

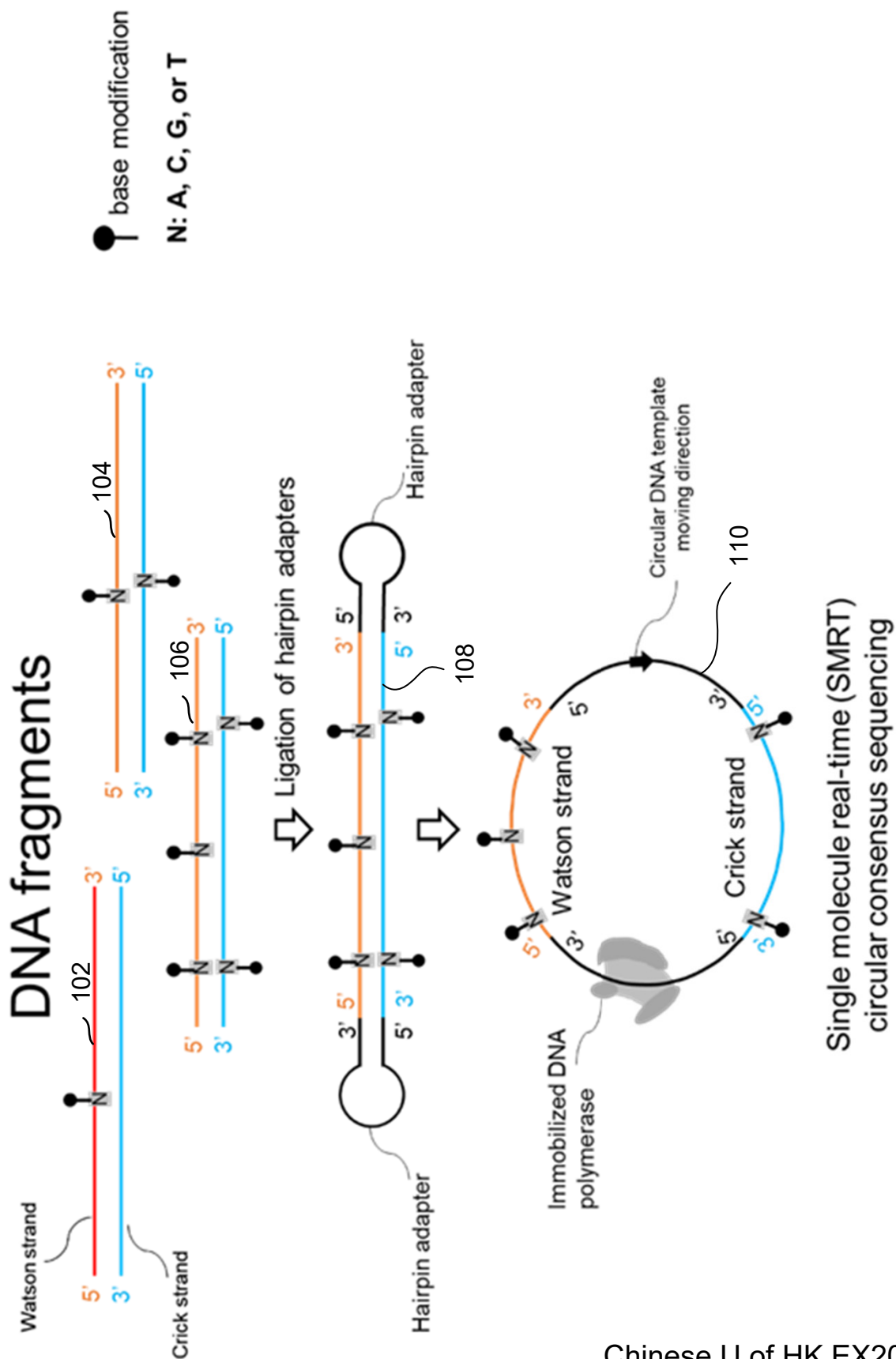


FIG. 1







FIG. 4

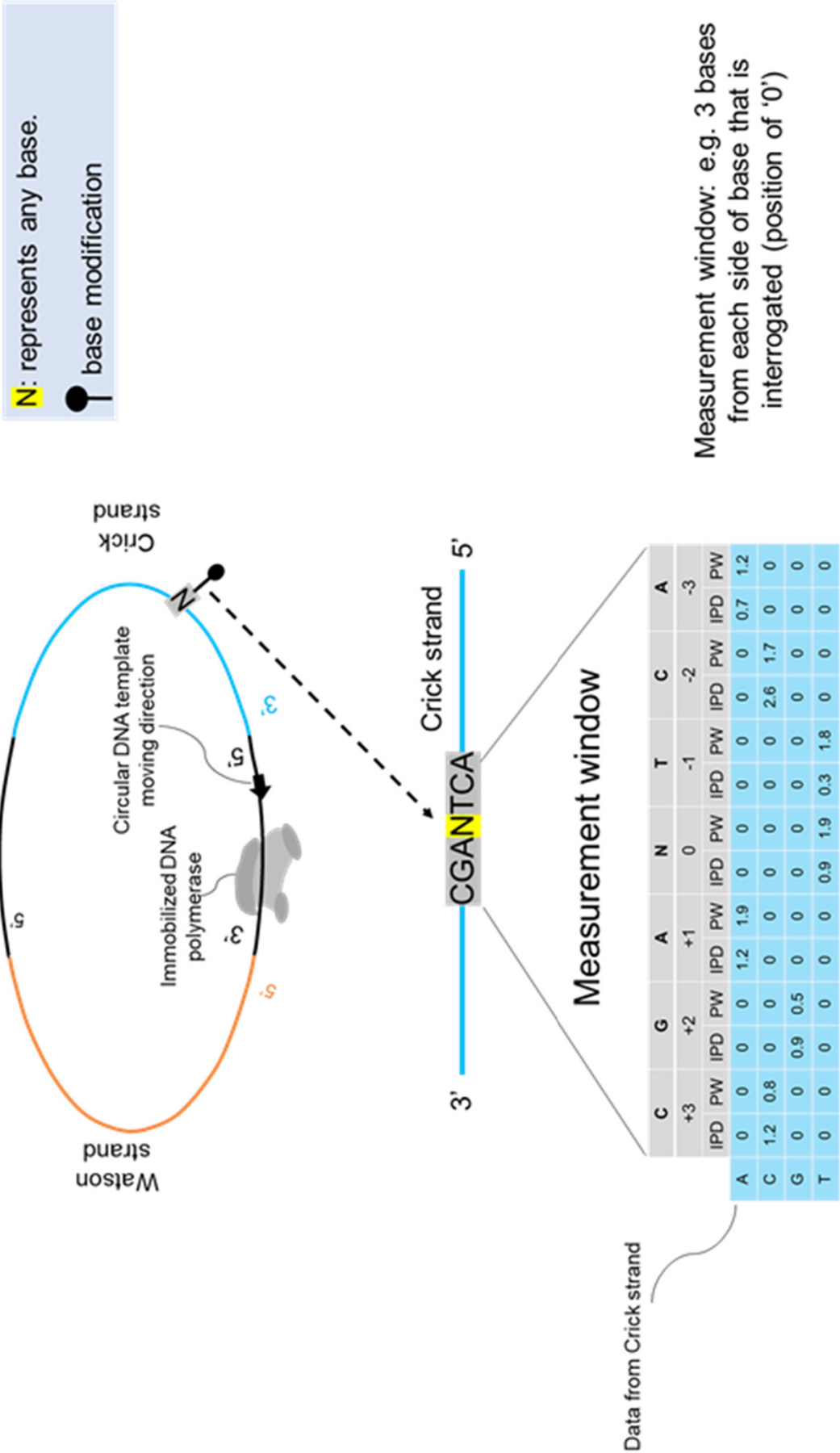


FIG. 5



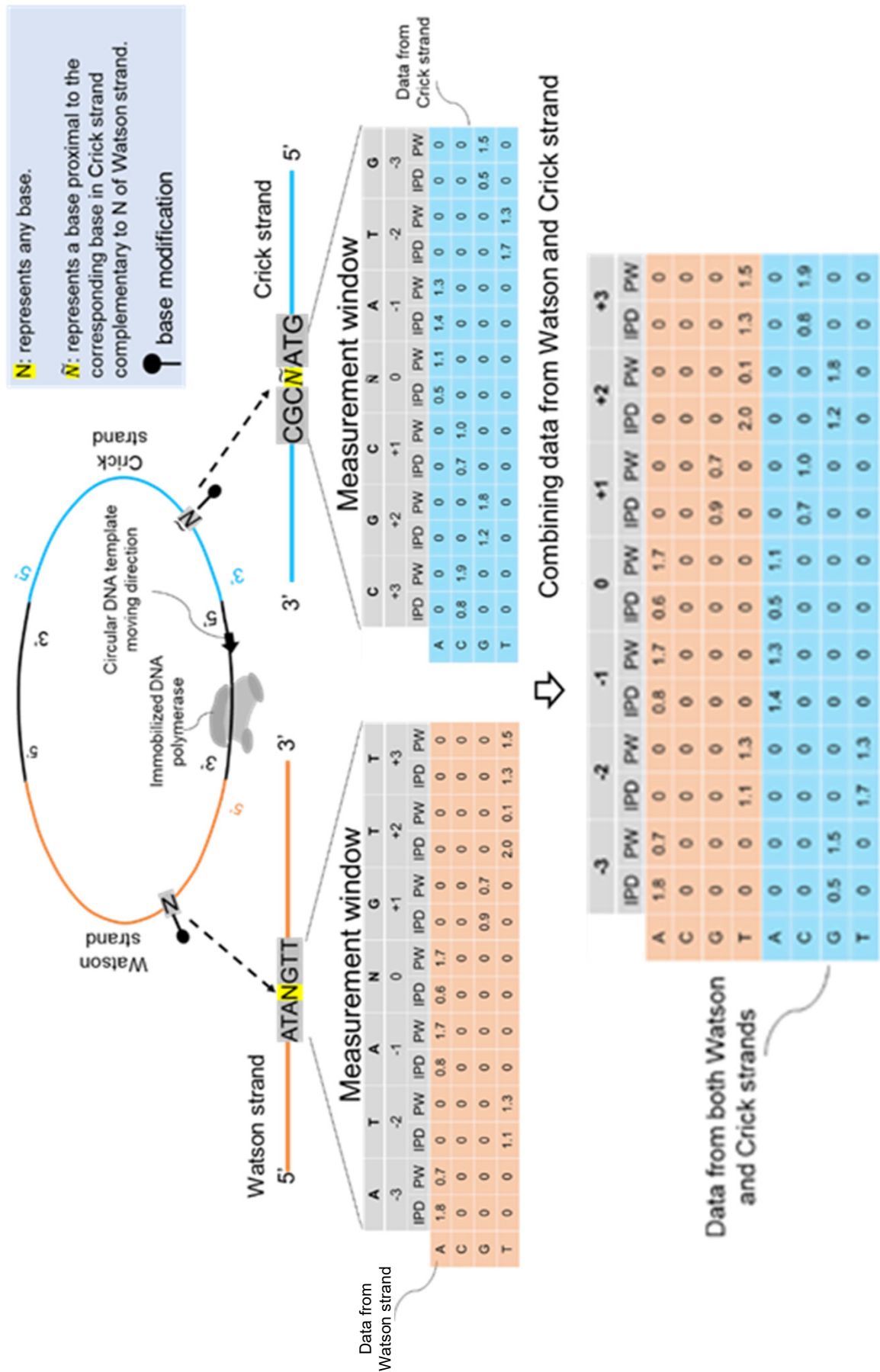


FIG. 7

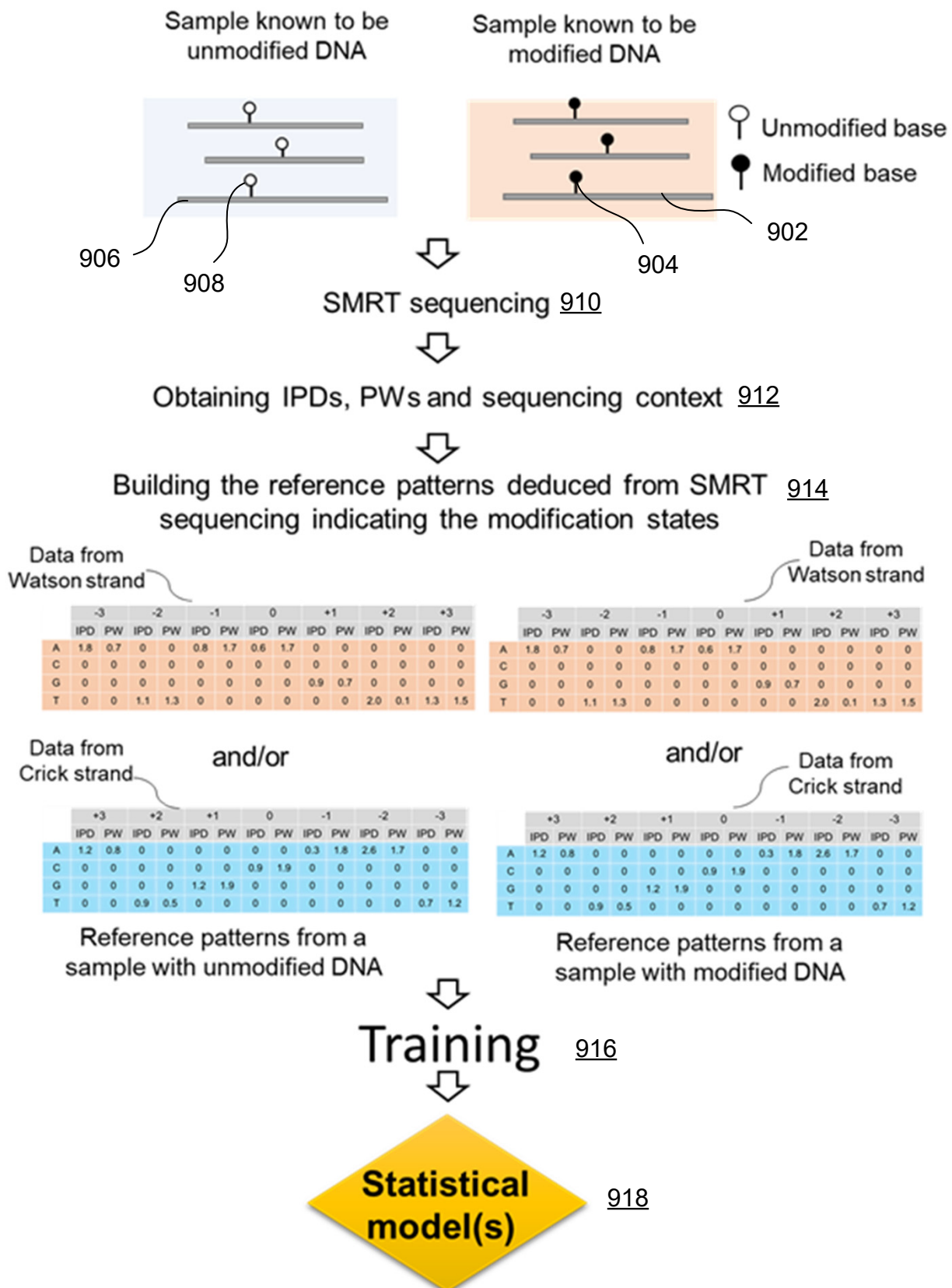


FIG. 9

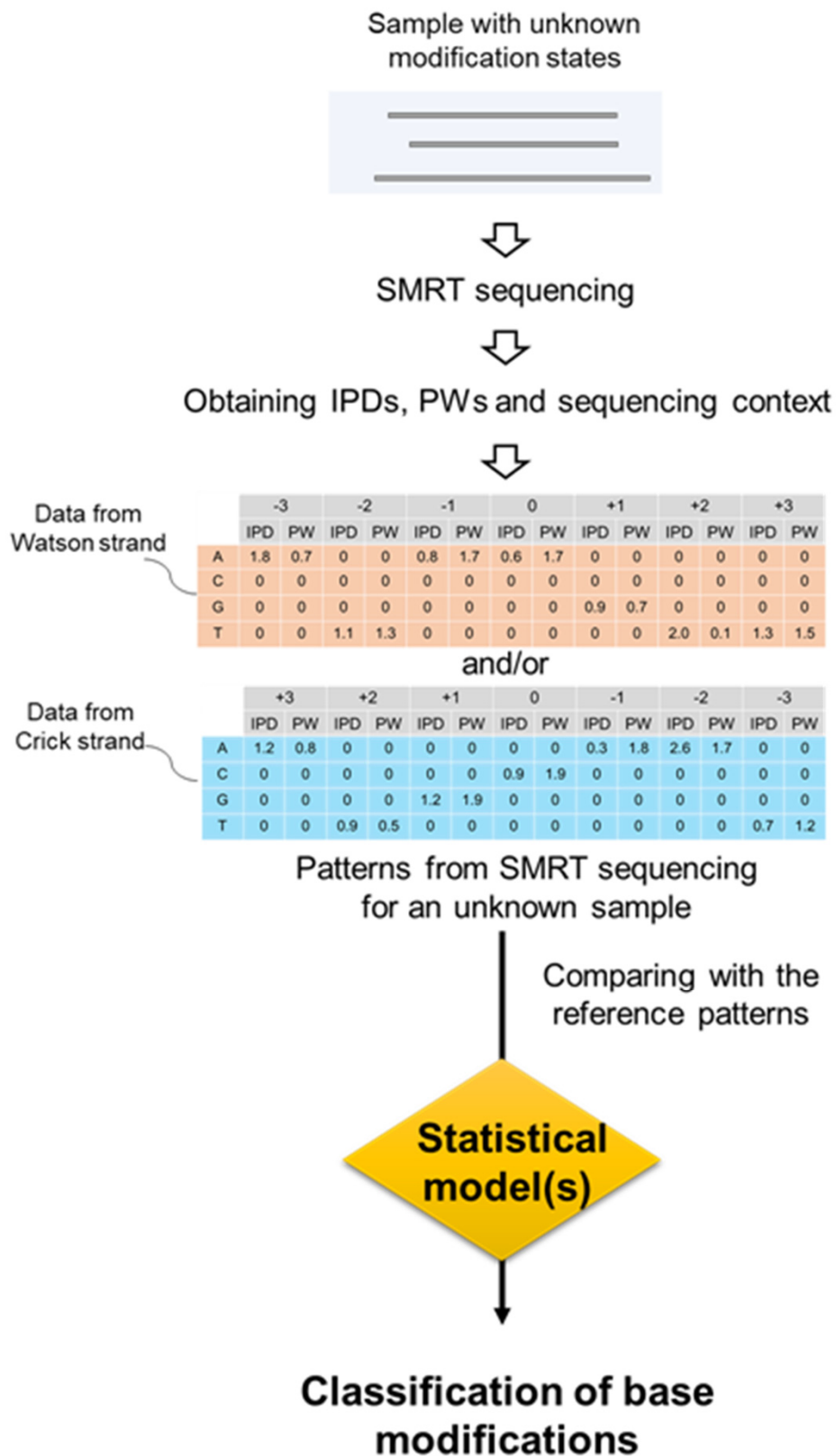


FIG. 10

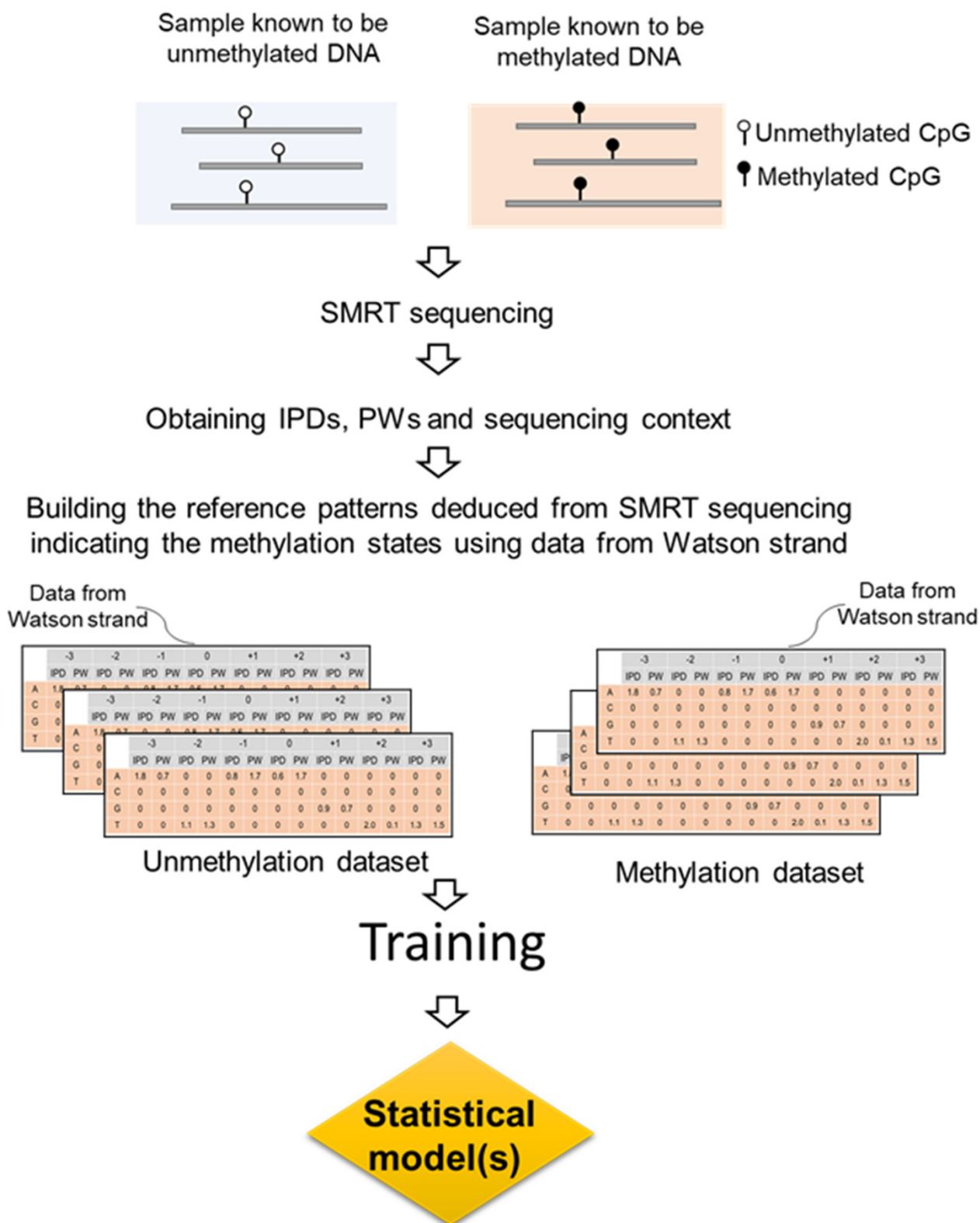


FIG. 11

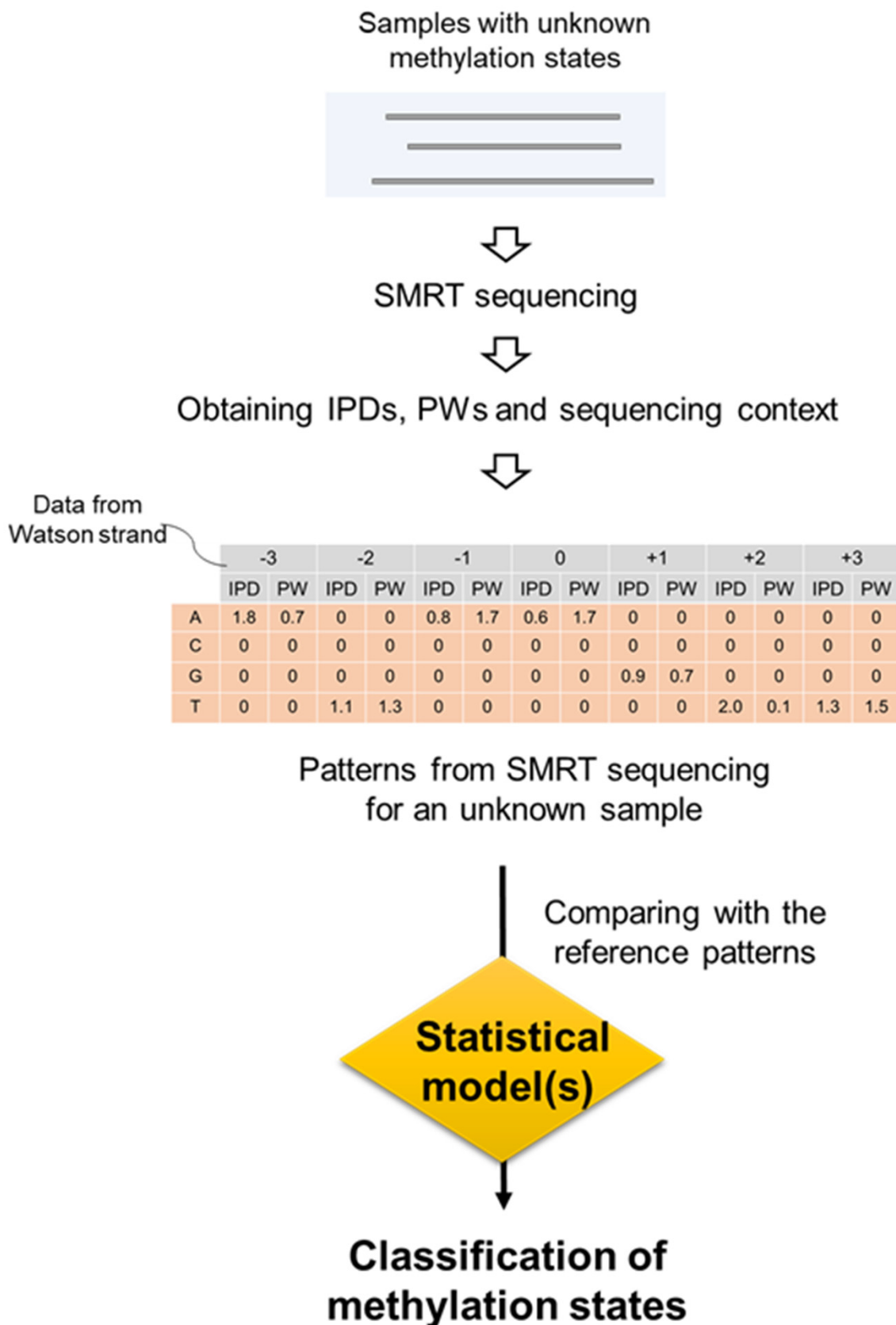


FIG. 12

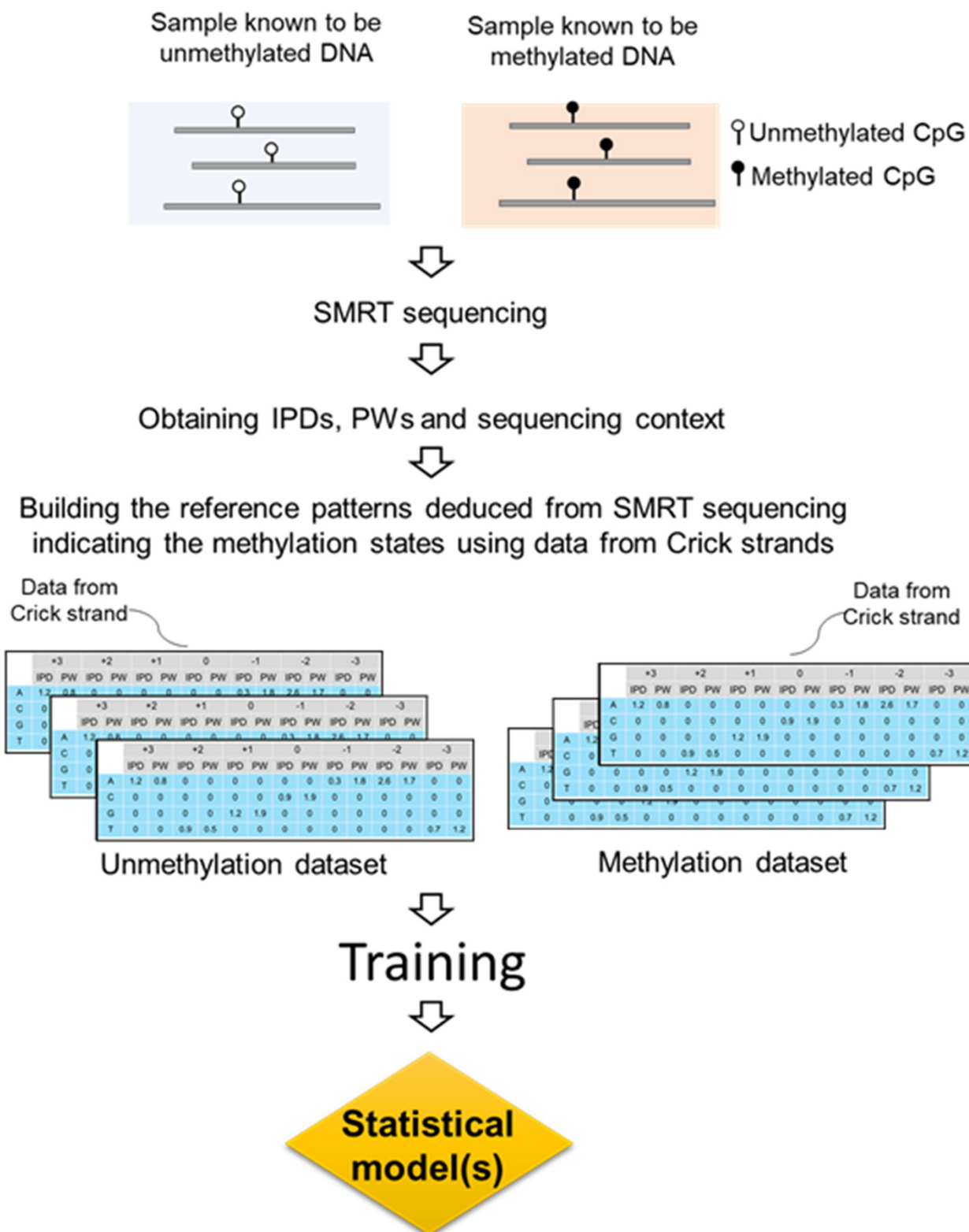


