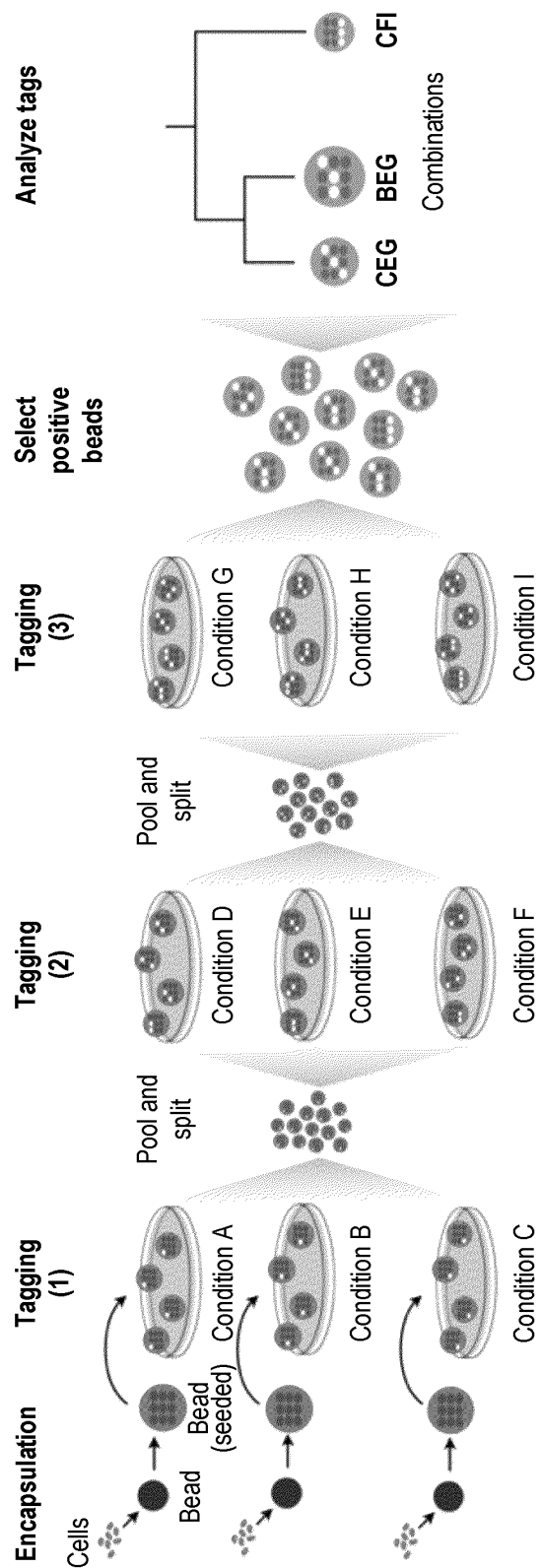




Schematic of the current CombiCult 2.0 approach.

