

FIG. 1

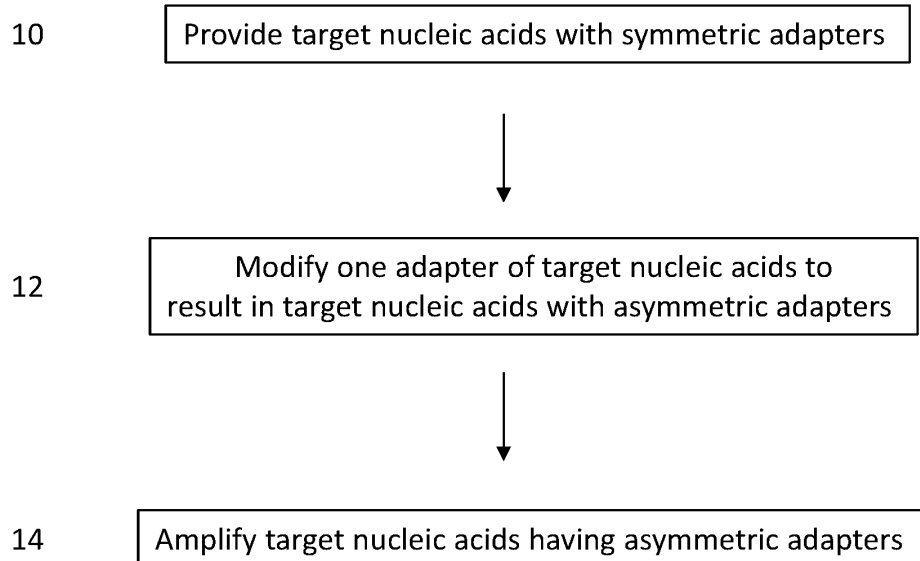


FIG. 2

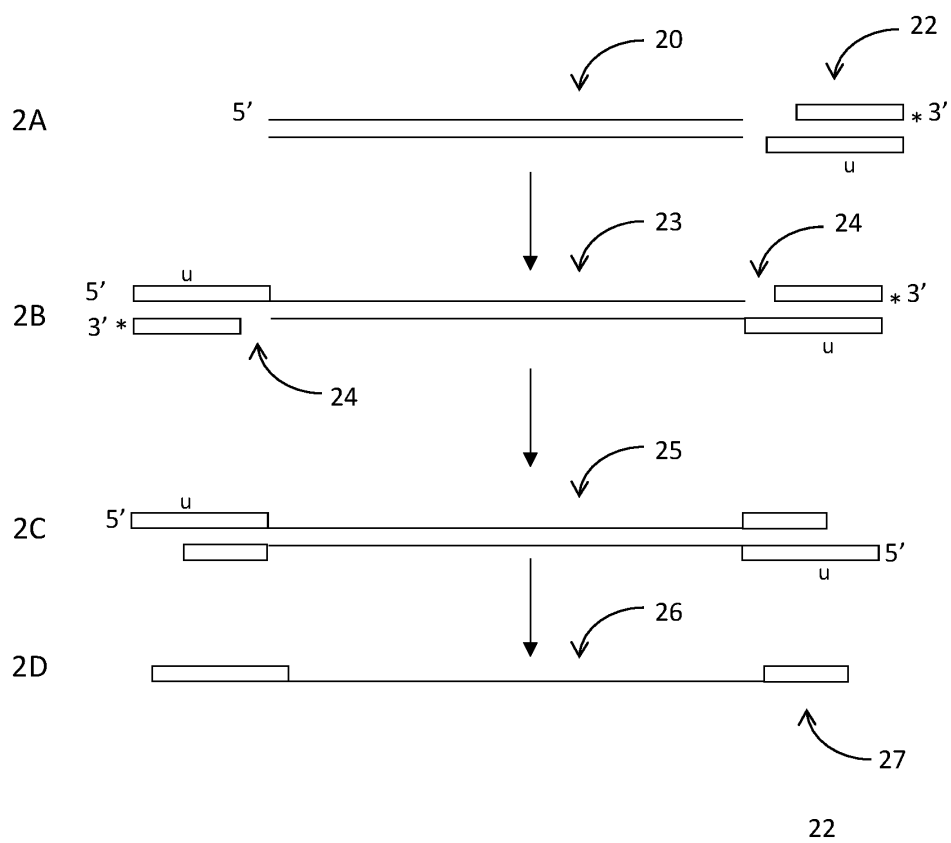


FIG. 3

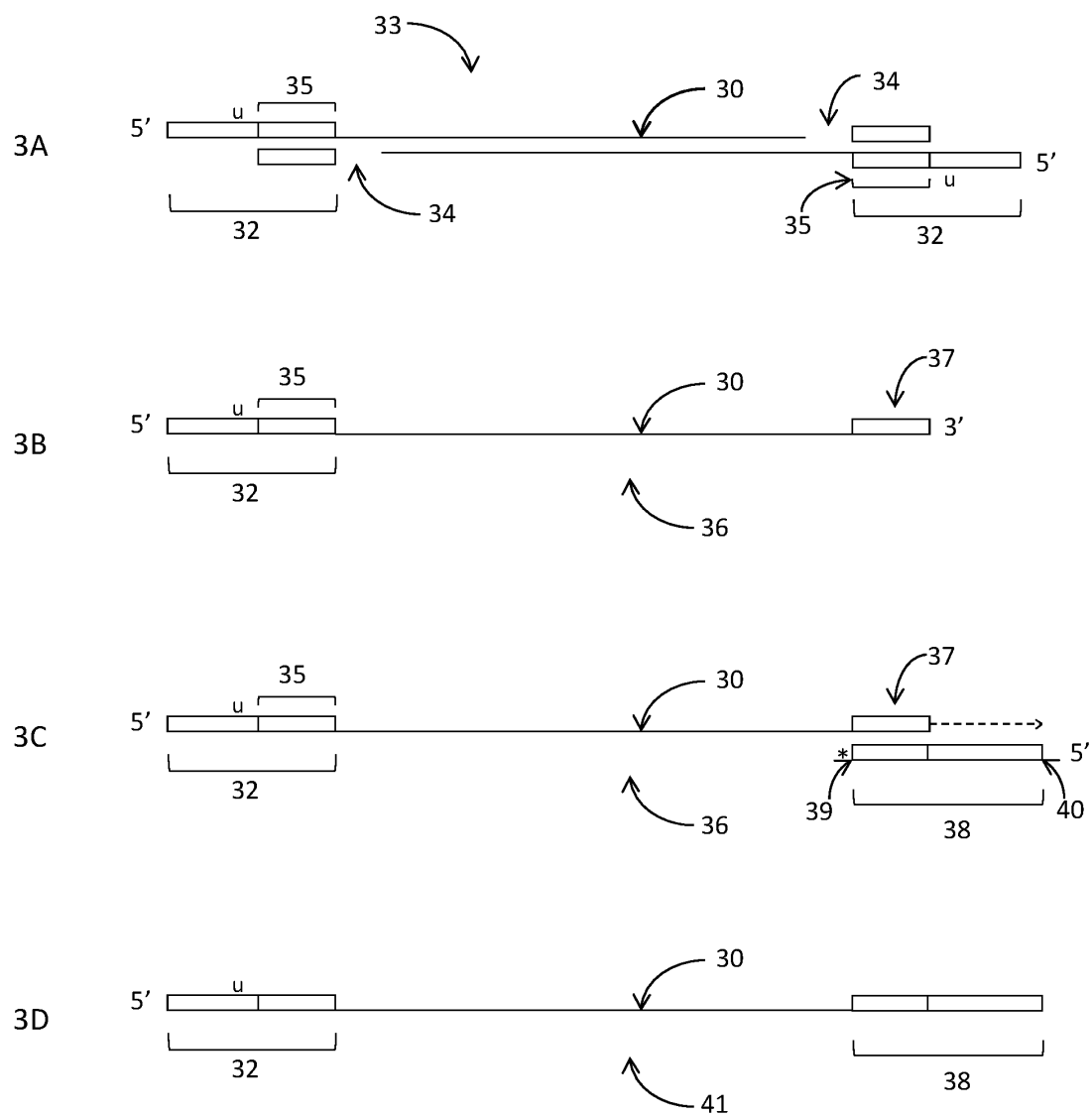
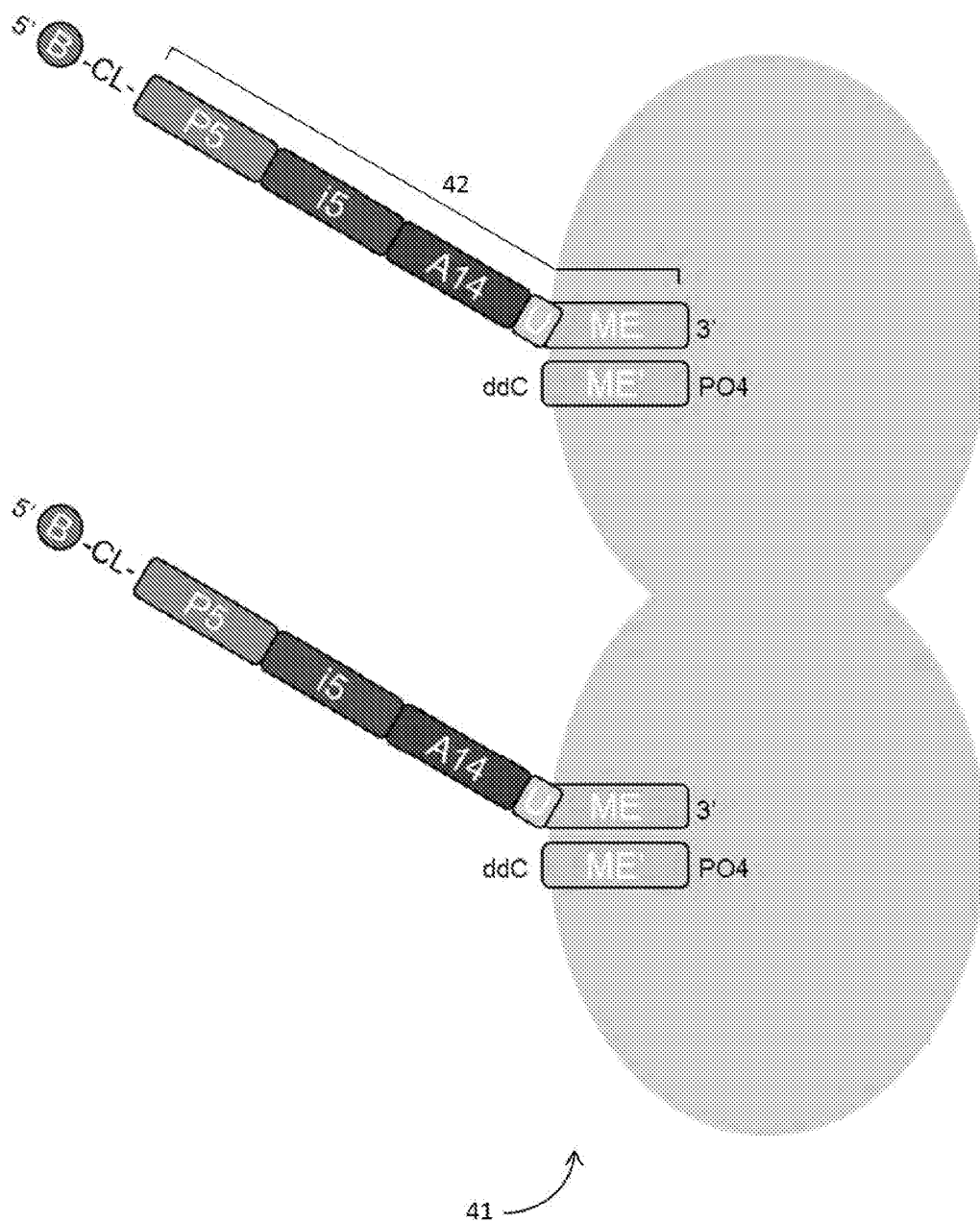