FIG. 13

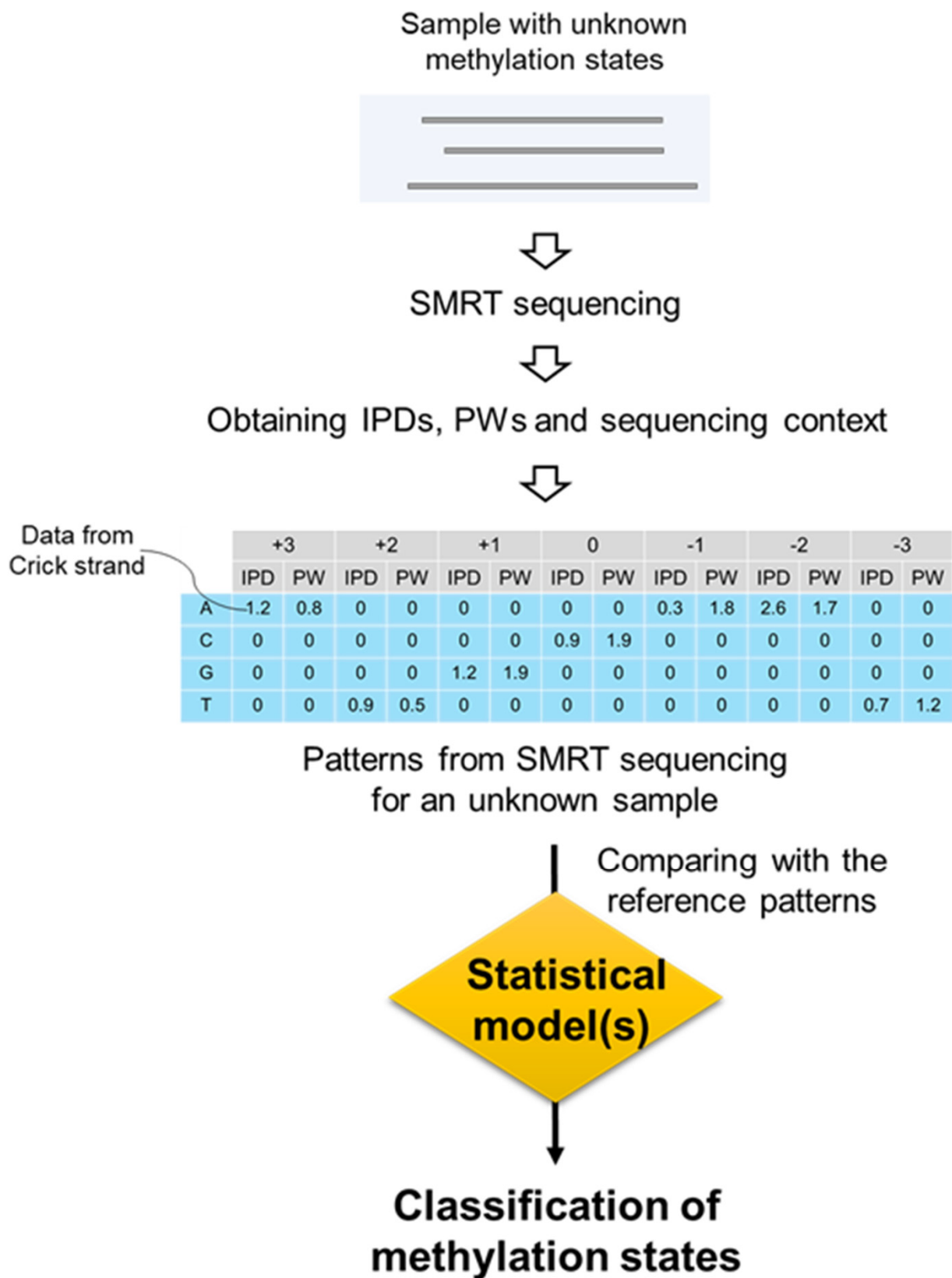


FIG.14

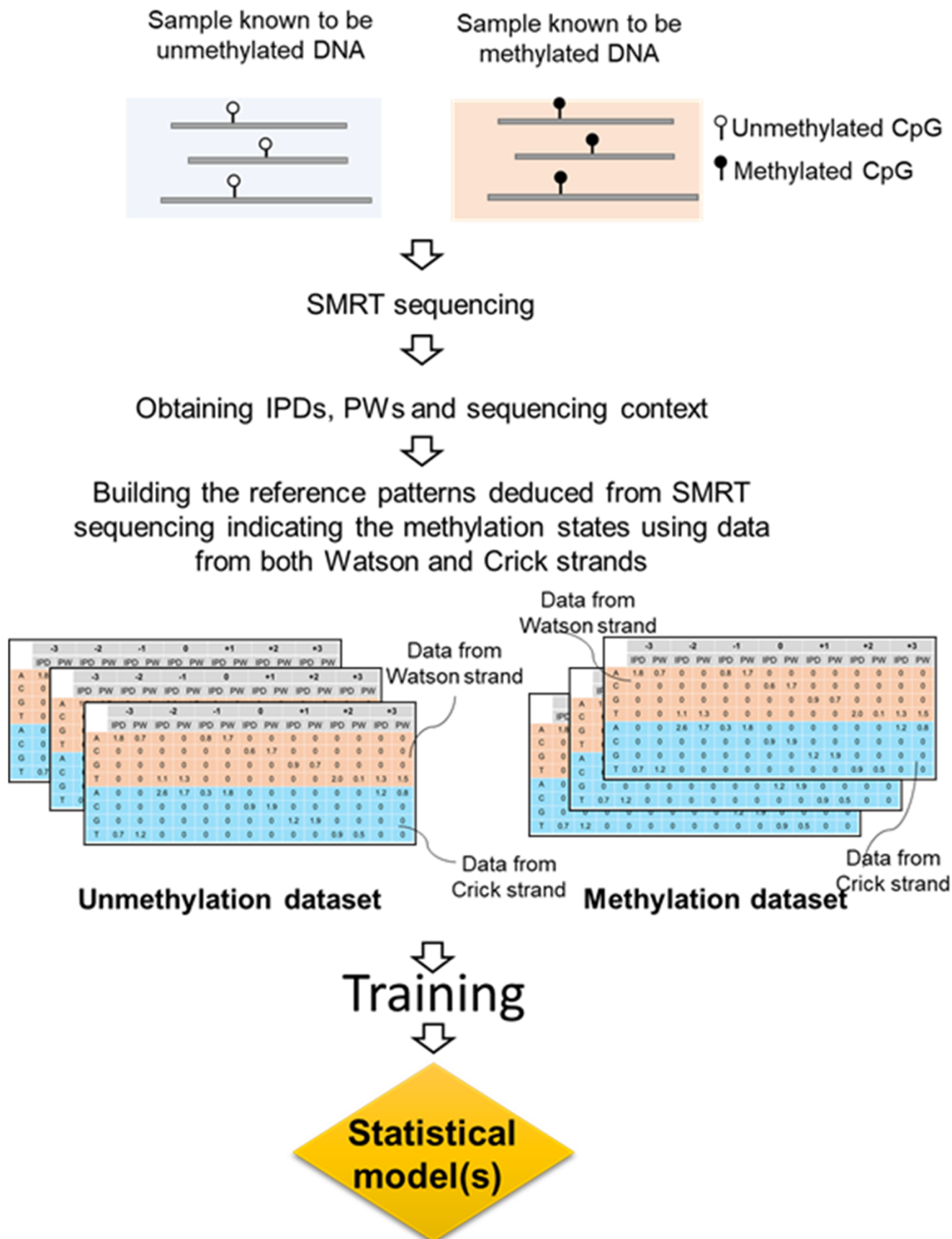


FIG. 15

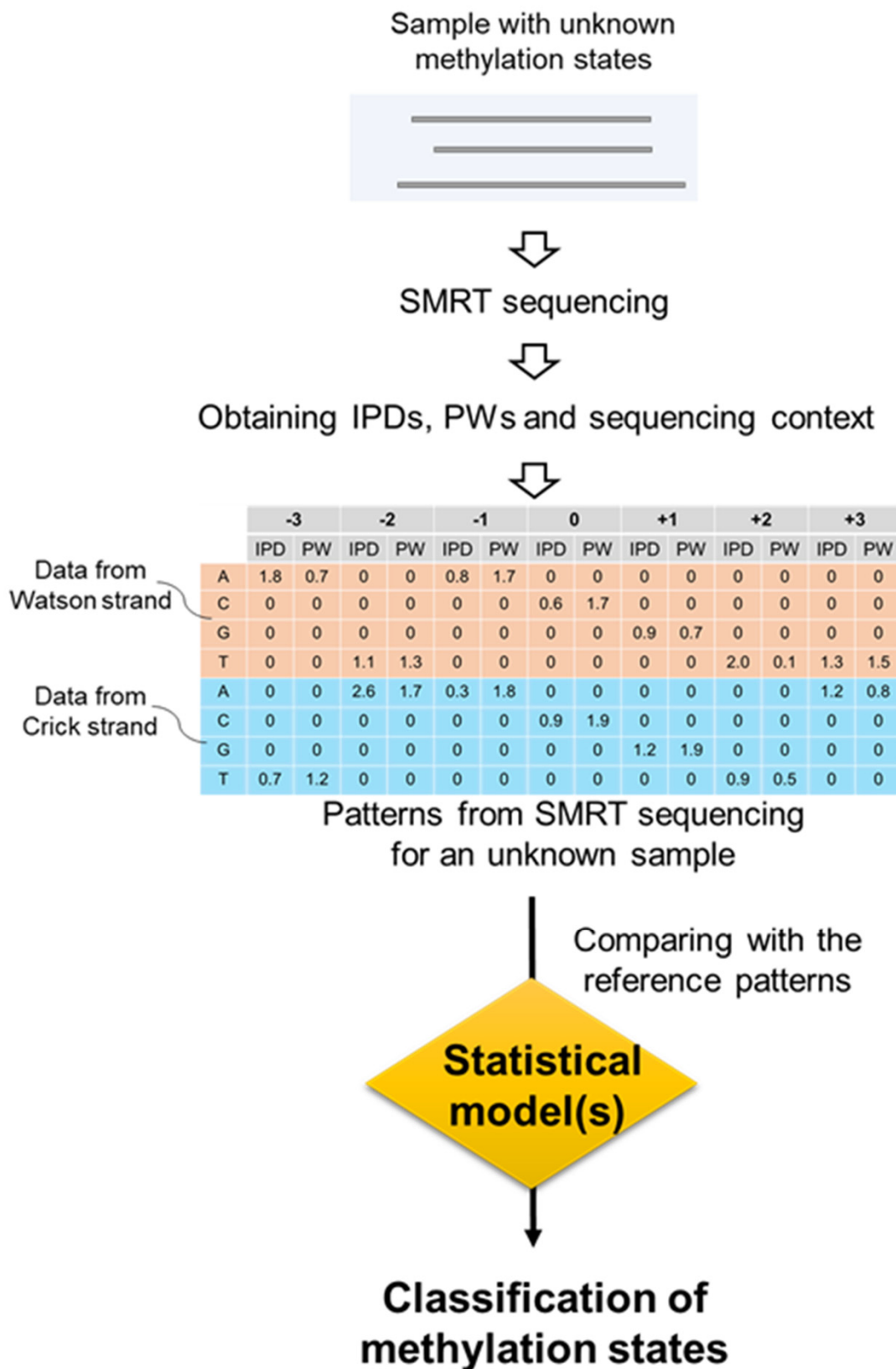


FIG. 16

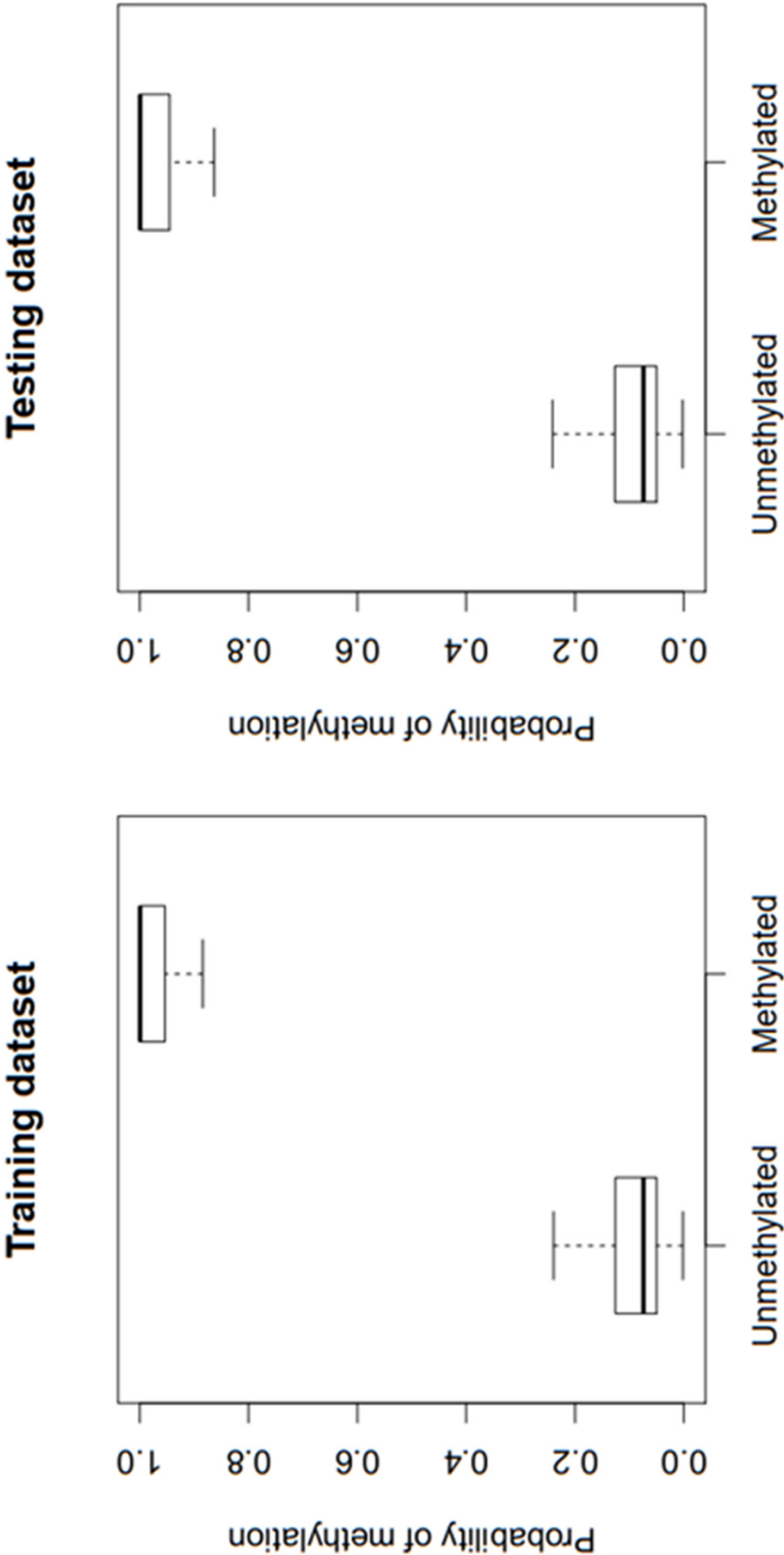


FIG. 17A

FIG. 17B

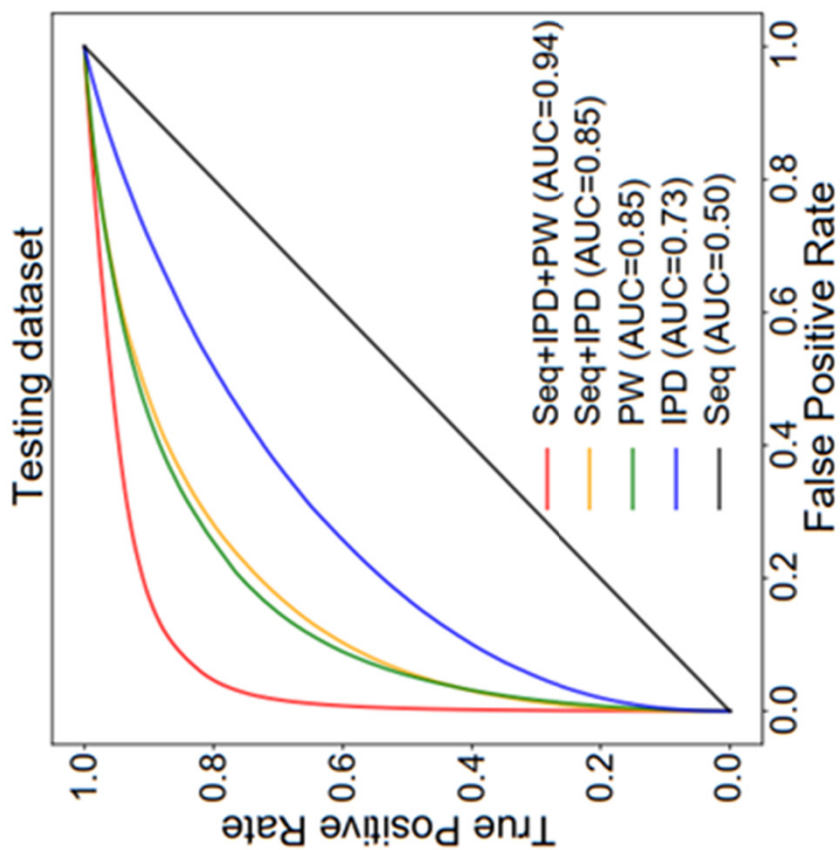


FIG. 18B

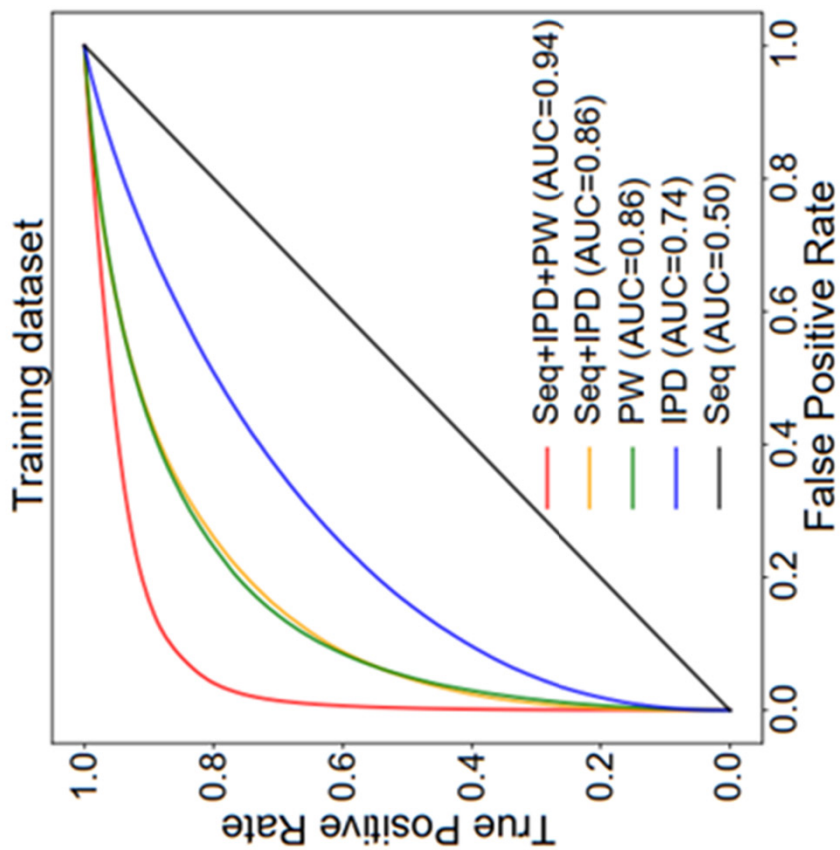


FIG. 18A

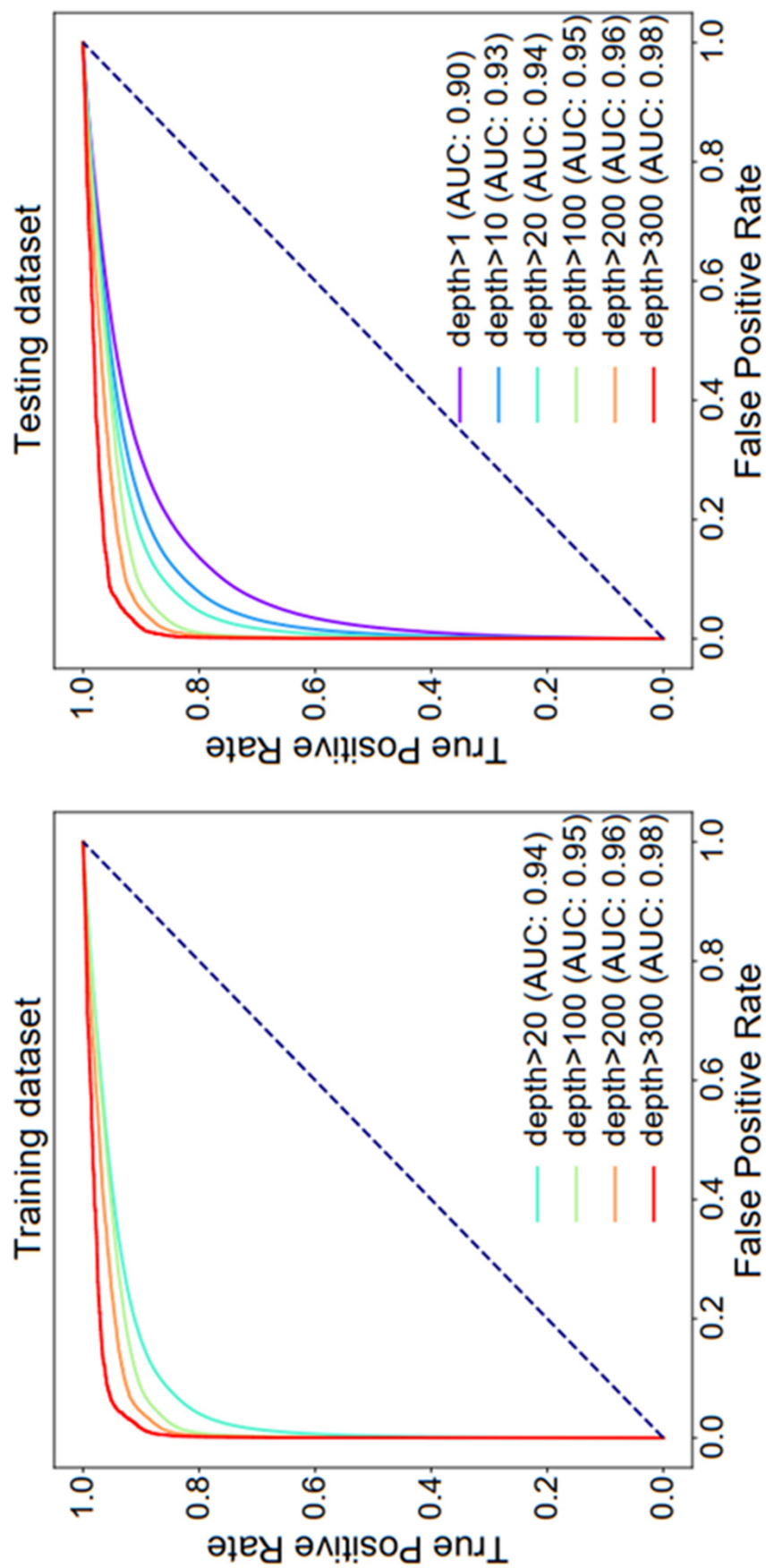


FIG. 19B

FIG. 19A

