

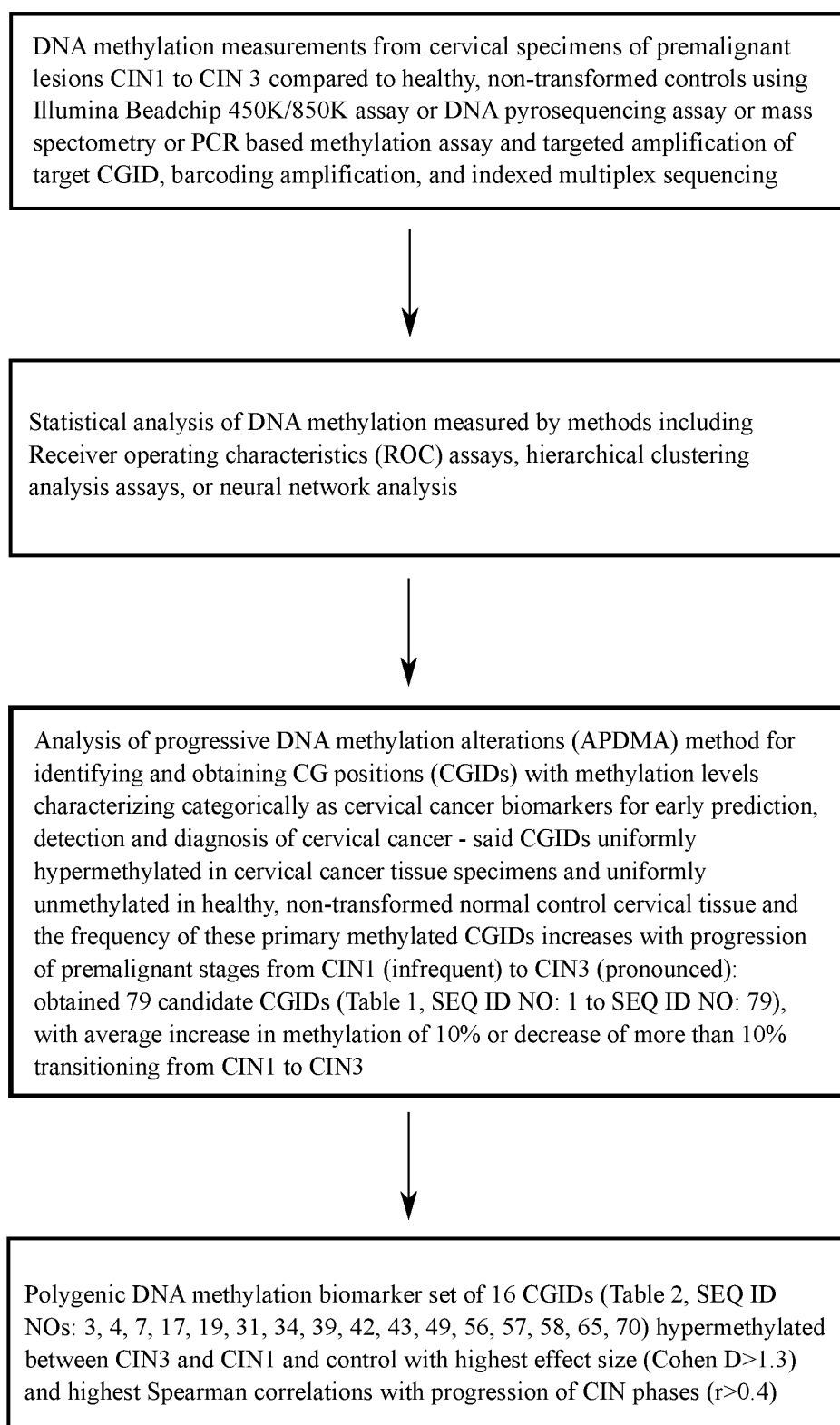


