

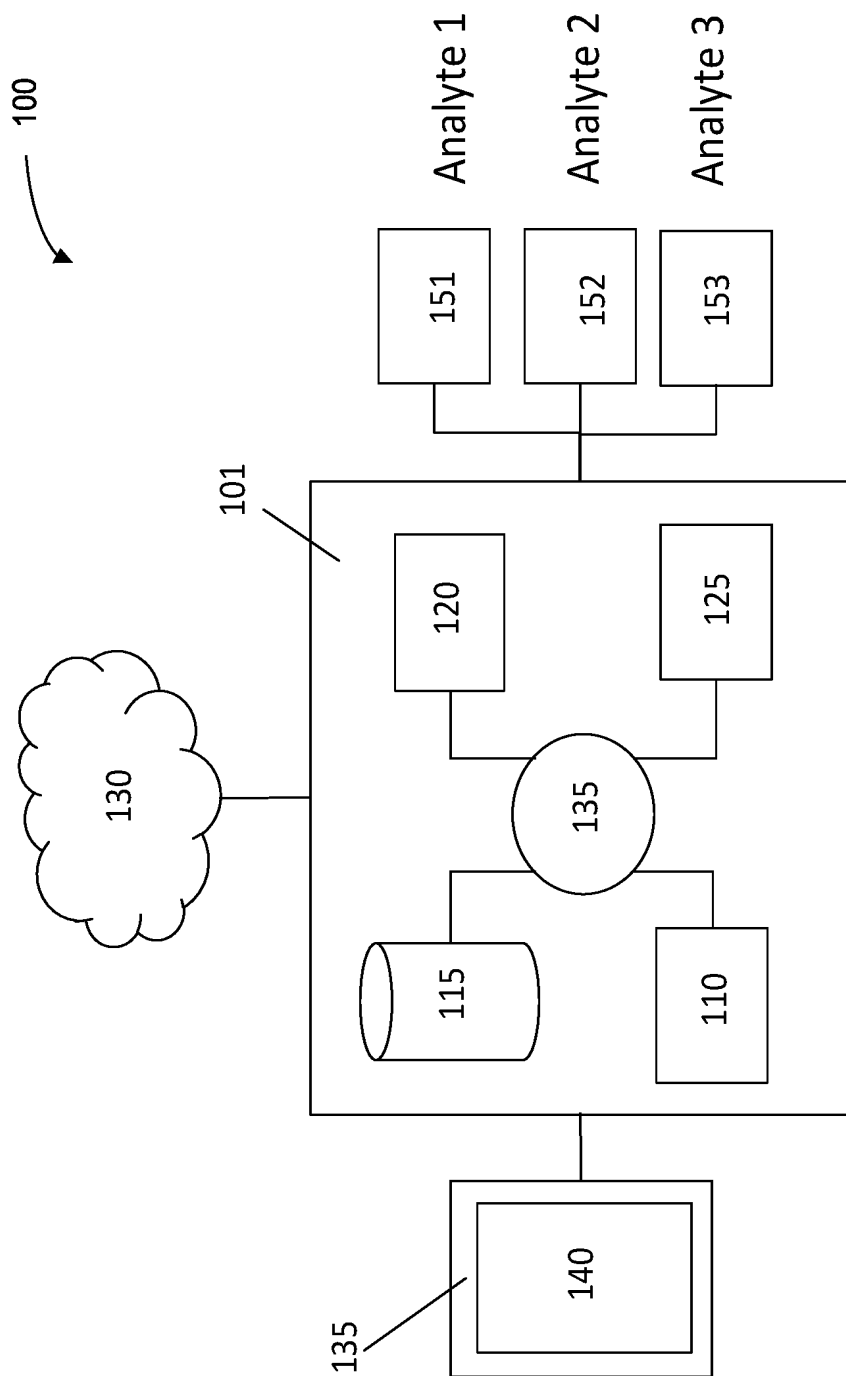
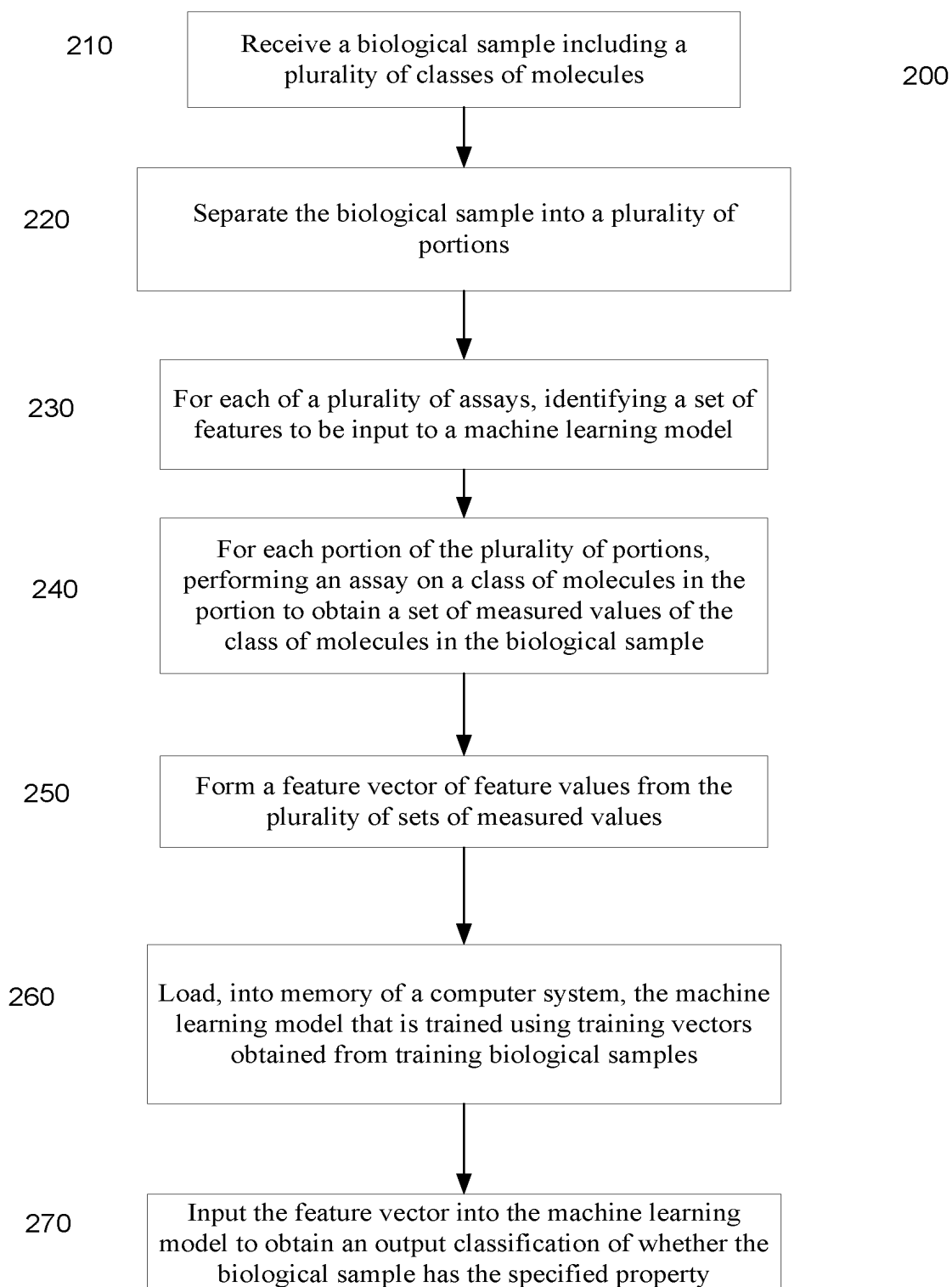


FIG. 1

**FIG. 2**

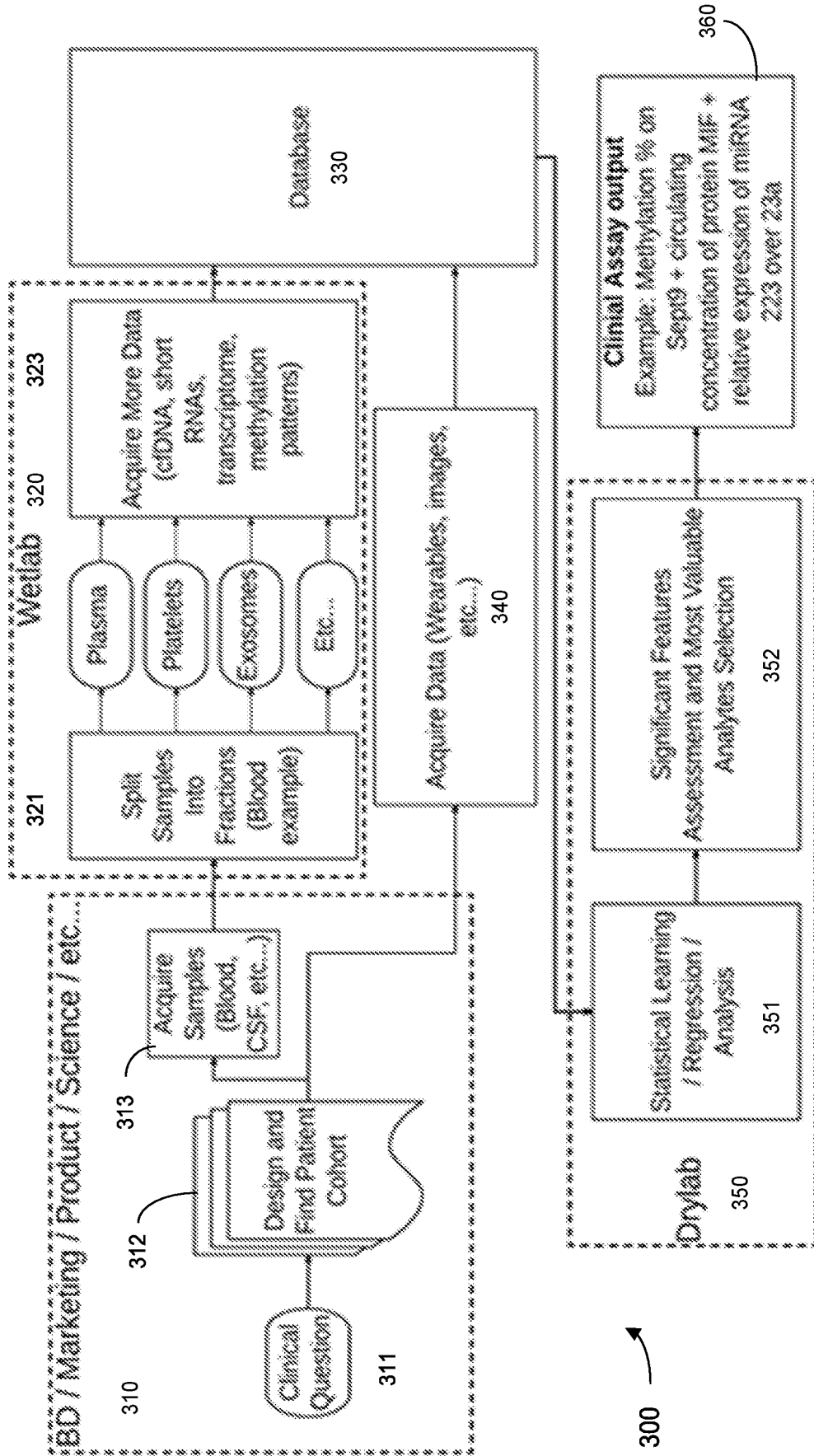


FIG. 3

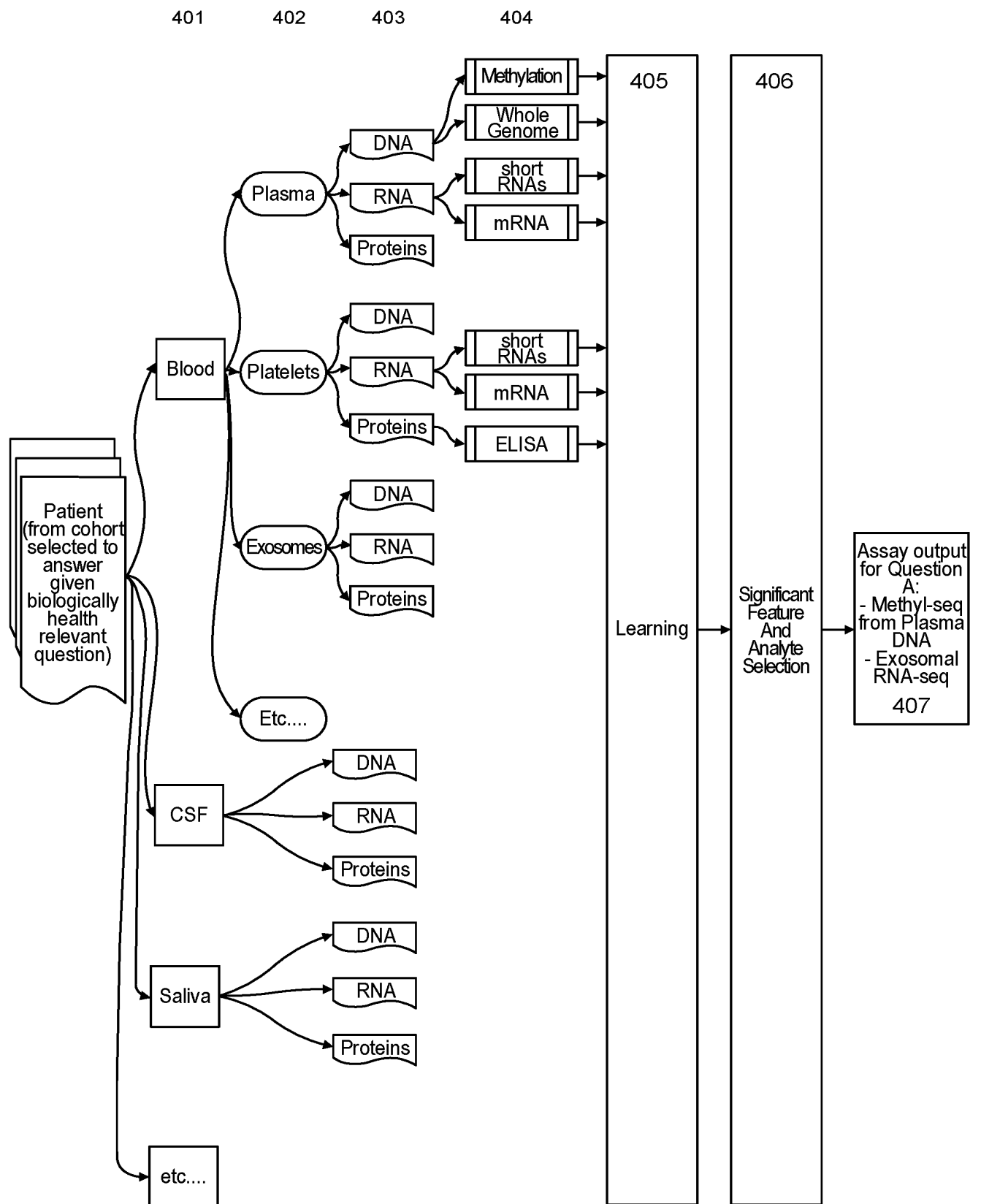
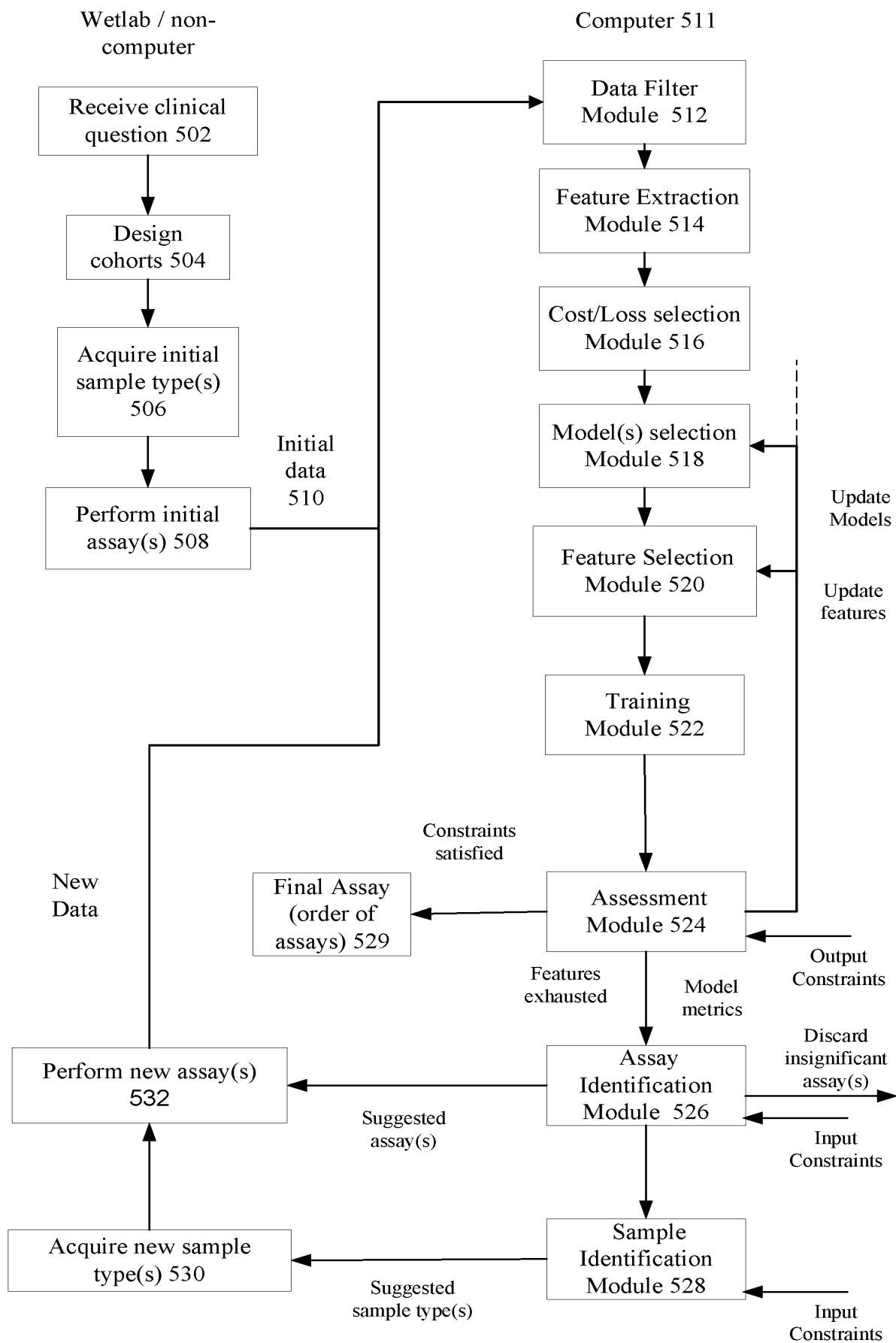


FIG. 4

**FIG. 5**

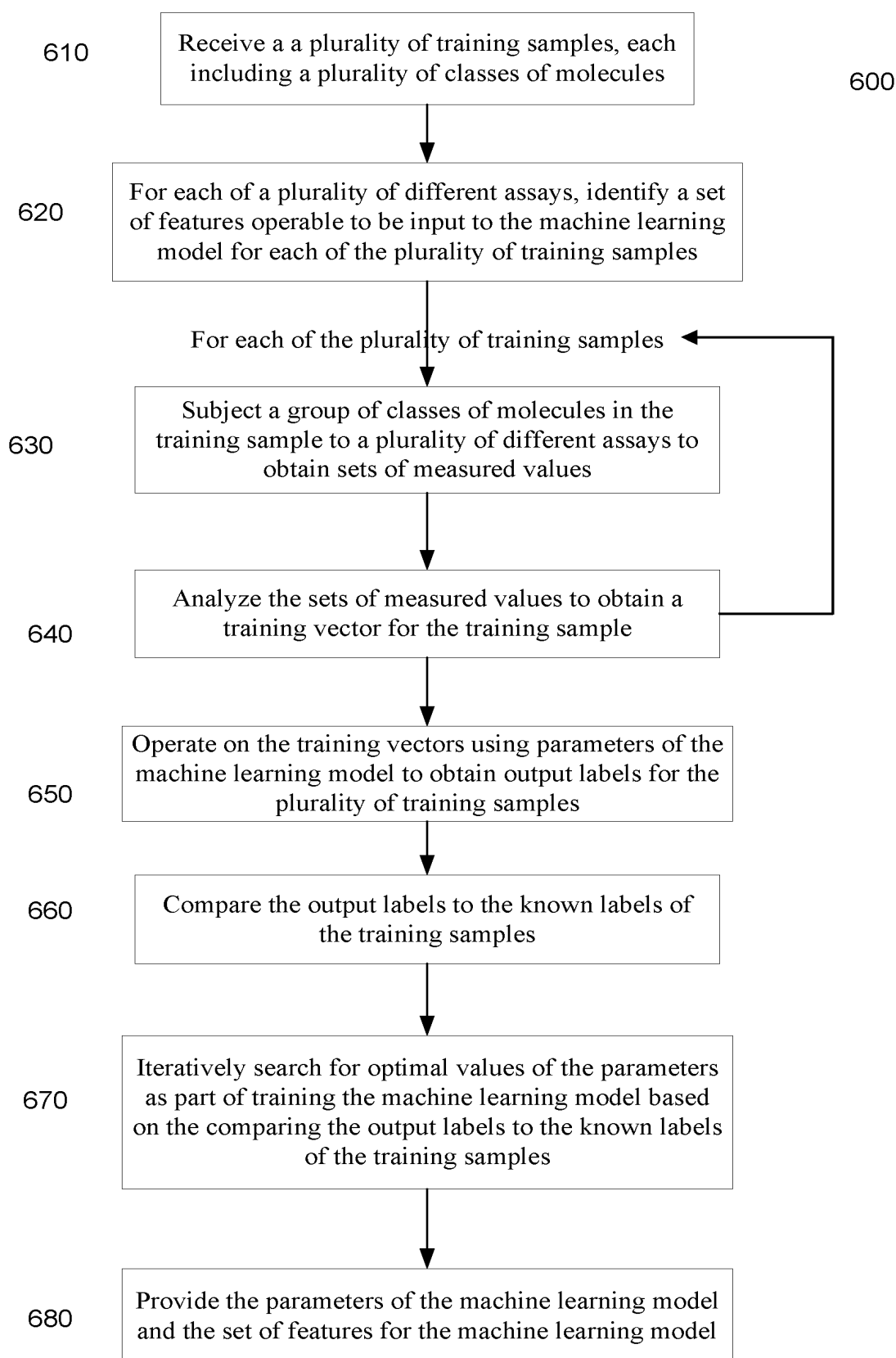
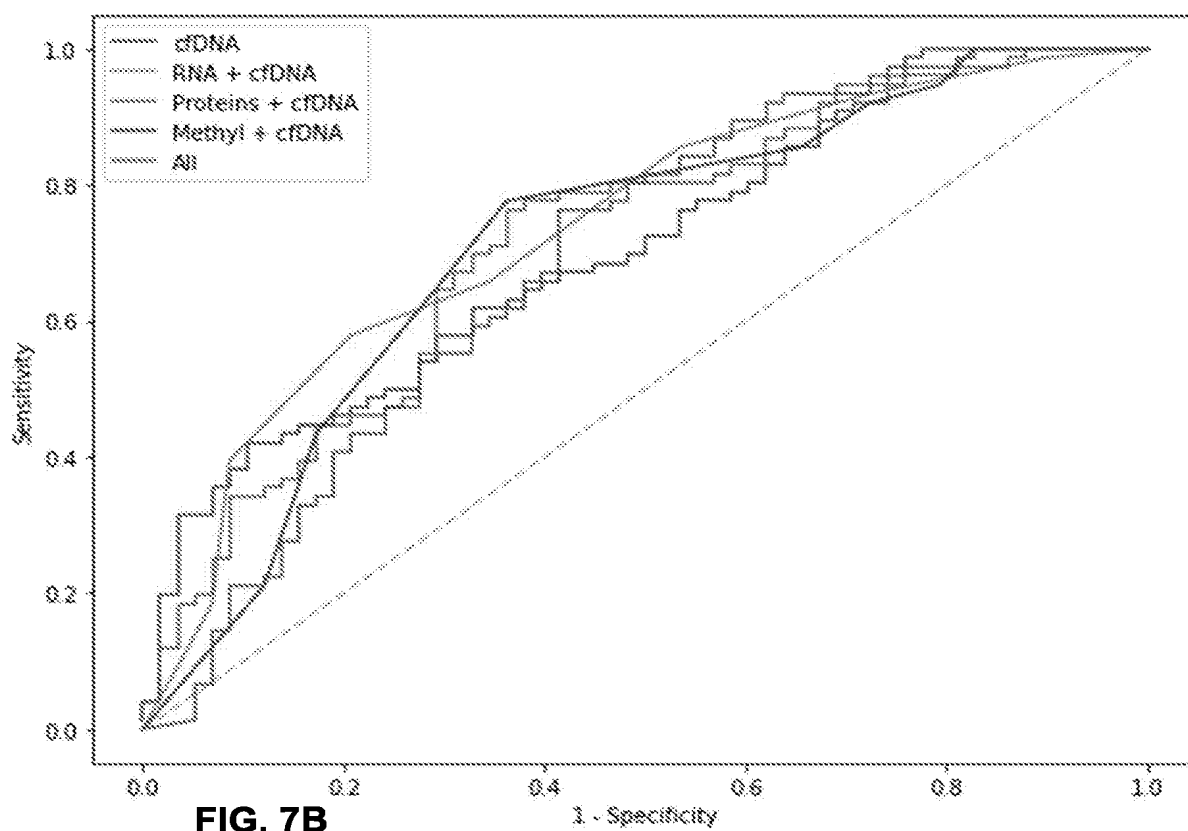
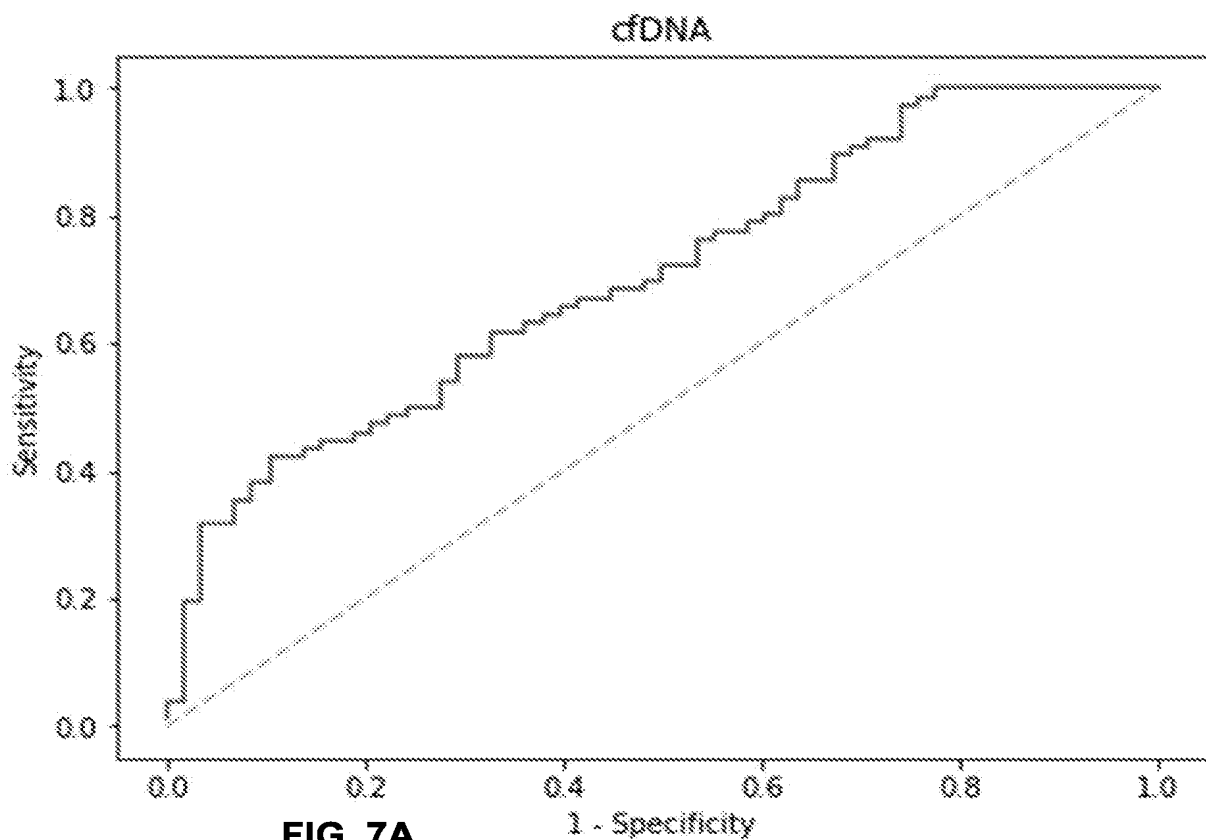


