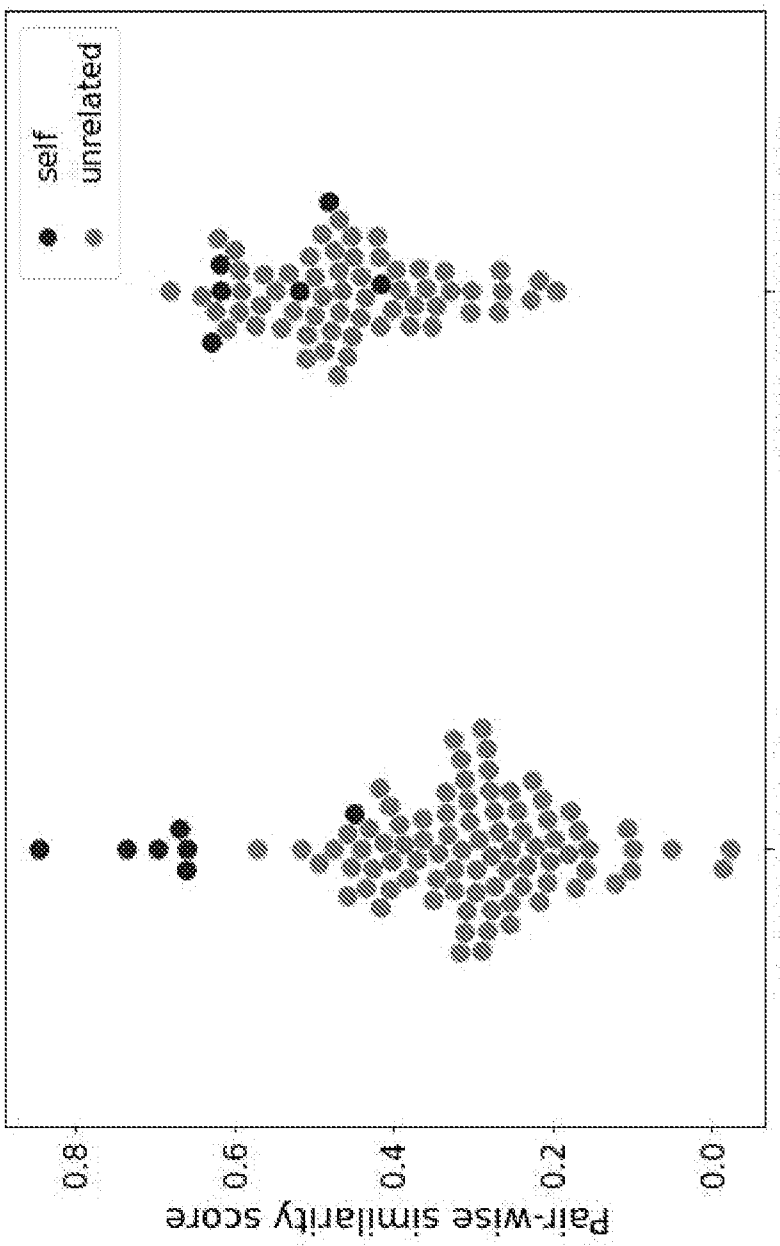

self
unrelated
Pair-wise similarity score
0.0
0.2
0.4
0.6
0.8
Fragmentation-free
DRS-WGA based
Random Fragmentation
Library preparation method

FIG. 1

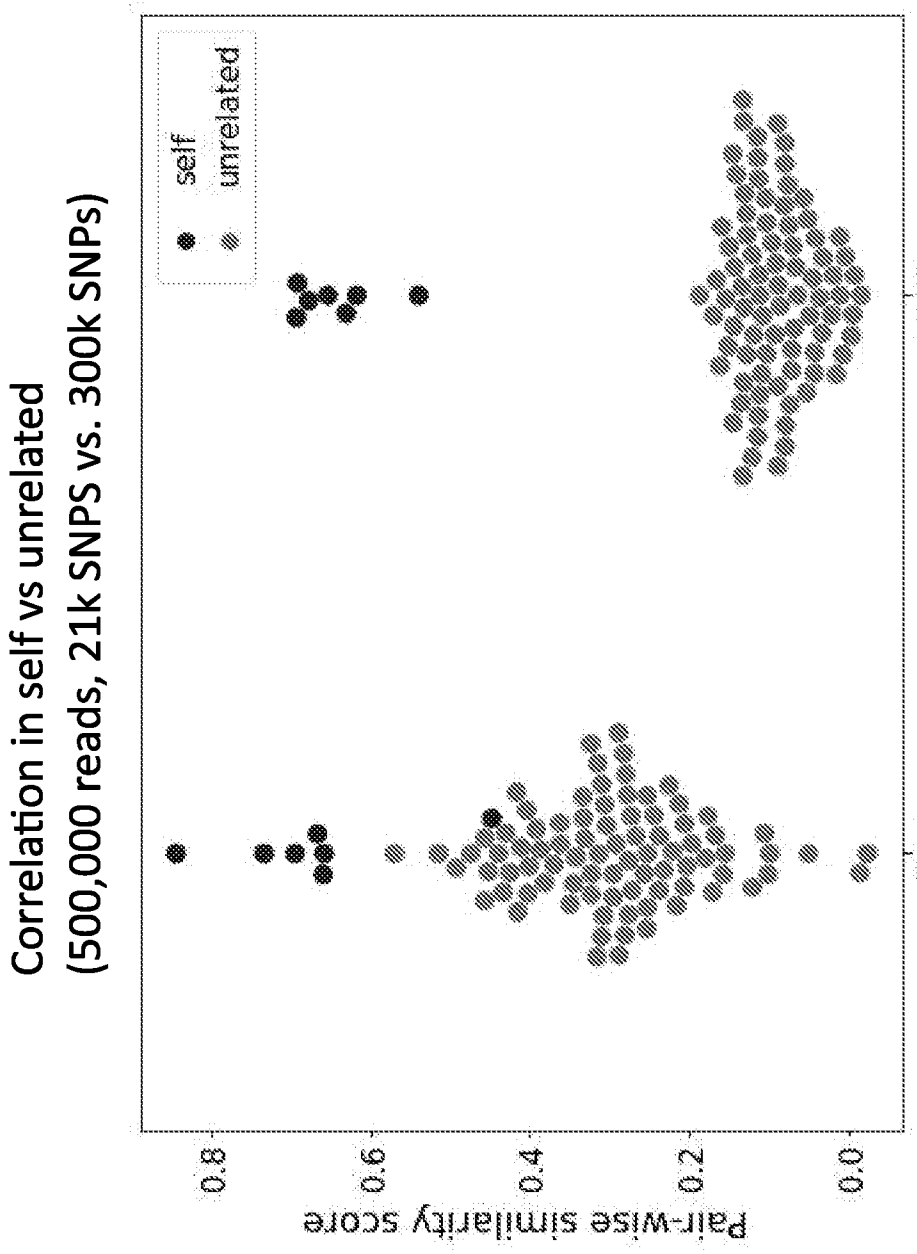

Correlation in self vs unrelated
(500,000 reads, 21k SNPS vs. 300k SNPs)
self
unrelated
Pair-wise similarity score
0.0
0.2
0.4
0.6
0.8
21k
300k
SNP set

