

FIG. 1

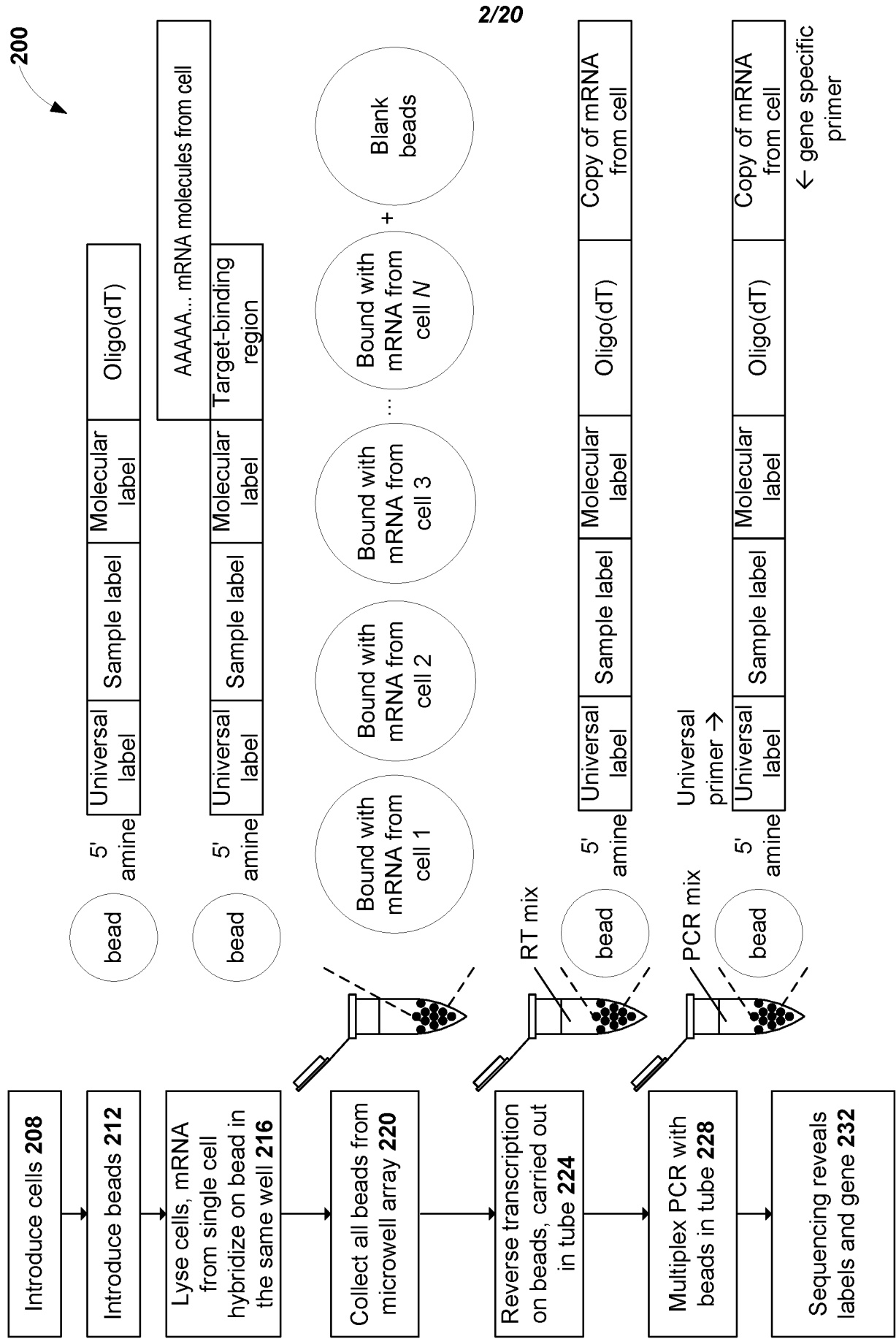
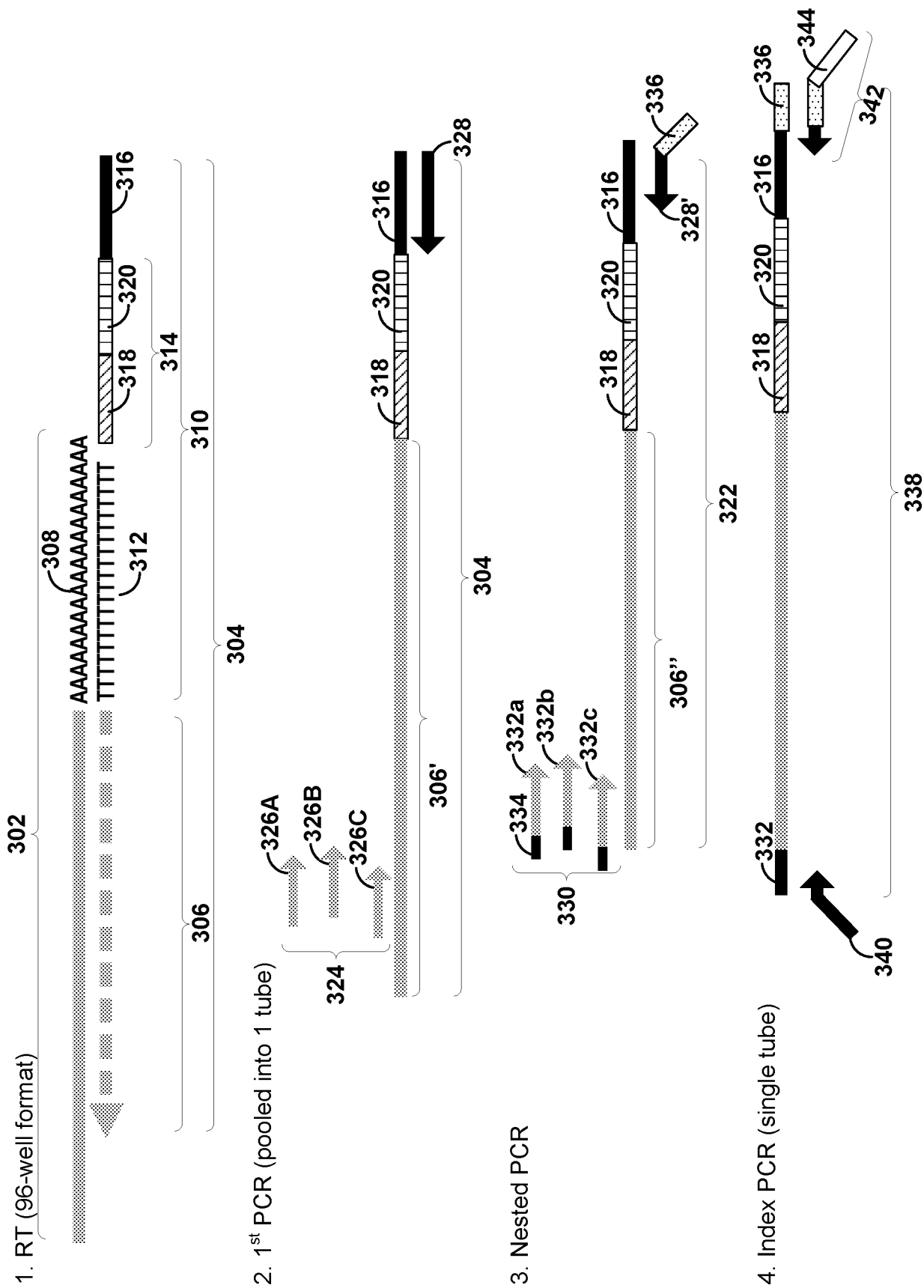
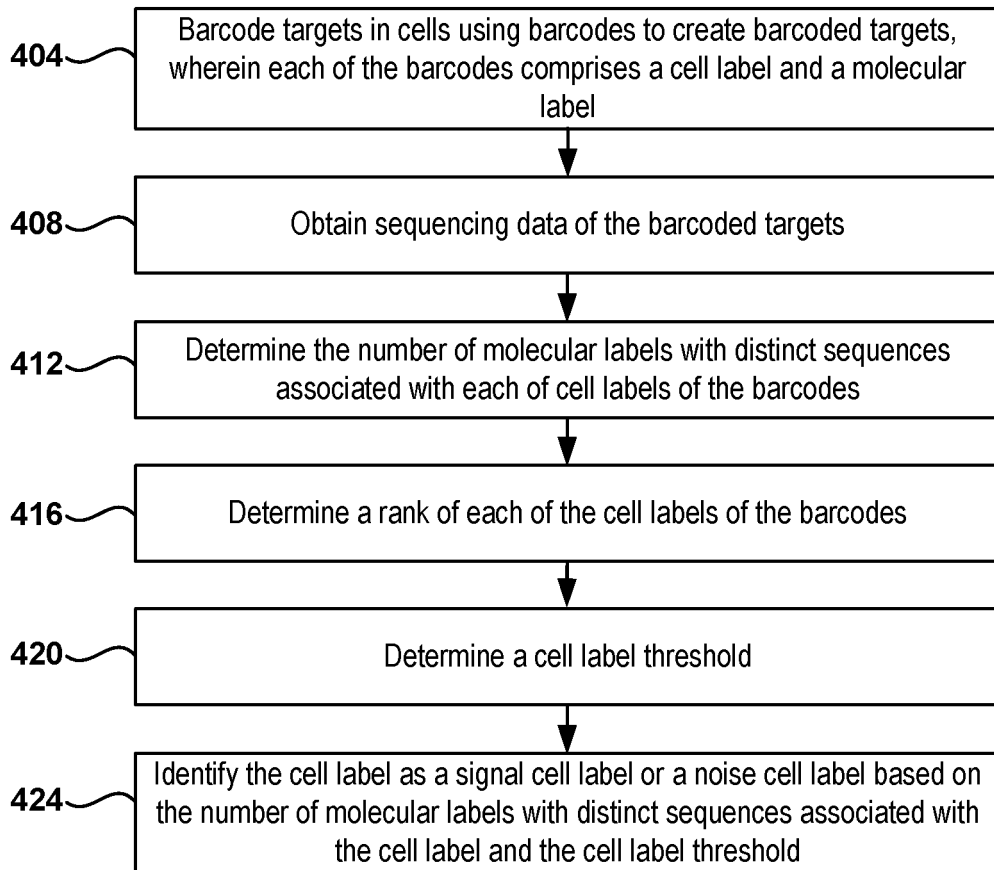