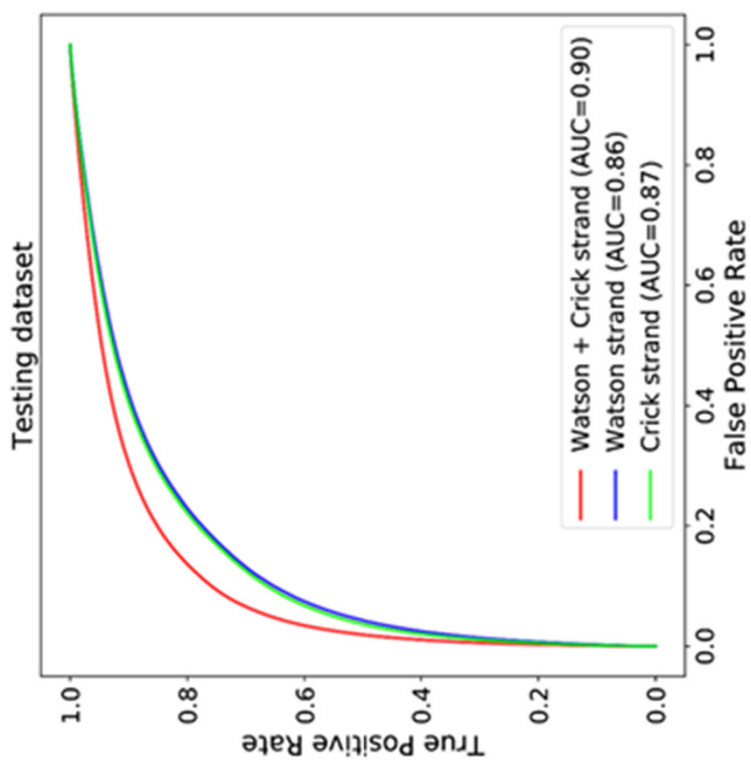


FIG. 20B

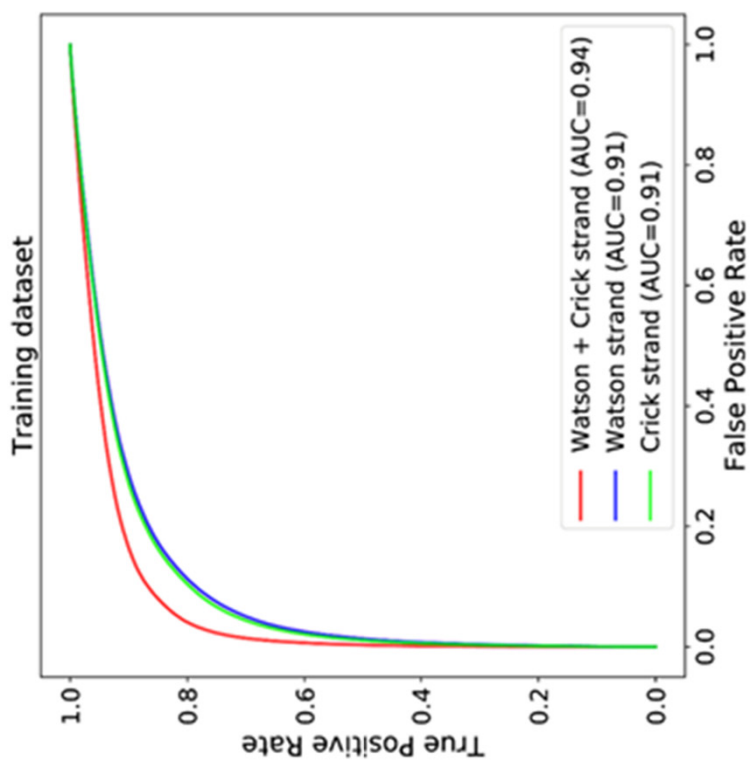


FIG. 20A

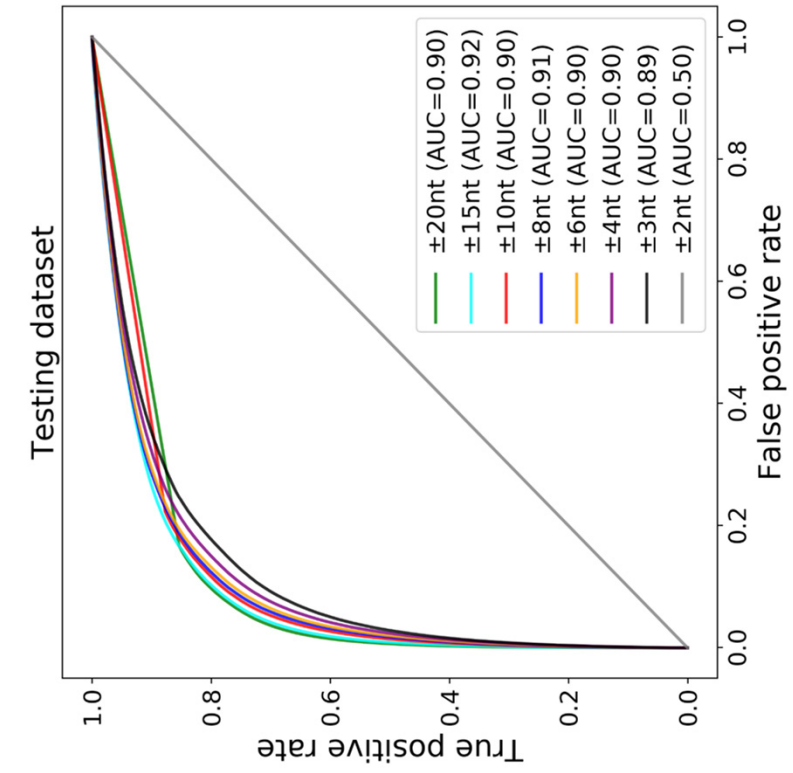


FIG. 21B

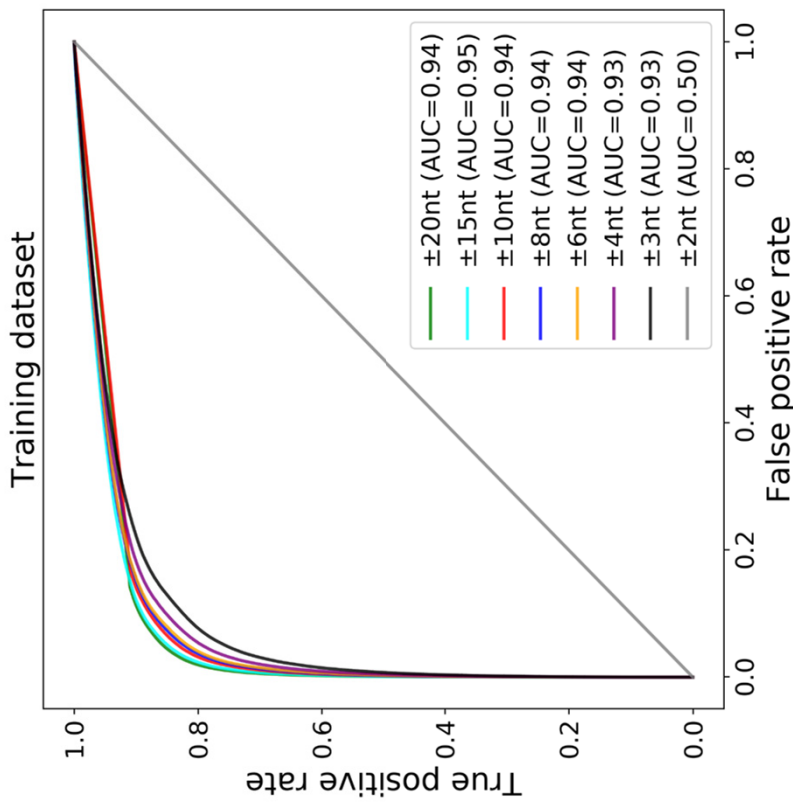


FIG. 21A

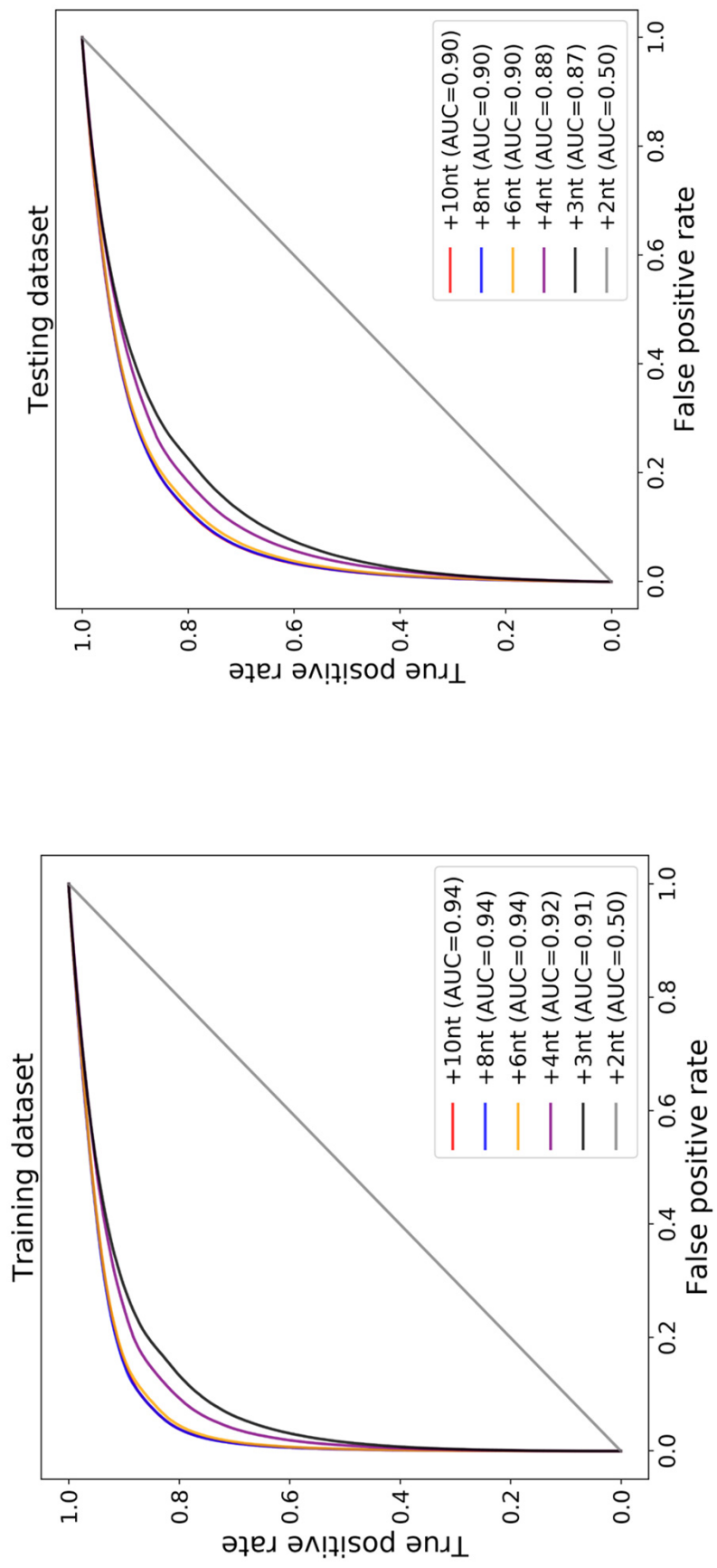


FIG. 22A

FIG. 22B

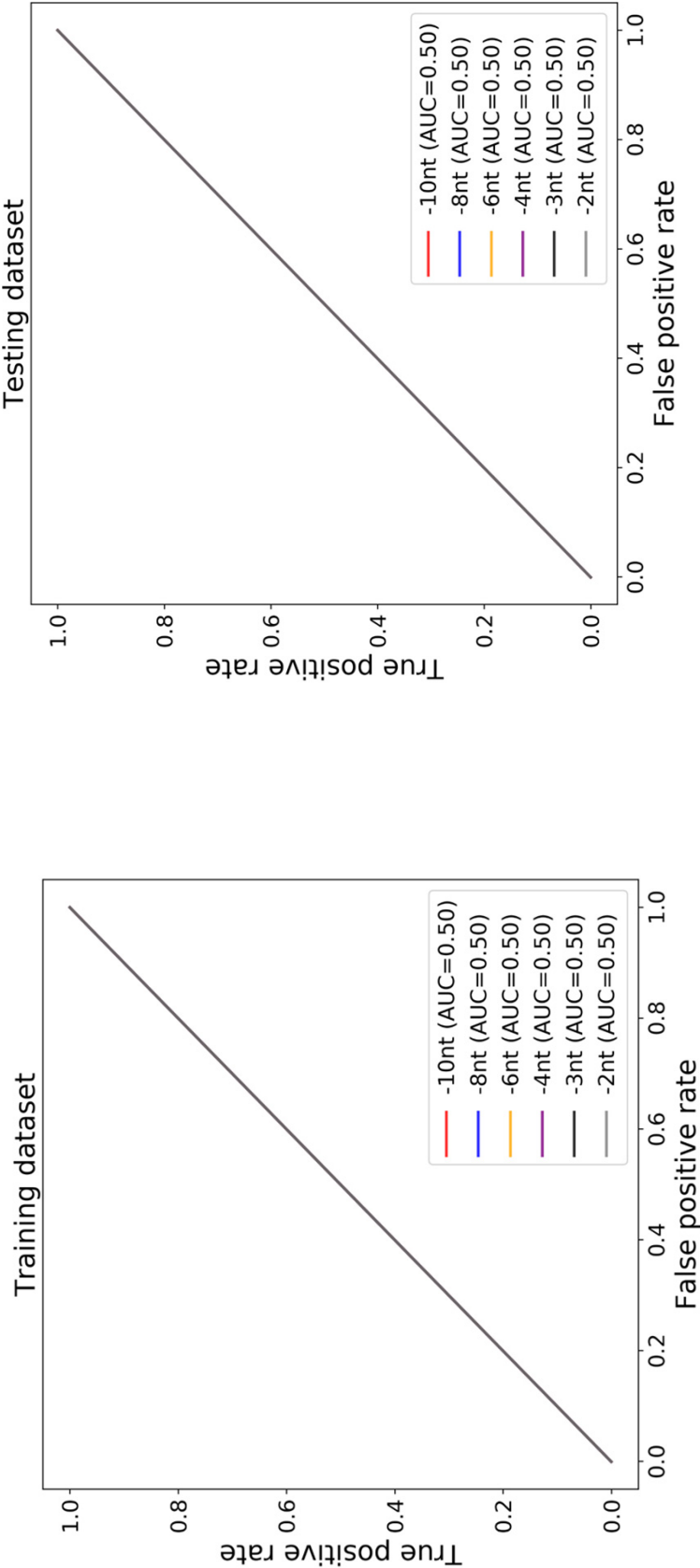


FIG. 23A

FIG. 23B

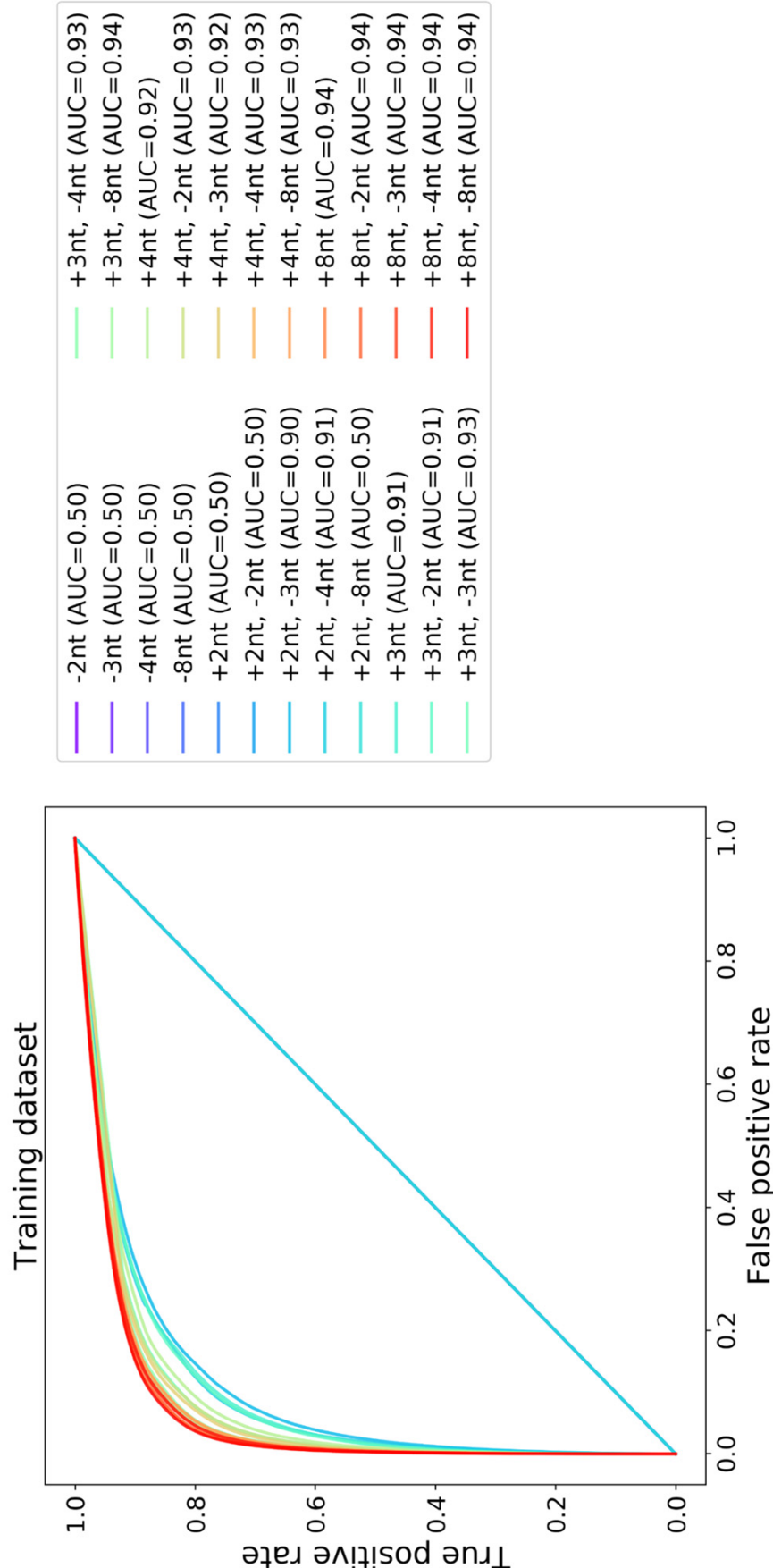


FIG. 24

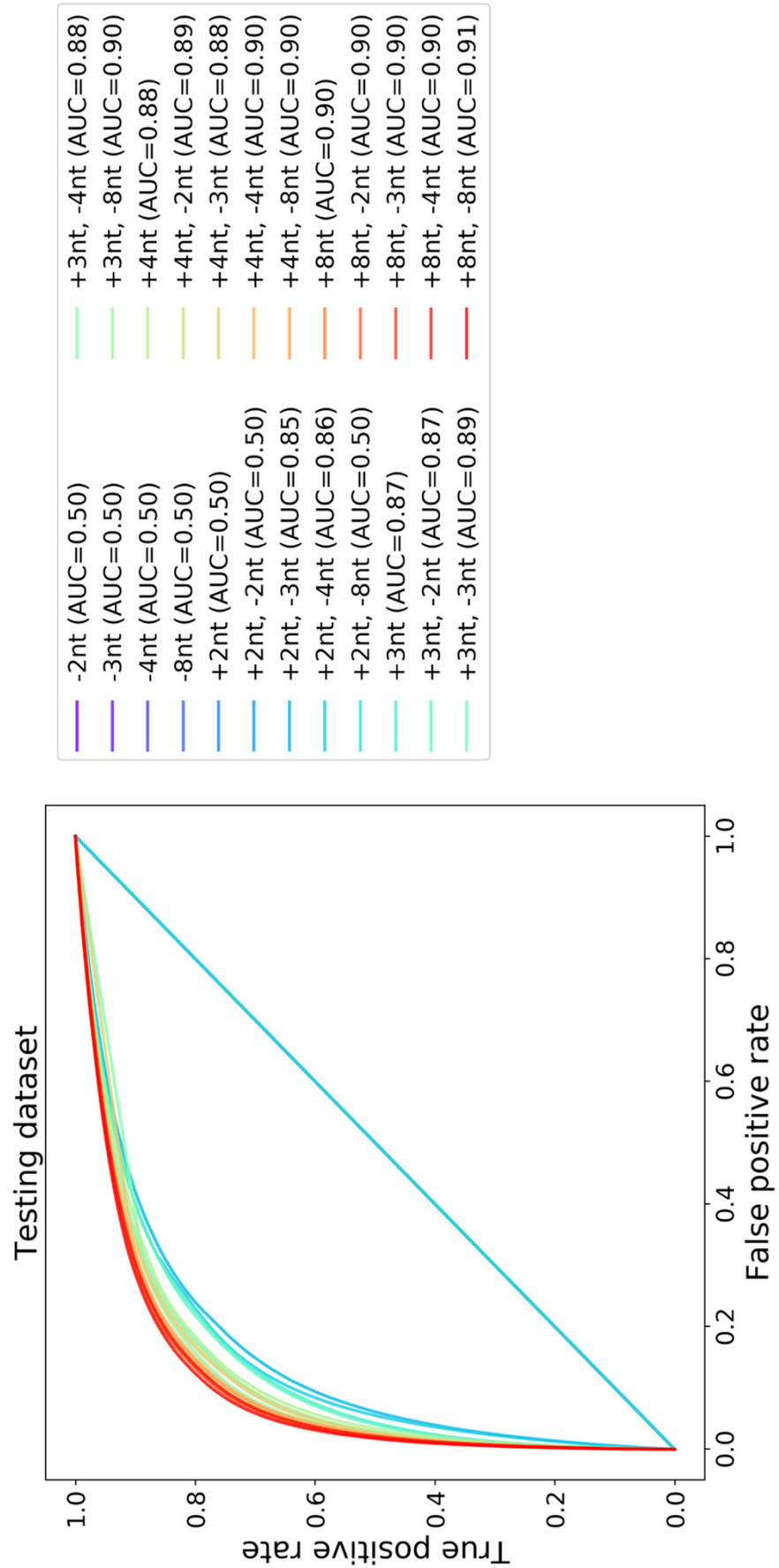


