

FIG. 1A

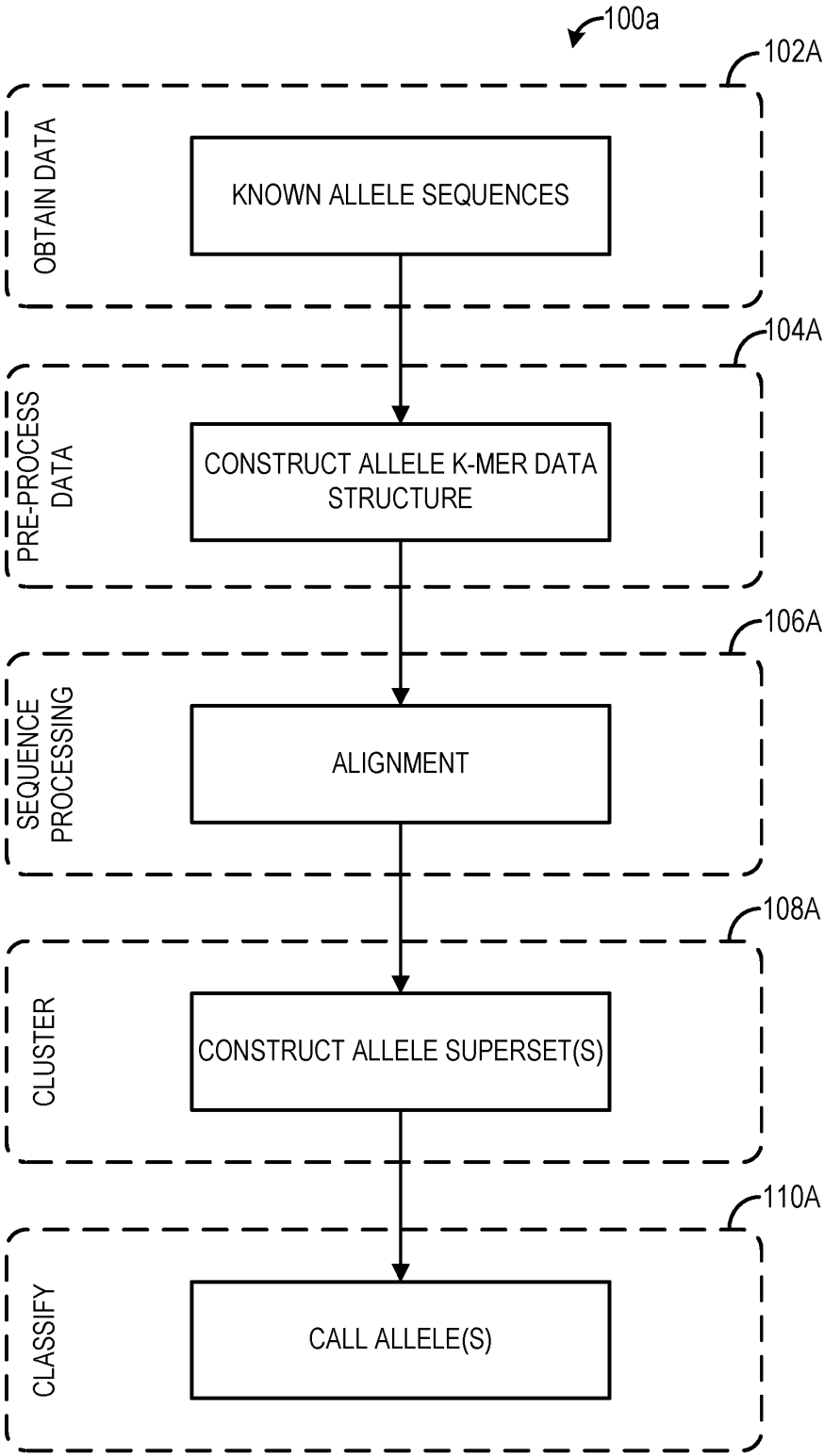


FIG. 1B

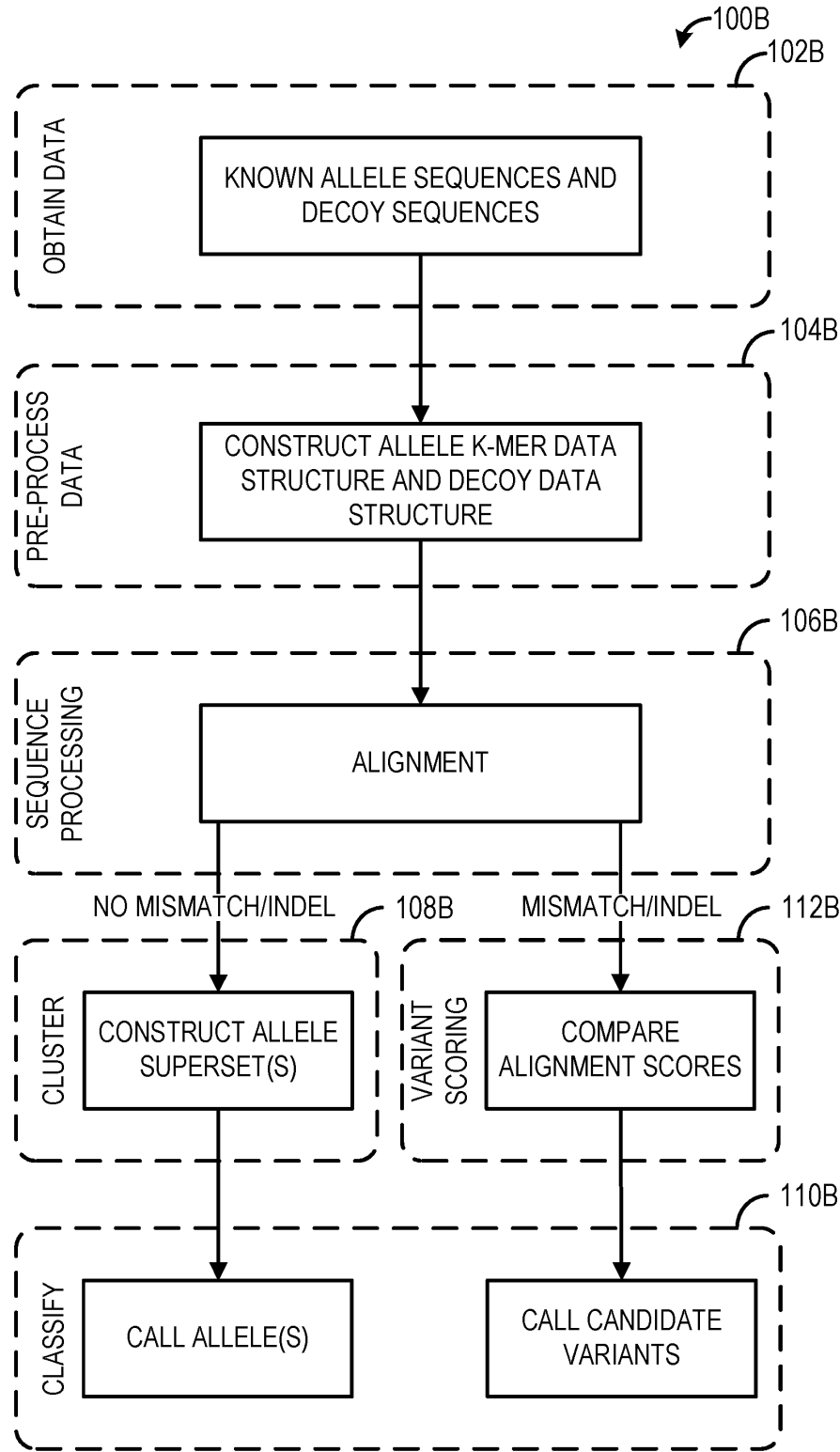
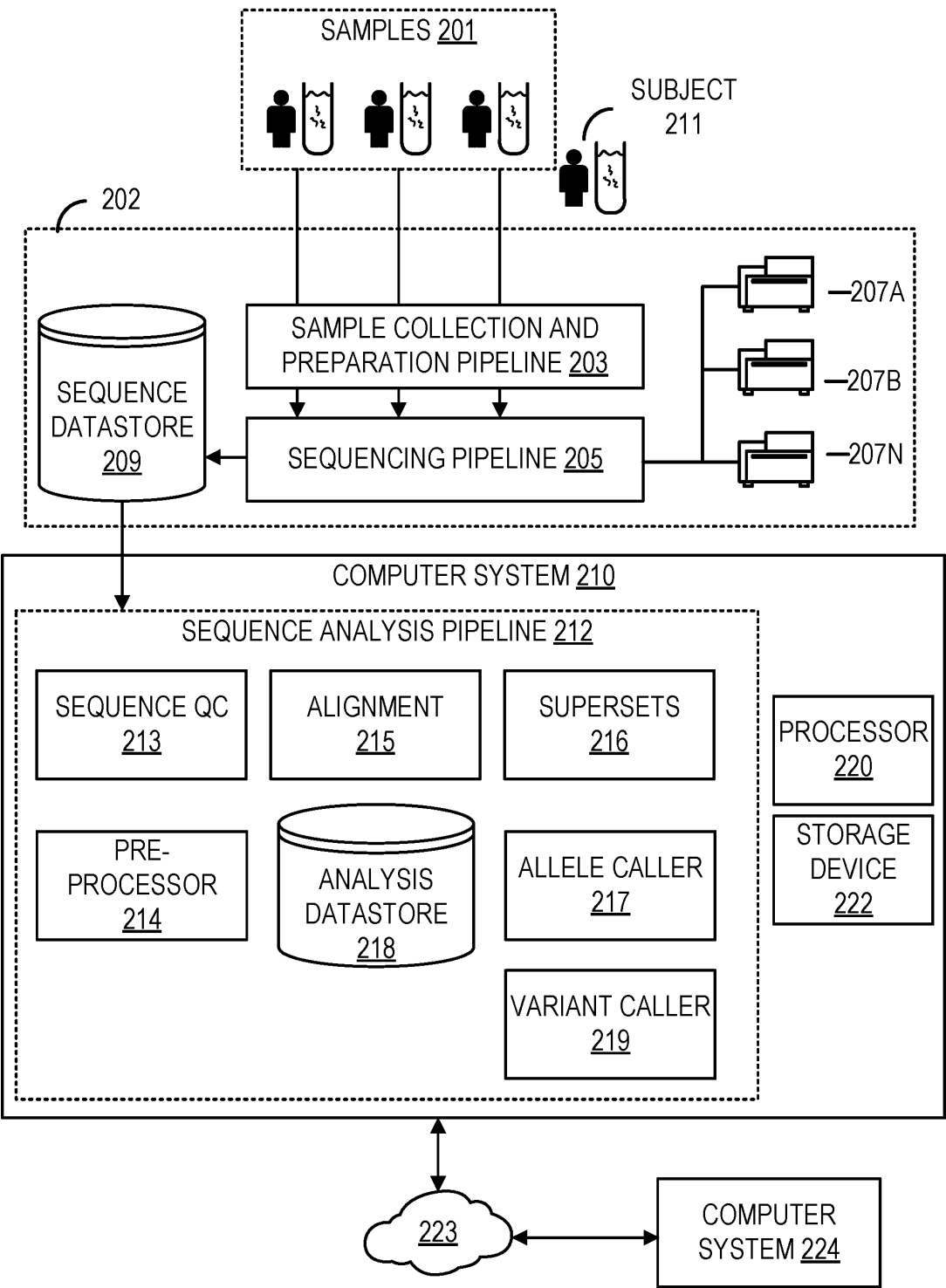


