Fig. 1

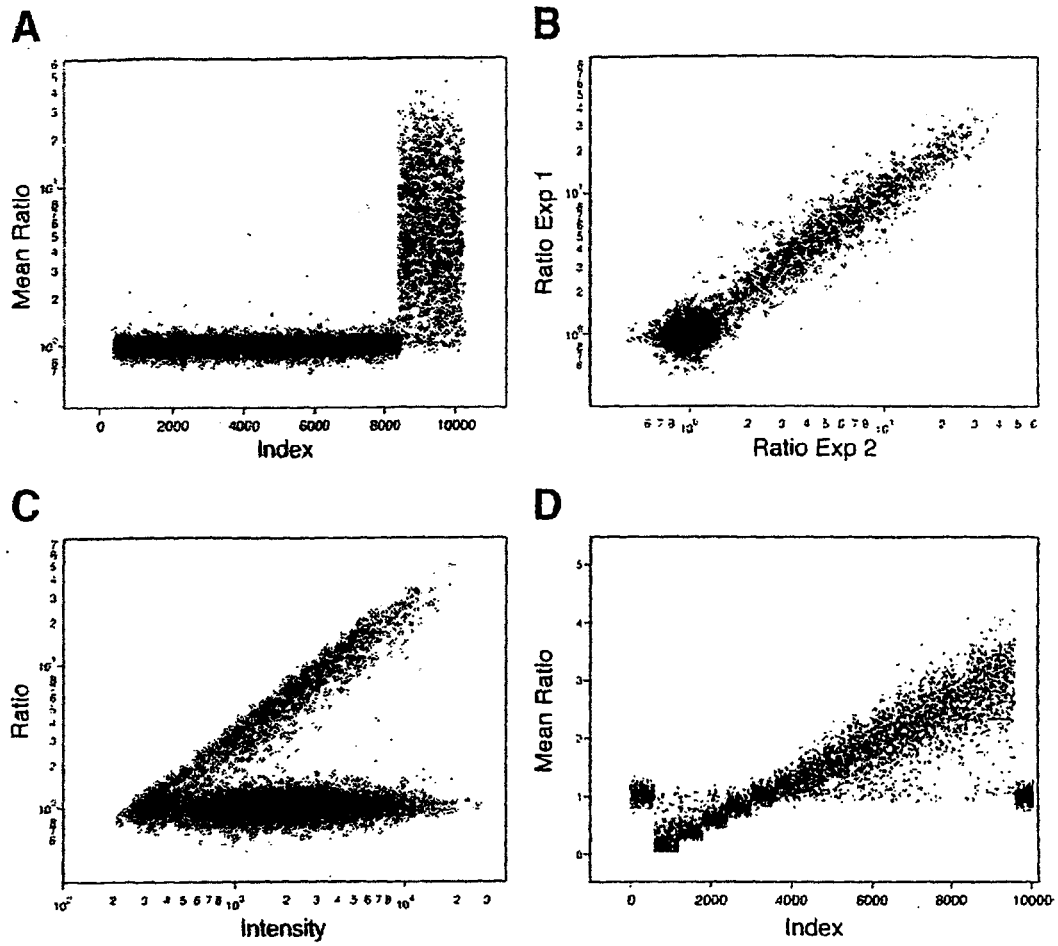
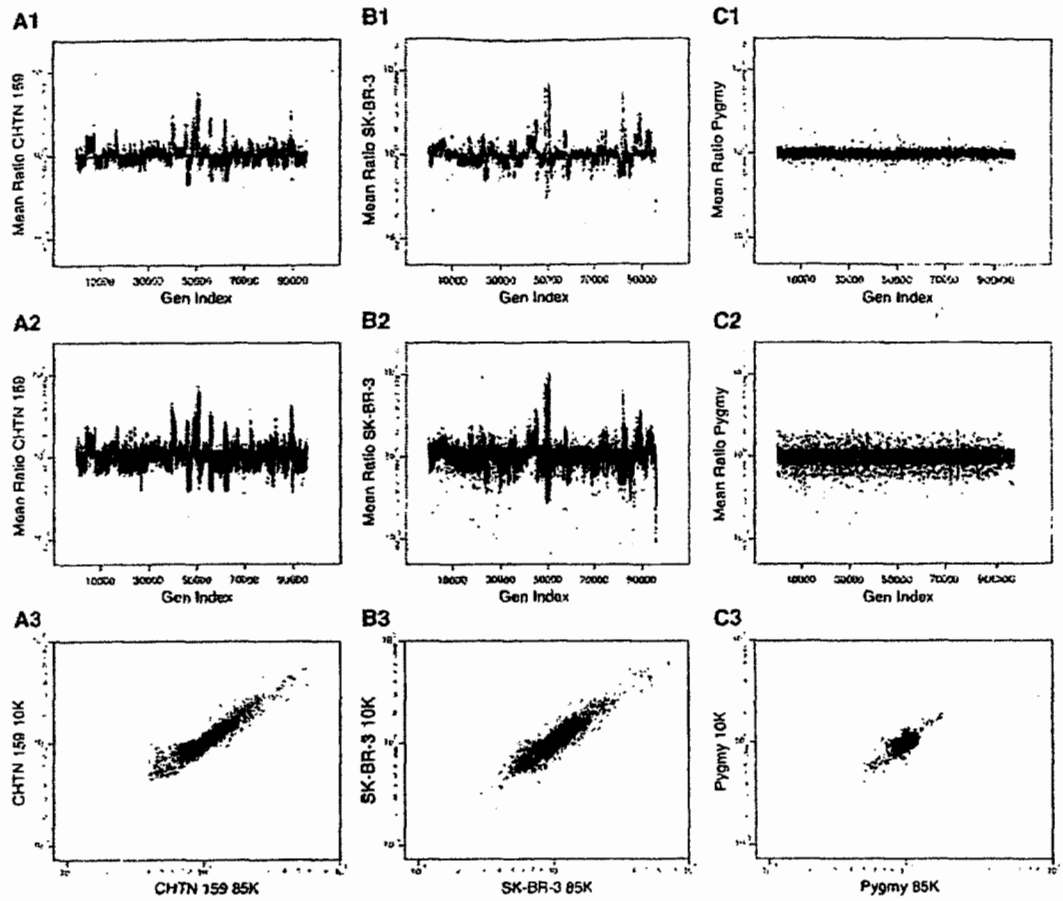

A
Mean Ratio
Index
B
Ratio Exp 1
Ratio Exp 2
C
Ratio
Intensity
D
Mean Ratio
Index

Fig. 2


A1
Mean Ratio CHTN 159
Gen Index
B1
Mean Ratio SK-BR-3
Gen Index
C1
Mean Ratio Pygmy
Gen Index
A2
Mean Ratio CHTN 159
Gen Index
B2
Mean Ratio SK-BR-3
Gen Index
C2
Mean Ratio Pygmy
Gen Index
A3
CHTN 159 10K
CHTN 159 85K
B3
SK-BR-3 10K
SK-BR-3 85K
C3
Pygmy 10K
Pygmy 85K