FIG. 1

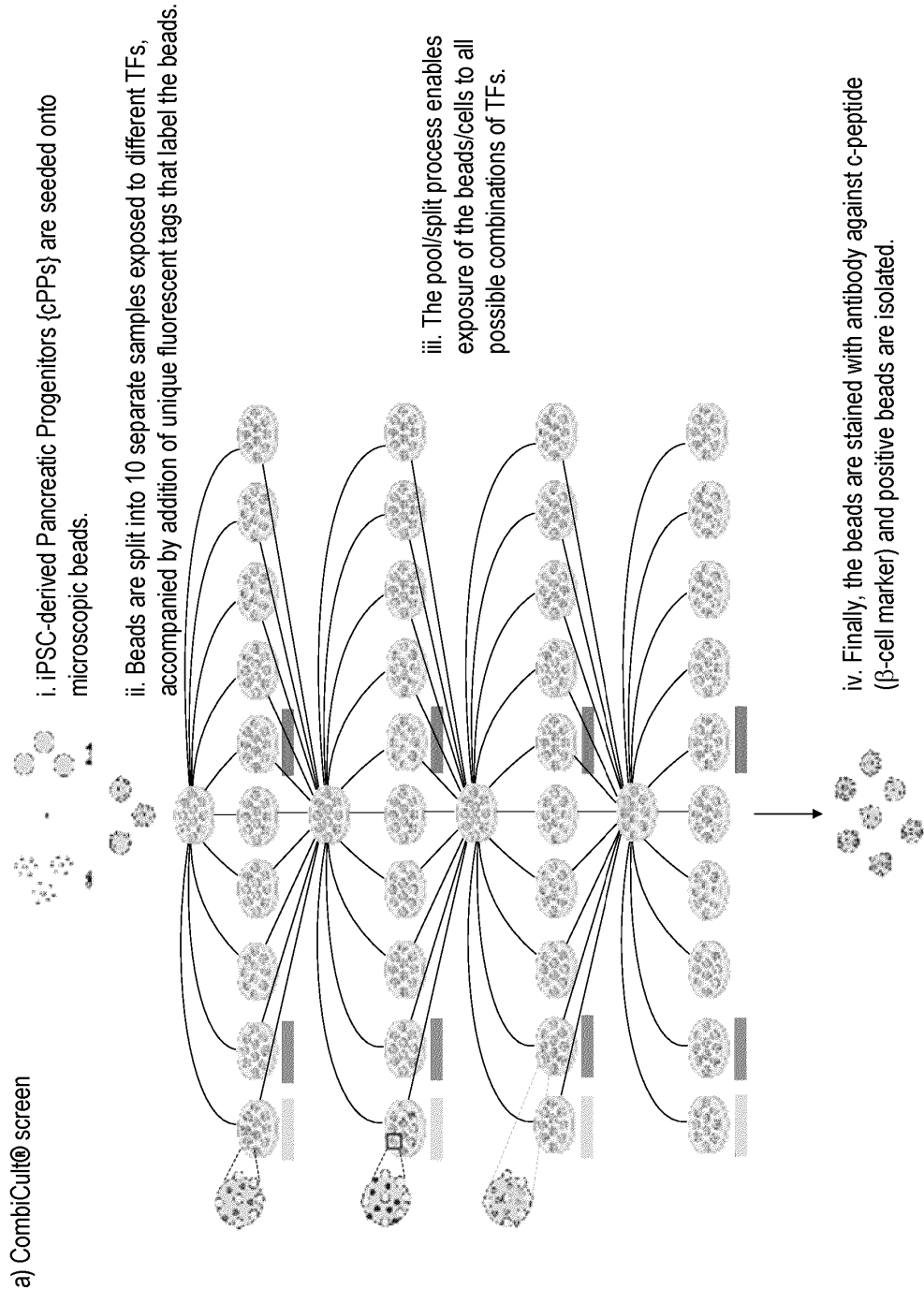


FIG. 2a

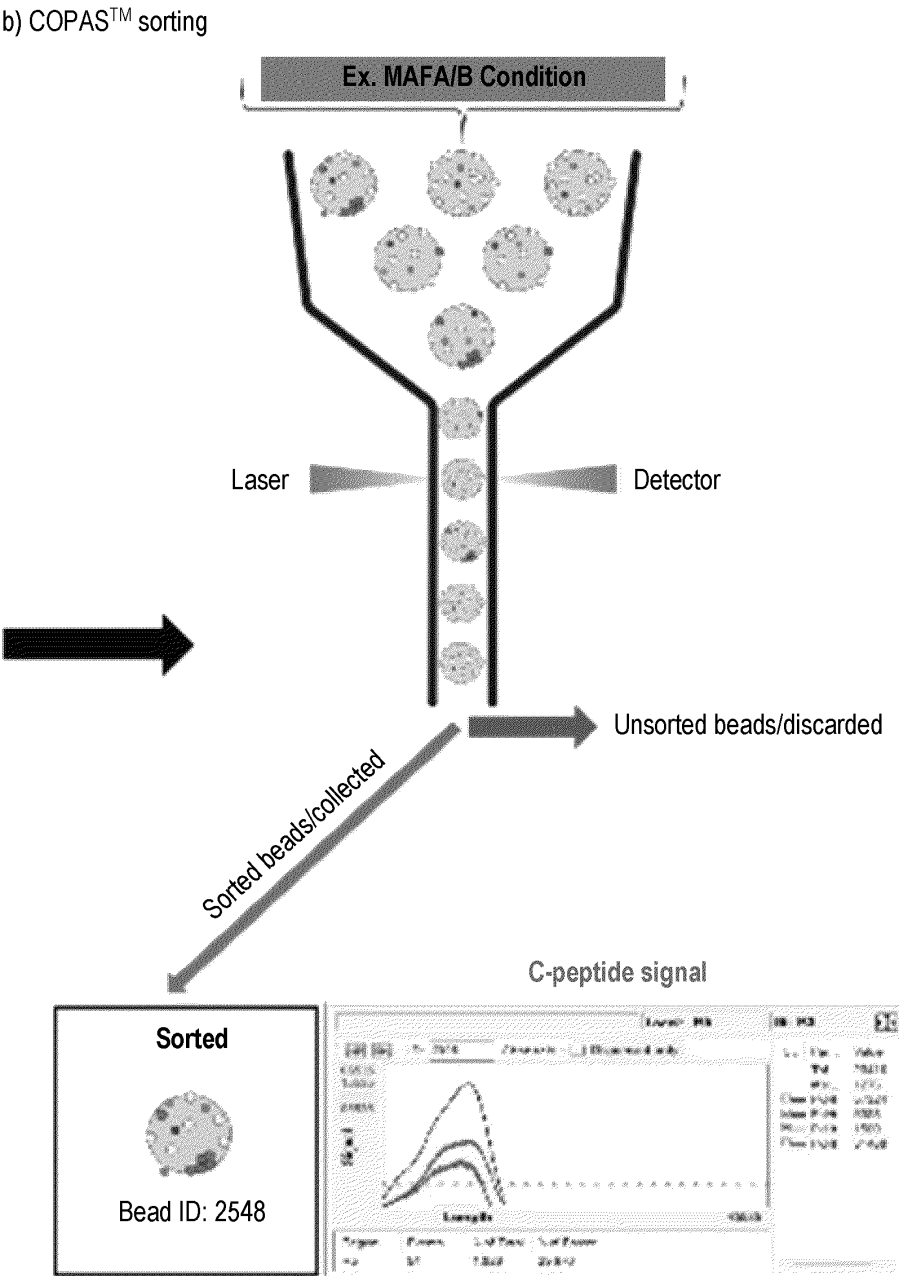


FIG. 2b