FIG. 2



300 ↗

KMER SEQUENCE	# ALLELES	ALLELE ID	START	ALLELE ID	START	...
AAAAAAAAAAAAAAAA...TCTGGAGAAAAAAAAGAAAAGGG	8	12187	3851	12189	3719	...
AAAAAAAAAAAAAAAA...AGGAAGCAGAGGGAAGTAAAC	1	11319	3658			...
AAAAAAAAAAAAAAAA...TTCCTCAAGTCCACTCTGAGT	6	11388	376	11389	376	...
AAAAAAAAAAAAAAAA...CTGGAGAAAAAAAAGAAAAGGGC	9	12187	4002	12188	3852	...
...	...	...	...	...	...	...

FIG. 3

FIG. 4

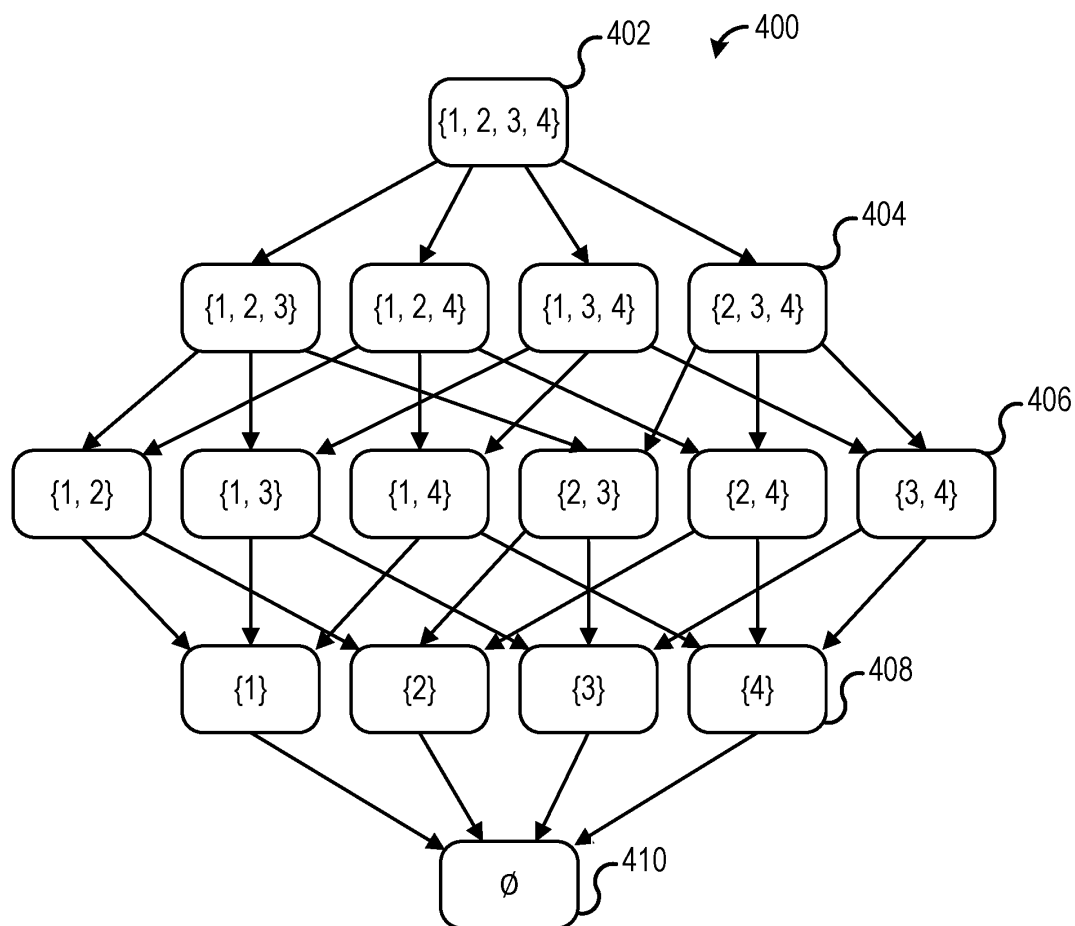


FIG. 5

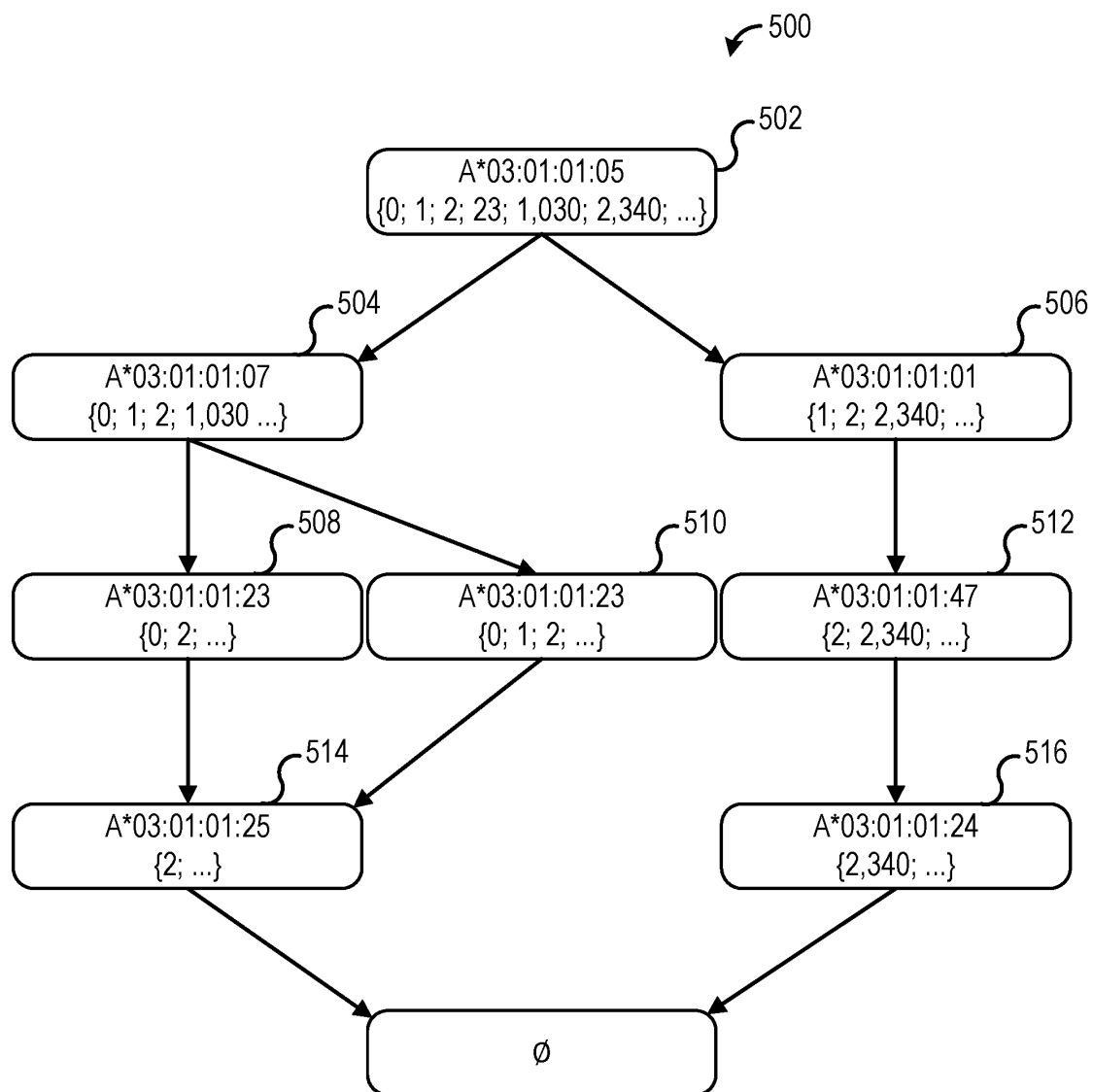


FIG. 6

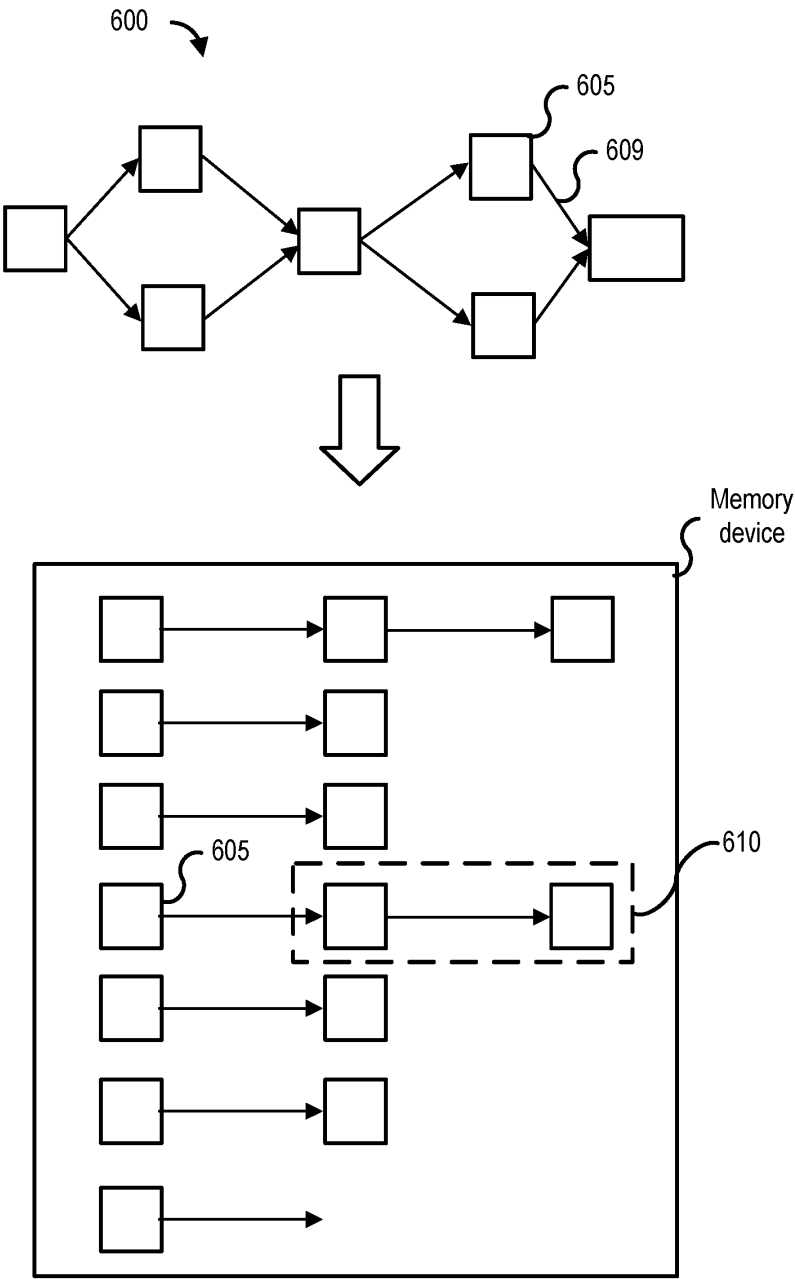


FIG. 7

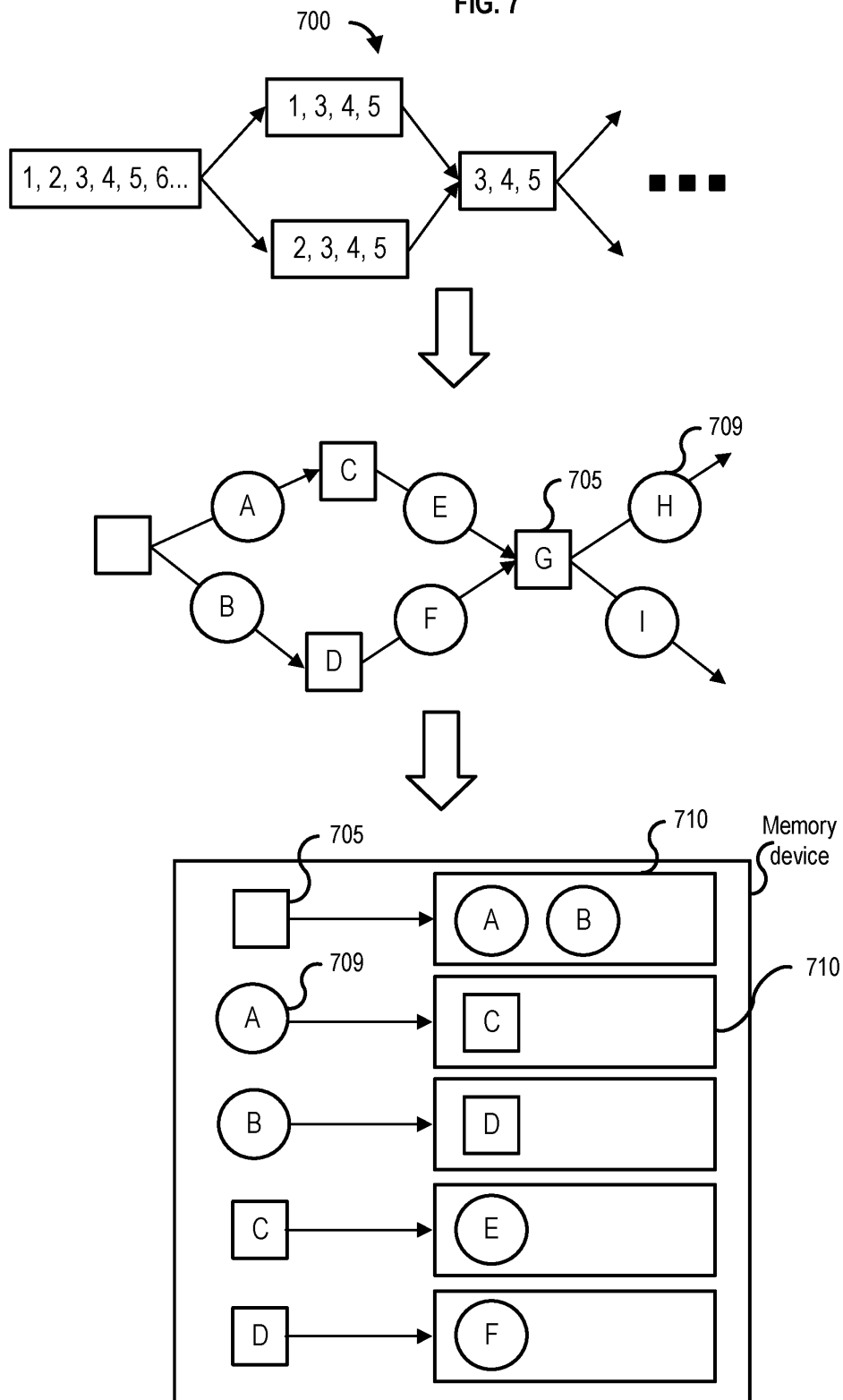
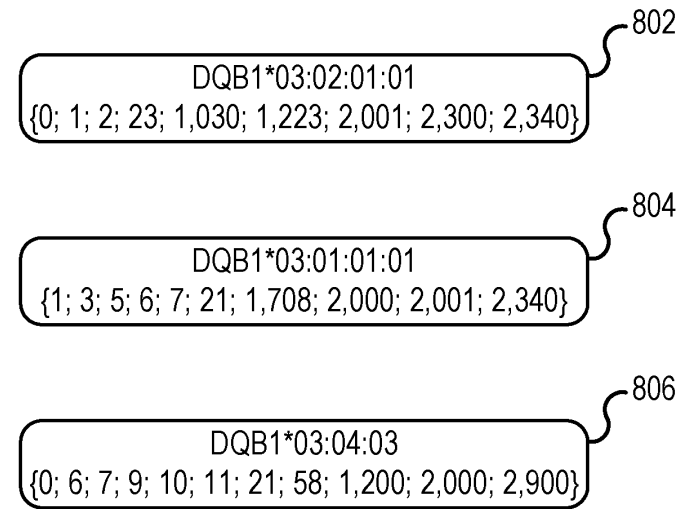


