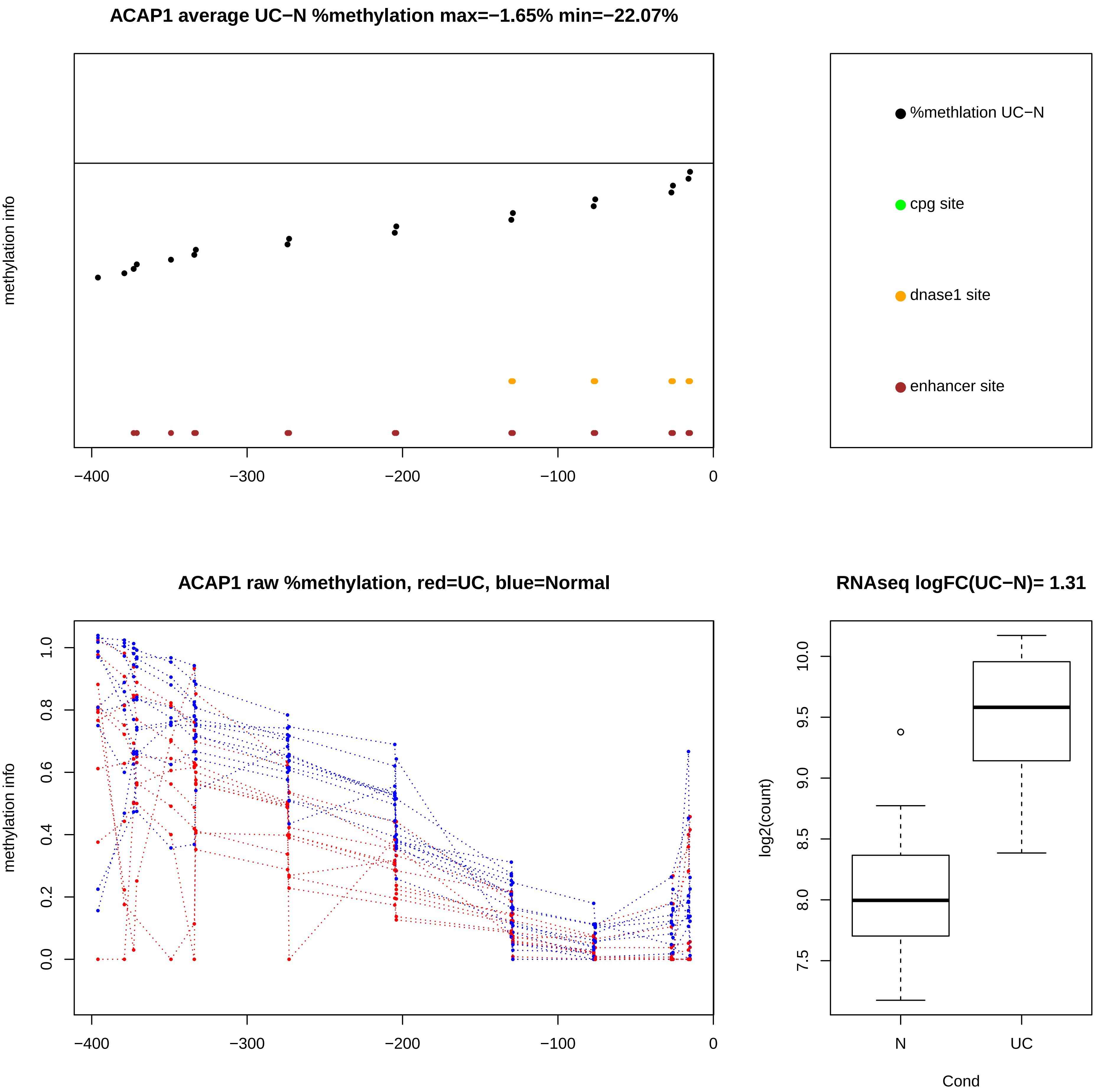
Supplementary Data 3. Relationship between the raw methylation data per sample, average difference between groups, and relationship to the TSS and transcript expression.

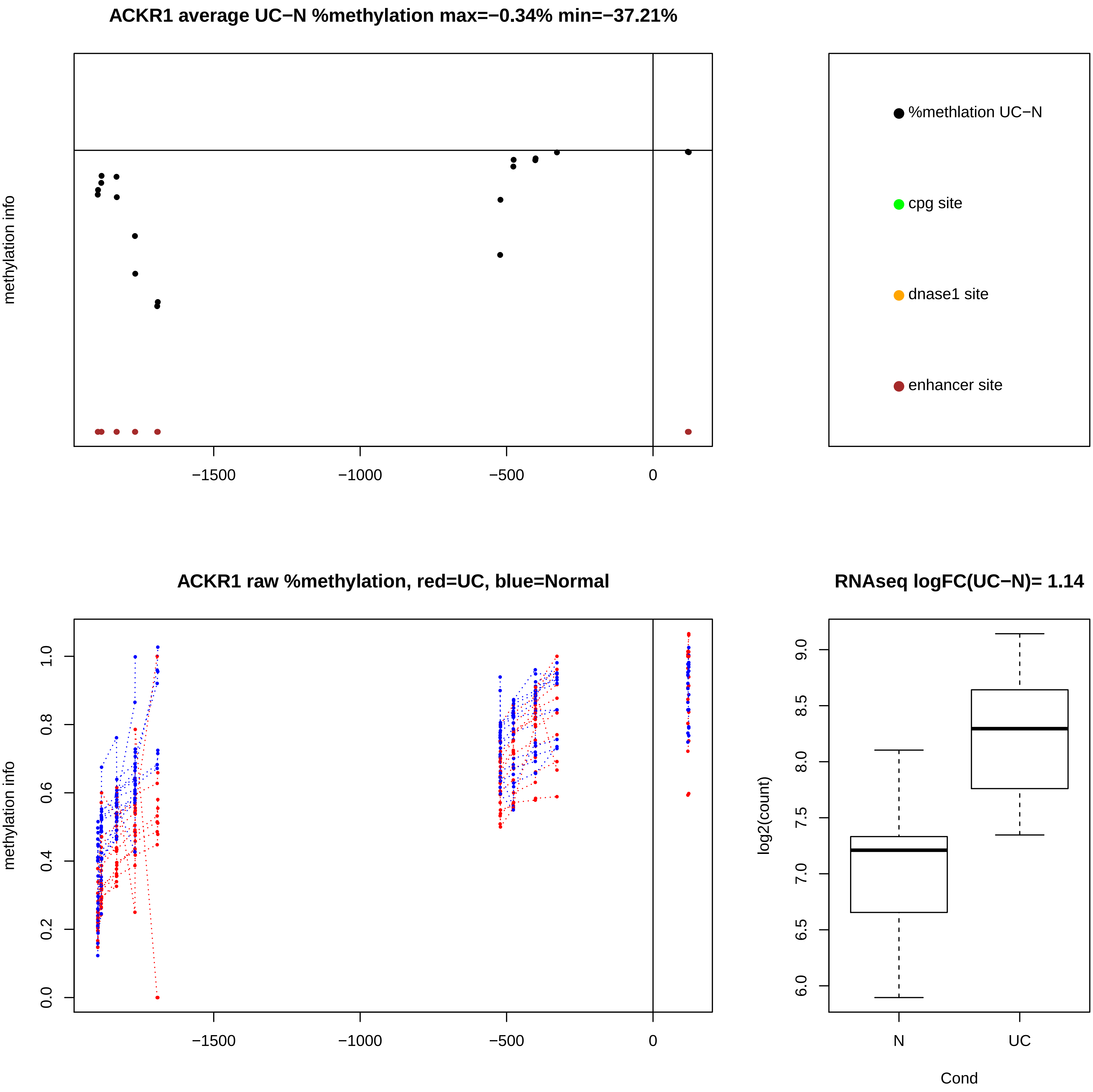
Top left panel: The Y axis represents difference in relative methylation between the ulcerative colitis and normal groups. The X-axis shows the position relative to the TSS site defined as 0. Negative numbers are upstream of TSS, positive numbers downstream.
Top right panel: Legend of top left panel.
Bottom left panel: The raw methylation data per patient. The X scale is the same as the top left panel. The Y-axis shows relative methylation, 1 for 100% methylated, 0 for not methylated, 0.5 for 50% methylated.
A point represent the relative methylation value for a sample at a particular location. Dotted lines connect same samples between positions. Red points and dotted lines are from Ulcerative Colitis samples, blue from normal samples.
Bottom right panel: Shows a boxplot of the normalized log2 values of the transcript corresponding to the promoter.



ACAP1 average UC−N %methylation max=−1.65% min=−22.07%

ACAP1 raw %methylation, red=UC, blue=Normal

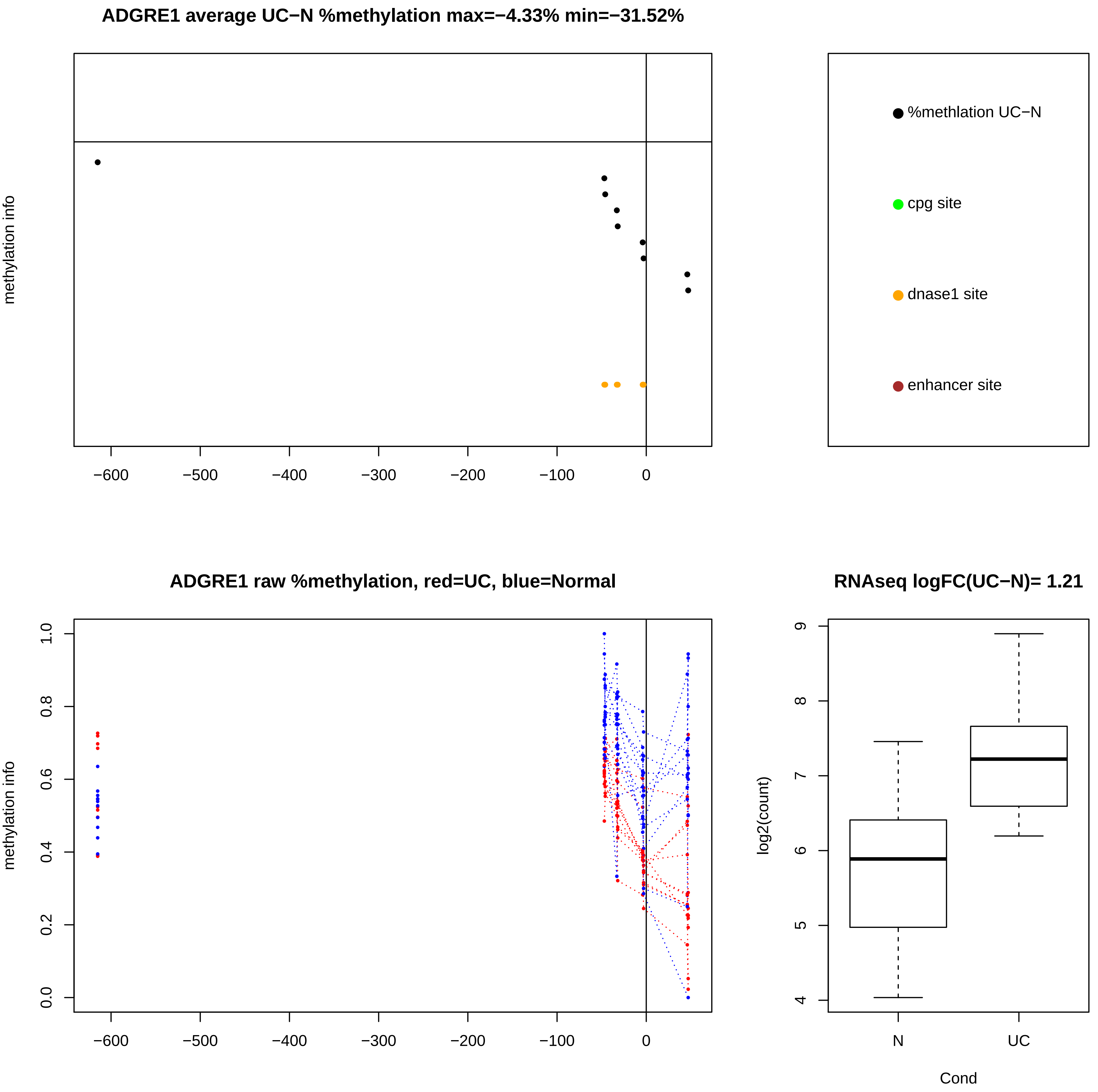
RNAseq logFC(UC−N)= 1.31



ACKR1 average UC−N %methylation max=−0.34% min=−37.21%

ACKR1 raw %methylation, red=UC, blue=Normal

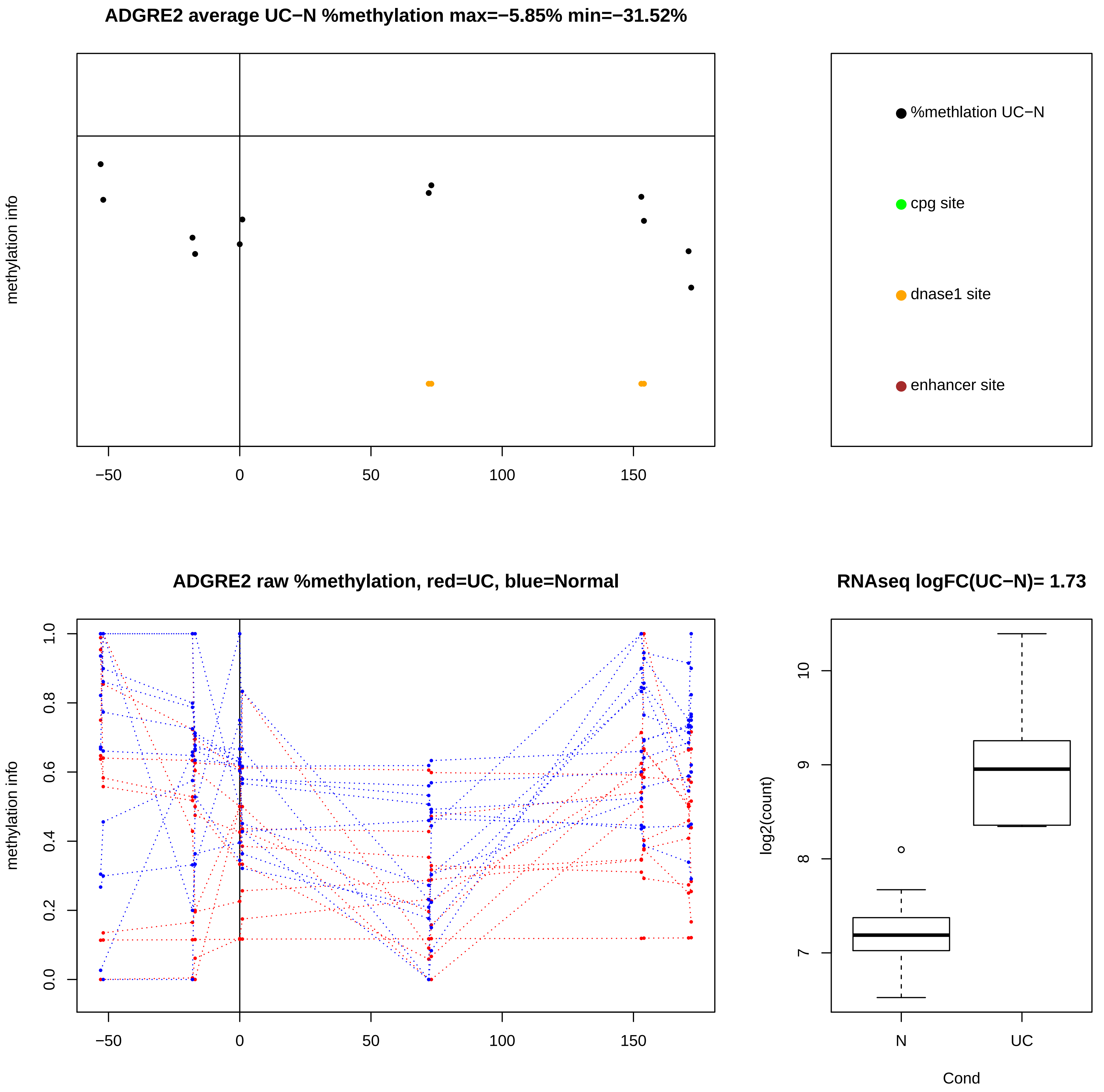
RNAseq logFC(UC−N)= 1.14



ADGRE1 average UC−N %methylation max=−4.33% min=−31.52%

ADGRE1 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.21

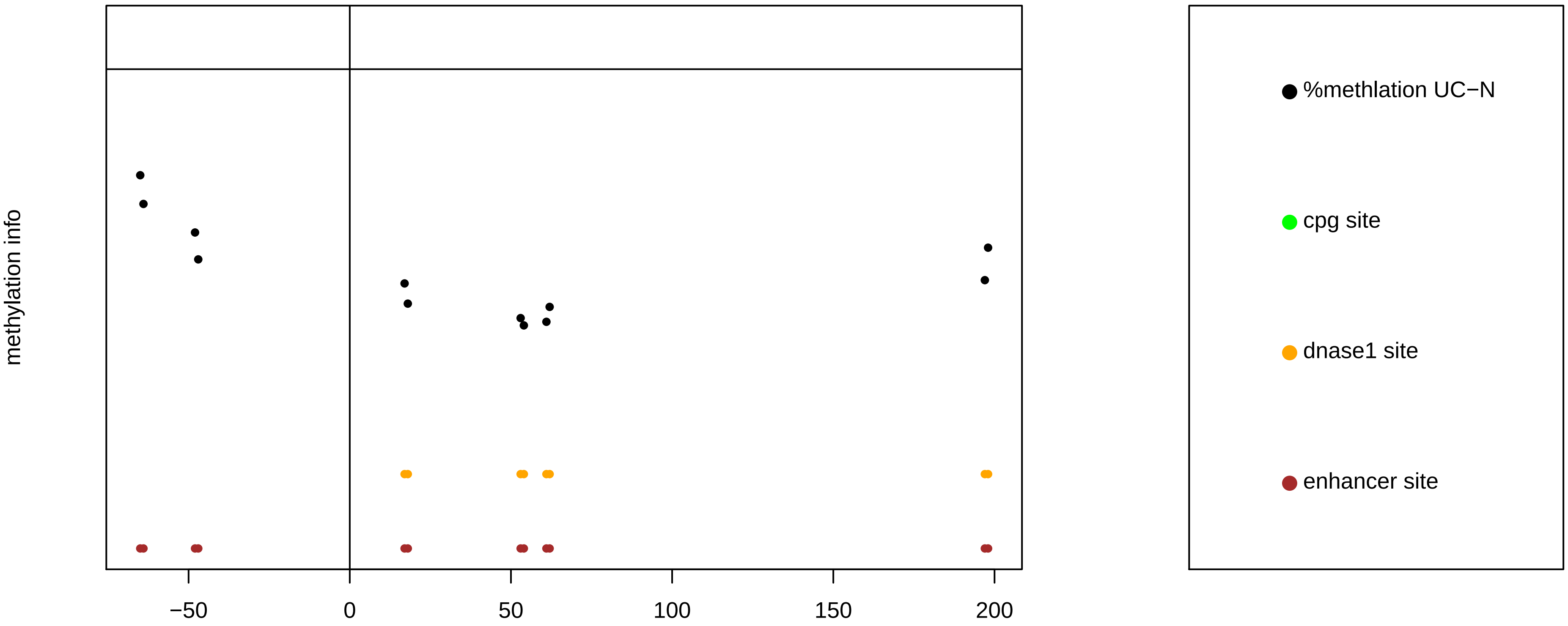


ADGRE2 average UC−N %methylation max=−5.85% min=−31.52%

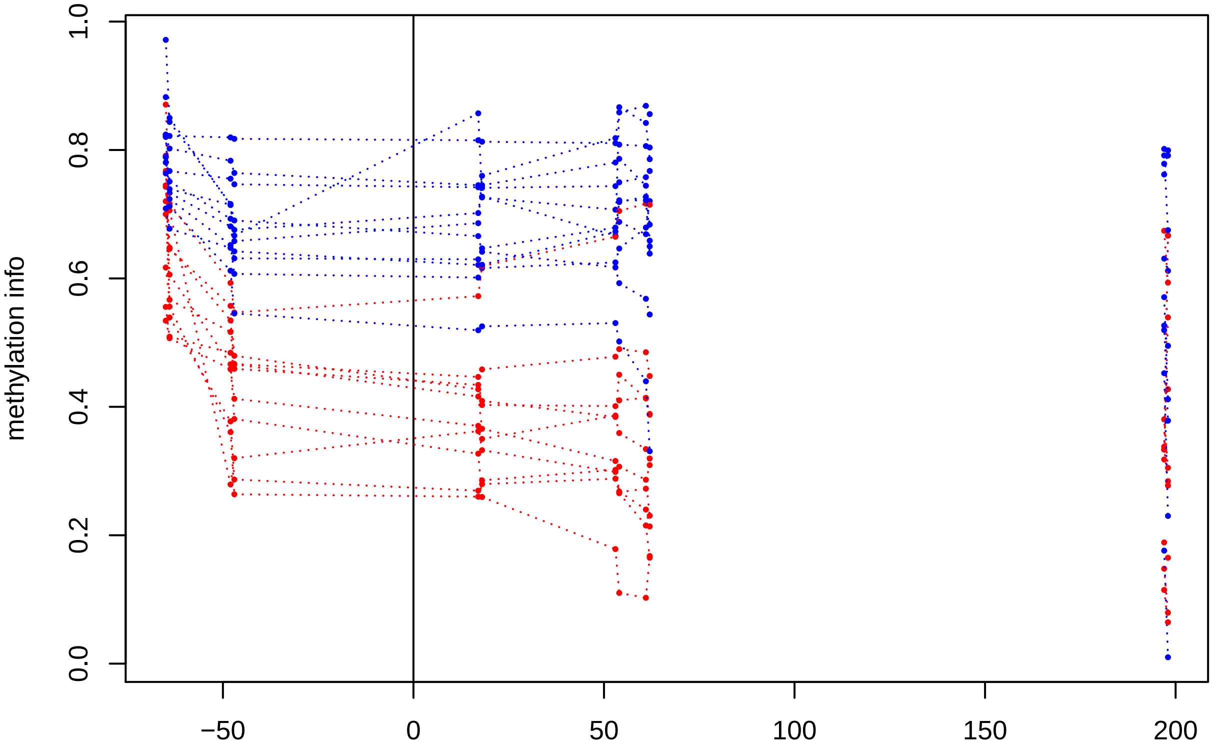
ADGRE2 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.73

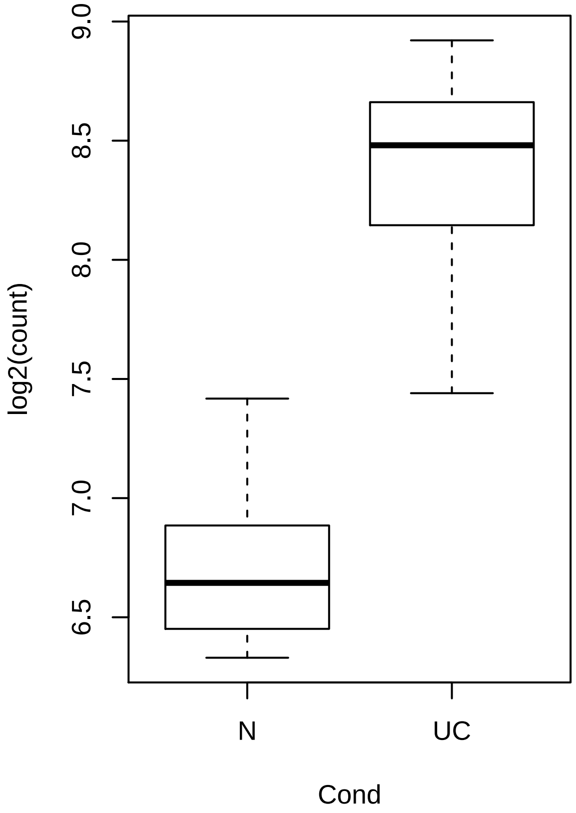
ADGRG5 average UC−N %methylation max=−14.26% min=−34.46%

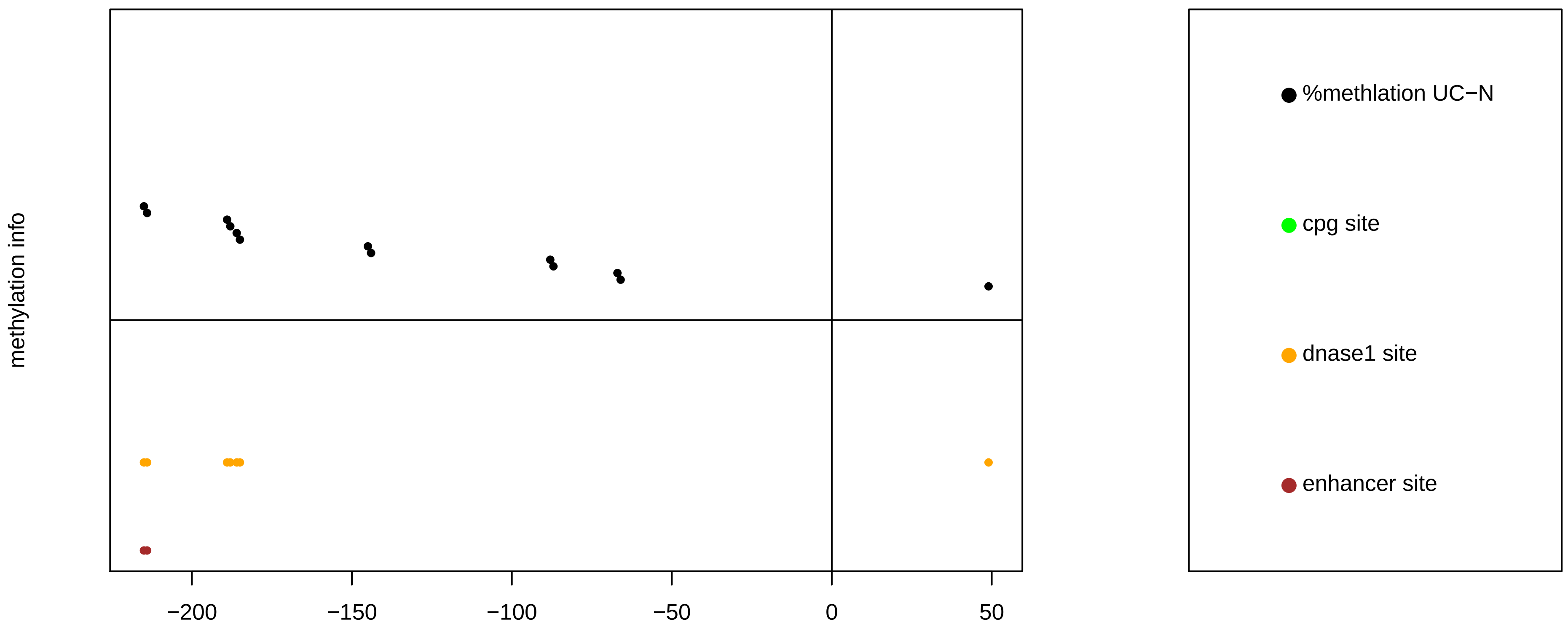


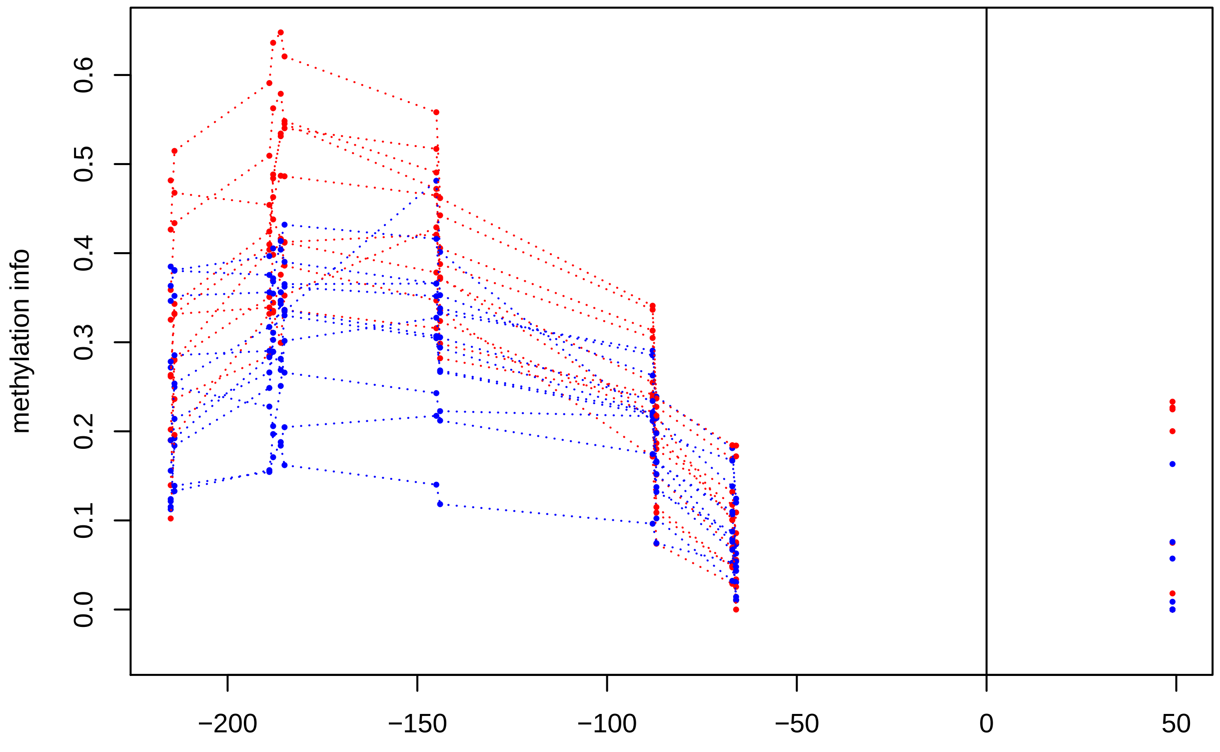
ADGRG5 raw %methylation, red=UC, blue=Normal

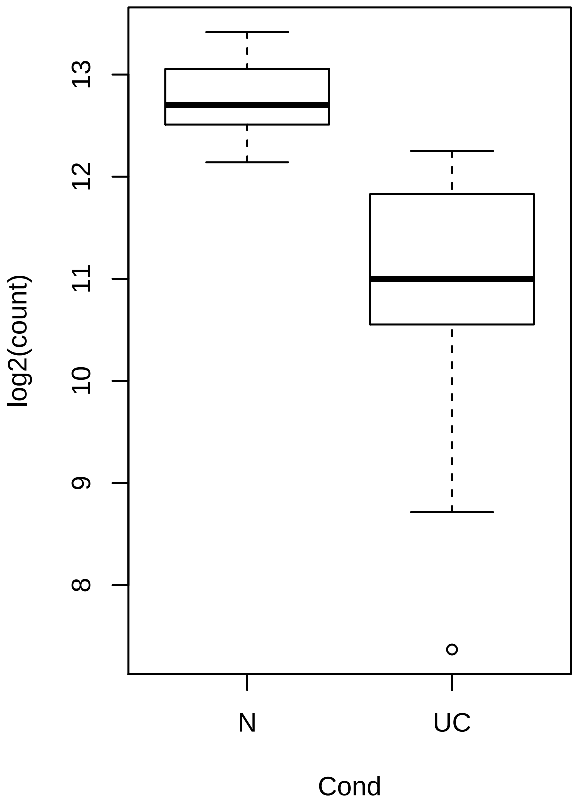


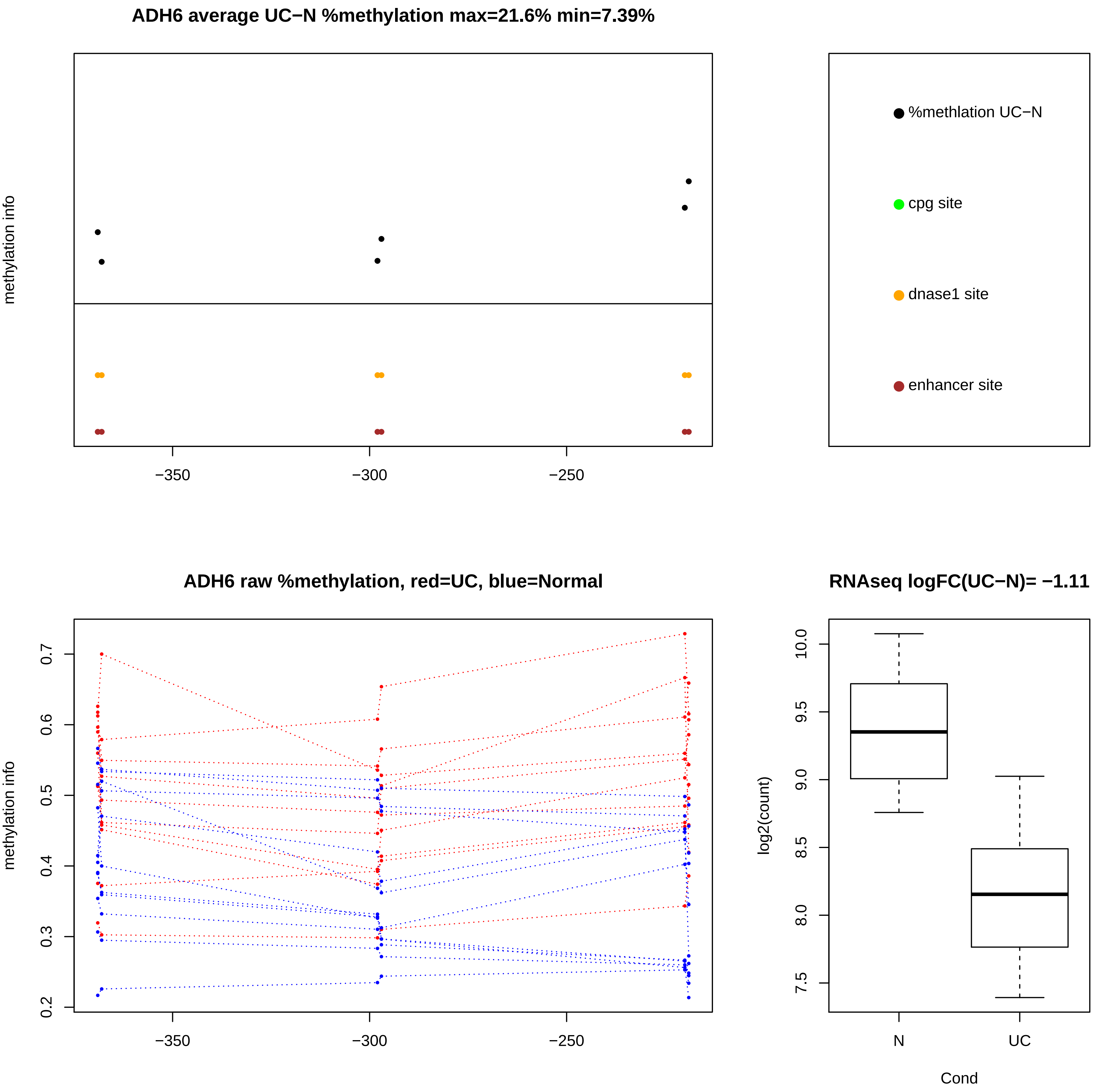
RNAseq logFC(UC−N)= 1.54




ADH1C average UC−N %methylation max=12.93% min=3.83%


ADH1C raw %methylation, red=UC, blue=Normal

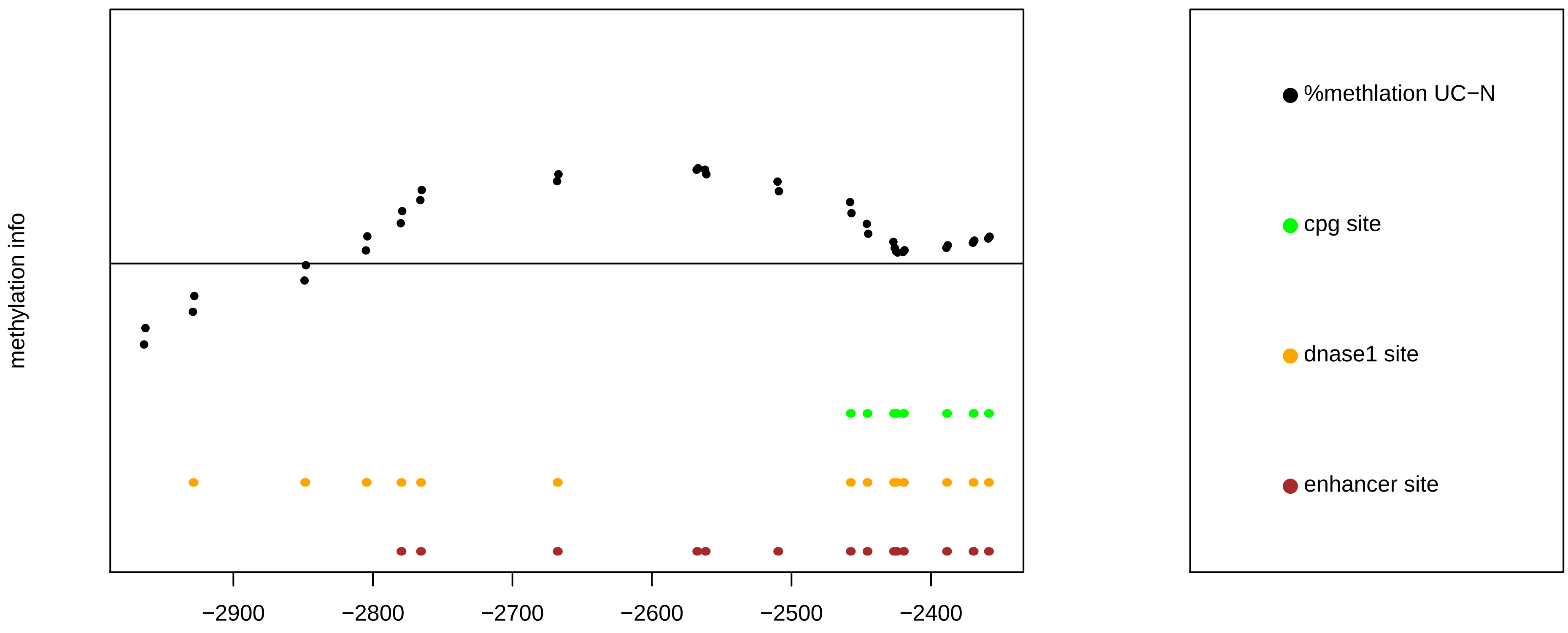

RNAseq logFC(UC−N)= −1.25


ADH6 average UC−N %methylation max=21.6% min=7.39%

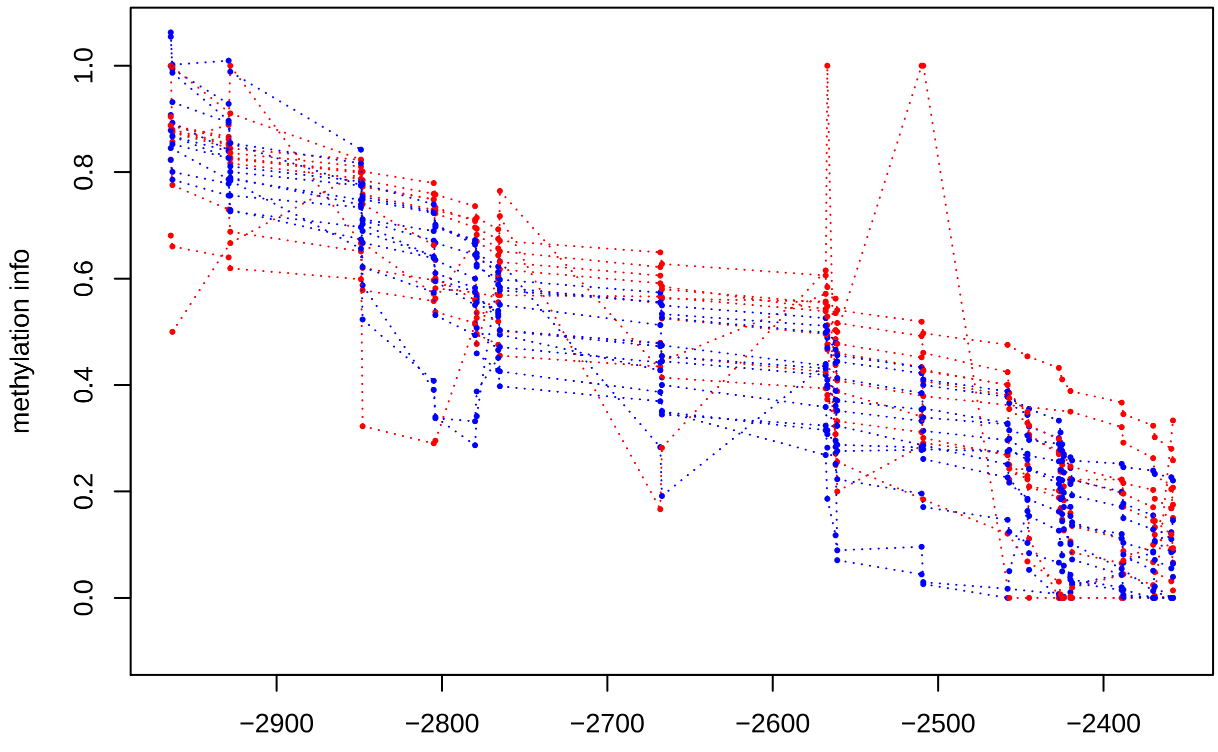
ADH6 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= −1.11

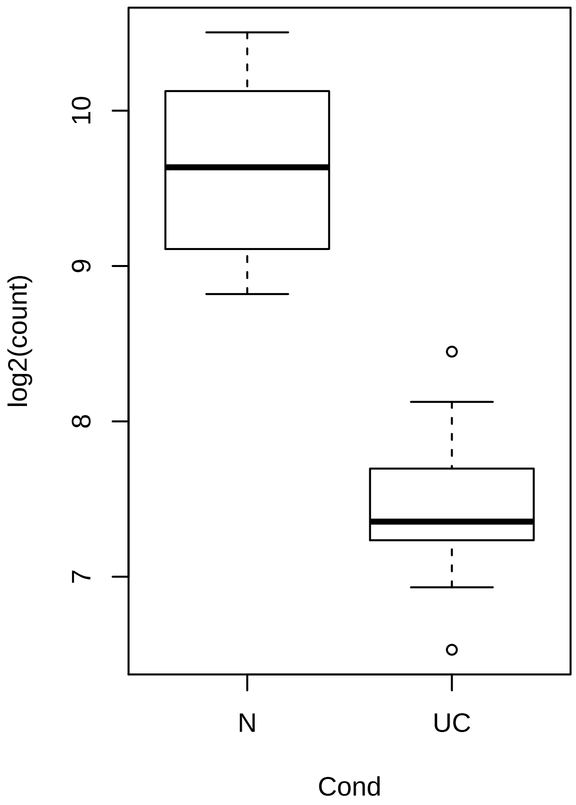
ADIRF average UC−N %methylation max=13.83% min=−11.74%

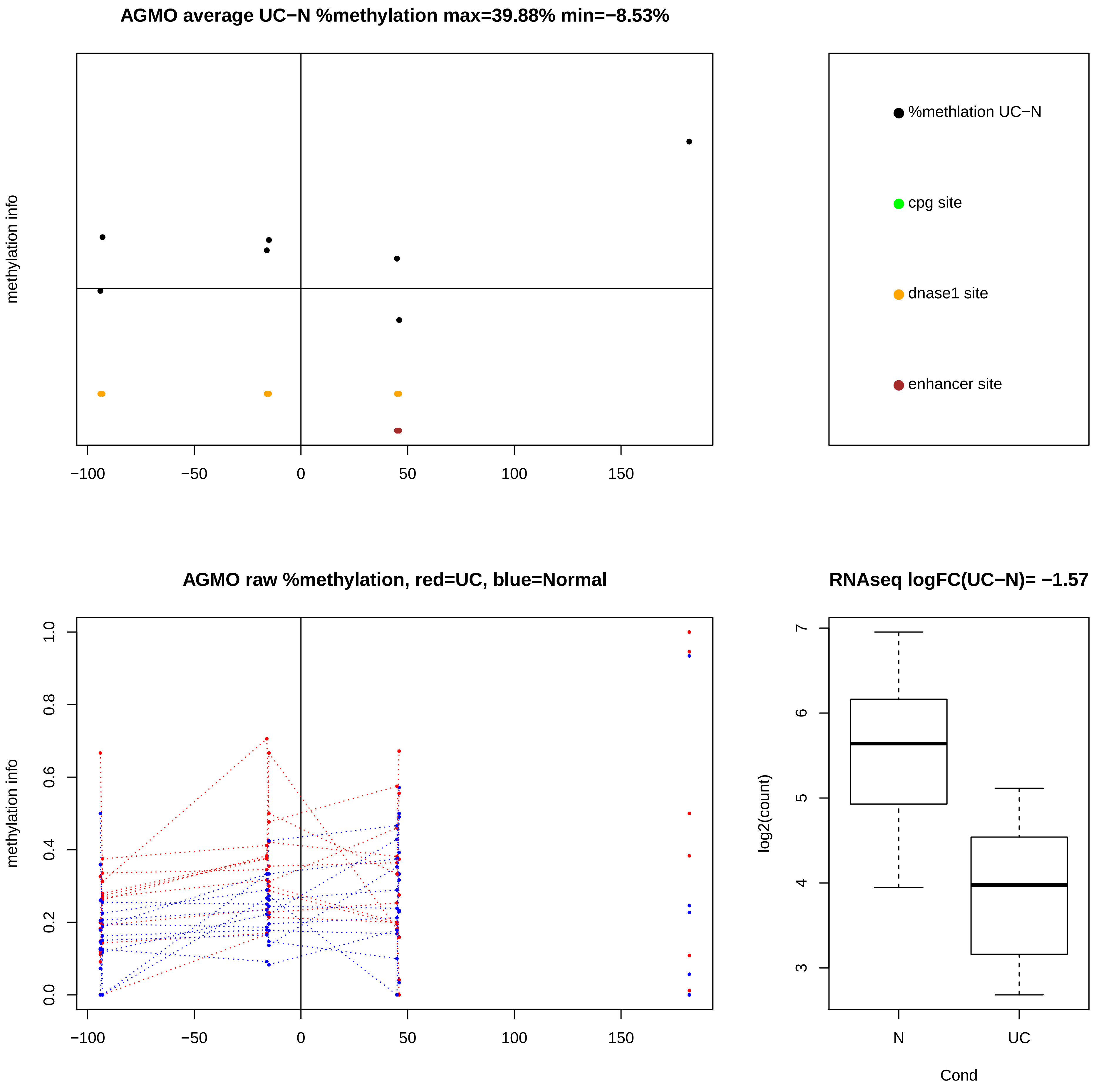


ADIRF raw %methylation, red=UC, blue=Normal

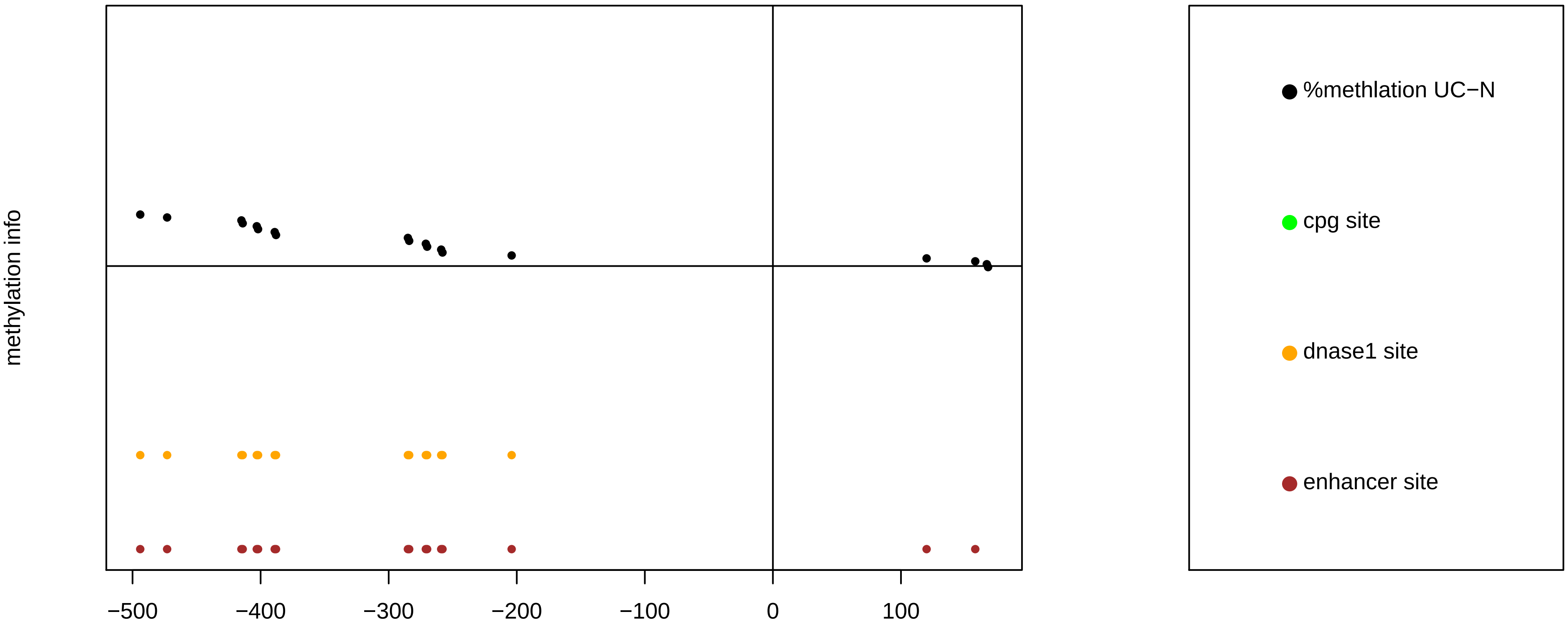


RNAseq logFC(UC−N)= −1.88

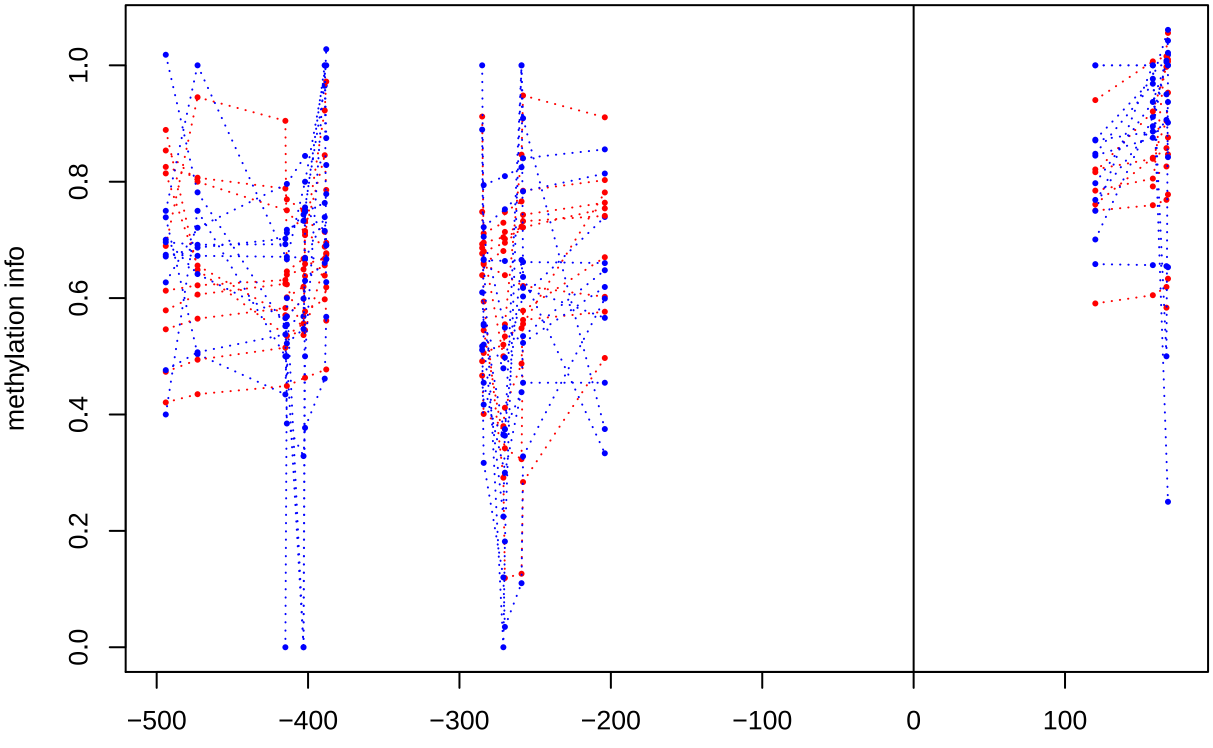



AGMO average UC−N %methylation max=39.88% min=−8.53%
methylation info
−100
−50
0
50
100
150
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
AGMO raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−100
−50
0
50
100
150
RNAseq logFC(UC−N)= −1.57
log2(count)
3
4
5
6
7
N
UC
Cond

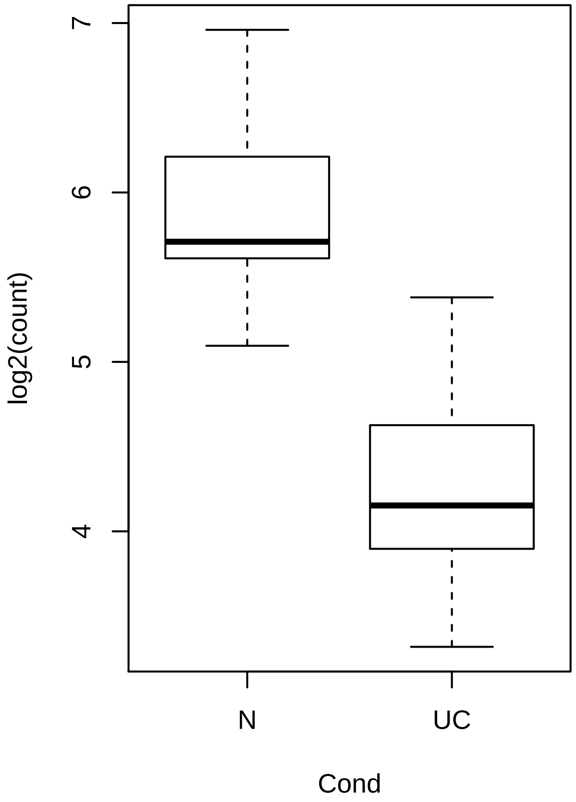
ALOX12B average UC−N %methylation max=5.48% min=−0.12%

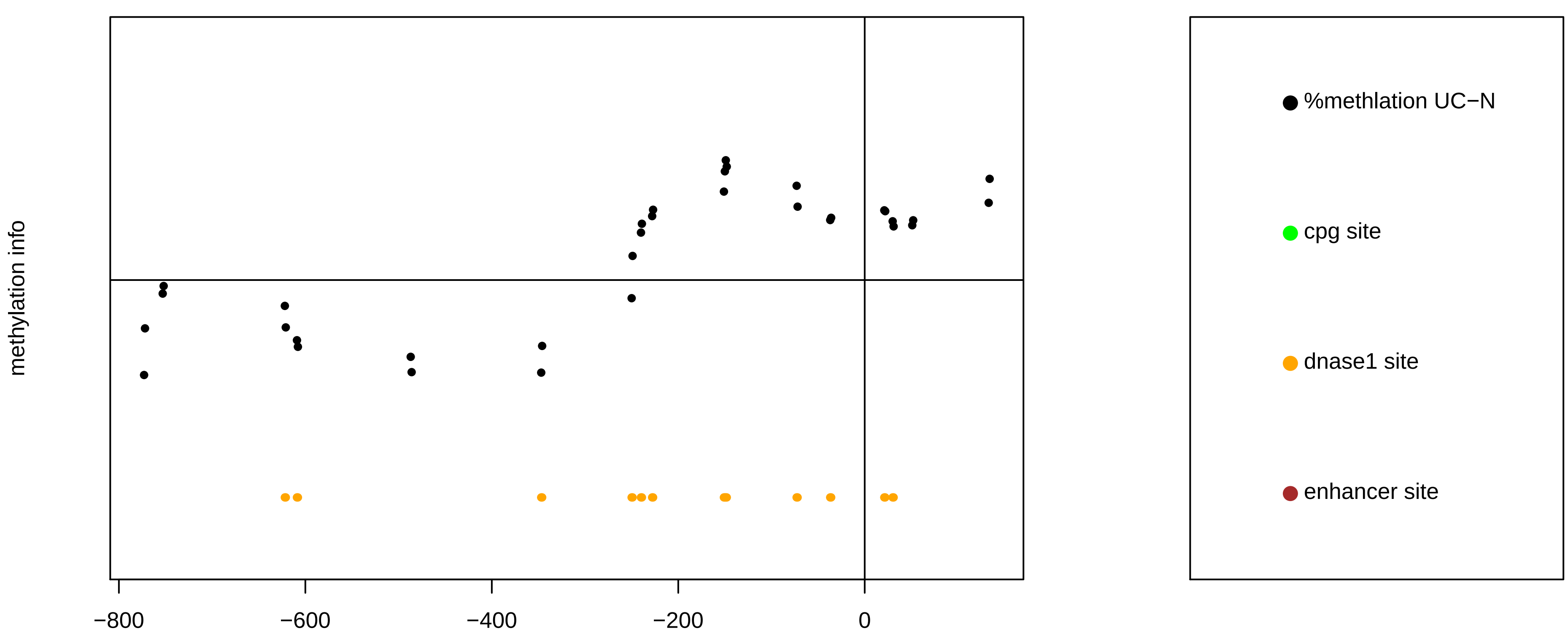


ALOX12B raw %methylation, red=UC, blue=Normal

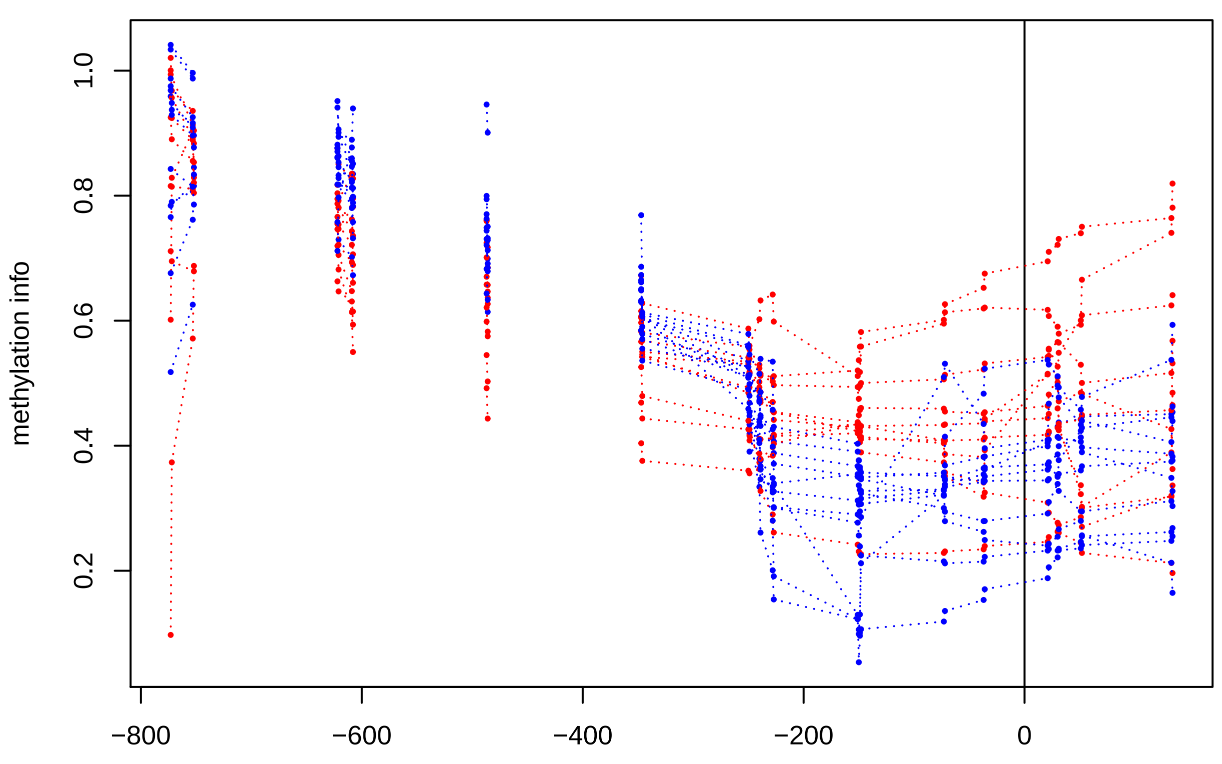


RNAseq logFC(UC−N)= −1.47

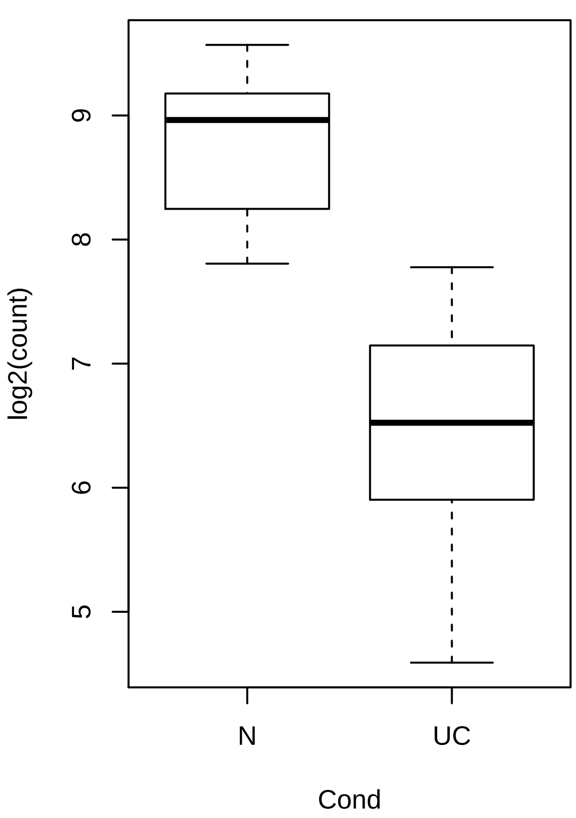




ALPI average UC−N %methylation max=19.58% min=−15.52%

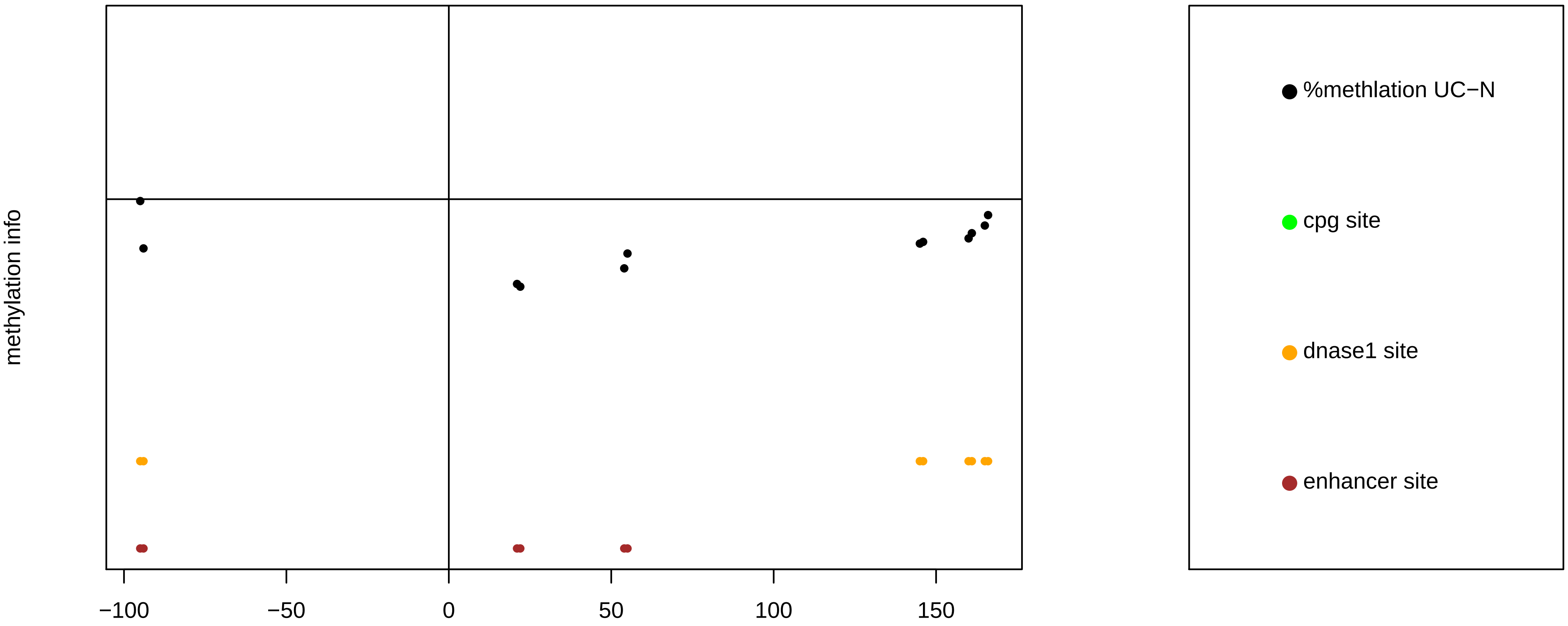


ALPI raw %methylation, red=UC, blue=Normal

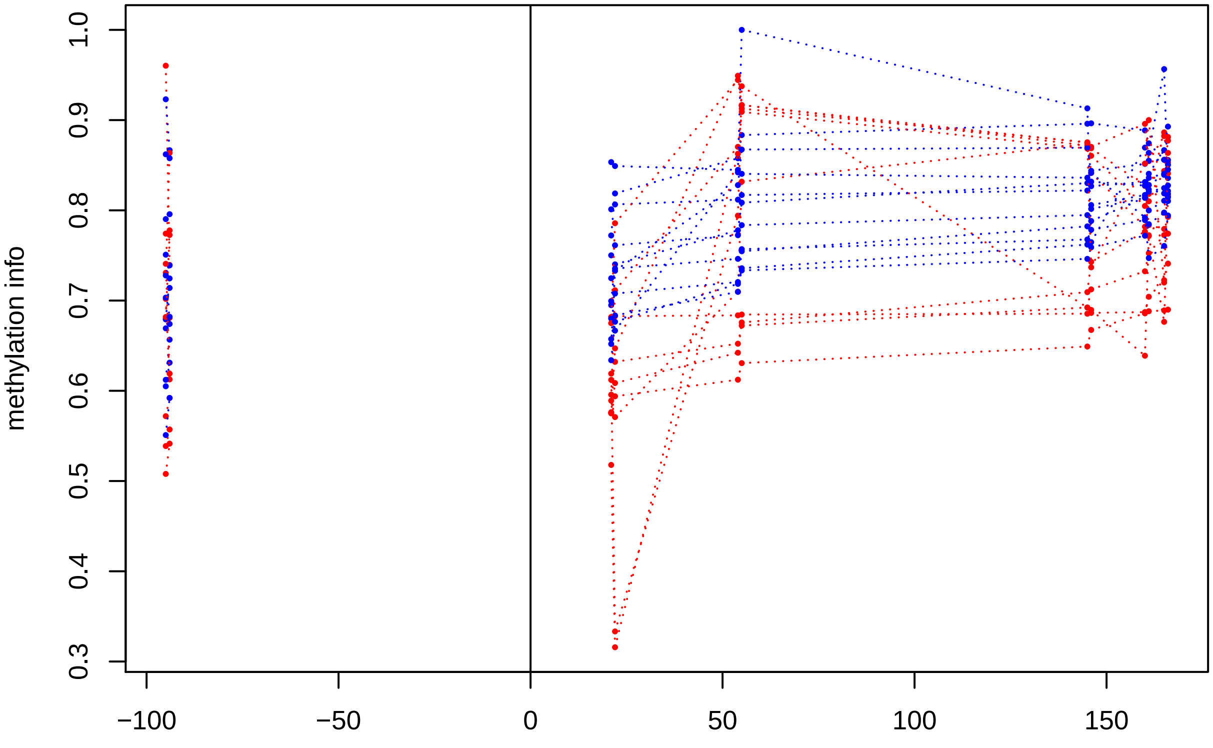


RNAseq logFC(UC−N)= −1.91

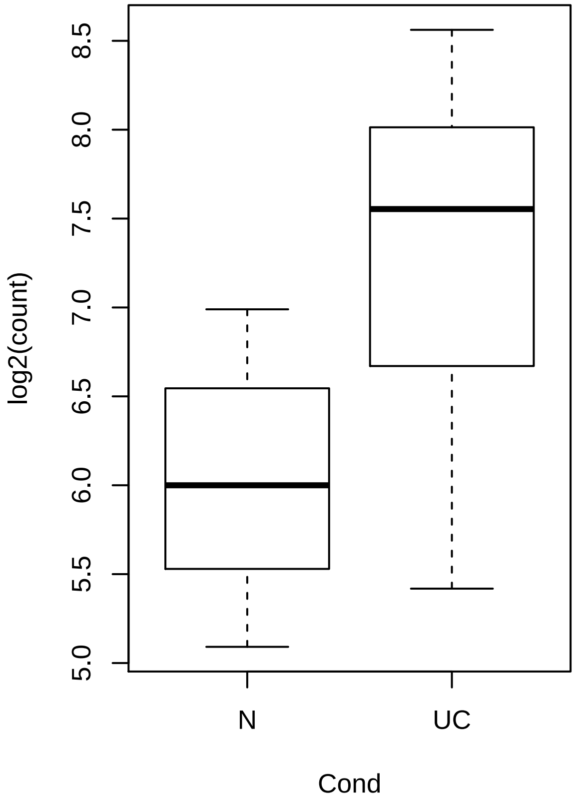
ALPK2 average UC−N %methylation max=−0.21% min=−10.02%



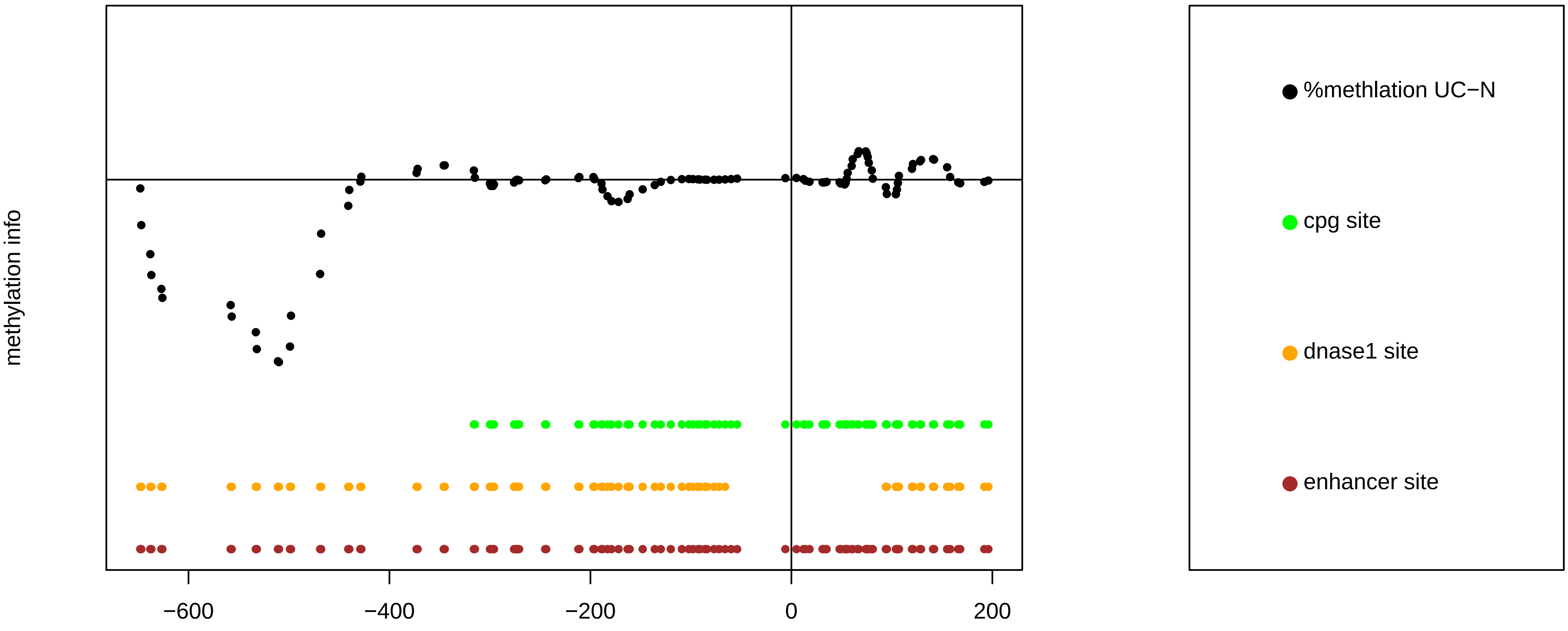
ALPK2 raw %methylation, red=UC, blue=Normal



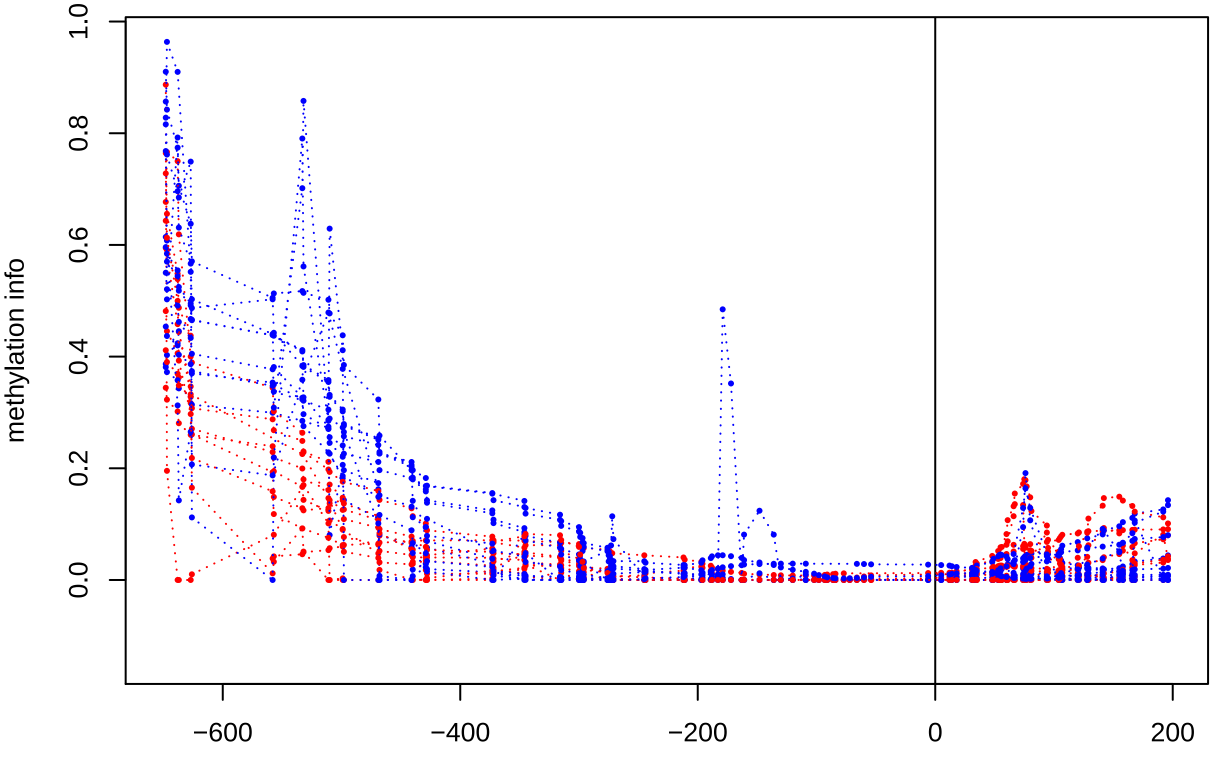
RNAseq logFC(UC−N)= 1.22



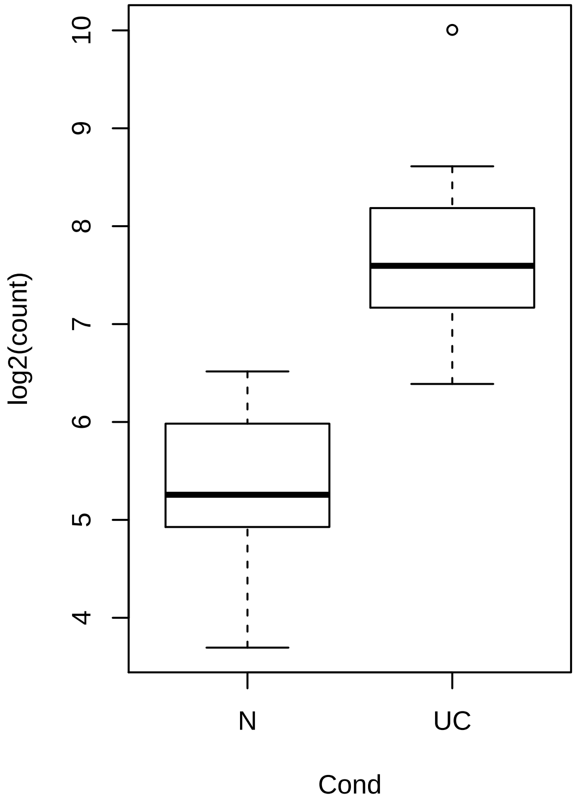
ALPL average UC−N %methylation max=4.56% min=−29.27%

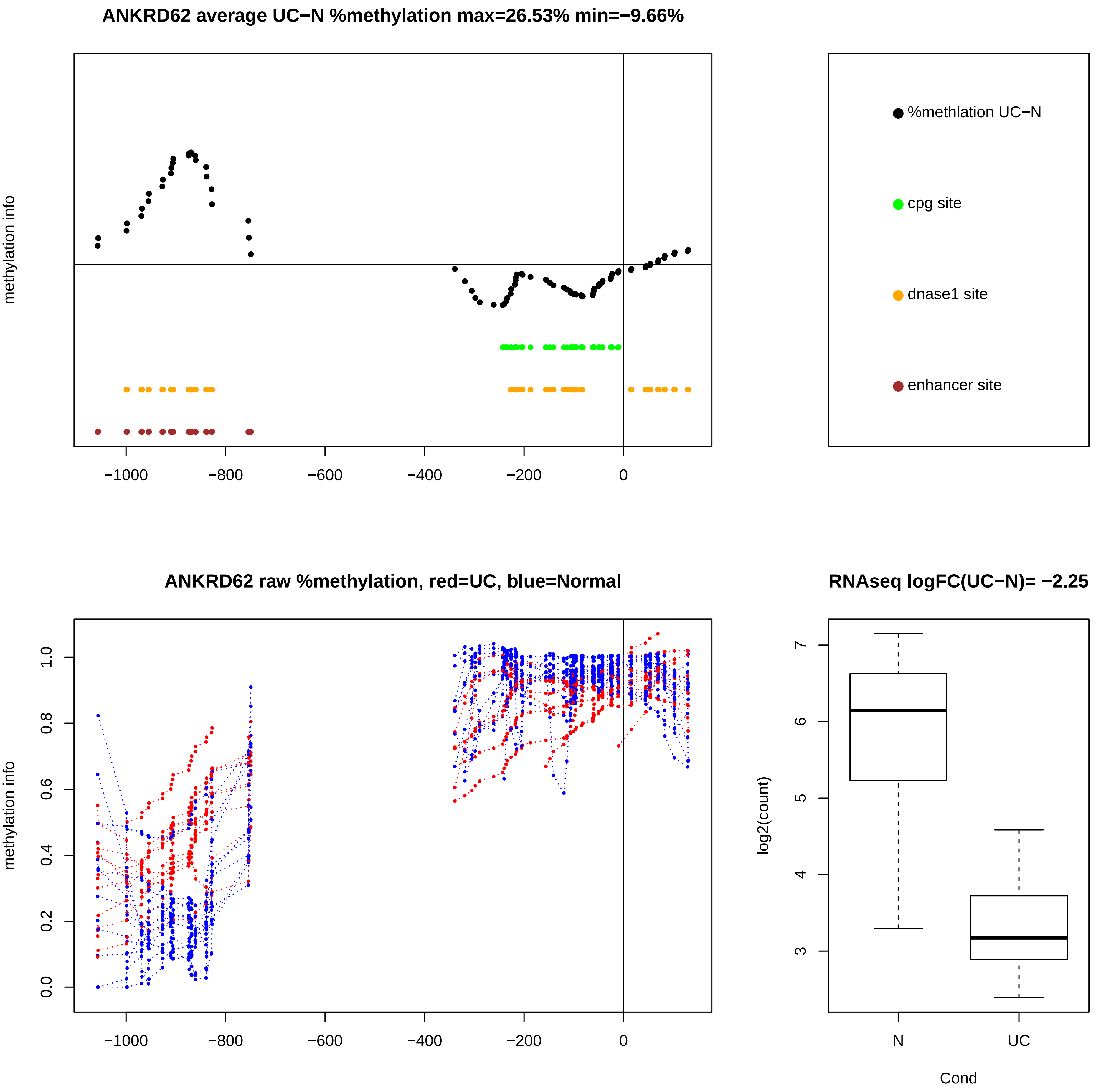


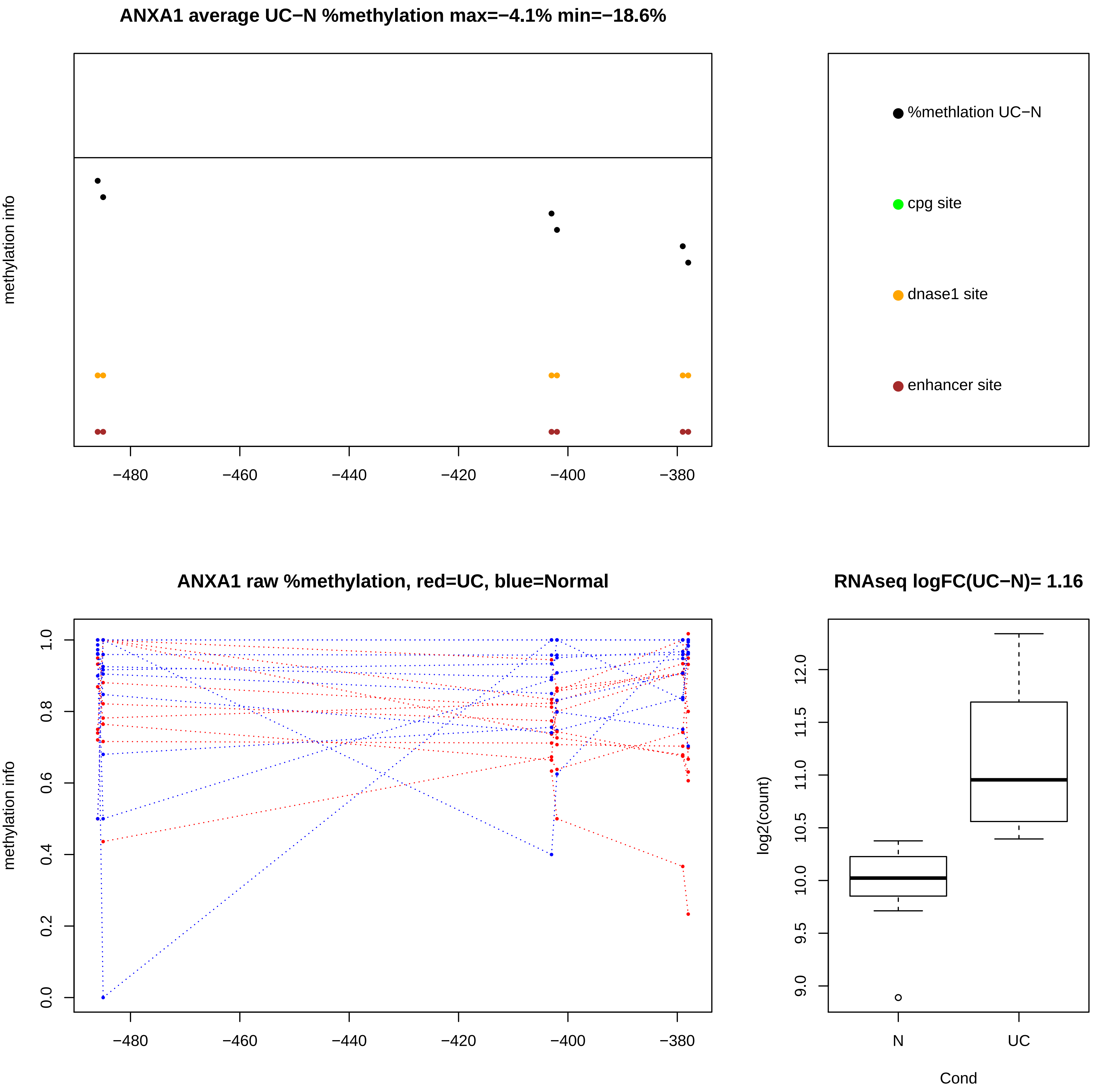
ALPL raw %methylation, red=UC, blue=Normal

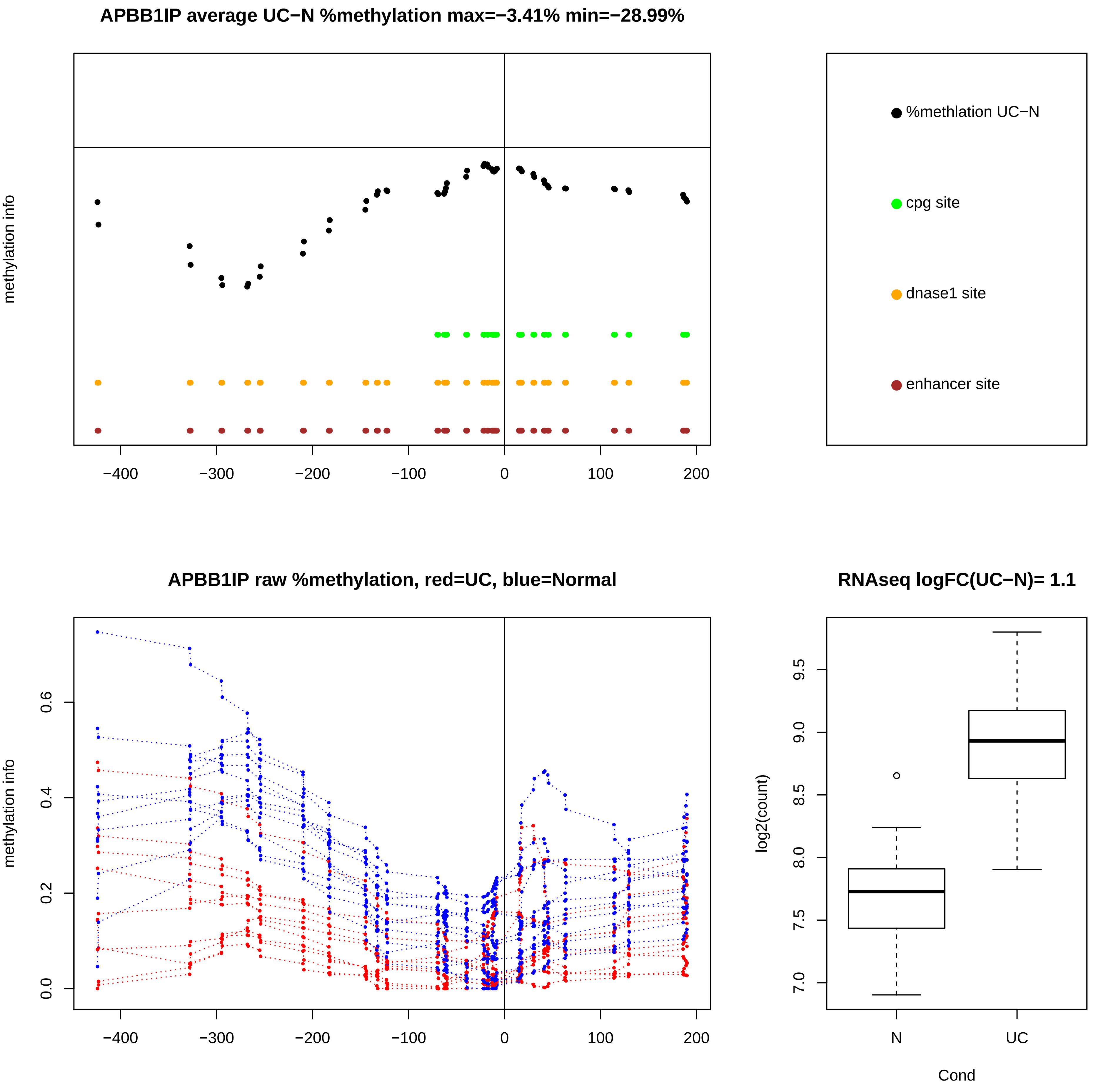


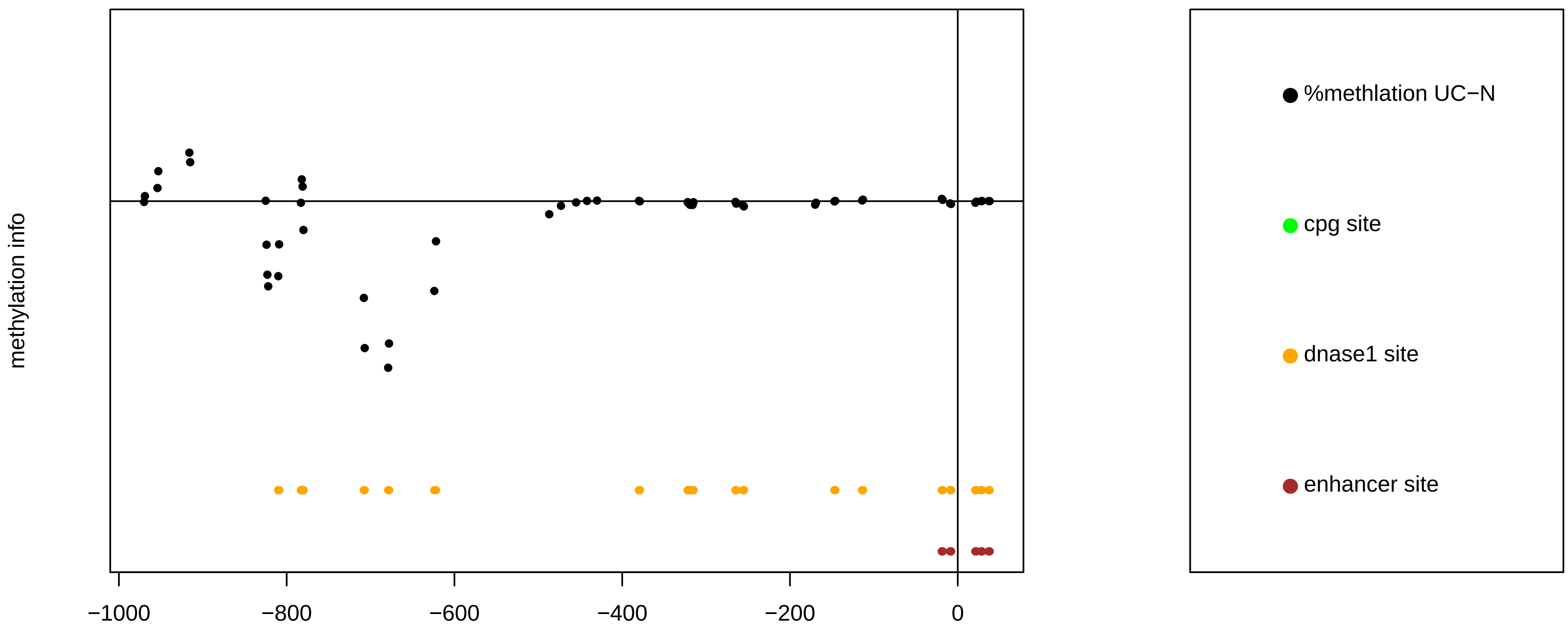
RNAseq logFC(UC−N)= 2.23

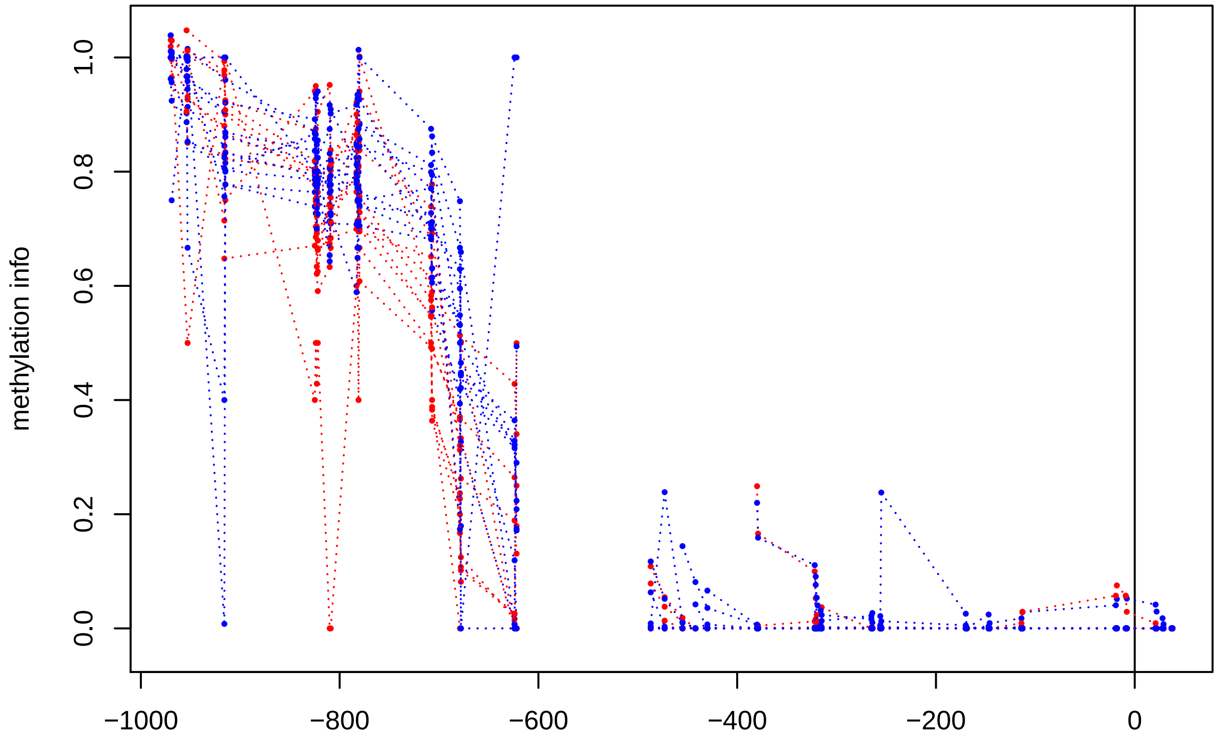


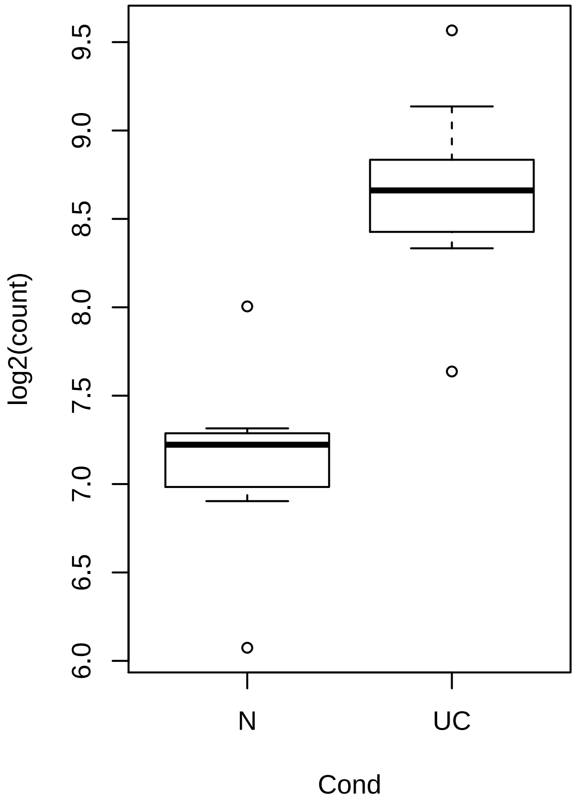

ANKRD62 average UC−N %methylation max=26.53% min=−9.66%
methylation info
−1000
−800
−600
−400
−200
0
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
ANKRD62 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−1000
−800
−600
−400
−200
0
RNAseq logFC(UC−N)= −2.25
log2(count)
3
4
5
6
7
N
UC
Cond

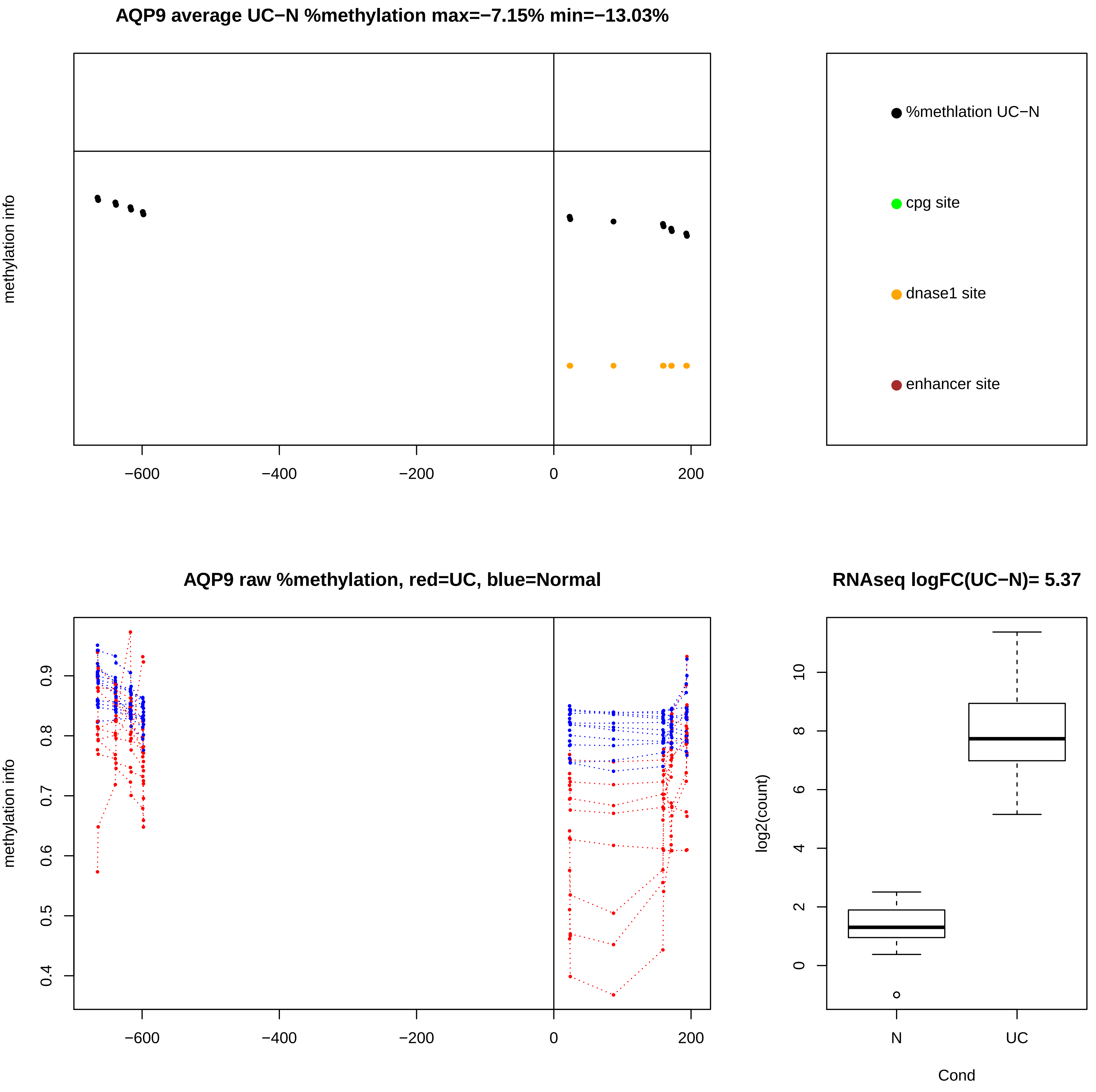

ANXA1 average UC−N %methylation max=−4.1% min=−18.6%
methylation info
−480
−460
−440
−420
−400
−380
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
ANXA1 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−480
−460
−440
−420
−400
−380
RNAseq logFC(UC−N)= 1.16
log2(count)
9.0
9.5
10.0
10.5
11.0
11.5
12.0
N
UC
Cond

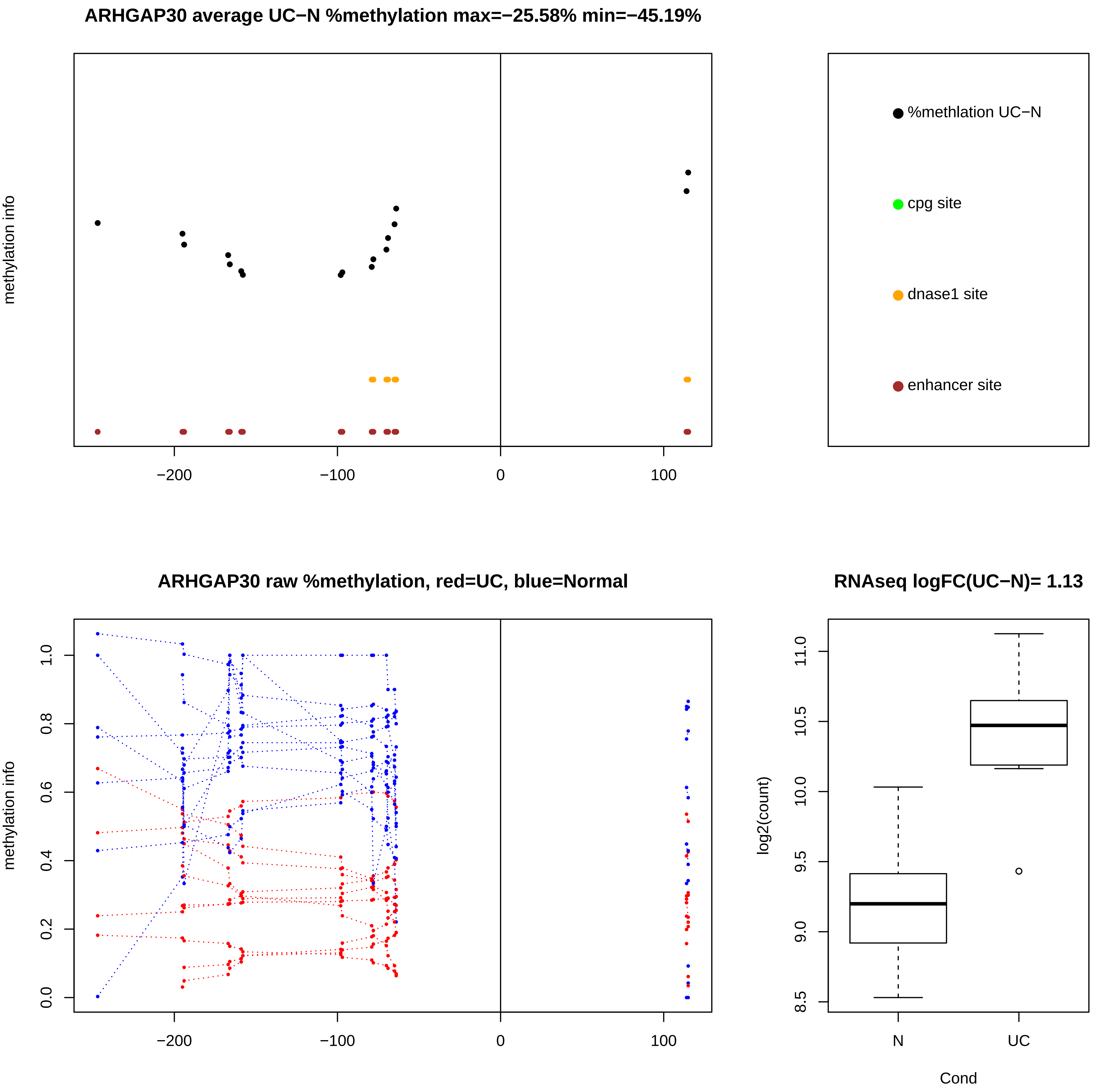

APBB1IP average UC−N %methylation max=−3.41% min=−28.99%
methylation info
−400
−300
−200
−100
0
100
200
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
APBB1IP raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
−400
−300
−200
−100
0
100
200
RNAseq logFC(UC−N)= 1.1
log2(count)
7.0
7.5
8.0
8.5
9.0
9.5
N
UC
Cond

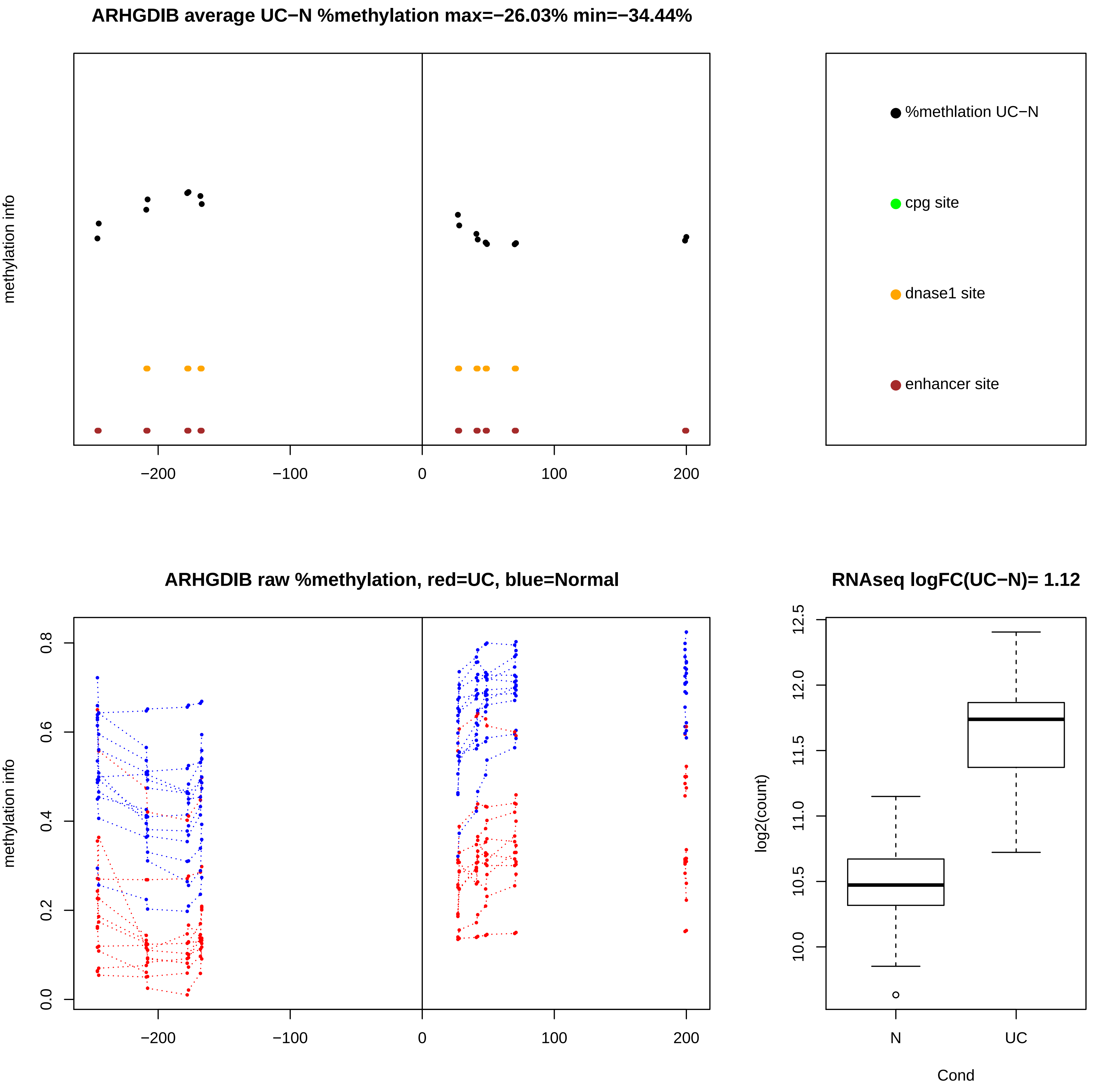

APOBEC3G average UC−N %methylation max=7.92% min=−27.22%


APOBEC3G raw %methylation, red=UC, blue=Normal


RNAseq logFC(UC−N)= 1.36


AQP9 average UC−N %methylation max=−7.15% min=−13.03%
methylation info
−600
−400
−200
0
200
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
AQP9 raw %methylation, red=UC, blue=Normal
methylation info
0.4
0.5
0.6
0.7
0.8
0.9
−600
−400
−200
0
200
RNAseq logFC(UC−N)= 5.37
log2(count)
0
2
4
6
8
10
N
UC
Cond


ARHGAP30 average UC−N %methylation max=−25.58% min=−45.19%
methylation info
−200
−100
0
100
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
ARHGAP30 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−200
−100
0
100
RNAseq logFC(UC−N)= 1.13
log2(count)
8.5
9.0
9.5
10.0
10.5
11.0
N
UC
Cond

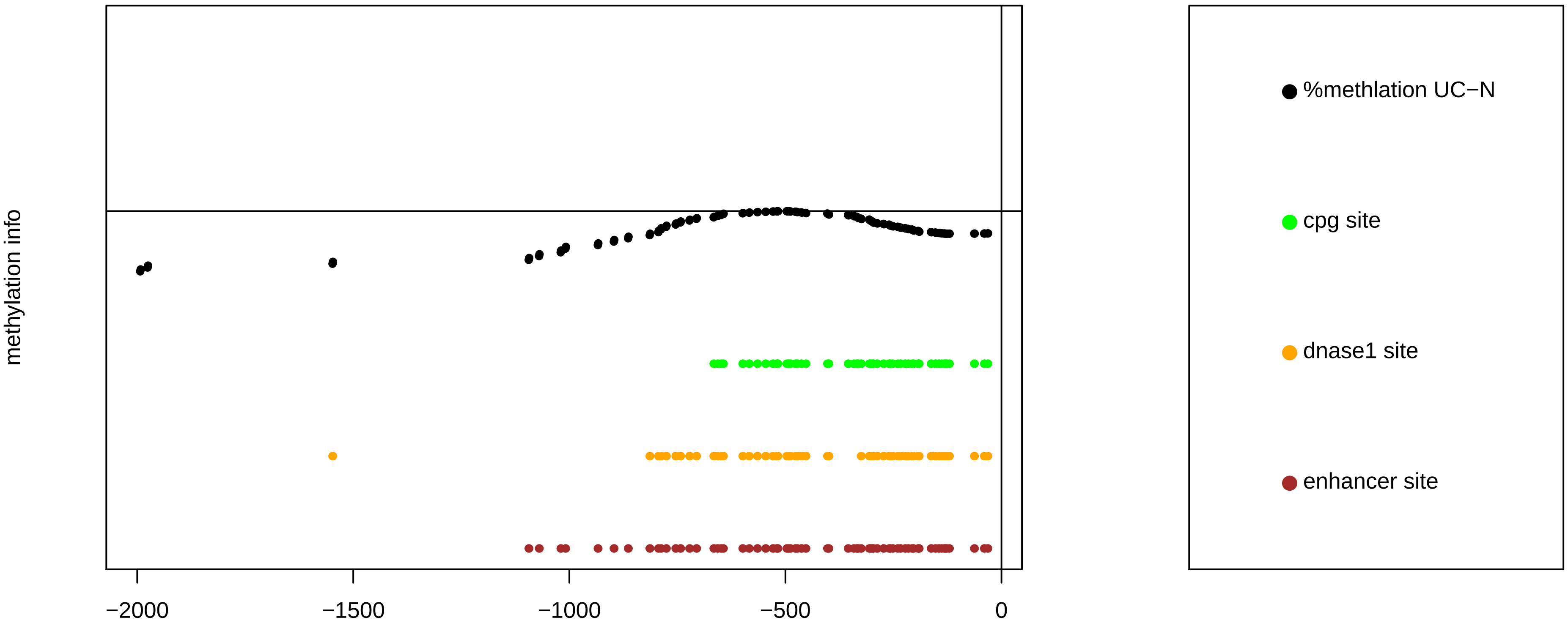


ARHGDIB average UC−N %methylation max=−26.03% min=−34.44%

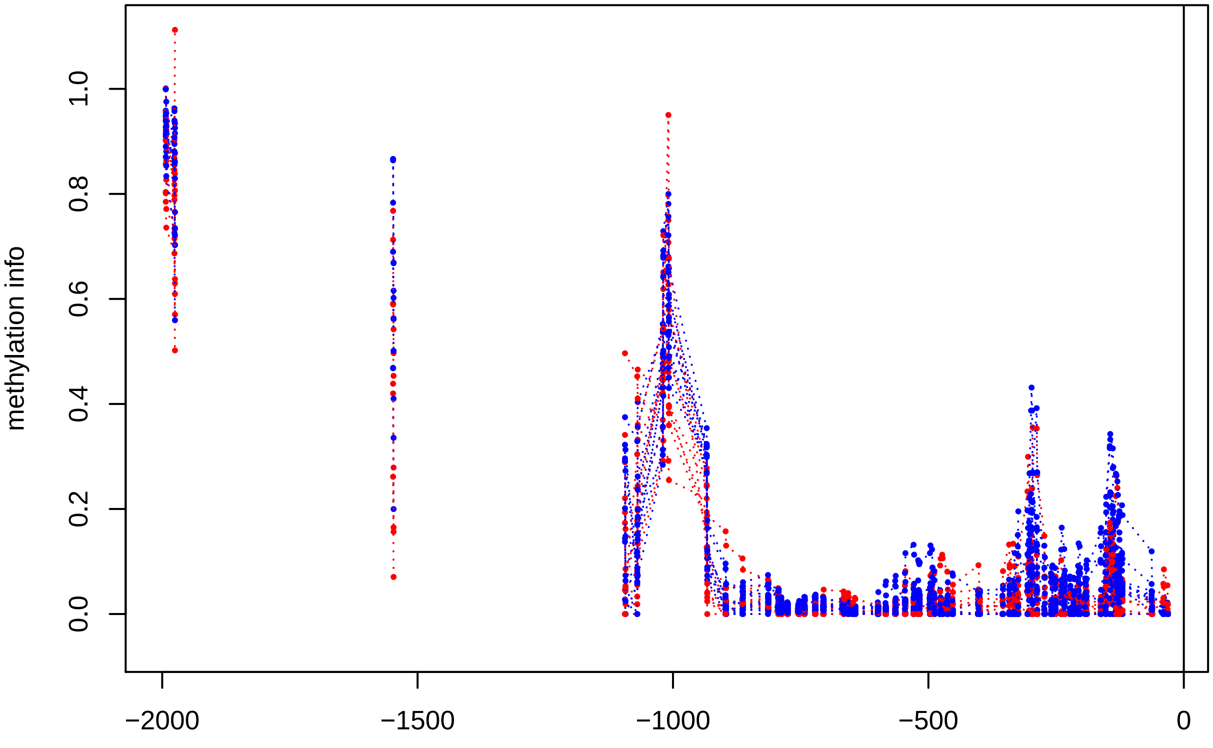
ARHGDIB raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.12

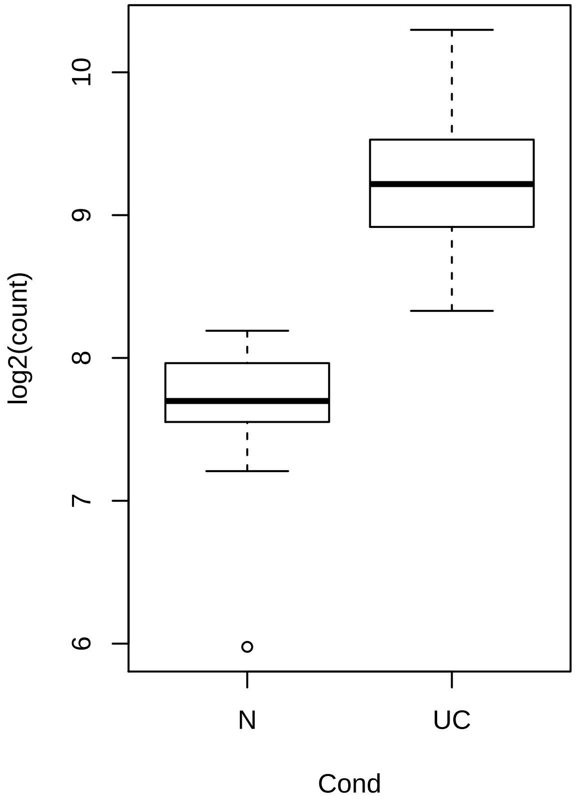
BASP1 average UC−N %methylation max=−0.02% min=−6.52%



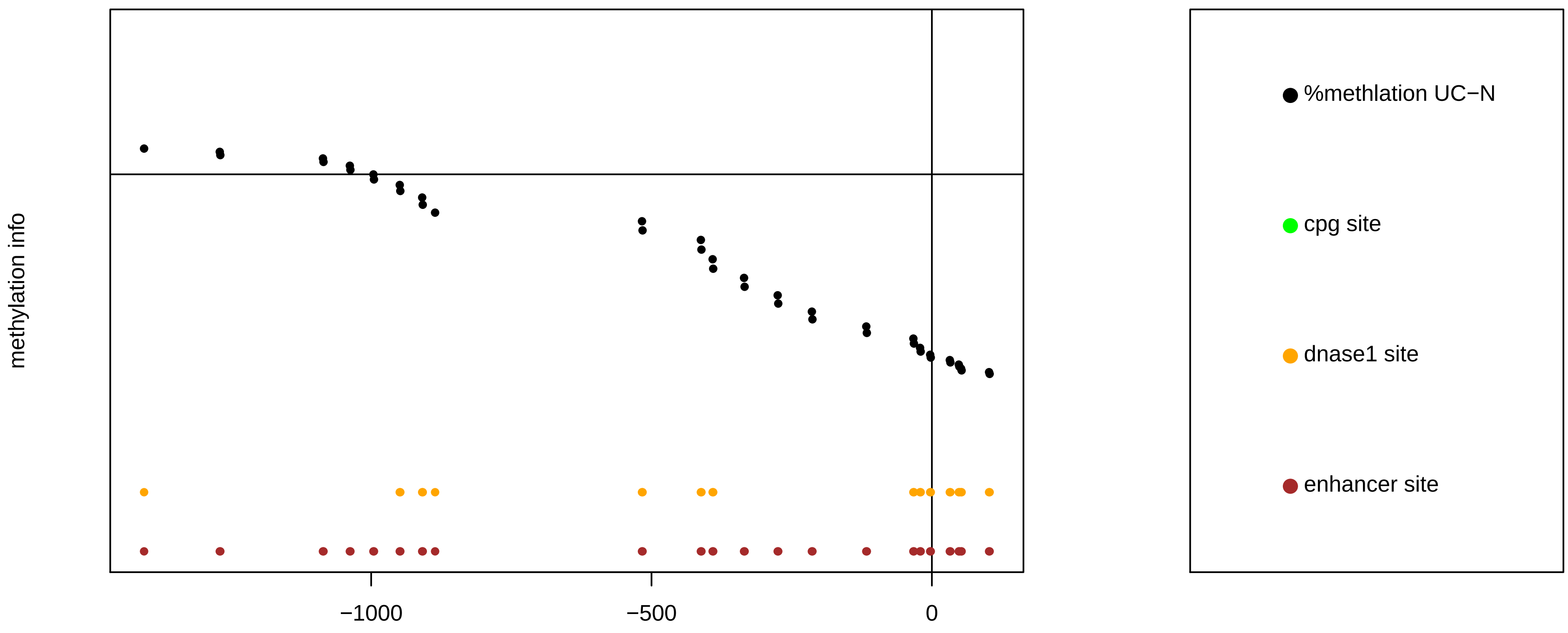
BASP1 raw %methylation, red=UC, blue=Normal



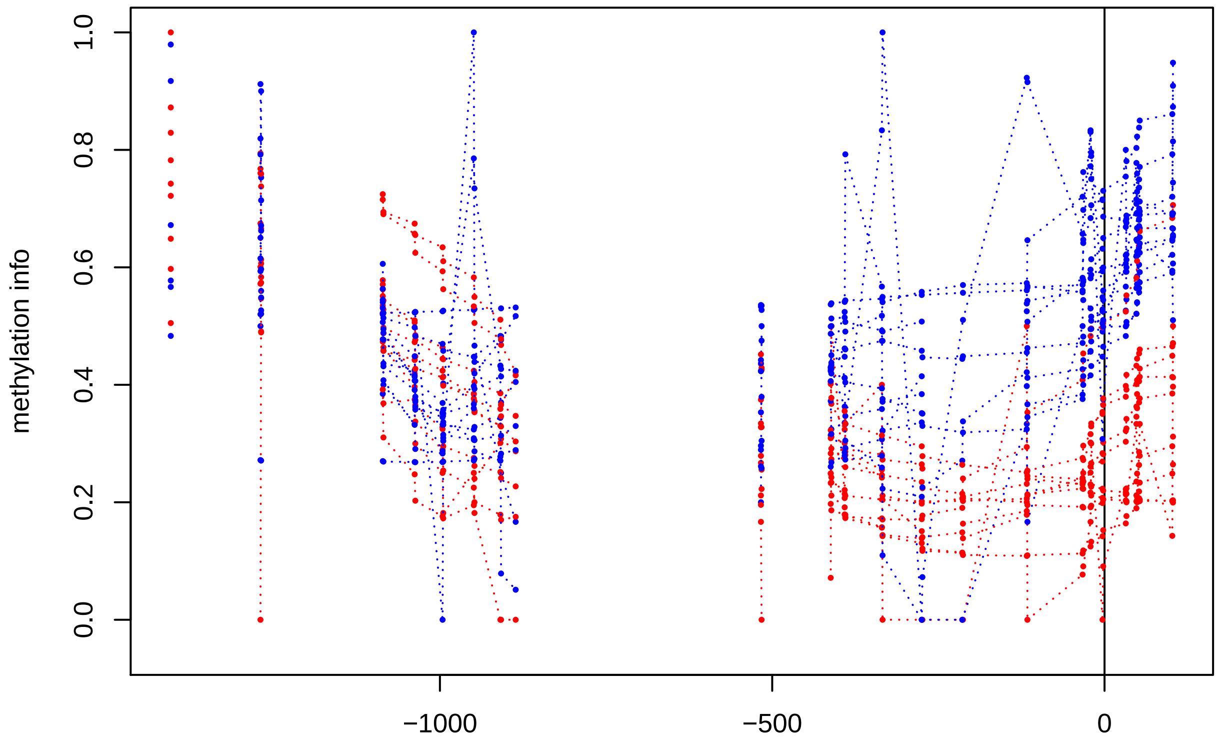
RNAseq logFC(UC−N)= 1.48



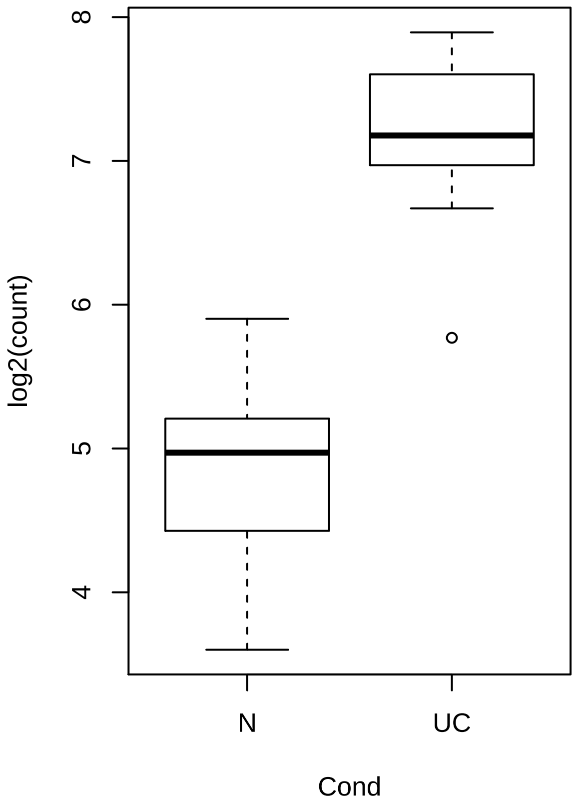
BATF average UC−N %methylation max=4.36% min=−33.74%

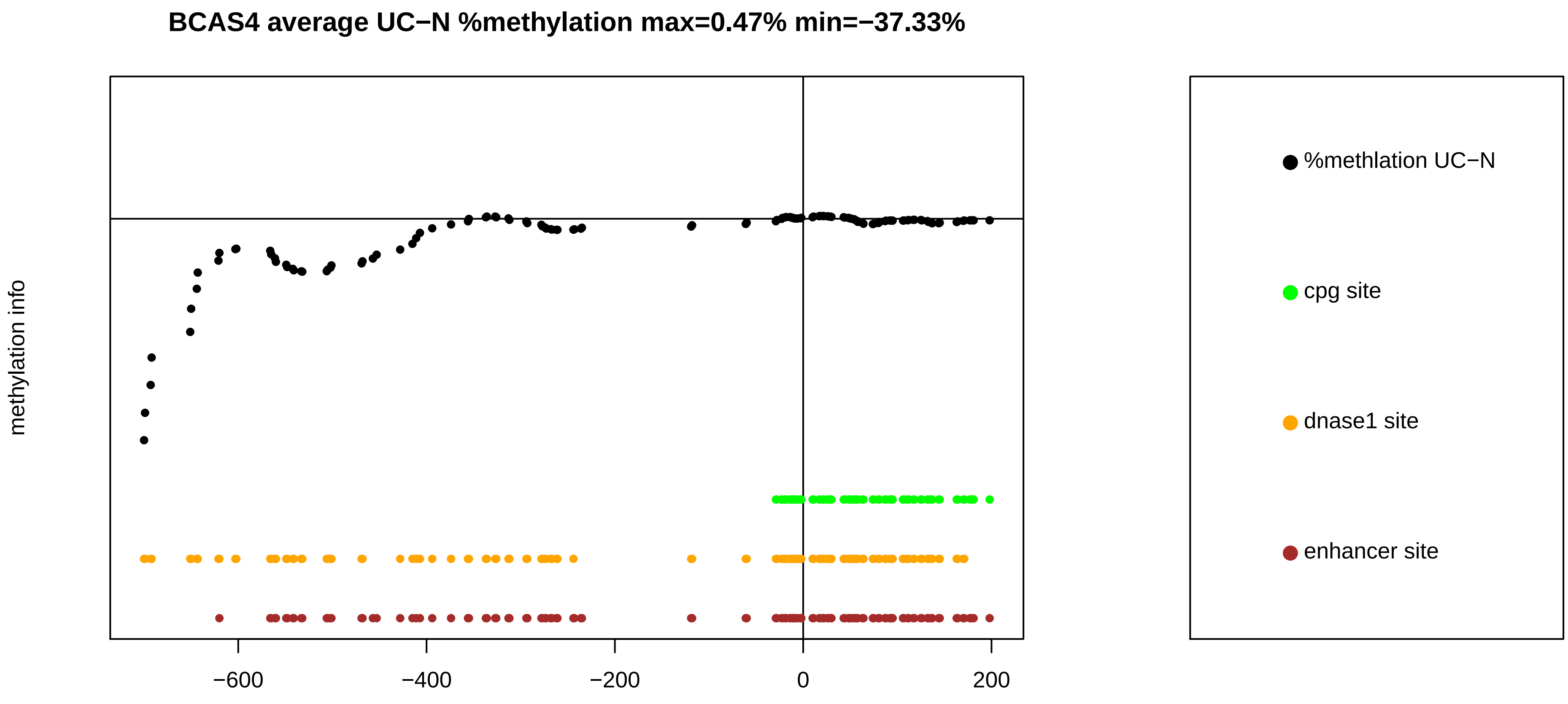


BATF raw %methylation, red=UC, blue=Normal

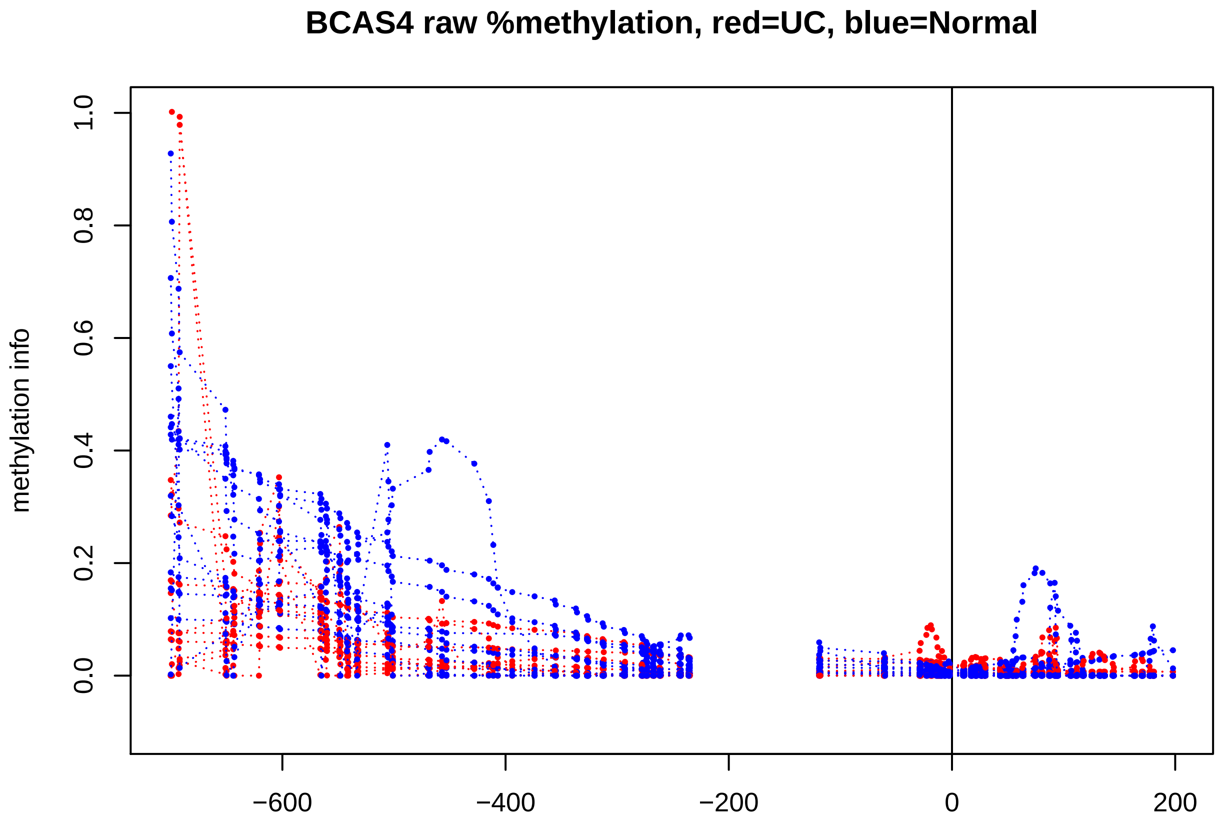


RNAseq logFC(UC−N)= 2.1

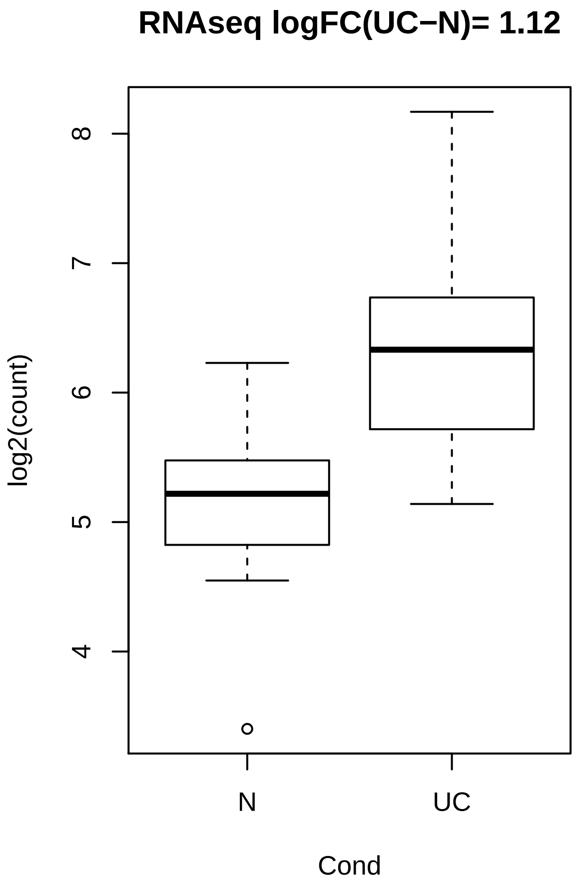




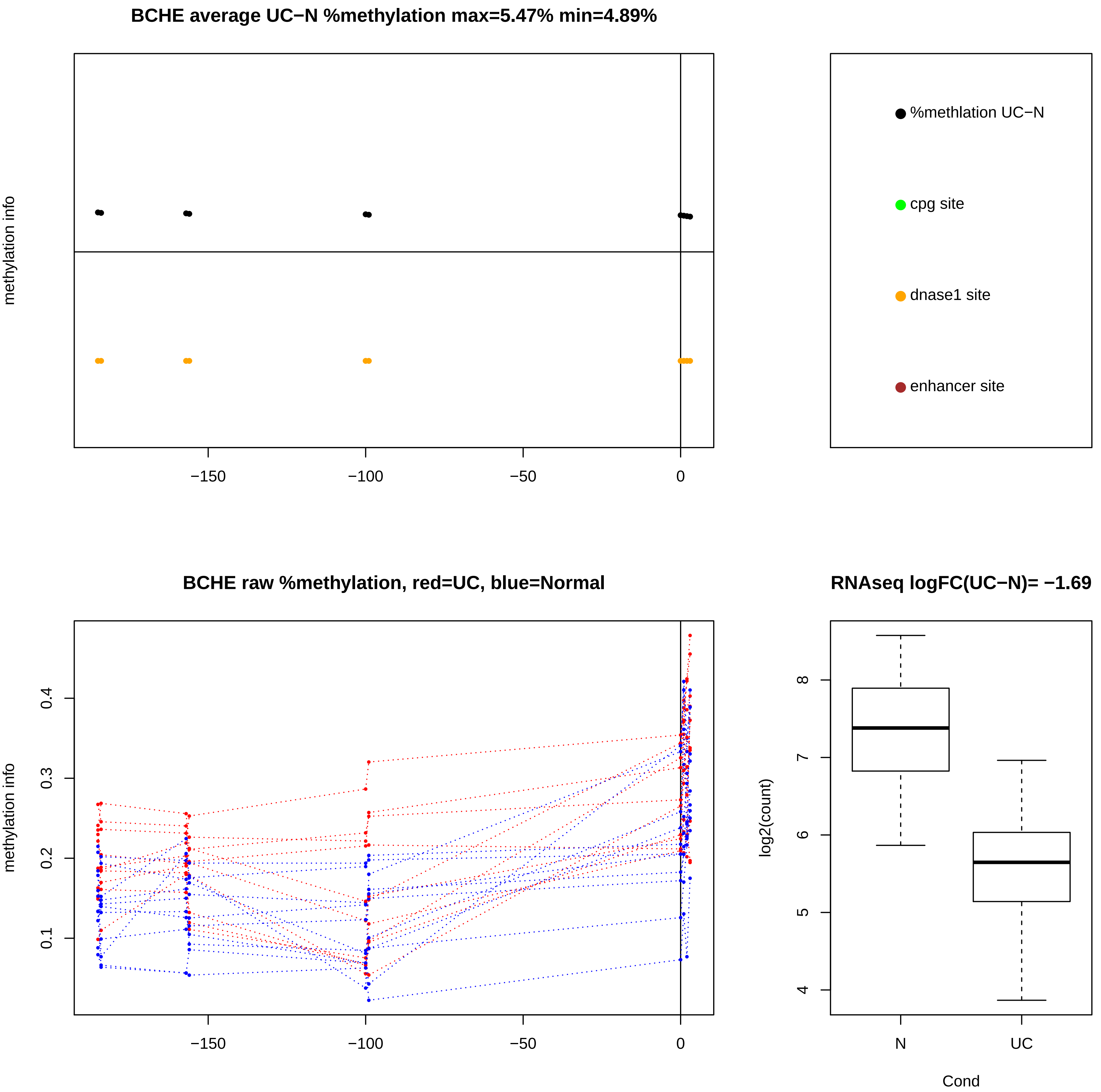
BCAS4 average UC−N %methylation max=0.47% min=−37.33%



BCAS4 raw %methylation, red=UC, blue=Normal

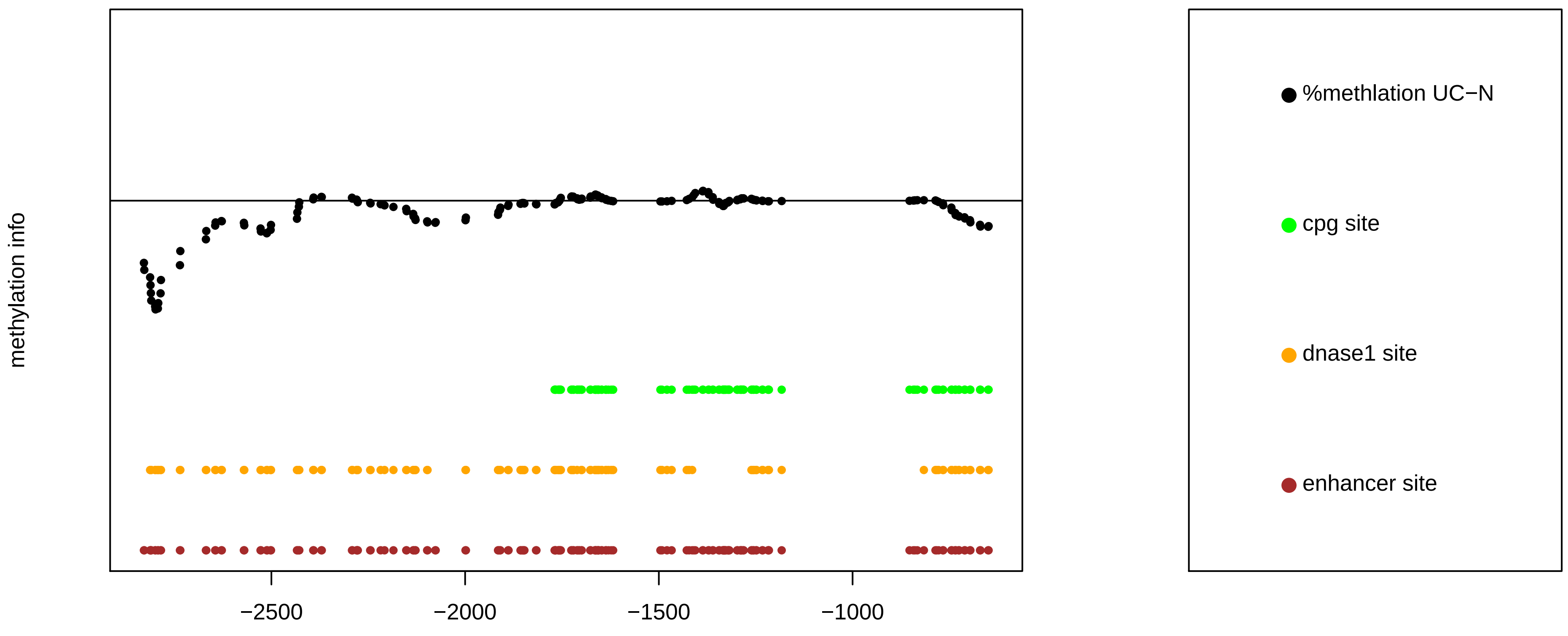


RNAseq logFC(UC−N)= 1.12

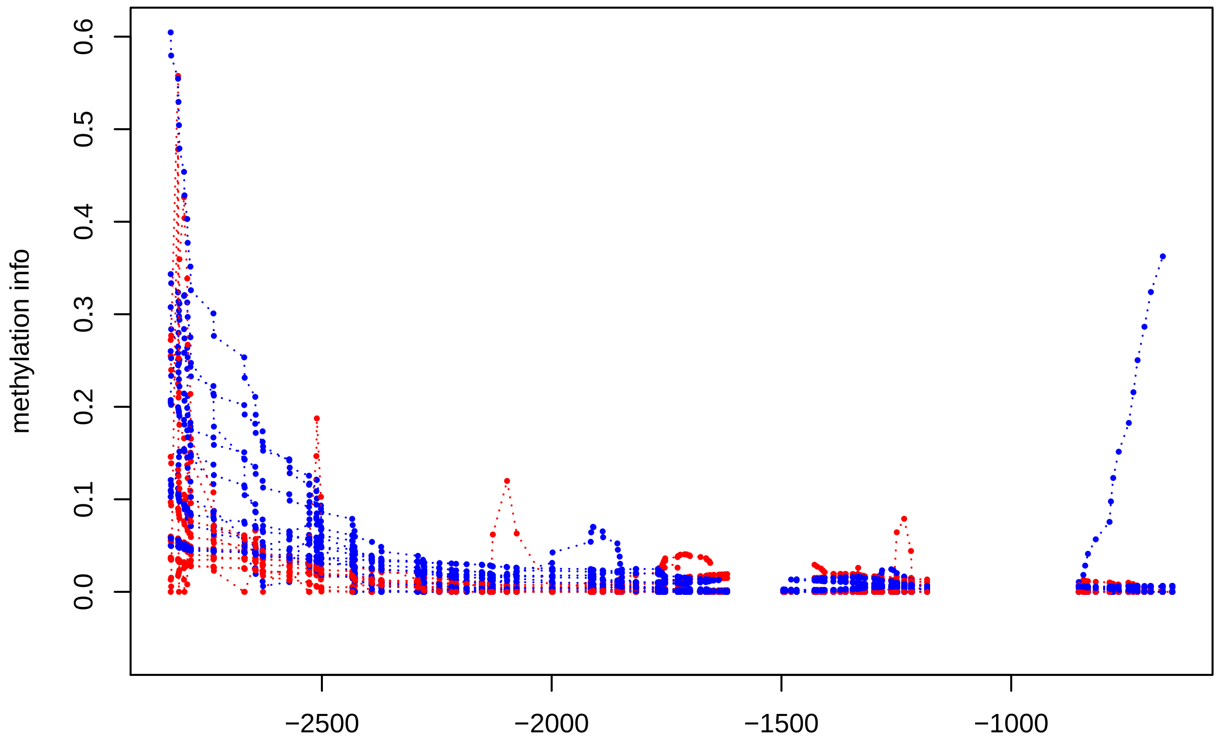

BCHE average UC−N %methylation max=5.47% min=4.89%

BCHE raw %methylation, red=UC, blue=Normal

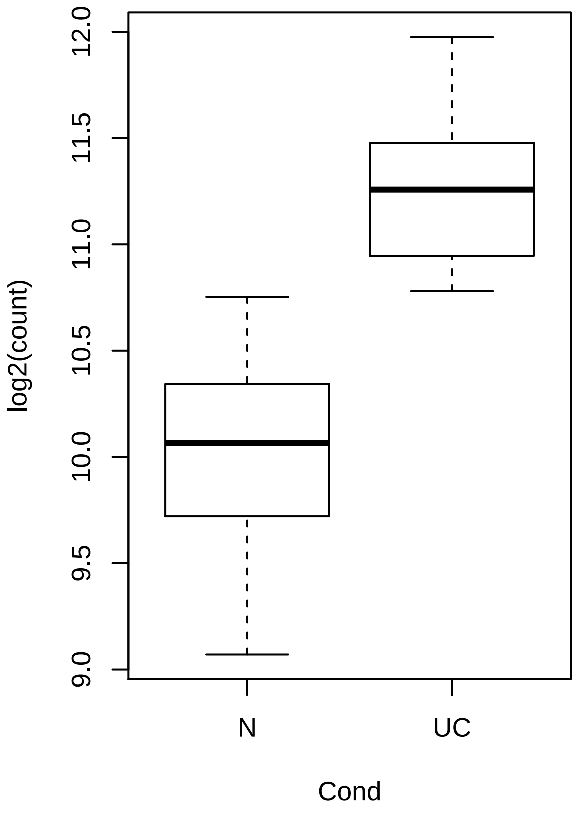
RNAseq logFC(UC−N)= −1.69



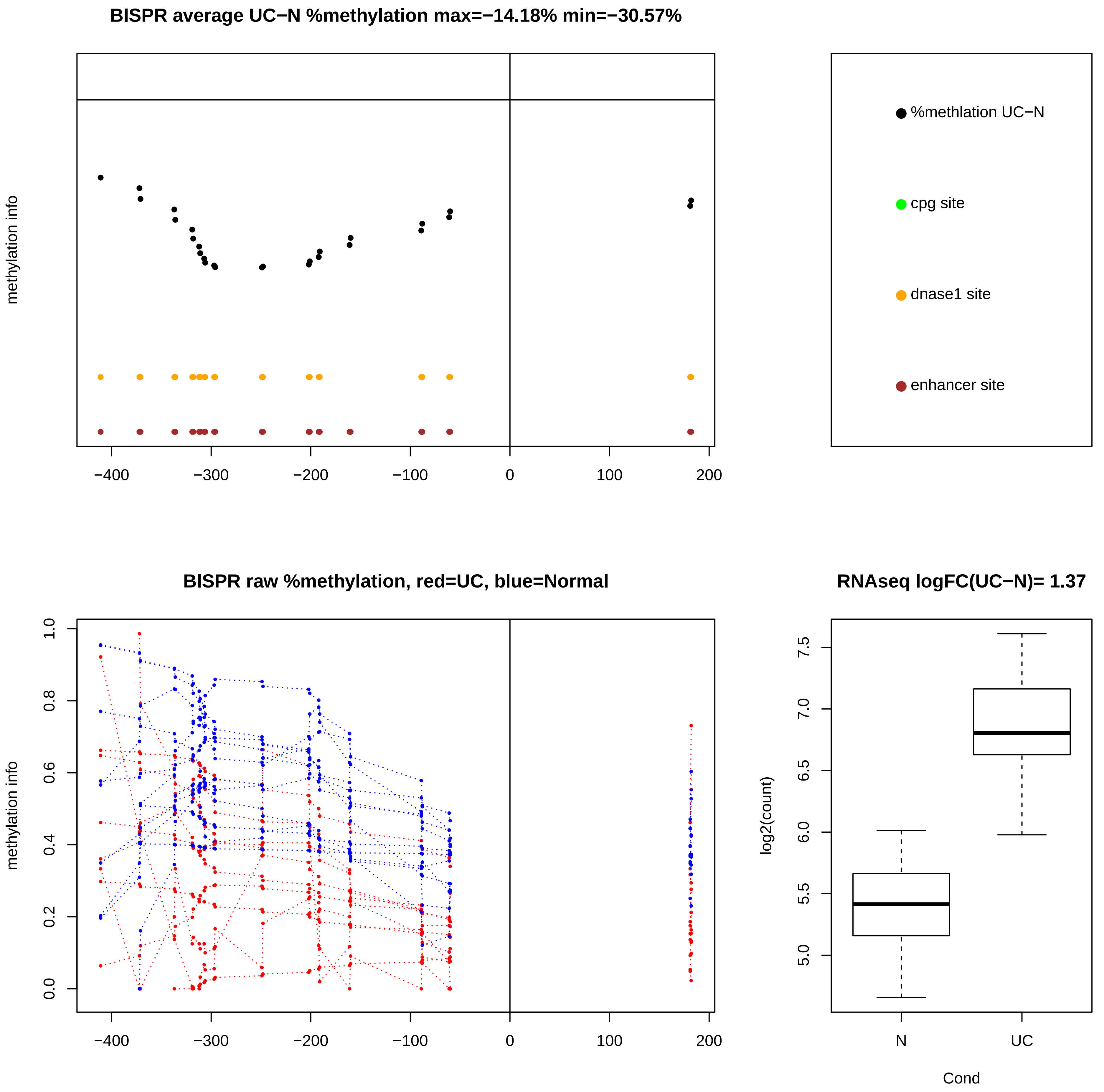
BHLHE40 average UC−N %methylation max=1.23% min=−13.54%



BHLHE40 raw %methylation, red=UC, blue=Normal



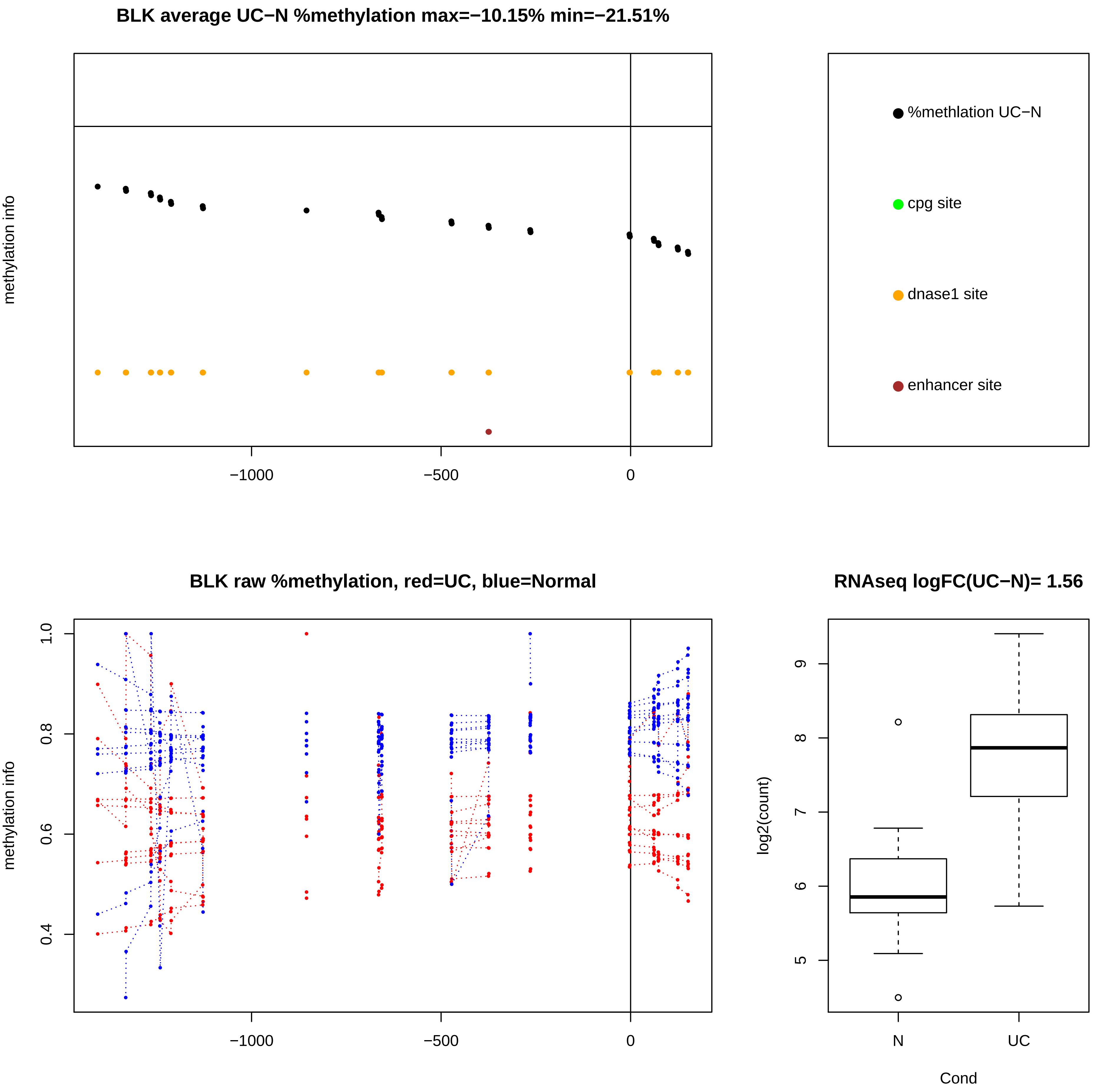
RNAseq logFC(UC−N)= 1.05



BISPR average UC−N %methylation max=−14.18% min=−30.57%

BISPR raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.37

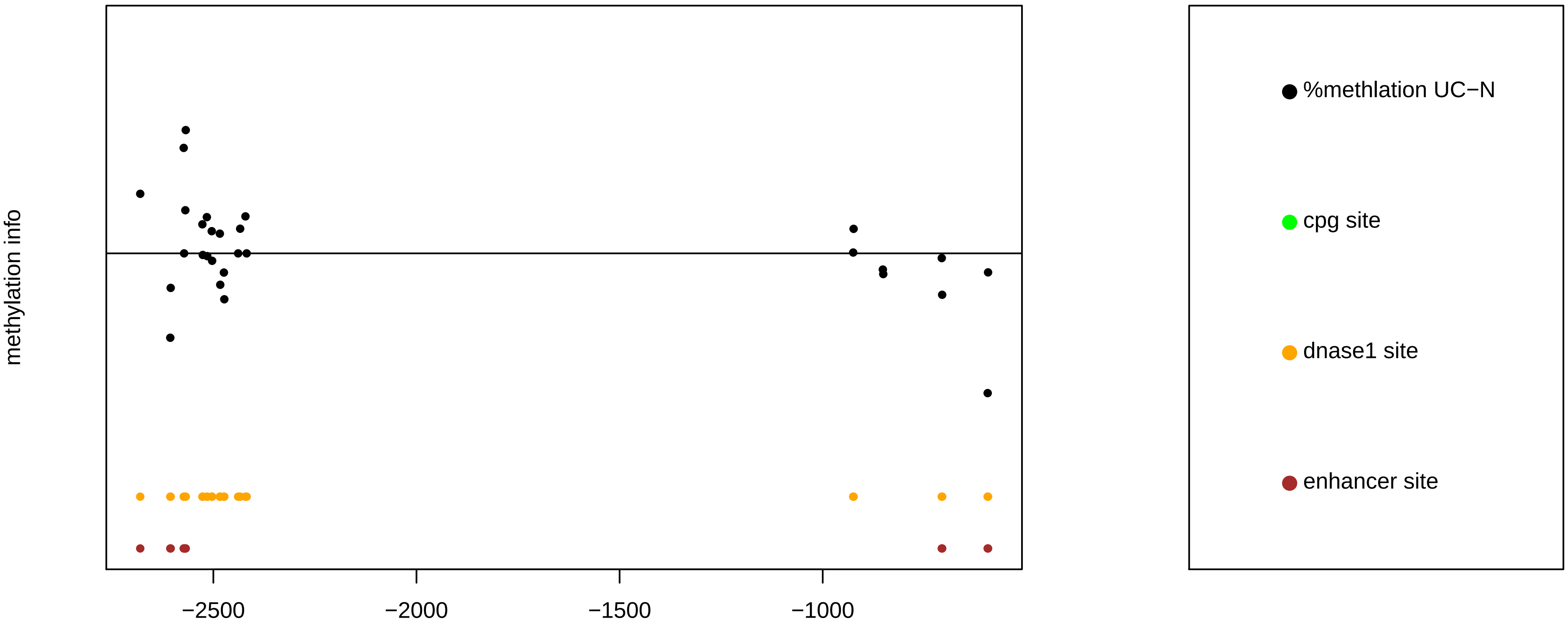


BLK average UC−N %methylation max=−10.15% min=−21.51%

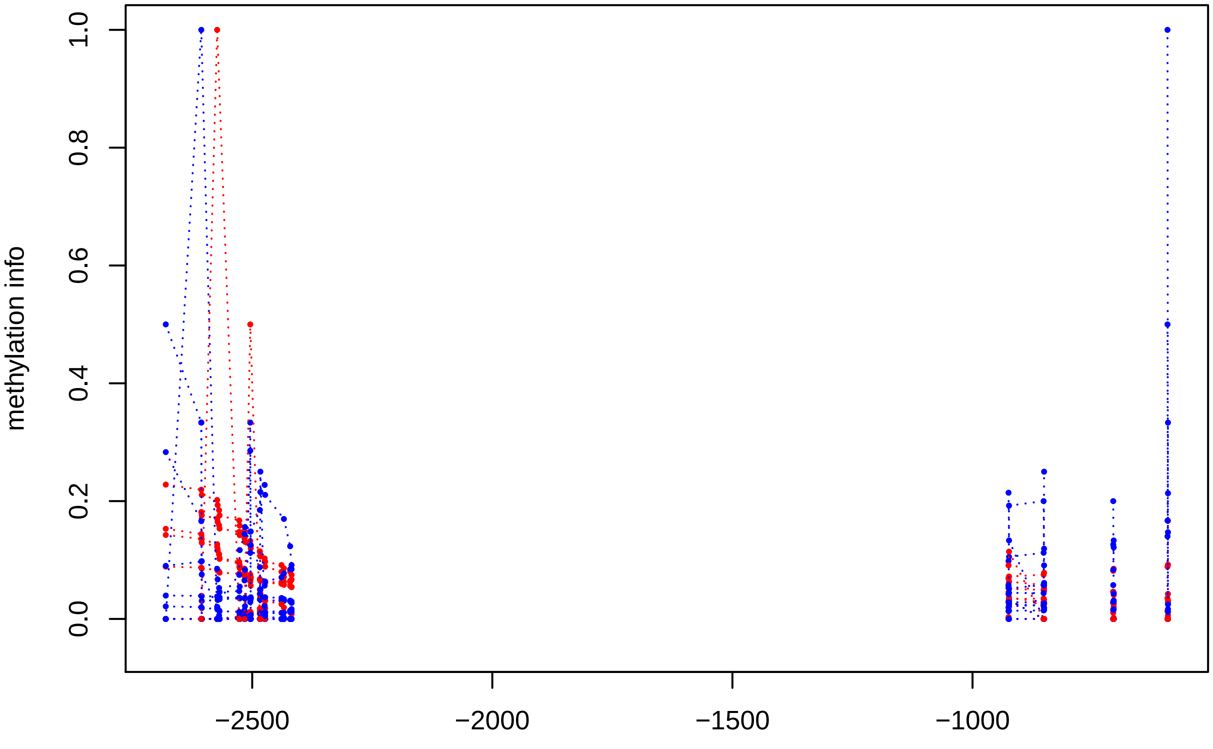
BLK raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.56

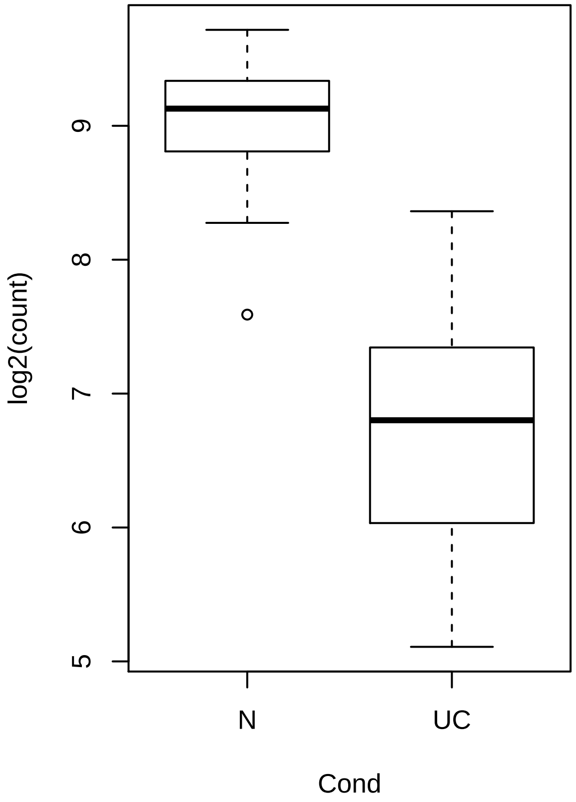
BRINP3 average UC−N %methylation max=23.81% min=−26.98%



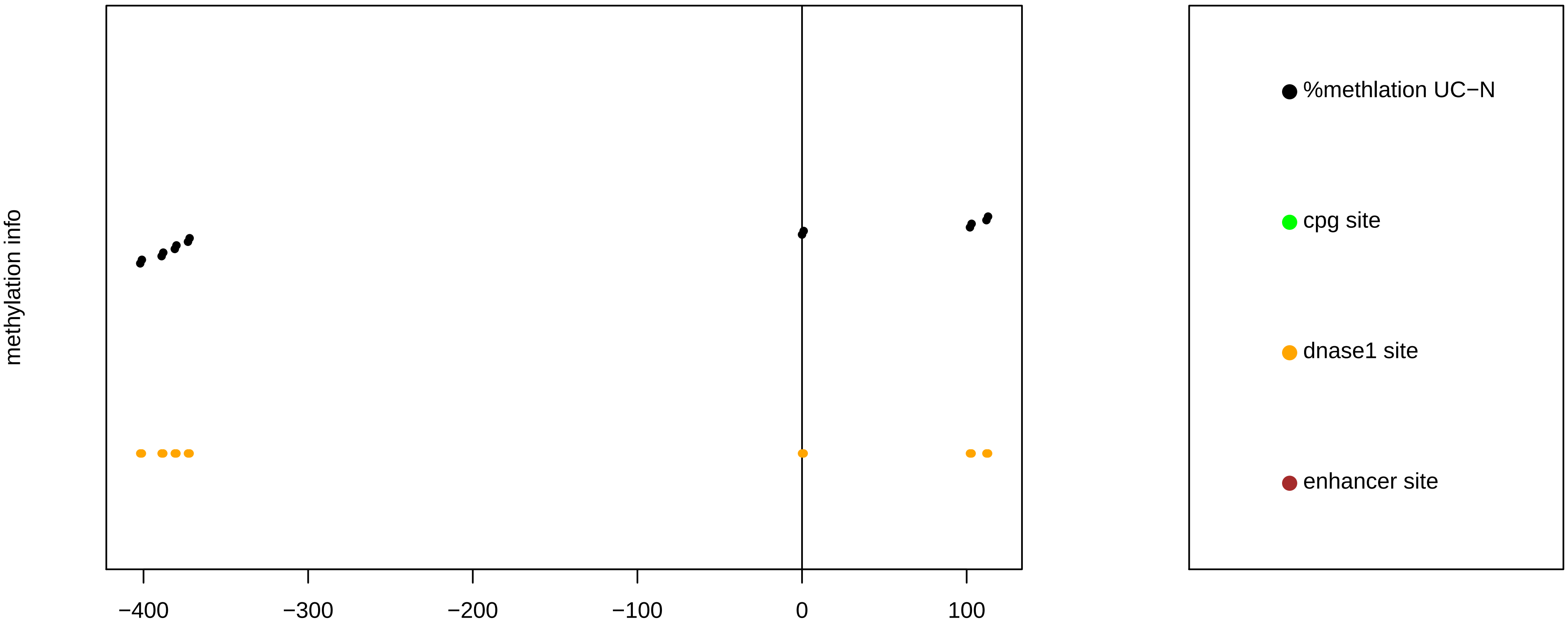
BRINP3 raw %methylation, red=UC, blue=Normal



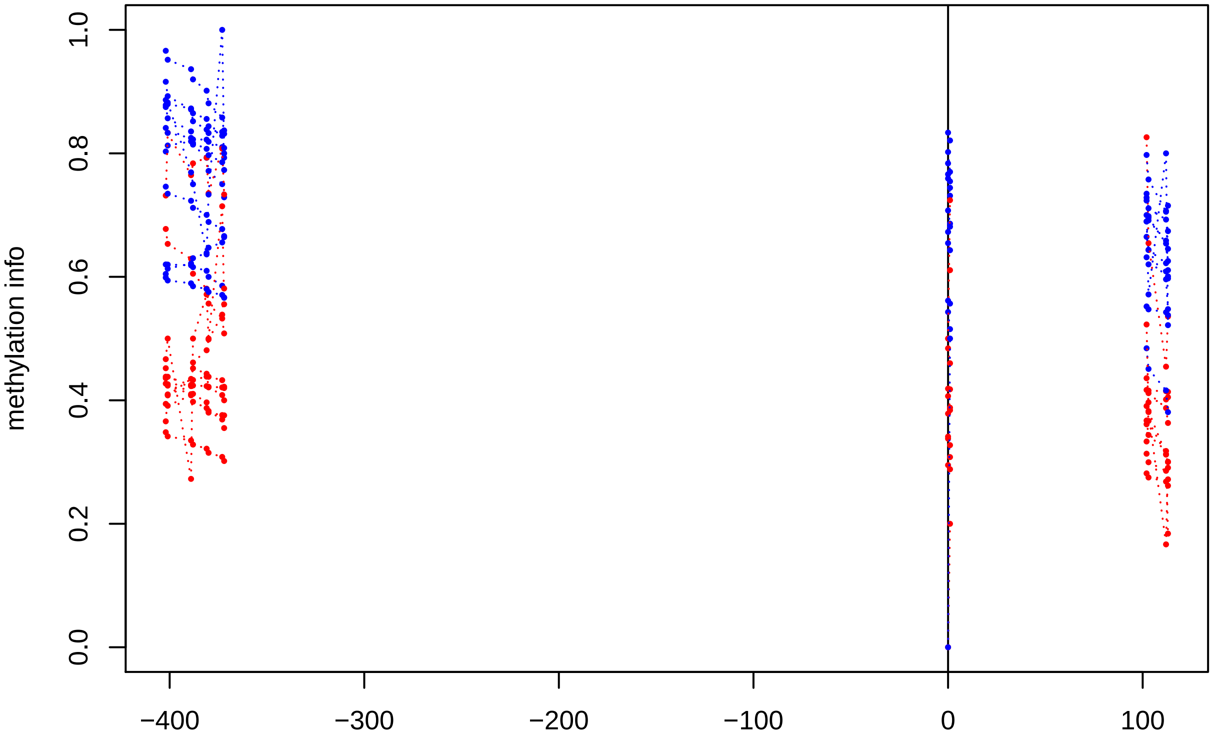
RNAseq logFC(UC−N)= −1.74



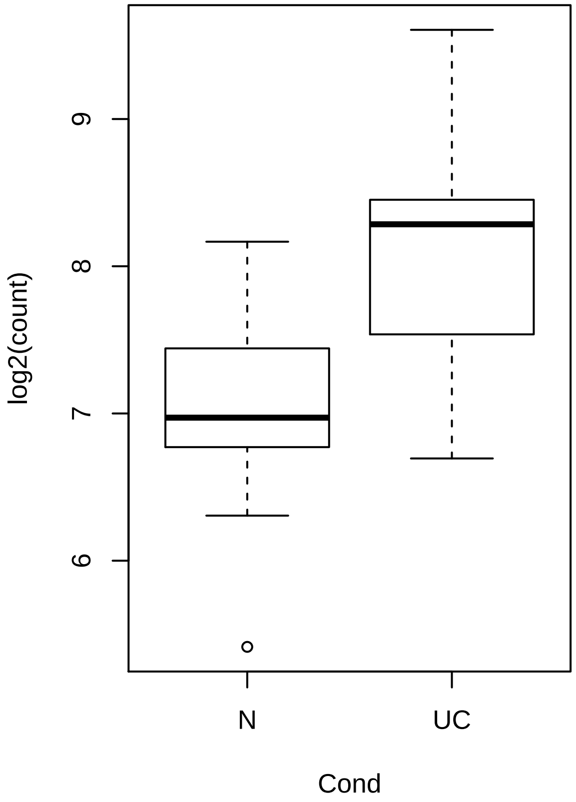
BTLA average UC−N %methylation max=−25.48% min=−30.41%

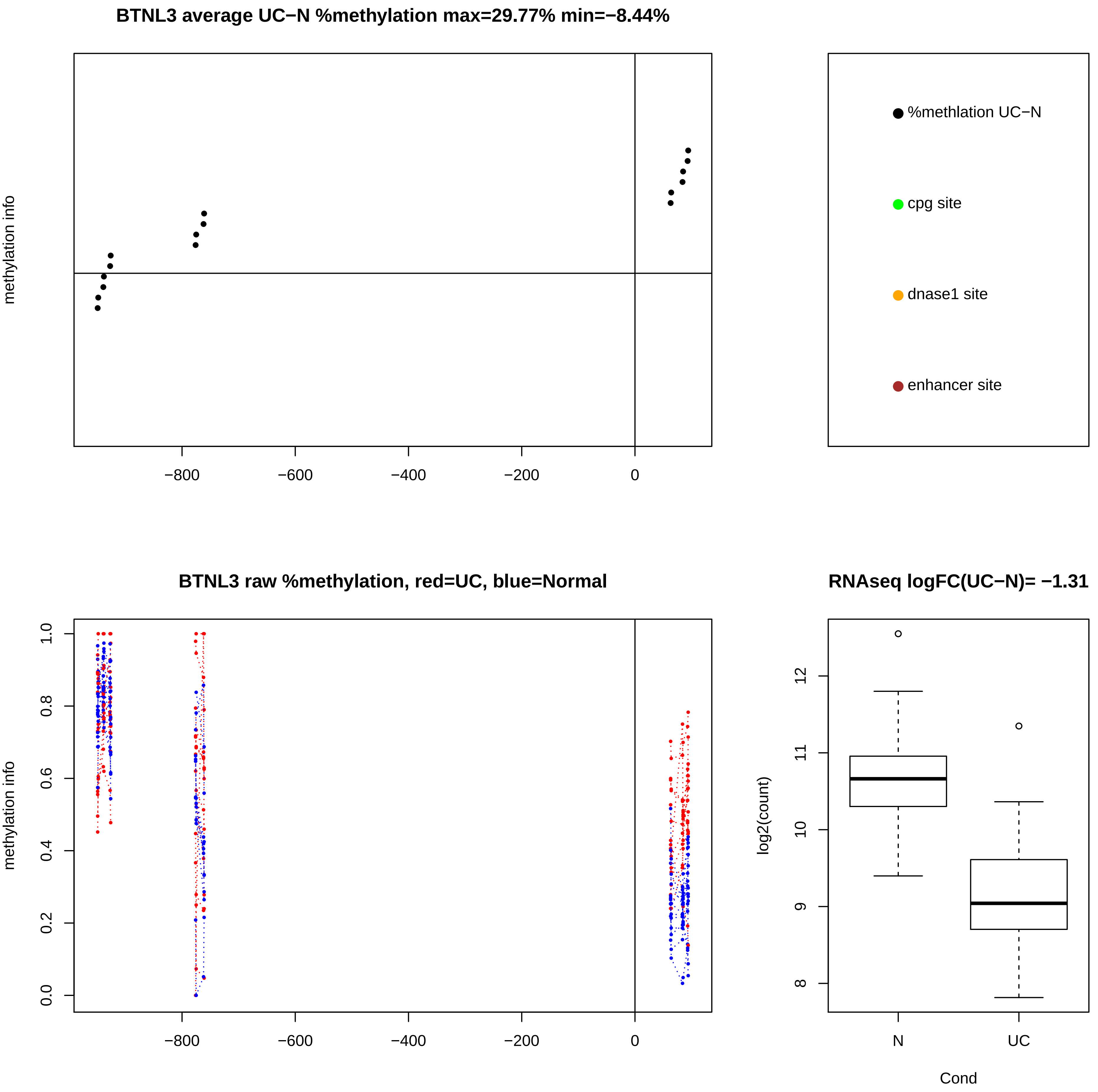


BTLA raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 1.14

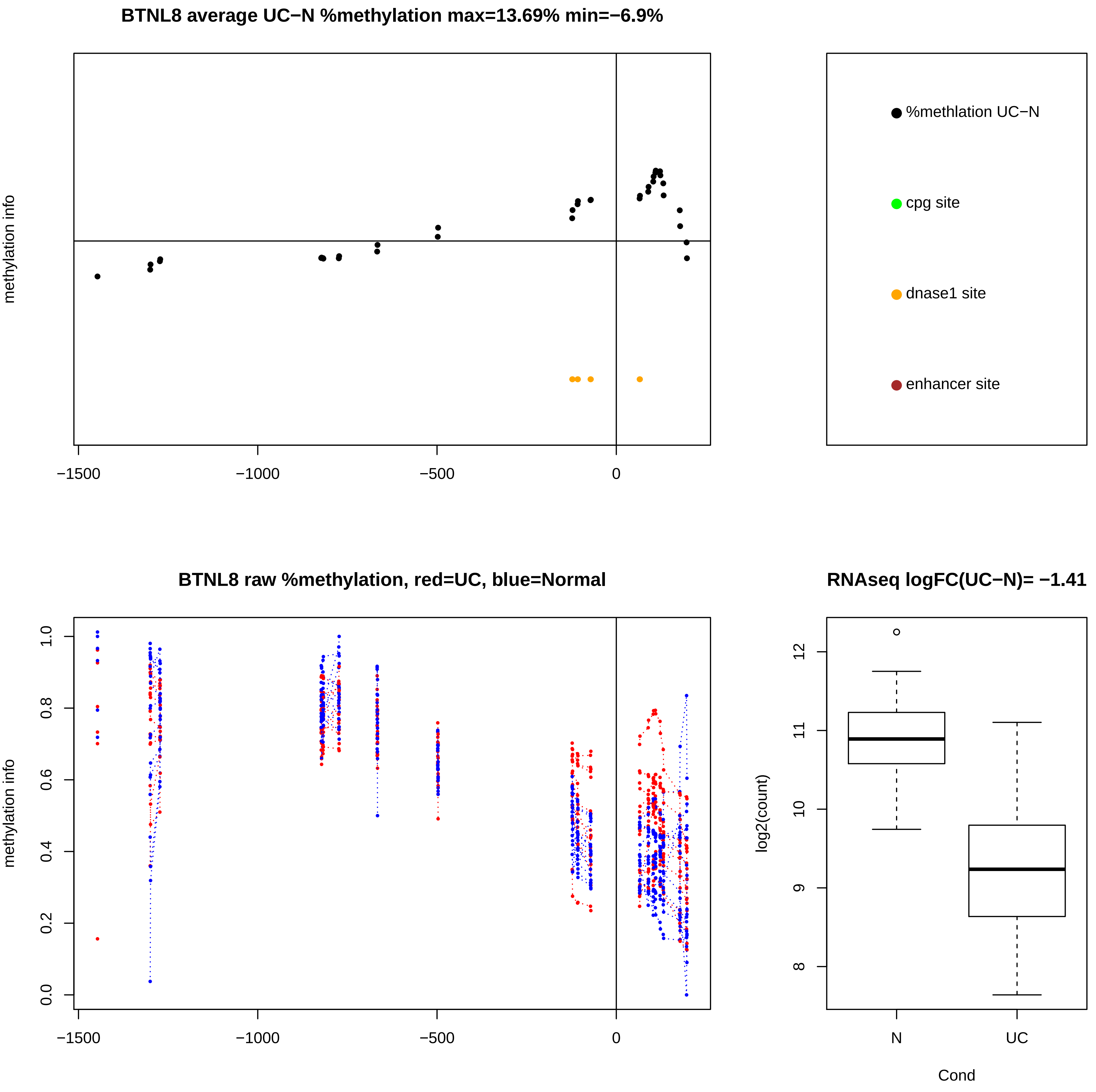


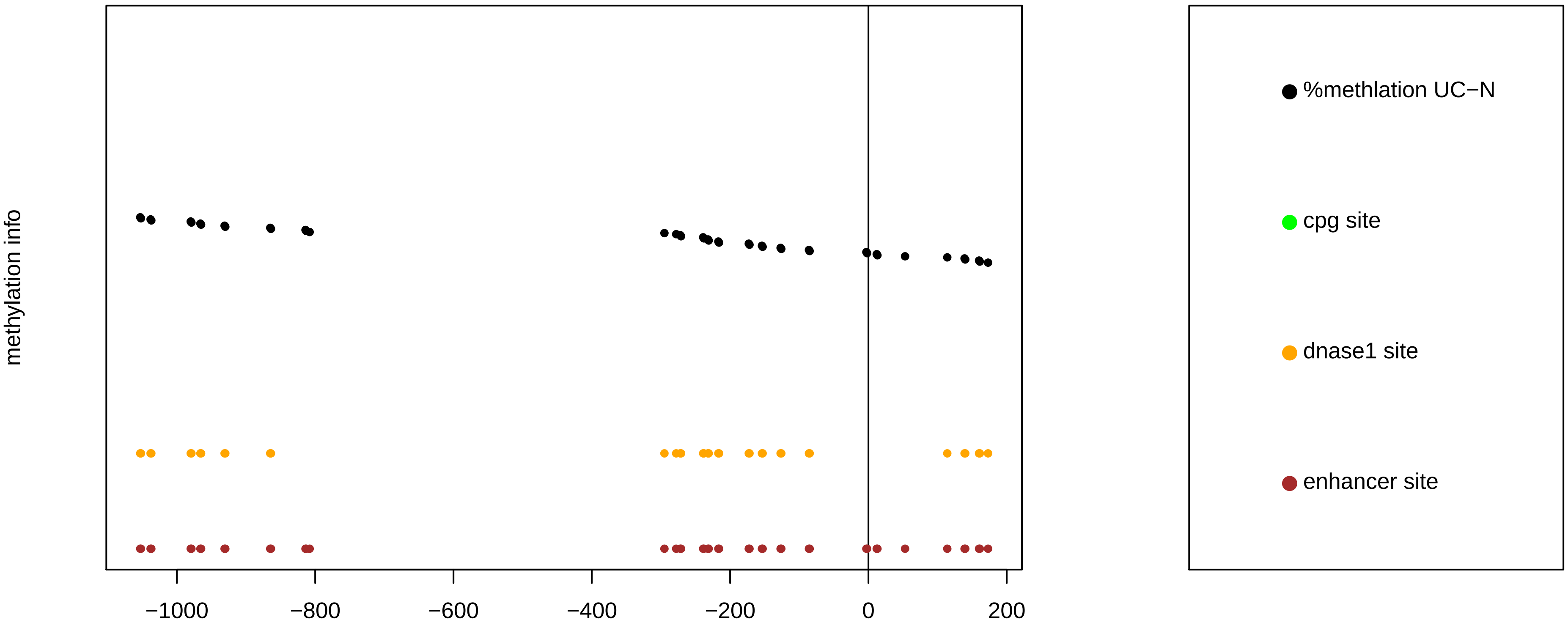


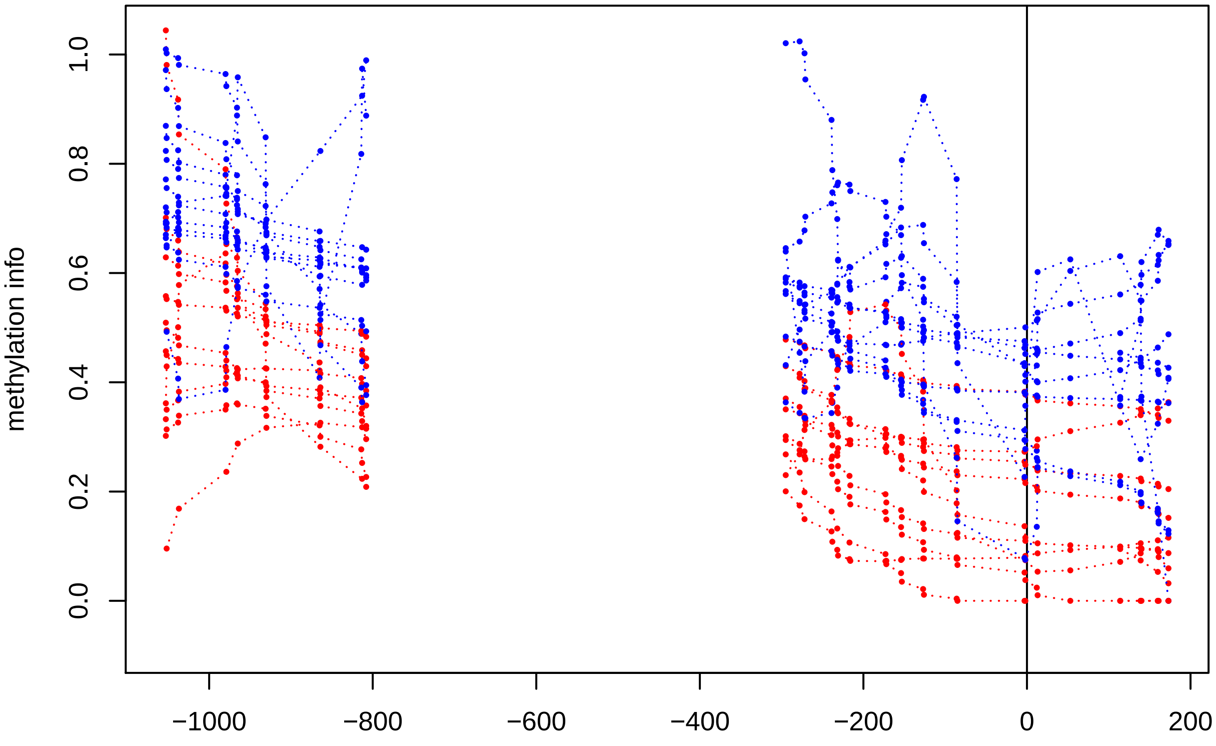
BTNL3 average UC−N %methylation max=29.77% min=−8.44%

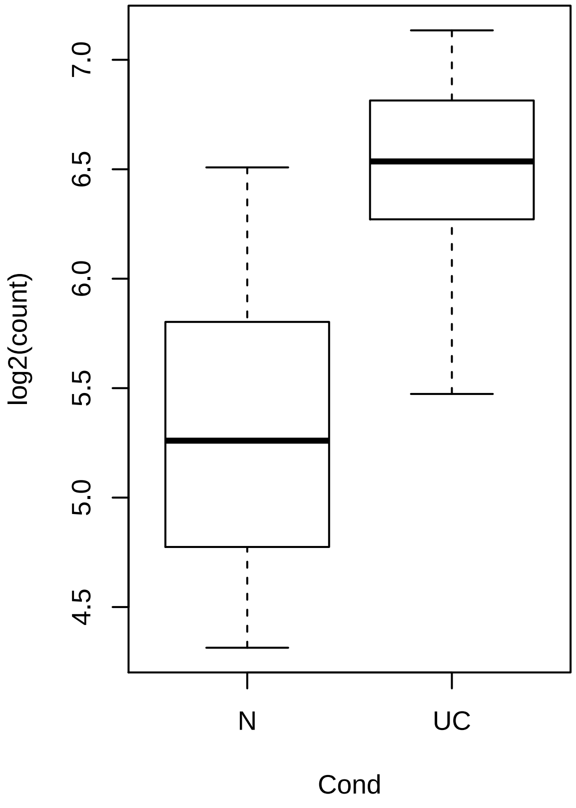
BTNL3 raw %methylation, red=UC, blue=Normal

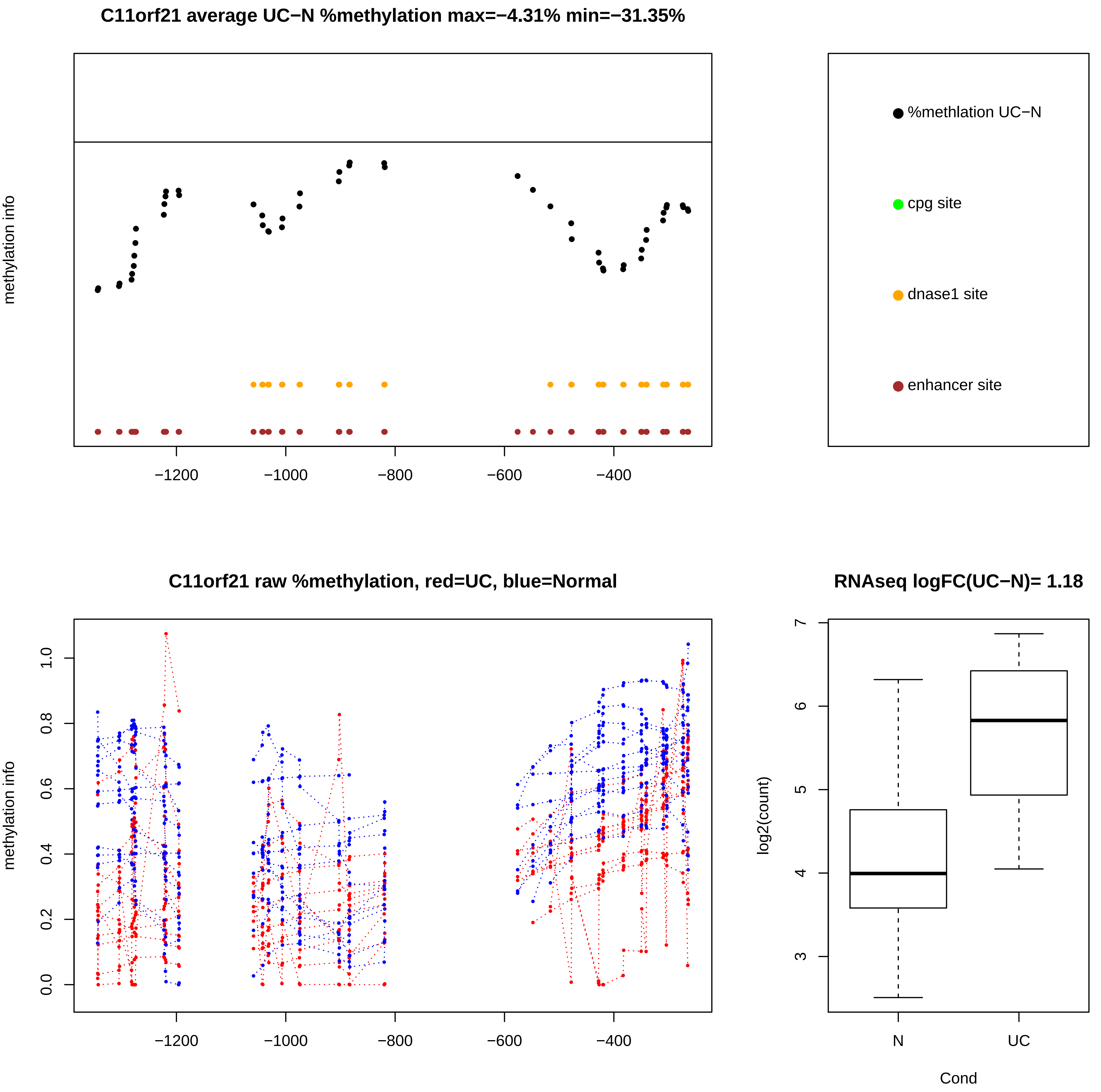
RNAseq logFC(UC−N)= −1.31


BTNL8 average UC−N %methylation max=13.69% min=−6.9%
methylation info
−1500
−1000
−500
0
%methlation UC−N
cpg site
dnase1 site
enhancer site
BTNL8 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−1500
−1000
−500
0
RNAseq logFC(UC−N)= −1.41
log2(count)
8
9
10
11
12
N
UC
Cond


BZRAP1−AS1 average UC−N %methylation max=−22.54% min=−27.3%


BZRAP1−AS1 raw %methylation, red=UC, blue=Normal

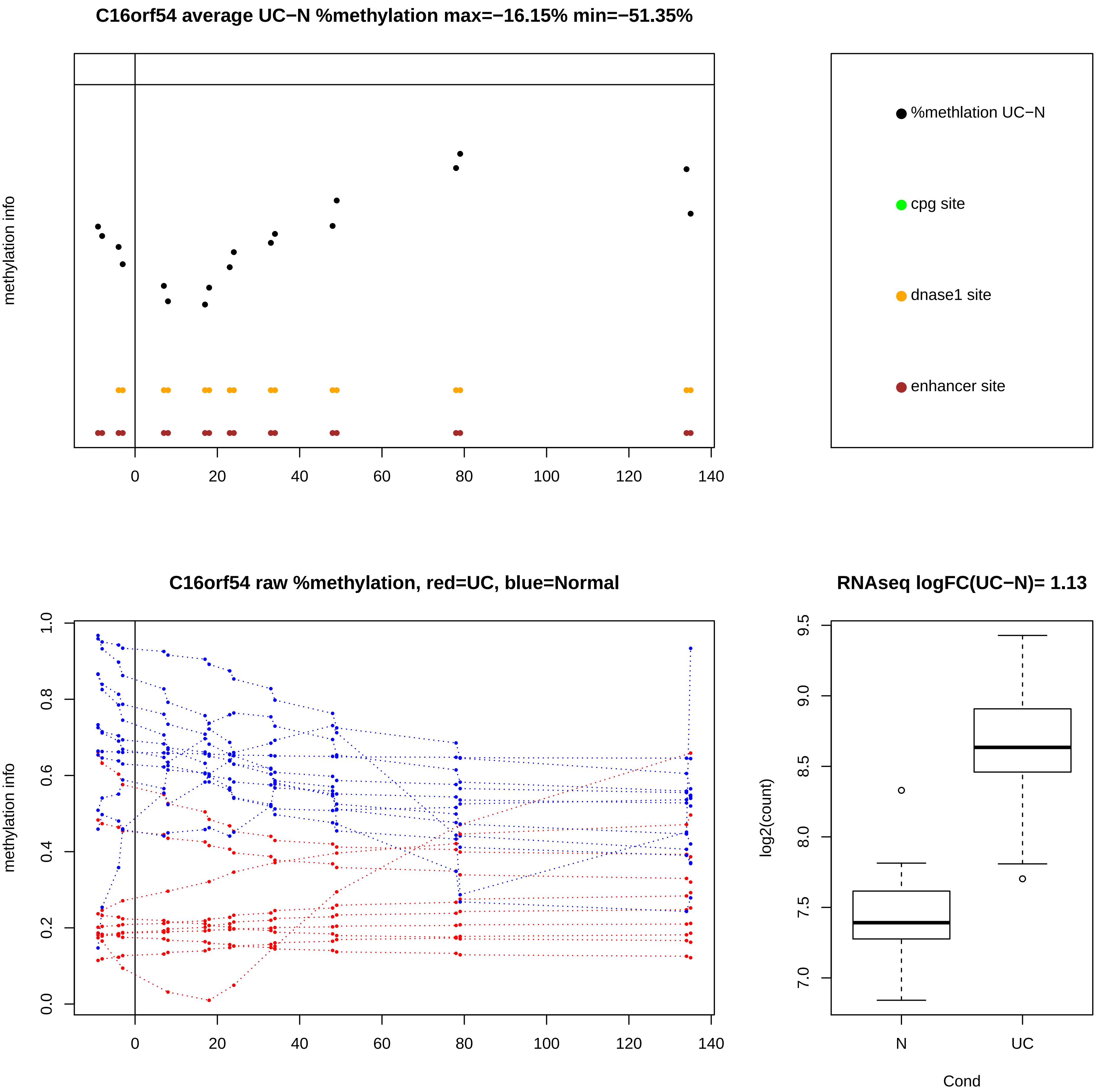

RNAseq logFC(UC−N)= 1.07



C11orf21 average UC−N %methylation max=−4.31% min=−31.35%

C11orf21 raw %methylation, red=UC, blue=Normal

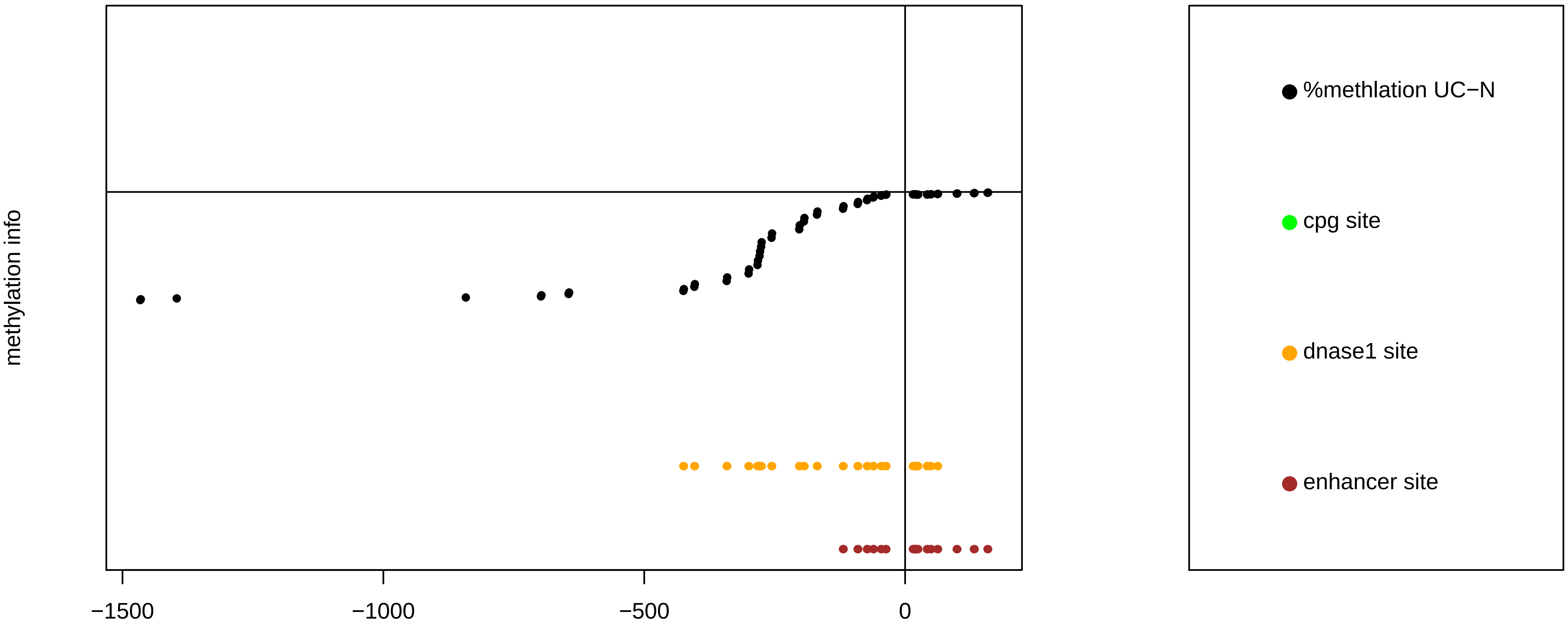
RNAseq logFC(UC−N)= 1.18


C16orf54 average UC−N %methylation max=−16.15% min=−51.35%

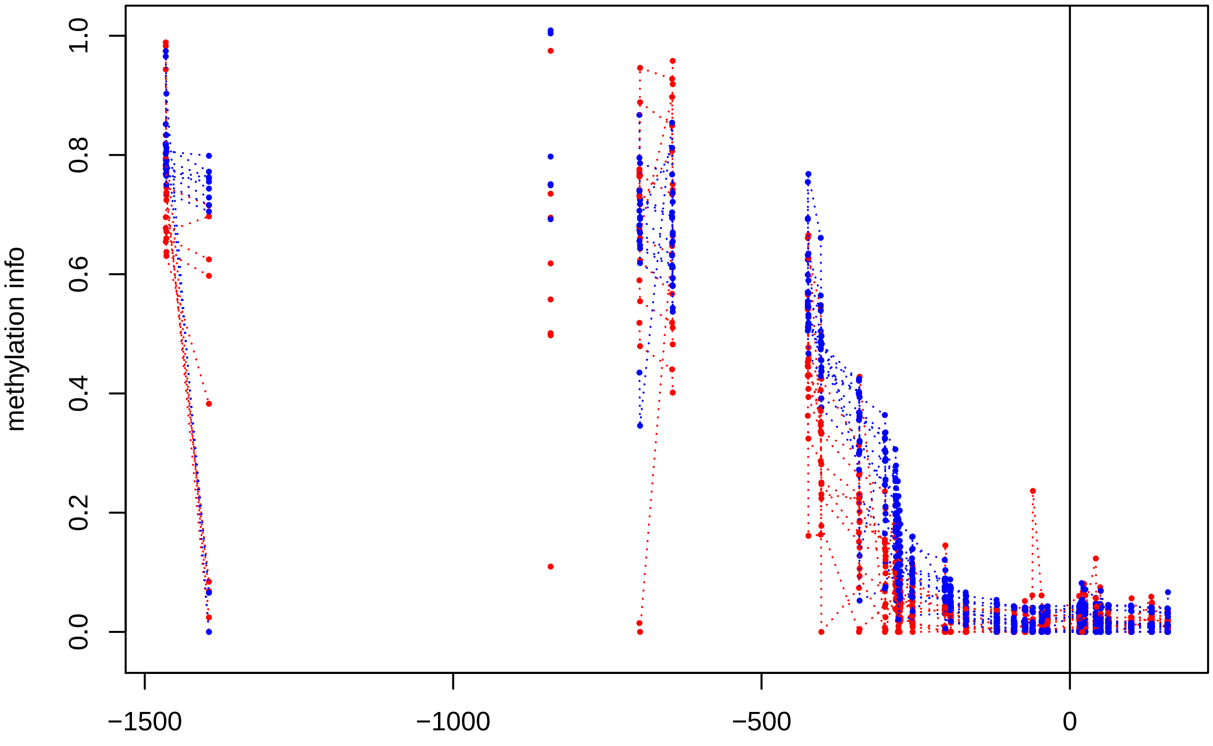
C16orf54 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.13

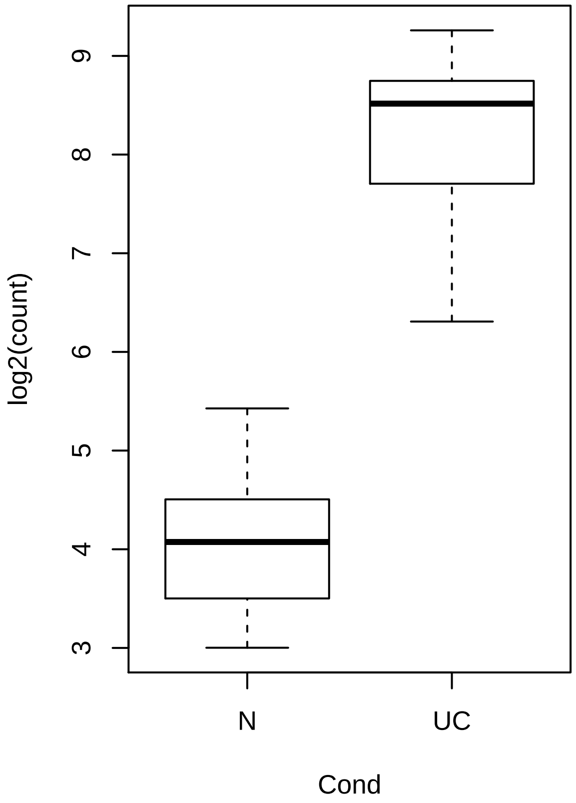
C2CD4A average UC−N %methylation max=−0.07% min=−13.02%

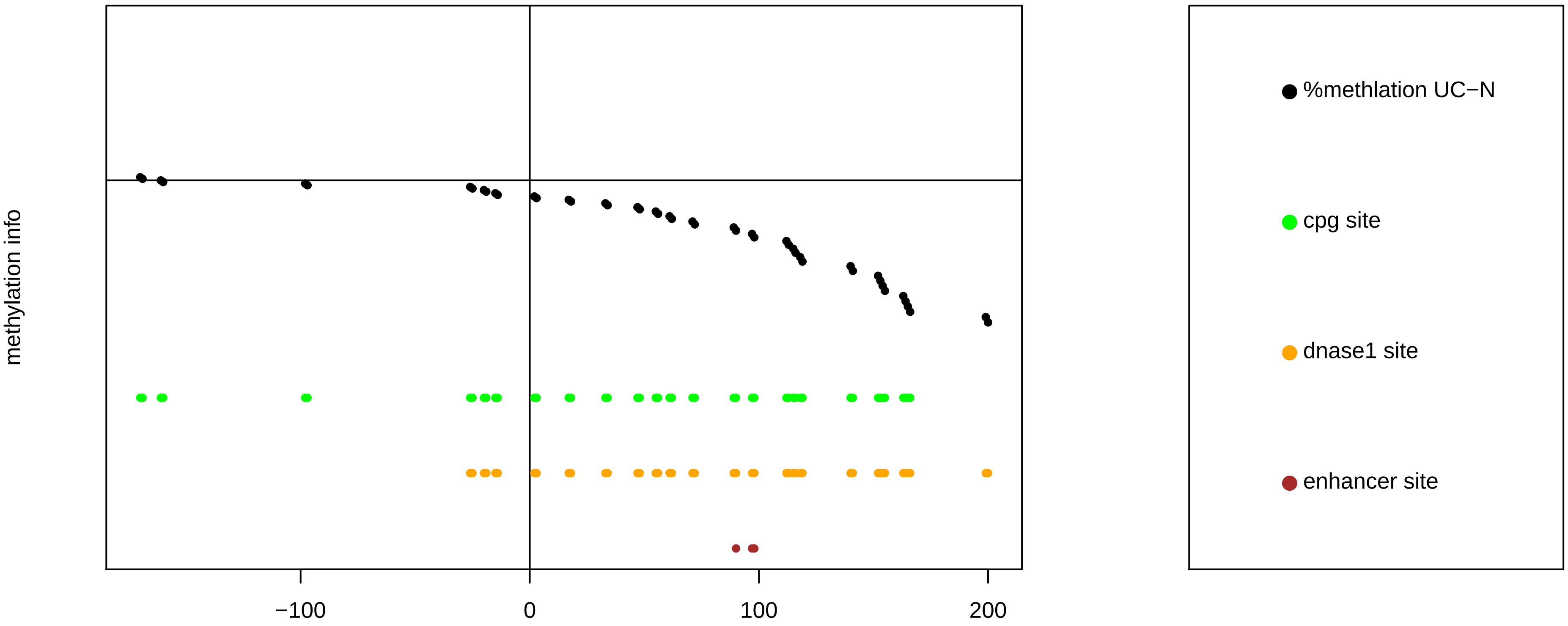


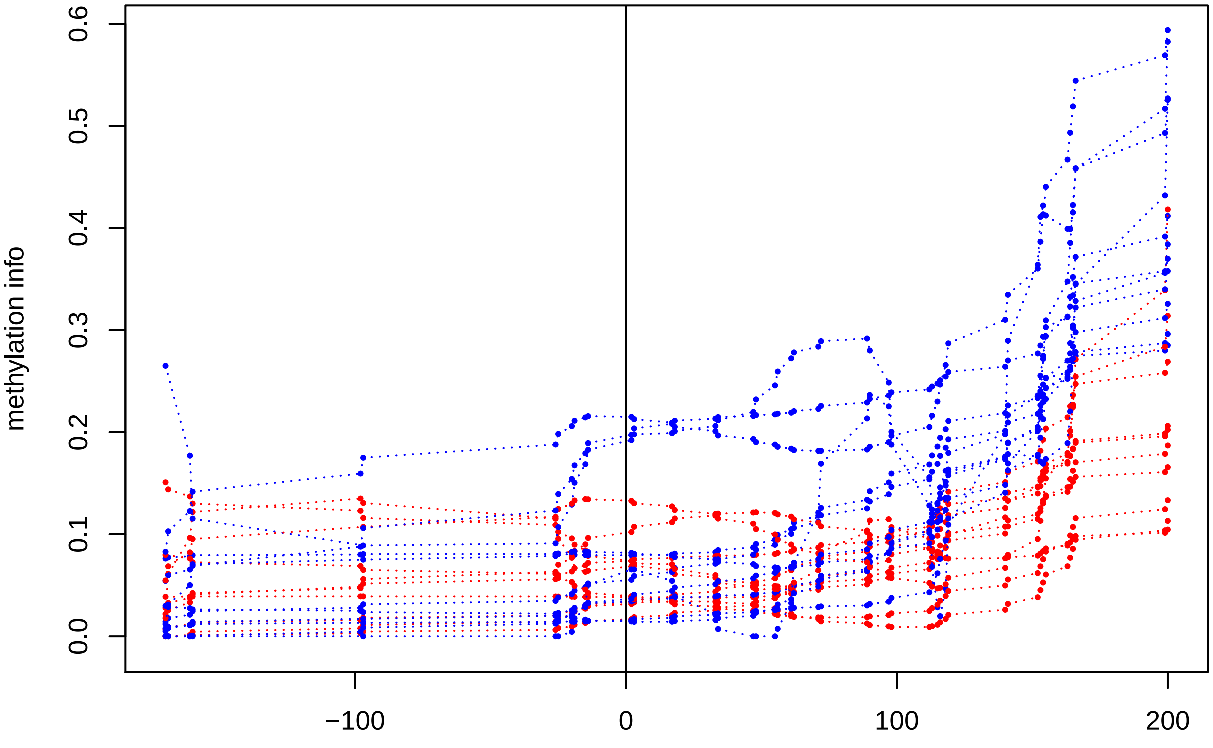
C2CD4A raw %methylation, red=UC, blue=Normal

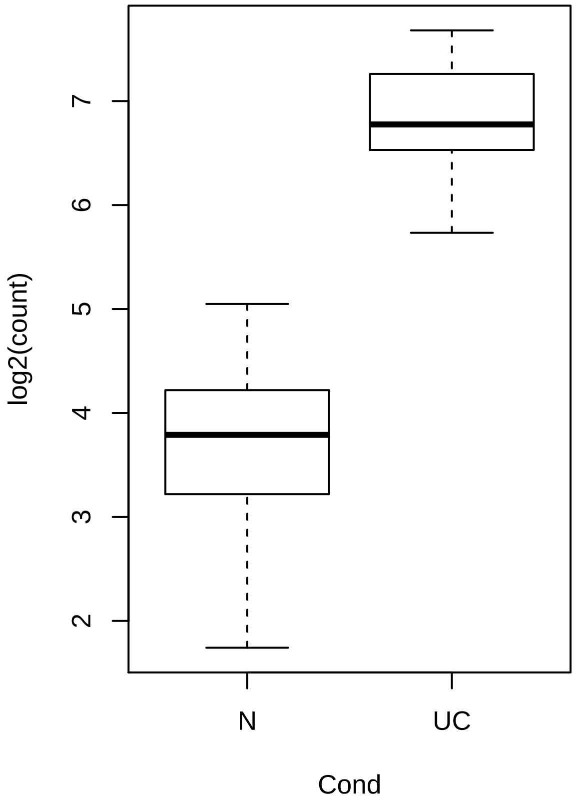


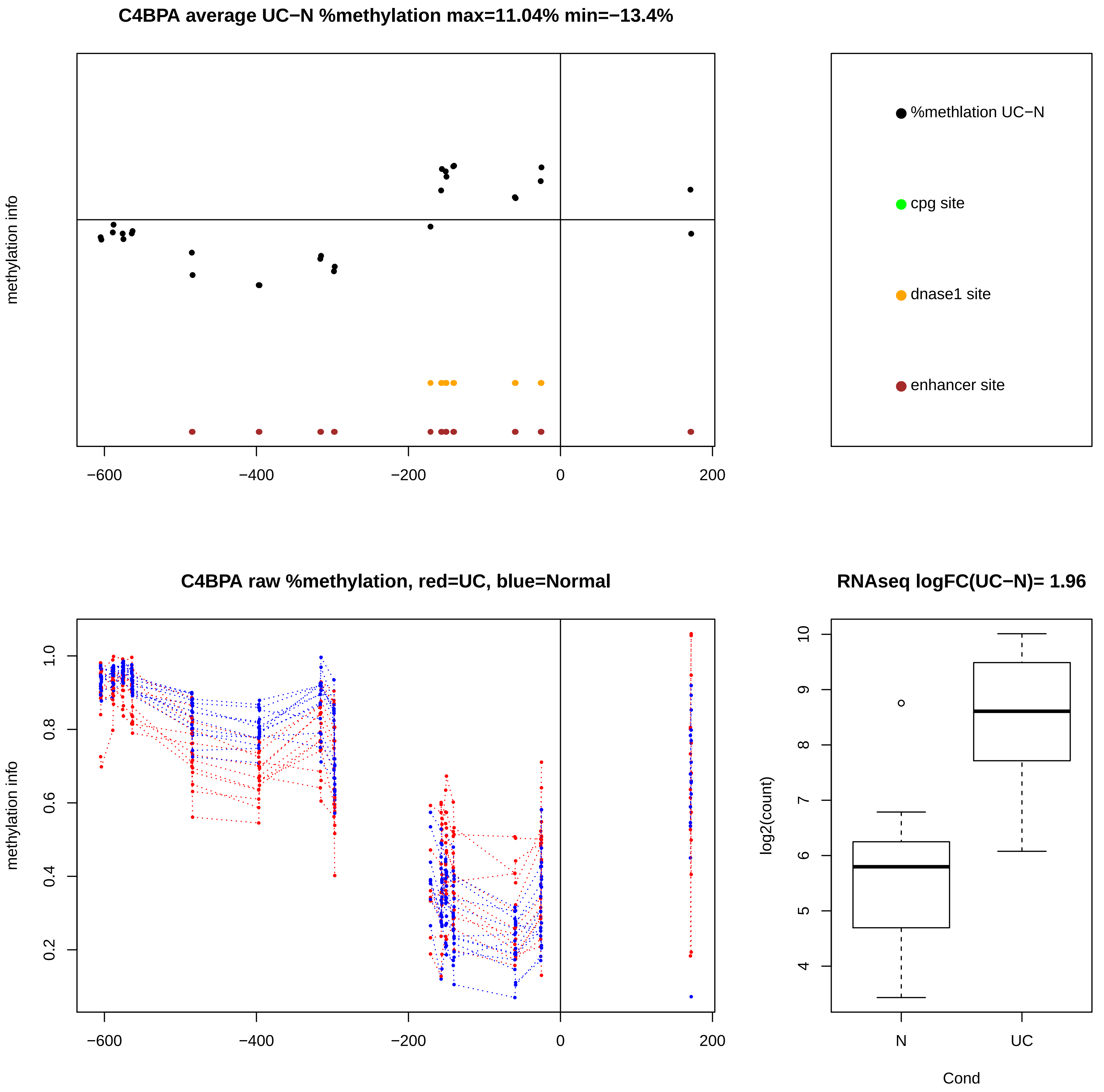
RNAseq logFC(UC−N)= 3.72




C2CD4B average UC−N %methylation max=0.41% min=−18.86%


C2CD4B raw %methylation, red=UC, blue=Normal

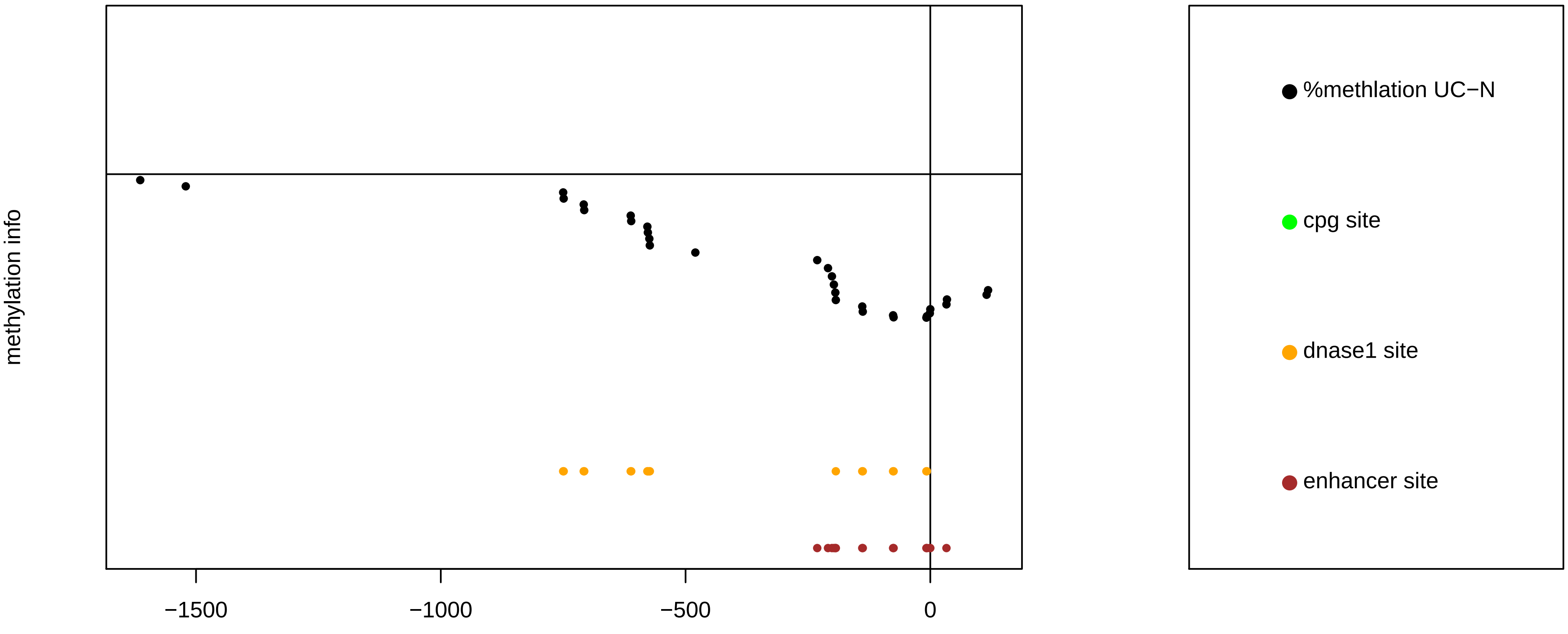

RNAseq logFC(UC−N)= 2.79



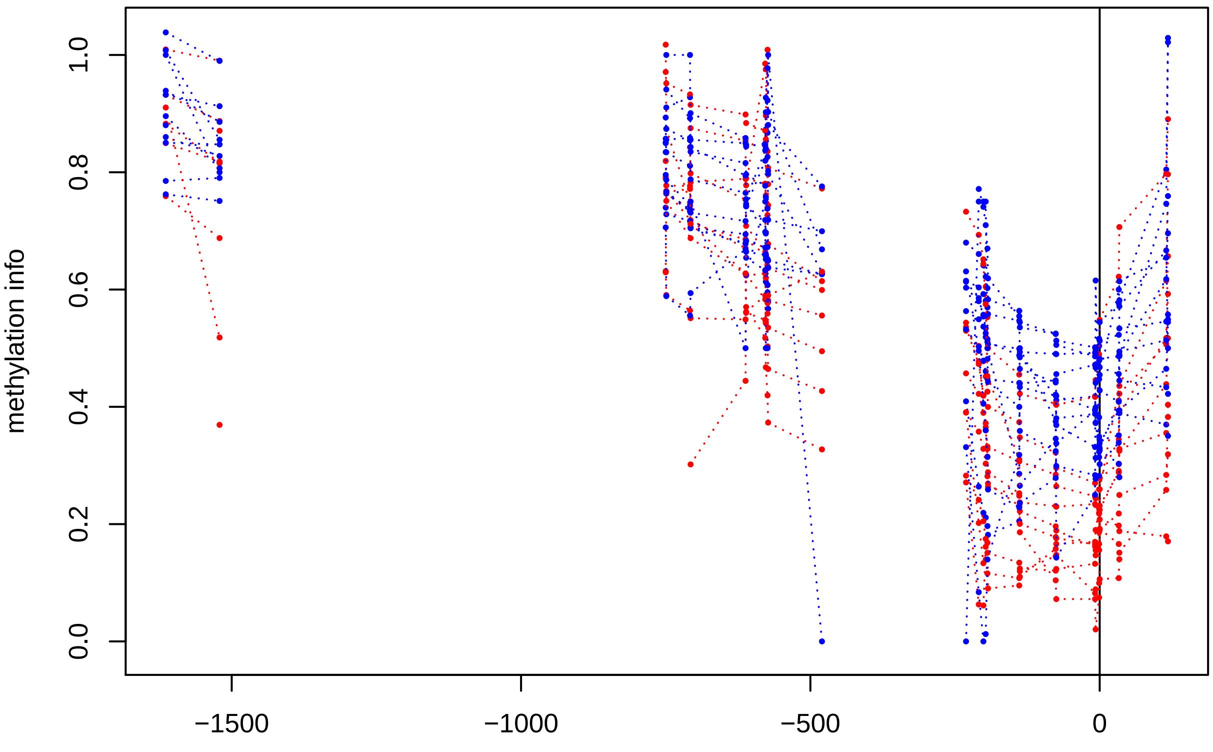
C4BPA average UC−N %methylation max=11.04% min=−13.4%

C4BPA raw %methylation, red=UC, blue=Normal

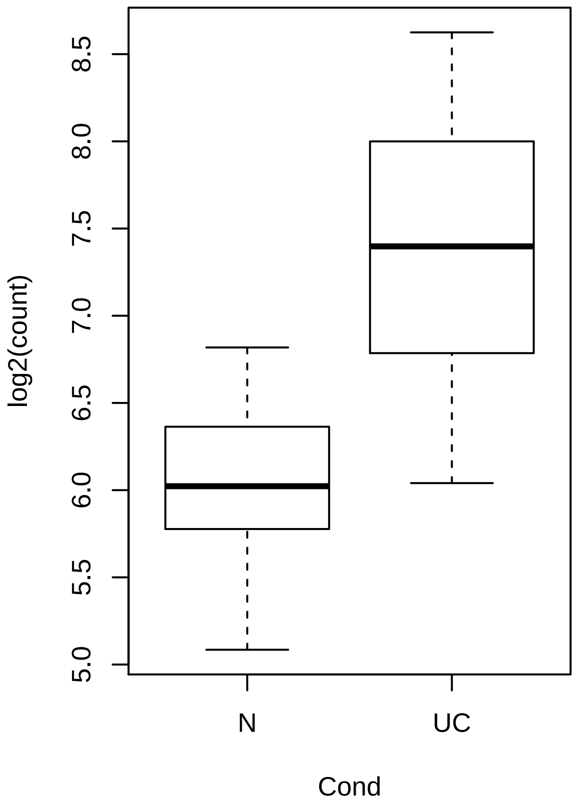
RNAseq logFC(UC−N)= 1.96



C5AR1 average UC−N %methylation max=−0.77% min=−18.68%

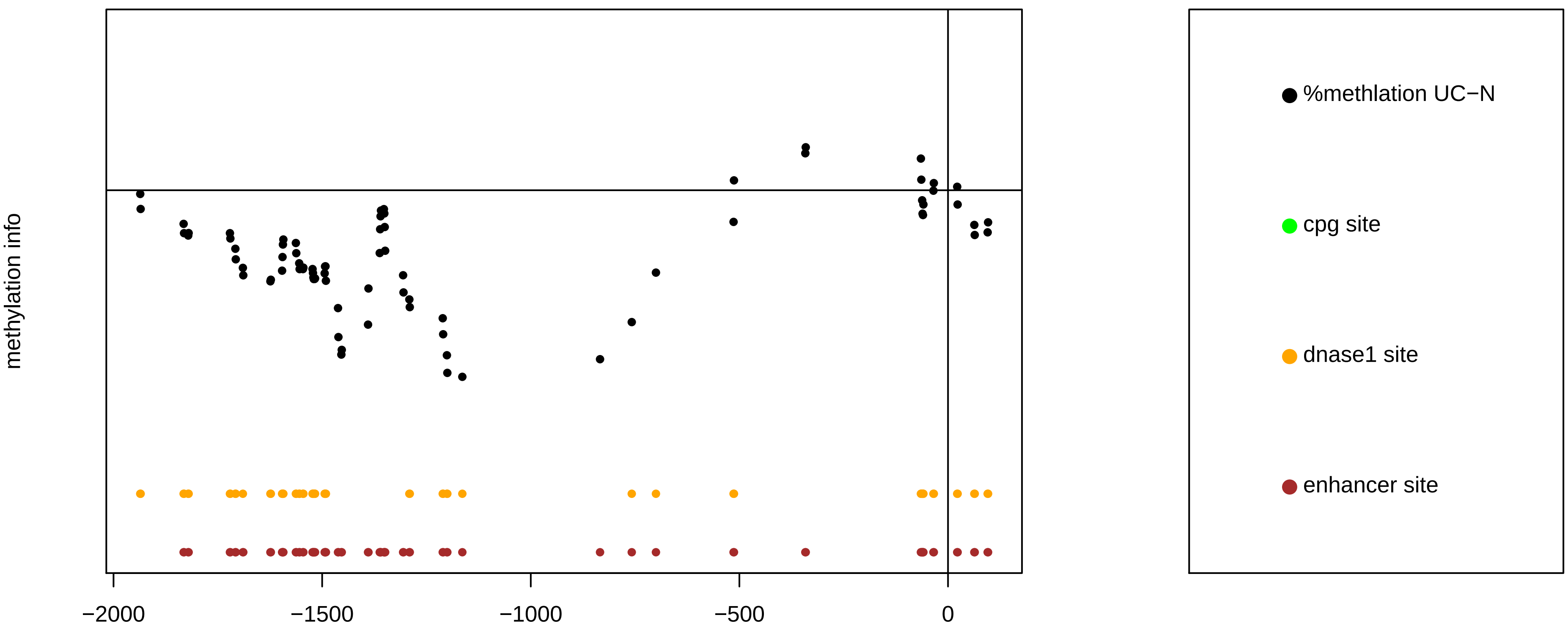


C5AR1 raw %methylation, red=UC, blue=Normal

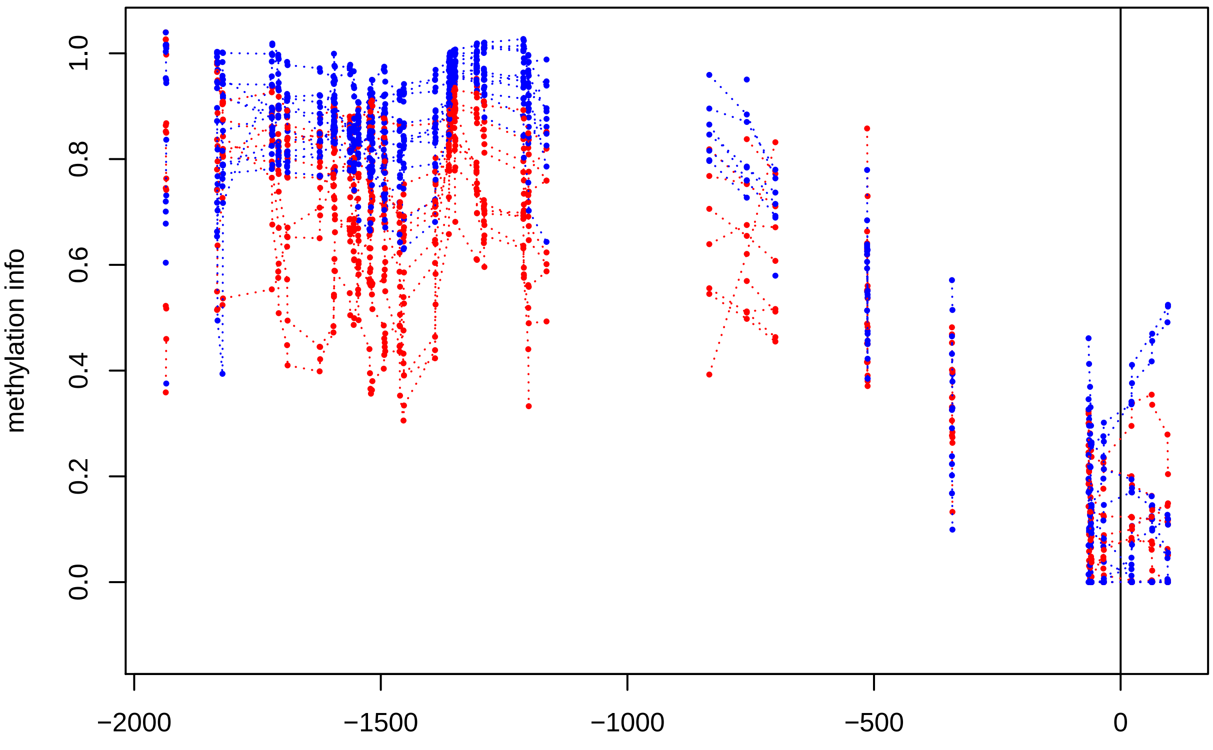


RNAseq logFC(UC−N)= 1.18

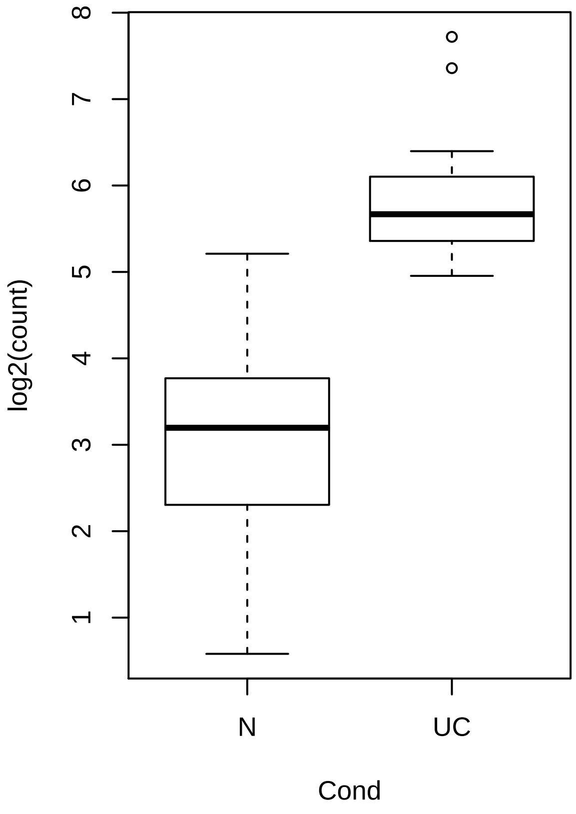
C6orf223 average UC−N %methylation max=7.35% min=−31.91%



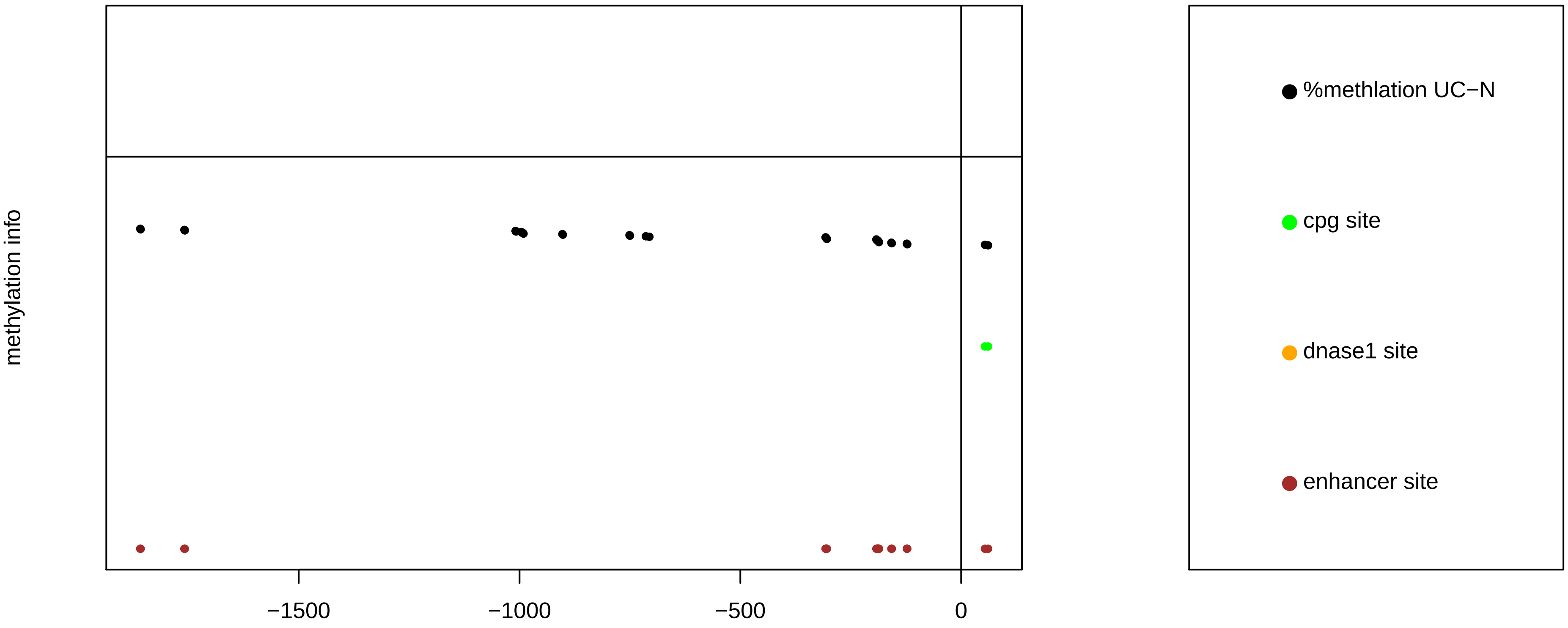
C6orf223 raw %methylation, red=UC, blue=Normal



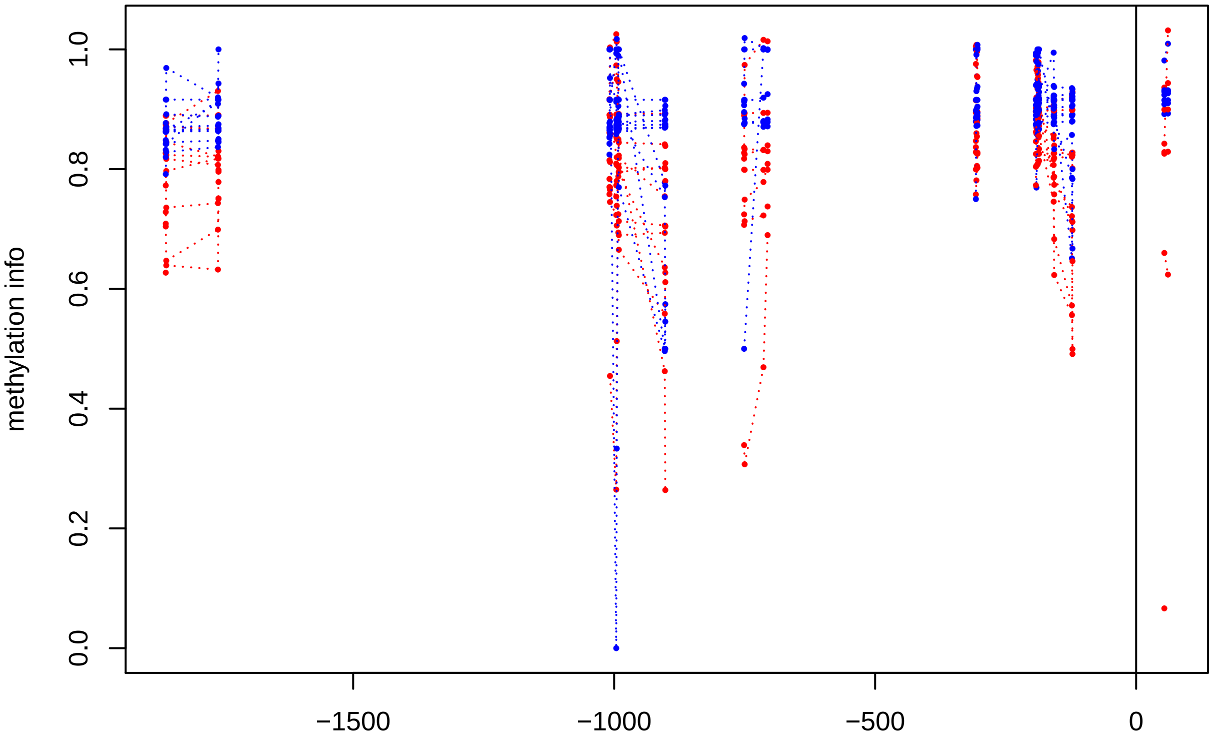
RNAseq logFC(UC−N)= 2.31



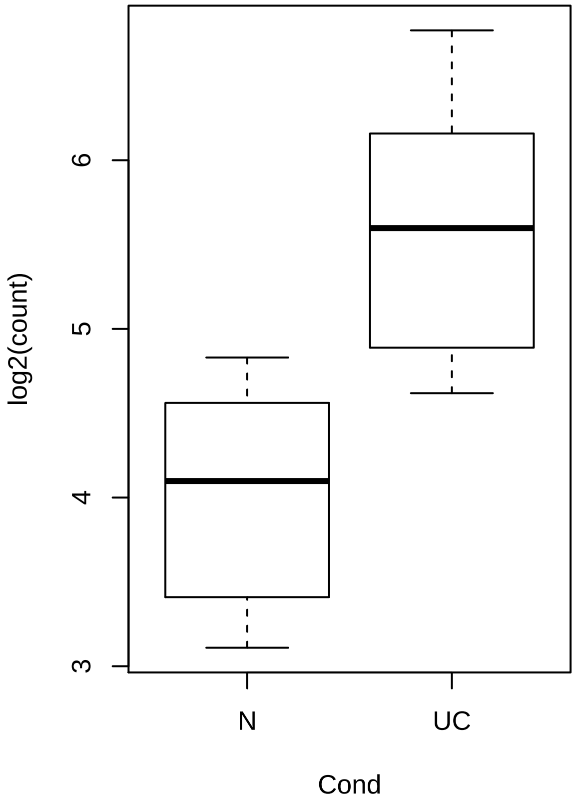
CACNA1E average UC−N %methylation max=−7.13% min=−8.76%

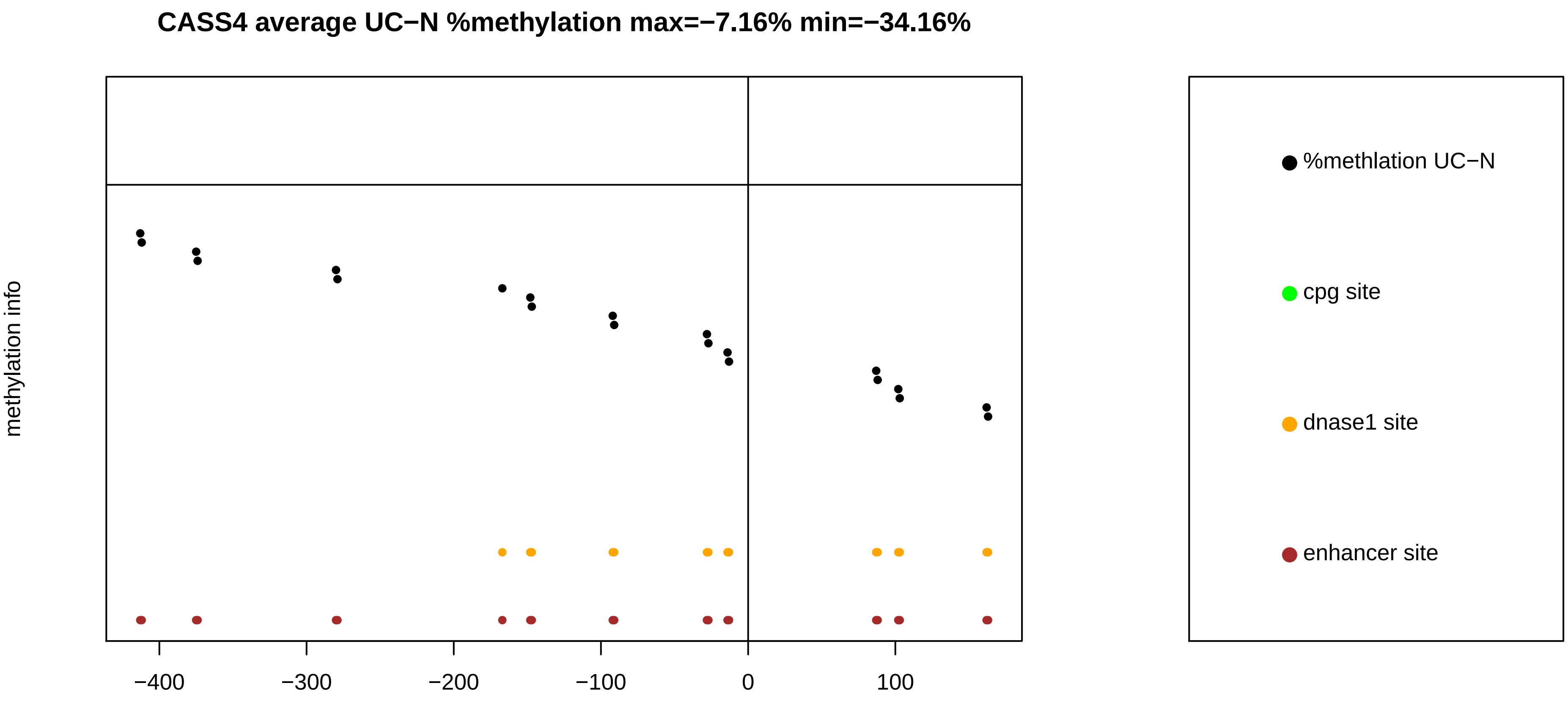


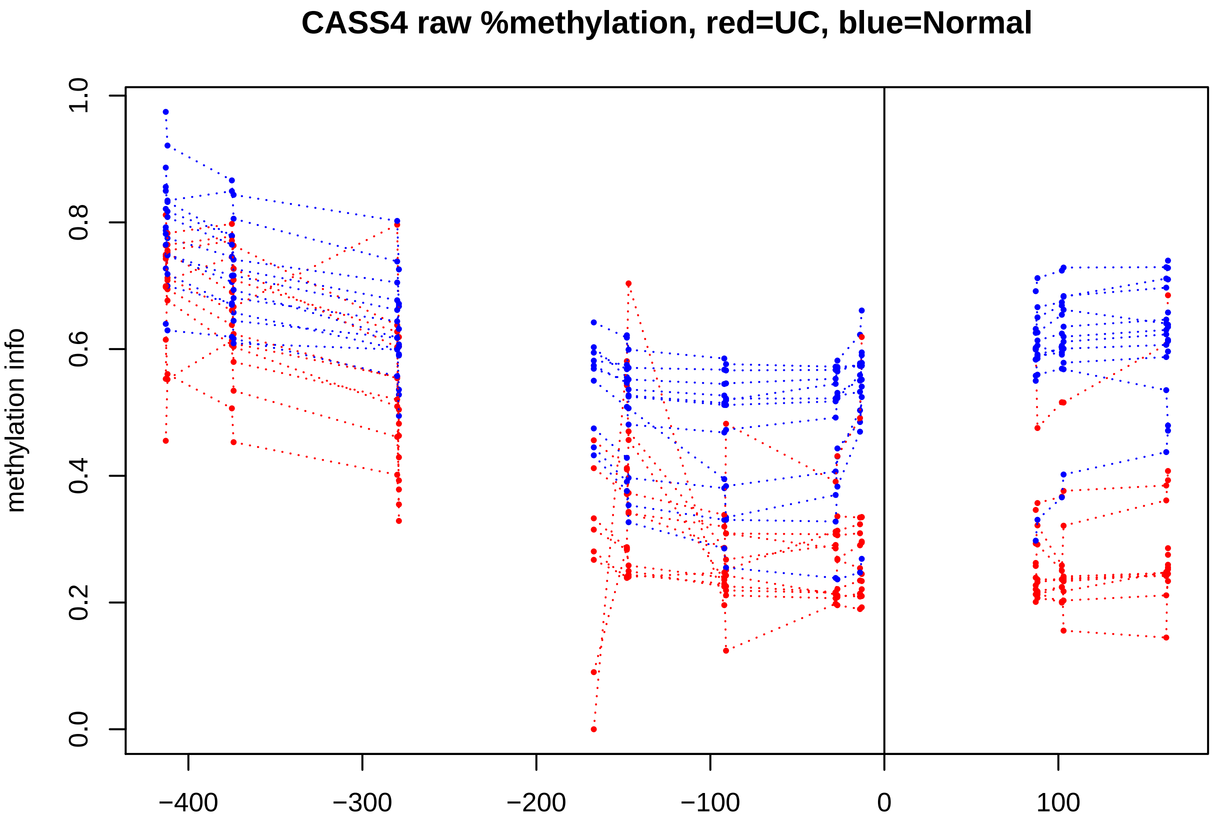
CACNA1E raw %methylation, red=UC, blue=Normal