FIG. 2

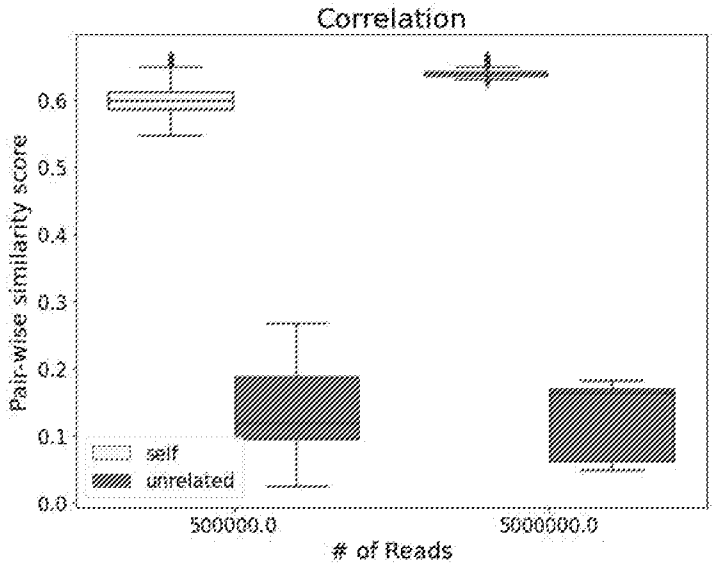


FIG. 3A

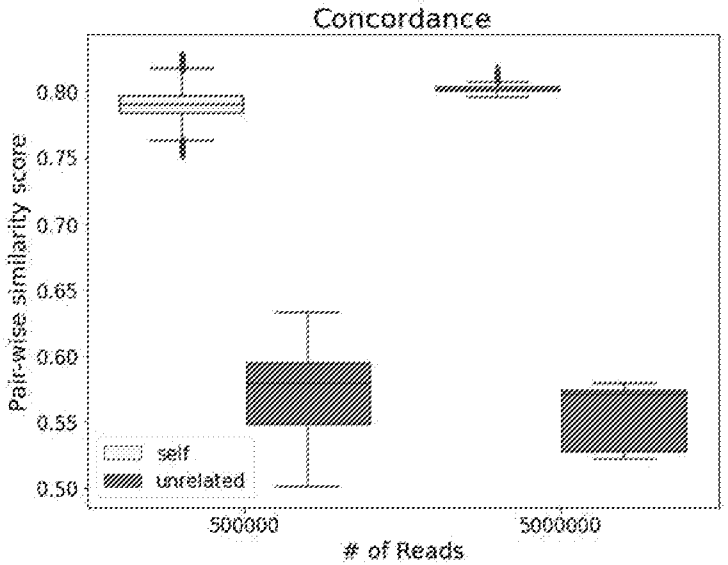


FIG. 3B

AvHet threholds:
500,000 reads: 0.46
5M reads: 0.49

FIG. 4A

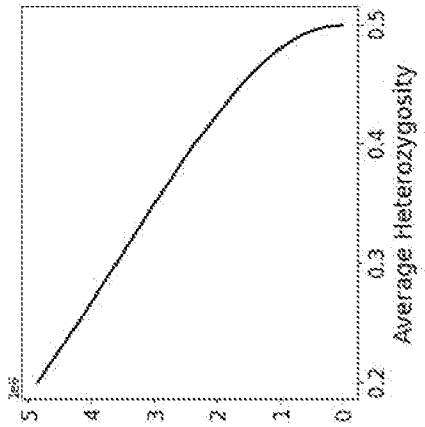


FIG. 4B

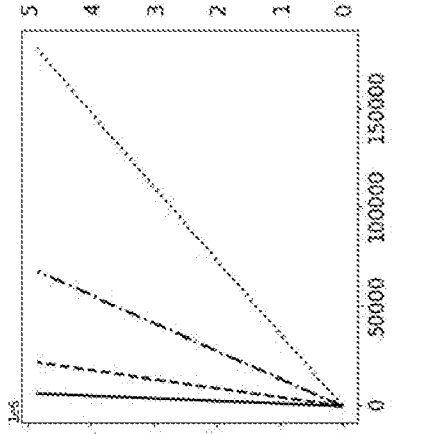


FIG. 4C

FIG. 4D

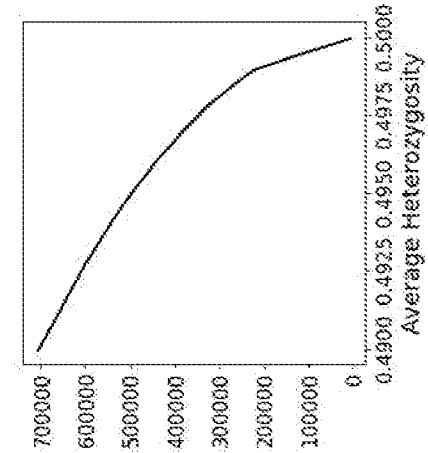


FIG. 4E

