

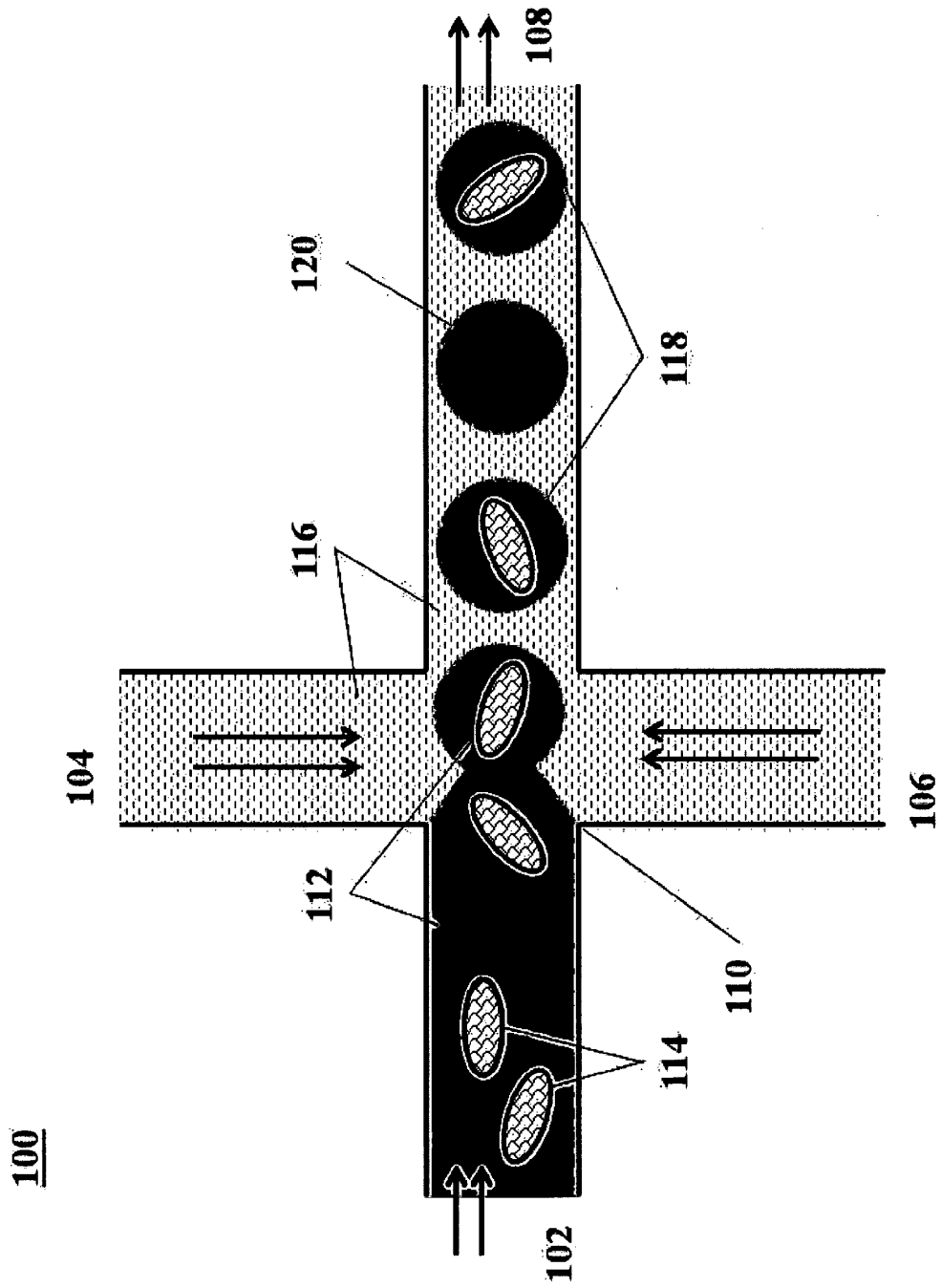


FIG. 1

200

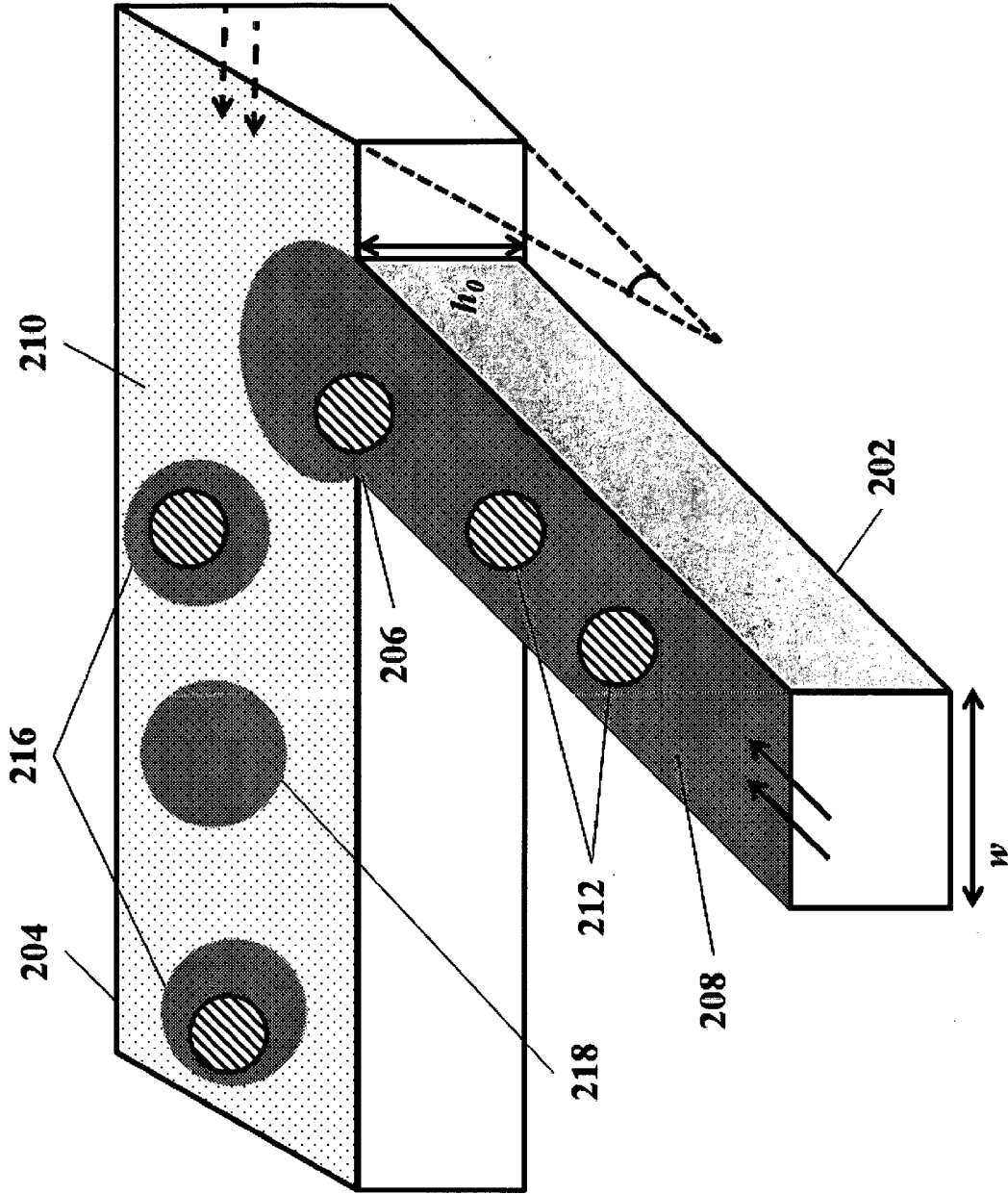


FIG. 2

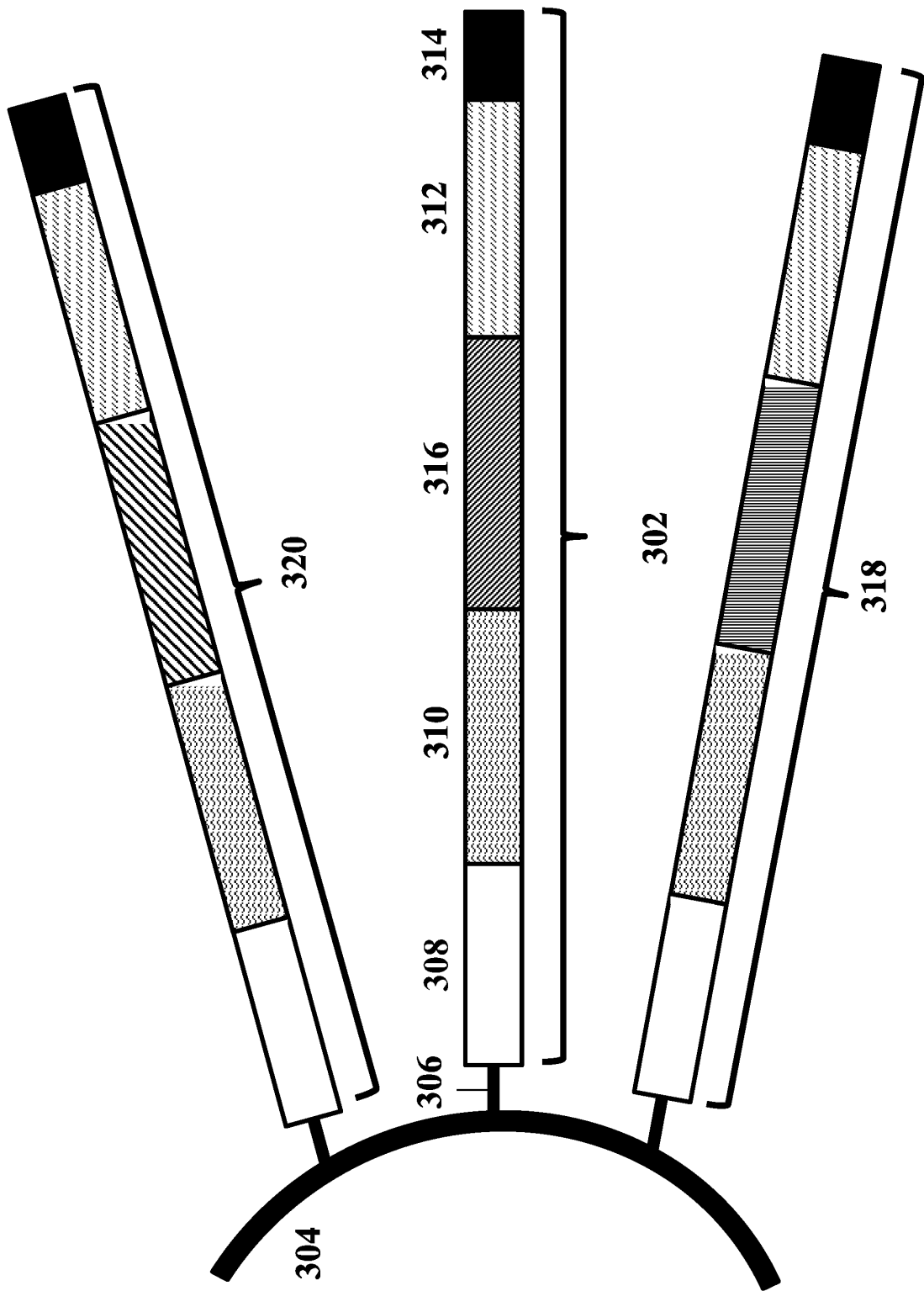


FIG. 3

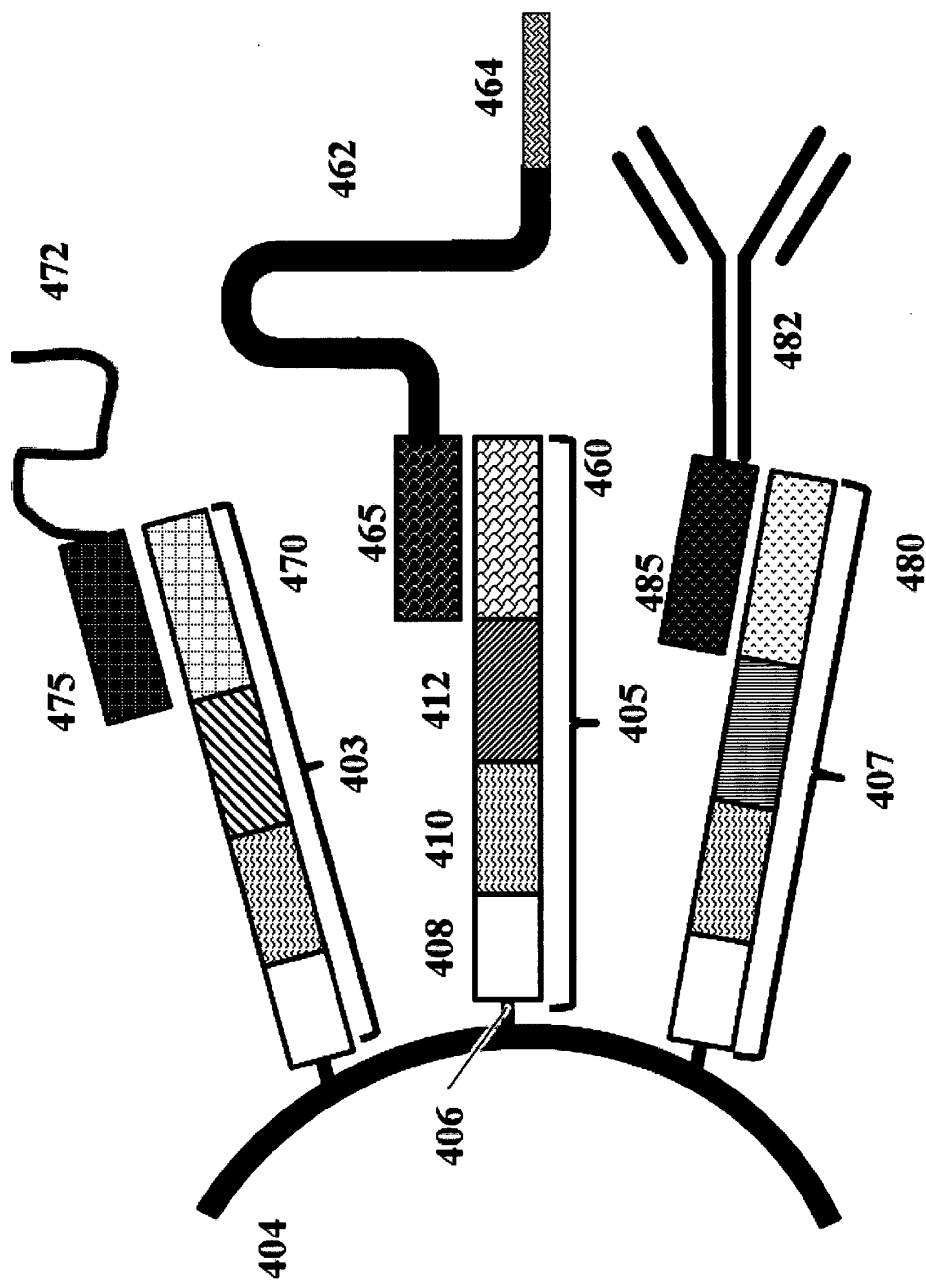


FIG. 4

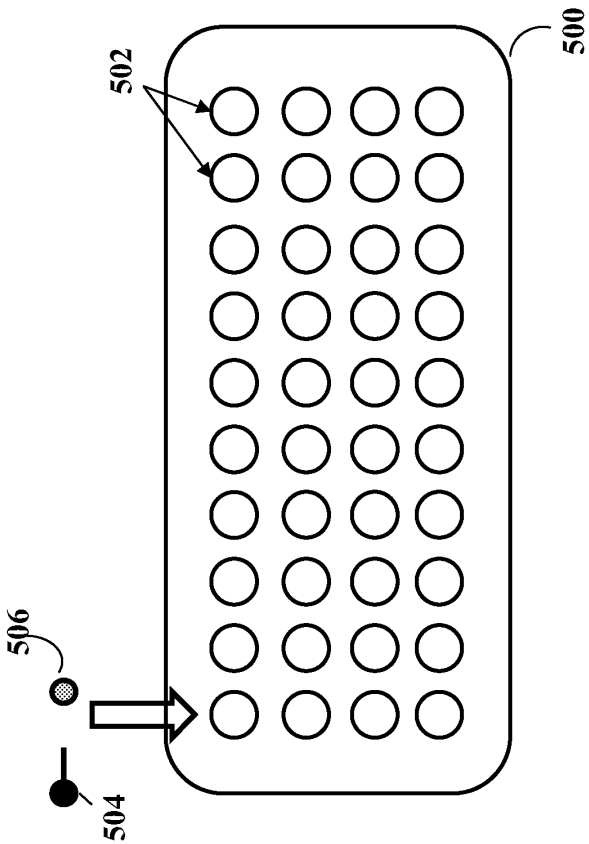


FIG. 5

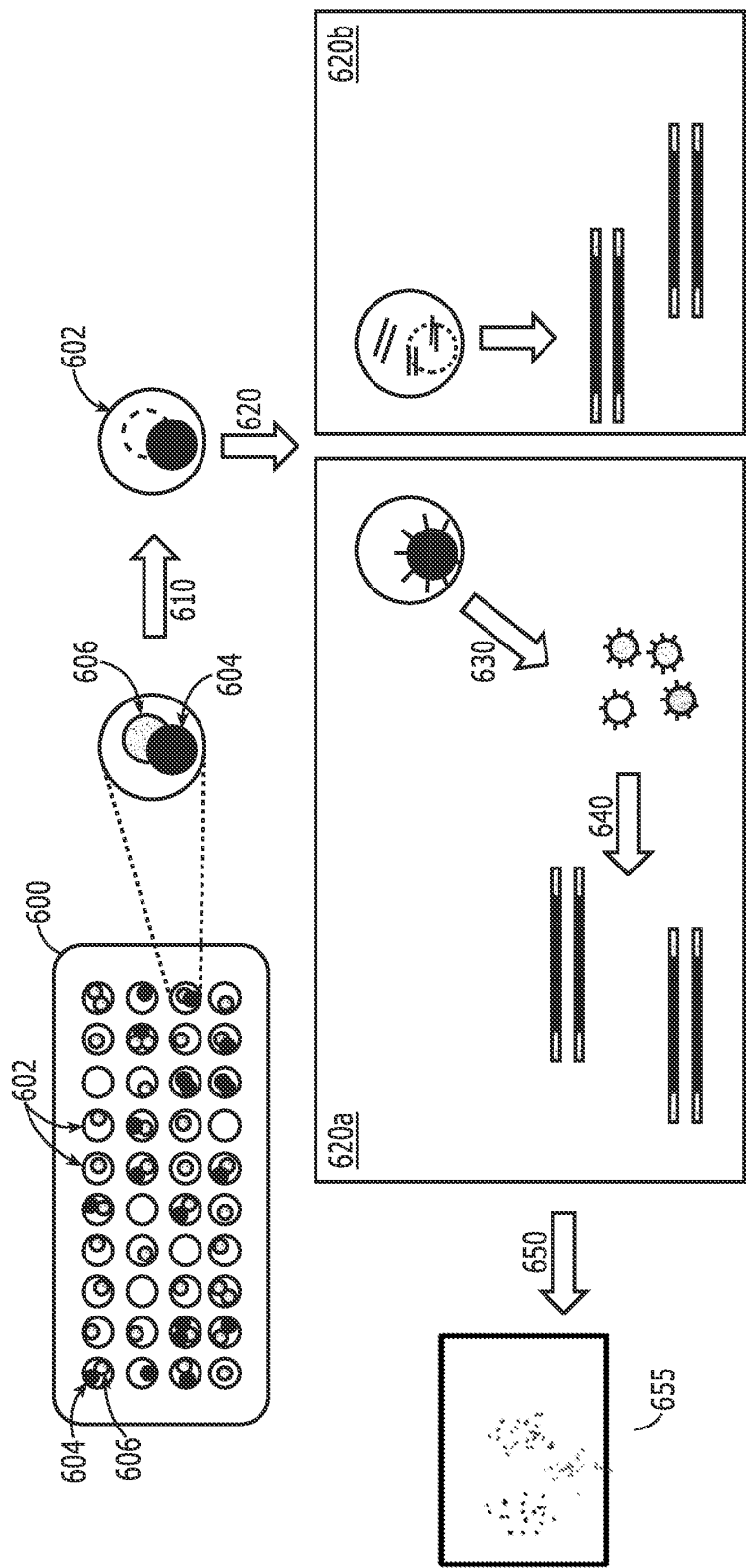


FIG. 6

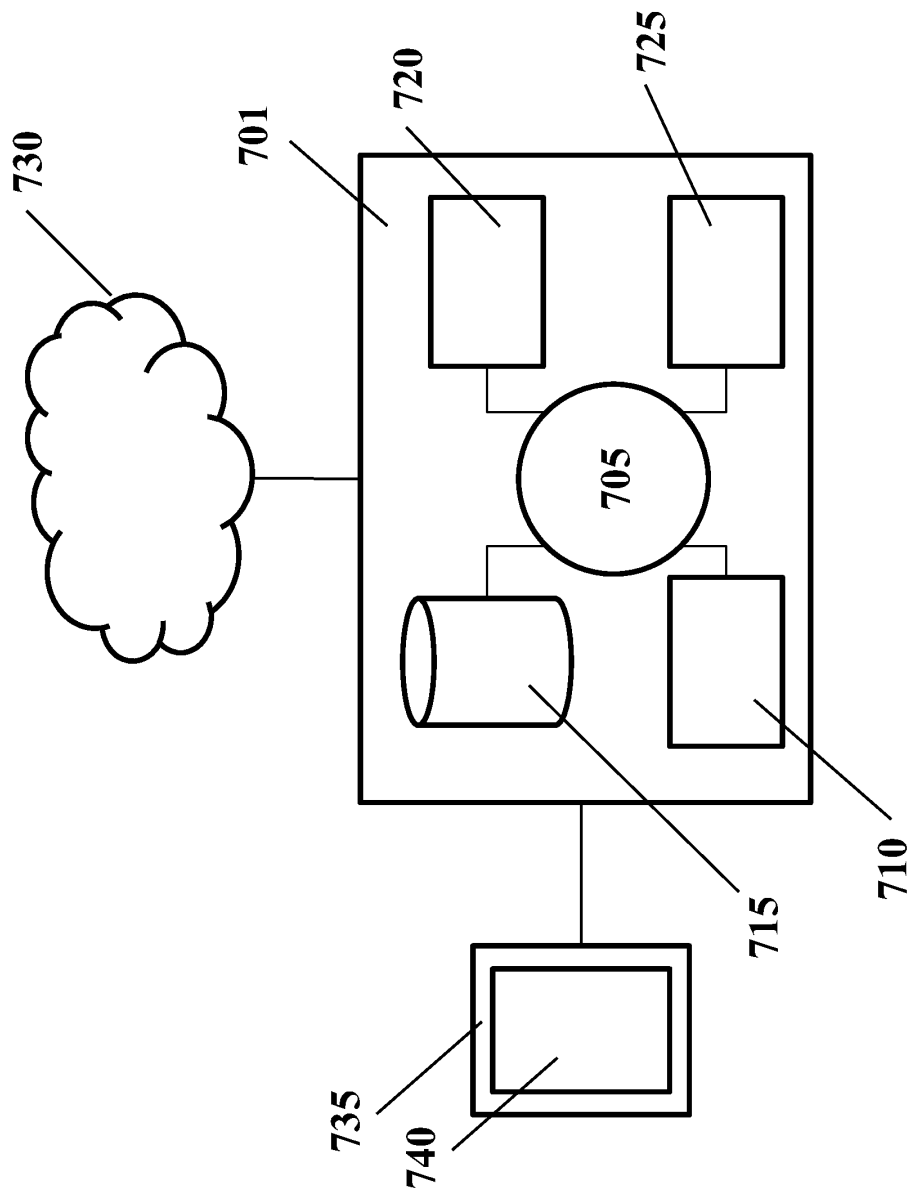


FIG. 7

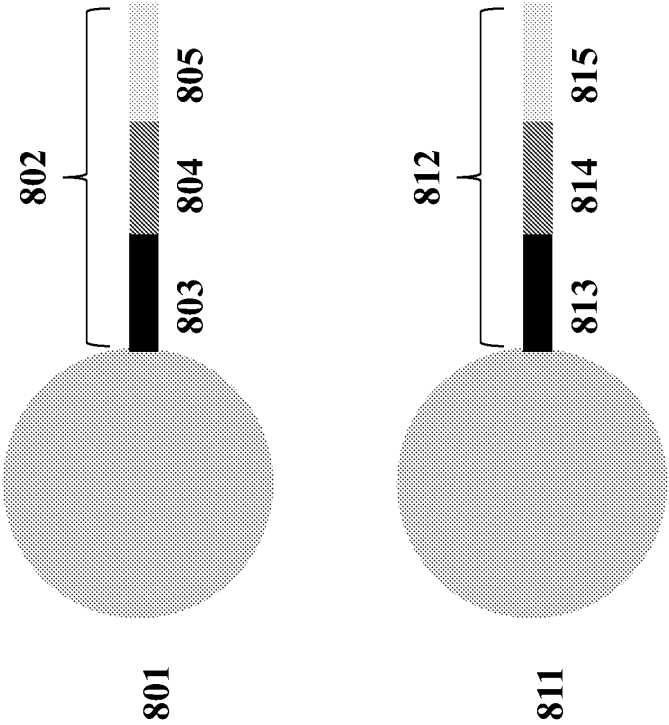