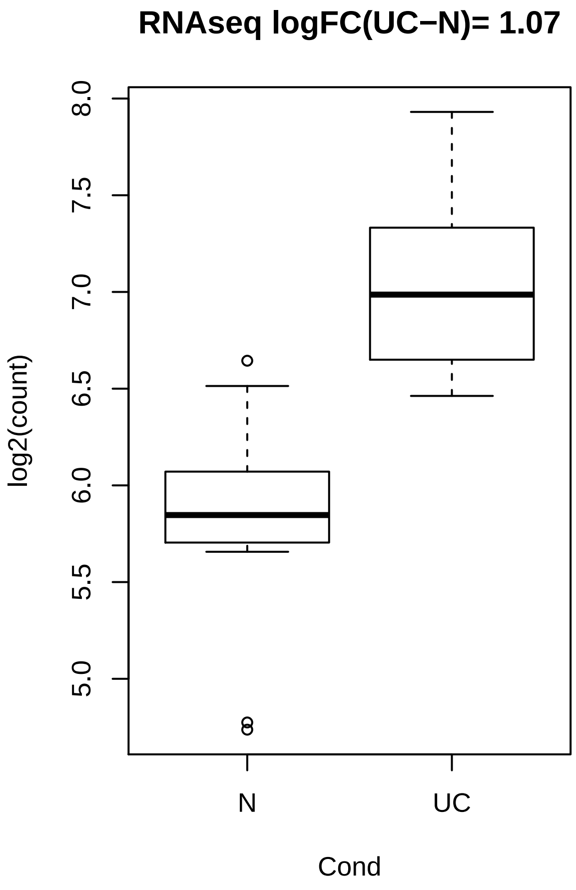


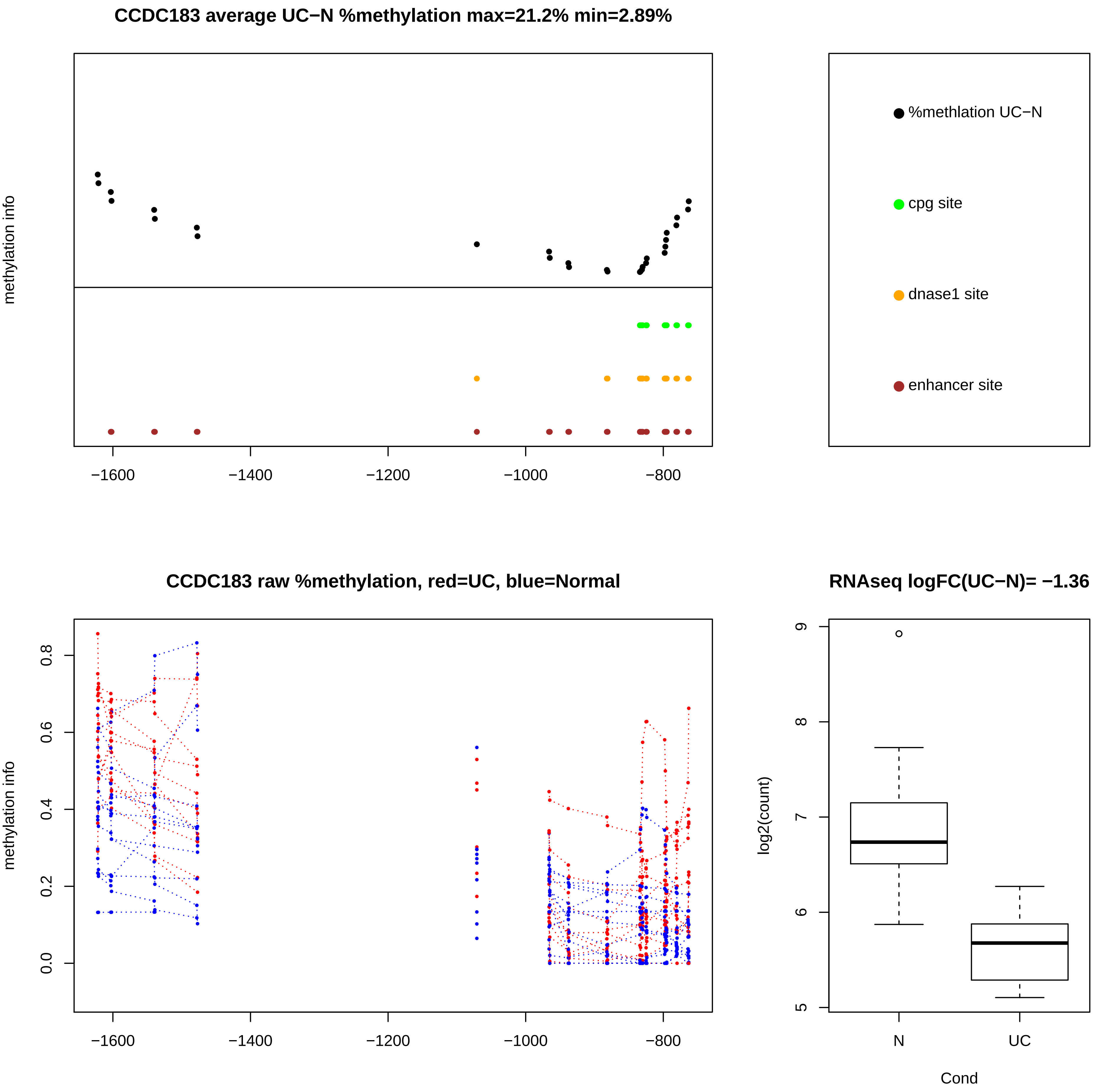
RNAseq logFC(UC−N)= 1.47

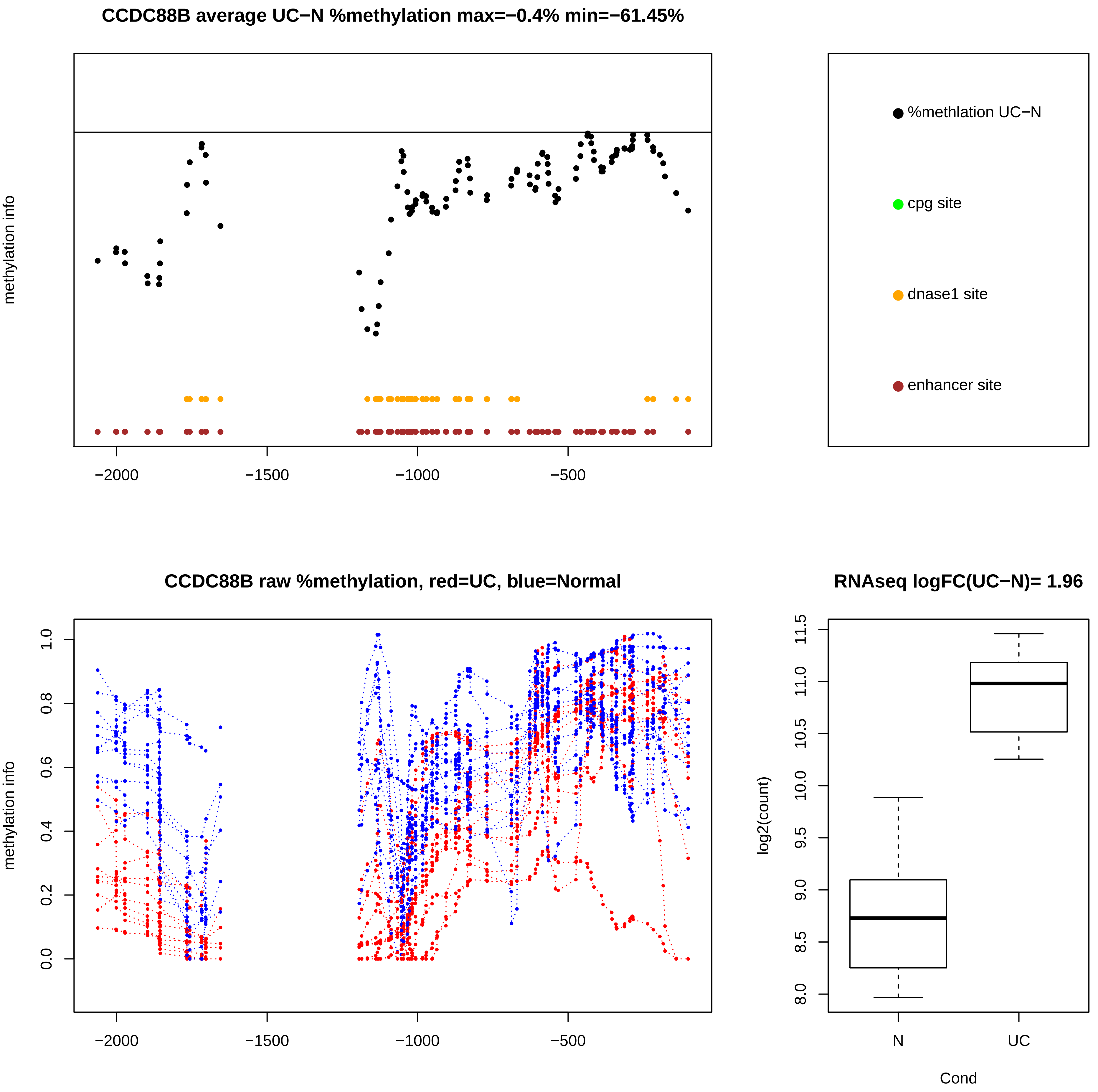



CASS4 average UC−N %methylation max=−7.16% min=−34.16%


CASS4 raw %methylation, red=UC, blue=Normal


RNAseq logFC(UC−N)= 1.07

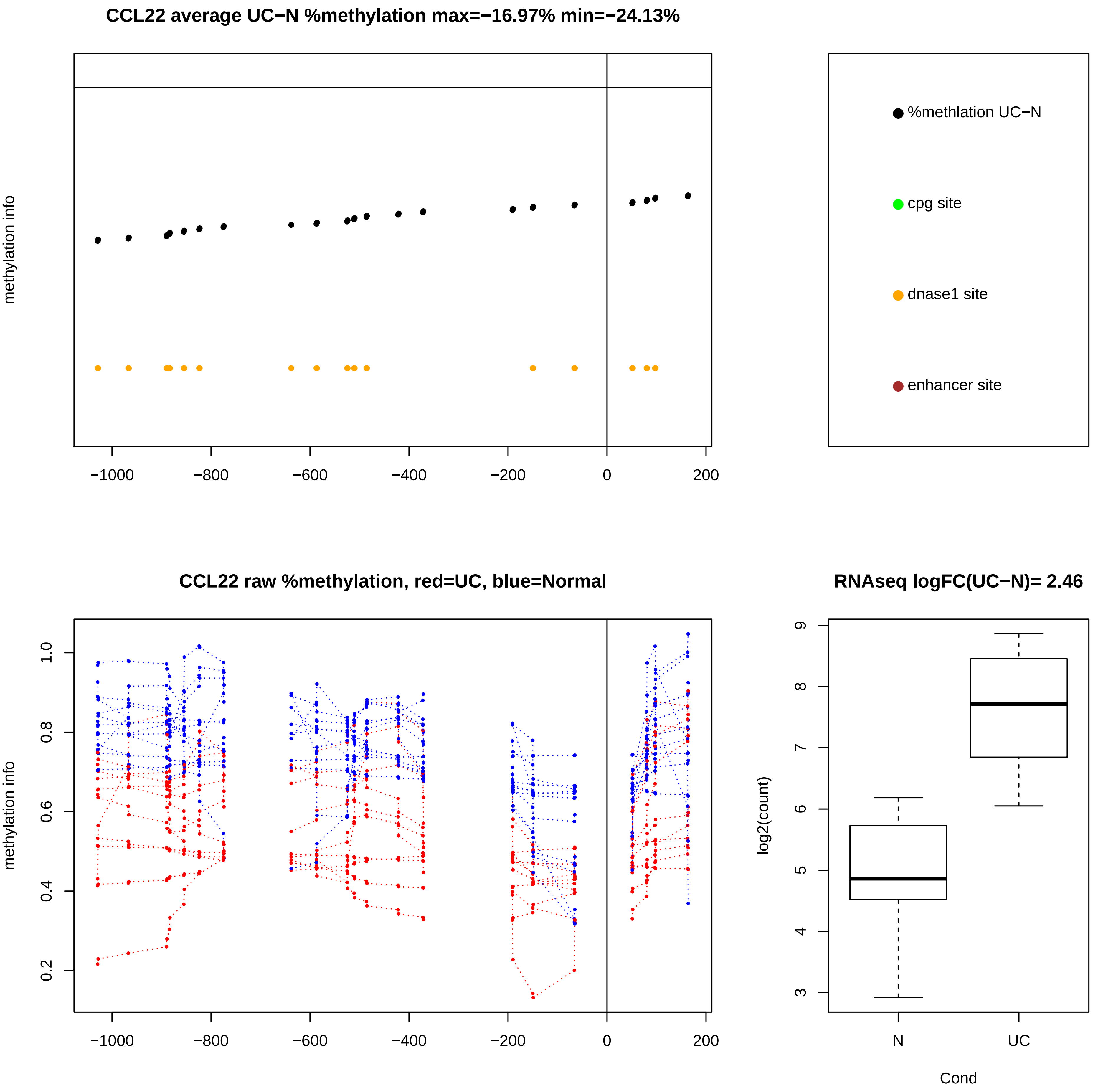

CCDC183 average UC−N %methylation max=21.2% min=2.89%
methylation info
−1600
−1400
−1200
−1000
−800
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
CCDC183 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
−1600
−1400
−1200
−1000
−800
RNAseq logFC(UC−N)= −1.36
log2(count)
5
6
7
8
9
N
UC
Cond



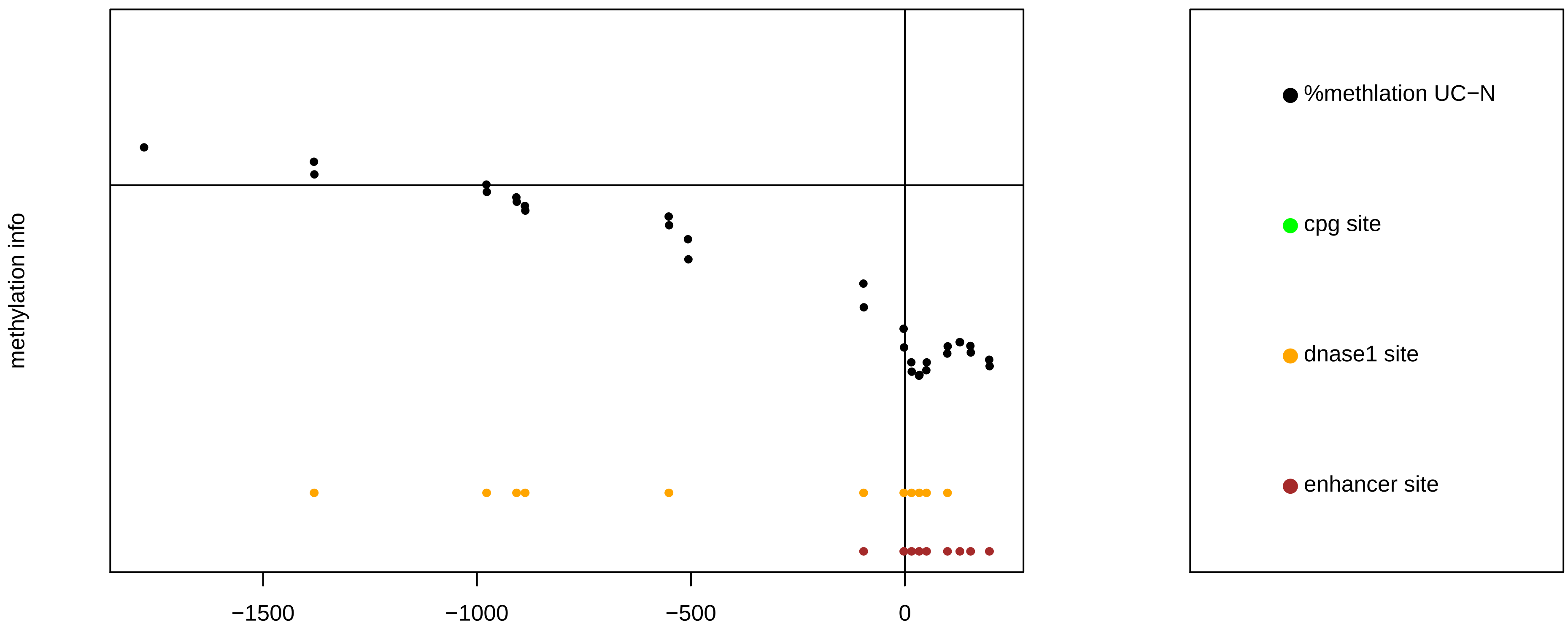
CCDC88B average UC−N %methylation max=−0.4% min=−61.45%

CCDC88B raw %methylation, red=UC, blue=Normal

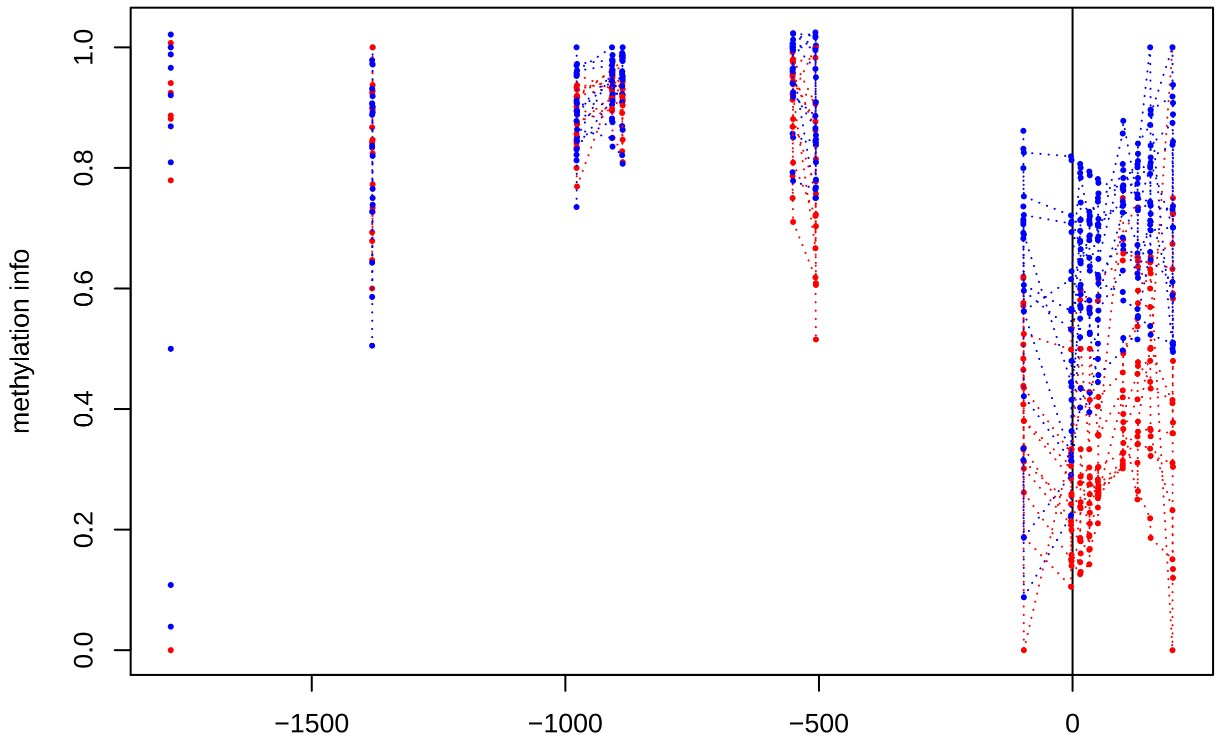
RNAseq logFC(UC−N)= 1.96


CCL22 average UC−N %methylation max=−16.97% min=−24.13%
methylation info
−1000
−800
−600
−400
−200
0
200
%methlation UC−N
cpg site
dnase1 site
enhancer site
CCL22 raw %methylation, red=UC, blue=Normal
methylation info
0.2
0.4
0.6
0.8
1.0
−1000
−800
−600
−400
−200
0
200
RNAseq logFC(UC−N)= 2.46
log2(count)
3
4
5
6
7
8
9
N
UC
Cond

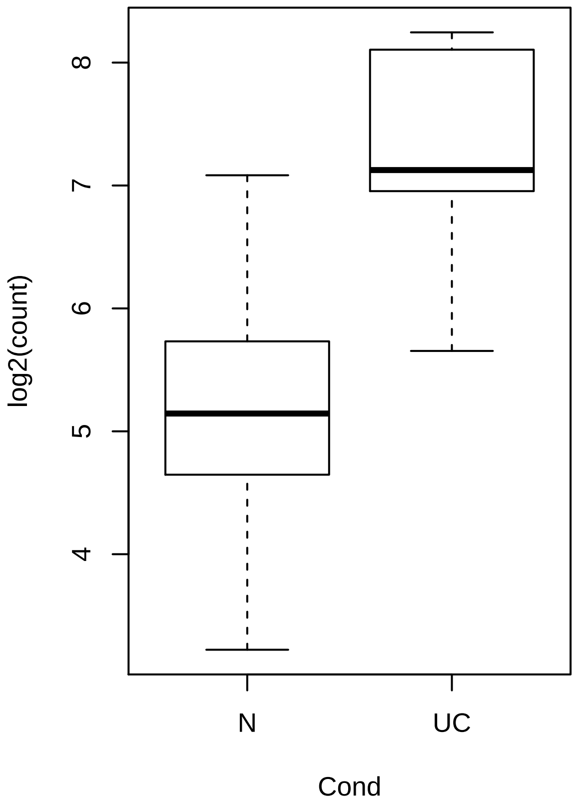
CCR4 average UC−N %methylation max=6.47% min=−32.55%

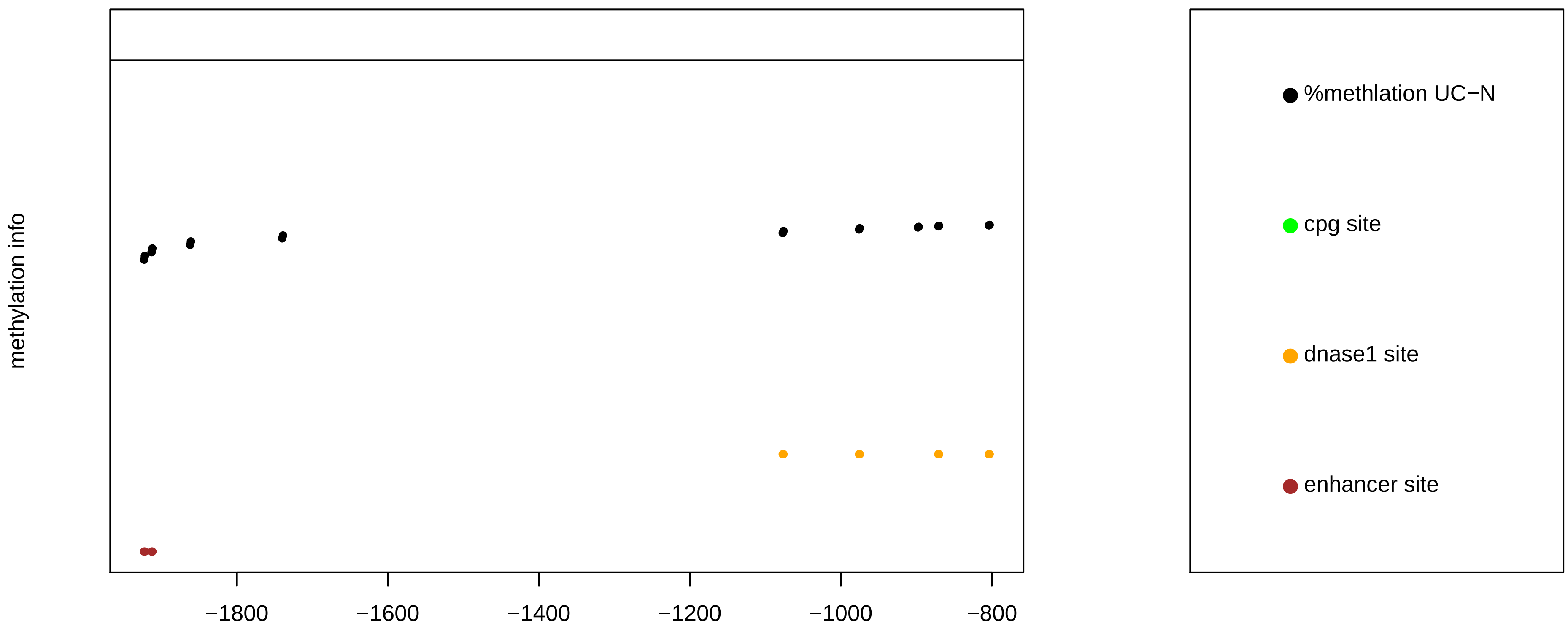


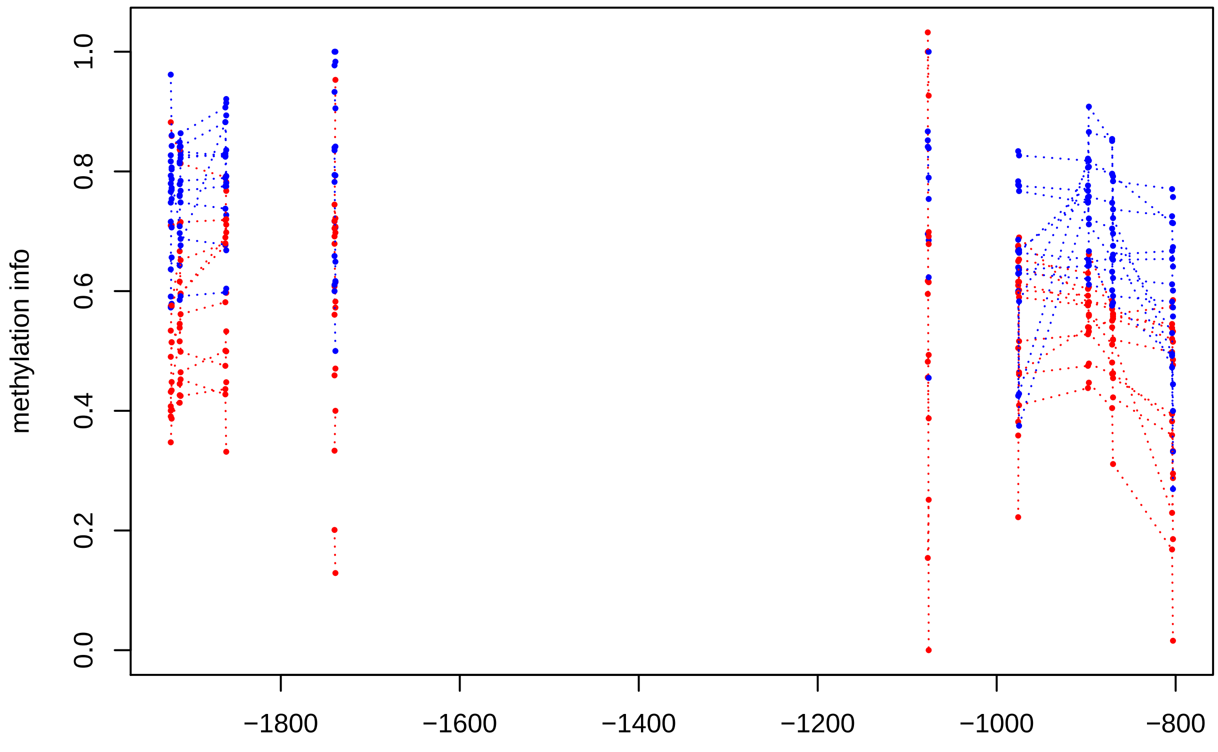
CCR4 raw %methylation, red=UC, blue=Normal

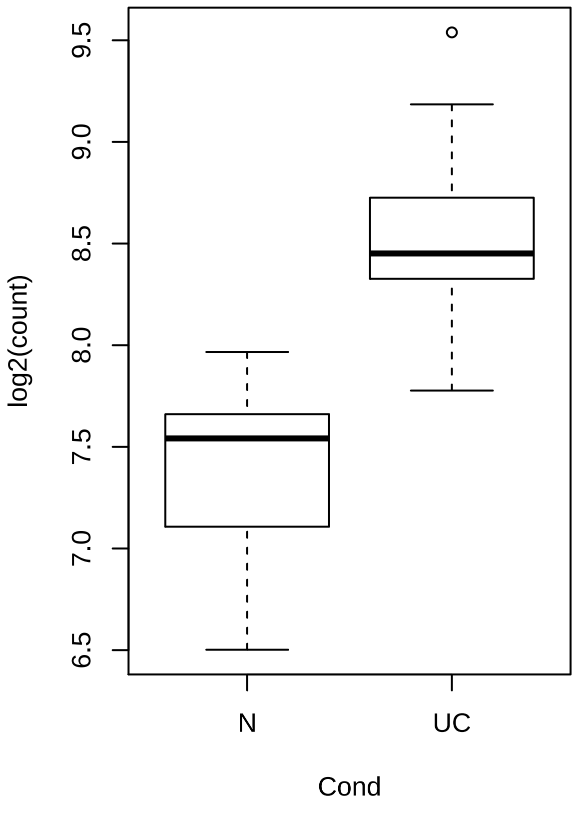


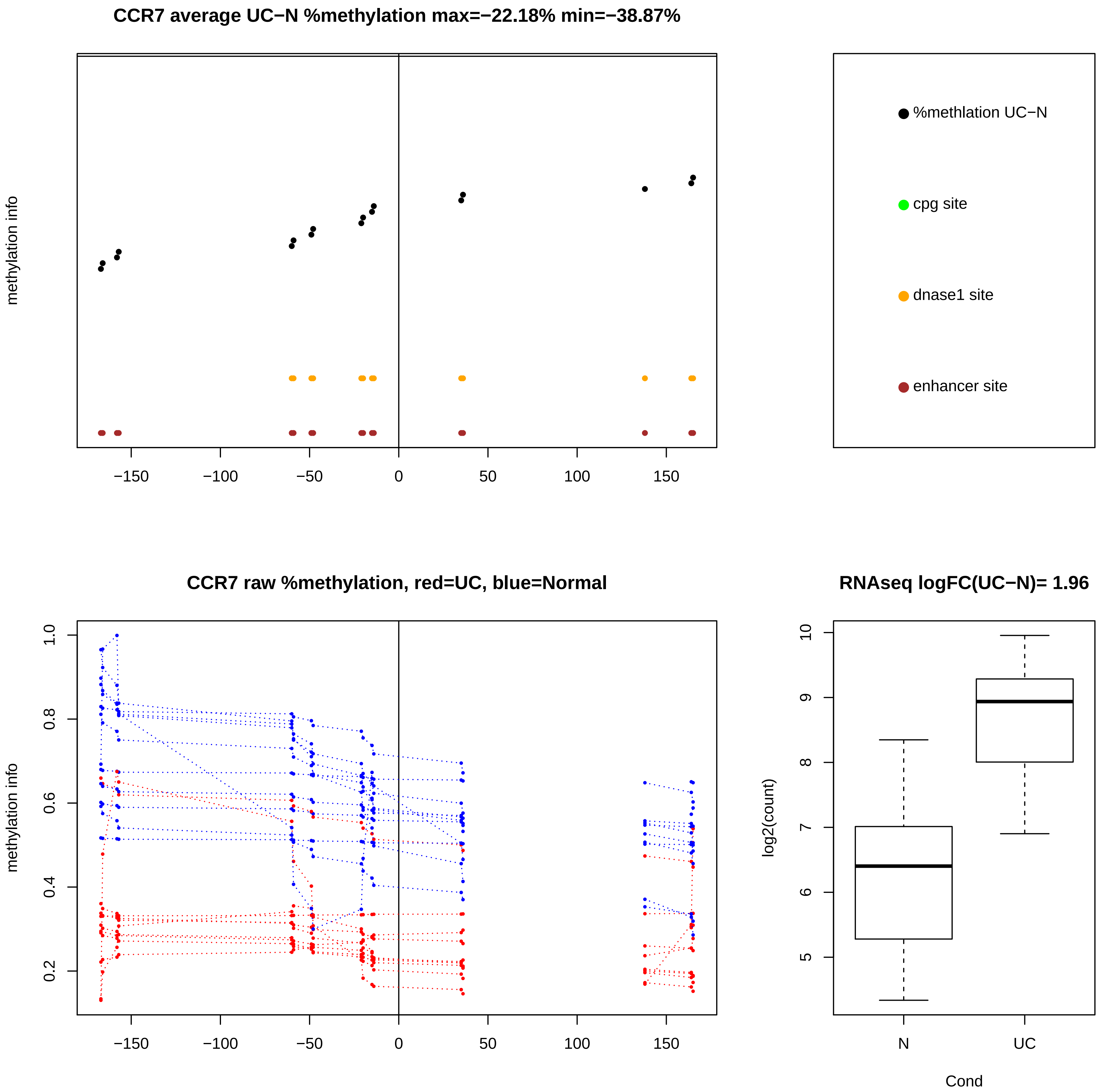
RNAseq logFC(UC−N)= 1.7

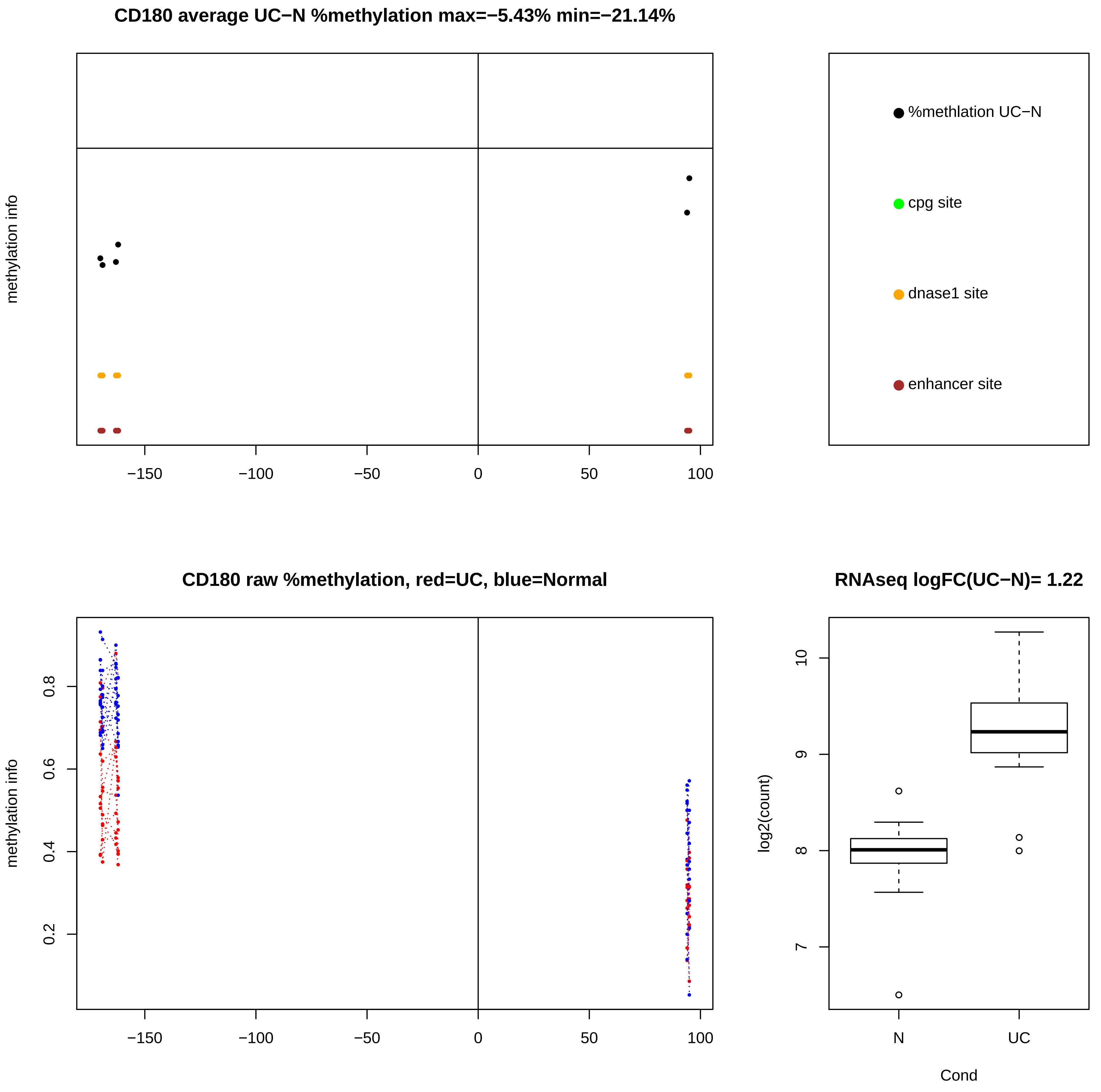



CCR5 average UC−N %methylation max=−16.94% min=−20.51%


CCR5 raw %methylation, red=UC, blue=Normal


RNAseq logFC(UC−N)= 1.09

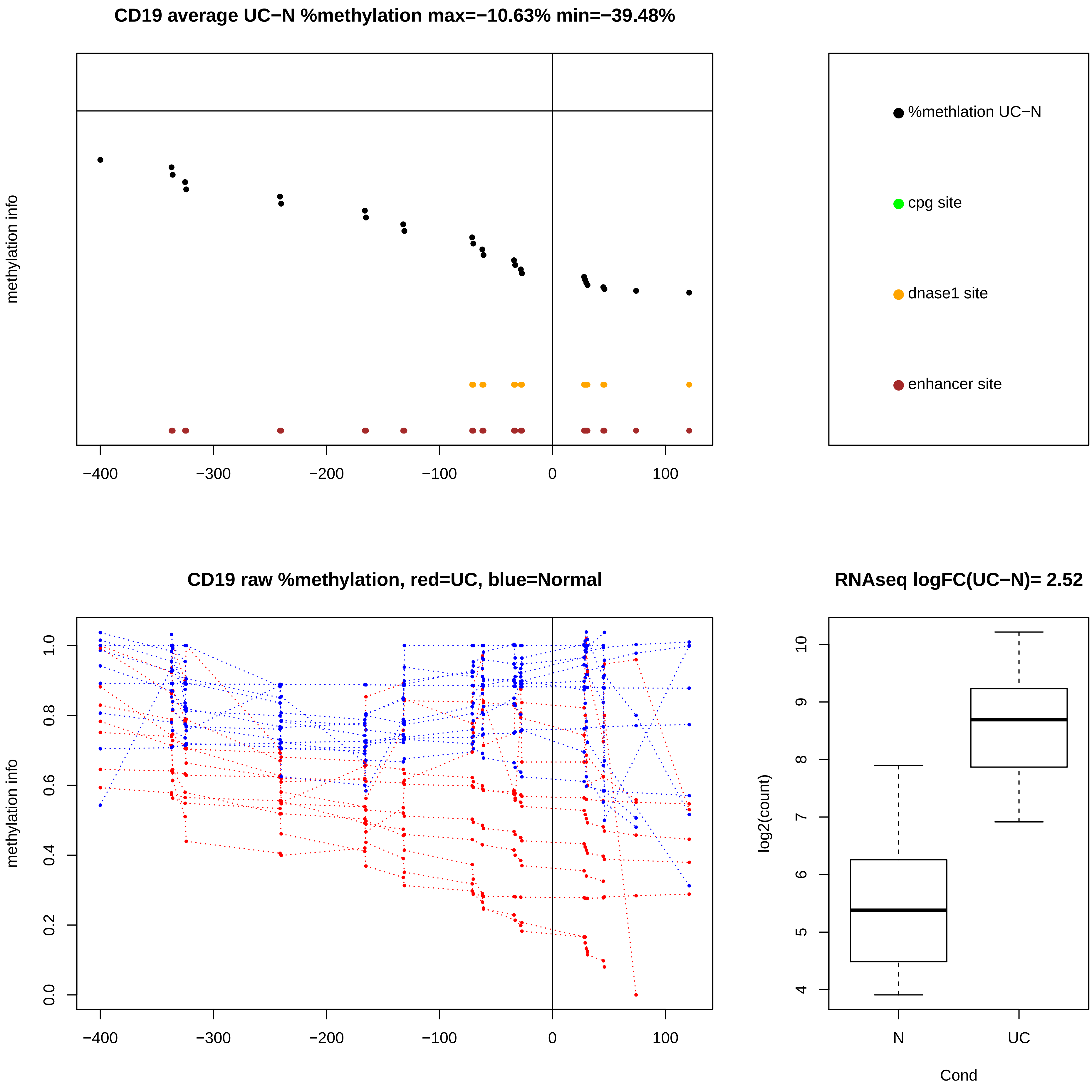

CCR7 average UC−N %methylation max=−22.18% min=−38.87%
methylation info
−150
−100
−50
0
50
100
150
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
CCR7 raw %methylation, red=UC, blue=Normal
methylation info
0.2
0.4
0.6
0.8
1.0
−150
−100
−50
0
50
100
150
RNAseq logFC(UC−N)= 1.96
log2(count)
5
6
7
8
9
10
N
UC
Cond



CD180 average UC−N %methylation max=−5.43% min=−21.14%

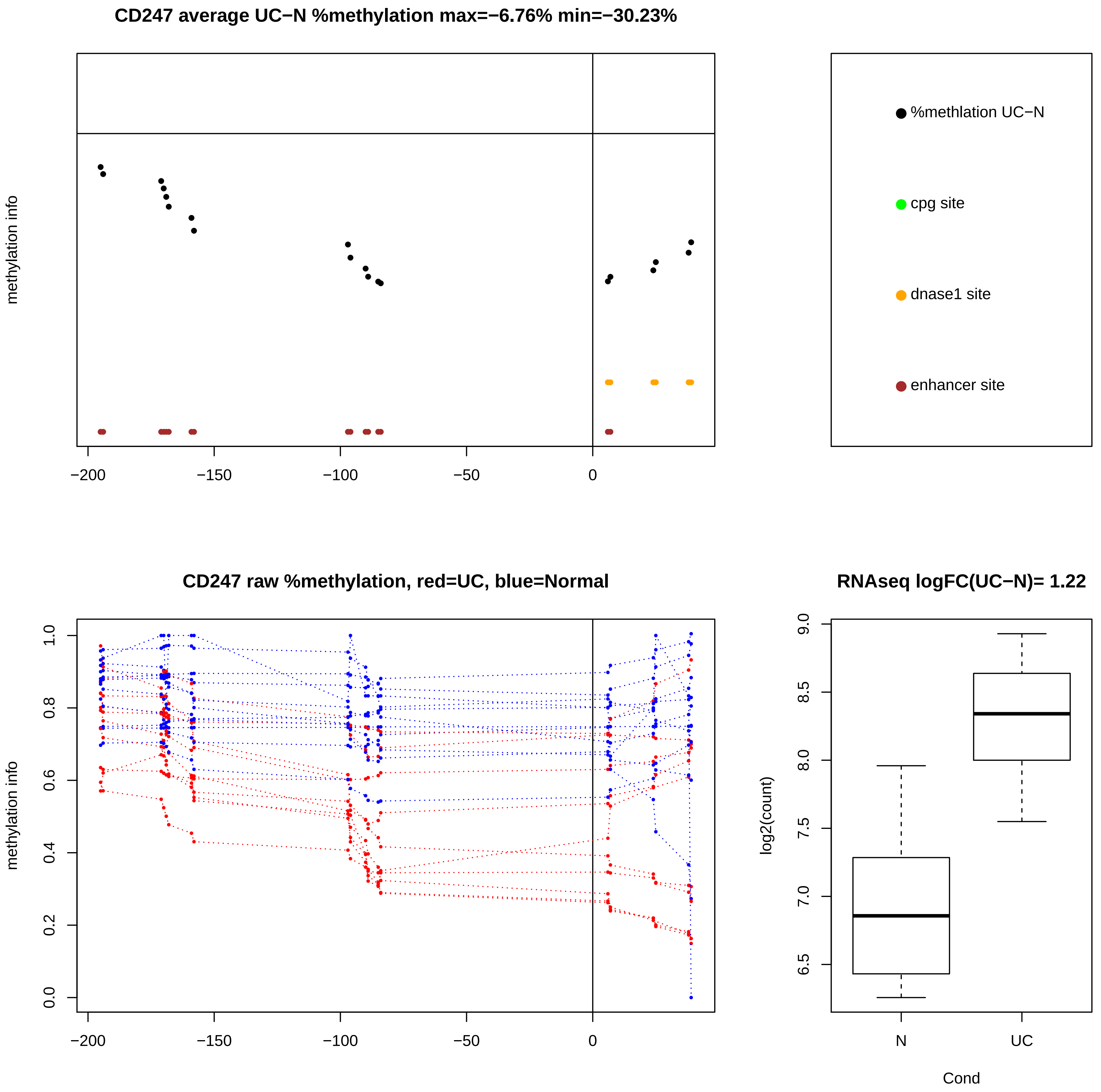
CD180 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.22


CD19 average UC−N %methylation max=−10.63% min=−39.48%

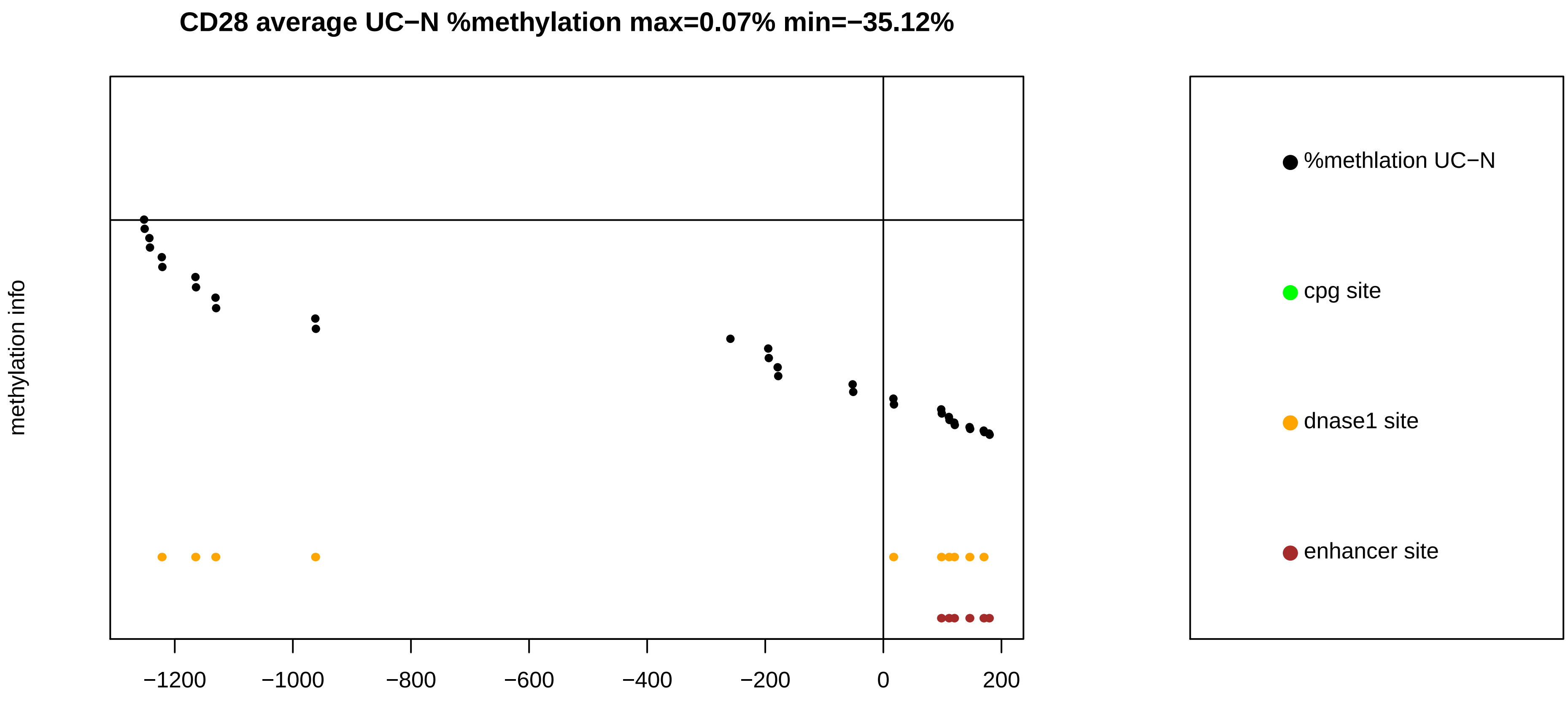
CD19 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 2.52

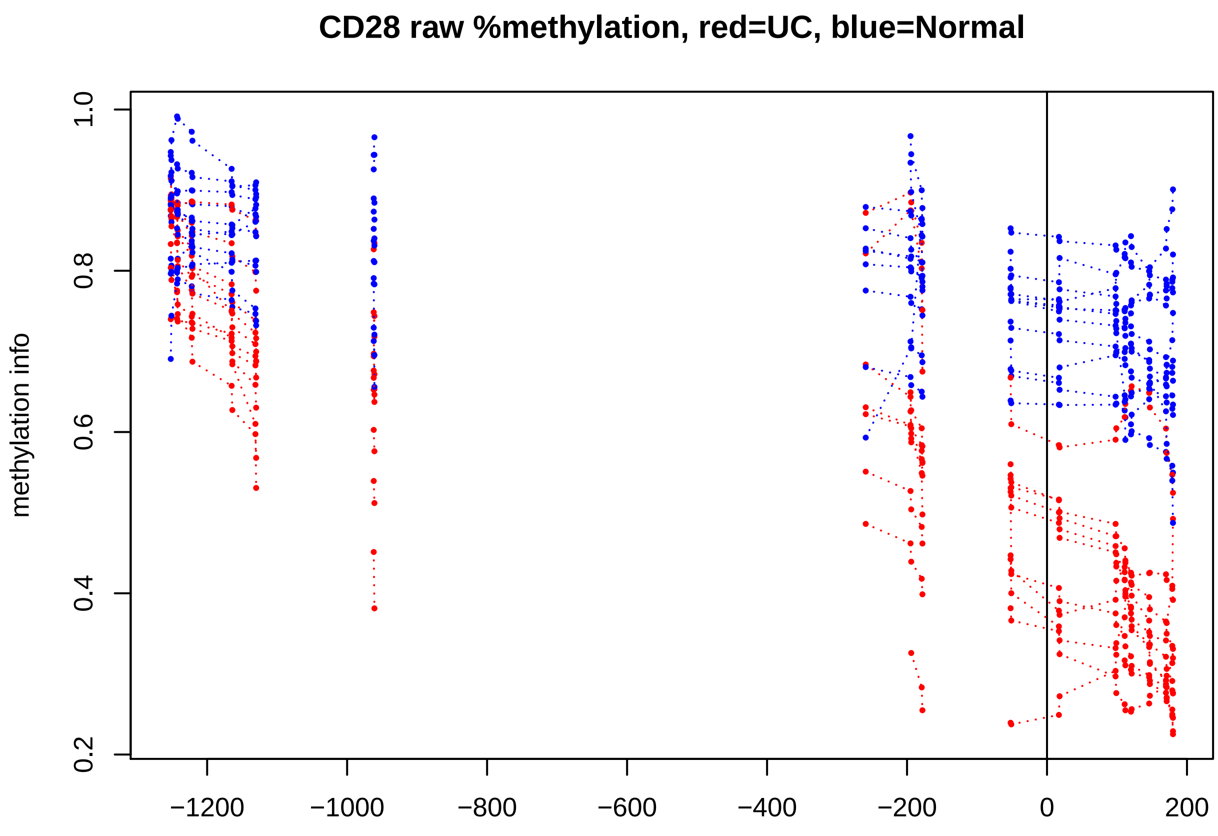

CD247 average UC−N %methylation max=−6.76% min=−30.23%

CD247 raw %methylation, red=UC, blue=Normal

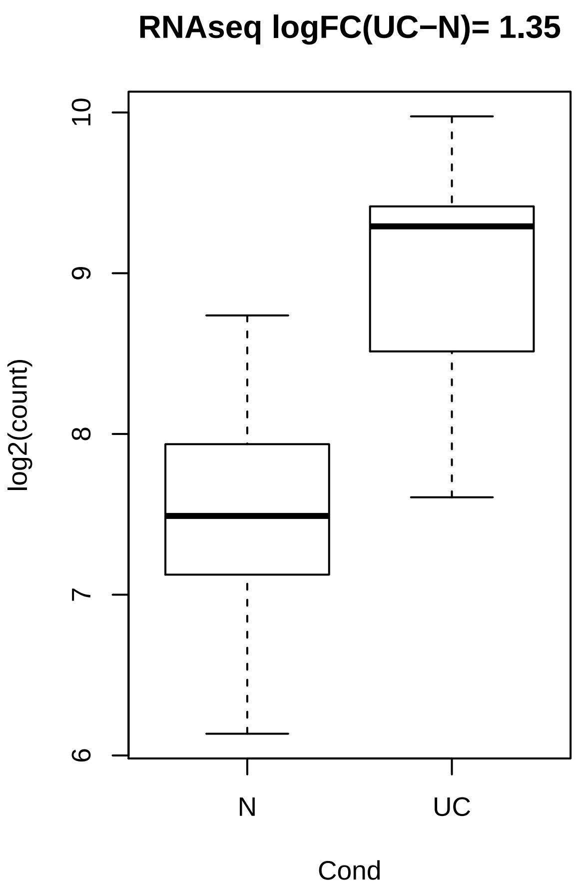
RNAseq logFC(UC−N)= 1.22



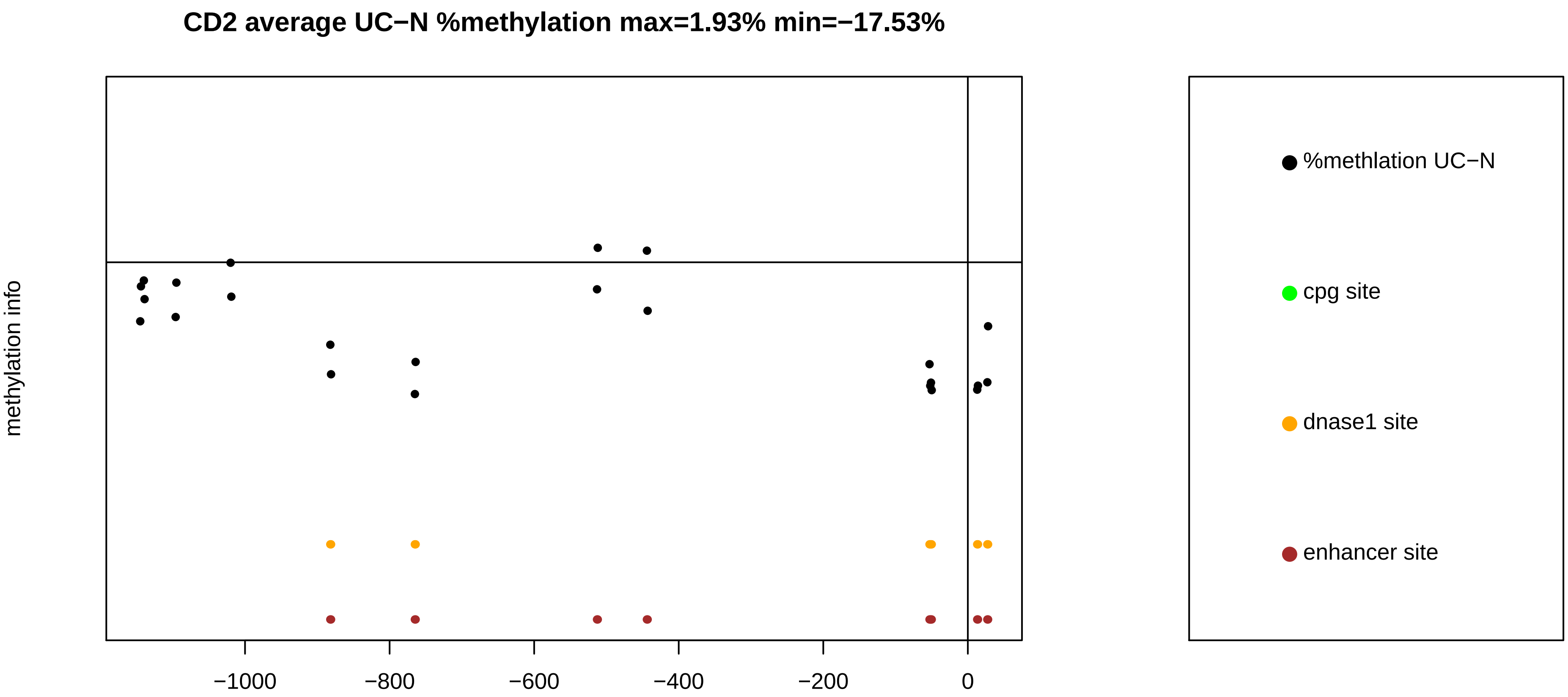
CD28 average UC−N %methylation max=0.07% min=−35.12%



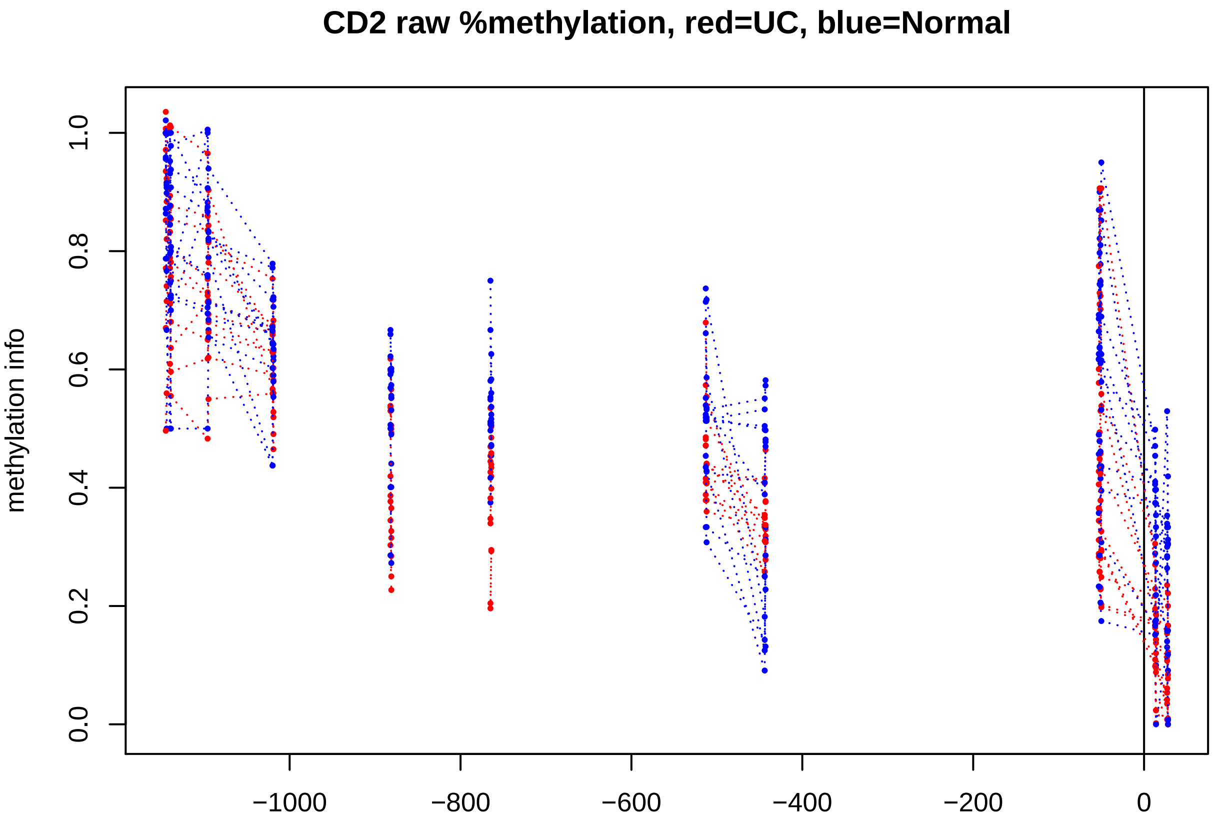
CD28 raw %methylation, red=UC, blue=Normal



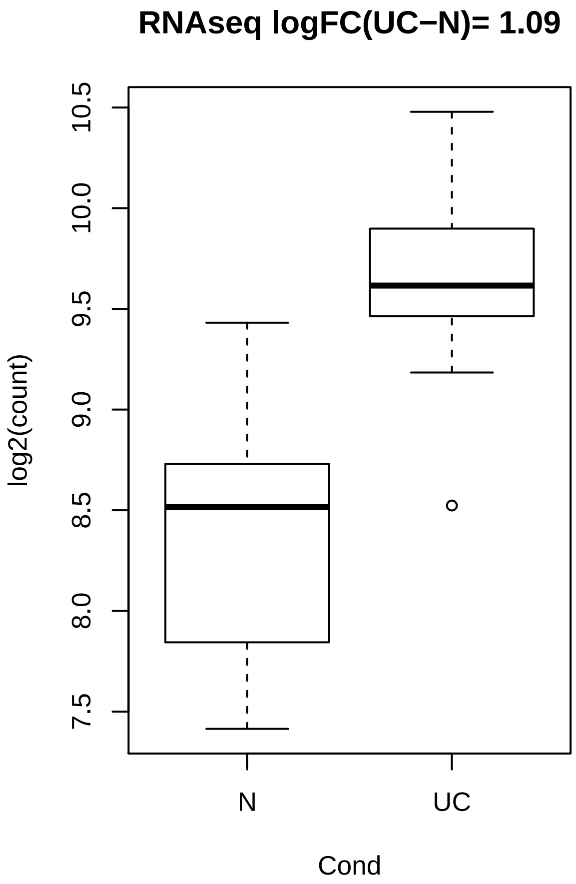
RNAseq logFC(UC−N)= 1.35



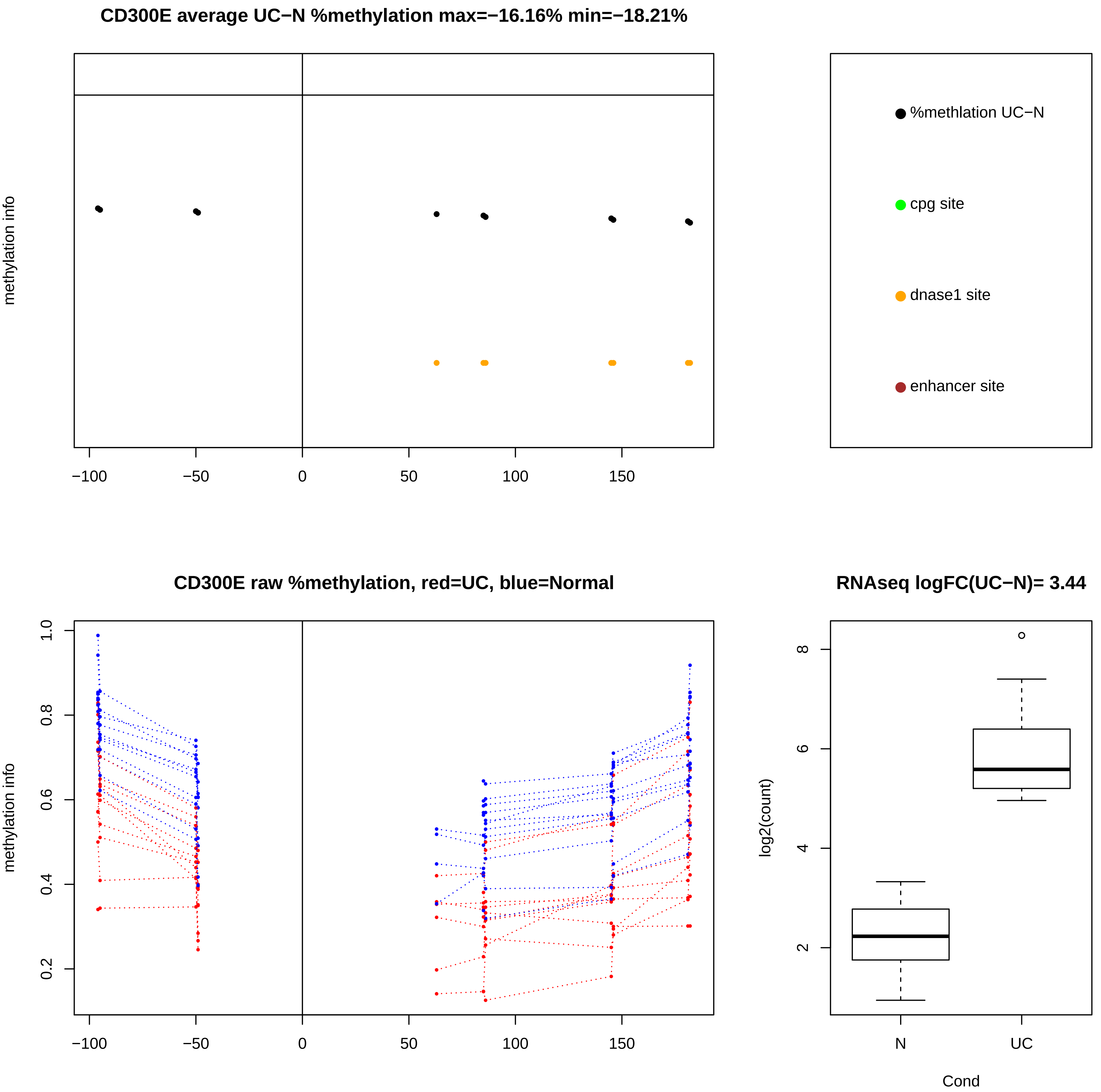
CD2 average UC−N %methylation max=1.93% min=−17.53%



CD2 raw %methylation, red=UC, blue=Normal



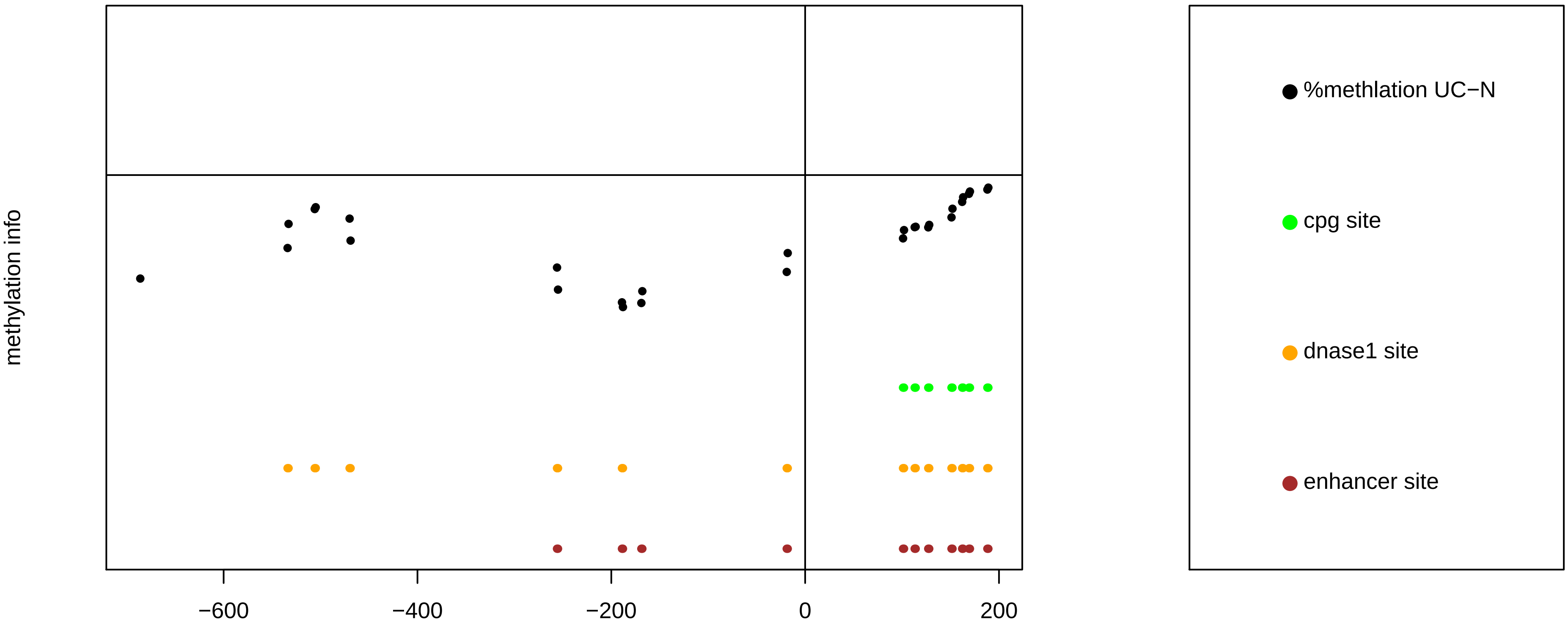
RNAseq logFC(UC−N)= 1.09



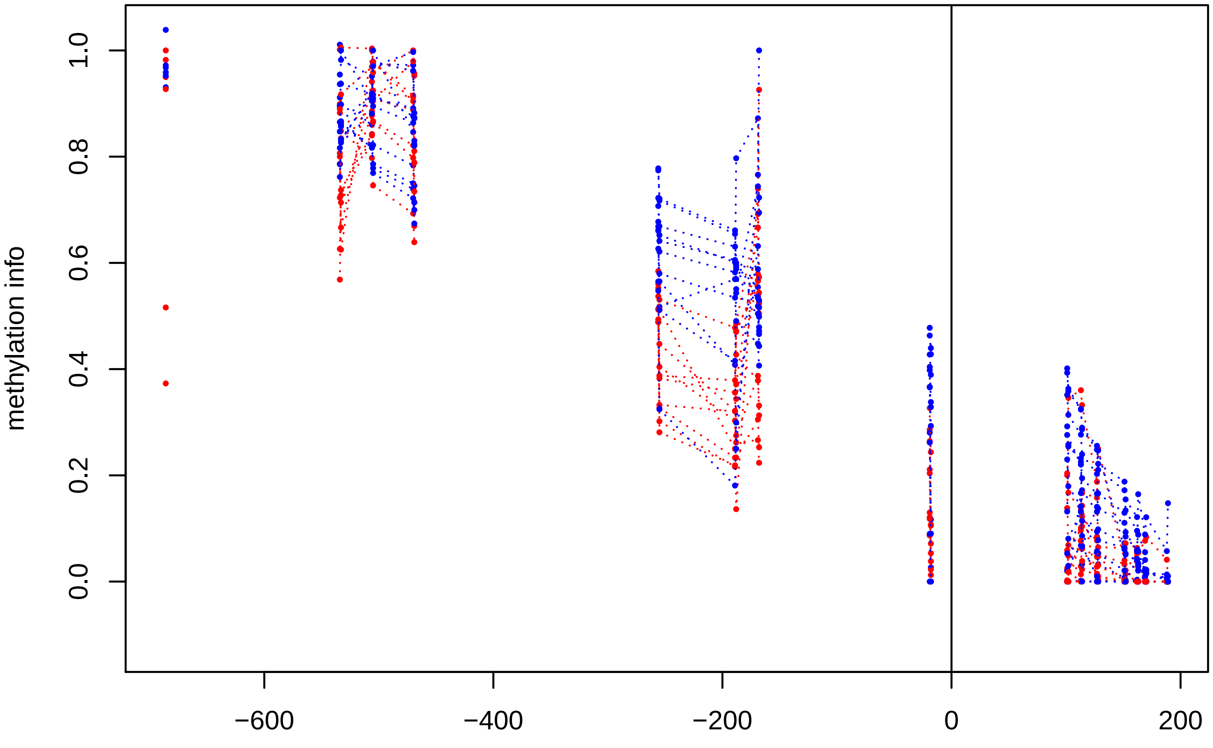
CD300E average UC−N %methylation max=−16.16% min=−18.21%

CD300E raw %methylation, red=UC, blue=Normal

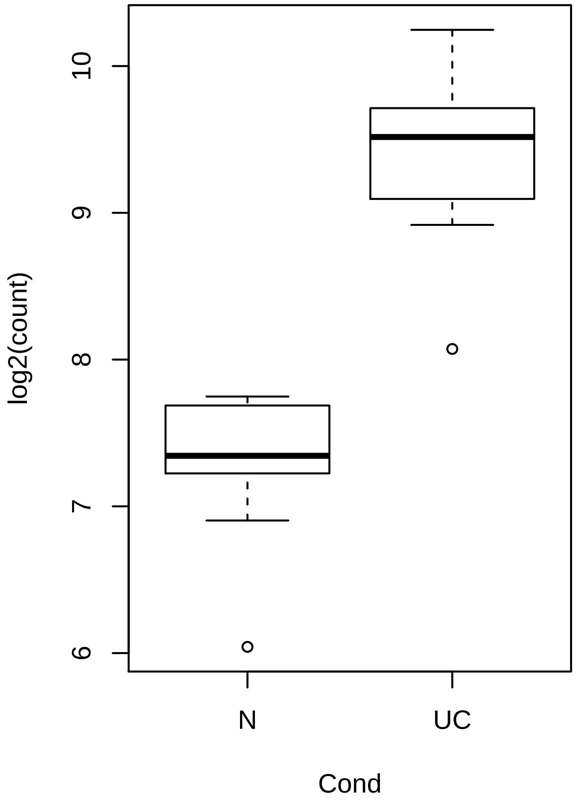
RNAseq logFC(UC−N)= 3.44



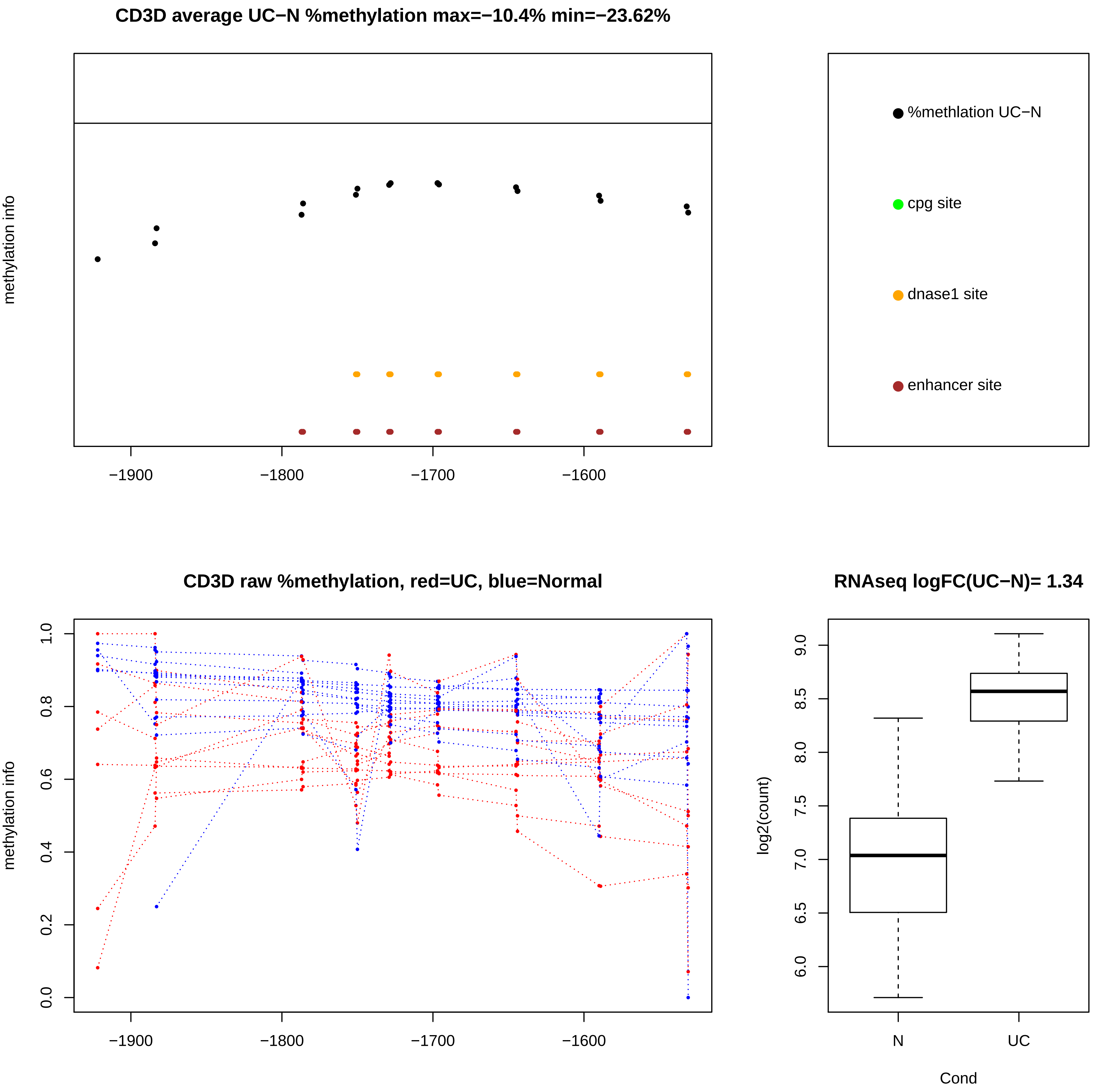
CD38 average UC−N %methylation max=−1.56% min=−16.39%

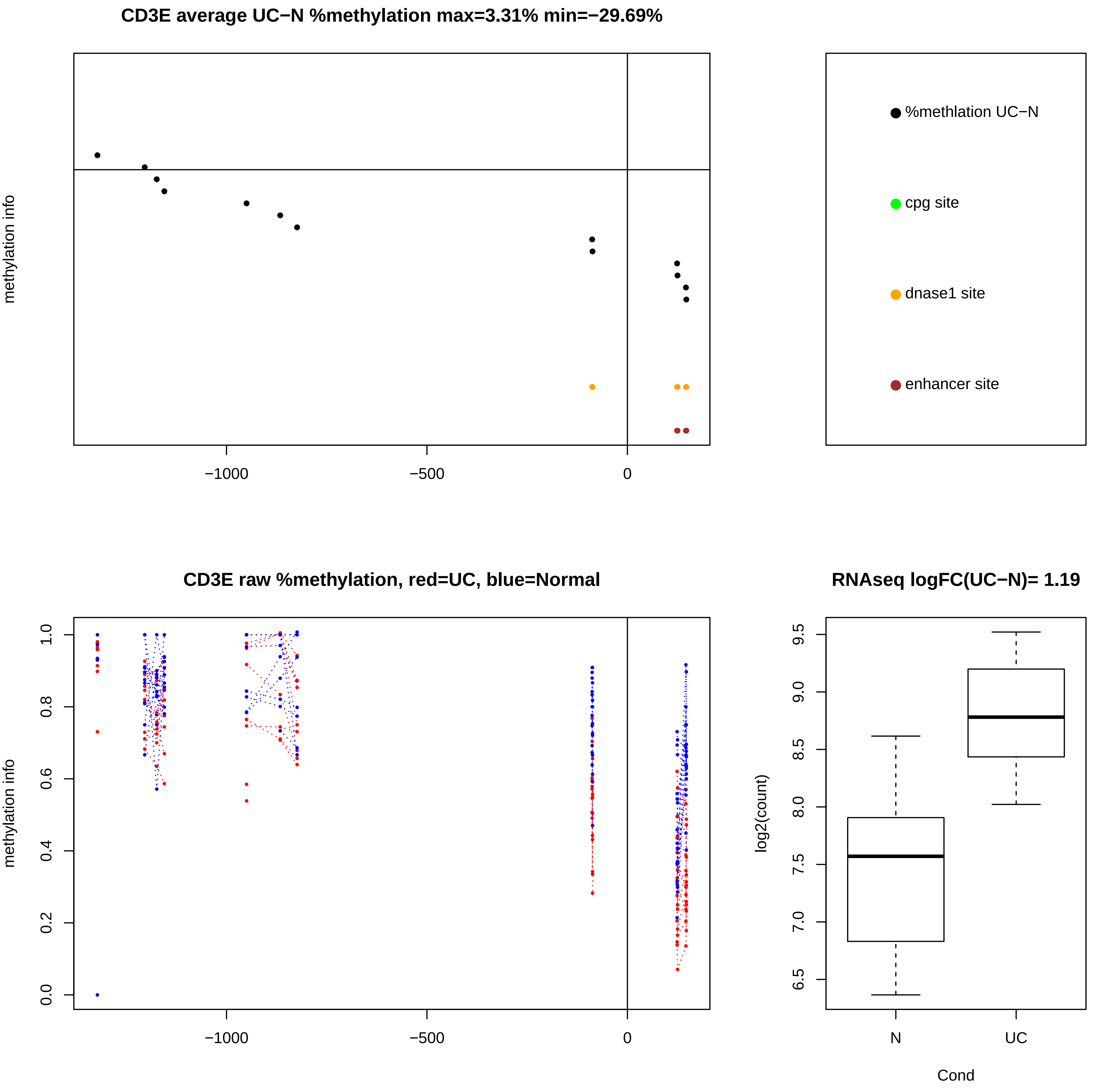


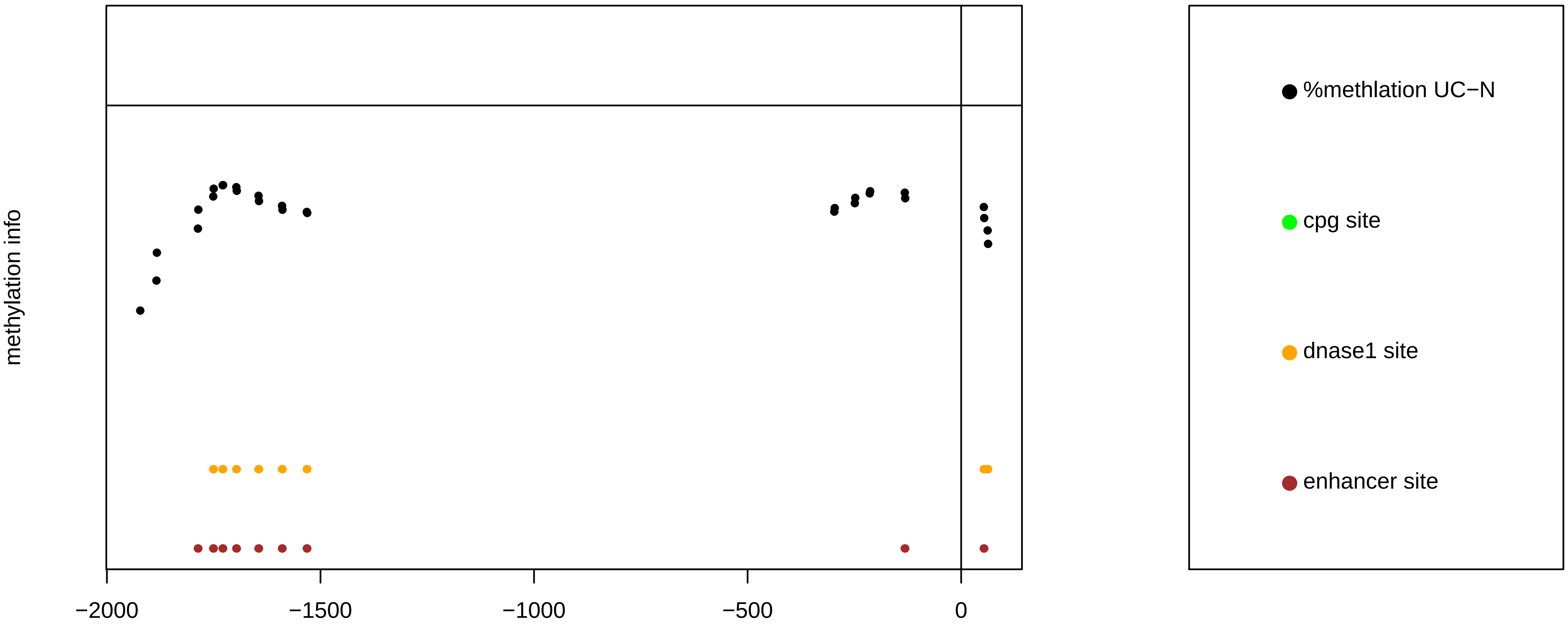
CD38 raw %methylation, red=UC, blue=Normal



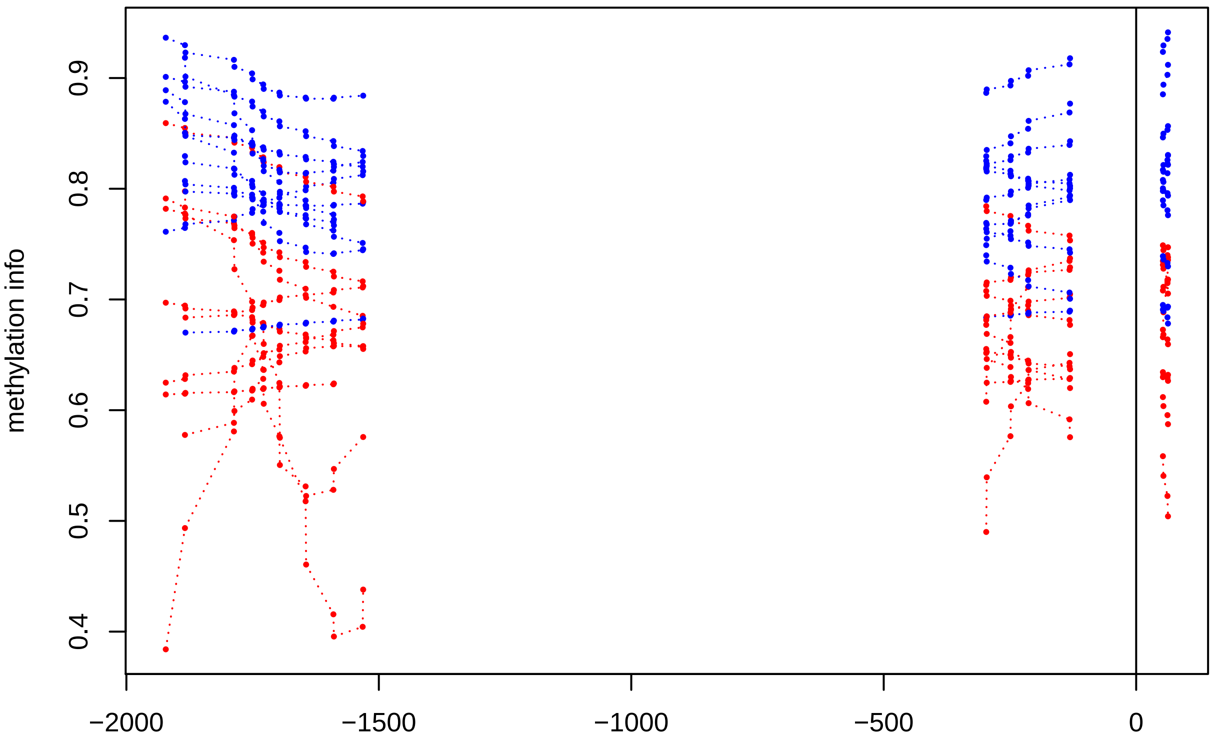
RNAseq logFC(UC−N)= 1.88


CD3D average UC−N %methylation max=−10.4% min=−23.62%
methylation info
−1900
−1800
−1700
−1600
%methlation UC−N
cpg site
dnase1 site
enhancer site
CD3D raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−1900
−1800
−1700
−1600
RNAseq logFC(UC−N)= 1.34
log2(count)
6.0
6.5
7.0
7.5
8.0
8.5
9.0
N
UC
Cond

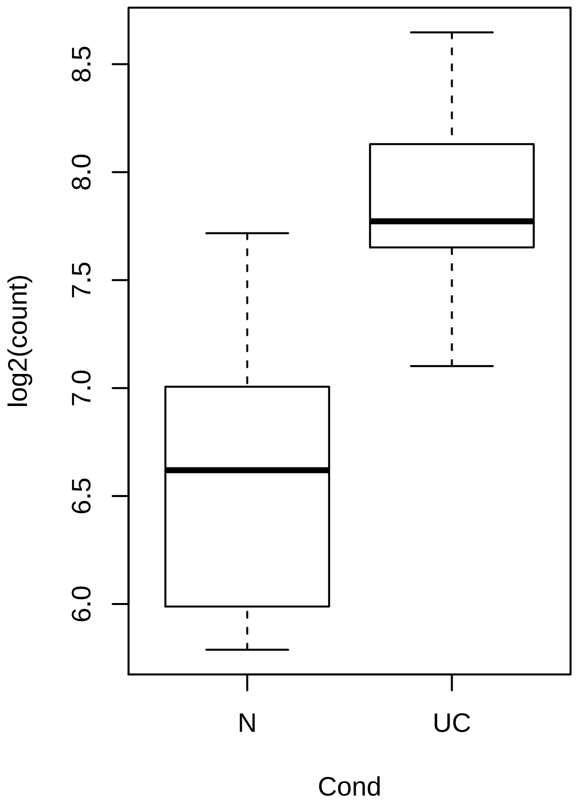

CD3E average UC−N %methylation max=3.31% min=−29.69%
methylation info
−1000
−500
0
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
CD3E raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−1000
−500
0
RNAseq logFC(UC−N)= 1.19
log2(count)
6.5
7.0
7.5
8.0
8.5
9.0
9.5
N
UC
Cond



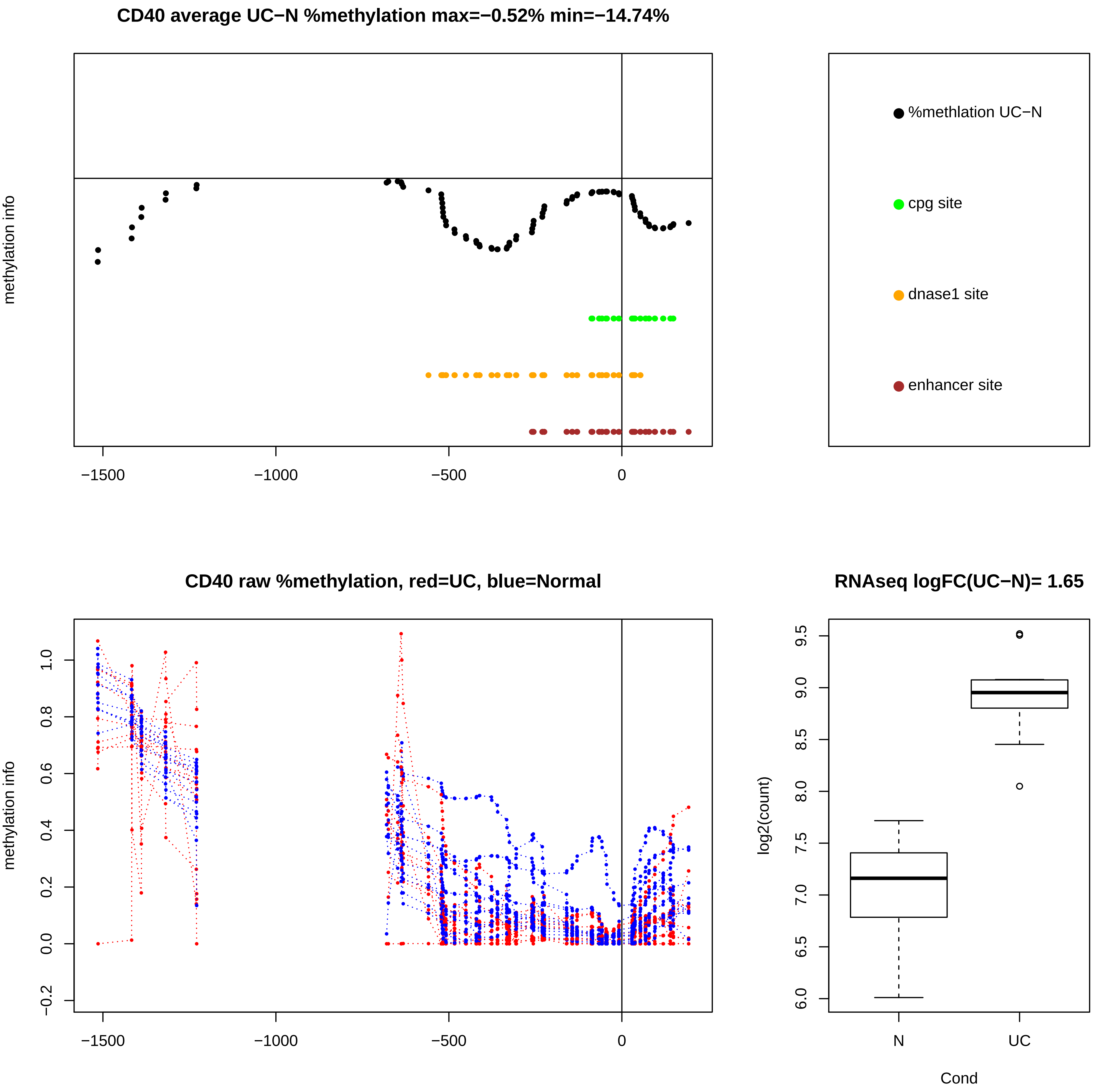
CD3G average UC−N %methylation max=−10.04% min=−25.87%



CD3G raw %methylation, red=UC, blue=Normal

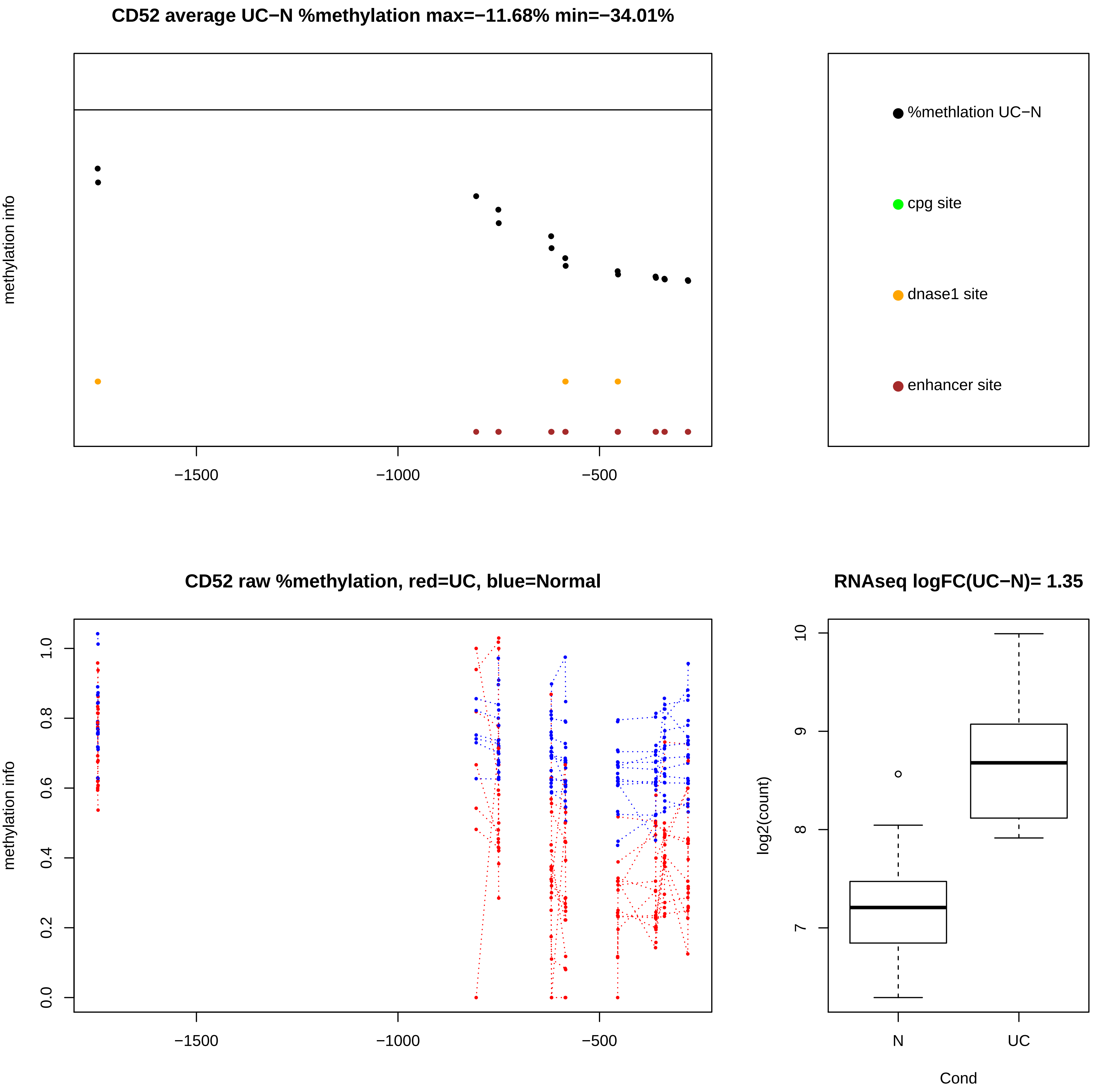


RNAseq logFC(UC−N)= 1.09


CD40 average UC−N %methylation max=−0.52% min=−14.74%

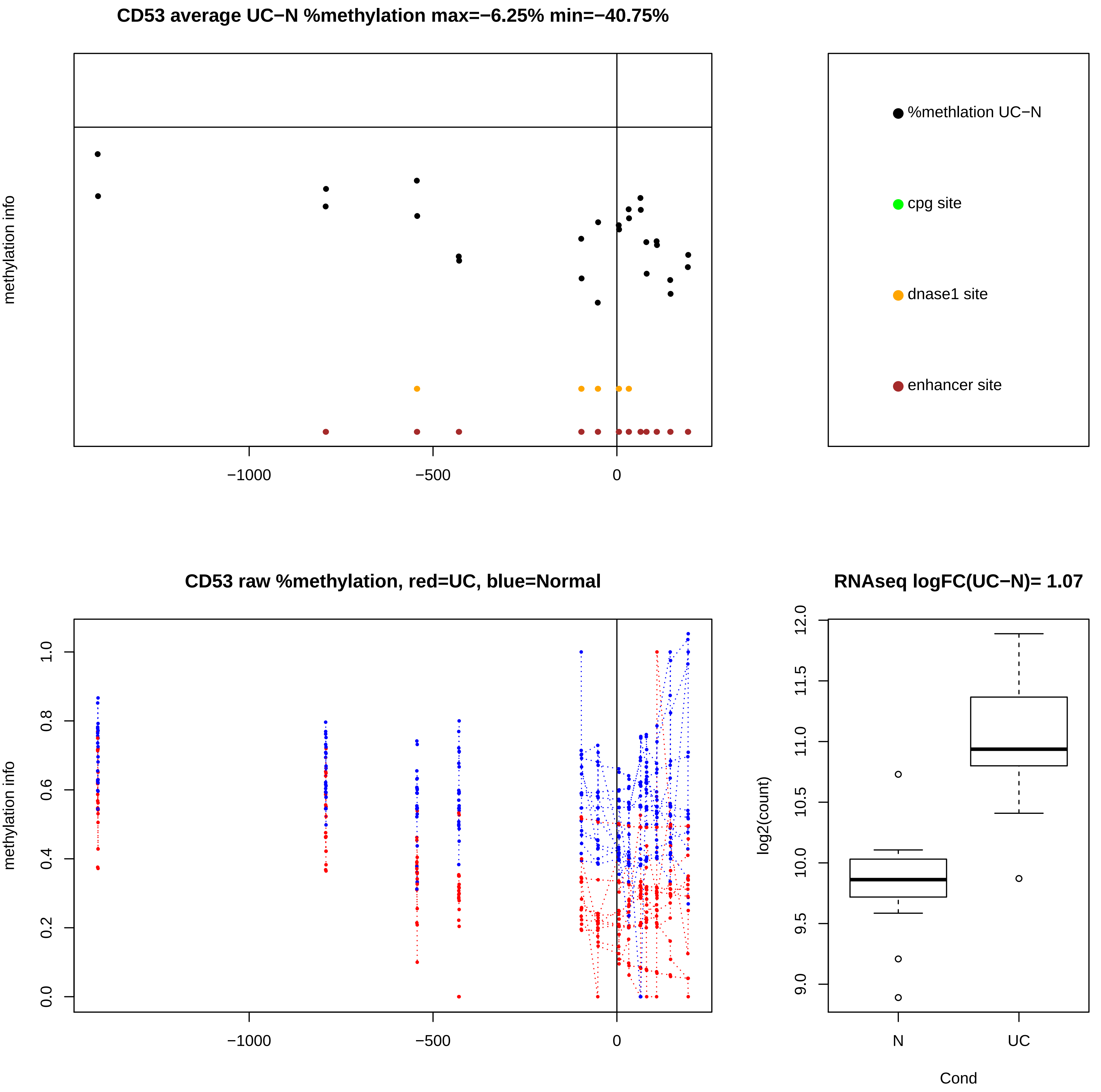
CD40 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.65


CD52 average UC−N %methylation max=−11.68% min=−34.01%

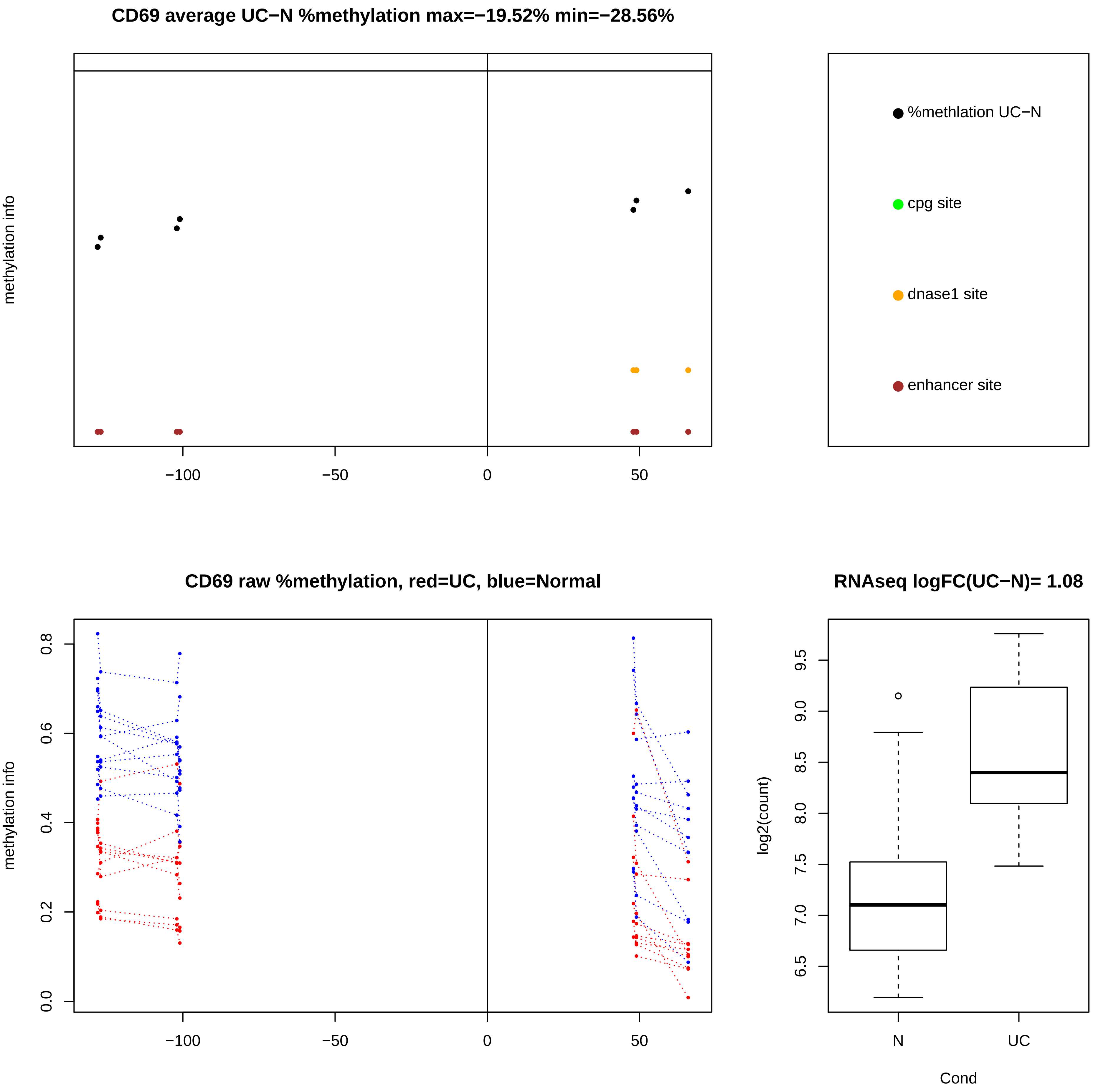
CD52 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.35


CD53 average UC−N %methylation max=−6.25% min=−40.75%

CD53 raw %methylation, red=UC, blue=Normal

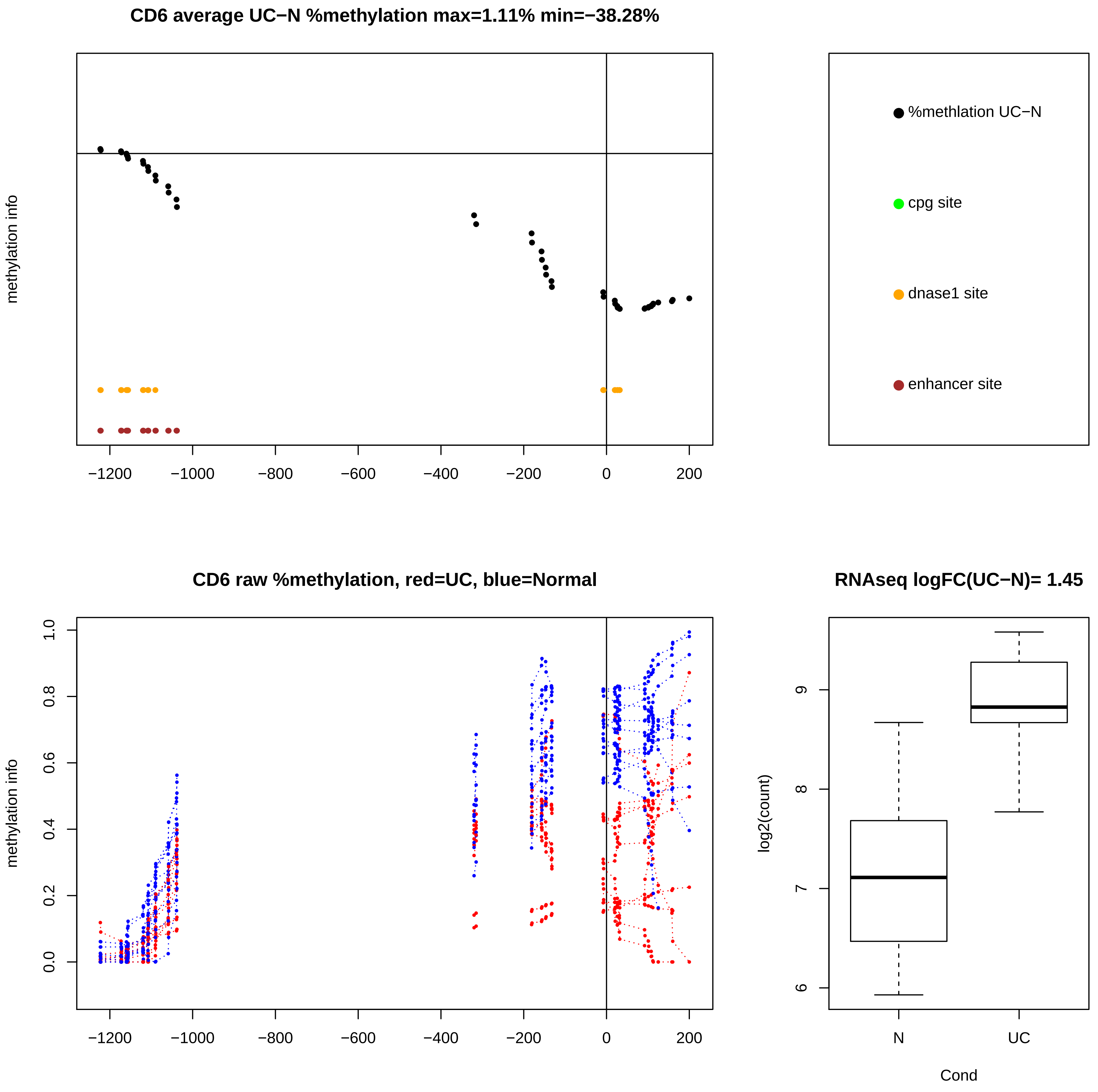
RNAseq logFC(UC−N)= 1.07

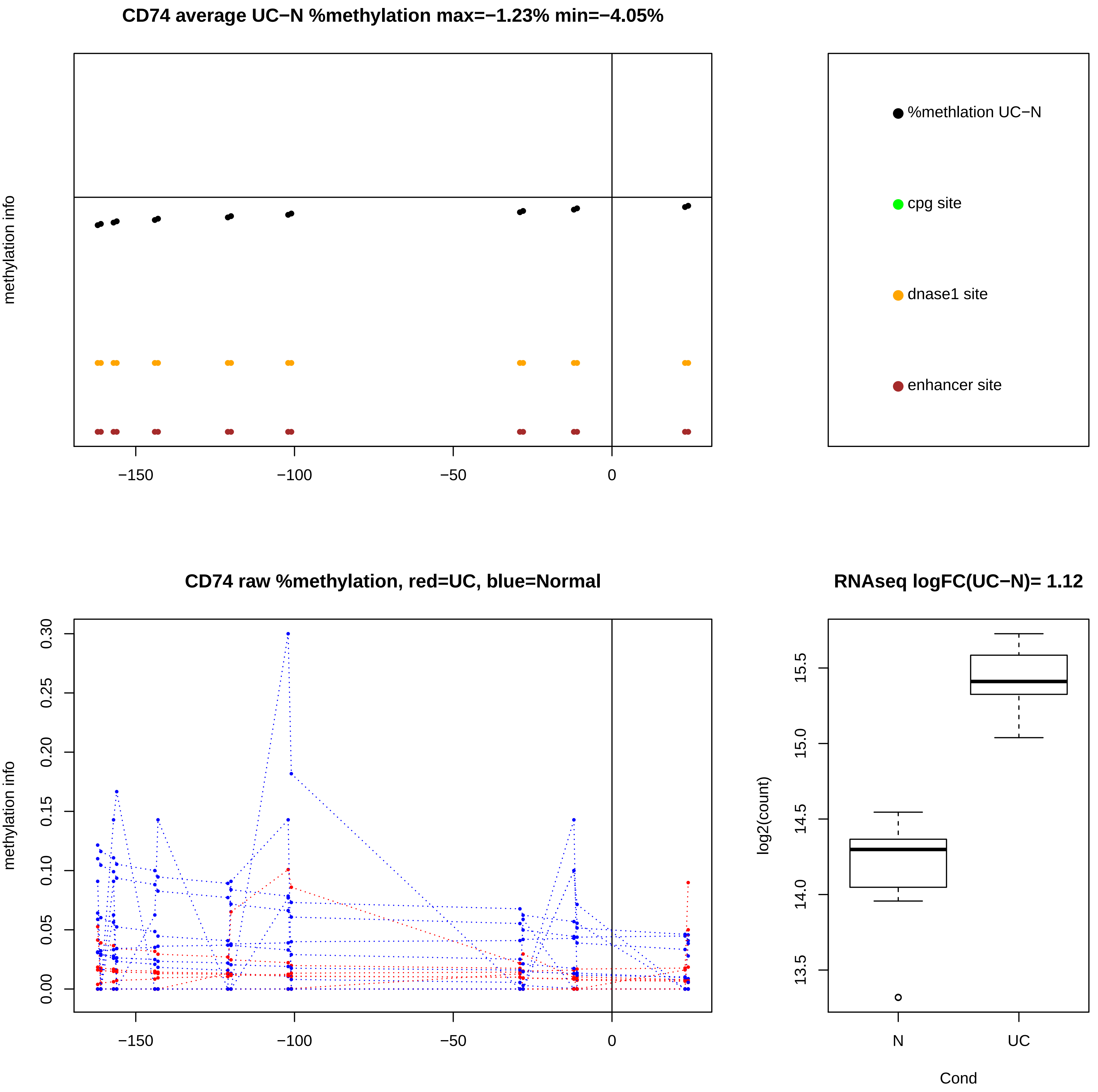


CD69 average UC−N %methylation max=−19.52% min=−28.56%

CD69 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.08

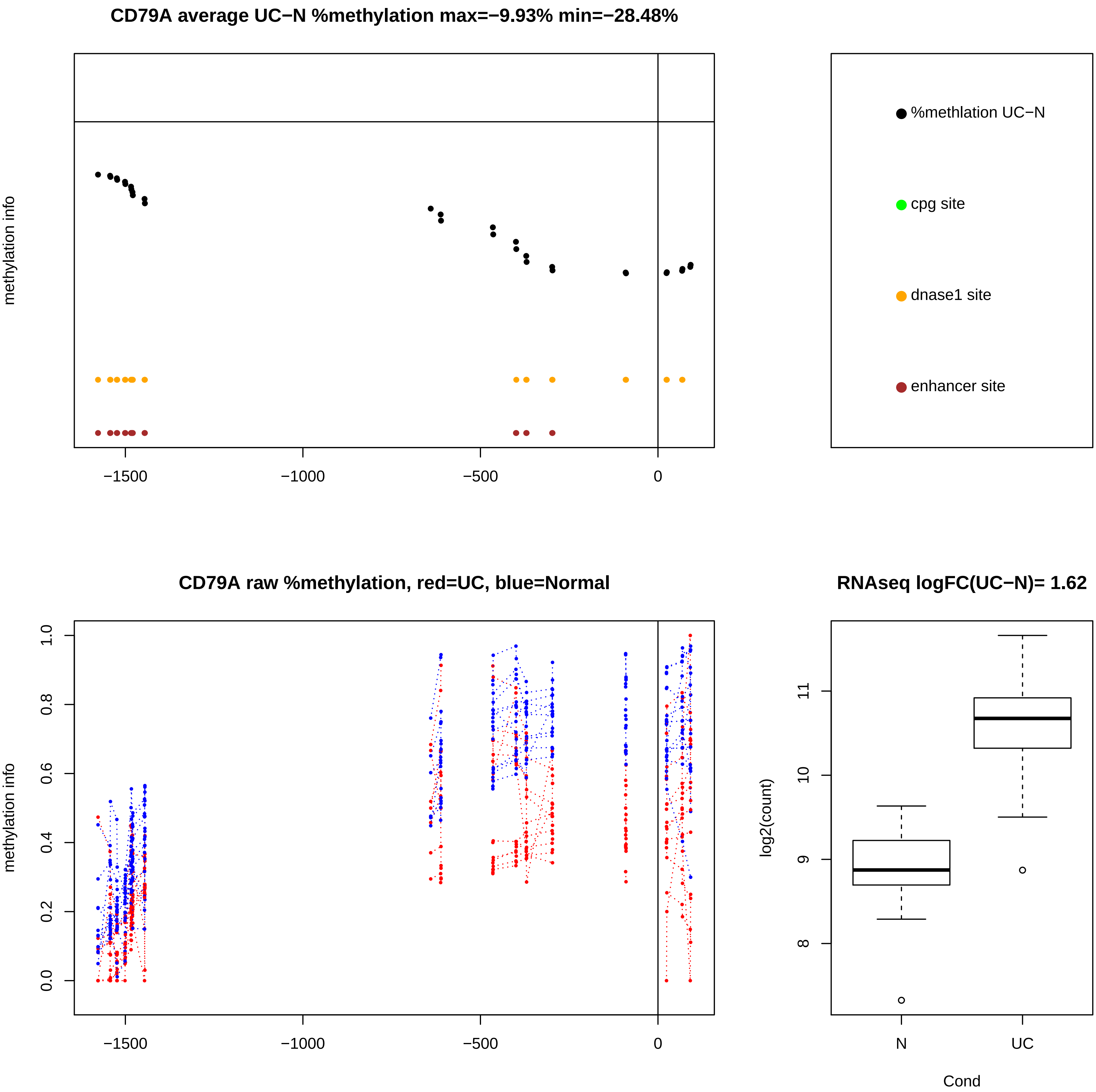

CD6 average UC−N %methylation max=1.11% min=−38.28%
methylation info
−1200
−1000
−800
−600
−400
−200
0
200
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
CD6 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−1200
−1000
−800
−600
−400
−200
0
200
RNAseq logFC(UC−N)= 1.45
log2(count)
6
7
8
9
N
UC
Cond



CD74 average UC−N %methylation max=−1.23% min=−4.05%

CD74 raw %methylation, red=UC, blue=Normal

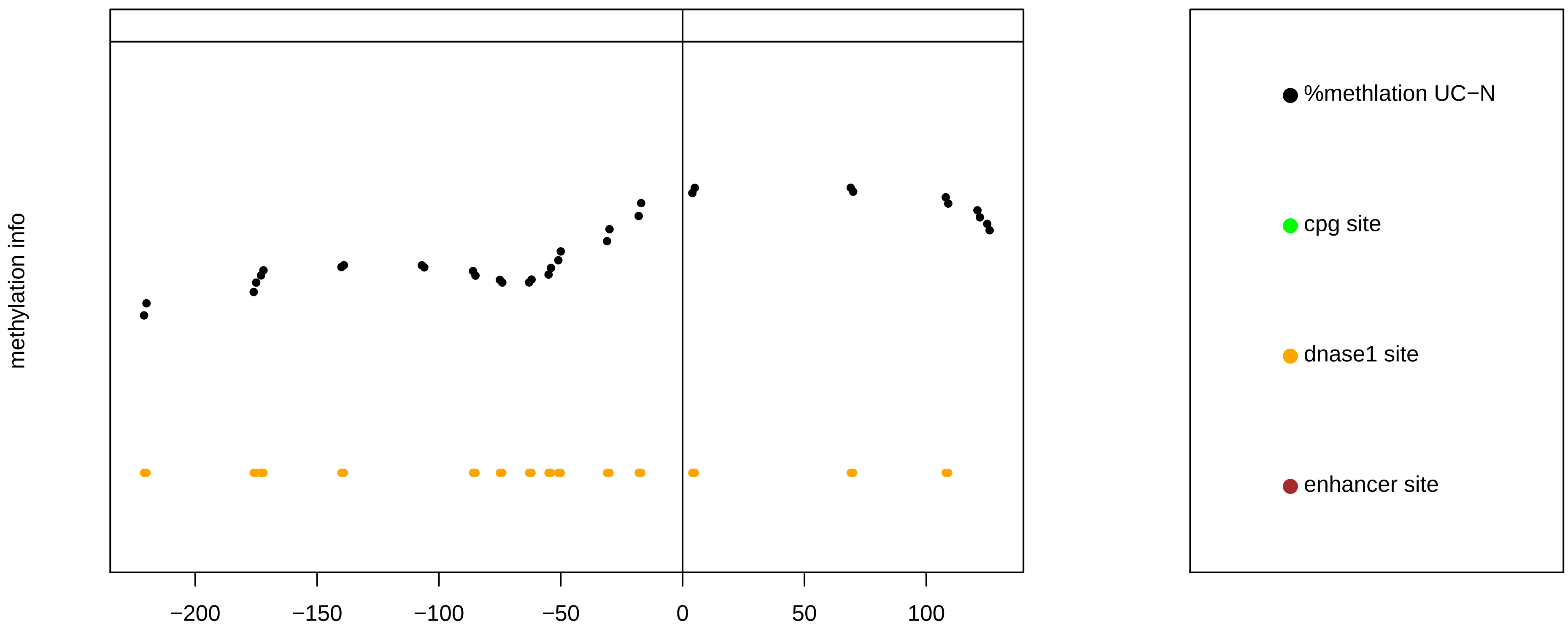
RNAseq logFC(UC−N)= 1.12



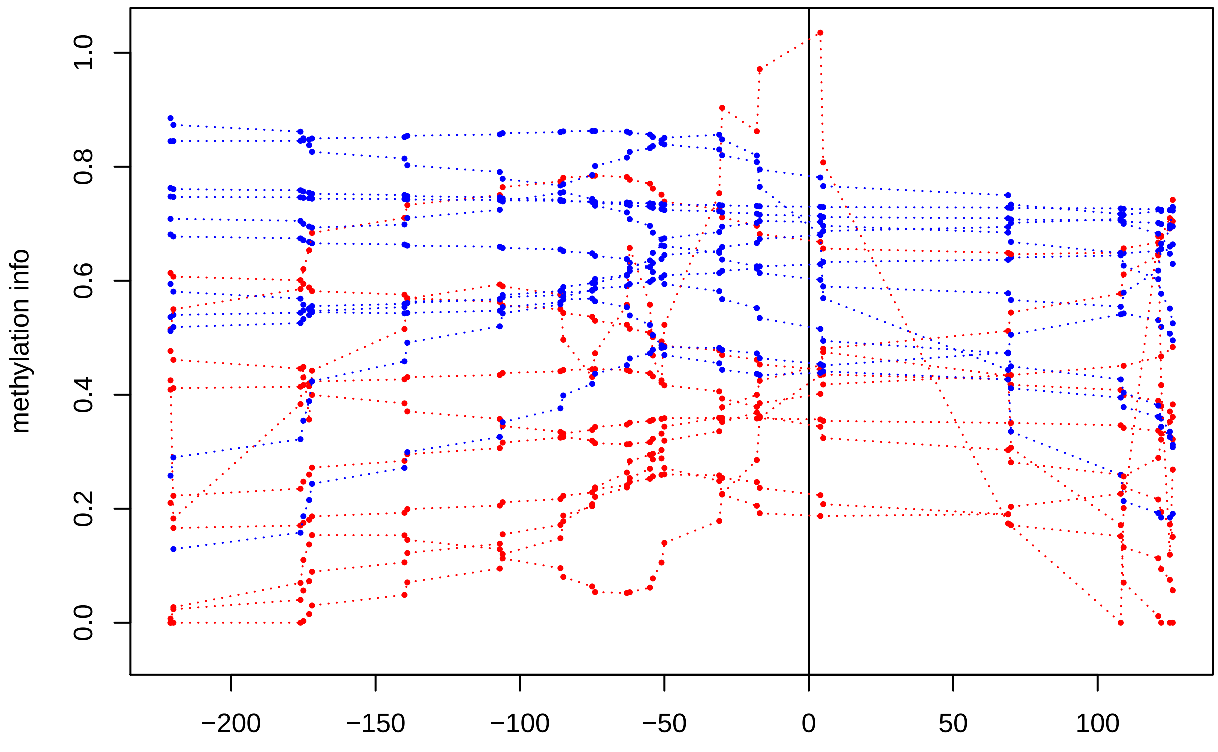
CD79A average UC−N %methylation max=−9.93% min=−28.48%

CD79A raw %methylation, red=UC, blue=Normal

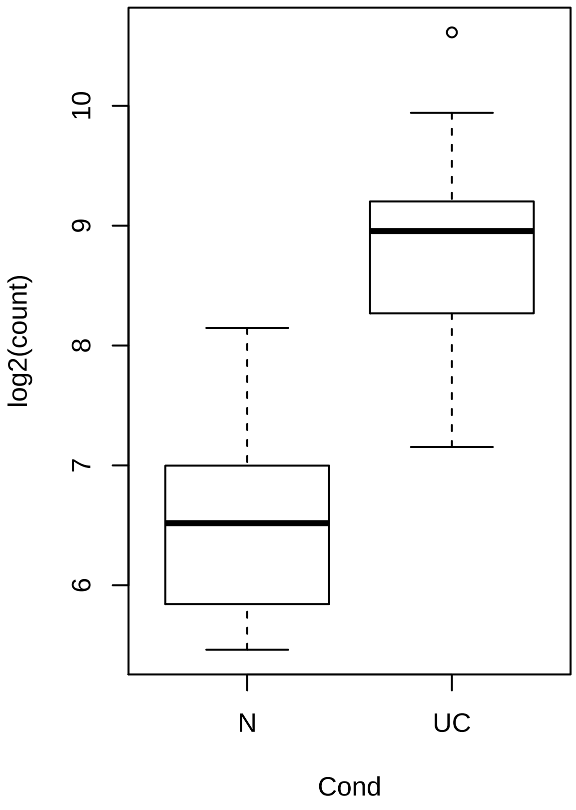
RNAseq logFC(UC−N)= 1.62



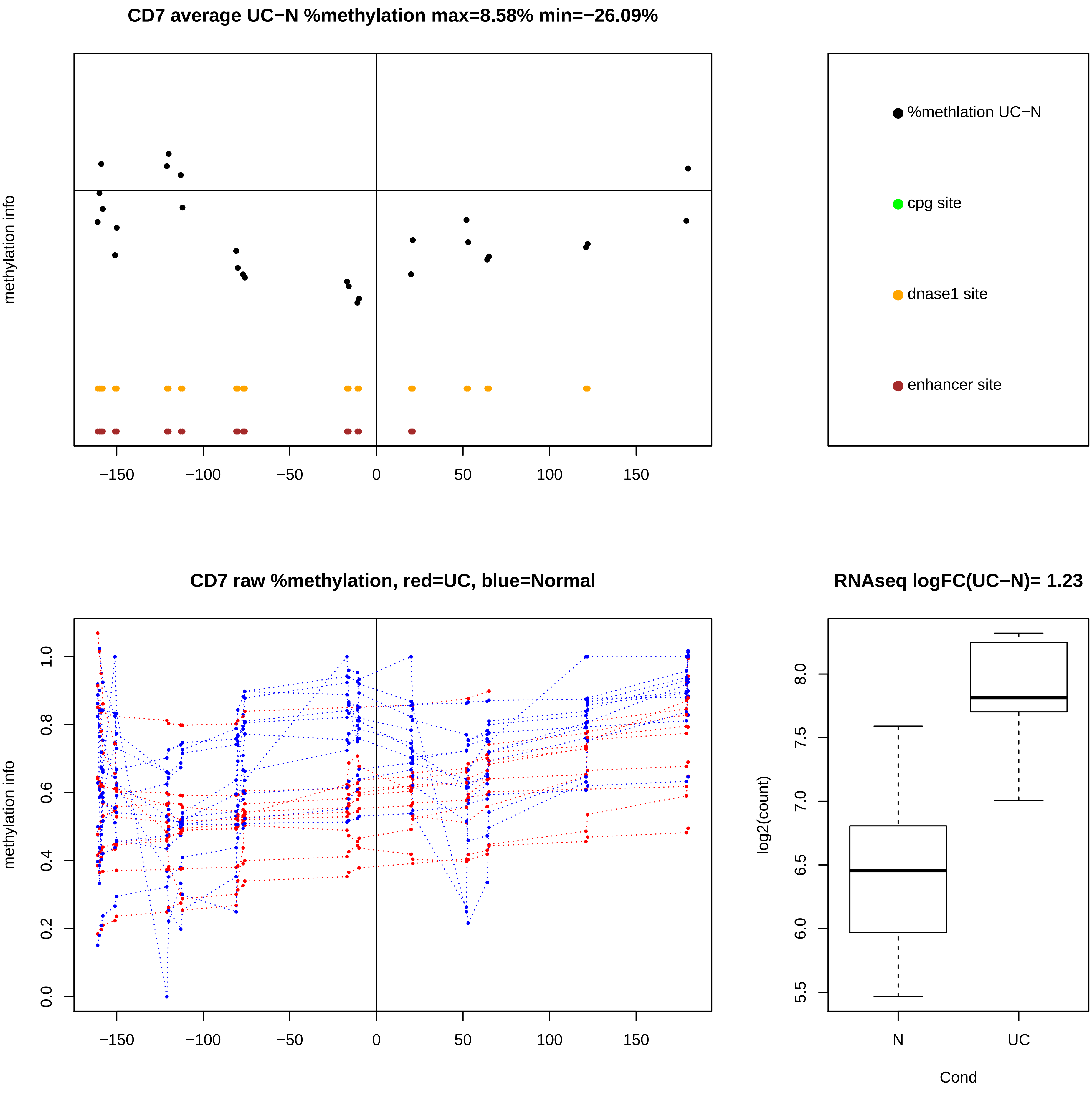
CD79B average UC−N %methylation max=−18.55% min=−34.77%



CD79B raw %methylation, red=UC, blue=Normal



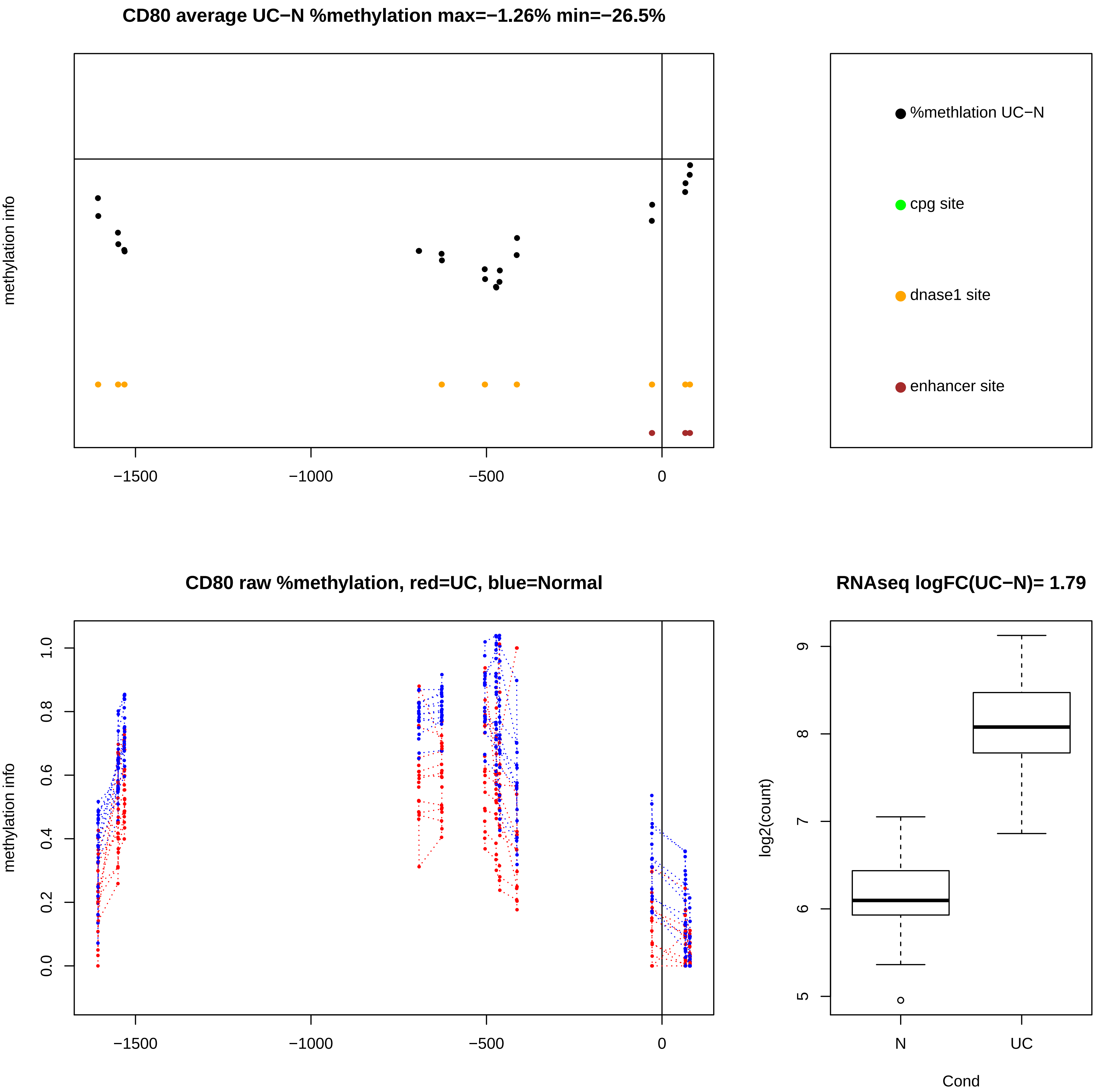
RNAseq logFC(UC−N)= 2.07



CD7 average UC−N %methylation max=8.58% min=−26.09%

CD7 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.23

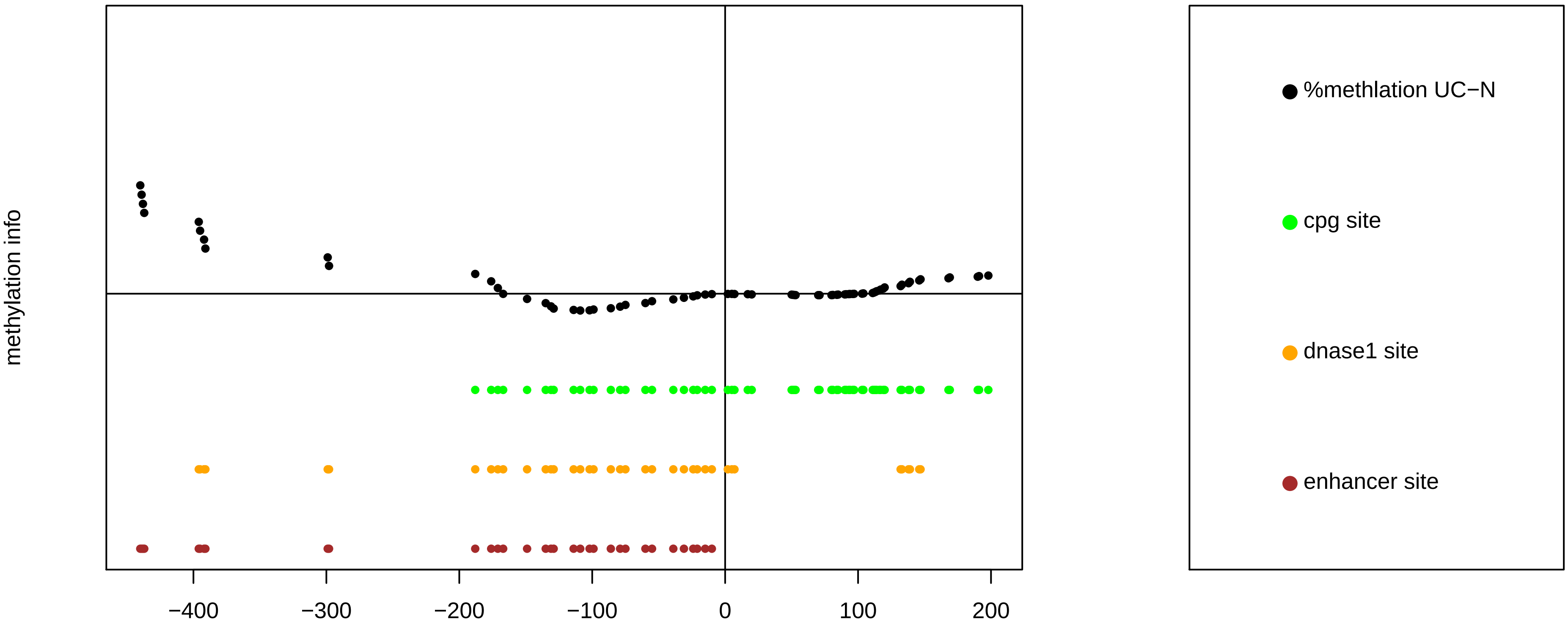


CD80 average UC−N %methylation max=−1.26% min=−26.5%

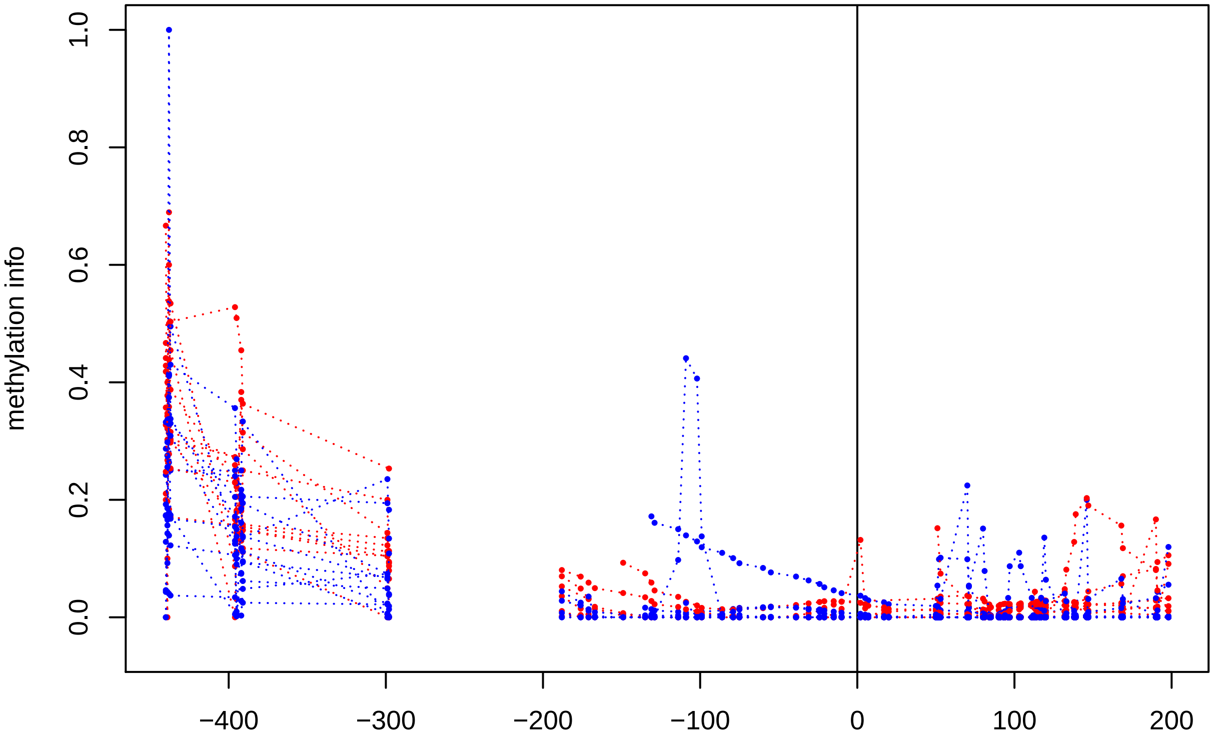
CD80 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.79

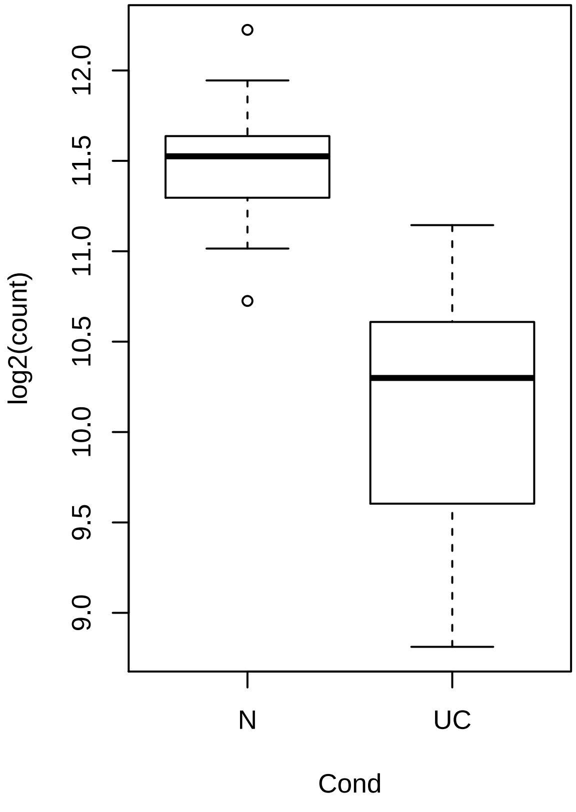
CDHR1 average UC−N %methylation max=13.65% min=−2.11%

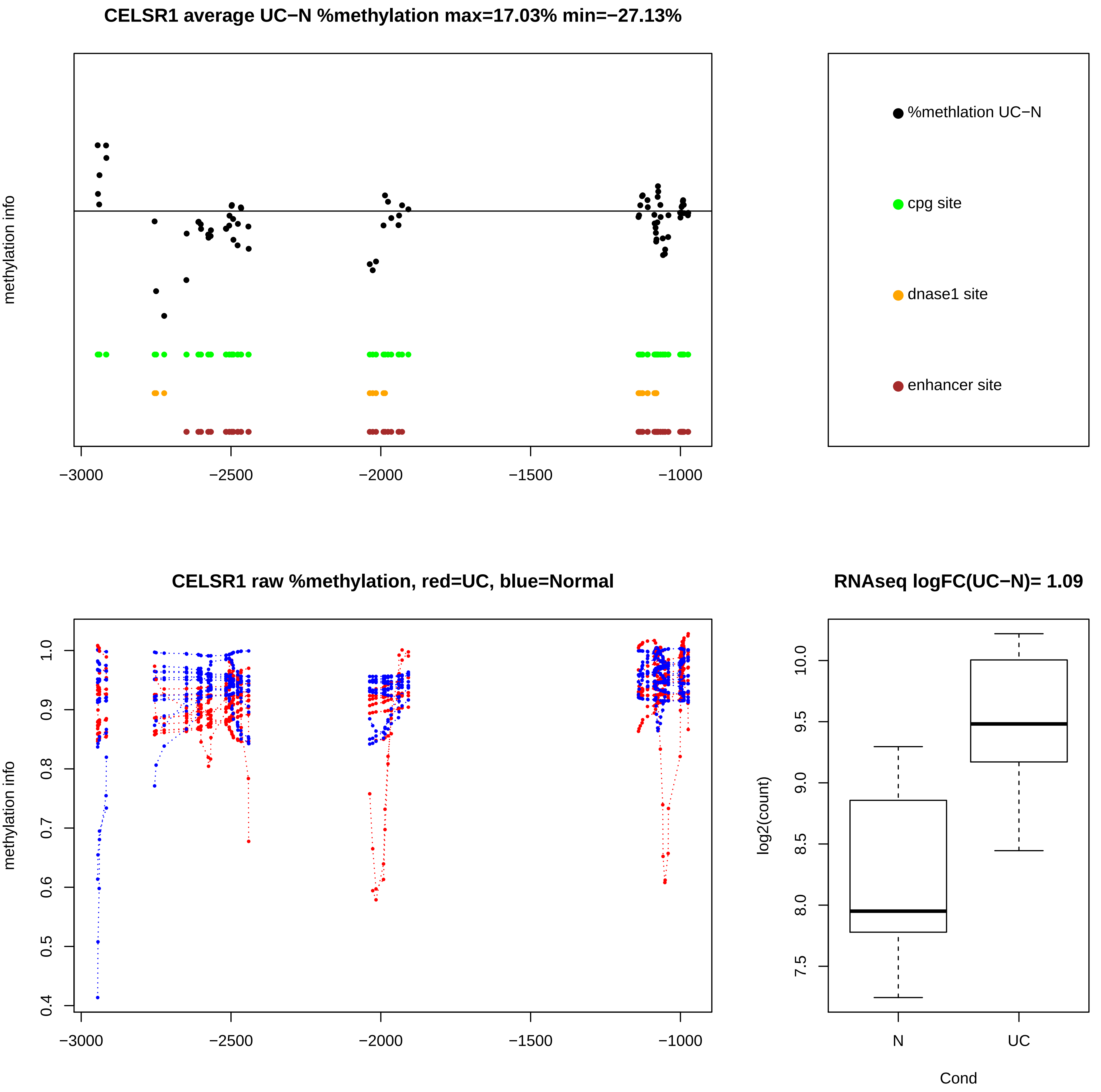


CDHR1 raw %methylation, red=UC, blue=Normal



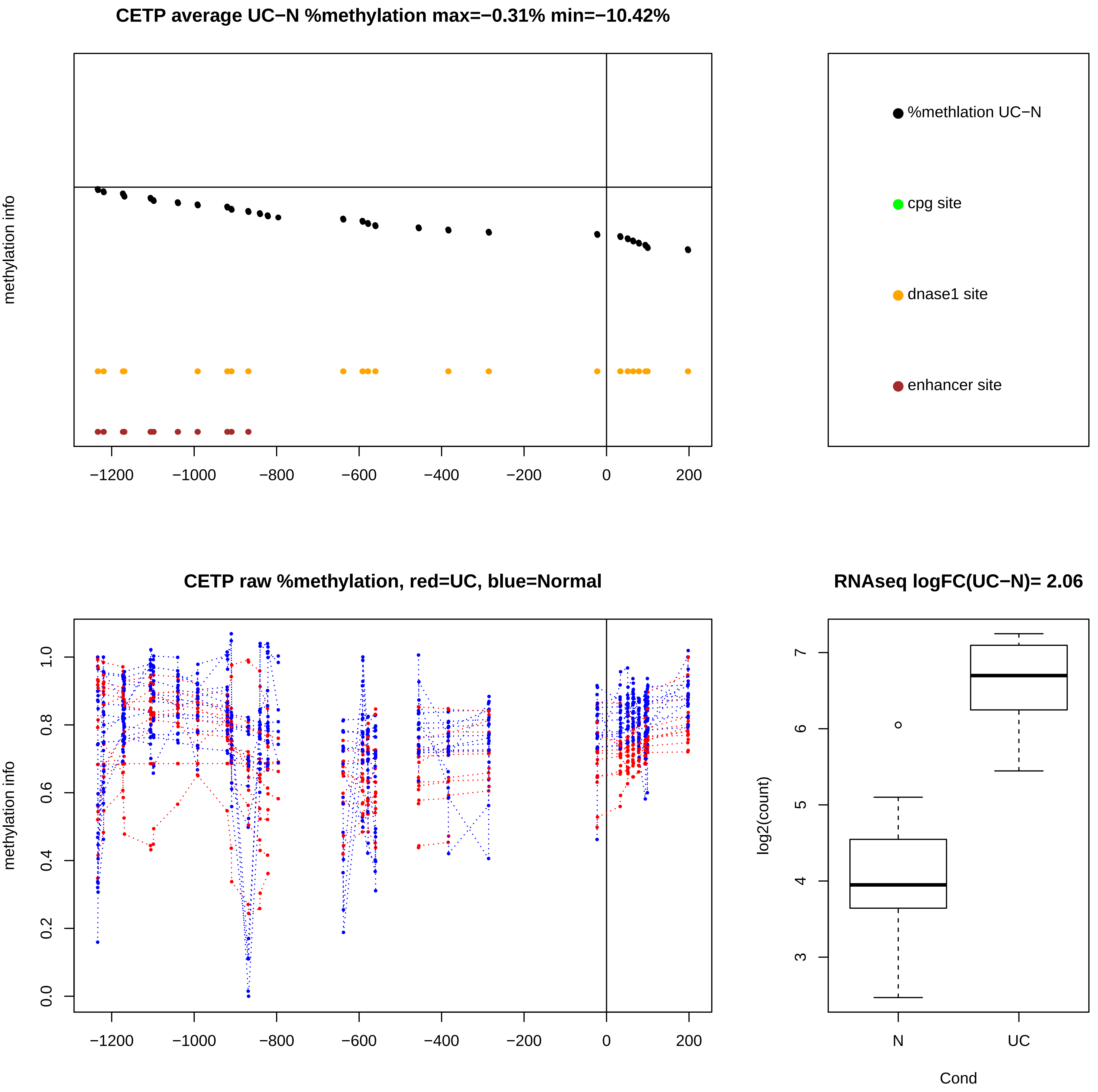
RNAseq logFC(UC−N)= −1.06



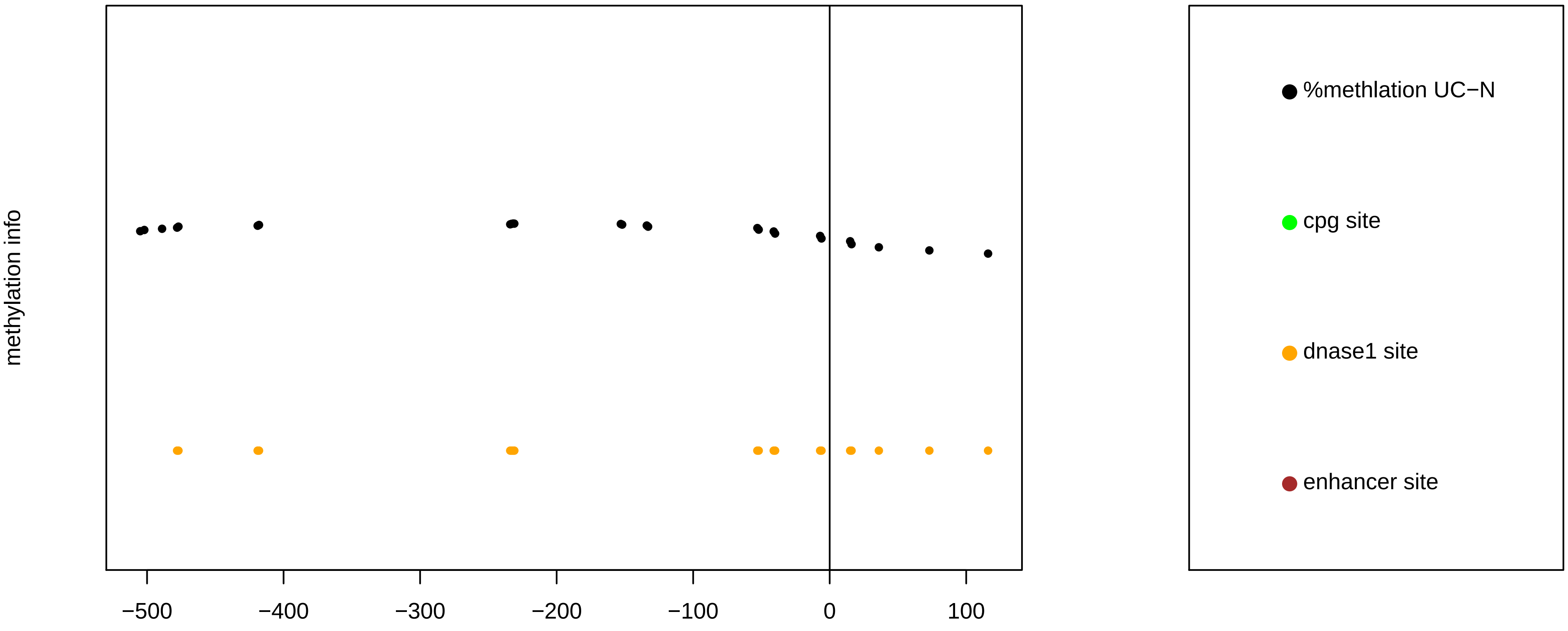

CELSR1 average UC−N %methylation max=17.03% min=−27.13%

CELSR1 raw %methylation, red=UC, blue=Normal

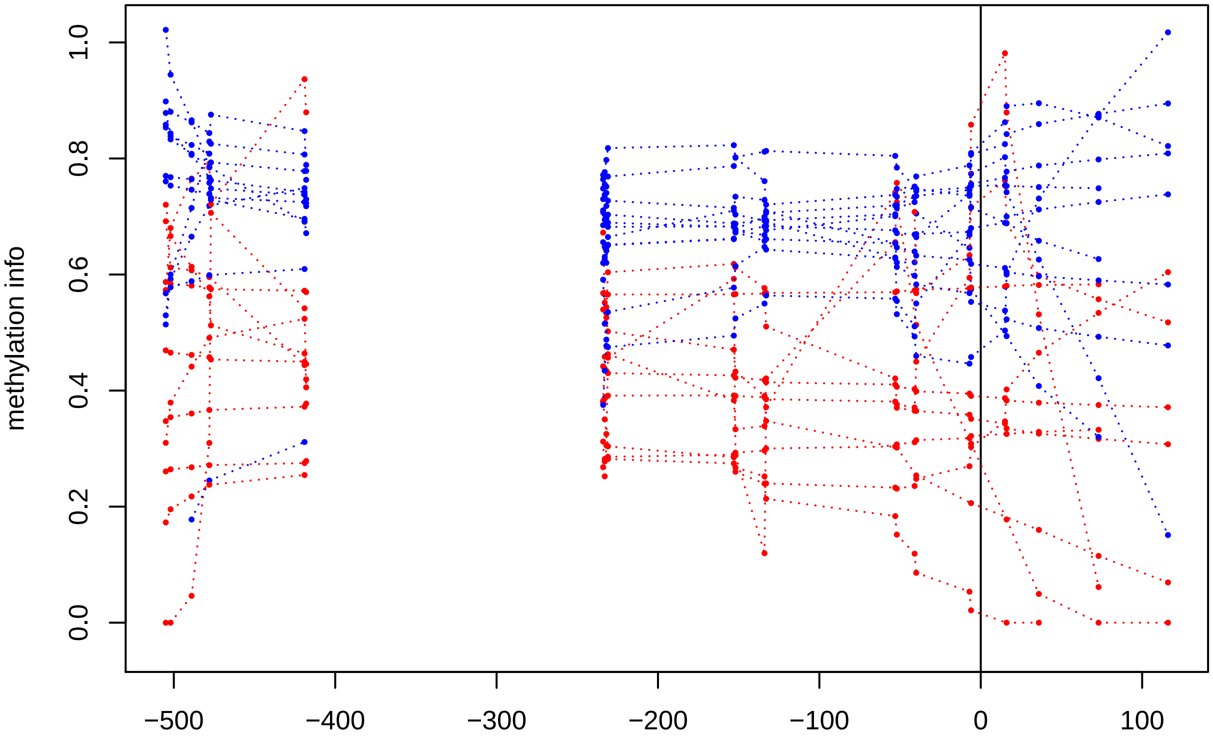
RNAseq logFC(UC−N)= 1.09


CETP average UC−N %methylation max=−0.31% min=−10.42%
methylation info
−1200
−1000
−800
−600
−400
−200
0
200
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
CETP raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−1200
−1000
−800
−600
−400
−200
0
200
RNAseq logFC(UC−N)= 2.06
log2(count)
3
4
5
6
7
N
UC
Cond

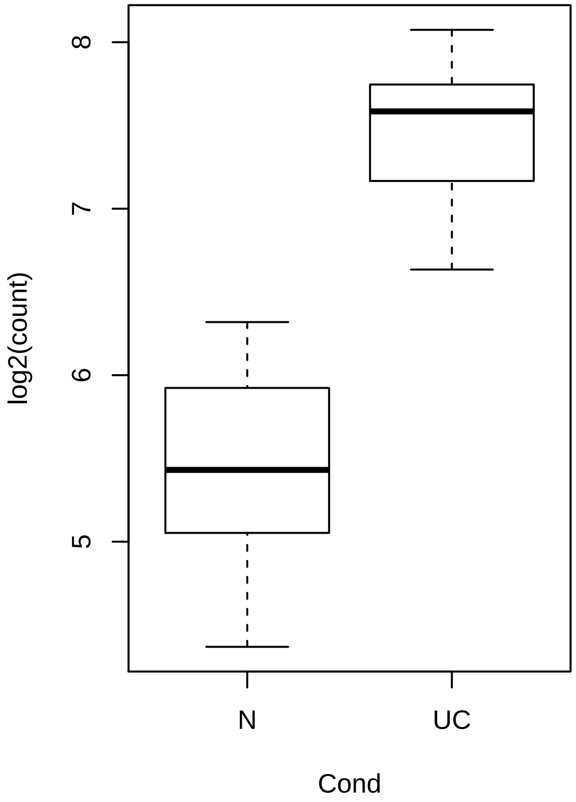
CFP average UC−N %methylation max=−26.69% min=−29.74%

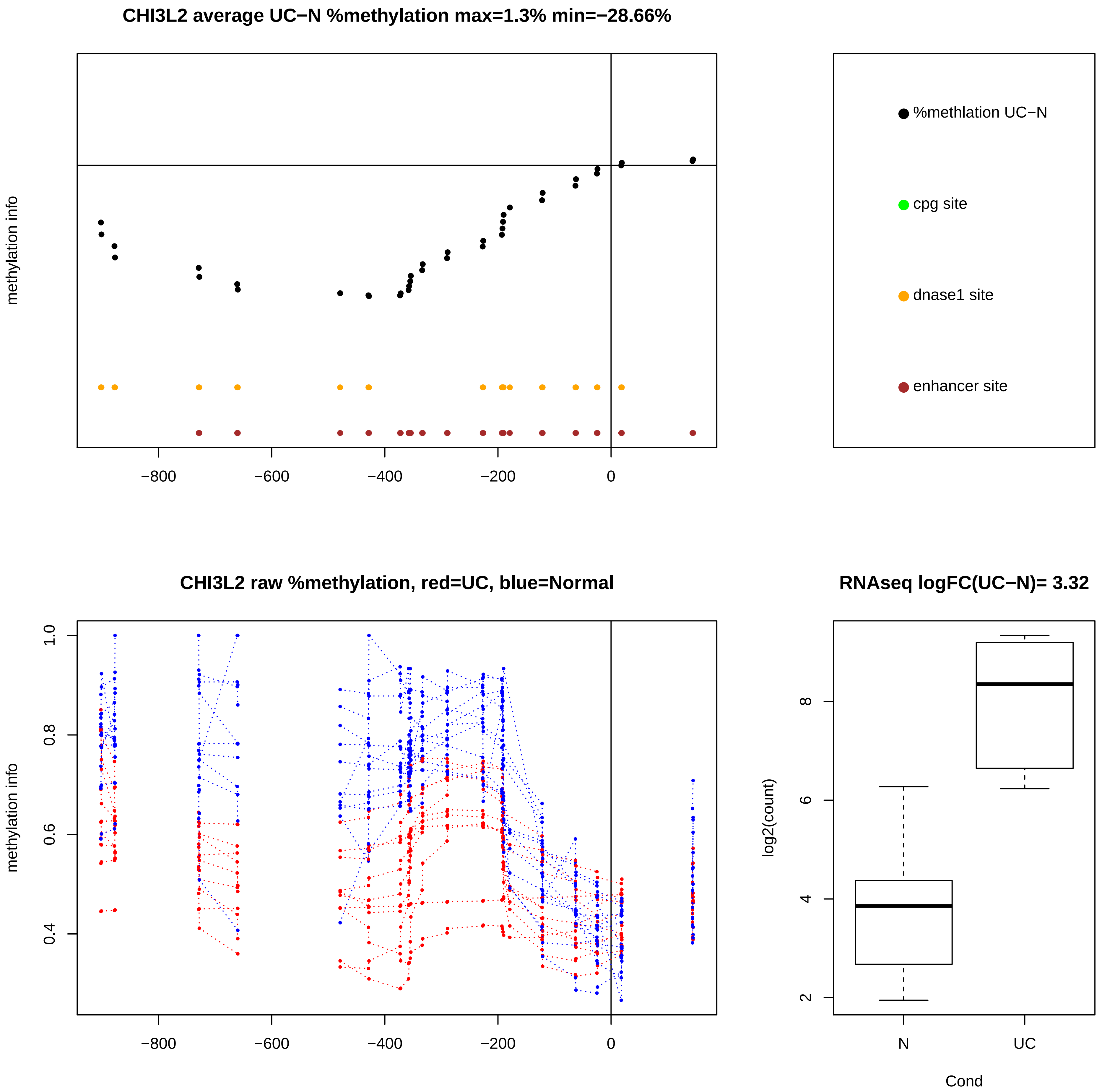


CFP raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 1.82

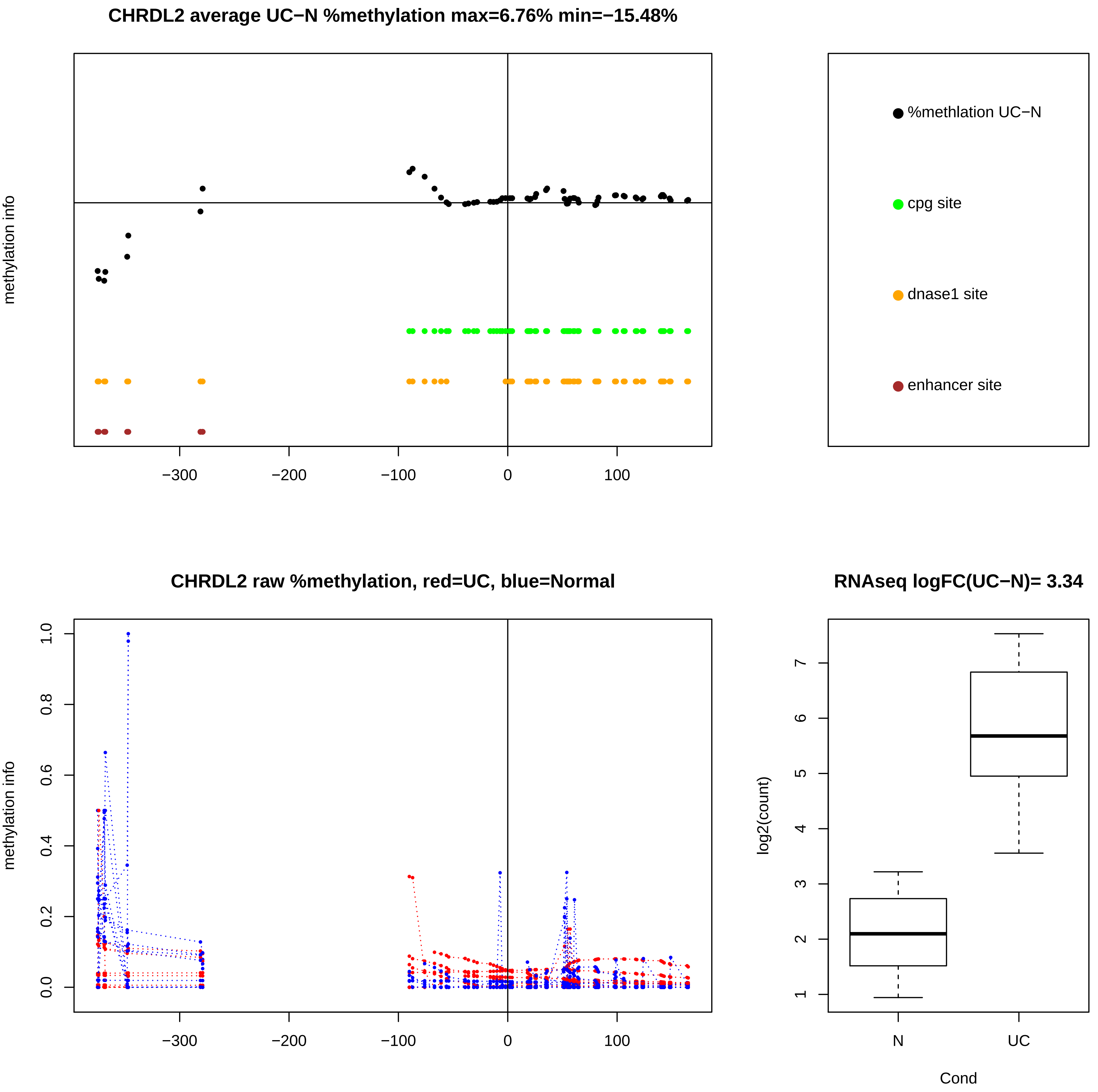




CHI3L2 average UC−N %methylation max=1.3% min=−28.66%

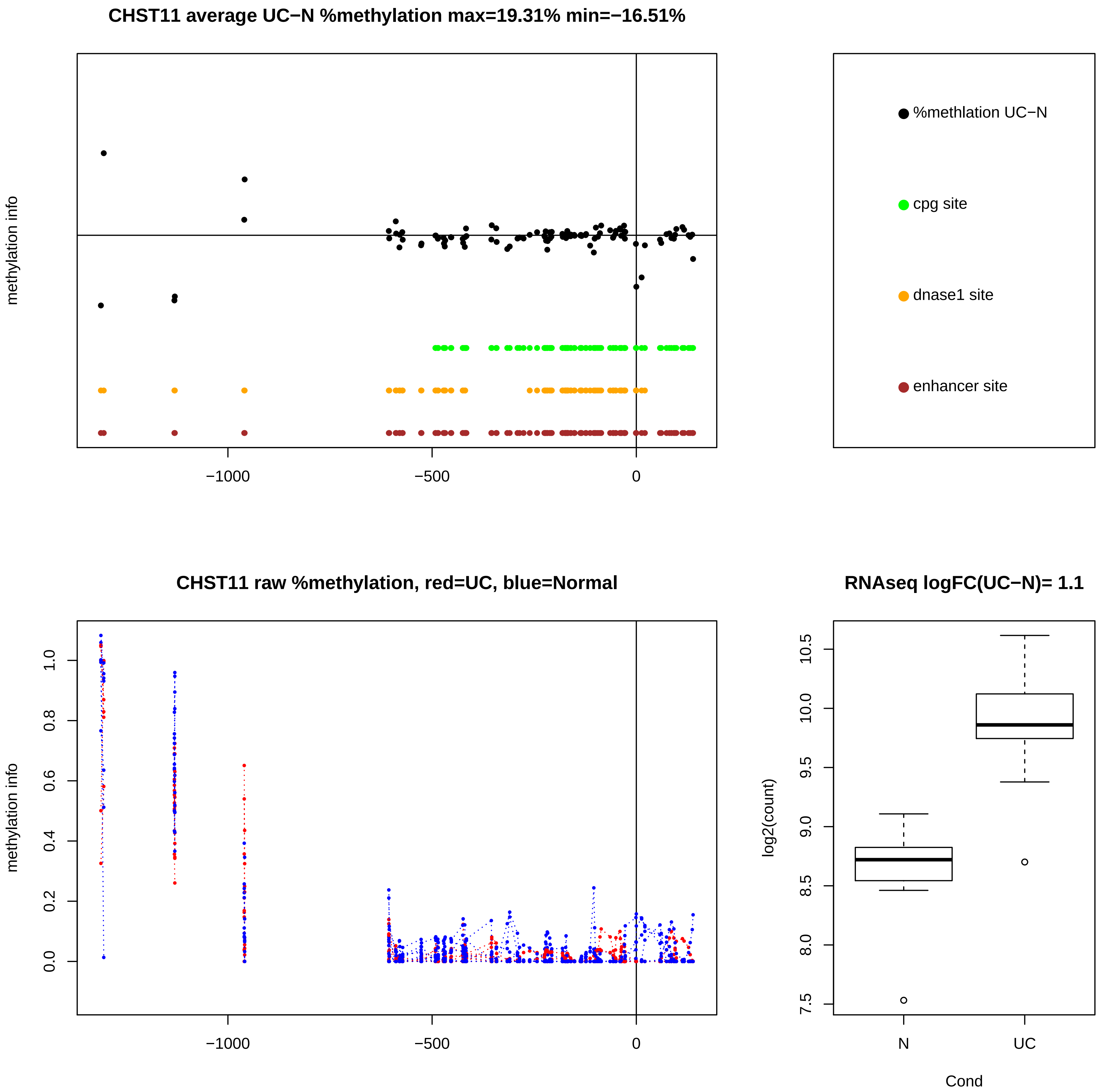
CHI3L2 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 3.32


CHRDL2 average UC−N %methylation max=6.76% min=−15.48%

CHRDL2 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 3.34

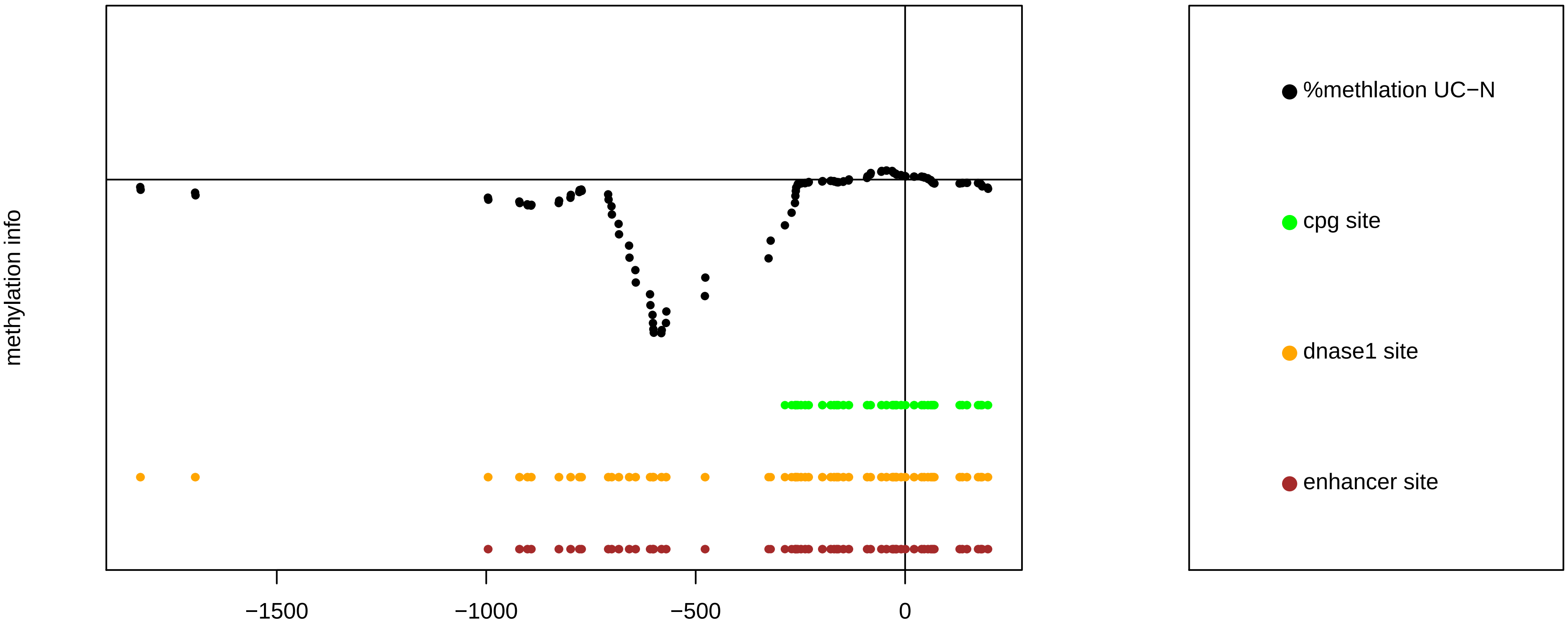


CHST11 average UC−N %methylation max=19.31% min=−16.51%

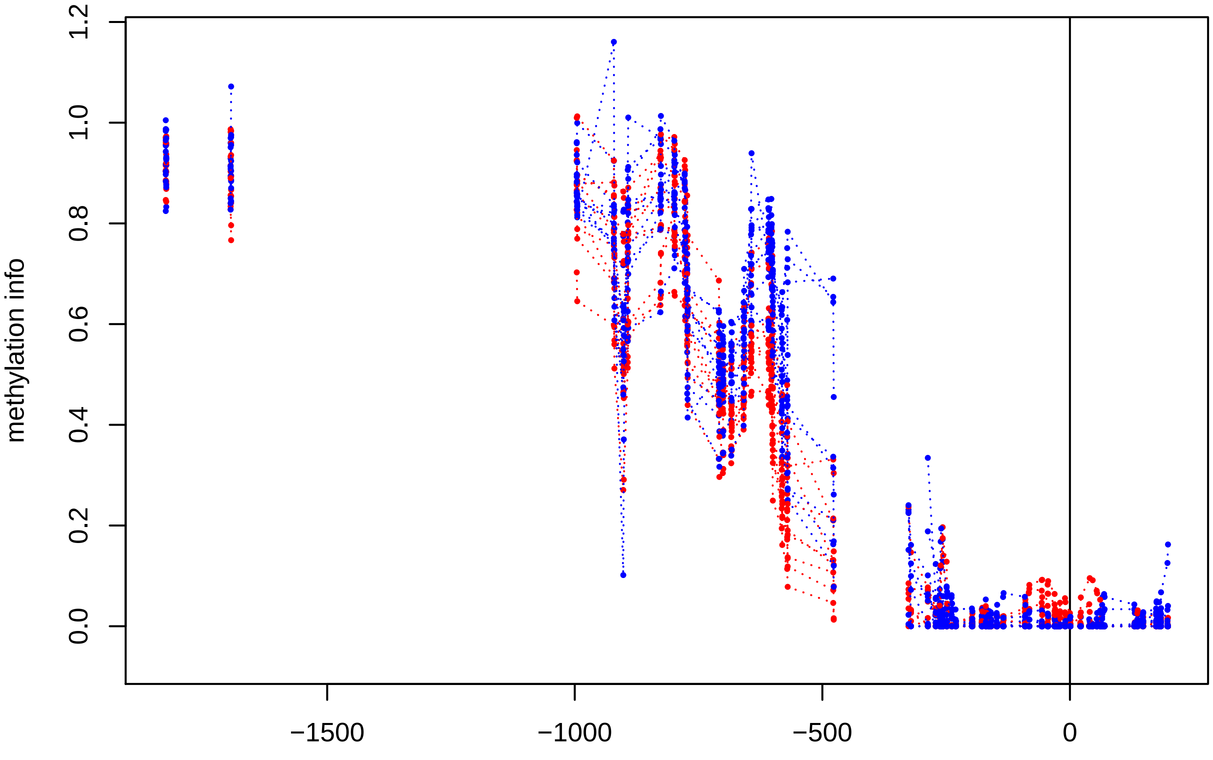
CHST11 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.1

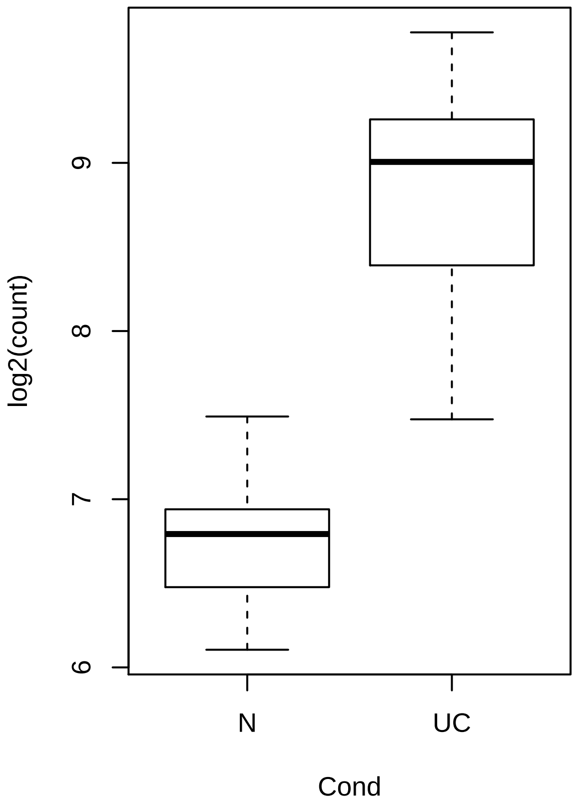
CHST2 average UC−N %methylation max=1.26% min=−21.33%



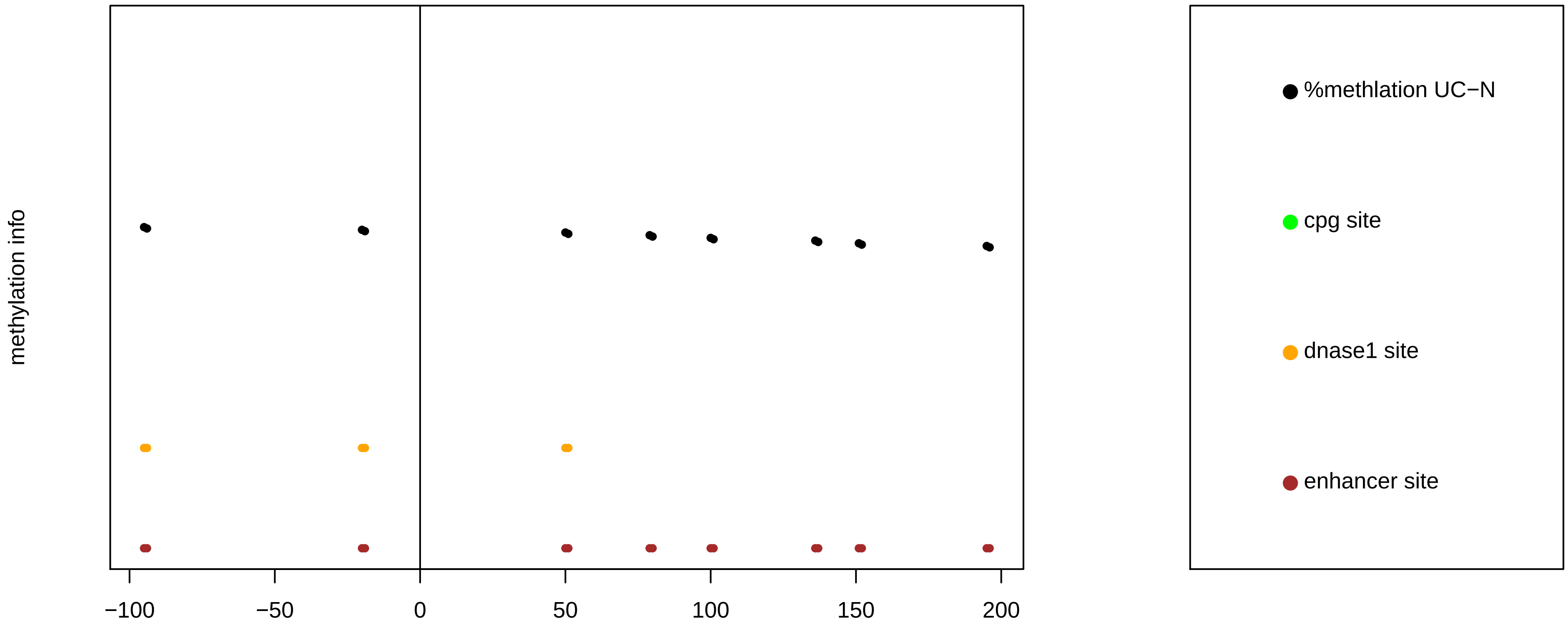
CHST2 raw %methylation, red=UC, blue=Normal



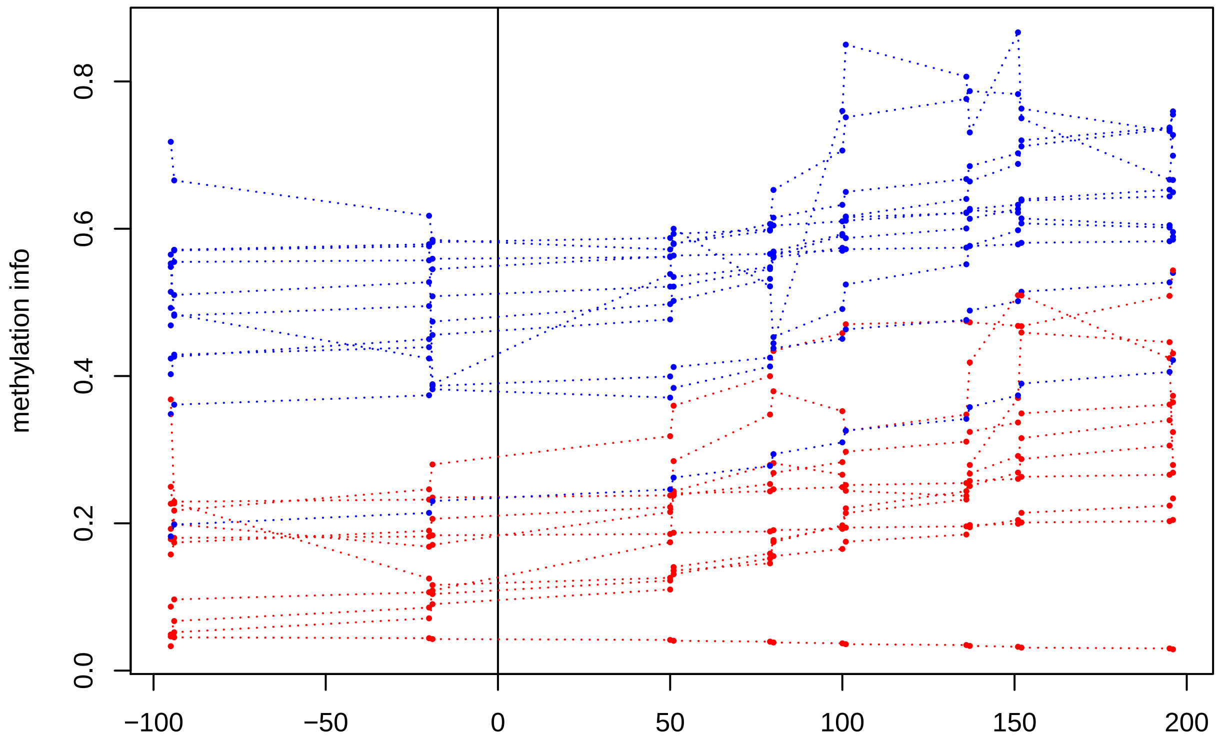
RNAseq logFC(UC−N)= 2.04



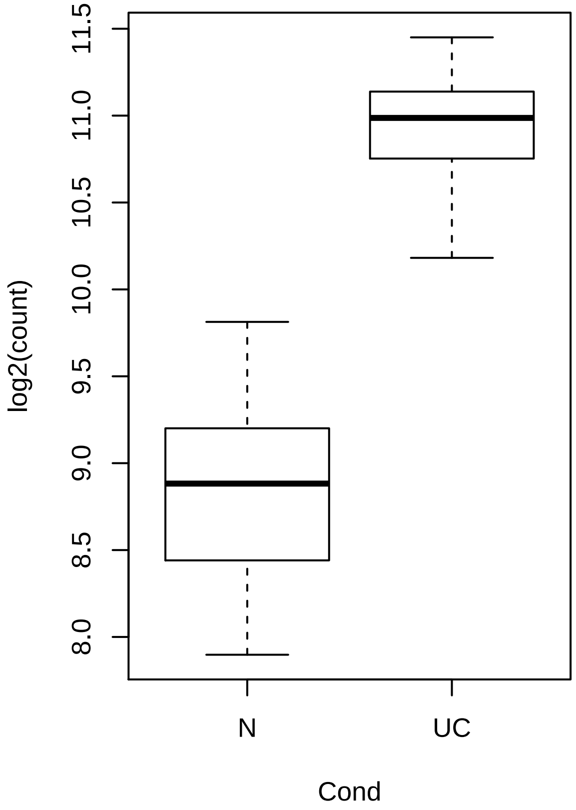
CIITA average UC−N %methylation max=−31.3% min=−33.31%



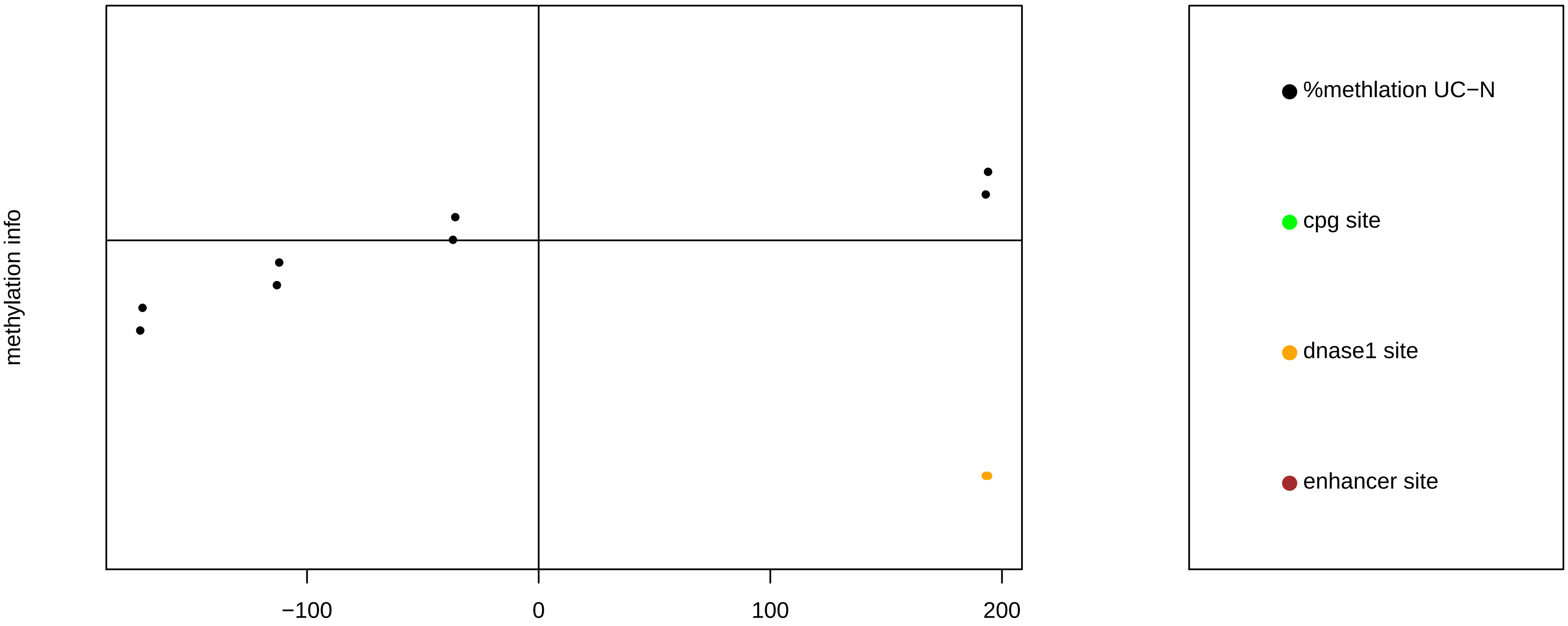
CIITA raw %methylation, red=UC, blue=Normal



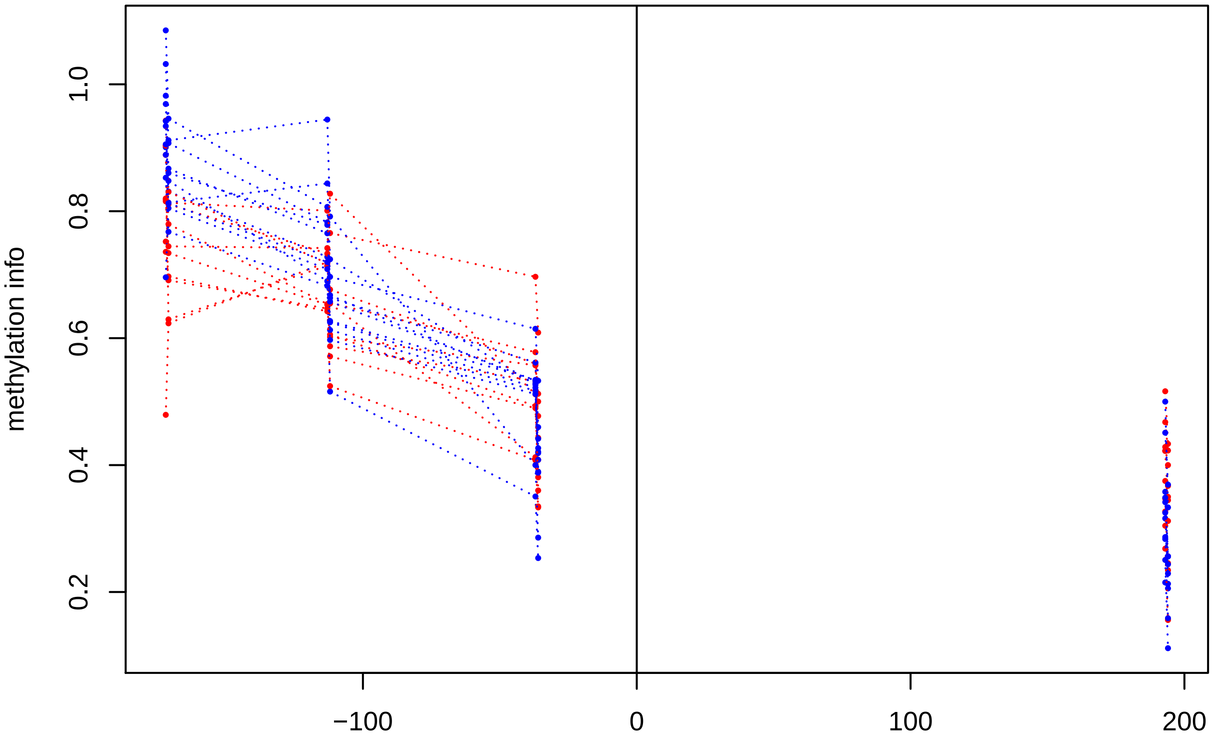
RNAseq logFC(UC−N)= 1.81



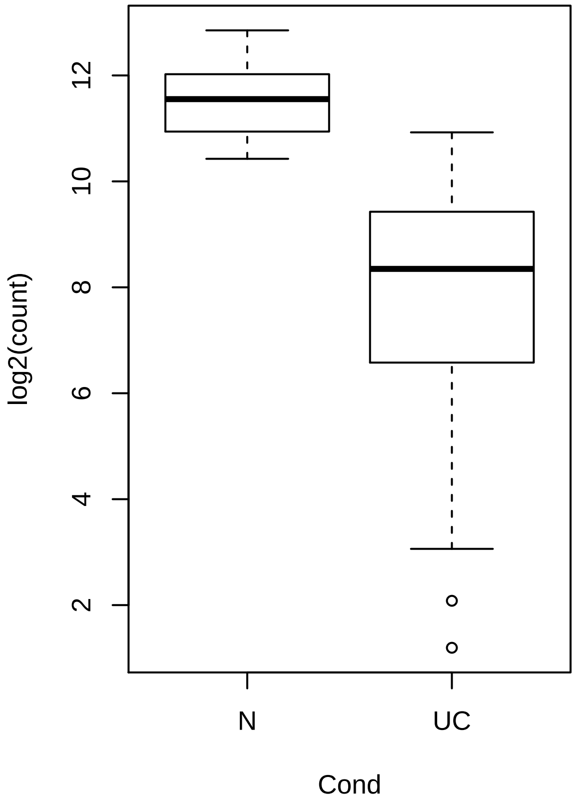
CLDN8 average UC−N %methylation max=9.44% min=−12.41%

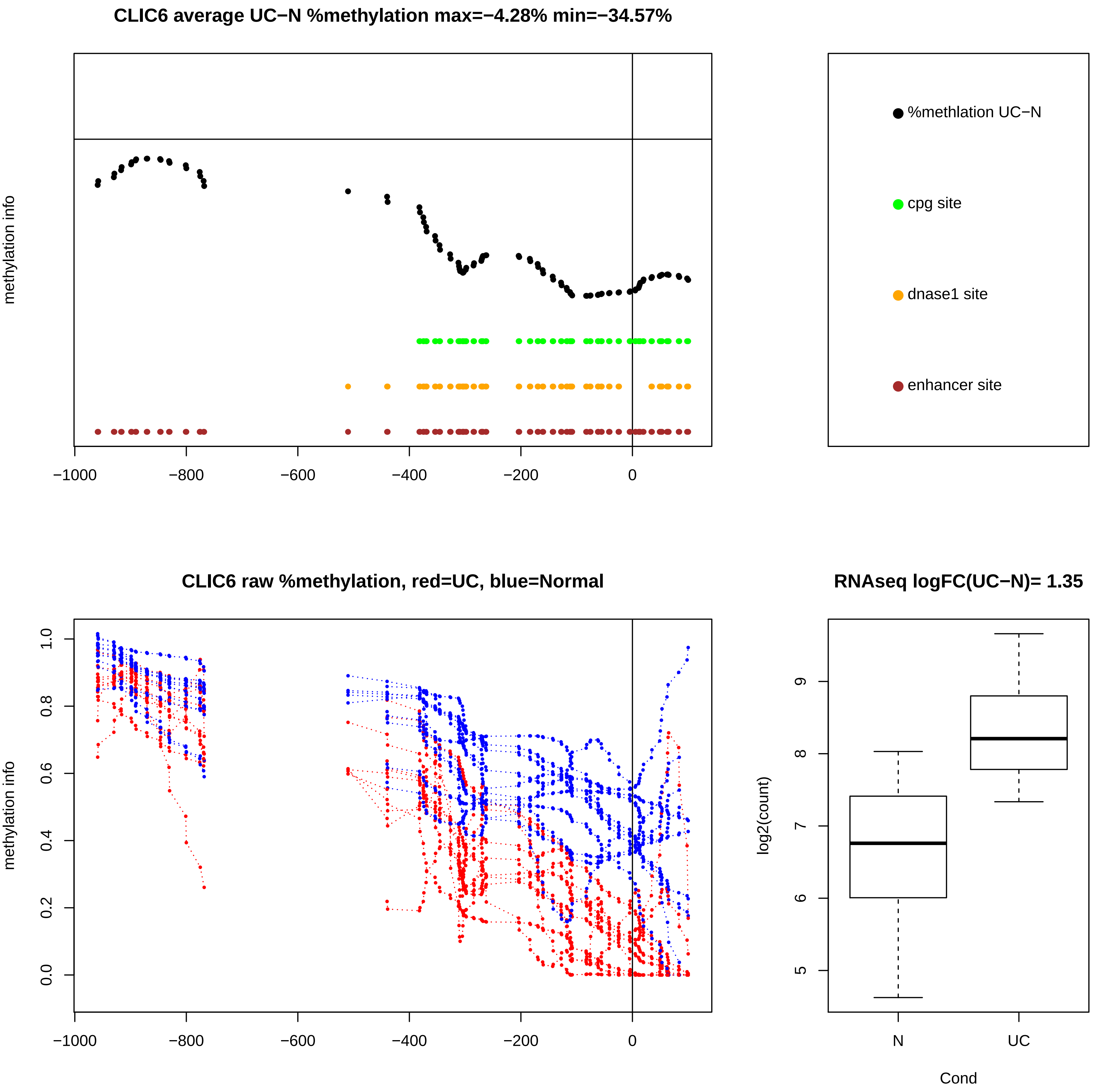


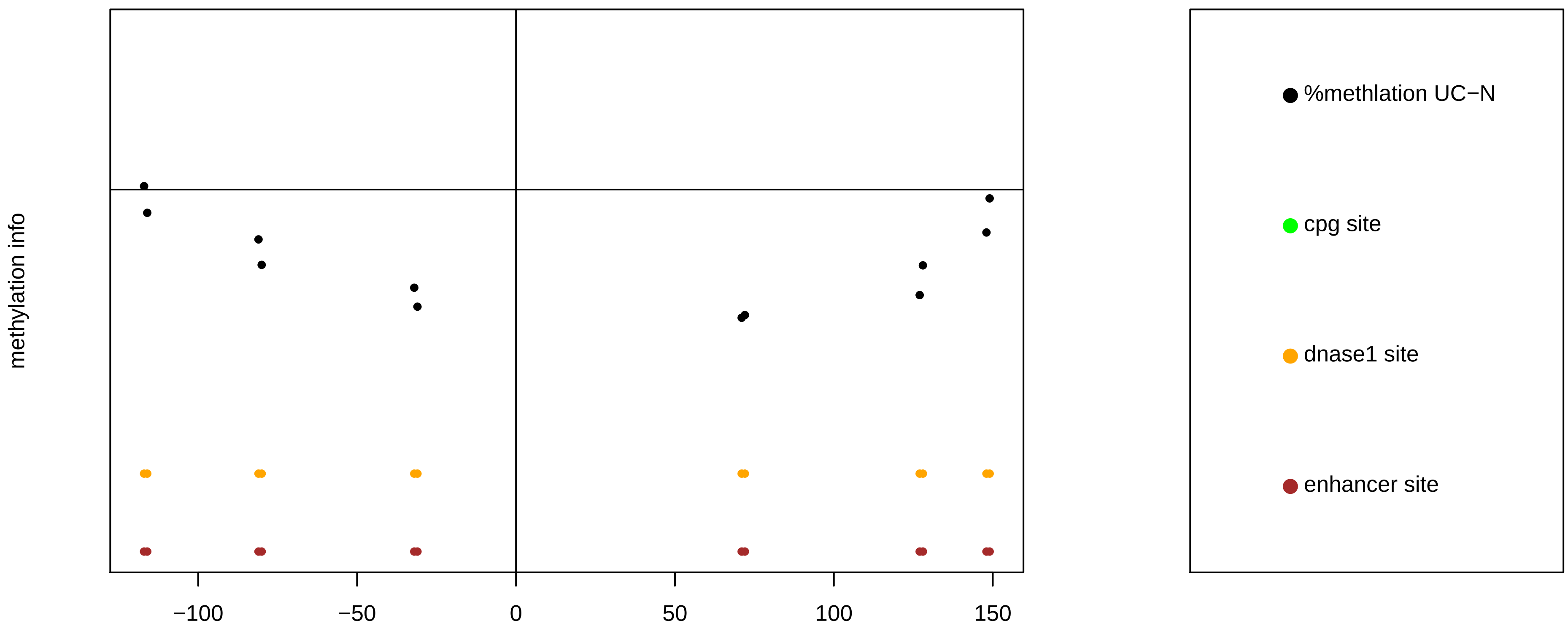
CLDN8 raw %methylation, red=UC, blue=Normal

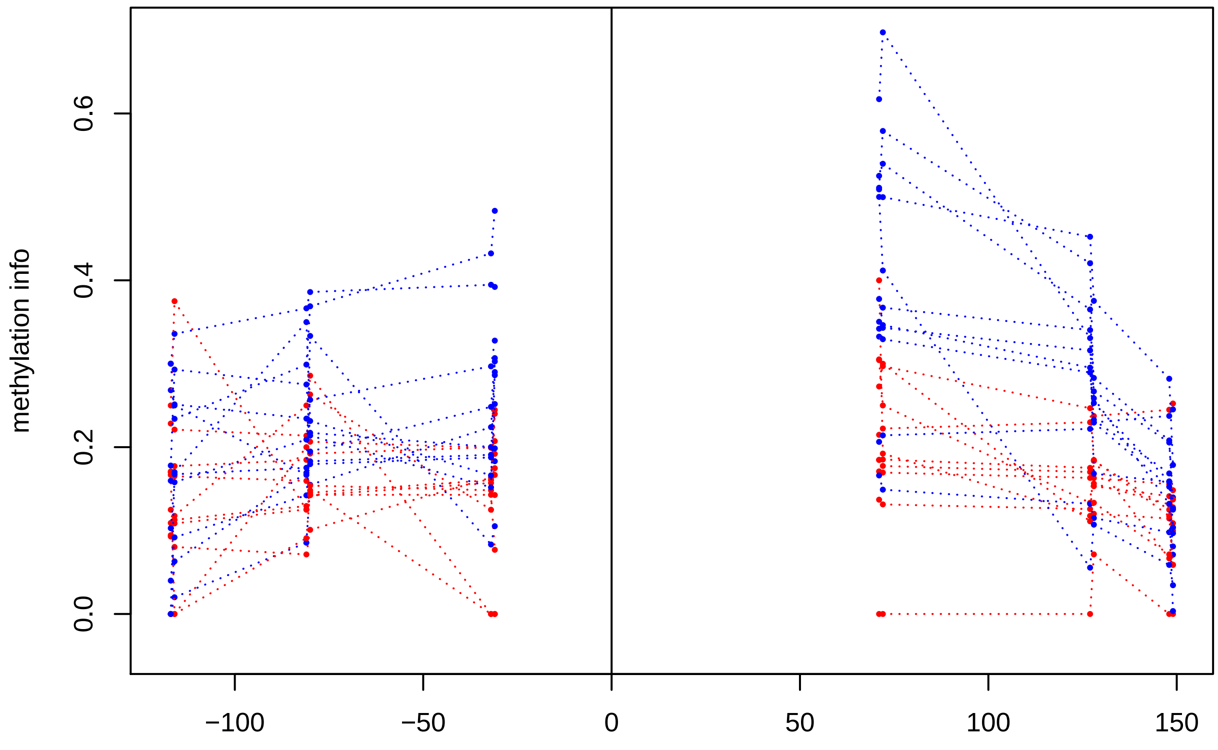


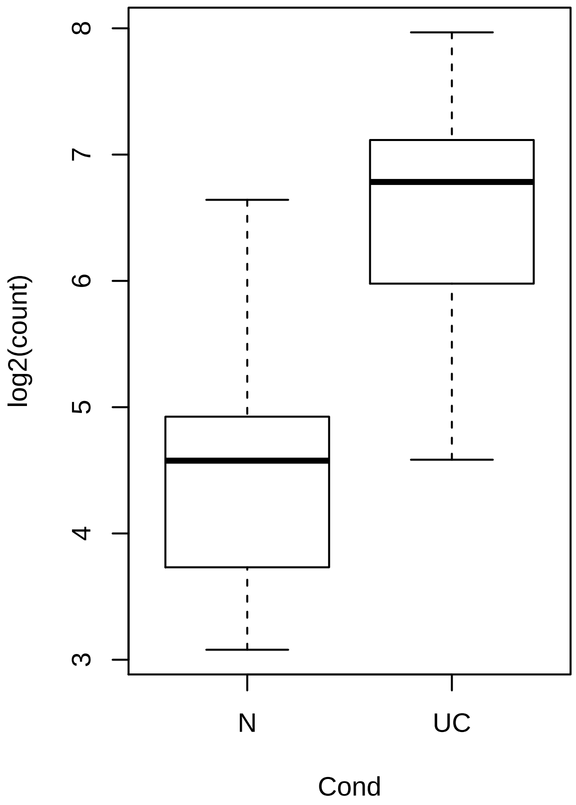
RNAseq logFC(UC−N)= −1.9



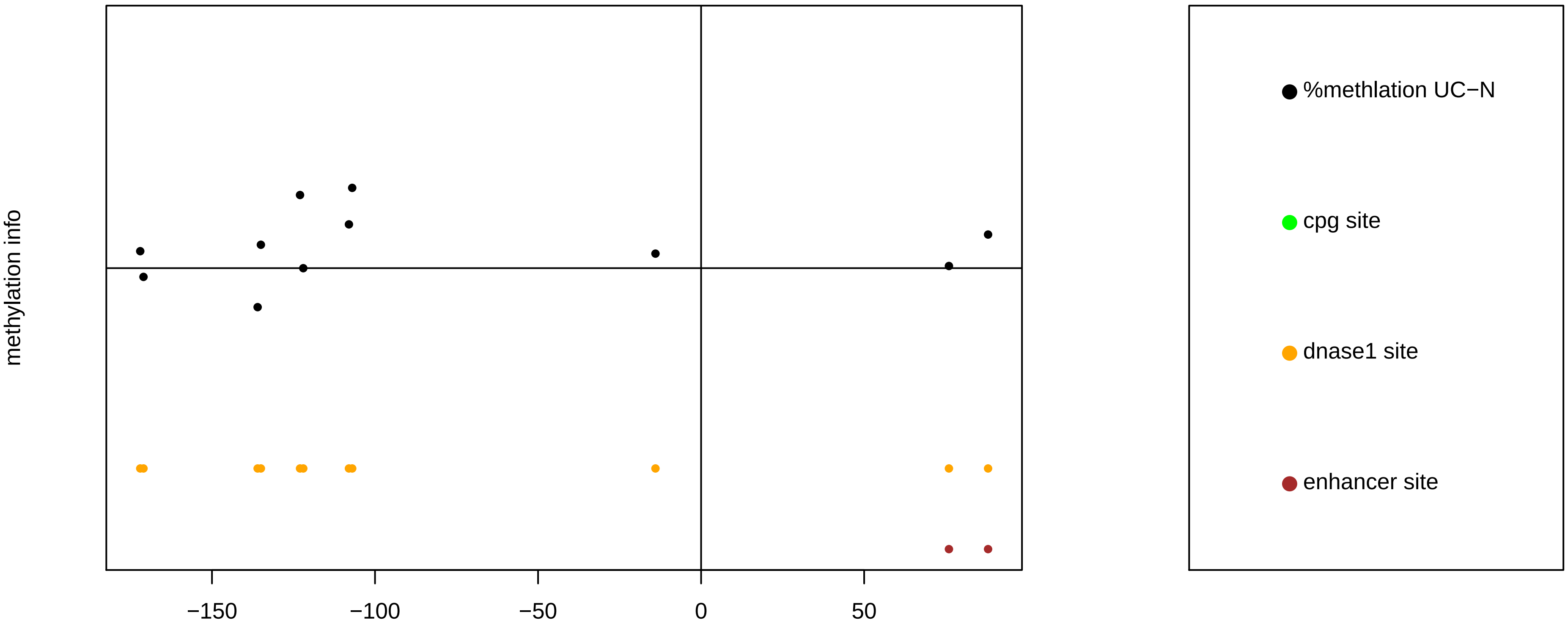

CLIC6 average UC−N %methylation max=−4.28% min=−34.57%
methylation info
−1000
−800
−600
−400
−200
0
%methlation UC−N
cpg site
dnase1 site
enhancer site
CLIC6 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−1000
−800
−600
−400
−200
0
RNAseq logFC(UC−N)= 1.35
log2(count)
5
6
7
8
9
N
UC
Cond


CNR2 average UC−N %methylation max=0.44% min=−16.45%

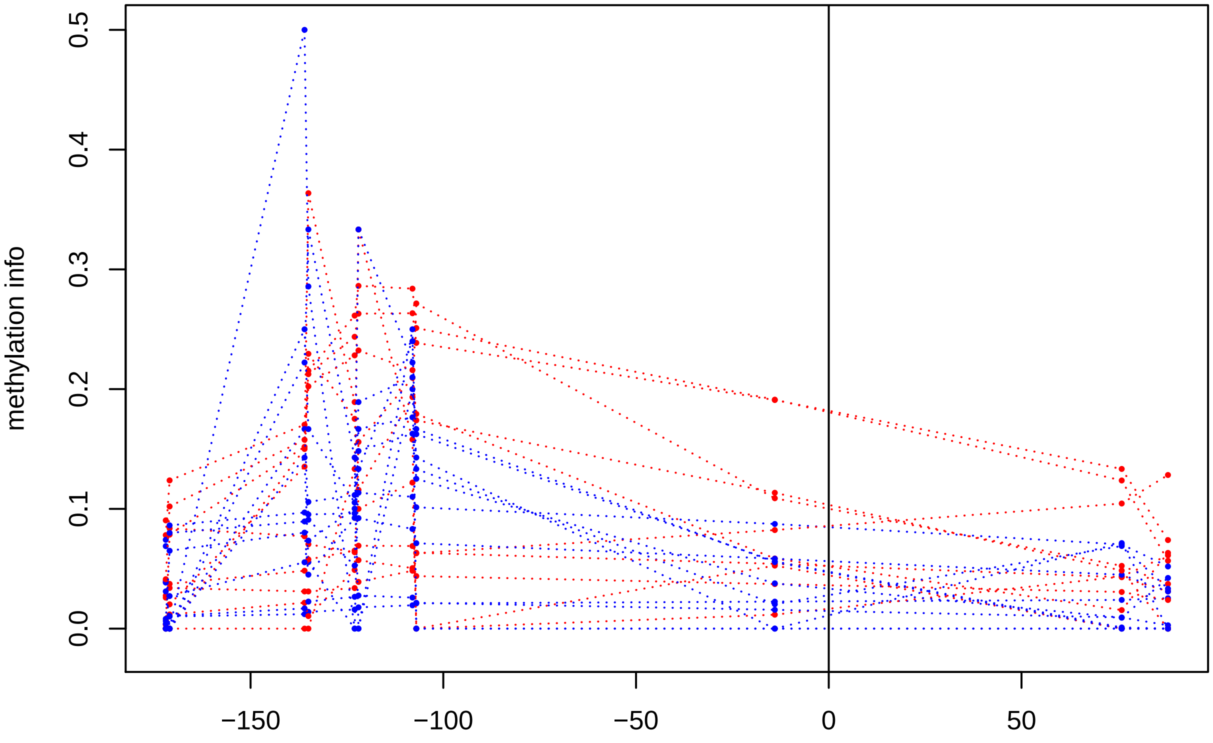

CNR2 raw %methylation, red=UC, blue=Normal


RNAseq logFC(UC−N)= 1.68

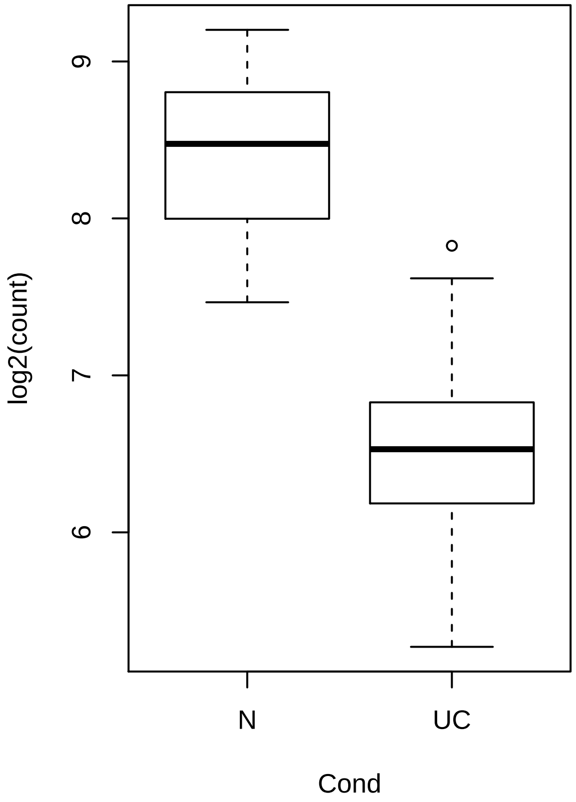
CPA6 average UC−N %methylation max=9.95% min=−4.83%

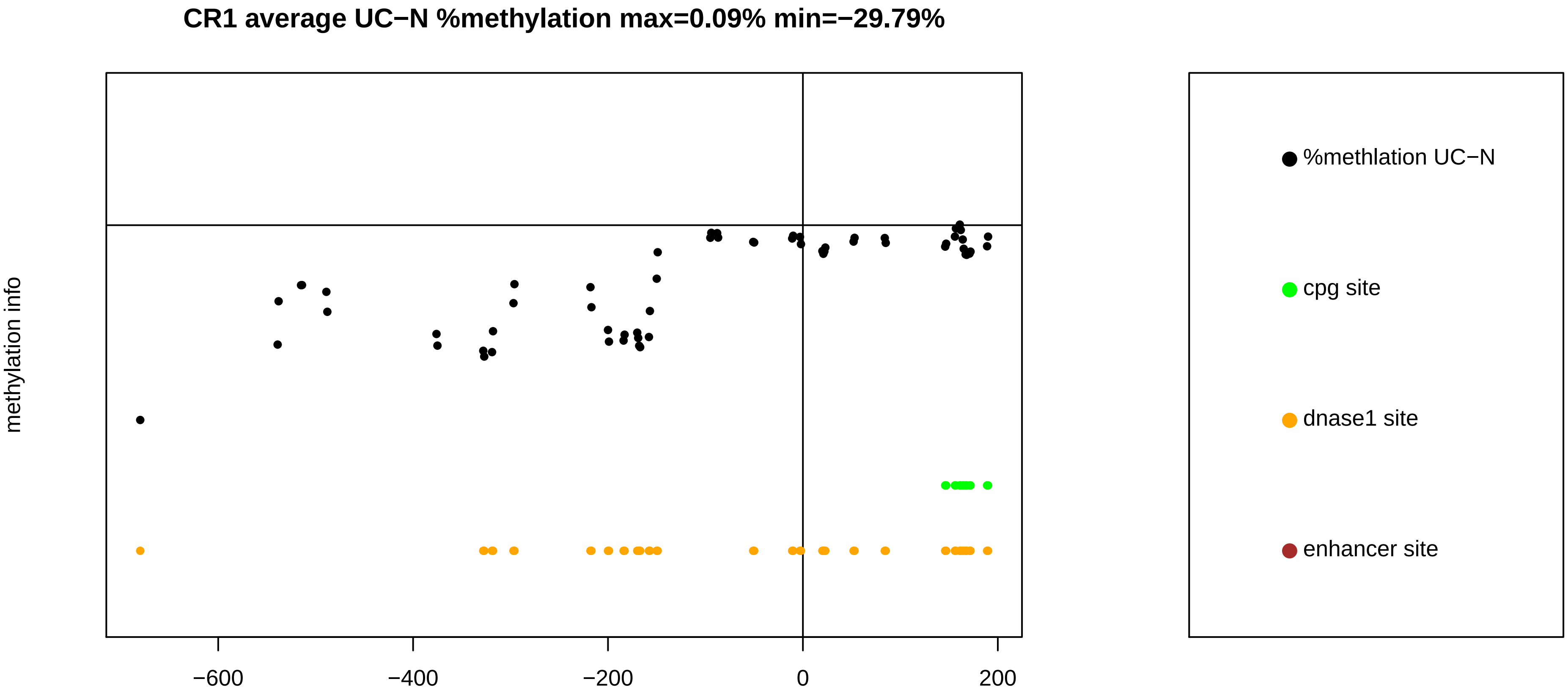


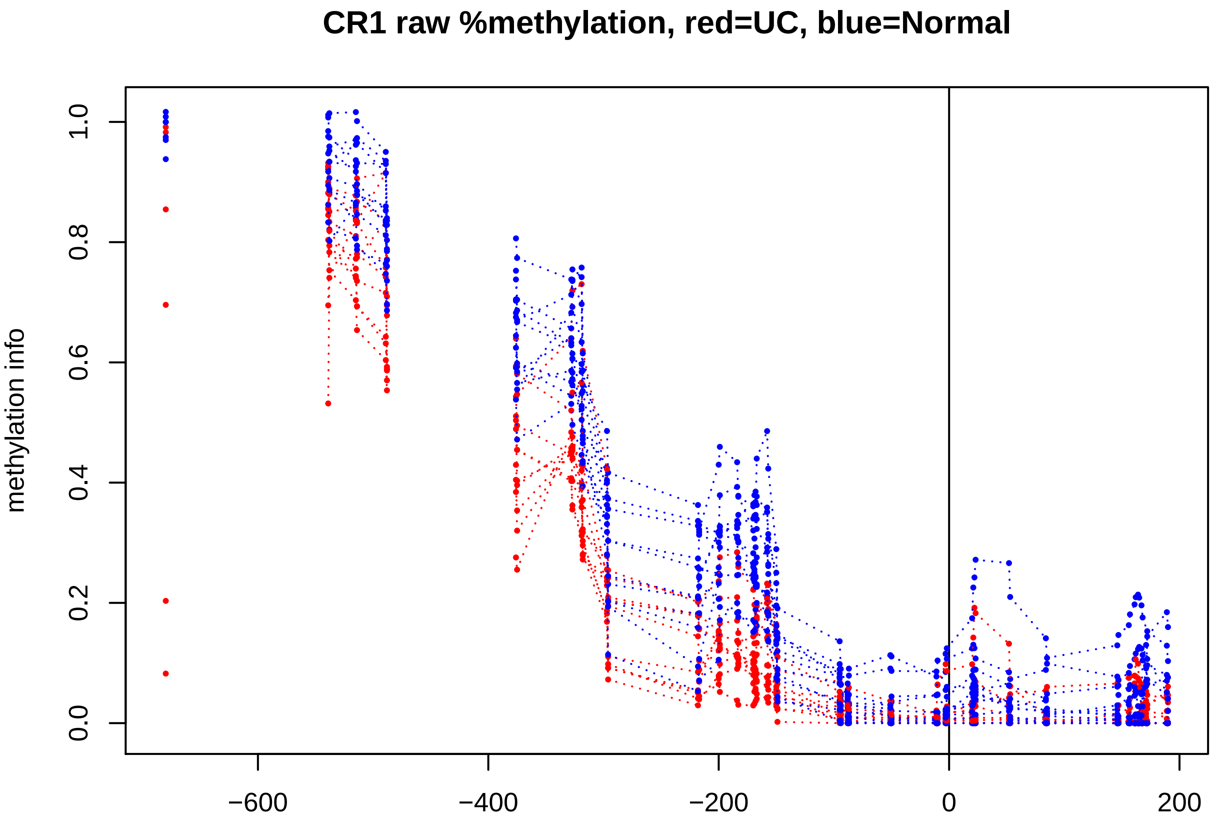
CPA6 raw %methylation, red=UC, blue=Normal

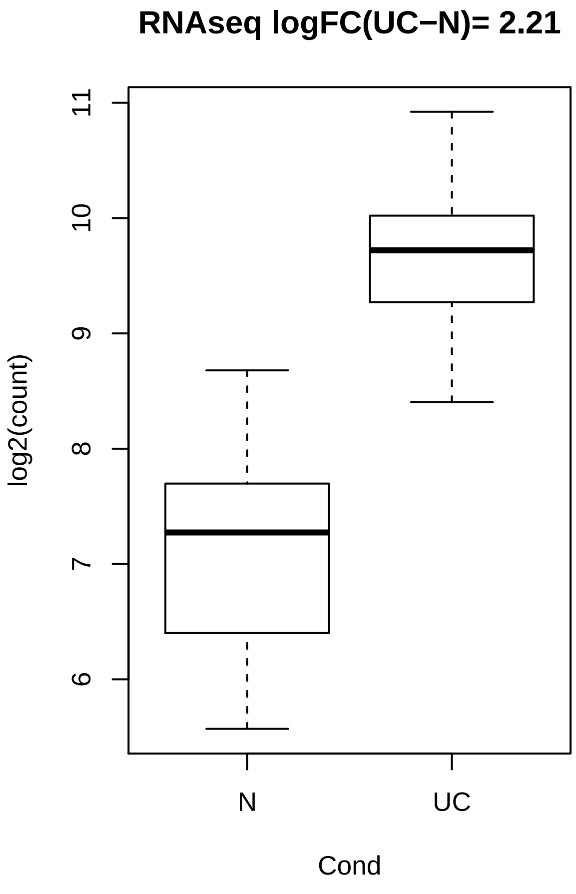


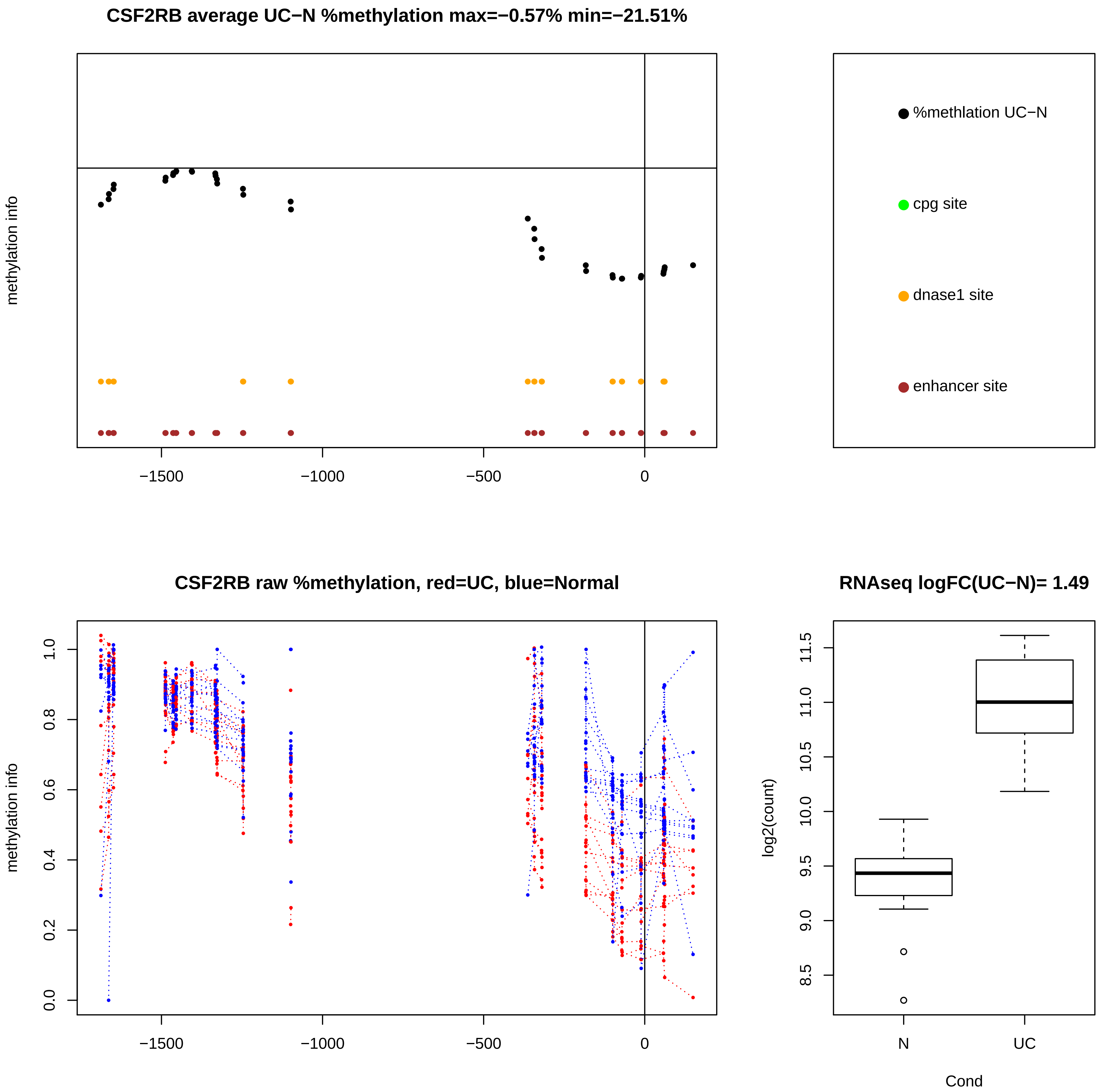
RNAseq logFC(UC−N)= −1.38




CR1 average UC−N %methylation max=0.09% min=−29.79%


CR1 raw %methylation, red=UC, blue=Normal

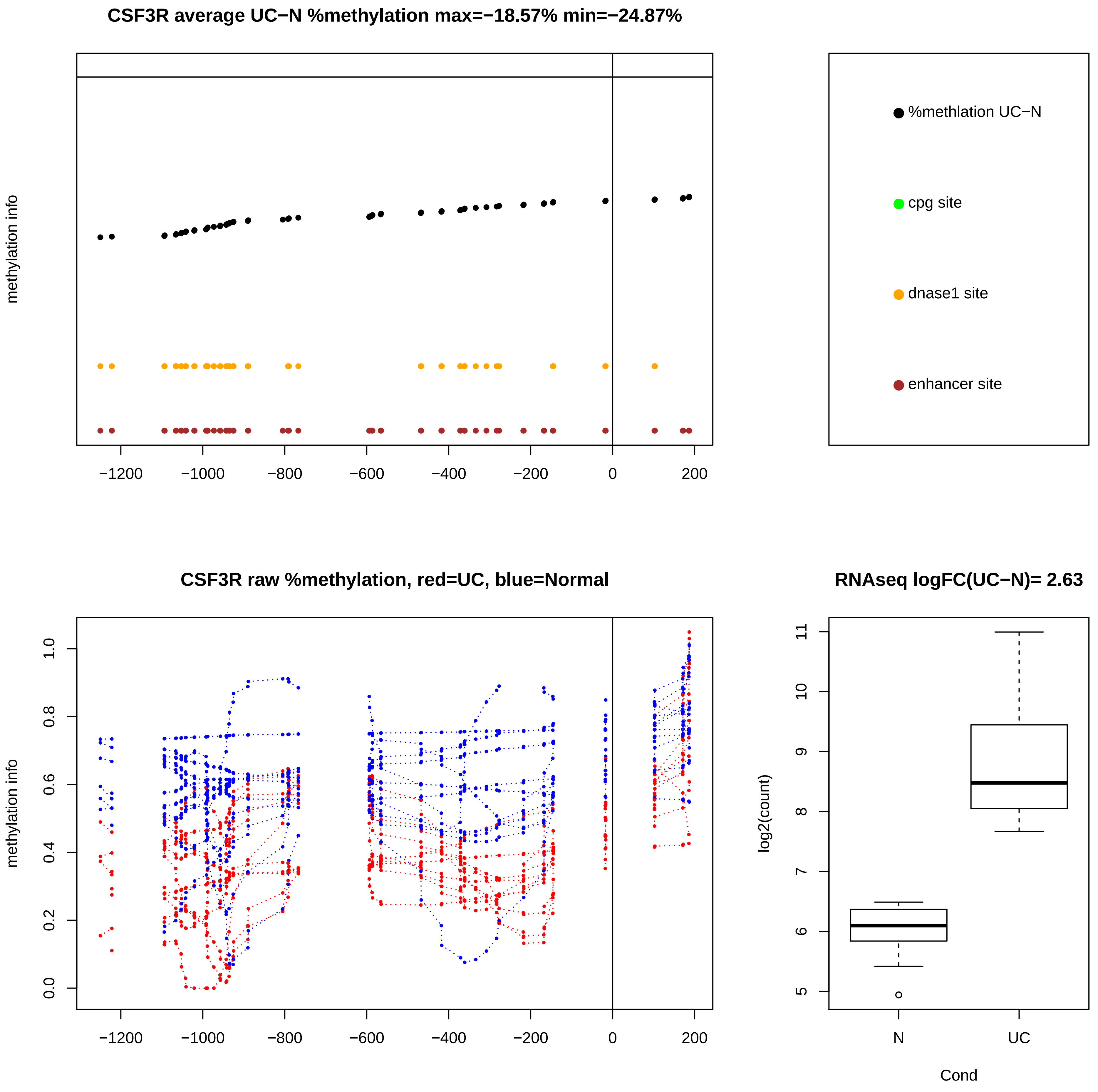

RNAseq logFC(UC−N)= 2.21



CSF2RB average UC−N %methylation max=−0.57% min=−21.51%

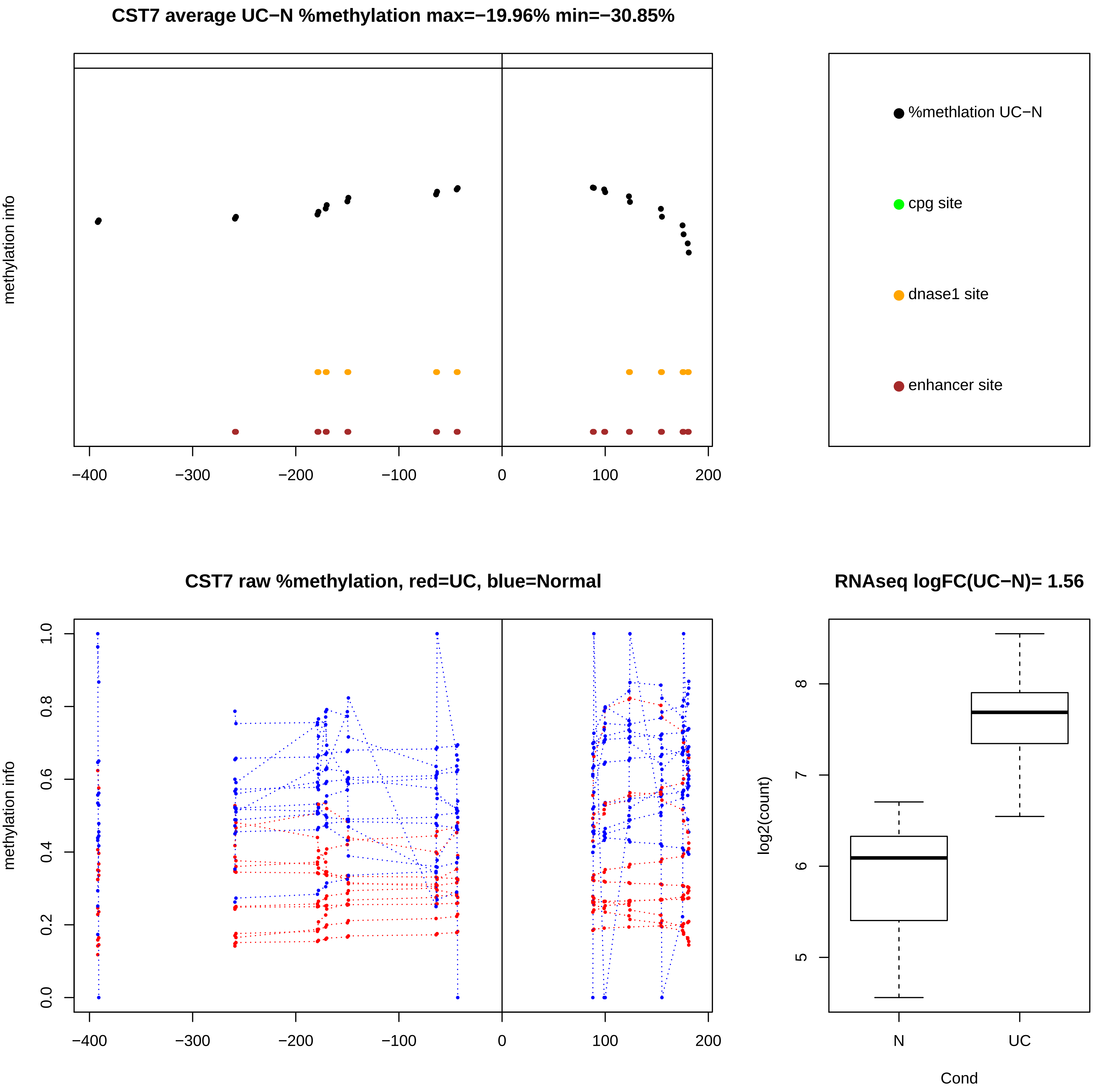
CSF2RB raw %methylation, red=UC, blue=Normal

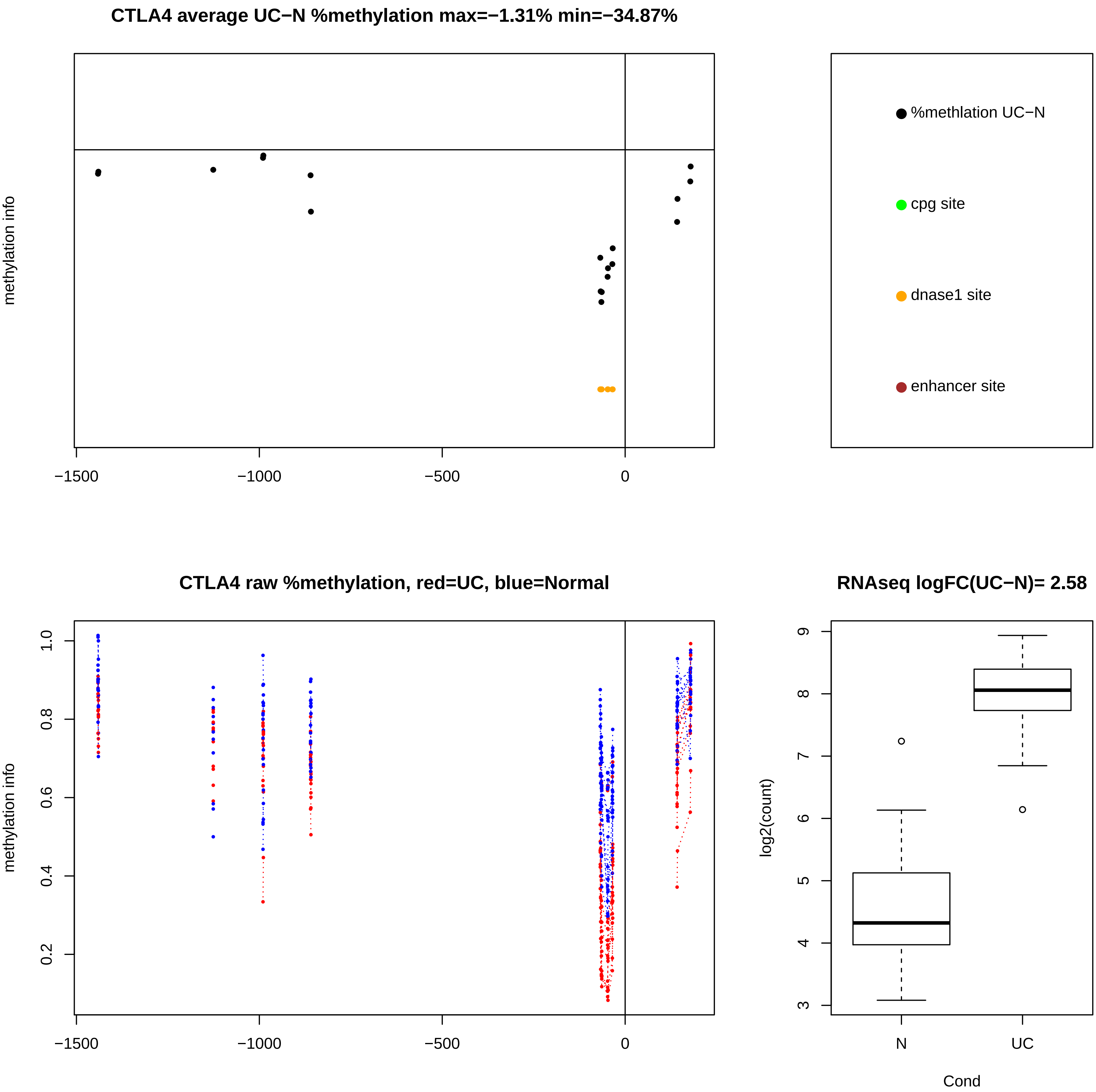
RNAseq logFC(UC−N)= 1.49

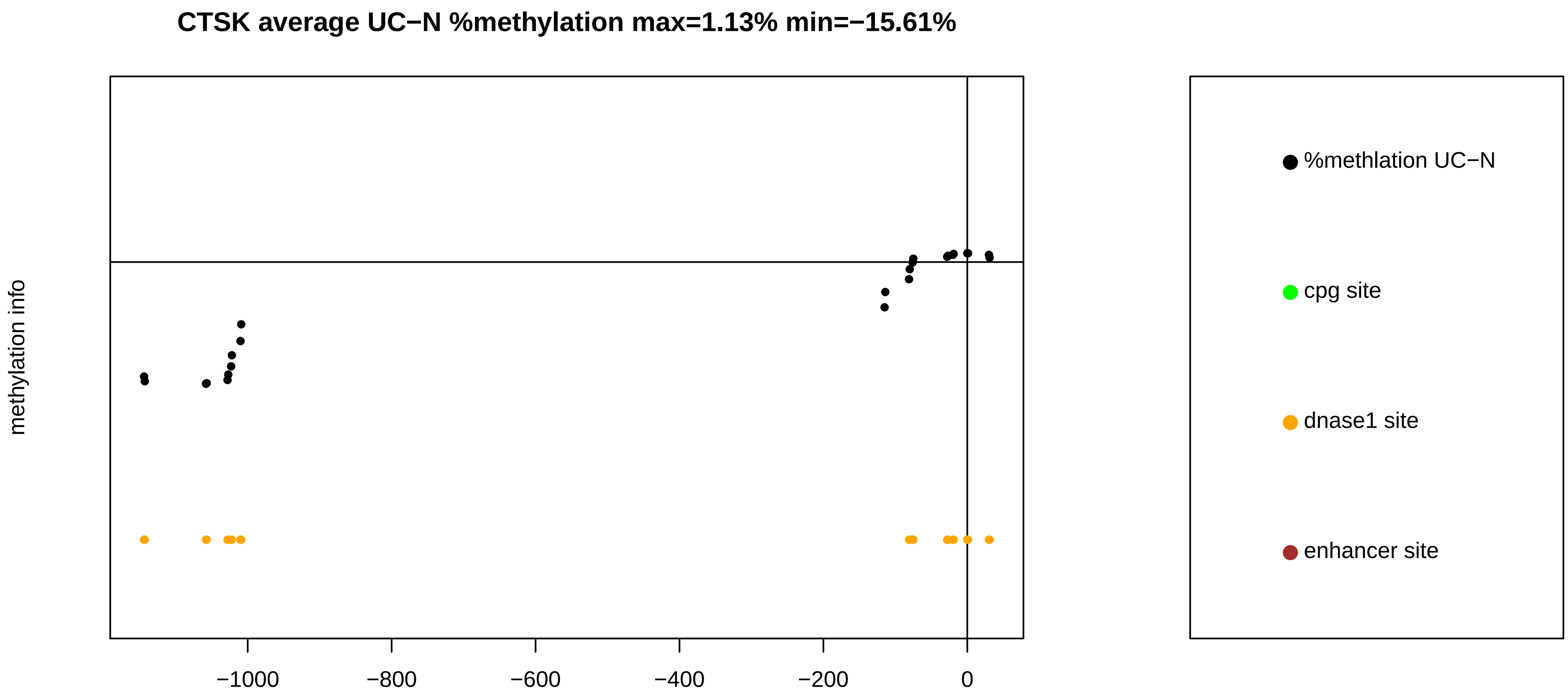

CSF3R average UC−N %methylation max=−18.57% min=−24.87%

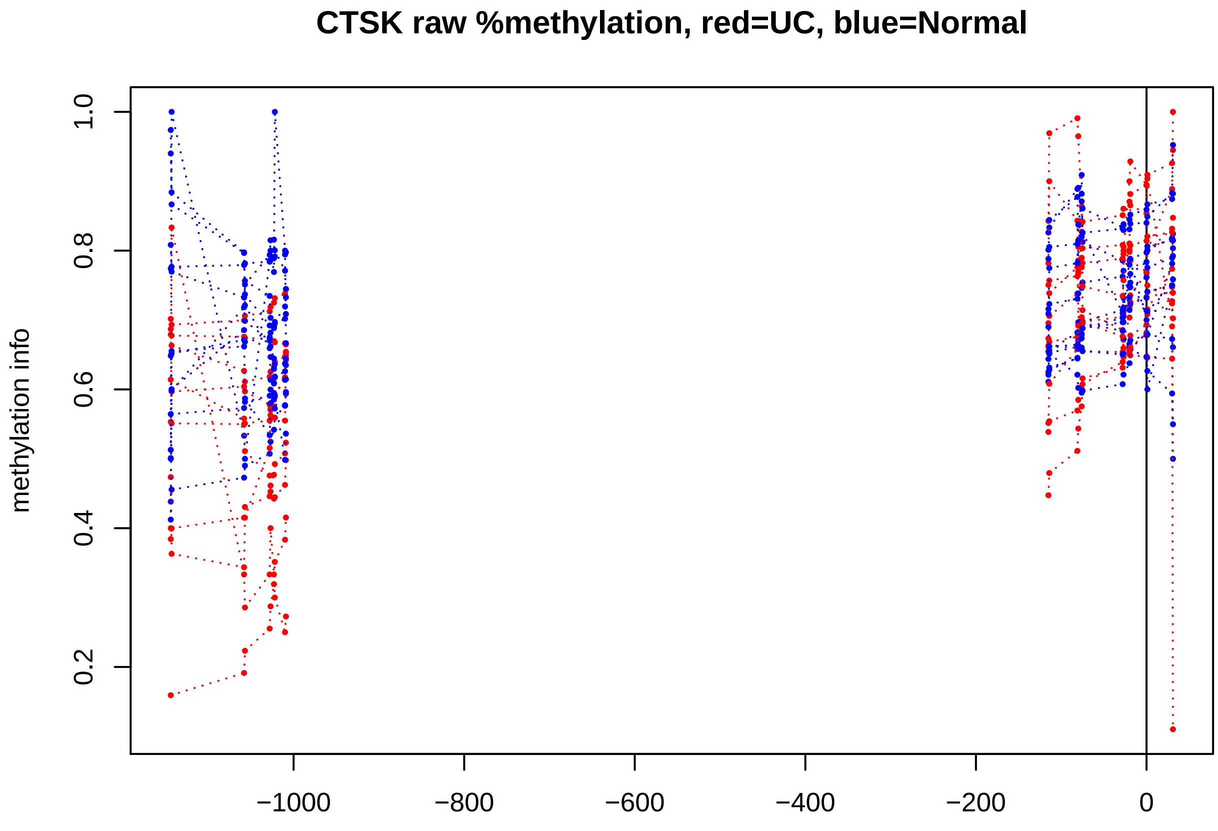
CSF3R raw %methylation, red=UC, blue=Normal