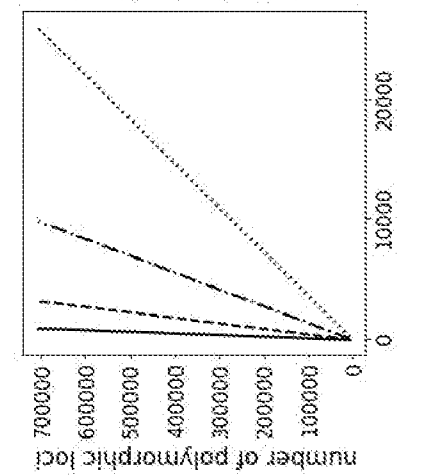


FIG. 4F

FIG. 5A

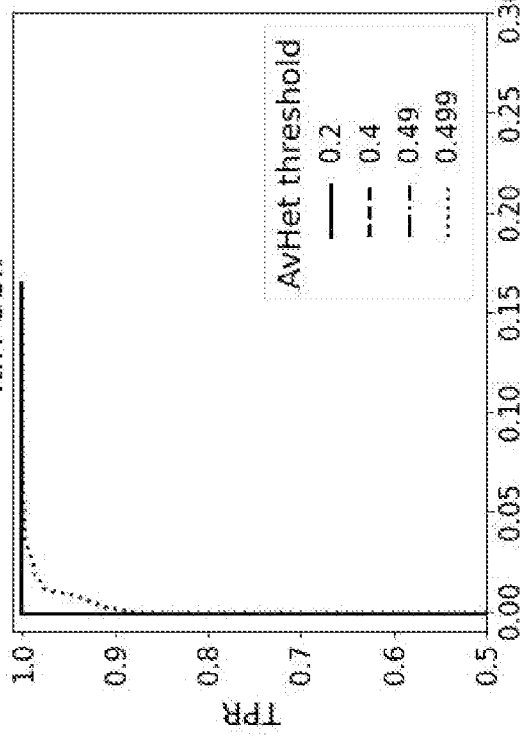


FIG. 5B

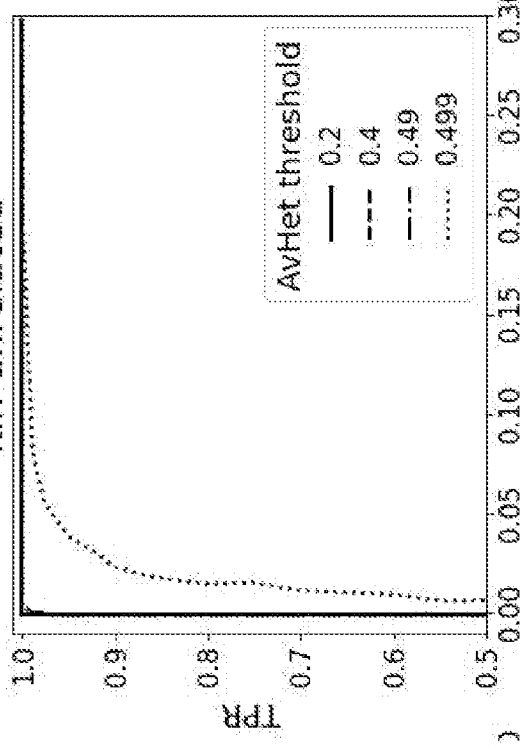


FIG. 5C

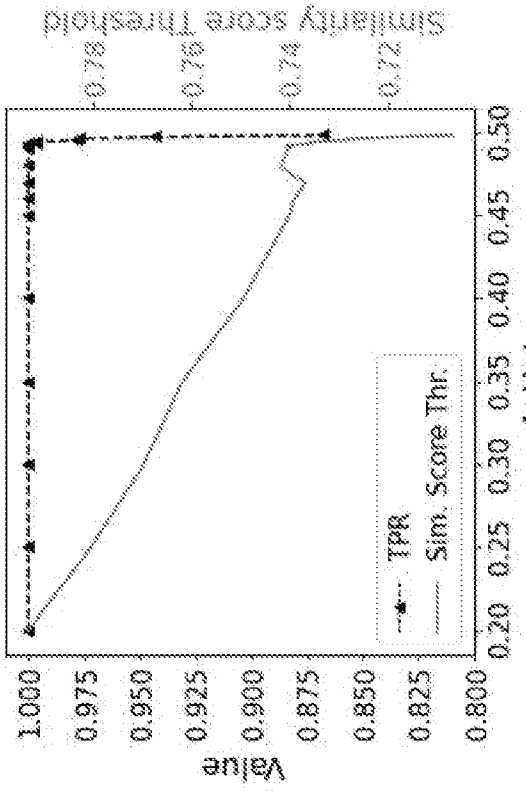
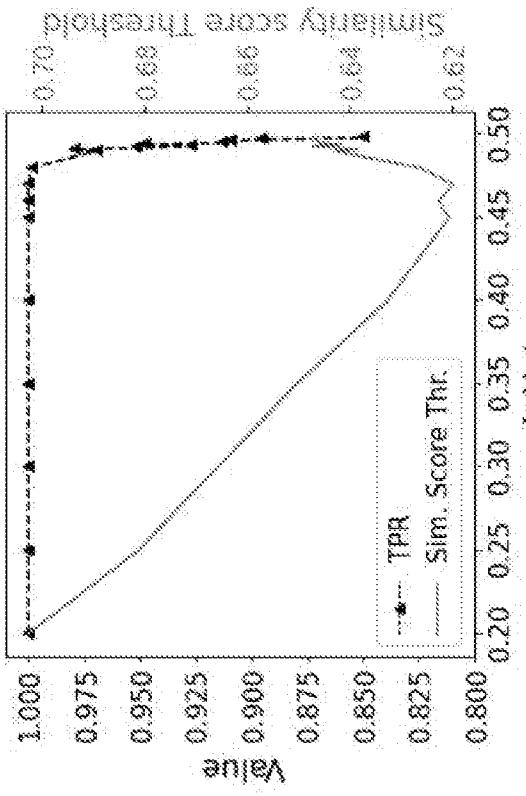


FIG. 5D



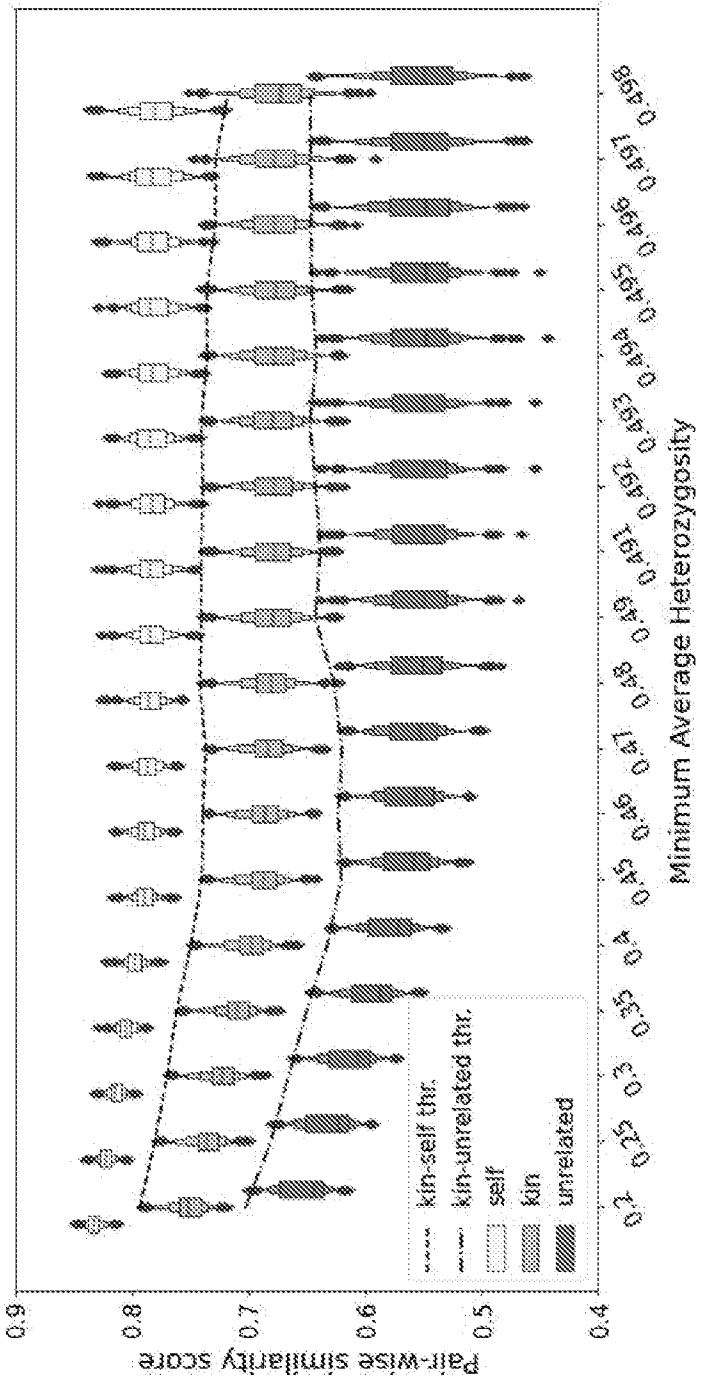


FIG. 6

thresholds at different AvHet for which PPV > 0.999.