FIG. 8A

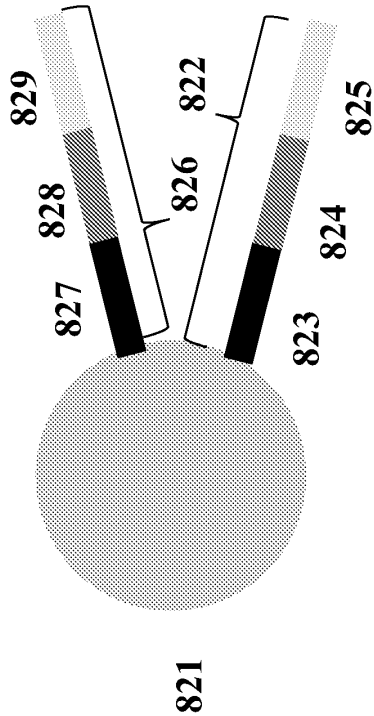


FIG. 8B

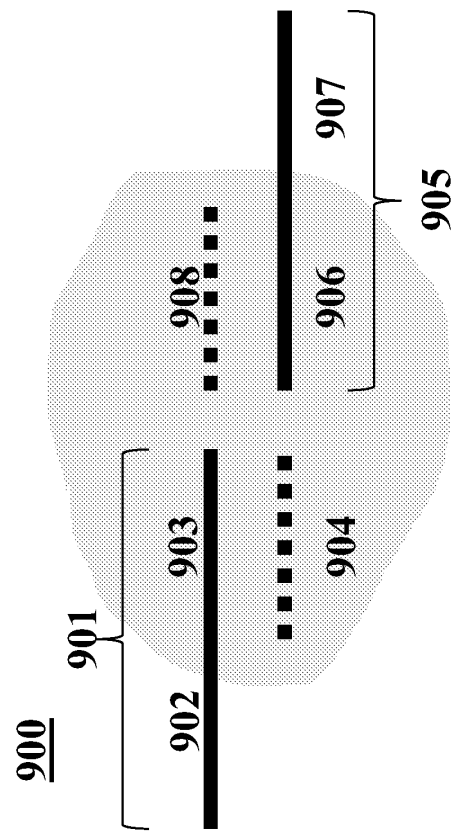


FIG. 9

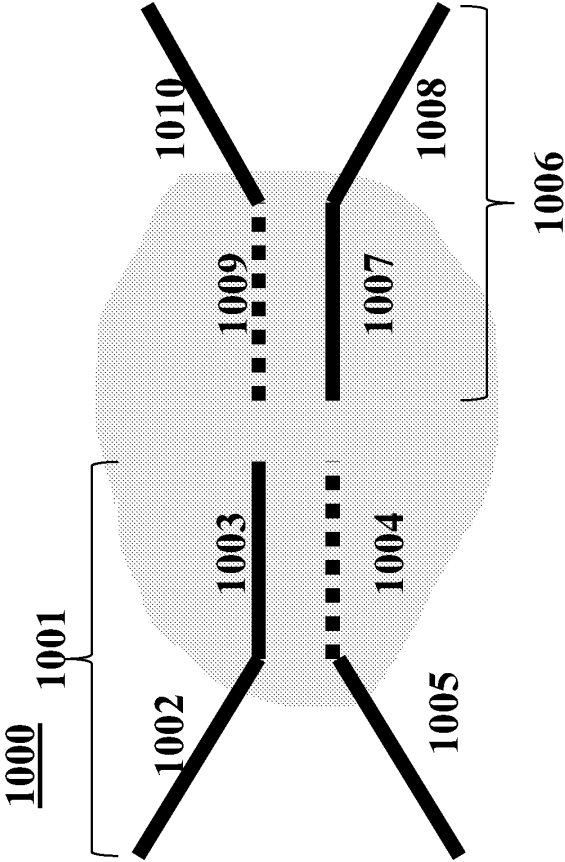


FIG. 10

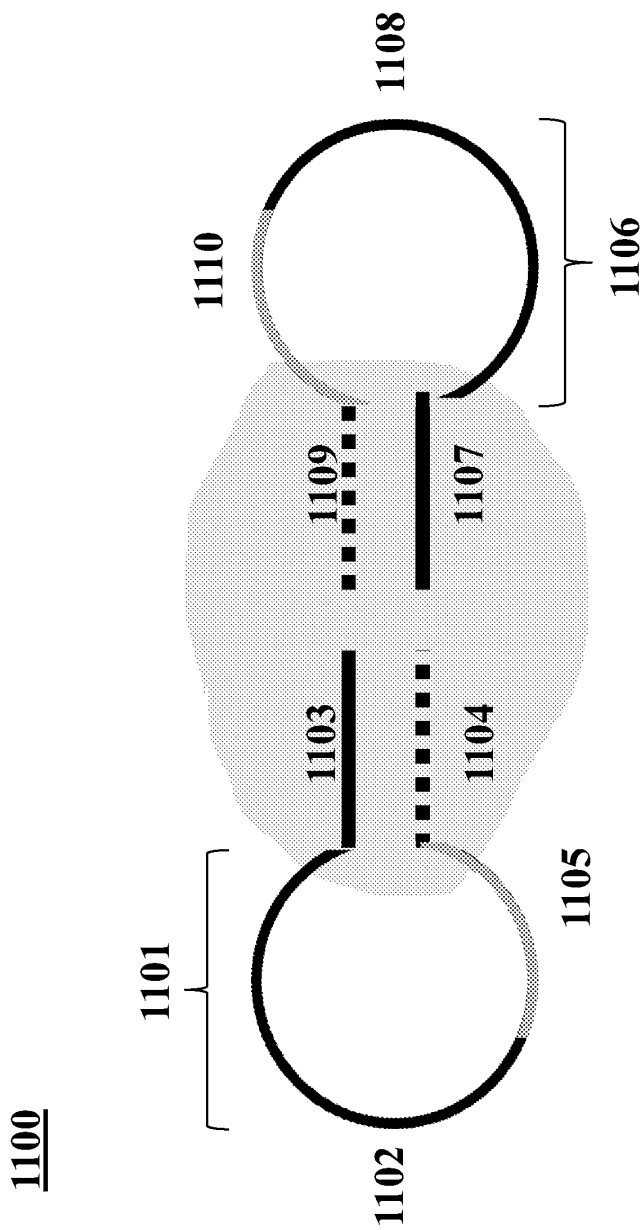
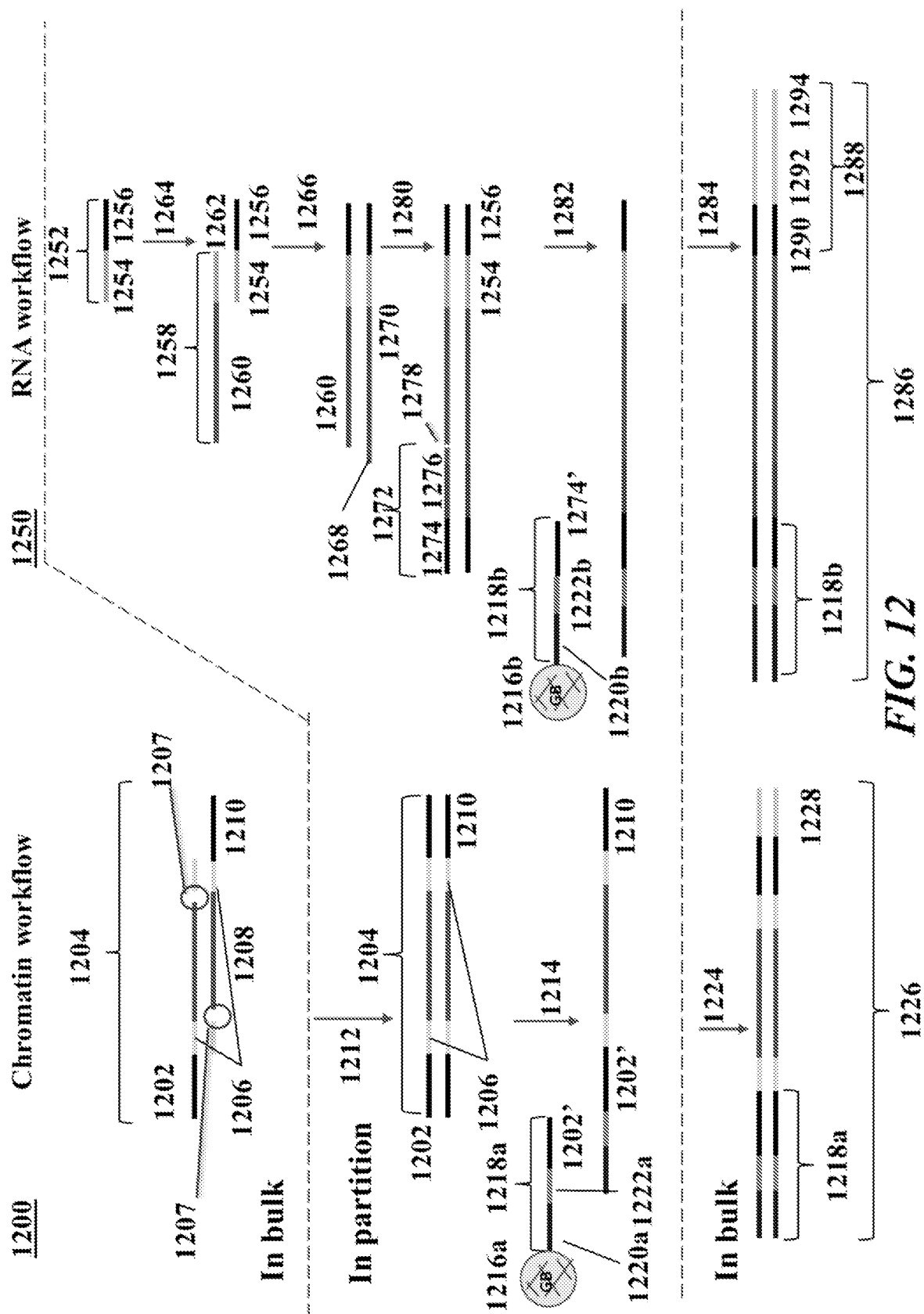
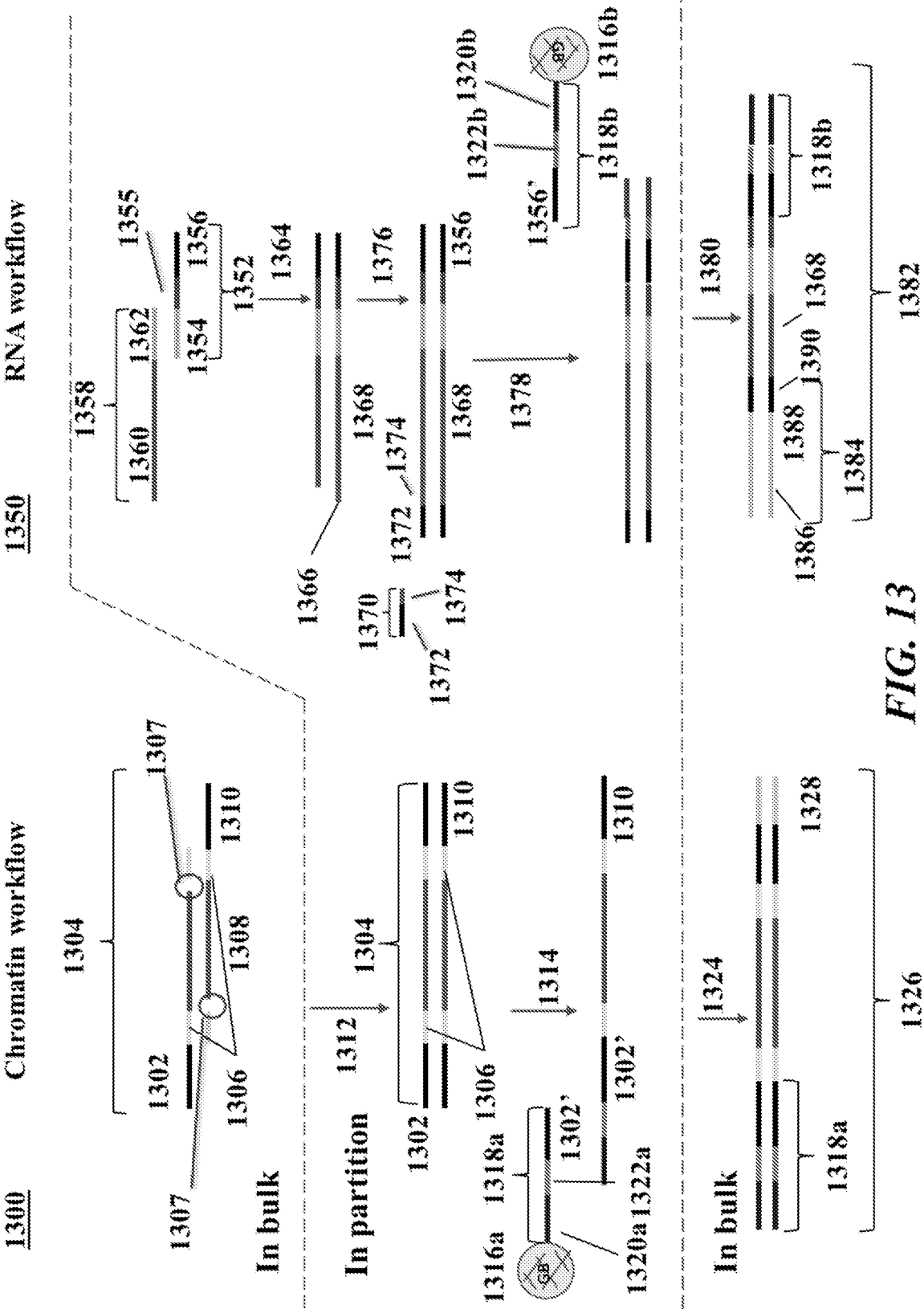
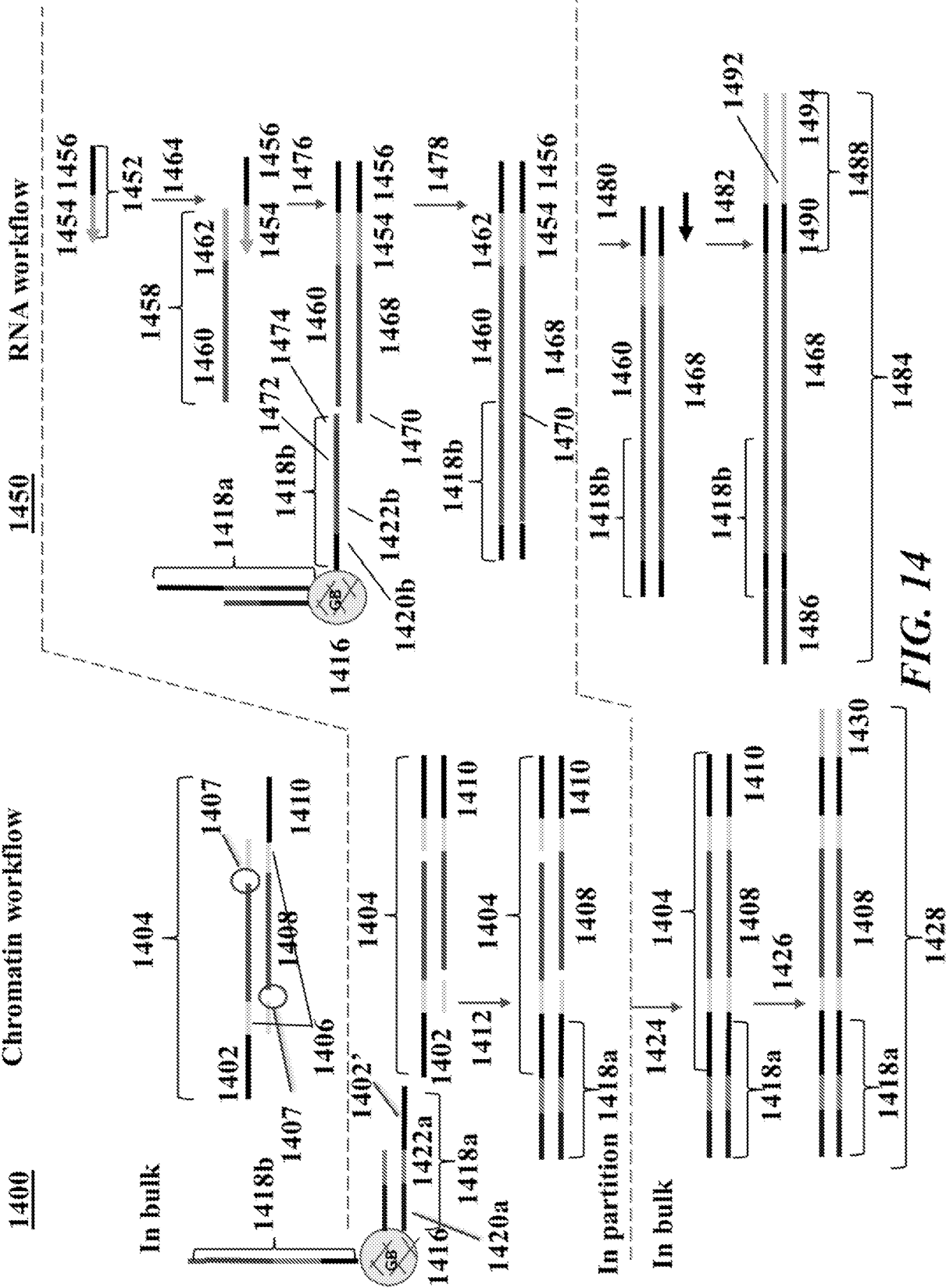
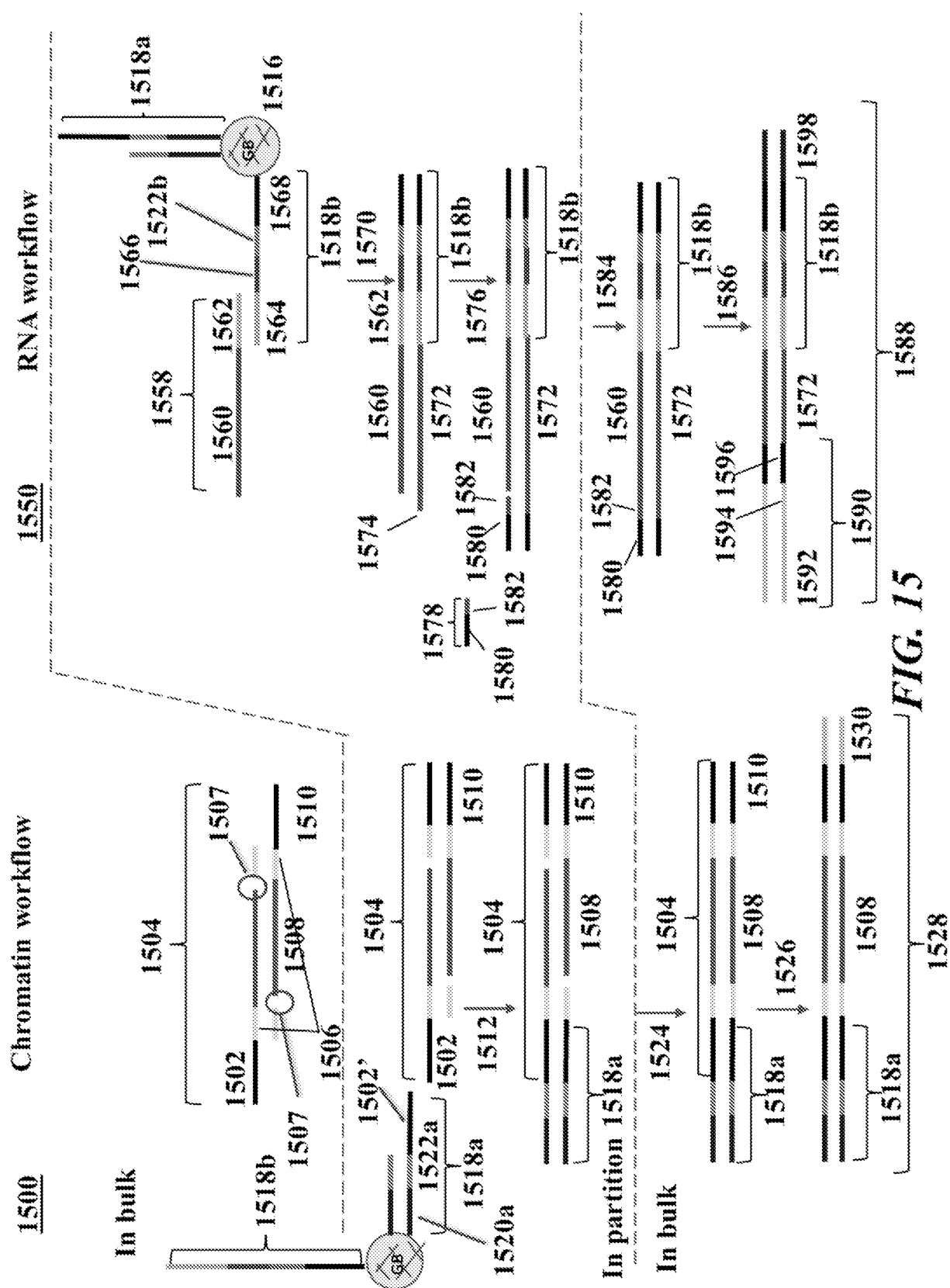