FIG. 25

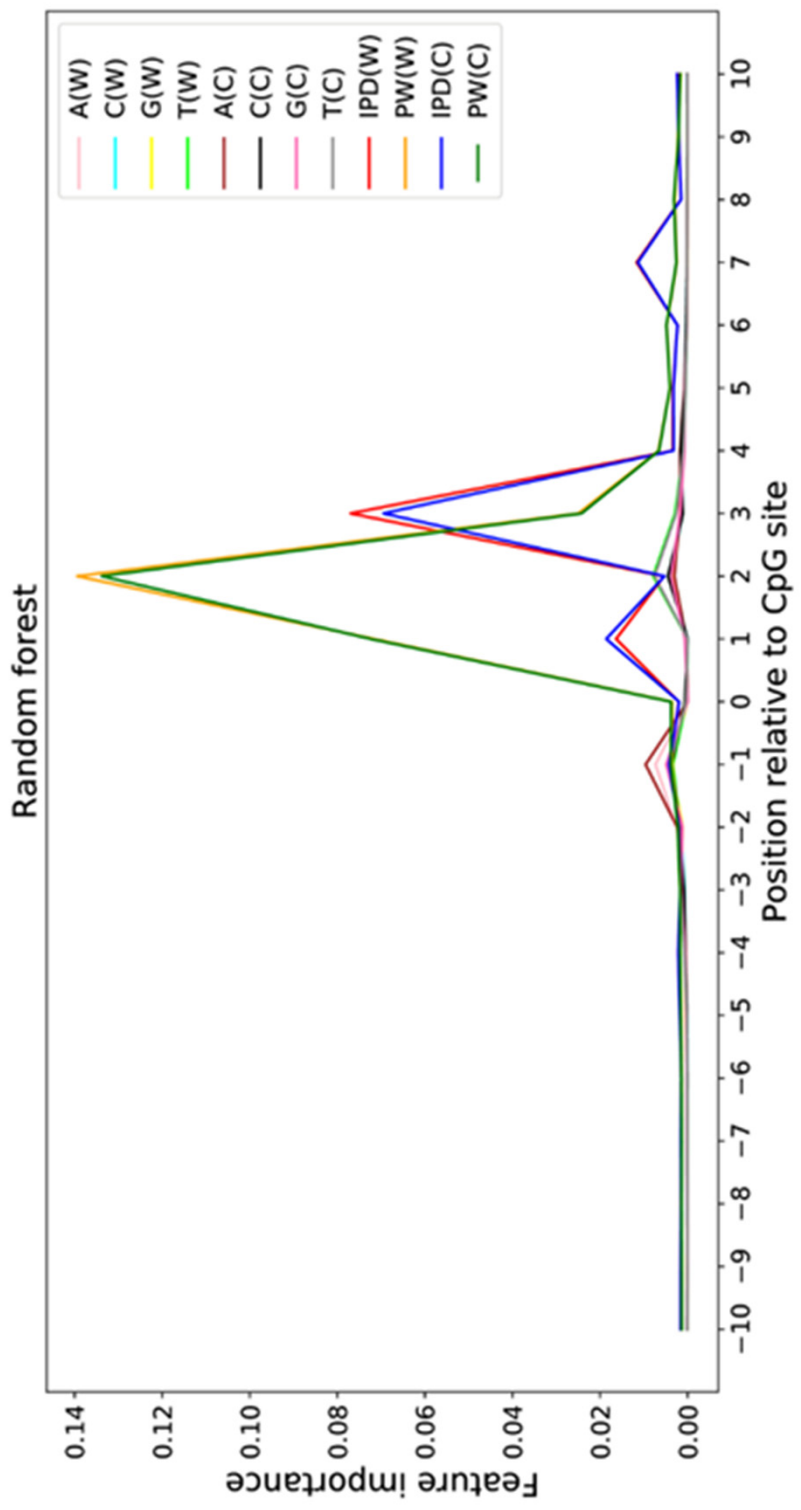


FIG. 26

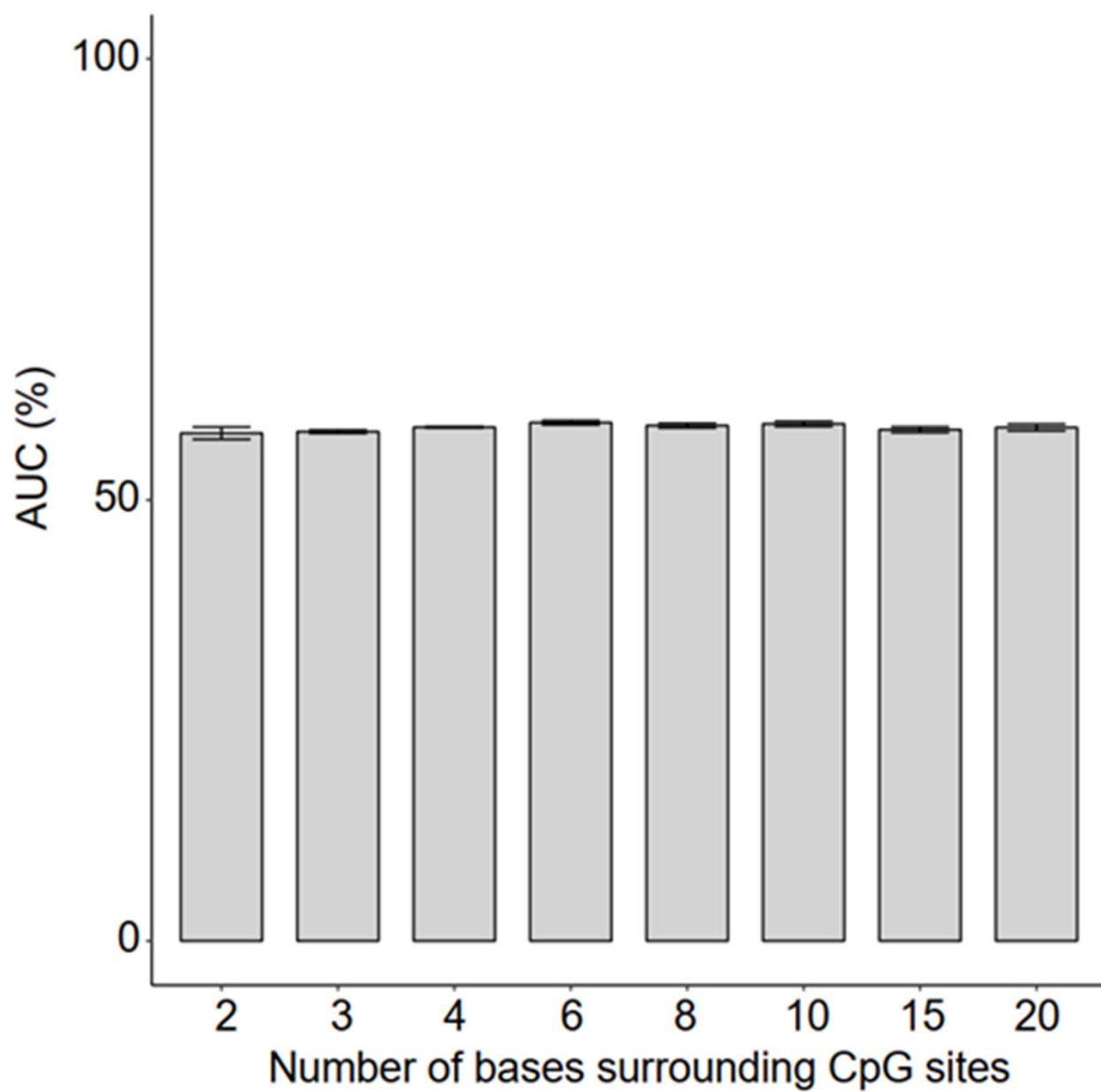


FIG. 27

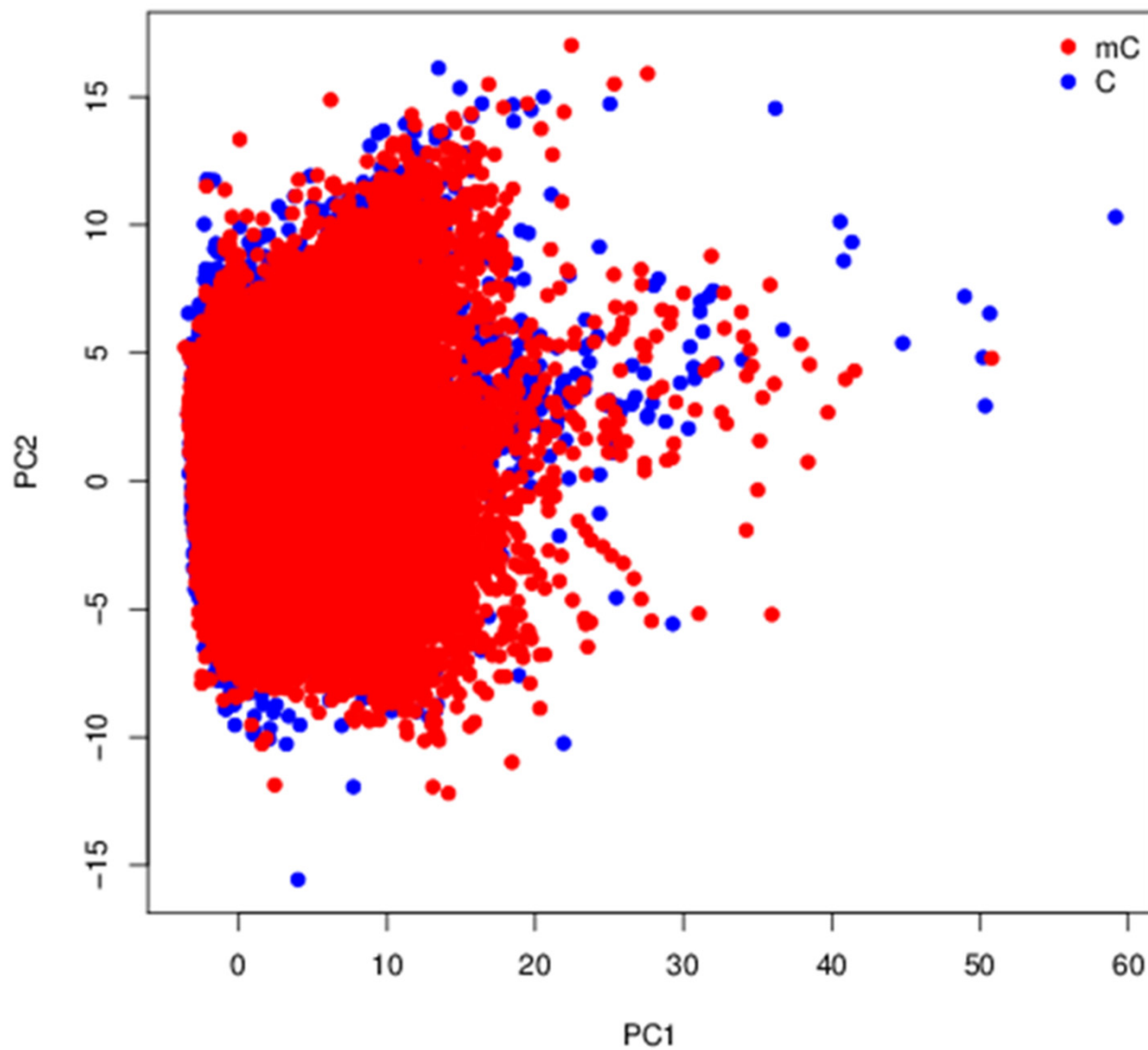


FIG. 28

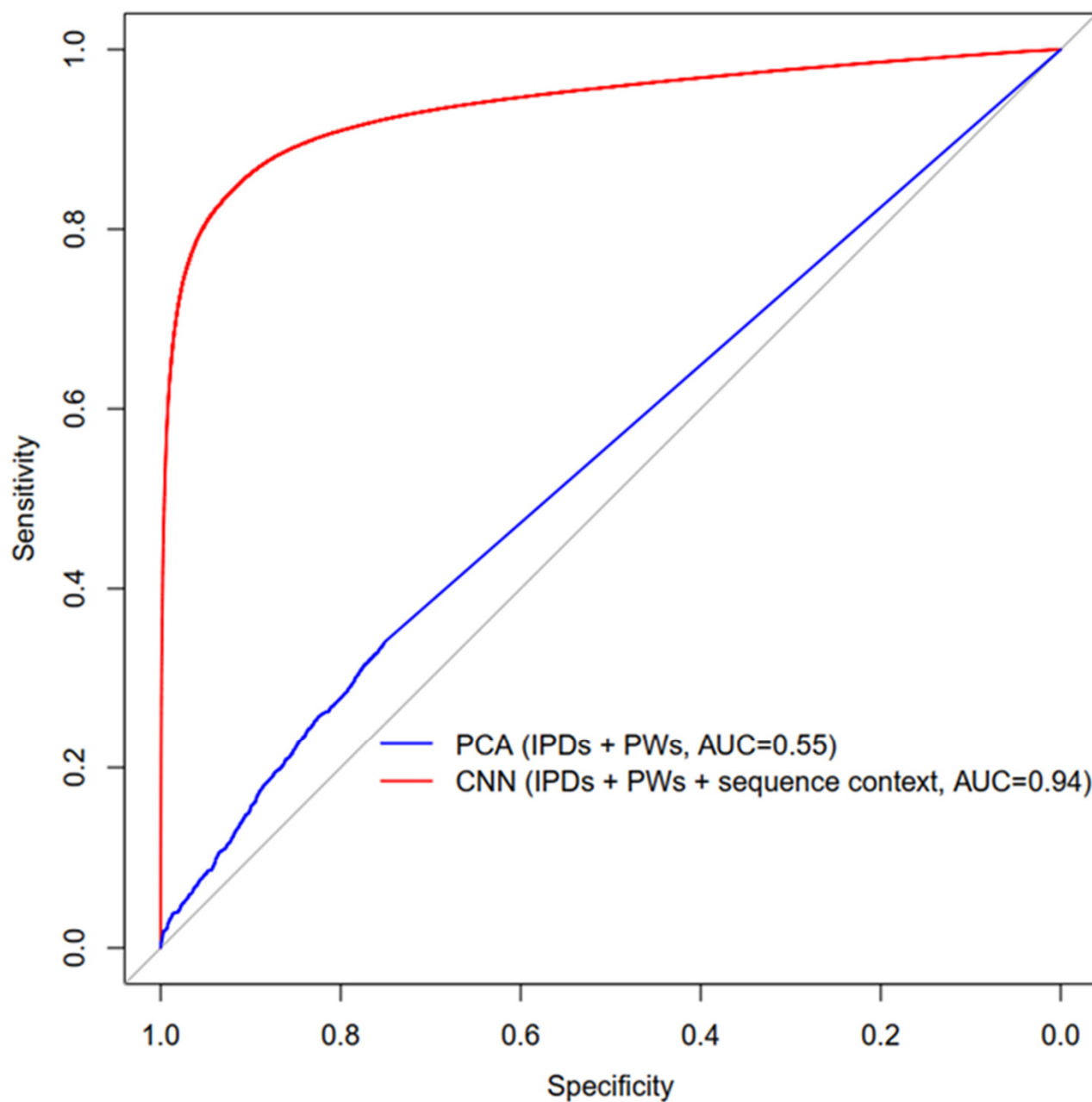


FIG. 29

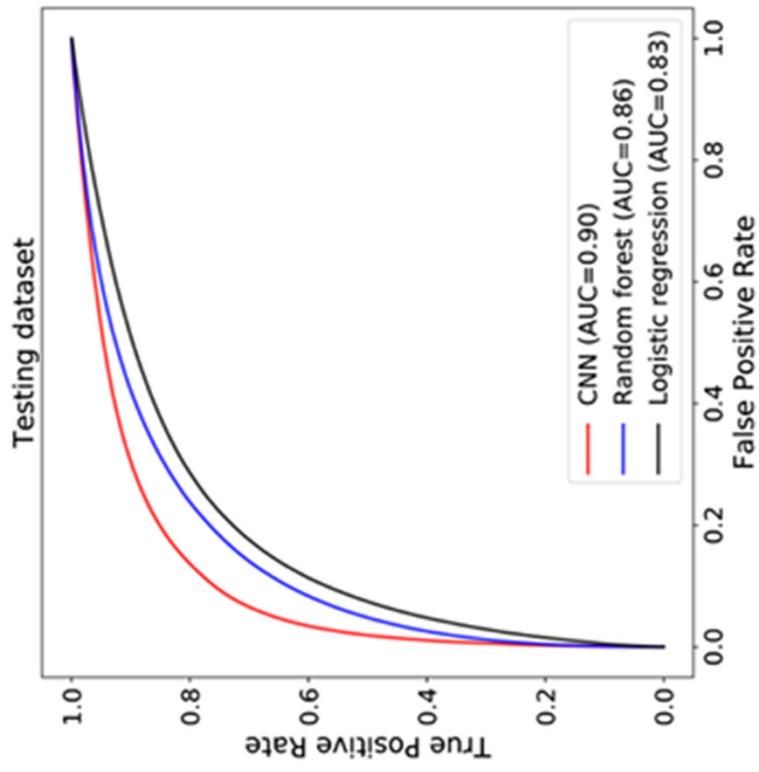


FIG. 30B

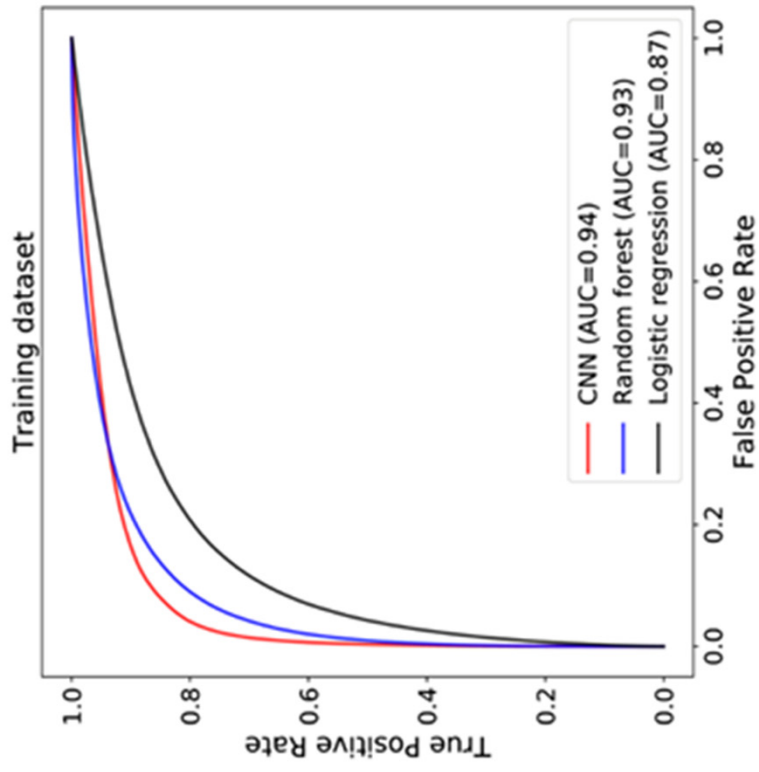
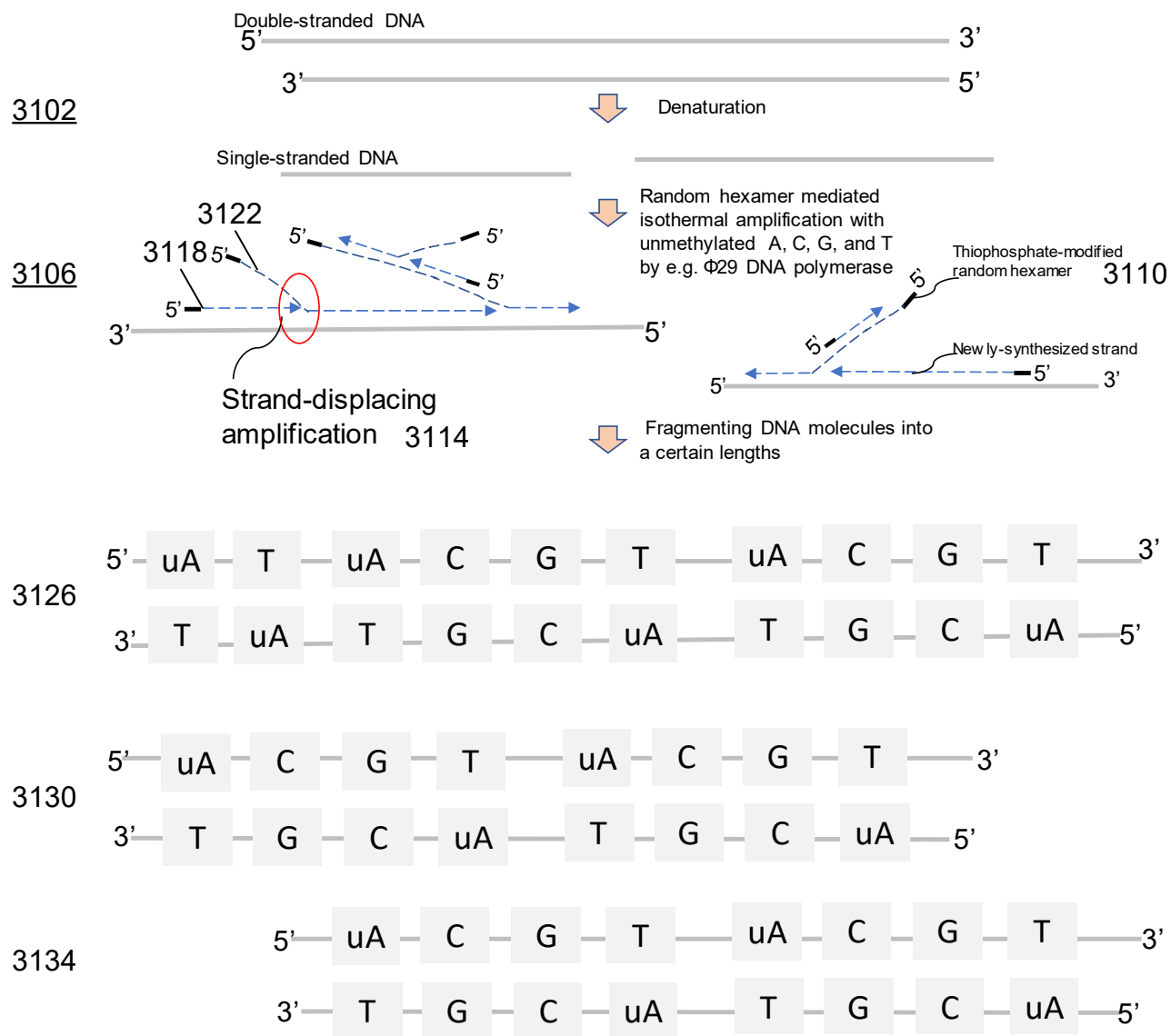
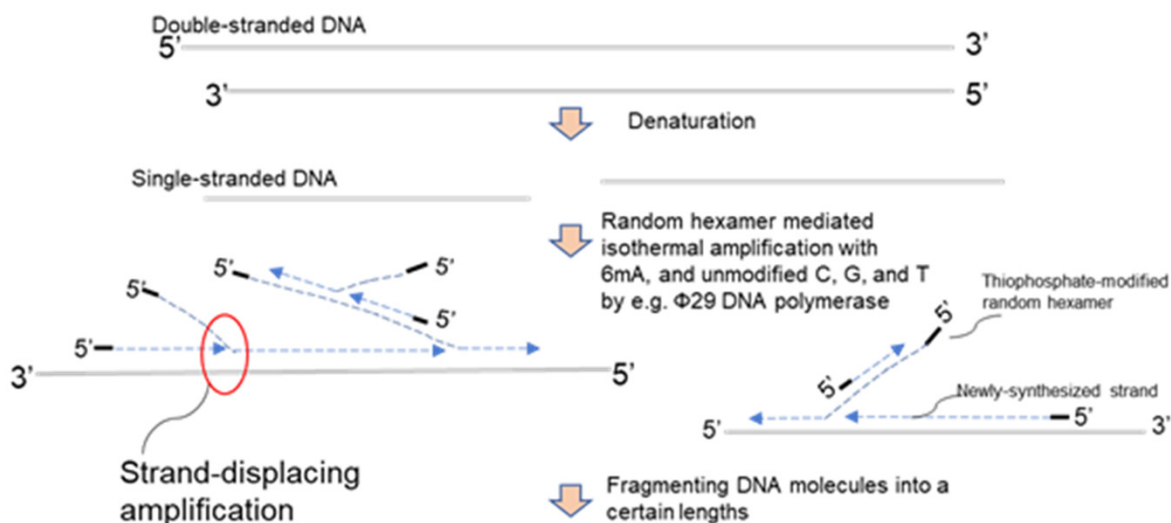