FIG. 6

Classification performance



5261

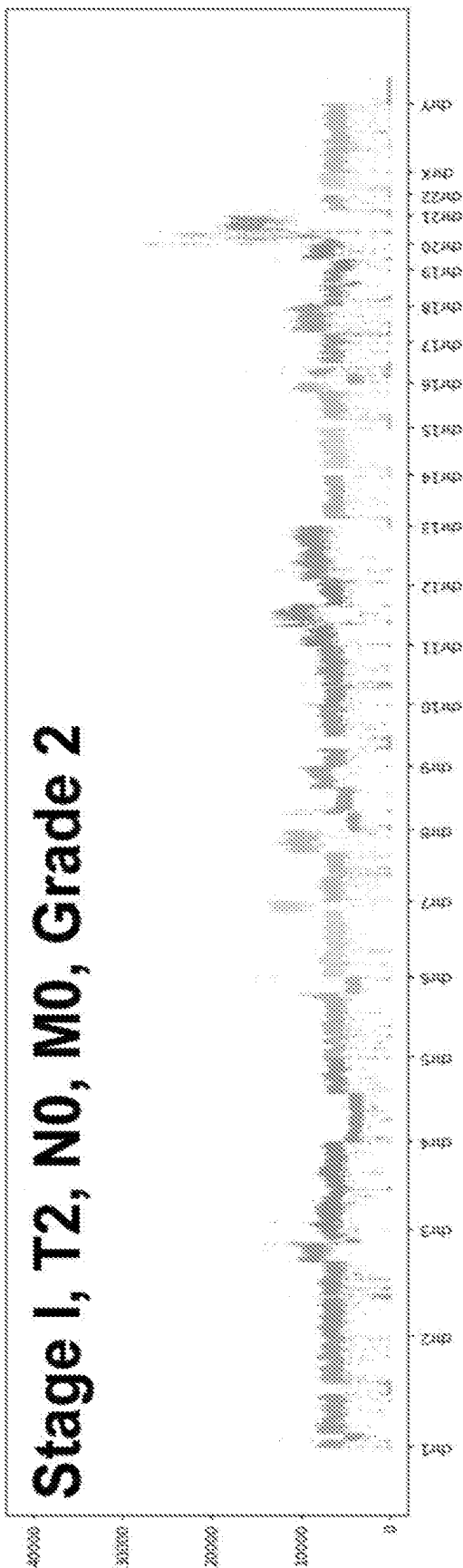


FIG. 8A

5262

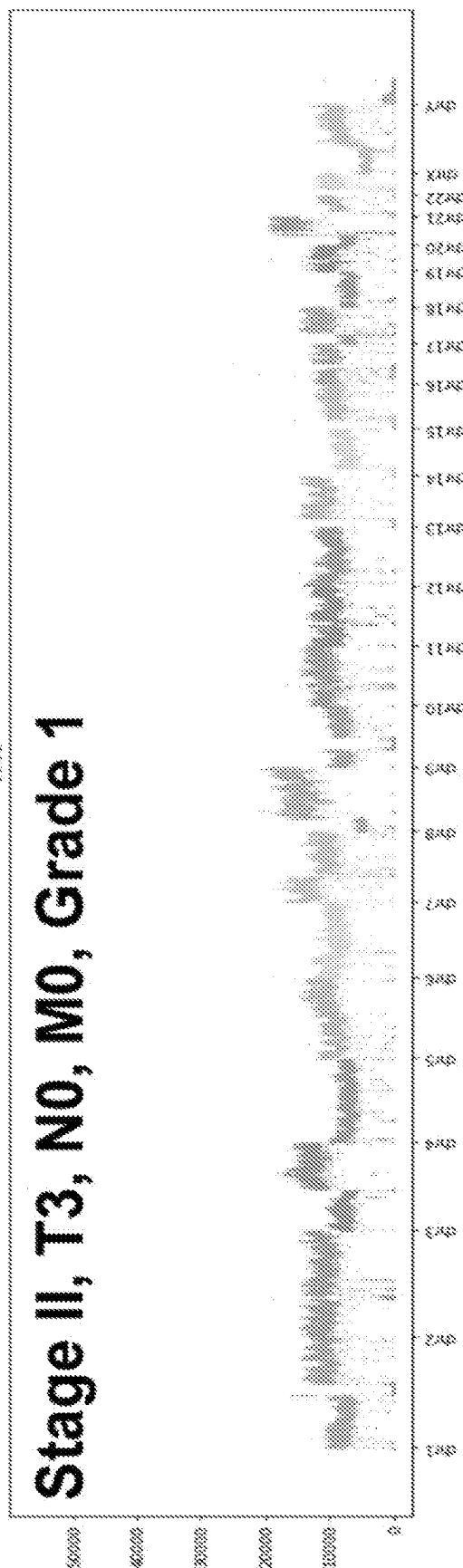


FIG. 8B

9121

Stage II, T3, N0, M0, Grade 2

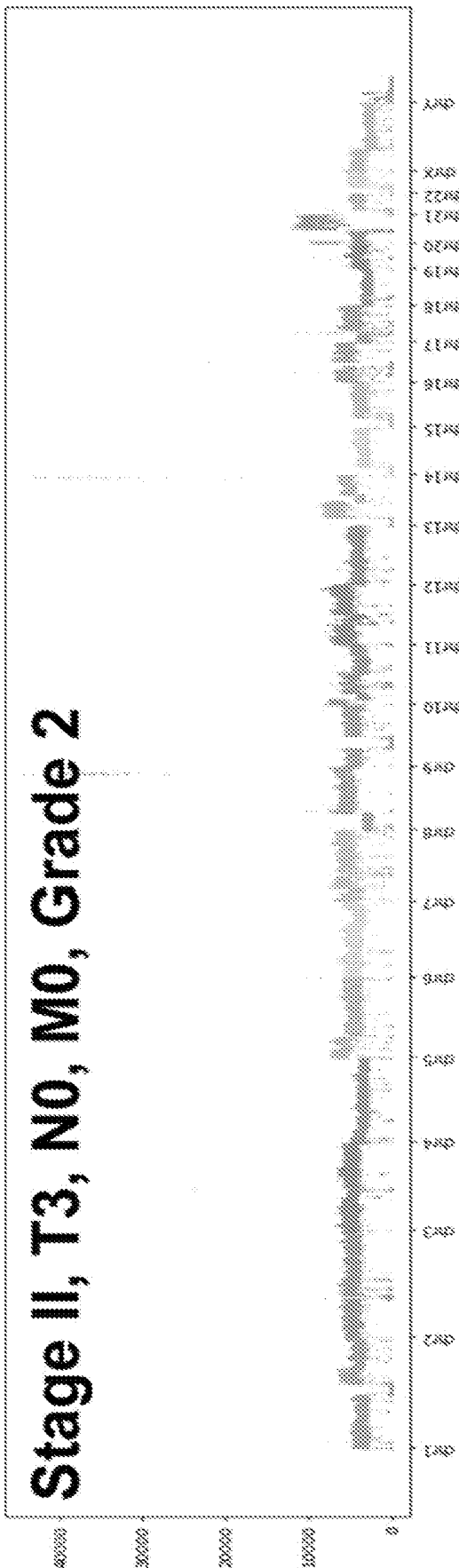


FIG. 8C

7034

Stage III, T3, N2, M0, Grade 2

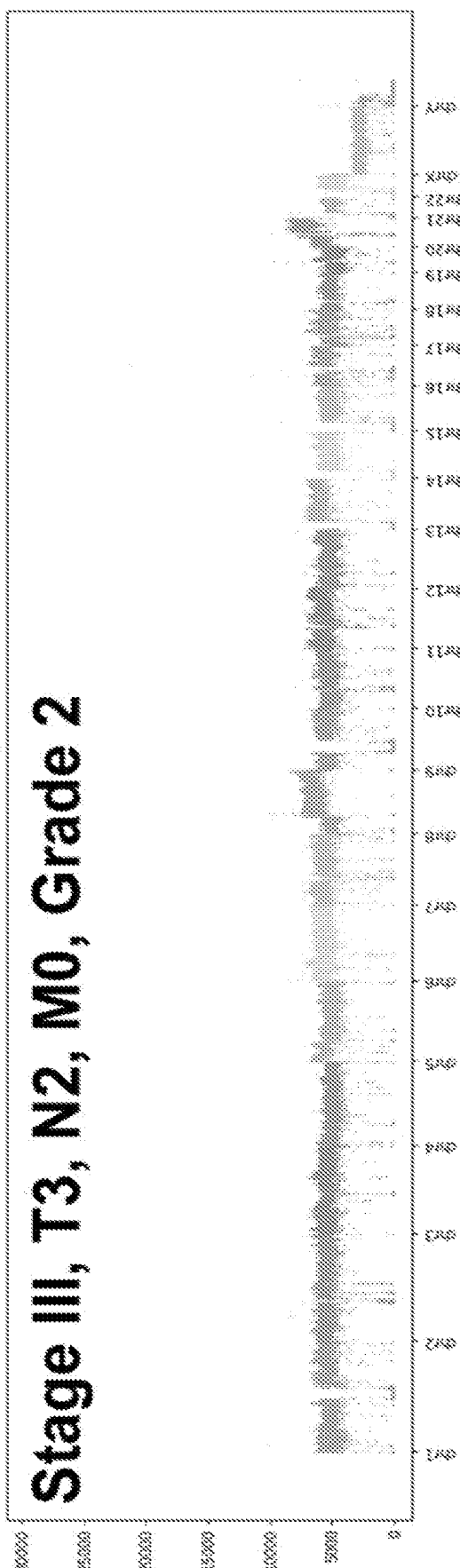


FIG. 8D

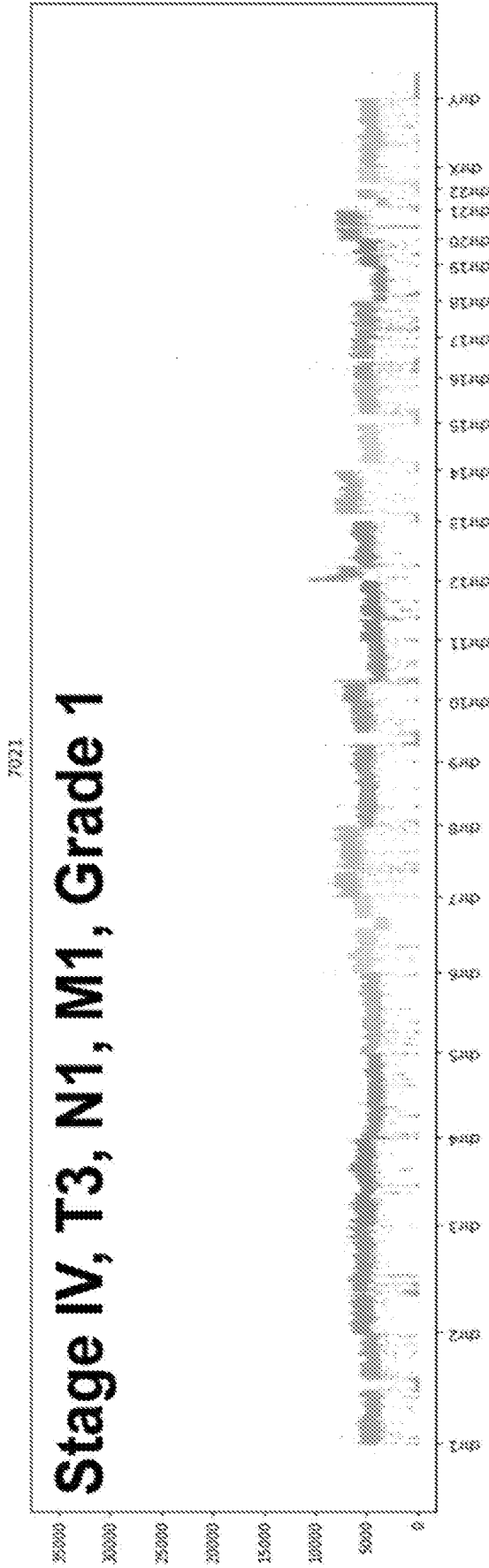


FIG. 8E

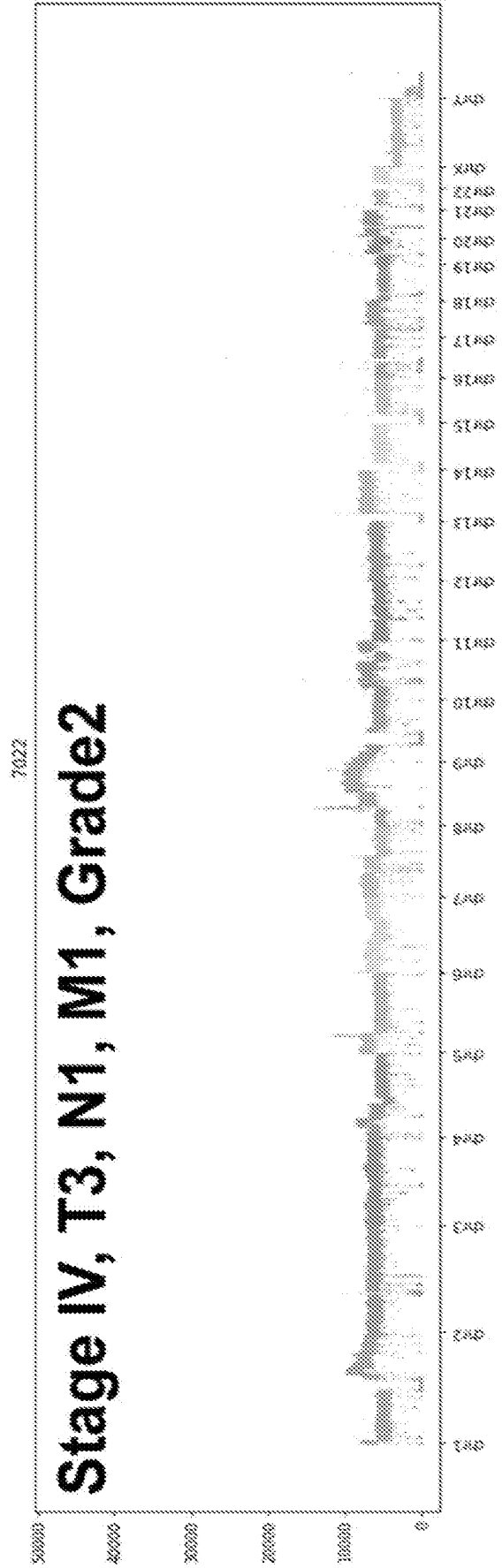


FIG. 8F

7023

Stage IV, T3, N1, M1, Grade 2

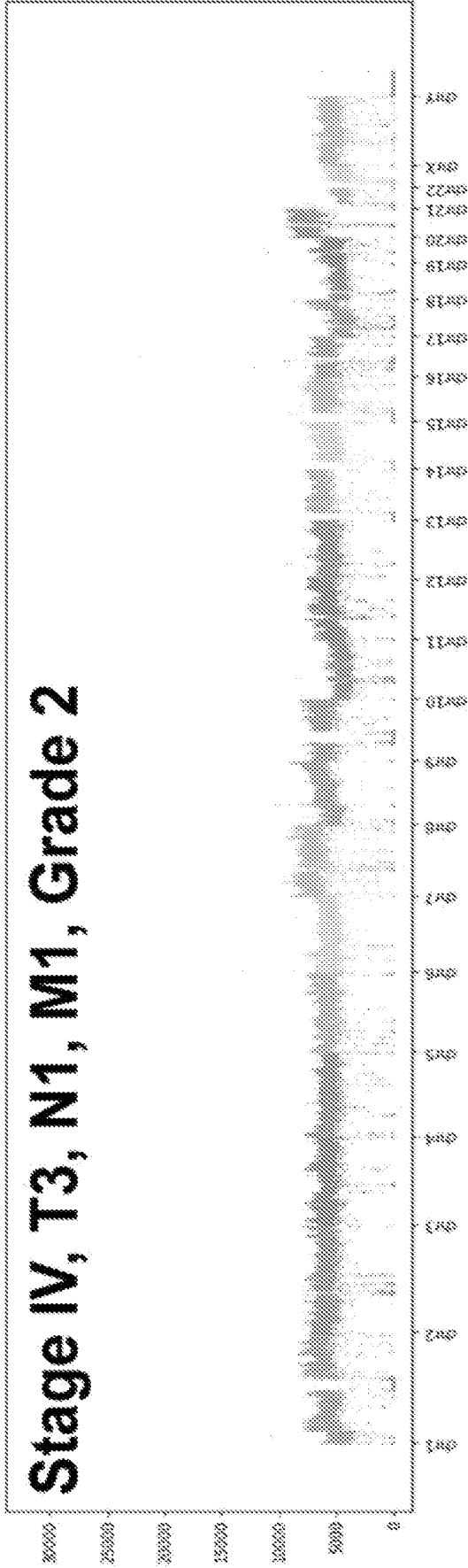


FIG. 8G

7024

Stage IV, T3, Nx, M1

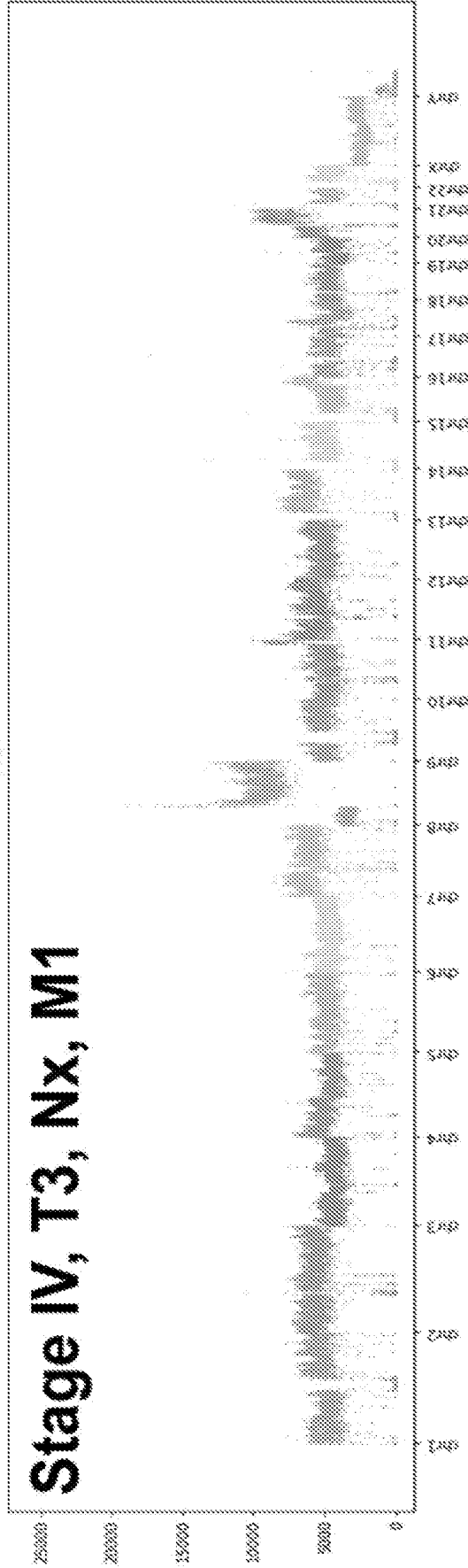


FIG. 8H

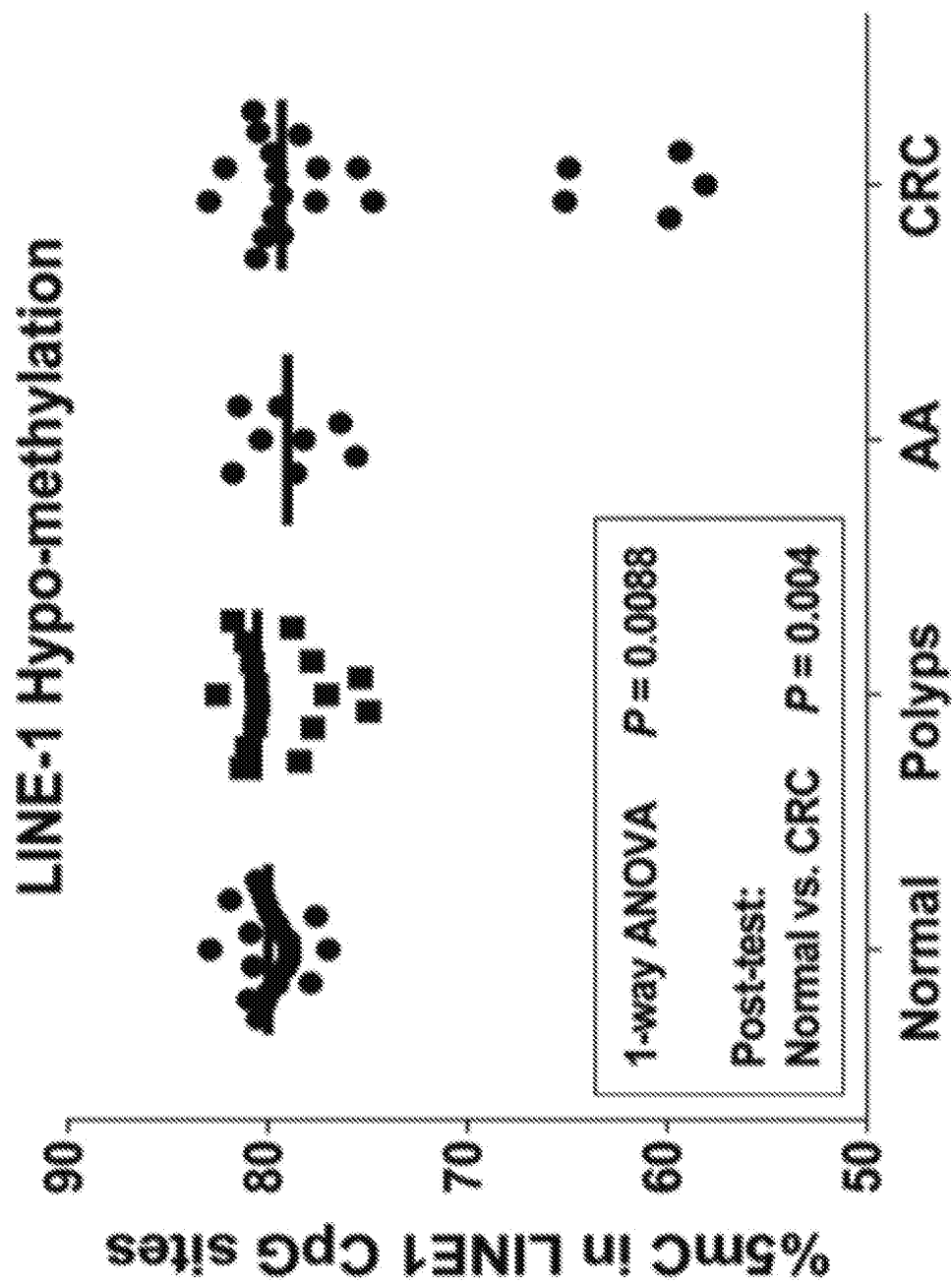


FIG. 9

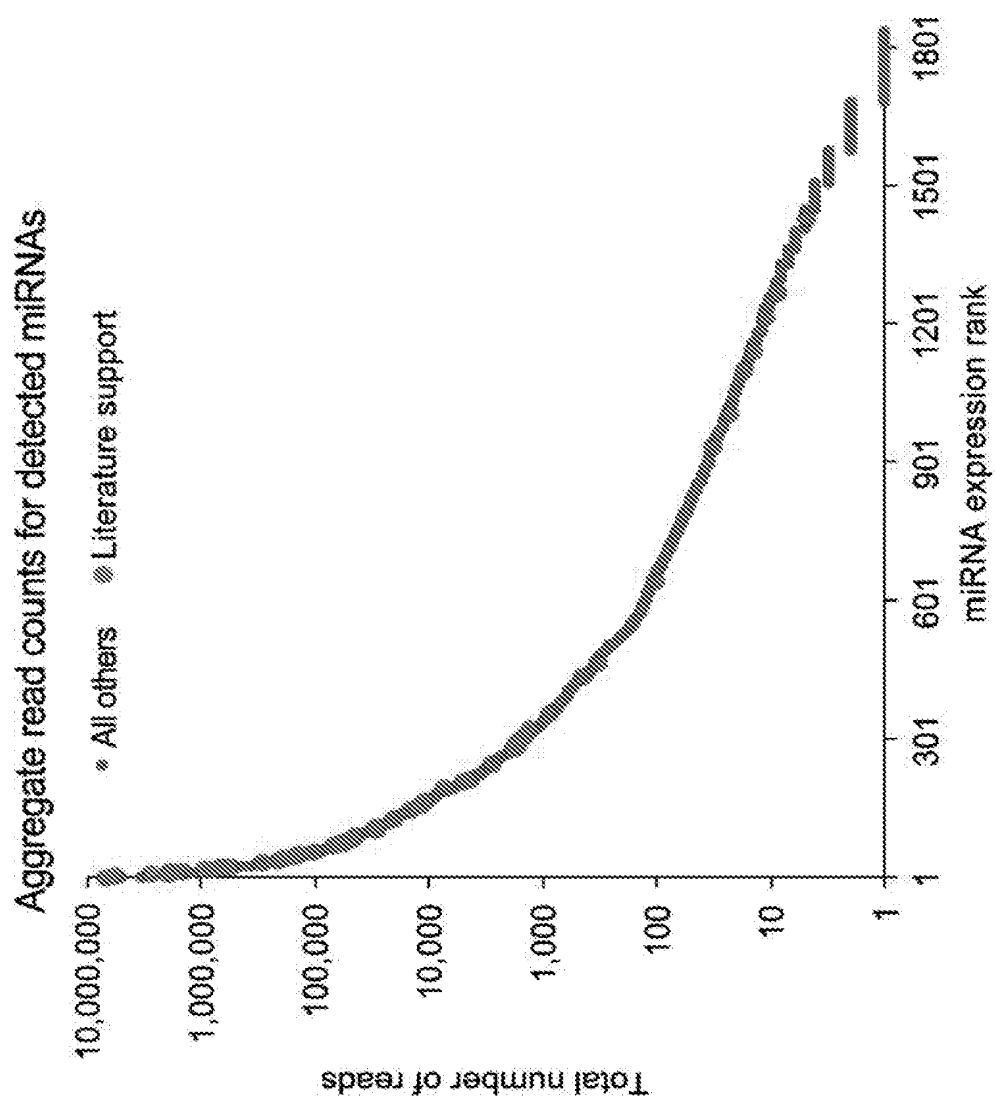


FIG. 10

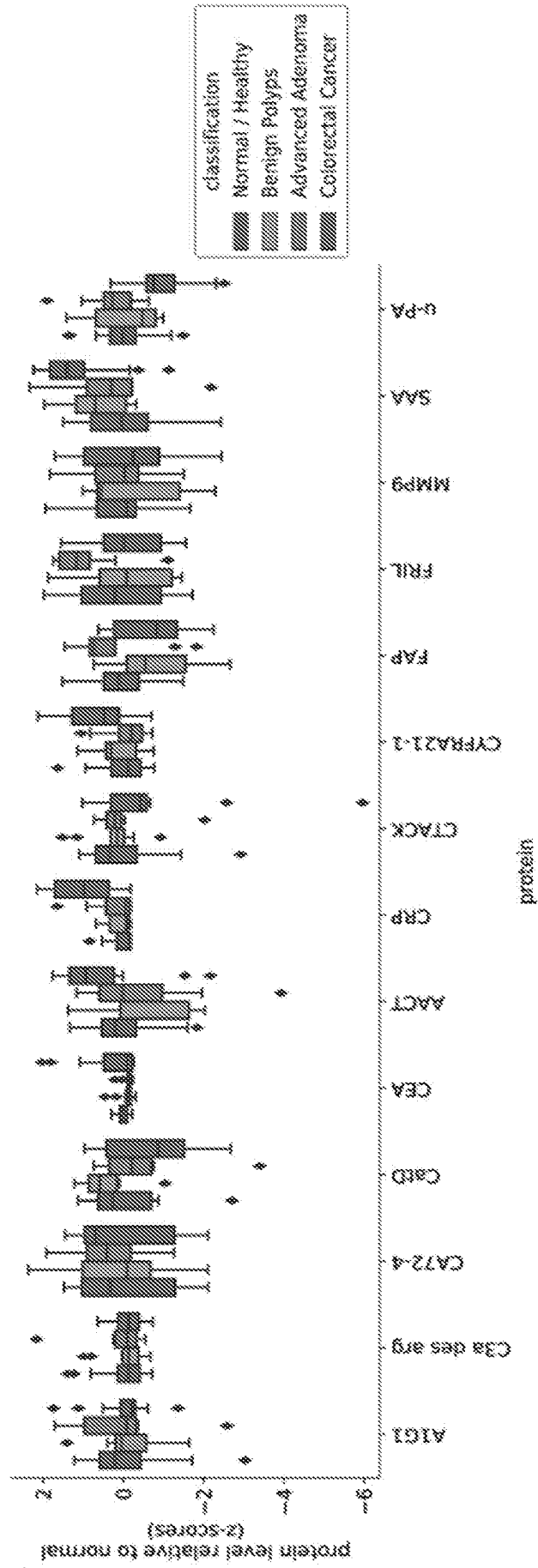
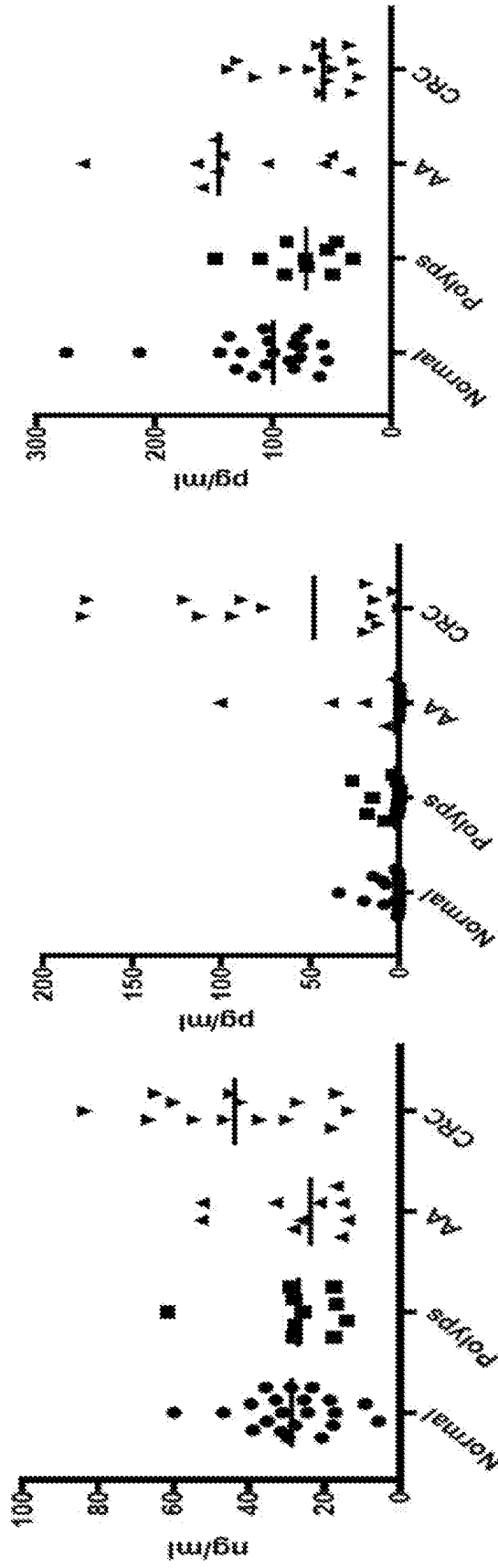


FIG. 11A

AACT

CRP

FAP



1-way ANOVA $P=0.024$

1-way ANOVA $P<0.0001$

1-way ANOVA $P=0.014$

Post-test:

Post-test:

Post-test:

Normal vs. CRC adj. $P=0.034$

Normal vs. CRC adj. $P<0.0001$

AA vs. CRC adj. $P=0.020$

AA vs. CRC. adj. $P=0.006$

FIG. 11B

FIG. 11C

FIG. 11D

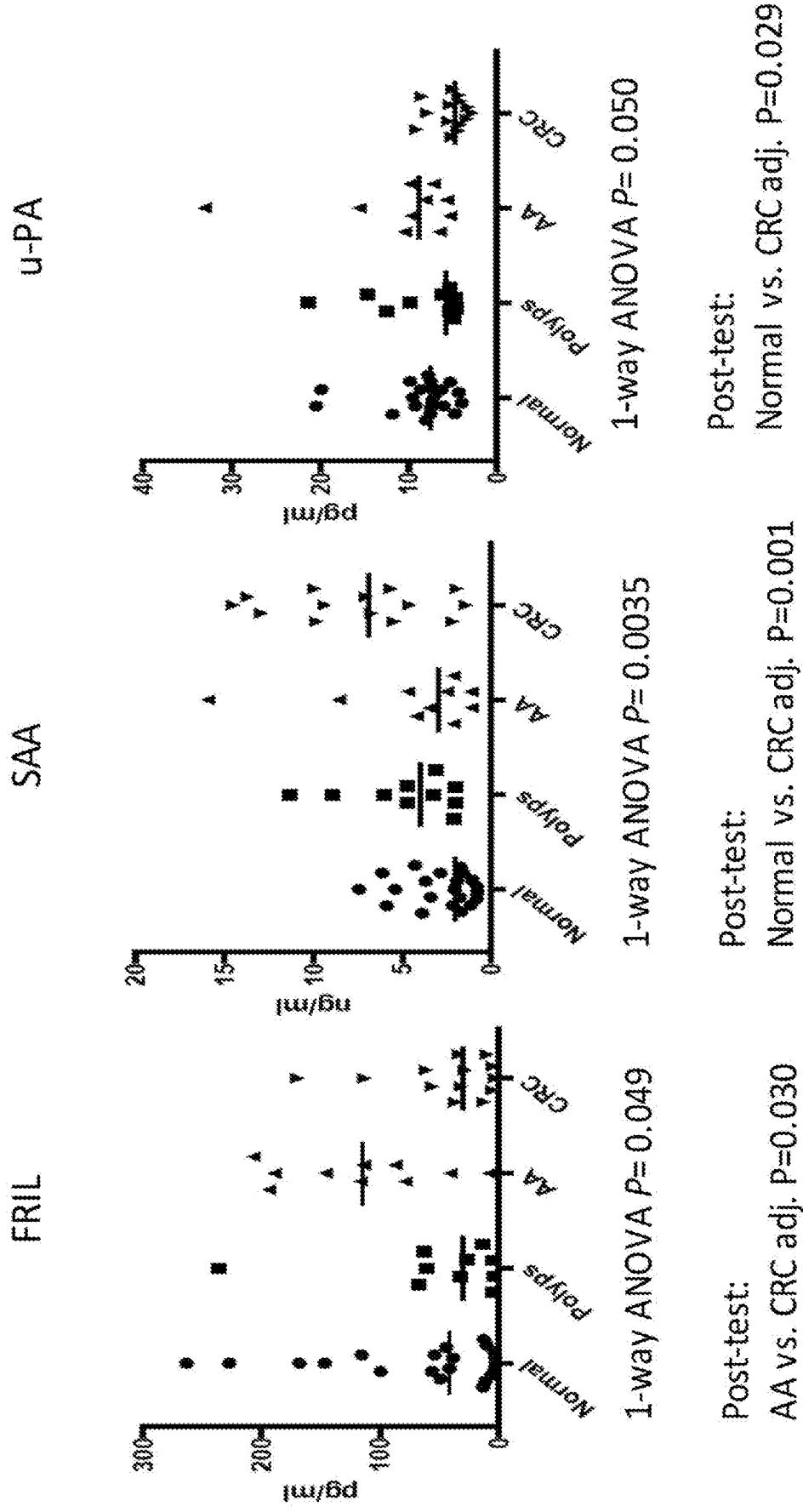


FIG. 11E

FIG. 11F

FIG. 11G

FIG. 12A

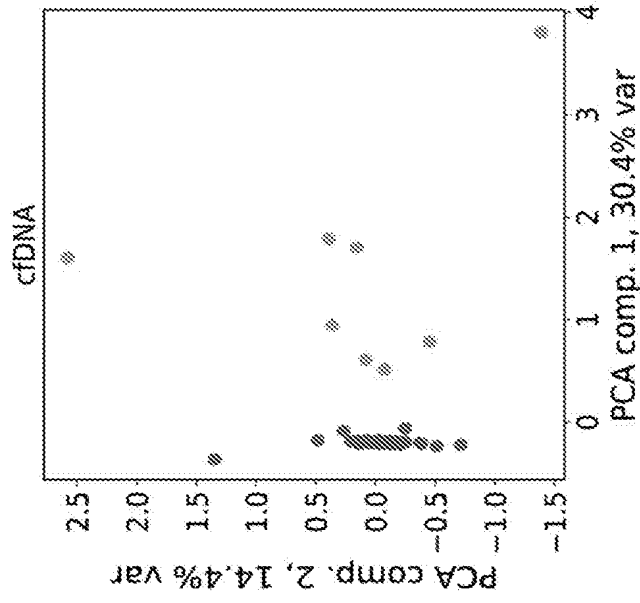


FIG. 12B

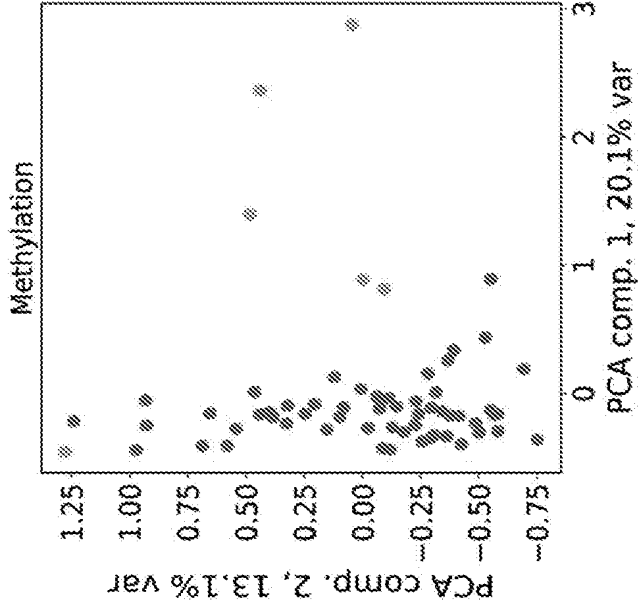


FIG. 12C

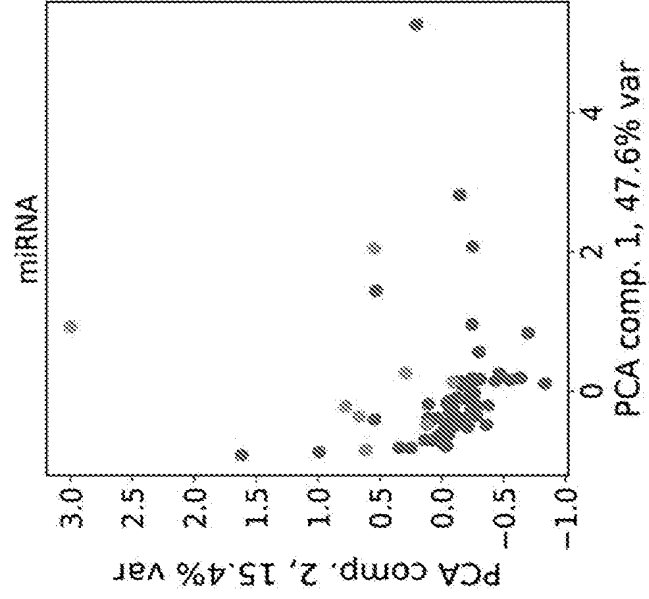


FIG. 12D

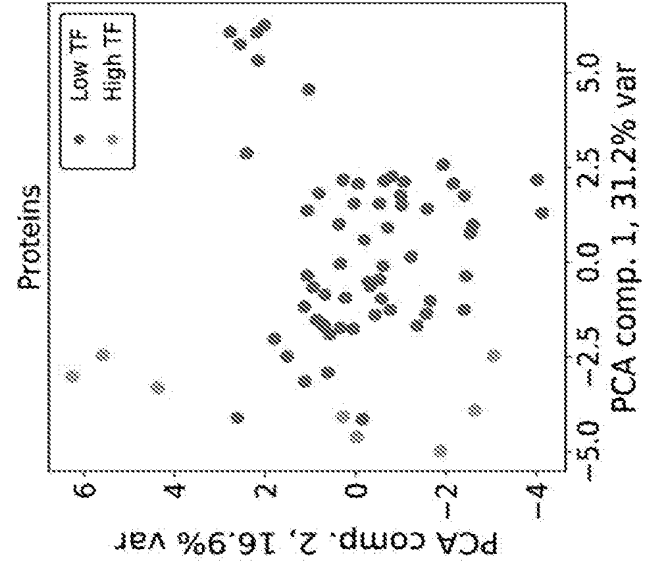


FIG. 12E

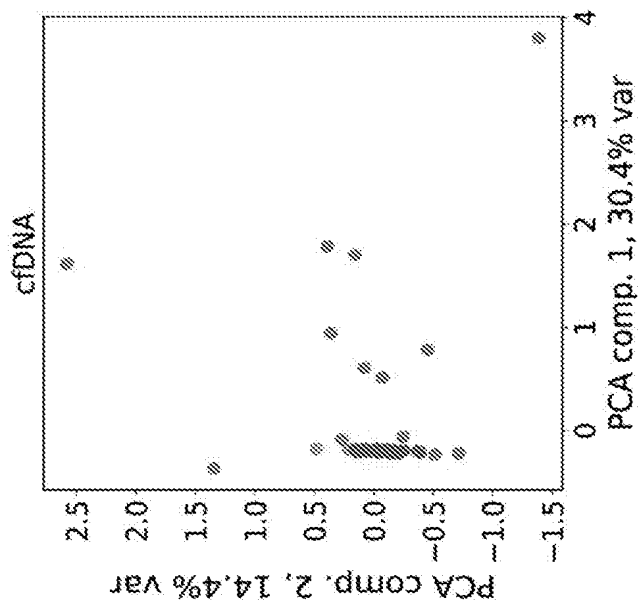


FIG. 12F

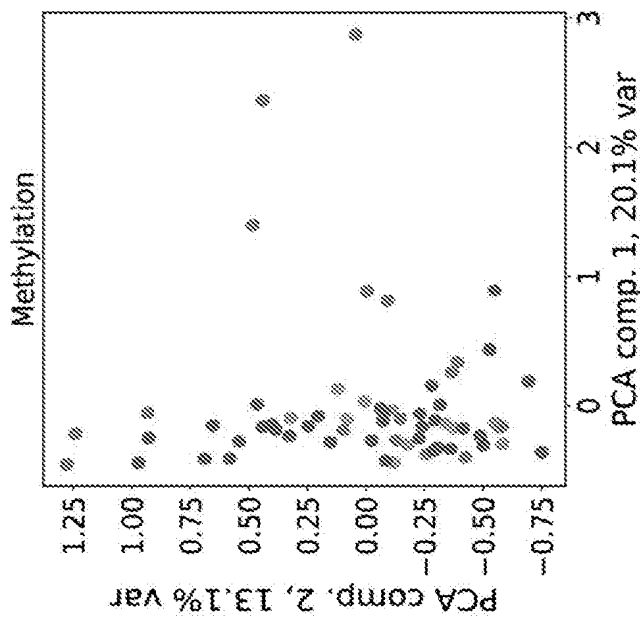


FIG. 12G

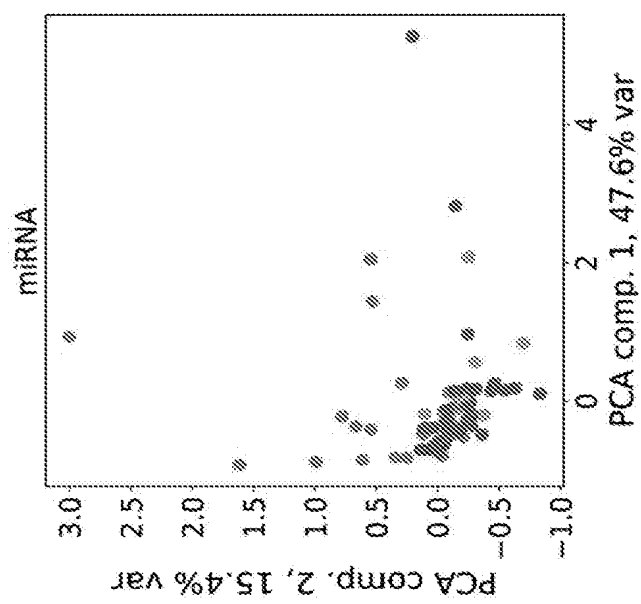
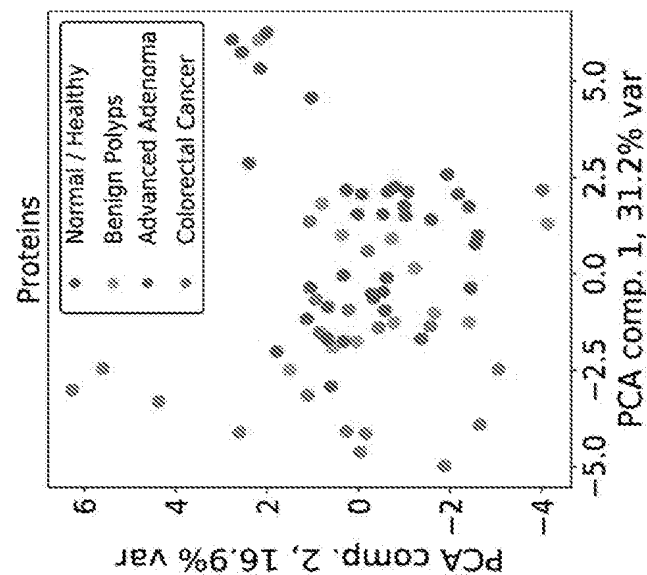


FIG. 12H



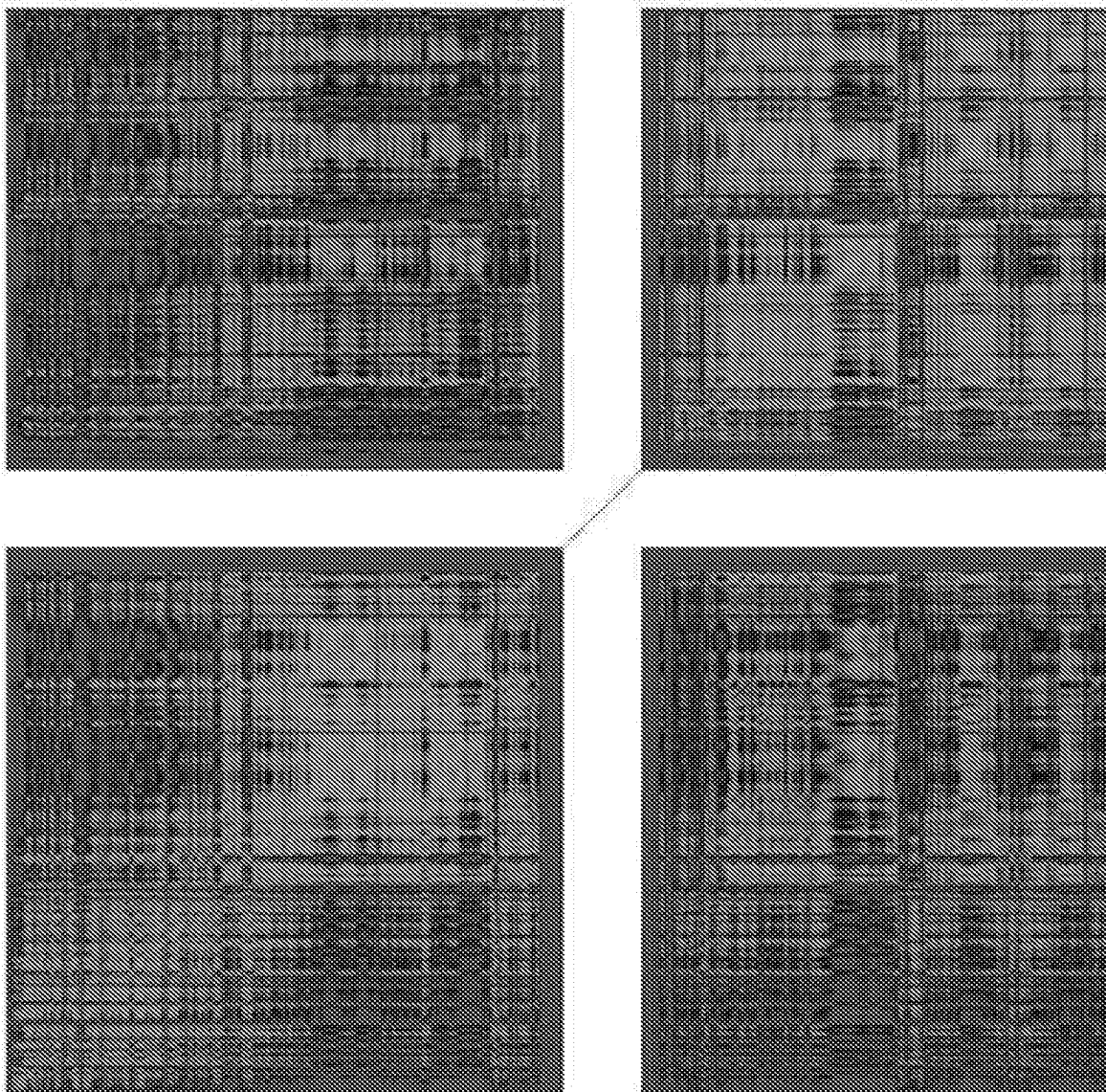


FIG. 13

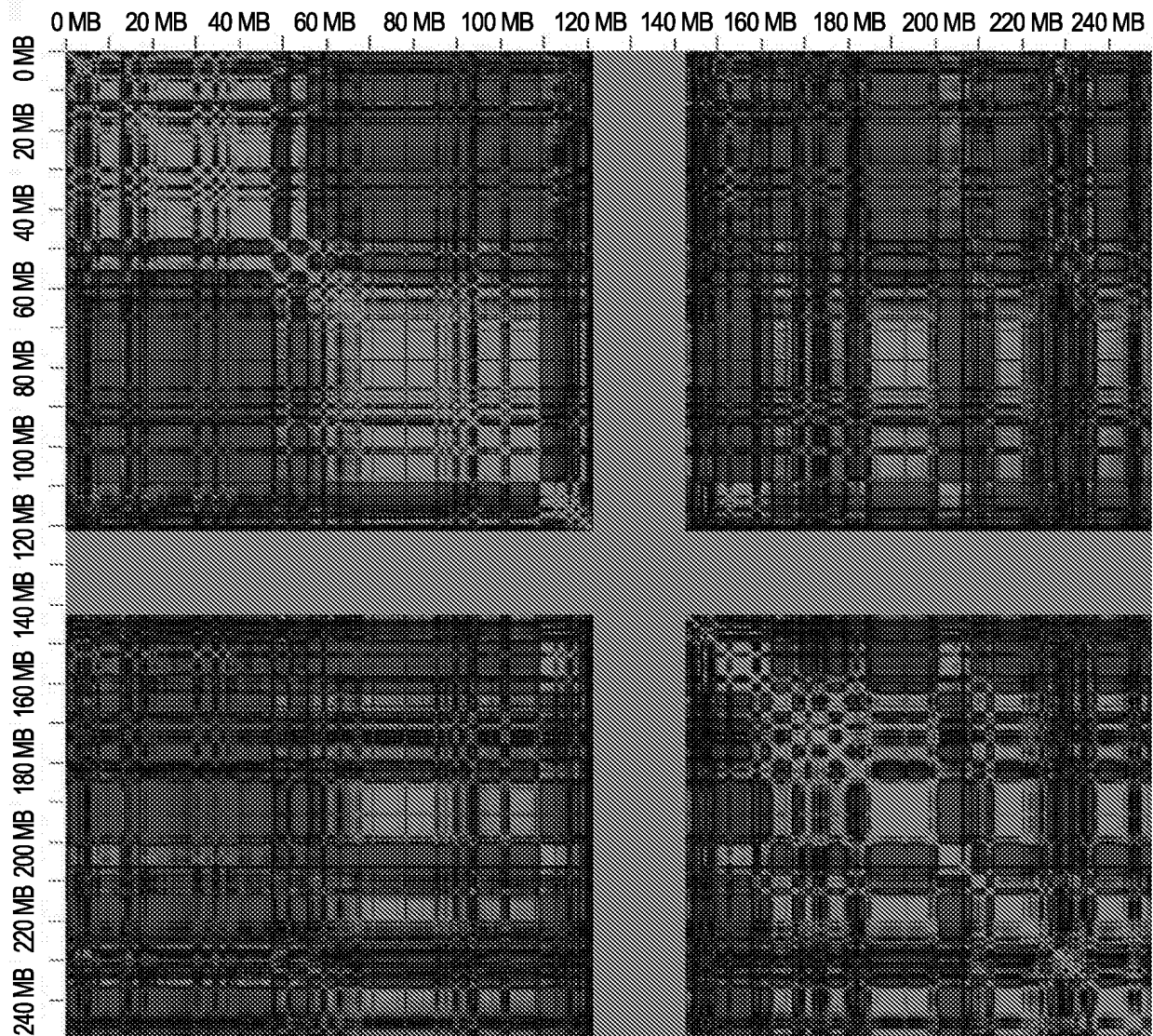


FIG. 14

Pearson Correlation Coefficient

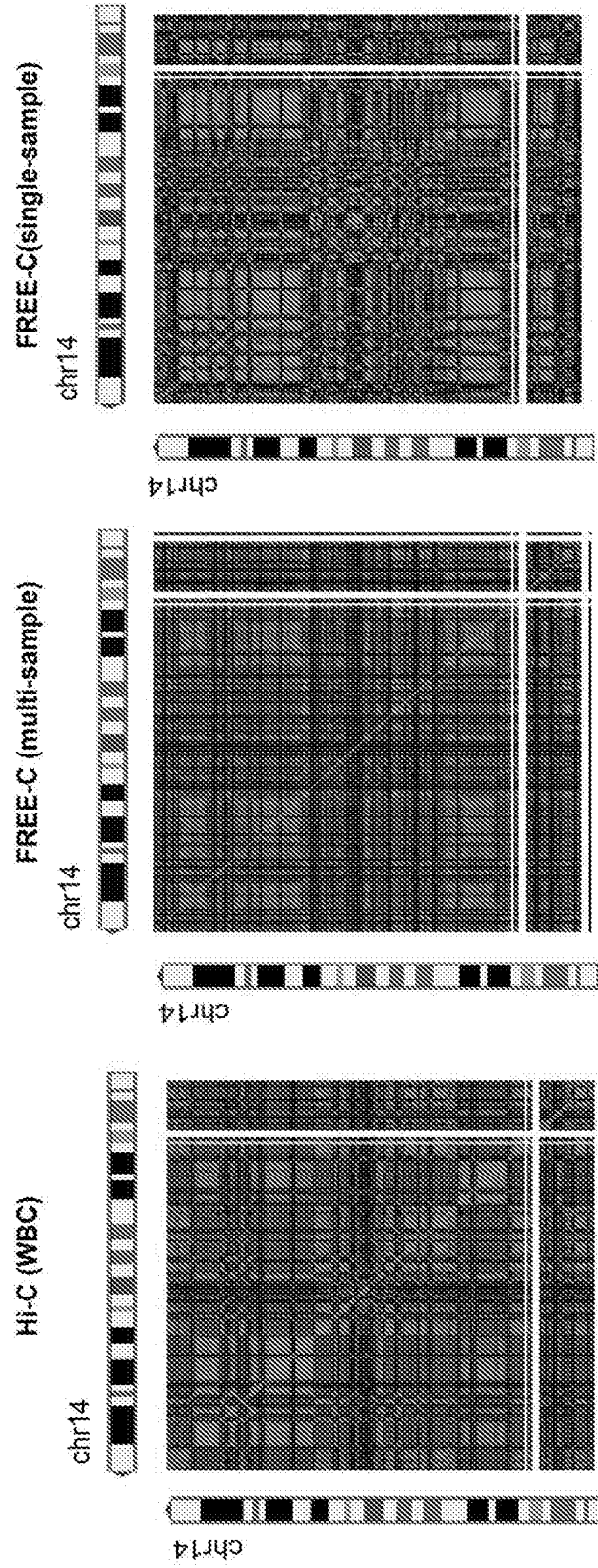


FIG. 15C

FIG. 15B

FIG. 15A

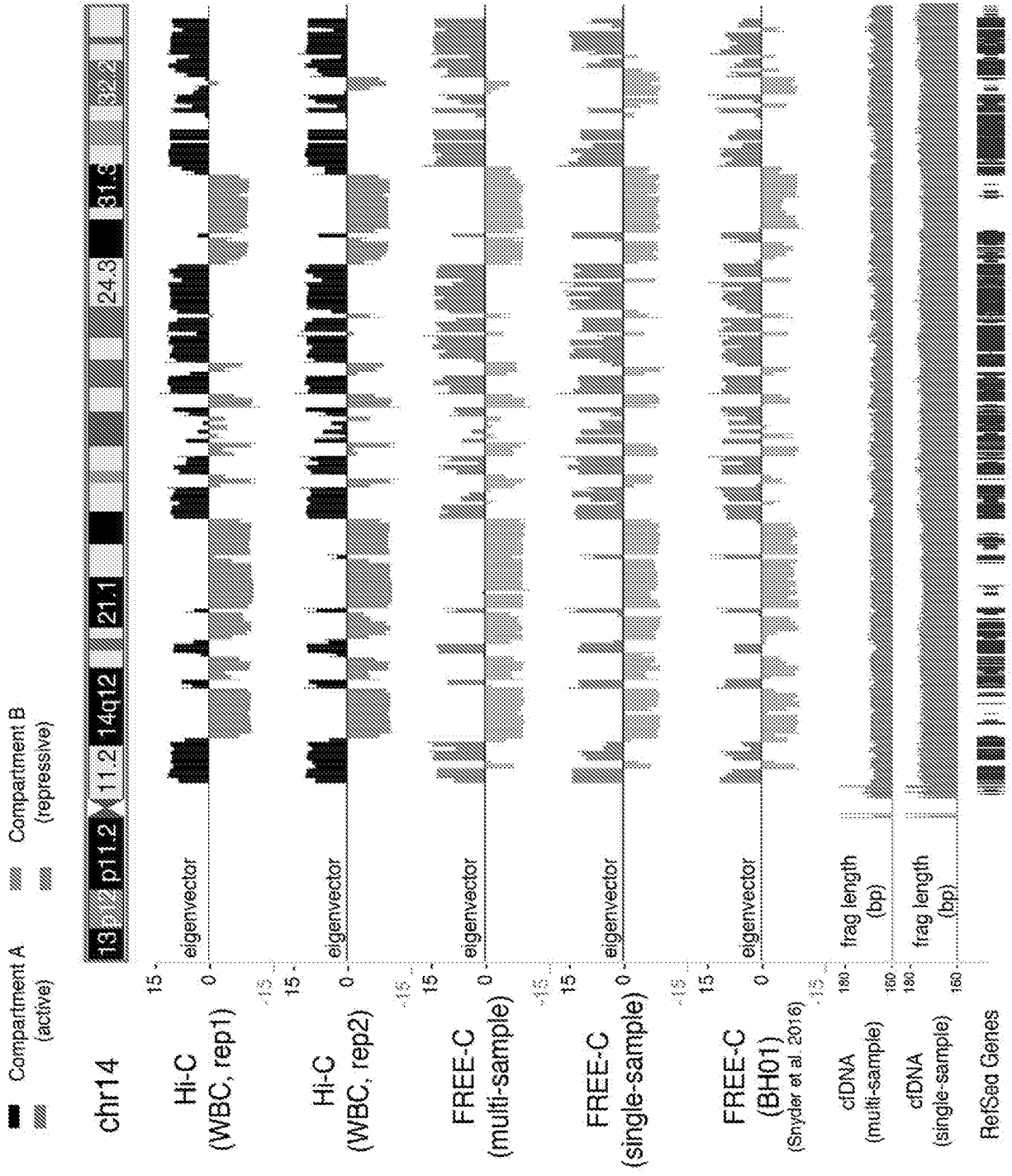
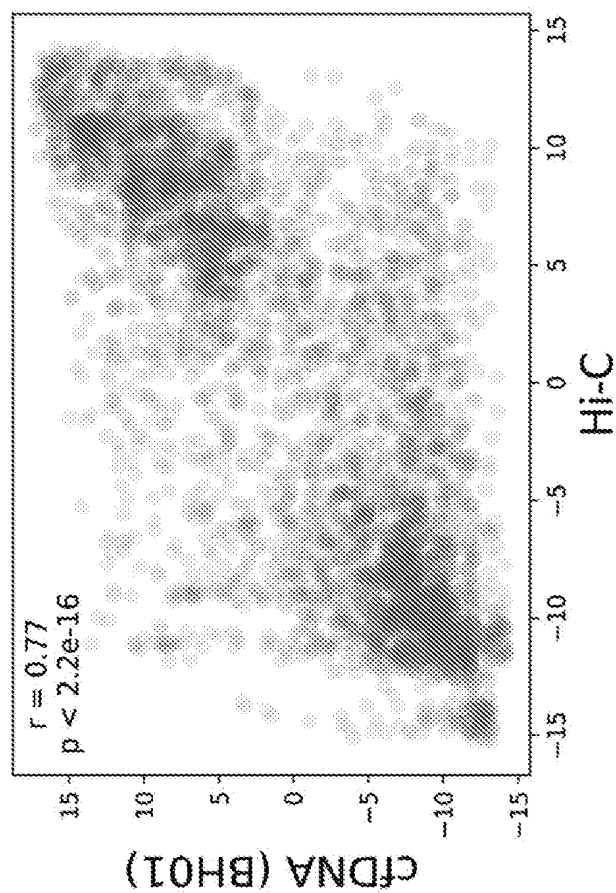


FIG. 15D

single-sample FREE-C vs. Hi-C
(genome wide)



multi-sample FREE-C vs. Hi-C
(genome wide)

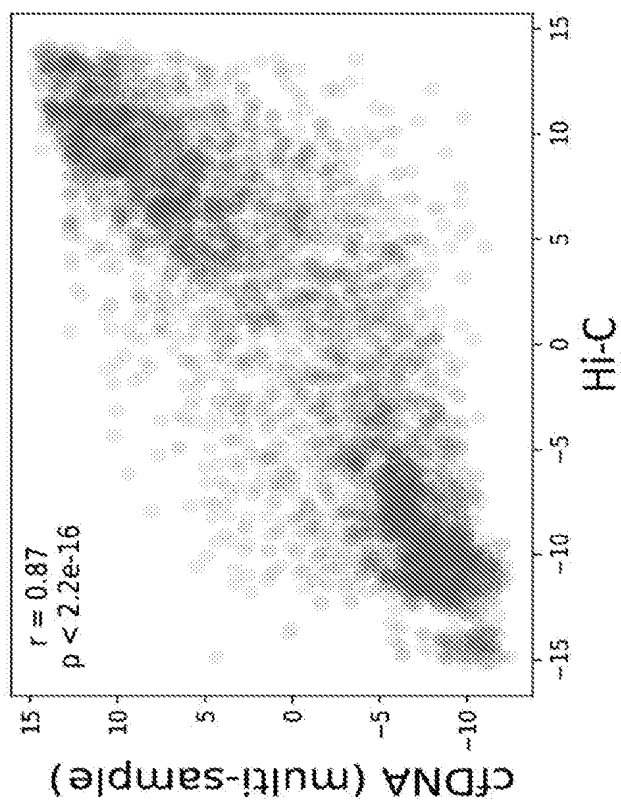
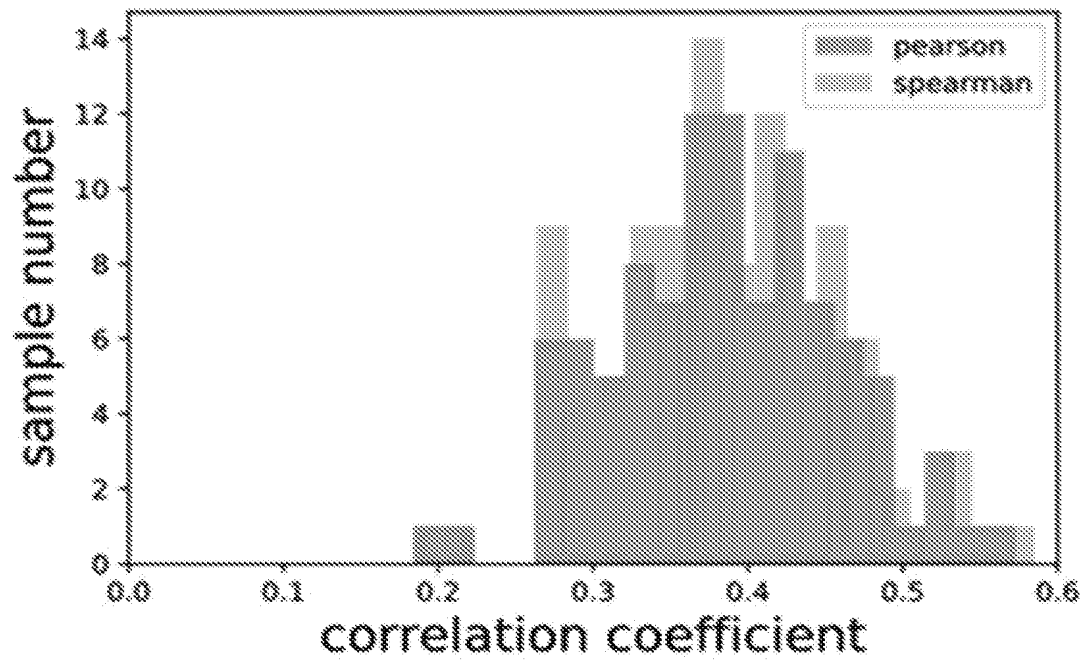
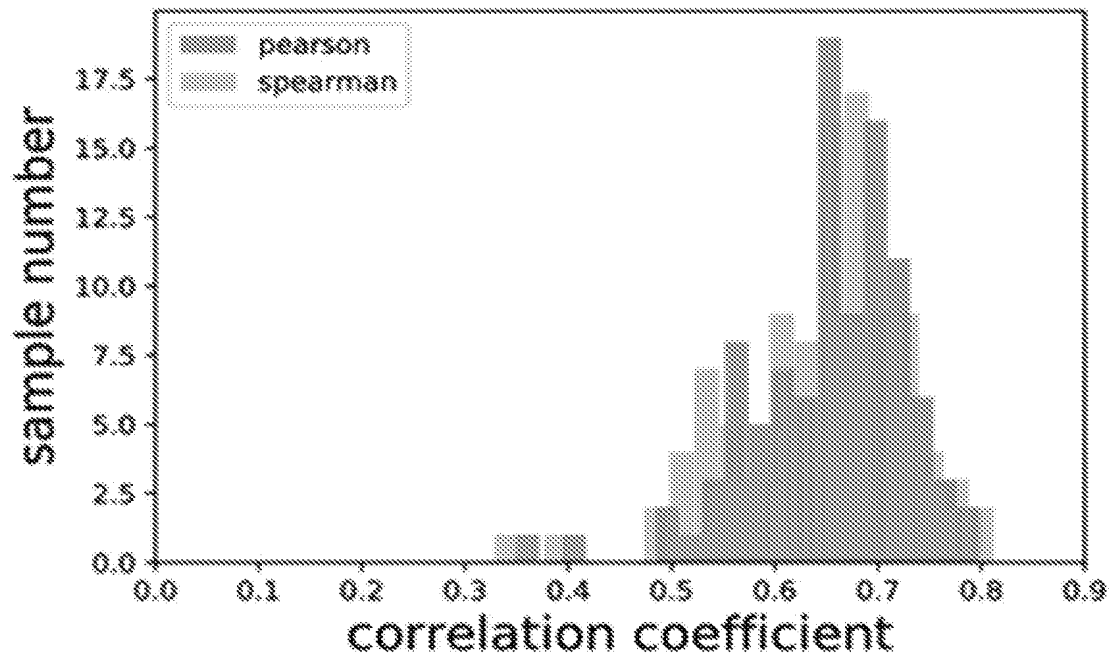