c) Isolation of tags

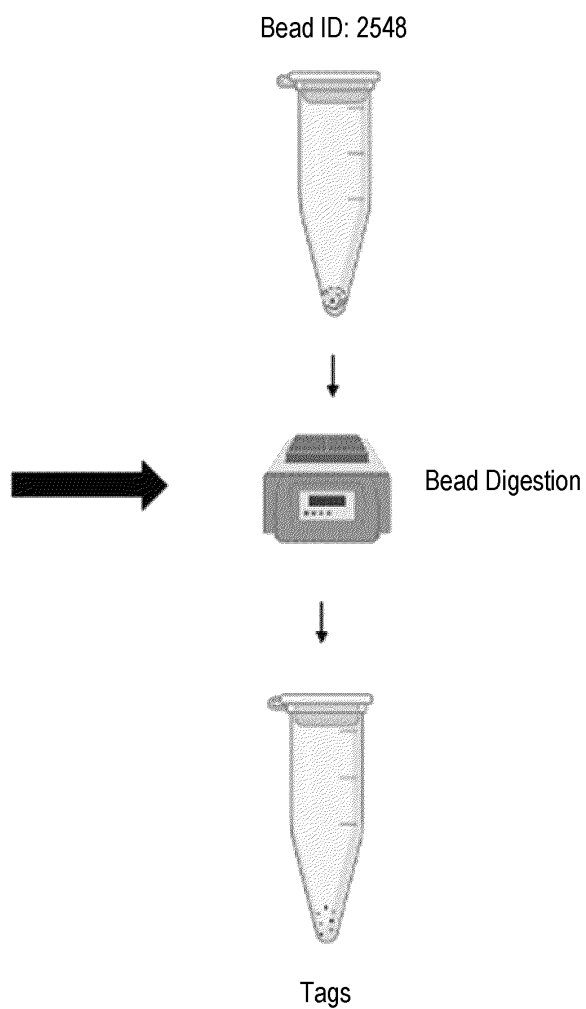
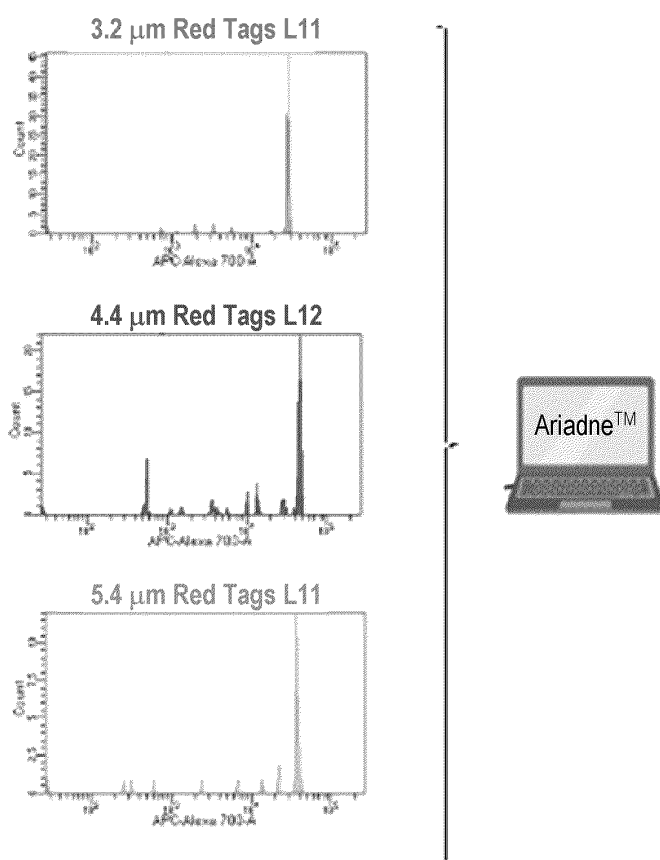