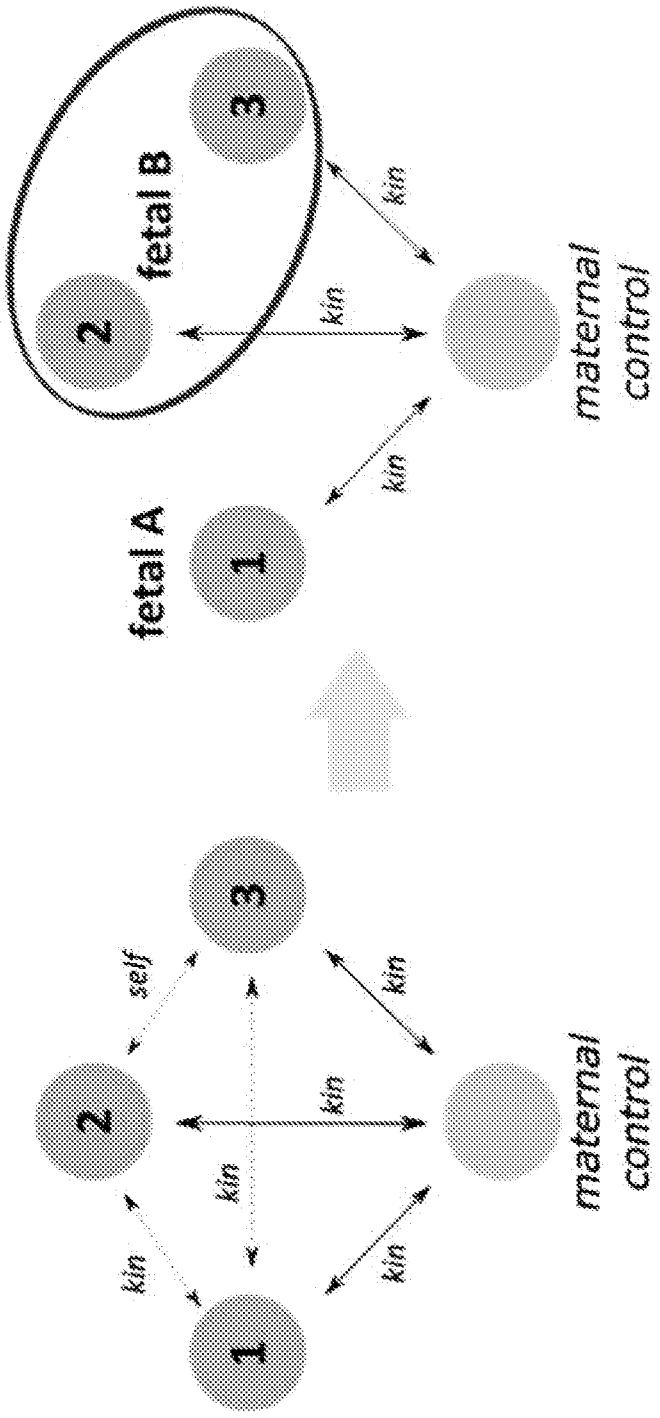


FIG. 7

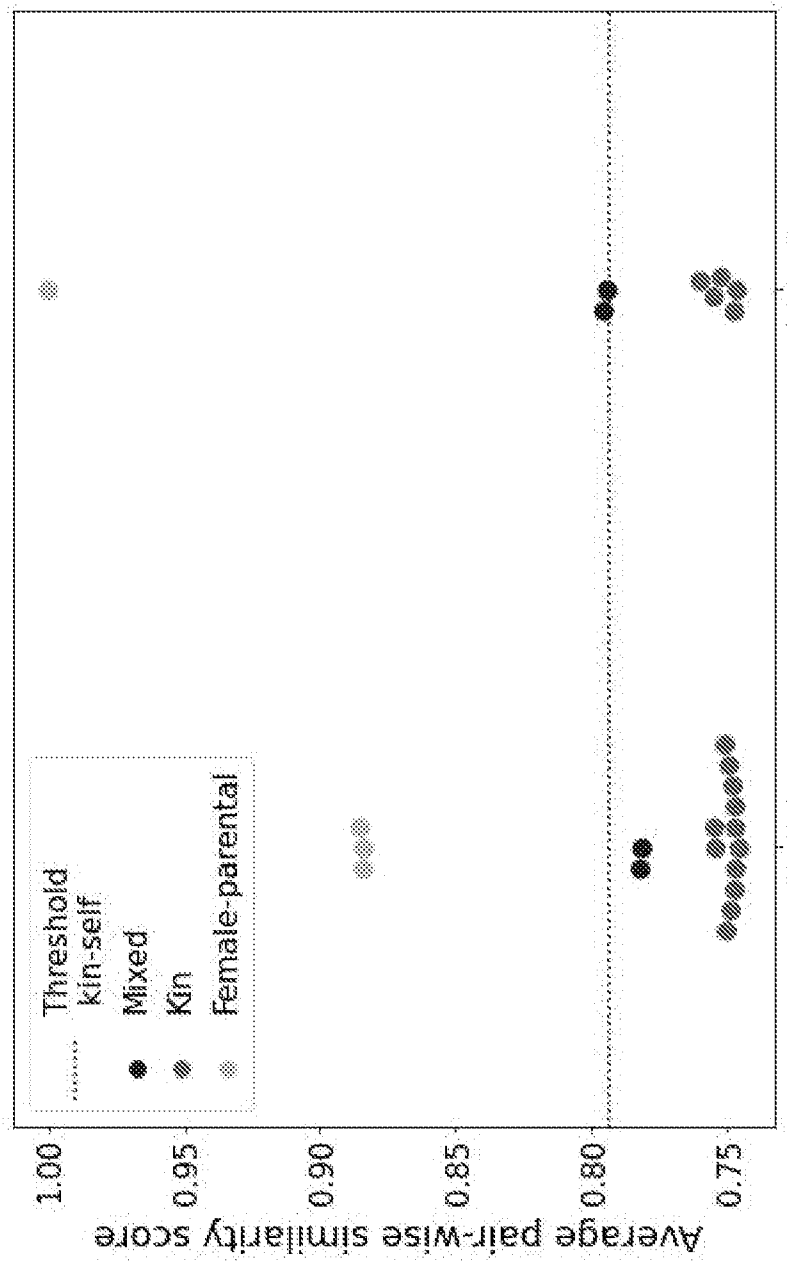

Threshold kin-self
Mixed
Kin
Female-parental
1.00
0.95
0.90
0.85
0.80
0.75
Average pair-wise similarity score
OB1368
OB1383
Sample