FIG. 2



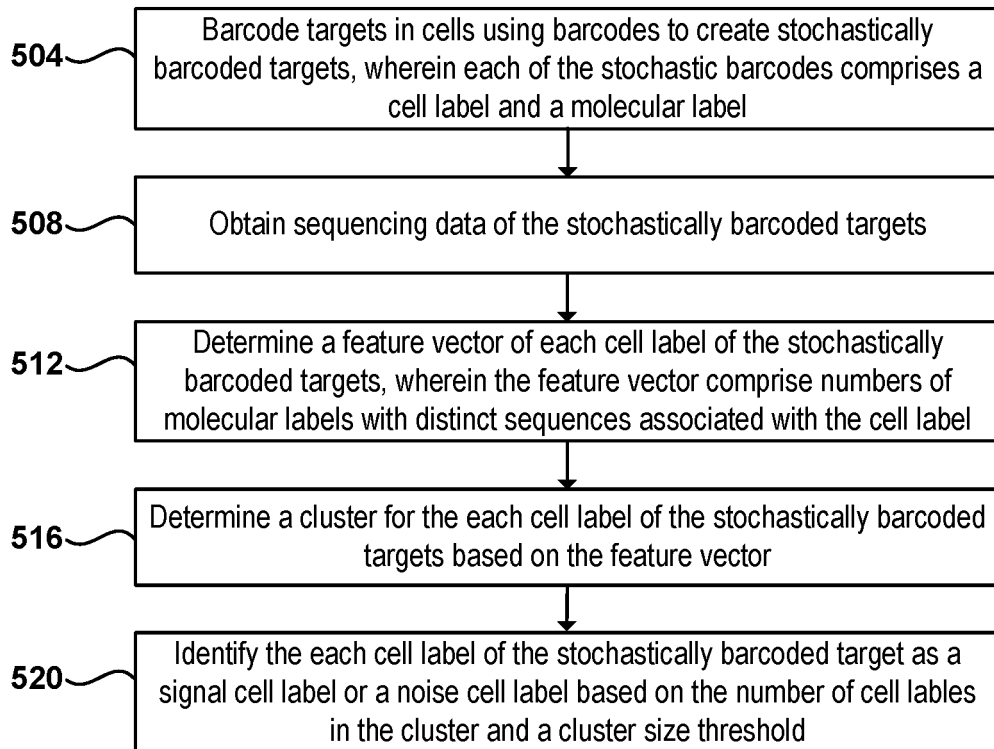
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400

