

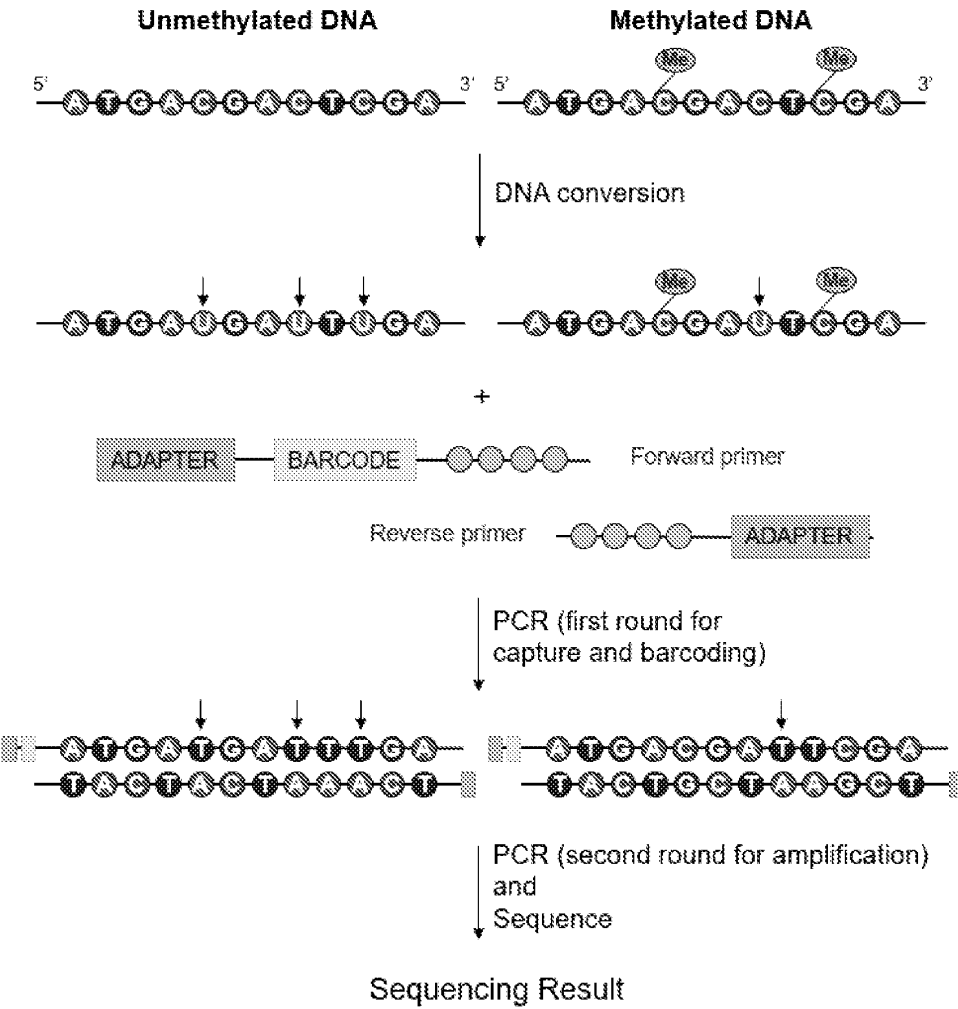


Fig. 1

CLIP4_methyl_2F ACACGACGCTCTTCCGATCTNNNNNNNNNN
GGGTTYGGAGAGGTGTG

CLIP4_methyl_2R GACGTGTGCTCTTCCGATCT CCTACCTCCTCCRAATCCTC

Indexed Illumina P5 Primers

F-1:

AATGATACGGCGACCACCGAGATCTACACCTAGCGCTACACTCTTCCCTACAC
GACGCTCTTCCGATC*T

Indexed Illumina P7 Primers

R-1:

CAAGCAGAAGACGGCATACGAGATAACCGCGGTGACTGGAGTTCAGACGTGT
GCTCTTCCGATC*T

Fig. 2

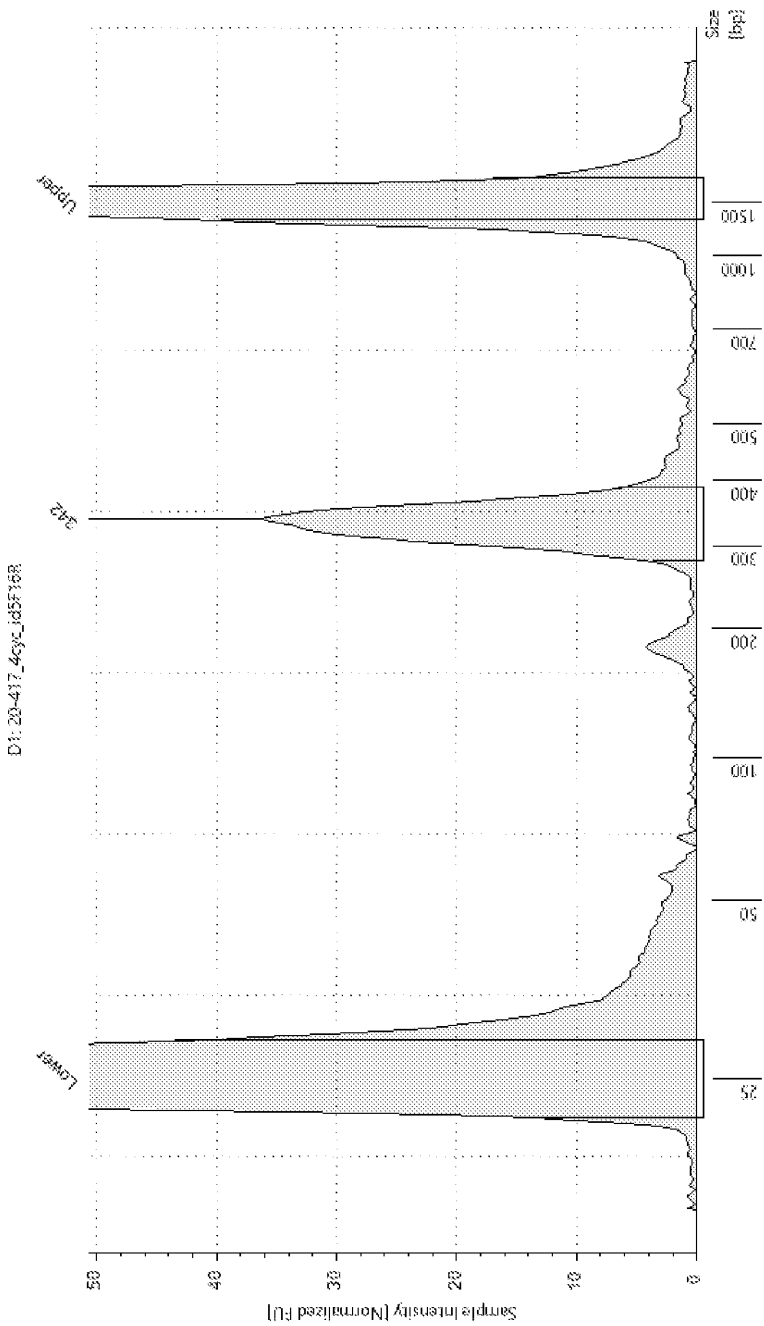


Fig. 3

