

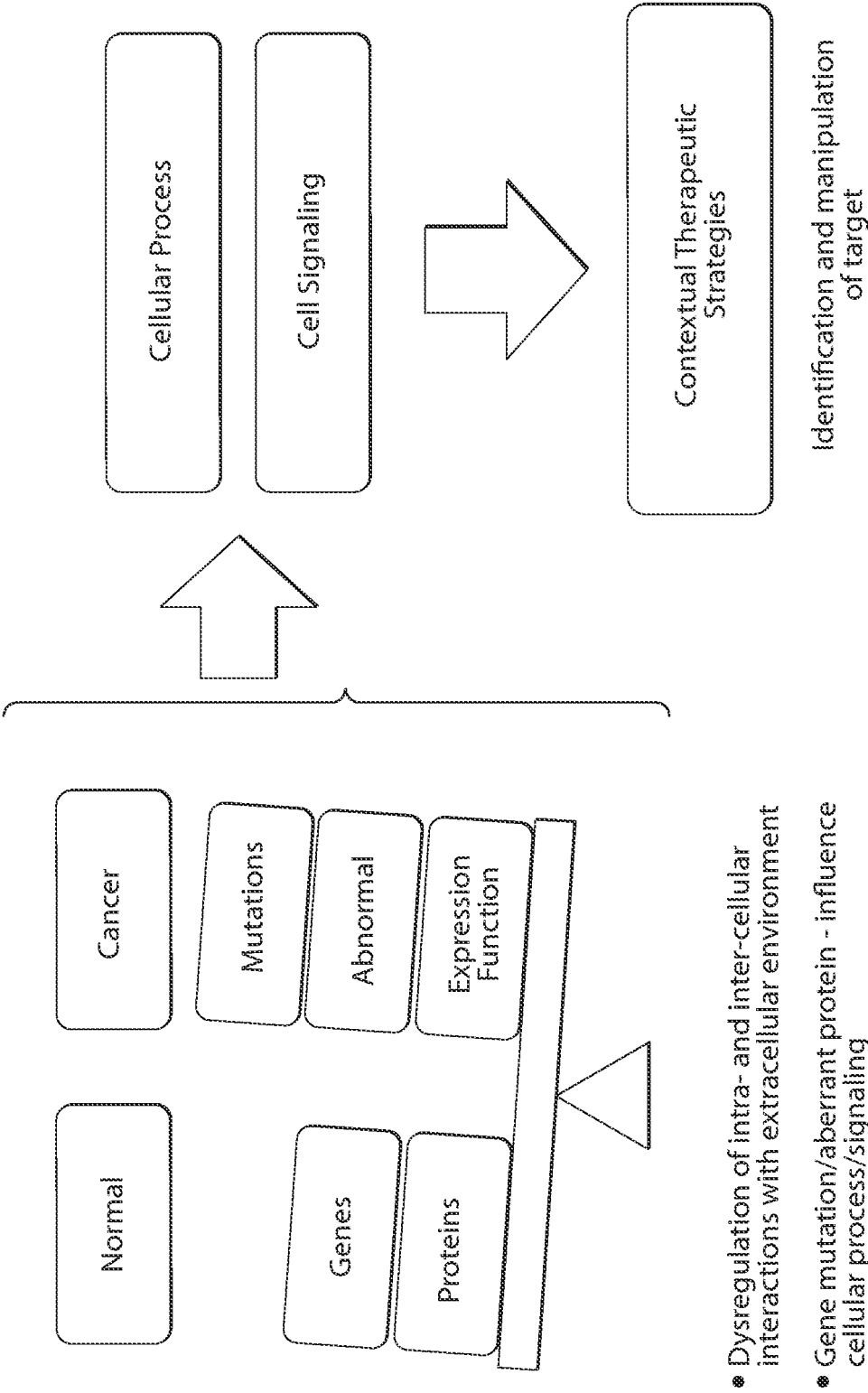


Fig. 1

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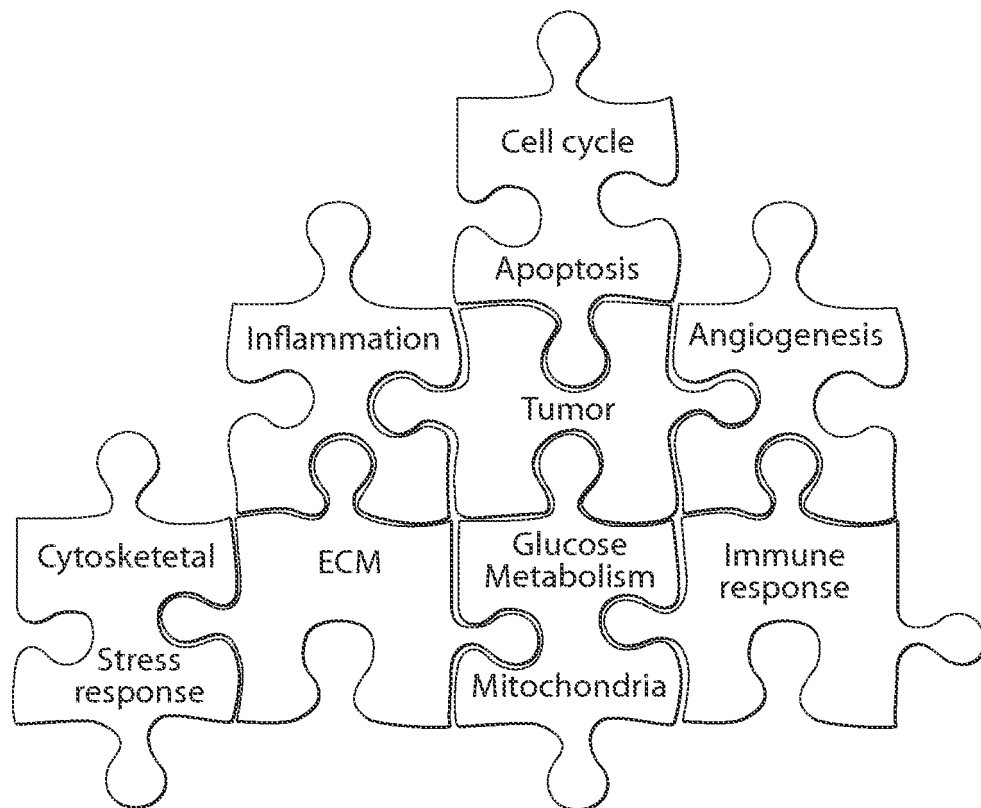


Fig. 2

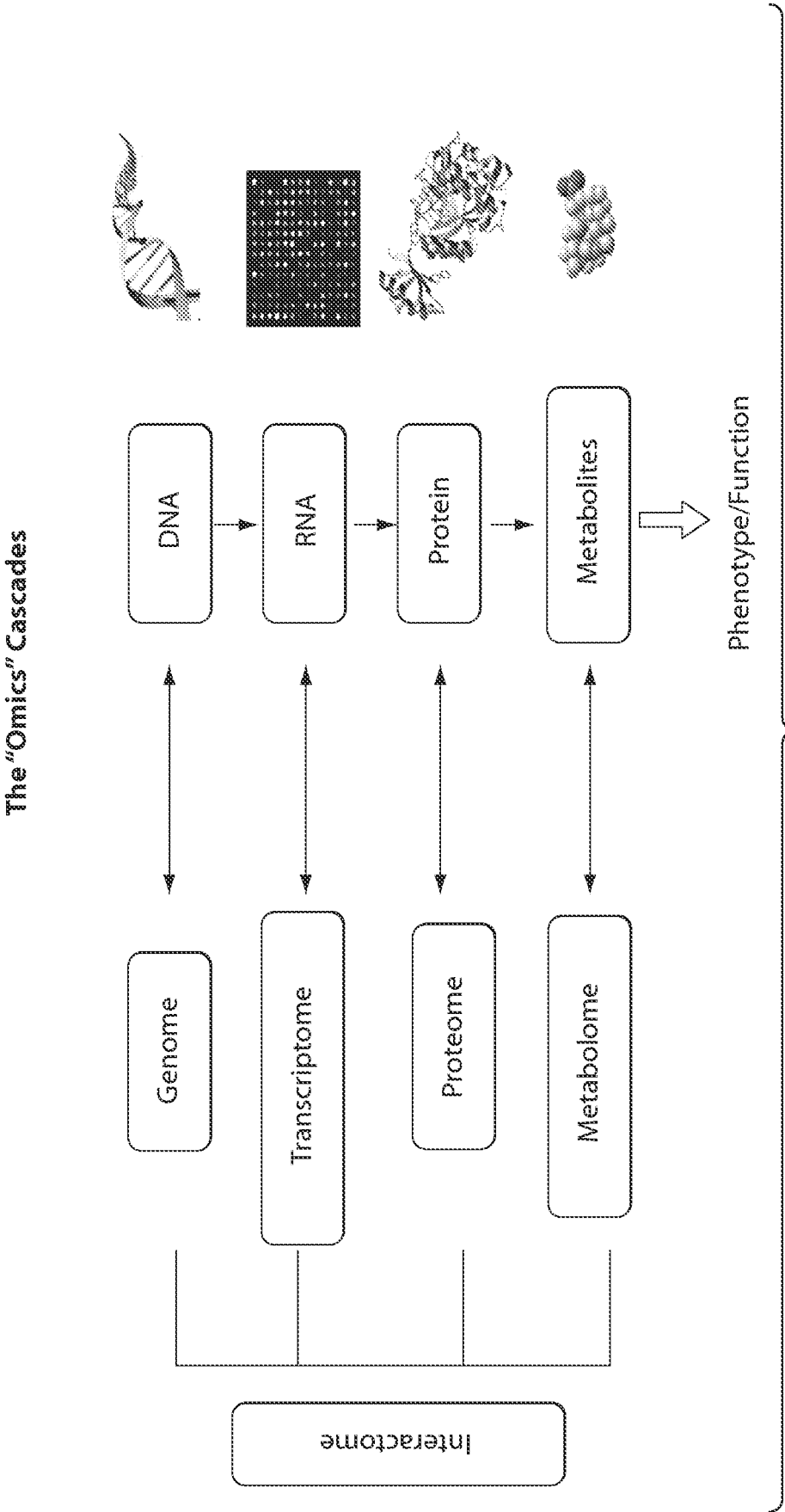


Fig. 3

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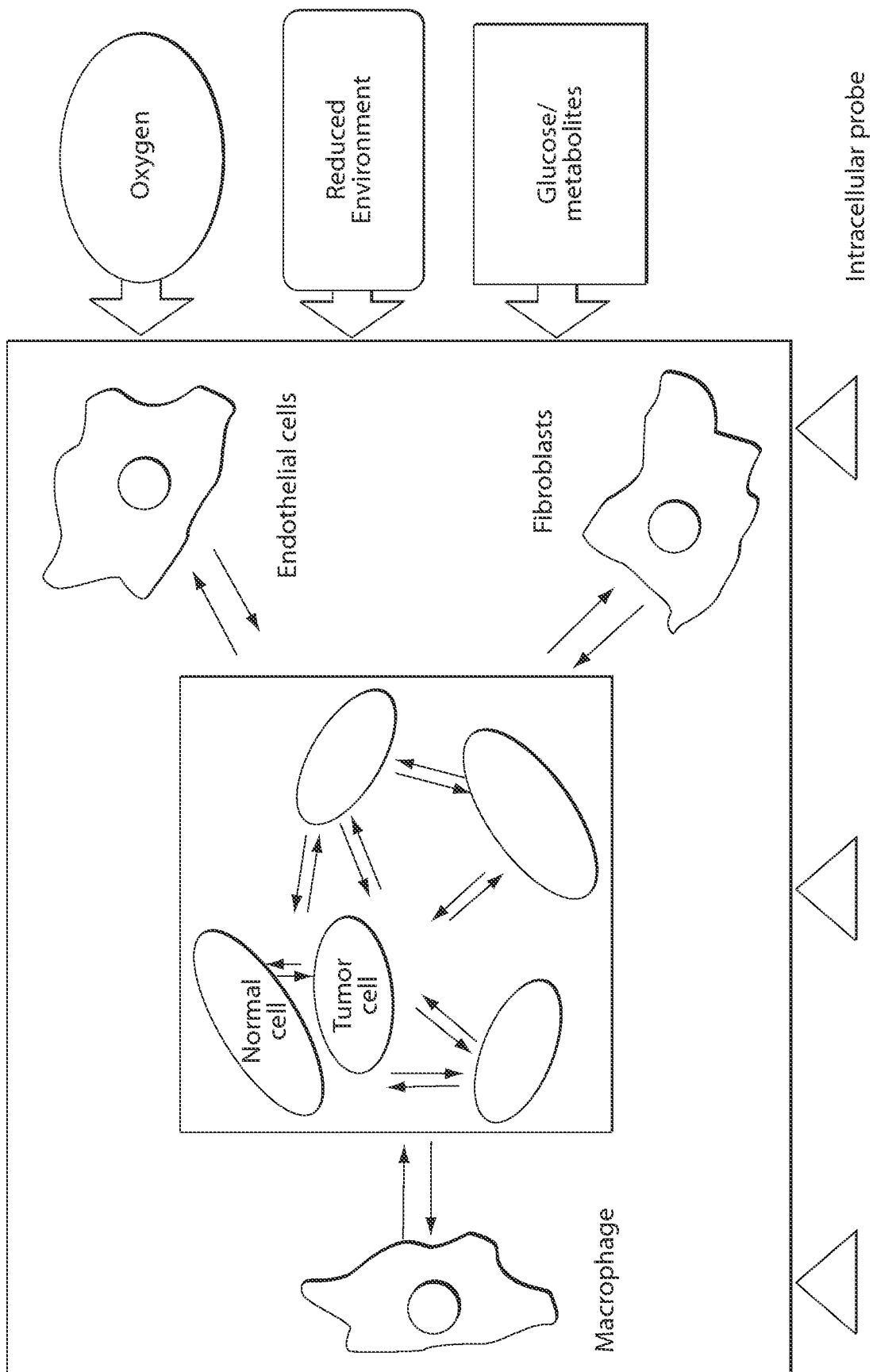


Fig. 4

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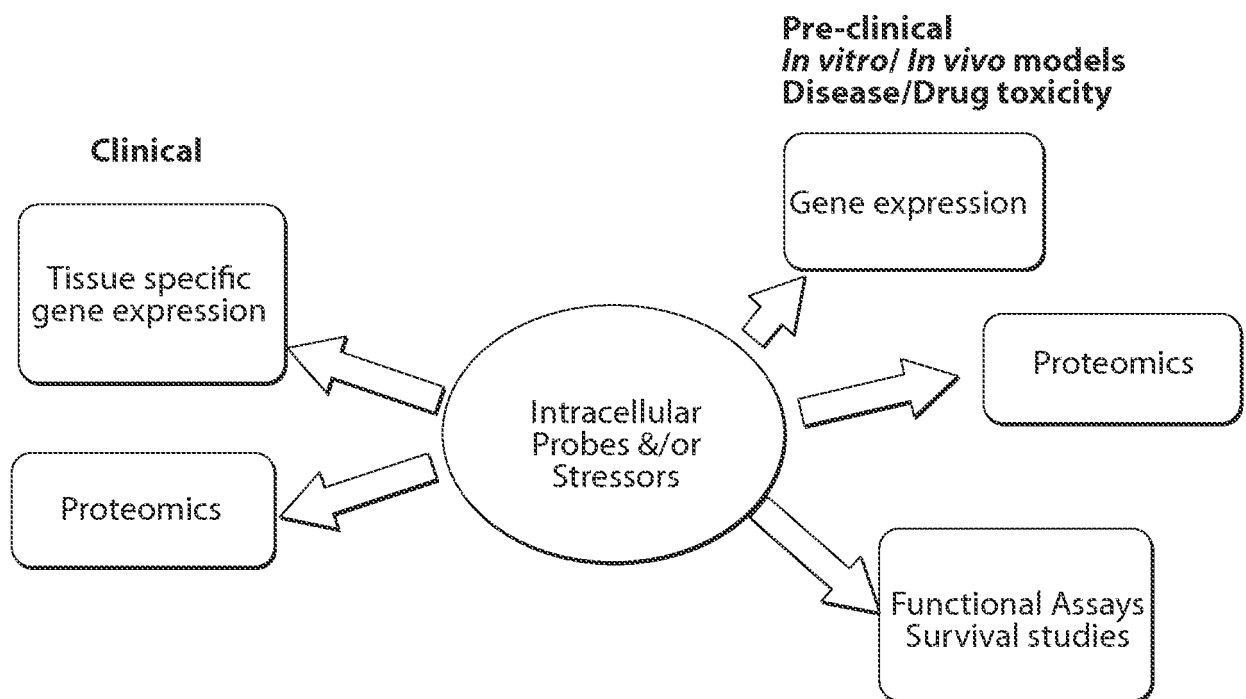


Fig. 5

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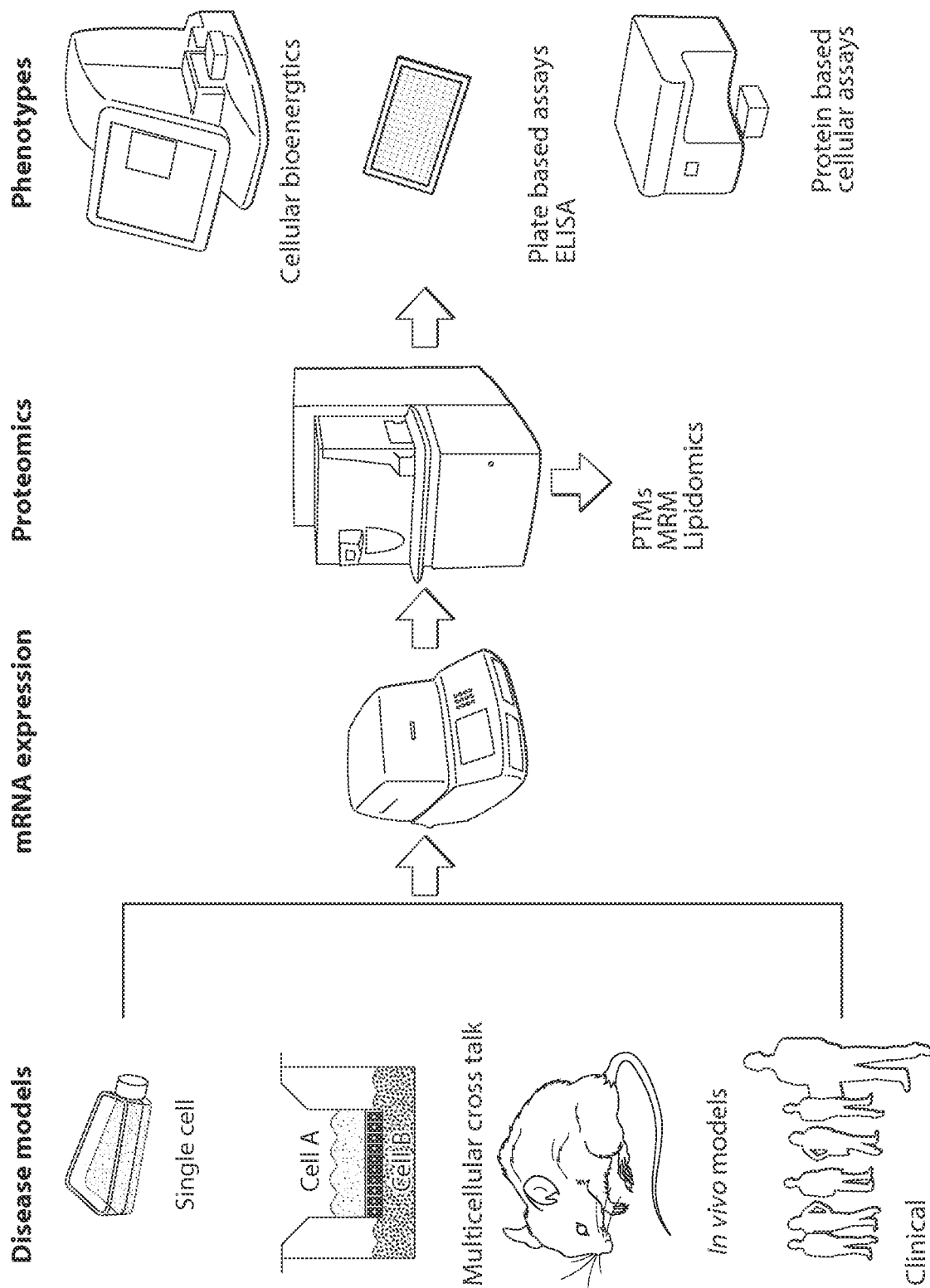