FIG. 8



ROOT NODES	CUMULATIVE DISTINCT FRAGMENTS
802 + 804	16
802 + 806	19
804 + 806	17

FIG. 9

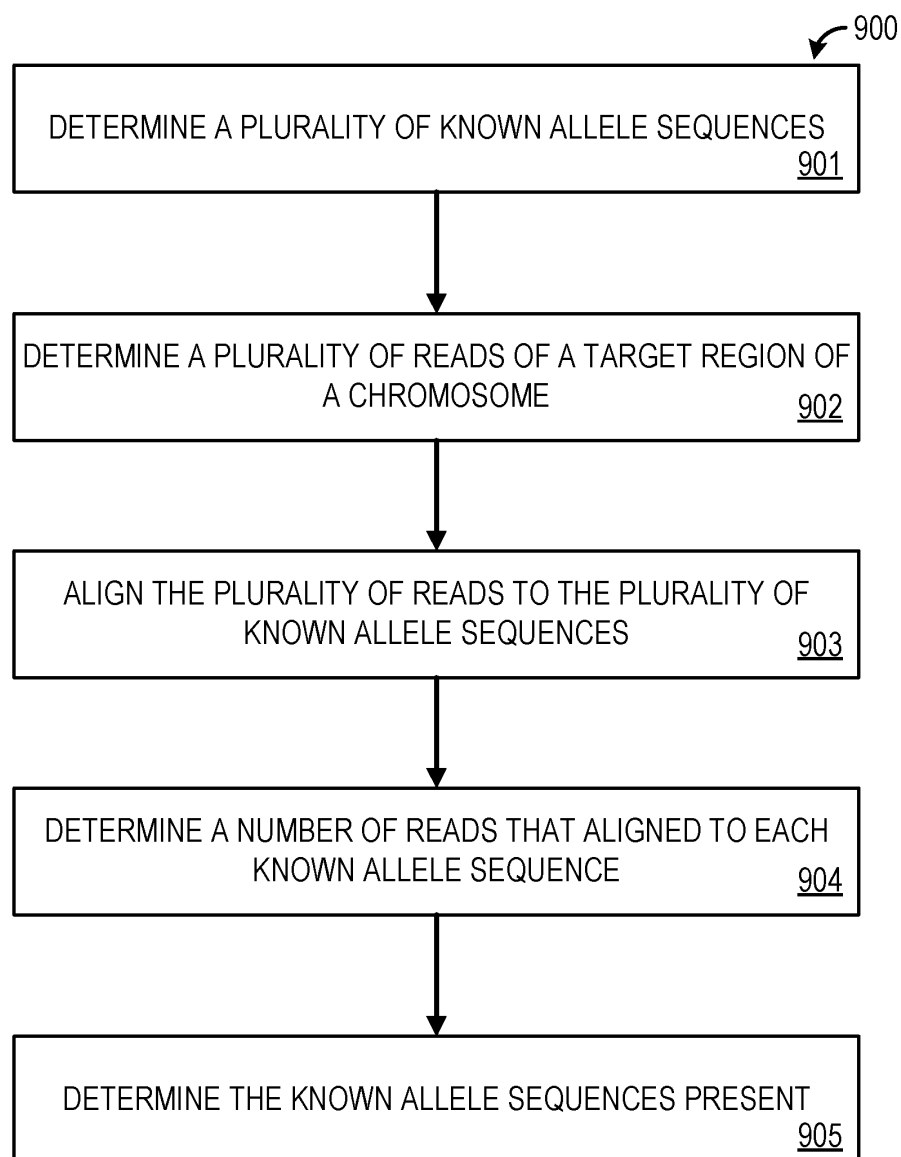
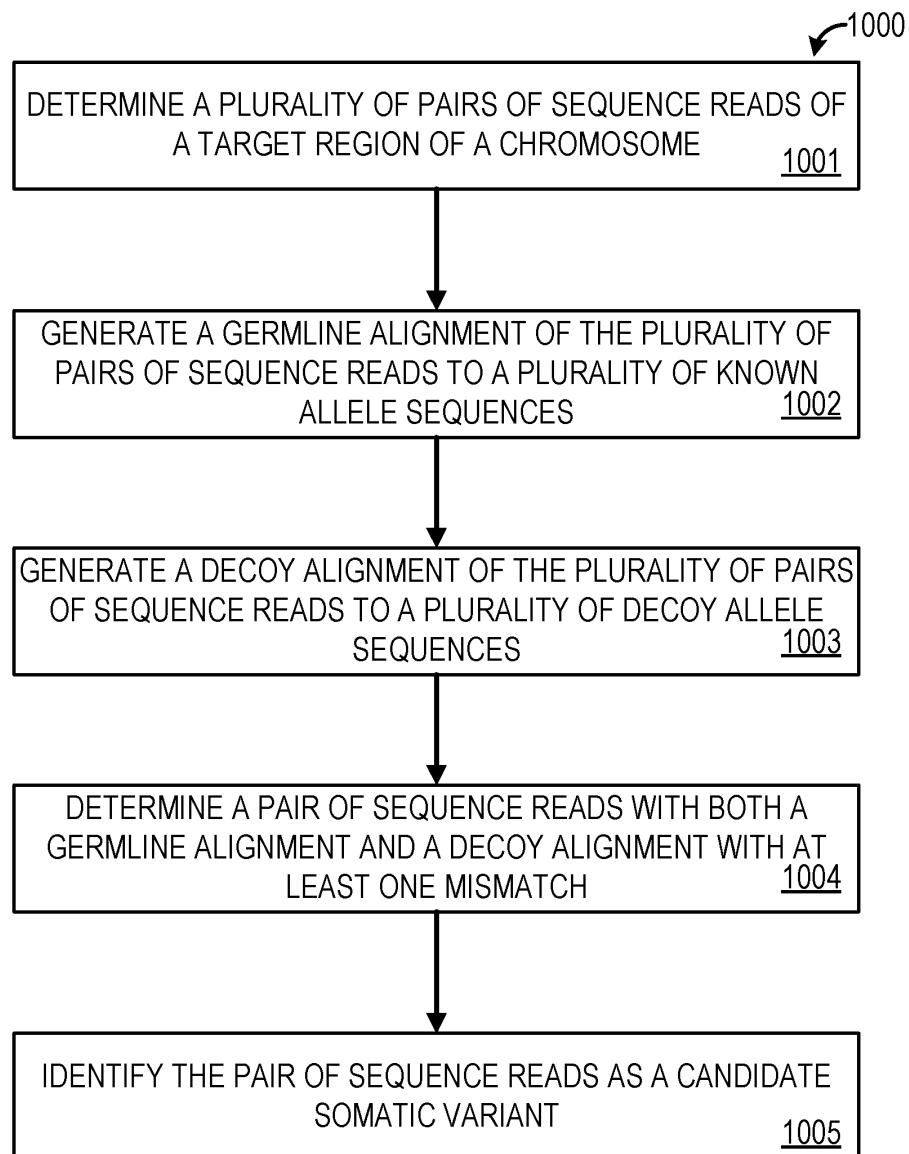


