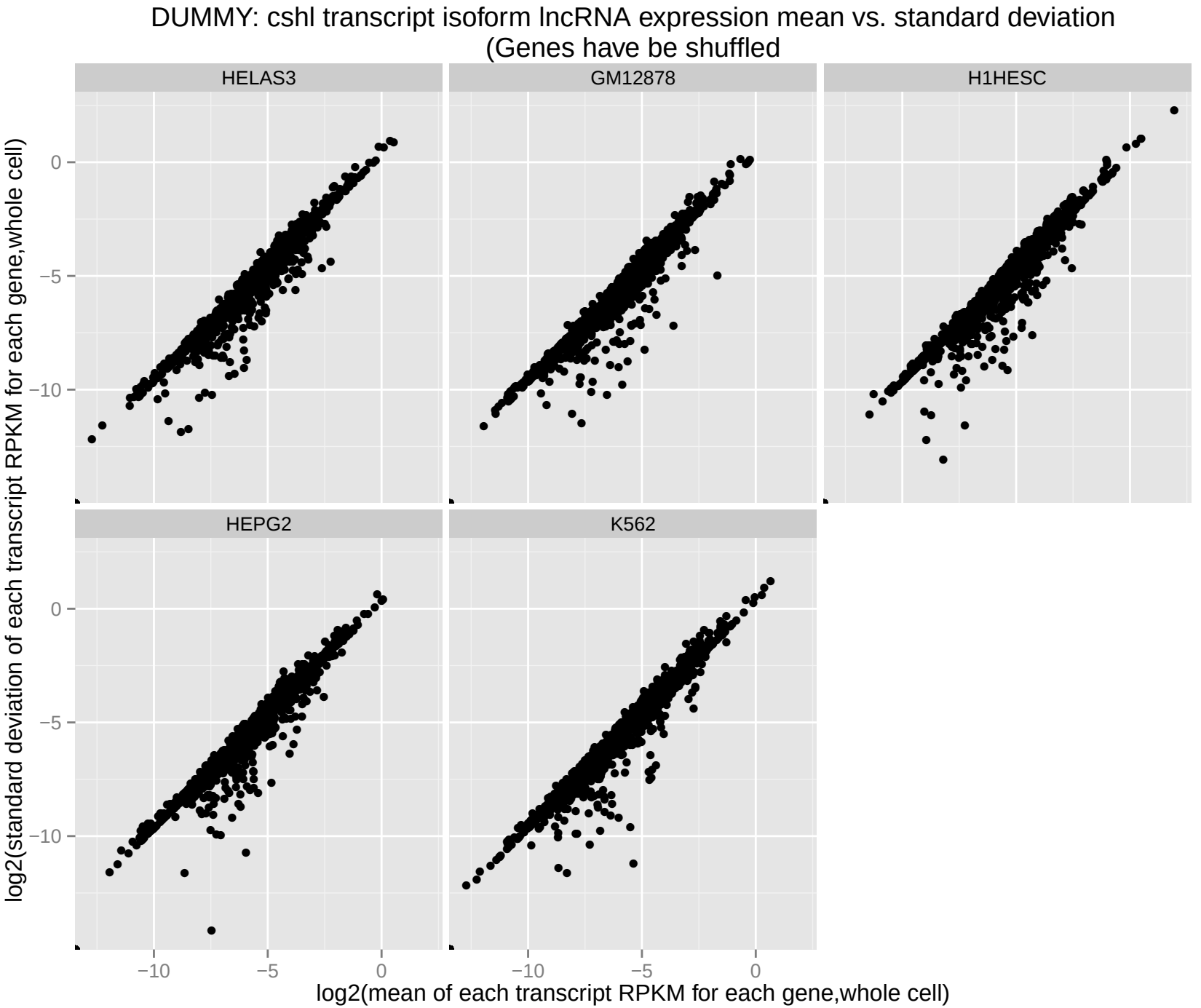

log(stdev)
2
1
0
0.0
0.5
1.0
1.5
2.0
log(mean)