Fig. 6

7/62

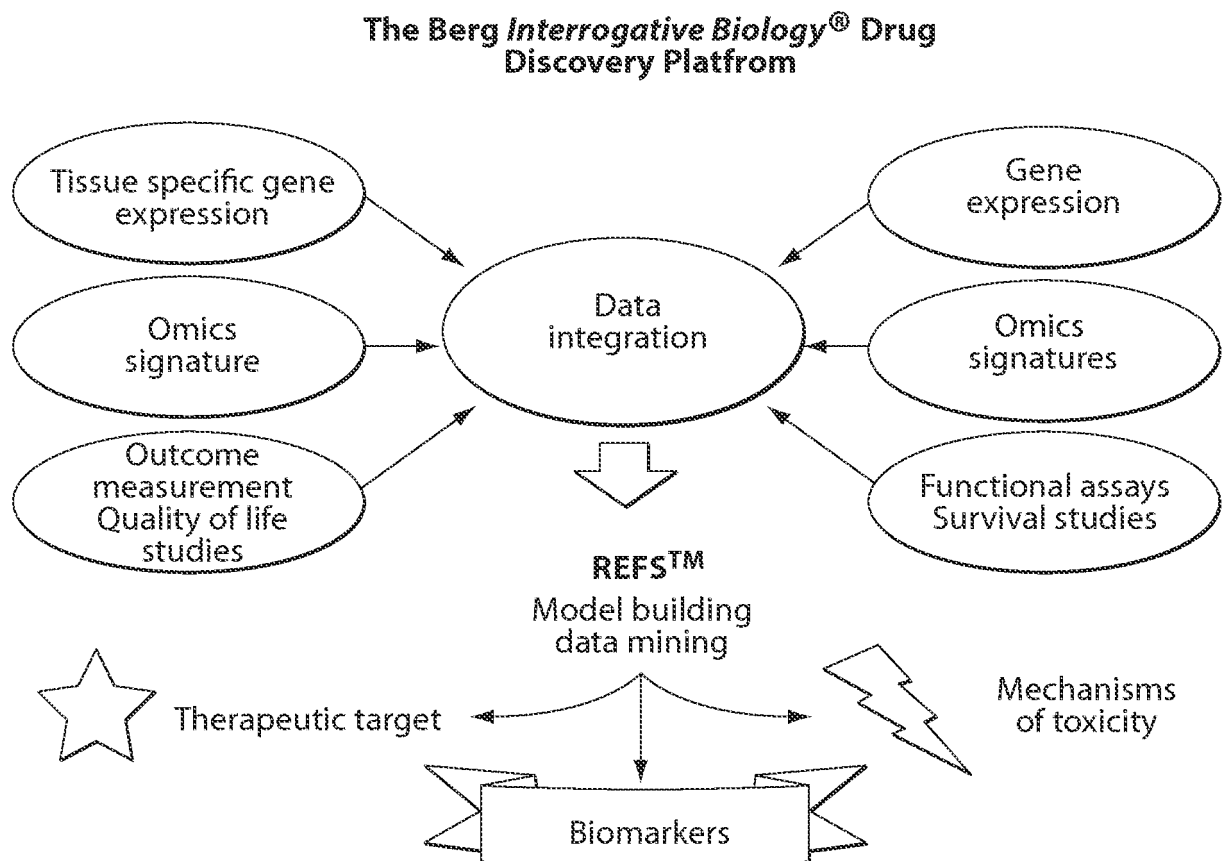


Fig. 7

8/62

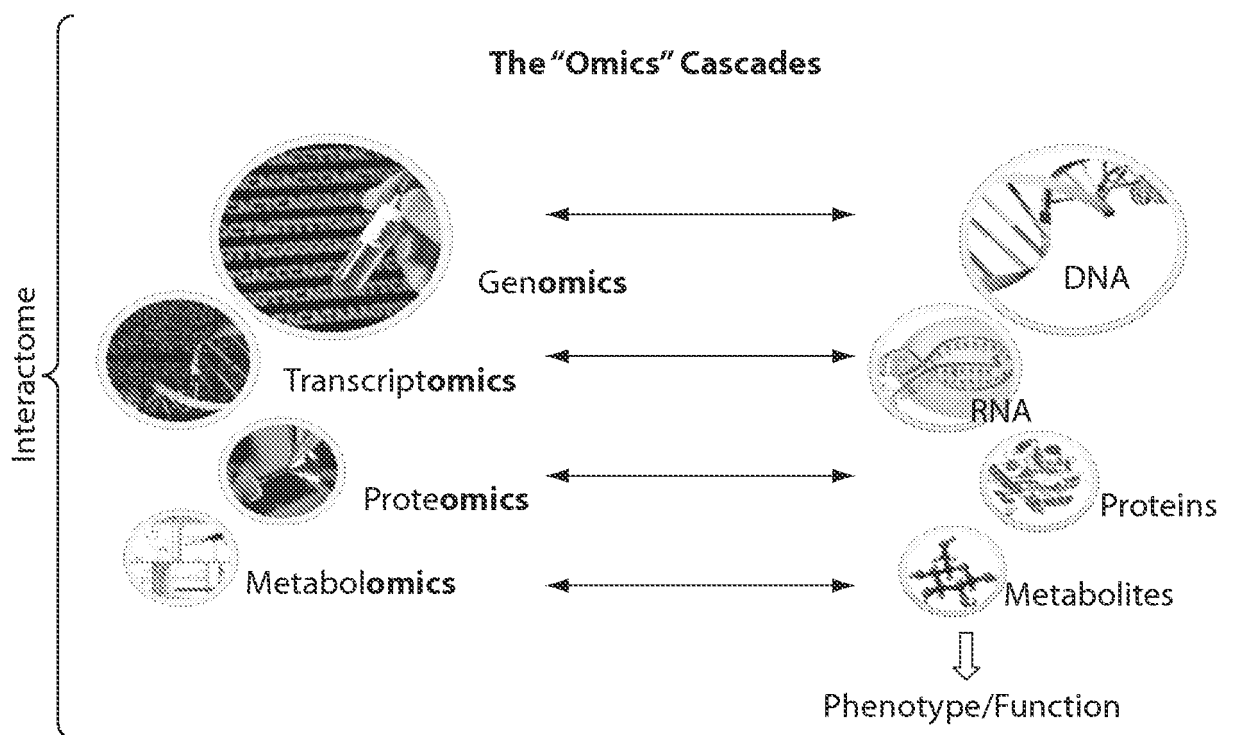


Fig. 8

9/62

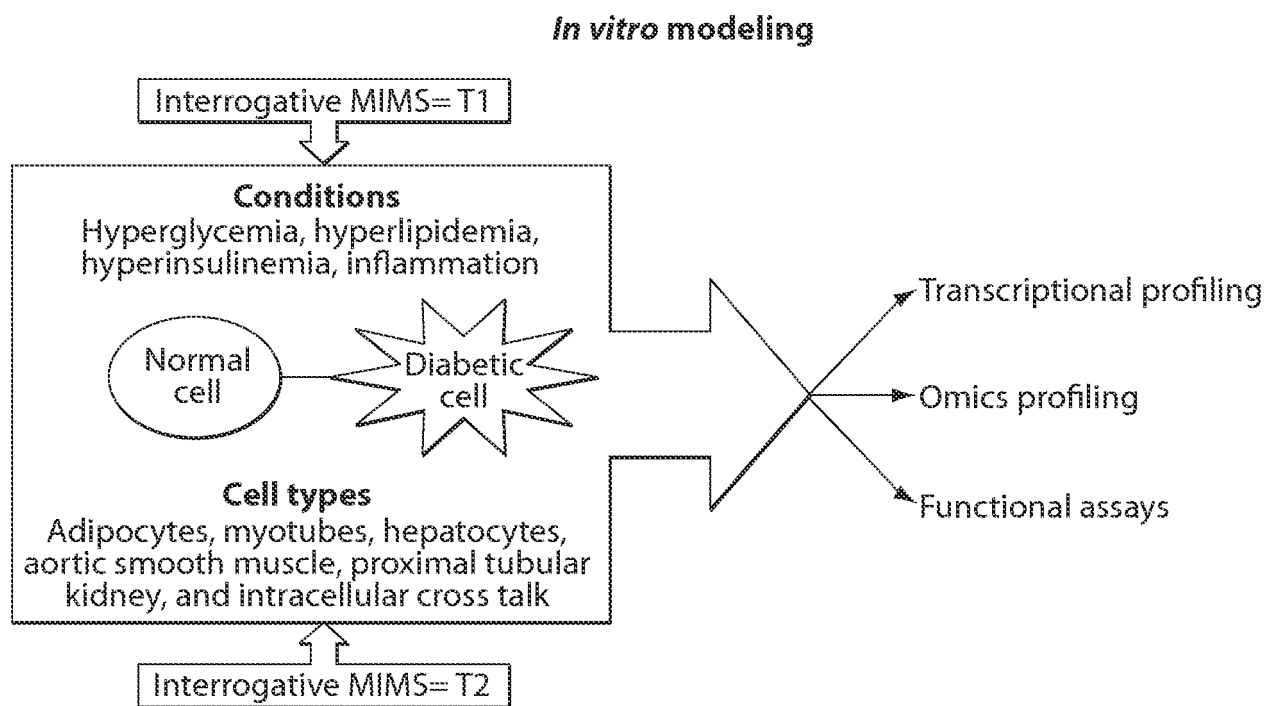


Fig. 9

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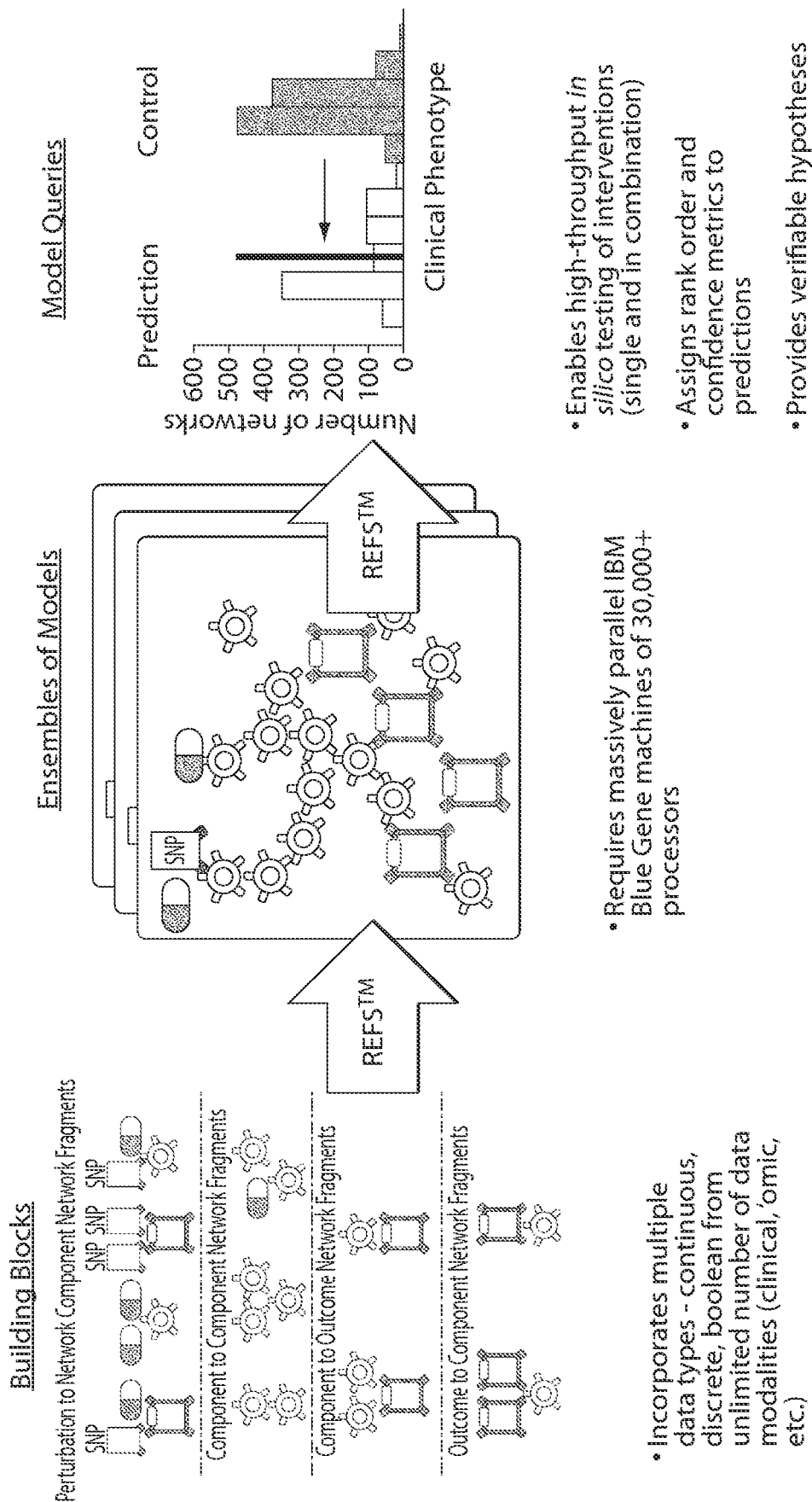
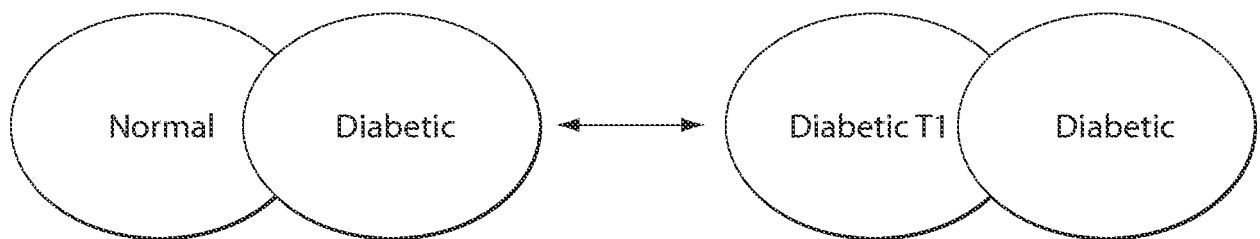


Fig. 10

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(Normal vs. Diabetic) Vs. (Diabetic T1 vs. Diabetic)



Compare the unique edges of **Normal** in the normal vs. disease delta network with the unique edges of **Disease T1** in the disease vs. disease T1 delta network. Edges in the intersection of normal and disease T1 are disease edges that were restored to normal when treated with T1.

Fig. 11

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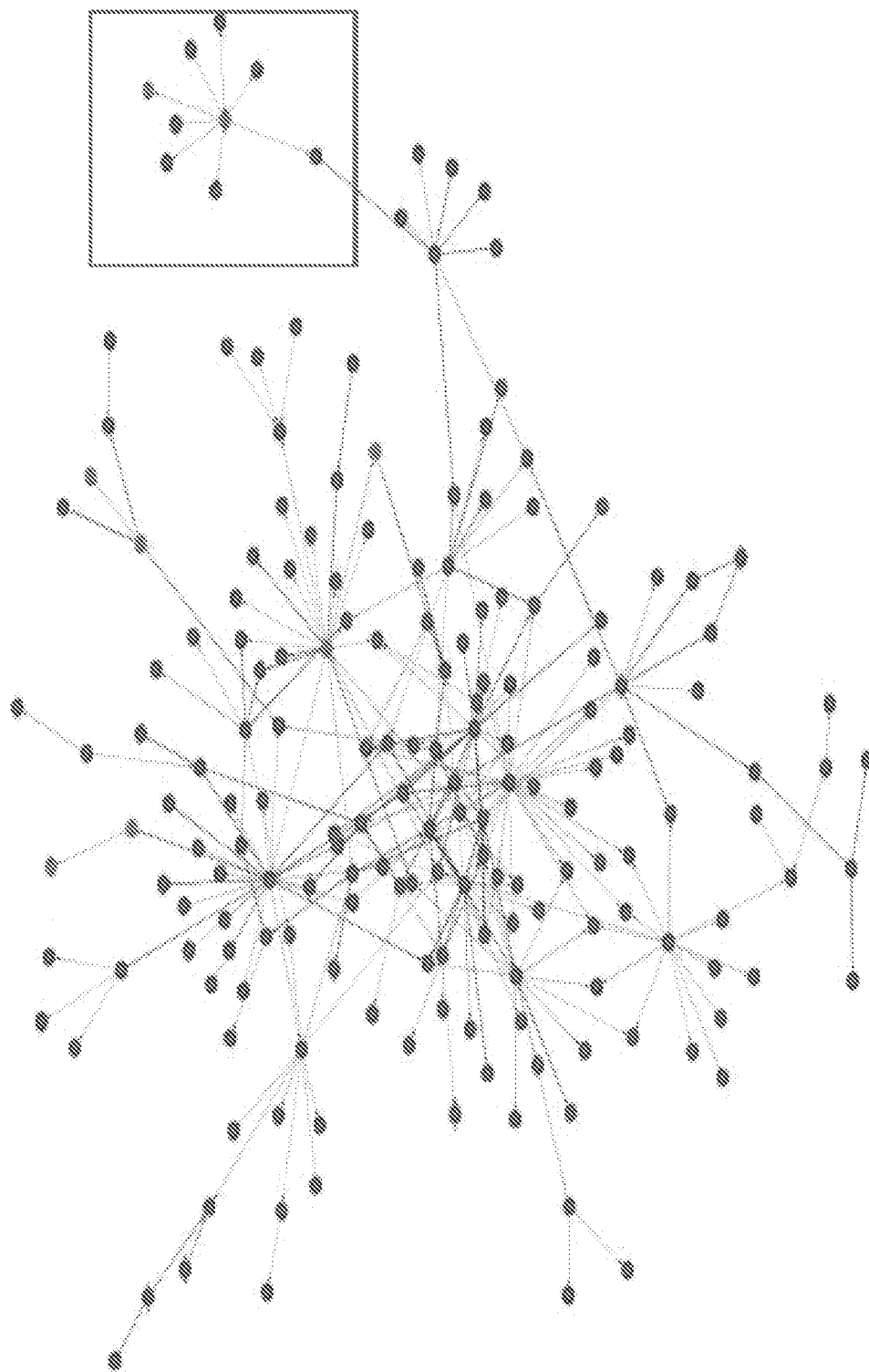