**FIG. 4**

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500

**FIG. 5**

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600a

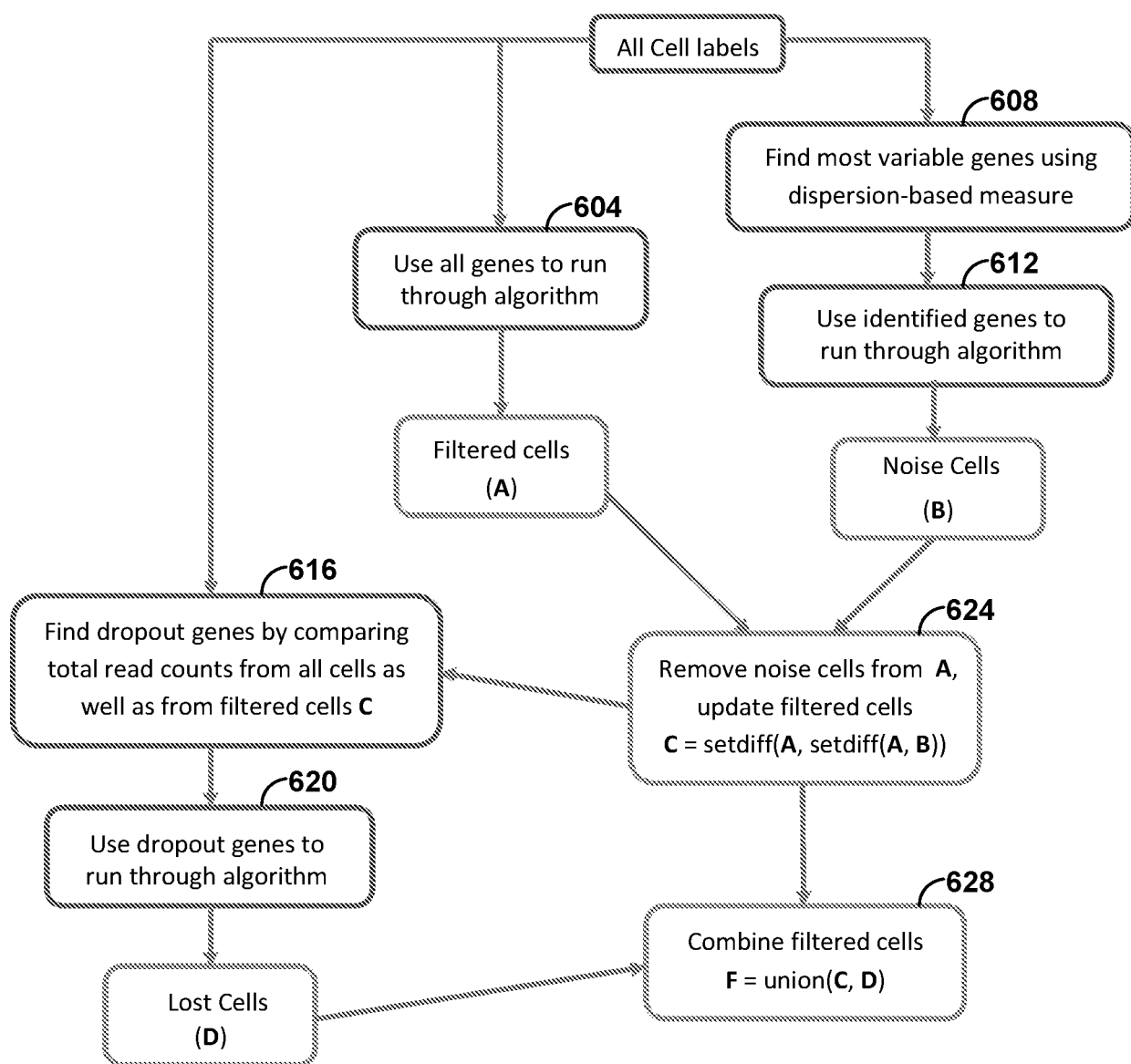
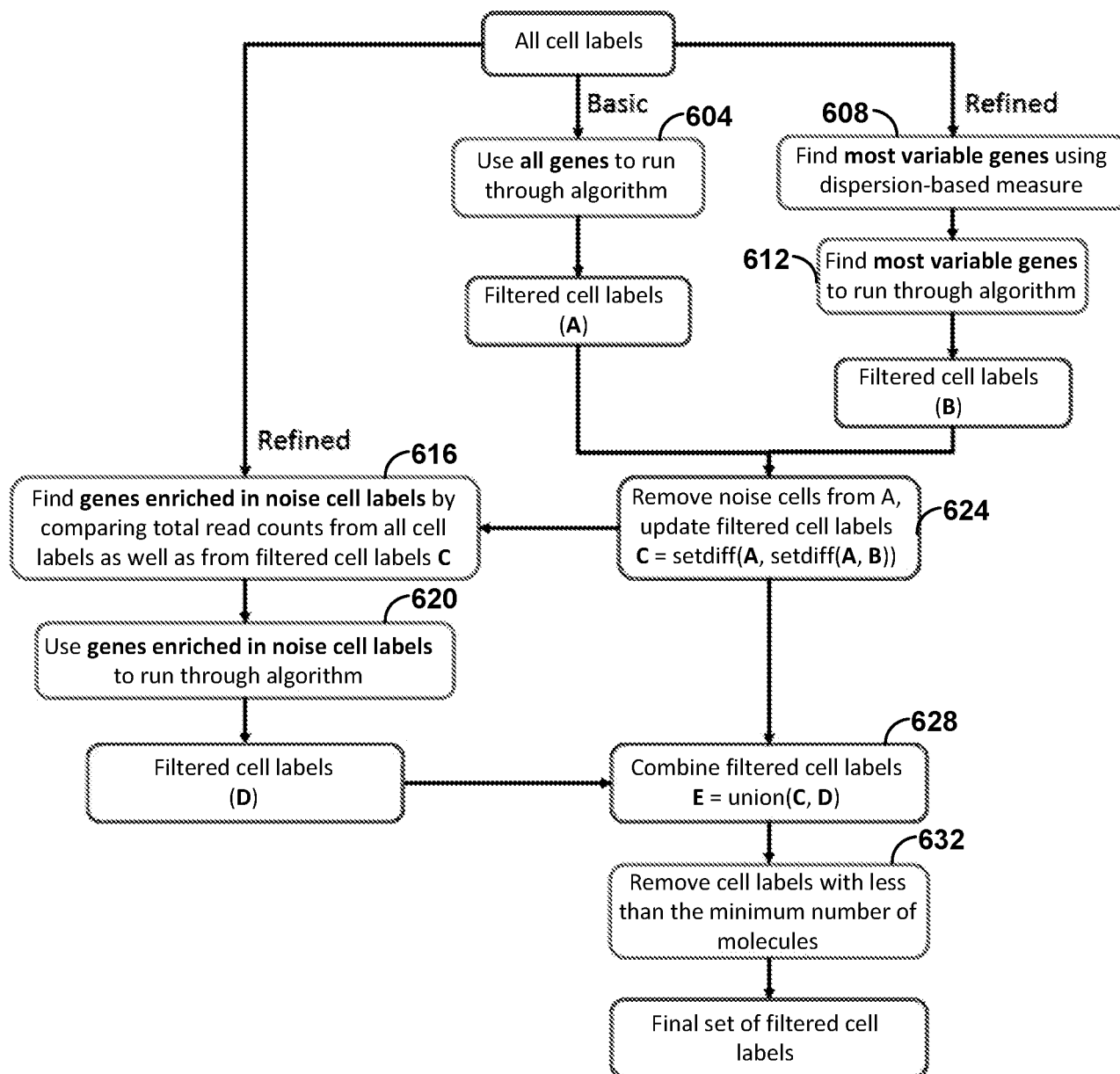
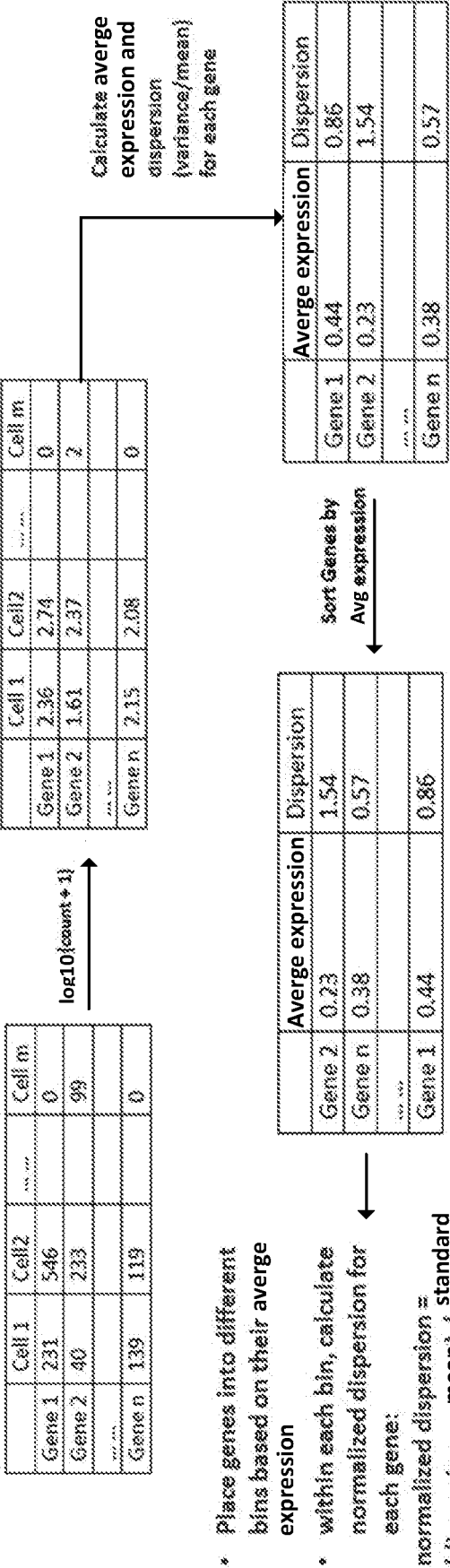


FIG. 6A

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**FIG. 6B**



- * Place genes into different bins based on their average expression
- * within each bin, calculate normalized dispersion for each gene:
$$\text{normalized dispersion} = \frac{\text{dispersion} - \text{mean}}{\text{standard deviation}}$$
- * Select most variable genes based on normalized dispersion