FIGURE 1

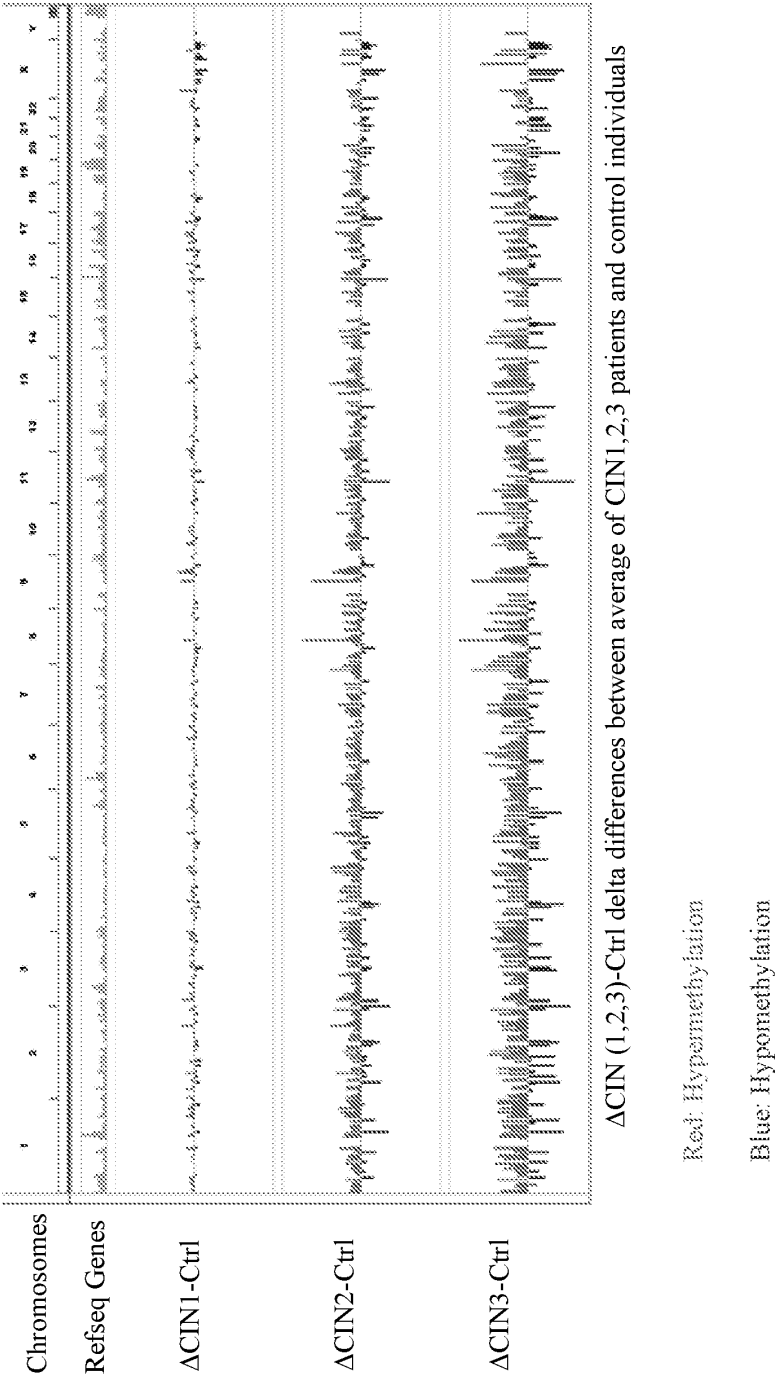