FIG. 15E

FIG. 15F

Pixel level**FIG. 16A****Compartment level****FIG. 16B**

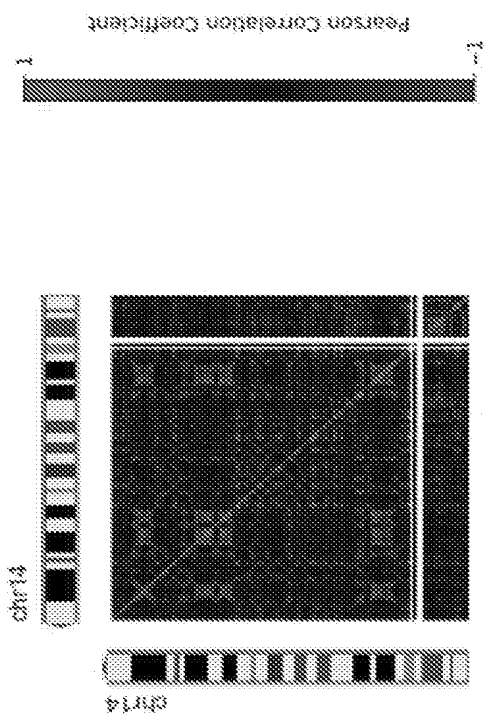


FIG. 17B

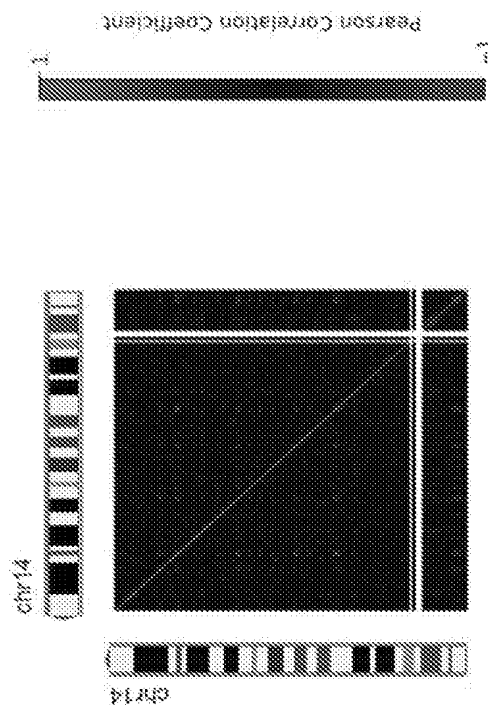


FIG. 17D

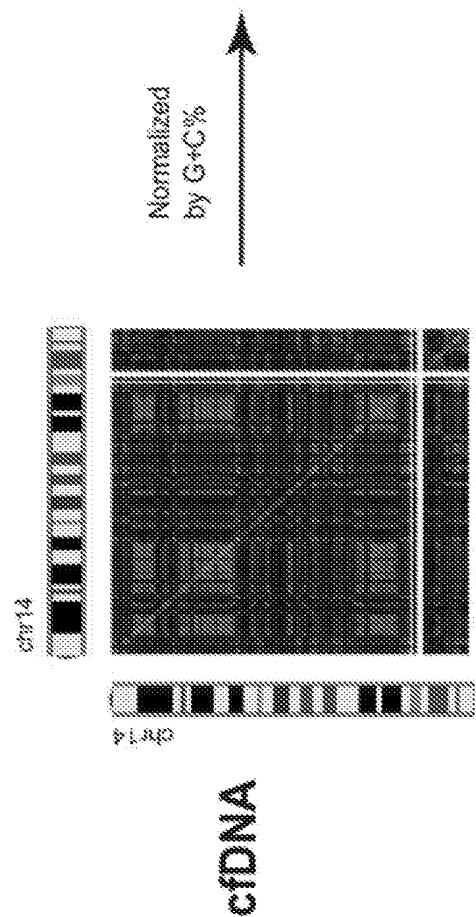


FIG. 17A

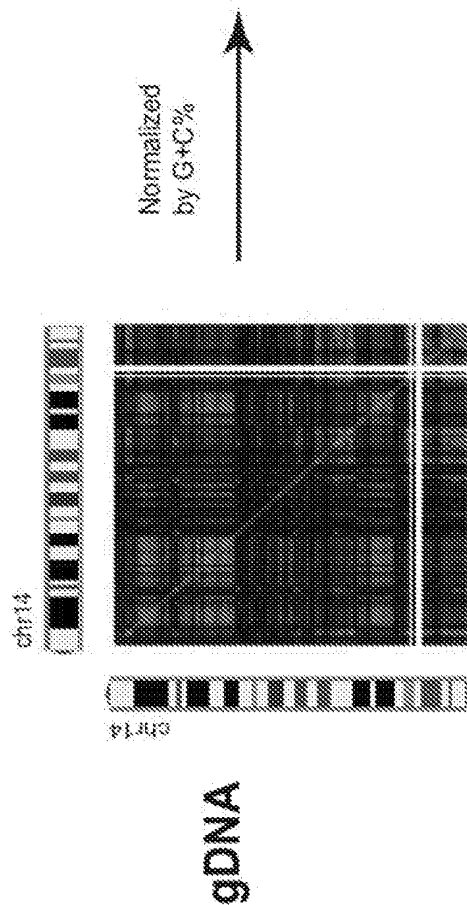


FIG. 17C

Normalized
by G+C%

Normalized
by G+C%

cfDNA

gDNA

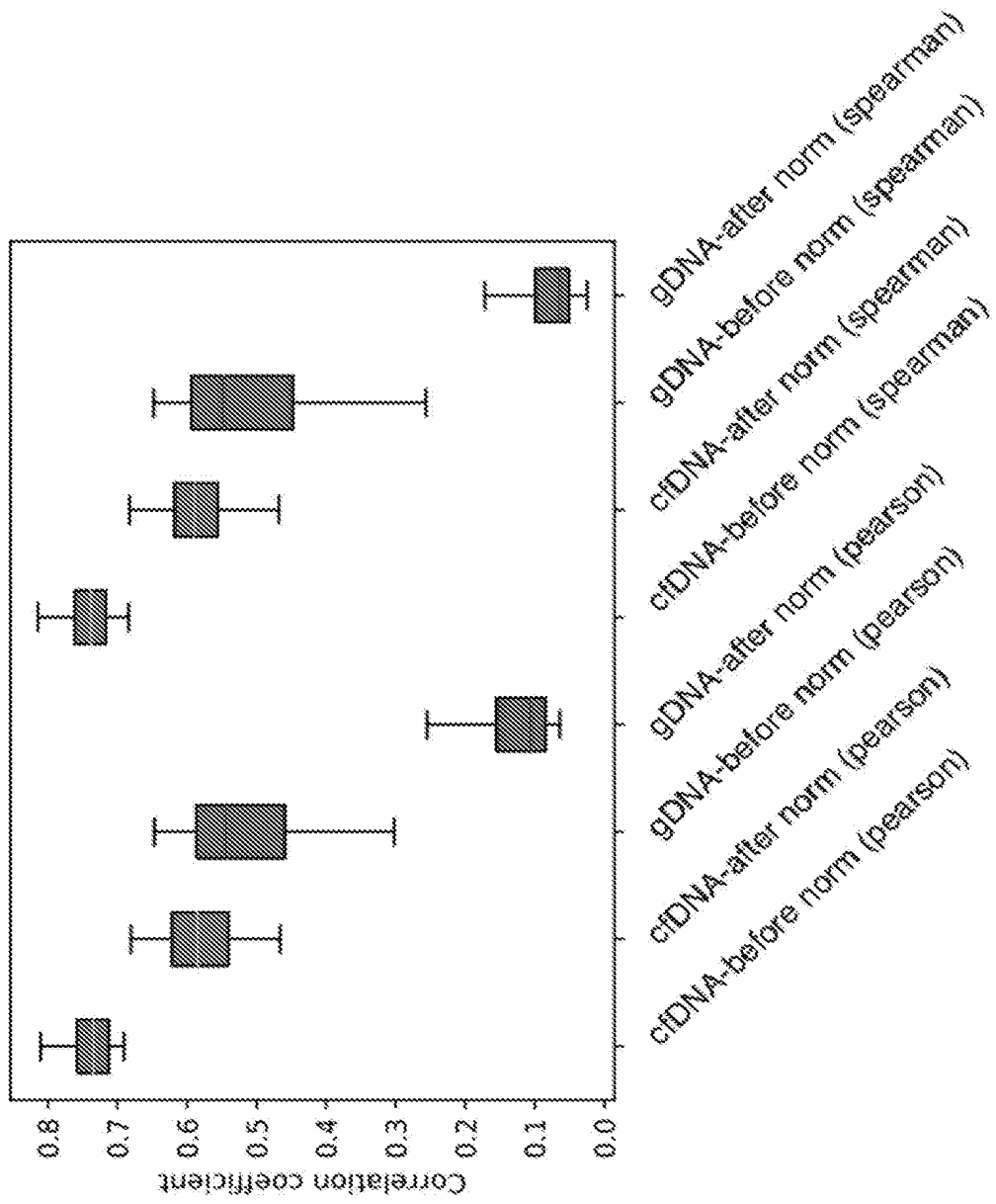


FIG. 17E

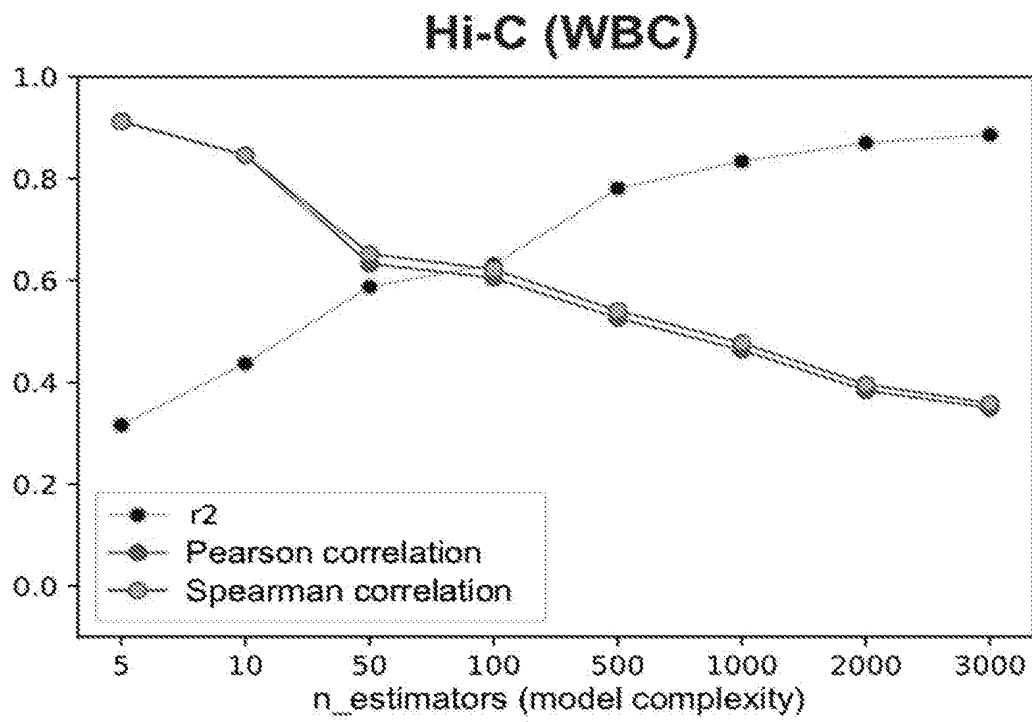


FIG. 18A

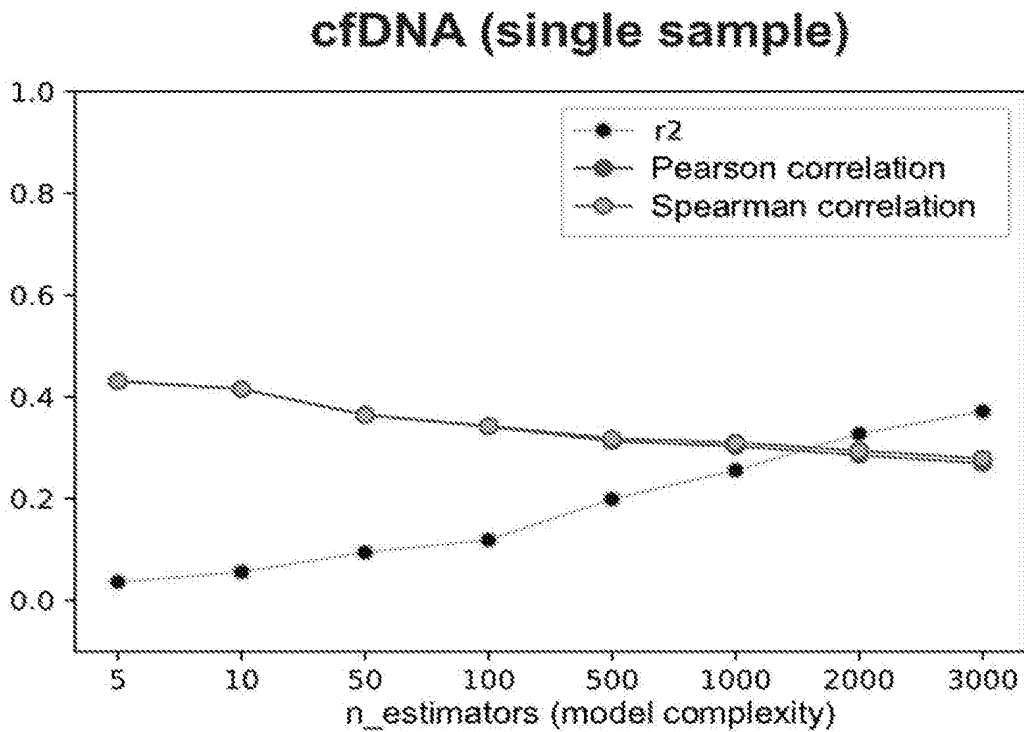


FIG. 18B

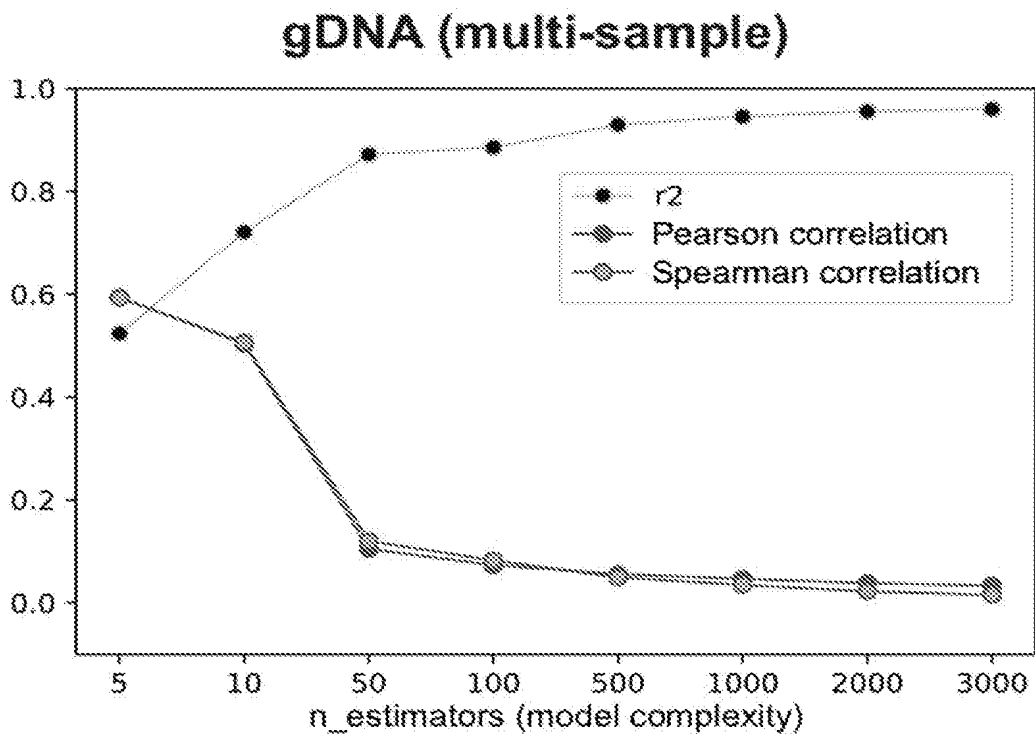


FIG. 18C

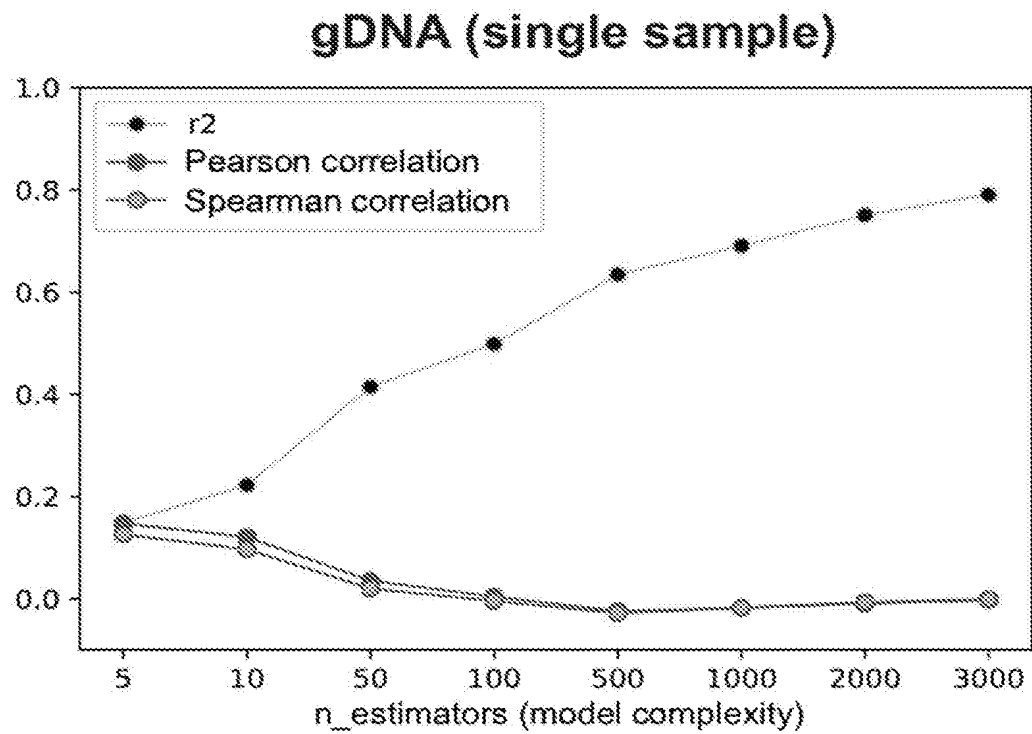


FIG. 18D

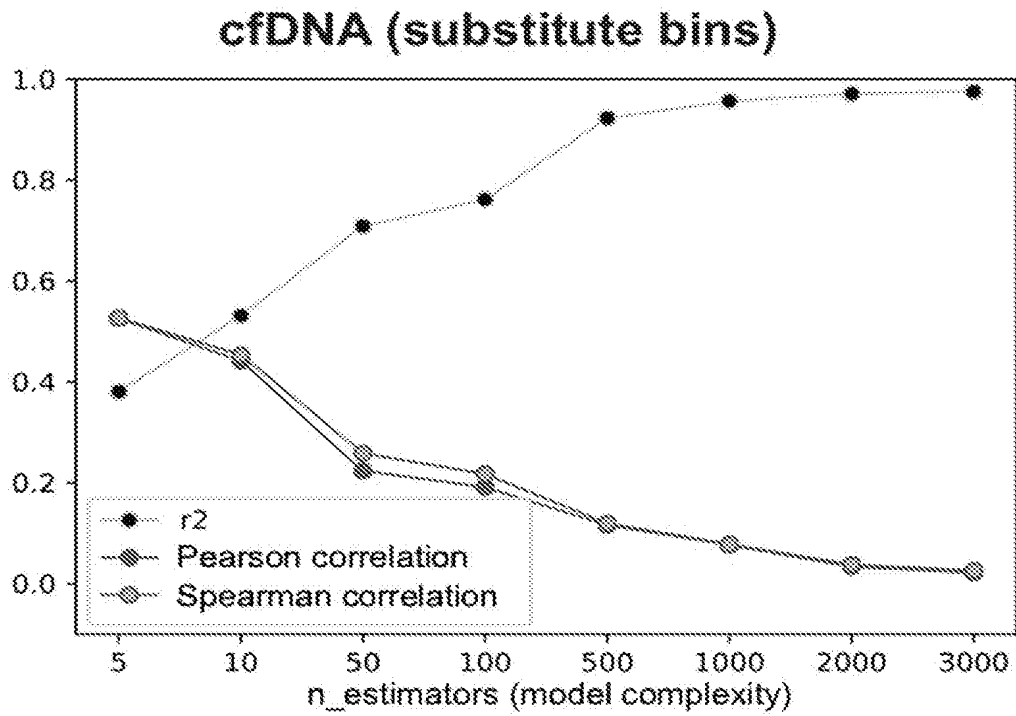


FIG. 18E

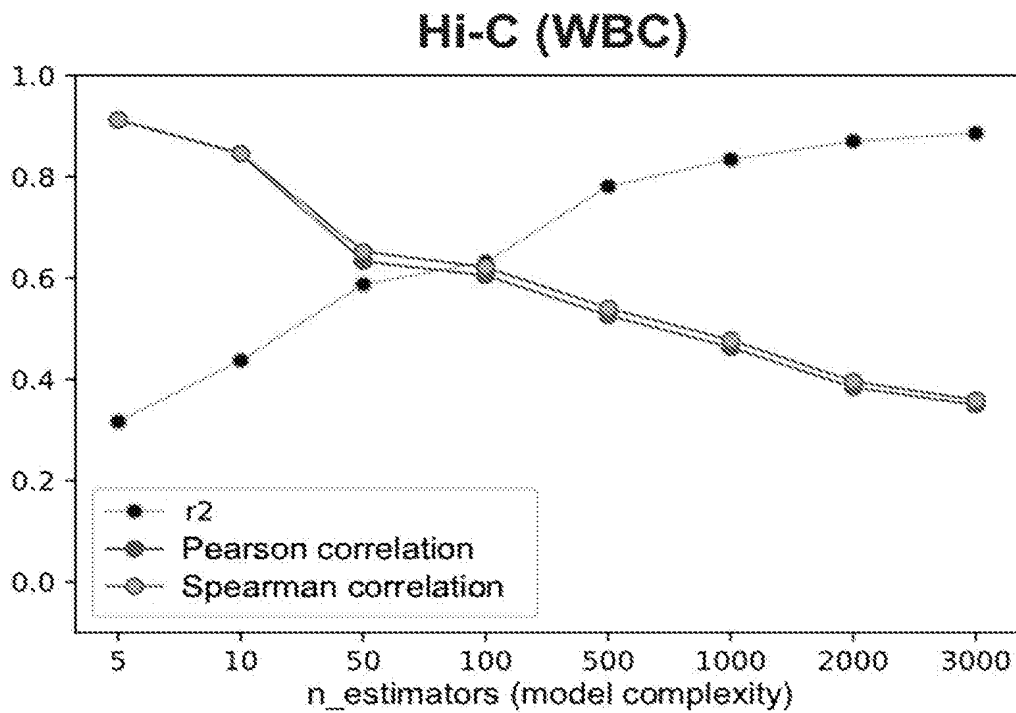


FIG. 18F

cfDNA
(shuffle individuals)

chr14: $r = 0.001$

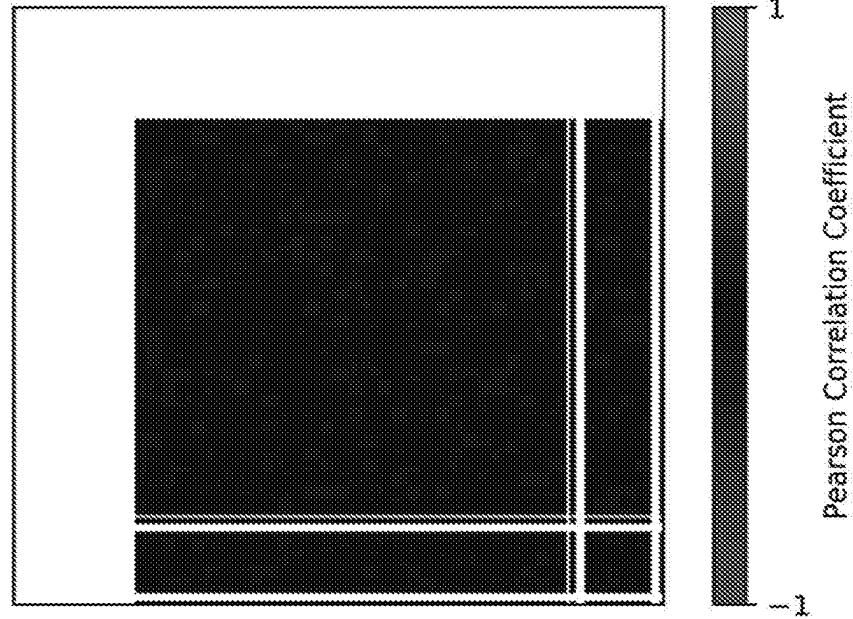


FIG. 19A

cfDNA
(18 samples within same batch)

chr14: $r = 0.72$

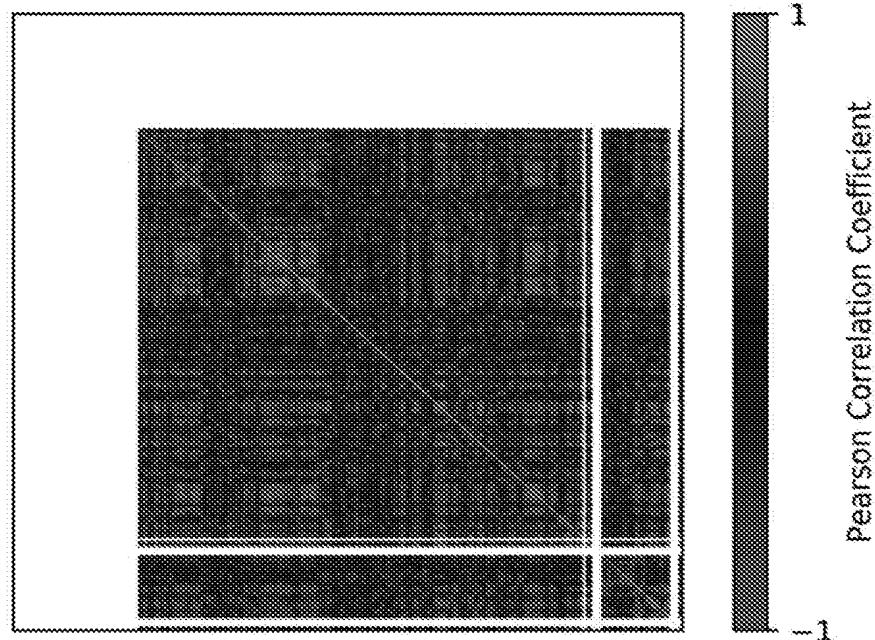


FIG. 19B

cfDNA
(18 samples from different batch)

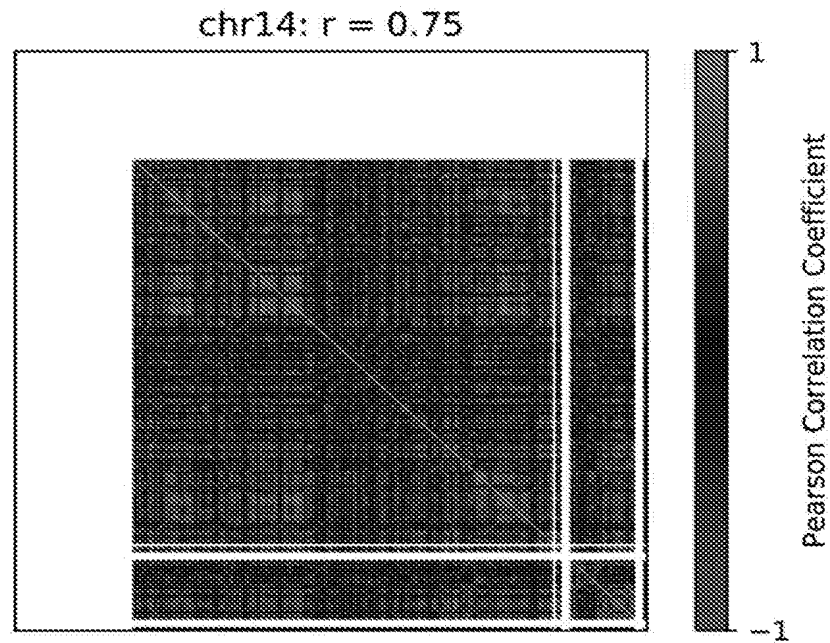


FIG. 19C

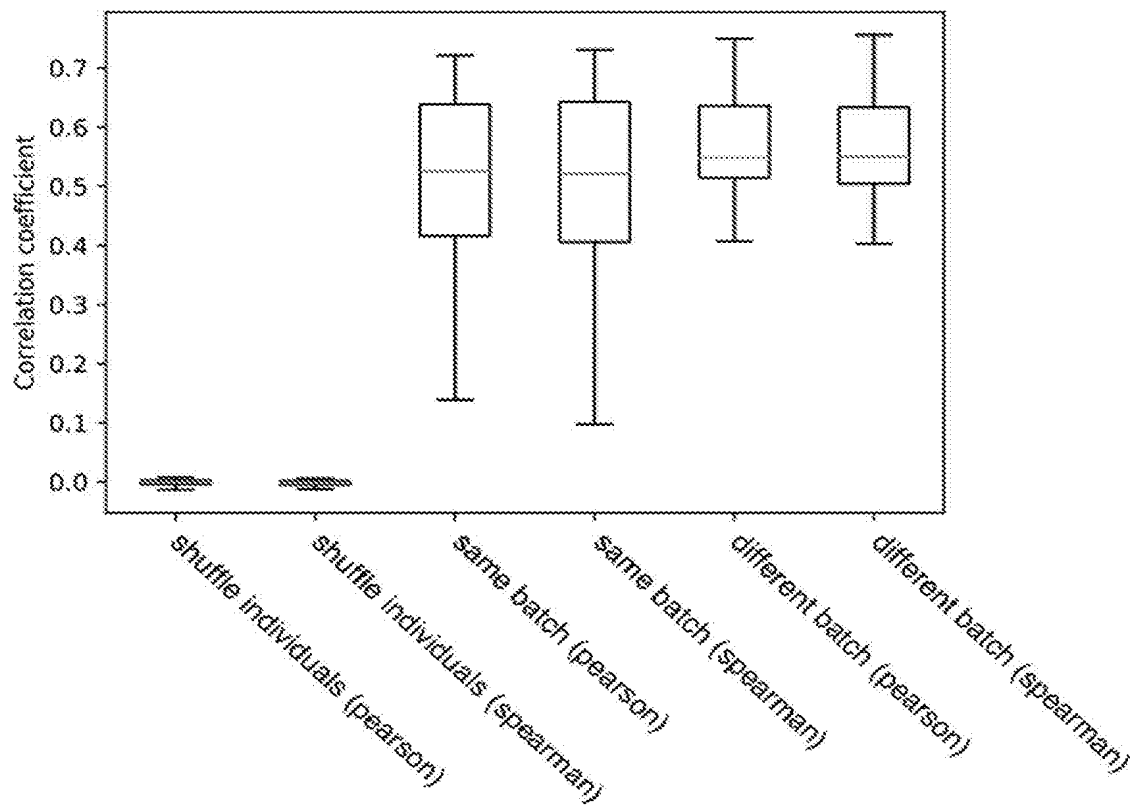


FIG. 19D

FIG. 20A

Randomly choosing n samples to estimate corr. matrices for 20 times,
500kb, Pearson correlations

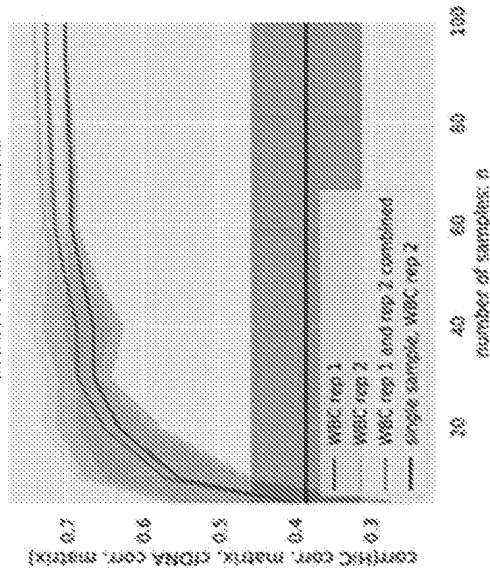


FIG. 20B

Randomly choosing n samples to estimate corr. matrices for 20 times,
500kb, Spearman correlations

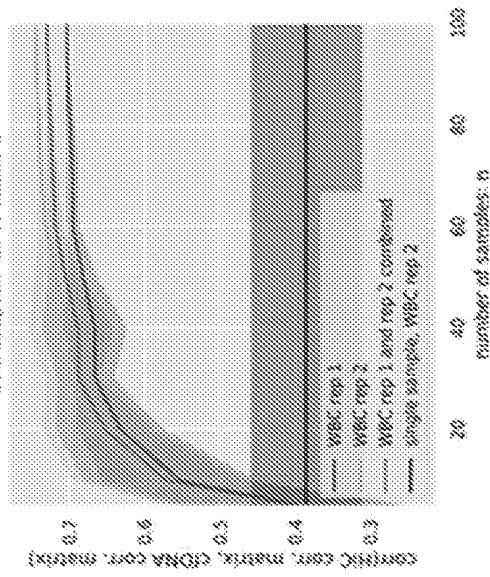


FIG. 20C

Randomly choosing n samples to estimate corr. matrices for 20 times,
500kb, Pearson correlations

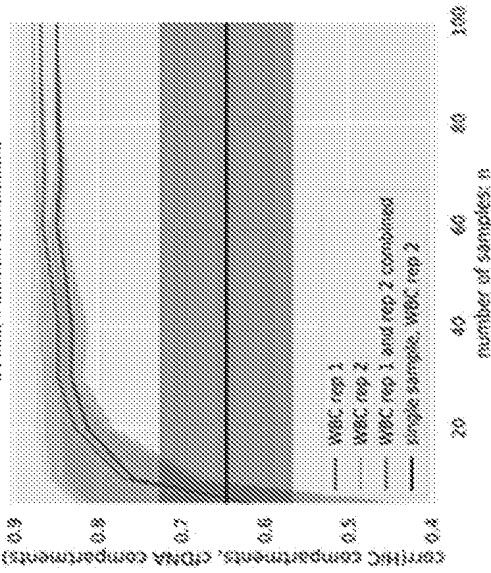
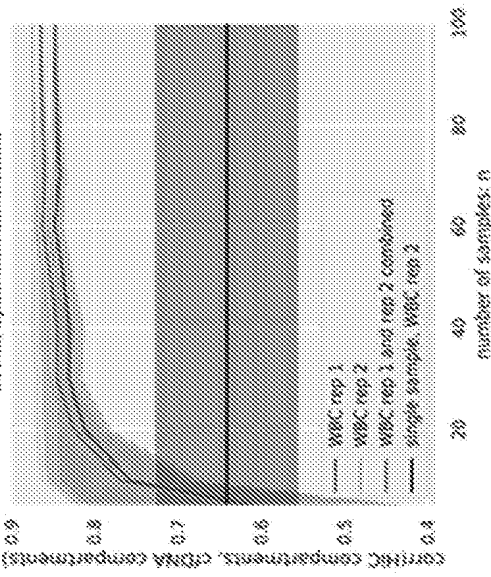


FIG. 20D

Randomly choosing n samples to estimate corr. matrices for 20 times,
500kb, Spearman correlations