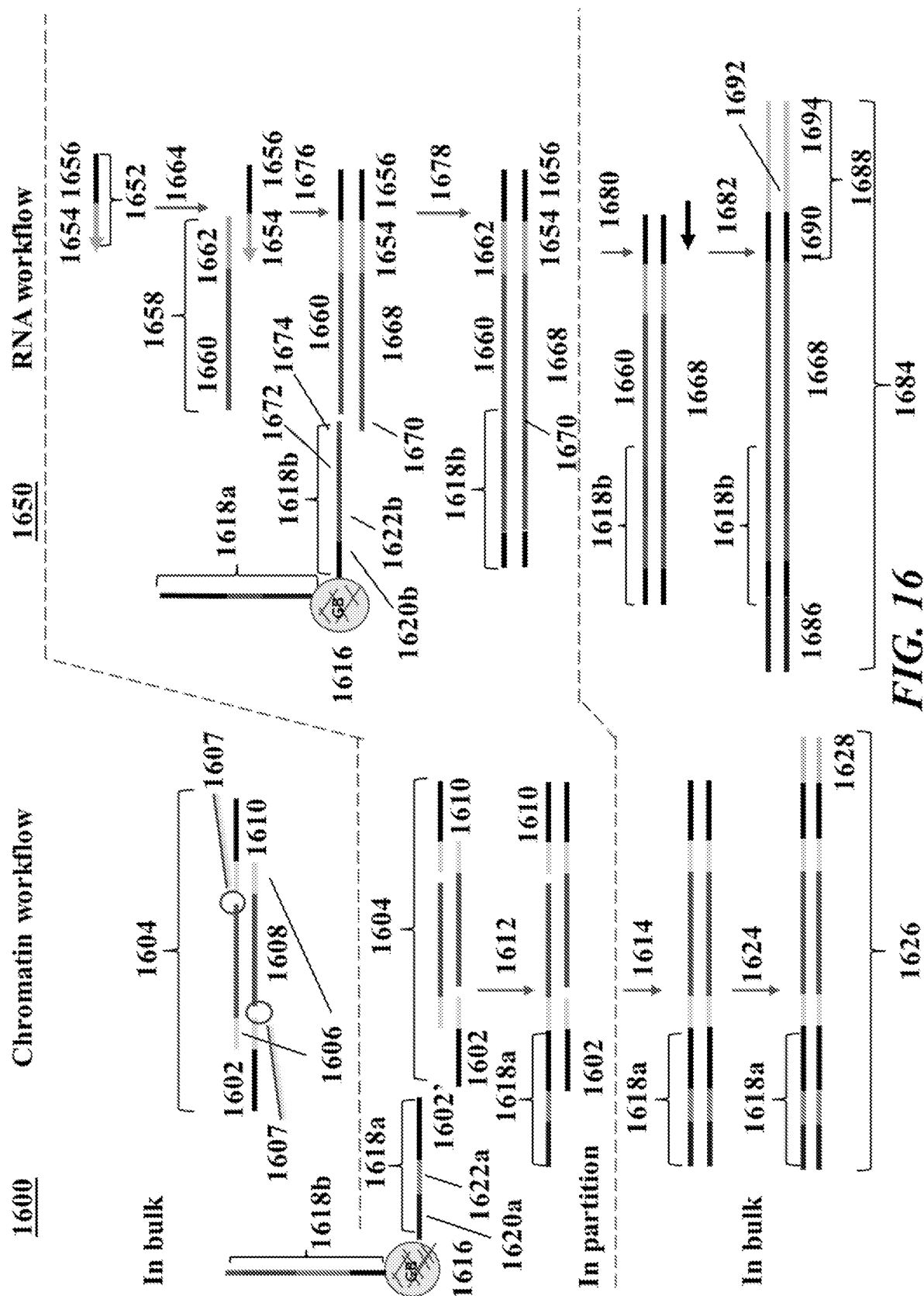
FIG. 11











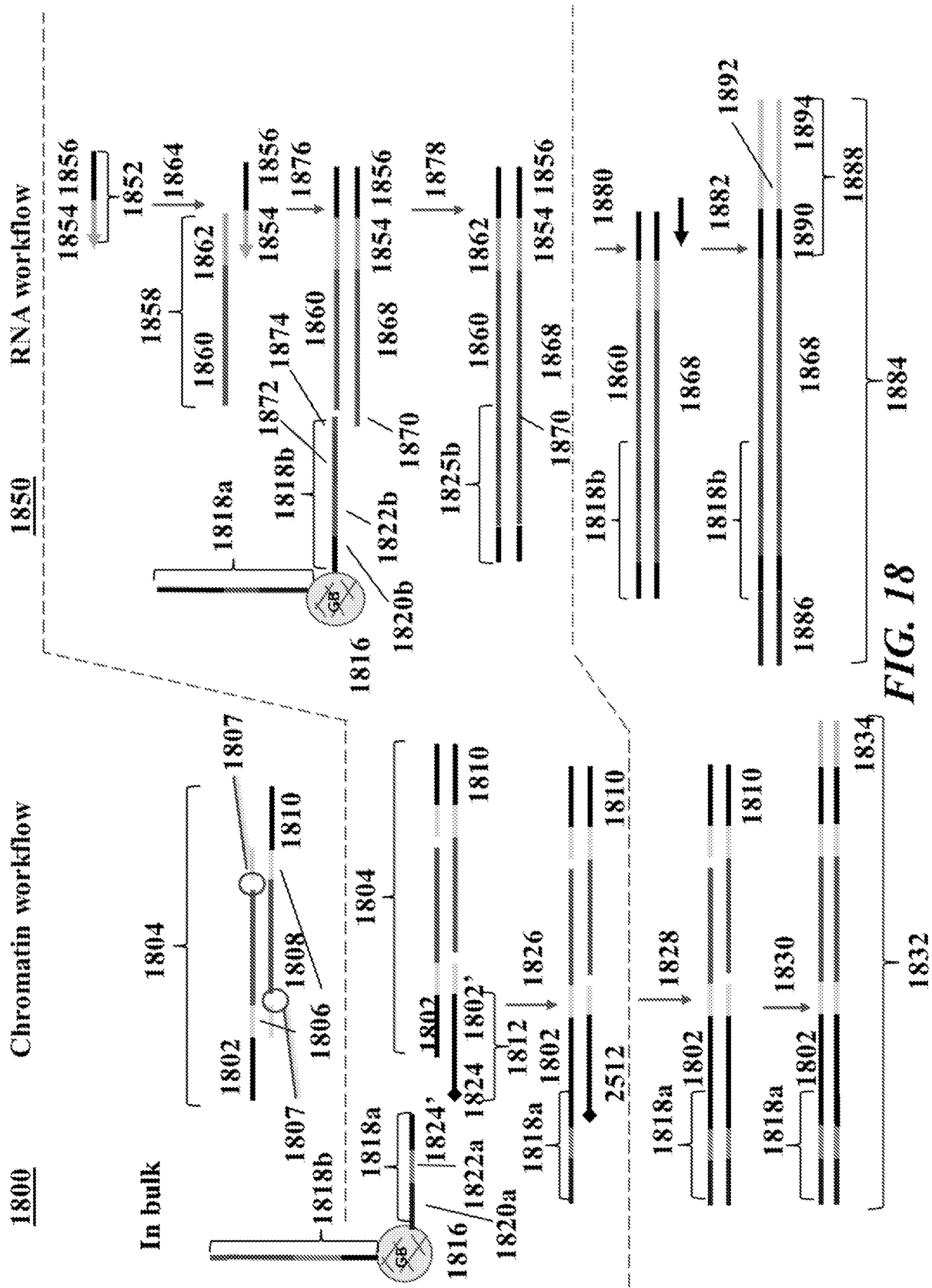
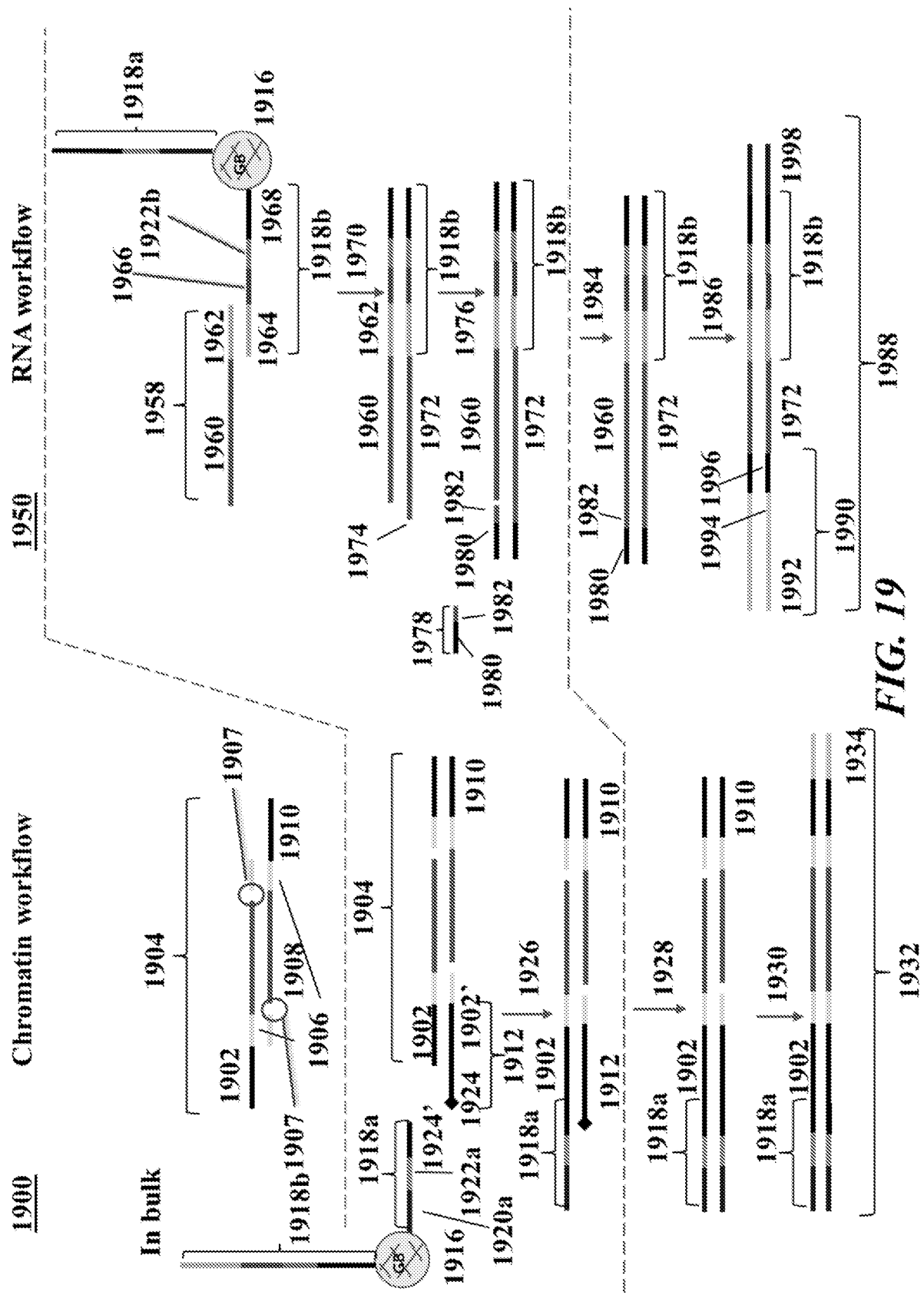
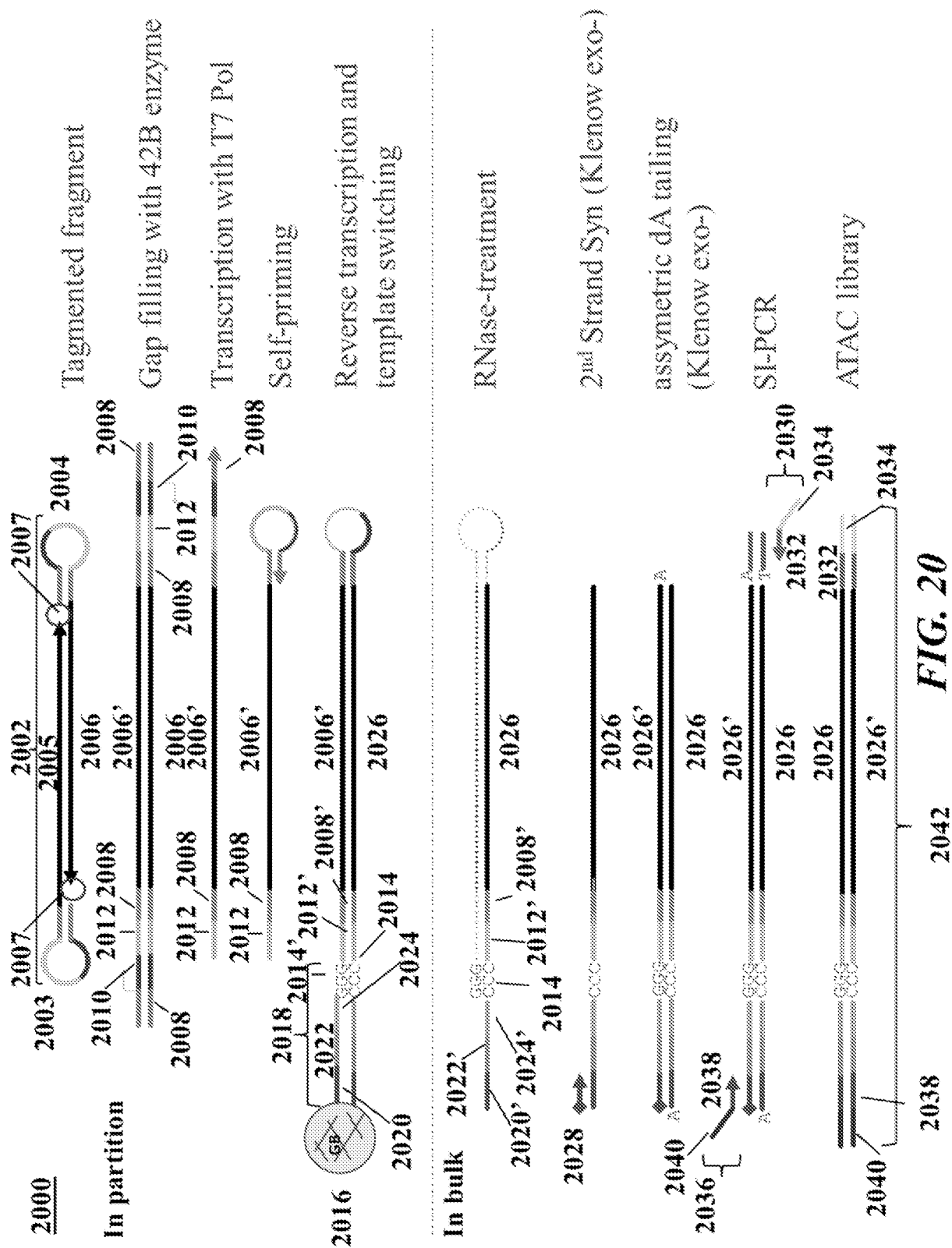