FIG. 2c

d) Tags analysis

*FIG. 2d*

e) Ariadne™ Bioinformatics

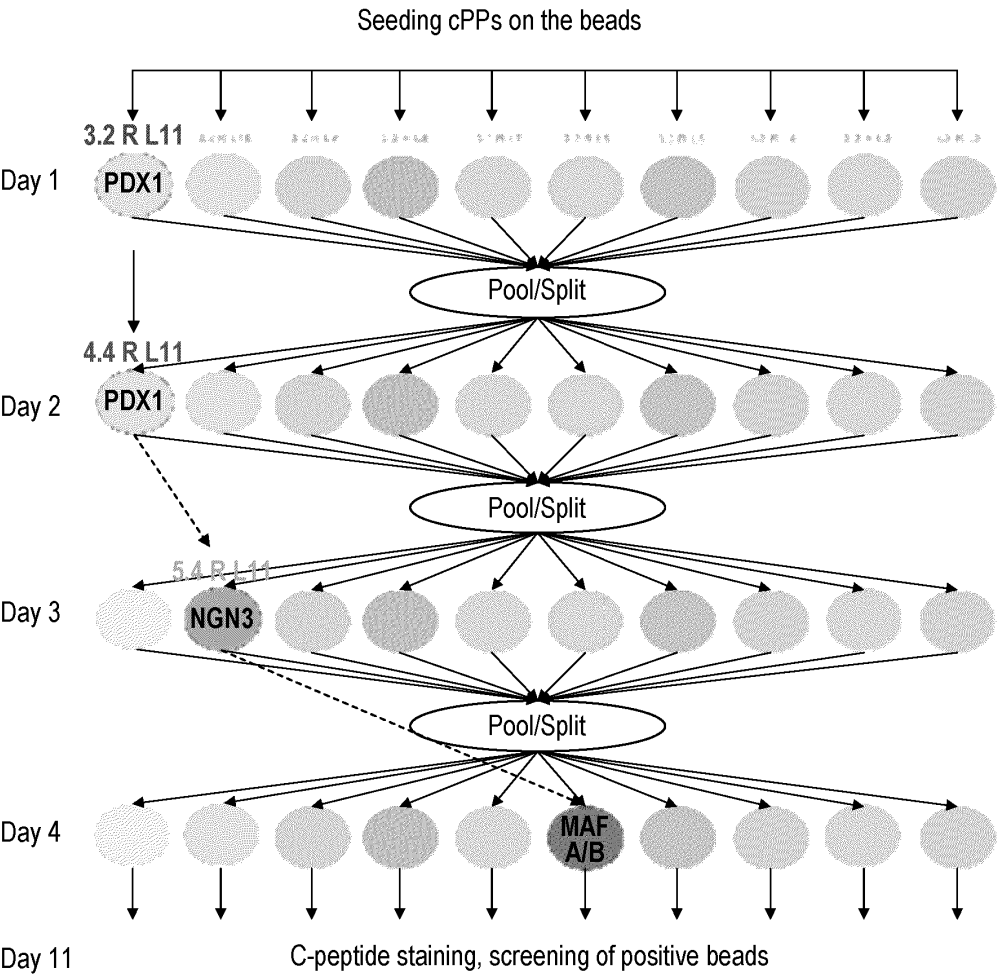
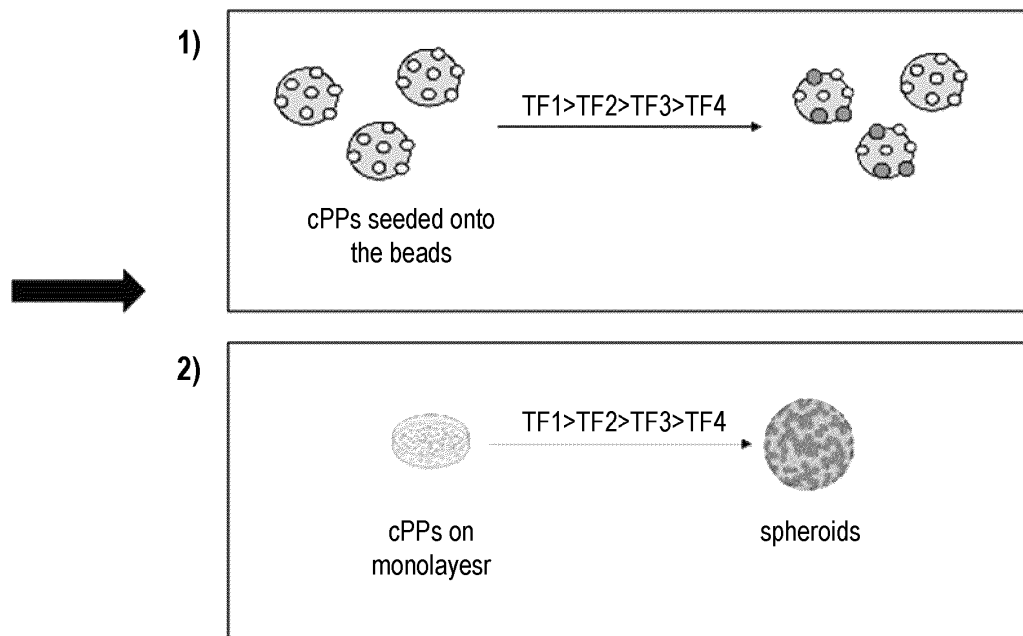
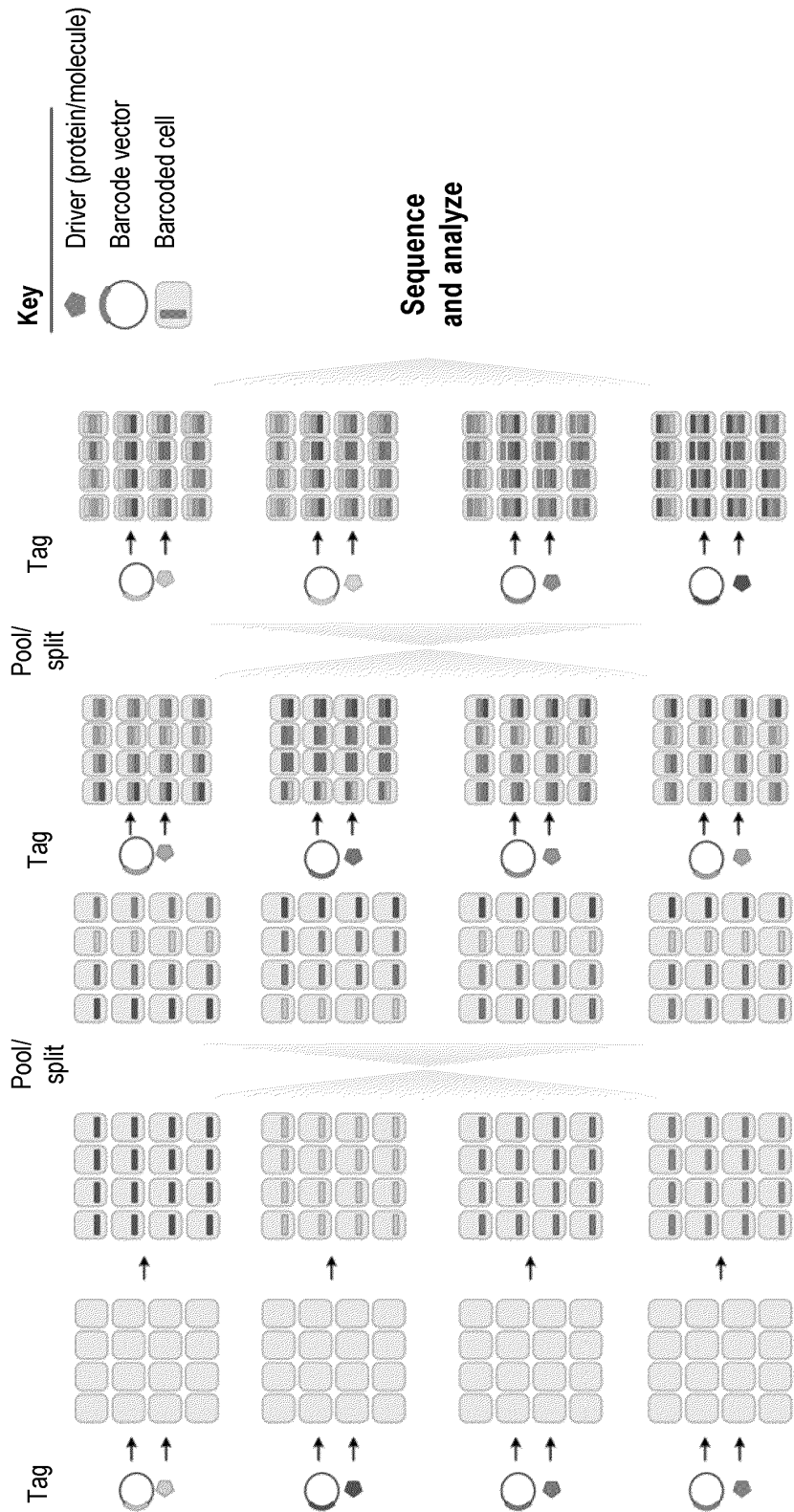


