

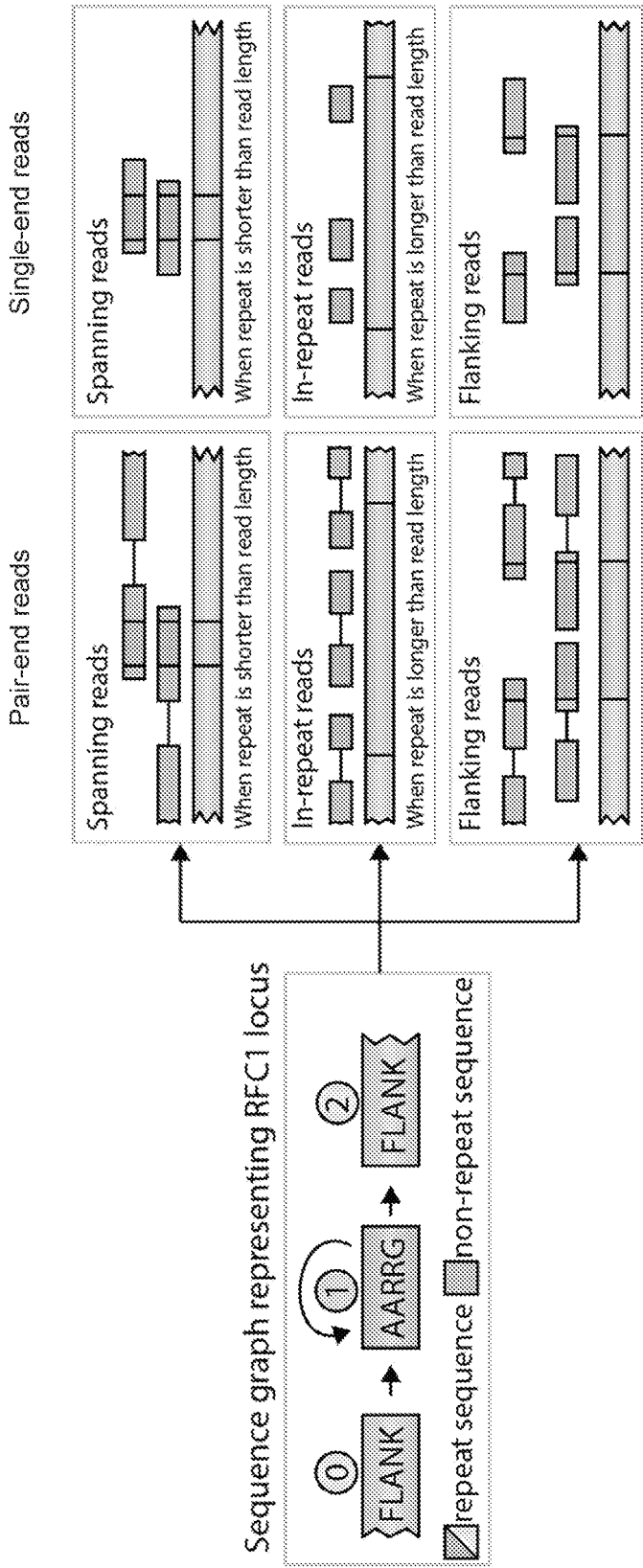
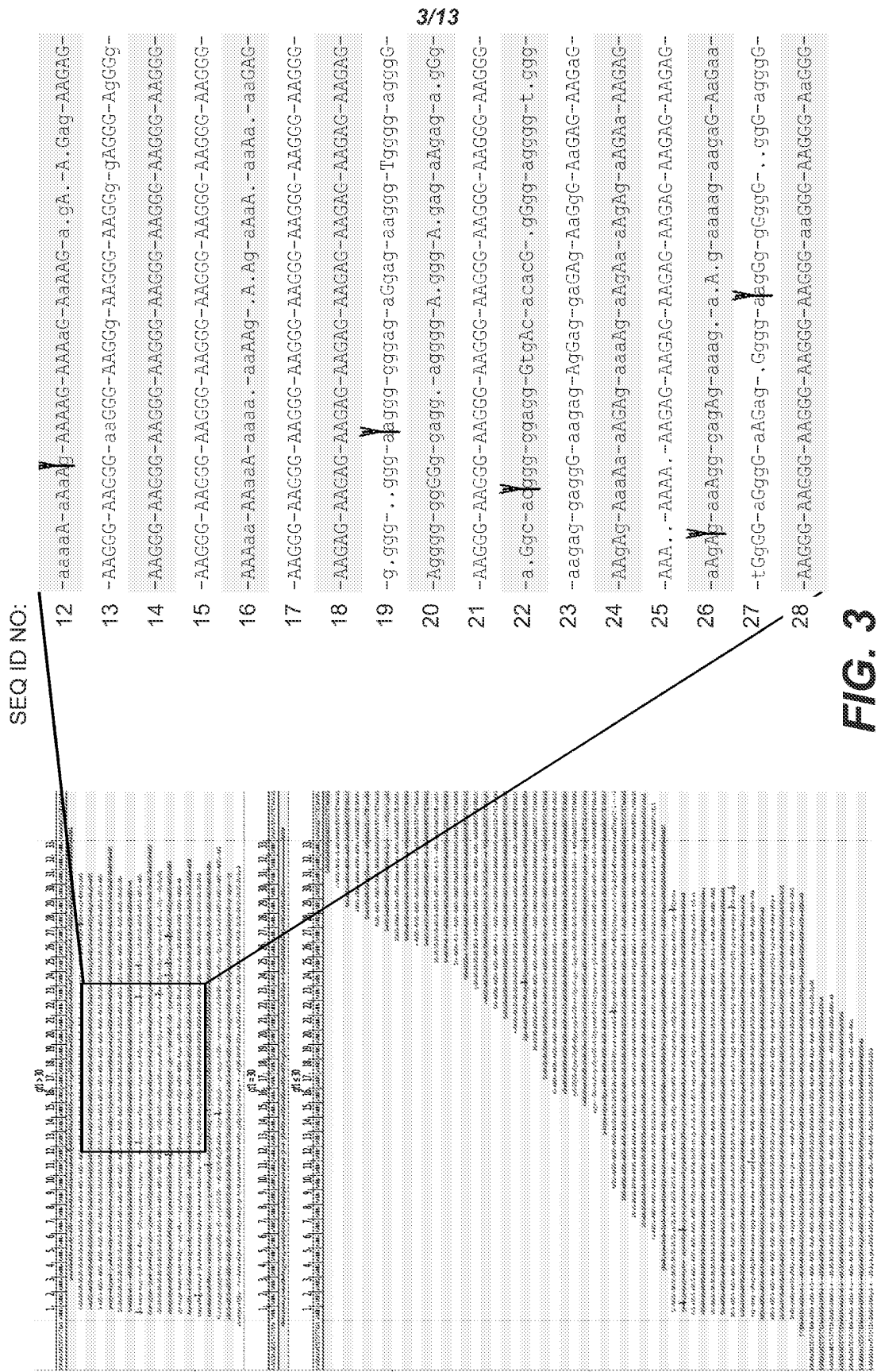