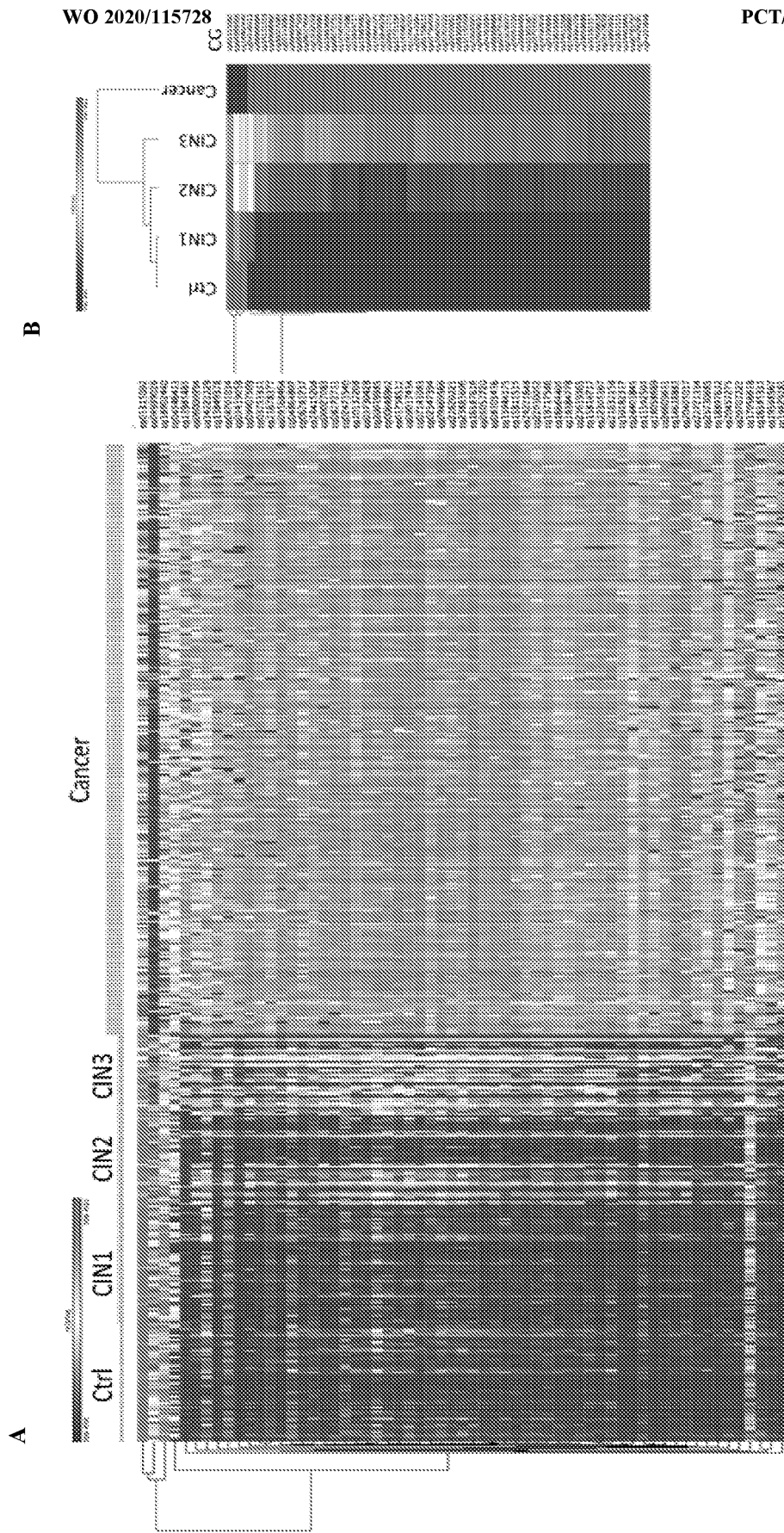


