

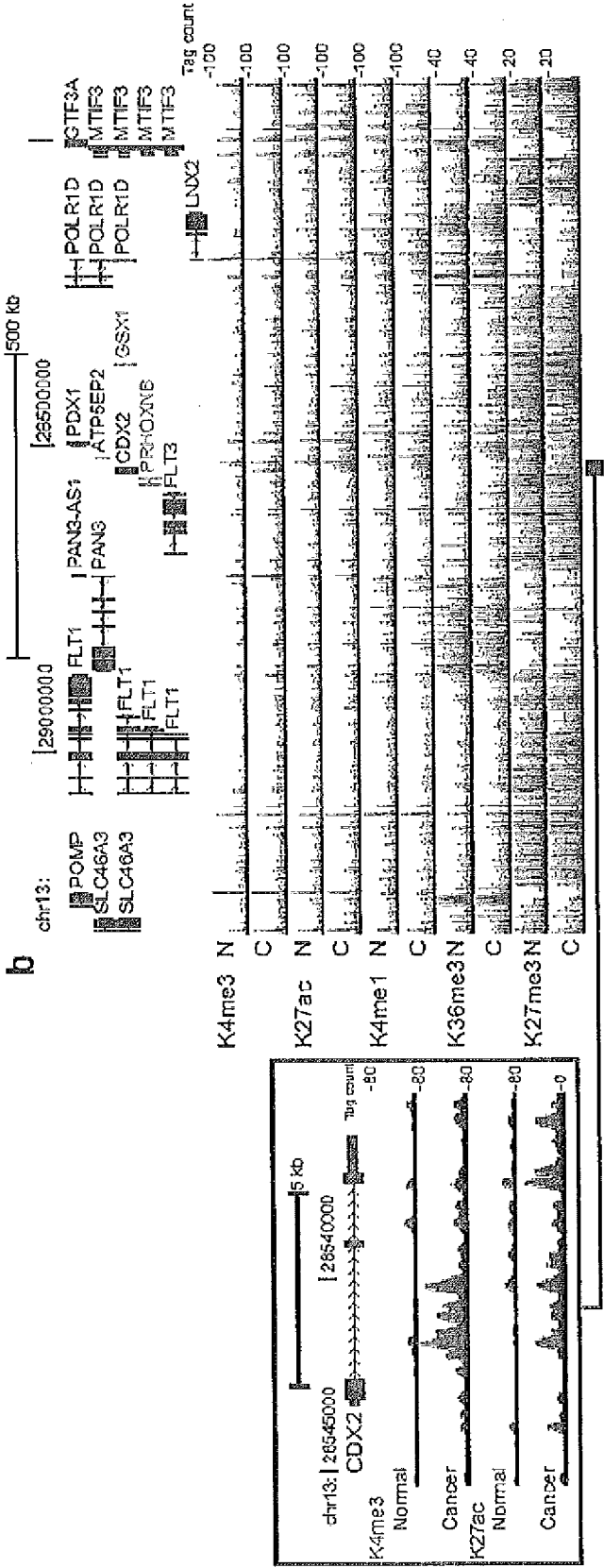
1/ 60

FIG. 1

a

Histone H3 modification	Genomic region
K4me3	Promoters
K4me1	Enhancers and promoters
K27ac	Active regulatory elements
K36me3	Transcribed regions
K27me3	Repressive

FIG. 1



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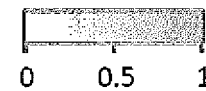
FIG. 1

d

2000721		2nd set overlap				
Normal		K4me3	K4me1	K27ac	K36me3	K27me3
1st set	K4me3	1.00	0.38	0.60	0.32	0.15
	K4me1	0.36	1.00	0.35	0.31	0.10
	K27ac	0.79	0.47	1.00	0.37	0.08
	K36me3	0.34	0.30	0.30	1.00	0.07
	K27me3	0.07	0.05	0.03	0.03	1.00

2000721		2nd set overlap				
Cancer		K4me3	K4me1	K27ac	K36me3	K27me3
1st set	K4me3	1.00	0.74	0.85	0.28	0.28
	K4me1	0.33	1.00	0.47	0.26	0.21
	K27ac	0.63	0.77	1.00	0.31	0.25
	K36me3	0.30	0.53	0.40	1.00	0.18
	K27me3	0.09	0.15	0.11	0.06	1.00

Fraction of 1st set region overlapping with 2nd set region



e

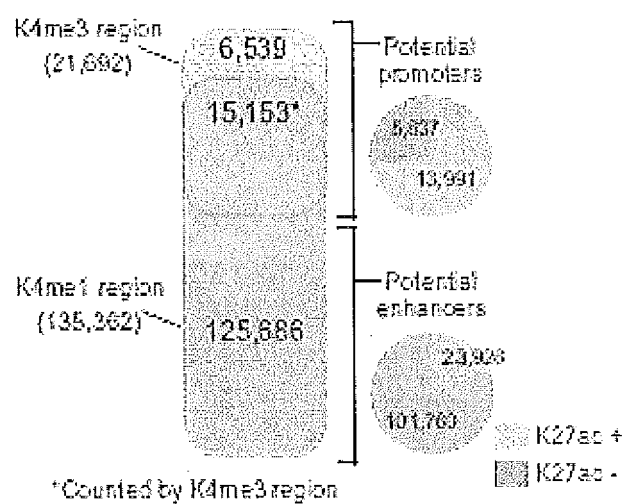
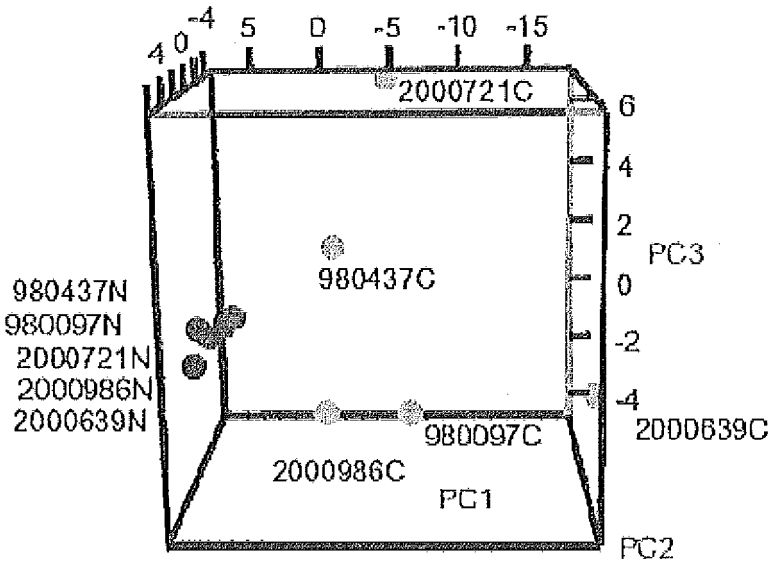


FIG. 1

f

Promoter region K4me3



g

Enhancer region K4me1

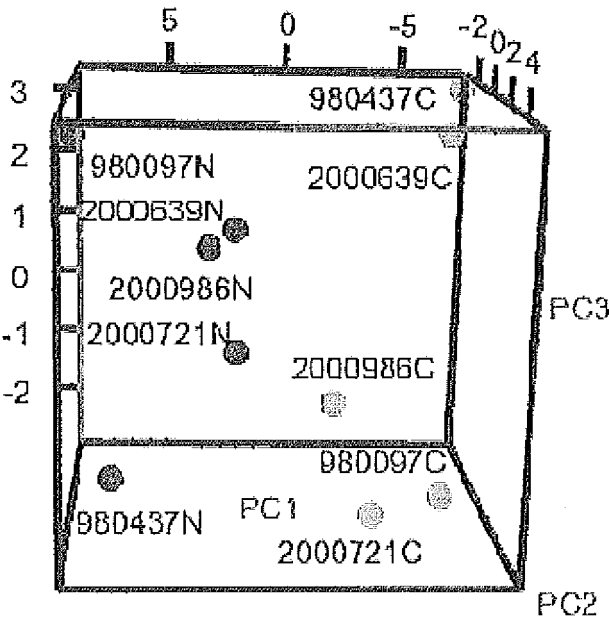


Fig. 1

h

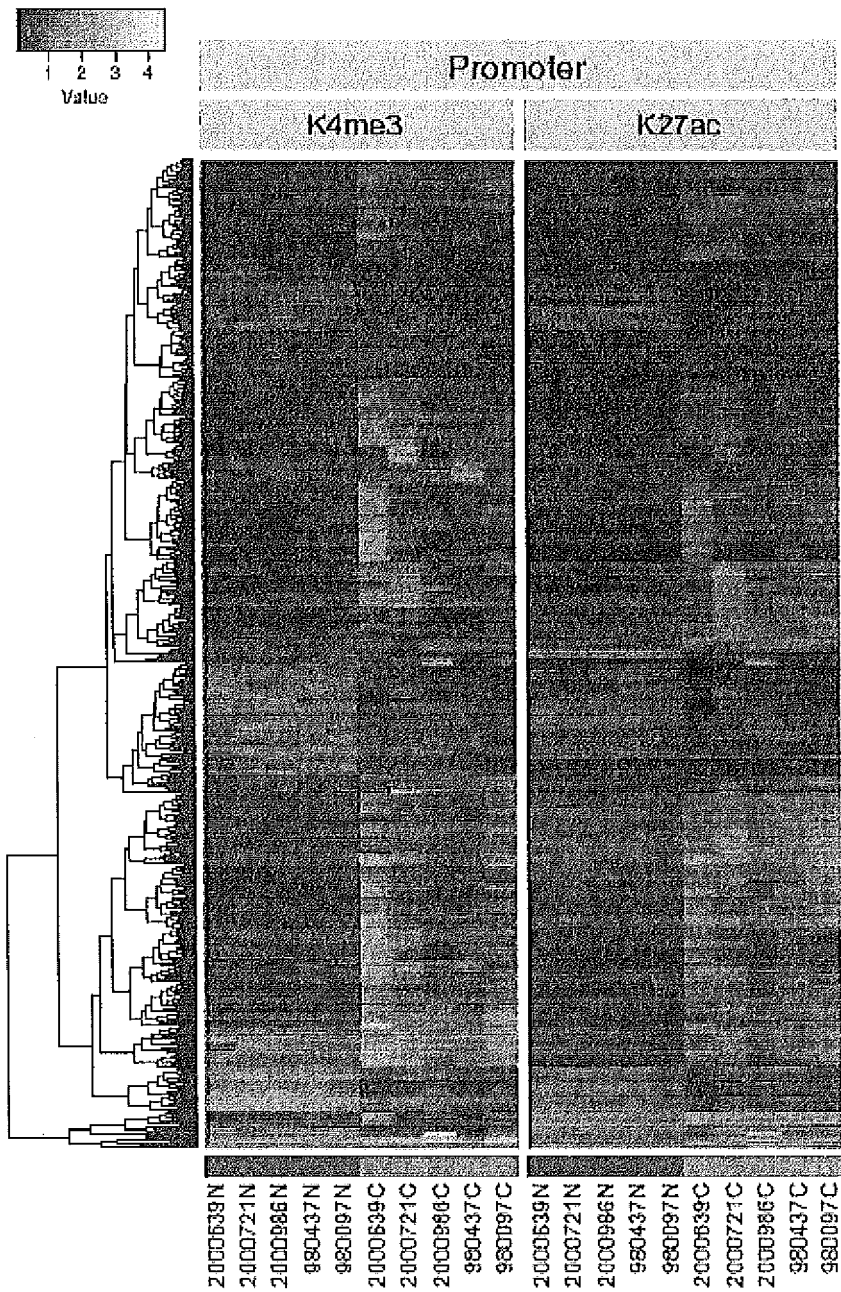
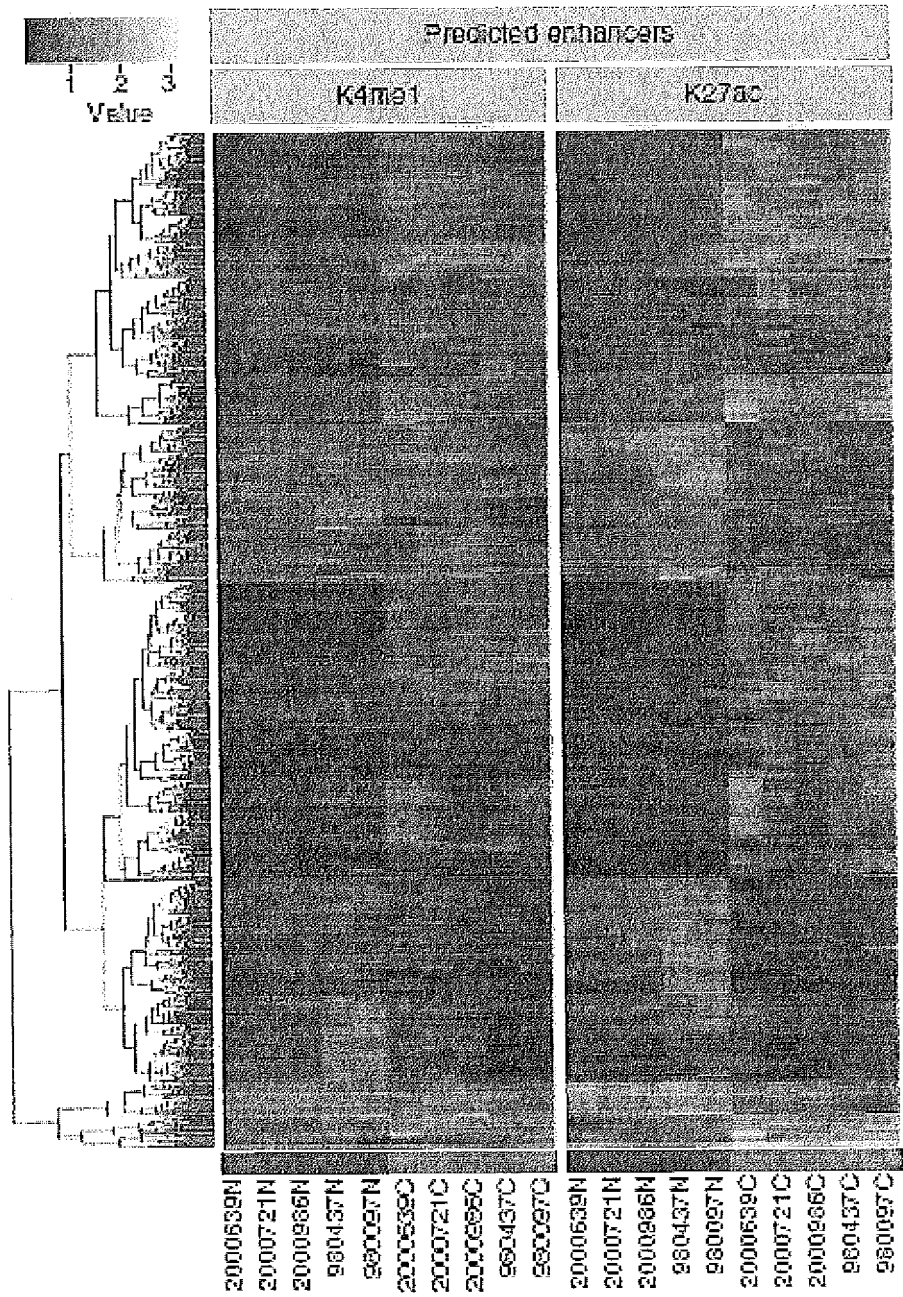


Fig. 1

i



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FIG. 2

a

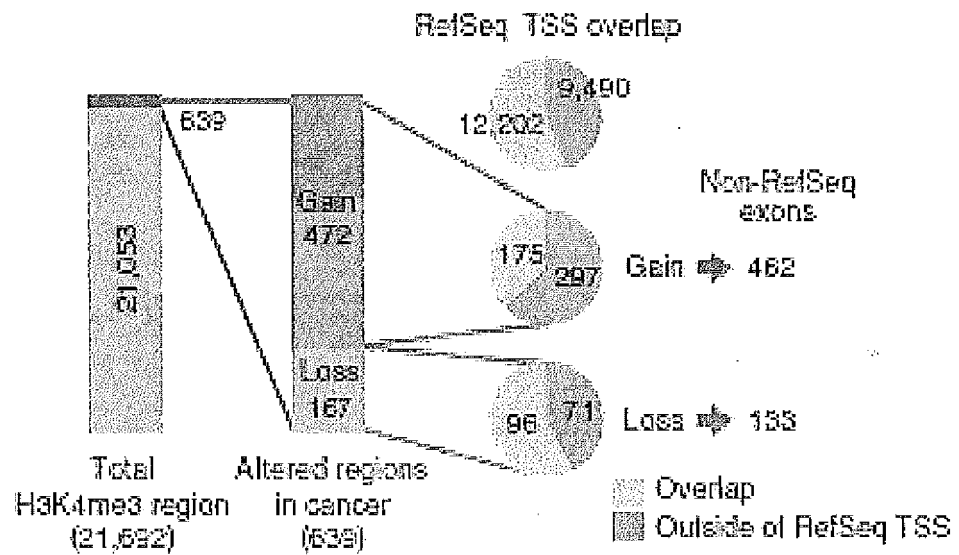
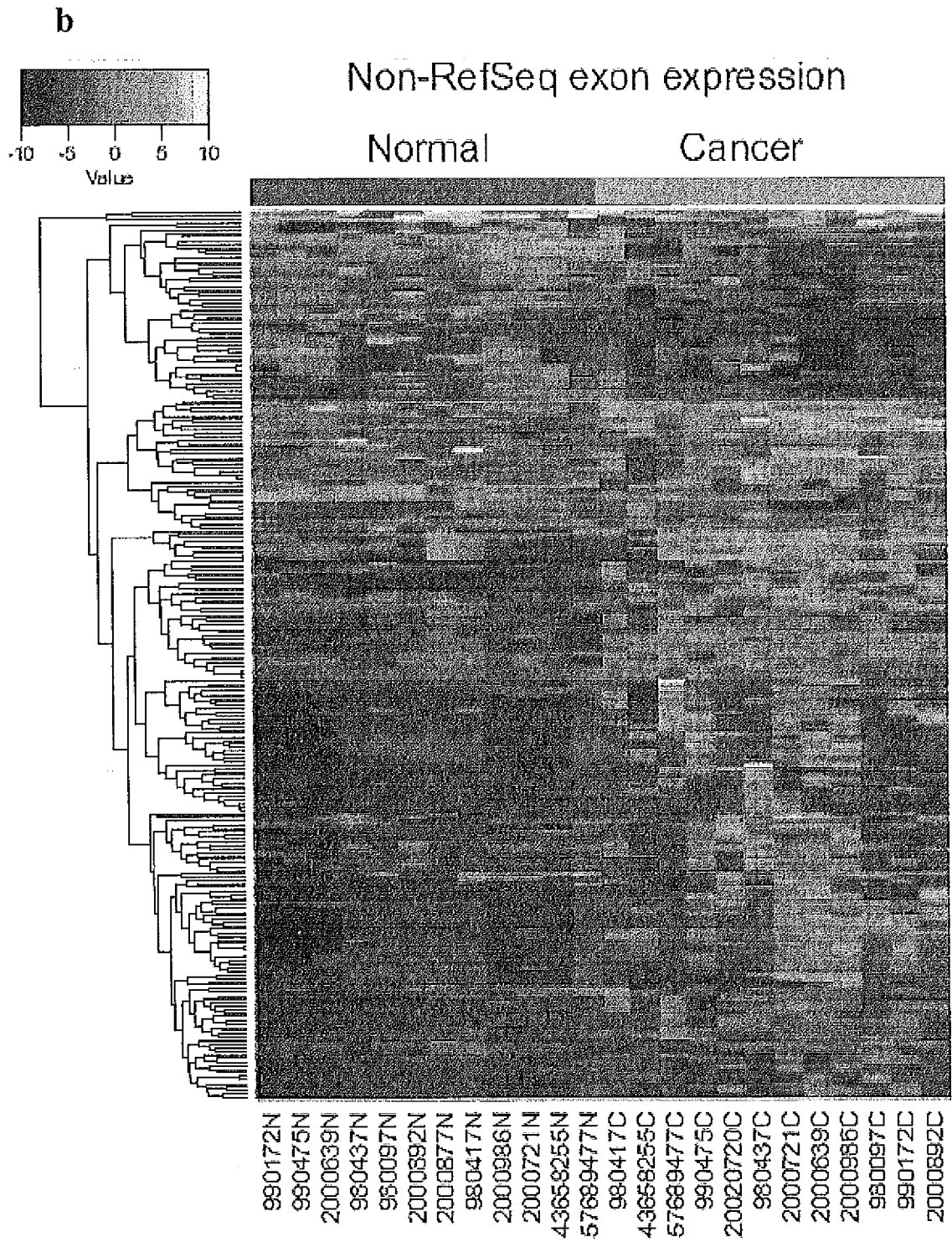