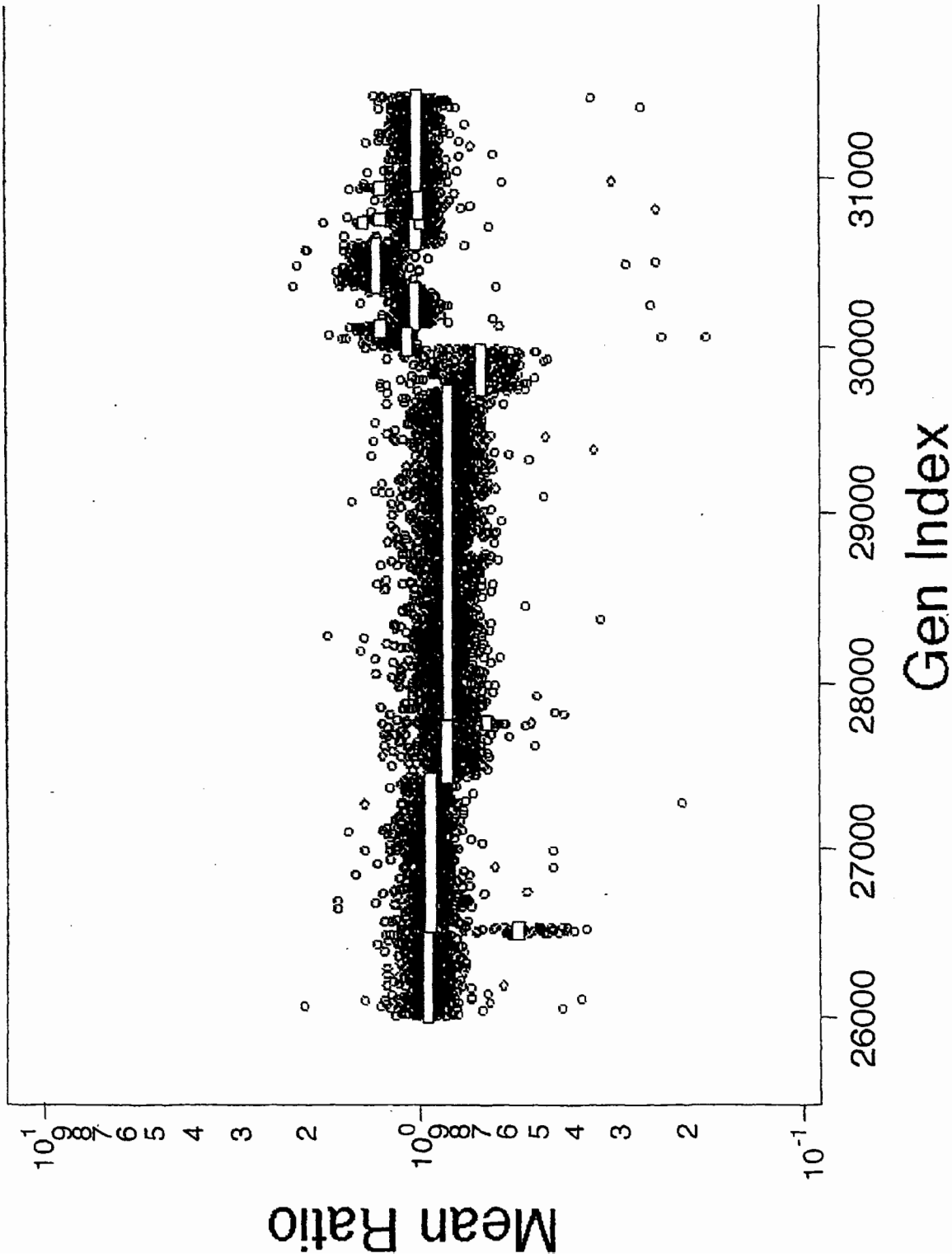

Mean Ratio
10^{1}
8
7
6
5
4
3
2
10^{0}
8
7
6
5
4
3
2
10^{-1}
26000
27000
28000
29000
30000
31000
Gen Index

