

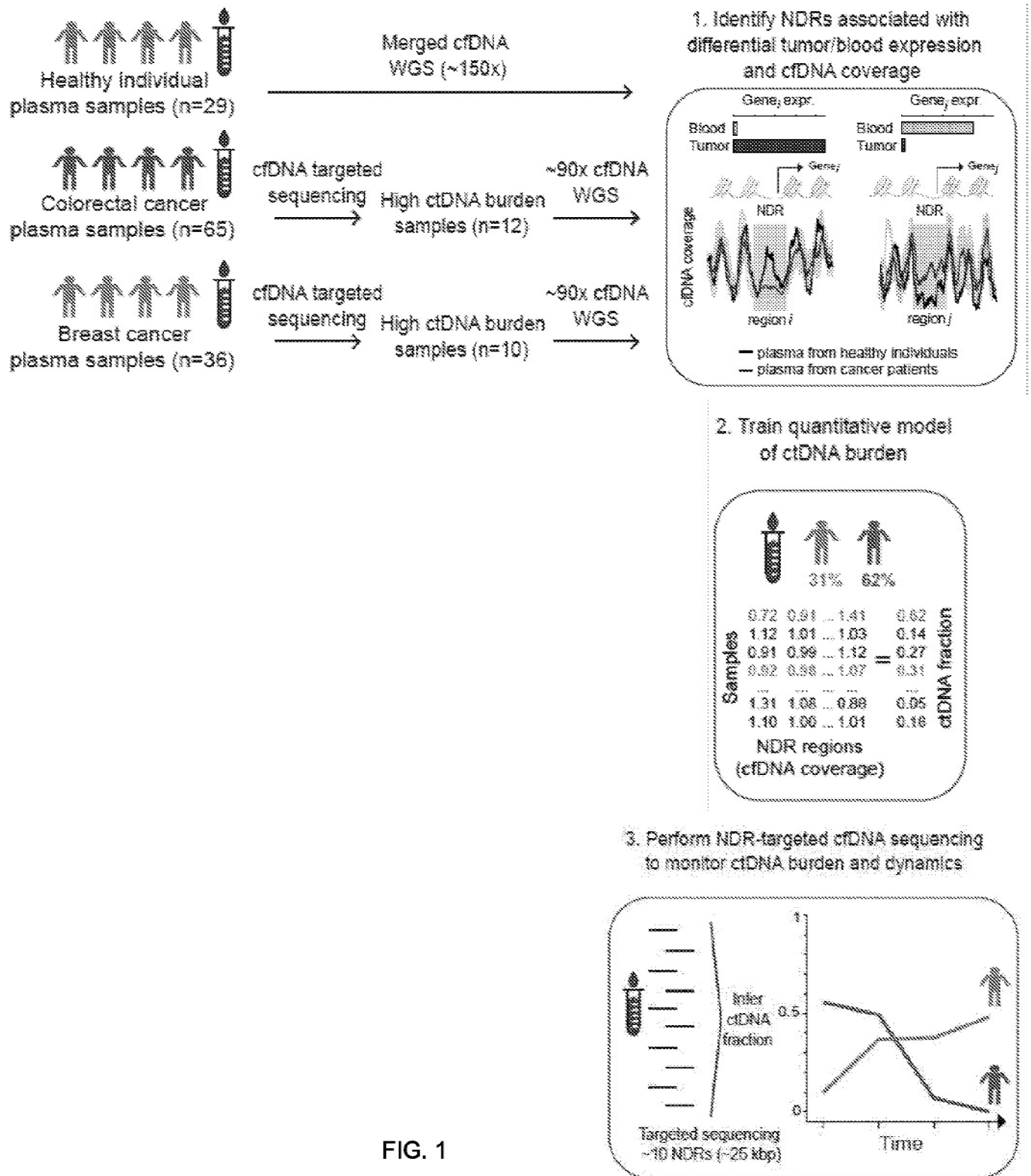
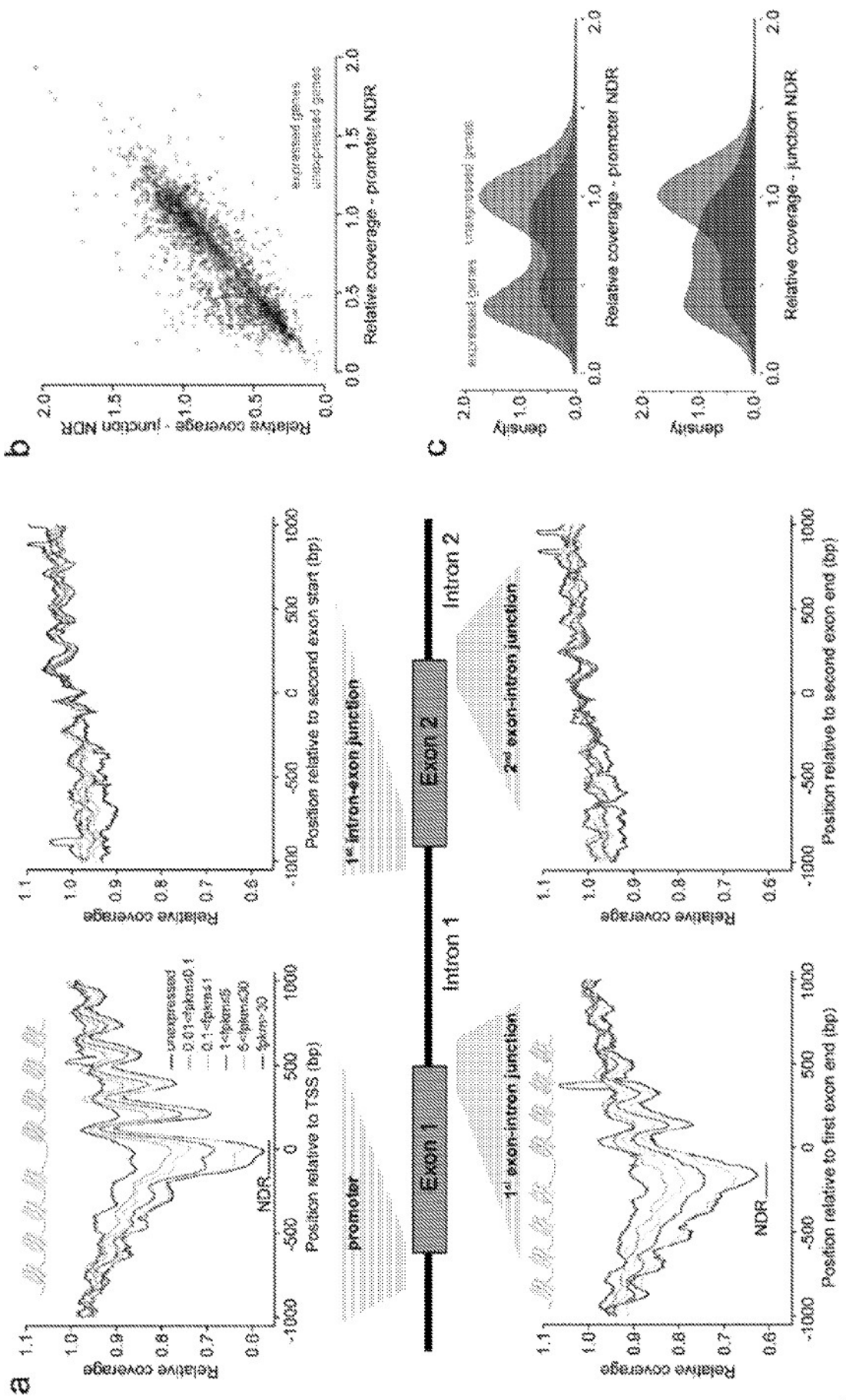


FIG. 1



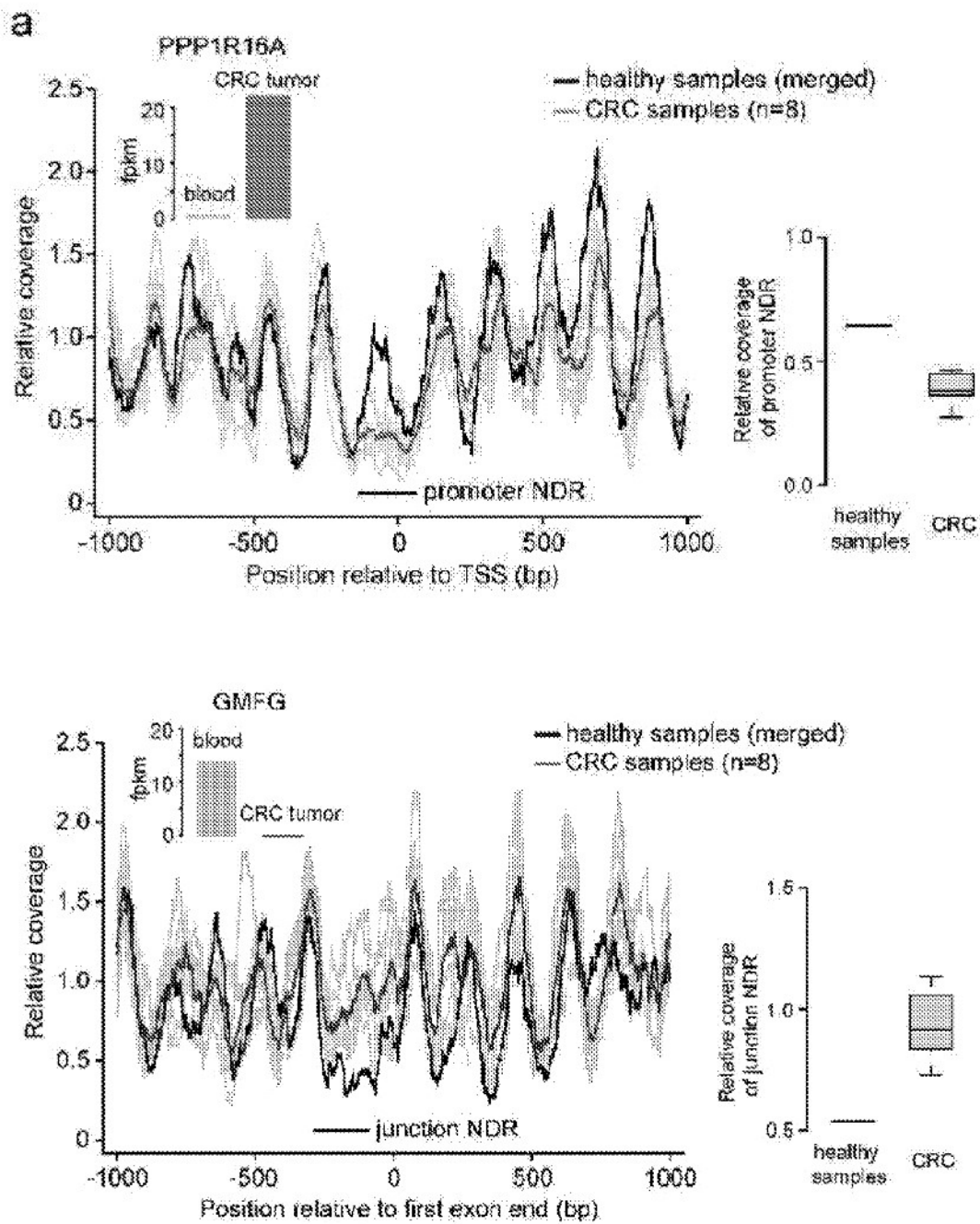


FIG. 3

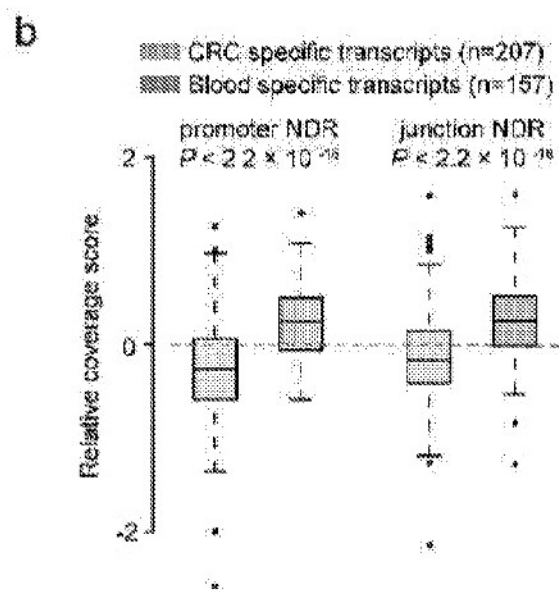


FIG. 3 (continued)