FIG. 8

FIG. 9A

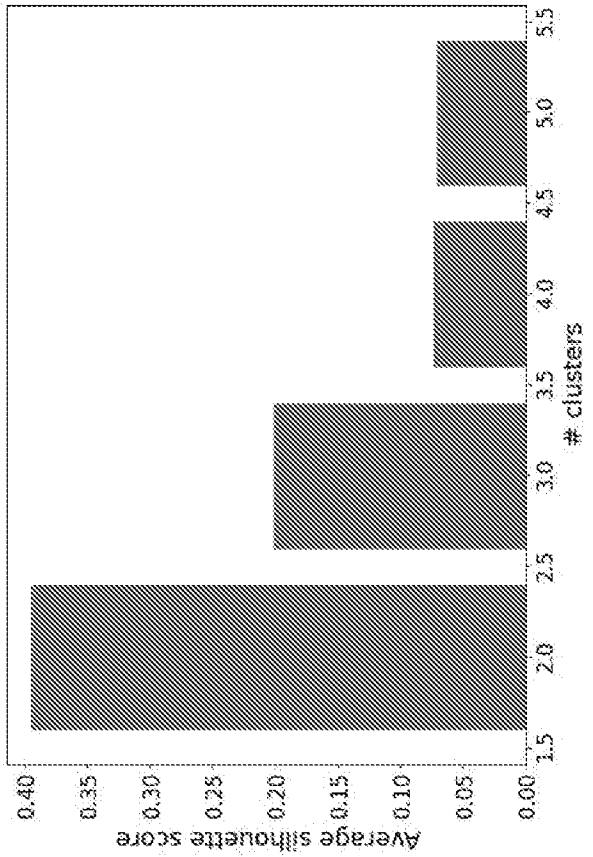


FIG. 9B

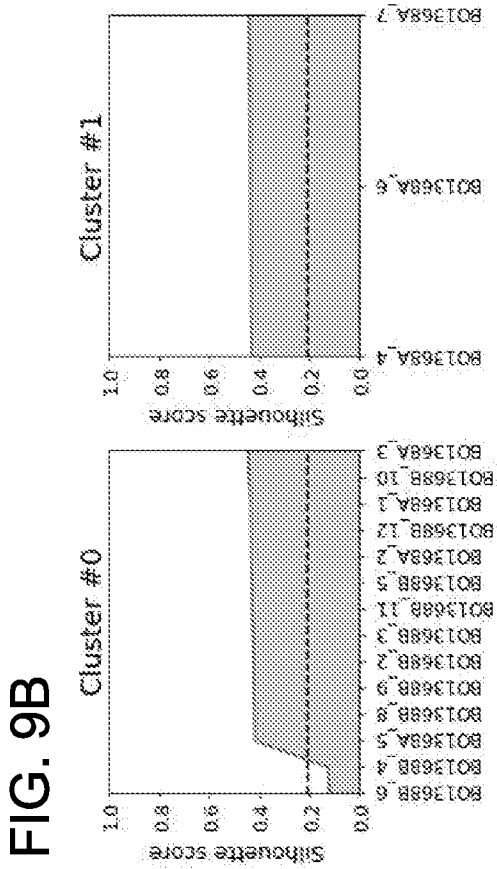


FIG. 9C

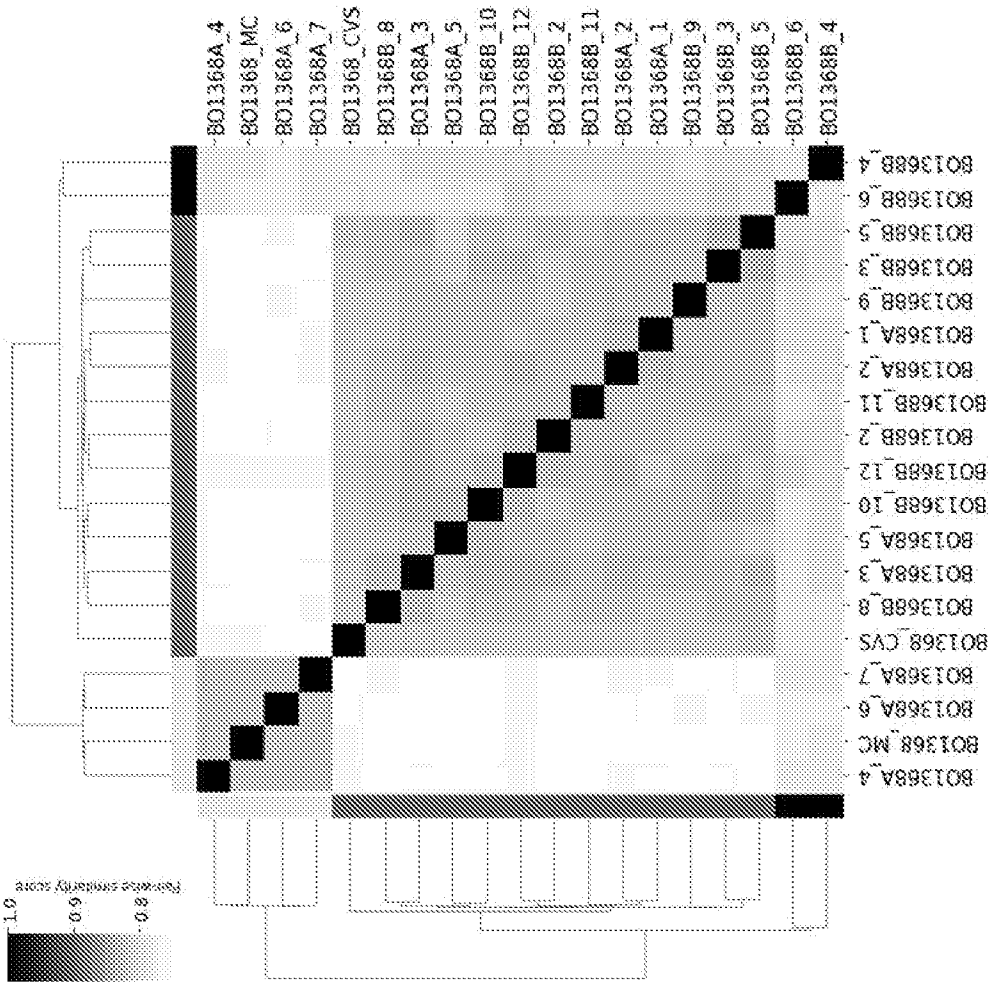


FIG. 10A

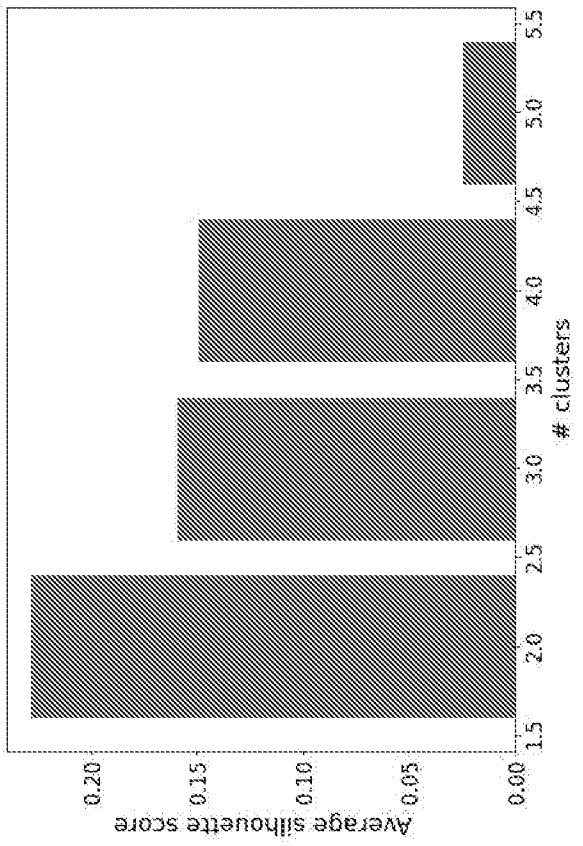


FIG. 10B

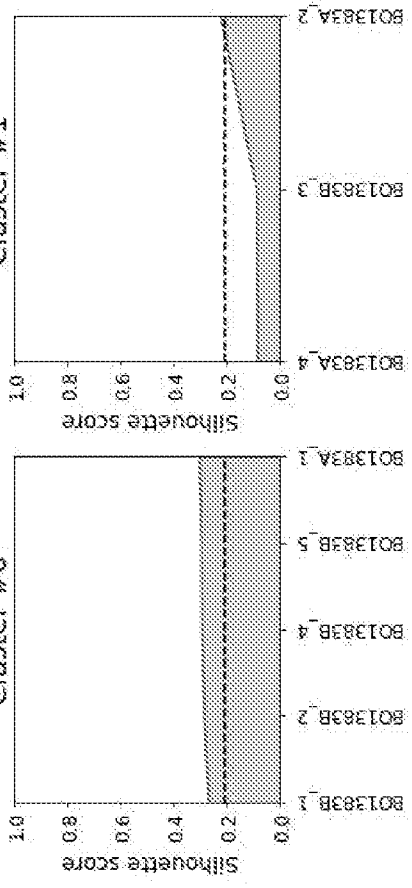
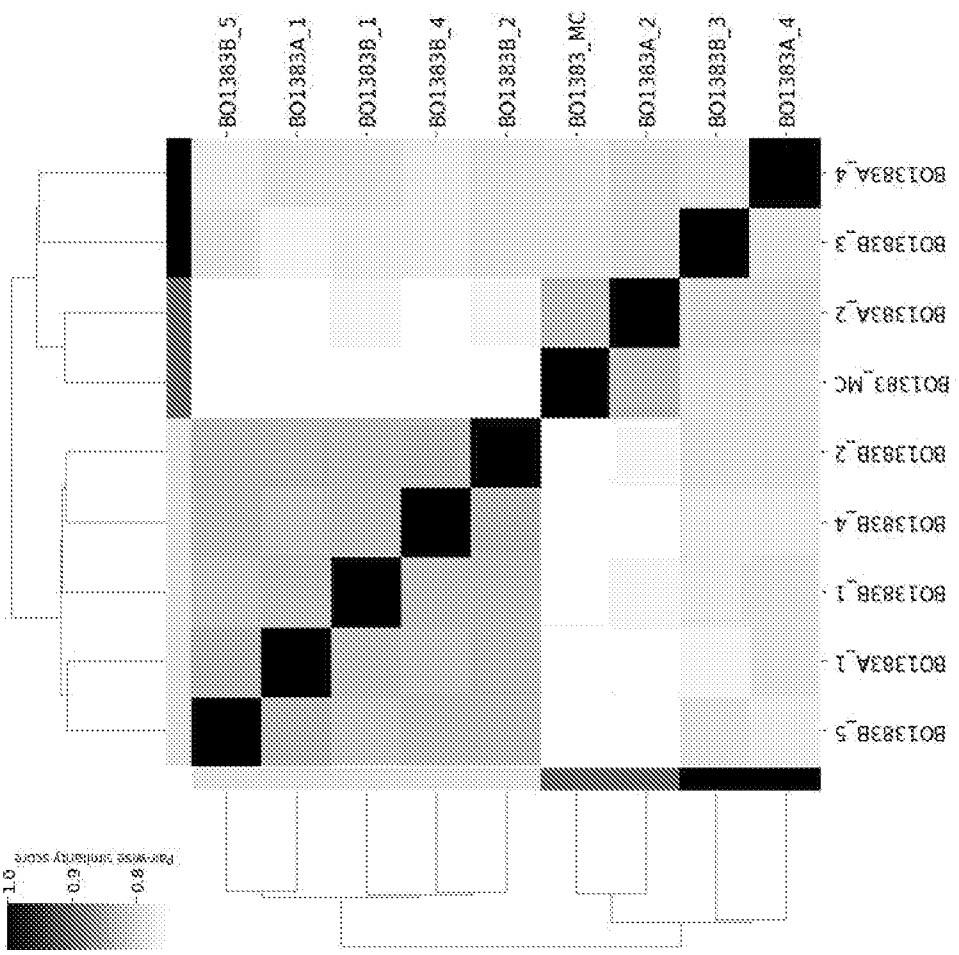