FIG. 3A

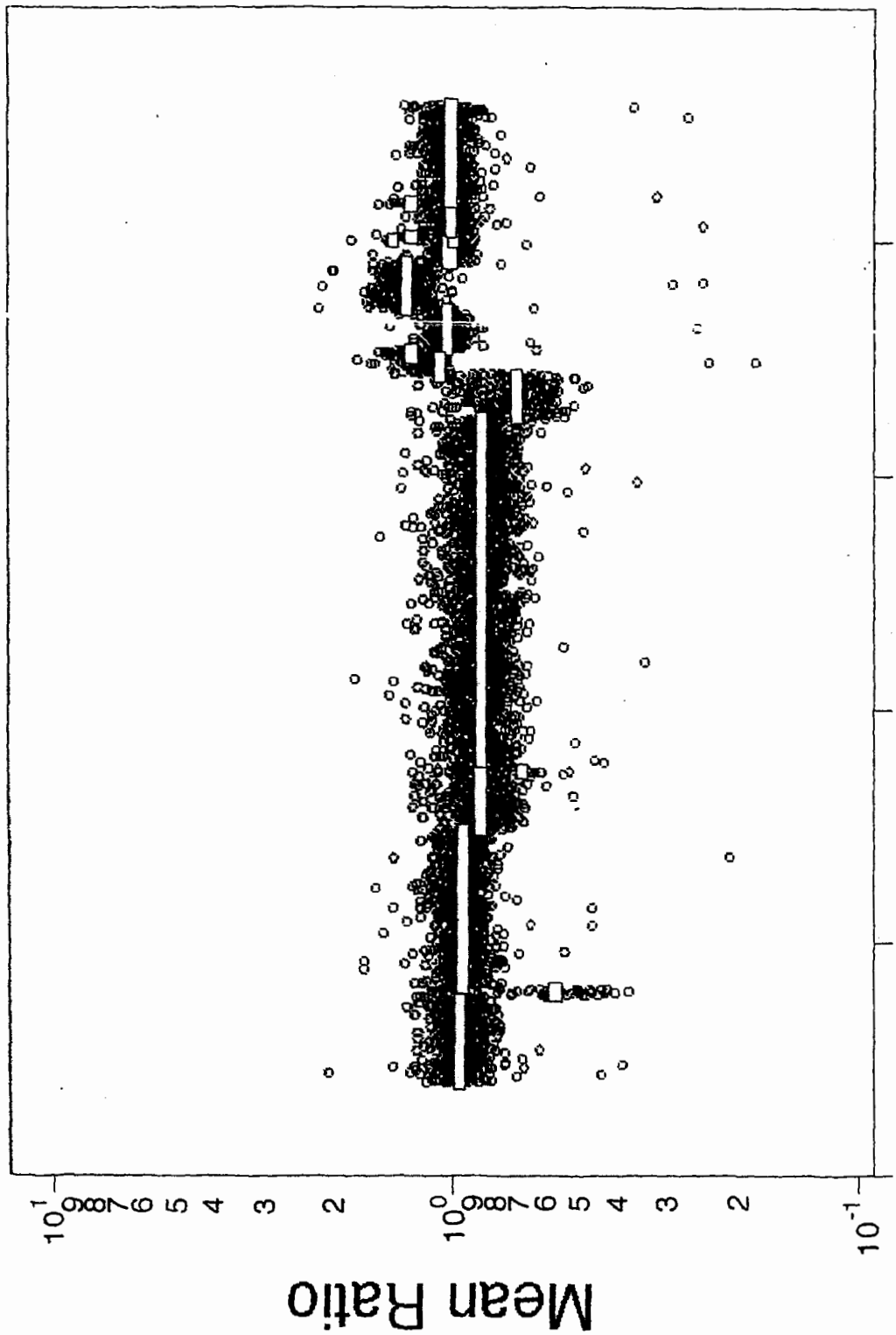


FIG. 3B

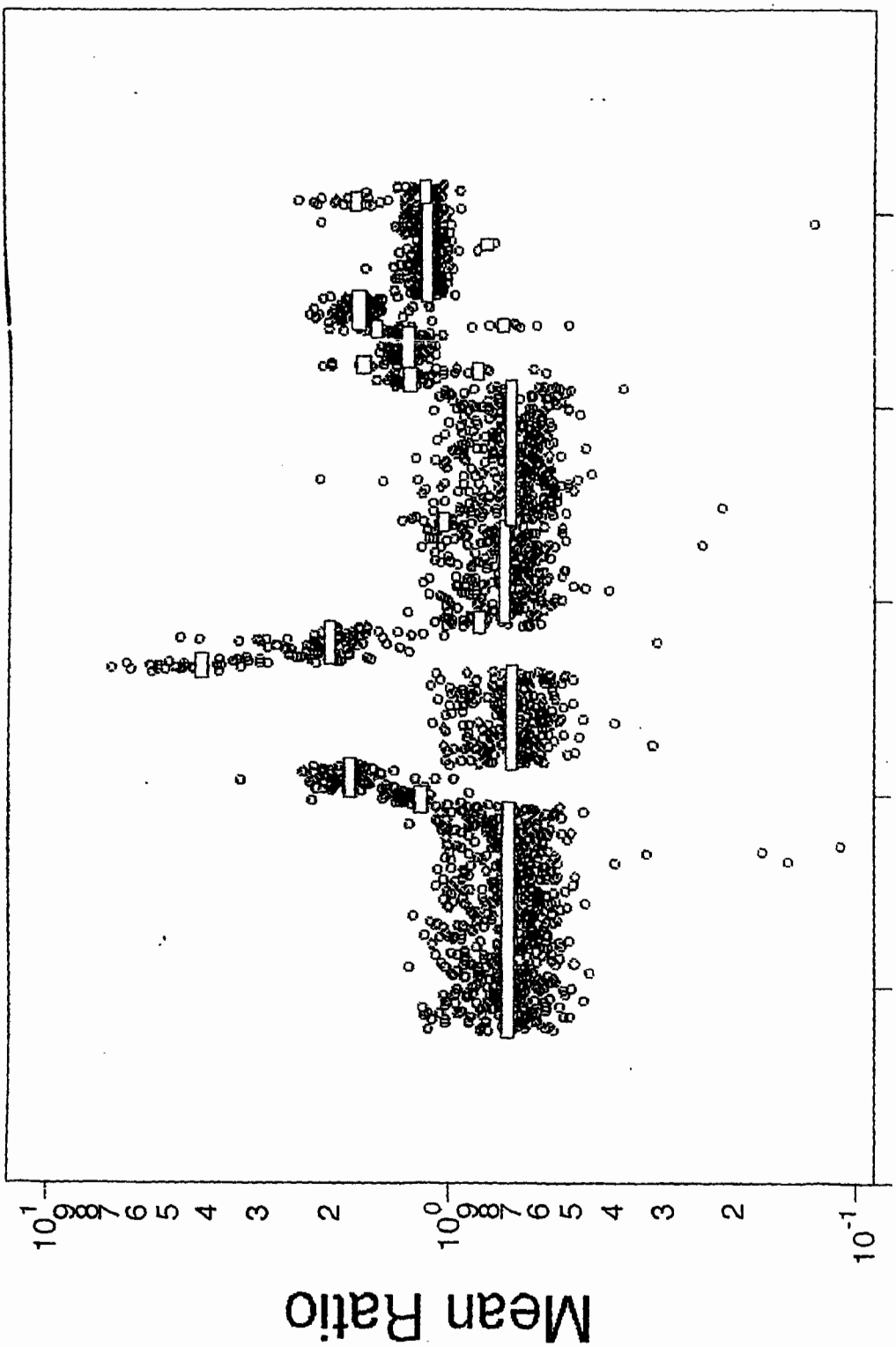

Mean Ratio
Gen Index
41000
42000
42000
43000
44000
45000
10^{1}
10^{0}
10^{-1}

FIG. 3C

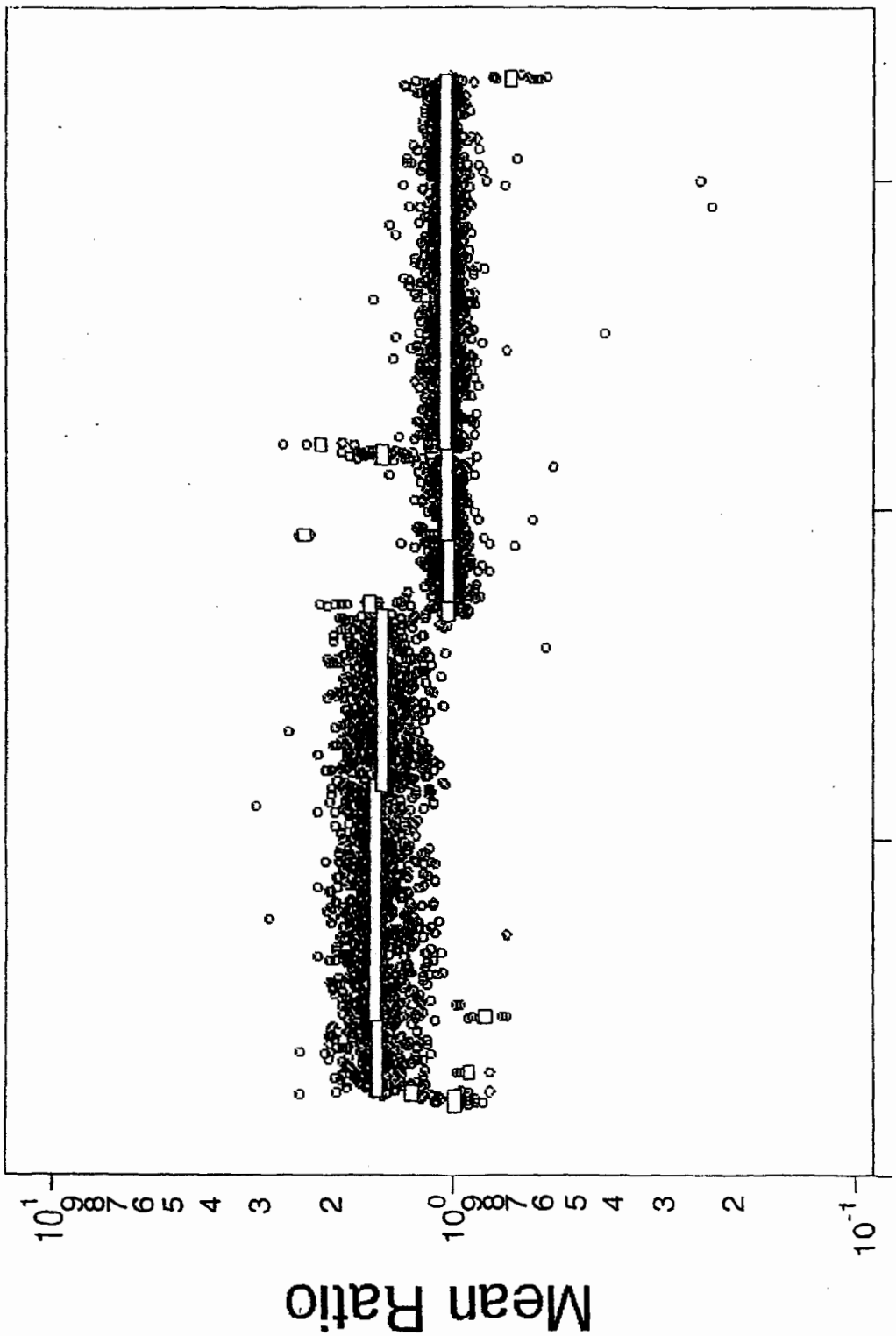
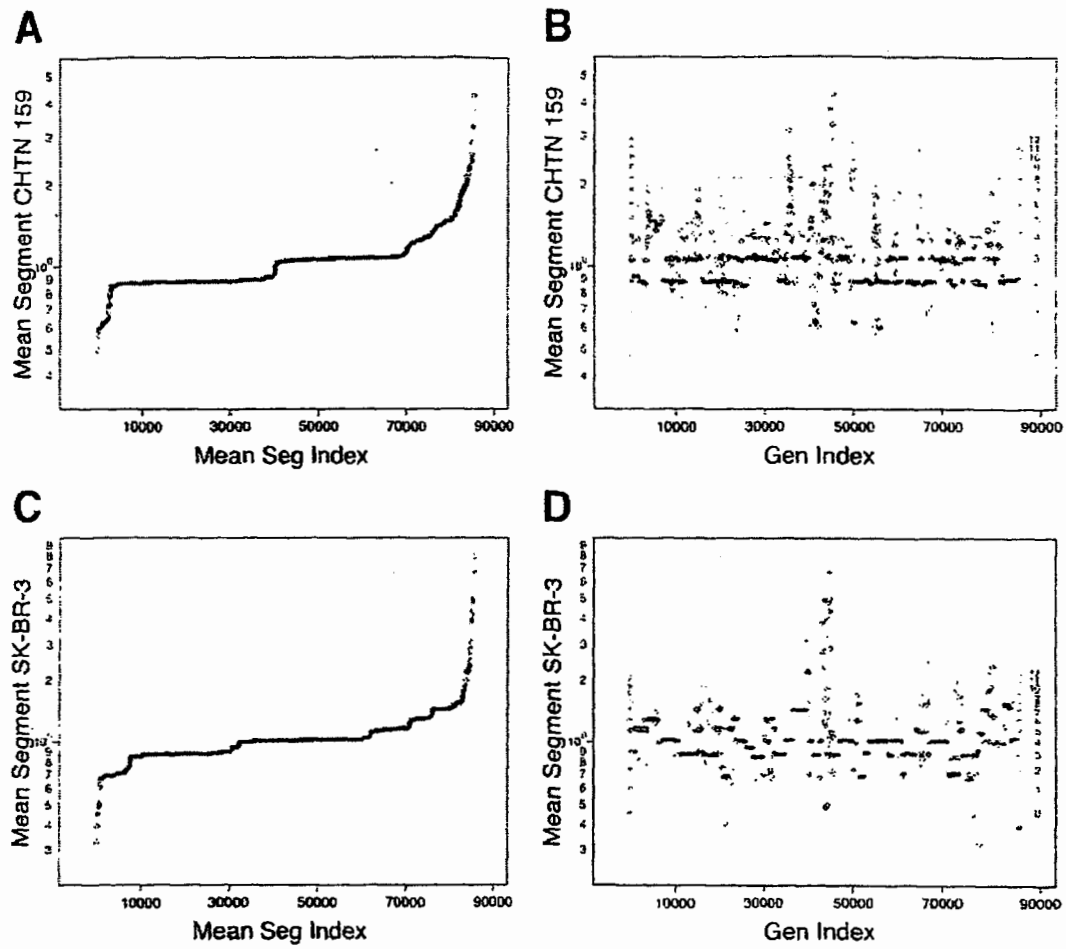


FIG. 3D

Fig. 4


A
Mean Segment CHTN 159
Mean Seg Index
B
Mean Segment CHTN 159
Gen Index
C
Mean Segment SK-BR-3
Mean Seg Index
D
Mean Segment SK-BR-3
Gen Index