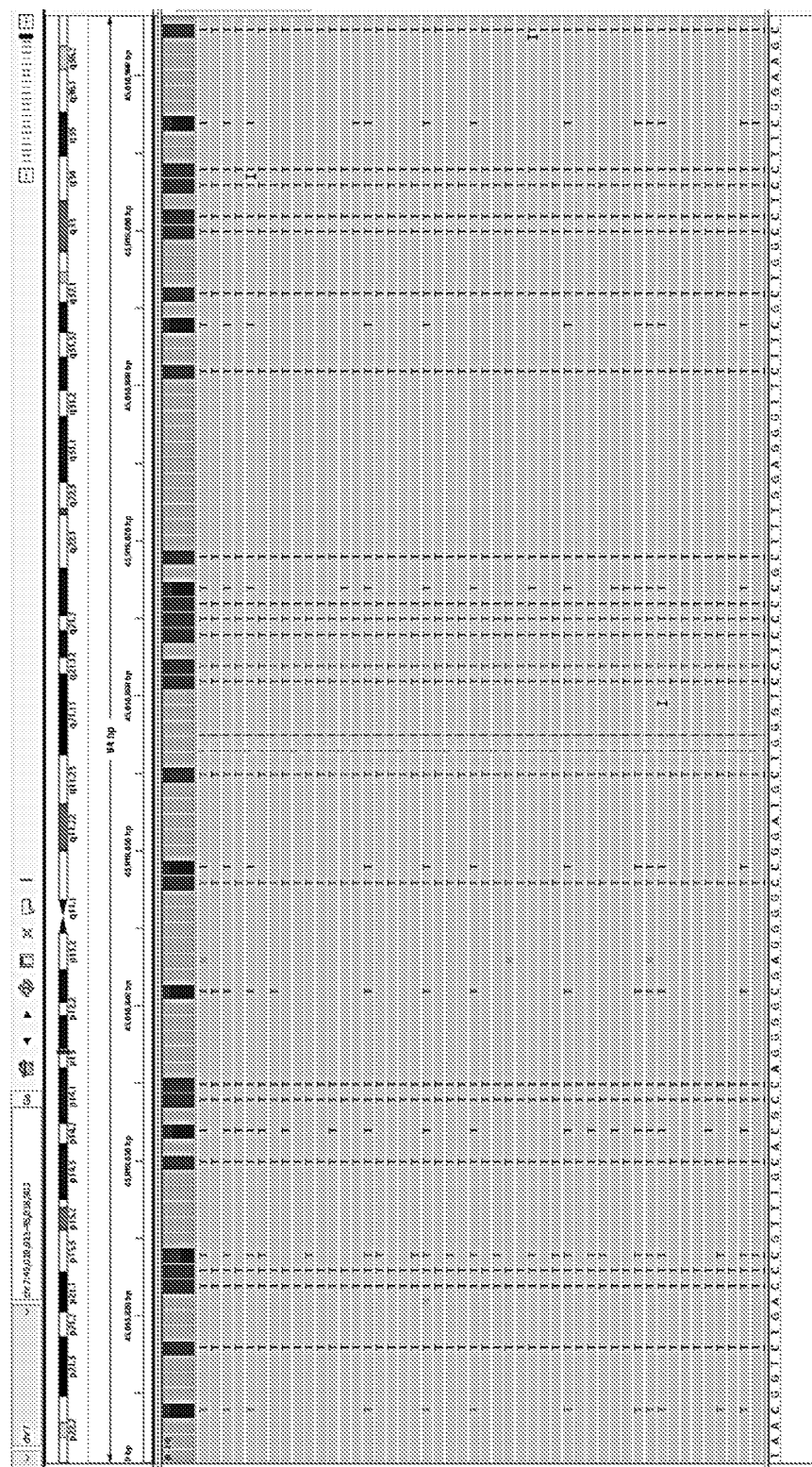
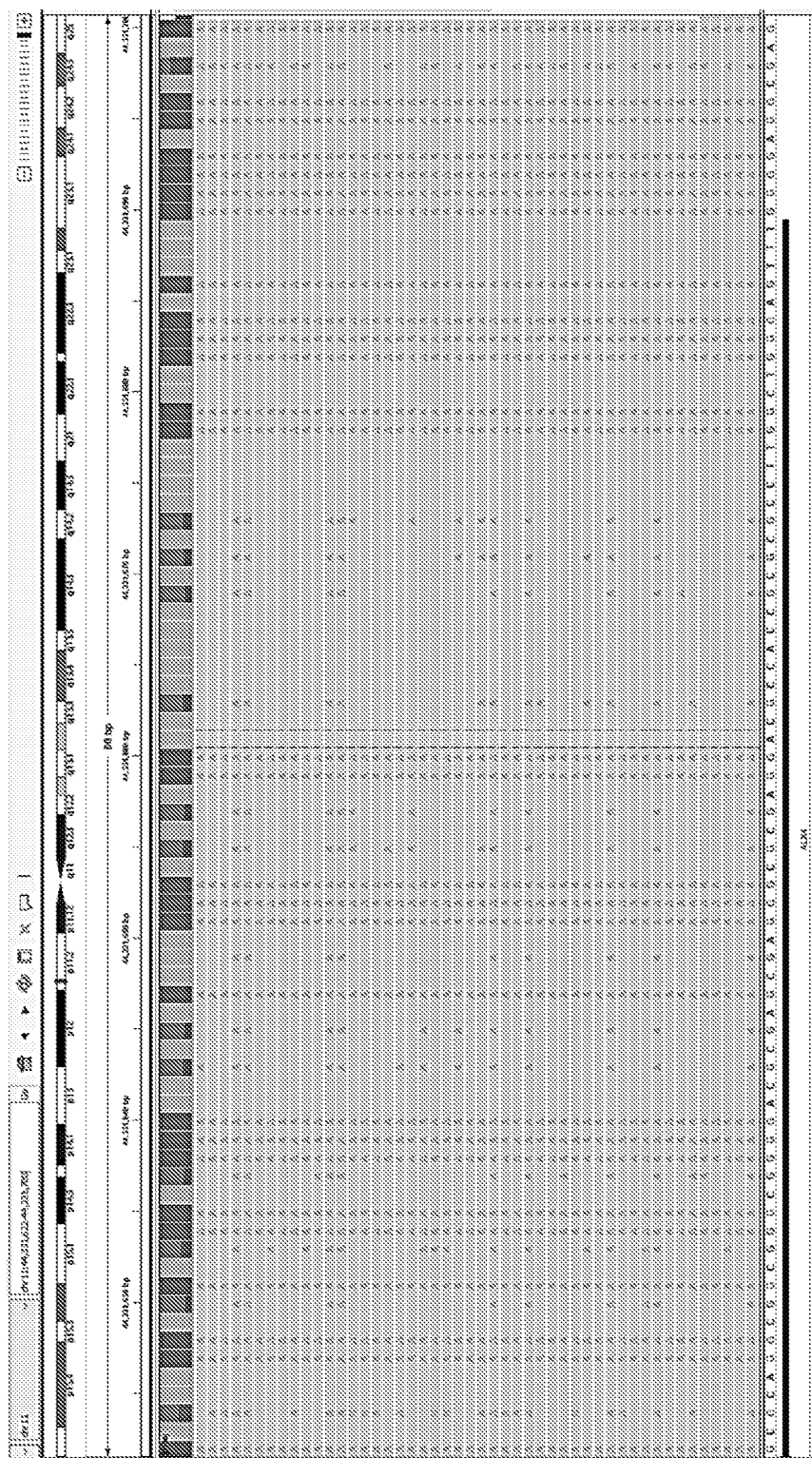