Fig. 12

13/62

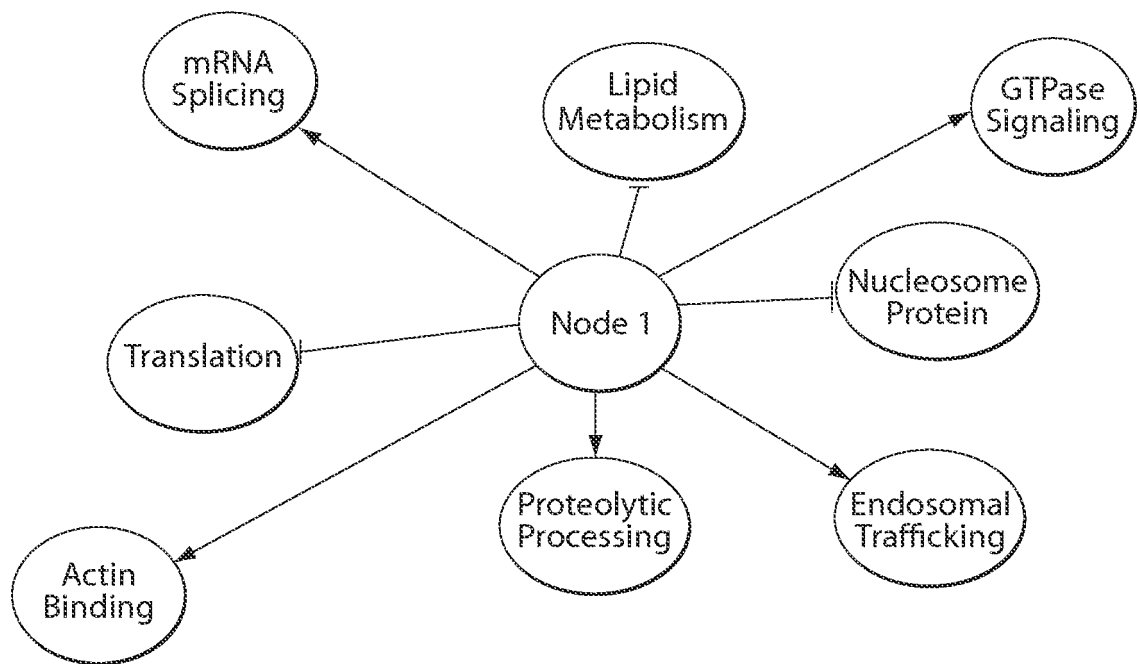


Fig. 13

14/62

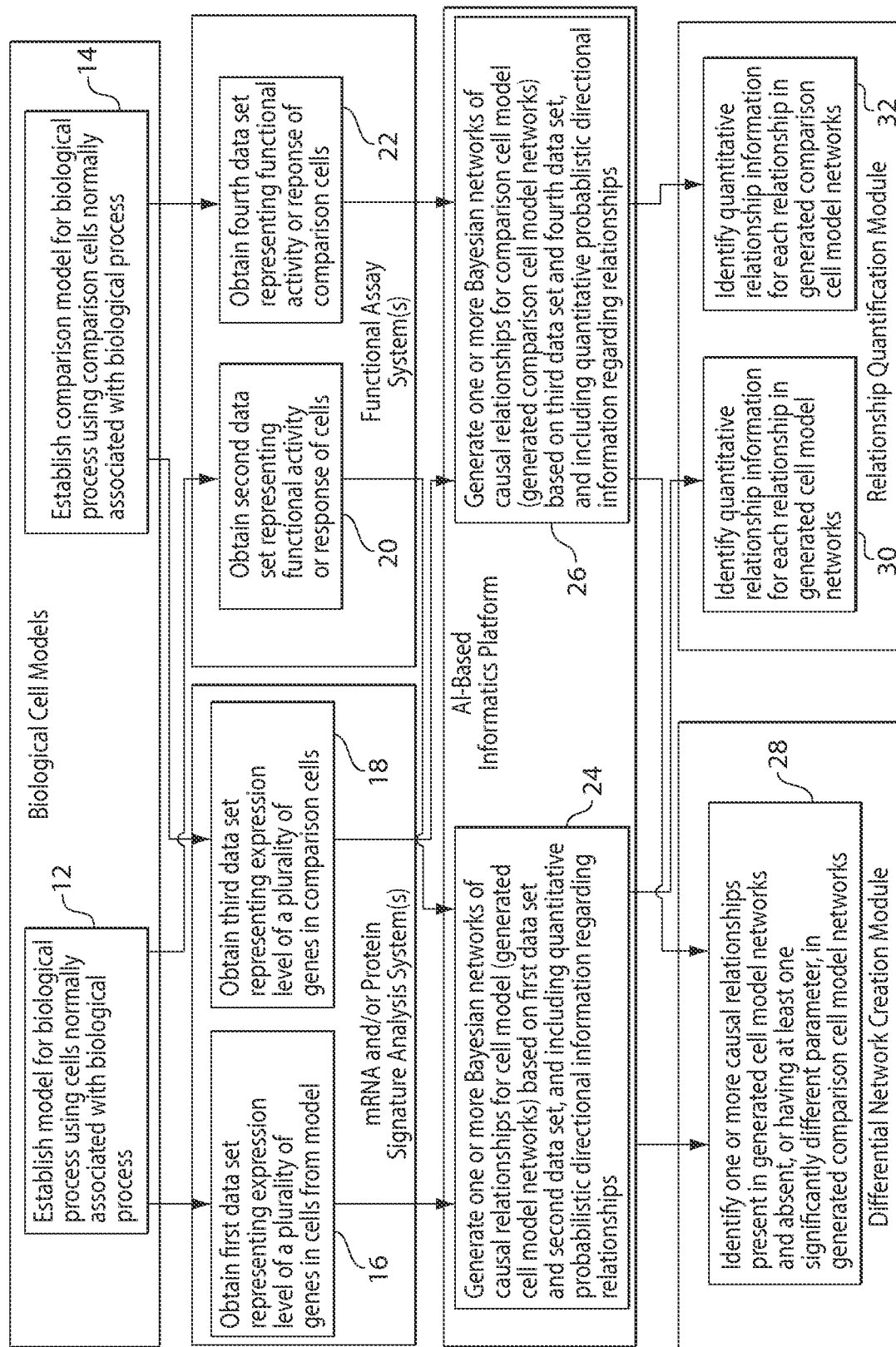


Fig. 14

15/62

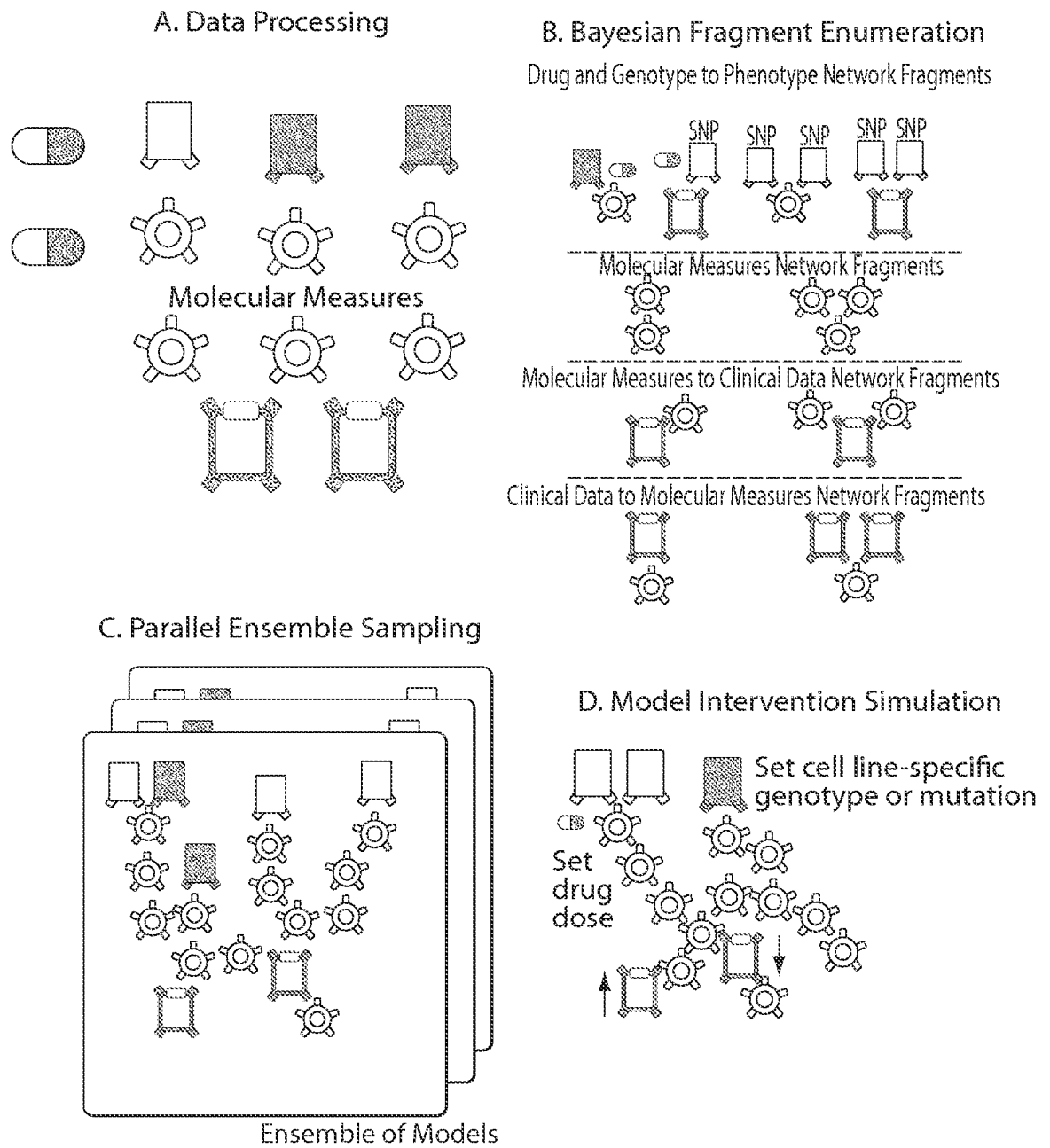


Fig. 15

16/62

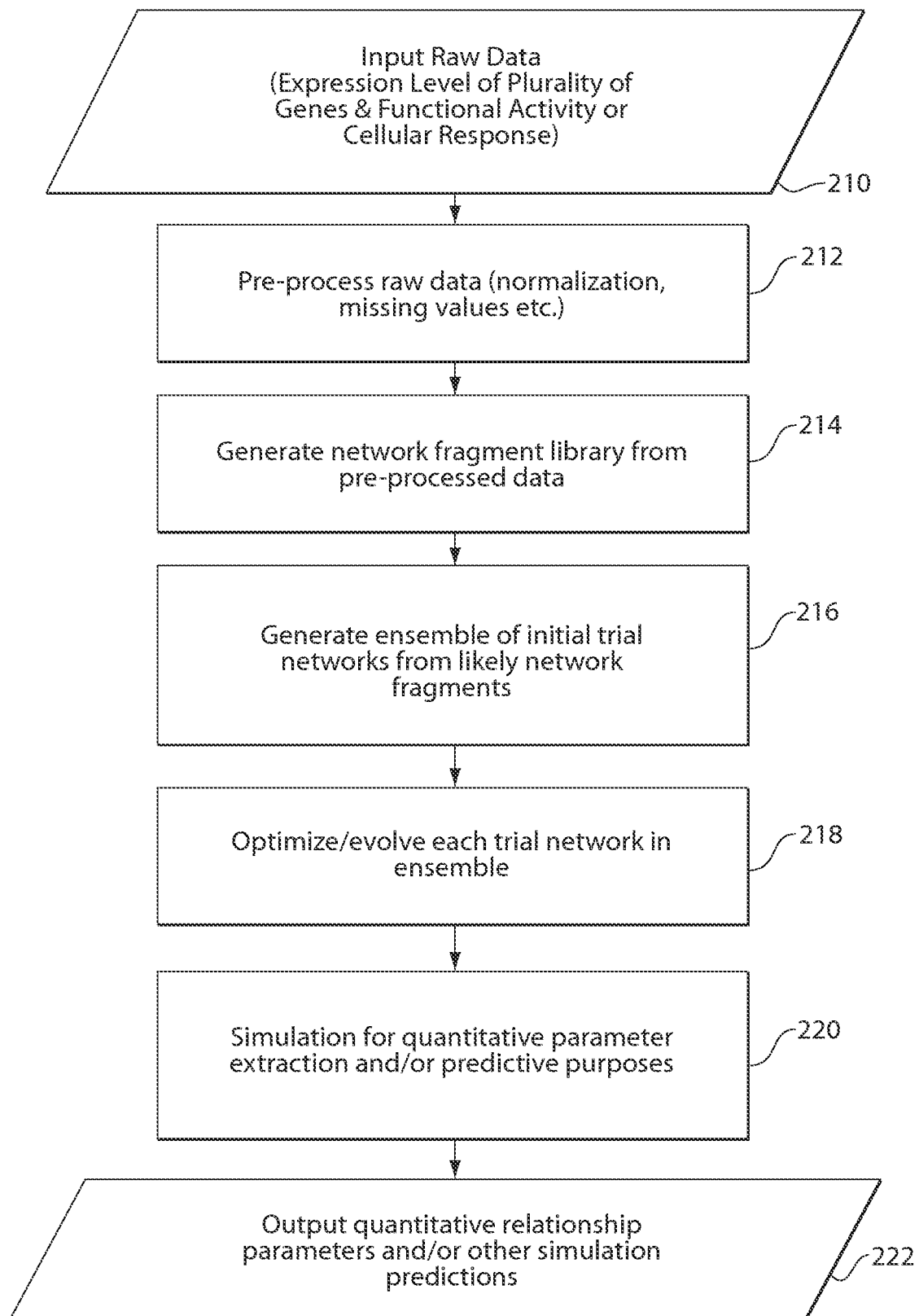


Fig. 16

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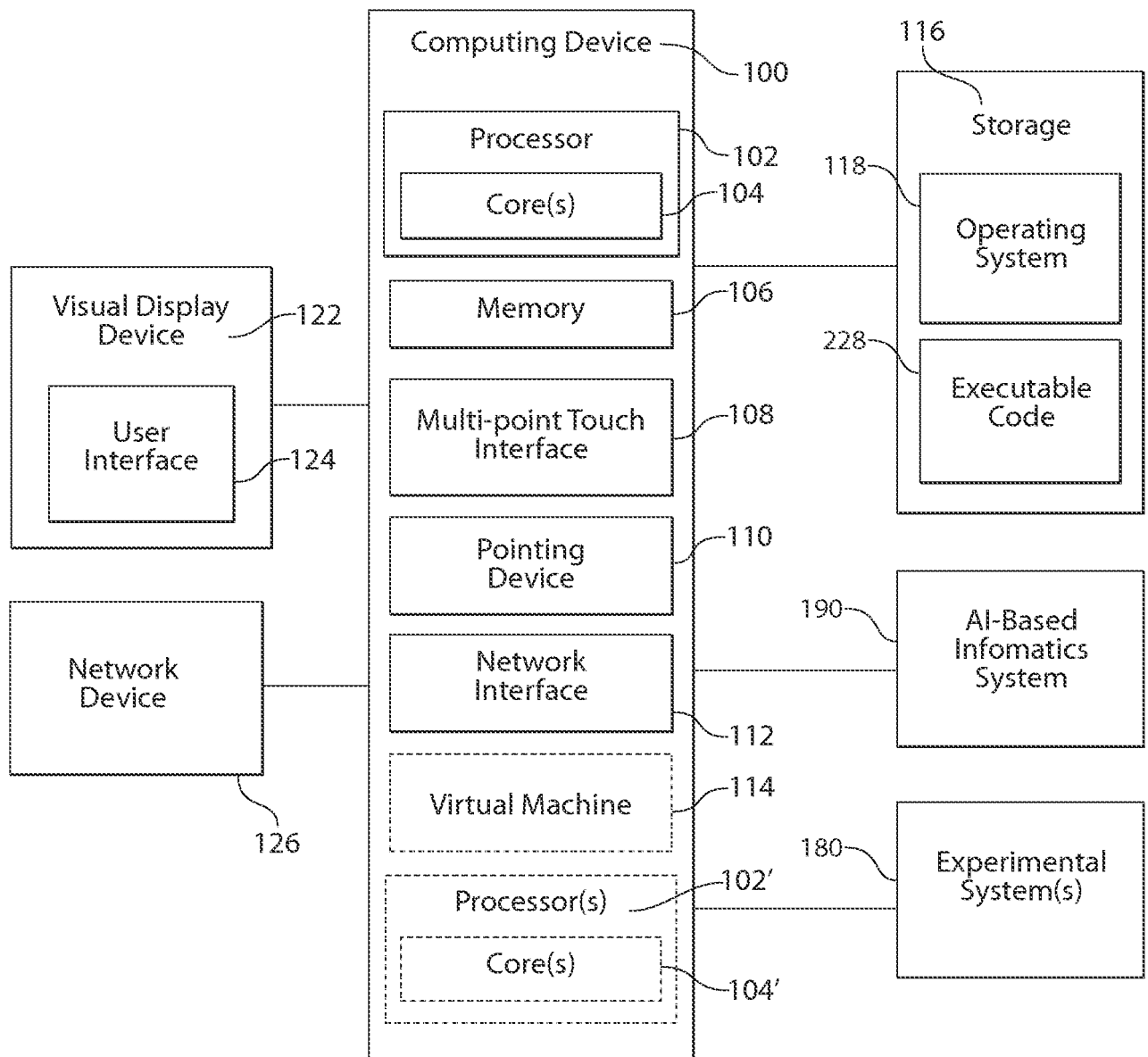


Fig. 17

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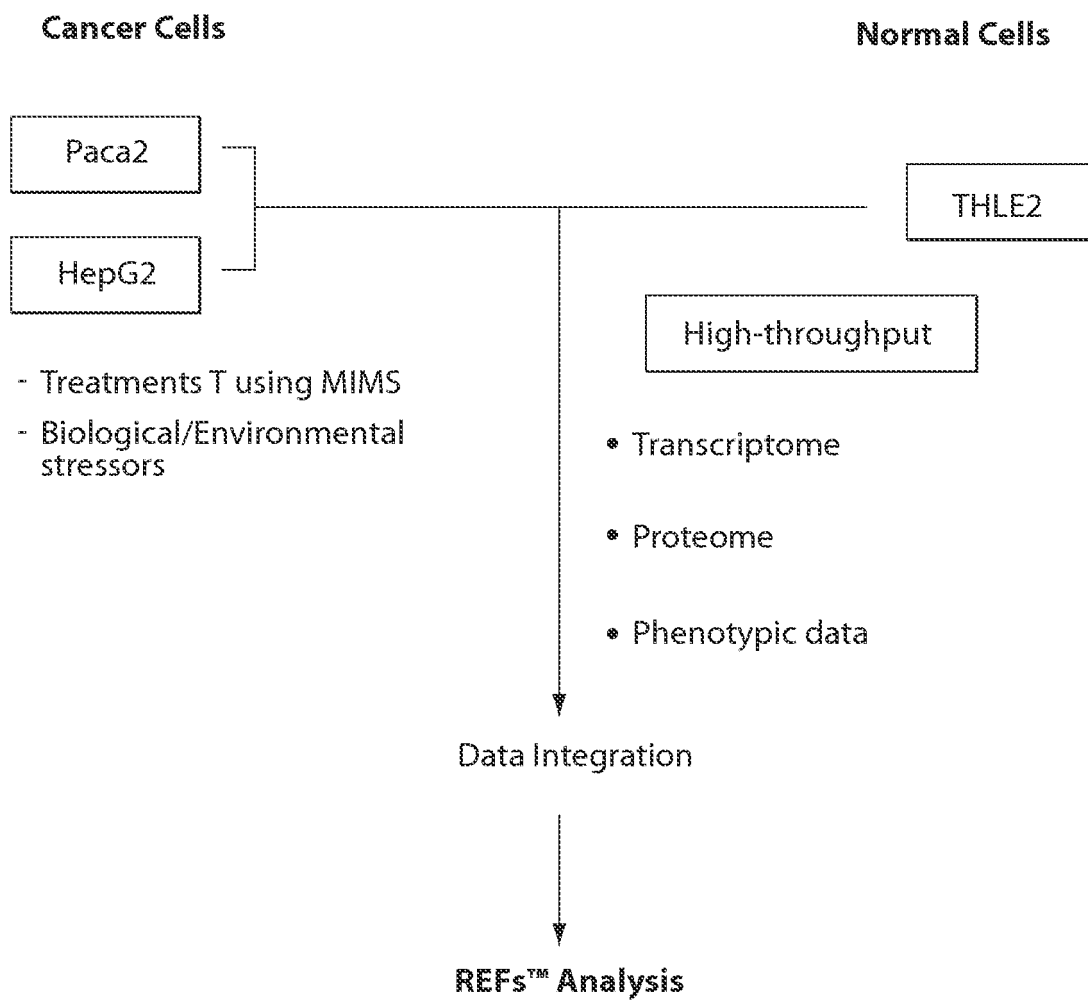