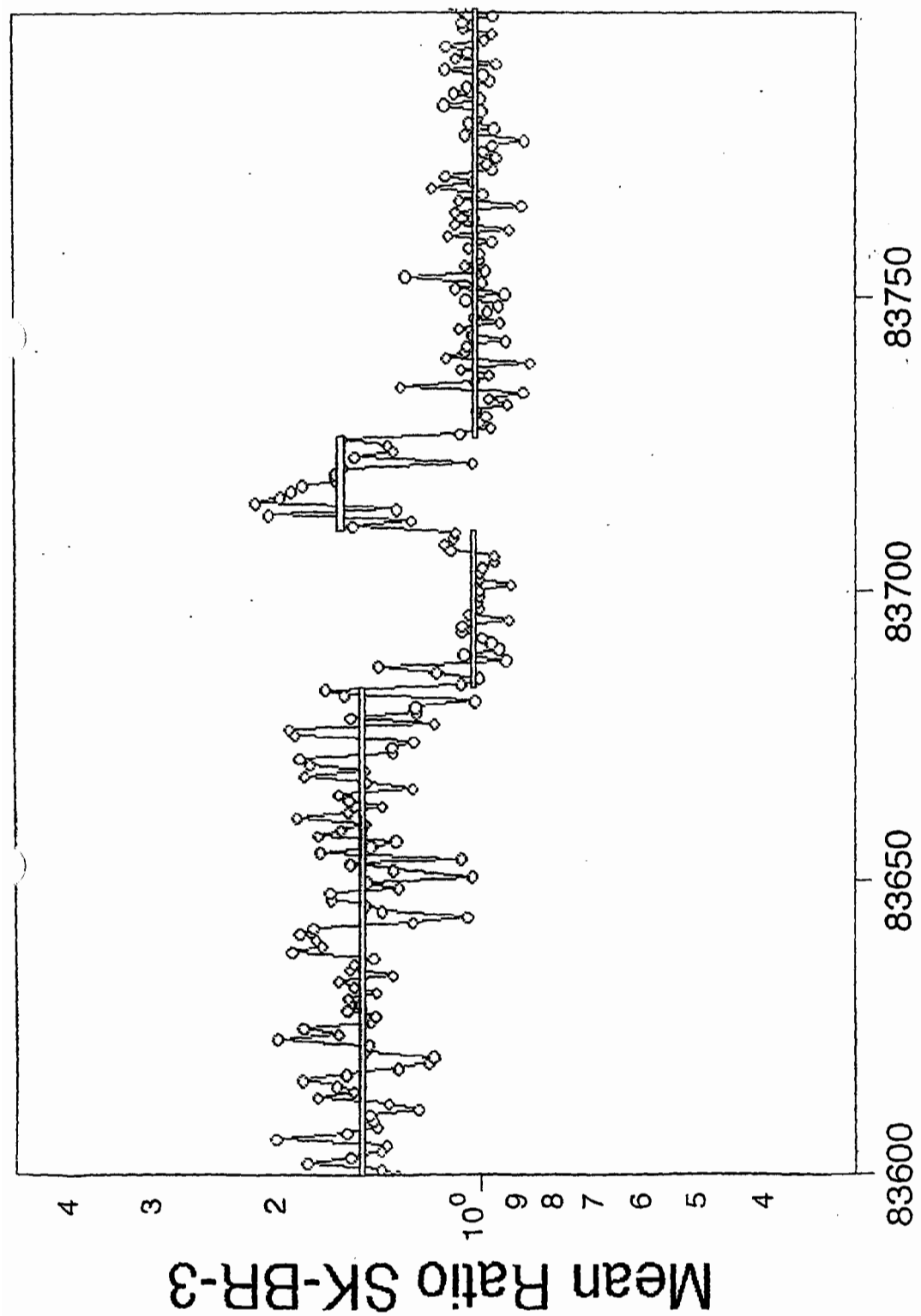

Mean Ratio SK-BR-3
4
3
2
10^0
9
8
7
6
5
4
83600
83650
83700
83750
Gen Index

FIG. 5A


Mean Ratio SK-BR-3
2
10^1
8
7
6
5
4
3
2
10^0
8
7
6
44900
44950
45000
45050
45100
45150
Gen Index