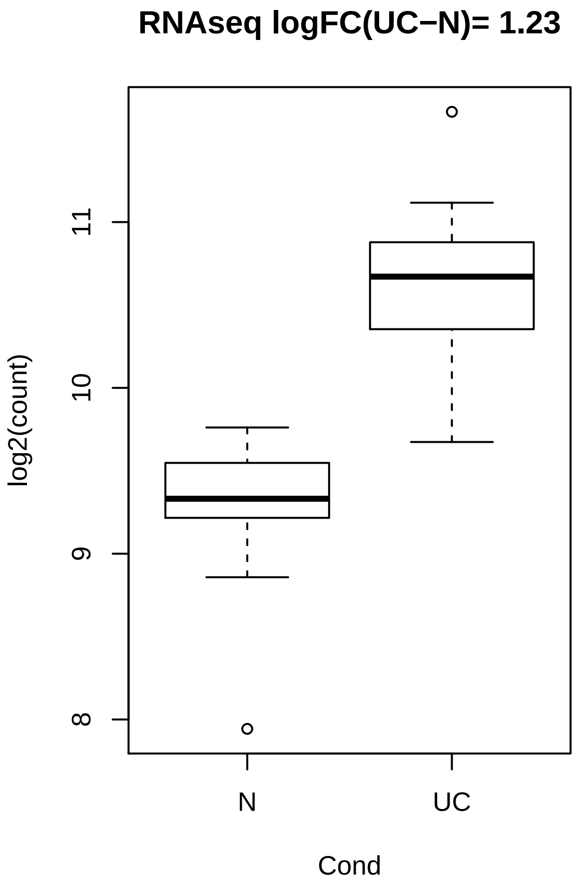
RNAseq logFC(UC−N)= 2.63

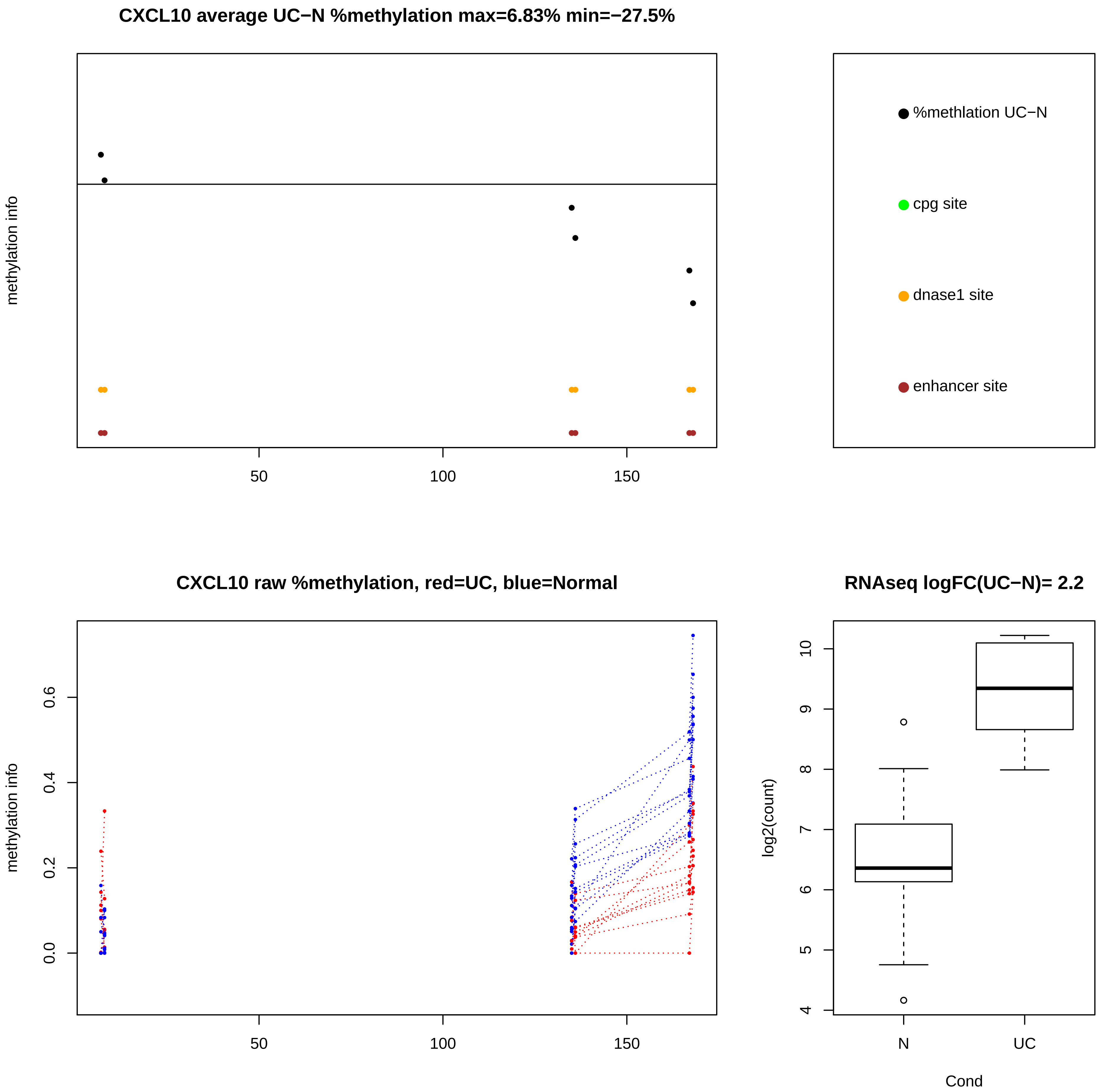

CST7 average UC−N %methylation max=−19.96% min=−30.85%
methylation info
−400
−300
−200
−100
0
100
200
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
CST7 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−400
−300
−200
−100
0
100
200
RNAseq logFC(UC−N)= 1.56
log2(count)
5
6
7
8
N
UC
Cond




CTSK average UC−N %methylation max=1.13% min=−15.61%
methylation info
−1000
−800
−600
−400
−200
0
%methlation UC−N
cpg site
dnase1 site
enhancer site


CTSK raw %methylation, red=UC, blue=Normal
methylation info
1.0
0.8
0.6
0.4
0.2
−1000
−800
−600
−400
−200
0


RNAseq logFC(UC−N)= 1.23
log2(count)
11
10
9
8
N
UC
Cond

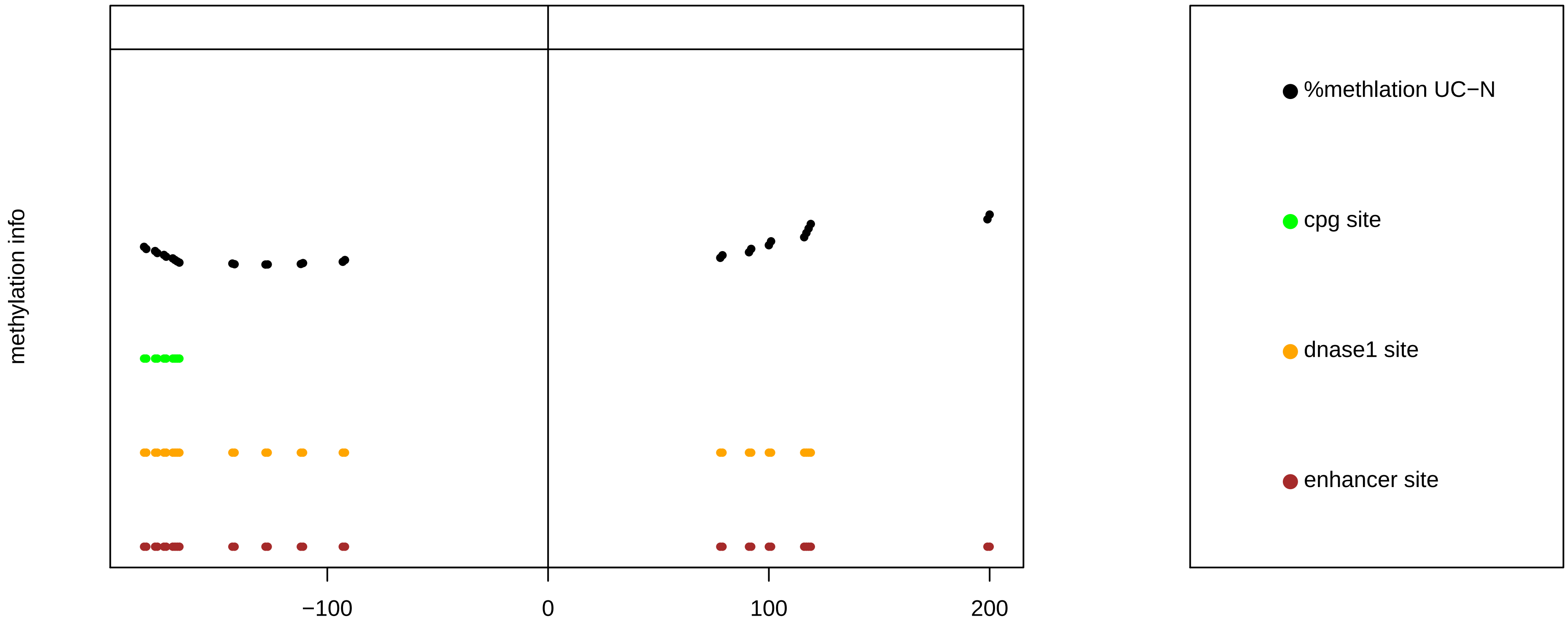


CXCL10 average UC−N %methylation max=6.83% min=−27.5%

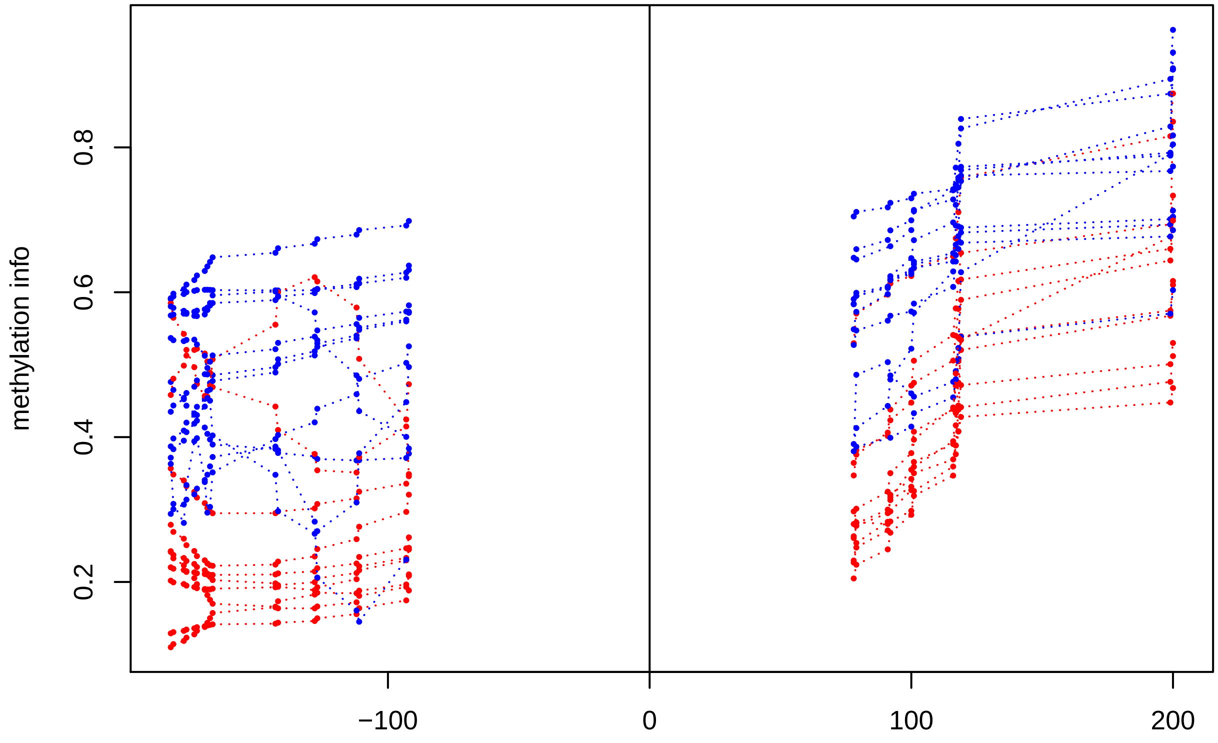
CXCL10 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 2.2

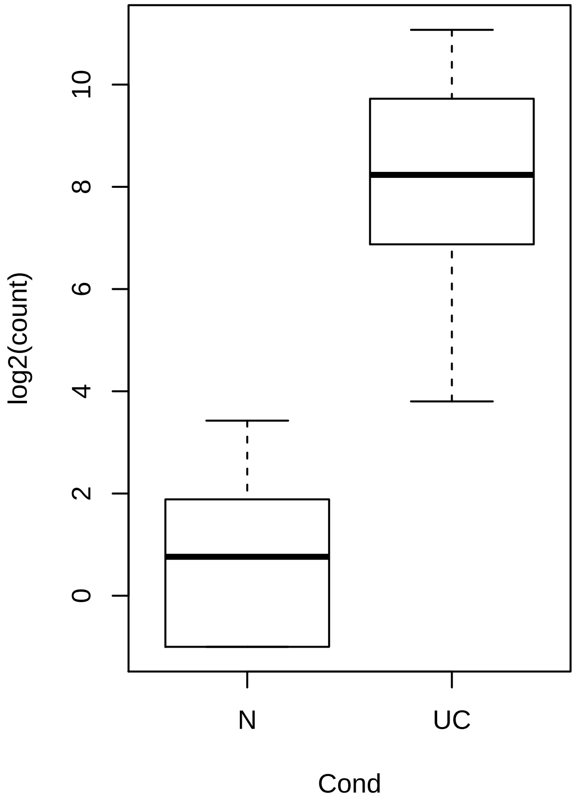
CXCL5 average UC−N %methylation max=−17.57% min=−22.88%

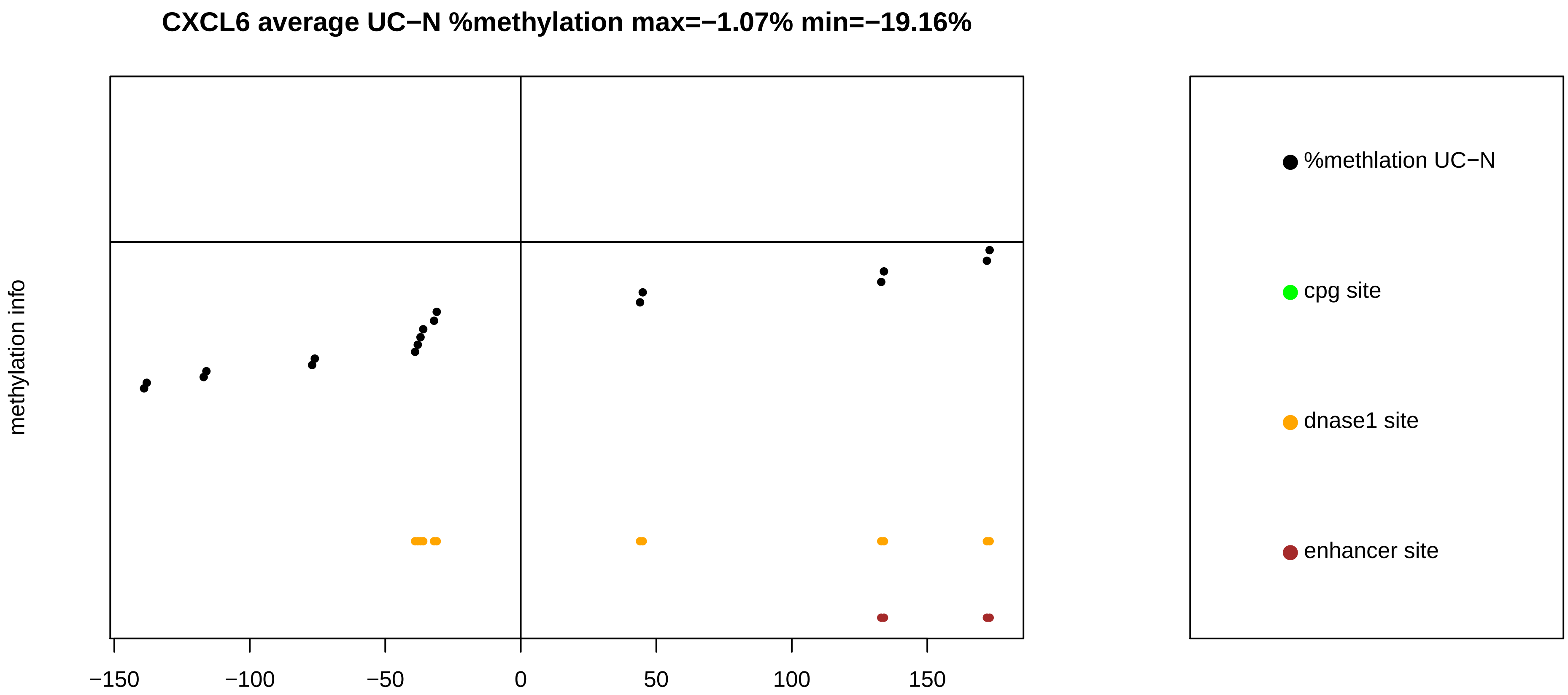


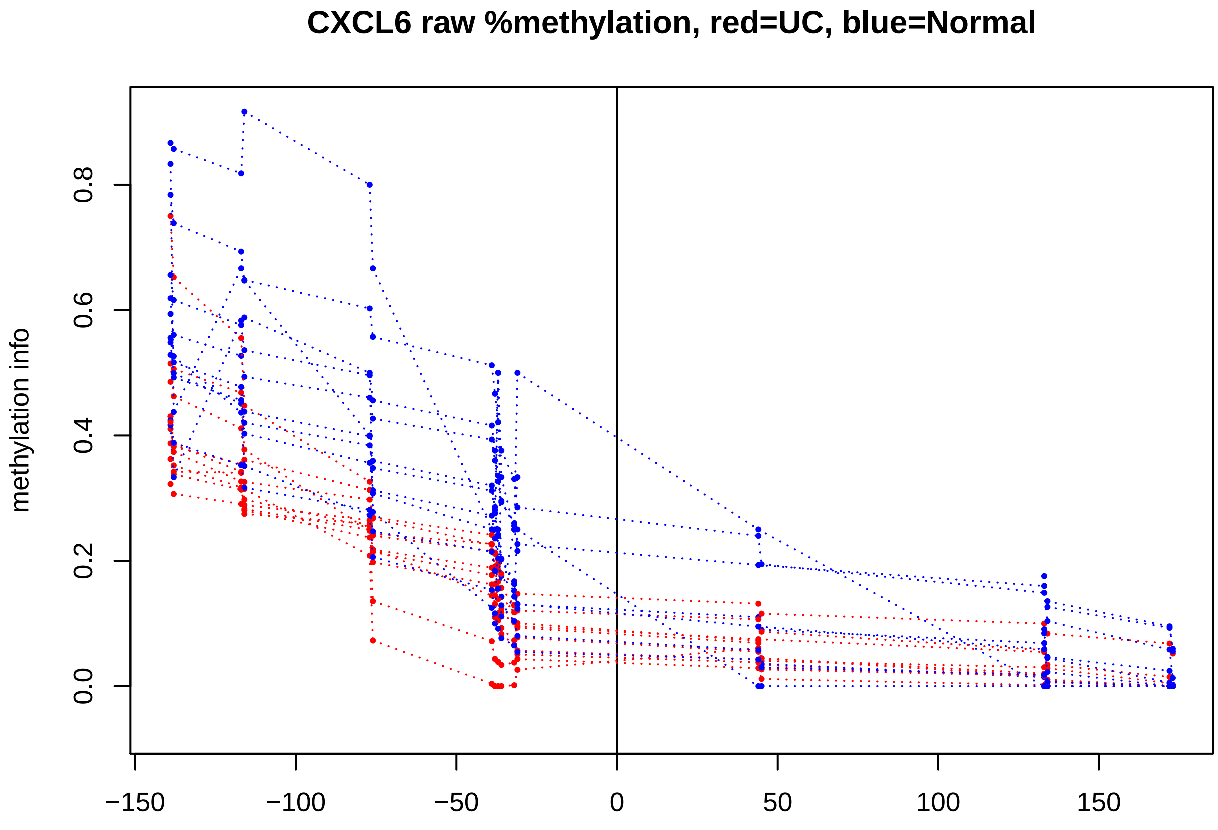
CXCL5 raw %methylation, red=UC, blue=Normal

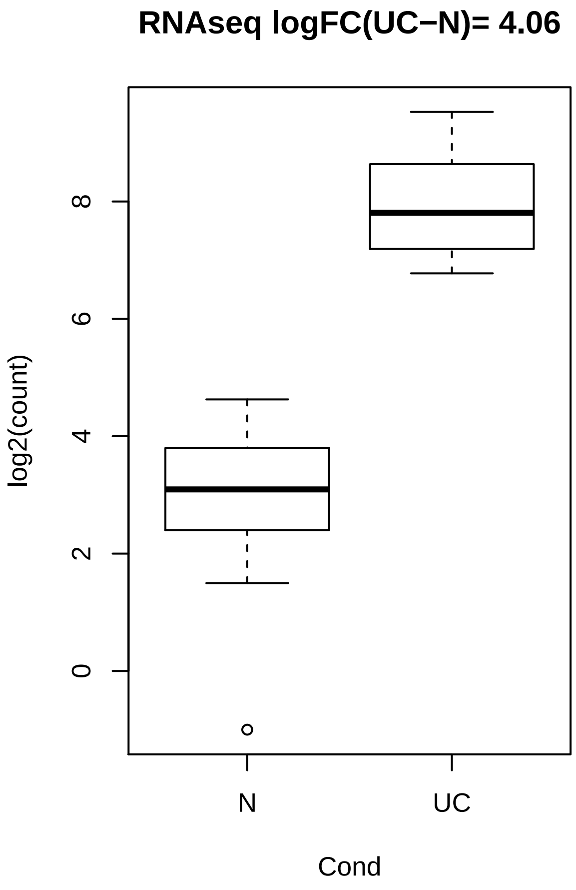


RNAseq logFC(UC−N)= 4.63

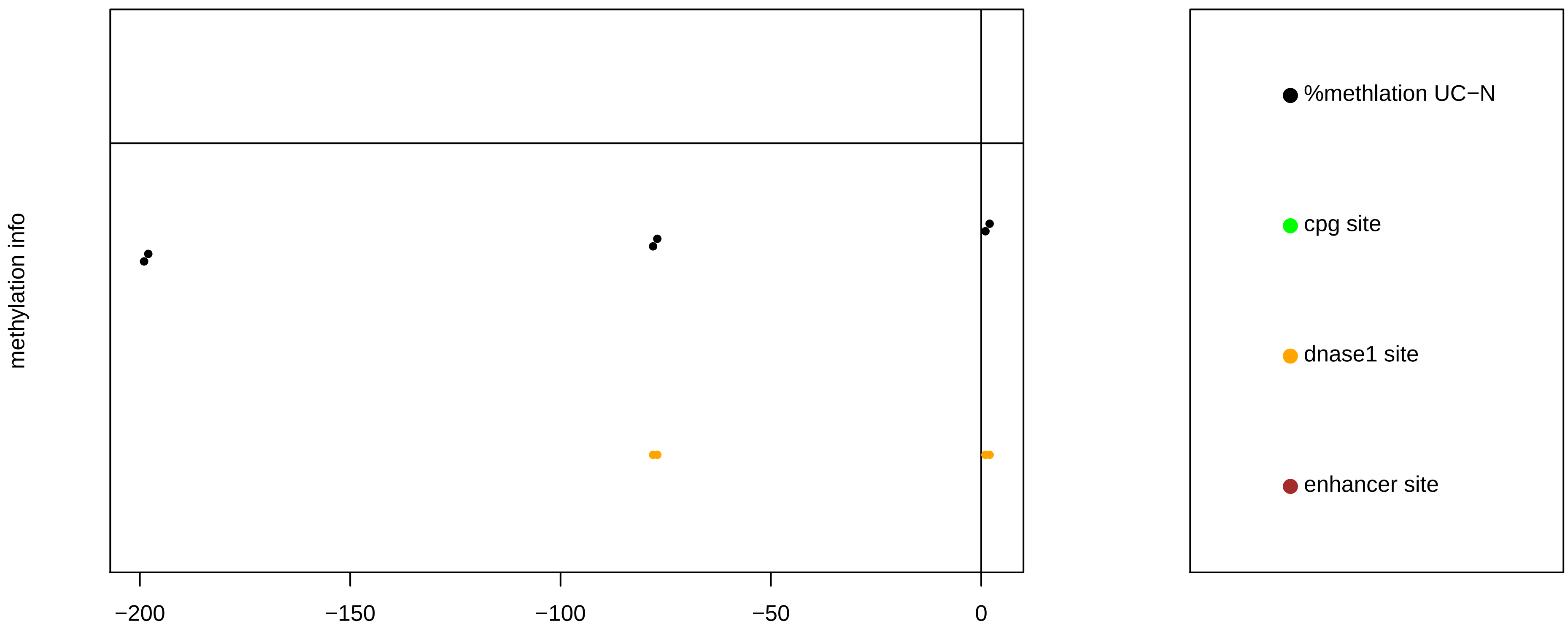



CXCL6 average UC−N %methylation max=−1.07% min=−19.16%

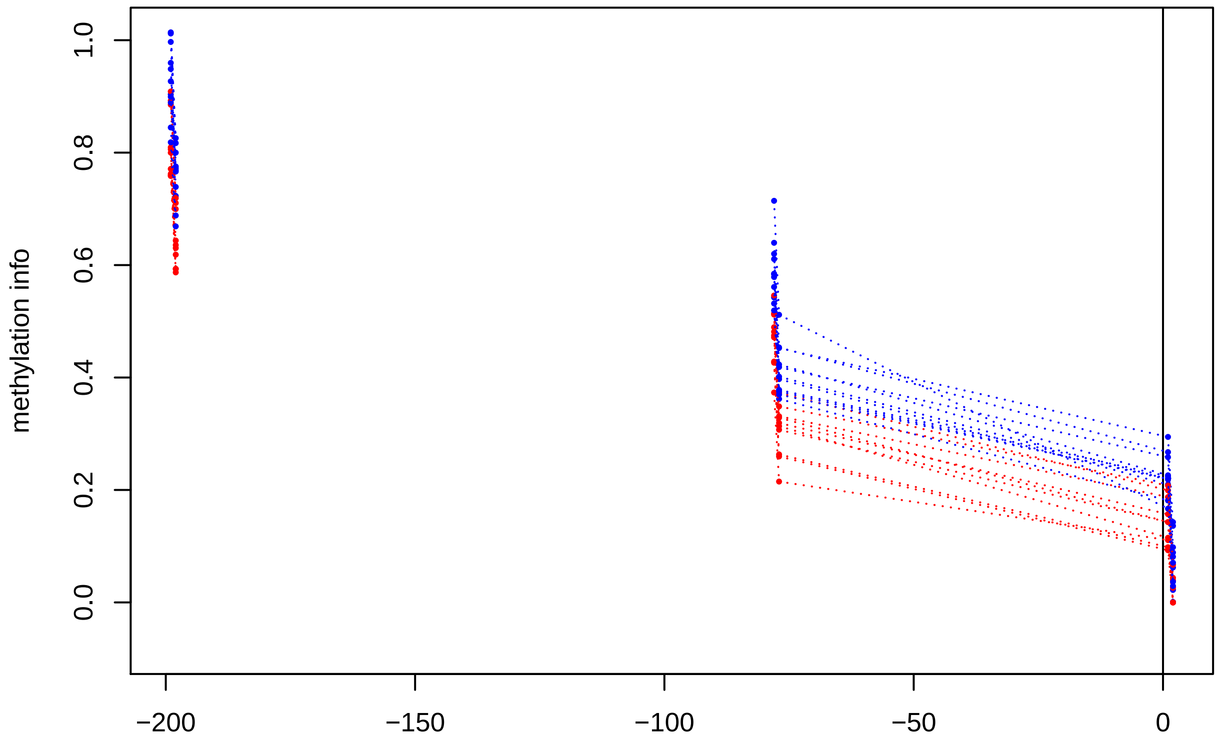

CXCL6 raw %methylation, red=UC, blue=Normal


RNAseq logFC(UC−N)= 4.06

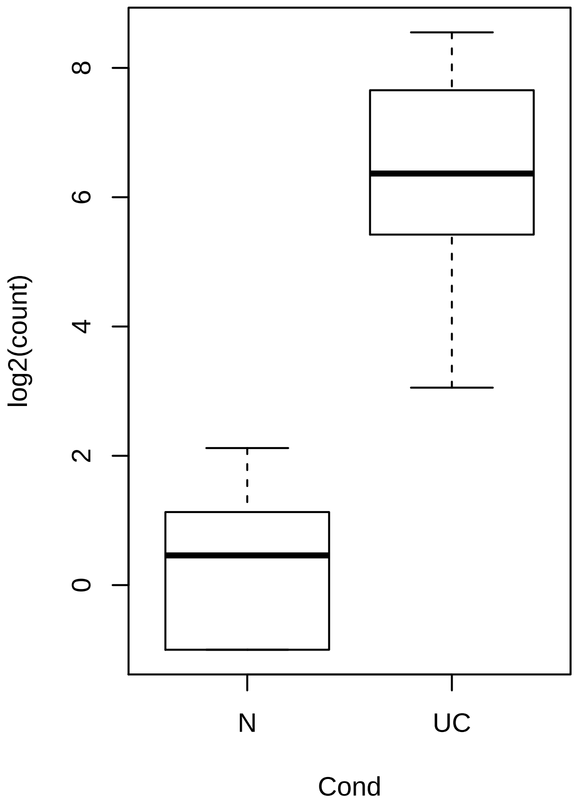
CXCR1 average UC−N %methylation max=−8.32% min=−12.22%

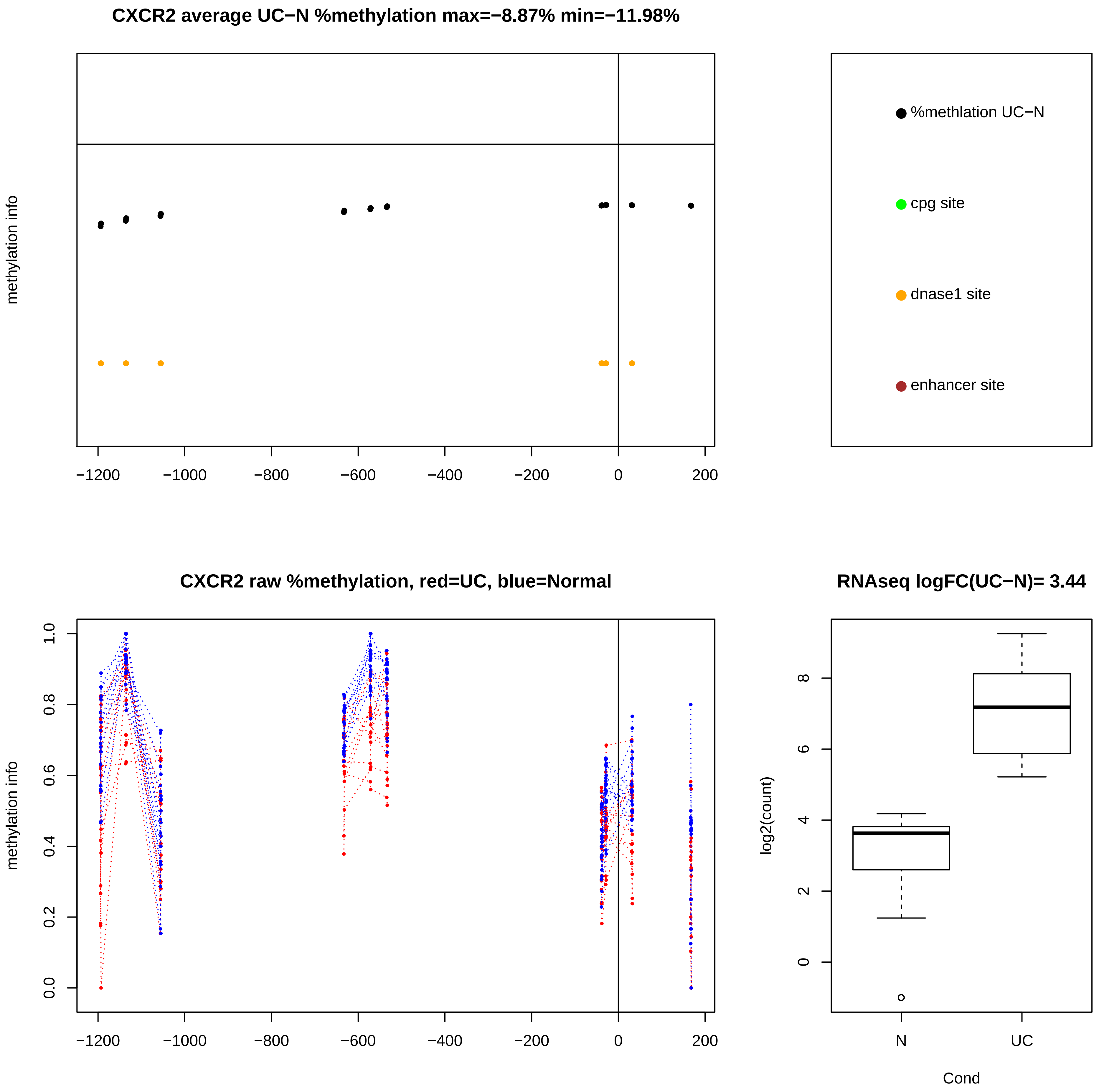


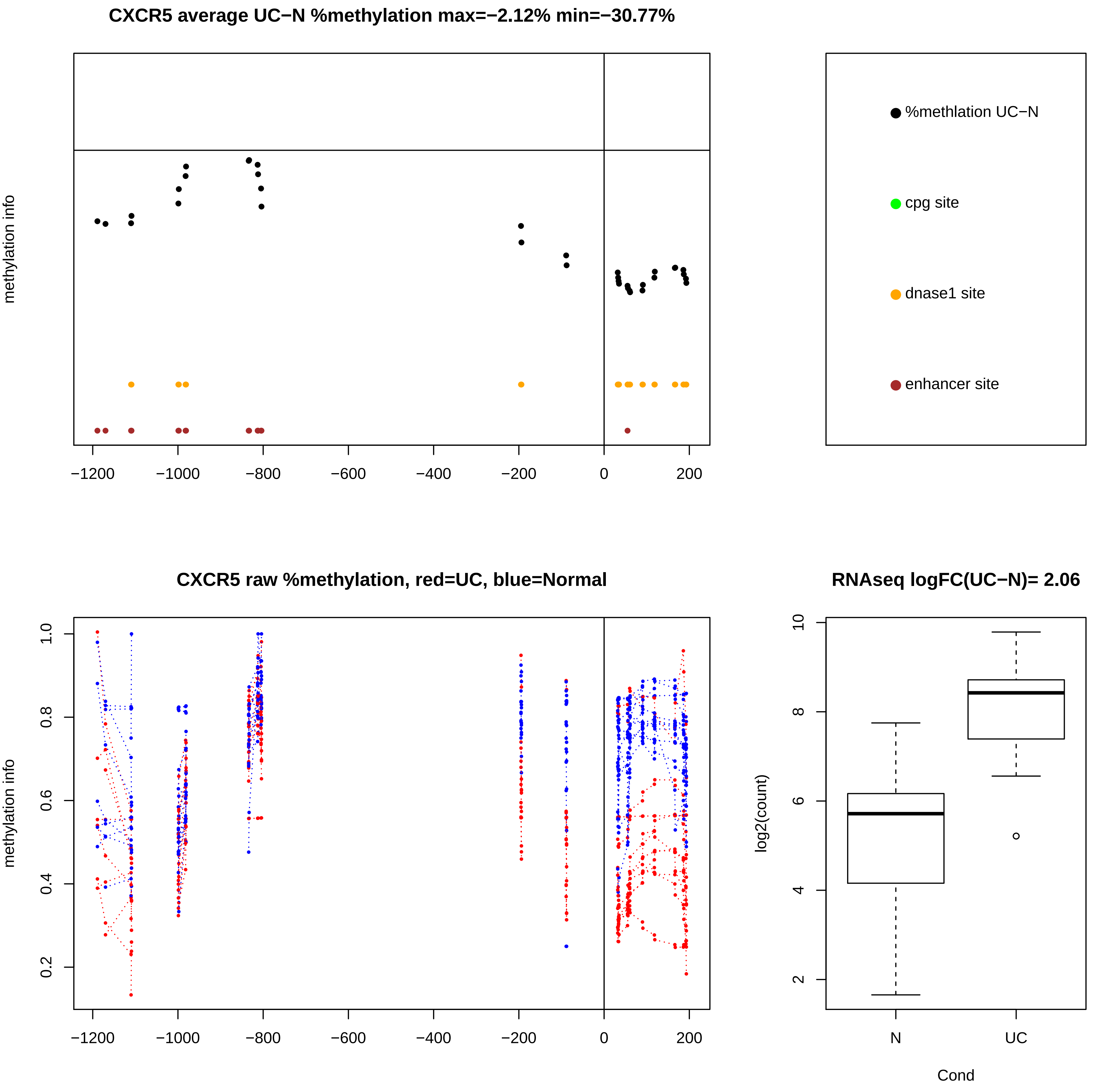
CXCR1 raw %methylation, red=UC, blue=Normal

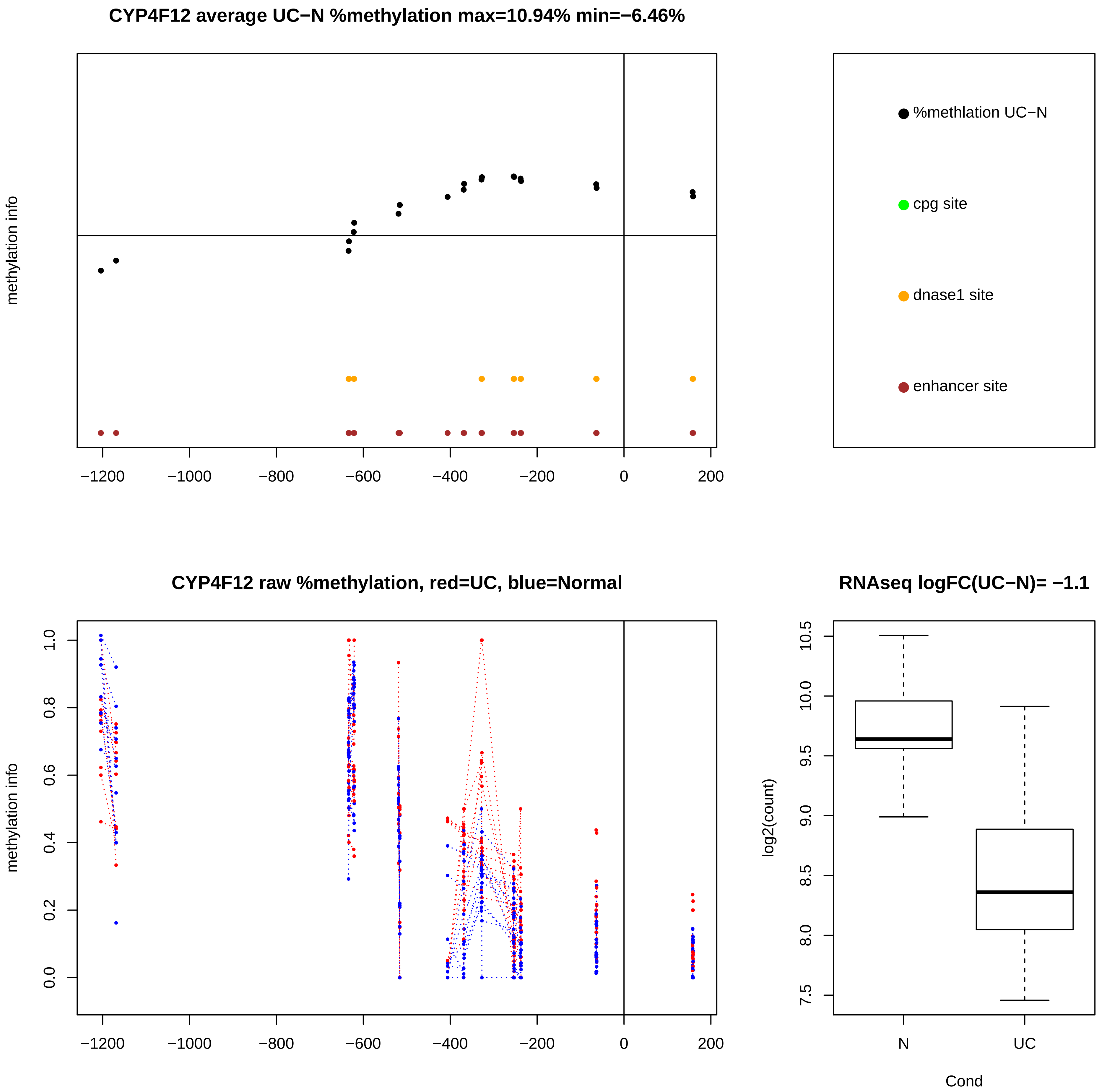


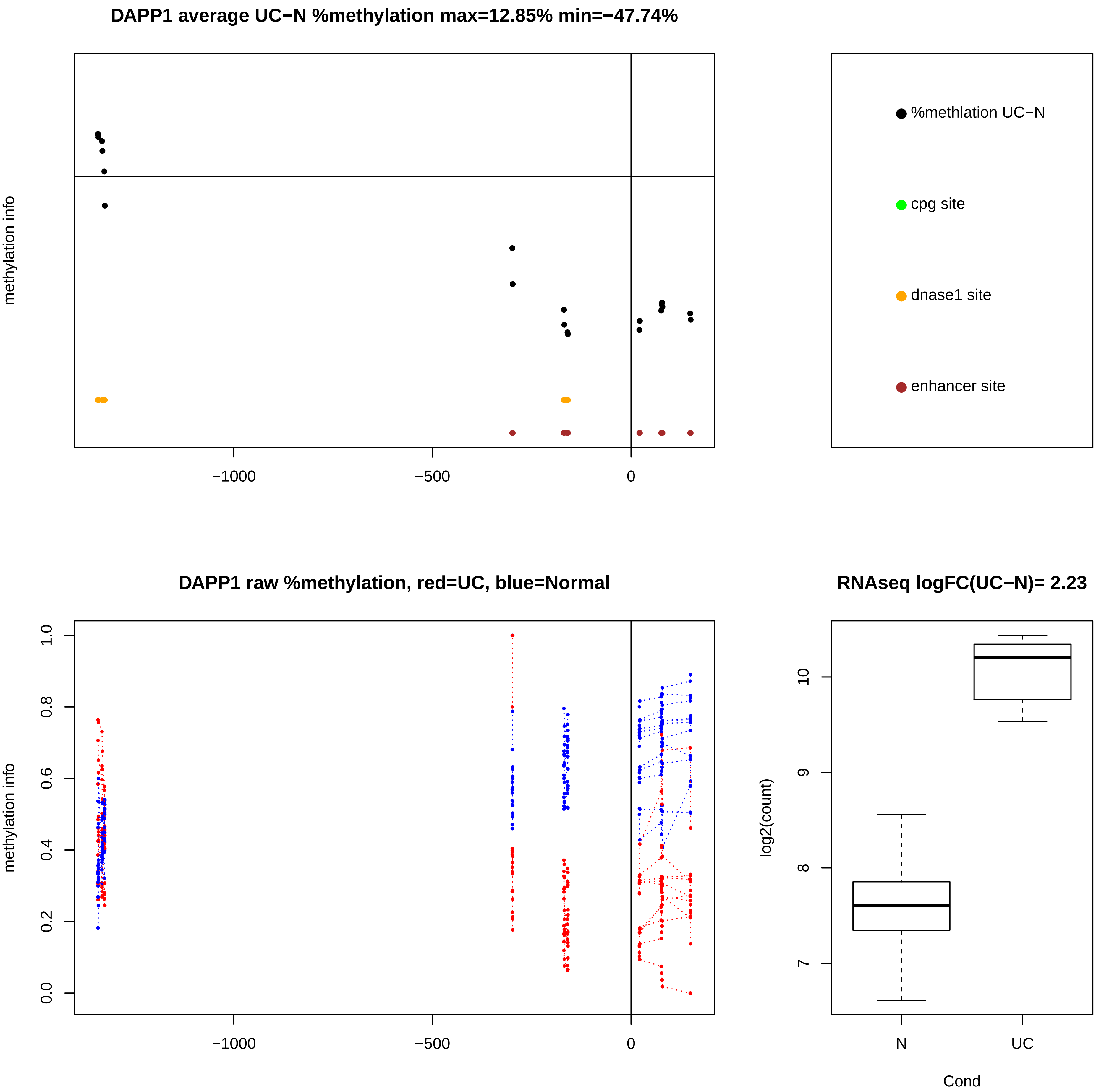
RNAseq logFC(UC−N)= 4.64




CXCR2 average UC−N %methylation max=−8.87% min=−11.98%
methylation info
−1200
−1000
−800
−600
−400
−200
0
200
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
CXCR2 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−1200
−1000
−800
−600
−400
−200
0
200
RNAseq logFC(UC−N)= 3.44
log2(count)
0
2
4
6
8
N
UC
Cond

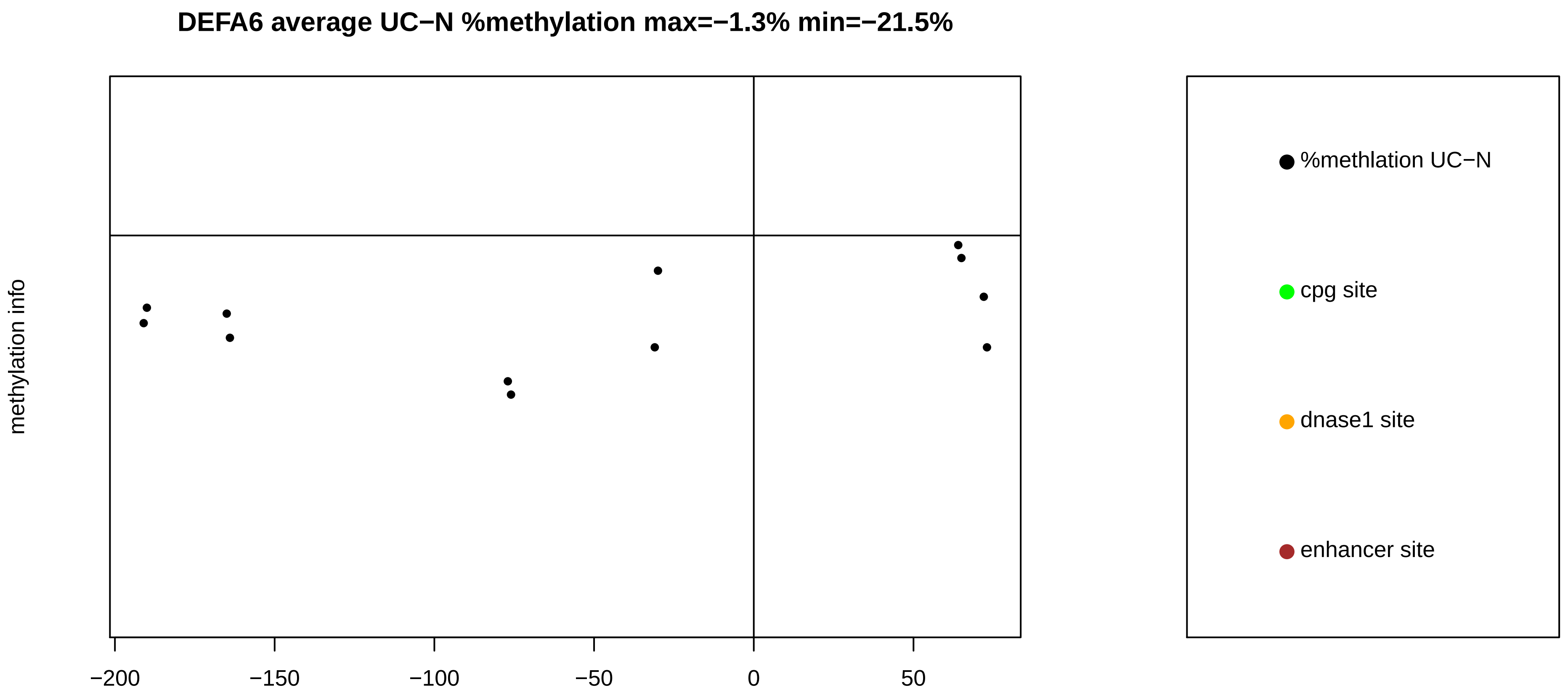

CXCR5 average UC−N %methylation max=−2.12% min=−30.77%
methylation info
−1200
−1000
−800
−600
−400
−200
0
200
%methlation UC−N
cpg site
dnase1 site
enhancer site
CXCR5 raw %methylation, red=UC, blue=Normal
methylation info
0.2
0.4
0.6
0.8
1.0
−1200
−1000
−800
−600
−400
−200
0
200
RNAseq logFC(UC−N)= 2.06
log2(count)
2
4
6
8
10
N
UC
Cond

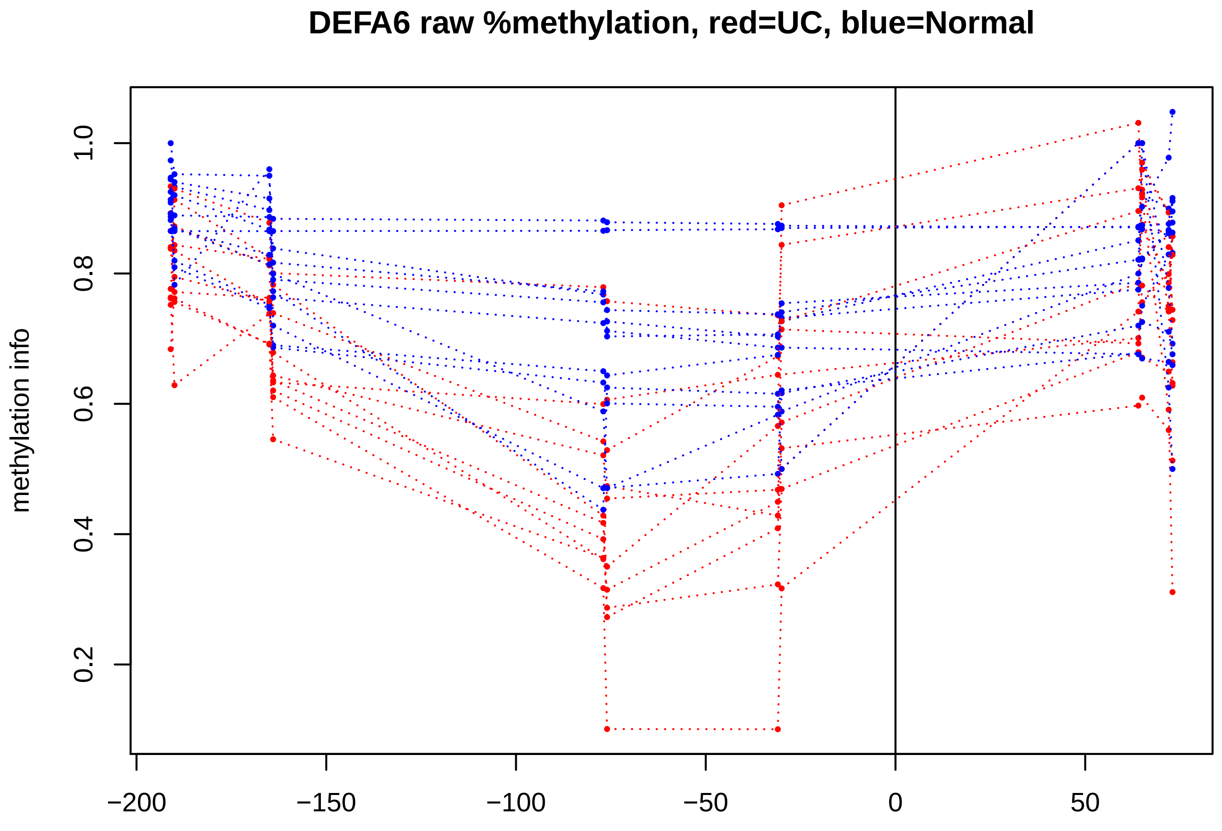

CYP4F12 average UC−N %methylation max=10.94% min=−6.46%
methylation info
−1200
−1000
−800
−600
−400
−200
0
200
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
CYP4F12 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−1200
−1000
−800
−600
−400
−200
0
200
RNAseq logFC(UC−N)= −1.1
log2(count)
7.5
8.0
8.5
9.0
9.5
10.0
10.5
N
UC
Cond

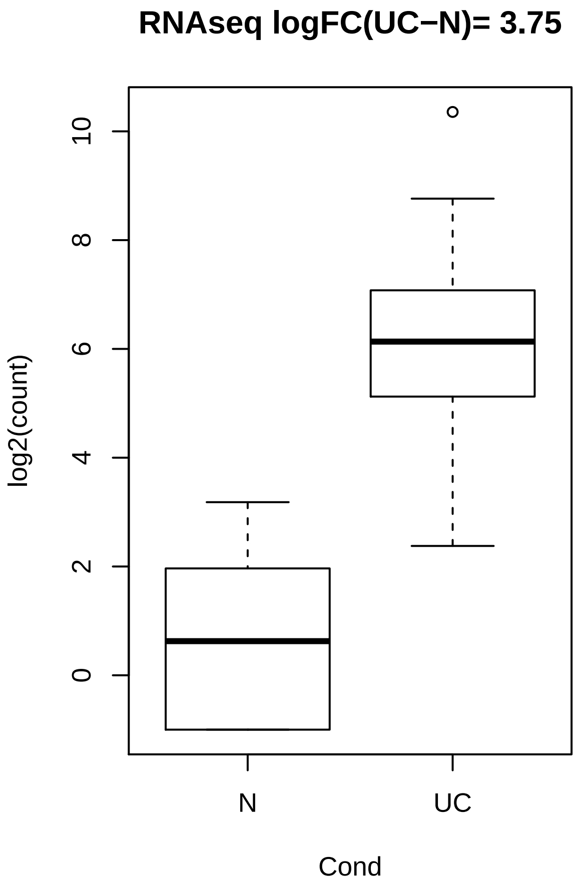

DAPP1 average UC−N %methylation max=12.85% min=−47.74%

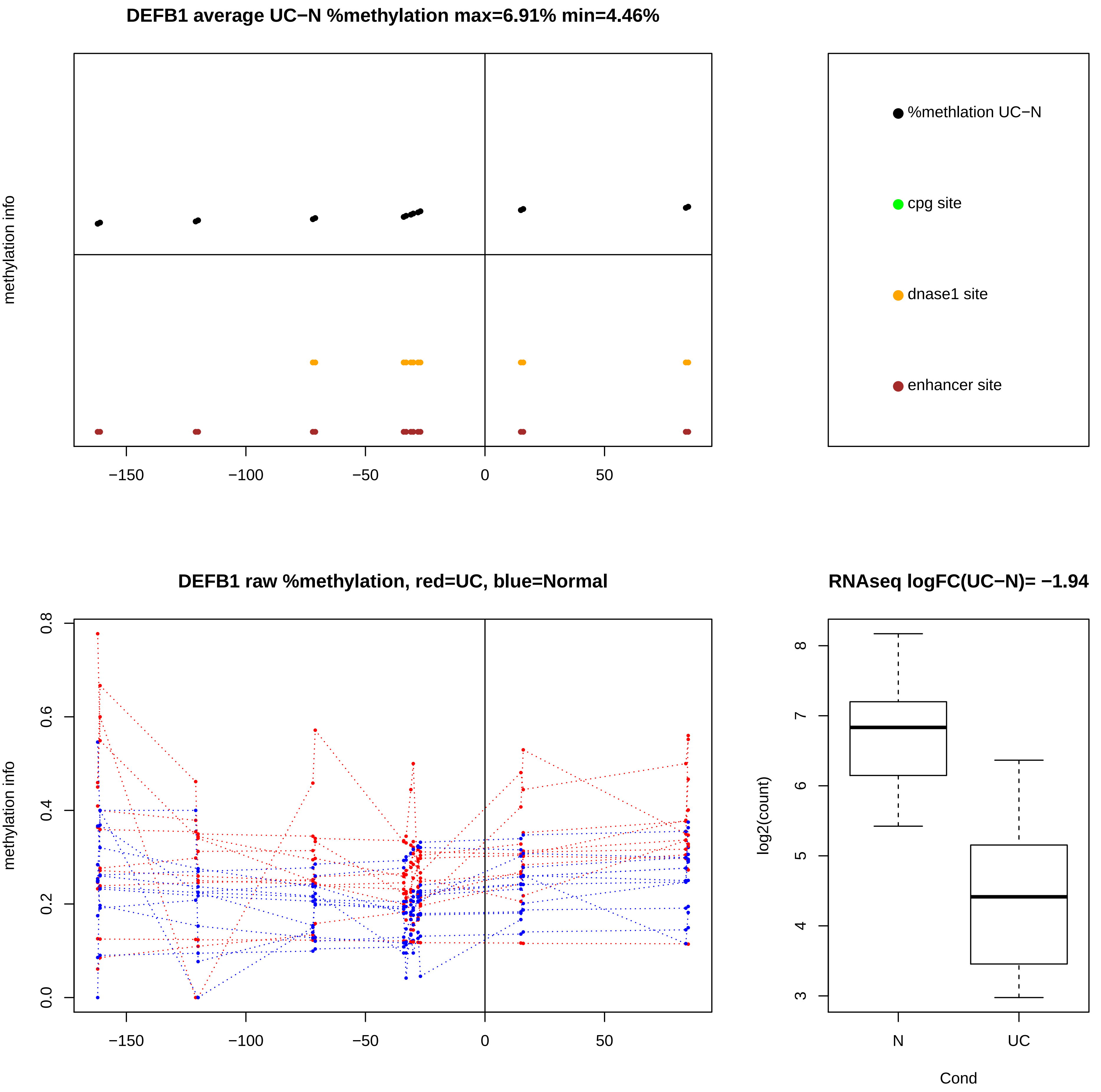
DAPP1 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 2.23


DEFA6 average UC−N %methylation max=−1.3% min=−21.5%


DEFA6 raw %methylation, red=UC, blue=Normal

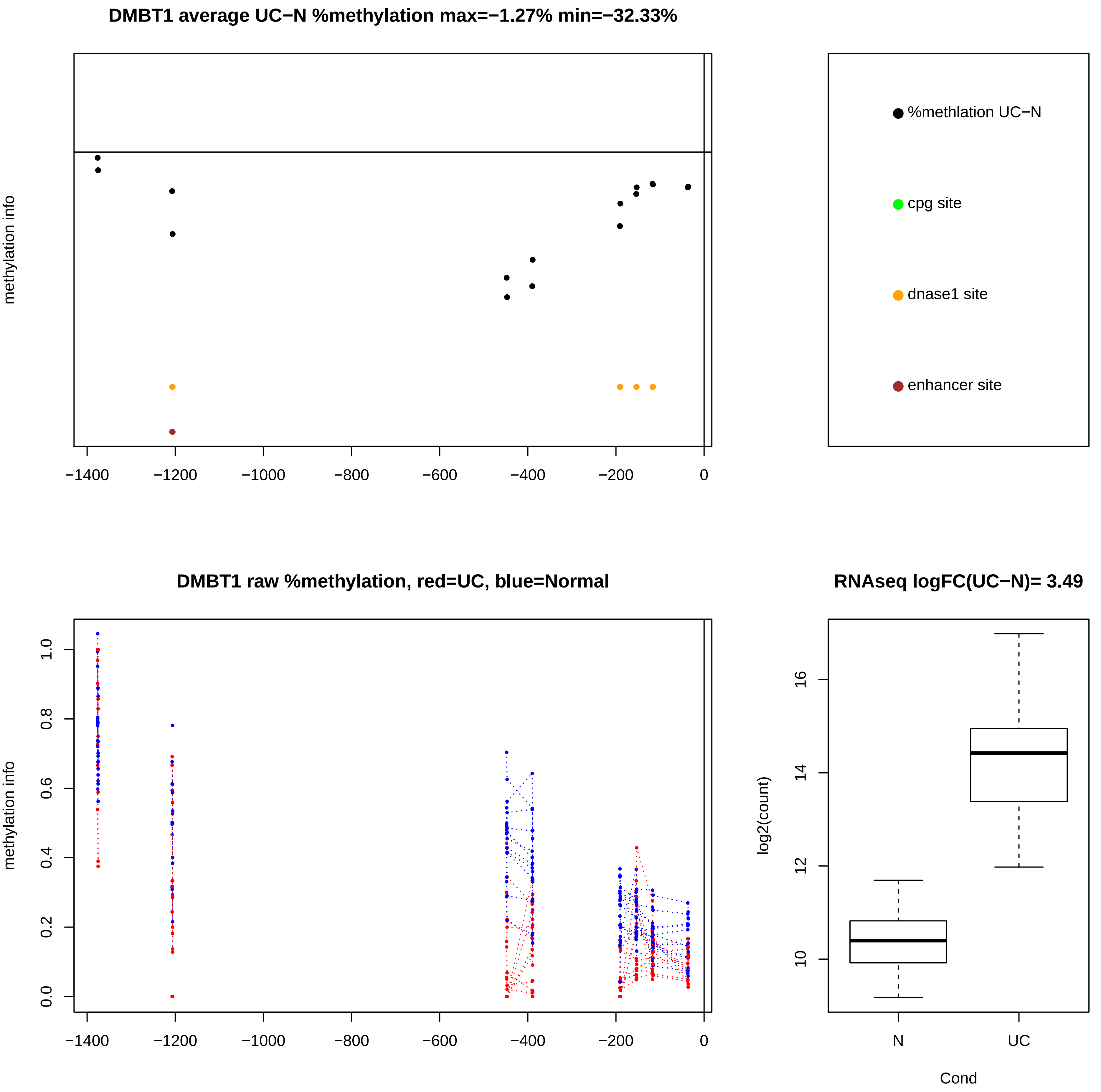

RNAseq logFC(UC−N)= 3.75



DEFB1 average UC−N %methylation max=6.91% min=4.46%

DEFB1 raw %methylation, red=UC, blue=Normal

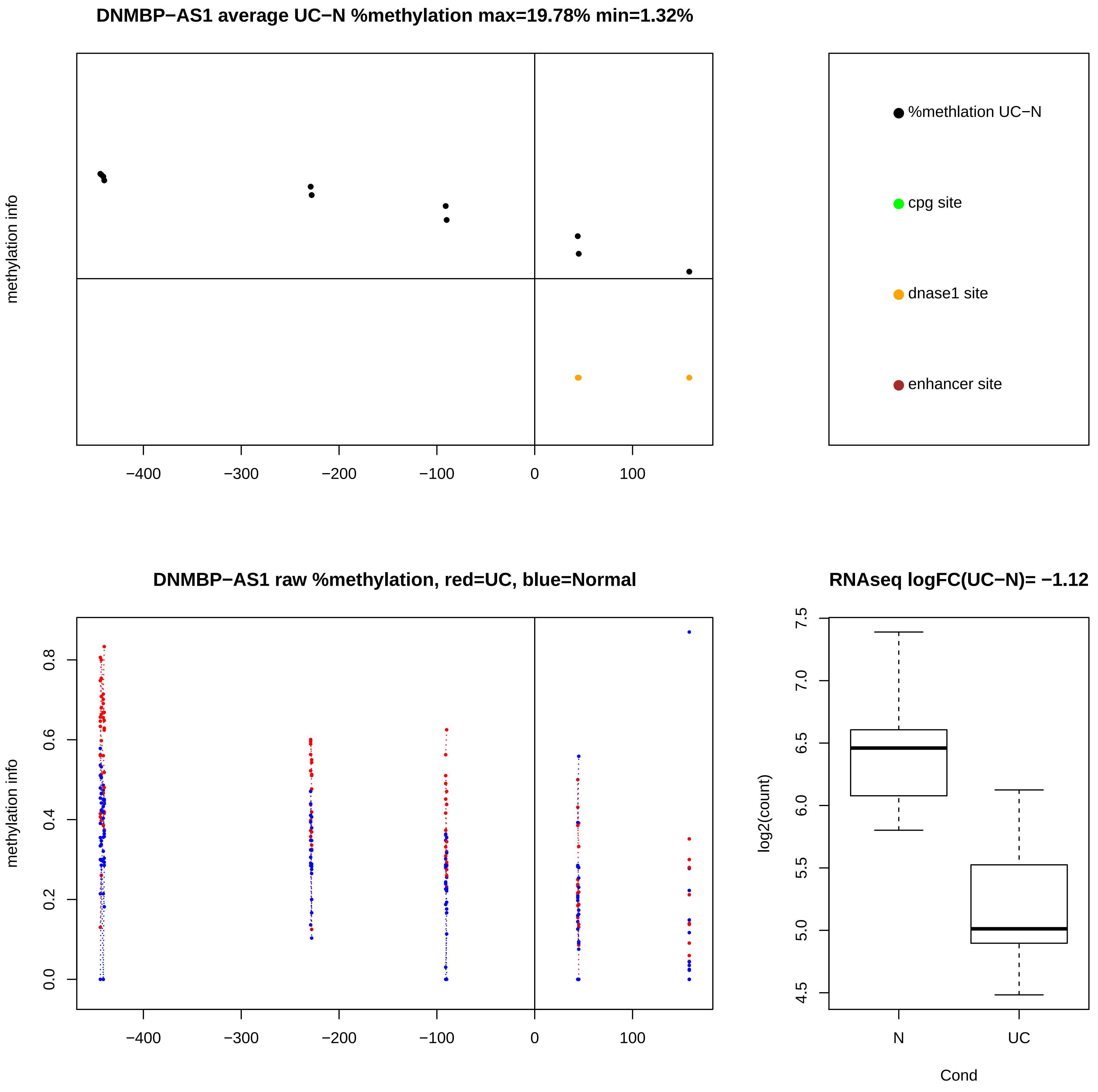
RNAseq logFC(UC−N)= −1.94



DMBT1 average UC−N %methylation max=−1.27% min=−32.33%

DMBT1 raw %methylation, red=UC, blue=Normal

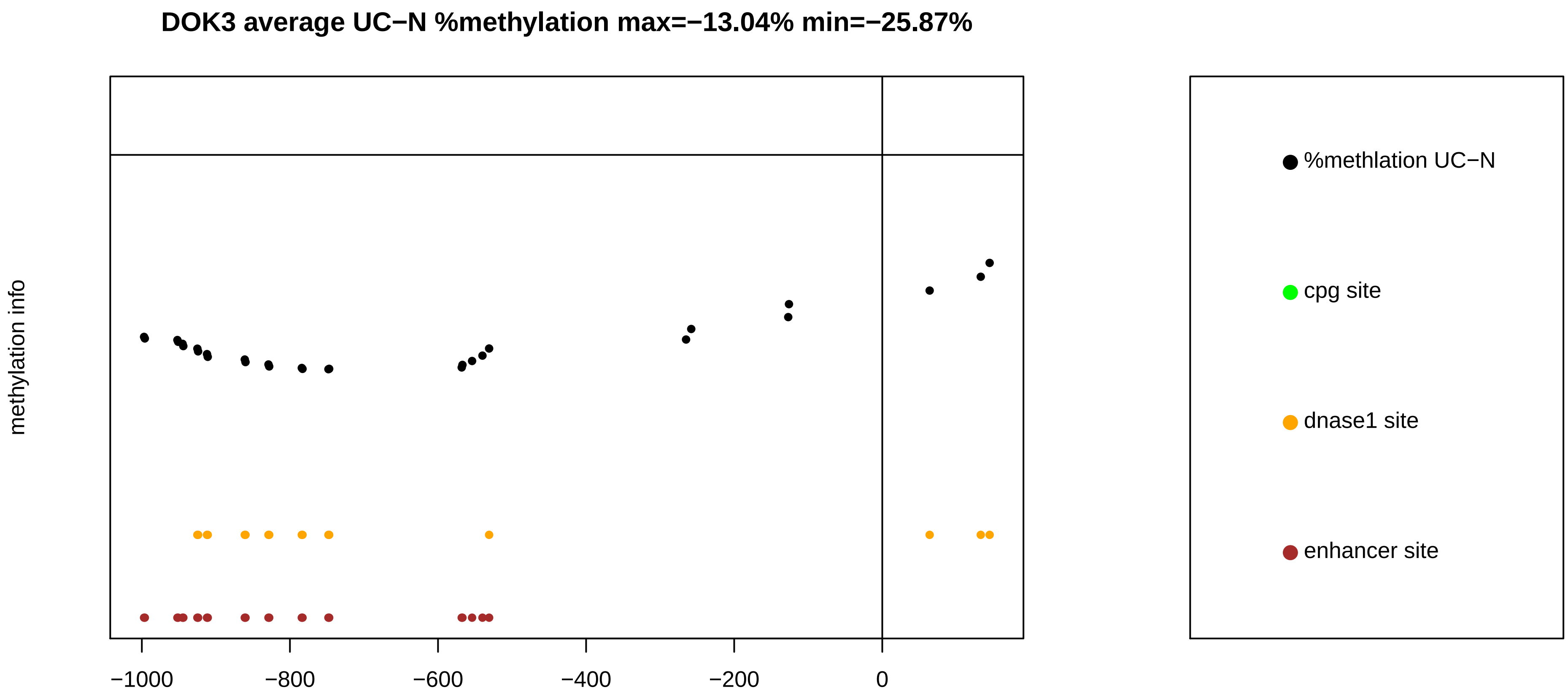
RNAseq logFC(UC−N)= 3.49



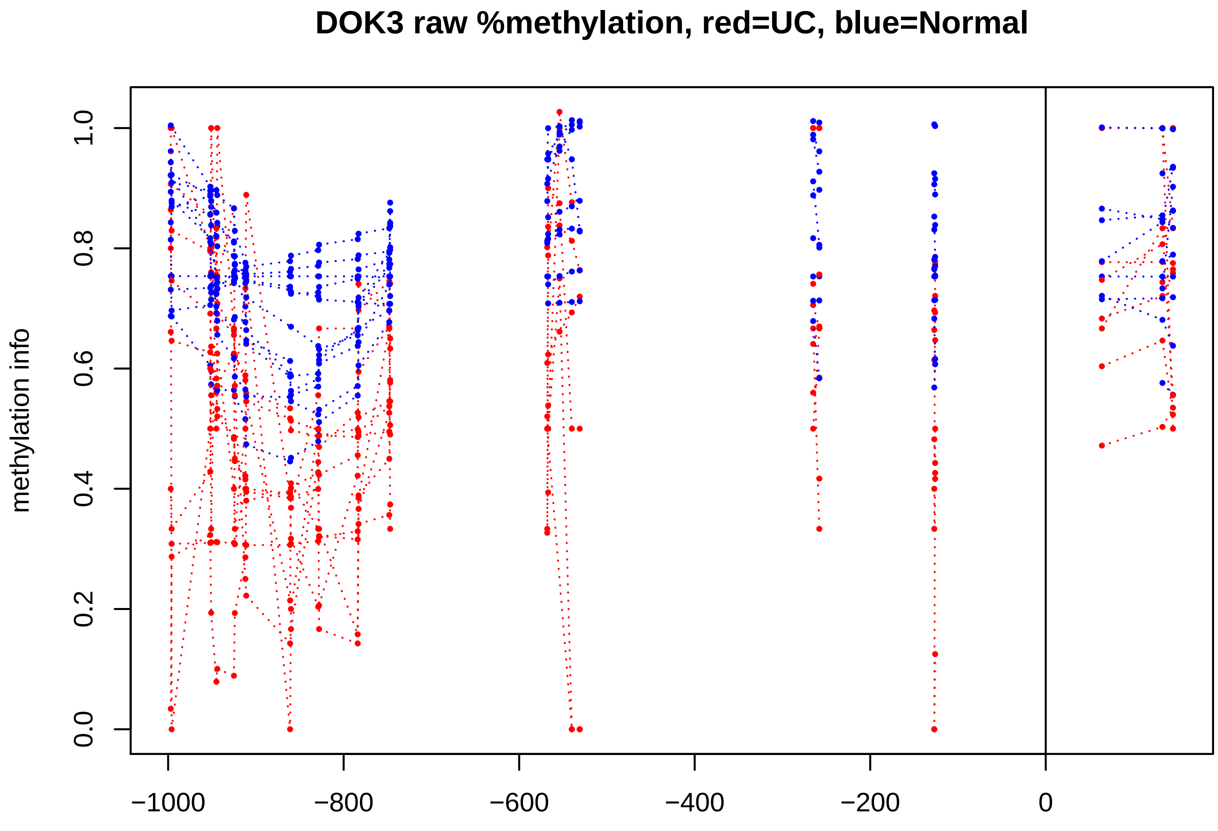
DNMBP−AS1 average UC−N %methylation max=19.78% min=1.32%

DNMBP−AS1 raw %methylation, red=UC, blue=Normal

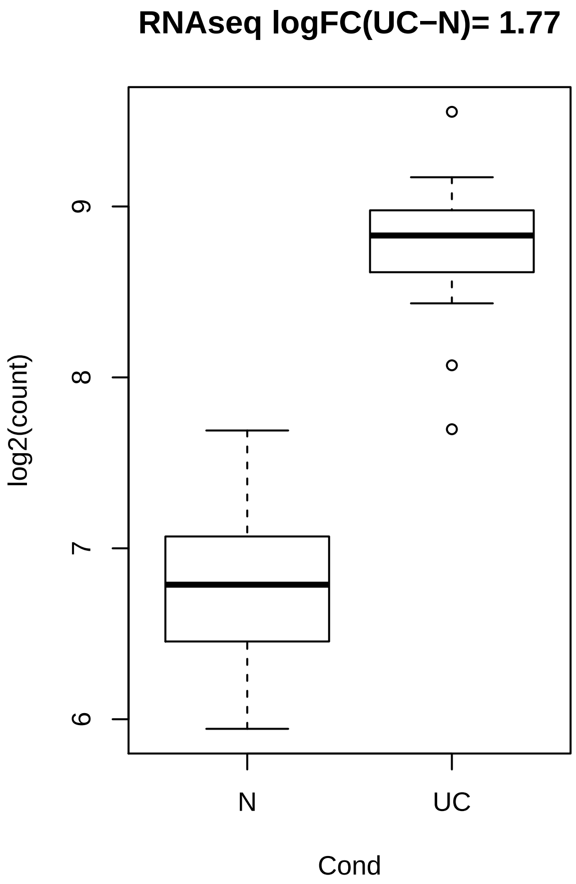
RNAseq logFC(UC−N)= −1.12



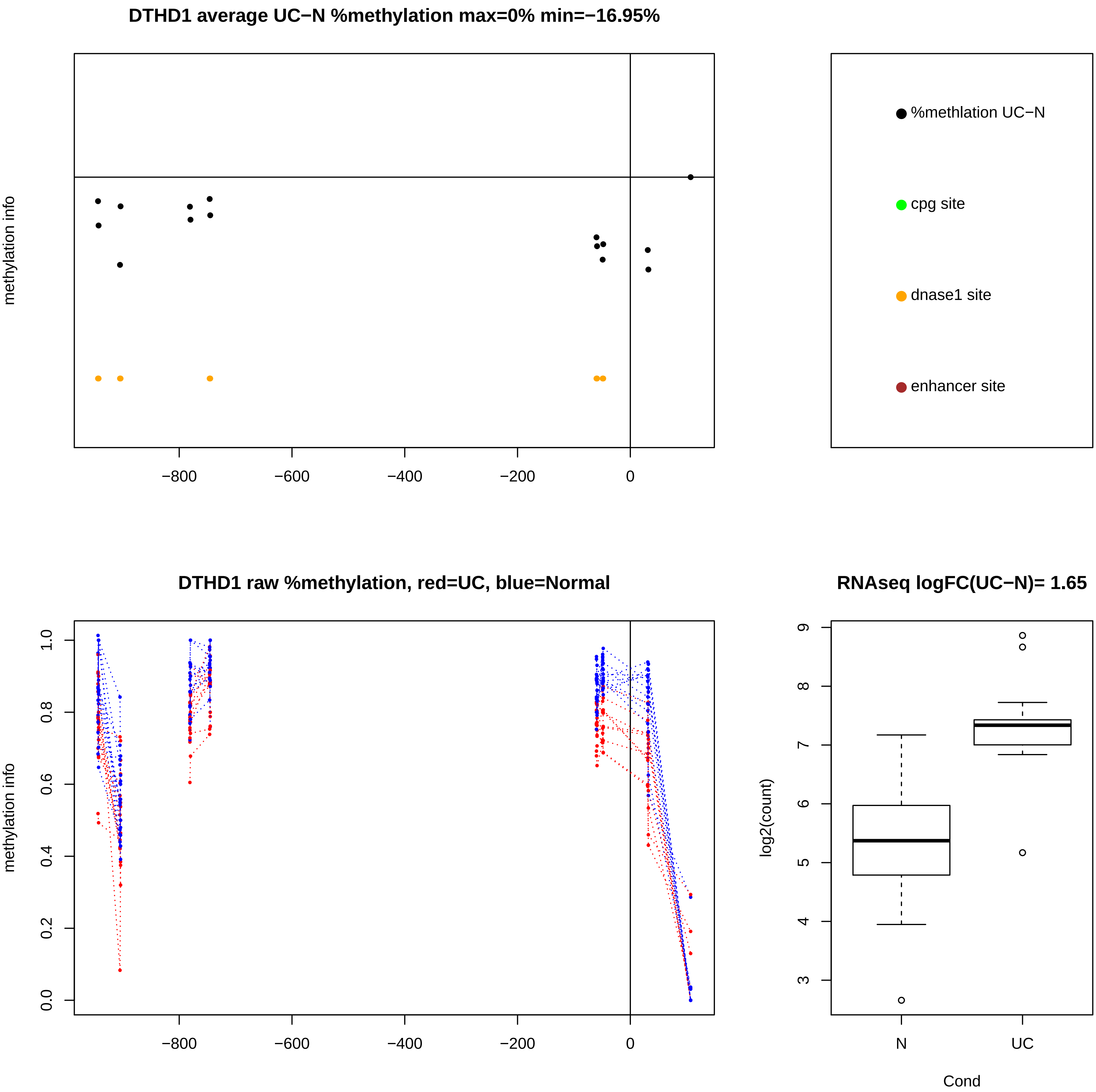
DOK3 average UC−N %methylation max=−13.04% min=−25.87%

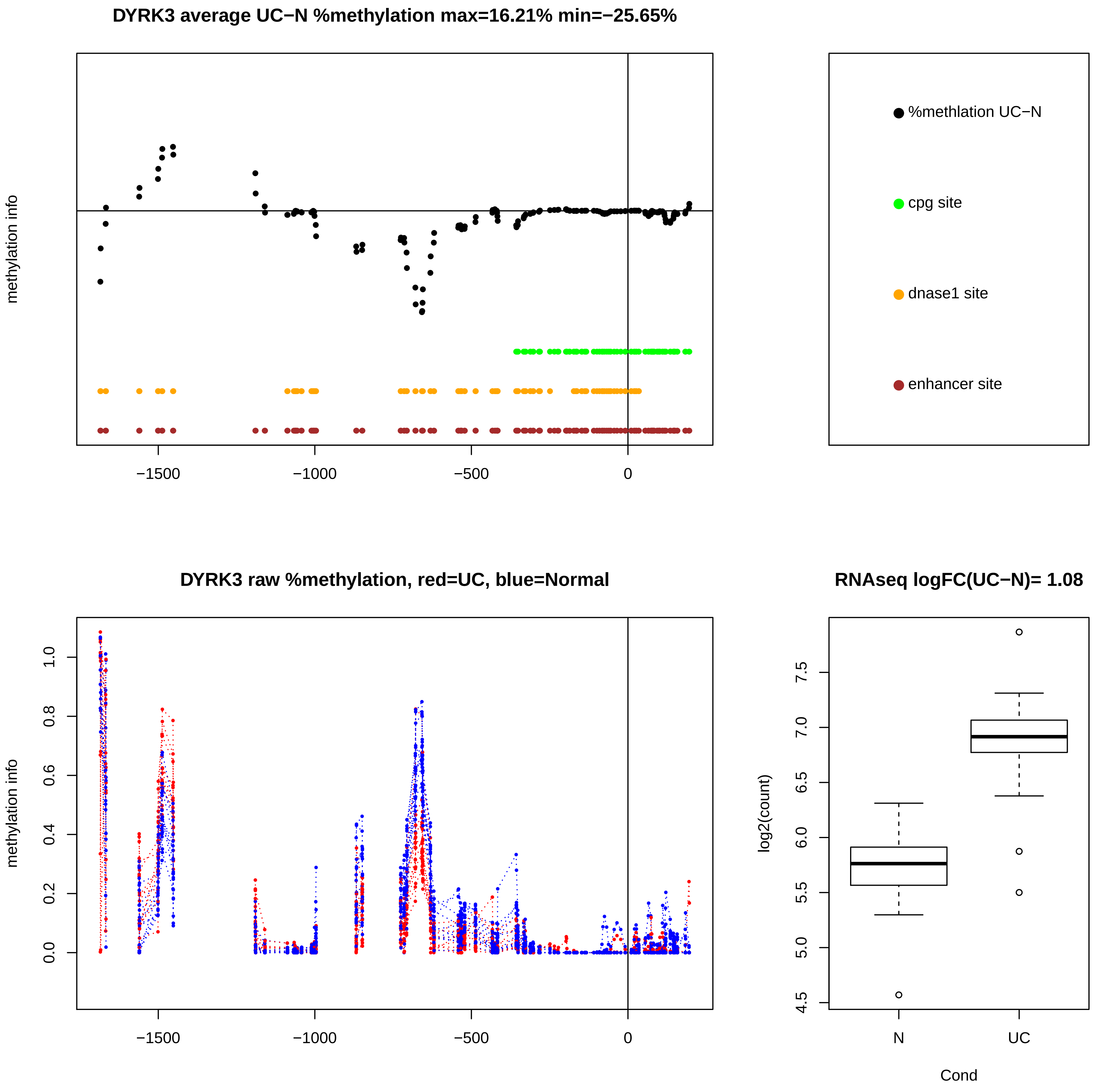


DOK3 raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 1.77

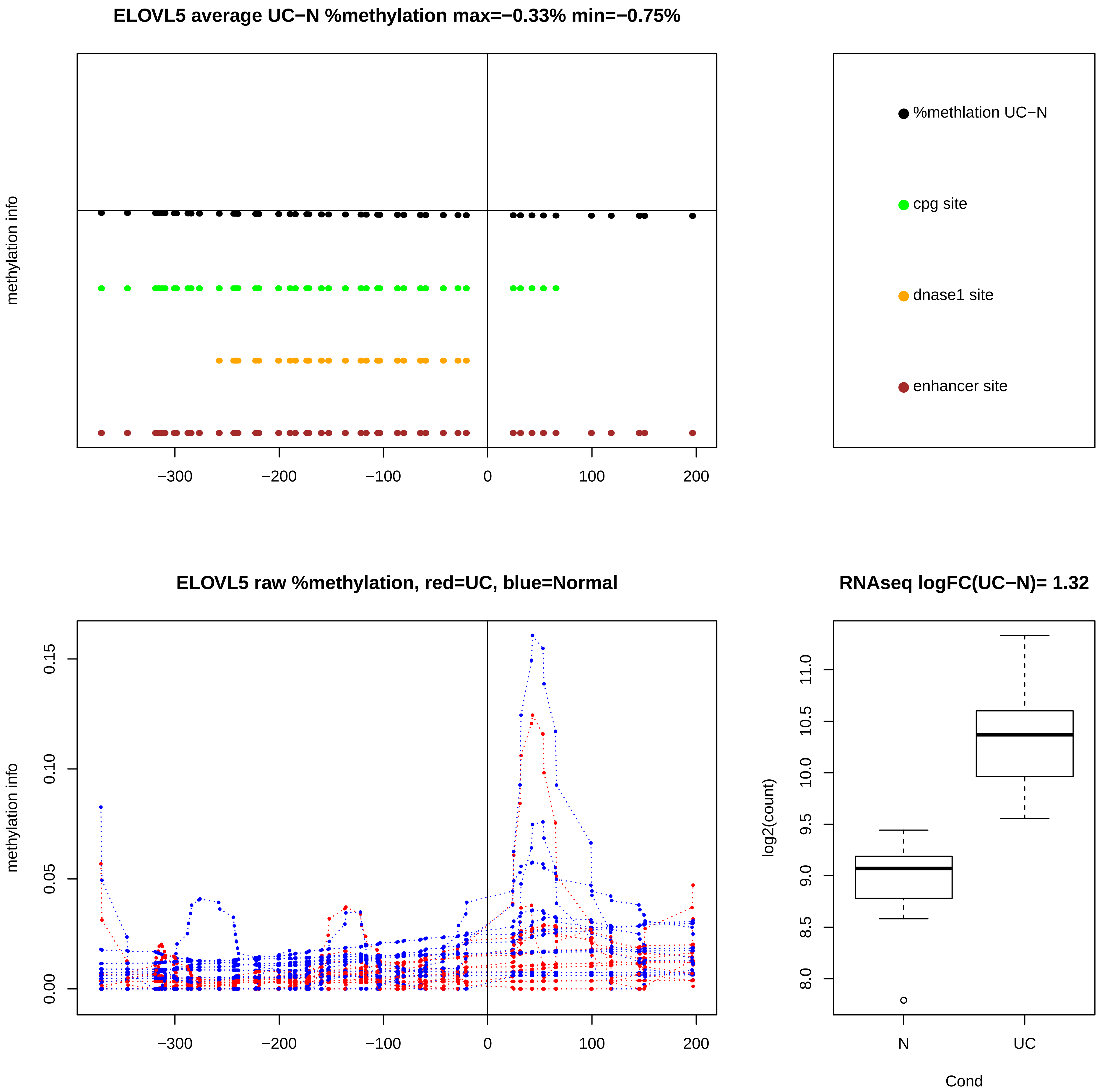

DTHD1 average UC−N %methylation max=0% min=−16.95%
methylation info
−800
−600
−400
−200
0
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
DTHD1 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−800
−600
−400
−200
0
RNAseq logFC(UC−N)= 1.65
log2(count)
3
4
5
6
7
8
9
N
UC
Cond

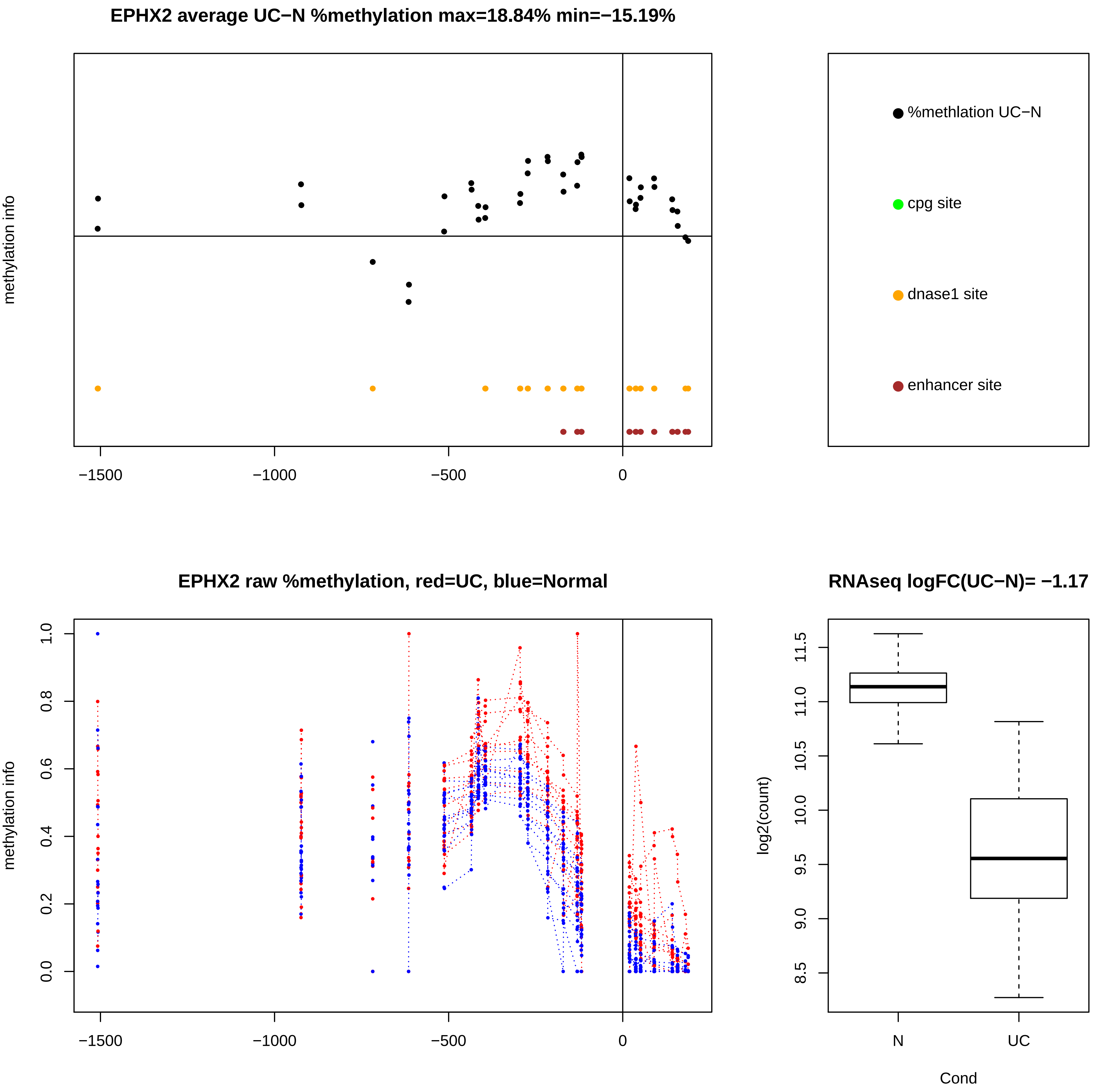


DYRK3 average UC−N %methylation max=16.21% min=−25.65%

DYRK3 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.08

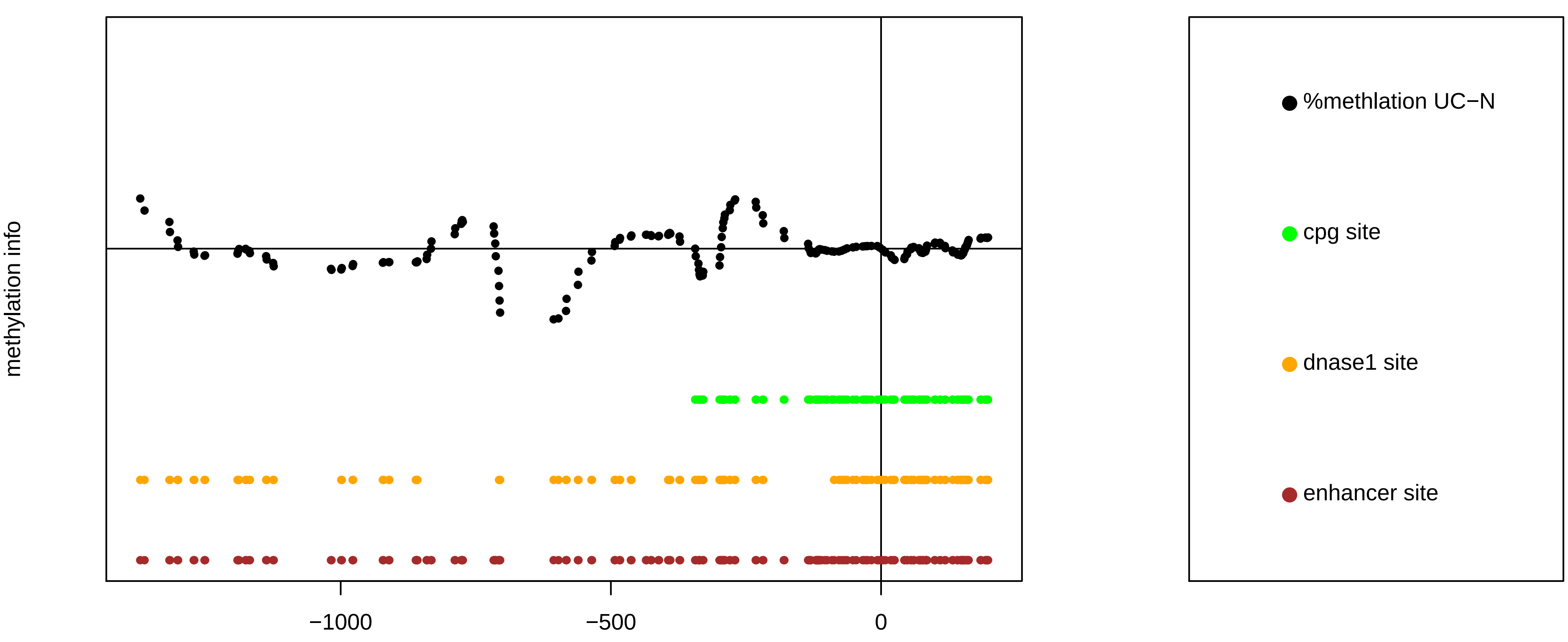

ELOVL5 average UC−N %methylation max=−0.33% min=−0.75%
methylation info
−300
−200
−100
0
100
200
%methlation UC−N
cpg site
dnase1 site
enhancer site
ELOVL5 raw %methylation, red=UC, blue=Normal
methylation info
0.00
0.05
0.10
0.15
−300
−200
−100
0
100
200
RNAseq logFC(UC−N)= 1.32
log2(count)
8.0
8.5
9.0
9.5
10.0
10.5
11.0
N
UC
Cond

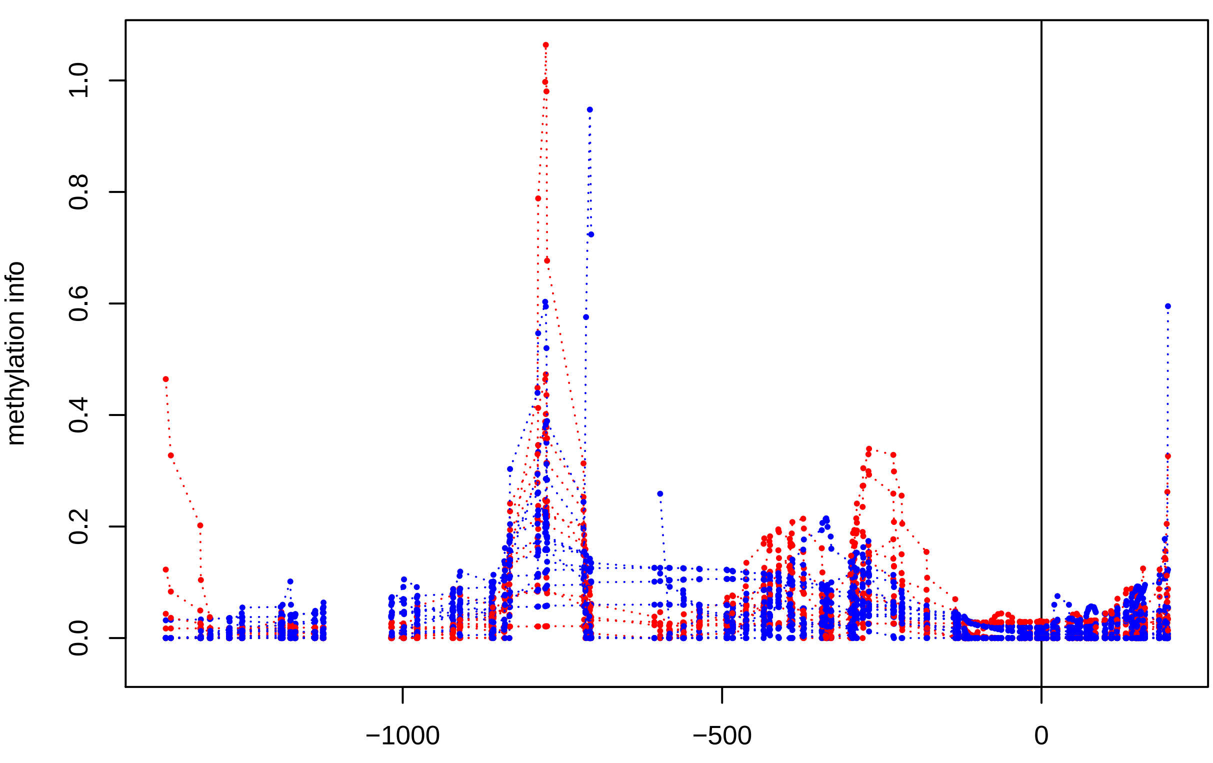


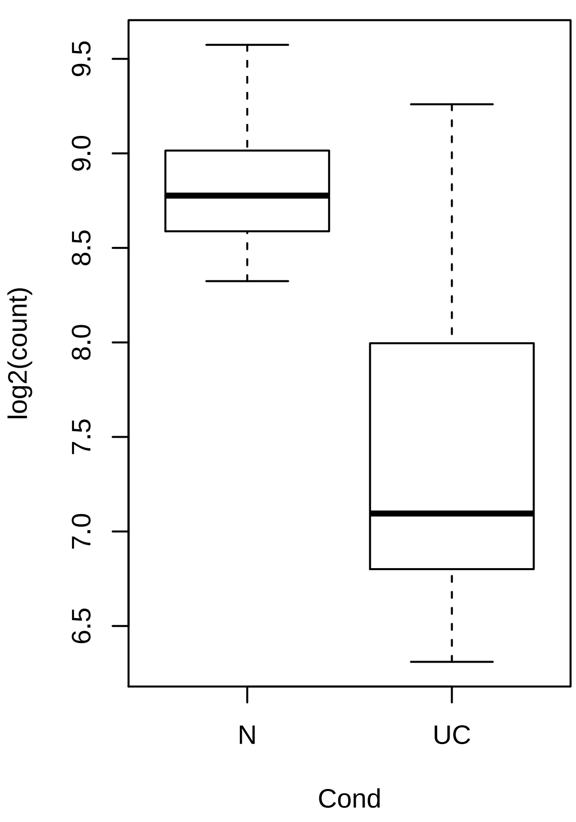
EPHX2 average UC−N %methylation max=18.84% min=−15.19%

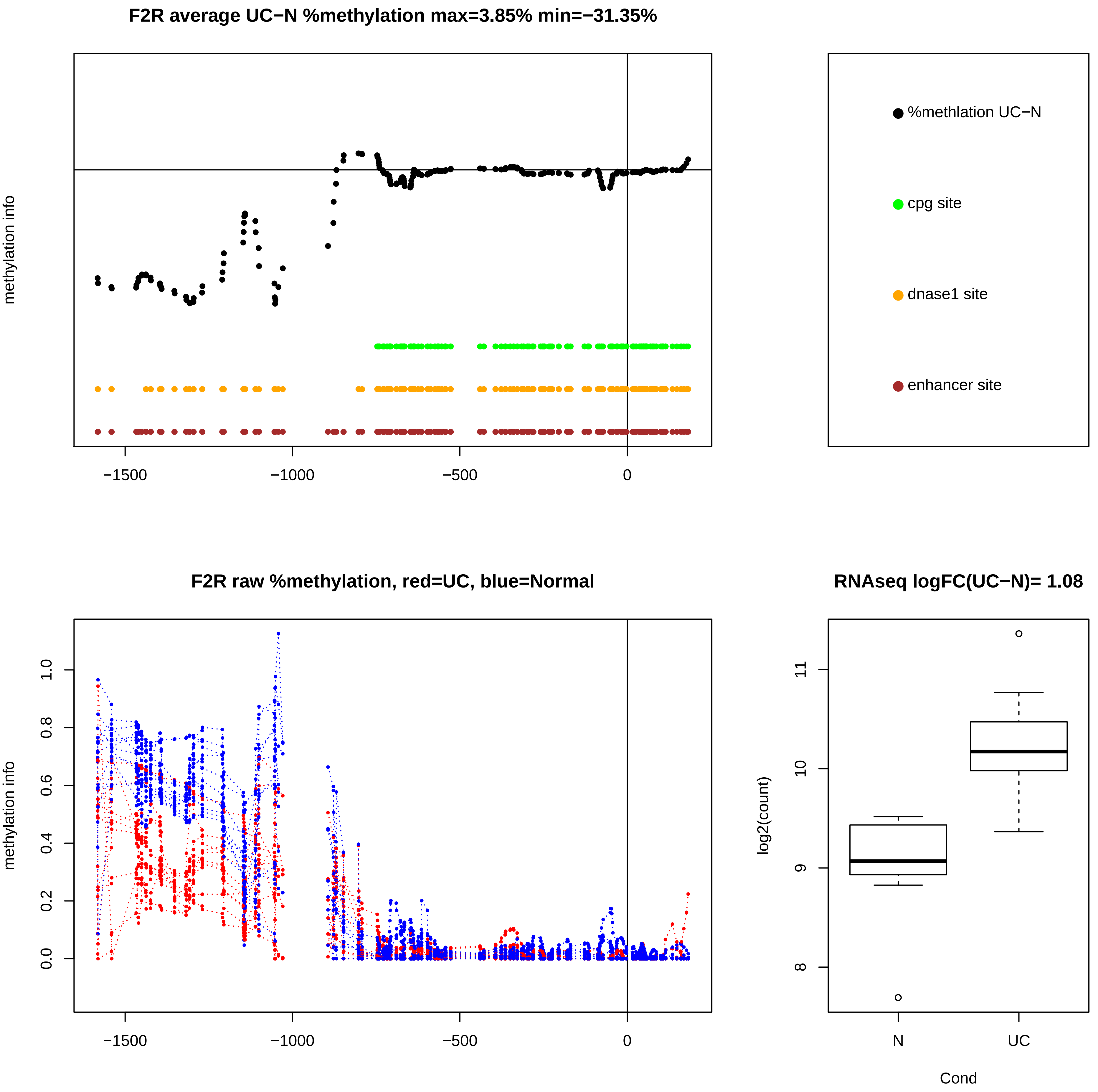
EPHX2 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= −1.17

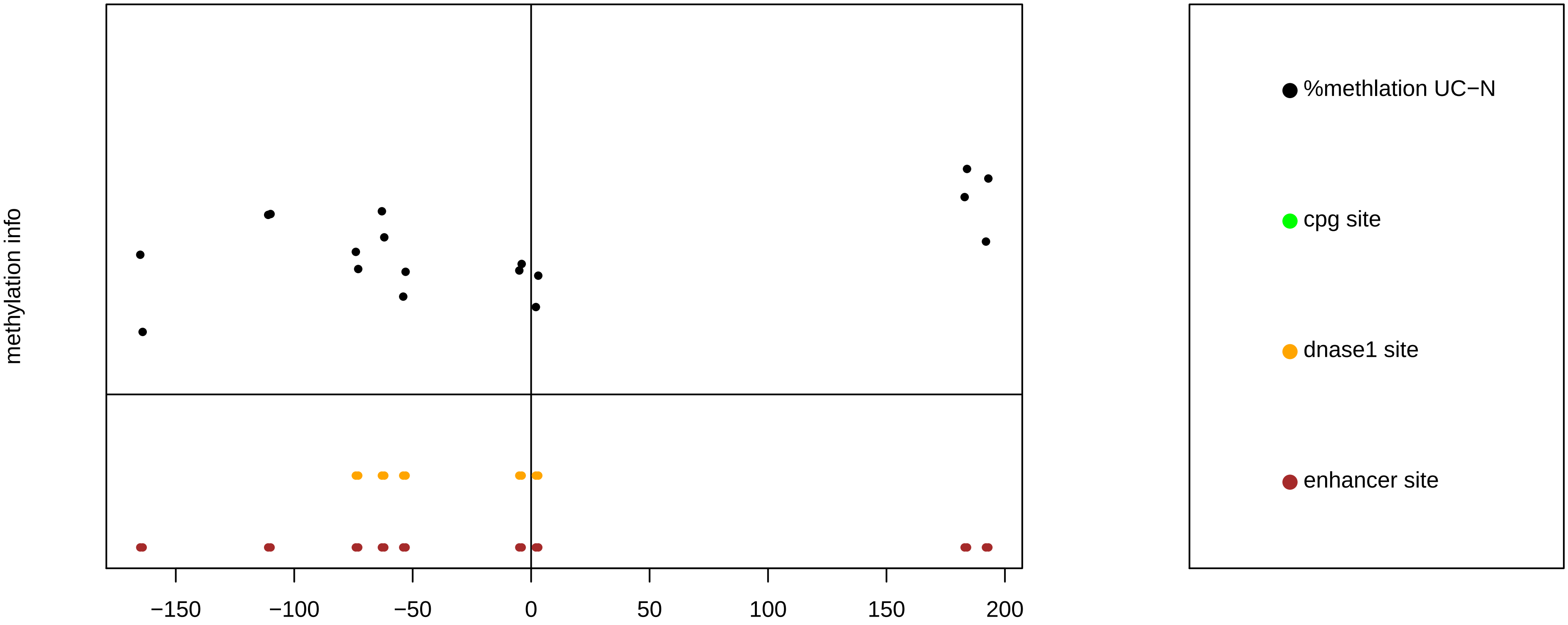

ESPN average UC−N %methylation max=6.25% min=−8.81%


ESPN raw %methylation, red=UC, blue=Normal

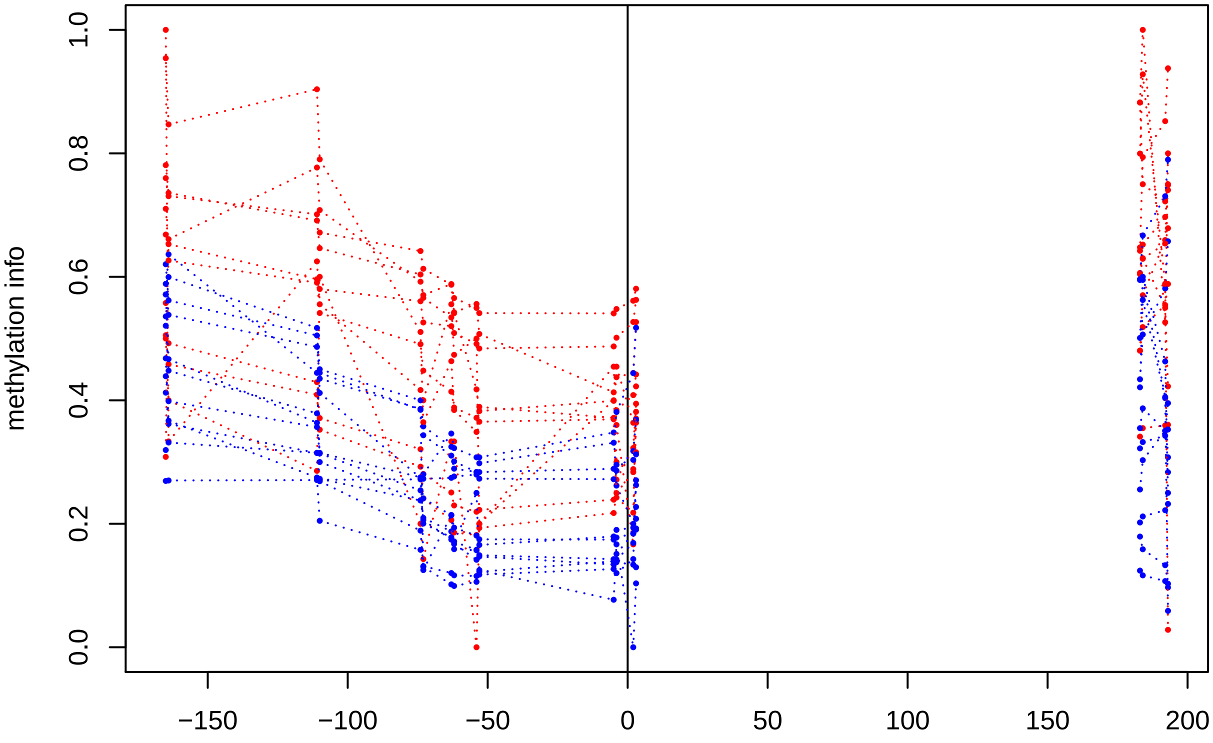

RNAseq logFC(UC−N)= −1.07


F2R average UC−N %methylation max=3.85% min=−31.35%
methylation info
−1500
−1000
−500
0
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
F2R raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−1500
−1000
−500
0
RNAseq logFC(UC−N)= 1.08
log2(count)
8
9
10
11
N
UC
Cond

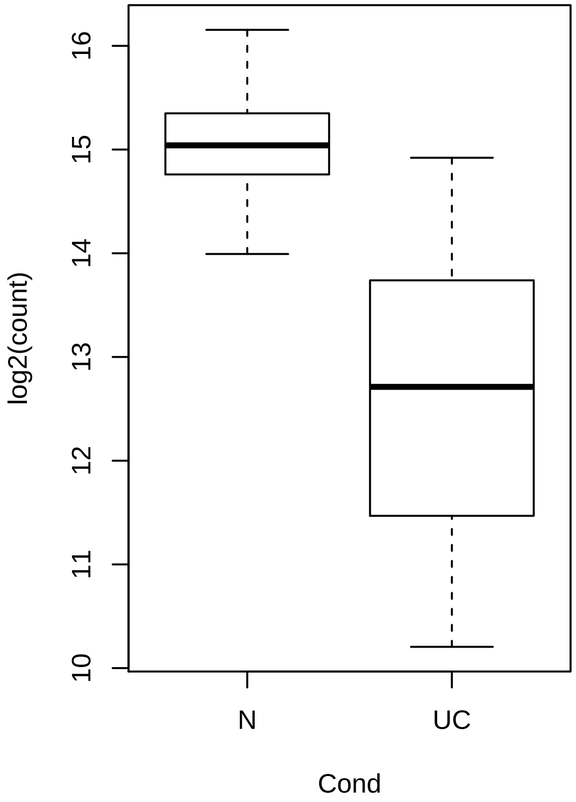
FABP1 average UC−N %methylation max=31.39% min=8.7%

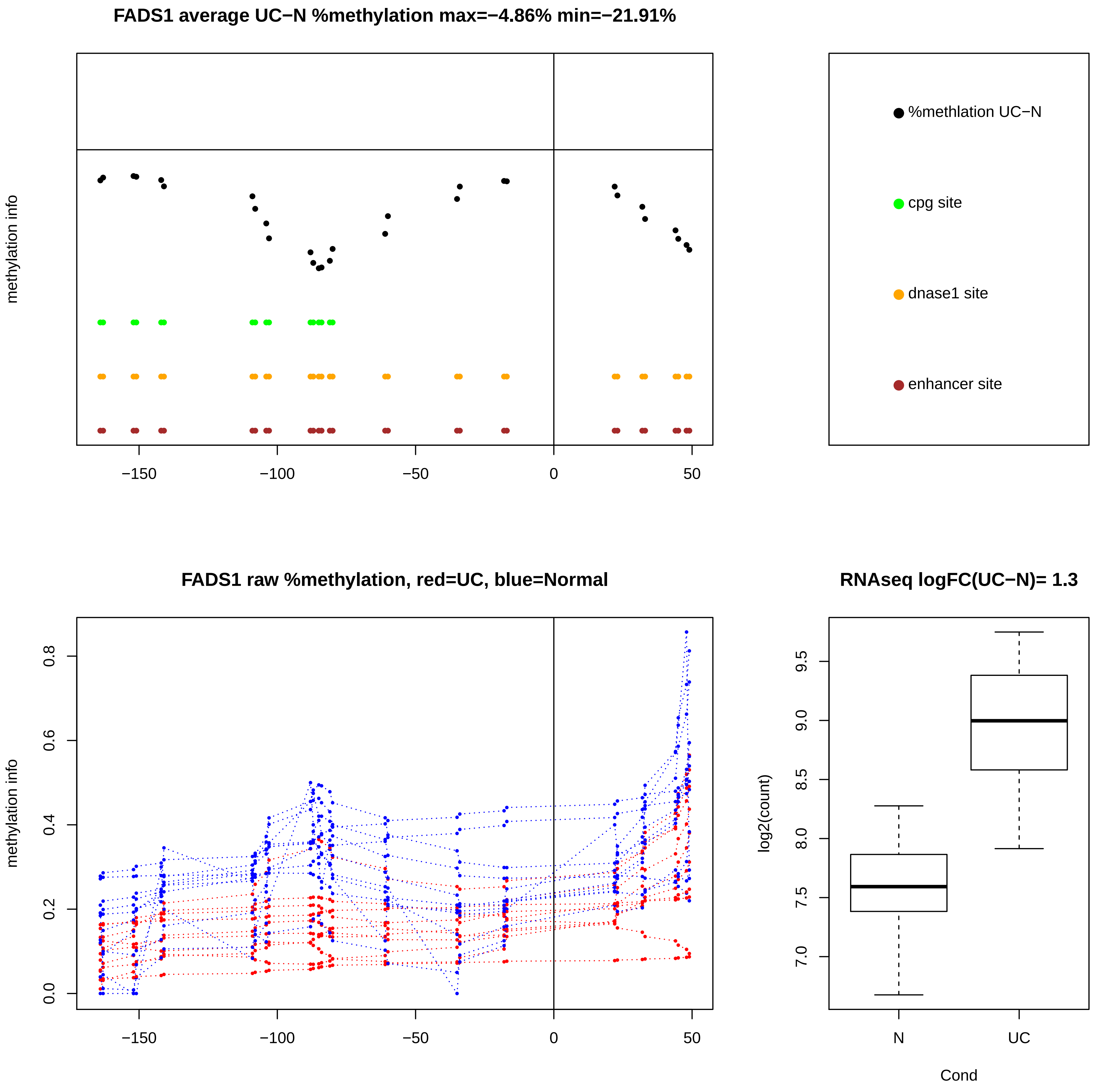


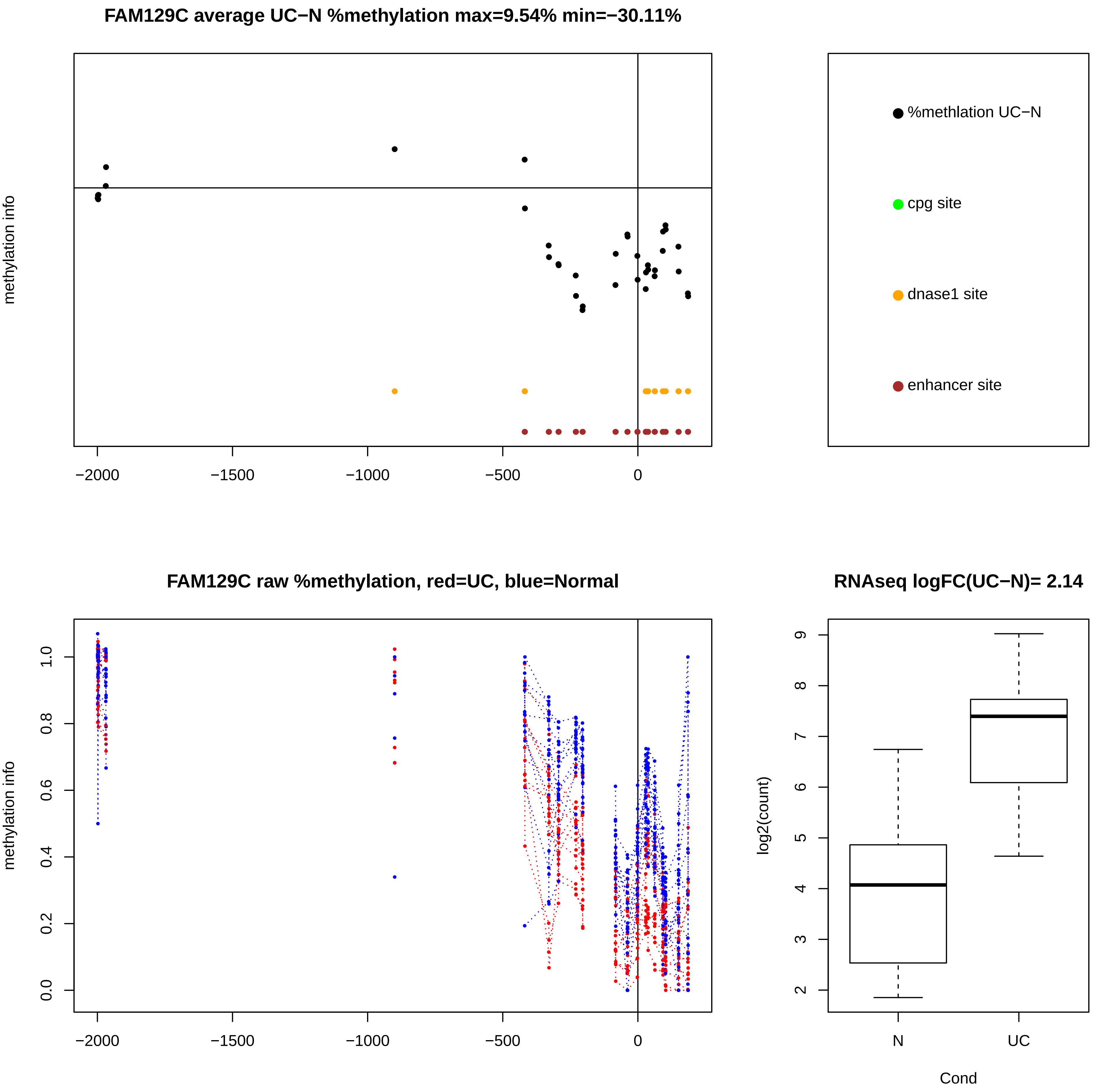
FABP1 raw %methylation, red=UC, blue=Normal

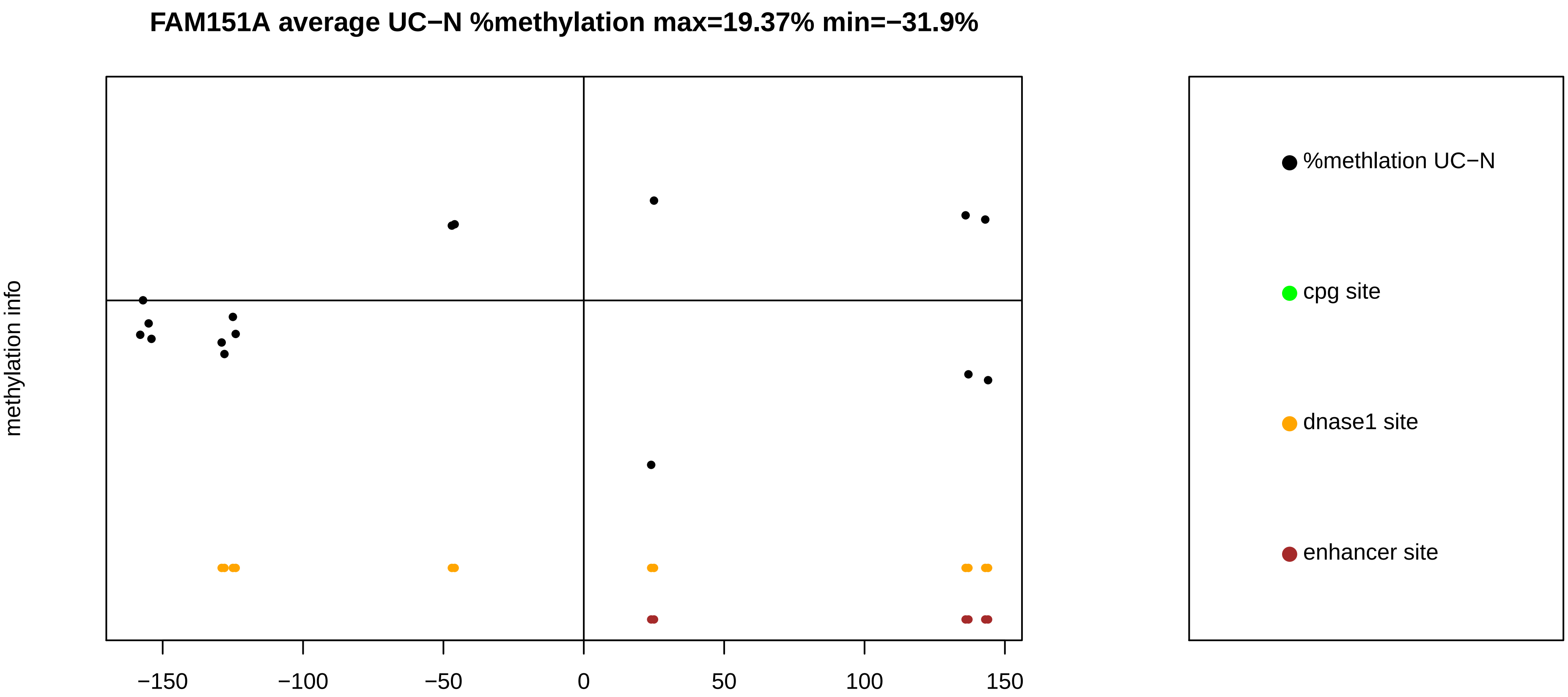


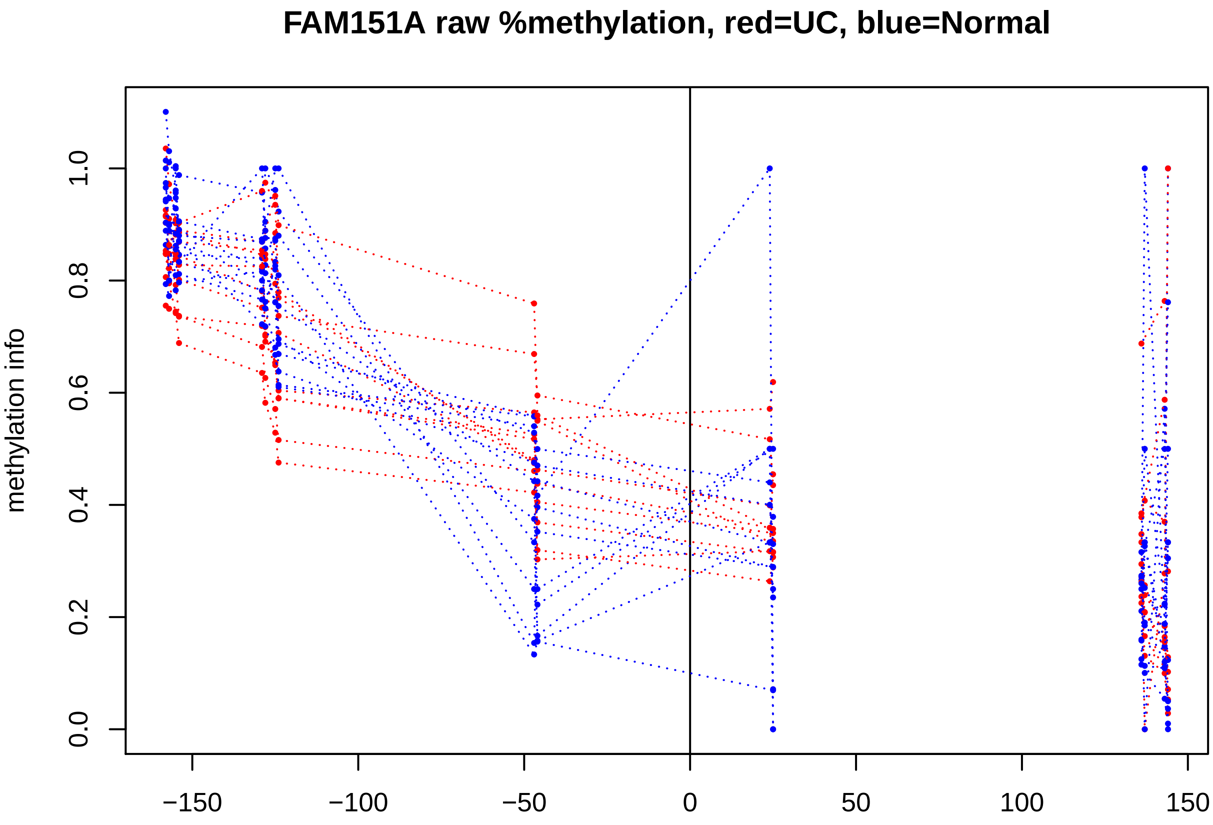
RNAseq logFC(UC−N)= −1.66

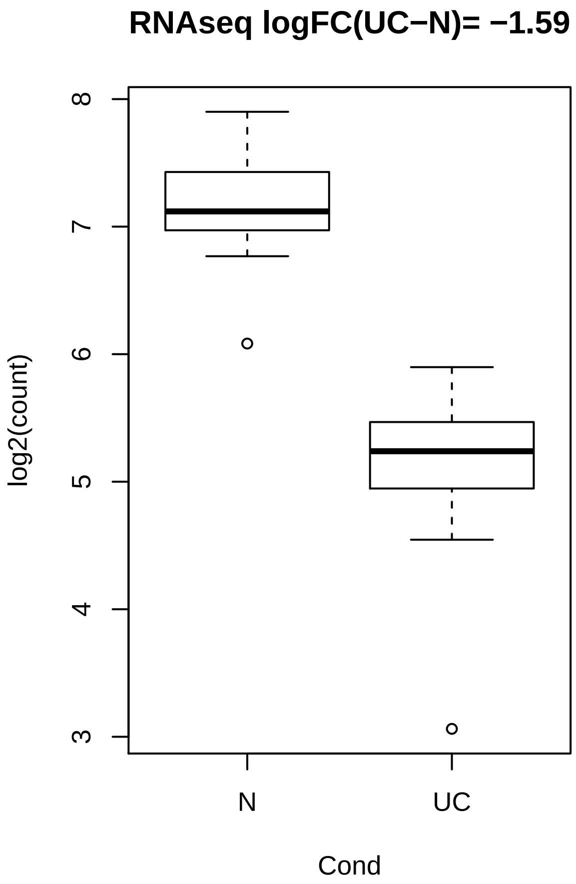


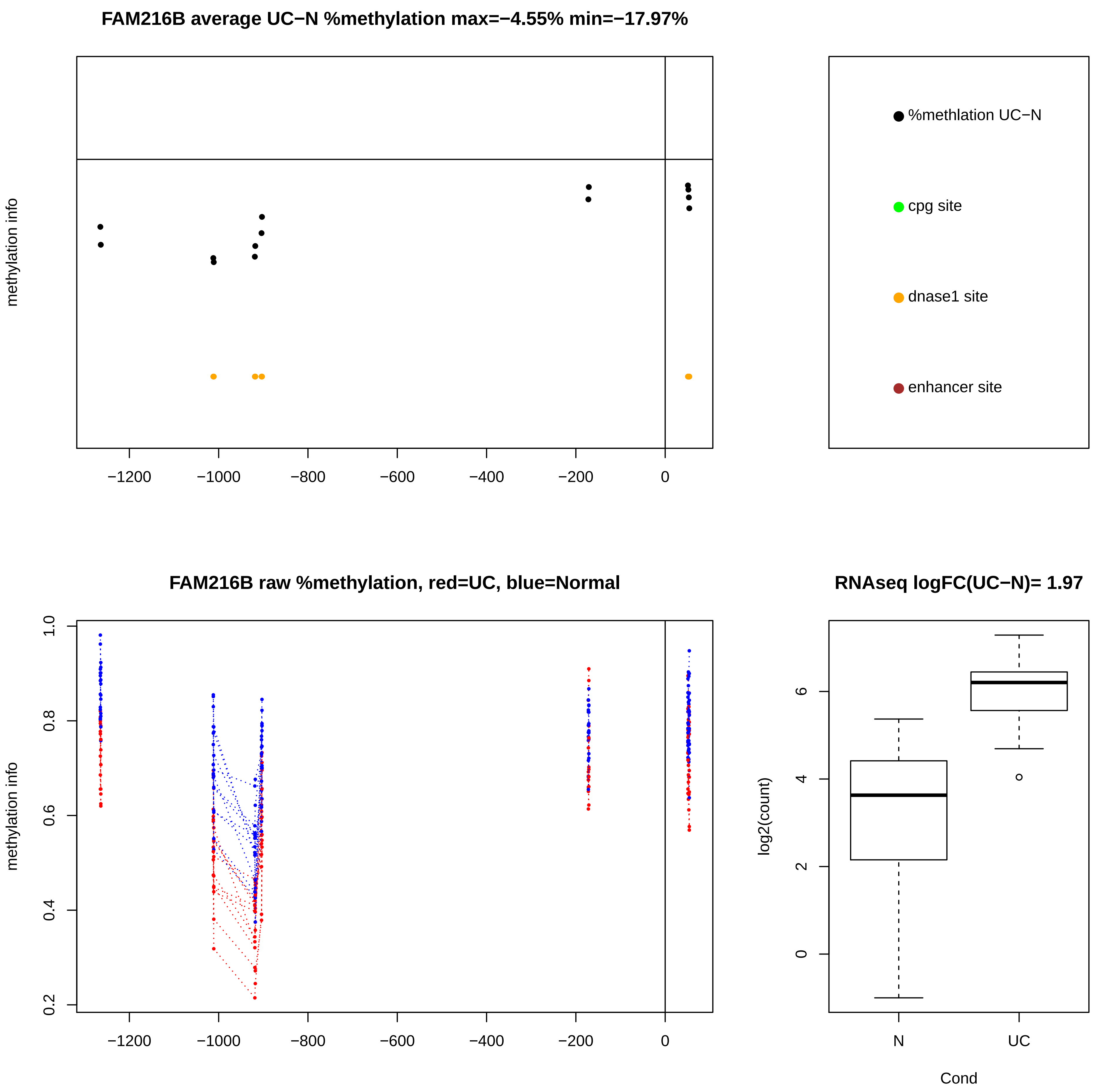

FADS1 average UC−N %methylation max=−4.86% min=−21.91%
methylation info
−150
−100
−50
0
50
%methlation UC−N
cpg site
dnase1 site
enhancer site
FADS1 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
−150
−100
−50
0
50
RNAseq logFC(UC−N)= 1.3
log2(count)
7.0
7.5
8.0
8.5
9.0
9.5
N
UC
Cond


FAM129C average UC−N %methylation max=9.54% min=−30.11%
methylation info
−2000
−1500
−1000
−500
0
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
FAM129C raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−2000
−1500
−1000
−500
0
RNAseq logFC(UC−N)= 2.14
log2(count)
2
3
4
5
6
7
8
9
N
UC
Cond

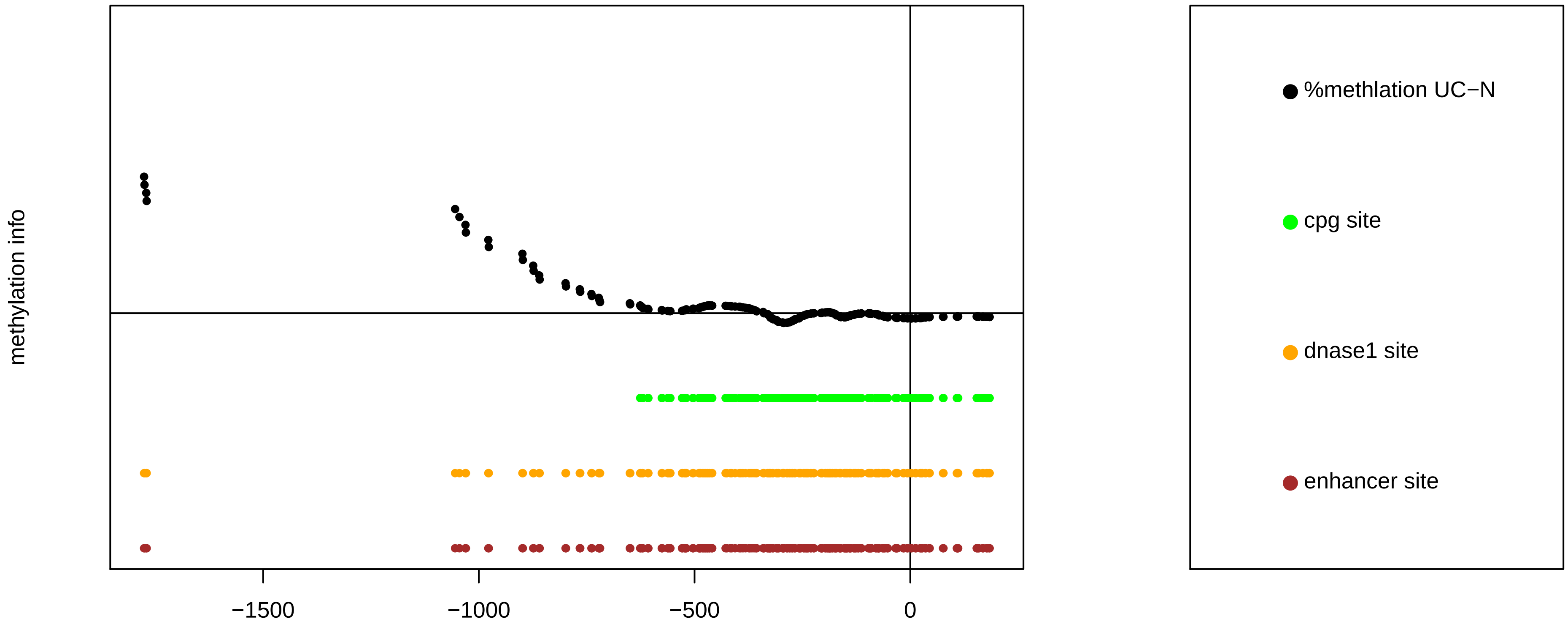

FAM151A average UC−N %methylation max=19.37% min=−31.9%
methylation info
−150
−100
−50
0
50
100
150
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site


FAM151A raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−150
−100
−50
0
50
100
150

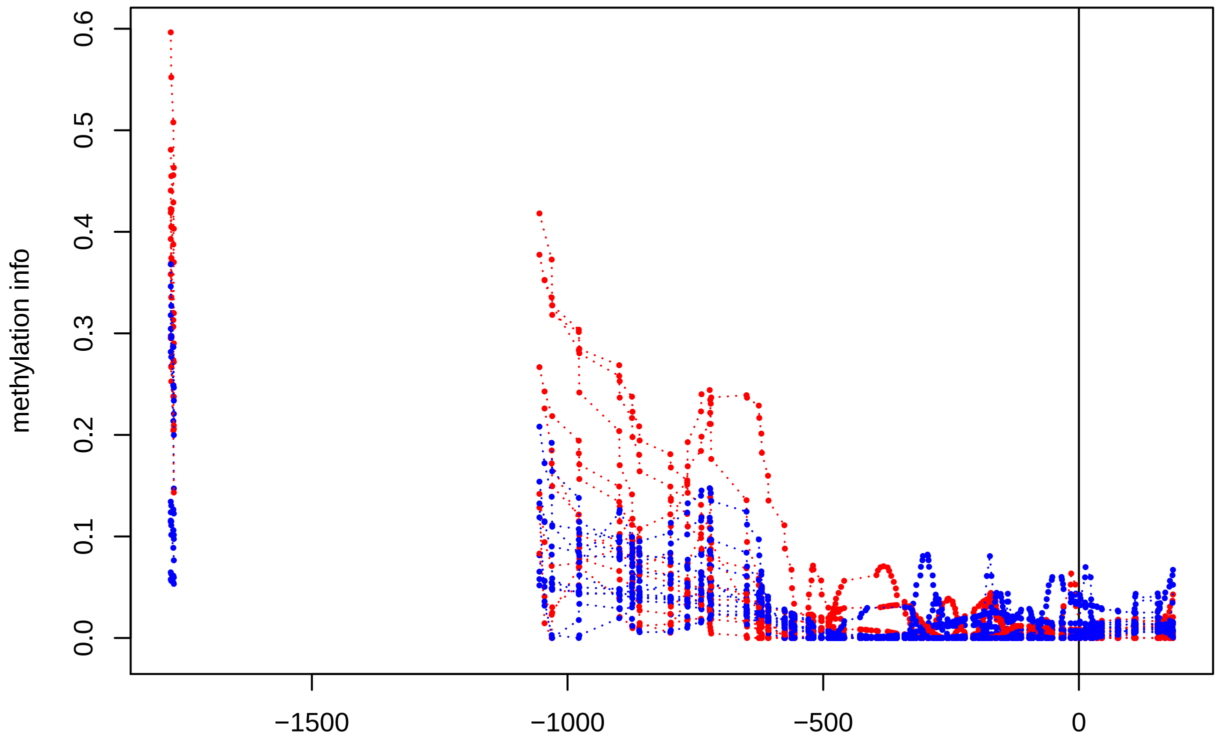

RNAseq logFC(UC−N)= −1.59
log2(count)
3
4
5
6
7
8
N
UC
Cond


FAM216B average UC−N %methylation max=−4.55% min=−17.97%
methylation info
−1200
−1000
−800
−600
−400
−200
0
%methlation UC−N
cpg site
dnase1 site
enhancer site
FAM216B raw %methylation, red=UC, blue=Normal
methylation info
0.2
0.4
0.6
0.8
1.0
−1200
−1000
−800
−600
−400
−200
0
RNAseq logFC(UC−N)= 1.97
log2(count)
0
2
4
6
N
UC
Cond

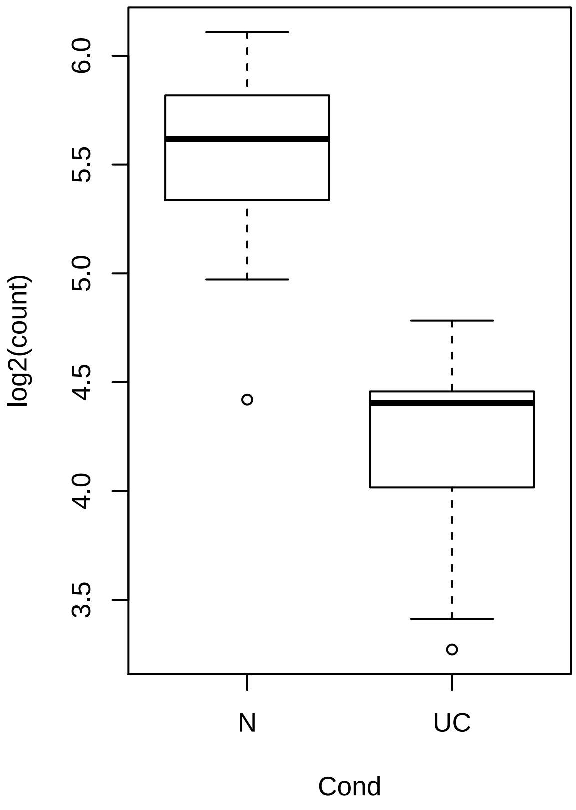
FAM47E average UC−N %methylation max=18.17% min=−1.3%

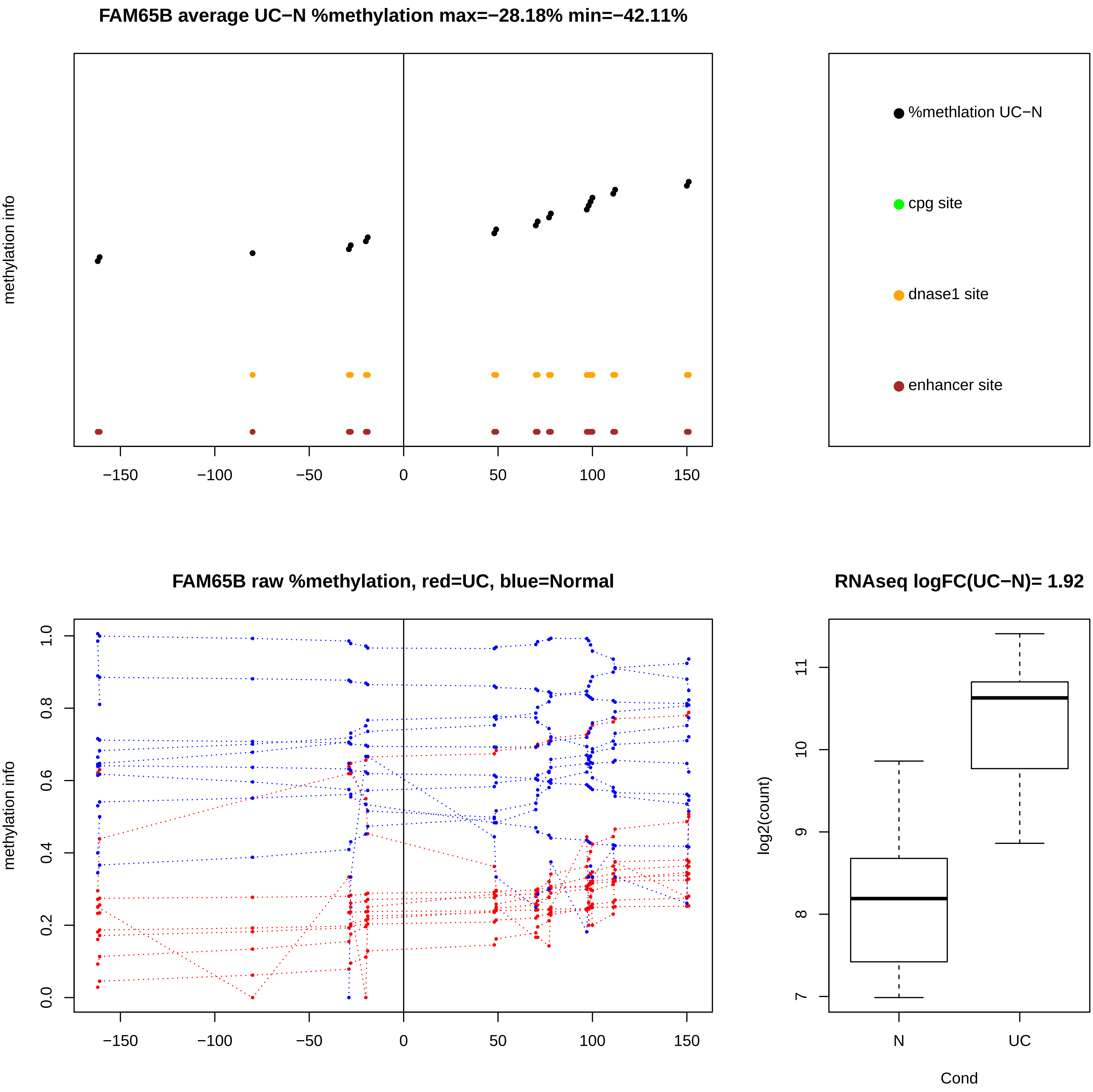


FAM47E raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= −1.29

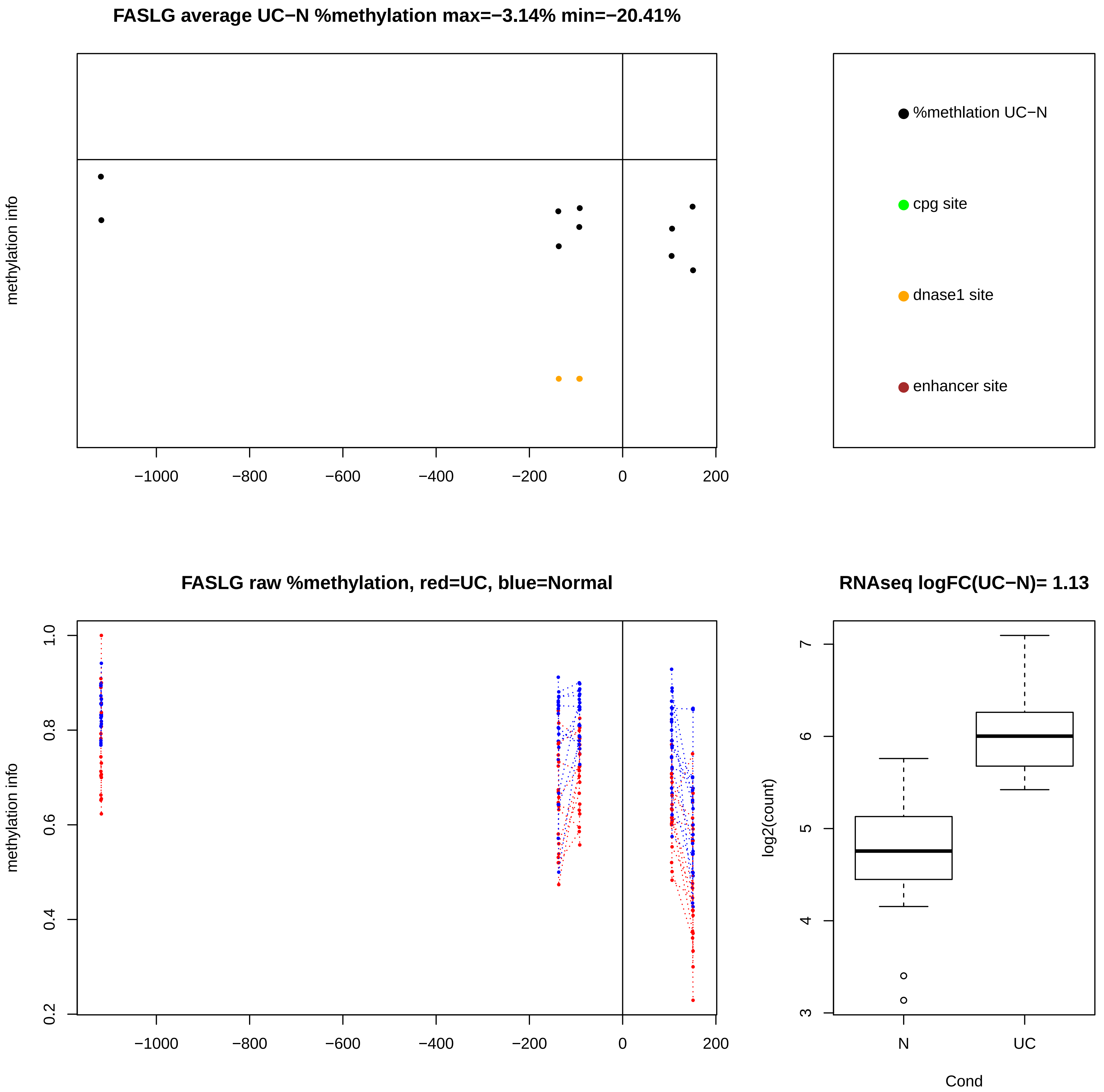


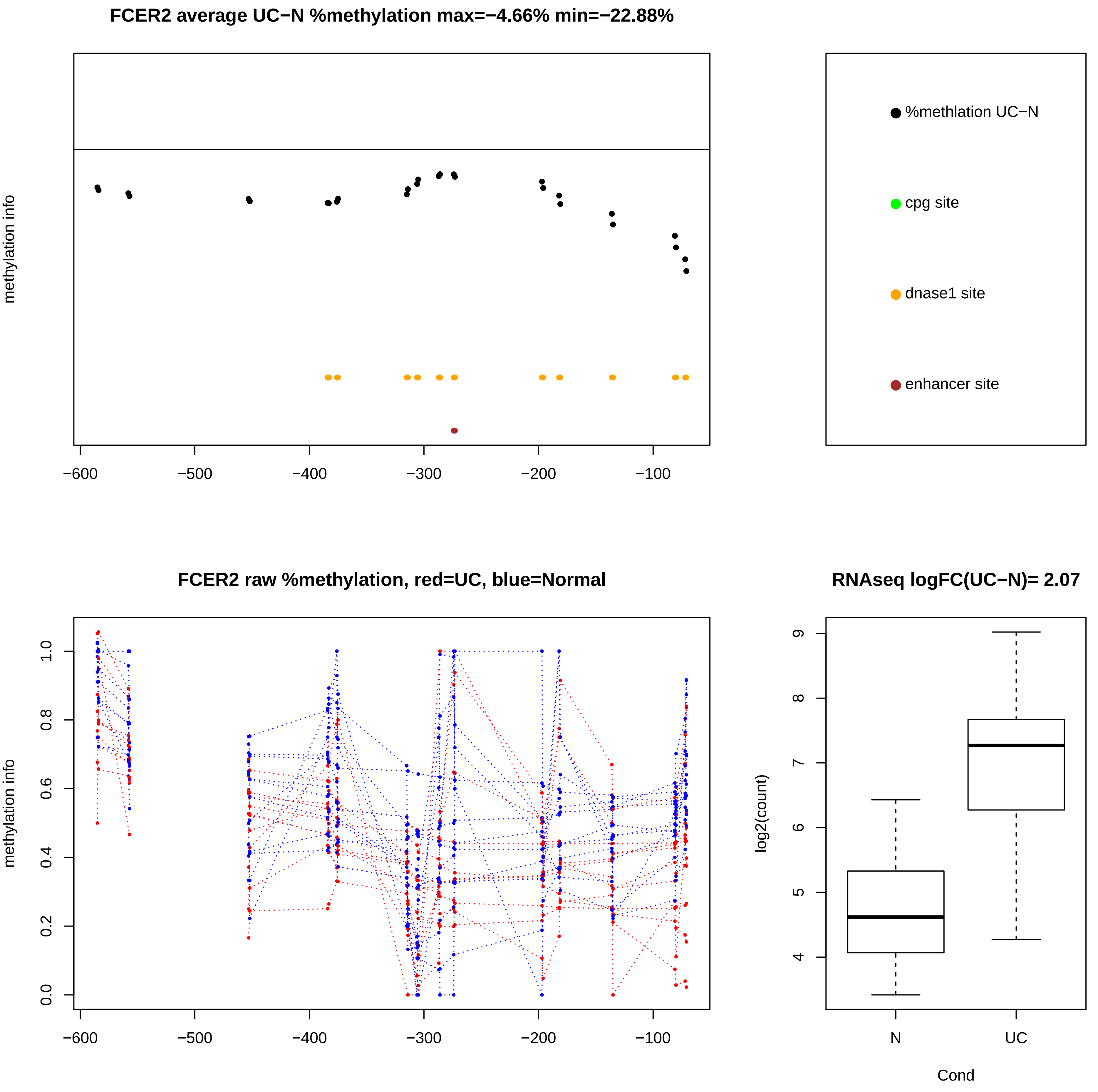


FAM65B average UC−N %methylation max=−28.18% min=−42.11%

FAM65B raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.92

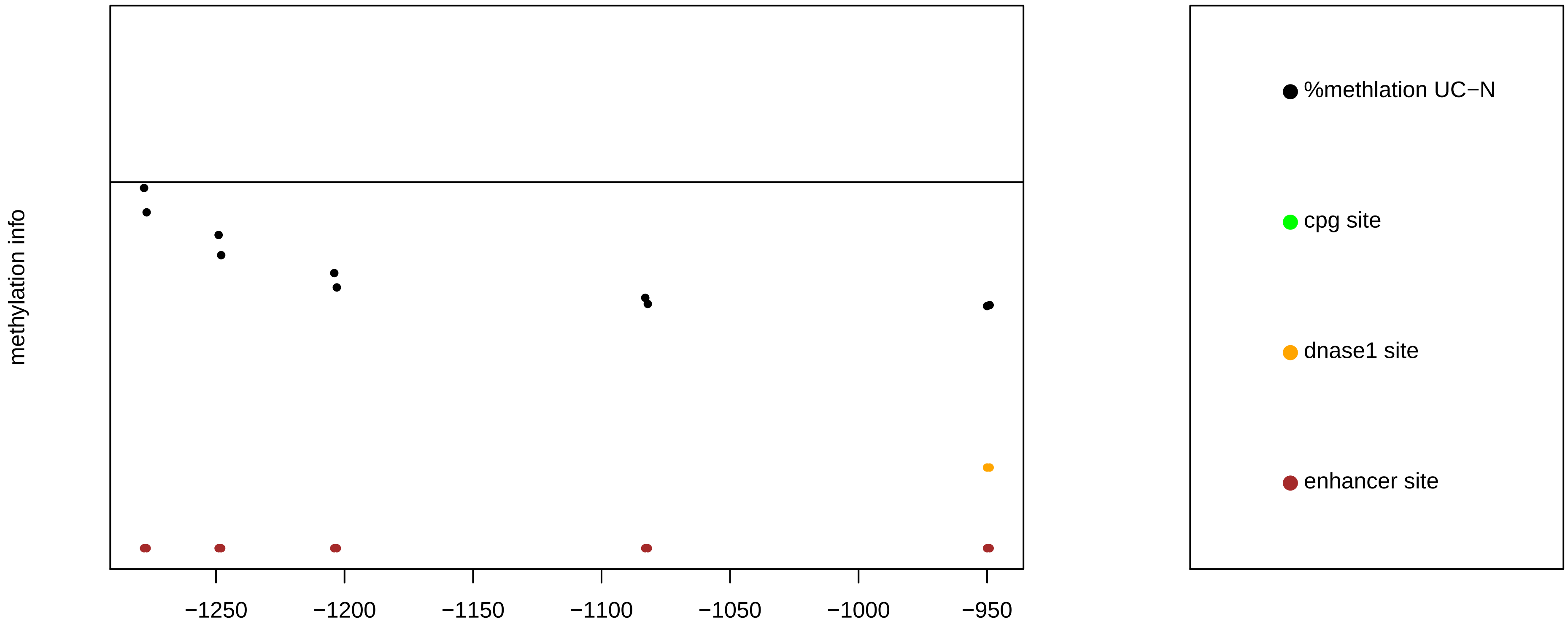

FASLG average UC−N %methylation max=−3.14% min=−20.41%
methylation info
−1000
−800
−600
−400
−200
0
200
%methlation UC−N
cpg site
dnase1 site
enhancer site
FASLG raw %methylation, red=UC, blue=Normal
methylation info
0.2
0.4
0.6
0.8
1.0
−1000
−800
−600
−400
−200
0
200
RNAseq logFC(UC−N)= 1.13
log2(count)
3
4
5
6
7
N
UC
Cond


FCER2 average UC−N %methylation max=−4.66% min=−22.88%

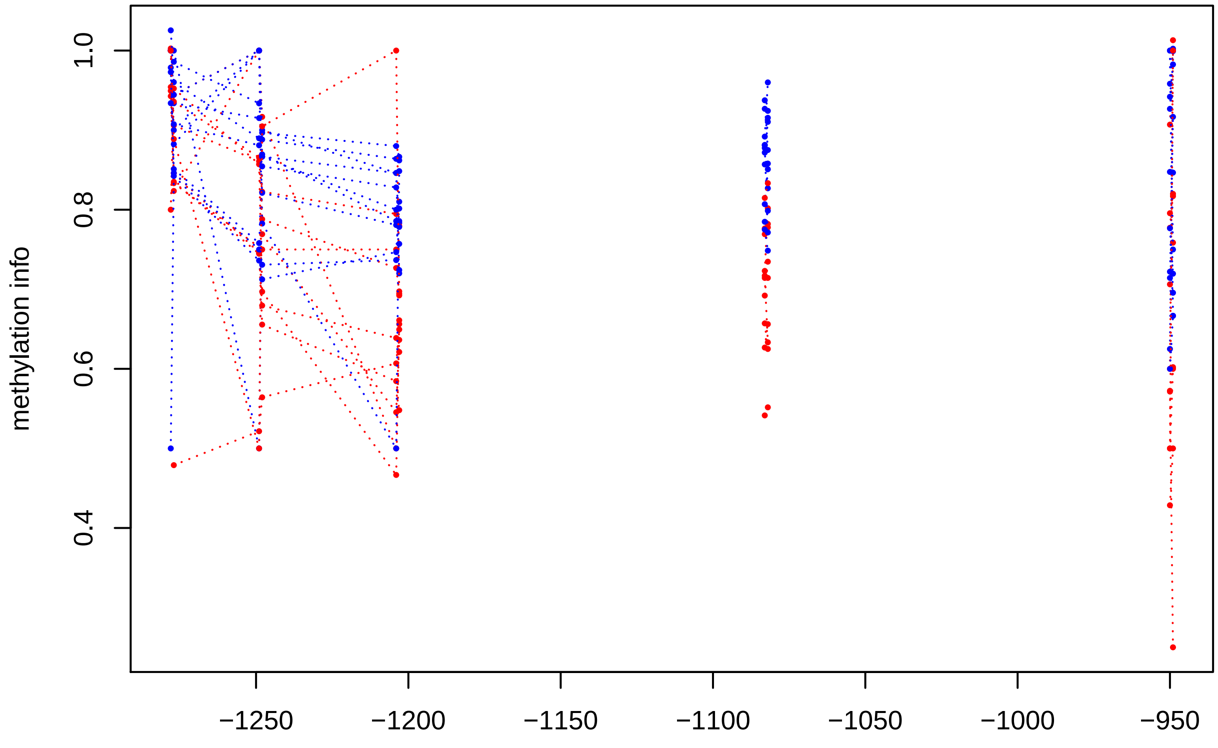
FCER2 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 2.07

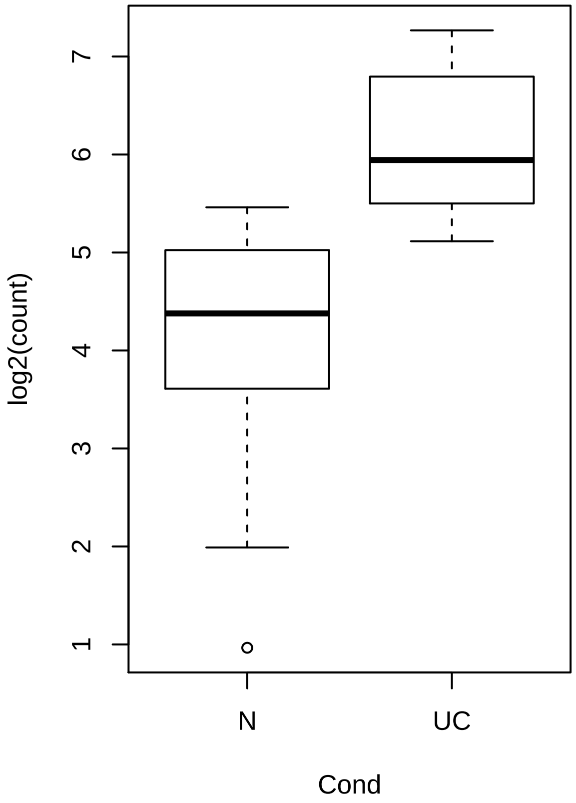
FCGR1A average UC−N %methylation max=−0.72% min=−15.35%

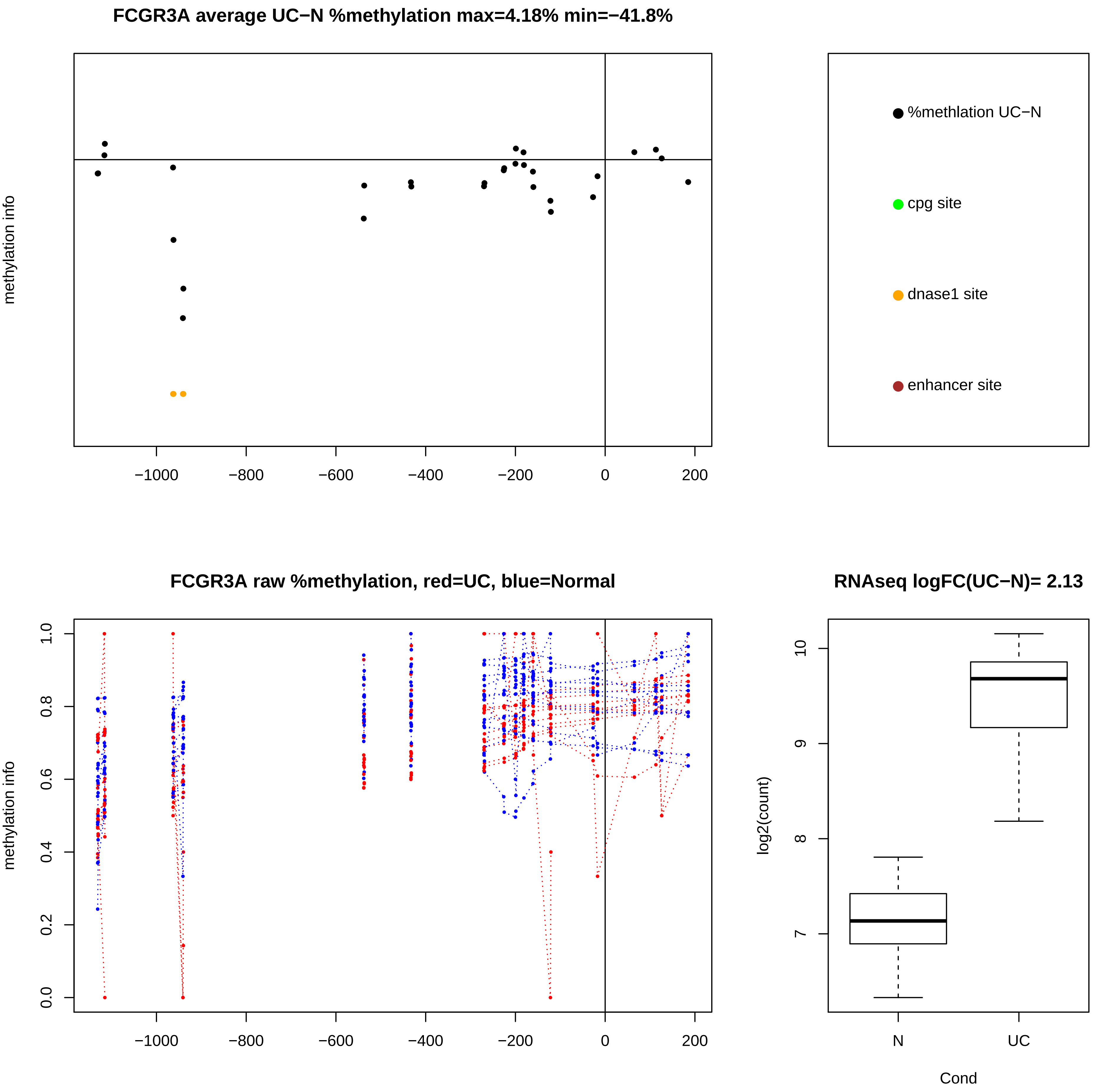


FCGR1A raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 1.5

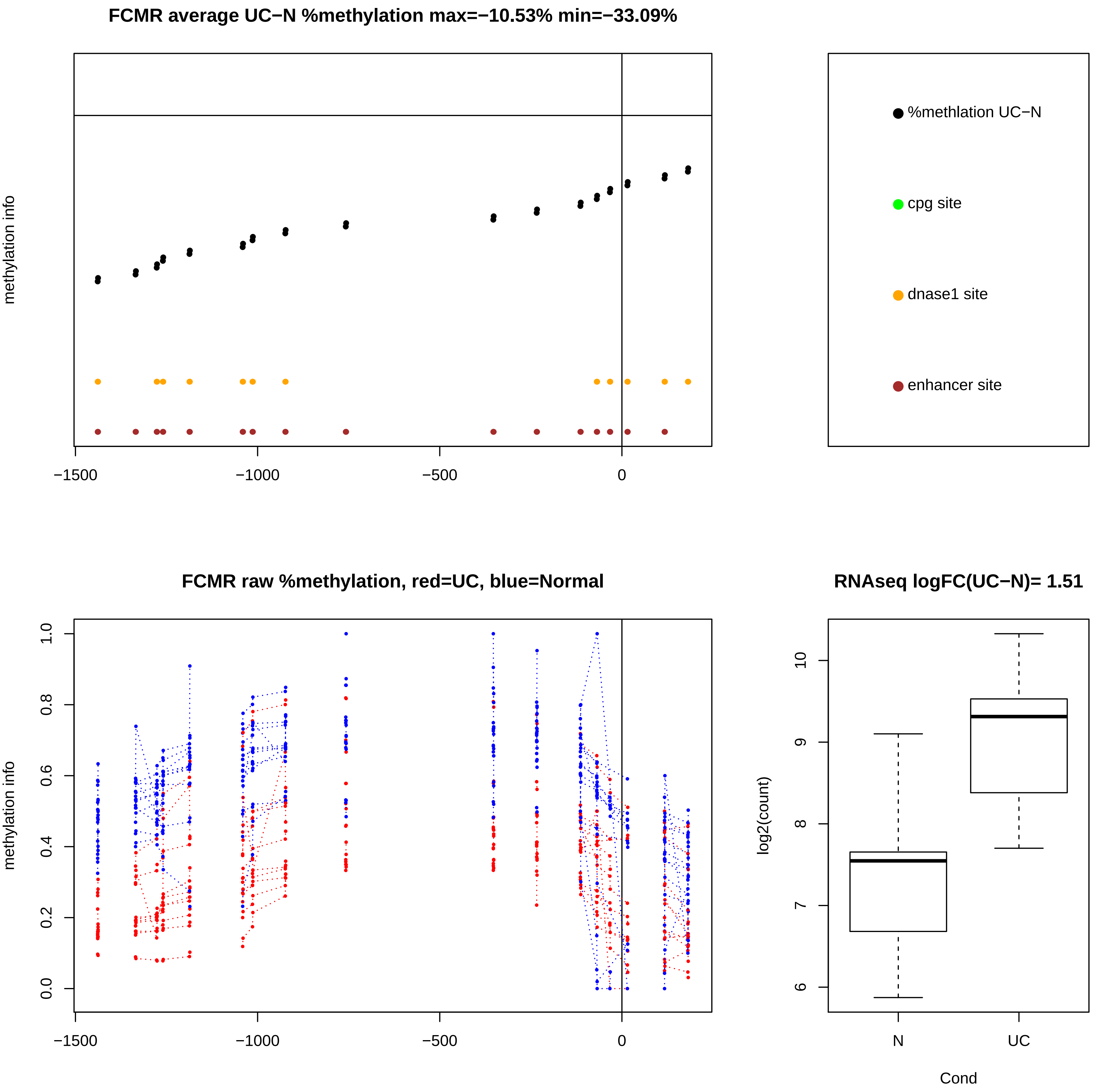


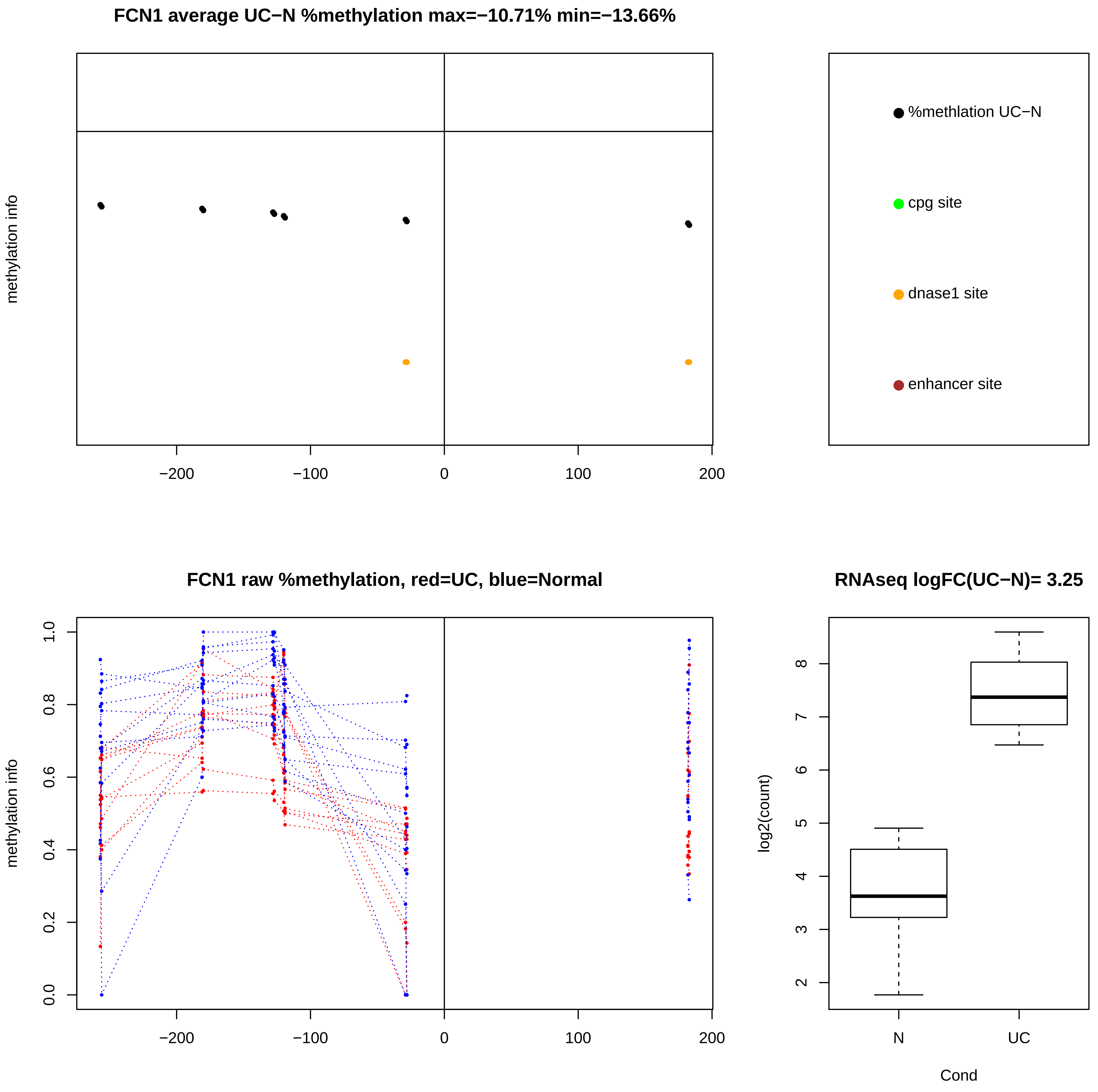


FCGR3A average UC−N %methylation max=4.18% min=−41.8%

FCGR3A raw %methylation, red=UC, blue=Normal

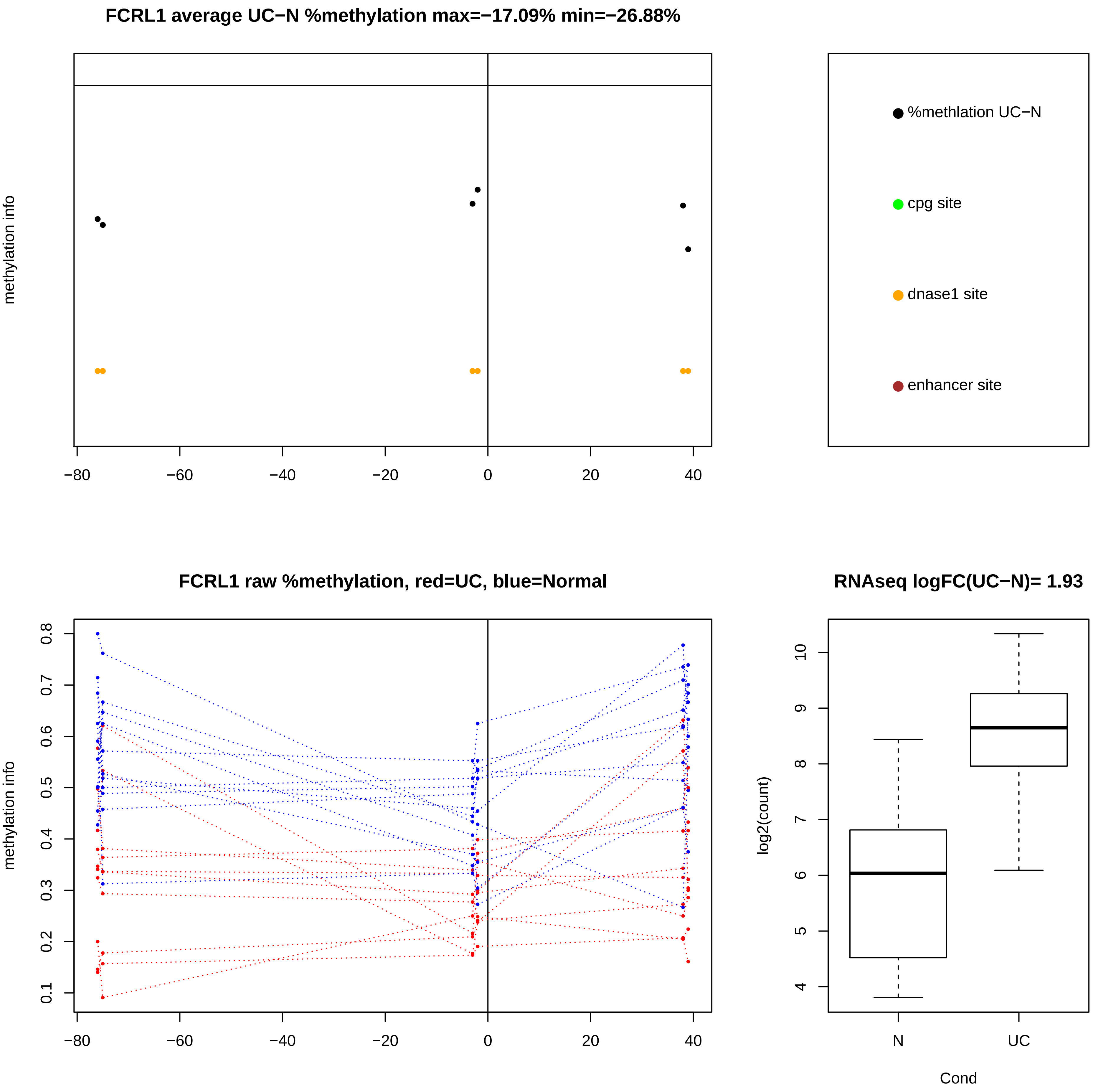
RNAseq logFC(UC−N)= 2.13


FCMR average UC−N %methylation max=−10.53% min=−33.09%
methylation info
−1500
−1000
−500
0
%methlation UC−N
cpg site
dnase1 site
enhancer site
FCMR raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−1500
−1000
−500
0
RNAseq logFC(UC−N)= 1.51
log2(count)
6
7
8
9
10
N
UC
Cond


FCN1 average UC−N %methylation max=−10.71% min=−13.66%

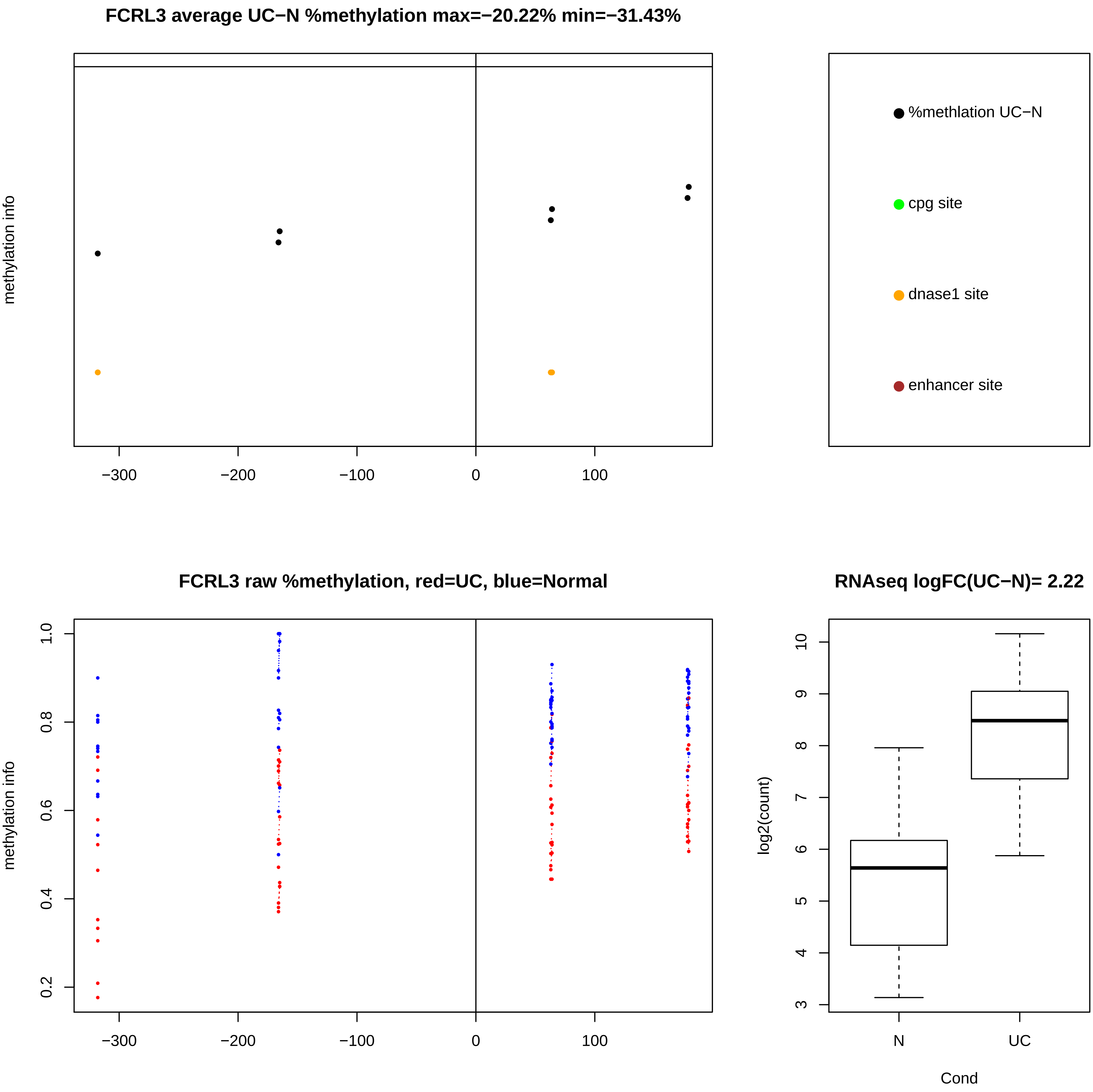
FCN1 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 3.25

 FCRL1 average UC−N %methylation max=−17.09% min=−26.88%

FCRL1 raw %methylation, red=UC, blue=Normal

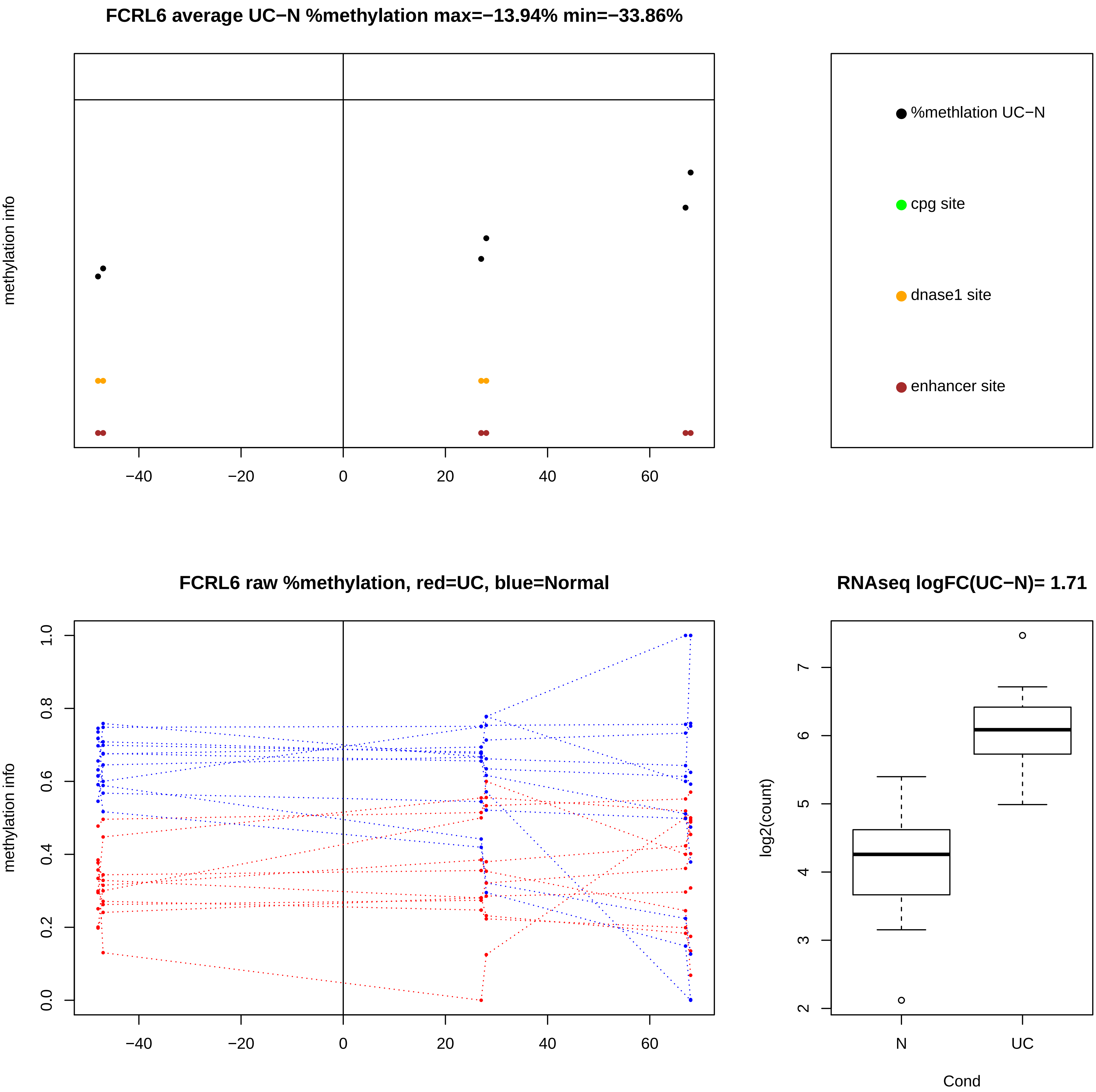
RNAseq logFC(UC−N)= 1.93

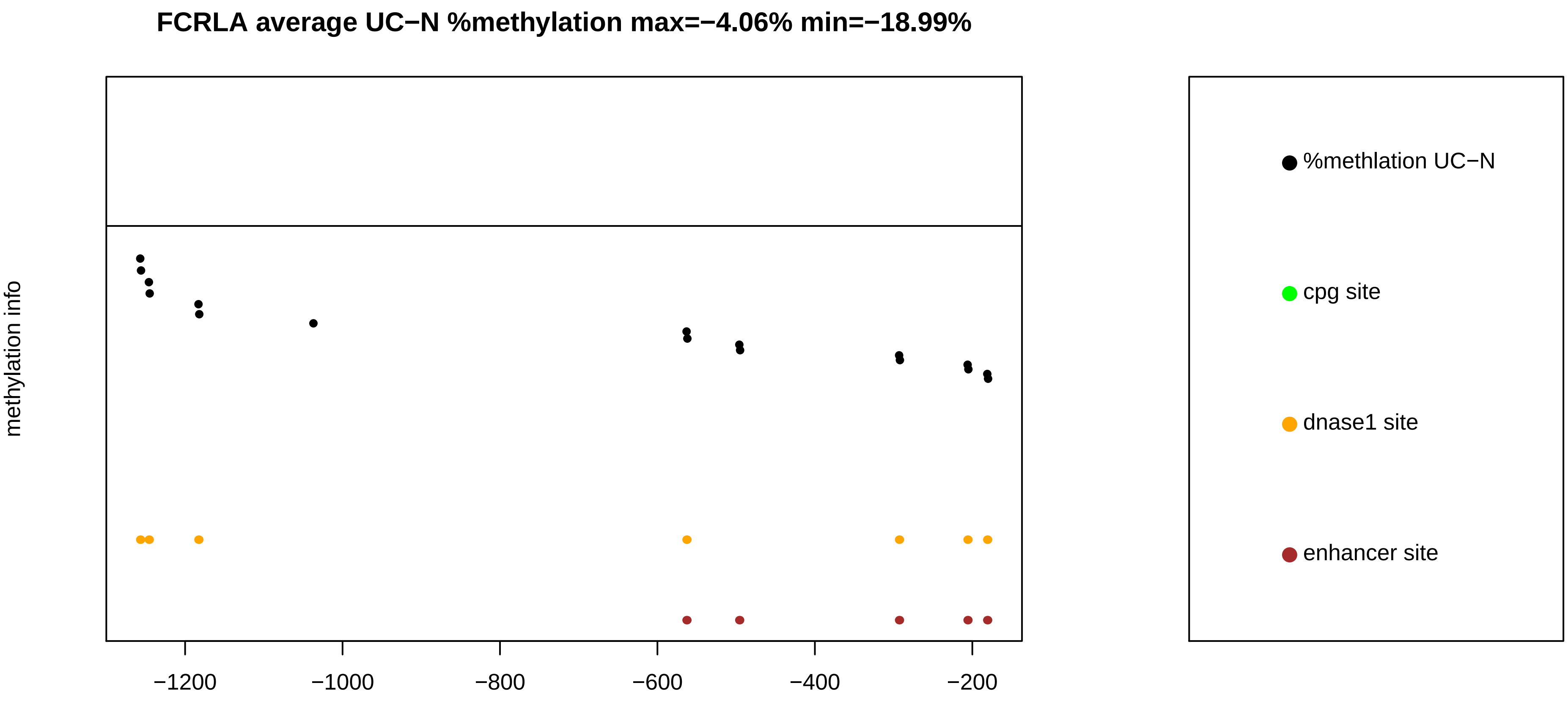


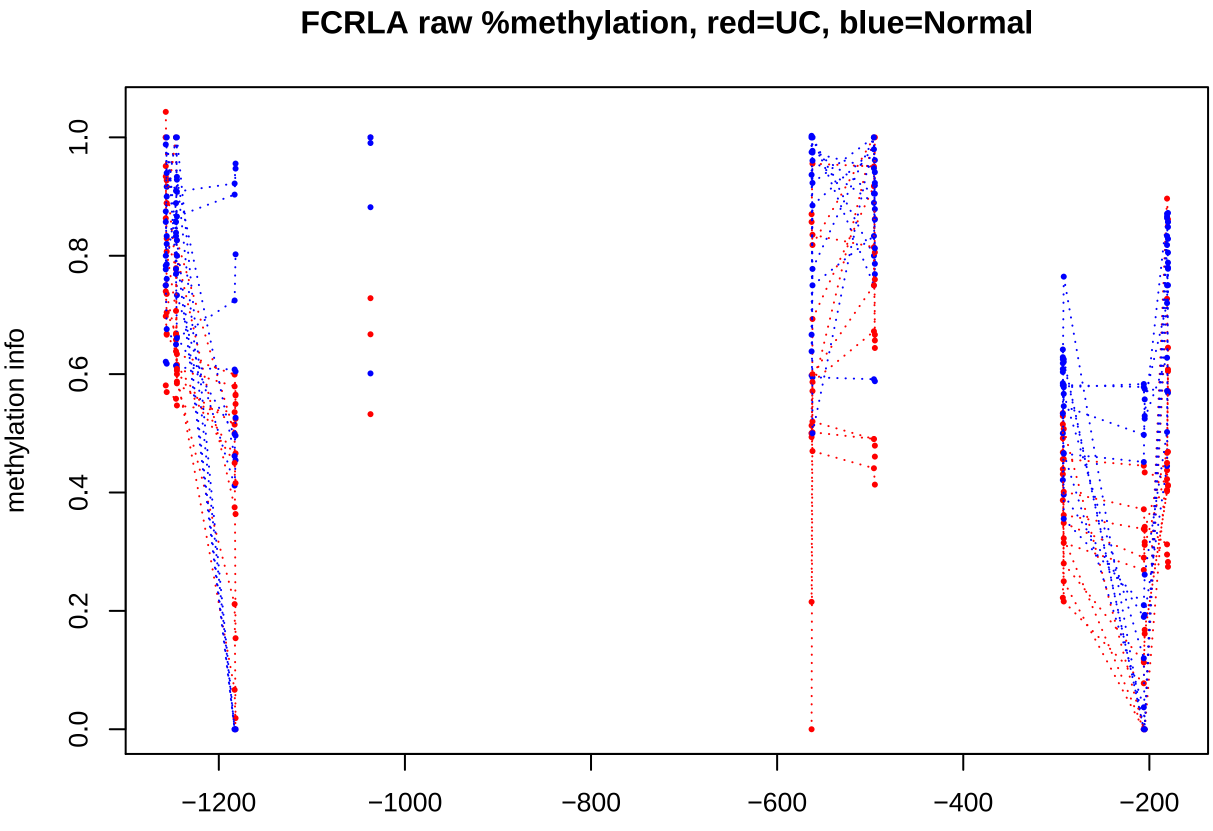
FCRL3 average UC−N %methylation max=−20.22% min=−31.43%

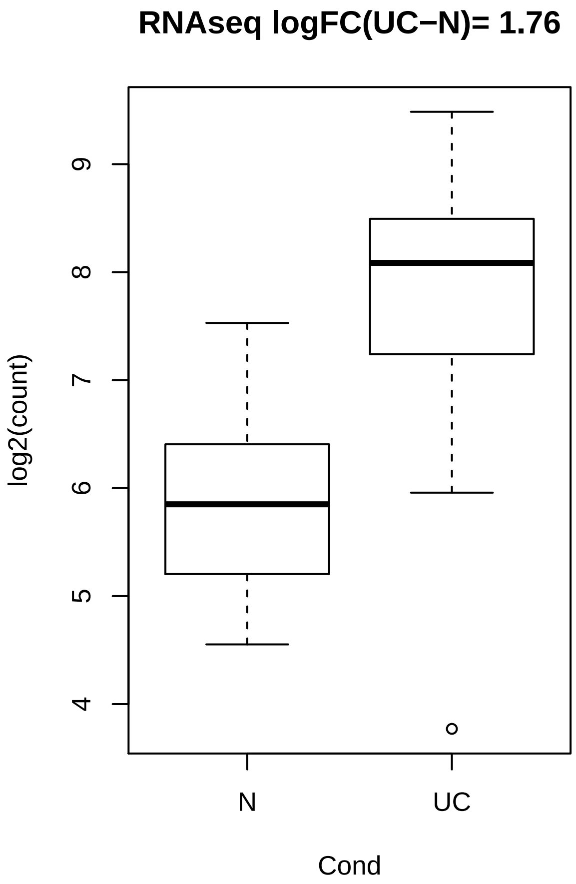
FCRL3 raw %methylation, red=UC, blue=Normal

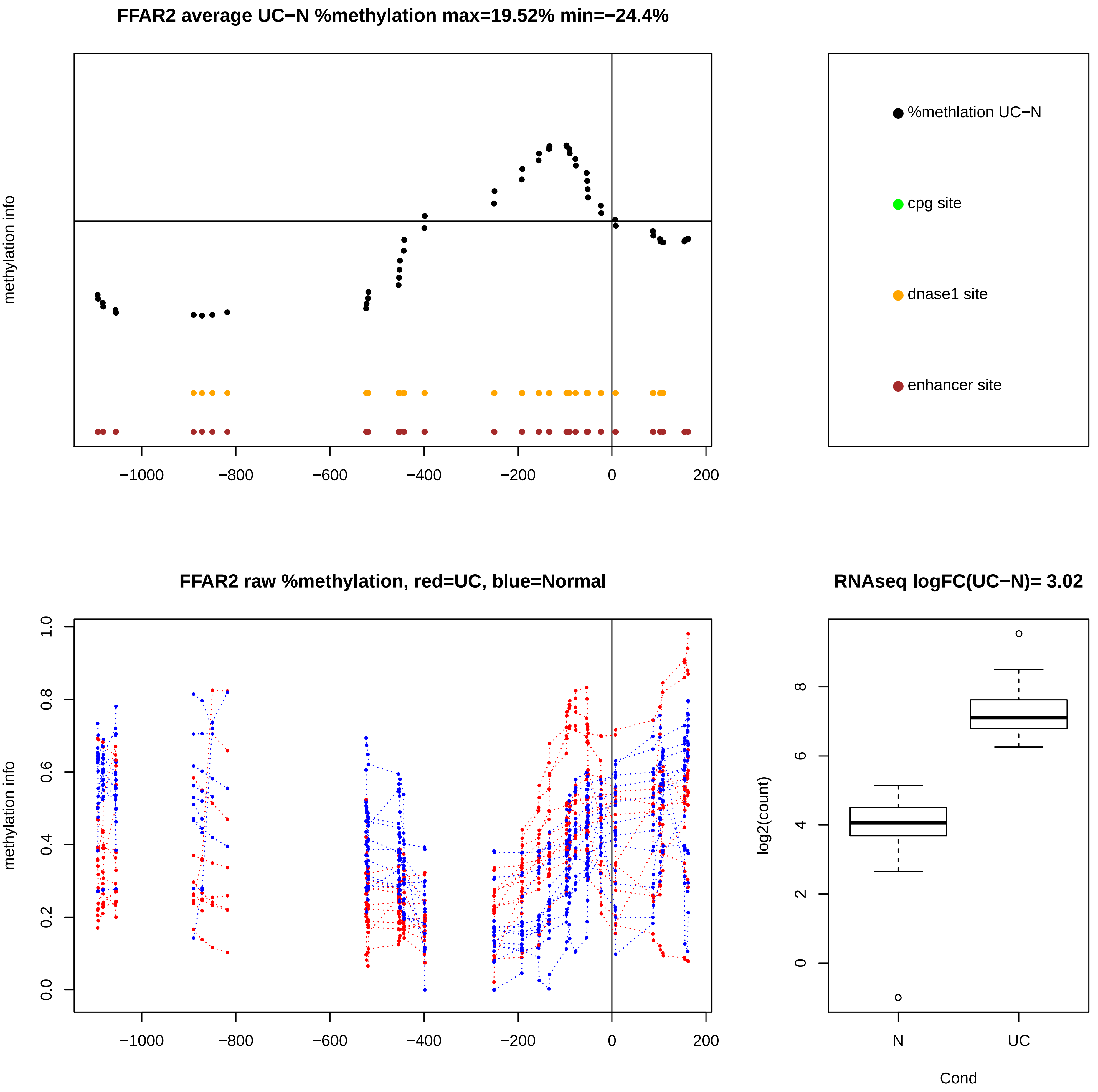
RNAseq logFC(UC−N)= 2.22

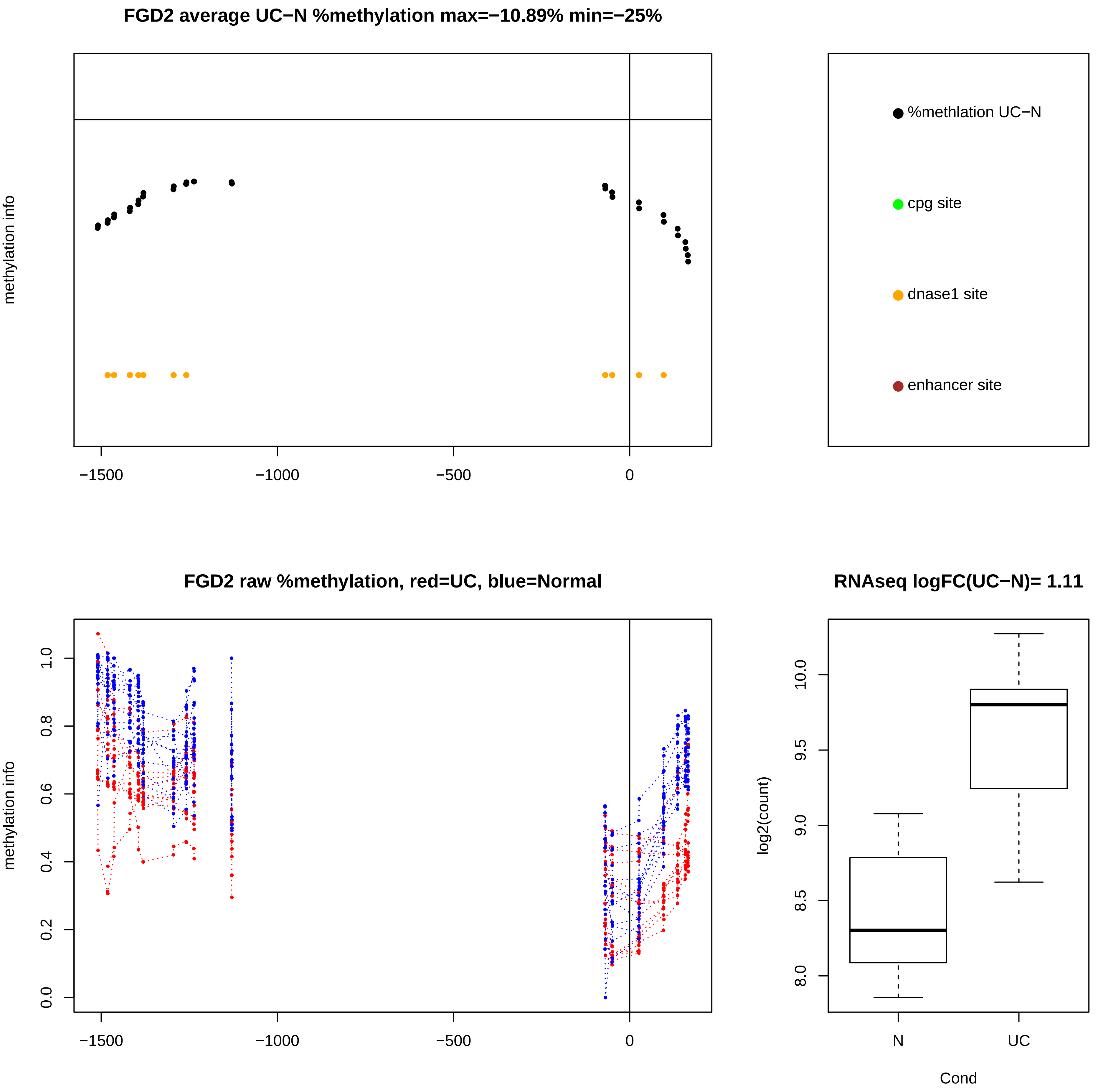

FCRL6 average UC−N %methylation max=−13.94% min=−33.86%
methylation info
−40
−20
0
20
40
60
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
FCRL6 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−40
−20
0
20
40
60
RNAseq logFC(UC−N)= 1.71
log2(count)
2
3
4
5
6
7
N
UC
Cond


FCRLA average UC−N %methylation max=−4.06% min=−18.99%


FCRLA raw %methylation, red=UC, blue=Normal


RNAseq logFC(UC−N)= 1.76


FFAR2 average UC−N %methylation max=19.52% min=−24.4%
methylation info
−1000
−800
−600
−400
−200
0
200
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
FFAR2 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−1000
−800
−600
−400
−200
0
200
RNAseq logFC(UC−N)= 3.02
log2(count)
0
2
4
6
8
N
UC
Cond

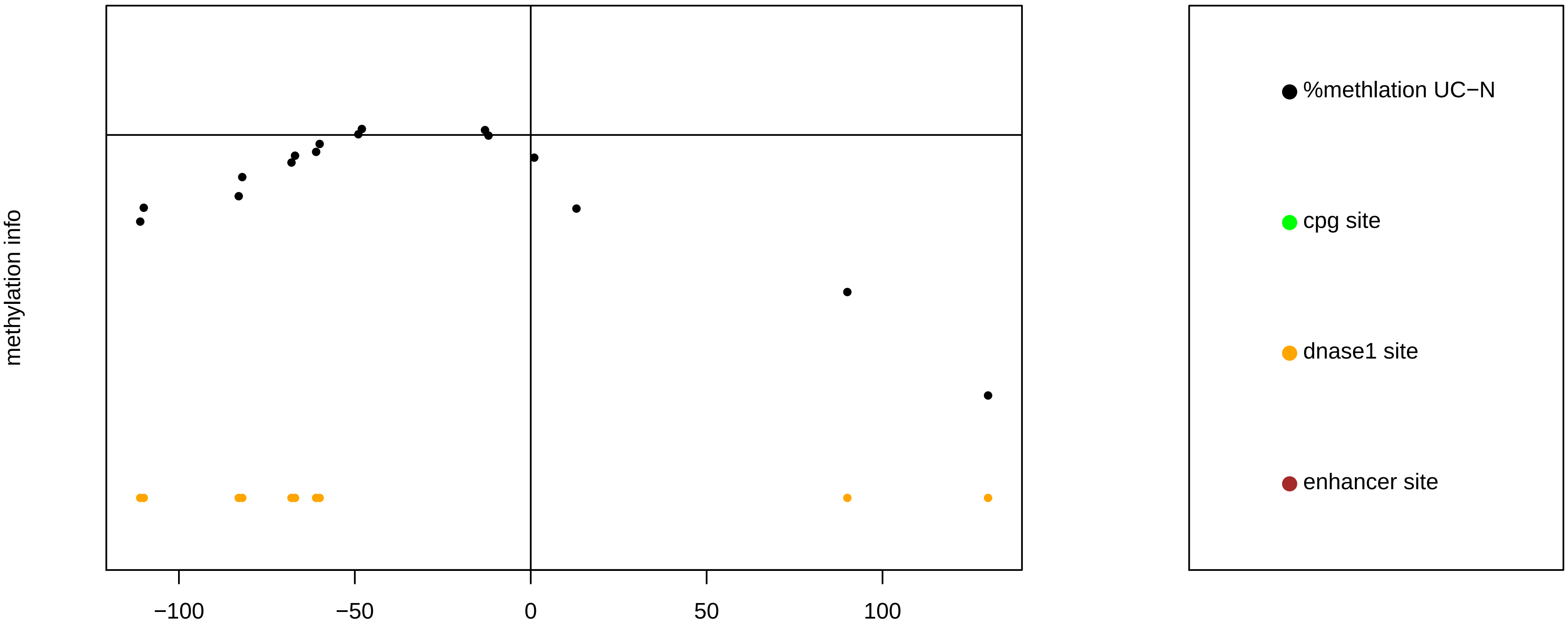


FGD2 average UC−N %methylation max=−10.89% min=−25%

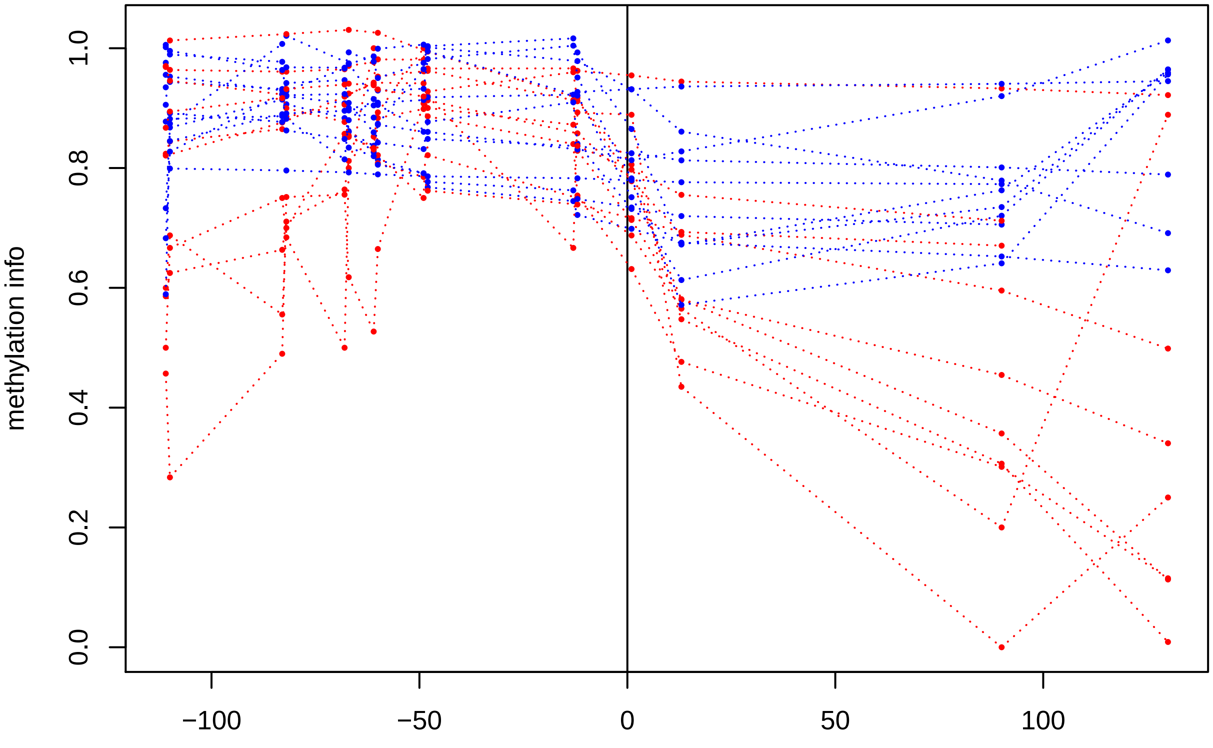
FGD2 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.11

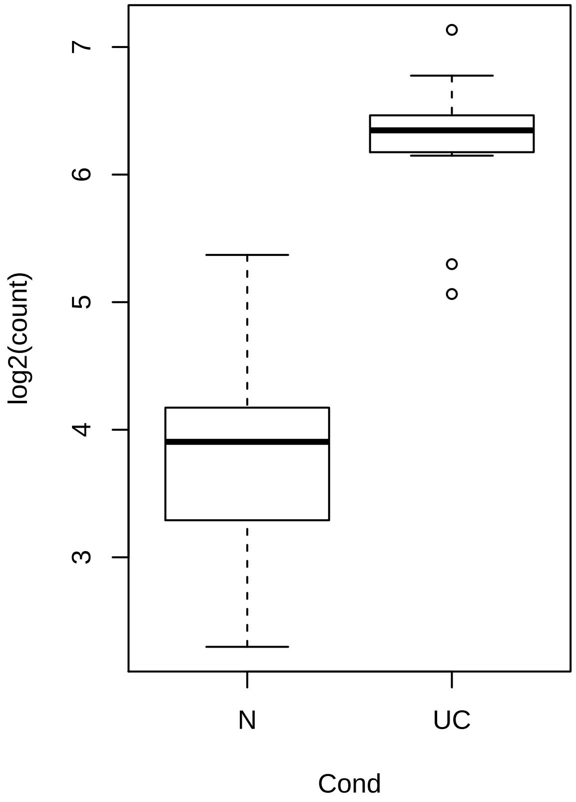
FOXP3 average UC−N %methylation max=1.16% min=−50.87%

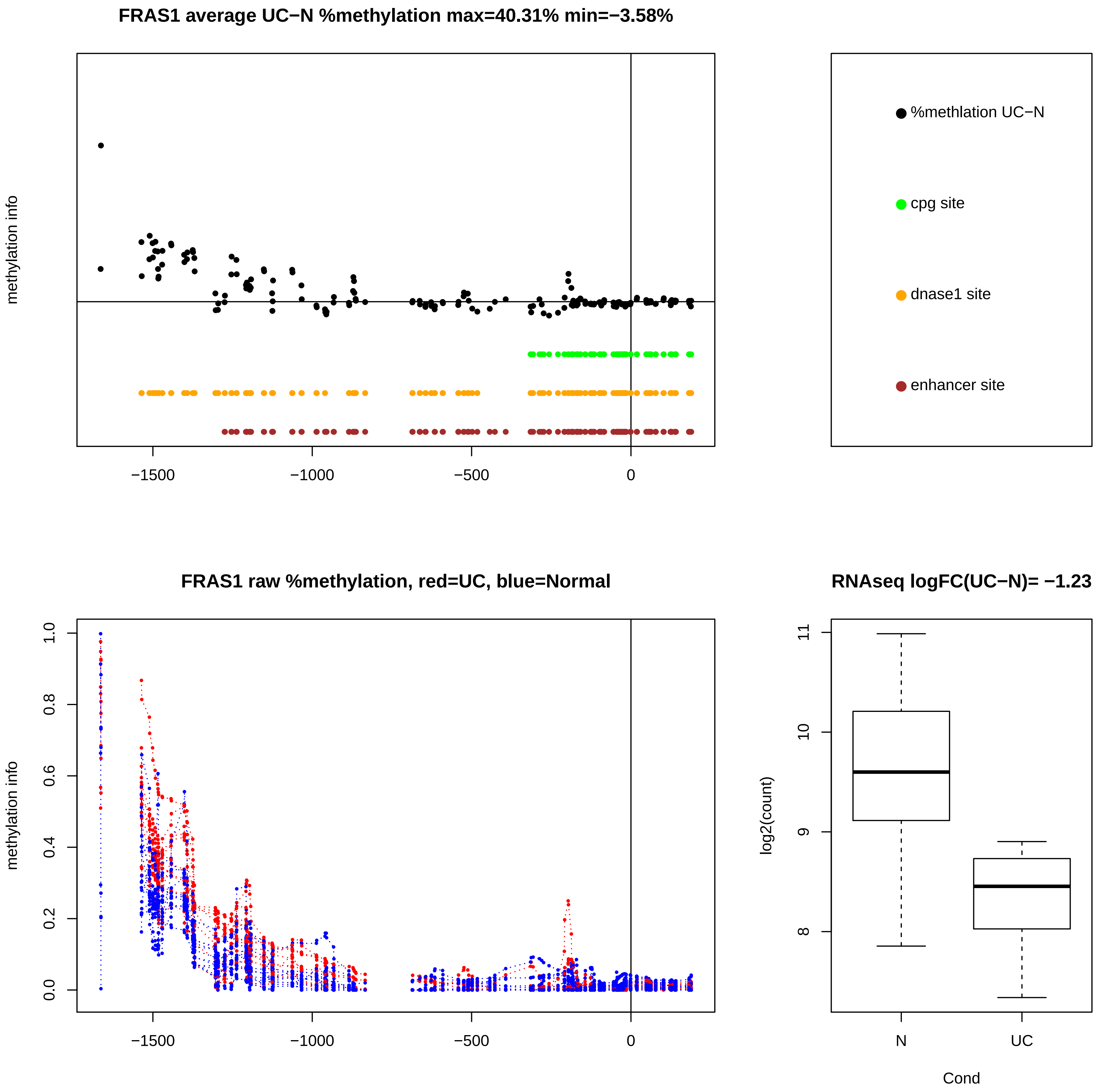


FOXP3 raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 2.11

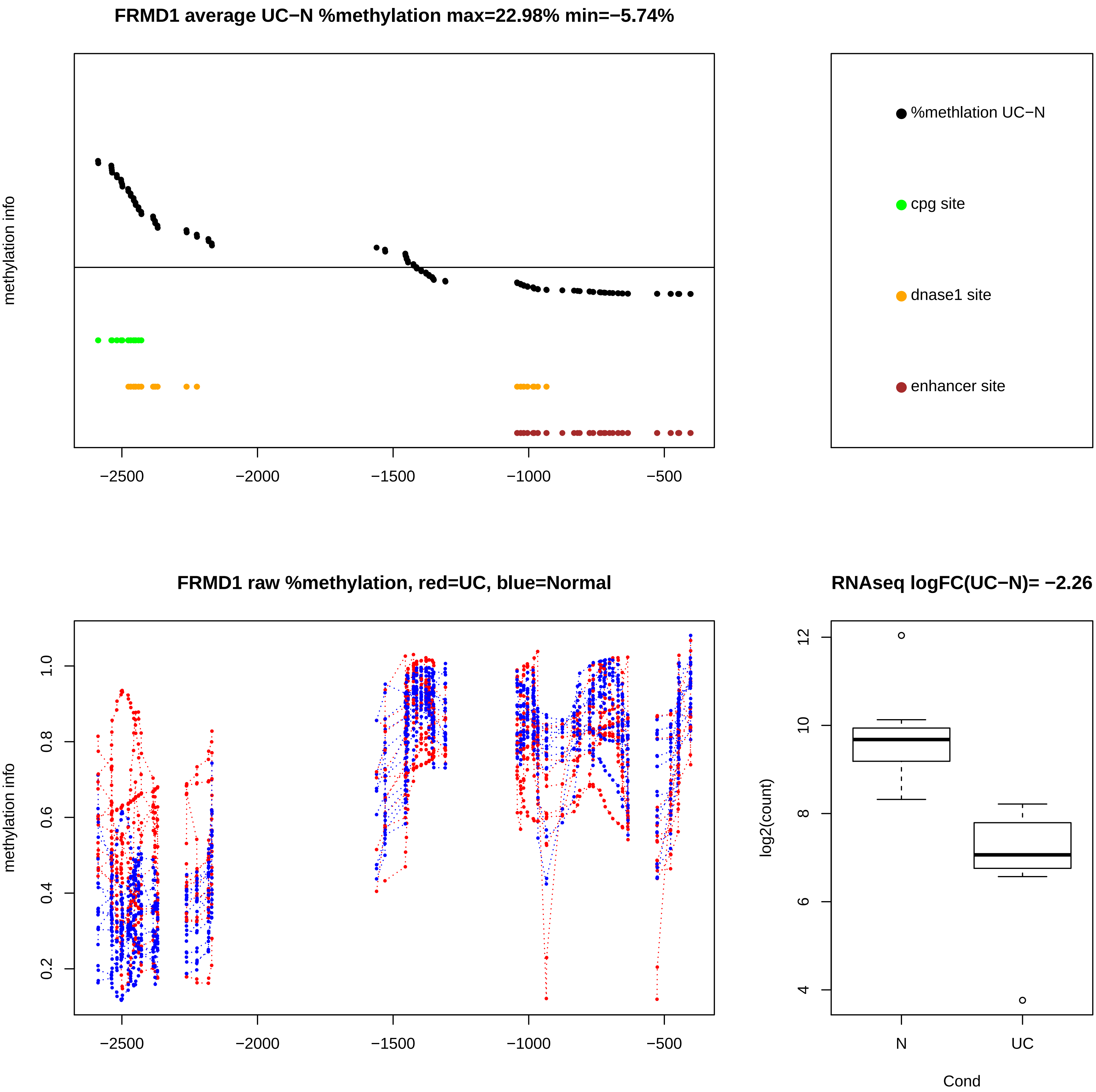




FRAS1 average UC−N %methylation max=40.31% min=−3.58%

FRAS1 raw %methylation, red=UC, blue=Normal

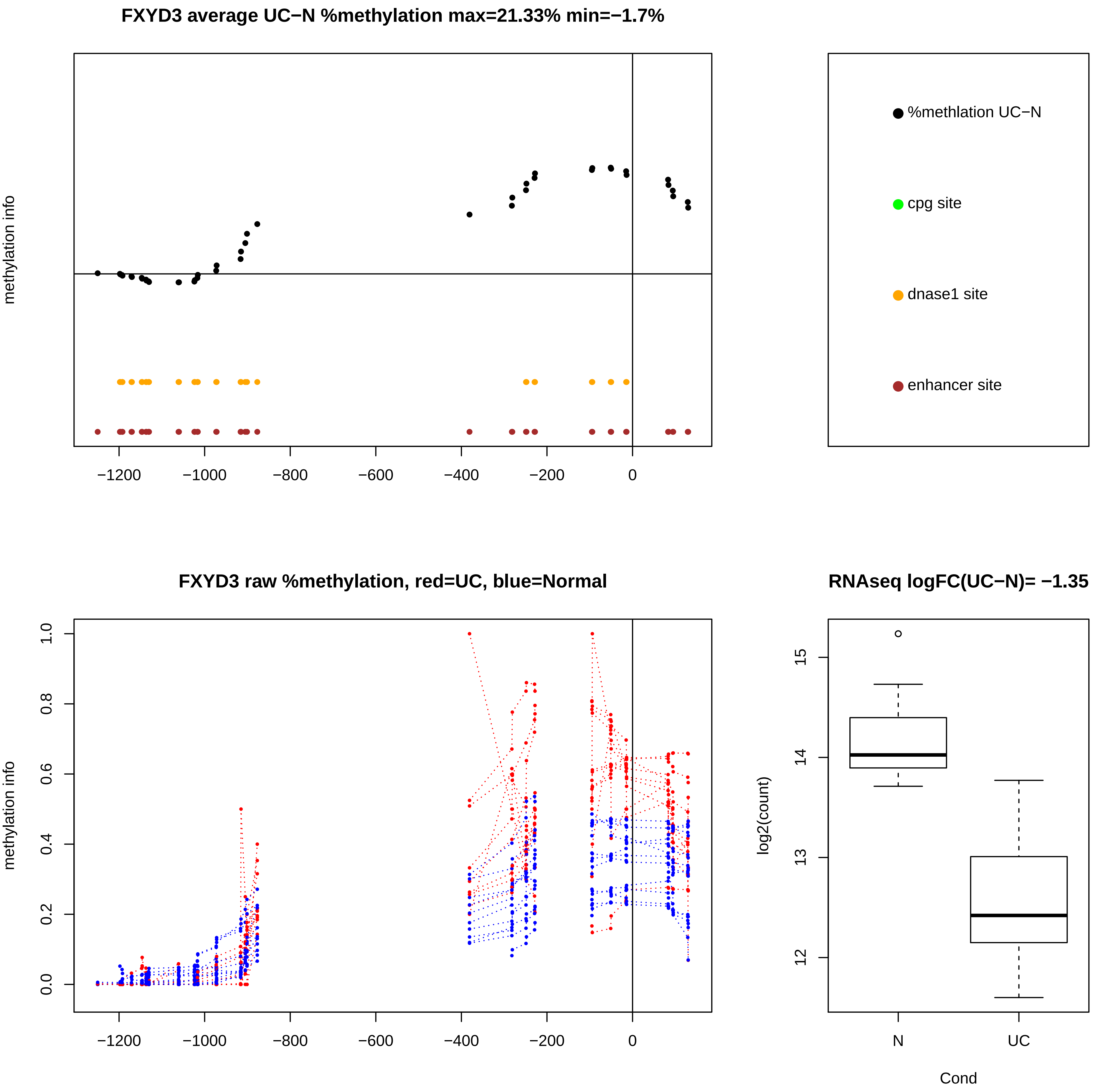
RNAseq logFC(UC−N)= −1.23



FRMD1 average UC−N %methylation max=22.98% min=−5.74%

FRMD1 raw %methylation, red=UC, blue=Normal

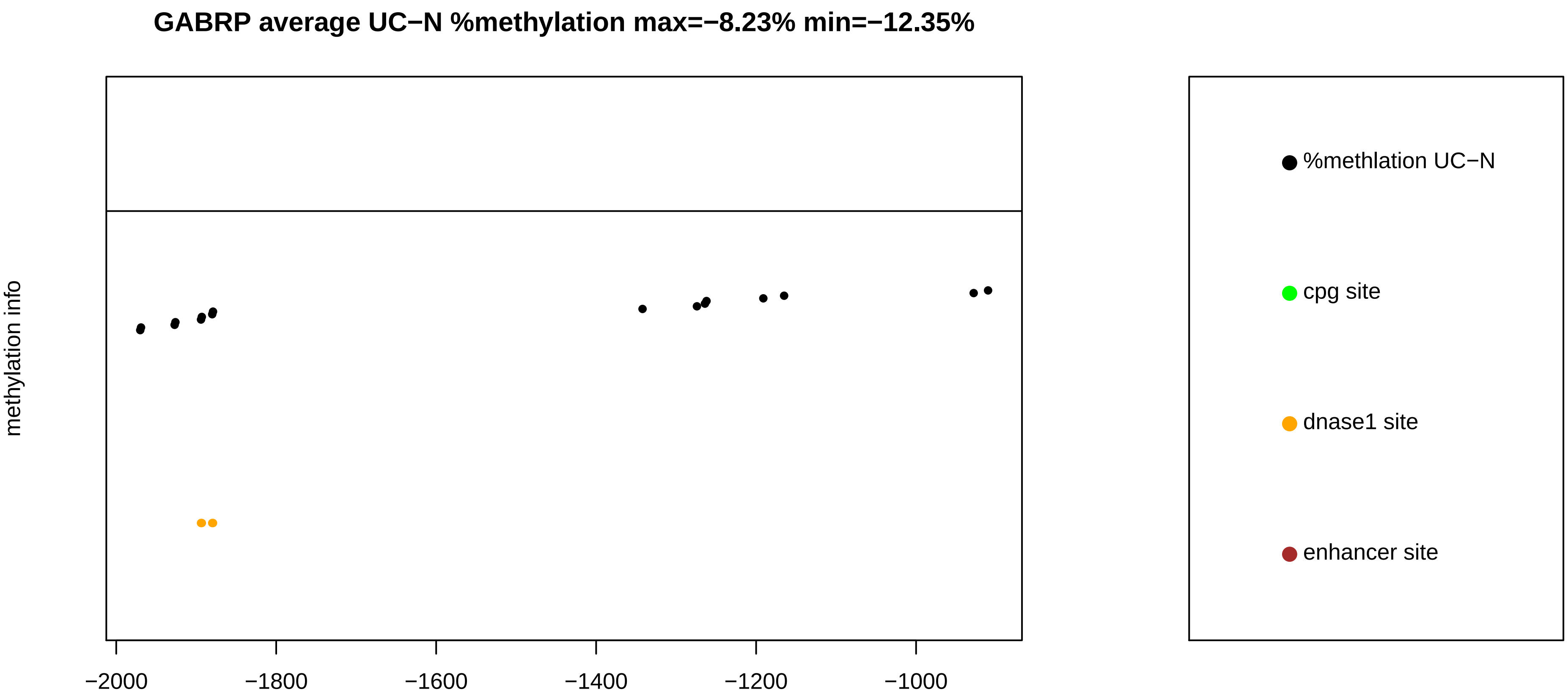
RNAseq logFC(UC−N)= −2.26



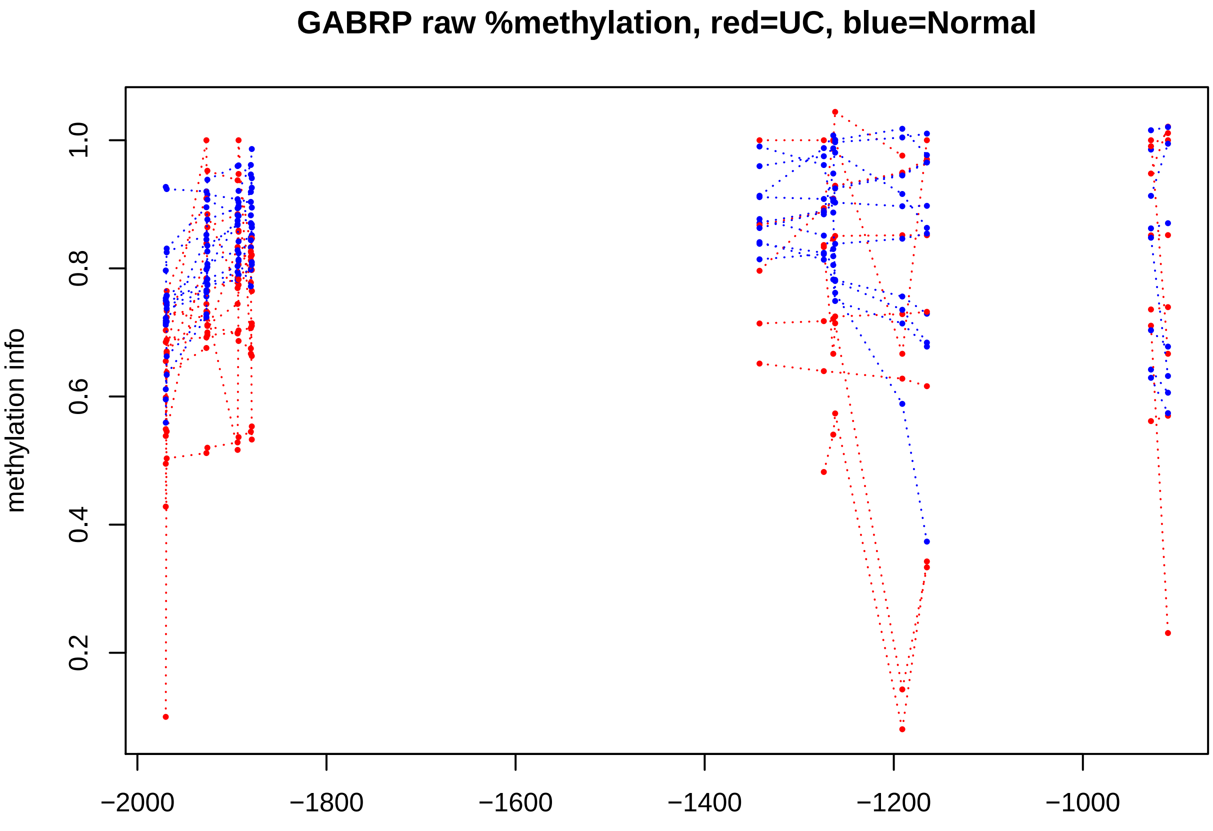
FXYD3 average UC−N %methylation max=21.33% min=−1.7%

FXYD3 raw %methylation, red=UC, blue=Normal

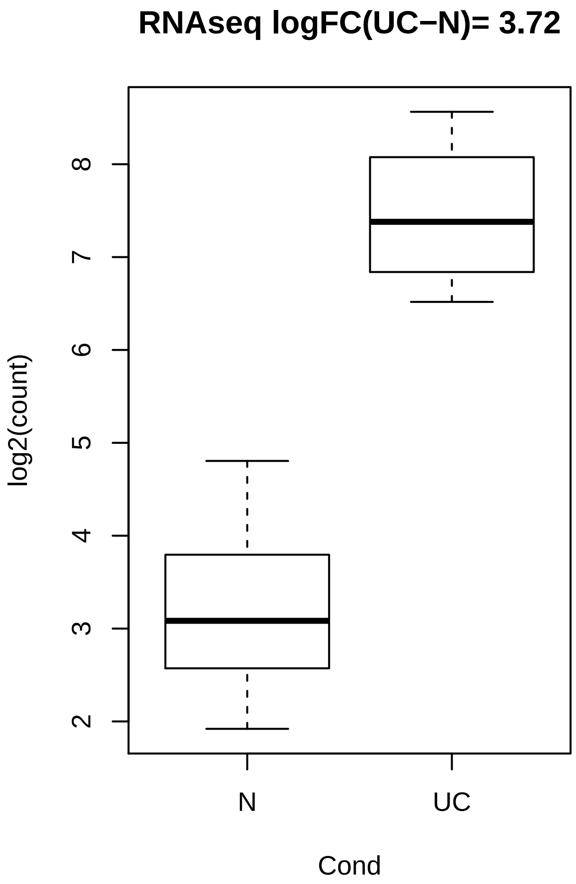
RNAseq logFC(UC−N)= −1.35



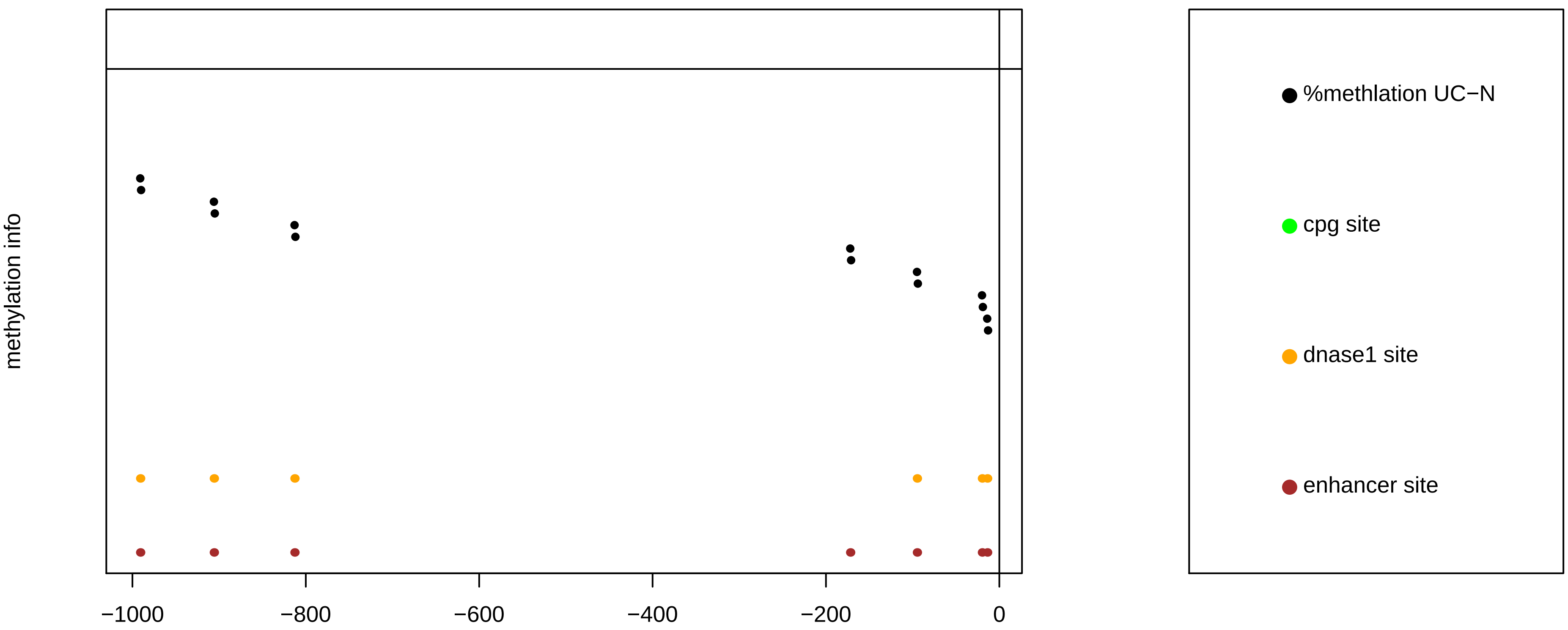
GABRP average UC−N %methylation max=−8.23% min=−12.35%

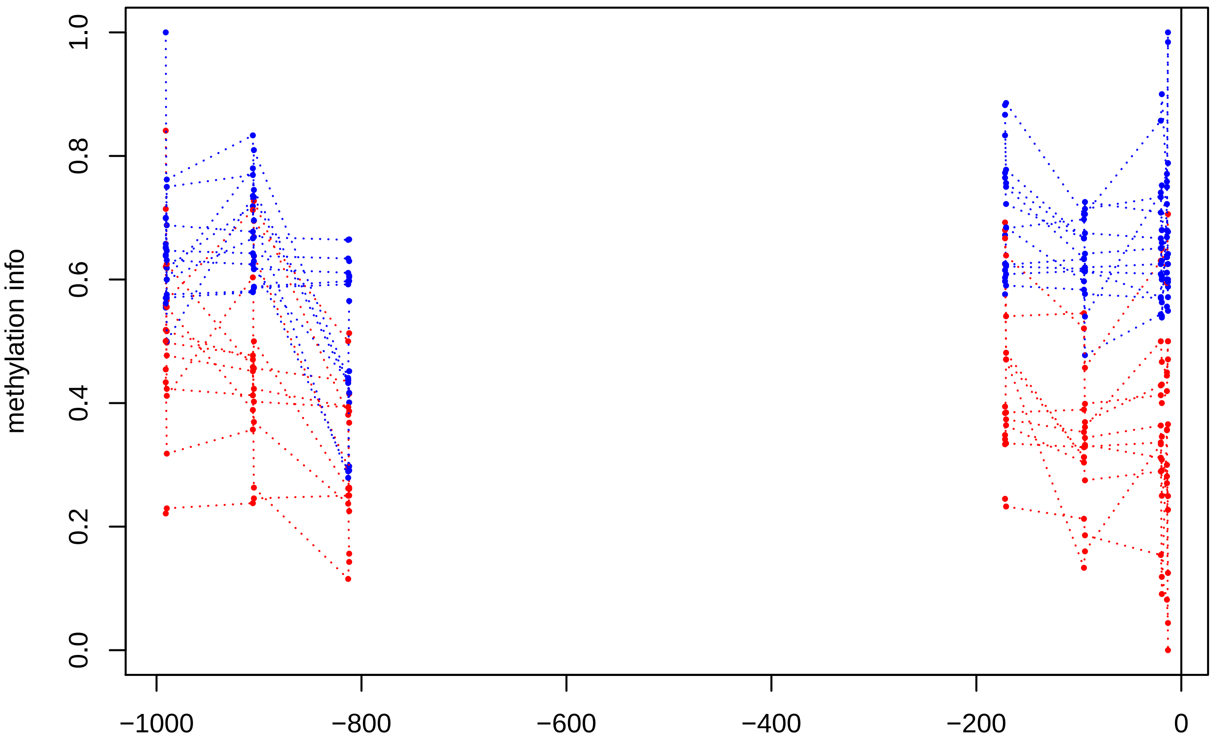


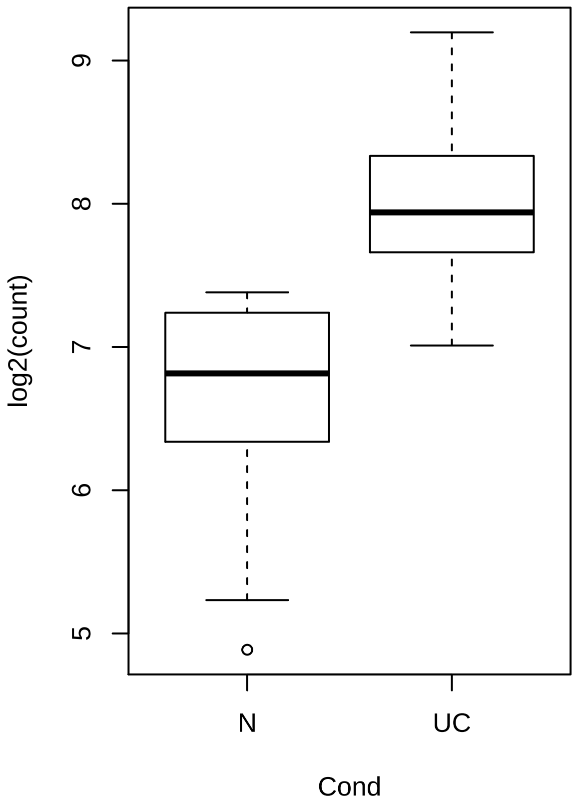
GABRP raw %methylation, red=UC, blue=Normal

