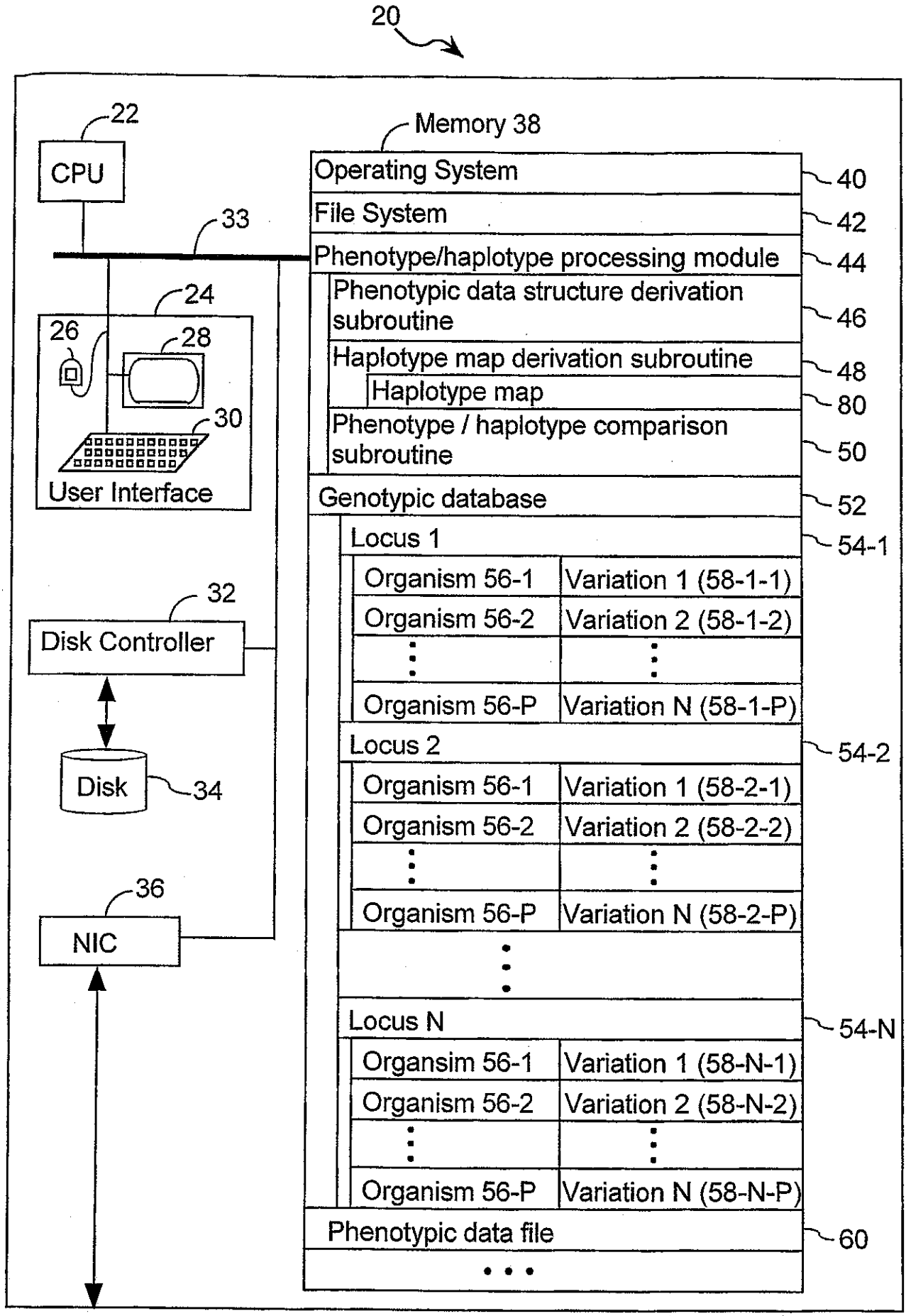

20
22
CPU
33
24
26
28
30
User Interface
32
Disk Controller
Disk
34
36
NIC
Memory 38
Operating System
40
File System
42
Phenotype/haplotype processing module
44
Phenotypic data structure derivation subroutine
46
Haplotype map derivation subroutine
48
Haplotype map
80
Phenotype / haplotype comparison subroutine
50
Genotypic database
52
Locus 1
54-1
Organism 56-1
Variation 1 (58-1-1)
Organism 56-2
Variation 2 (58-1-2)
Organism 56-P
Variation N (58-1-P)
Locus 2
54-2
Organism 56-1
Variation 1 (58-2-1)
Organism 56-2
Variation 2 (58-2-2)
Organism 56-P
Variation N (58-2-P)
Locus N
54-N
Organsim 56-1
Variation 1 (58-N-1)
Organism 56-2
Variation 2 (58-N-2)
Organism 56-P
Variation N (58-N-P)
Phenotypic data file
60