FIG. 10



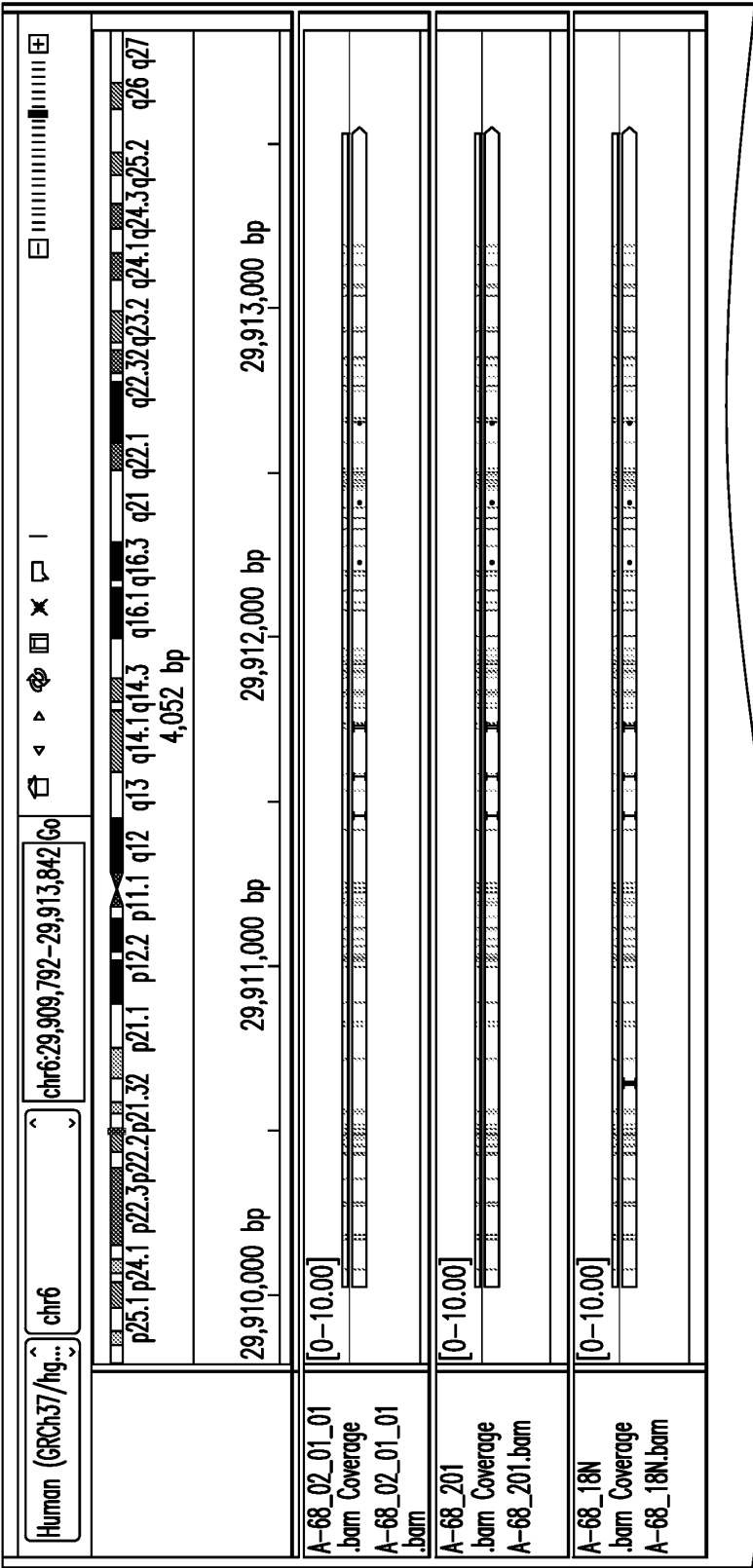


FIG. 11

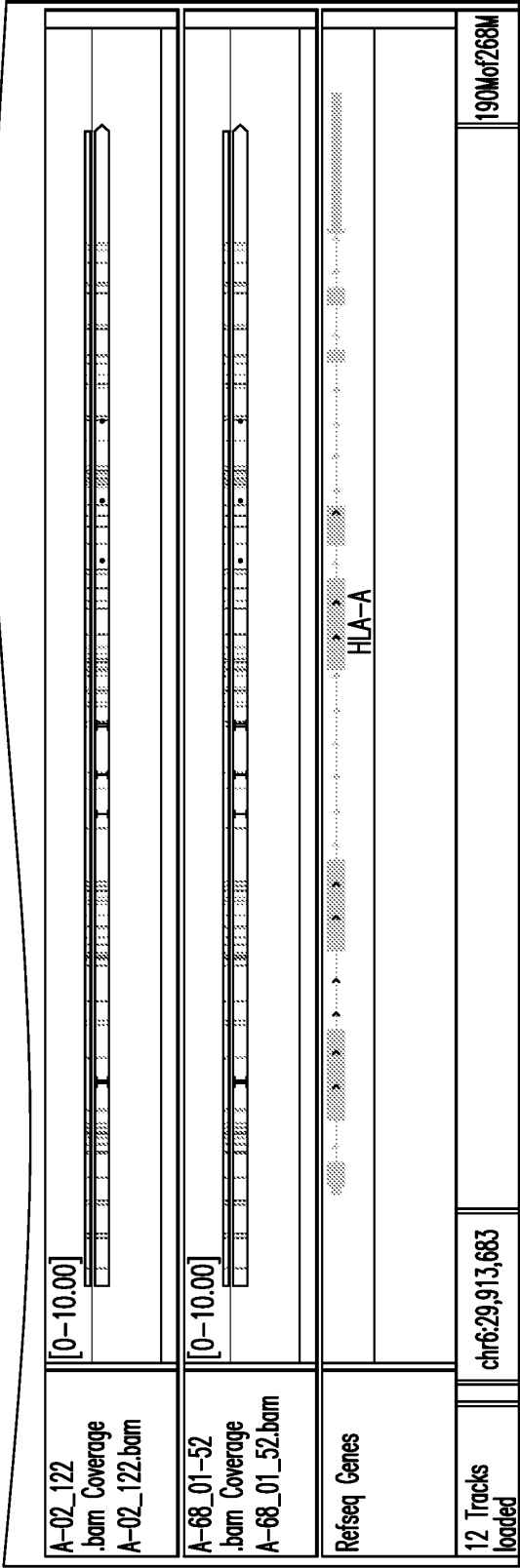
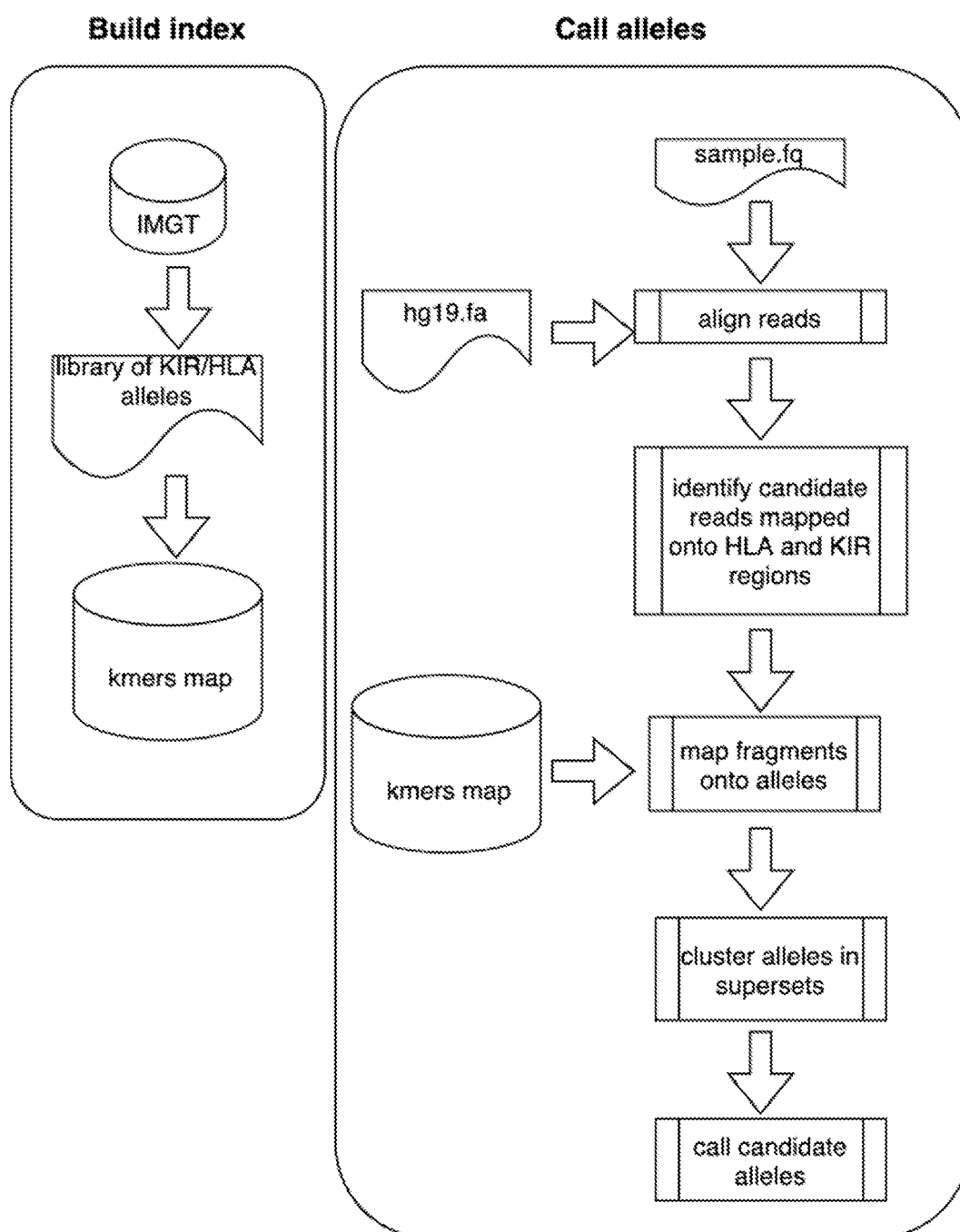