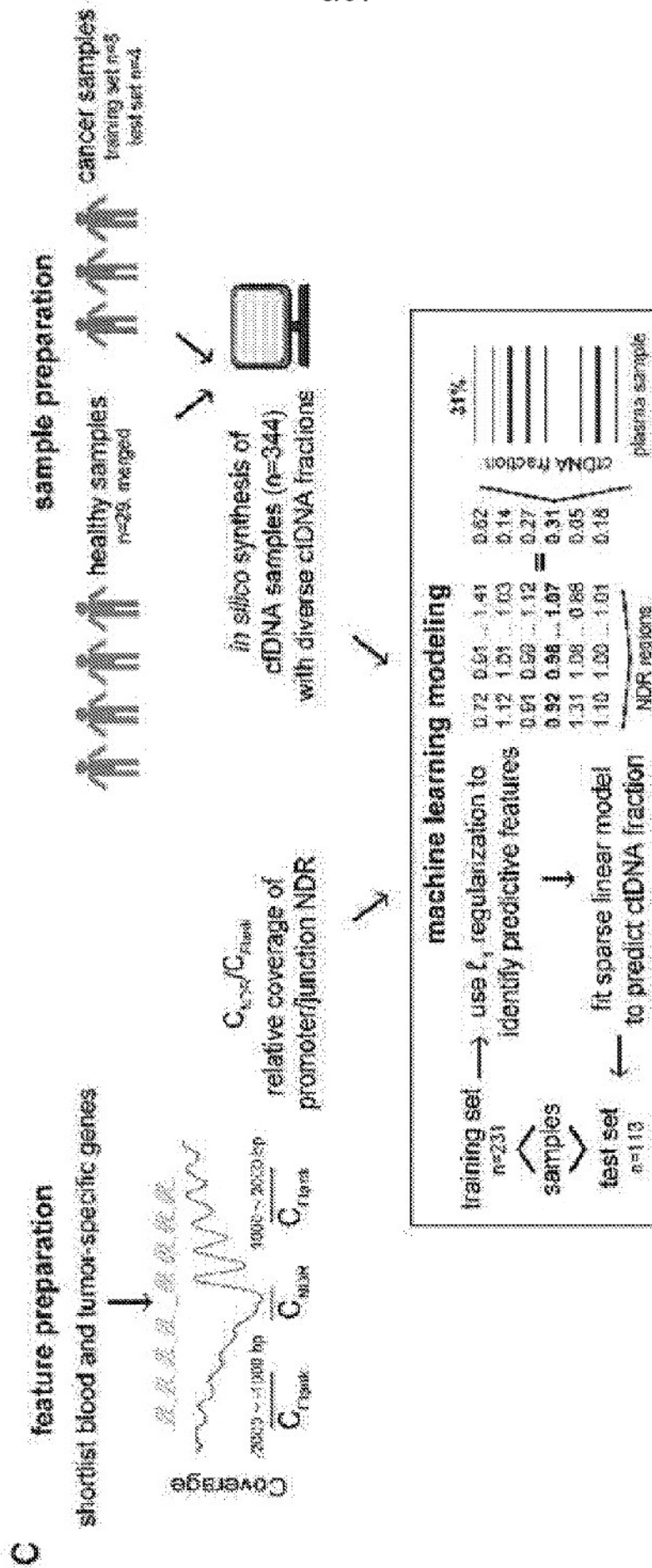


FIG. 3 (continued)

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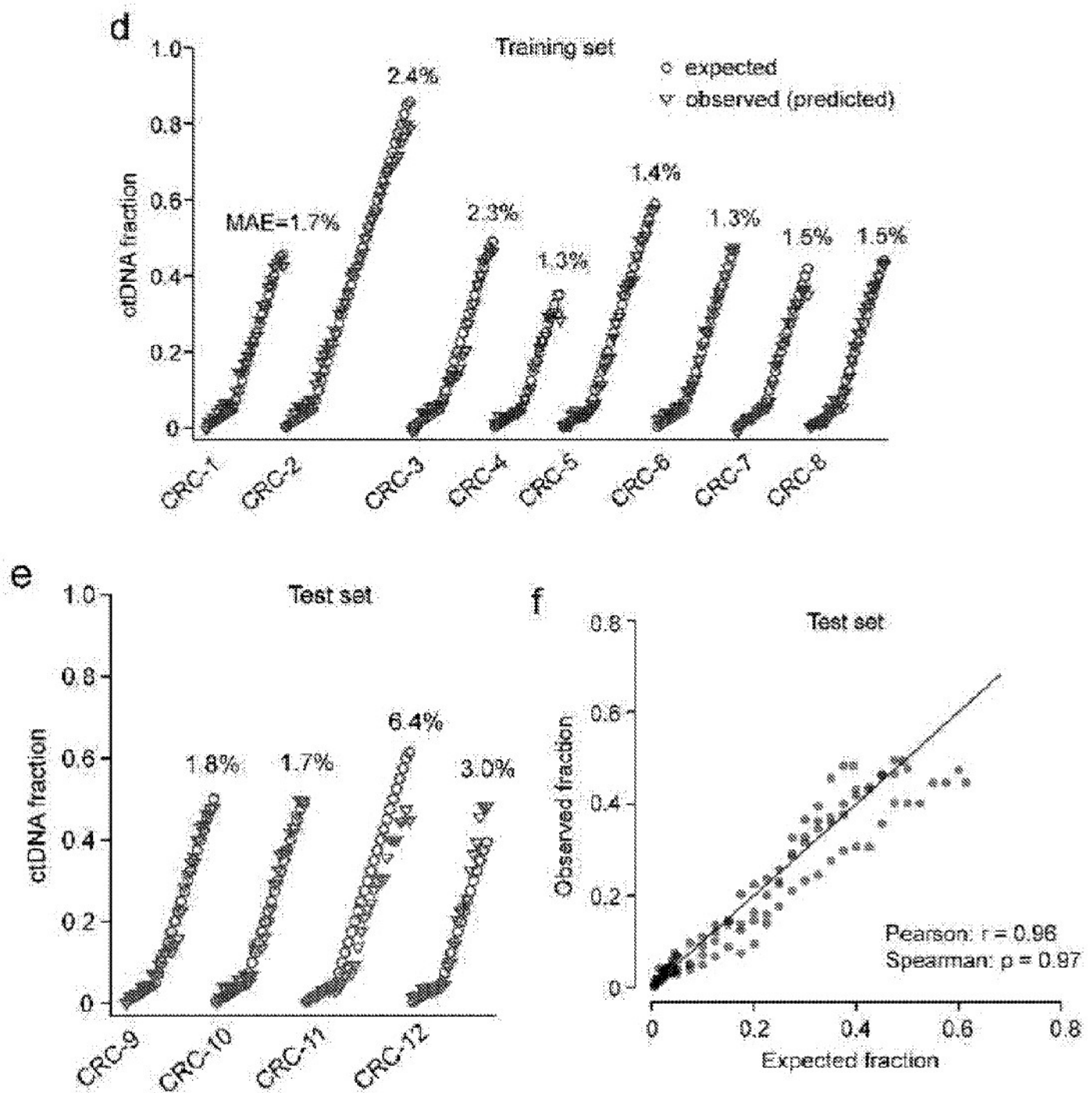


FIG. 3 (continued)

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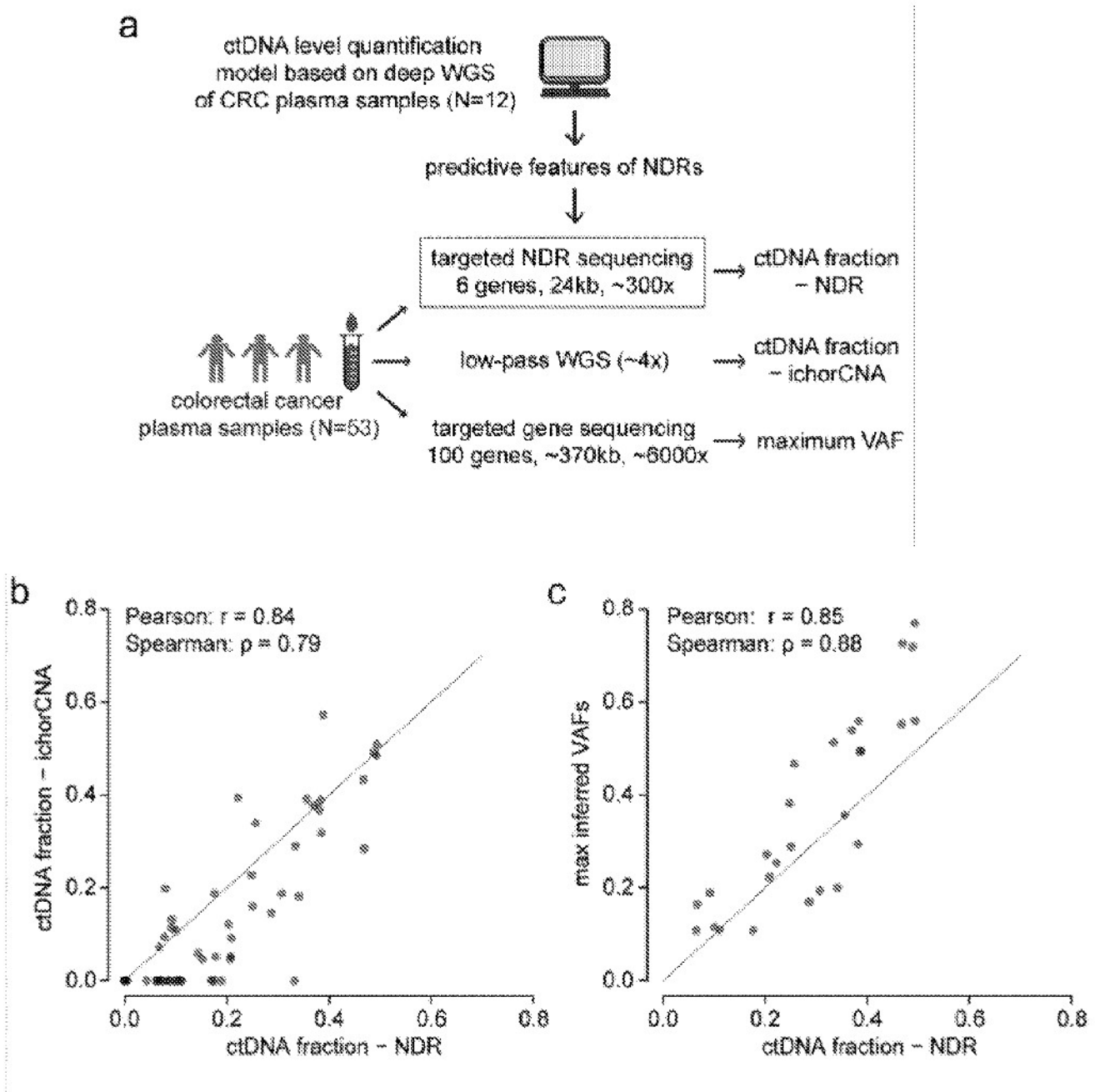


FIG. 4

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d

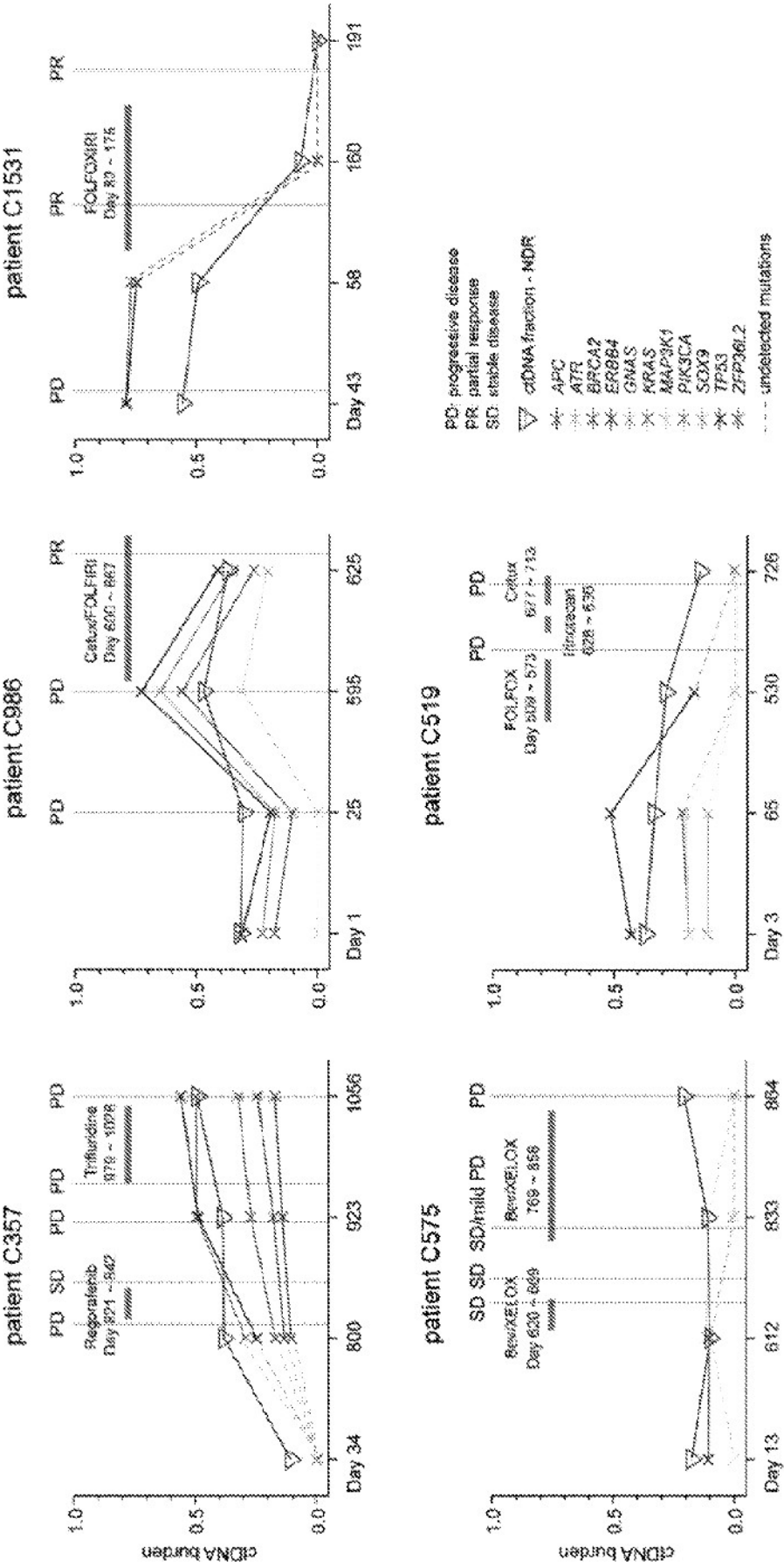


FIG. 4 (continued)