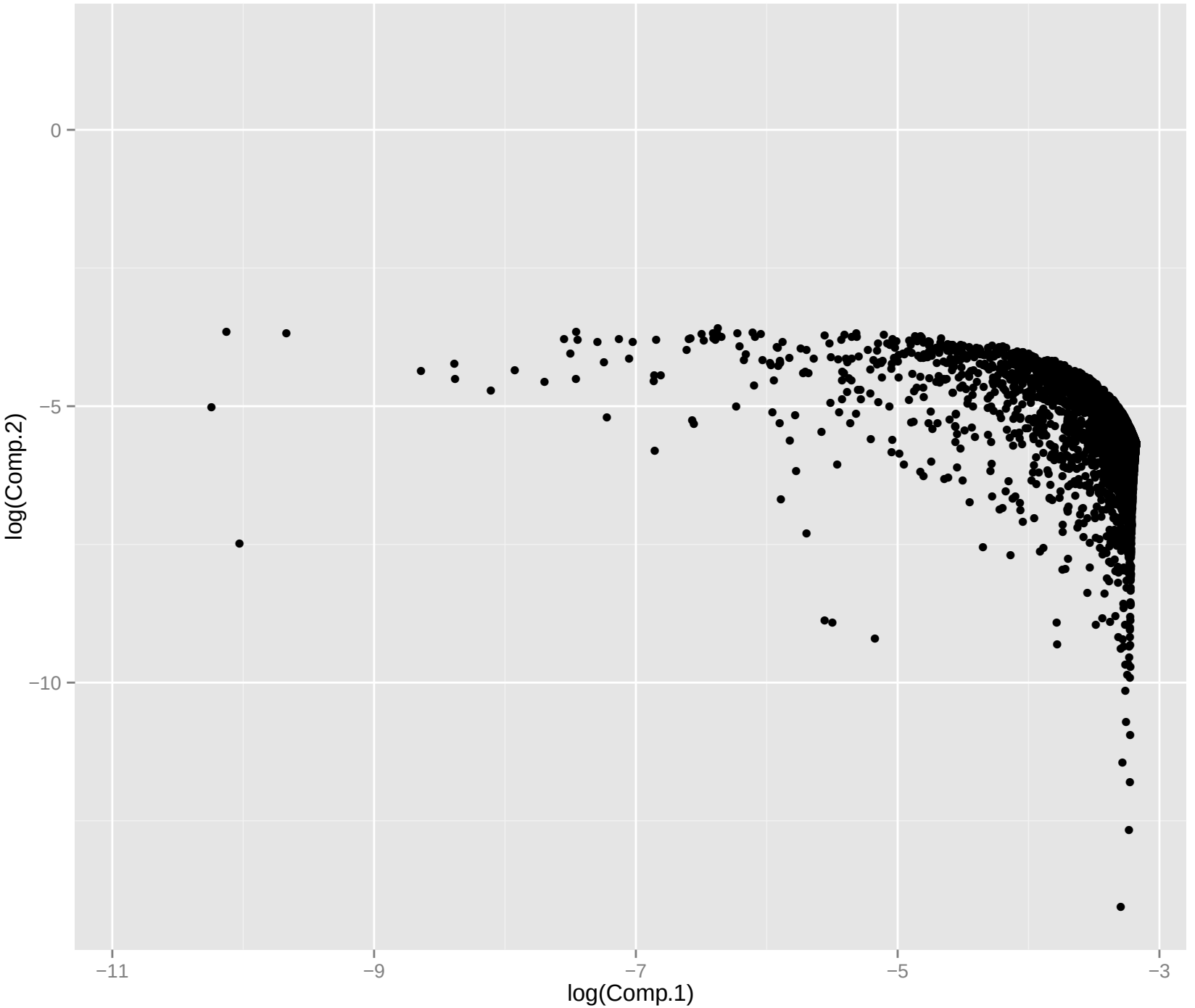

12.5
10.0
7.5
5.0
2.5
stdev
2.5
5.0
7.5
10.0
mean


5e+15
4e+15
3e+15
2e+15
1e+15
0e+00
stdev
0.0e+00
5.0e+14
1.0e+15
1.5e+15
mean


40
30
20
10
0
log2(stdev)
0
10
20
30
log2(mean)


cshl transcript isoform lncRNA expression mean vs. standard deviation
Genes have be shuffled
HELAS3
GM12878
H1HESC
HEPG2
K562
0
−5
−10
log2(standard deviation of each transcript RPKM for each gene,whole cell)
log2(mean of each transcript RPKM for each gene,whole cell)


DUMMY: cshl transcript isoform lncRNA expression mean vs. standard deviation
(Genes have be shuffled
HELAS3
GM12878
H1HESC
HEPG2
K562
0
−5
−10
log2(standard deviation of each transcript RPKM for each gene,whole cell)
log2(mean of each transcript RPKM for each gene,whole cell)


0
−5
−10
log(Comp.2)
−11
−9
−7
−5
−3
log(Comp.1)