FIGURE 2



Red: Hypermethylation
Blue: Hypomethylation

FIGURE 3

A

Call:

lm(formula = CG ~ cg03419058 * cg13944175, data = mydata)

Residuals:

Min	1Q	Median	3Q	Max
-0.267834	-0.004006	-0.000922	0.003339	0.259895

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-0.259395	0.008266	-31.38	<2e-16 ***
cg03419058	2.082067	0.075762	27.48	<2e-16 ***
cg13944175	2.098529	0.026368	79.58	<2e-16 ***
cg03419058:cg13944175	-3.466222	0.134114	-25.84	<2e-16 ***

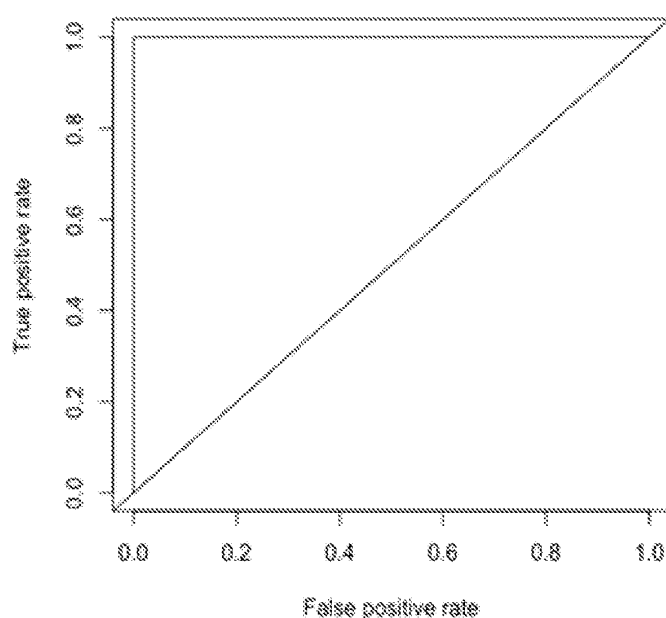
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.04126 on 320 degrees of freedom

Multiple R-squared: 0.9879, Adjusted R-squared: 0.9878

F-statistic: 8703 on 3 and 320 DF, p-value: < 2.2e-16

B

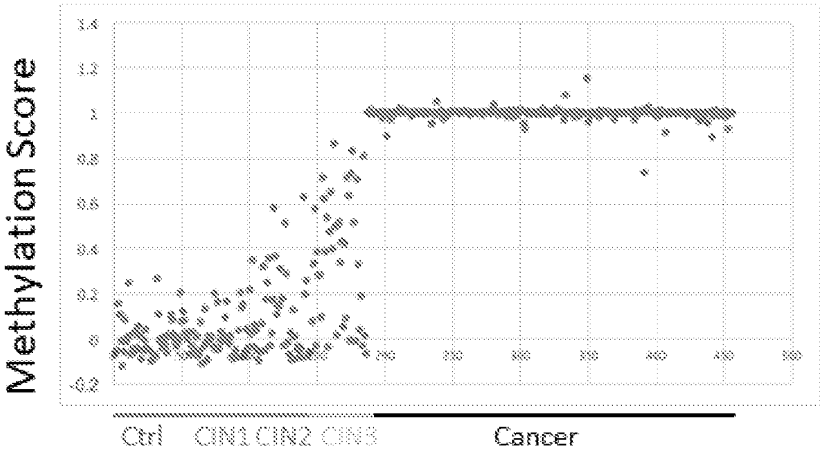


C

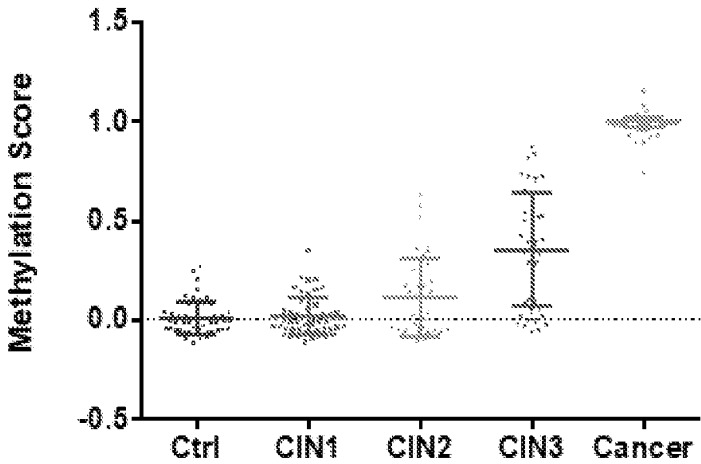
sensitivity	1
specificity	1
accuracy	1
AUC	1