FIG. 2e

f) Validation

*FIG. 2f*



A schematic of the viral barcoding approach

FIG. 3

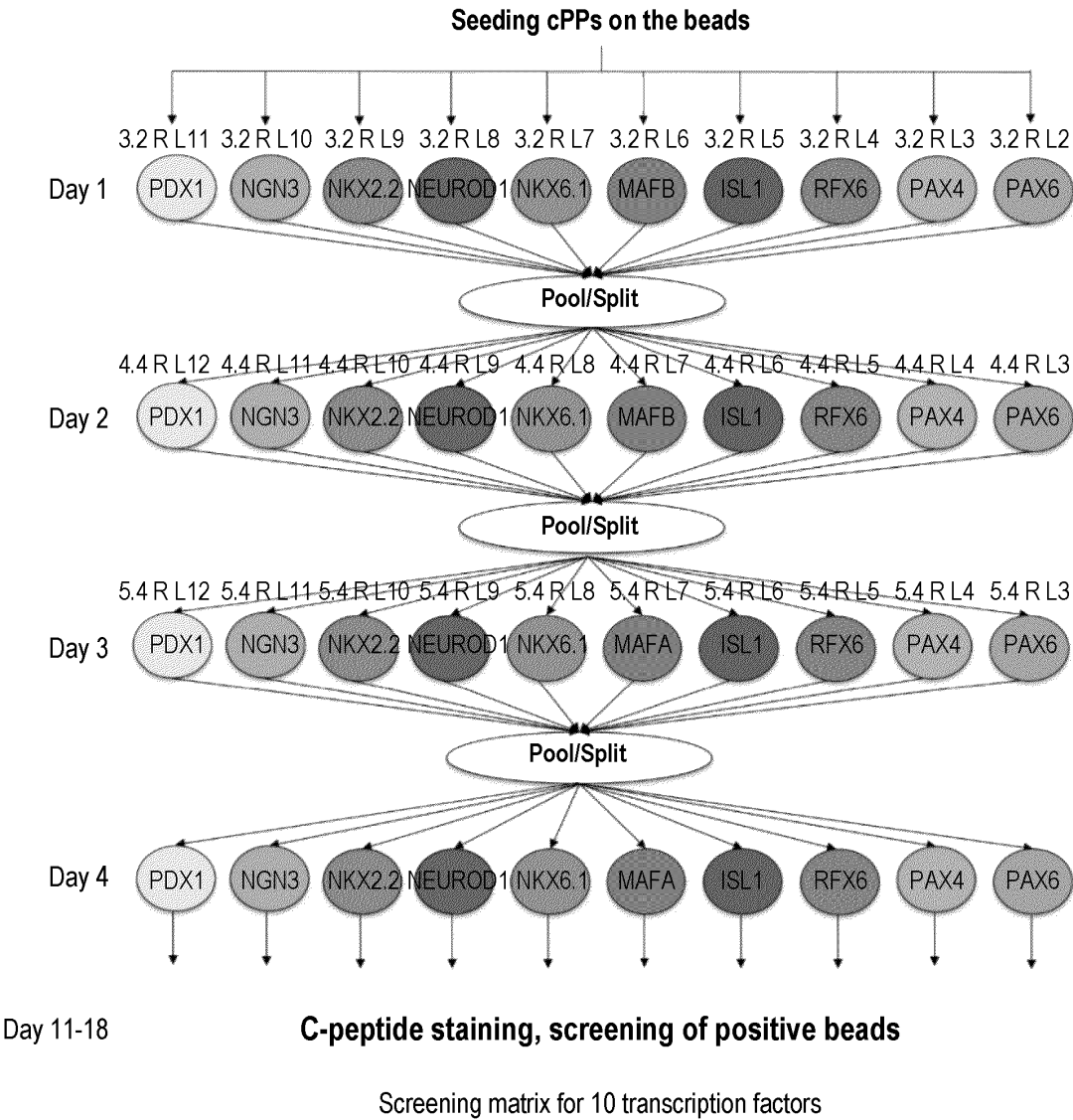
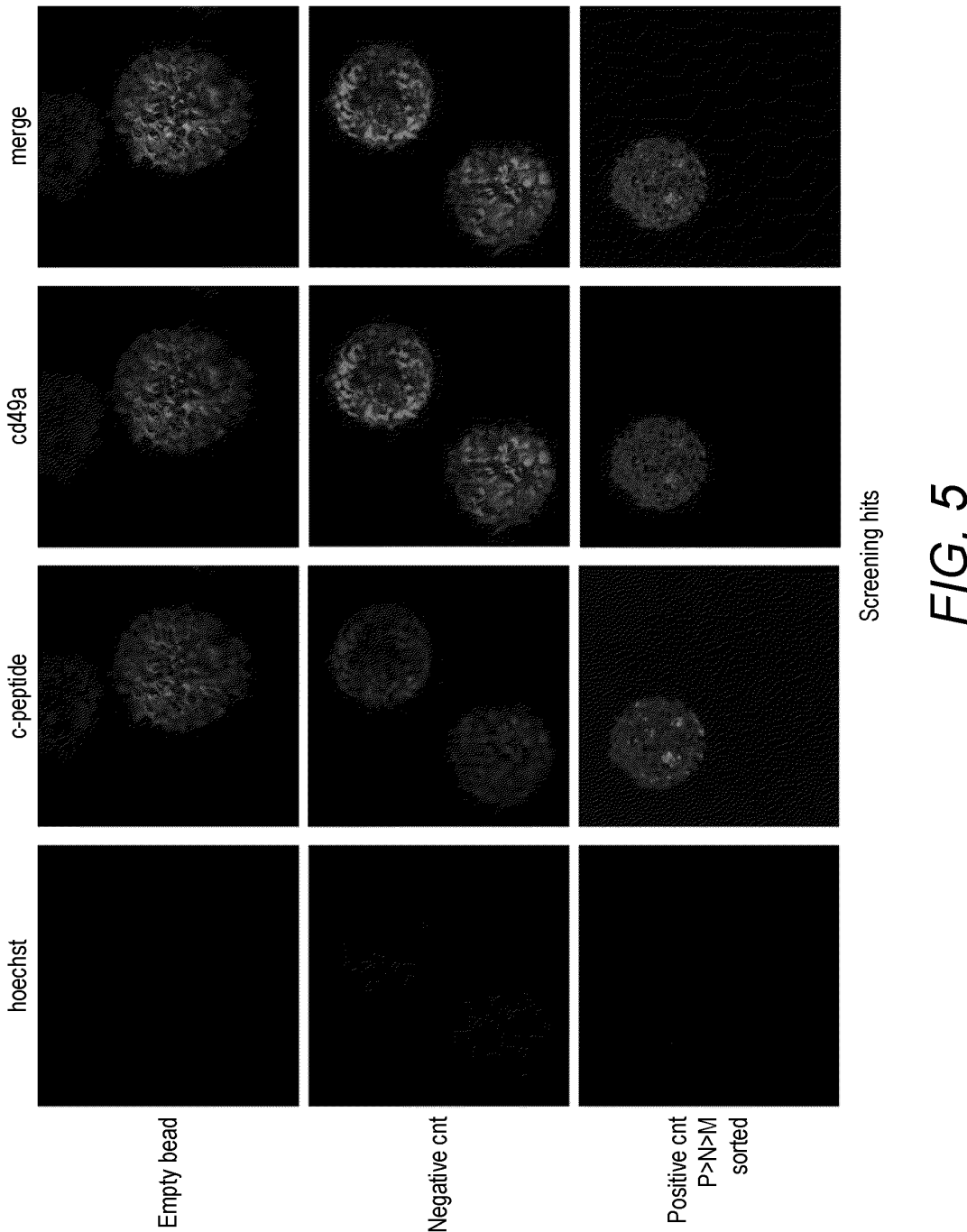