FIG. 18





2100

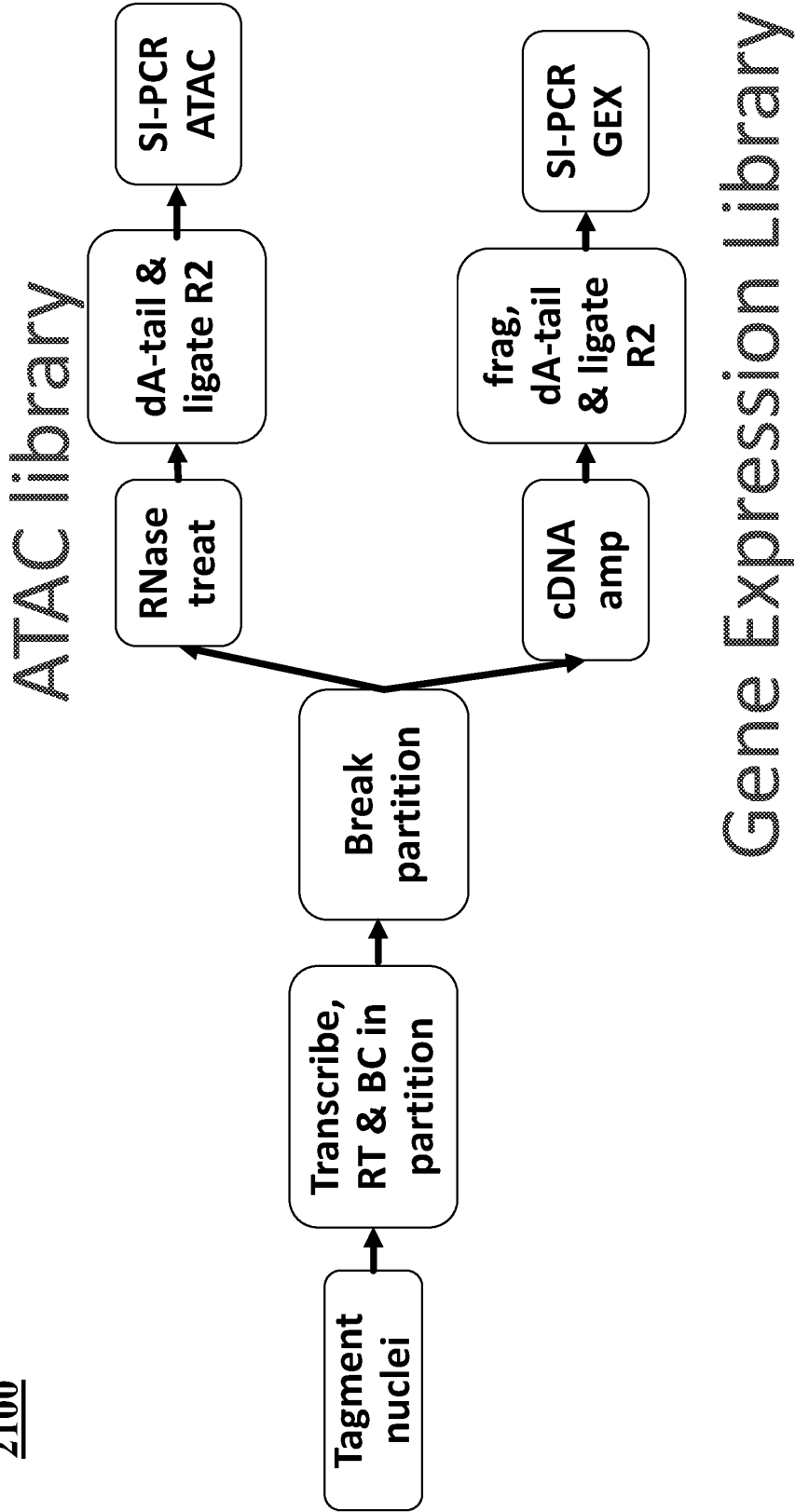


FIG. 21

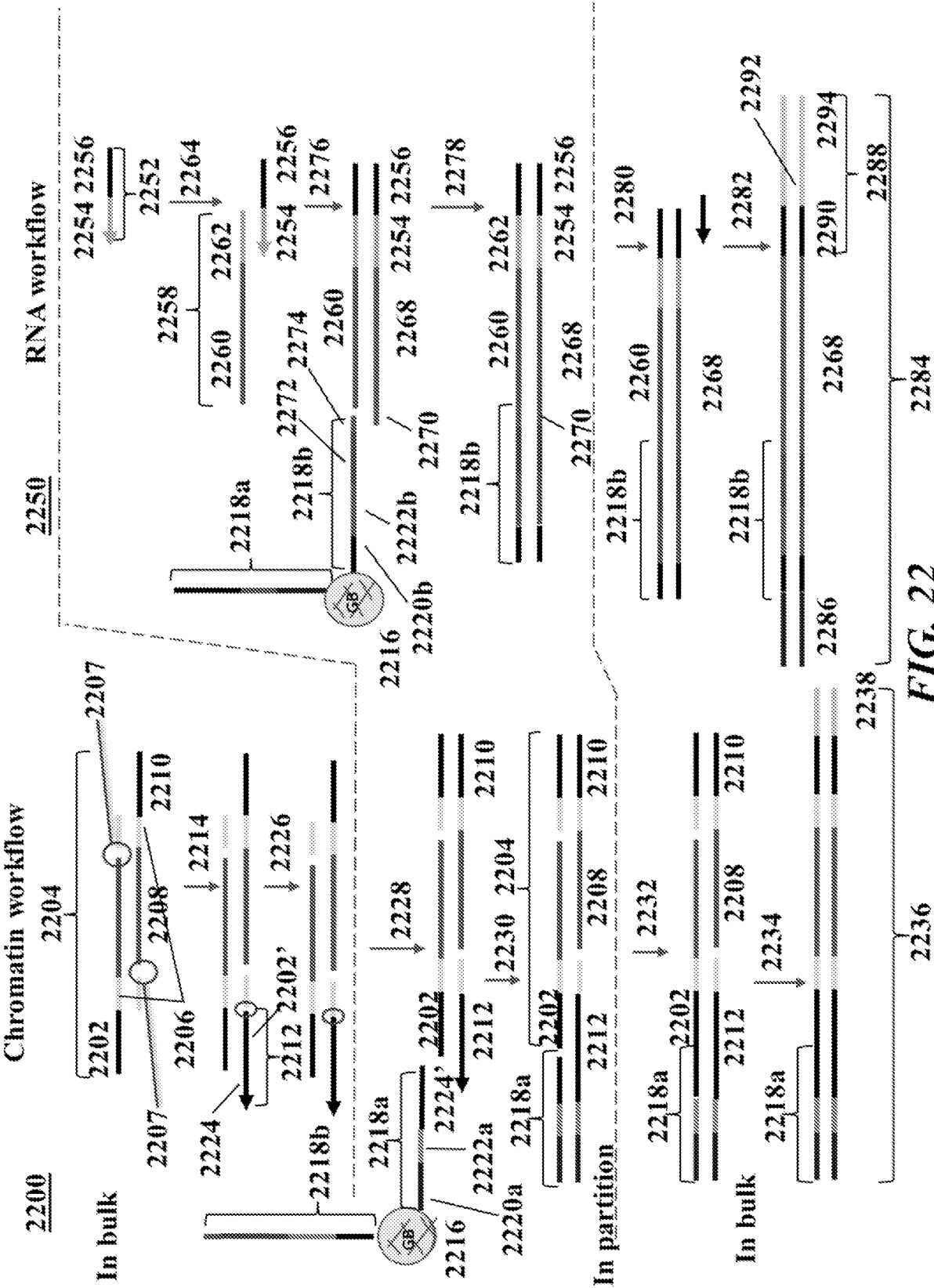


FIG. 22

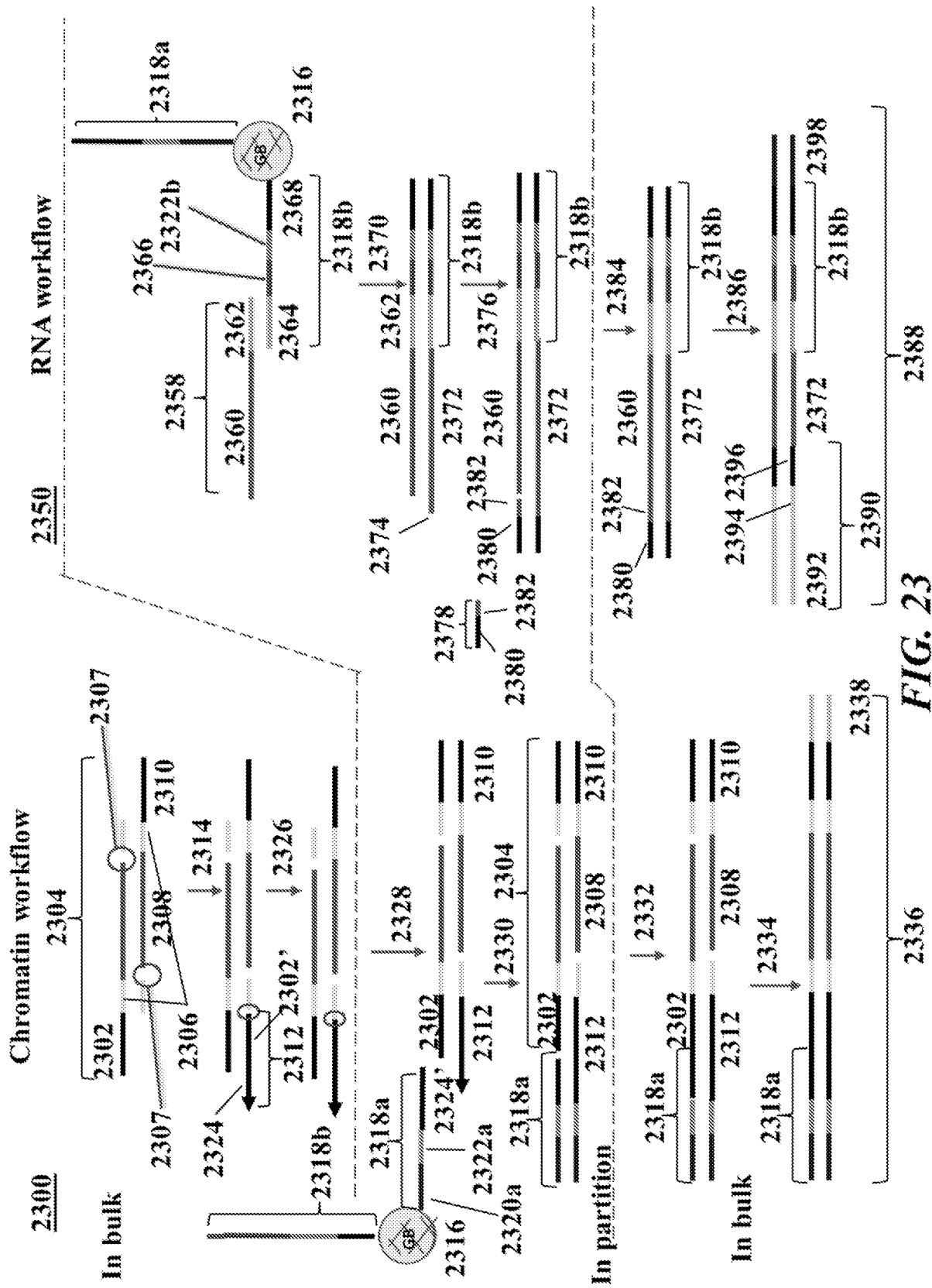


FIG. 23

Profiling Different Modalities to Gain Better Understanding of Complex Biological Systems

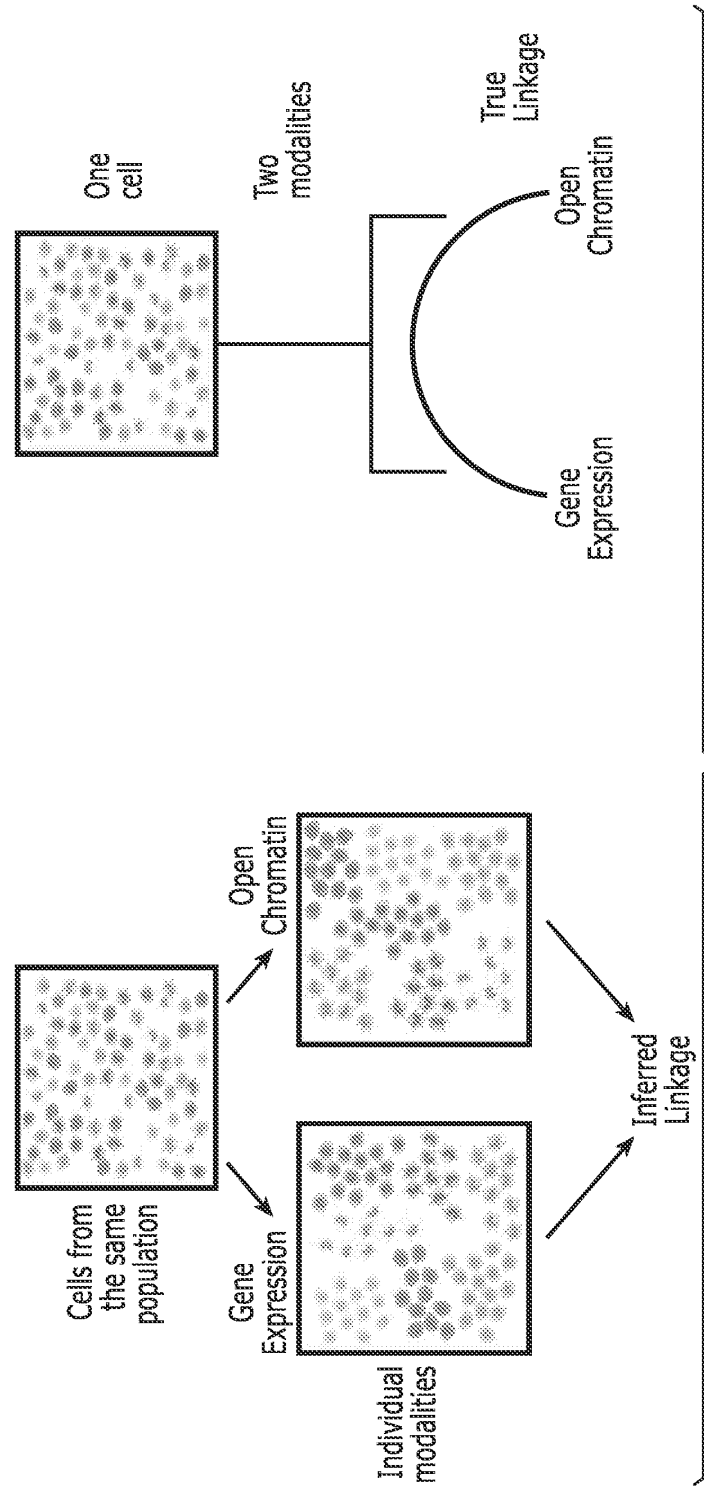


FIG. 24

Two Modalities - One Simple Workflow

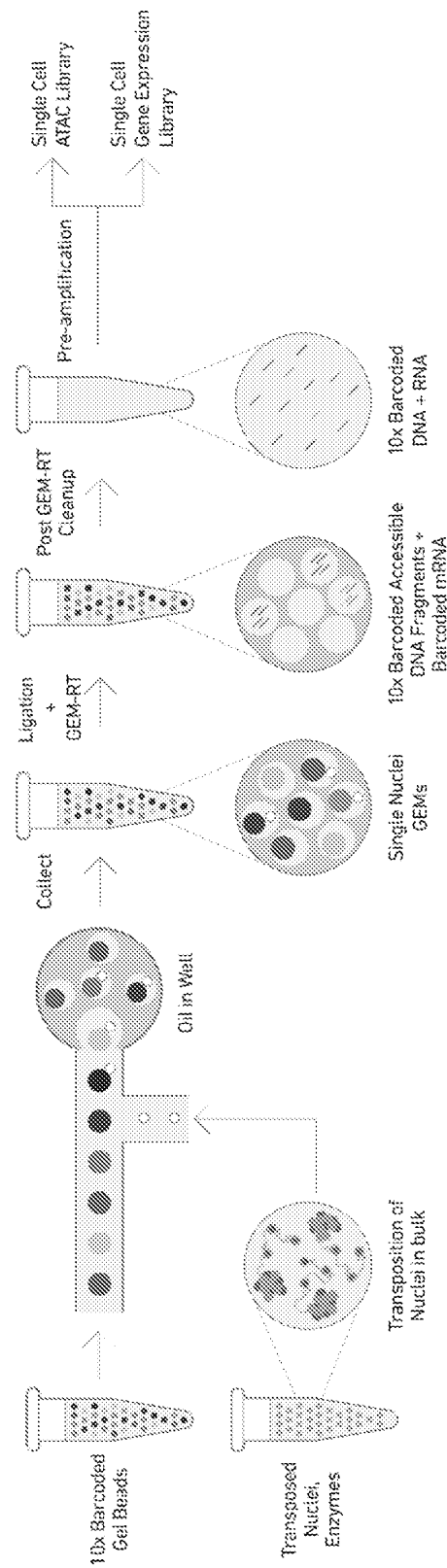


FIG. 25

Joint ATAC and Gene Expression Profiling of 24,000 Peripheral Blood Mononuclear Cells (PBMCs)

Gene Expression Annotation Using Expressed Markers

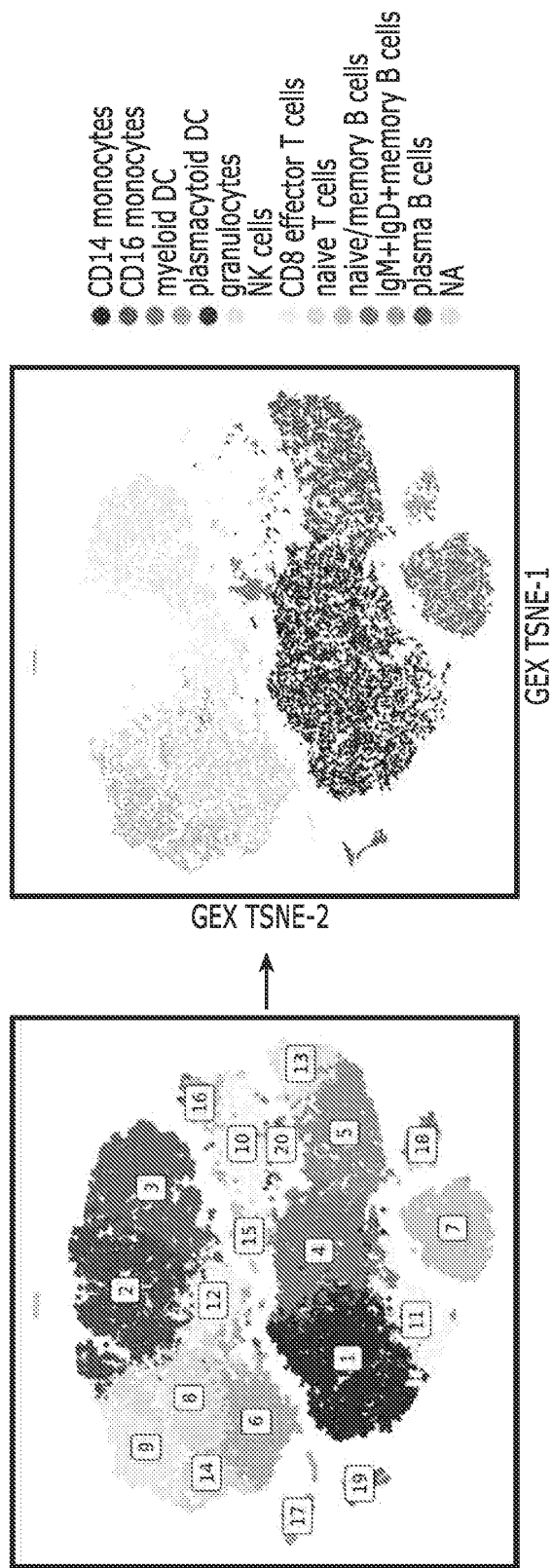


FIG. 26

Joint ATAC and Gene Expression Profiling of PBMCs

Open Chromatin Annotation Using TF Accessibility

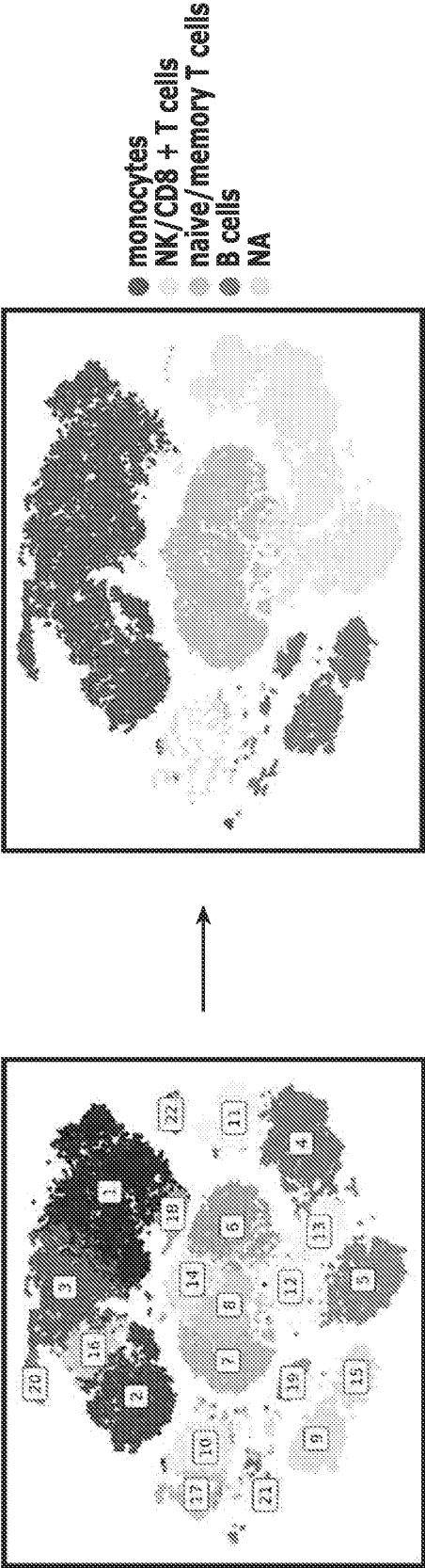
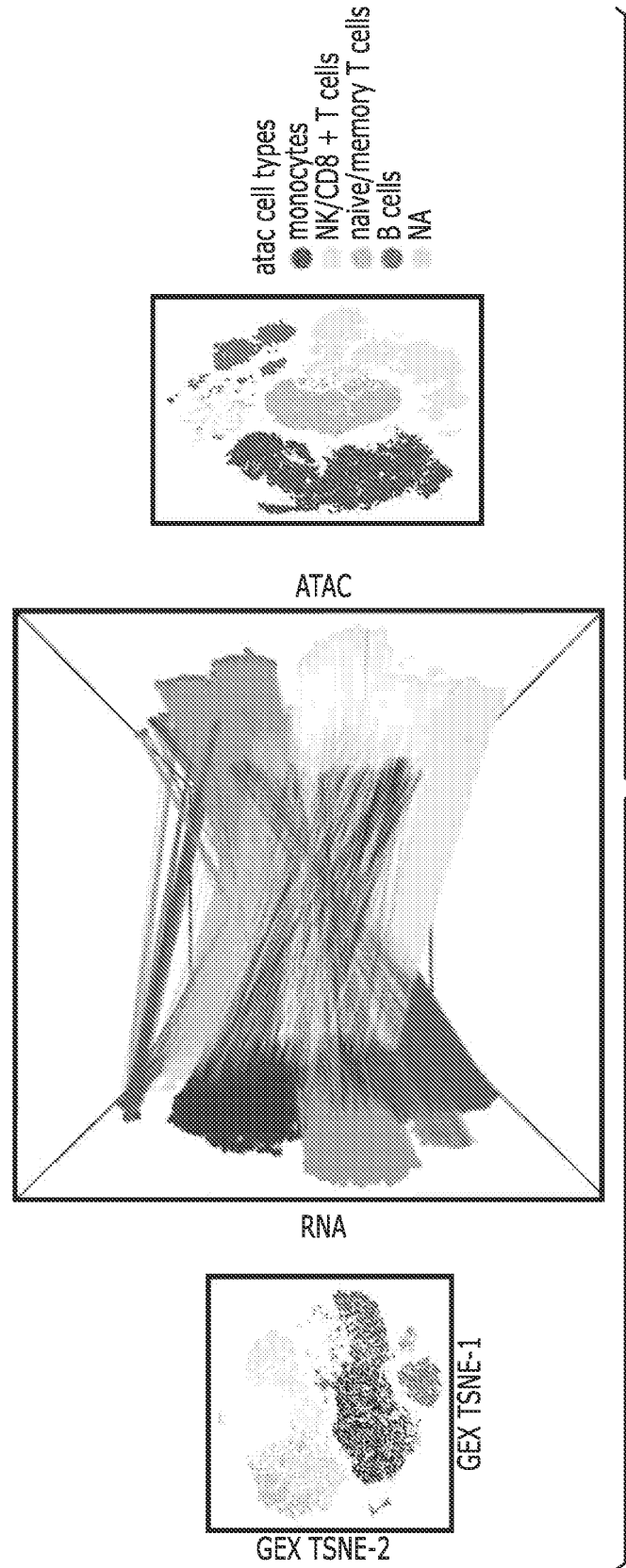