FIGURE 4

A



B



Control, n = 54
CIN1, n = 50
CIN2, n = 40
CIN3, n = 42
Cervical cancer, n = 270

FIGURE 5

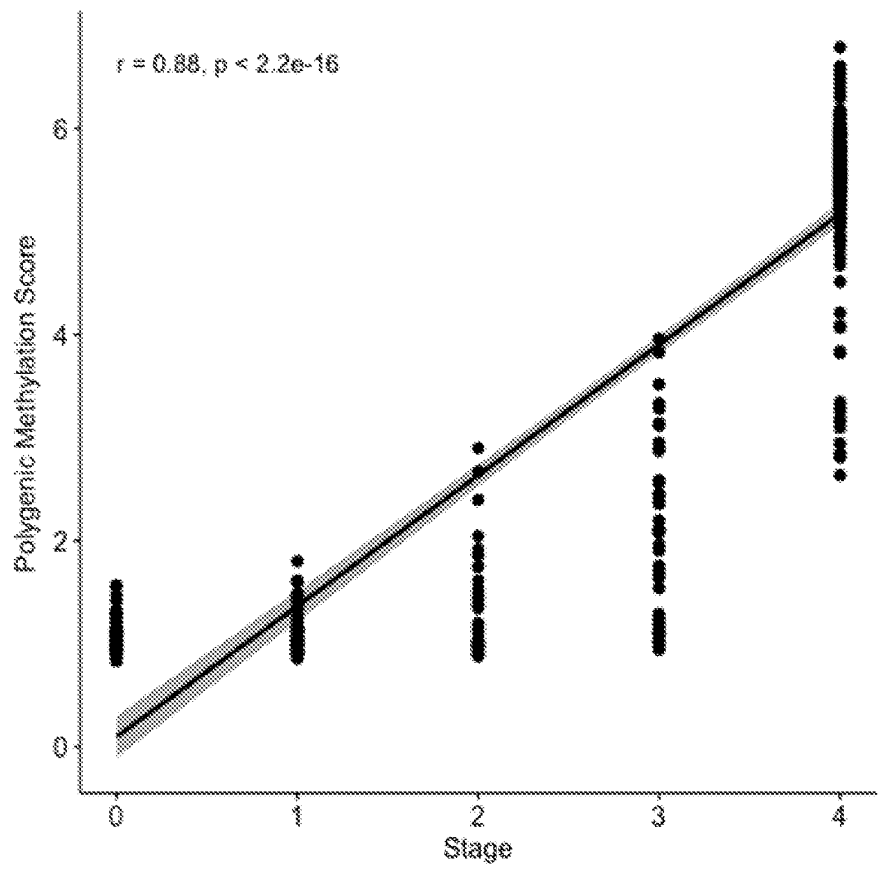


FIGURE 6

A

Pearson's product-moment correlation

```
data: mydata$Stage and mydata$Polygenic_Score
t = 37.422, df = 496, p-value < 2.2e-16
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.8344742 0.8807004
sample estimates:
      cor
0.8593325

> res$p.value
[1] 1.486279e-146
> res$estimate
      cor
0.8593325
```