FIG. 10C



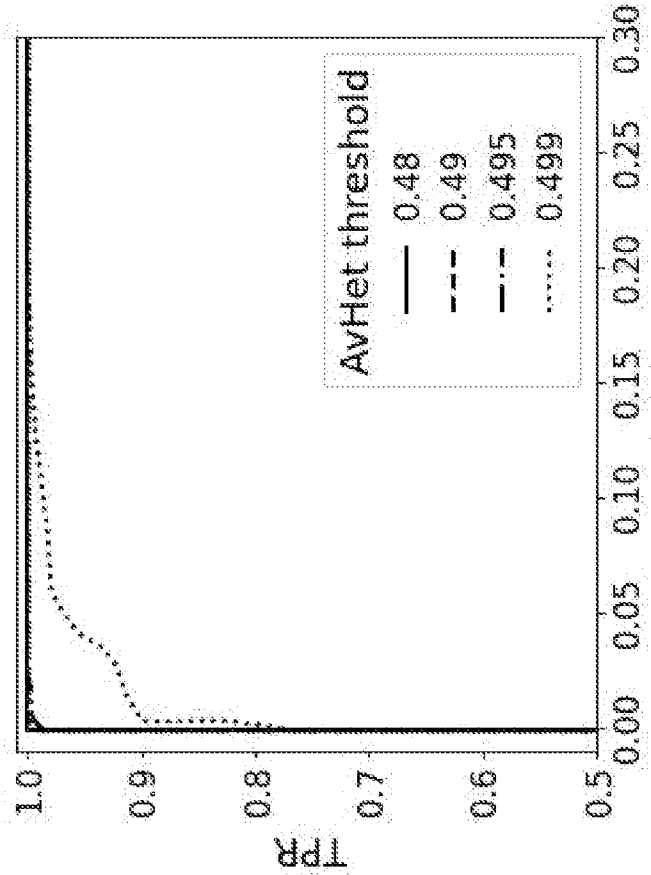


FIG. 11A

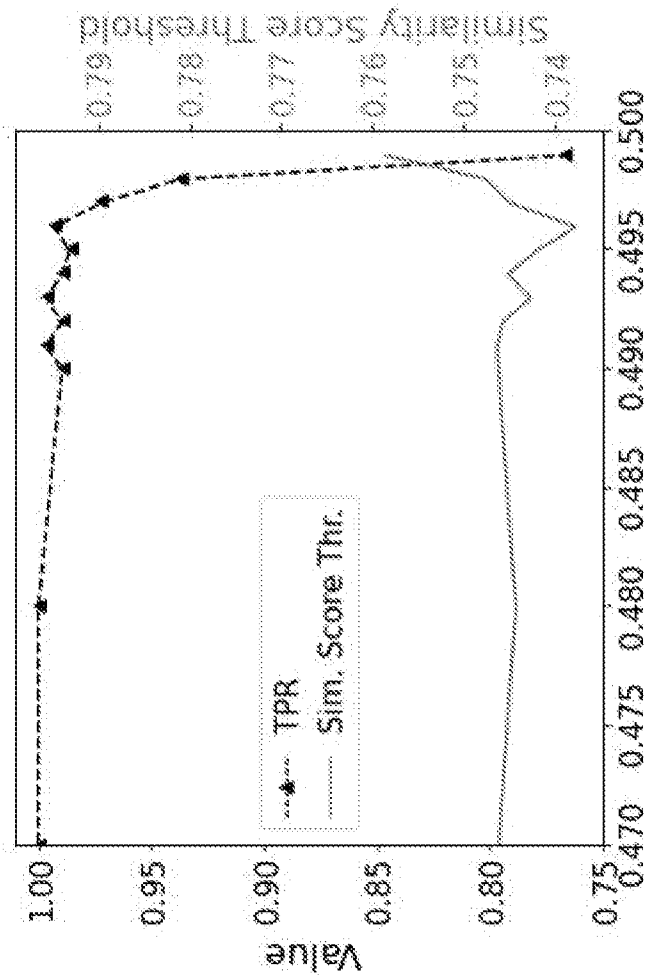


FIG. 11B

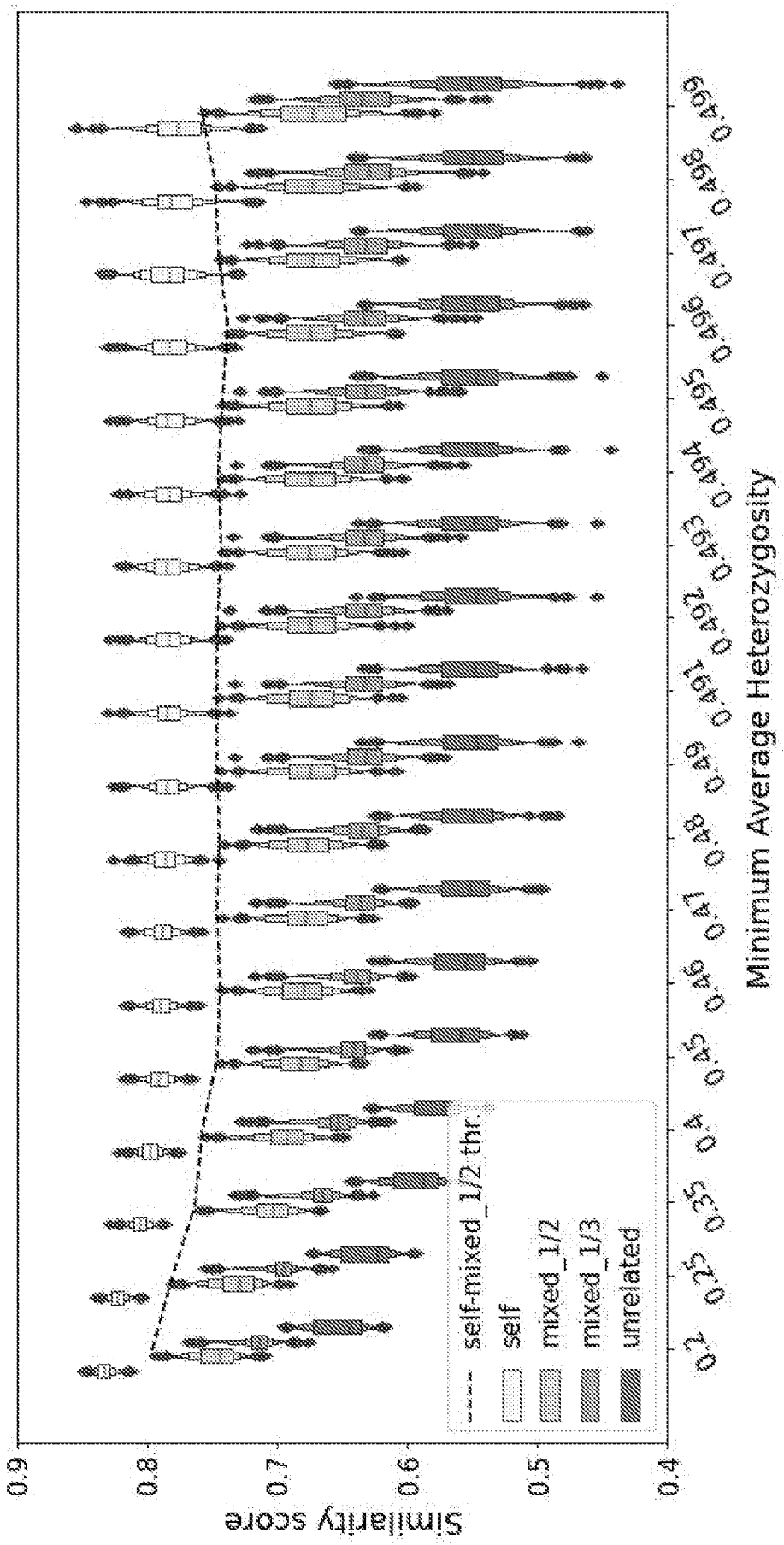

Similarity score
0.9
0.8
0.7
0.6
0.5
0.4
self-mixed_1/2 thr.
self
mixed_1/2
mixed_1/3
unrelated
0.2
0.25
0.3
0.35