FIG. 1

SEQ ID NO:

1 G-AAGGG-AAGGG-AAGGG-AAGGG-AAGGG-AAGGG-AAGGG-AAGGG-AAGGG-
2 aGGG-aAGGG-AAGGG-AAGGG-AaGGG-AAGGG-AAGGG-AaGGG-caGGG-cAGGG-
3 AGGG-AAGGG-AAGGG-AAGGG-AAGGG-AAGGG-AAGGG-AAGGG-AAGGG-
4 -AAGG-aAGGG-AAGGG-aAGGG-AAGGG-aAGGG-aAGGG-aAGGG-aAGGG-
5 -AAGGG-AAGGG-AAGGG-AAGGG-AAGGG-AAGGG-AAGGG-AAGGG-AAGGG-
6 -AaGGG-AAGGG-AAGGG-AAGGG-AAGGG-AAGGG-AAGGG-aAGGG-AAGGG-
7 -AAGGG-AAGGG-AAGGG-AAGGG-aAGGG-AAGGG-AAGGG-AAGGG-AAGGG-
8 -AAGGG-AAGGG-AAGGG-AAGGG-AAGGG-AAGGG-AAGGG-AAGGG-AAGGG-
9 -acggG-.GgGg-c.ggg-caGGG-gGgGg-.GgGg-TgGgGg-ggggG-.g.ggg-
10 -gGGG-aGGG-gGGGg-GgGGG-gGGGg-GgGGG-gGGGg-GGGGg-GaGGG-gGGGg-
11 -GaGgG-gGgGg-a.GGg-aGgGg-GagGg-aagGg-GgGgG-g.GGg-AGGag-.gGg-aaGGG-