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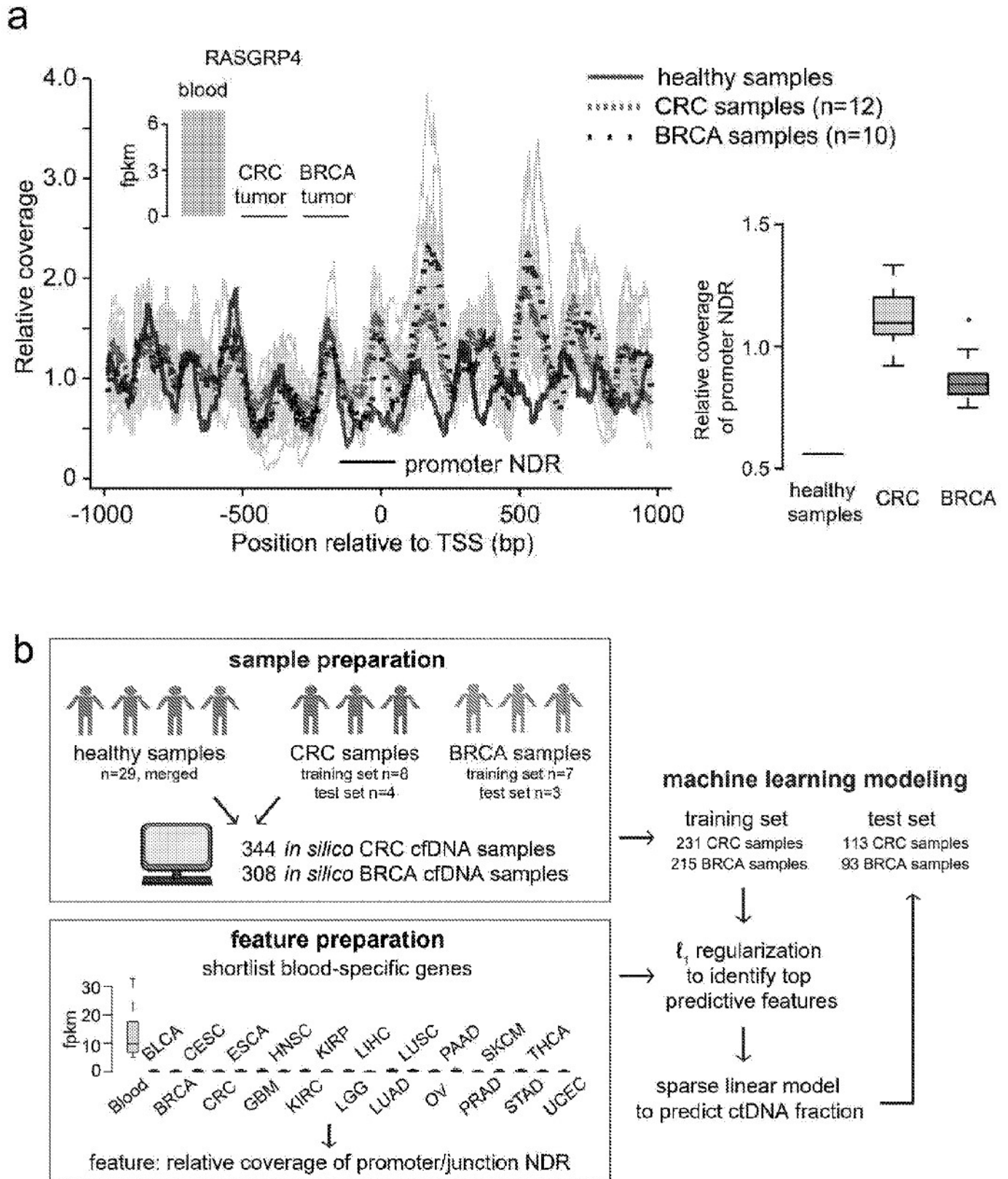


FIG. 5

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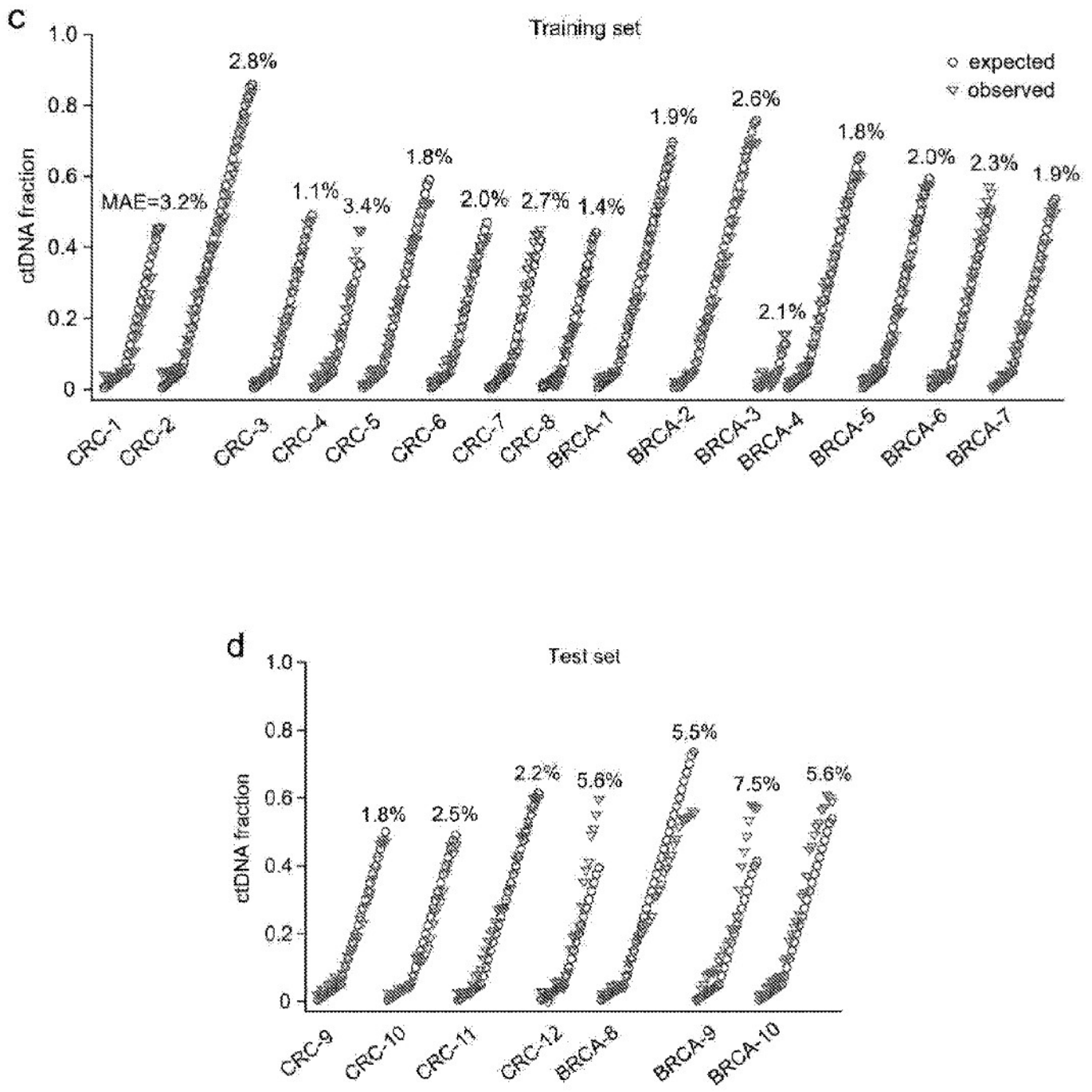


FIG. 5 (continued)

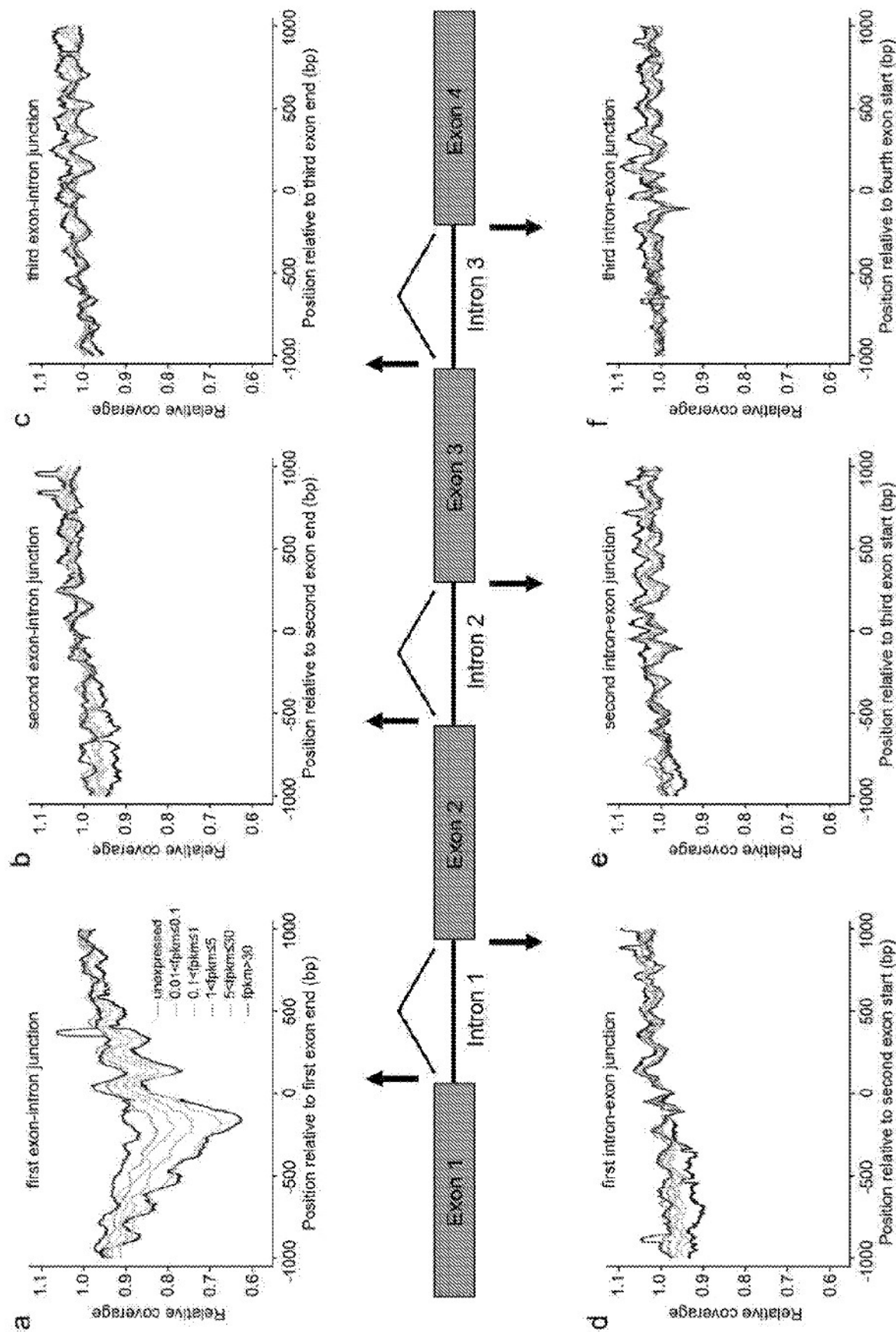


FIG. 6

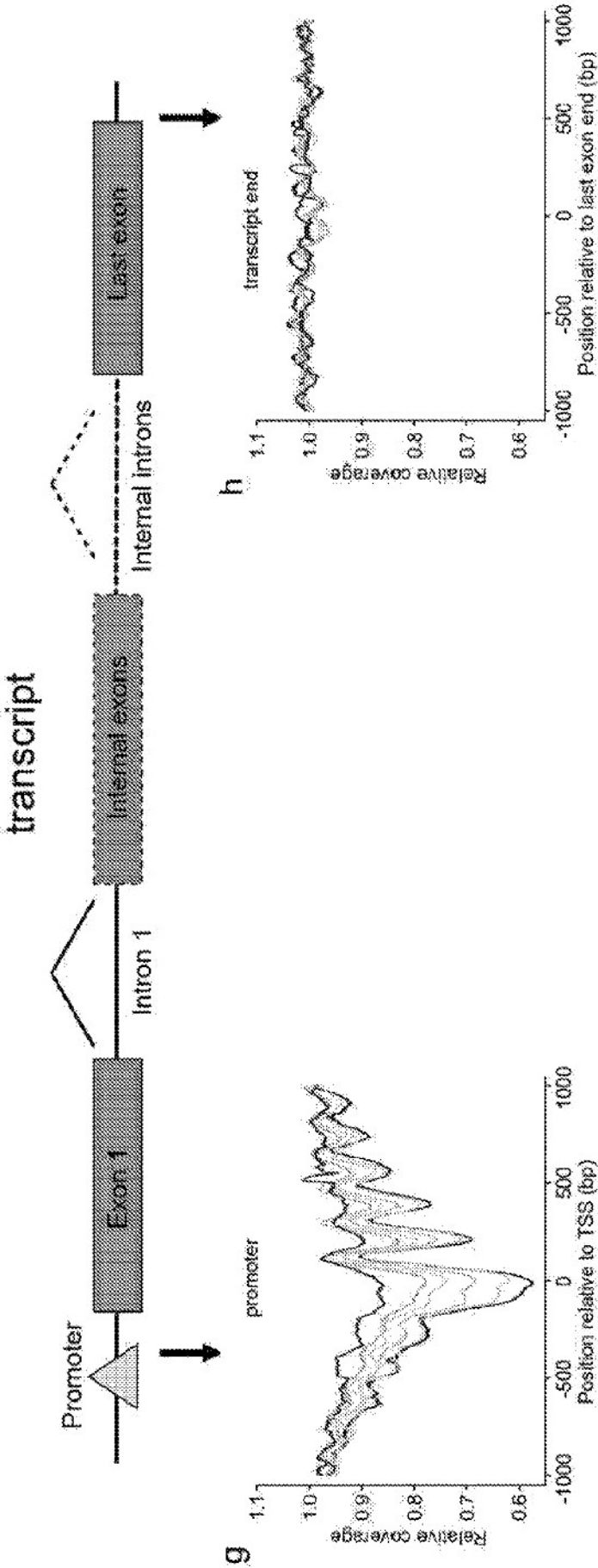


FIG. 6 (continued)