FIG. 4A



5/37

FIG. 4B

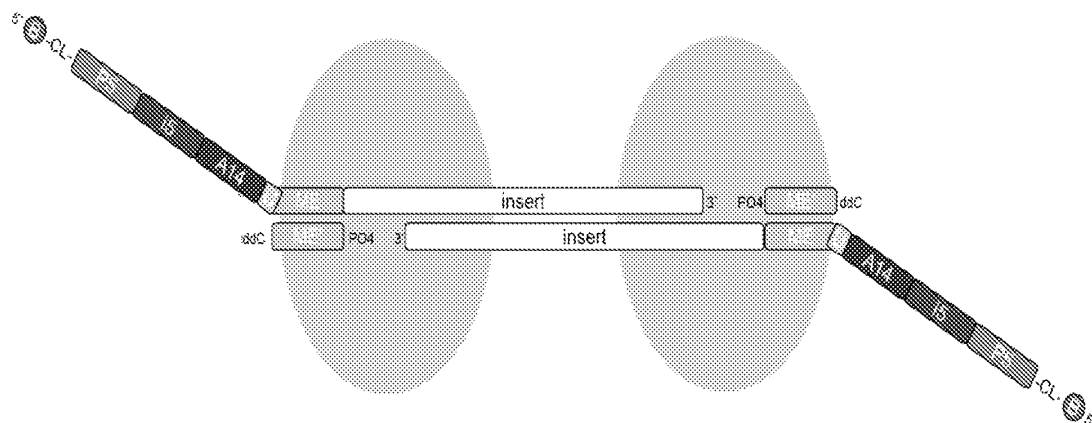


FIG. 4C

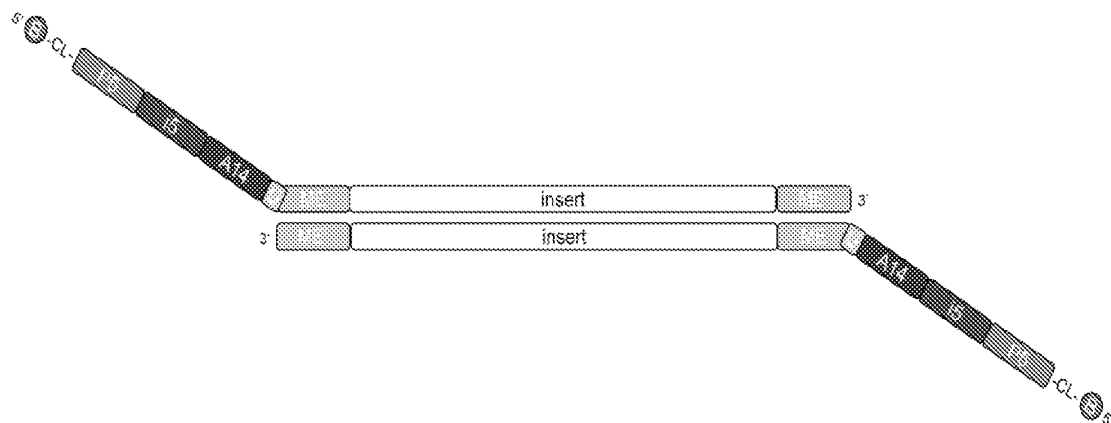


FIG. 4D

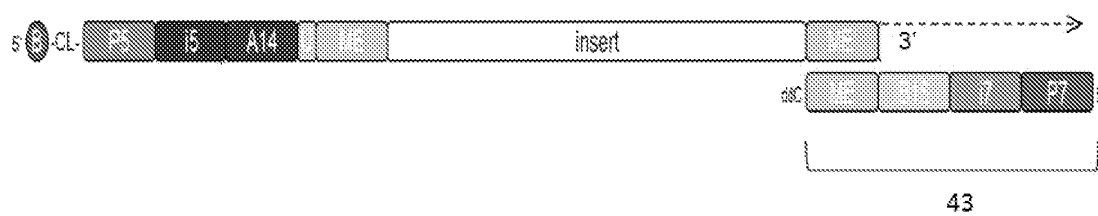
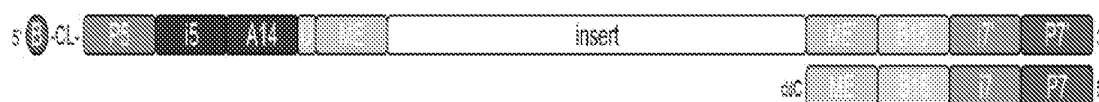
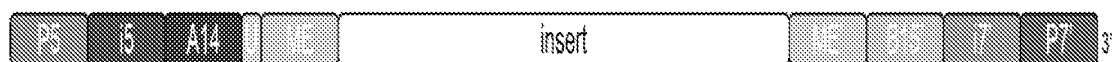


FIG. 4E



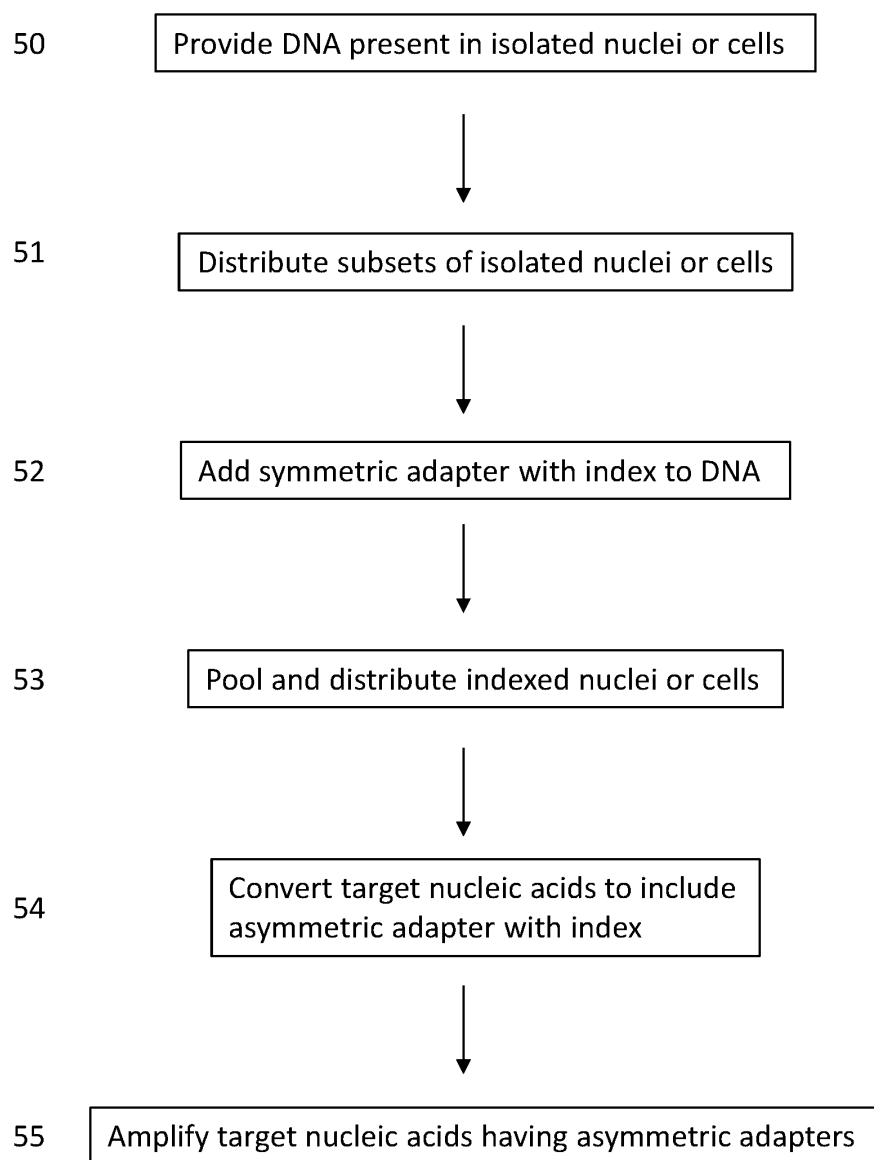
7/37

FIG. 4F



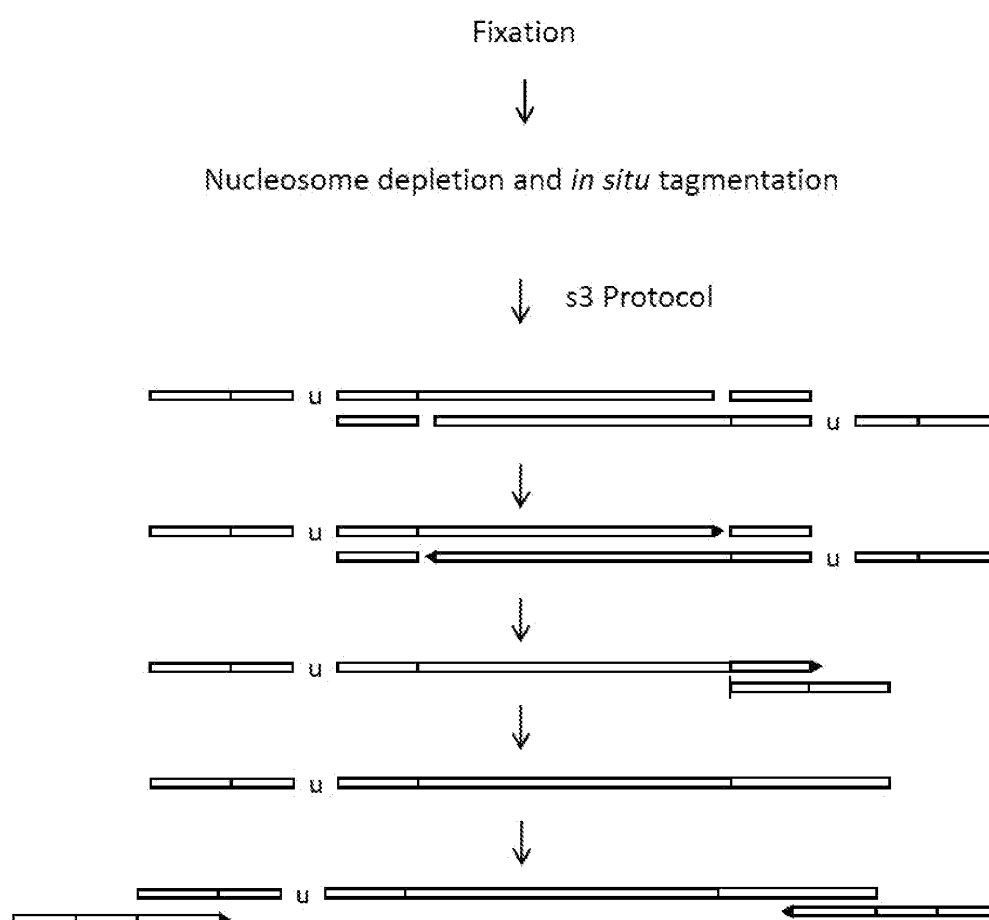
8/37

FIG. 5



9/37

FIG. 6



10/37

FIG. 7

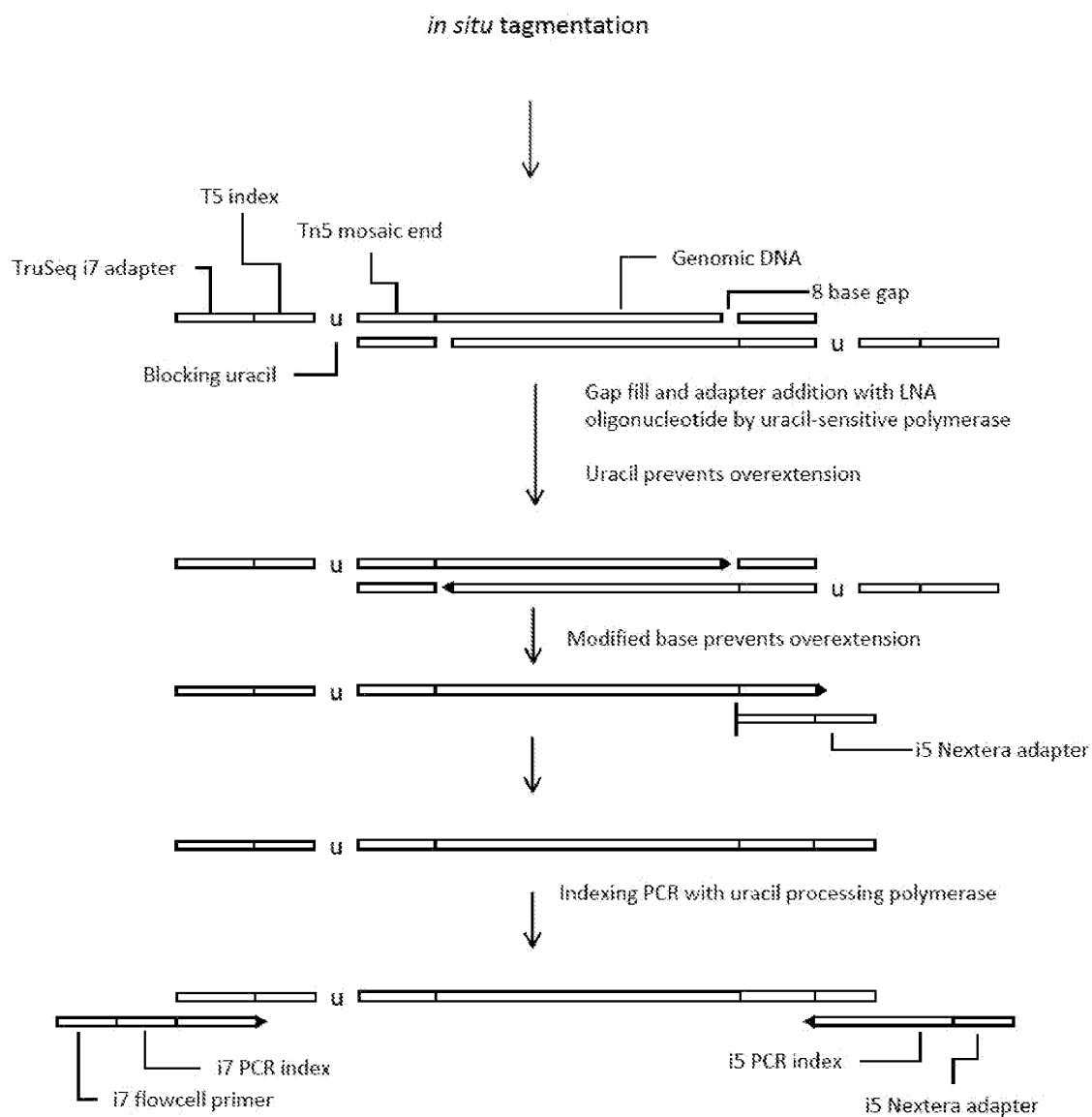


FIG. 8A

Indexed Reversed Transcription (96x)