FIG. 1

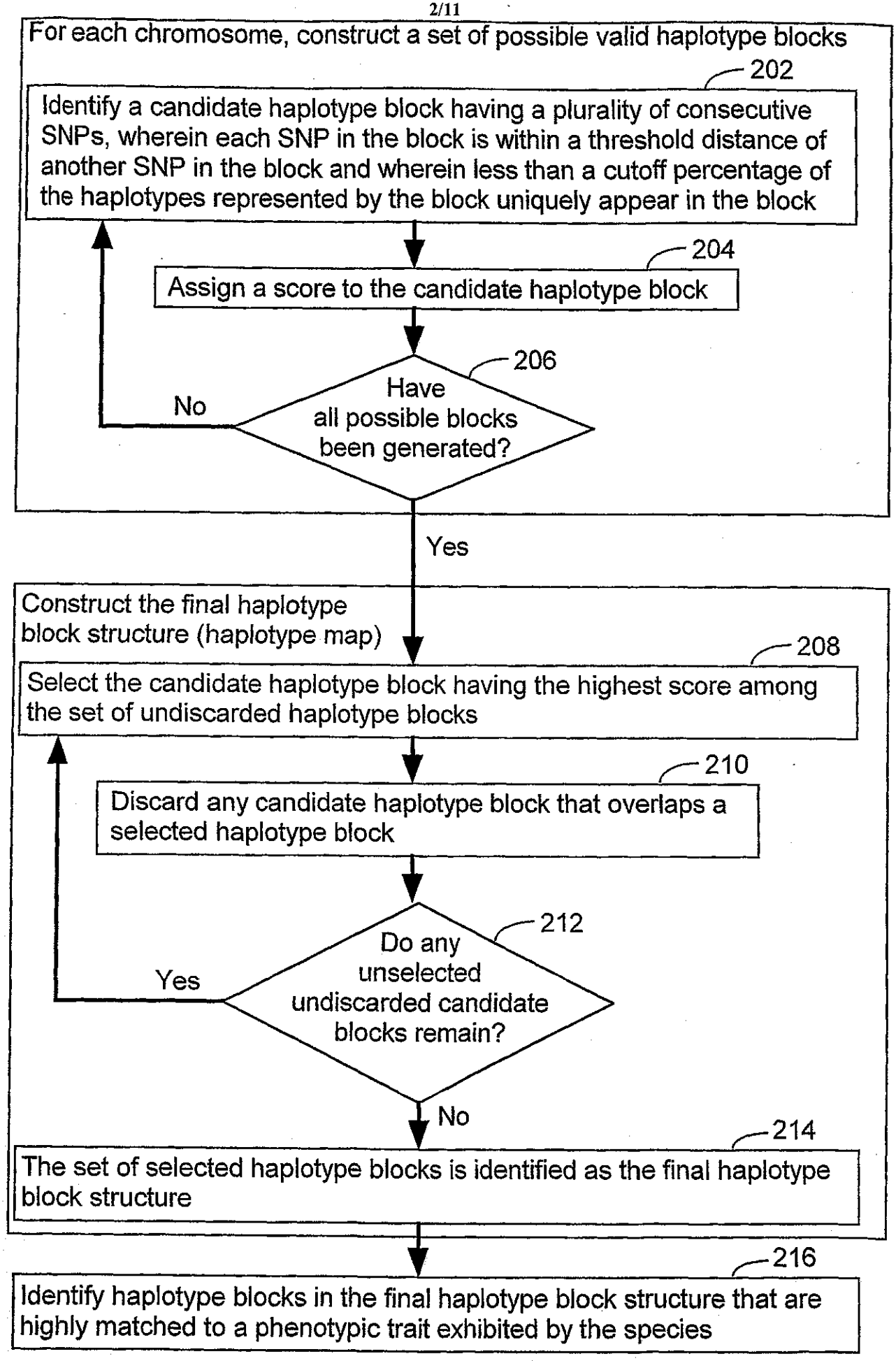

For each chromosome, construct a set of possible valid haplotype blocks
202
Identify a candidate haplotype block having a plurality of consecutive SNPs, wherein each SNP in the block is within a threshold distance of another SNP in the block and wherein less than a cutoff percentage of the haplotypes represented by the block uniquely appear in the block
204
Assign a score to the candidate haplotype block
206
Have all possible blocks been generated?
No
Yes
Construct the final haplotype block structure (haplotype map)
208
Select the candidate haplotype block having the highest score among the set of undiscarded haplotype blocks
210
Discard any candidate haplotype block that overlaps a selected haplotype block
212
Do any unselected undiscarded candidate blocks remain?
Yes
No
214
The set of selected haplotype blocks is identified as the final haplotype block structure
216
Identify haplotype blocks in the final haplotype block structure that are highly matched to a phenotypic trait exhibited by the species