FIG. 27

Concordance between the two Read-Outs



Concordance between the two Read-Outs

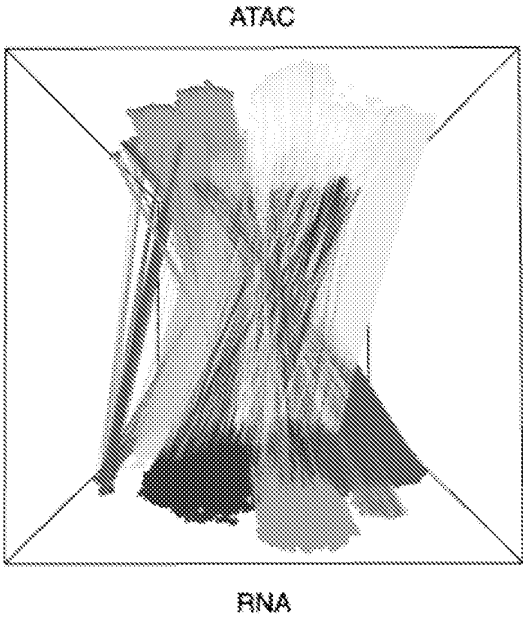
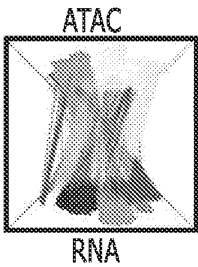


FIG. 29A

Concordance between the two Read-Outs



FIG. 29B



Further Annotate your ATAC Populations
Transfer Gene Expression Marker-derived Annotation into ATAC Populations

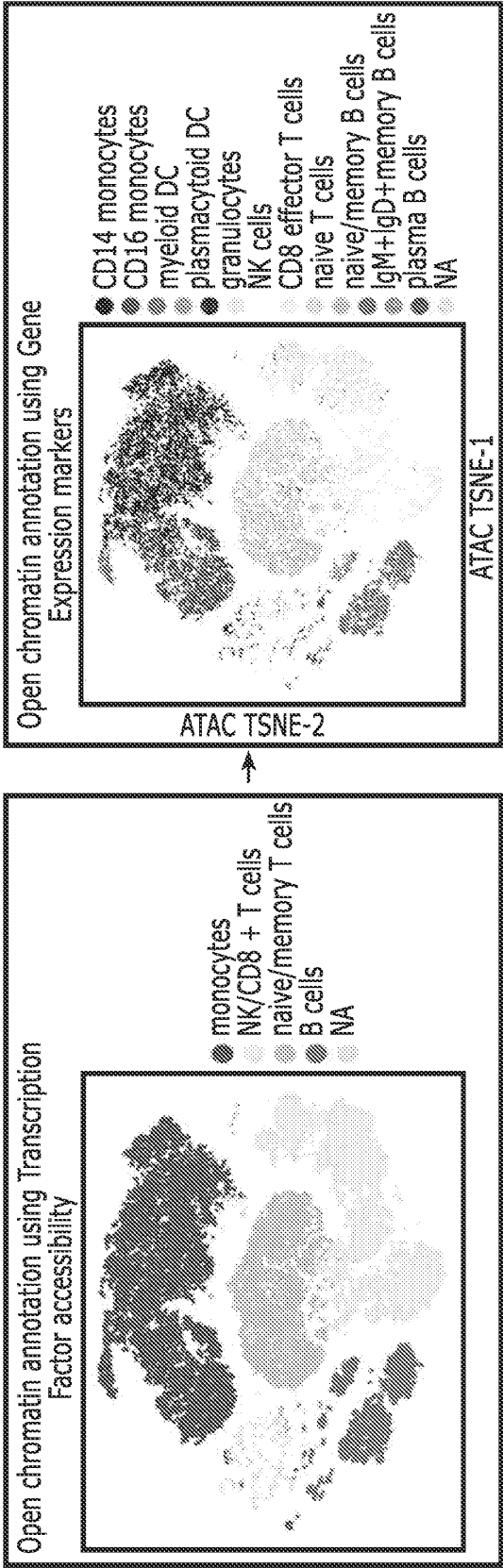


FIG. 30

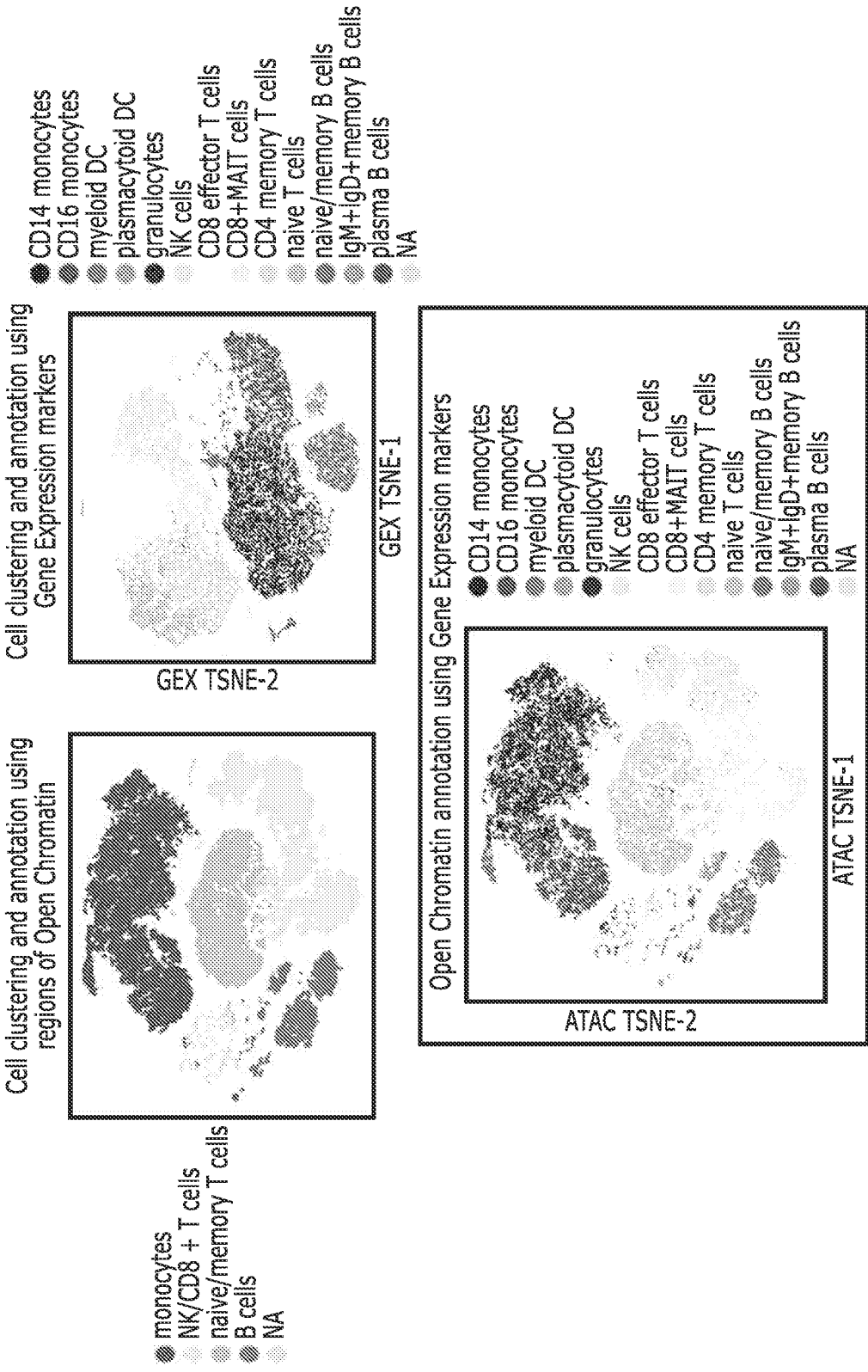


FIG. 31

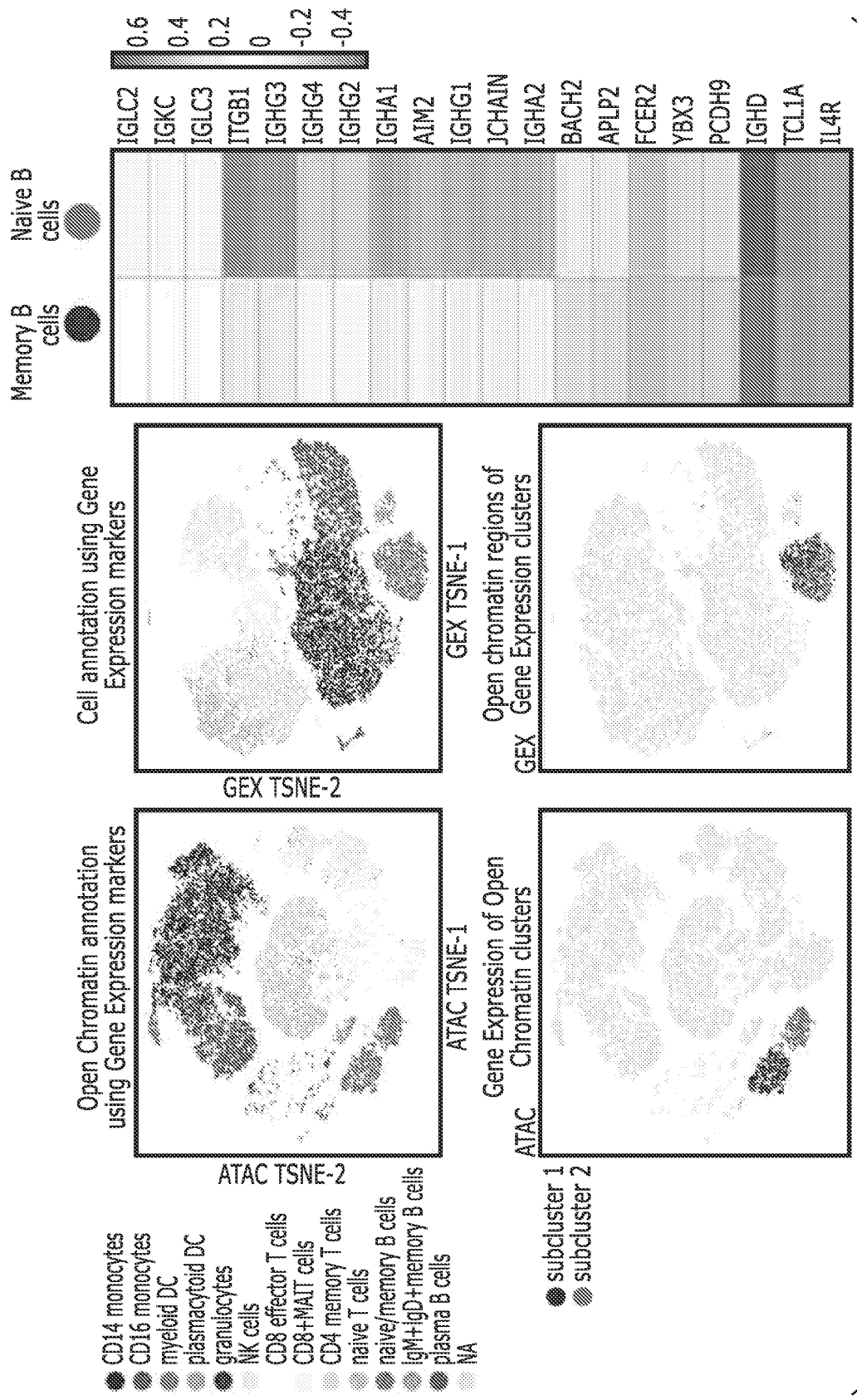


FIG. 32

Case Study - B Cell Lymphoma

Functional characterization of a small B cell lymphoma and its signaling pathways

Pathology report

Lymph node tumor

Diagnosis: Diffuse small lymphocytic lymphoma of the lymph node

Tumor location: Lymph node, Intra-abdominal

Diagnosis details: IHC: CD20(+), CD3(-)

Comments: Malignant lymphoma, small B cell, diffuse type

Profile ~9,000 nuclei through Single Cell ATAC + Gene Expression analysis

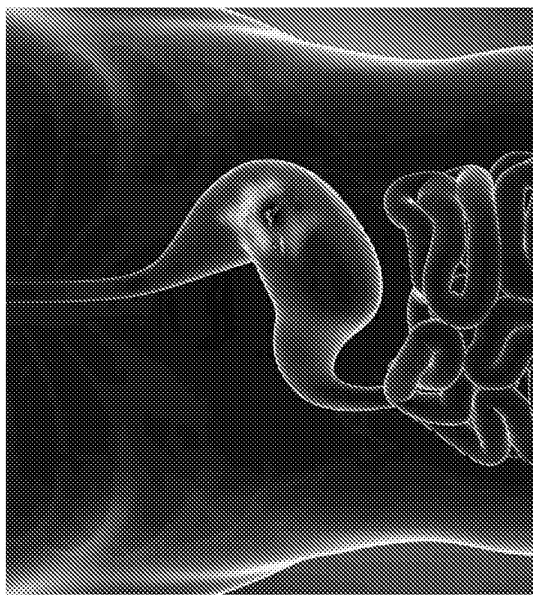
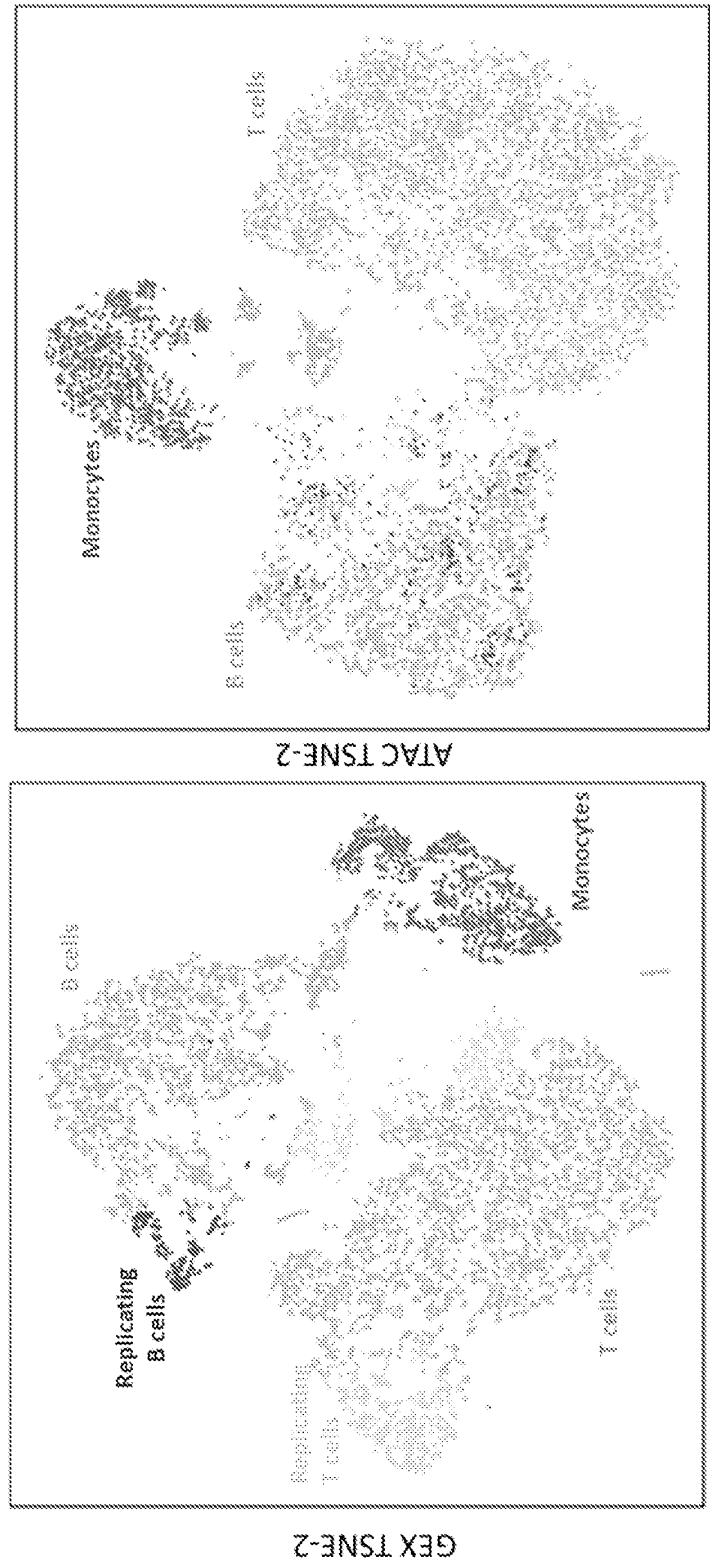


FIG. 33

Cell type annotation using gene expression
markers and transcription factor (TF) accessibility