Fig. 4(a)



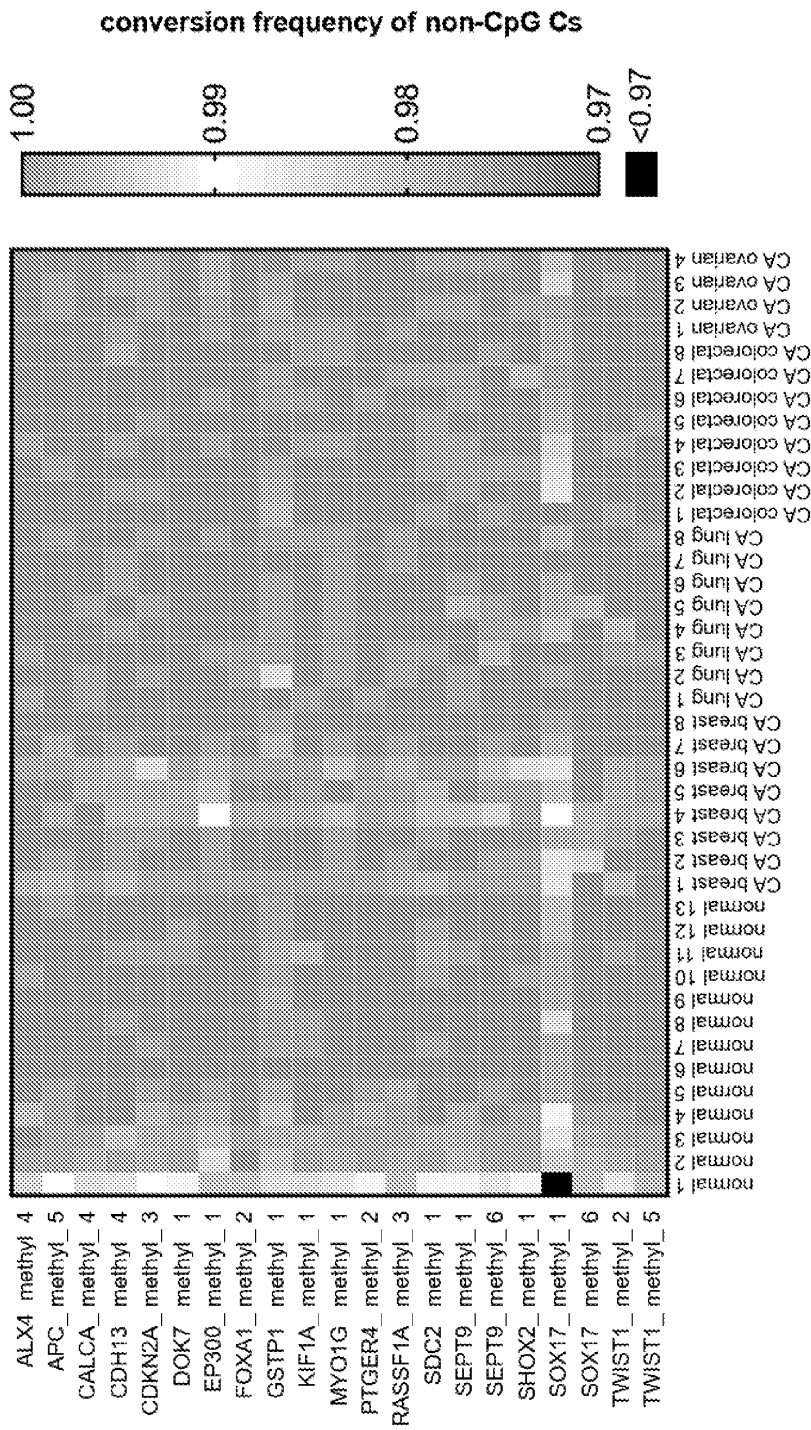


Fig. 5

7/13

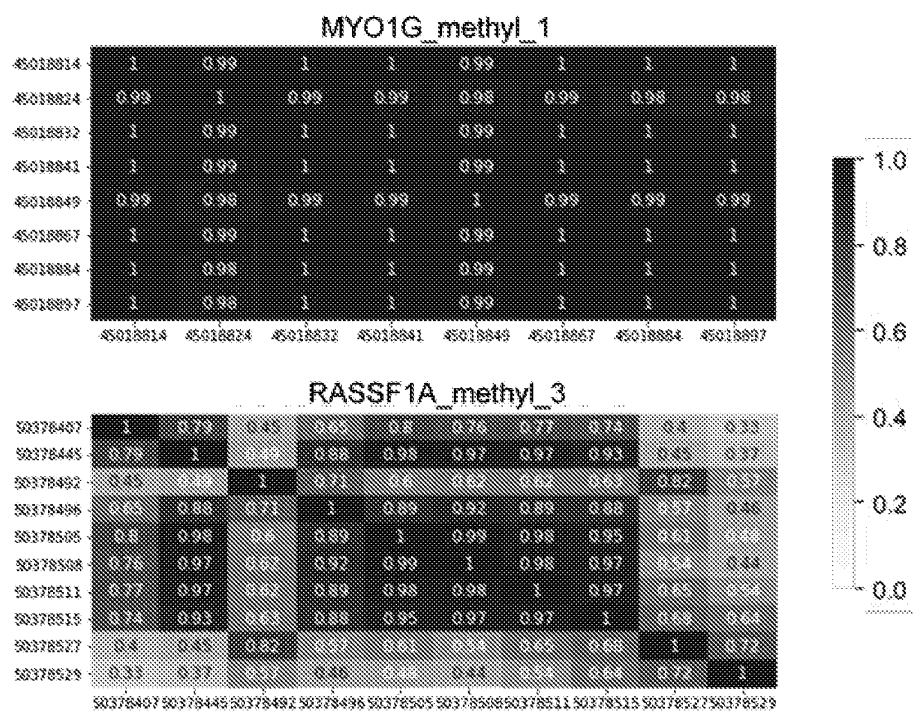


Fig. 6

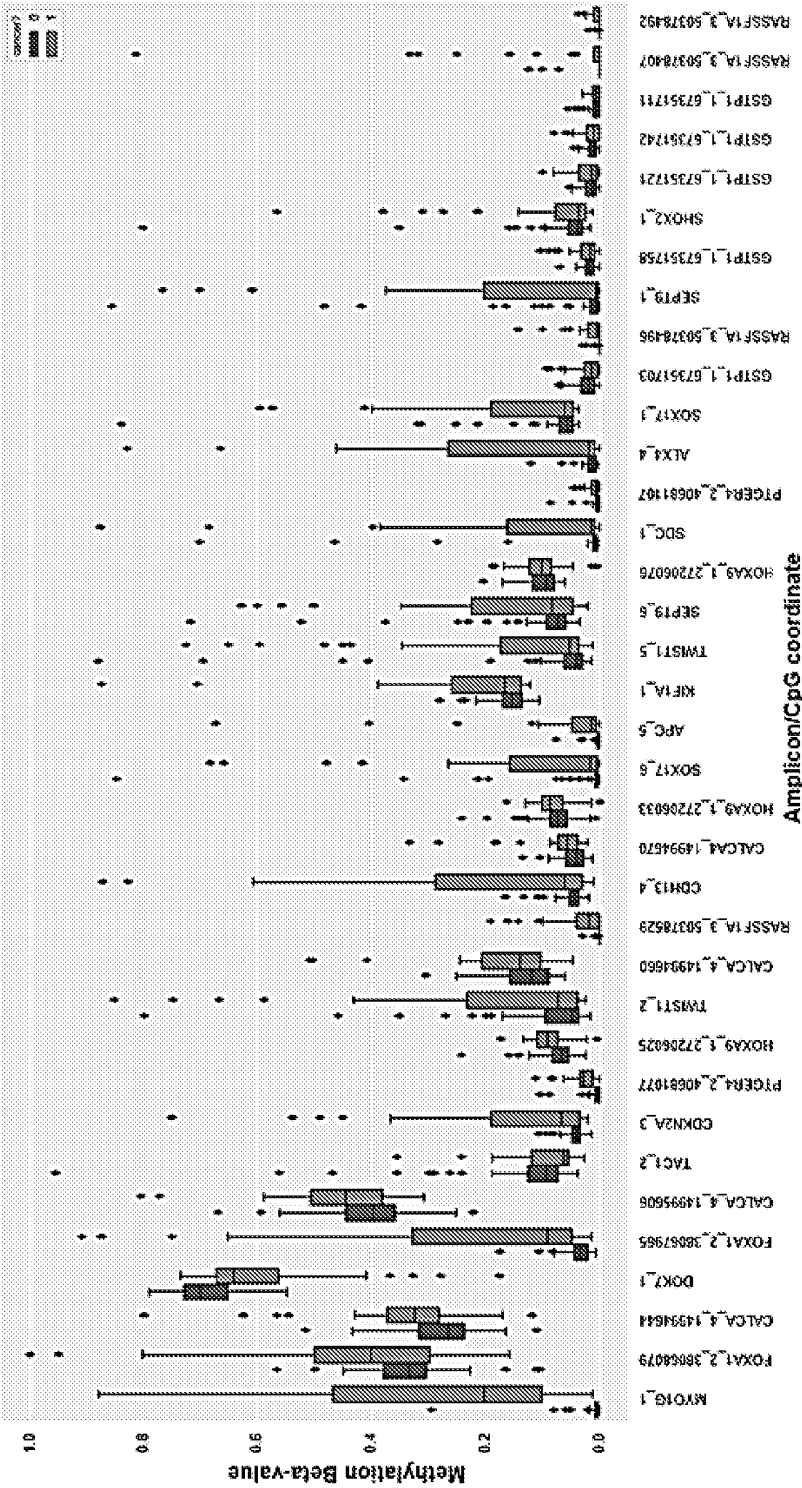


Fig. 7