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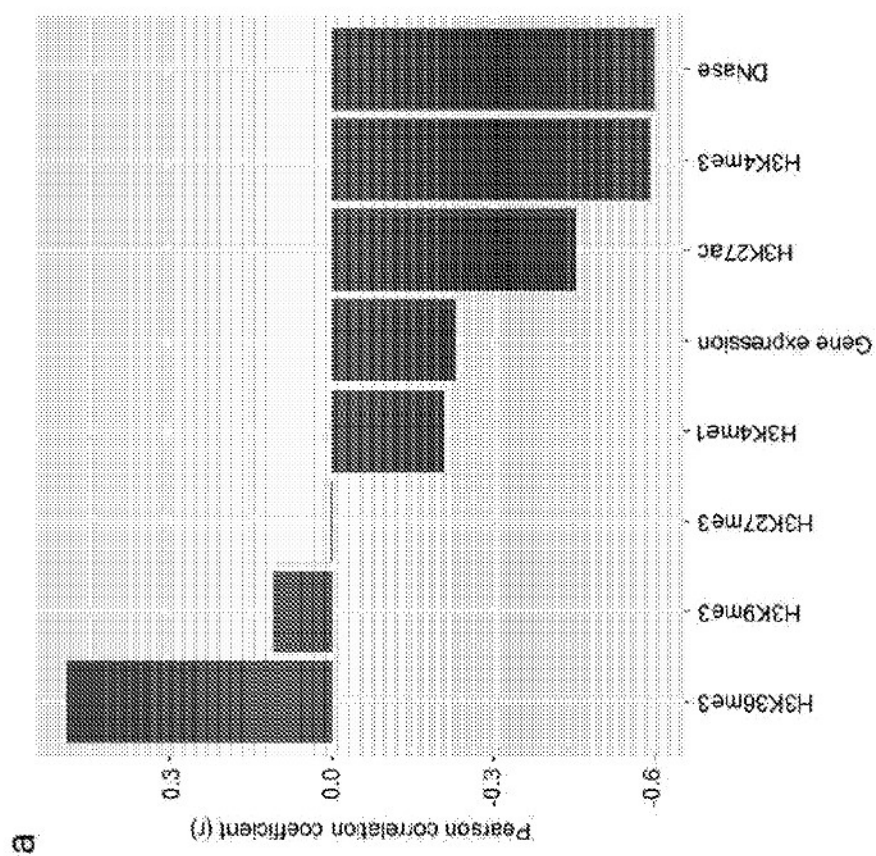
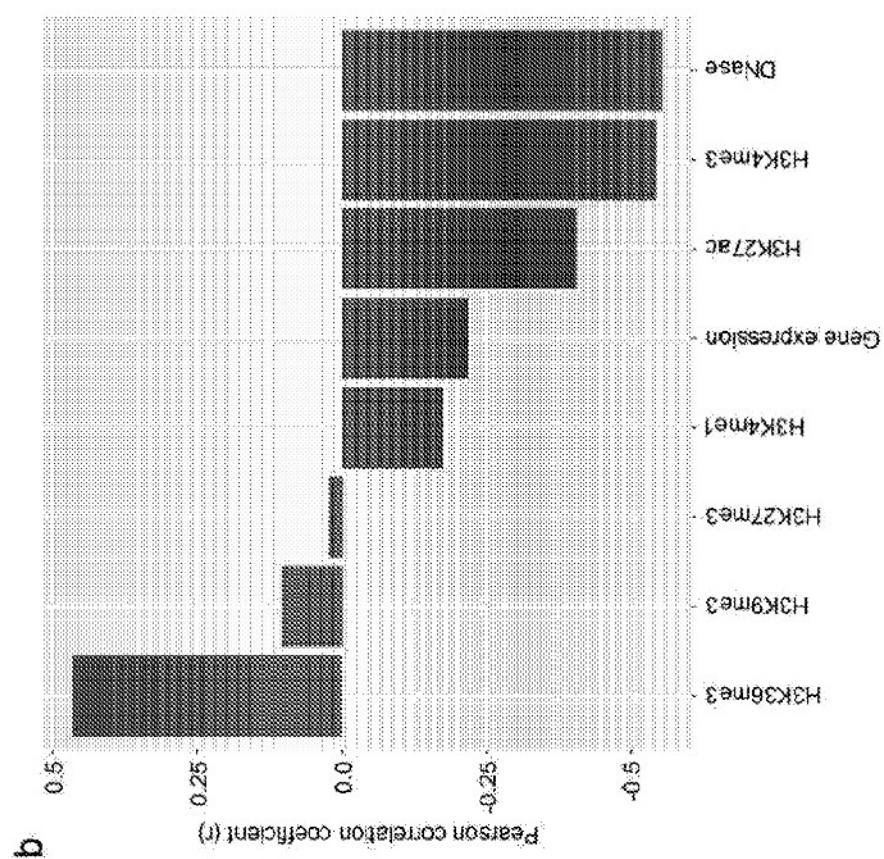


FIG. 7

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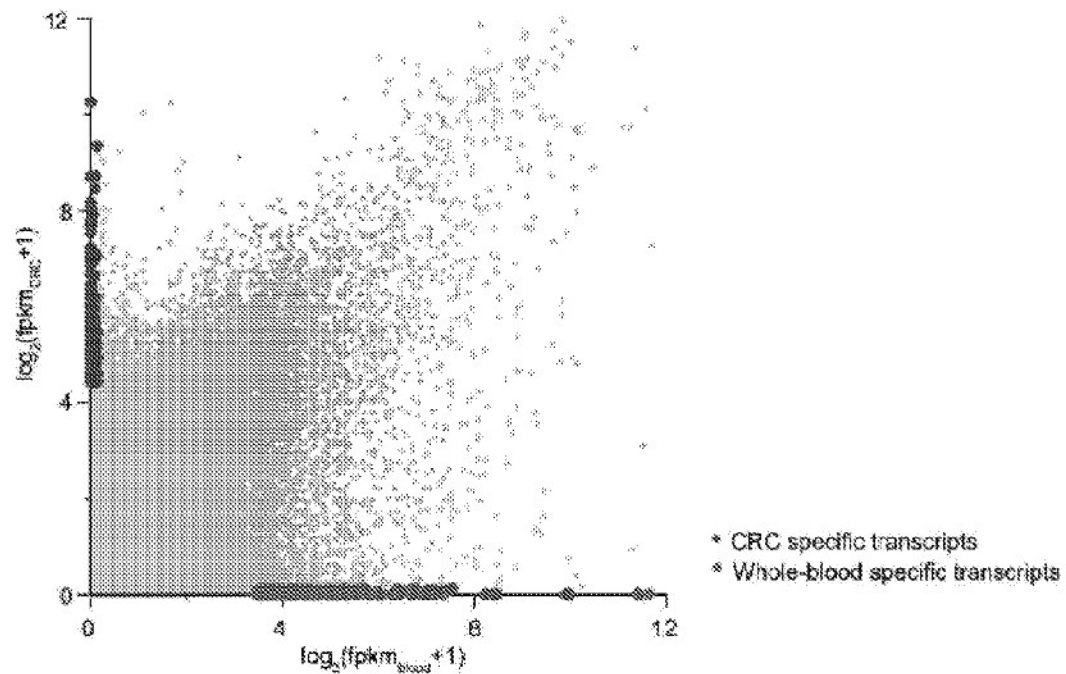