0.4
0.45
0.46
0.47
0.48
0.49
0.491
0.492
0.493
0.494
0.495
0.496
0.497
0.498
0.499
Minimum Average Heterozygosity

FIG. 12

FIG. 13A

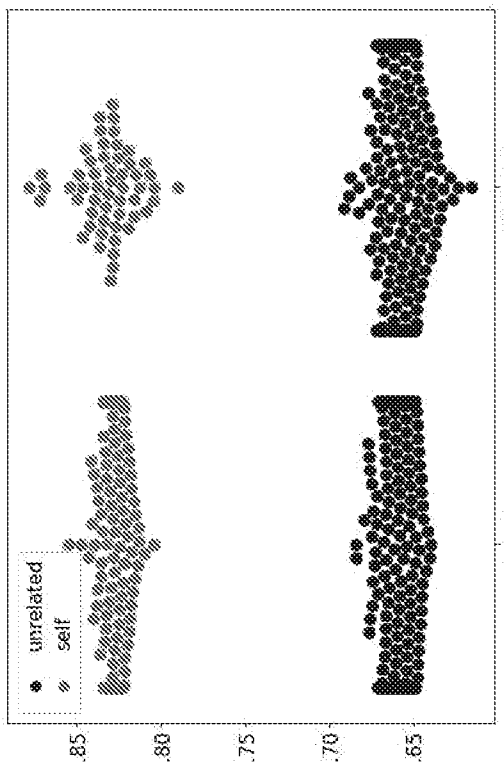


FIG. 13B

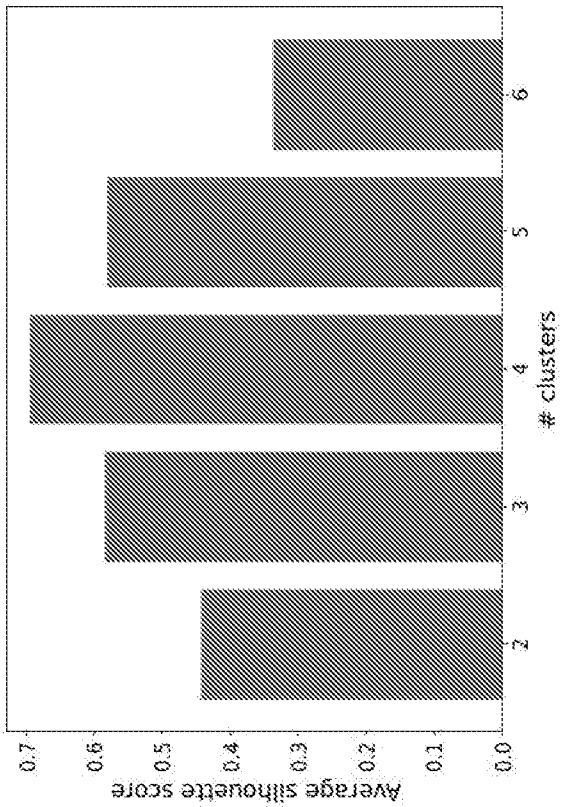
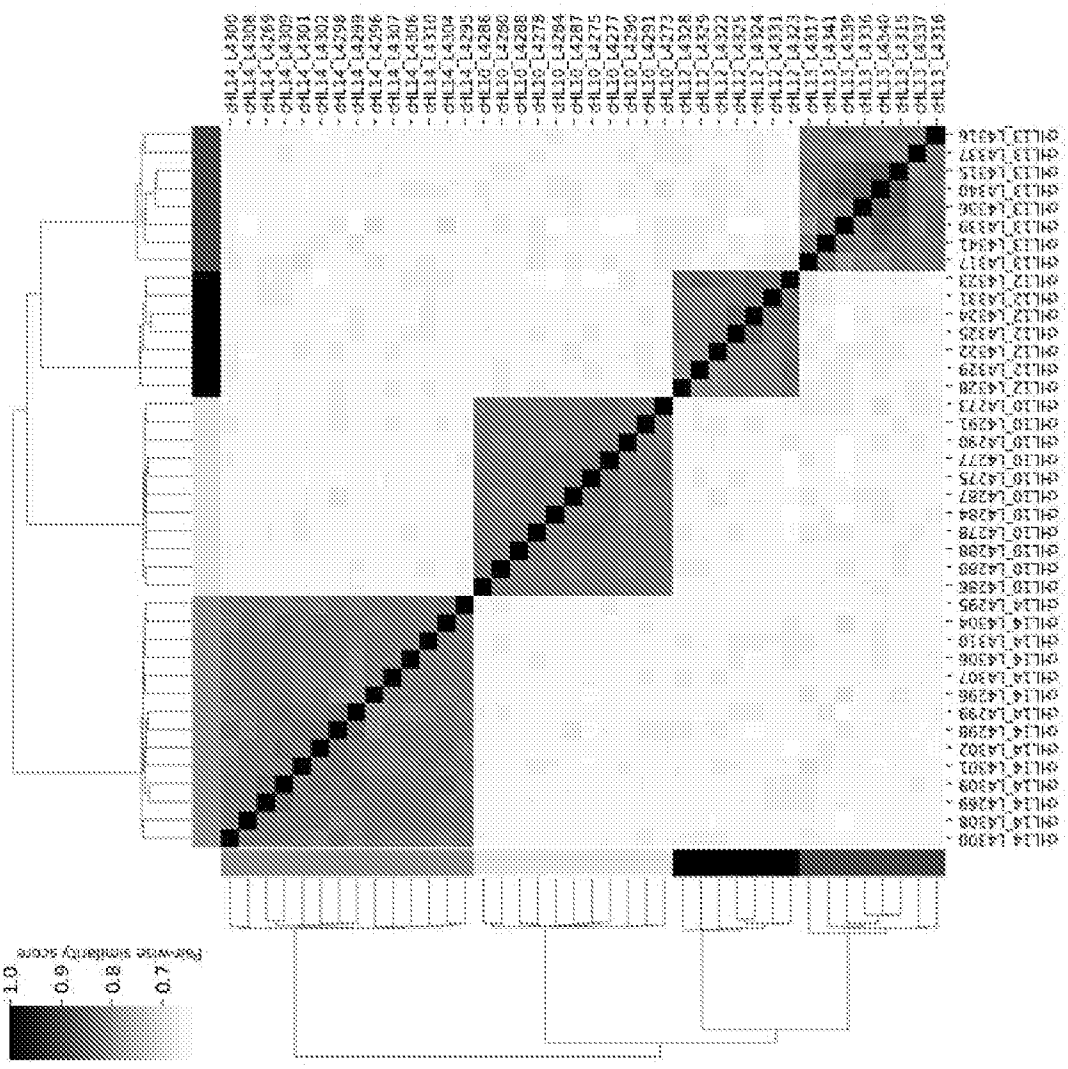