GEX TSNE-1

ATAC TSNE-1

FIG. 34

Parsing out Tumor from Normal B cells
Using mutational load and BANK1 pathway

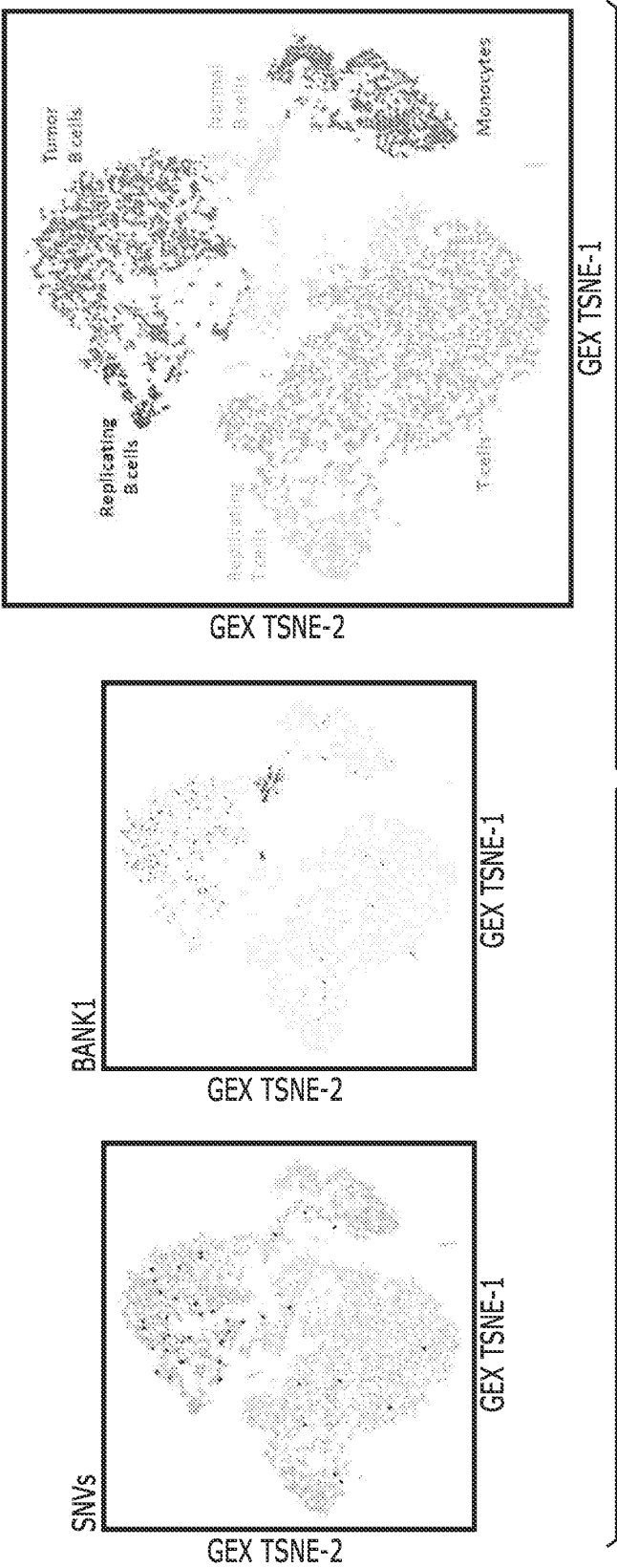


FIG. 35

Use Gene Expression Annotation to Annotate ATAC Populations

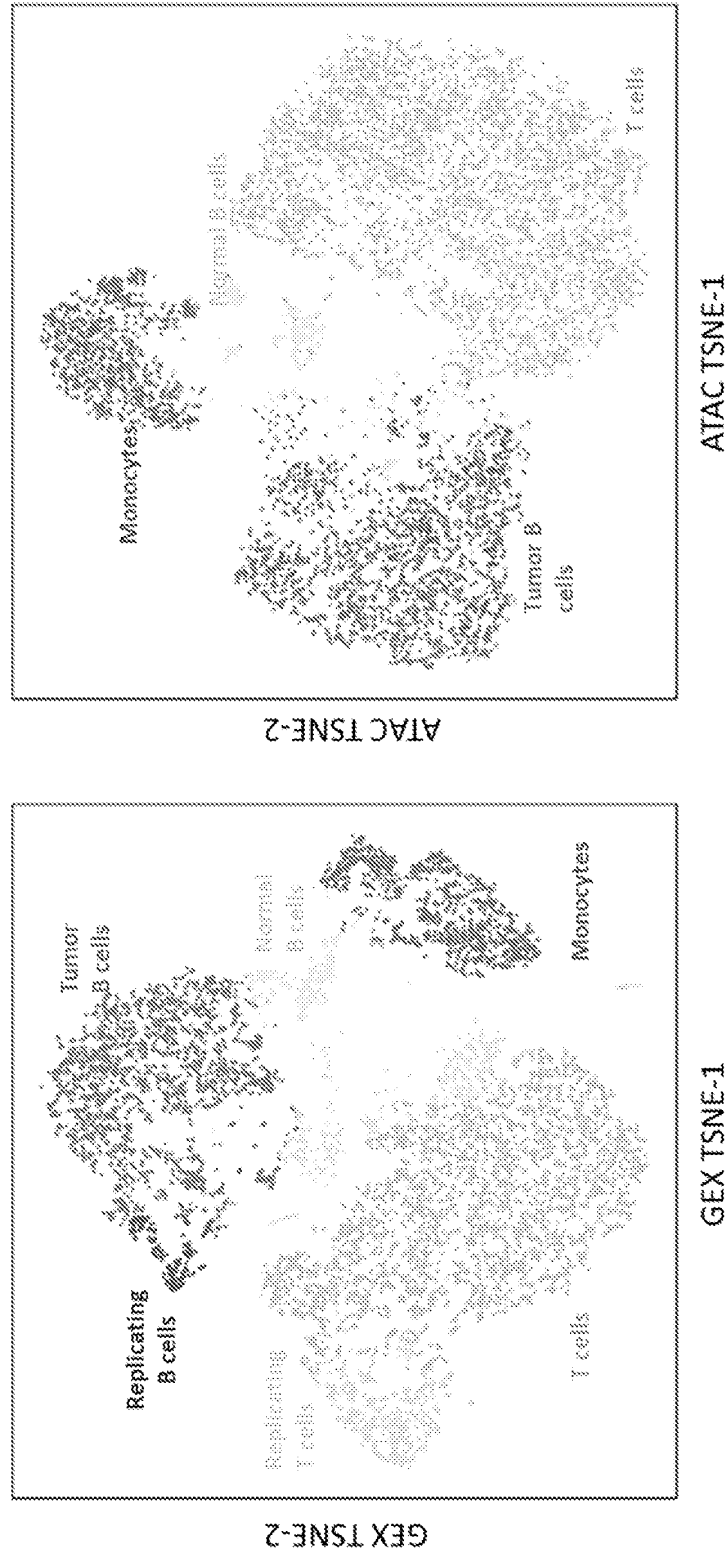


FIG. 36

Differential gene expression analysis between normal
and tumor B cells

Top 10 positively and negatively
differentially expressed genes

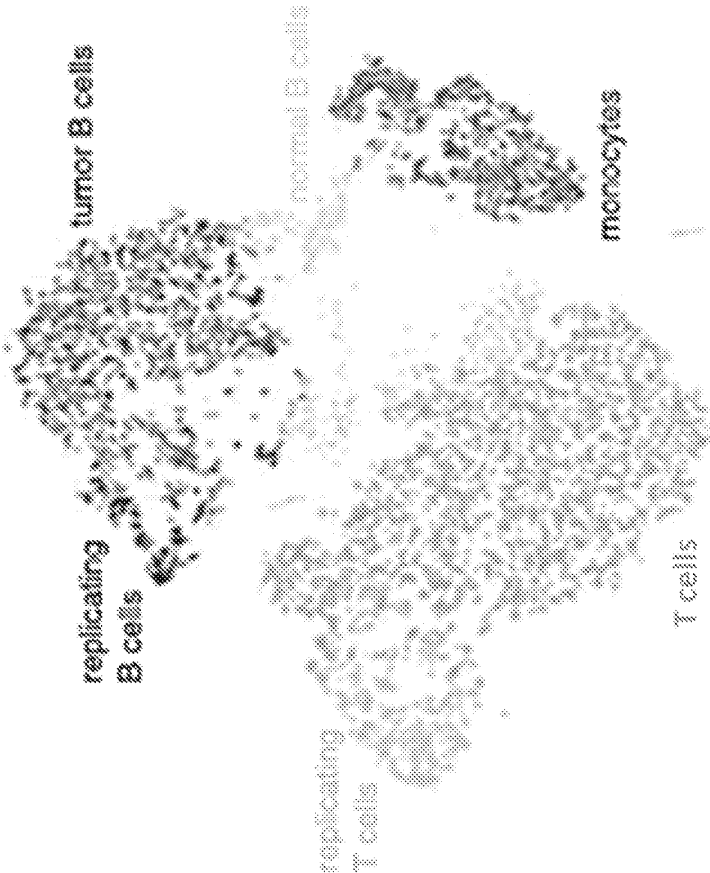
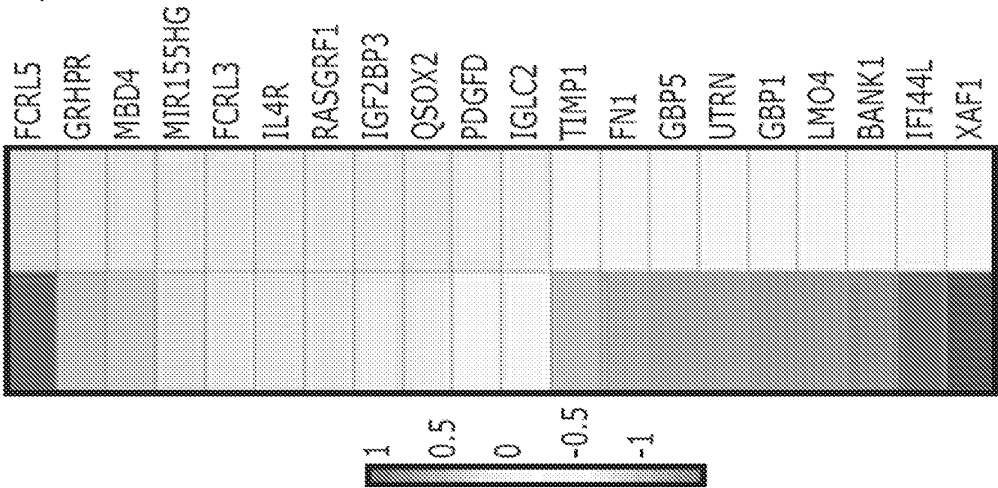
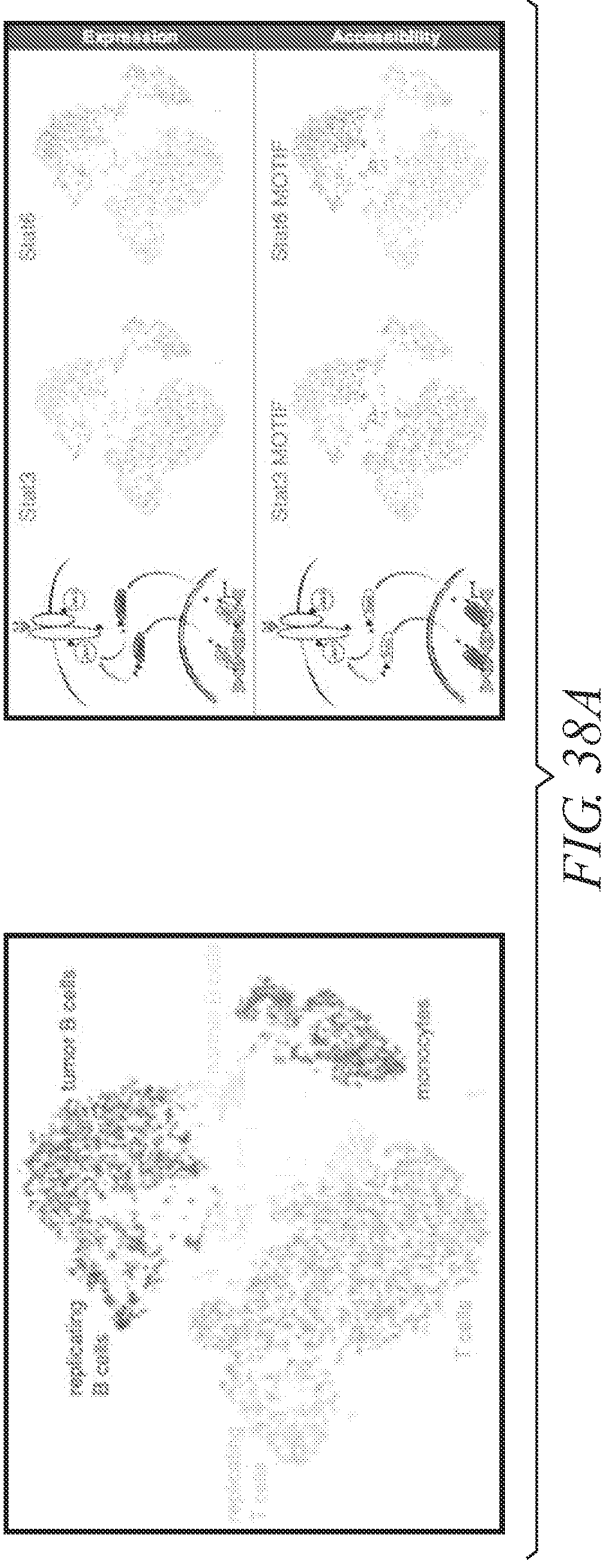


FIG. 37

When Gene Expression doesn't tell the whole story
STAT proteins accumulate in cytoplasm but are only active upon nuclear translocations