FIG. 11 Continued

FIG. 12



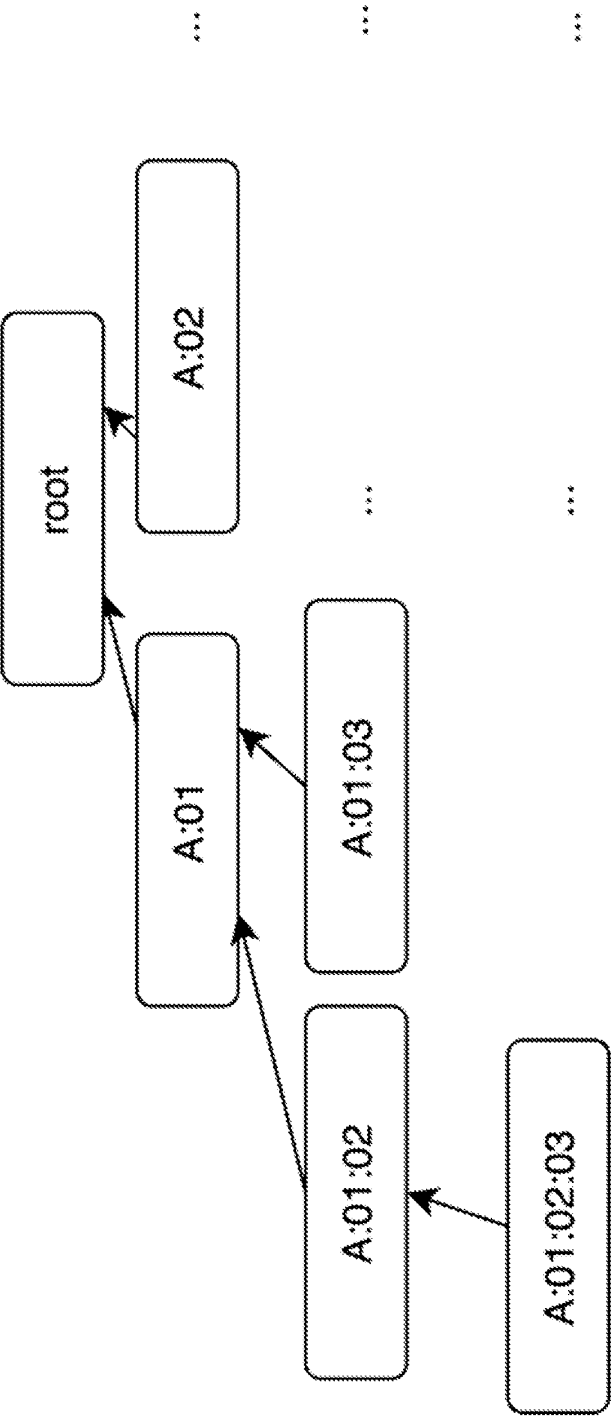


FIG. 13

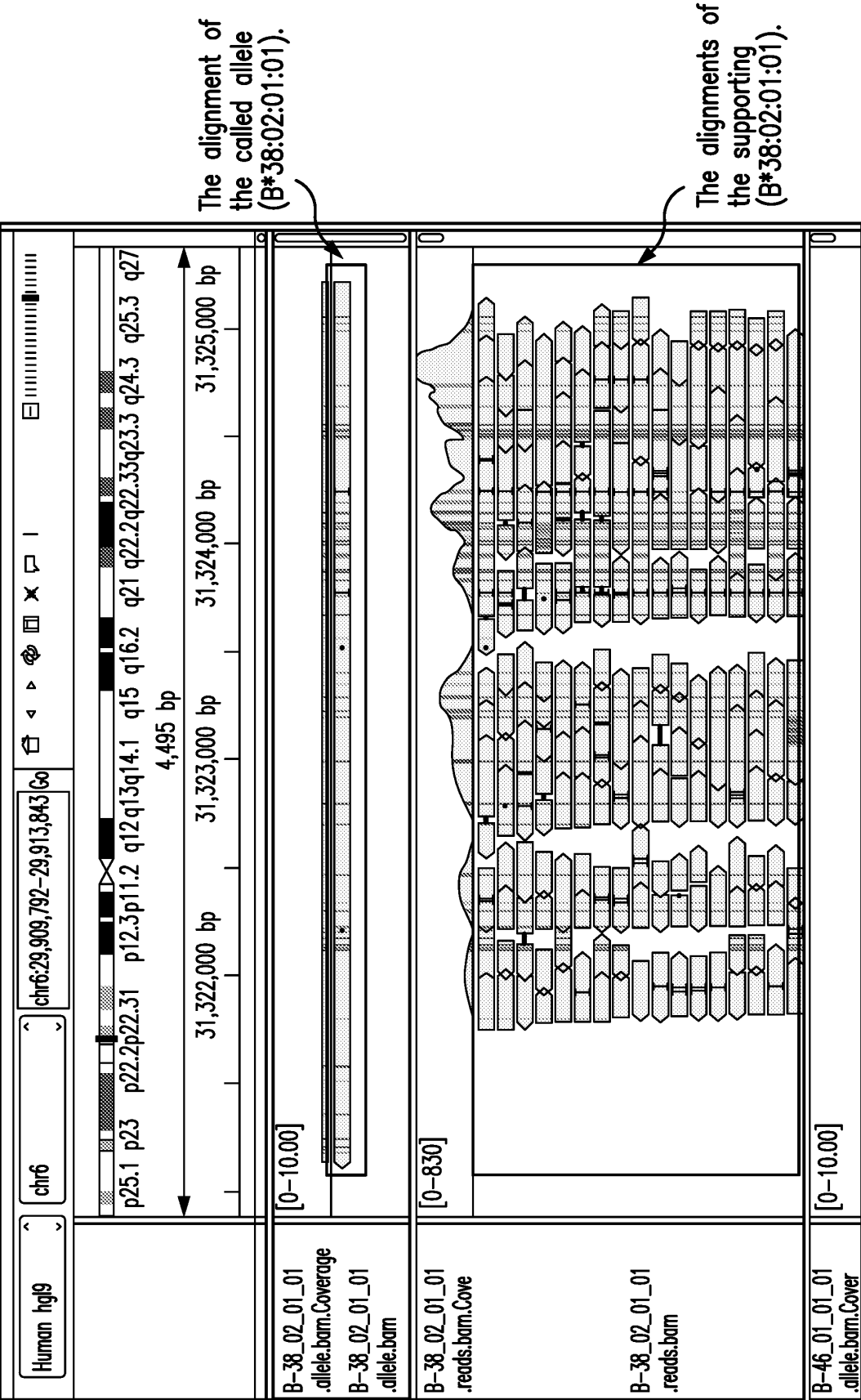


FIG. 14

<i>locus</i>	Regular					Difficult				
	<i>n</i>	<i>FN</i>	<i>FP</i>	<i>sens. (%)</i>	<i>HISAT-genotype sens. (%)</i>	<i>n</i>	<i>FN</i>	<i>FP</i>	<i>sens. (%)</i>	<i>HISAT-genotype sens. (%)</i>
A	200	4	3	98.00	62.50	200	0	0	100.00	85.50
B	200	4	4	98.00	56.00	200	0	0	100.00	87.50
C	200	3	3	98.50	64.00	200	0	0	100.00	88.00
DPA1	200	2	2	99.00	83.50	200	0	0	100.00	96.50
DPB1	200	0	0	100.00	75.00	200	0	0	100.00	100.00
DQA1	200	5	5	97.50	82.50	200	0	0	100.00	87.00
DQB1	200	3	3	98.50	72.50	200	0	0	100.00	95.50
DRB1	200	0	0	100.00	96.50	0				
DRB3	200	0	0	100.00		0				
DRB4	200	0	0	100.00		0				
DRB5	200	0	0	100.00		0				
E	200	0	0	100.00	50.00	0				