FIG. 8

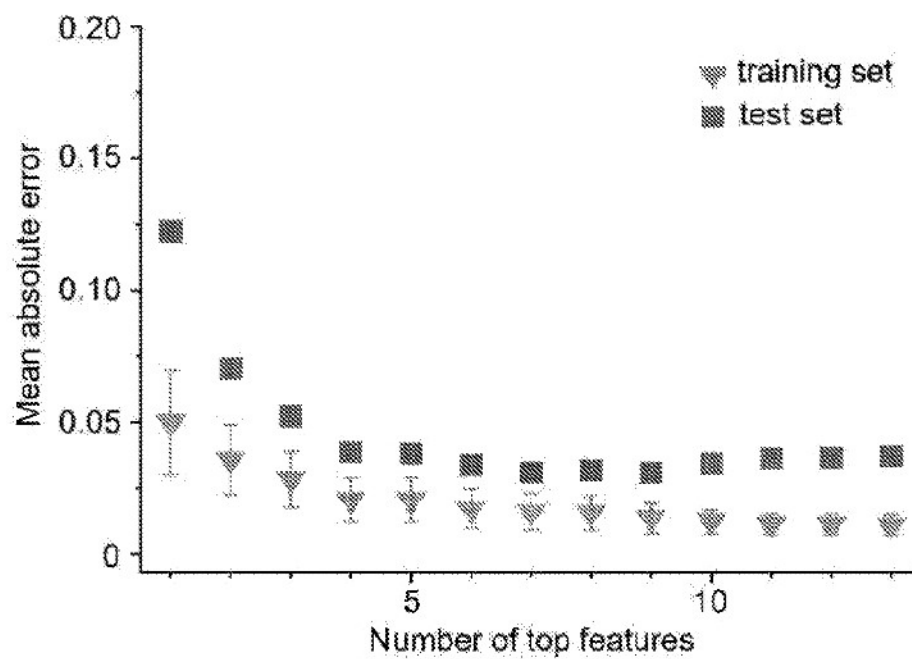


FIG. 9

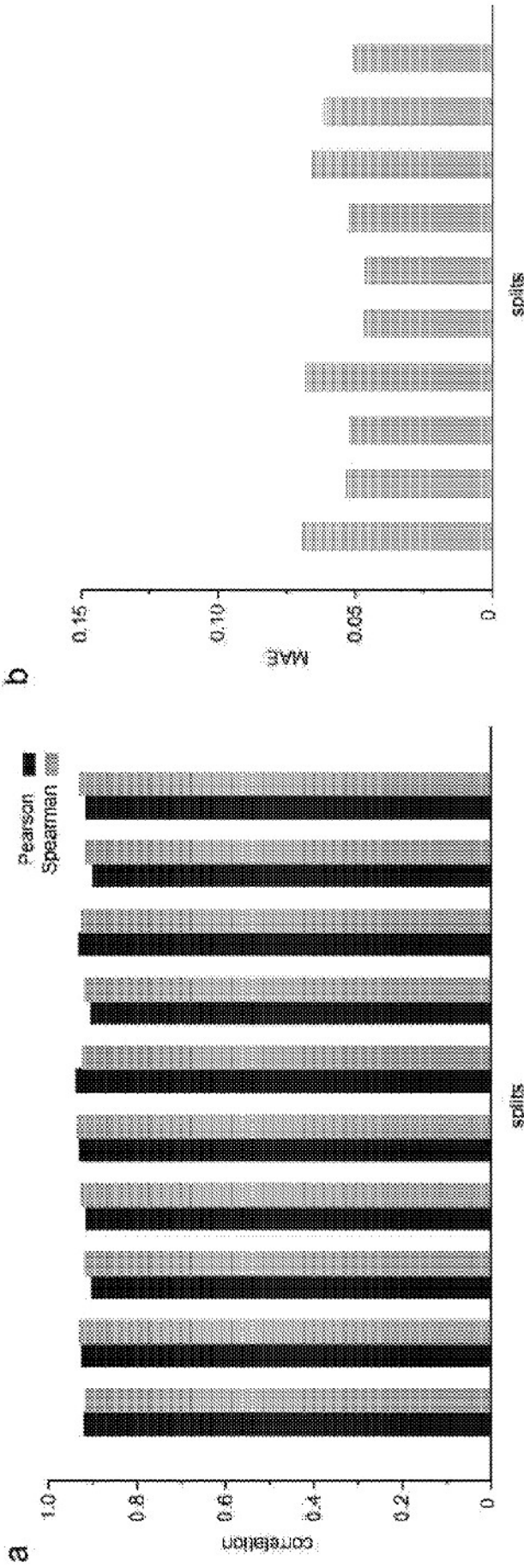


FIG. 10

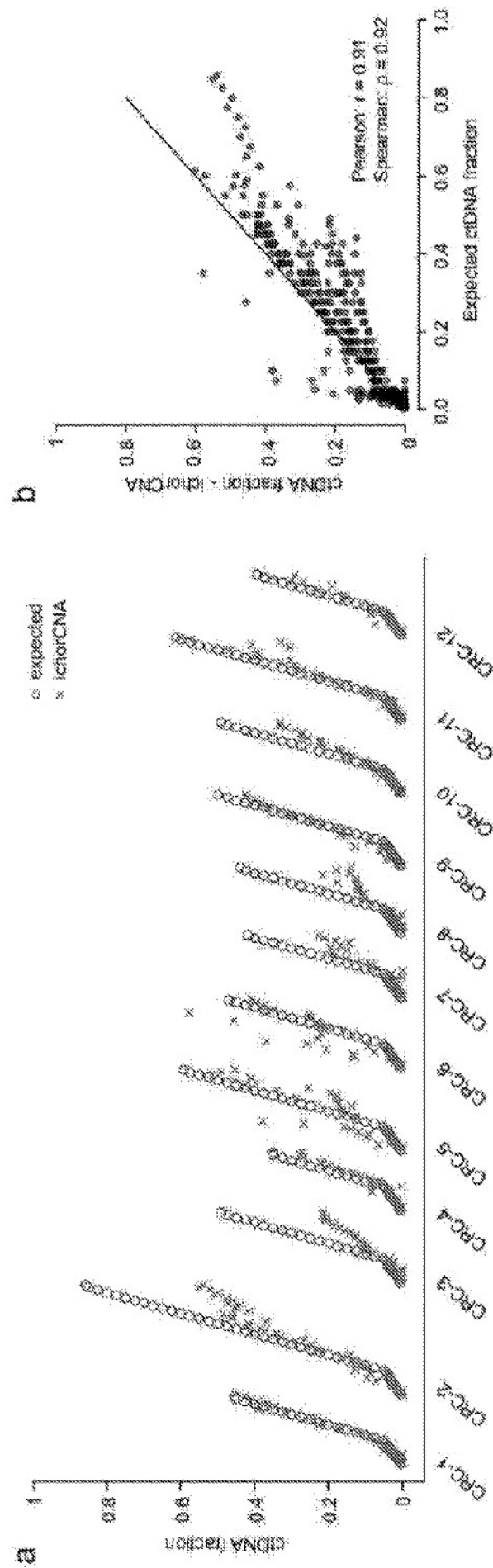


FIG. 11

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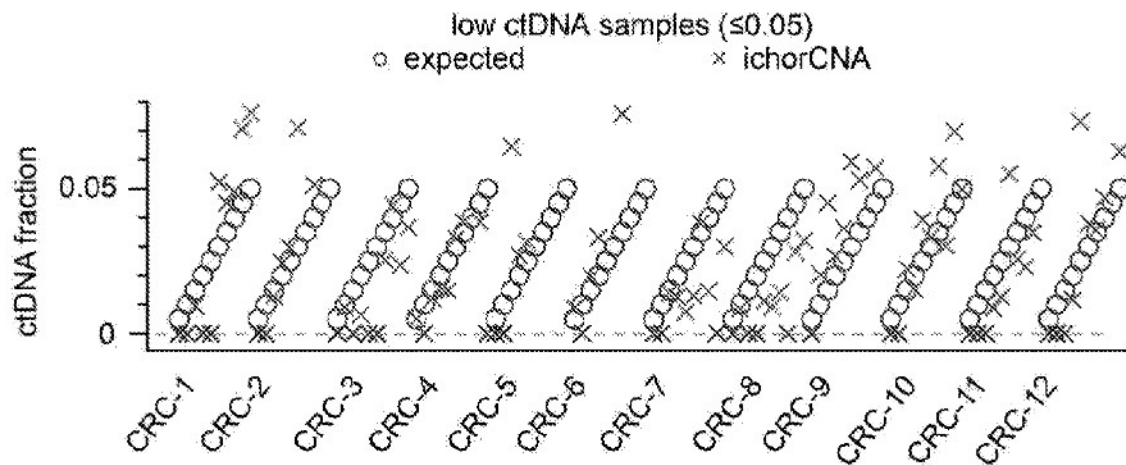


FIG. 12

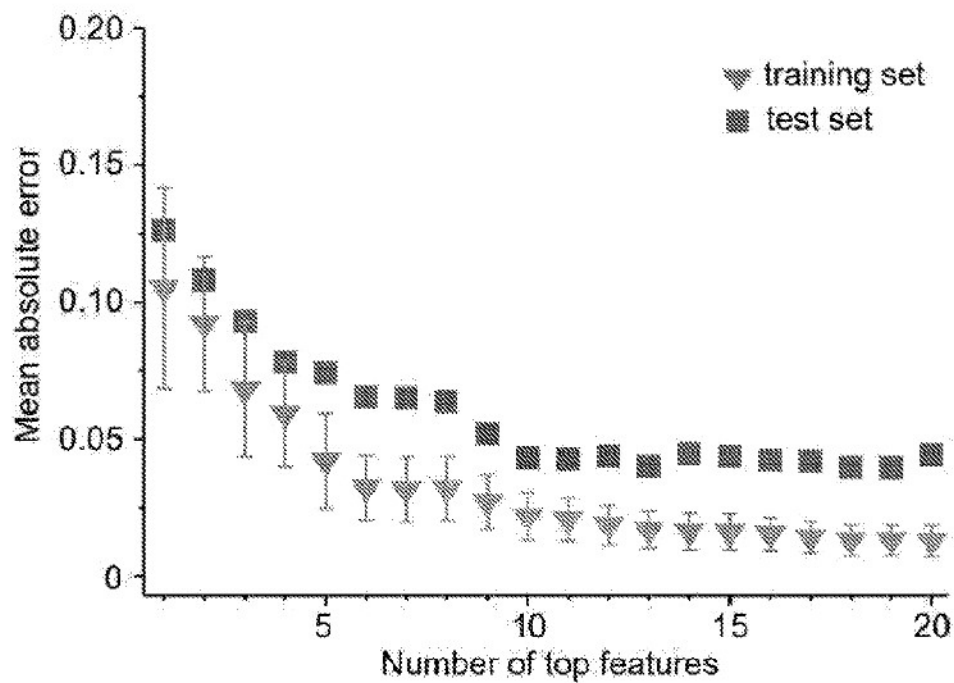


FIG. 13

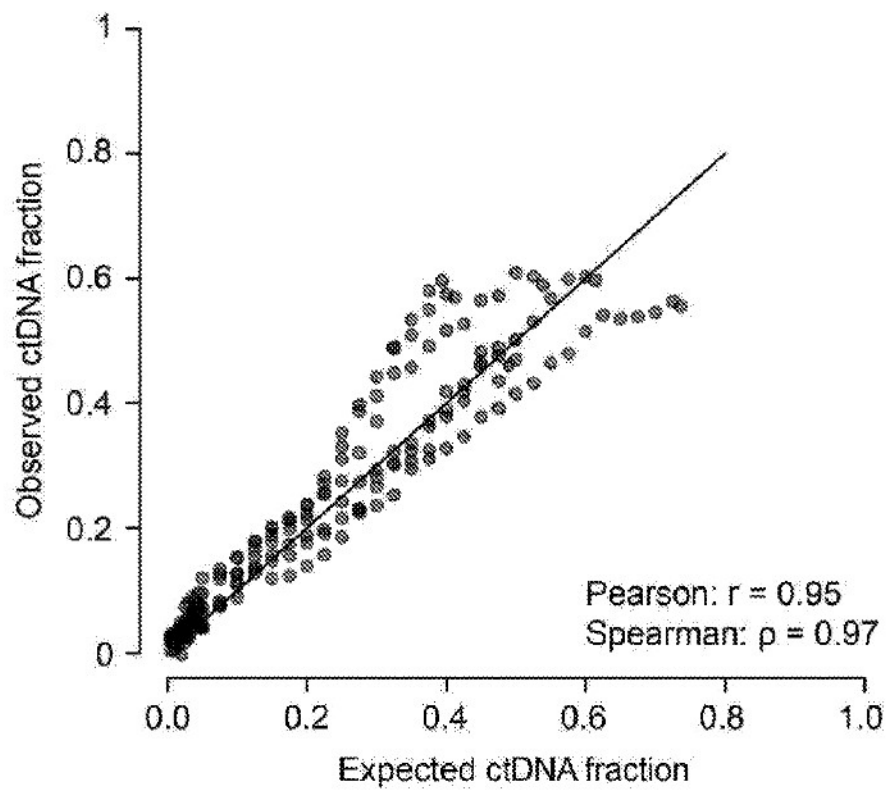
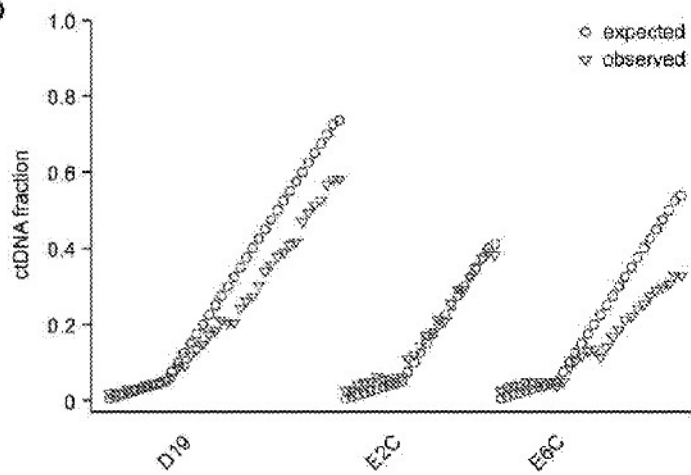


FIG. 14

a

Gene	Transcript	Chr	Site	Region	Expr.	FPKM _{blood}	FPKM _{BRCA}	Pr
NUPR1	ENST00000395641	16	28550329	promoter	tumor	0.45	106.68	1
MLPH	ENST00000338530	2	238396080	junction	tumor	0.00	68.32	0.996
PTK7	ENST00000230419	6	43044305	junction	tumor	0.00	15.65	0.989
PROM2	ENST00000317620	2	95940577	junction	tumor	0.02	21.64	0.972
HID1	ENST00000425042	17	72968686	junction	tumor	0.23	38.07	0.968
TPD52	ENST00000379097	8	80992550	junction	tumor	0.50	70.34	0.961
SORD	ENST00000267814	15	45315547	junction	tumor	0.93	11.37	0.960
HOXC10	ENST00000303460	12	54378970	promoter	tumor	0.00	12.67	0.952