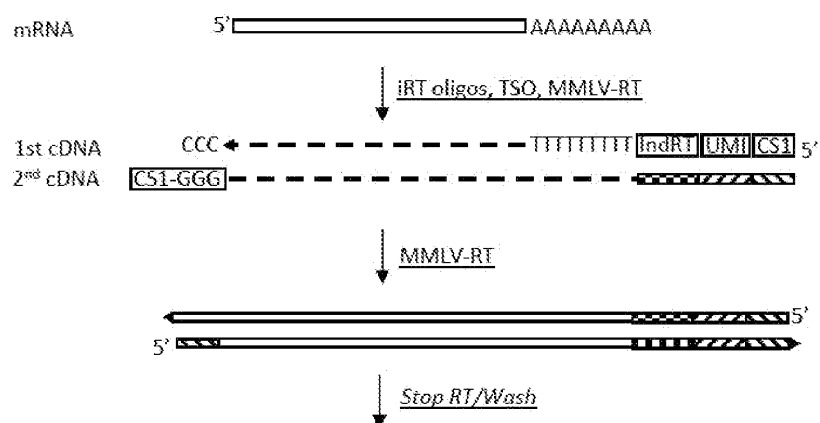


FIG. 8B

Indexed Tagmentation with i7 TSM in the same wells (96x)

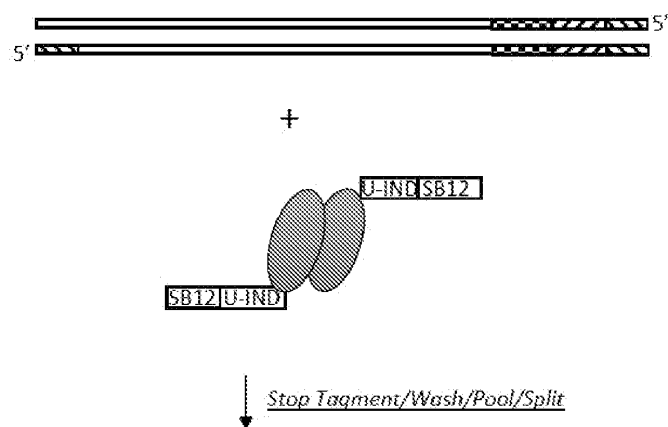


FIG. 8C Convert adapters BB -> AB

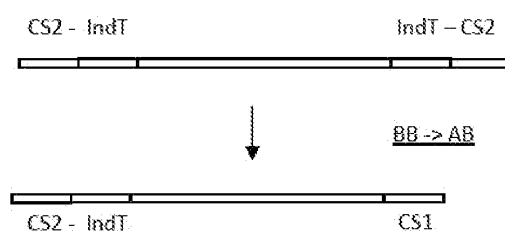
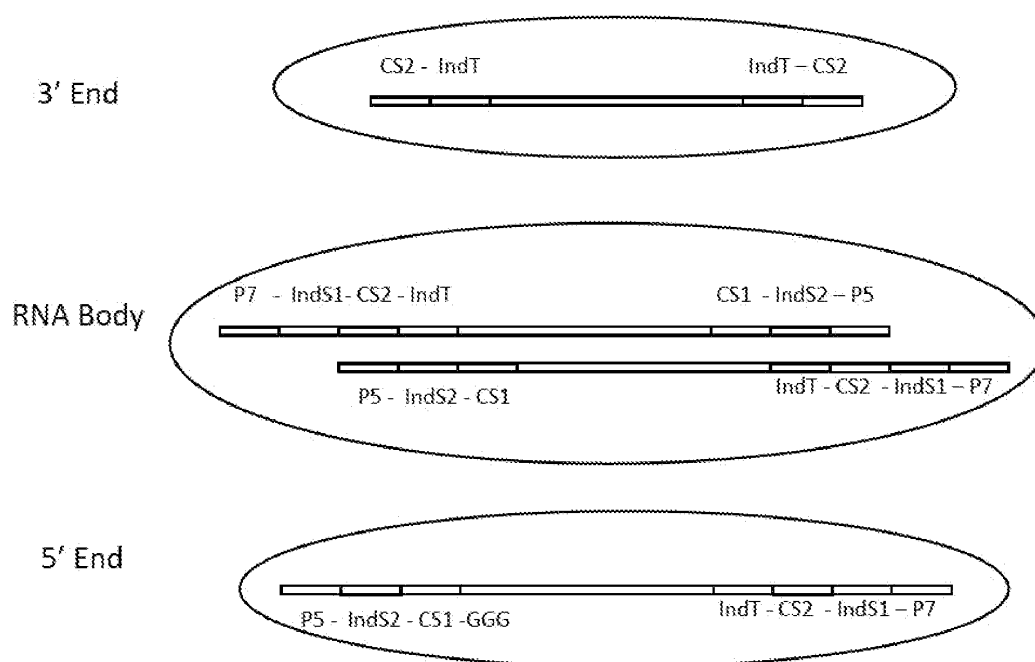


FIG. 8D Indexed PCR (96x/384x/1536x)



13/37

FIG. 9

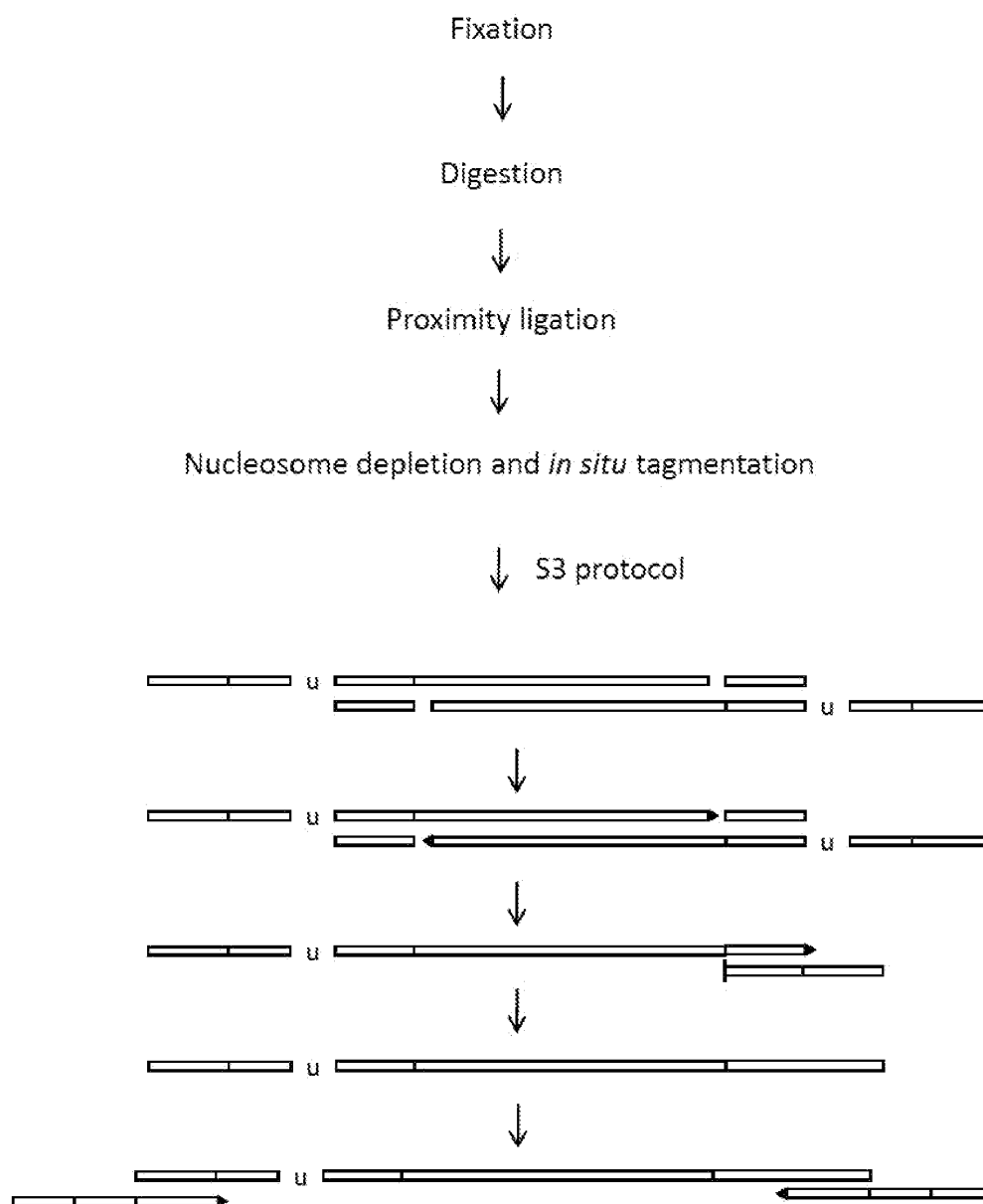
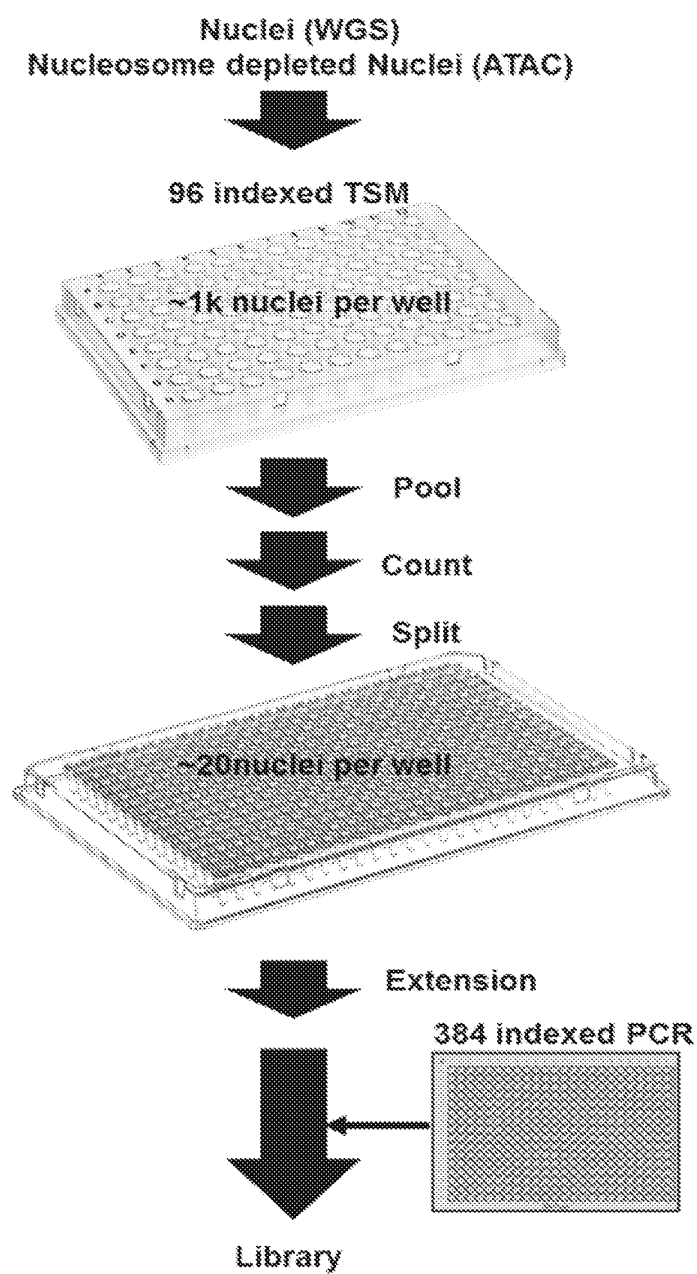