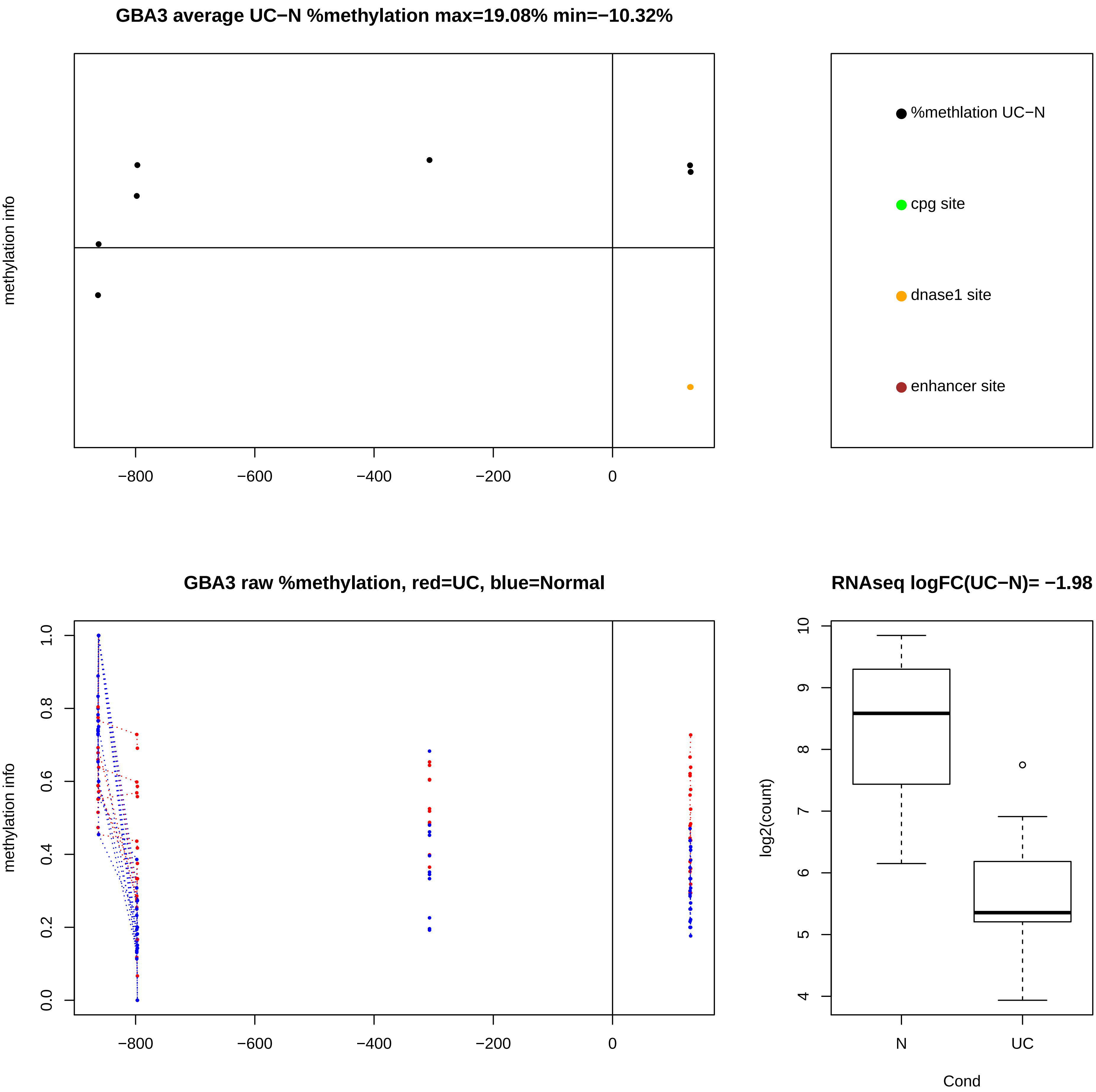


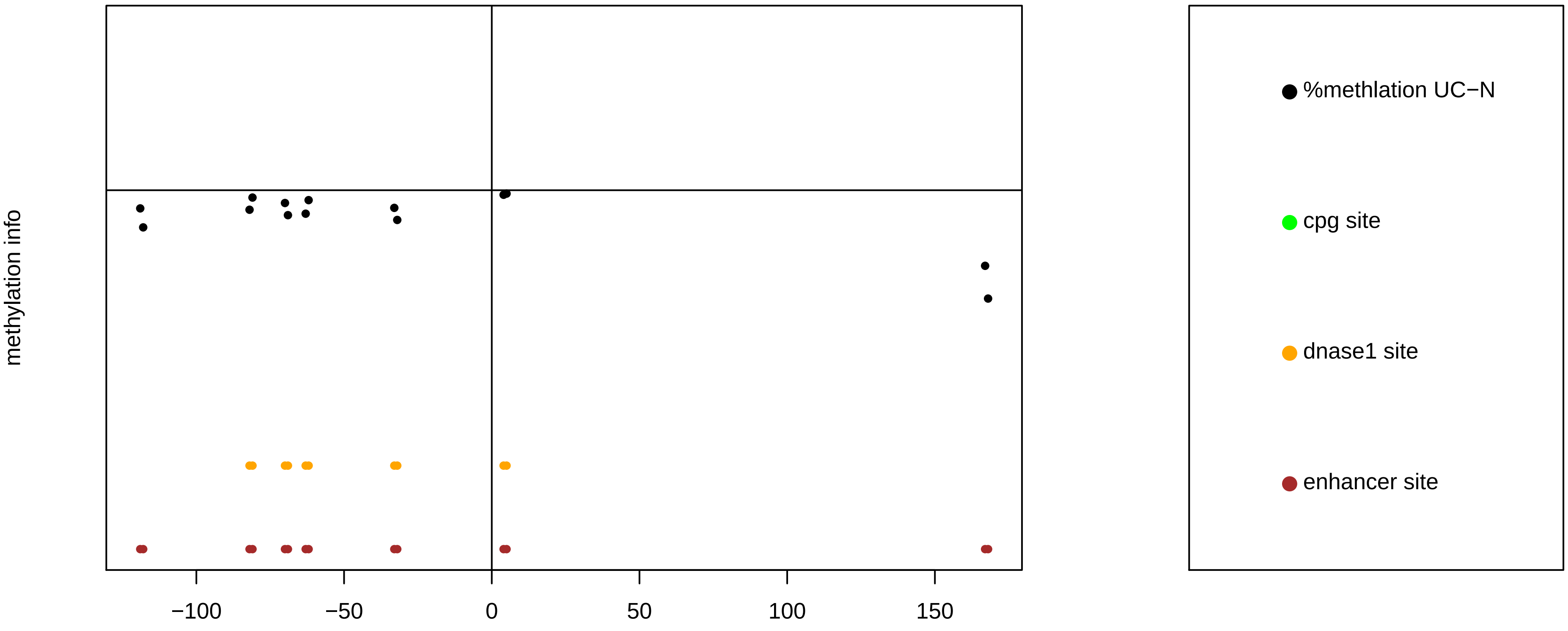
RNAseq logFC(UC−N)= 3.72


GAPT average UC−N %methylation max=−14.78% min=−35.32%

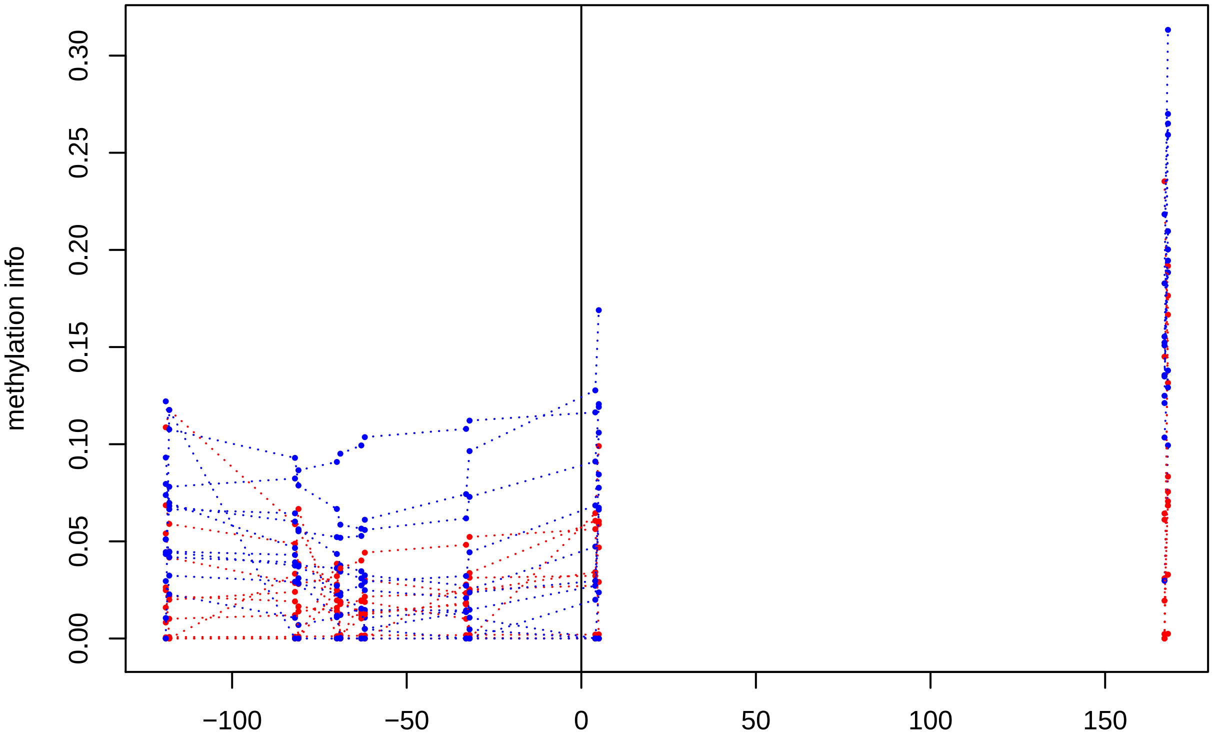

GAPT raw %methylation, red=UC, blue=Normal


RNAseq logFC(UC−N)= 1.22

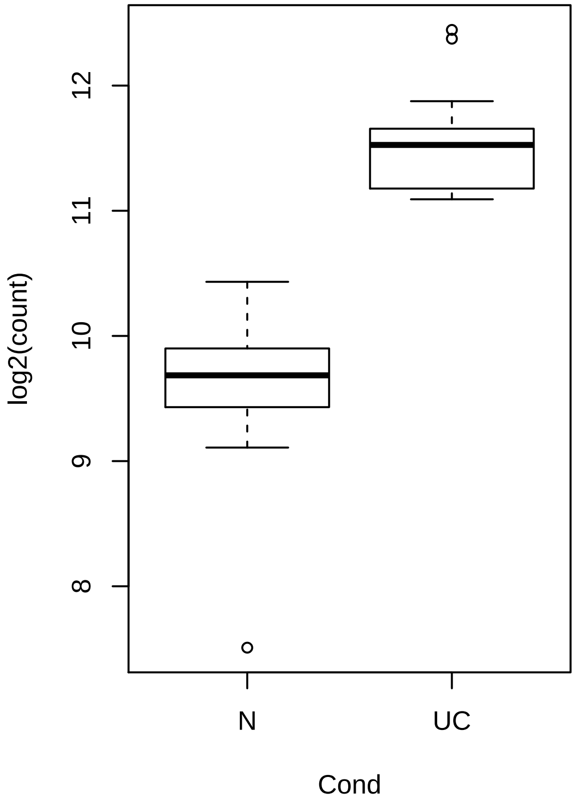

GBA3 average UC−N %methylation max=19.08% min=−10.32%
methylation info
−800
−600
−400
−200
0
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
GBA3 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−800
−600
−400
−200
0
RNAseq logFC(UC−N)= −1.98
log2(count)
4
5
6
7
8
9
10
N
UC
Cond



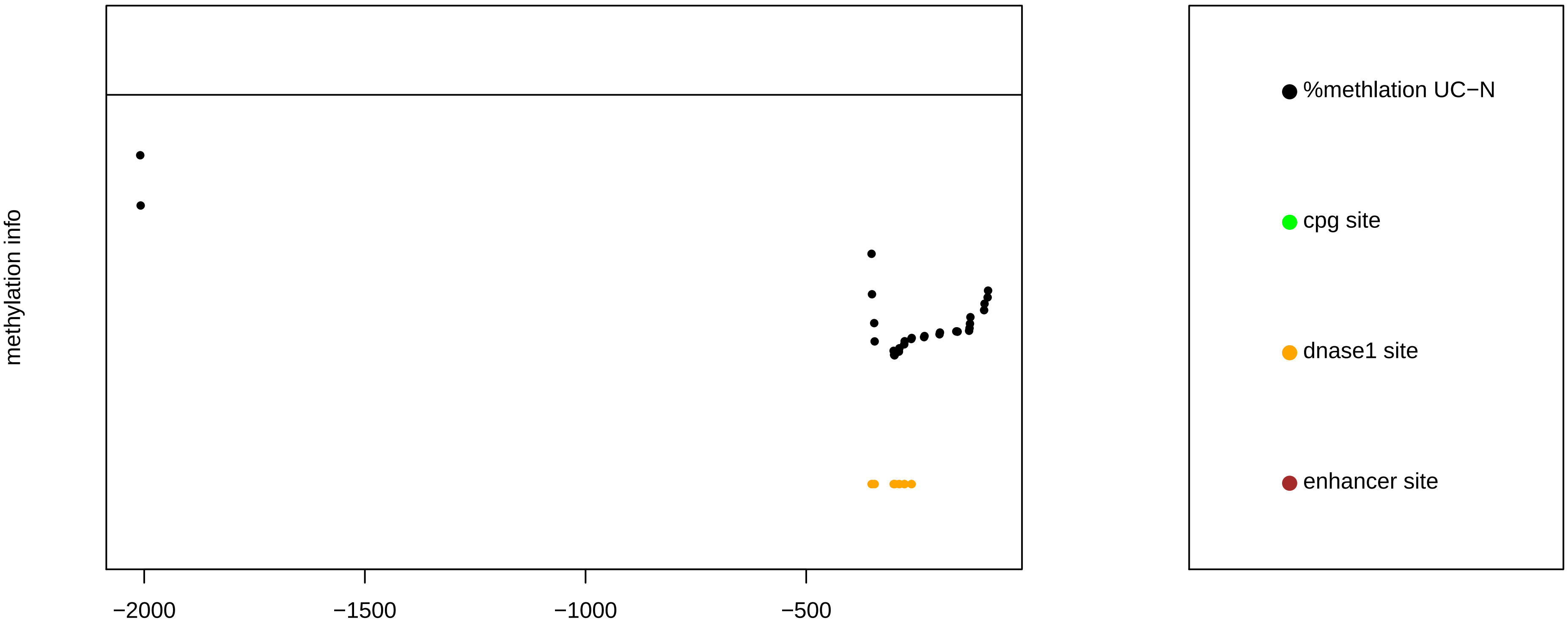
GBP4 average UC−N %methylation max=−0.4% min=−12.97%

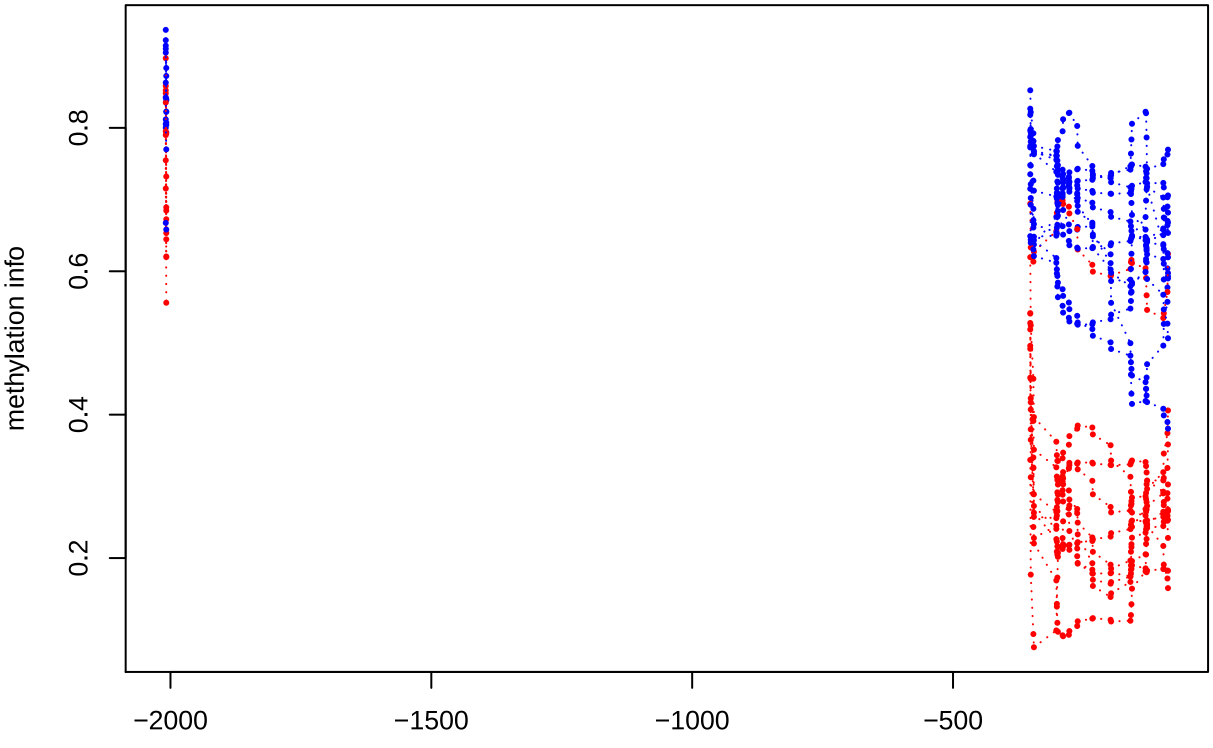


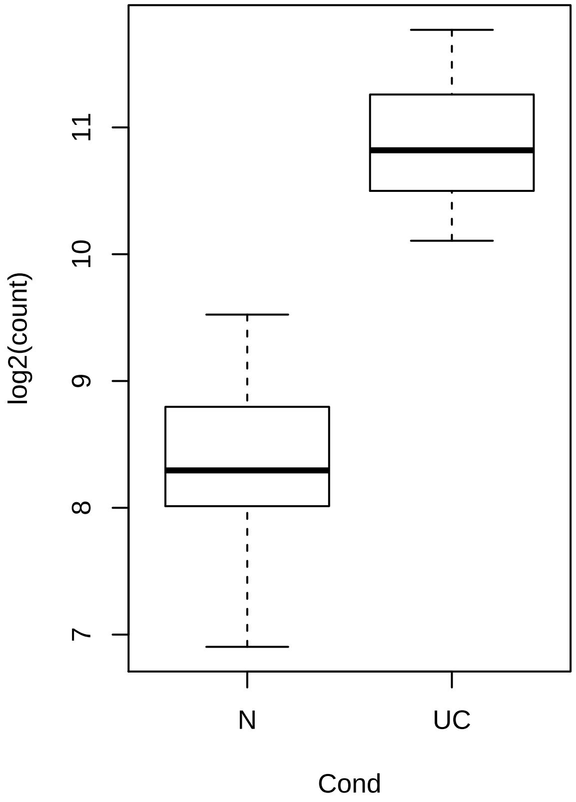
GBP4 raw %methylation, red=UC, blue=Normal

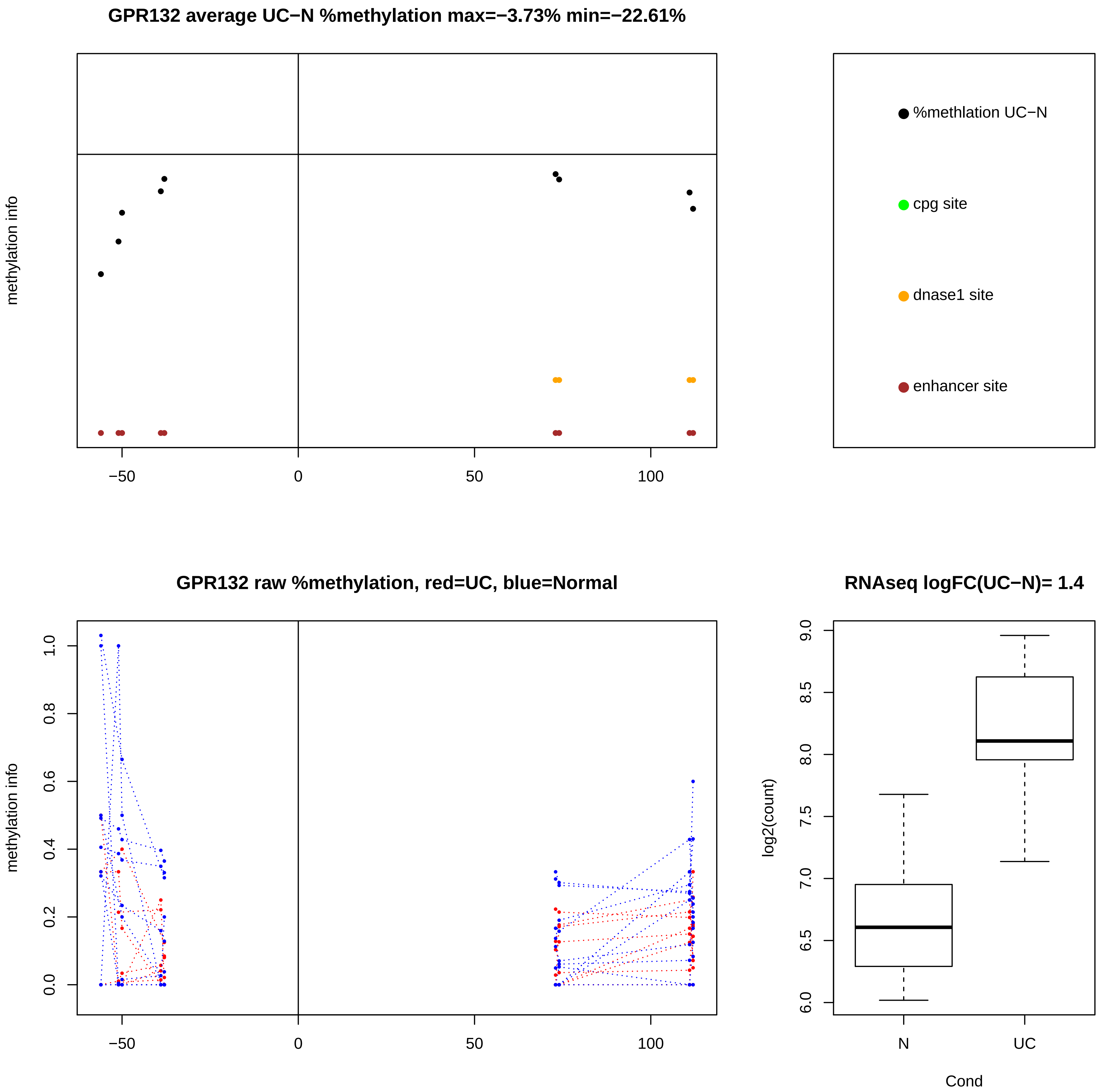


RNAseq logFC(UC−N)= 1.74


GBP5 average UC−N %methylation max=−9.39% min=−40.48%

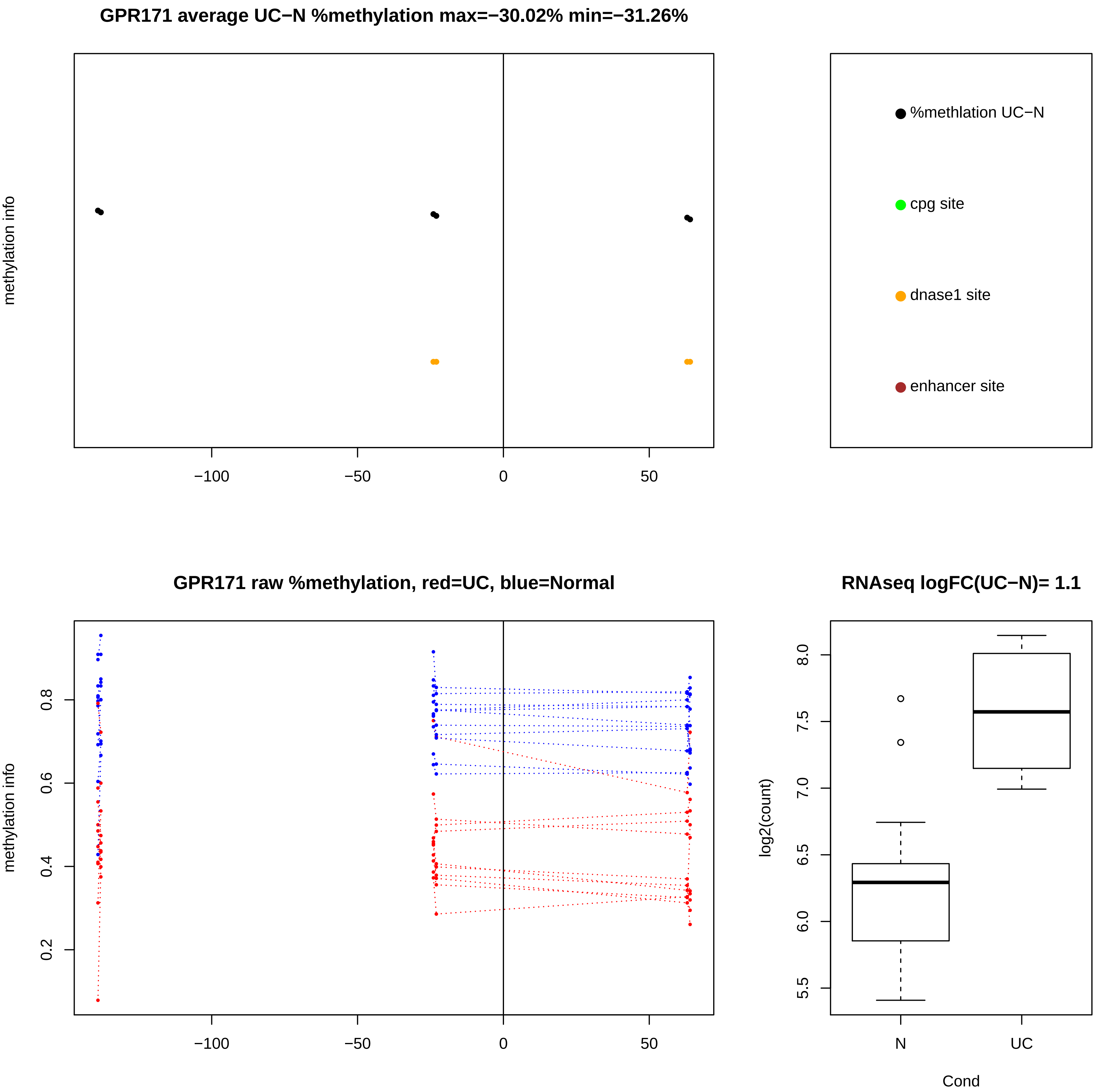

GBP5 raw %methylation, red=UC, blue=Normal


RNAseq logFC(UC−N)= 2.22

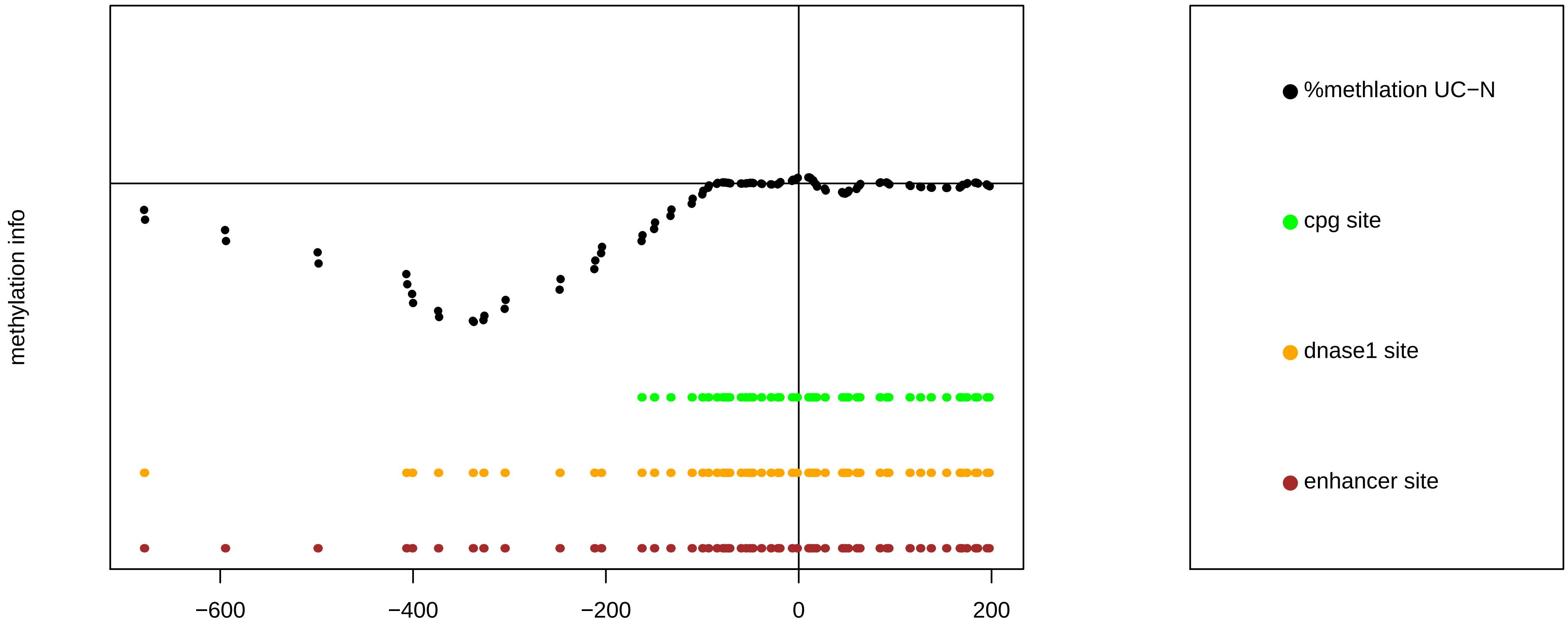

GPR132 average UC−N %methylation max=−3.73% min=−22.61%

GPR132 raw %methylation, red=UC, blue=Normal

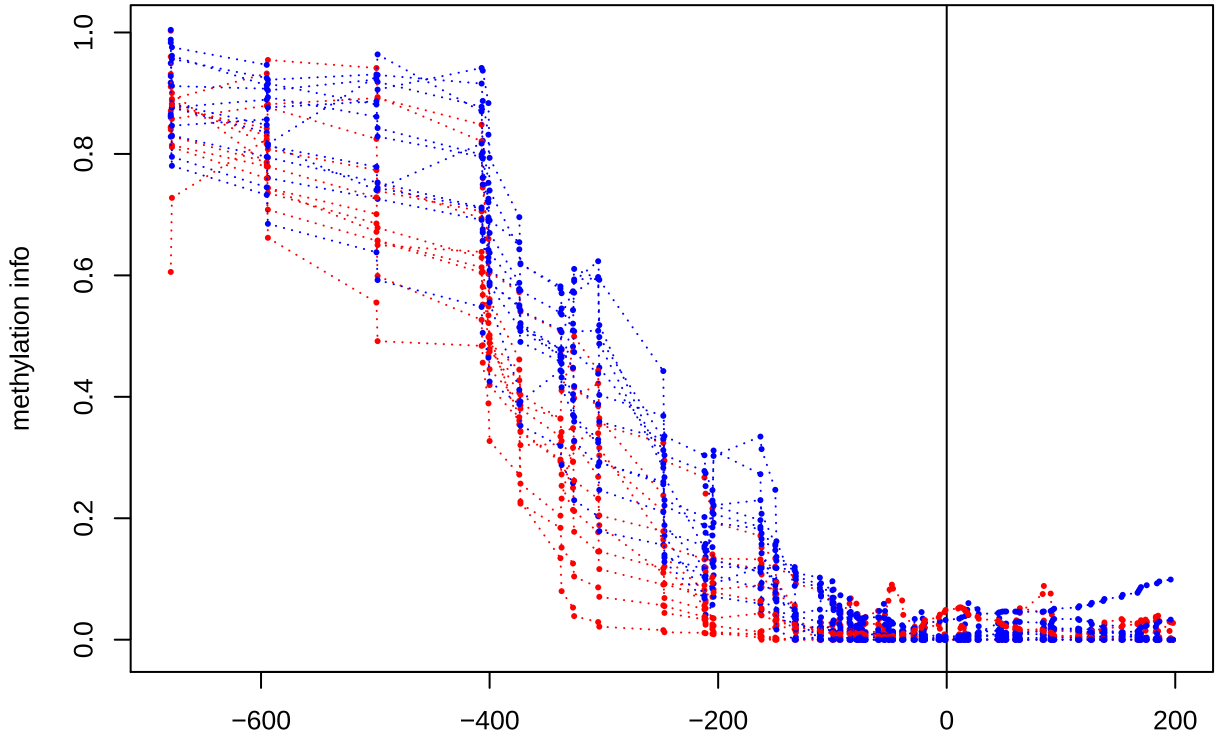
RNAseq logFC(UC−N)= 1.4


GPR171 average UC−N %methylation max=−30.02% min=−31.26%
methylation info
−100
−50
0
50
%methlation UC−N
cpg site
dnase1 site
enhancer site
GPR171 raw %methylation, red=UC, blue=Normal
methylation info
0.2
0.4
0.6
0.8
−100
−50
0
50
RNAseq logFC(UC−N)= 1.1
log2(count)
5.5
6.0
6.5
7.0
7.5
8.0
N
UC
Cond

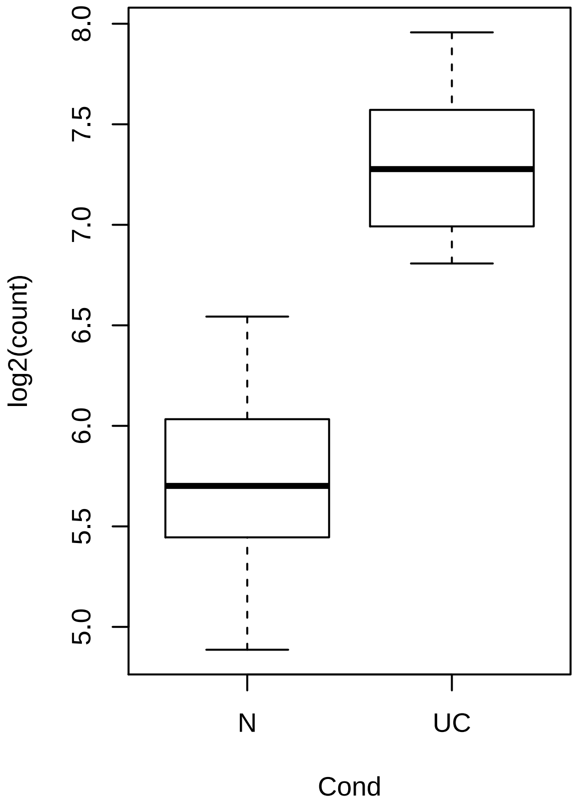
GPX7 average UC−N %methylation max=0.8% min=−18.35%

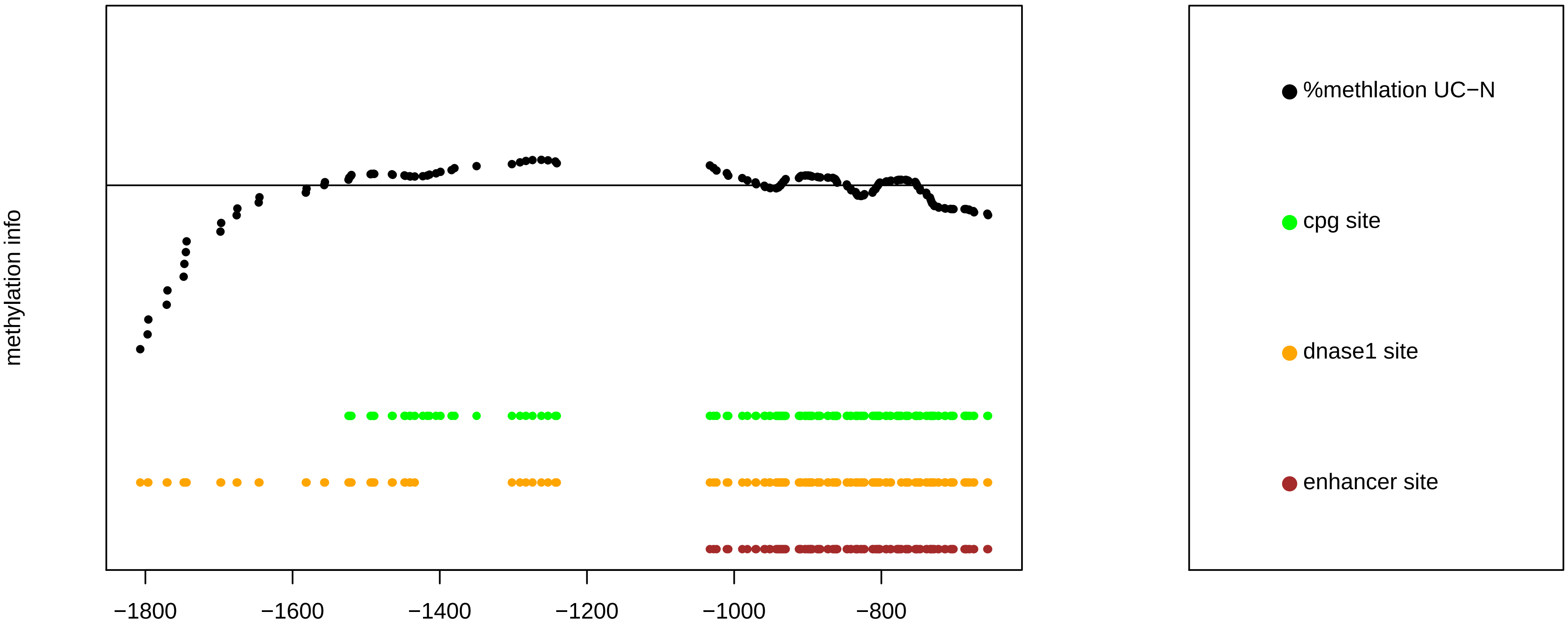


GPX7 raw %methylation, red=UC, blue=Normal

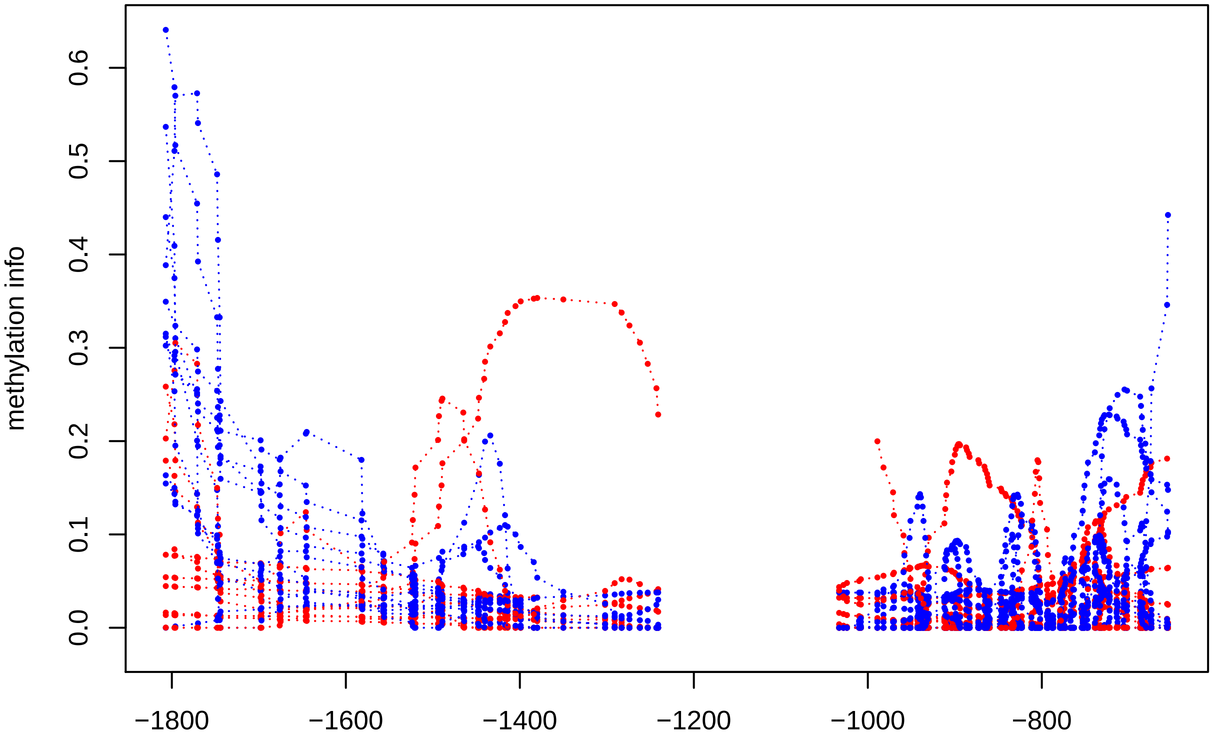


RNAseq logFC(UC−N)= 1.5

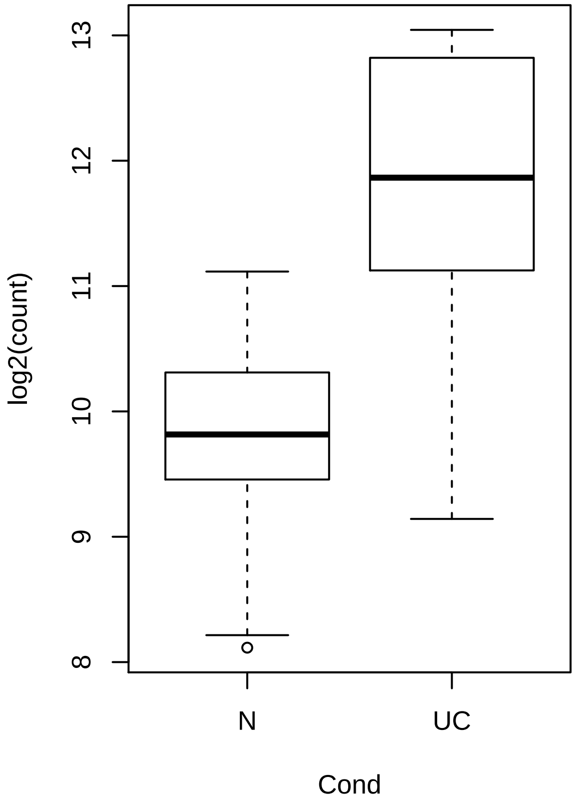




GREM1 average UC−N %methylation max=3.82% min=−24.59%

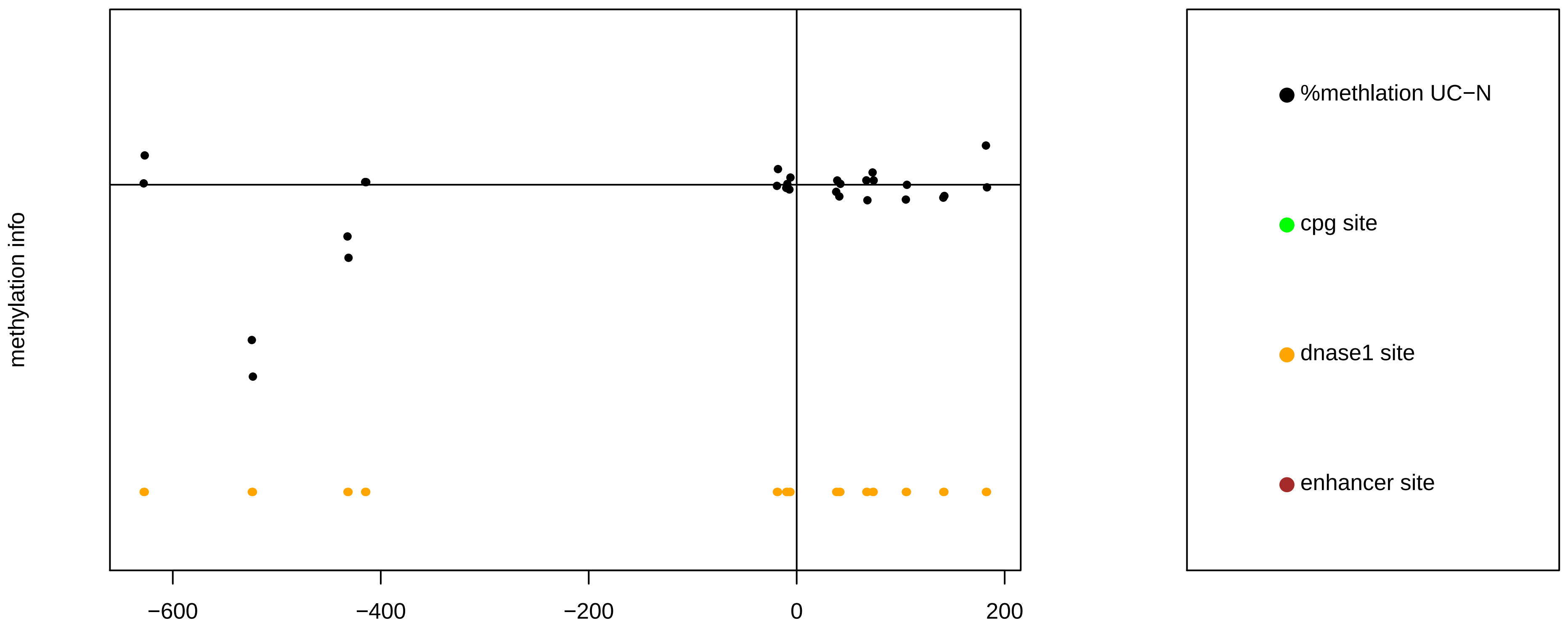


GREM1 raw %methylation, red=UC, blue=Normal

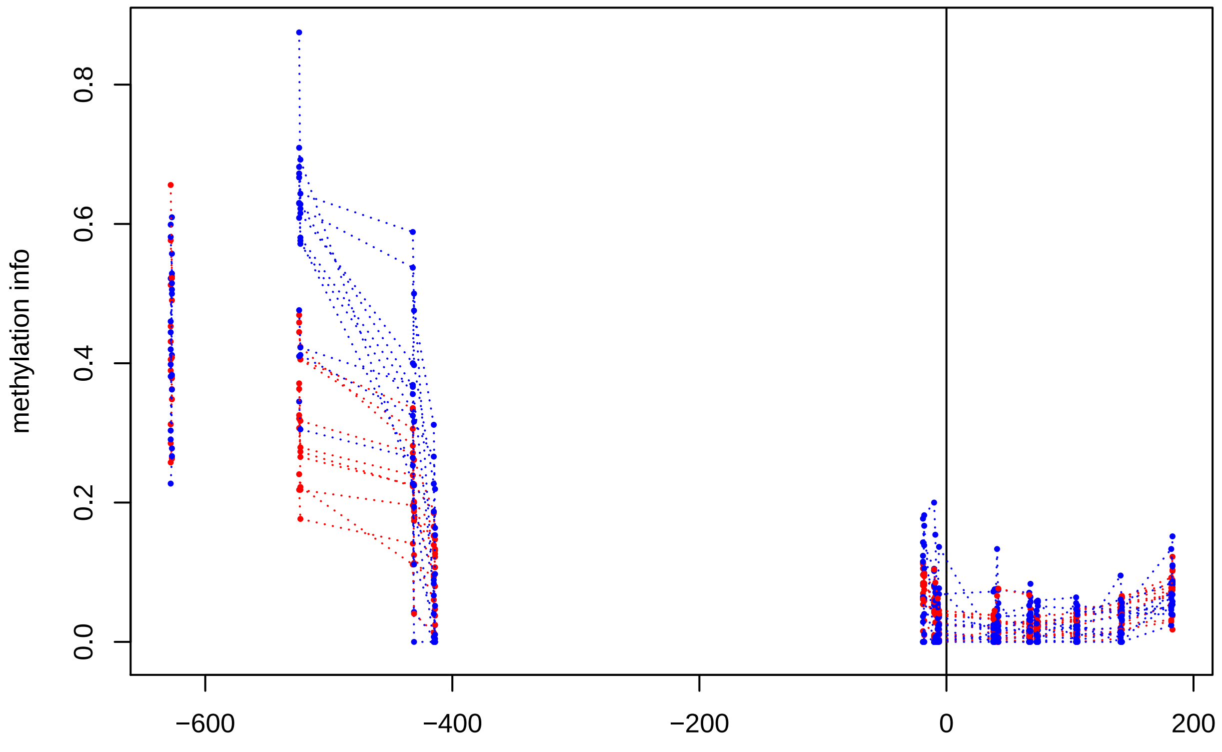


RNAseq logFC(UC−N)= 1.81

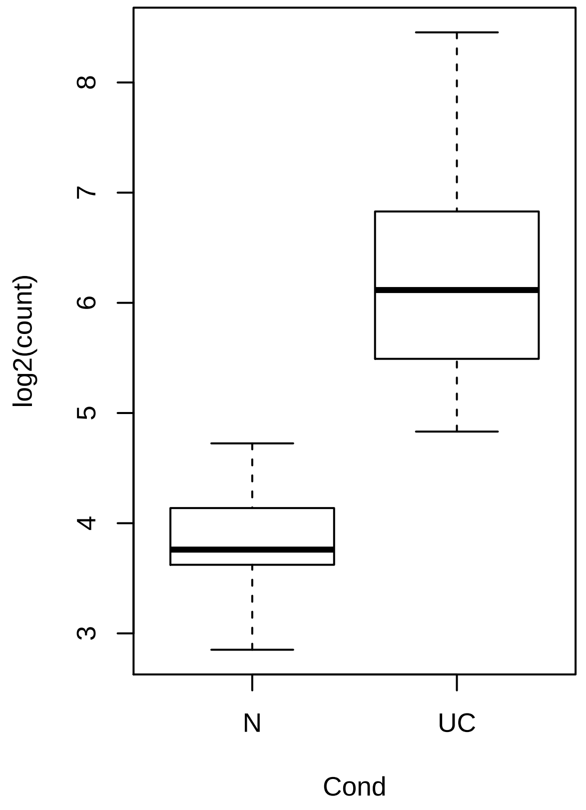
GRHL3 average UC−N %methylation max=6.8% min=−33.27%

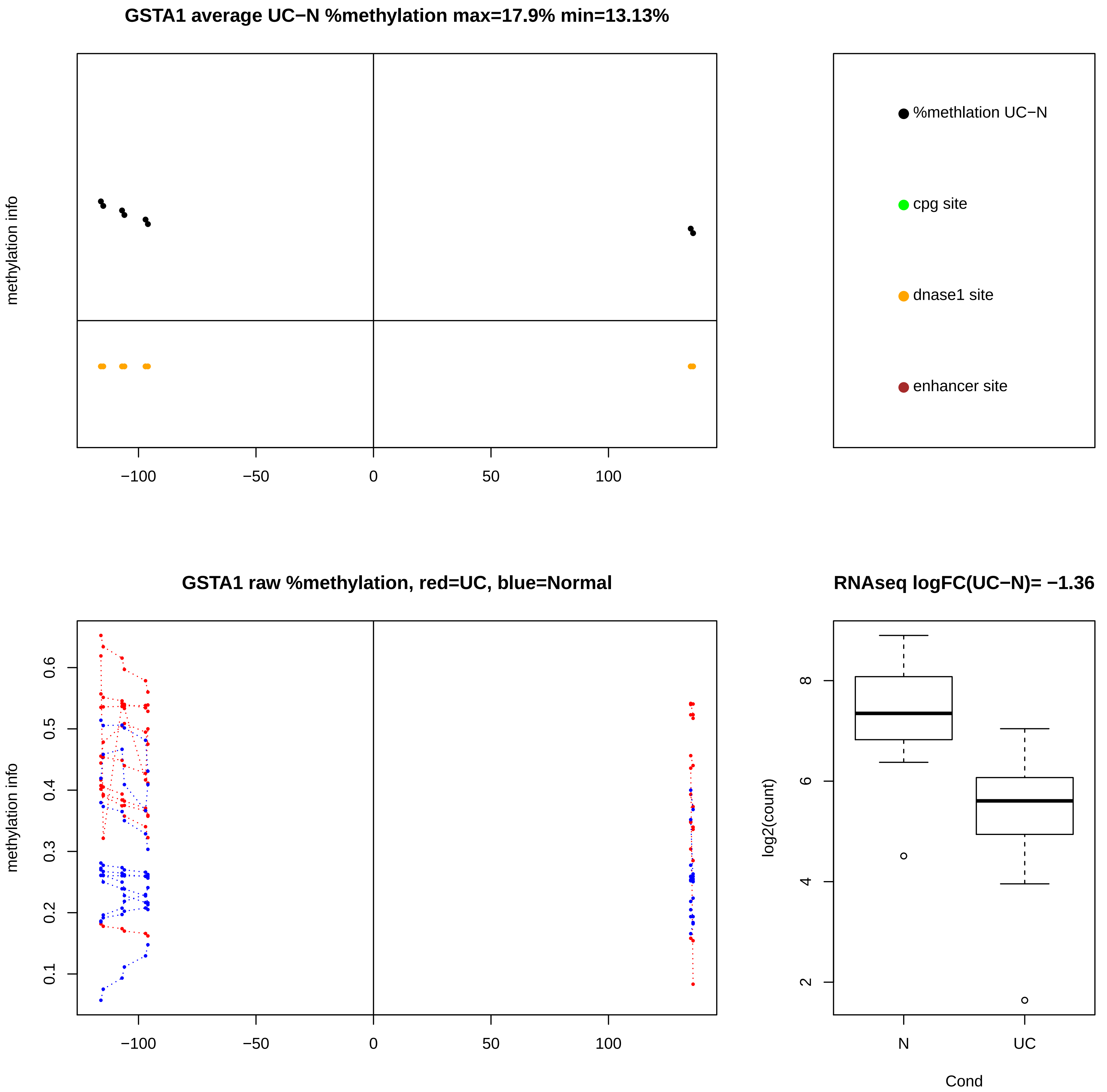


GRHL3 raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 2.27

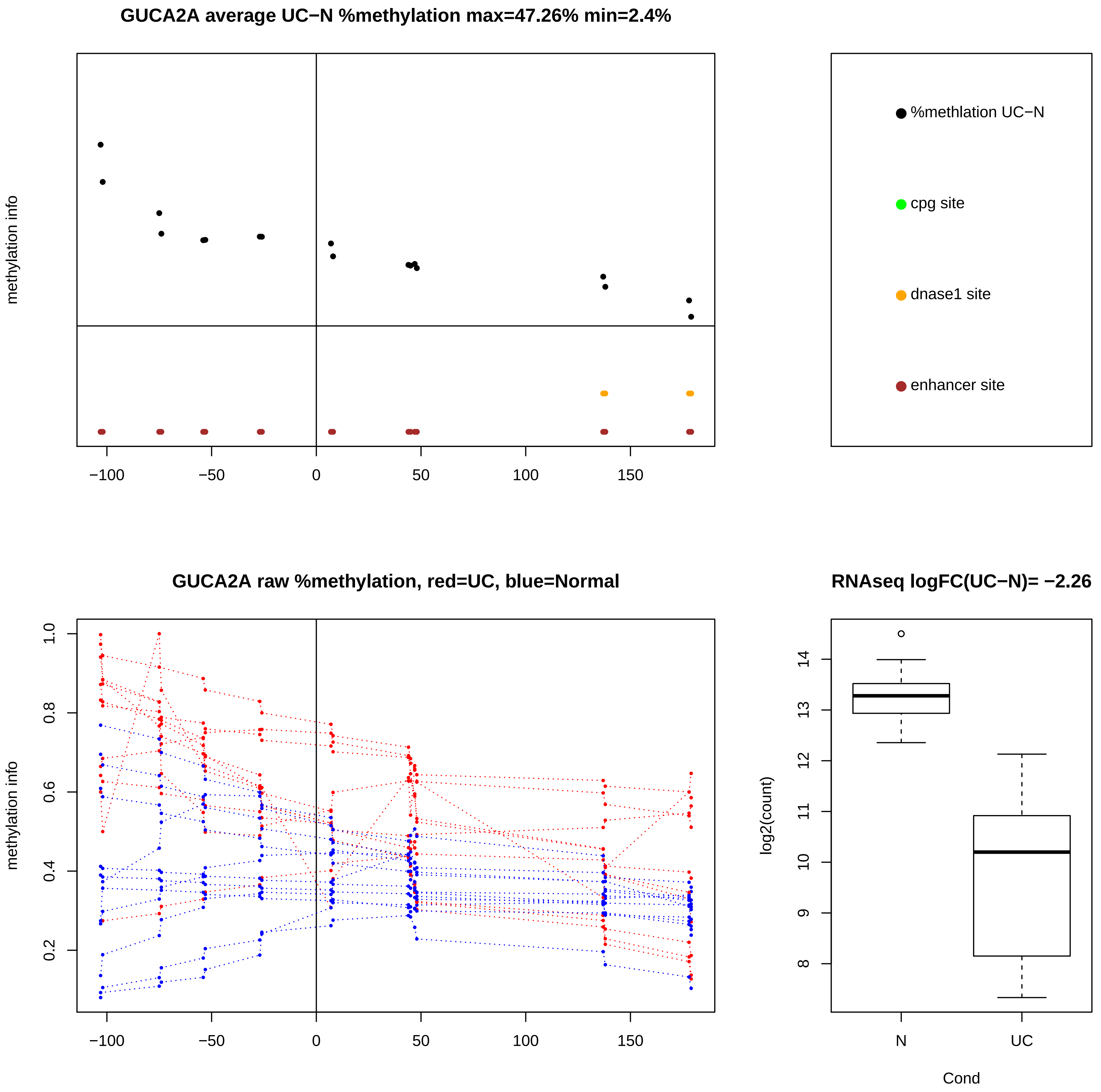


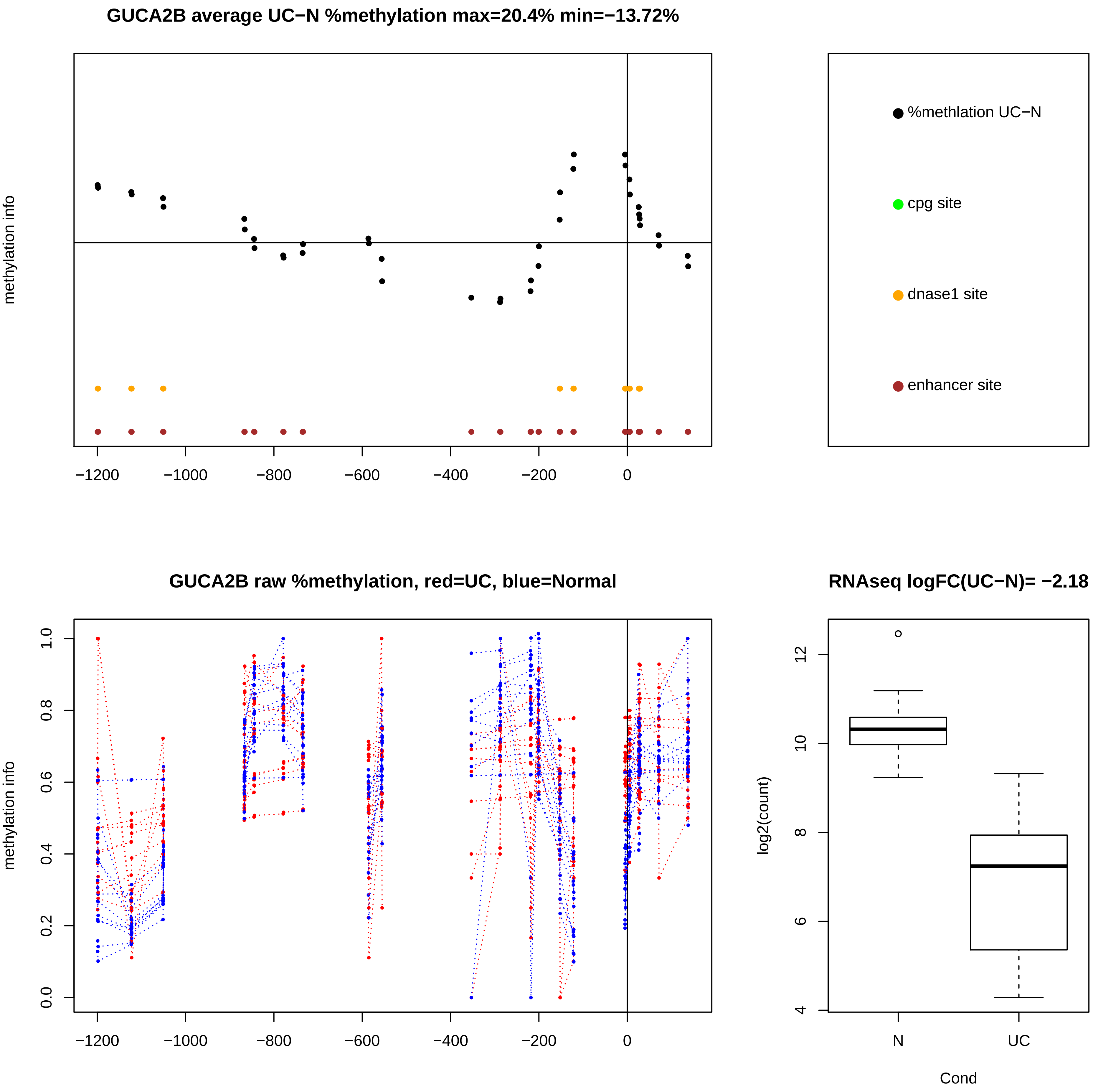


GSTA1 average UC−N %methylation max=17.9% min=13.13%

GSTA1 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= −1.36

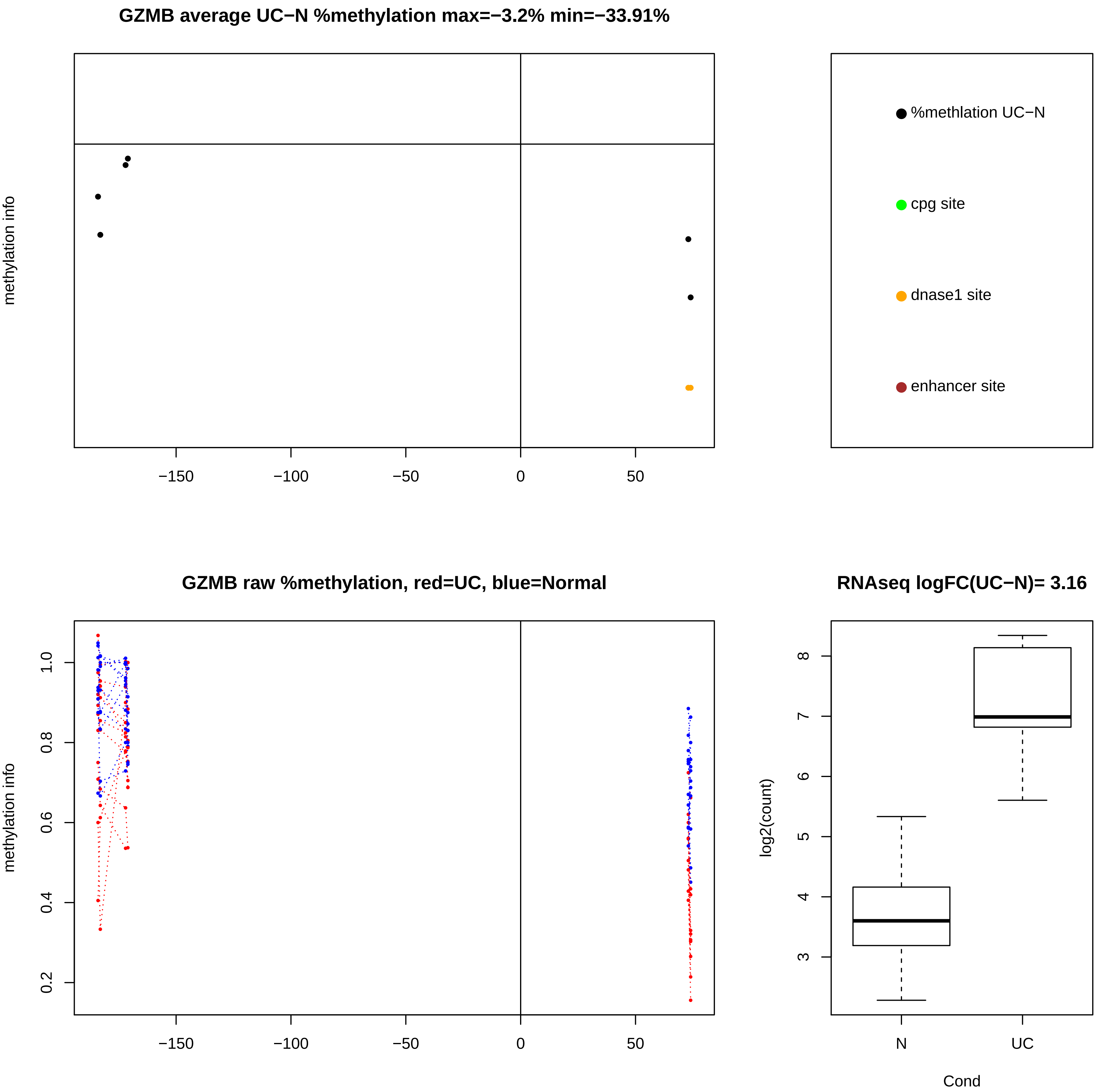

GUCA2A average UC−N %methylation max=47.26% min=2.4%
methylation info
−100
−50
0
50
100
150
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
GUCA2A raw %methylation, red=UC, blue=Normal
methylation info
0.2
0.4
0.6
0.8
1.0
−100
−50
0
50
100
150
RNAseq logFC(UC−N)= −2.26
log2(count)
8
9
10
11
12
13
14
N
UC
Cond



GUCA2B average UC−N %methylation max=20.4% min=−13.72%

GUCA2B raw %methylation, red=UC, blue=Normal

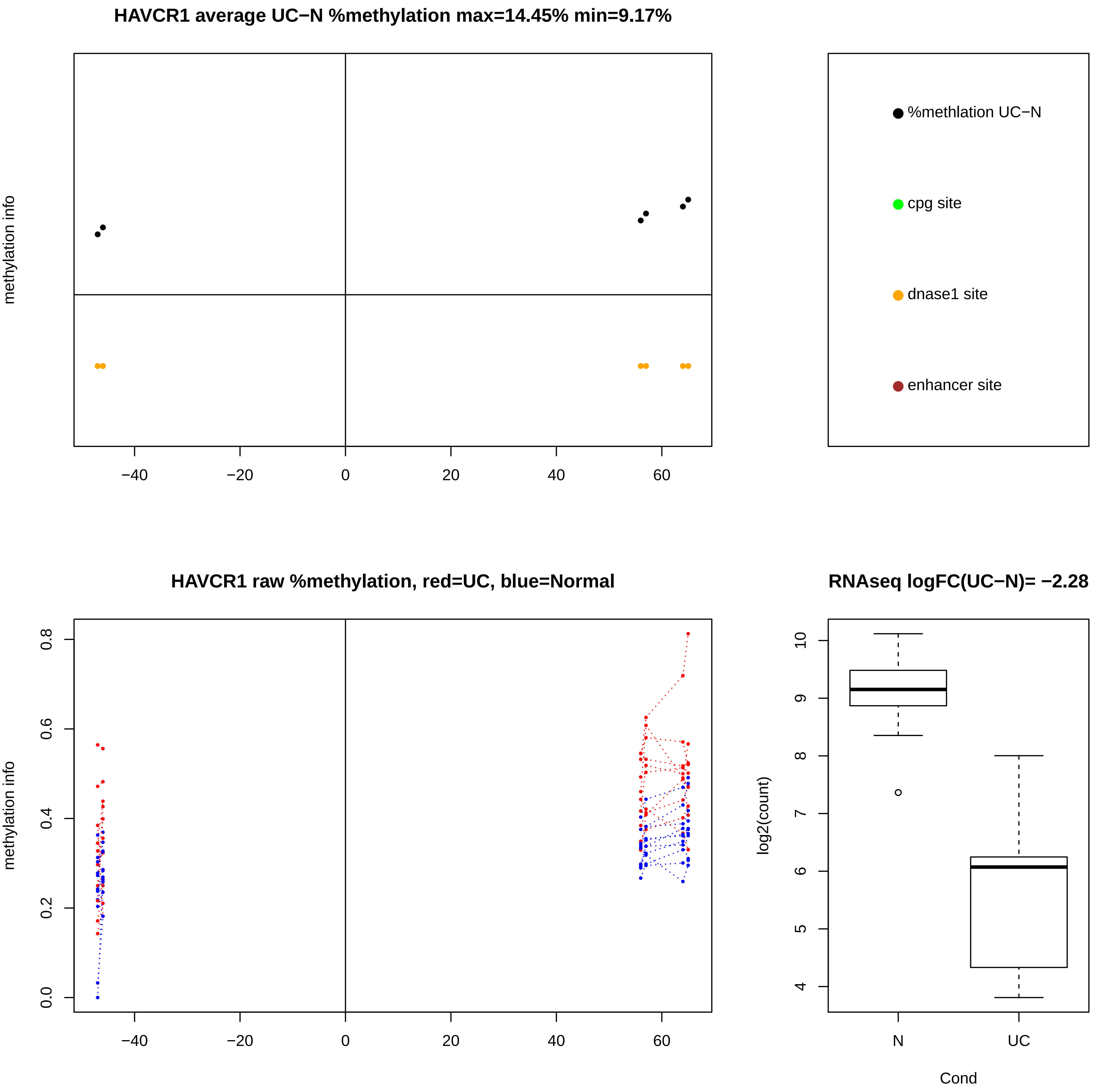
RNAseq logFC(UC−N)= −2.18



GZMB average UC−N %methylation max=−3.2% min=−33.91%

GZMB raw %methylation, red=UC, blue=Normal

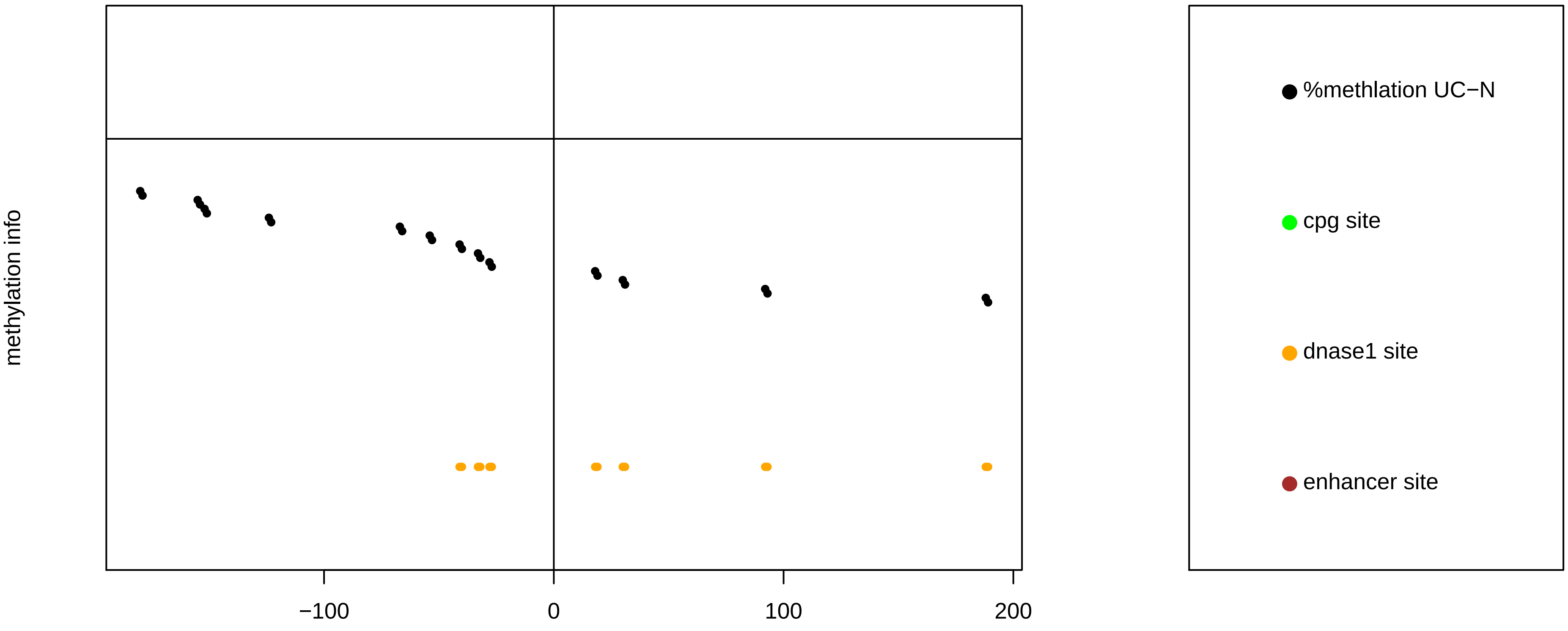
RNAseq logFC(UC−N)= 3.16


HAVCR1 average UC−N %methylation max=14.45% min=9.17%

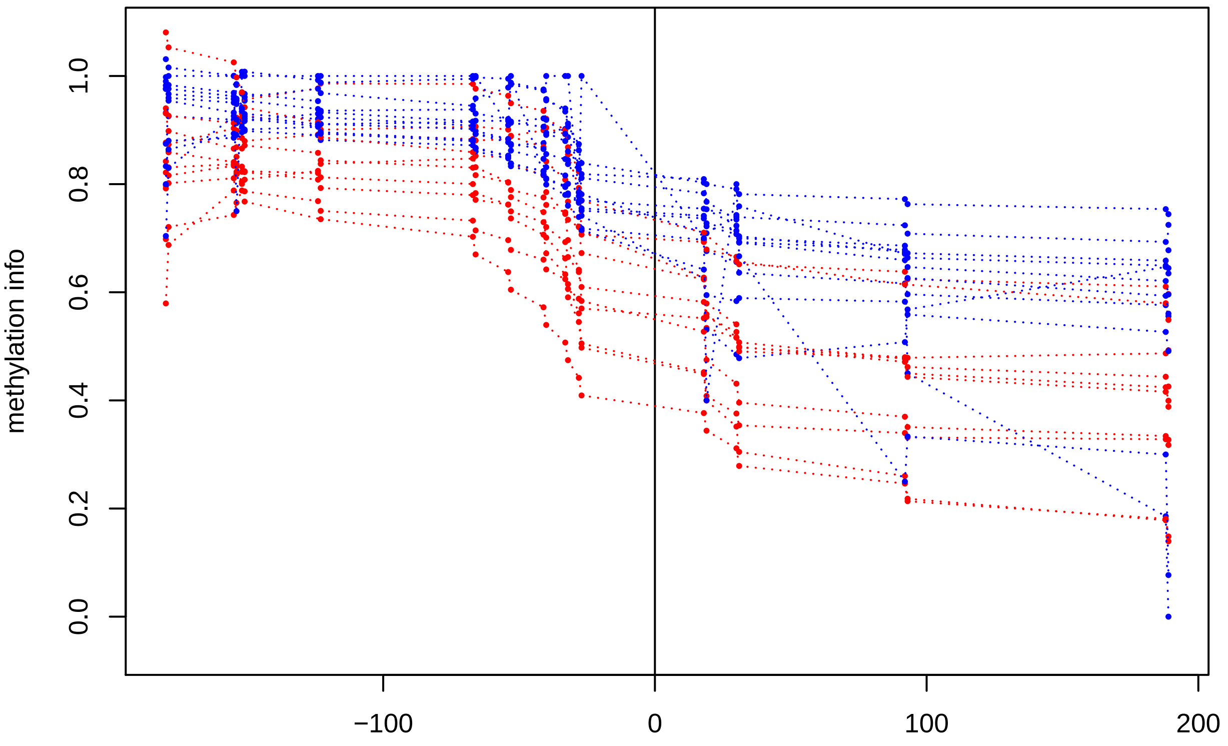
HAVCR1 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= −2.28

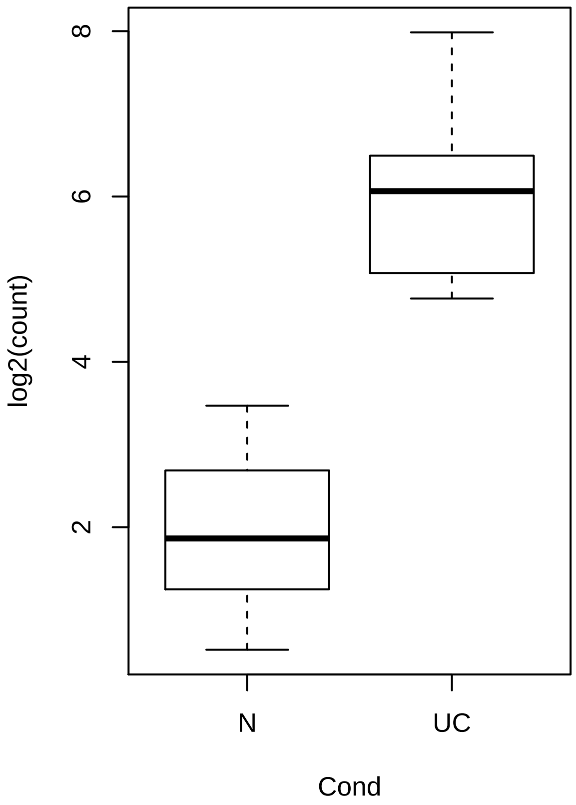
HCAR2 average UC−N %methylation max=−6.35% min=−19.88%

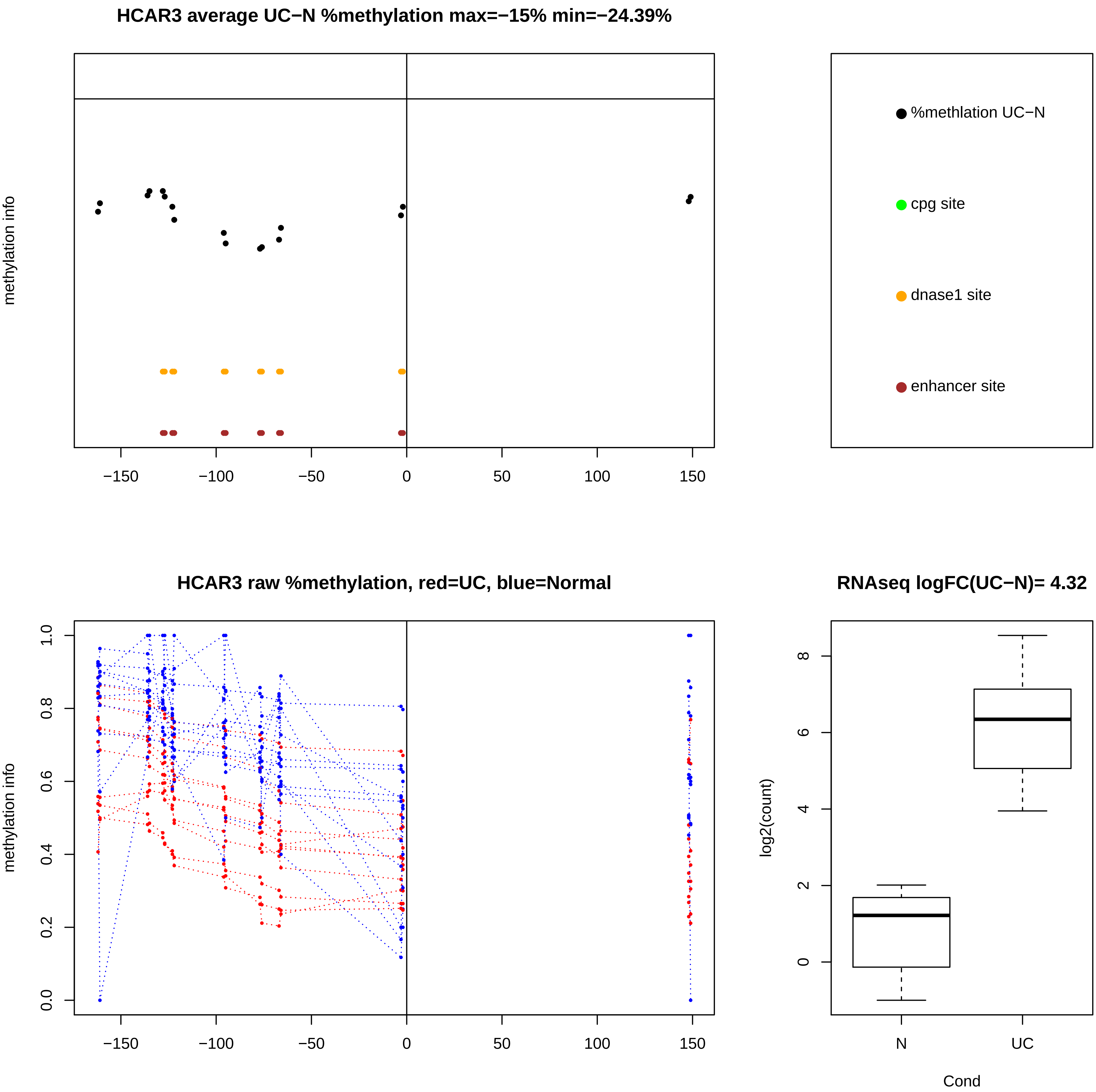


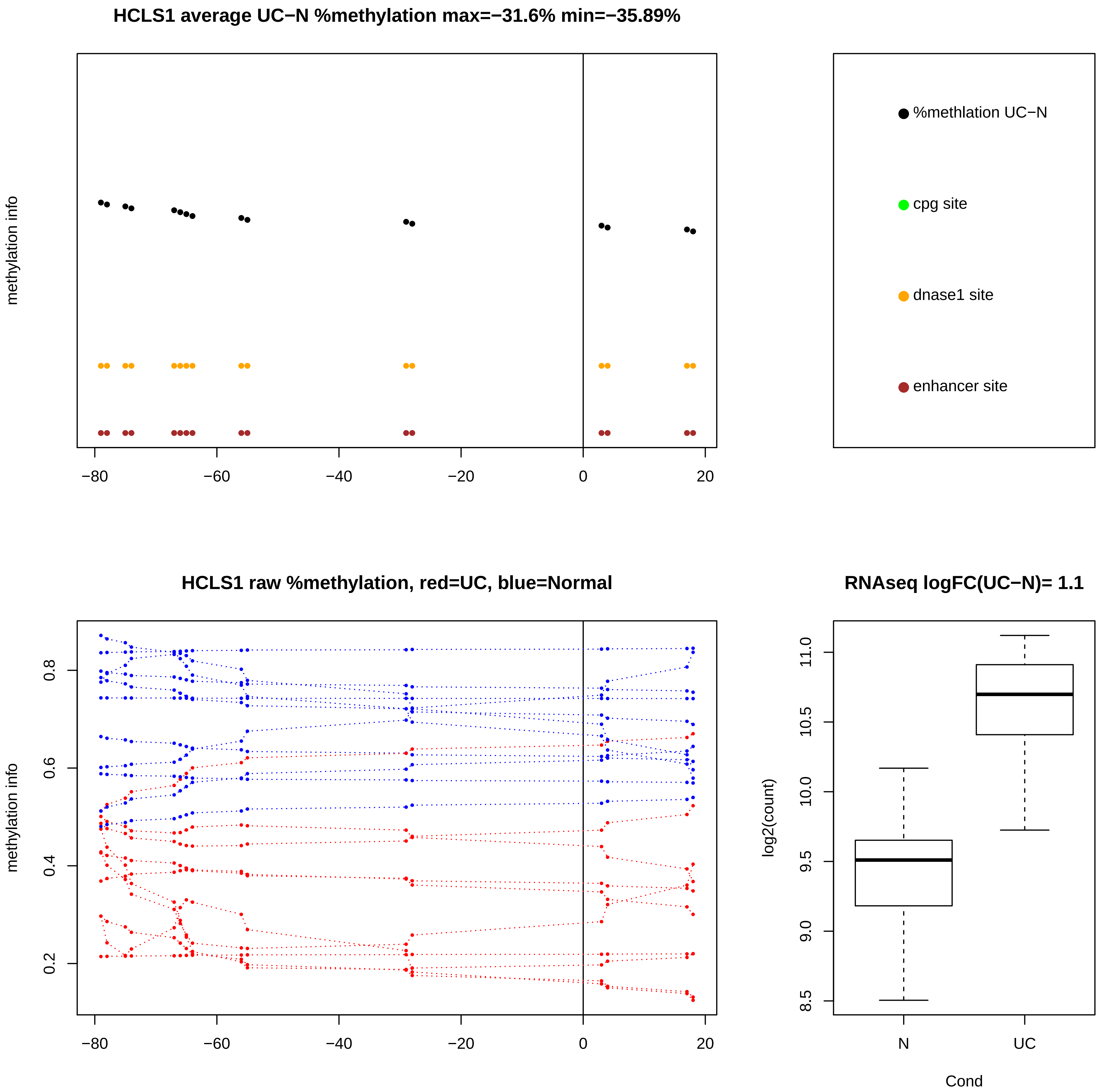
HCAR2 raw %methylation, red=UC, blue=Normal

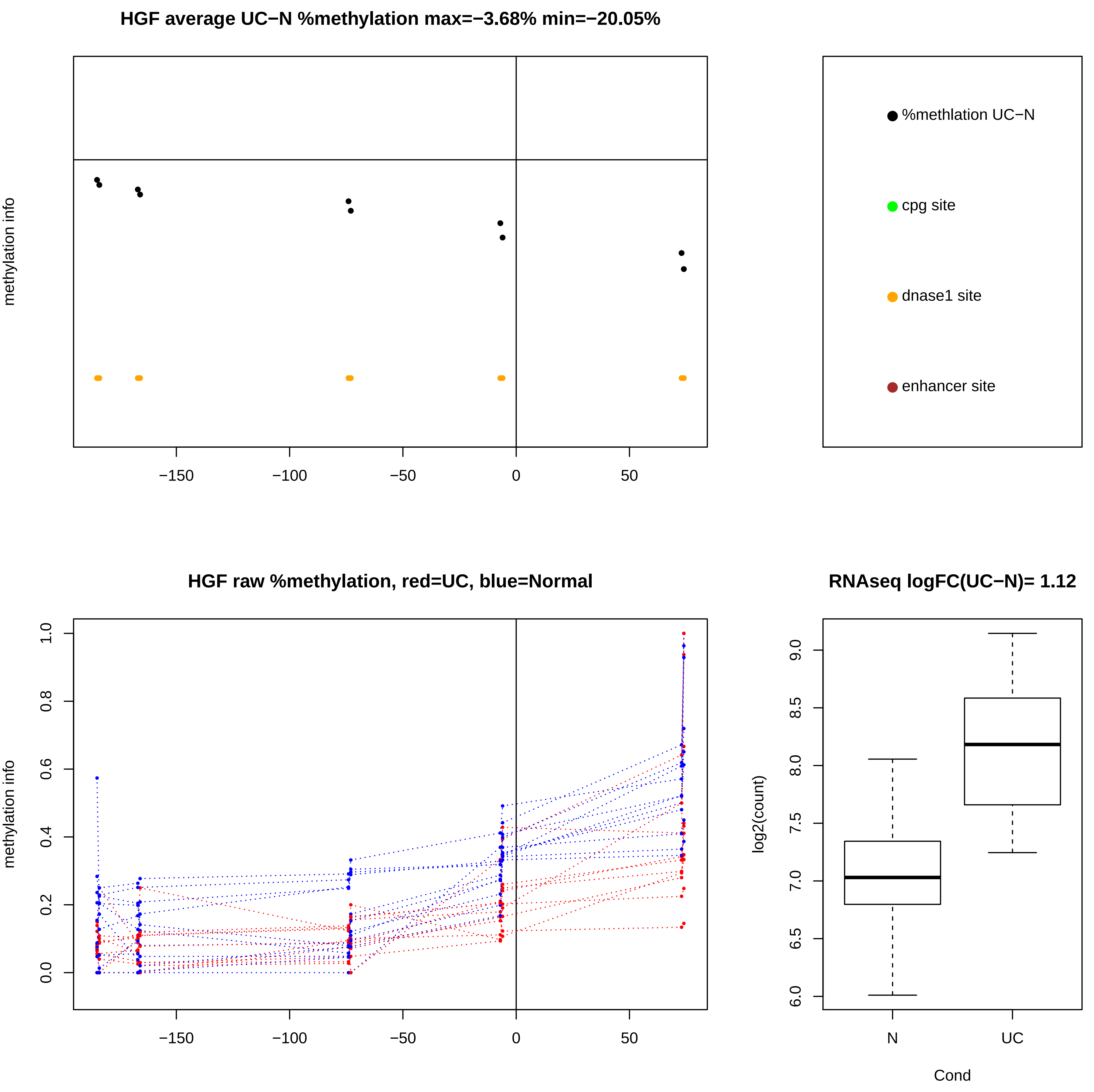


RNAseq logFC(UC−N)= 3.58



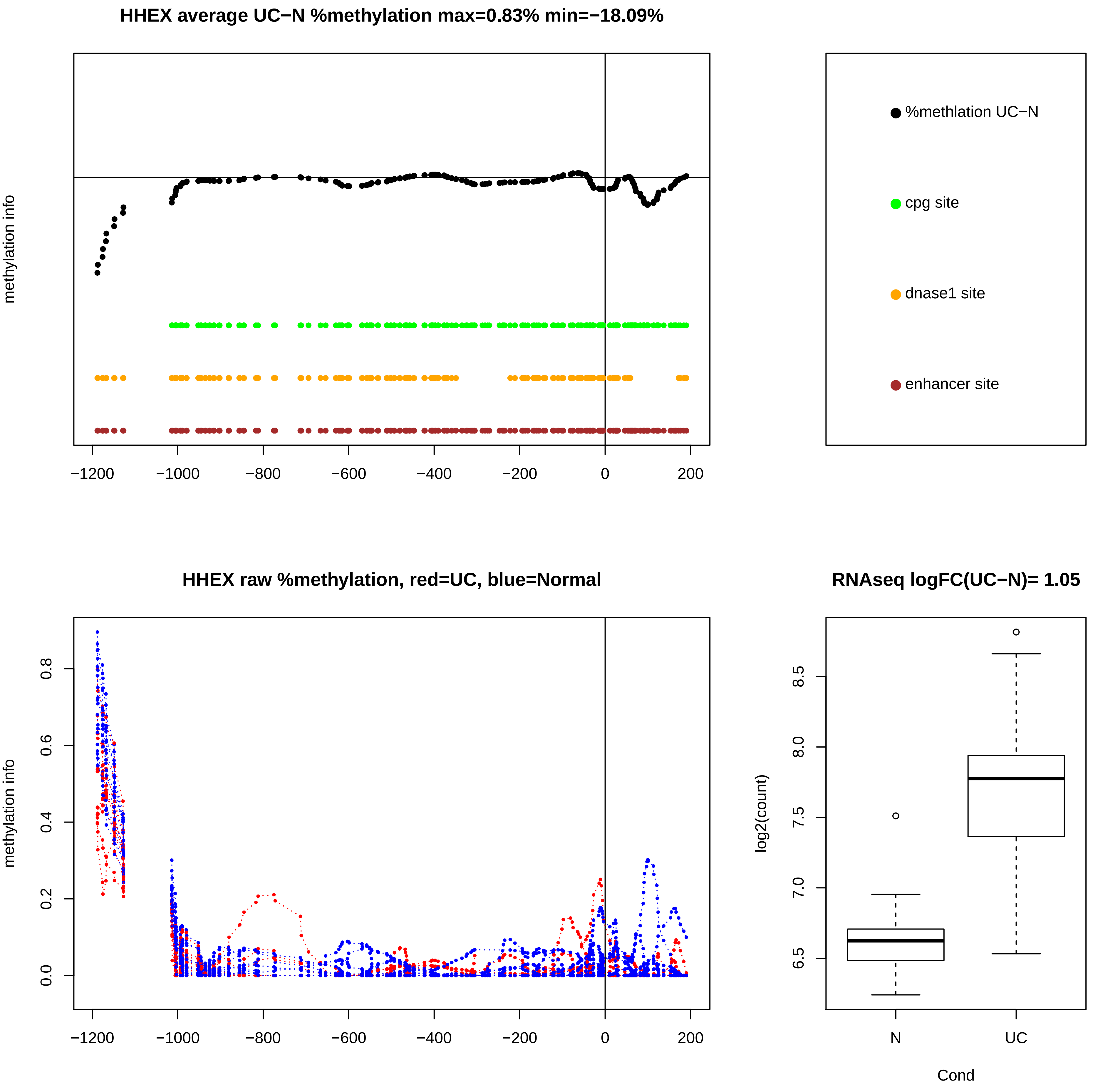

HCAR3 average UC−N %methylation max=−15% min=−24.39%
methylation info
−150
−100
−50
0
50
100
150
%methlation UC−N
cpg site
dnase1 site
enhancer site
HCAR3 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−150
−100
−50
0
50
100
150
RNAseq logFC(UC−N)= 4.32
log2(count)
0
2
4
6
8
N
UC
Cond

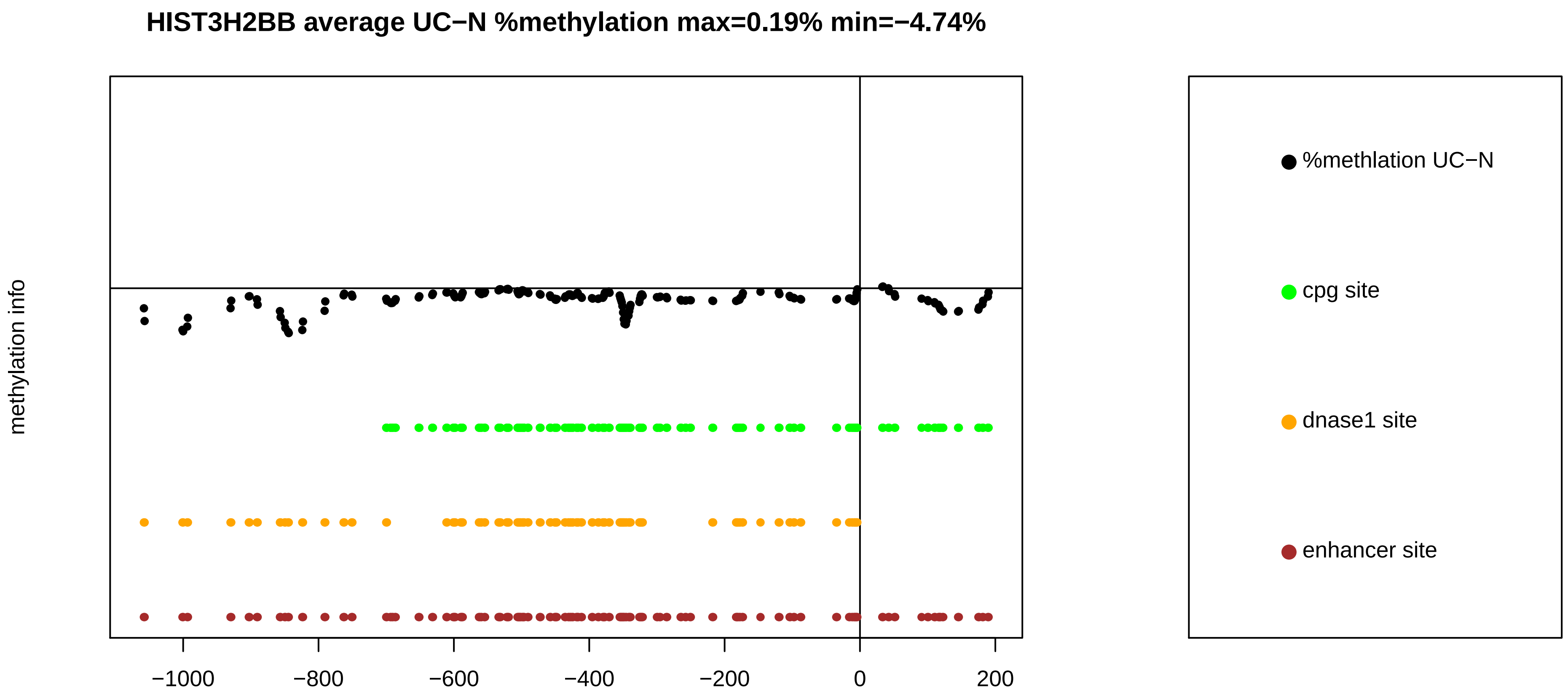

HCLS1 average UC−N %methylation max=−31.6% min=−35.89%
methylation info
−80
−60
−40
−20
0
20
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
HCLS1 raw %methylation, red=UC, blue=Normal
methylation info
0.2
0.4
0.6
0.8
−80
−60
−40
−20
0
20
RNAseq logFC(UC−N)= 1.1
log2(count)
8.5
9.0
9.5
10.0
10.5
11.0
N
UC
Cond

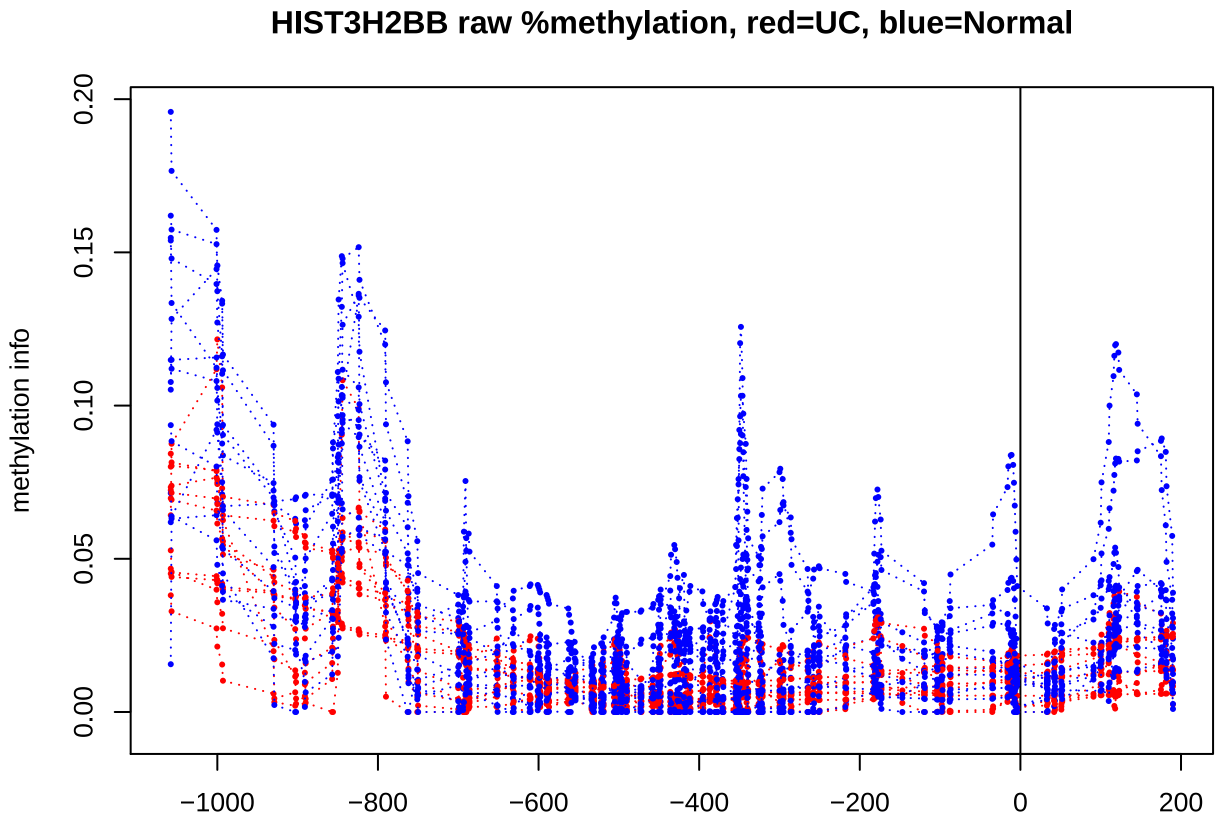

HGF average UC−N %methylation max=−3.68% min=−20.05%

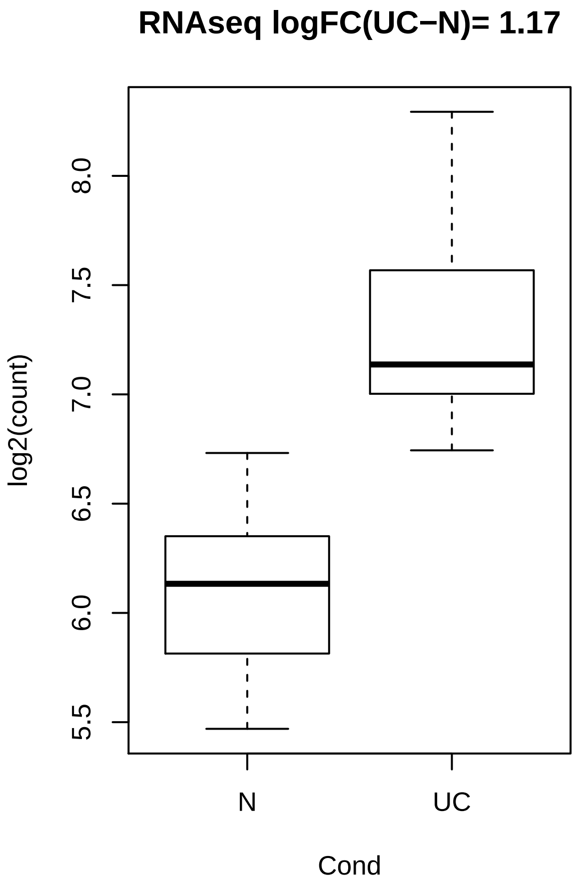
HGF raw %methylation, red=UC, blue=Normal

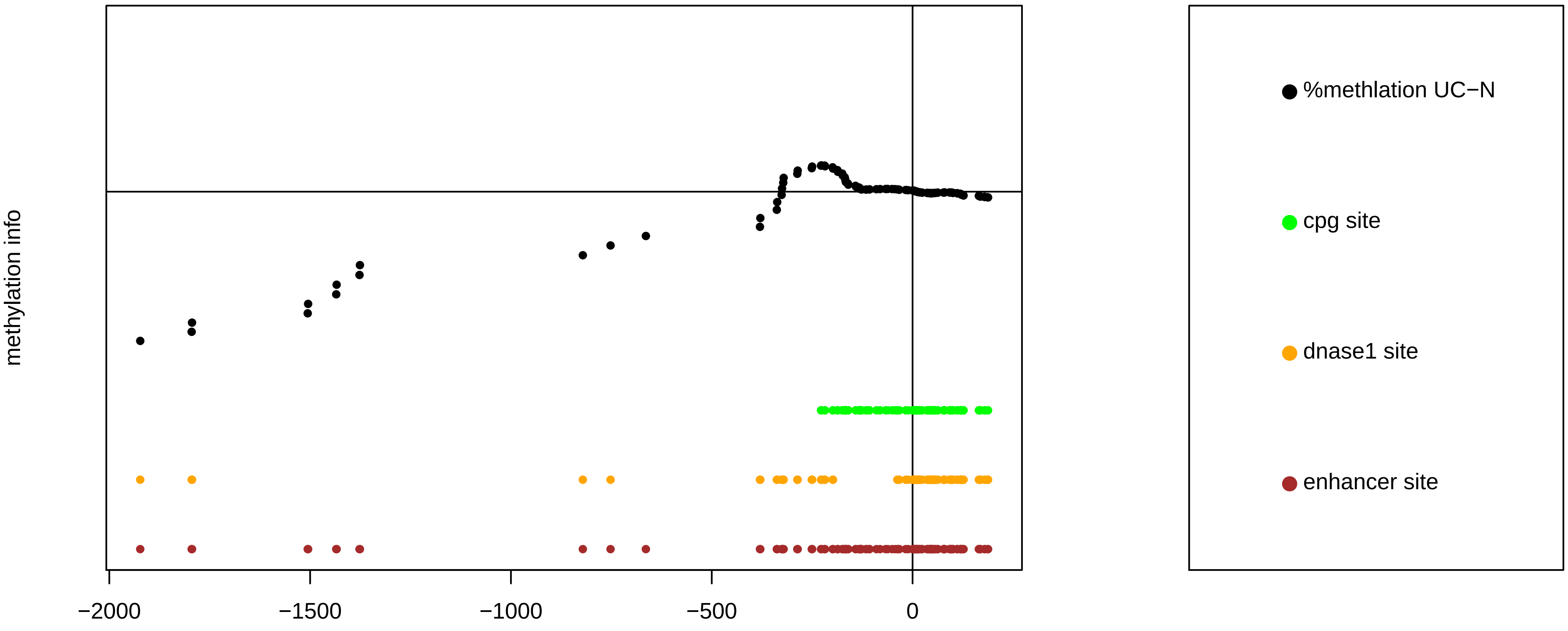
RNAseq logFC(UC−N)= 1.12

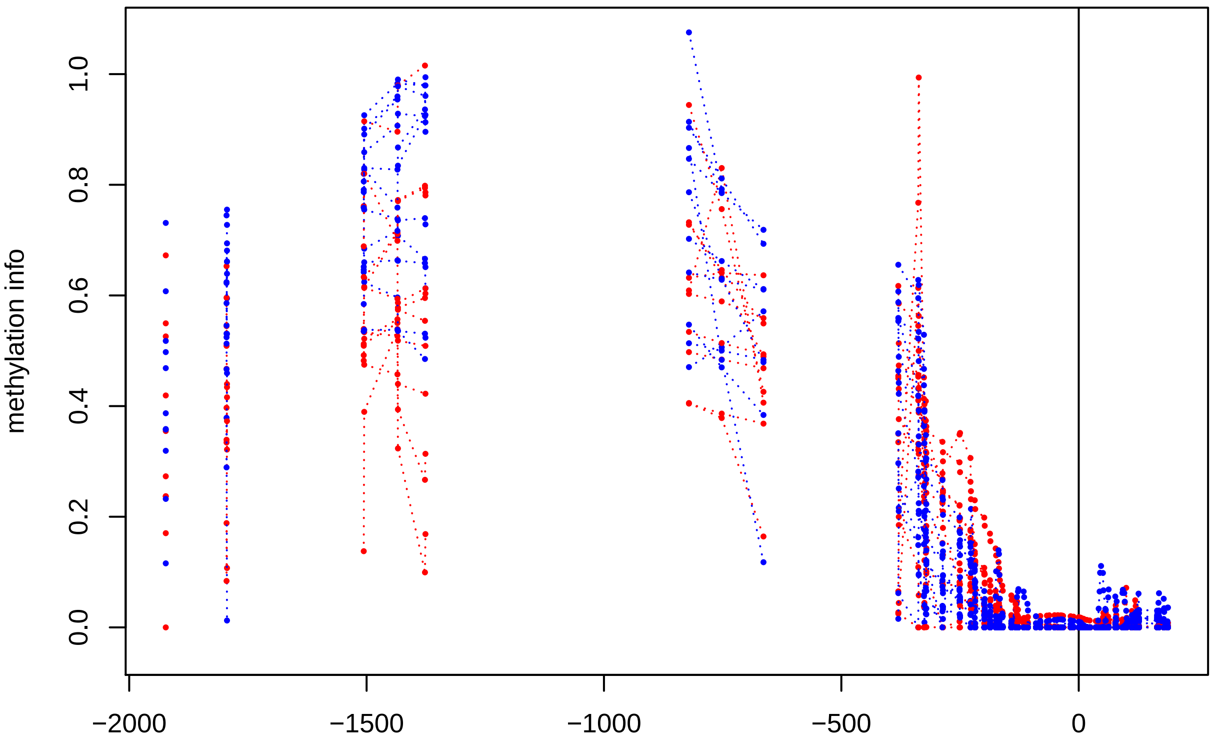

HHEX average UC−N %methylation max=0.83% min=−18.09%
methylation info
−1200
−1000
−800
−600
−400
−200
0
200
%methlation UC−N
cpg site
dnase1 site
enhancer site
HHEX raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
−1200
−1000
−800
−600
−400
−200
0
200
RNAseq logFC(UC−N)= 1.05
log2(count)
6.5
7.0
7.5
8.0
8.5
N
UC
Cond

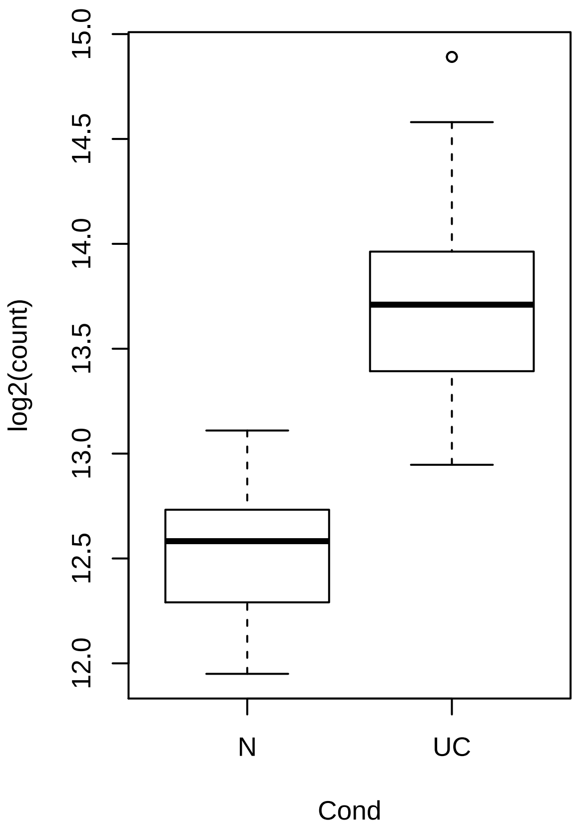

HIST3H2BB average UC−N %methylation max=0.19% min=−4.74%
methylation info
−1000
−800
−600
−400
−200
0
200
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site


HIST3H2BB raw %methylation, red=UC, blue=Normal
methylation info
0.00
0.05
0.10
0.15
0.20
−1000
−800
−600
−400
−200
0
200

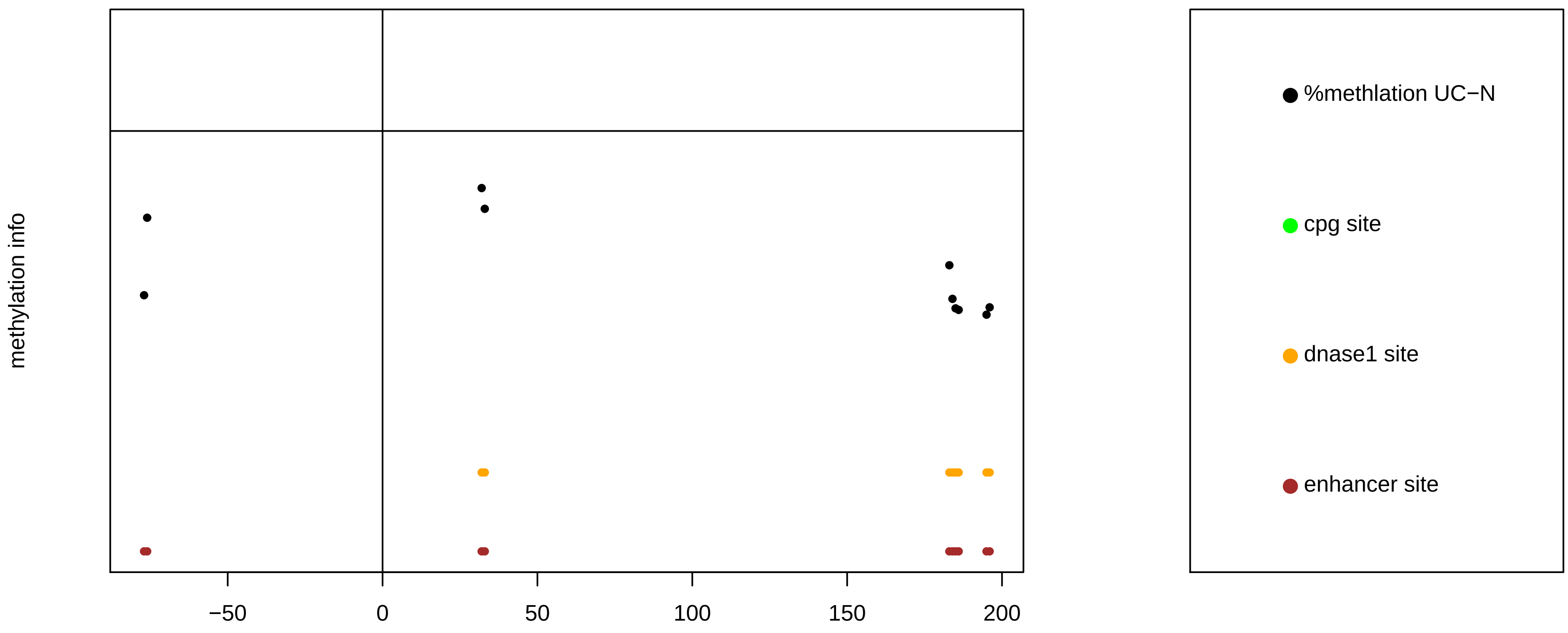

RNAseq logFC(UC−N)= 1.17
log2(count)
5.5
6.0
6.5
7.0
7.5
8.0
N
UC
Cond


HK2 average UC−N %methylation max=3.79% min=−21.5%

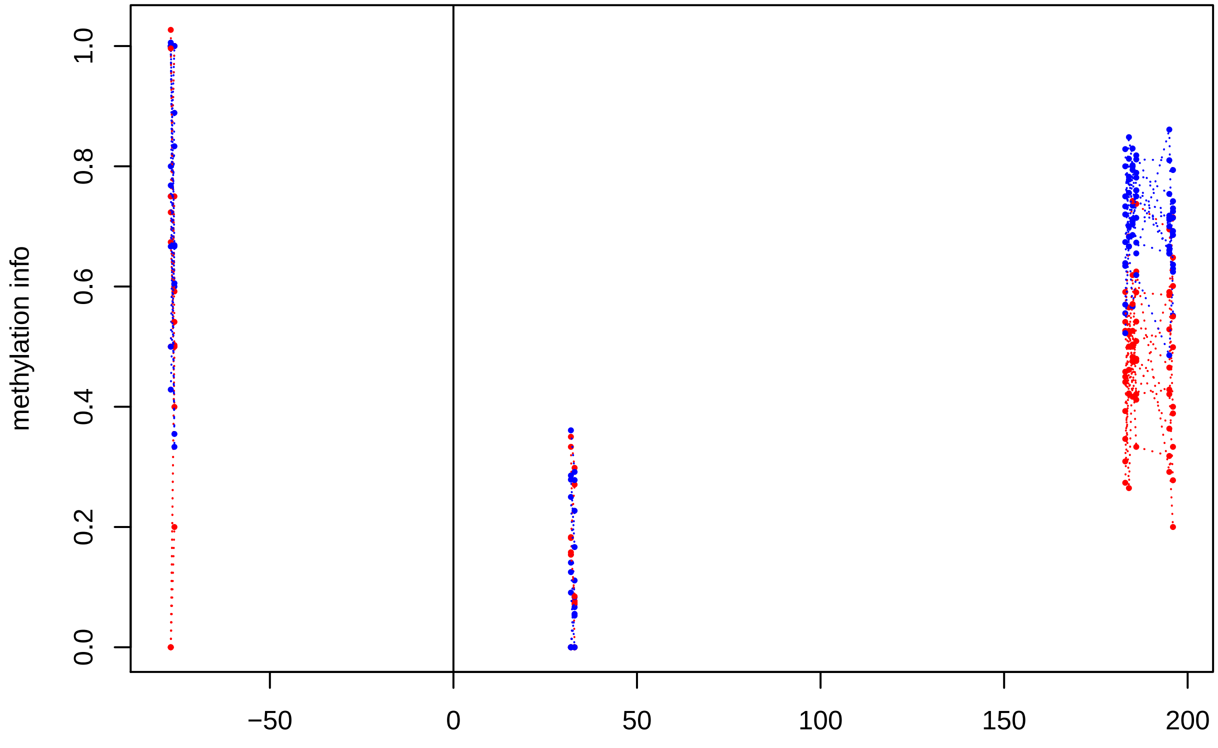

HK2 raw %methylation, red=UC, blue=Normal


RNAseq logFC(UC−N)= 1.24

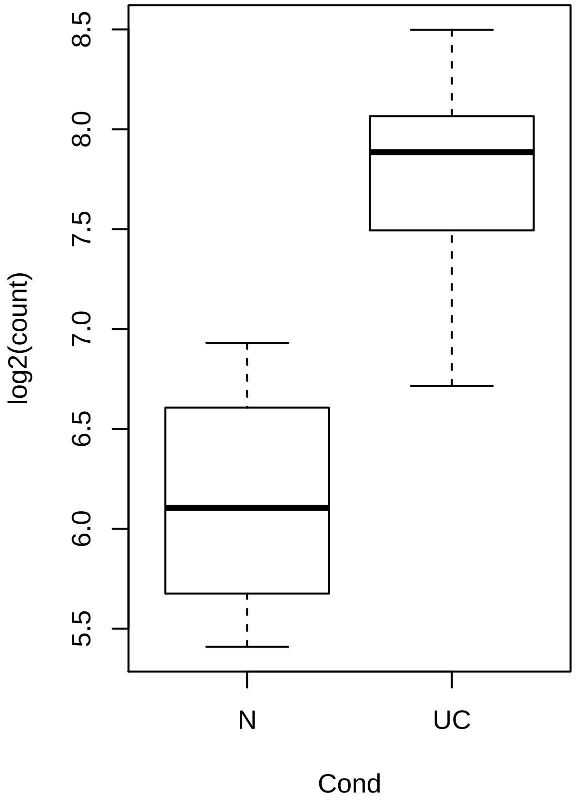
HK3 average UC−N %methylation max=−7.23% min=−23.28%

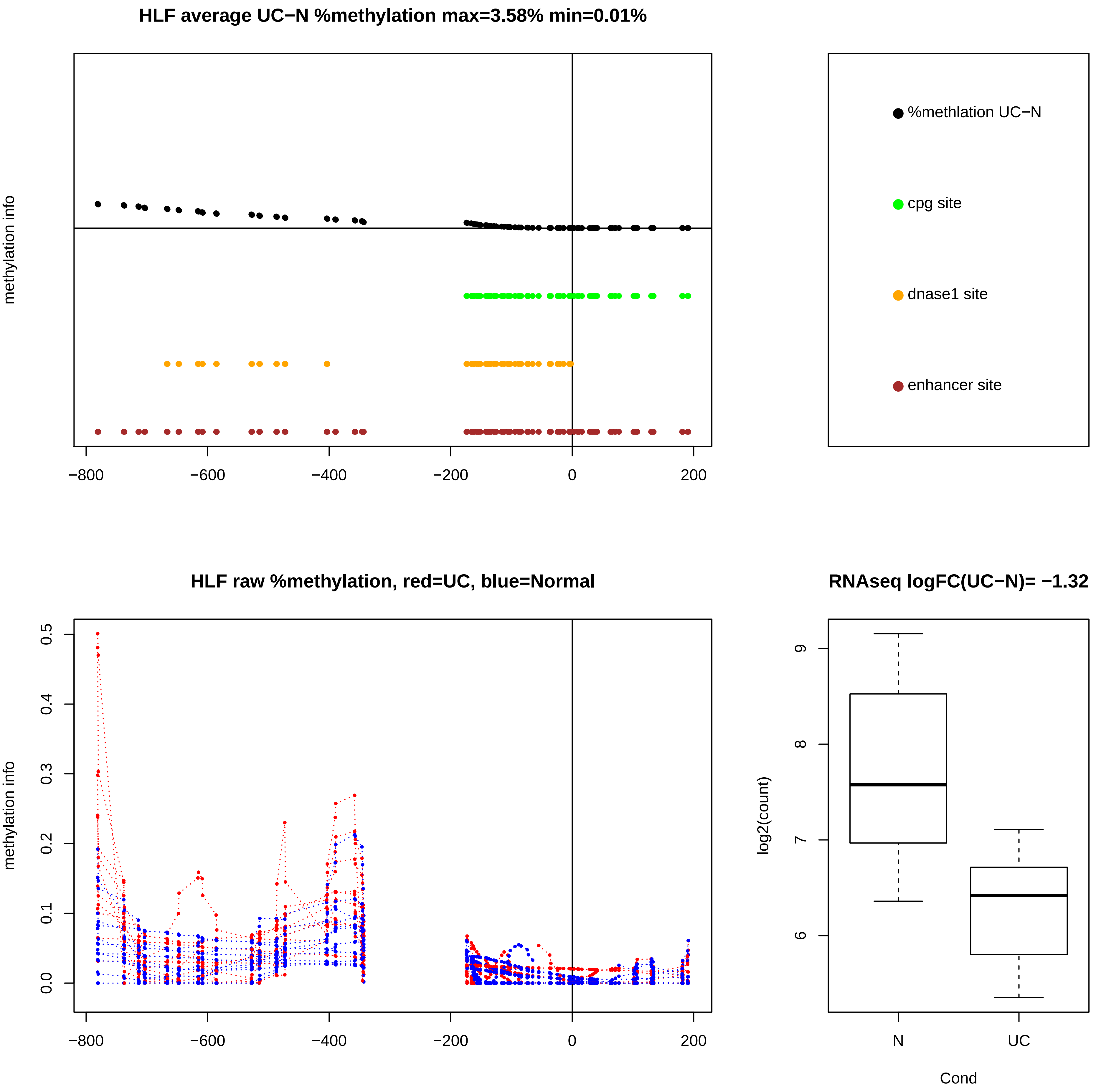


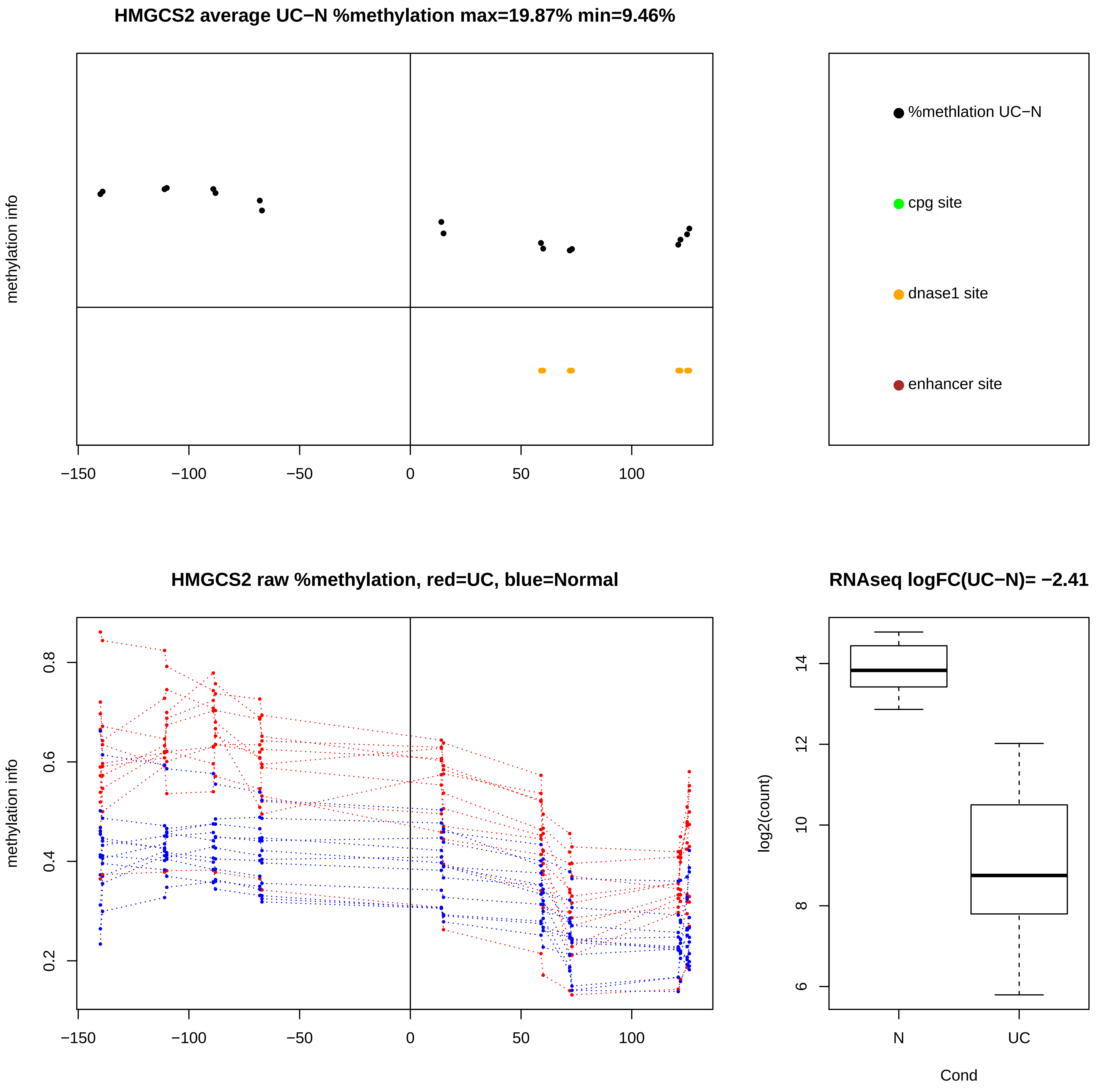
HK3 raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 1.41



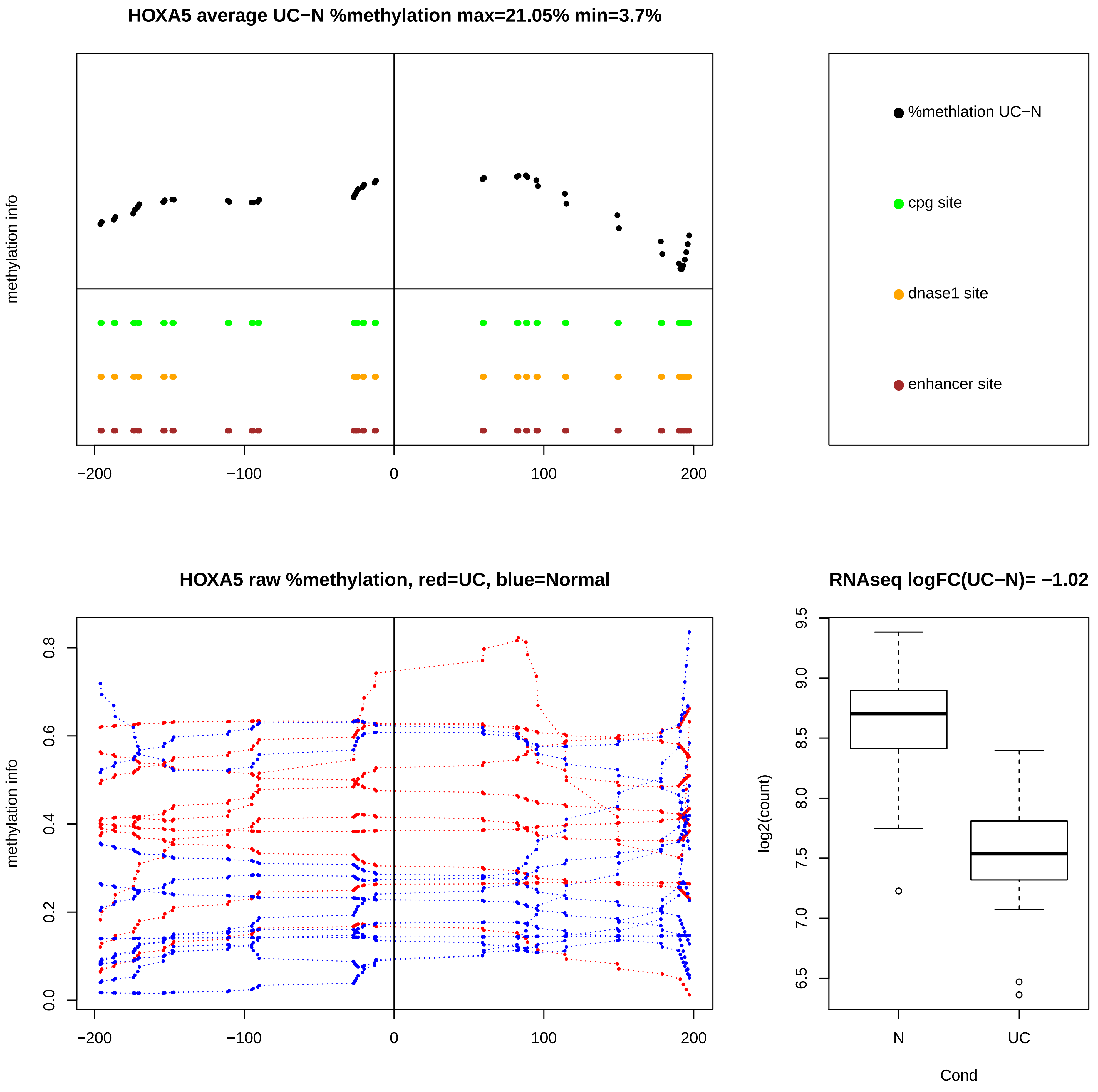

HLF average UC−N %methylation max=3.58% min=0.01%
methylation info
−800
−600
−400
−200
0
200
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
HLF raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.1
0.2
0.3
0.4
0.5
−800
−600
−400
−200
0
200
RNAseq logFC(UC−N)= −1.32
log2(count)
6
7
8
9
N
UC
Cond

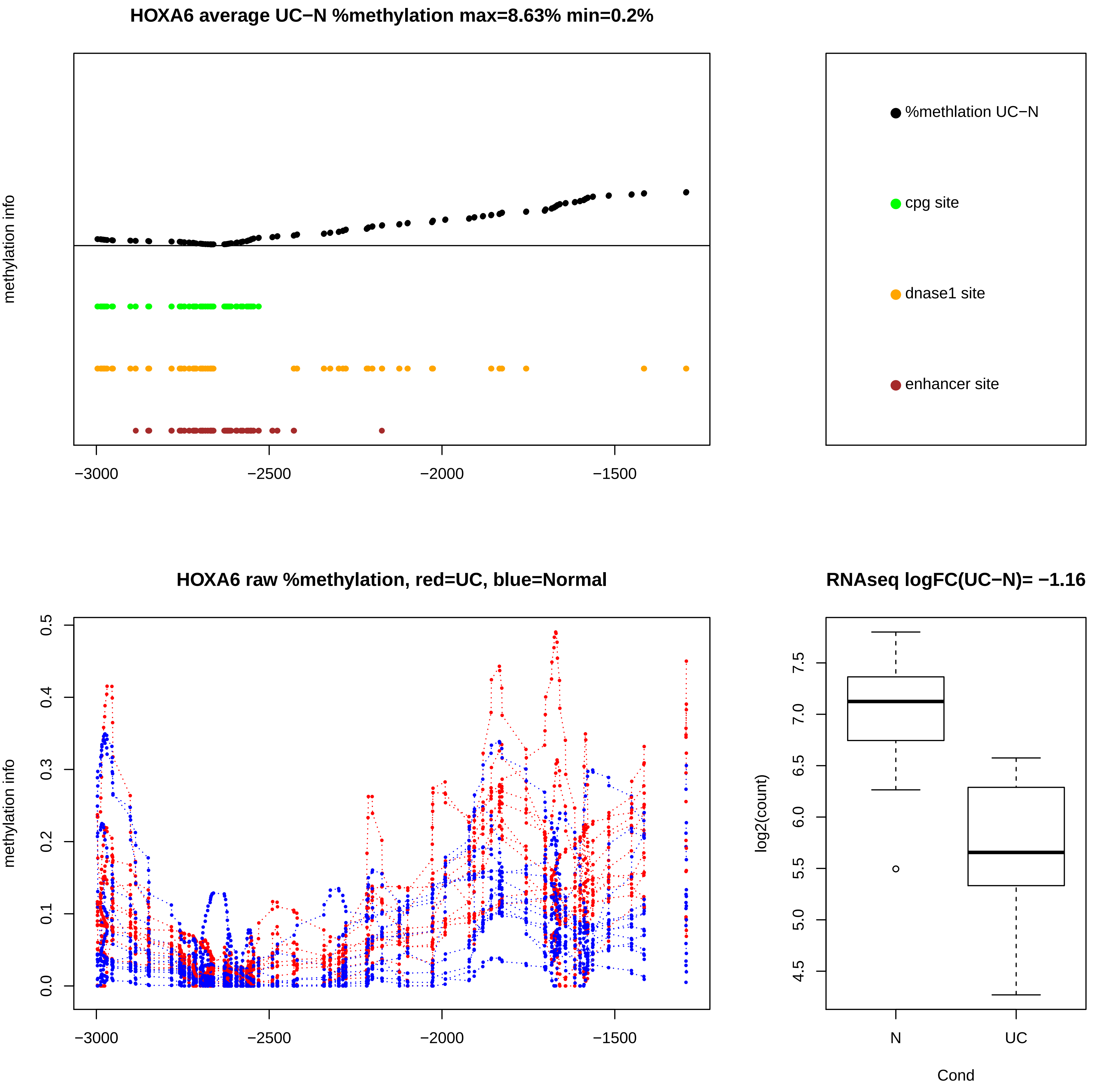


HMGCS2 average UC−N %methylation max=19.87% min=9.46%

HMGCS2 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= −2.41

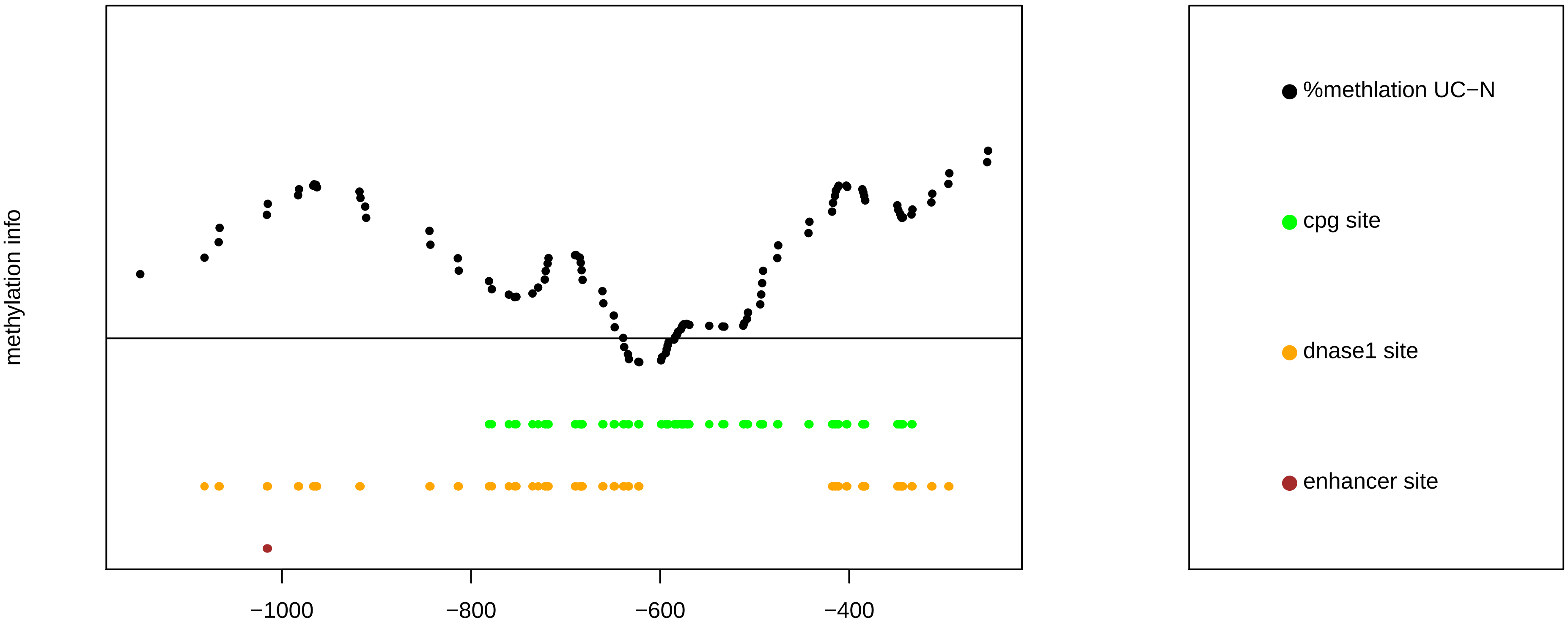

HOXA5 average UC−N %methylation max=21.05% min=3.7%
methylation info
−200
−100
0
100
200
%methlation UC−N
cpg site
dnase1 site
enhancer site
HOXA5 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
−200
−100
0
100
200
RNAseq logFC(UC−N)= −1.02
log2(count)
6.5
7.0
7.5
8.0
8.5
9.0
9.5
N
UC
Cond



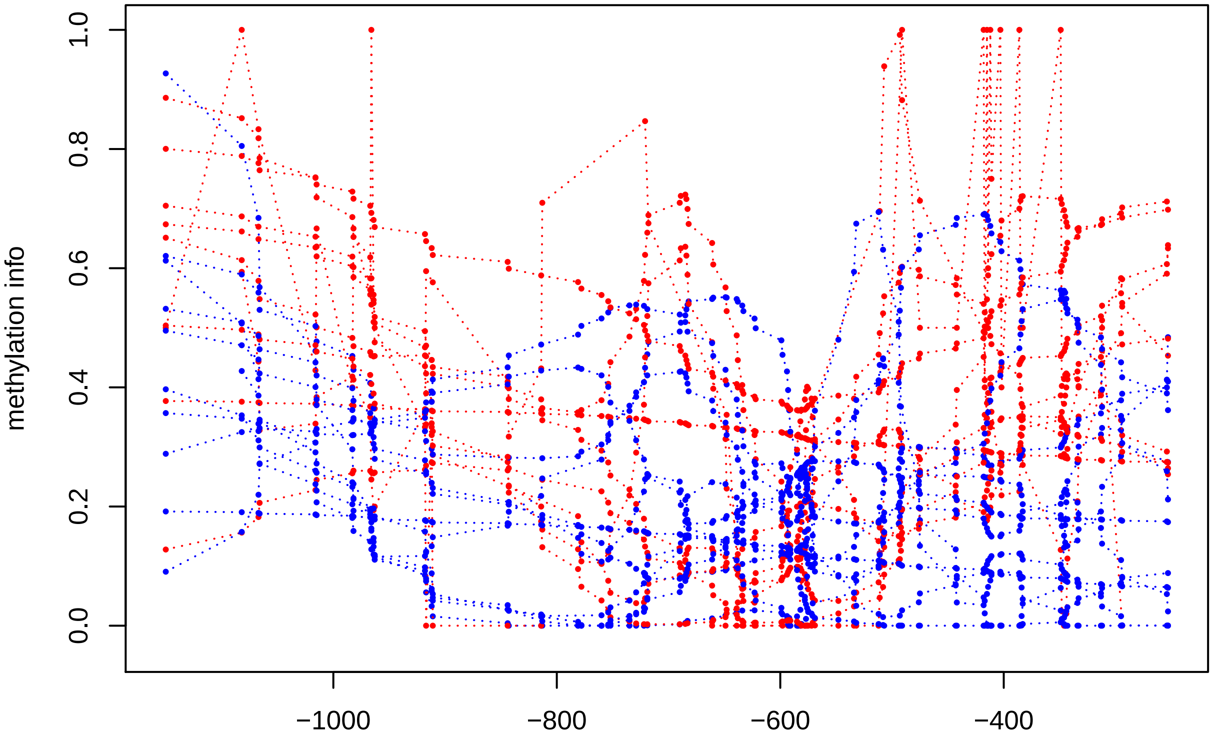
HOXA6 average UC−N %methylation max=8.63% min=0.2%

HOXA6 raw %methylation, red=UC, blue=Normal

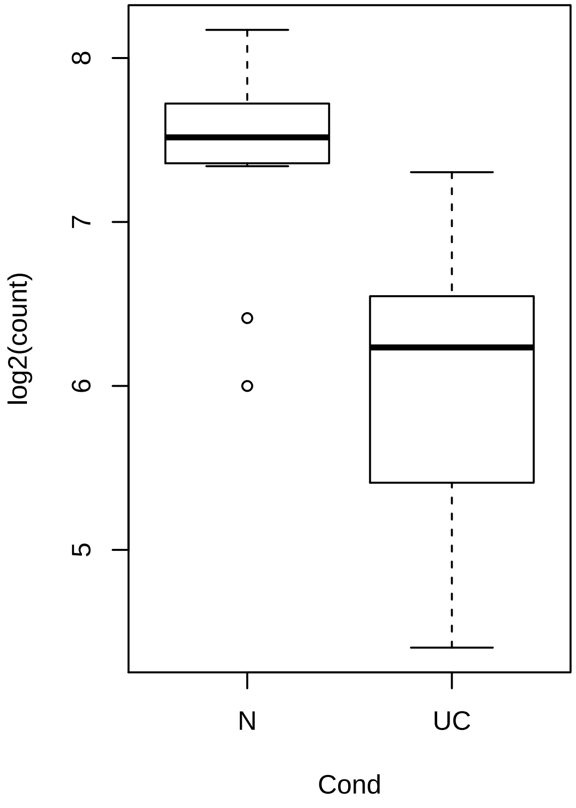
RNAseq logFC(UC−N)= −1.16



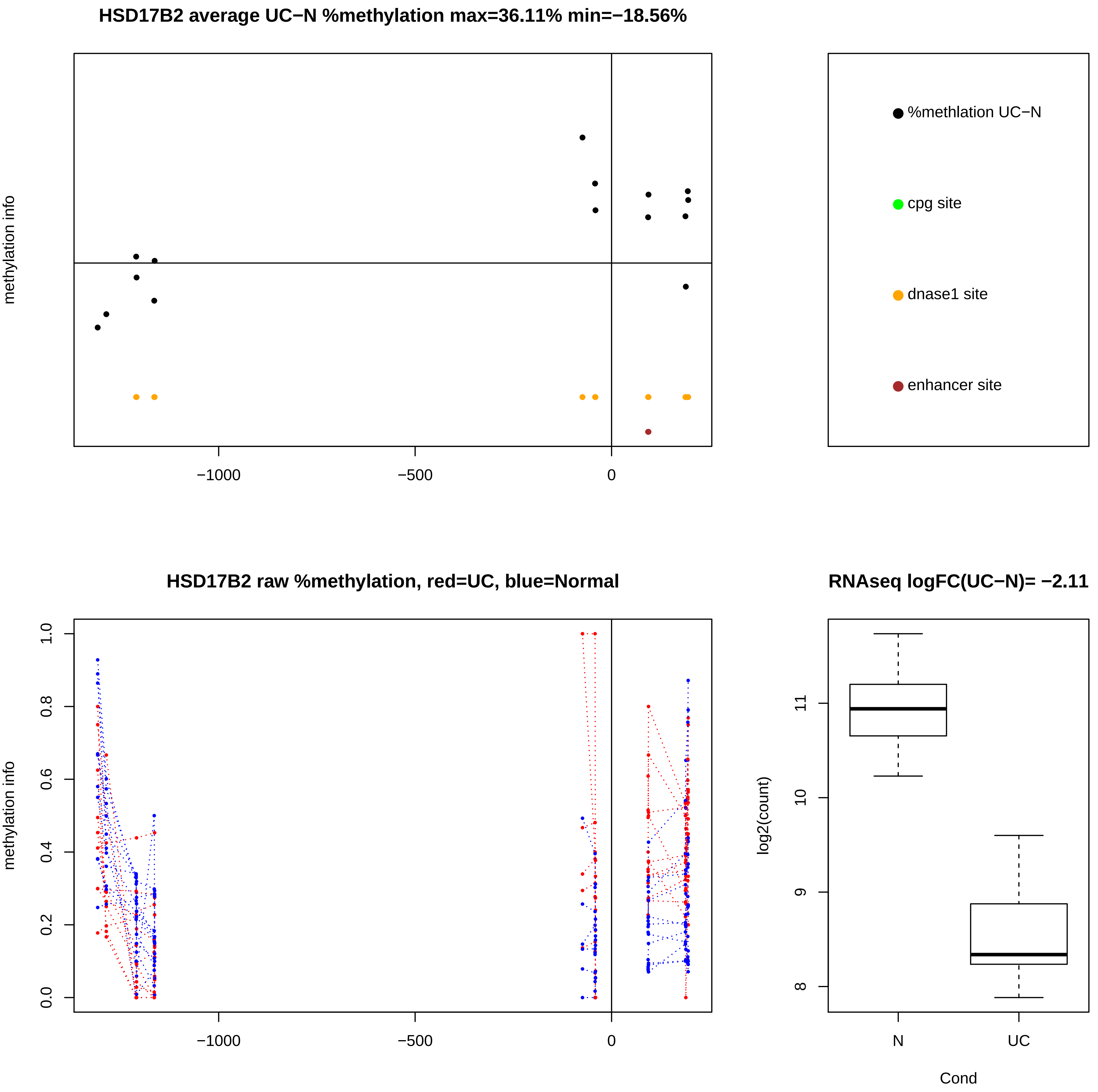
HOXA−AS3 average UC−N %methylation max=30.2% min=−3.83%



HOXA−AS3 raw %methylation, red=UC, blue=Normal

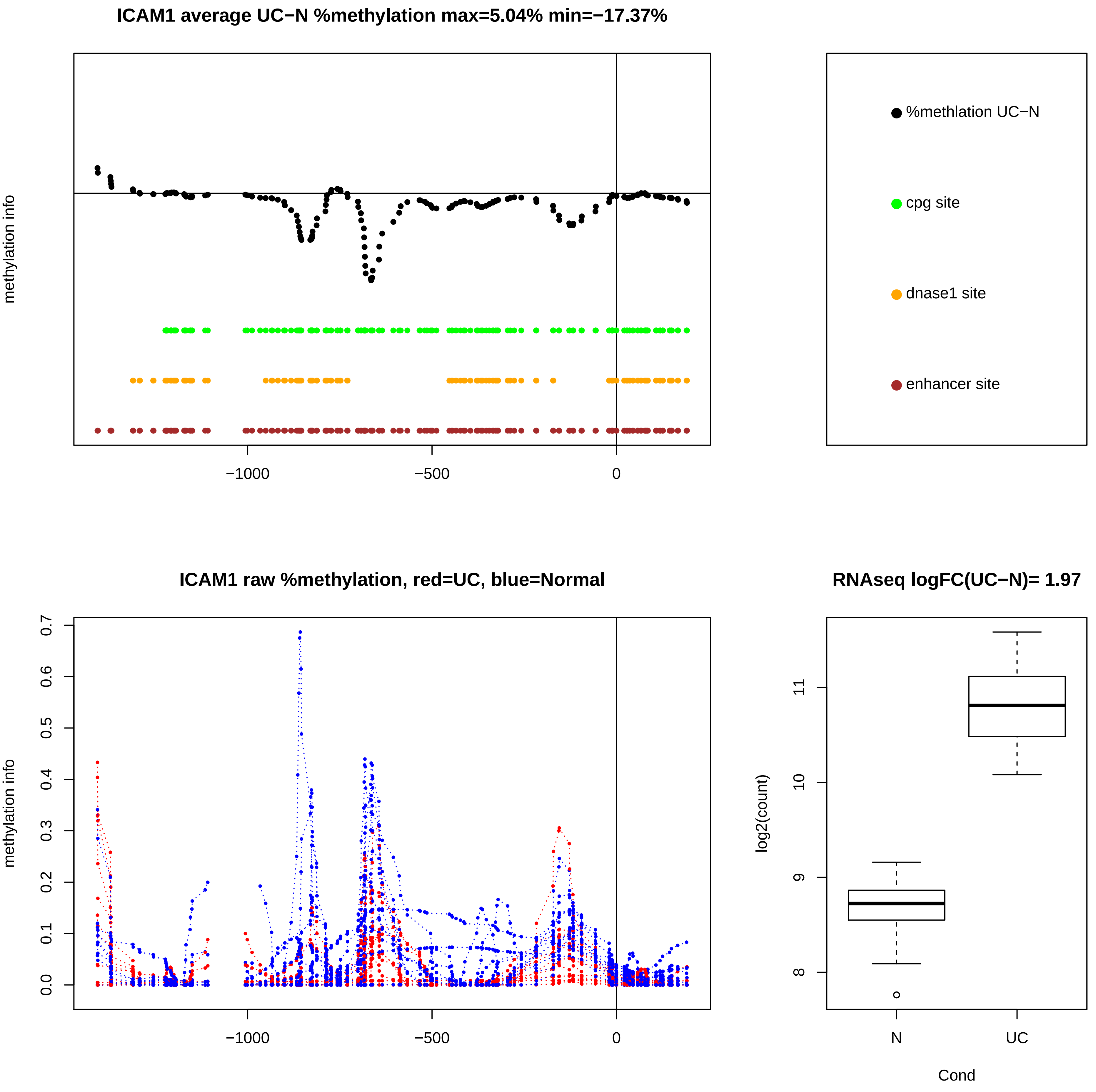


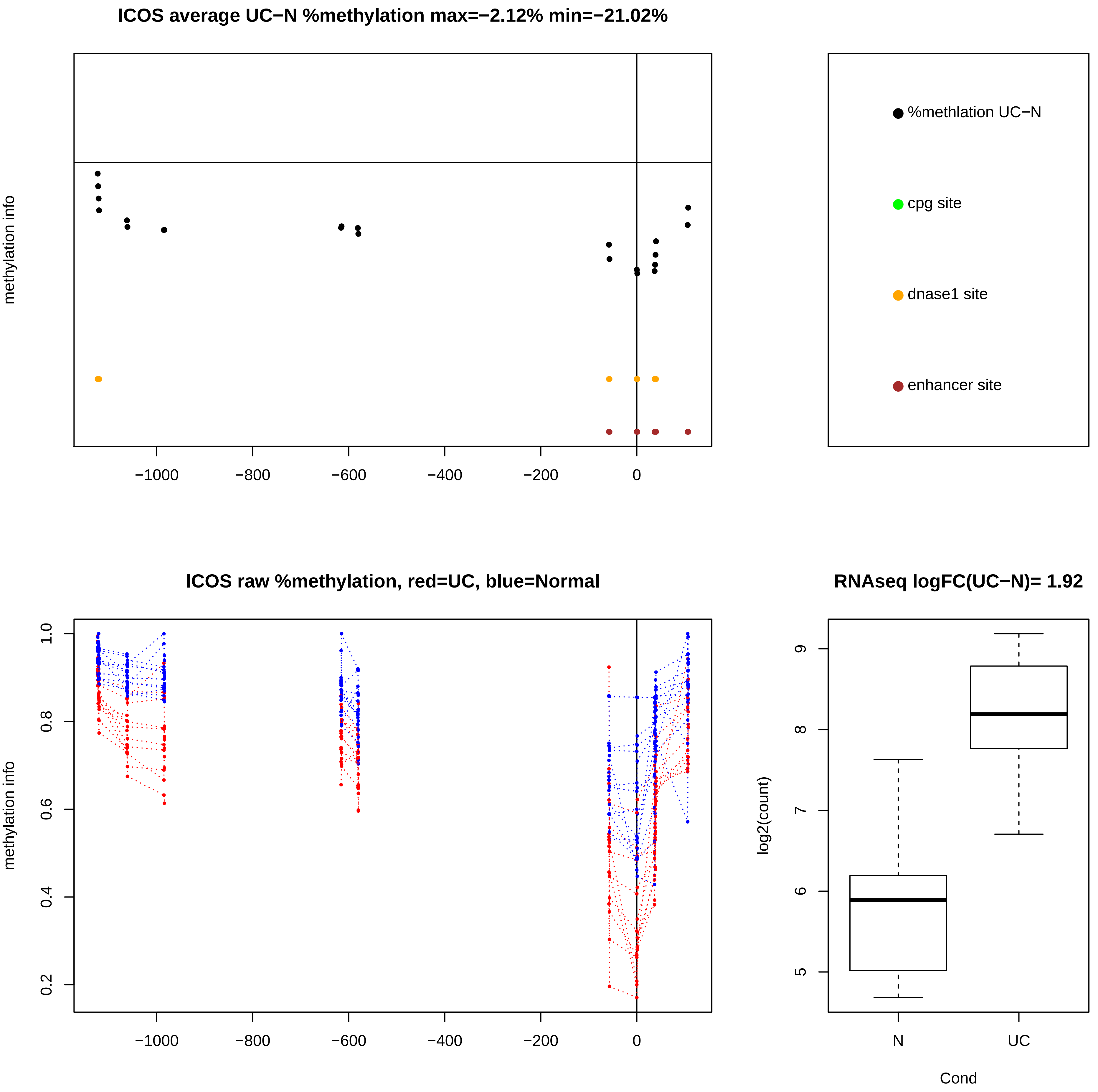
RNAseq logFC(UC−N)= −1.16

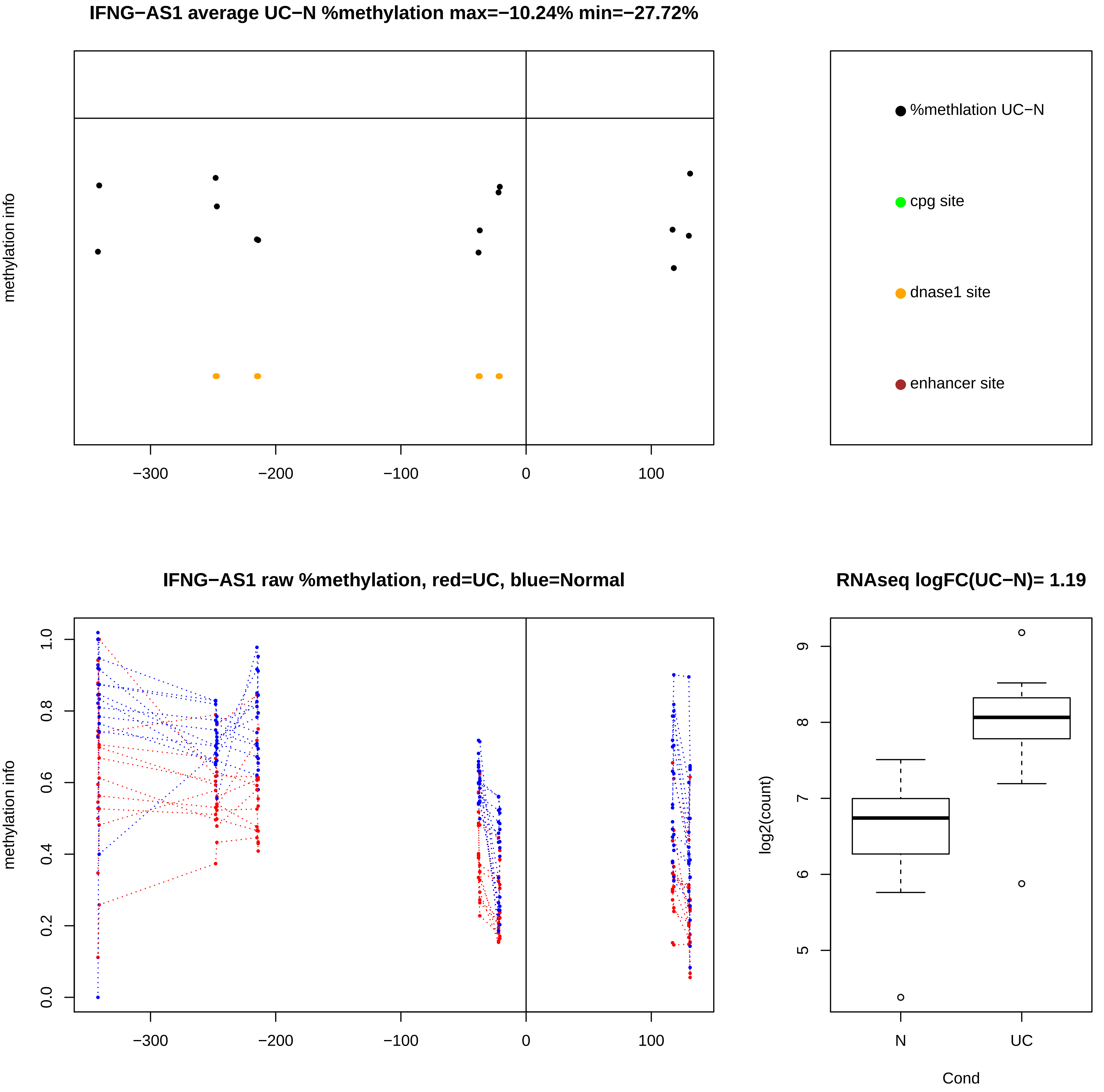

HSD17B2 average UC−N %methylation max=36.11% min=−18.56%

HSD17B2 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= −2.11


ICAM1 average UC−N %methylation max=5.04% min=−17.37%
methylation info
−1000
−500
0
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
ICAM1 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
−1000
−500
0
RNAseq logFC(UC−N)= 1.97
log2(count)
8
9
10
11
N
UC
Cond

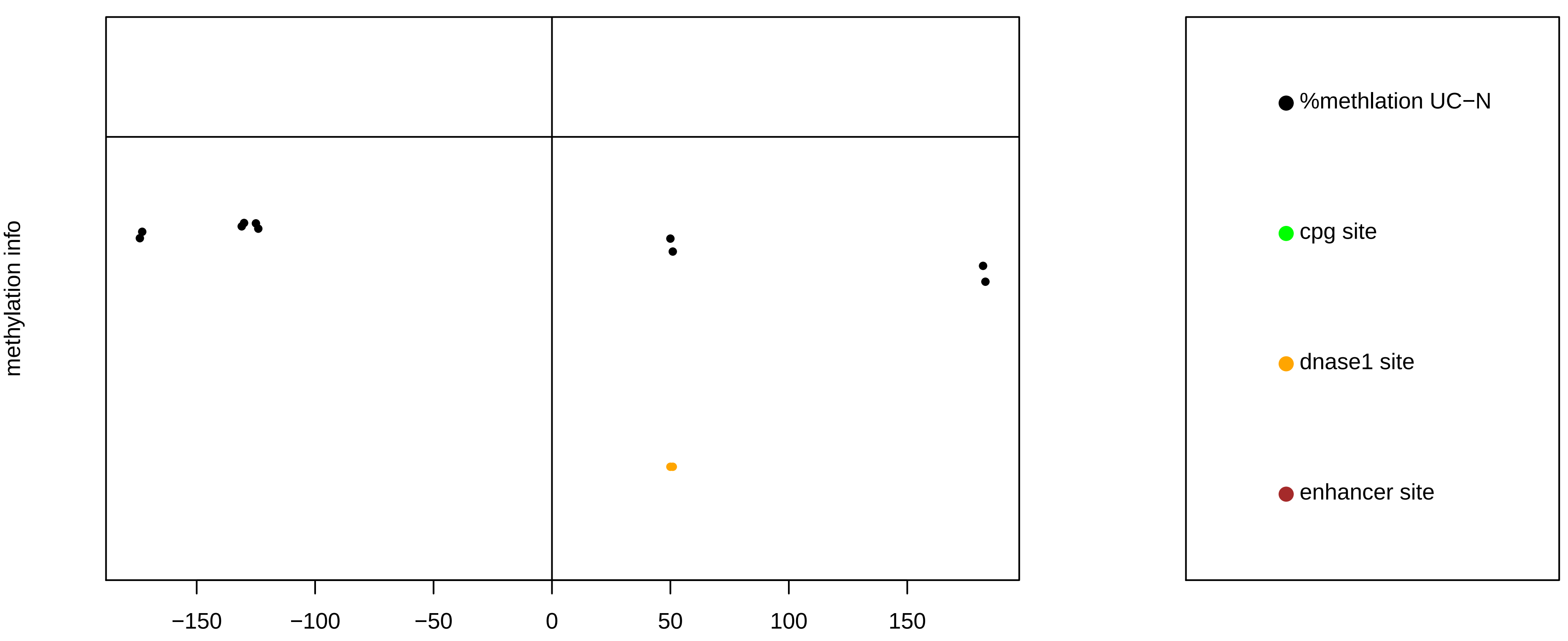

ICOS average UC−N %methylation max=−2.12% min=−21.02%
methylation info
−1000
−800
−600
−400
−200
0
%methlation UC−N
cpg site
dnase1 site
enhancer site
ICOS raw %methylation, red=UC, blue=Normal
methylation info
0.2
0.4
0.6
0.8
1.0
−1000
−800
−600
−400
−200
0
RNAseq logFC(UC−N)= 1.92
log2(count)
5
6
7
8
9
N
UC
Cond

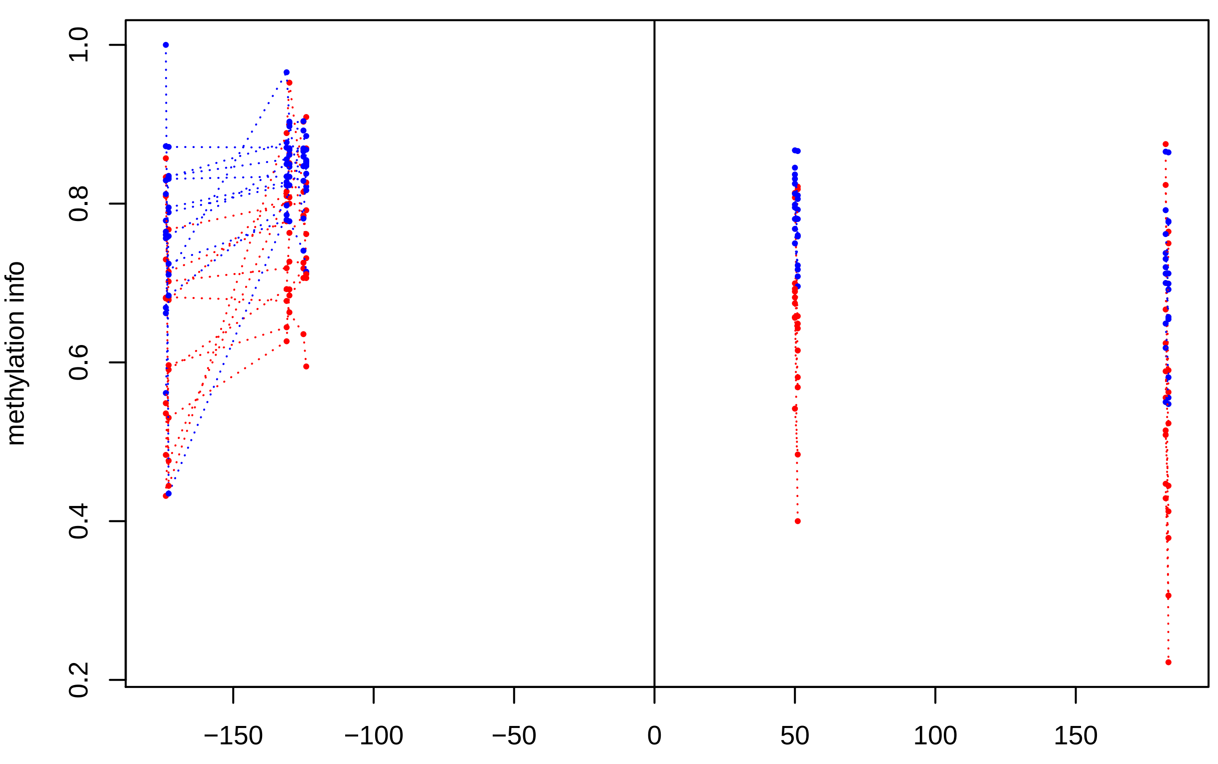


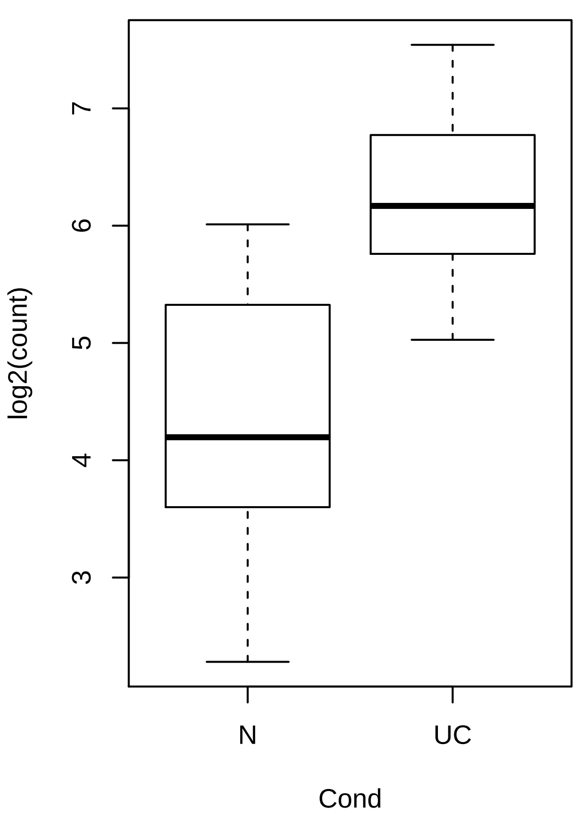
IFNG−AS1 average UC−N %methylation max=−10.24% min=−27.72%

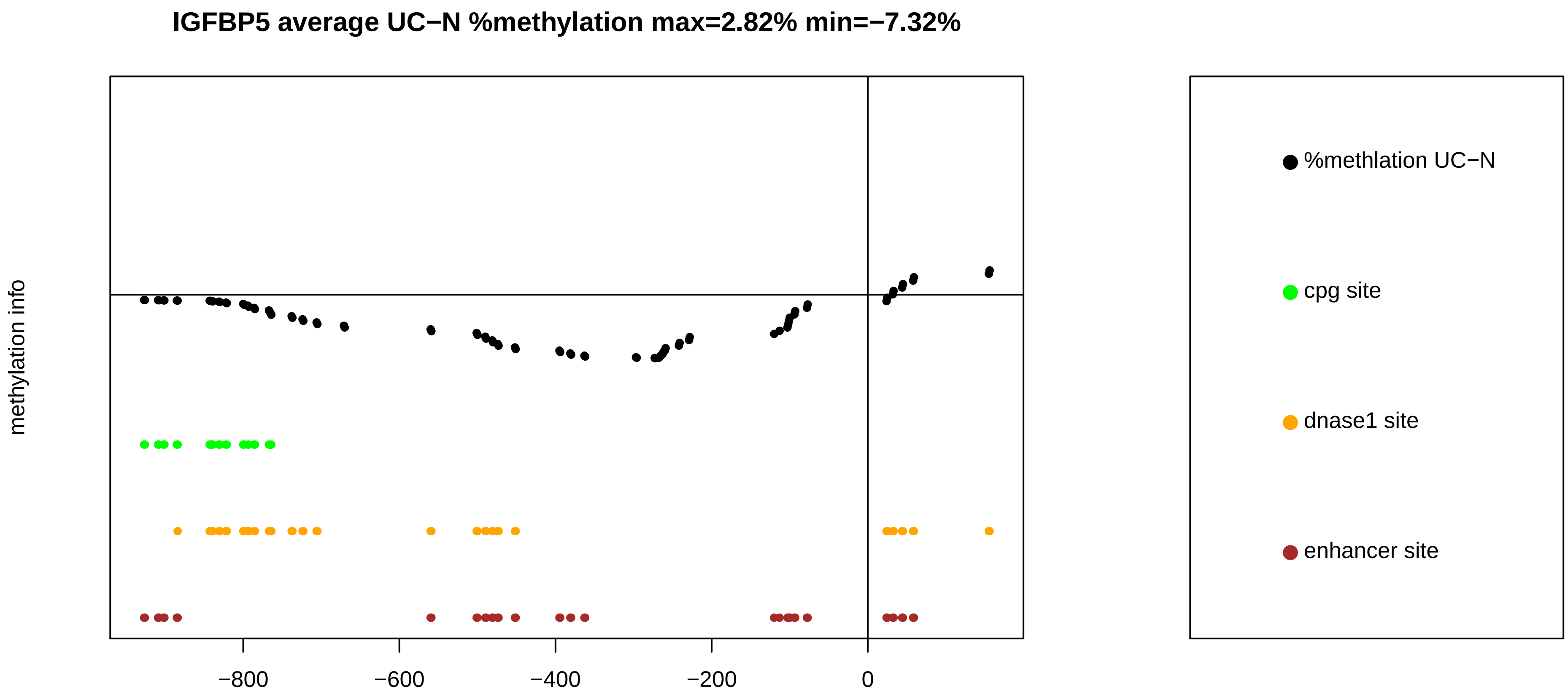
IFNG−AS1 raw %methylation, red=UC, blue=Normal

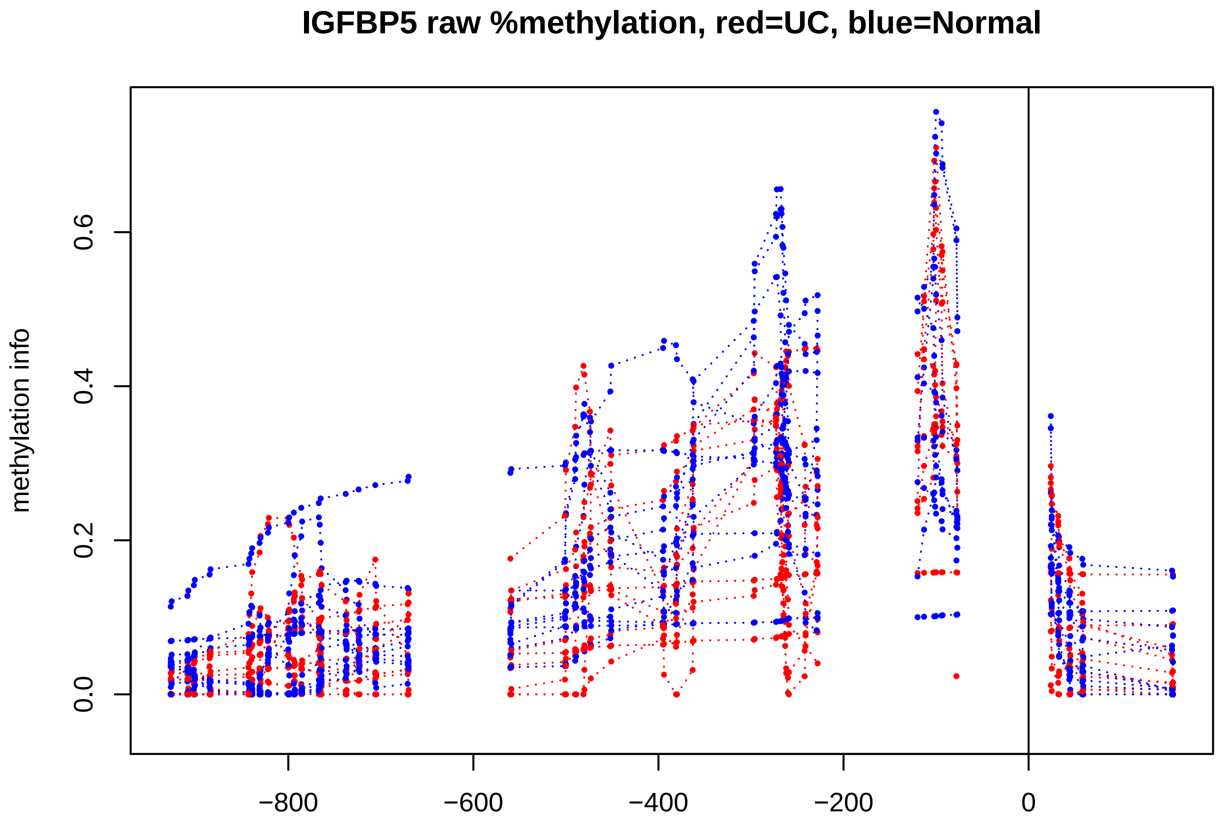
RNAseq logFC(UC−N)= 1.19

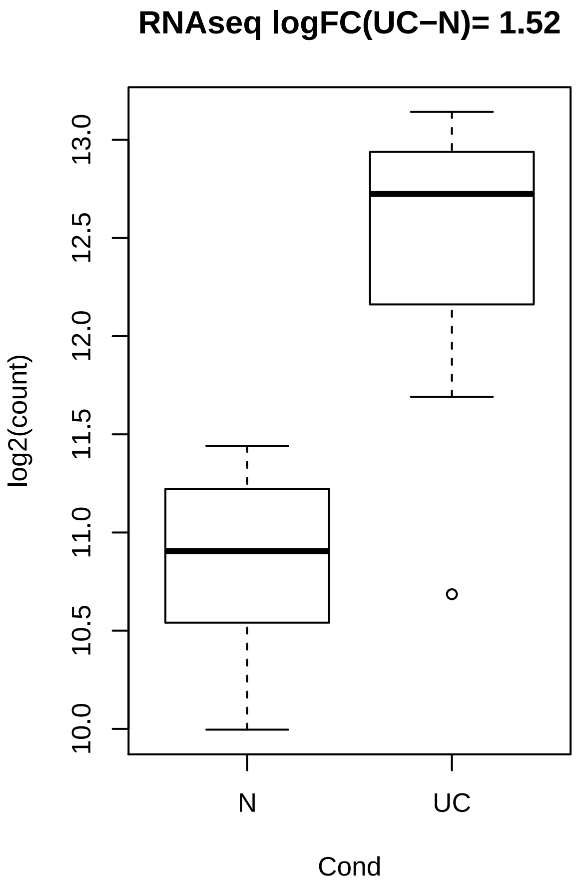

IFNG average UC−N %methylation max=−9.3% min=−15.65%

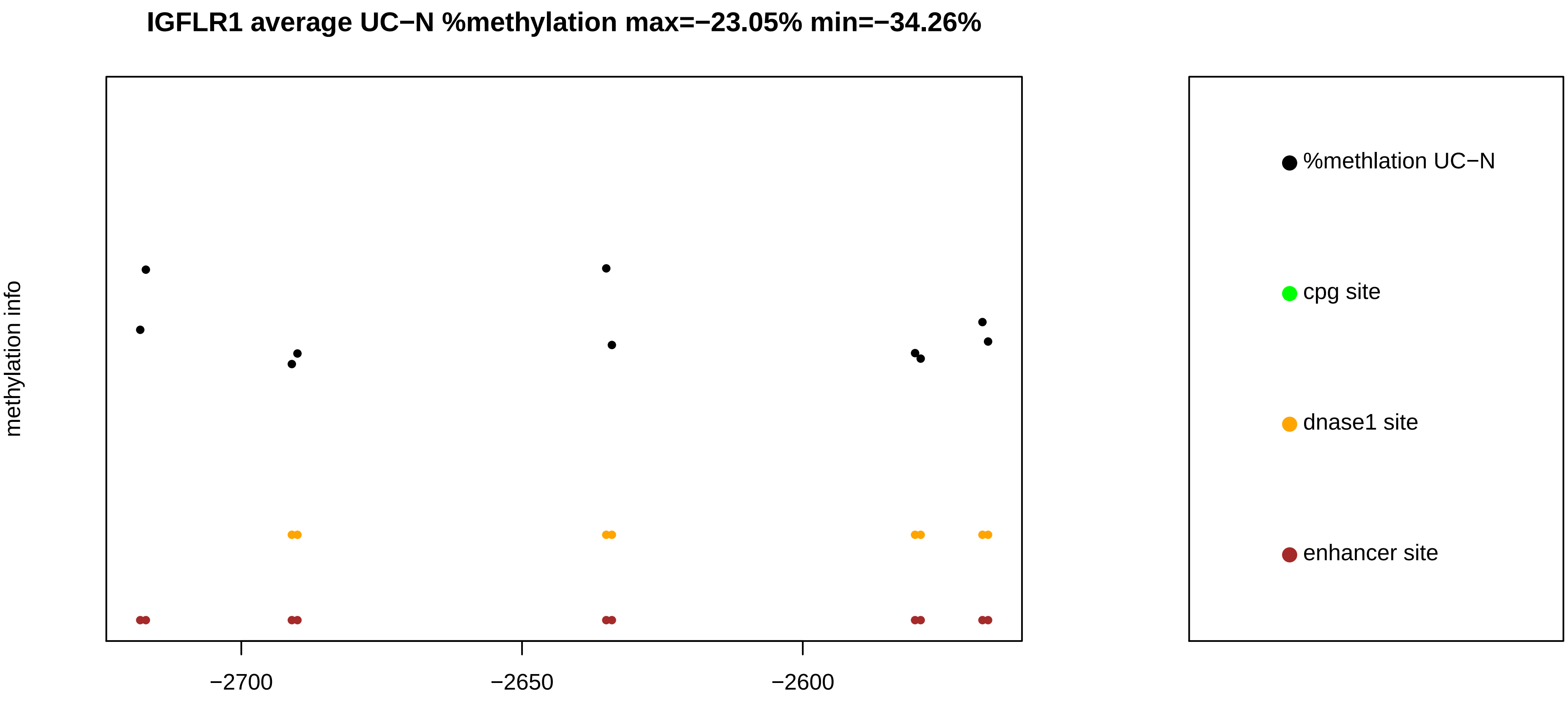

IFNG raw %methylation, red=UC, blue=Normal

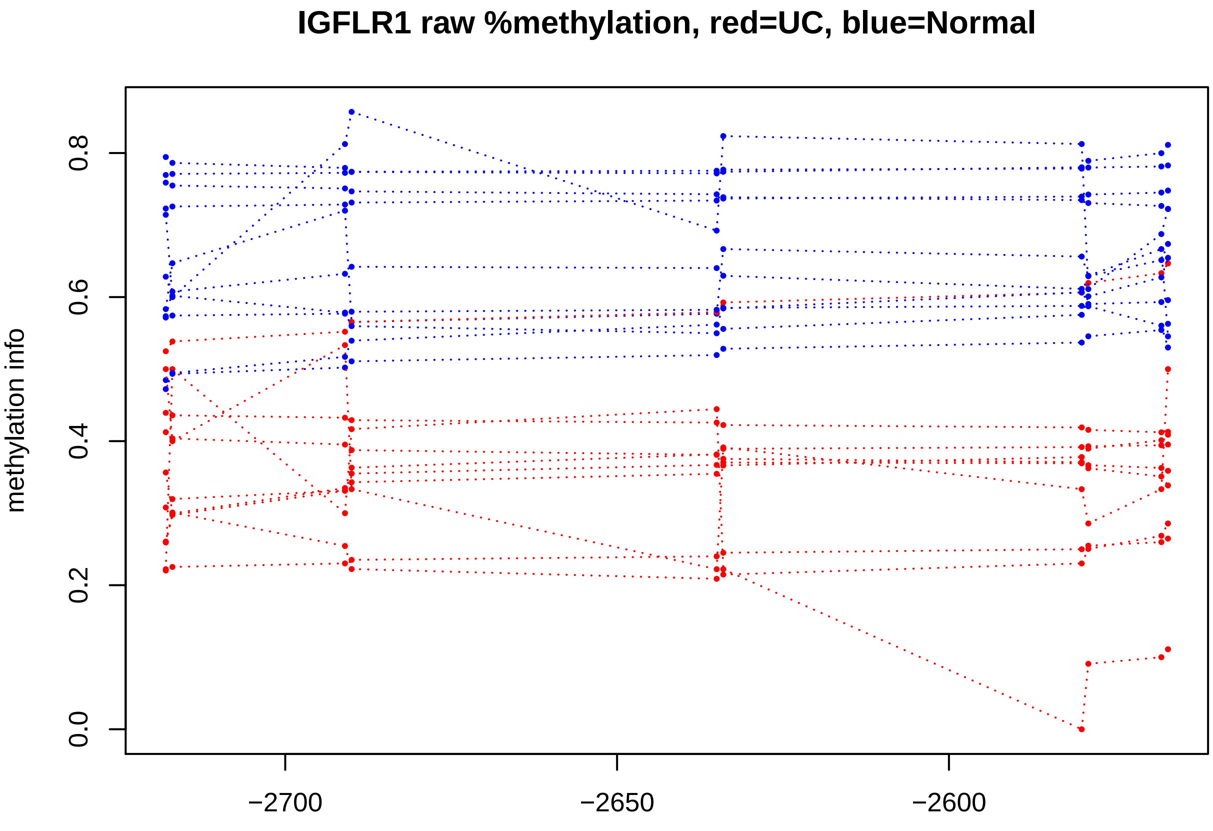

RNAseq logFC(UC−N)= 1.54

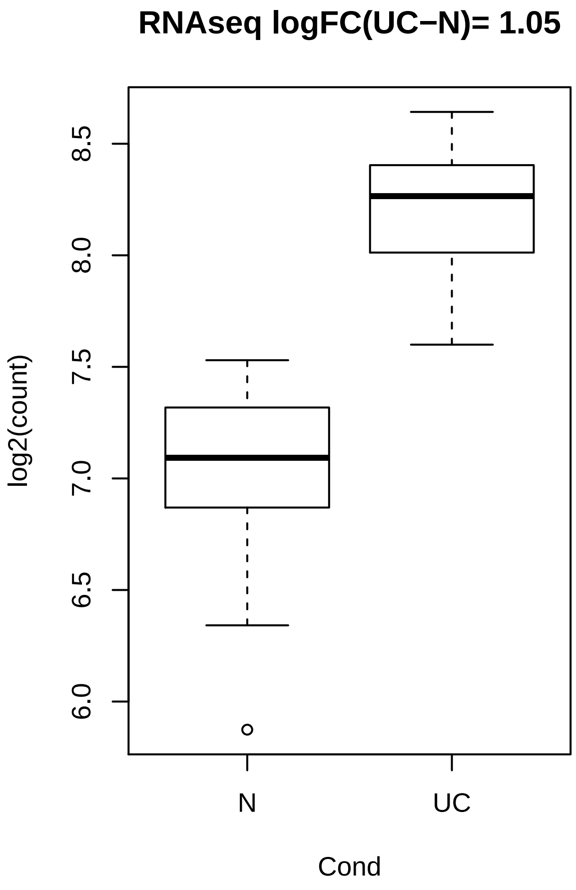

IGFBP5 average UC−N %methylation max=2.82% min=−7.32%

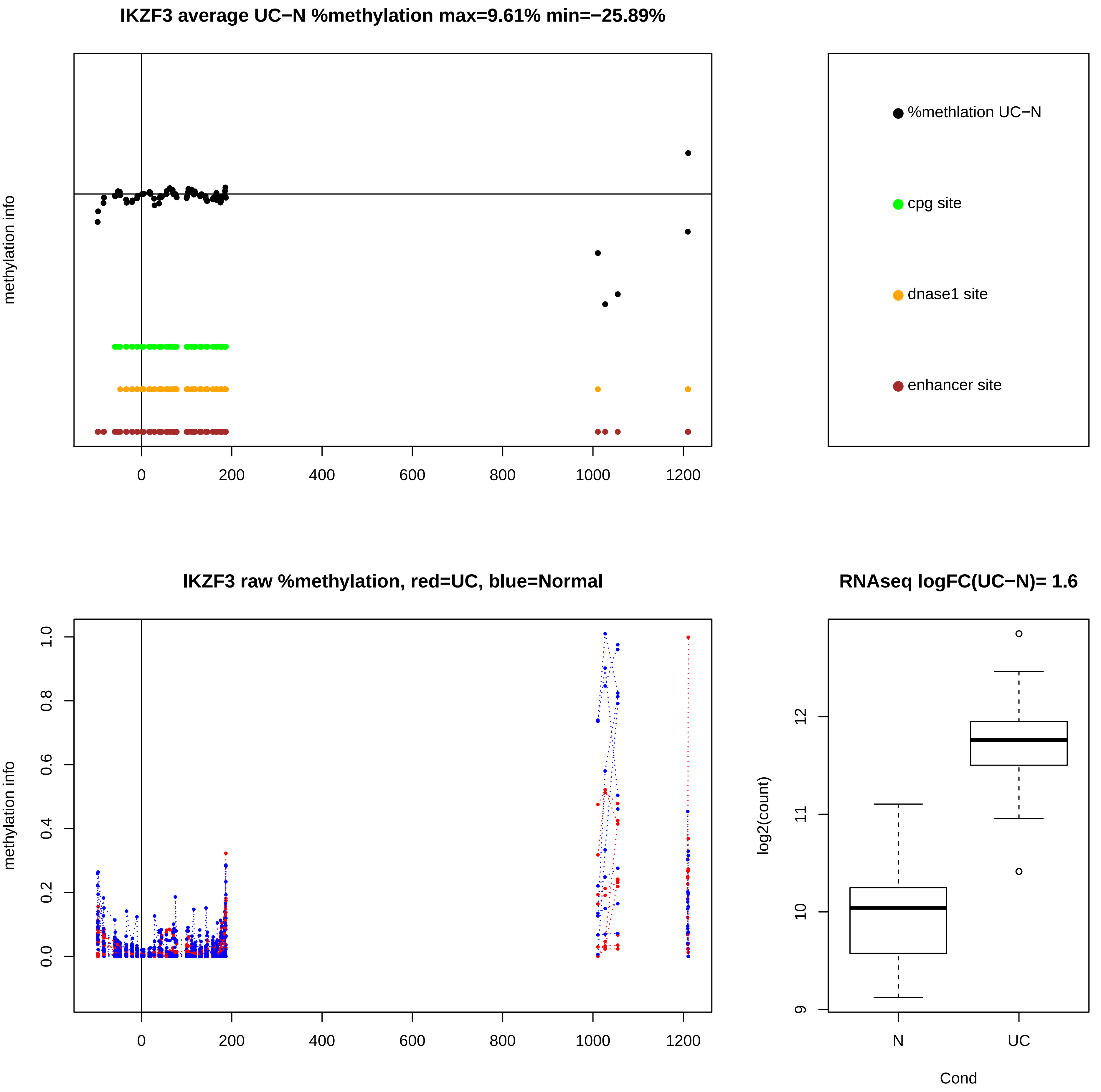

IGFBP5 raw %methylation, red=UC, blue=Normal

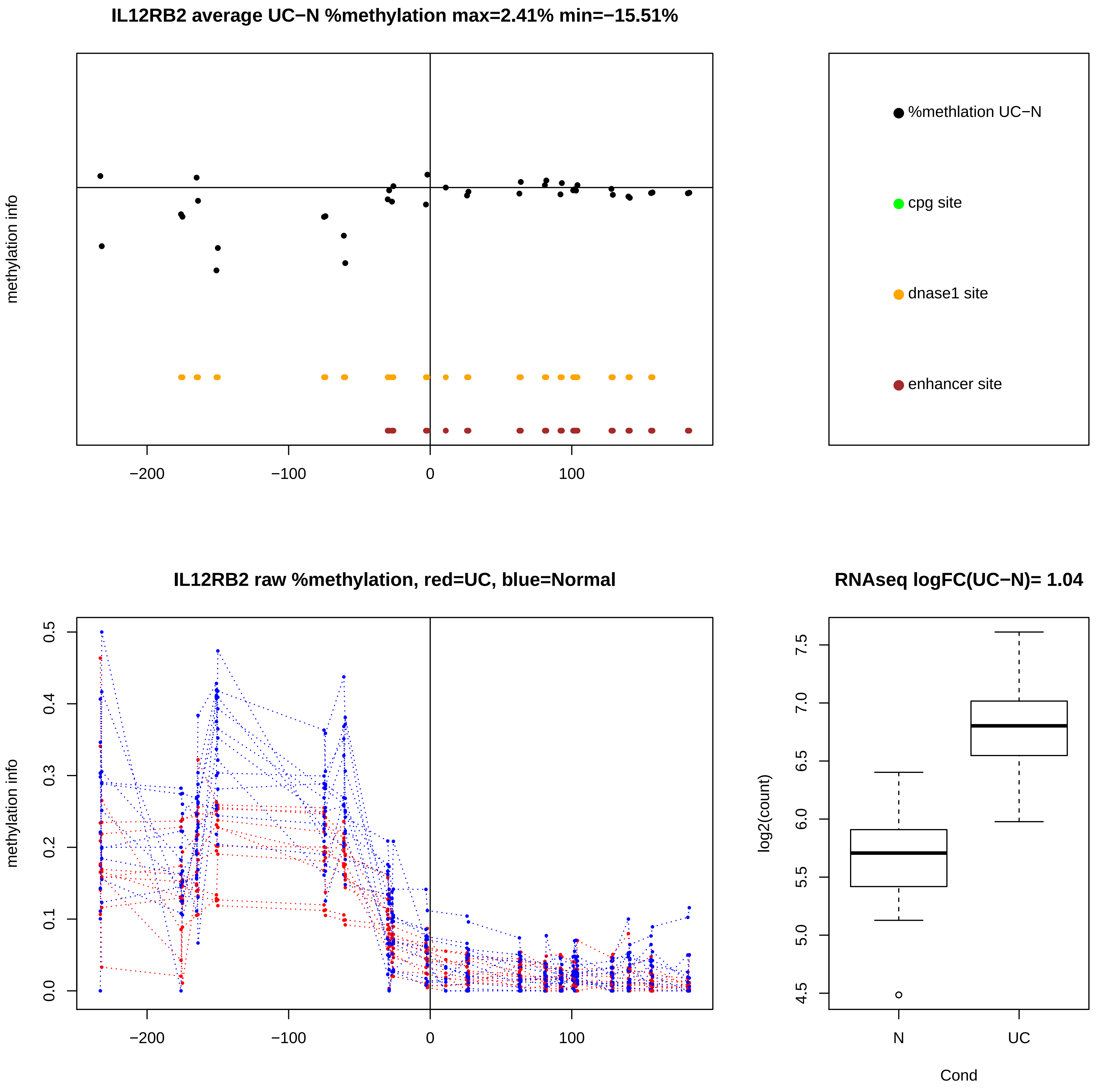

RNAseq logFC(UC−N)= 1.52

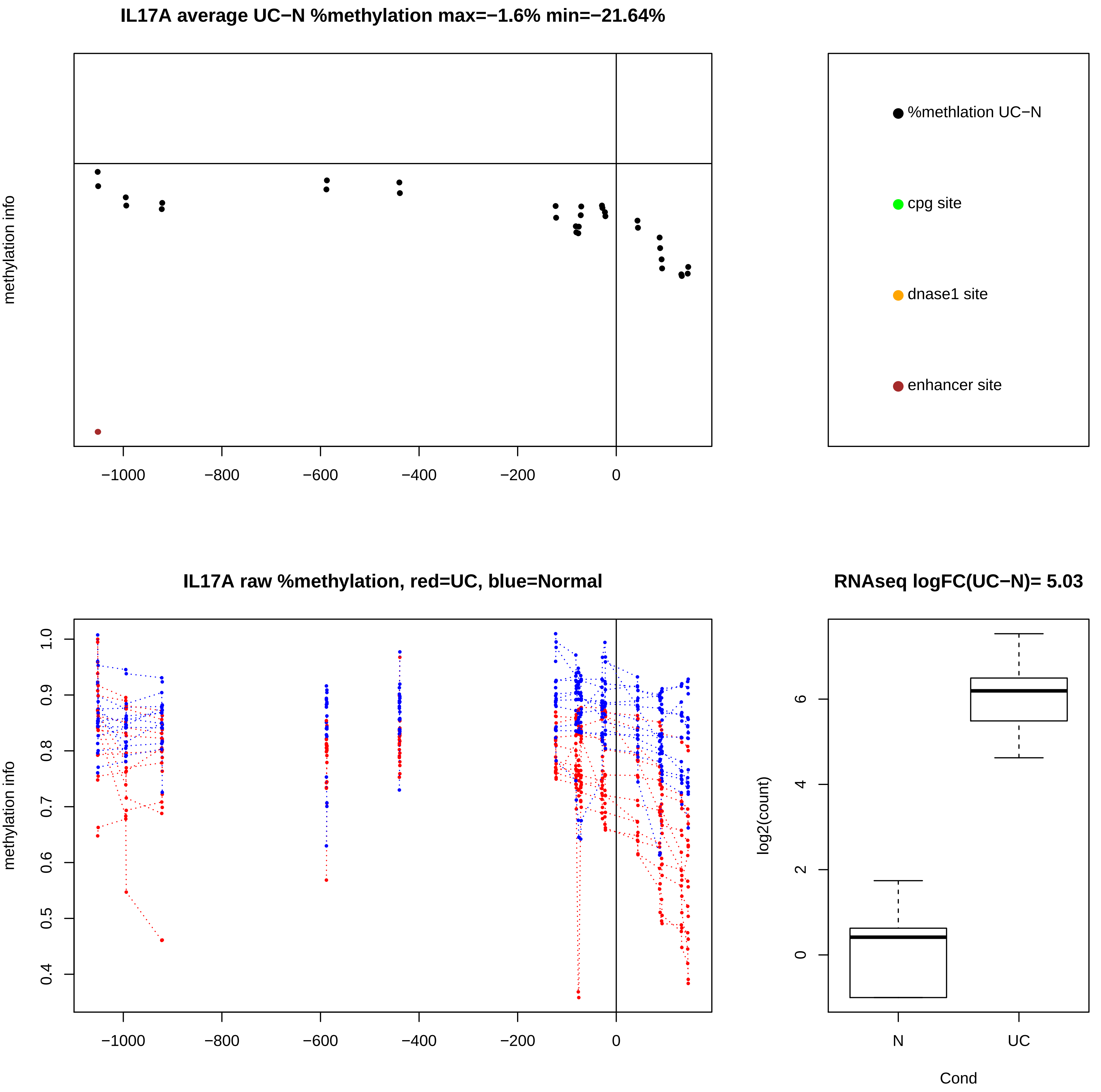

IGFLR1 average UC−N %methylation max=−23.05% min=−34.26%


IGFLR1 raw %methylation, red=UC, blue=Normal


RNAseq logFC(UC−N)= 1.05


IKZF3 average UC−N %methylation max=9.61% min=−25.89%
methylation info
0
200
400
600
800
1000
1200
%methlation UC−N
cpg site
dnase1 site
enhancer site
IKZF3 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
0
200
400
600
800
1000
1200
RNAseq logFC(UC−N)= 1.6
log2(count)
9
10
11
12
N
UC
Cond

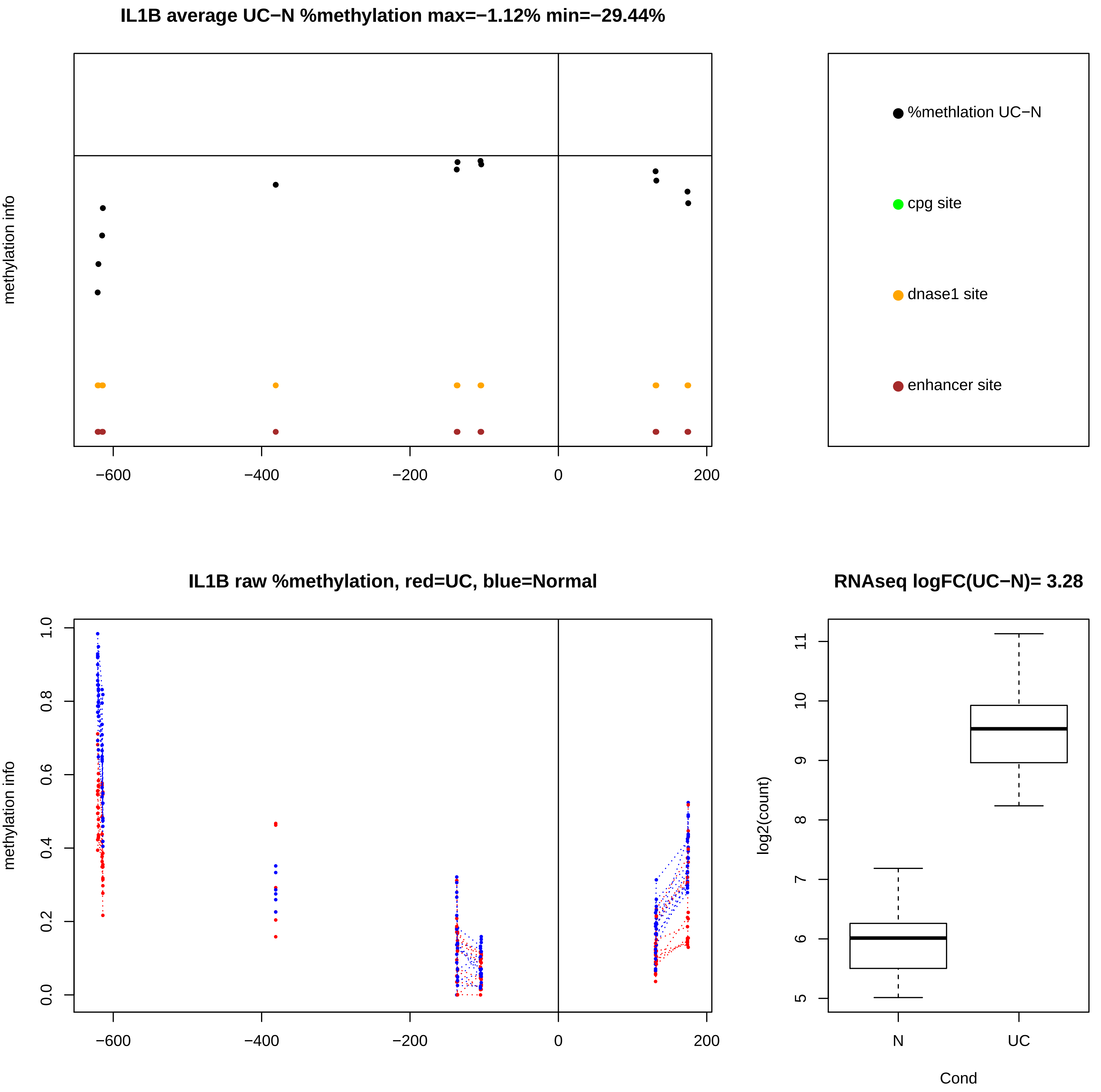

IL12RB2 average UC−N %methylation max=2.41% min=−15.51%
methylation info
−200
−100
0
100
%methlation UC−N
cpg site
dnase1 site
enhancer site
IL12RB2 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.1
0.2
0.3
0.4
0.5
−200
−100
0
100
RNAseq logFC(UC−N)= 1.04
log2(count)
4.5
5.0
5.5
6.0
6.5
7.0
7.5
N
UC
Cond

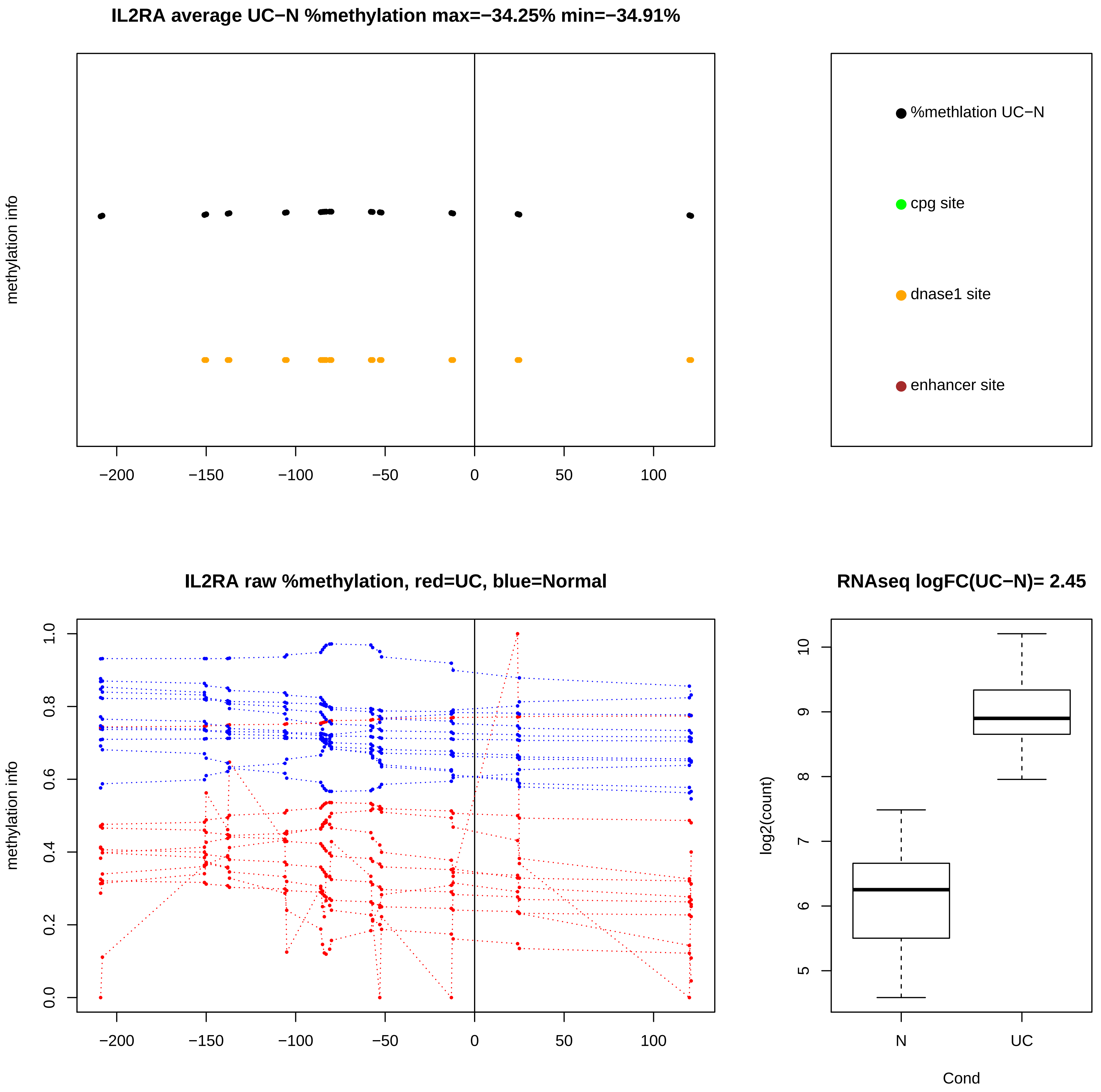


IL17A average UC−N %methylation max=−1.6% min=−21.64%

IL17A raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 5.03


IL1B average UC−N %methylation max=−1.12% min=−29.44%
methylation info
−600
−400
−200
0
200
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
IL1B raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−600
−400
−200
0
200
RNAseq logFC(UC−N)= 3.28
log2(count)
5
6
7
8
9
10
11
N
UC
Cond

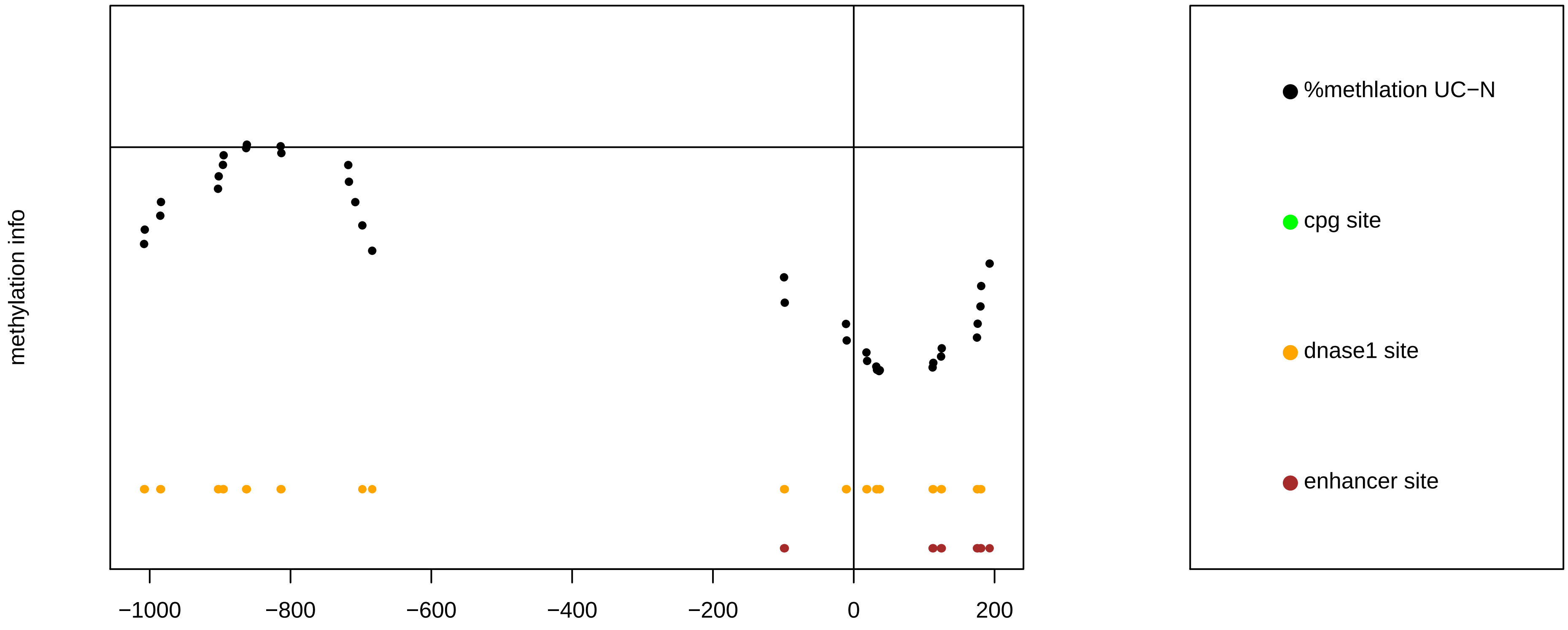


IL2RA average UC−N %methylation max=−34.25% min=−34.91%

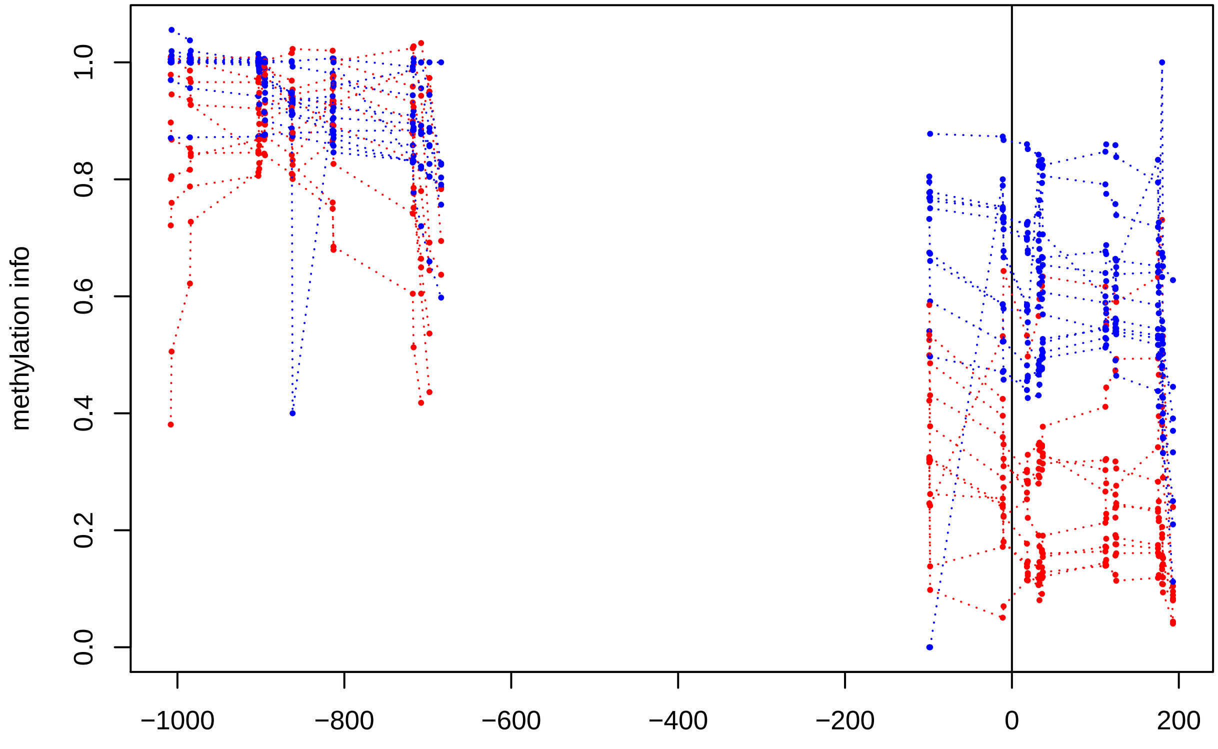
IL2RA raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 2.45

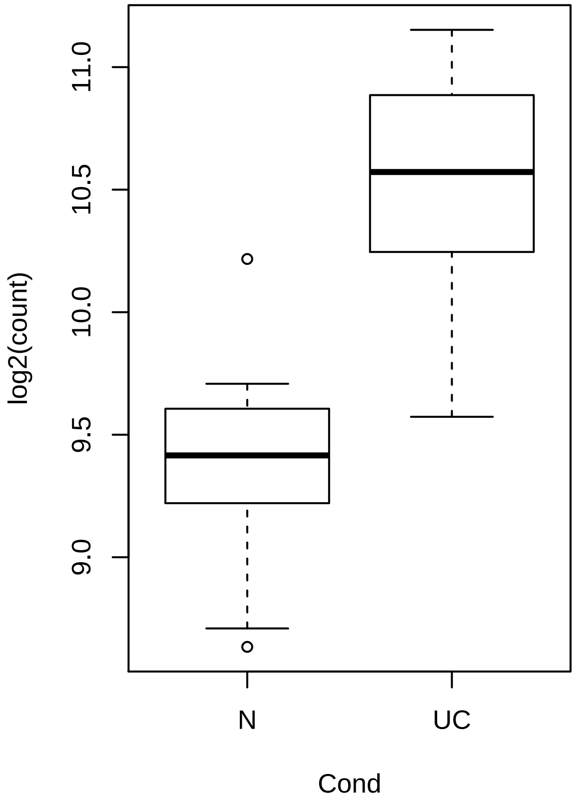
INPP5D average UC−N %methylation max=0.43% min=−37.9%

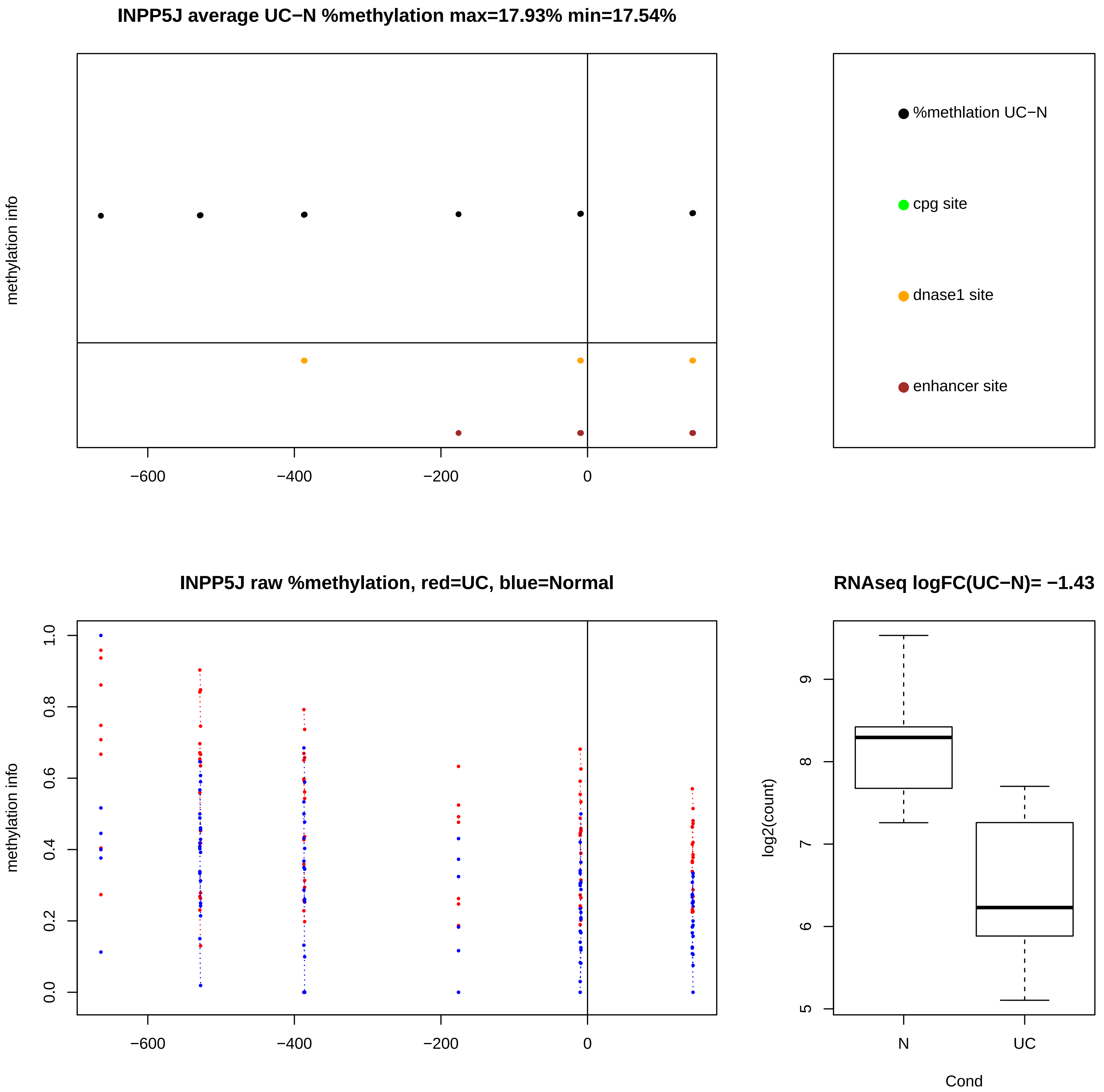


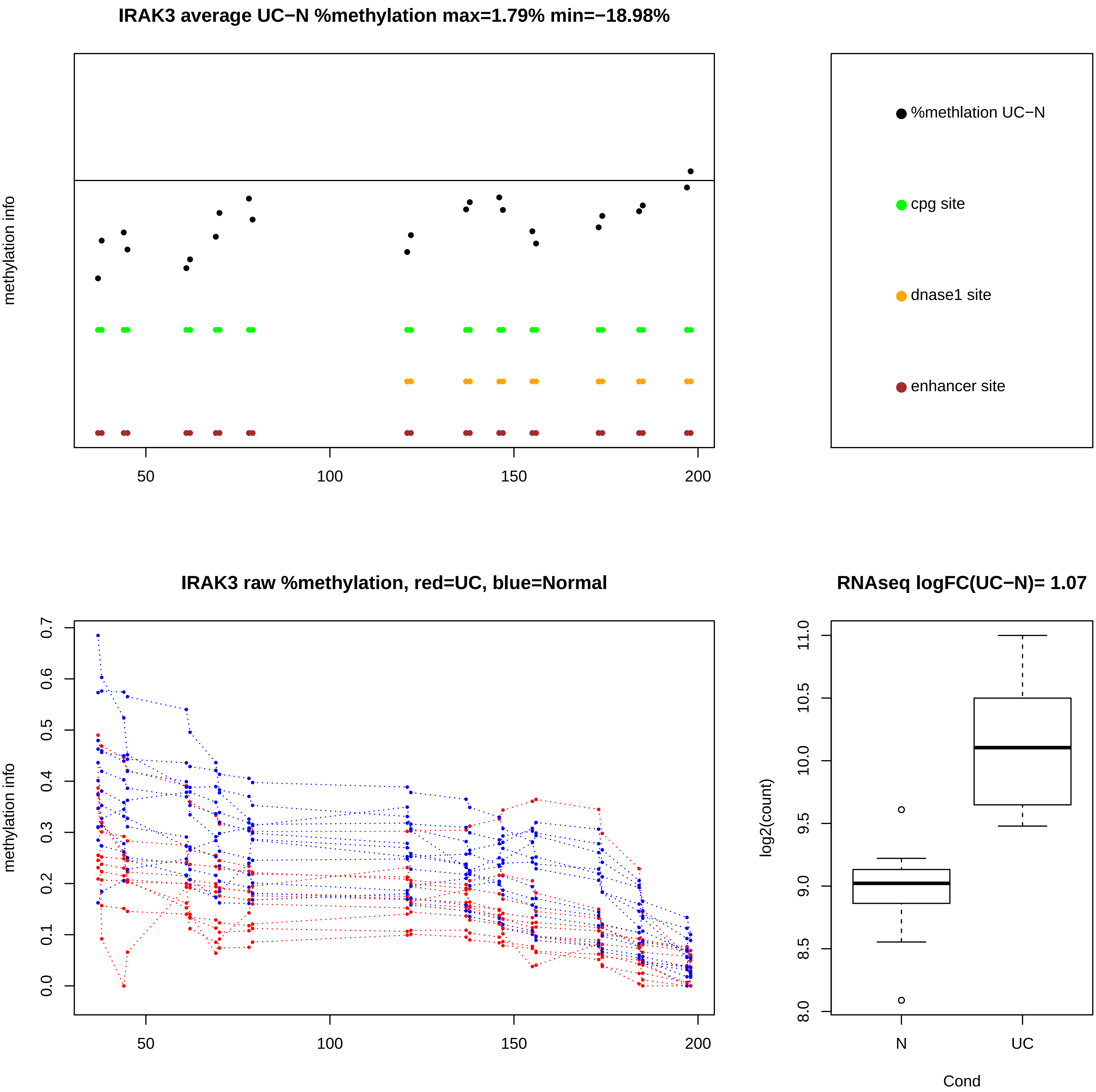
INPP5D raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 1.07



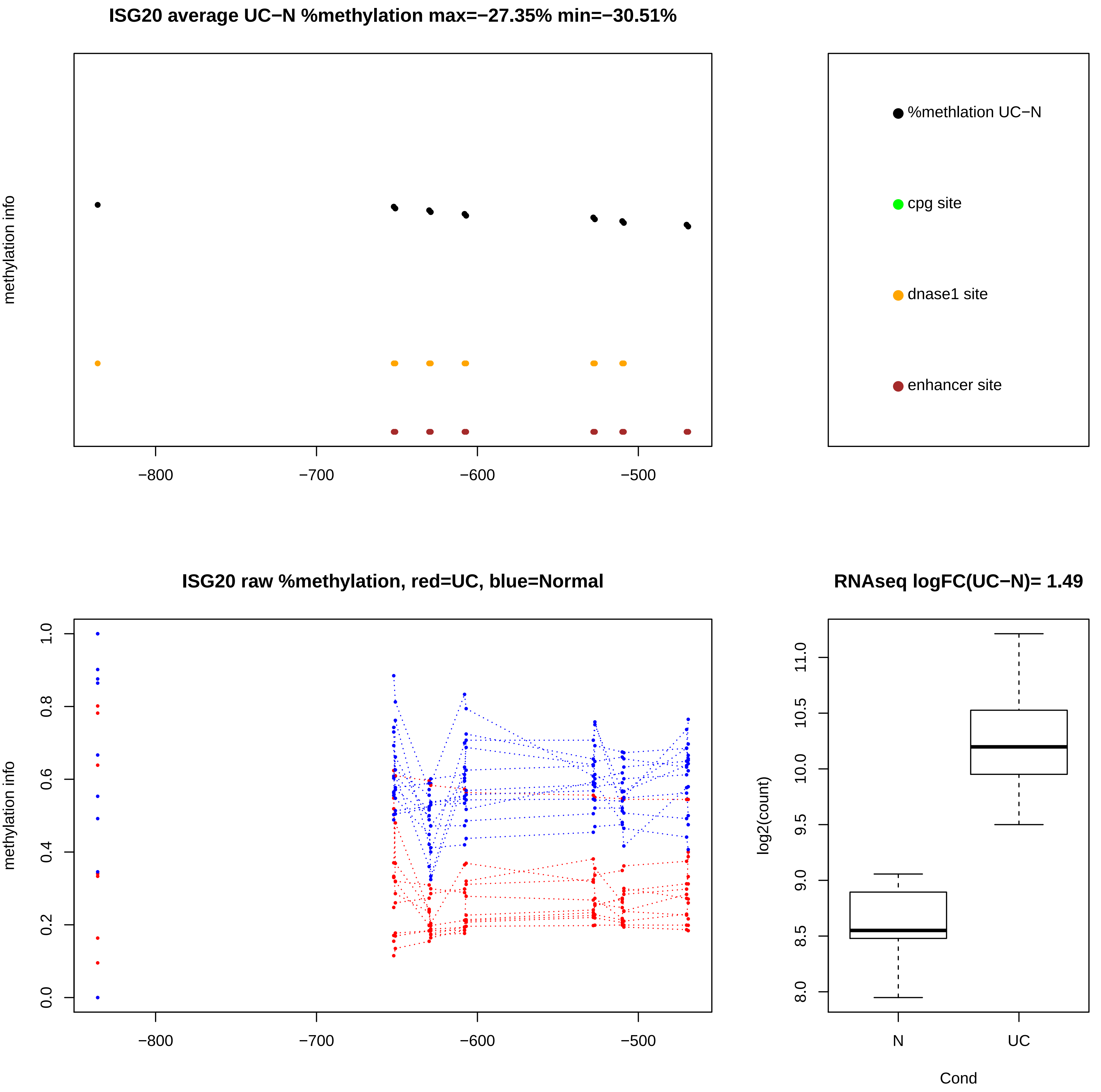

INPP5J average UC−N %methylation max=17.93% min=17.54%
methylation info
-600
-400
-200
0
%methlation UC−N
cpg site
dnase1 site
enhancer site
INPP5J raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
-600
-400
-200
0
RNAseq logFC(UC−N)= −1.43
log2(count)
5
6
7
8
9
N
UC
Cond



IRAK3 average UC−N %methylation max=1.79% min=−18.98%

IRAK3 raw %methylation, red=UC, blue=Normal

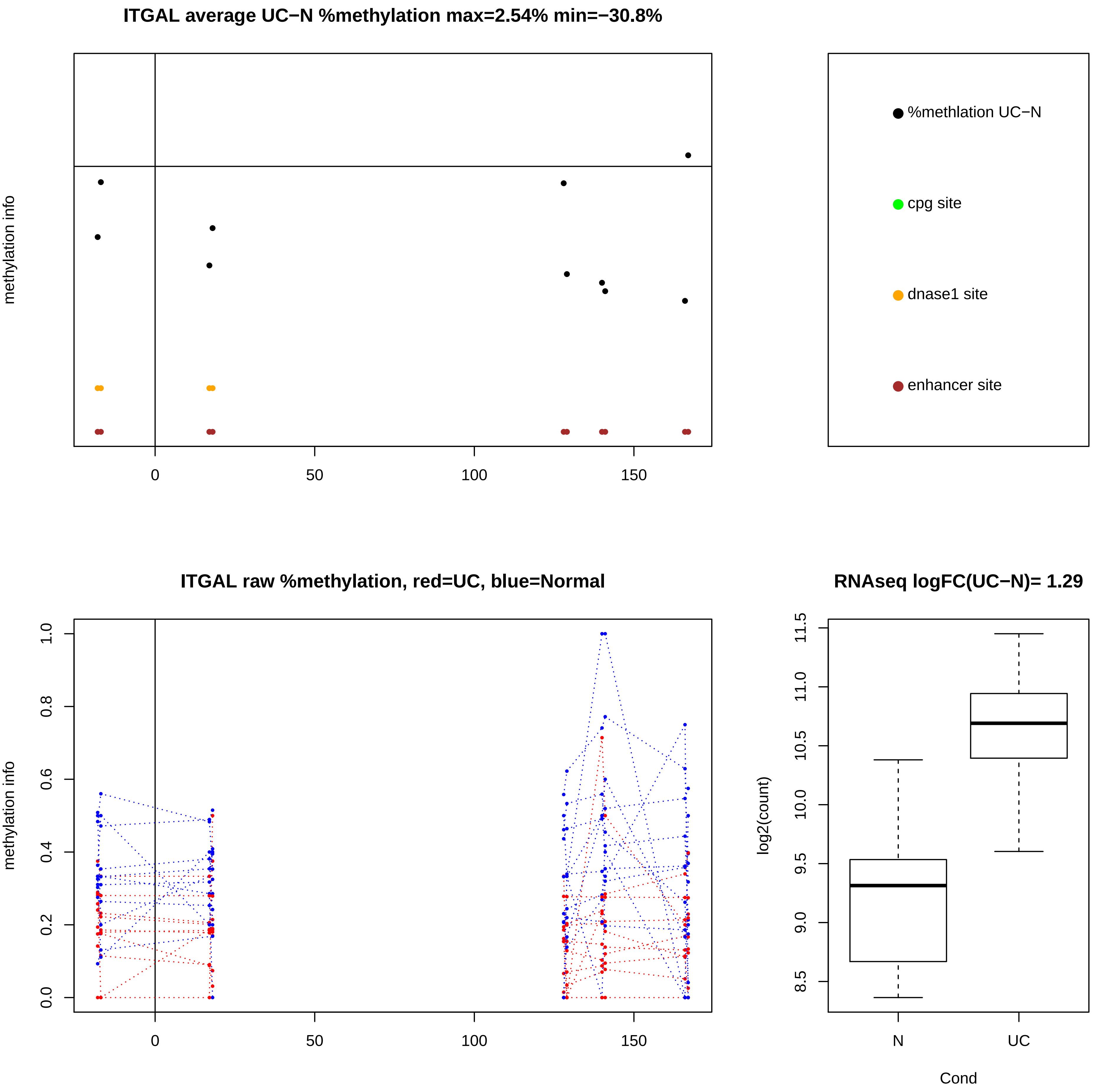
RNAseq logFC(UC−N)= 1.07



ISG20 average UC−N %methylation max=−27.35% min=−30.51%

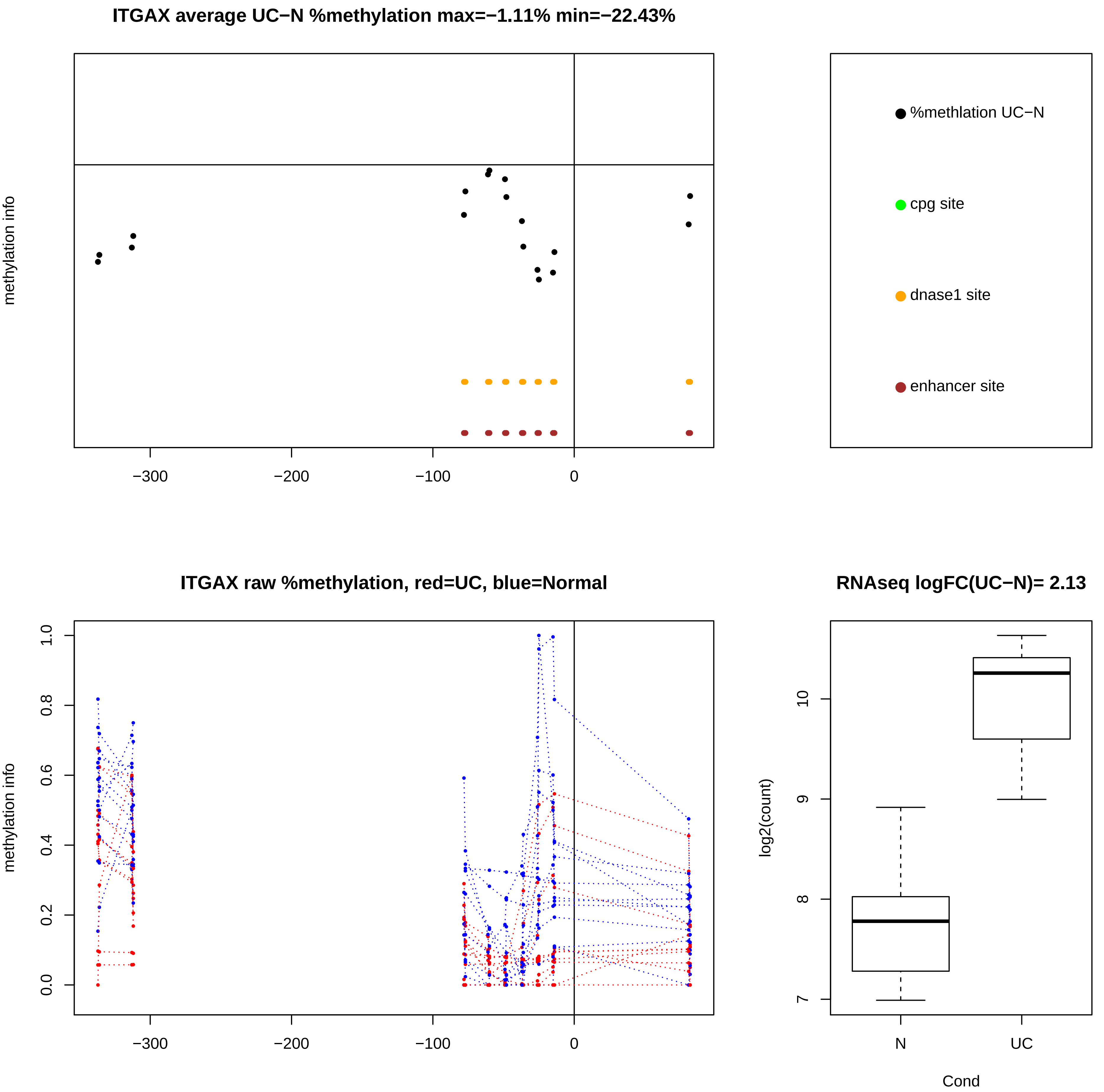
ISG20 raw %methylation, red=UC, blue=Normal

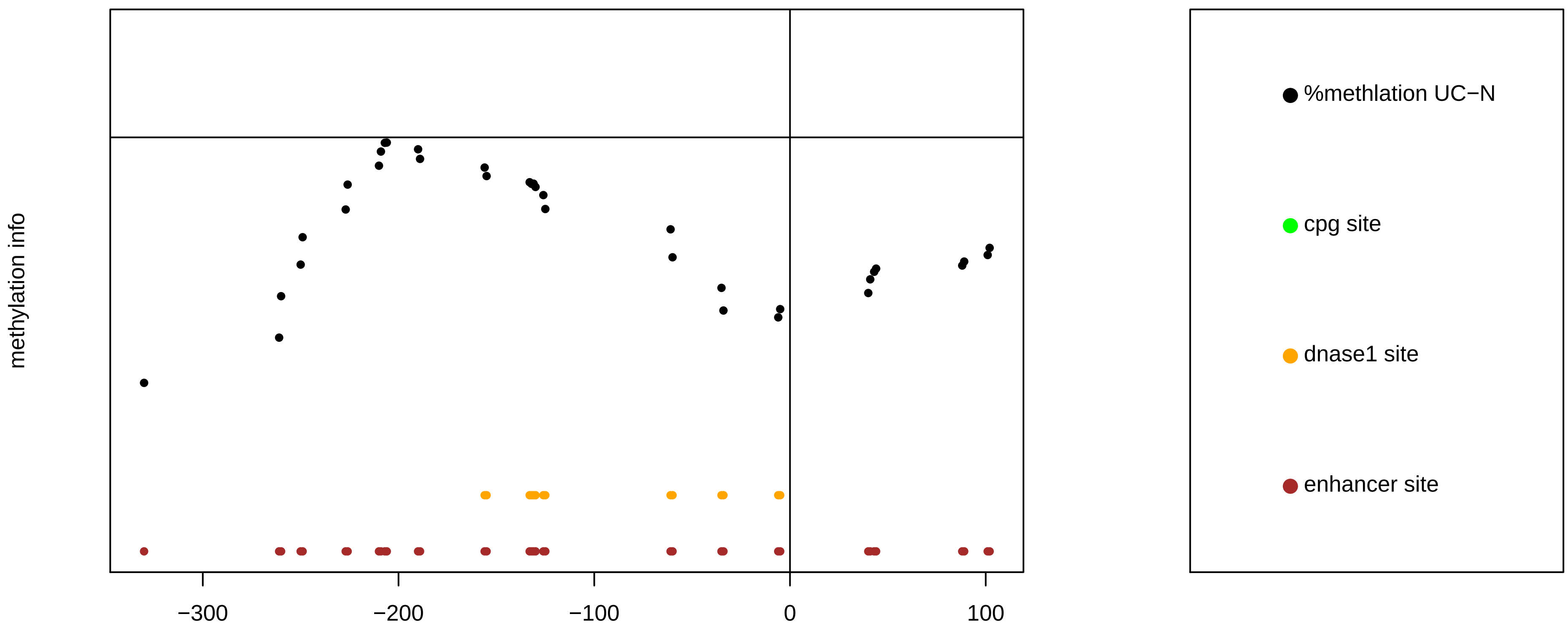
RNAseq logFC(UC−N)= 1.49


ITGAL average UC−N %methylation max=2.54% min=−30.8%

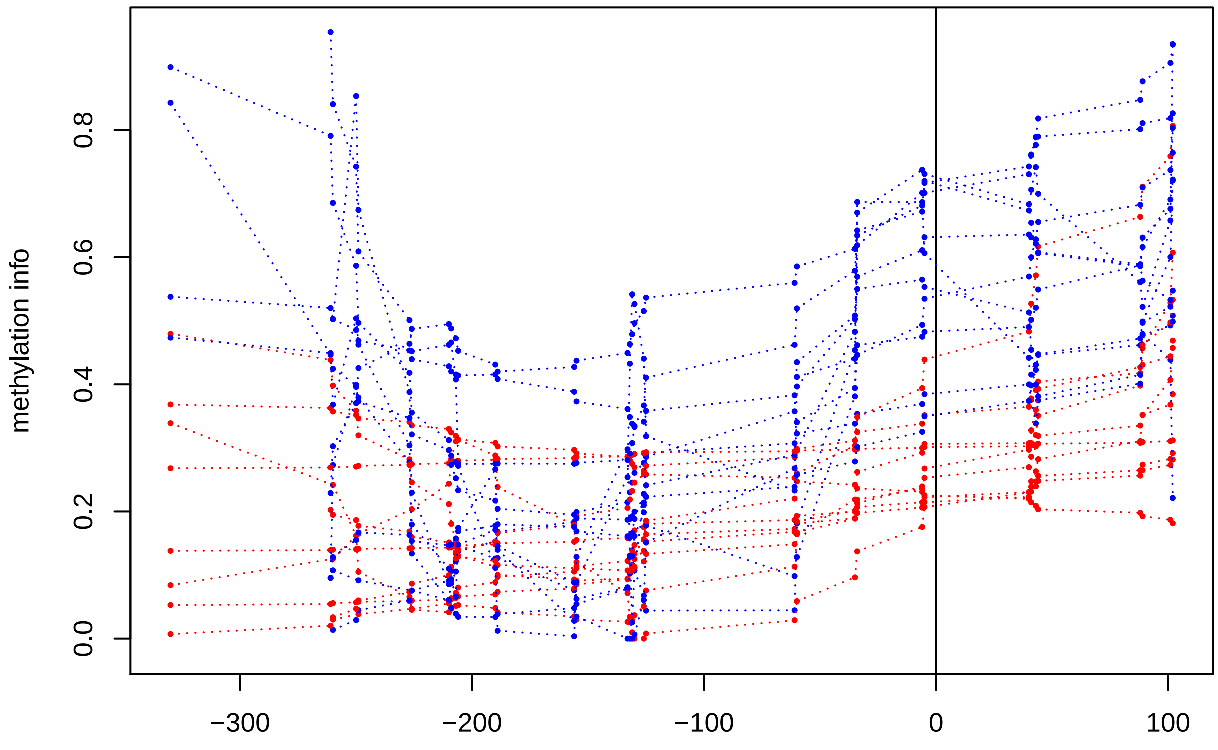
ITGAL raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.29

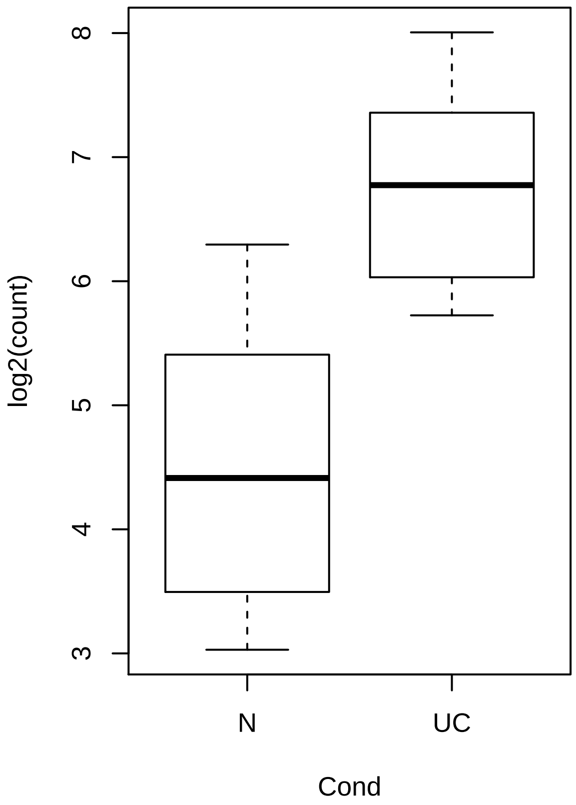

ITGAX average UC−N %methylation max=−1.11% min=−22.43%
methylation info
−300
−200
−100
0
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
ITGAX raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−300
−200
−100
0
RNAseq logFC(UC−N)= 2.13
log2(count)
7
8
9
10
N
UC
Cond