FIG. 5B

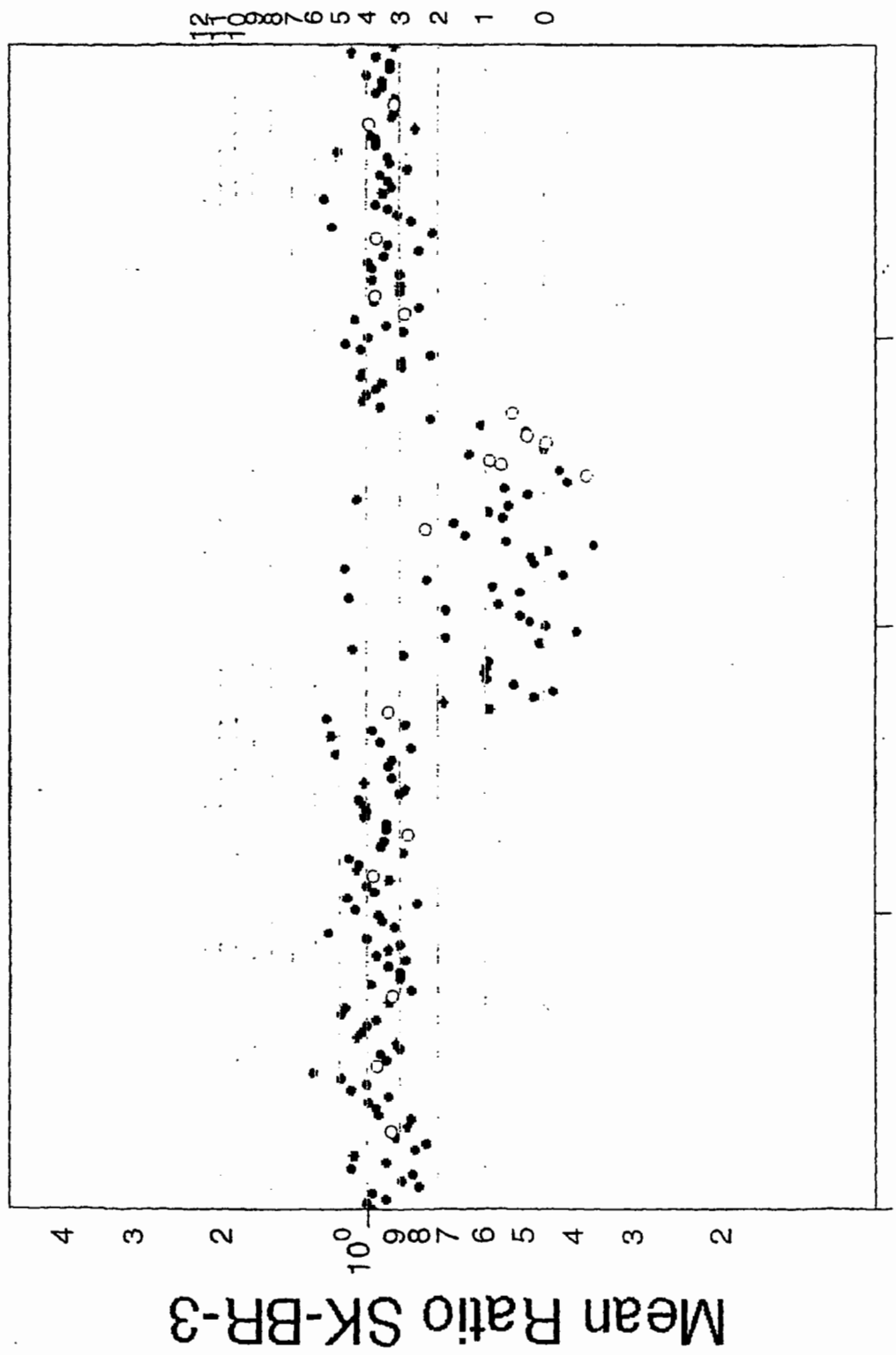


FIG. 5C

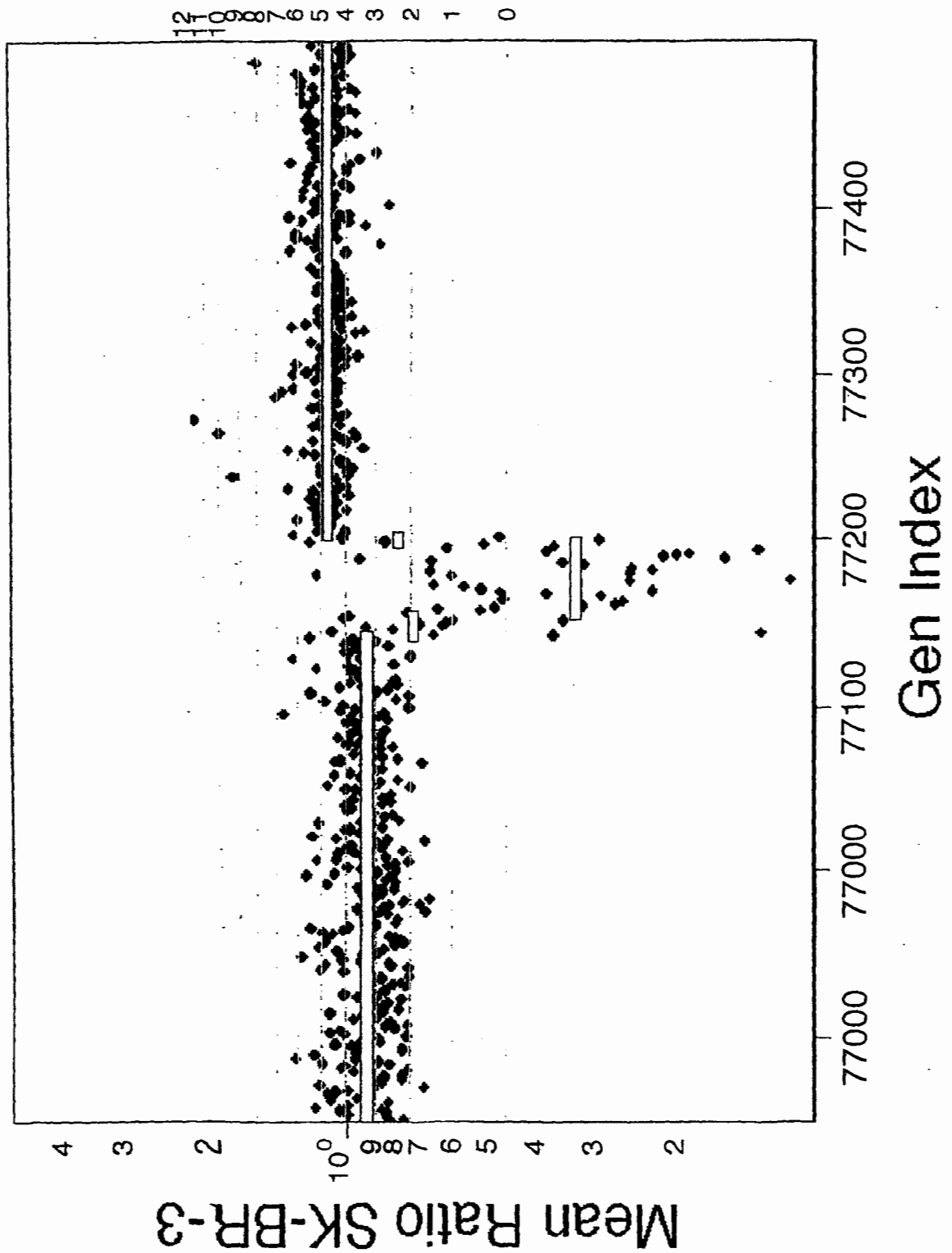


FIG. 5D

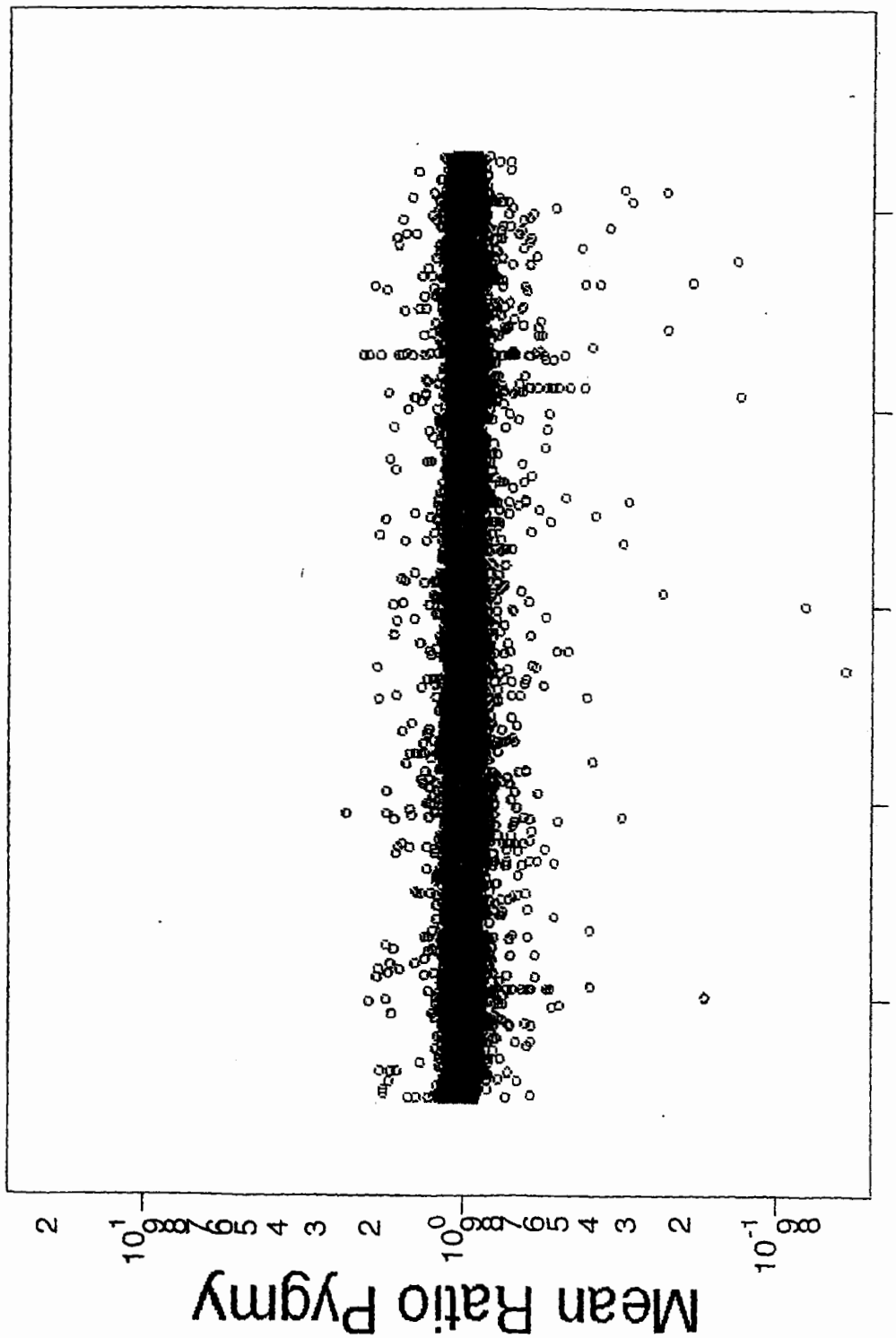


FIG. 6A

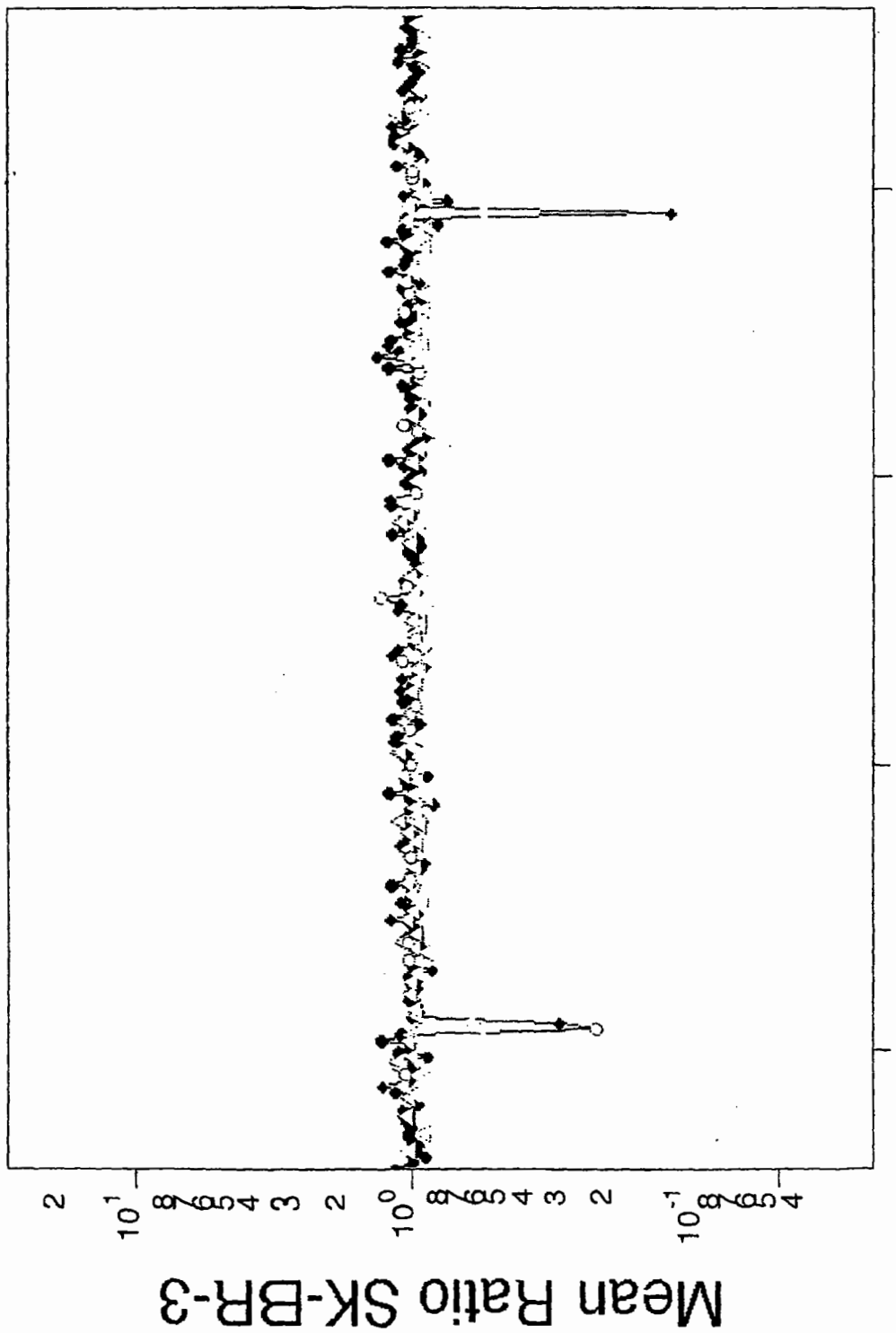


FIG. 6B

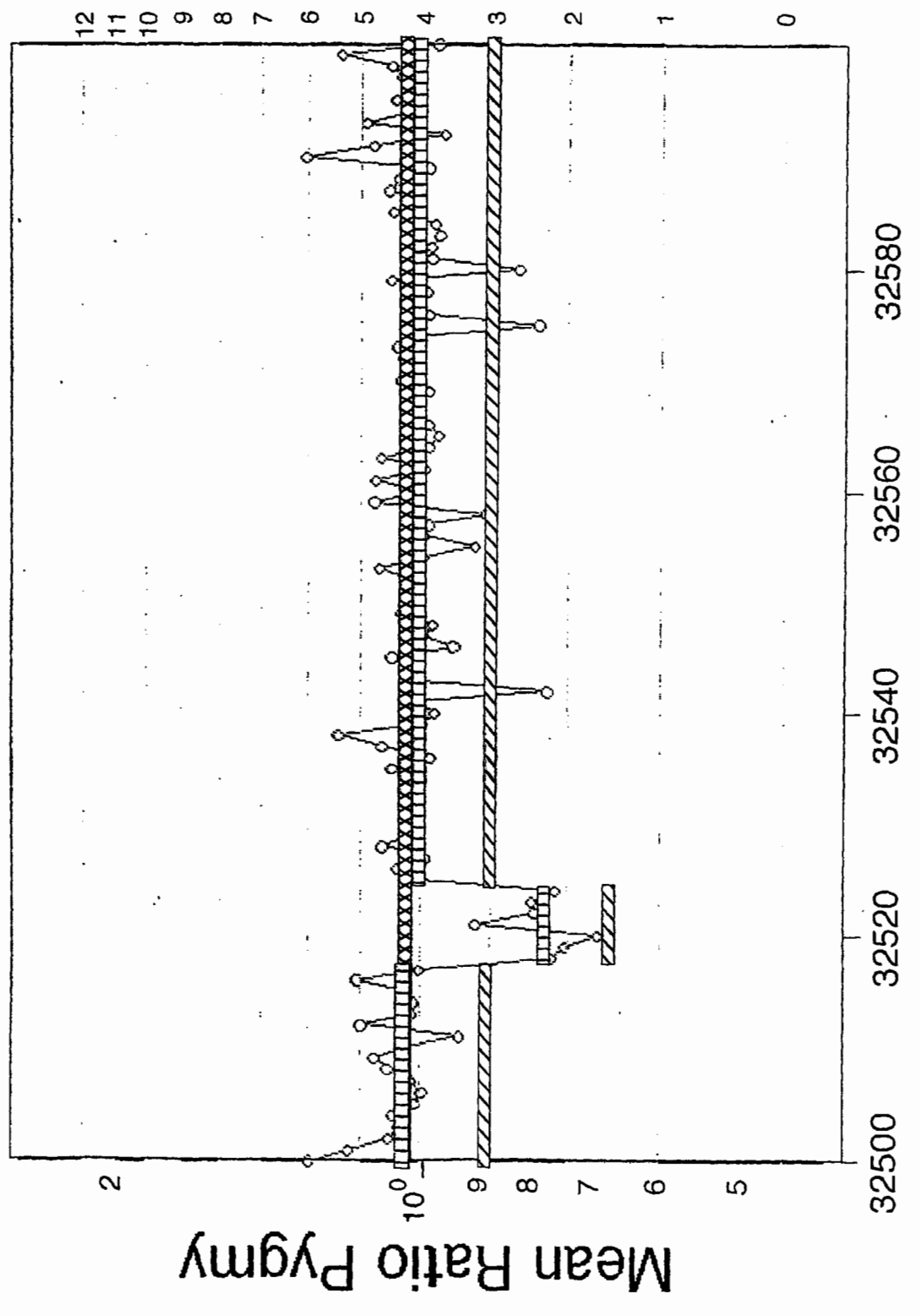