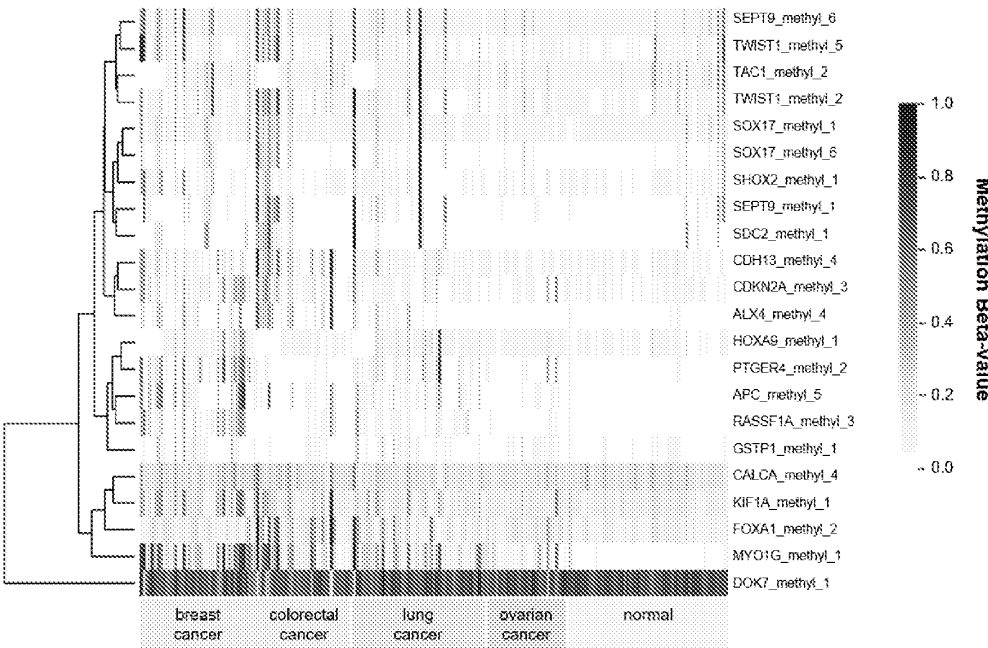


Fig. 8

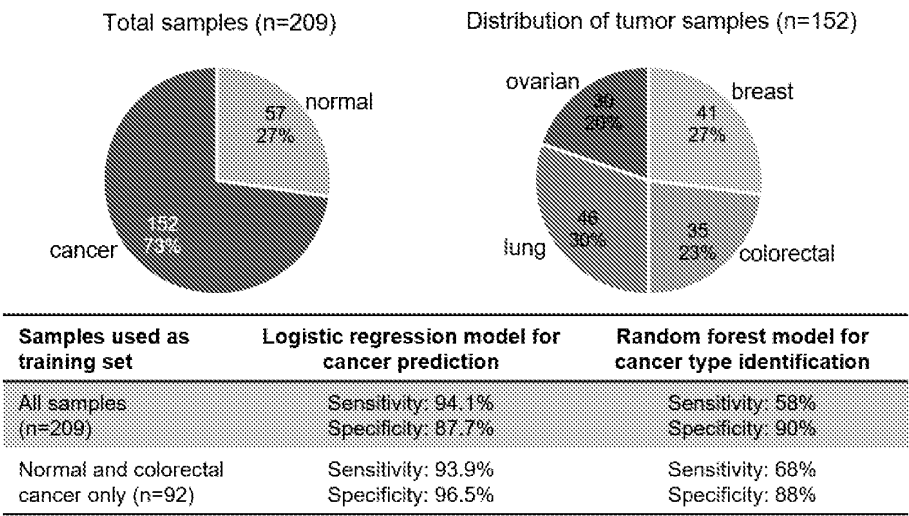


Fig. 9

11/13

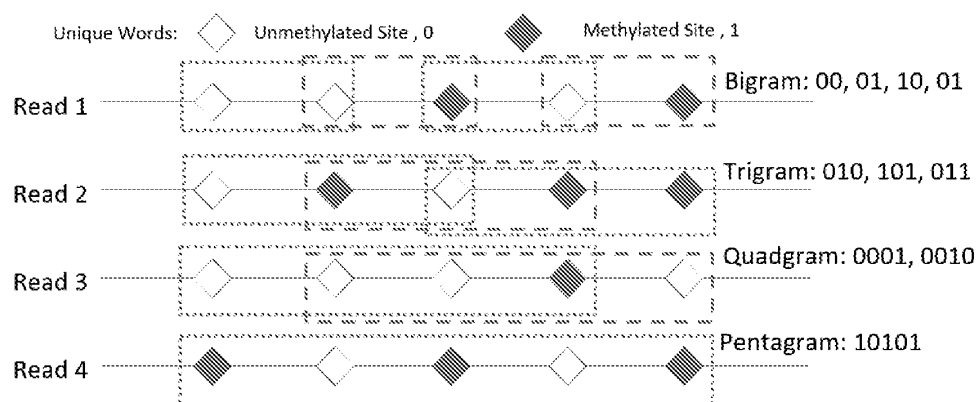


Fig. 10

12/13

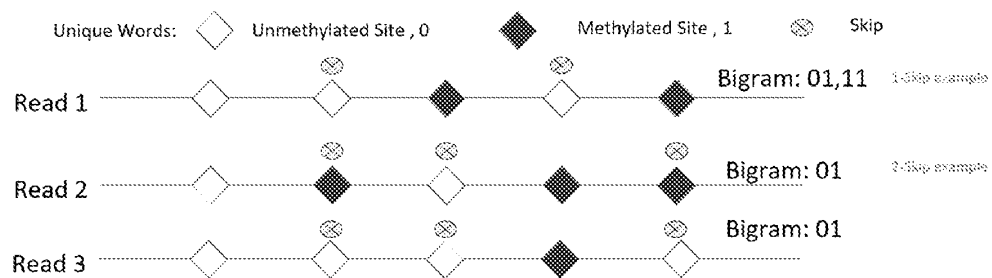


Fig. 11

Methylation data	Early-stage lung cancer sensitivity (%)	Late-stage lung cancer sensitivity (%)
Methylation amplicon frequency (mAF)	33.96	86.21
Methylation N-gram	54.72	81.61
Methylation Skip-gram	43.40	83.91
Biomarkers	35.85	82.76
Ensemble mAF+Biomarkers+N-gram	79.49	91.07
CEA	46.15	73.21
Combined [Ensemble mAF+Biomarkers+N-gram] + CEA	84.64	94.64

Fig. 12