FIG. 30A



Whole-genome amplified DNA products

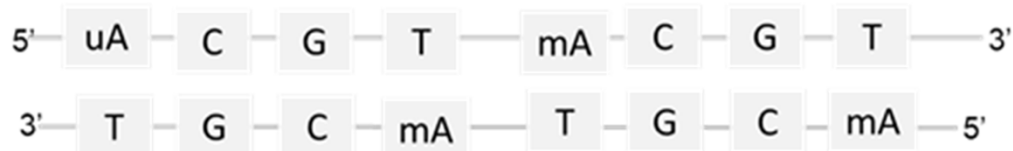
FIG. 31A



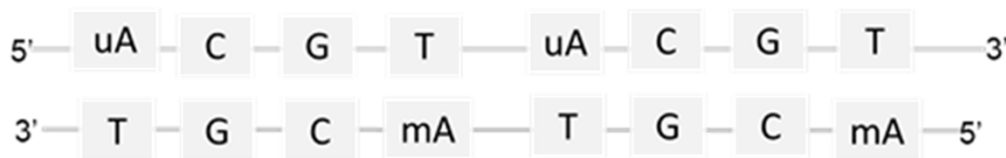
(I)



(II)



(III)



(IV)



Whole-genome amplified DNA products

FIG. 31B

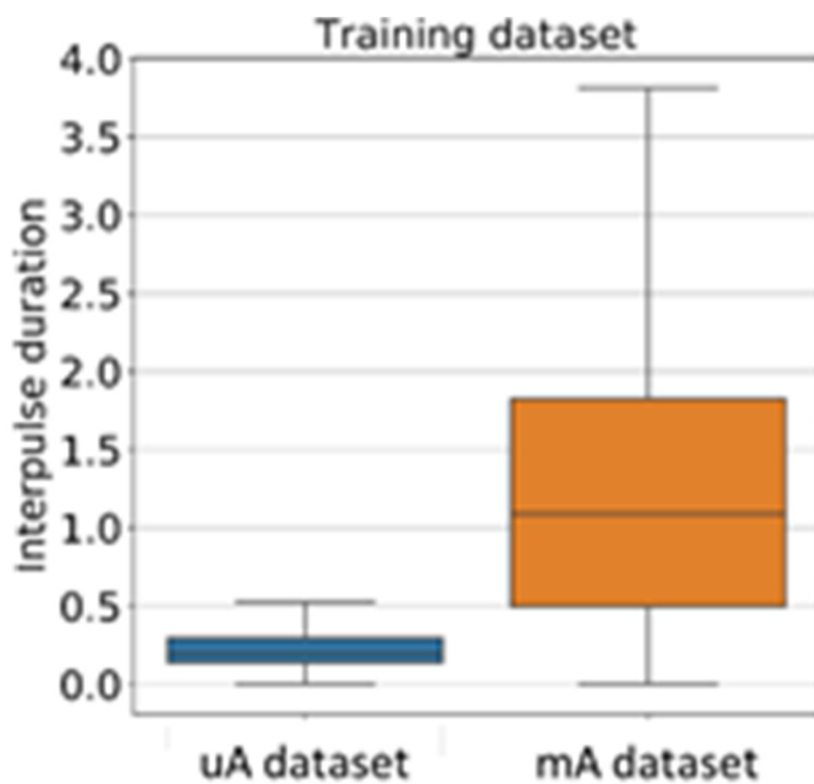


FIG. 32A

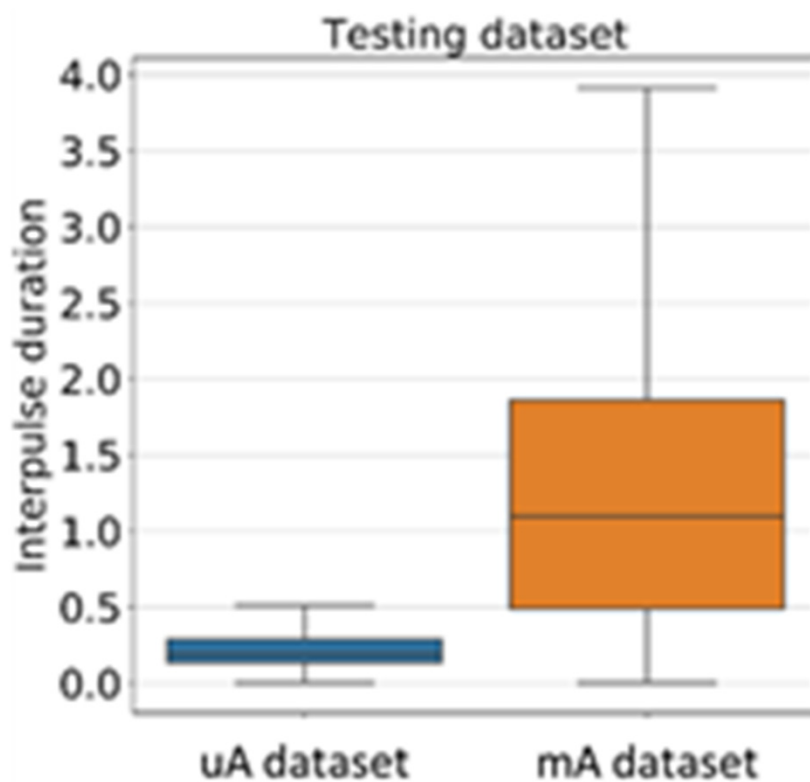


FIG. 32B

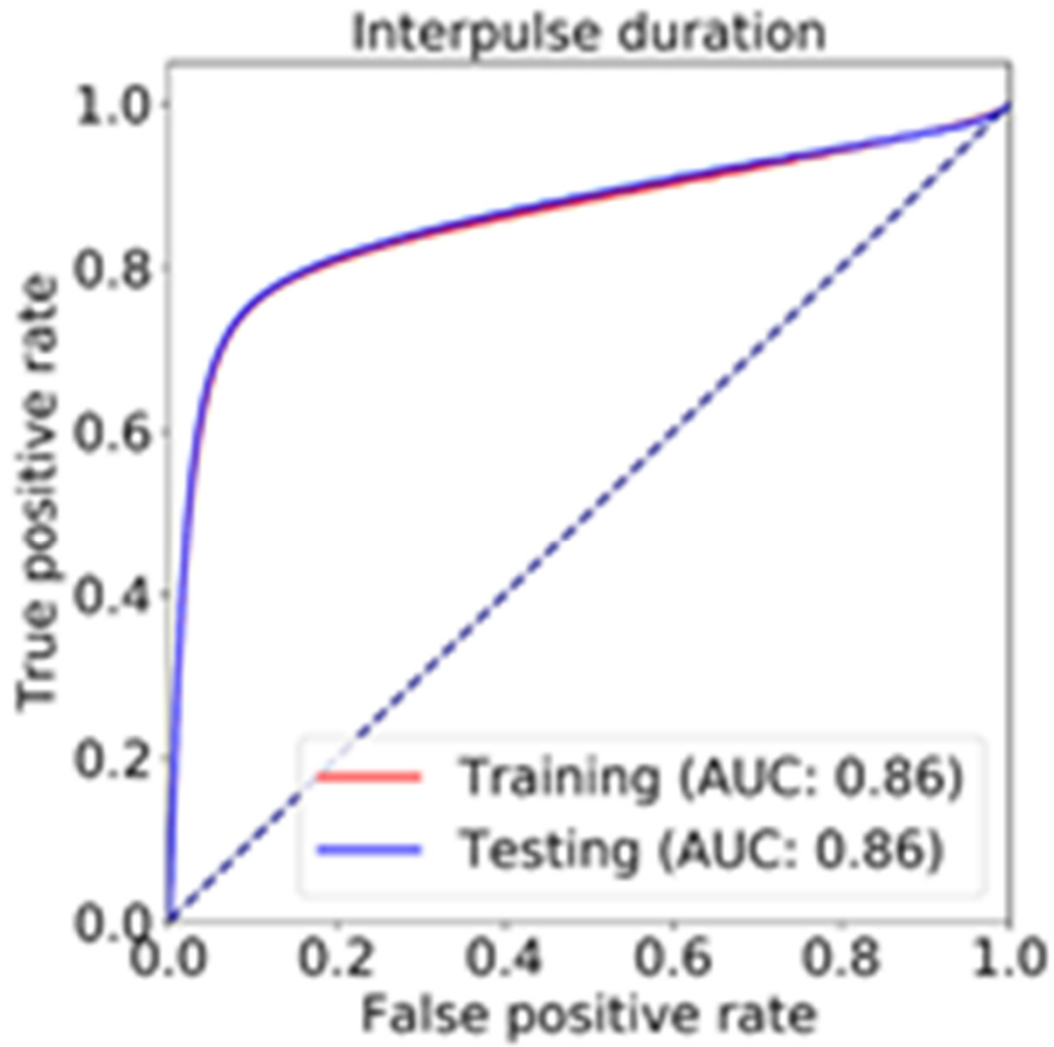


FIG. 32C

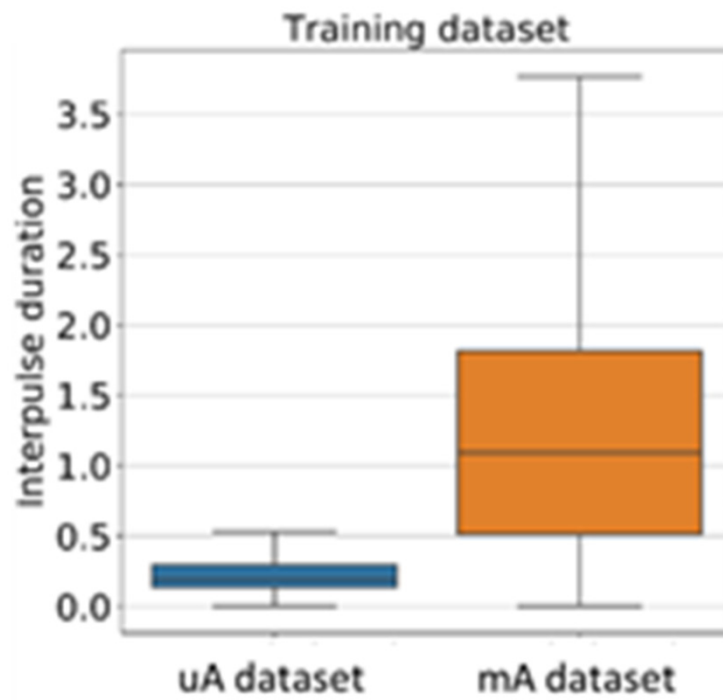


FIG. 33A

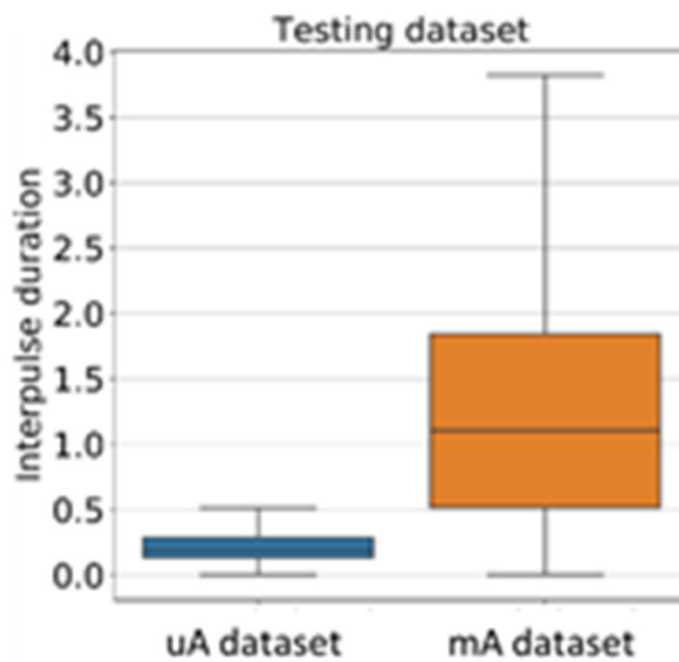


FIG. 33B

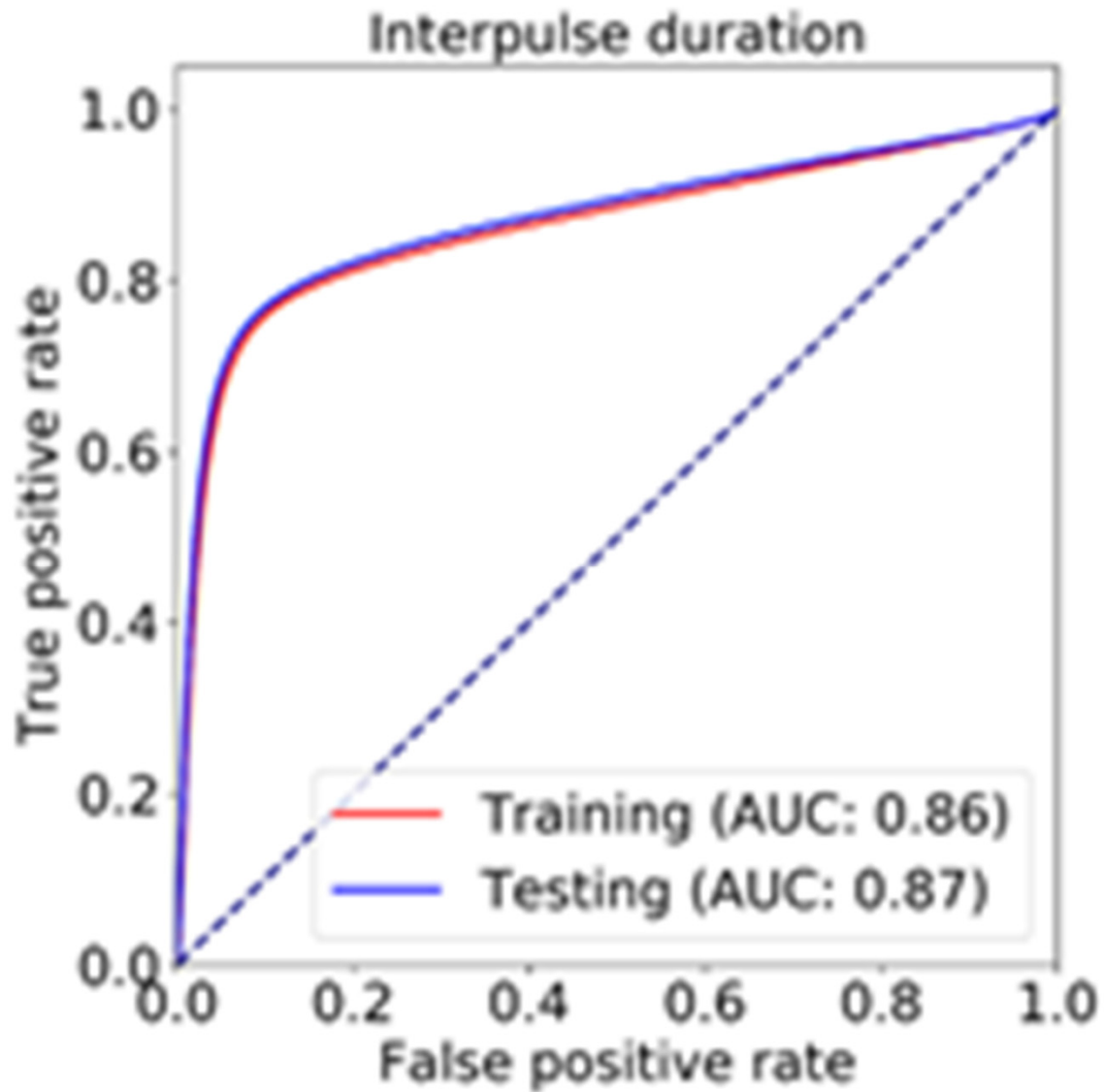


FIG. 33C



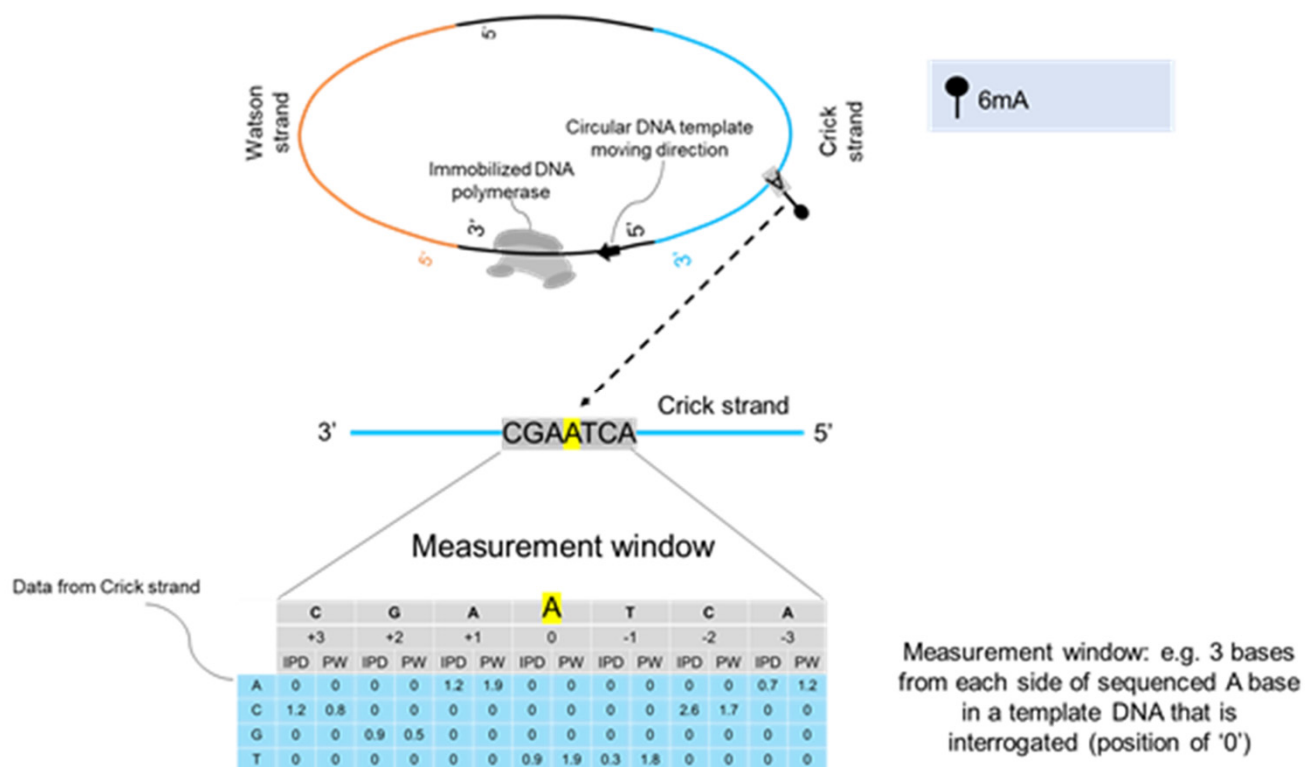


FIG.35

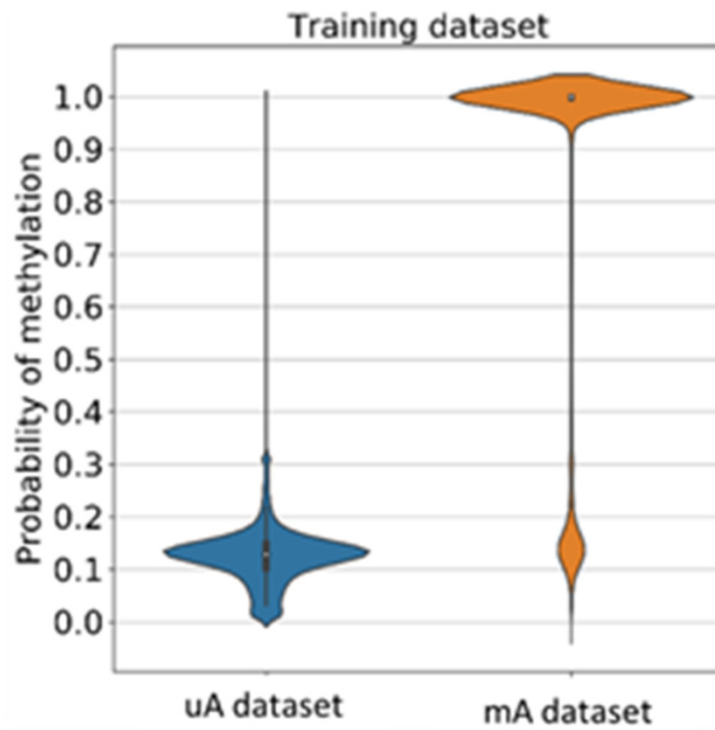


FIG. 36A



FIG. 36B