ITGB2−AS1 average UC−N %methylation max=−0.93% min=−43.72%

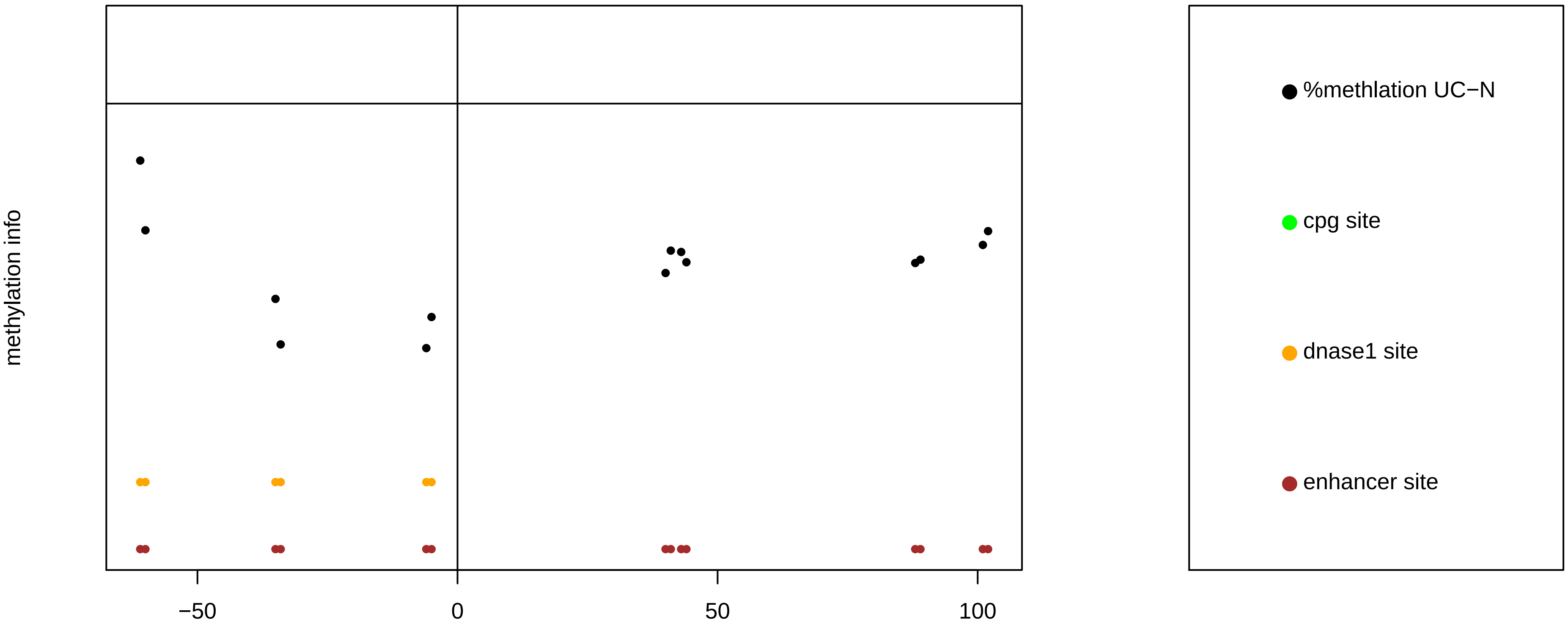


ITGB2−AS1 raw %methylation, red=UC, blue=Normal

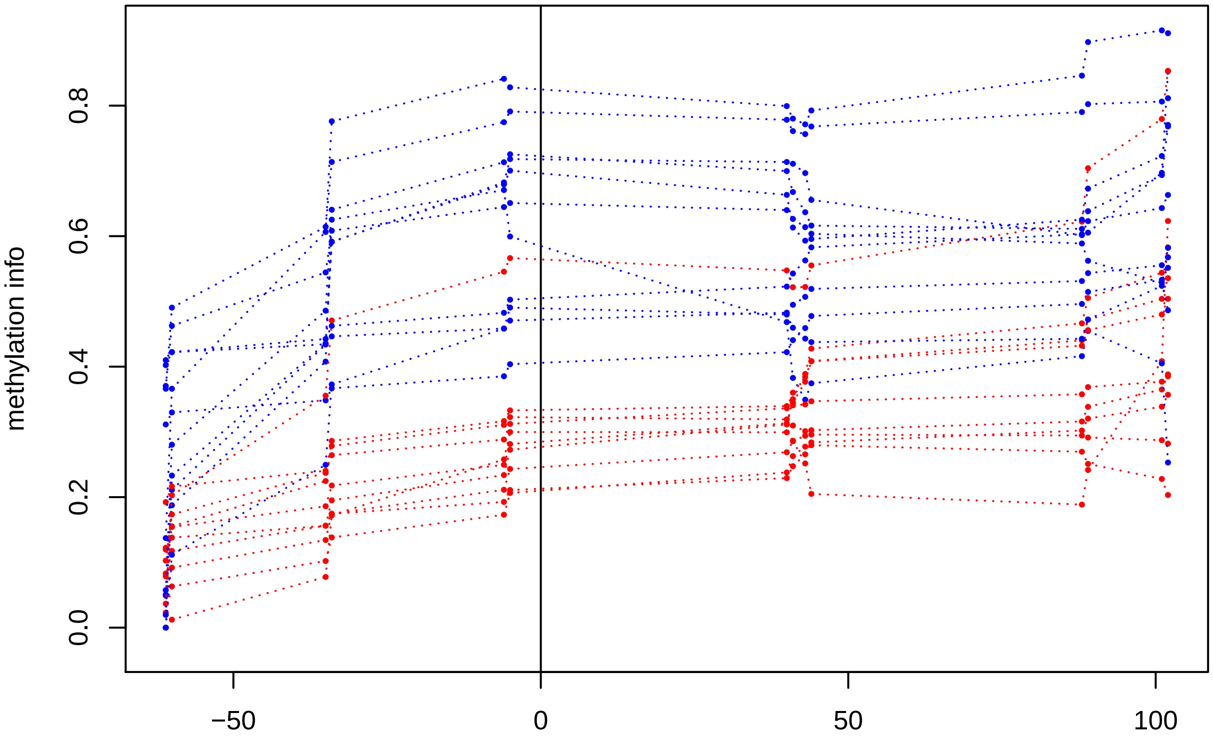


RNAseq logFC(UC−N)= 1.79

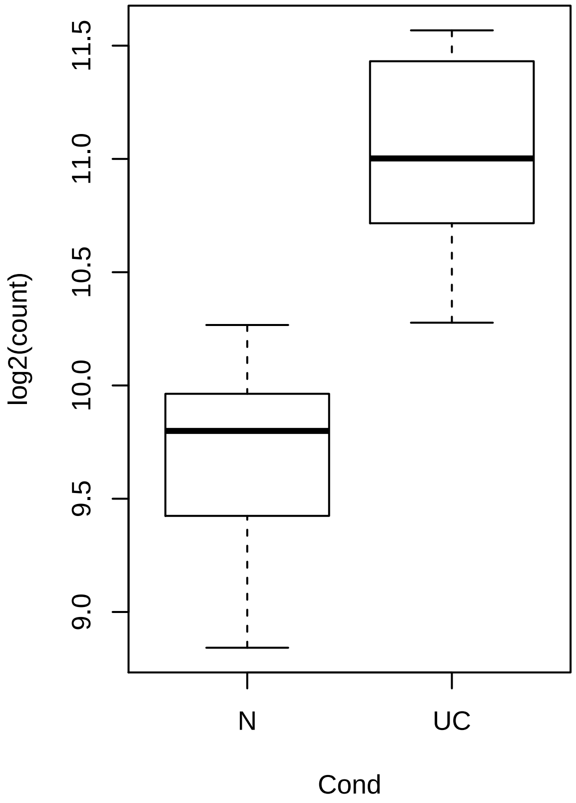
ITGB2 average UC−N %methylation max=−8.5% min=−36.49%

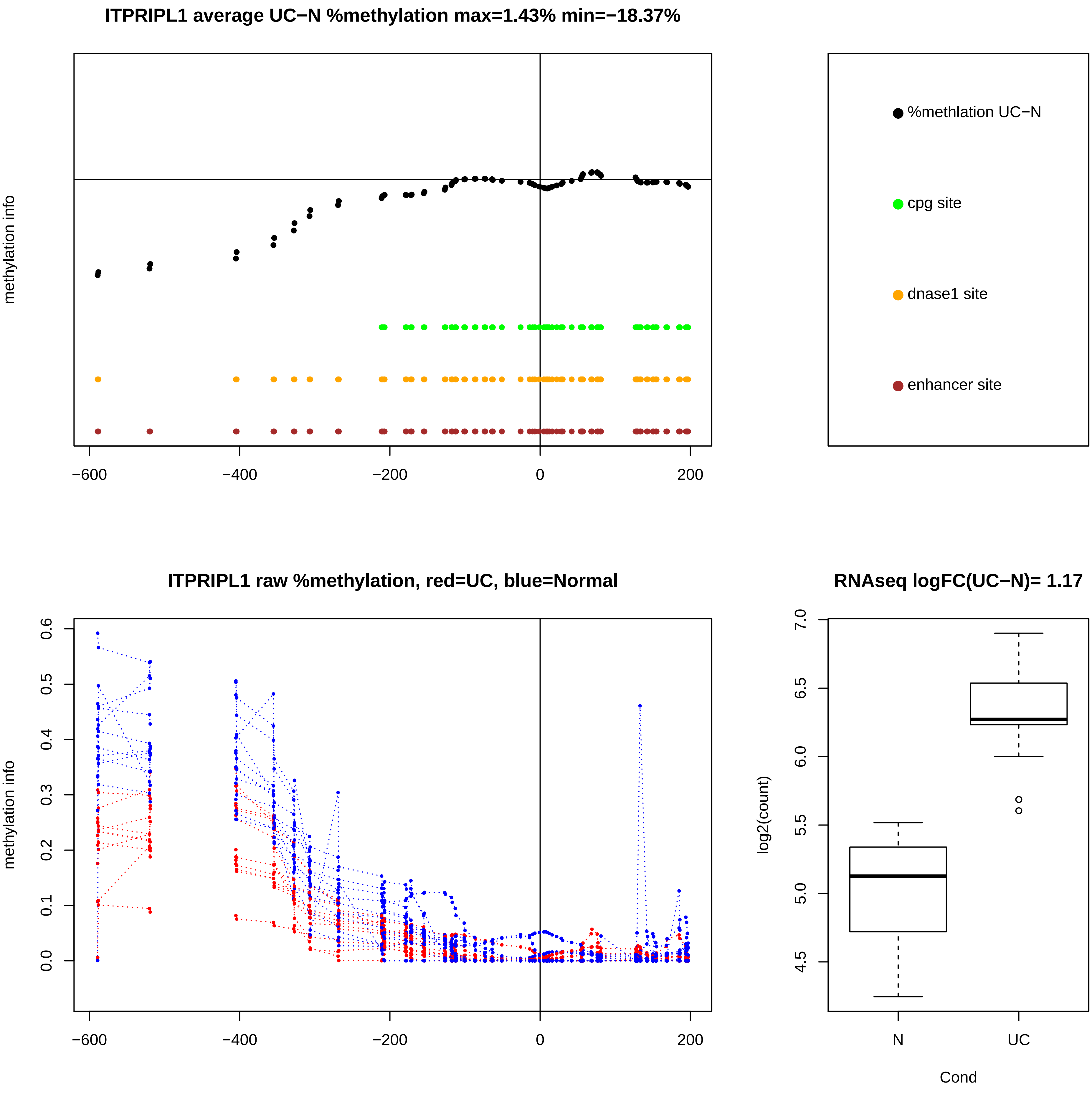


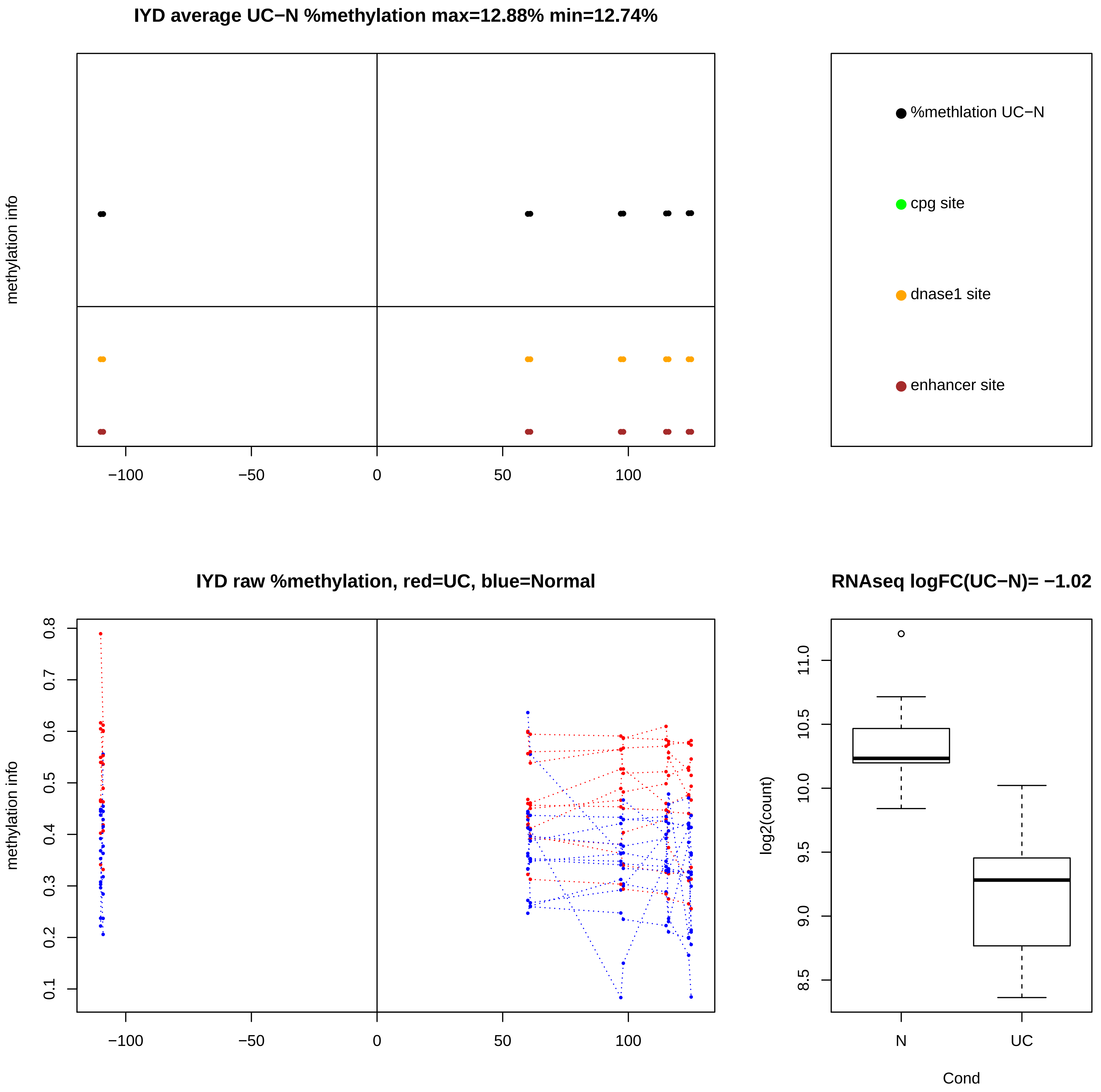
ITGB2 raw %methylation, red=UC, blue=Normal

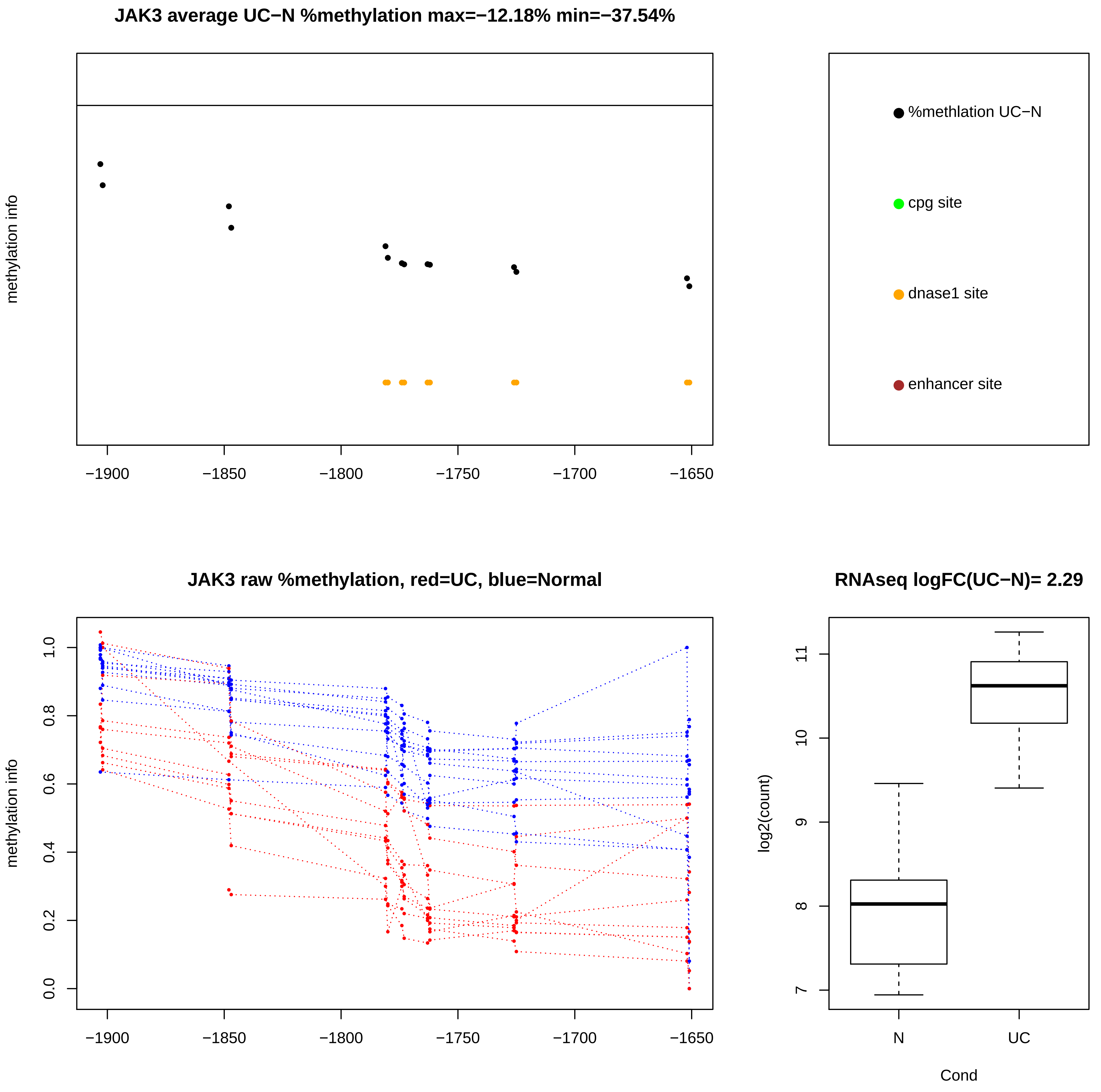


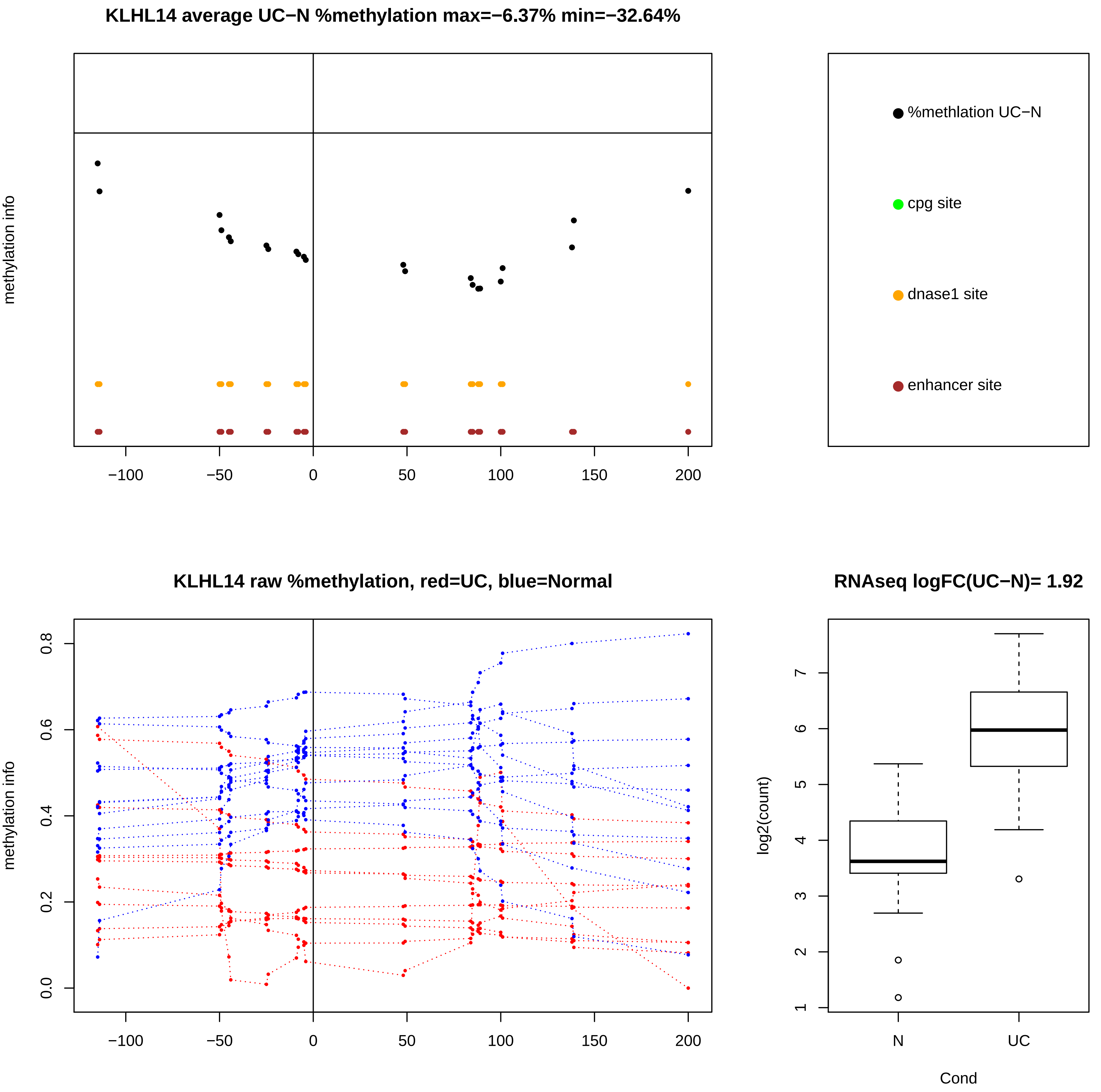
RNAseq logFC(UC−N)= 1.23



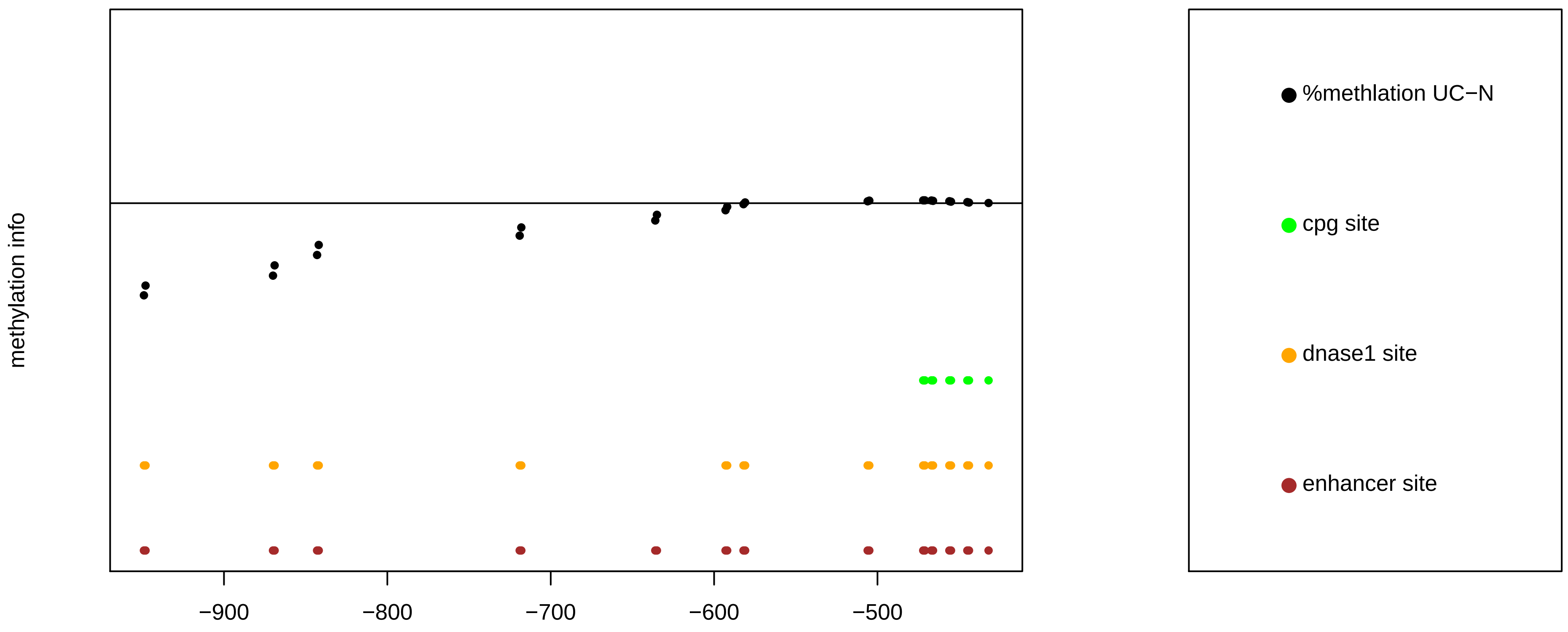

ITPRIPL1 average UC−N %methylation max=1.43% min=−18.37%
methylation info
−600
−400
−200
0
200
%methlation UC−N
cpg site
dnase1 site
enhancer site
ITPRIPL1 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.1
0.2
0.3
0.4
0.5
0.6
−600
−400
−200
0
200
RNAseq logFC(UC−N)= 1.17
log2(count)
4.5
5.0
5.5
6.0
6.5
7.0
N
UC
Cond


IYD average UC−N %methylation max=12.88% min=12.74%
methylation info
−100
−50
0
50
100
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
IYD raw %methylation, red=UC, blue=Normal
methylation info
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
−100
−50
0
50
100
RNAseq logFC(UC−N)= −1.02
log2(count)
8.5
9.0
9.5
10.0
10.5
11.0
N
UC
Cond

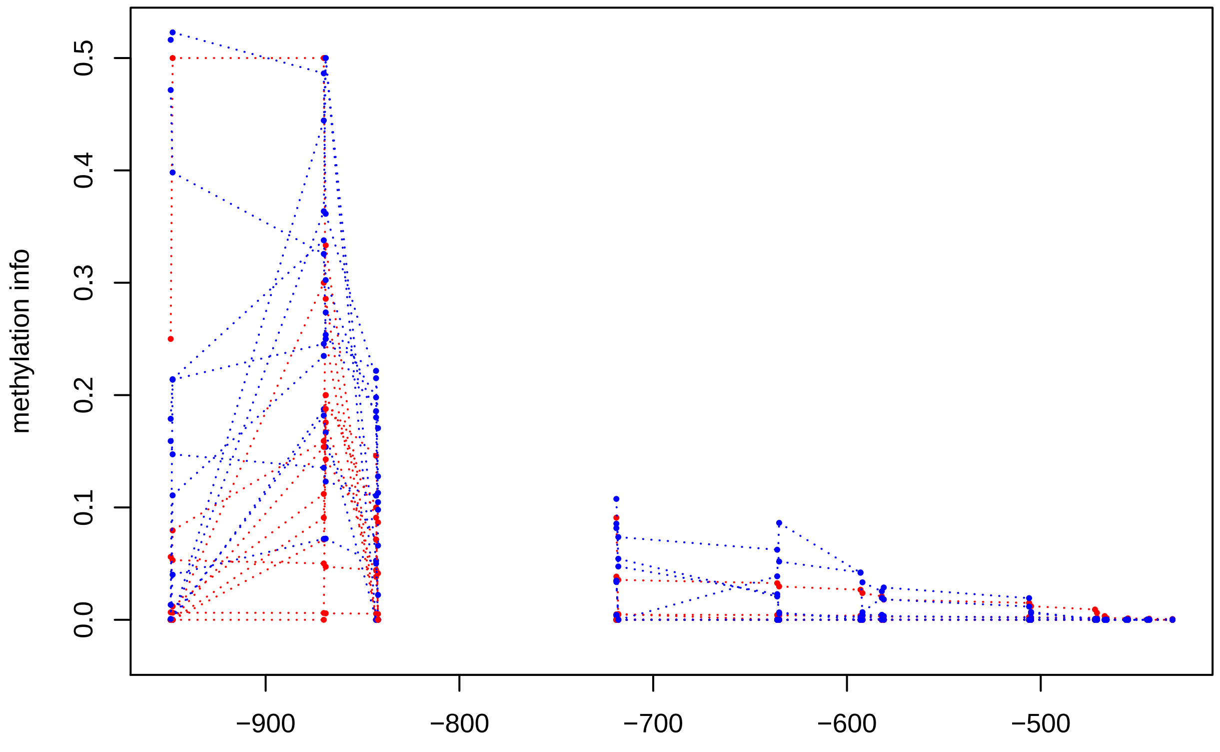

JAK3 average UC−N %methylation max=−12.18% min=−37.54%
methylation info
−1900
−1850
−1800
−1750
−1700
−1650
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
JAK3 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−1900
−1850
−1800
−1750
−1700
−1650
RNAseq logFC(UC−N)= 2.29
log2(count)
7
8
9
10
11
N
UC
Cond


KLHL14 average UC−N %methylation max=−6.37% min=−32.64%
methylation info
−100
−50
0
50
100
150
200
%methlation UC−N
cpg site
dnase1 site
enhancer site
KLHL14 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
RNAseq logFC(UC−N)= 1.92
log2(count)
1
2
3
4
5
6
7
N
UC
Cond

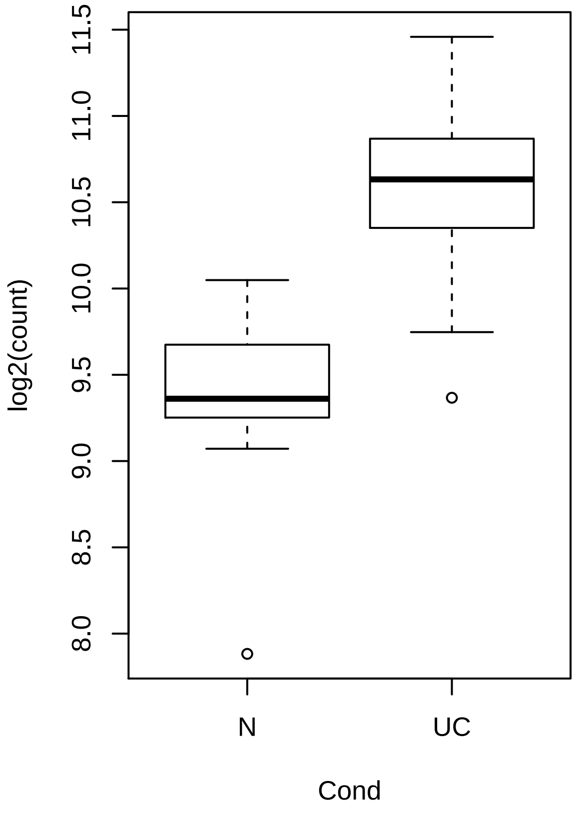
KLHL5 average UC−N %methylation max=0.34% min=−10.83%

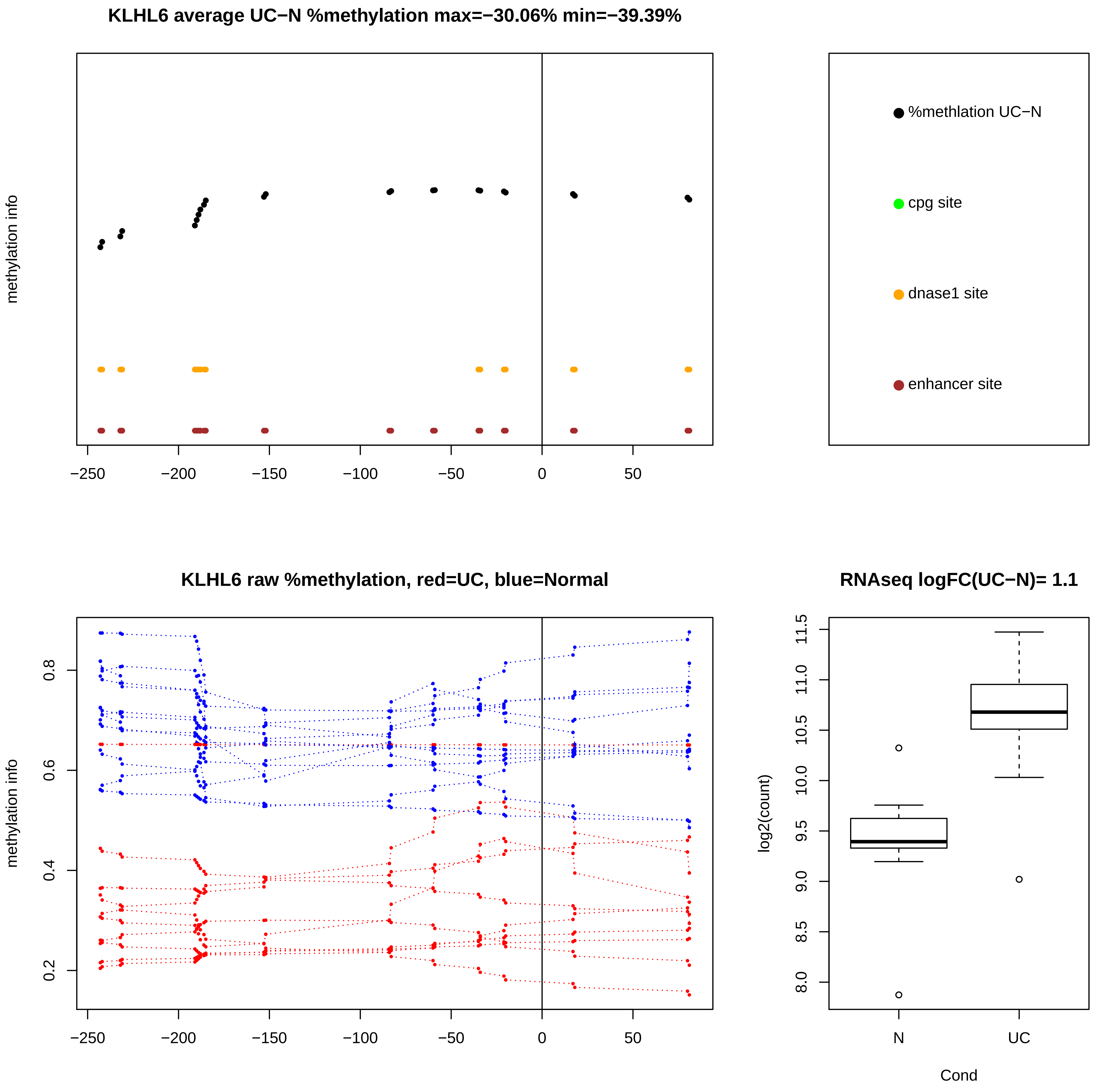


KLHL5 raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 1.09

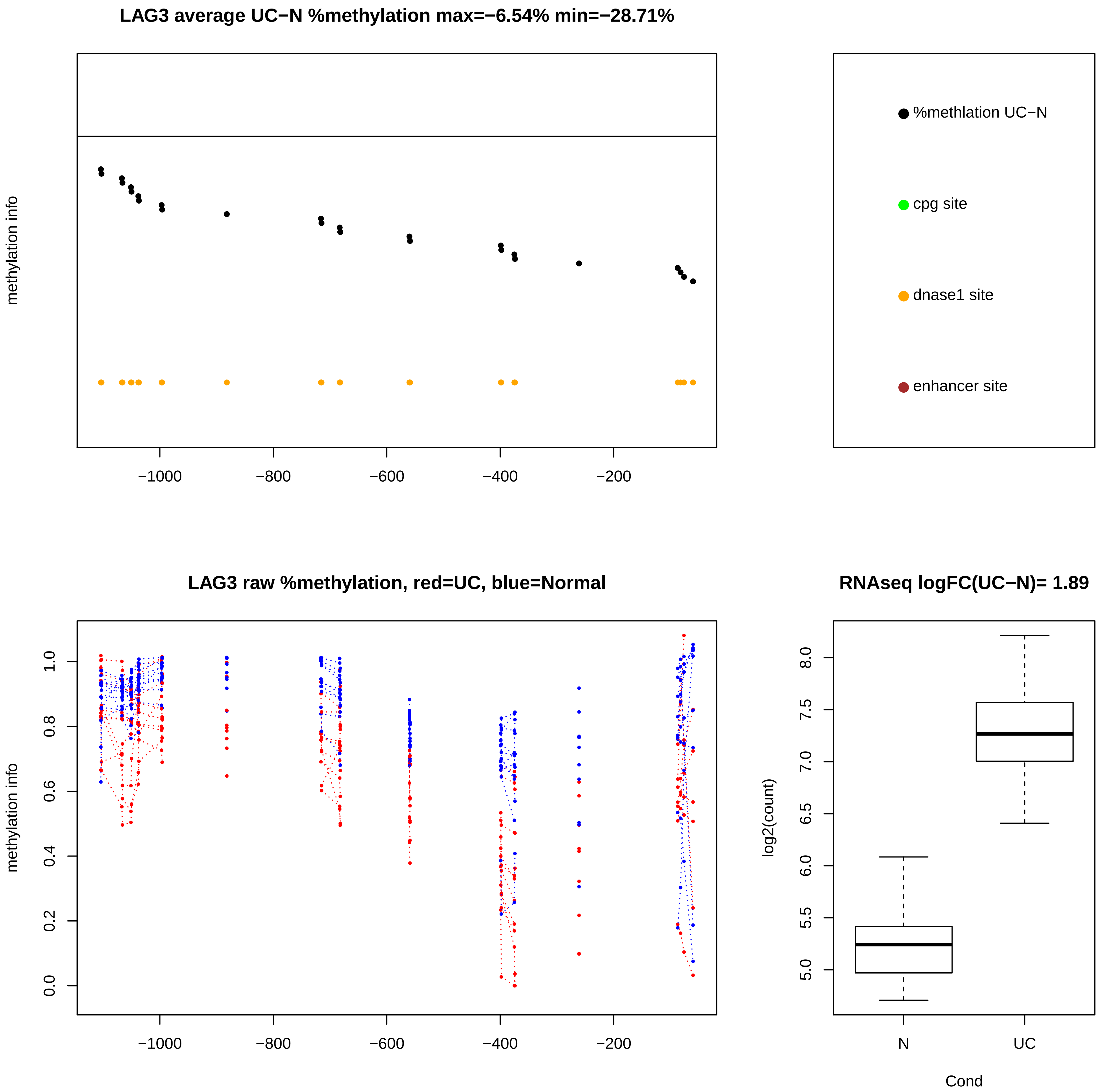


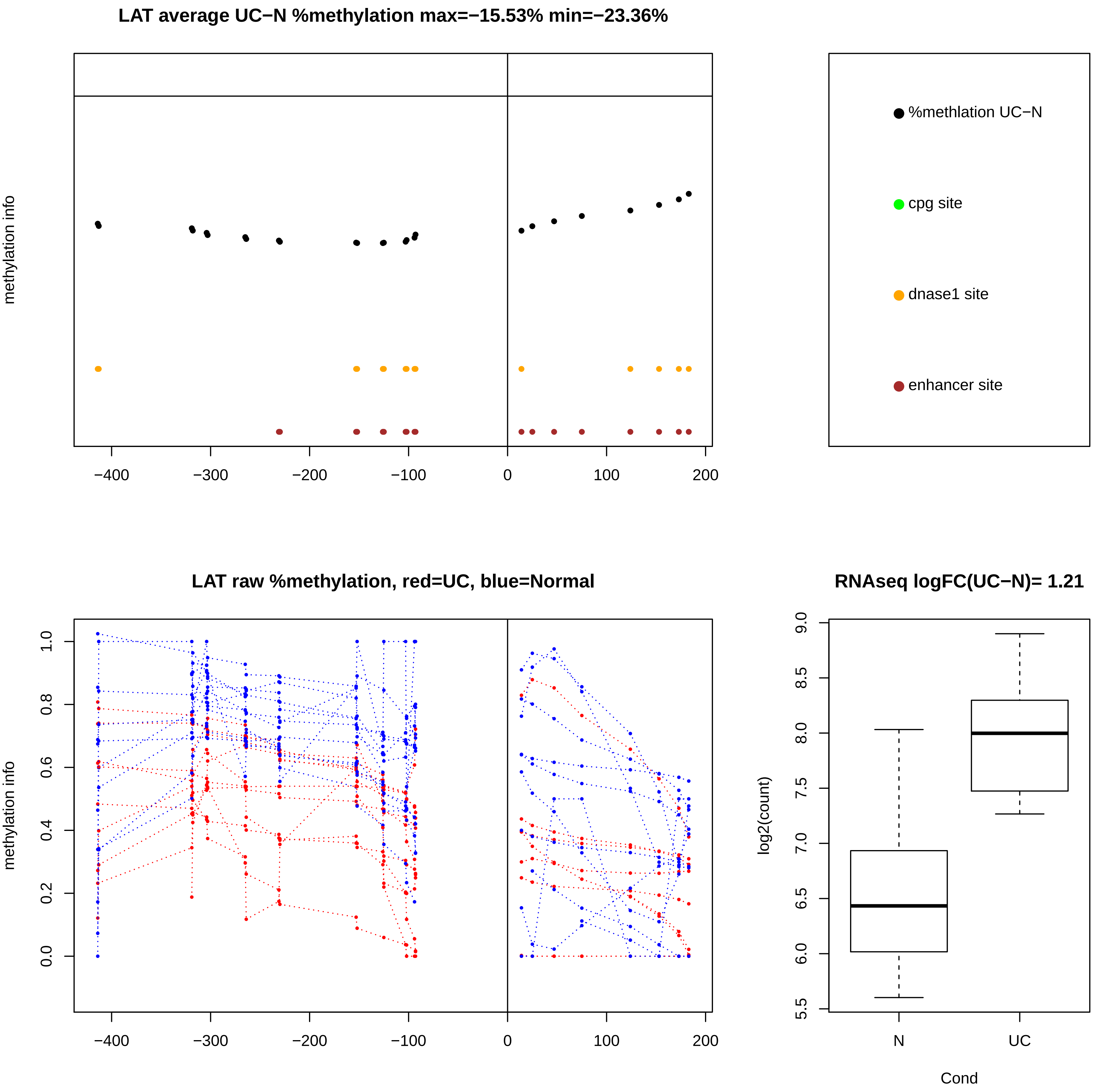


KLHL6 average UC−N %methylation max=−30.06% min=−39.39%

KLHL6 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.1

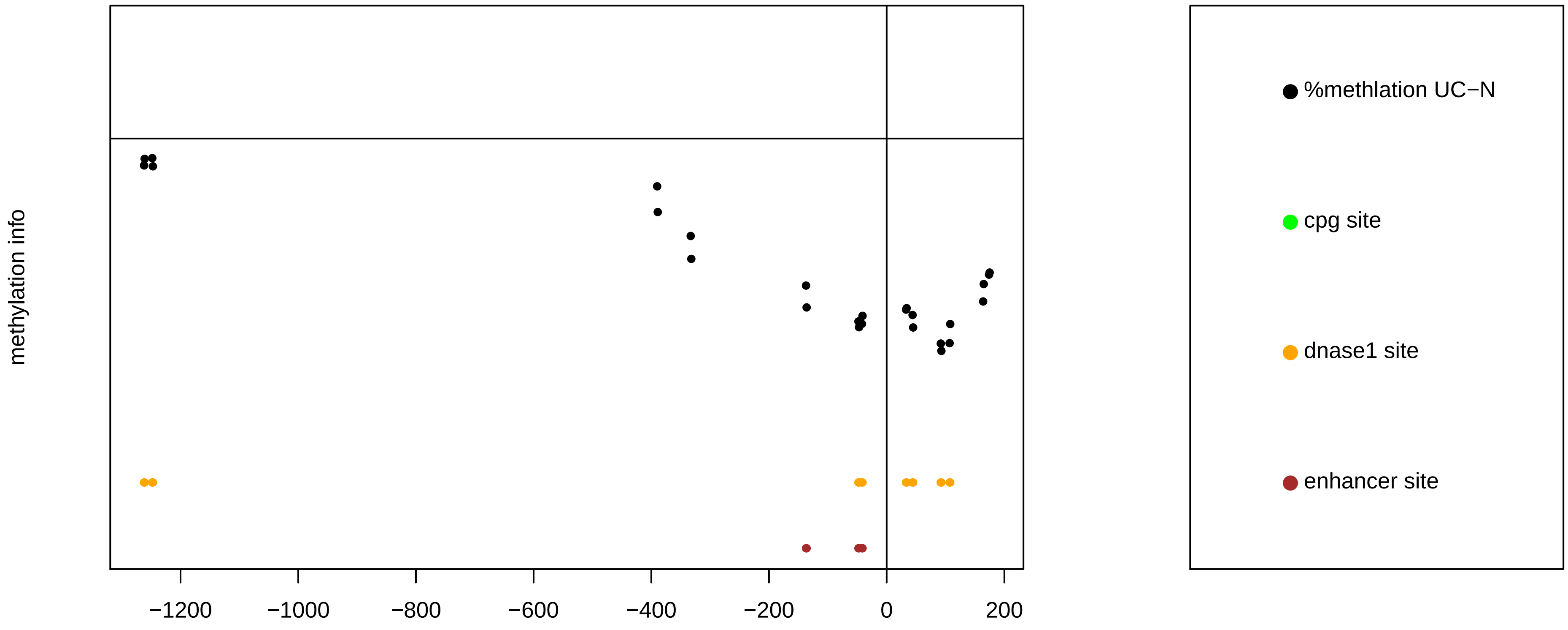

LAG3 average UC−N %methylation max=−6.54% min=−28.71%
methylation info
−1000
−800
−600
−400
−200
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
LAG3 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−1000
−800
−600
−400
−200
RNAseq logFC(UC−N)= 1.89
log2(count)
5.0
5.5
6.0
6.5
7.0
7.5
8.0
N
UC
Cond



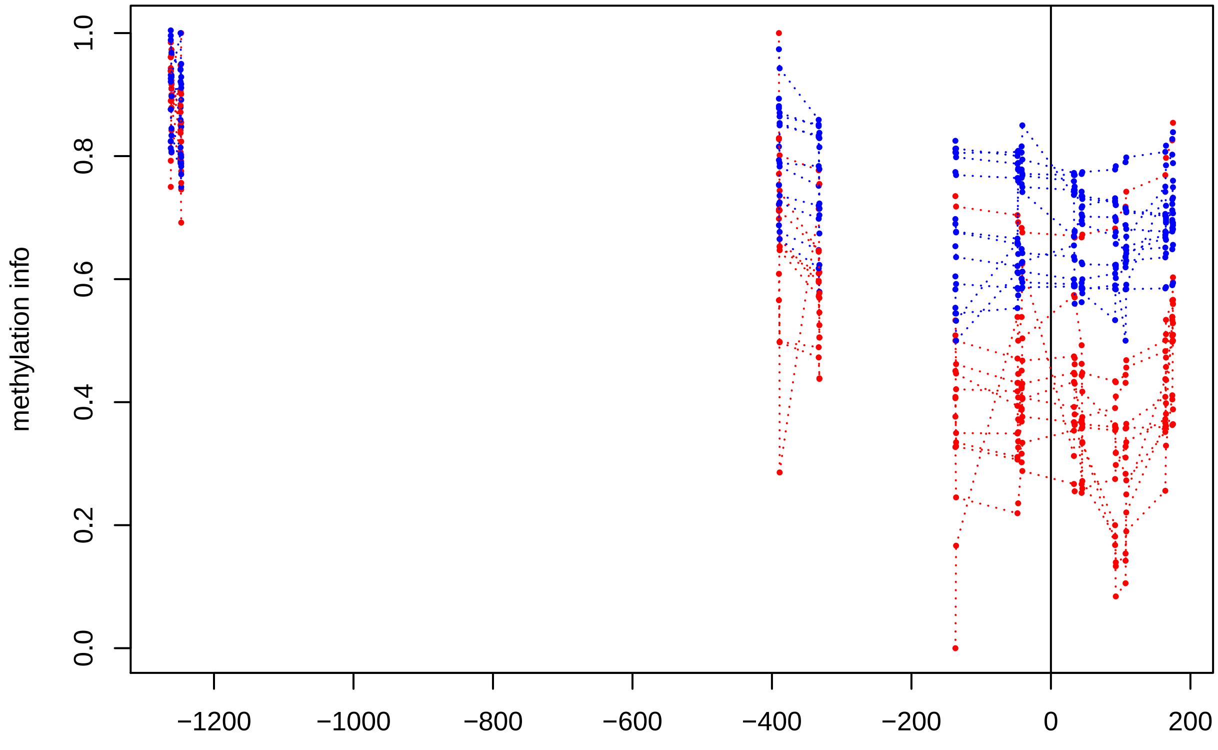
LAT average UC−N %methylation max=−15.53% min=−23.36%

LAT raw %methylation, red=UC, blue=Normal

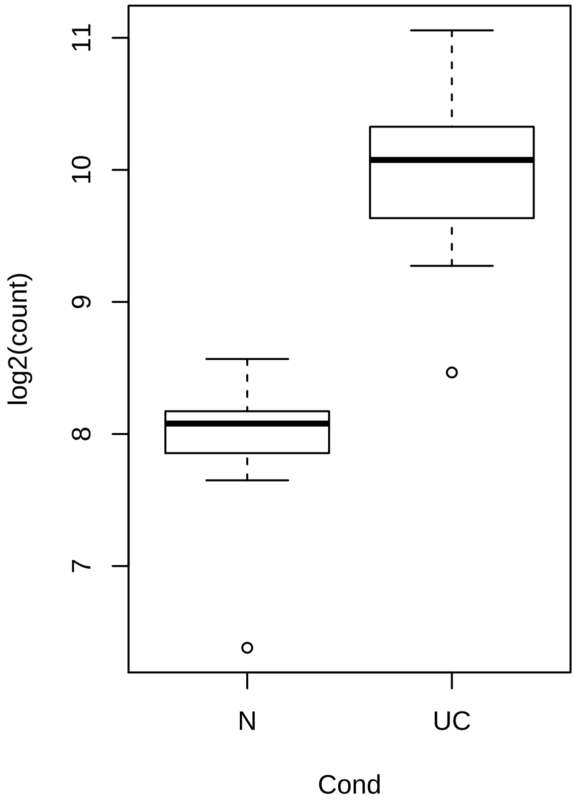
RNAseq logFC(UC−N)= 1.21



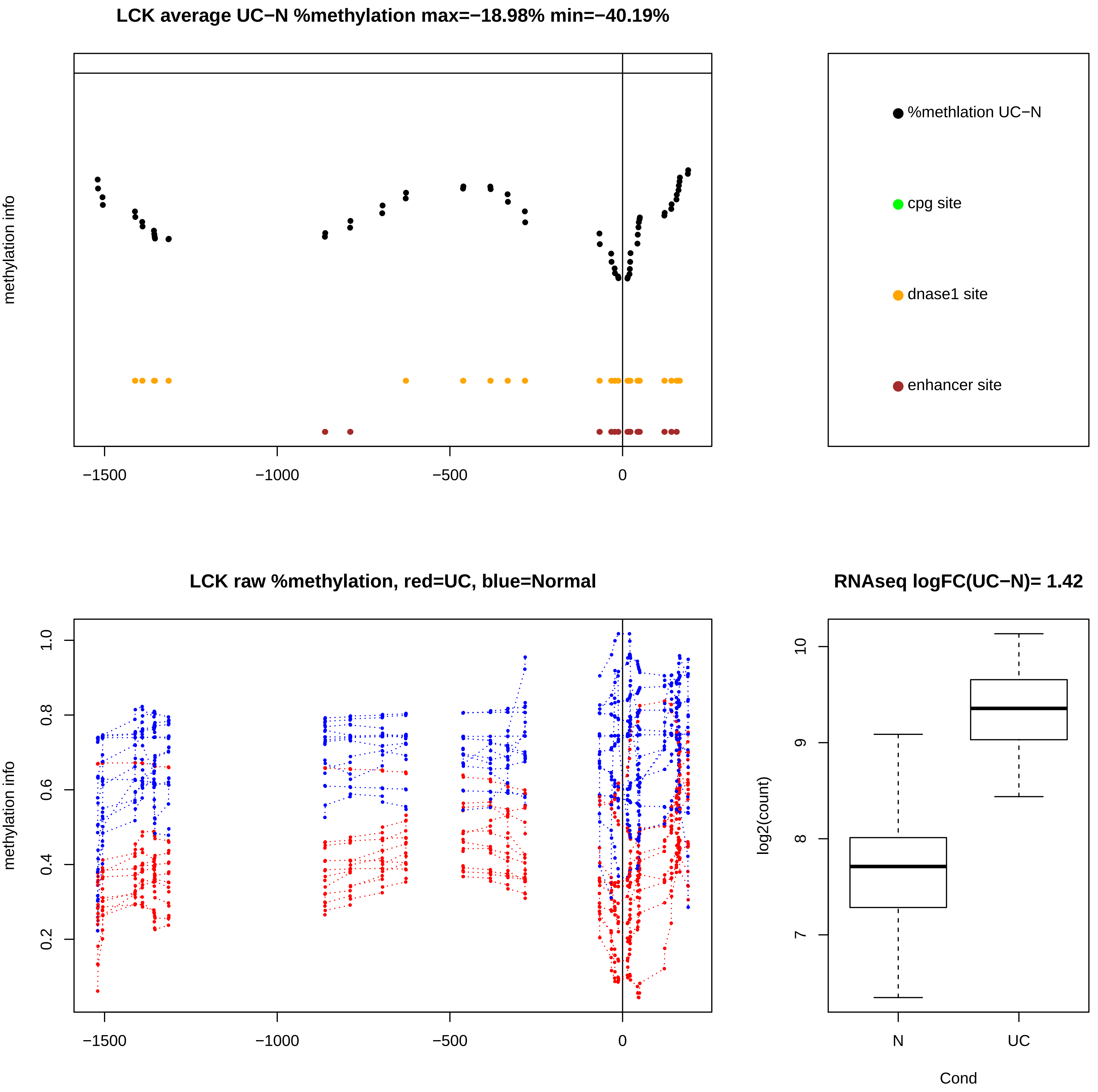
LAX1 average UC−N %methylation max=−2.97% min=−32.28%

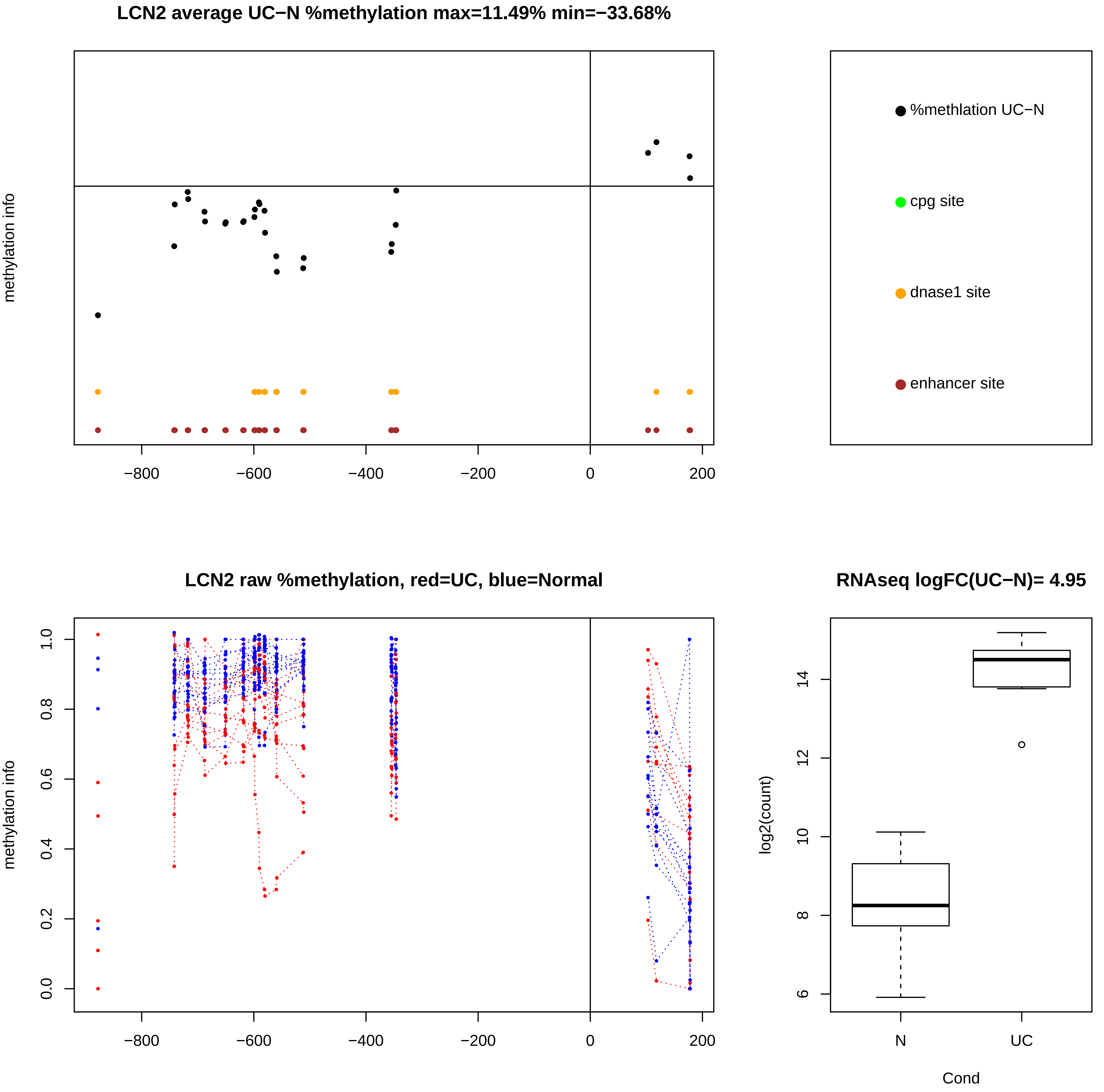


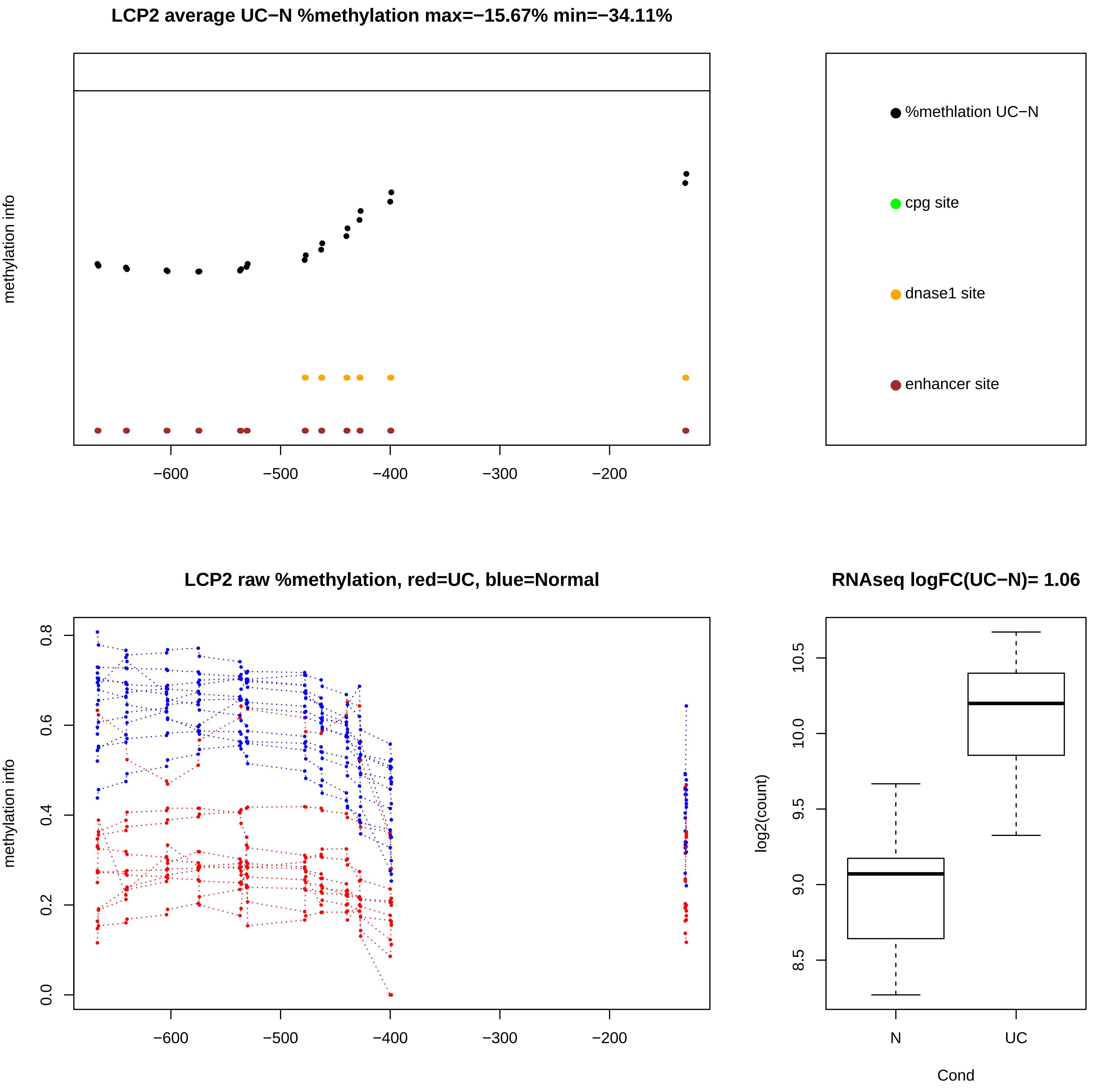
LAX1 raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 1.88


LCK average UC−N %methylation max=−18.98% min=−40.19%
methylation info
−1500
−1000
−500
0
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
LCK raw %methylation, red=UC, blue=Normal
methylation info
0.2
0.4
0.6
0.8
1.0
−1500
−1000
−500
0
RNAseq logFC(UC−N)= 1.42
log2(count)
7
8
9
10
N
UC
Cond

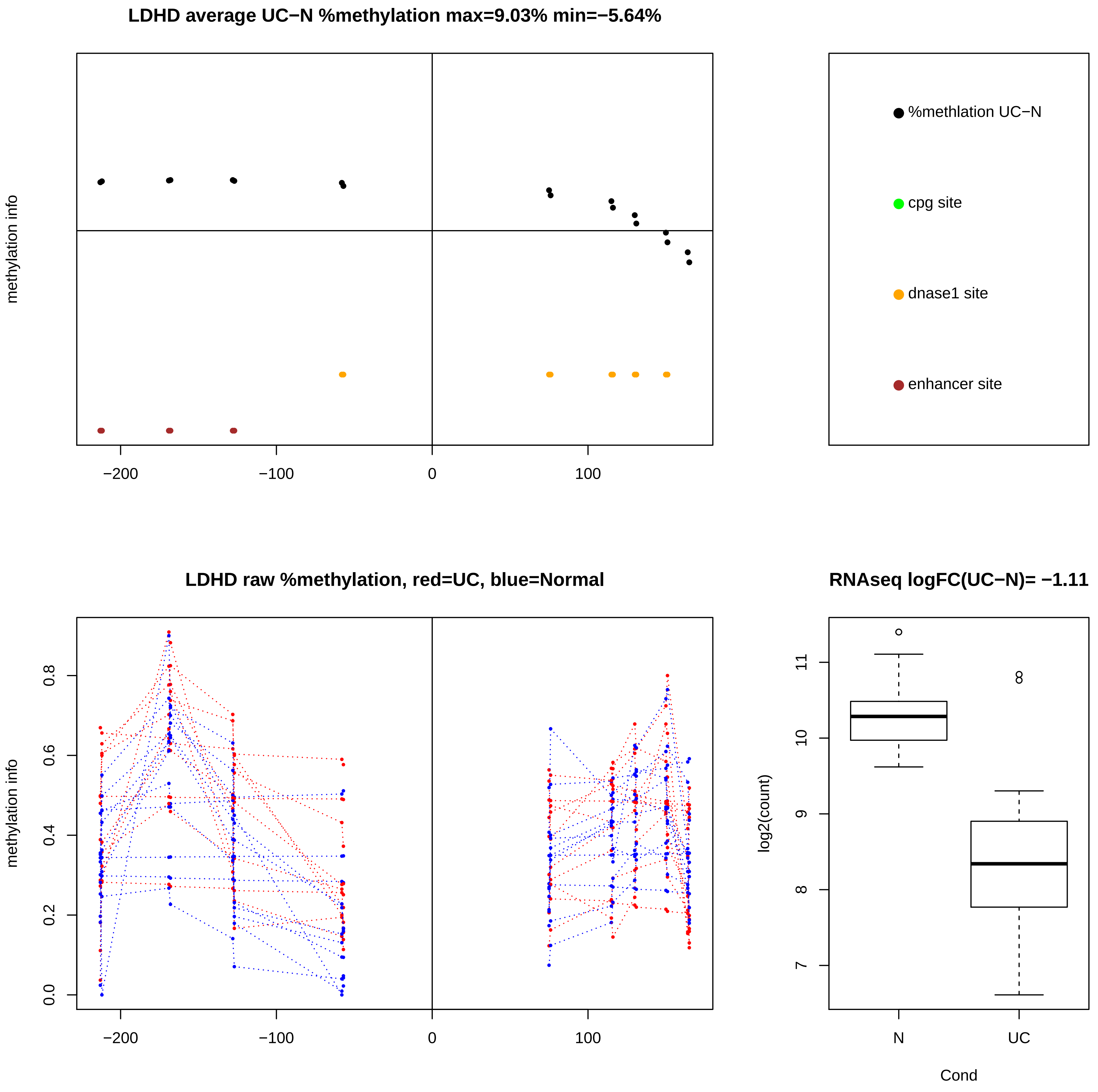

LCN2 average UC−N %methylation max=11.49% min=−33.68%
methylation info
−800
−600
−400
−200
0
200
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
LCN2 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−800
−600
−400
−200
0
200
RNAseq logFC(UC−N)= 4.95
log2(count)
6
8
10
12
14
N
UC
Cond



LCP2 average UC−N %methylation max=−15.67% min=−34.11%

LCP2 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.06

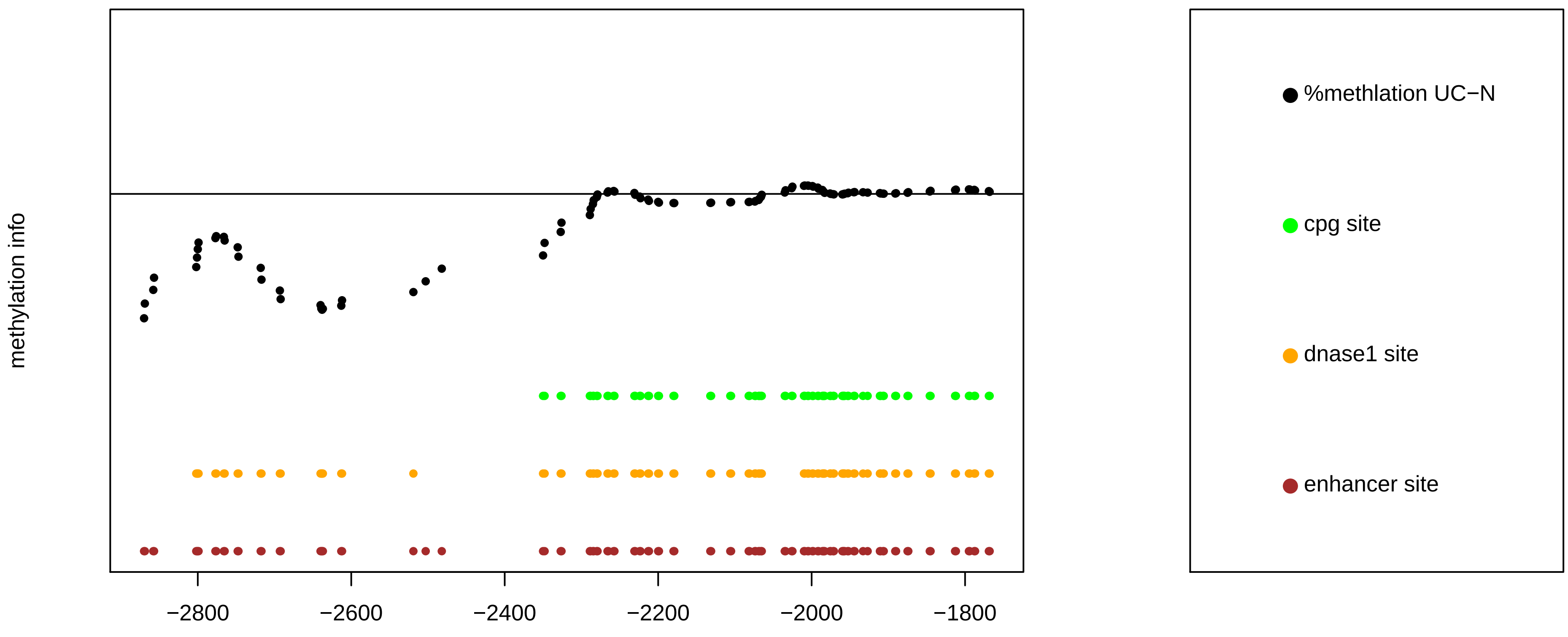


LDHD average UC−N %methylation max=9.03% min=−5.64%

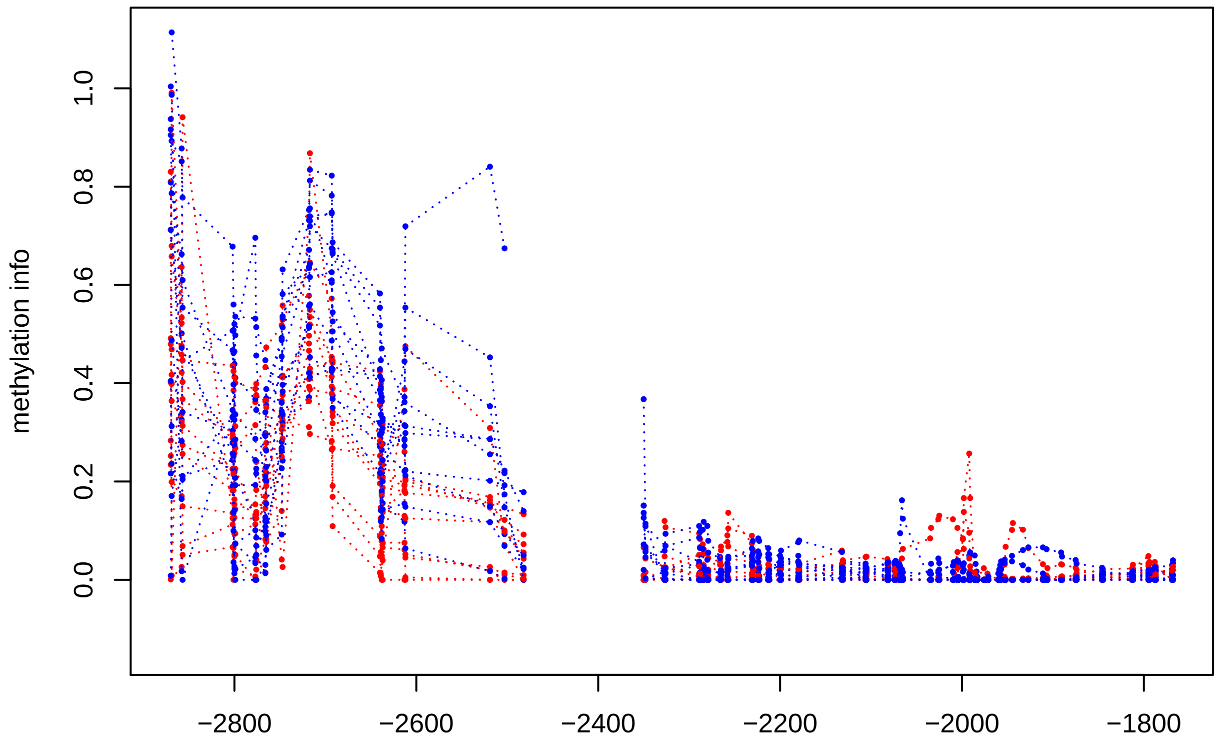
LDHD raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= −1.11

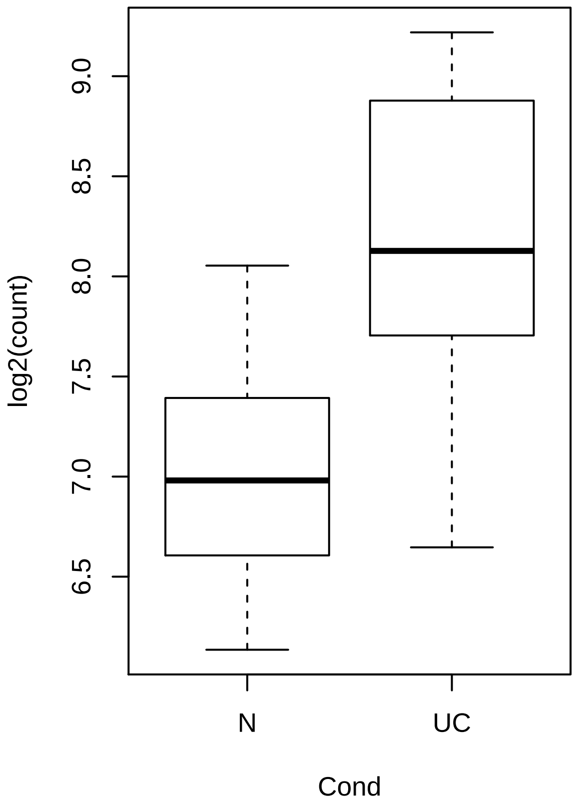
LEF1 average UC−N %methylation max=1.08% min=−16.02%

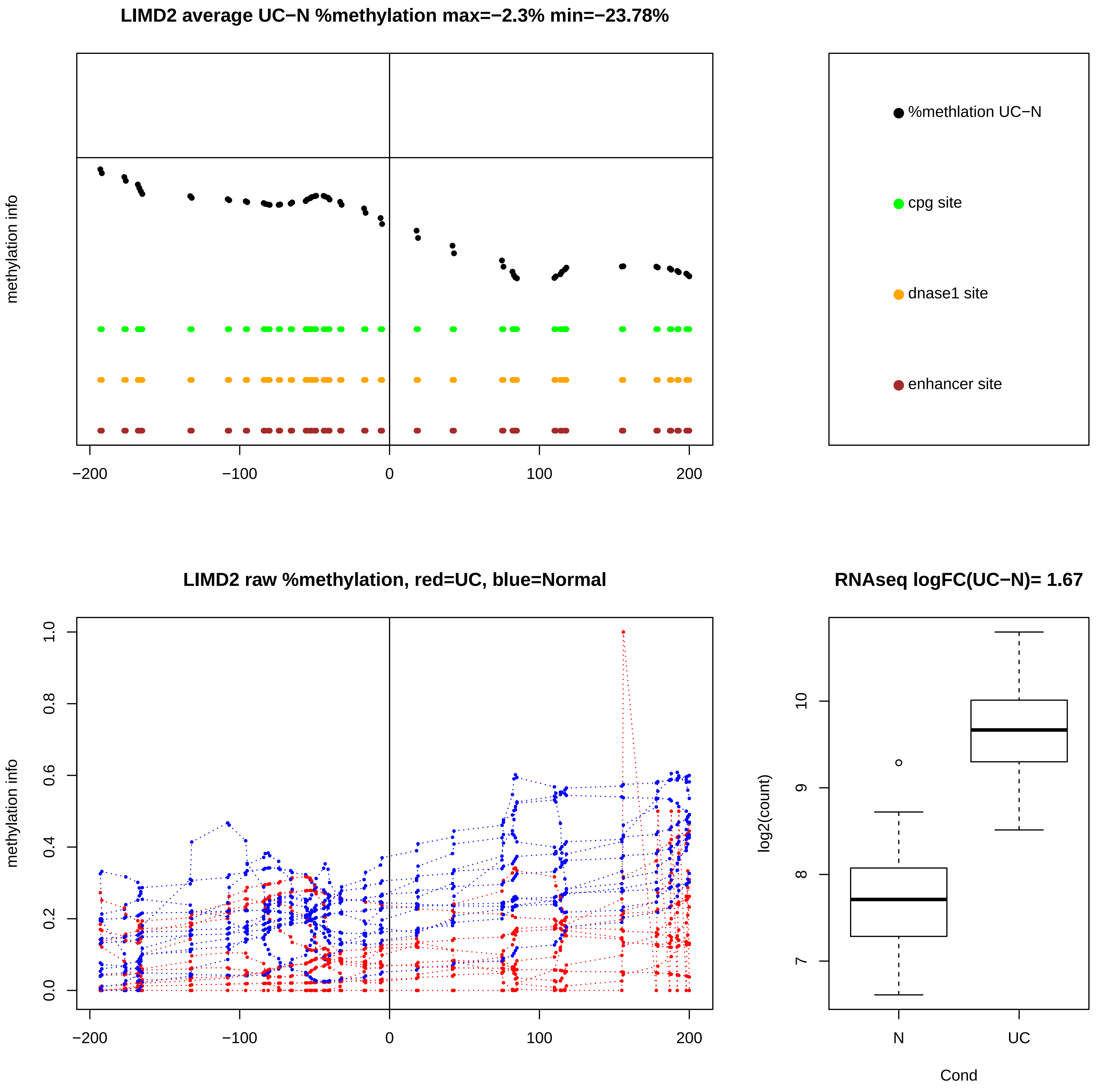


LEF1 raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 1.16



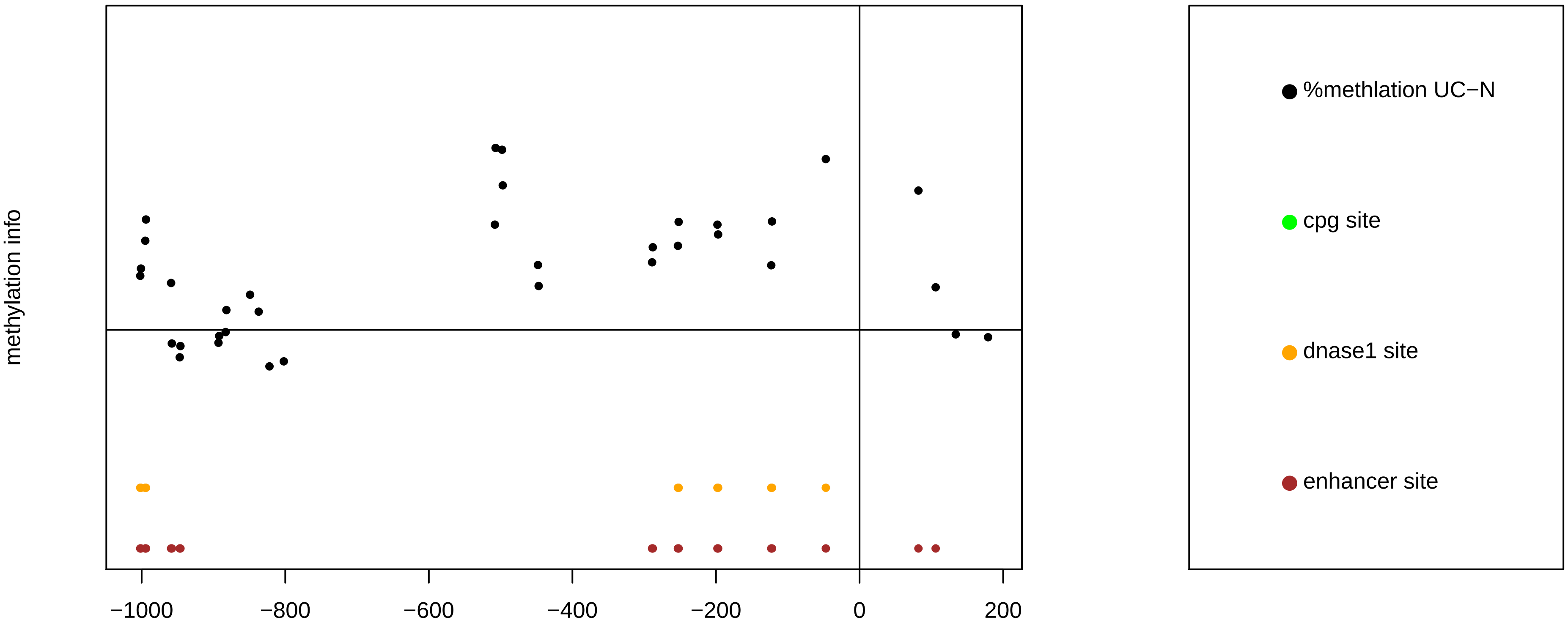


LIMD2 average UC−N %methylation max=−2.3% min=−23.78%

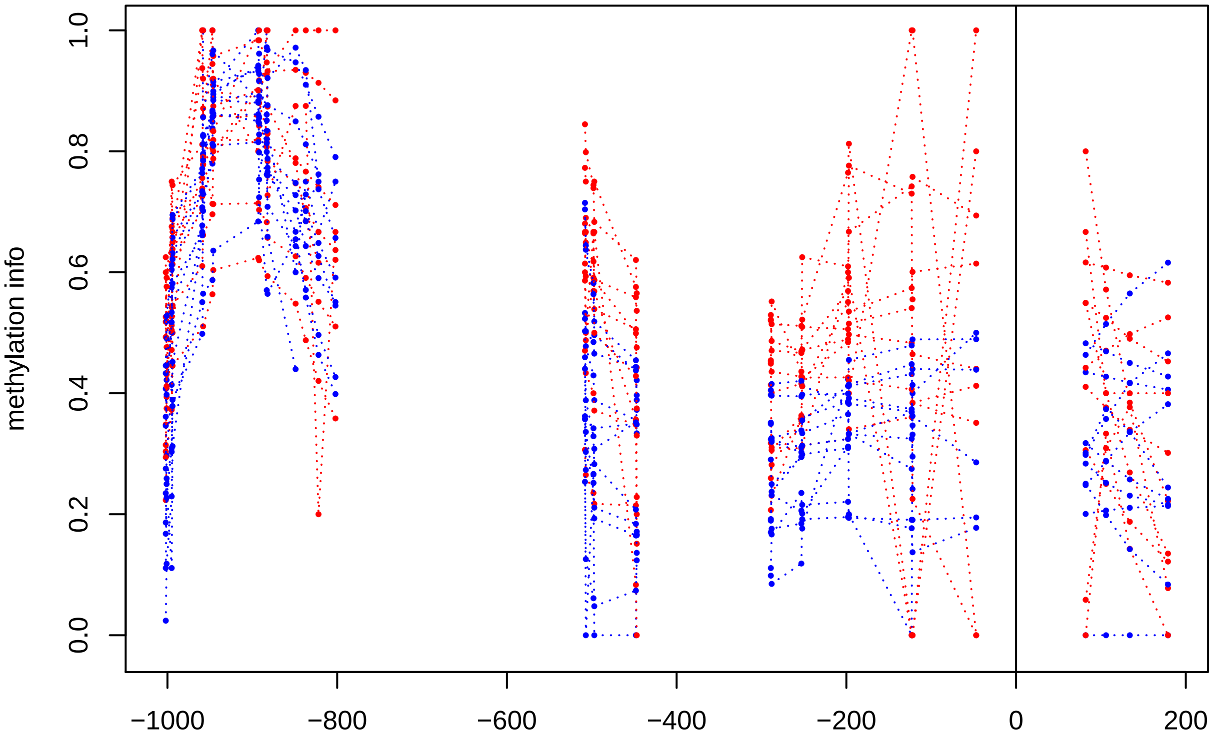
LIMD2 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.67

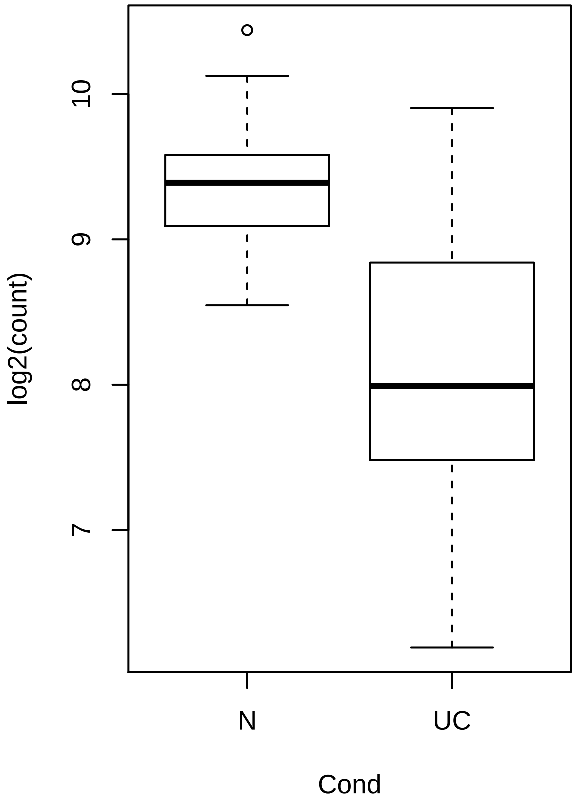
LINC00483 average UC−N %methylation max=29.98% min=−6.01%

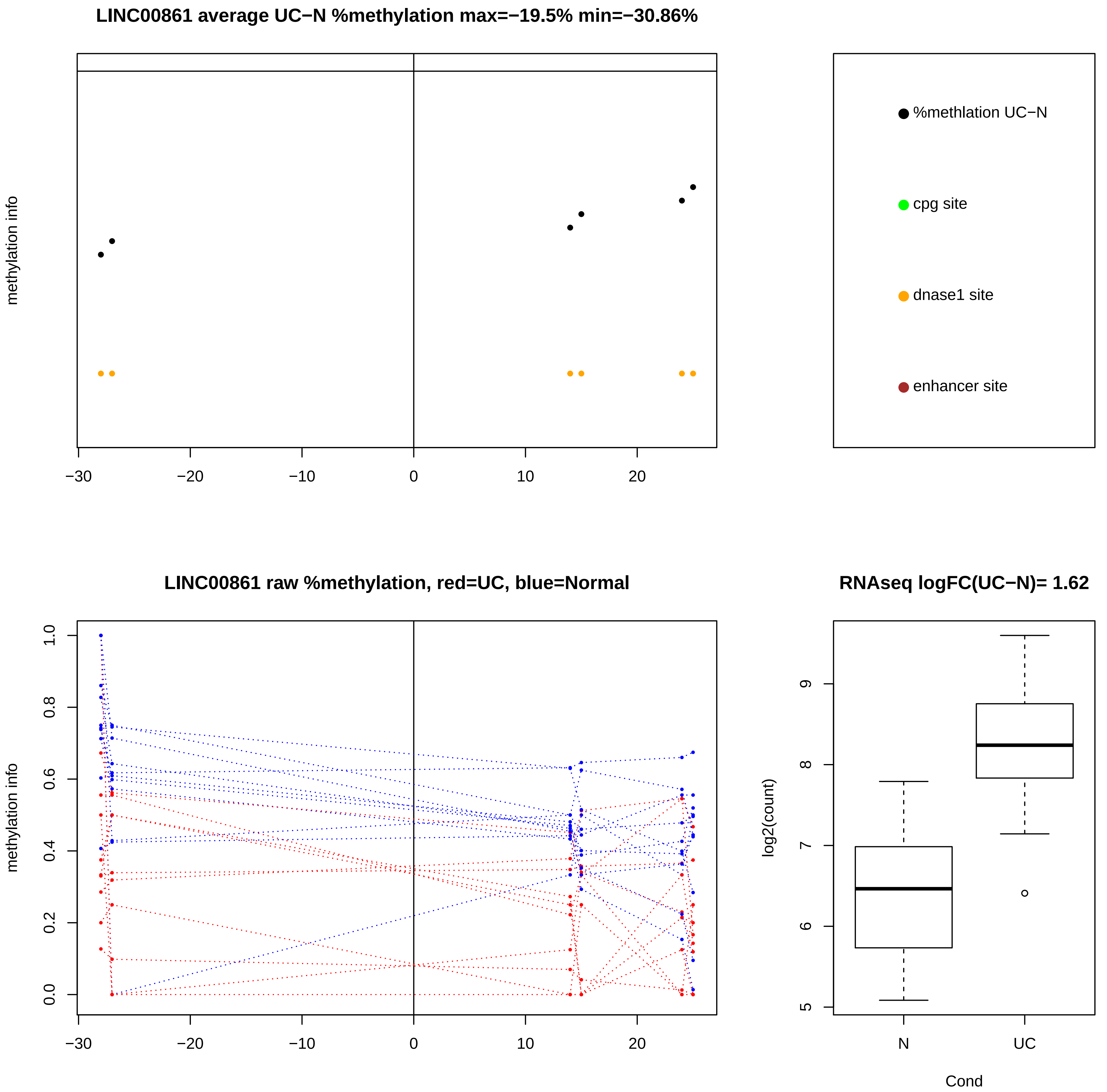


LINC00483 raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= −1.07



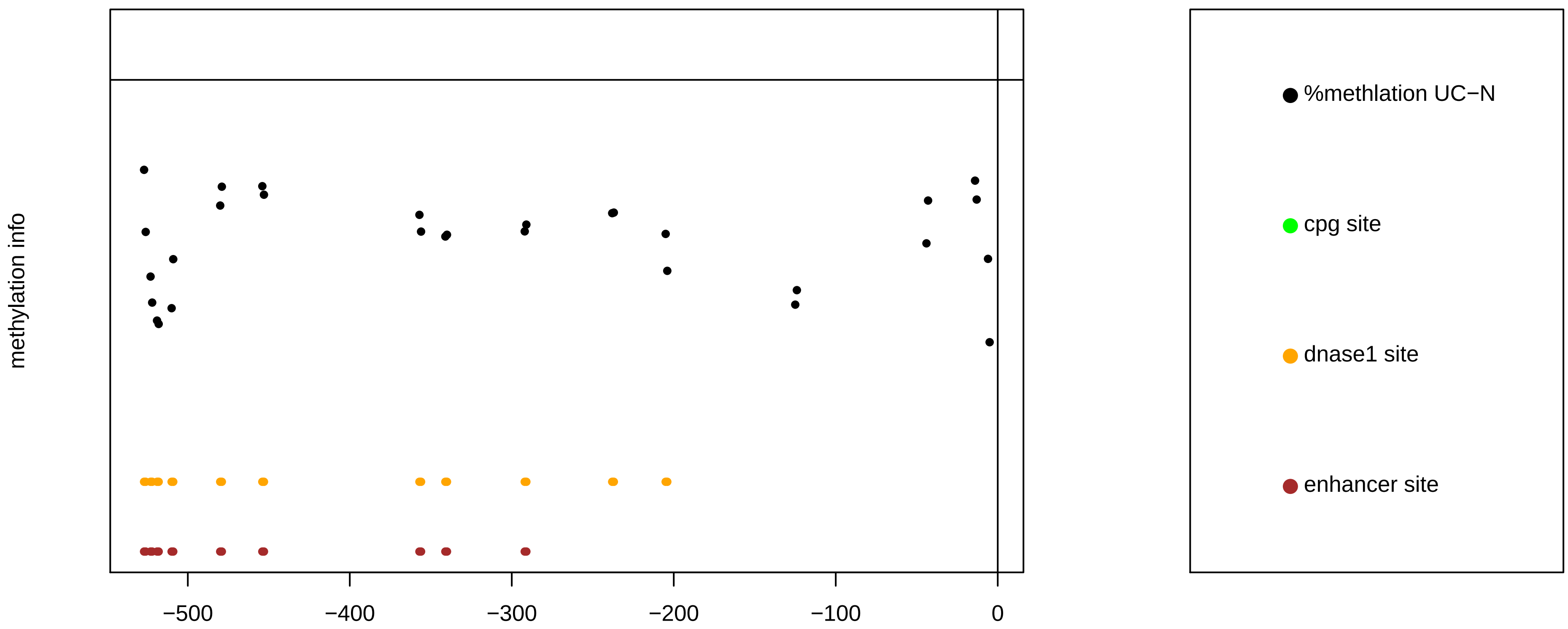


LINC00861 average UC−N %methylation max=−19.5% min=−30.86%

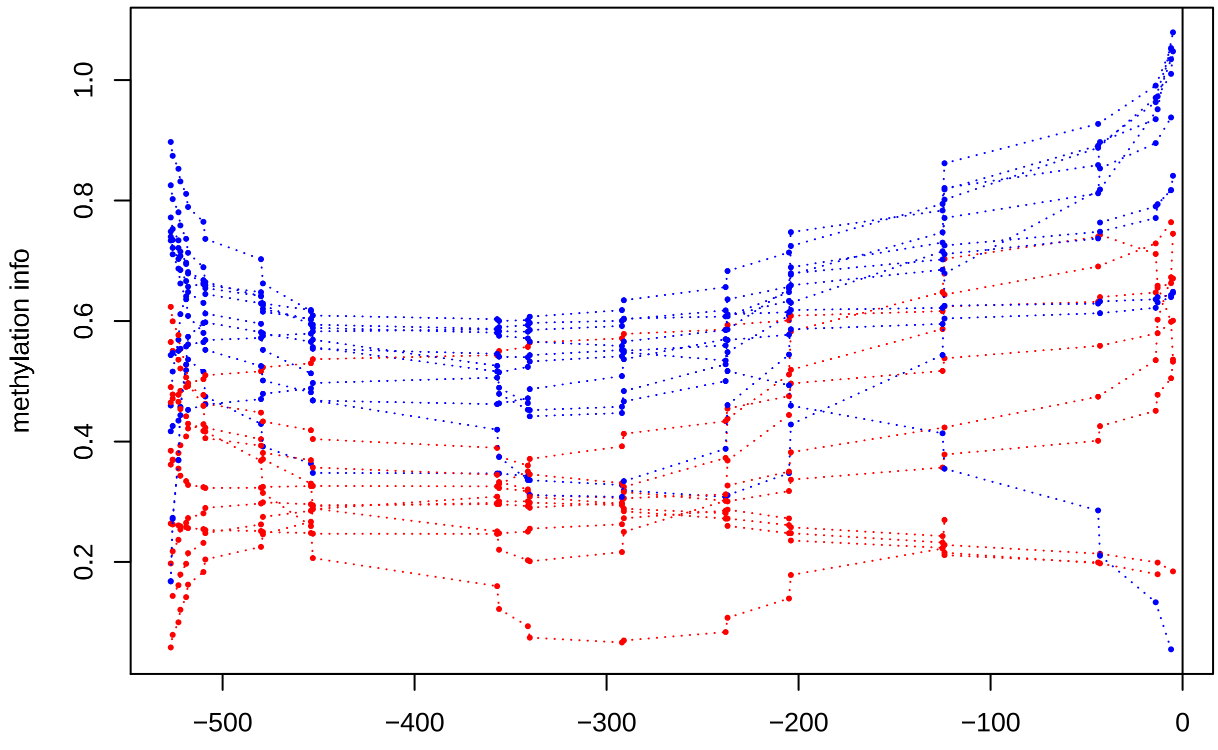
LINC00861 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.62

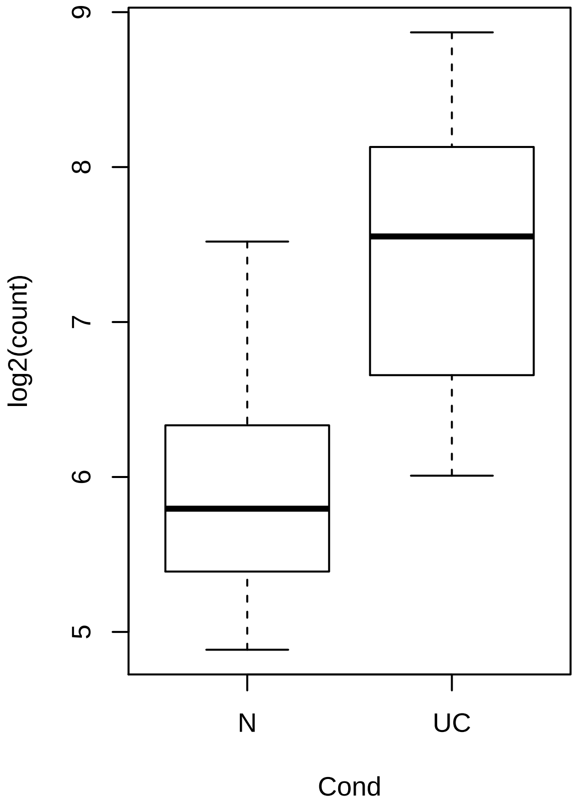
LINC00926 average UC−N %methylation max=−12.89% min=−37.59%

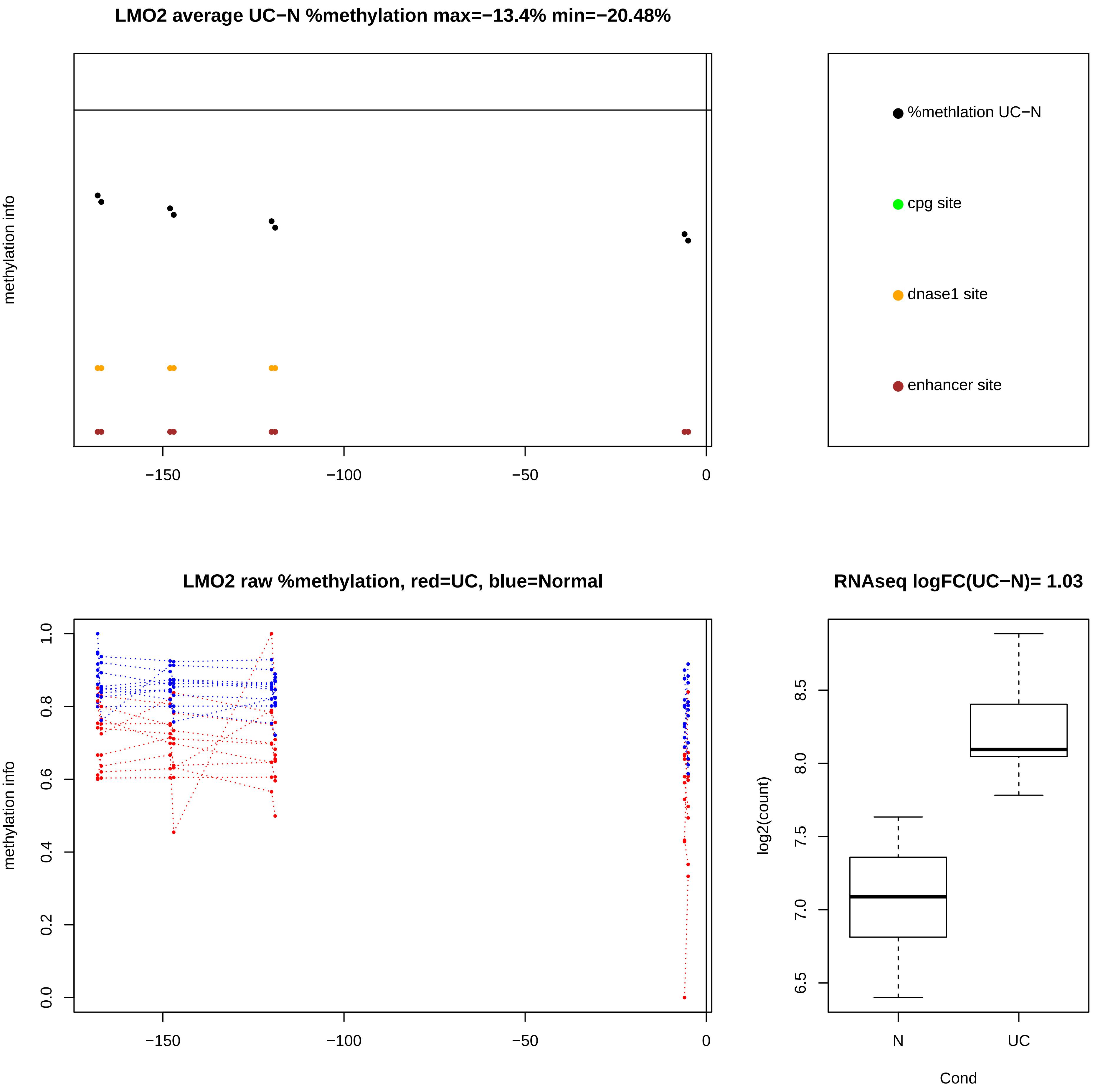


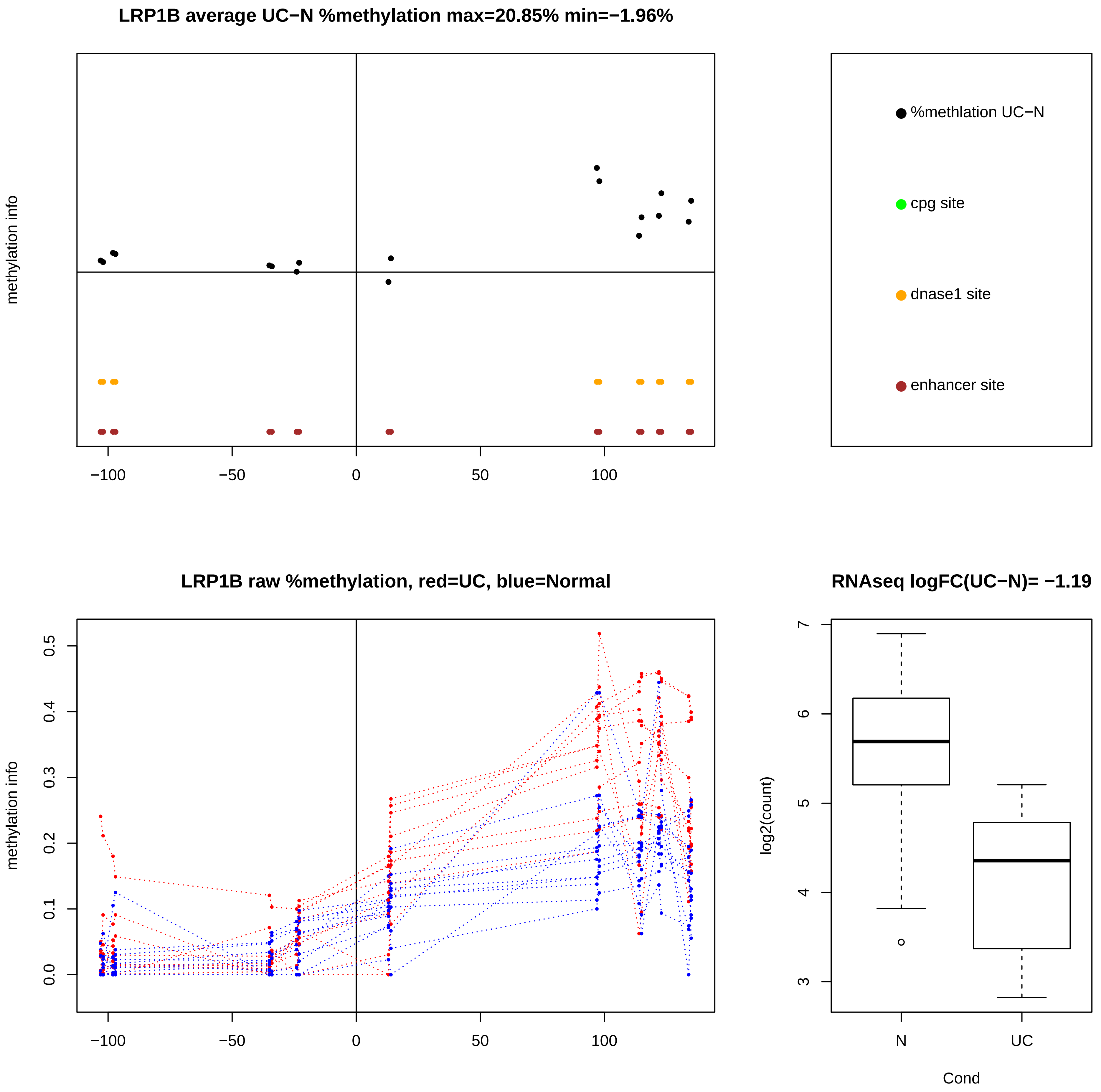
LINC00926 raw %methylation, red=UC, blue=Normal

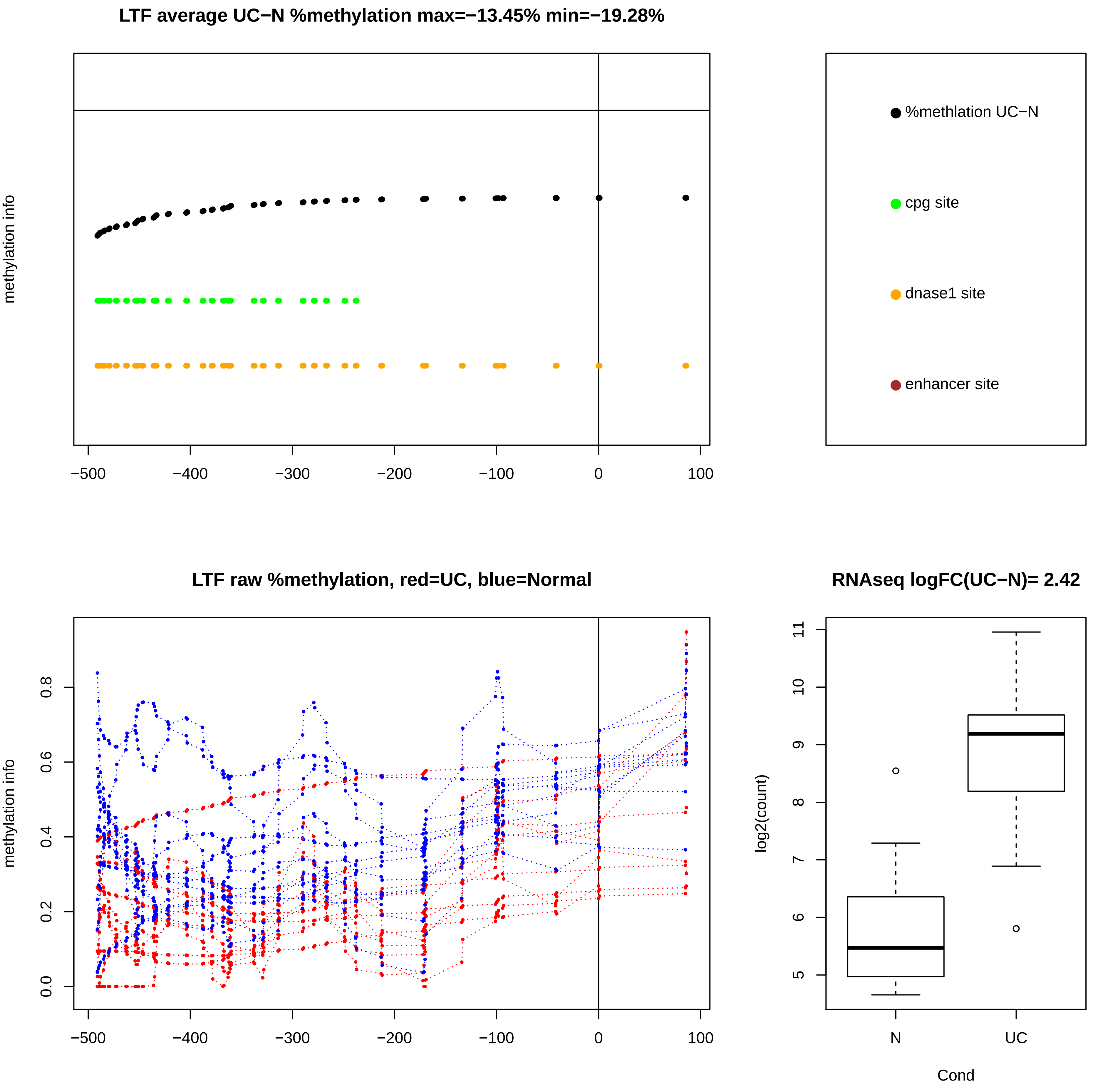


RNAseq logFC(UC−N)= 1.36




LMO2 average UC−N %methylation max=−13.4% min=−20.48%
methylation info
−150
−100
−50
0
%methlation UC−N
cpg site
dnase1 site
enhancer site
LMO2 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−150
−100
−50
0
RNAseq logFC(UC−N)= 1.03
log2(count)
6.5
7.0
7.5
8.0
8.5
N
UC
Cond

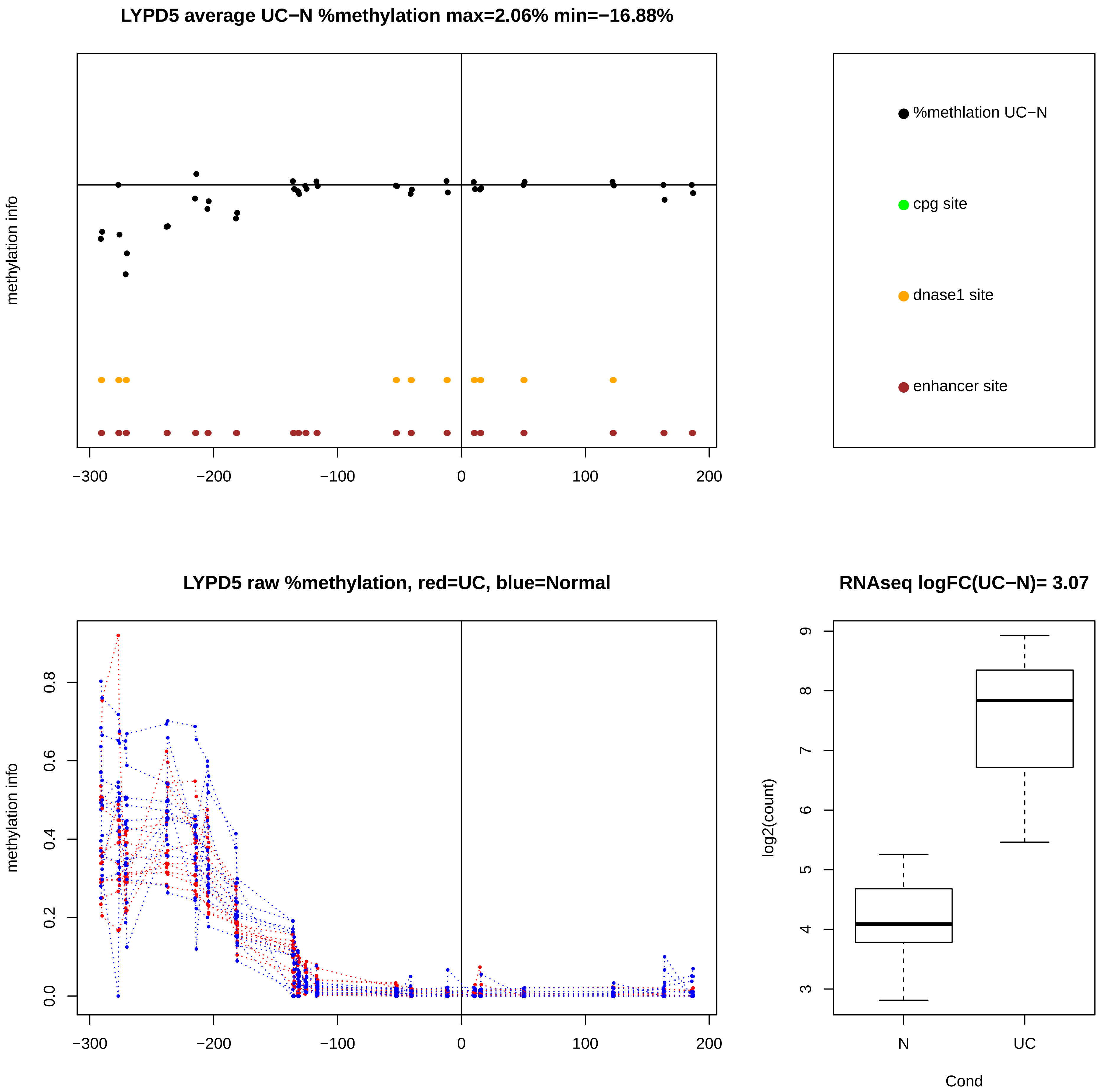

LRP1B average UC−N %methylation max=20.85% min=−1.96%
methylation info
−100
−50
0
50
100
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
LRP1B raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.1
0.2
0.3
0.4
0.5
−100
−50
0
50
100
RNAseq logFC(UC−N)= −1.19
log2(count)
3
4
5
6
7
N
UC
Cond



LTF average UC−N %methylation max=−13.45% min=−19.28%

LTF raw %methylation, red=UC, blue=Normal

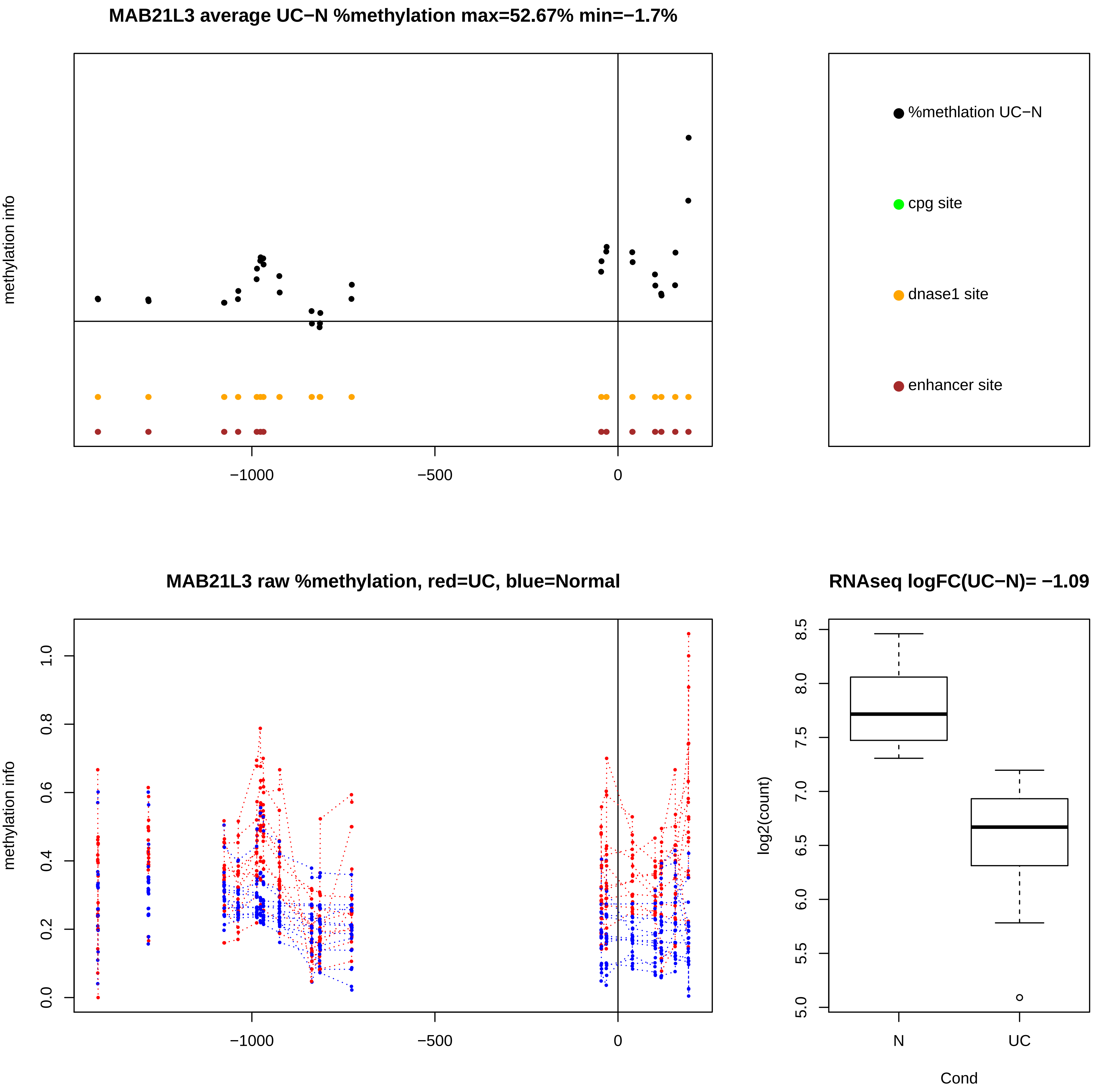
RNAseq logFC(UC−N)= 2.42



LYPD5 average UC−N %methylation max=2.06% min=−16.88%

LYPD5 raw %methylation, red=UC, blue=Normal

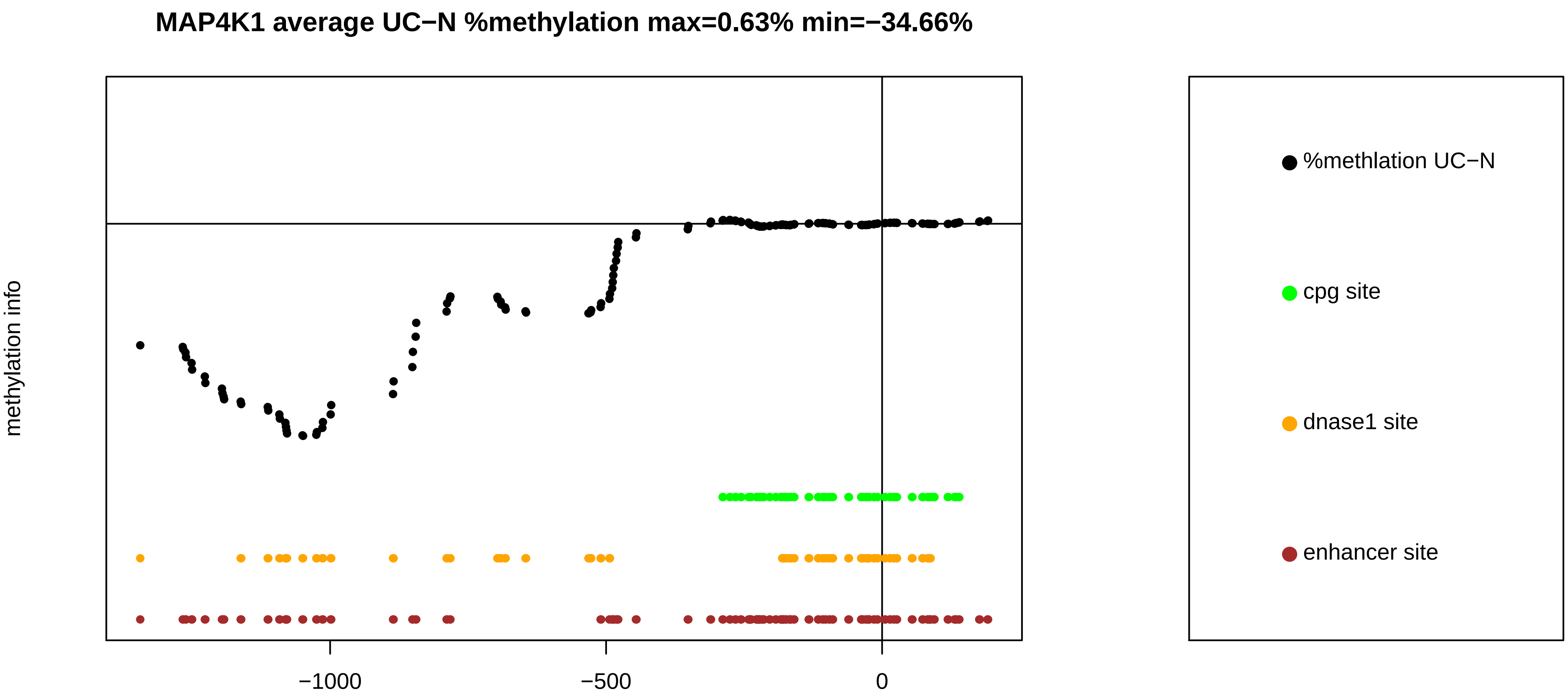
RNAseq logFC(UC−N)= 3.07

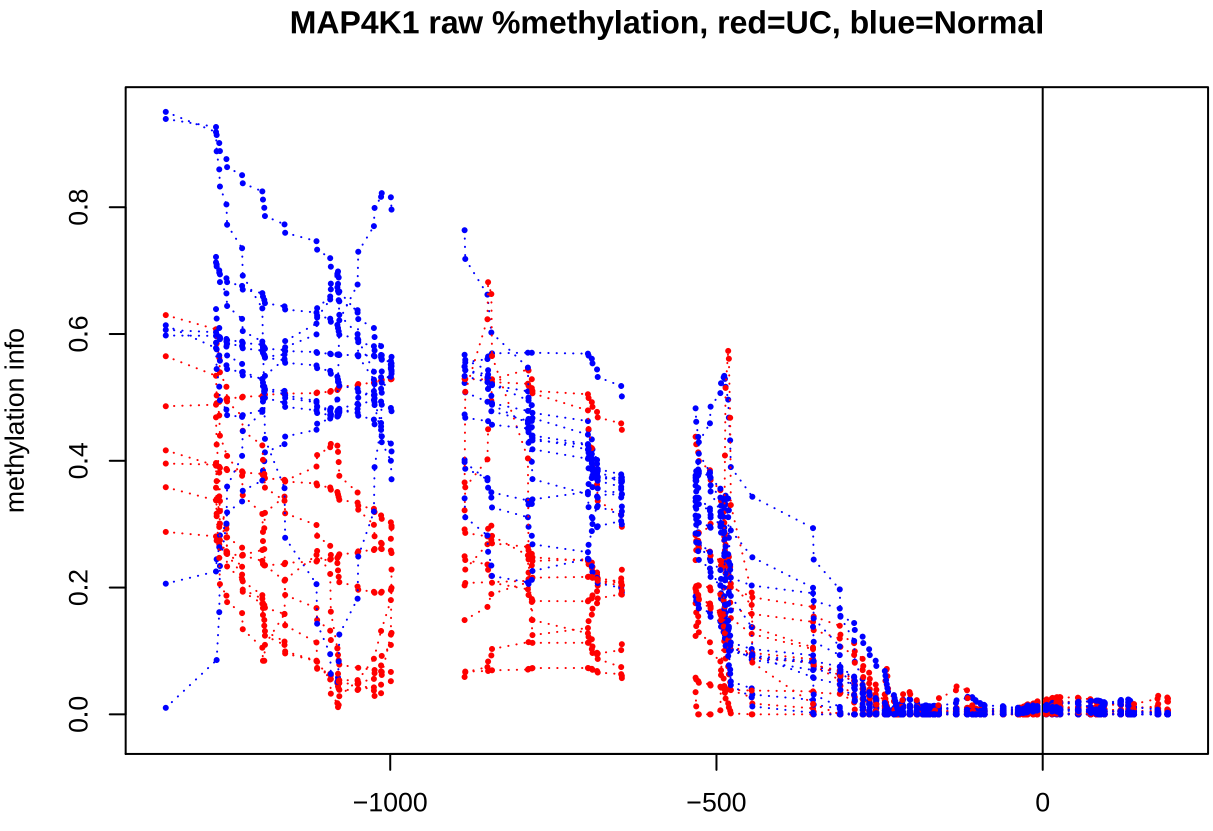


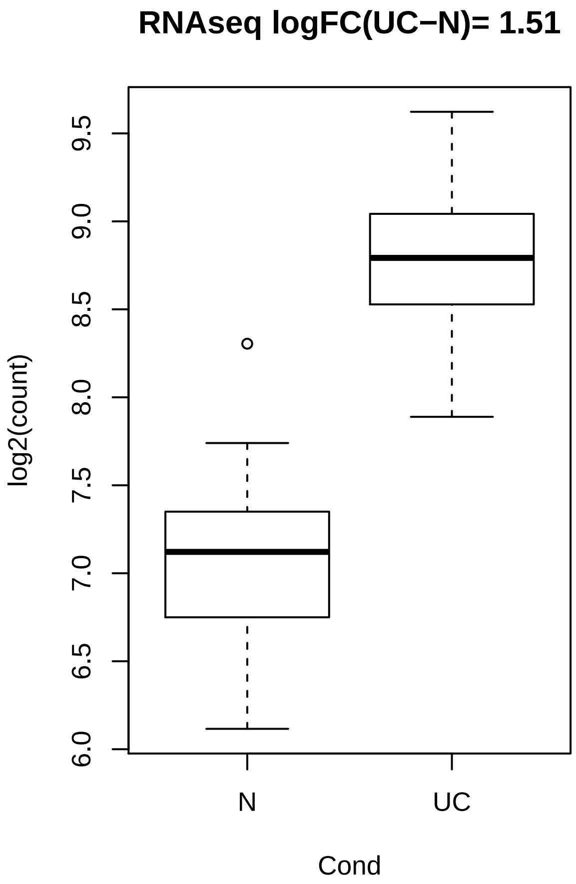
MAB21L3 average UC−N %methylation max=52.67% min=−1.7%

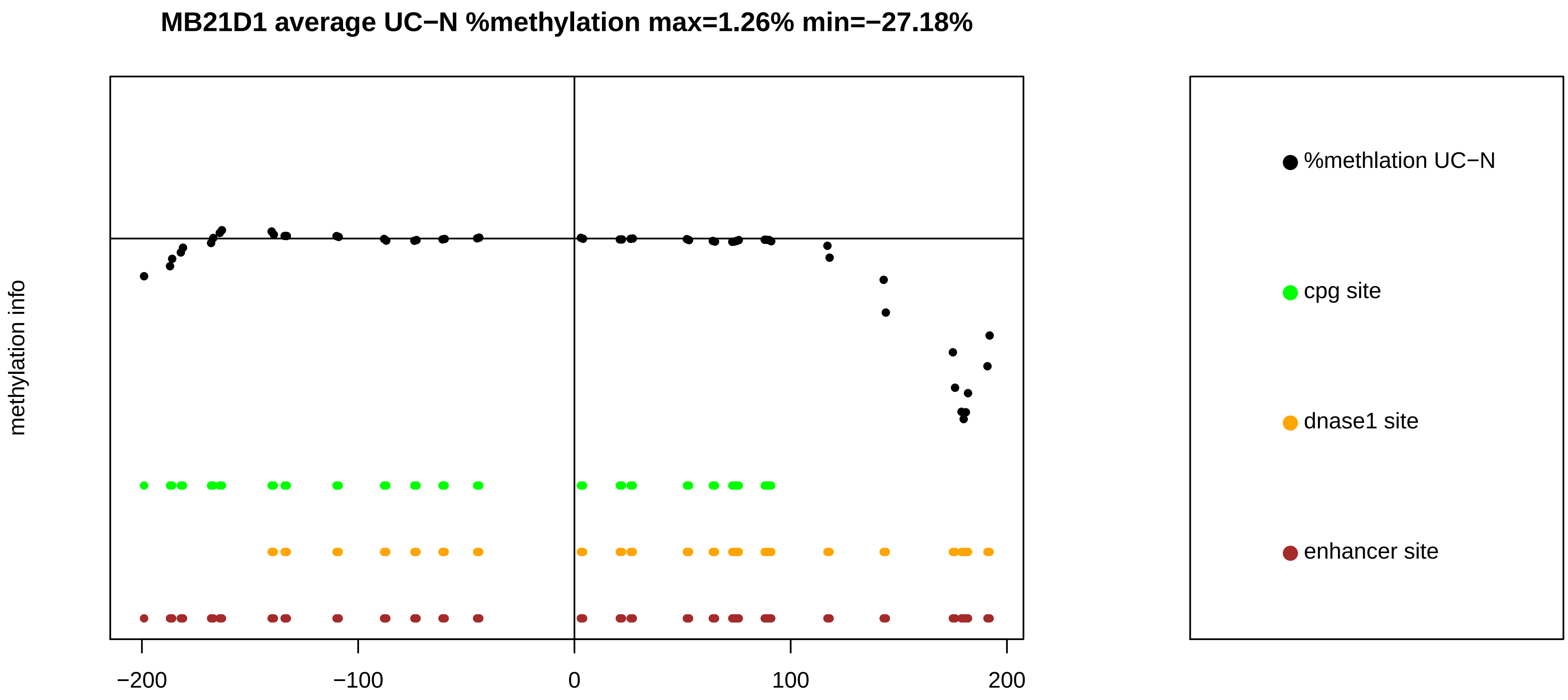
MAB21L3 raw %methylation, red=UC, blue=Normal

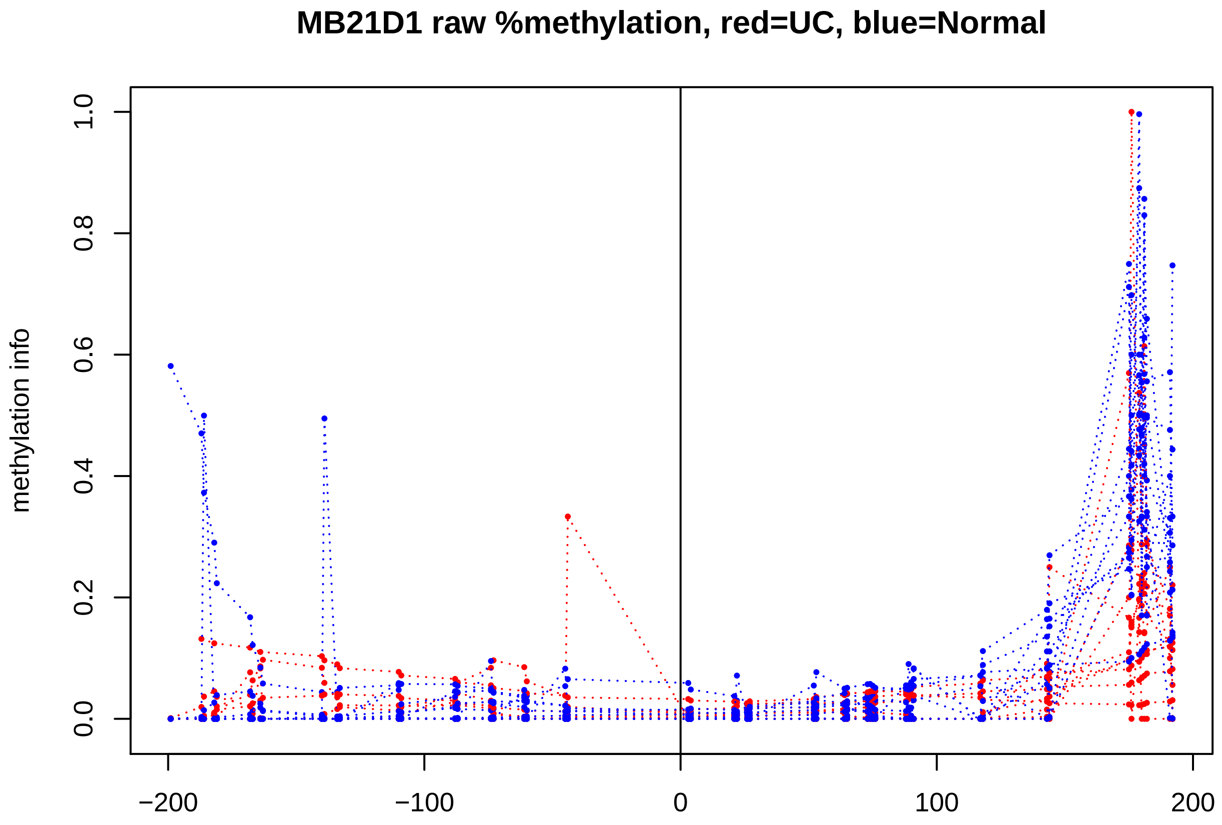
RNAseq logFC(UC−N)= −1.09

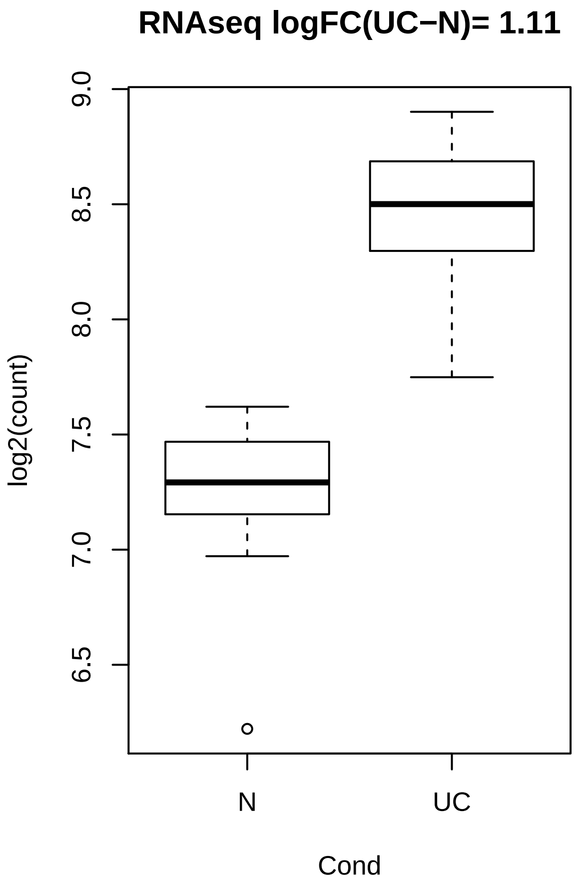

MAP4K1 average UC−N %methylation max=0.63% min=−34.66%
methylation info
−1000
−500
0
%methlation UC−N
cpg site
dnase1 site
enhancer site

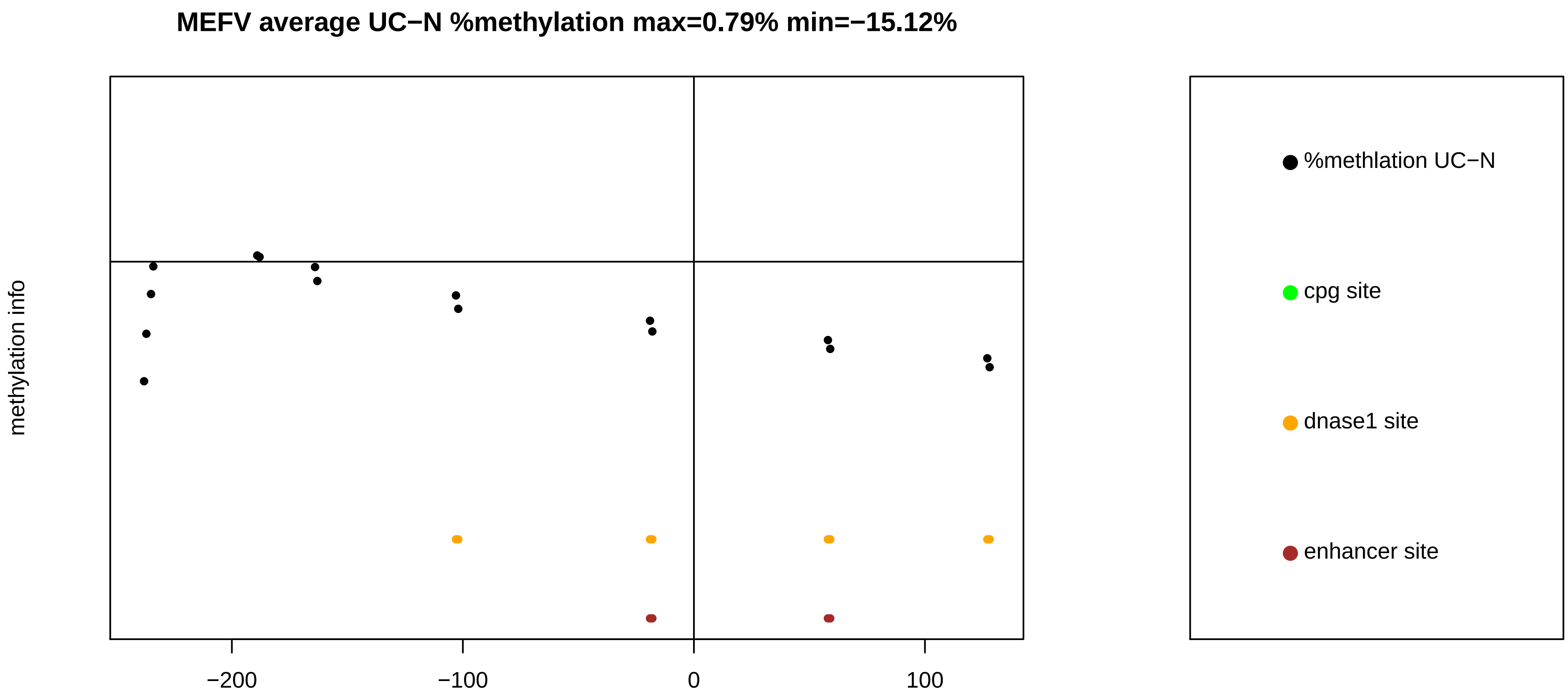

MAP4K1 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
−1000
−500
0

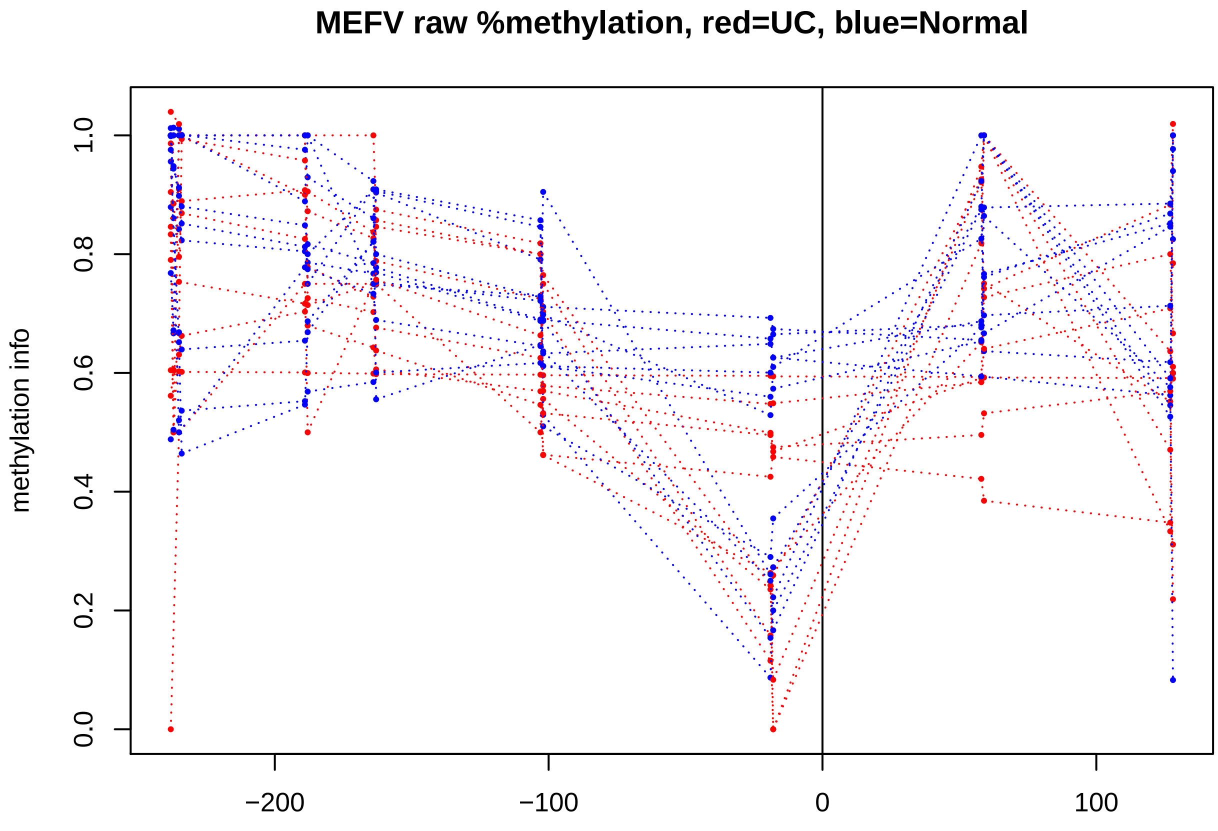

RNAseq logFC(UC−N)= 1.51
log2(count)
6.0
6.5
7.0
7.5
8.0
8.5
9.0
9.5
N
UC
Cond

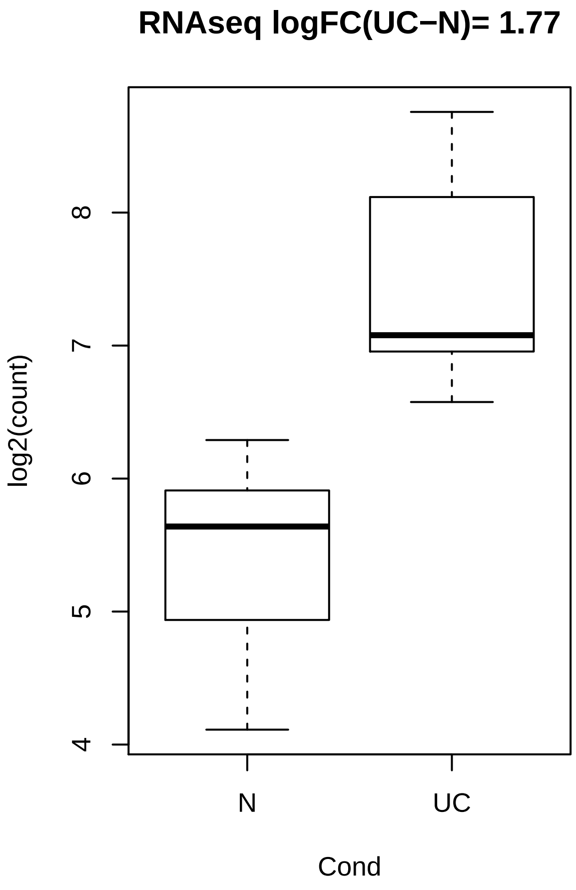

MB21D1 average UC−N %methylation max=1.26% min=−27.18%

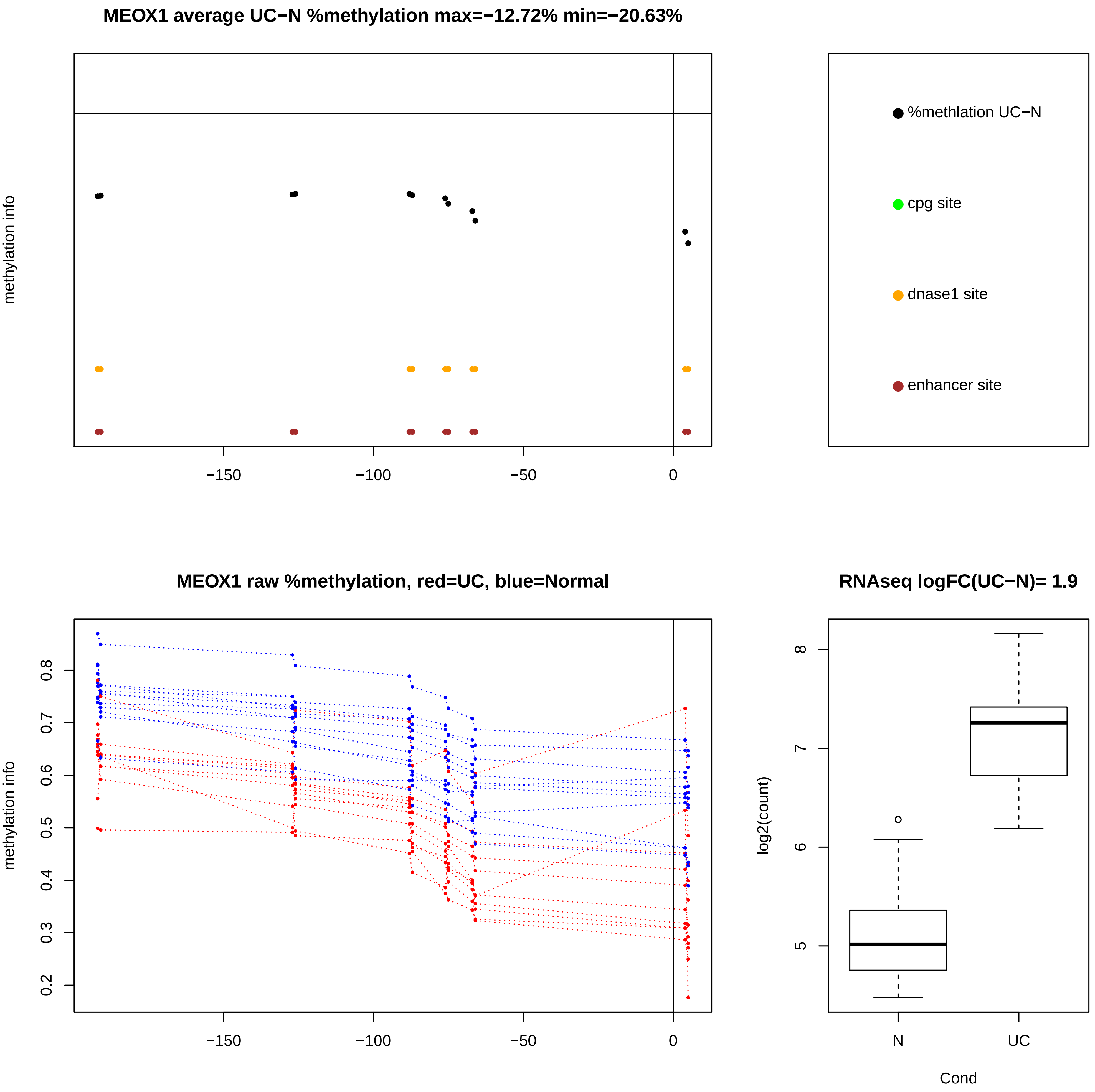

MB21D1 raw %methylation, red=UC, blue=Normal

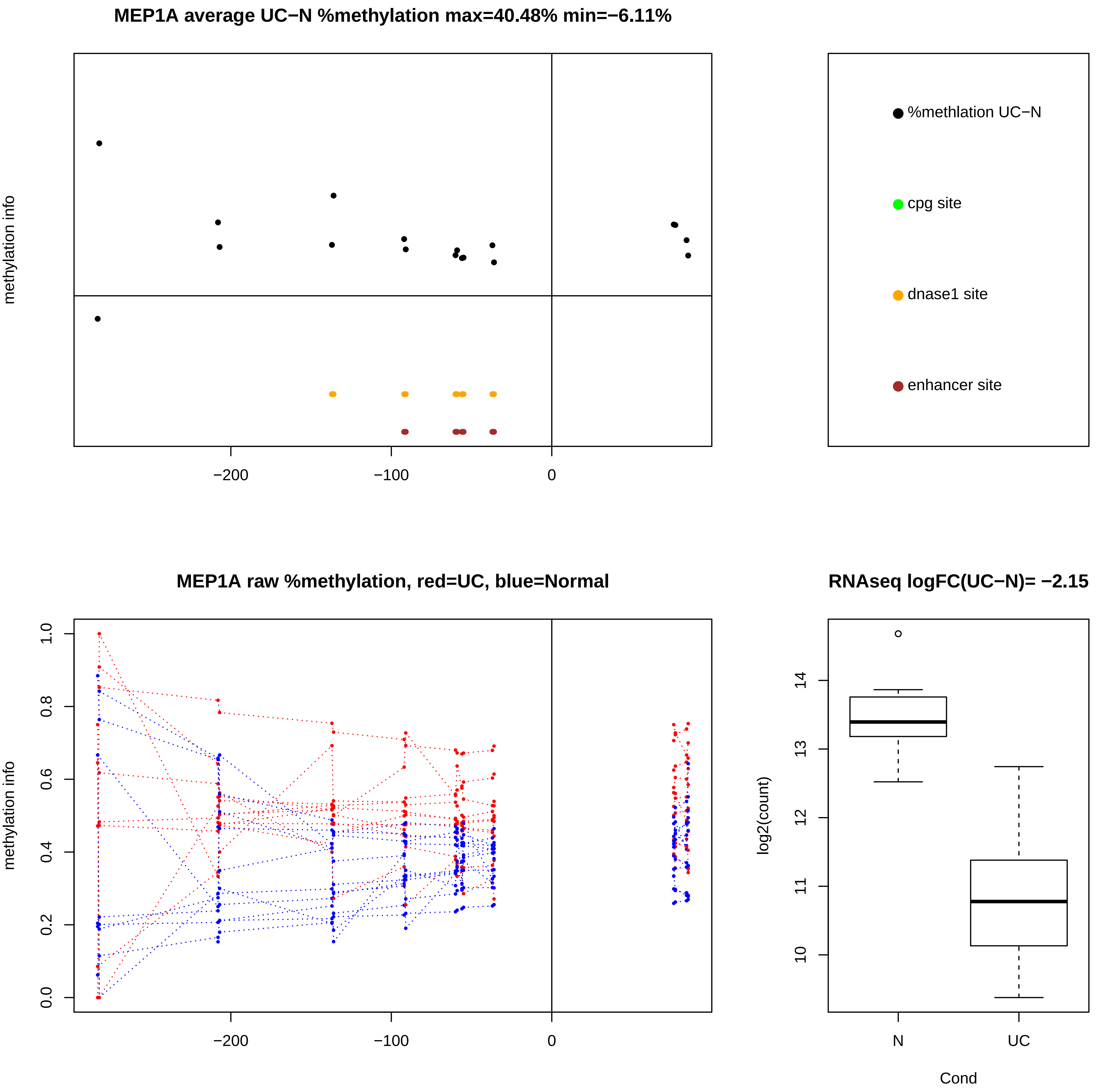

RNAseq logFC(UC−N)= 1.11


MEFV average UC−N %methylation max=0.79% min=−15.12%
methylation info
−200
−100
0
100
%methlation UC−N
cpg site
dnase1 site
enhancer site


MEFV raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−200
−100
0
100


RNAseq logFC(UC−N)= 1.77
log2(count)
4
5
6
7
8
N
UC
Cond

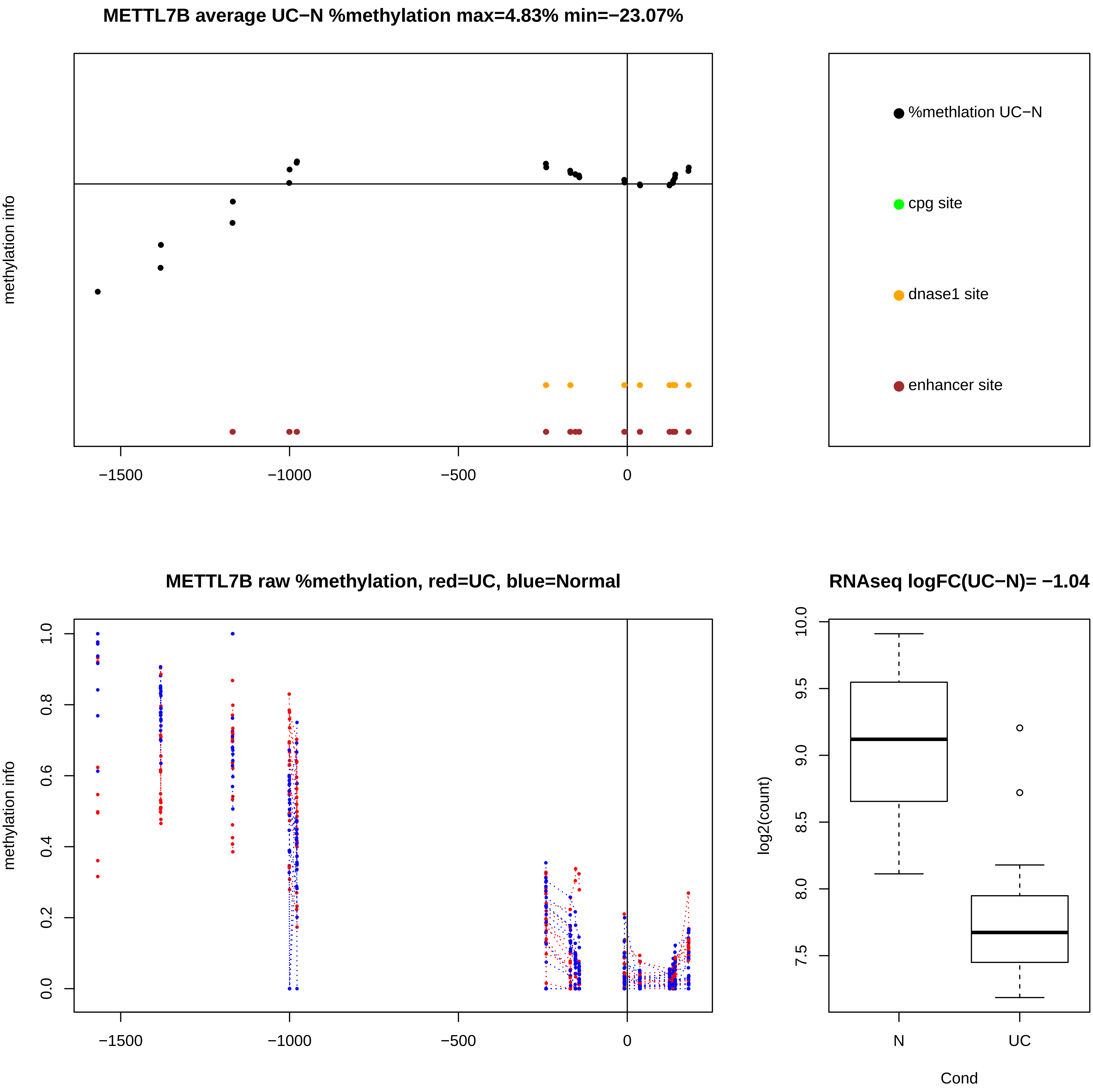

MEOX1 average UC−N %methylation max=−12.72% min=−20.63%
methylation info
−150
−100
−50
0
%methlation UC−N
cpg site
dnase1 site
enhancer site
MEOX1 raw %methylation, red=UC, blue=Normal
methylation info
0.2
0.3
0.4
0.5
0.6
0.7
0.8
−150
−100
−50
0
RNAseq logFC(UC−N)= 1.9
log2(count)
5
6
7
8
N
UC
Cond



MEP1A average UC−N %methylation max=40.48% min=−6.11%

MEP1A raw %methylation, red=UC, blue=Normal

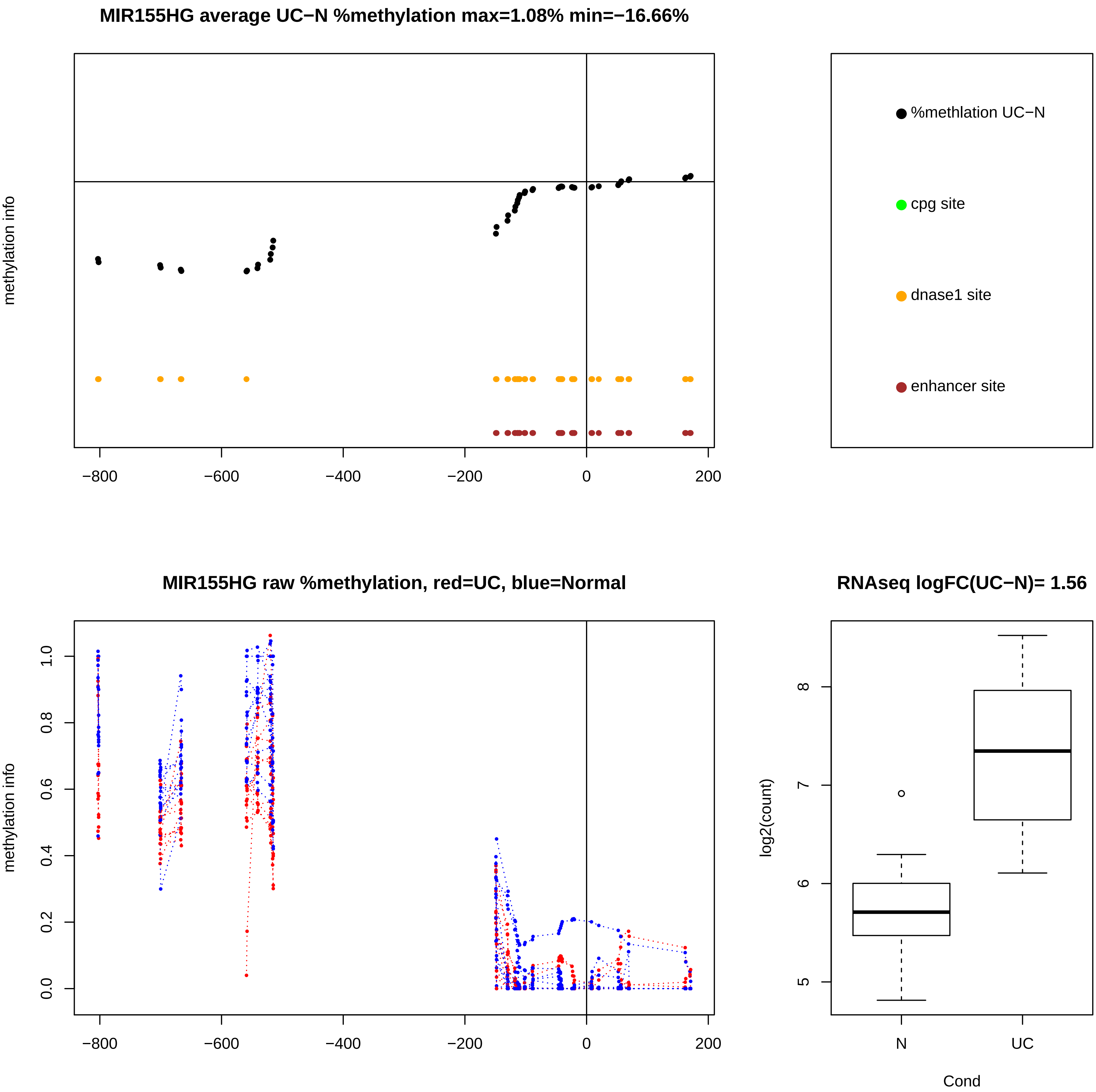
RNAseq logFC(UC−N)= −2.15



METTL7B average UC−N %methylation max=4.83% min=−23.07%

METTL7B raw %methylation, red=UC, blue=Normal

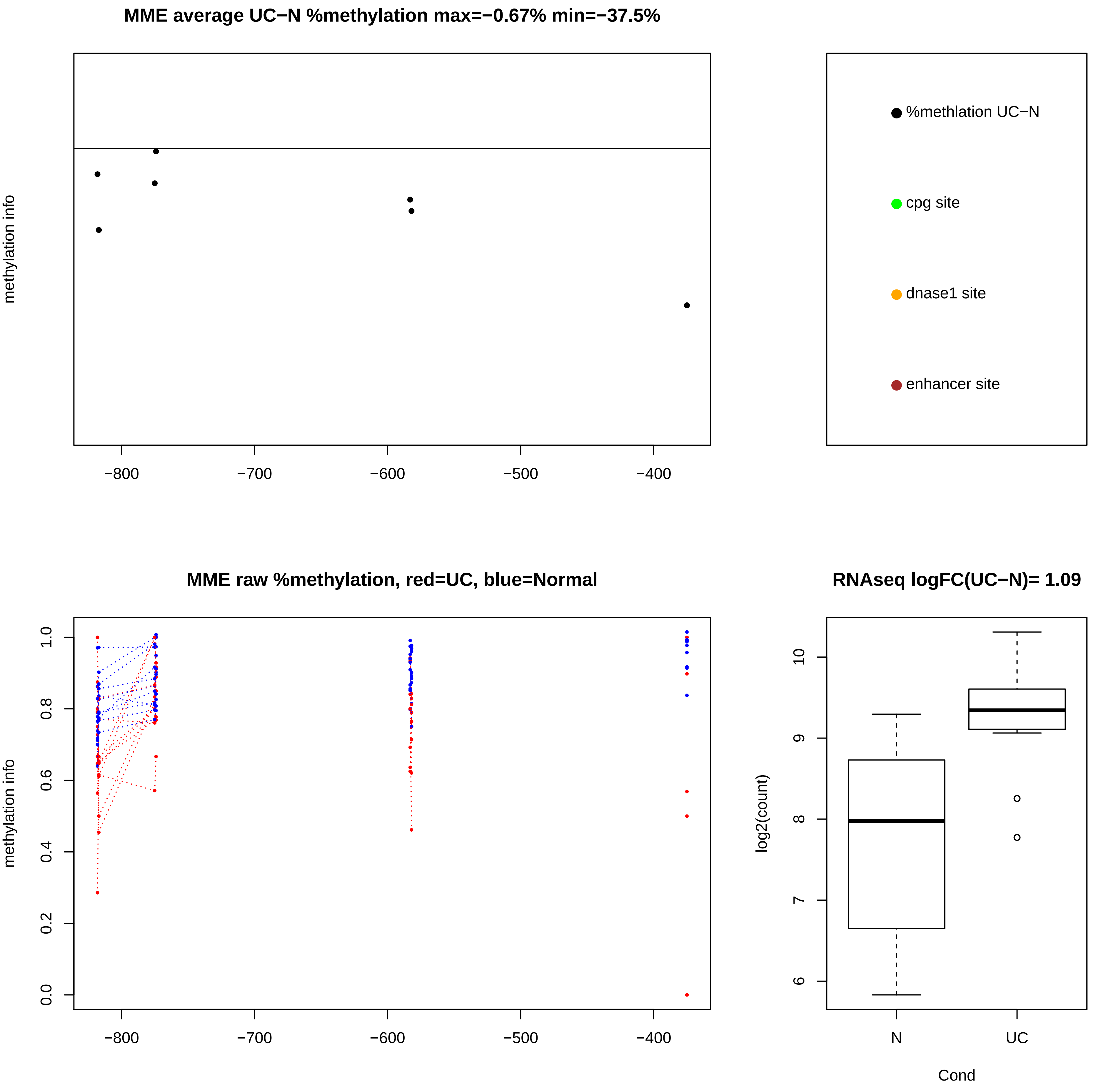
RNAseq logFC(UC−N)= −1.04



MIR155HG average UC−N %methylation max=1.08% min=−16.66%

MIR155HG raw %methylation, red=UC, blue=Normal

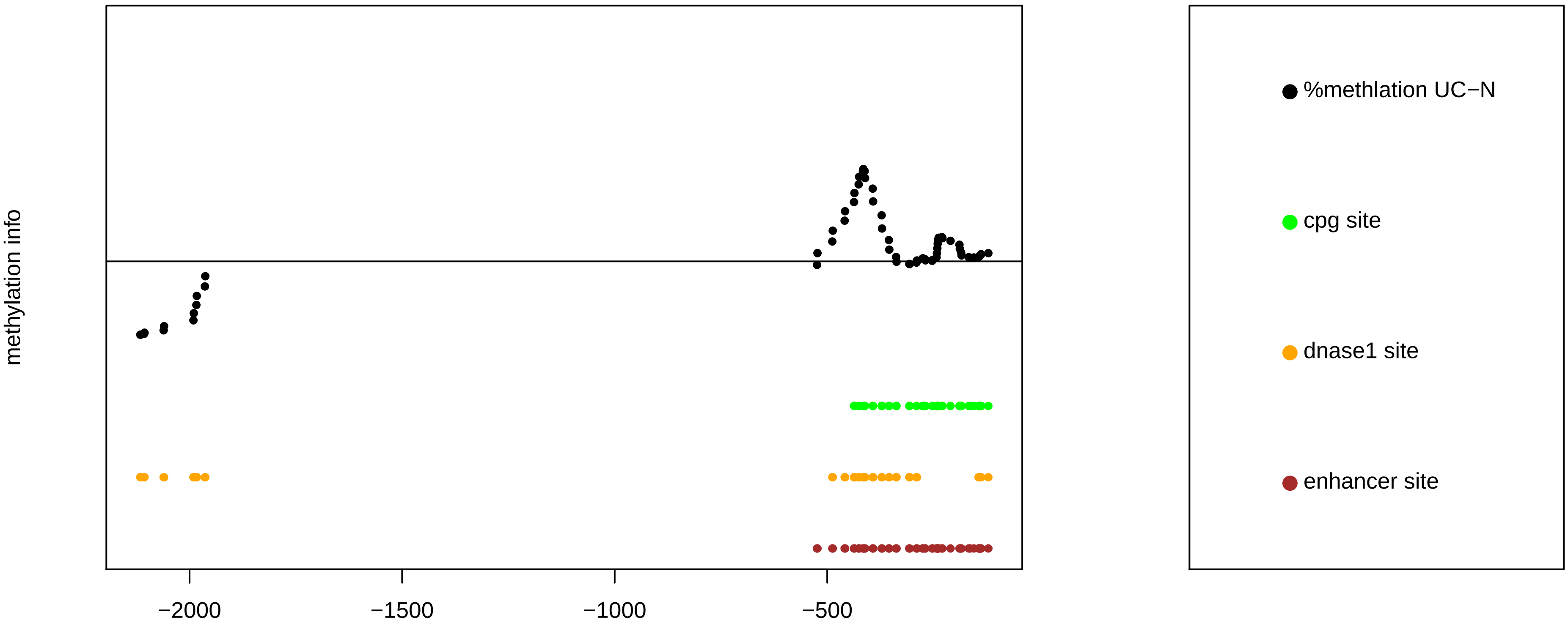
RNAseq logFC(UC−N)= 1.56



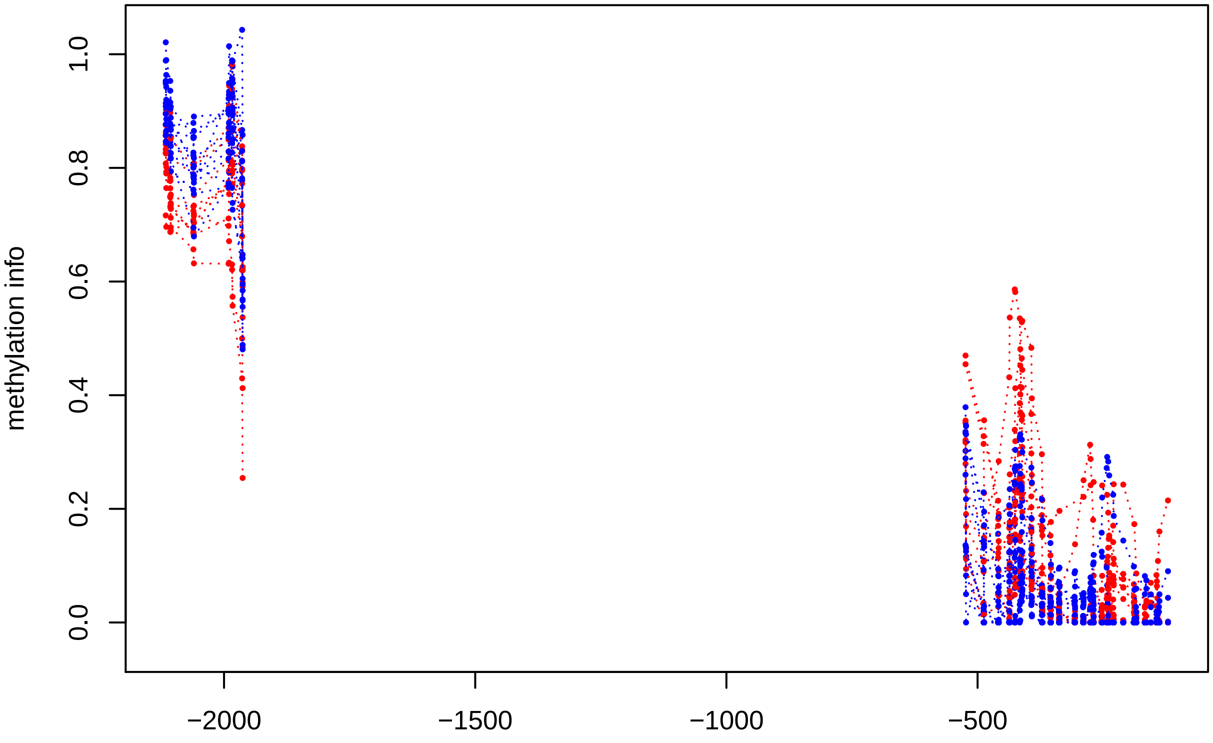
MME average UC−N %methylation max=−0.67% min=−37.5%

MME raw %methylation, red=UC, blue=Normal

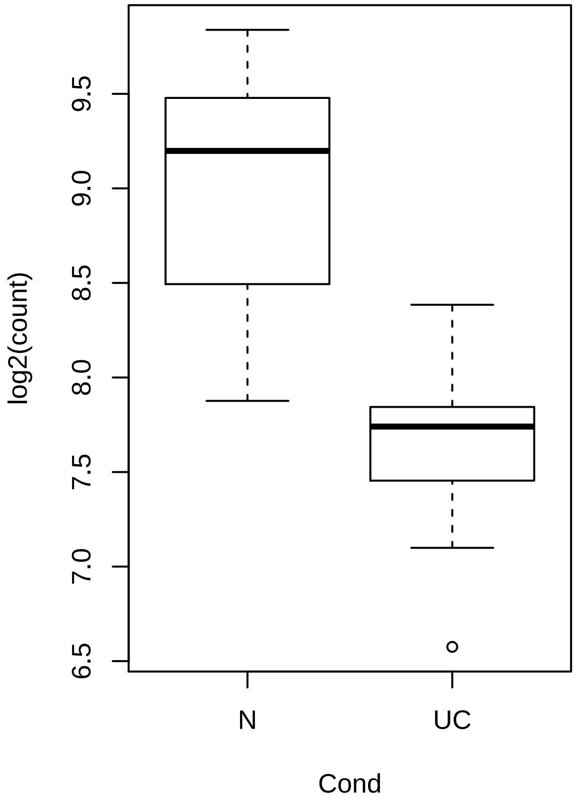
RNAseq logFC(UC−N)= 1.09



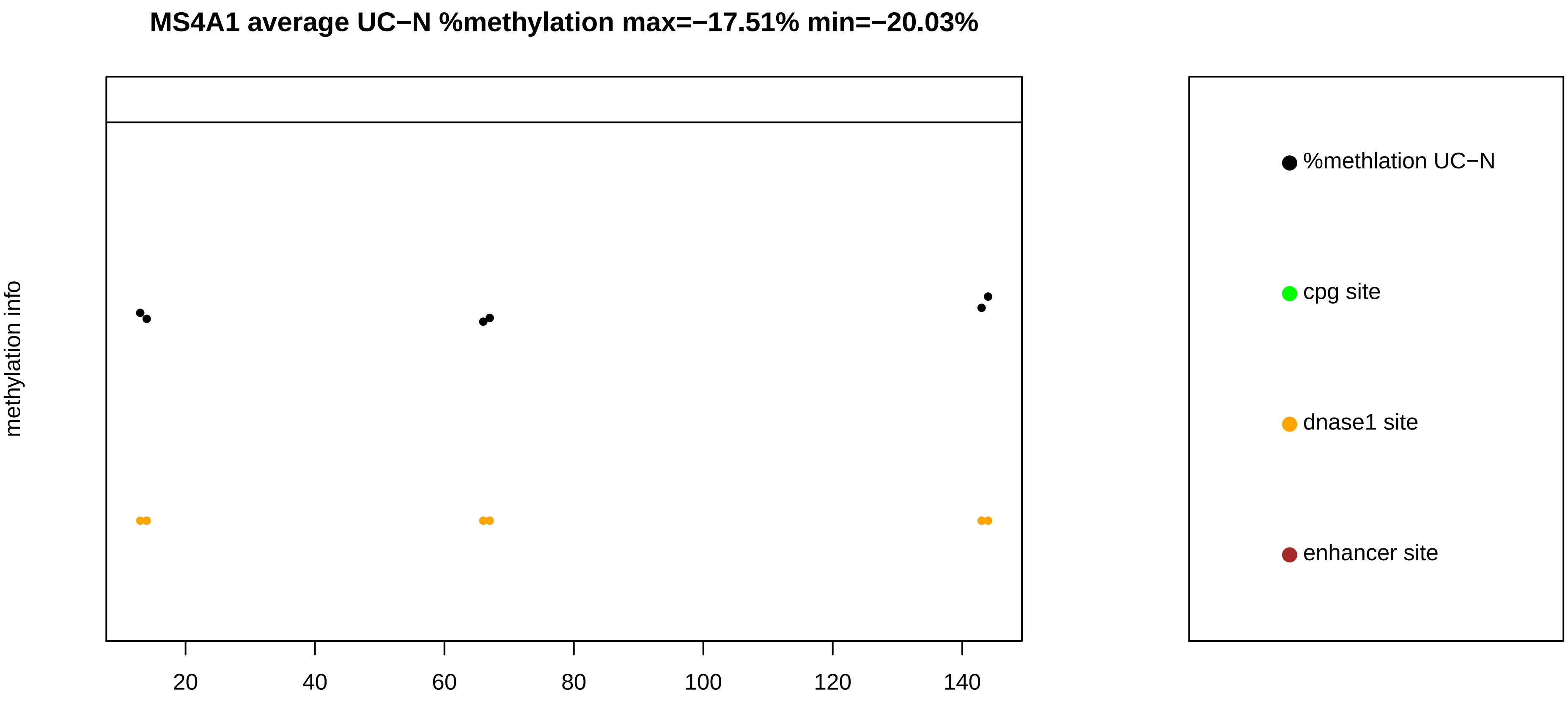
MOCS1 average UC−N %methylation max=12.96% min=−10.29%



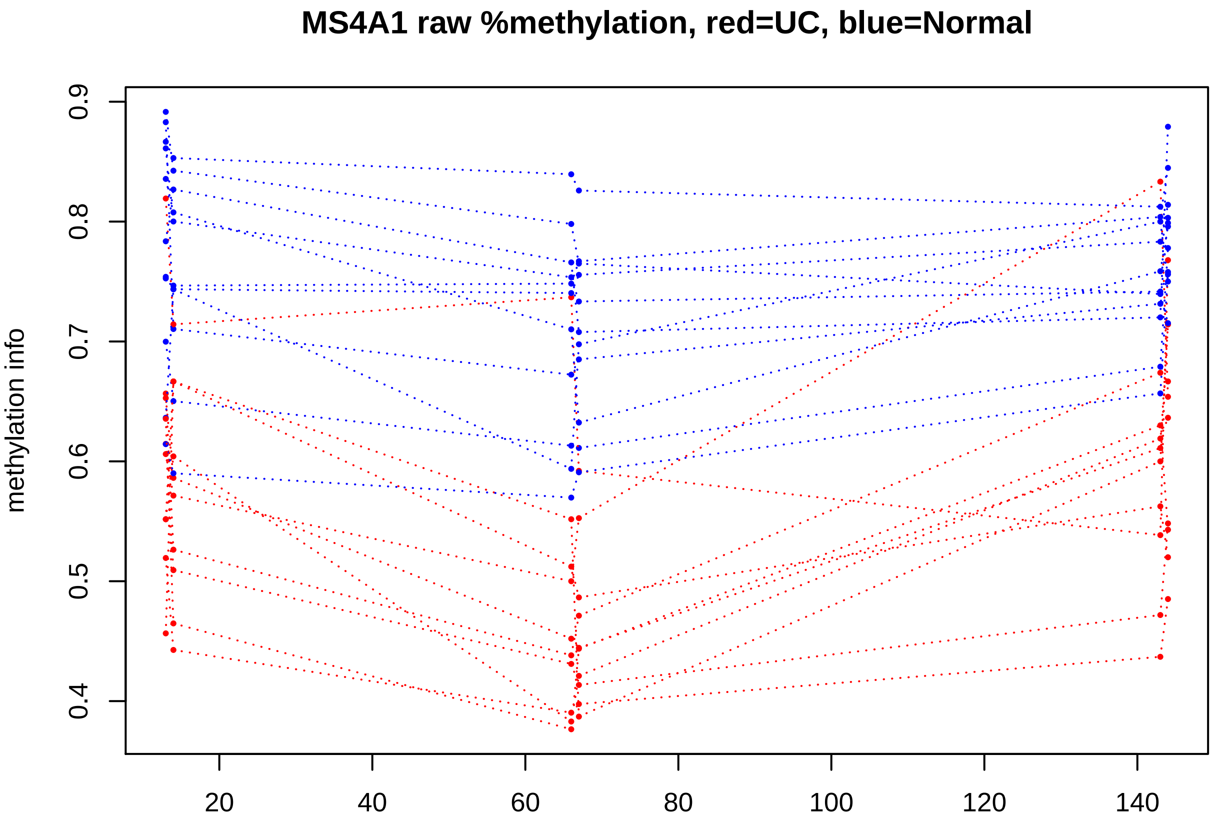
MOCS1 raw %methylation, red=UC, blue=Normal



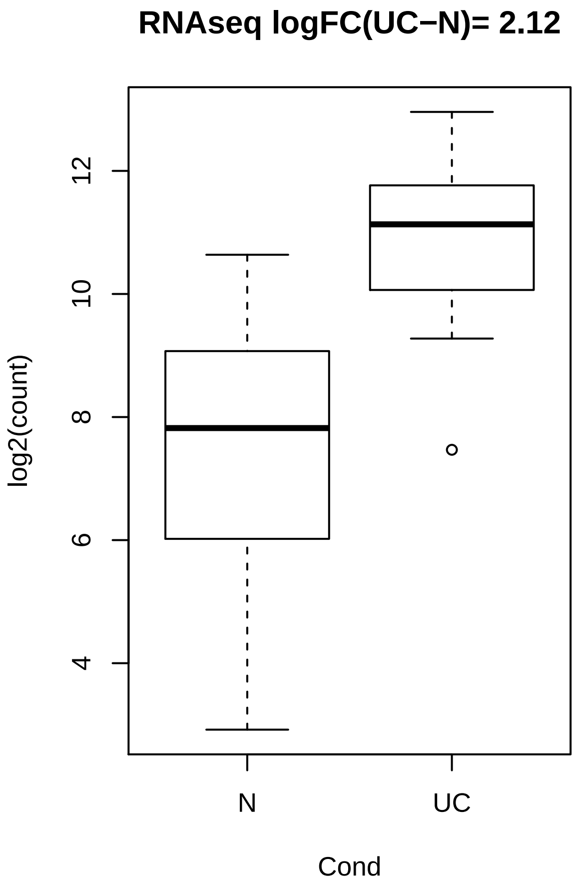
RNAseq logFC(UC−N)= −1.27



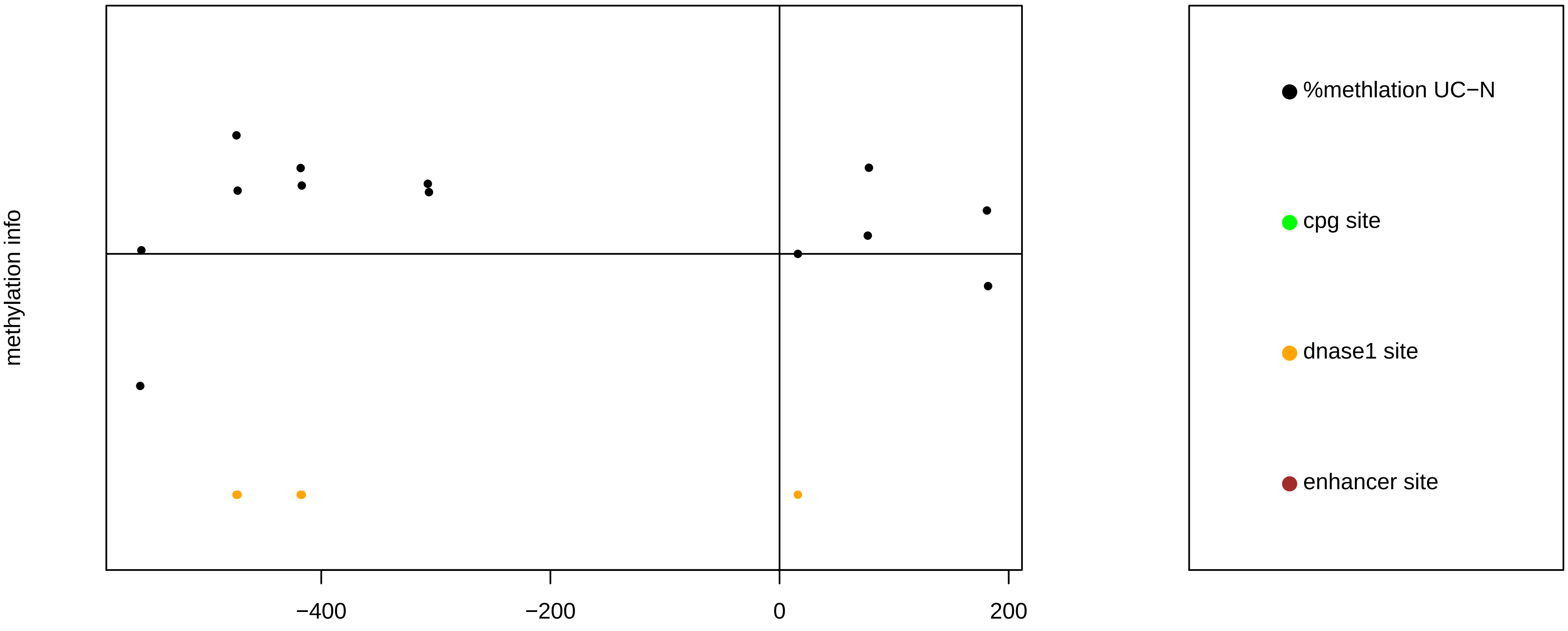
MS4A1 average UC−N %methylation max=−17.51% min=−20.03%

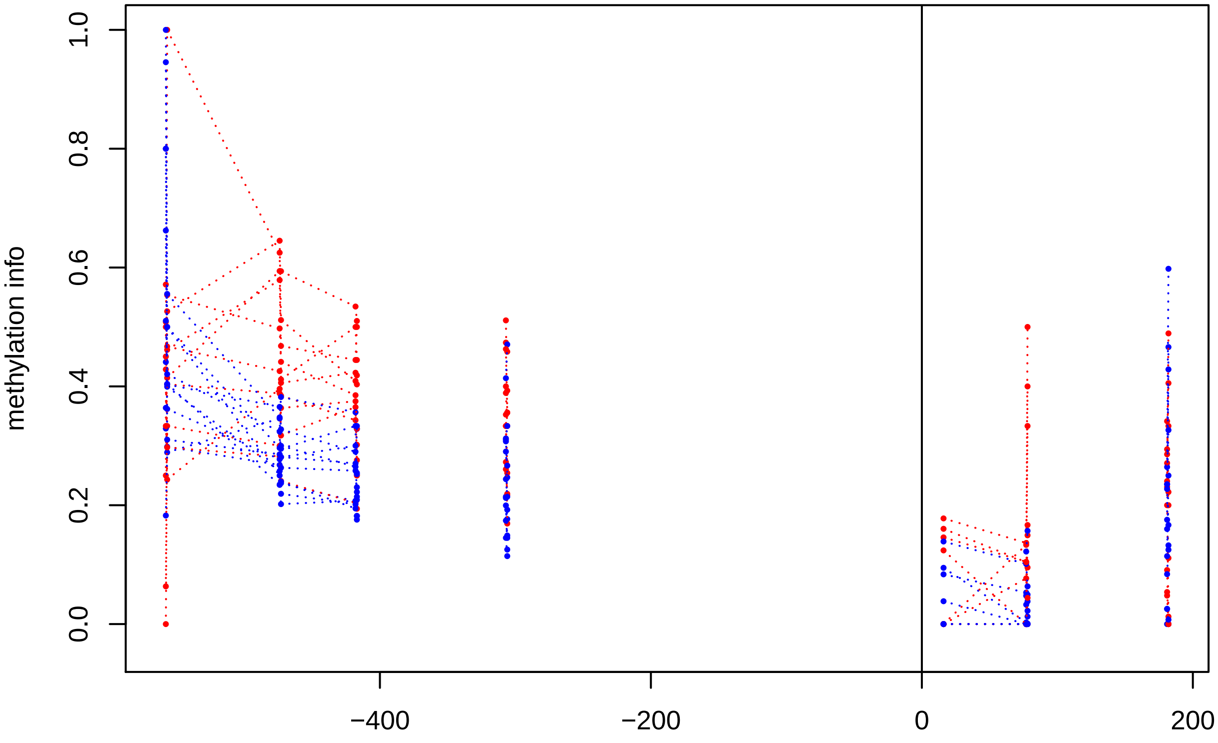


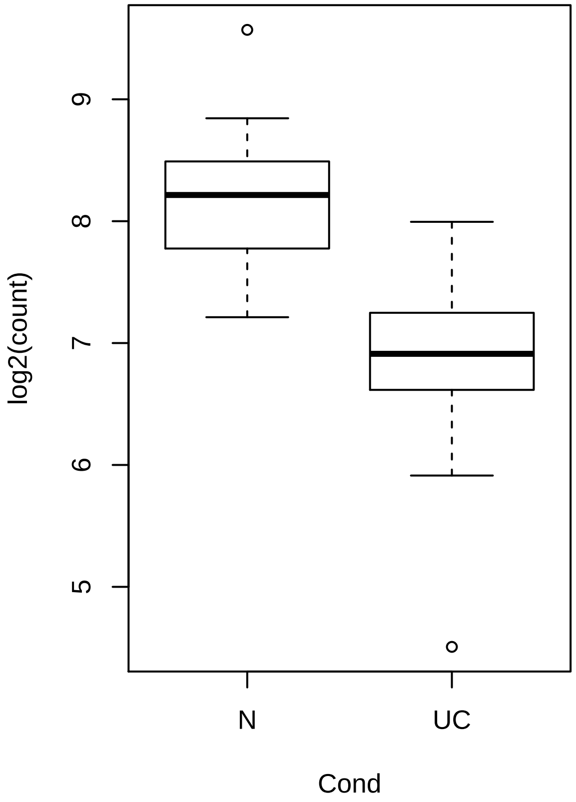
MS4A1 raw %methylation, red=UC, blue=Normal



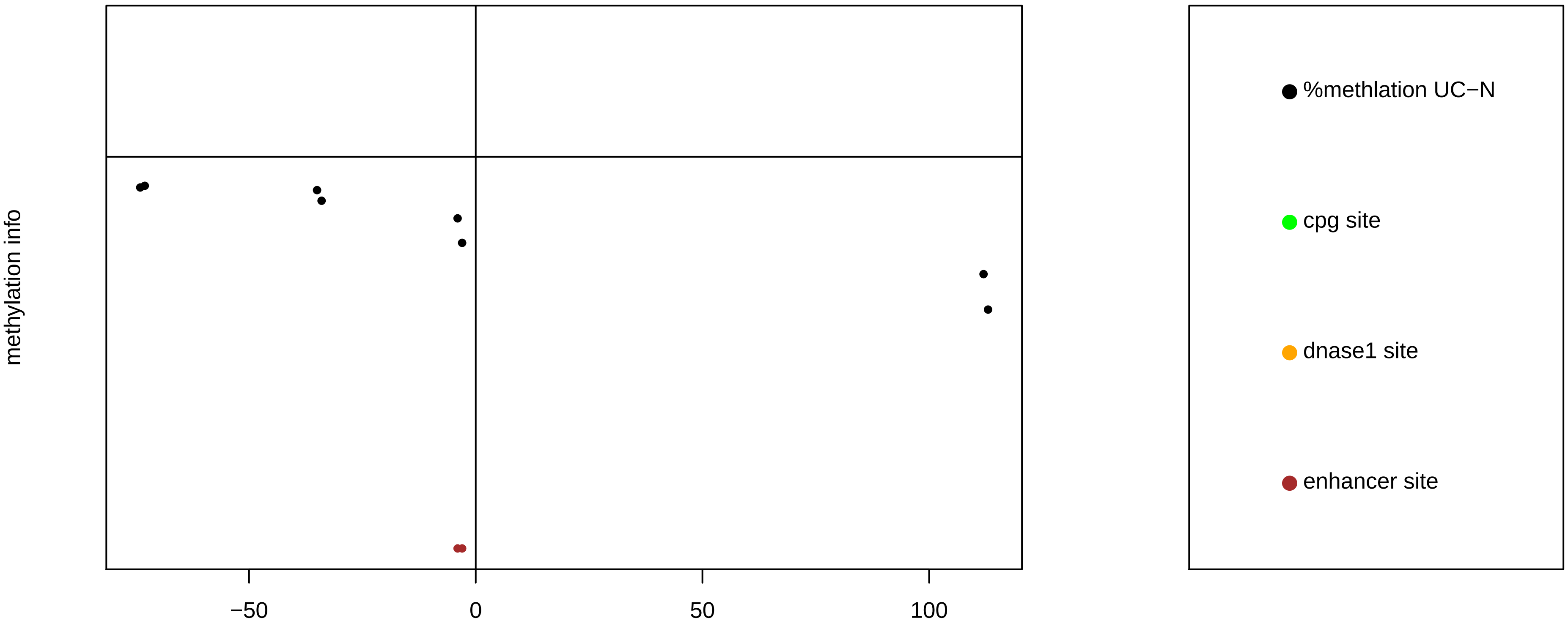
RNAseq logFC(UC−N)= 2.12


MS4A8 average UC−N %methylation max=21.79% min=−24.28%

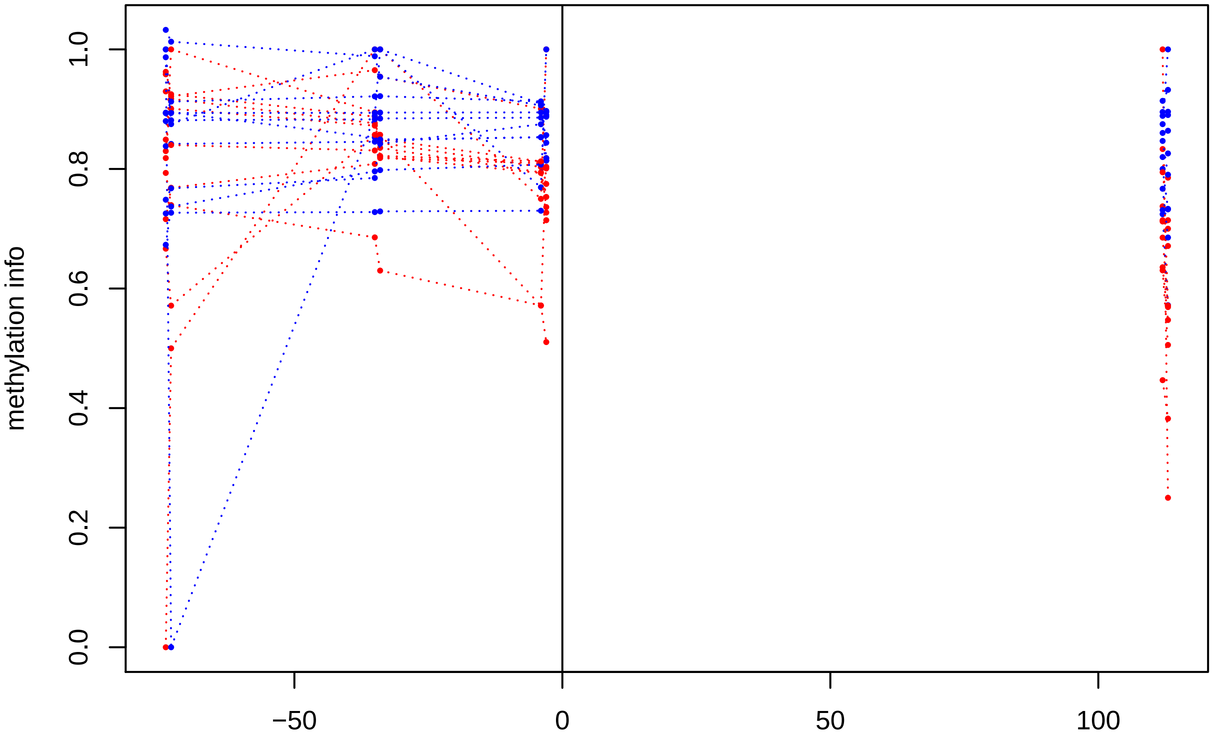

MS4A8 raw %methylation, red=UC, blue=Normal


RNAseq logFC(UC−N)= −1.18

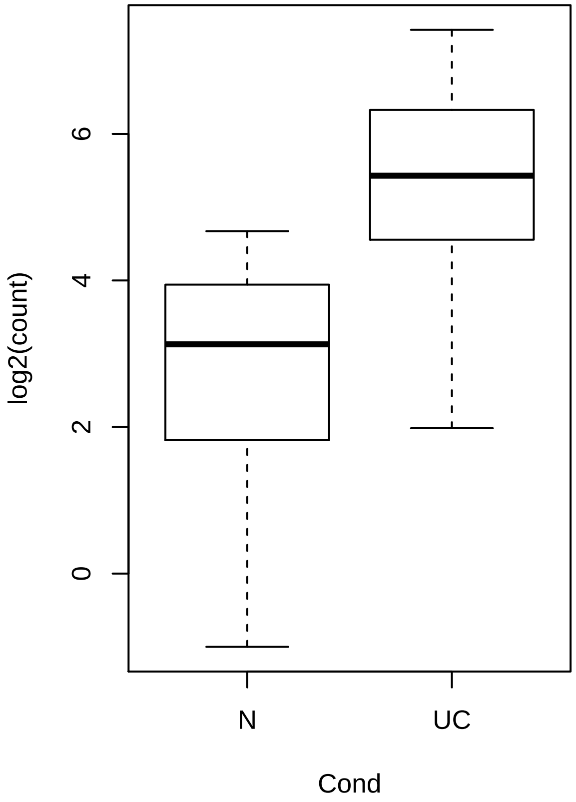
MUC16 average UC−N %methylation max=−3.64% min=−19.19%

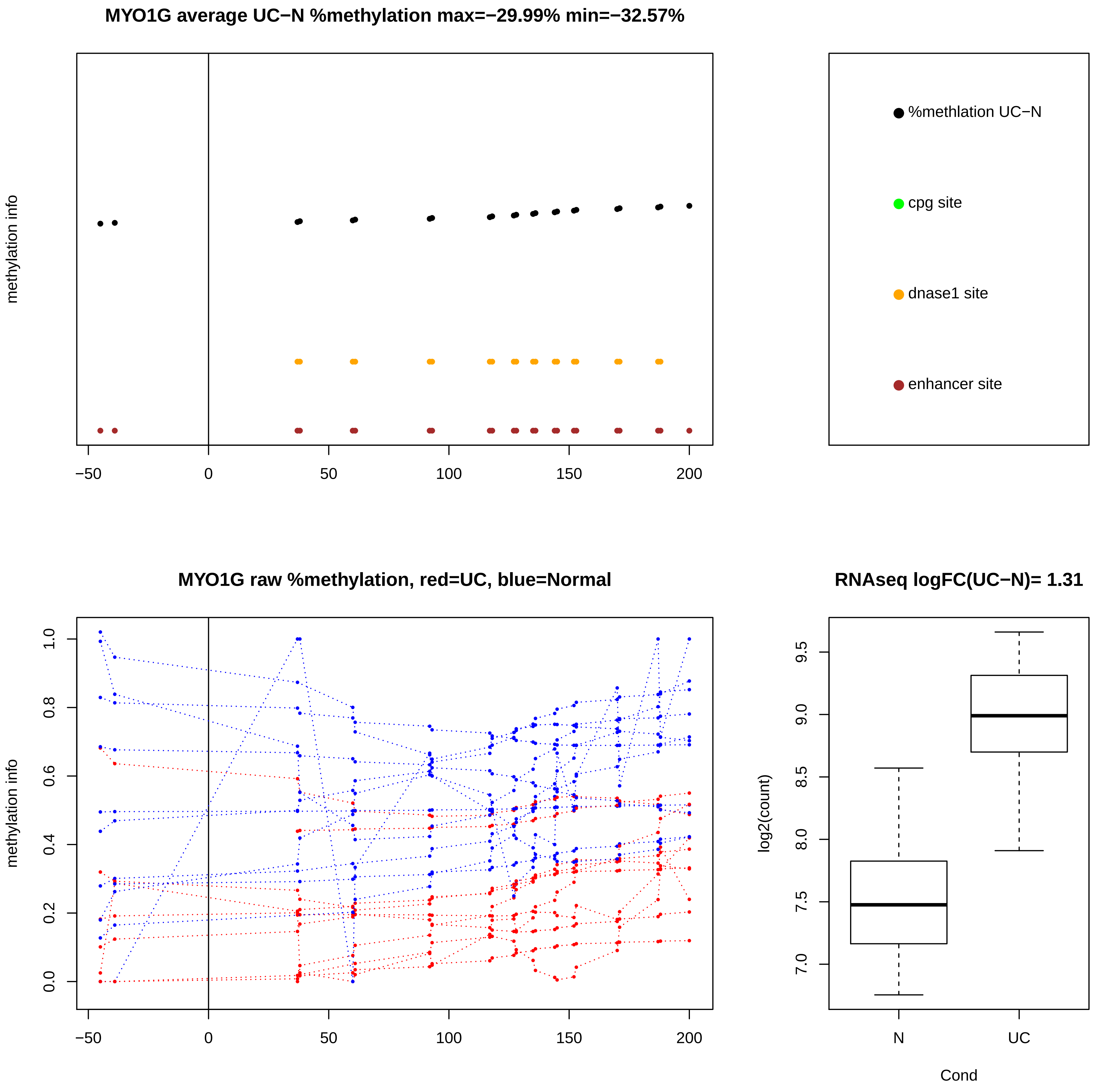


MUC16 raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 2.16

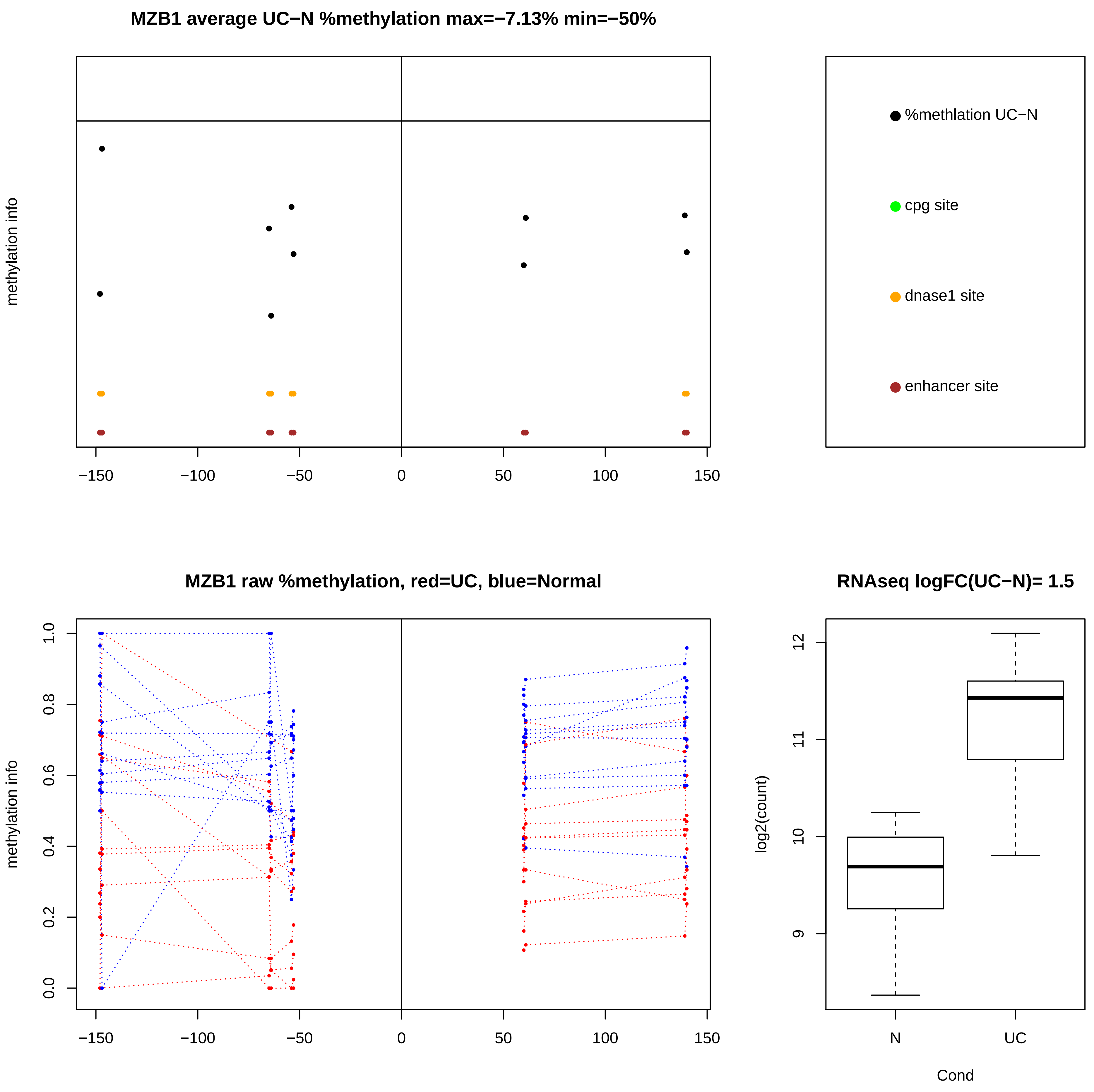




MYO1G average UC−N %methylation max=−29.99% min=−32.57%

MYO1G raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.31

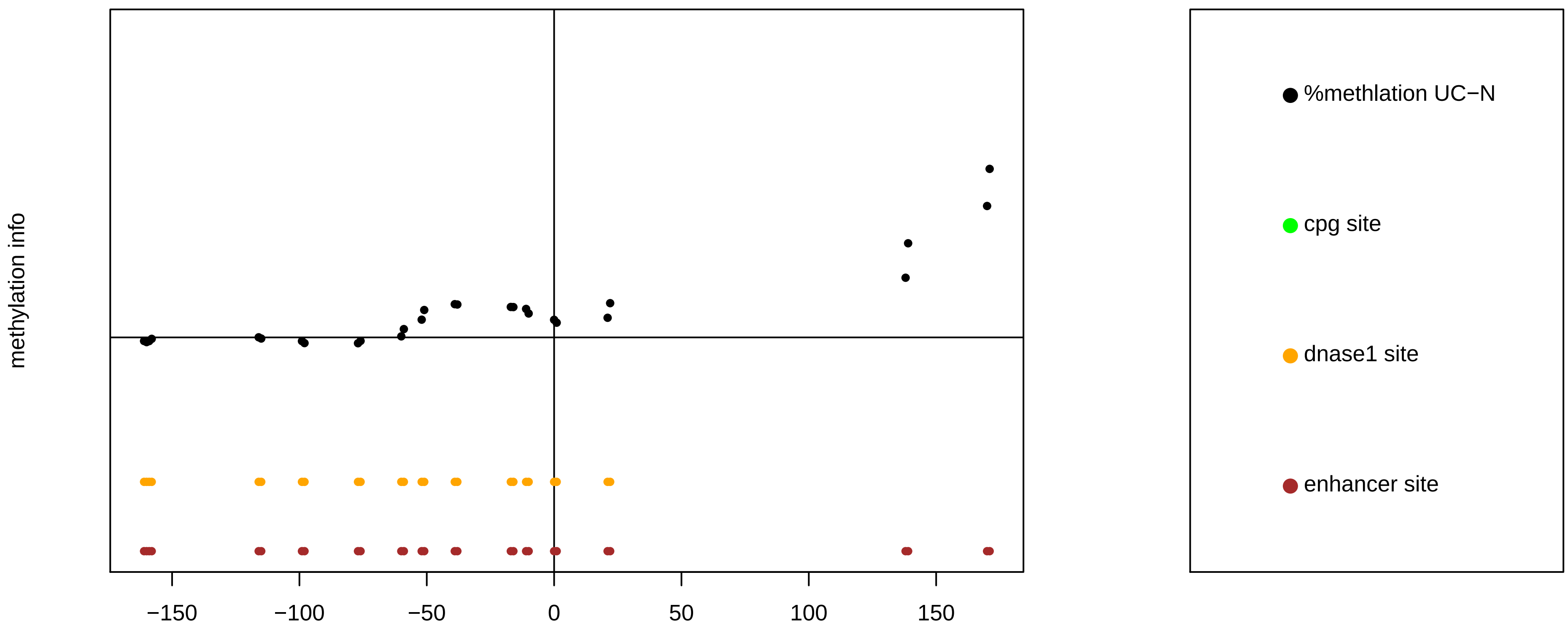


MZB1 average UC−N %methylation max=−7.13% min=−50%

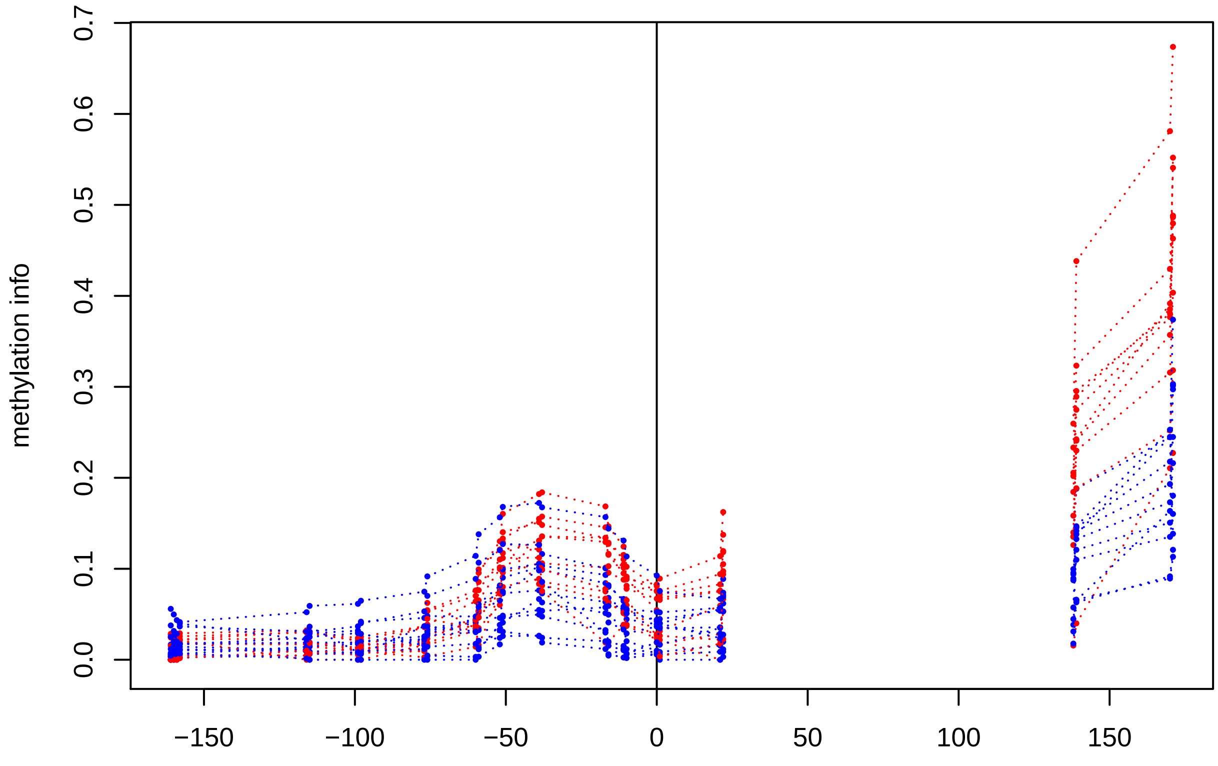
MZB1 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.5

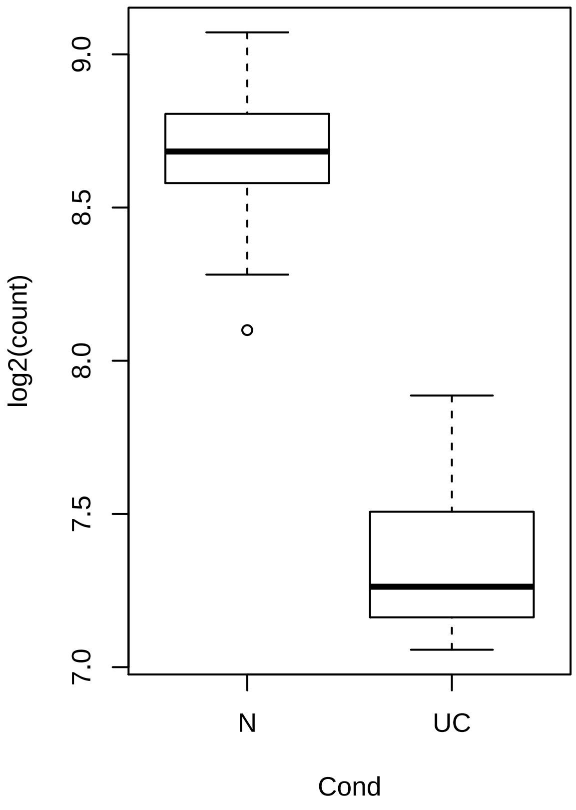
NCKAP5 average UC−N %methylation max=24.32% min=−0.84%

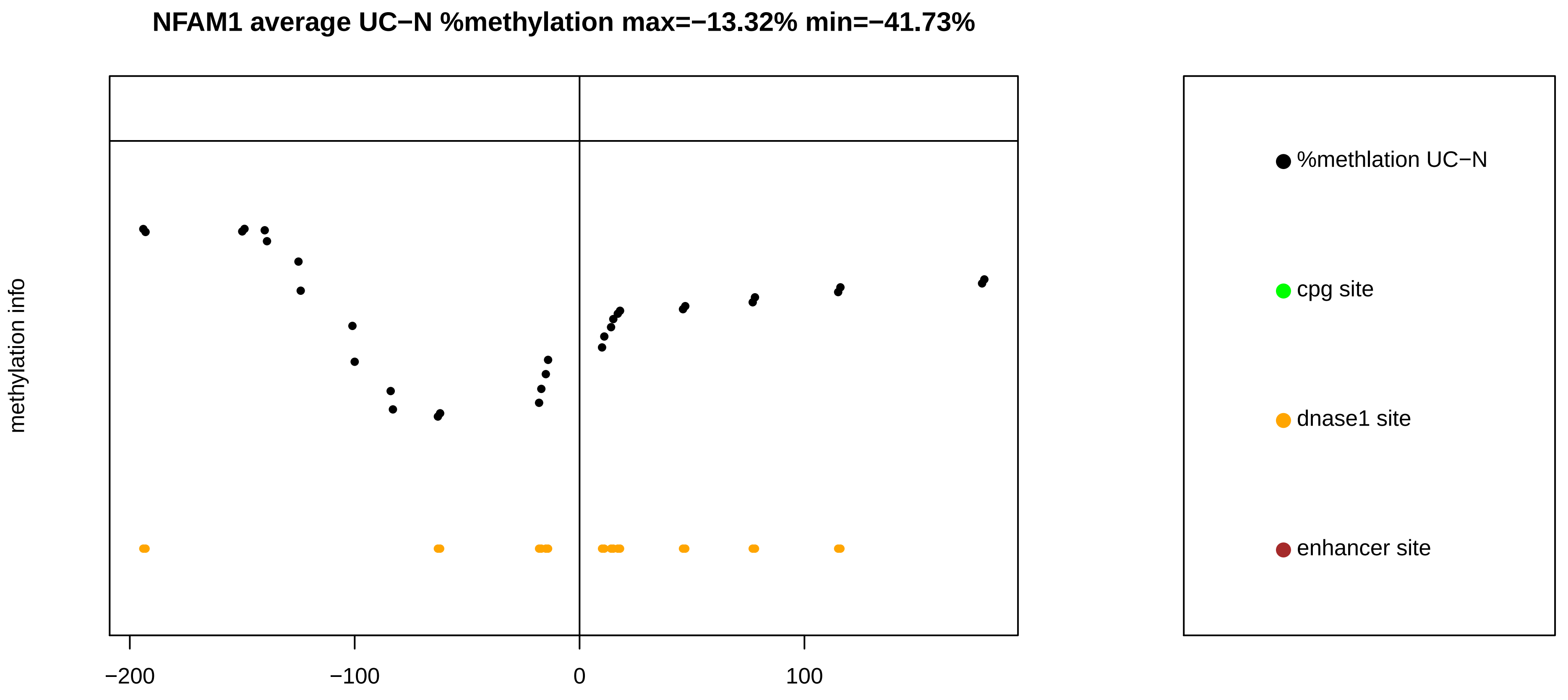


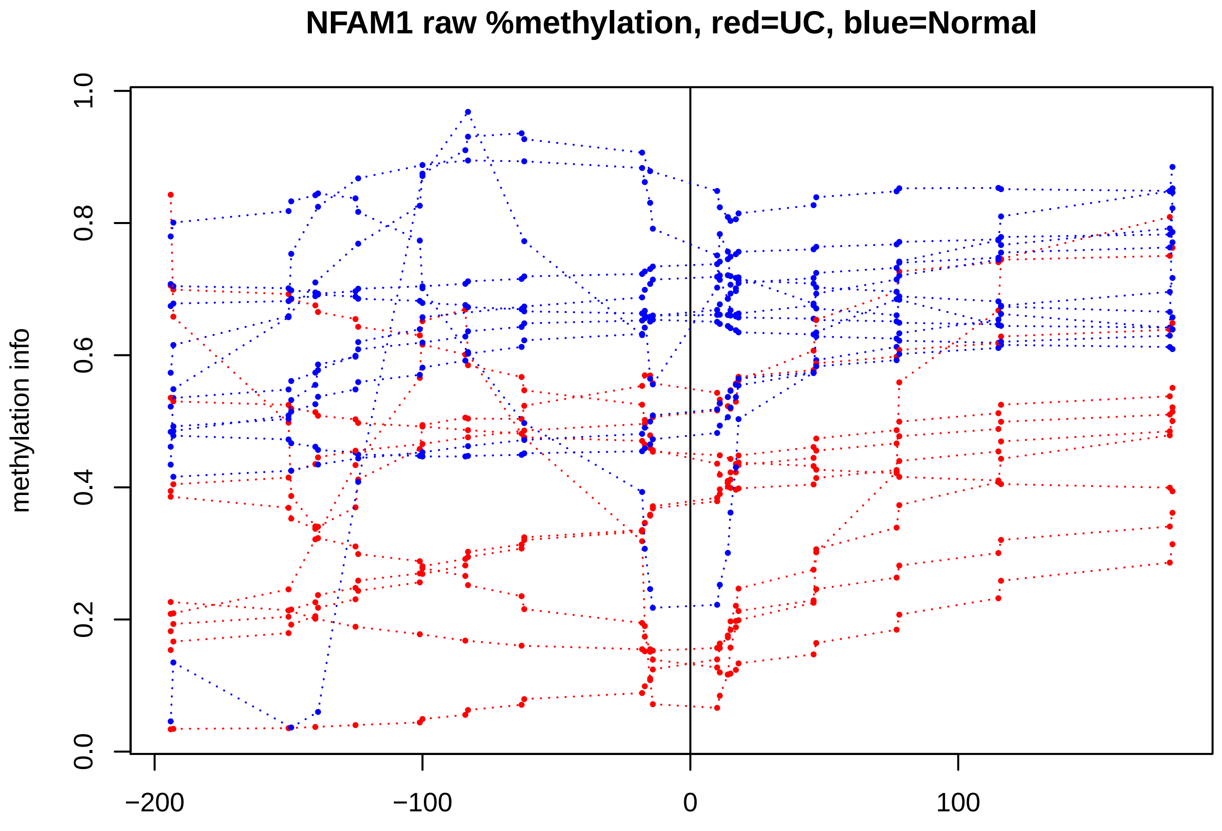
NCKAP5 raw %methylation, red=UC, blue=Normal

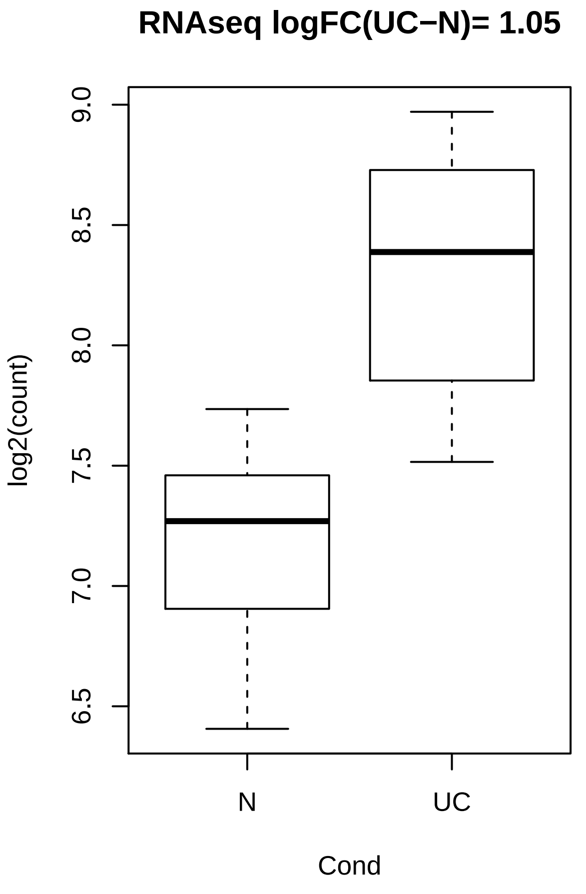


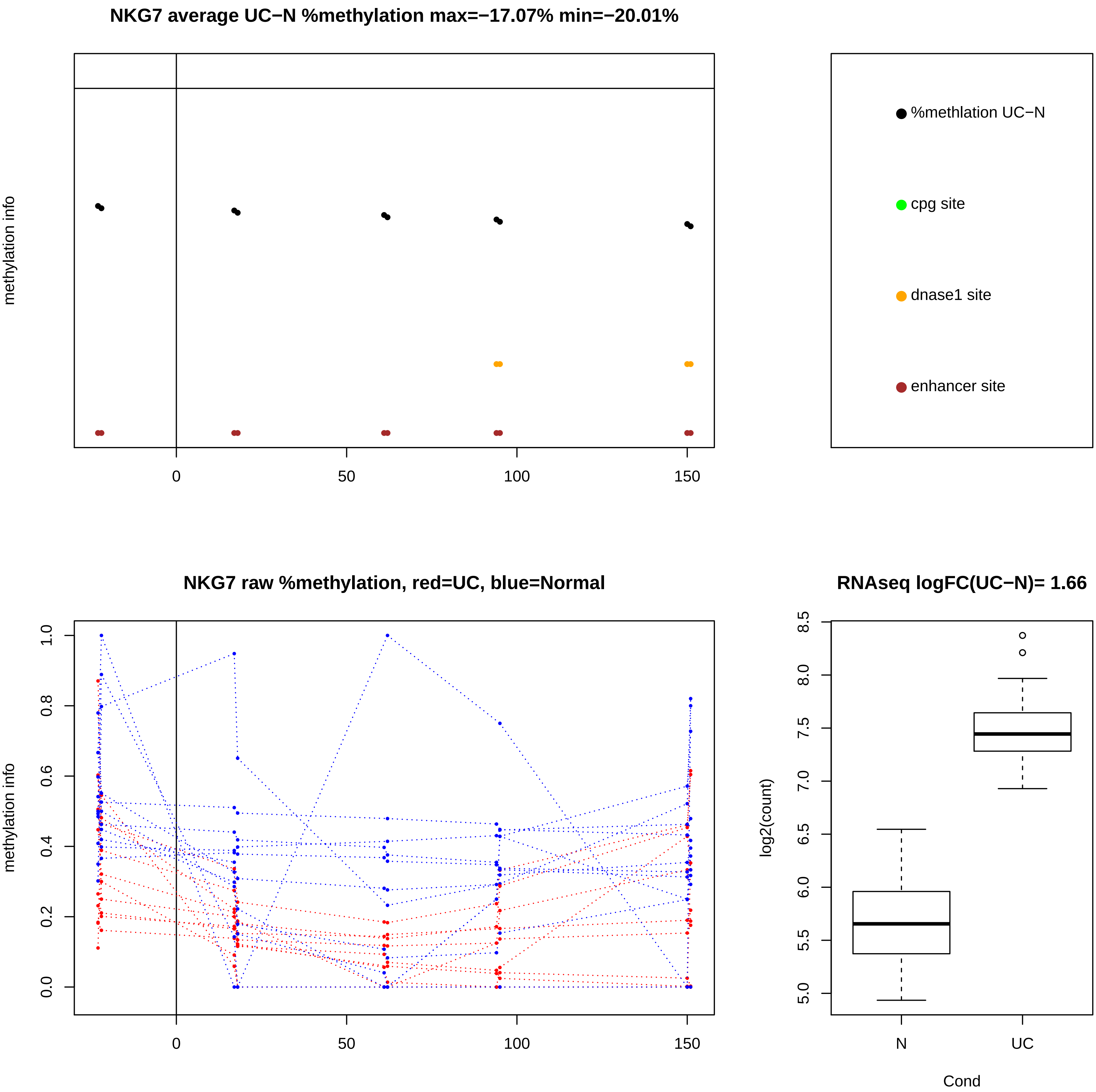
RNAseq logFC(UC−N)= −1.21




NFAM1 average UC−N %methylation max=−13.32% min=−41.73%
methylation info
−200
−100
0
100
%methlation UC−N
cpg site
dnase1 site
enhancer site


NFAM1 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−200
−100
0
100

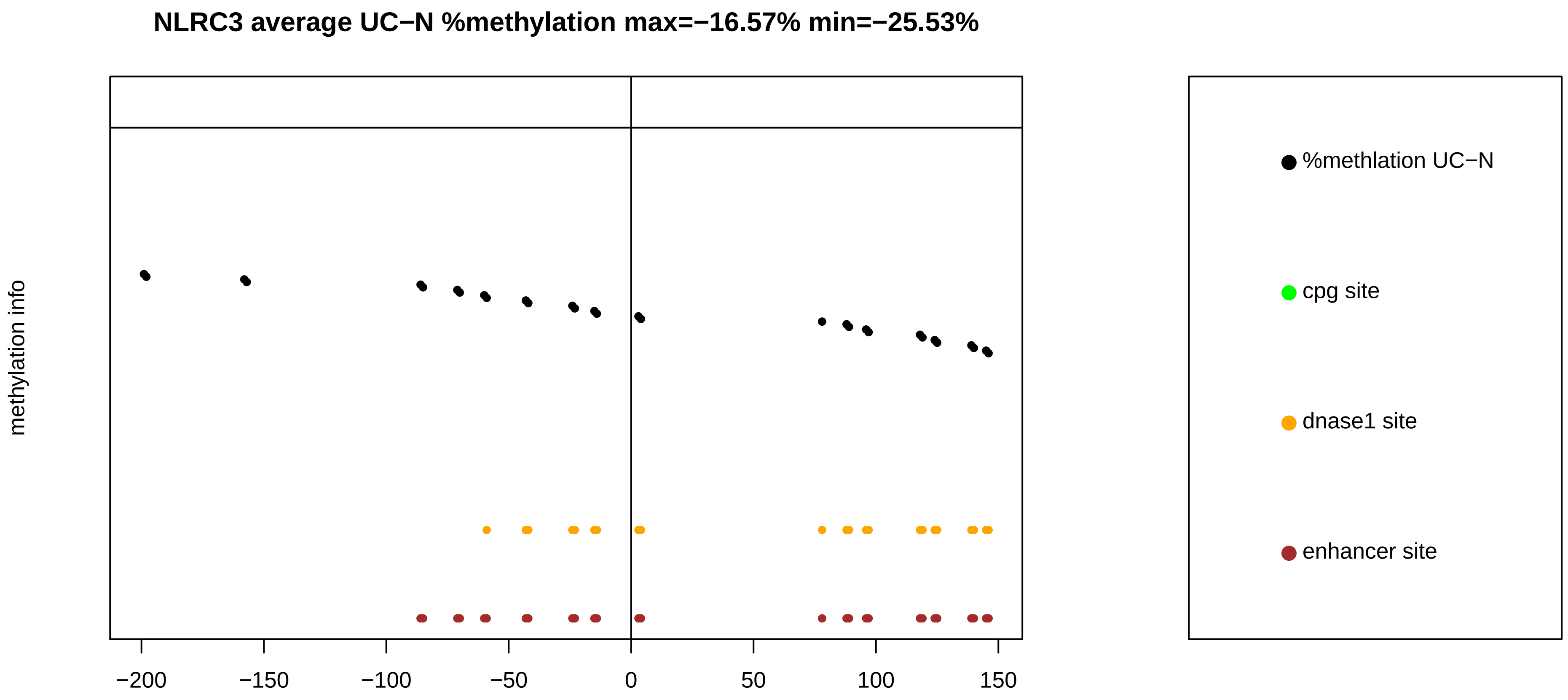

RNAseq logFC(UC−N)= 1.05
log2(count)
6.5
7.0
7.5
8.0
8.5
9.0
N
UC
Cond

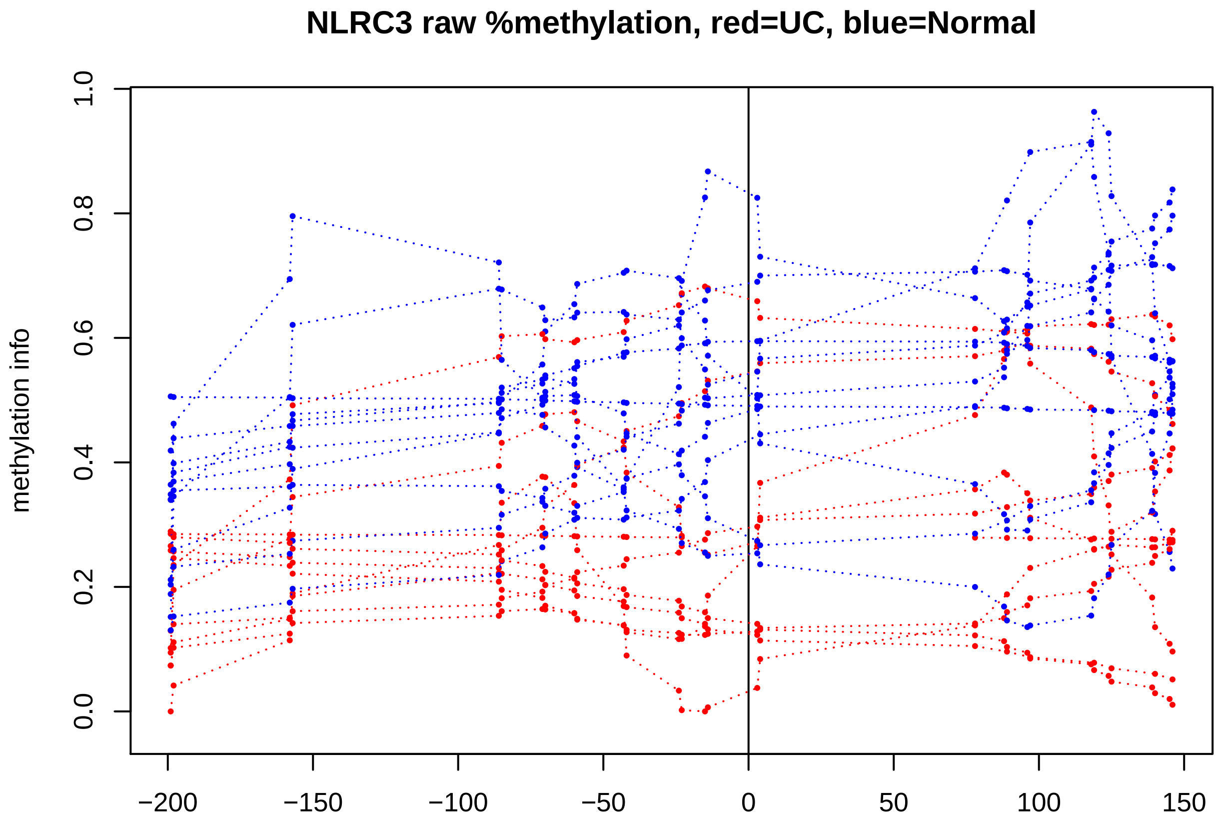


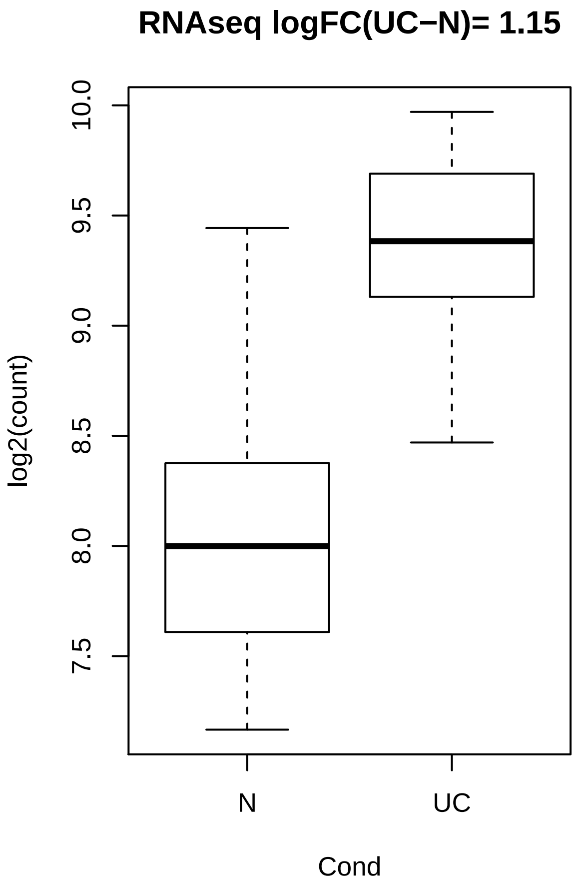
NKG7 average UC−N %methylation max=−17.07% min=−20.01%

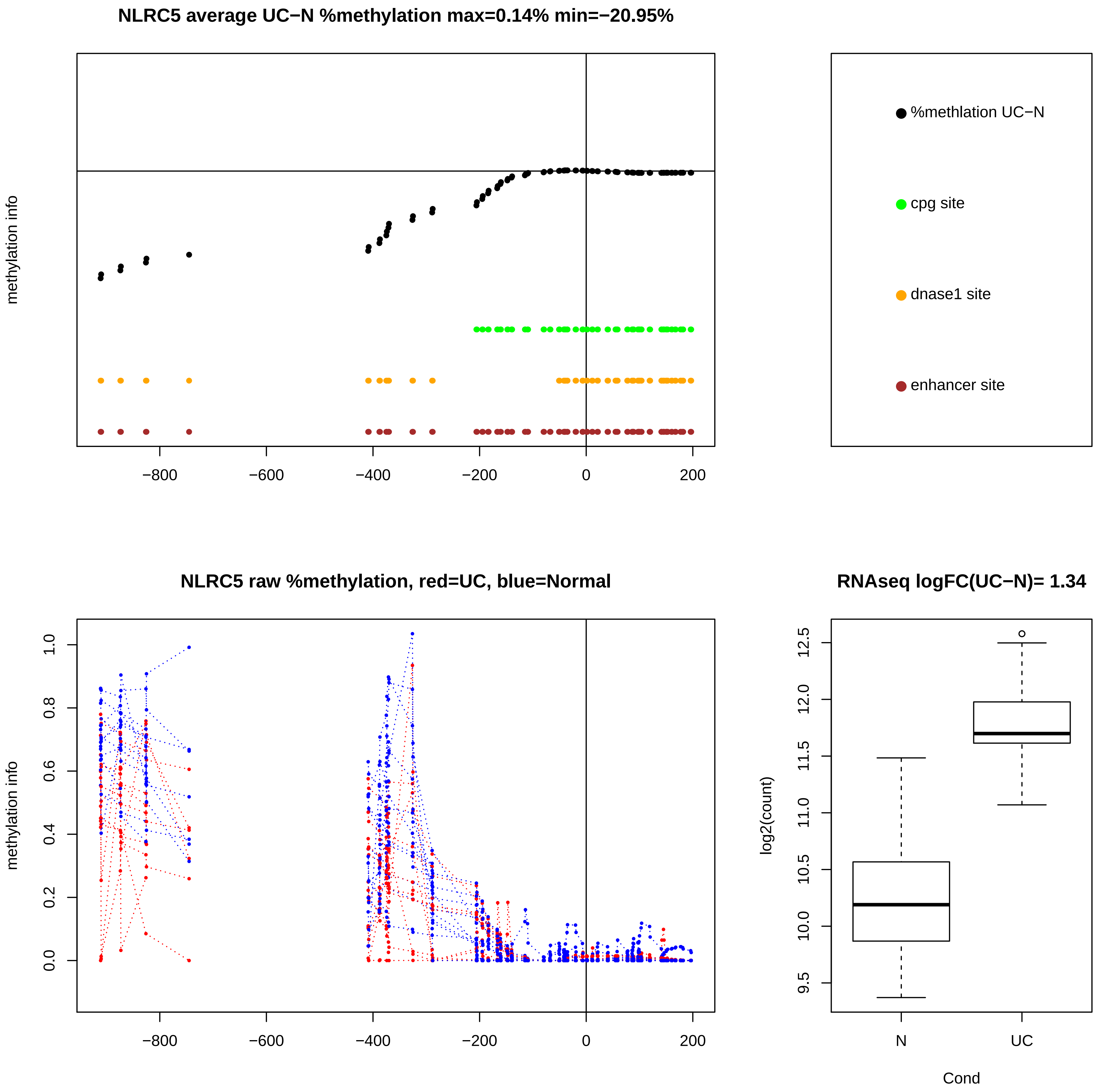
NKG7 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.66


NLRC3 average UC−N %methylation max=−16.57% min=−25.53%


NLRC3 raw %methylation, red=UC, blue=Normal


RNAseq logFC(UC−N)= 1.15

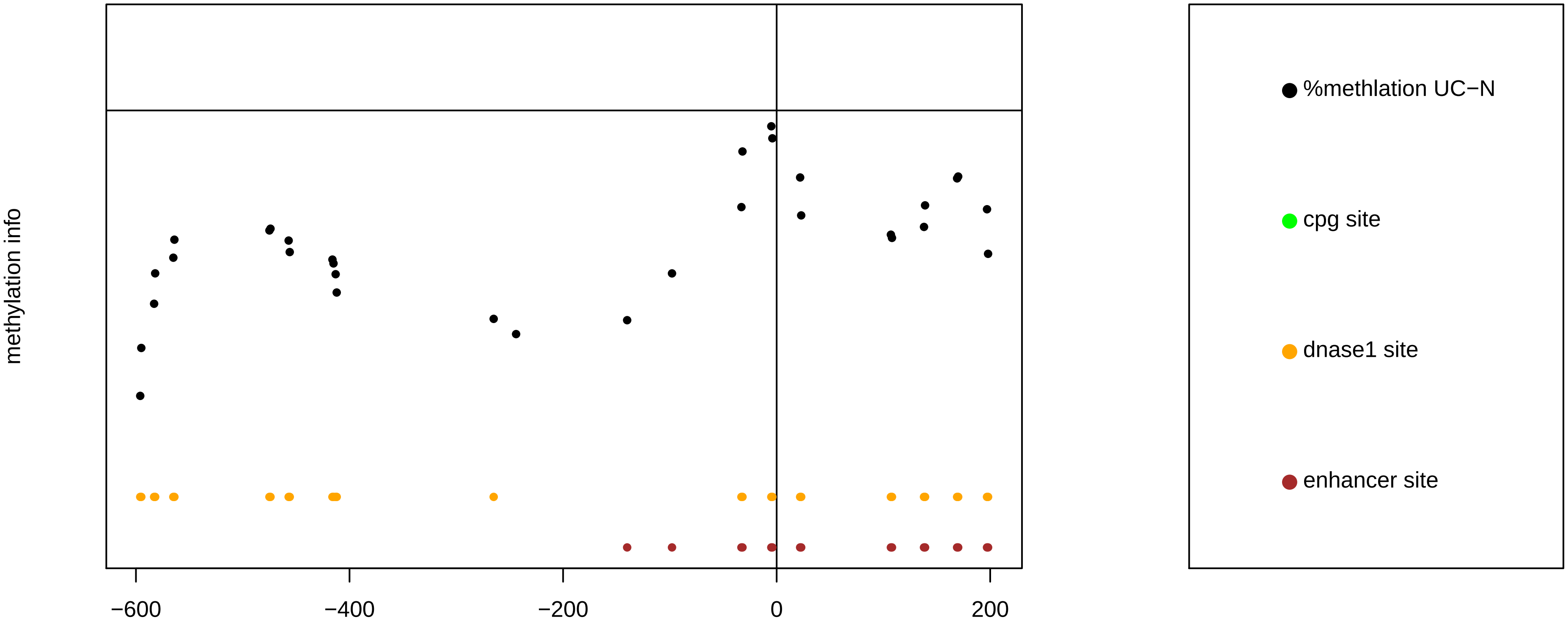


NLRC5 average UC−N %methylation max=0.14% min=−20.95%

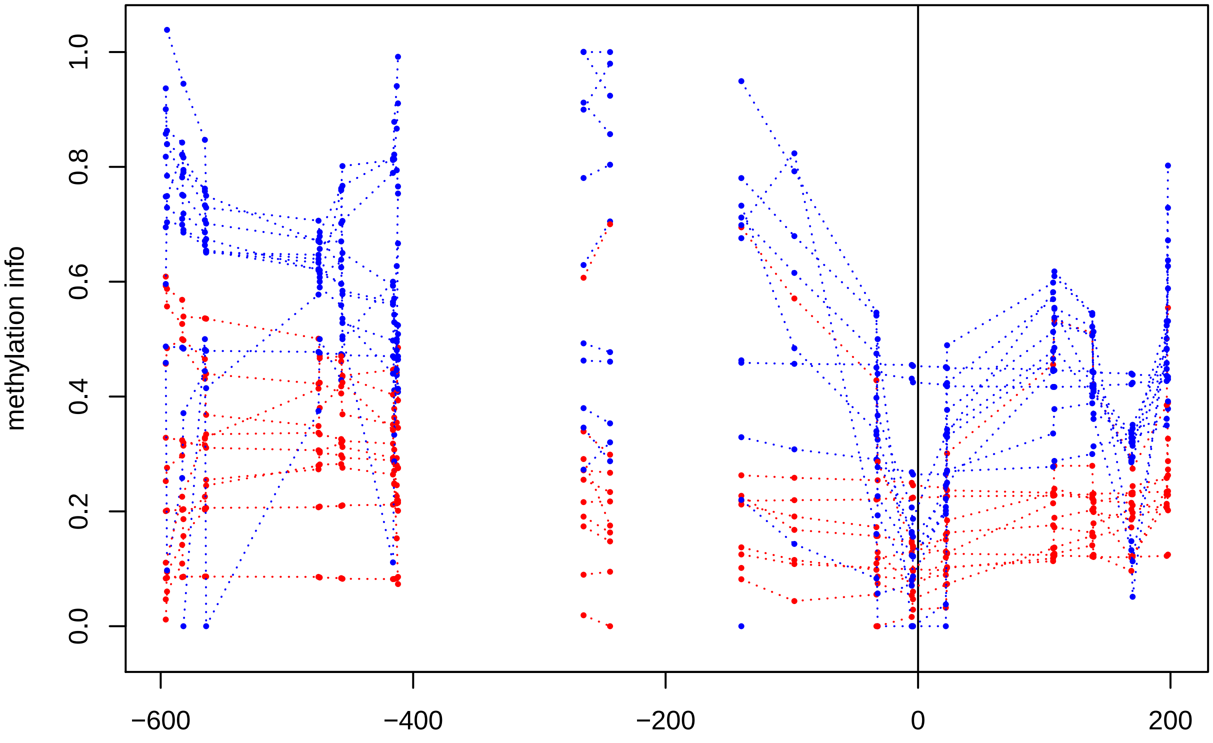
NLRC5 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.34

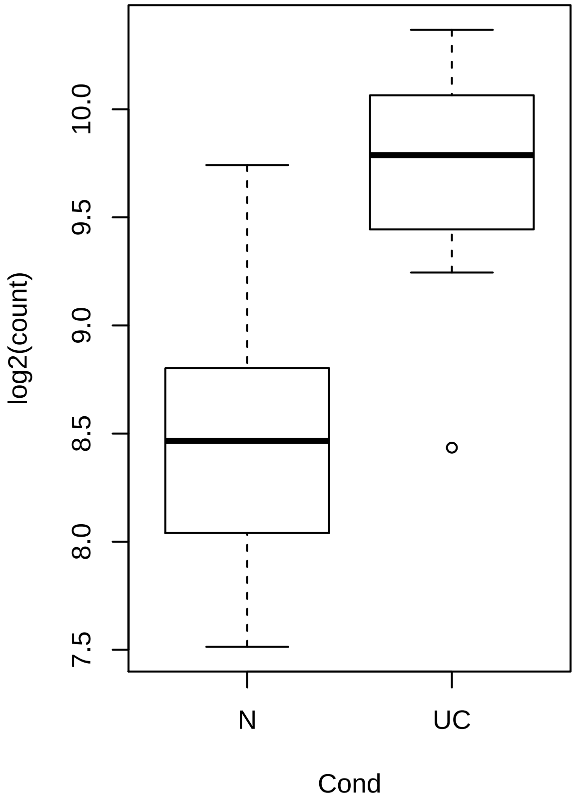
NLRP1 average UC−N %methylation max=−3.13% min=−56.51%