Fig. 18

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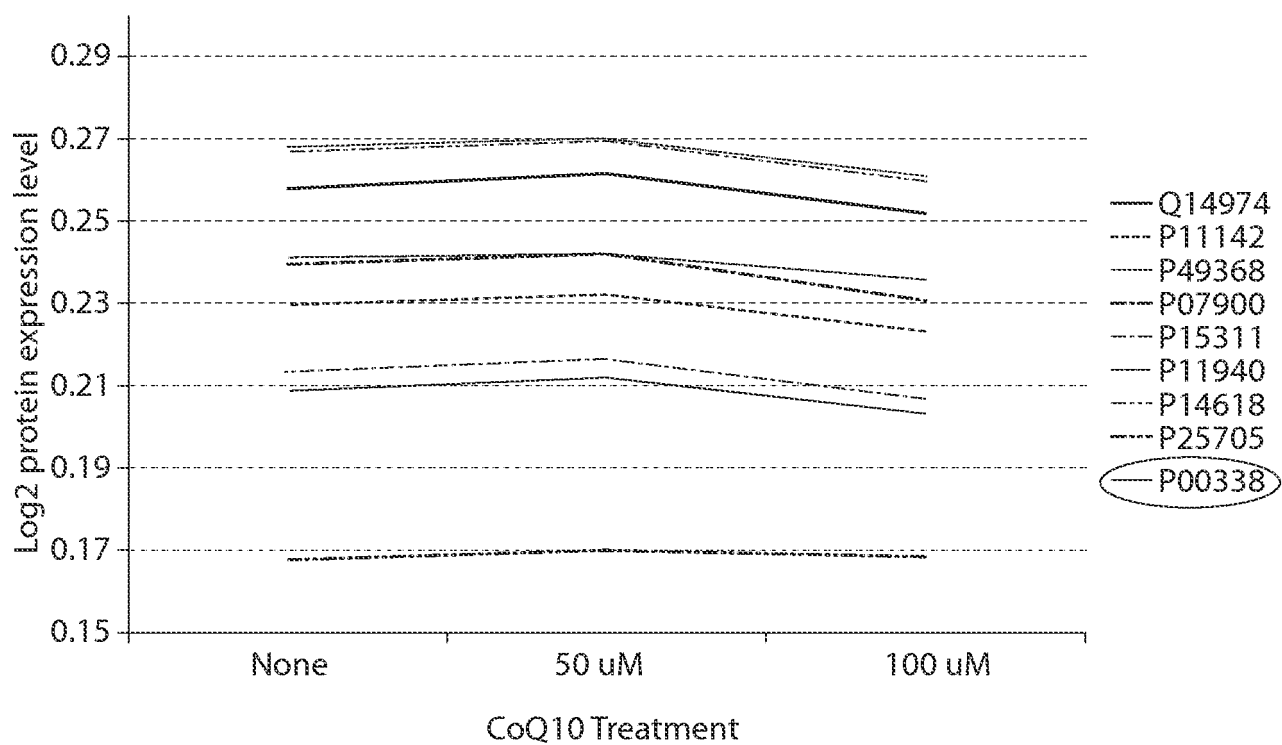


Fig. 19

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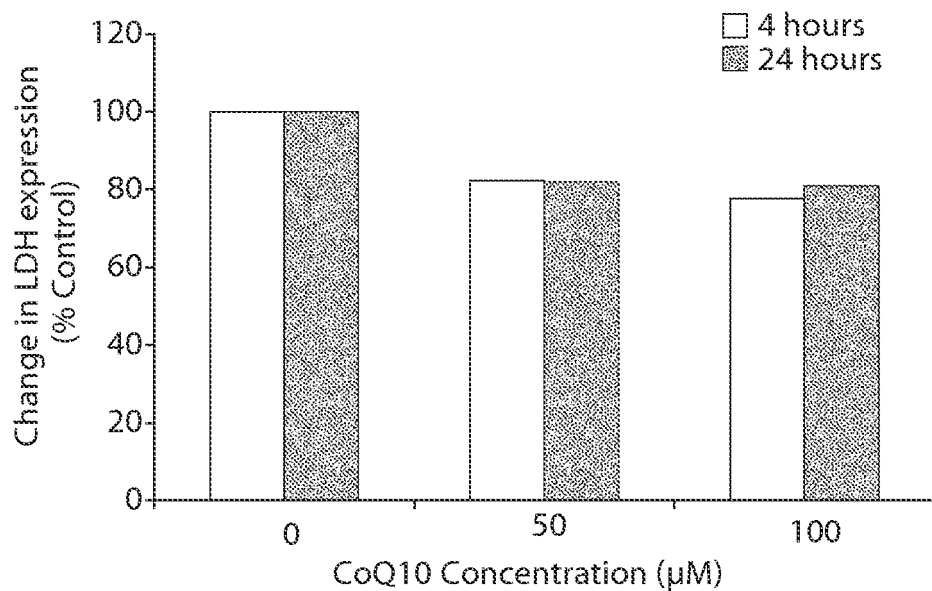
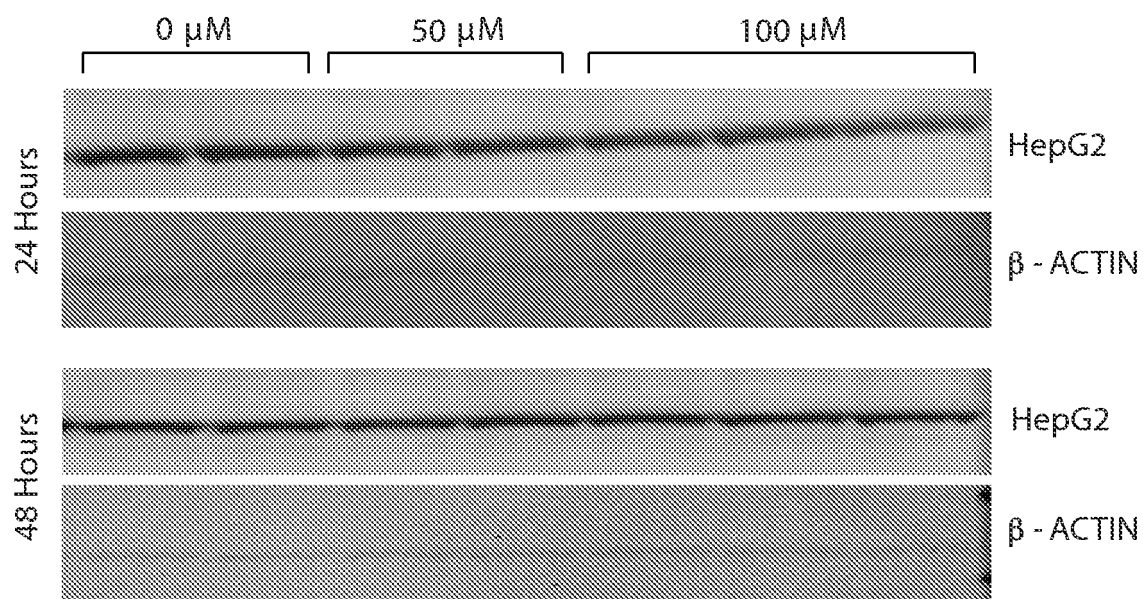


Fig. 20

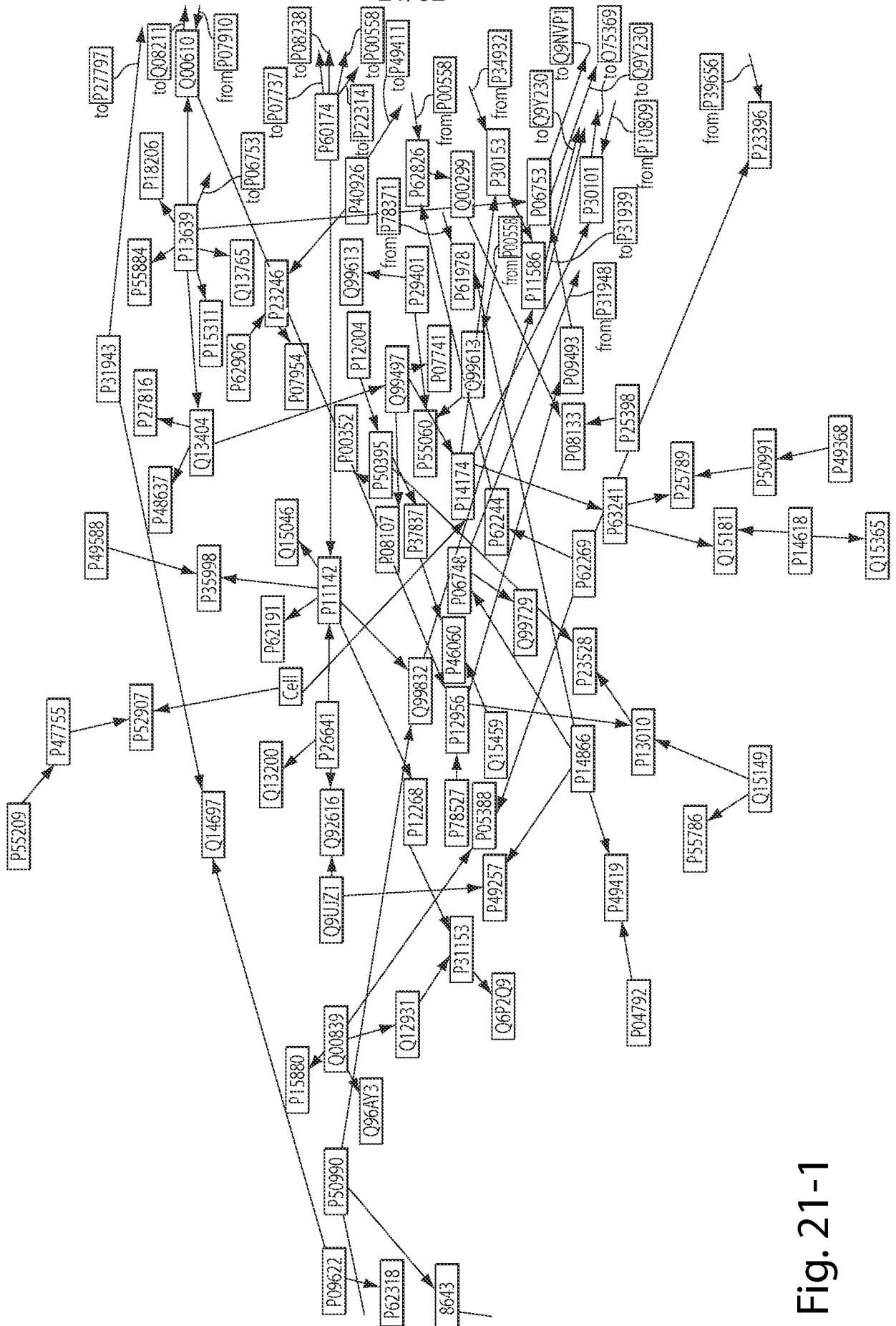


Fig. 21-1

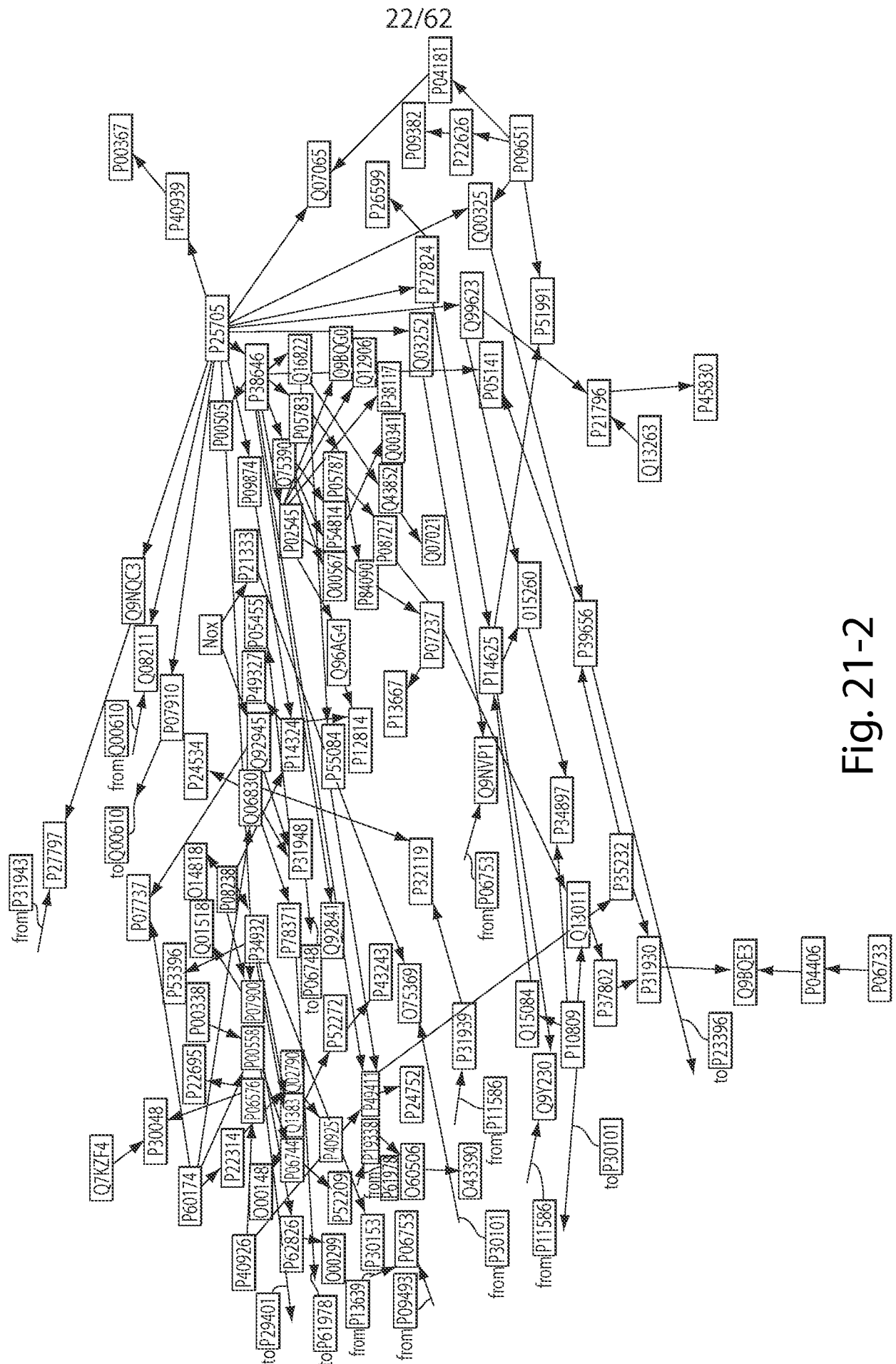


Fig. 21-2

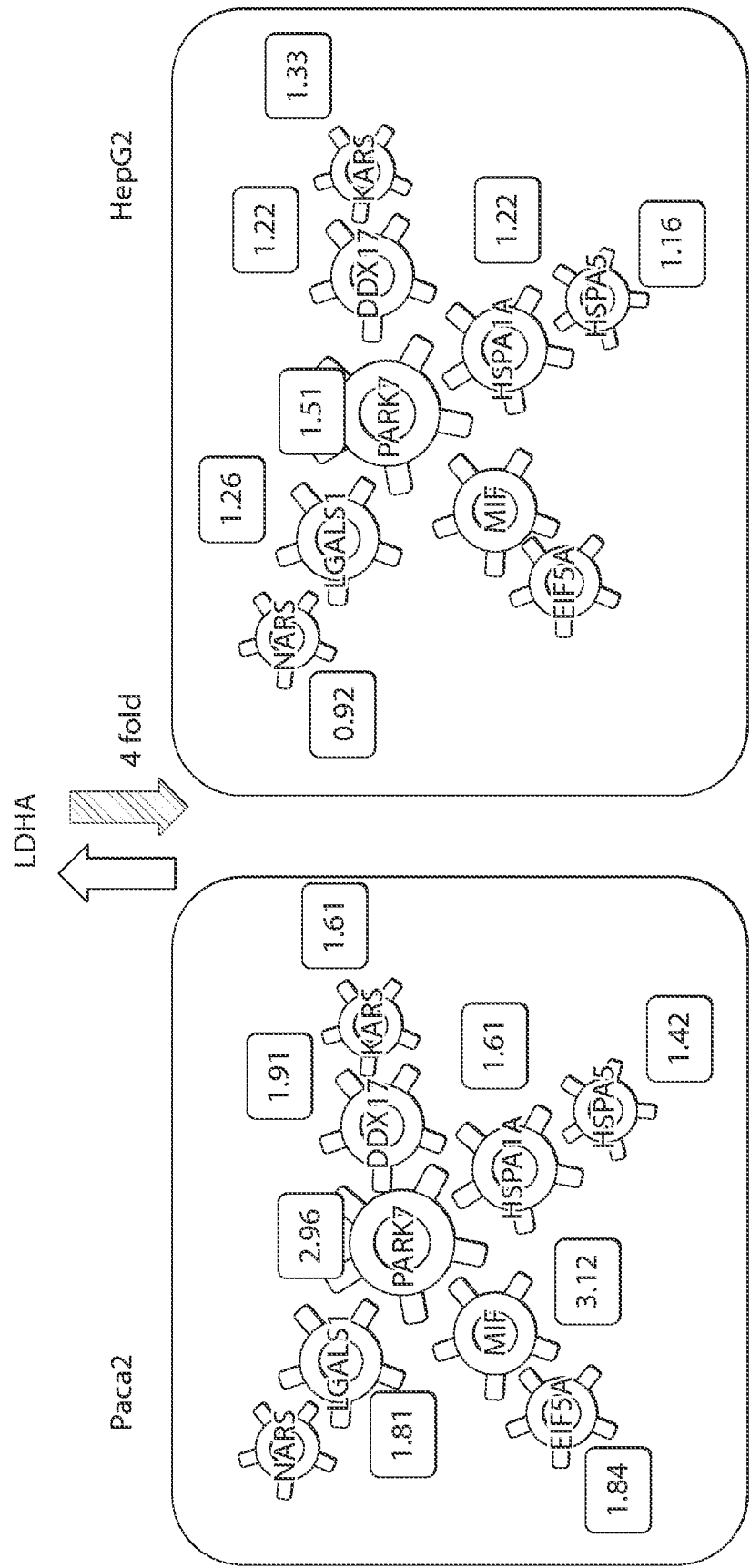


Fig. 22

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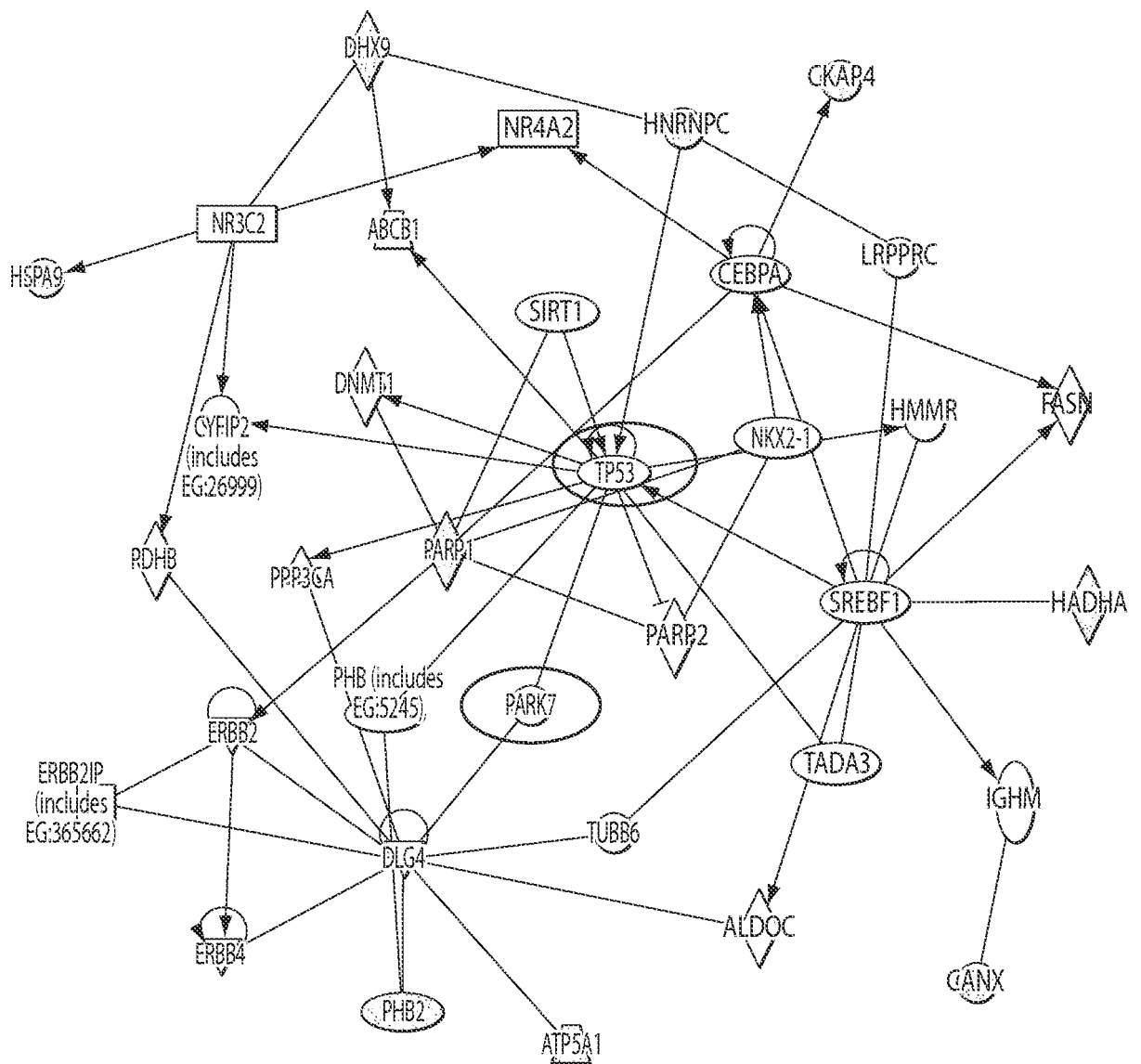