FIG. 2



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Fig. 2

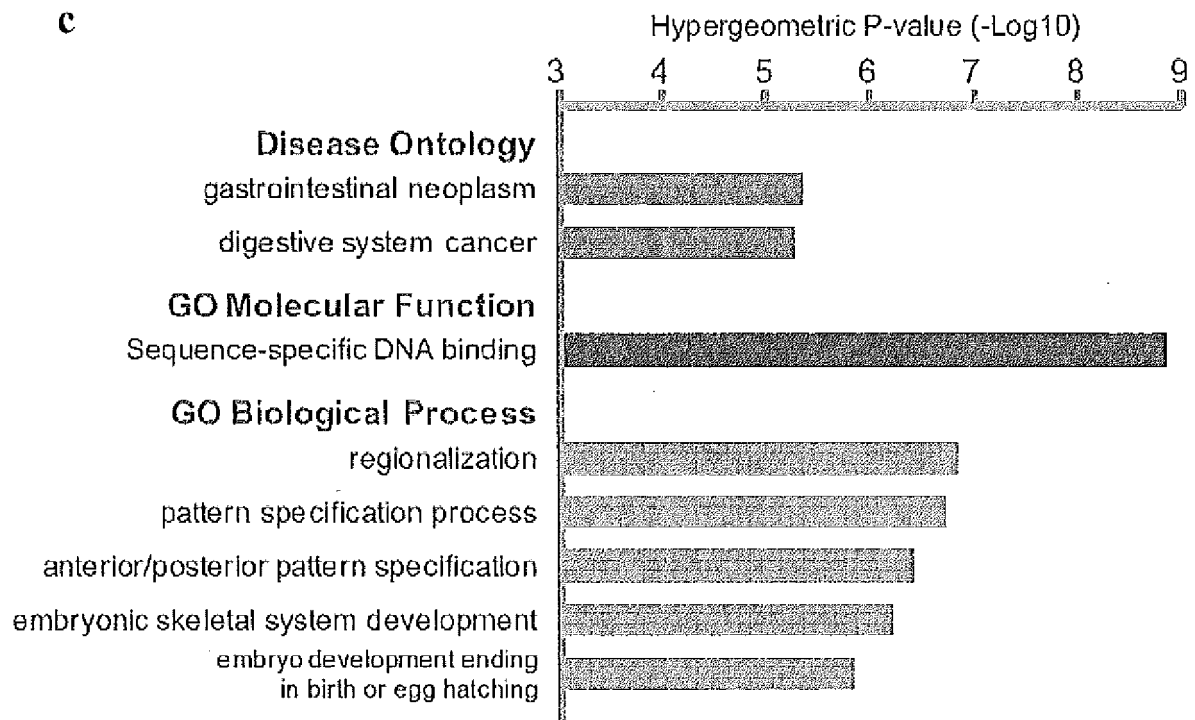


Fig. 2

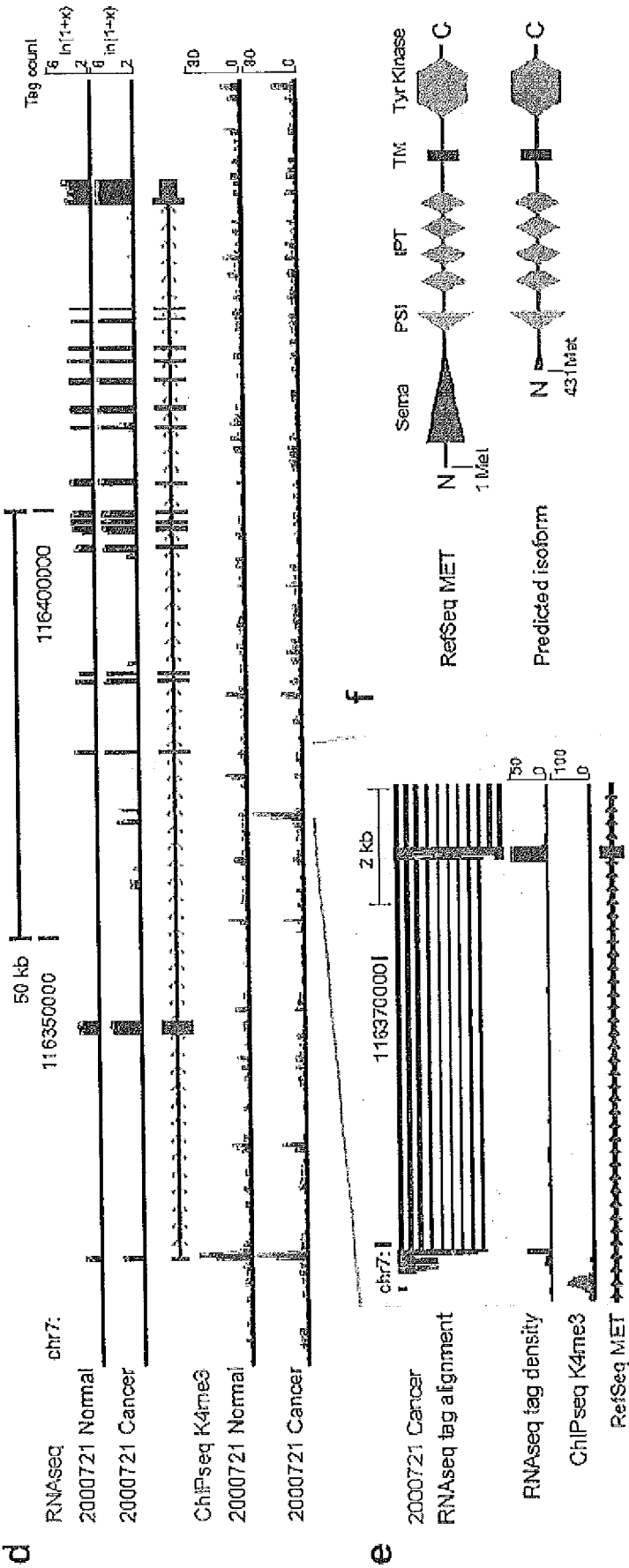
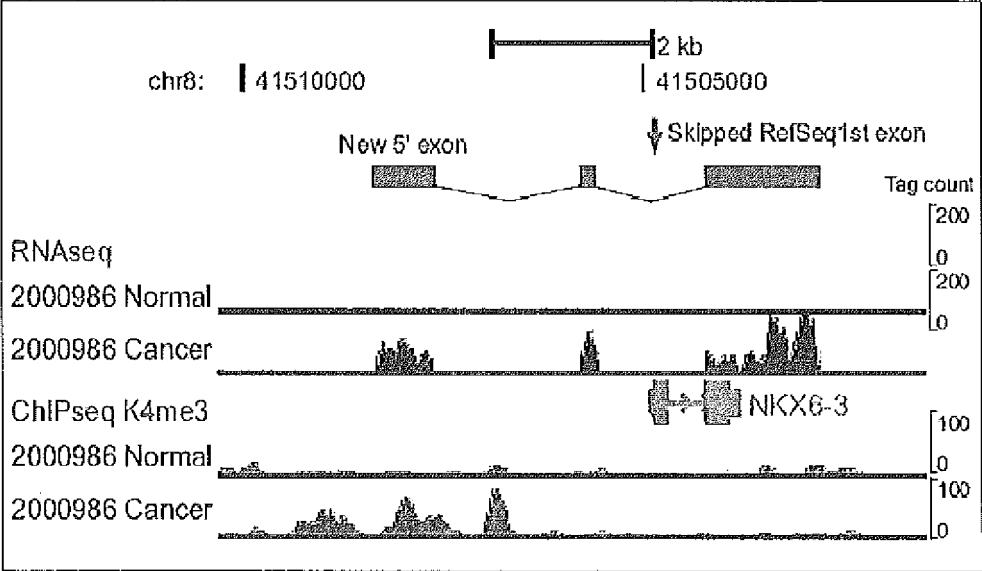
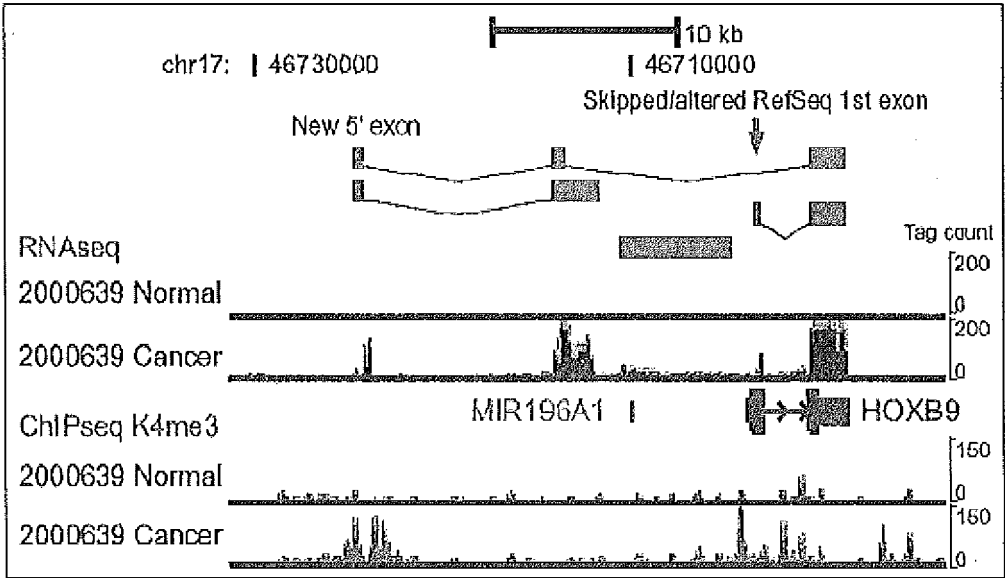


Fig. 2

g



h



12/ 60

Fig. 2

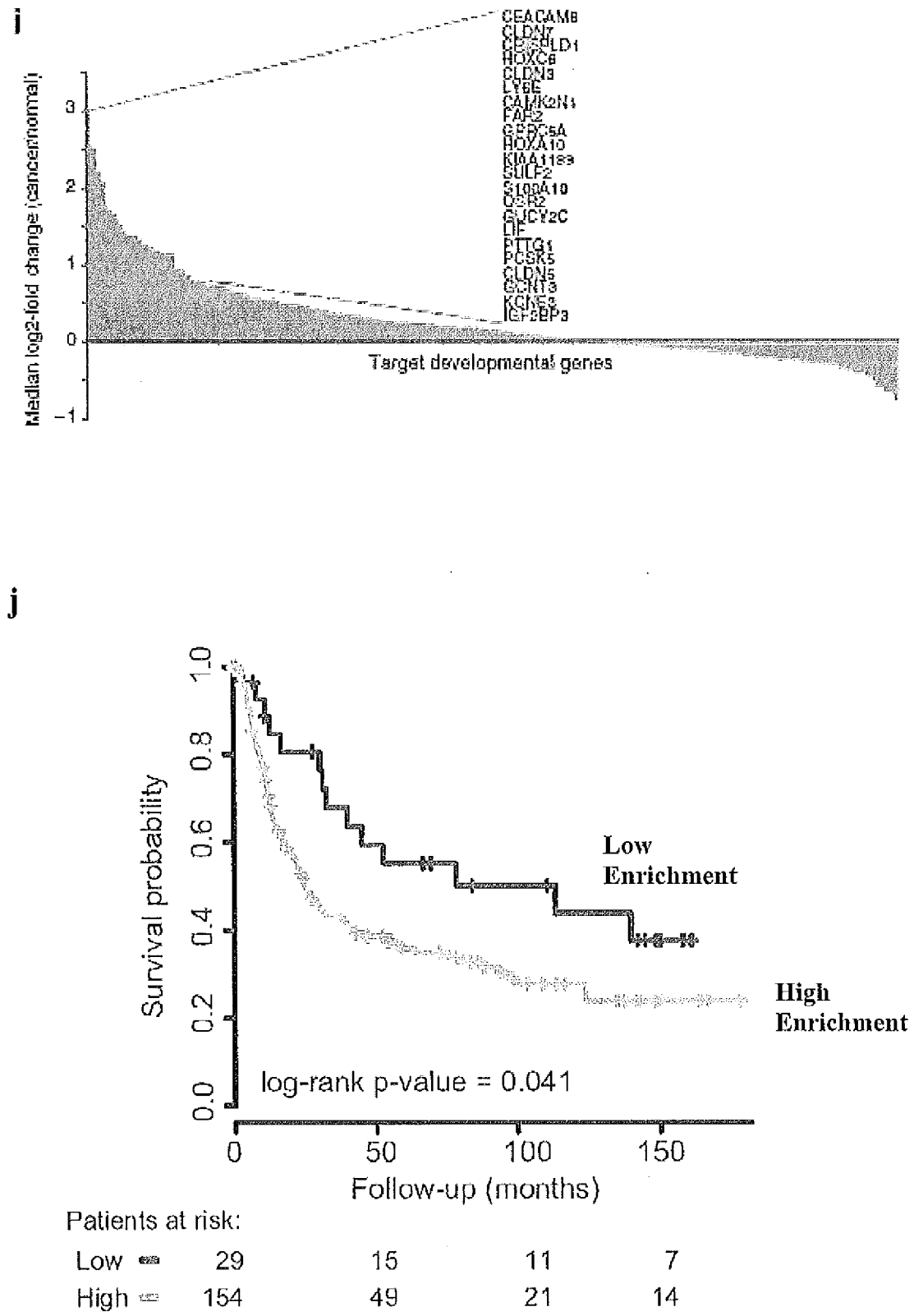


Fig. 3

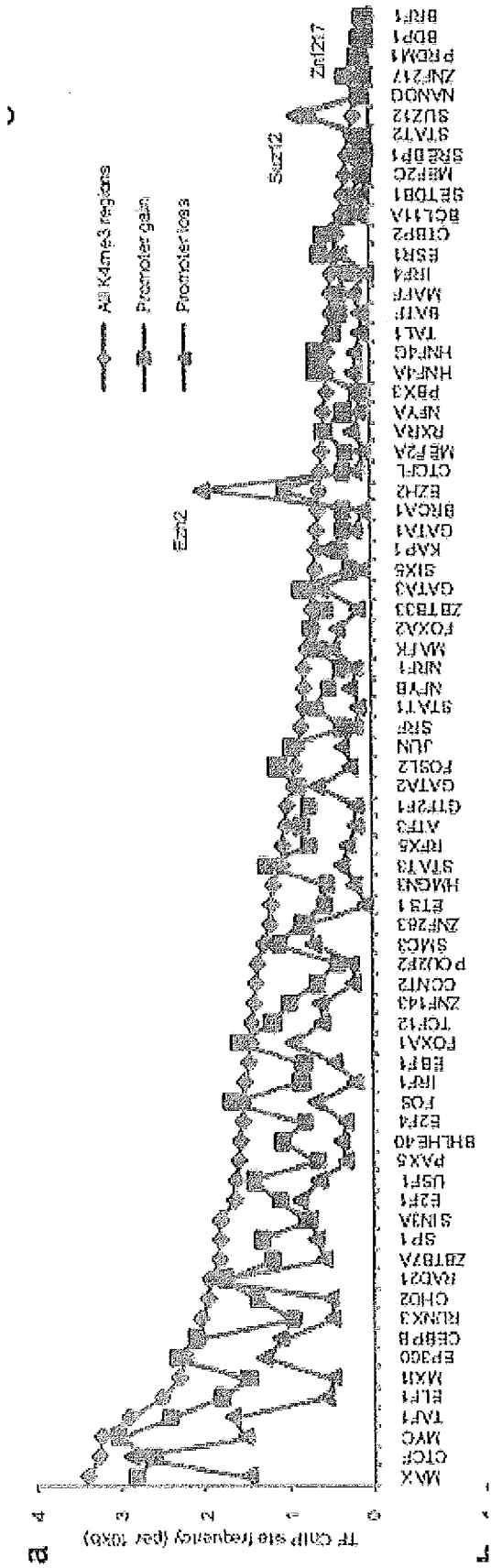


Fig. 3

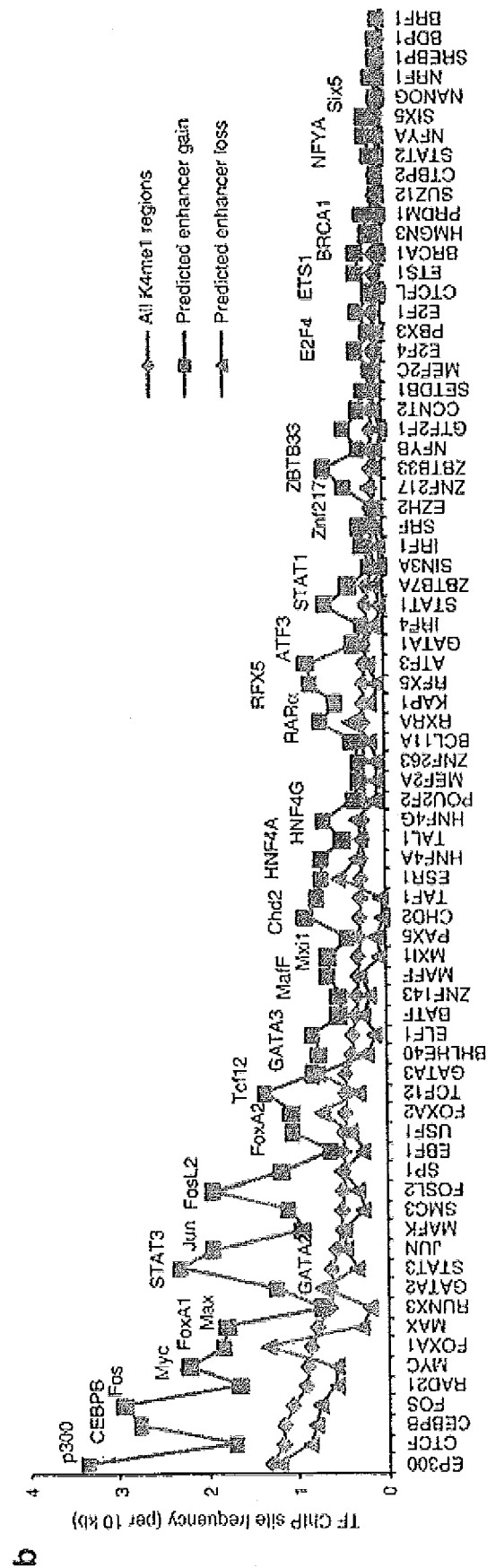
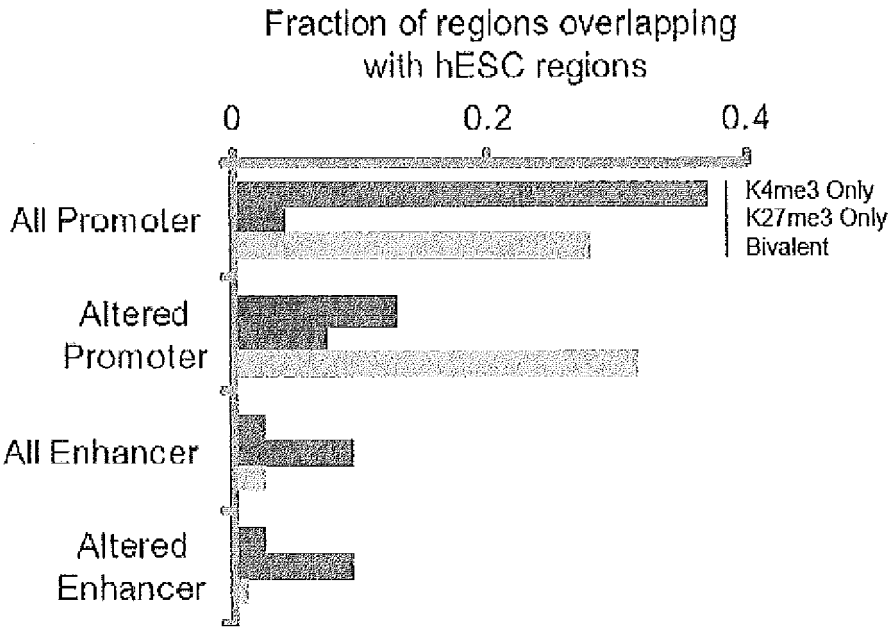
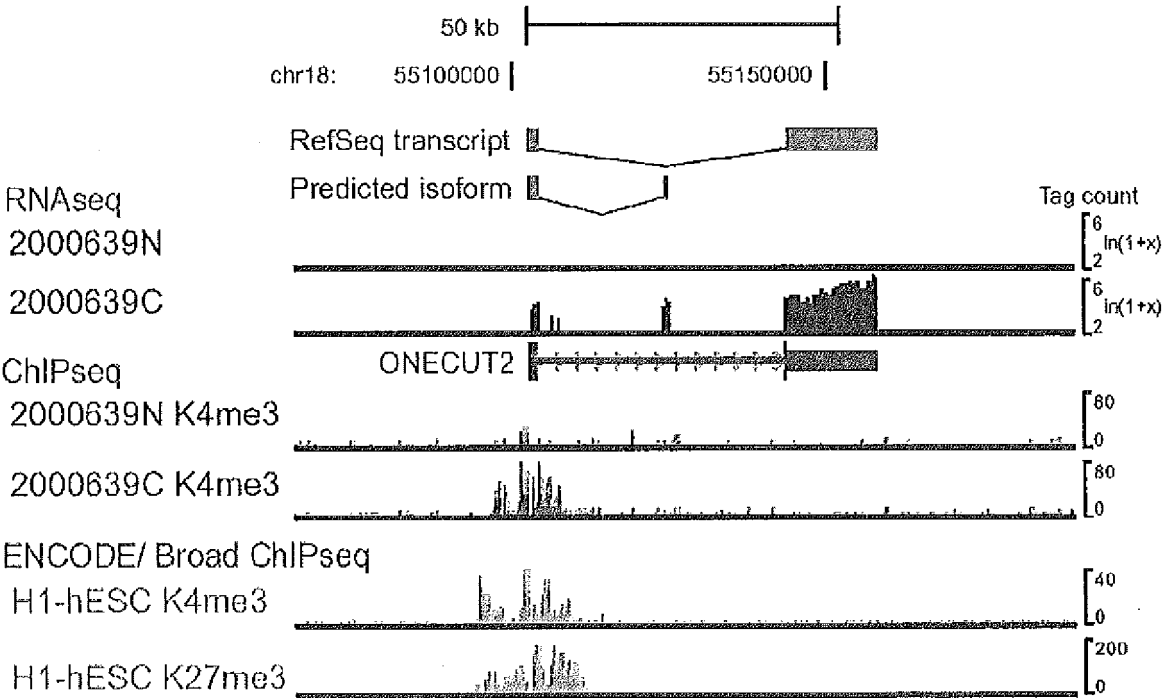