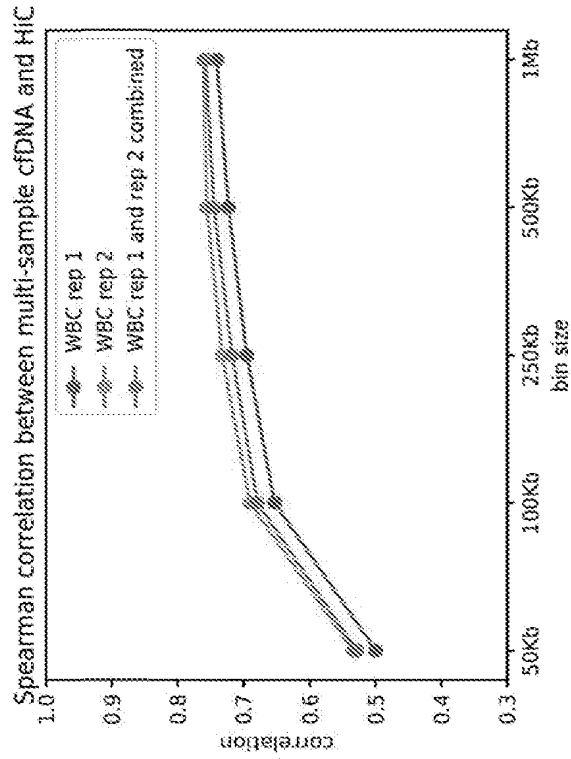


FIG. 21B

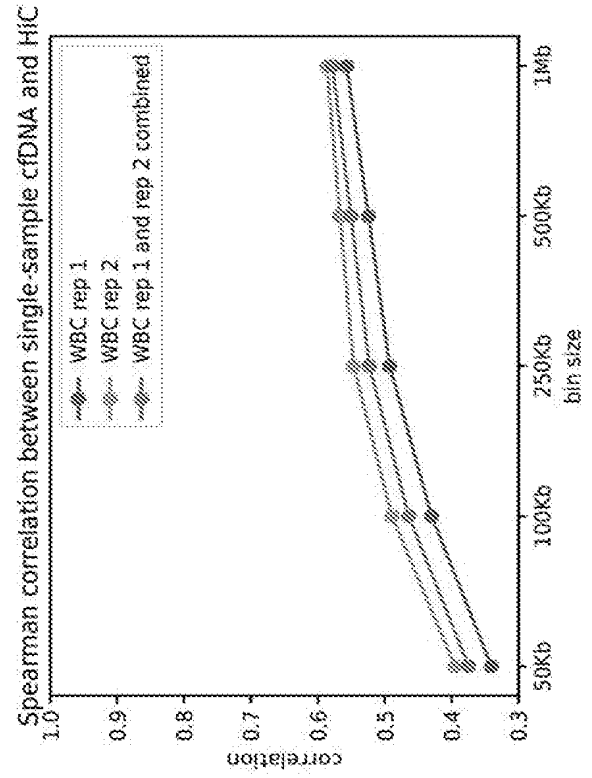


FIG. 21D

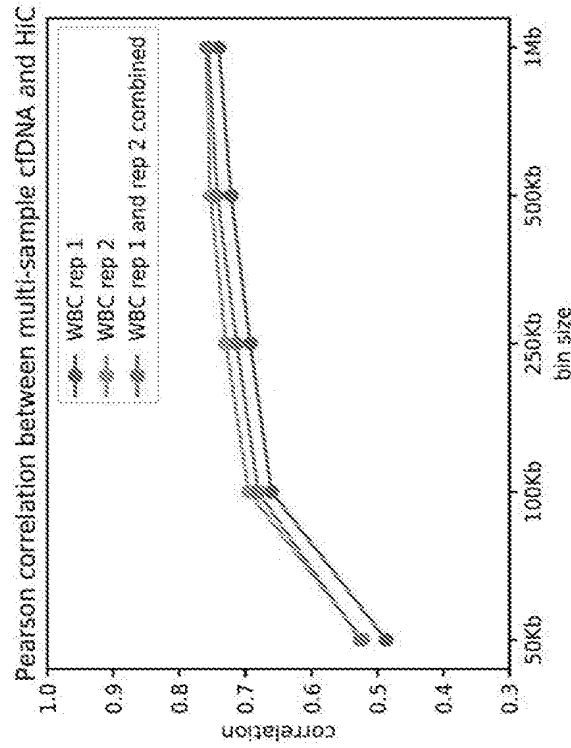


FIG. 21A

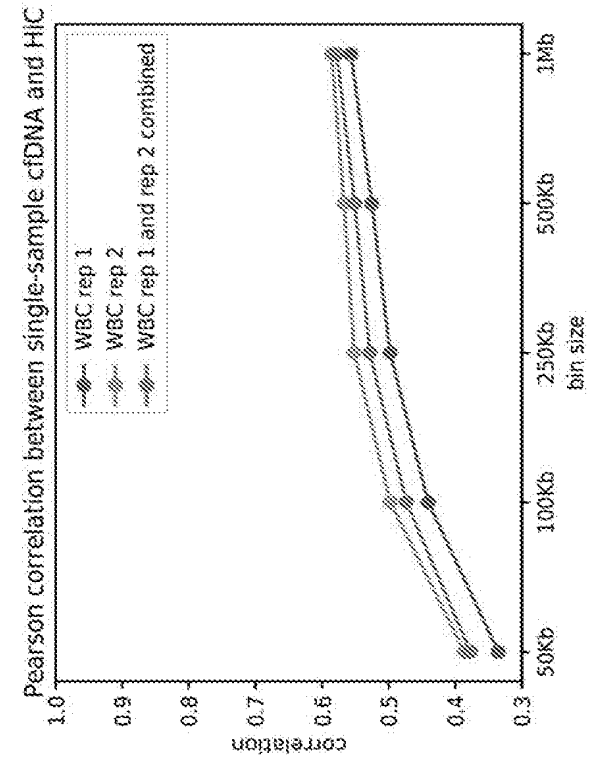


FIG. 21C

Pearson correlation between compartments of multi-sample cfDNA and HiC

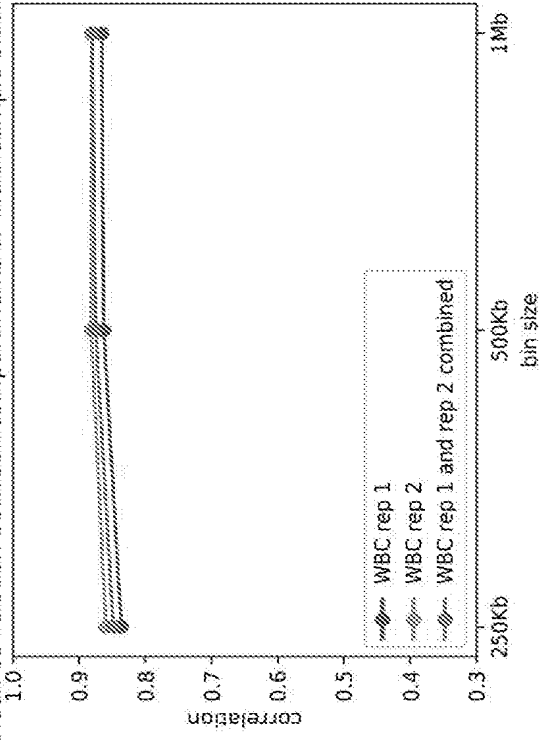


FIG. 21E

Spearman correlation between compartments of multi-sample cfDNA and HiC

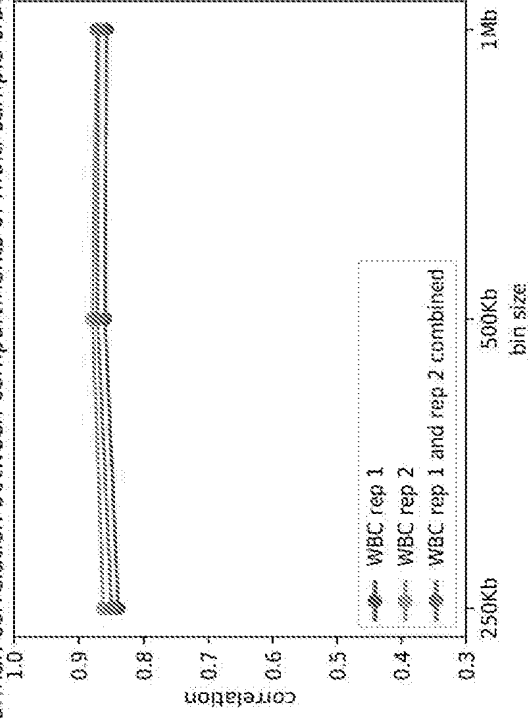


FIG. 21F

Pearson correlation between compartments of single-sample cfDNA and HiC

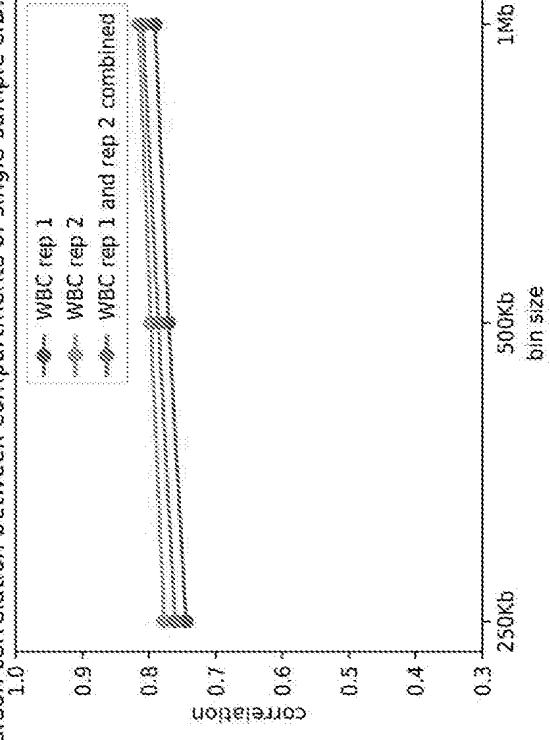


FIG. 21G

Spearman correlation between compartments of single-sample cfDNA and HiC

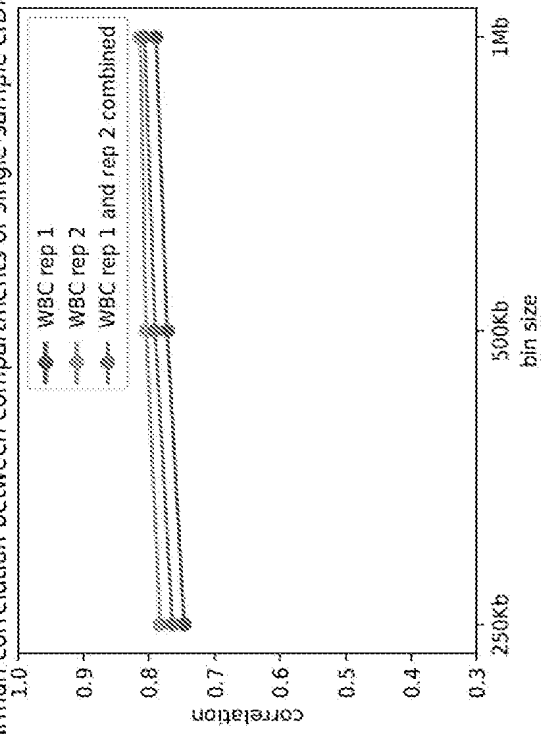


FIG. 21H

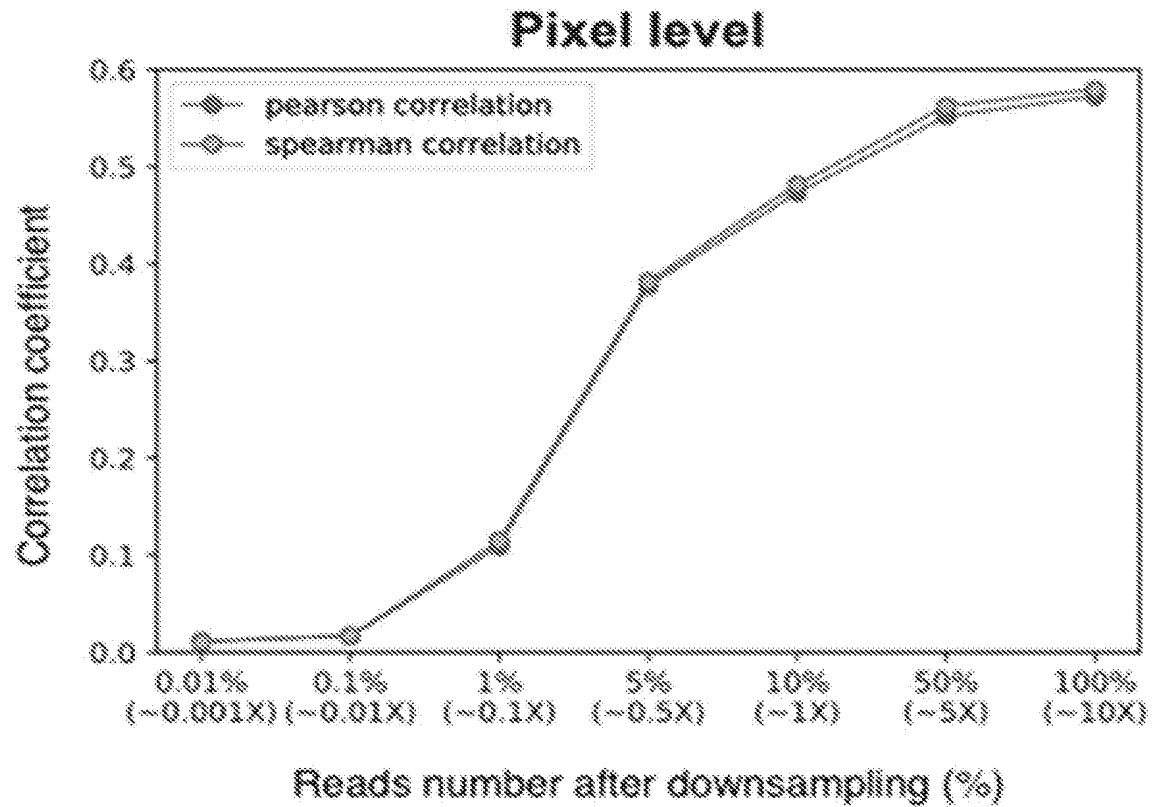


FIG. 22A

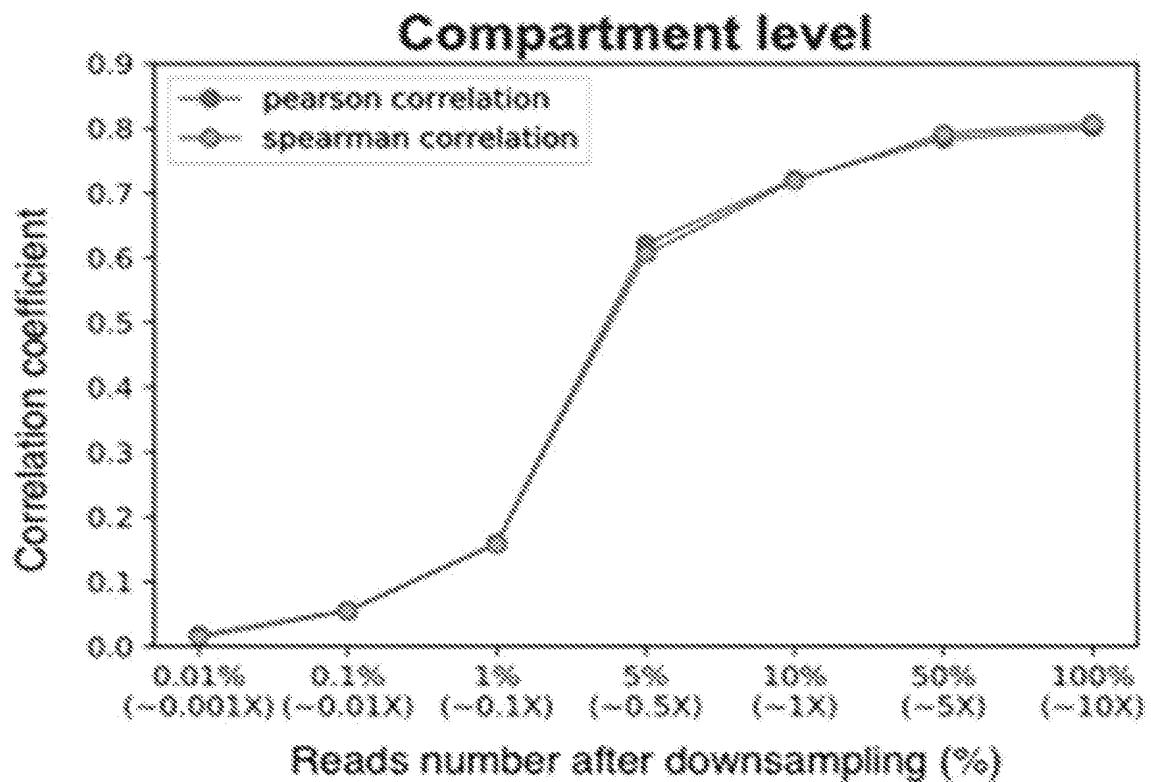


FIG. 22B

FIG. 23A

PCA

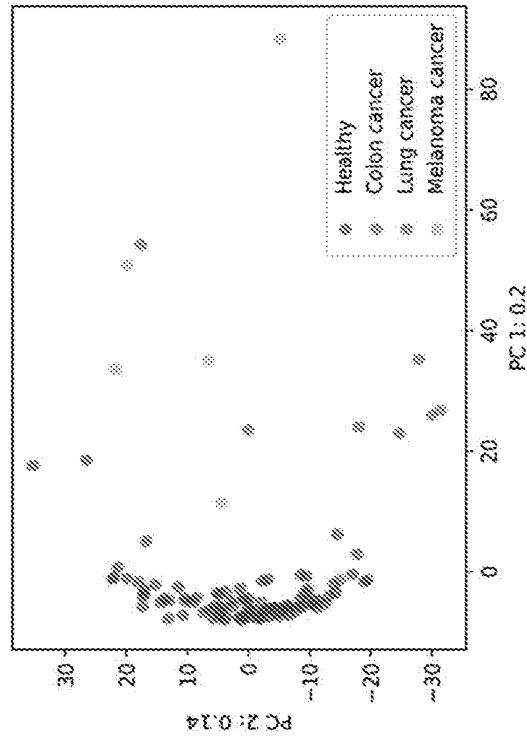


FIG. 23B

CCA (random 1)

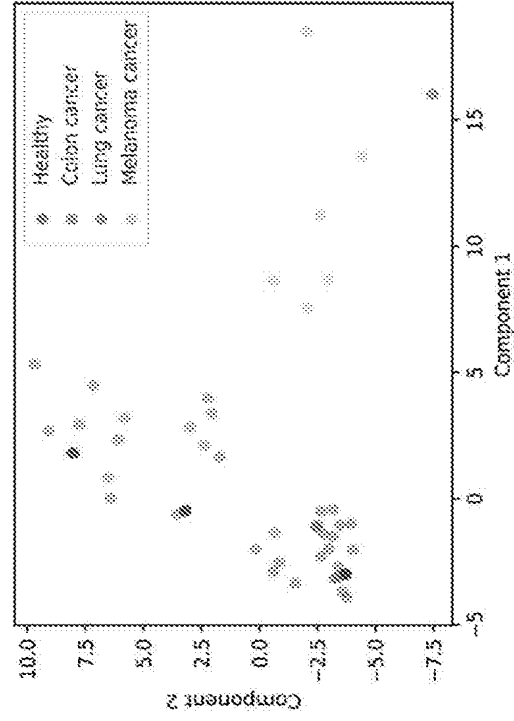


FIG. 23C

CCA (random 2)

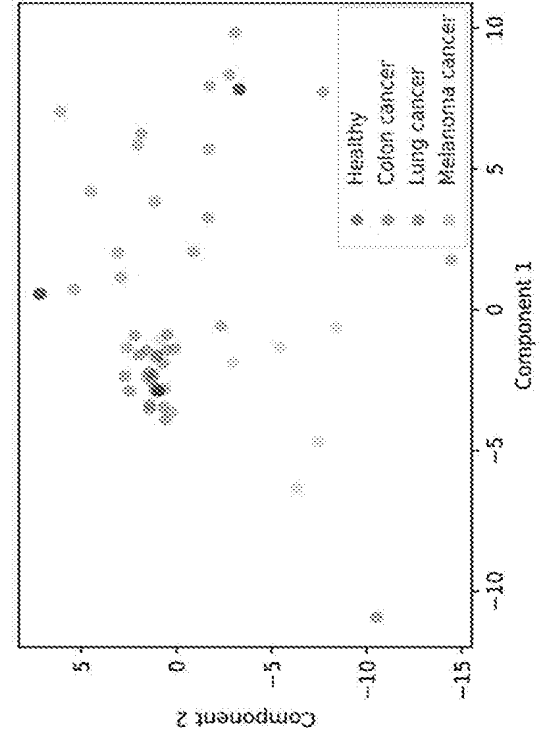


FIG. 23D

CCA (random 3)

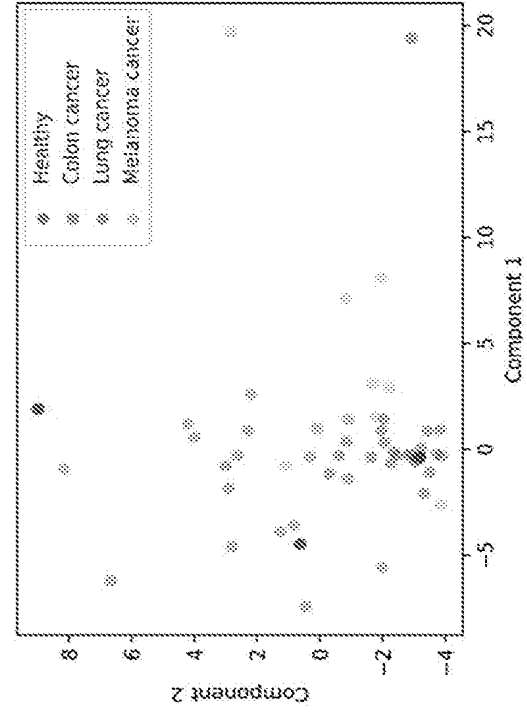


FIG. 23B

FIG. 23C

FIG. 23E

CCA (random 4)

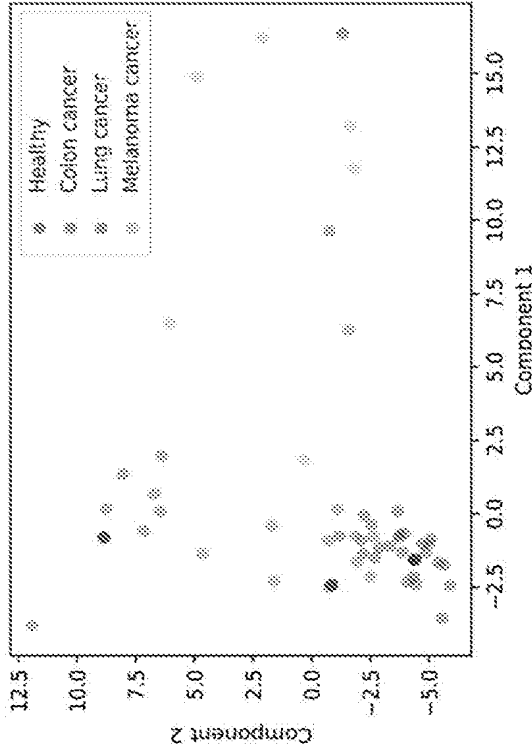
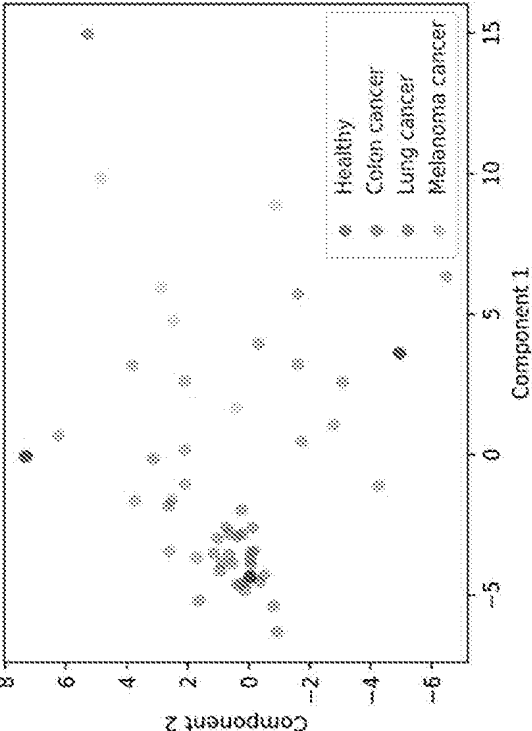


FIG. 23F

CCA (random 5)



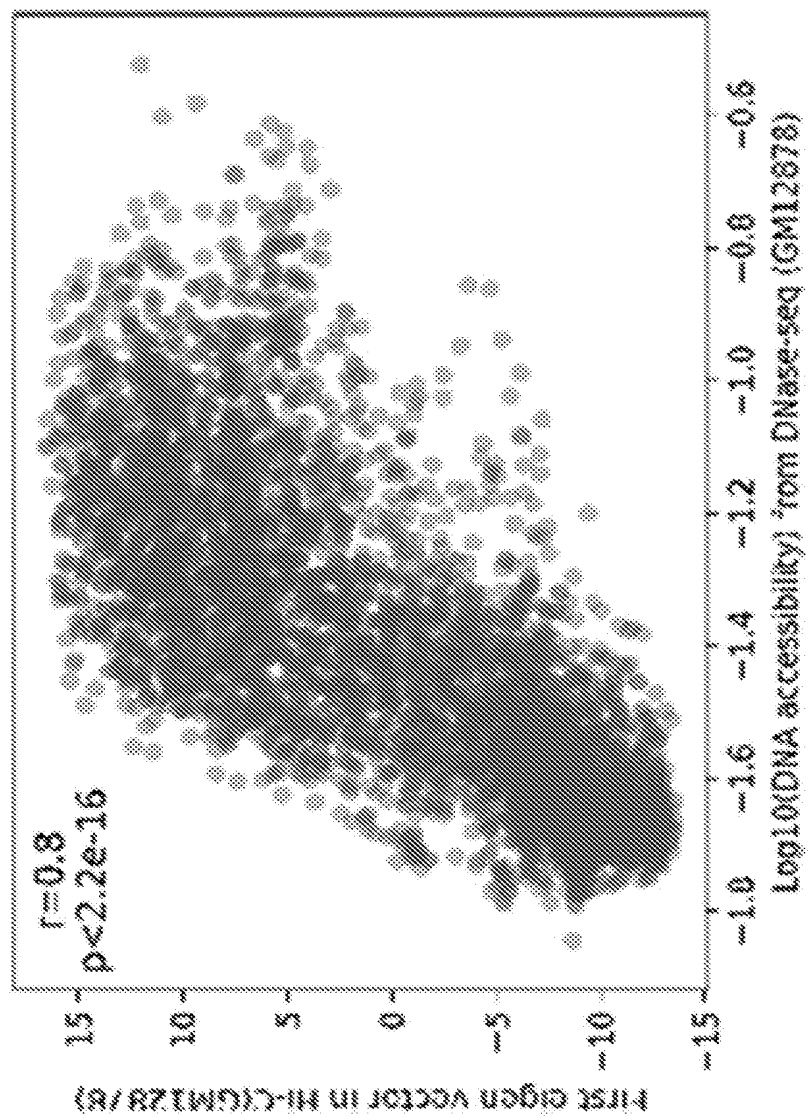


FIG. 24

FIG. 25A

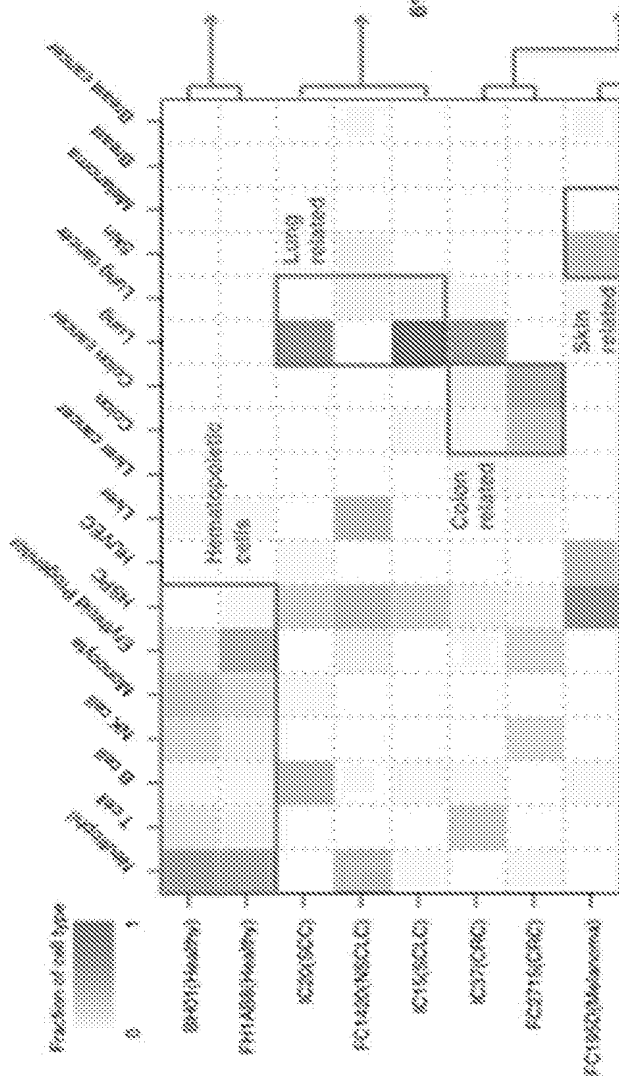


FIG. 25B

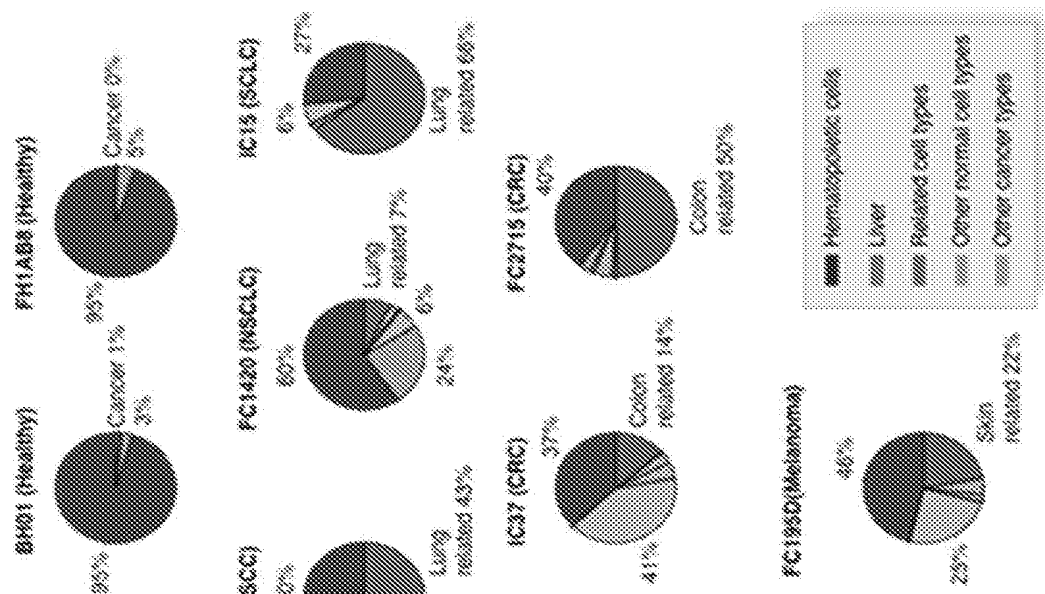
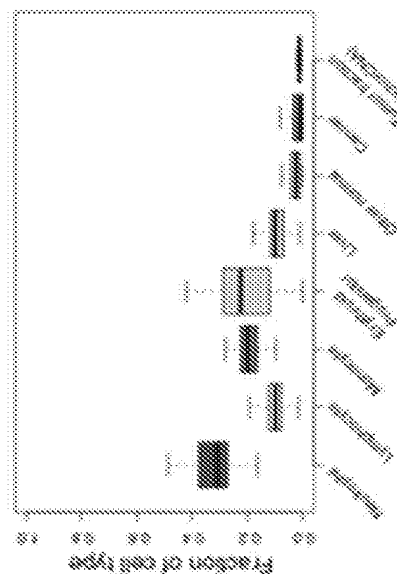