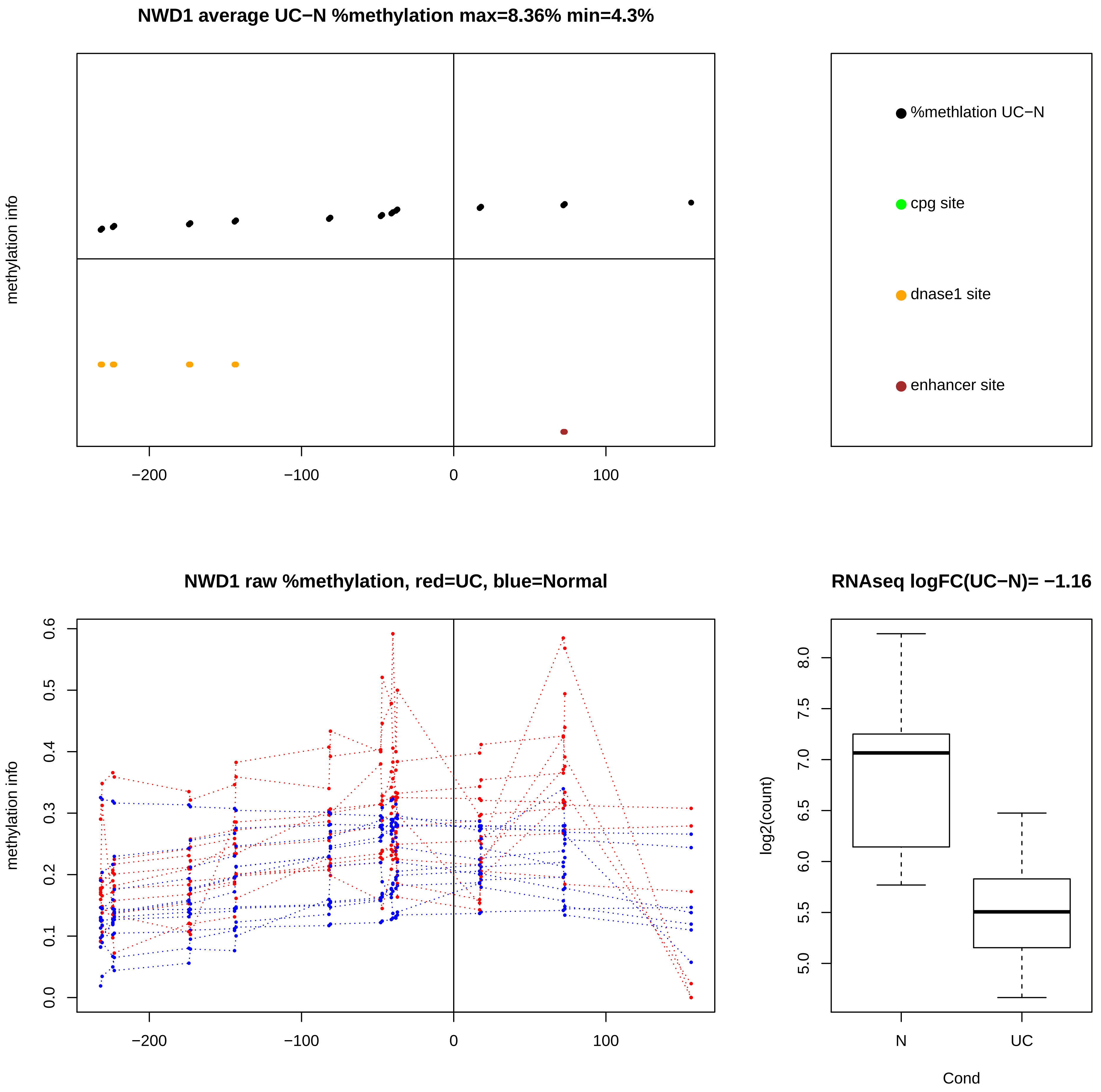


NLRP1 raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 1.06

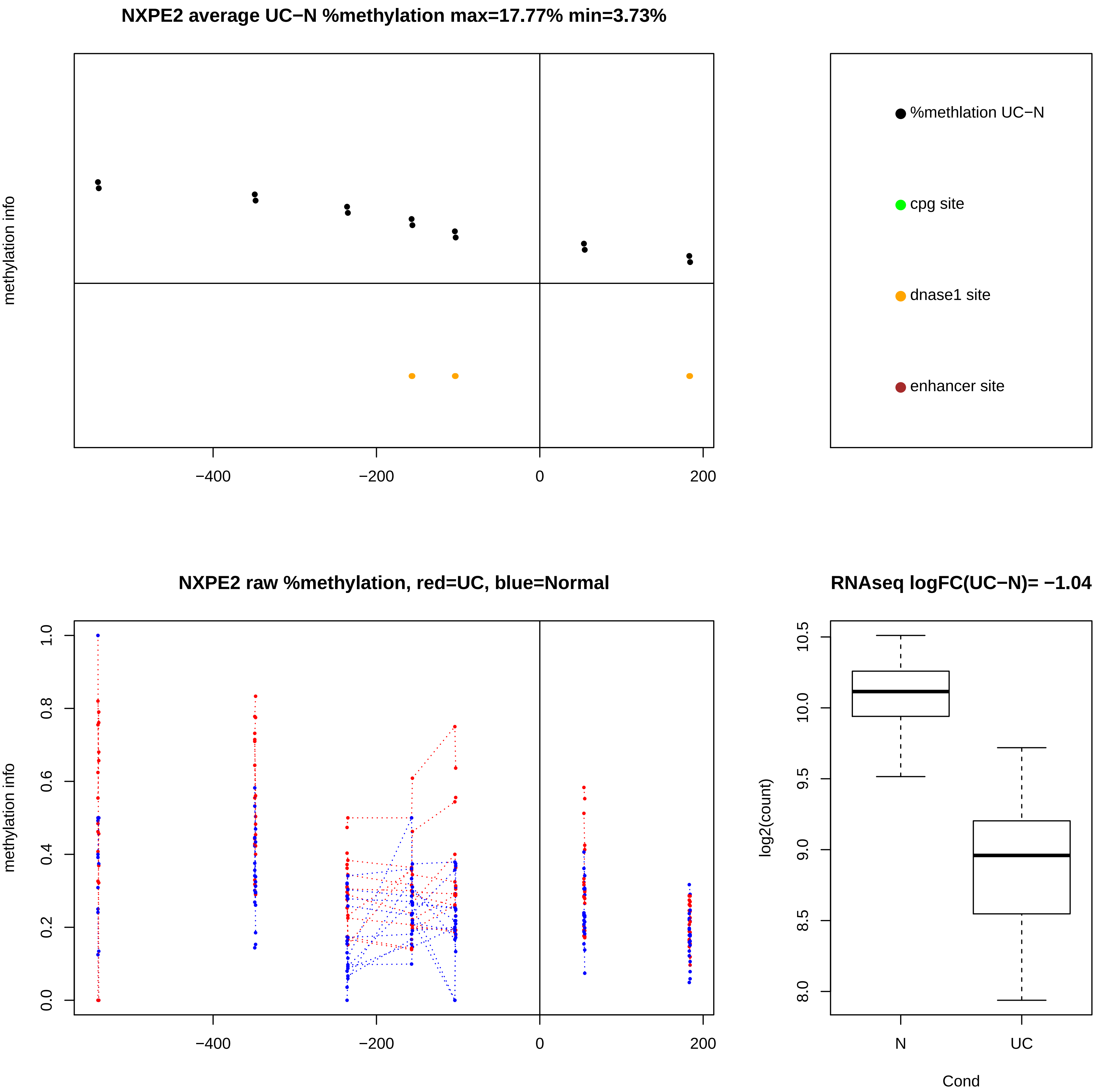




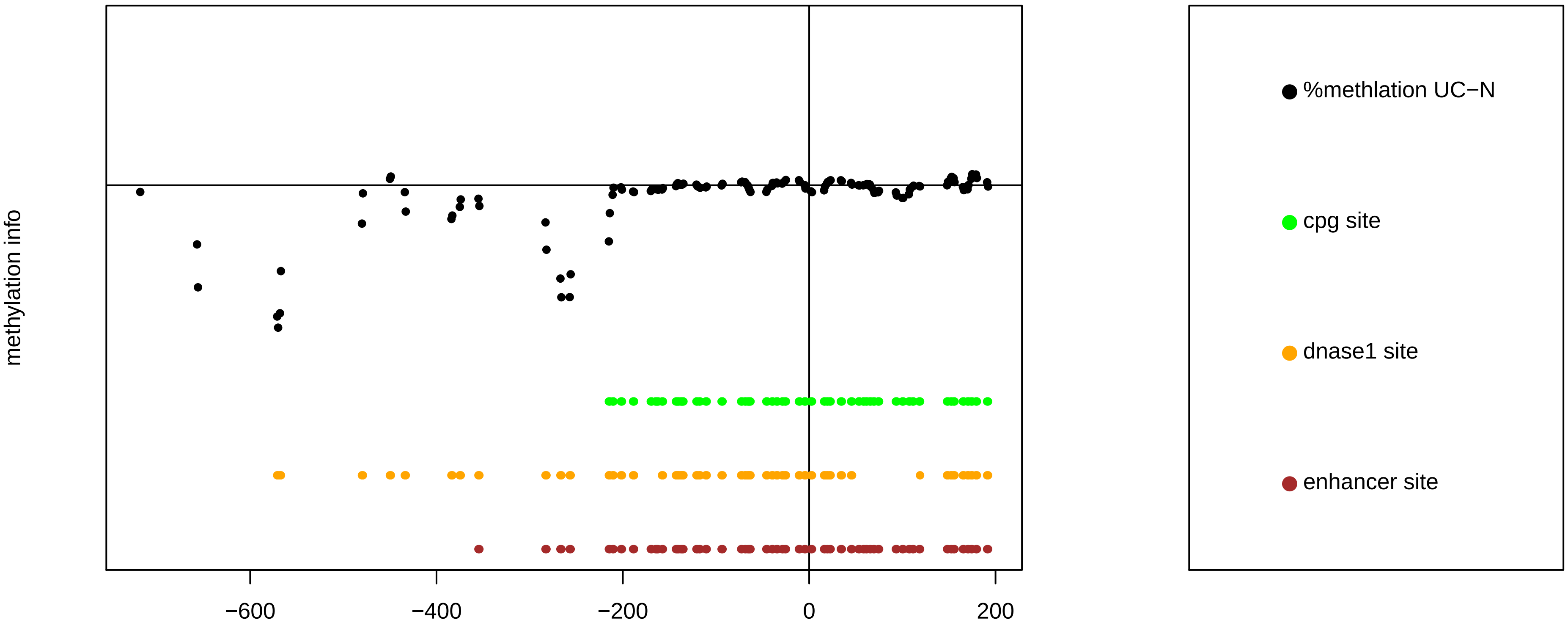
NWD1 average UC−N %methylation max=8.36% min=4.3%

NWD1 raw %methylation, red=UC, blue=Normal

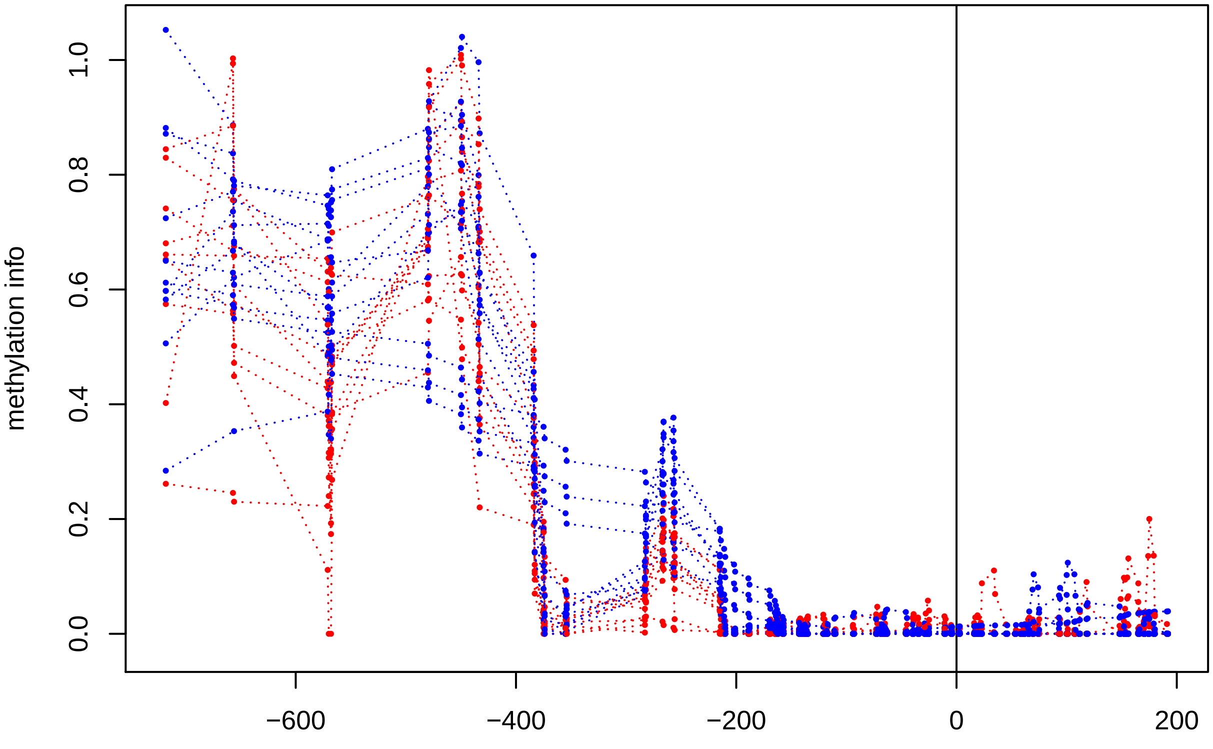
RNAseq logFC(UC−N)= −1.16


NXPE2 average UC−N %methylation max=17.77% min=3.73%
methylation info
−400
−200
0
200
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
NXPE2 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−400
−200
0
200
RNAseq logFC(UC−N)= −1.04
log2(count)
8.0
8.5
9.0
9.5
10.0
10.5
N
UC
Cond

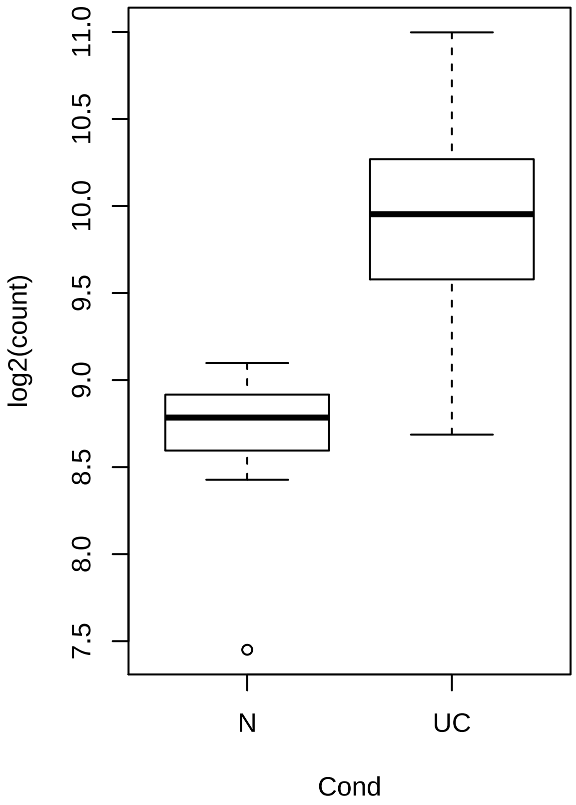
NXPE3 average UC−N %methylation max=1.5% min=−19.29%

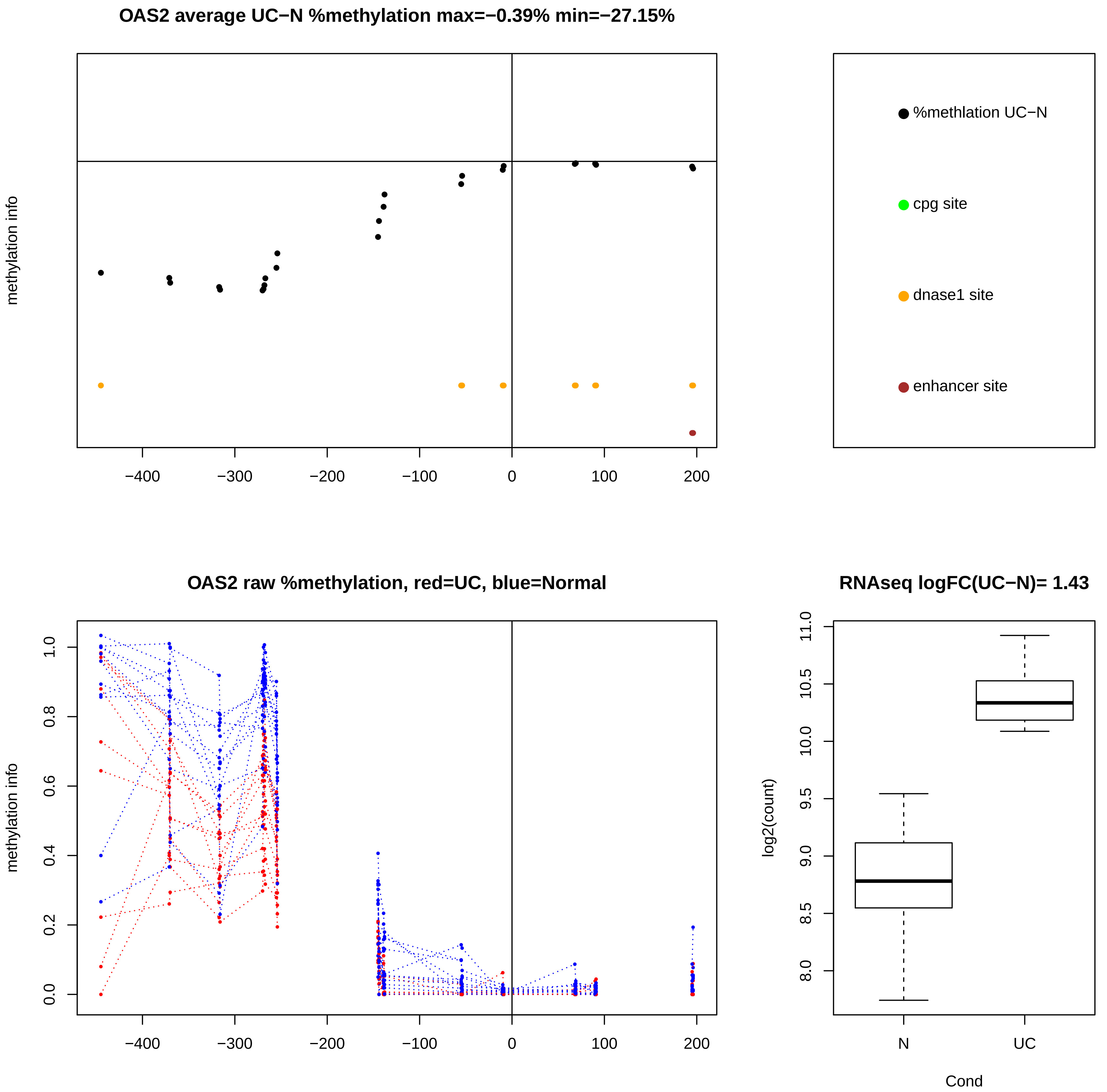


NXPE3 raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 1.12

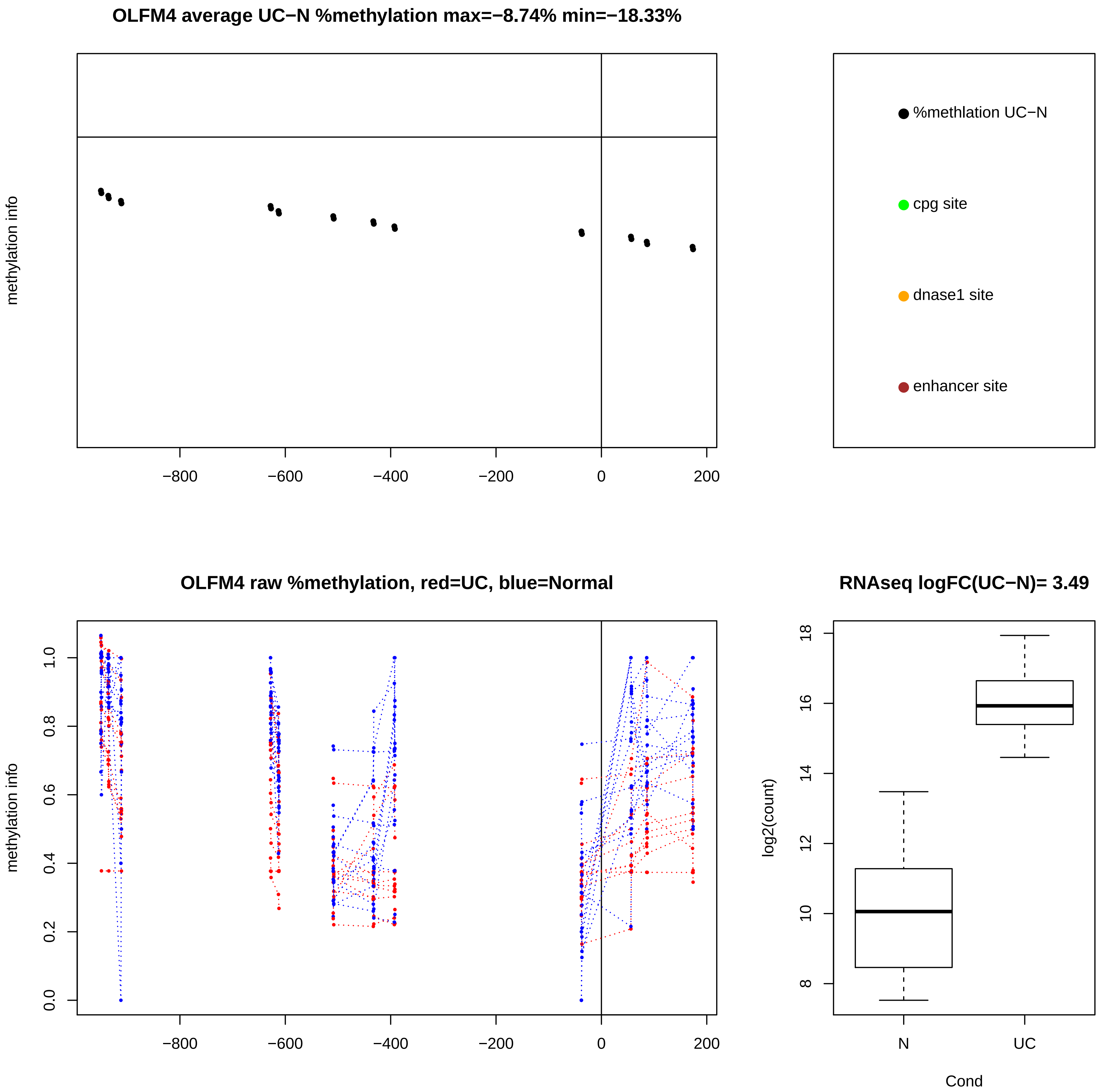




OAS2 average UC−N %methylation max=−0.39% min=−27.15%

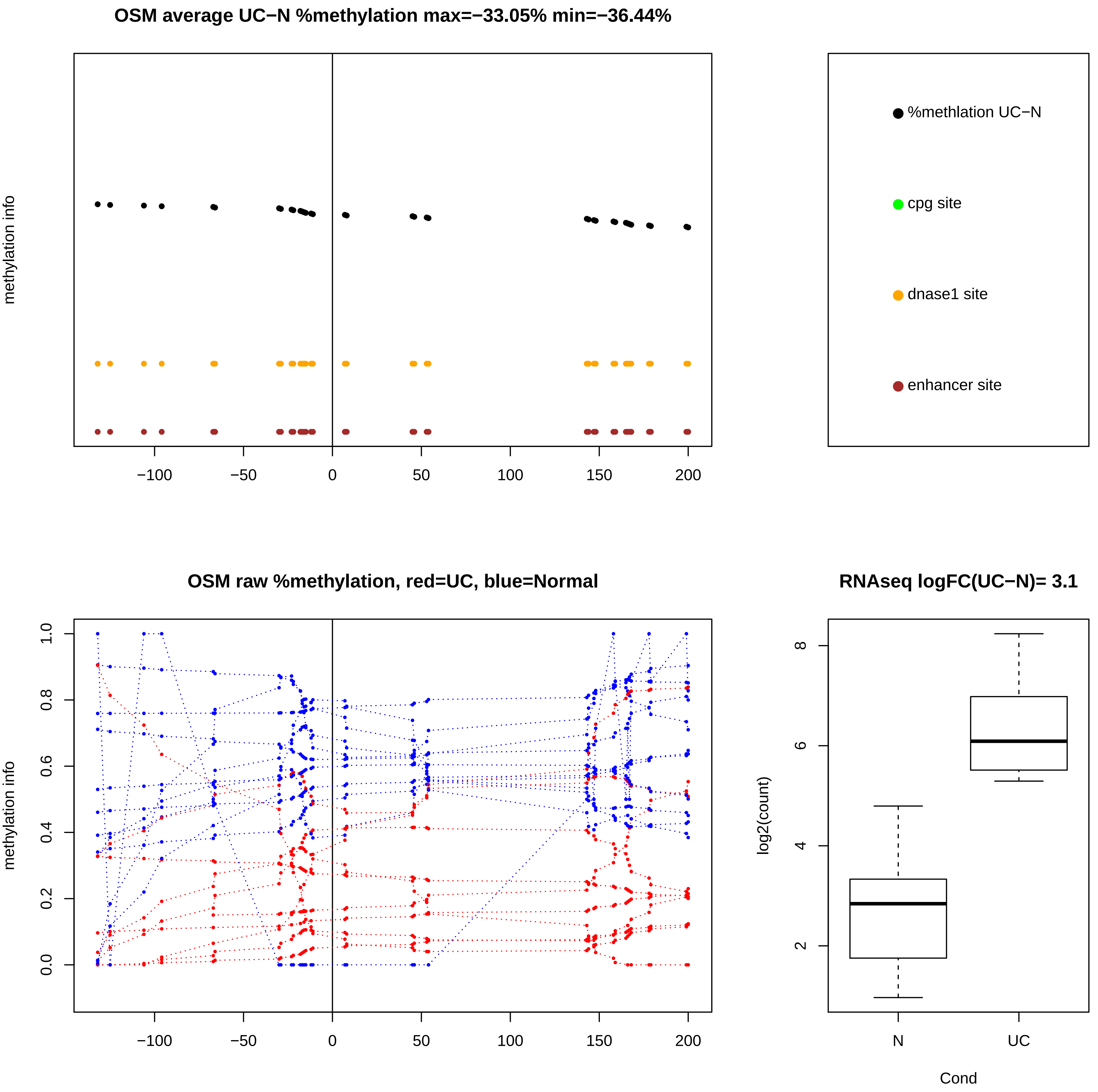
OAS2 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.43


OLFM4 average UC−N %methylation max=−8.74% min=−18.33%

OLFM4 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 3.49

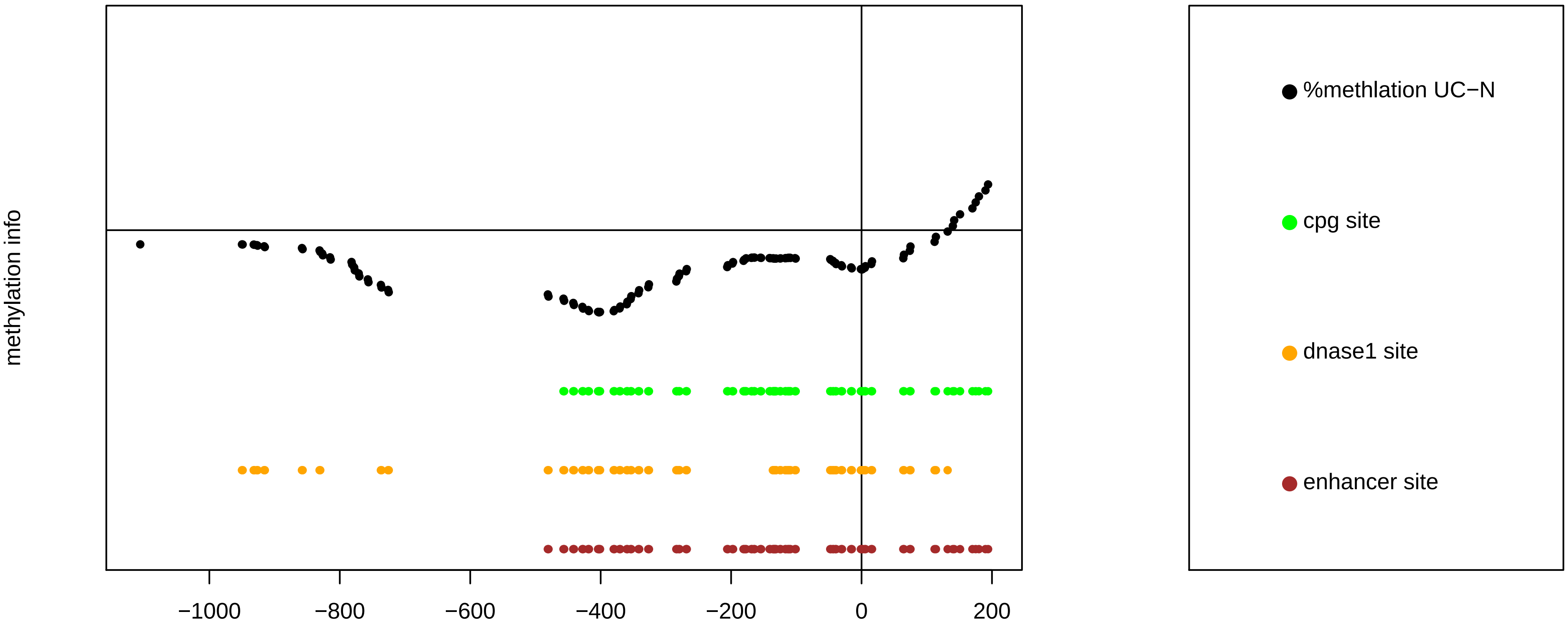


OSM average UC−N %methylation max=−33.05% min=−36.44%

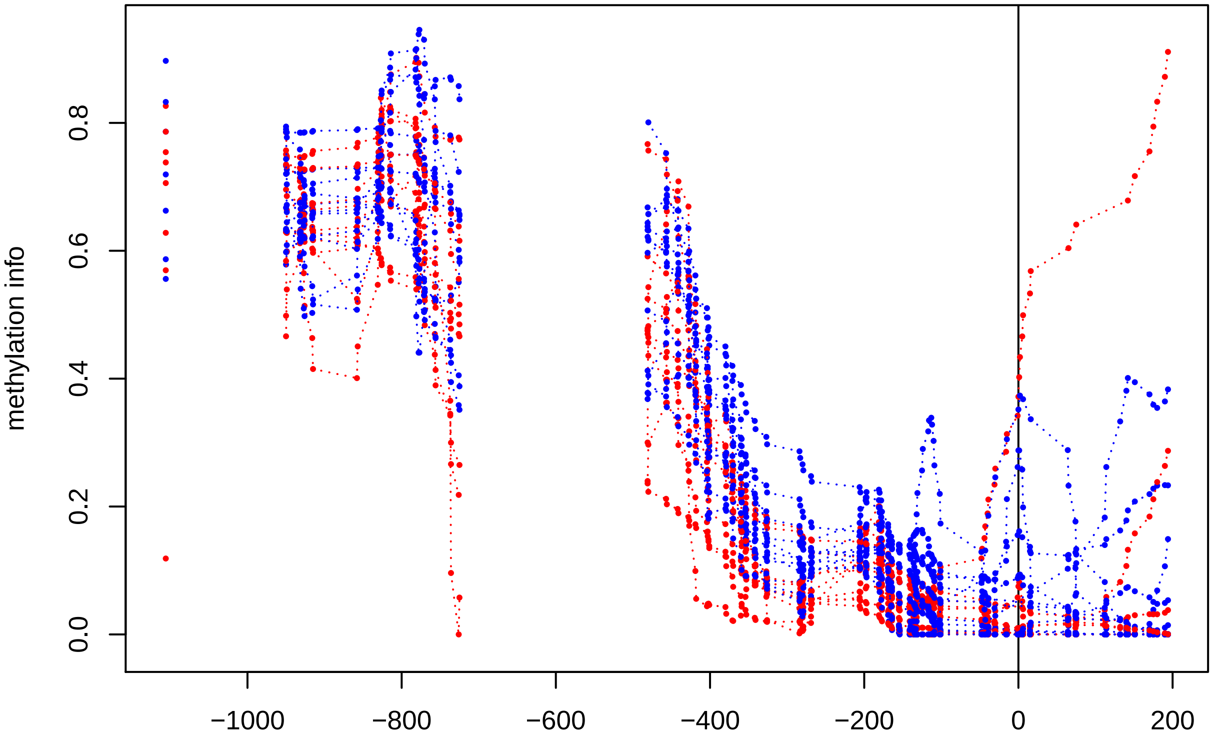
OSM raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 3.1

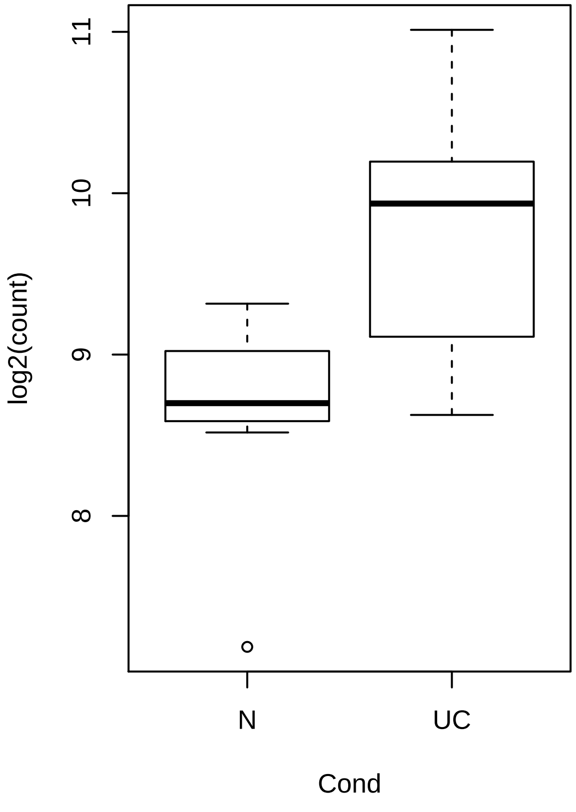
OSMR average UC−N %methylation max=5.8% min=−10.4%



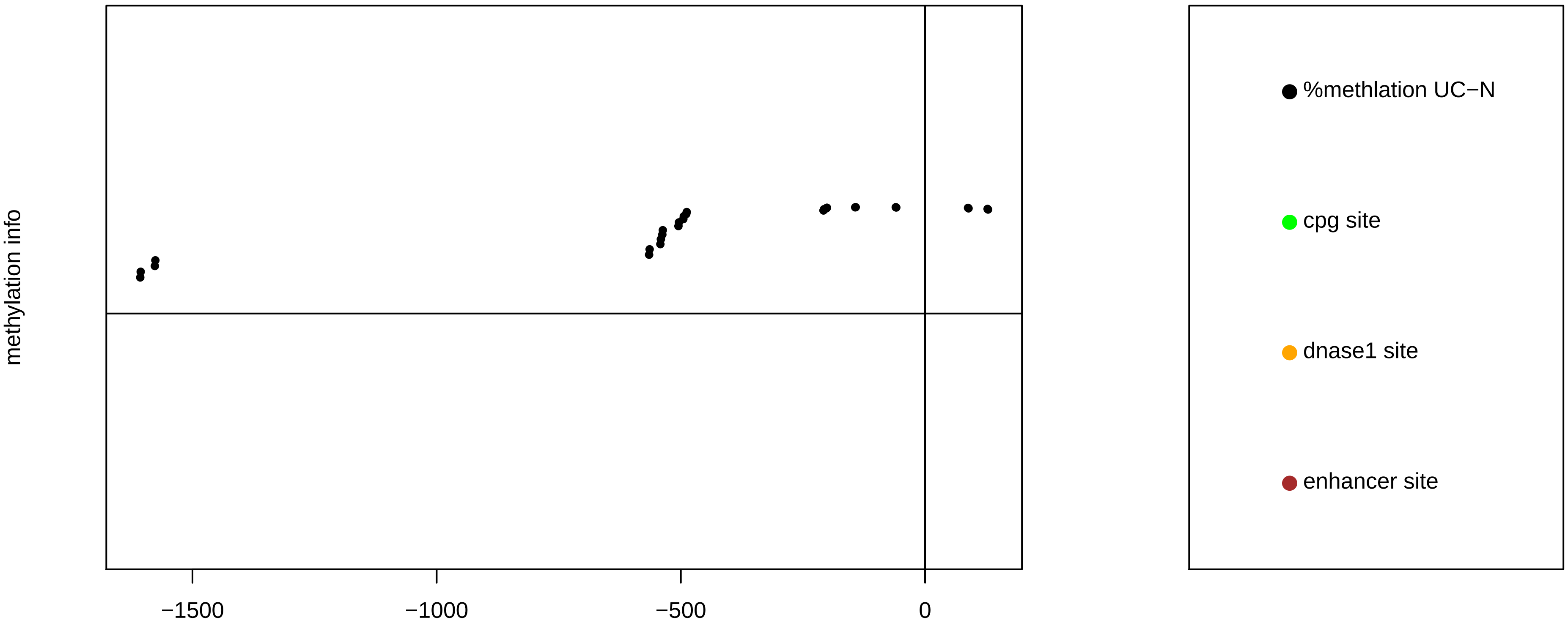
OSMR raw %methylation, red=UC, blue=Normal



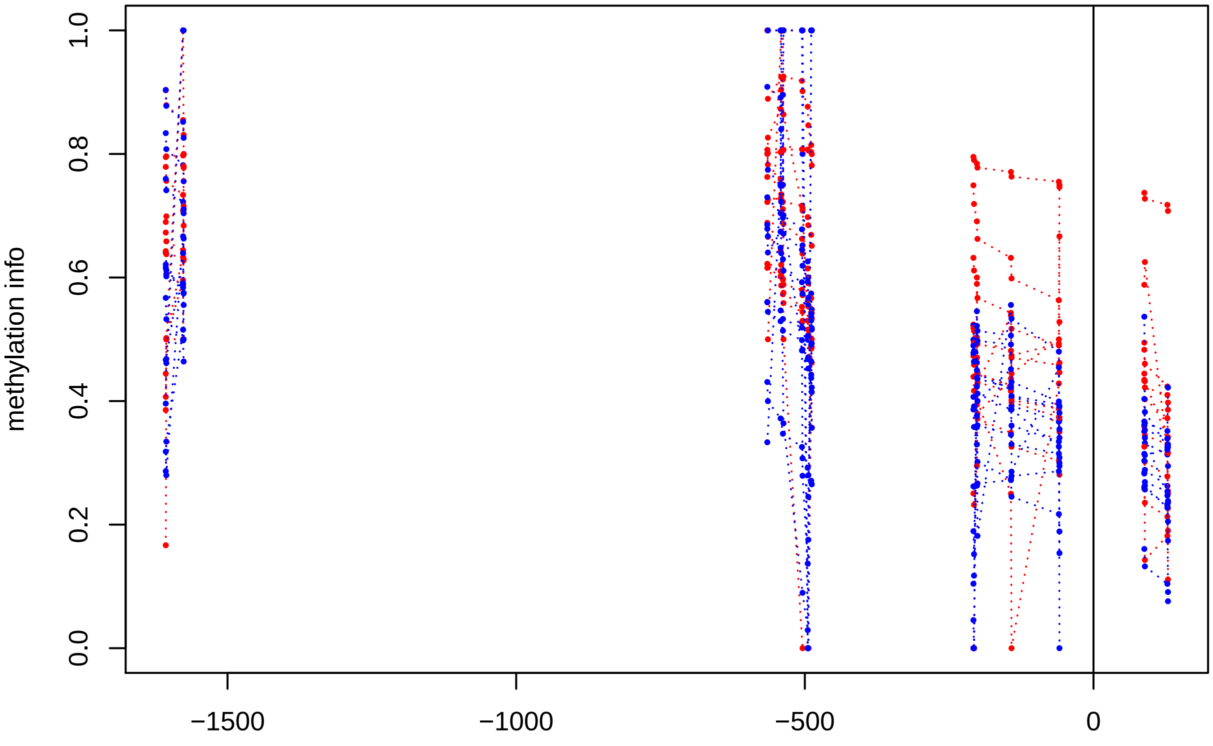
RNAseq logFC(UC−N)= 1.1



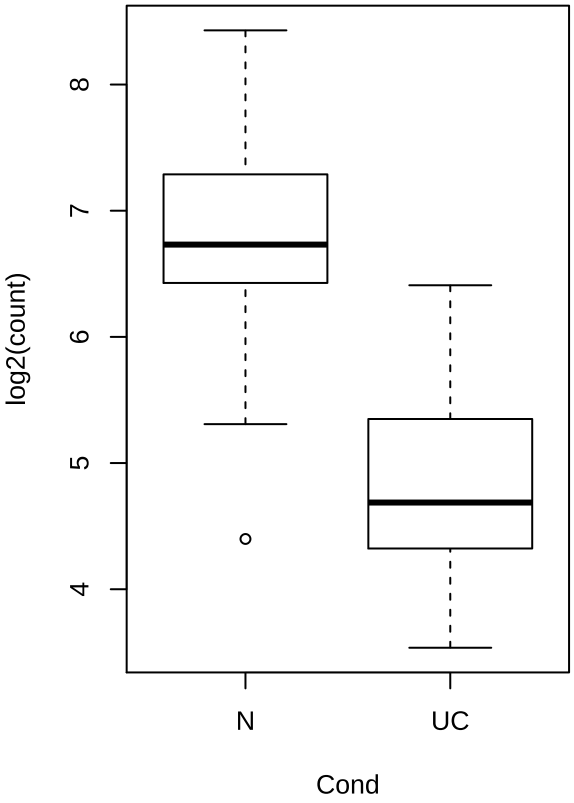
OTC average UC−N %methylation max=11.77% min=3.99%

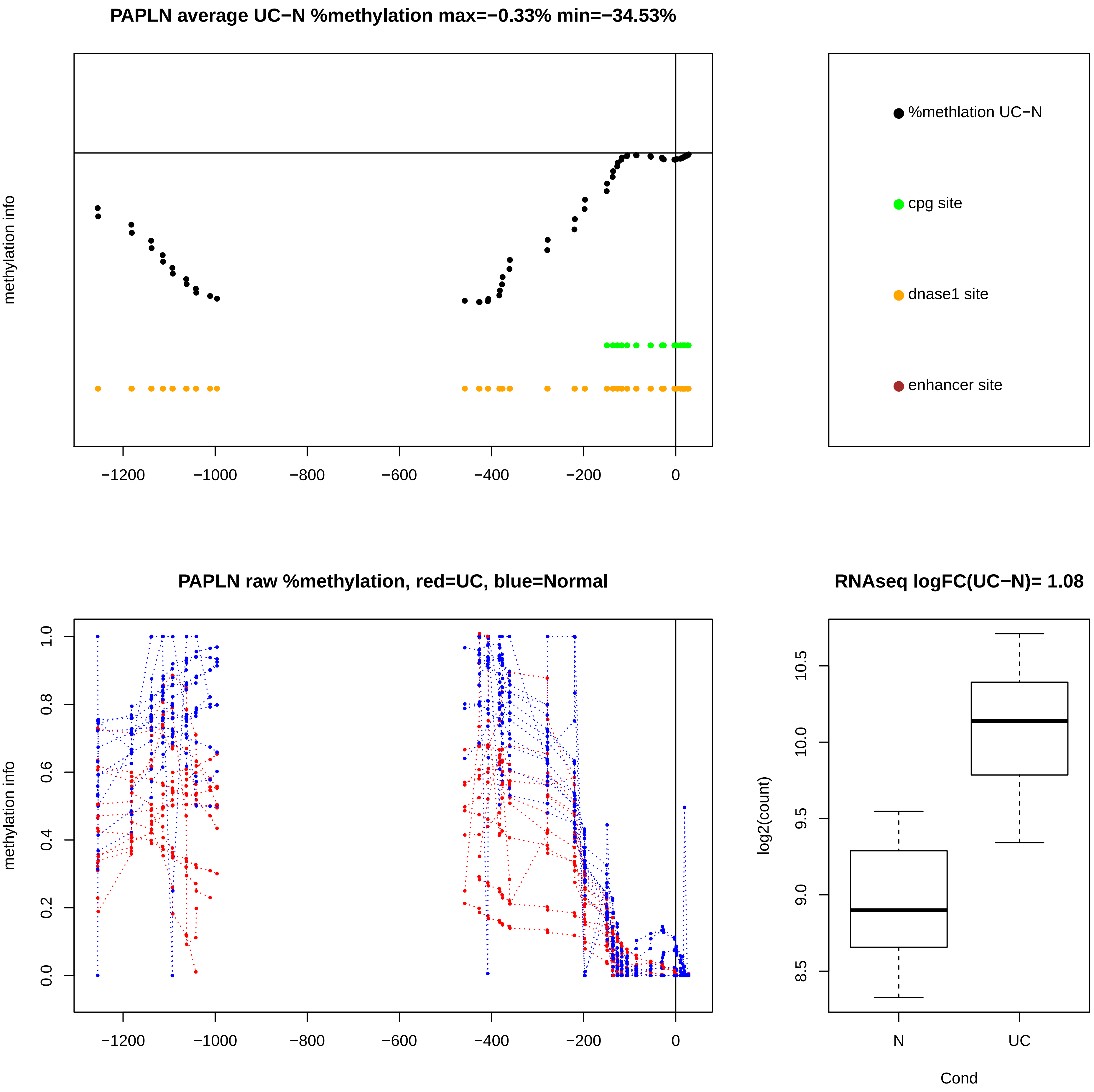


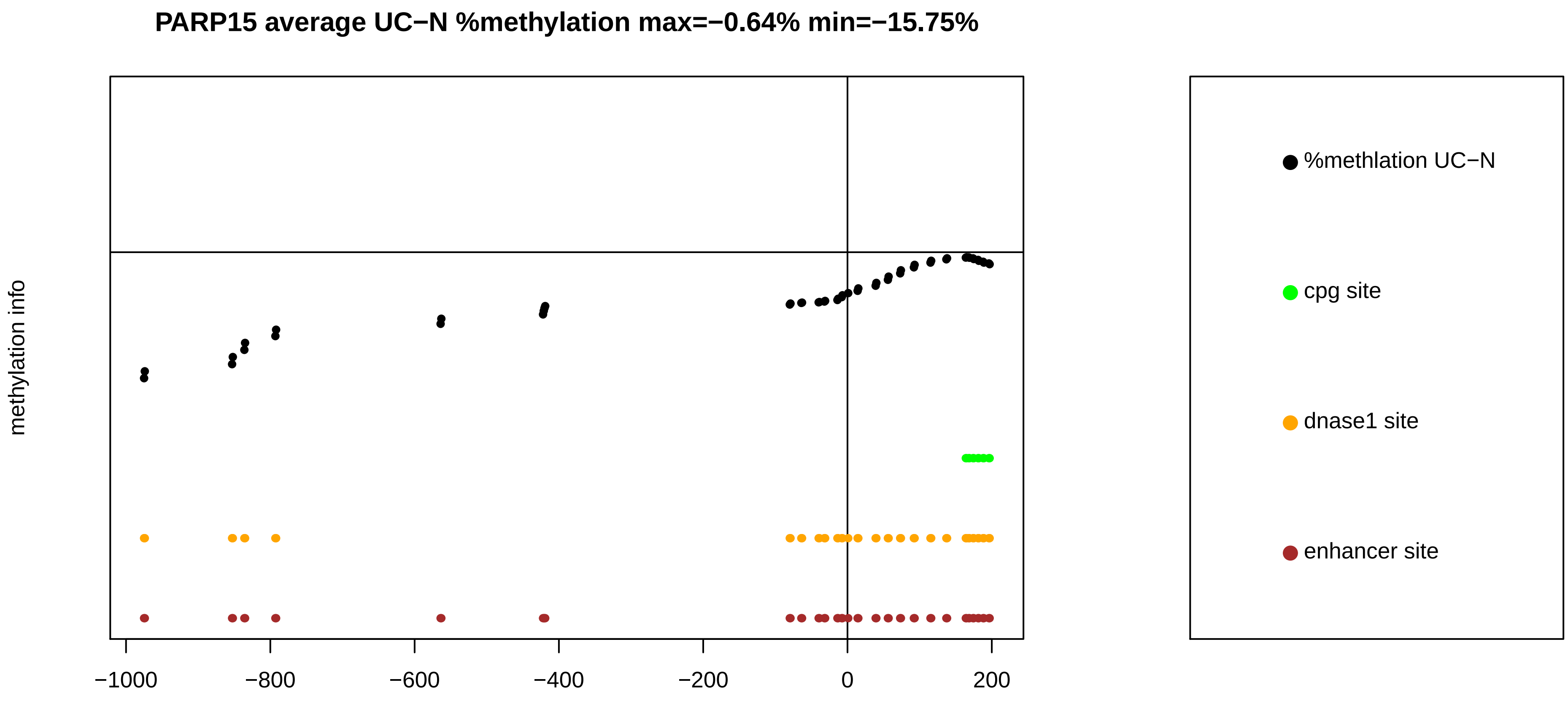
OTC raw %methylation, red=UC, blue=Normal



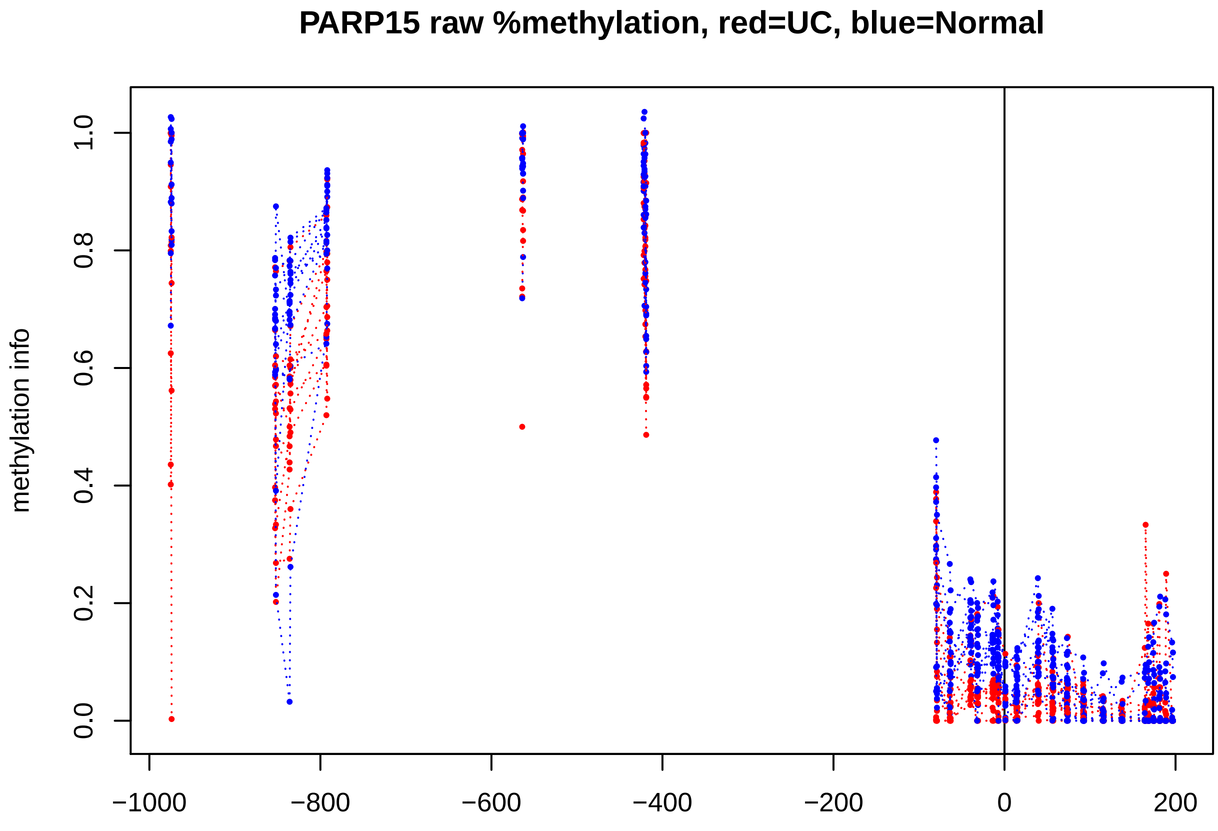
RNAseq logFC(UC−N)= −1.68



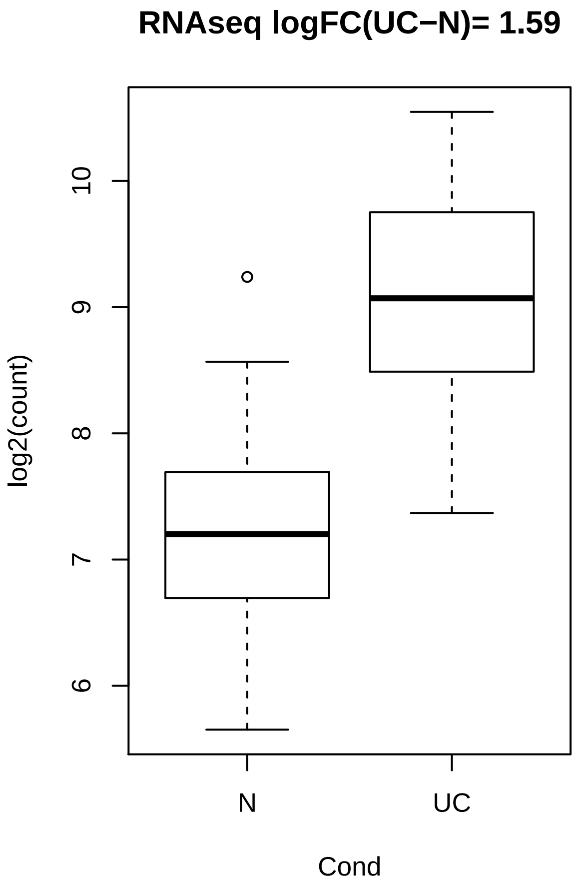

PAPLN average UC−N %methylation max=−0.33% min=−34.53%
methylation info
−1200
−1000
−800
−600
−400
−200
0
%methlation UC−N
cpg site
dnase1 site
enhancer site
PAPLN raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−1200
−1000
−800
−600
−400
−200
0
RNAseq logFC(UC−N)= 1.08
log2(count)
8.5
9.0
9.5
10.0
10.5
N
UC
Cond



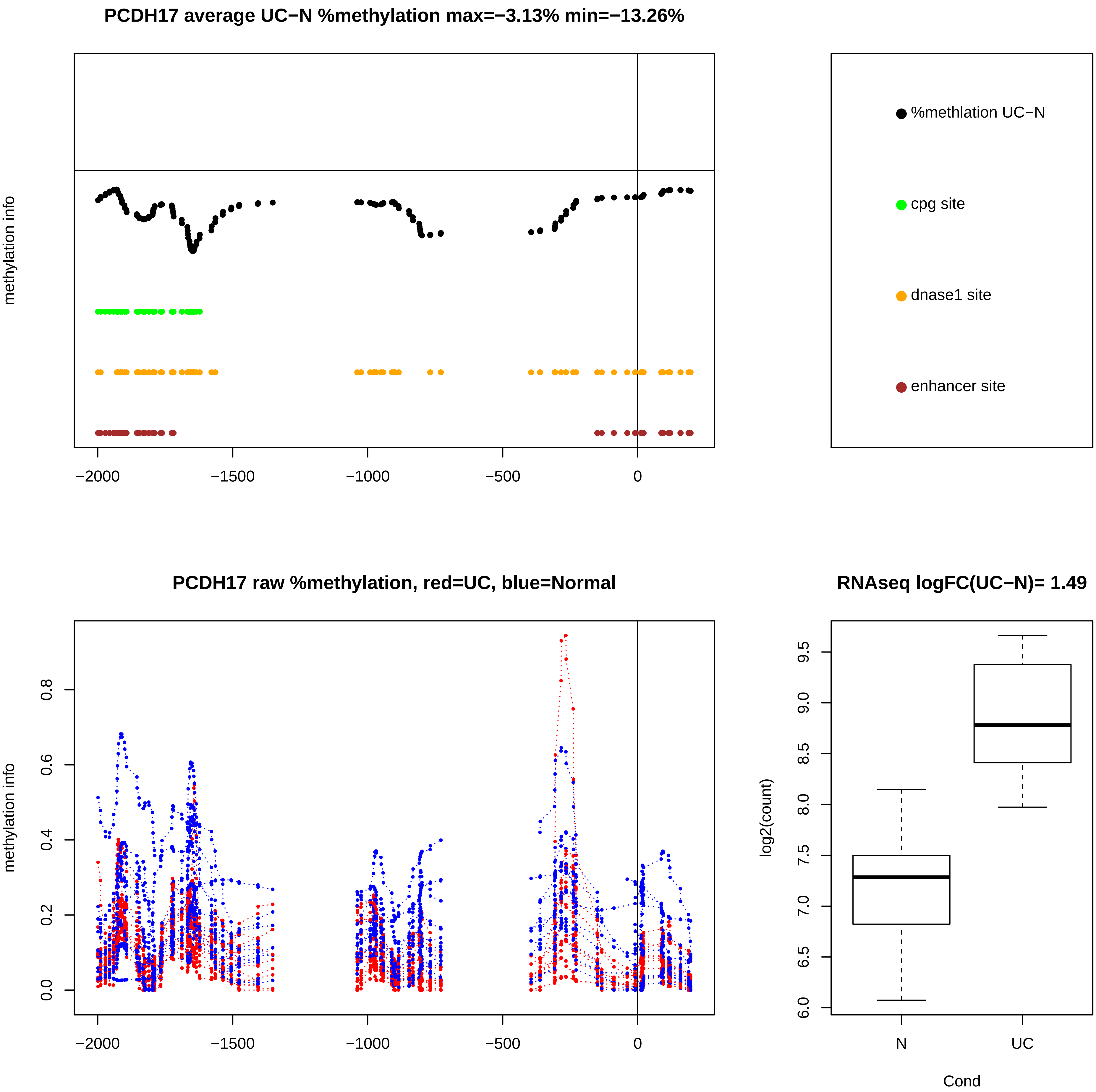
PARP15 average UC−N %methylation max=−0.64% min=−15.75%



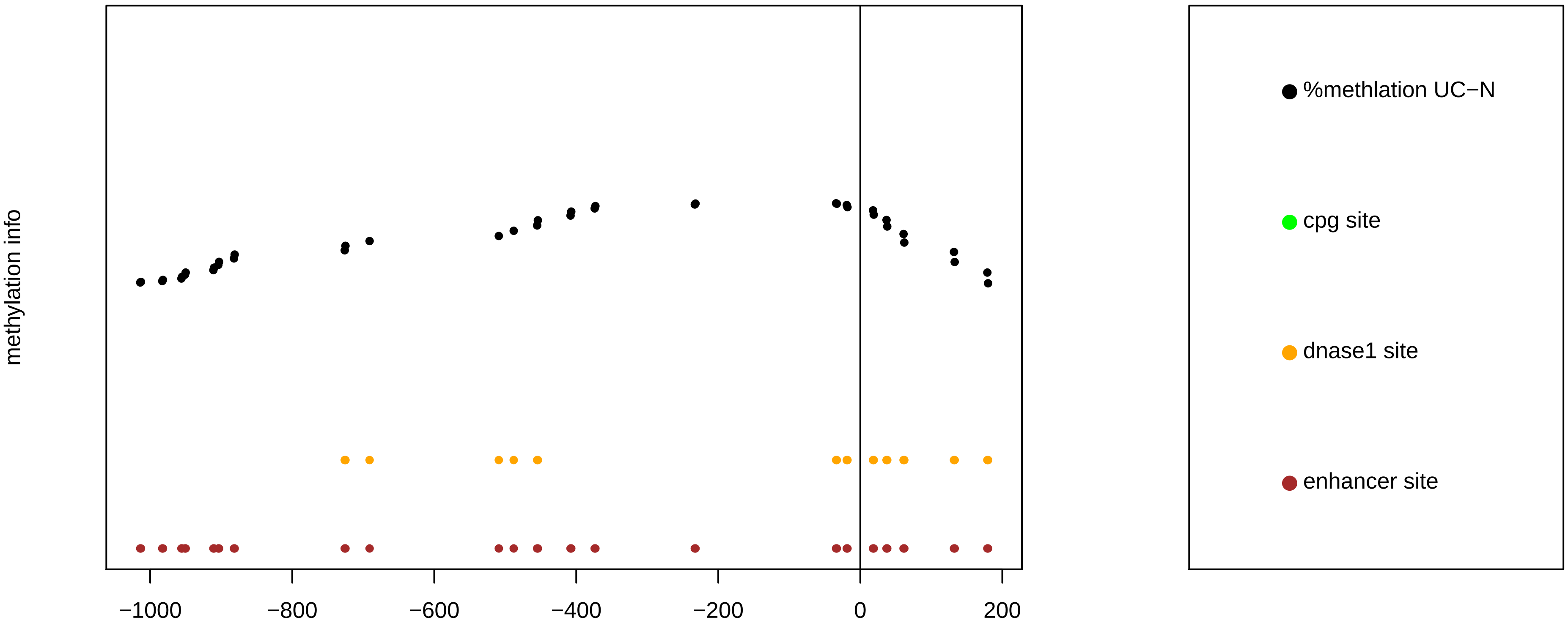
PARP15 raw %methylation, red=UC, blue=Normal



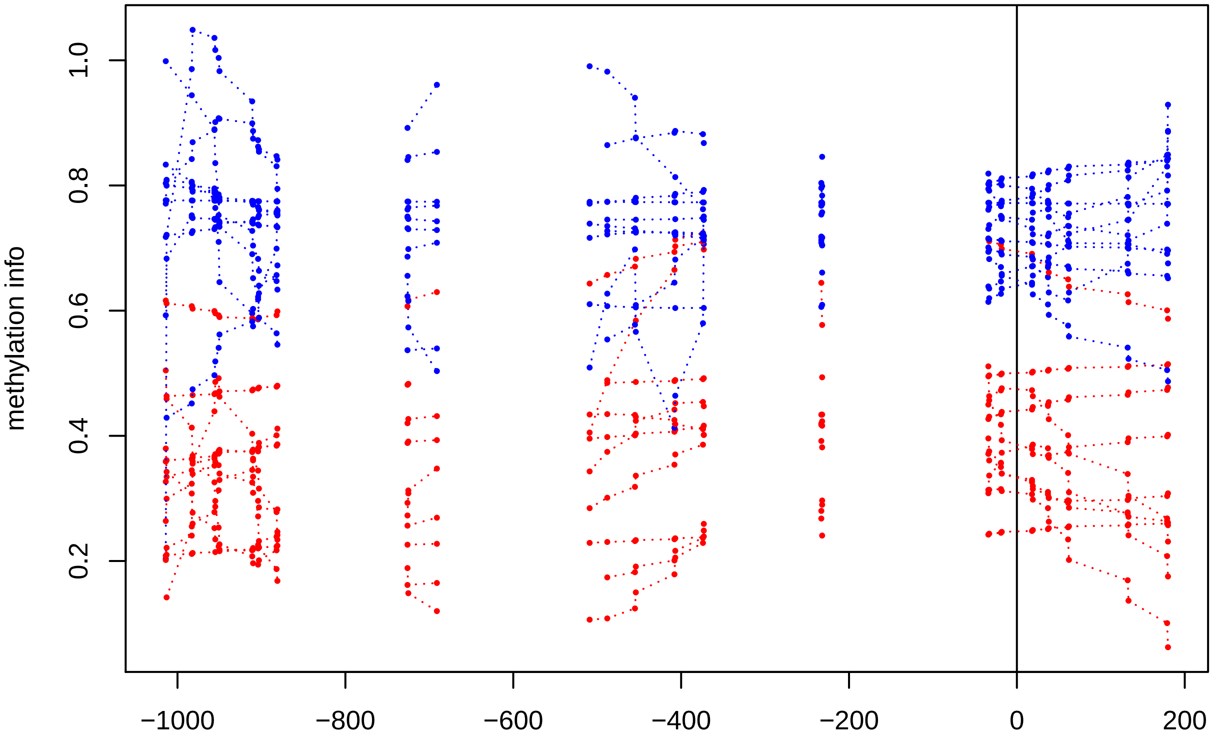
RNAseq logFC(UC−N)= 1.59


PCDH17 average UC−N %methylation max=−3.13% min=−13.26%
methylation info
−2000
−1500
−1000
−500
0
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
PCDH17 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
−2000
−1500
−1000
−500
0
RNAseq logFC(UC−N)= 1.49
log2(count)
6.0
6.5
7.0
7.5
8.0
8.5
9.0
9.5
N
UC
Cond

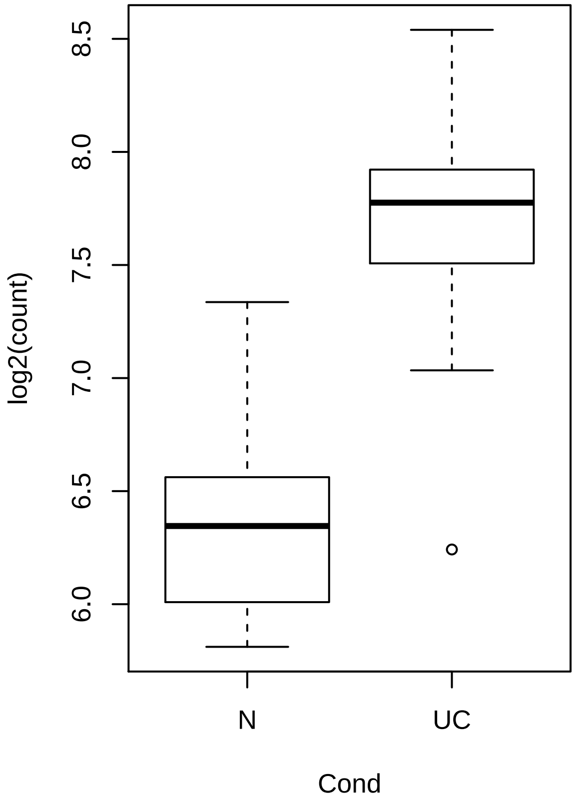
PCED1B average UC−N %methylation max=−31.56% min=−40.61%

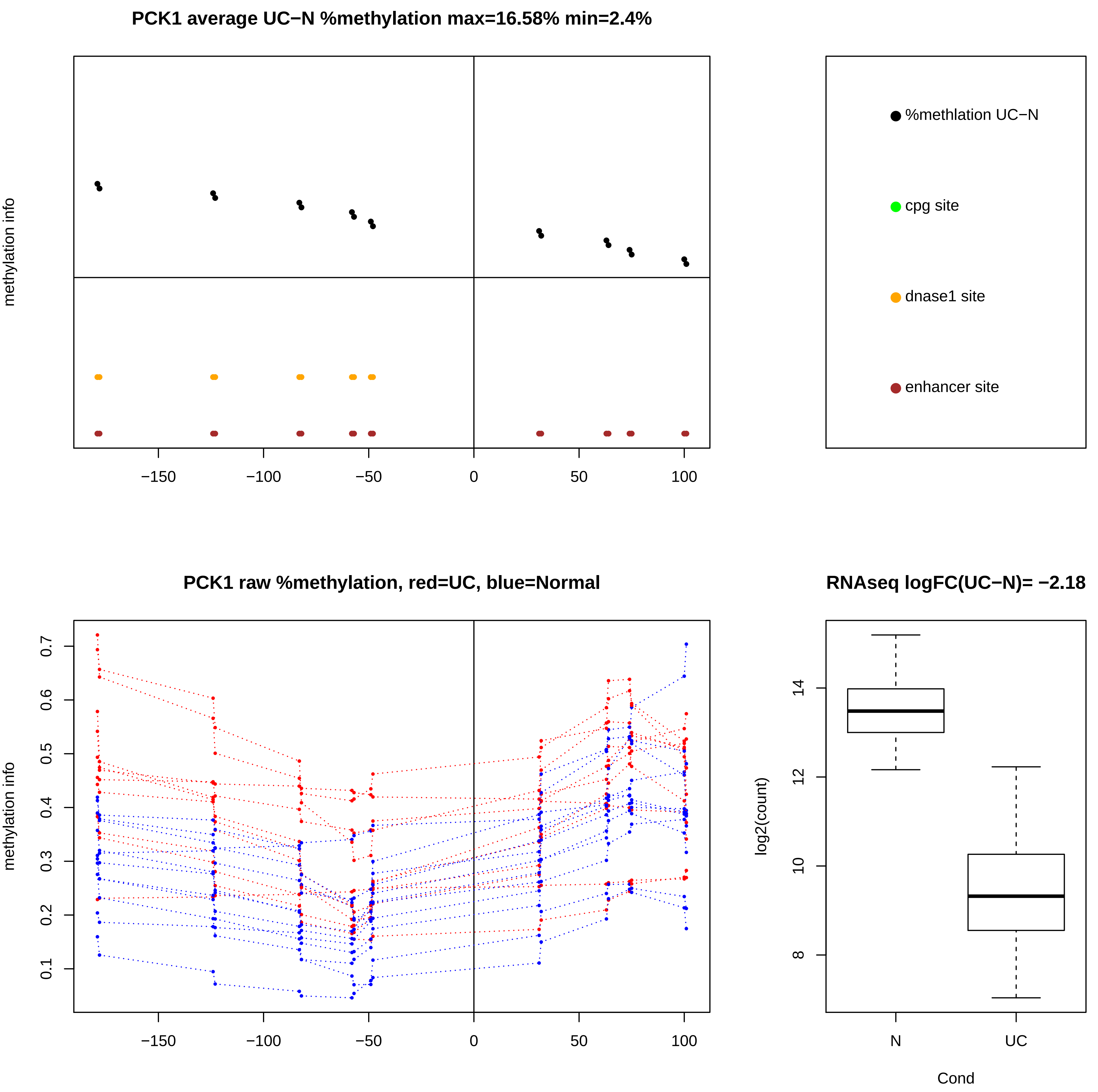


PCED1B raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 1.25

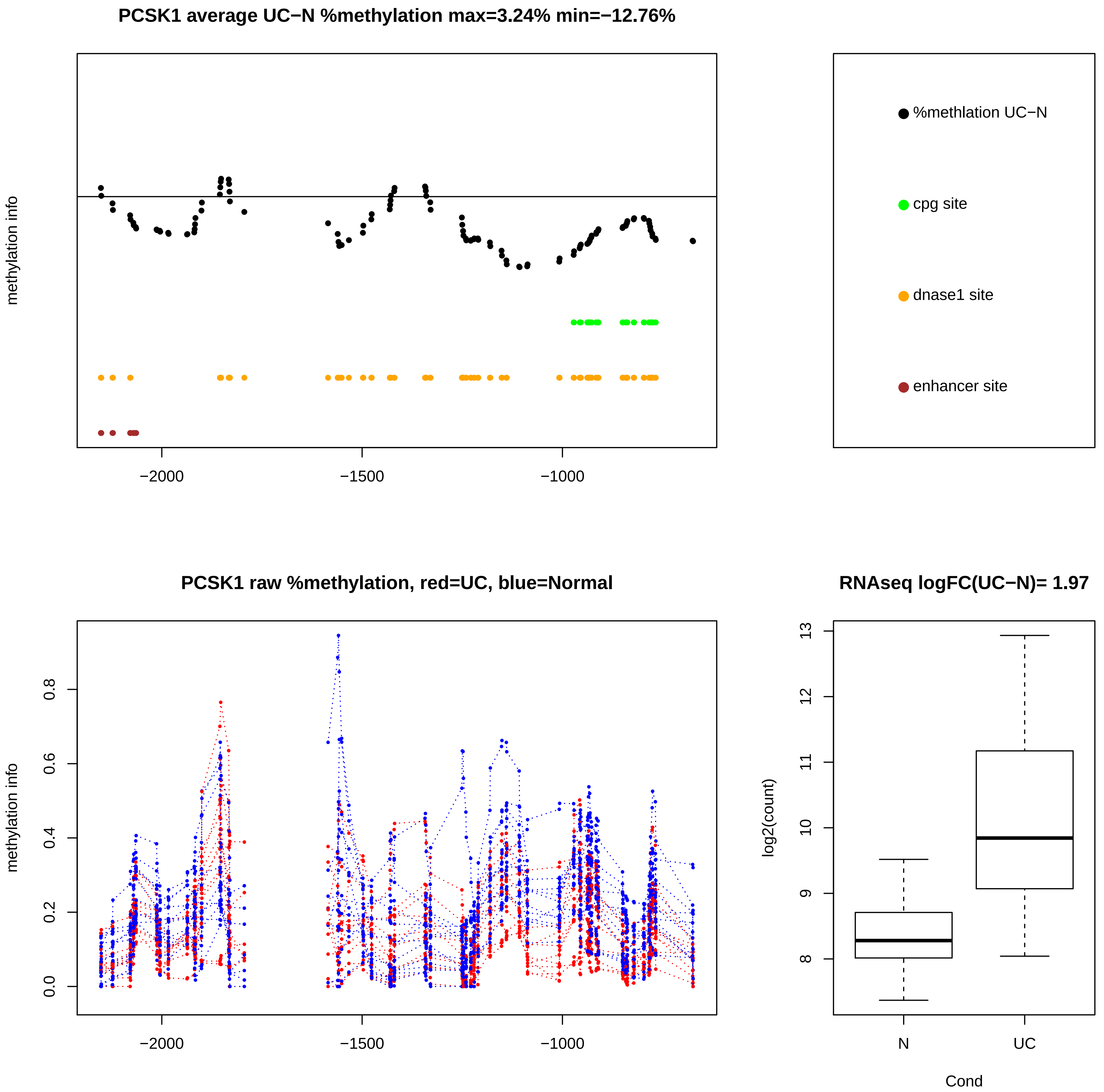


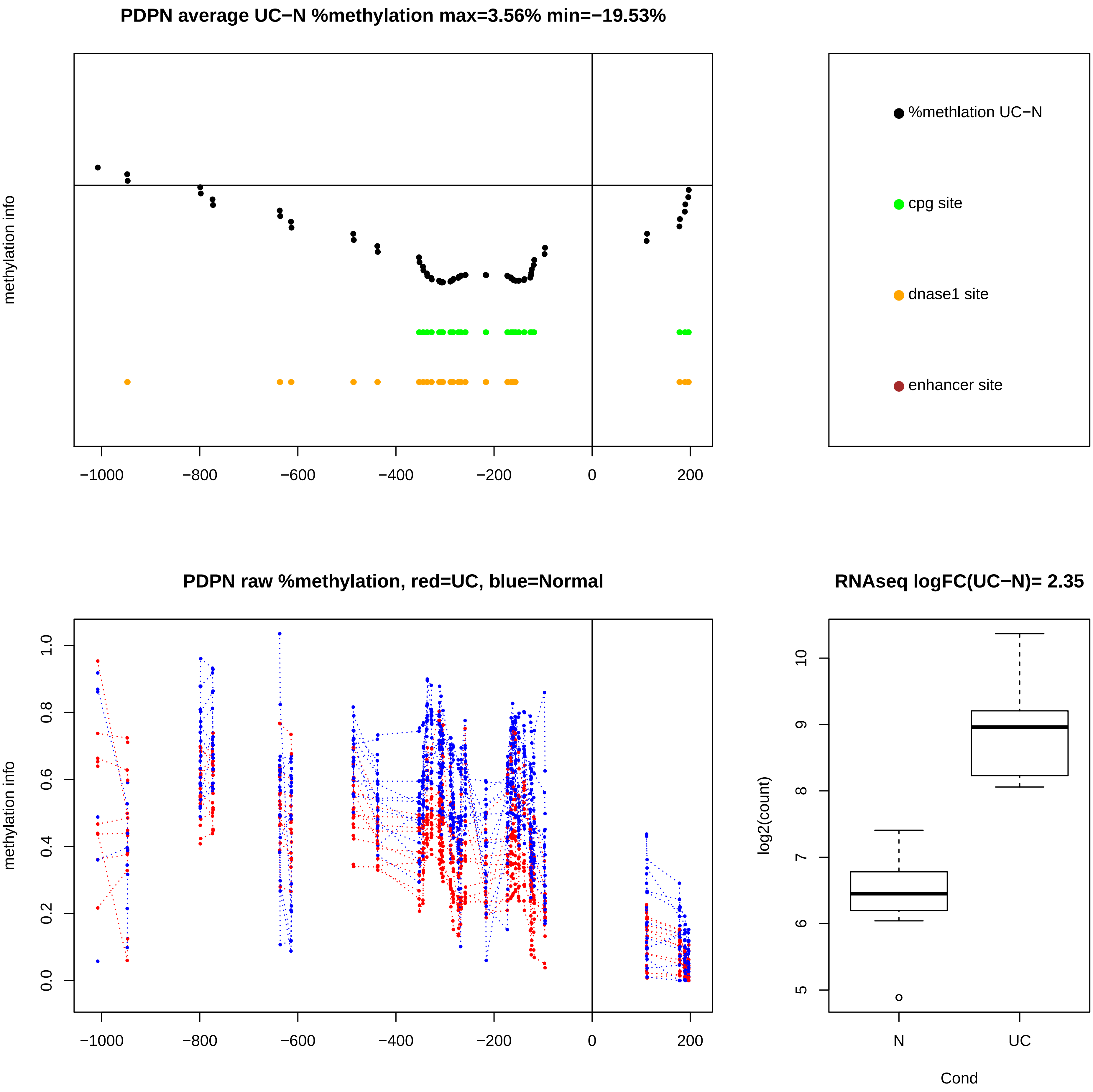


PCK1 average UC−N %methylation max=16.58% min=2.4%

PCK1 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= −2.18


PCSK1 average UC−N %methylation max=3.24% min=−12.76%
methylation info
−2000
−1500
−1000
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
PCSK1 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
−2000
−1500
−1000
RNAseq logFC(UC−N)= 1.97
log2(count)
8
9
10
11
12
13
N
UC
Cond

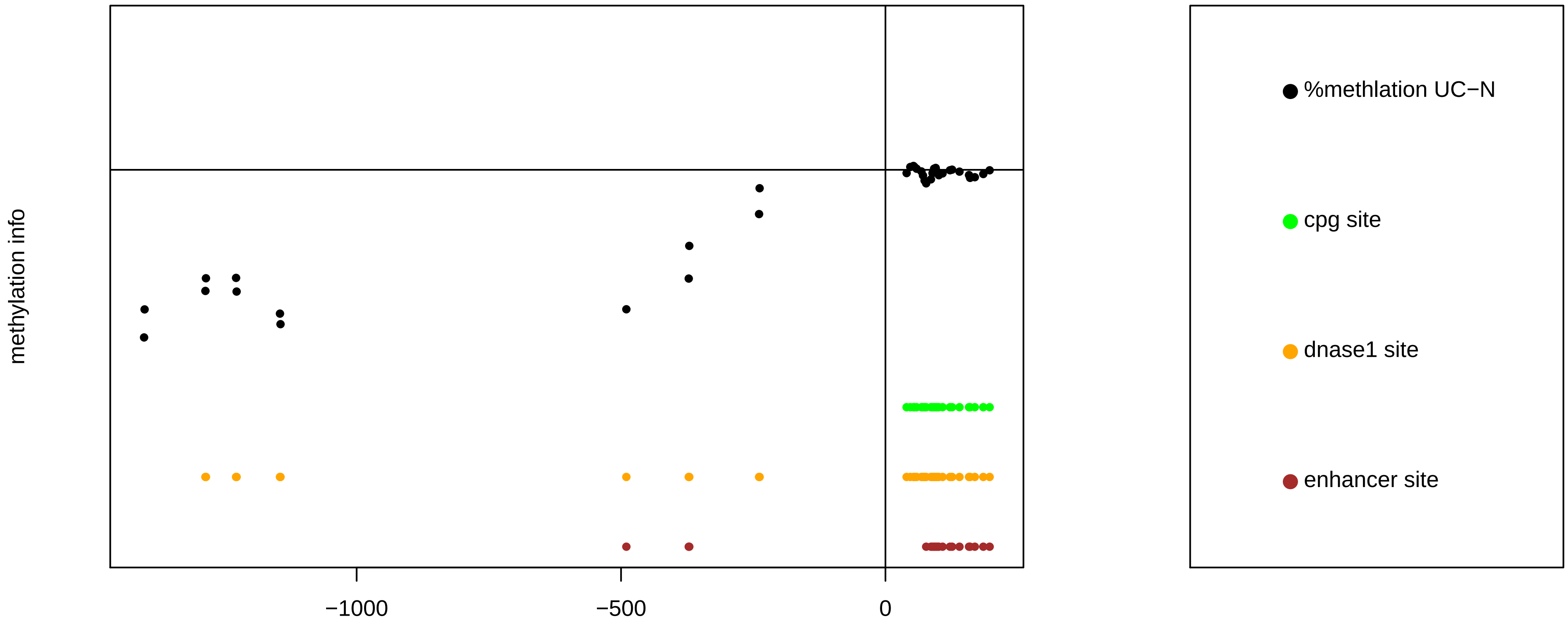


PDPN average UC−N %methylation max=3.56% min=−19.53%

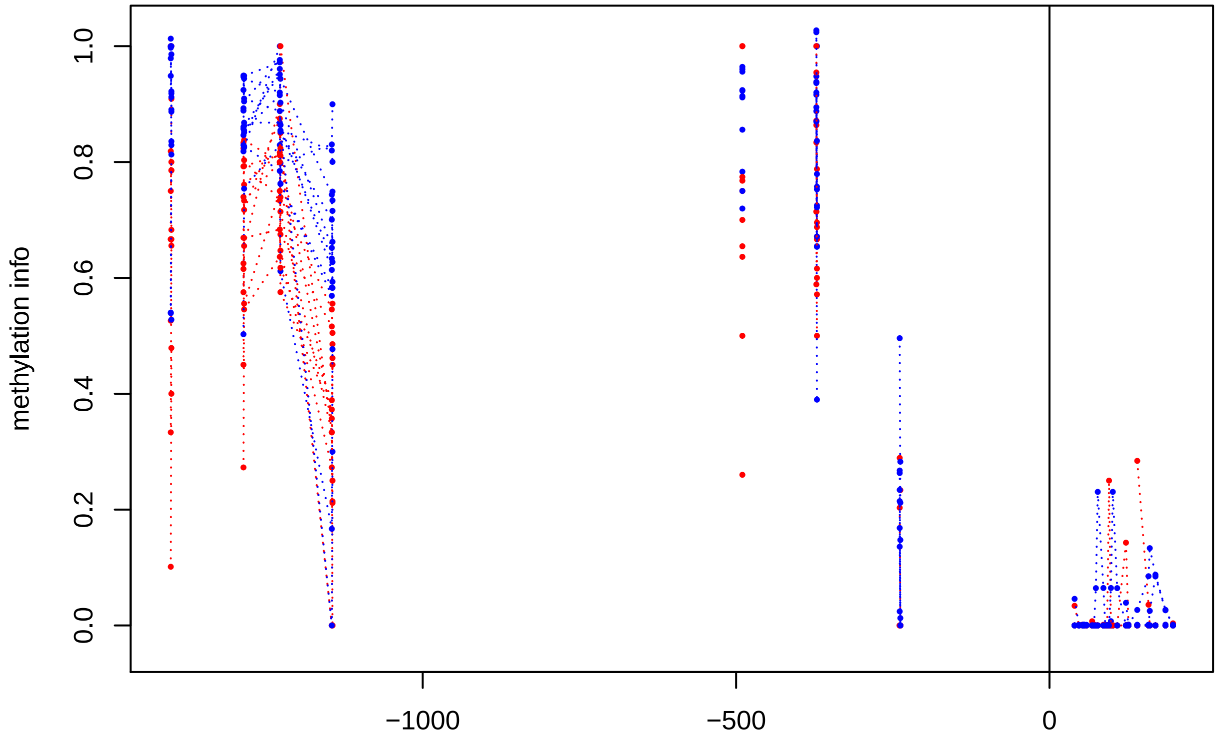
PDPN raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 2.35

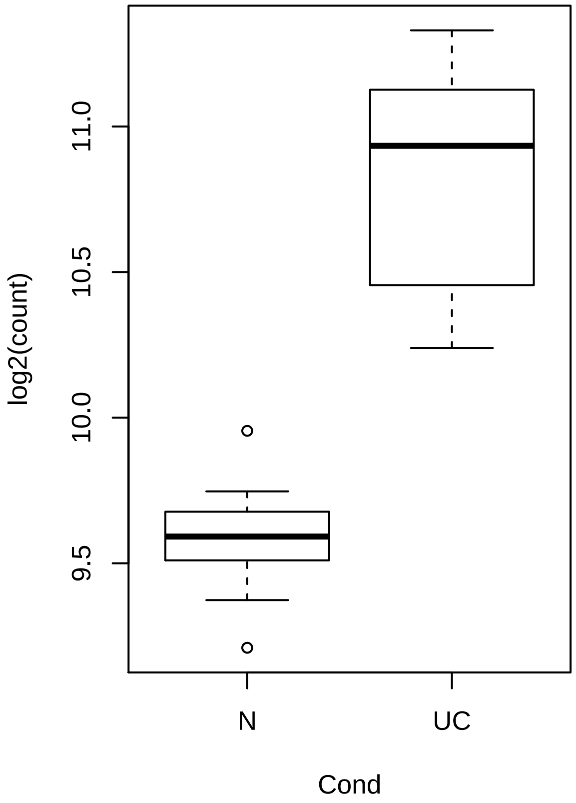
PEA15 average UC−N %methylation max=0.56% min=−24.03%

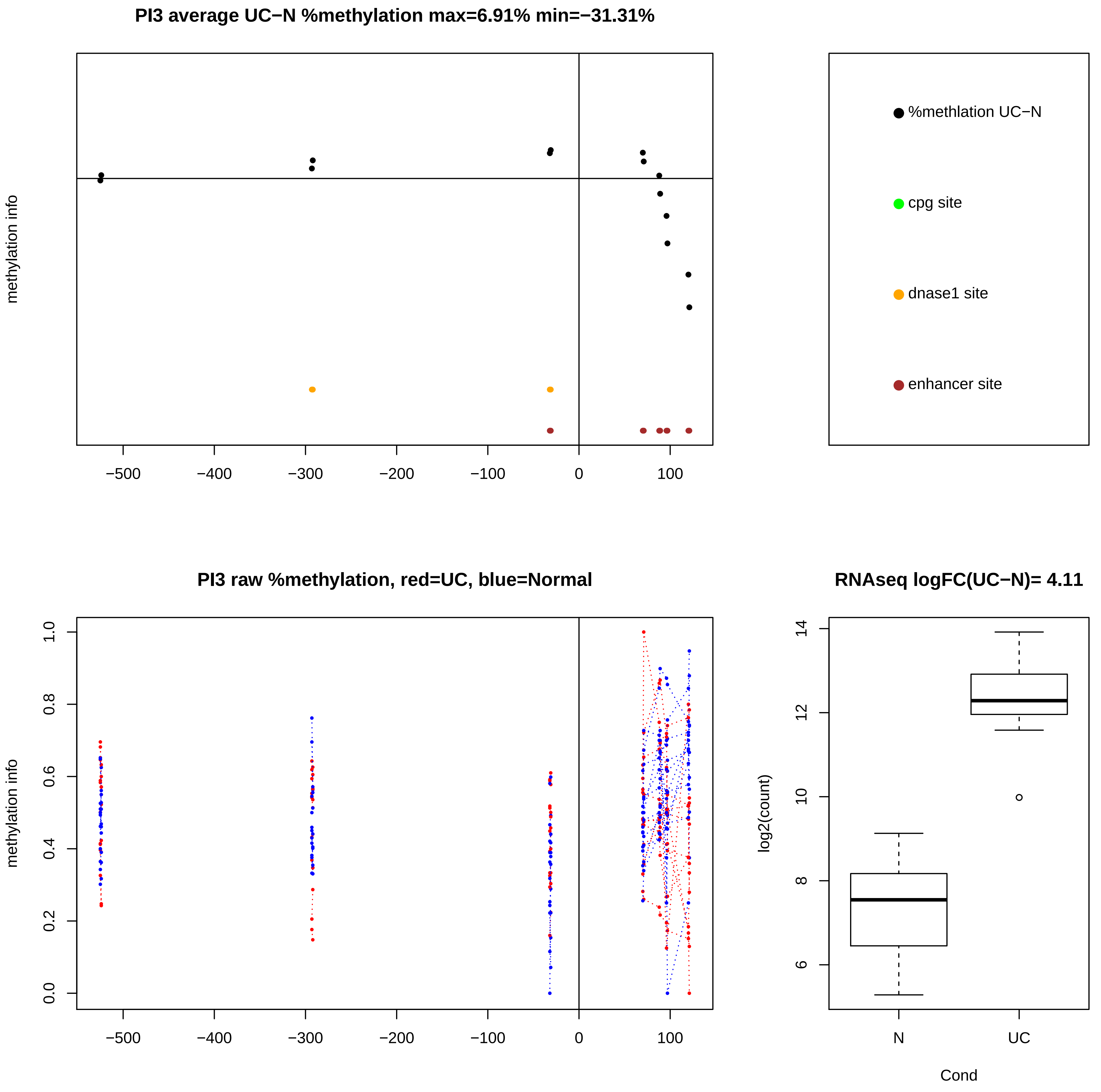


PEA15 raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 1.17

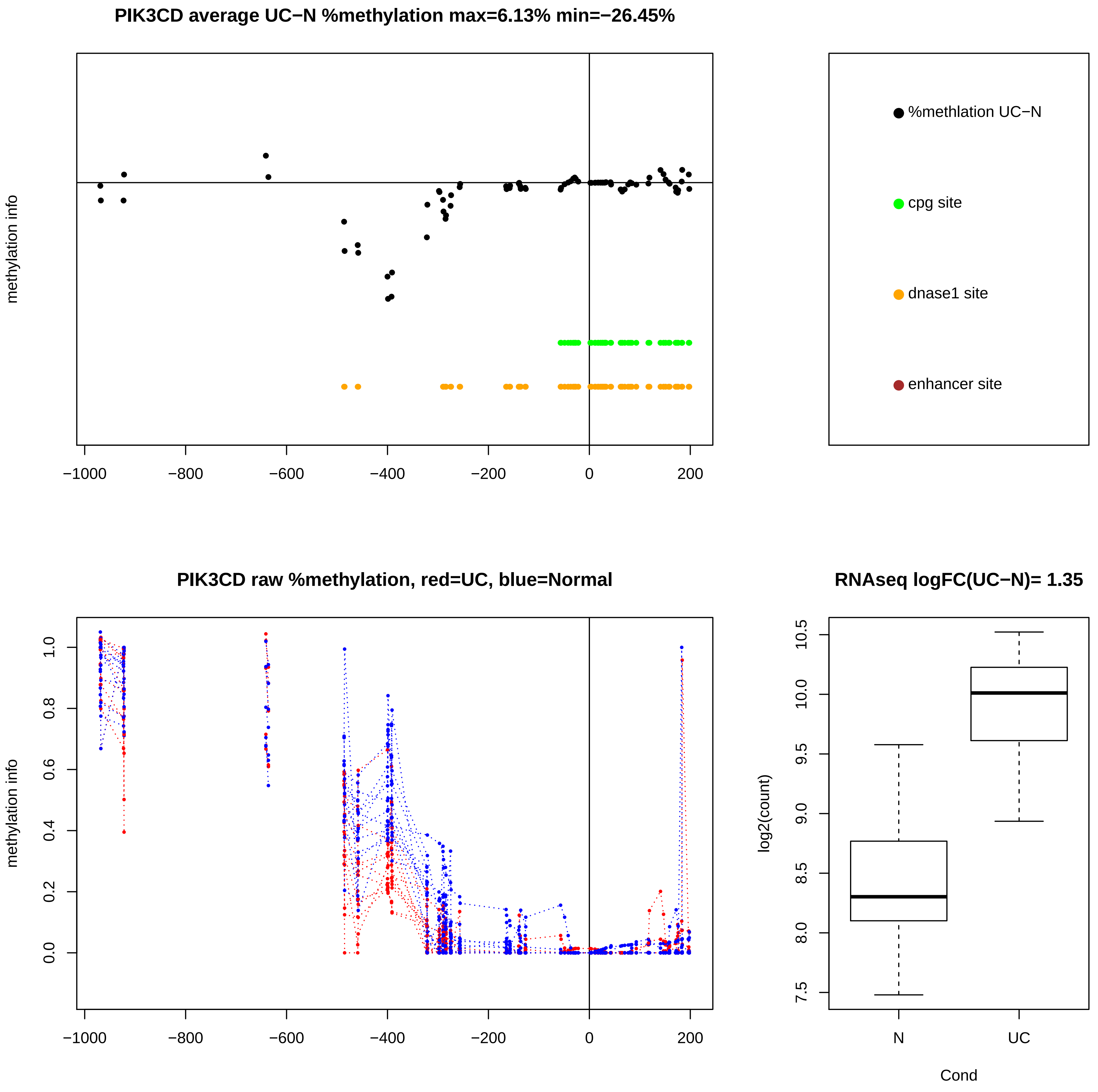


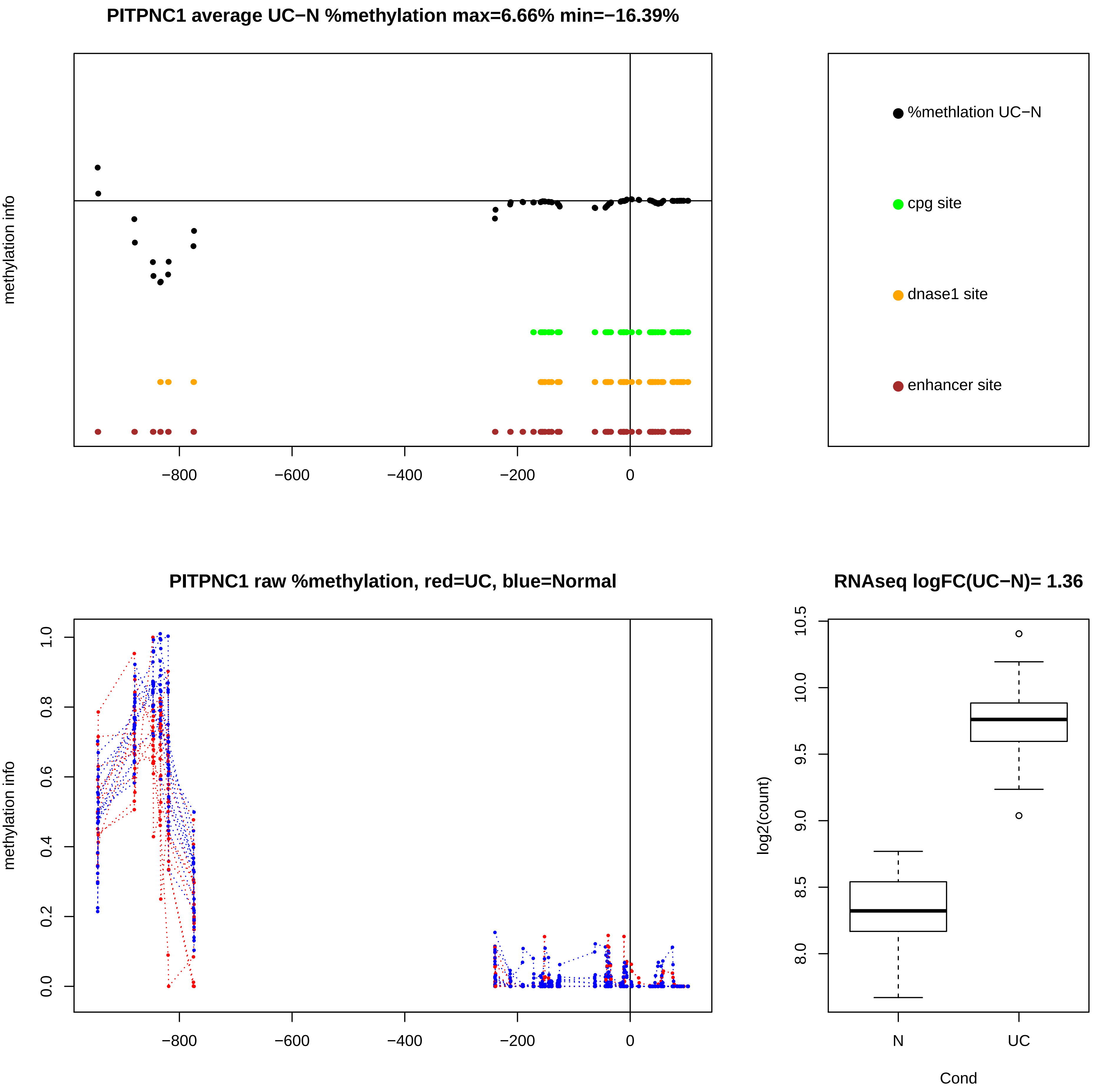


PI3 average UC−N %methylation max=6.91% min=−31.31%

PI3 raw %methylation, red=UC, blue=Normal

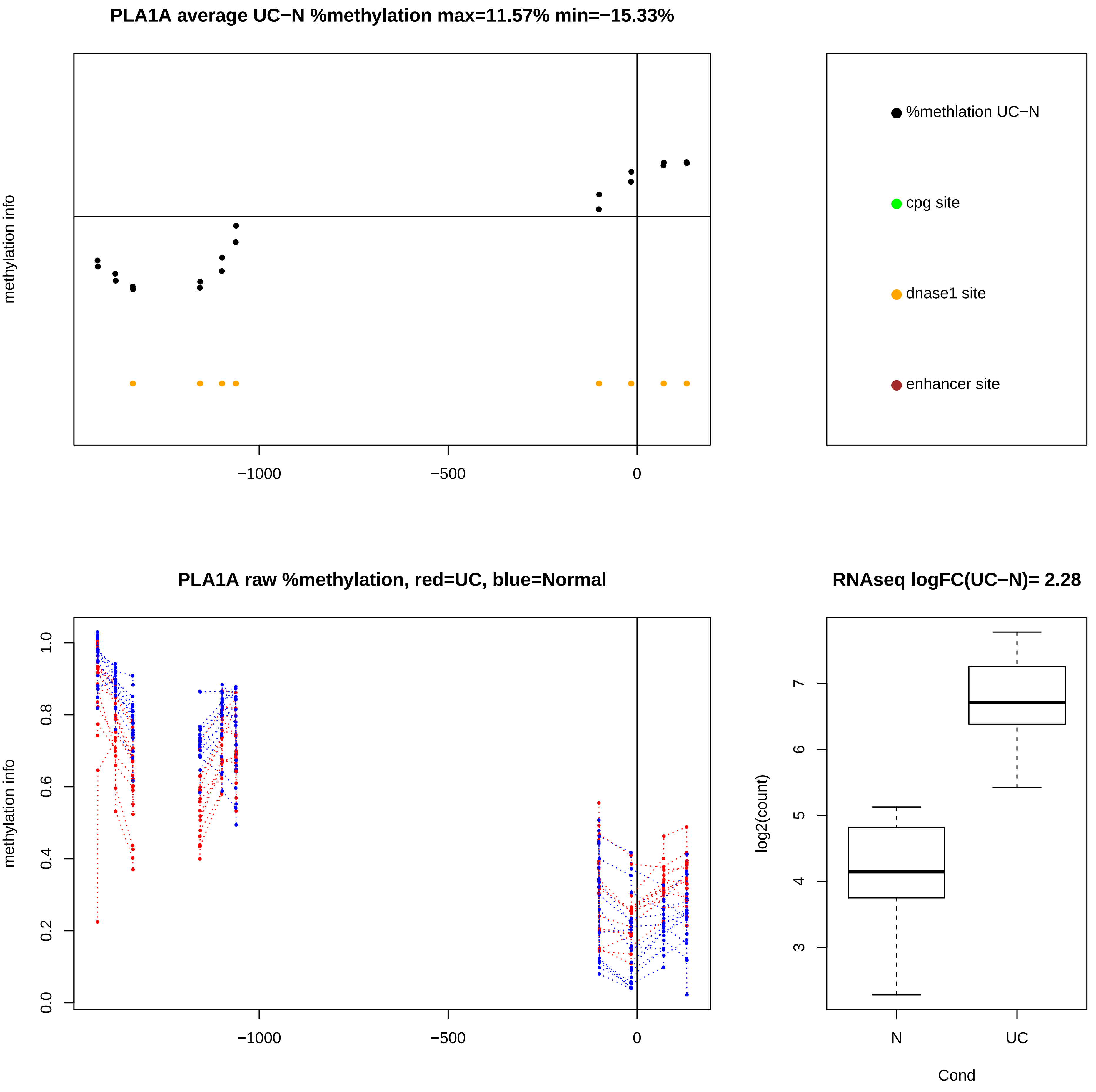
RNAseq logFC(UC−N)= 4.11

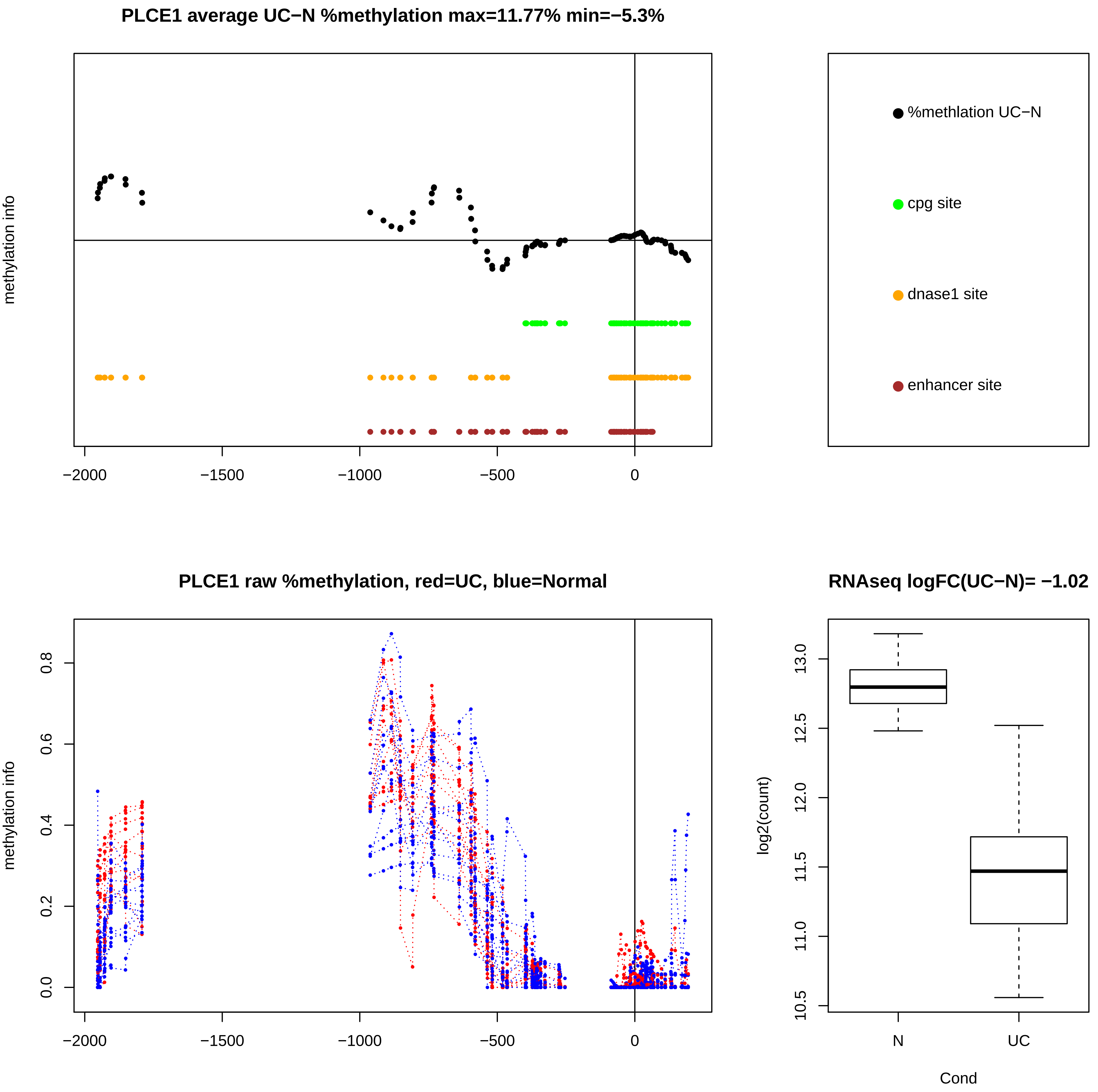

PIK3CD average UC−N %methylation max=6.13% min=−26.45%
methylation info
−1000
−800
−600
−400
−200
0
200
%methlation UC−N
cpg site
dnase1 site
enhancer site
PIK3CD raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−1000
−800
−600
−400
−200
0
200
RNAseq logFC(UC−N)= 1.35
log2(count)
7.5
8.0
8.5
9.0
9.5
10.0
10.5
N
UC
Cond

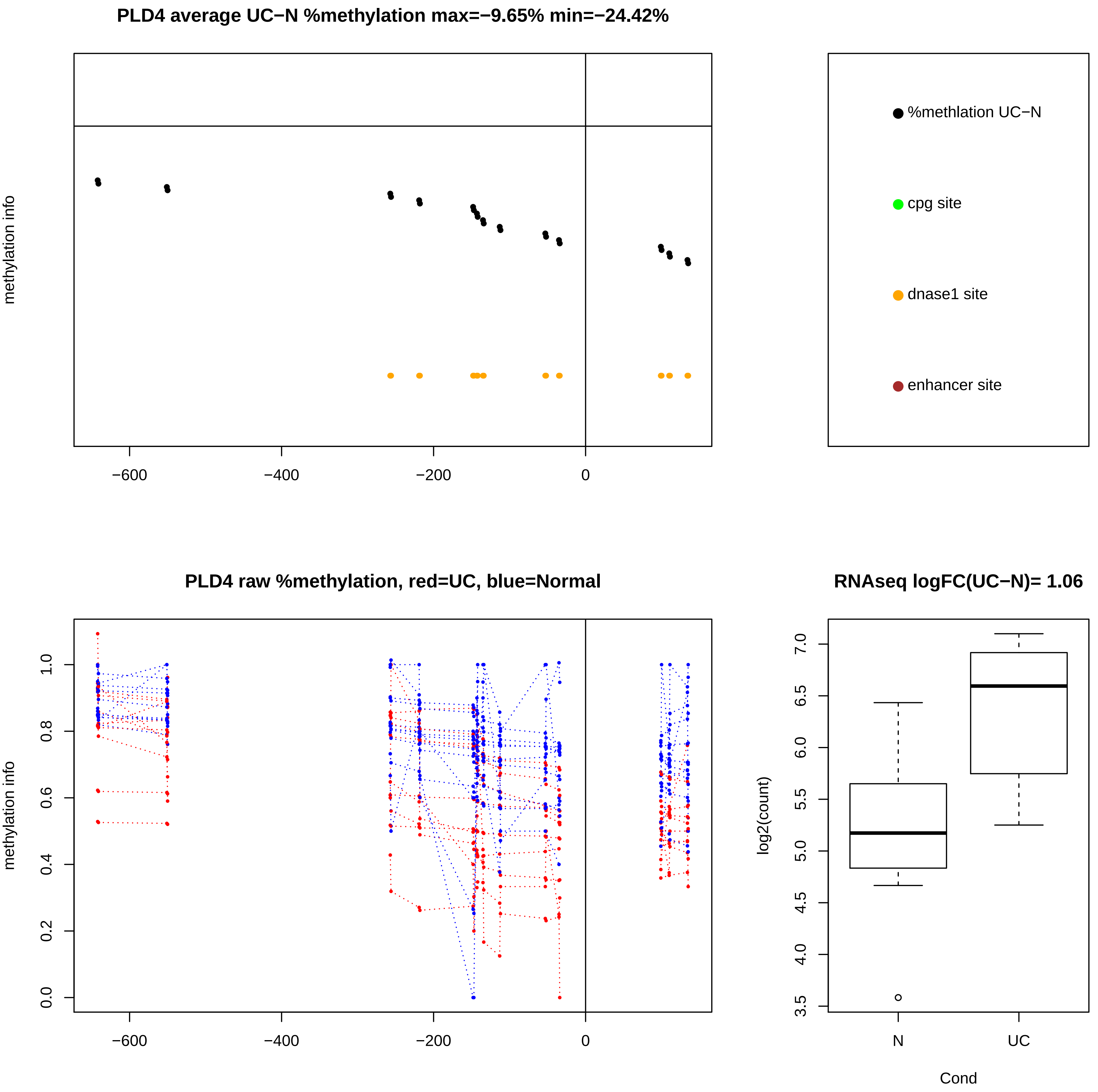

PITPNC1 average UC−N %methylation max=6.66% min=−16.39%

PITPNC1 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.36


PLA1A average UC−N %methylation max=11.57% min=−15.33%
methylation info
−1000
−500
0
%methlation UC−N
cpg site
dnase1 site
enhancer site
PLA1A raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−1000
−500
0
RNAseq logFC(UC−N)= 2.28
log2(count)
3
4
5
6
7
N
UC
Cond

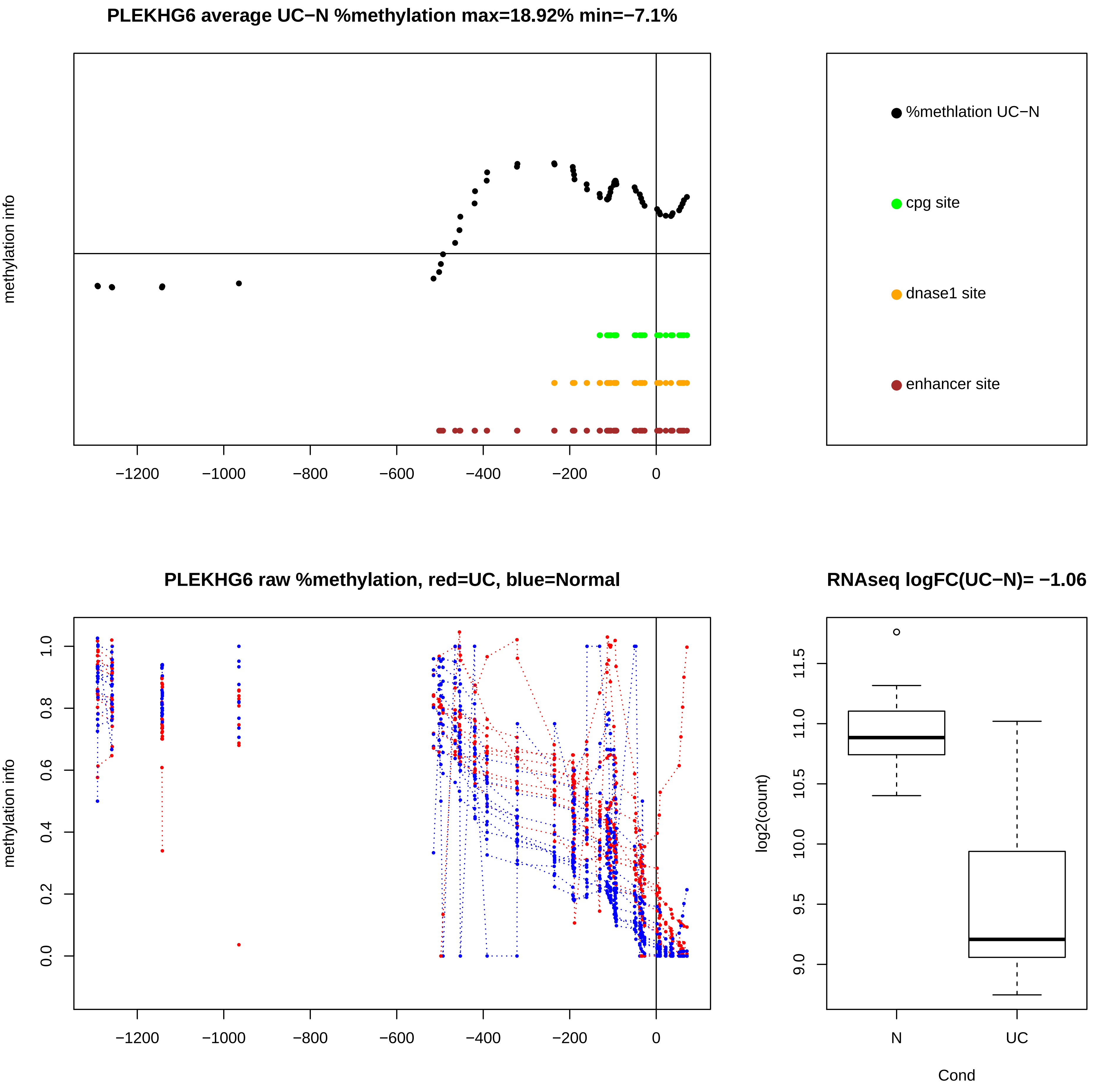

PLCE1 average UC−N %methylation max=11.77% min=−5.3%
methylation info
−2000
−1500
−1000
−500
0
%methlation UC−N
cpg site
dnase1 site
enhancer site
PLCE1 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
−2000
−1500
−1000
−500
0
RNAseq logFC(UC−N)= −1.02
log2(count)
10.5
11.0
11.5
12.0
12.5
13.0
N
UC
Cond

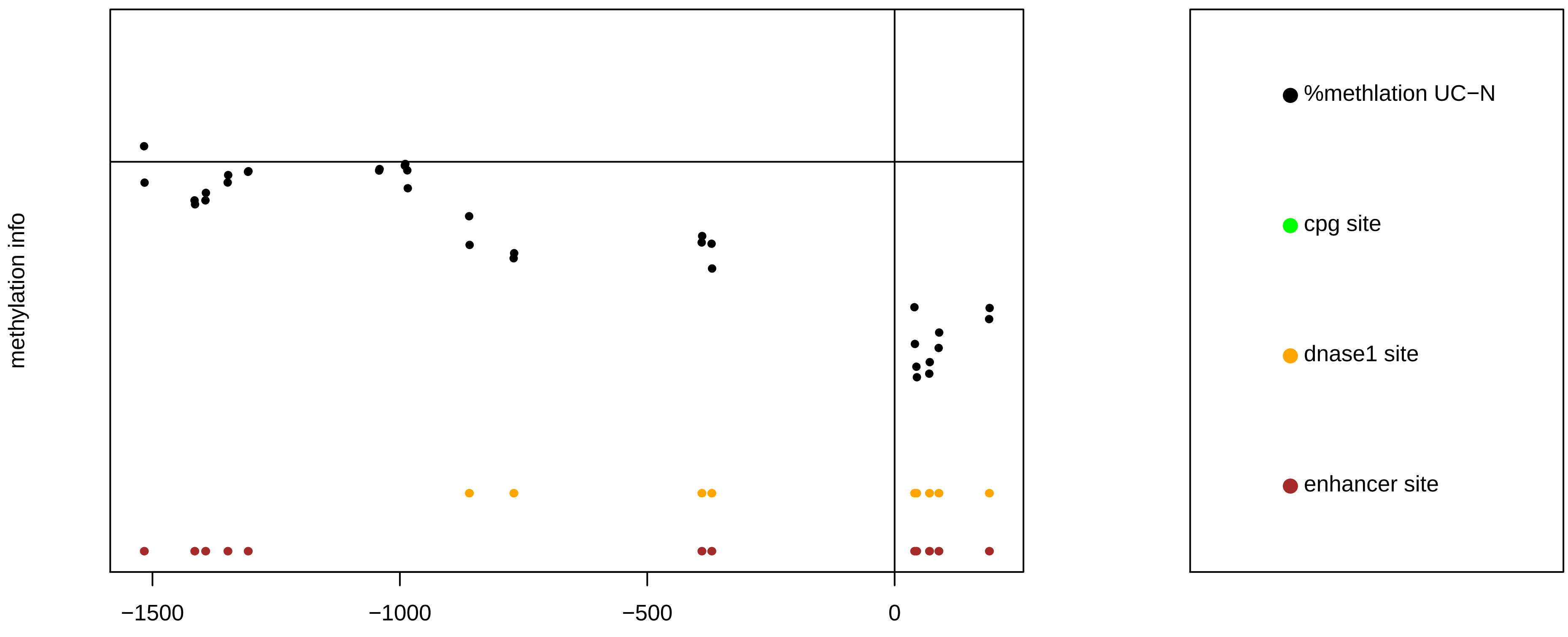


PLD4 average UC−N %methylation max=−9.65% min=−24.42%

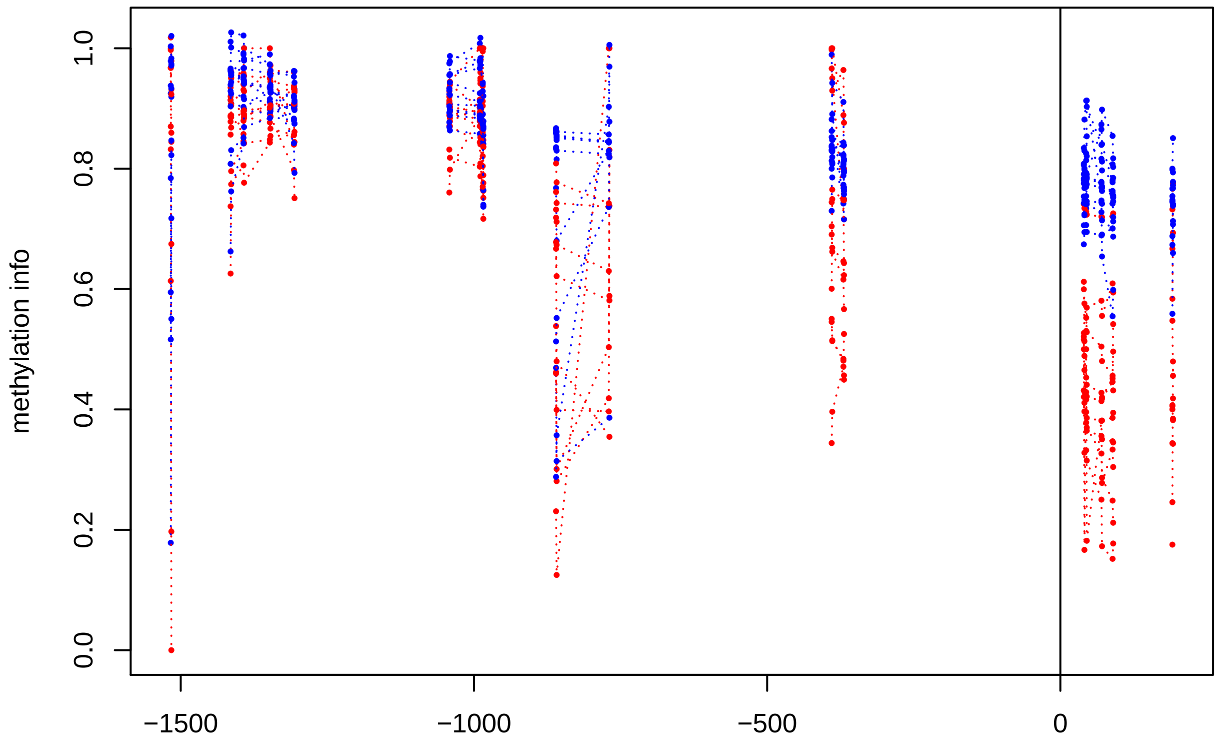
PLD4 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.06

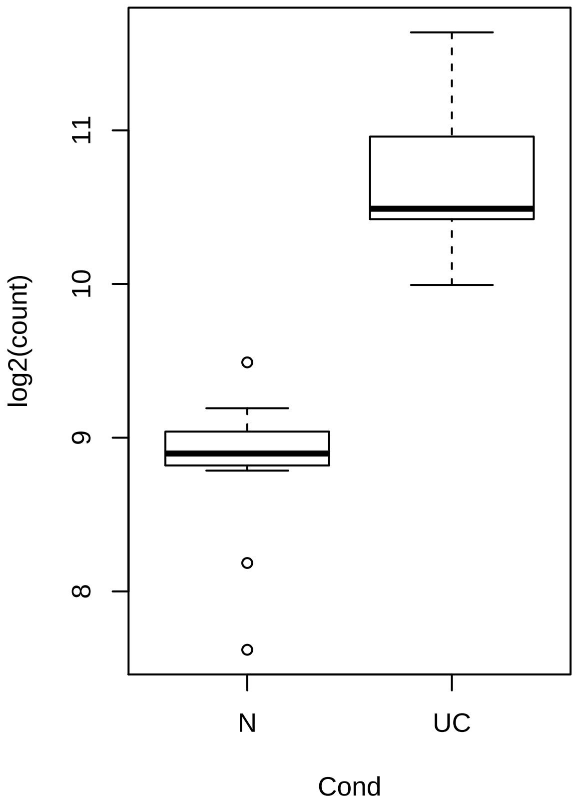

PLEKHG6 average UC−N %methylation max=18.92% min=−7.1%
methylation info
−1200
−1000
−800
−600
−400
−200
0
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
PLEKHG6 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−1200
−1000
−800
−600
−400
−200
0
RNAseq logFC(UC−N)= −1.06
log2(count)
9.0
9.5
10.0
10.5
11.0
11.5
N
UC
Cond



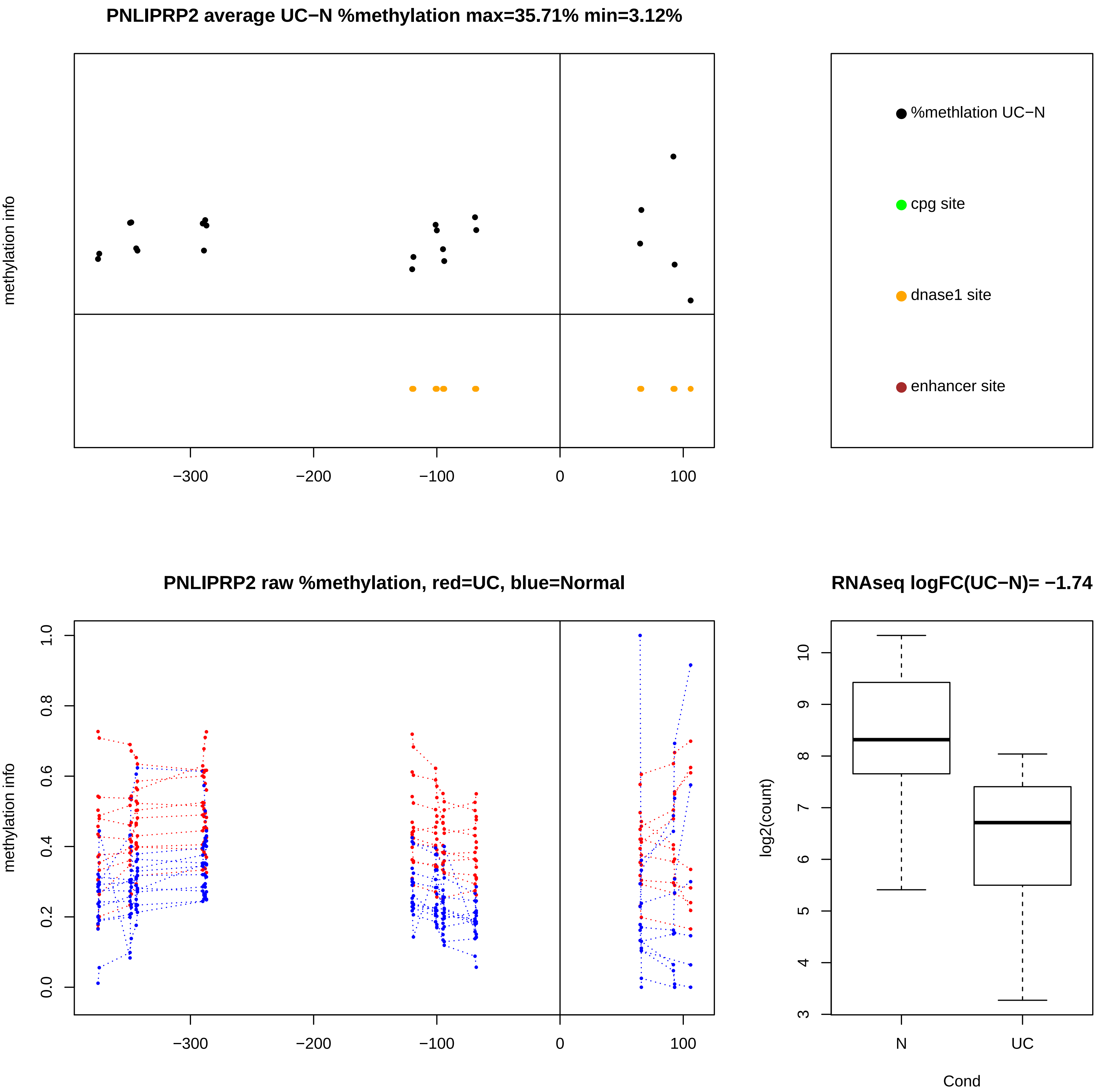
PLEK average UC−N %methylation max=2.69% min=−37.16%



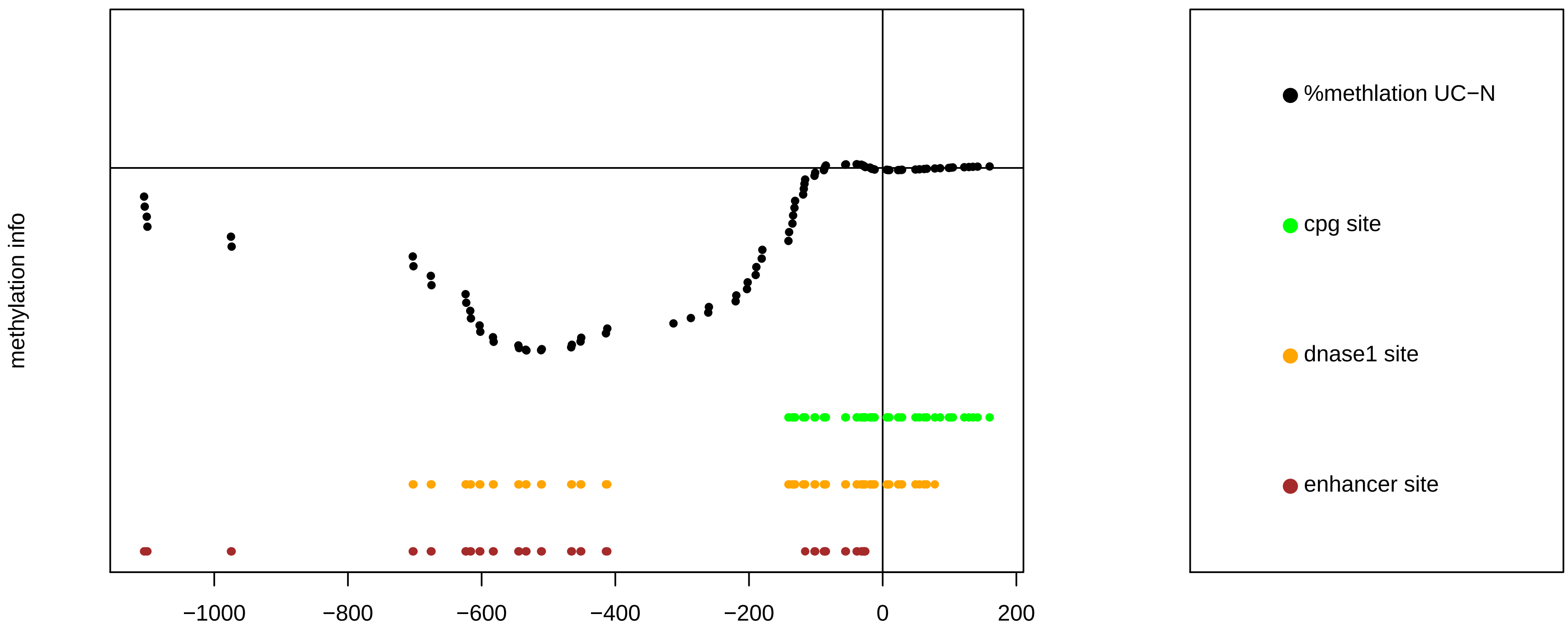
PLEK raw %methylation, red=UC, blue=Normal



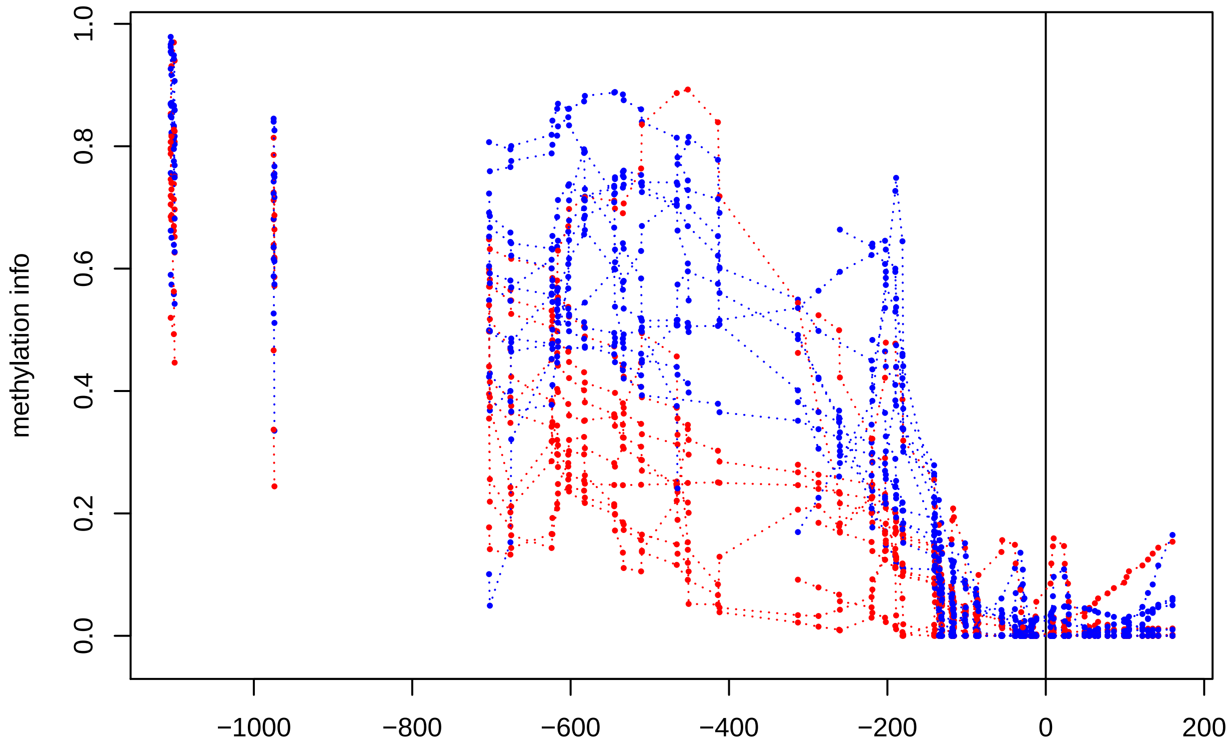
RNAseq logFC(UC−N)= 1.69


PNLIPRP2 average UC−N %methylation max=35.71% min=3.12%
methylation info
−300
−200
−100
0
100
%methlation UC−N
cpg site
dnase1 site
enhancer site
PNLIPRP2 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−300
−200
−100
0
100
RNAseq logFC(UC−N)= −1.74
log2(count)
3
4
5
6
7
8
9
10
N
UC
Cond

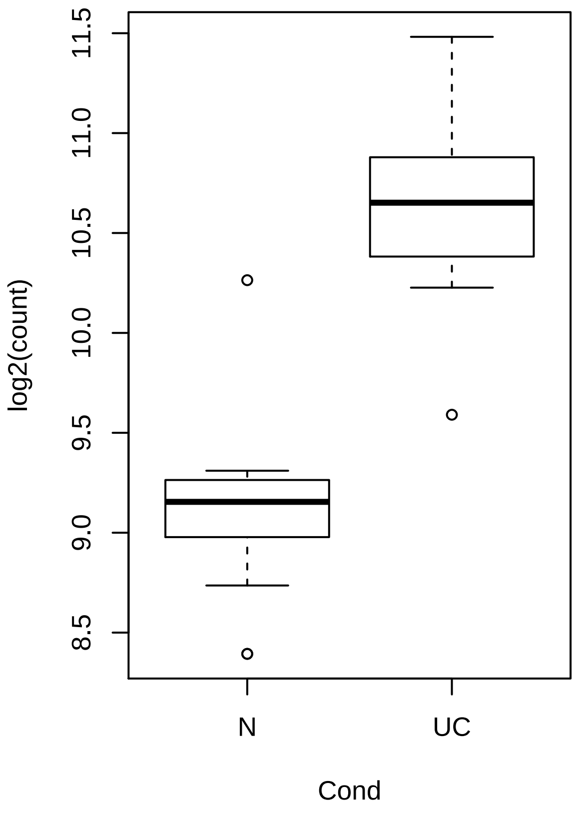
PPP1R16B average UC−N %methylation max=0.55% min=−27.24%

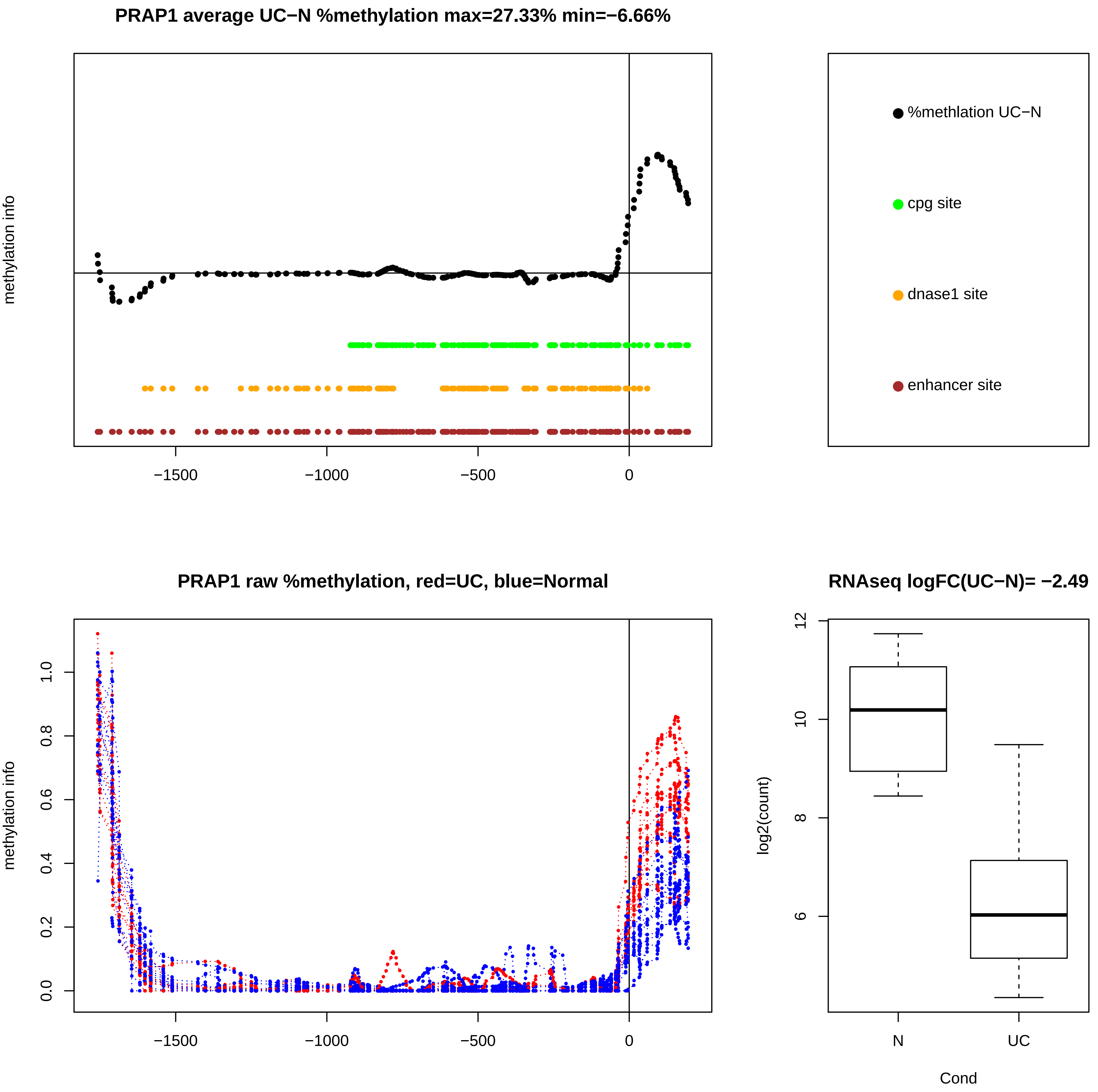


PPP1R16B raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 1.41



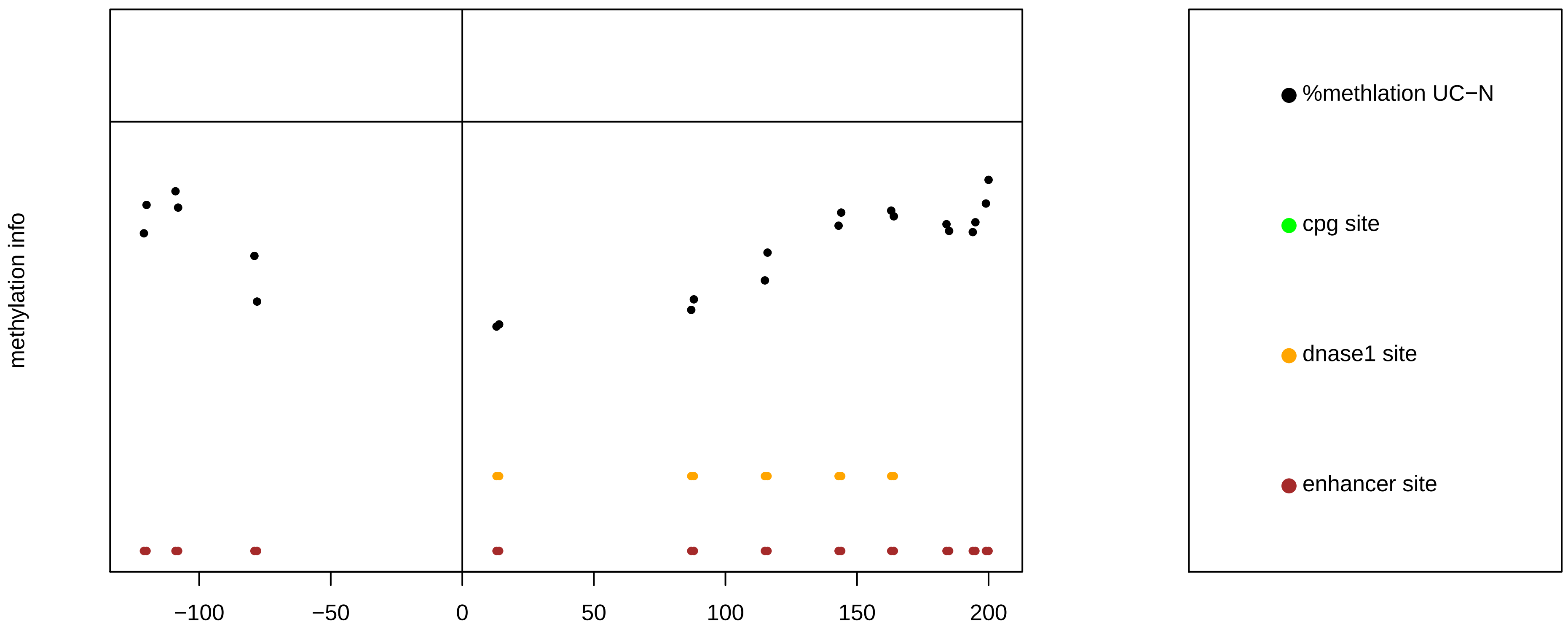


PRAP1 average UC−N %methylation max=27.33% min=−6.66%

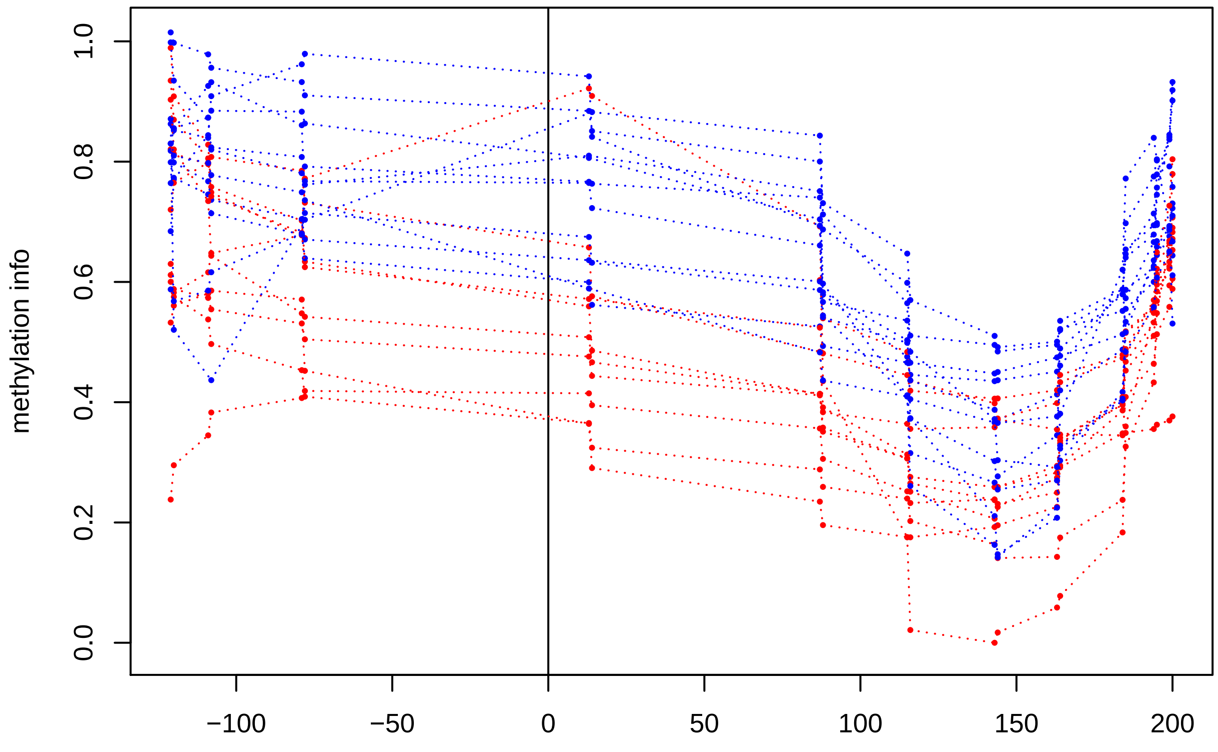
PRAP1 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= −2.49

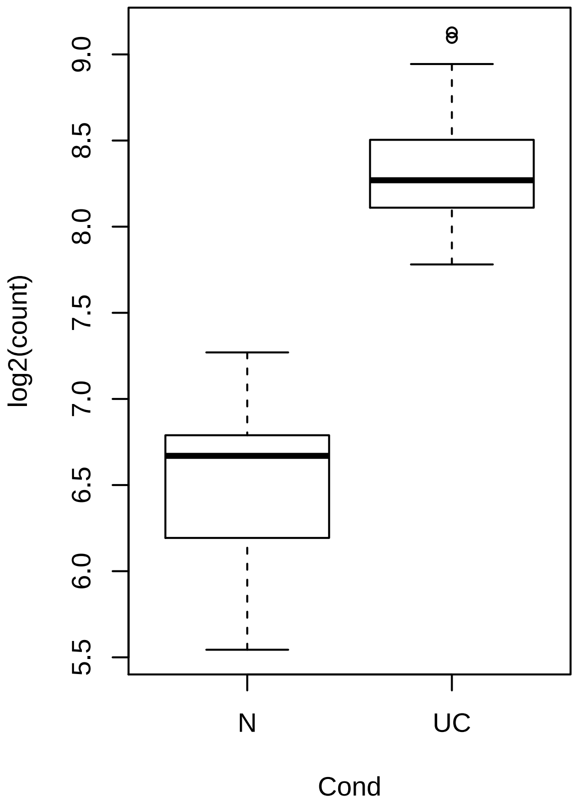
PRF1 average UC−N %methylation max=−7.77% min=−27.39%



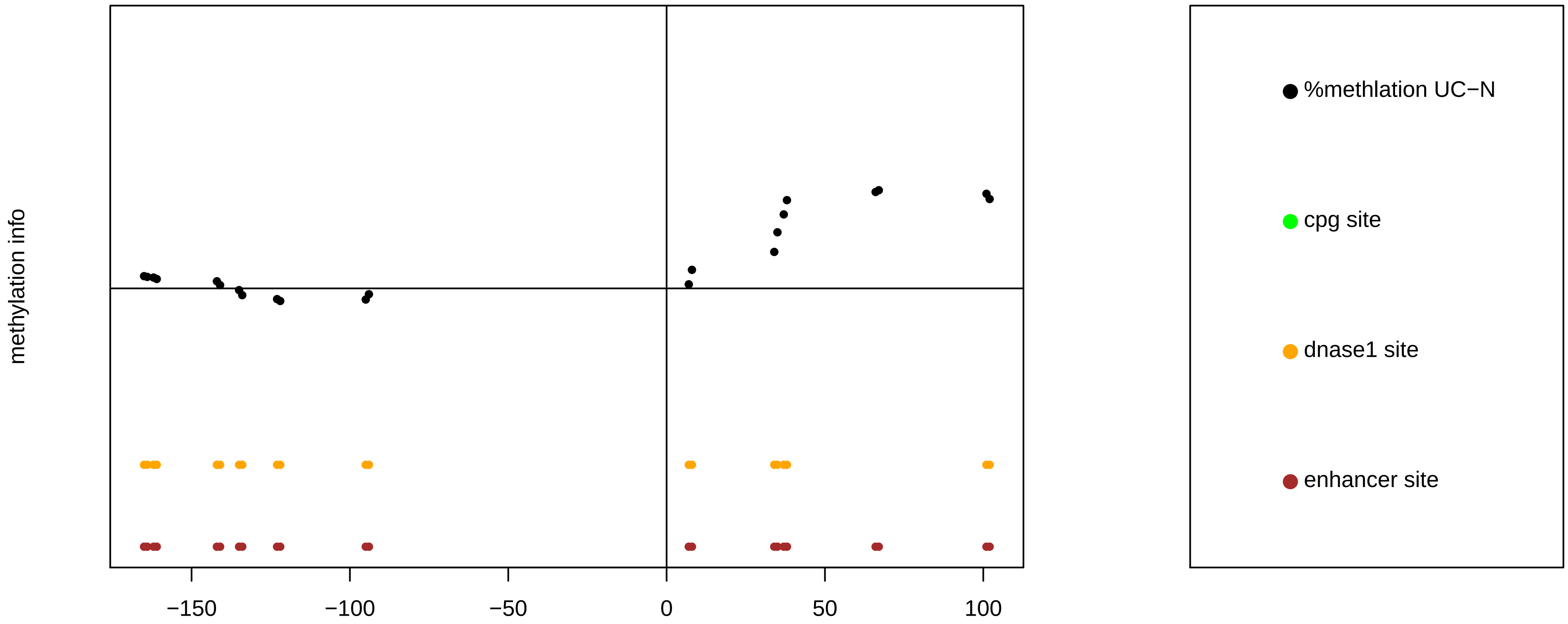
PRF1 raw %methylation, red=UC, blue=Normal



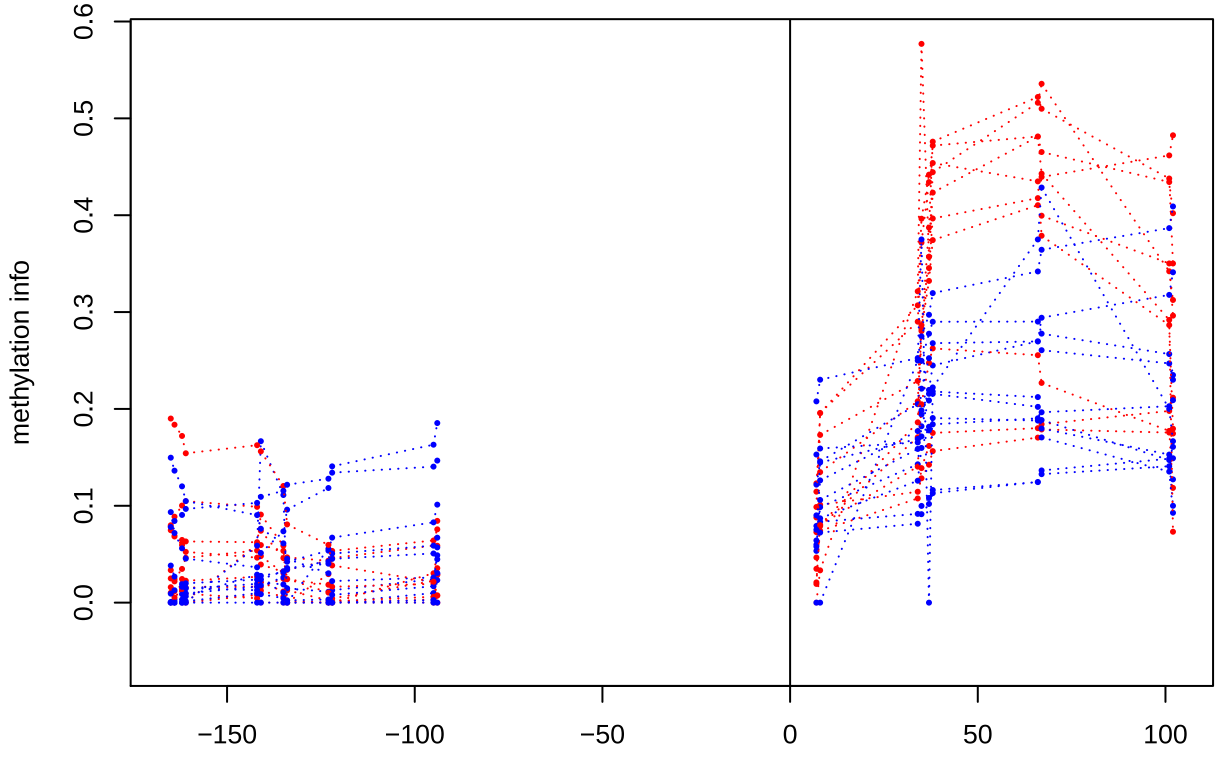
RNAseq logFC(UC−N)= 1.68



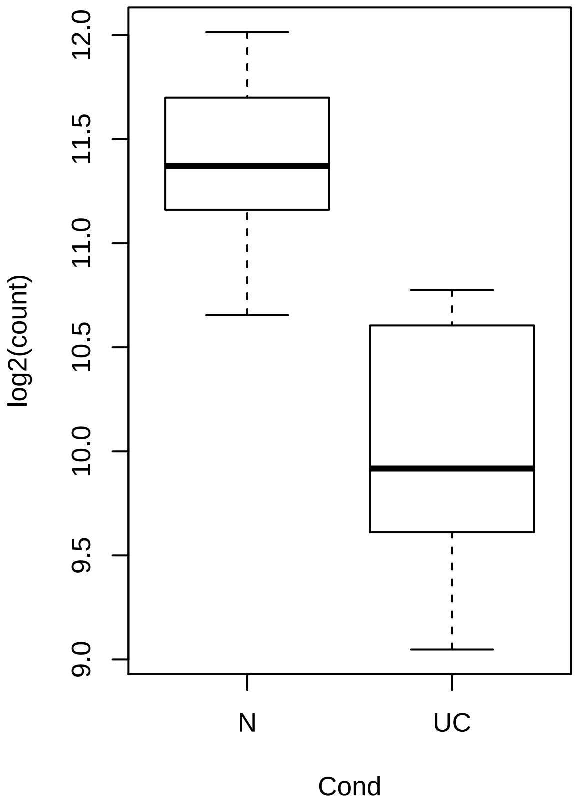
PRLR average UC−N %methylation max=11.99% min=−1.54%

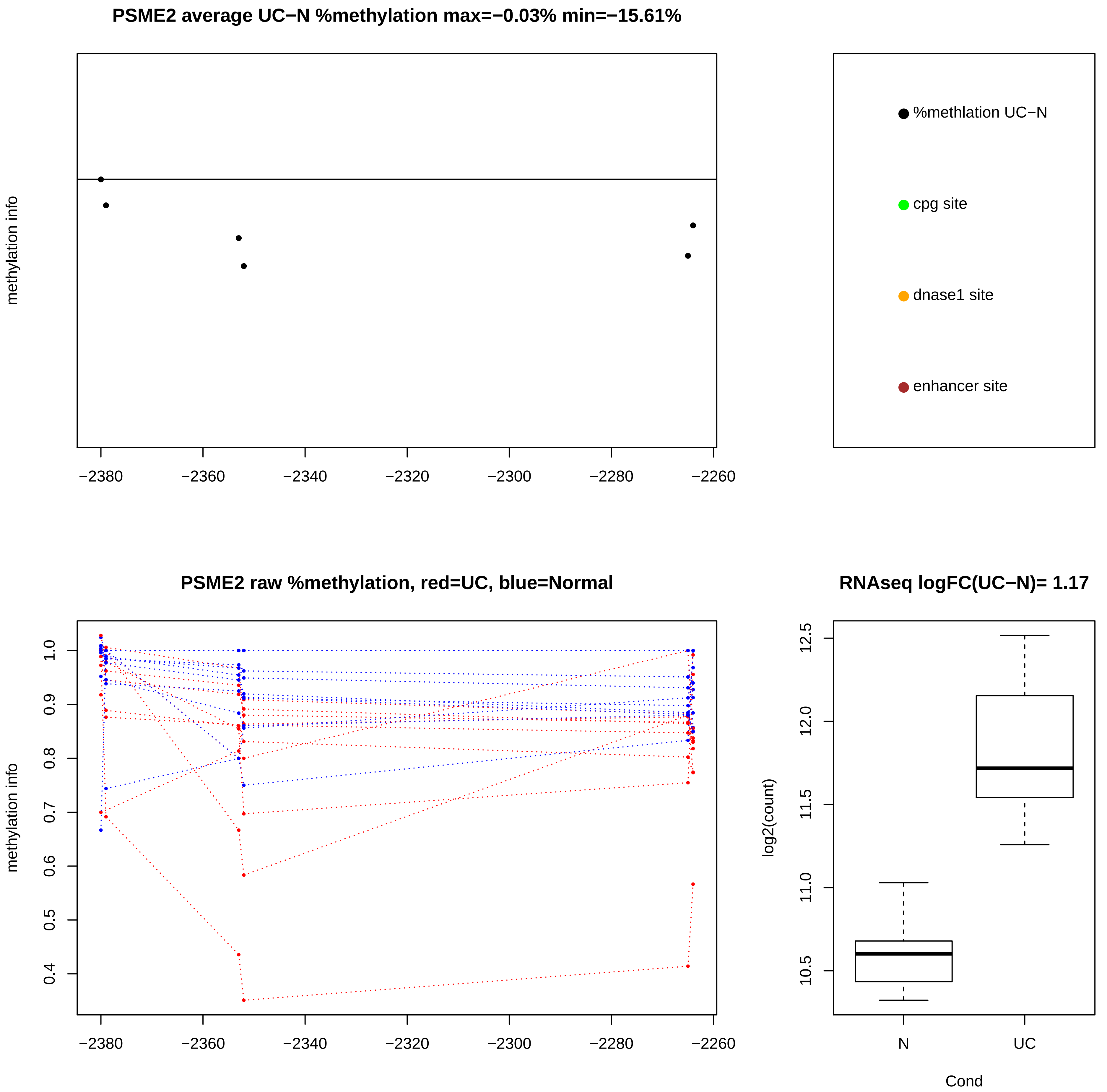


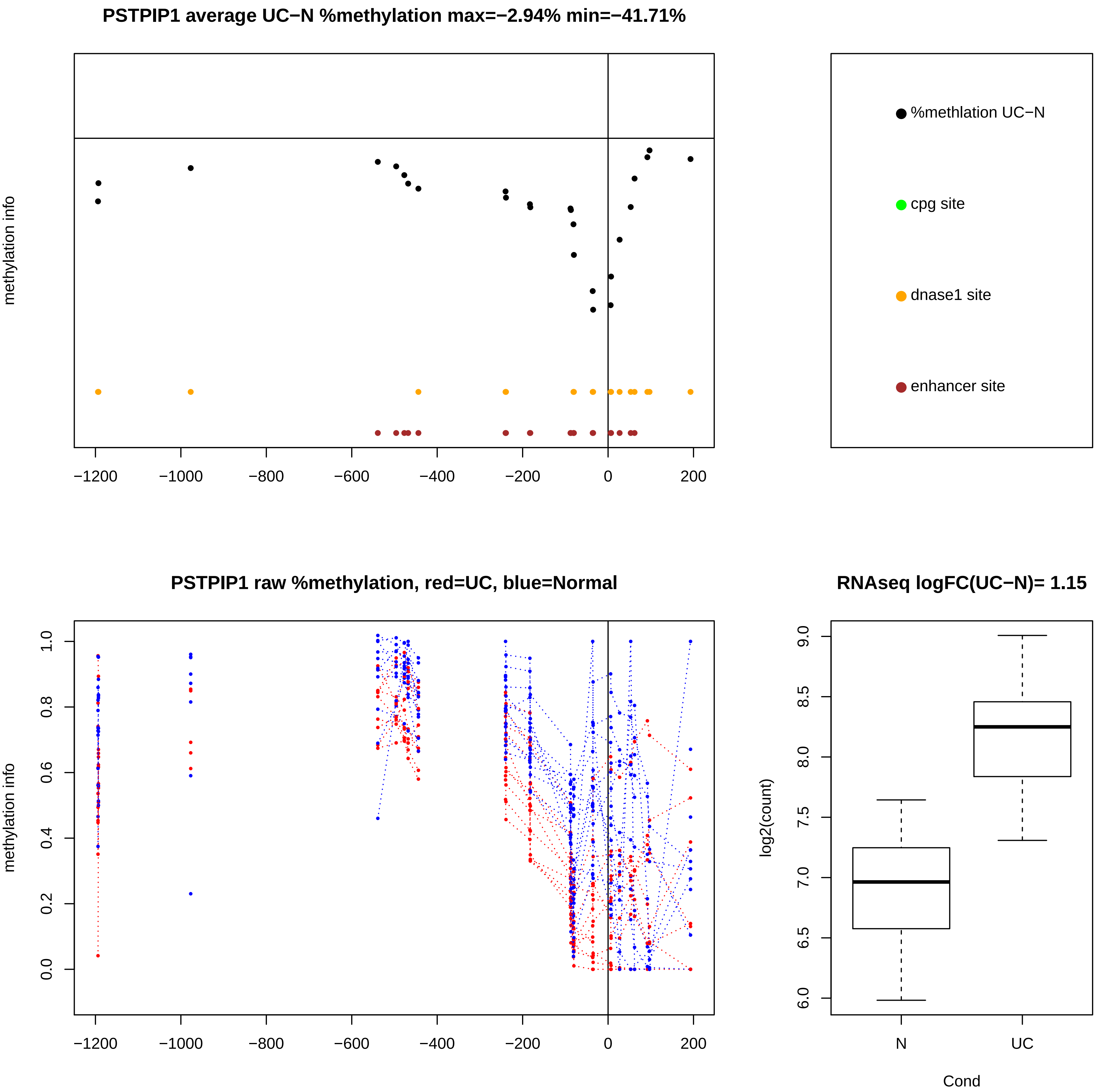
PRLR raw %methylation, red=UC, blue=Normal



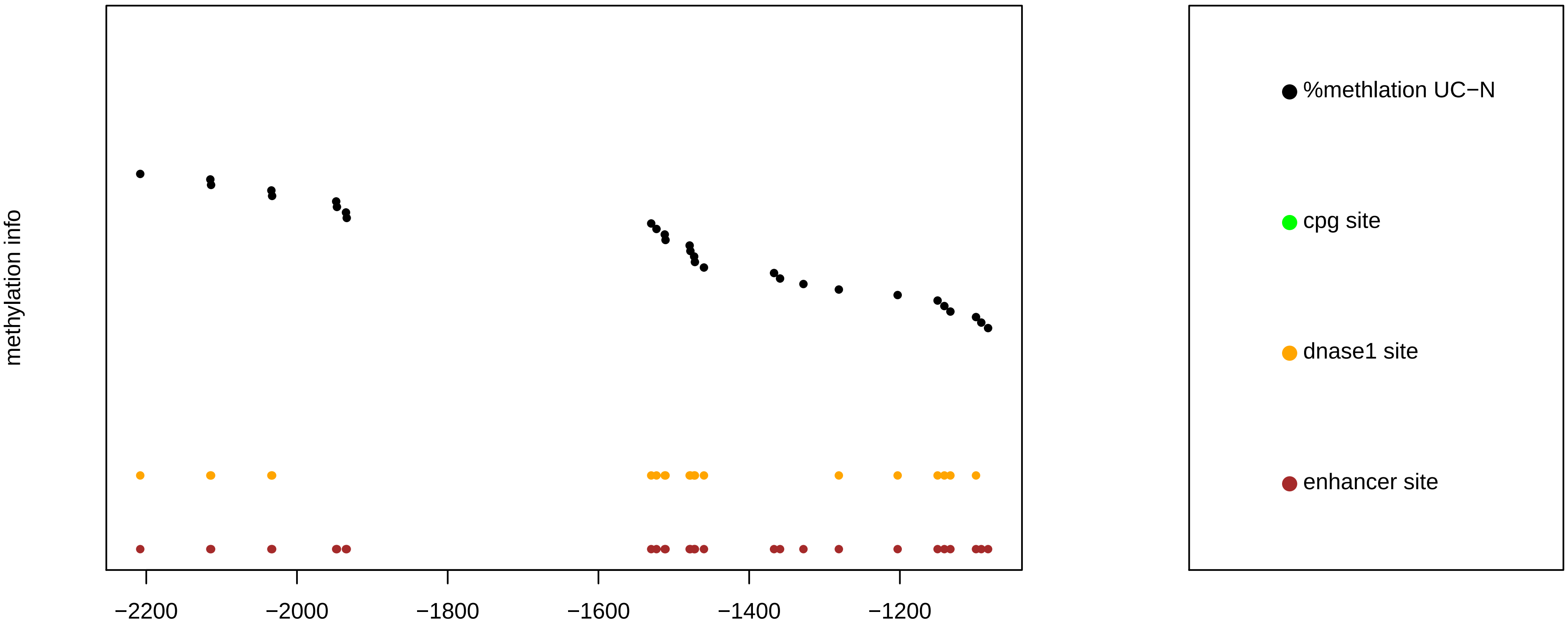
RNAseq logFC(UC−N)= −1.06



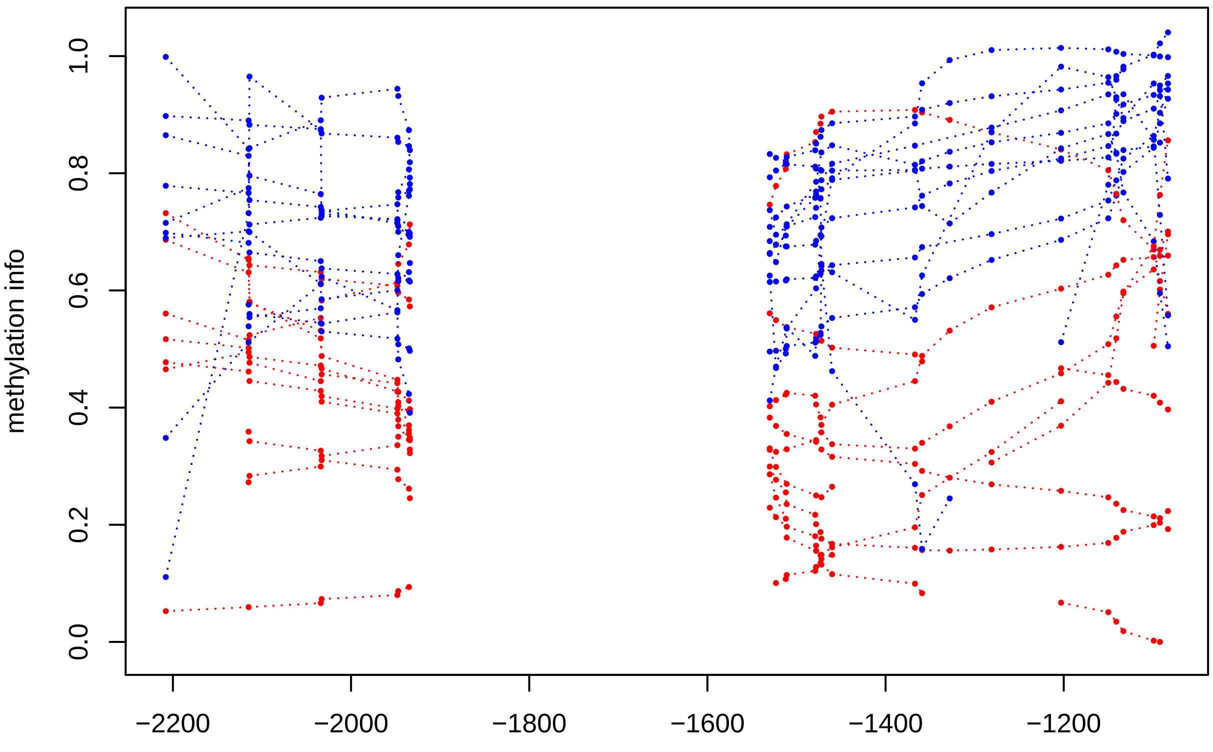

PSME2 average UC−N %methylation max=−0.03% min=−15.61%
methylation info
−2380
−2360
−2340
−2320
−2300
−2280
−2260
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
PSME2 raw %methylation, red=UC, blue=Normal
methylation info
1.0
0.9
0.8
0.7
0.6
0.5
0.4
−2380
−2360
−2340
−2320
−2300
−2280
−2260
RNAseq logFC(UC−N)= 1.17
log2(count)
12.5
12.0
11.5
11.0
10.5
N
UC
Cond


PSTPIP1 average UC−N %methylation max=−2.94% min=−41.71%
methylation info
−1200
−1000
−800
−600
−400
−200
0
200
%methlation UC−N
cpg site
dnase1 site
enhancer site
PSTPIP1 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−1200
−1000
−800
−600
−400
−200
0
200
RNAseq logFC(UC−N)= 1.15
log2(count)
6.0
6.5
7.0
7.5
8.0
8.5
9.0
N
UC
Cond

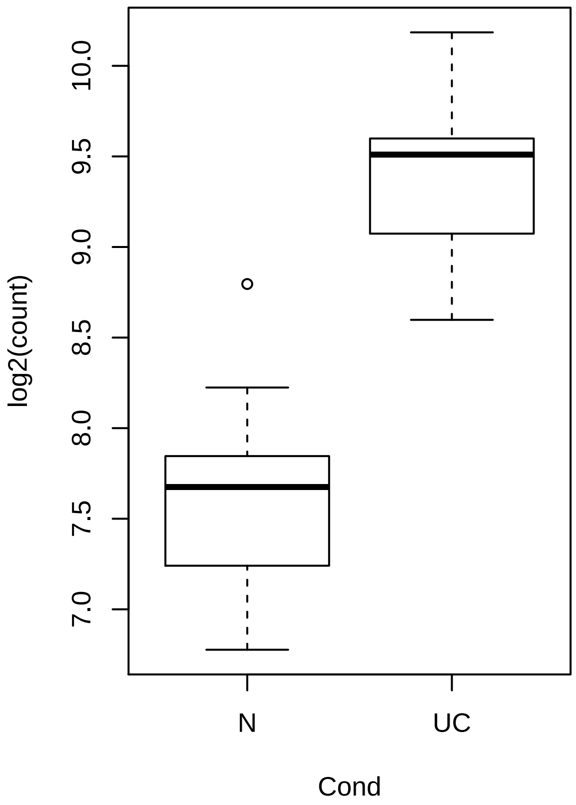
PTPN7 average UC−N %methylation max=−23.31% min=−44.24%



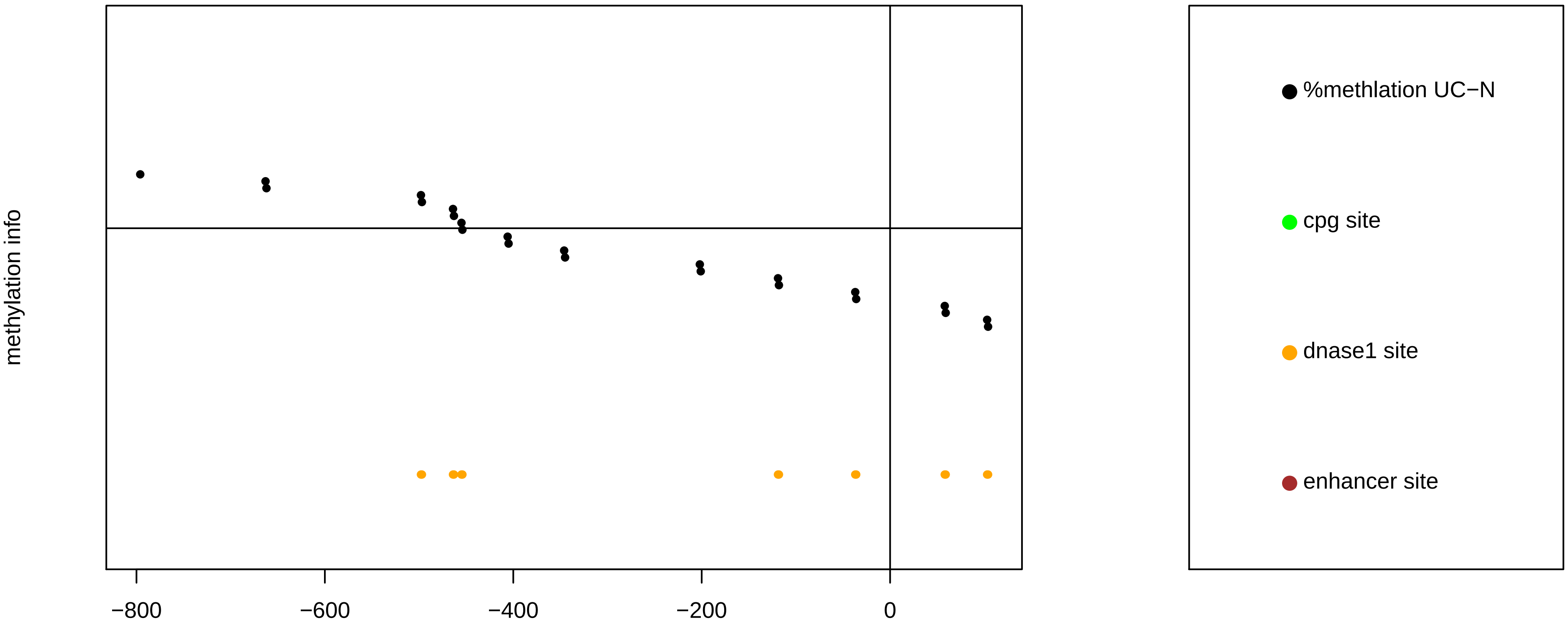
PTPN7 raw %methylation, red=UC, blue=Normal



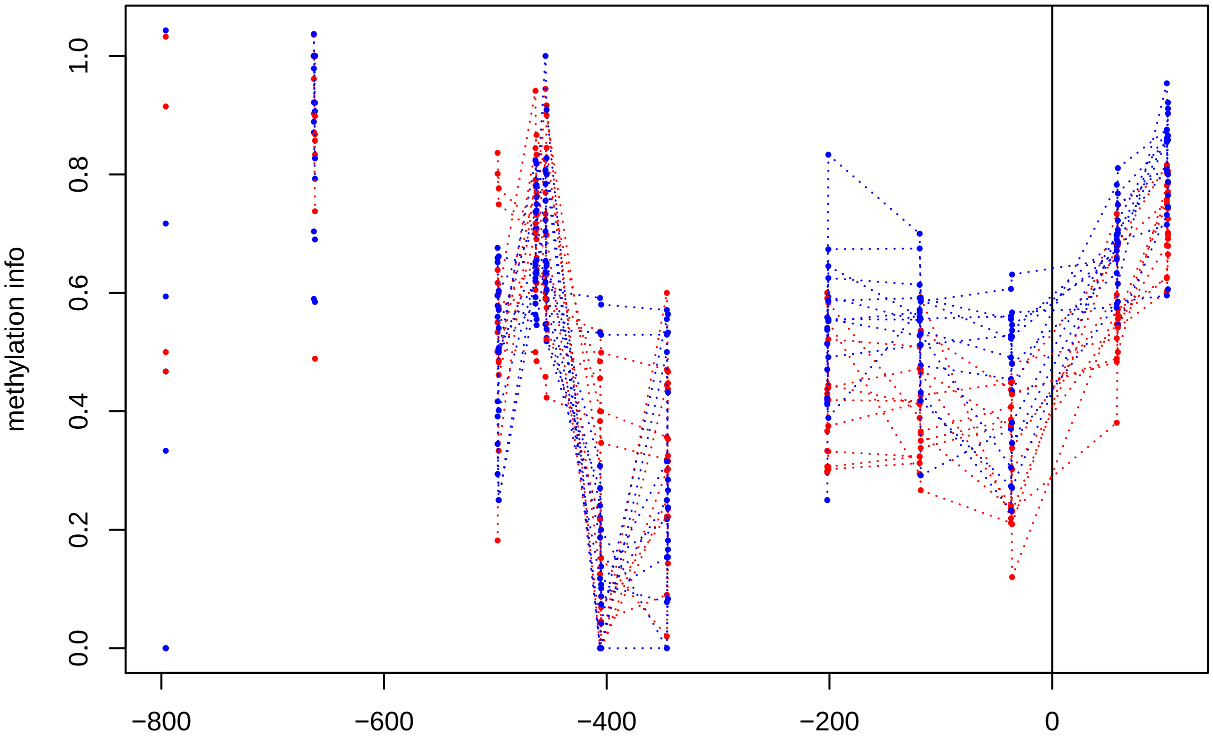
RNAseq logFC(UC−N)= 1.62



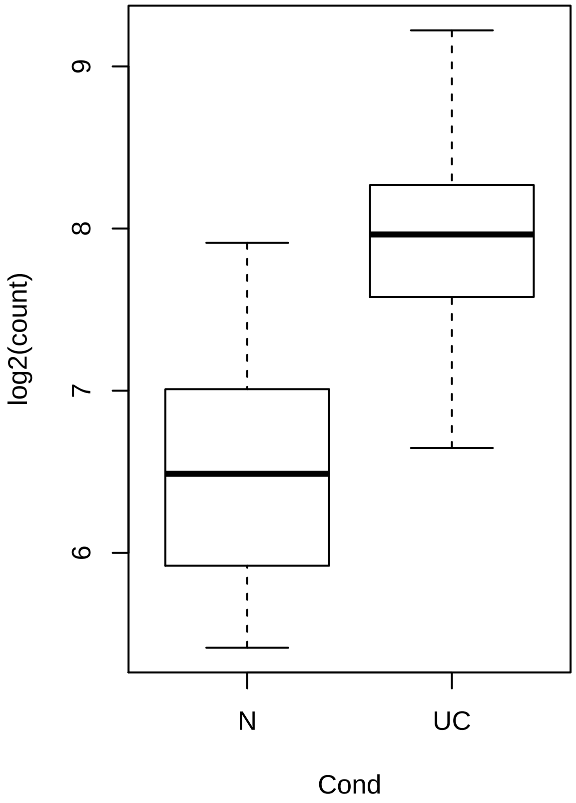
PYHIN1 average UC−N %methylation max=7.29% min=−13.32%

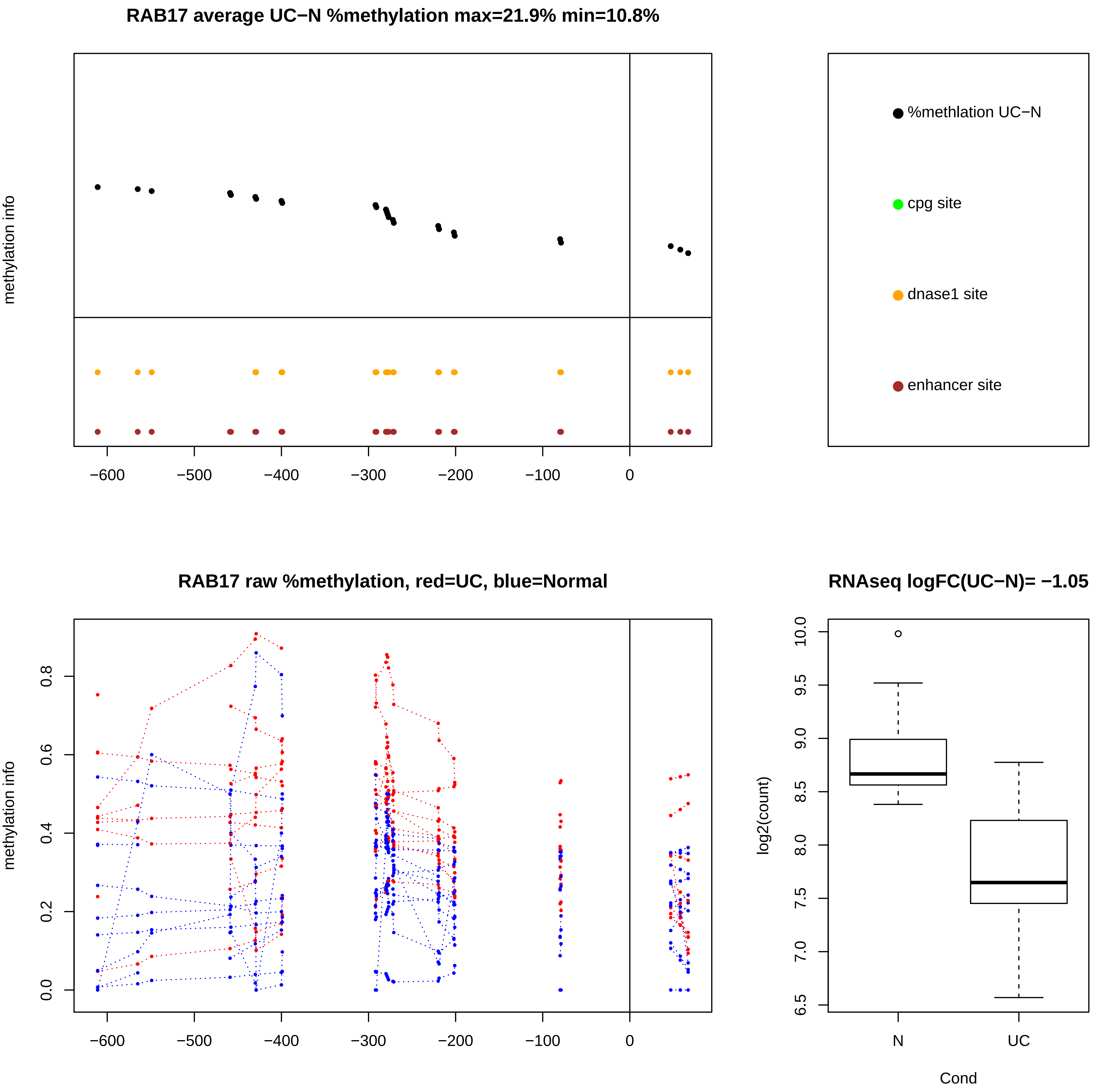


PYHIN1 raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 1.24

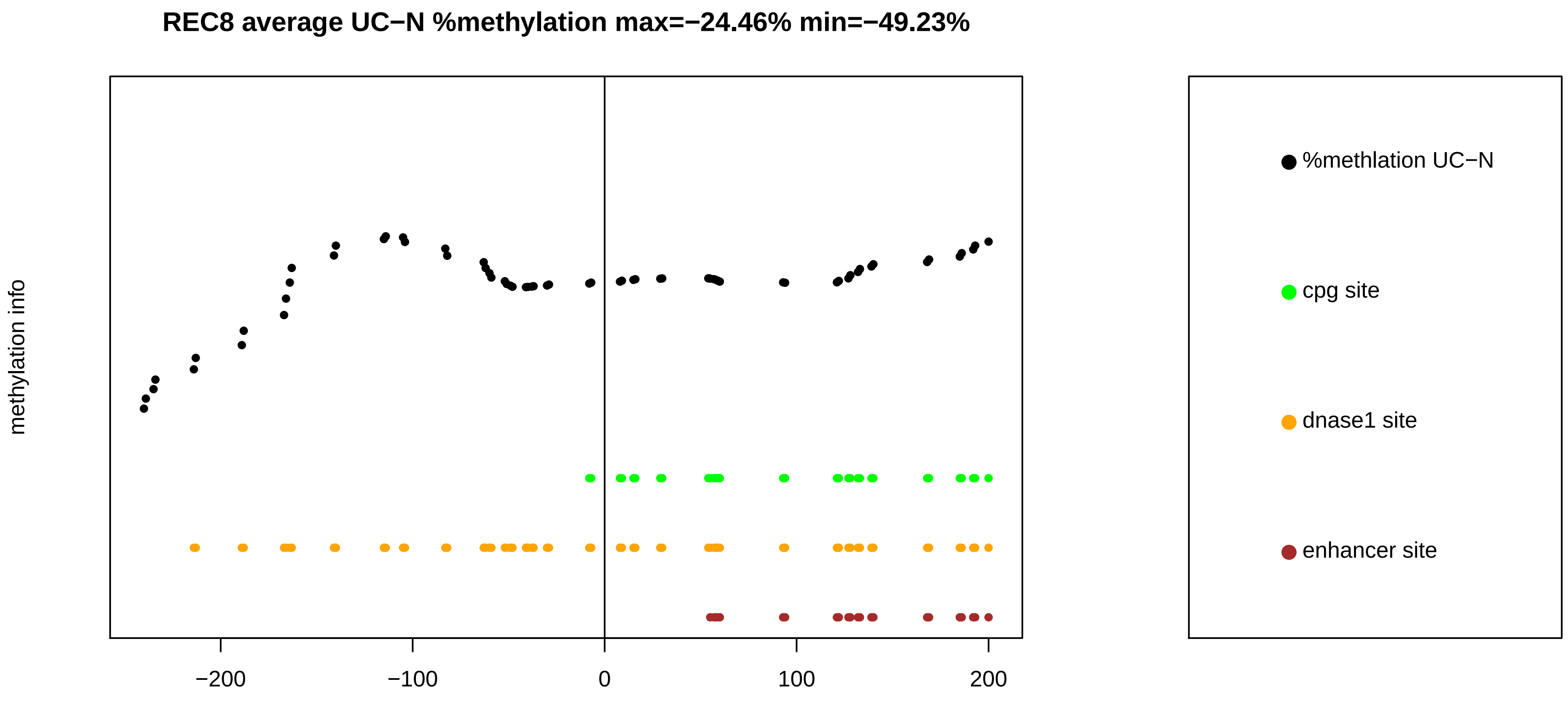




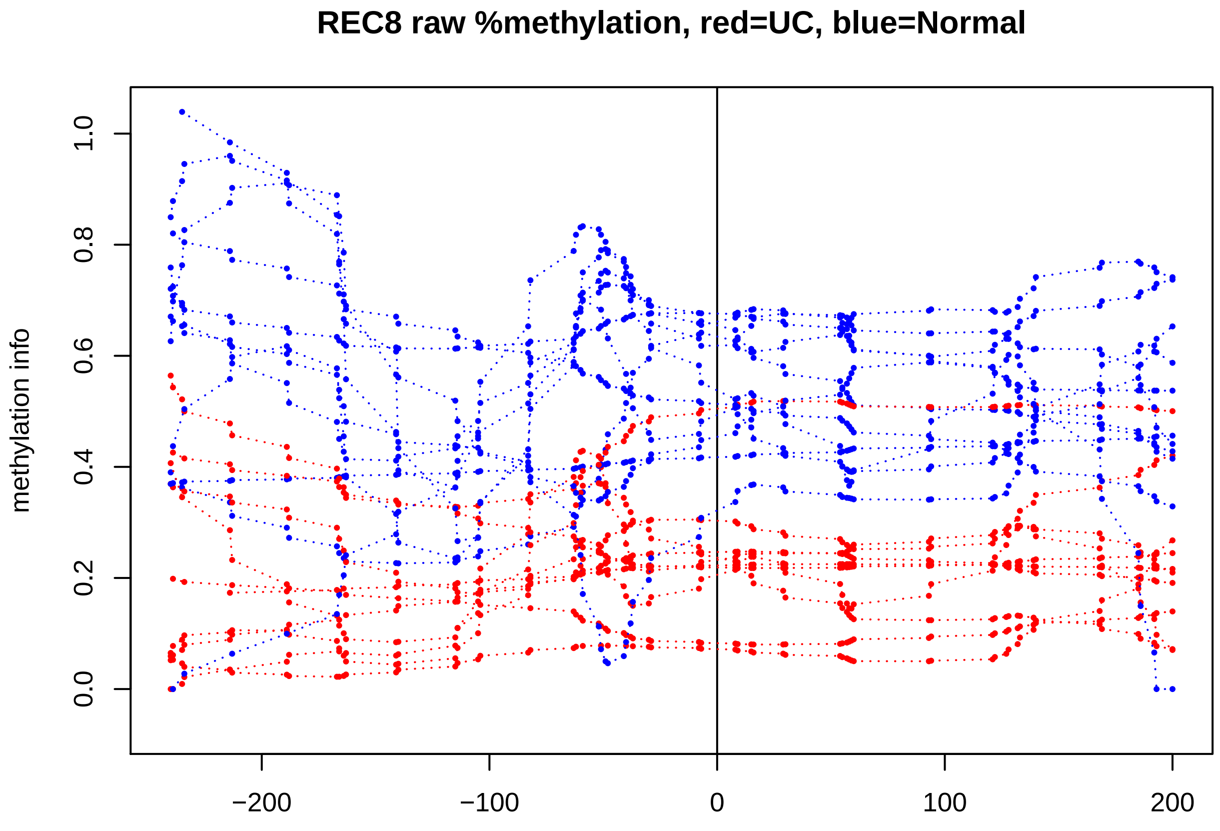
RAB17 average UC−N %methylation max=21.9% min=10.8%

RAB17 raw %methylation, red=UC, blue=Normal

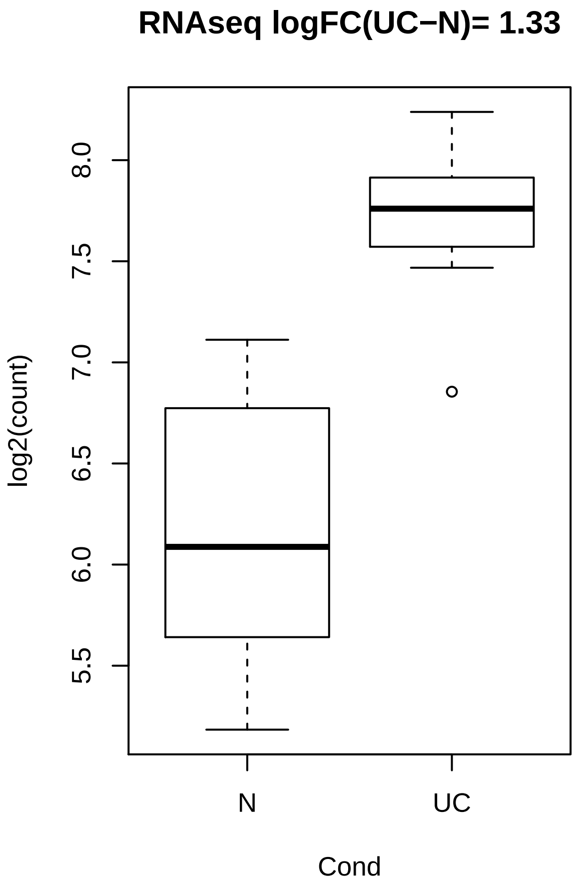
RNAseq logFC(UC−N)= −1.05



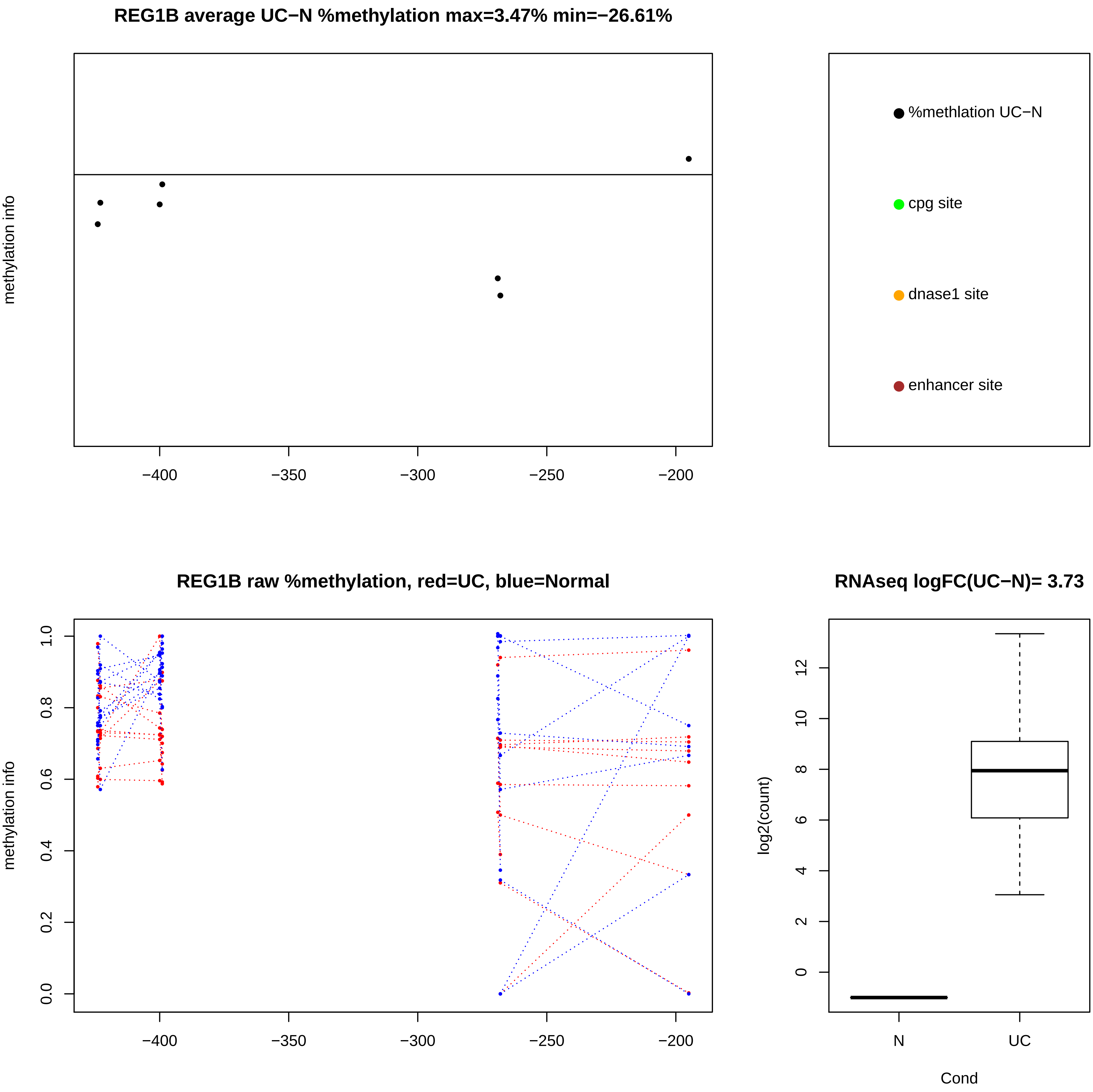
REC8 average UC−N %methylation max=−24.46% min=−49.23%



REC8 raw %methylation, red=UC, blue=Normal



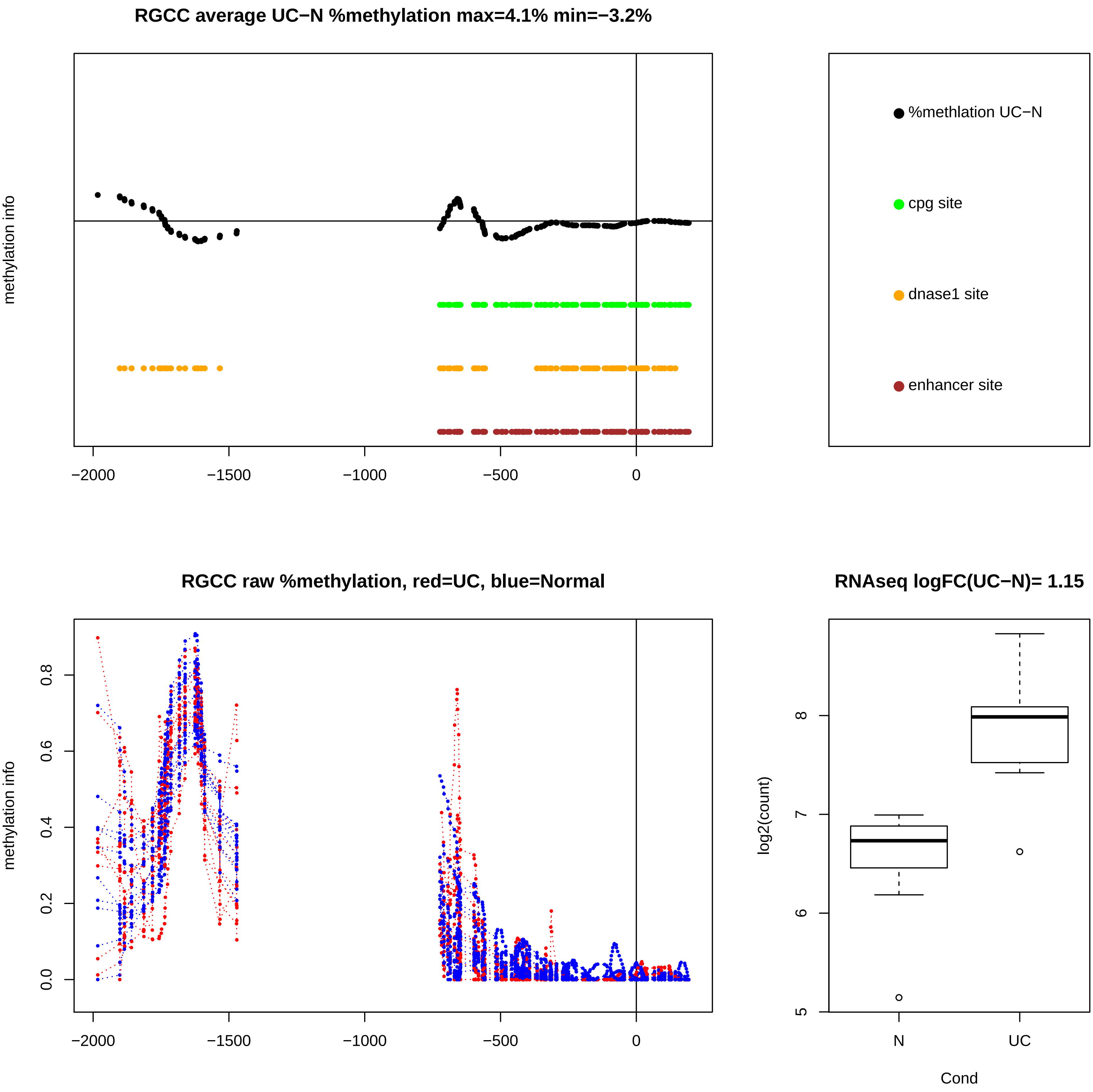
RNAseq logFC(UC−N)= 1.33



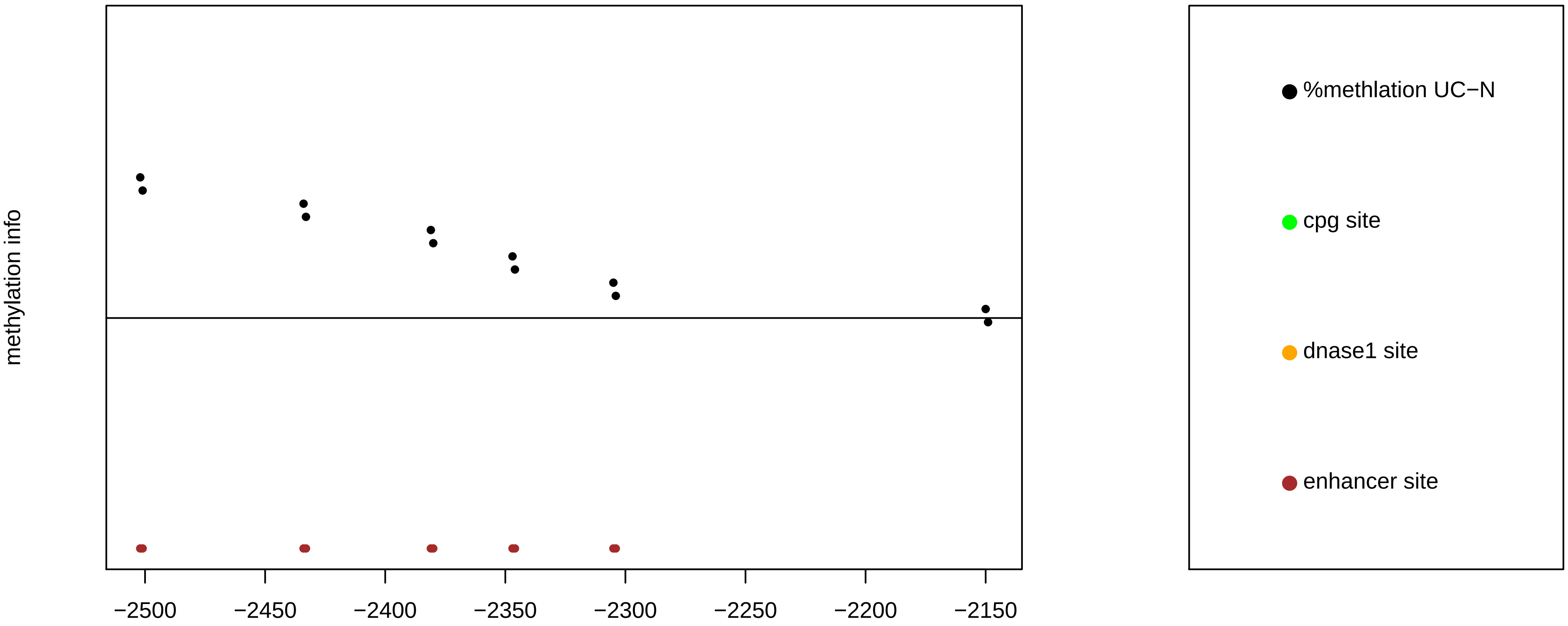
REG1B average UC−N %methylation max=3.47% min=−26.61%

REG1B raw %methylation, red=UC, blue=Normal

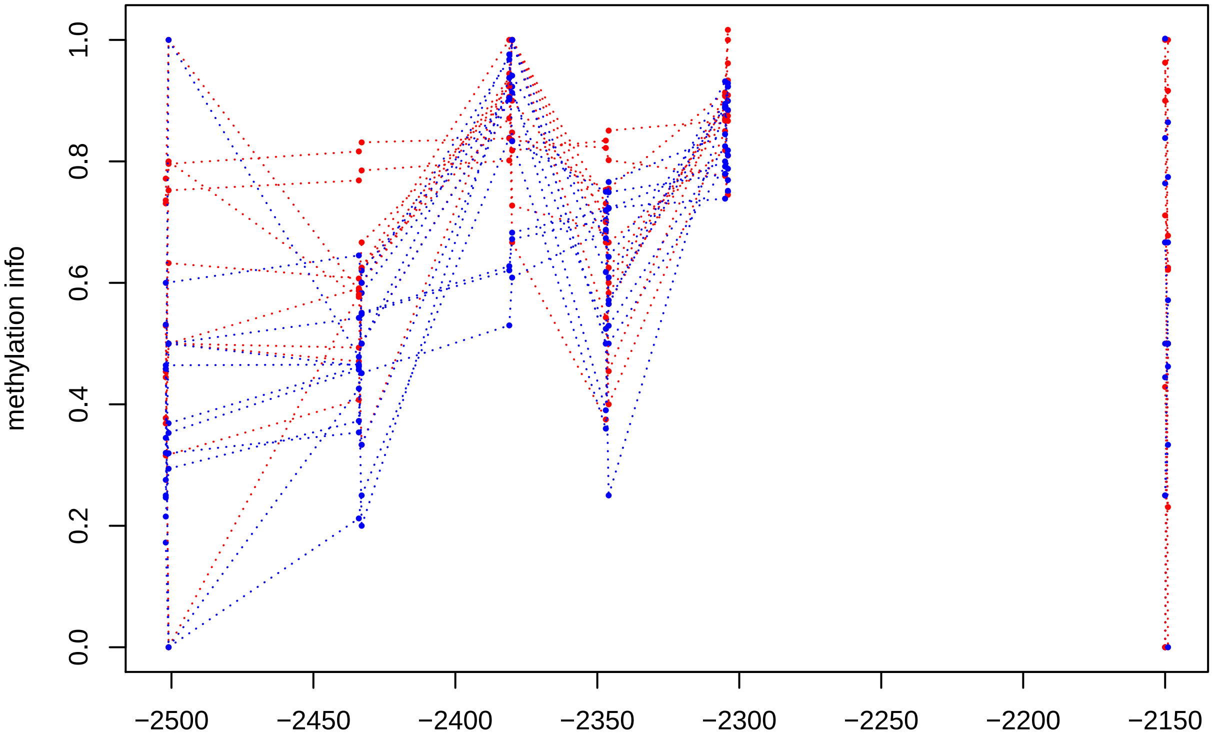
RNAseq logFC(UC−N)= 3.73


RGCC average UC−N %methylation max=4.1% min=−3.2%
methylation info
−2000
−1500
−1000
−500
0
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
RGCC raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
−2000
−1500
−1000
−500
0
RNAseq logFC(UC−N)= 1.15
log2(count)
5
6
7
8
N
UC
Cond

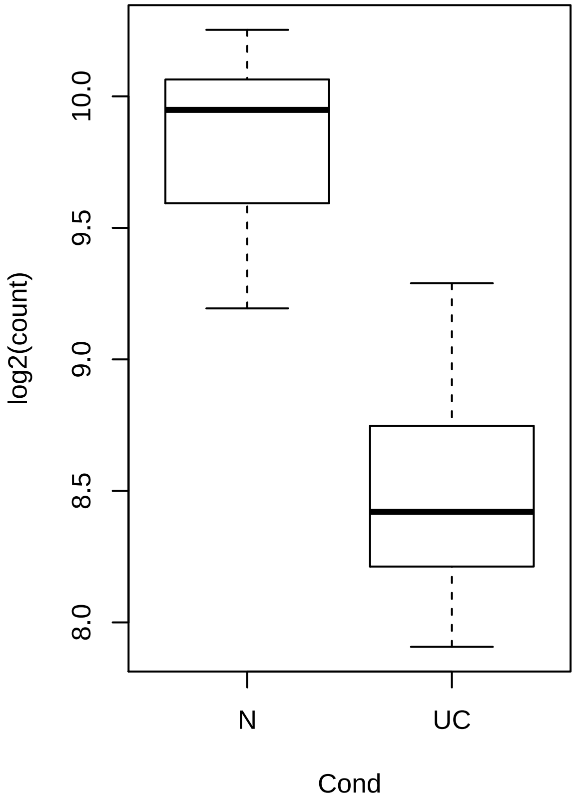
RMDN2 average UC−N %methylation max=18.65% min=−0.55%



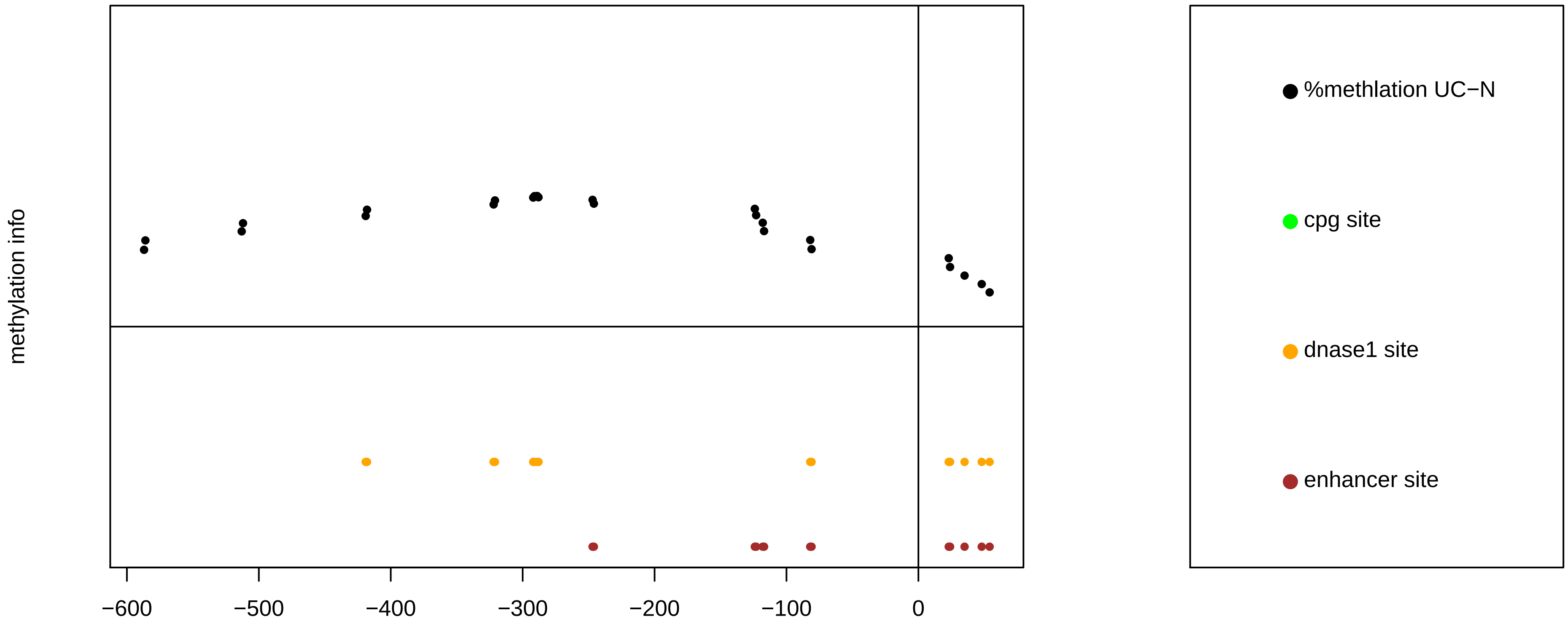
RMDN2 raw %methylation, red=UC, blue=Normal



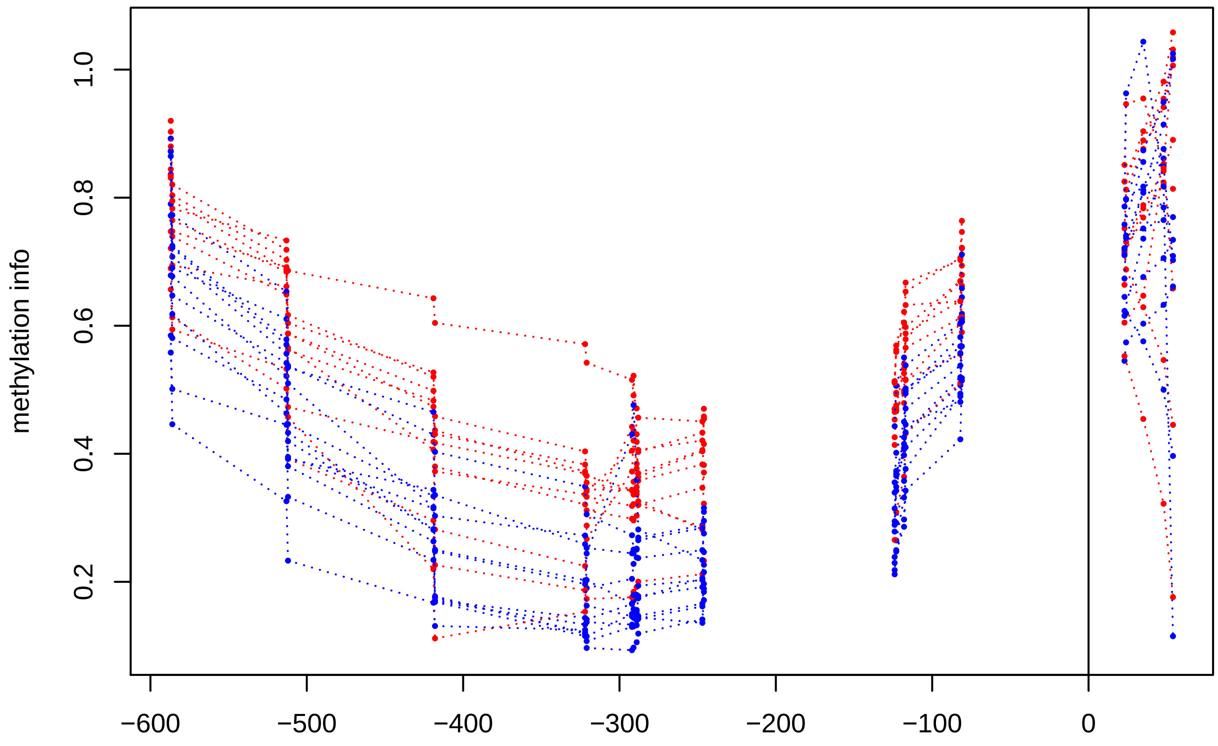
RNAseq logFC(UC−N)= −1.23



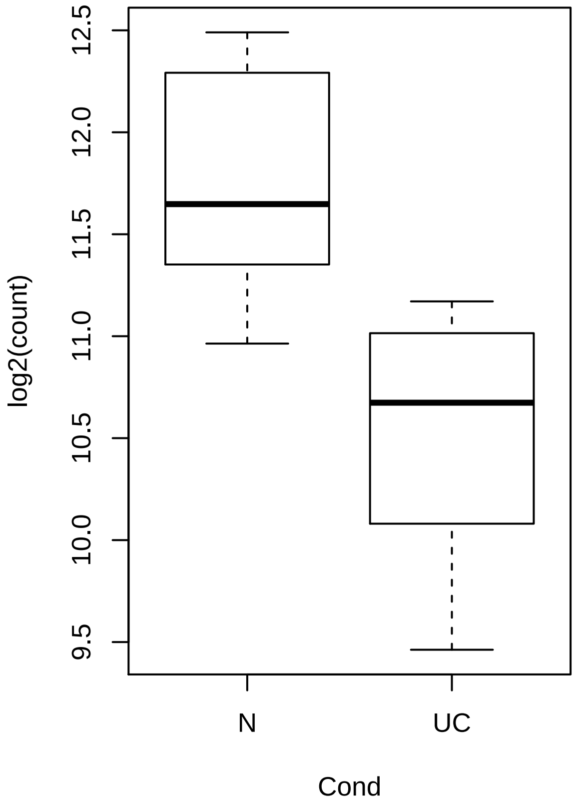
RNASE1 average UC−N %methylation max=15.41% min=4.04%



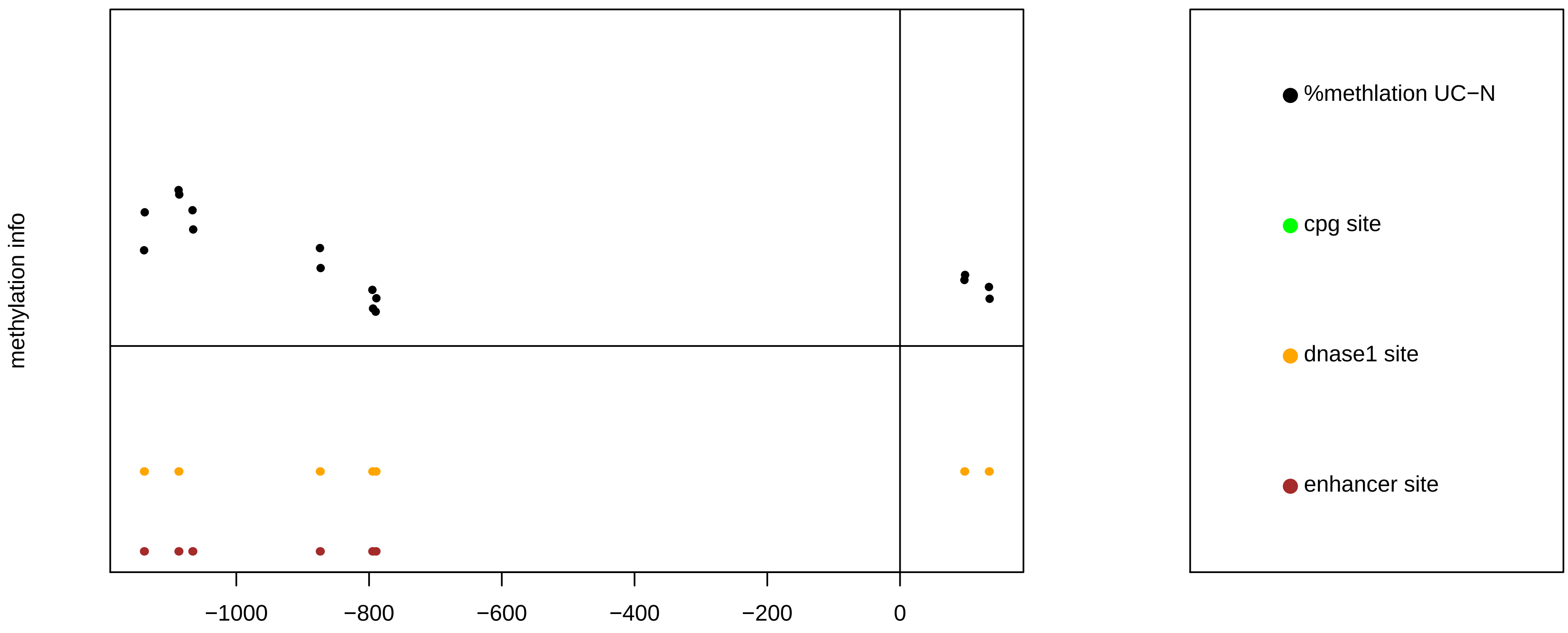
RNASE1 raw %methylation, red=UC, blue=Normal



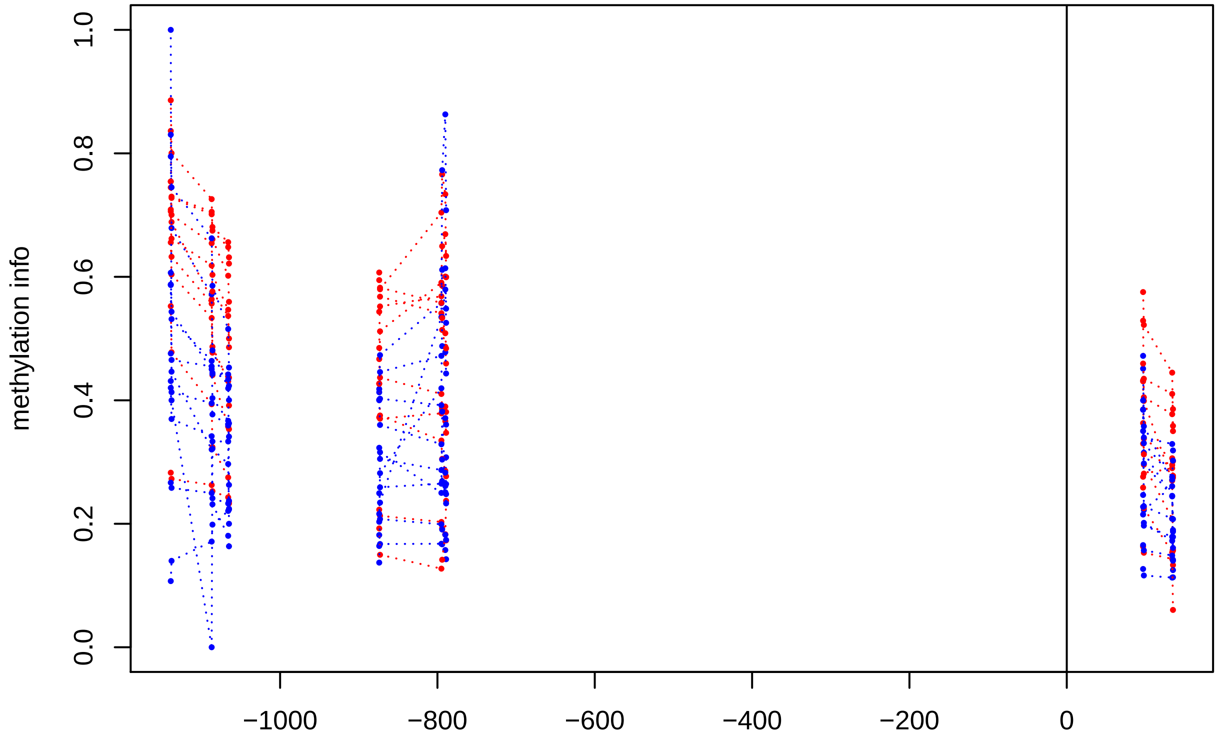
RNAseq logFC(UC−N)= −1.06



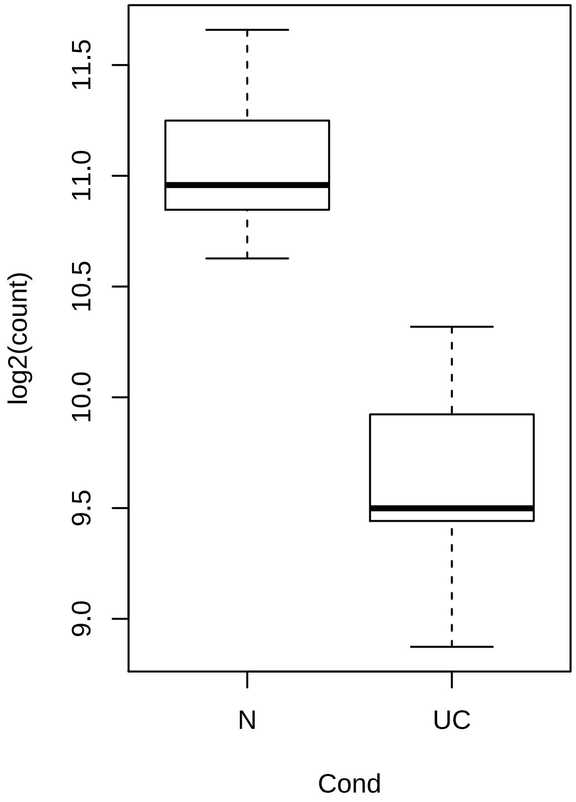
RNF128 average UC−N %methylation max=19.52% min=4.3%

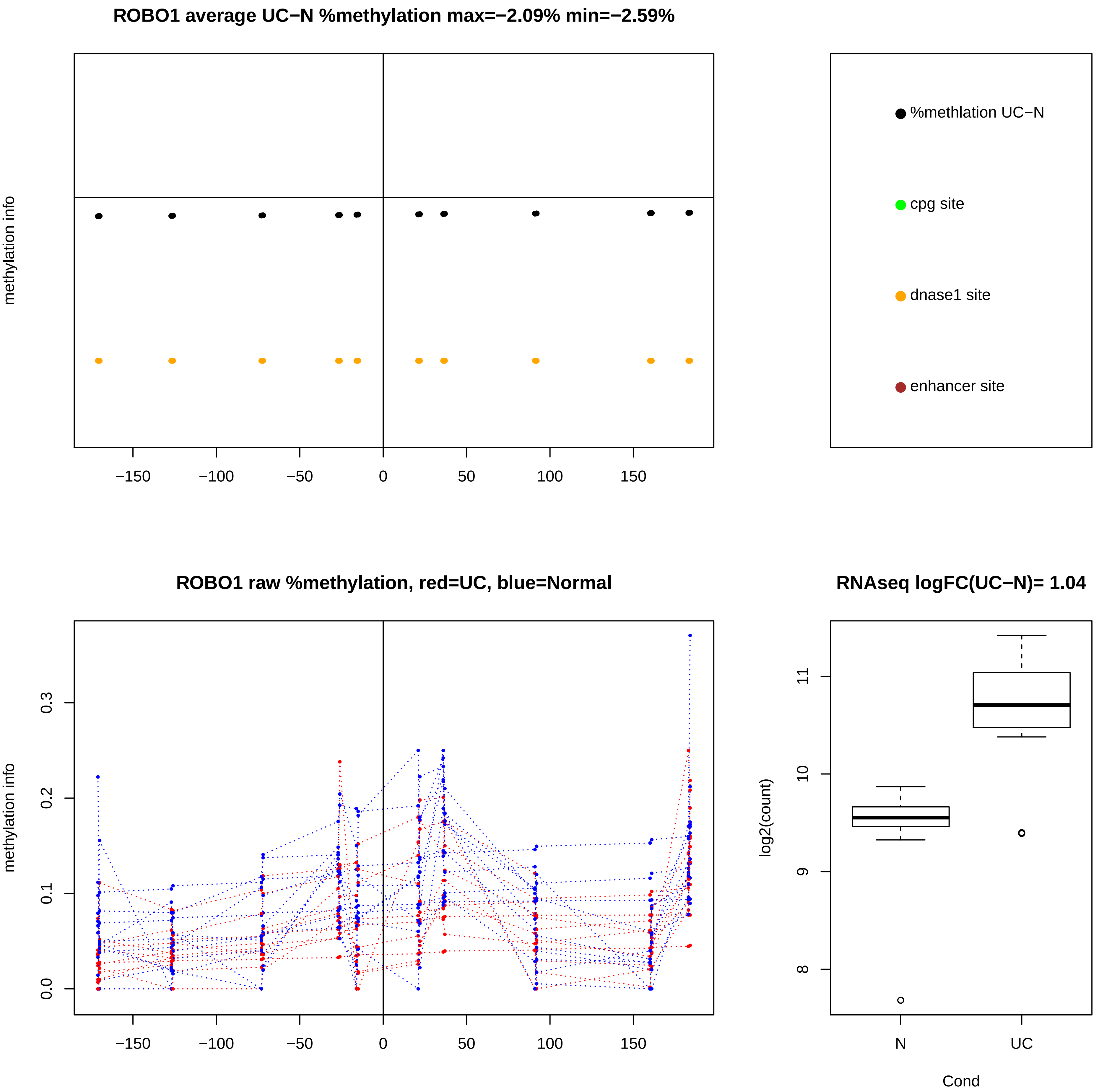


RNF128 raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= −1.29

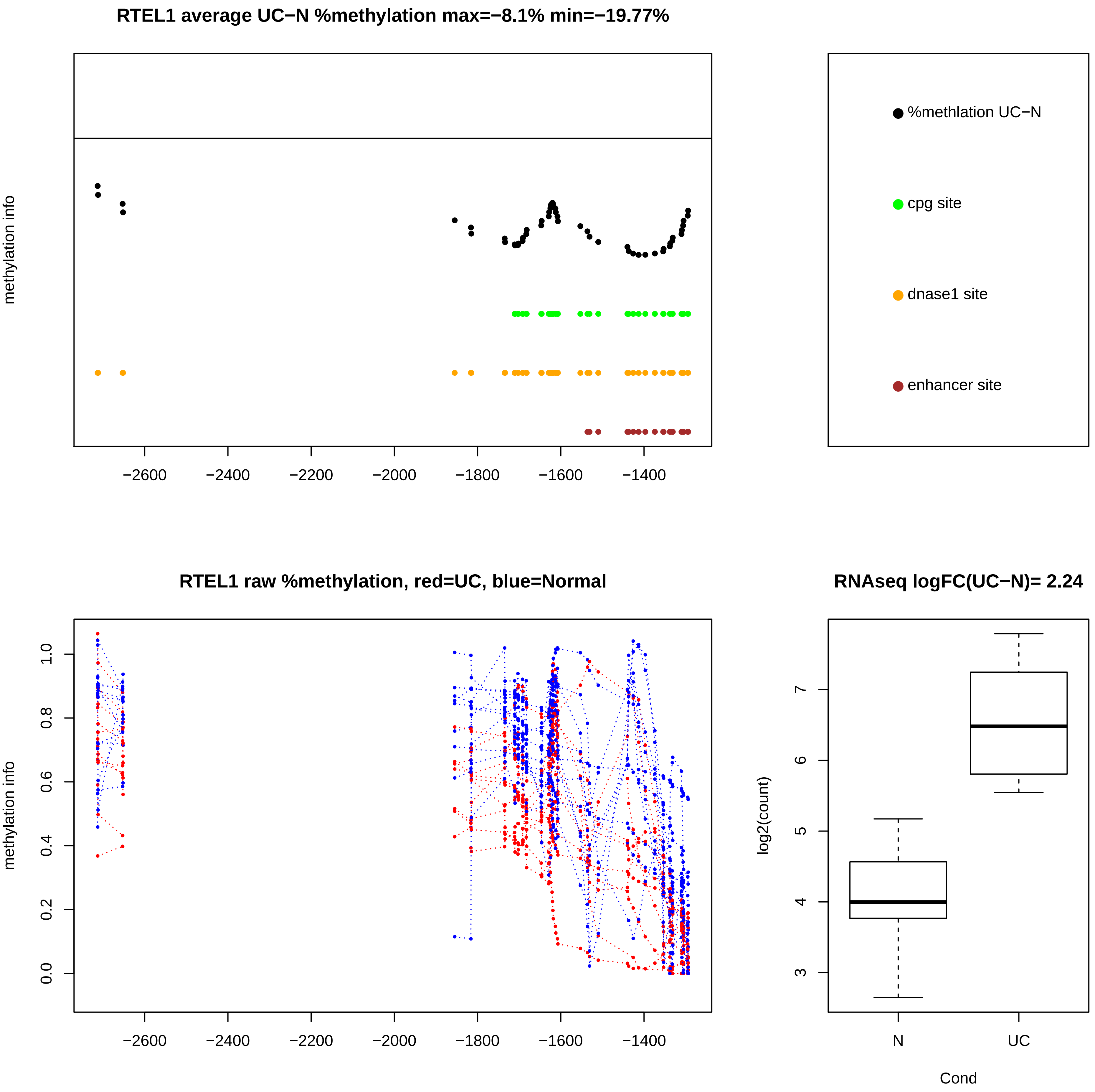




ROBO1 average UC−N %methylation max=−2.09% min=−2.59%

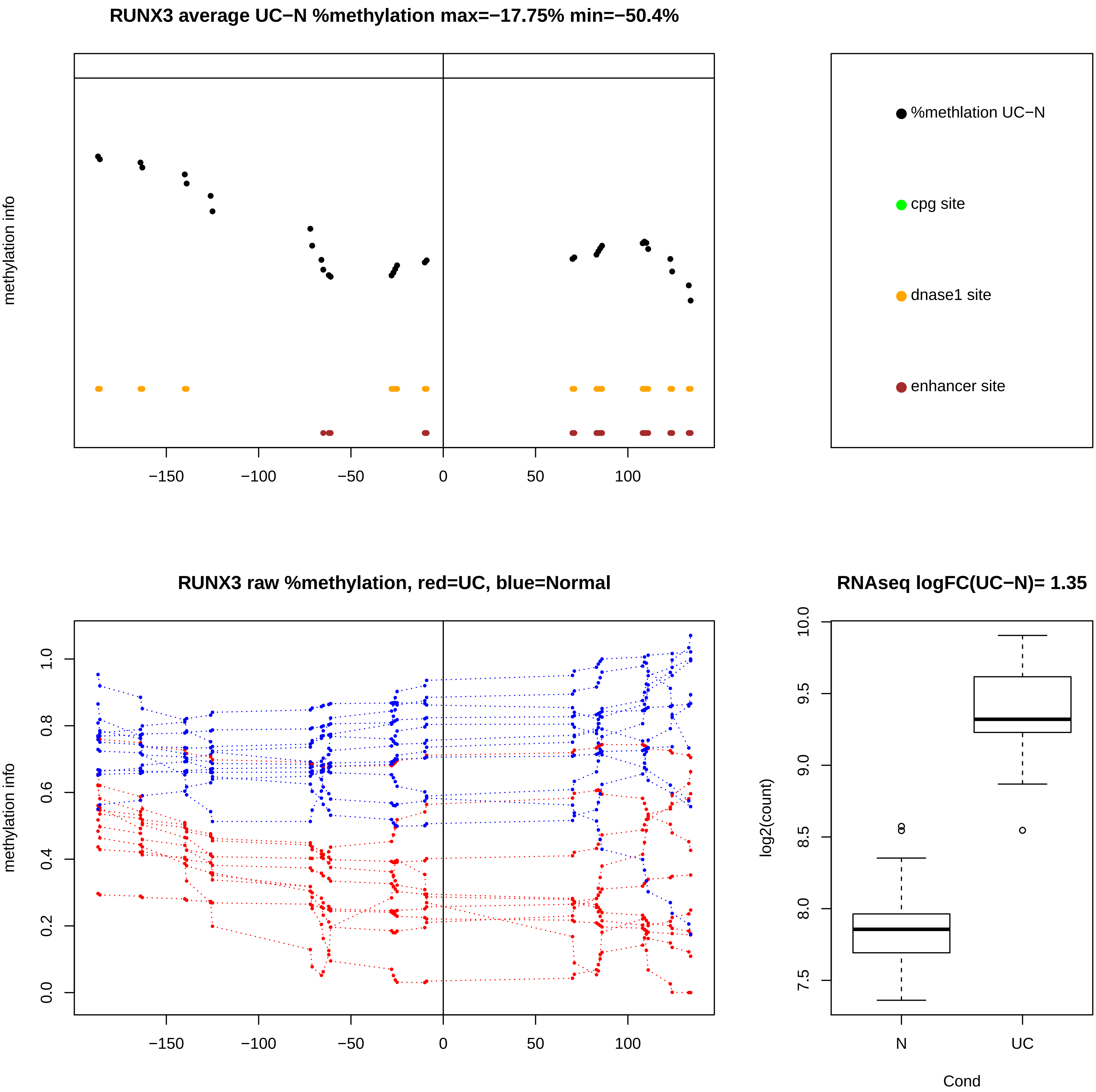
ROBO1 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.04


RTEL1 average UC−N %methylation max=−8.1% min=−19.77%

RTEL1 raw %methylation, red=UC, blue=Normal

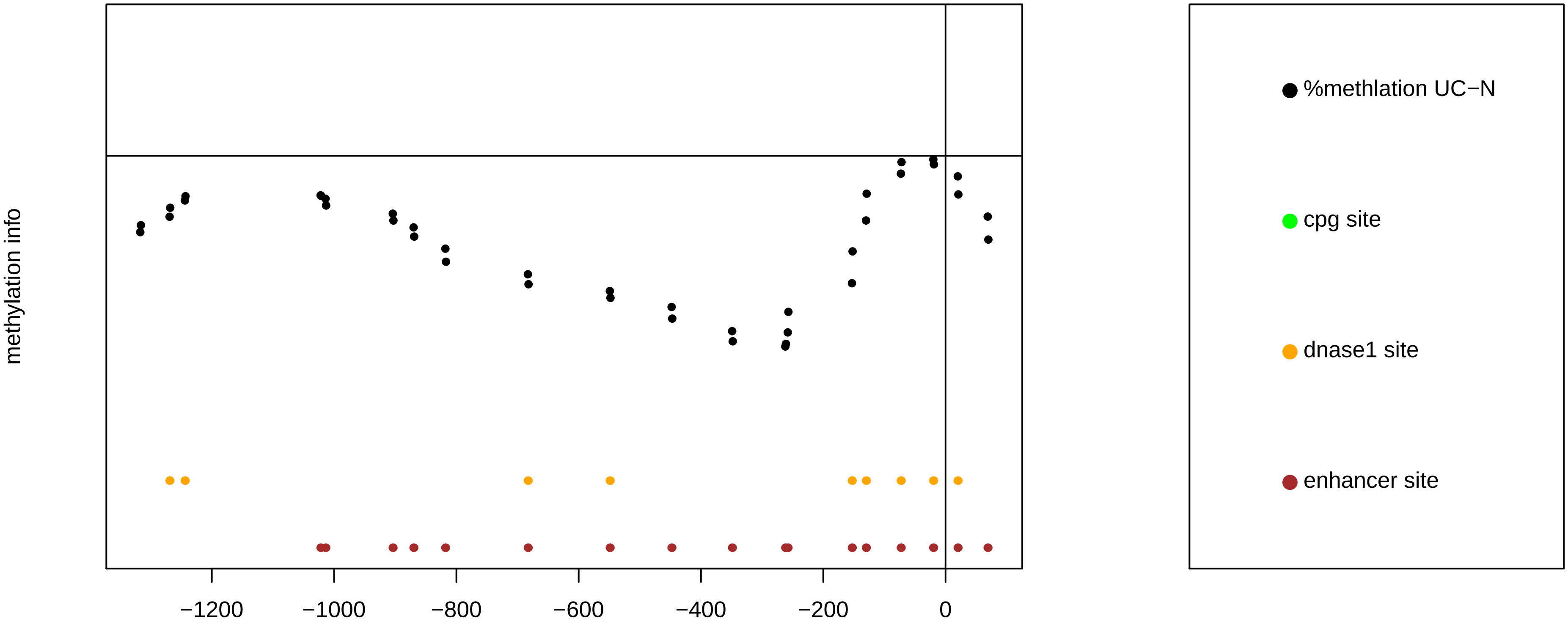
RNAseq logFC(UC−N)= 2.24


RUNX3 average UC−N %methylation max=−17.75% min=−50.4%

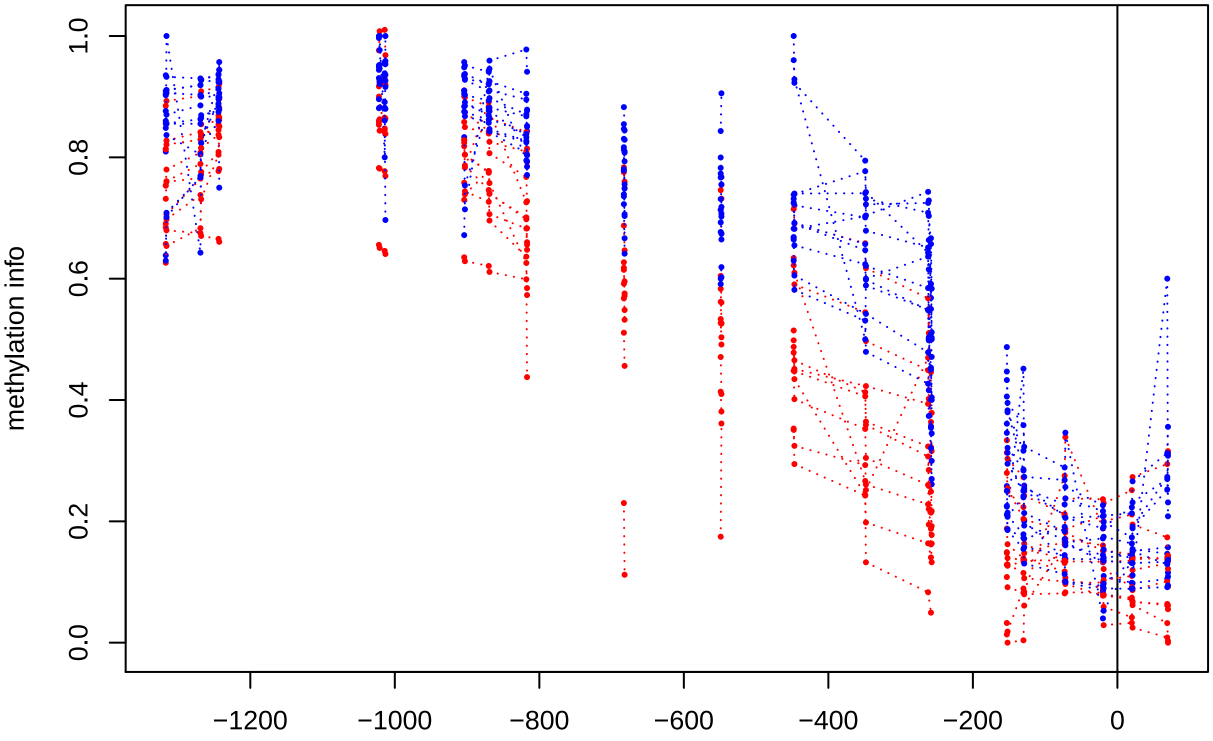
RUNX3 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.35

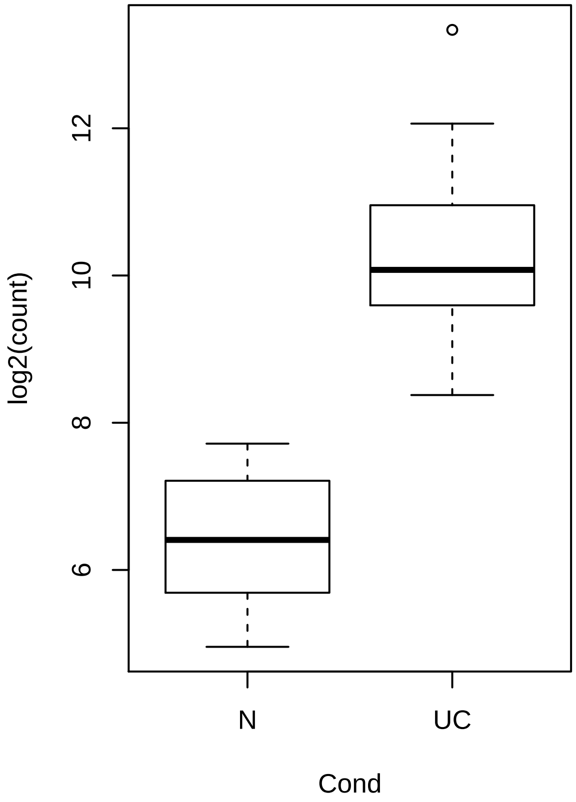
S100A9 average UC−N %methylation max=−0.54% min=−28.44%