FIG. 2



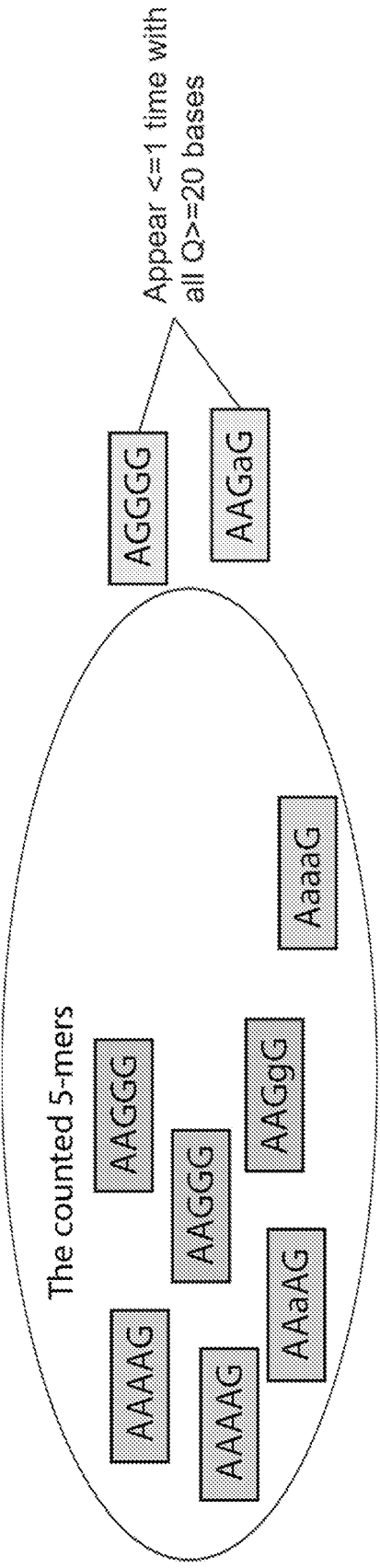


FIG. 4A

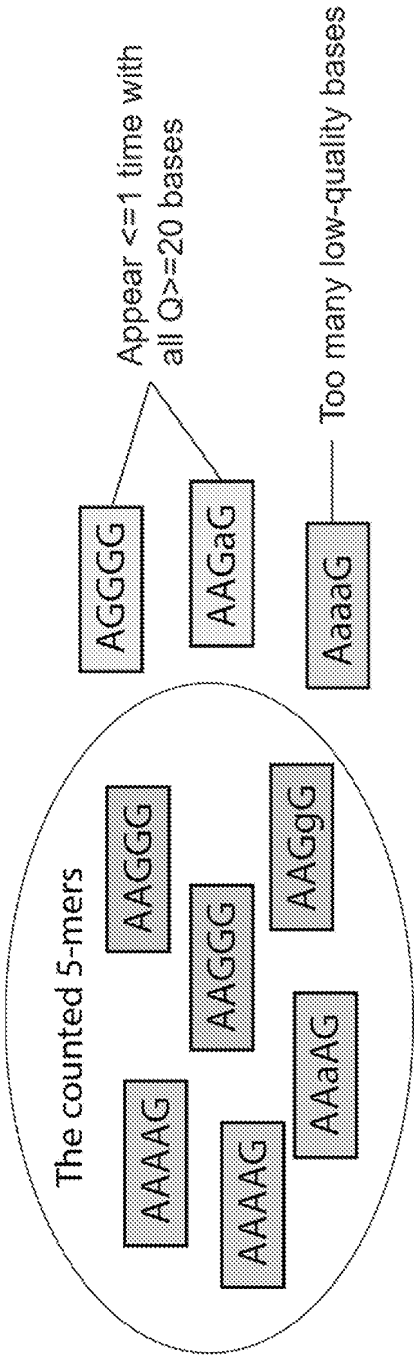


FIG. 4B

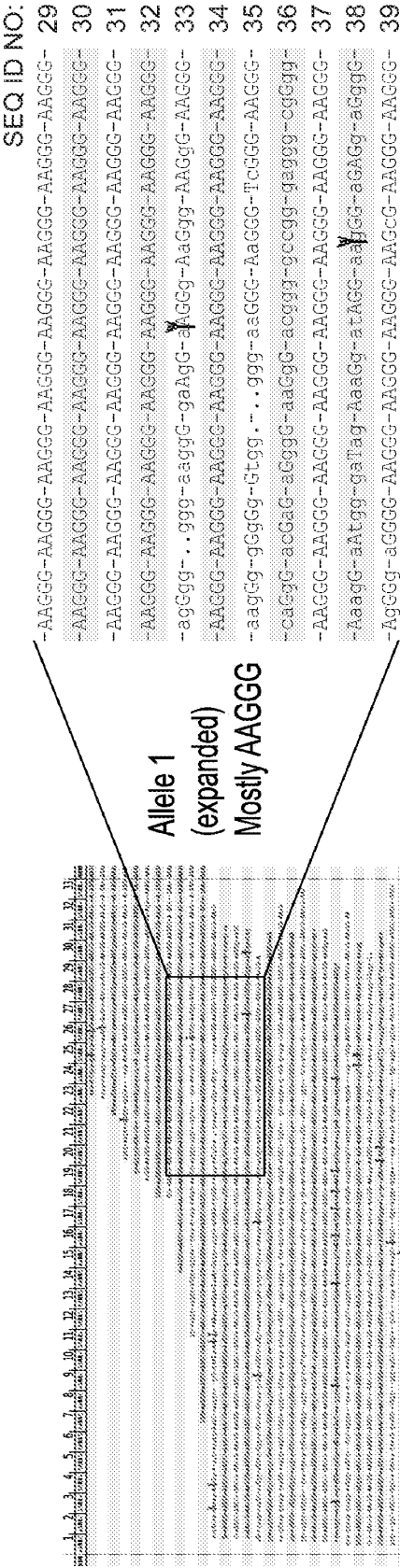
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When looking at two haplotypes together, it was observed:

%AAGG = 75%

%AAAAG = 20%

FIG. 5A



By doing 5-mer counting on the expanded allele only, it was observed:

%AAGGG = 93% %GGGGG = 7%

%AAAAG = 0%

FIG. 5B

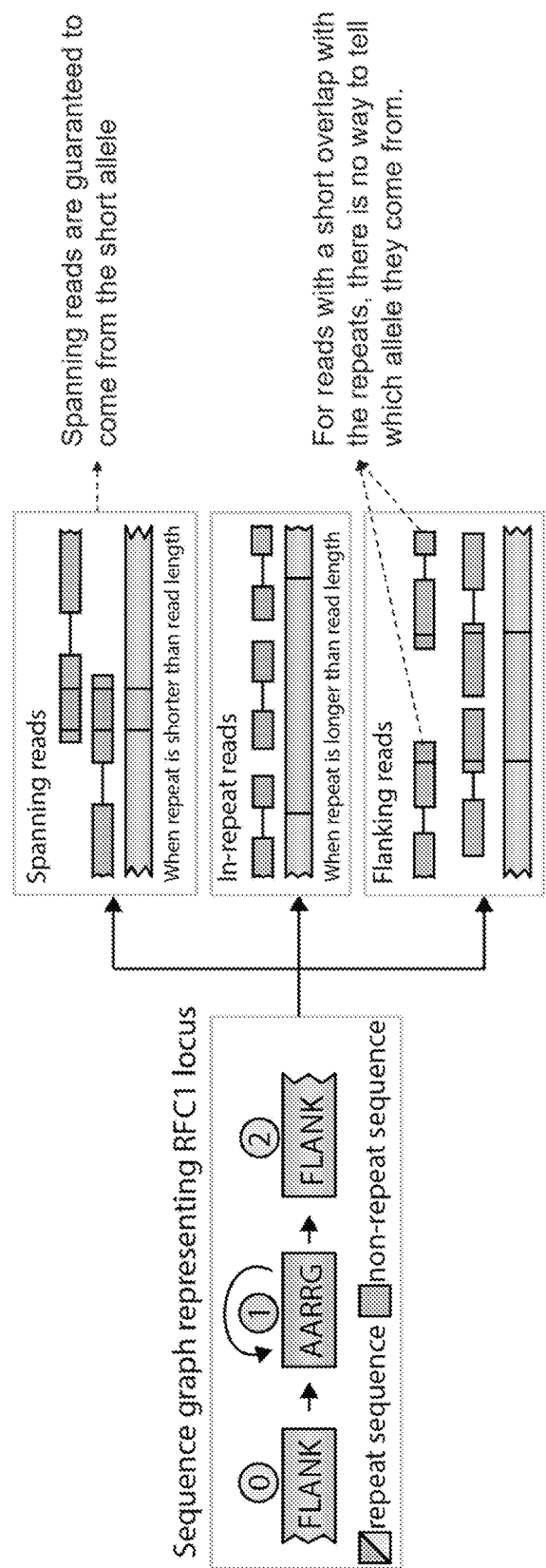


FIG. 6A