FIG. 7

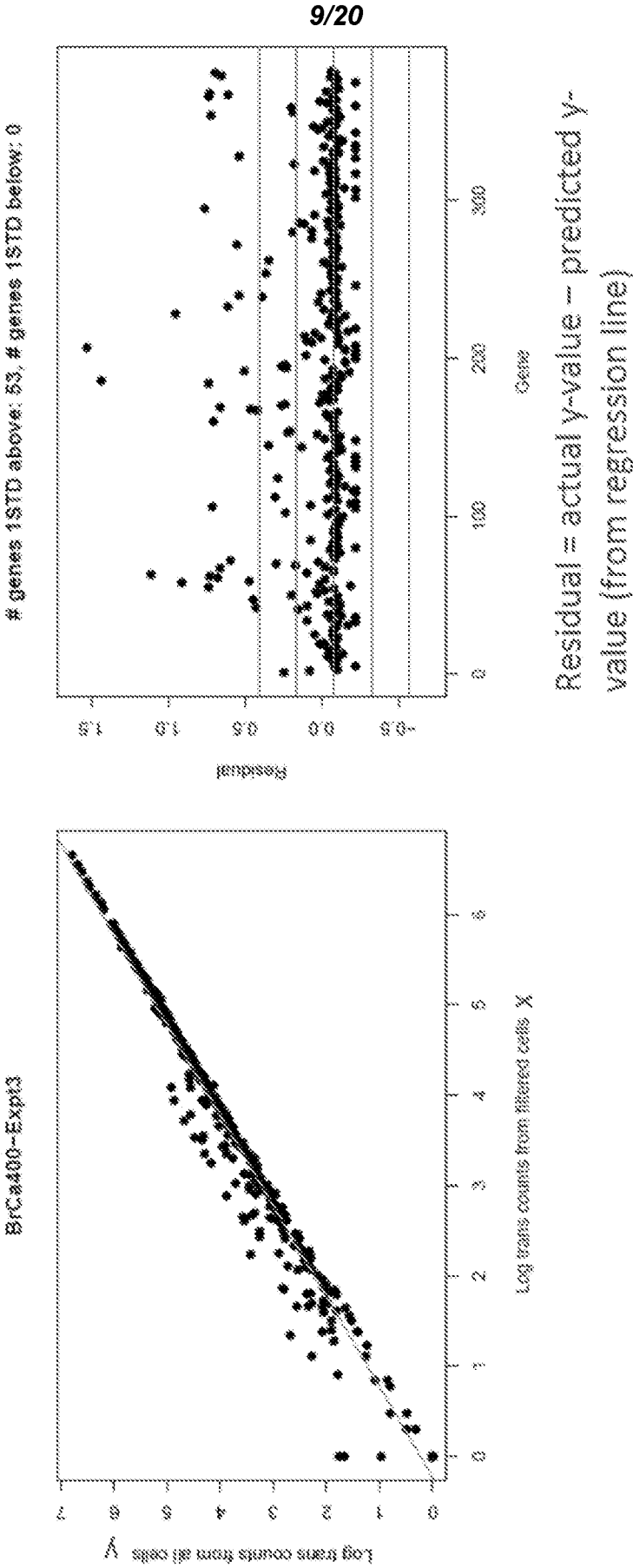


FIG. 8A

FIG. 8B

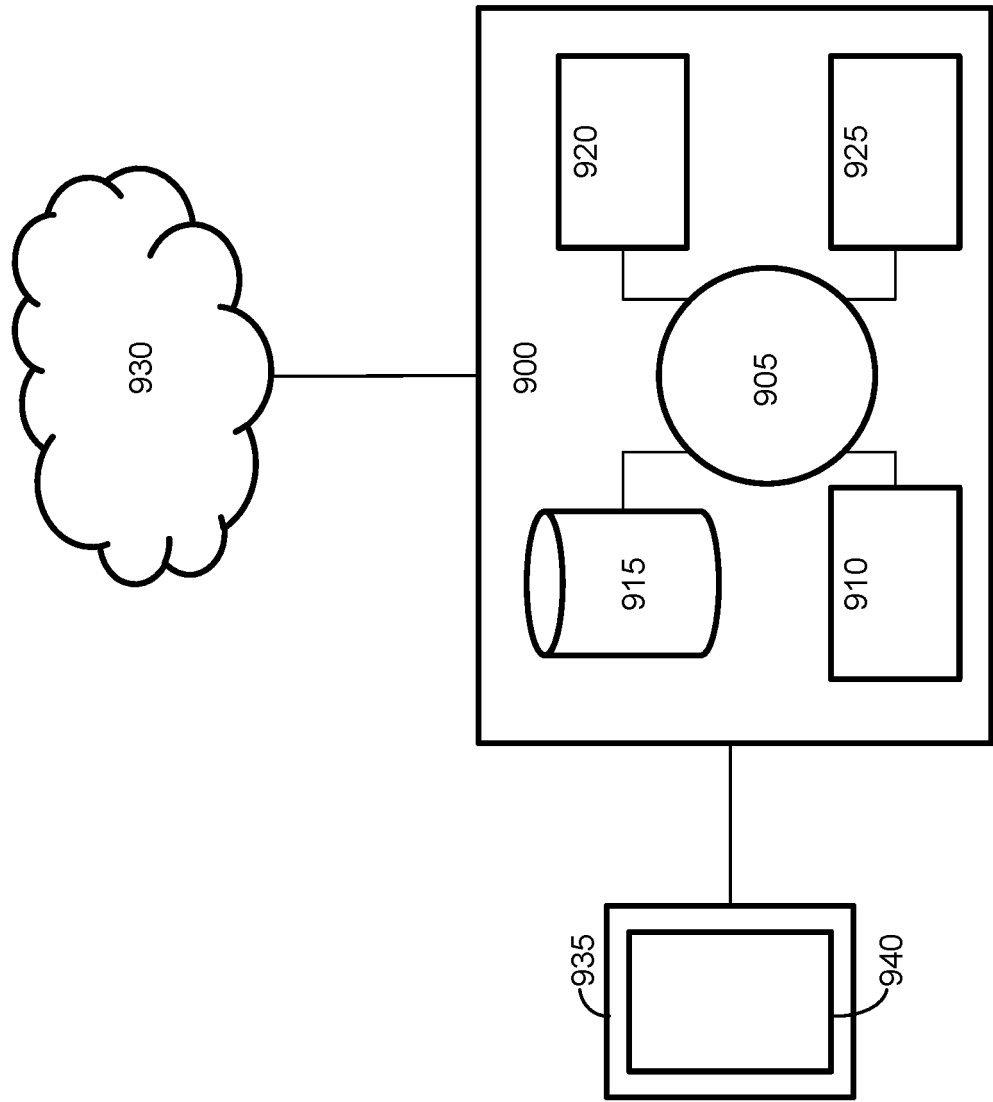


FIG. 9

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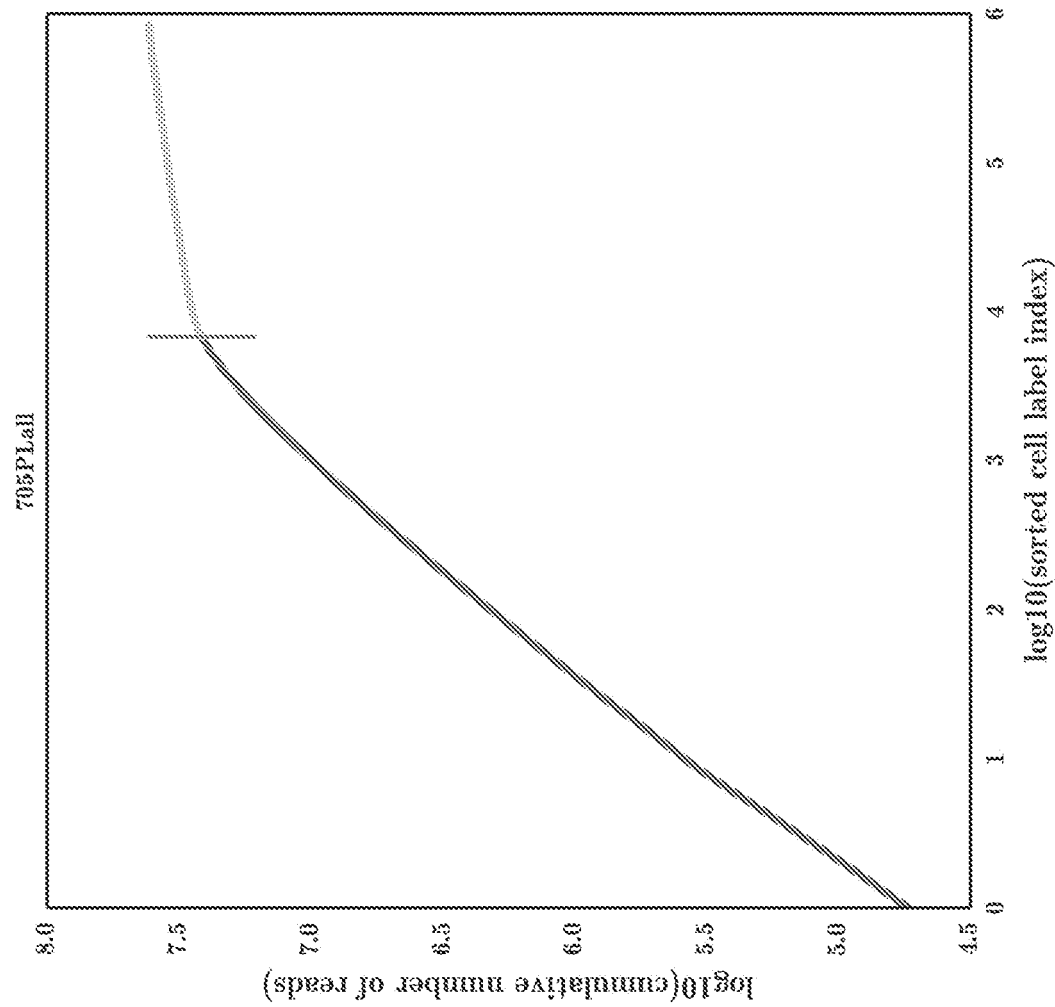


FIG. 10

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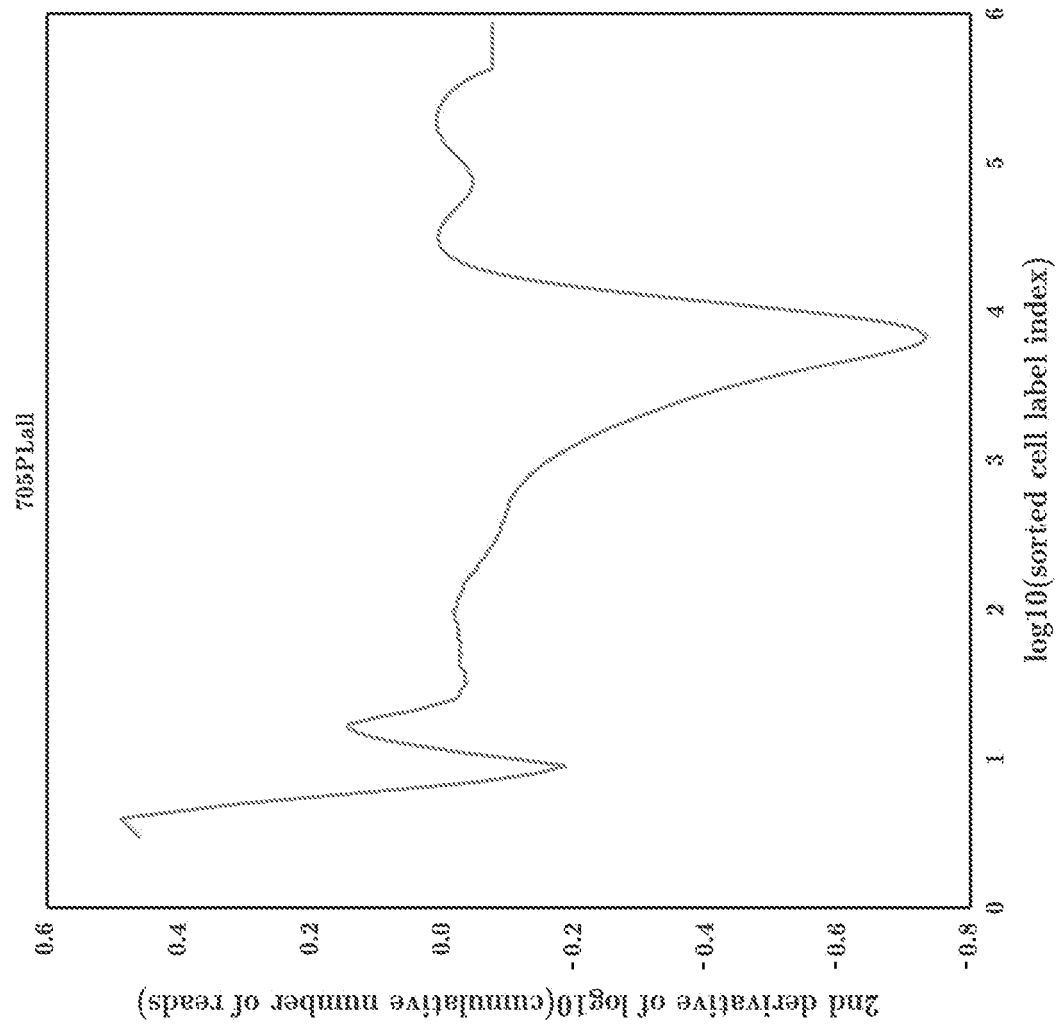