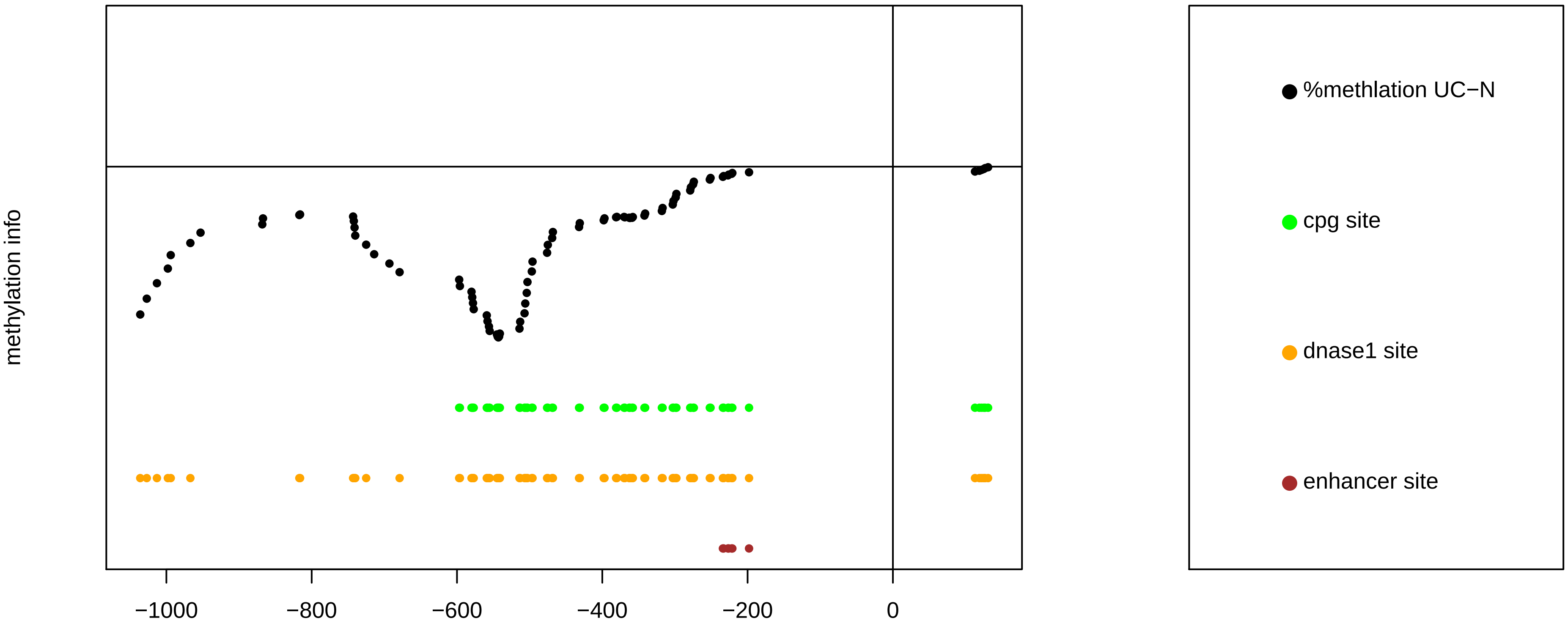
S100A9 raw %methylation, red=UC, blue=Normal



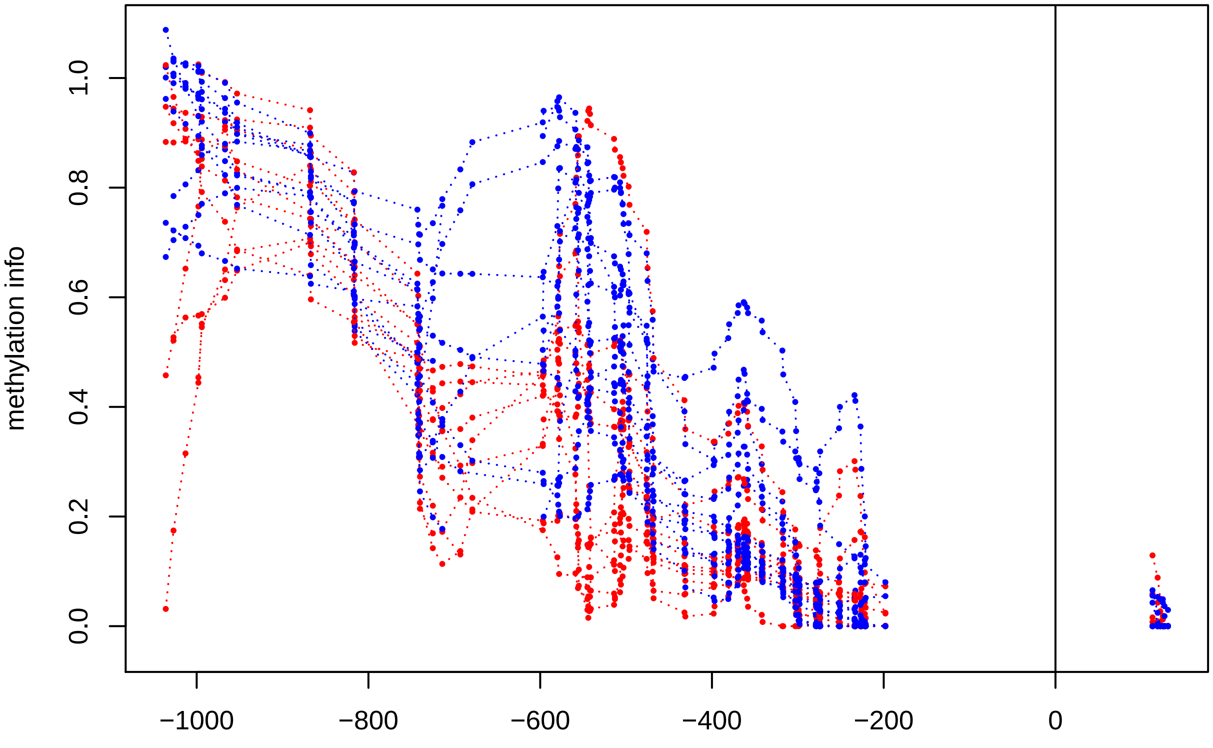
RNAseq logFC(UC−N)= 3.46



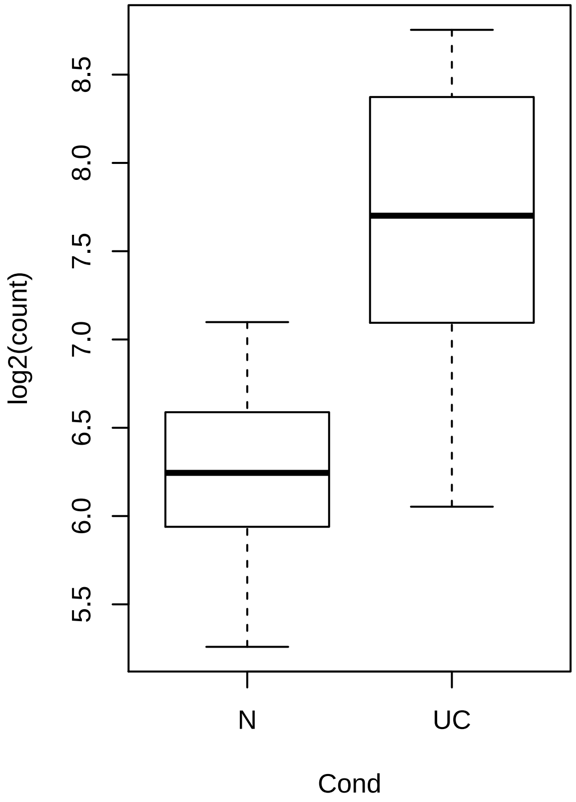
S1PR3 average UC−N %methylation max=−0.08% min=−24.27%

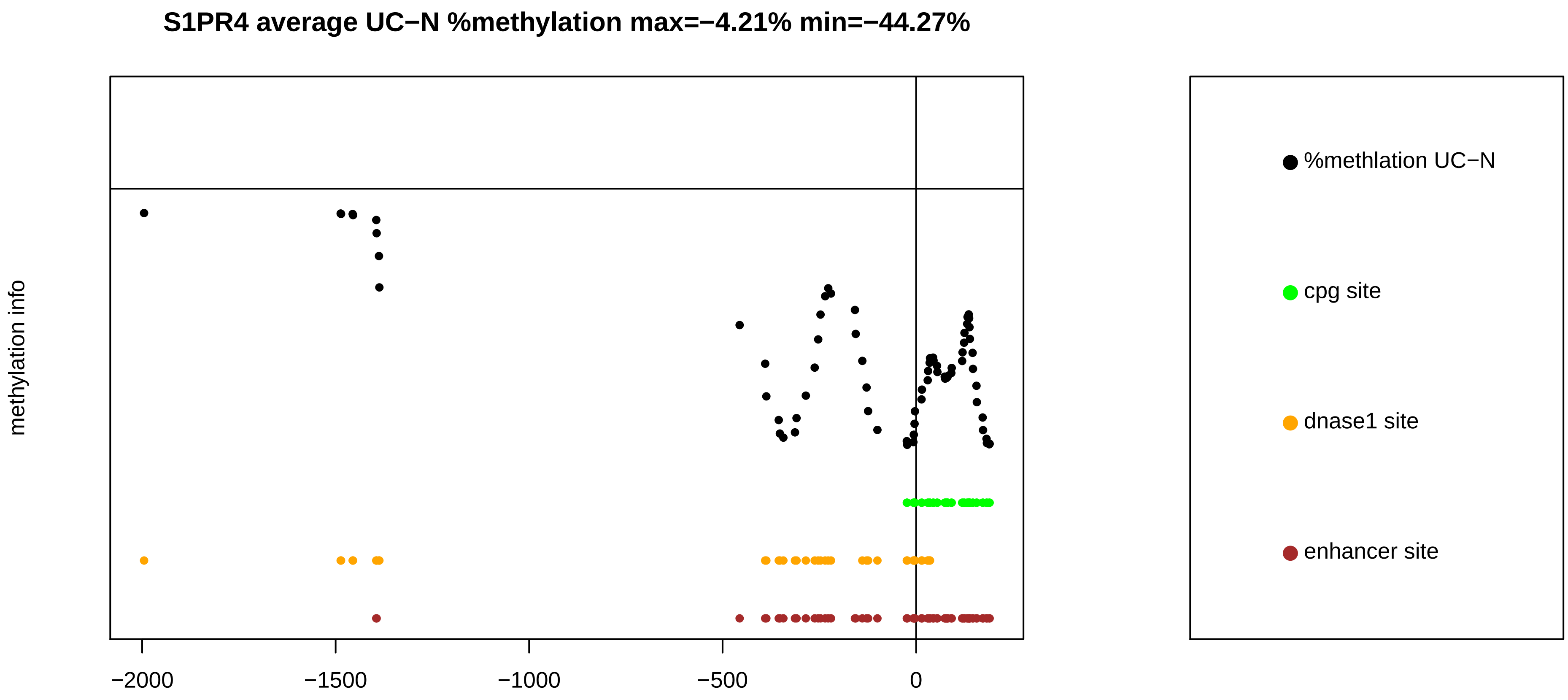


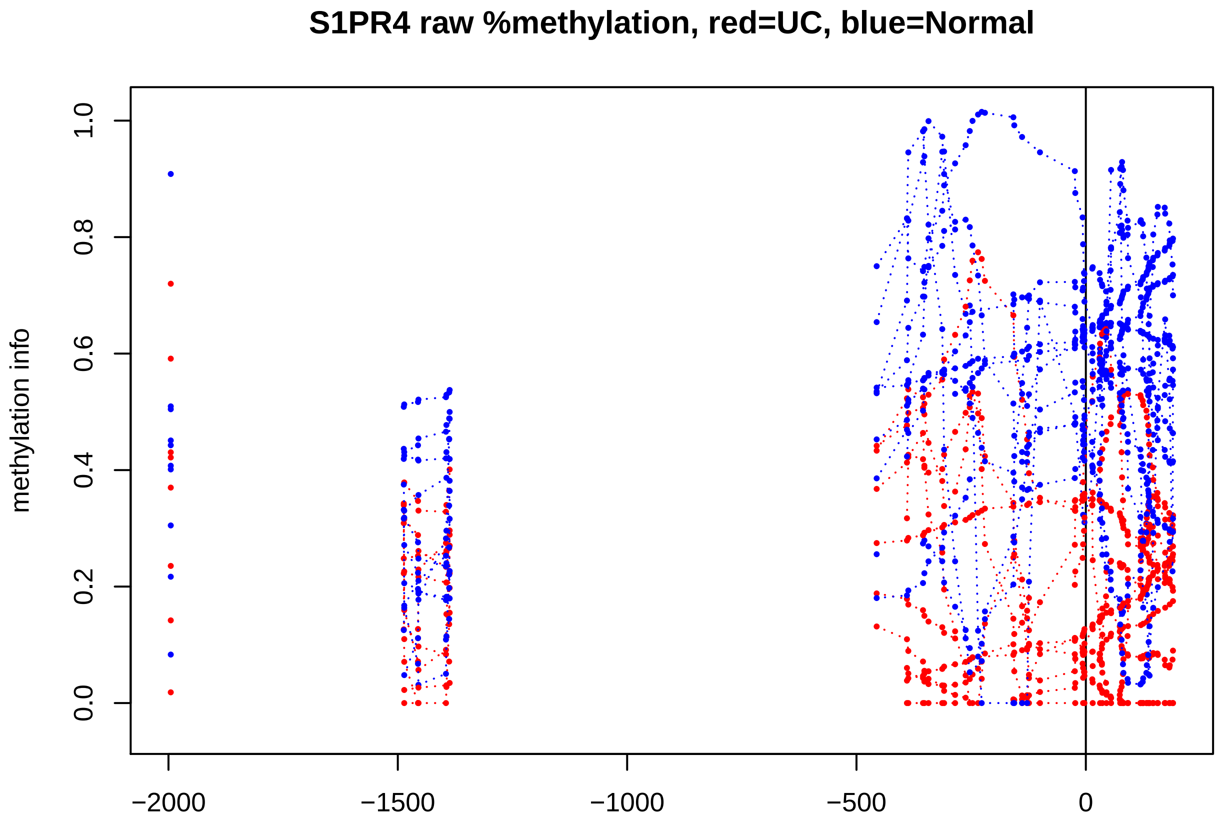
S1PR3 raw %methylation, red=UC, blue=Normal

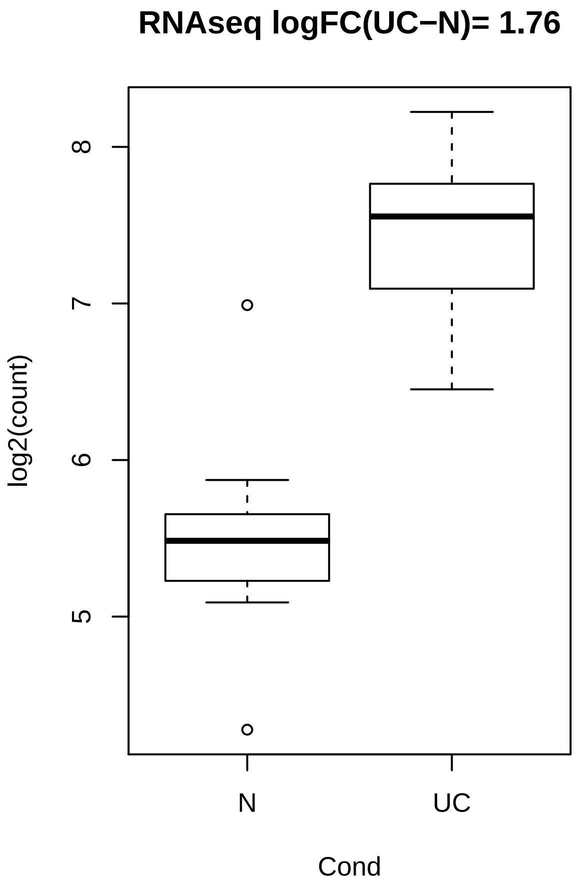


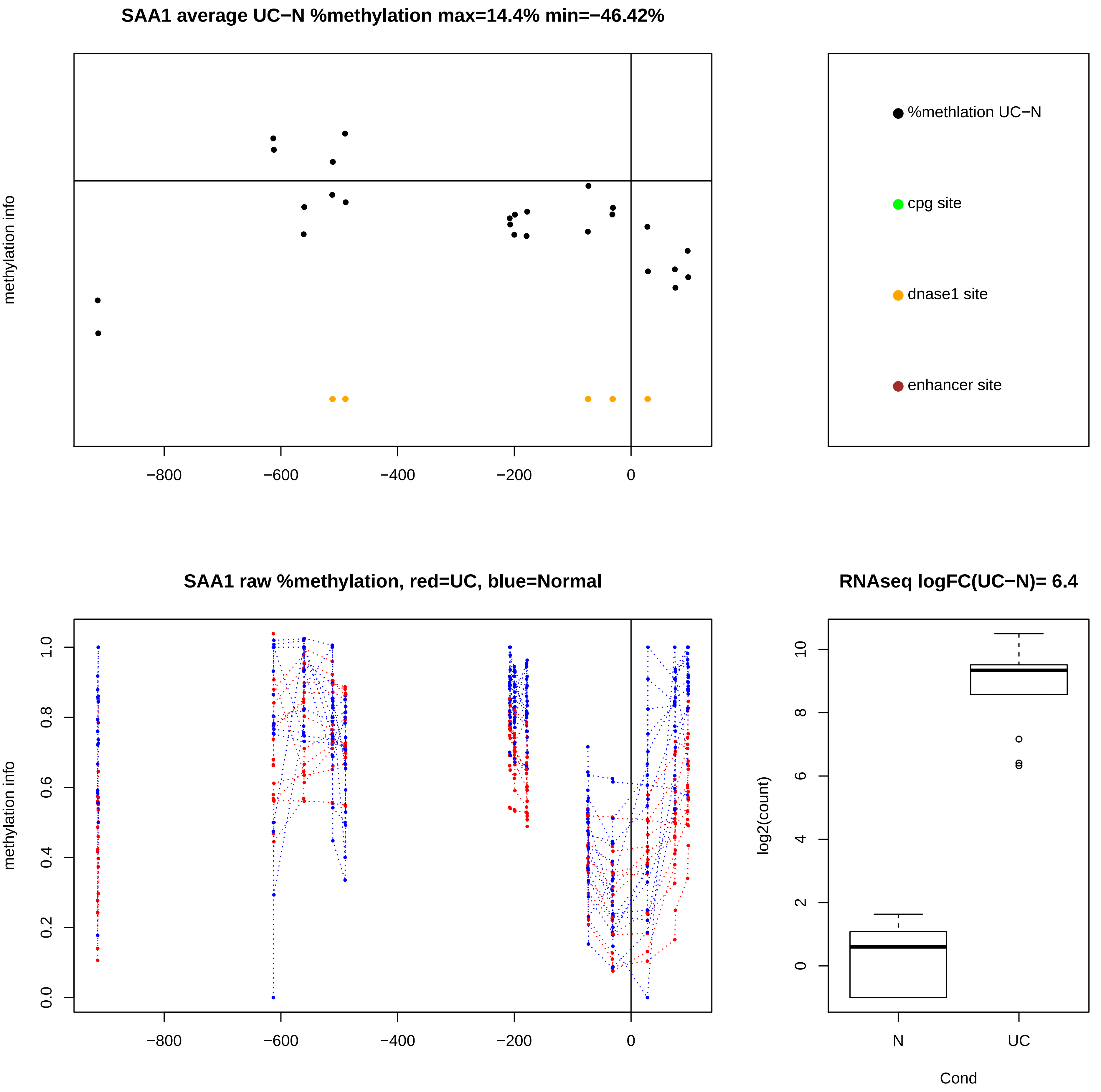
RNAseq logFC(UC−N)= 1.39




S1PR4 average UC−N %methylation max=−4.21% min=−44.27%


S1PR4 raw %methylation, red=UC, blue=Normal

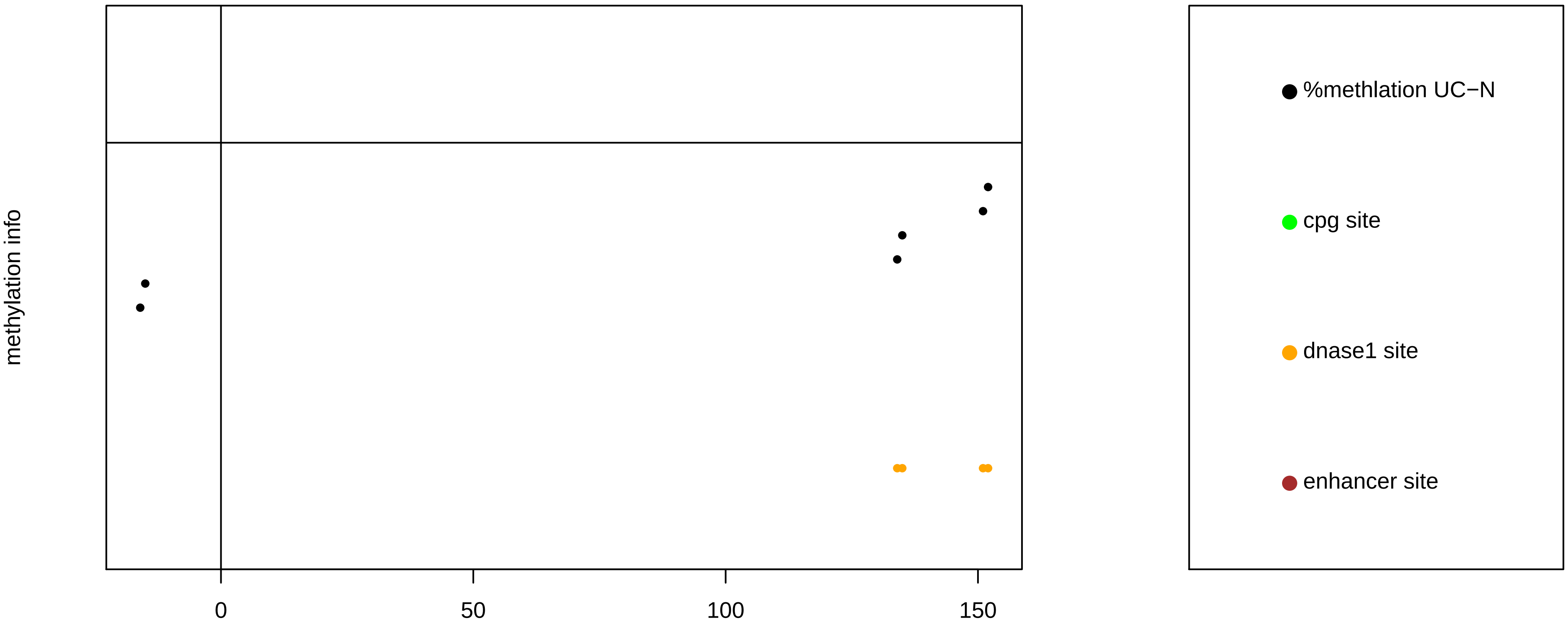

RNAseq logFC(UC−N)= 1.76


SAA1 average UC−N %methylation max=14.4% min=−46.42%

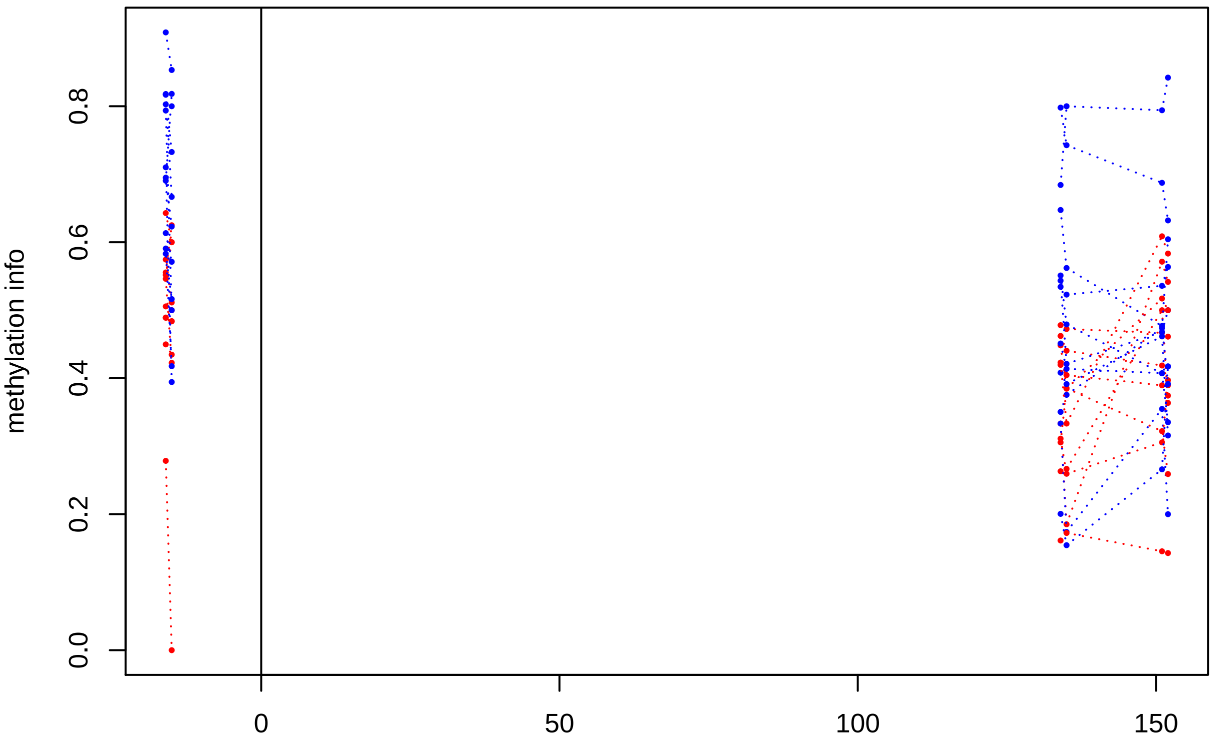
SAA1 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 6.4

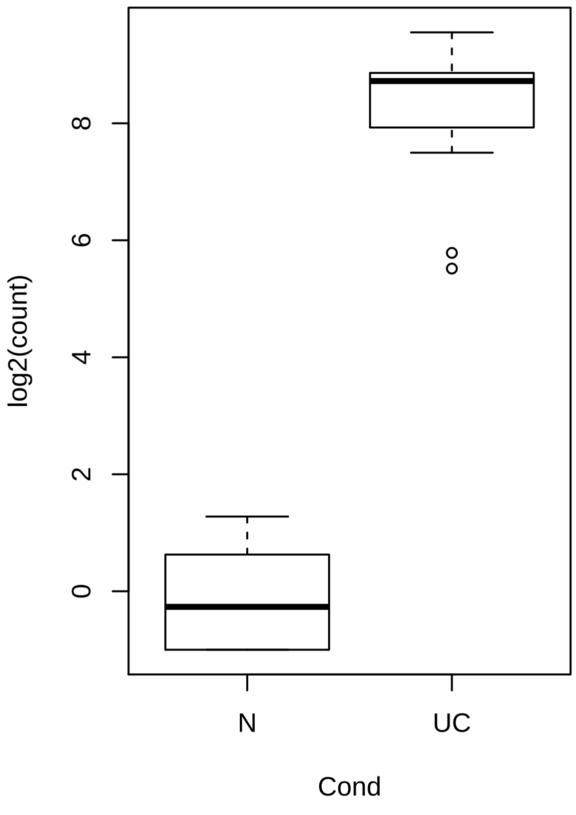
SAA2 average UC−N %methylation max=−5.52% min=−20.55%

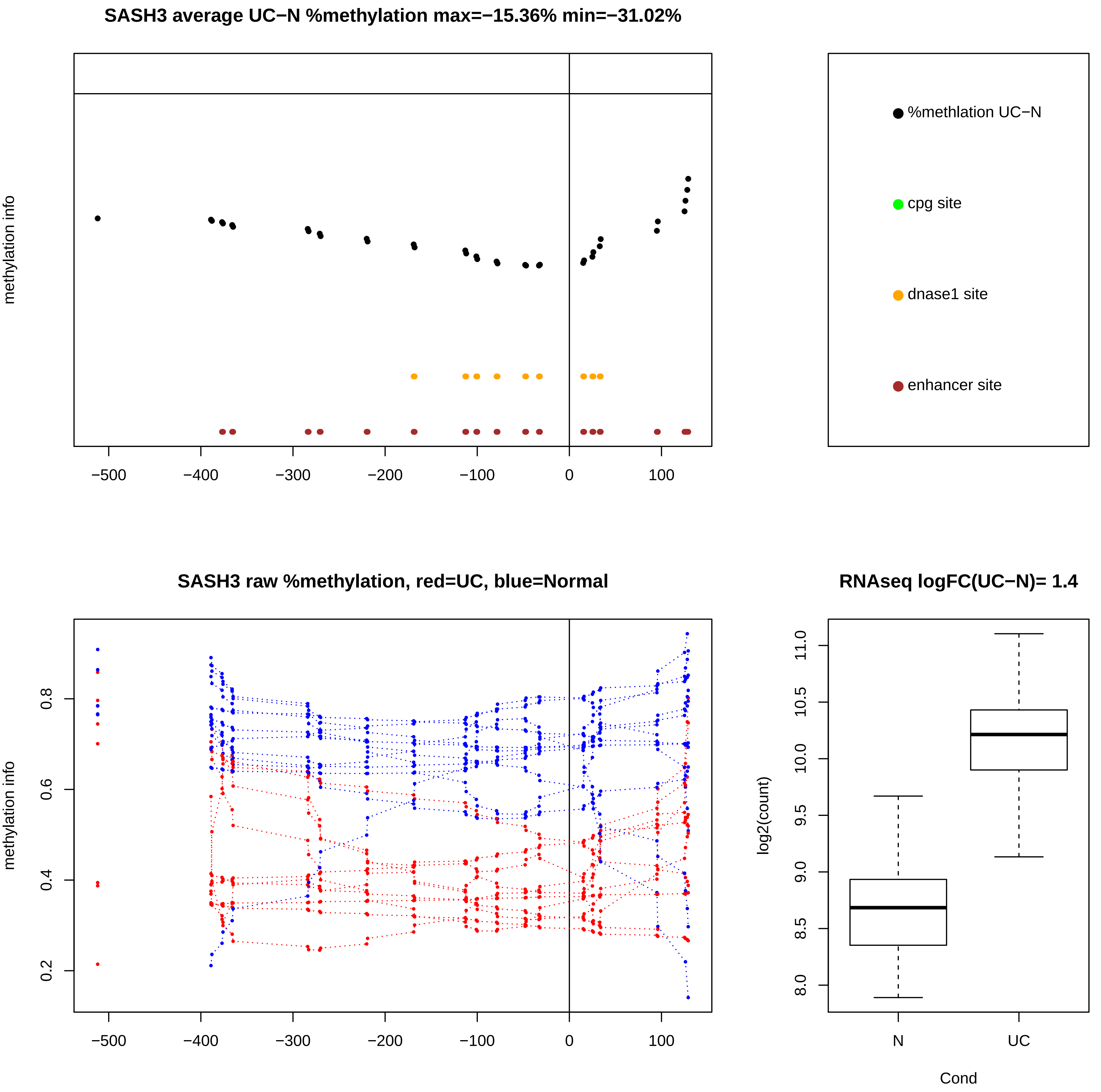


SAA2 raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 6.23

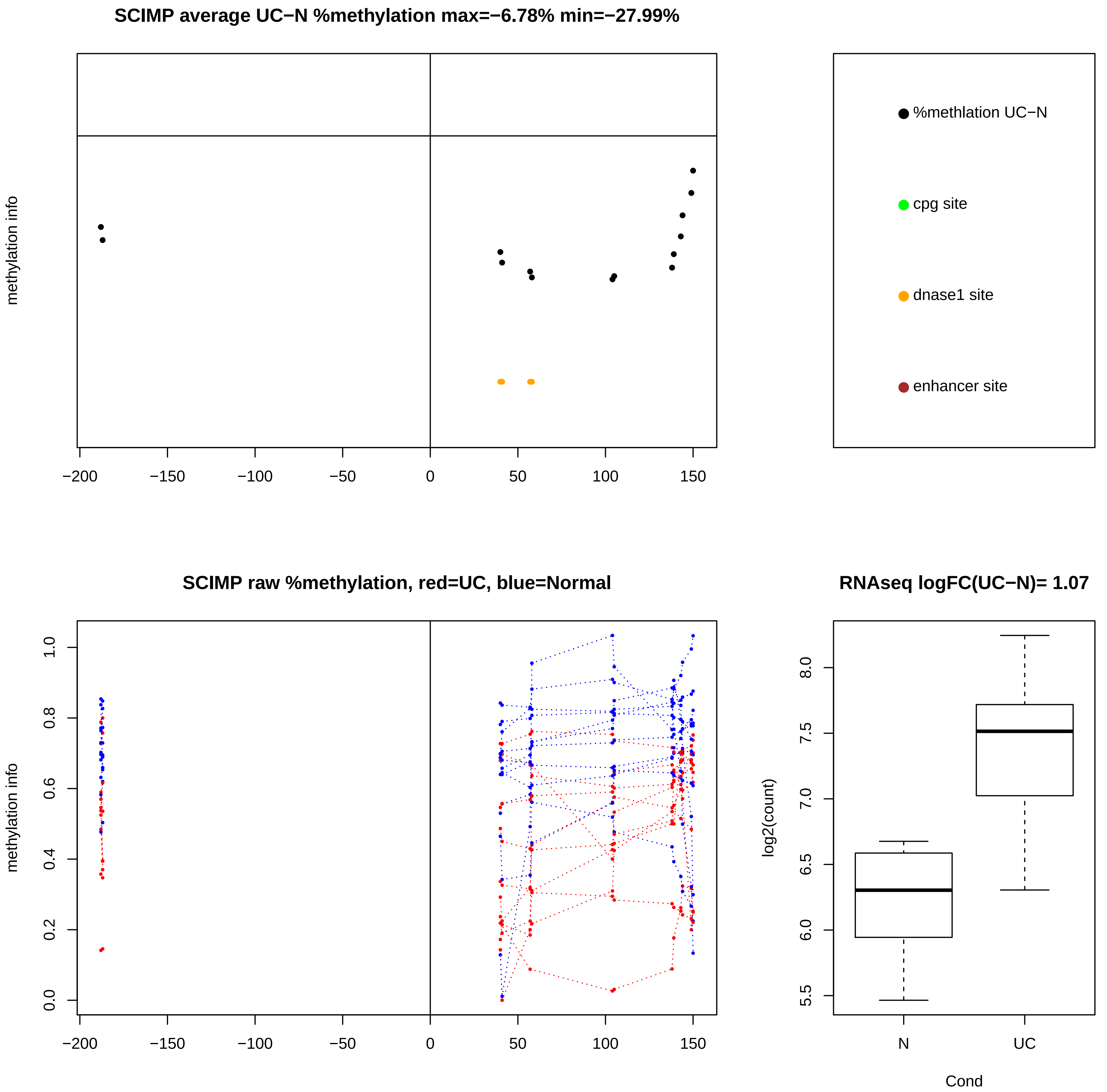


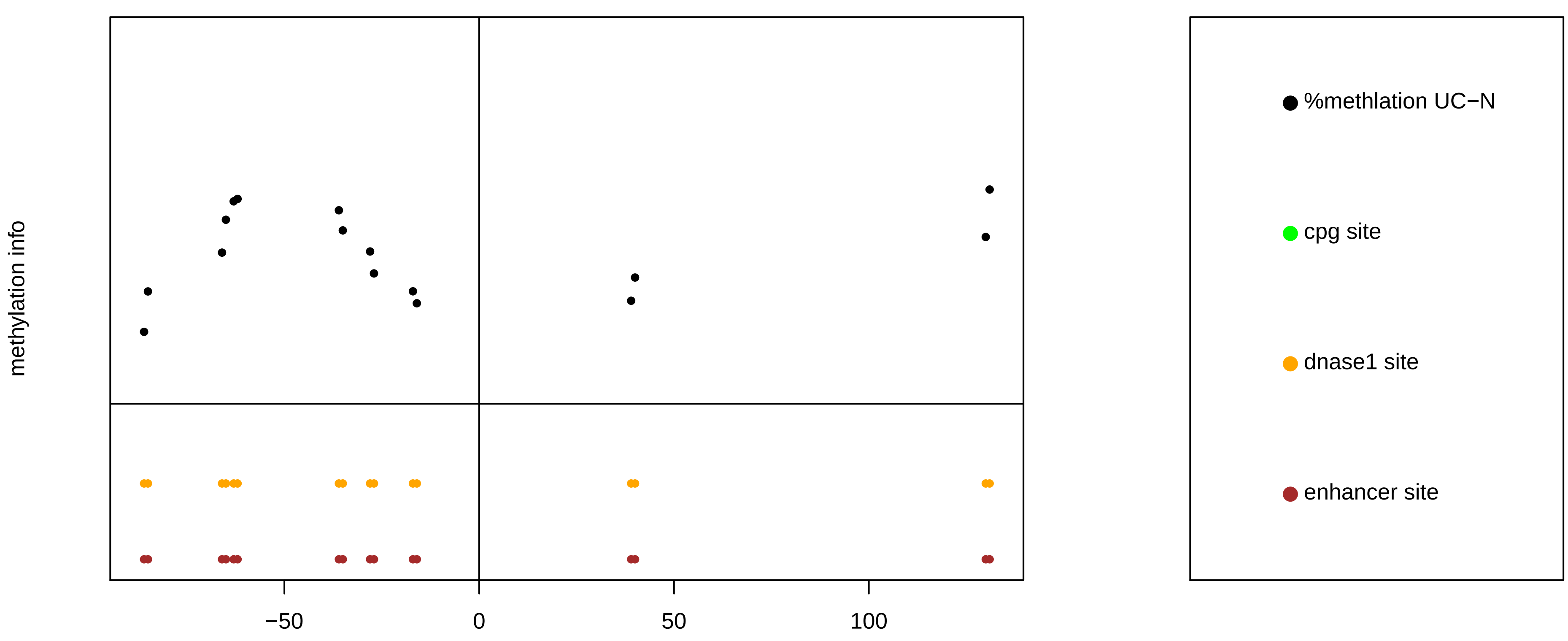


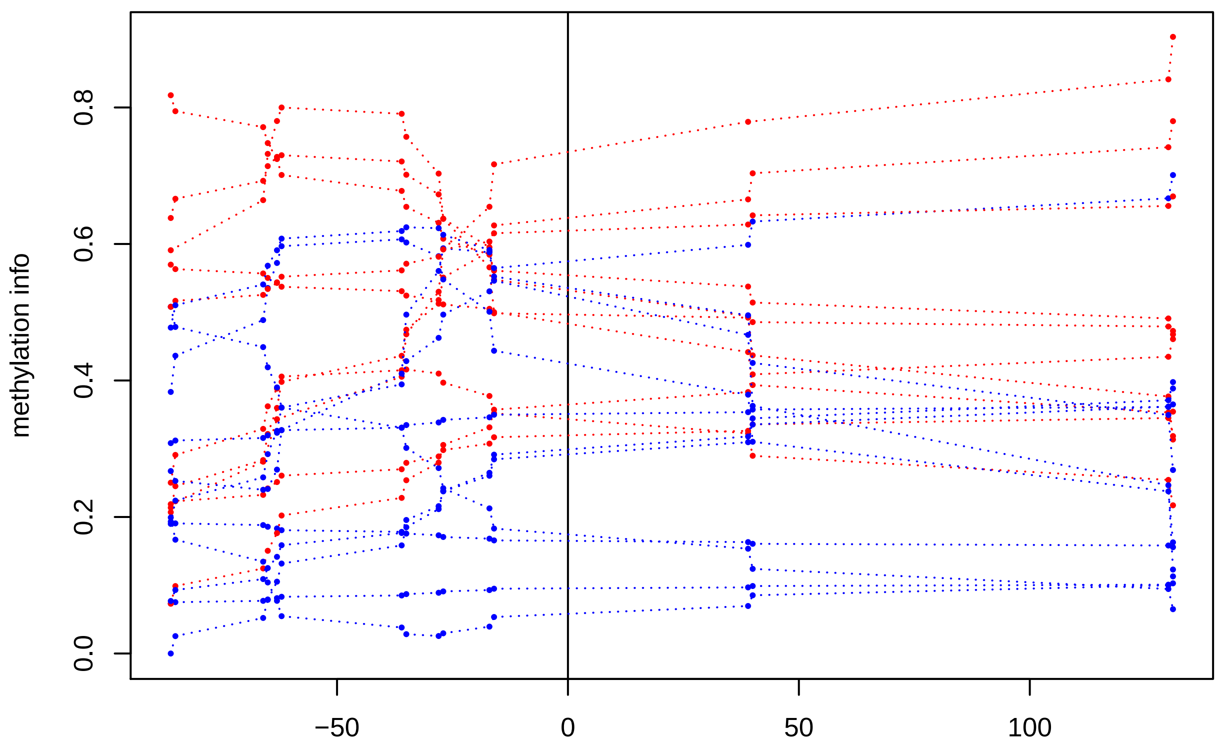
SASH3 average UC−N %methylation max=−15.36% min=−31.02%

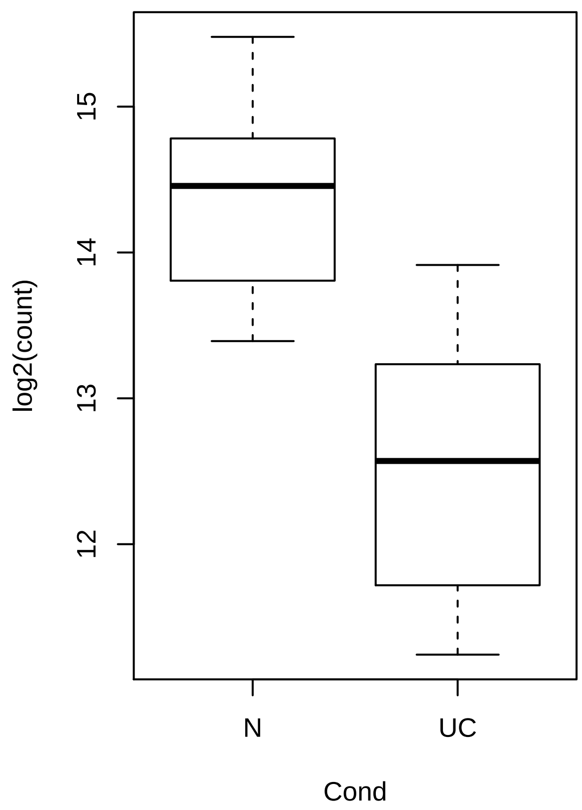
SASH3 raw %methylation, red=UC, blue=Normal

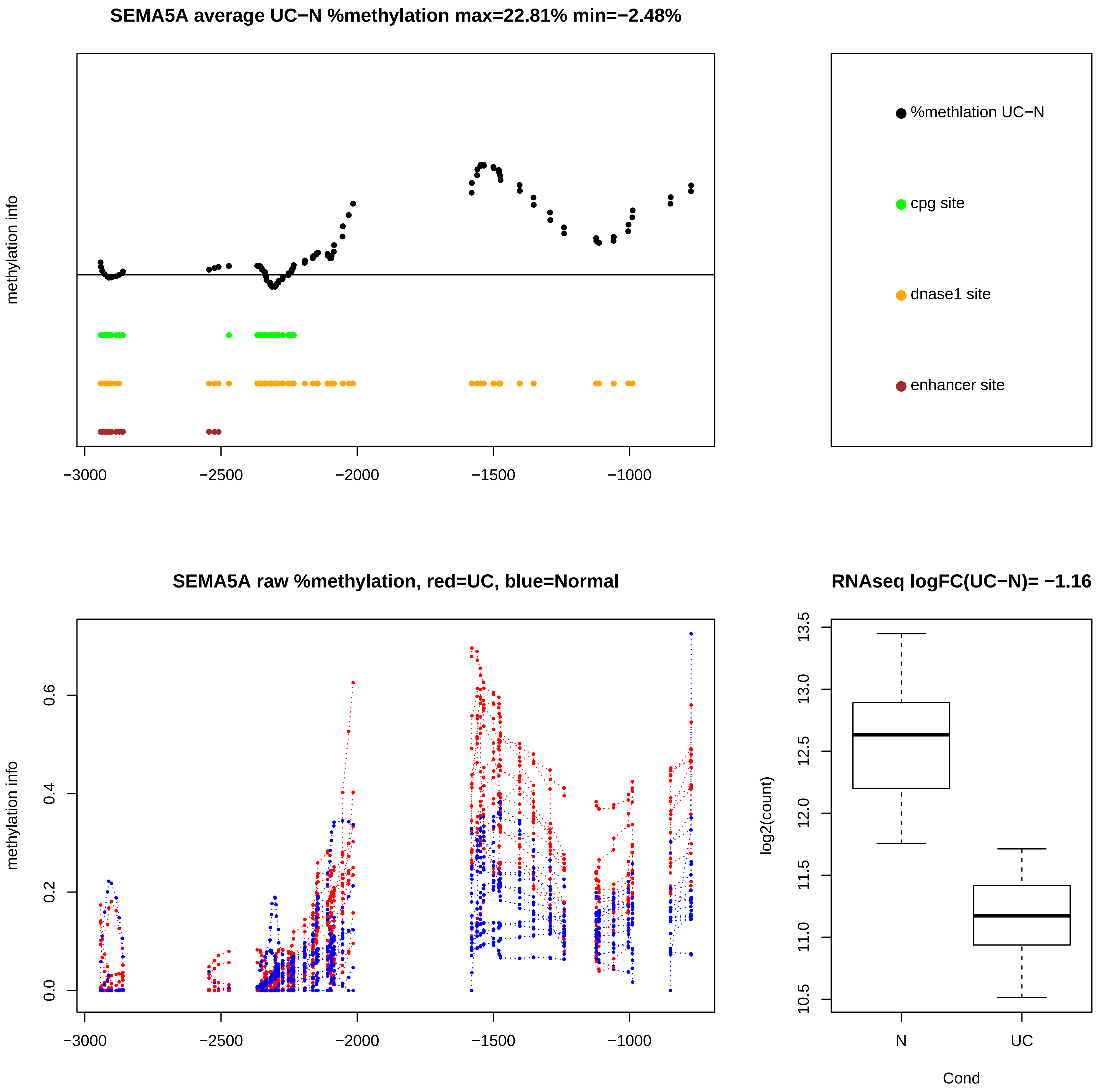
RNAseq logFC(UC−N)= 1.4


SCIMP average UC−N %methylation max=−6.78% min=−27.99%
methylation info
−200
−150
−100
−50
0
50
100
150
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
SCIMP raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−200
−150
−100
−50
0
50
100
150
RNAseq logFC(UC−N)= 1.07
log2(count)
5.5
6.0
6.5
7.0
7.5
8.0
N
UC
Cond


SELENBP1 average UC−N %methylation max=28.26% min=9.49%


SELENBP1 raw %methylation, red=UC, blue=Normal

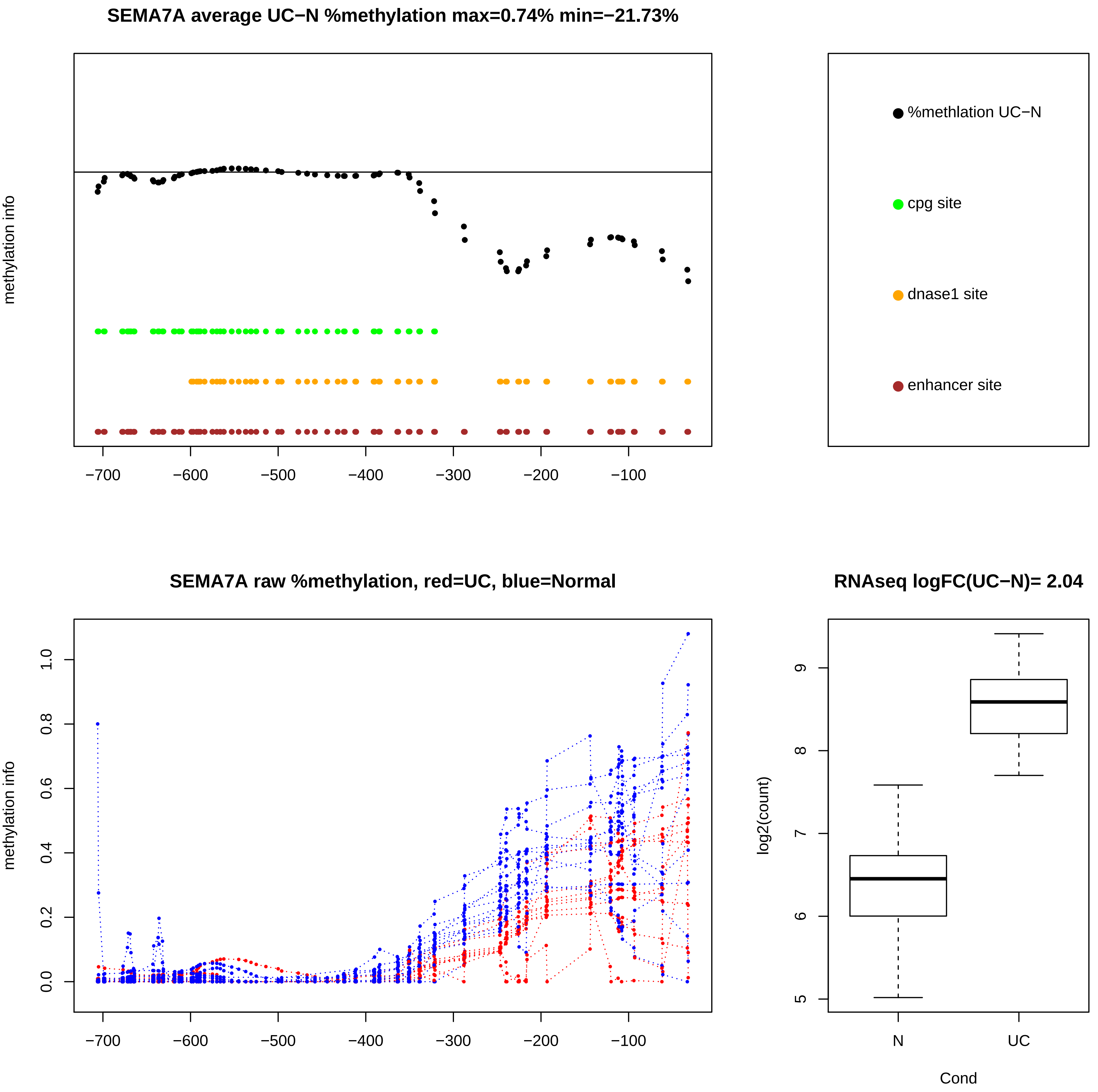

RNAseq logFC(UC−N)= −1.41



SEMA5A average UC−N %methylation max=22.81% min=−2.48%

SEMA5A raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= −1.16

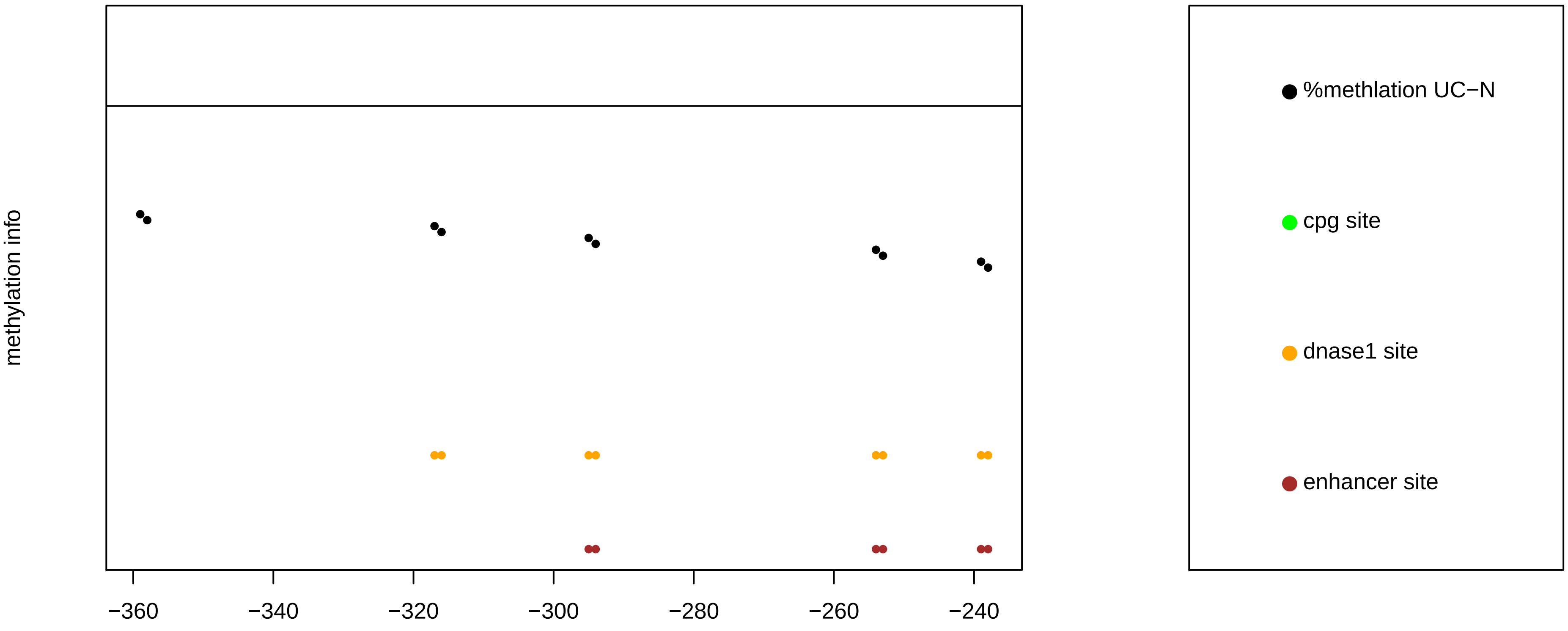


SEMA7A average UC−N %methylation max=0.74% min=−21.73%

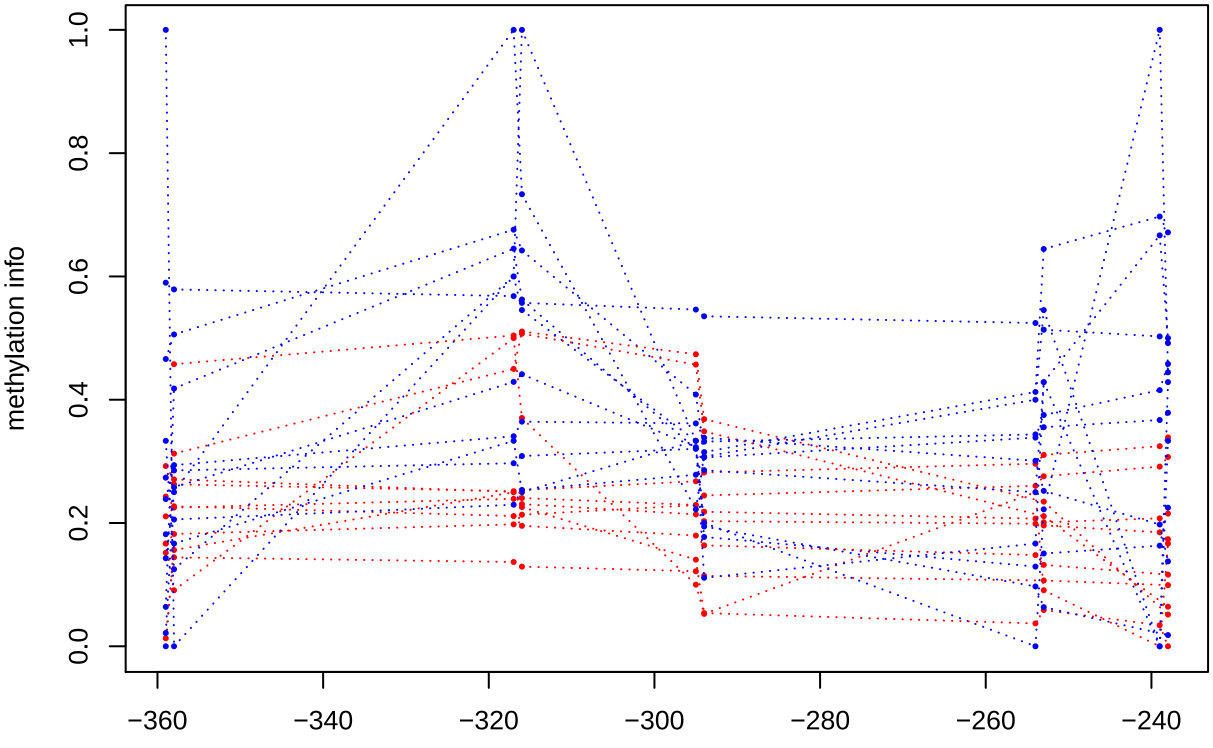
SEMA7A raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 2.04

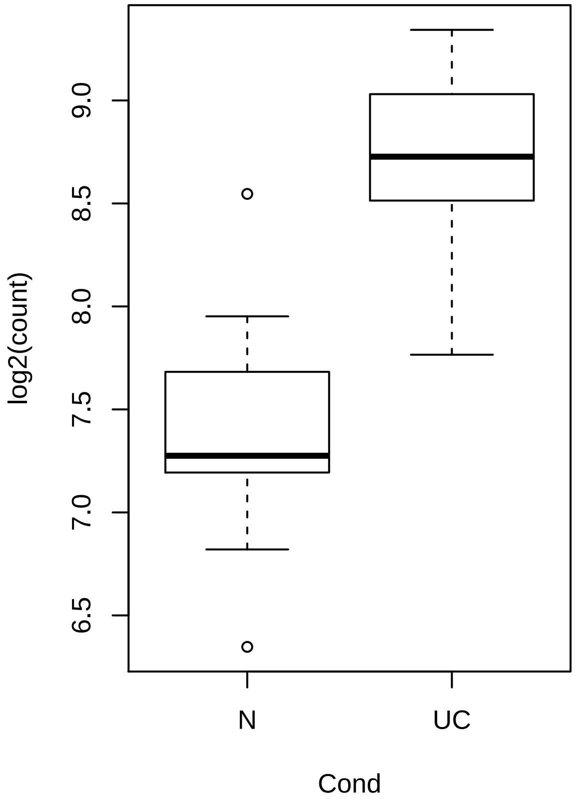
SEPT1 average UC−N %methylation max=−11.54% min=−17.22%

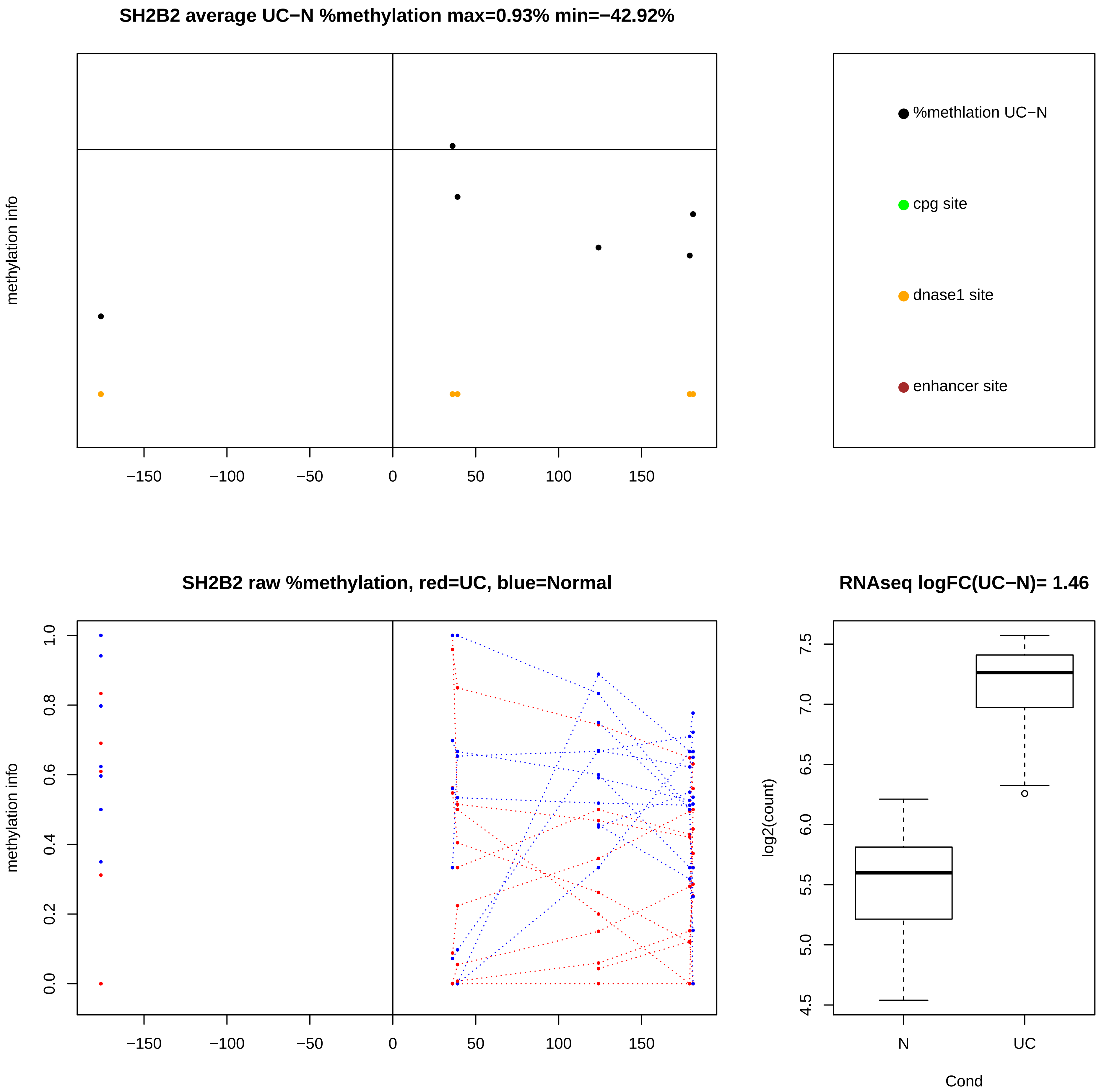


SEPT1 raw %methylation, red=UC, blue=Normal

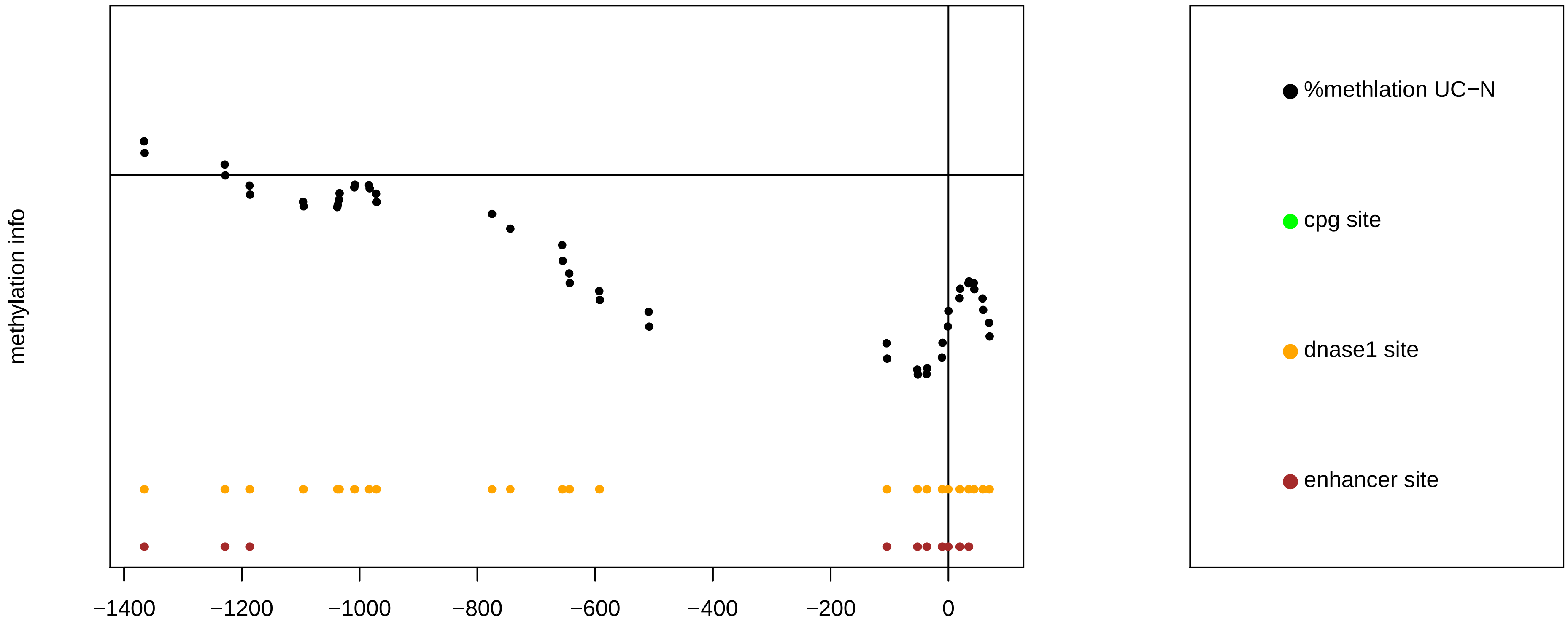


RNAseq logFC(UC−N)= 1.21

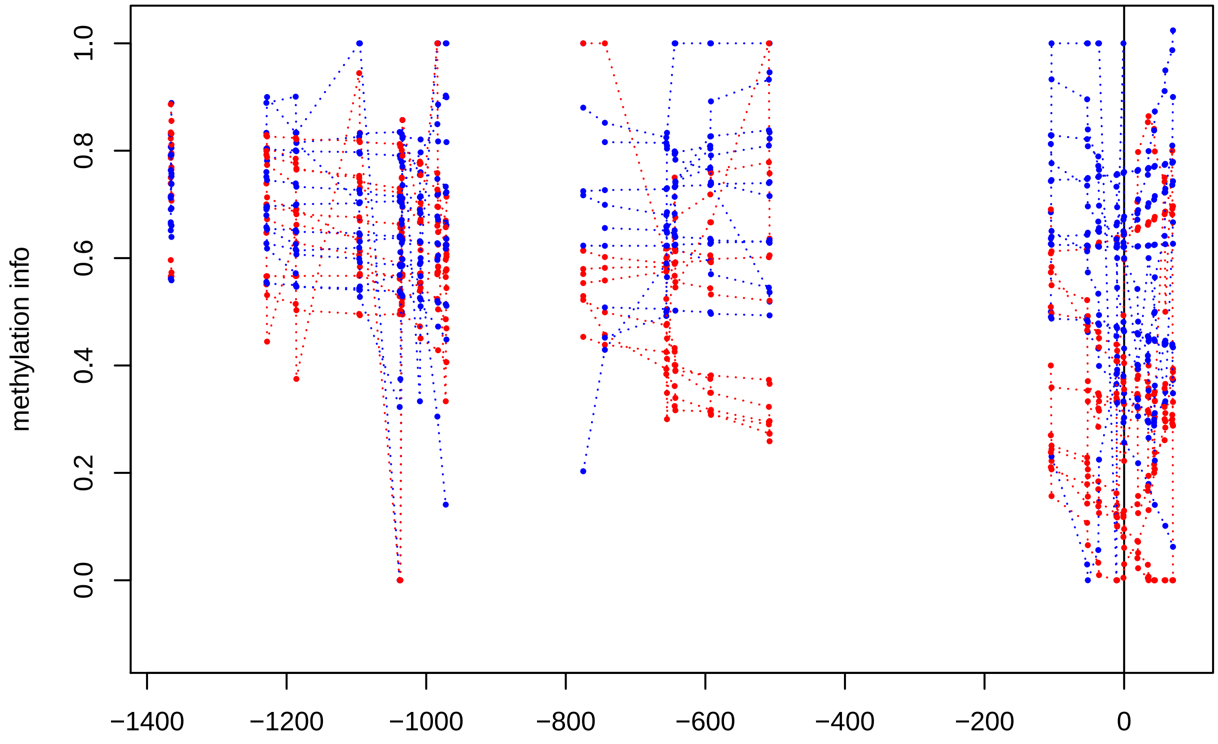



SH2B2 average UC−N %methylation max=0.93% min=−42.92%
methylation info
−150
−100
−50
0
50
100
150
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
SH2B2 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−150
−100
−50
0
50
100
150
RNAseq logFC(UC−N)= 1.46
log2(count)
4.5
5.0
5.5
6.0
6.5
7.0
7.5
N
UC
Cond

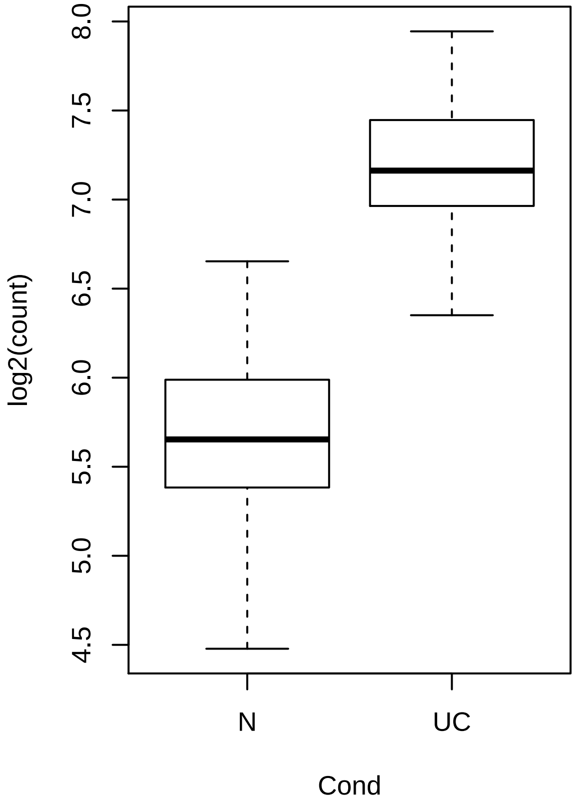
SH2D2A average UC−N %methylation max=5.85% min=−34.77%

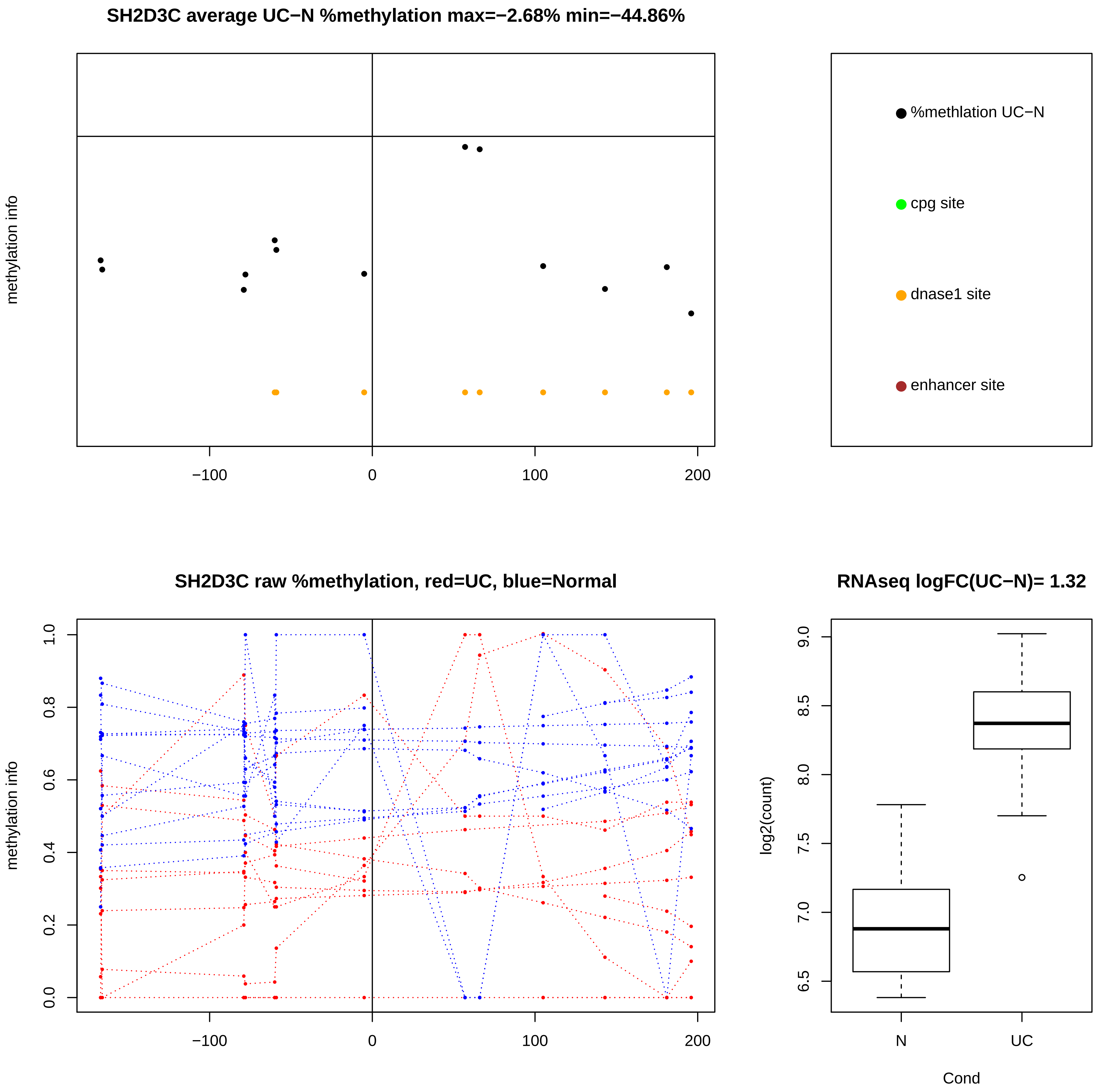


SH2D2A raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 1.37



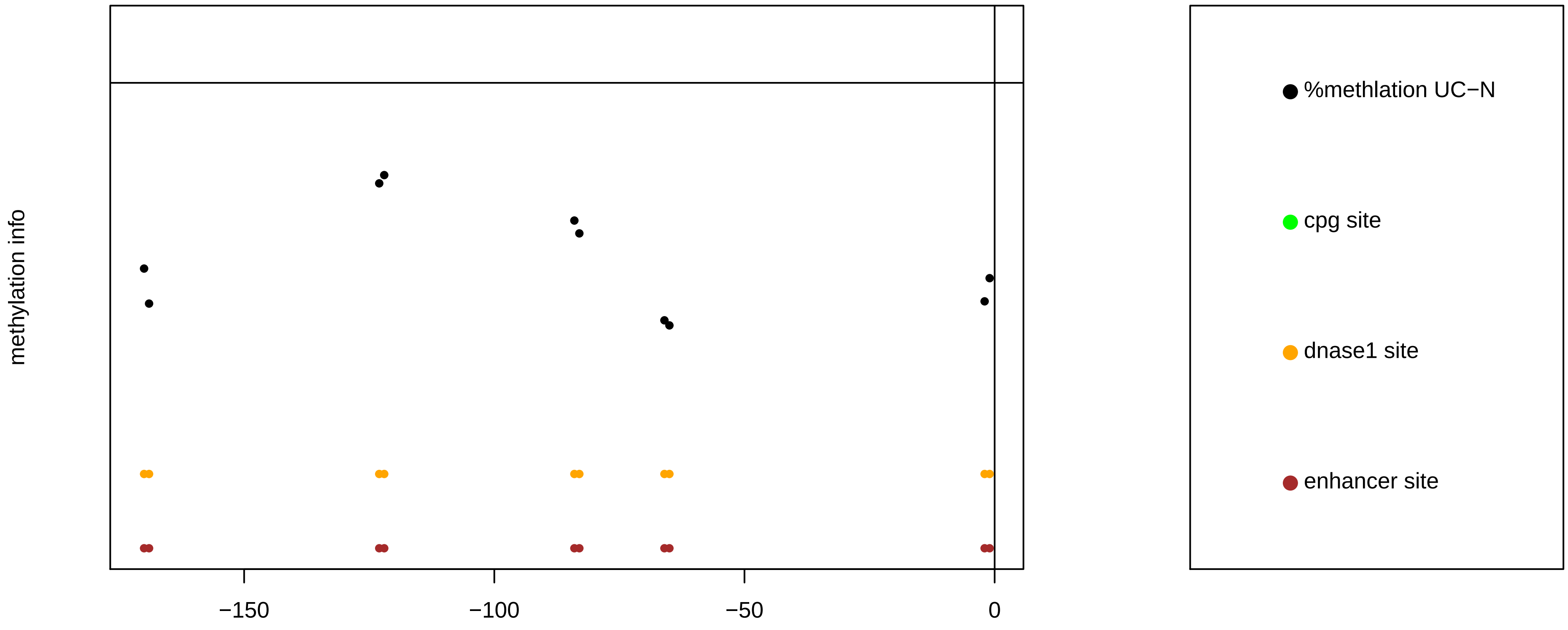


SH2D3C average UC−N %methylation max=−2.68% min=−44.86%

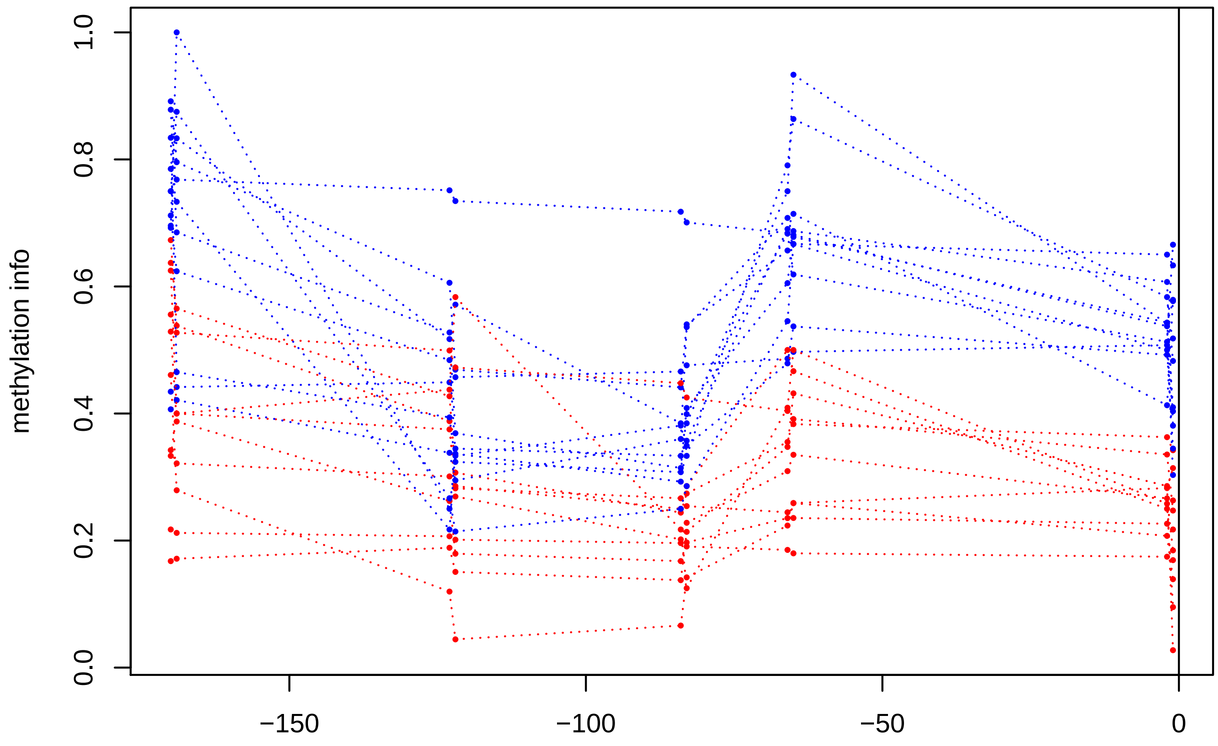
SH2D3C raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.32

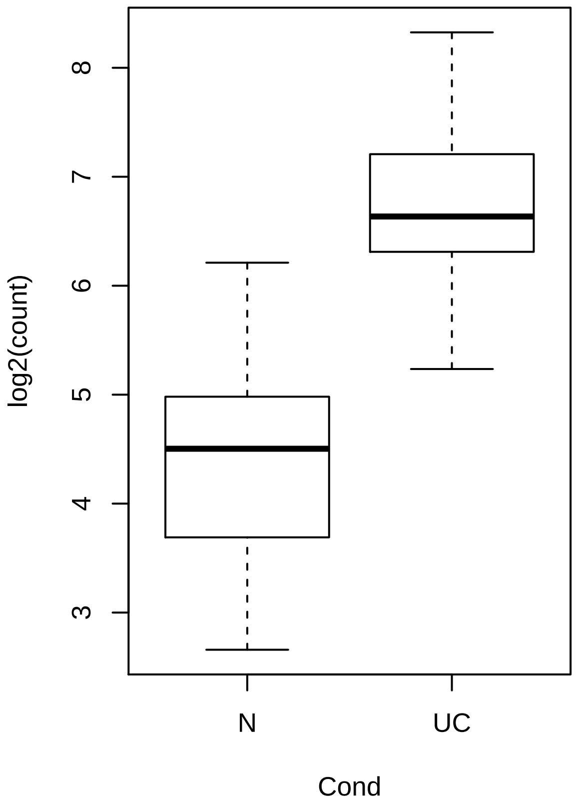
SIRPB1 average UC−N %methylation max=−12.42% min=−32.65%

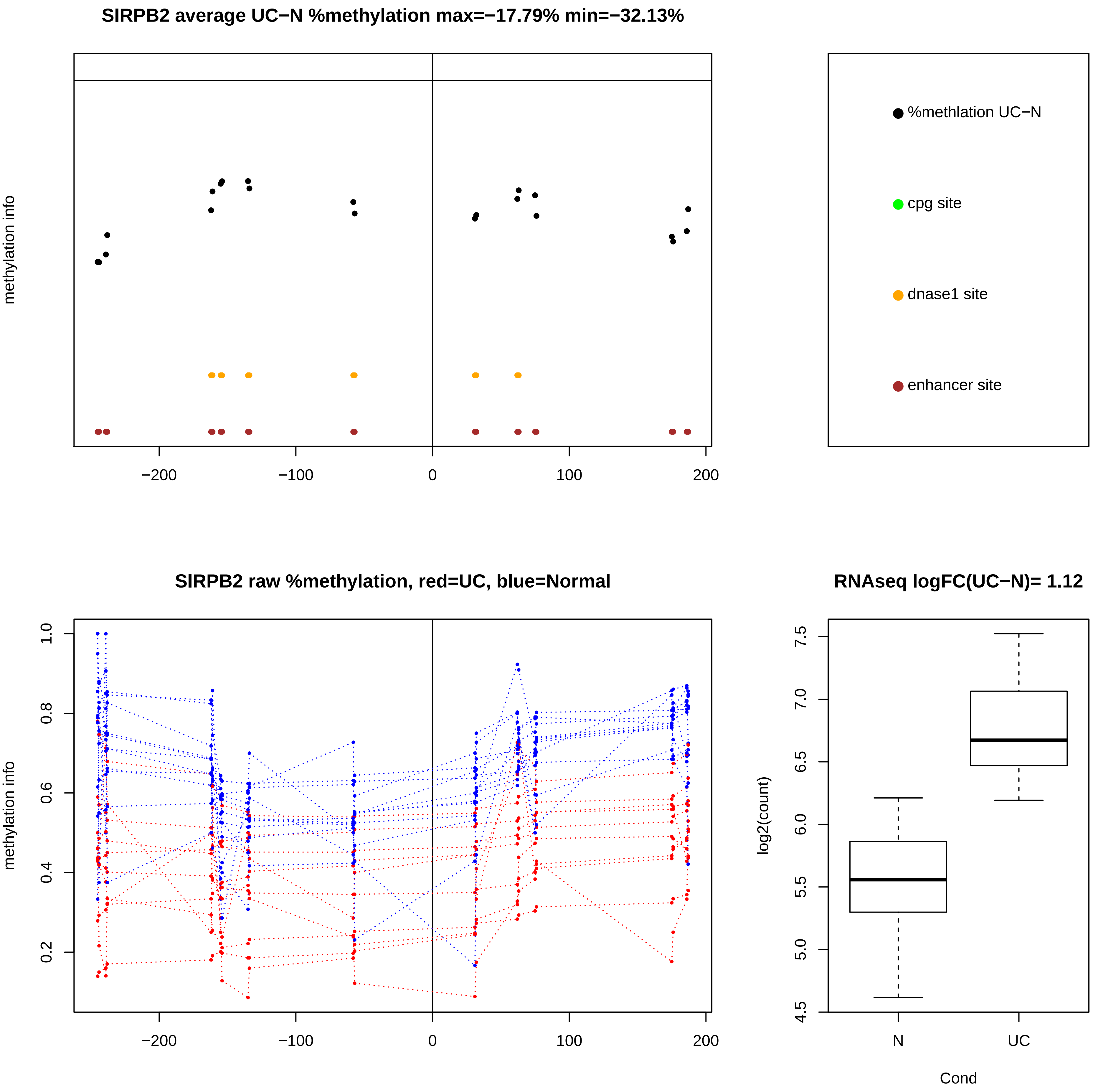


SIRPB1 raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 1.91



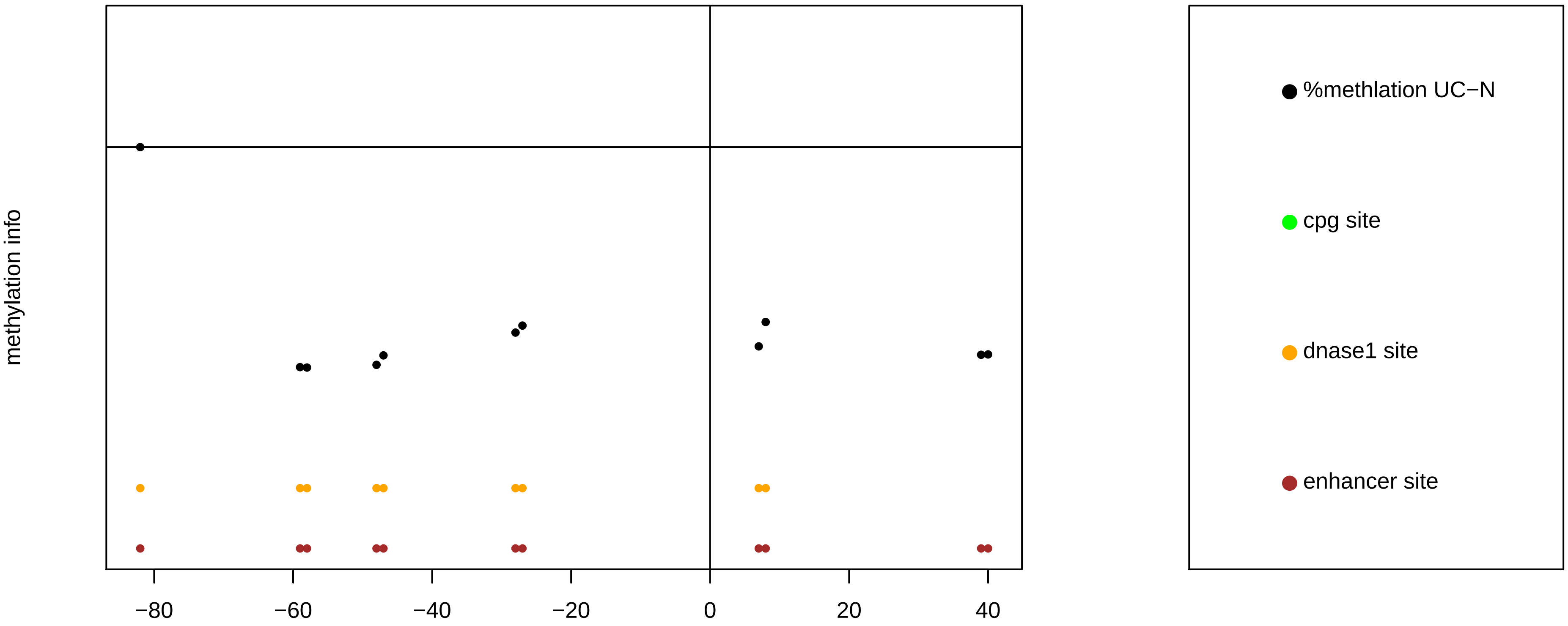


SIRPB2 average UC−N %methylation max=−17.79% min=−32.13%

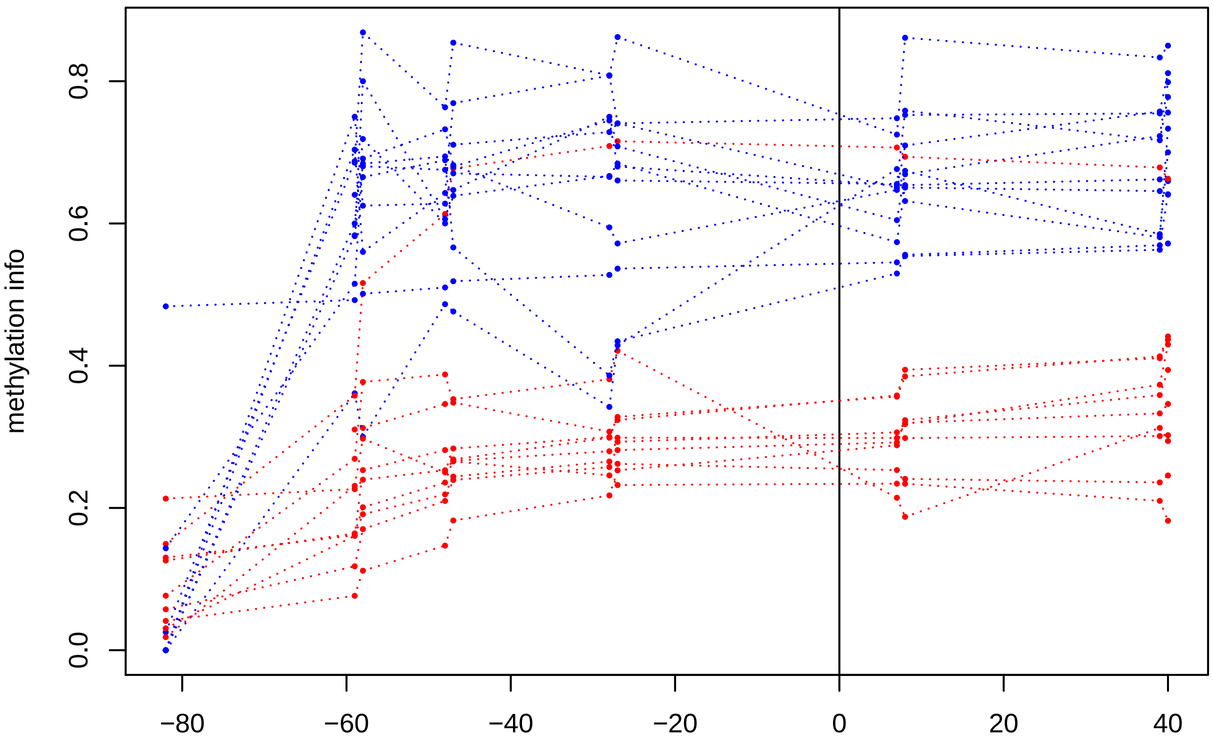
SIRPB2 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.12

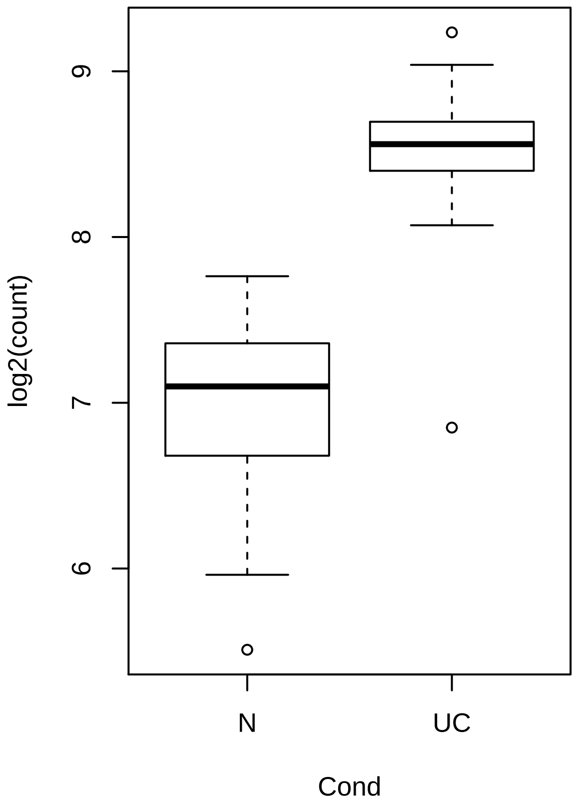
SLAMF1 average UC−N %methylation max=0% min=−36.55%



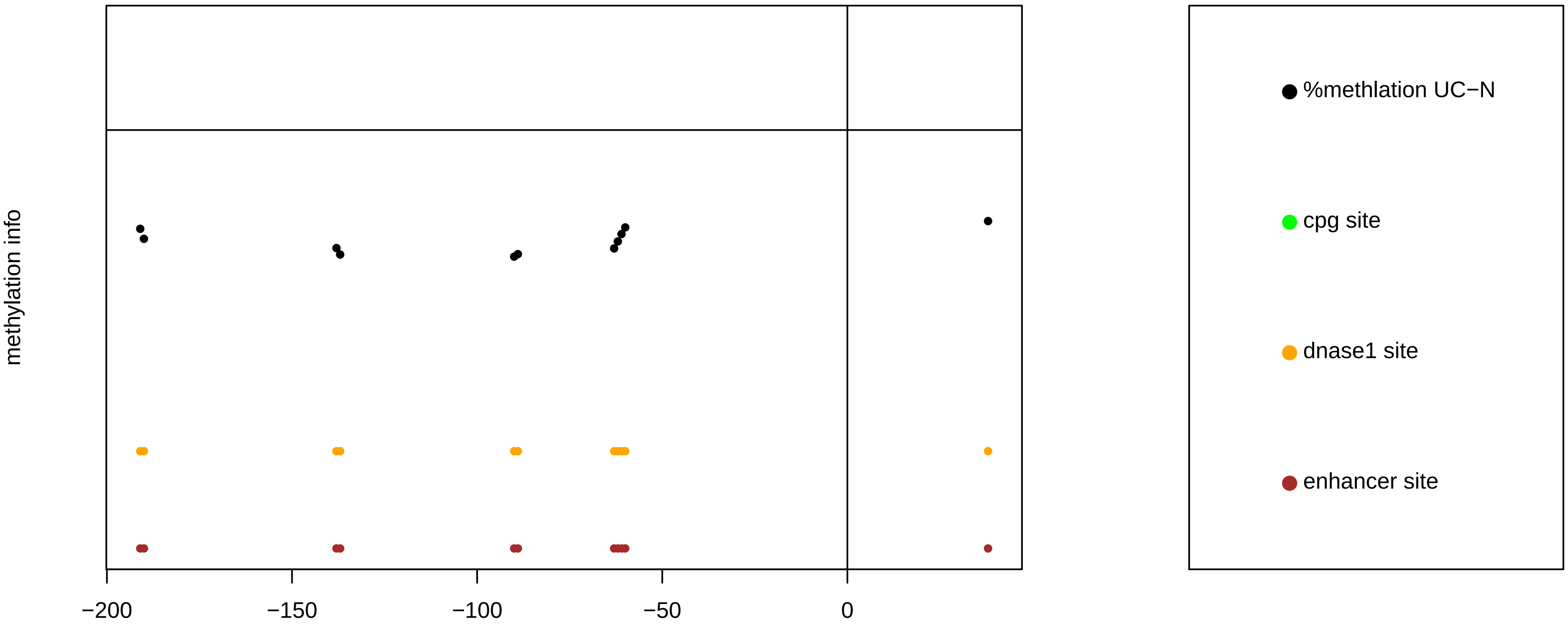
SLAMF1 raw %methylation, red=UC, blue=Normal



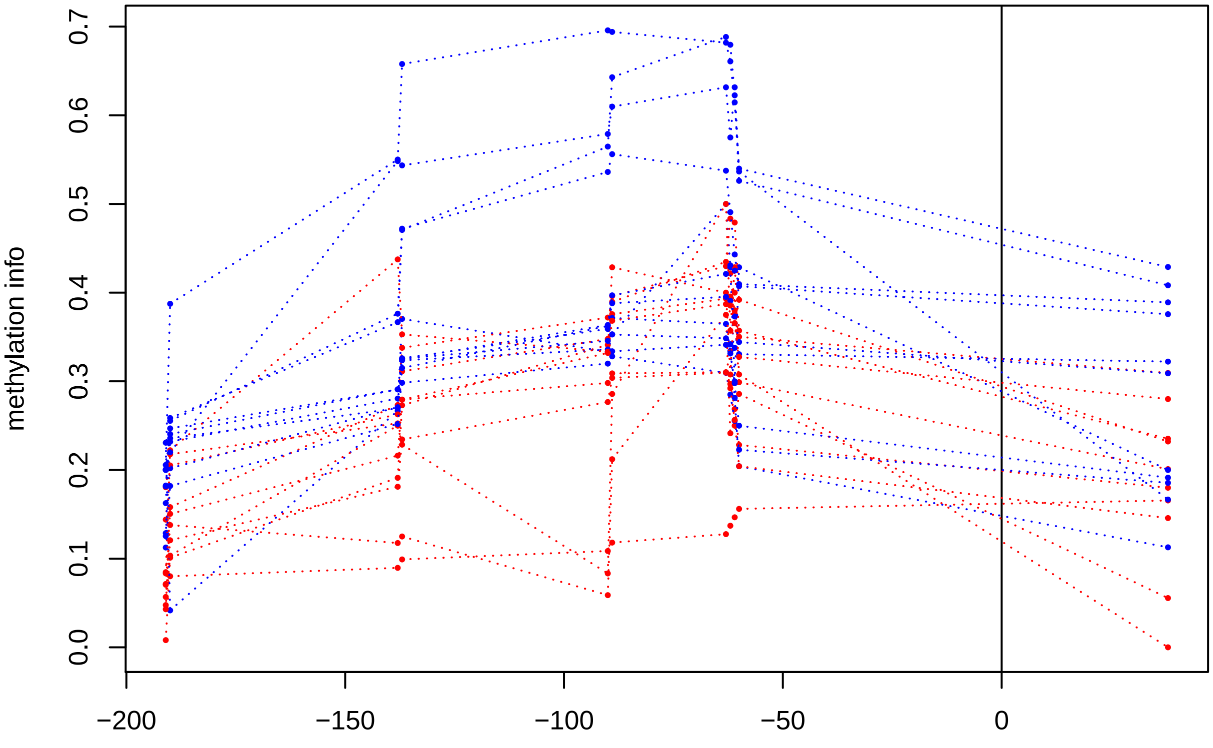
RNAseq logFC(UC−N)= 1.34



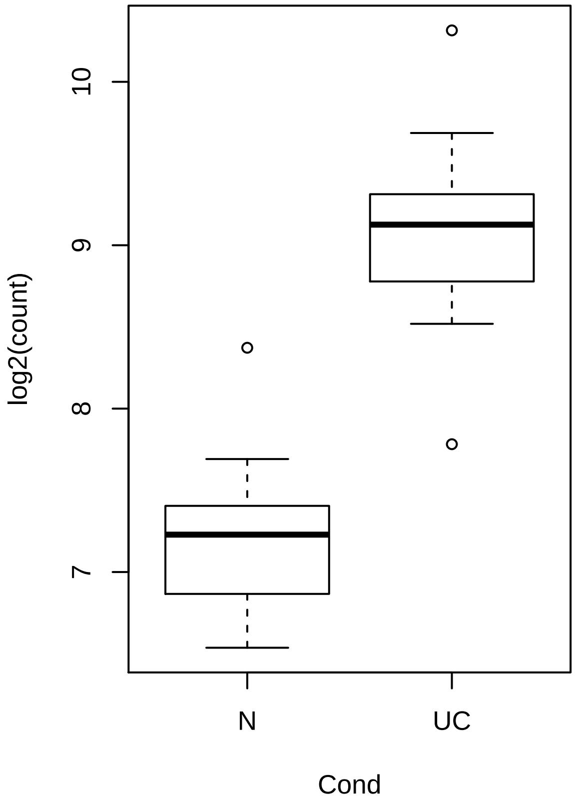
SLAMF6 average UC−N %methylation max=−9.36% min=−13.01%

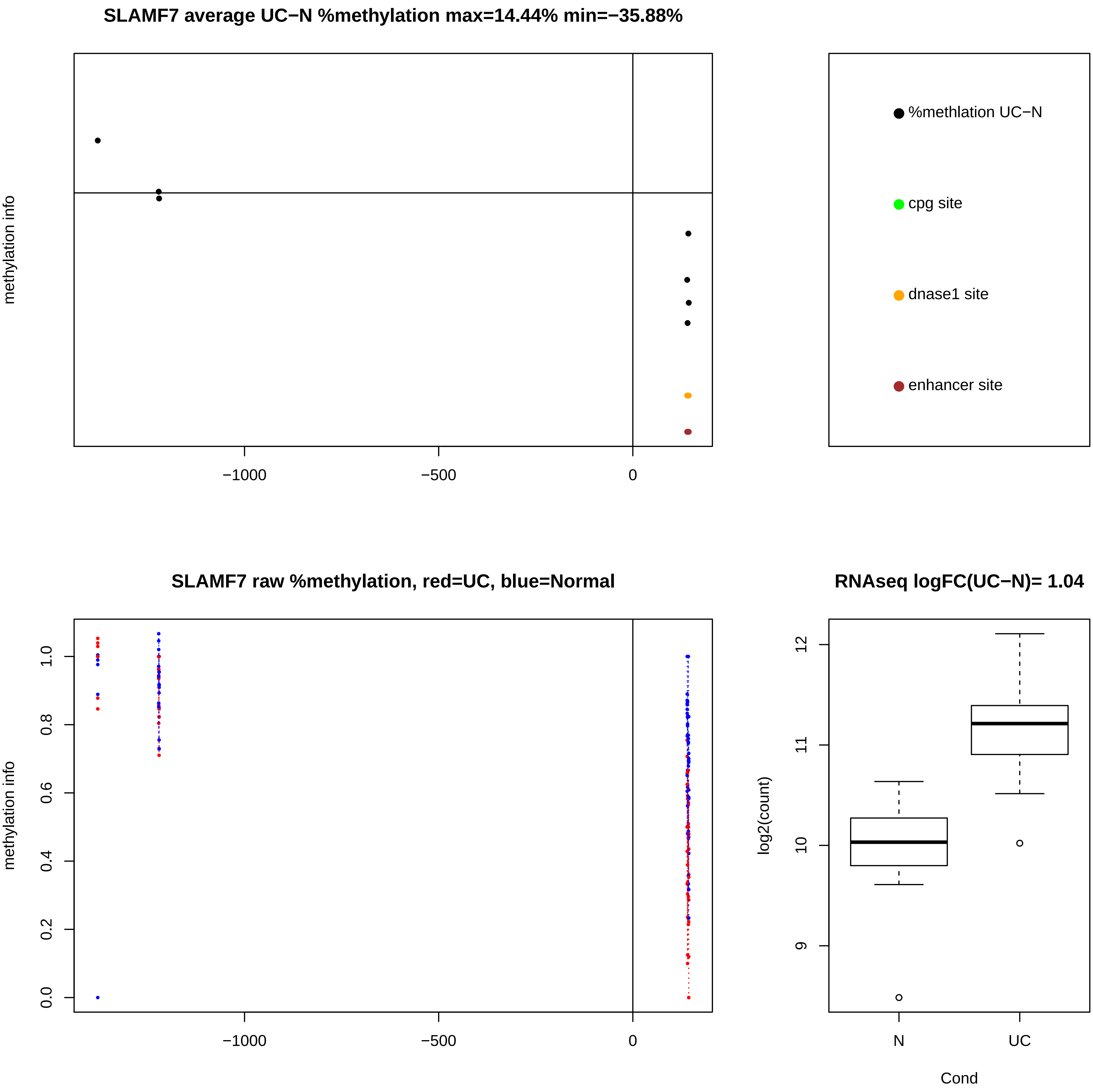


SLAMF6 raw %methylation, red=UC, blue=Normal



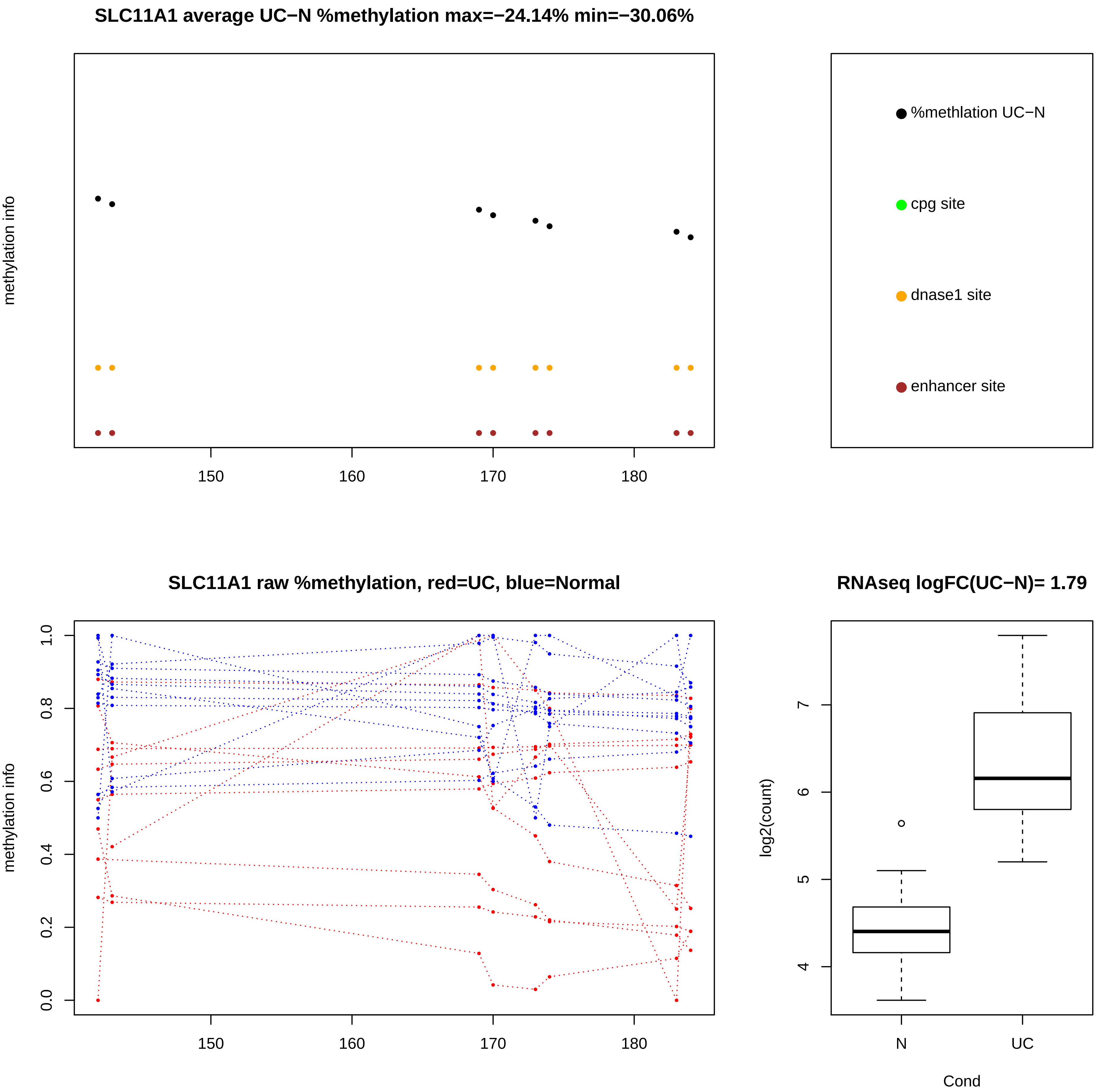
RNAseq logFC(UC−N)= 1.72




SLAMF7 average UC−N %methylation max=14.44% min=−35.88%

SLAMF7 raw %methylation, red=UC, blue=Normal

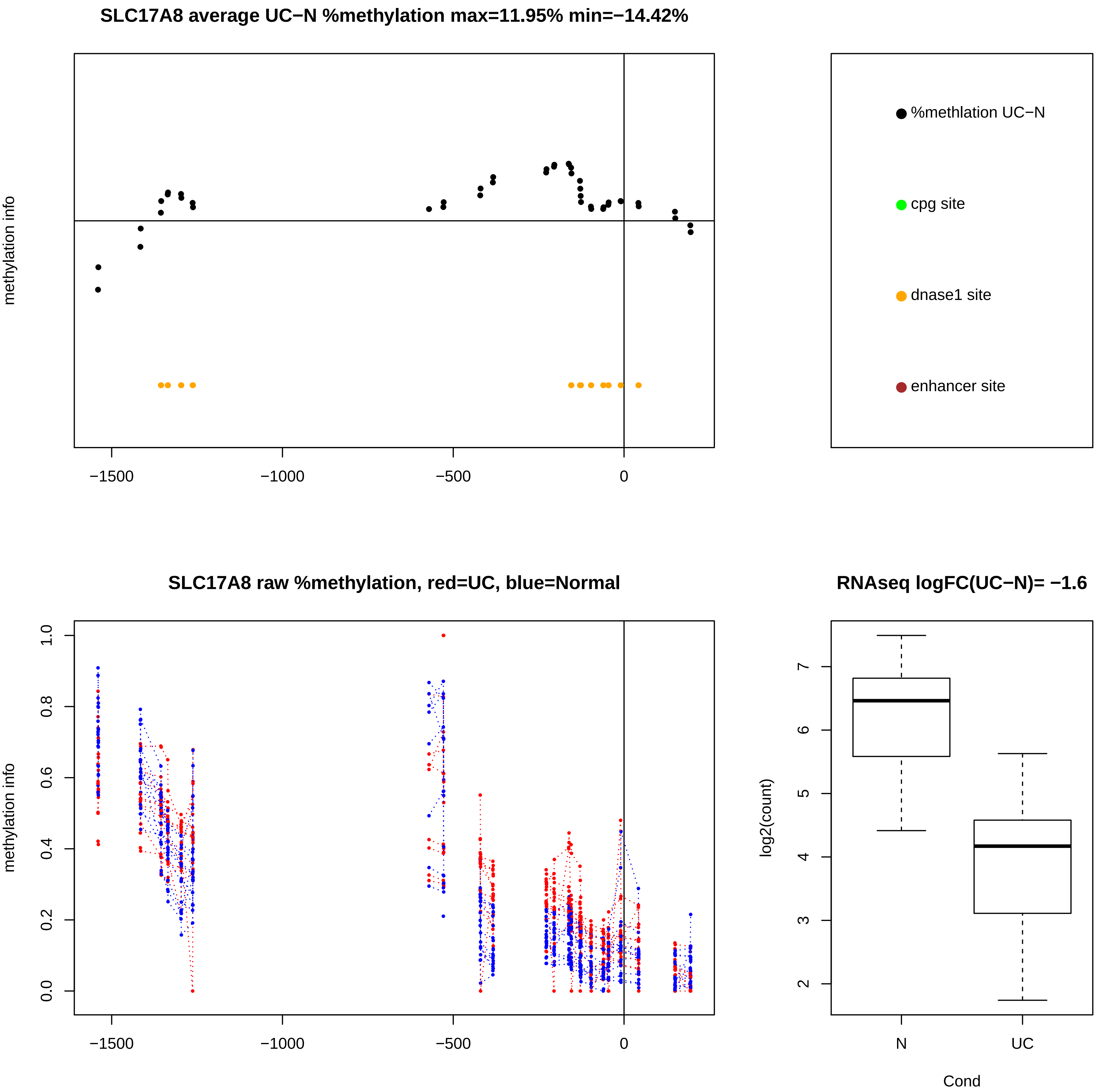
RNAseq logFC(UC−N)= 1.04

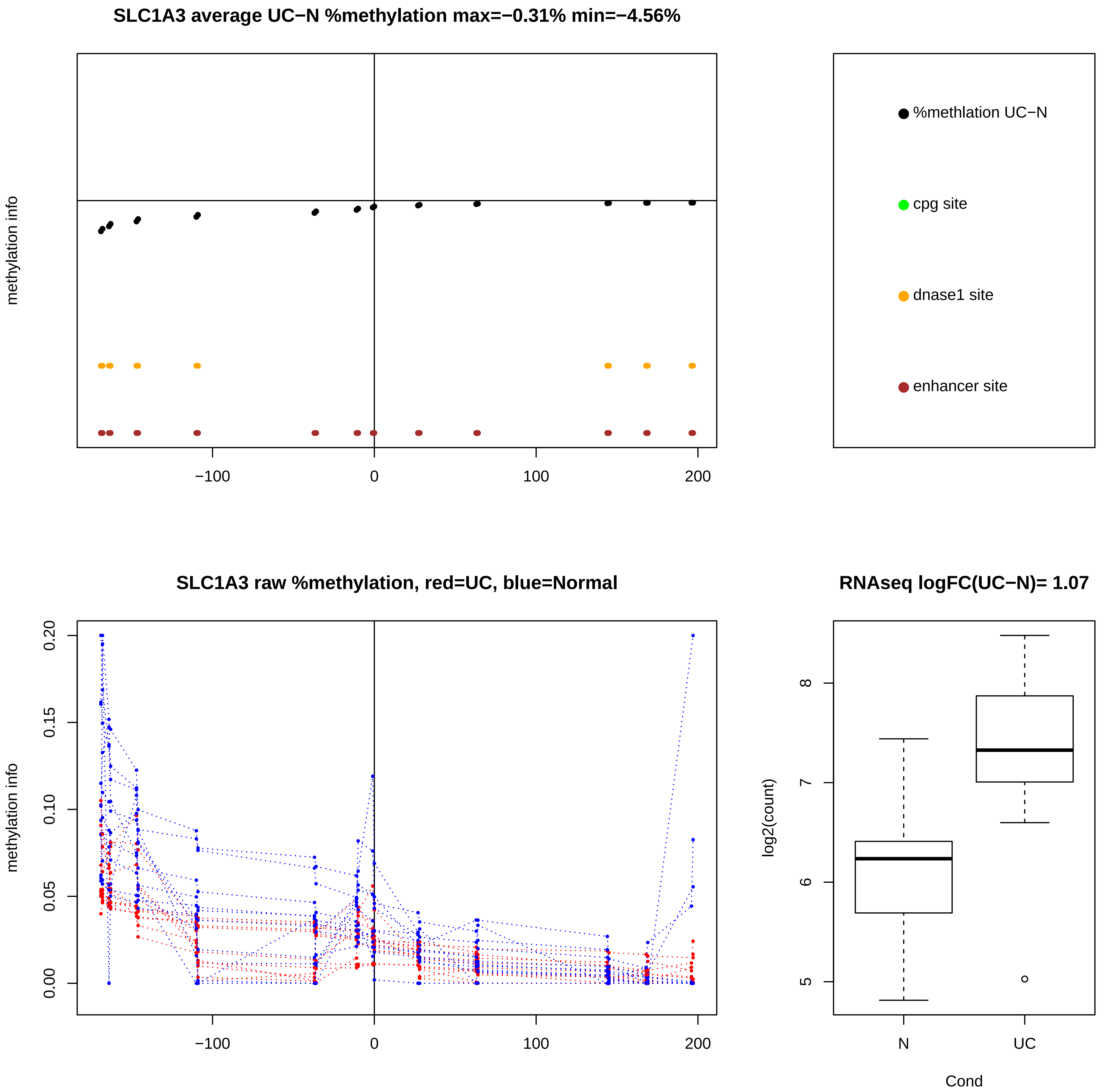


SLC11A1 average UC−N %methylation max=−24.14% min=−30.06%

SLC11A1 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.79

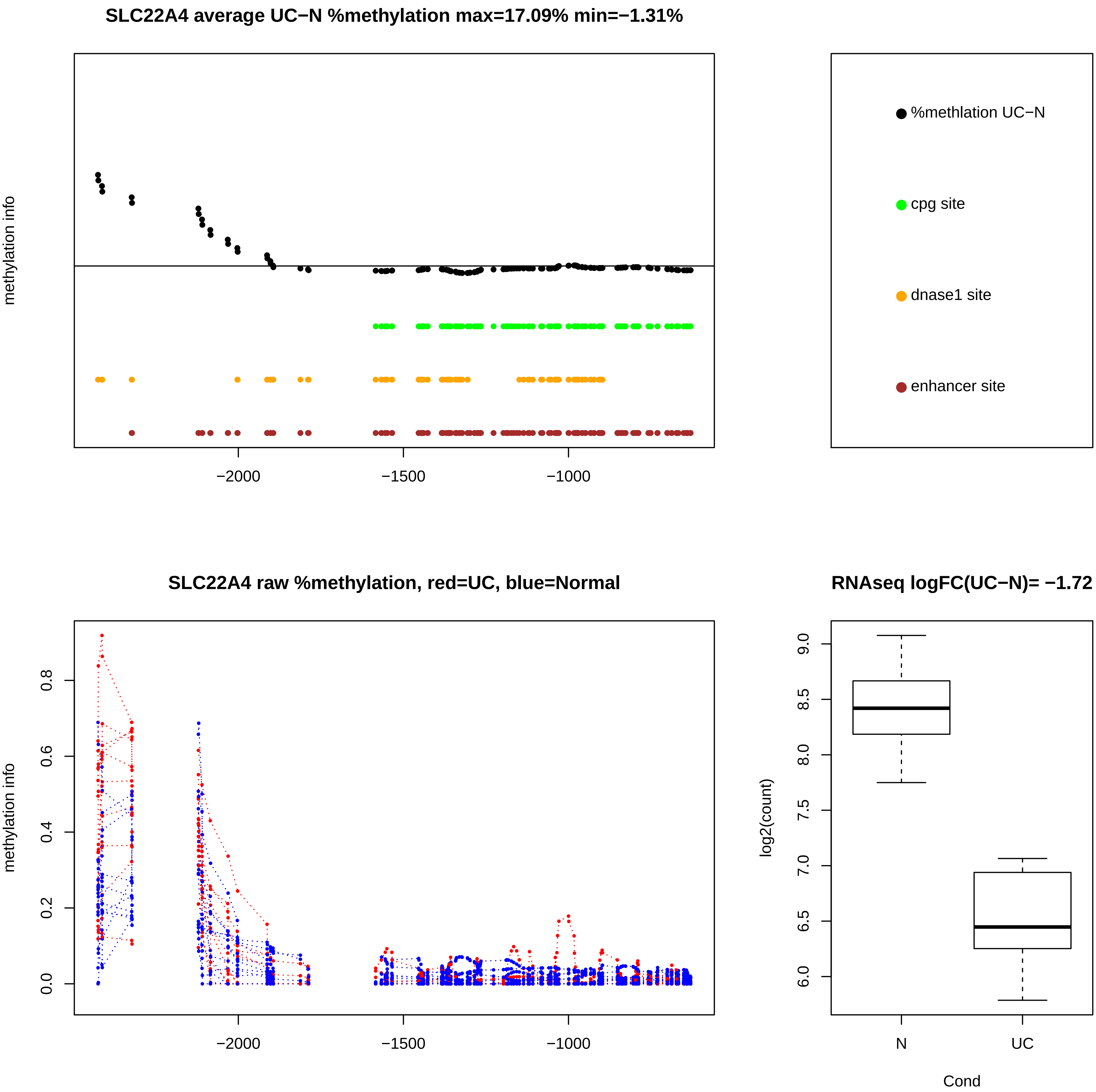

SLC17A8 average UC−N %methylation max=11.95% min=−14.42%
methylation info
−1500
−1000
−500
0
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
SLC17A8 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−1500
−1000
−500
0
RNAseq logFC(UC−N)= −1.6
log2(count)
2
3
4
5
6
7
N
UC
Cond



SLC1A3 average UC−N %methylation max=−0.31% min=−4.56%

SLC1A3 raw %methylation, red=UC, blue=Normal

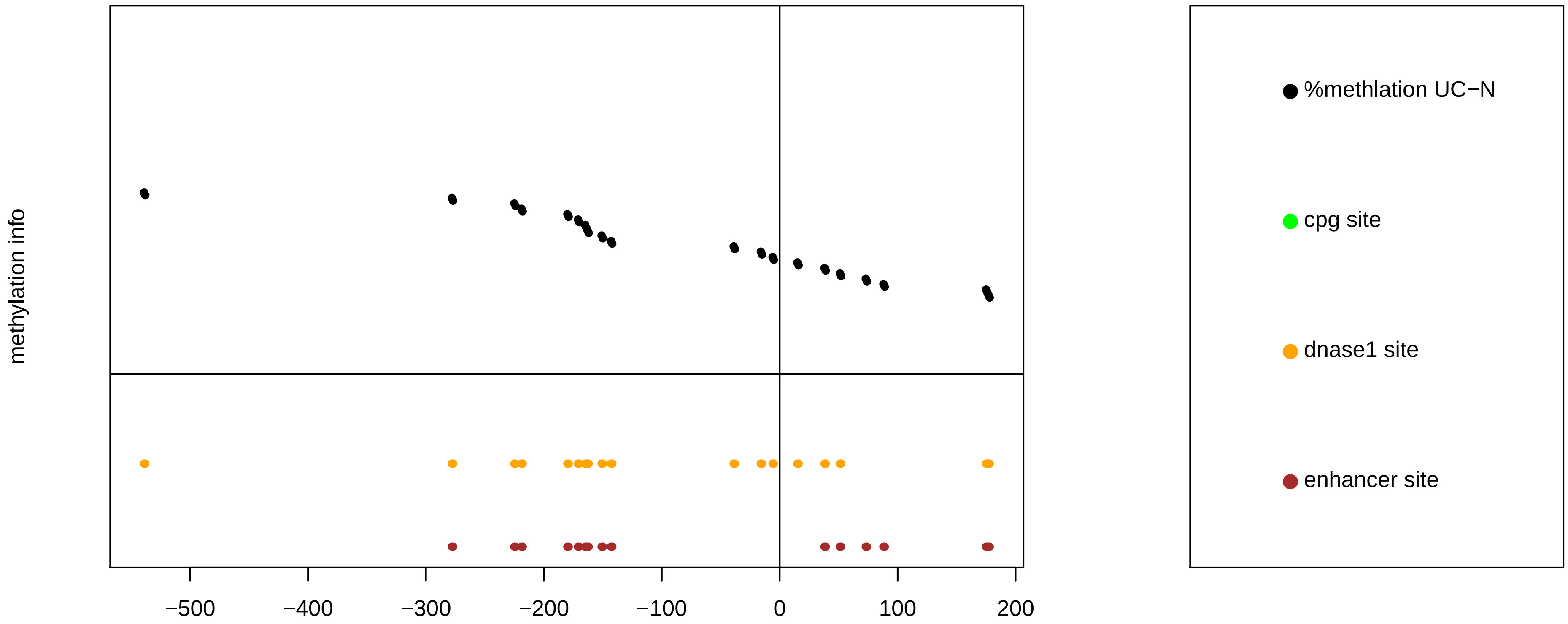
RNAseq logFC(UC−N)= 1.07



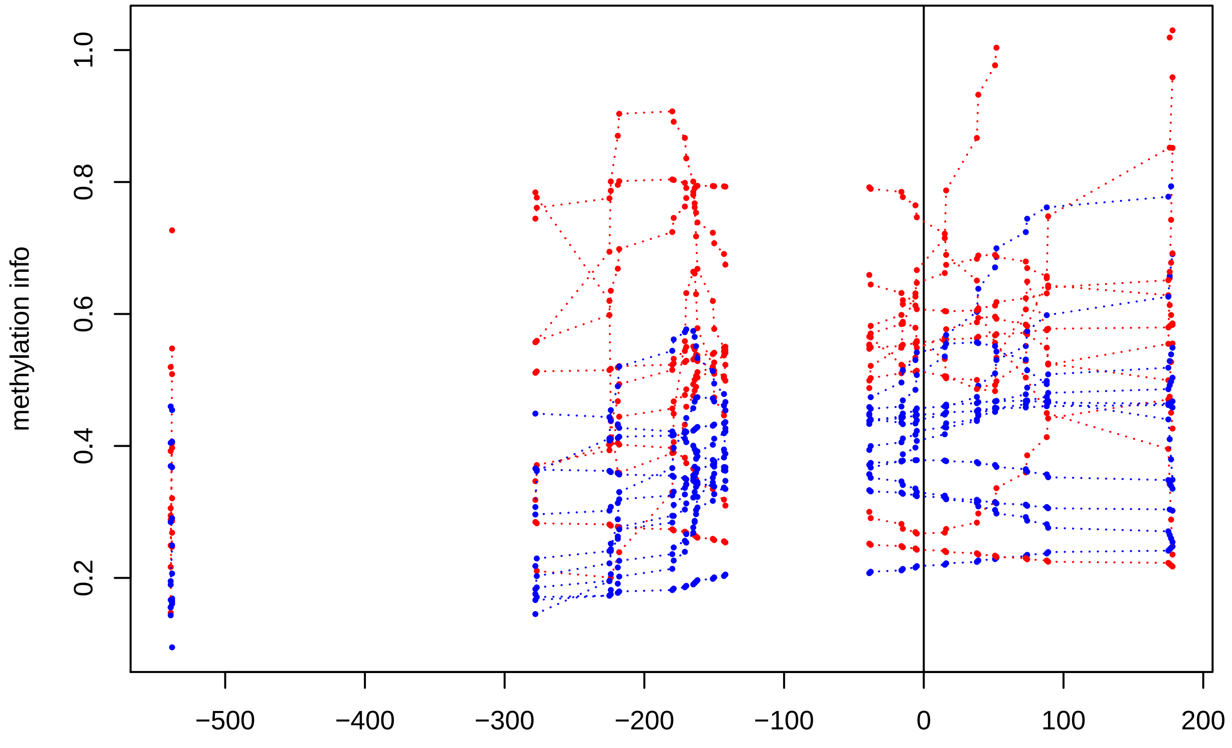
SLC22A4 average UC−N %methylation max=17.09% min=−1.31%

SLC22A4 raw %methylation, red=UC, blue=Normal

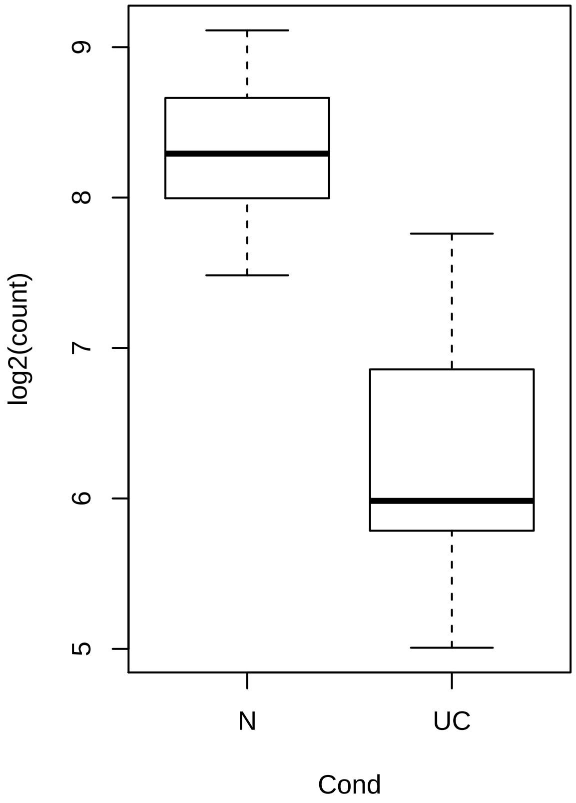
RNAseq logFC(UC−N)= −1.72



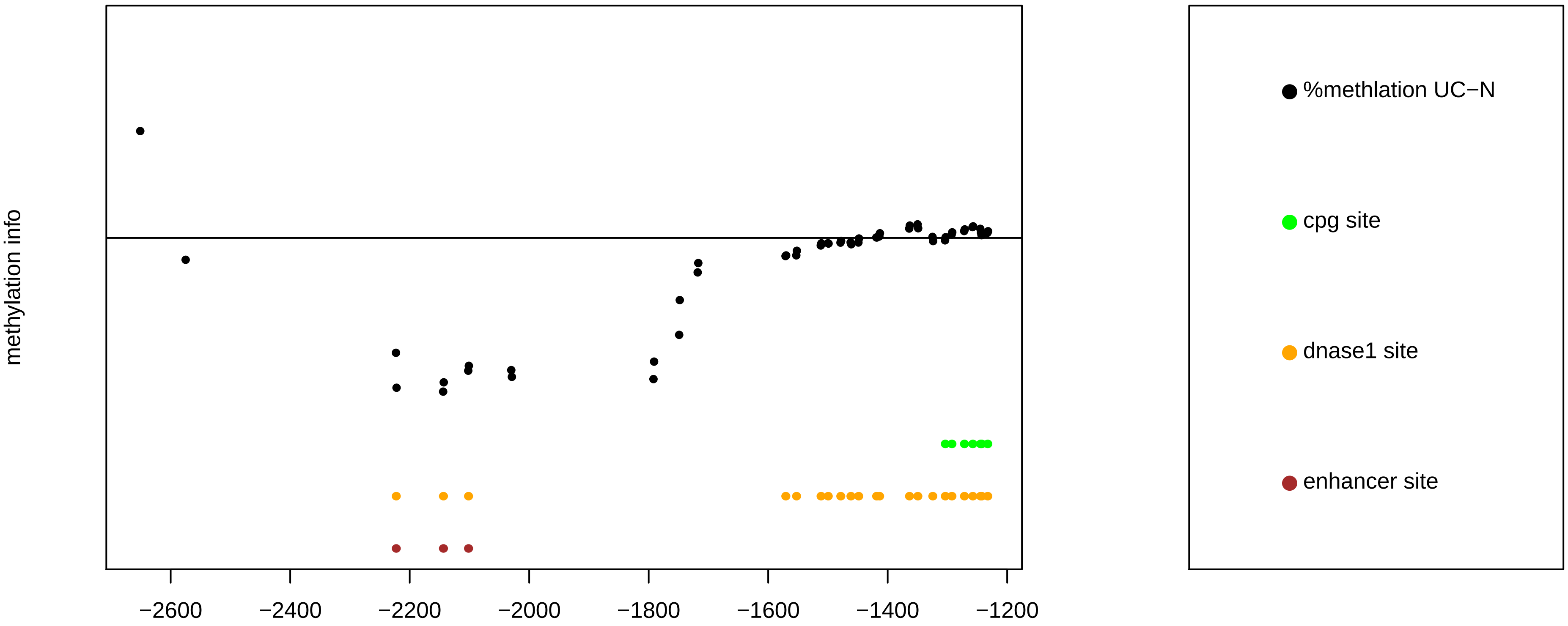
SLC25A34 average UC−N %methylation max=21.86% min=9.21%



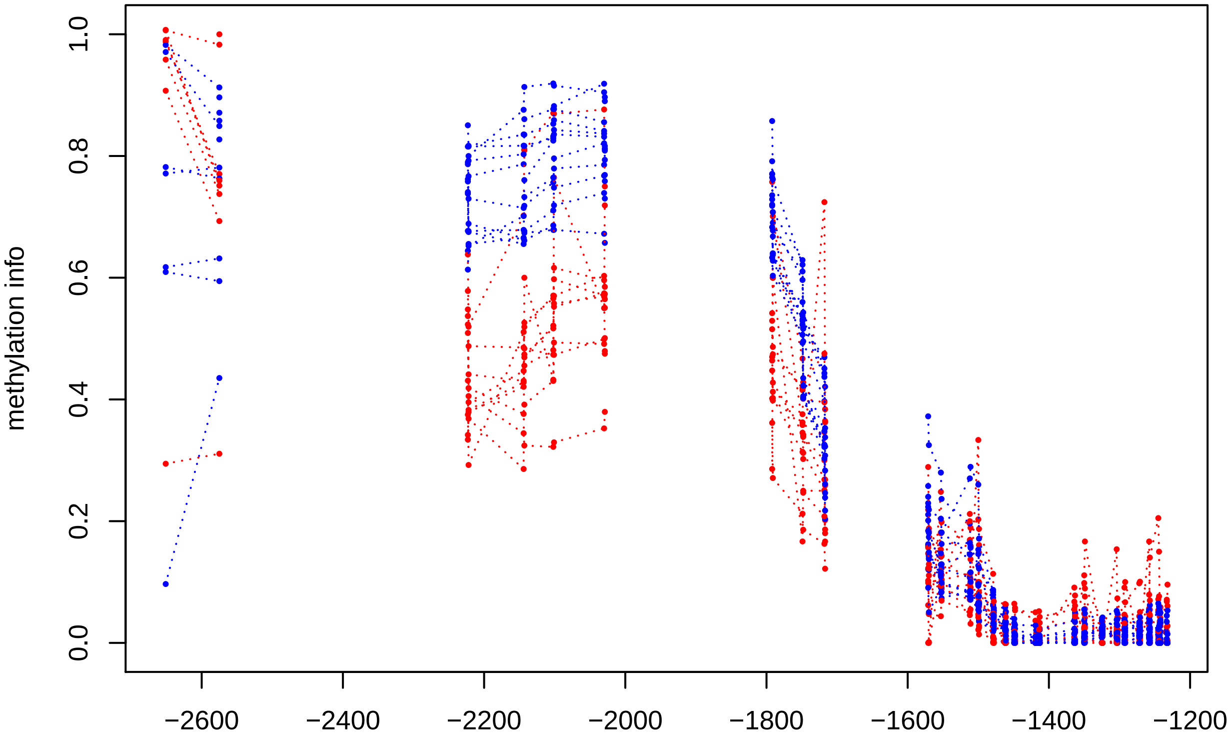
SLC25A34 raw %methylation, red=UC, blue=Normal



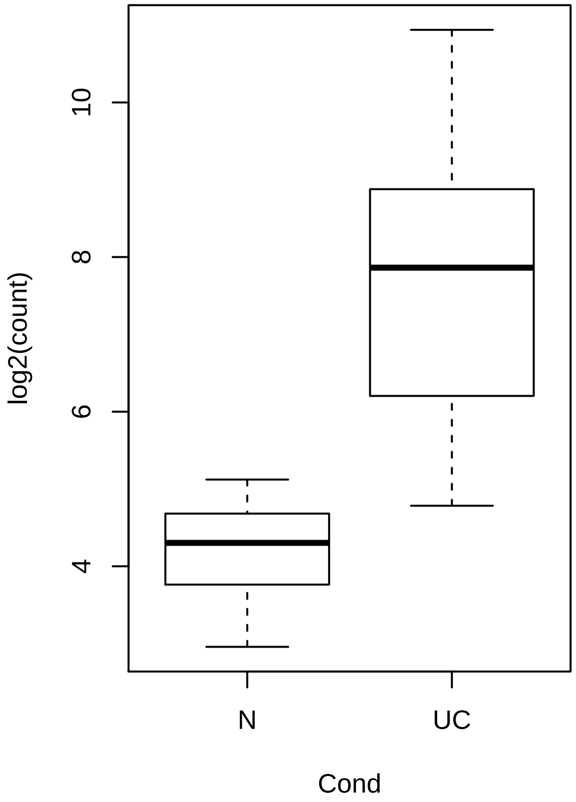
RNAseq logFC(UC−N)= −1.76



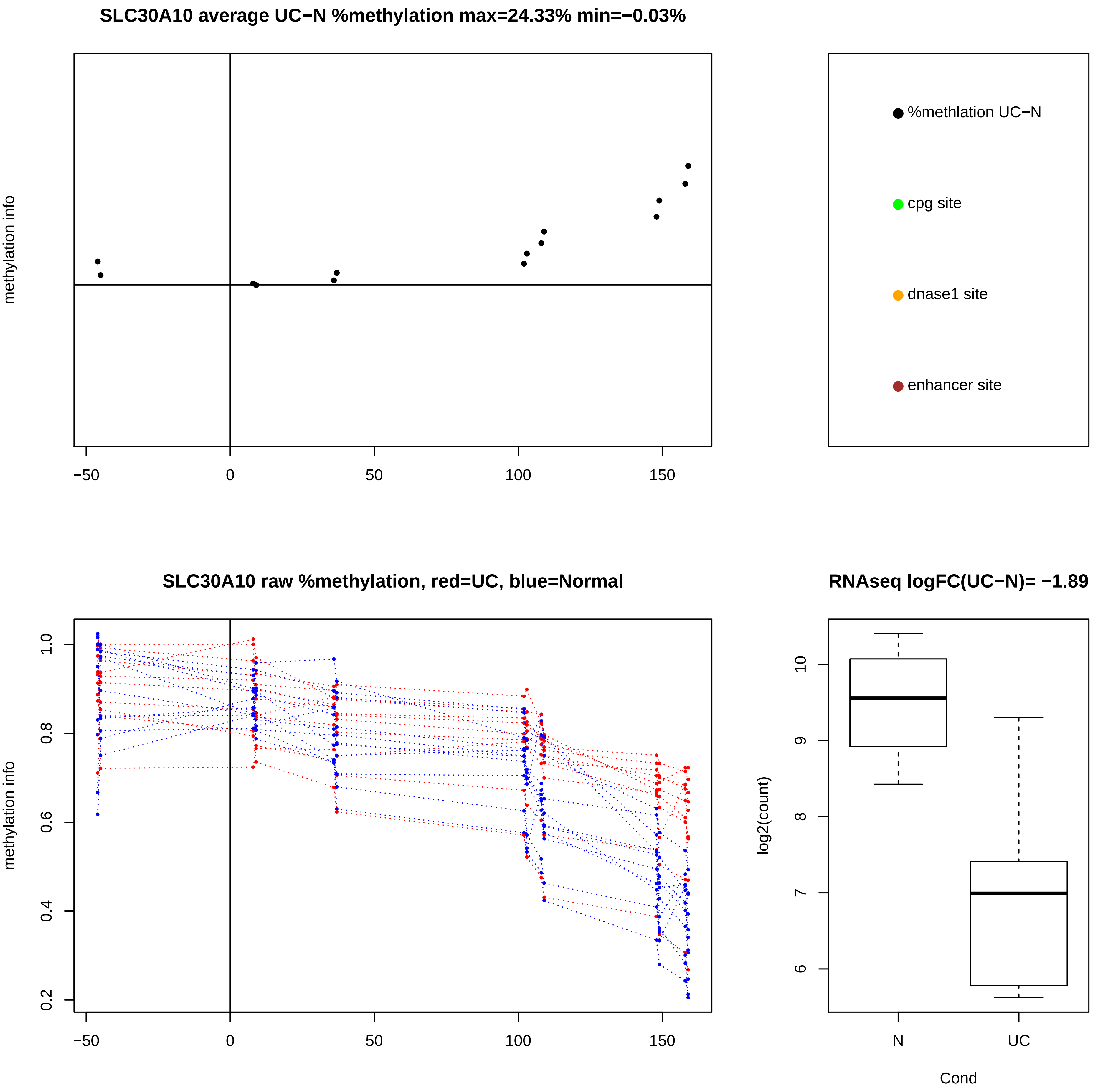
SLC26A4 average UC−N %methylation max=20.45% min=−29.4%



SLC26A4 raw %methylation, red=UC, blue=Normal



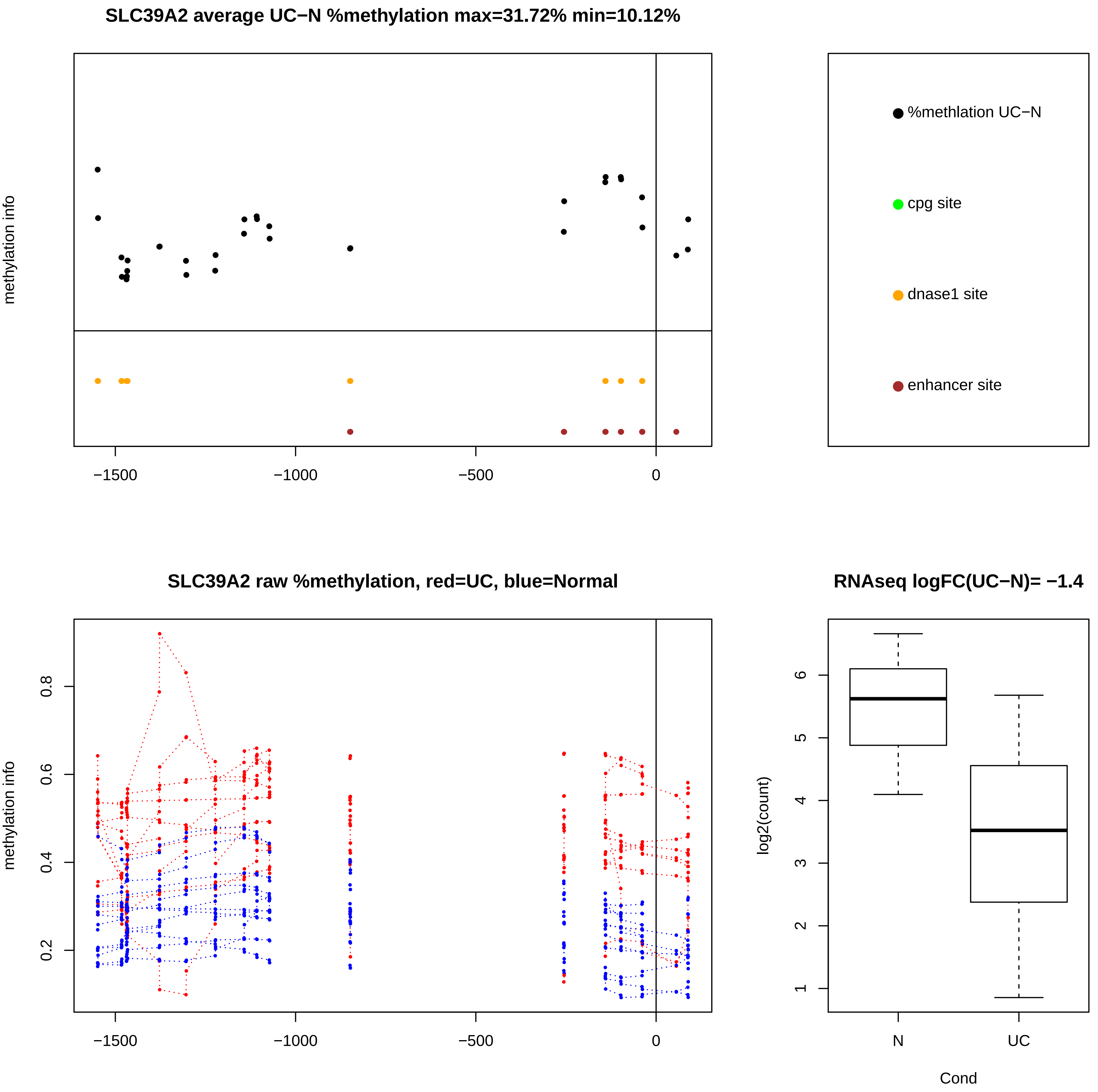
RNAseq logFC(UC−N)= 3.28



SLC30A10 average UC−N %methylation max=24.33% min=−0.03%

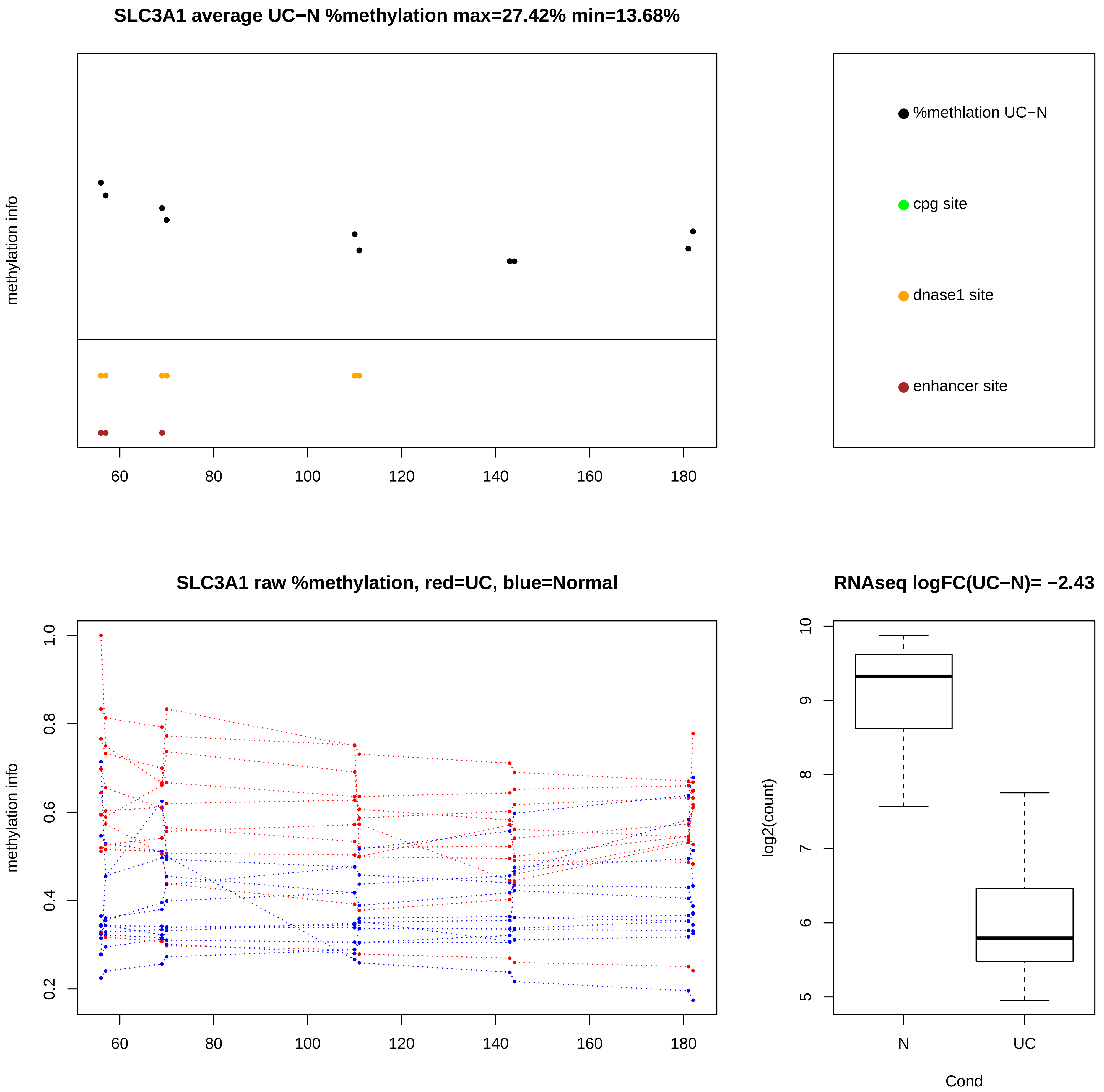
SLC30A10 raw %methylation, red=UC, blue=Normal

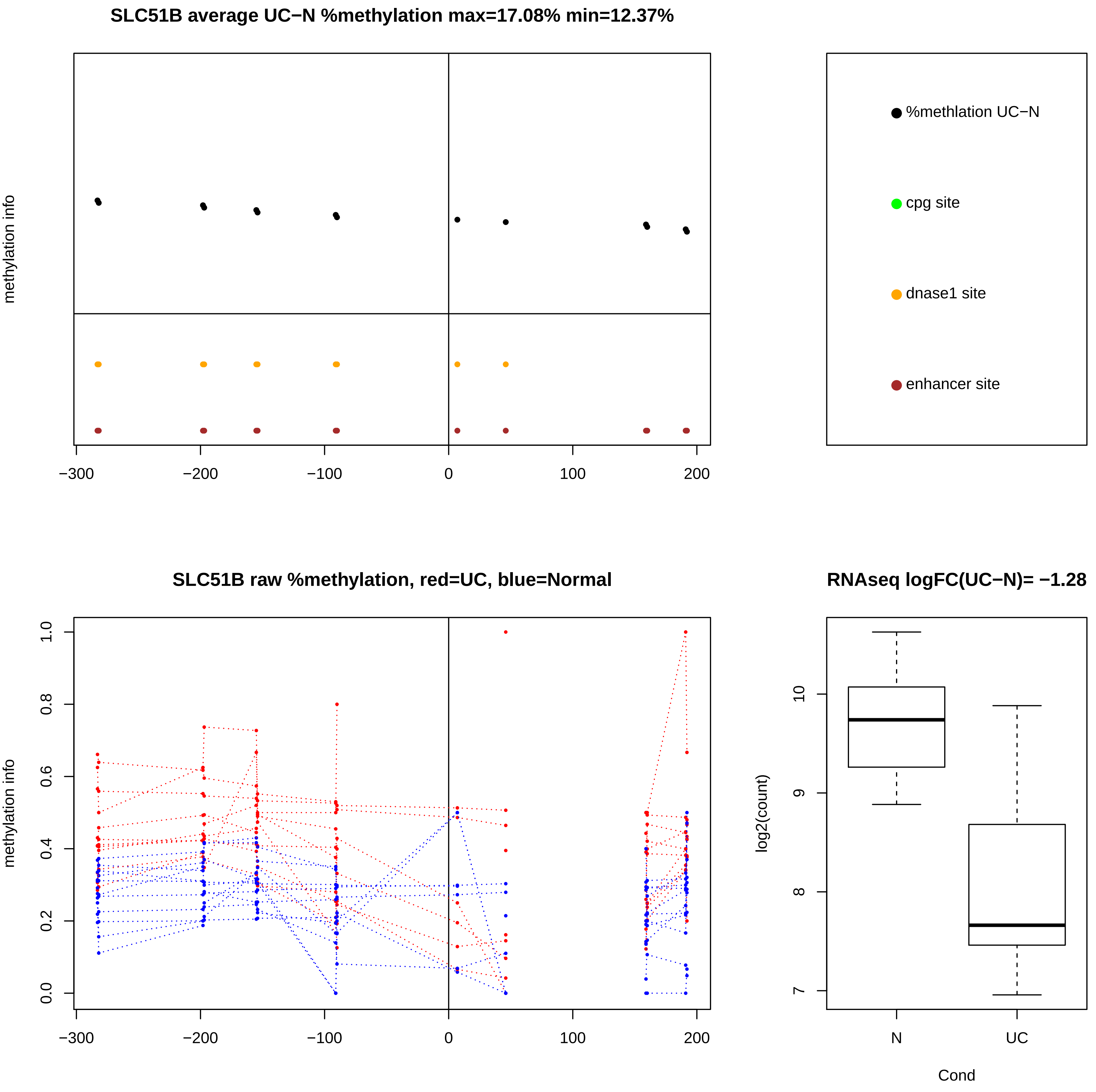
RNAseq logFC(UC−N)= −1.89


SLC39A2 average UC−N %methylation max=31.72% min=10.12%

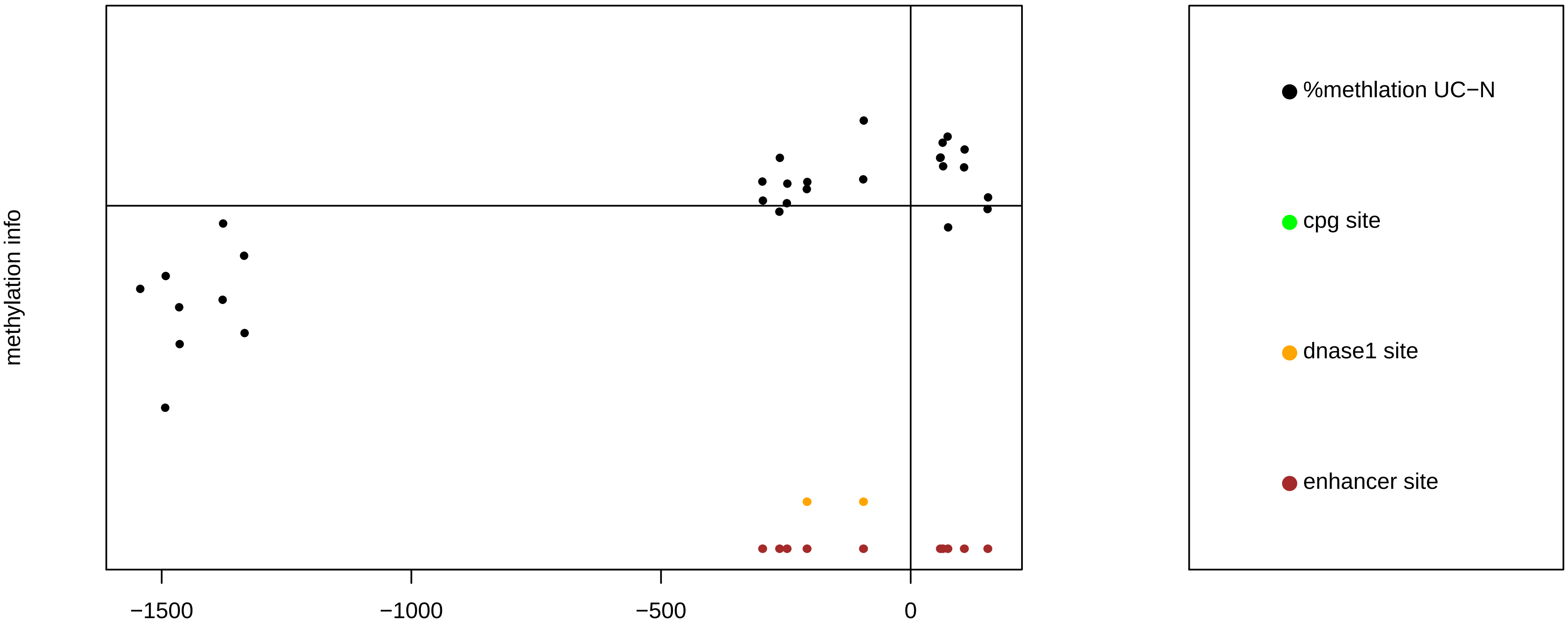
SLC39A2 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= −1.4

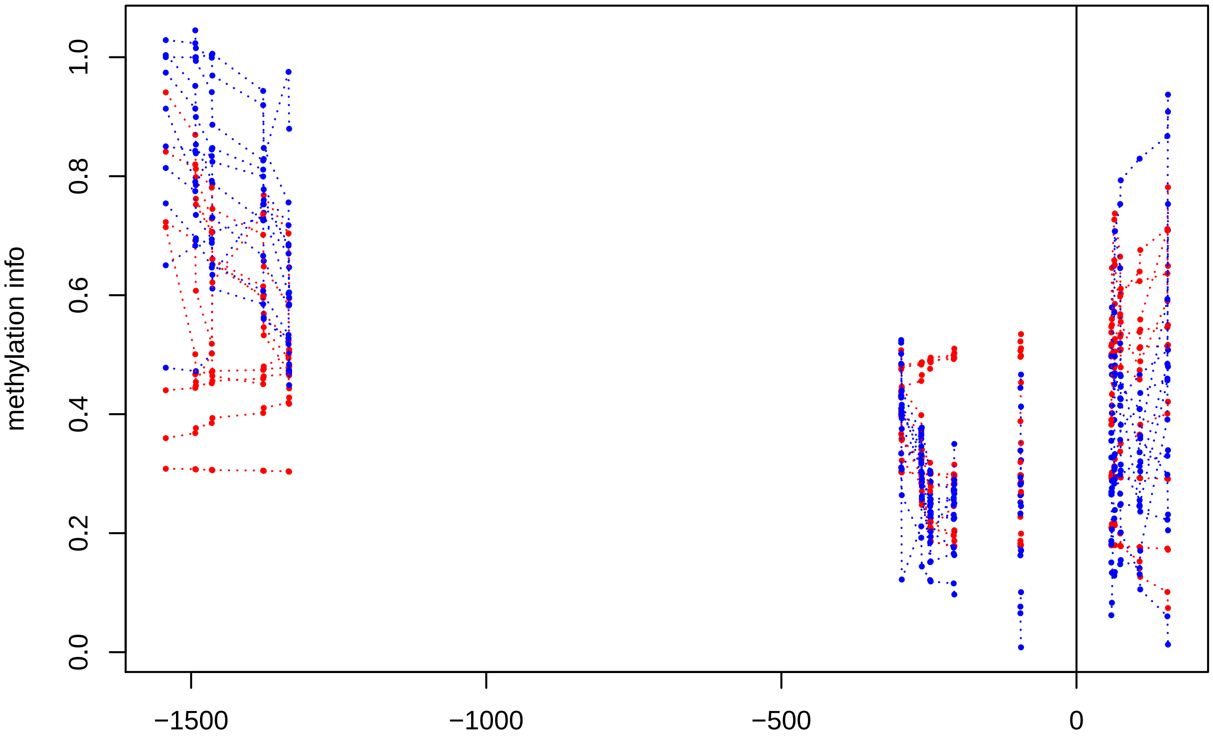

SLC3A1 average UC−N %methylation max=27.42% min=13.68%
methylation info
60
80
100
120
140
160
180
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
SLC3A1 raw %methylation, red=UC, blue=Normal
methylation info
0.2
0.4
0.6
0.8
1.0
60
80
100
120
140
160
180
RNAseq logFC(UC−N)= −2.43
log2(count)
5
6
7
8
9
10
N
UC
Cond


SLC51B average UC−N %methylation max=17.08% min=12.37%
methylation info
−300
−200
−100
0
100
200
%methlation UC−N
cpg site
dnase1 site
enhancer site
SLC51B raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−300
−200
−100
0
100
200
RNAseq logFC(UC−N)= −1.28
log2(count)
7
8
9
10
N
UC
Cond

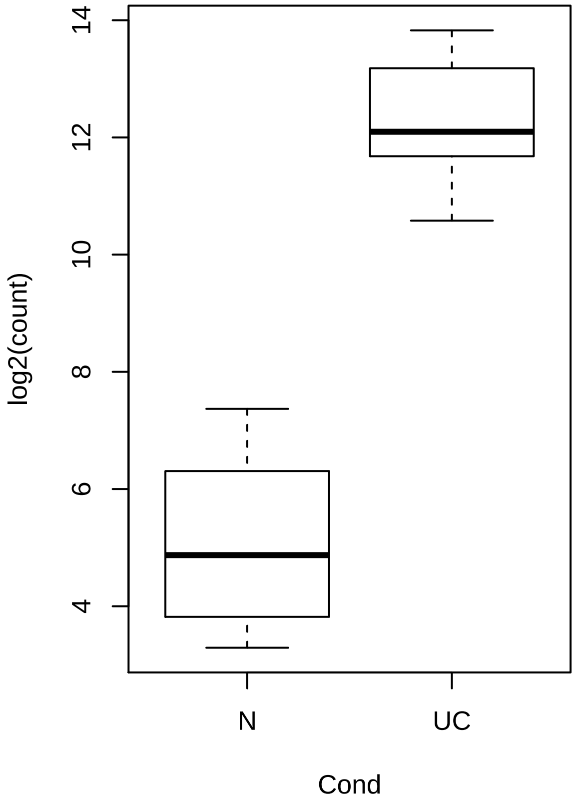
SLC6A14 average UC−N %methylation max=18.13% min=−42.97%



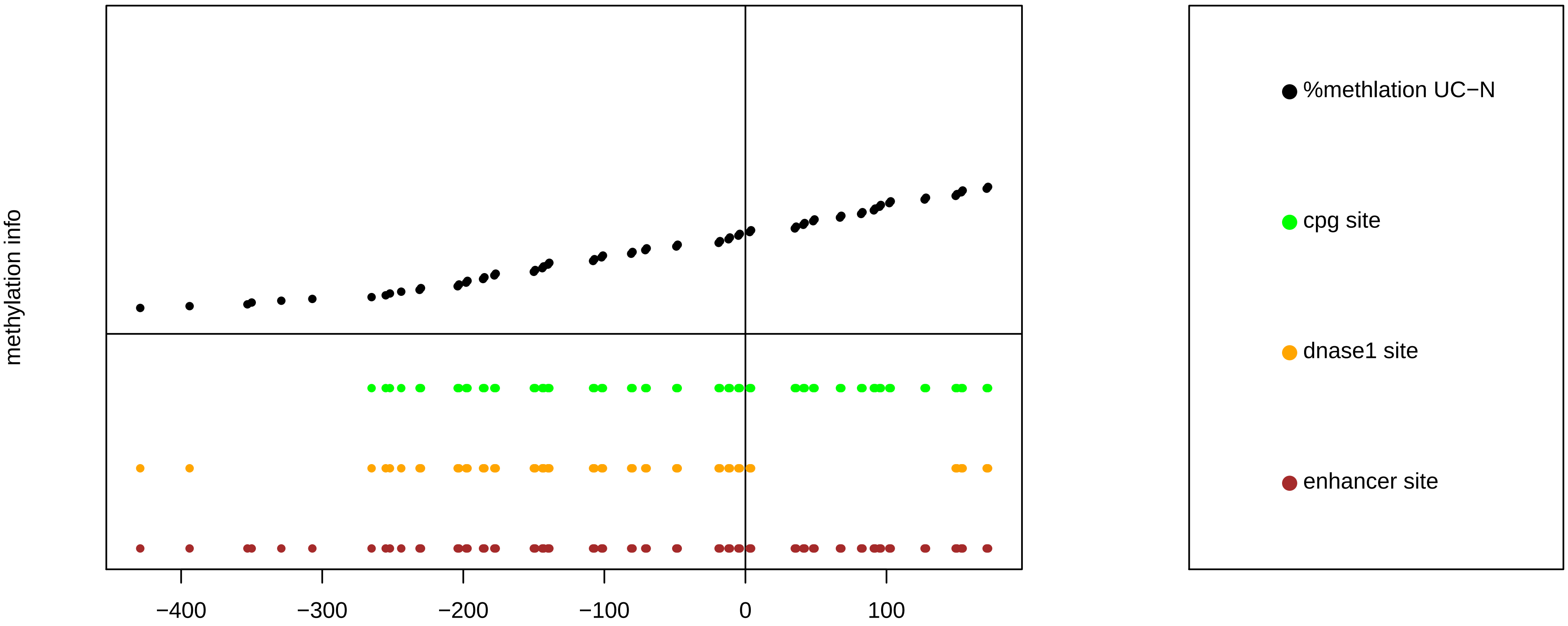
SLC6A14 raw %methylation, red=UC, blue=Normal



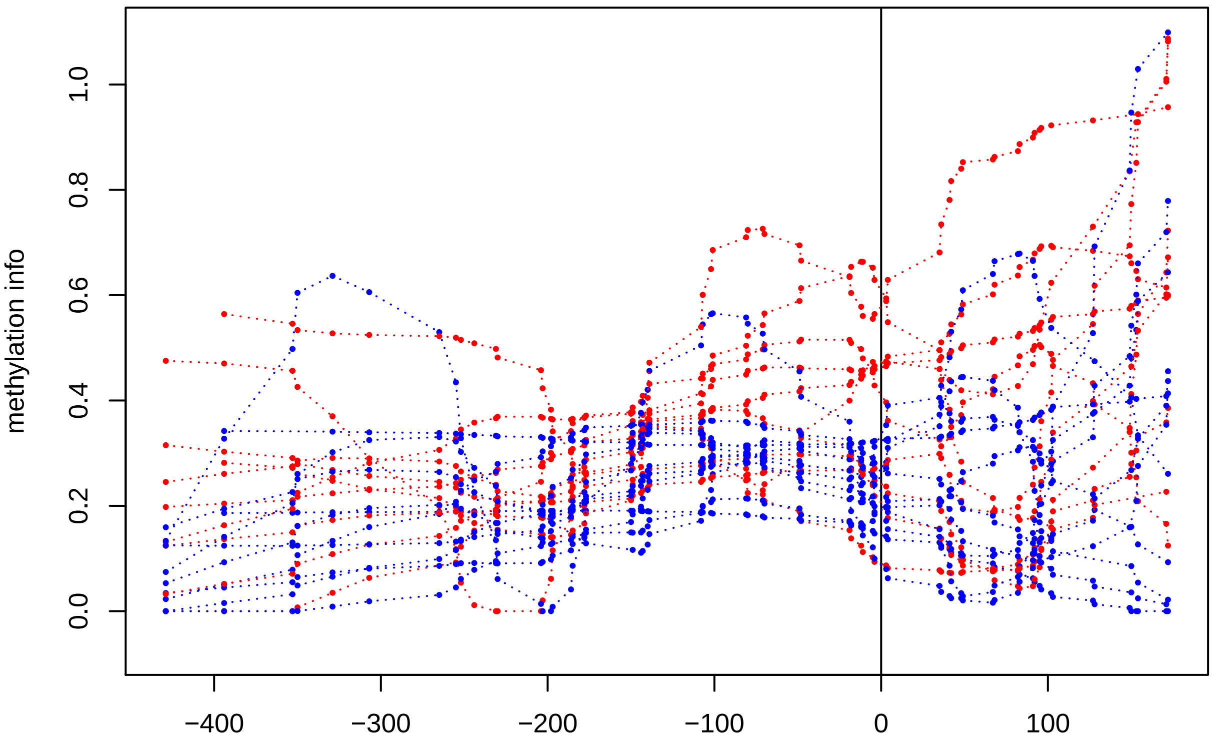
RNAseq logFC(UC−N)= 5.66



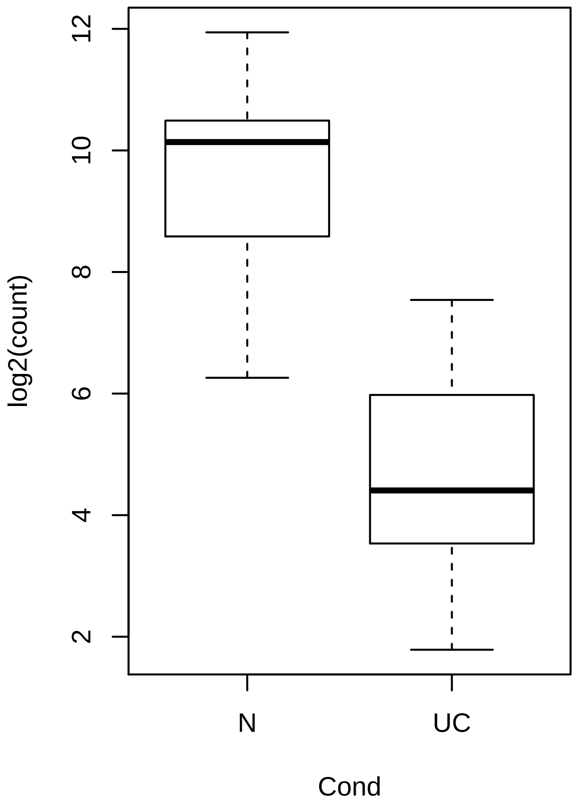
SLC6A19 average UC−N %methylation max=18.34% min=3.24%

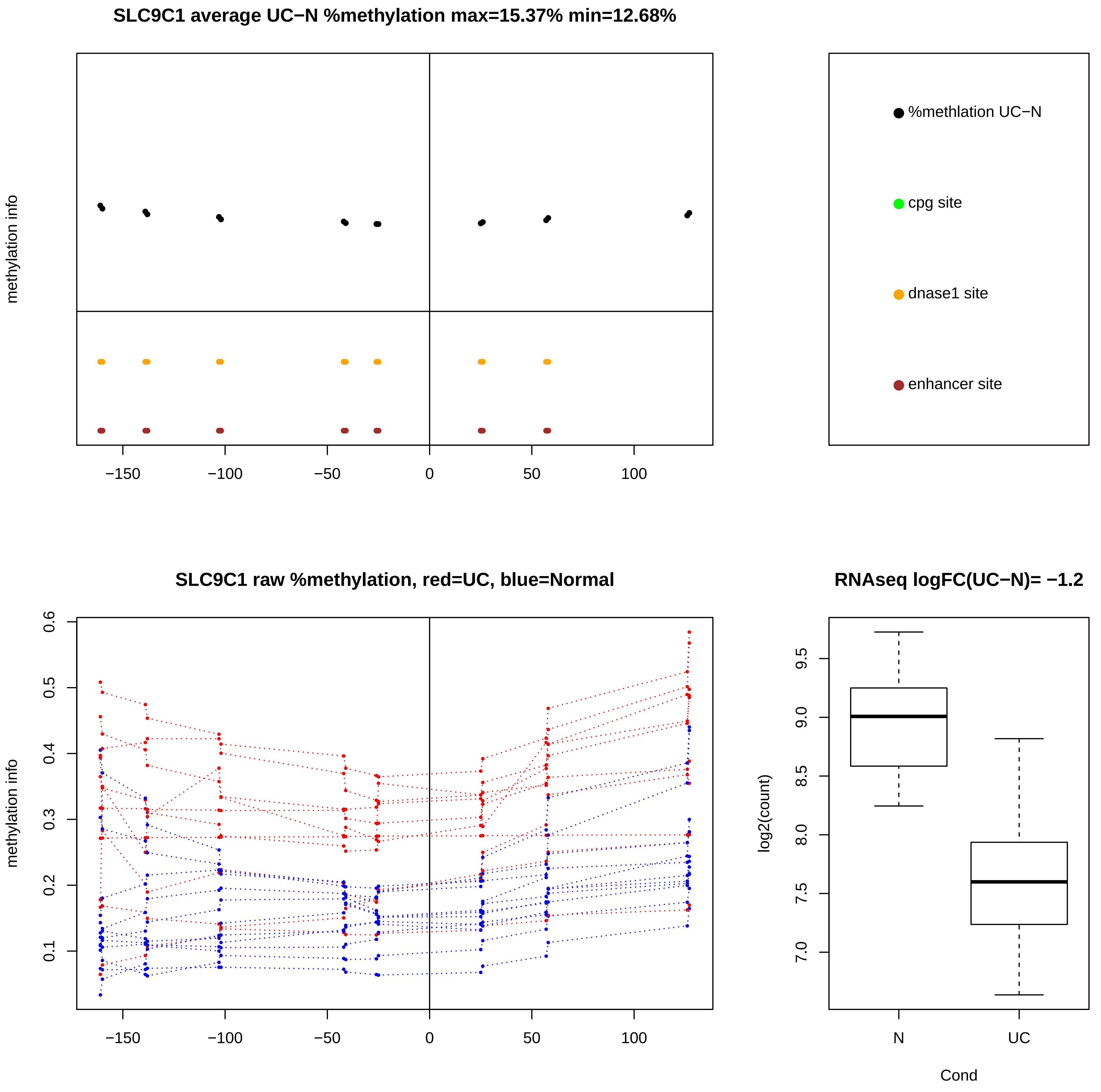


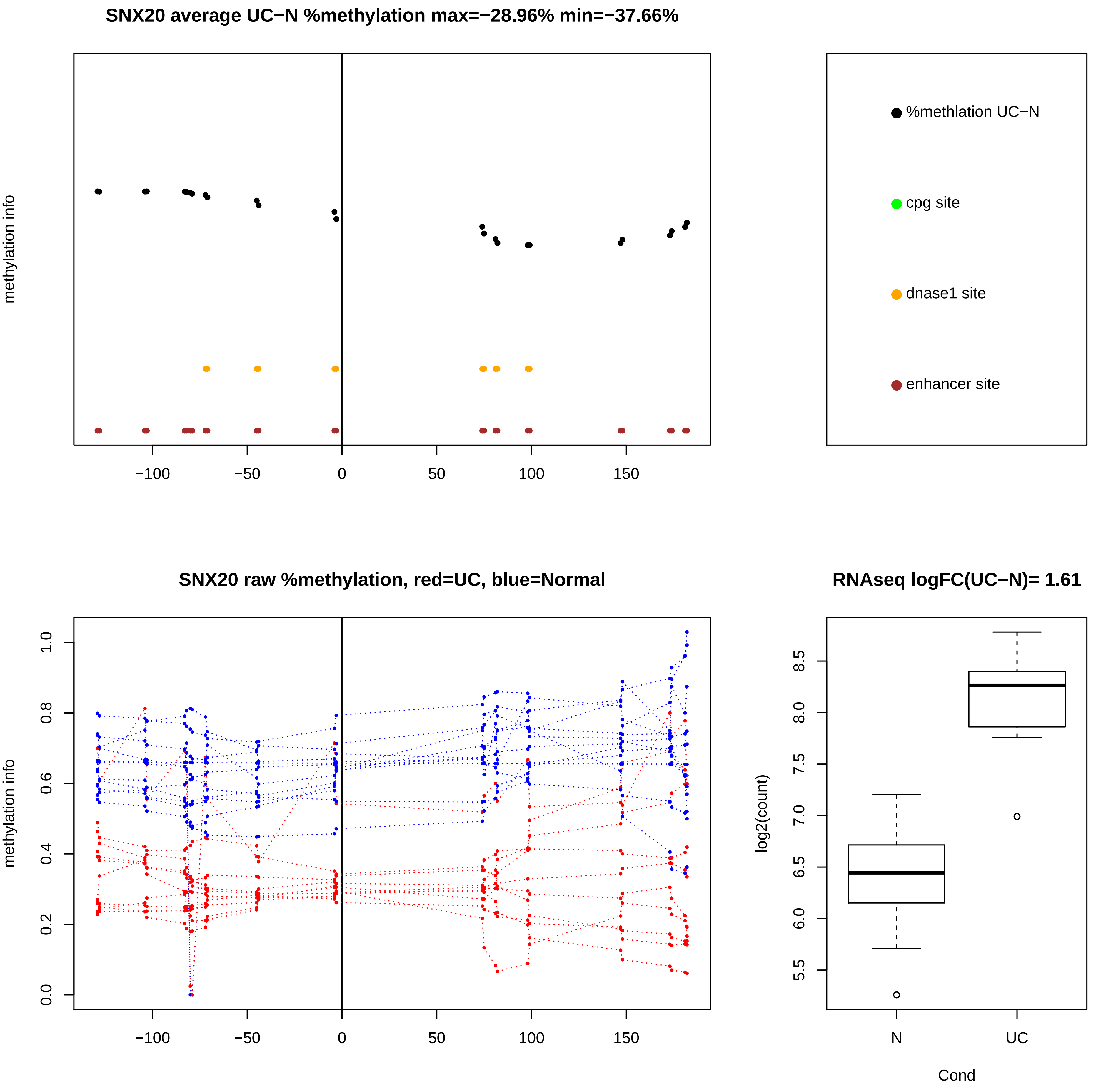
SLC6A19 raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= −2.82



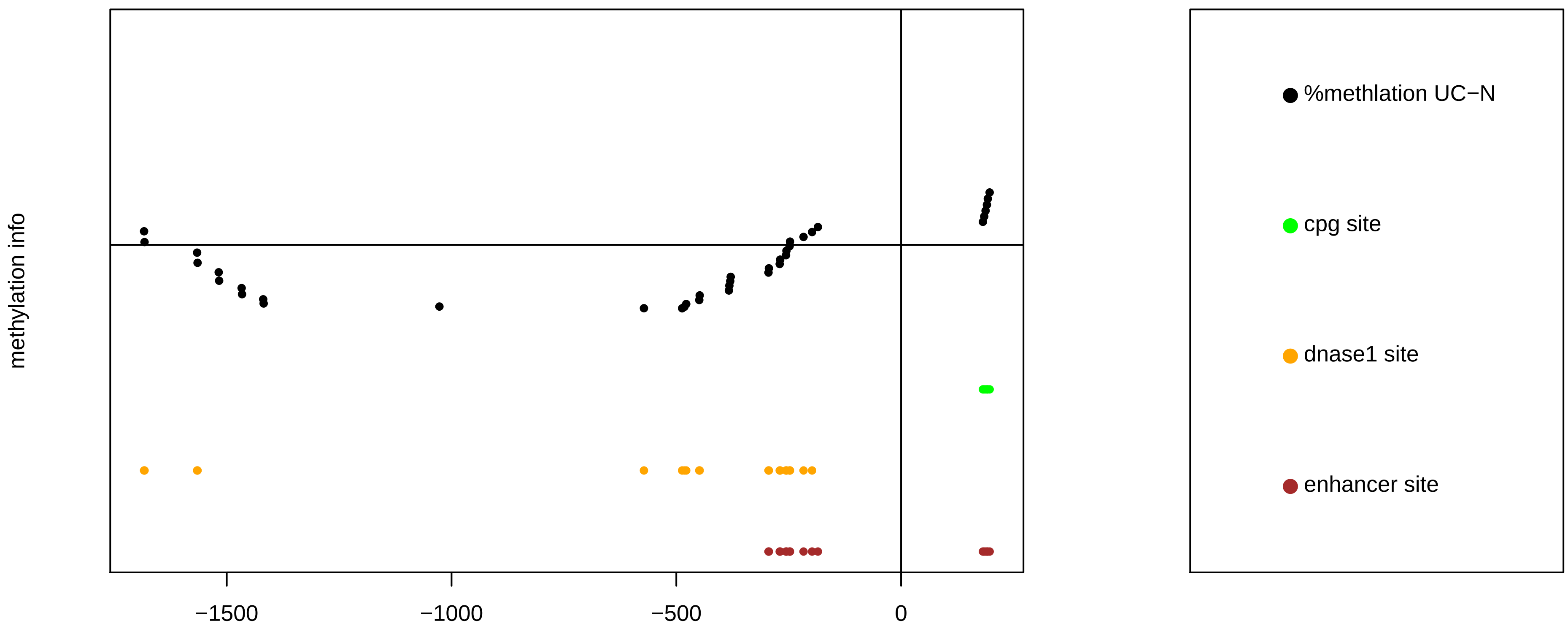

SLC9C1 average UC−N %methylation max=15.37% min=12.68%
methylation info
−150
−100
−50
0
50
100
%methlation UC−N
cpg site
dnase1 site
enhancer site
SLC9C1 raw %methylation, red=UC, blue=Normal
methylation info
0.1
0.2
0.3
0.4
0.5
0.6
−150
−100
−50
0
50
100
RNAseq logFC(UC−N)= −1.2
log2(count)
7.0
7.5
8.0
8.5
9.0
9.5
N
UC
Cond



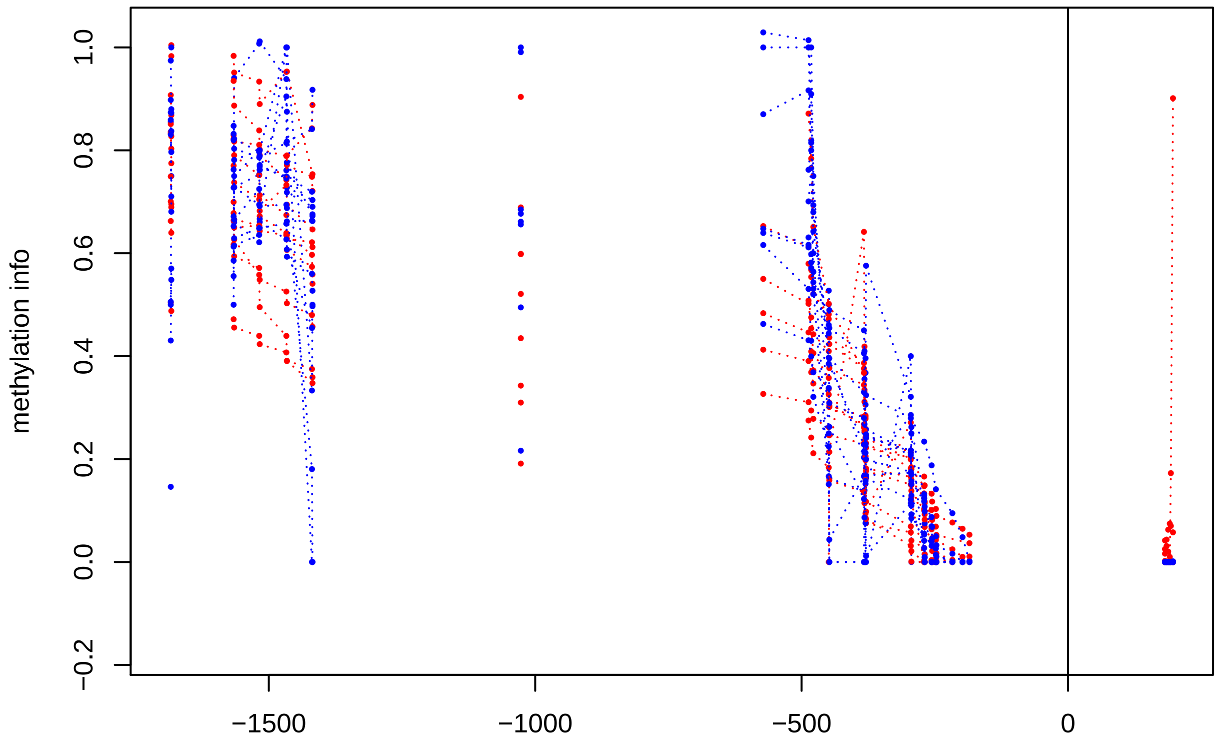
SNX20 average UC−N %methylation max=−28.96% min=−37.66%

SNX20 raw %methylation, red=UC, blue=Normal

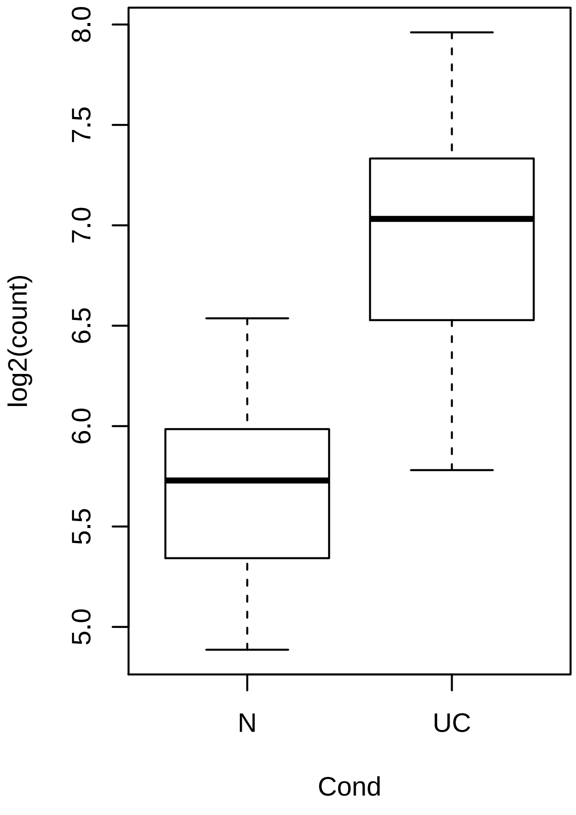
RNAseq logFC(UC−N)= 1.61



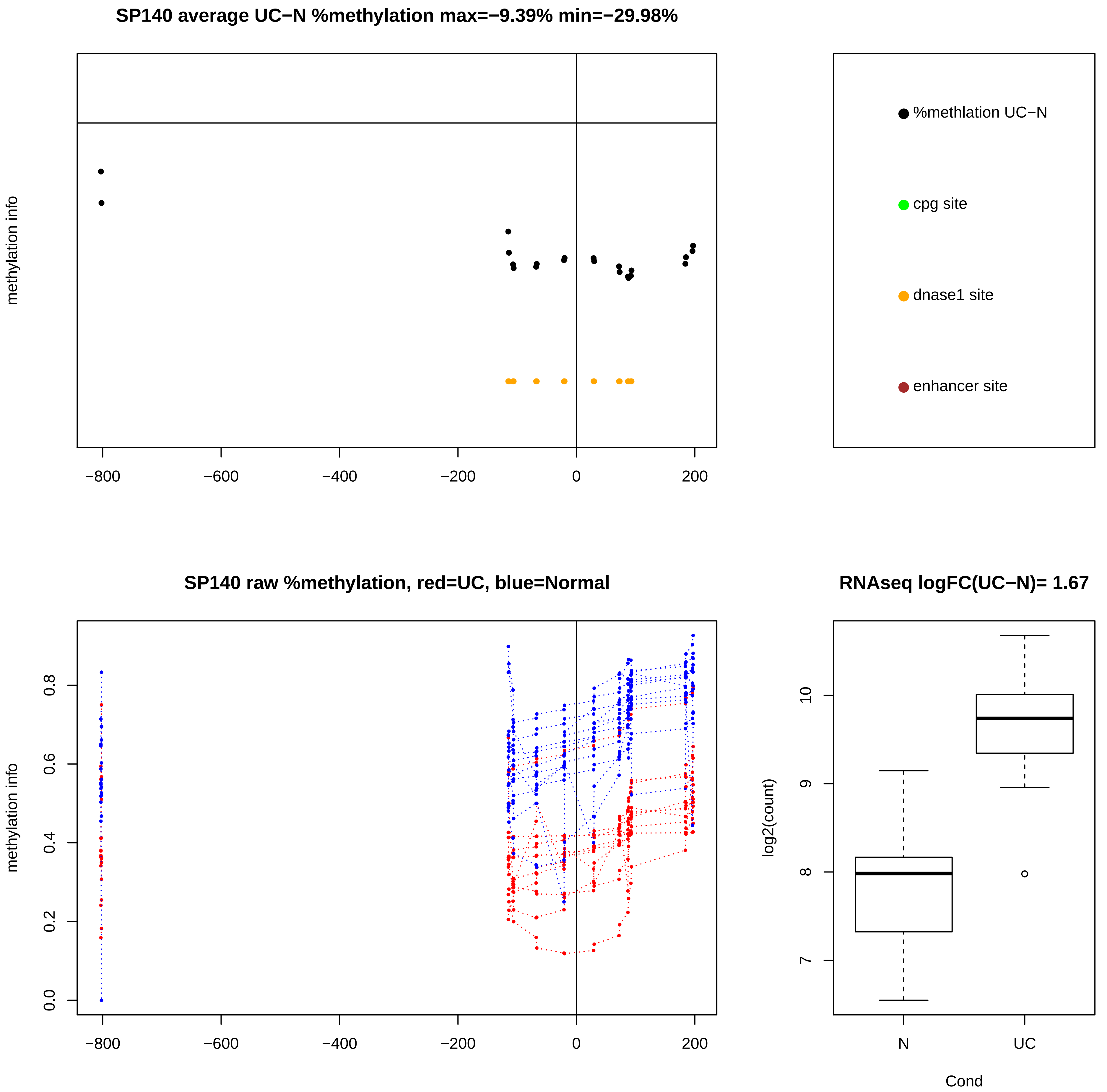
SORCS2 average UC−N %methylation max=6.46% min=−7.83%

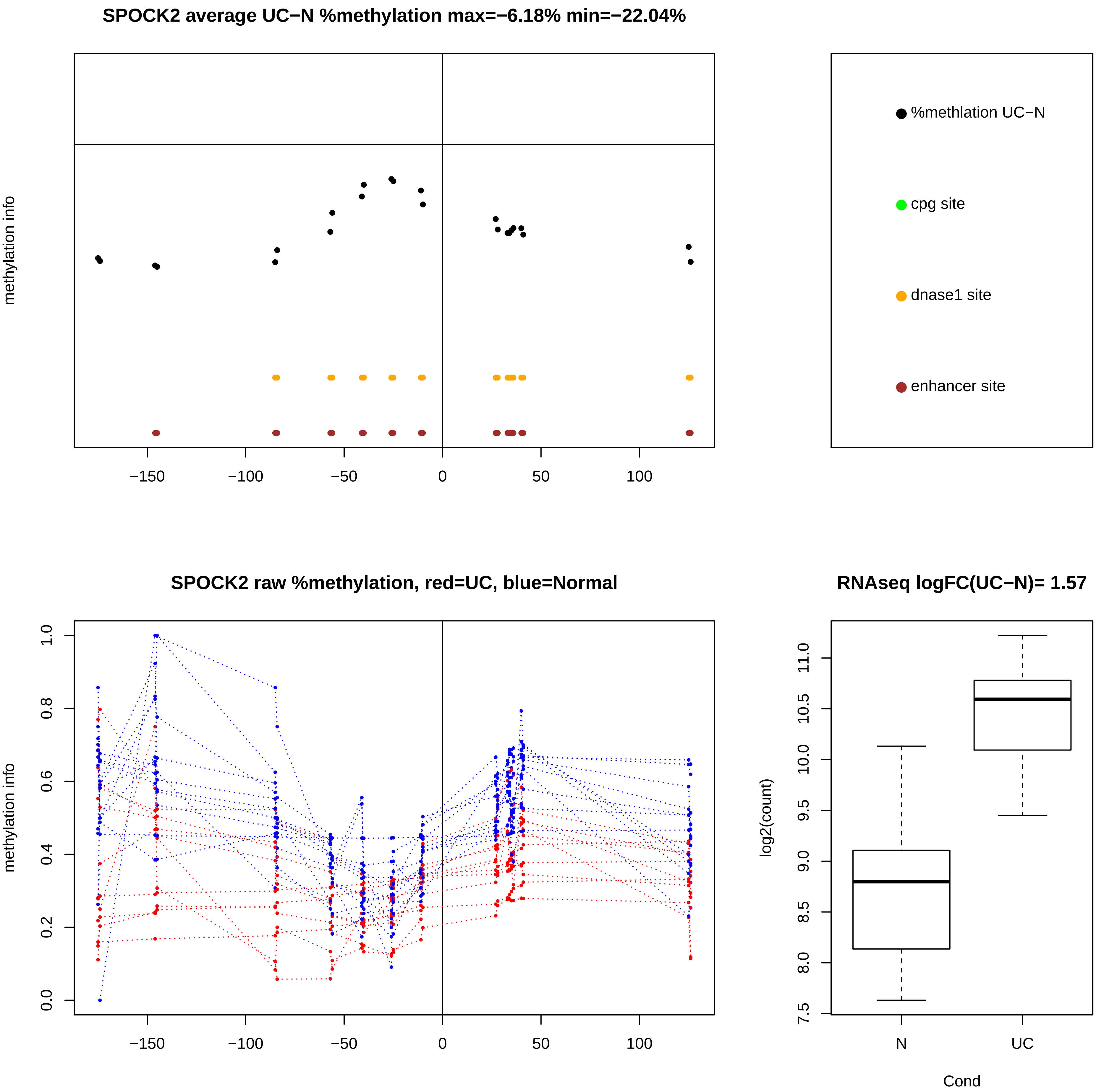


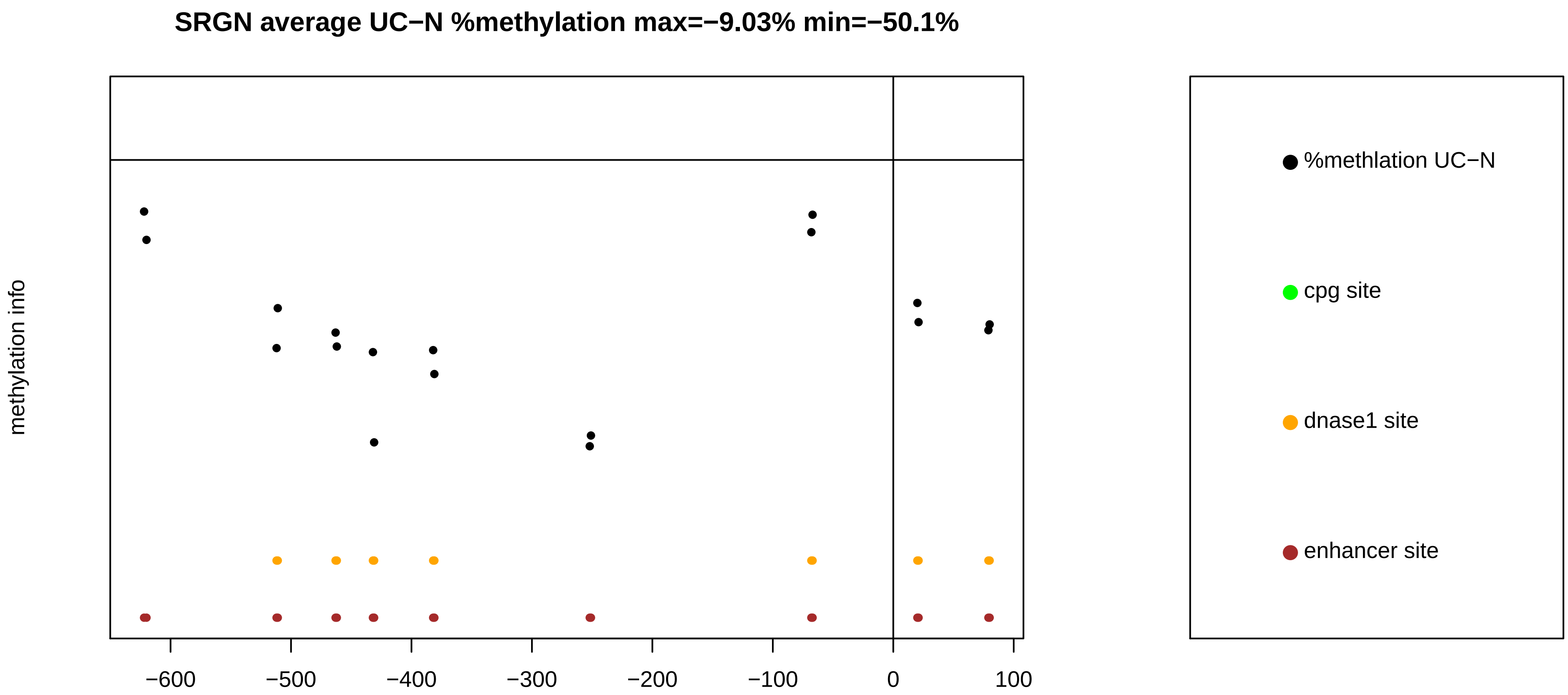
SORCS2 raw %methylation, red=UC, blue=Normal

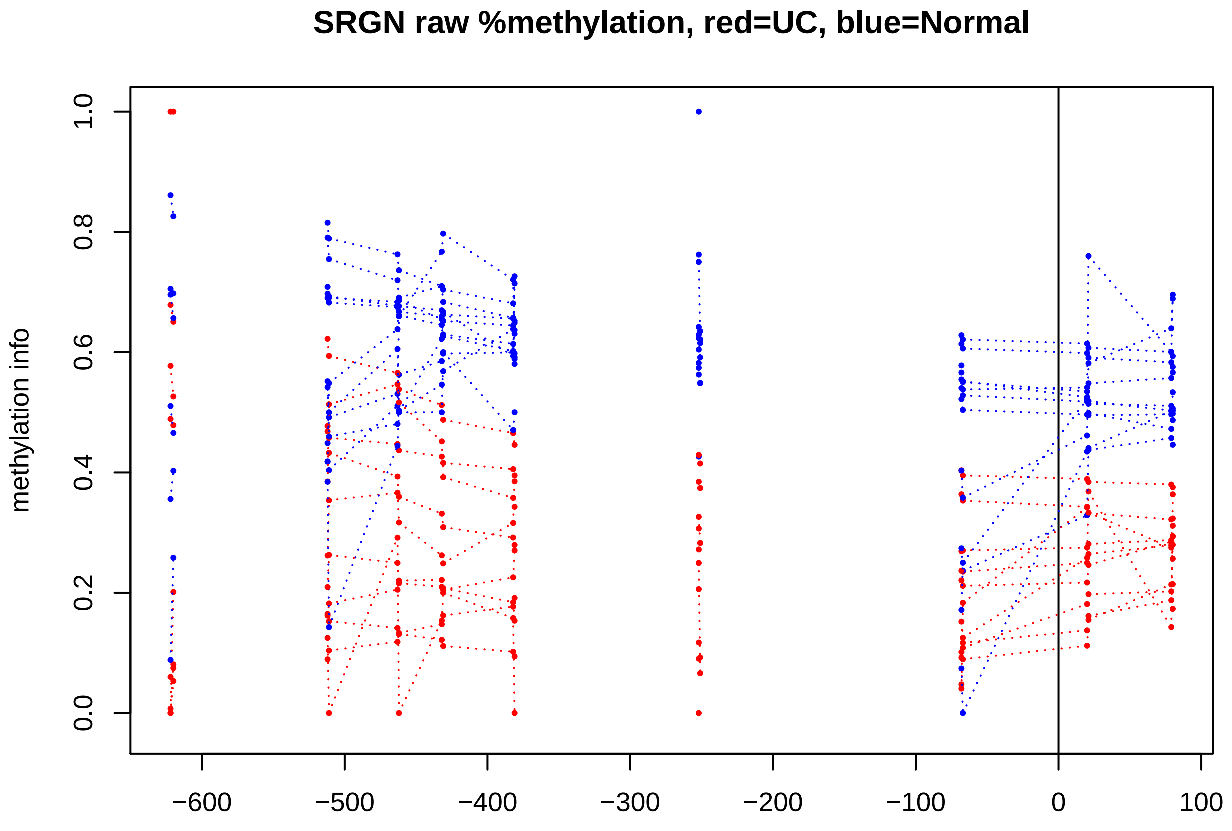


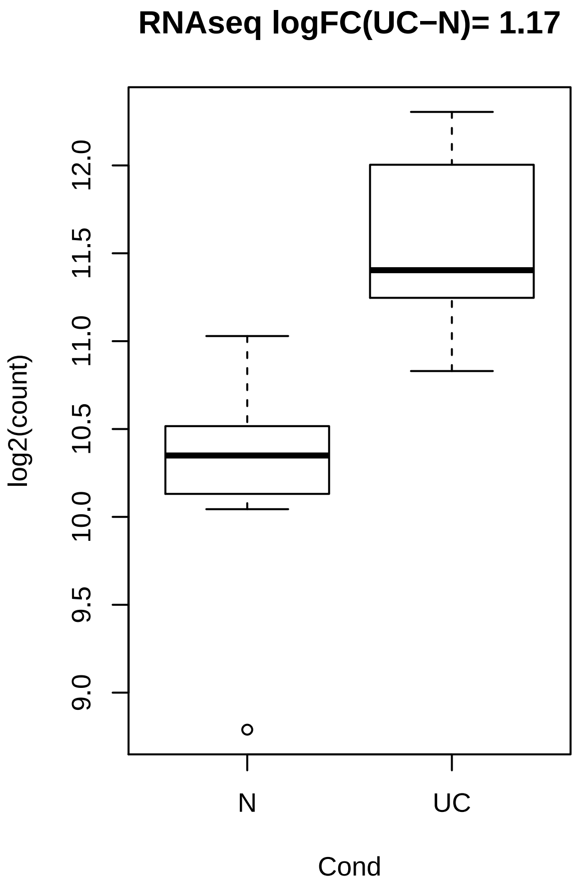
RNAseq logFC(UC−N)= 1.17

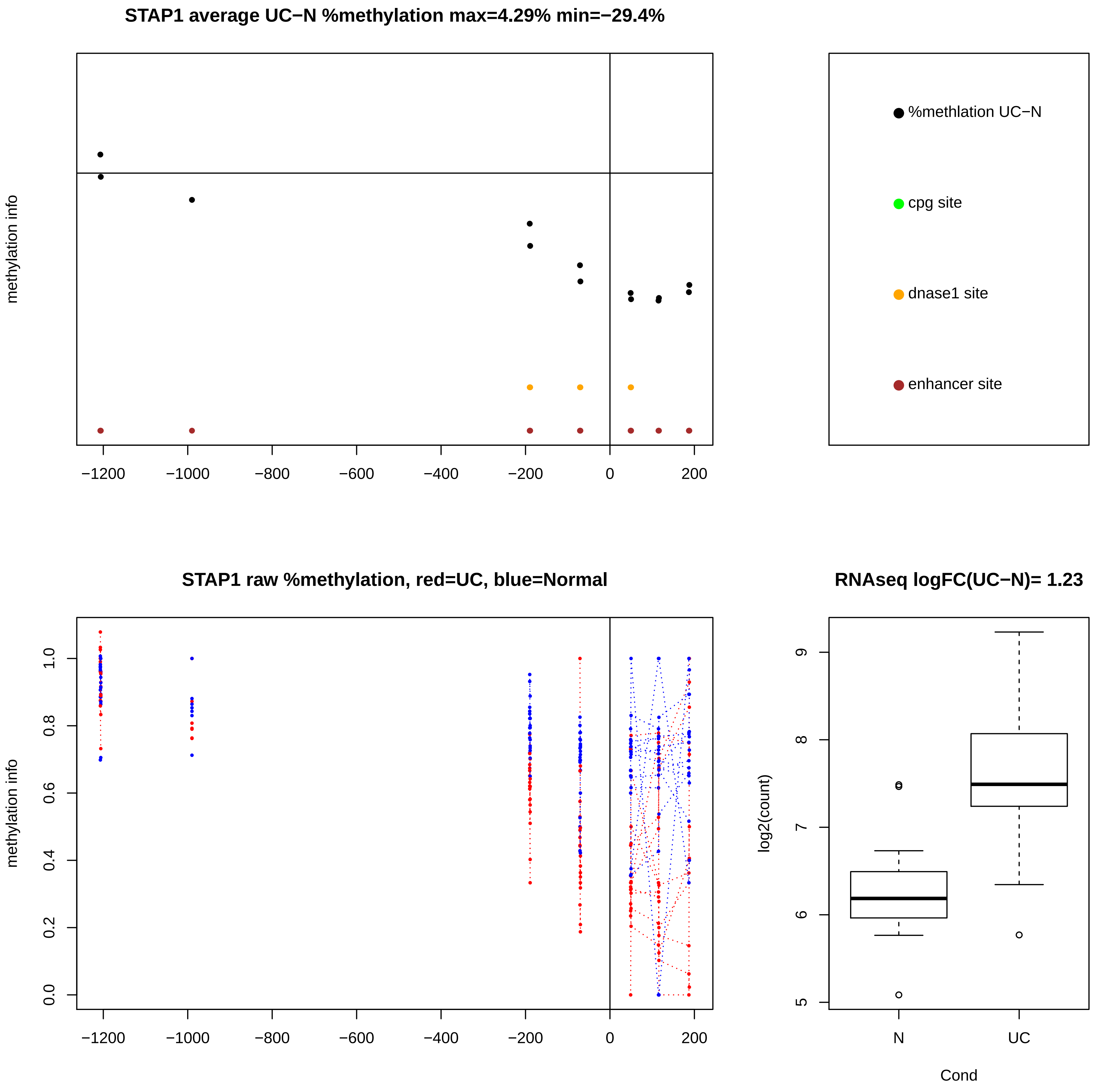

SP140 average UC−N %methylation max=−9.39% min=−29.98%
methylation info
−800
−600
−400
−200
0
200
%methlation UC−N
cpg site
dnase1 site
enhancer site
SP140 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
−800
−600
−400
−200
0
200
RNAseq logFC(UC−N)= 1.67
log2(count)
7
8
9
10
N
UC
Cond


SPOCK2 average UC−N %methylation max=−6.18% min=−22.04%
methylation info
−150
−100
−50
0
50
100
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
SPOCK2 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−150
−100
−50
0
50
100
RNAseq logFC(UC−N)= 1.57
log2(count)
7.5
8.0
8.5
9.0
9.5
10.0
10.5
11.0
N
UC
Cond


SRGN average UC−N %methylation max=−9.03% min=−50.1%


SRGN raw %methylation, red=UC, blue=Normal

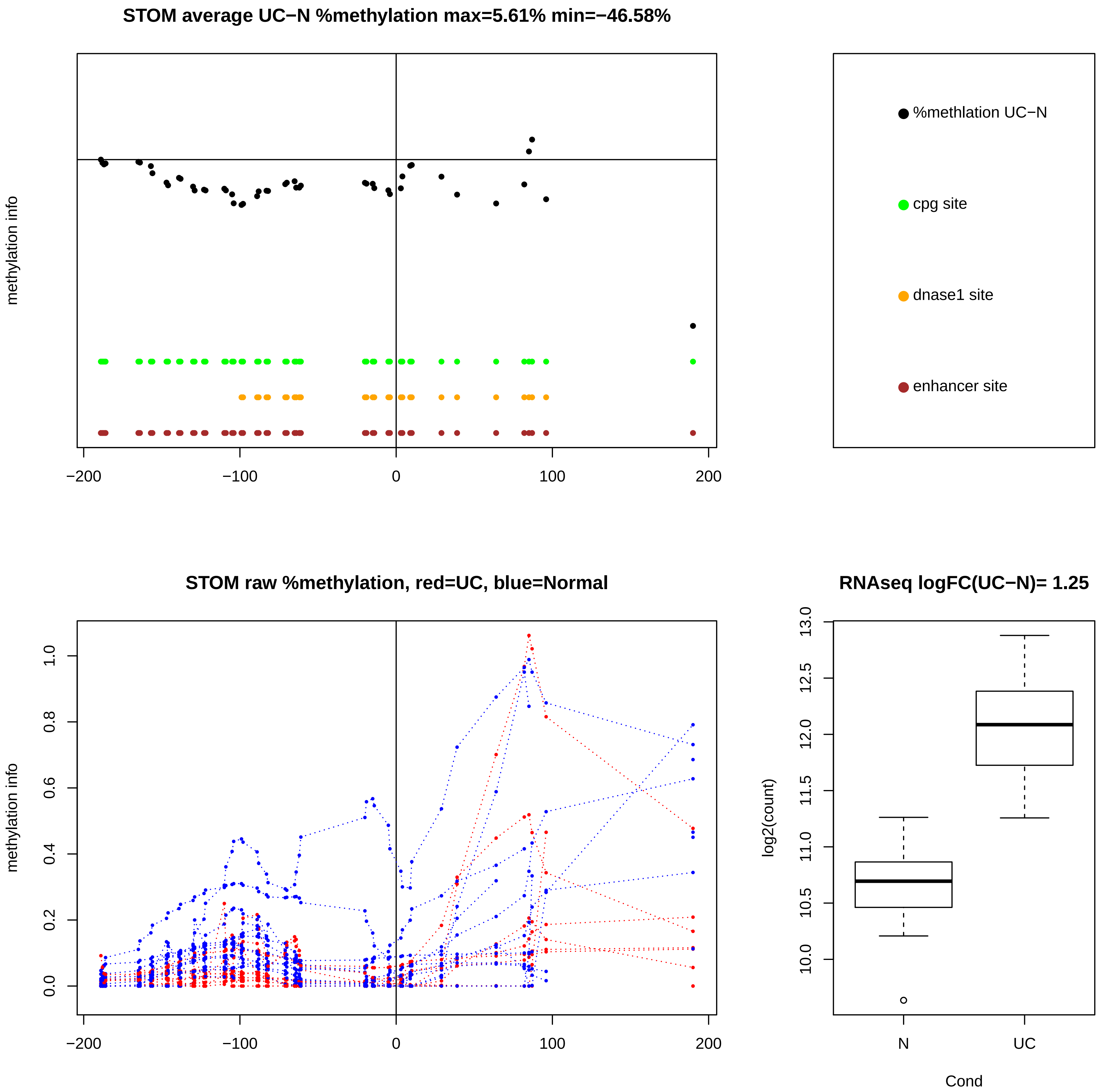

RNAseq logFC(UC−N)= 1.17

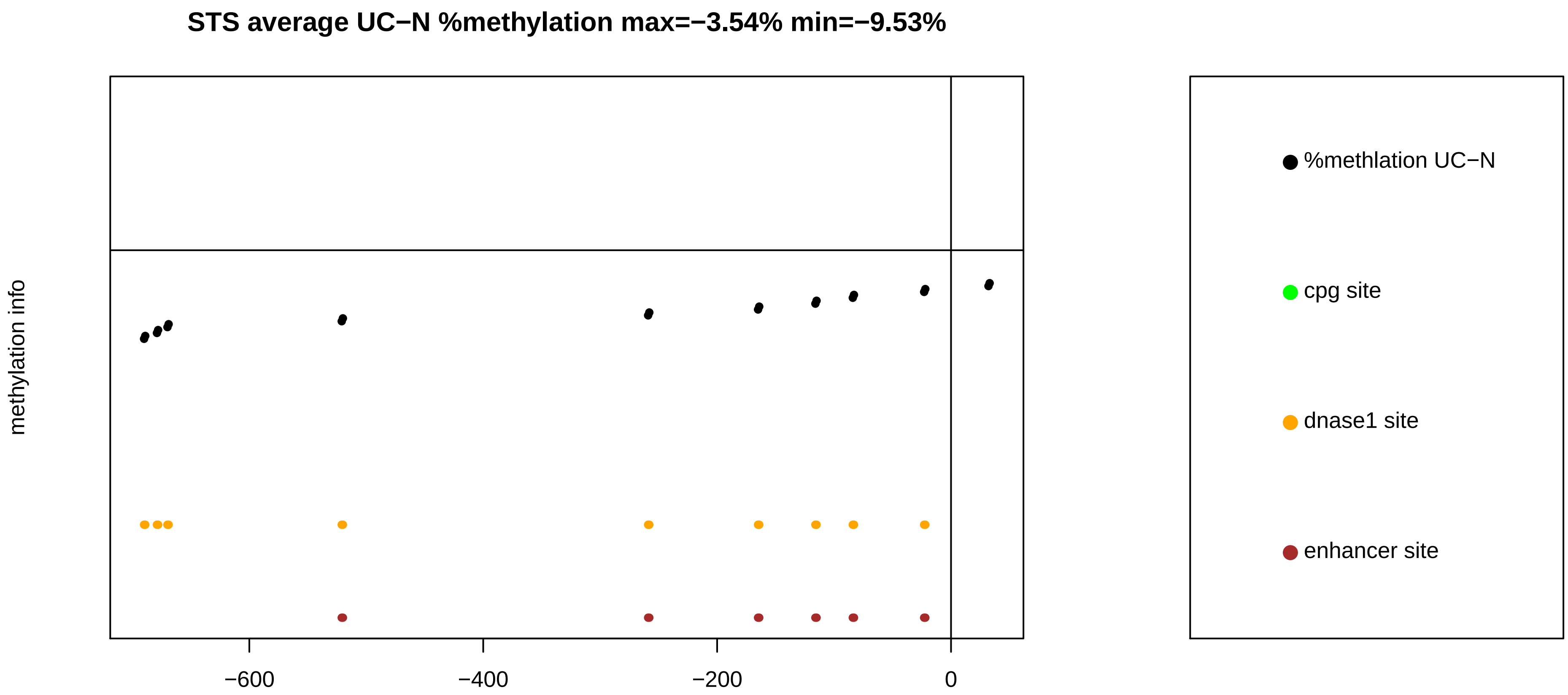


STAP1 average UC−N %methylation max=4.29% min=−29.4%

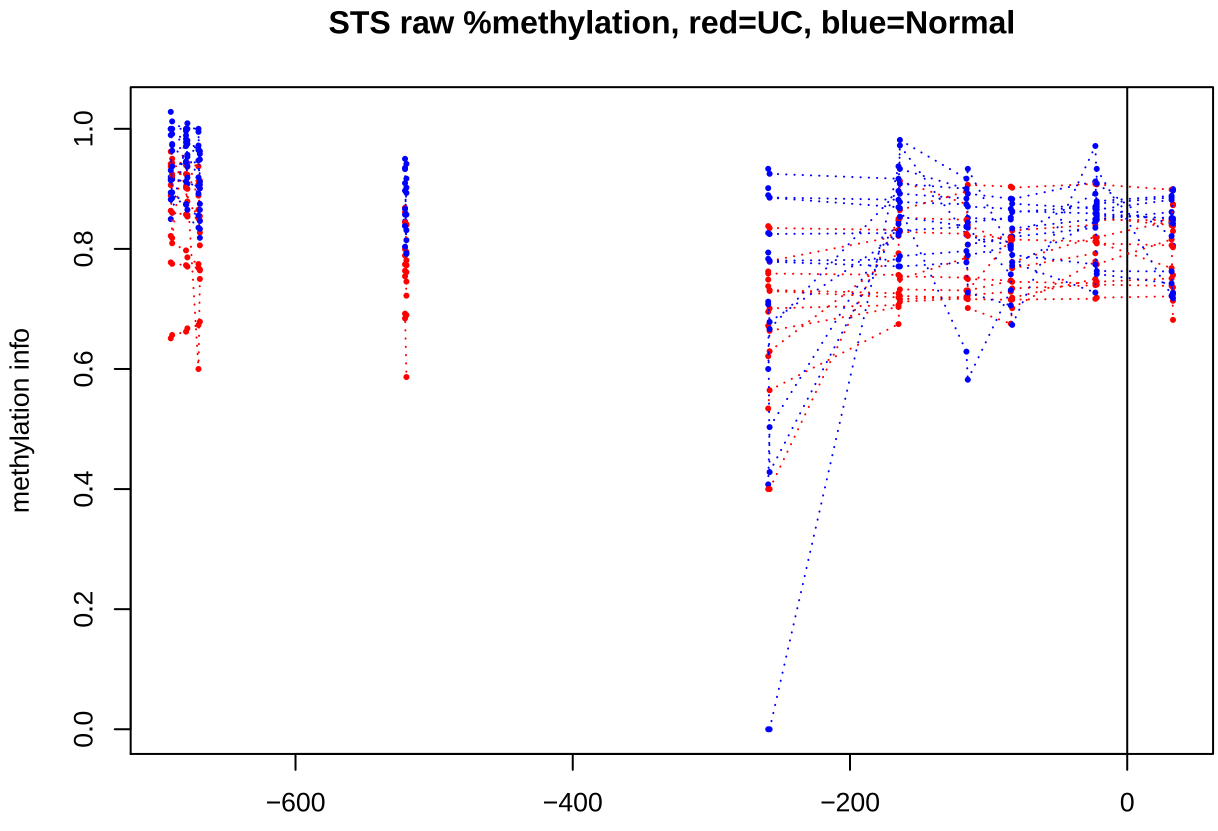
STAP1 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.23

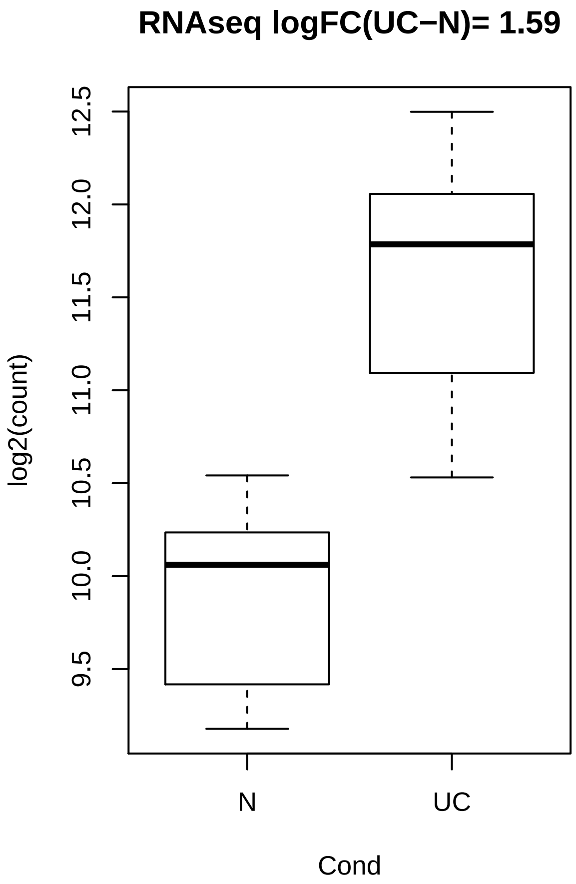

STOM average UC−N %methylation max=5.61% min=−46.58%
methylation info
−200
−100
0
100
200
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
STOM raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−200
−100
0
100
200
RNAseq logFC(UC−N)= 1.25
log2(count)
10.0
10.5
11.0
11.5
12.0
12.5
13.0
N
UC
Cond



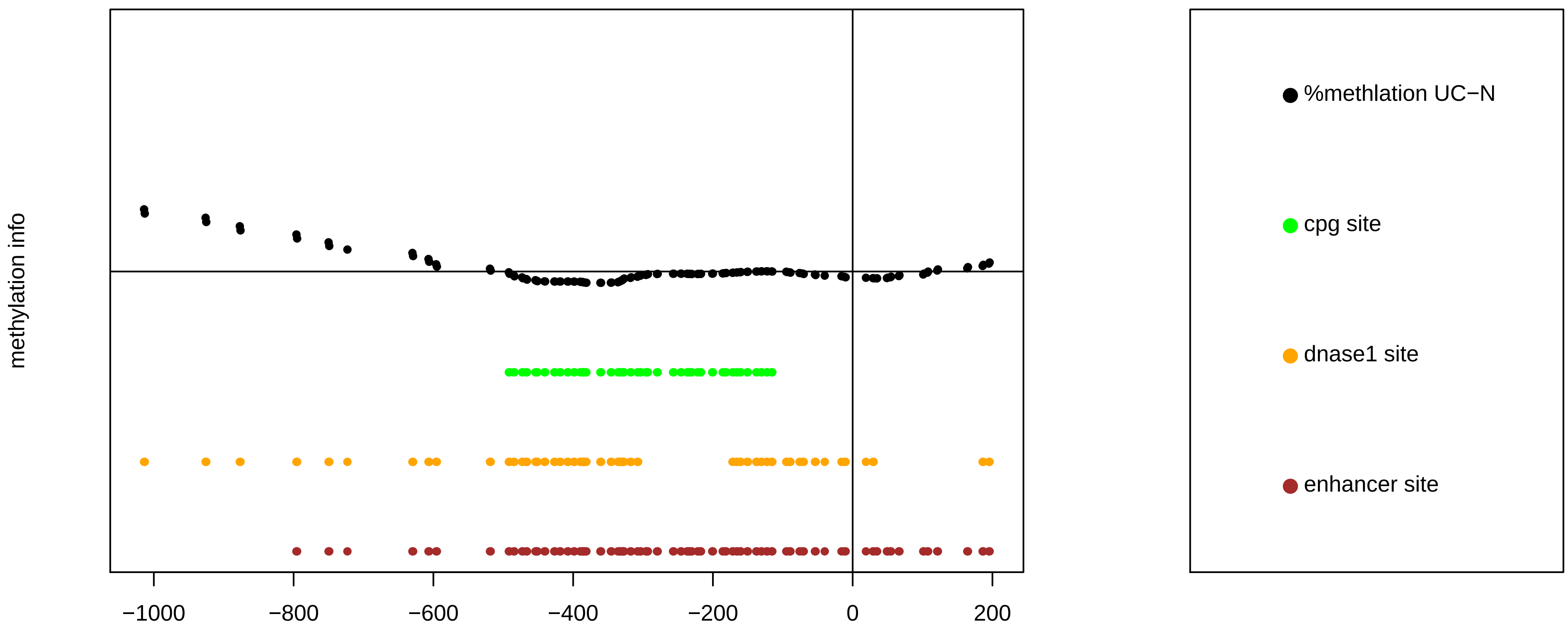
STS average UC−N %methylation max=−3.54% min=−9.53%

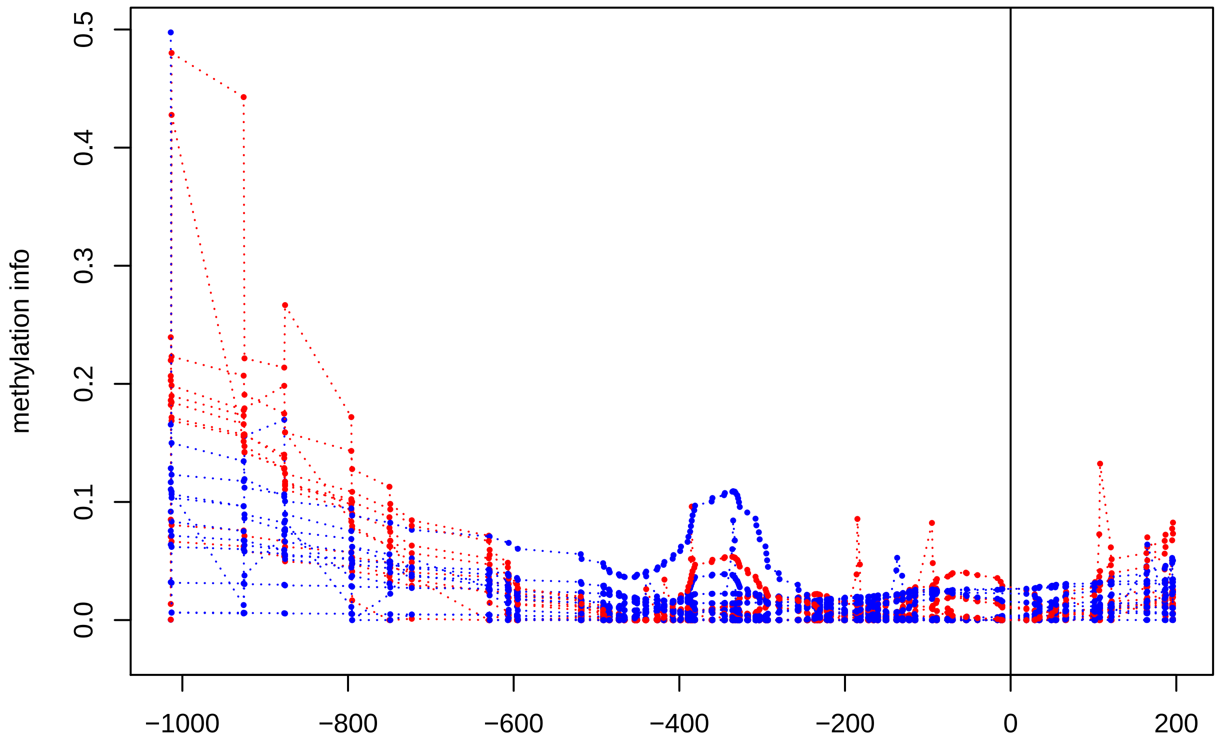


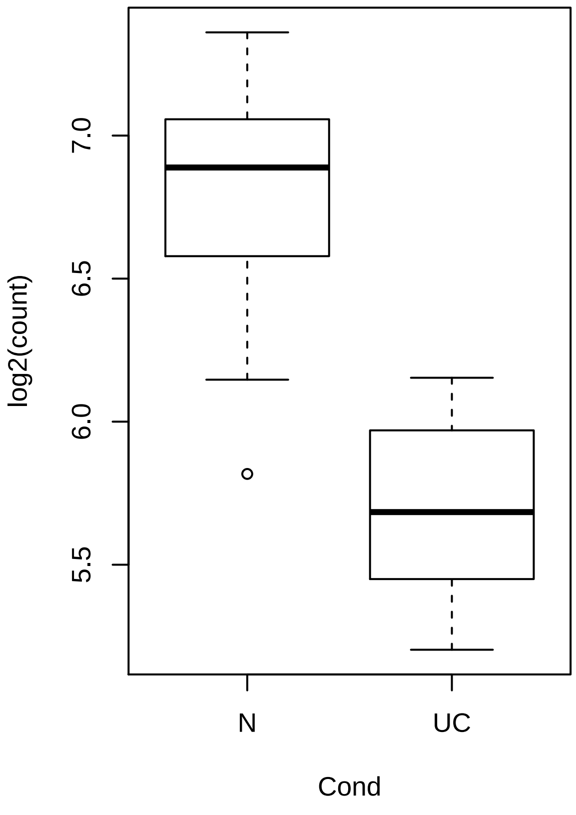
STS raw %methylation, red=UC, blue=Normal

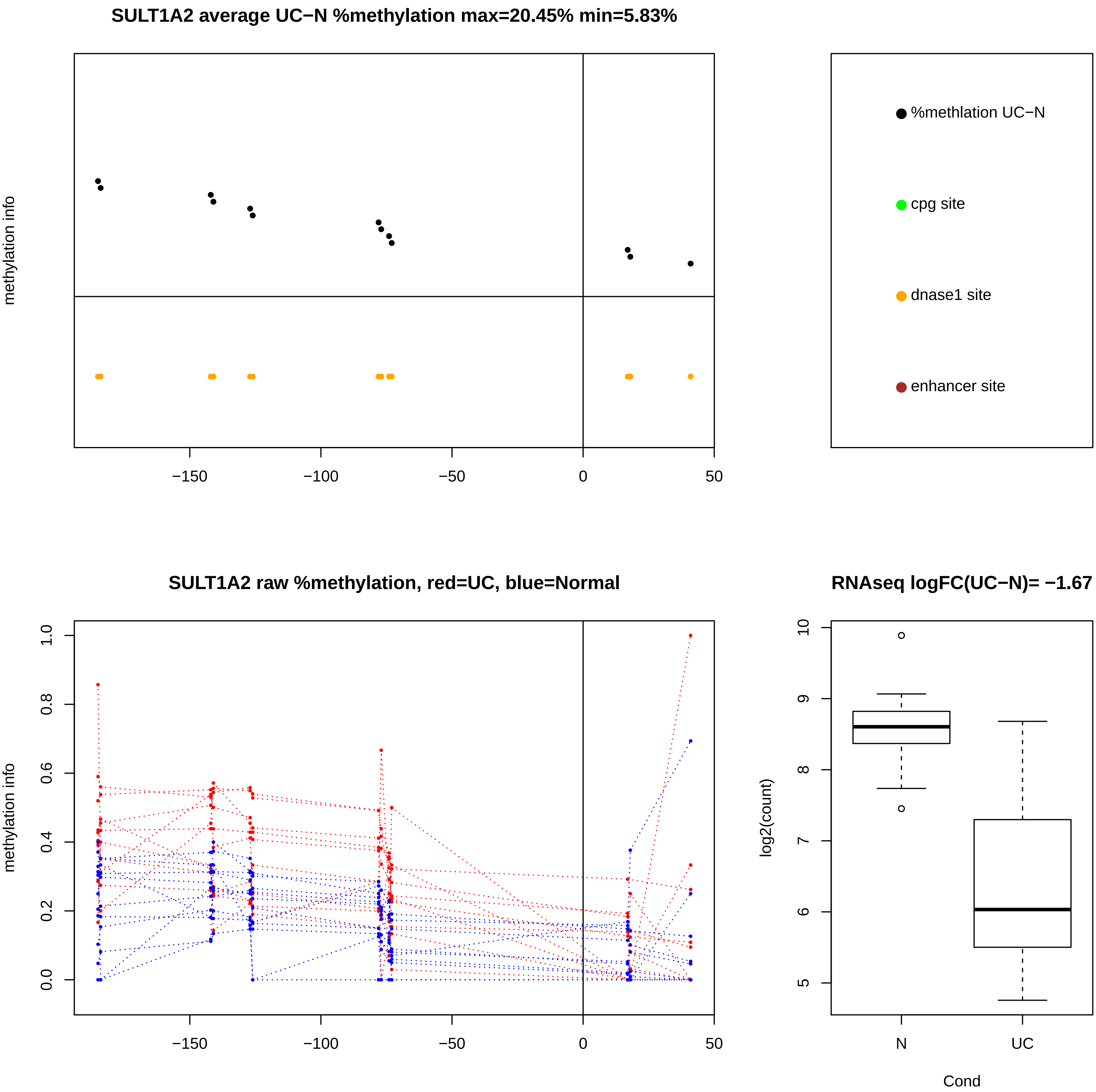


RNAseq logFC(UC−N)= 1.59


SUCLG2−AS1 average UC−N %methylation max=6.95% min=−1.26%


SUCLG2−AS1 raw %methylation, red=UC, blue=Normal

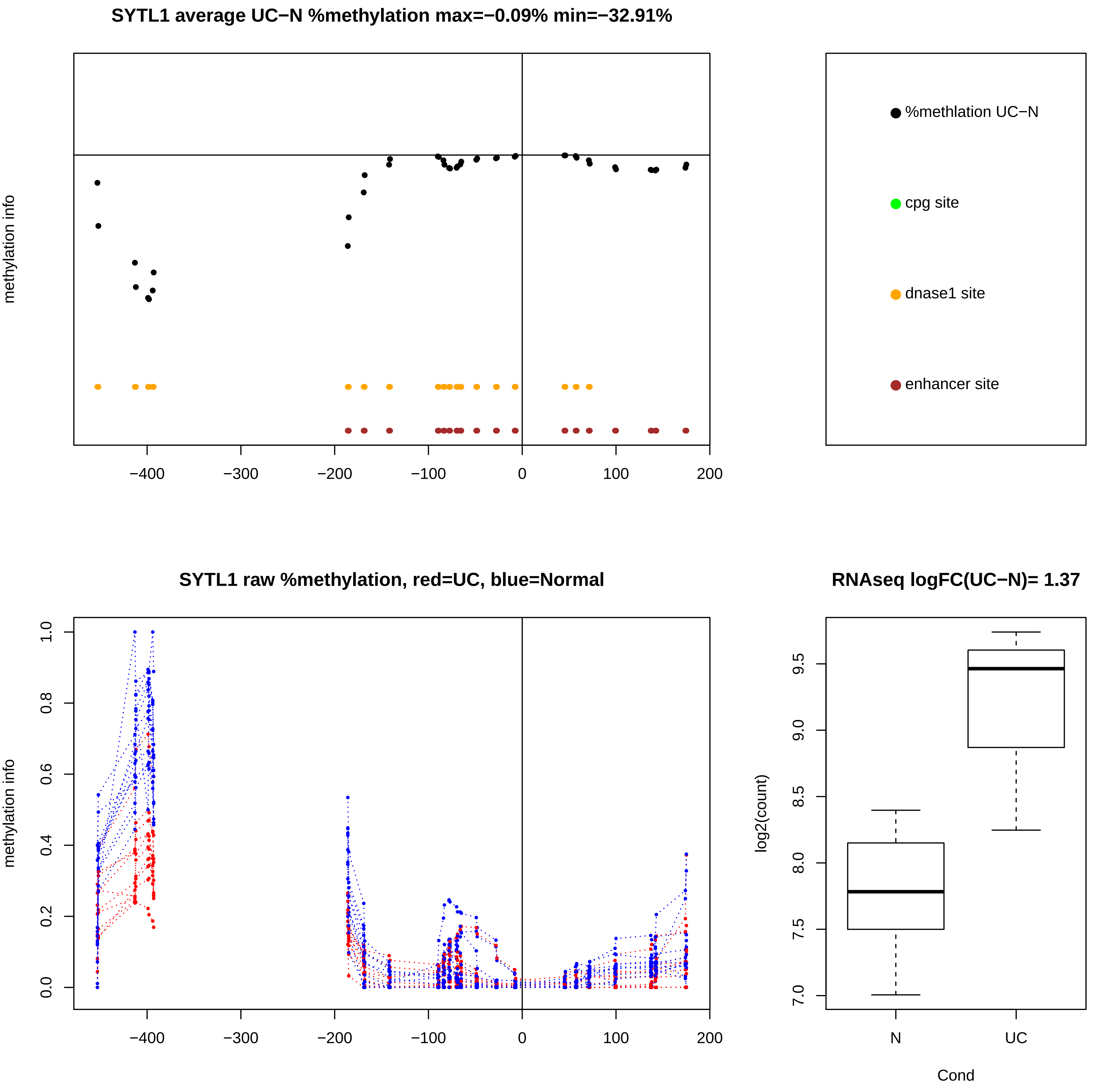

RNAseq logFC(UC−N)= −1.02



SULT1A2 average UC−N %methylation max=20.45% min=5.83%

SULT1A2 raw %methylation, red=UC, blue=Normal

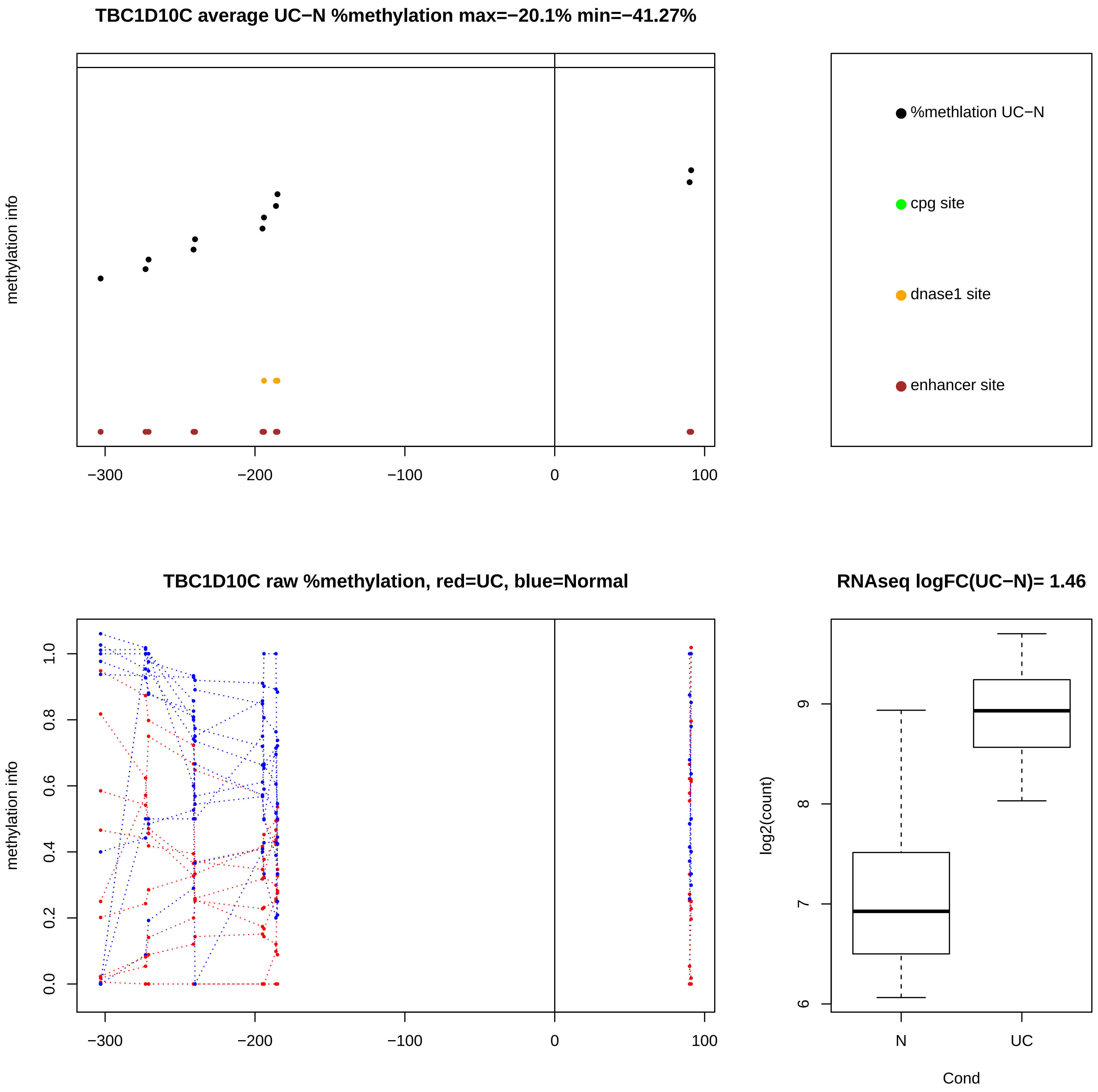
RNAseq logFC(UC−N)= −1.67

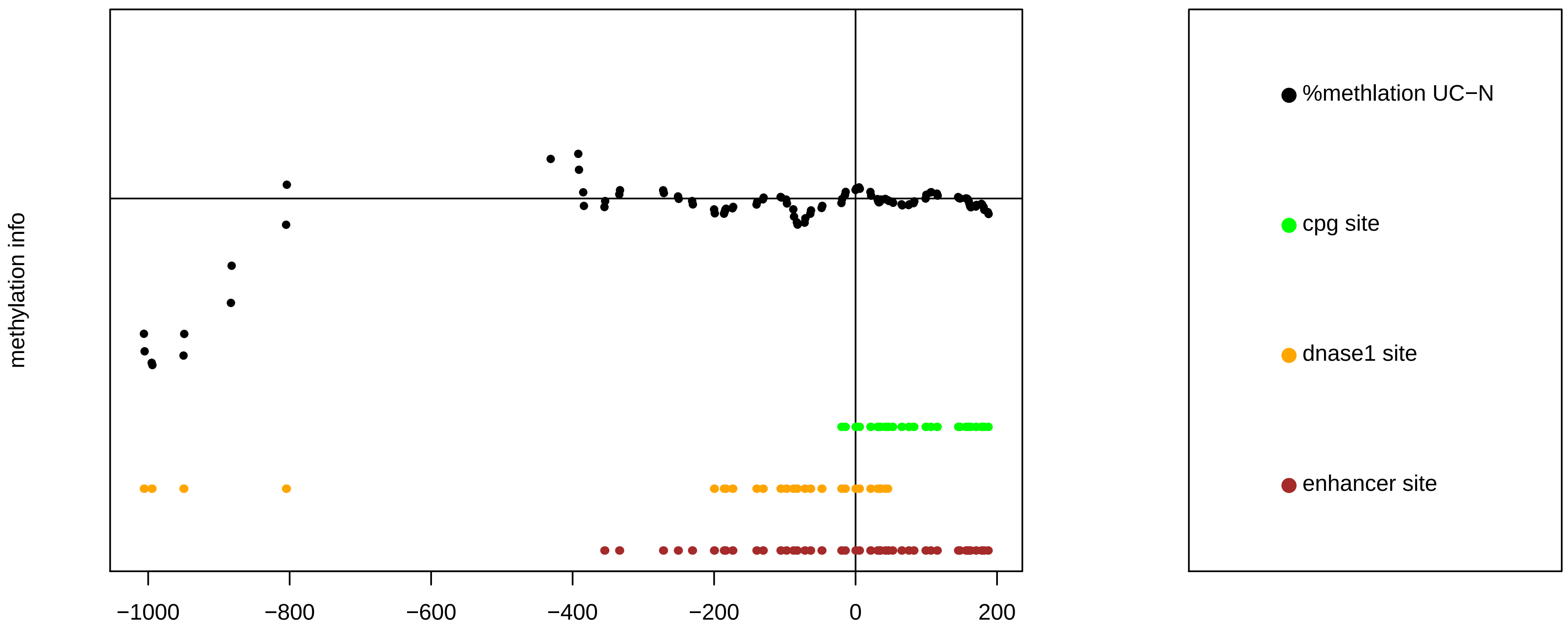


SYTL1 average UC−N %methylation max=−0.09% min=−32.91%

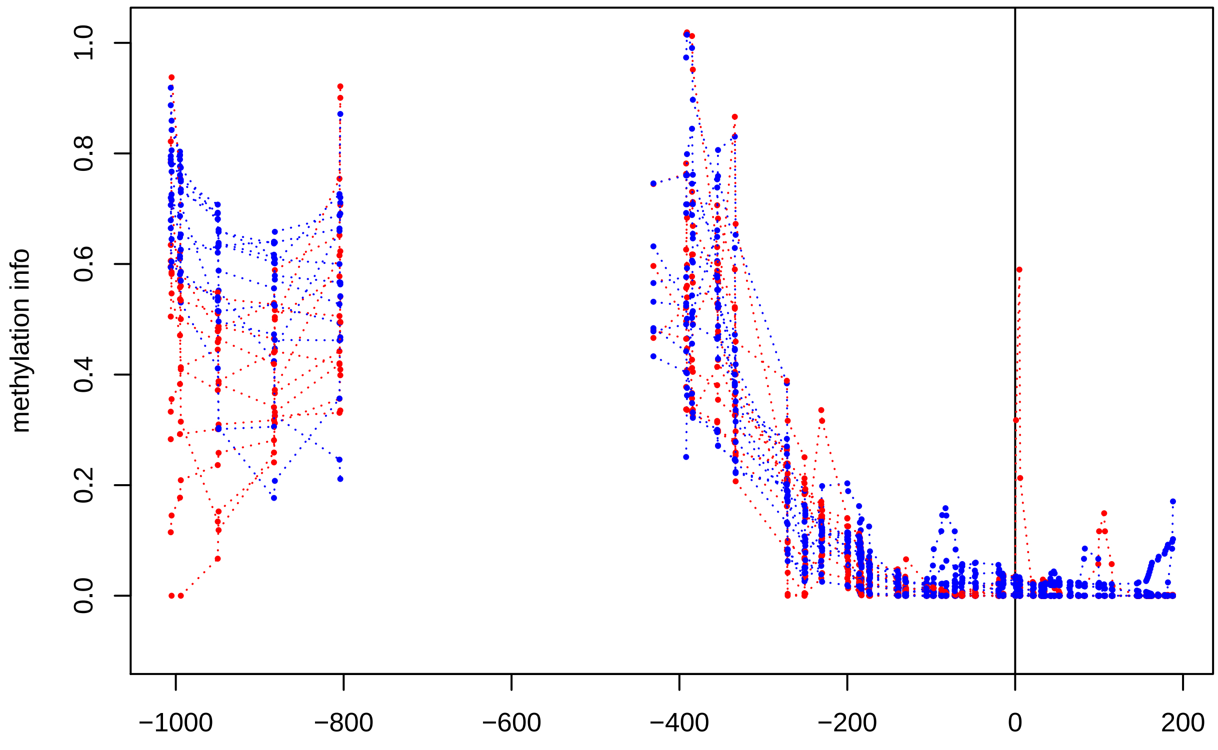
SYTL1 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.37