FIG. 4



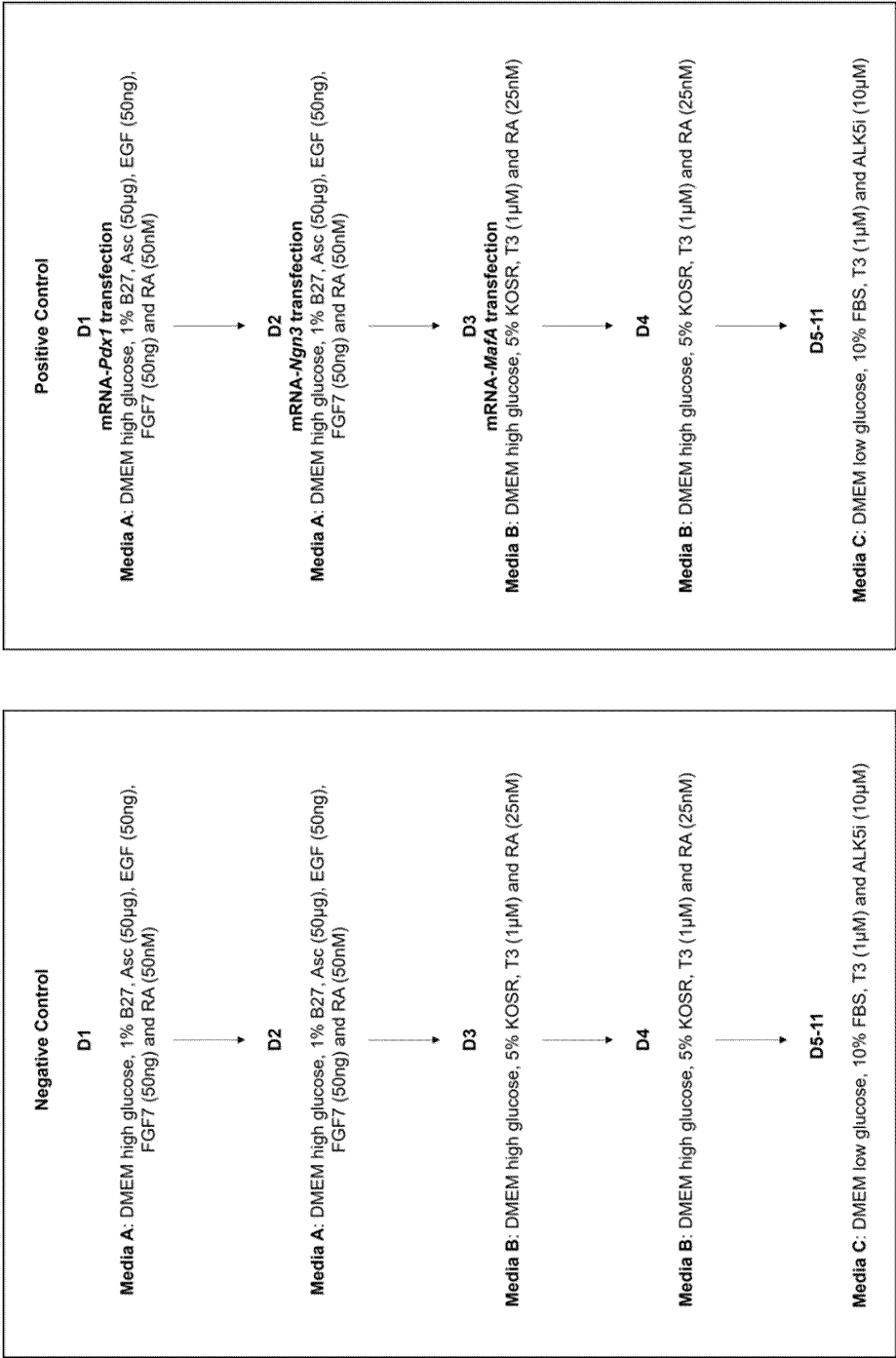