FIG. 25C

Healthy samples



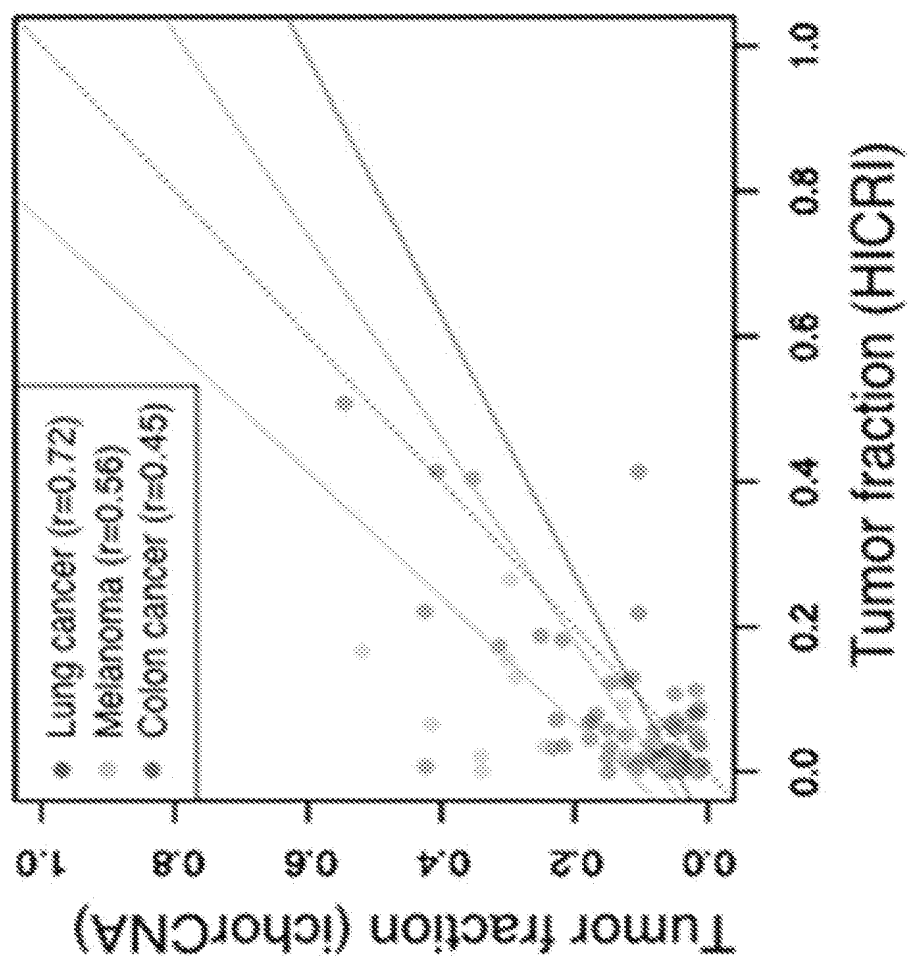


FIG. 26

FIG. 27A

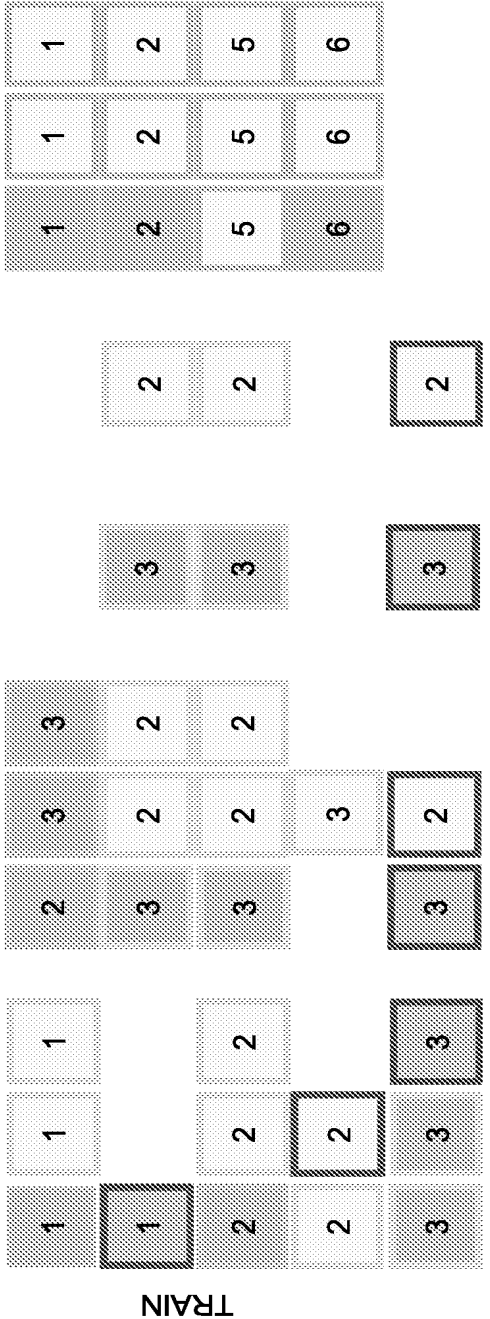
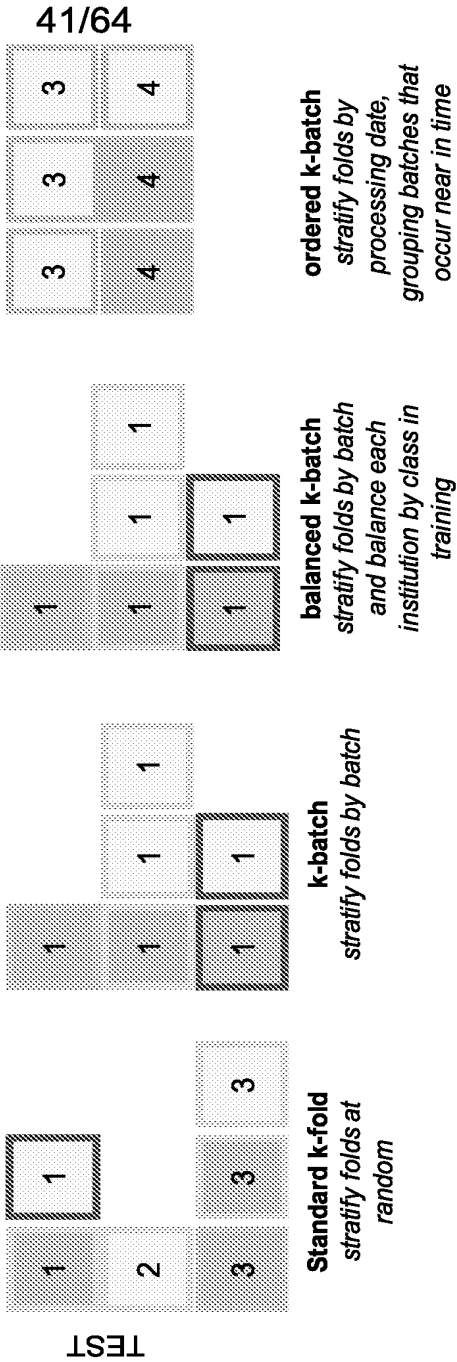