Mean Ratio Pygmy
Gen Index
32500
32520
32540
32560
32580
0
1
2
3
4
5
6
7
8
9
10
11
12

FIG. 6C

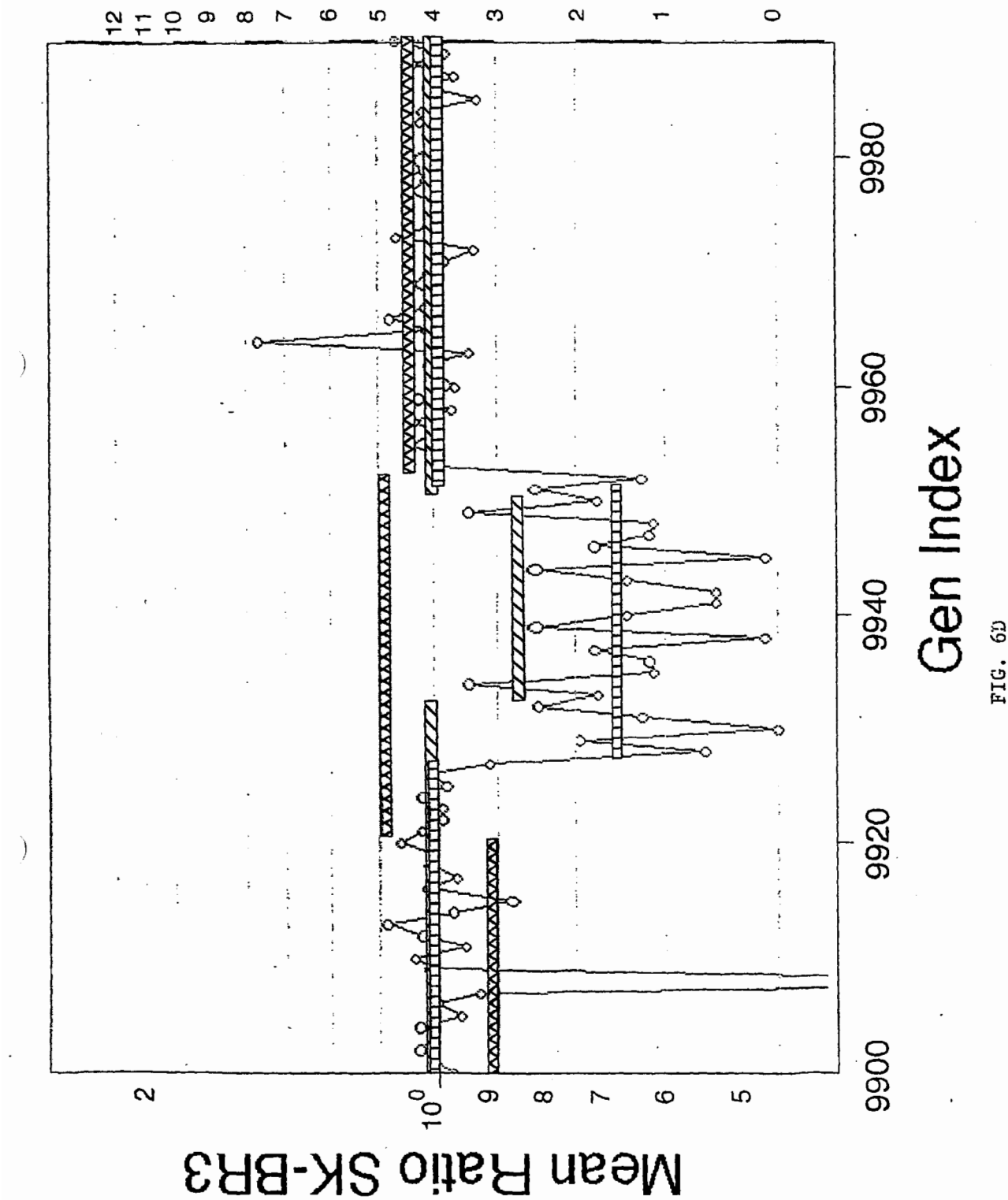

Mean Ratio SK-BR3
Gen Index
9900
9920
9940
9960
9980
0
1
2
3
4
5
6
7
8
9
10
11
12