FIG. 10



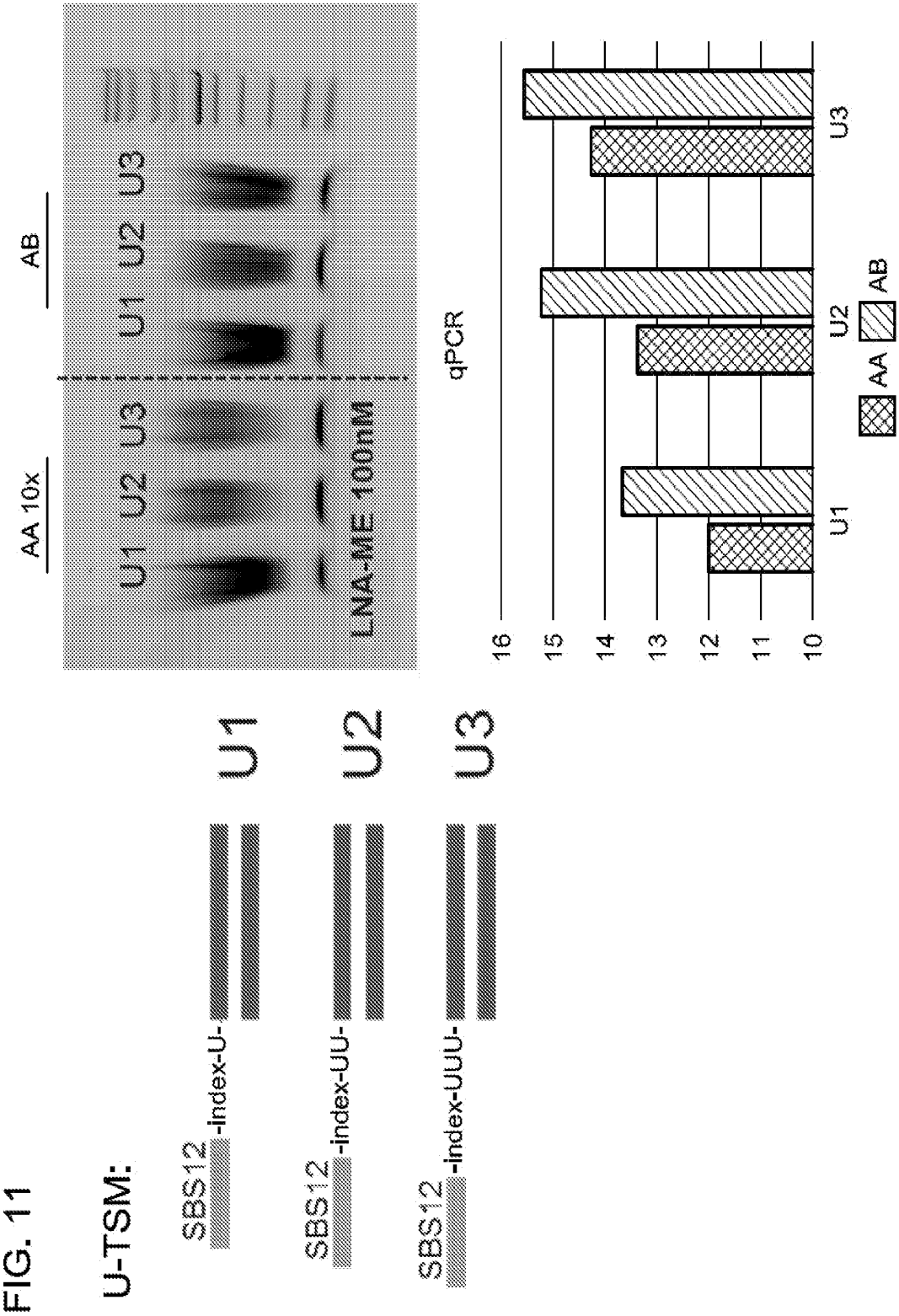
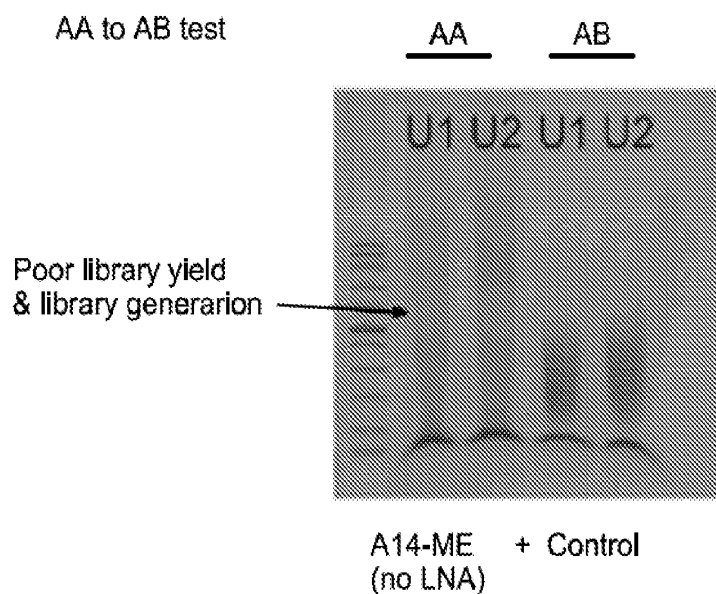


FIG. 12



- gDNA tagged by either AA TSM or AB TSM
- 0.01% SDS NPM 1st extension @72c
- Spike in A14-ME, 98c denature, 2nd extension @45c, 5x
- Add 0.1% TX-100 to neutralize SDS, Taq qPCR, 25x, and run gel

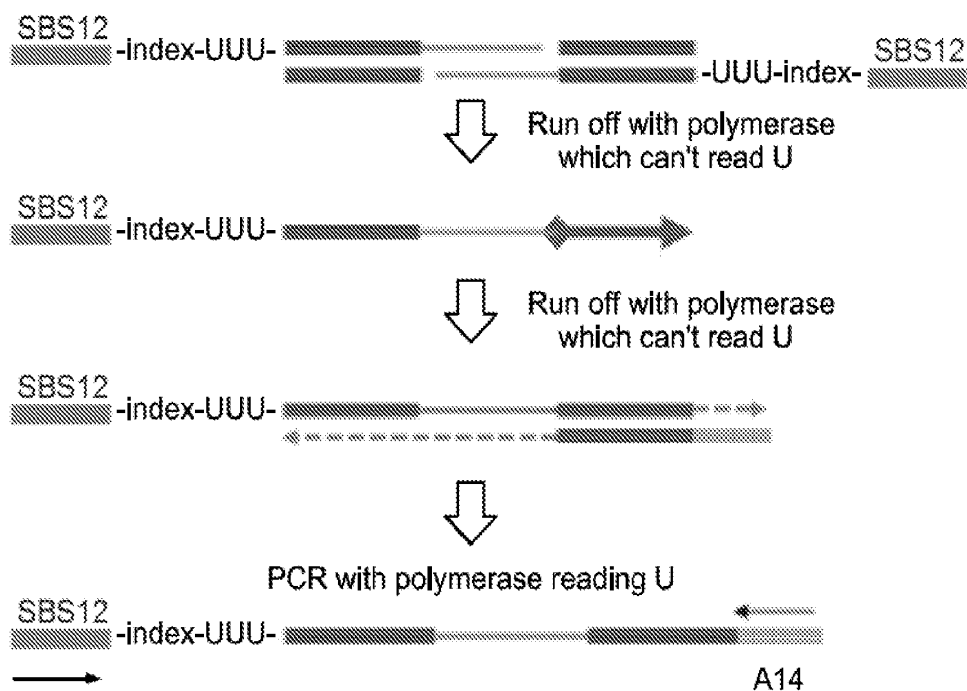
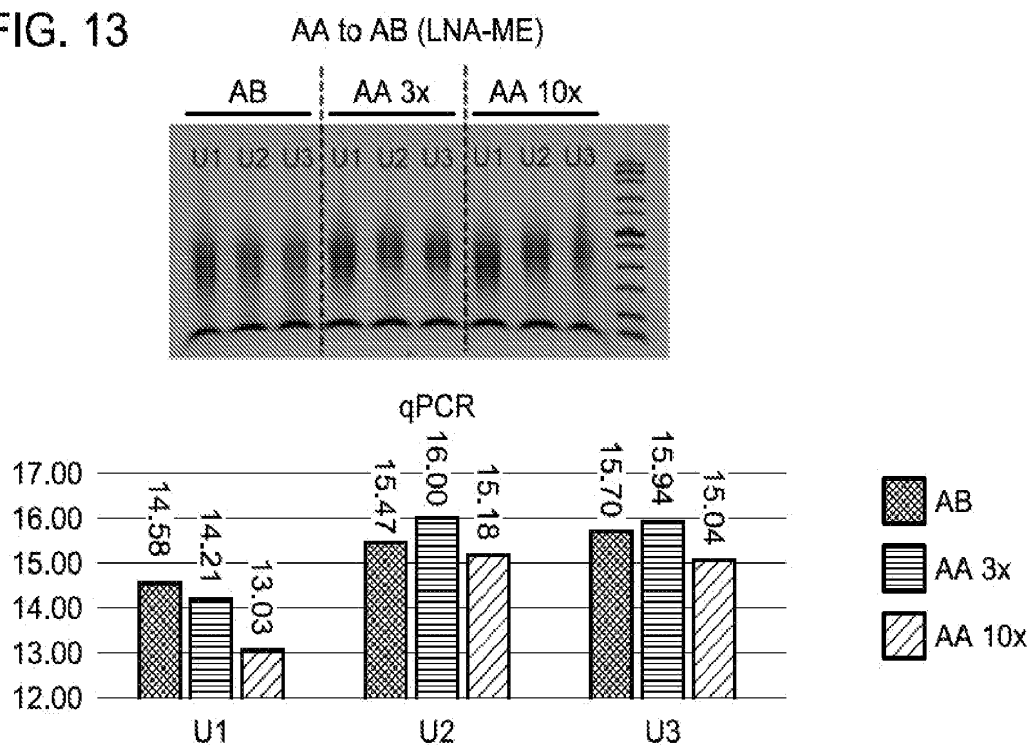
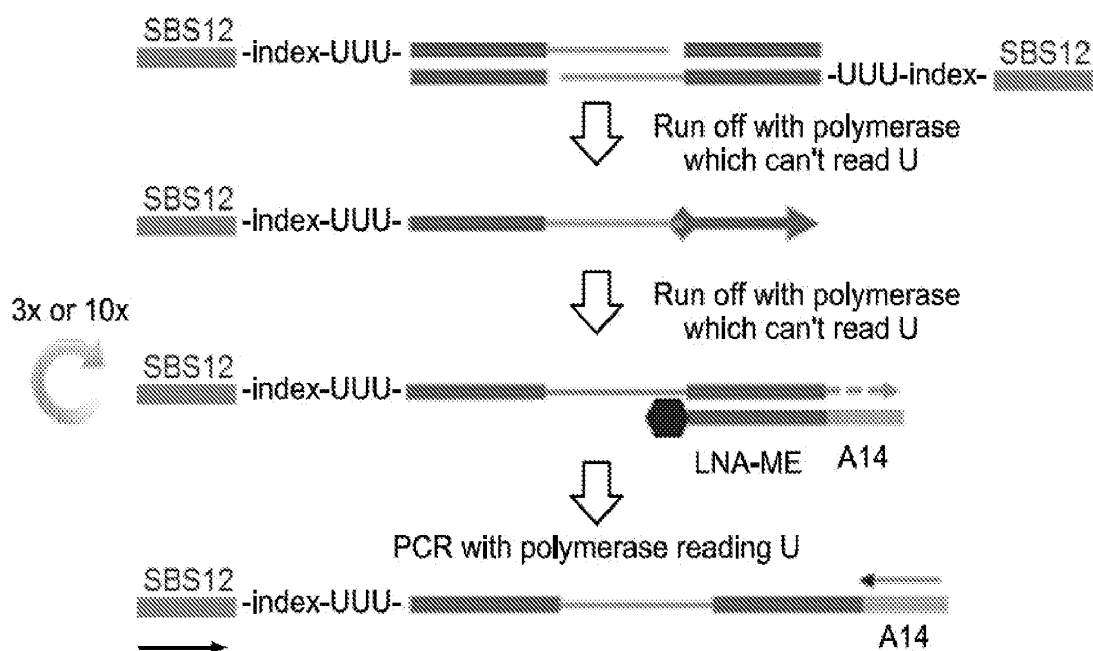