b



c

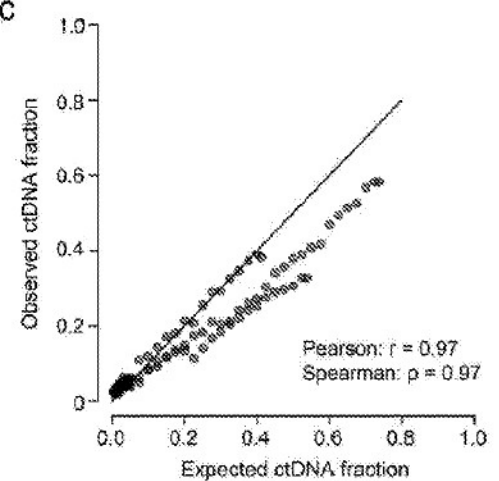


FIG. 15

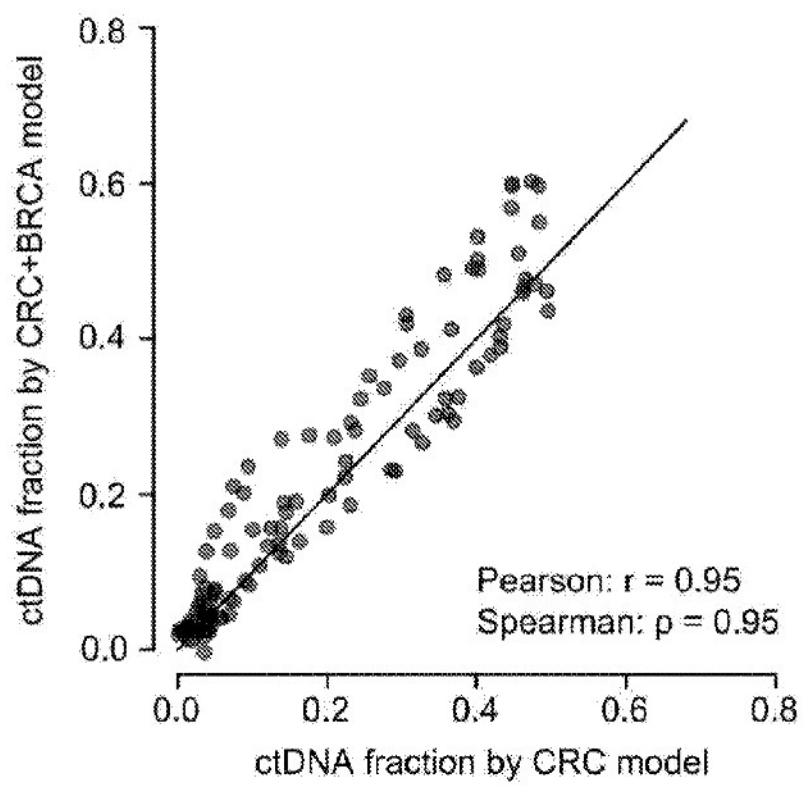


FIG. 16

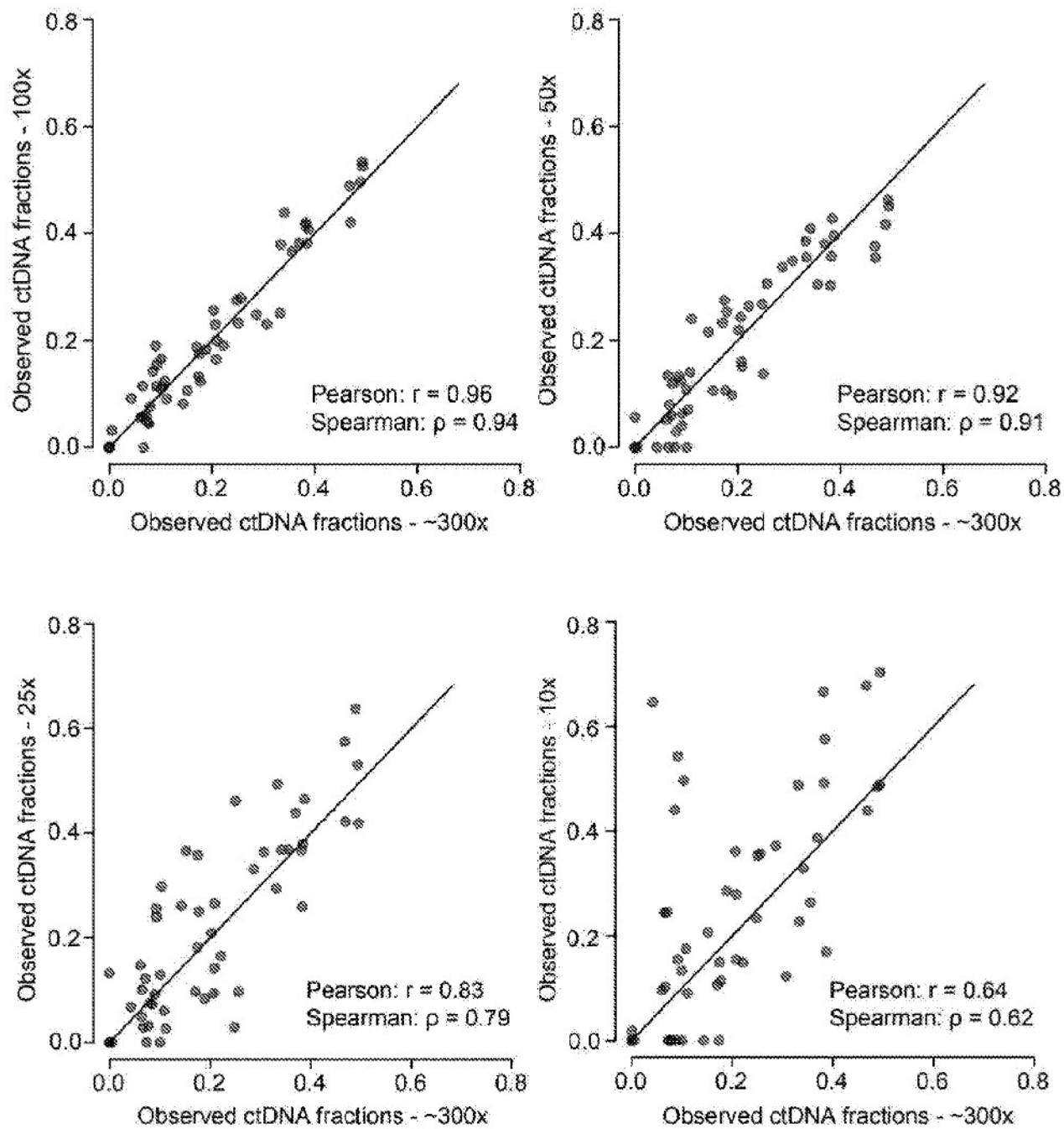


FIG. 17

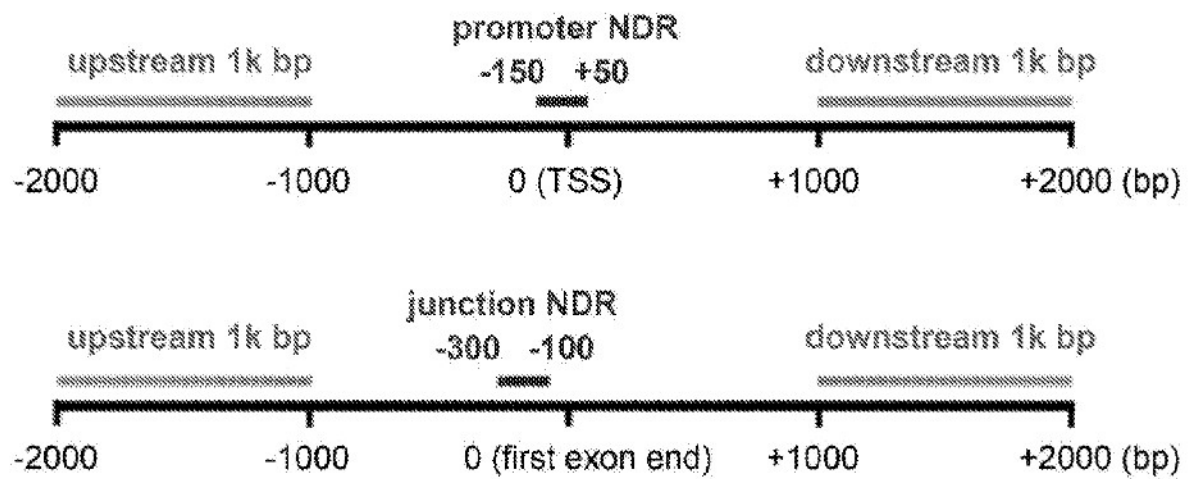


FIG. 18

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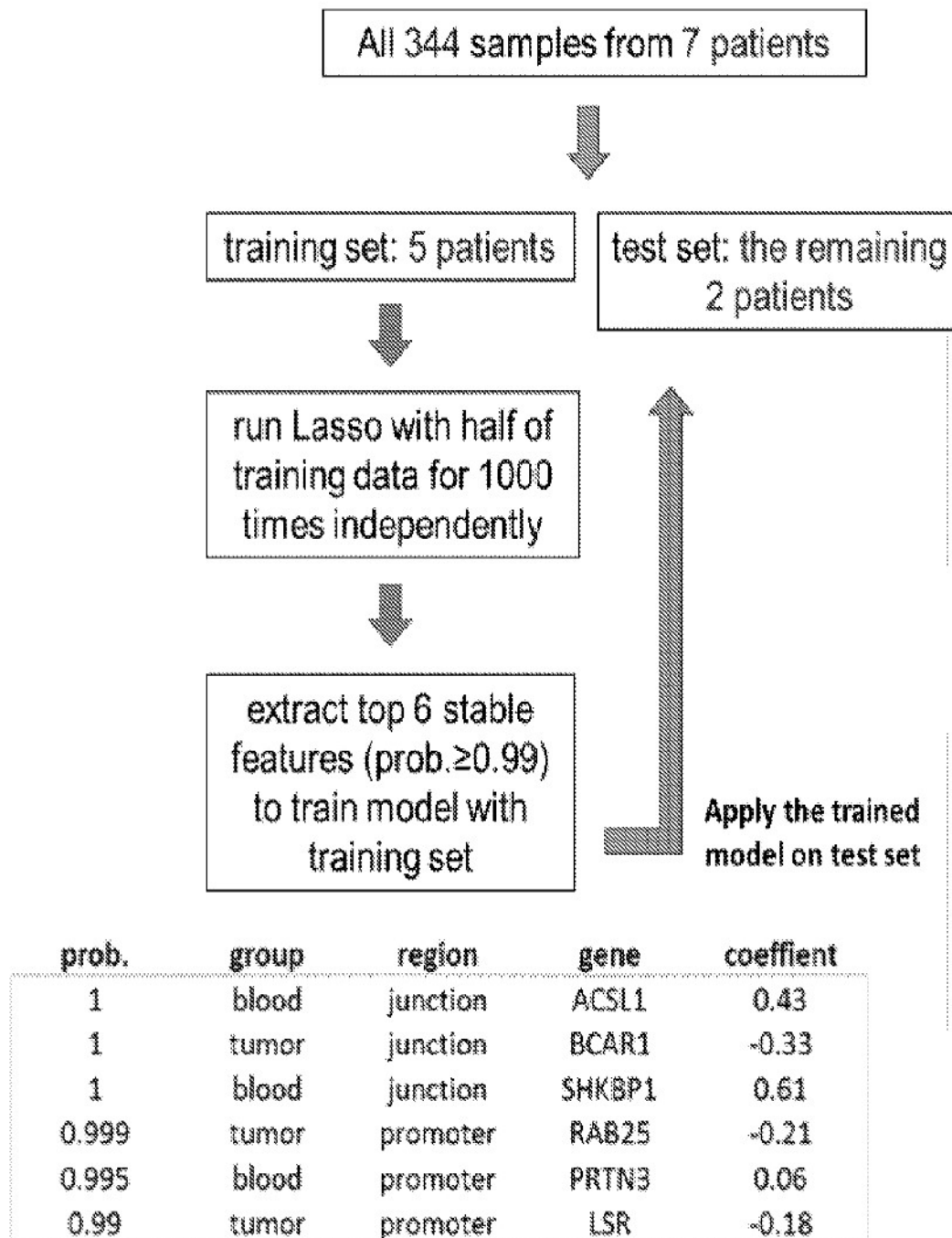
a

FIG. 19

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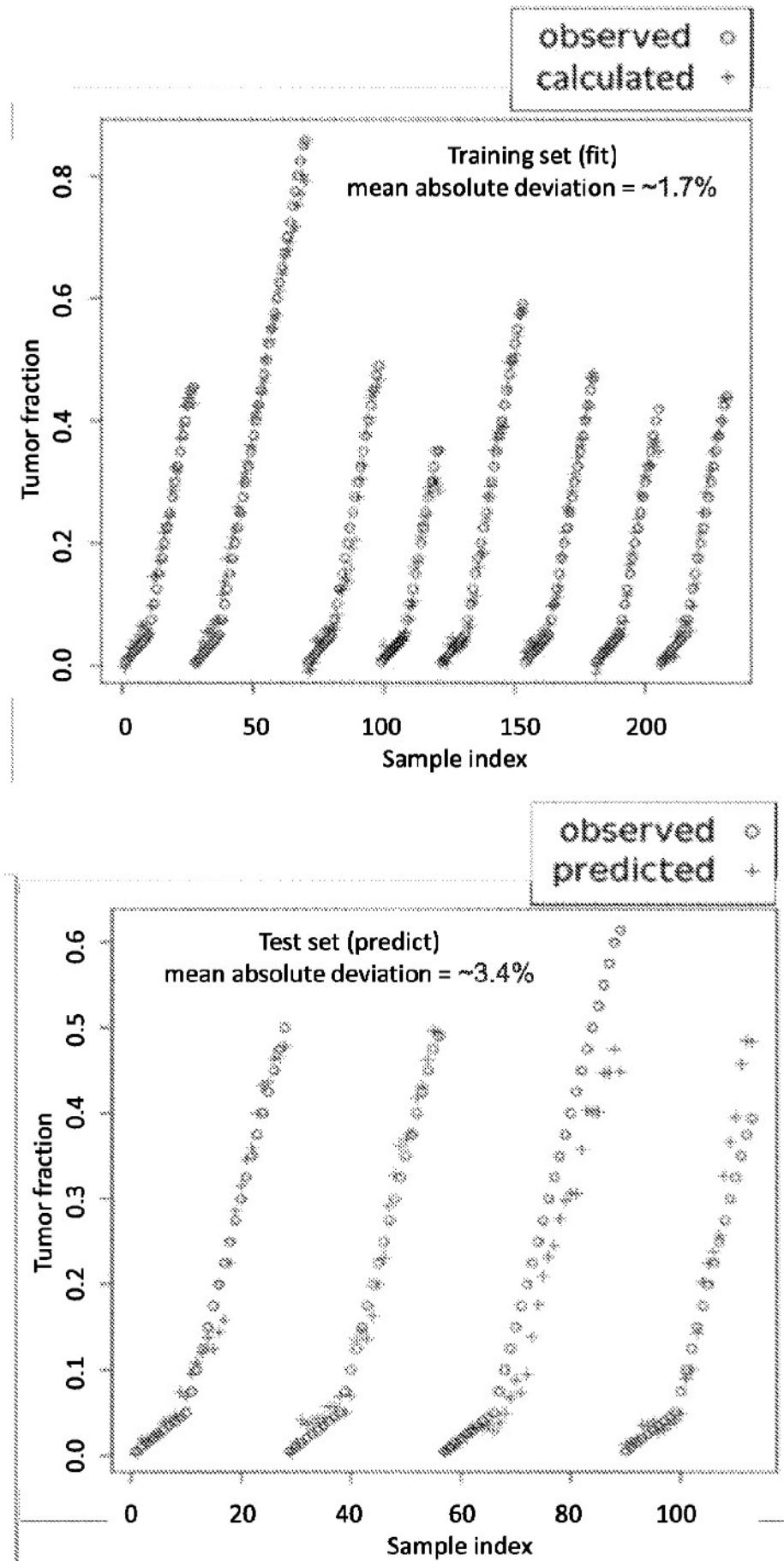
b