Fig. 23

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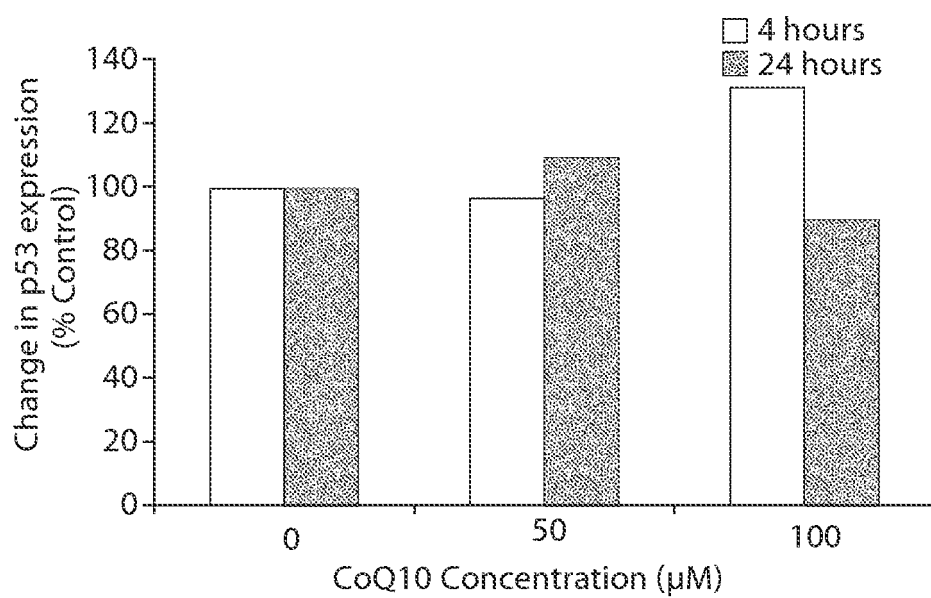
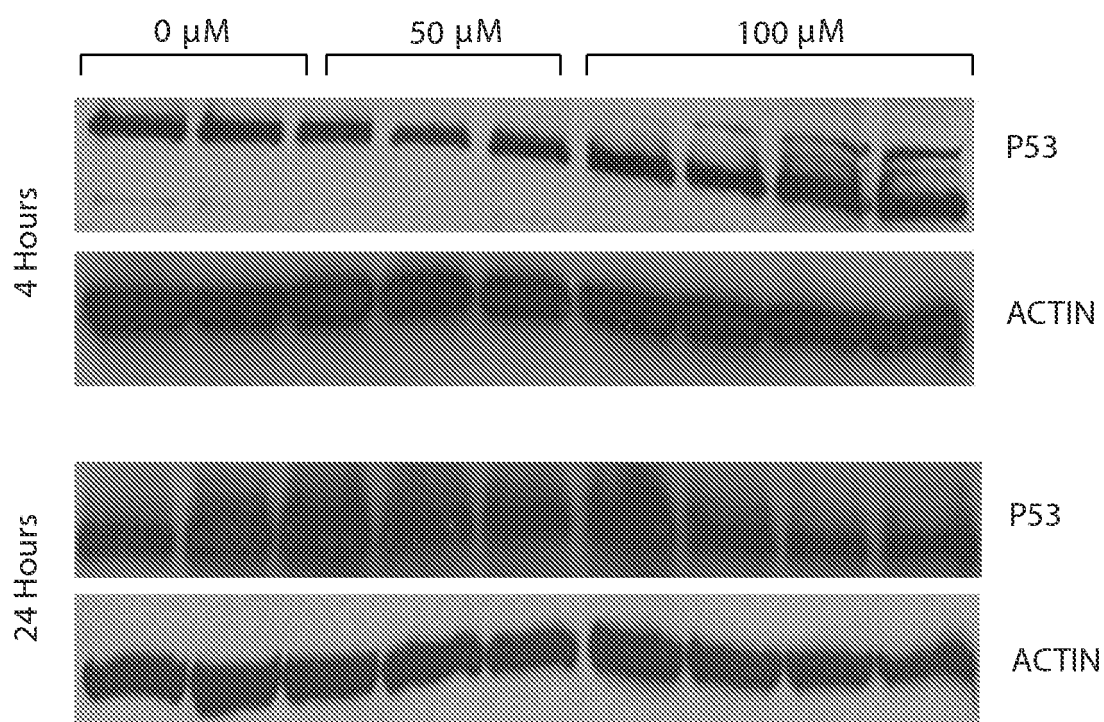


Fig. 24

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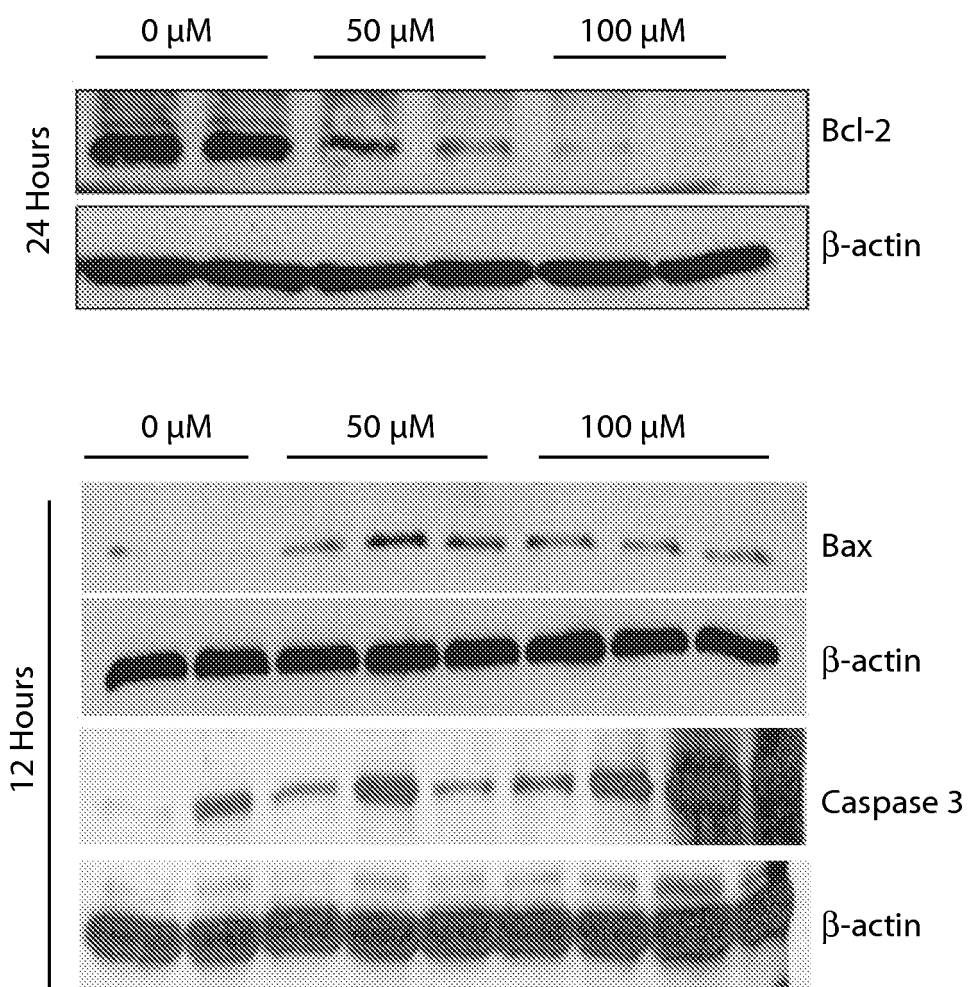


Fig. 25

27/62

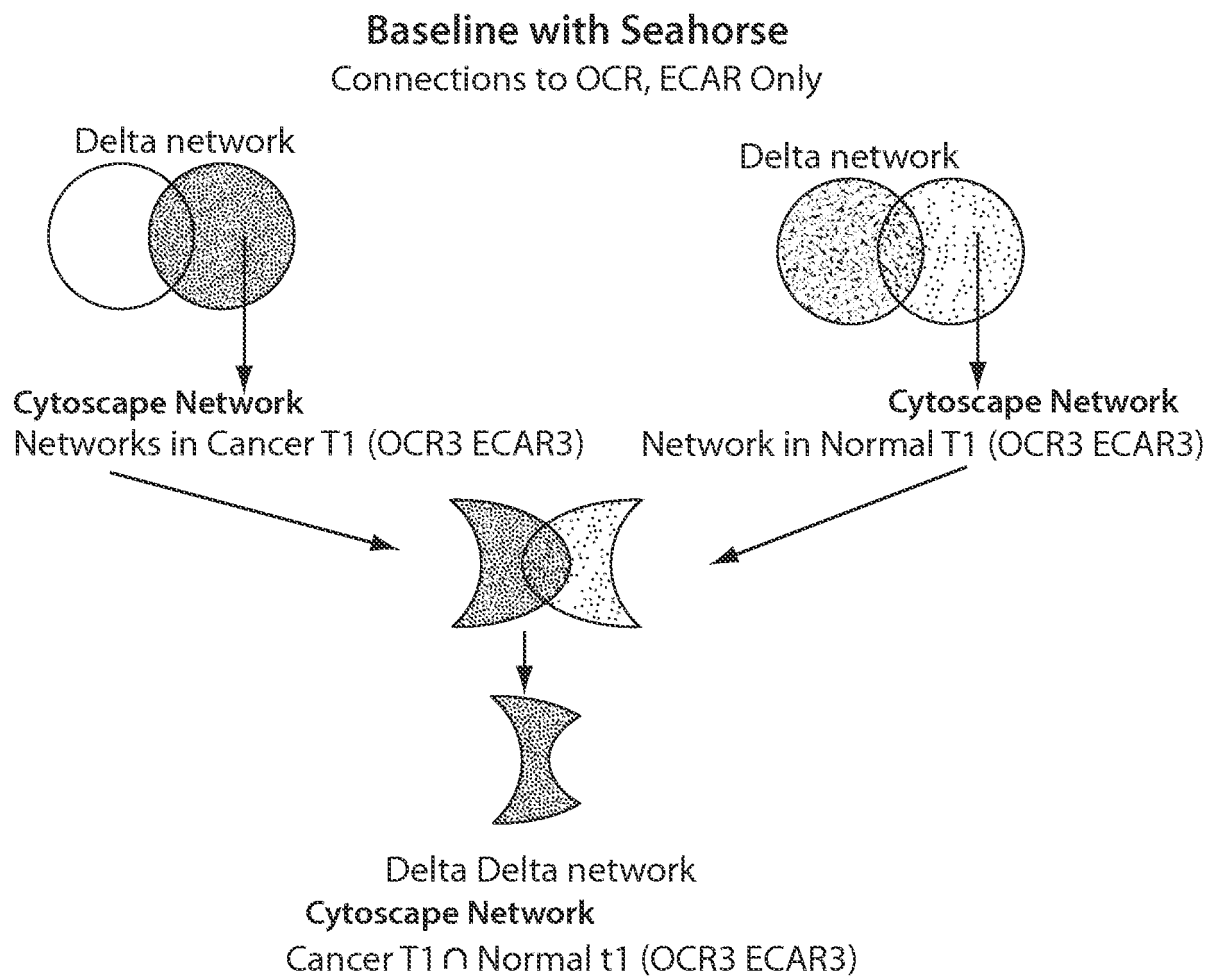


Fig. 26

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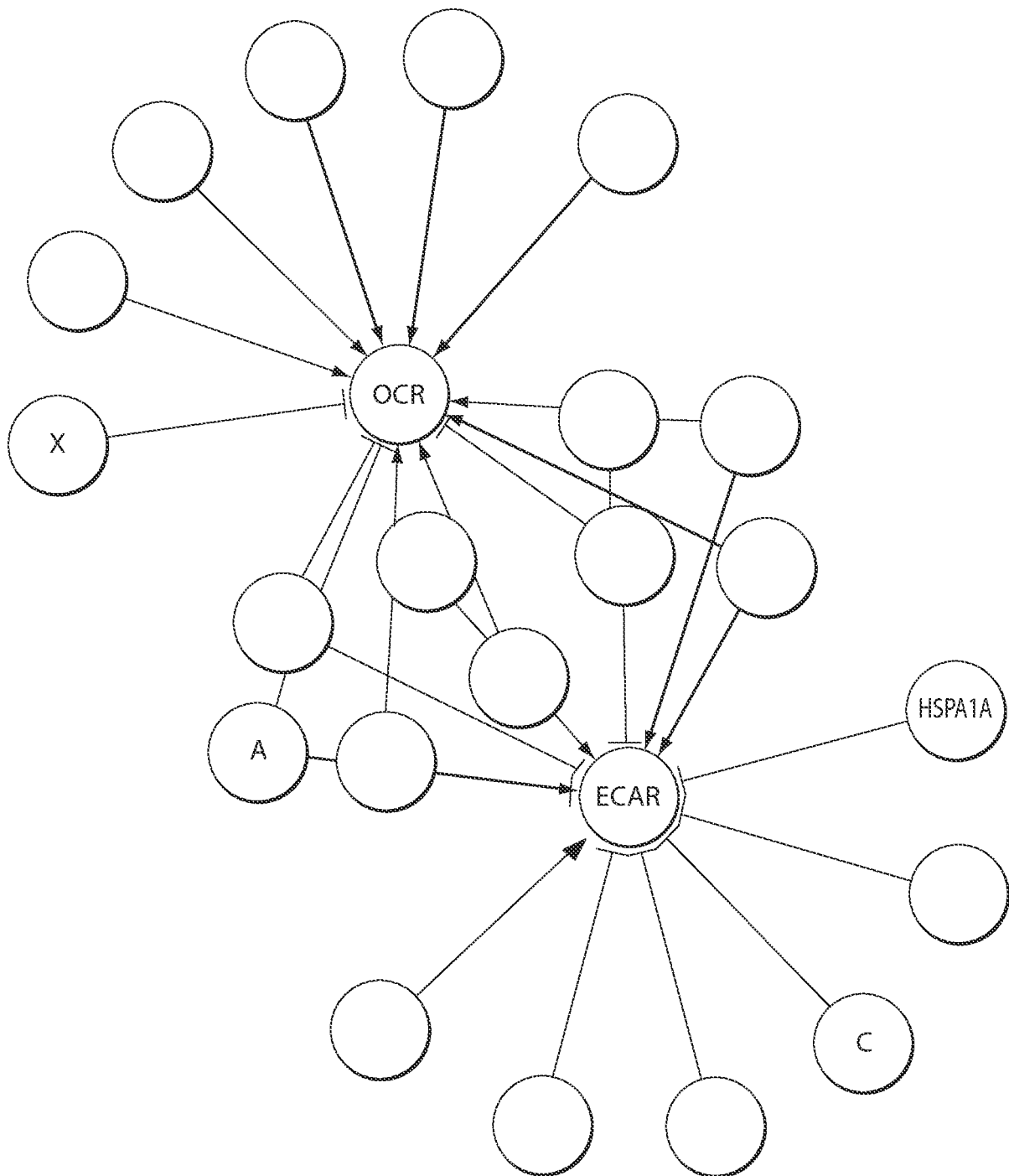