FIG. 6D

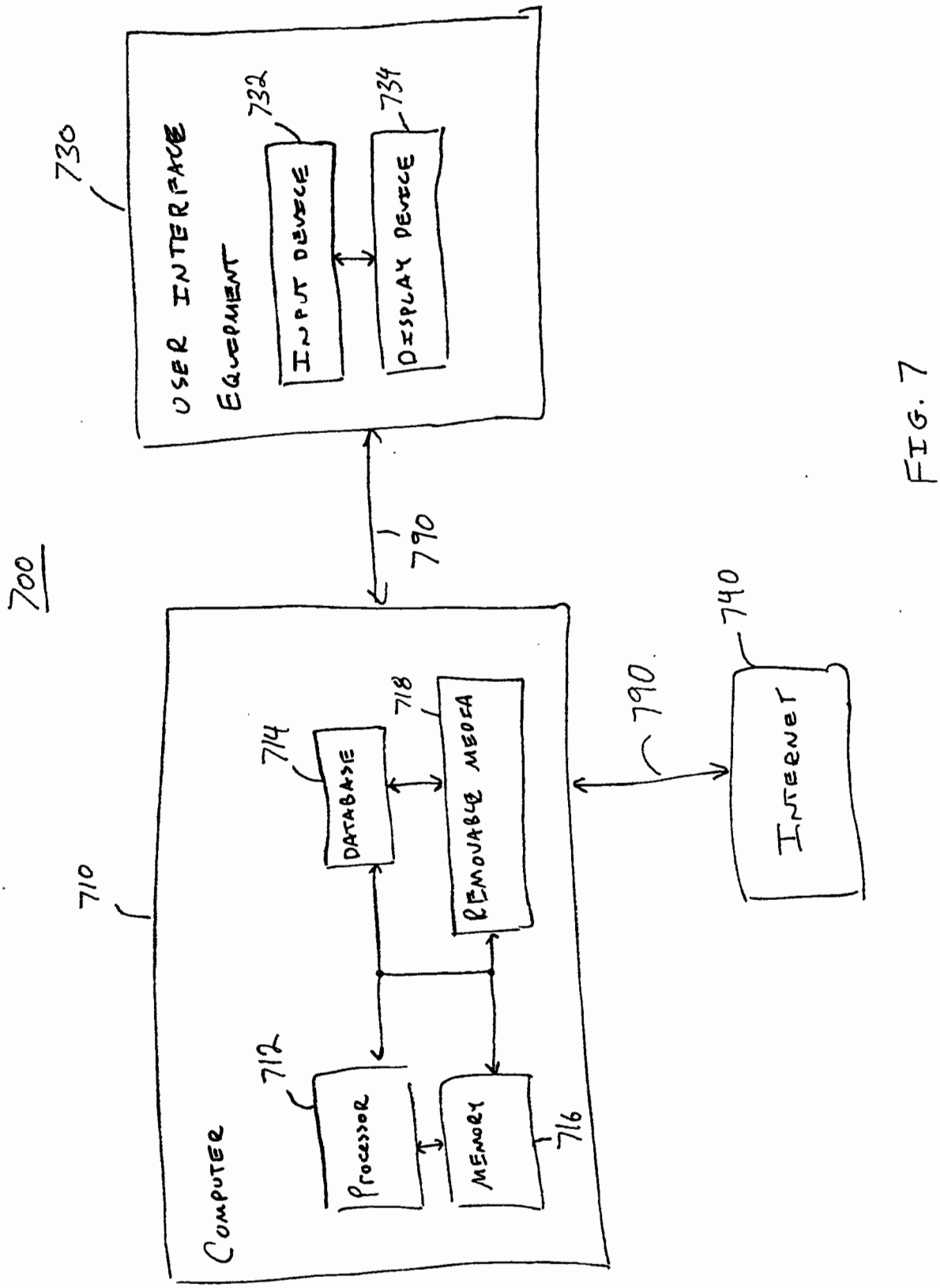

700
730
USER INTERFACE EQUIPMENT
732
INPUT DEVICE
734
DISPLAY DEVICE
790
710
COMPUTER
712
PROCESSOR
716
MEMORY
714
DATABASE
718
REMOVABLE MEDIA
790
740
INTERNET

FIG. 7

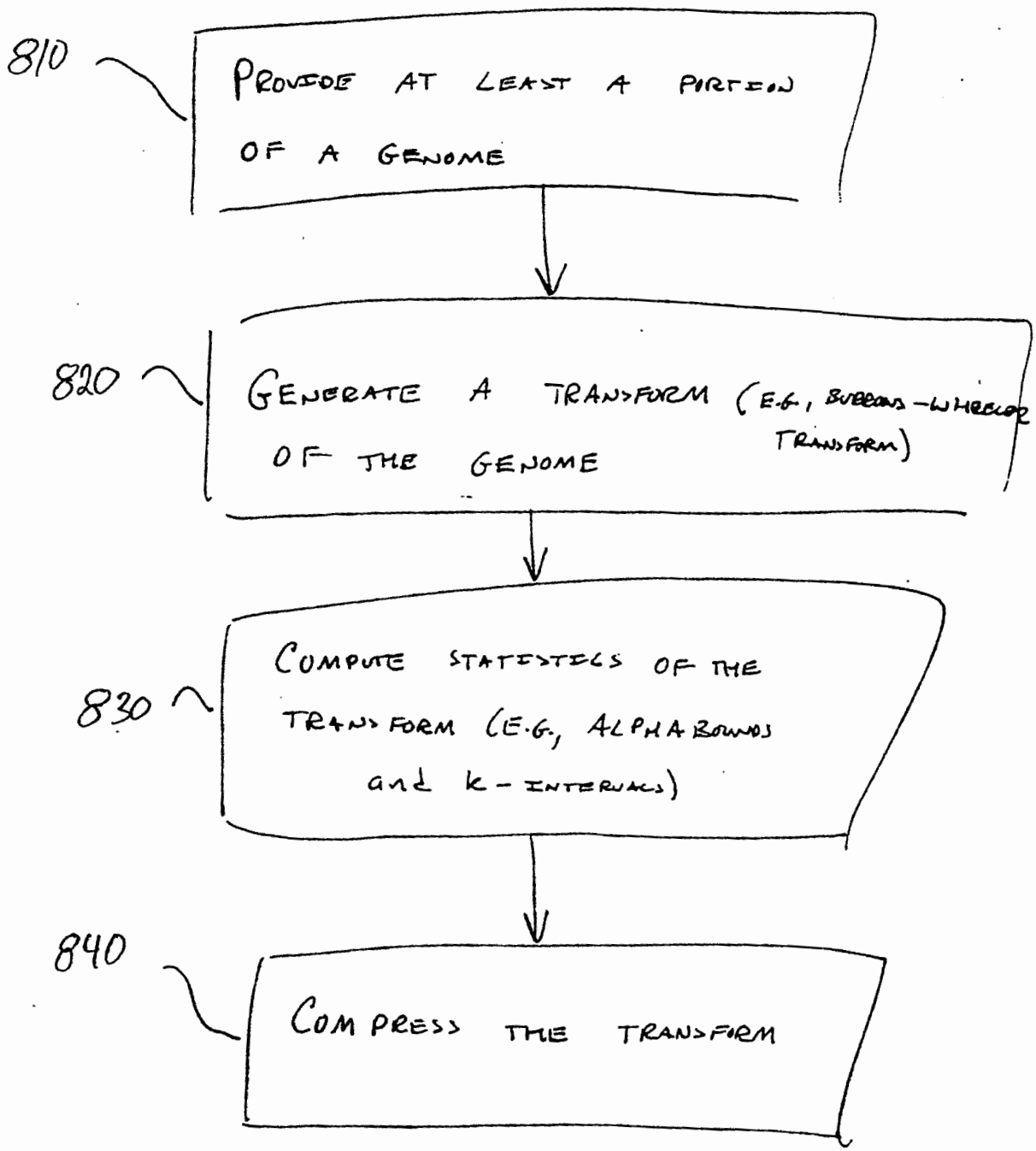

810
PROVIDE AT LEAST A PORTION OF A GENOME
820
GENERATE A TRANSFORM (E.G., BURROWS-WHEELER TRANSFORM) OF THE GENOME
830
COMPUTE STATISTICS OF THE TRANSFORM (E.G., ALPHABOUNDS and k-INTERVALS)
840
COMPRESS THE TRANSFORM

FIG. 8

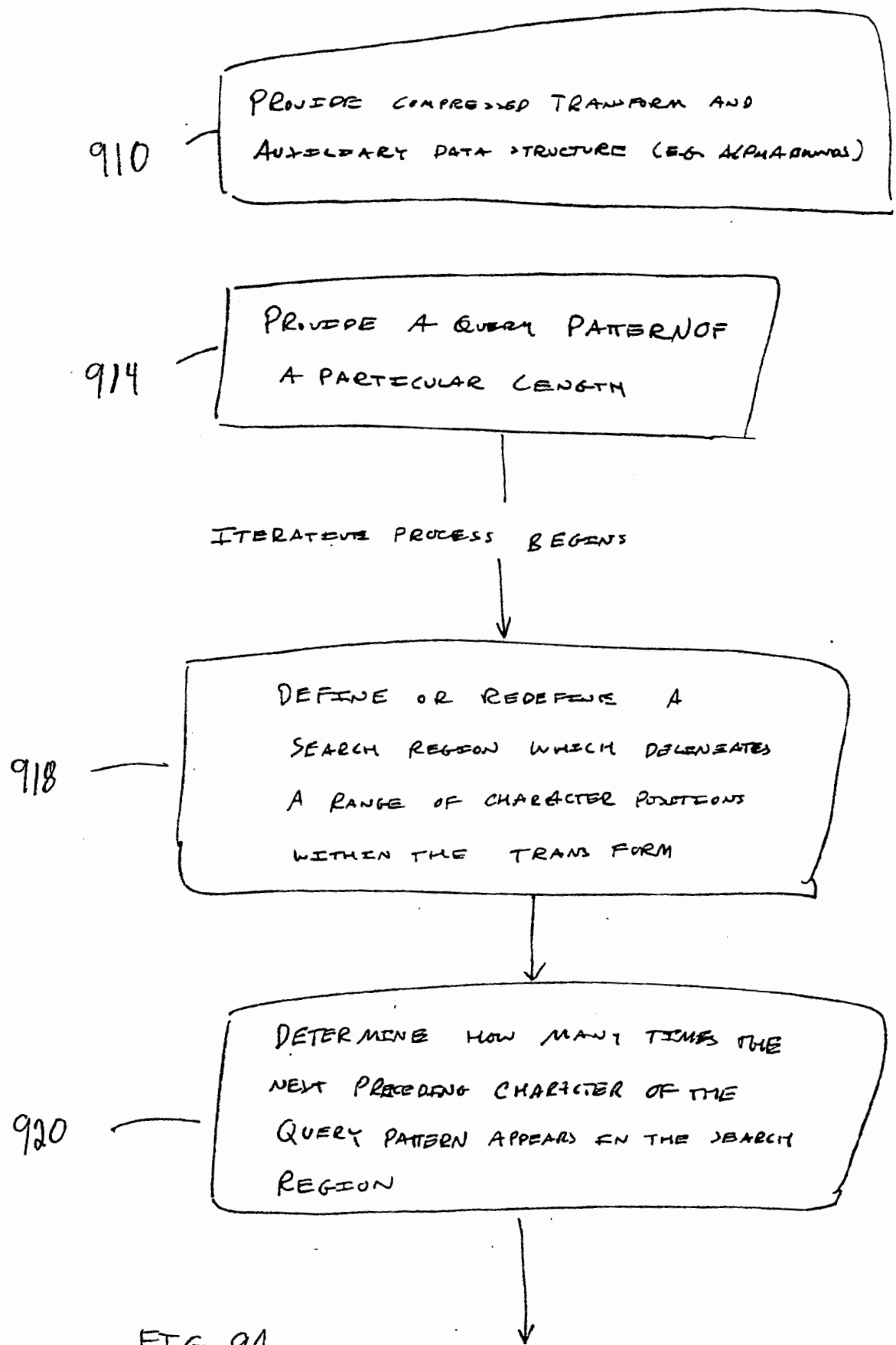

910
PROVIDE COMPRESSED TRANSFORM AND AUXILIARY DATA STRUCTURE (E.G. ALPHABANDS)
914
PROVIDE A QUERY PATTERN OF A PARTICULAR LENGTH
ITERATIVE PROCESS BEGINS
918
DEFINE OR REDEFINE A SEARCH REGION WHICH DELINEATES A RANGE OF CHARACTER POSITIONS WITHIN THE TRANSFORM
920
DETERMINE HOW MANY TIMES THE NEXT PRECEDING CHARACTER OF THE QUERY PATTERN APPEARS IN THE SEARCH REGION