FIG. 2

302

SNP#	A	B	C	D	E	F	G
SNP1	1	0	1	0	0	0	1
SNP2	1	0	1	0	1	1	0

304

Haplotype	Organism
1,1	A,C
0,0	B,D
0,1	E,F
1,0	G

FIG. 3A

306

SNP#	A	B	C	D	E	F	G
SNP1	1	0	1	0	0	0	1
SNP2	1	0	1	0	1	1	0
SNP3	1	0	1	0	1	1	0

304

Haplotype	Organism
1,1,1	A,C
0,0,0	B,D
0,1,1	E,F
1,0,0	G

FIG. 3B

310

SNP#	A	B	C	D	E	F	G
SNP1	1	0	1	0	0	0	1
SNP2	1	0	1	0	1	1	0
SNP3	1	0	1	0	1	1	0
SNP4	1	0	1	0	1	0	0

312

Haplotype	Organism
1,1,1,1	A,C
0,0,0,0	B,D
0,1,1,1	E
0,1,1,0	F
1,0,0,0	G

FIG. 3C

402

SNP#	A	B	C	D
SNP1	0	0	1	1
SNP2	1	1	0	0
SNP1	1	1	0	0
SNP2	0	0	1	1

Haplotype	Organism
0,1,1,0	A,B
1,0,0,1	C,D

FIG. 4A

406

SNP#	A	C	D	B
SNP1	1	1	1	0
SNP2	0	0	0	1
SNP1	1	1	1	0
SNP2	1	1	1	0

Haplotype	Organism
1,0,1,1	A,C,D
0,1,0,0	B

FIG. 4B

408

Phenotype	Value
P_A	6
P_B	7.5
P_C	20
P_D	22

FIG. 4C

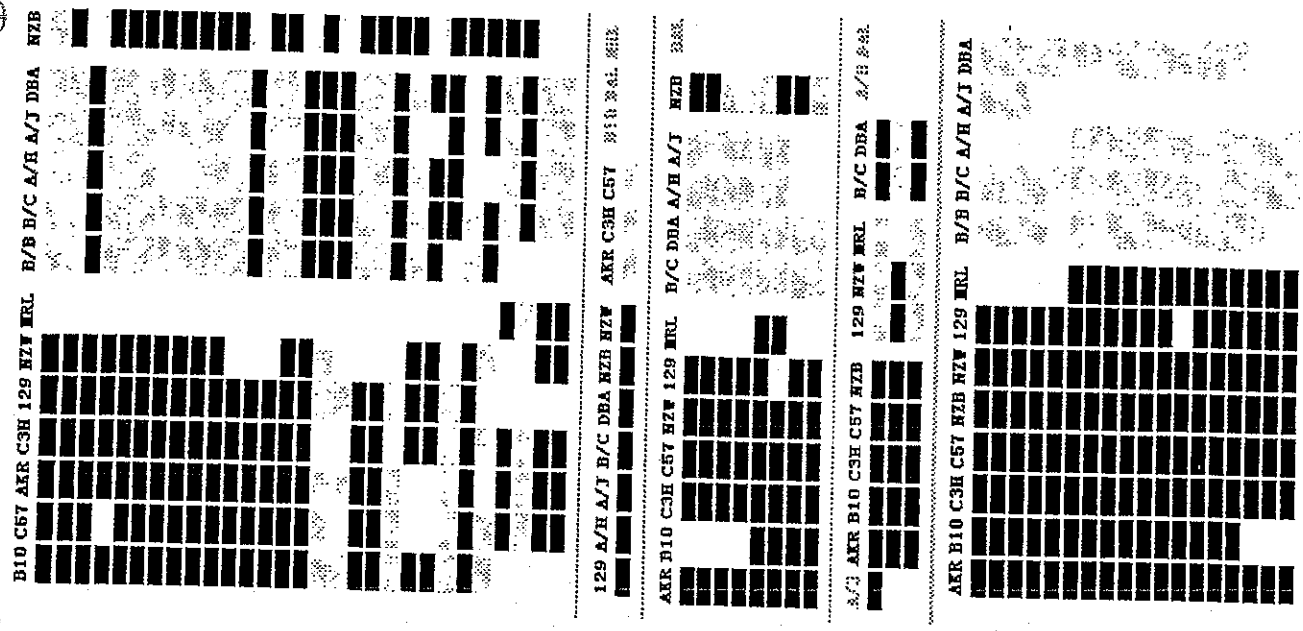

B10 C57 AKR C3H 129 NZW MRL
B/B B/C A/H A/J DBA NZB
129 A/H A/J B/C DBA NZB NZW
AKR C3H C57
AKR B10 C3H C57 NZW 129 MRL
B/C DBA A/H A/J NZB
AKR B10 C3H C57 NZB
129 NZW MRL B/C DBA
AKR B10 C3H C57 NZB NZW 129 MRL
B/B B/C A/H A/J DBA