FIG. 19 (continued)

Identify all predictive coverage features

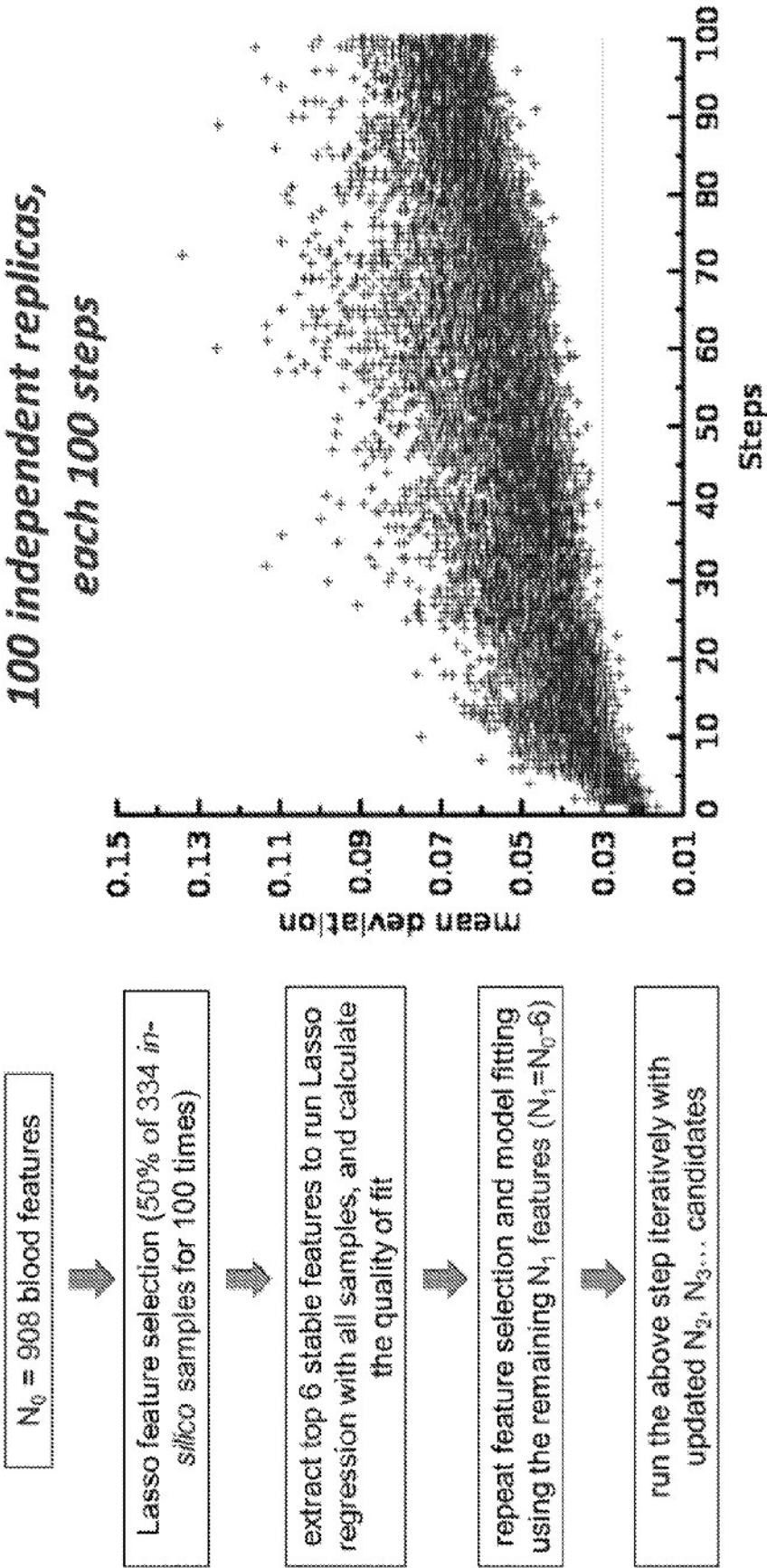


FIG. 20

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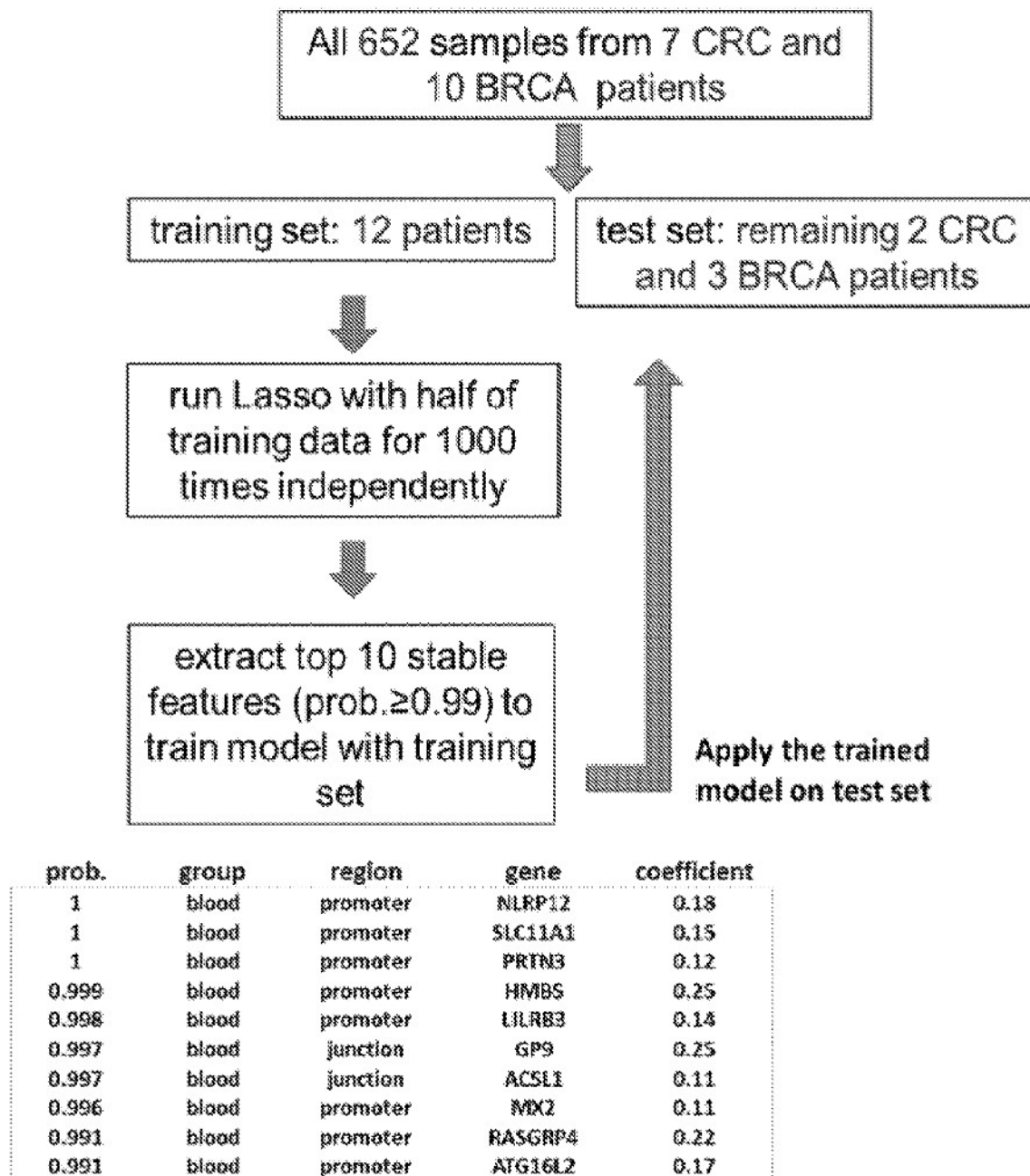


FIG. 21

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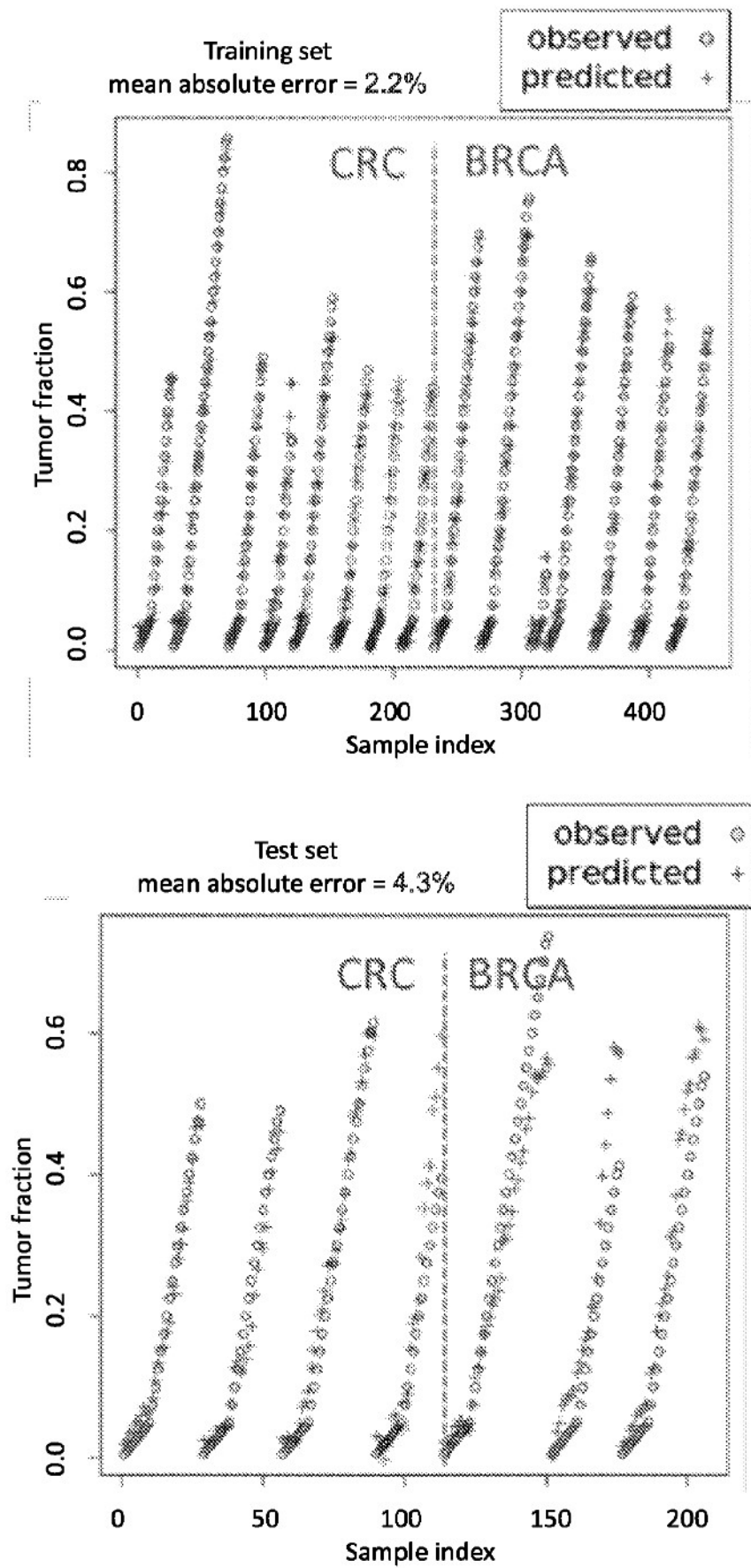


FIG. 21 (continued)

Identify all predictive coverage features (pan-cancer)