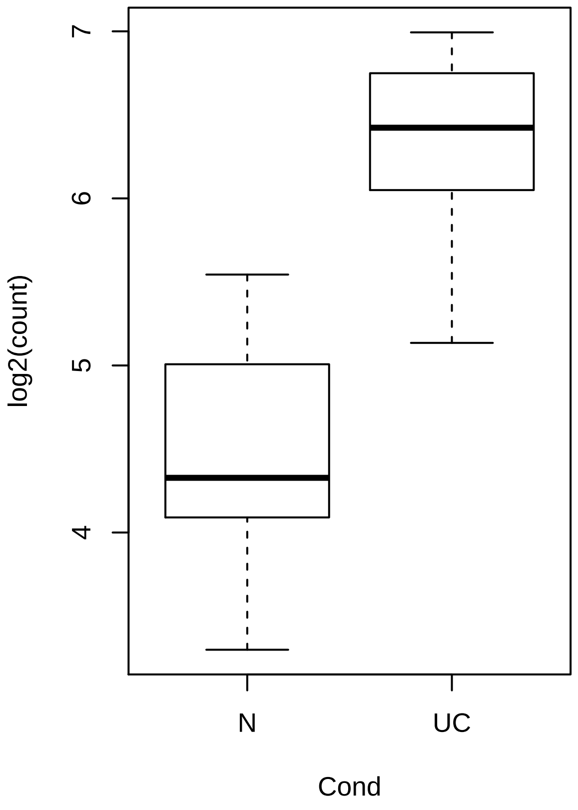

TBC1D10C average UC−N %methylation max=−20.1% min=−41.27%
methylation info
−300
−200
−100
0
100
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
TBC1D10C raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−300
−200
−100
0
100
RNAseq logFC(UC−N)= 1.46
log2(count)
6
7
8
9
N
UC
Cond



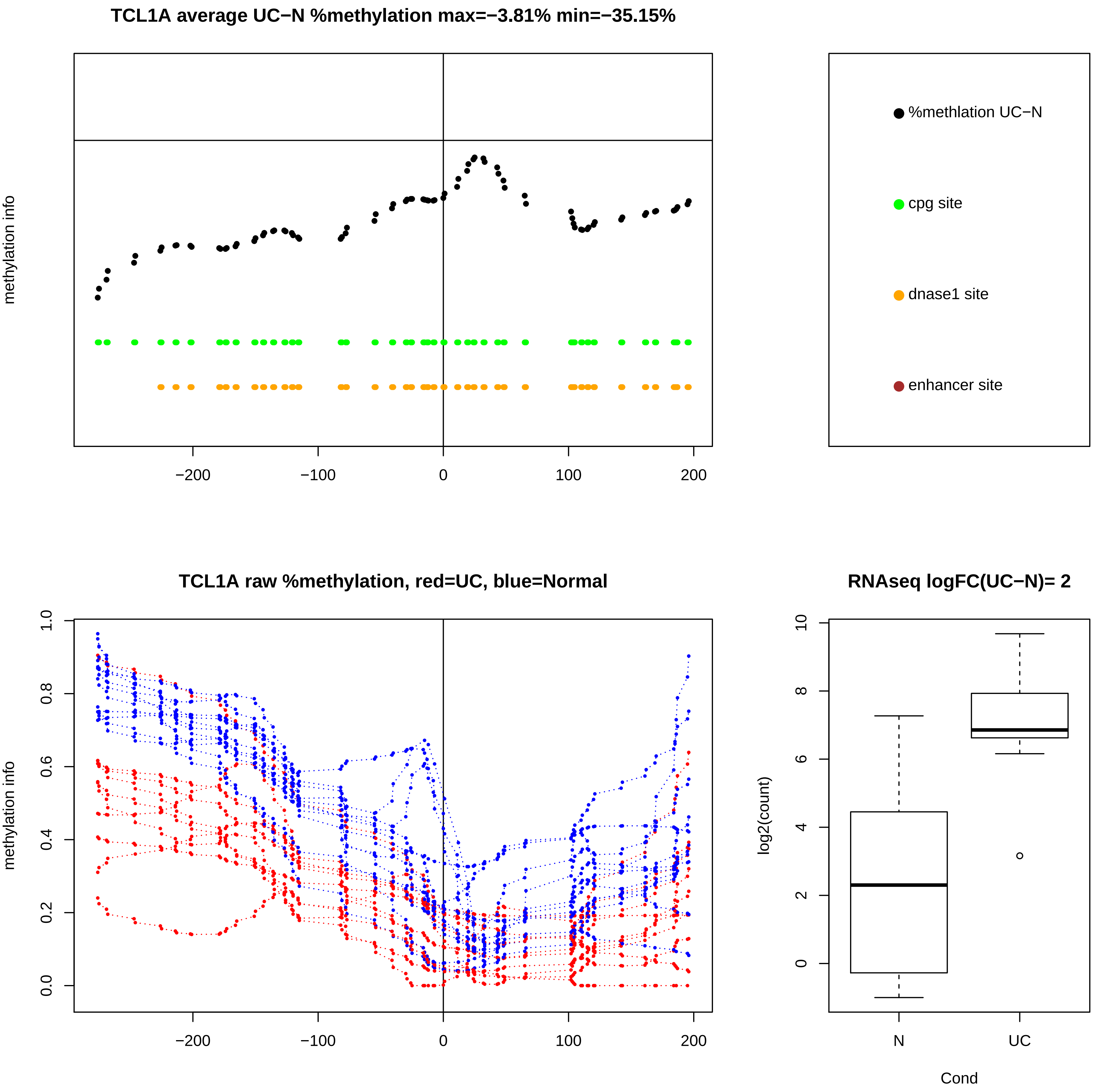
TBX21 average UC−N %methylation max=7.23% min=−26.94%



TBX21 raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 1.6

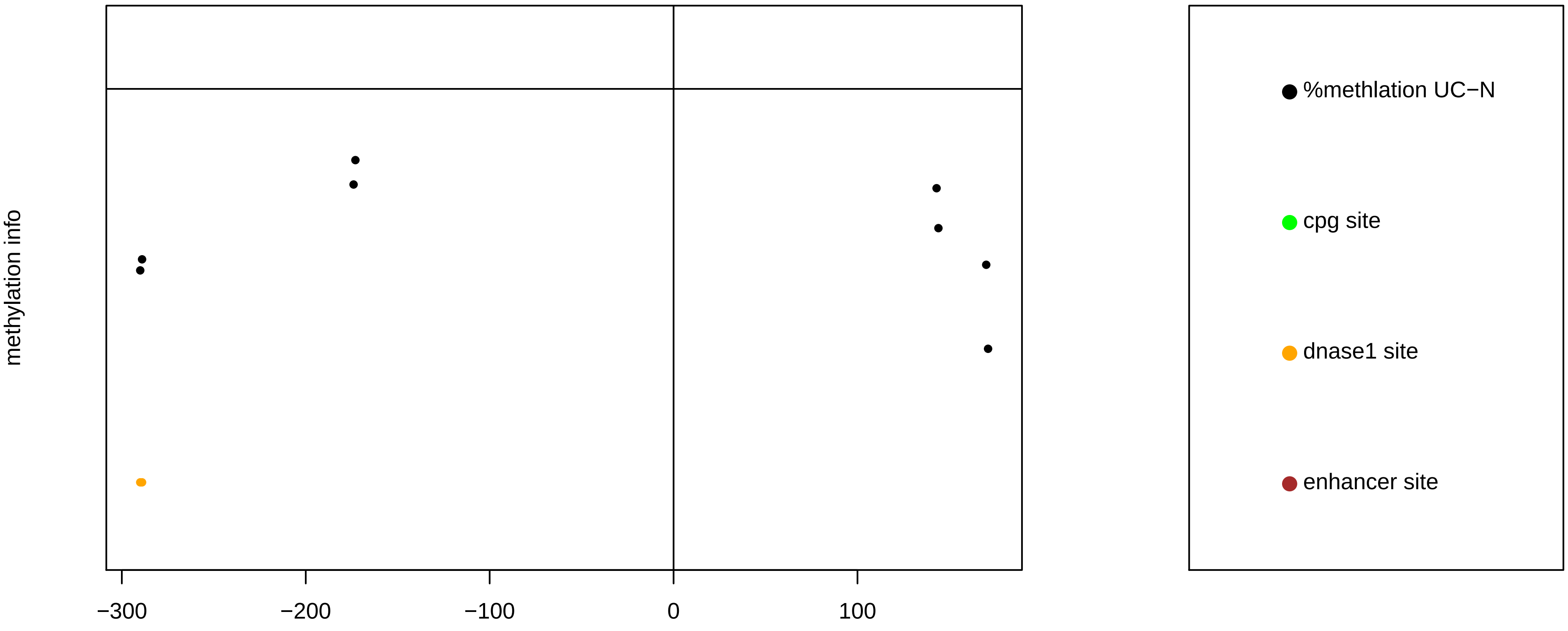


TCL1A average UC−N %methylation max=−3.81% min=−35.15%

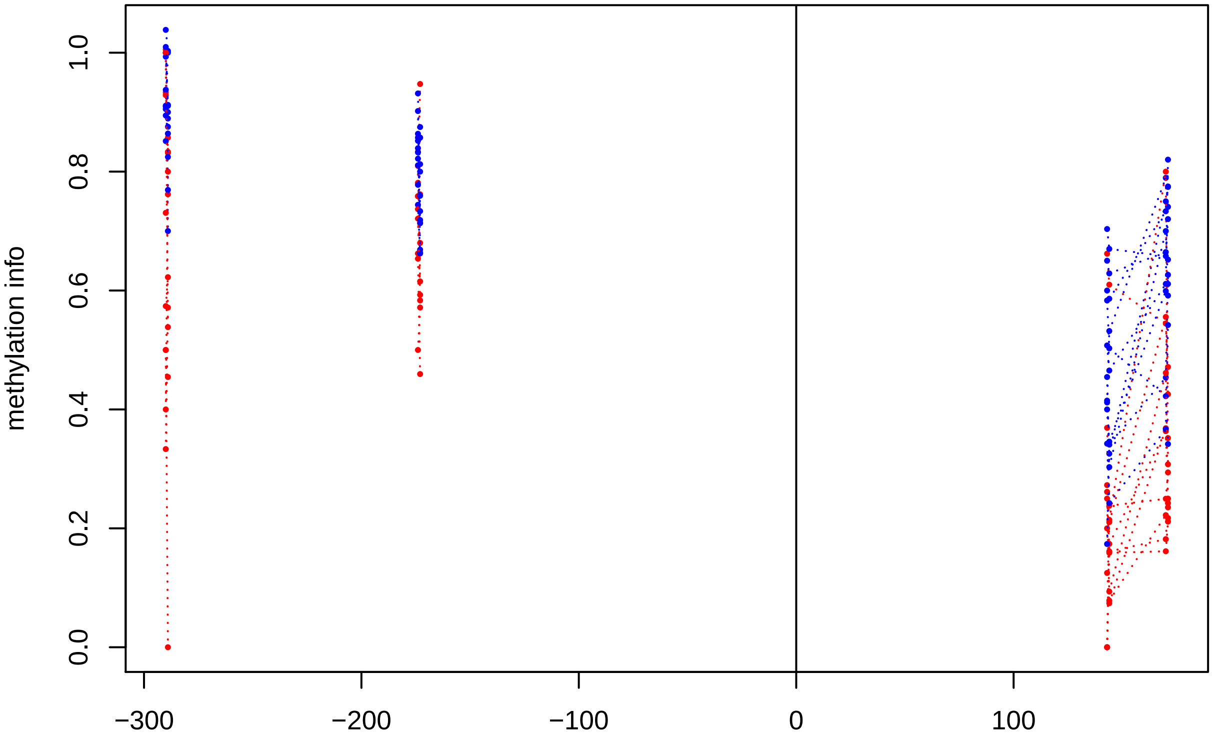
TCL1A raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 2

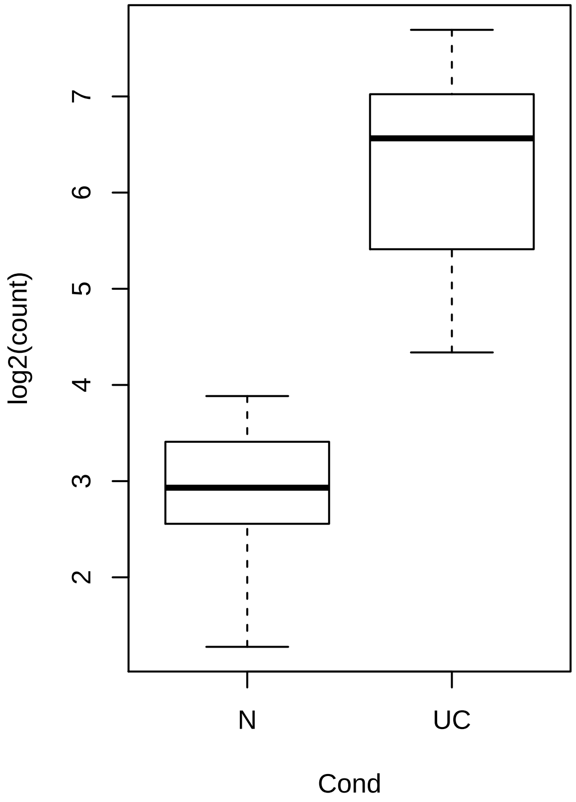
TCN1 average UC−N %methylation max=−10.67% min=−38.92%



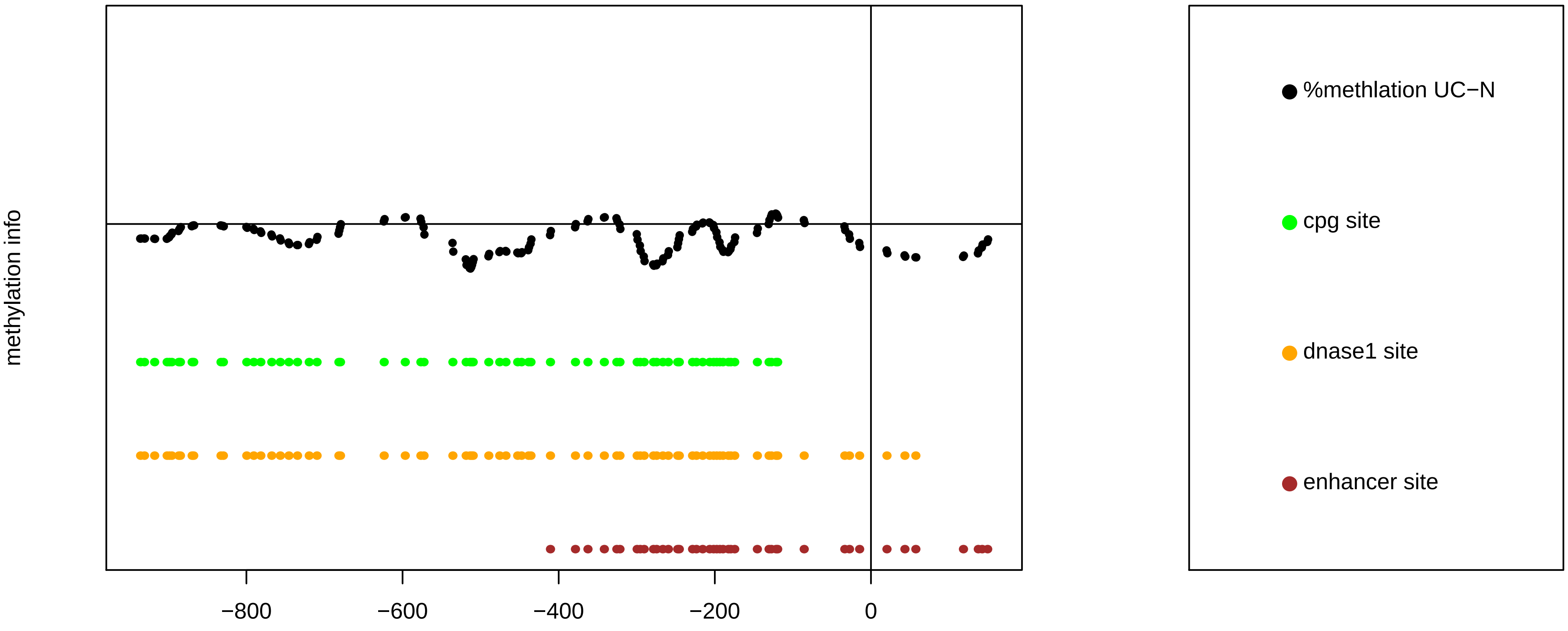
TCN1 raw %methylation, red=UC, blue=Normal



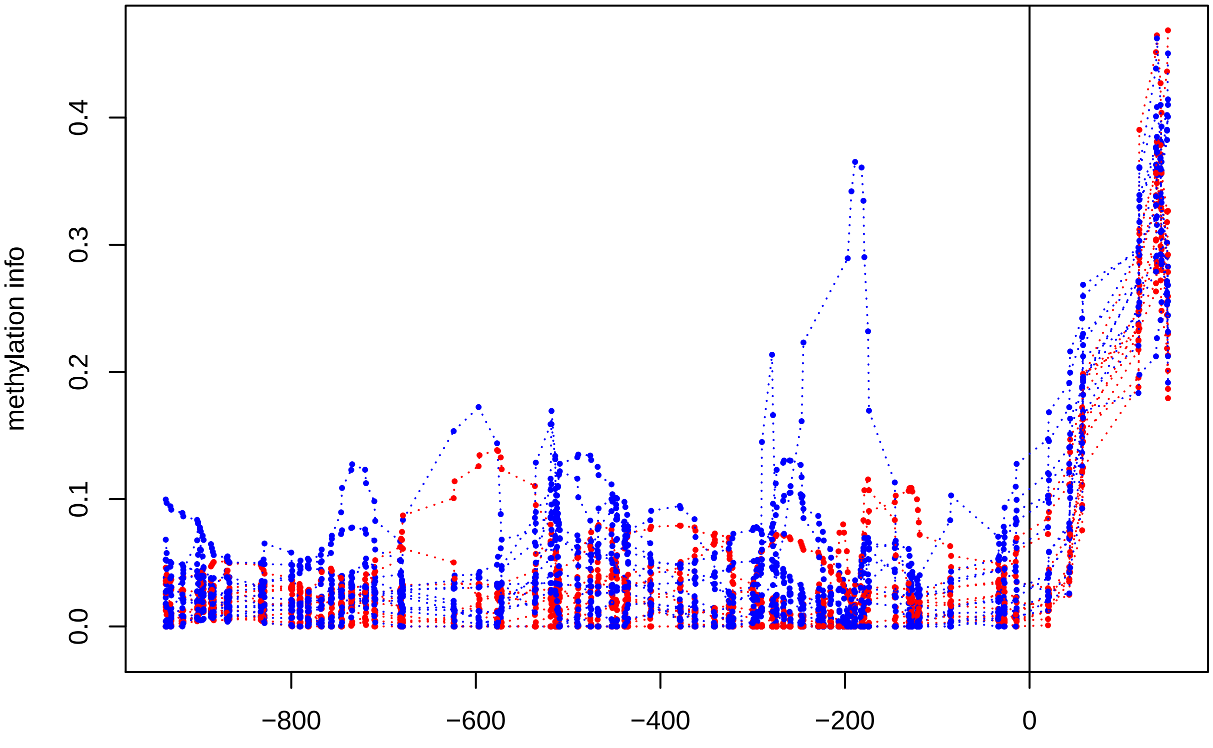
RNAseq logFC(UC−N)= 2.96



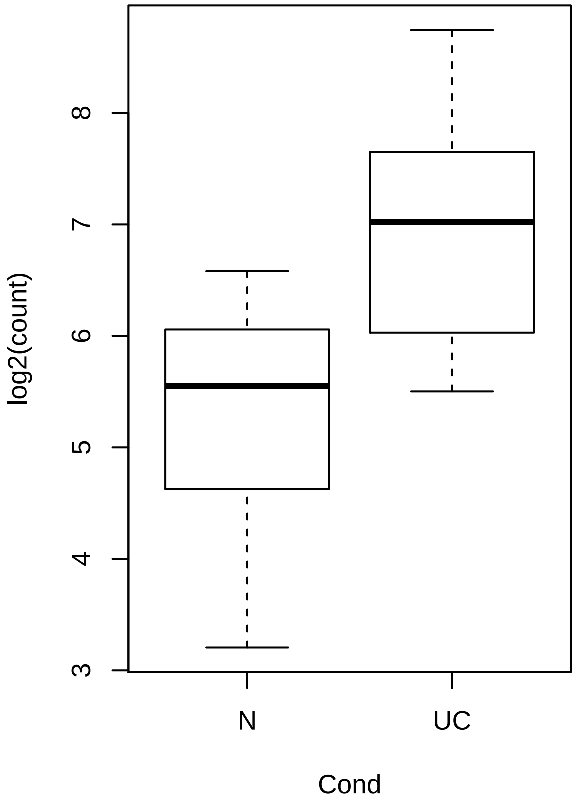
TFPI2 average UC−N %methylation max=1.11% min=−4.76%

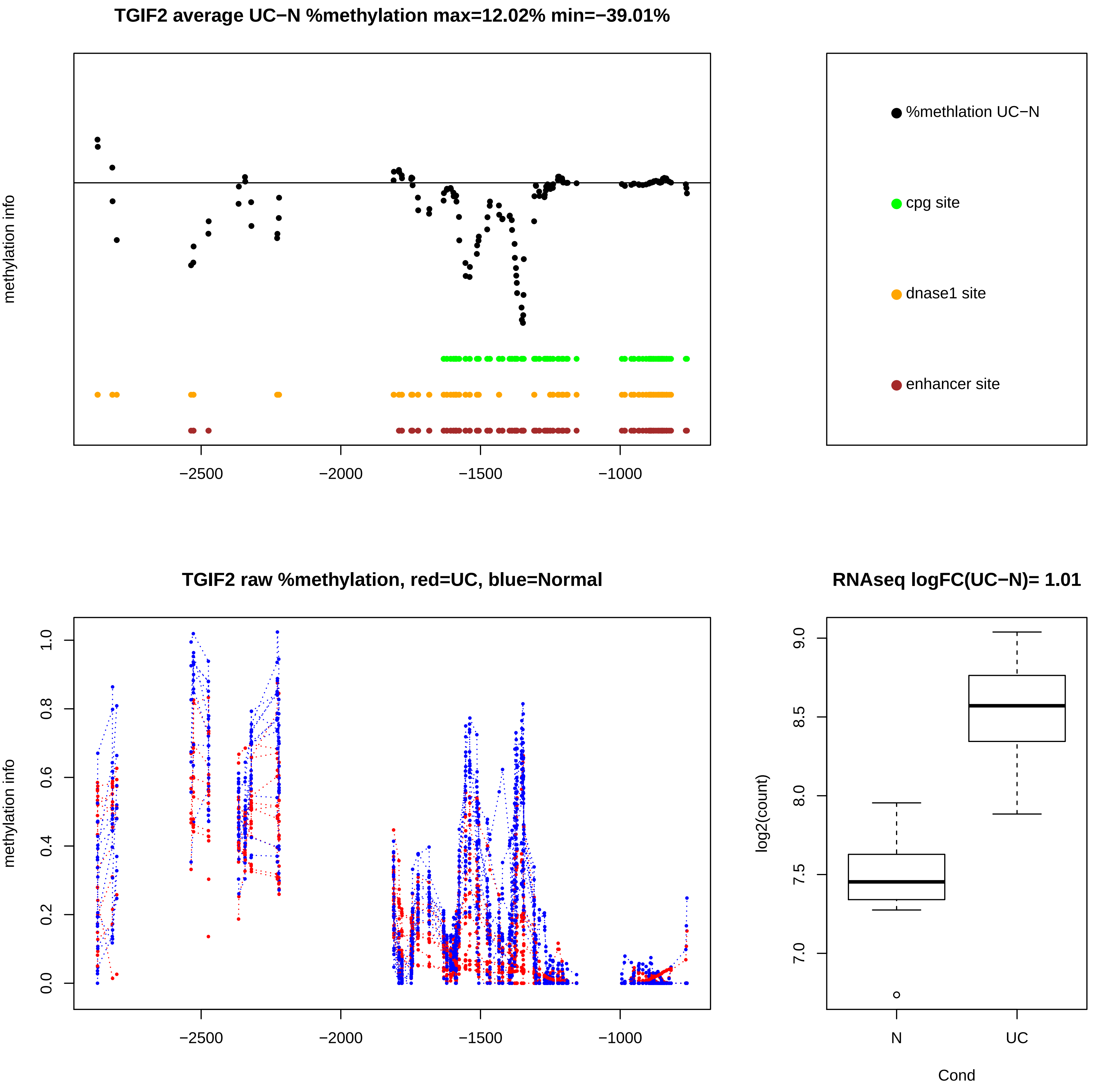


TFPI2 raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 1.64

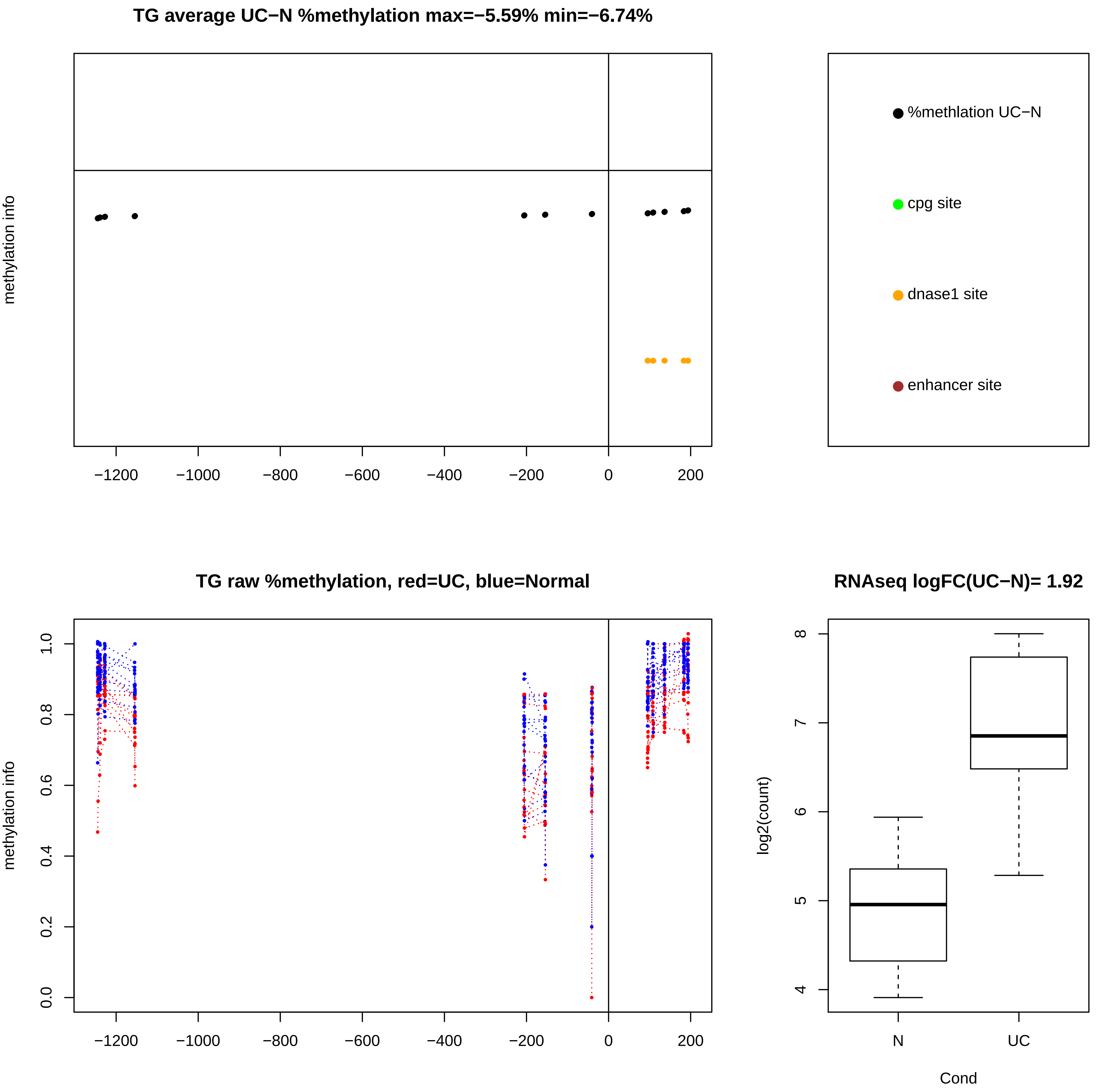




TGIF2 average UC−N %methylation max=12.02% min=−39.01%

TGIF2 raw %methylation, red=UC, blue=Normal

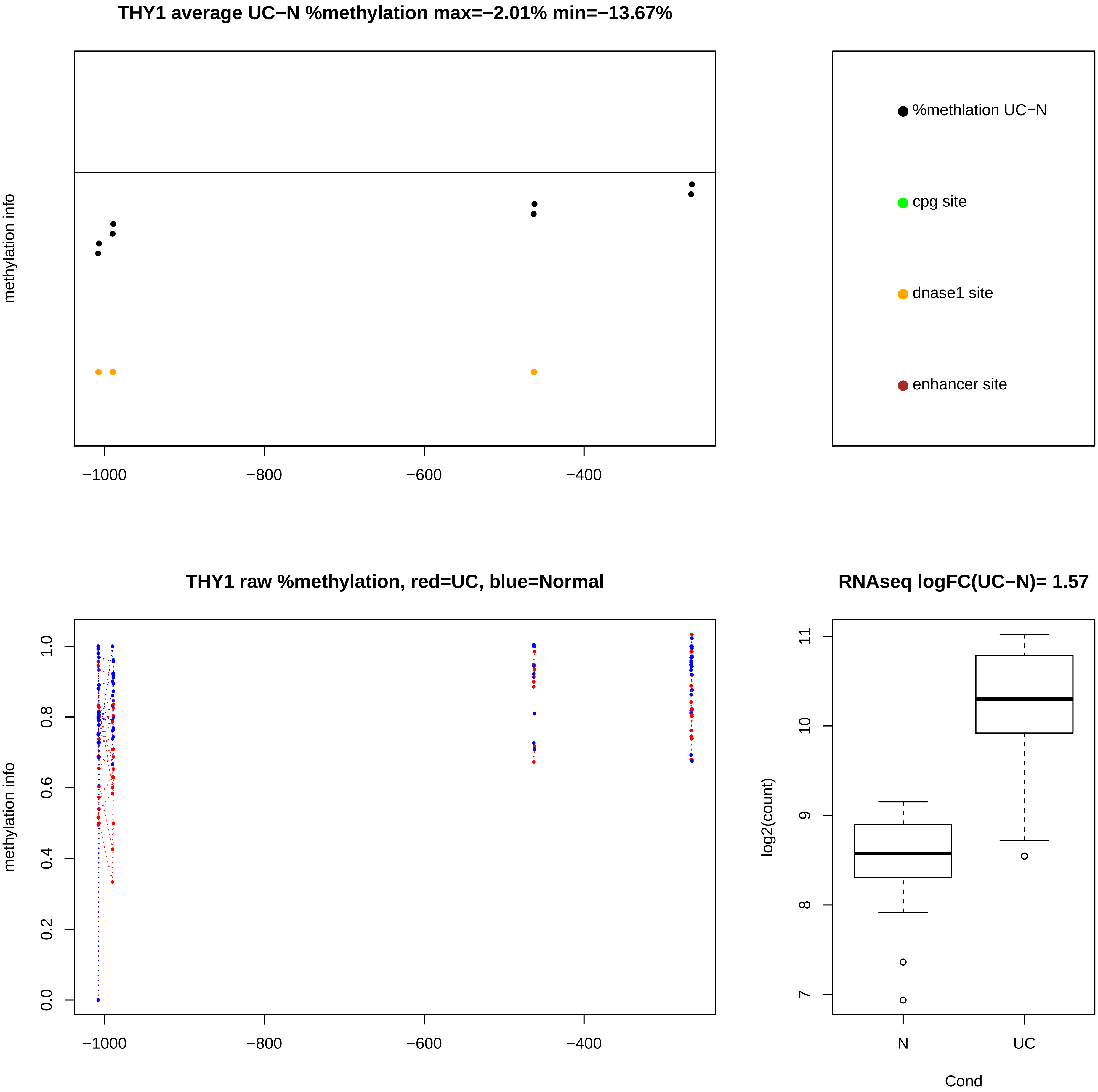
RNAseq logFC(UC−N)= 1.01



TG average UC−N %methylation max=−5.59% min=−6.74%

TG raw %methylation, red=UC, blue=Normal

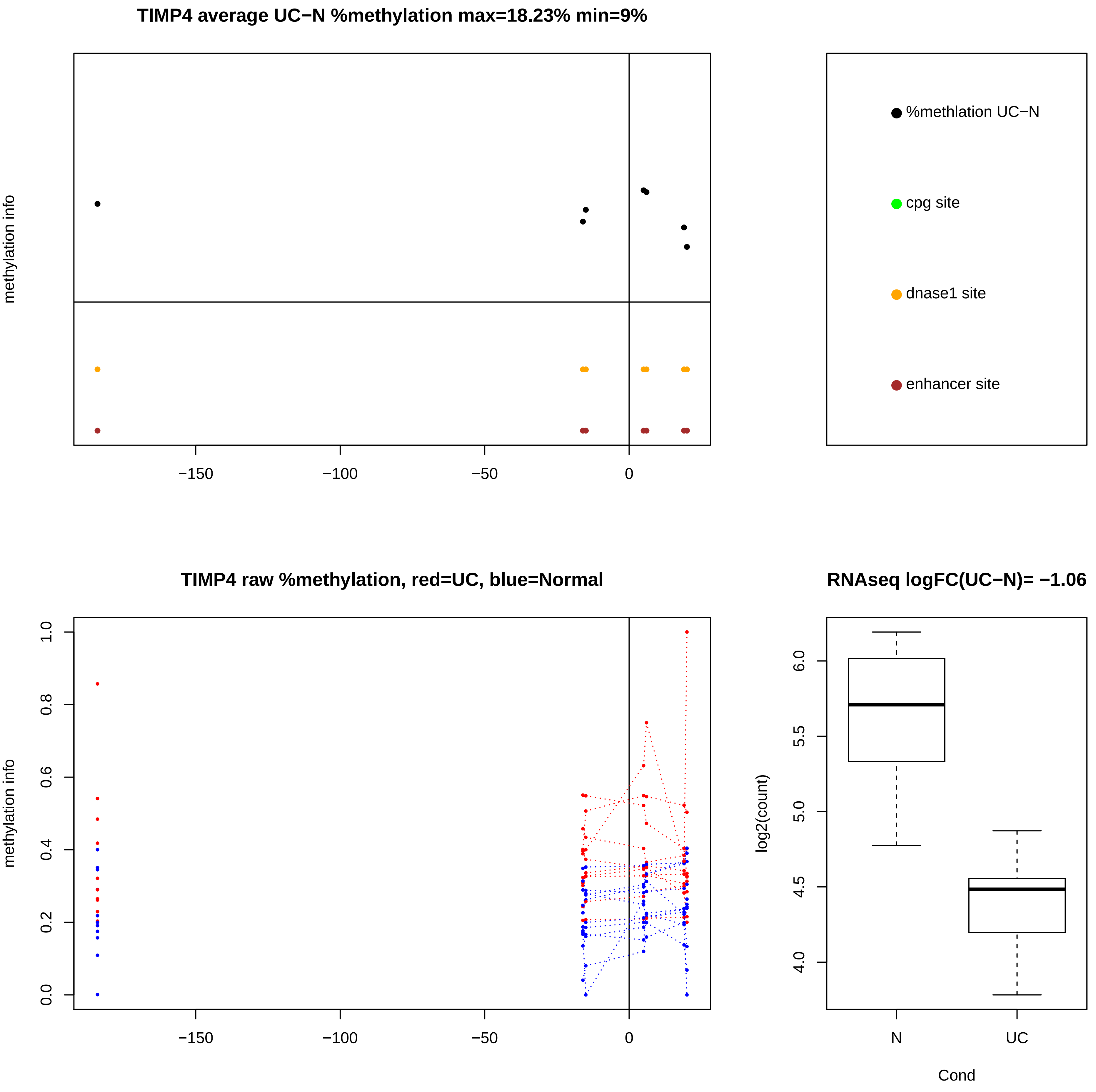
RNAseq logFC(UC−N)= 1.92



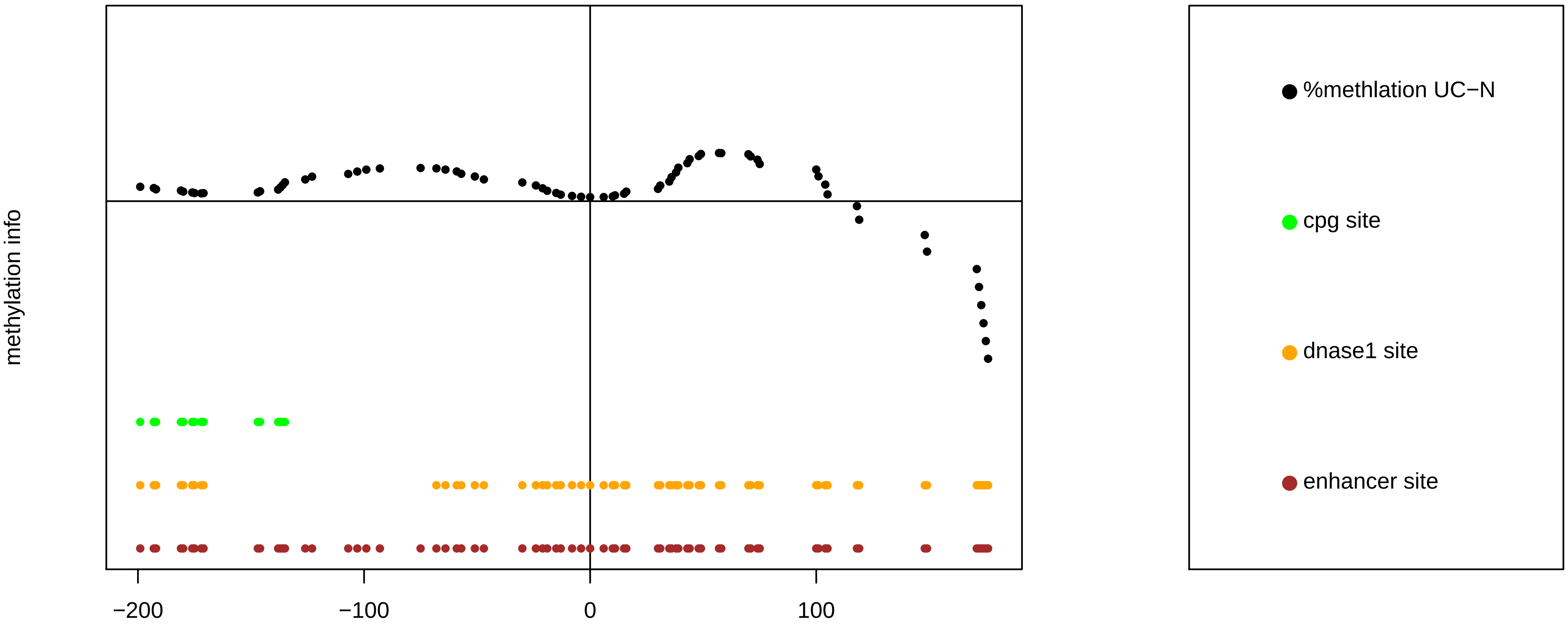
THY1 average UC−N %methylation max=−2.01% min=−13.67%

THY1 raw %methylation, red=UC, blue=Normal

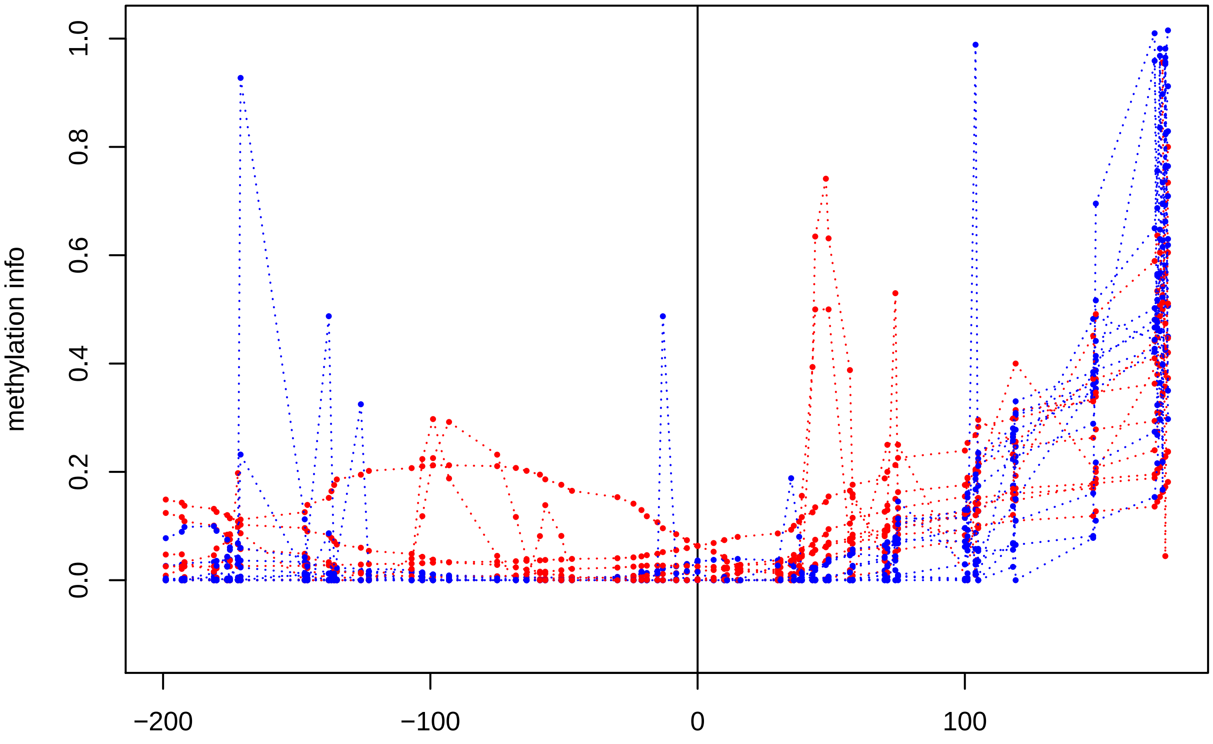
RNAseq logFC(UC−N)= 1.57


TIMP4 average UC−N %methylation max=18.23% min=9%
methylation info
−150
−100
−50
0
%methlation UC−N
cpg site
dnase1 site
enhancer site
TIMP4 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−150
−100
−50
0
RNAseq logFC(UC−N)= −1.06
log2(count)
4.0
4.5
5.0
5.5
6.0
N
UC
Cond

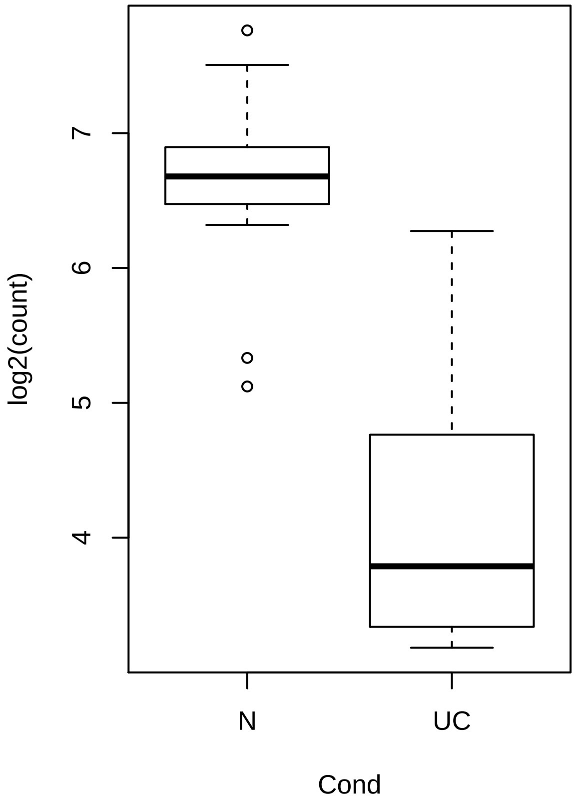
TINCR average UC−N %methylation max=7.62% min=−24.91%



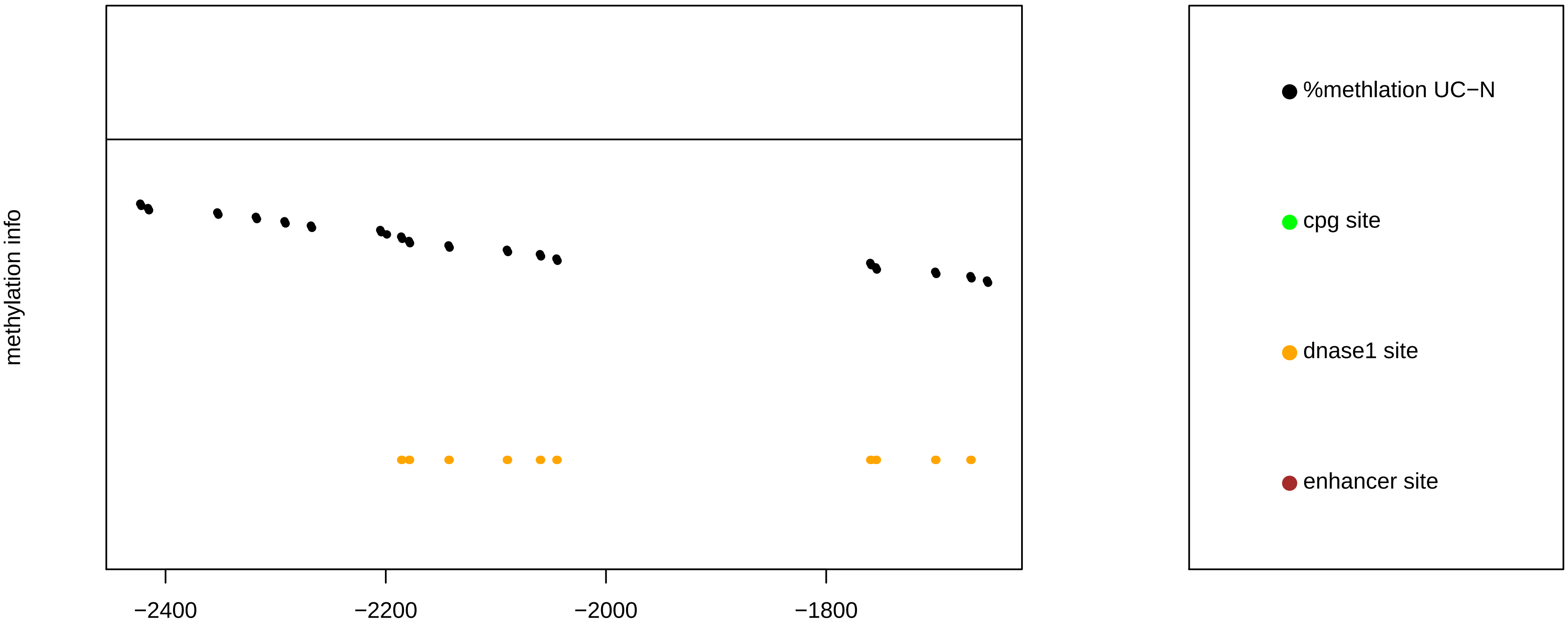
TINCR raw %methylation, red=UC, blue=Normal



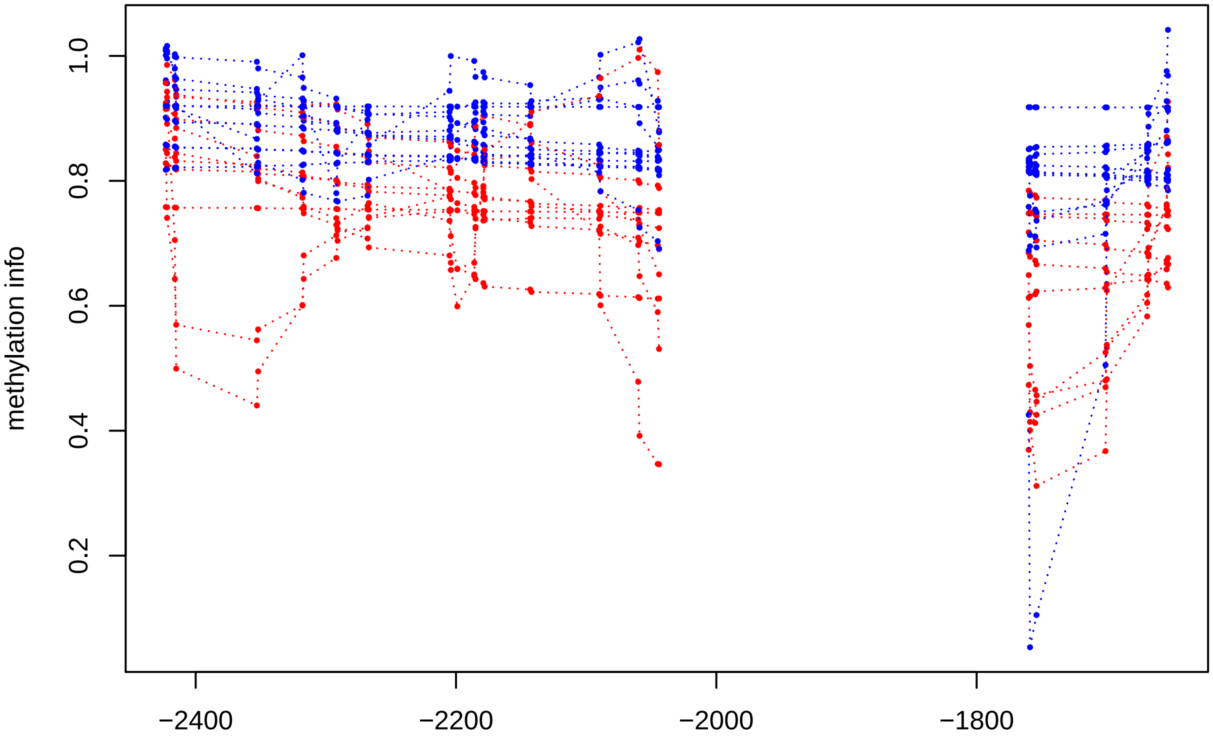
RNAseq logFC(UC−N)= −1.98



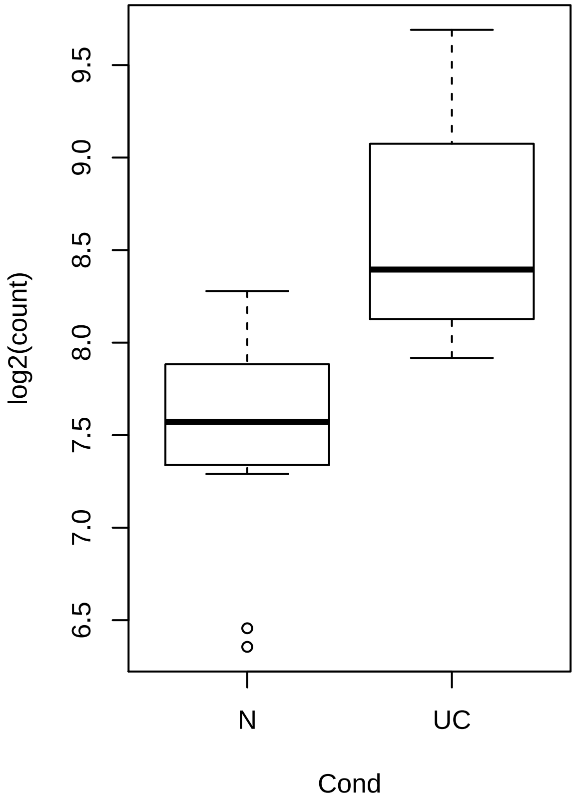
TLR8 average UC−N %methylation max=−7.25% min=−16.18%

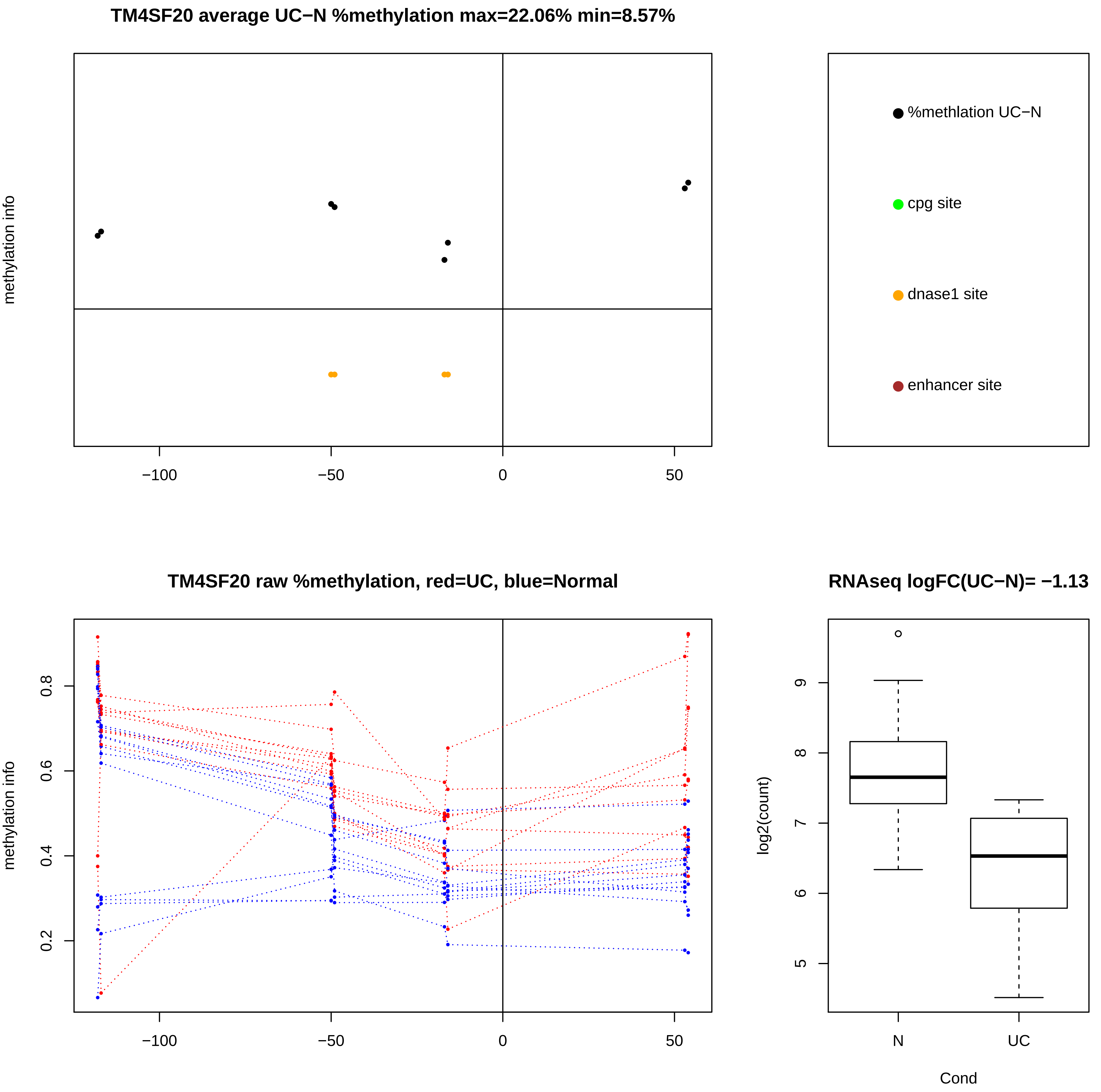


TLR8 raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 1.04

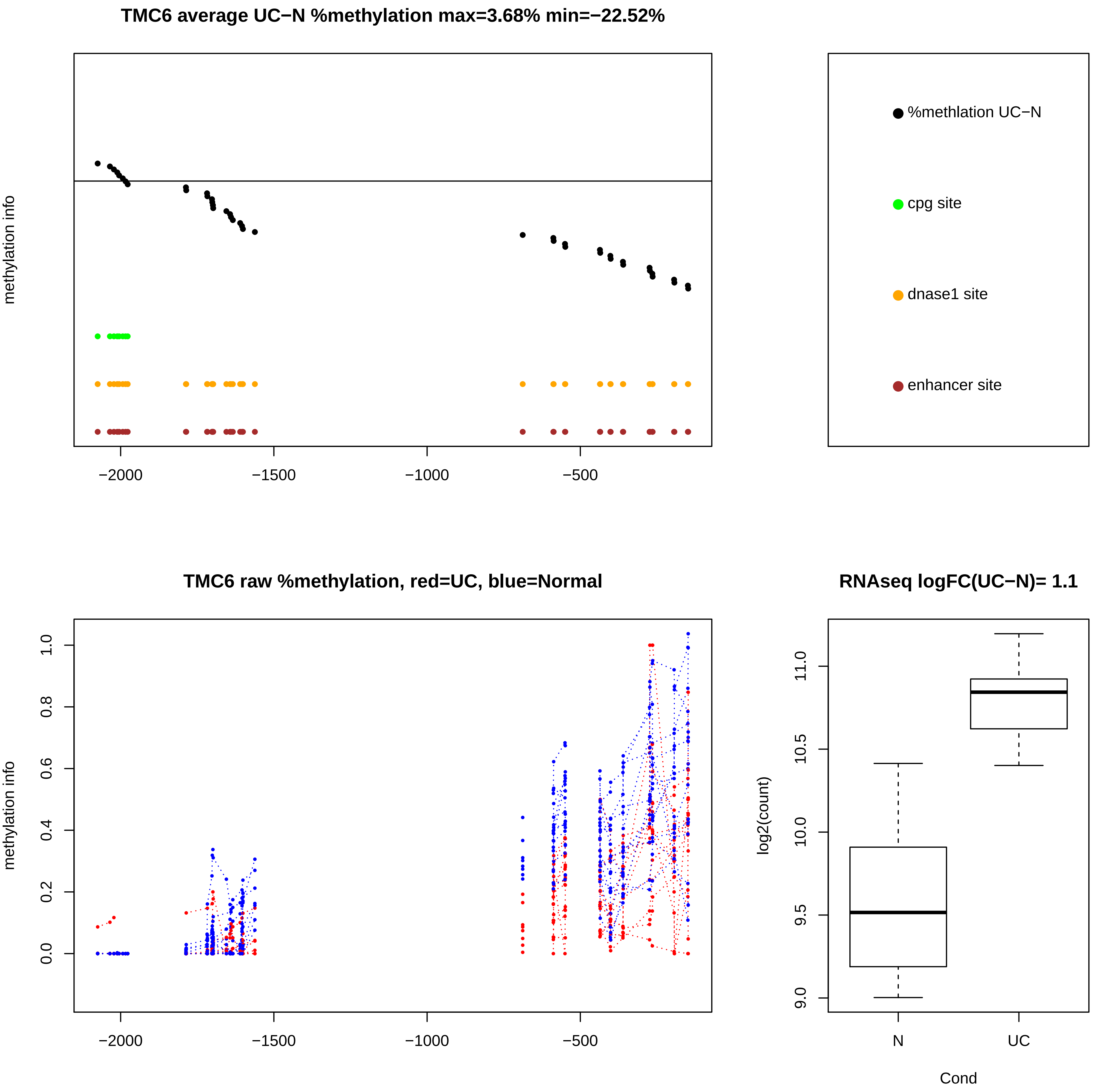




TM4SF20 average UC−N %methylation max=22.06% min=8.57%

TM4SF20 raw %methylation, red=UC, blue=Normal

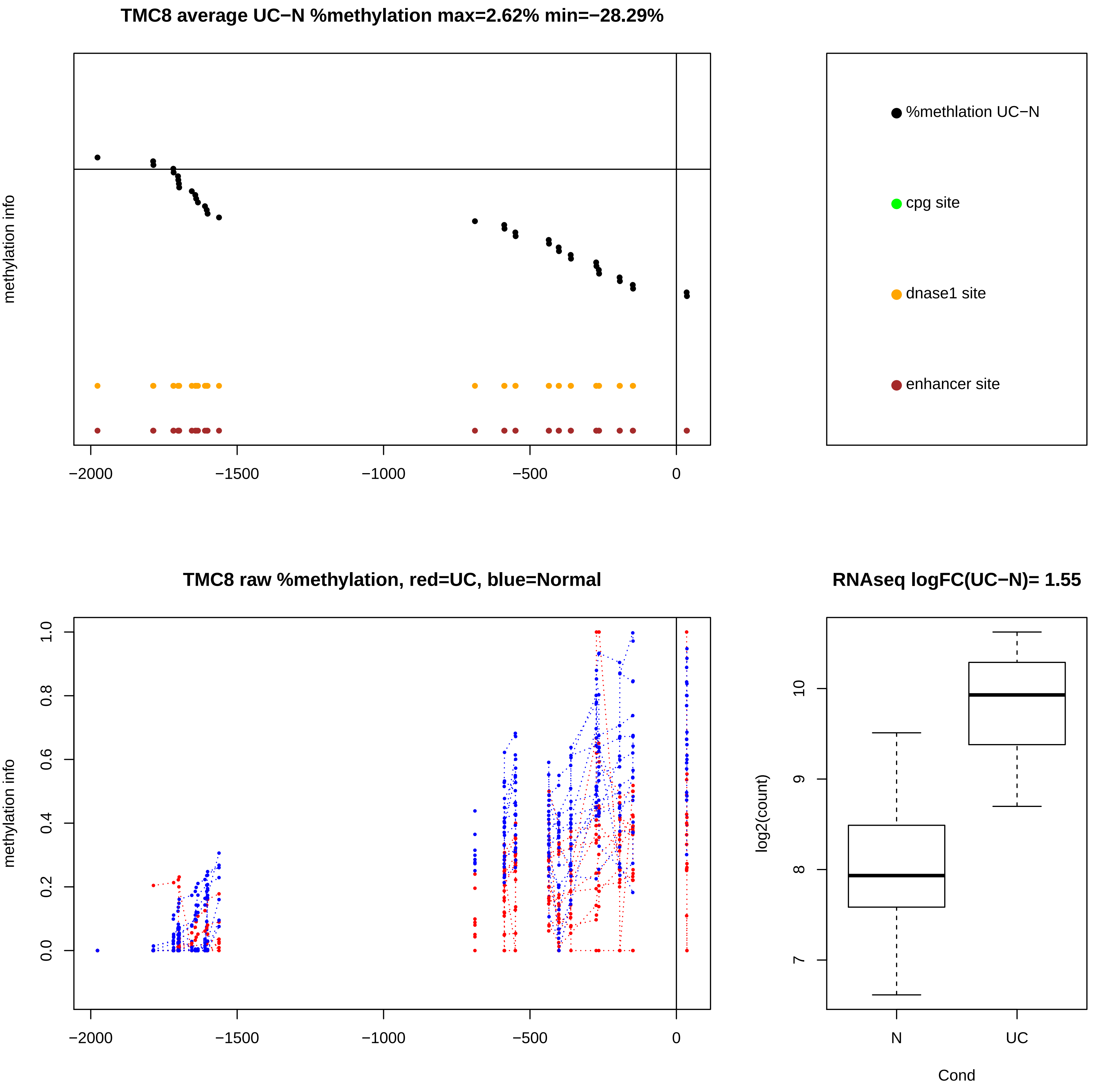
RNAseq logFC(UC−N)= −1.13



TMC6 average UC−N %methylation max=3.68% min=−22.52%

TMC6 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.1

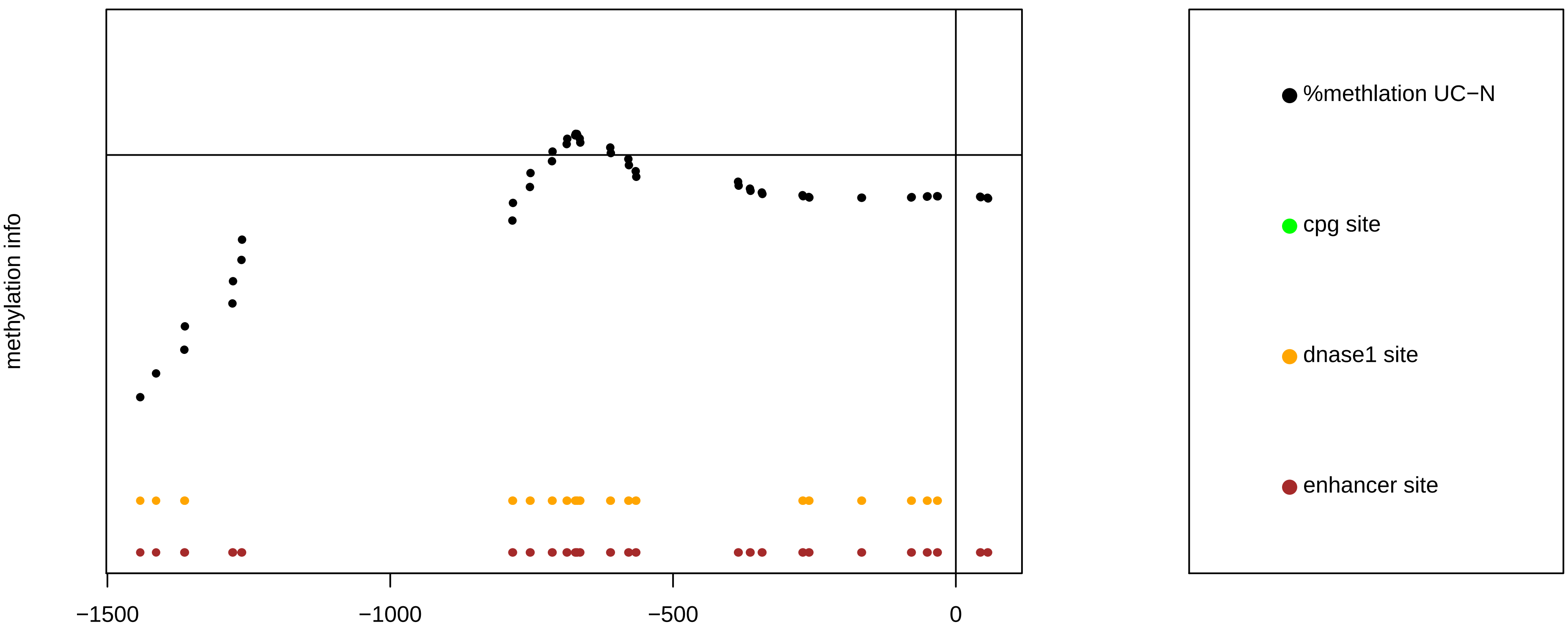


TMC8 average UC−N %methylation max=2.62% min=−28.29%

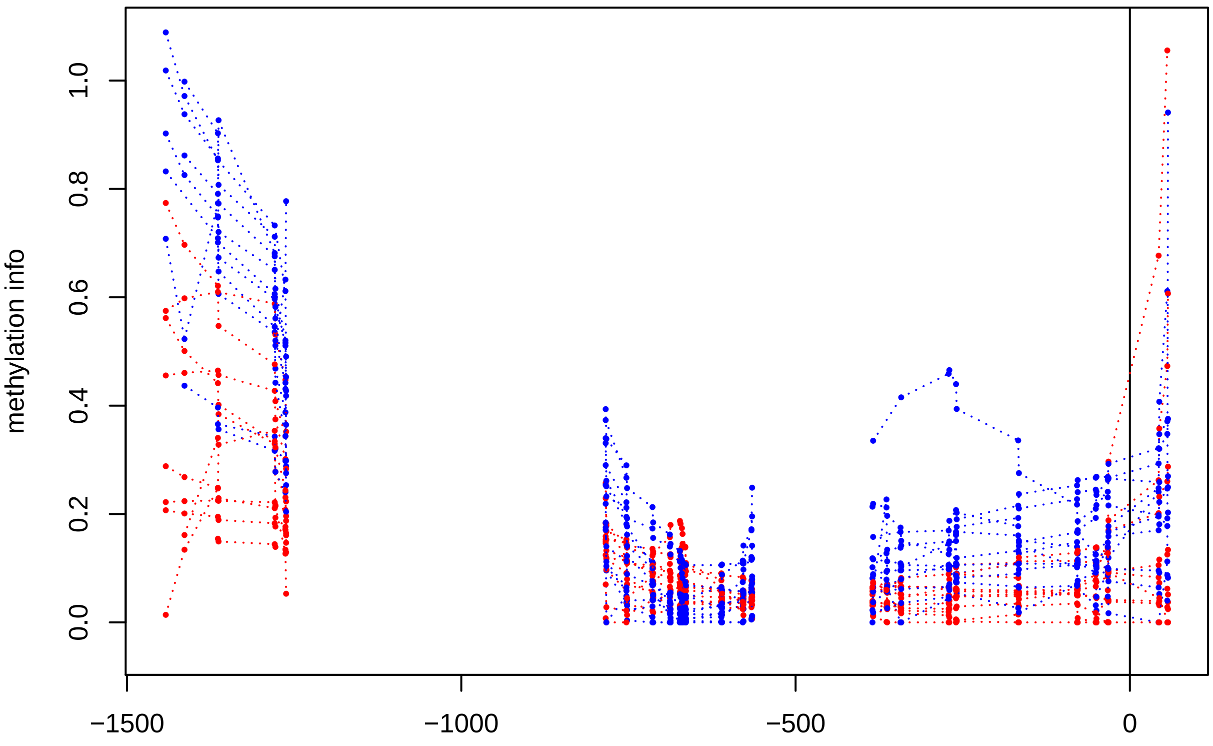
TMC8 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= 1.55

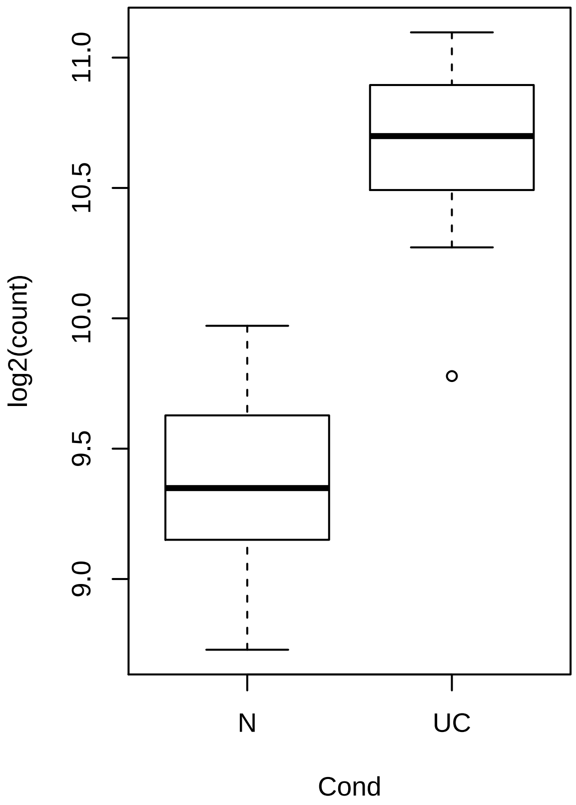
TMEM173 average UC−N %methylation max=4.09% min=−46.79%

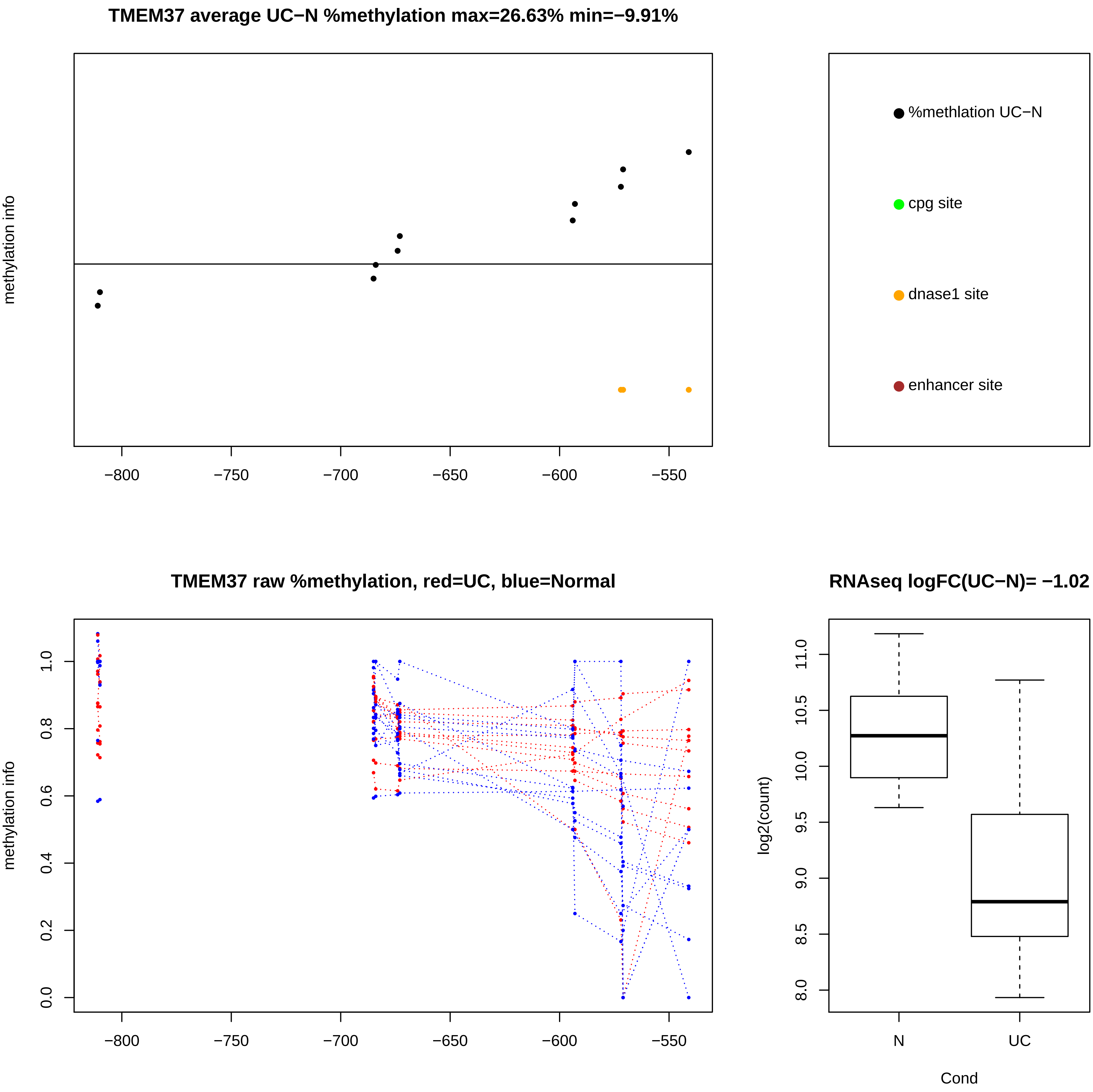


TMEM173 raw %methylation, red=UC, blue=Normal



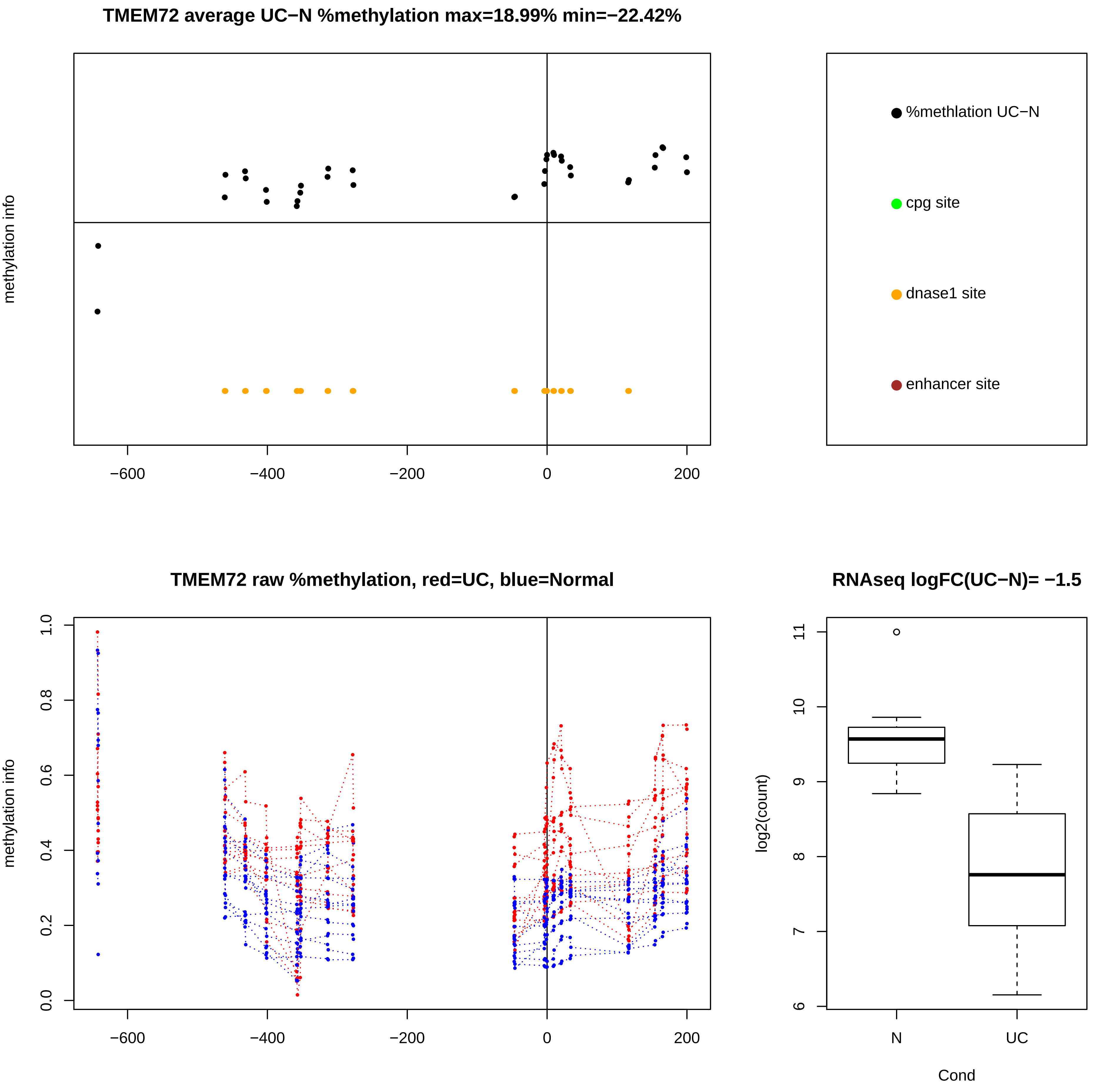
RNAseq logFC(UC−N)= 1.21




TMEM37 average UC−N %methylation max=26.63% min=−9.91%

TMEM37 raw %methylation, red=UC, blue=Normal

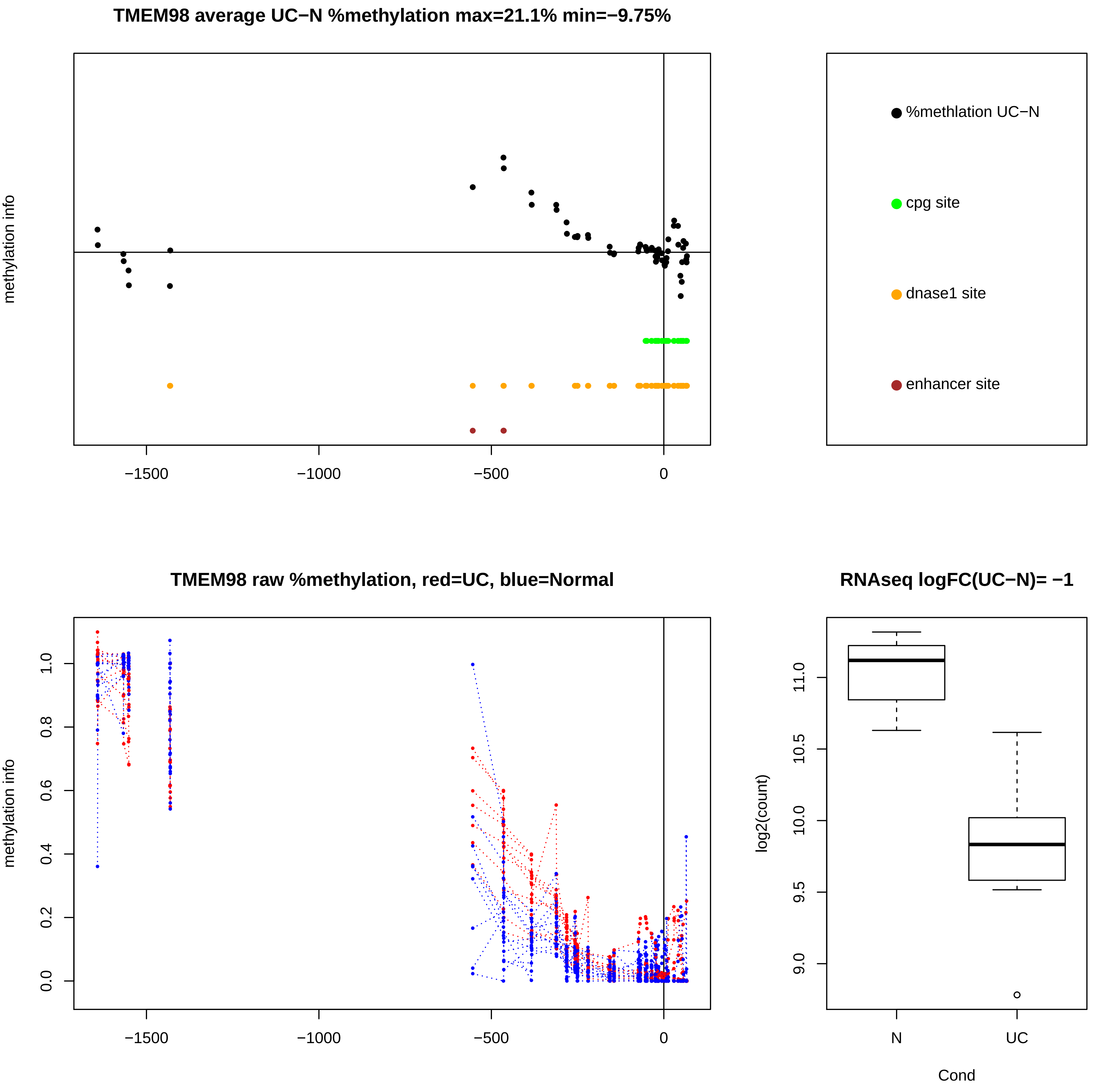
RNAseq logFC(UC−N)= −1.02



TMEM72 average UC−N %methylation max=18.99% min=−22.42%

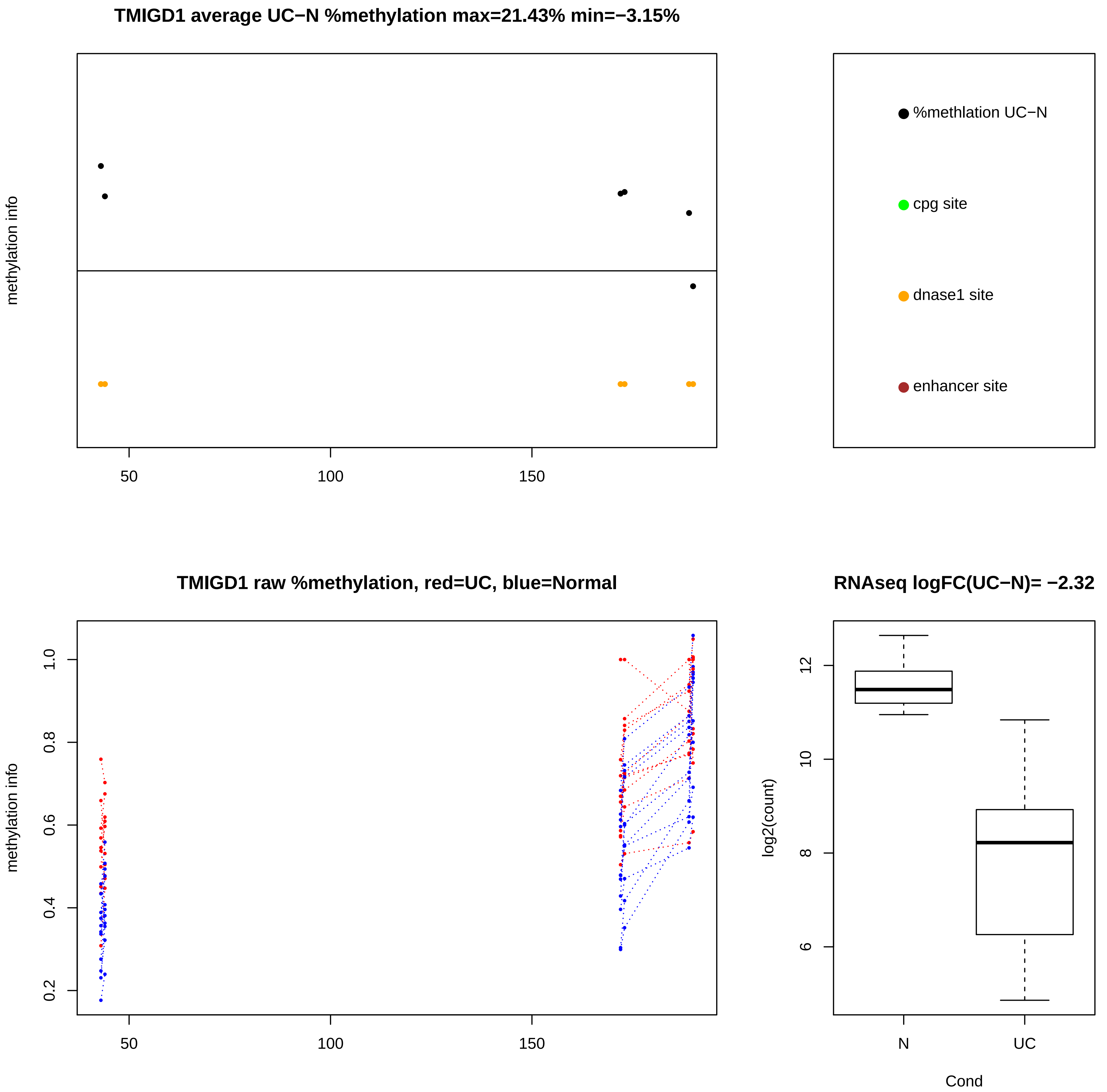
TMEM72 raw %methylation, red=UC, blue=Normal

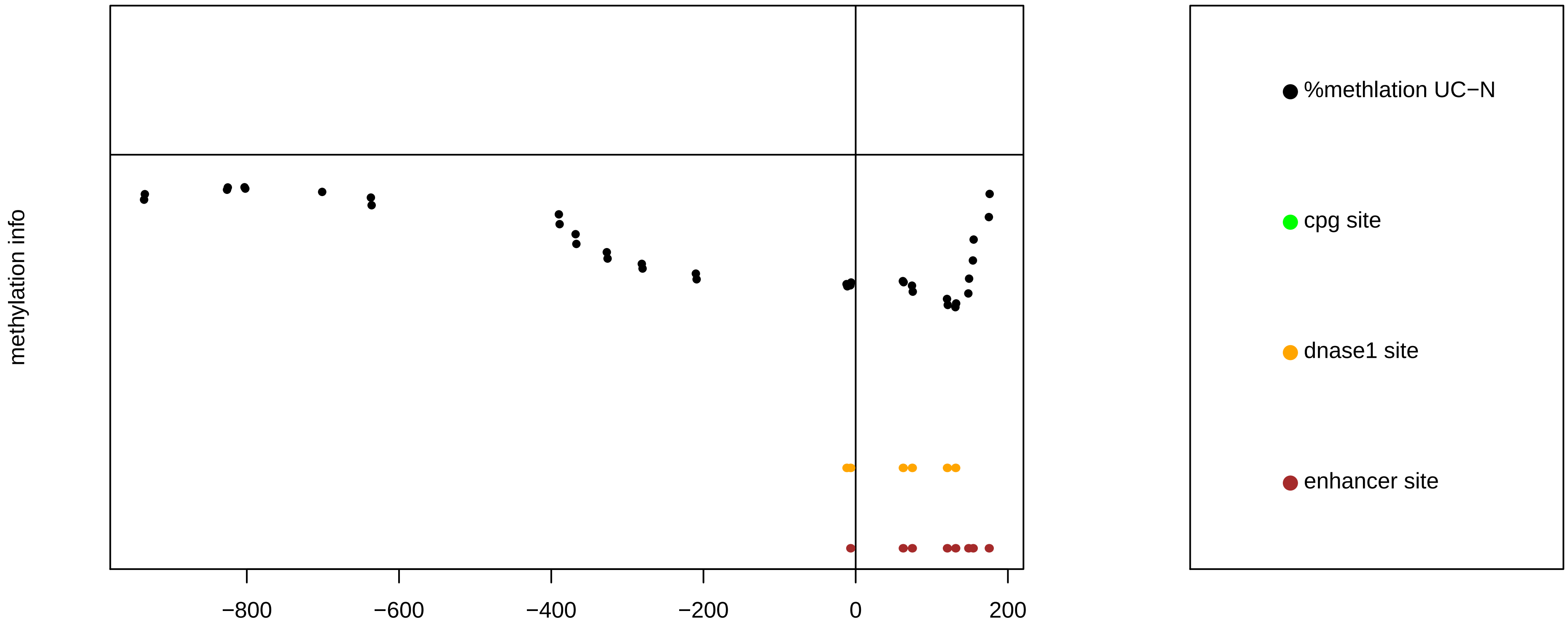
RNAseq logFC(UC−N)= −1.5

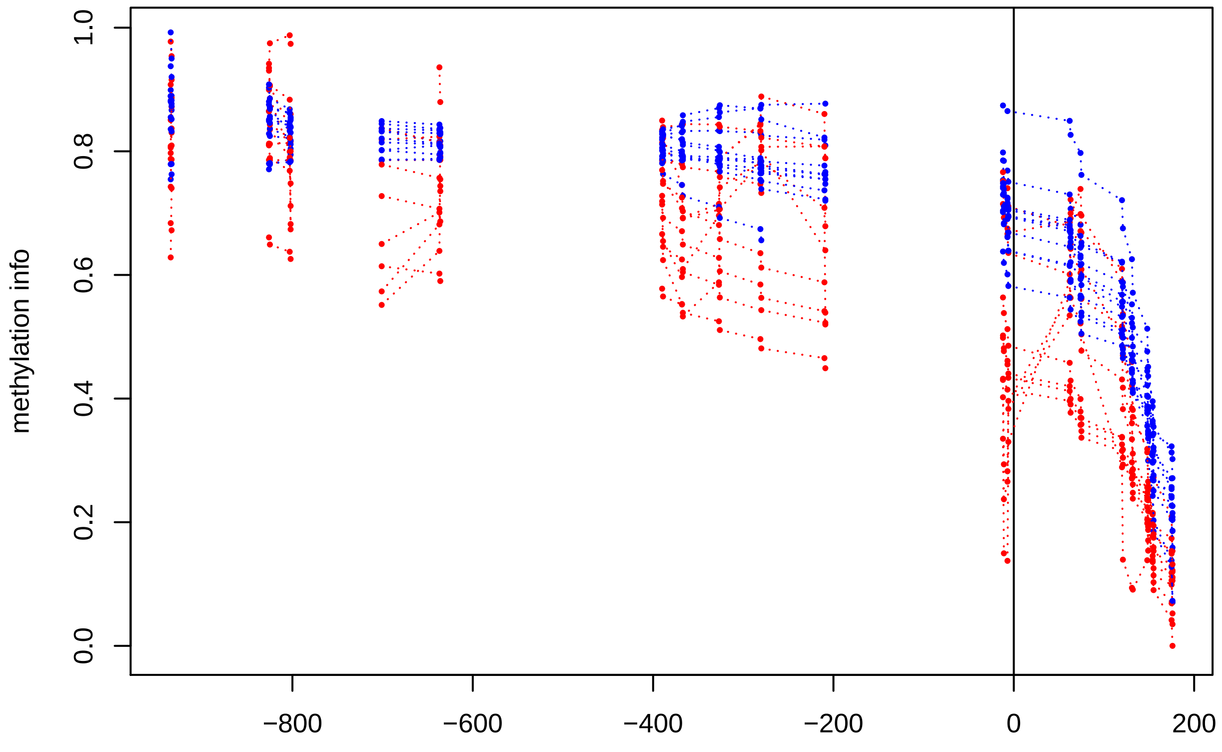

TMEM98 average UC−N %methylation max=21.1% min=−9.75%

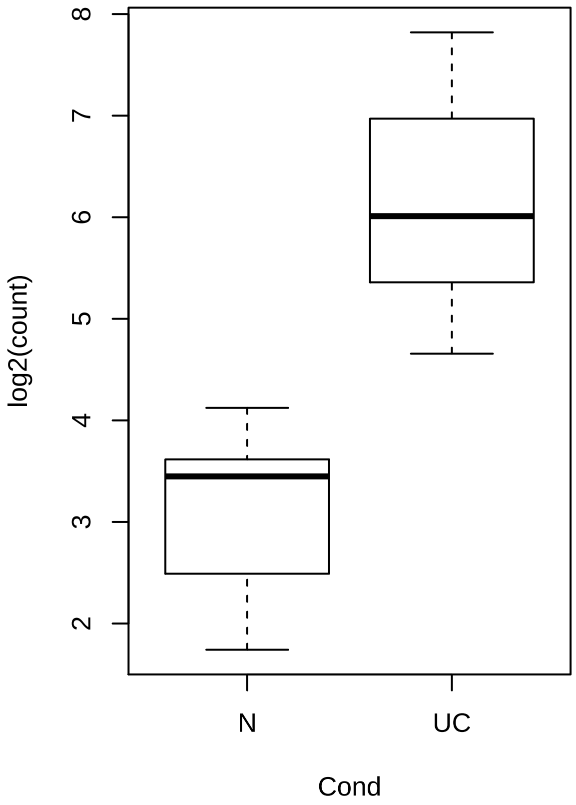
TMEM98 raw %methylation, red=UC, blue=Normal

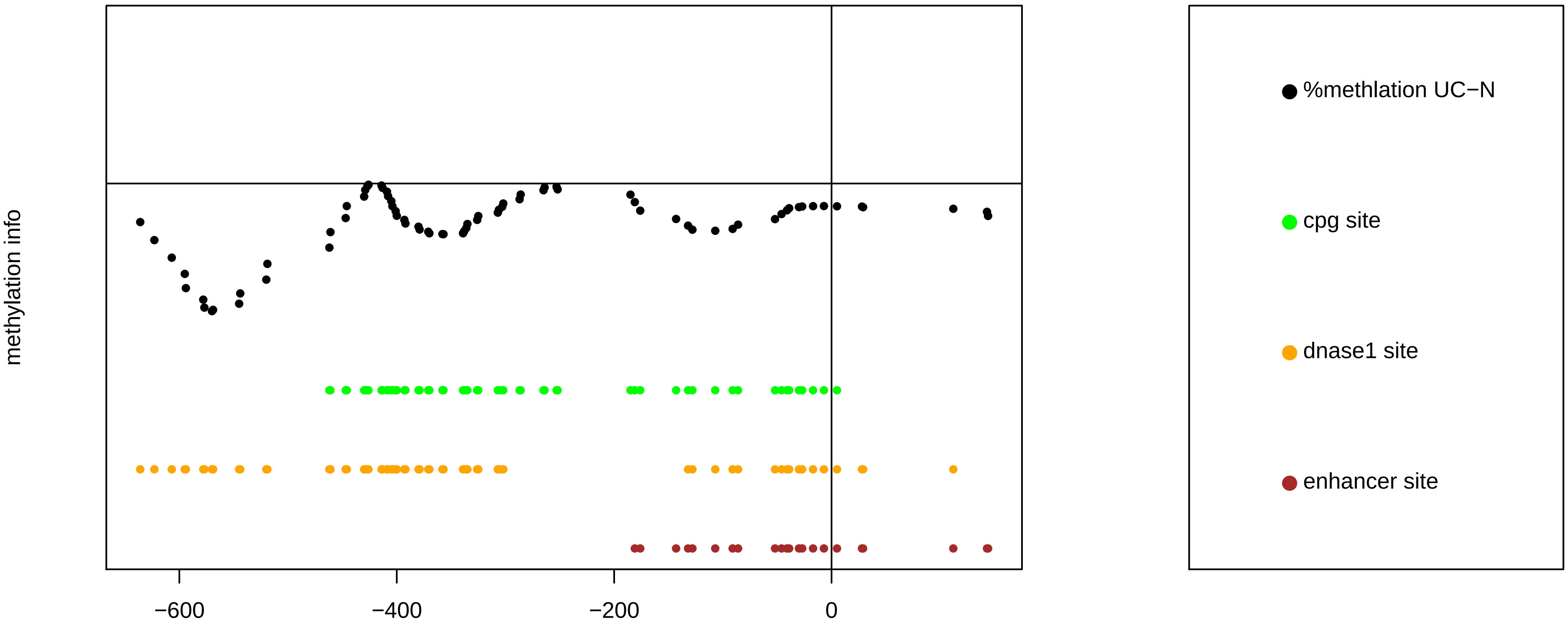
RNAseq logFC(UC−N)= −1

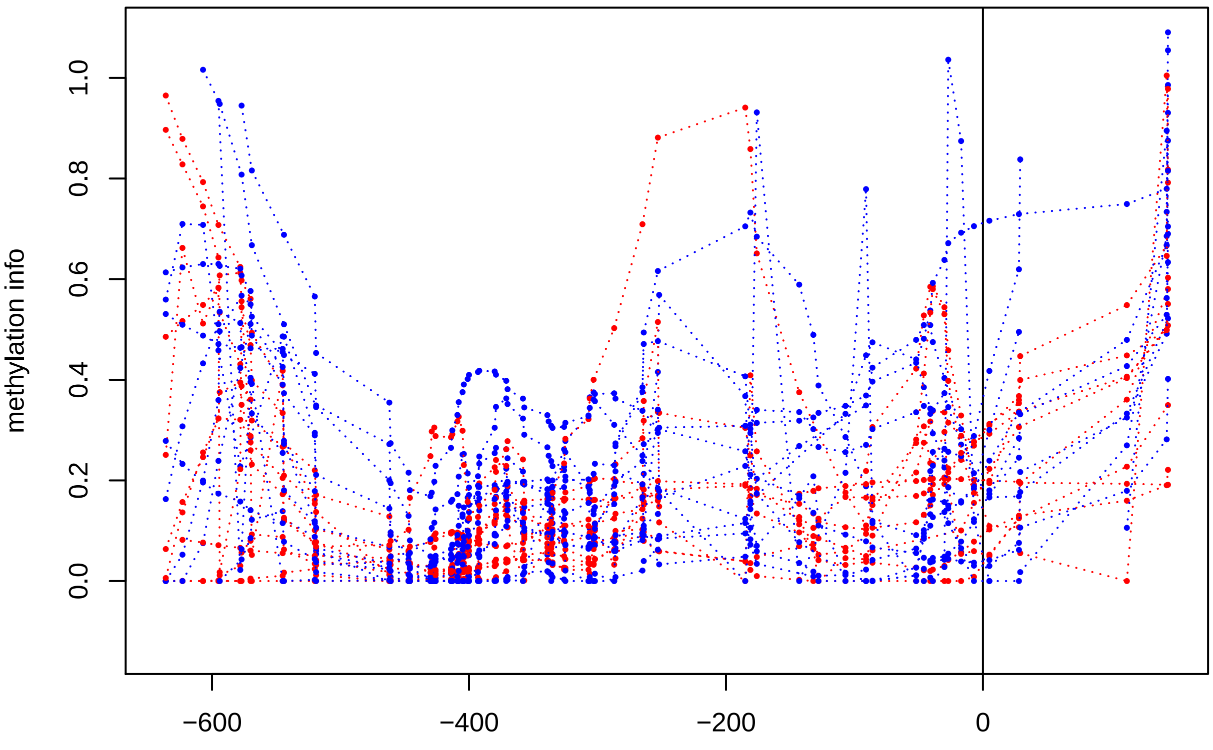

TMIGD1 average UC−N %methylation max=21.43% min=−3.15%
methylation info
50
100
150
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
TMIGD1 raw %methylation, red=UC, blue=Normal
methylation info
0.2
0.4
0.6
0.8
1.0
50
100
150
RNAseq logFC(UC−N)= −2.32
log2(count)
6
8
10
12
N
UC
Cond

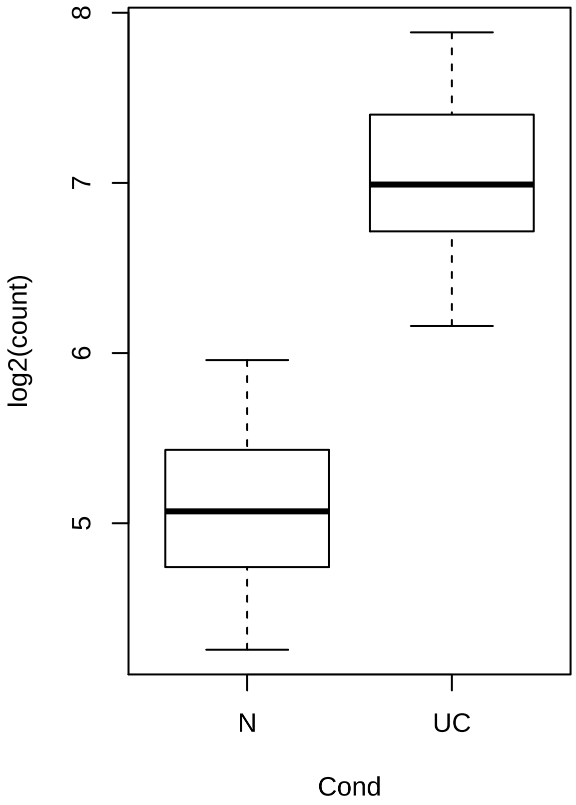

TNFRSF10C average UC−N %methylation max=−4.05% min=−18.97%

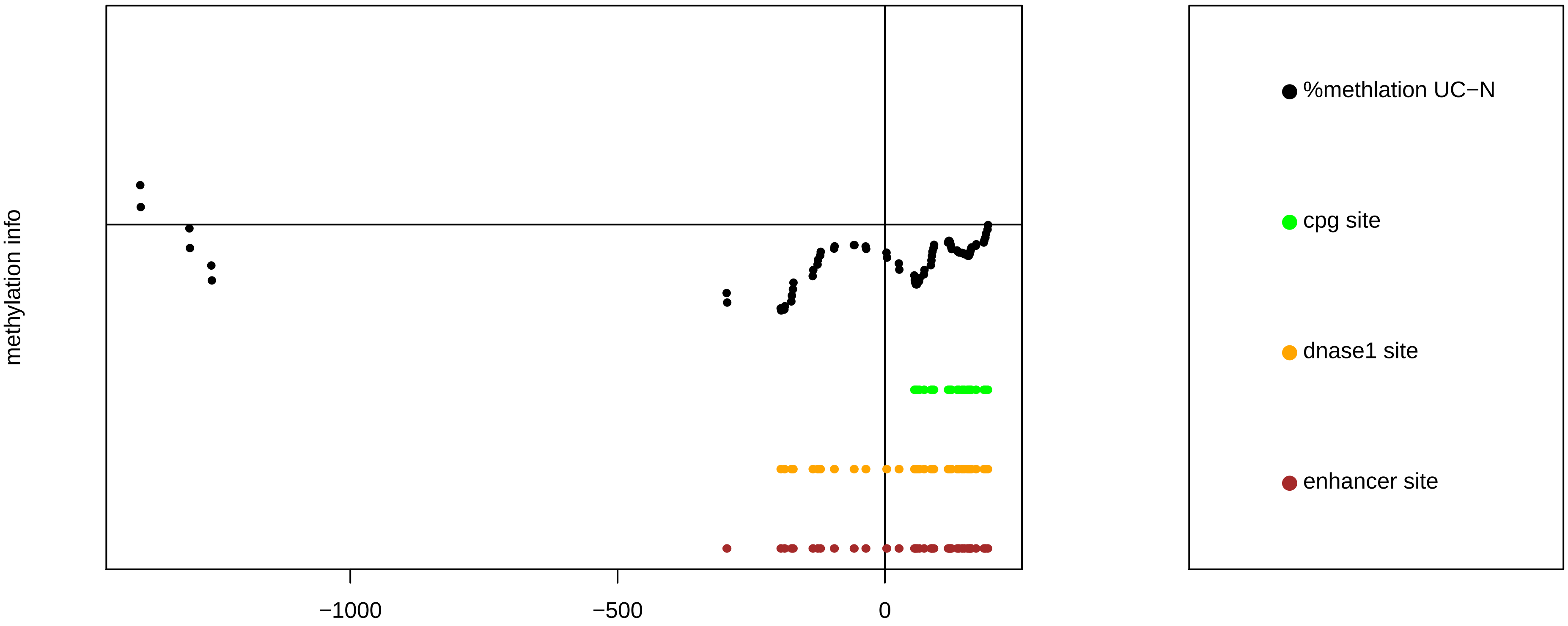

TNFRSF10C raw %methylation, red=UC, blue=Normal


RNAseq logFC(UC−N)= 2.71

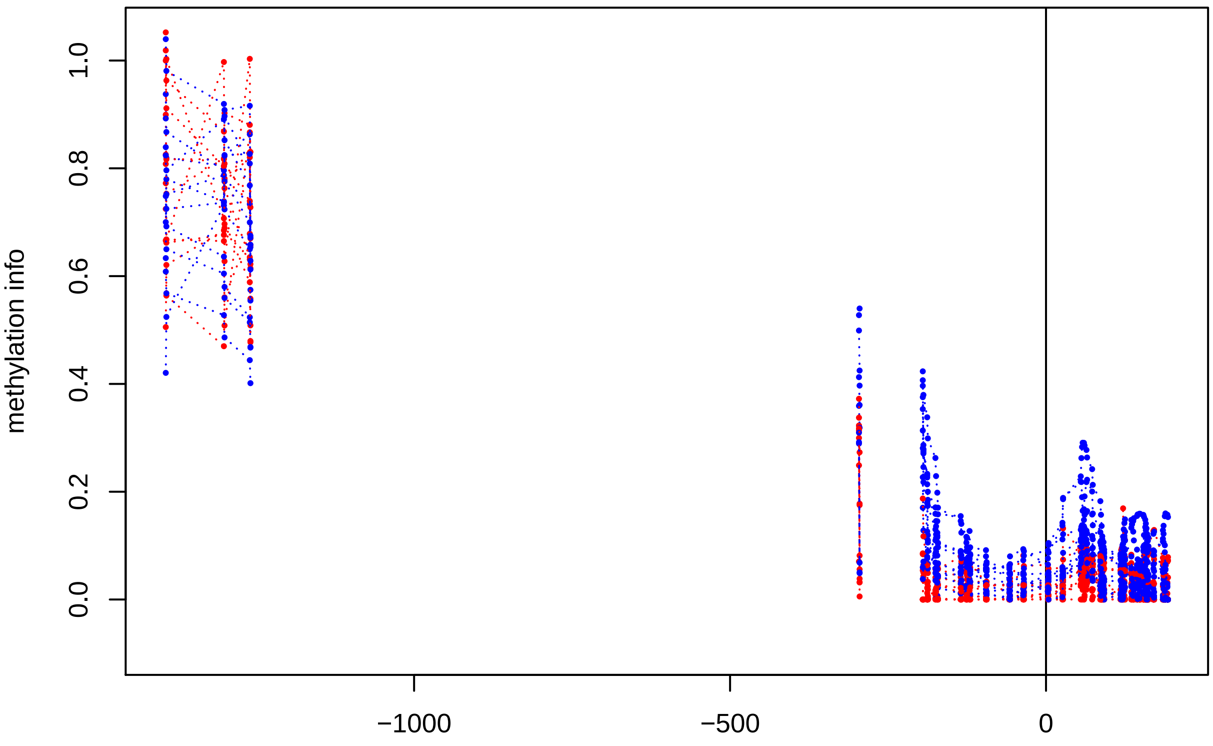

TNFRSF4 average UC−N %methylation max=−0.15% min=−16.13%


TNFRSF4 raw %methylation, red=UC, blue=Normal

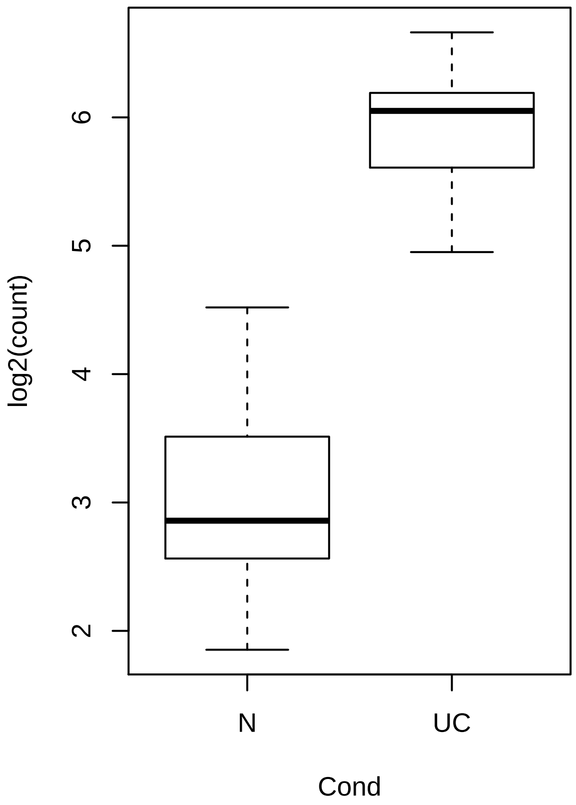

RNAseq logFC(UC−N)= 1.74



TNFRSF8 average UC−N %methylation max=4.97% min=−10.83%

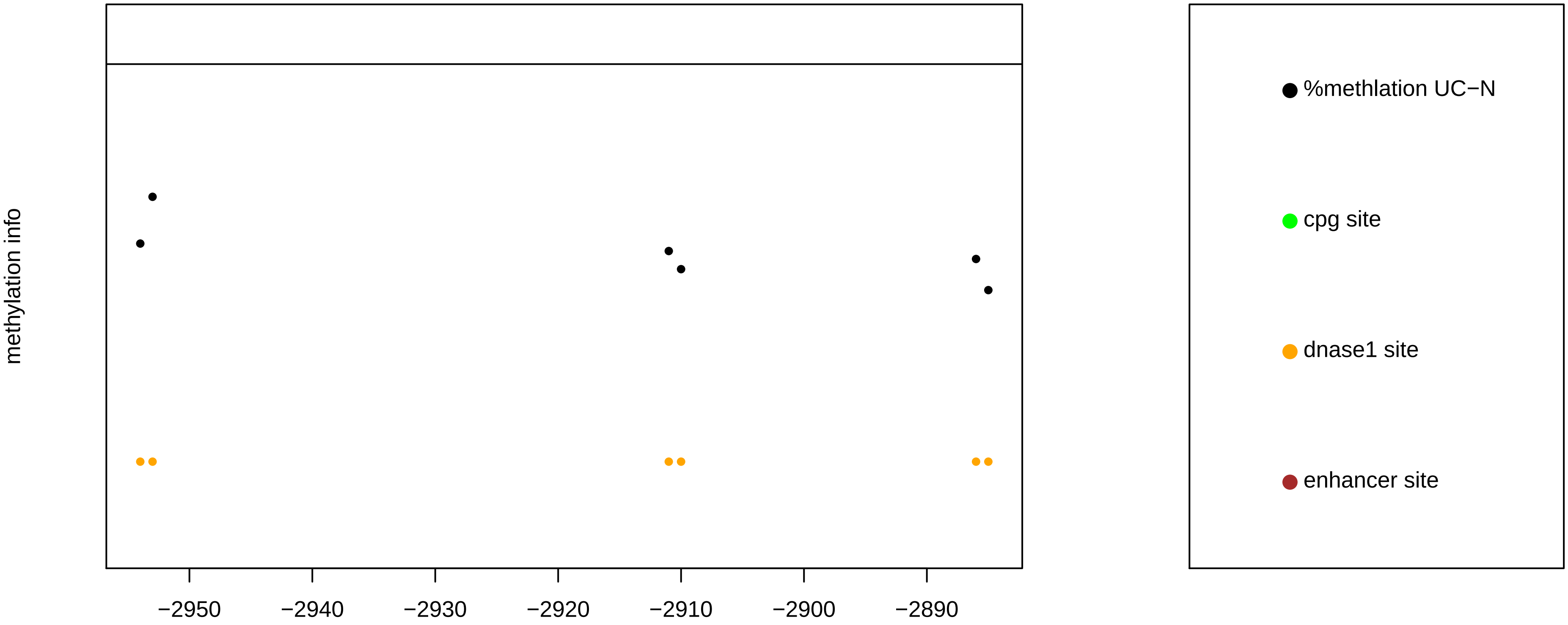


TNFRSF8 raw %methylation, red=UC, blue=Normal

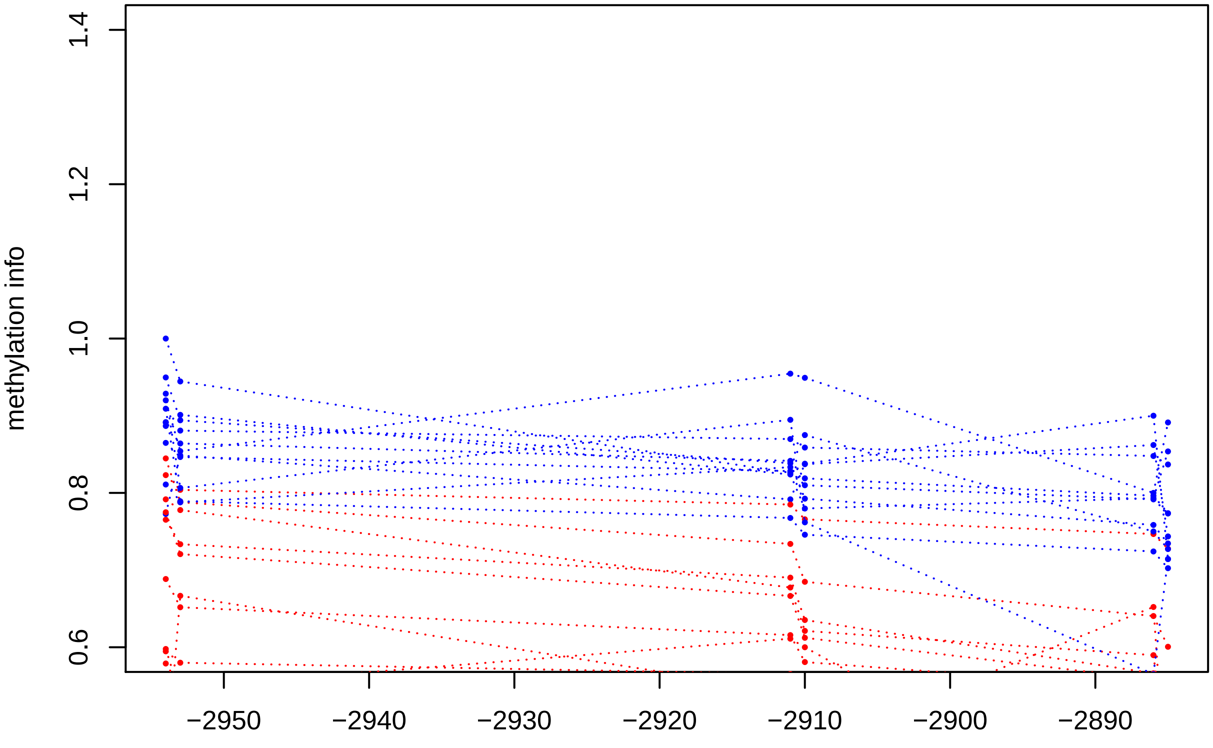


RNAseq logFC(UC−N)= 2.57

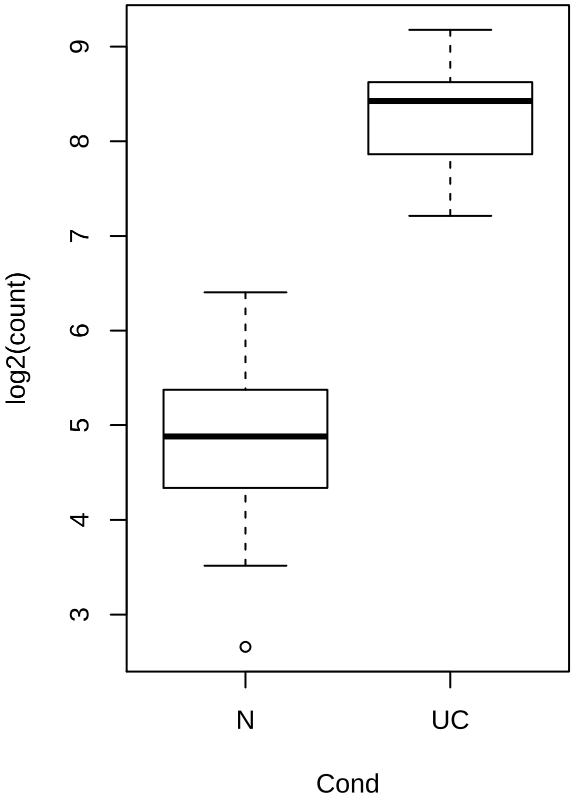
TNFRSF9 average UC−N %methylation max=−15.47% min=−26.35%



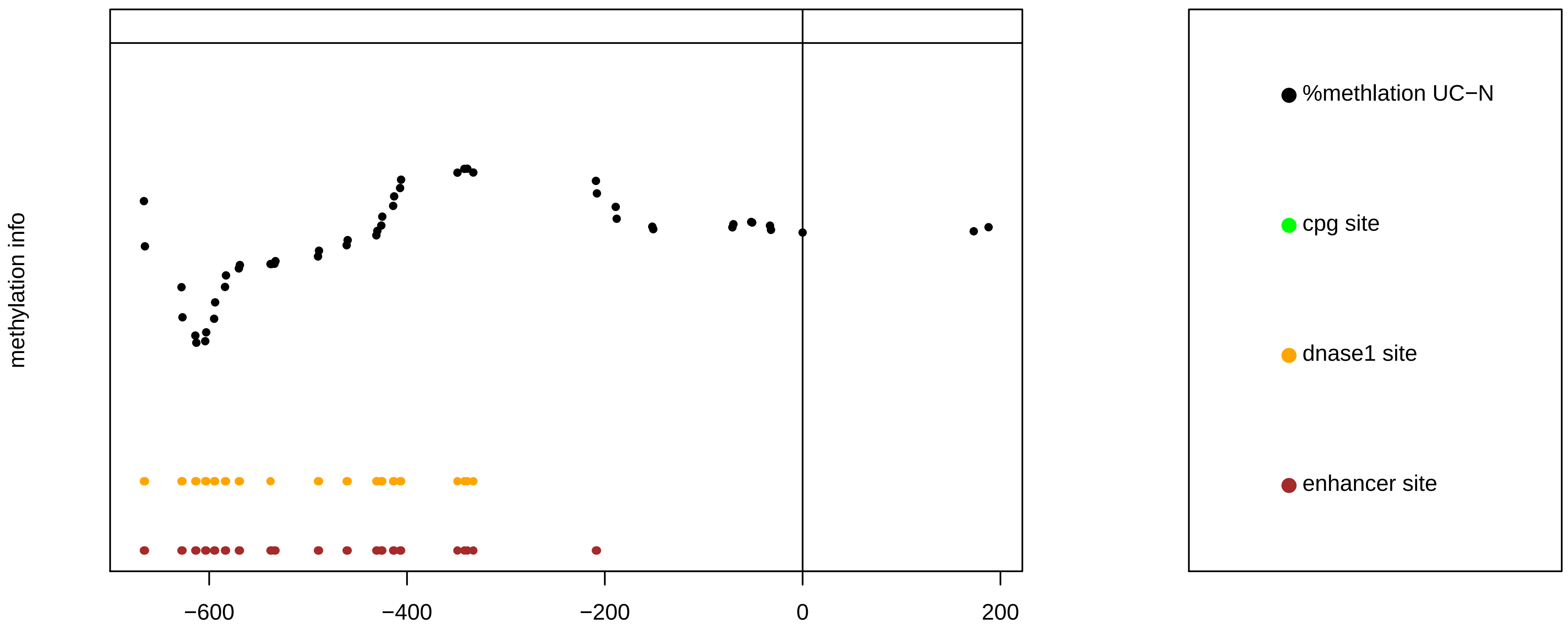
TNFRSF9 raw %methylation, red=UC, blue=Normal



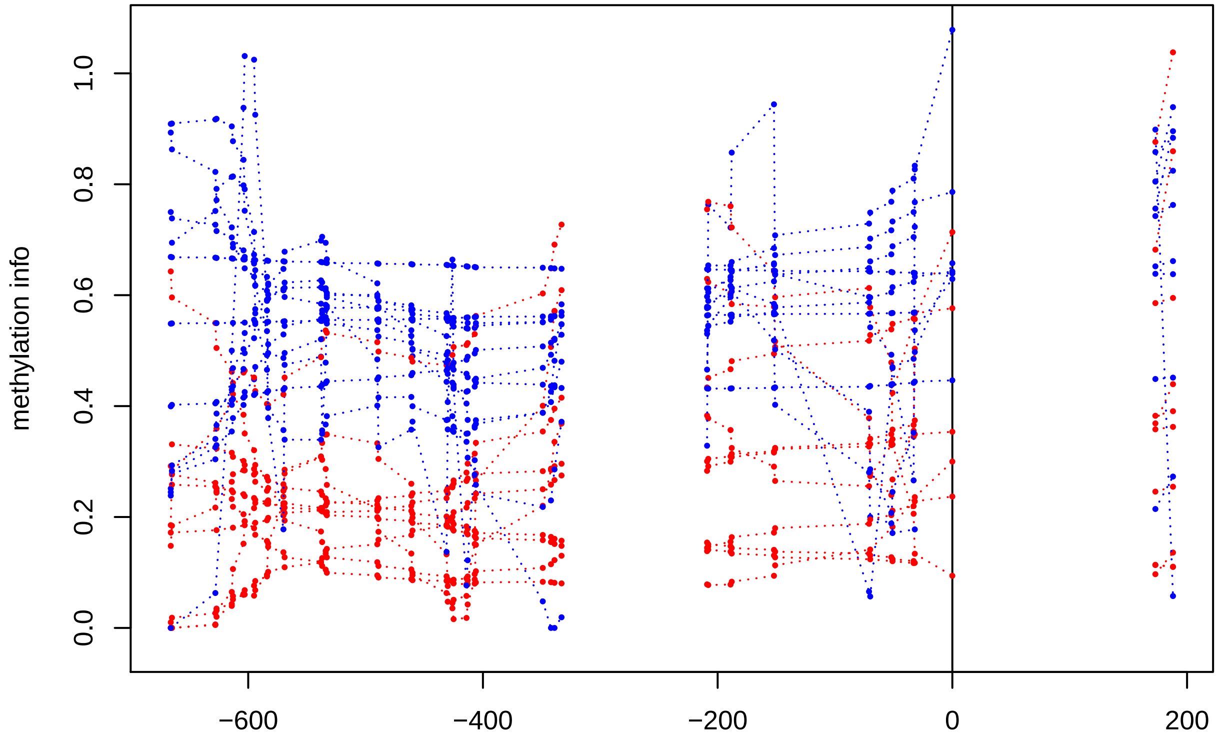
RNAseq logFC(UC−N)= 2.92



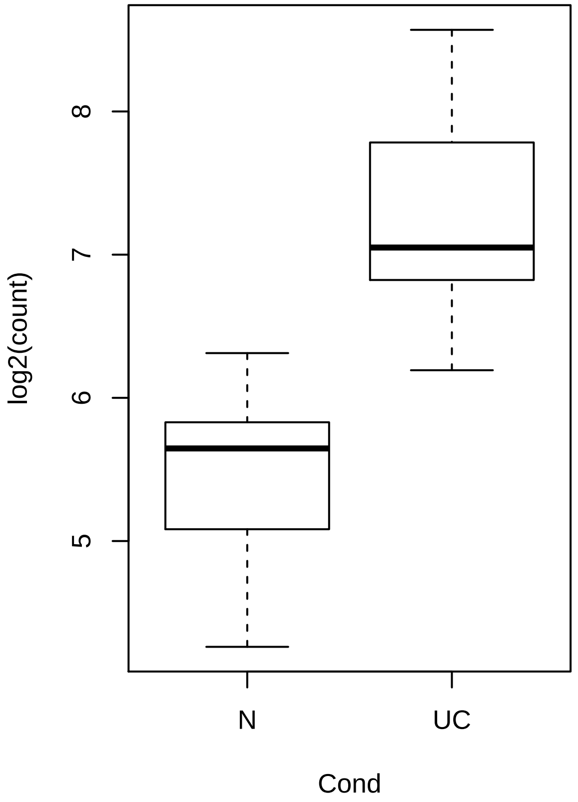
TNFSF14 average UC−N %methylation max=−18.15% min=−43.28%



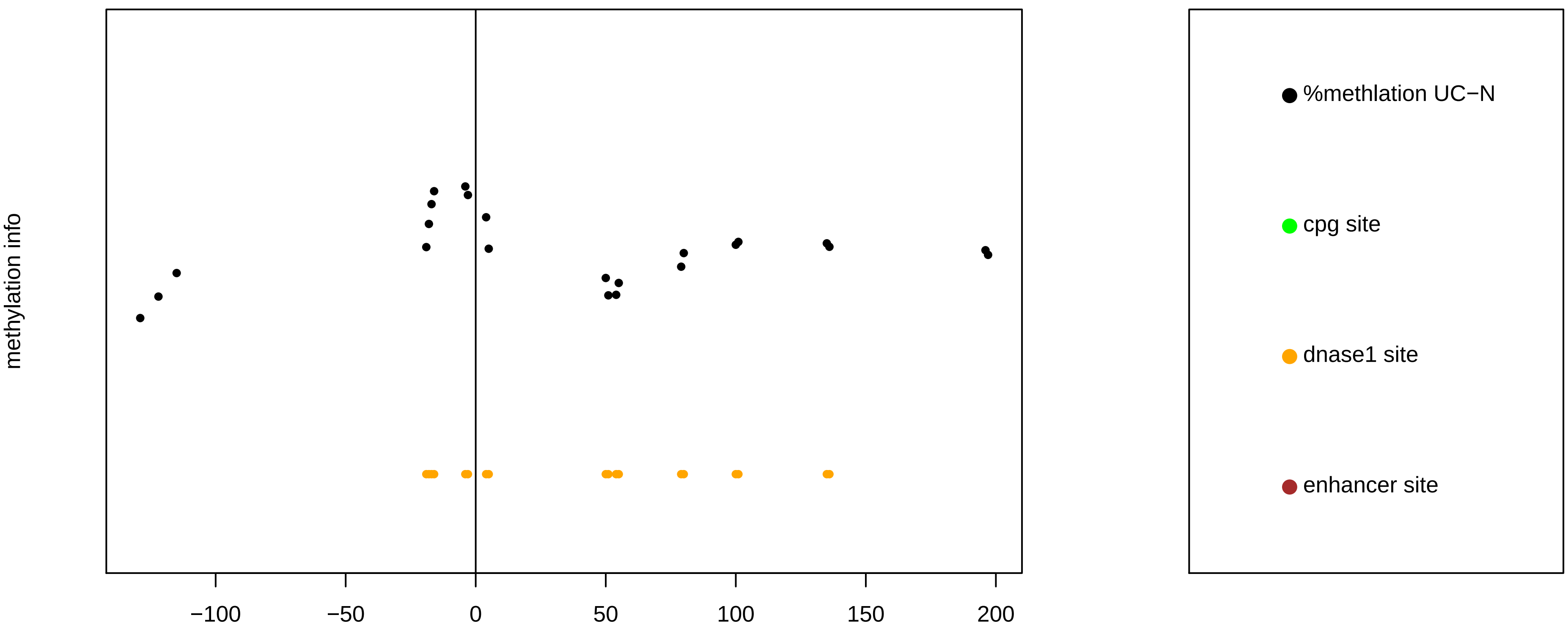
TNFSF14 raw %methylation, red=UC, blue=Normal



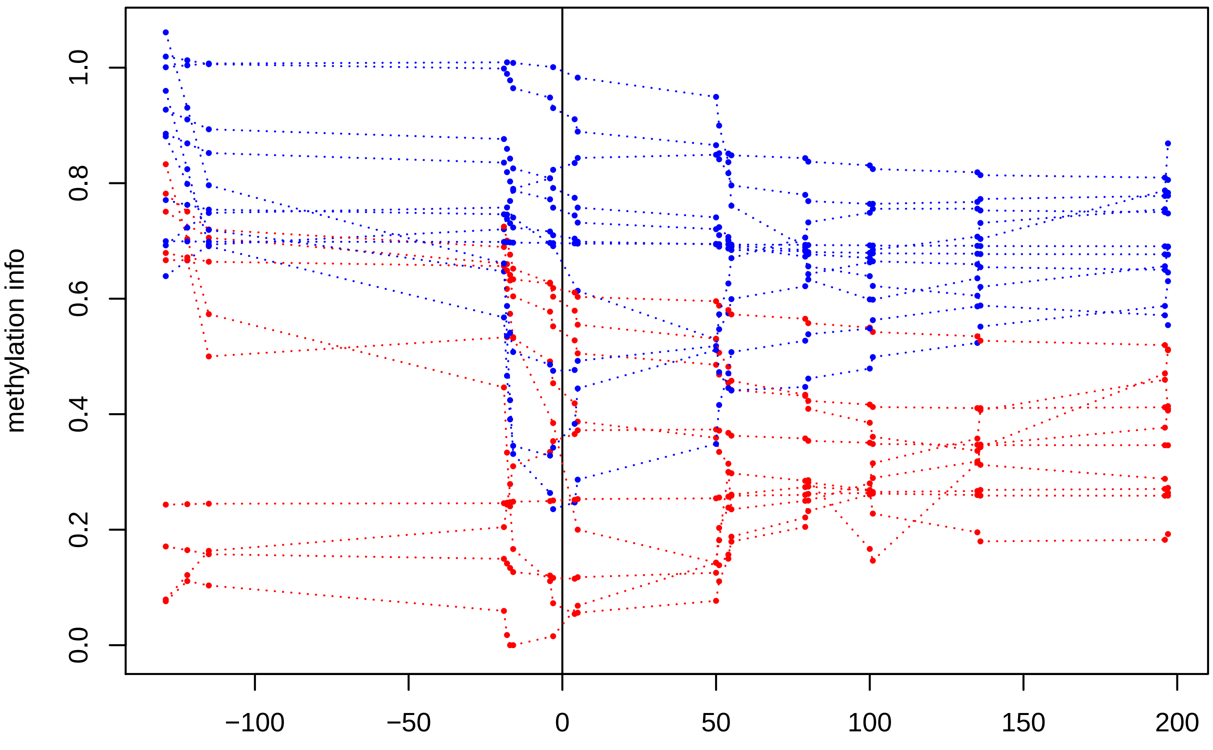
RNAseq logFC(UC−N)= 1.69



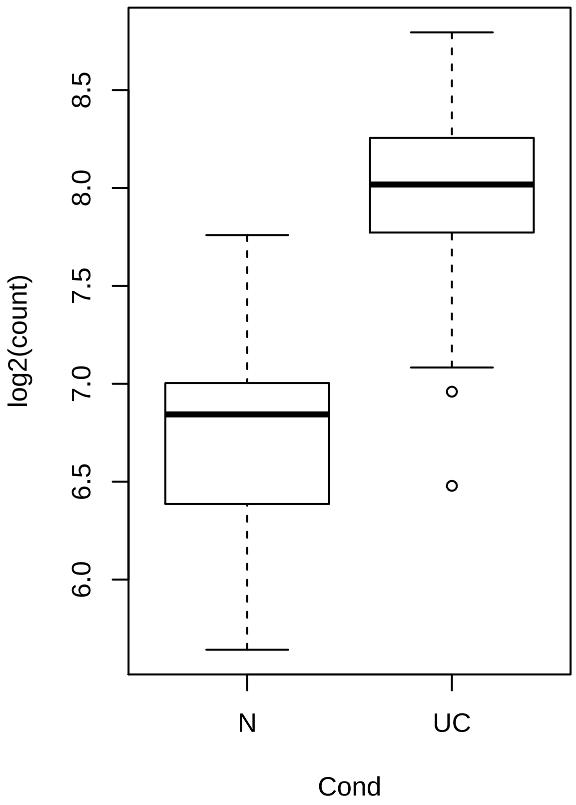
TNFSF8 average UC−N %methylation max=−25.8% min=−42.66%

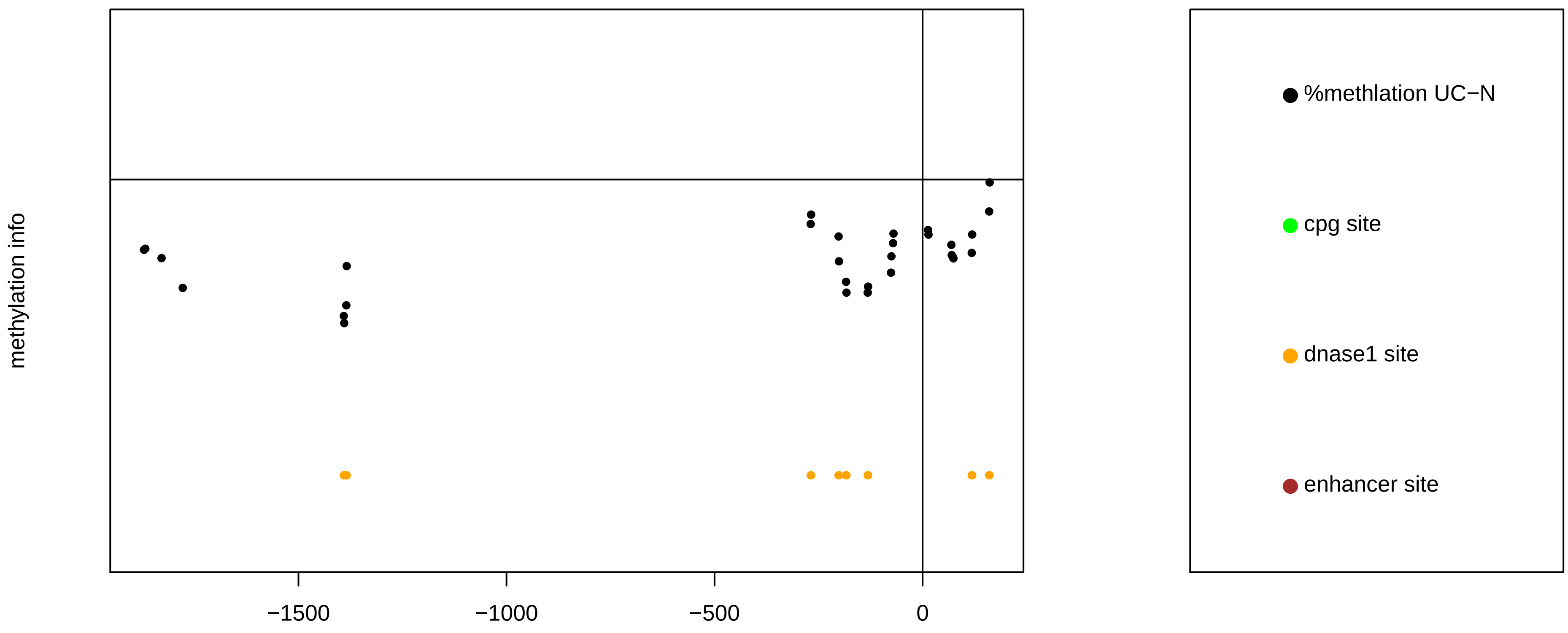


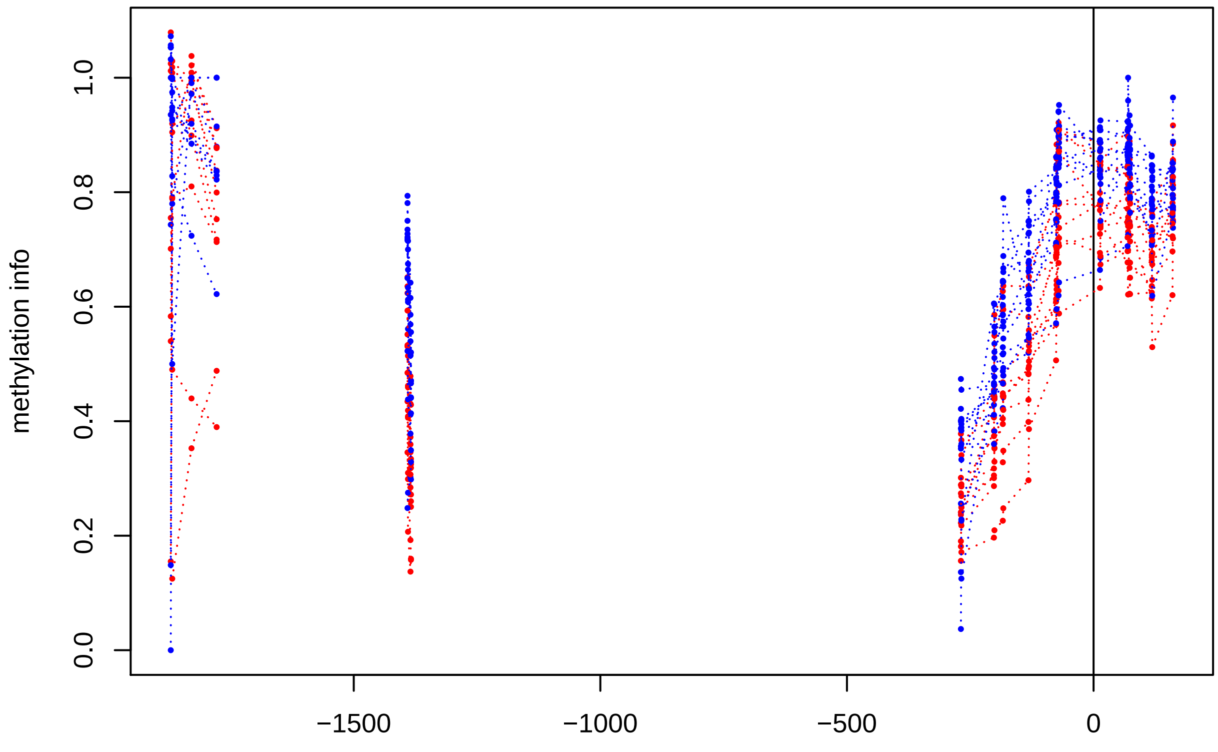
TNFSF8 raw %methylation, red=UC, blue=Normal

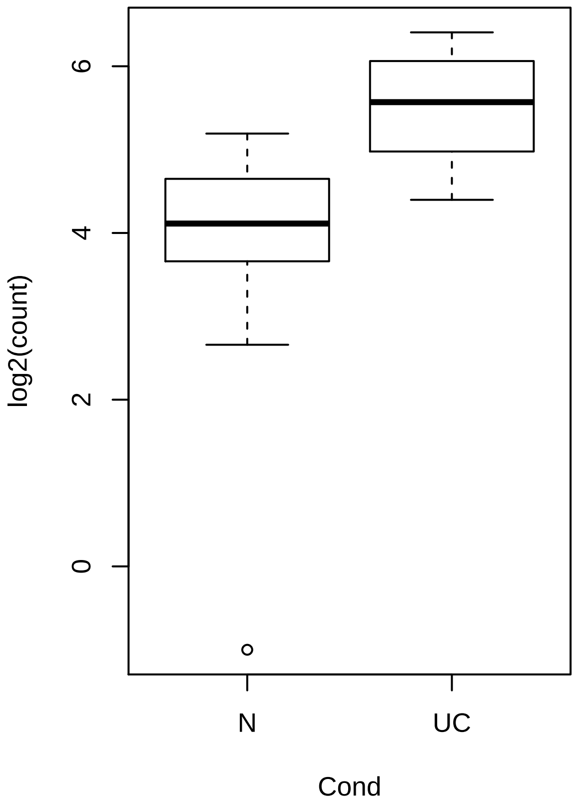


RNAseq logFC(UC−N)= 1.02

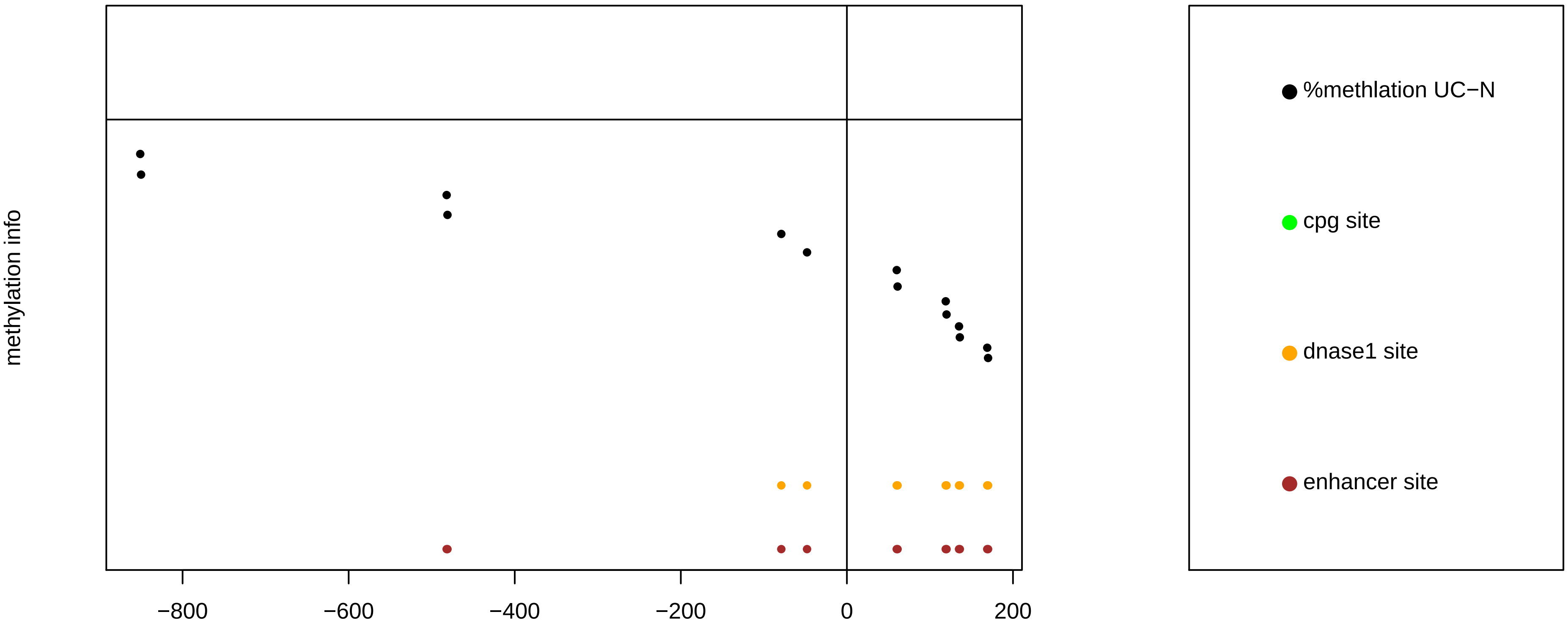



TP63 average UC−N %methylation max=−0.38% min=−18.88%

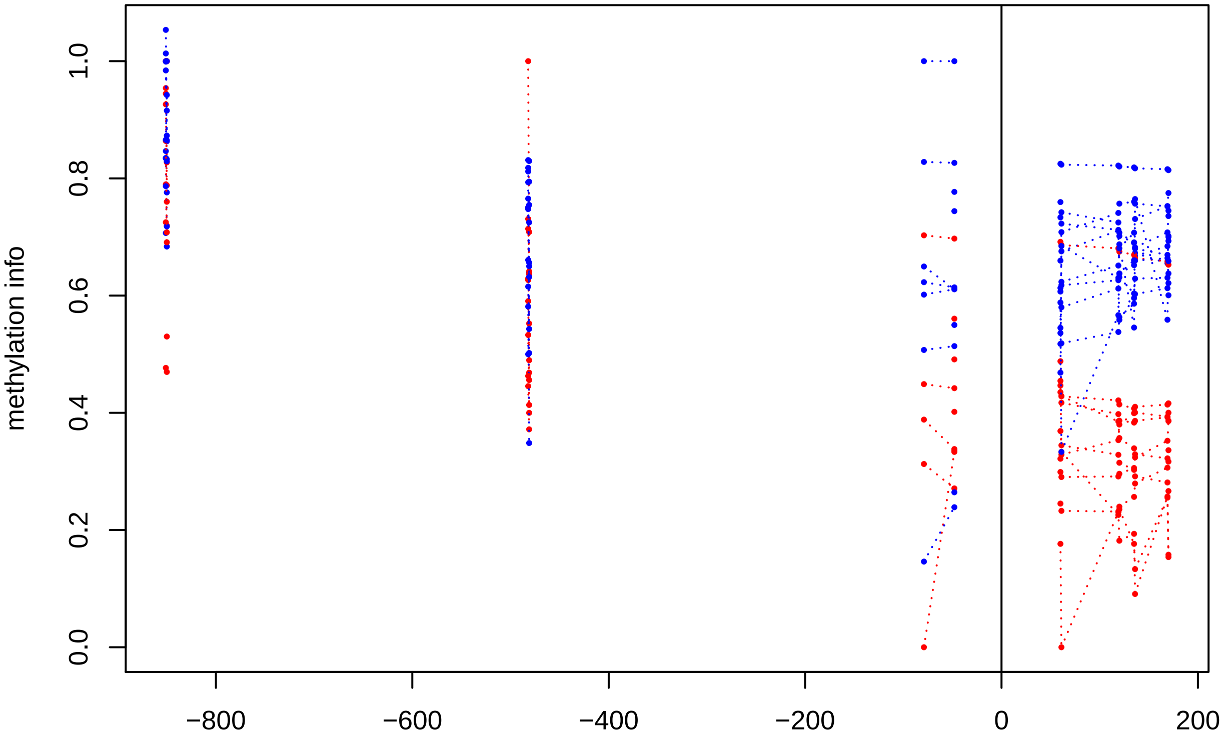

TP63 raw %methylation, red=UC, blue=Normal


RNAseq logFC(UC−N)= 1.25

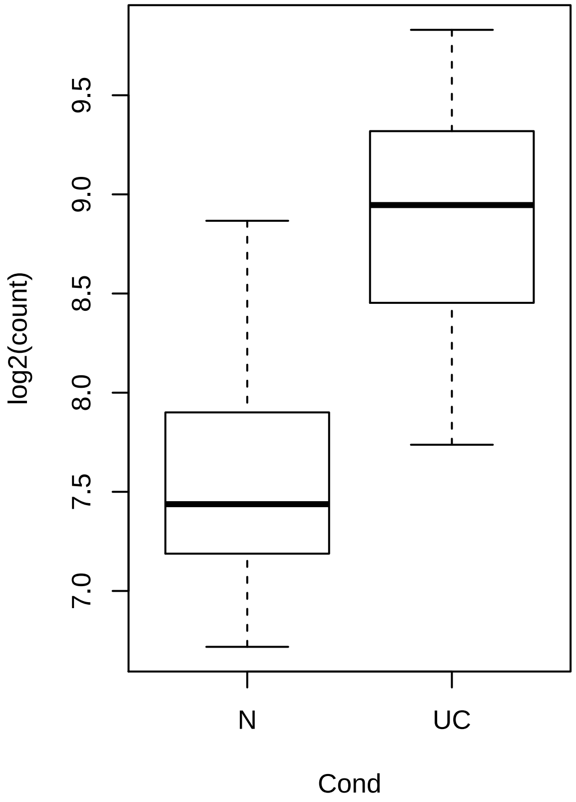
TRAF3IP3 average UC−N %methylation max=−5.4% min=−37.43%

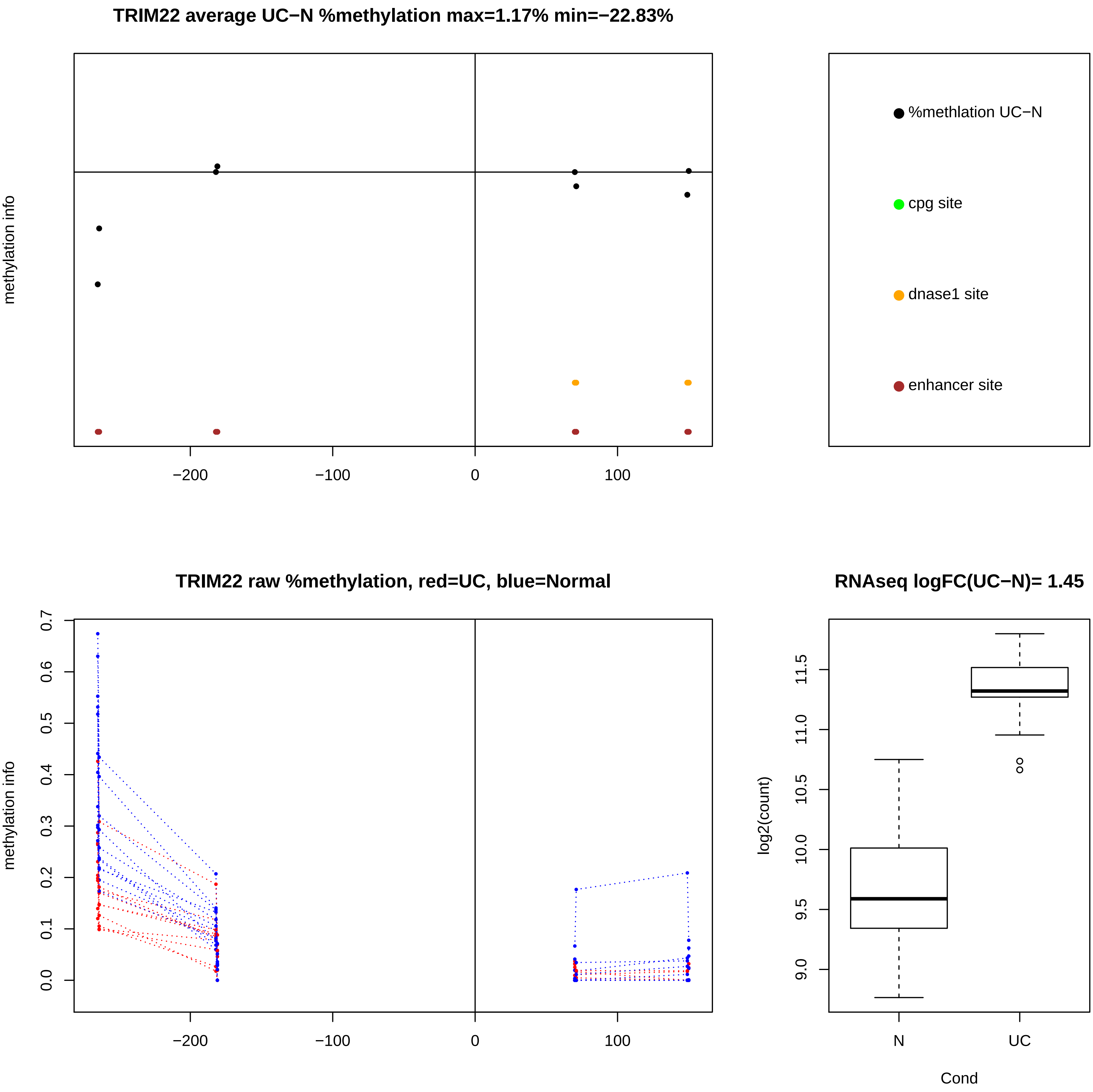


TRAF3IP3 raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 1.22

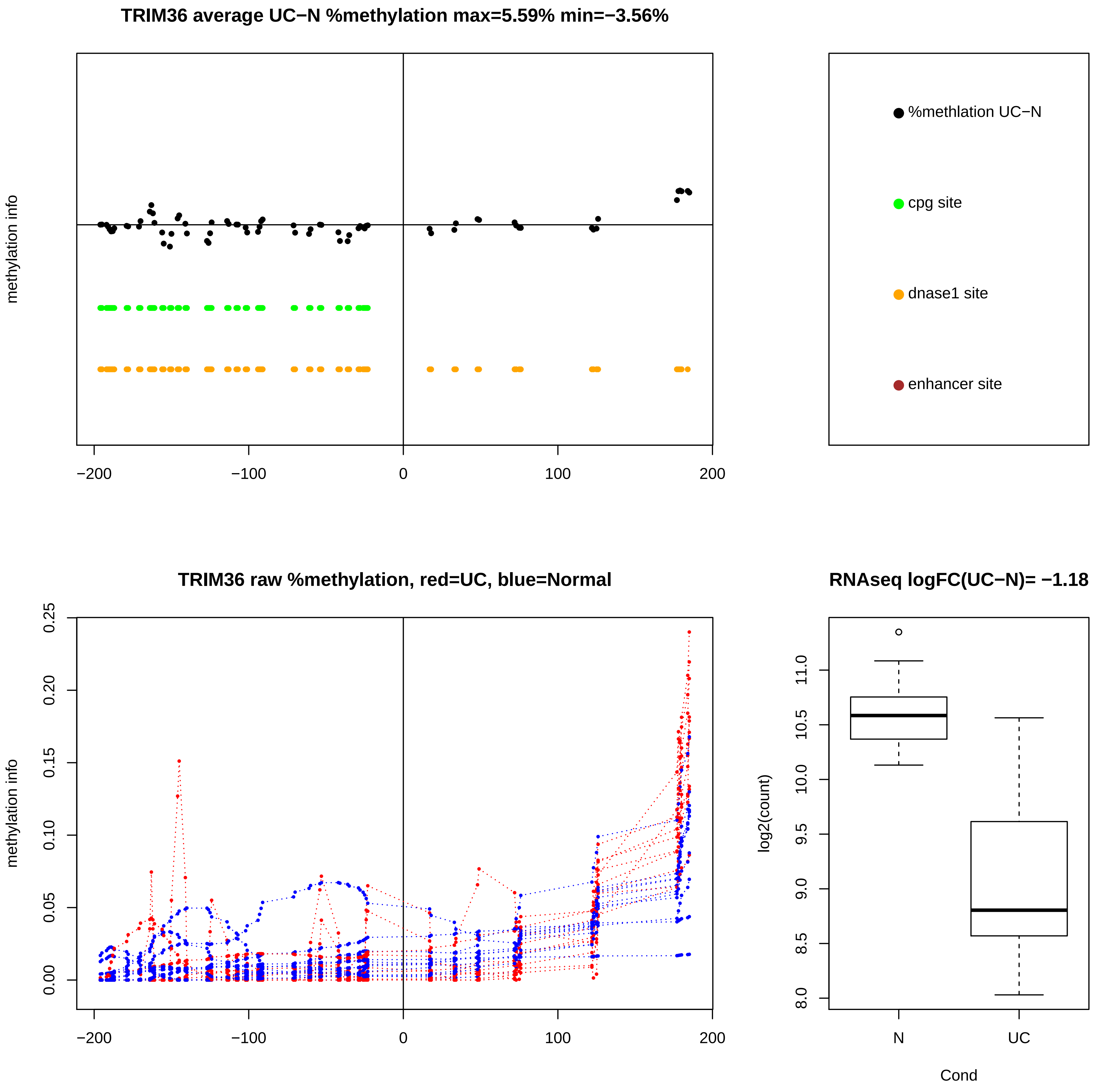




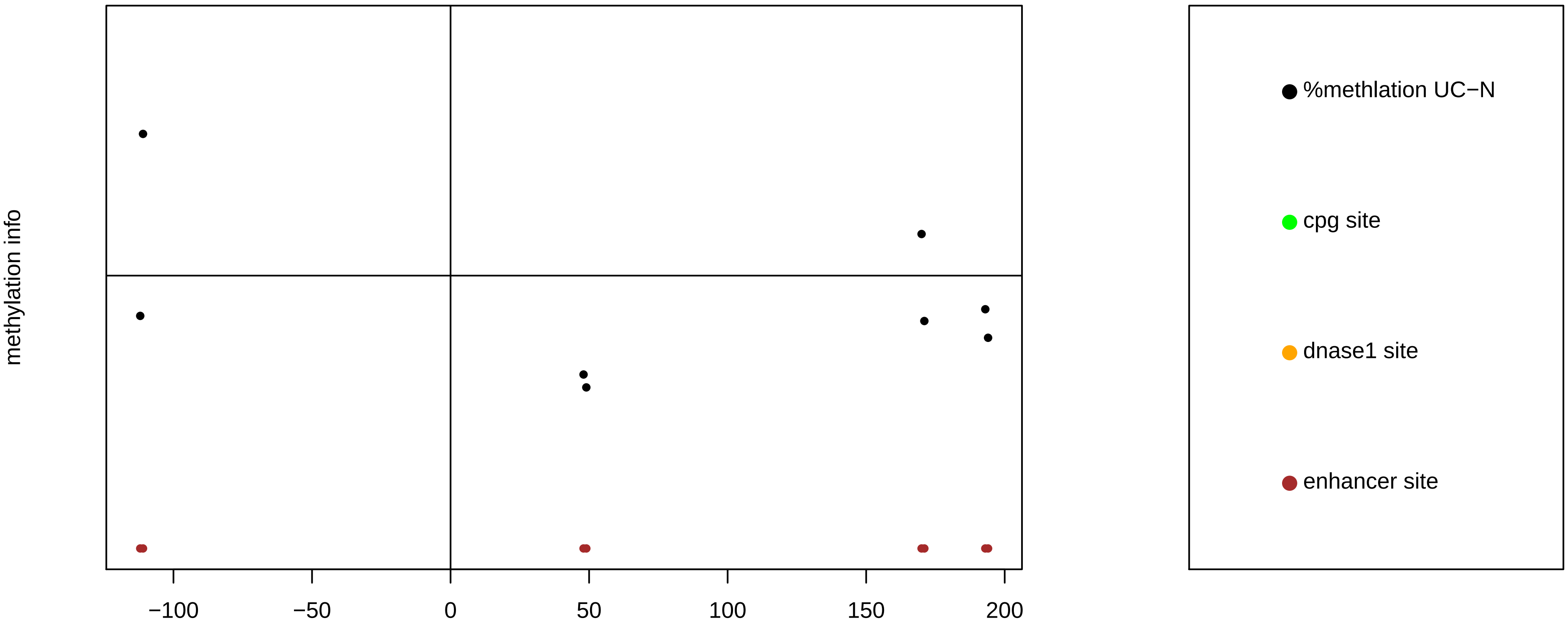
TRIM22 average UC−N %methylation max=1.17% min=−22.83%

TRIM22 raw %methylation, red=UC, blue=Normal

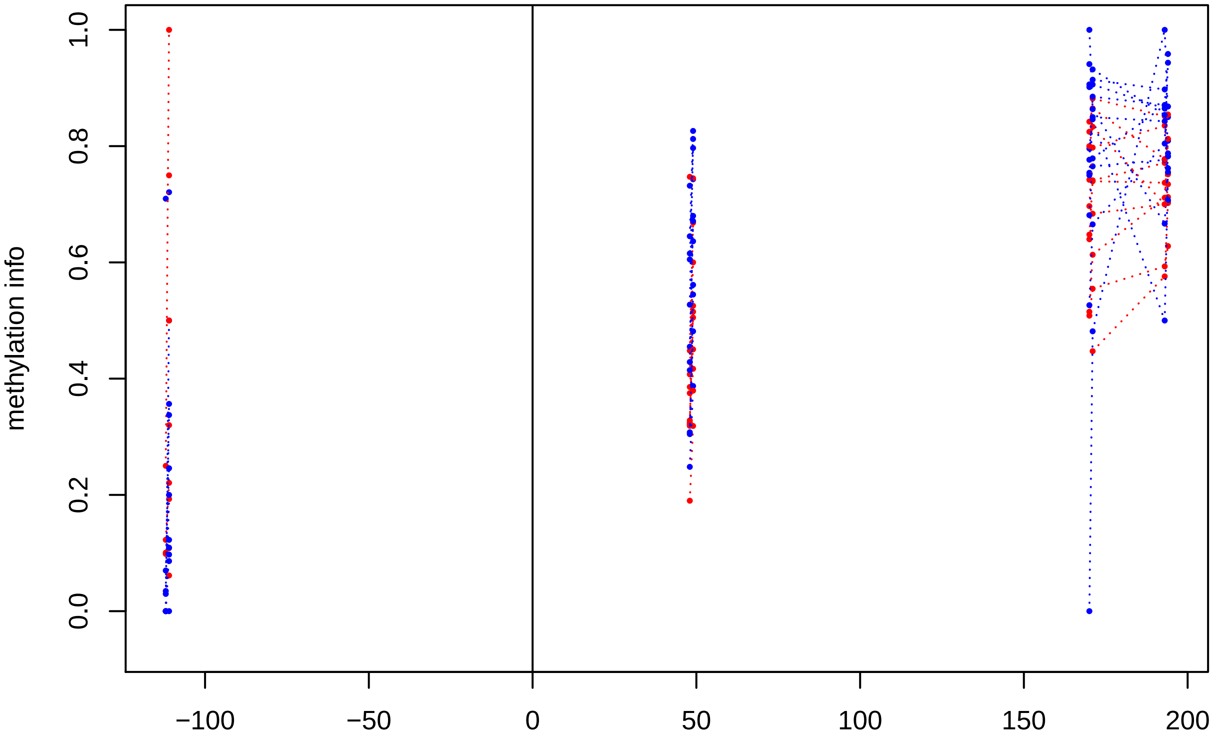
RNAseq logFC(UC−N)= 1.45


TRIM36 average UC−N %methylation max=5.59% min=−3.56%
methylation info
−200
−100
0
100
200
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
TRIM36 raw %methylation, red=UC, blue=Normal
methylation info
0.00
0.05
0.10
0.15
0.20
0.25
−200
−100
0
100
200
RNAseq logFC(UC−N)= −1.18
log2(count)
8.0
8.5
9.0
9.5
10.0
10.5
11.0
N
UC
Cond

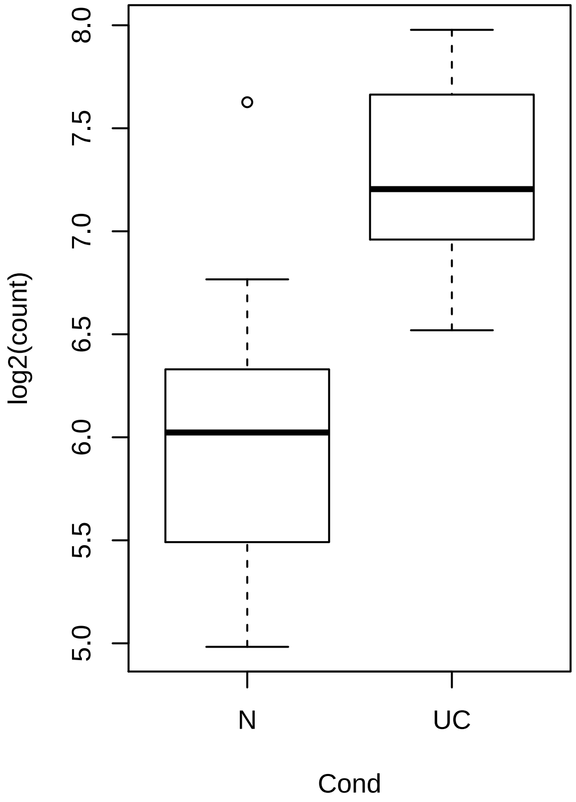
UBASH3A average UC−N %methylation max=26.4% min=−20.82%

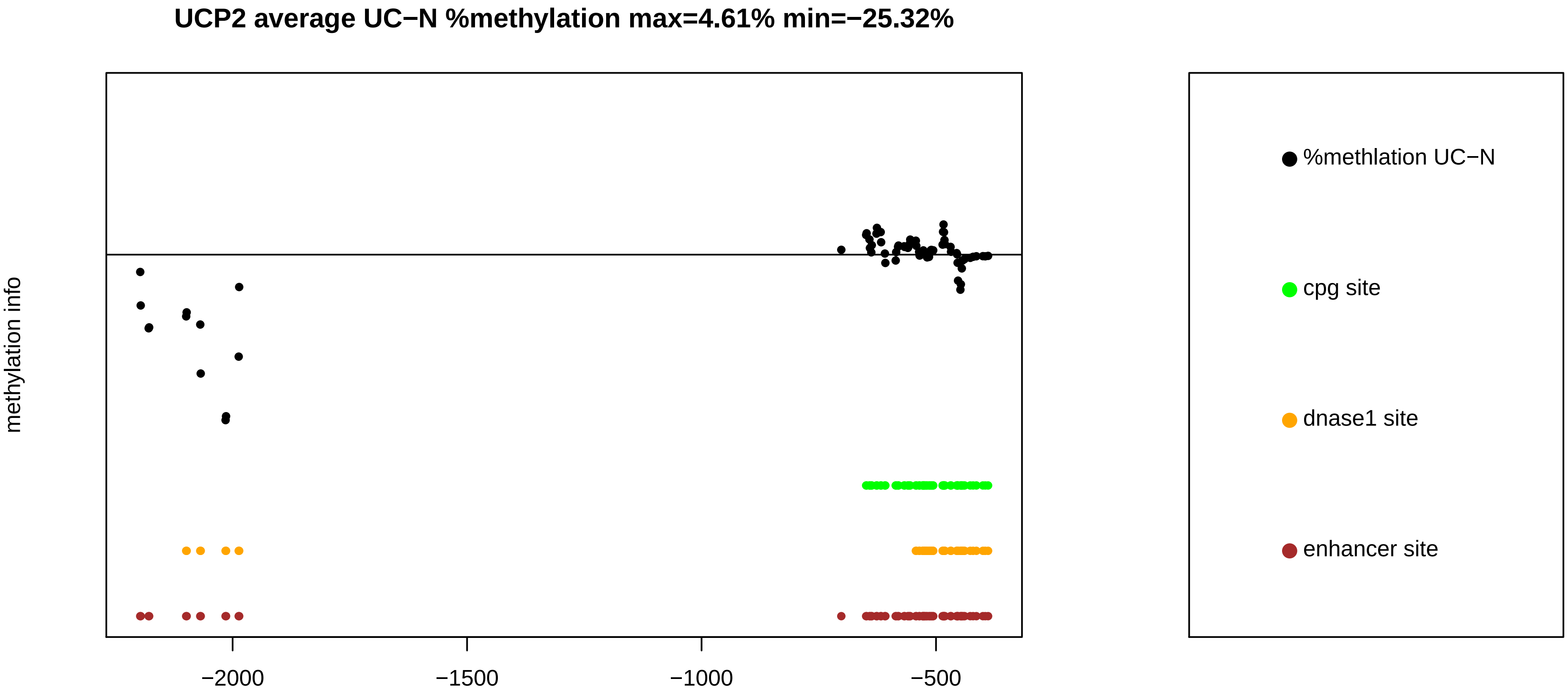


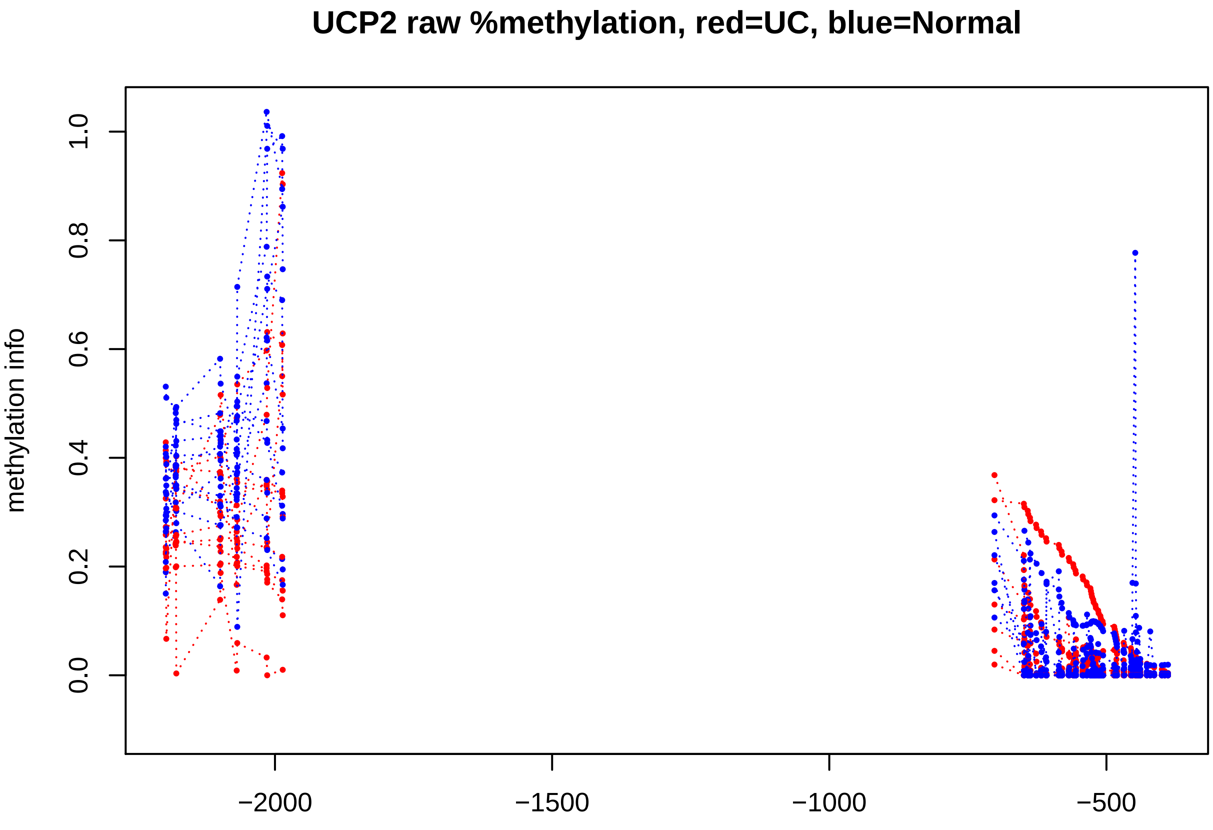
UBASH3A raw %methylation, red=UC, blue=Normal

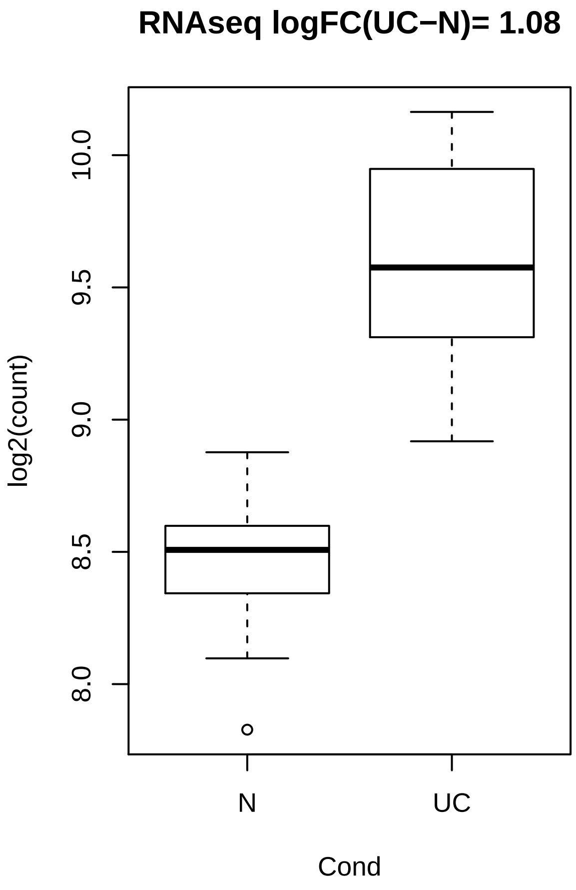


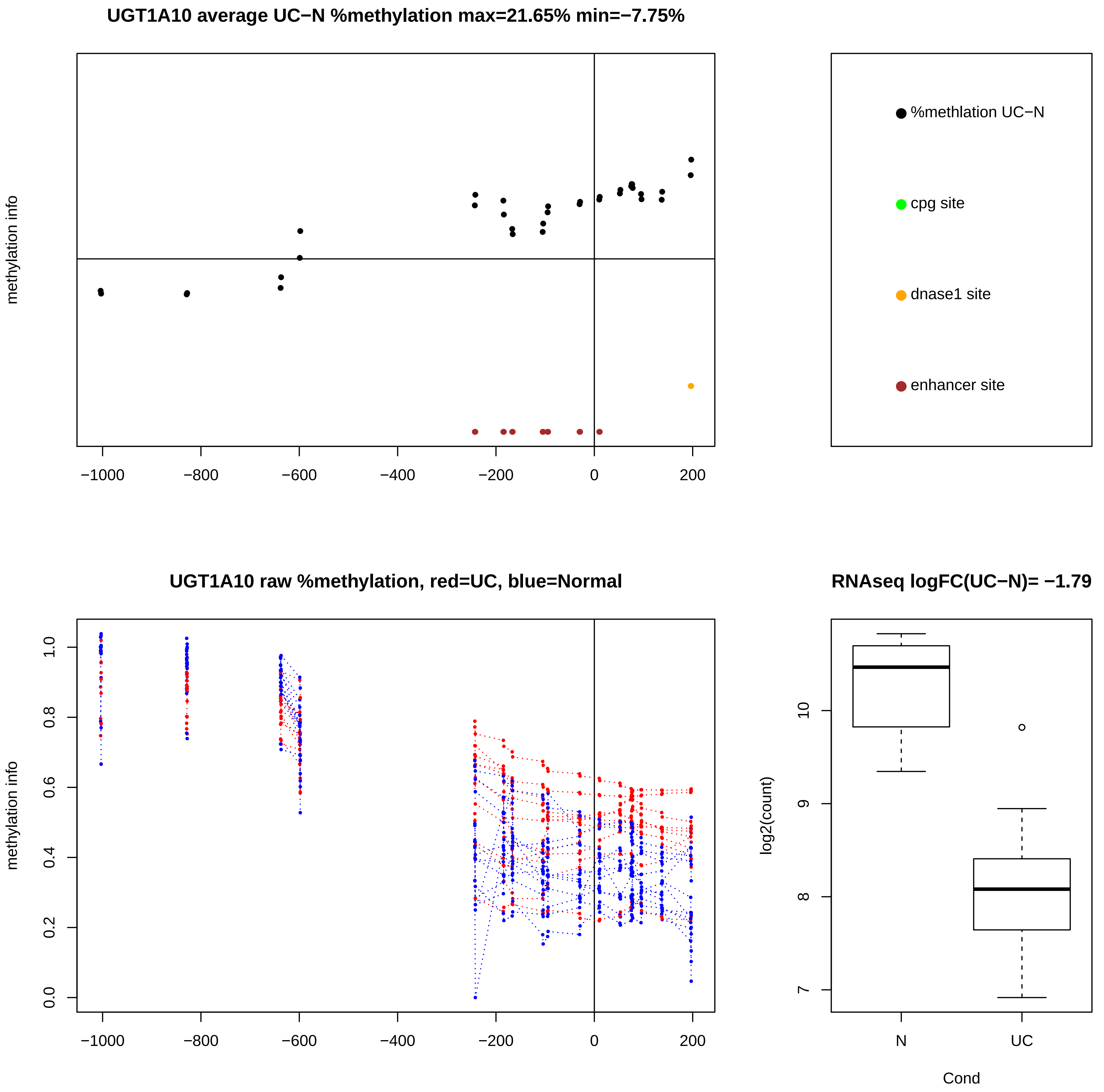
RNAseq logFC(UC−N)= 1.06

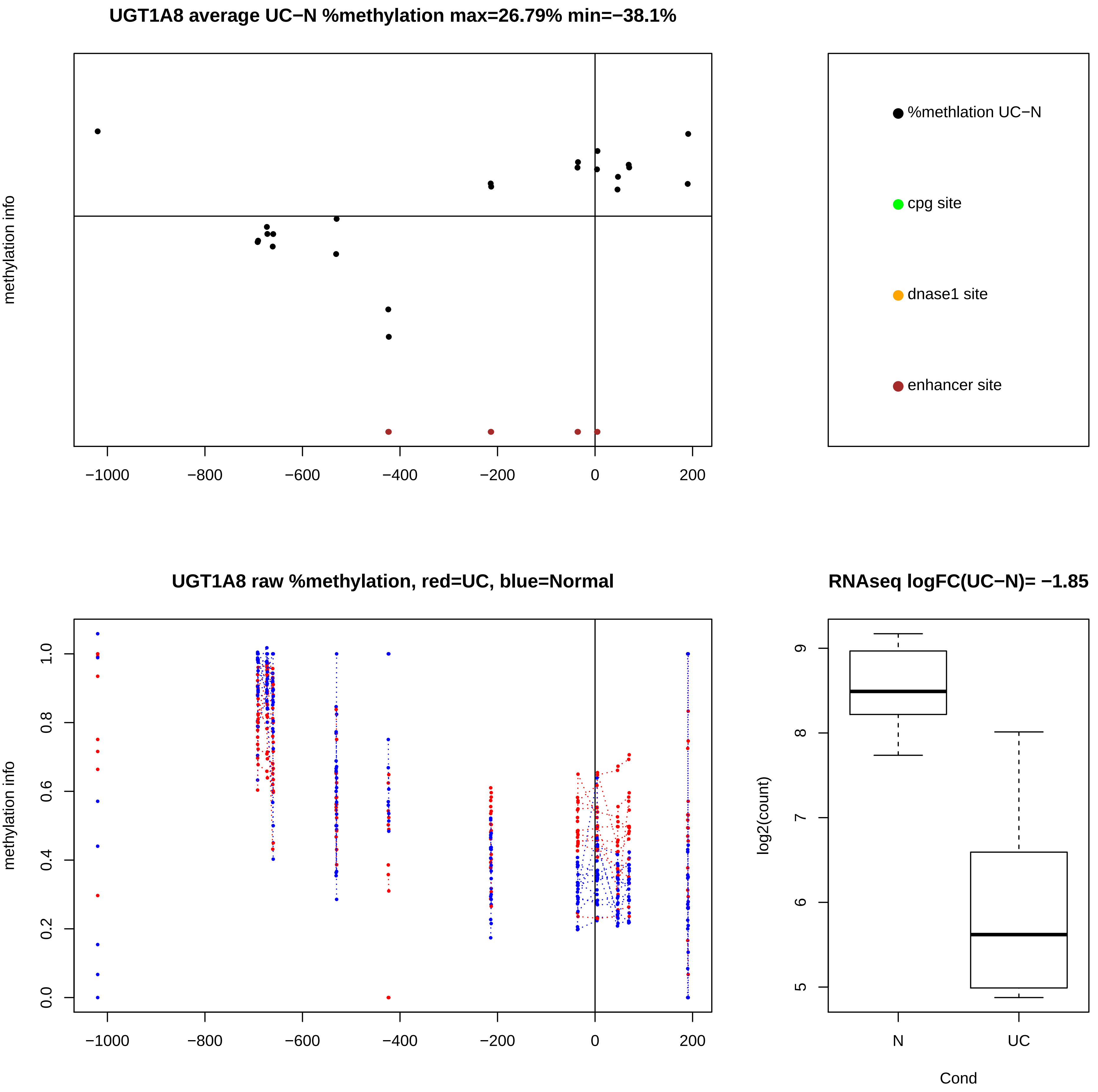



UCP2 average UC−N %methylation max=4.61% min=−25.32%


UCP2 raw %methylation, red=UC, blue=Normal


RNAseq logFC(UC−N)= 1.08


UGT1A10 average UC−N %methylation max=21.65% min=−7.75%
methylation info
−1000
−800
−600
−400
−200
0
200
● %methlation UC−N
● cpg site
● dnase1 site
● enhancer site
UGT1A10 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
0.8
1.0
−1000
−800
−600
−400
−200
0
200
RNAseq logFC(UC−N)= −1.79
log2(count)
7
8
9
10
N
UC
Cond

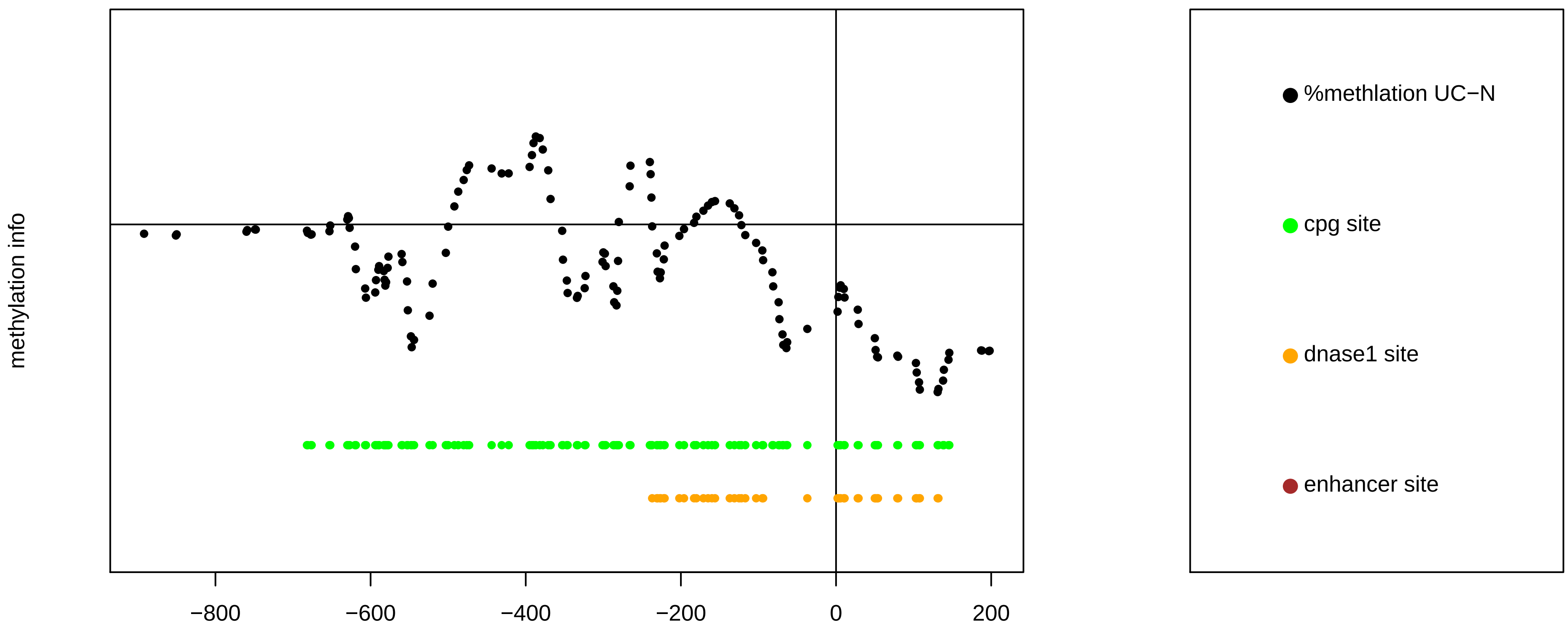


UGT1A8 average UC−N %methylation max=26.79% min=−38.1%

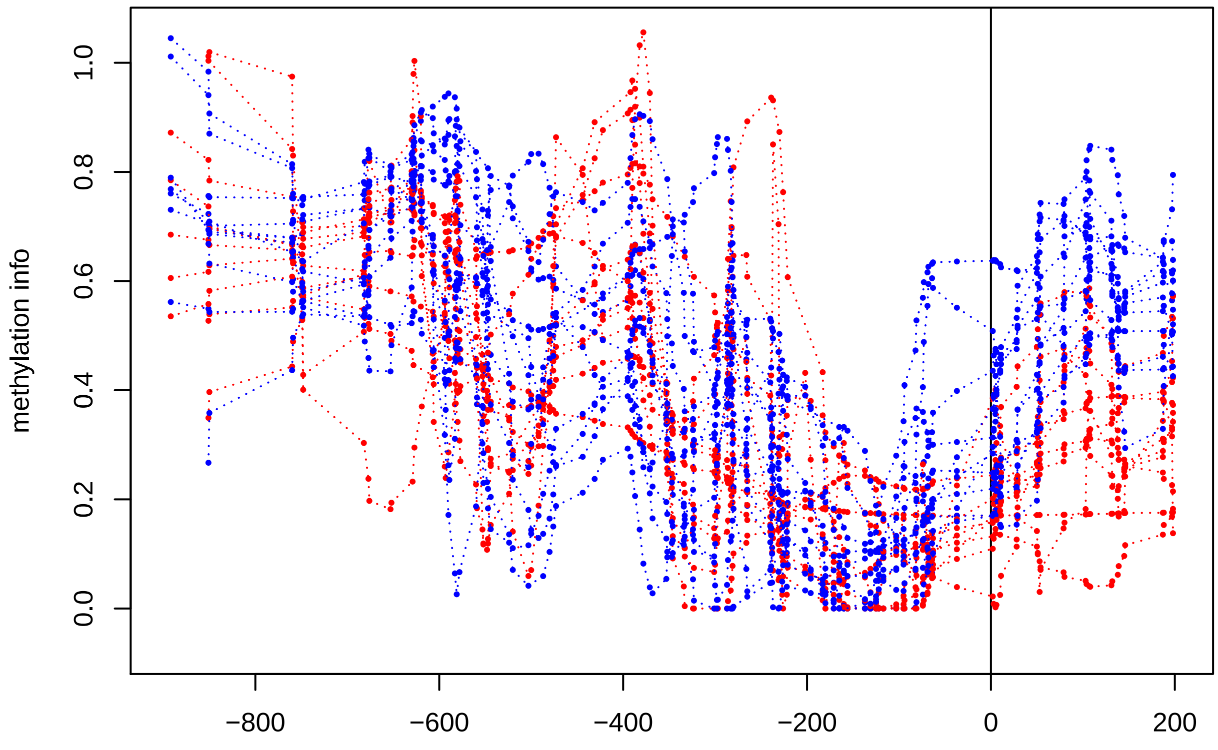
UGT1A8 raw %methylation, red=UC, blue=Normal

RNAseq logFC(UC−N)= −1.85

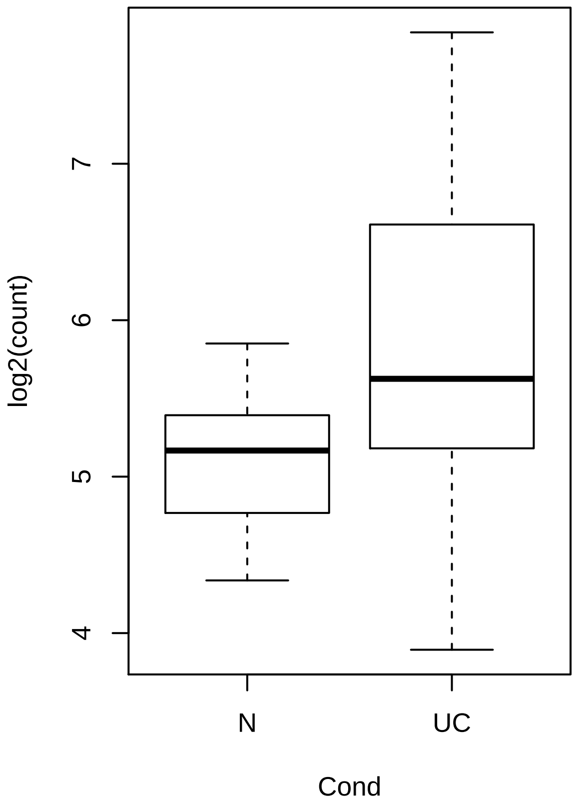
USP6 average UC−N %methylation max=16.56% min=−31.57%

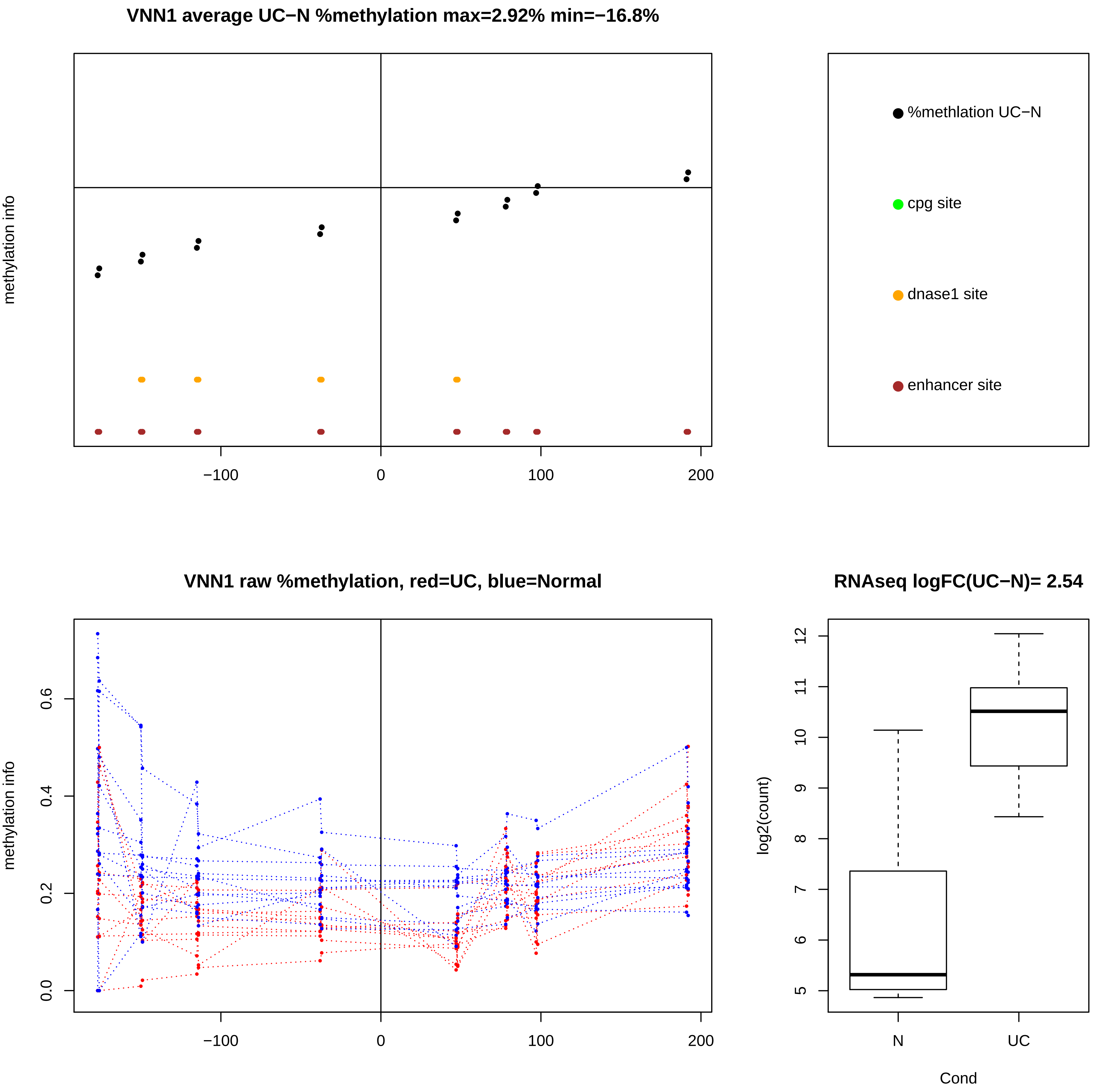


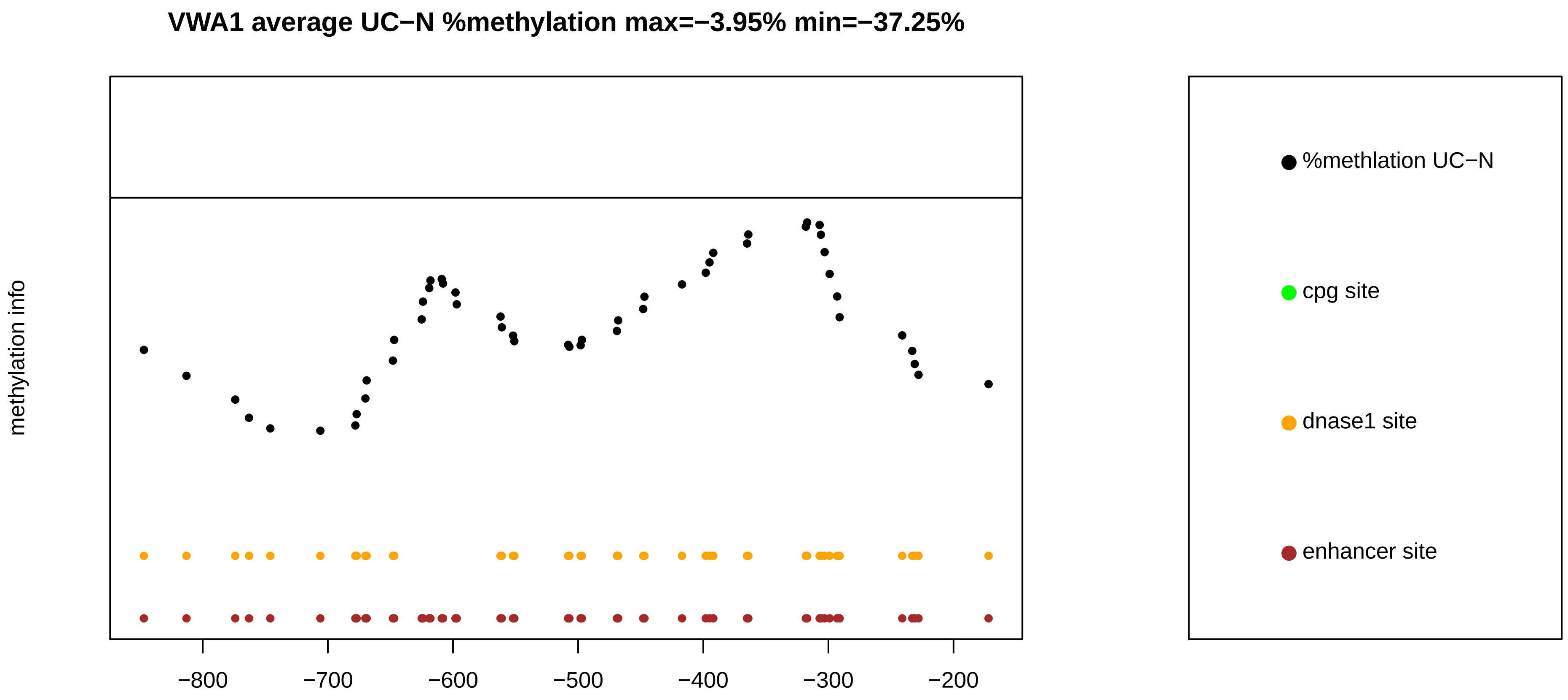
USP6 raw %methylation, red=UC, blue=Normal

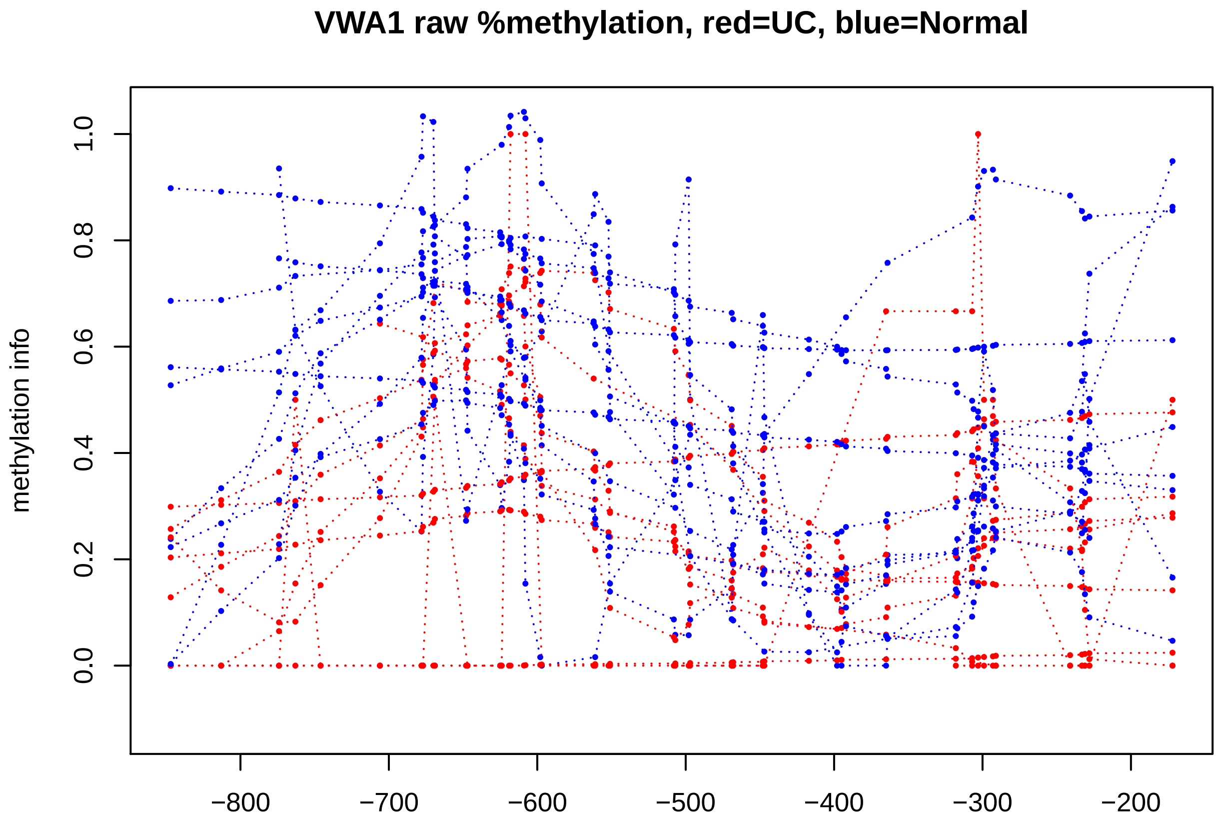


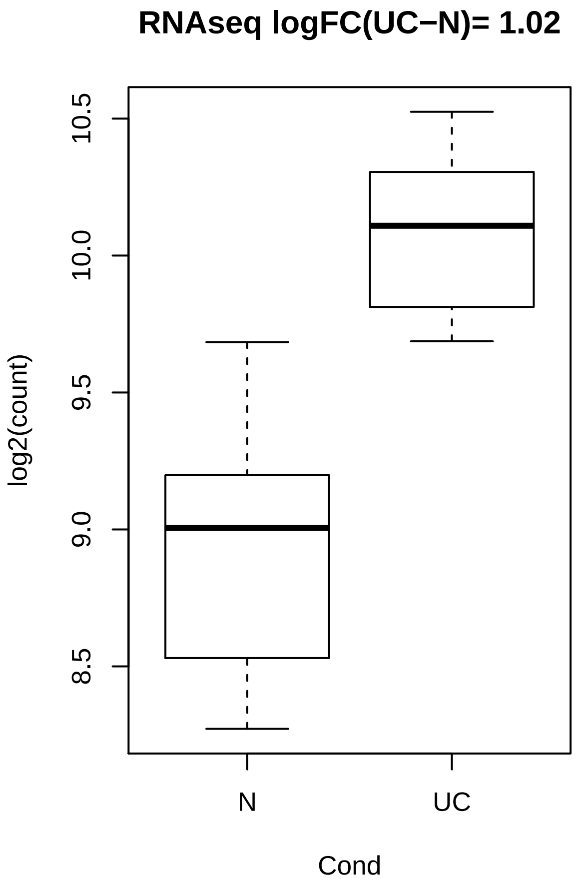
RNAseq logFC(UC−N)= 1.01



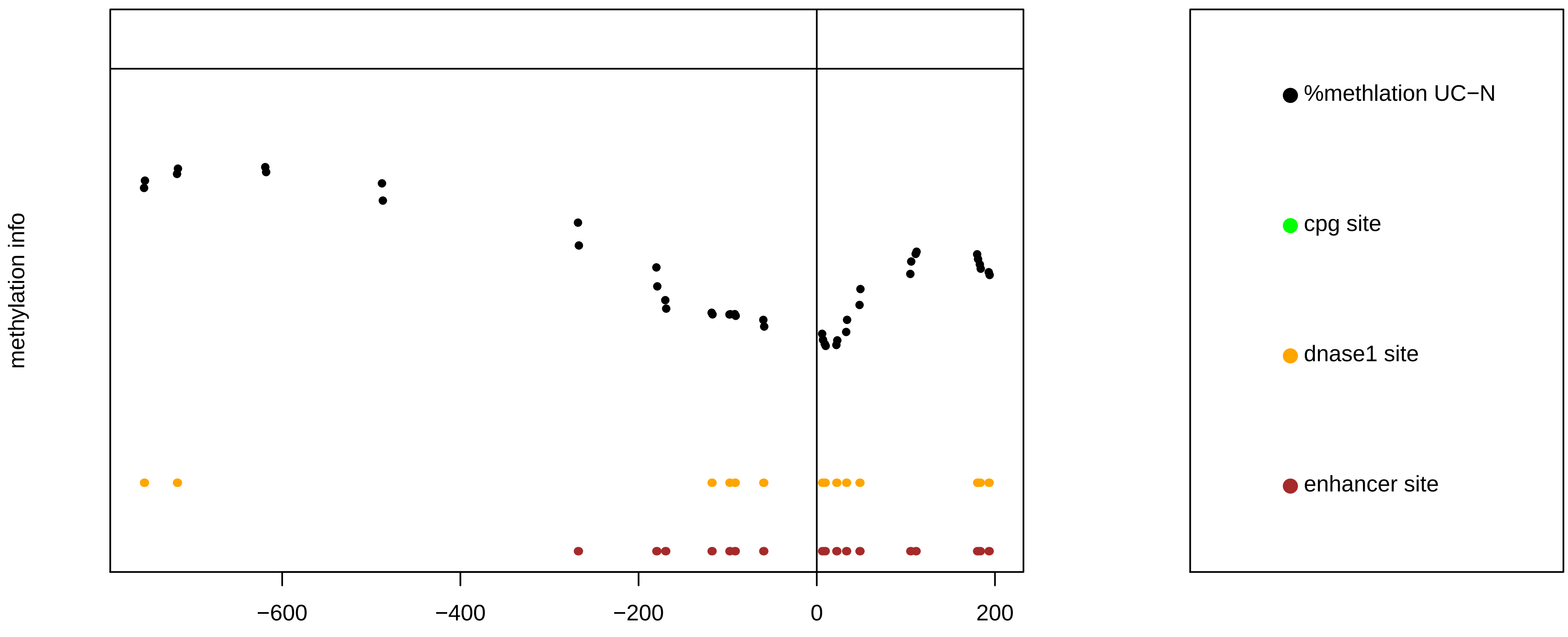

VNN1 average UC−N %methylation max=2.92% min=−16.8%
methylation info
−100
0
100
200
%methlation UC−N
cpg site
dnase1 site
enhancer site
VNN1 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.2
0.4
0.6
−100
0
100
200
RNAseq logFC(UC−N)= 2.54
log2(count)
5
6
7
8
9
10
11
12
N
UC
Cond


VWA1 average UC−N %methylation max=−3.95% min=−37.25%

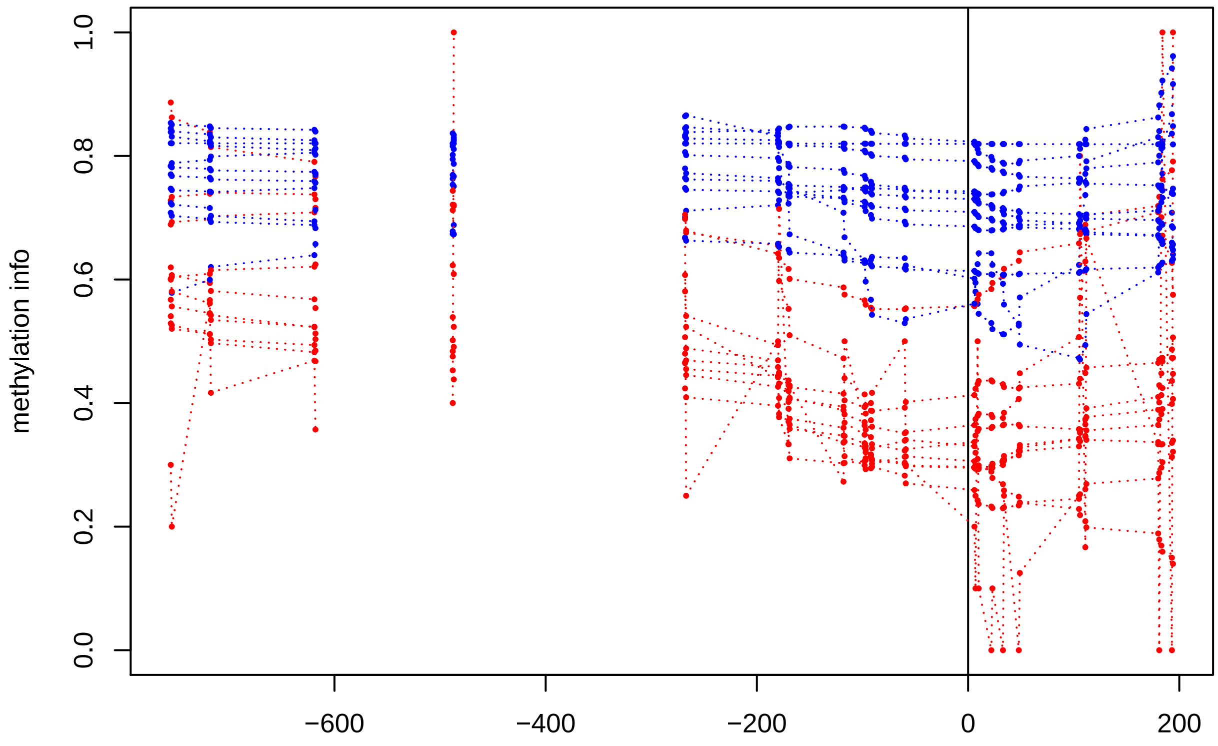

VWA1 raw %methylation, red=UC, blue=Normal


RNAseq logFC(UC−N)= 1.02

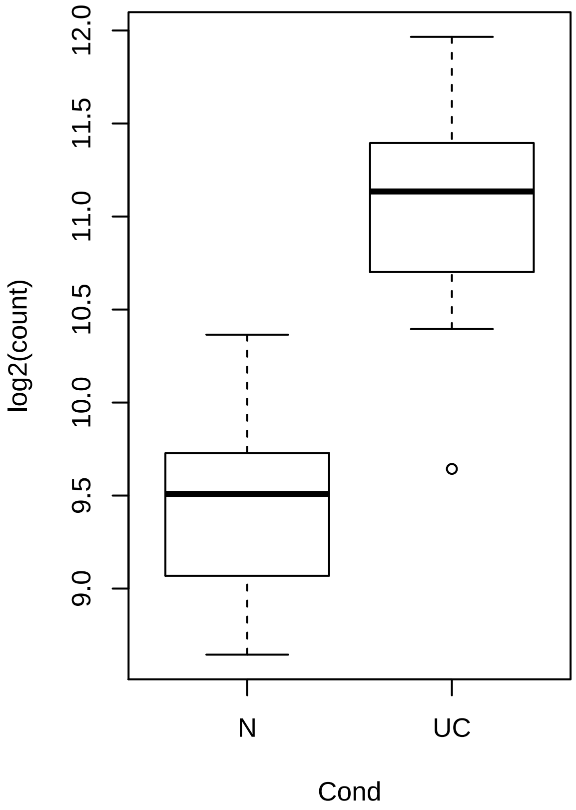
WDFY4 average UC−N %methylation max=−14.38% min=−40.51%



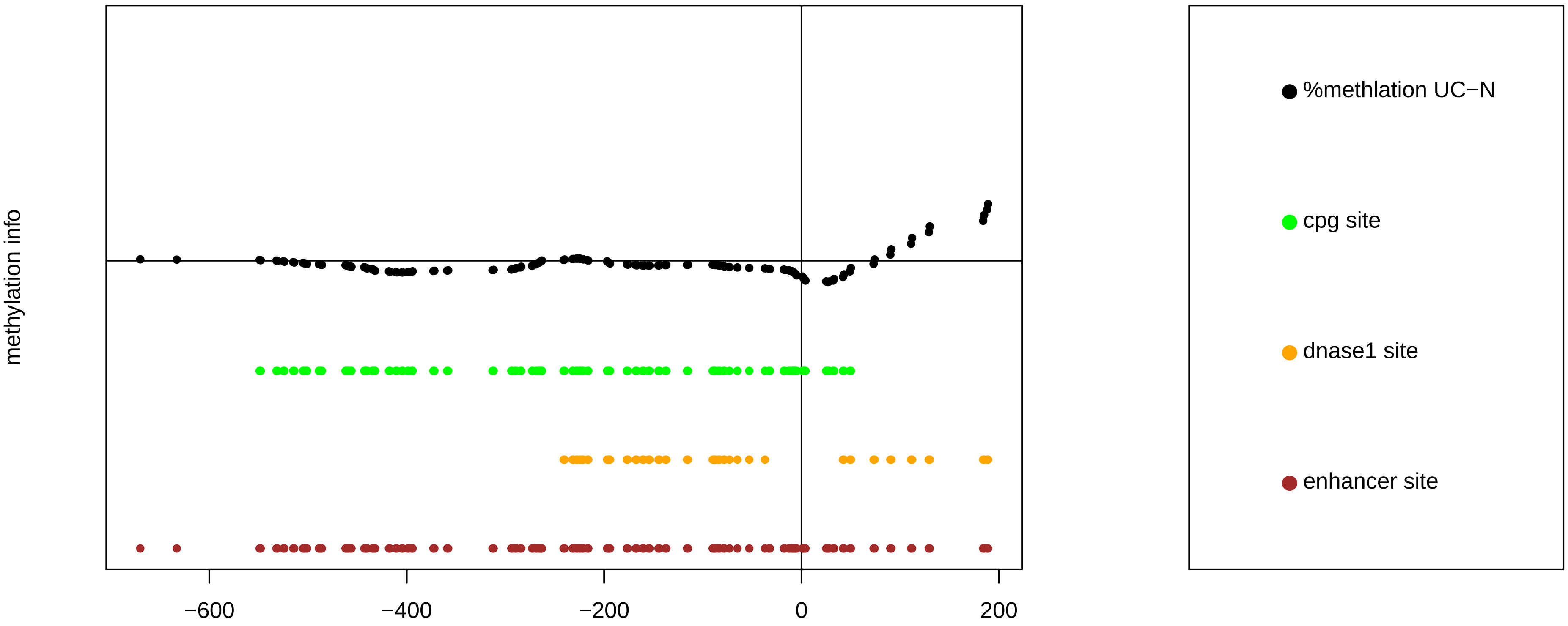
WDFY4 raw %methylation, red=UC, blue=Normal



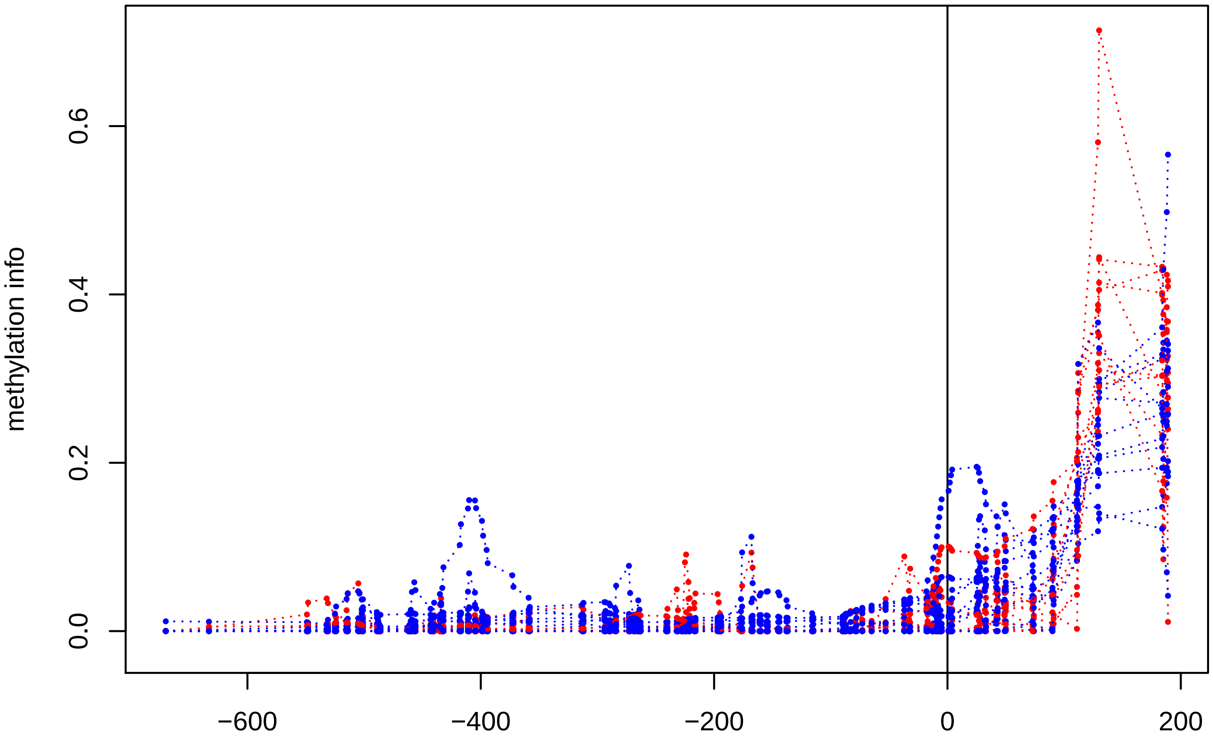
RNAseq logFC(UC−N)= 1.45



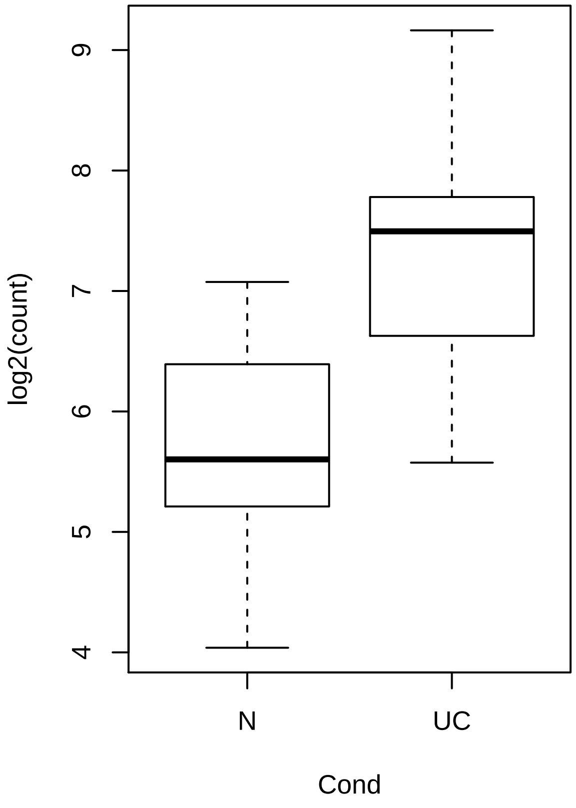
XKR9 average UC−N %methylation max=6.37% min=−2.4%



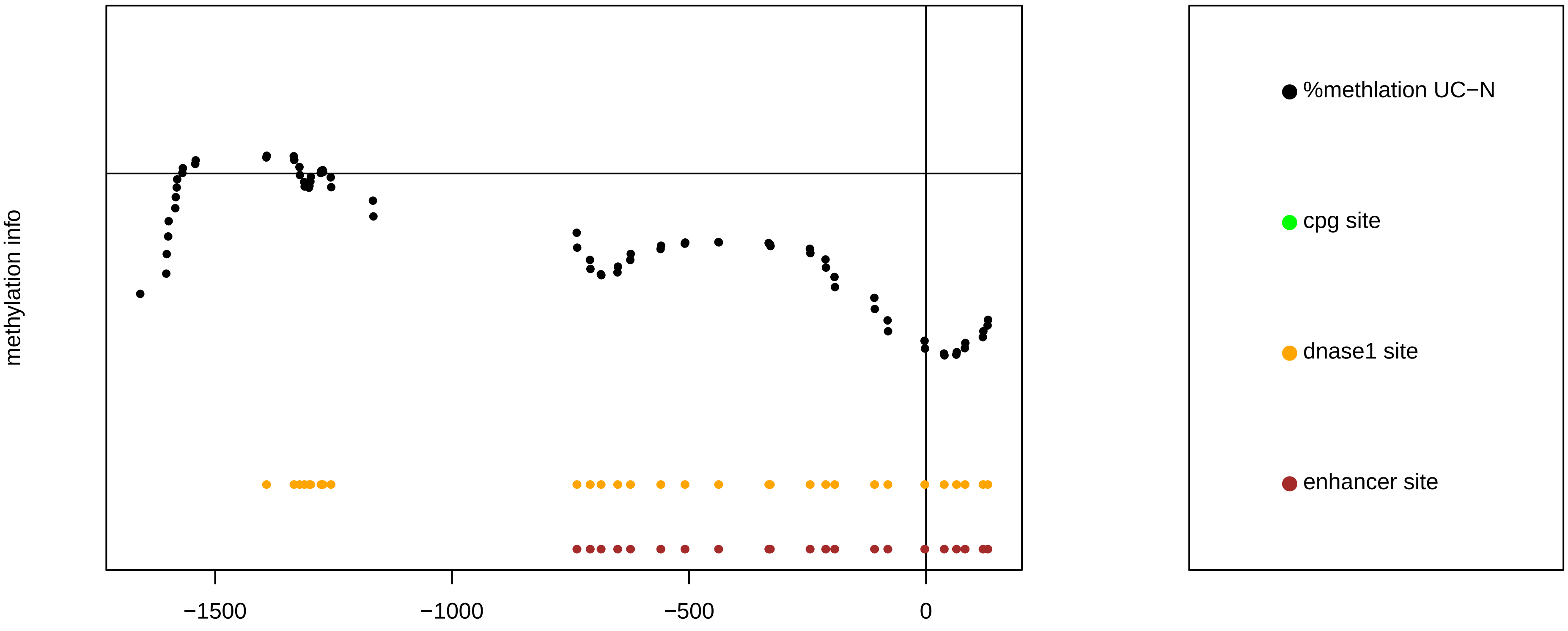
XKR9 raw %methylation, red=UC, blue=Normal



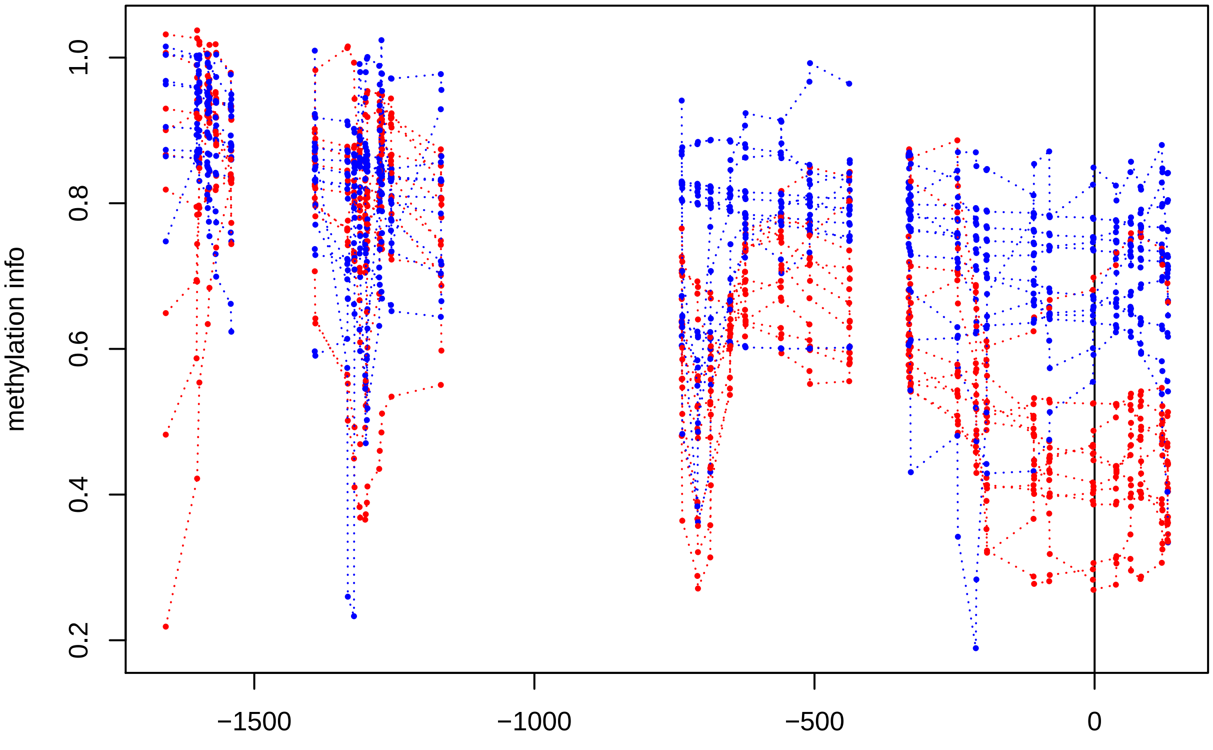
RNAseq logFC(UC−N)= 1.45



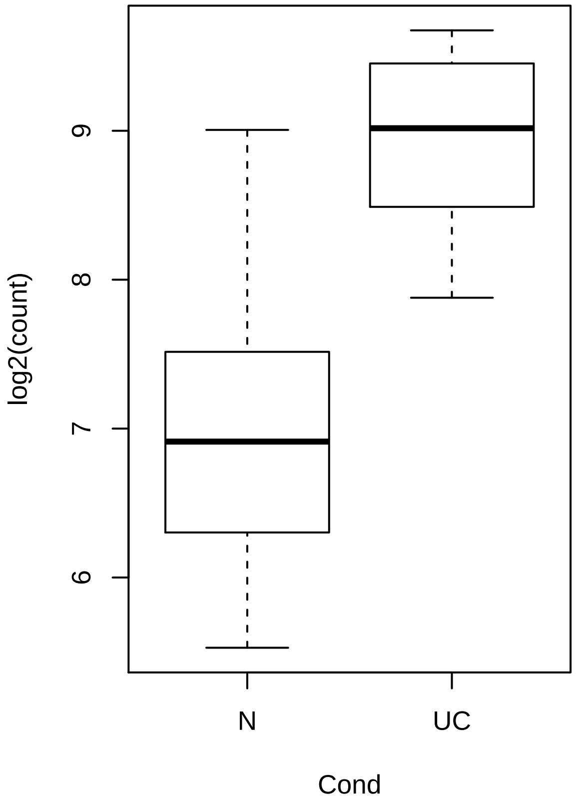
ZAP70 average UC−N %methylation max=2.75% min=−28.16%

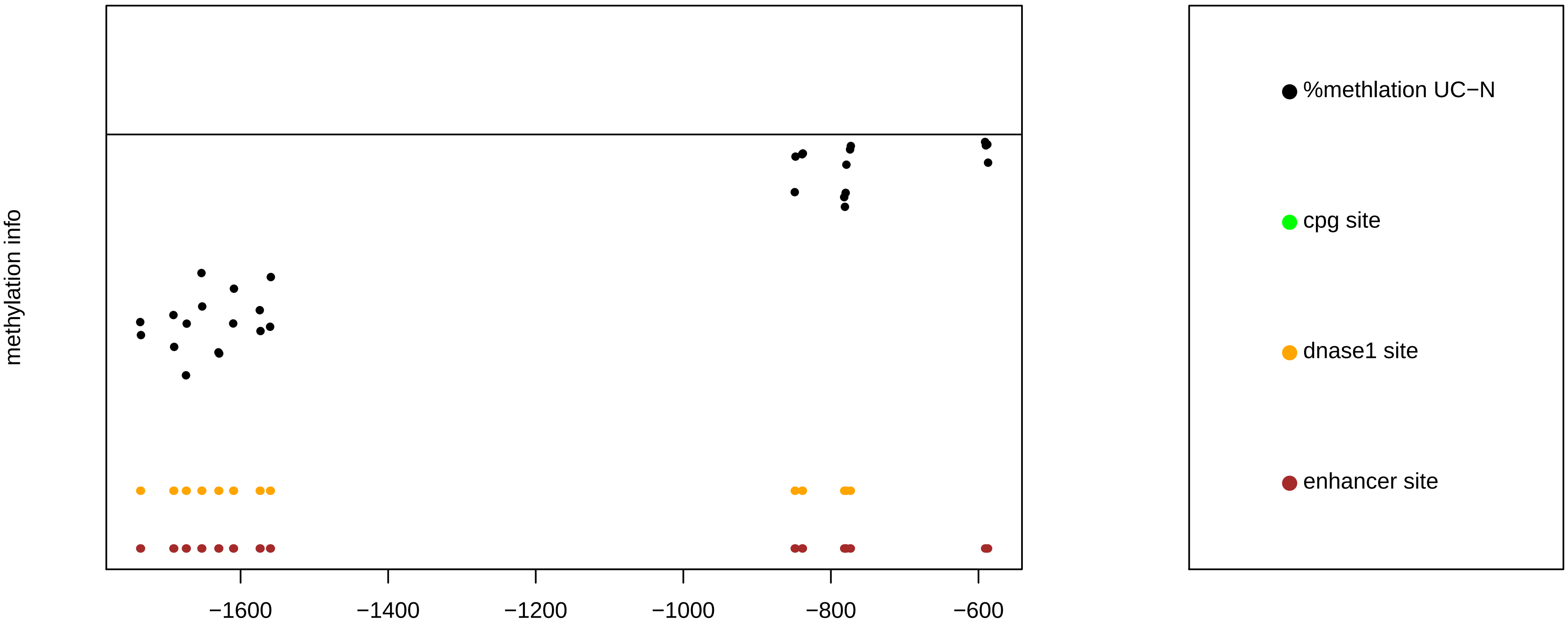


ZAP70 raw %methylation, red=UC, blue=Normal

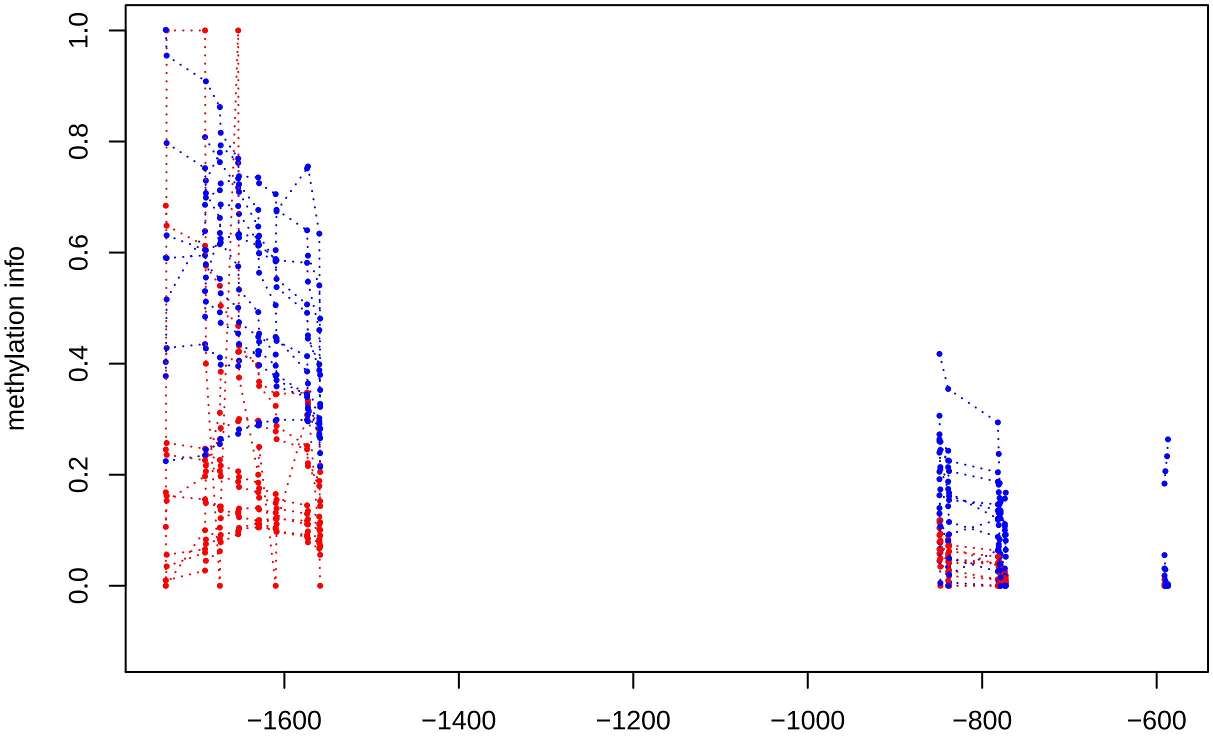


RNAseq logFC(UC−N)= 1.49

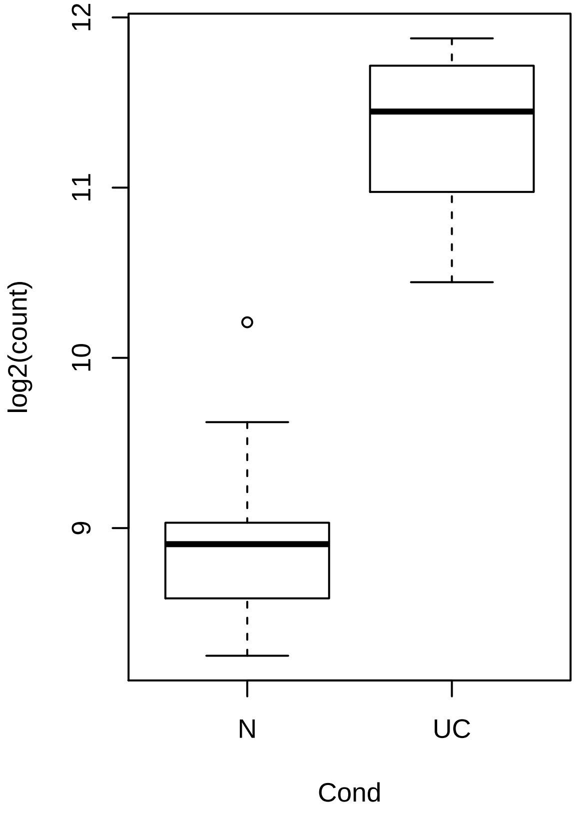




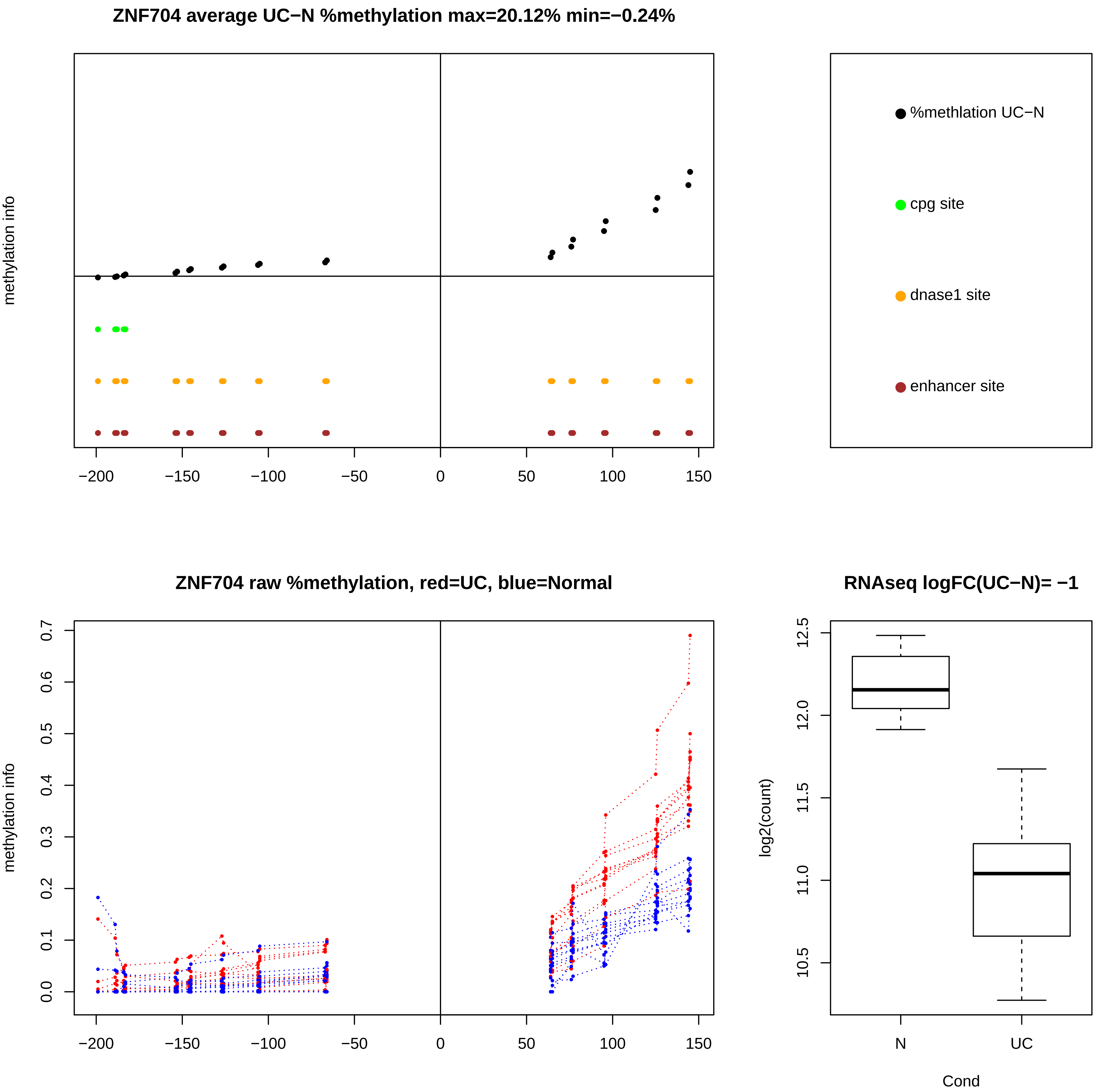
ZC3H12A average UC−N %methylation max=−1.3% min=−41.73%



ZC3H12A raw %methylation, red=UC, blue=Normal



RNAseq logFC(UC−N)= 2.19


ZNF704 average UC−N %methylation max=20.12% min=−0.24%
methylation info
−200
−150
−100
−50
0
50
100
150
%methlation UC−N
cpg site
dnase1 site
enhancer site
ZNF704 raw %methylation, red=UC, blue=Normal
methylation info
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
−200
−150
−100
−50
0
50
100
150
RNAseq logFC(UC−N)= −1
log2(count)
10.5
11.0
11.5
12.0
12.5
N
UC
Cond