Fig. 3

c



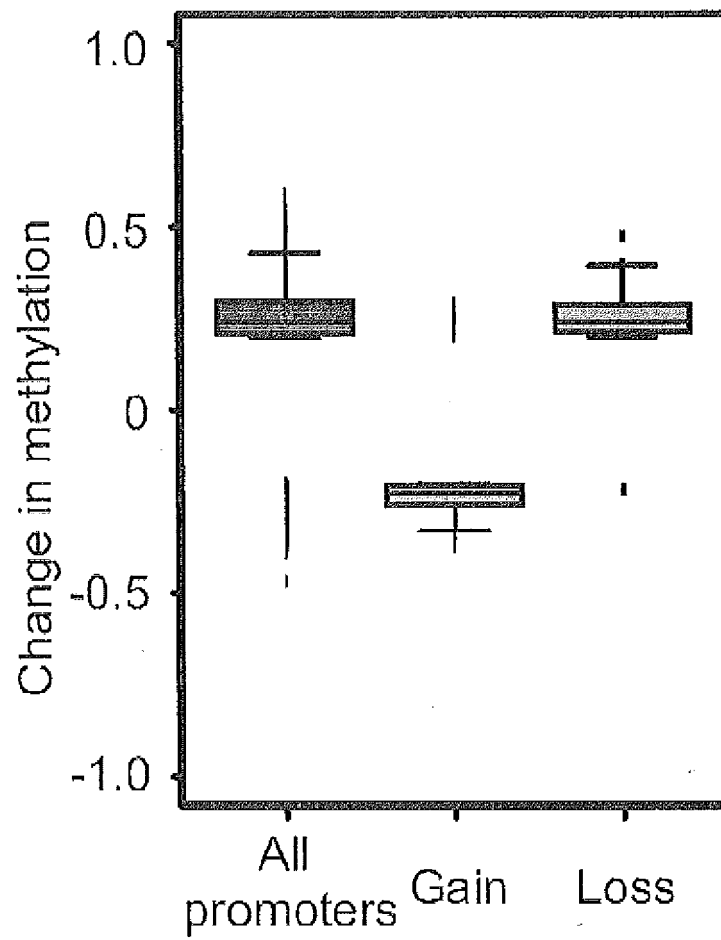
d



16/ 60

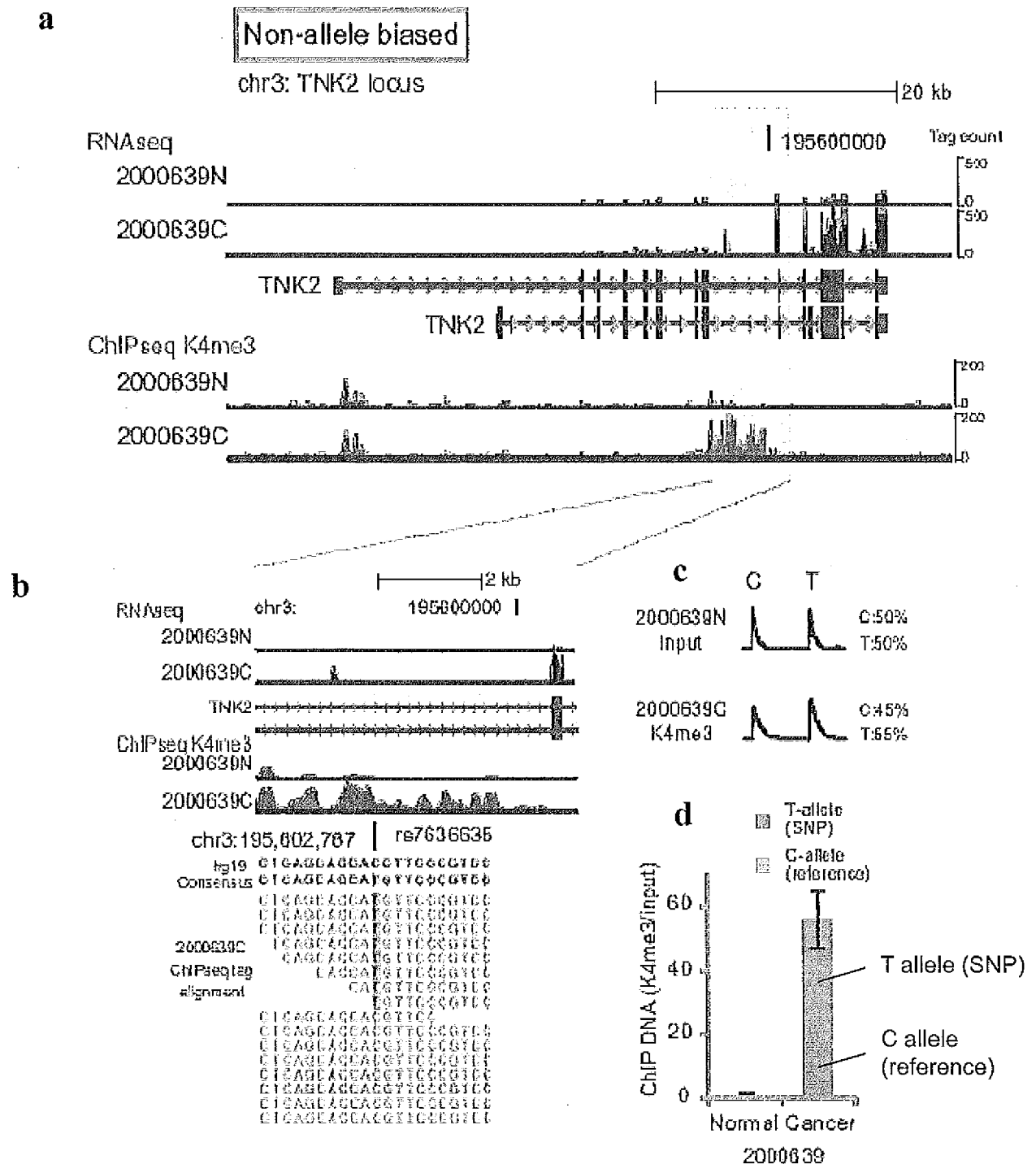
Fig. 3

e



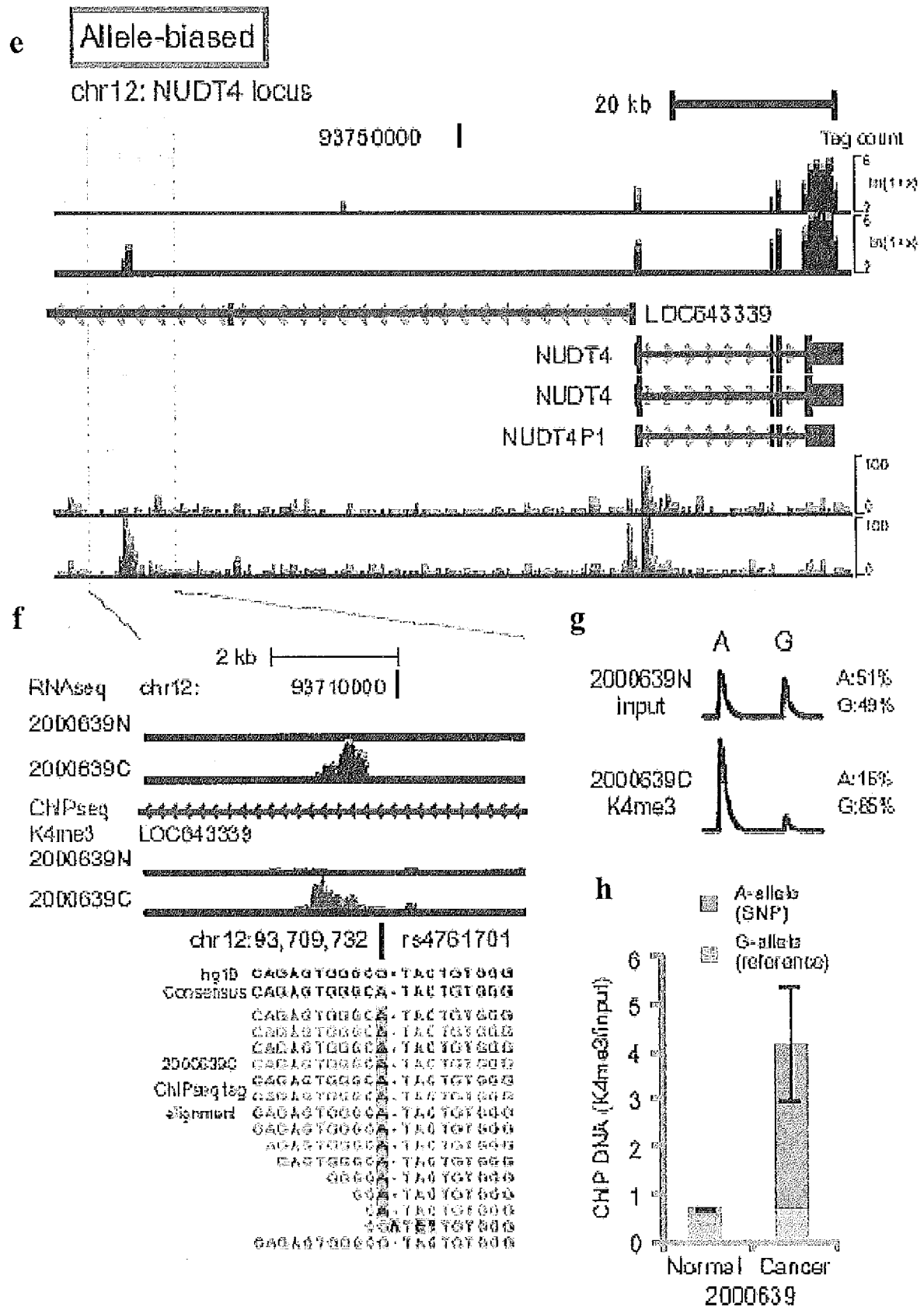
17/ 60

Fig. 4



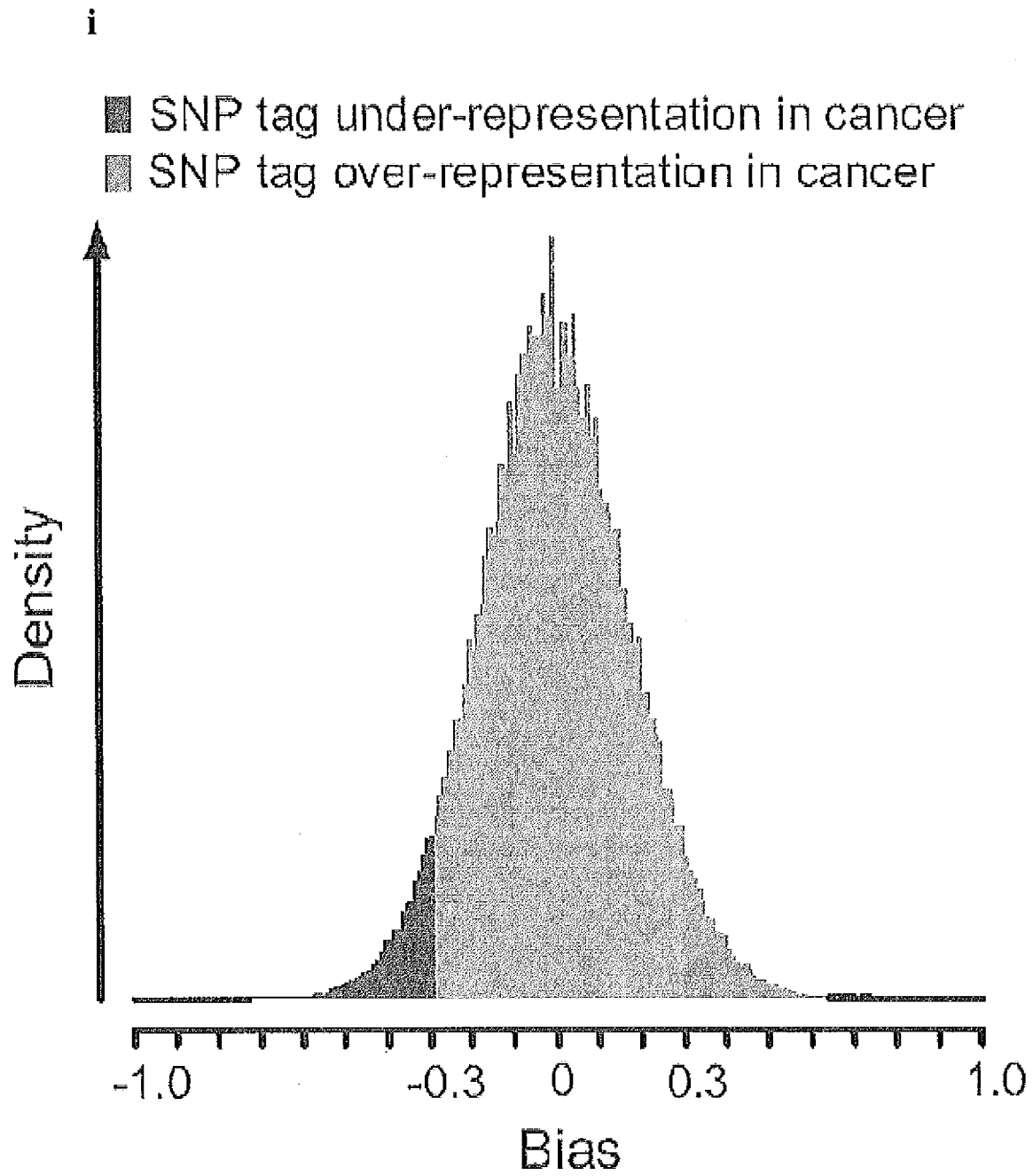
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Fig. 4



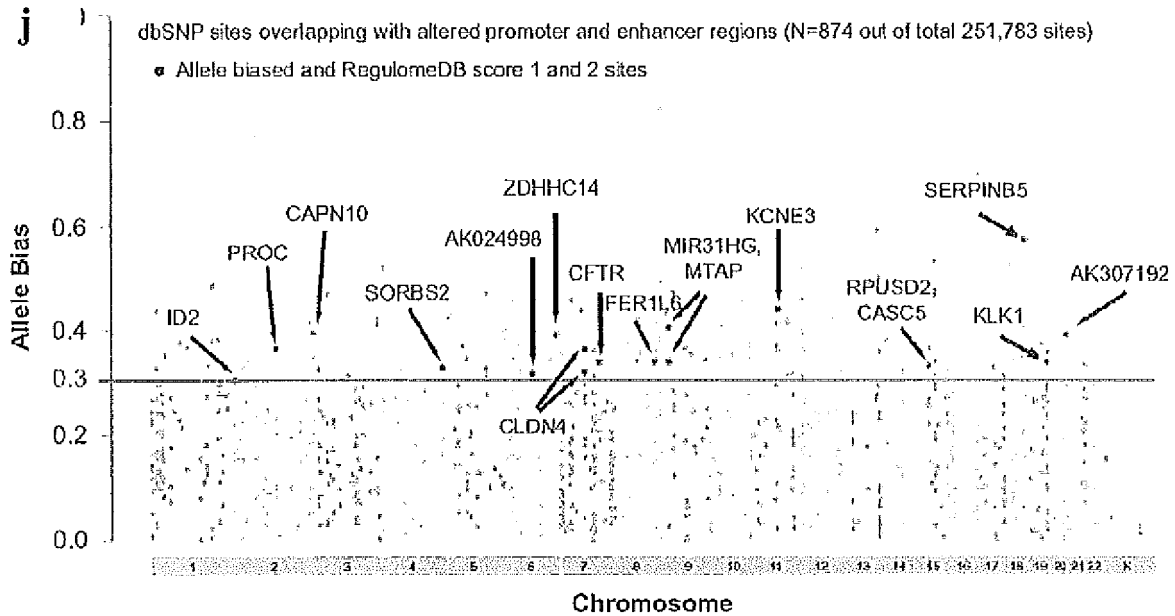
19/ 60

Fig. 4



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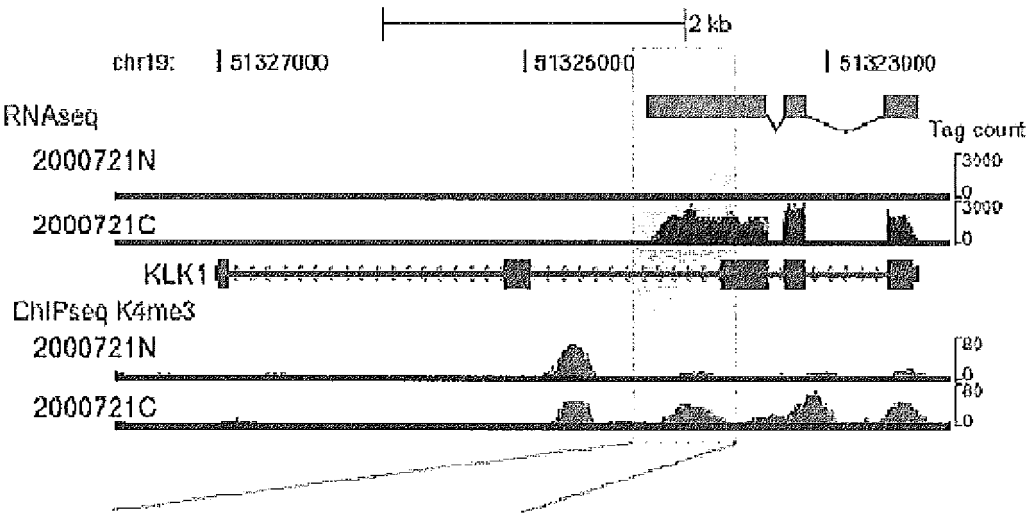
Fig. 4

**k**

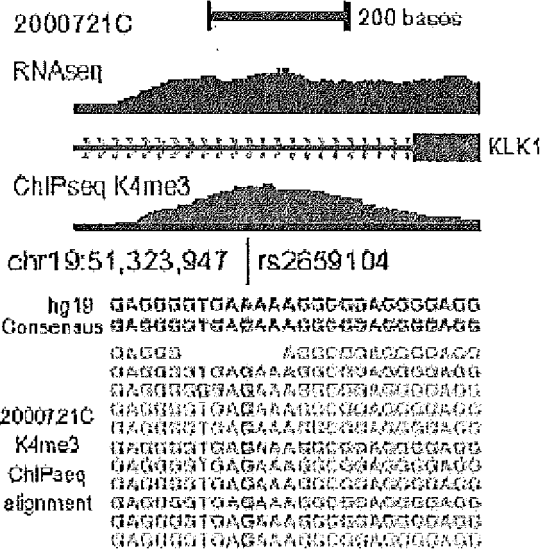
SNP	Bias	Nearest gene(s)	Score	Bound Protein	eQTL
rs10184180	+	ID2	2b	PAX5	
rs7580658	-	PROC	2b	TFAP2A, FOS, TRIM28, TFAP2C	-
rs7556712	-	CAPN10	2b	CTCF, HNF4A	-
rs1566347	+	SORBS2	2a	FOXA1, FOXA2, HEY1, HNF4G, EP300, TBP, HNF4A	-
rs577388	+	AK024998	1f	MAFF	C6orf160
rs4709360	+	ZDHHC14	1a	ELF1, HNF4A, HNF4G, TAF1, CEBPB, CDX2, HNF4A, FOXA1, EP300, RAD21, RXRA, SP1, JUND, MAFF, MAFK, RFX5, TCF4	ZDHHC14
rs7455225	-	CLDN4	1f	CTCF, RAD21, GATA2	WBSCR27
rs4458741	-	CLDN4	2b	CDX2, HNF4A, JUND, SP1, FOXA1, EP300, TBP	-
rs4148682	+	CFTR	2b	SUZ12	-
rs16899037	+	FER1L6	2b	EGR1	-
rs16938533	+	MIR31HG, MTAP	2b	STAT3, FOS, TBP, TCF4, EP300, GATA2, NR3C1, JUN, JUND	-
rs4307419	+	MIR31HG, MTAP	2b	STAT3, FOS, TBP, TCF4, EP300, GATA2, NR3C1, POLR2A, JUN, JUND	-
rs114596416	+	KCNE3	2b	ZNF263, CDX2	-
rs8036737	+	RPUSD2, CASC5	2c	SP1, NFYA, NFYB, FOS	-
rs3744942	+	SERPINB5	2b	POLR2A	
rs2659104	+	KLK1	1f	POLR2A	KLK1
rs6012888	+	AK307192	2b	GABPA	-

Fig. 4

l



m



n

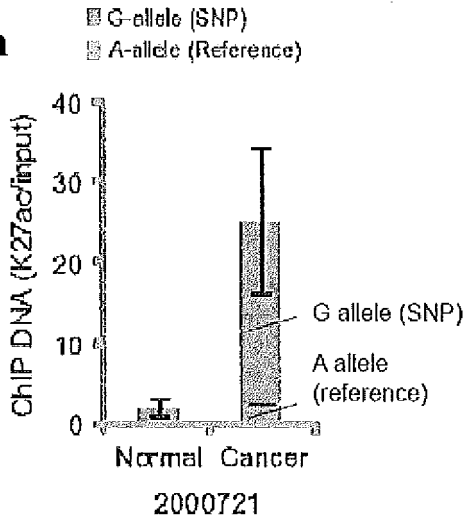
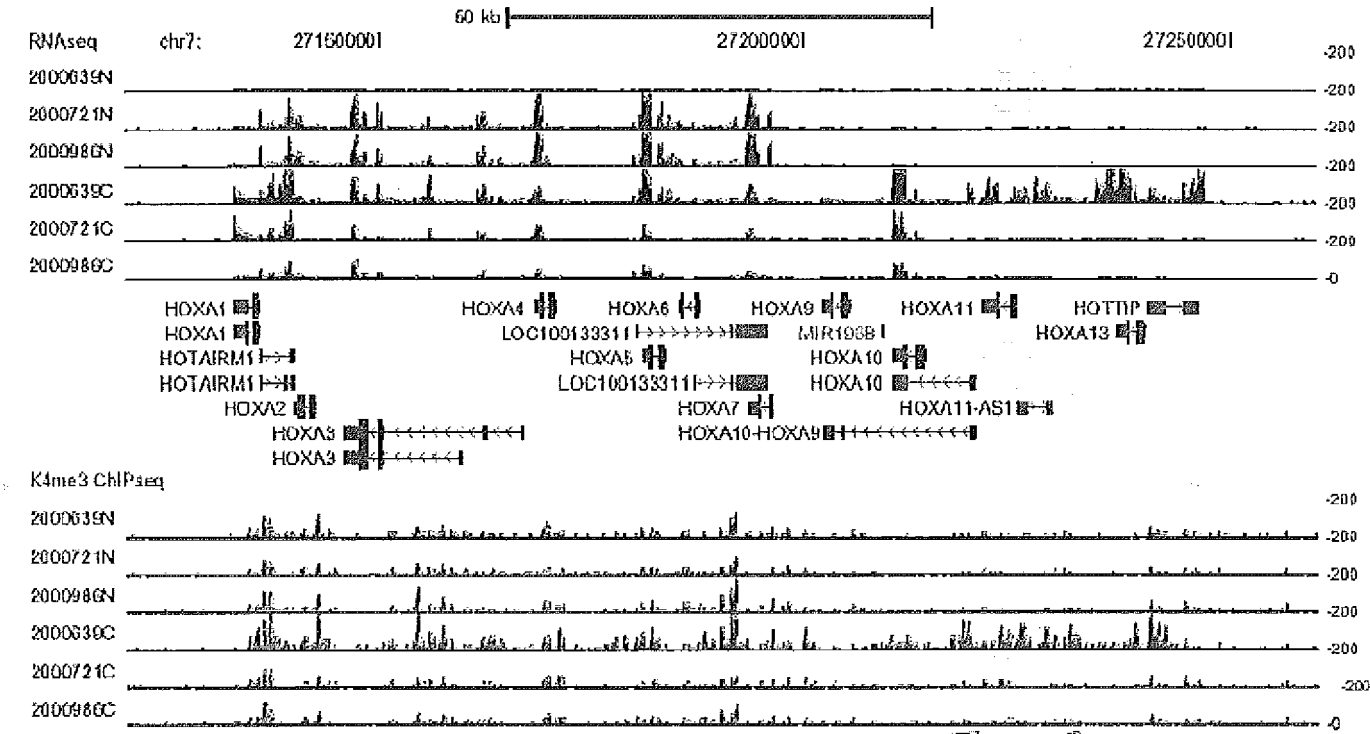