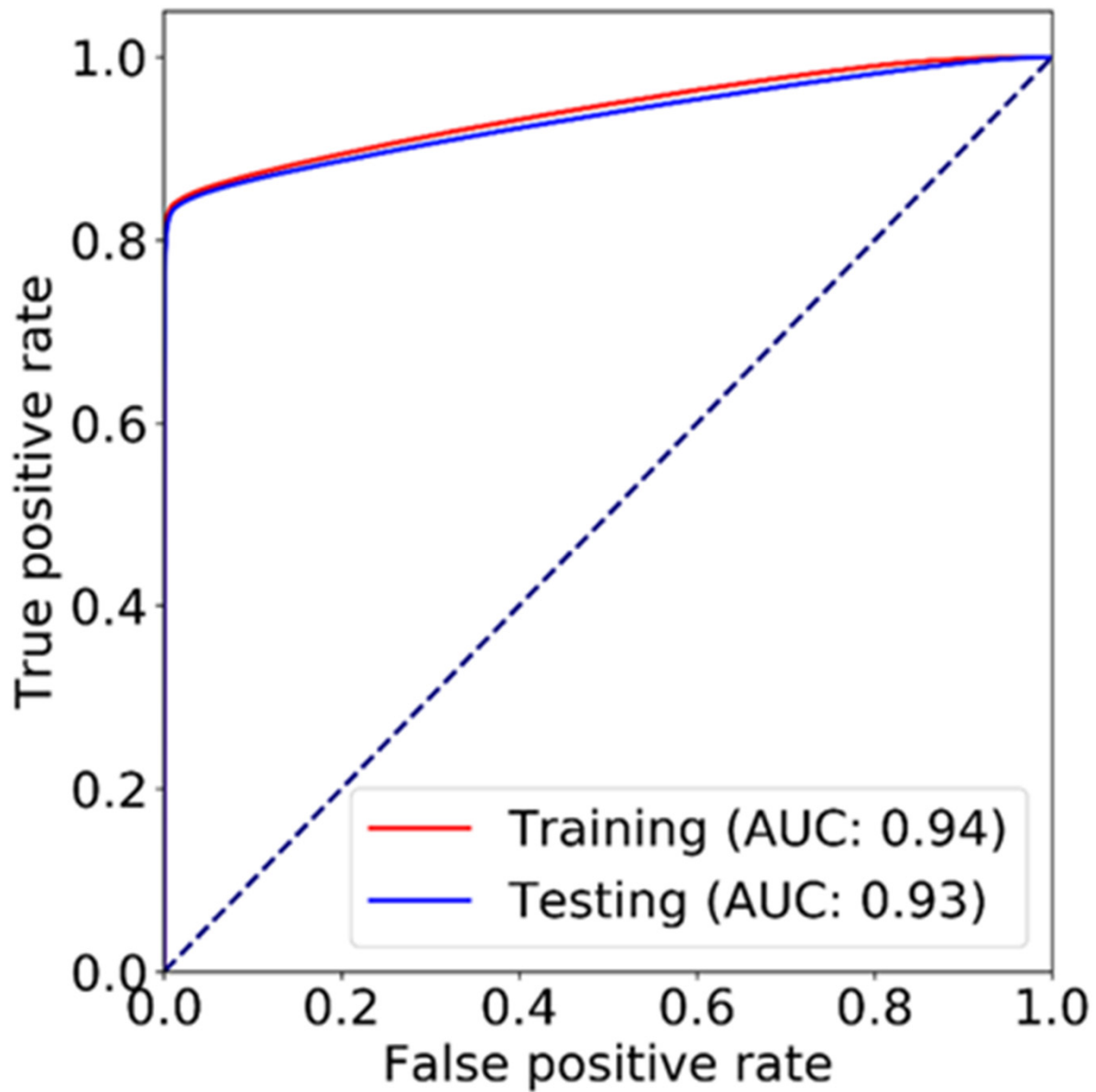


FIG. 37

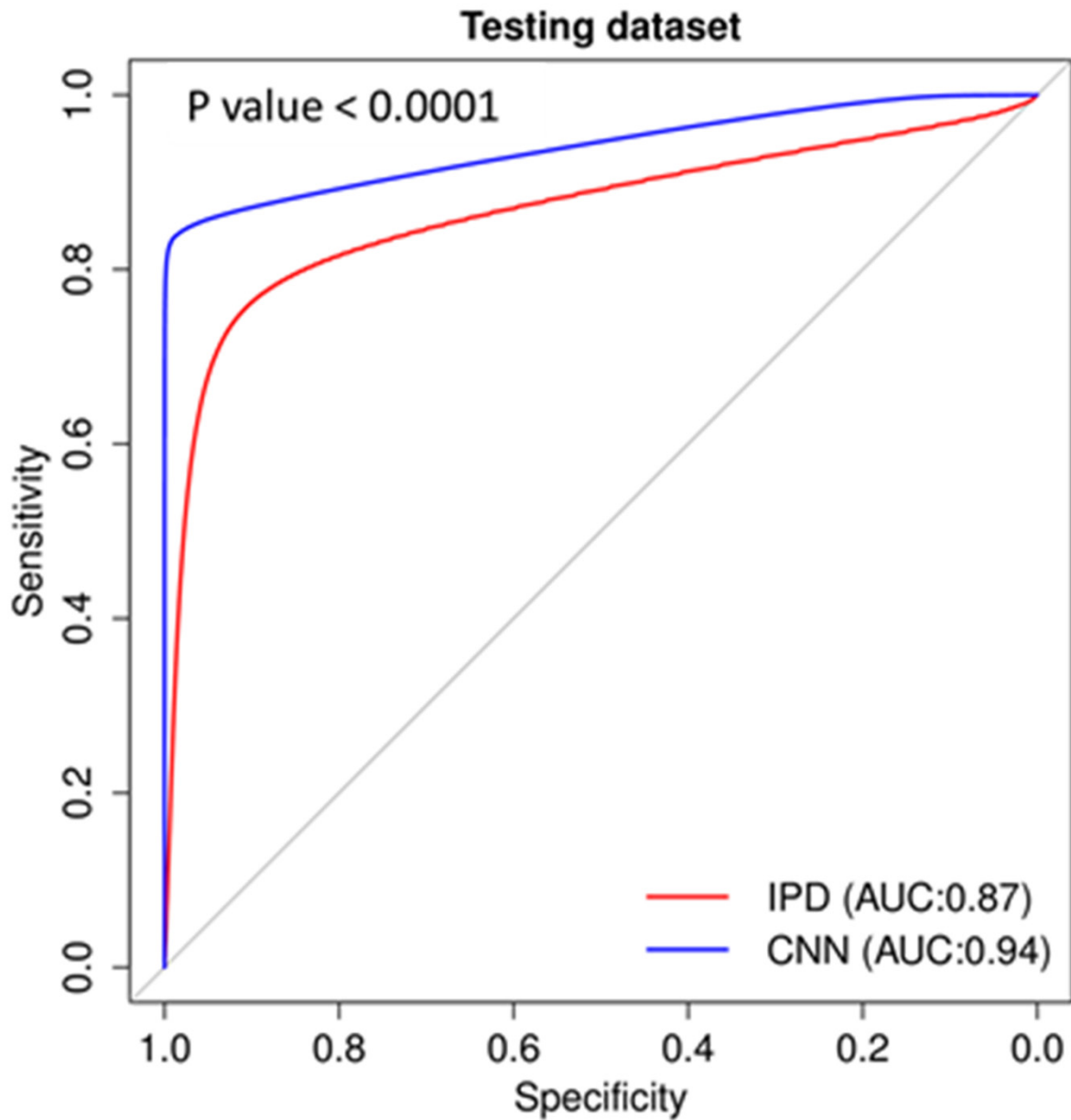


FIG. 38

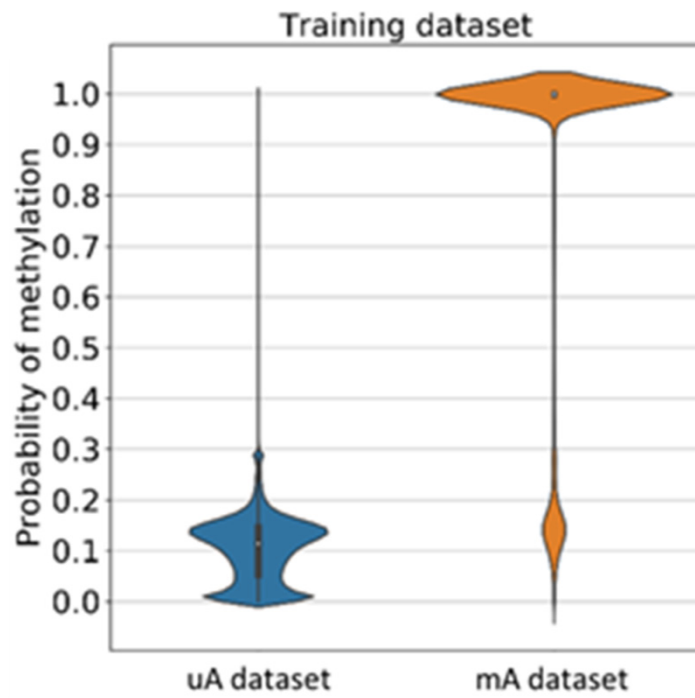


FIG. 39A



FIG. 39B

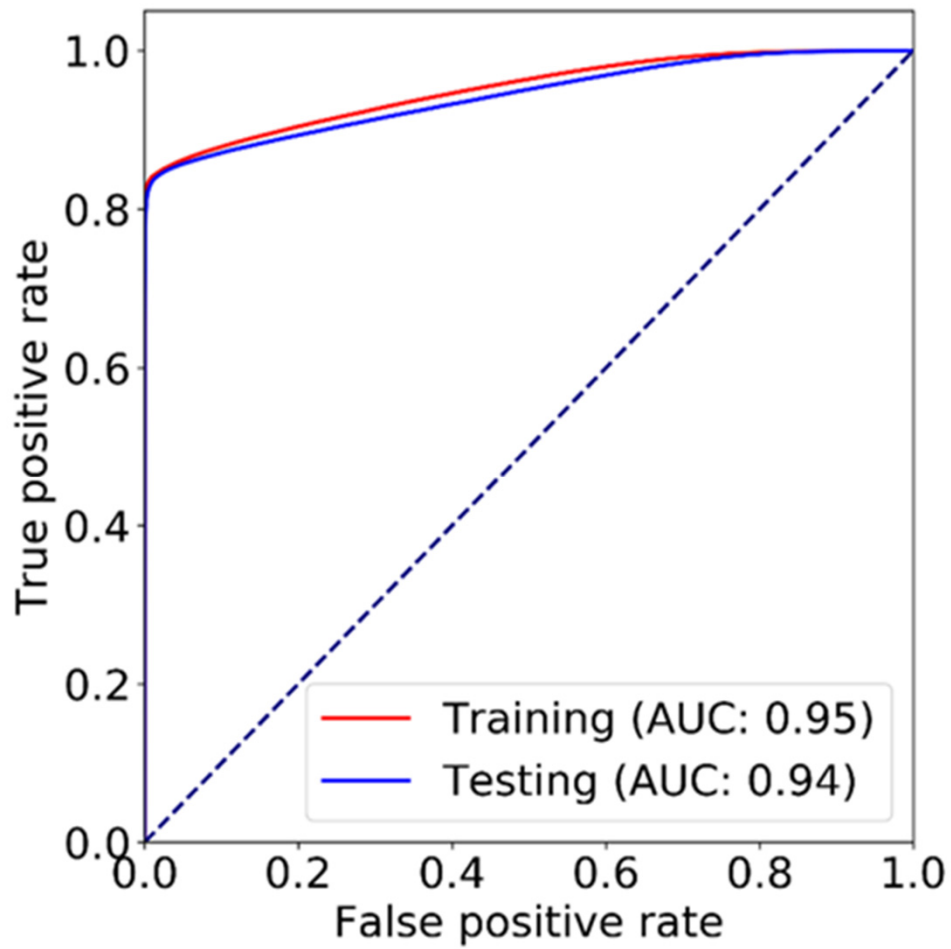


FIG. 40

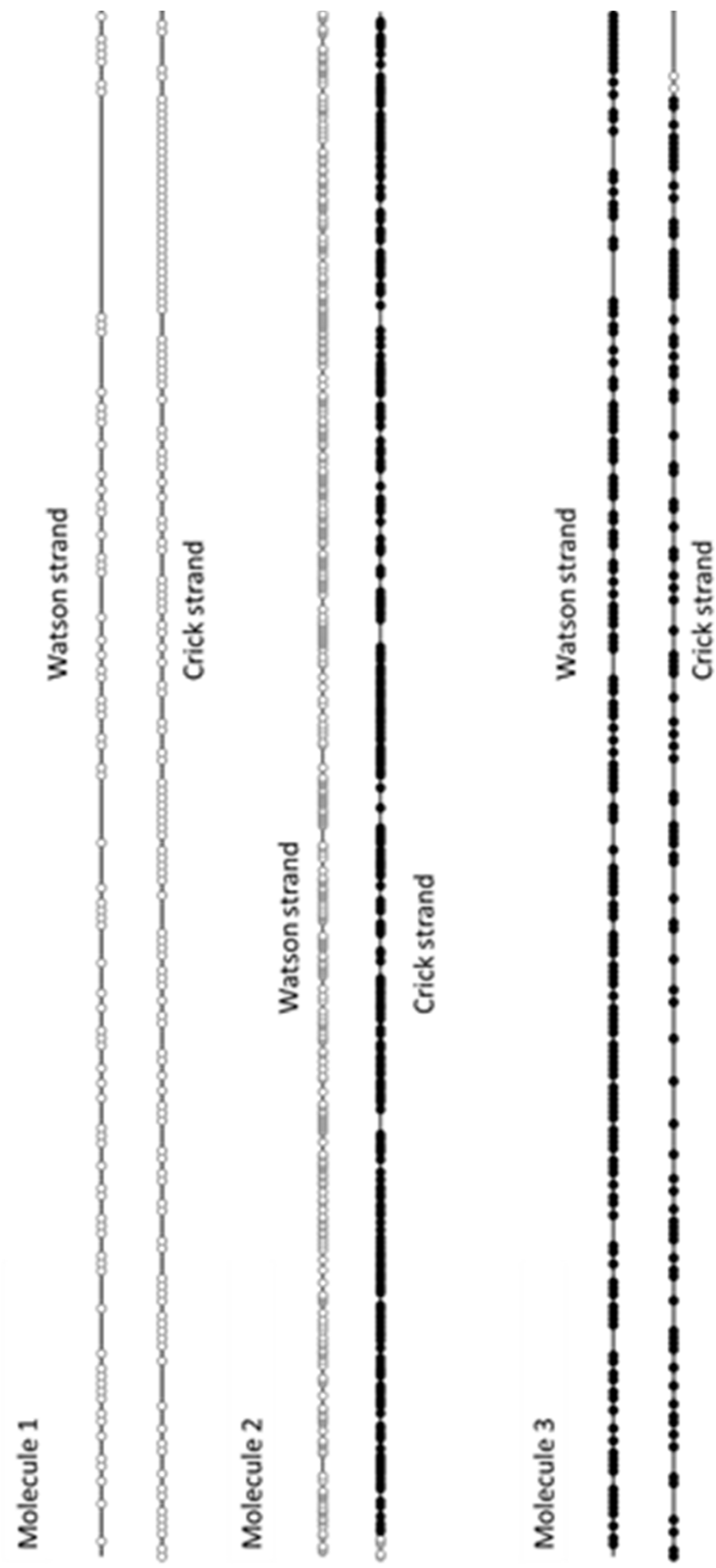


FIG. 41

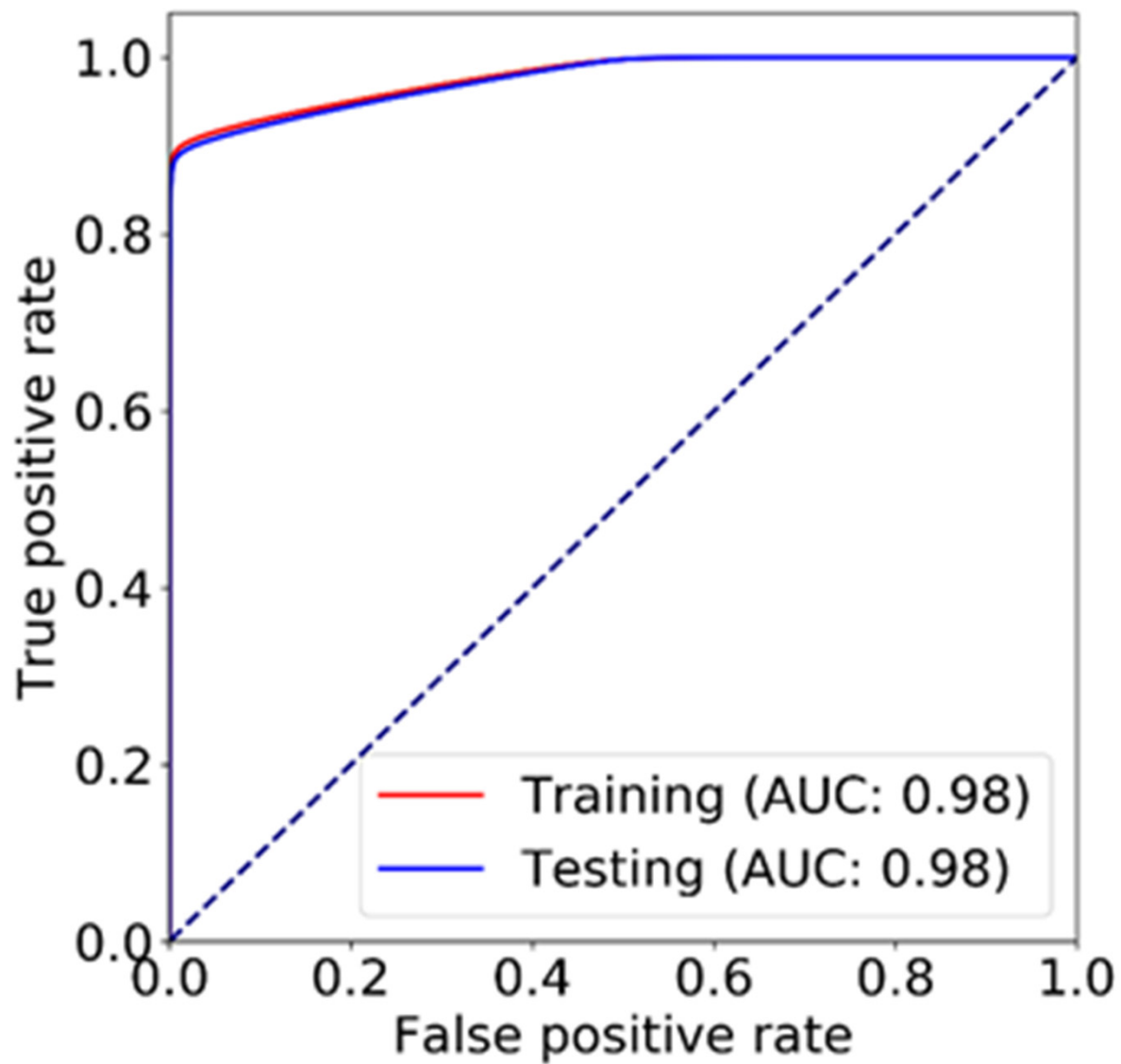


FIG. 42

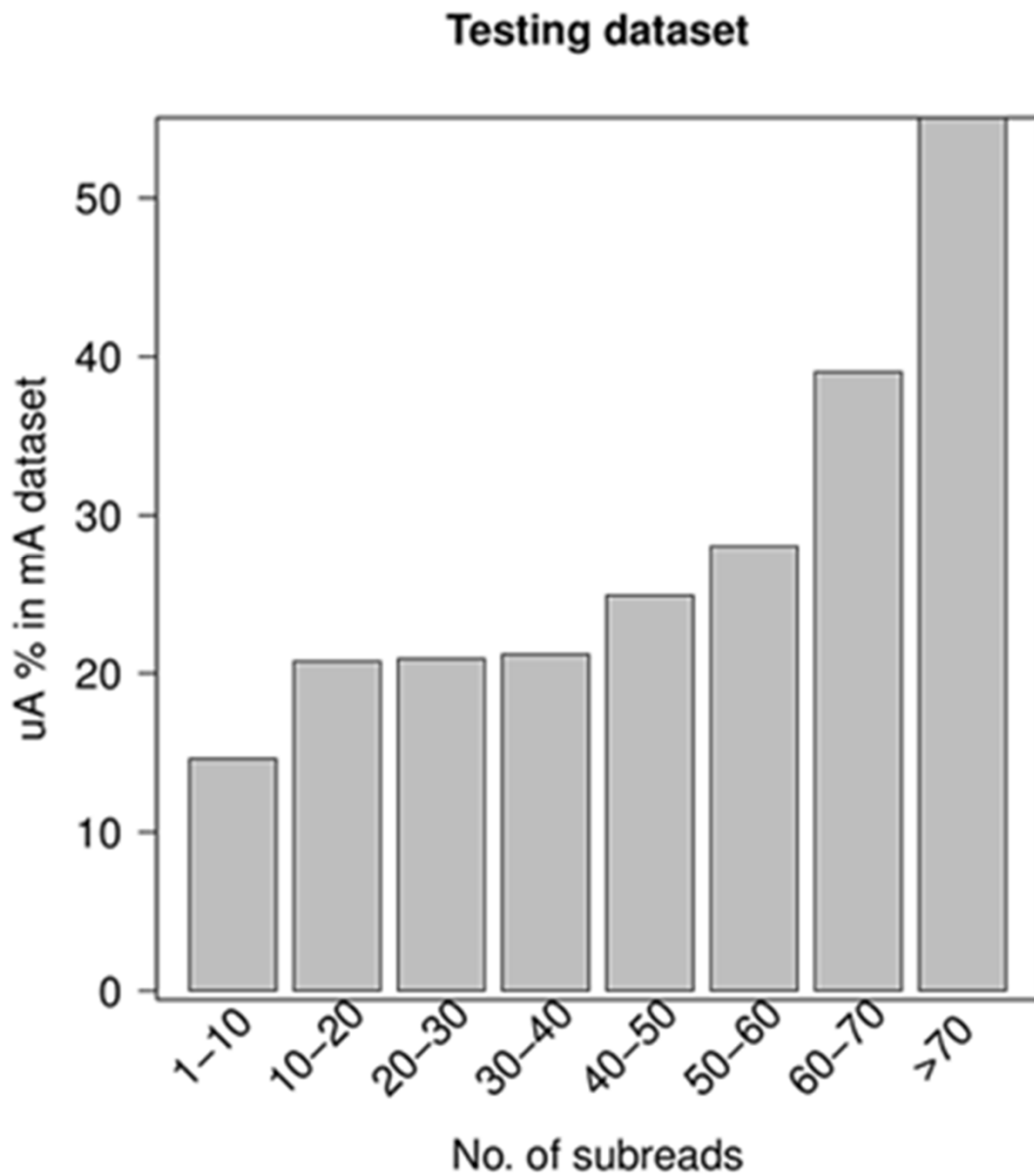


FIG. 43

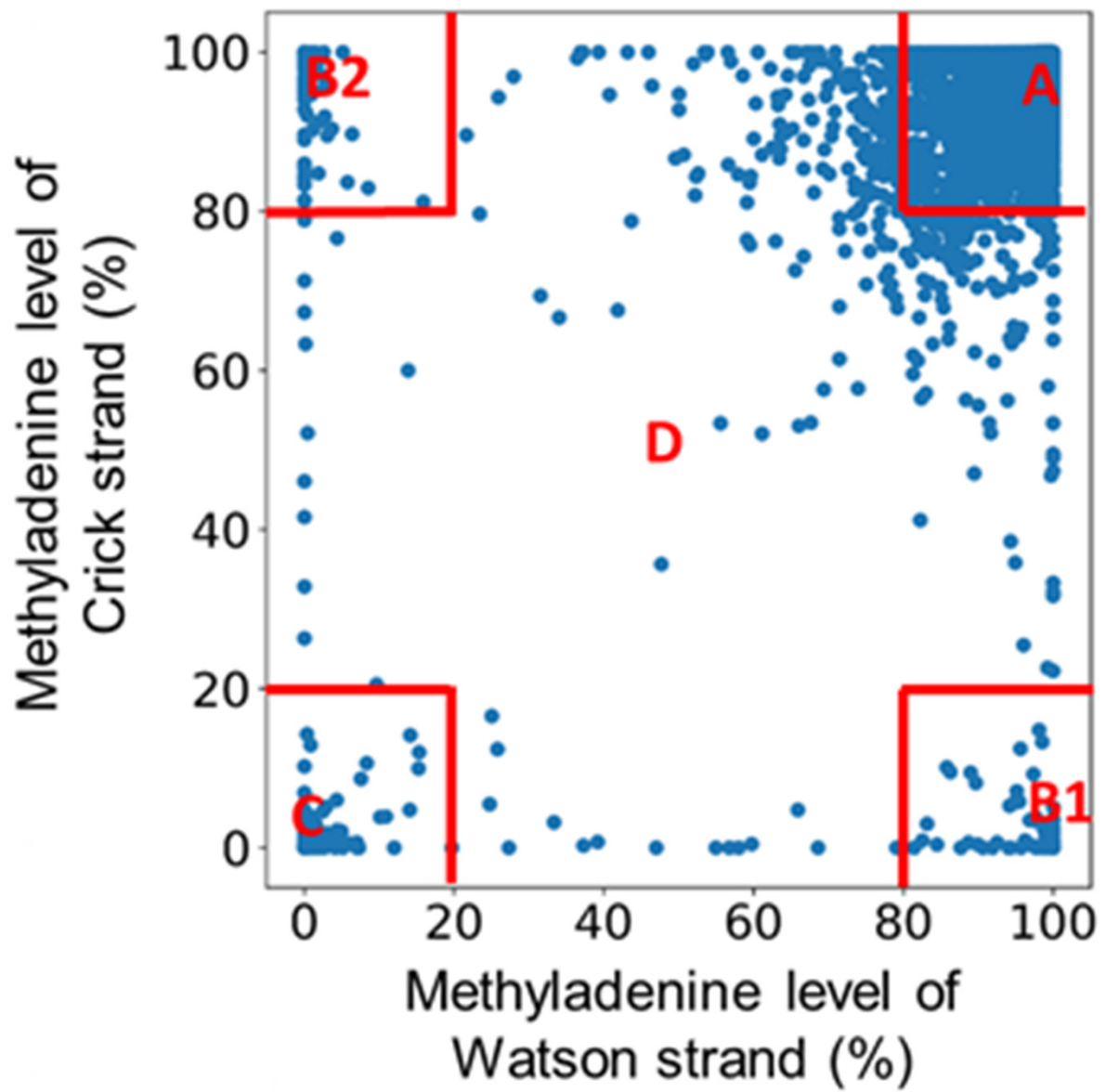


FIG.44

Categories	Training dataset	Testing dataset
Fully-unmethylated	283 (7.0%)	276 (7.0%)
Hemi-methylated	401 (10.0%)	389 (9.8%)
Fully-methylated	3194 (79.4%)	3142 (79.4%)
Interlacing methylation patterns	145 (3.6%)	148 (3.7%)