FIG. 13



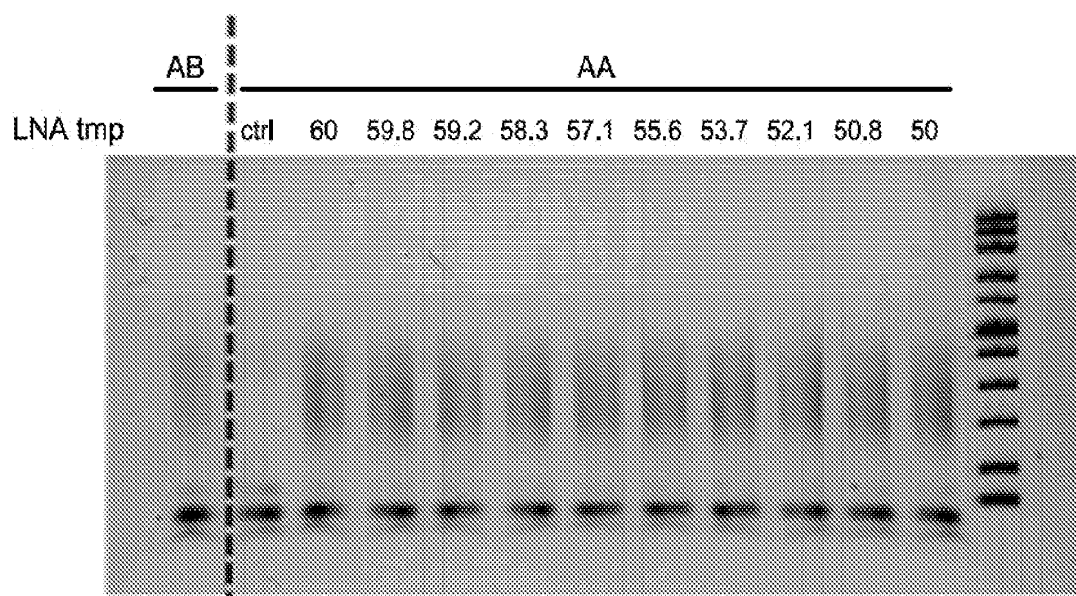
- gDNA tagged by either AA TSM (SBS12 TSM) or AB TSM (SBS12 TSM + A14 TSM)
- 0.01% SDS NPM 1st extension @72c
- Spike in A14-ME, 98c denature, 2nd extension @53c, 3x or 10x
- Add 0.1% TX-100 to neutralize SDS, Taq qPCR, 25x, and run gel



18/37

FIG. 14

LNA annealing optimization (for ATAC)



- ~15K nuclei; ~50 nuclei for qPCR
- AB as the positive control
- AA control is LNA_ME without extension
- LNA_ME extension for 11 repeats

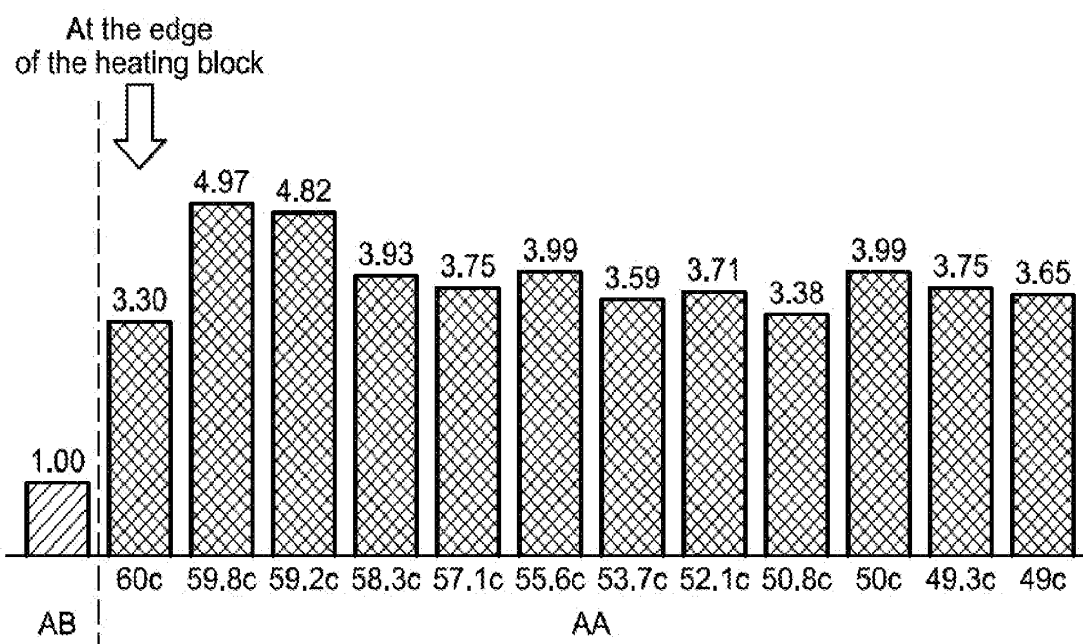


FIG. 15

b.

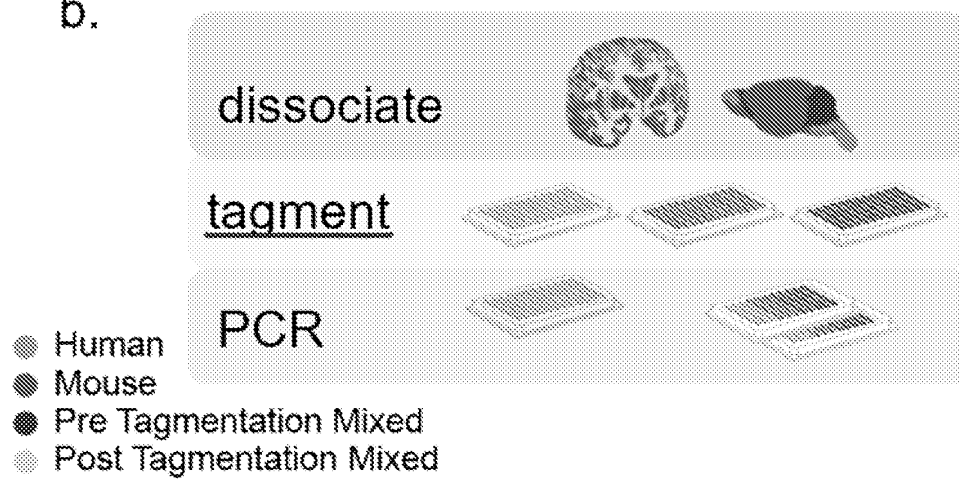
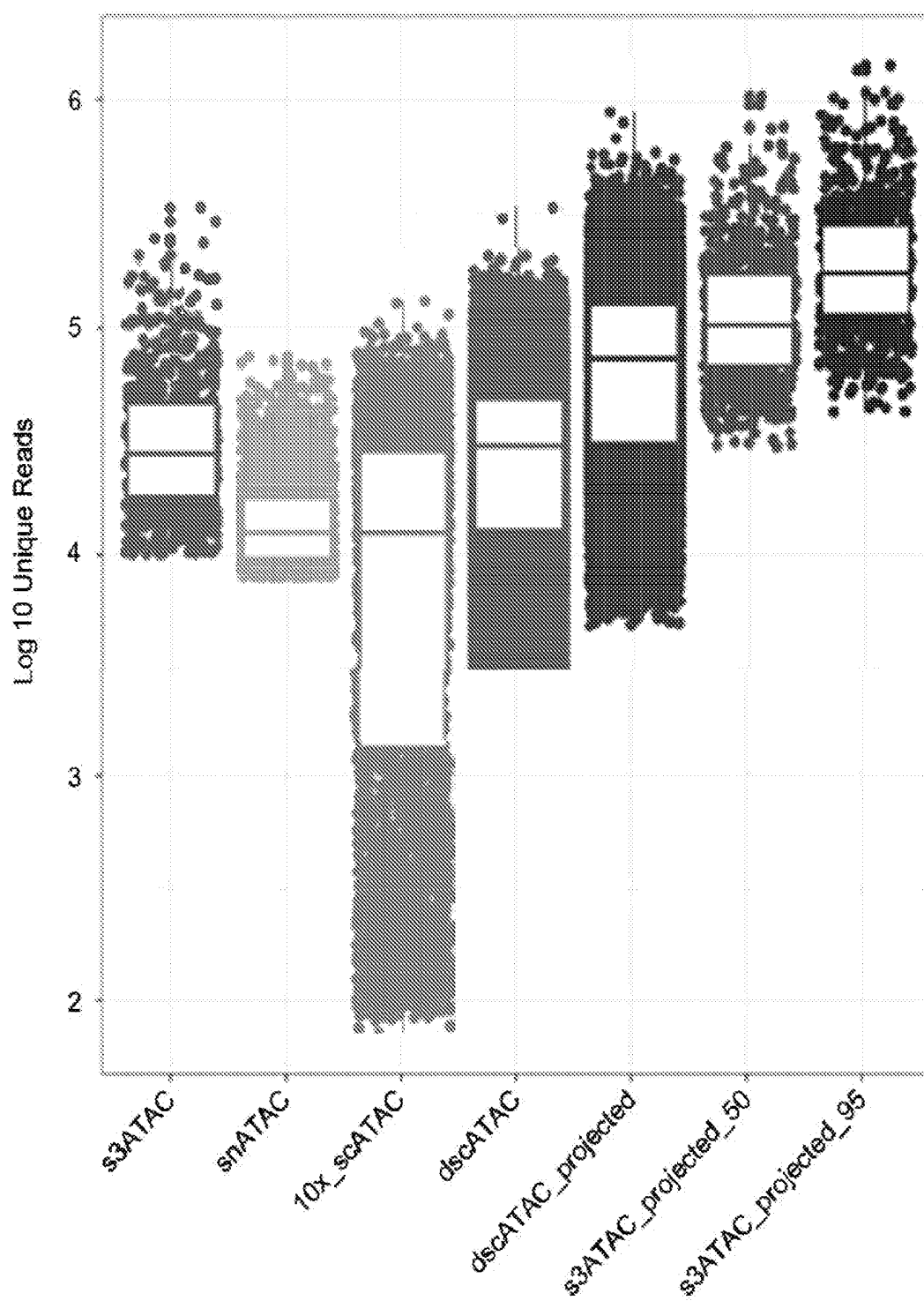


FIG. 16



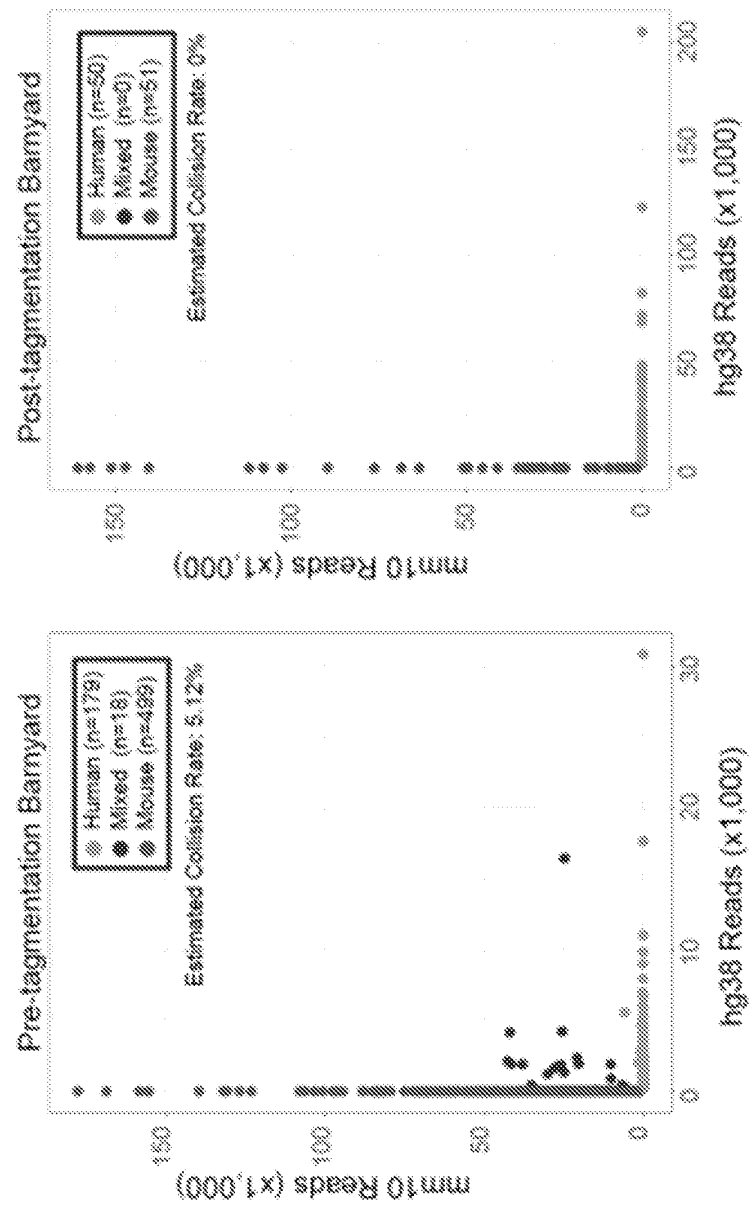
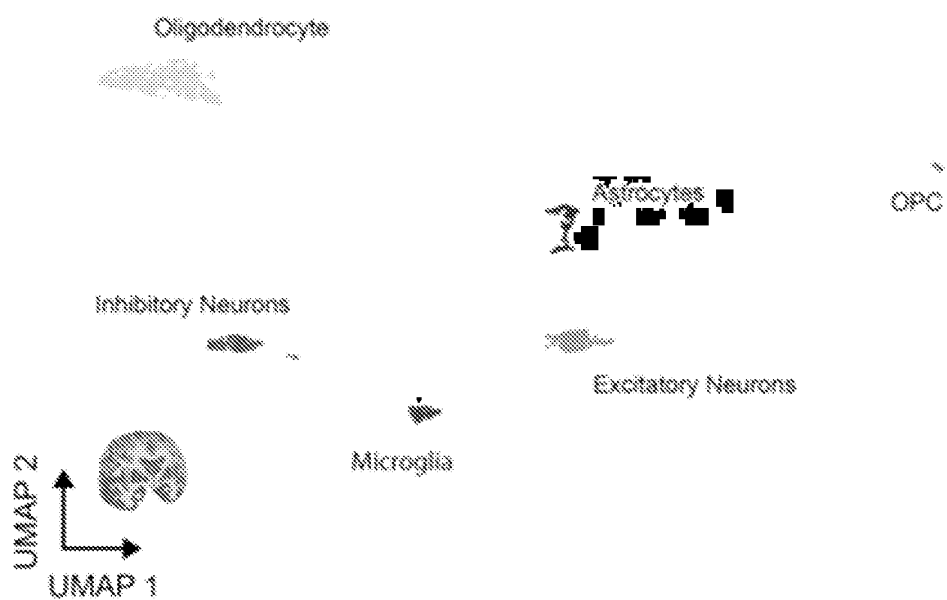