FIG. 27B



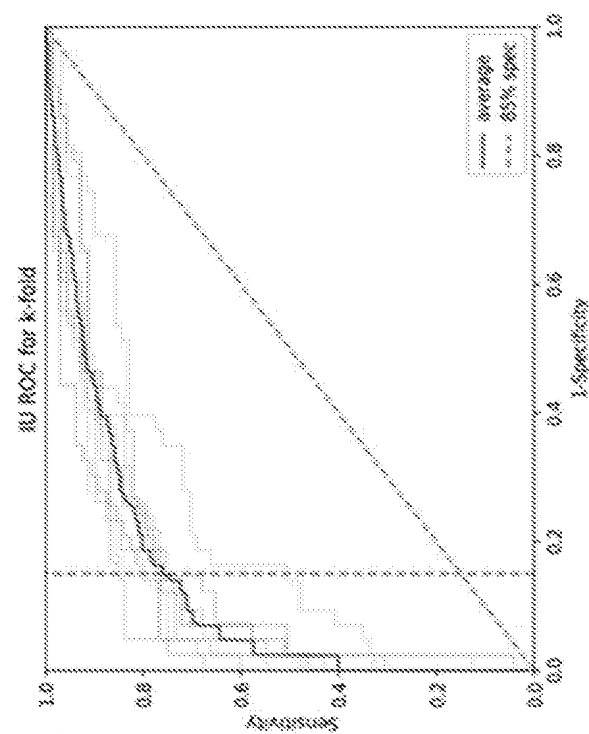


FIG. 28A

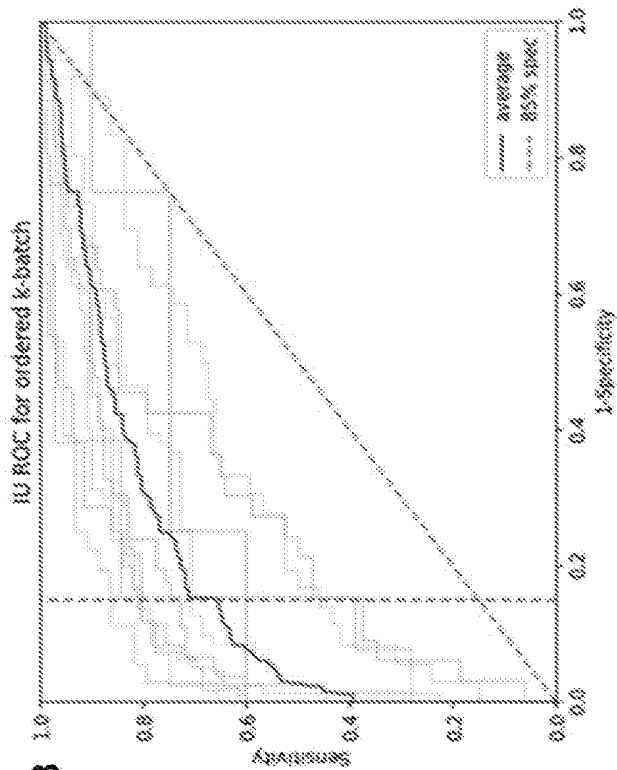


FIG. 28B

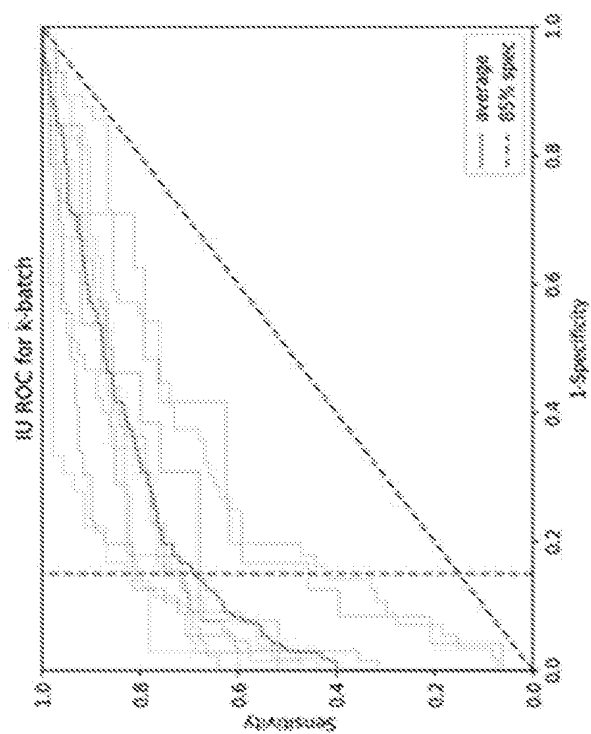


FIG. 28C

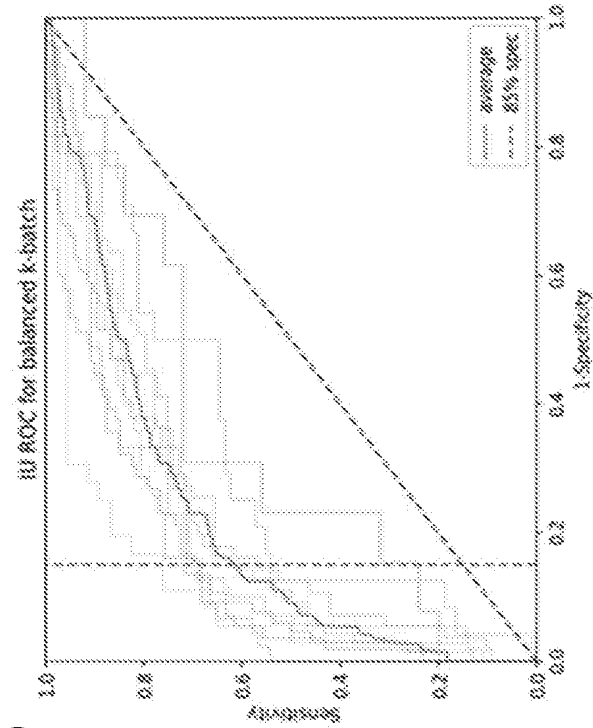


FIG. 28D

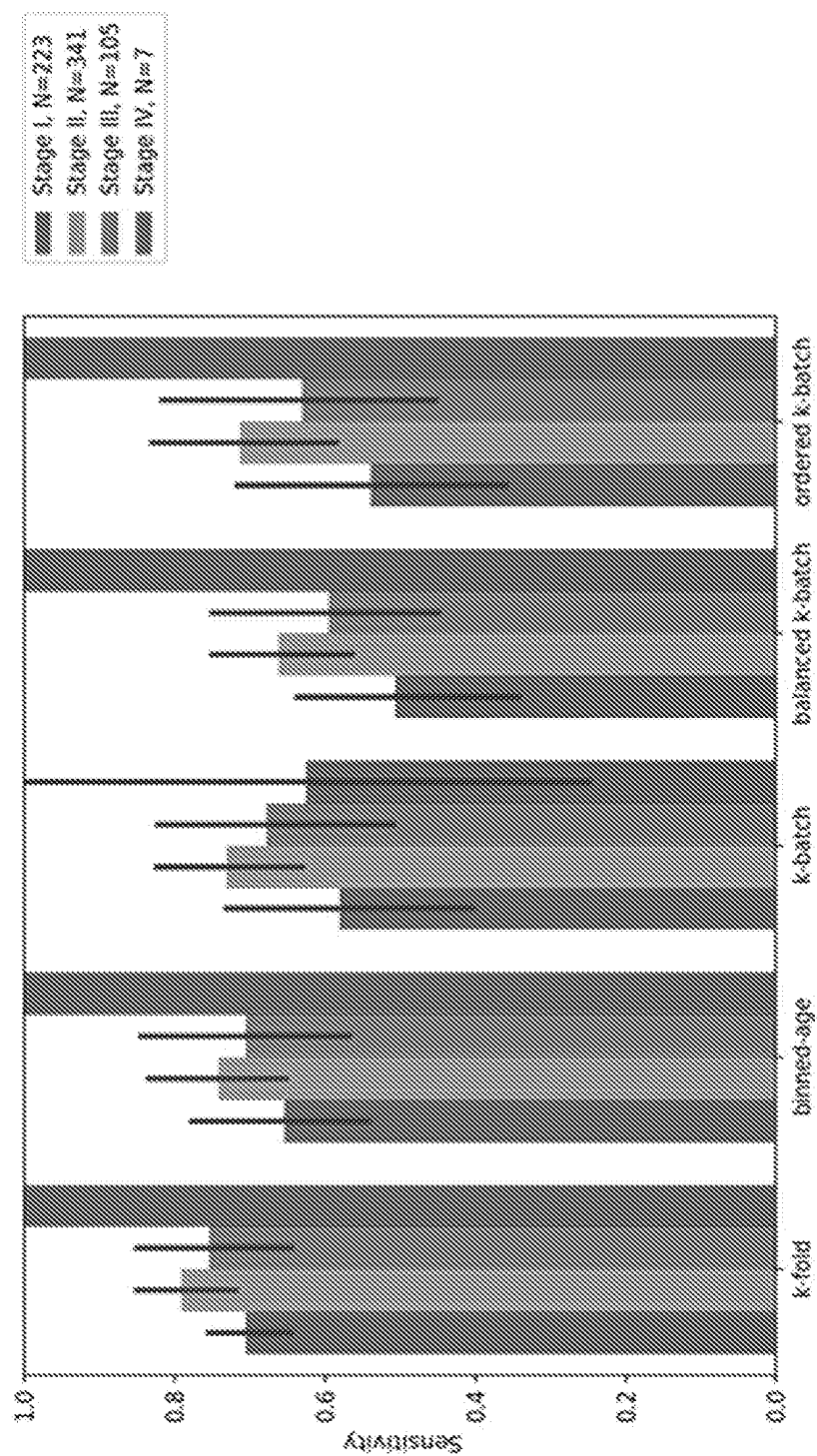


FIG. 28E

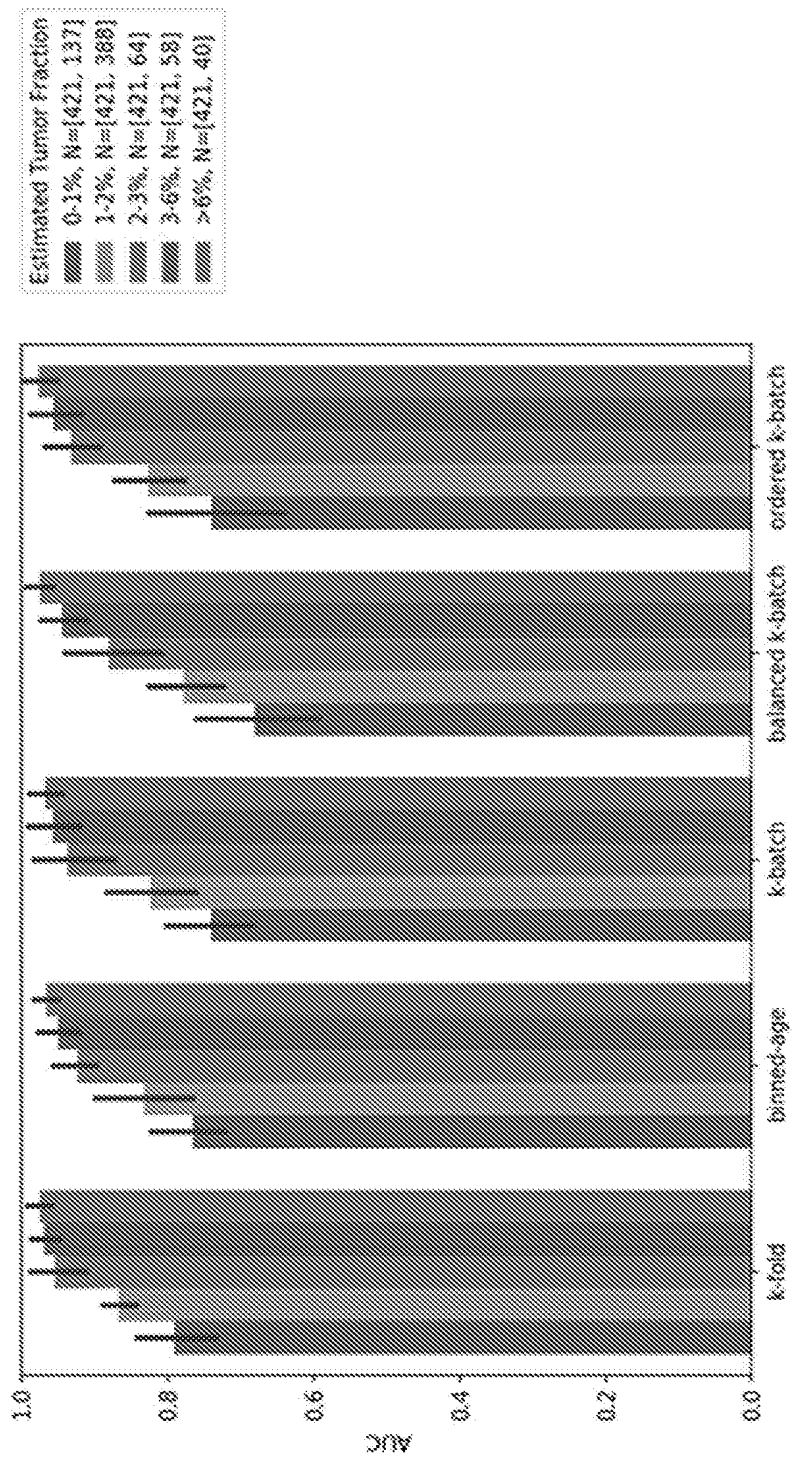


FIG. 28F

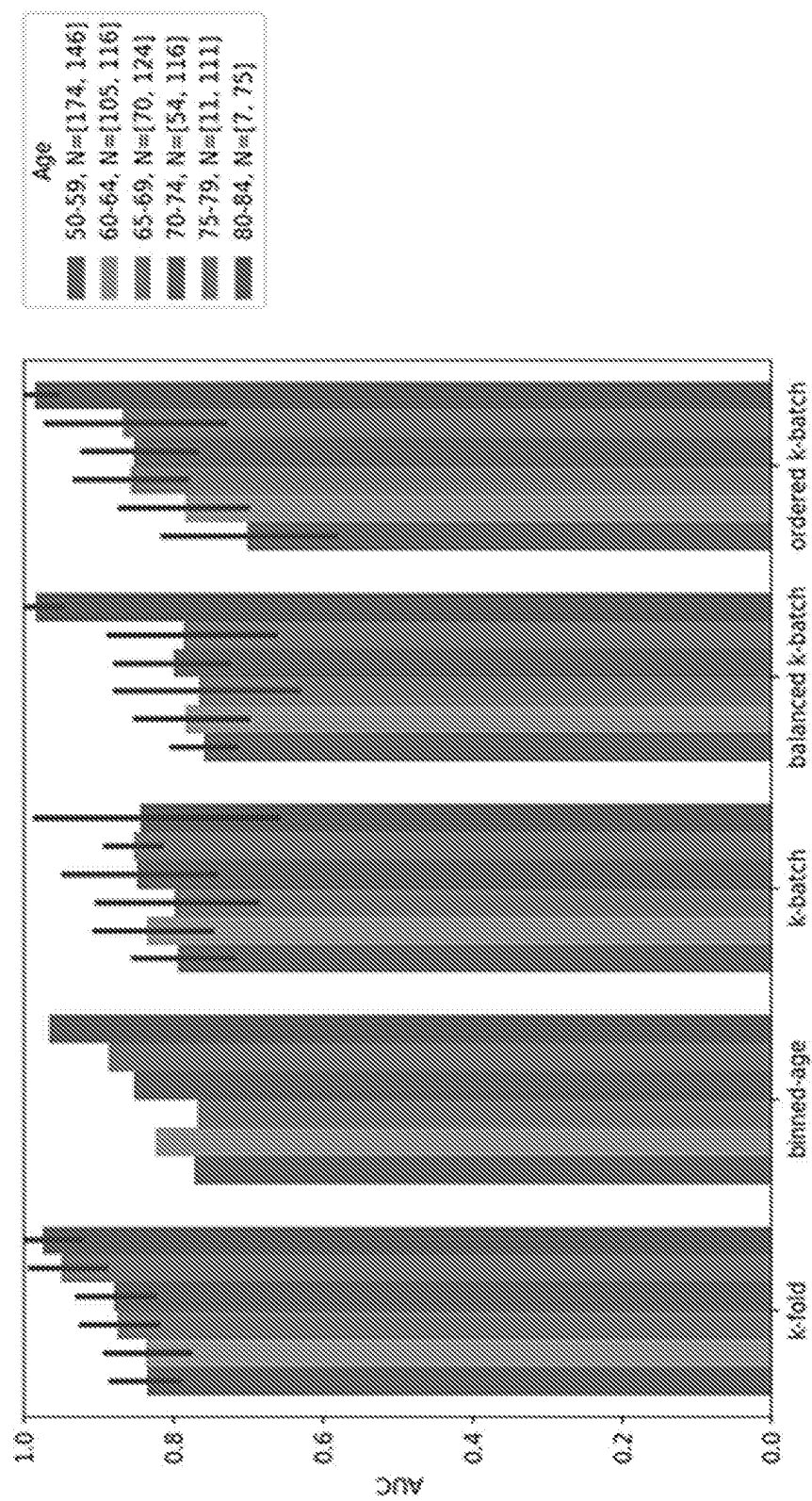


FIG. 28G

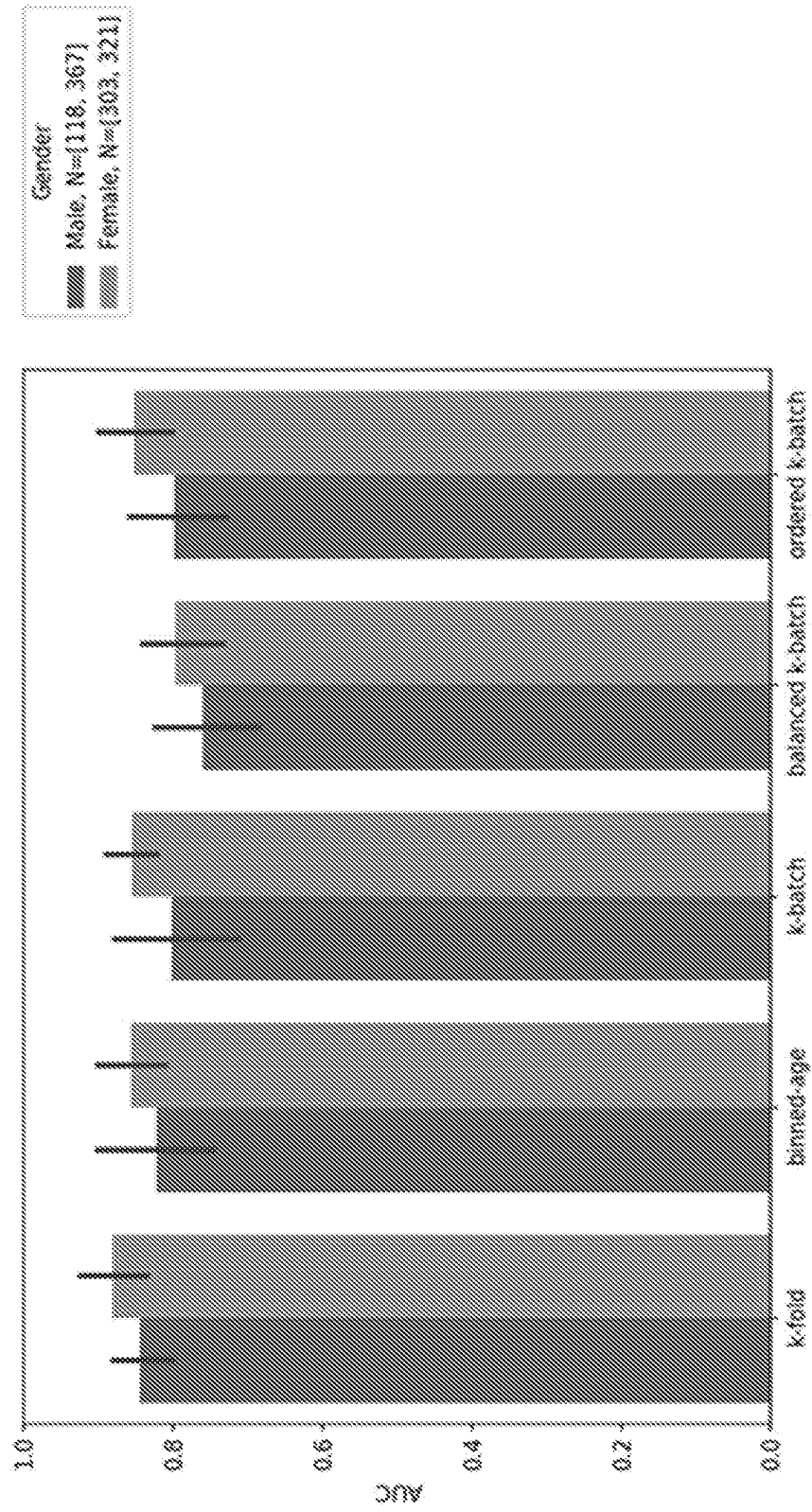


FIG. 28H

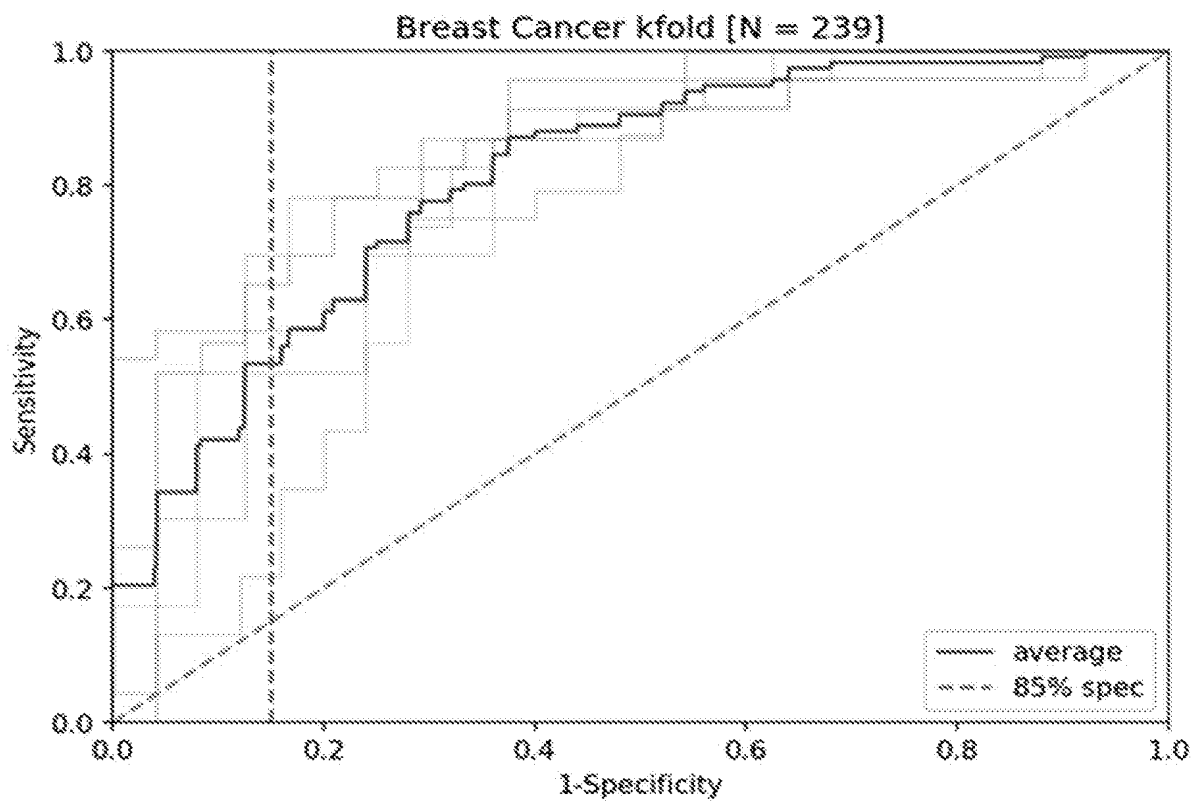


FIG. 29A

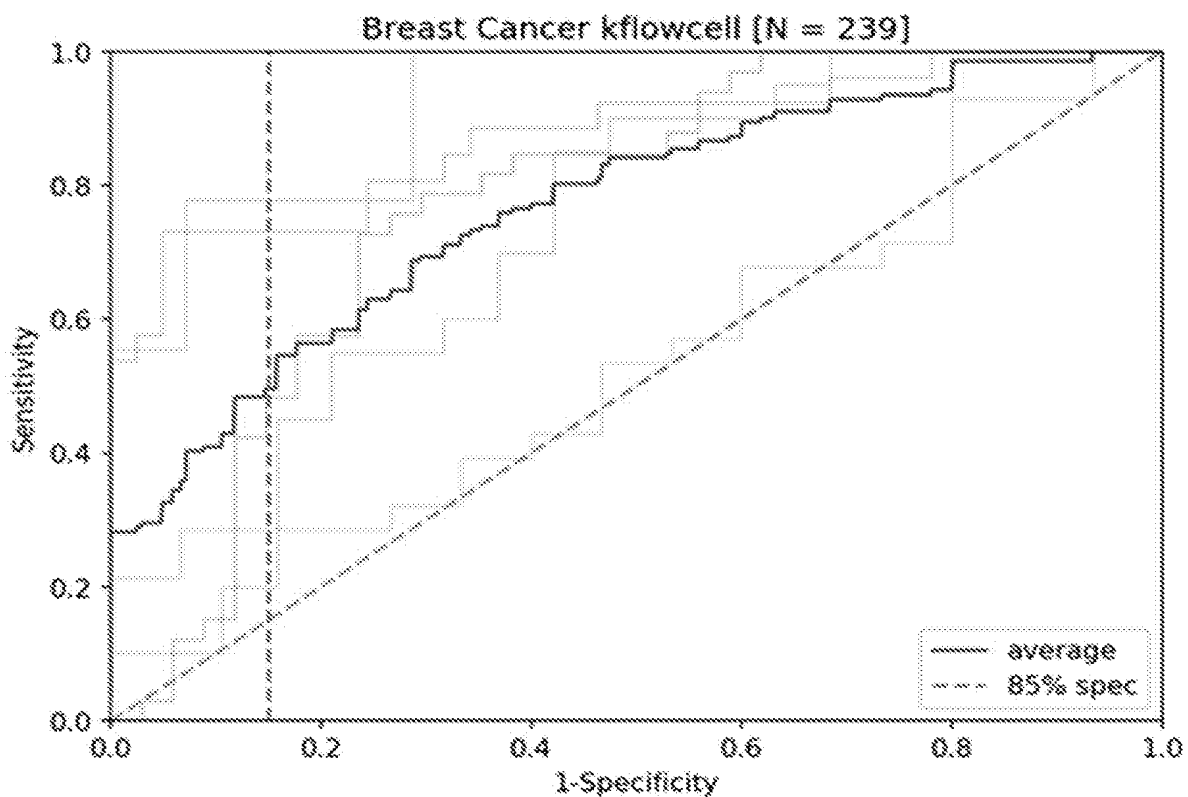


FIG. 29B

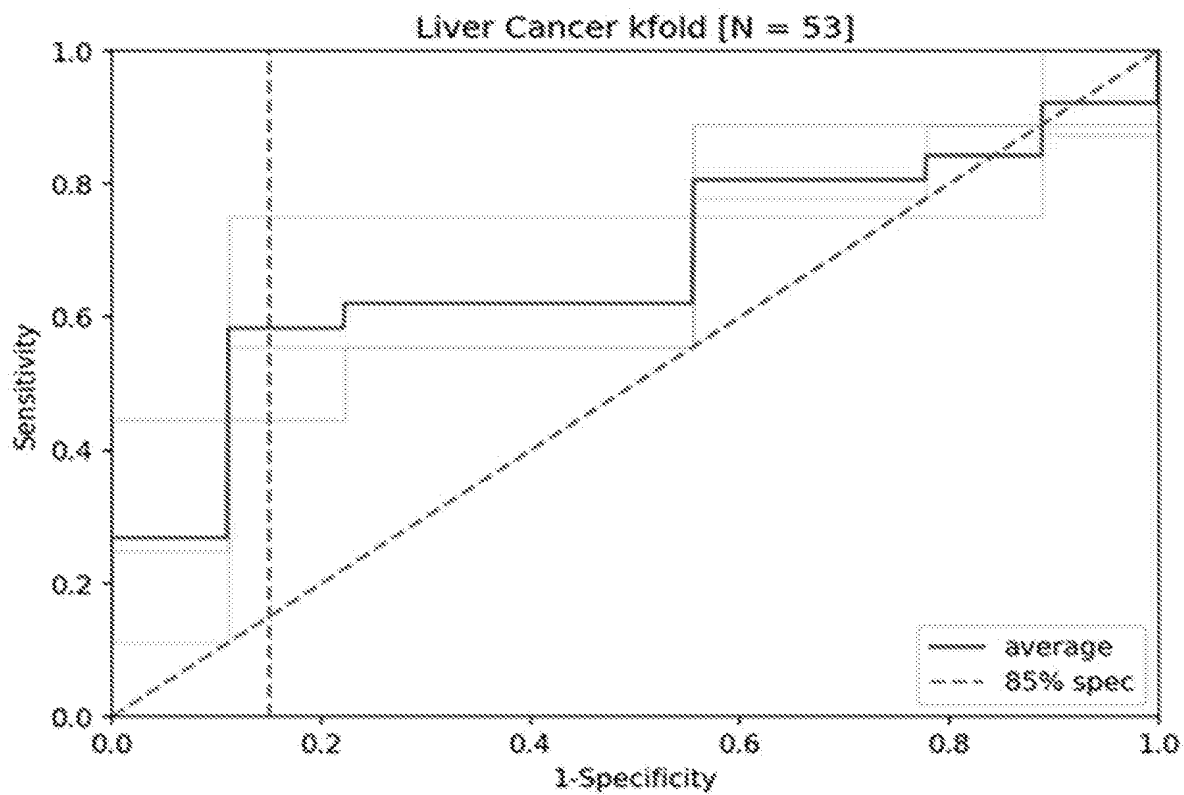


FIG. 29C

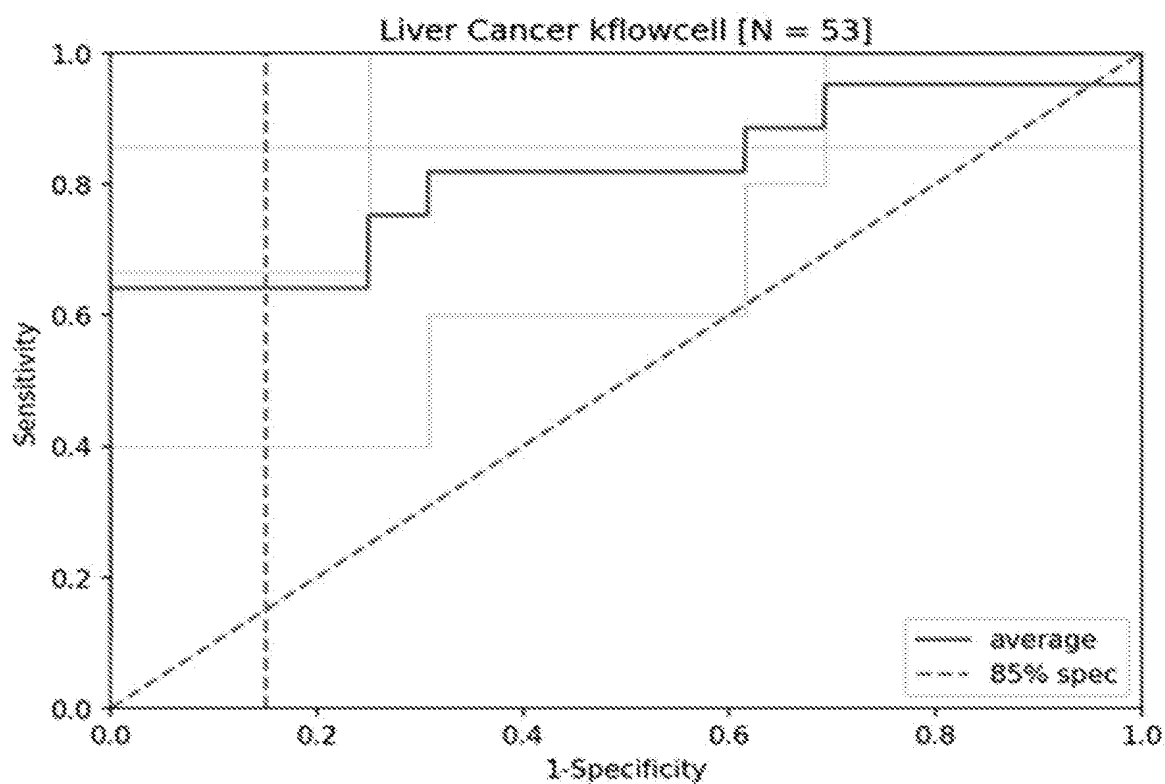


FIG. 29D

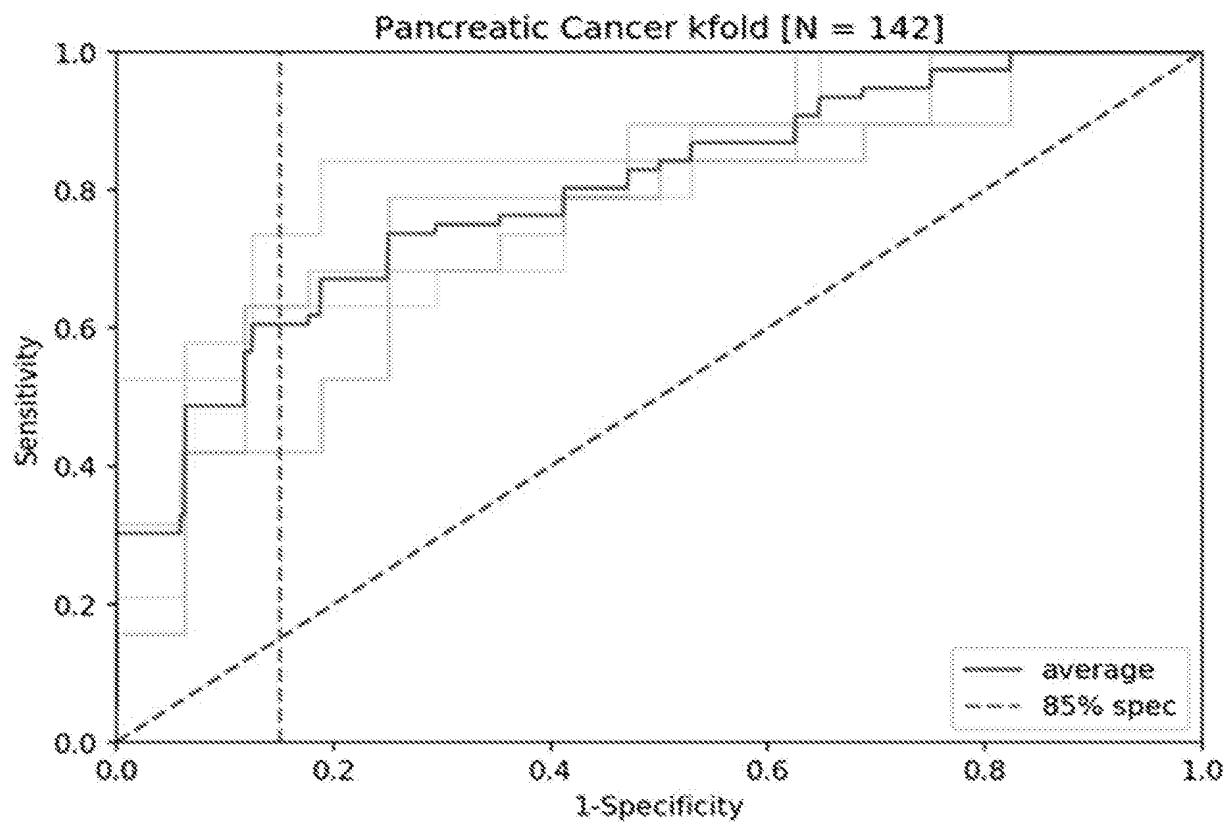


FIG. 29E

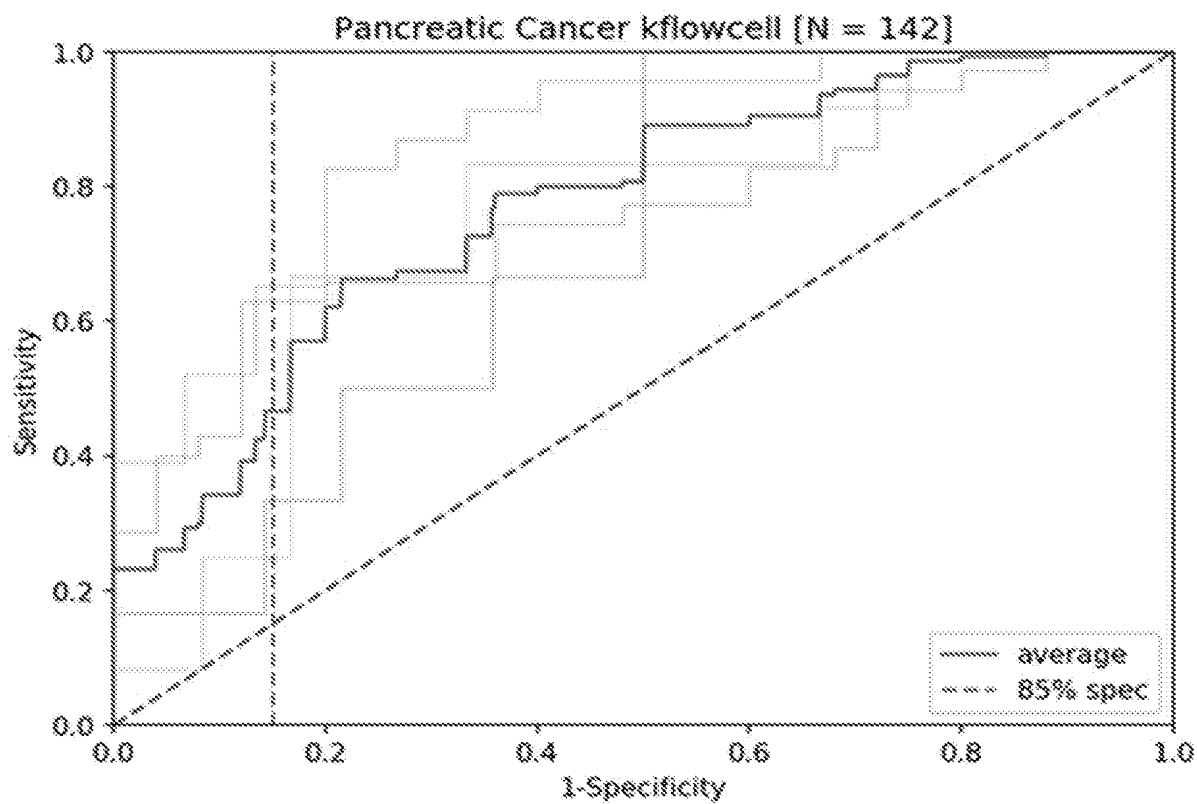


FIG. 29F

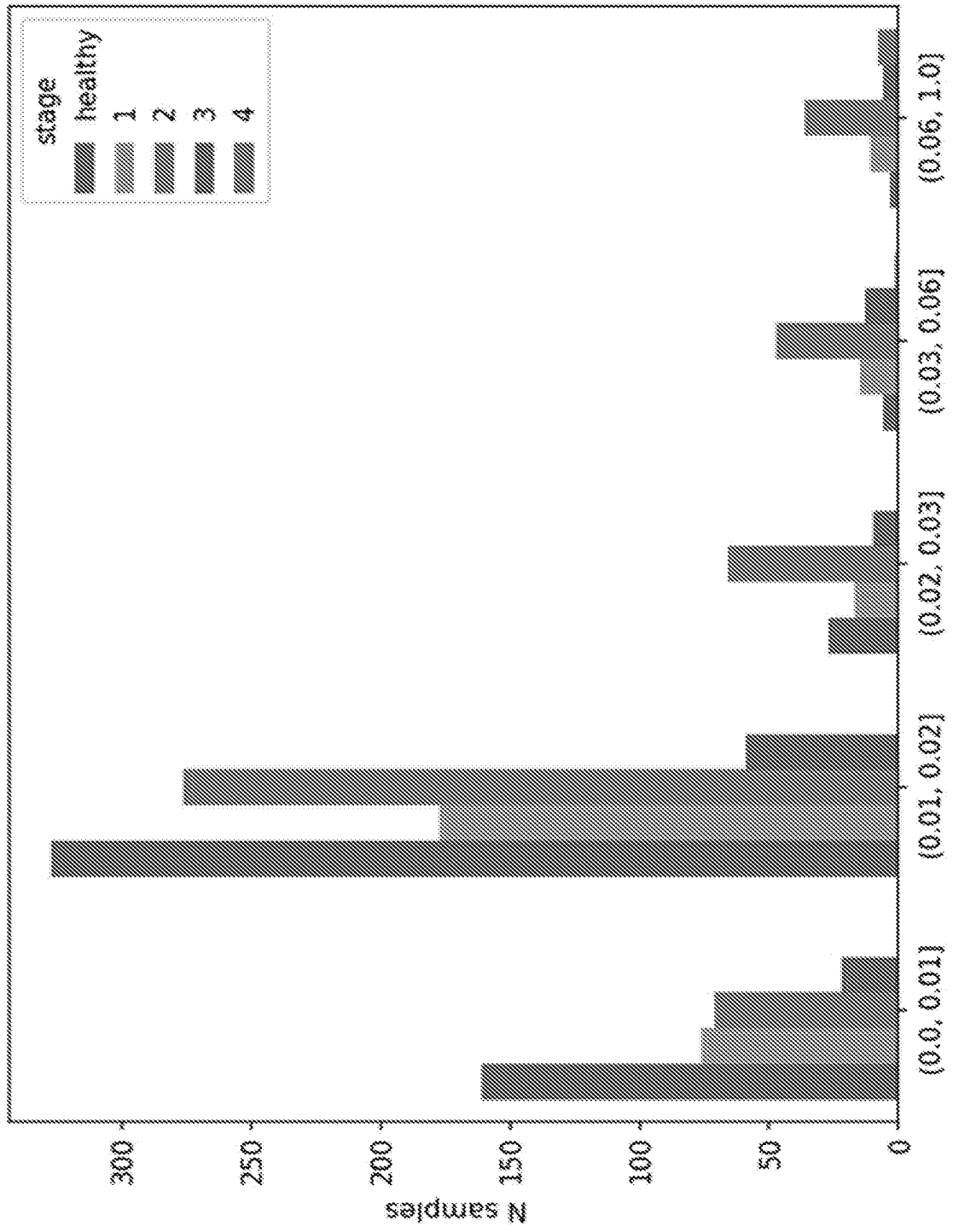


FIG. 30

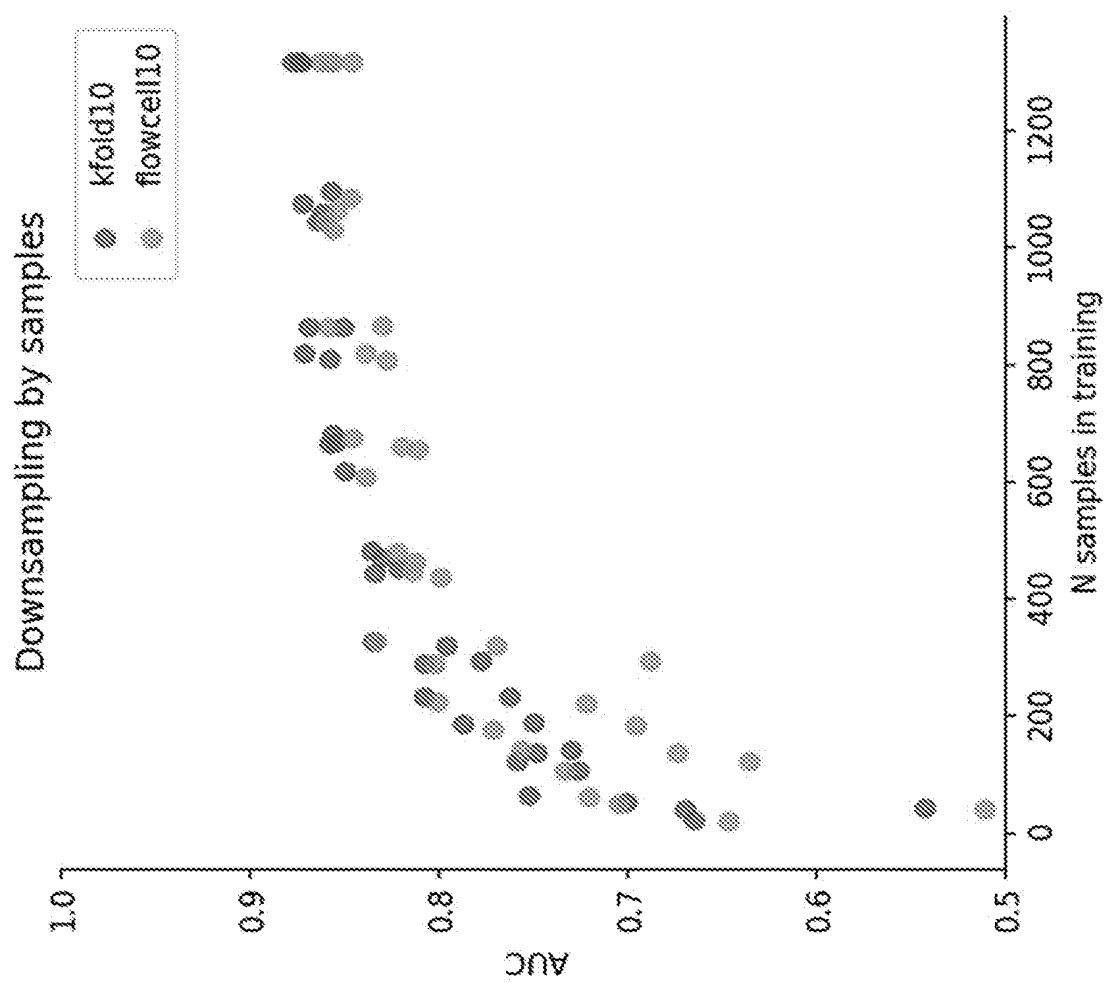


FIG. 31A

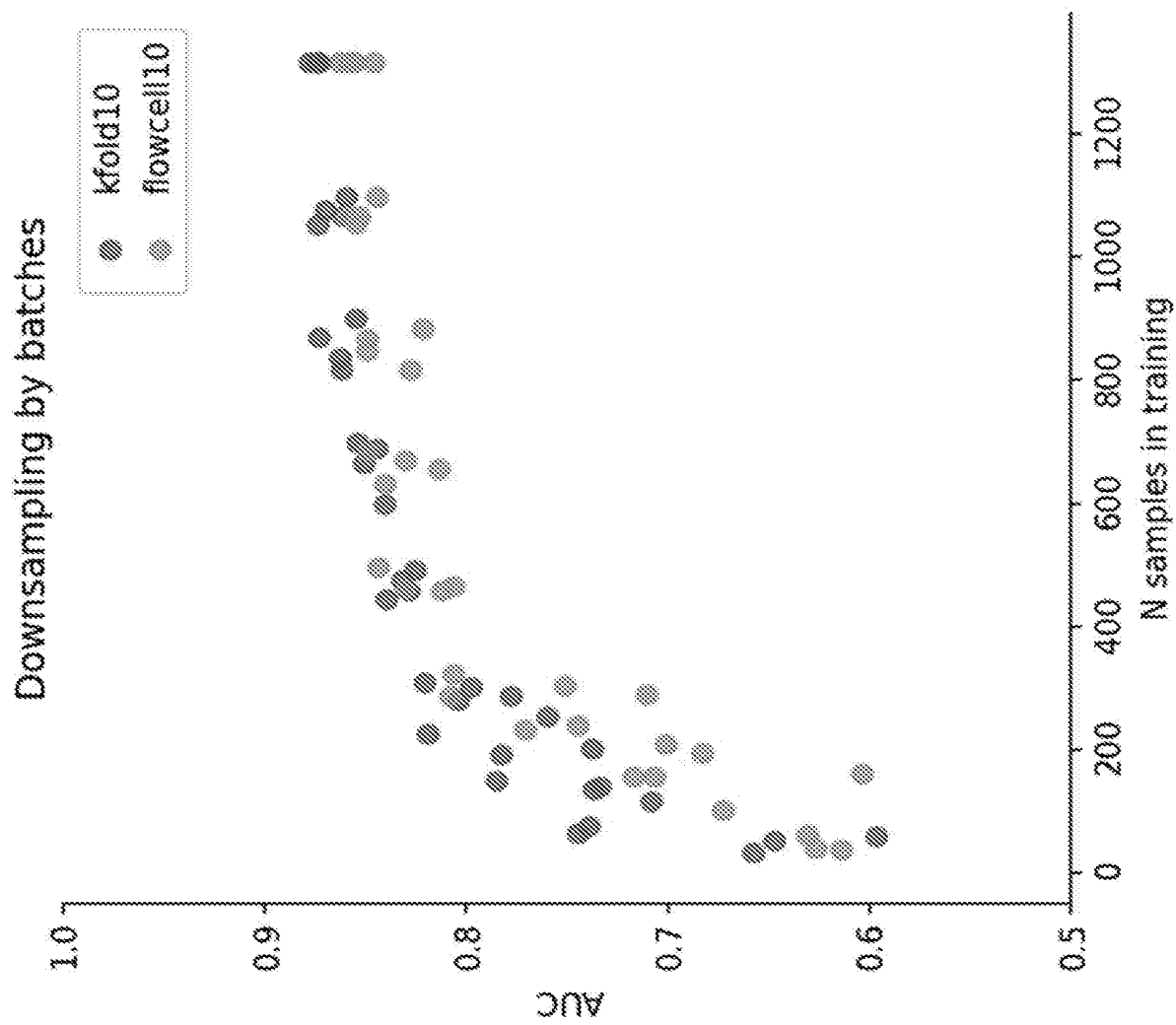


FIG. 31B

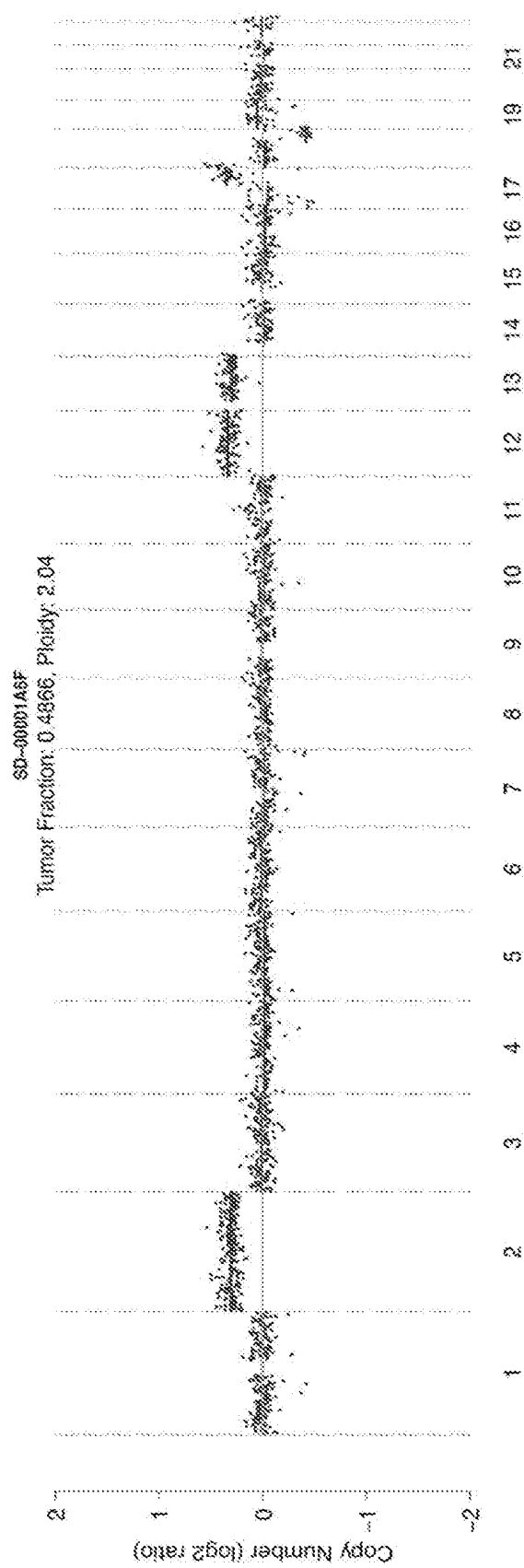


FIG. 32A

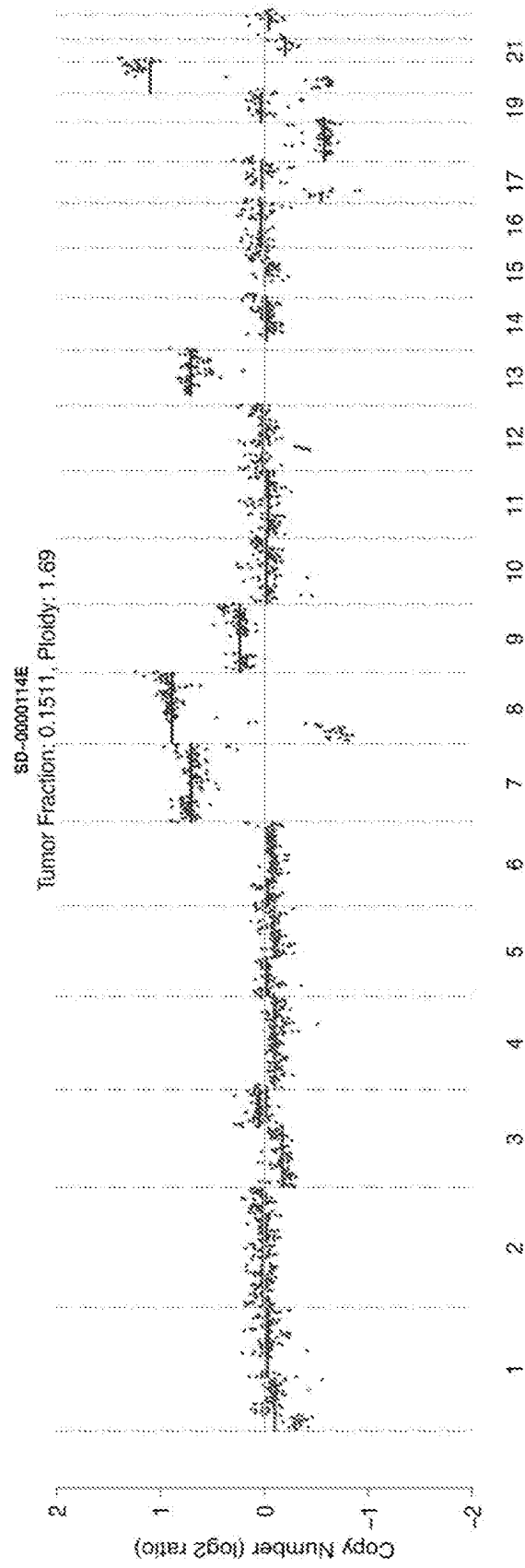


FIG. 32B

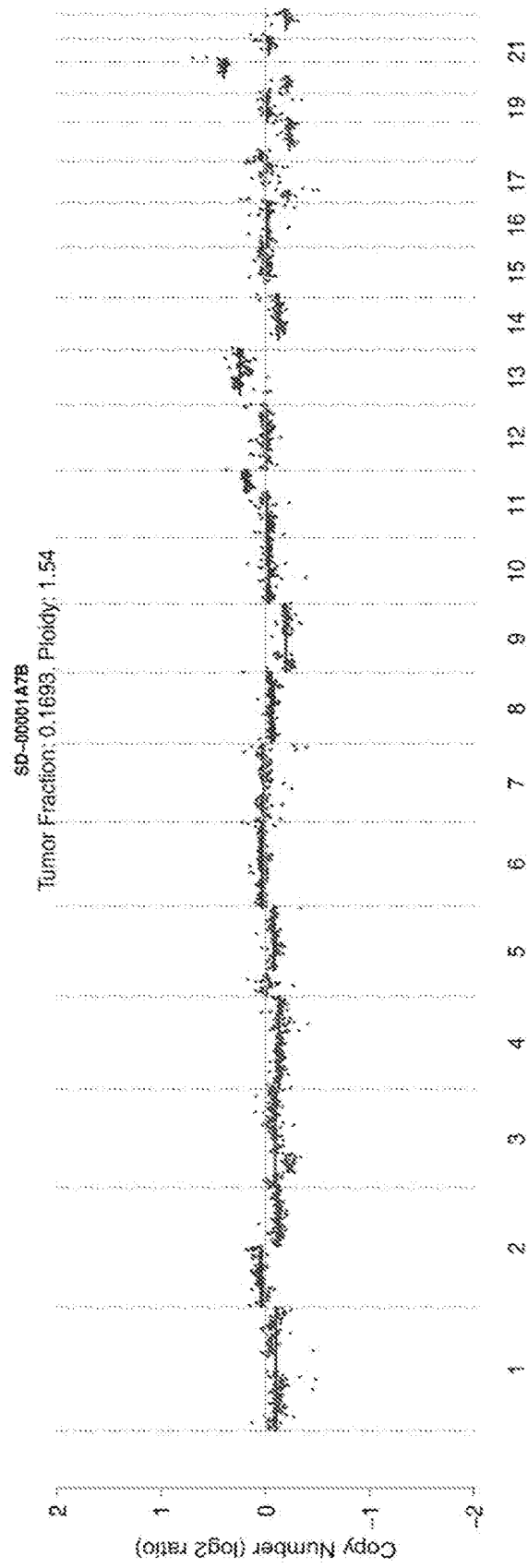


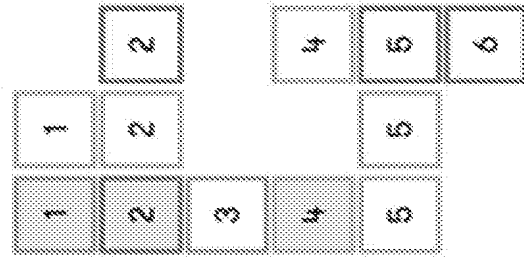
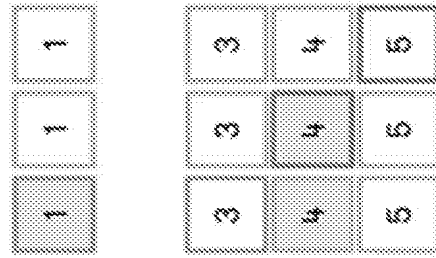
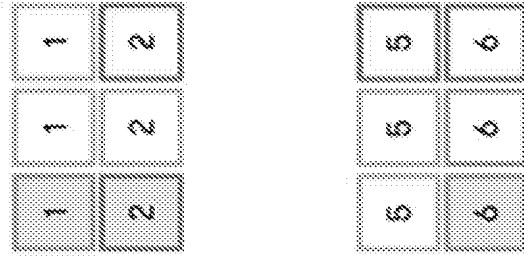
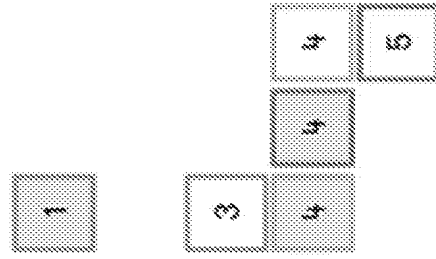
FIG. 32C

balanced k-batch
stratify folds by batch and
balance each institution
by class in training

ordered k-batch
stratify folds by processing
date after ordering batches
sequentially in time