Uncover Tumor-Specific Differentially Accessible
Chromatin Regions

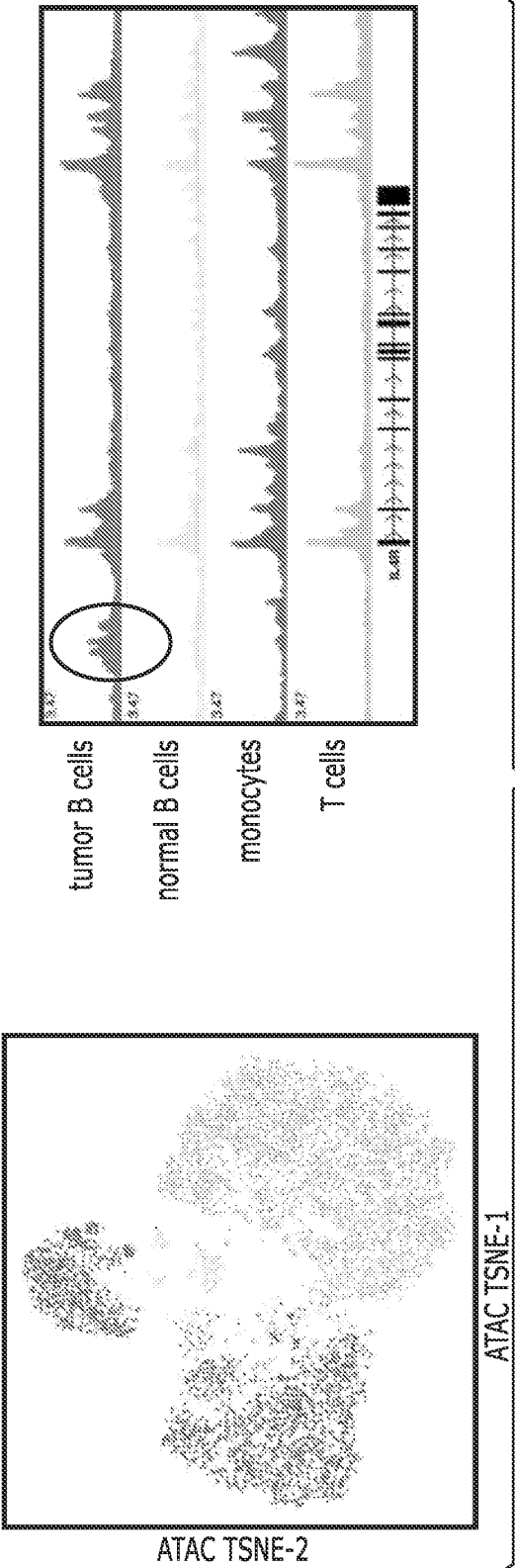


FIG. 38B

Discover novel open chromatin regions associated with specific cell states

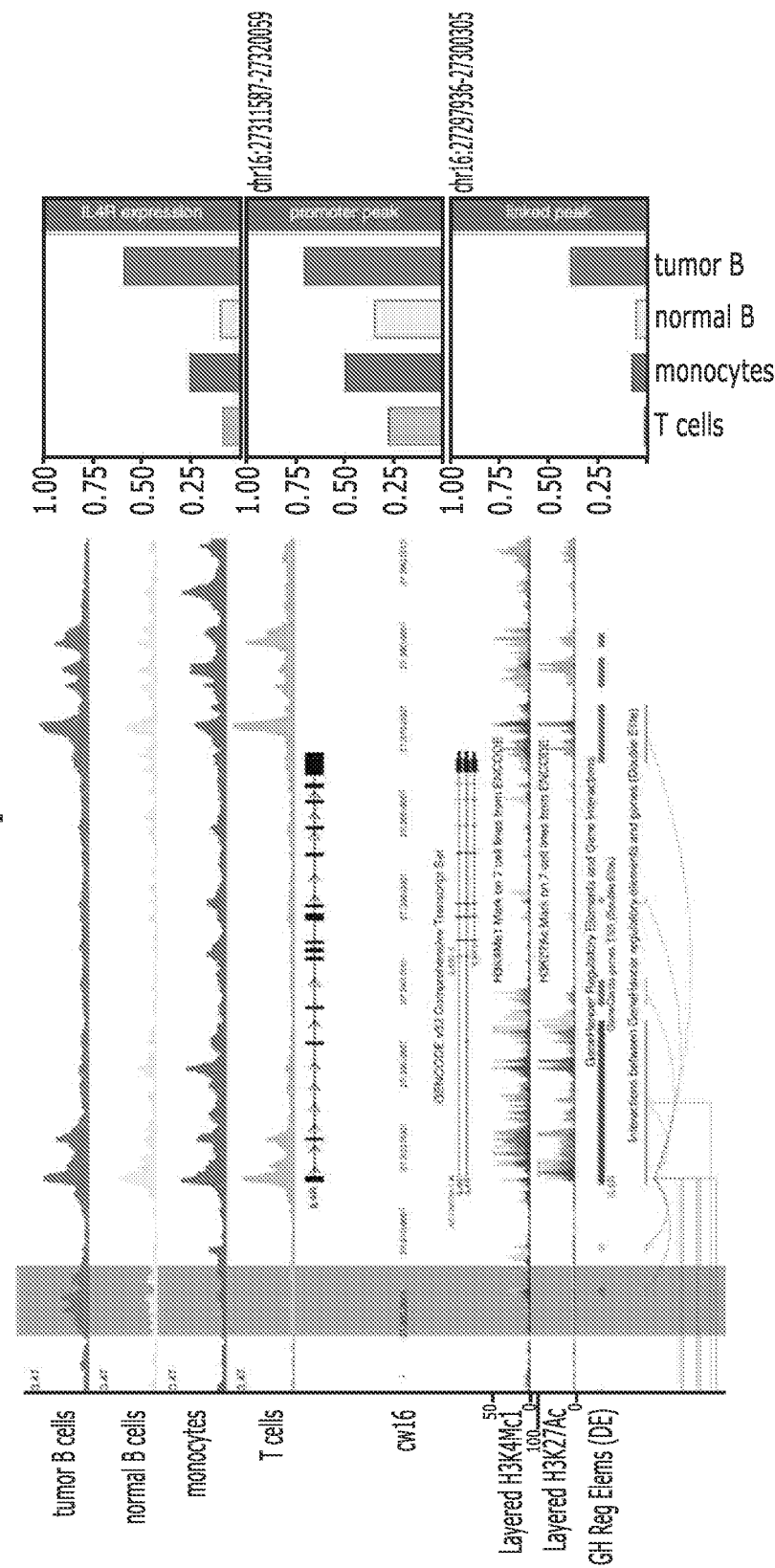


FIG. 38C

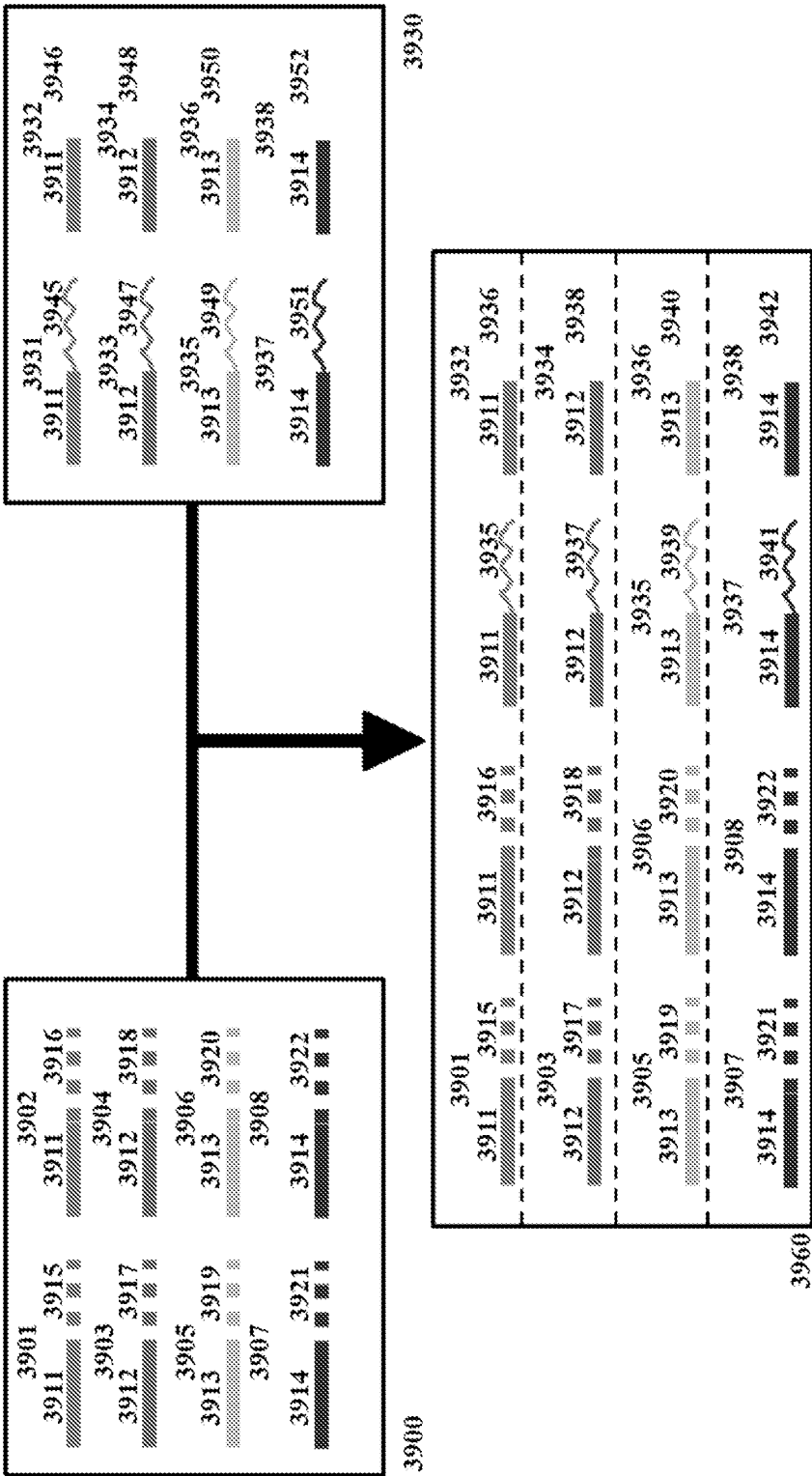


FIG. 39

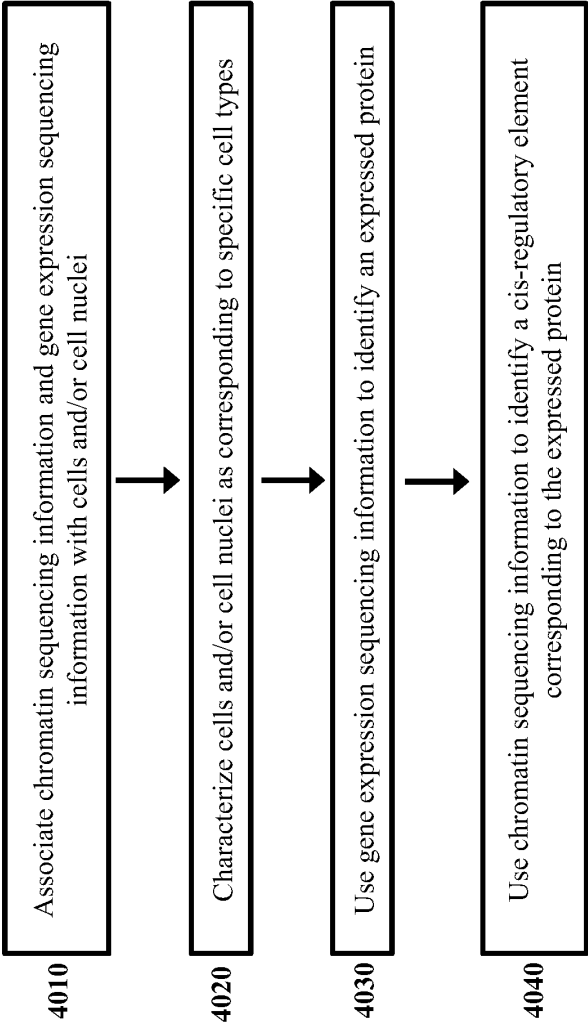


FIG. 40

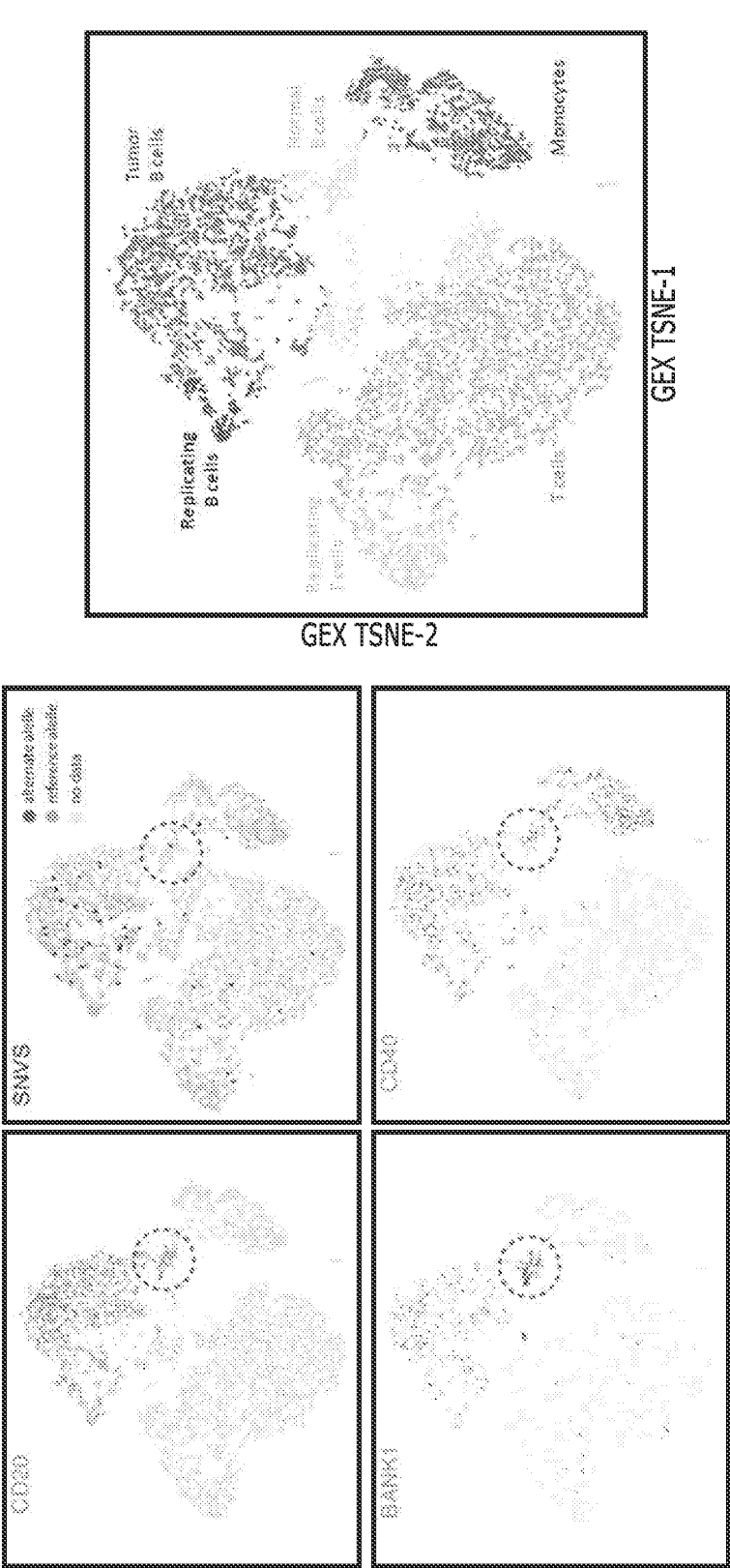


FIG. 41

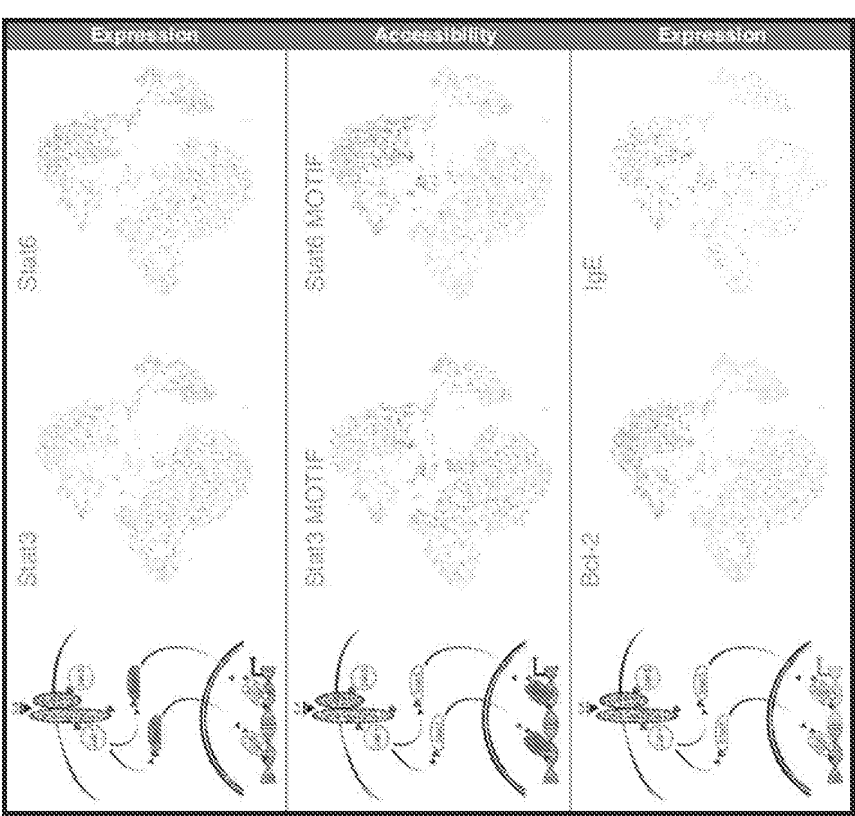
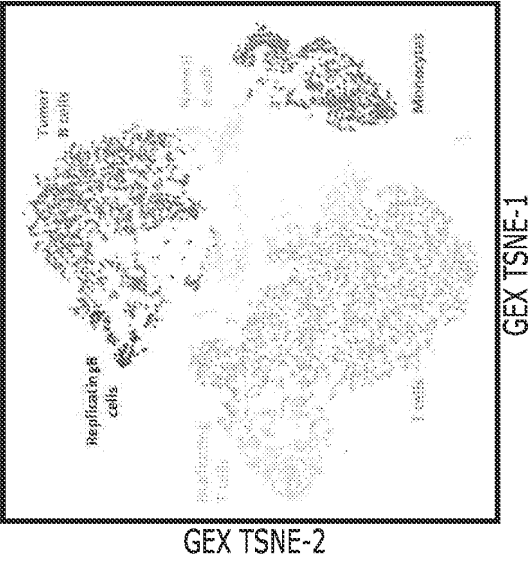