FIG. 11

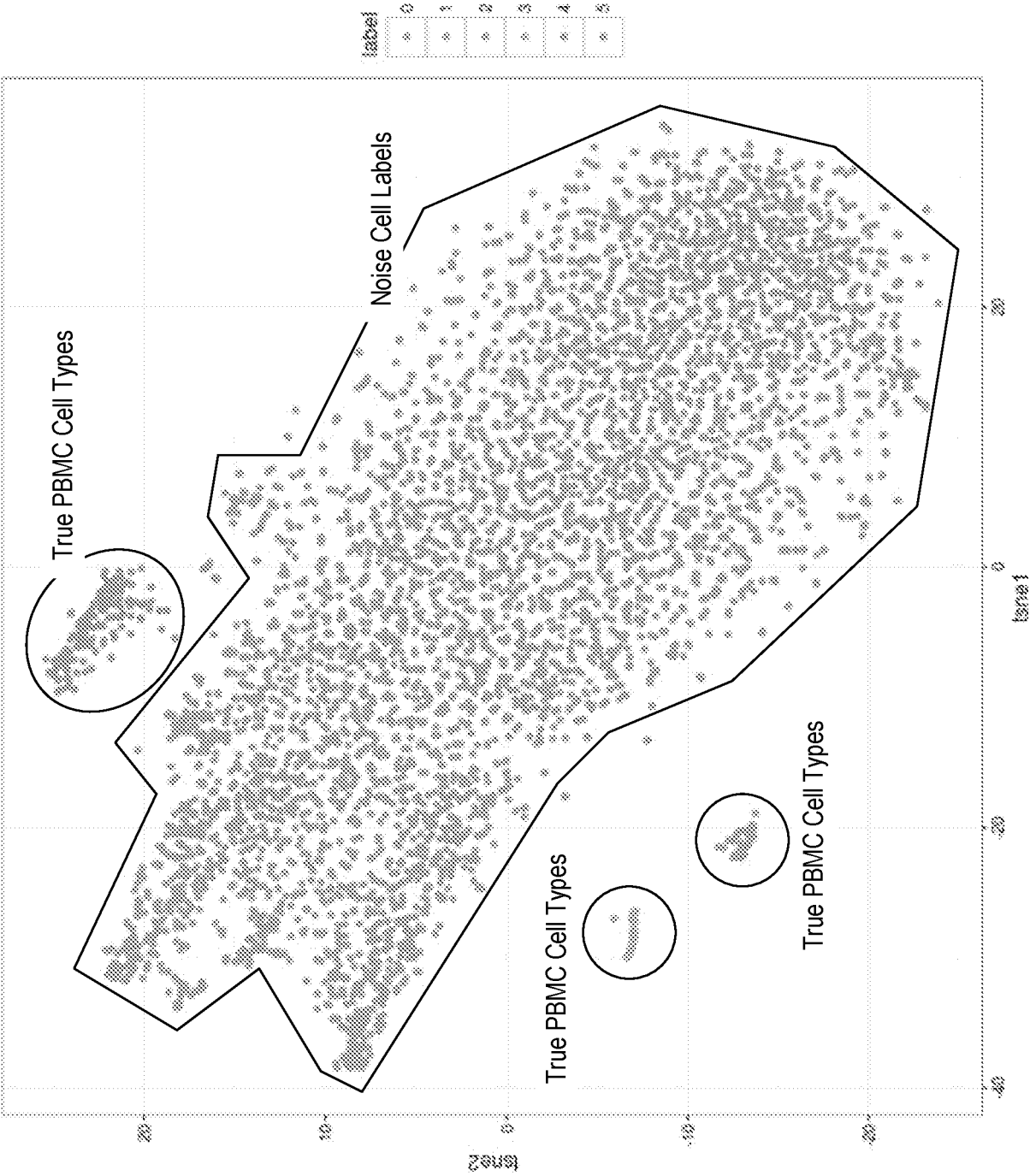


FIG. 12

One exemplary method (8017 cells identified)

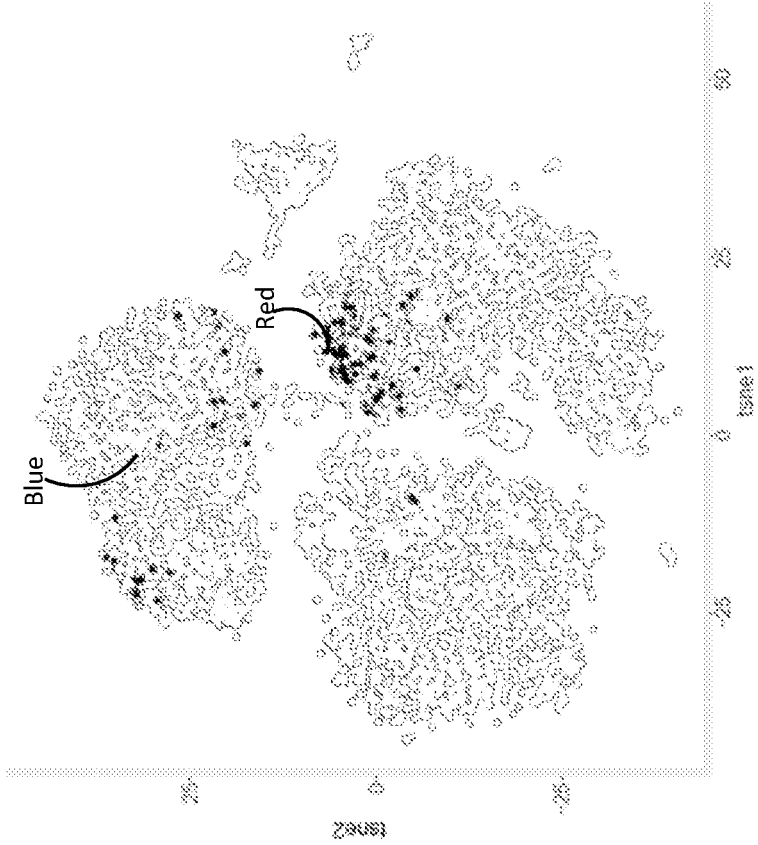
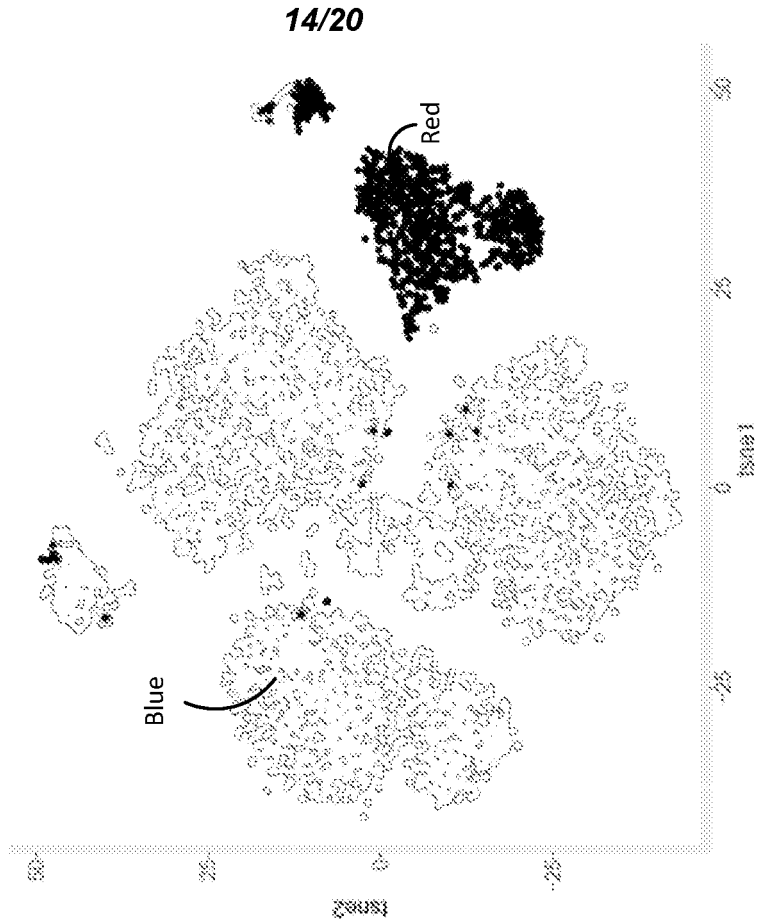