FIG. 45

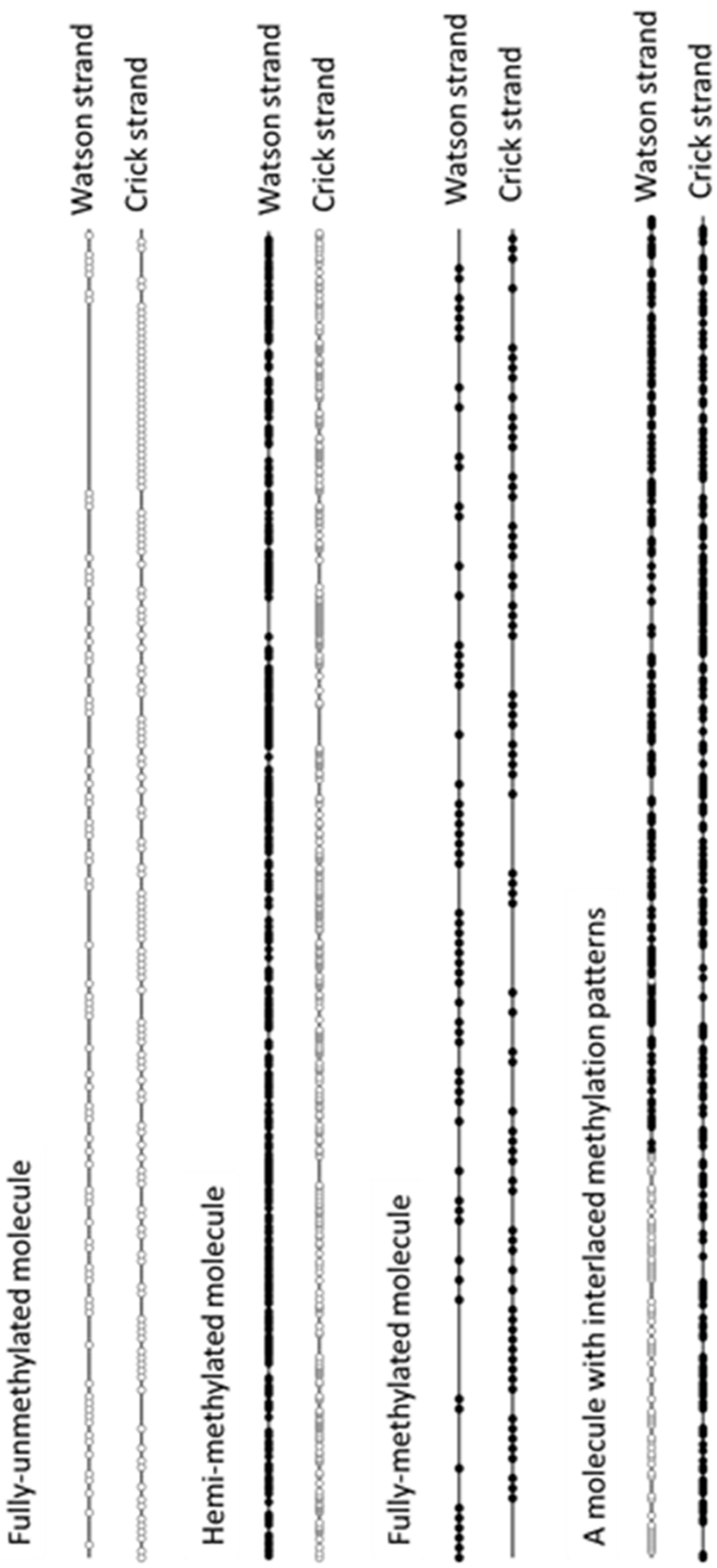


FIG. 46

ZMW hole number: m54276_180626_162240/40763503
Mapped location: chr1:113246546-113252811
Size: 6265

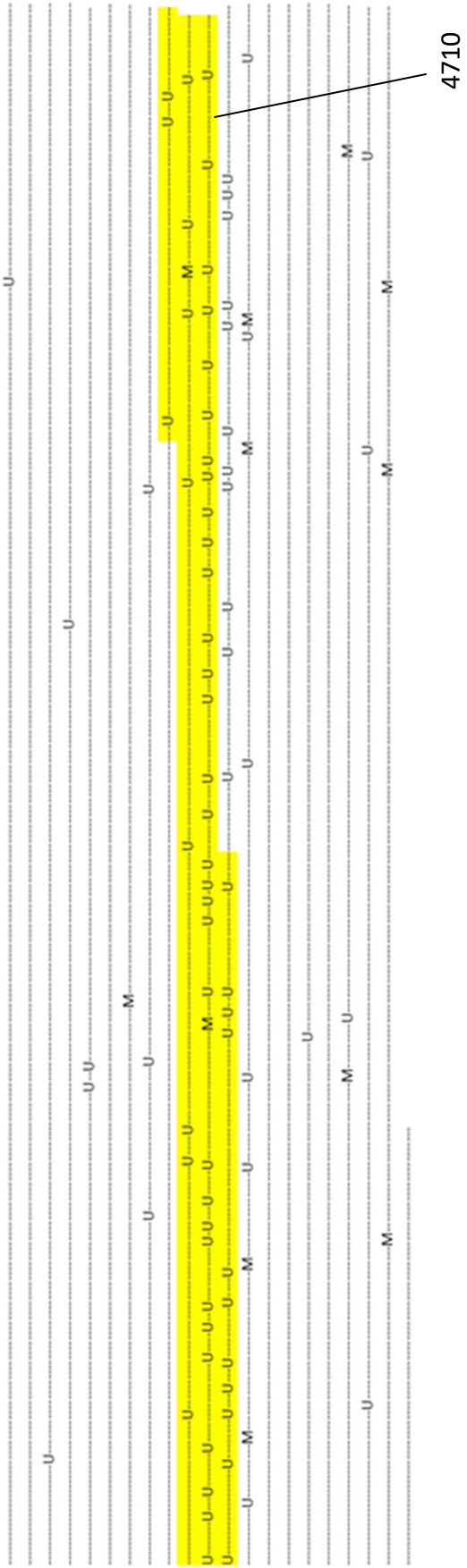


FIG. 47

Chromosomes	Start	End	Imprinted gene names	Length of CpG islands	Molecules sequenced by PacBio SMRT according to embodiments present in this disclosure	Methylation call for a molecule
chr11	2013333	2013617	H19	284	-M-----M-M-----U-U-----M-----M----- -U-----M-----M-----M-----M-----M----- M-----M-M-----U-----[T]-----M-----M----- --M-----	Methylated
chr11	2019565	2019863	H19	298	-M-M-----M-----M-----[C]-----M-M-----M----- M-----M-----M-----M-M-----M-----M-----M----- M-----M-M-----M-----M-----M-----M-M-----M-----	Methylated
chr11	32460586	32461004	WT1-AS/WT1	418	-U-U-----U-M-----[C]-----U-----U-----U-U----- U-----U-----U-U-U-----U-----U-----M-----U----- ---U-U-U-----U-----U-----U-----U-U-----U-----U----- ---M-----	Unmethylated
chr14	101192851	101193499	DLK1	648	-U-U-----U-----U-----U-----M-----U-----U----- -U-----U-----U-----U-----U-U-----U-U-----U----- -U-U-----U-----U-----U-----U-----U-U-----U----- M-----	Unmethylated
chr14	101201559	101201763	DLK1	204	-M-----U-----U-----M-----M-----M-----[T]----- ---M-----M-----M-----M-----M-----M-----M----- ---M-----M-----M-----M-----	Methylated
chr14	101292863	101293101	MEG3	238	--M-----M-----M-----U-----U-----M-----M----- -----M-----M-----M-----M-----	Methylated
chr15	25981176	25981392	ATP10A	216	*-----M-----M-----M-----M-----M----- M-----M-----M-----[T]-----M-M-----U----- *-[G]-----U-----U-----M-----M-----U-----U----- ---U-----U-----U-----U-----M-----M-----U----- ---U-U-----M-----U-----U-----U-----U----- ---	Methylated
chr2	80531367	80531719	LRRTM1	352		Unmethylated
chr7	79082174	79082427	MAGI2	253	*-U-----U-----[A]-M-U-----U-----U-----U----- U-----U-----*	Unmethylated