Fig. 27

29/62

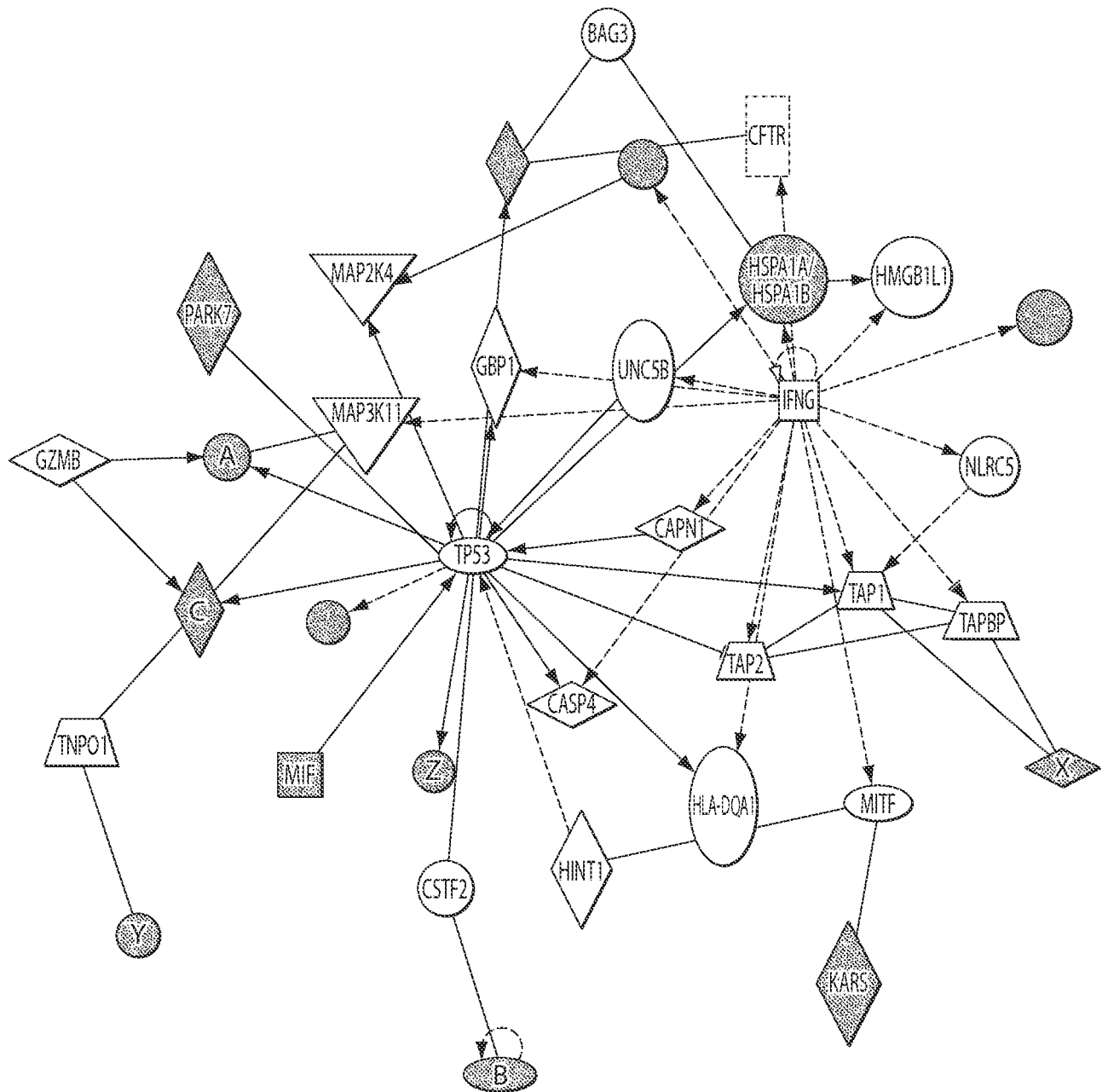


Fig. 28

30/62

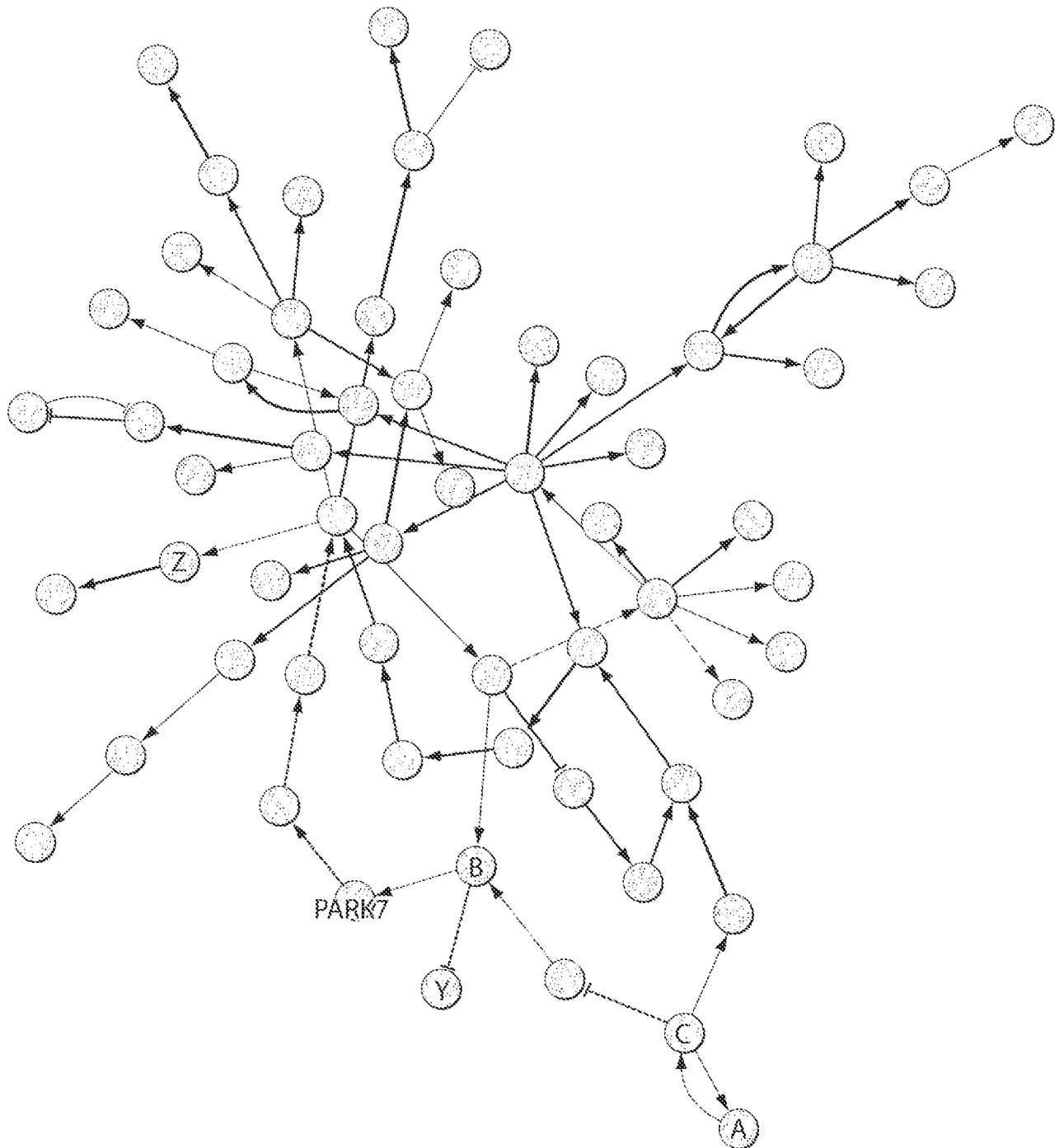


Fig. 29

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Delta-Delta Networks

DD_NG.vs.HG.vs.HGT1.cys

 $[NG \text{ vs. } HG] \text{ vs. } [HG \text{ vs. } HGT1]$

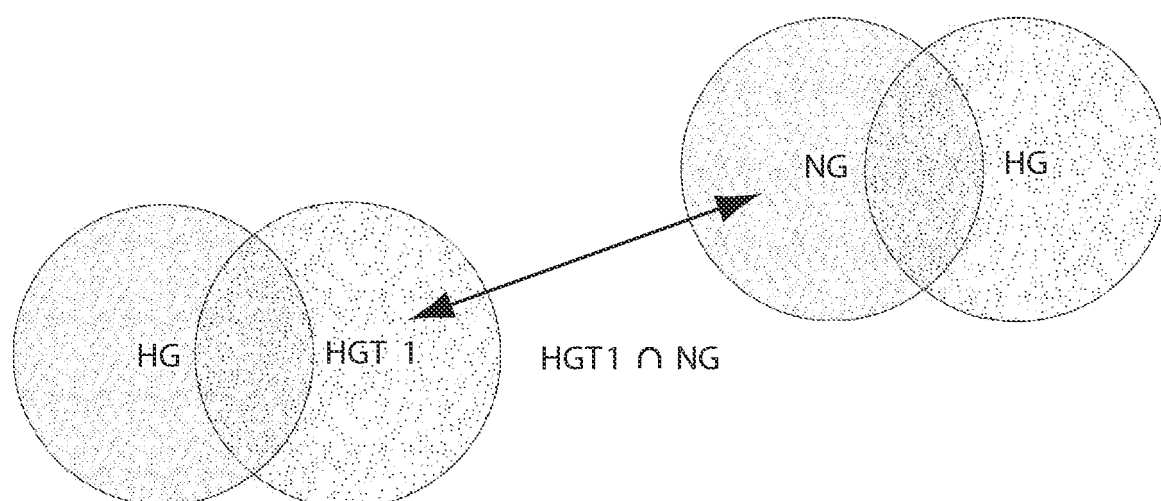


Fig. 30

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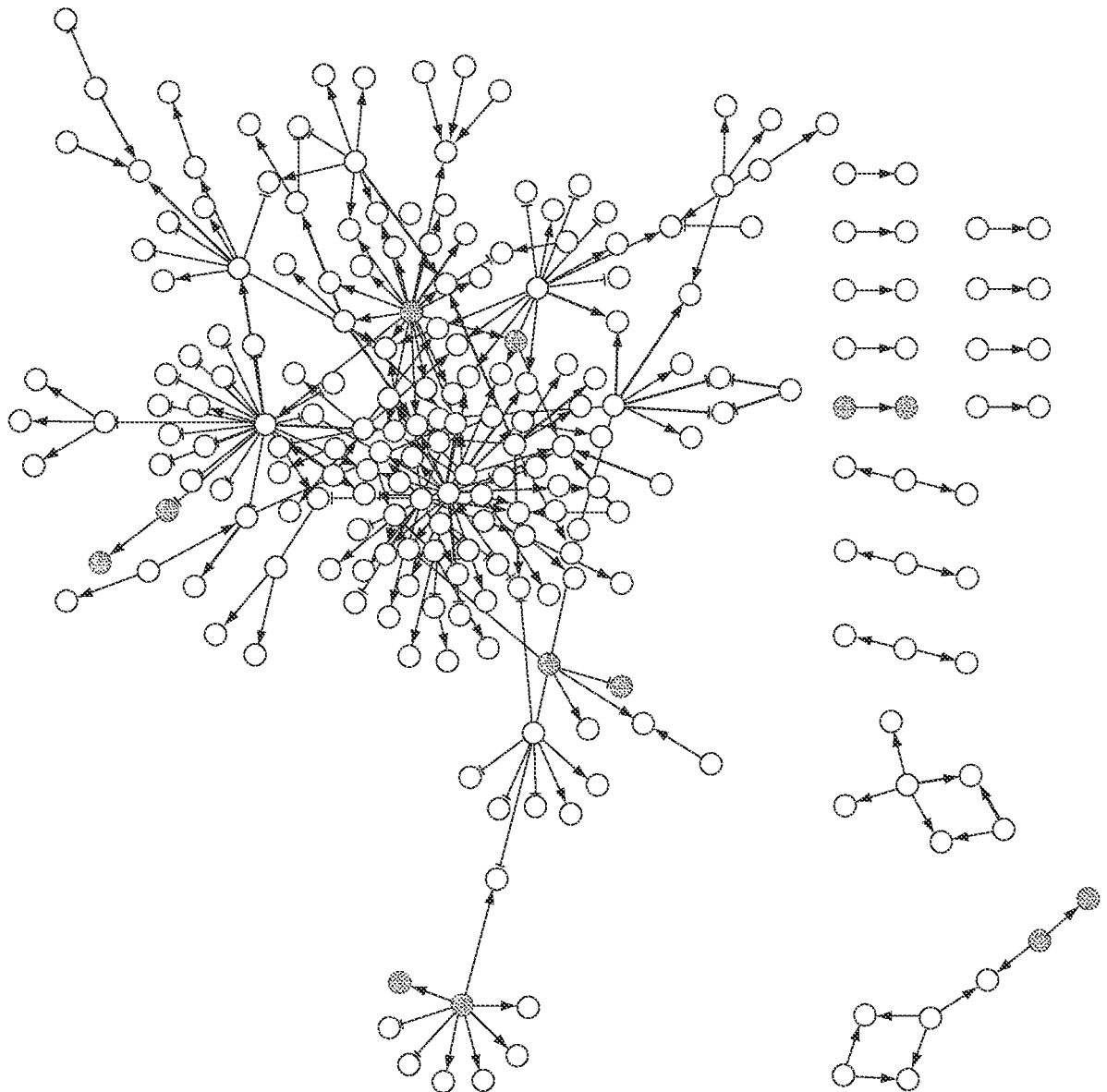


Fig. 31

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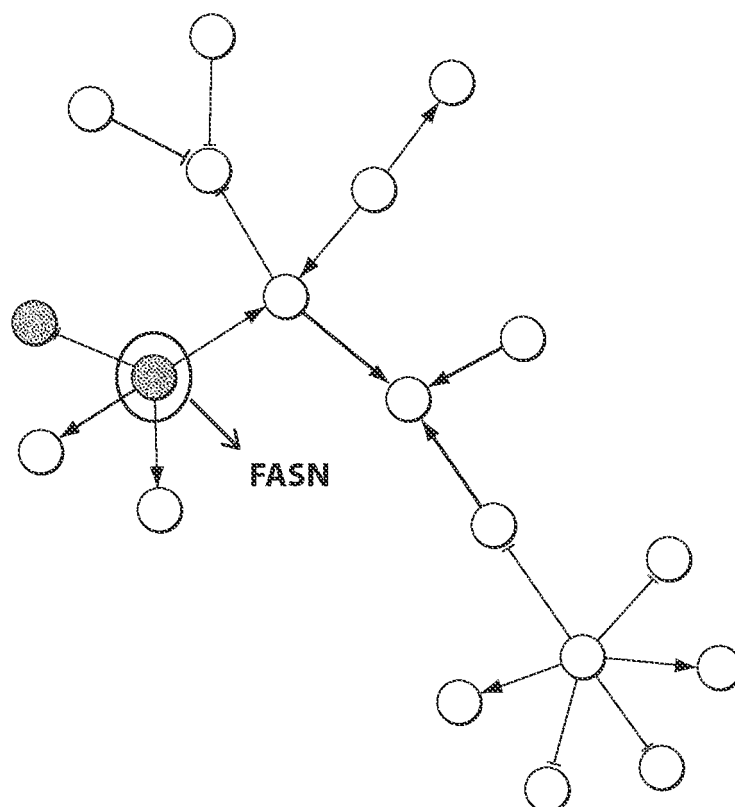


Fig. 32

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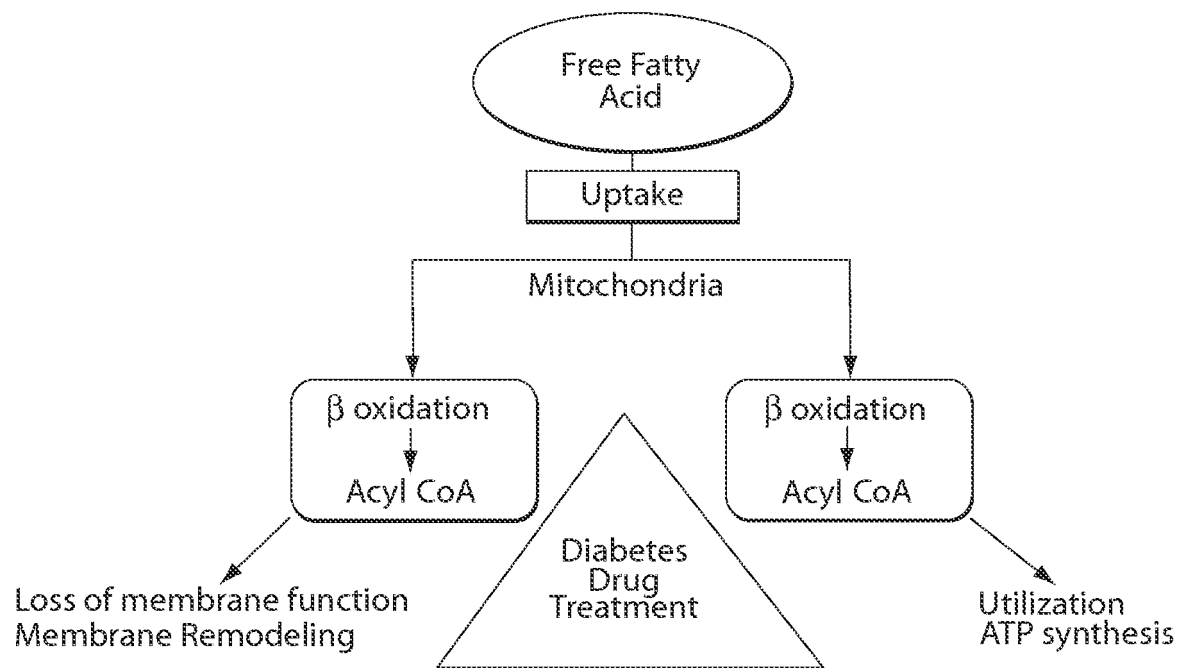


Fig. 33

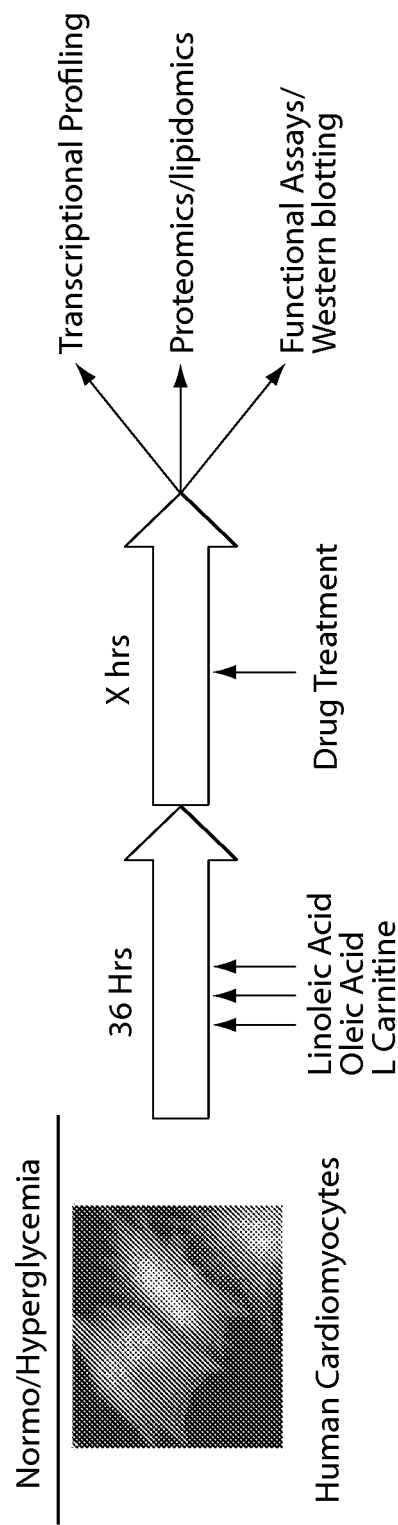


Fig. 34

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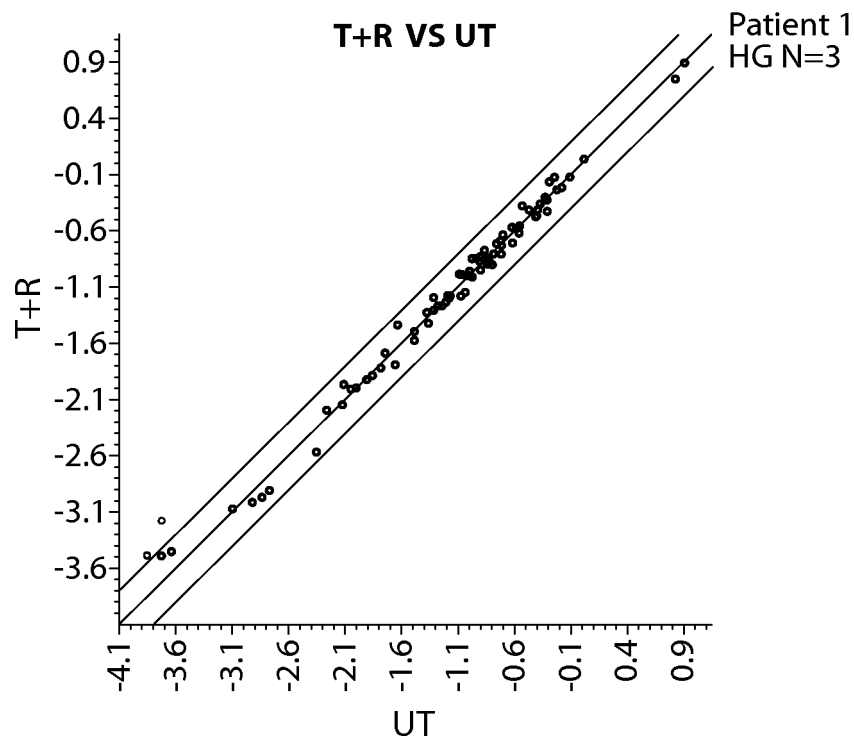
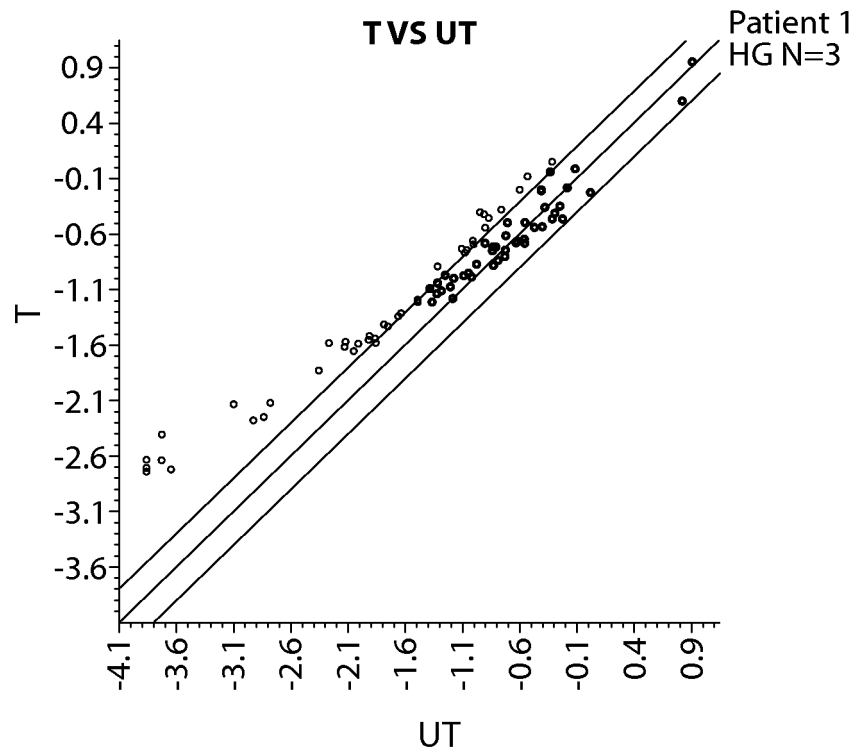