Fig. 5

a



b

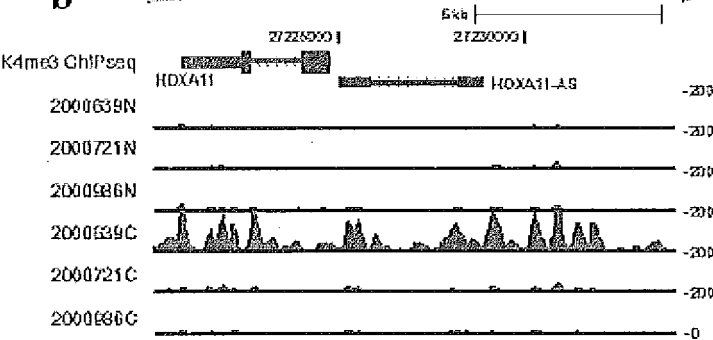


Fig. 5

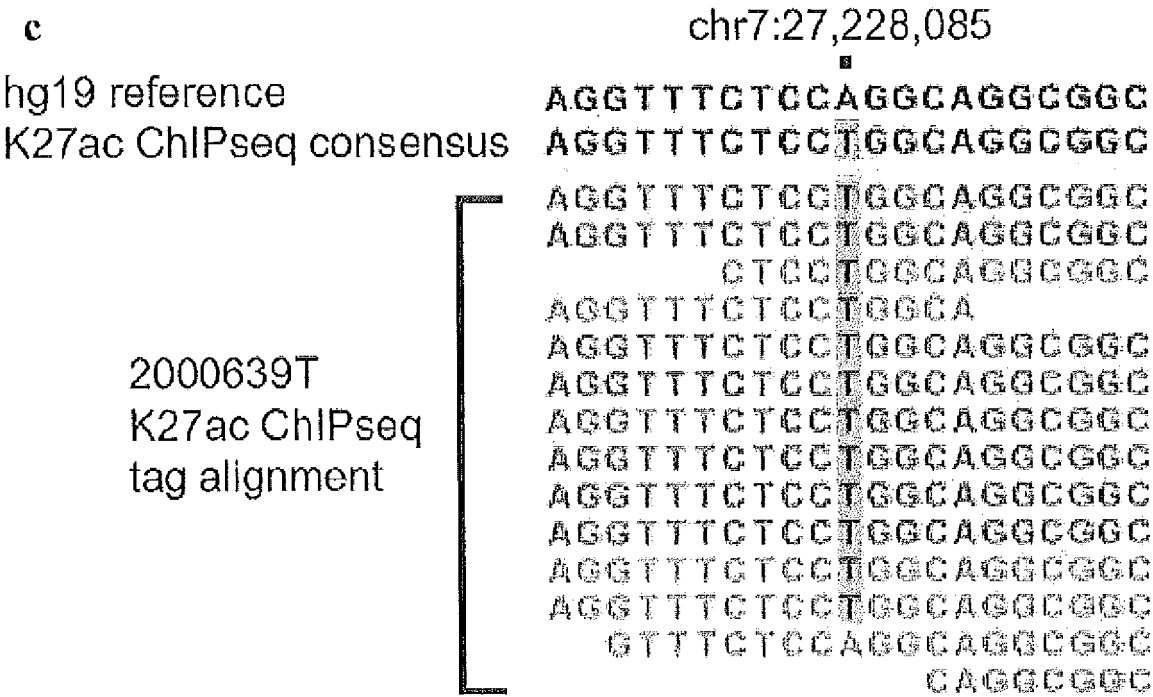
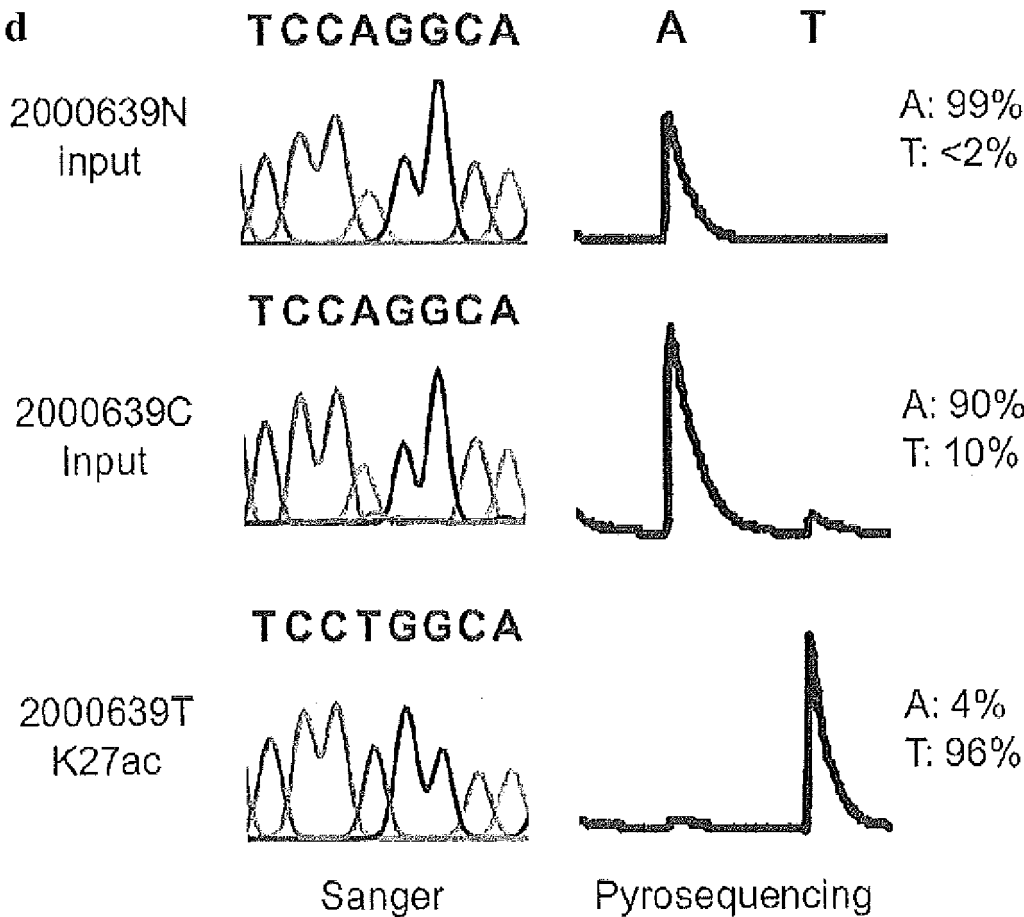


Fig. 5

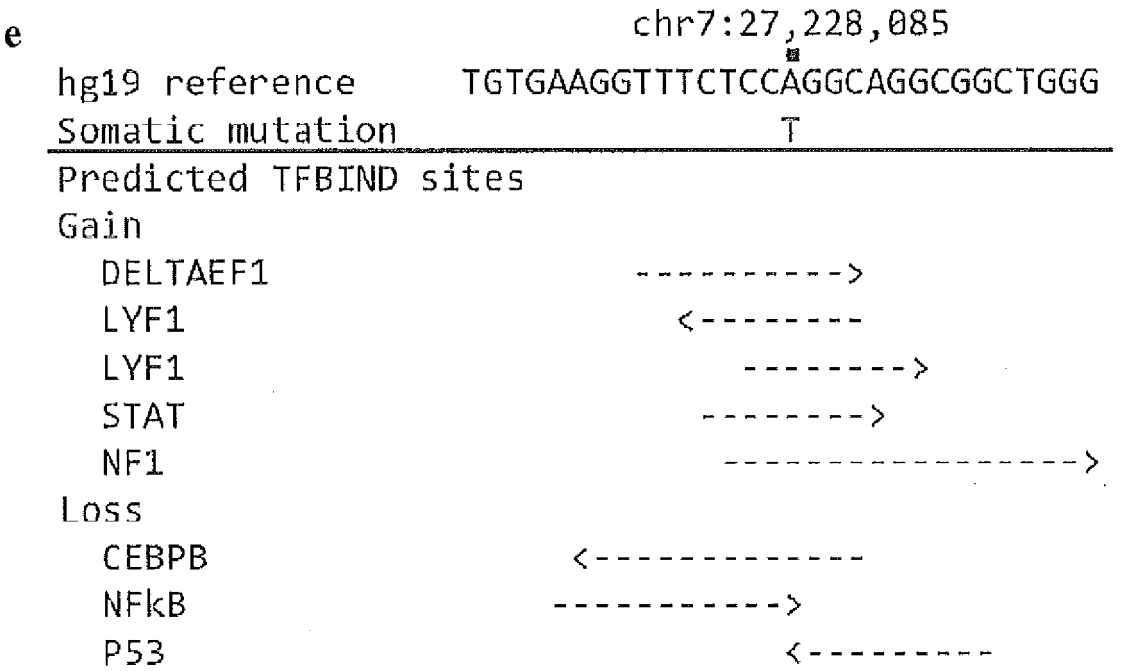
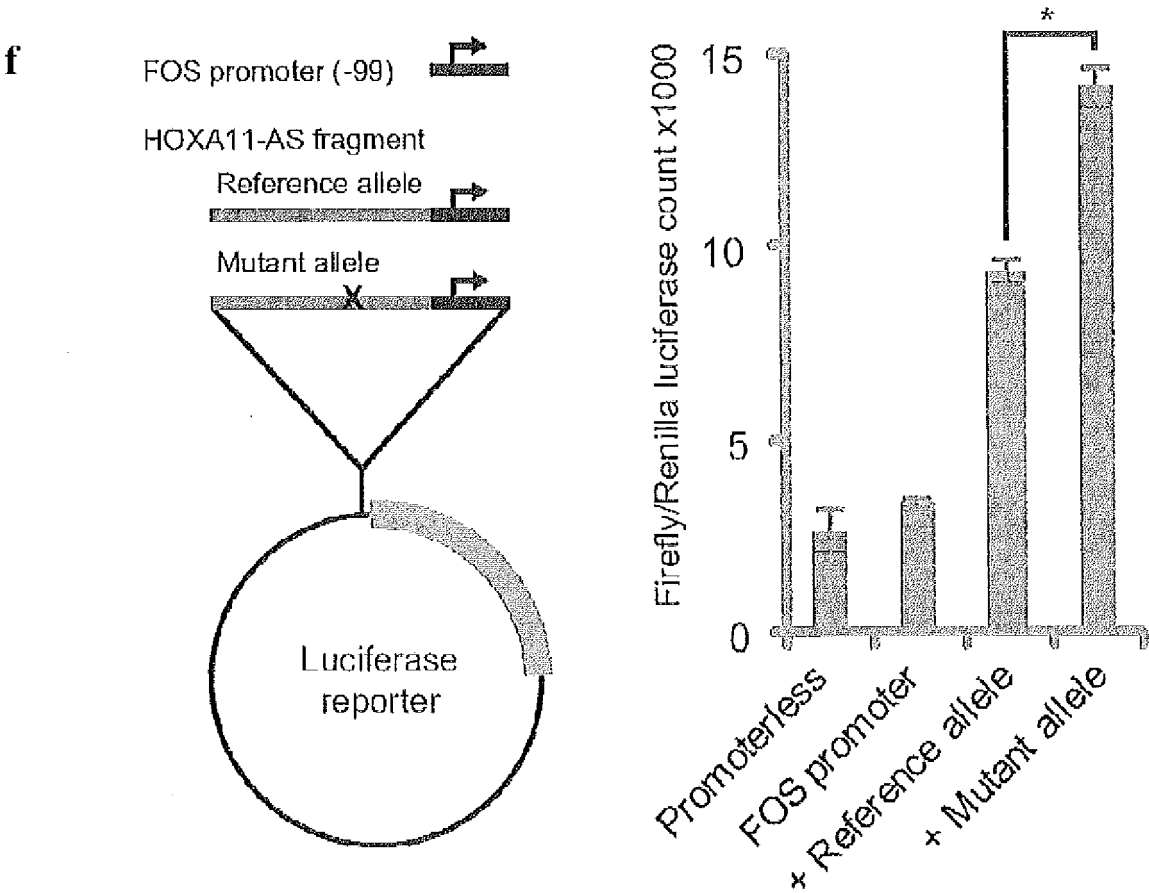
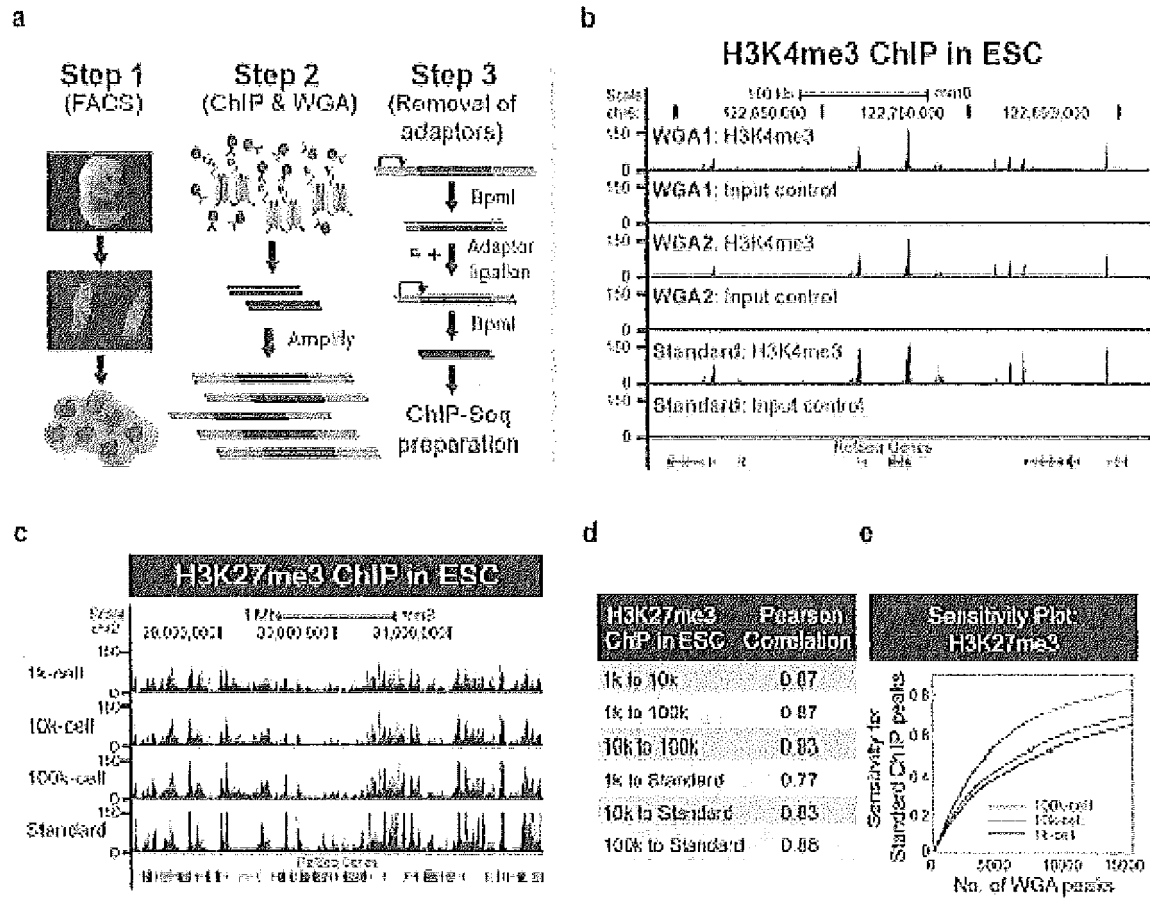


Fig. 6



From Ng et al. (2013) *Developmental Cell*

Fig. 7

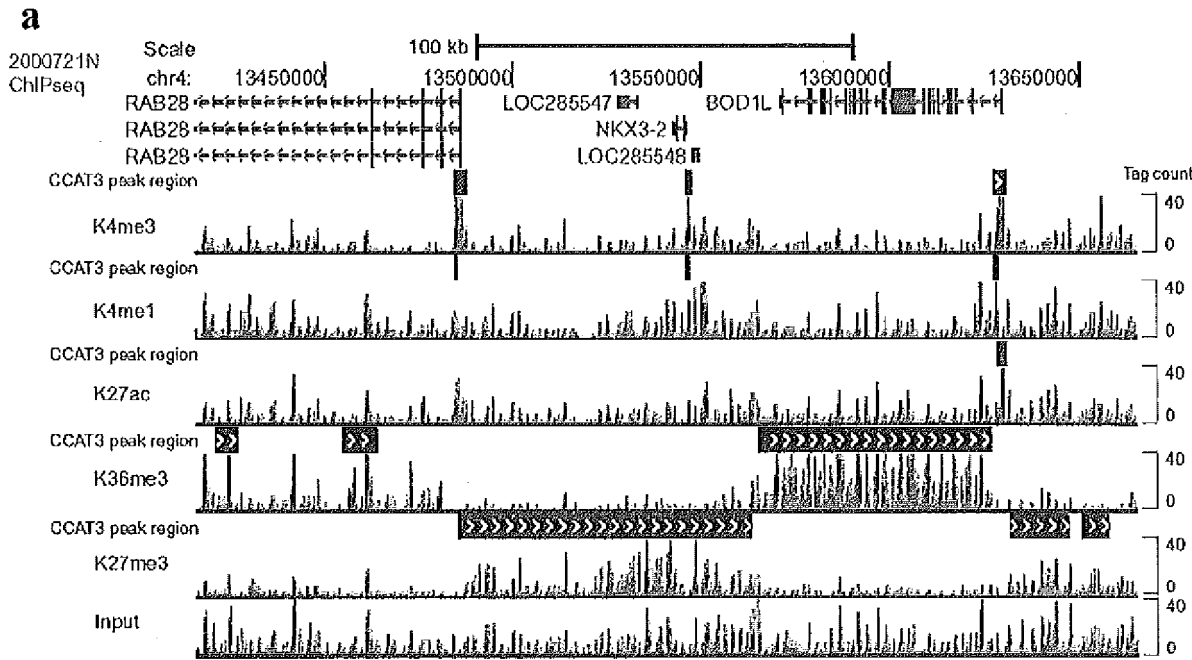
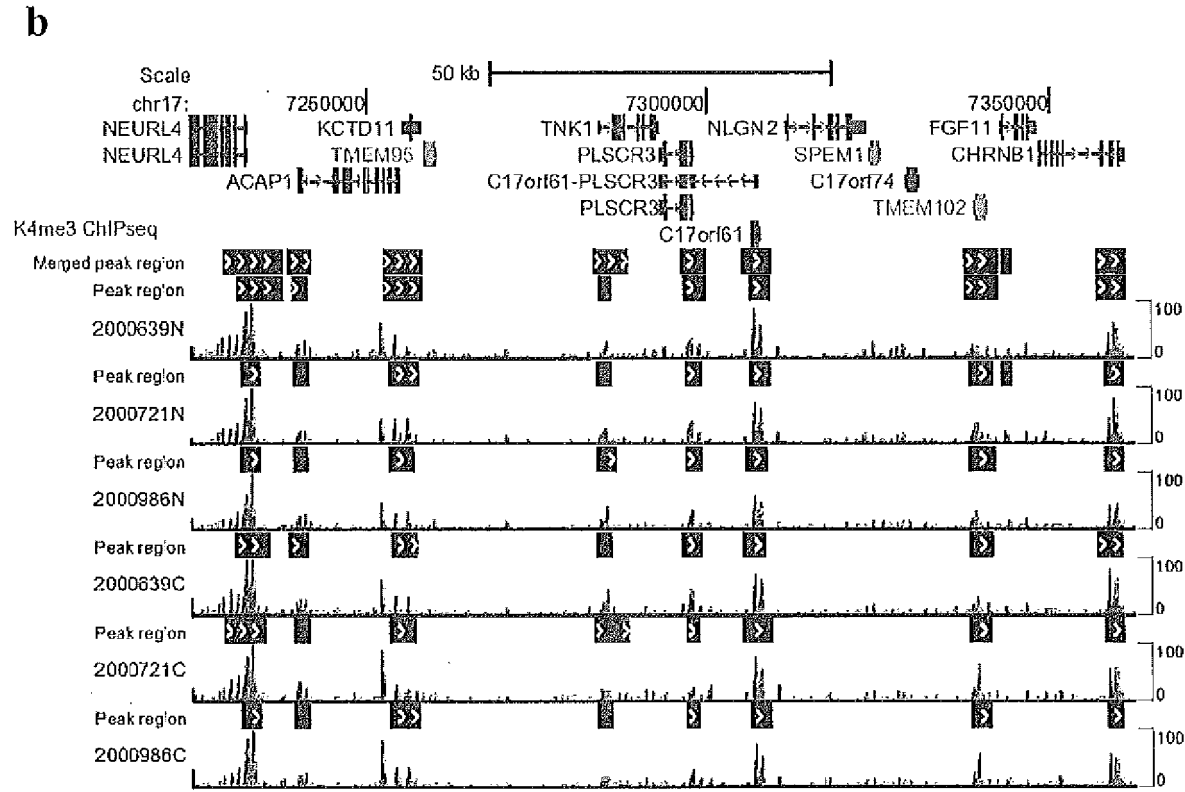


Fig. 8

a

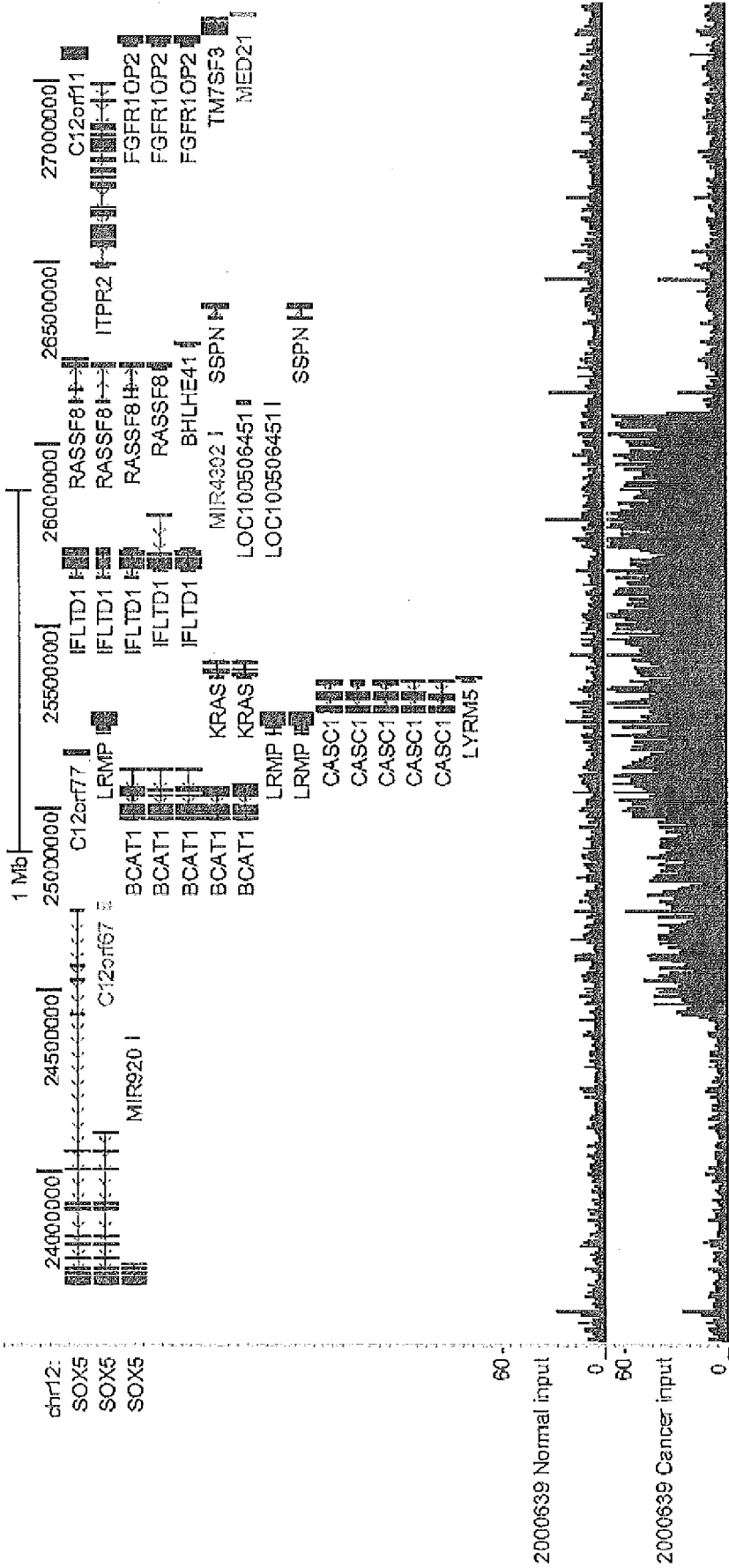
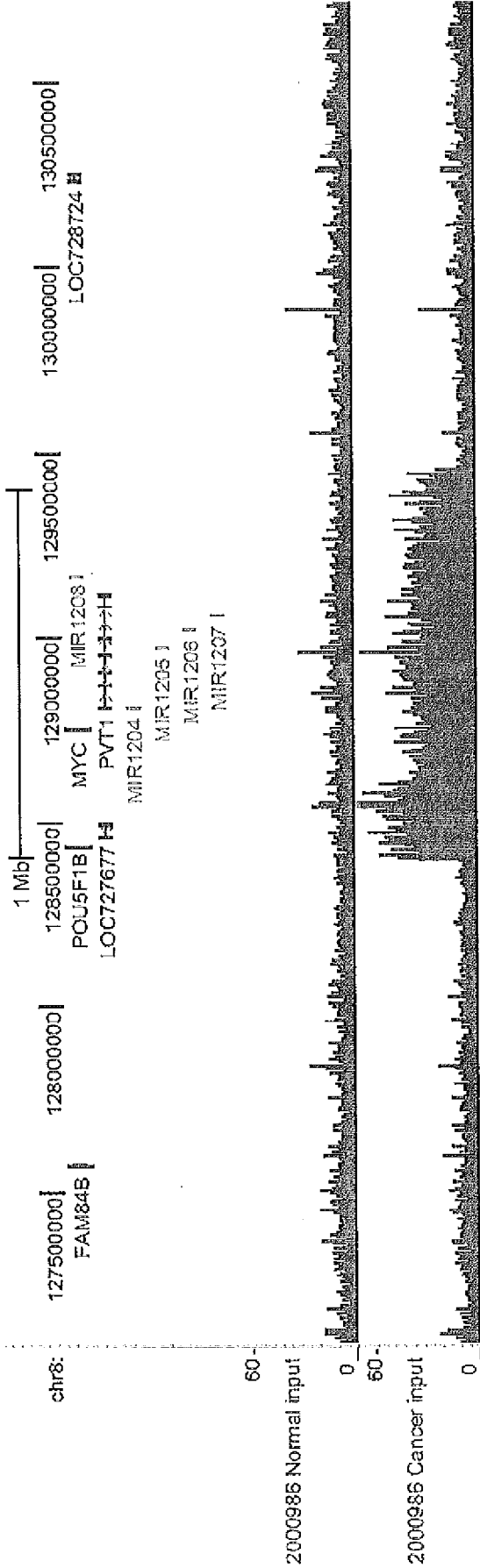