FIG. 13C



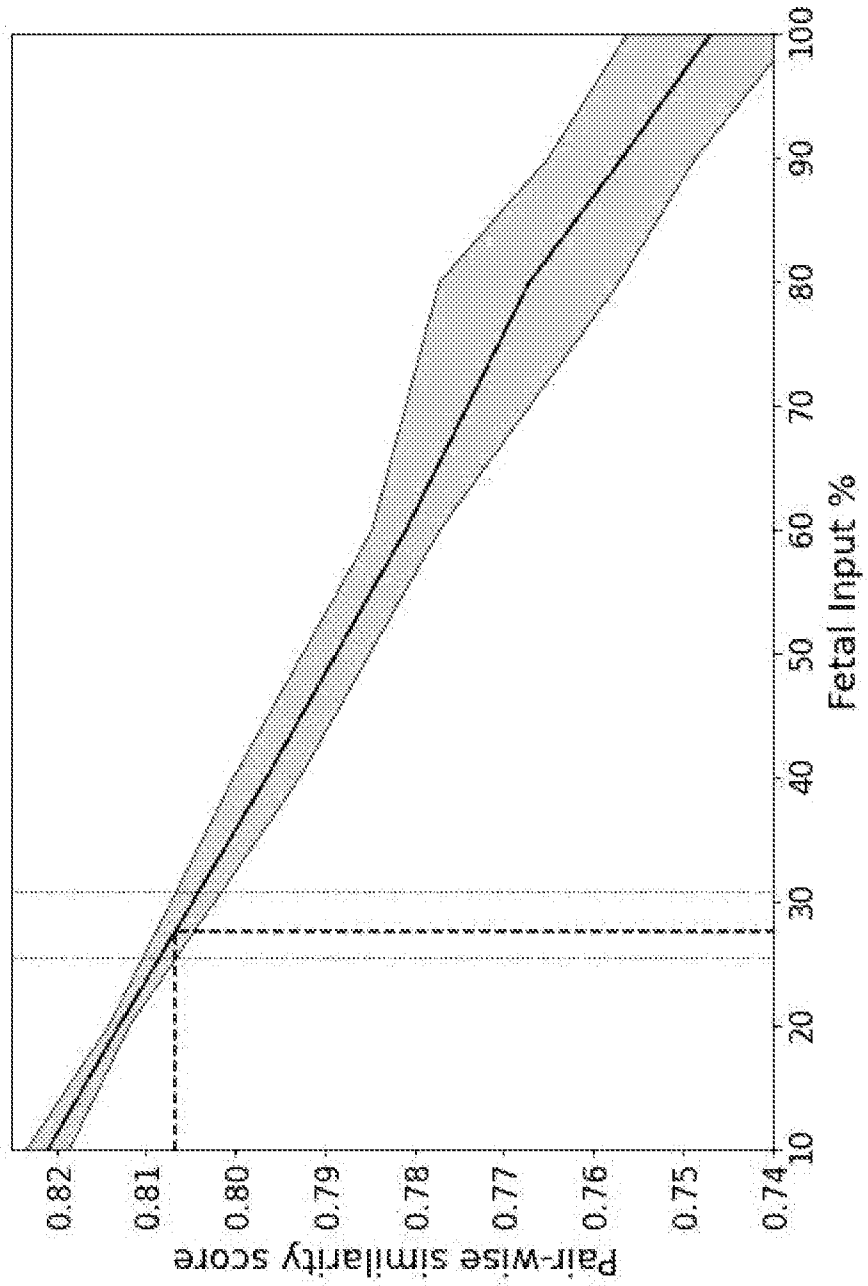

Pair-wise similarity score
0.82
0.81
0.80
0.79
0.78
0.77
0.76
0.75
0.74
10
20
30
40
50
60
70
80
90
100
Fetal Input %

FIG. 14

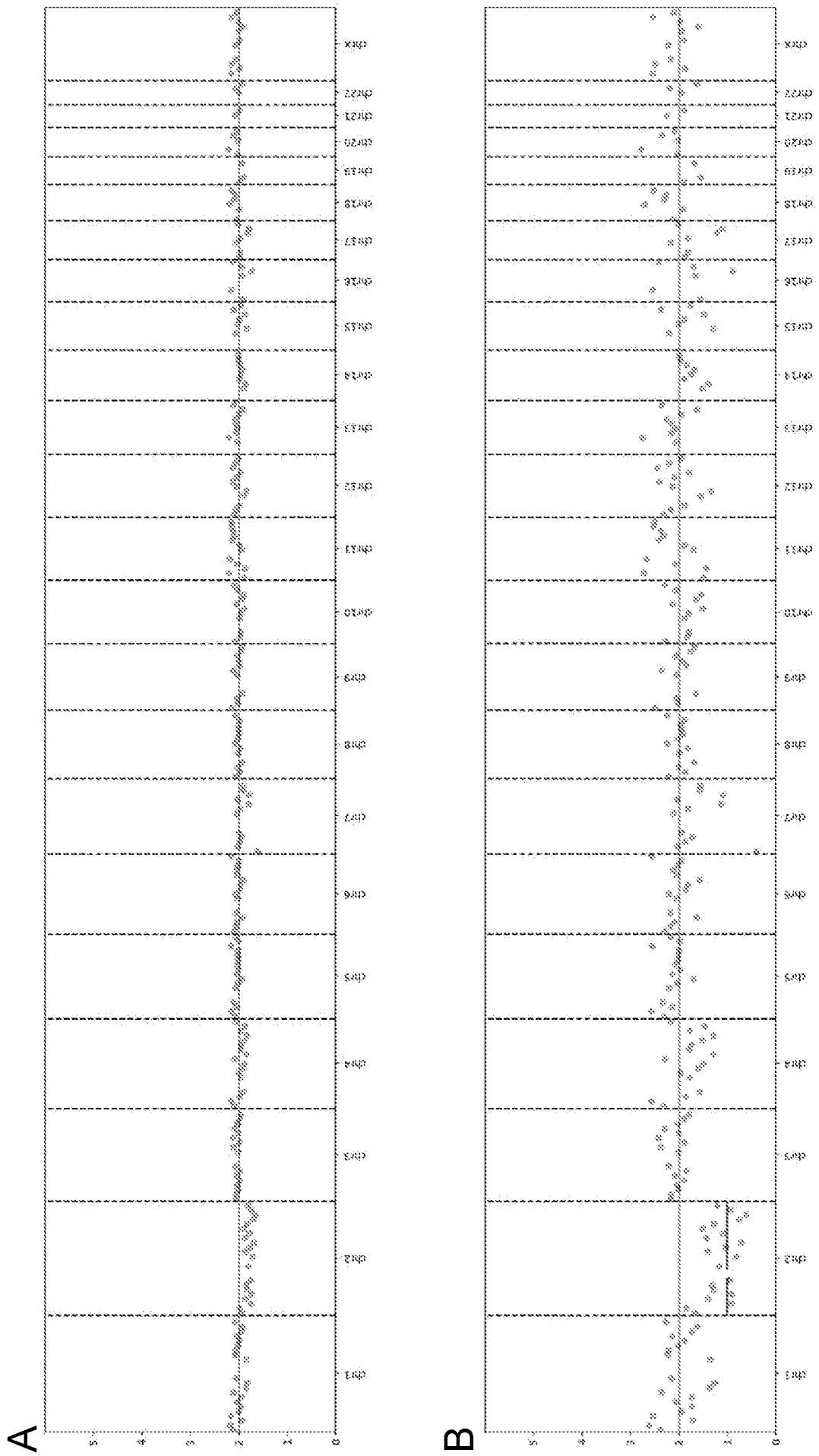


FIG. 15