FIG. 13A

Another exemplary method (9094 cells identified)



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FIG. 13B

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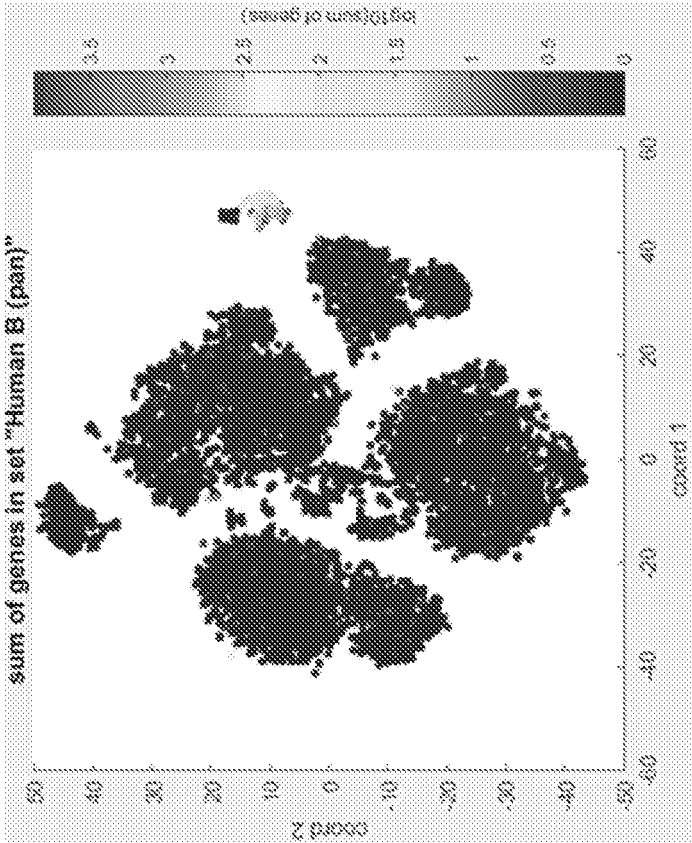


FIG. 14B

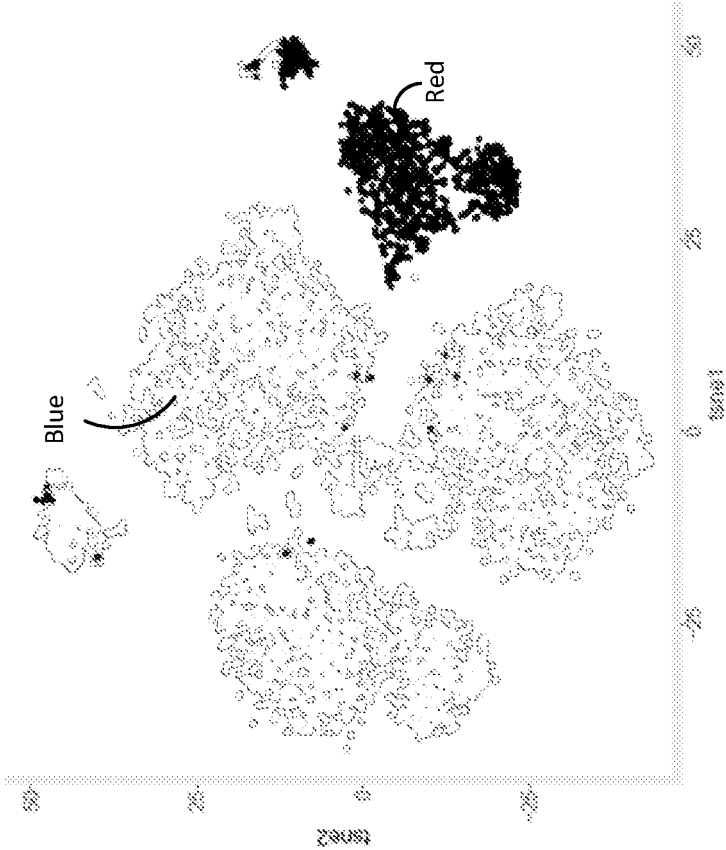


FIG. 14A

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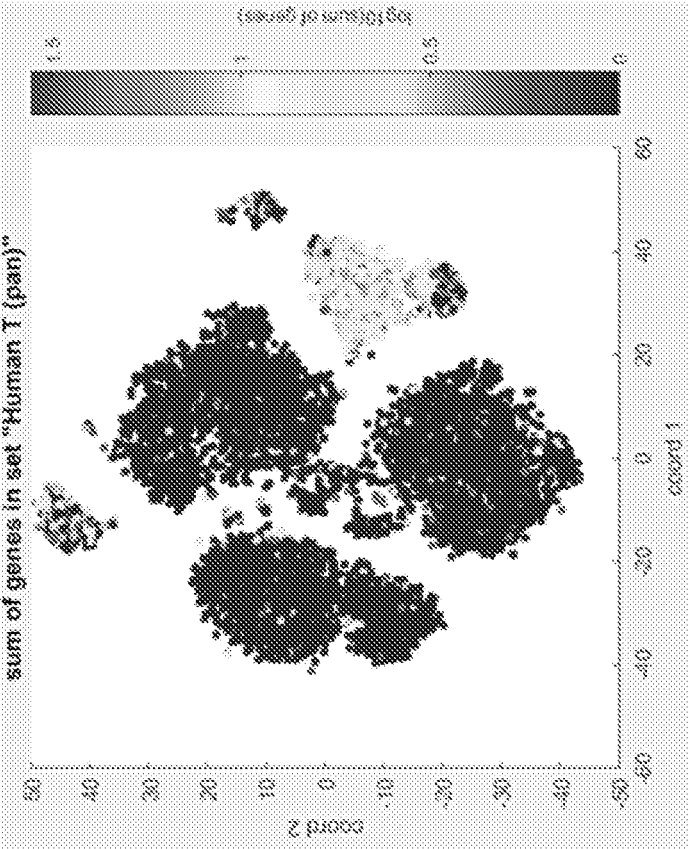