Figure 5

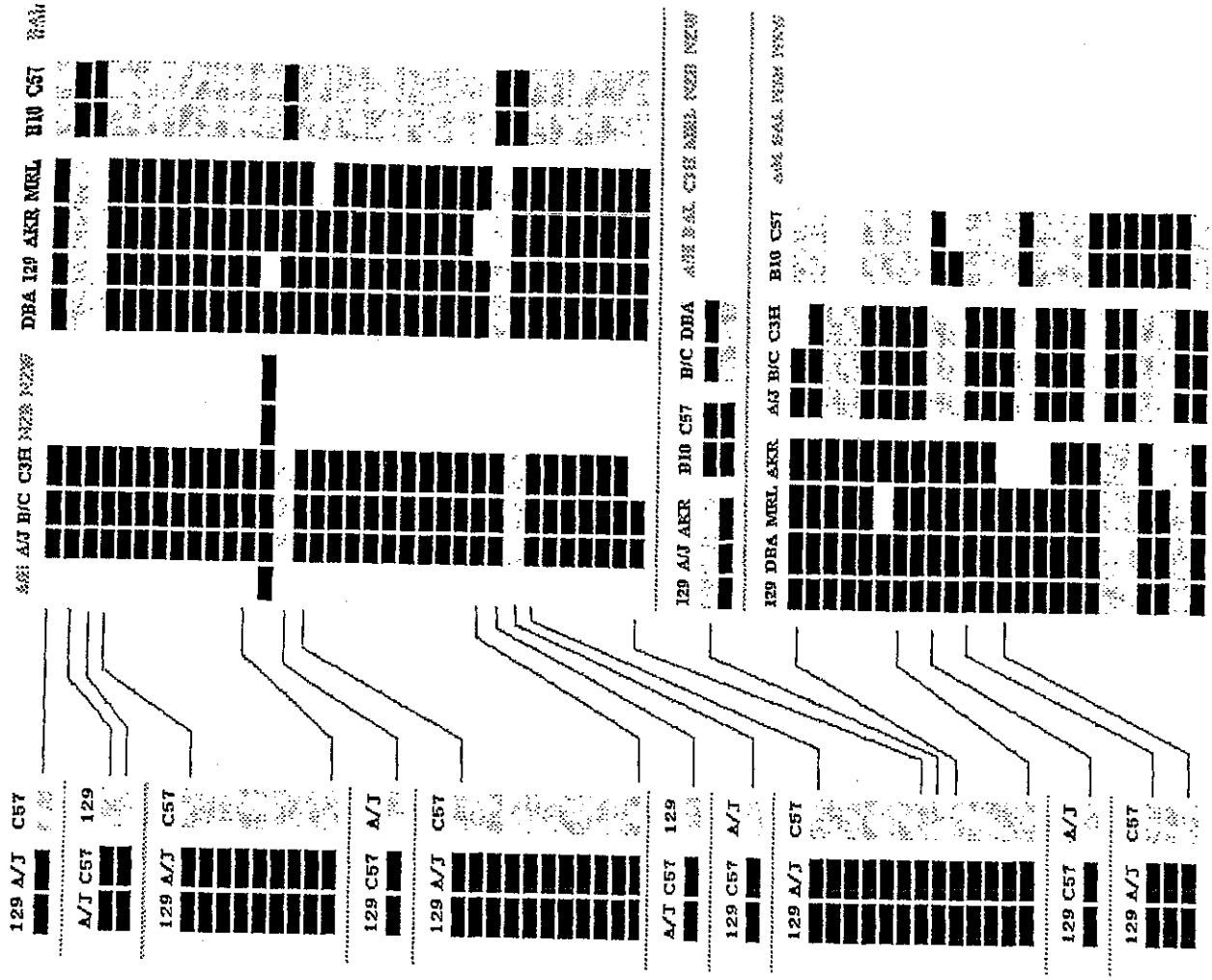


Figure 6B

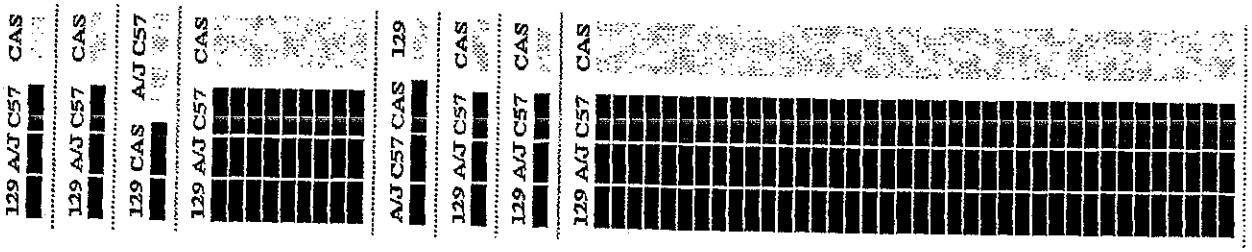


Figure 6A

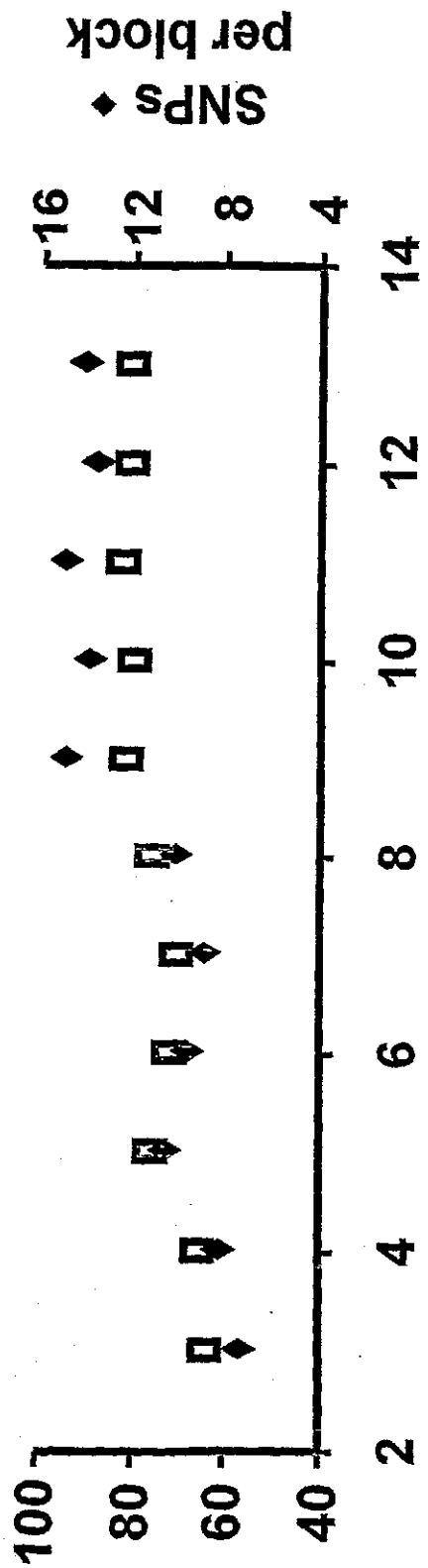


Figure 7A

Figure 7B

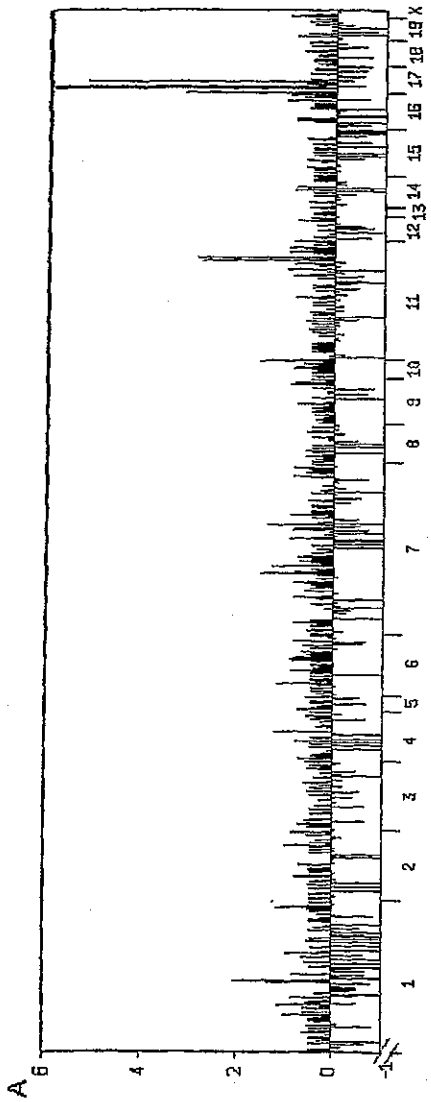


Figure 8A

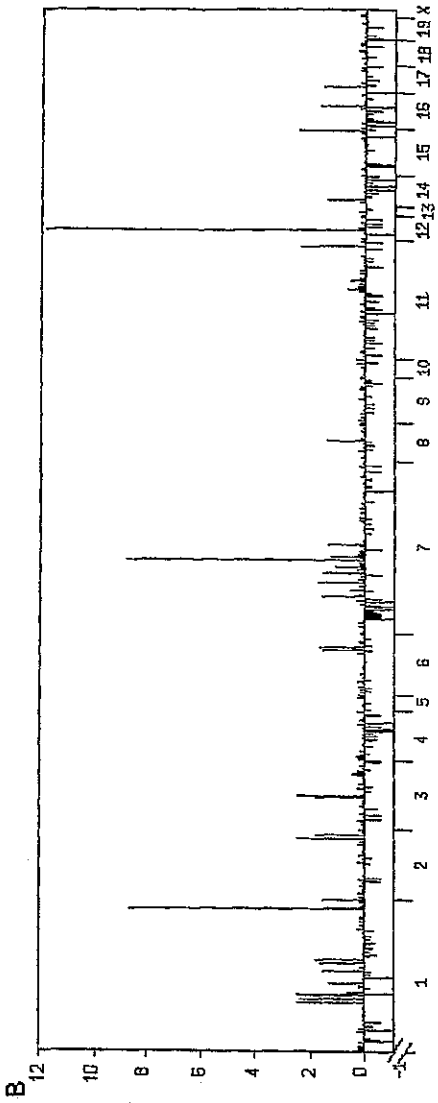


Figure 8B