FIG. 48

Methylation patterns present in a paternally imprinted region

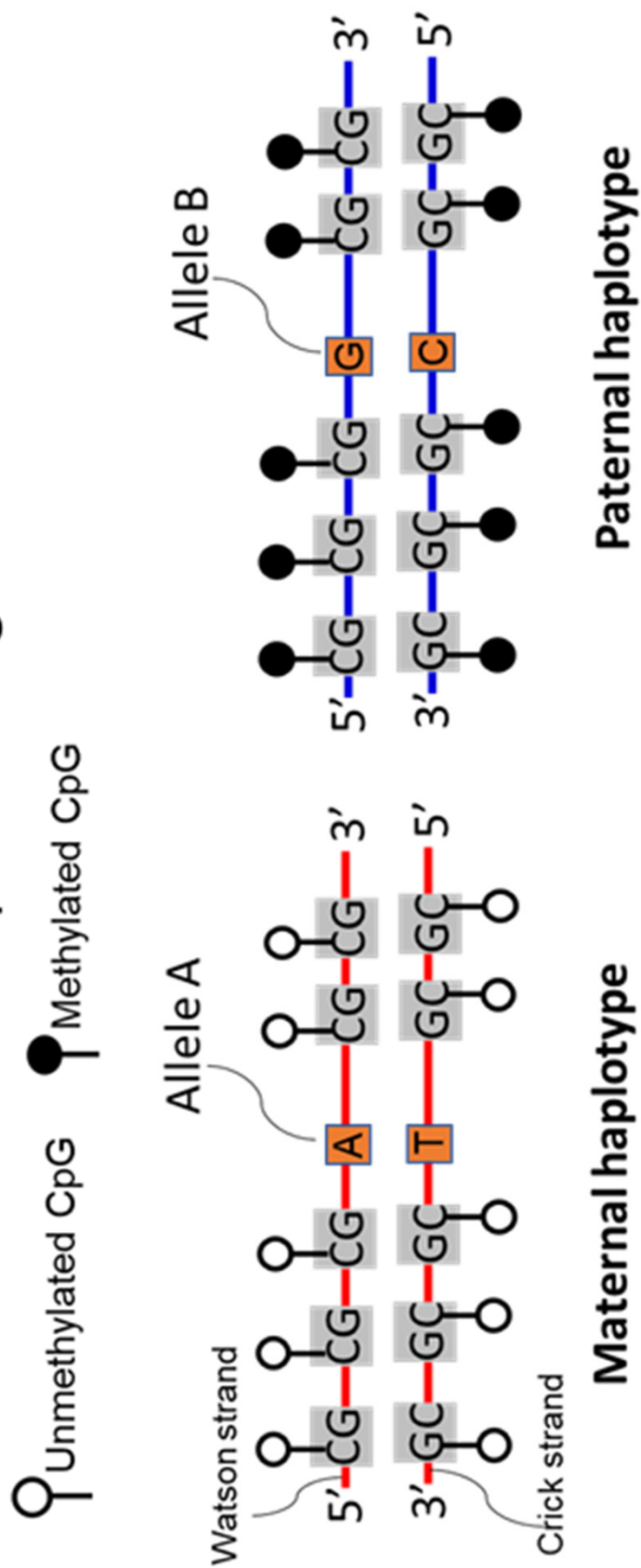


FIG. 49

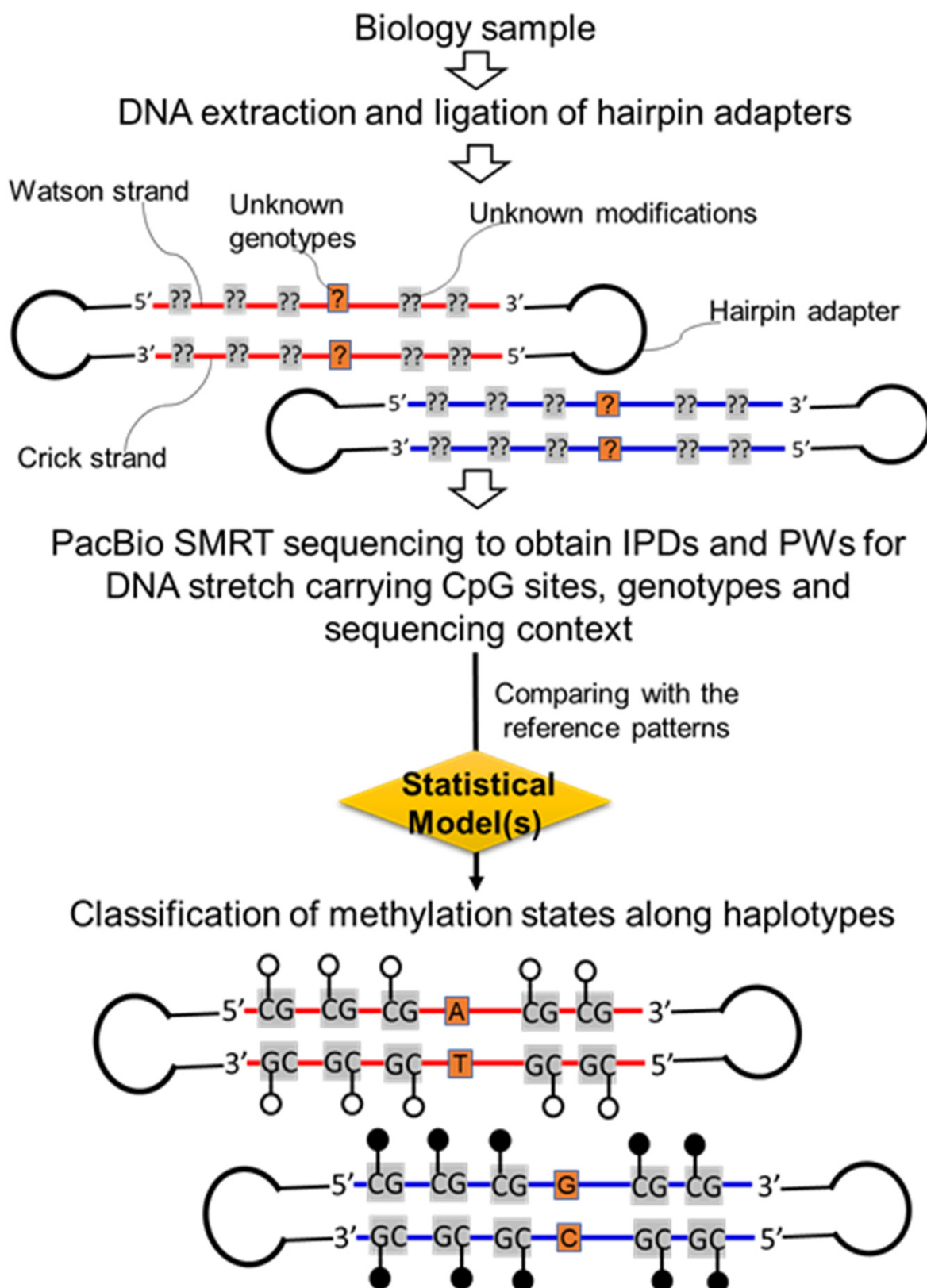


FIG. 50

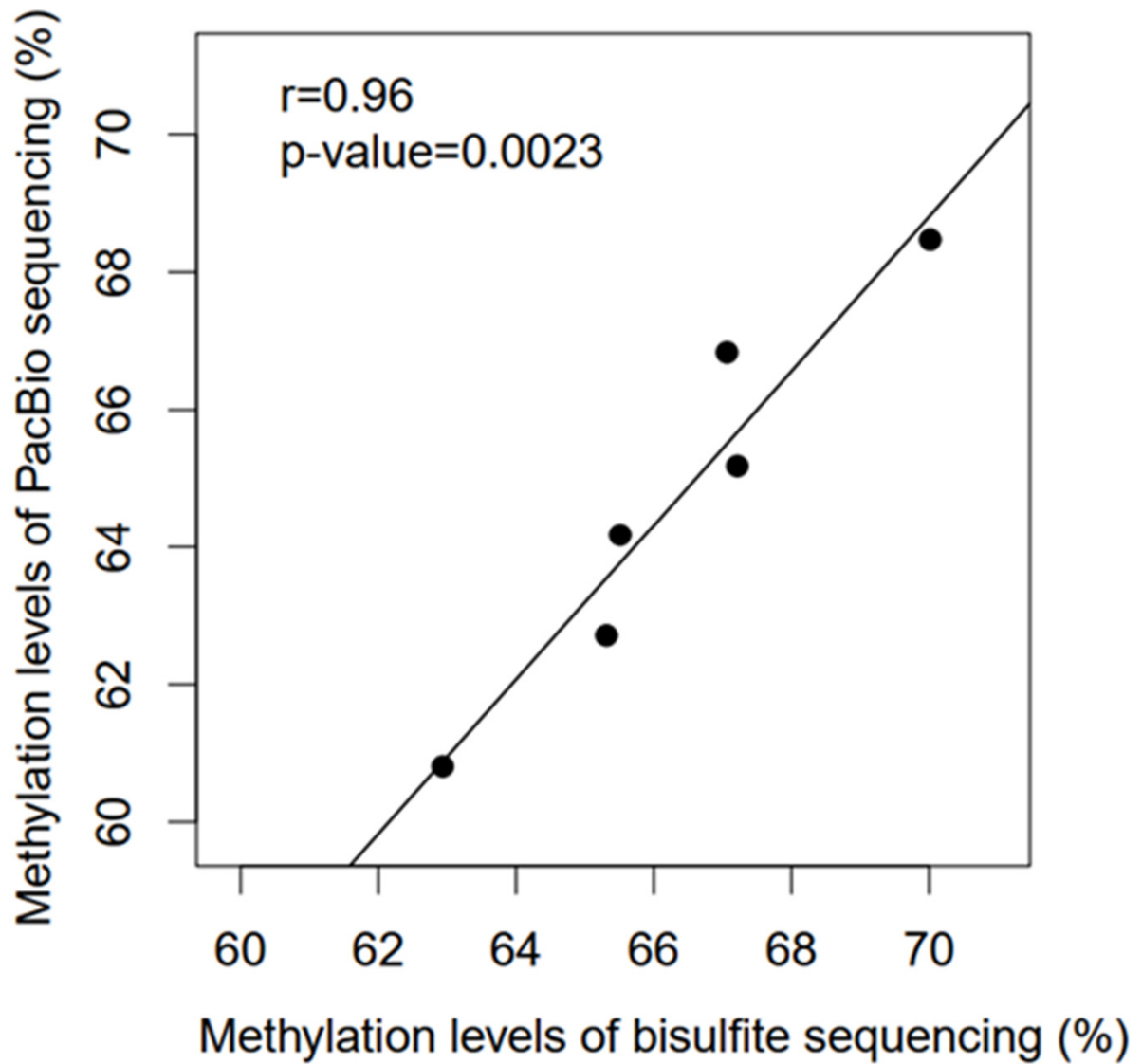


FIG. 51

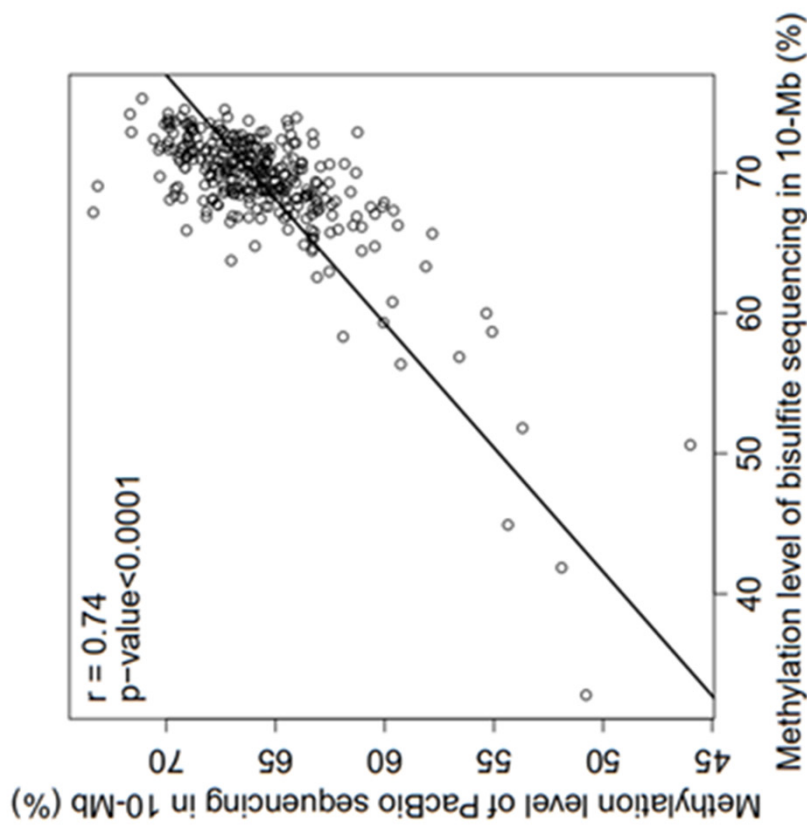


FIG. 52B

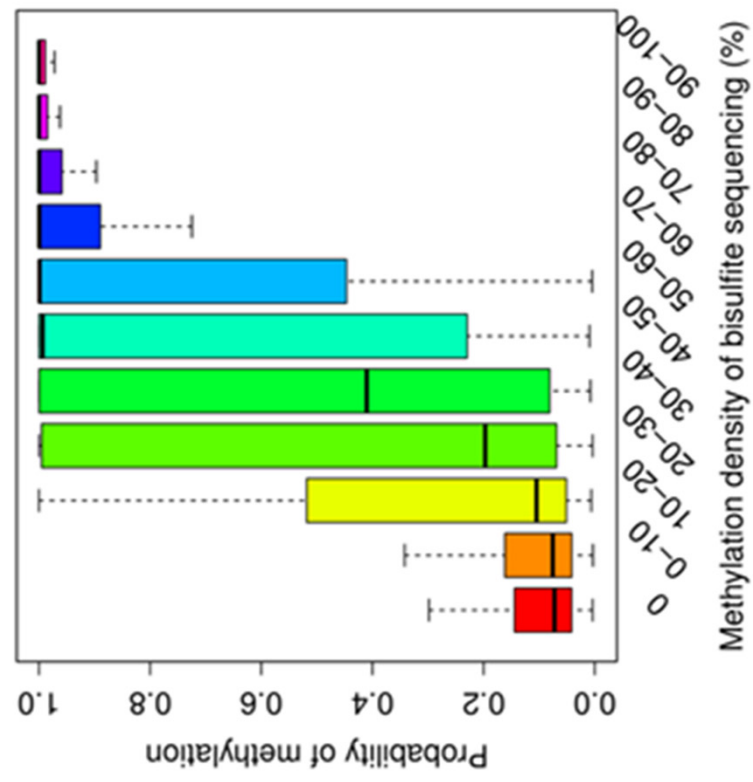


FIG. 52A

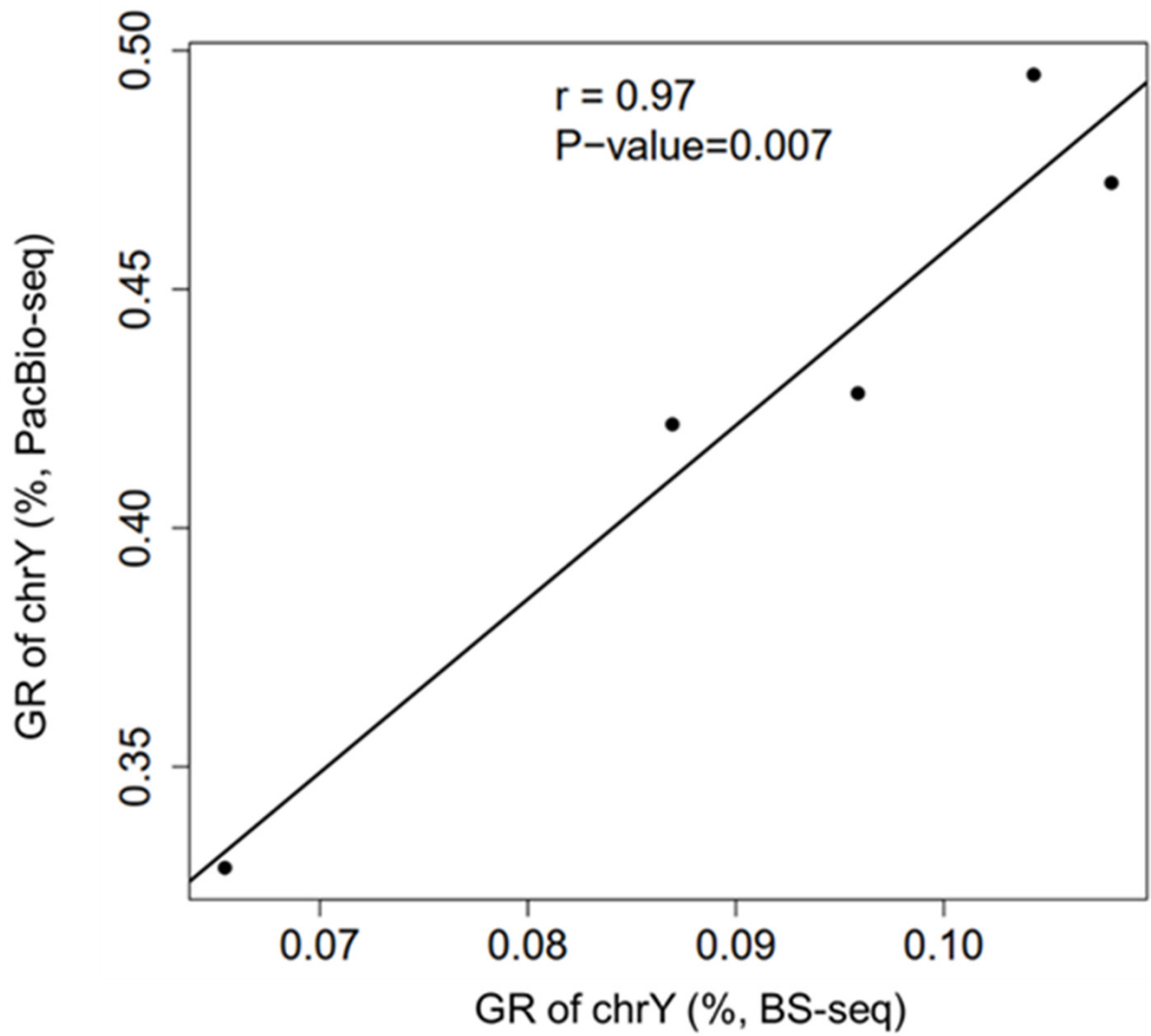


FIG. 53

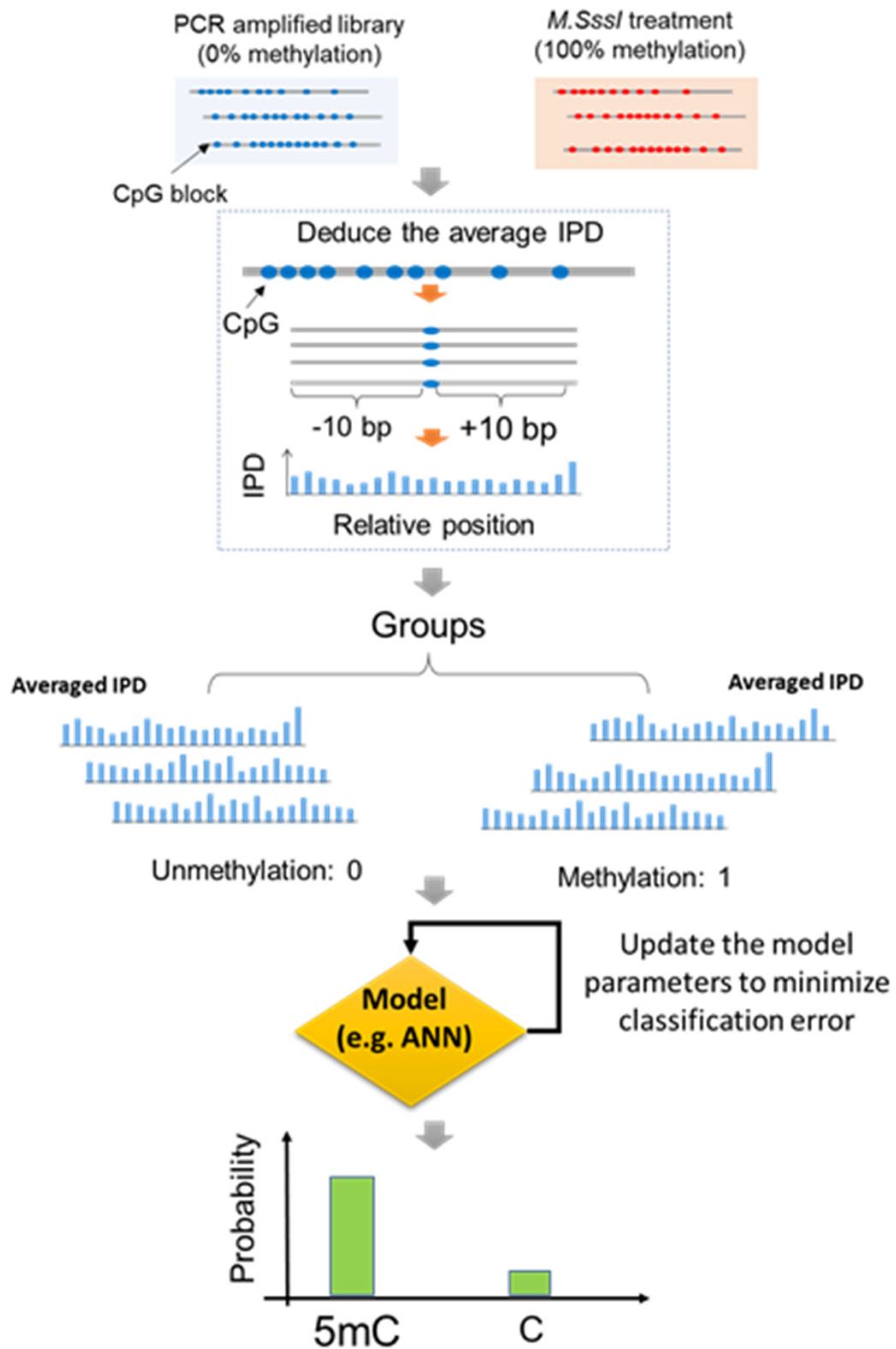


FIG. 54

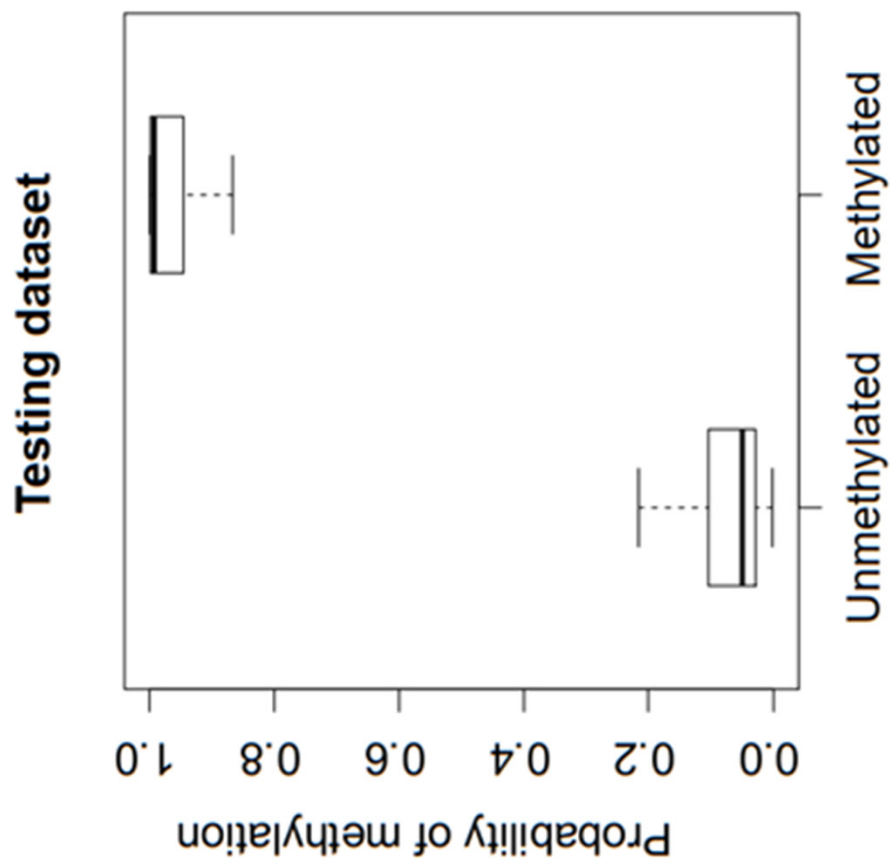


FIG. 55B

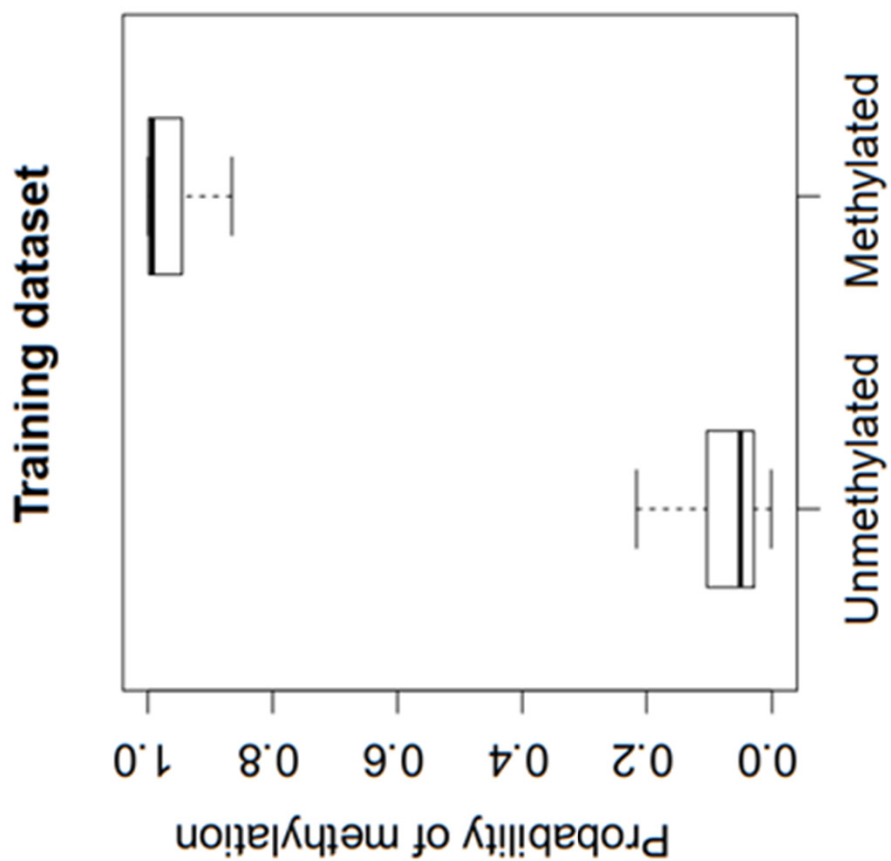


FIG. 55A

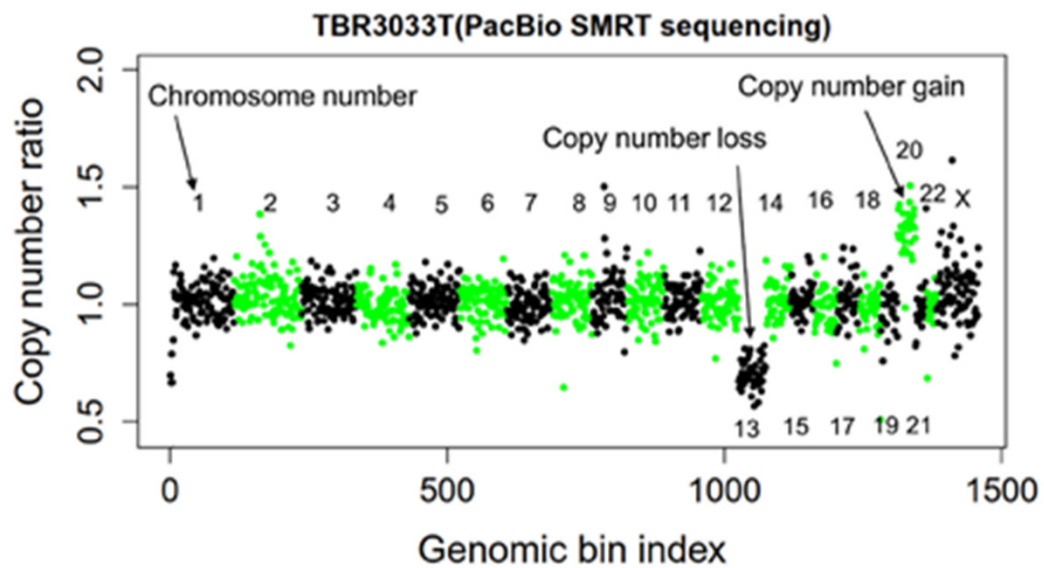


FIG. 56A

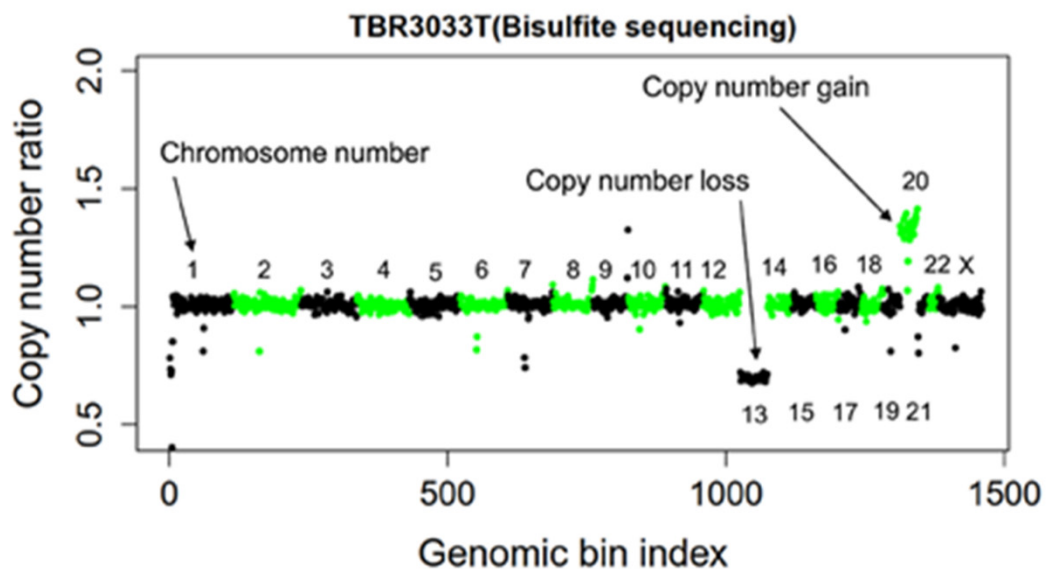


FIG. 56B

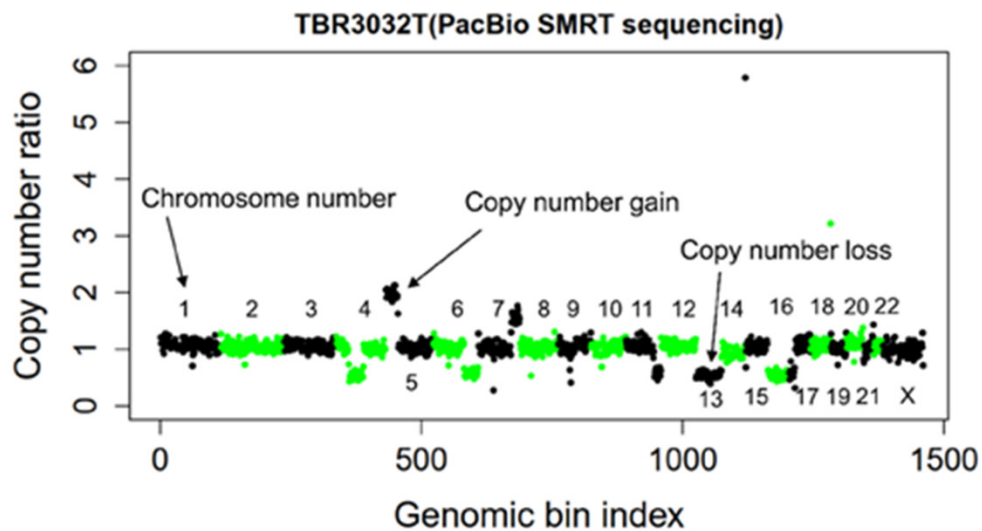


FIG. 57A

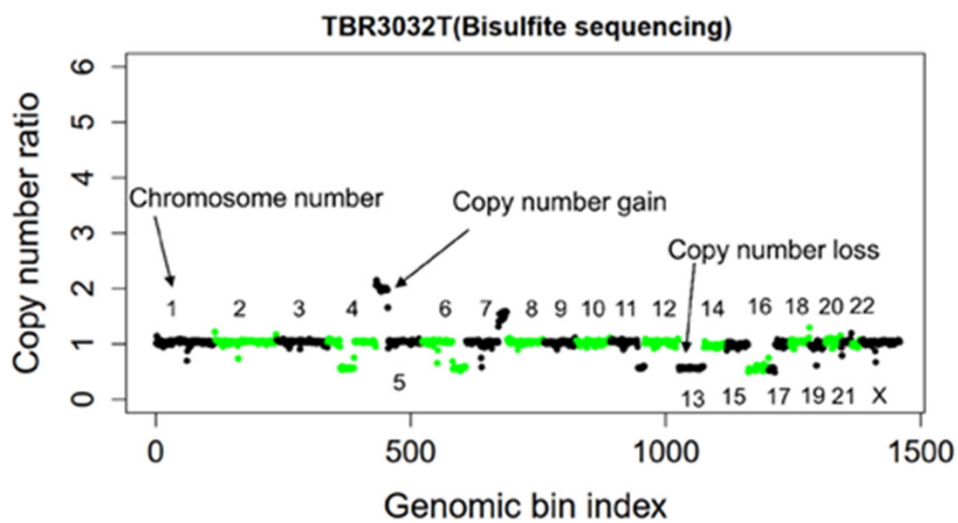


FIG. 57B

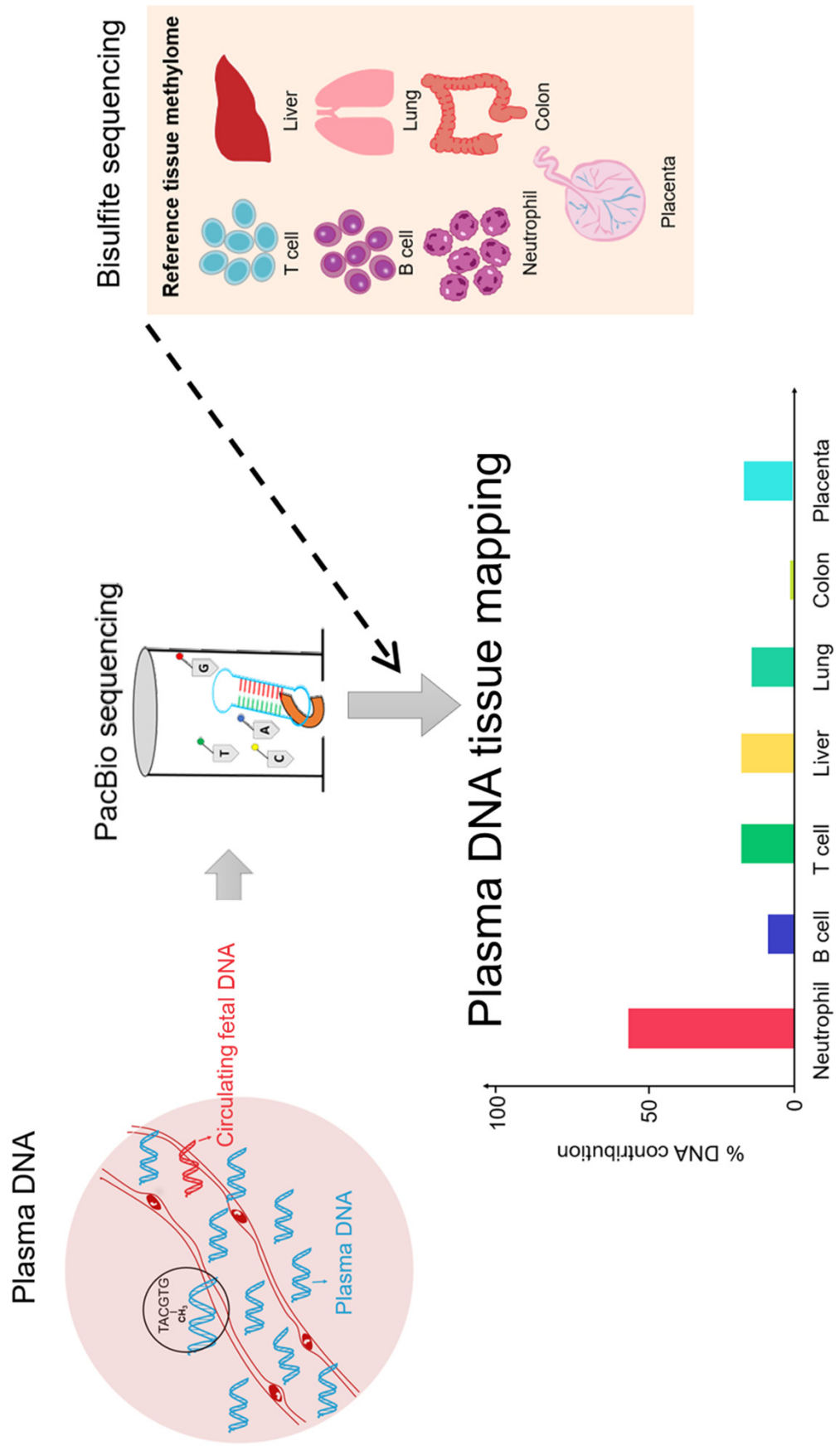


FIG. 58

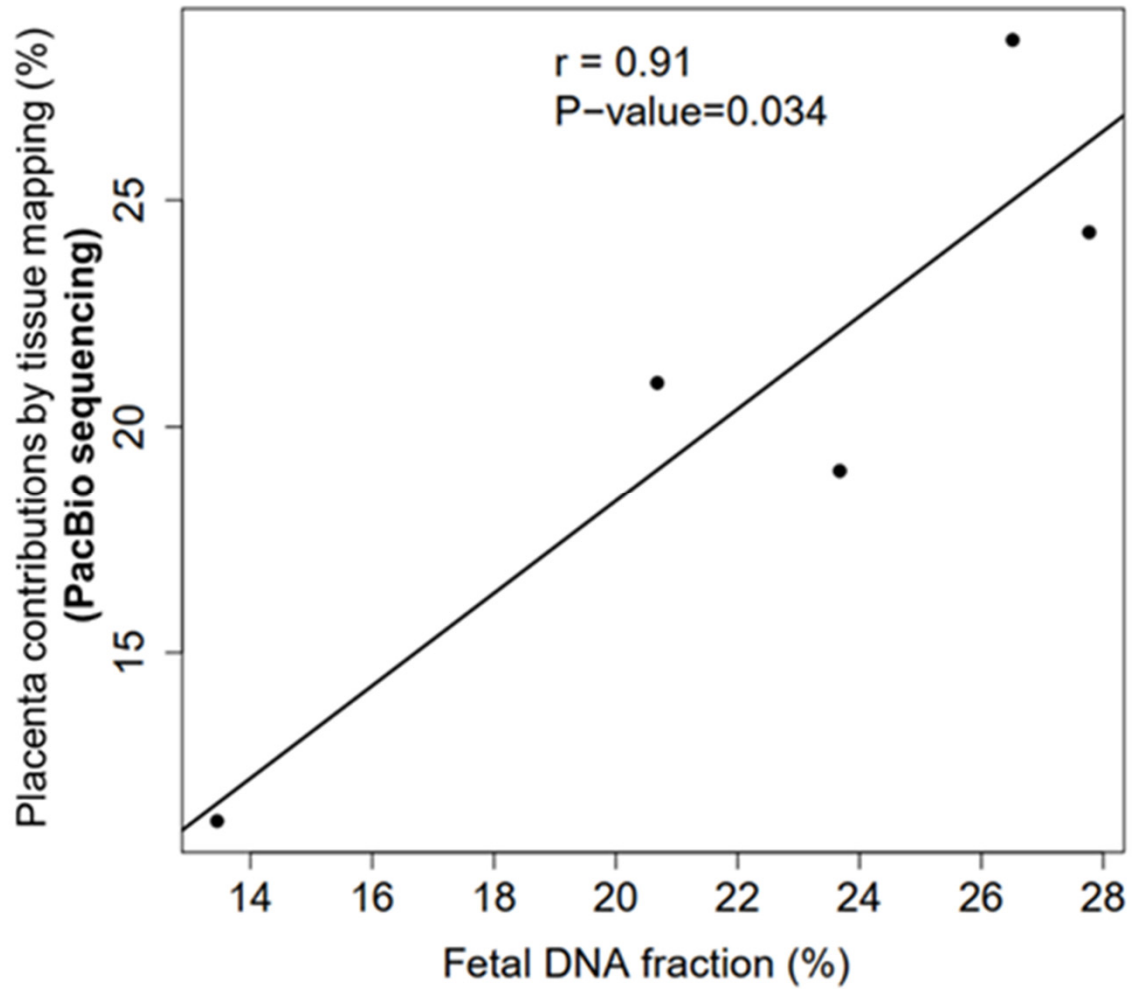


FIG. 59

Groups	Samples	Total subreads	Mapped subreads	Subread mappability (%)	Mean subread depth per SMRT well (x)	No. of SMRT wells	Mappable wells	Mappable well rate (%)
Maternal buffy coat	M13153w	39,006,460	30,673,525	78.6	13.4	3,157,310	2,295,002	72.7
Placenta	N13153	23,013,428	16,374,758	71.2	10.4	2,393,400	1,573,540	65.7
HCC tissues	TBR3032T	20,164,513	15,232,744	75.5	13.1	1,742,990	1,147,985	64.8
	TBR3033T	22,639,692	17,479,024	77.2	8.1	2,832,627	2,157,196	76.2
Adjacent normal tissues	TBR3033N	73,118,110	56,446,202	77.2	12.6	6,881,142	4,471,370	65.0
	TBR3032N	76,852,680	60,145,452	78.3	12.8	6,000,227	4,702,130	78.4
Buffy coat (healthy control subjects)	M1	44,777,423	28,325,587	63.3	7.7	7,316,000	3,659,996	50.0
	F2	49,840,758	32,994,645	66.2	8.6	7,215,112	3,823,329	53.0
	F1	40,012,804	24,717,289	61.8	6.5	7,301,768	3,800,392	52.0
	M2	152,530,411	88,596,520	58.1	7.7	21,794,606	11,563,500	53.1
HCC cell line	HepG2	47,308,982	34,581,721	73.1	7.3	6,220,000	4,750,581	76.4

FIG. 60