F	200	0	0	100.00	73.00	0				
G	200	1	1	99.50	93.00	200	0	0	100.00	100.00
	2800	22	21	99.21	73.50	1600	0	0	100.00	92.50

FIG. 15

<i>locus</i>	<i># of alleles</i>	<i>FN</i>	<i>FP</i>	<i>sens. (%)</i>
KIR2DL1	184	2	2	98.91
KIR2DL2	163	0	0	100.00
KIR2DL3	156	0	0	100.00
KIR2DL4	196	0	0	100.00
KIR2DL15A	196	56	60	71.43
KIR2DL5B	192	102	110	46.88
KIR2DP1	173	0	0	100.00
KIR2DS1	144	4	7	97.22
KIR2DS2	168	0	0	100.00
KIR2DS3	188	0	0	100.00
KIR2DS4	166	0	0	100.00
KIR2DS5	182	1	0	99.45
KIR3DL1	191	0	1	100.00
KIR3DL2	191	0	0	100.00
KIR3DL3	198	2	2	98.99
KIR3DP1	193	4	6	97.93
KIR3DS1	117	0	0	100.00
	2998	171	188	94.30

FIG. 16

	kmerizer	HISAT-genotype
# of loci	134	134
TP	133	134
FP	2	18

FIG. 17

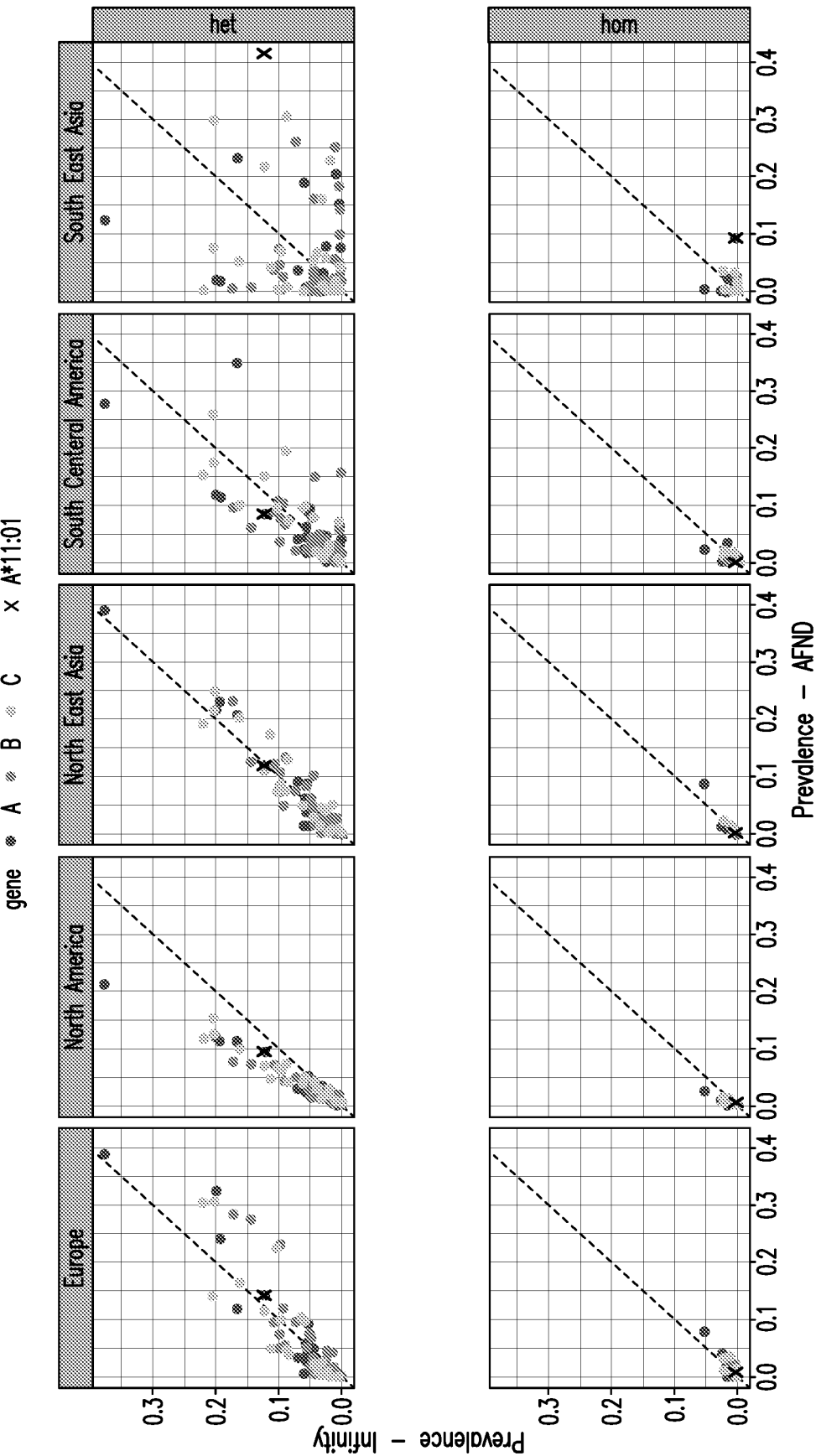
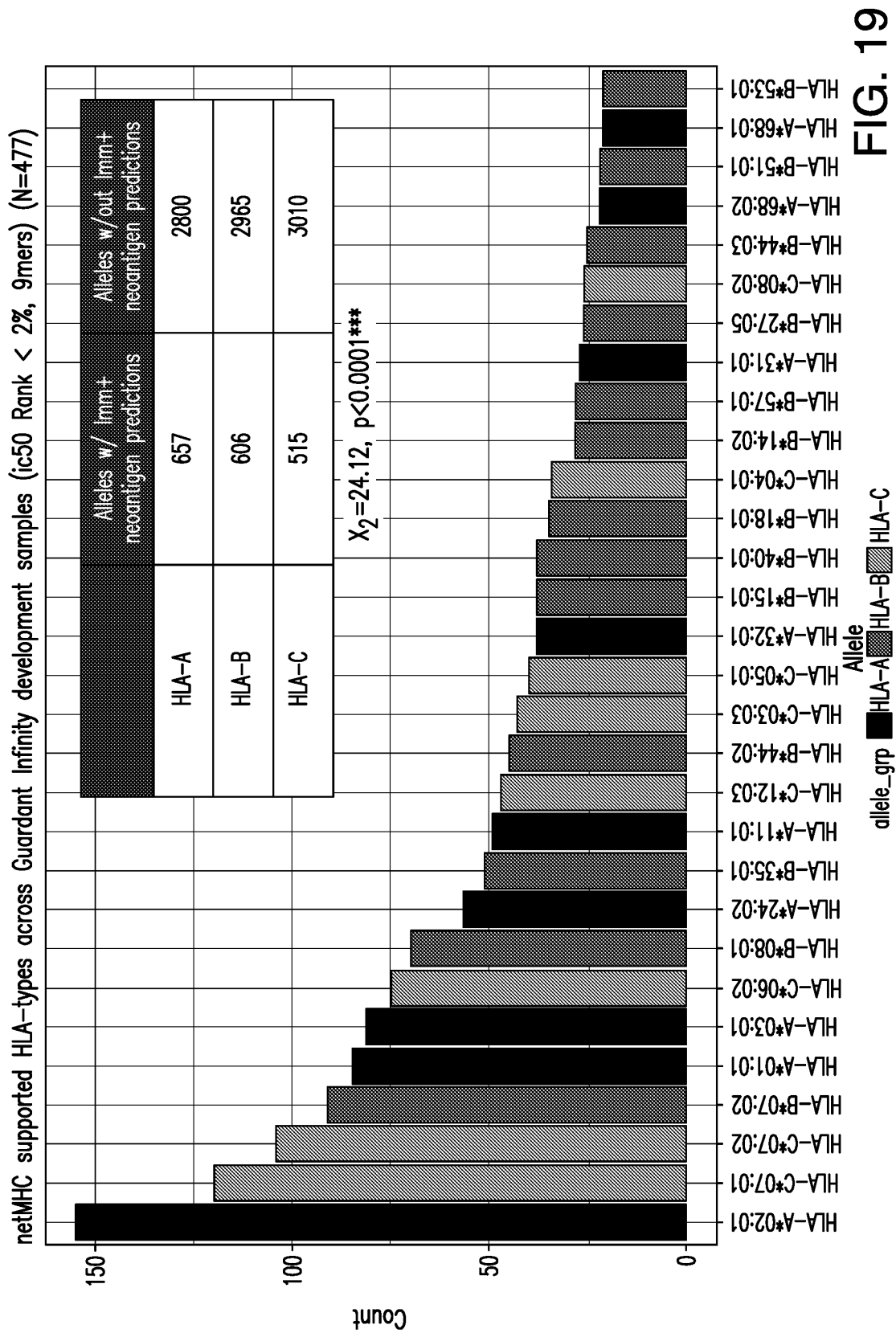