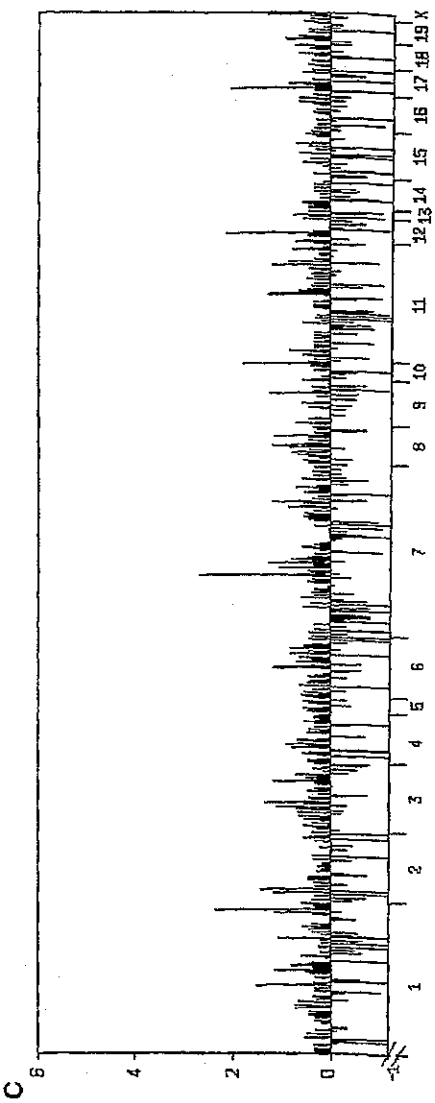


Figure 8C

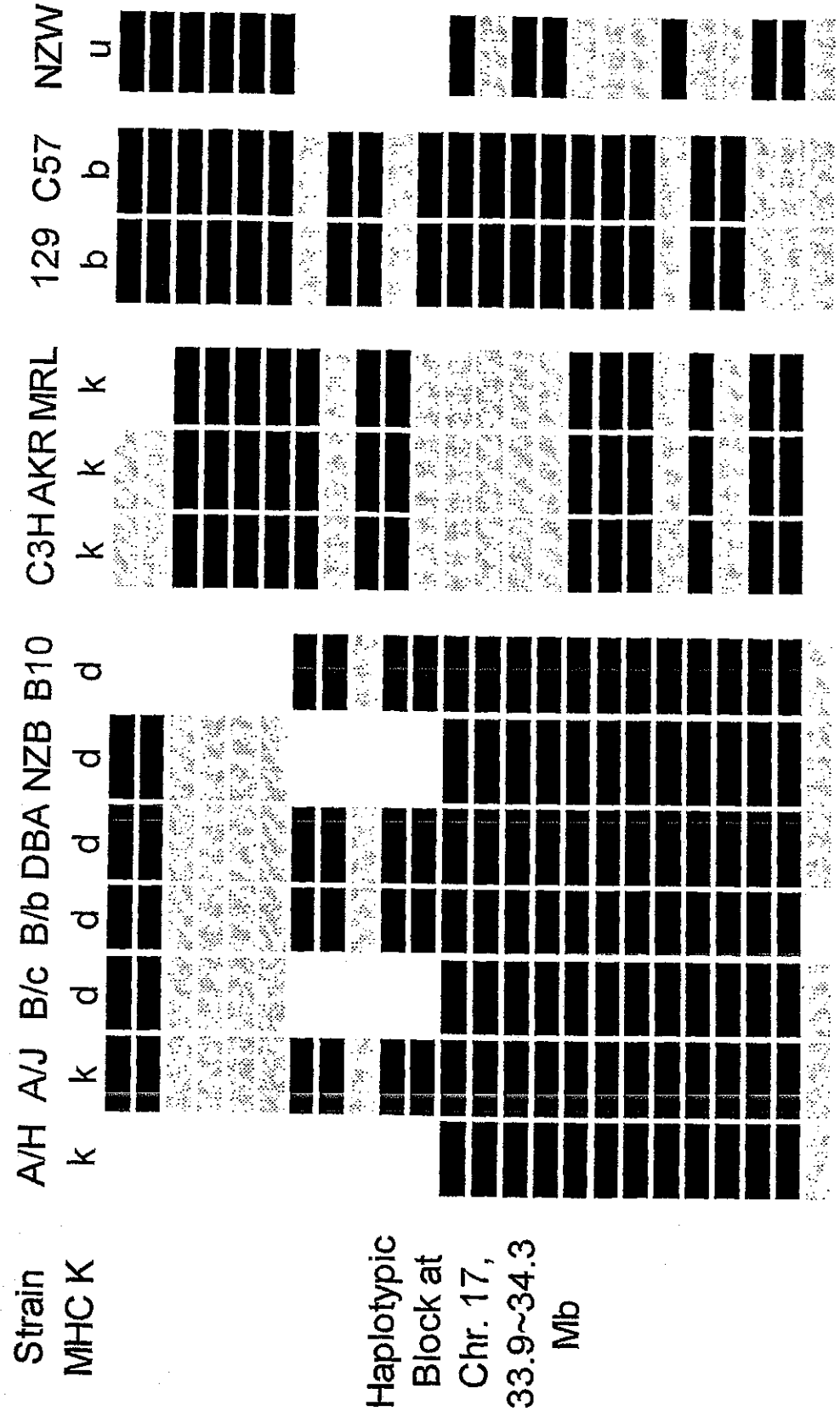
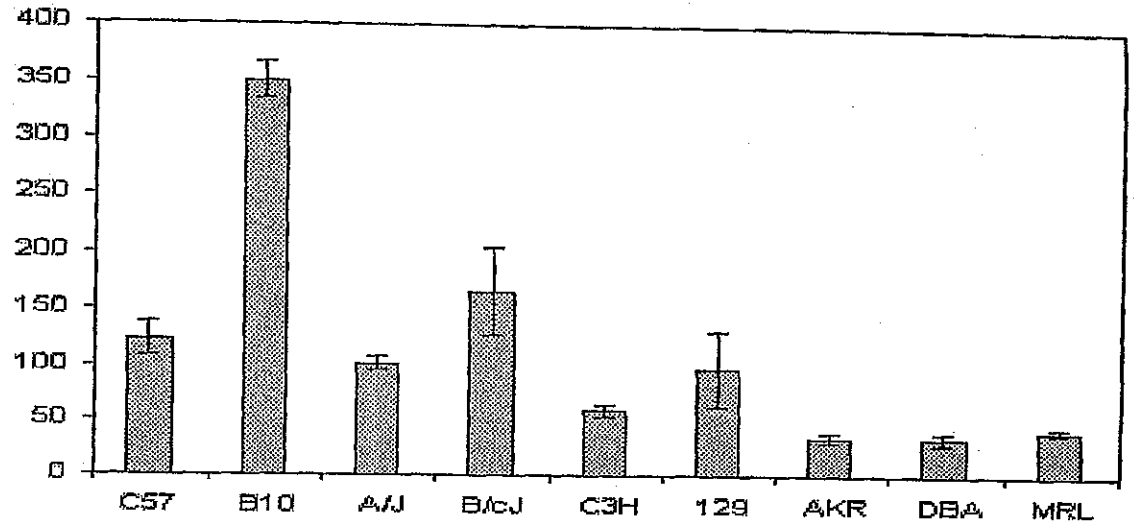

Strain
MHC K
Haplotypic Block at Chr. 17, 33.9~34.3 Mb
A/H k
A/J k
B/c d
B/b d
DBA d
NZB d
B10 d
C3H k
AKR k
MRL k
129 b
C57 b
NZW u

Figure 9

A

Figure 10A



B

Figure 10B

Mb	exon	C57	B10	A/J	B/cJ	C3H	129	AKR	DBA	MRL	codon change
29.625850	11	G	G	A	A	A	A	A	A	A	
29.625960	11	C	C	T	T	T	T	T	T	T	
29.625966	11	A	A	G	G	G	G	G	G	G	g
29.629122	10	C	C	T	T	T	C	C	C	C	f
29.629210	10	C	C	T	T	T	T	T	T	T	
29.629561	10	T	T	C	C	C	C	C	C		
29.629620	10	C	C	G	G	G	G	G	G	G	
29.629626	10	G	G	T	T	T	T	T	T	T	e
29.629713	10	A	A	G	G	G	G	G	G	G	
29.629795	10	C	C	T	T	T	T	T	T	T	d
29.629982	10	A	A	G	G	G	G	G	G	G	c
29.630005	10	C	C	T	T	T	T	T	T	T	
29.631538	9	G	G	G	G	G	A	A	A	A	b
29.631620	9	G	G	A	A	A	G	G	G	G	a
29.633542	7	C	C	T	T		T	T	T	T	
29.651742	2	C	C	T	T	T	C		C	C	