FIG. 17

22/37

FIG. 18



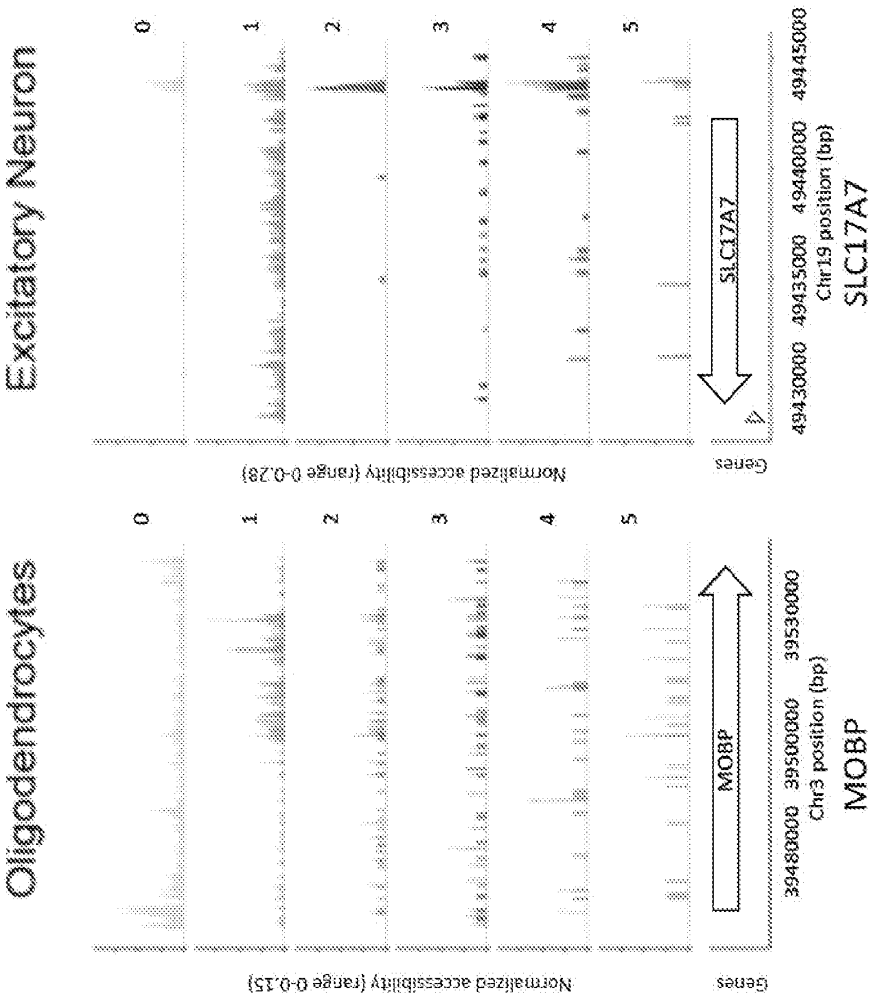


Fig. 19

24/37

Fig. 19 con't

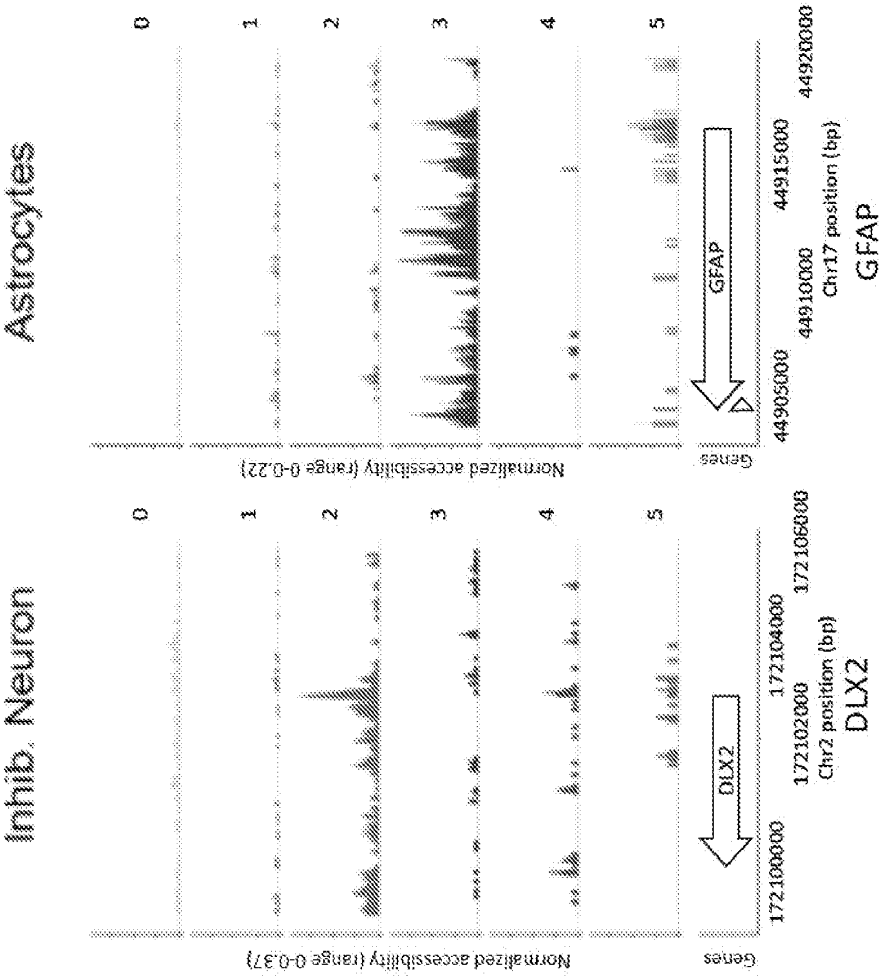
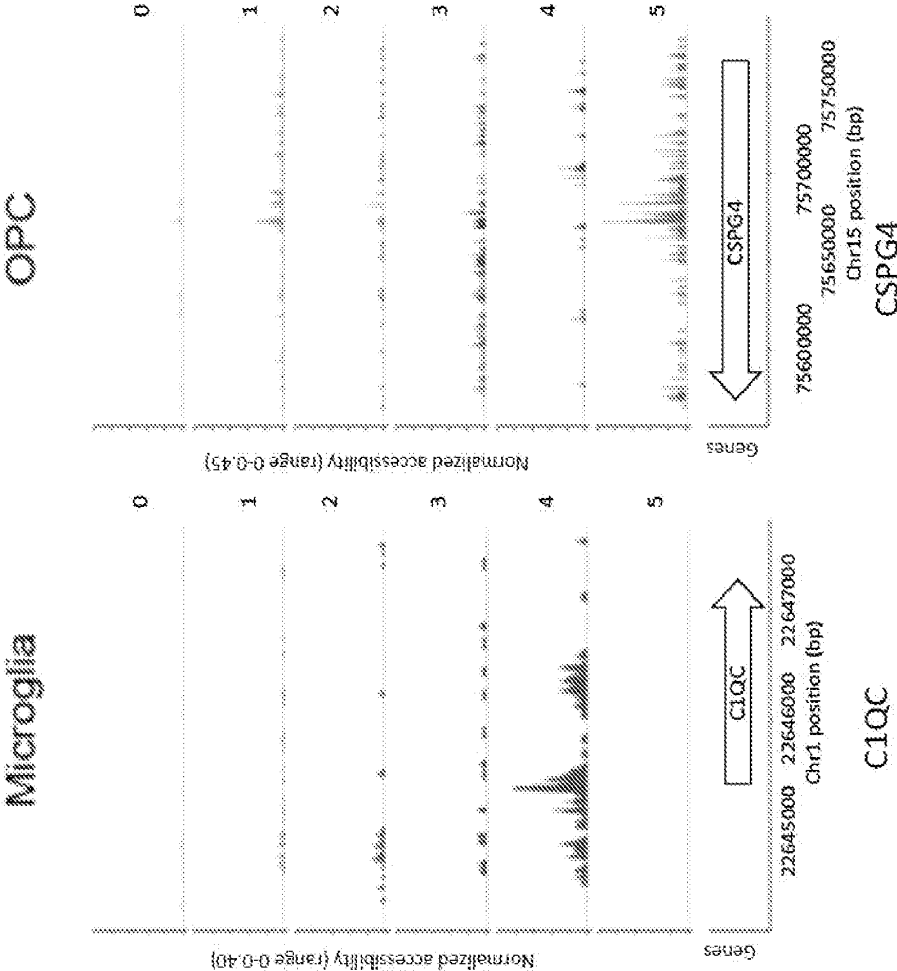


Fig. 19 con't



26/37

FIG. 20

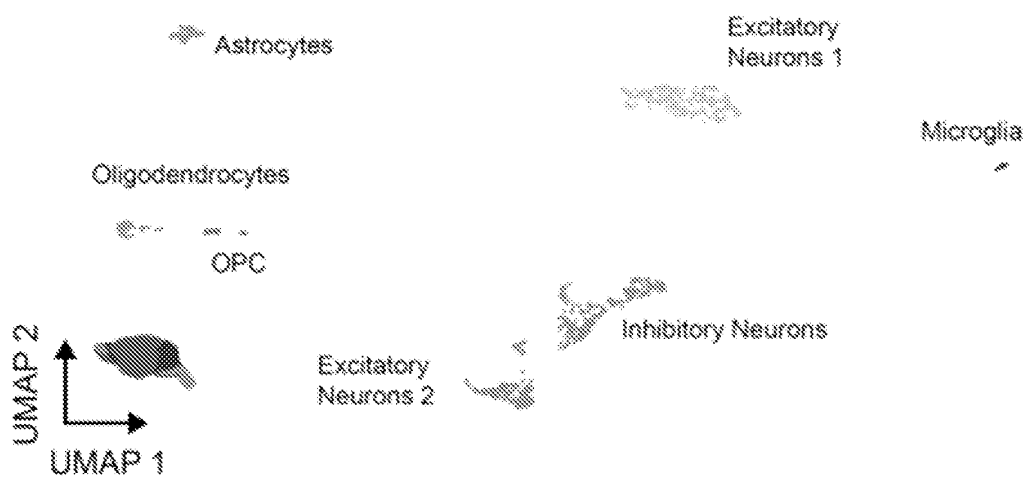
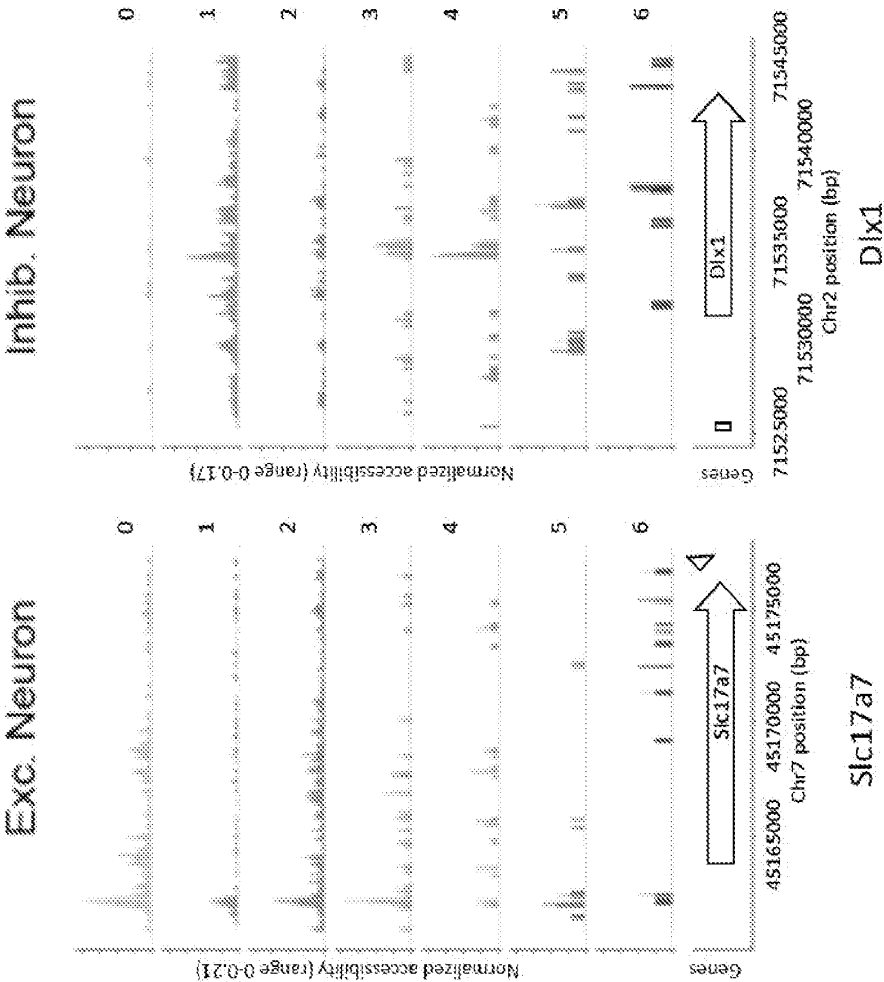