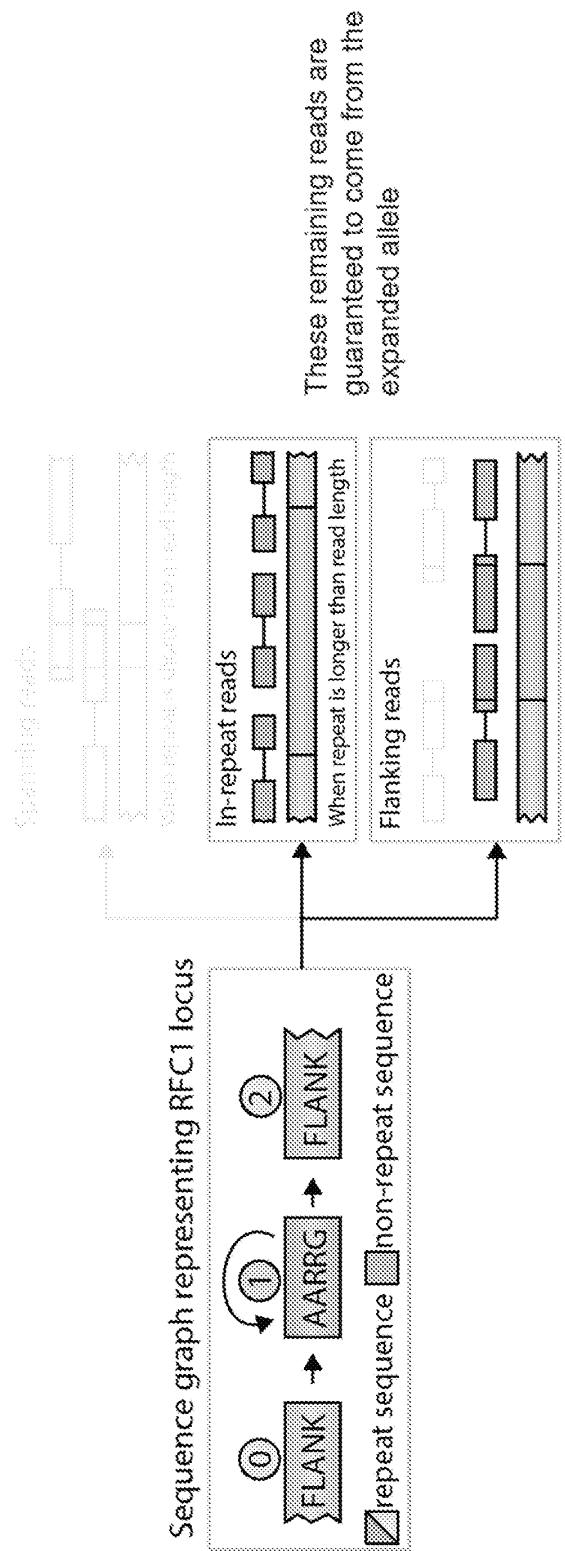


FIG. 6B

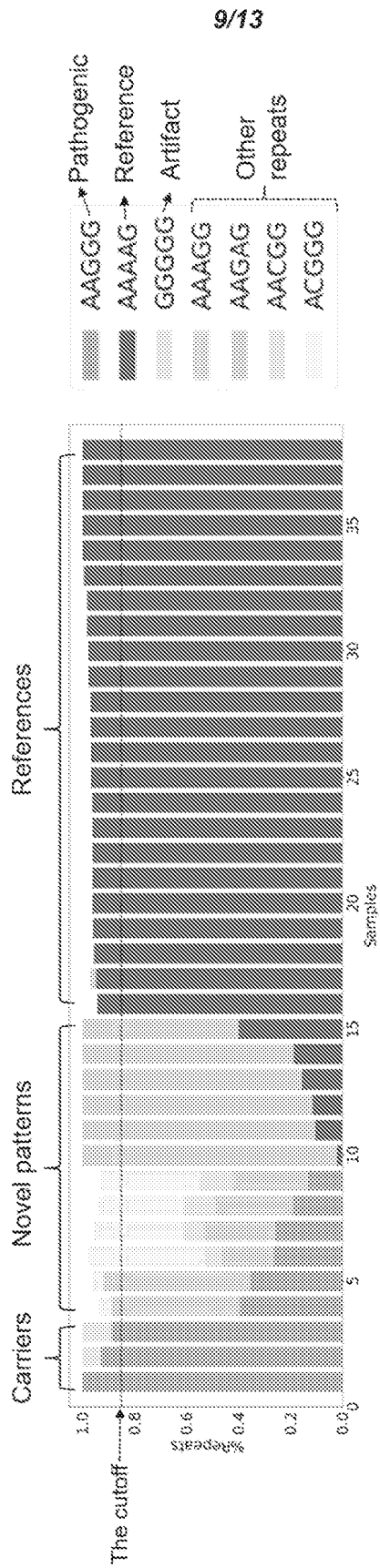