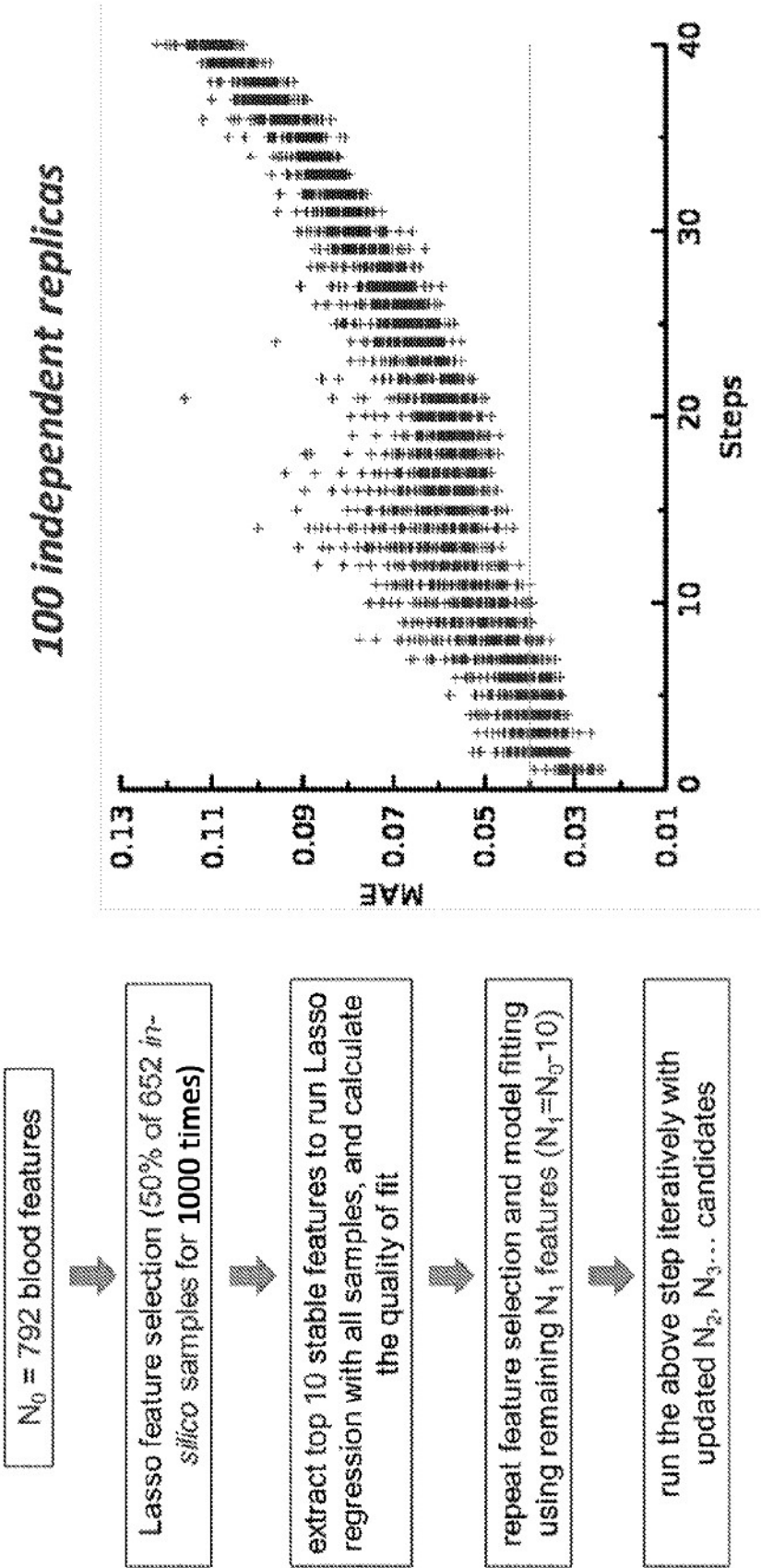


FIG. 22

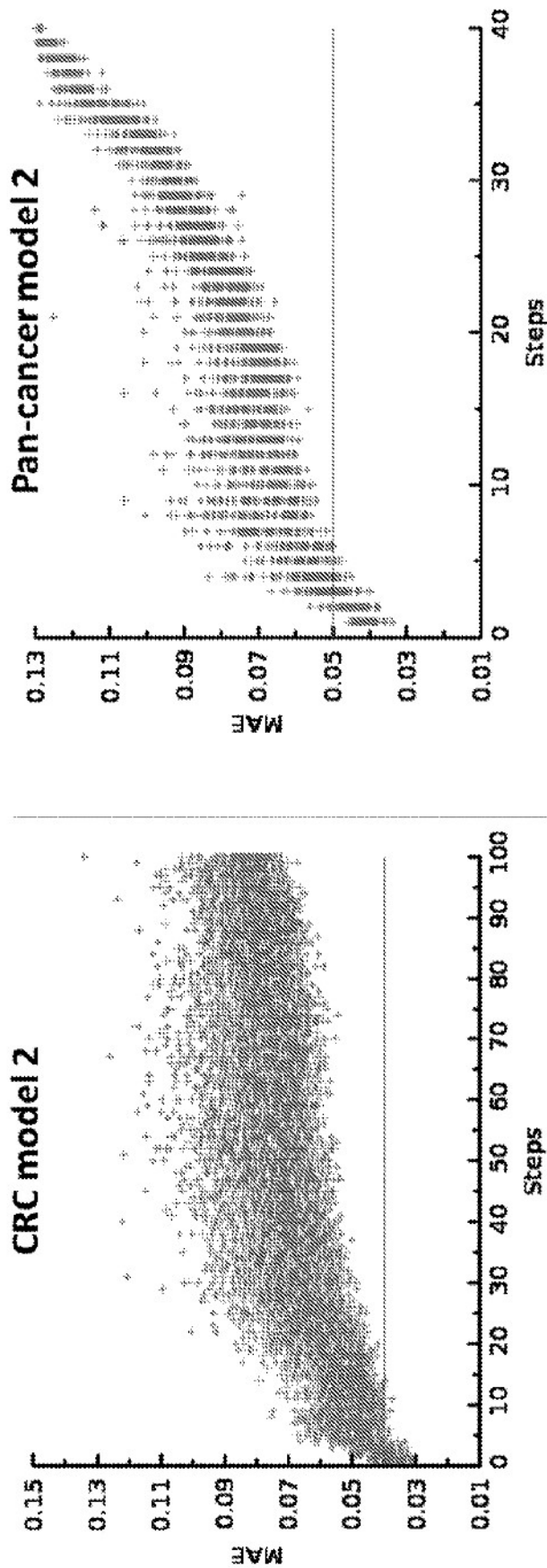


FIG. 23

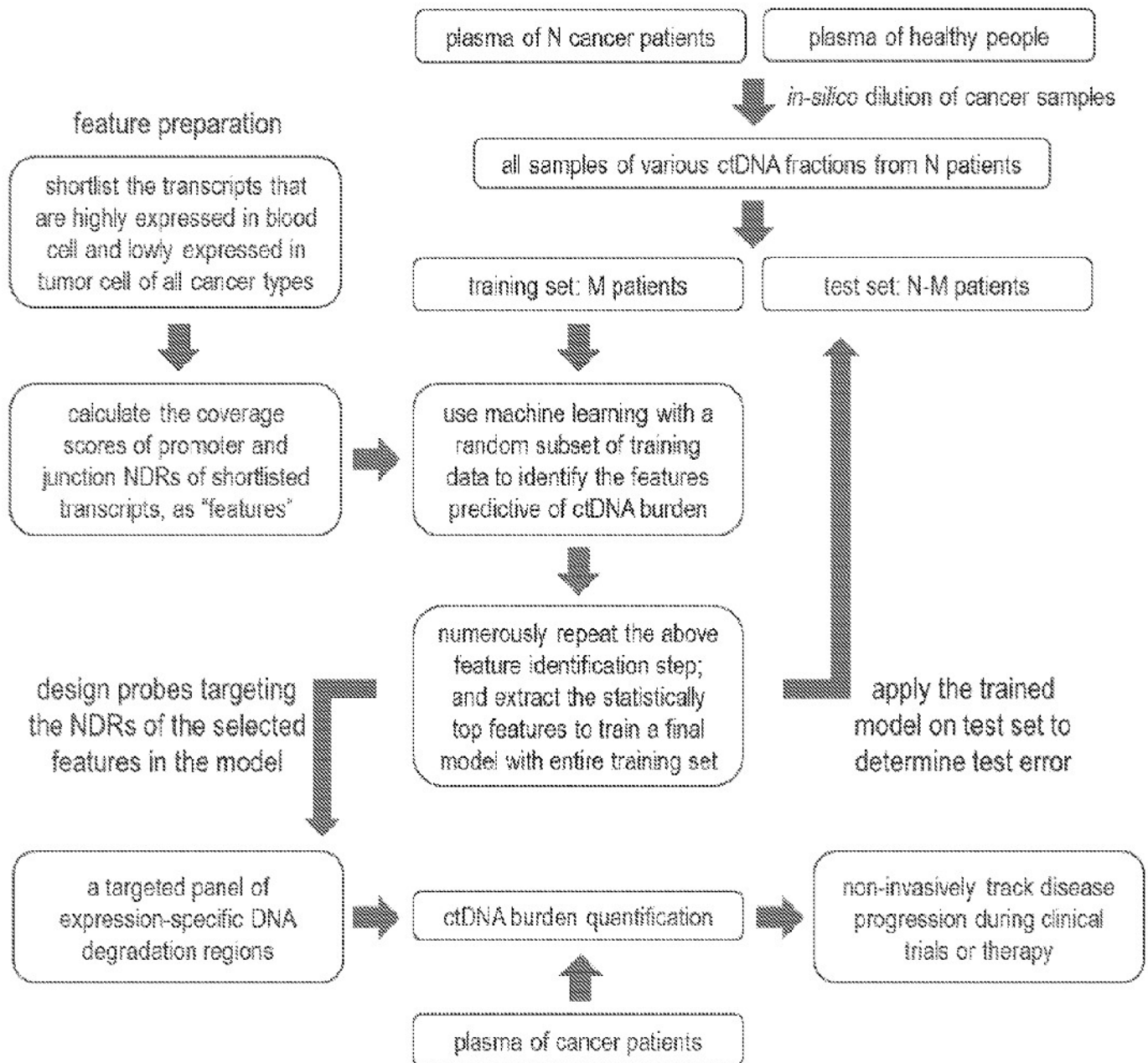


FIG. 24

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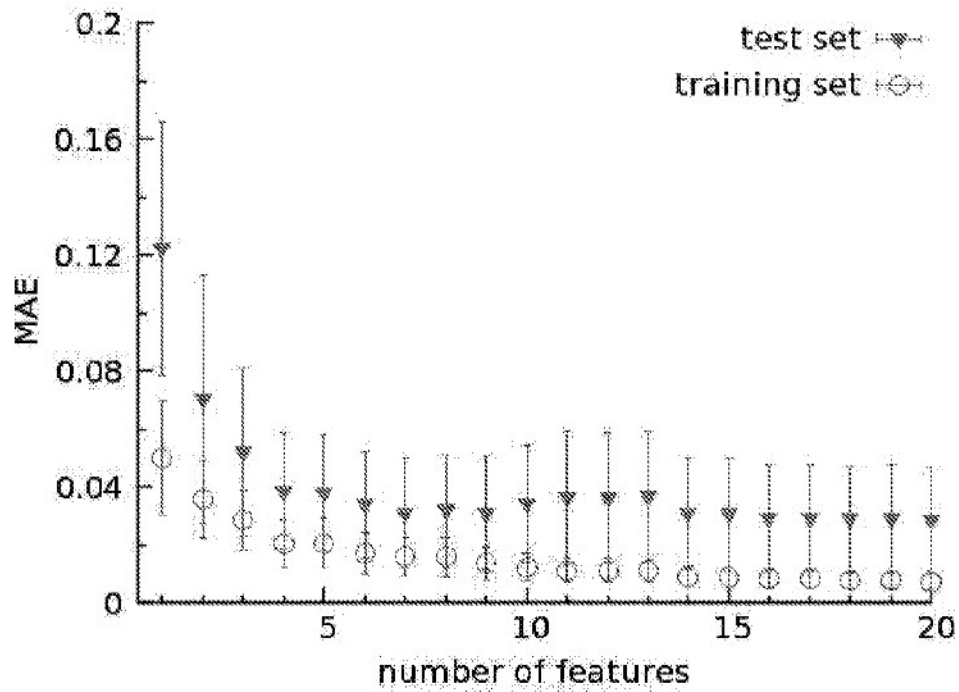


FIG. 25

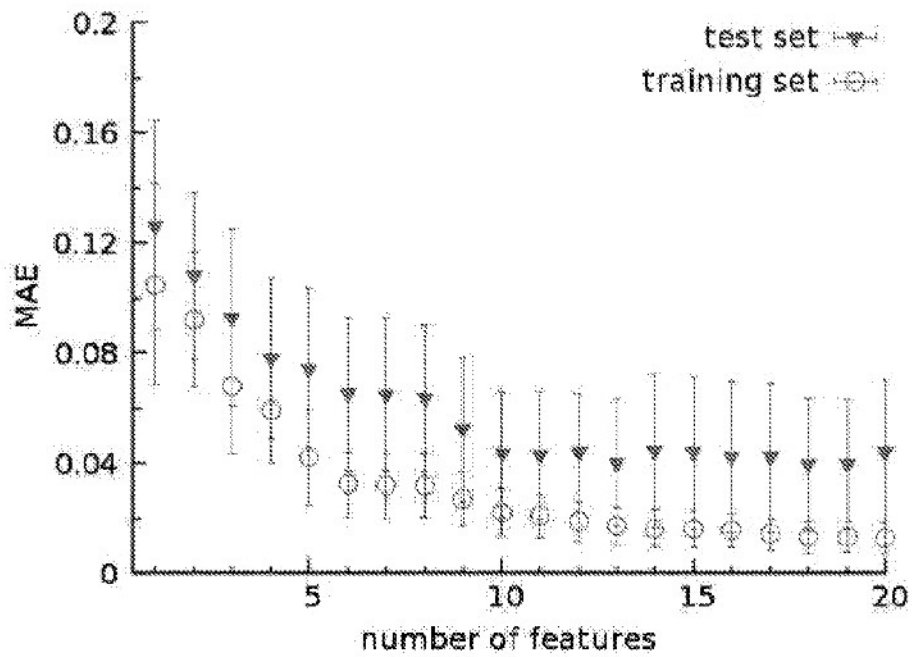


FIG. 26