FIG. 14 D

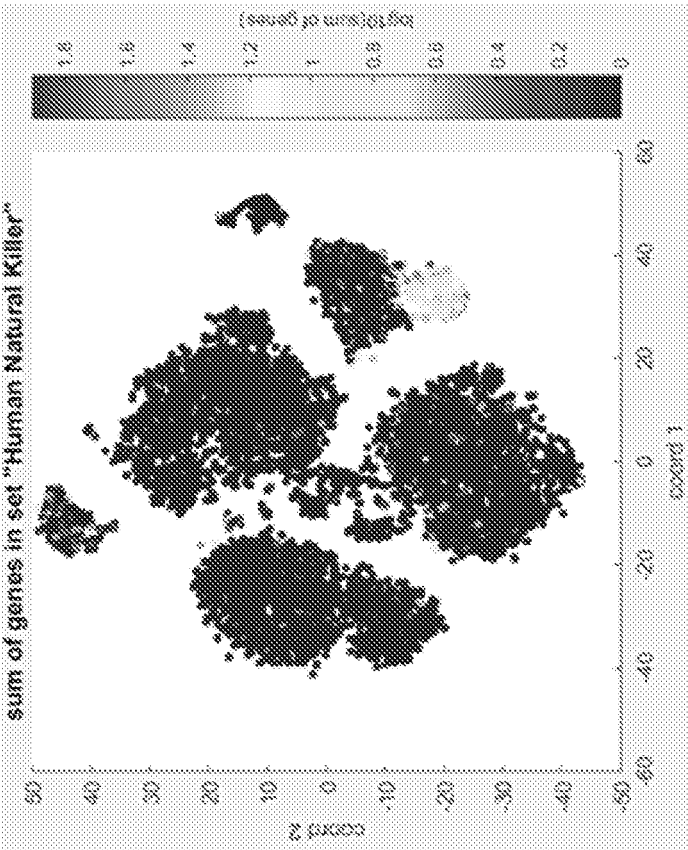
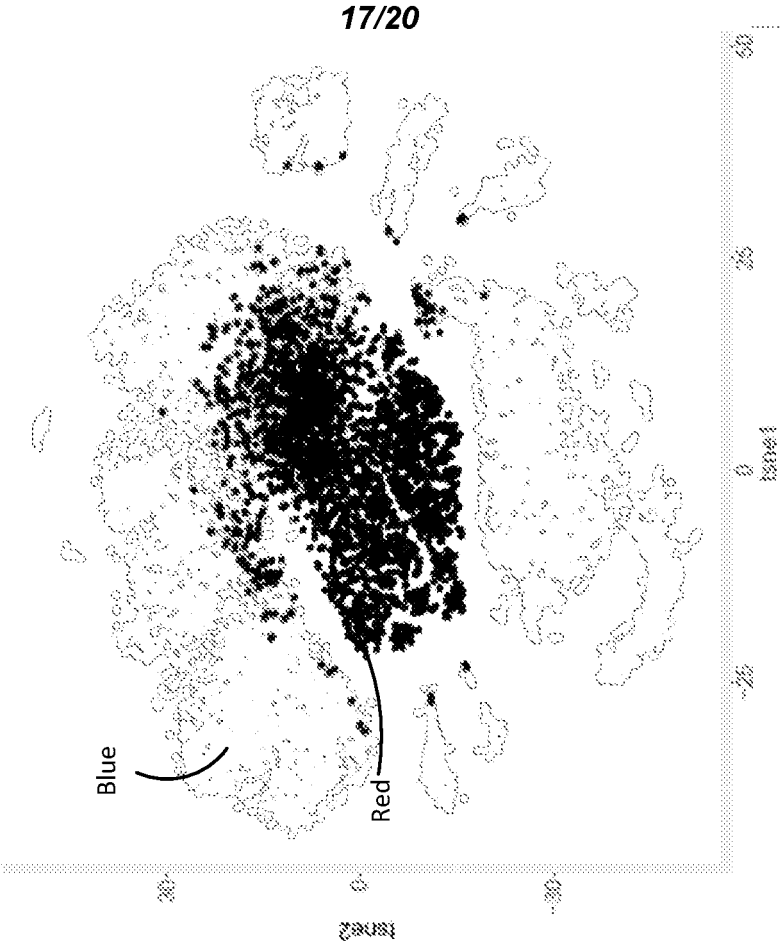


FIG. 14 C

Another exemplary method (16459 cells identified)



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One exemplary method (13950 cells identified)

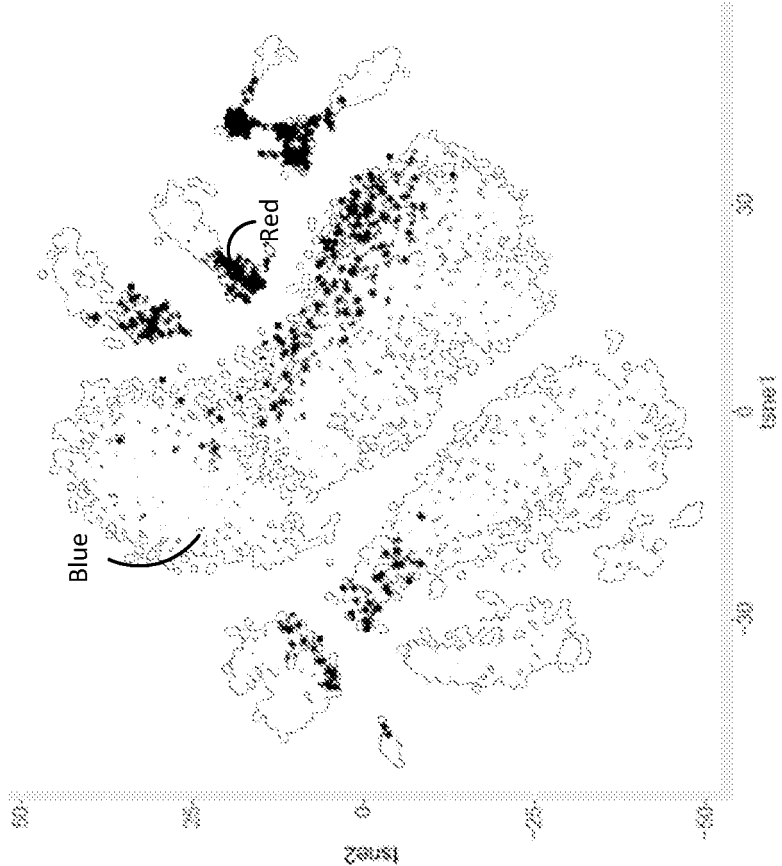


FIG. 15B

FIG. 15A

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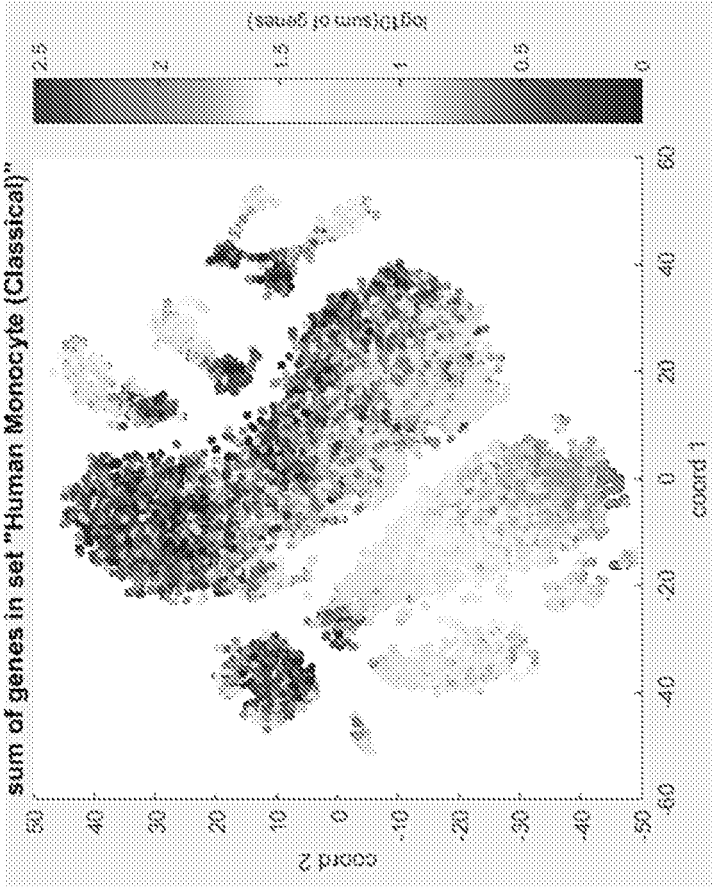