Fig. 35

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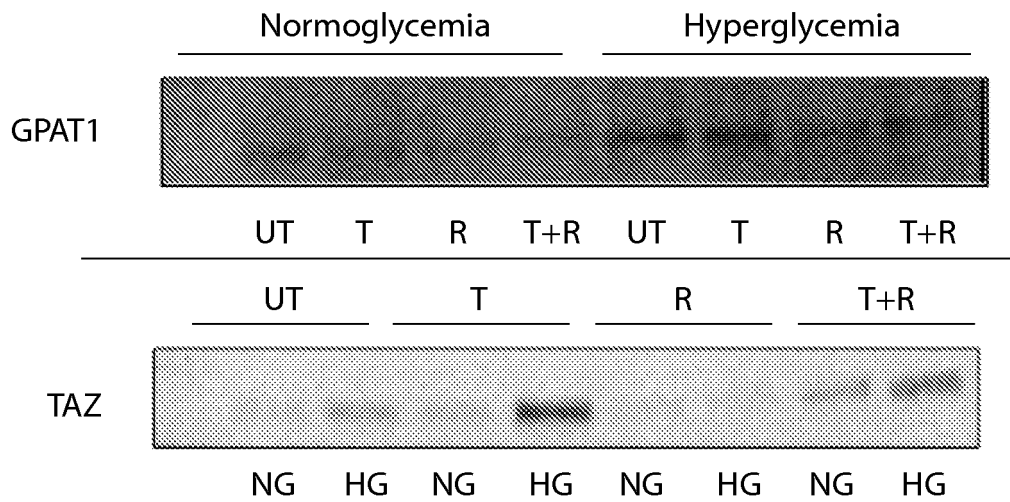


Fig. 36A

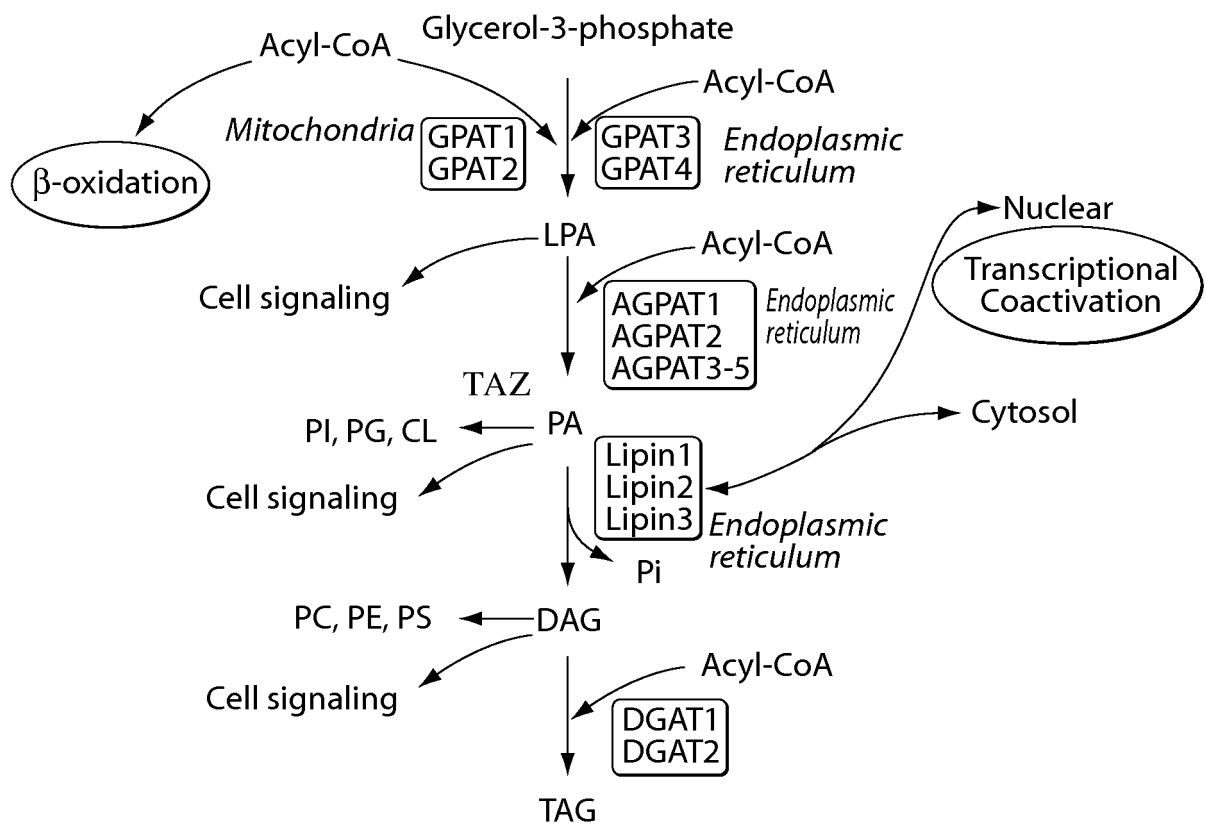


Fig. 36B

38/62

XFAssay_922011_1745.xls

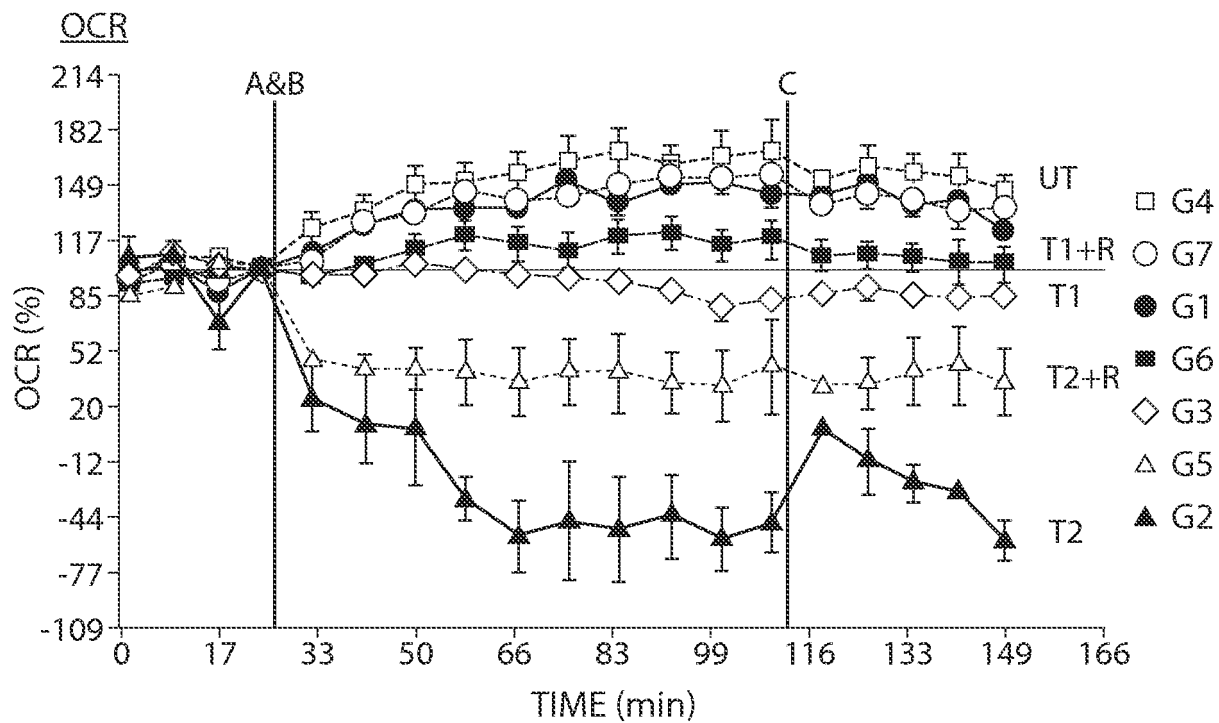


Fig. 37A

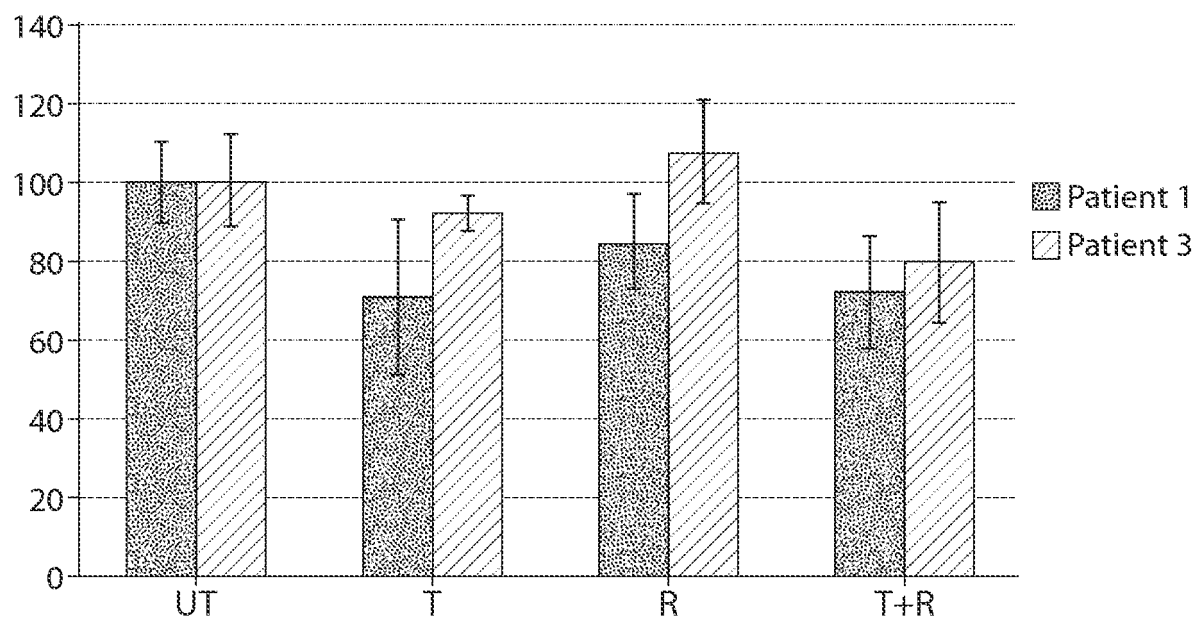


Fig. 37B

39/62

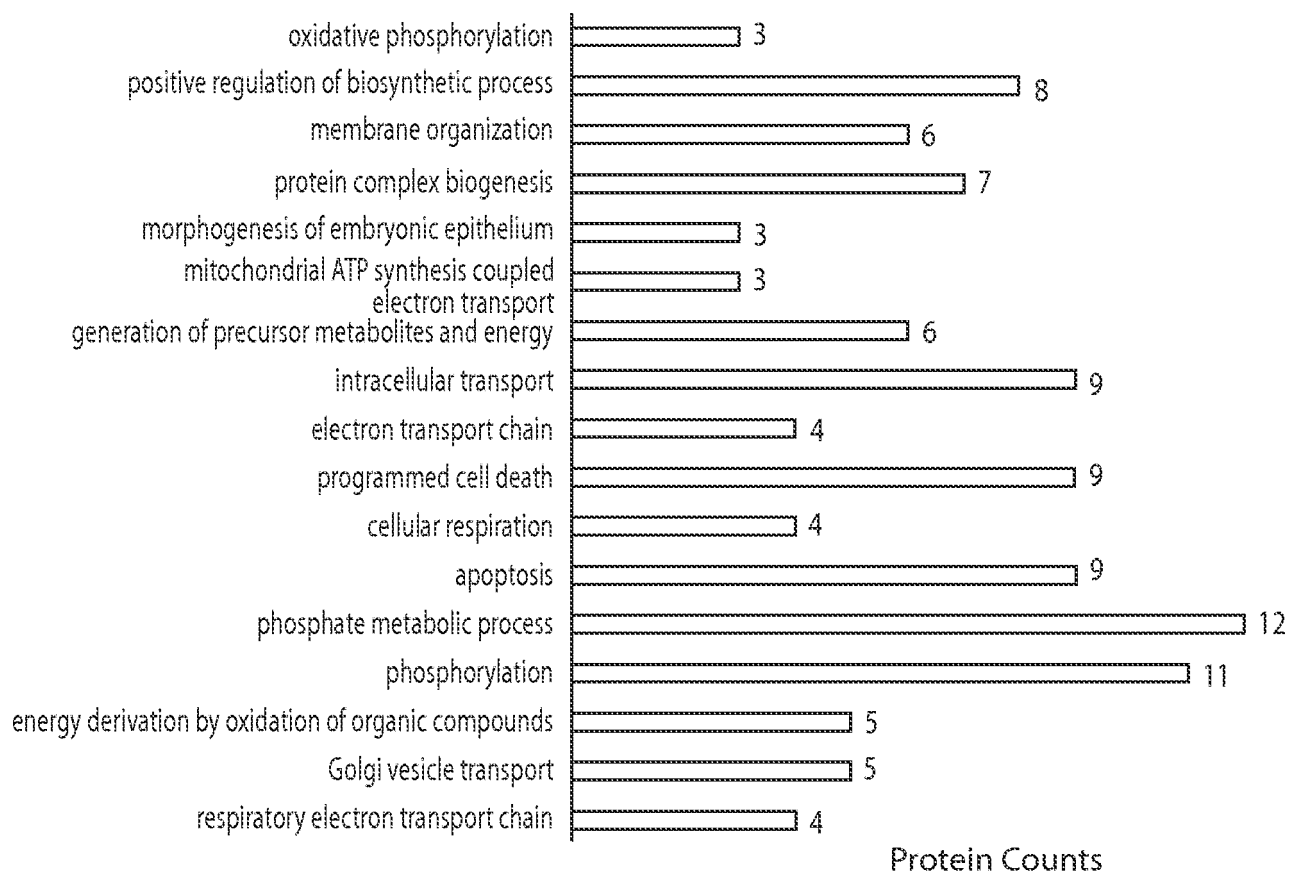


Fig. 38

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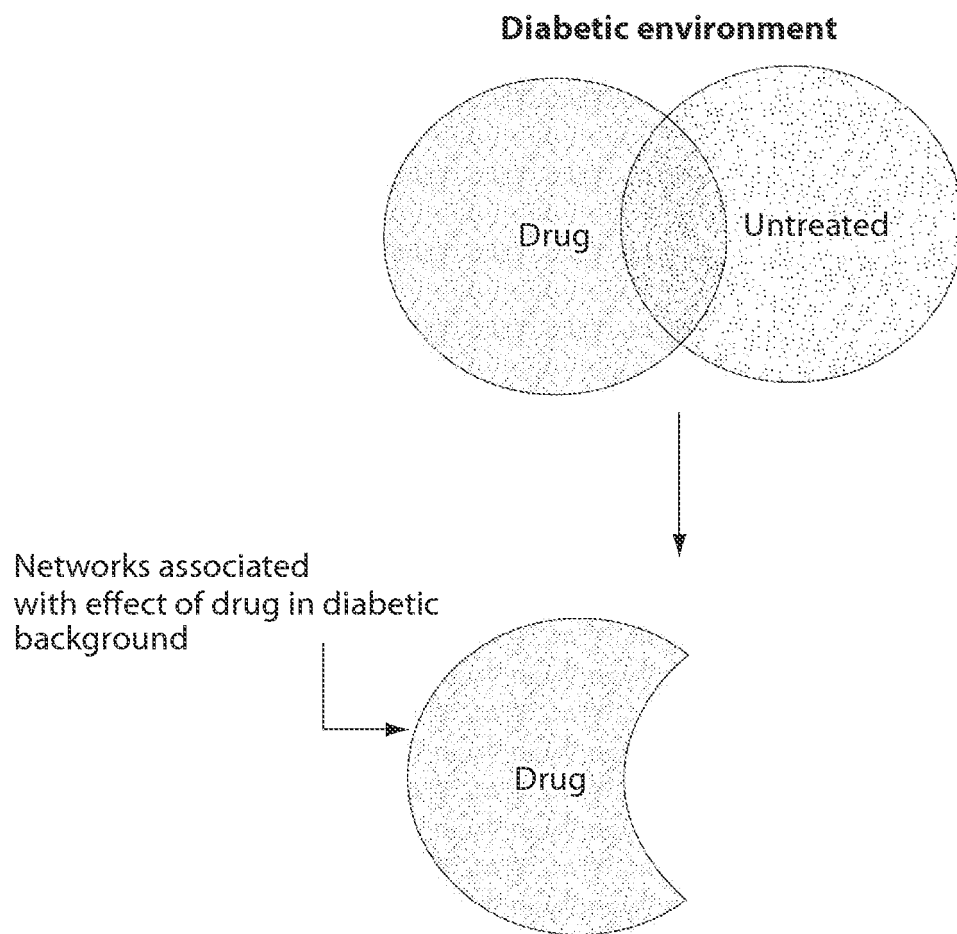