Fig. 8

b



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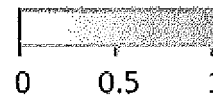
Fig. 9

a

		2nd set overlap				
Normal		K4me3	K4me1	K27ac	K36me3	K27me3
1st set	K4me3	1.00	0.30	0.73	0.19	0.06
	K4me1	0.40	1.00	0.49	0.19	0.04
	K27ac	0.75	0.35	1.00	0.21	0.03
	K36me3	0.28	0.20	0.29	1.00	0.02
	K27me3	0.07	0.04	0.04	0.02	1.00

		2nd set overlap				
Cancer		K4me3	K4me1	K27ac	K36me3	K27me3
1st set	K4me3	1.00	0.26	0.60	0.37	0.07
	K4me1	0.47	1.00	0.42	0.39	0.05
	K27ac	0.84	0.32	1.00	0.42	0.04
	K36me3	0.35	0.19	0.29	1.00	0.03
	K27me3	0.07	0.03	0.03	0.03	1.00

Fraction of 1st set region overlapping with 2nd set region

**b**

		2nd set overlap				
Normal		K4me3	K4me1	K27ac	K36me3	K27me3
1st set	K4me3	1.00	0.35	0.57	0.29	0.12
	K4me1	0.49	1.00	0.49	0.35	0.04
	K27ac	0.82	0.47	1.00	0.37	0.05
	K36me3	0.35	0.29	0.32	1.00	0.05
	K27me3	0.10	0.03	0.03	0.03	1.00

		2nd set overlap				
Cancer		K4me3	K4me1	K27ac	K36me3	K27me3
1st set	K4me3	1.00	0.56	0.73	0.25	0.08
	K4me1	0.40	1.00	0.45	0.25	0.05
	K27ac	0.74	0.62	1.00	0.29	0.05
	K36me3	0.26	0.34	0.30	1.00	0.04
	K27me3	0.06	0.05	0.04	0.03	1.00

Fraction of 1st set region overlapping with 2nd set region

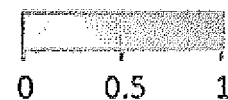
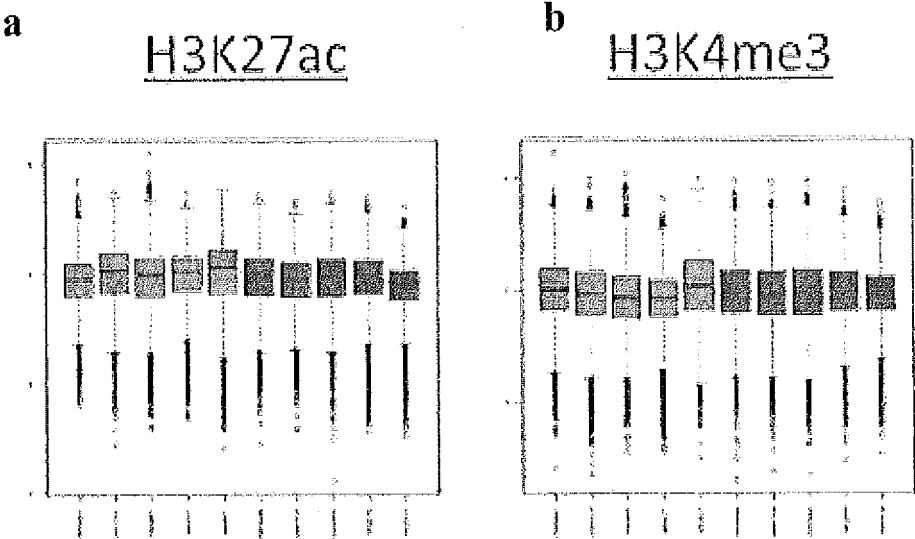


Fig. 10

Promoters



Enhancers

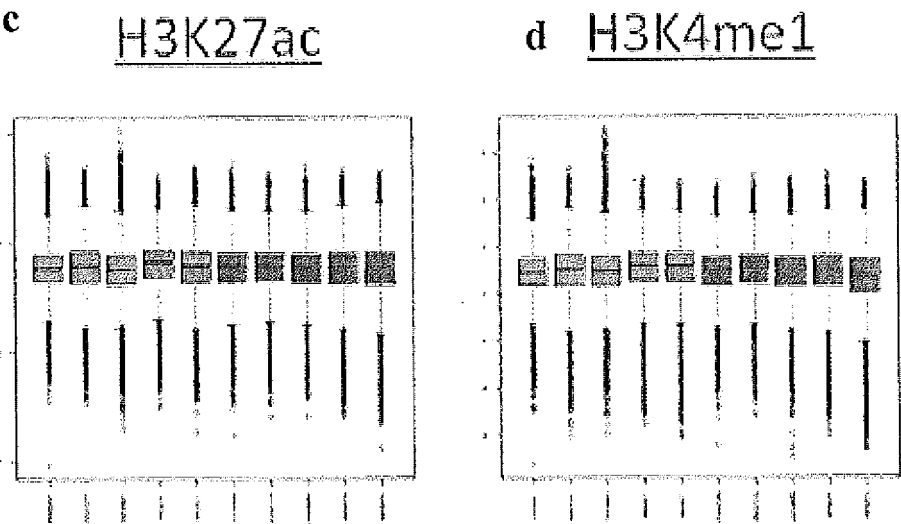


Fig. 10

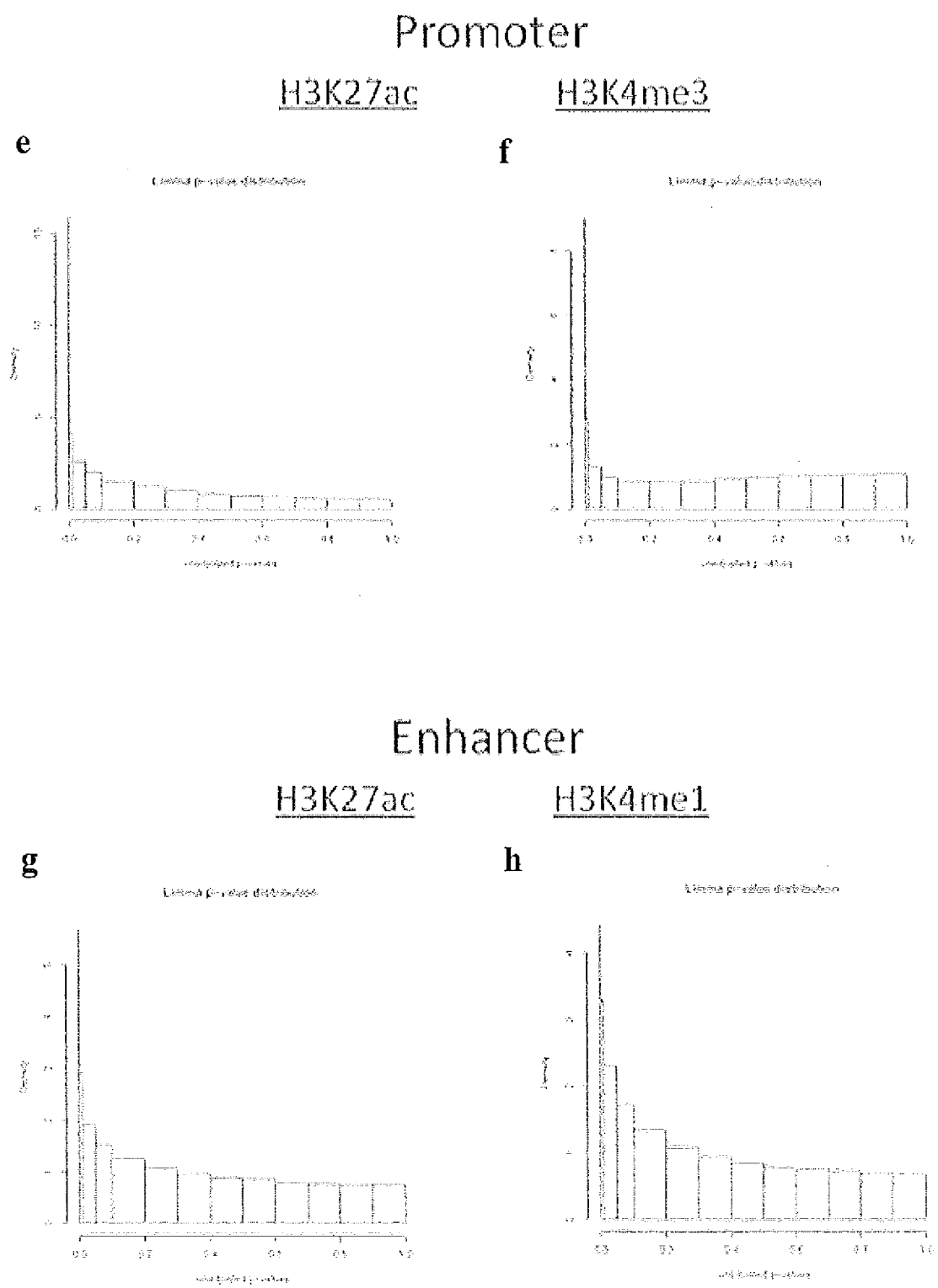
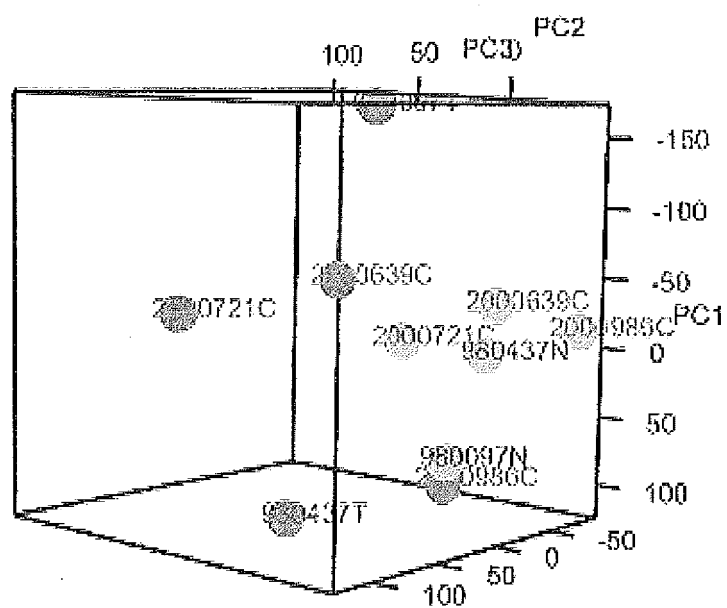


Fig. 11

Normal Cancer

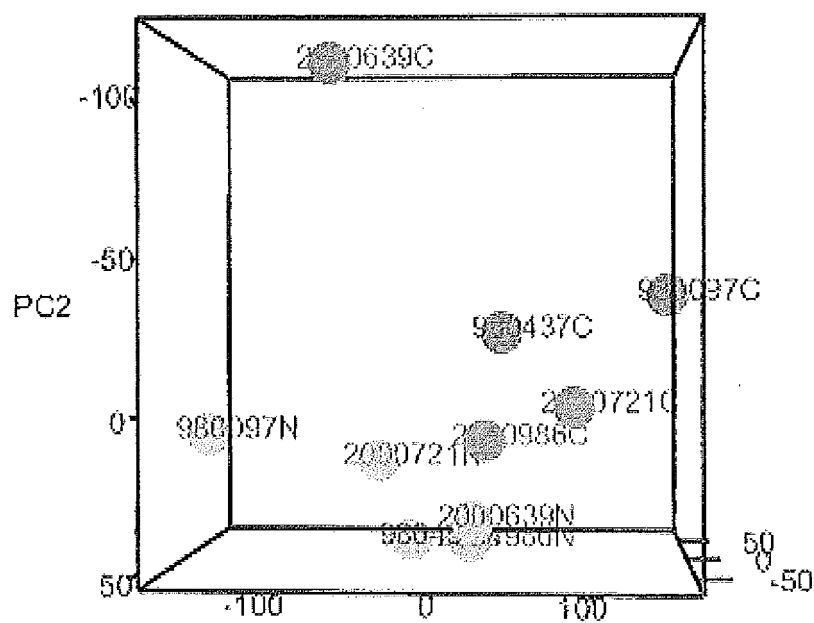
All promoter regions, K4me3 value



All promoter region, K27ac value

PC1

PC3

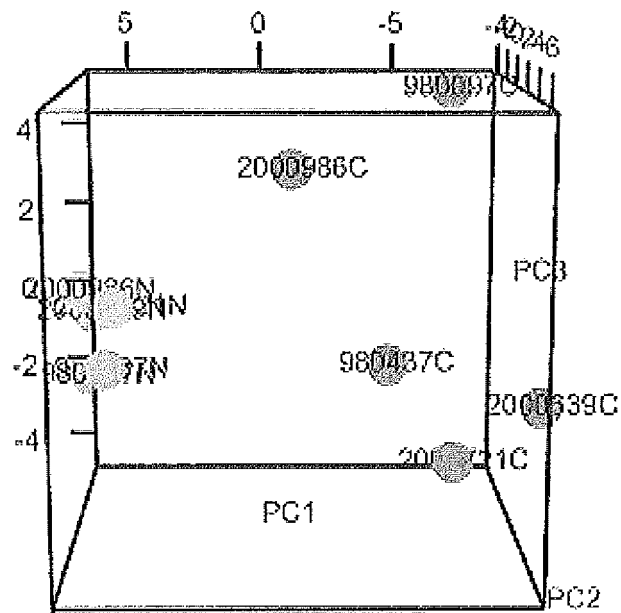


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Fig. 11

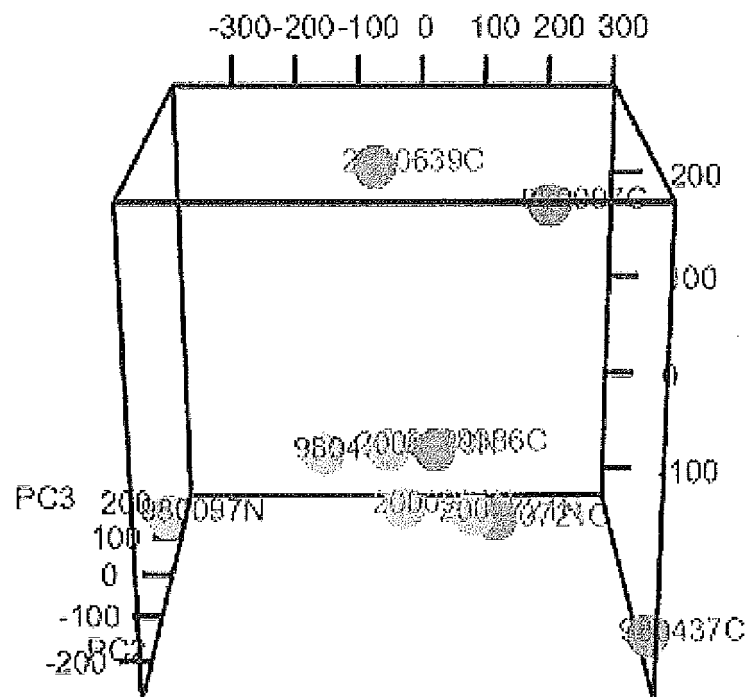
Altered promoter regions, K27ac value

c



All enhancer regions, K4me1 value

d

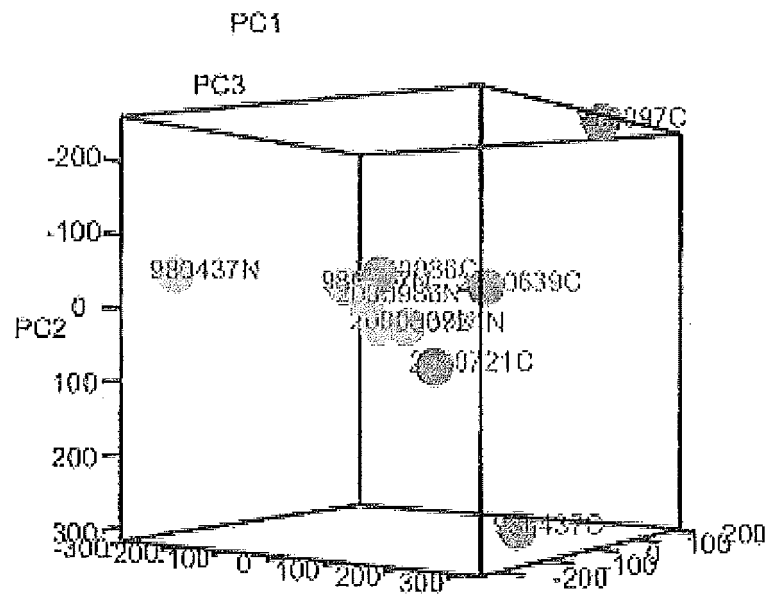


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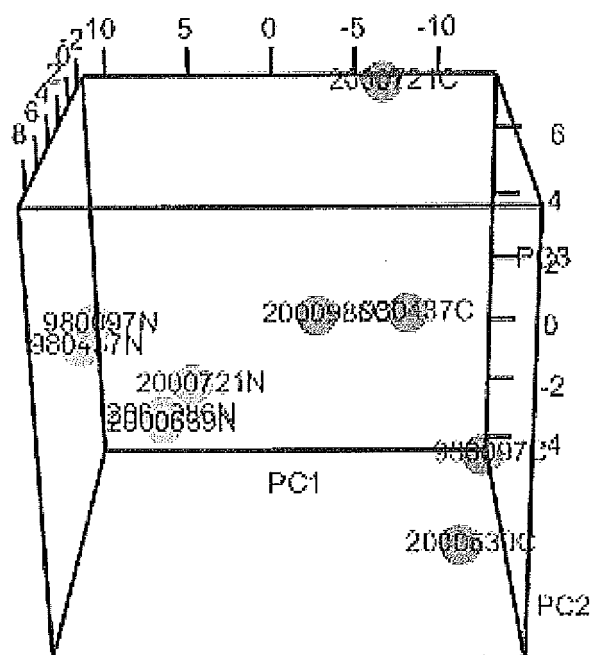
Fig. 11