FIG. 7

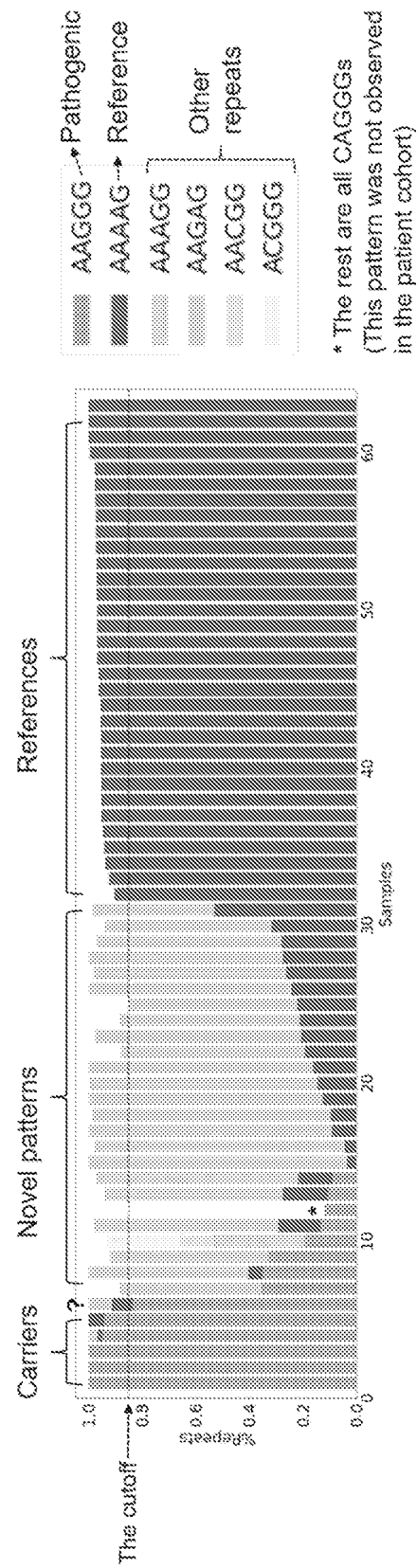
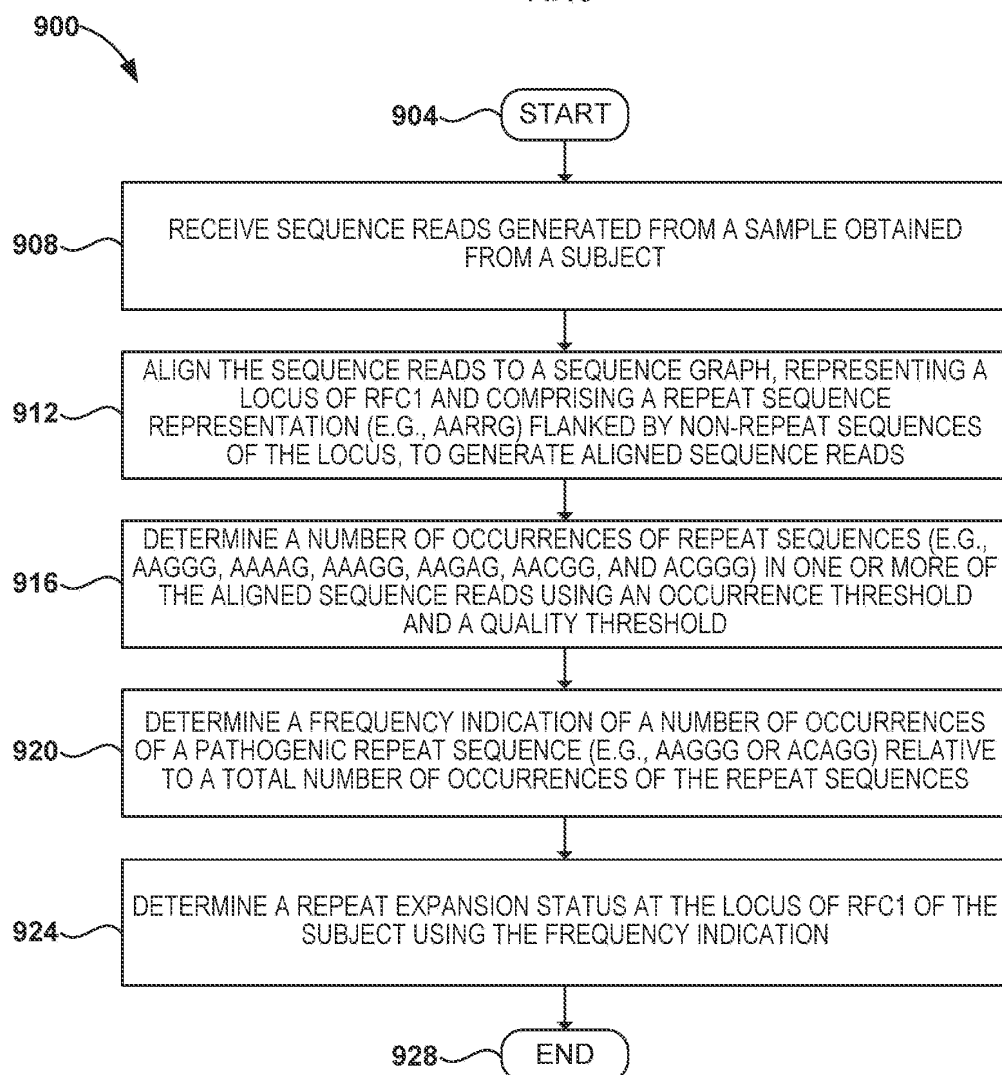