FIG. 9A

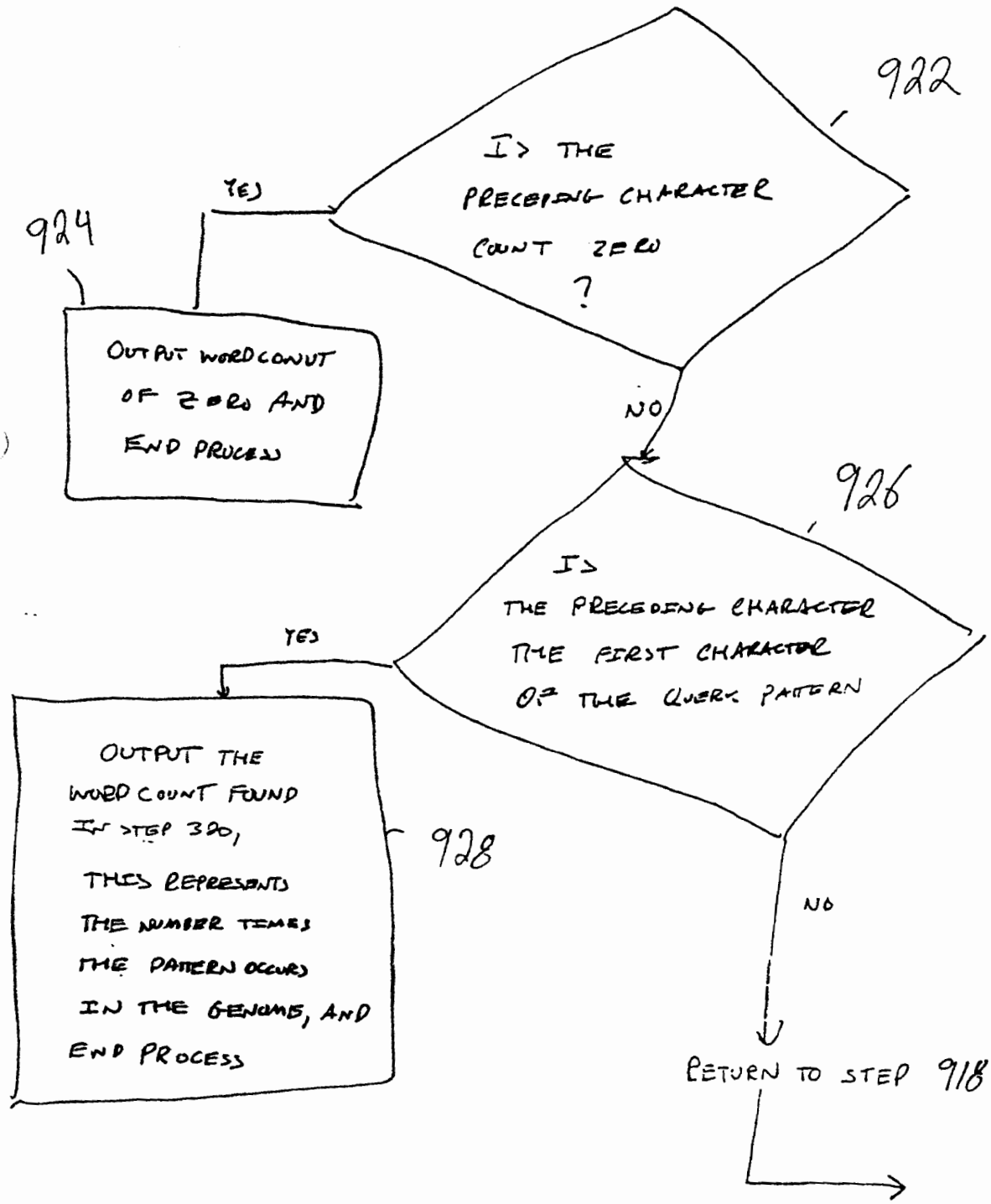

922
IS THE PRECEDING CHARACTER COUNT ZERO ?
YES
924
OUTPUT WORDCOUNT OF ZERO AND END PROCESS
NO
926
IS THE PRECEDING CHARACTER THE FIRST CHARACTER OF THE QUERY PATTERN
YES
OUTPUT THE WORD COUNT FOUND IN STEP 320, THIS REPRESENTS THE NUMBER TIMES THE PATTERN OCCURS IN THE GENOME, AND END PROCESS
928
NO
RETURN TO STEP 918

FIG. 9B

Position	Transform	
0	T	
1	G	
2	A	AG BLOCK
3	C	
4	C	
5	A	
6	T	
7	A	
8	A	
9	A	
10	G	

FIG. 10B

Position	Transform	
0	T	
1	G	
2	A	
3	C	
4	C	
5	A	
6	T	
7	A	G BLOCK
8	A	
9	A	
10	G	

FIG. 10A

0 1 2 3 4 5 6 7 8 9 10
A G A C A G T C A T $
10 → $ A G A C A G T C A T
2 → A C A G G T C A T $ A G
0 → A G A C A G T C A T $ A G G
4 → A G T C A T $ A G G A C
8 → A T $ A G G A C A G T C
3 → C A G T C A T $ A G G A C A
7 → C A T $ A G G T C A T $ A G
1 → G A C A G T C A T $ A G G A C
5 → G T C A T $ A G G A C A G T C
9 → T $ A G G A C A G T C A T
6 → T C A T $ A G G A C A G T C
3
7
COORDINATES THAT ARE CARRIED OVER TO THE TRANSFORM FROM THE SUFFIX ARRAY

FIG. 11

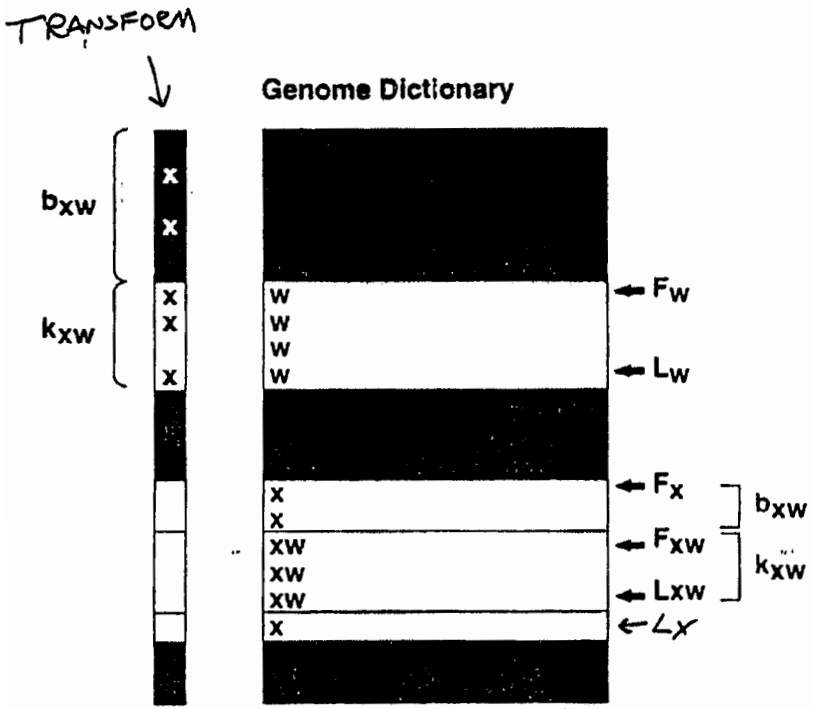


FIG. 12A

1. $W \leftarrow Z[N]$
2. $F_w, L_w \leftarrow$ alphabounds(W)
3. $k_w \leftarrow L_w - F_w + 1$
4. if $N = 1$, return k_w
5. for i in 1 to N-1
6. $X \leftarrow Z[N-i]$
7. $k_{xw} \leftarrow$ count of X's between F_w and L_w, inclusive, in the TRANSFORM
8. if $k_{xw} = 0$, return 0
9. $b_{xw} \leftarrow$ count of X's before F_w, in TRANSFORM
10. $F_x, L_x \leftarrow$ alphabounds (X)
11. $F_{xw} \leftarrow F_x + b_{xw}$
12. $L_{xw} \leftarrow F_{xw} + k_{xw} - 1$
13. $F_w \leftarrow F_{xw}$
14. $L_w \leftarrow L_{xw}$
15. return k_{xw}

FIG. 12B