Fig. 21



28/37

Fig. 21 con't

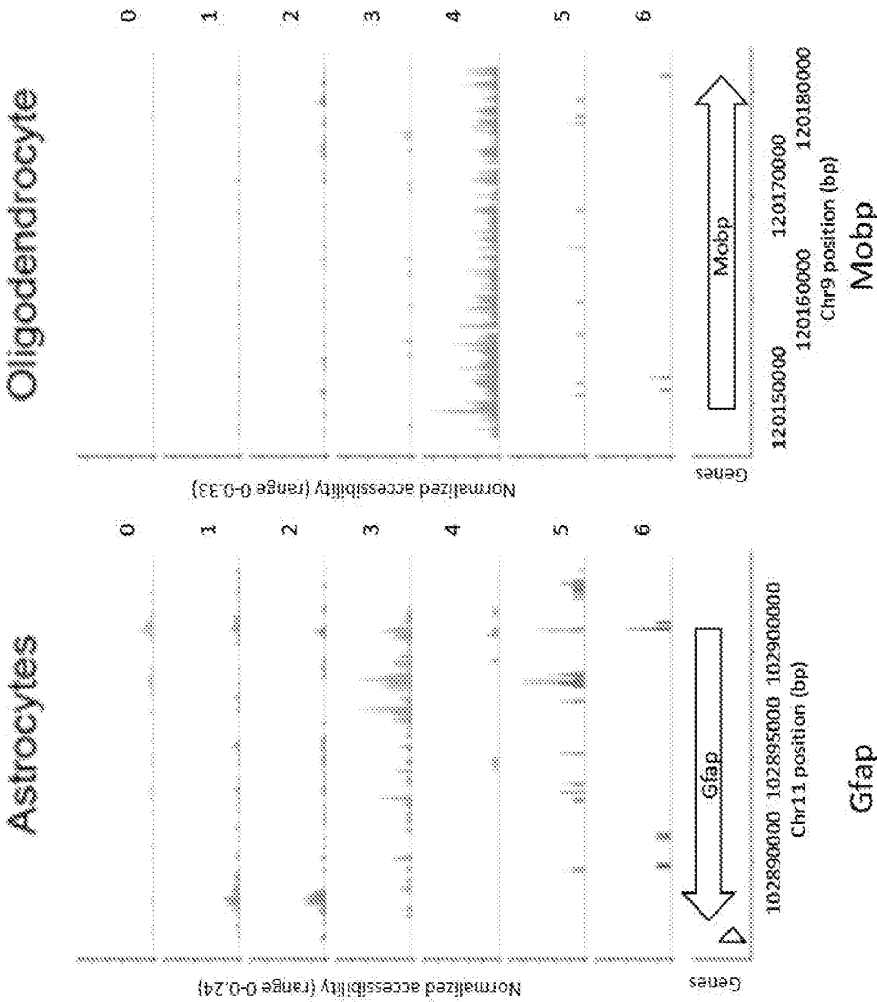
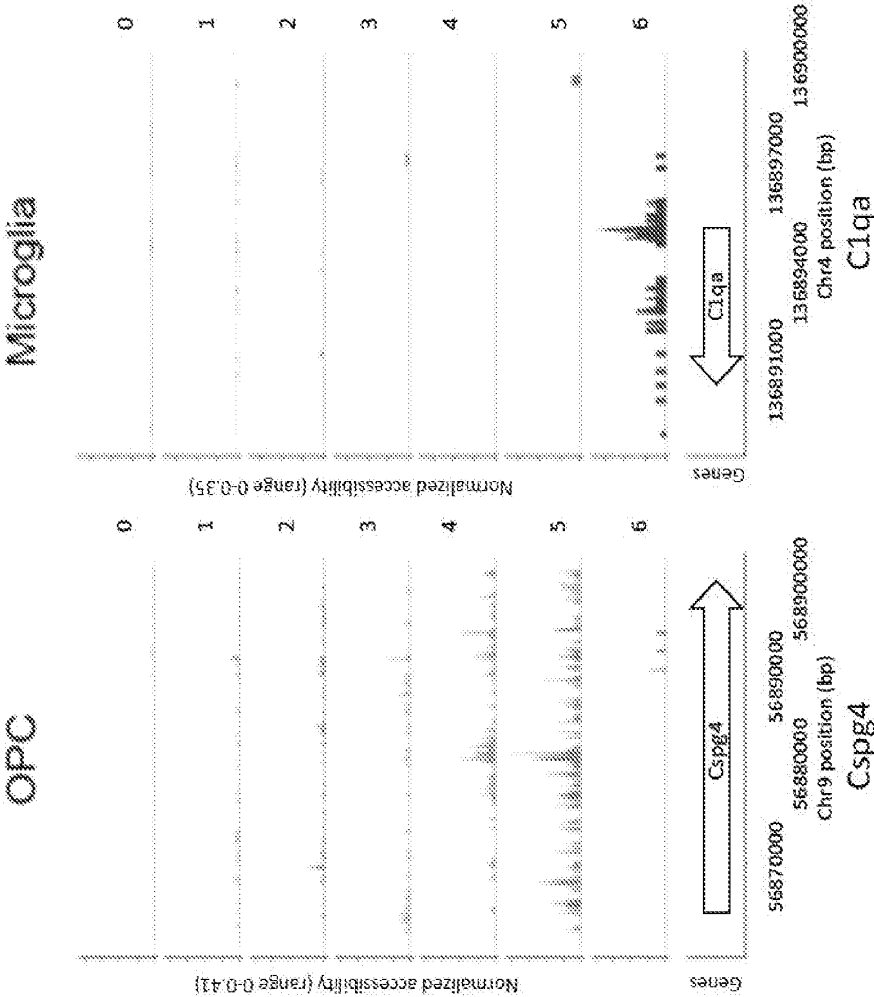
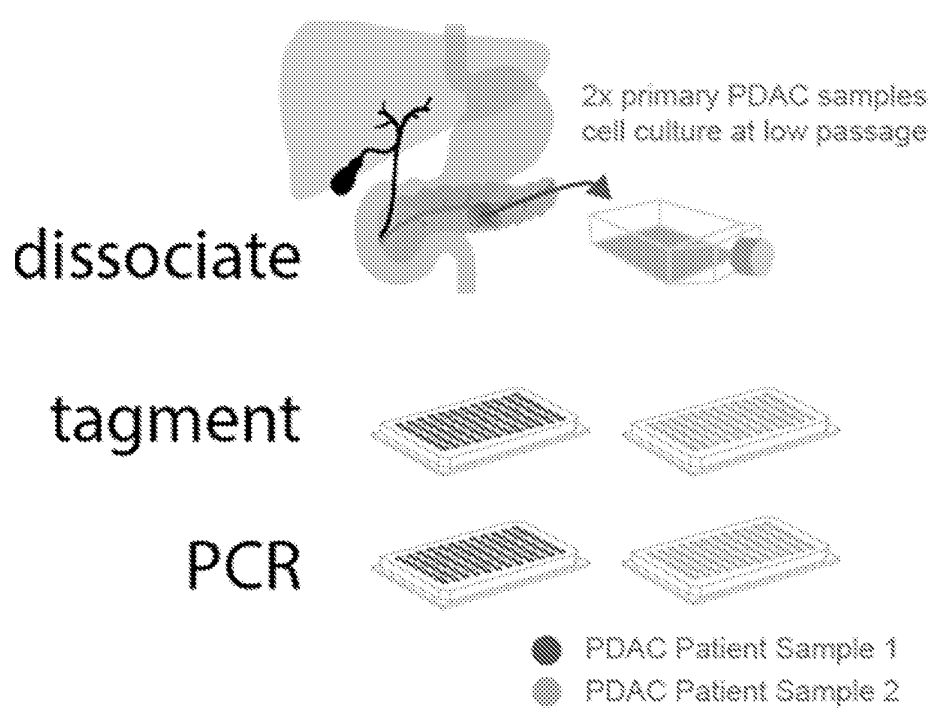