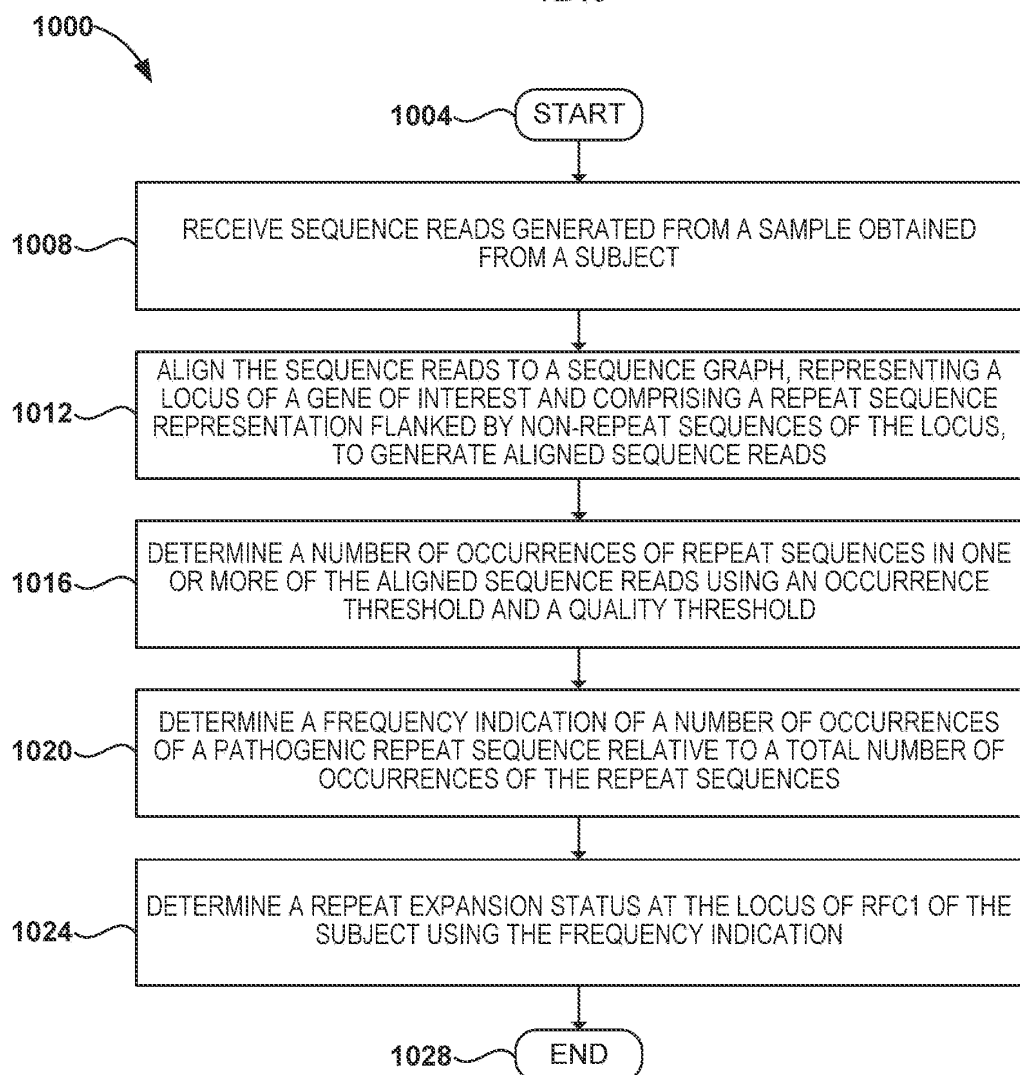
FIG. 8

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**FIG. 9**

SUBSTITUTE SHEET (RULE 26)