All enhancer regions, K27ac value

e



Altered enhancer regions, K27ac value



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Fig. 12

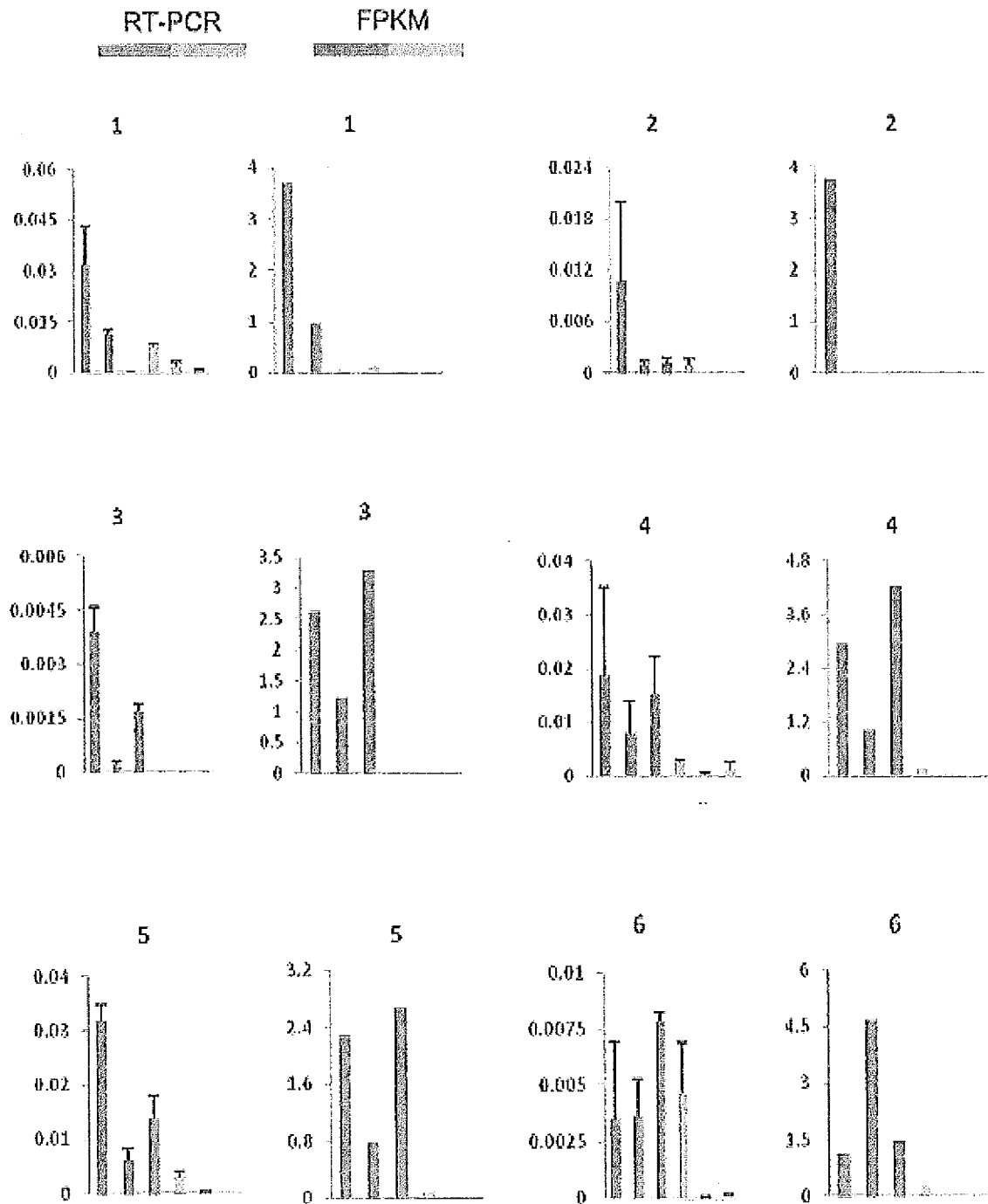
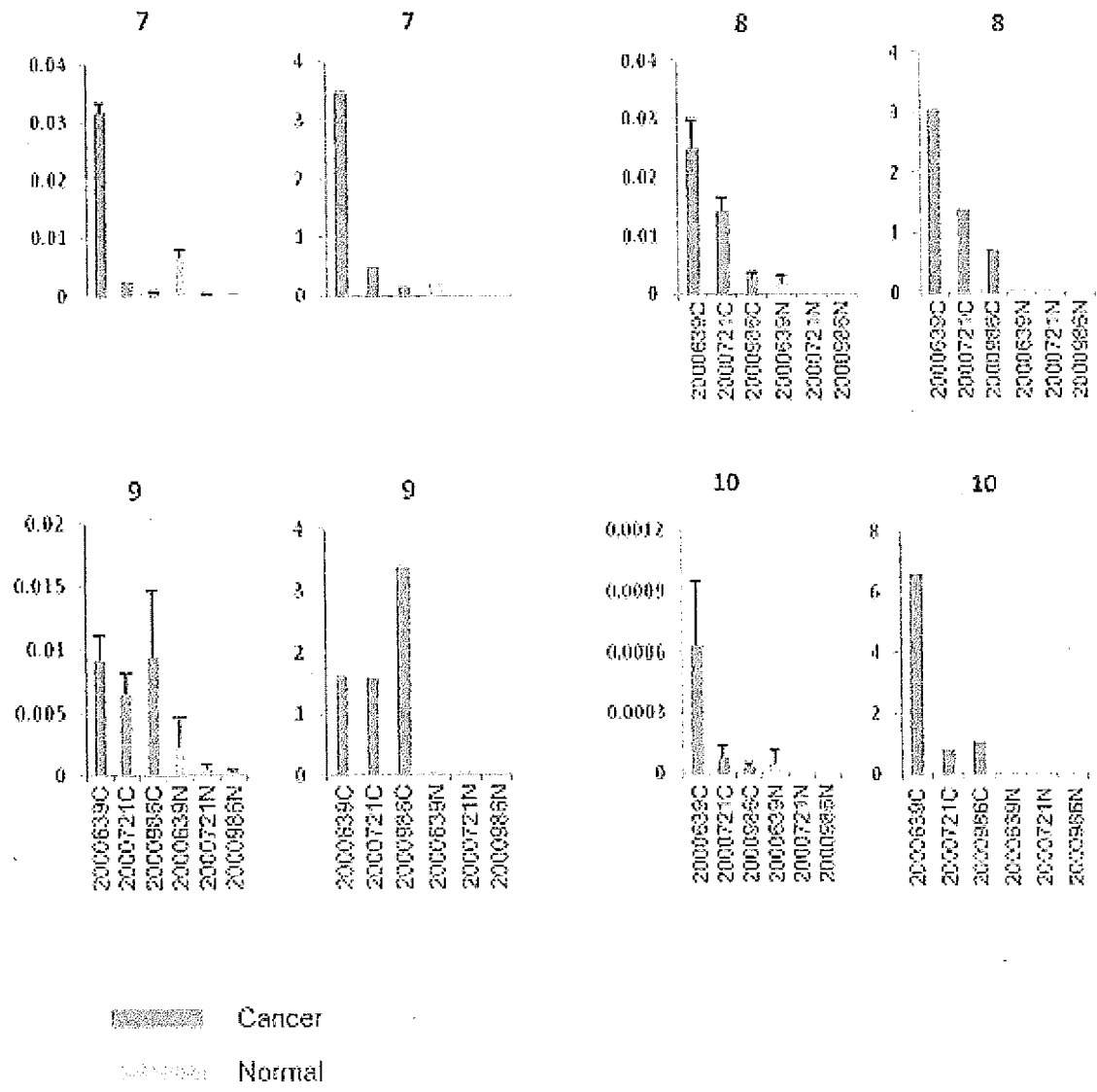


Fig. 12

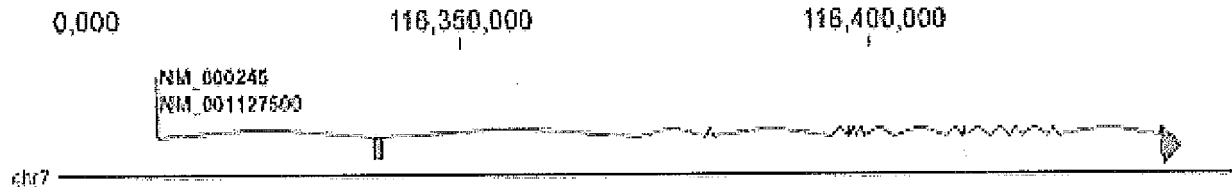


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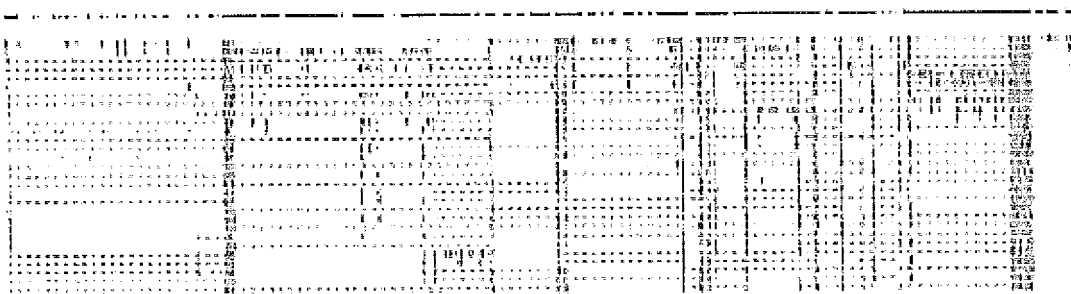
Fig. 13

a

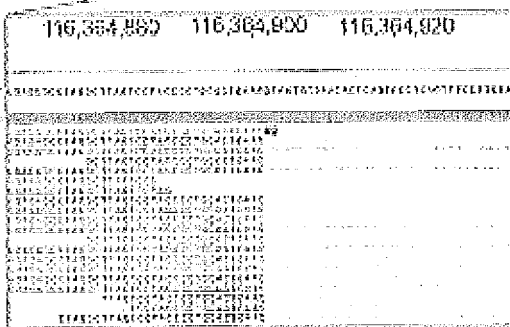
a MET Gene Locus



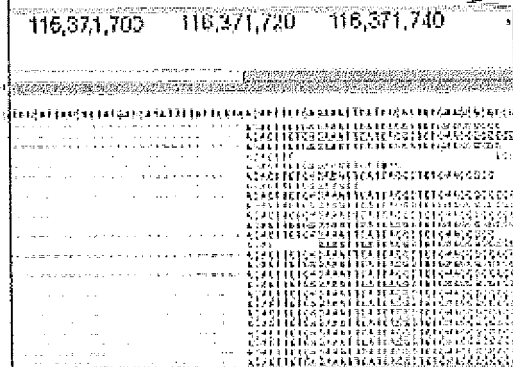
Consensus

2000721 Cancer
RNAseq tag alignment

b



c



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Fig. 13

d

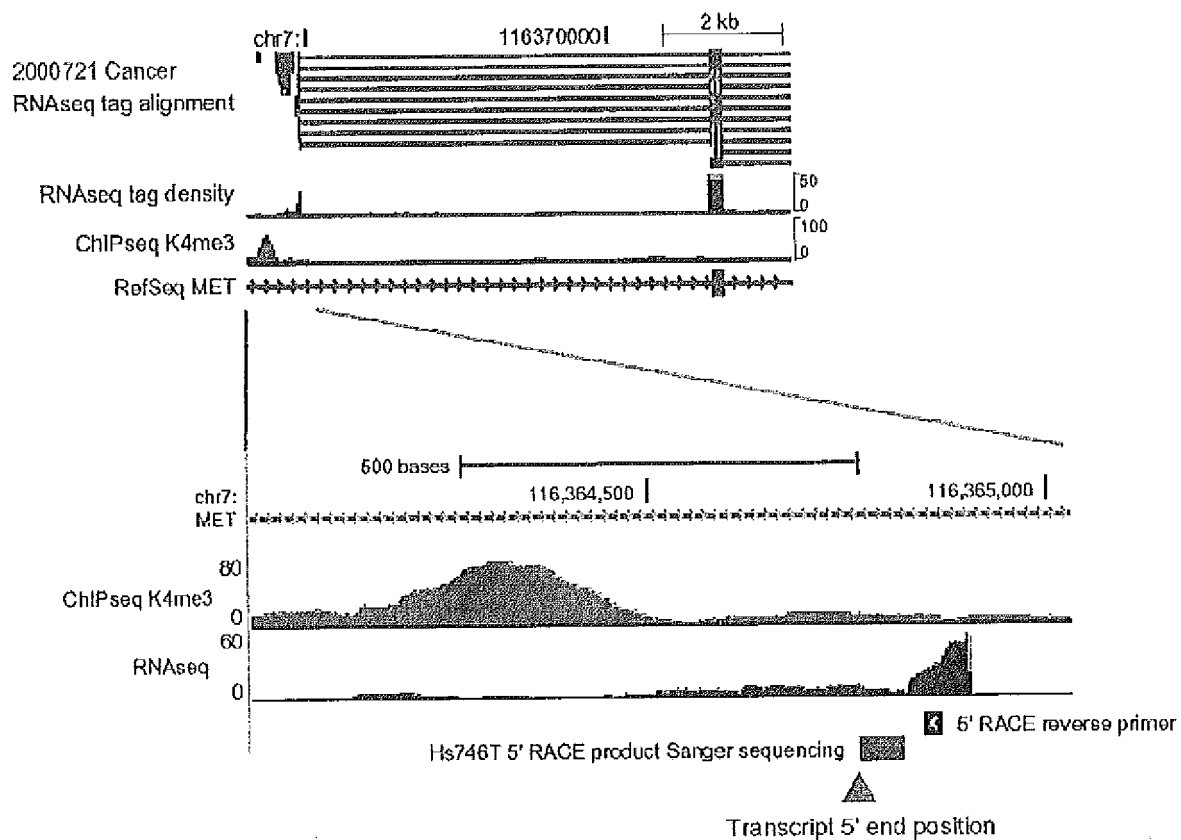
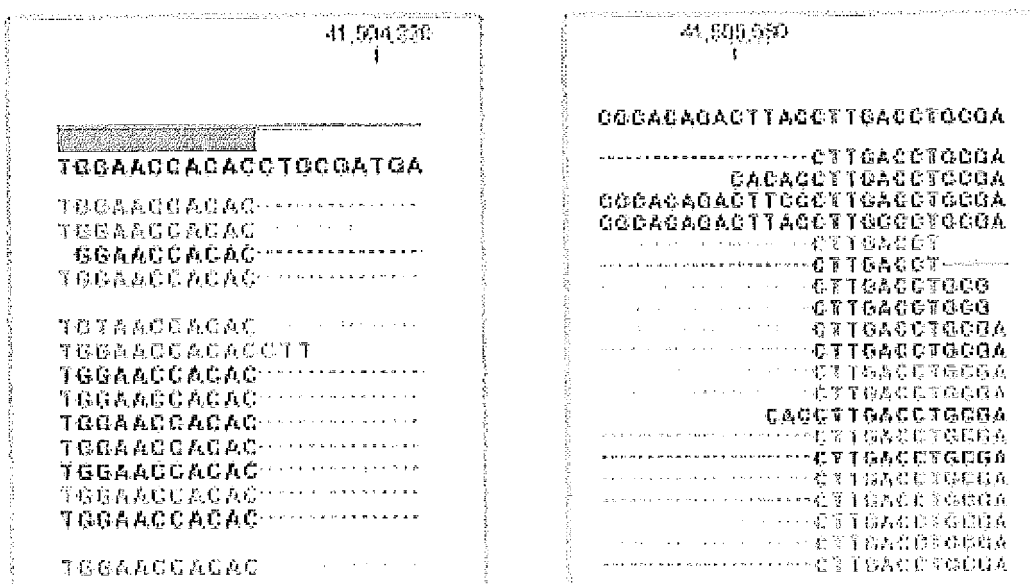