Group I Group II Group III

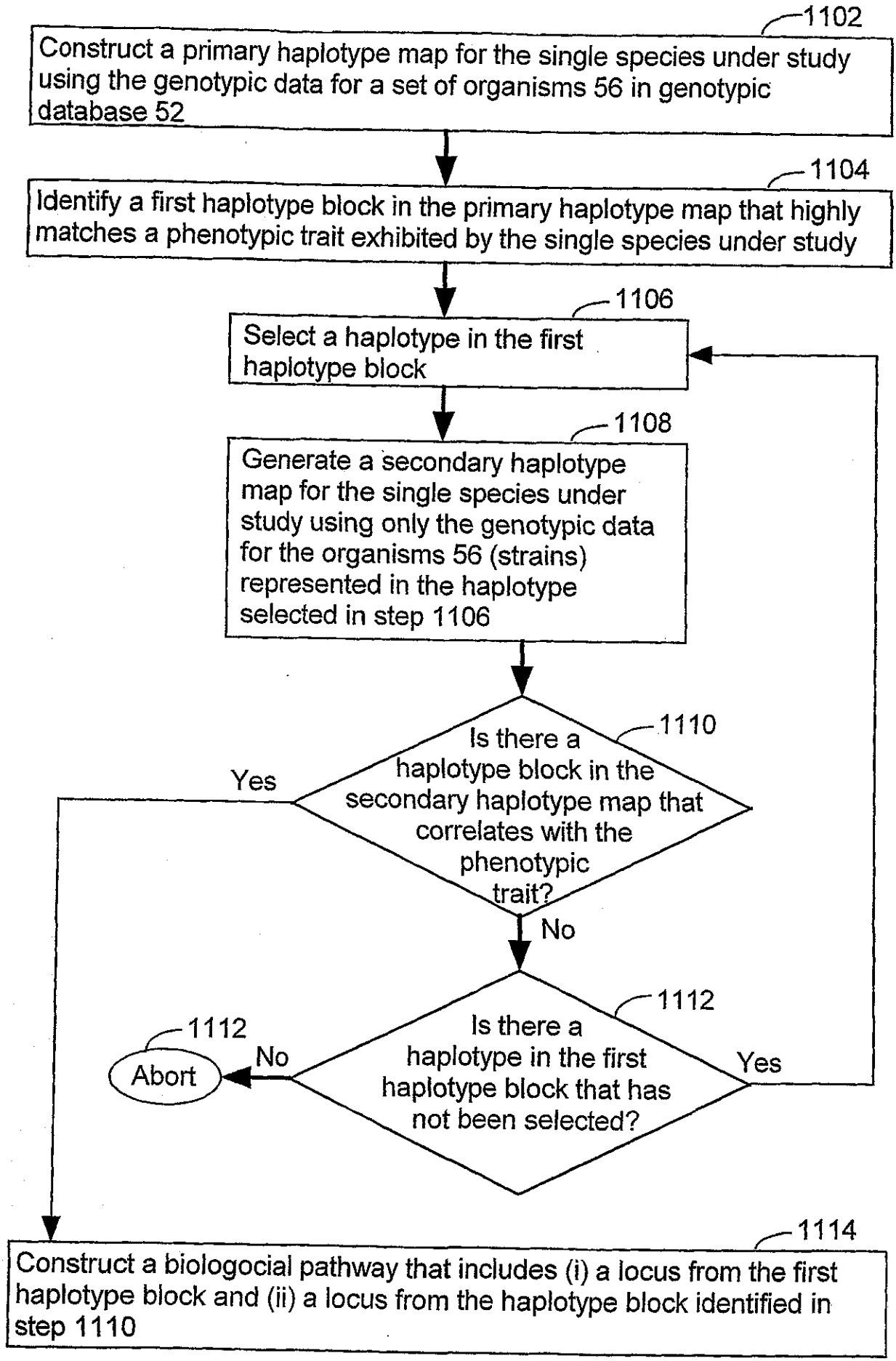

1102
Construct a primary haplotype map for the single species under study using the genotypic data for a set of organisms 56 in genotypic database 52
1104
Identify a first haplotype block in the primary haplotype map that highly matches a phenotypic trait exhibited by the single species under study
1106
Select a haplotype in the first haplotype block
1108
Generate a secondary haplotype map for the single species under study using only the genotypic data for the organisms 56 (strains) represented in the haplotype selected in step 1106
1110
Is there a haplotype block in the secondary haplotype map that correlates with the phenotypic trait?
Yes
No
1112
Is there a haplotype in the first haplotype block that has not been selected?
Yes
No
1112
Abort
1114
Construct a biologocial pathway that includes (i) a locus from the first haplotype block and (ii) a locus from the haplotype block identified in step 1110

FIG. 11