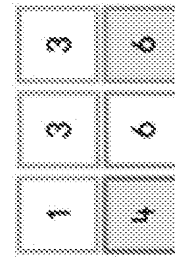
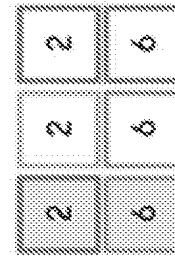
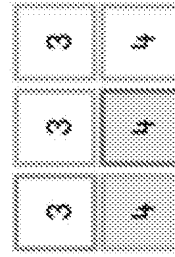
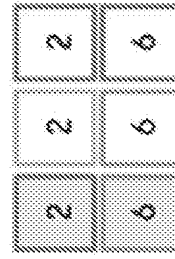
k-batch
stratify folds by batch

k-fold
stratify folds at random



TRAIN

FIG. 33A



TEST

FIG. 33B

Processing batch #

Institution A / B / C

Non-cancer control / cancer

1 2 3

1 2 3

1 2 3

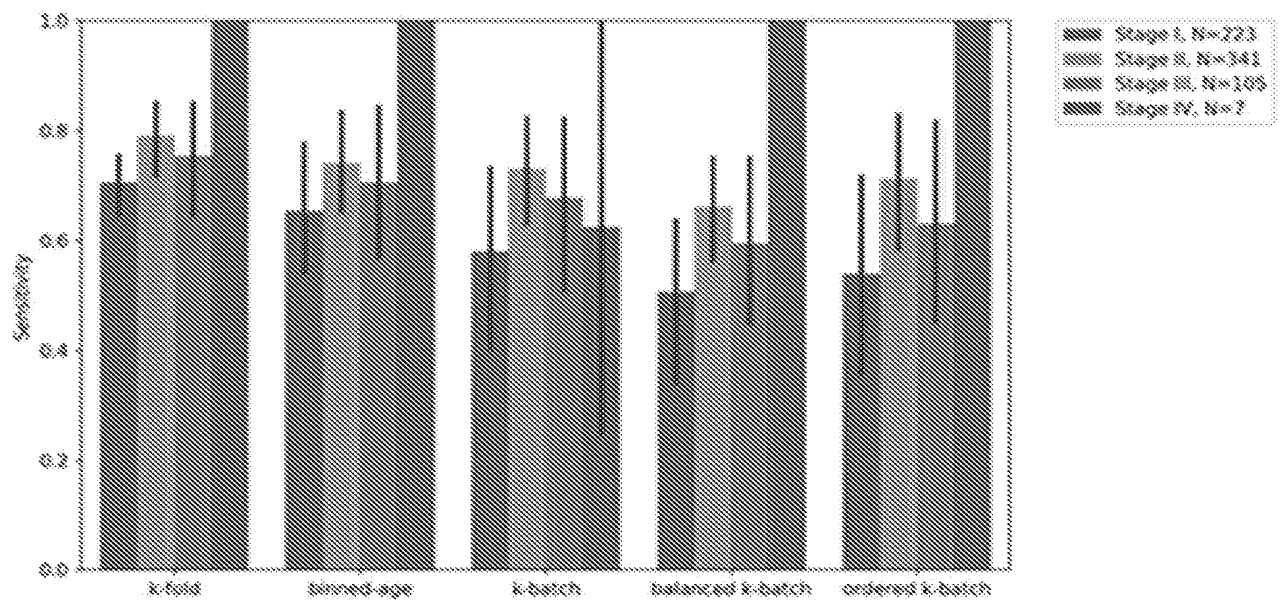


FIG. 34A

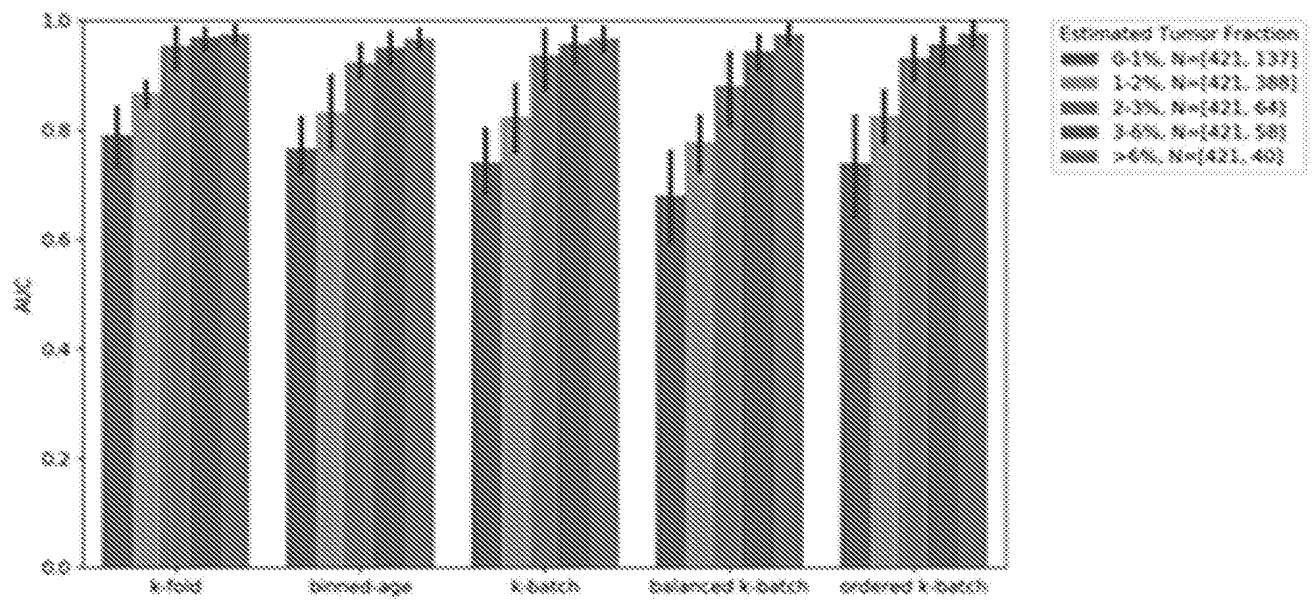


FIG. 34B

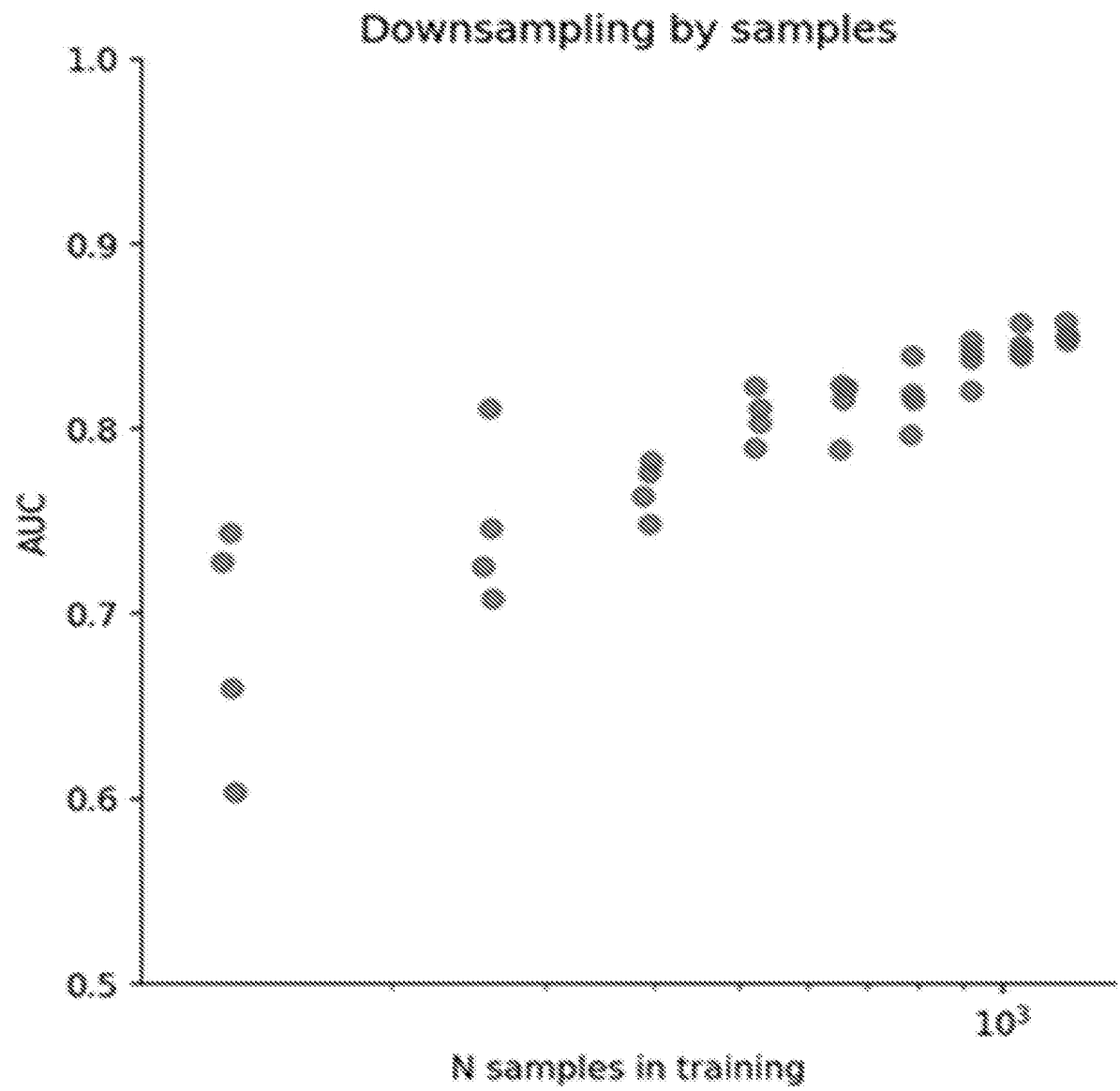


FIG. 34B

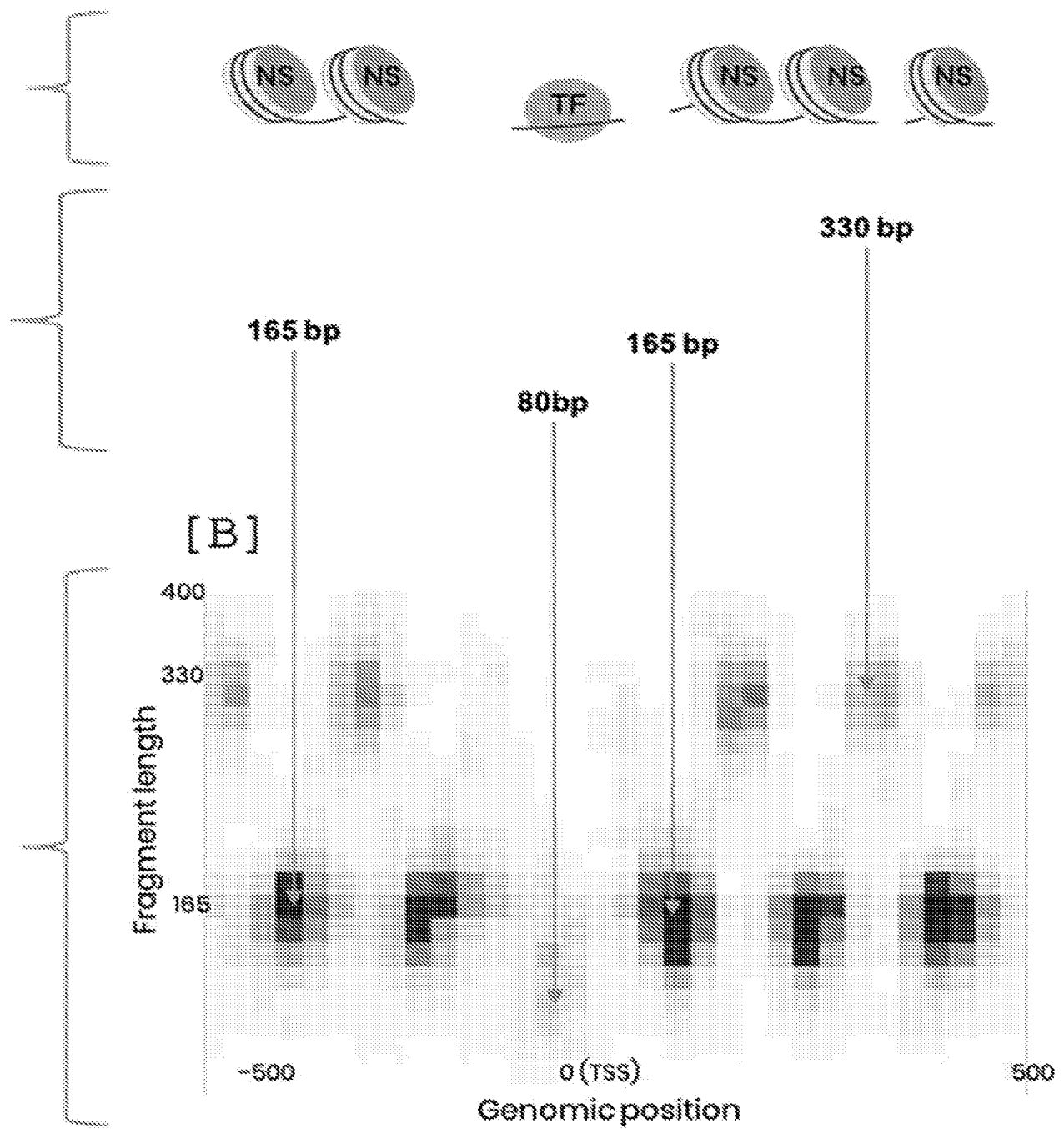


FIG. 35

TSS A

FIG. 36A

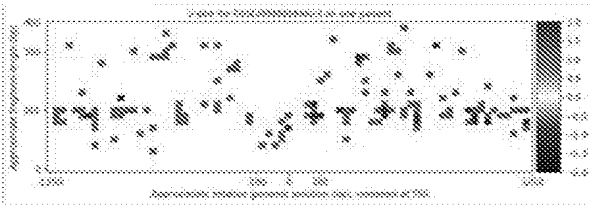


FIG. 36C

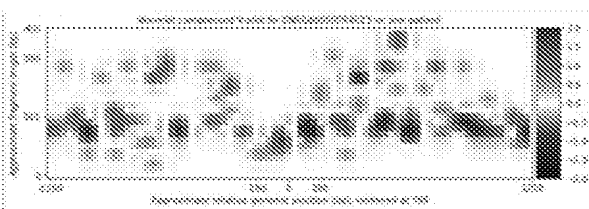


FIG. 36E

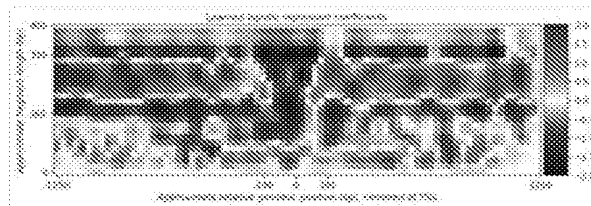
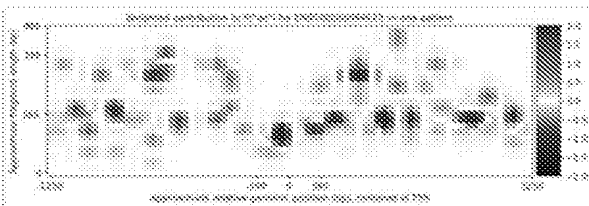


FIG. 36F



$$P(\text{on} \mid \text{TSS A}) = 0.83$$

TSS B

FIG. 36B

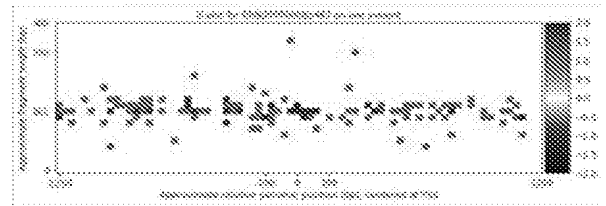


FIG. 36D

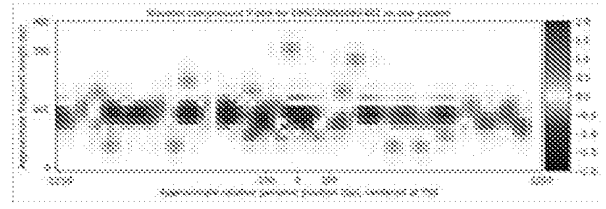
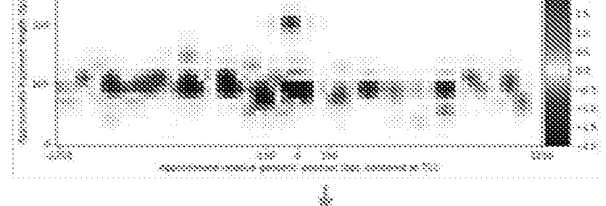


FIG. 36G



$$P(\text{on} \mid \text{TSS B}) = 0.01$$

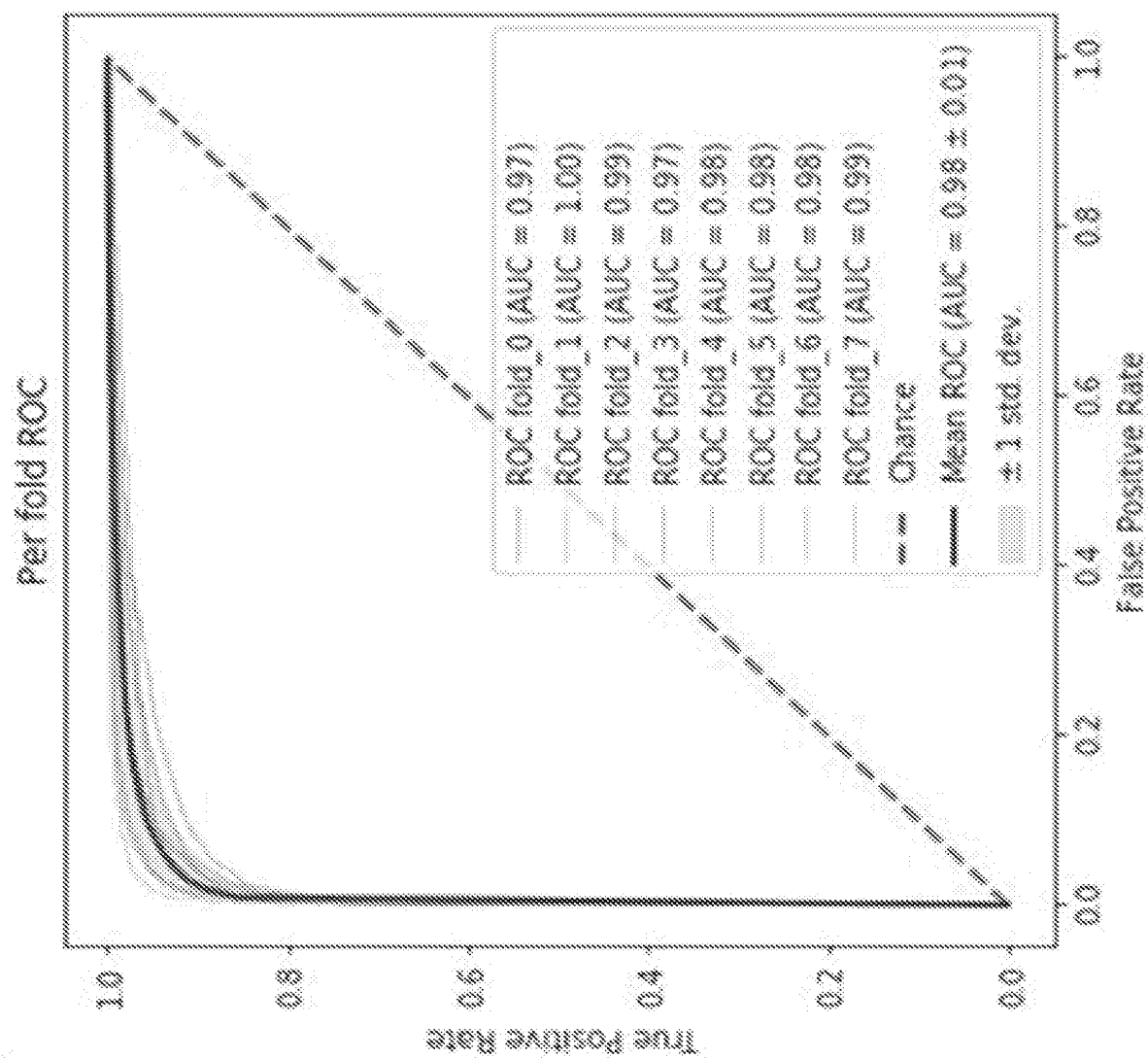


FIG. 37

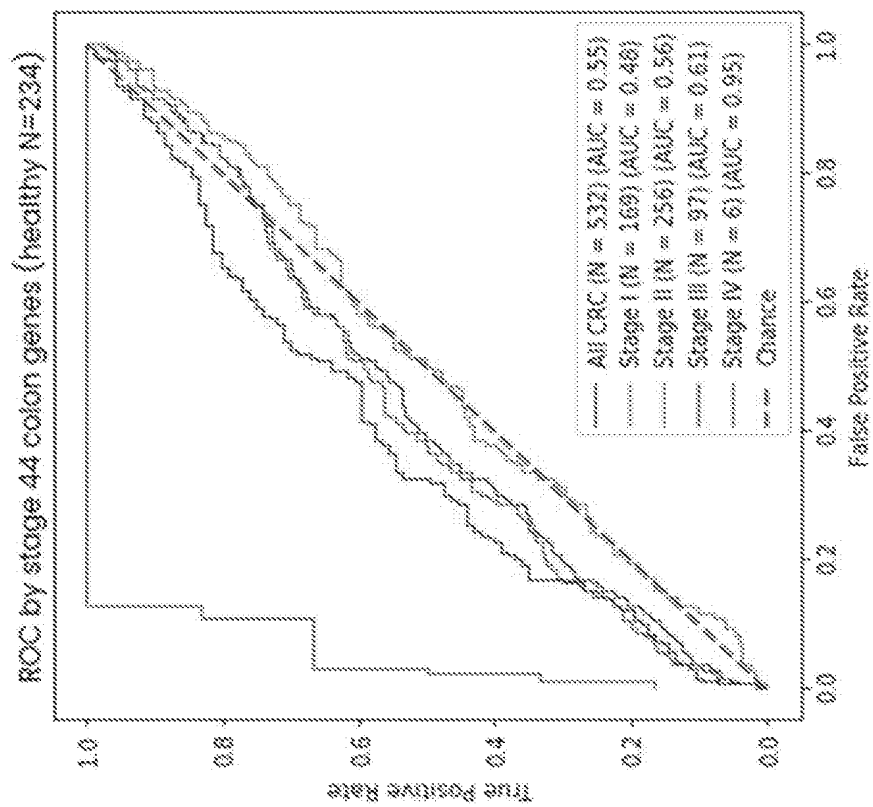


FIG. 38B

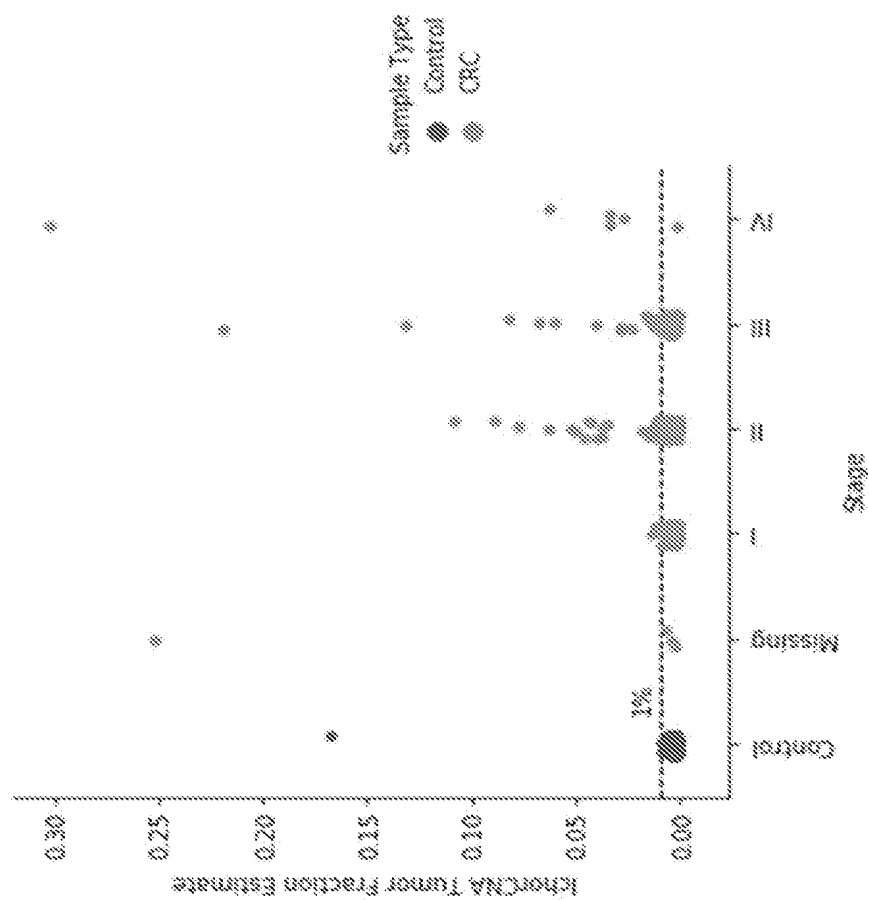


FIG. 38A

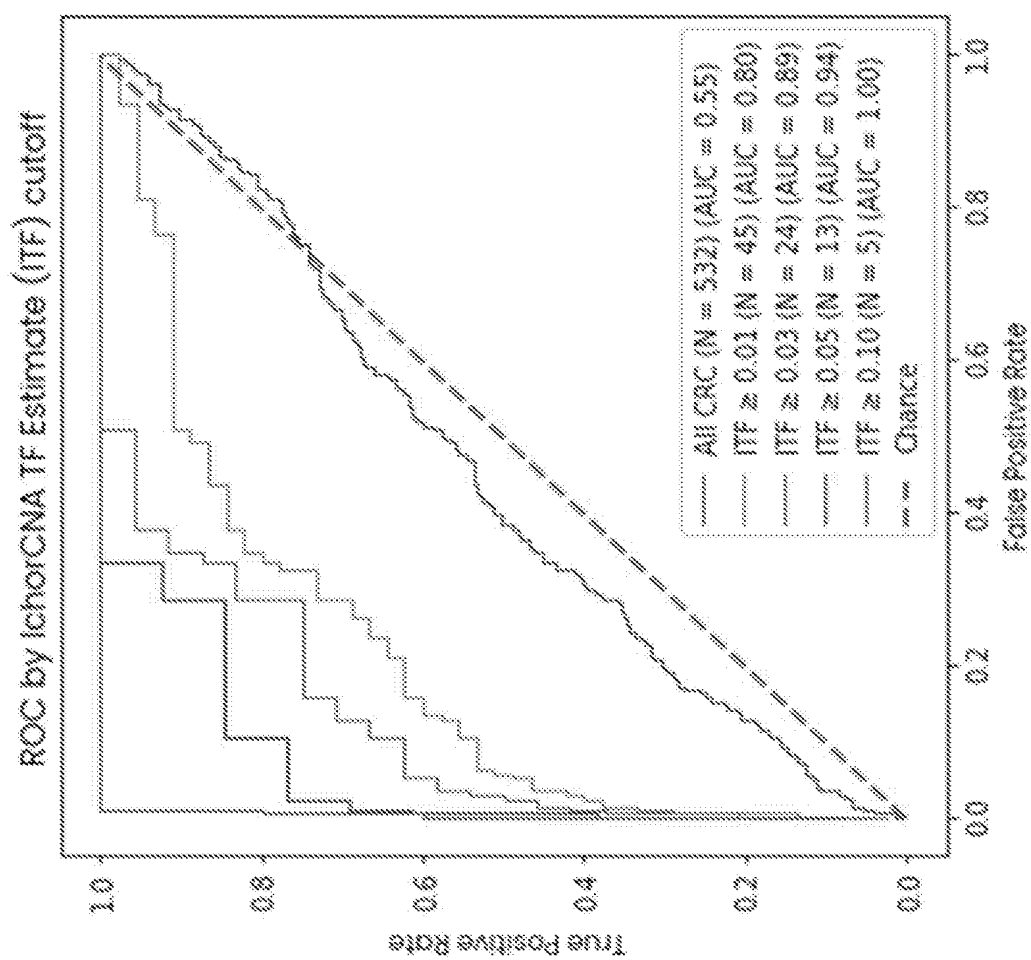


FIG. 38C

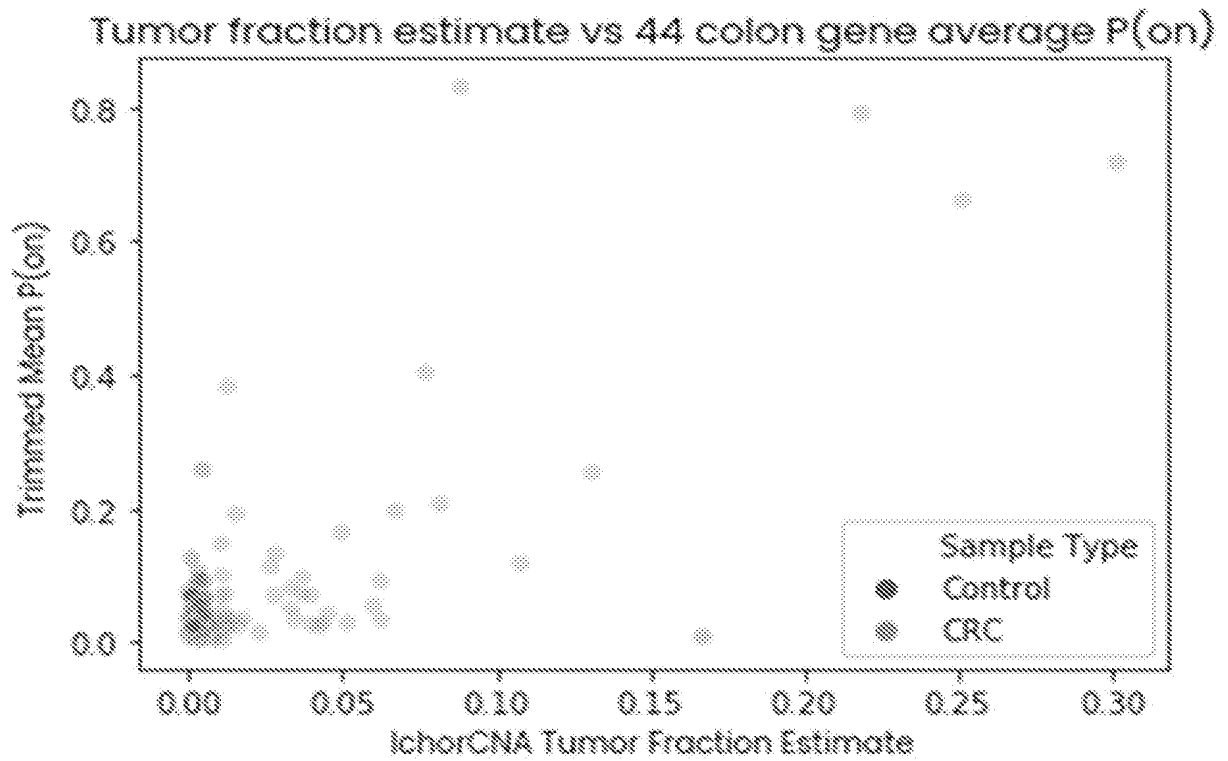


FIG. 39A

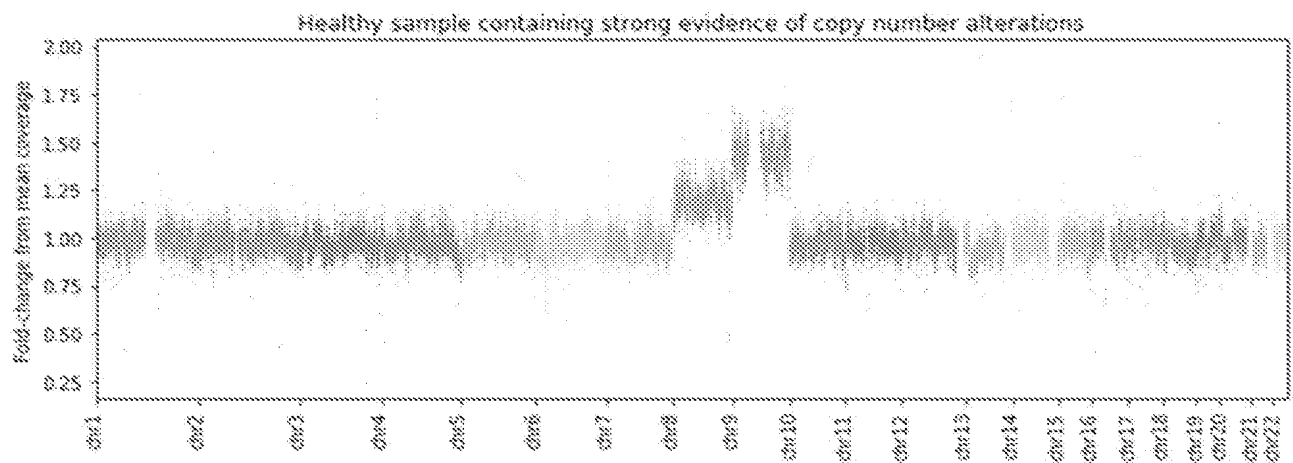


FIG. 39B