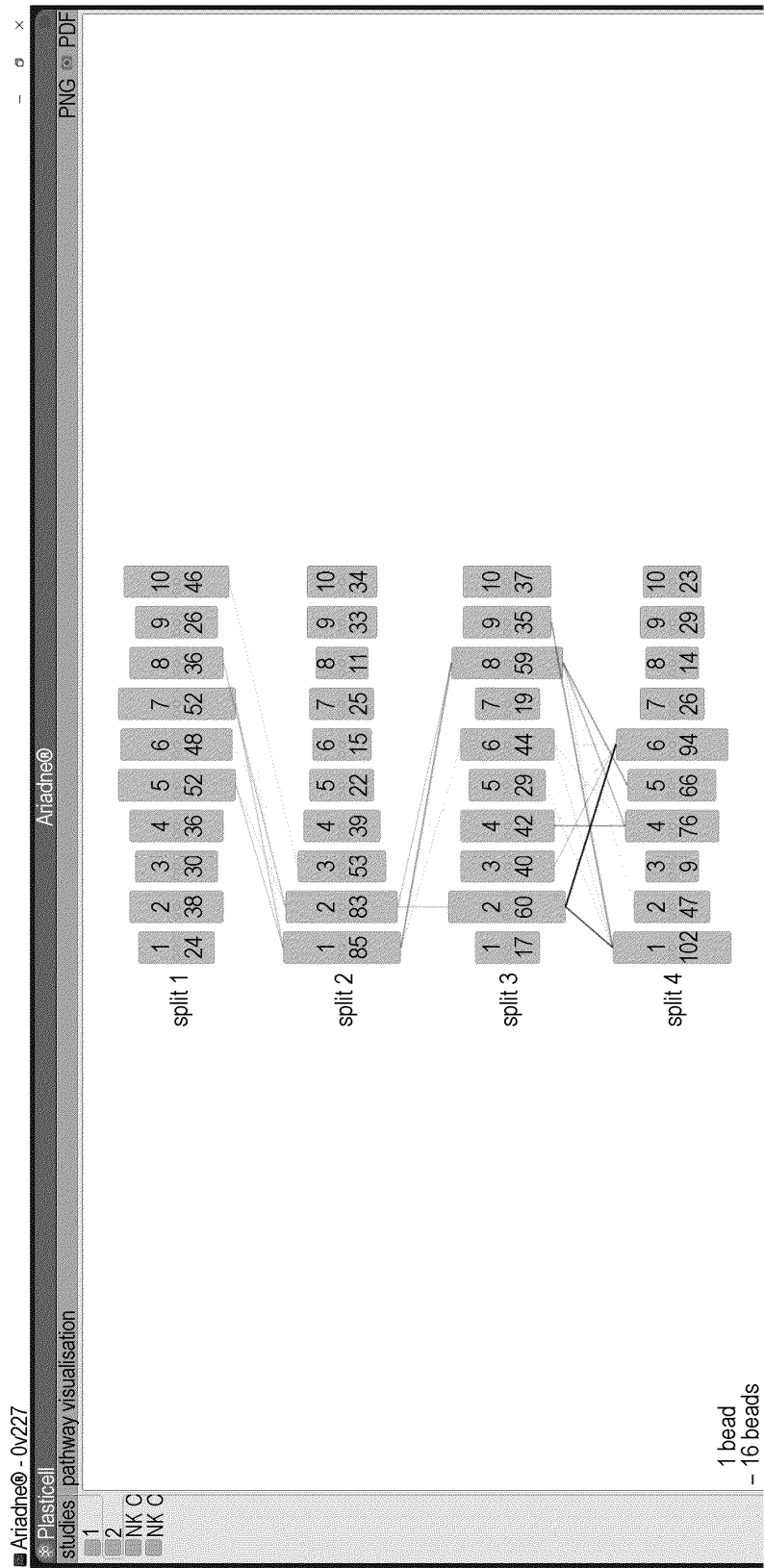
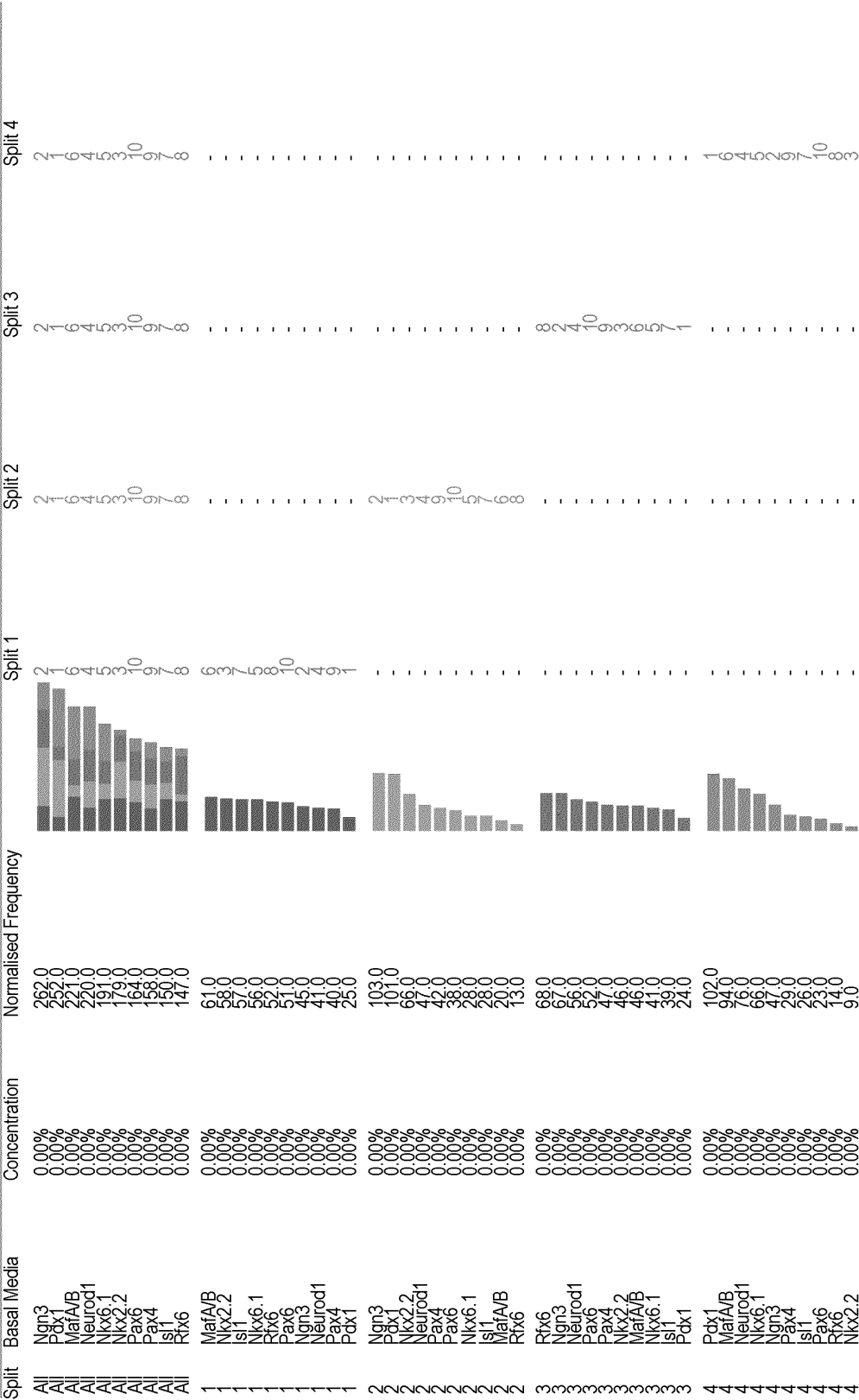