Fig. 14

NRX6-3 Gene Locus



c



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Fig. 14

d.

```

45 505,740      41 505,760
ACACAGGGGGGCTCTGGGGCTGGCAGG
CTCAGGGGGGCTCTGGGG
ACACAGGGGGGCTCTGGGG
GCTCAGGGGGCTCTGGGG
ACACAG
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ACACAGGGGGCTCTGGGG
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ACTCAGGGGGCTCTGGGG
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ACACAGGGGGCTCTGGGG
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ACACAGGGGGCTCTGGGG

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e

[illegible]

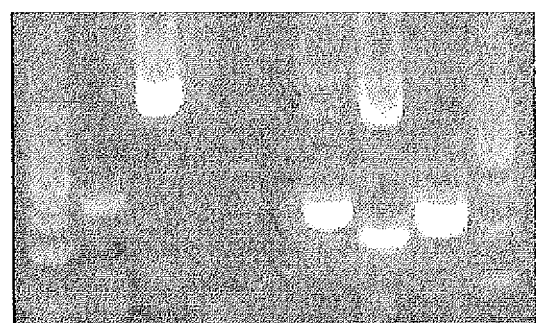
f

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g

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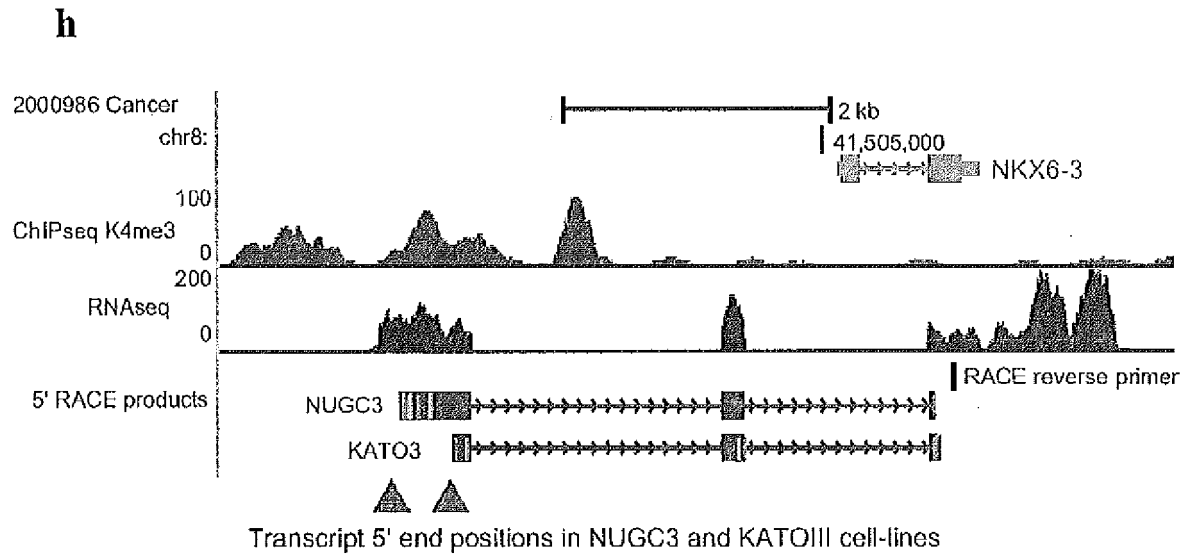
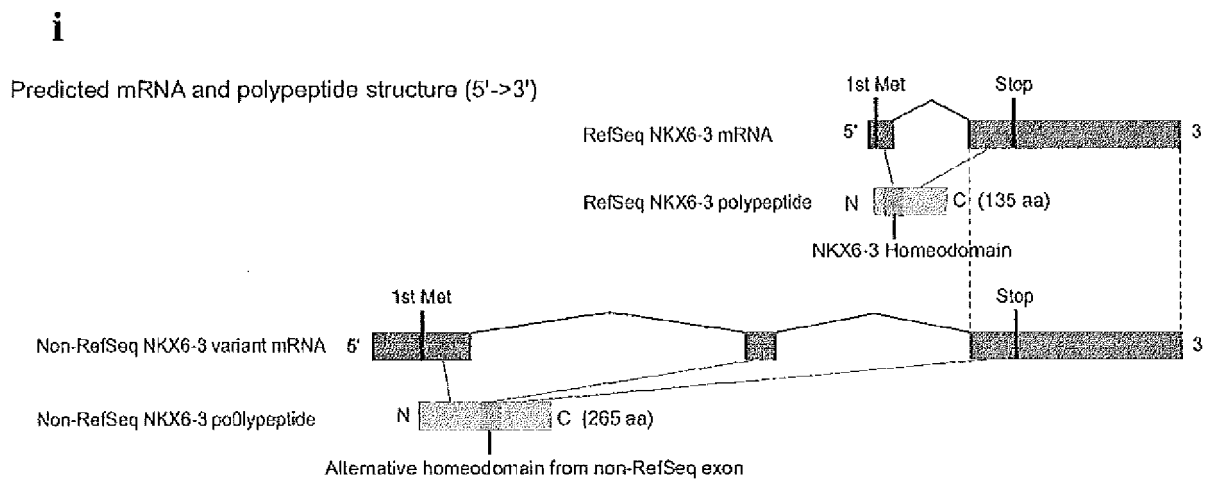
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400bp



1 2 3 4 5 6 7

41/ 60

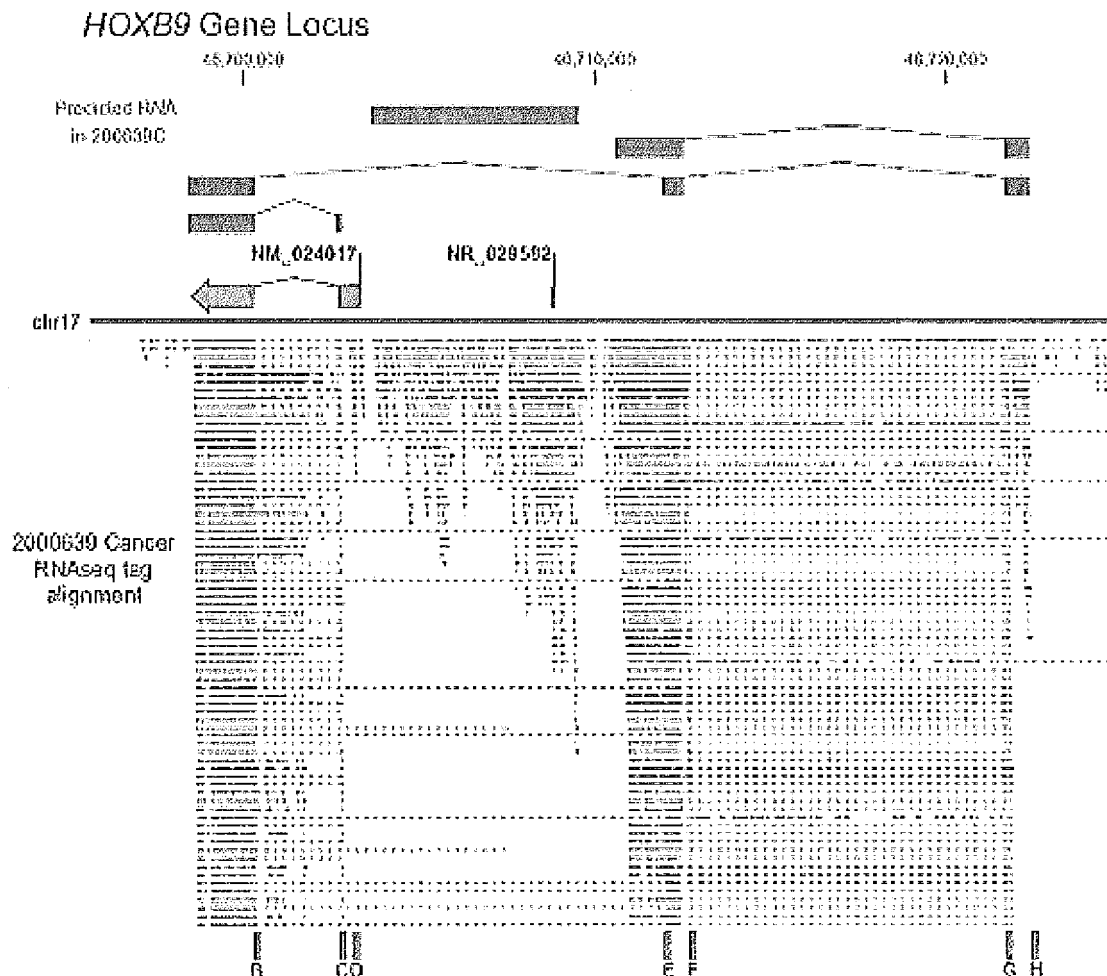
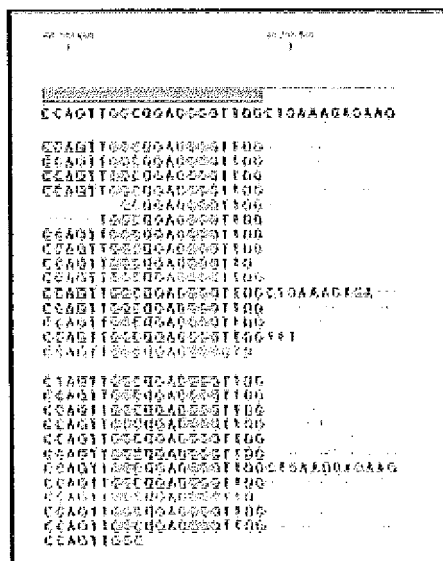
Fig. 14



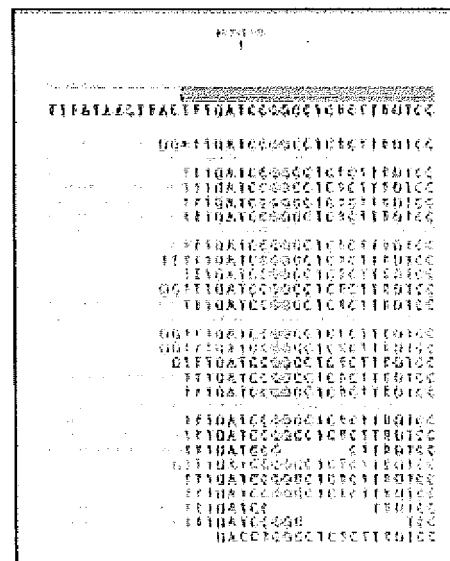
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Fig. 15

a

**b**

C



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Fig. 15

d

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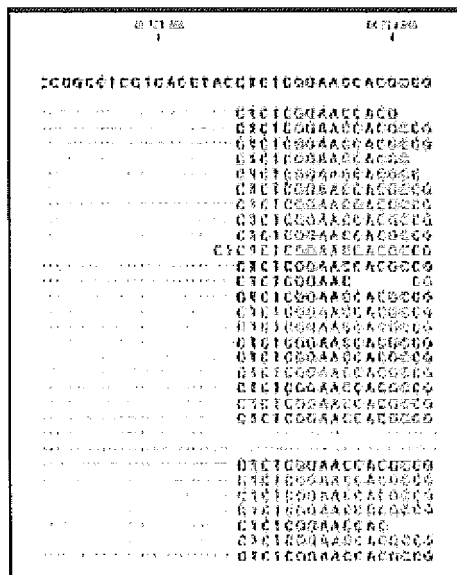
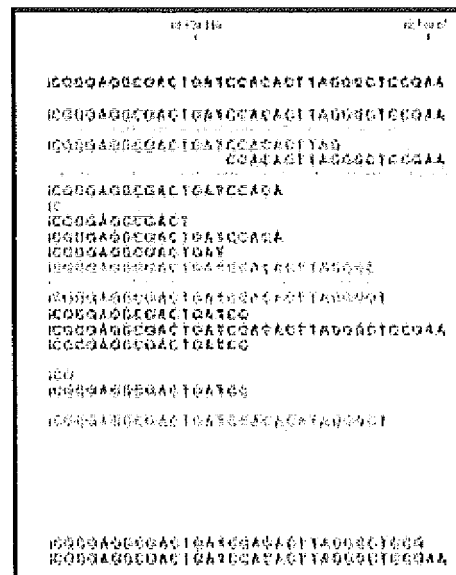
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Fig. 15

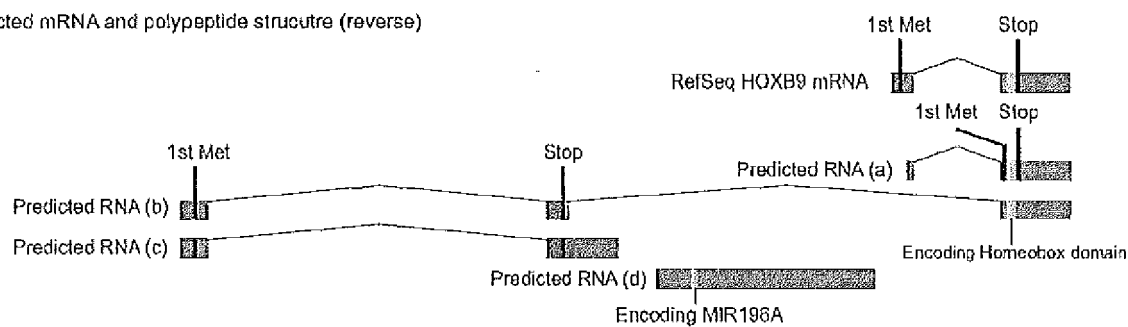
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h



i