FIG. 42



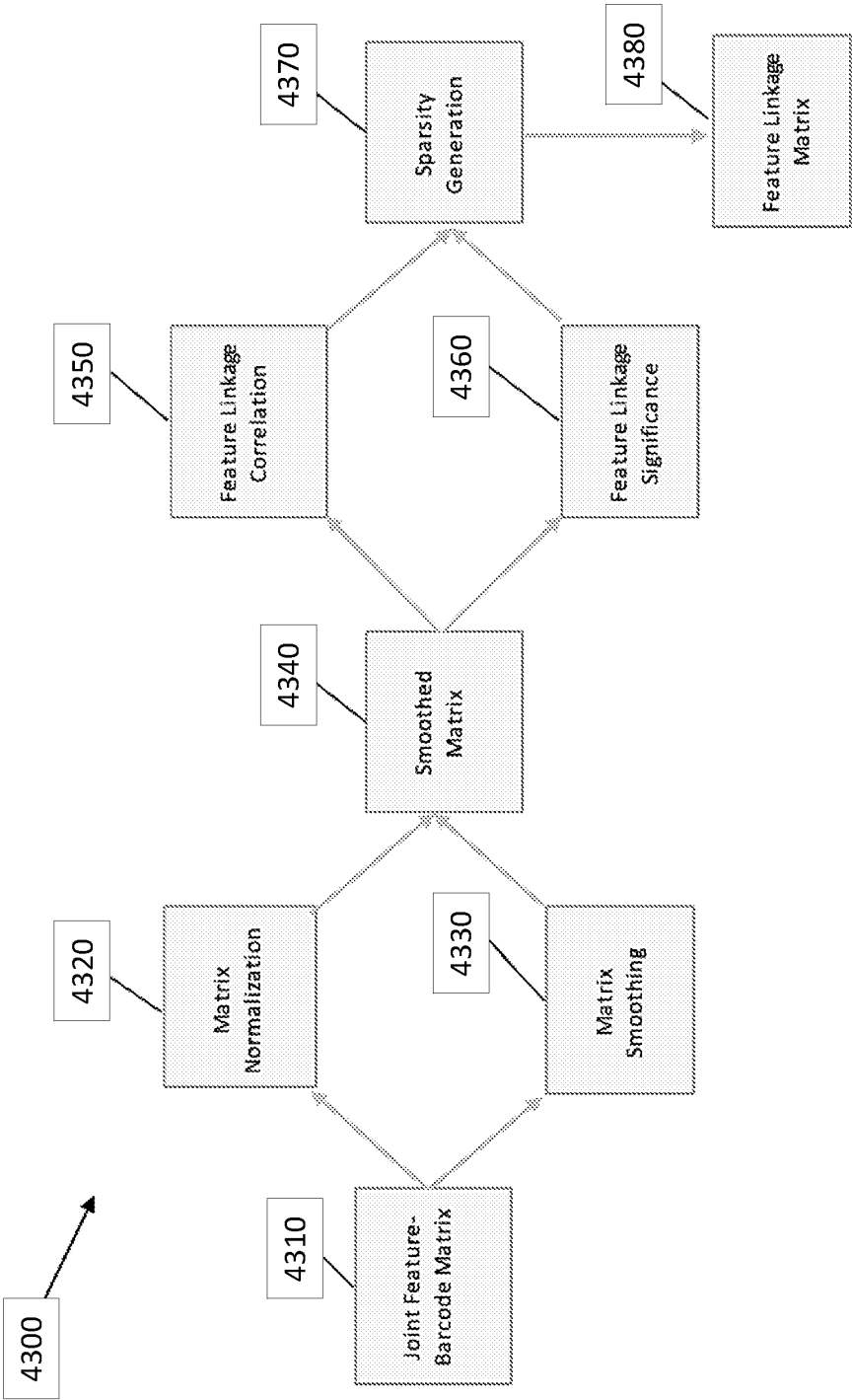


FIG. 43

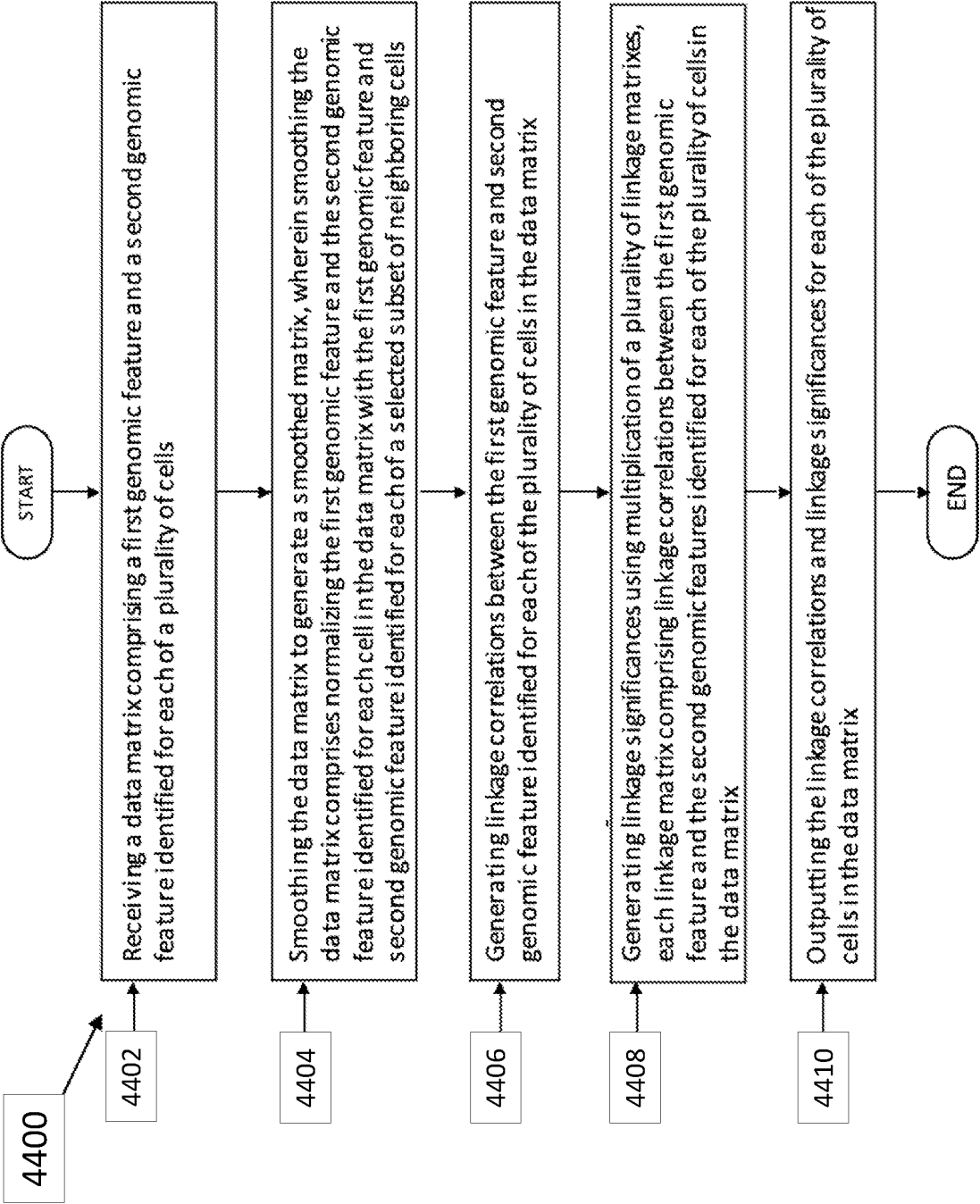


FIG. 44

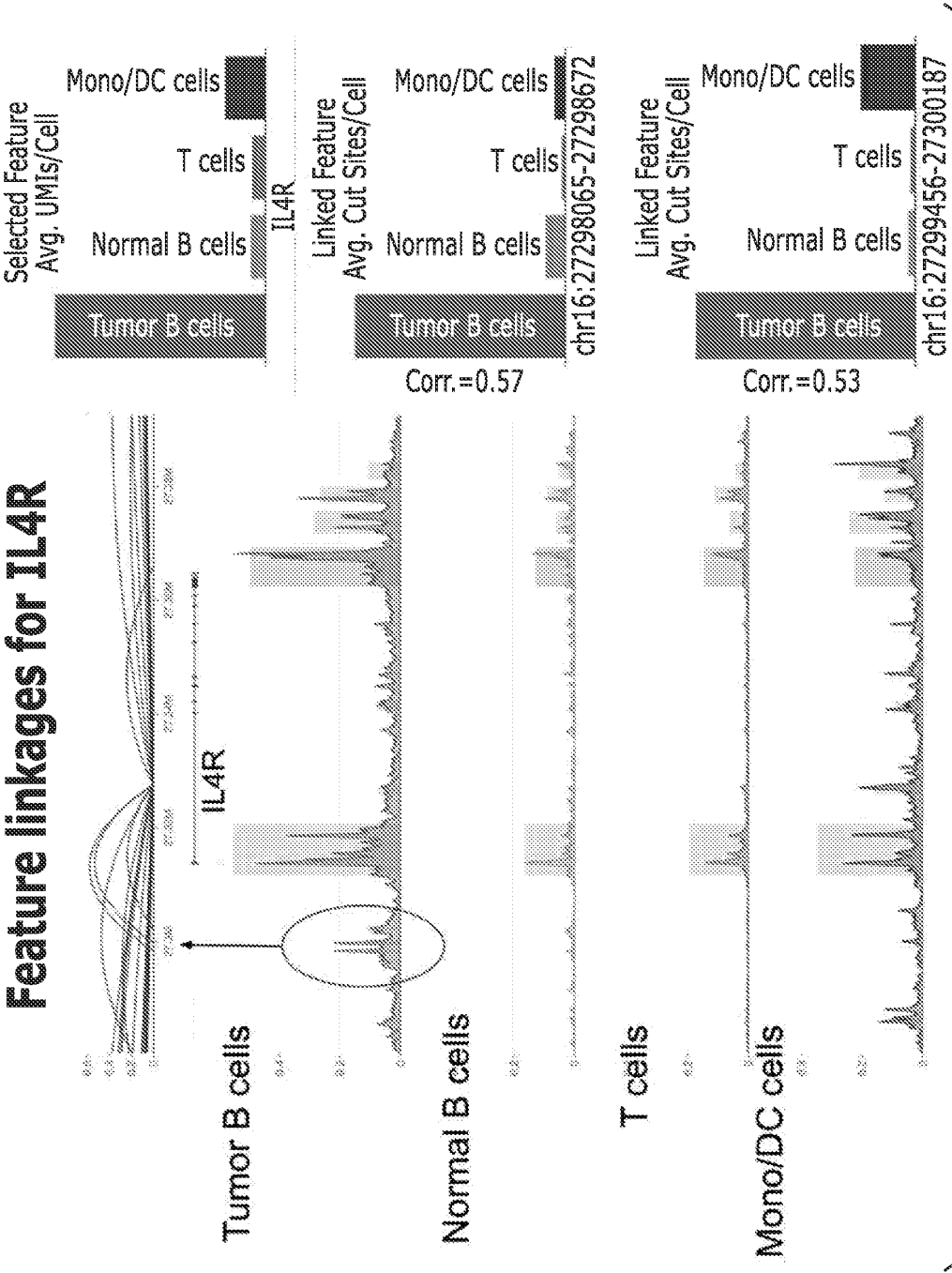


FIG. 45A

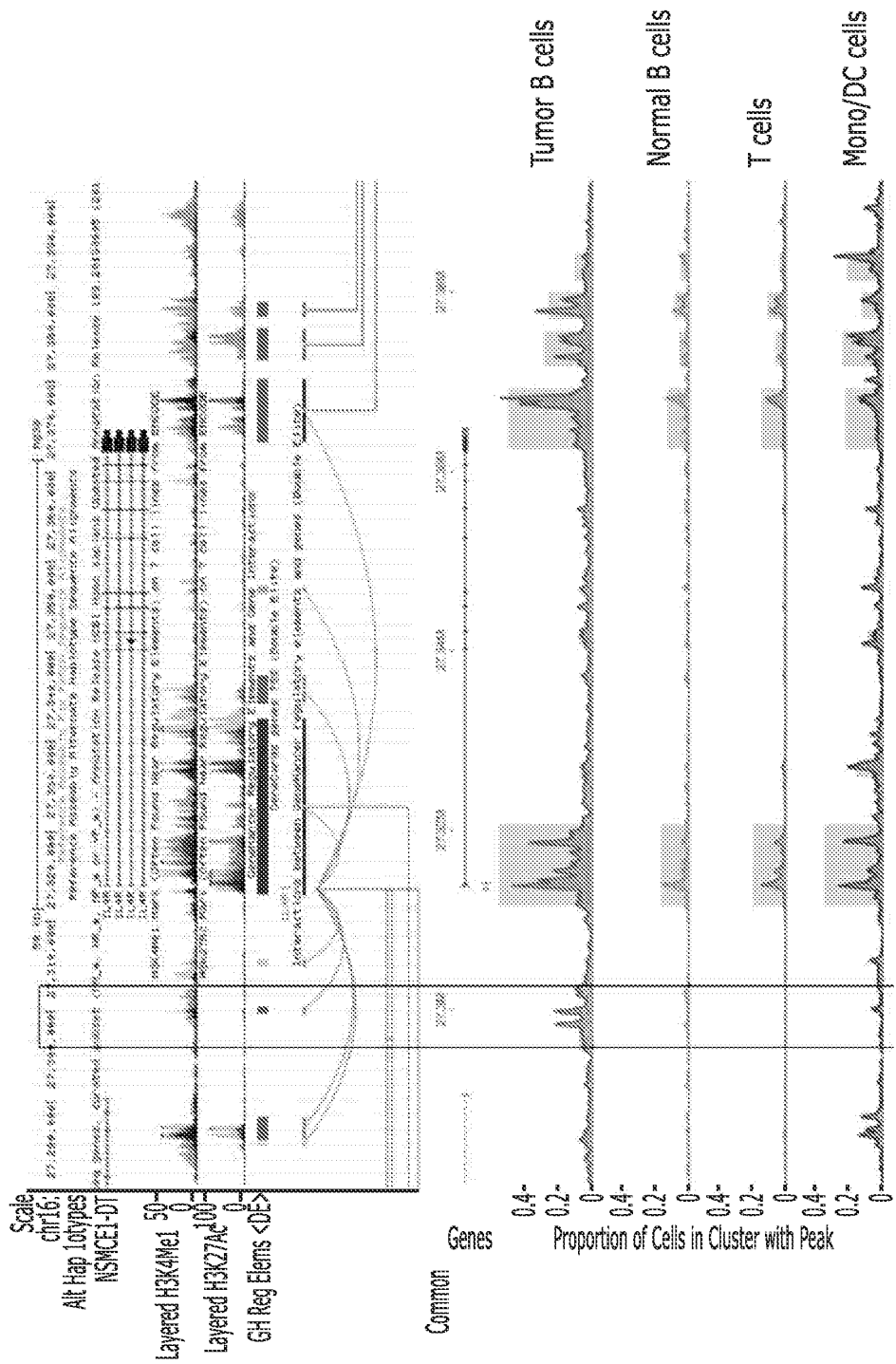
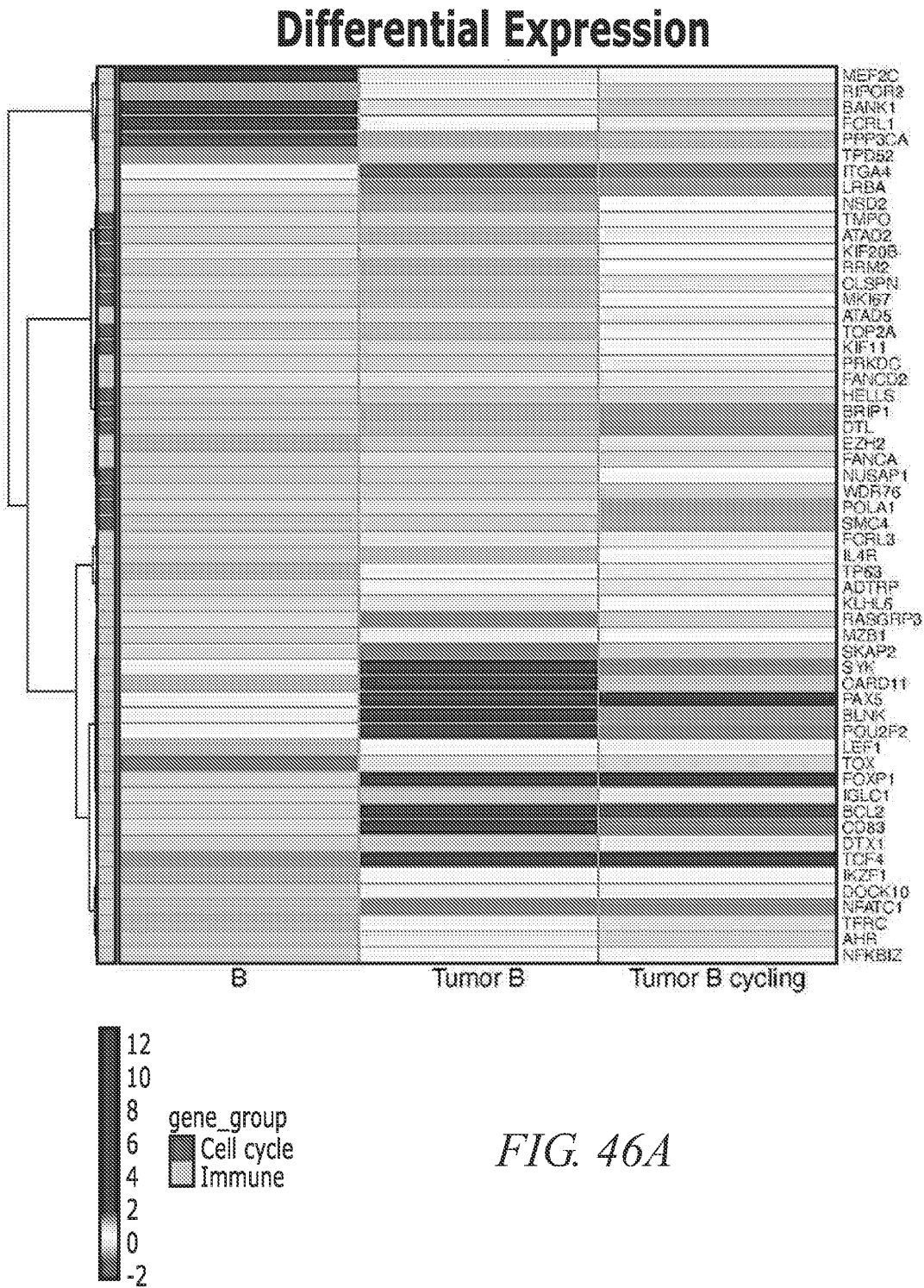
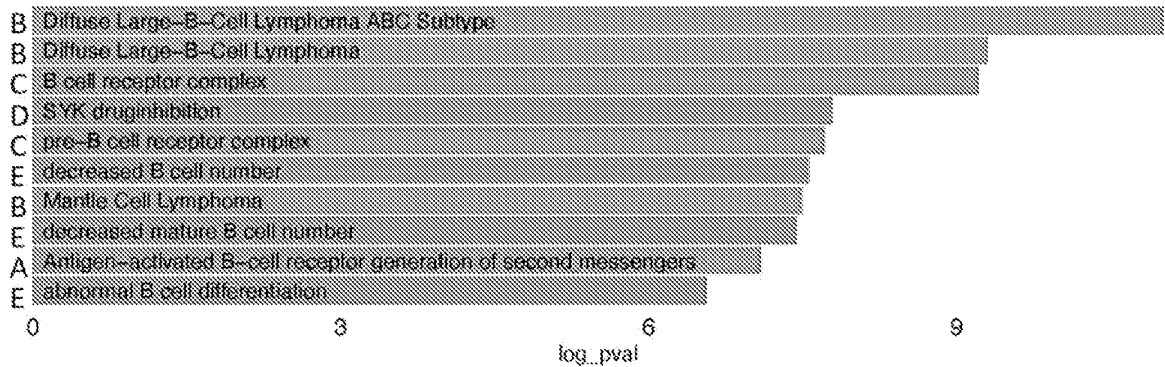


FIG. 45B



geneset

Ontologies & Pathways



geneset

Transcription

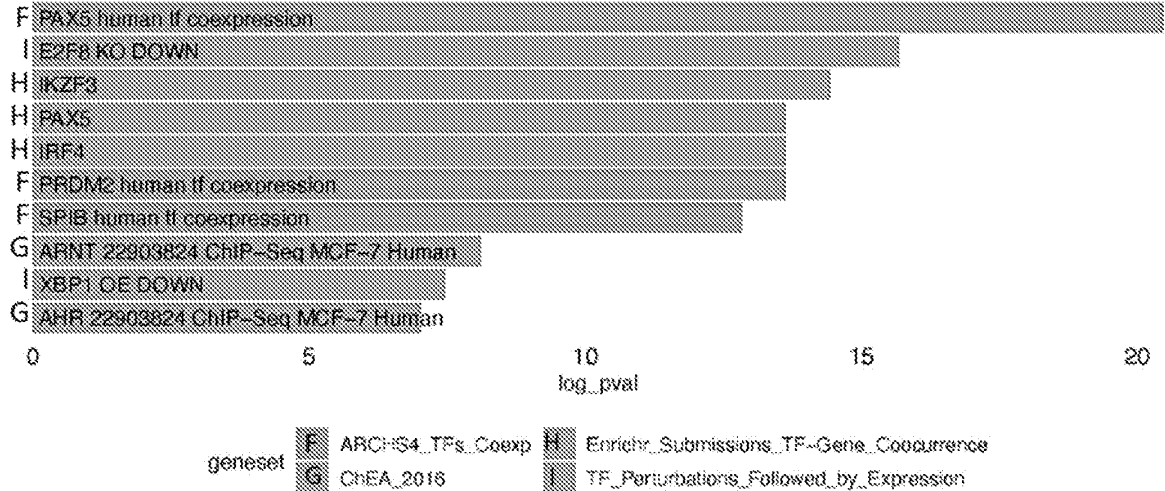


FIG. 46B

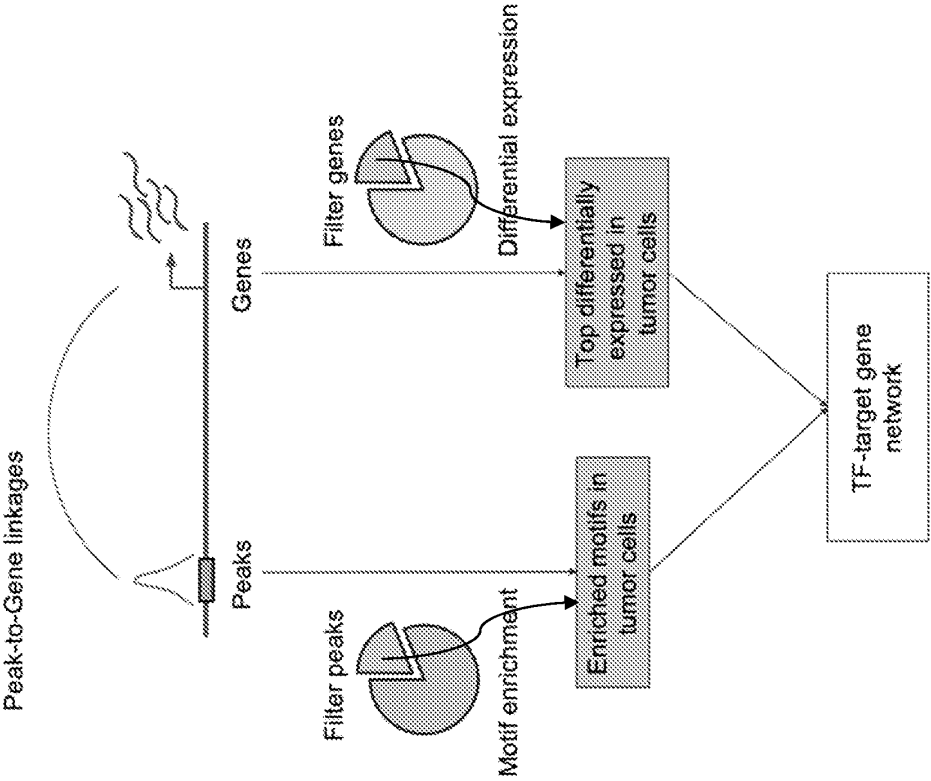


FIG. 47

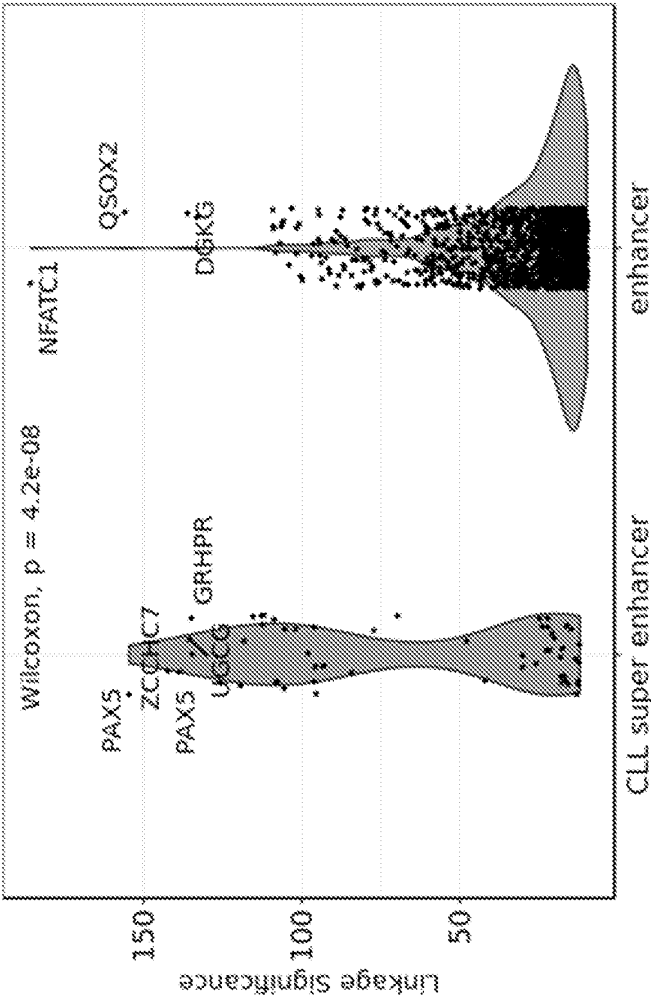
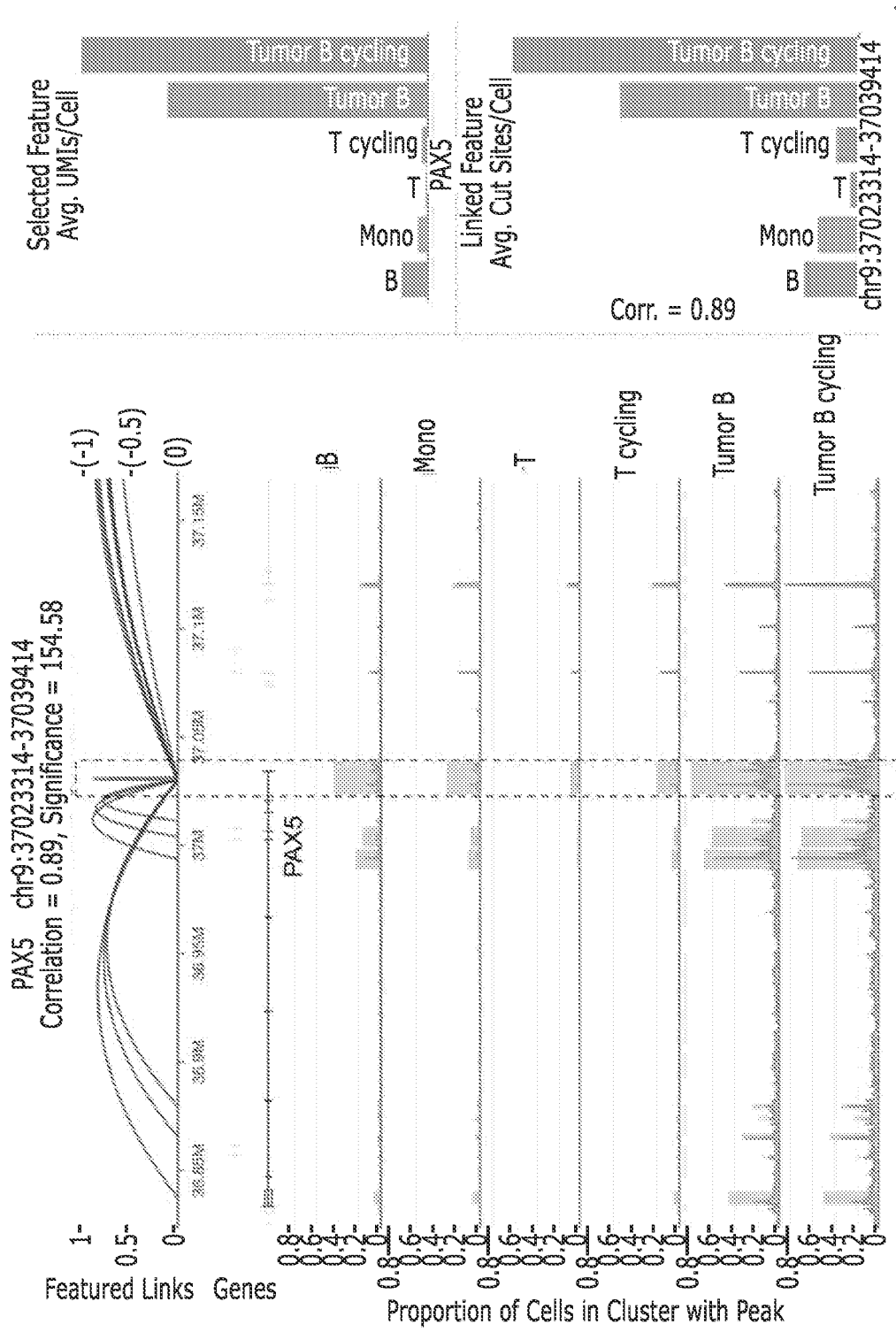


FIG. 48A



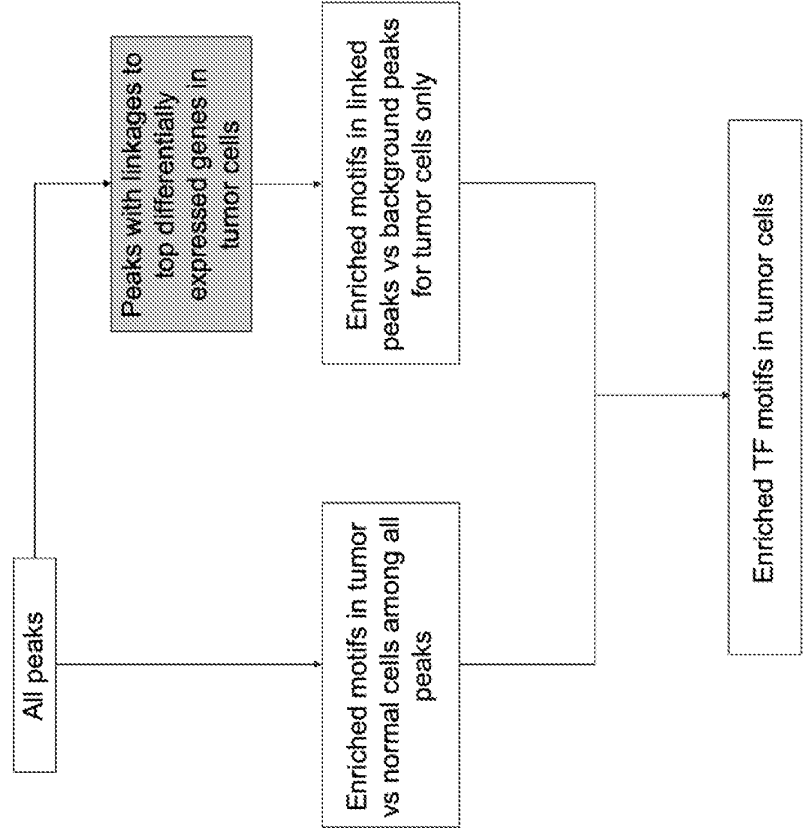


FIG. 49A

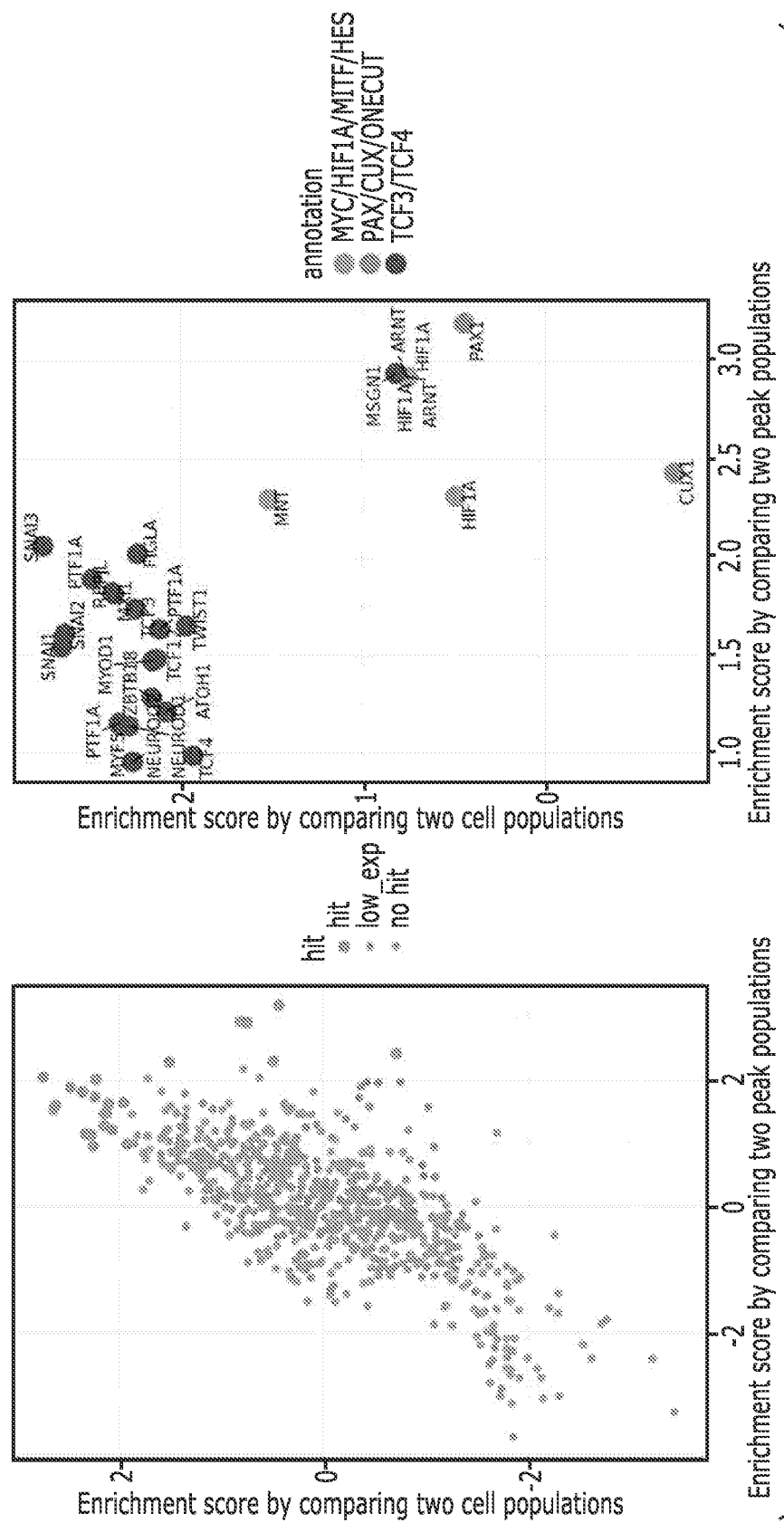


FIG. 49B