FIG. 16B

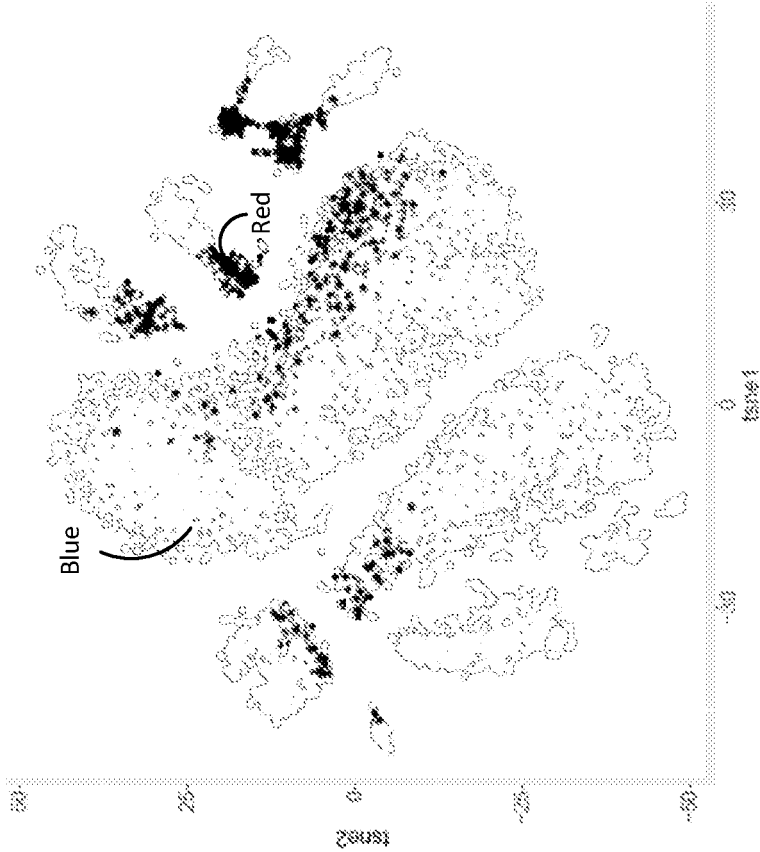


FIG. 16A

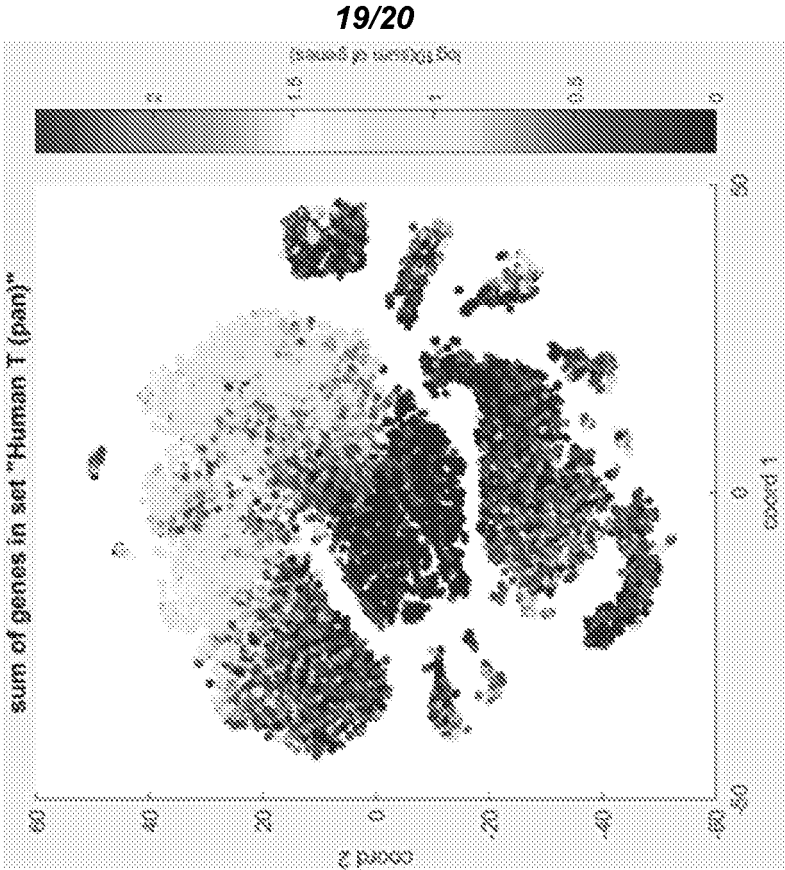


FIG. 17B

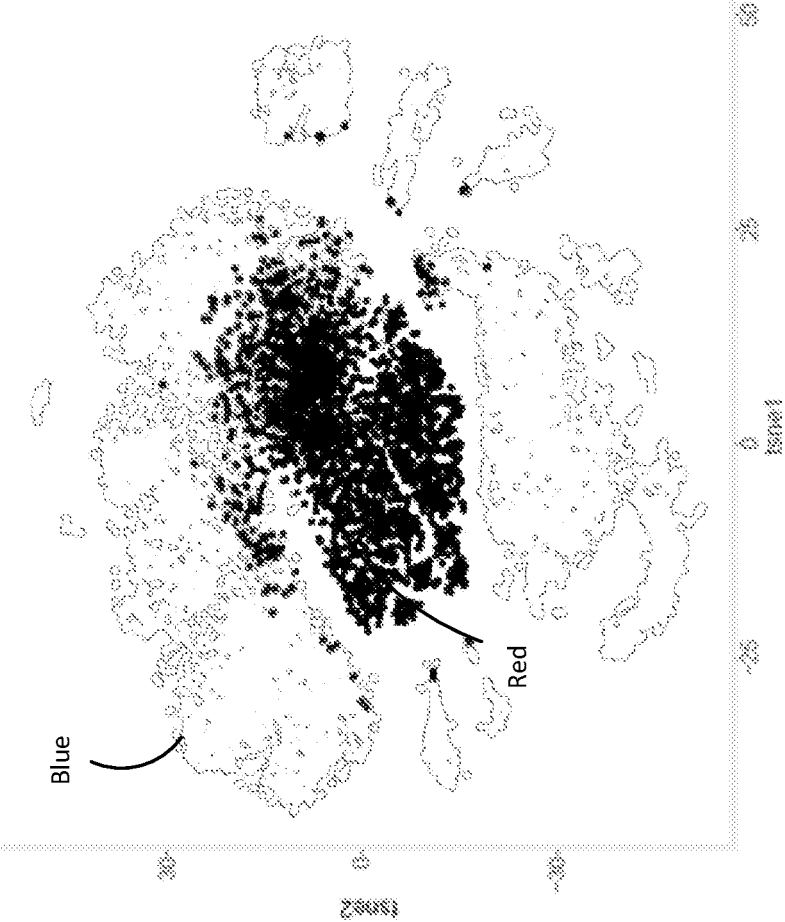


FIG. 17A

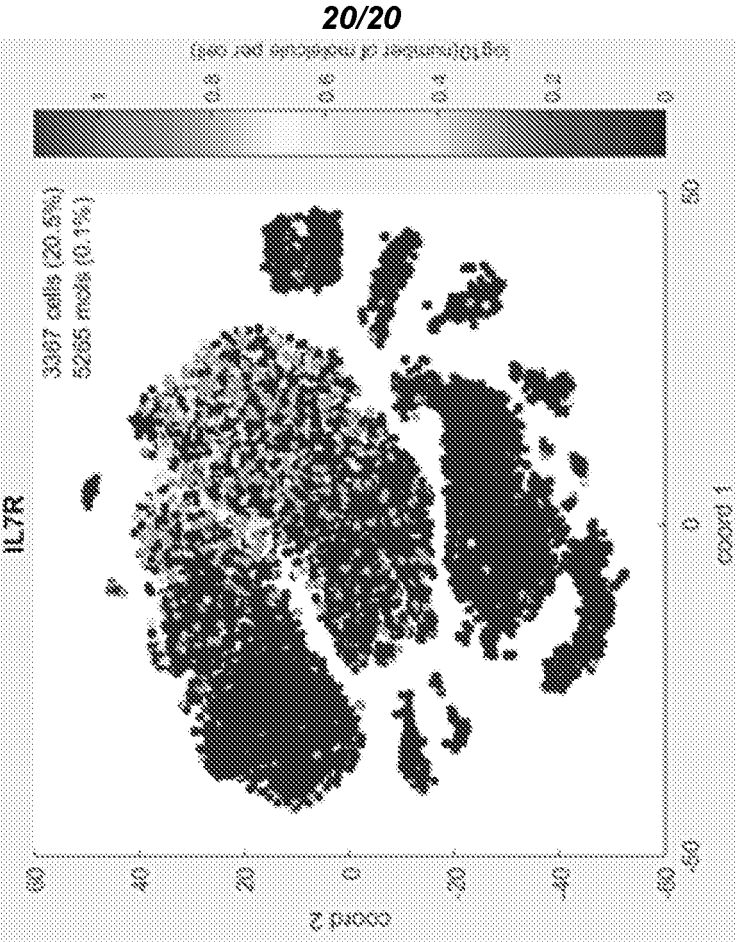


FIG. 17 D

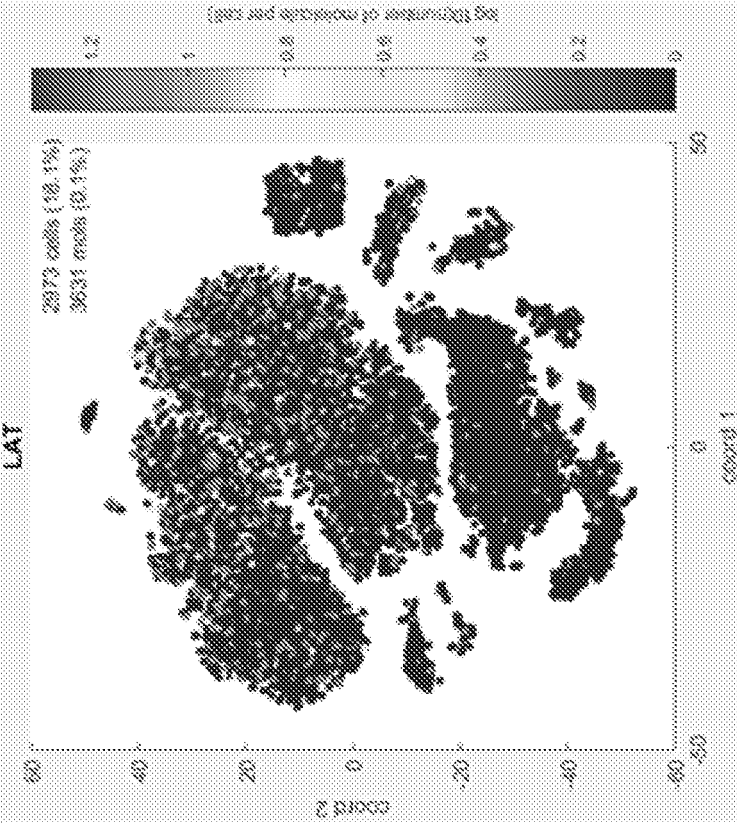


FIG. 17 C