FIG. 6



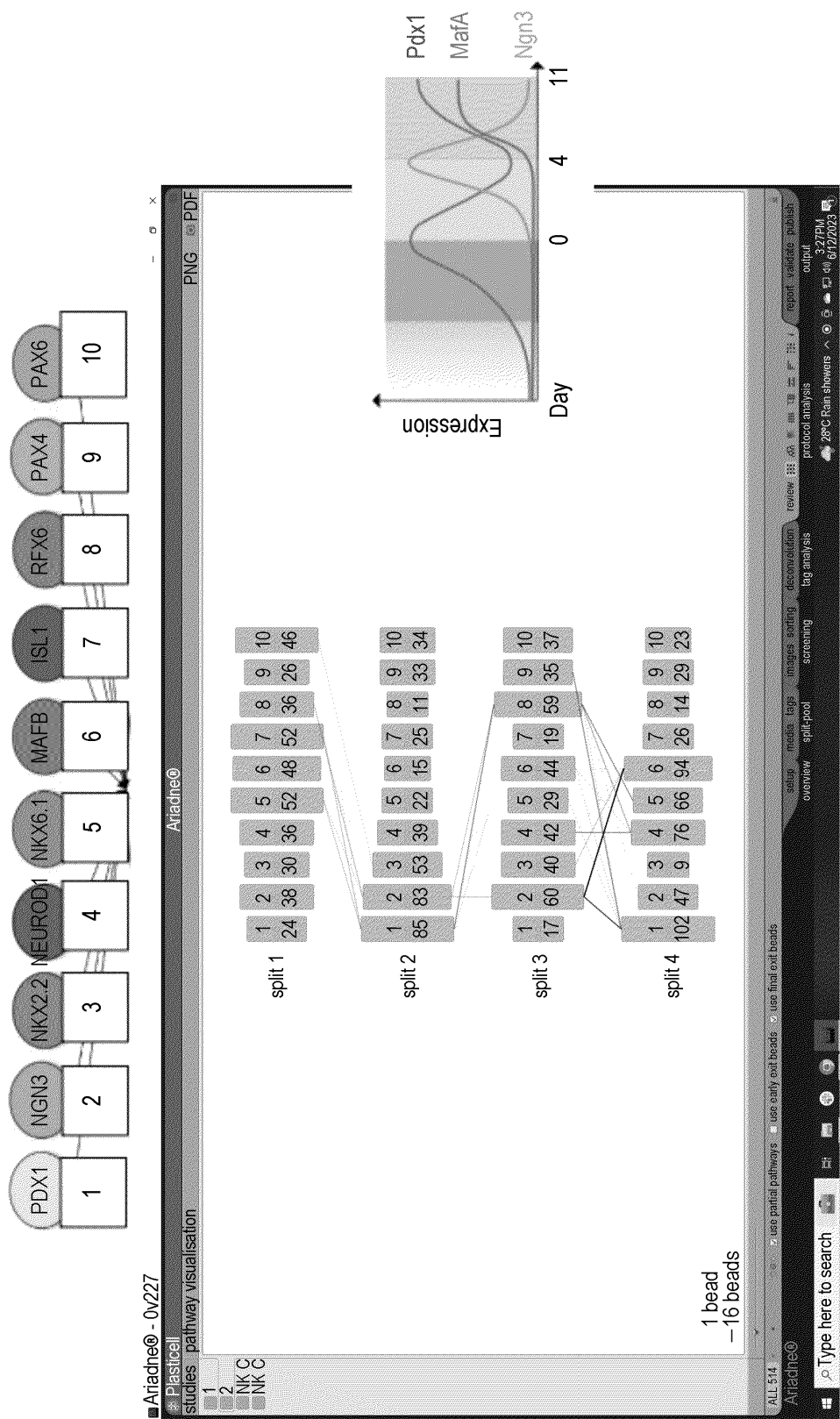
Transcription Factor Combinations leading to Reprogramming

FIG. 7A



Frequency of transcription factor addition in hits

FIG. 7B



Selection of transcription factors by computational analysis

FIG. 8