FIG. 18



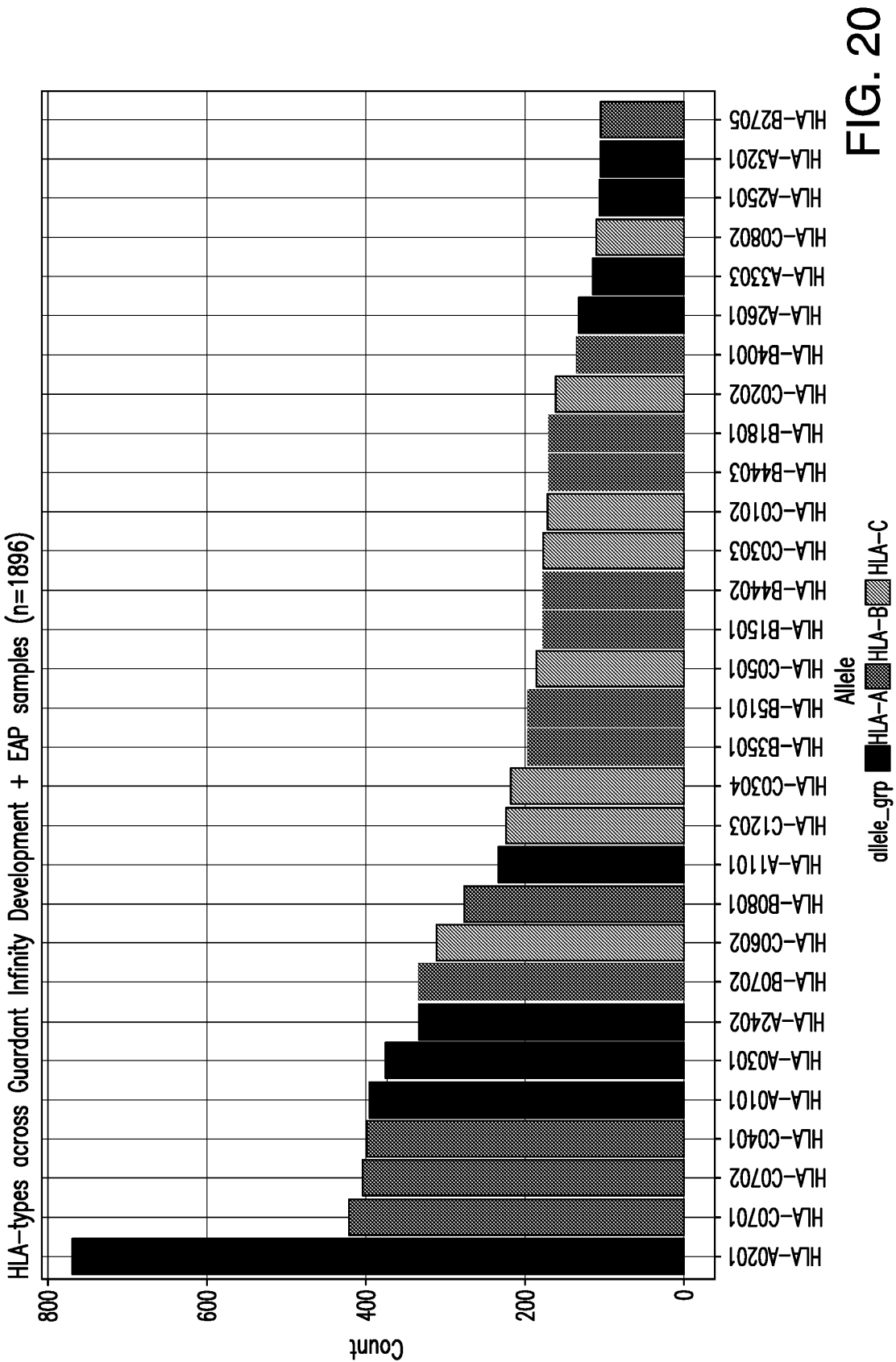


FIG. 20

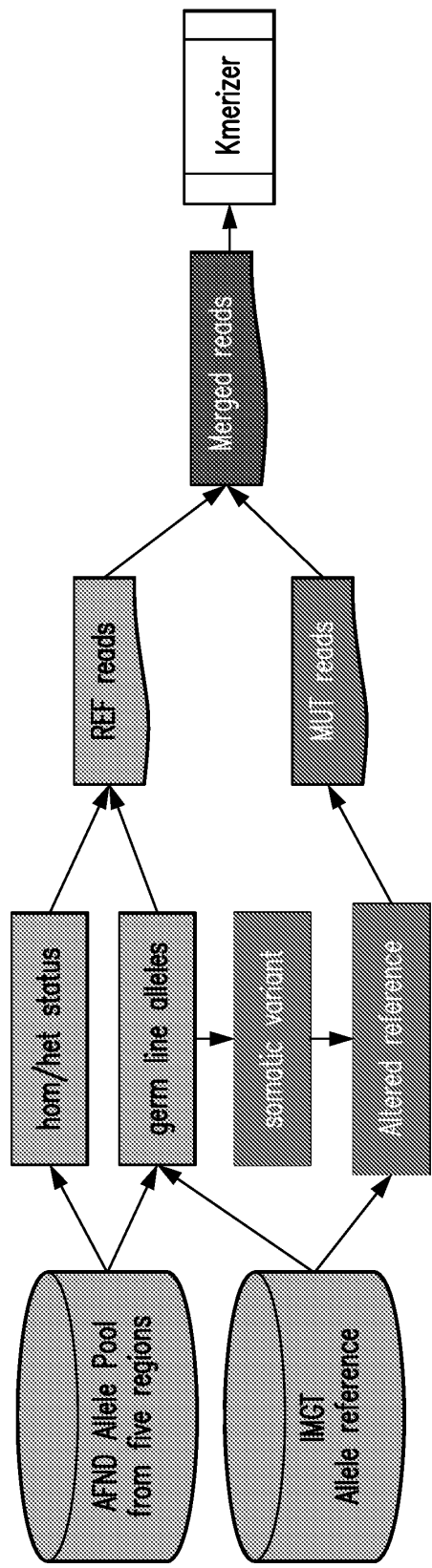


FIG. 21