Fig. 21 con't



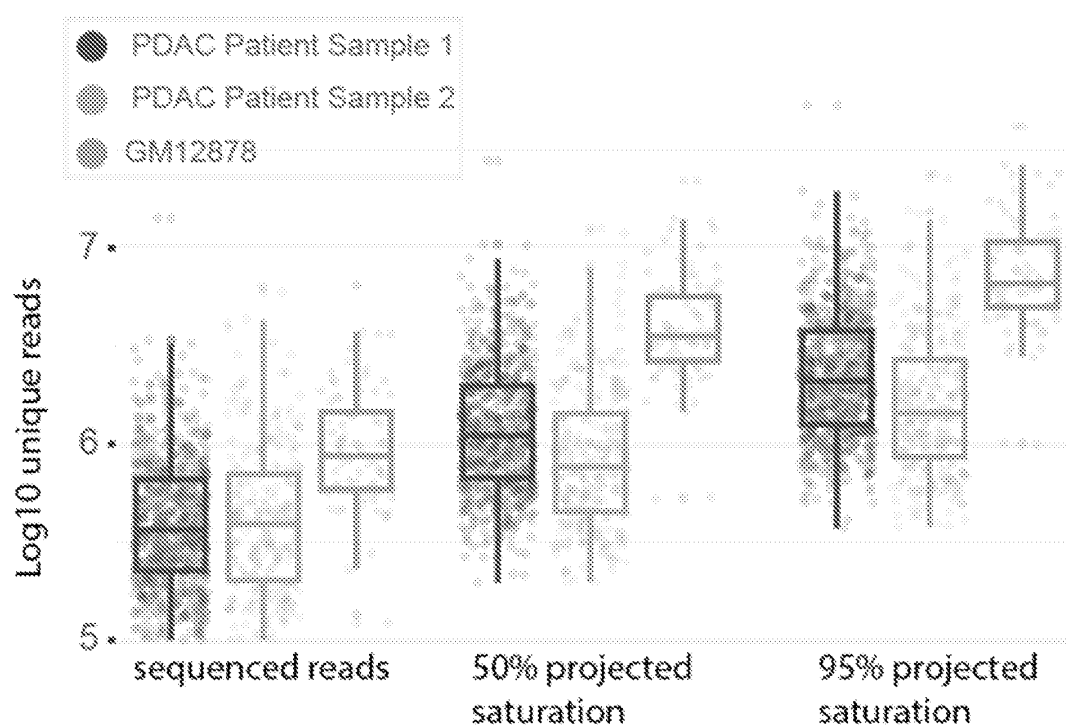
30/37

FIG. 22



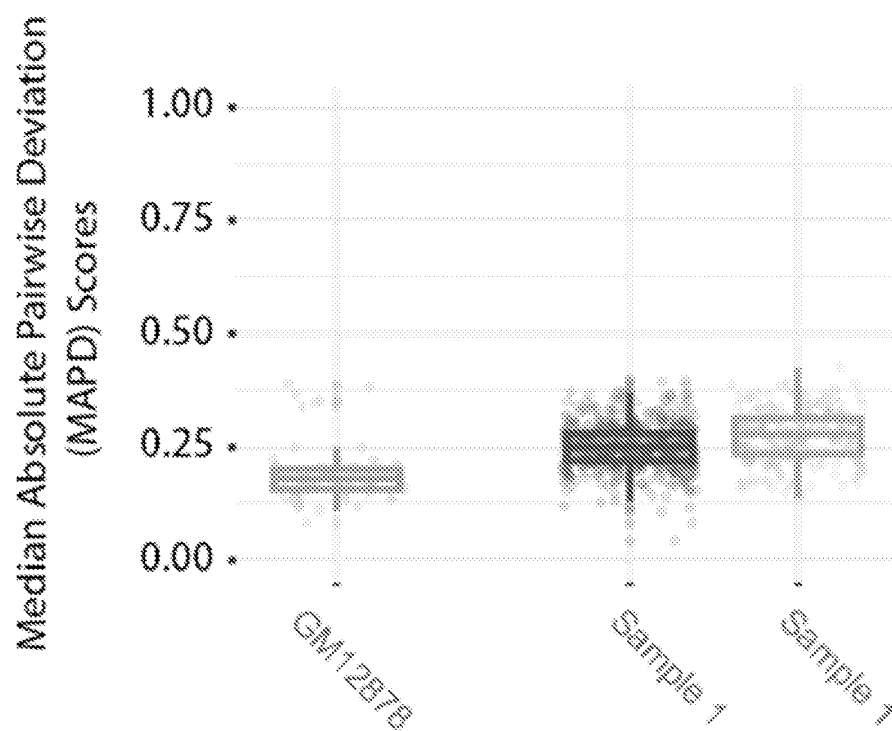
31/37

FIG. 23



32/37

FIG. 24



33/37

FIG. 25

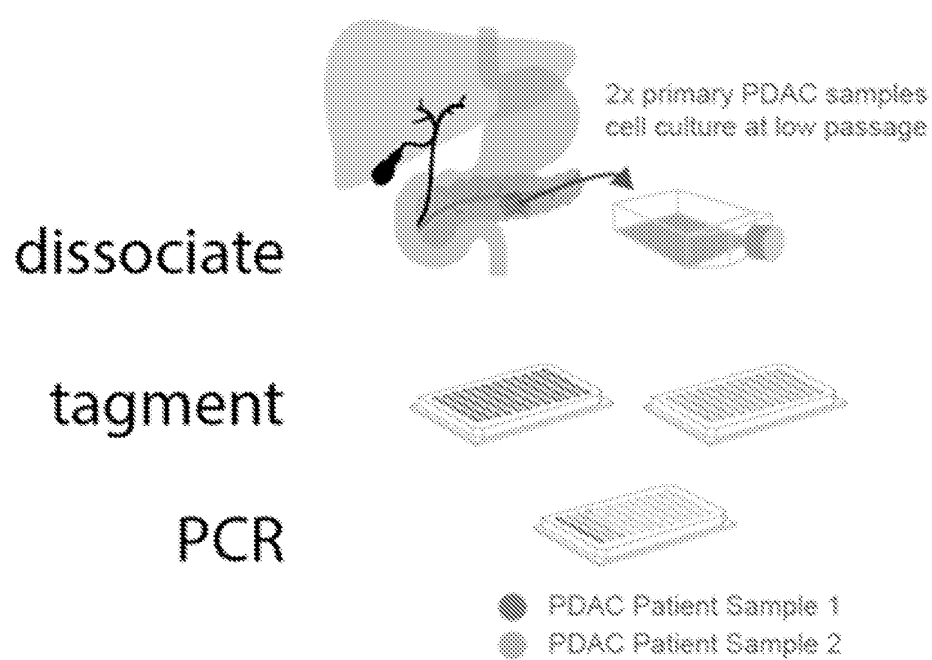
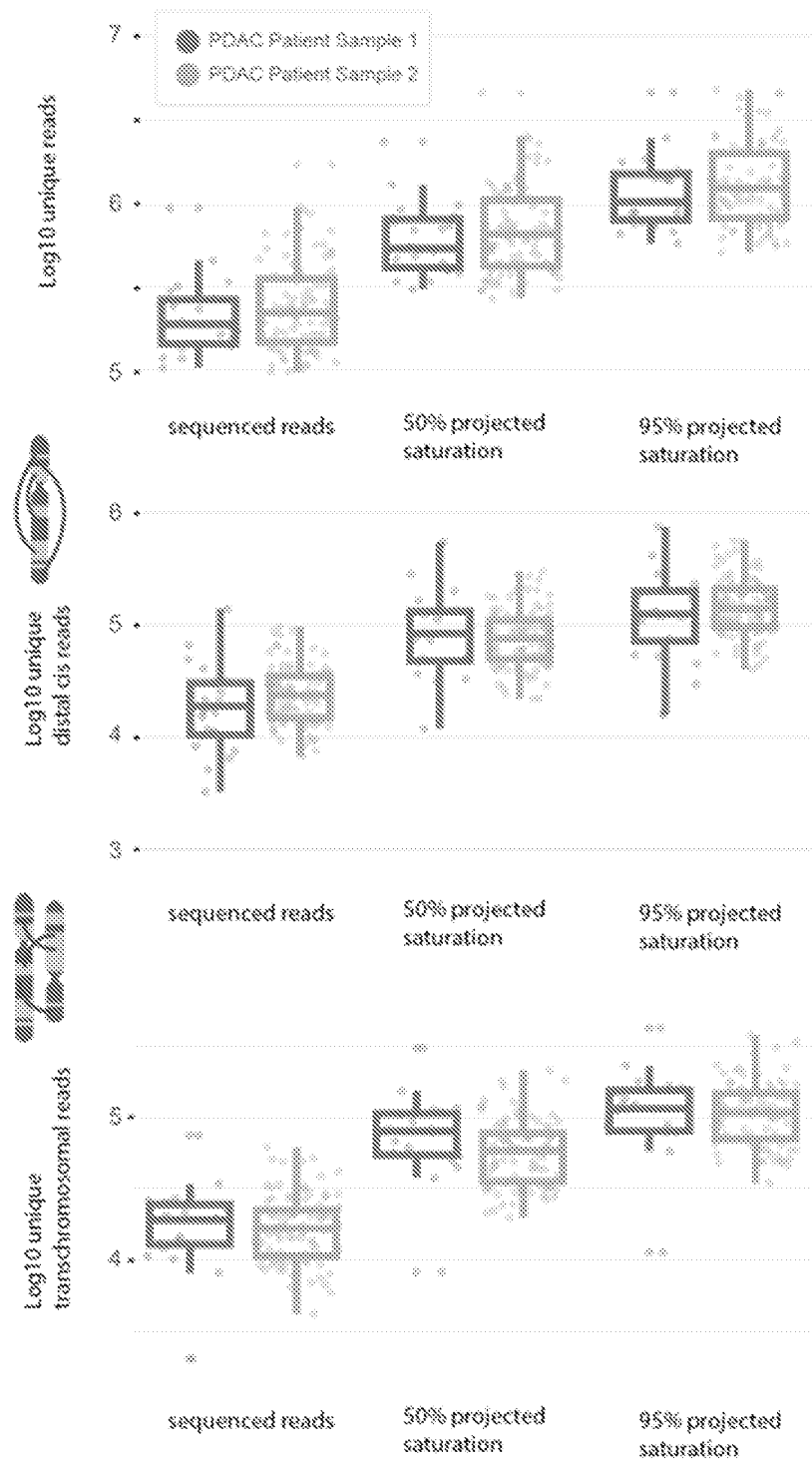
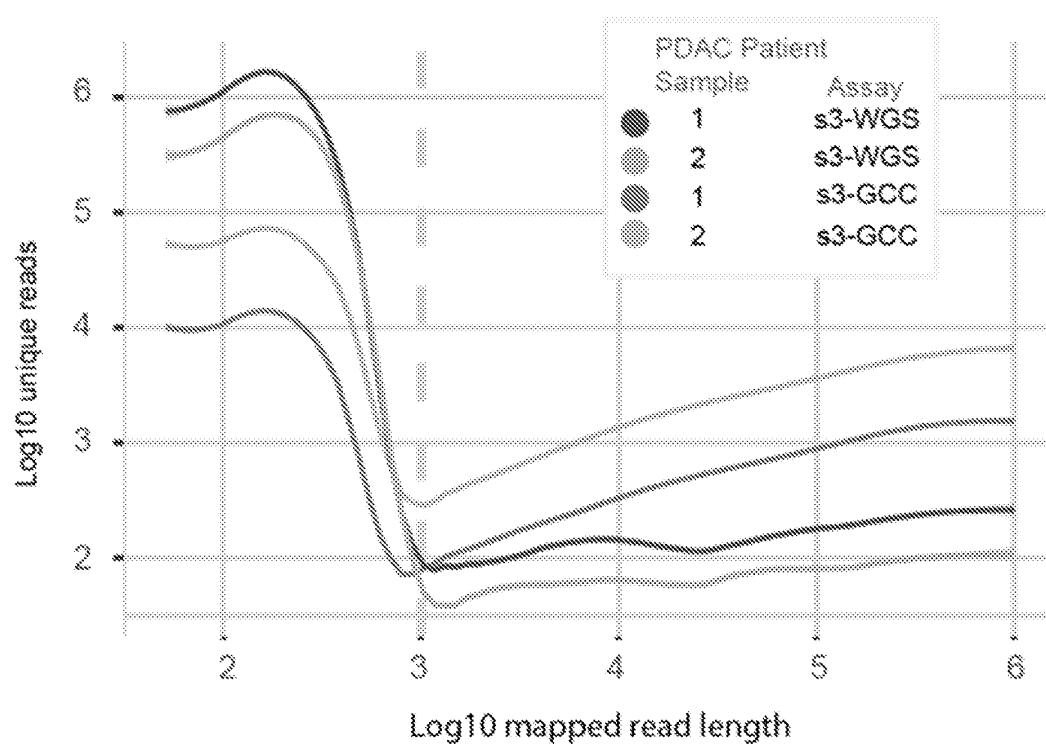


FIG. 26



35/37

FIG. 27



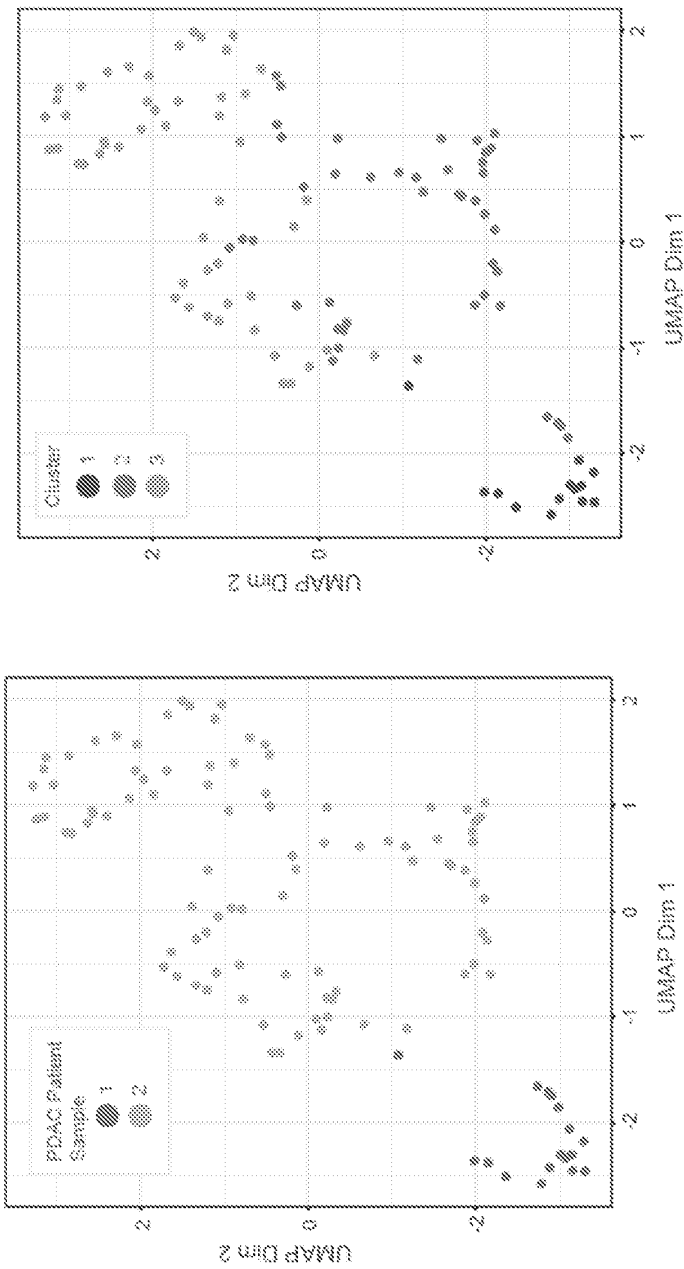


FIG. 28

37/37

FIG. 29

AATGATACGGCGACCACCGAGATCTACACTAGATCGCTCGT
CGGCAGCGTCUAGATGTGTATAAGAGACAG (SEQ ID NO: 1)

CAAGCAGAAGACGGCATACGAGATTCGCCTTAGTCTCGTGG
GCTCGGAGATGTGTATAAGAGACAG (SEQ ID NO: 2)

P5: AATGATACGGCGACCACCGAGATCTACAC (SEQ ID NO:3)

i5: TAGATCGC (SEQ ID NO:4)

P7: CAAGCAGAAGACGGCATACGAGA (SEQ ID NO:5)

i7: TTCGCCTTA (SEQ ID NO:6)

ME: AGATGTGTATAAGAGACAG (SEQ ID NO:7)

A14: TCGTCGGCAGCGTC (SEQ ID NO:8)

B15: GTCTCGTGGGCTCGG (SEQ ID NO:9)