Predicted mRNA and polypeptide structure (reverse)



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Fig. 16

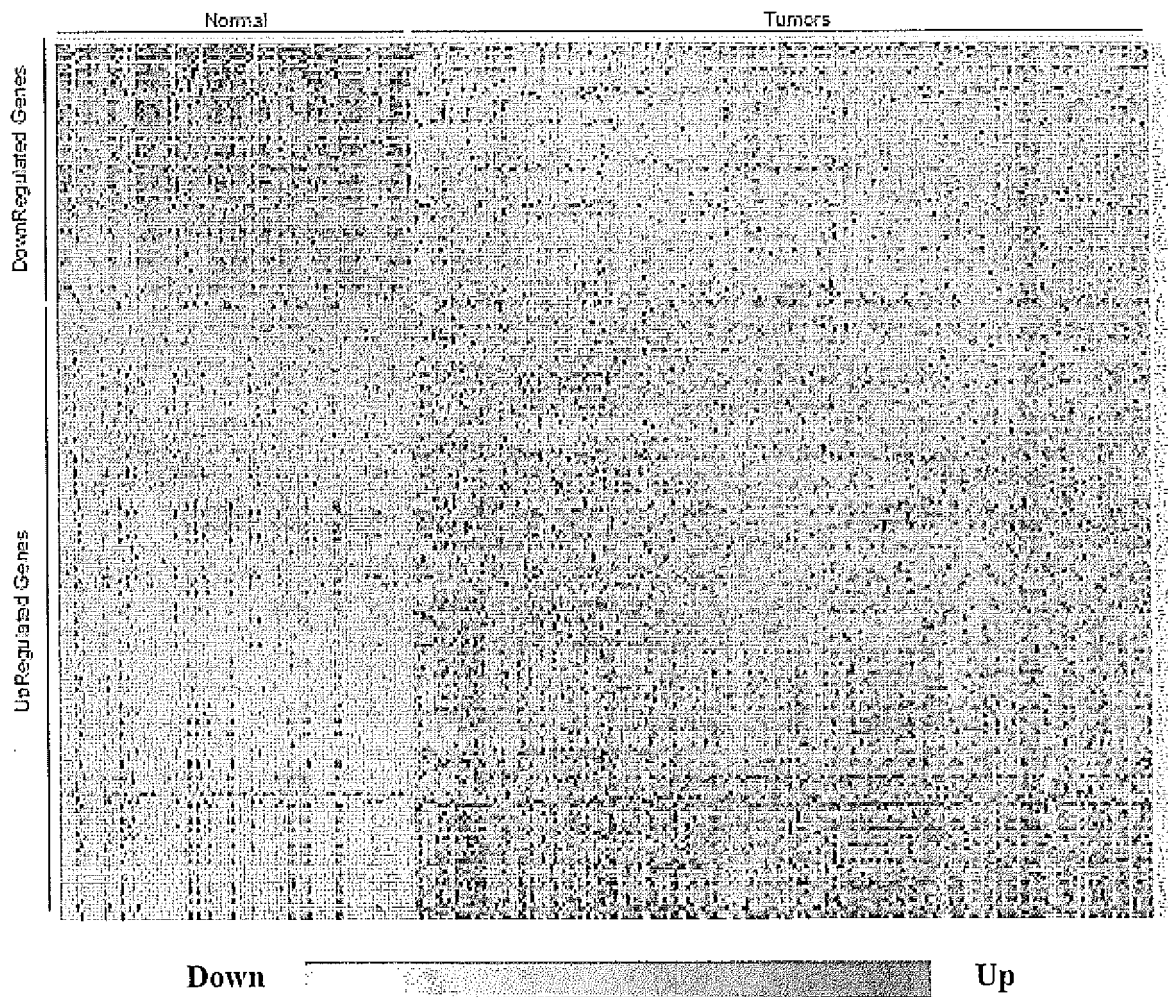
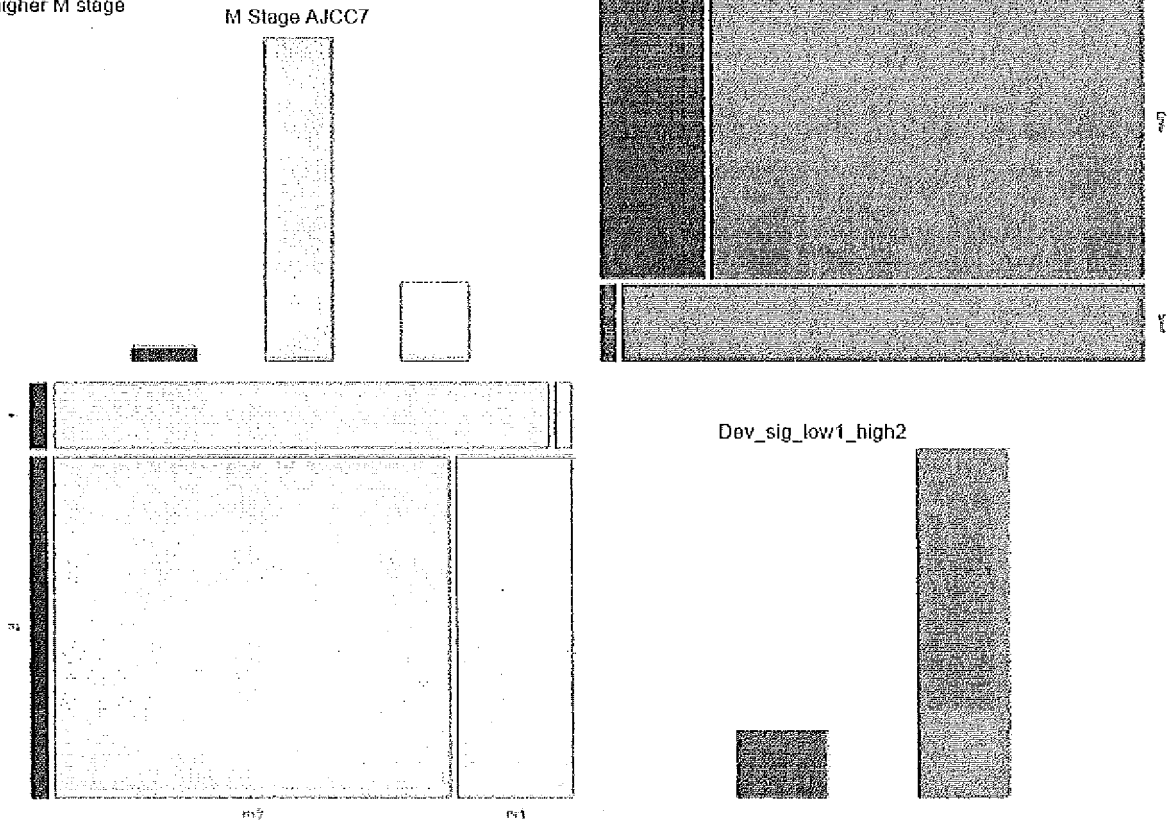


Fig. 17

a

Pearson Chi sq. p value = 0.03292
i.e. Higher dev.sig is significantly associated with
higher M stage



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Fig. 17

b

Pearson Chi sq. p value = 9.999e-05
 Excl. mixed: Laurens_intestinal1_Diffuse2_Mixed3
 Pearson Chi sq. p value = 9.999e-05
 i.e. Higher dev.sig is significantly associated with
 diffuse-type GC

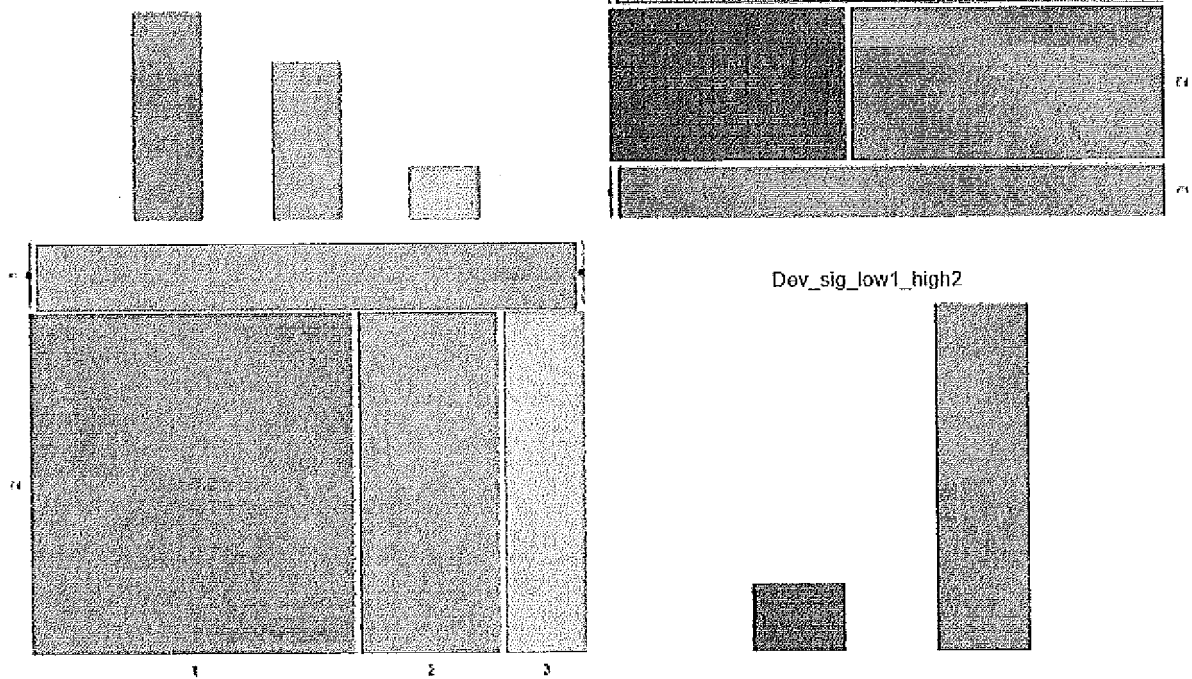


Fig. 17

c

Pearson Chi sq. p value = 1.684e-13
Excl. AMBI intrinsic_signature_GINT1_GDIFF2_AMBI
Pearson Chi sq. p value = 1.457e-11
i.e. Higher dev.sig is significantly associated with GDIFF-type GC

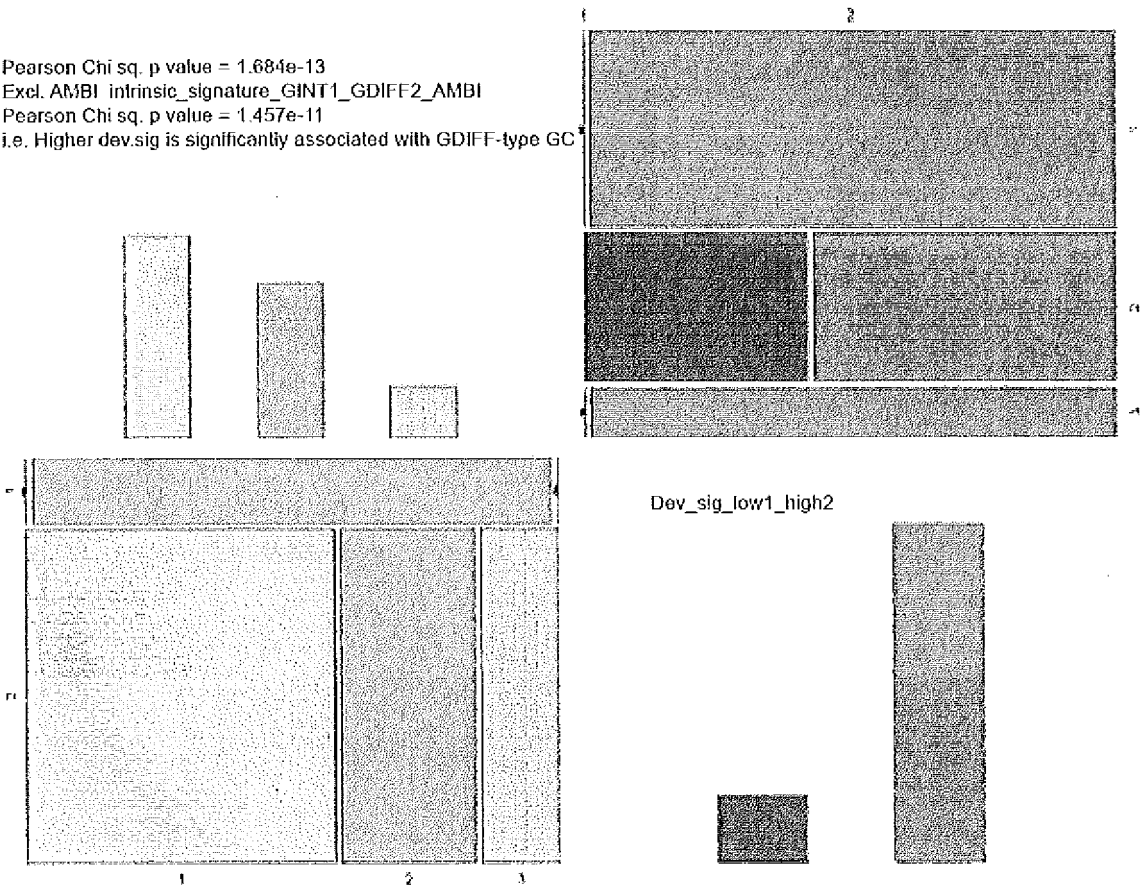


Fig. 18

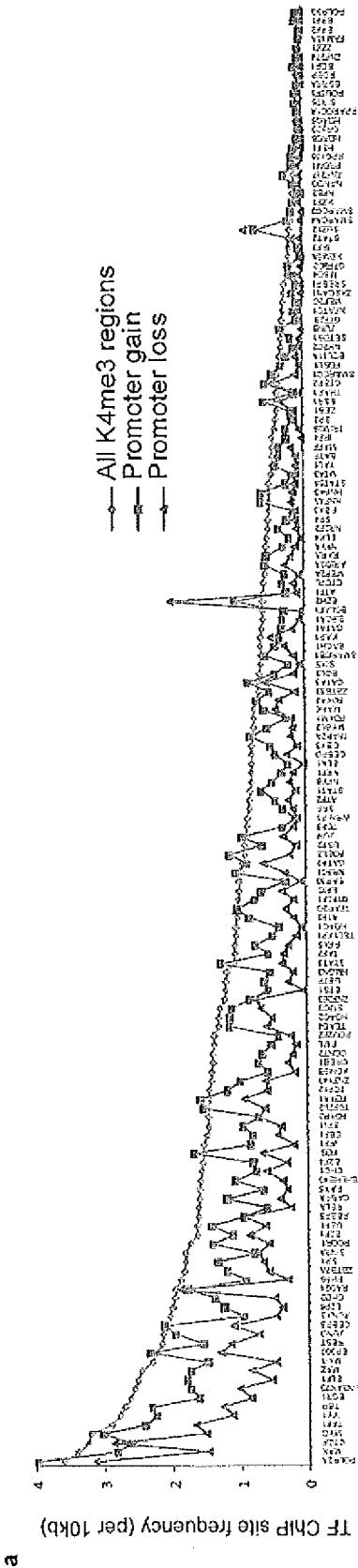


Fig. 18

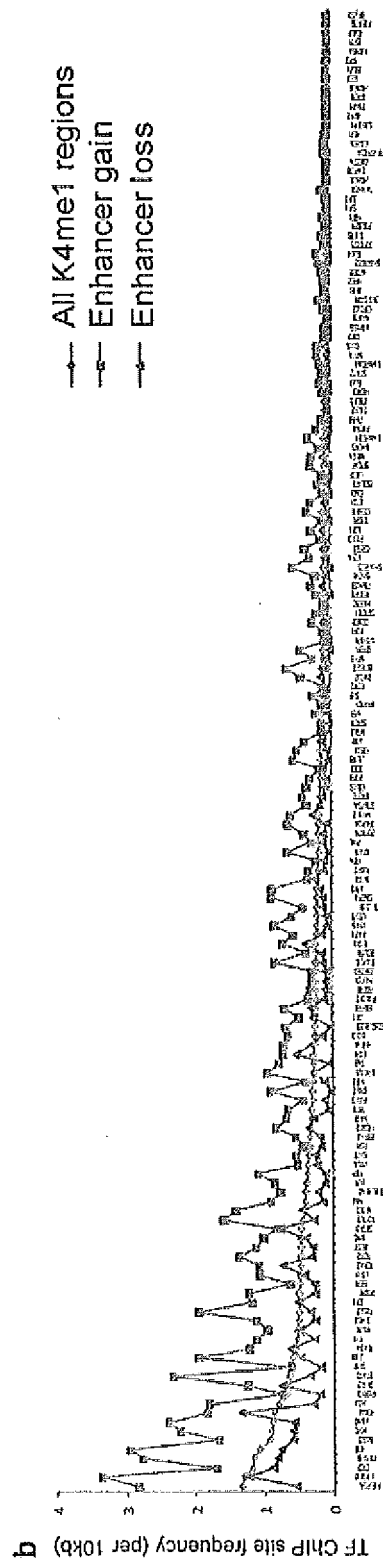


Fig. 19

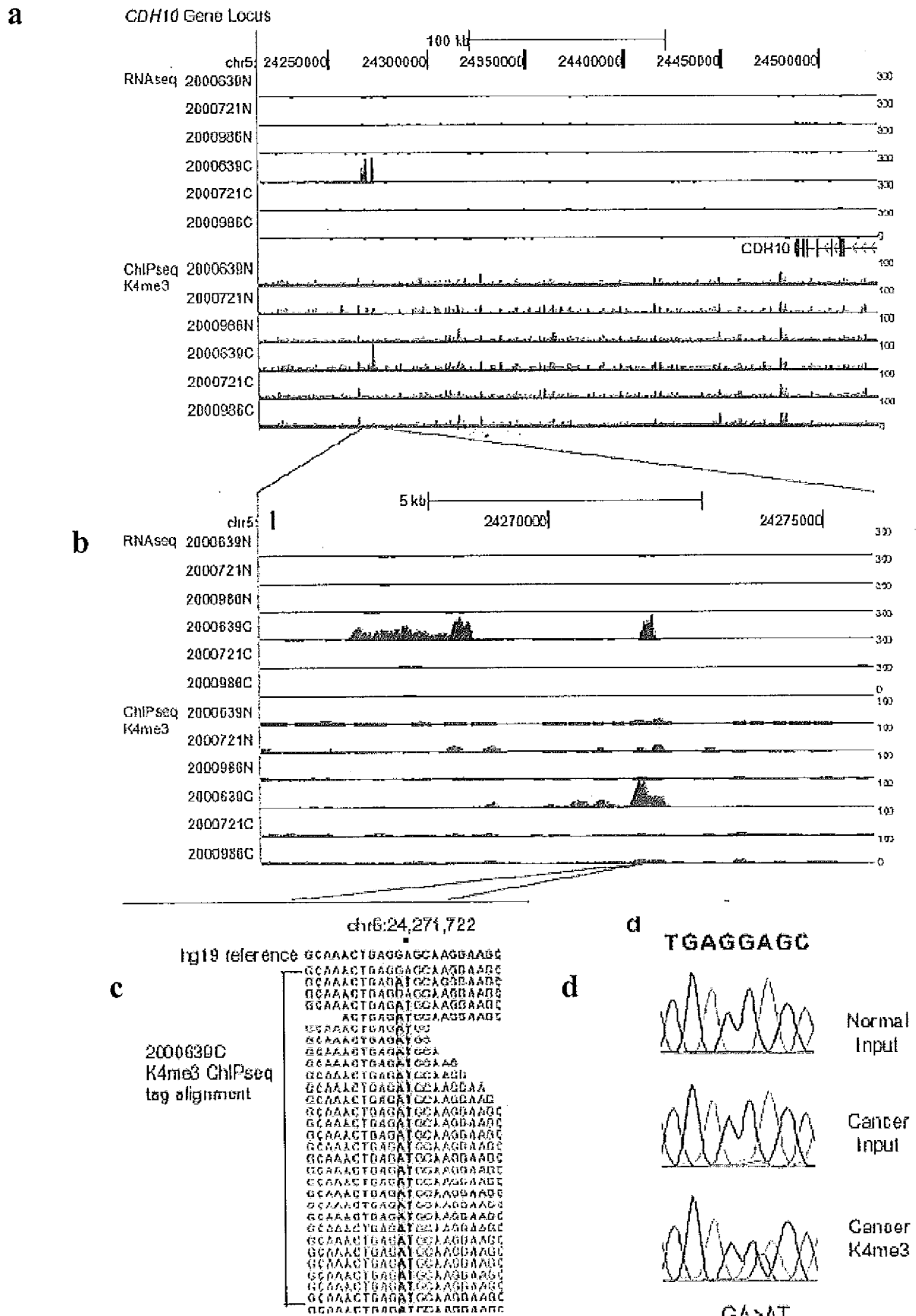


Fig. 20

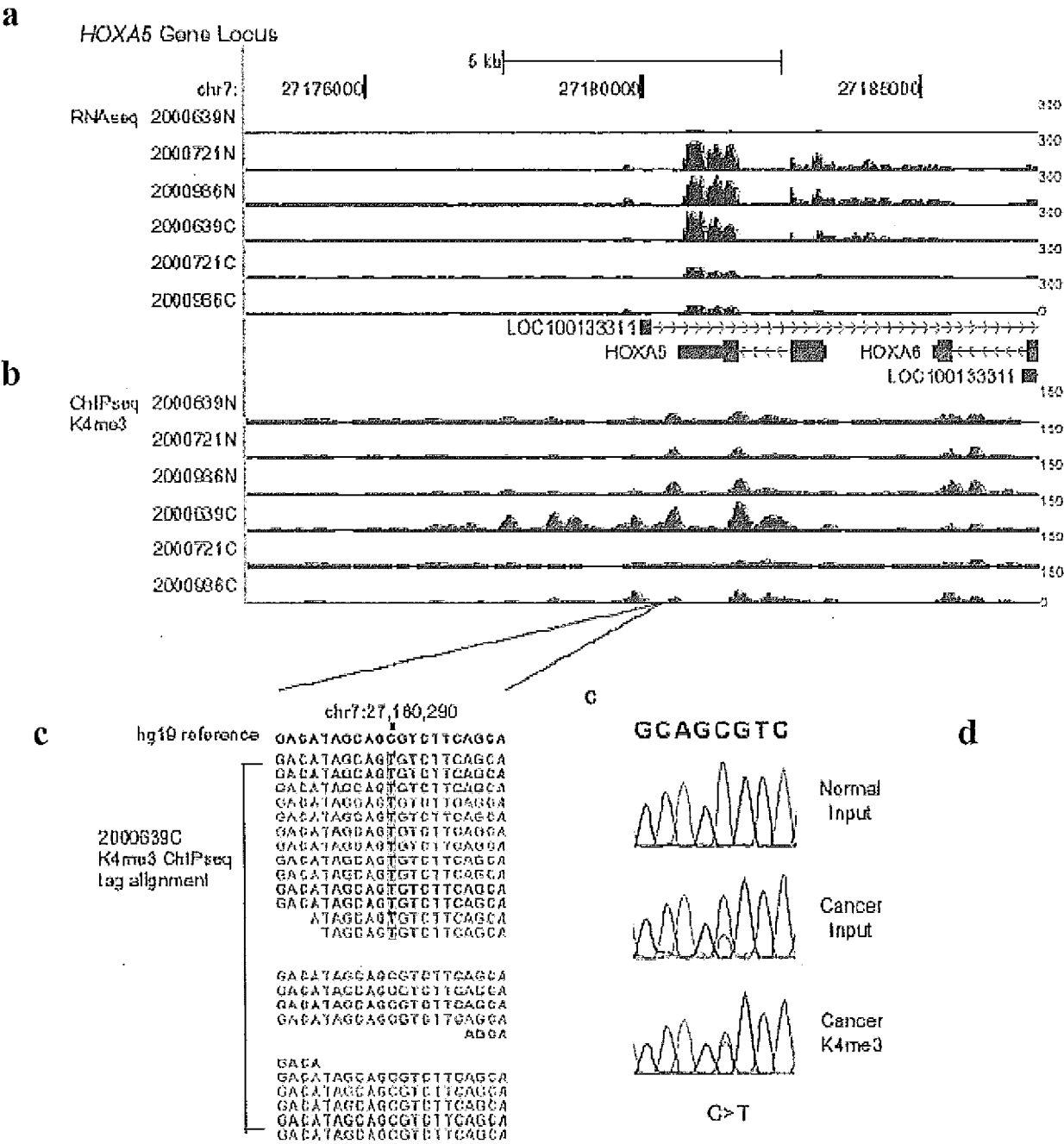
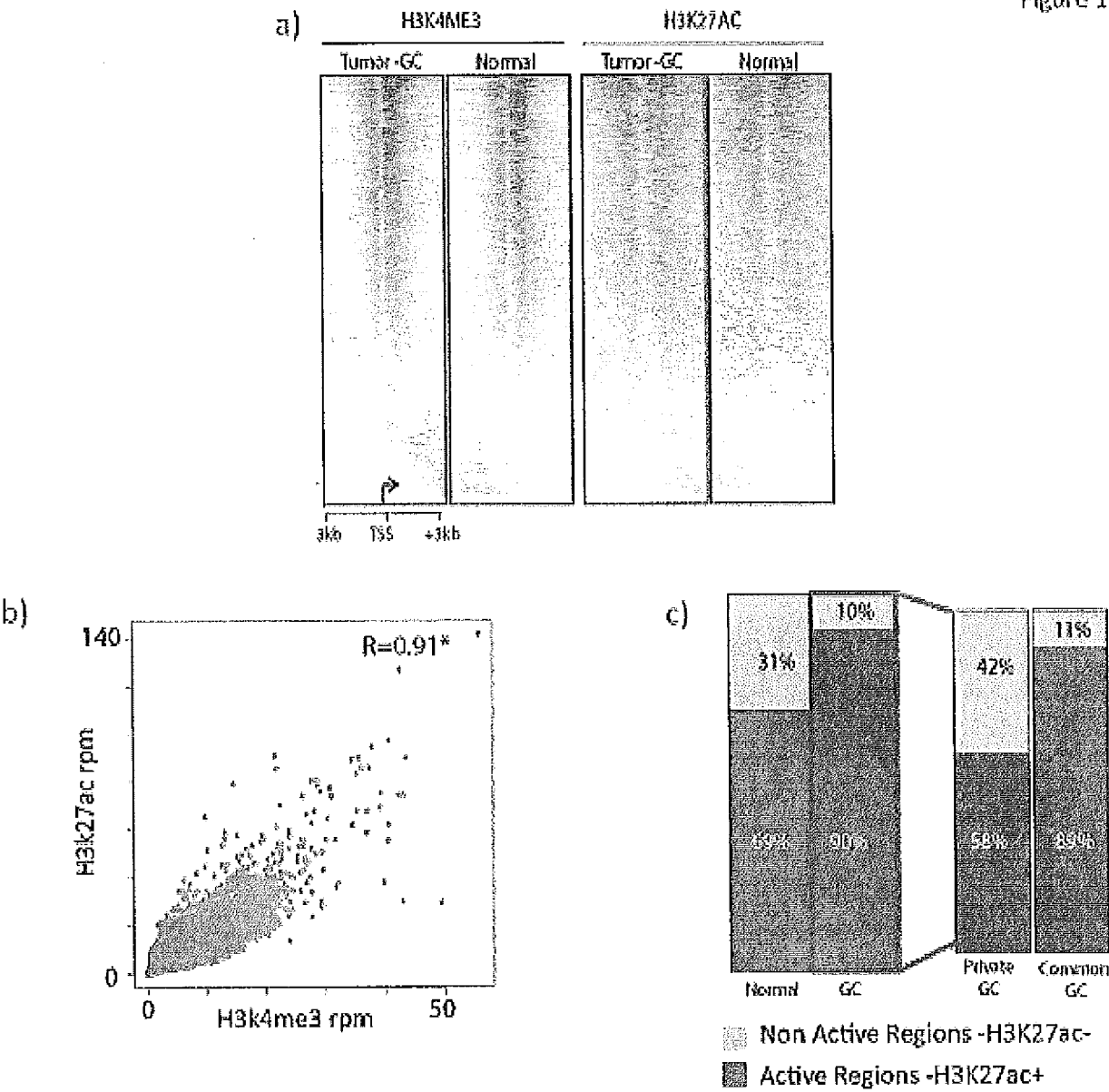


Fig. 22

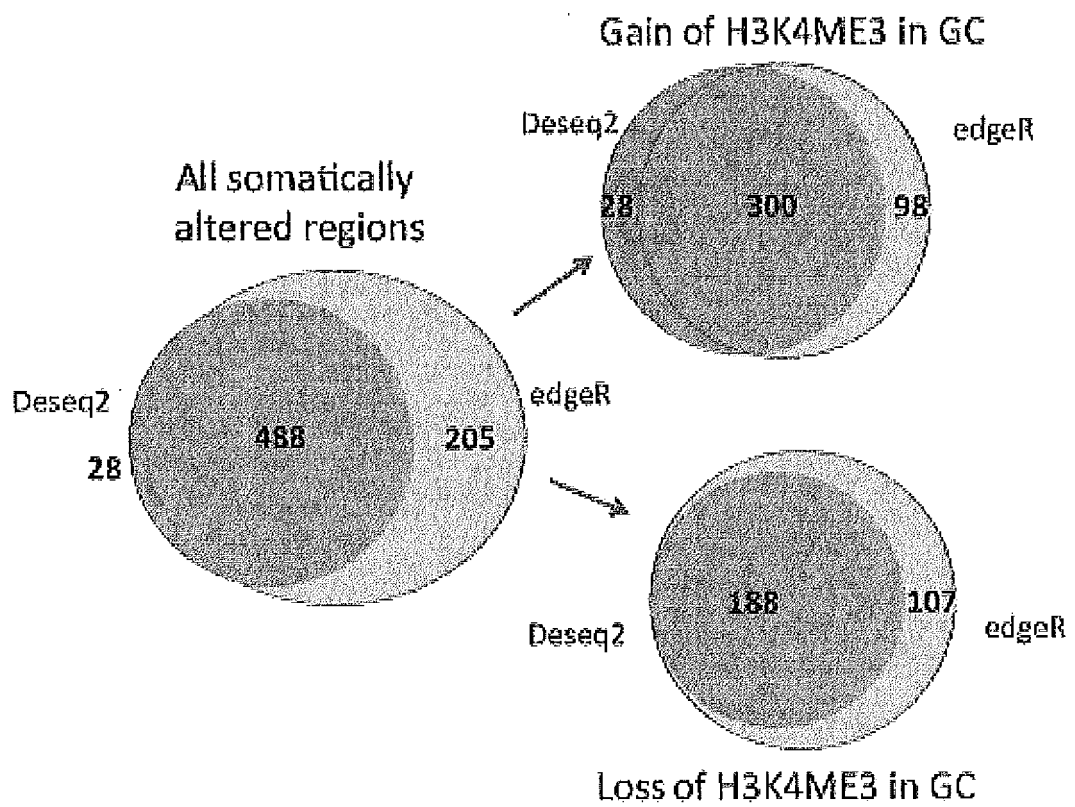
Figure 1



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Fig. 23

a)



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Fig. 23

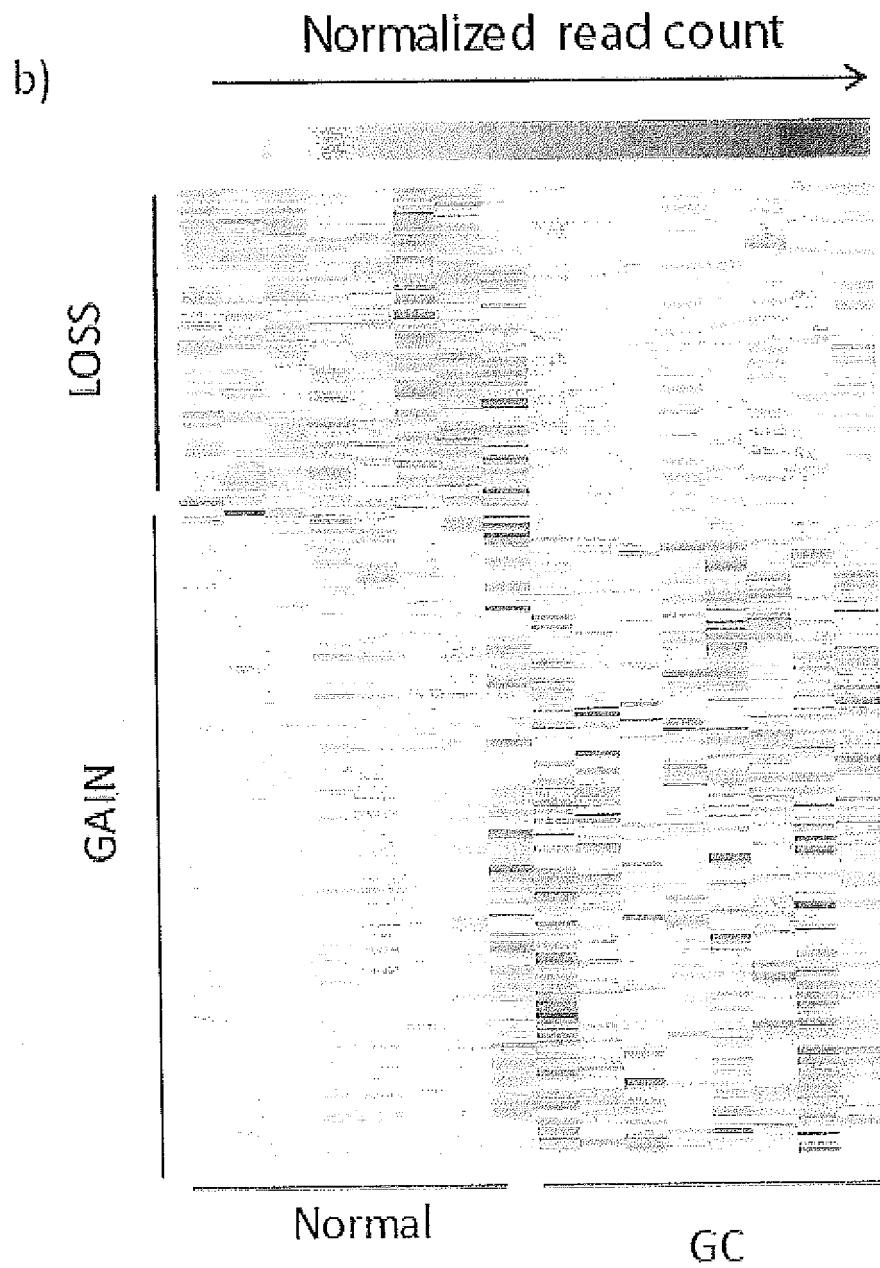


Fig 23.

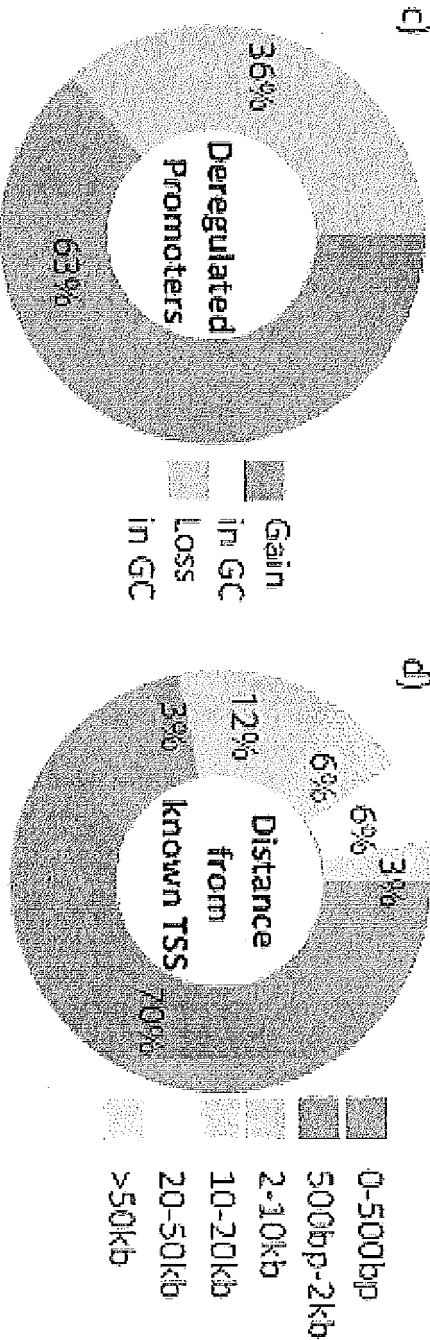


Fig 23.

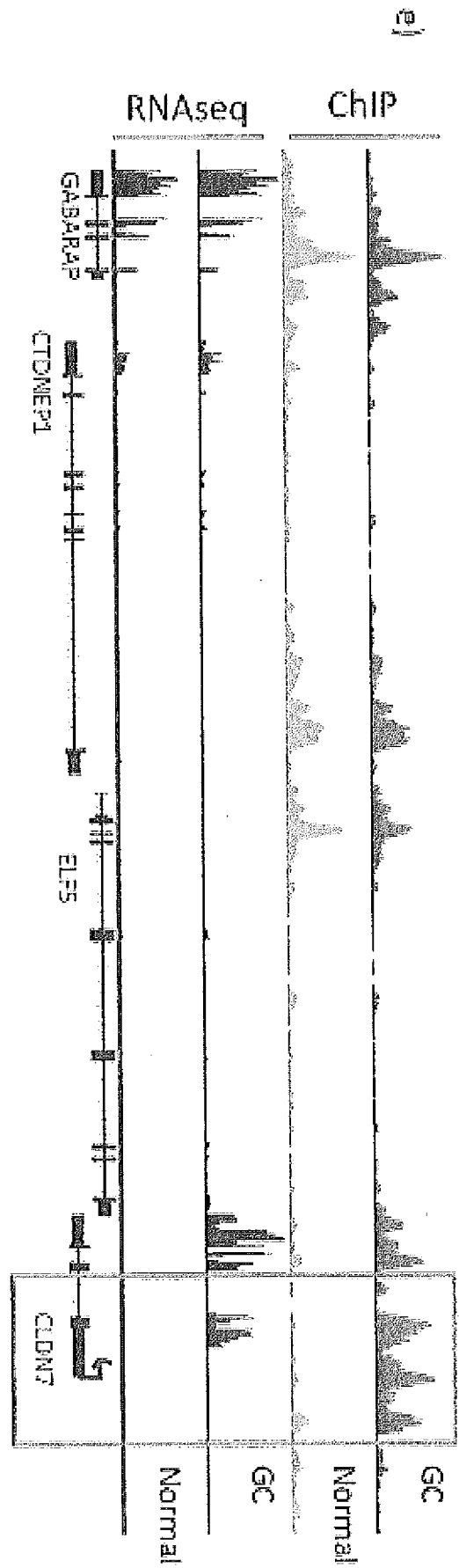


Fig. 24

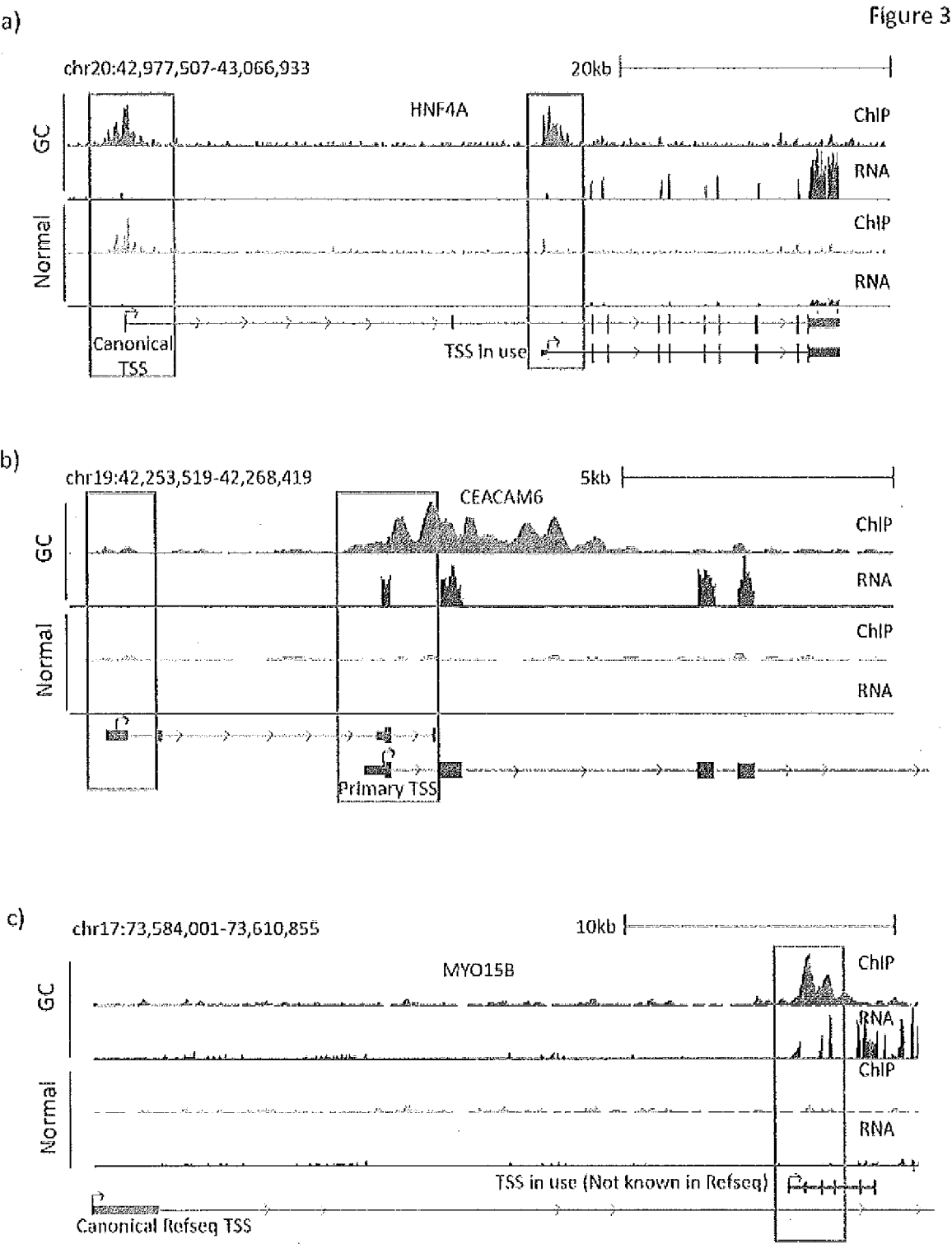


Fig. 25