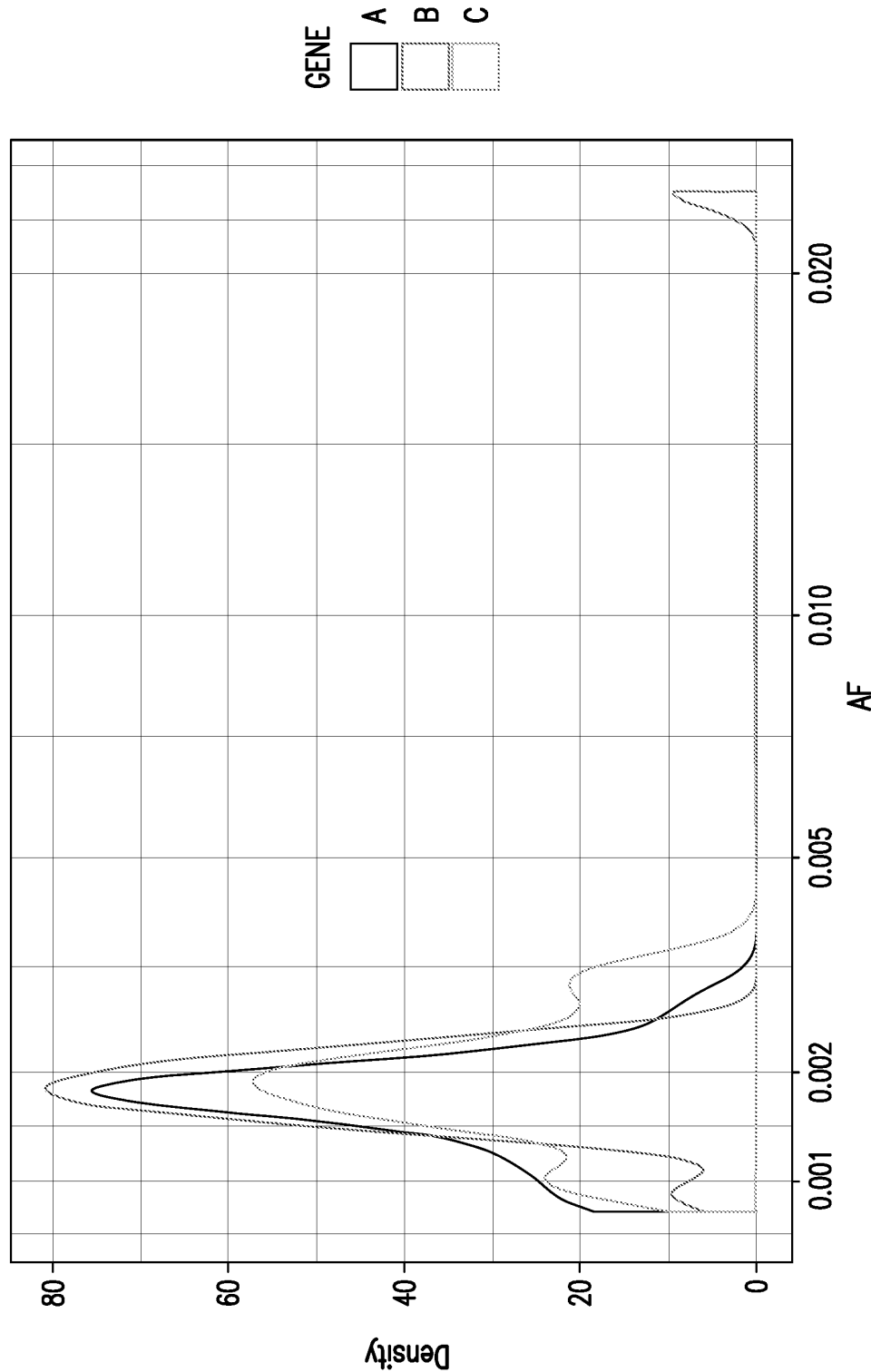


FIG. 22

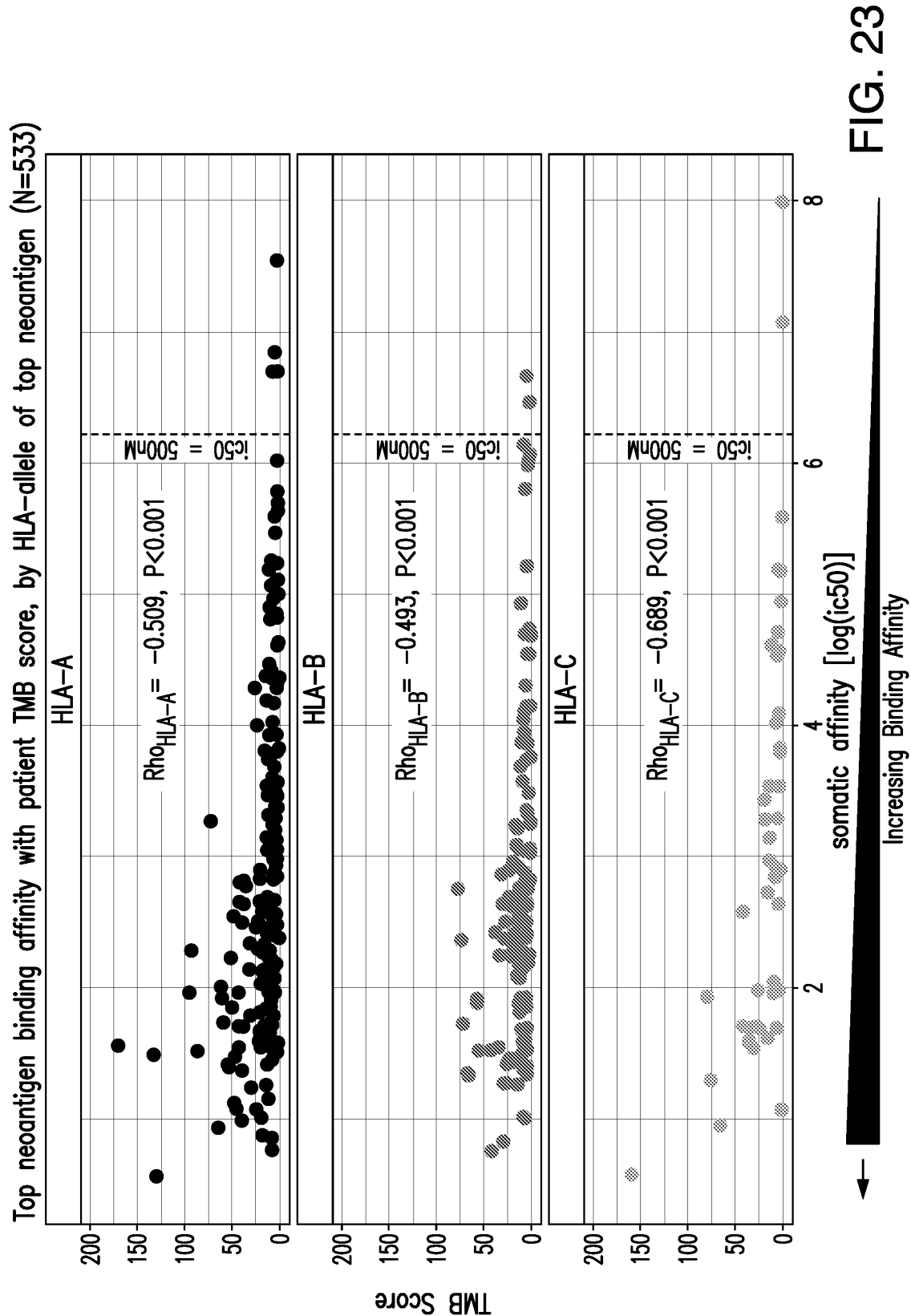


FIG. 23

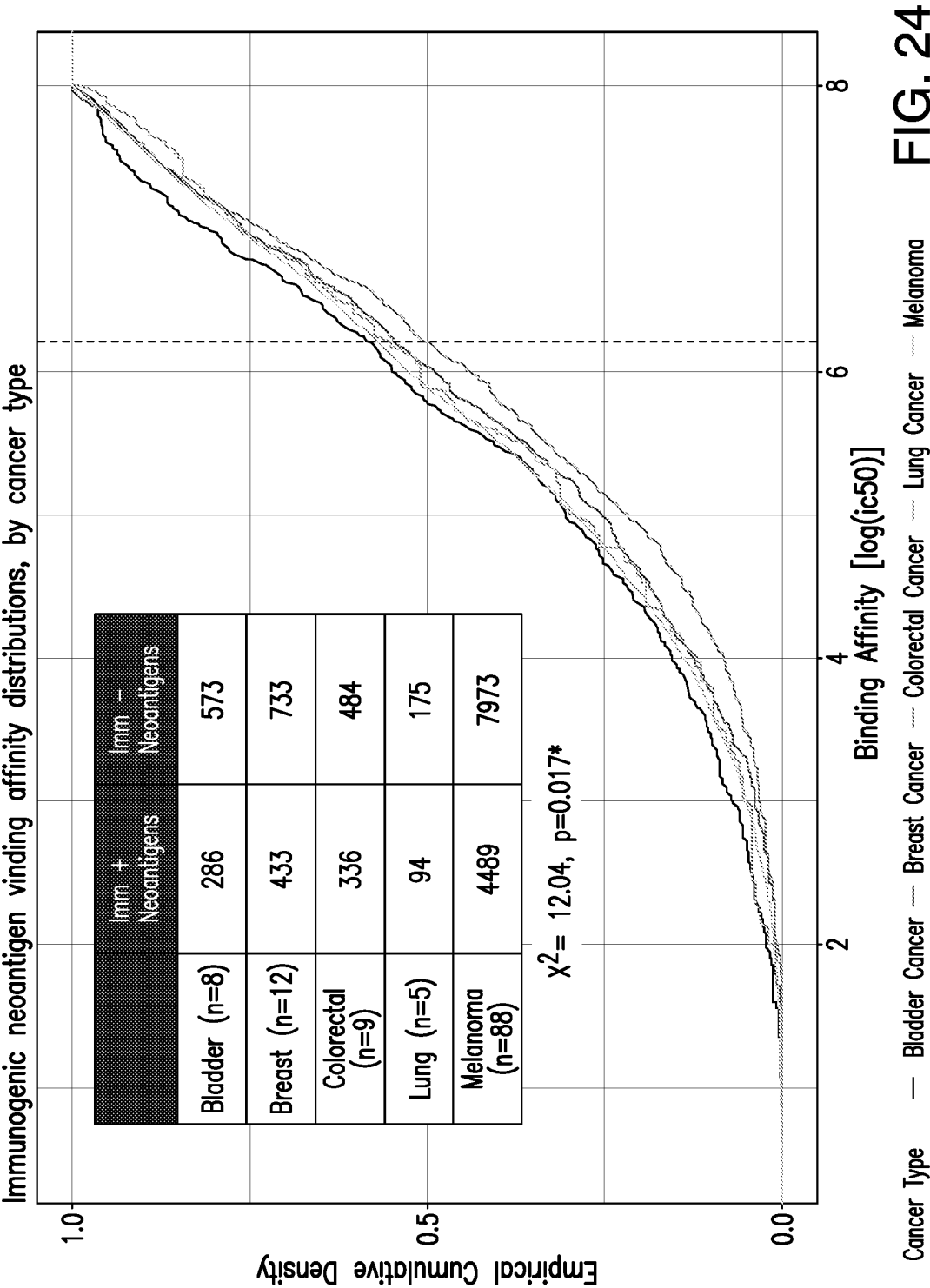


FIG. 24