B

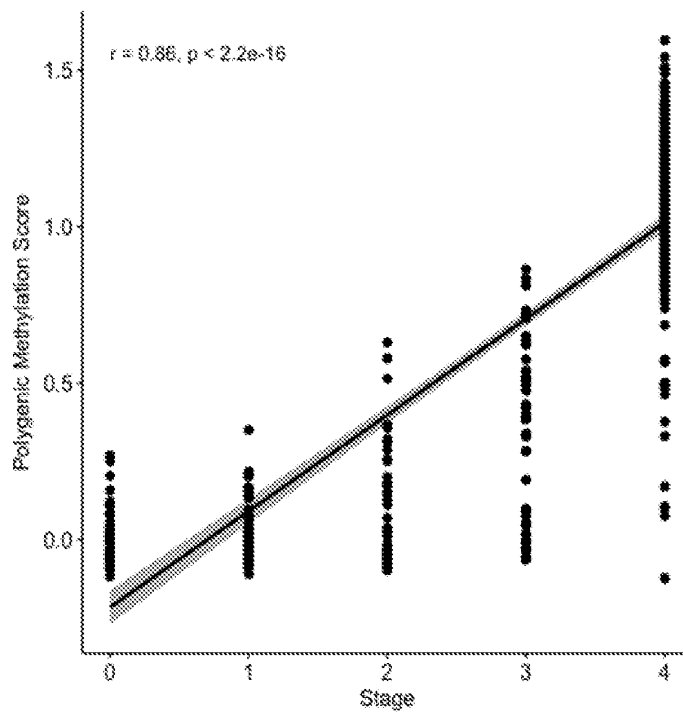


FIGURE 7

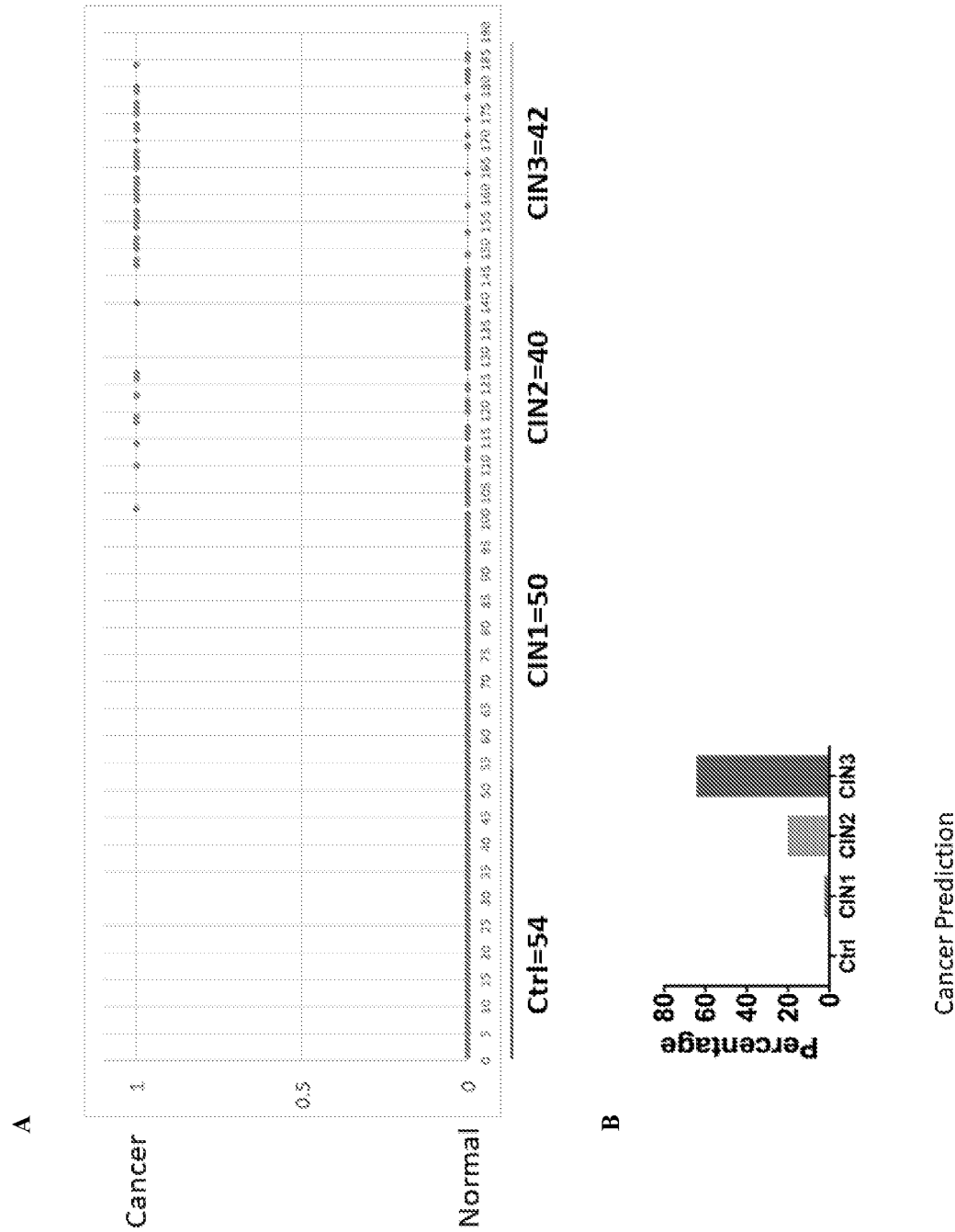


FIGURE 8