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**FIG. 10**

SUBSTITUTE SHEET (RULE 26)

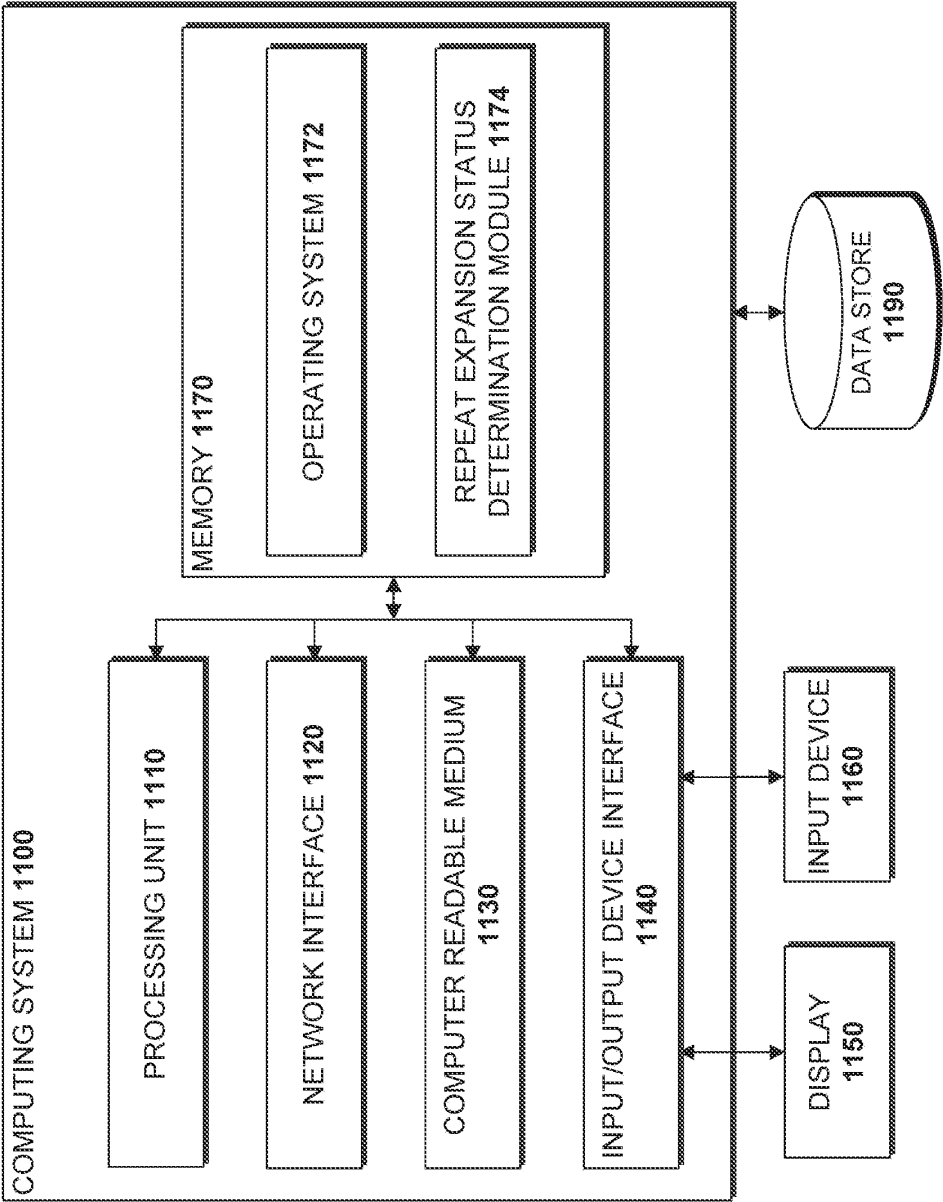


FIG. 11