Fig. 39

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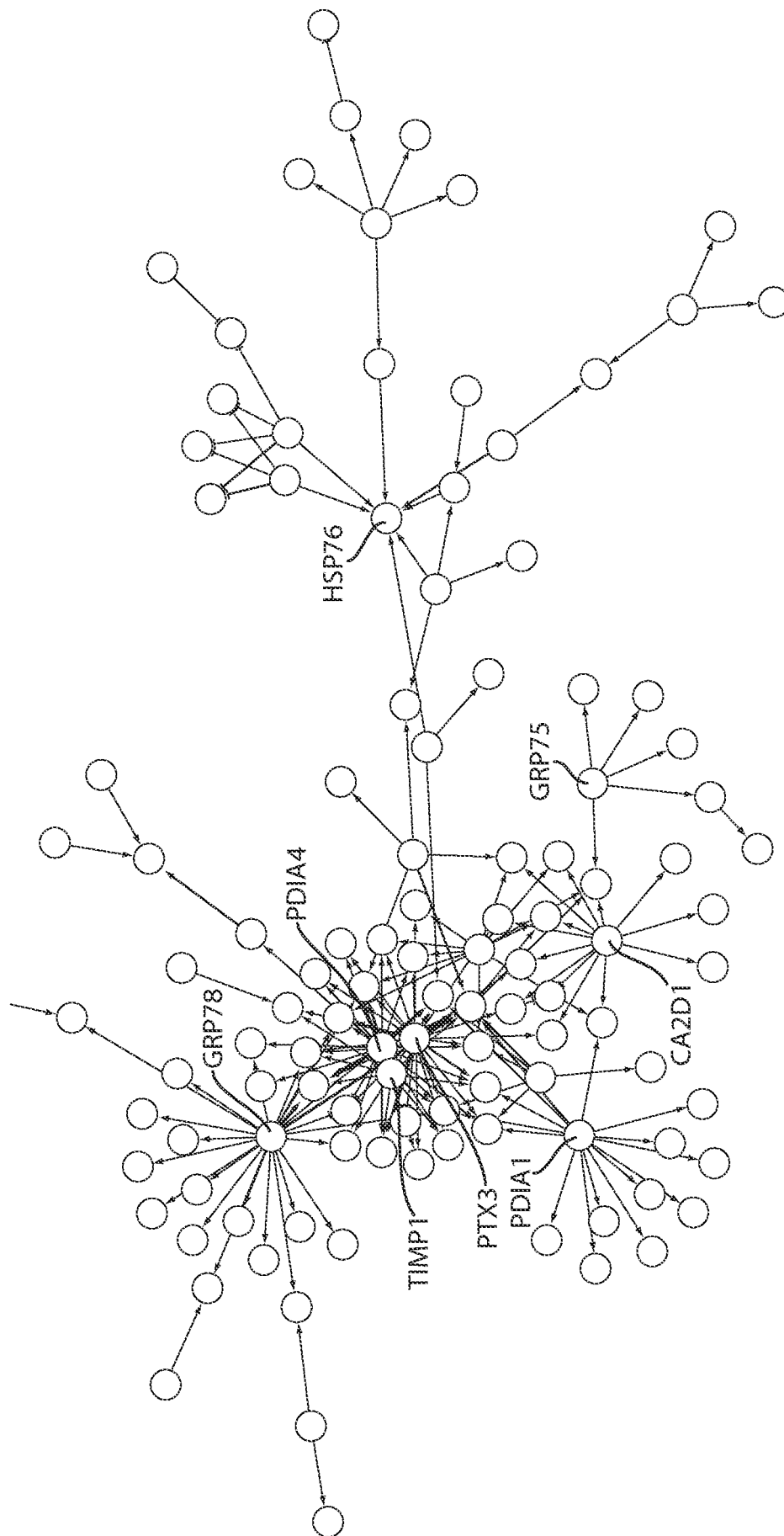
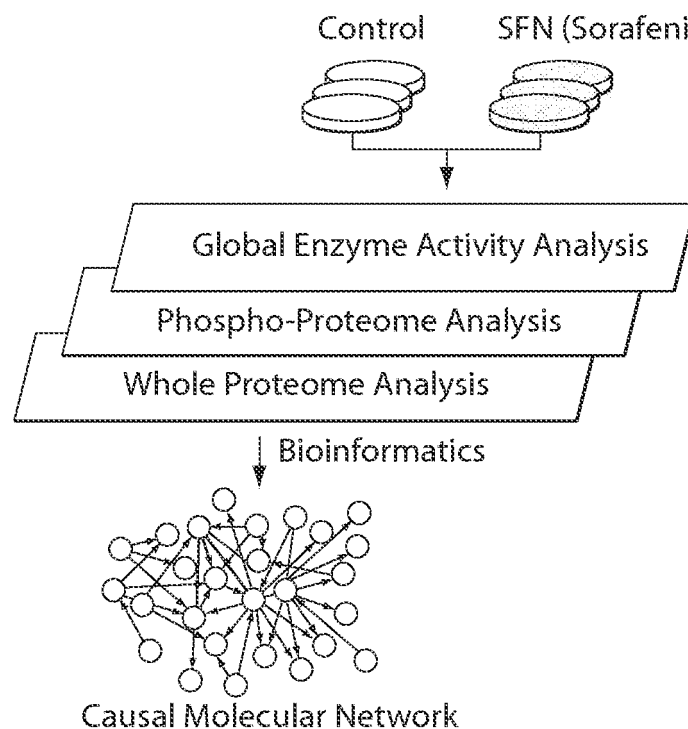


Fig. 40

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"Multi-Proteomics" techniques to elucidate enzyme/kinase activity



Applying "Multi-Proteomics" techniques to elucidate enzyme/kinase activity. Integration of multiple proteomics datasets generated from *in-vitro* model provides a unique system to understand causal relationship between enzymes/kinases and their metabolites/ substrates in the context of global changes in cellular proteome.

Fig. 41A

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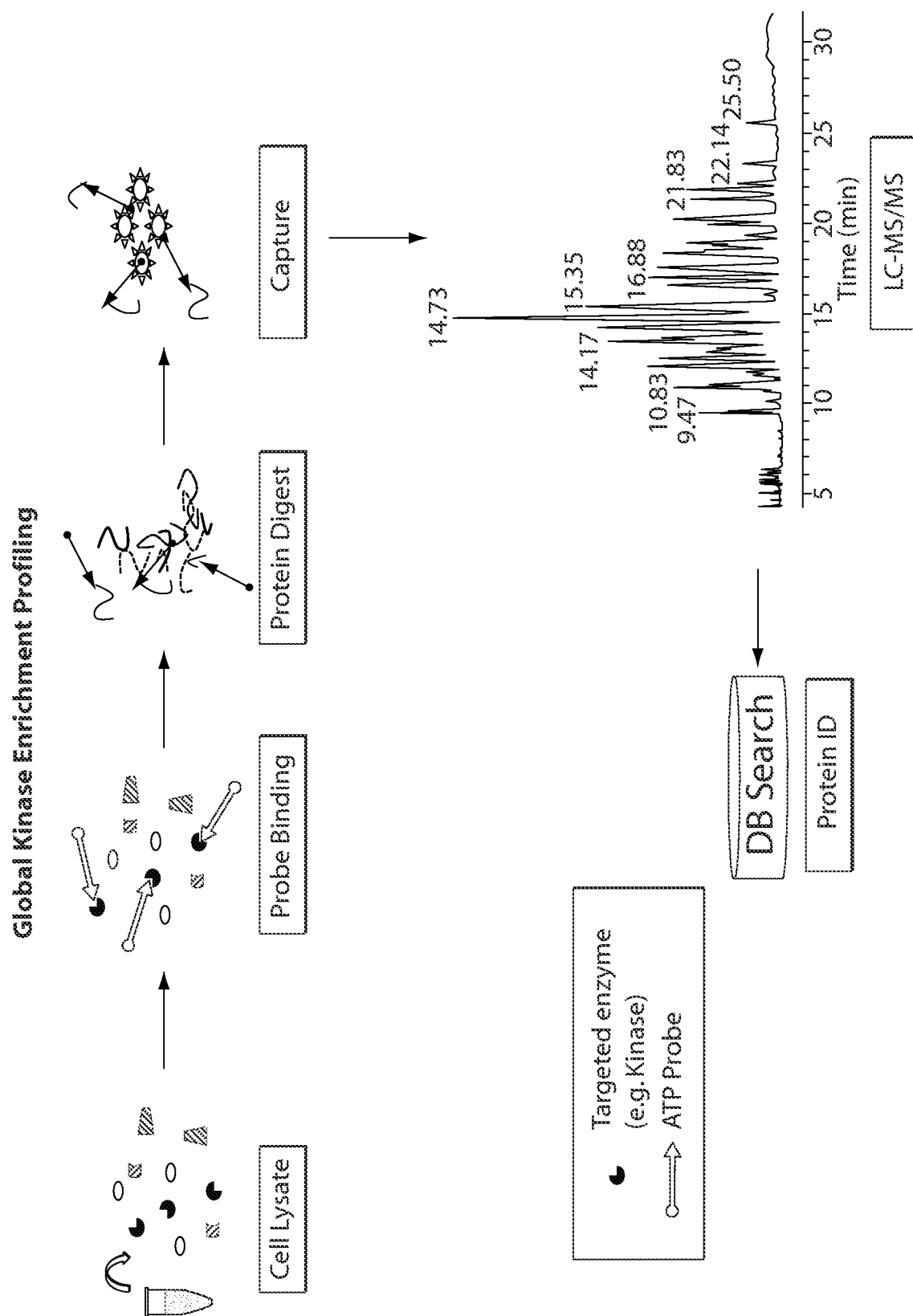


Fig. 41B

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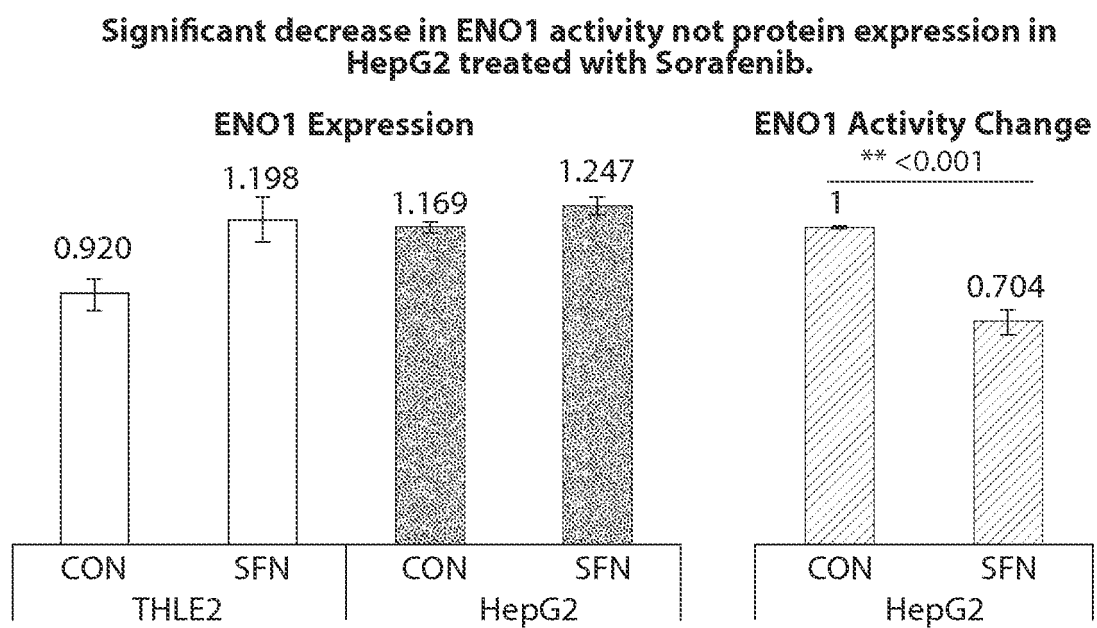


Fig. 42

45/62

Significant decrease in PGK1 activity not protein expression in HepG2 treated with Sorafenib.

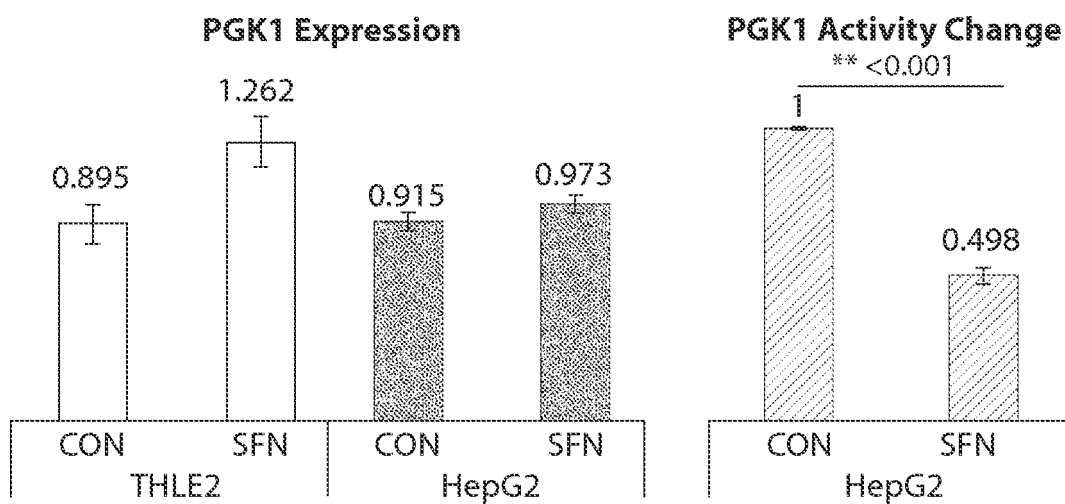


Fig. 43

Significant decrease in LDHA activity in HepG2 treated with Sorafenib.

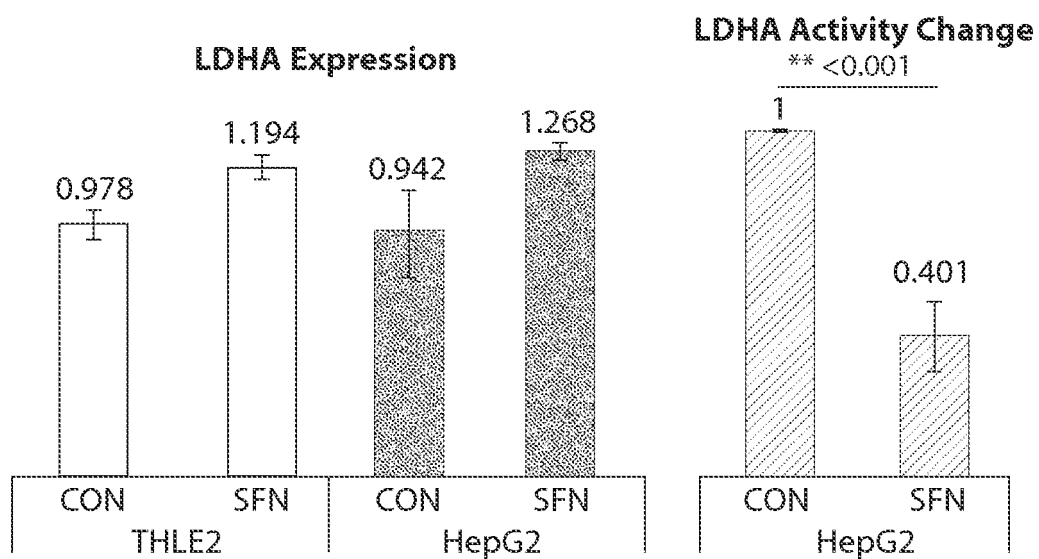


Fig. 44

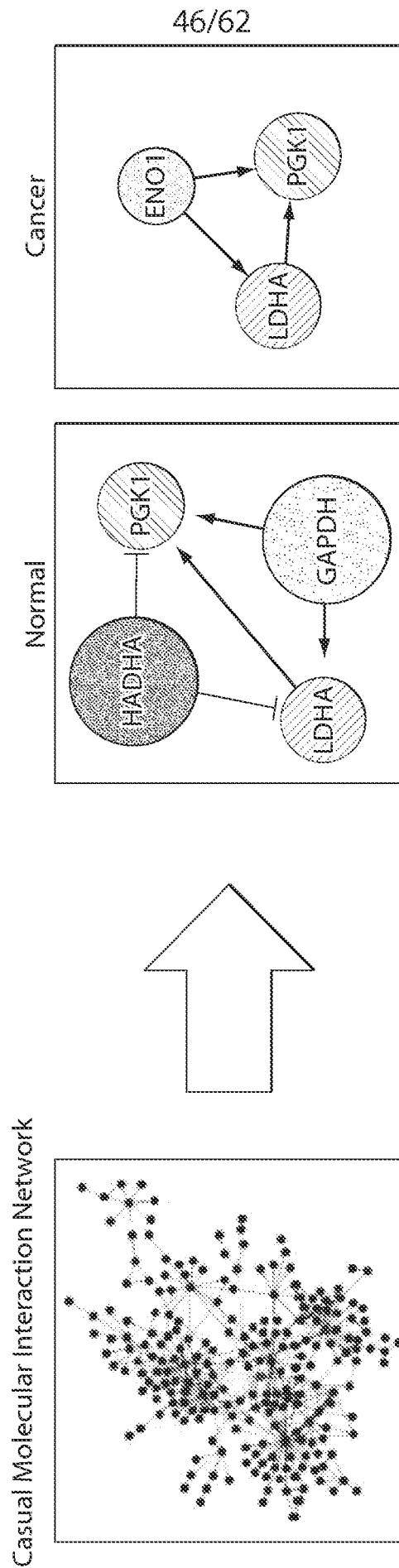


Fig. 45

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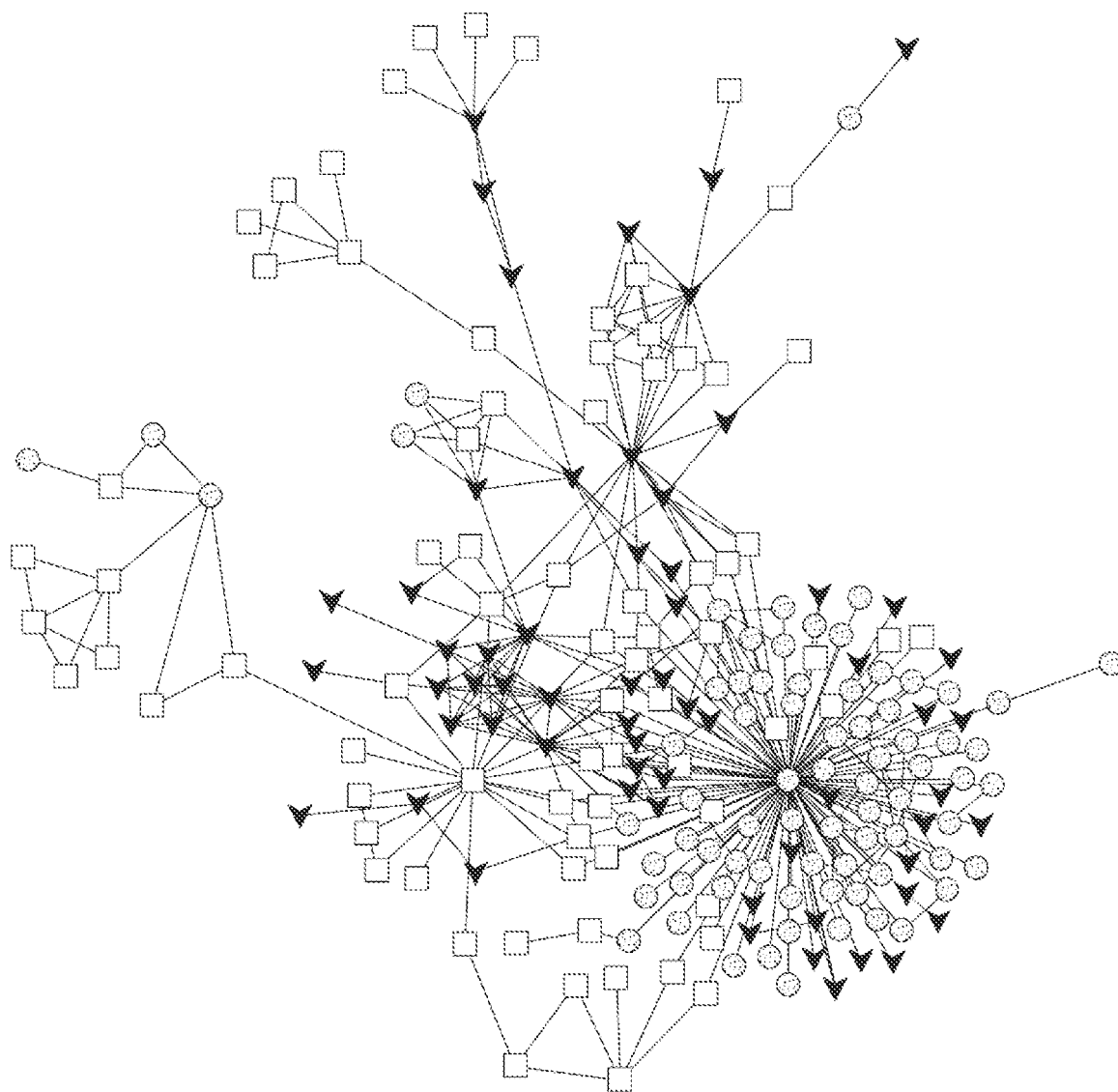


Fig. 46

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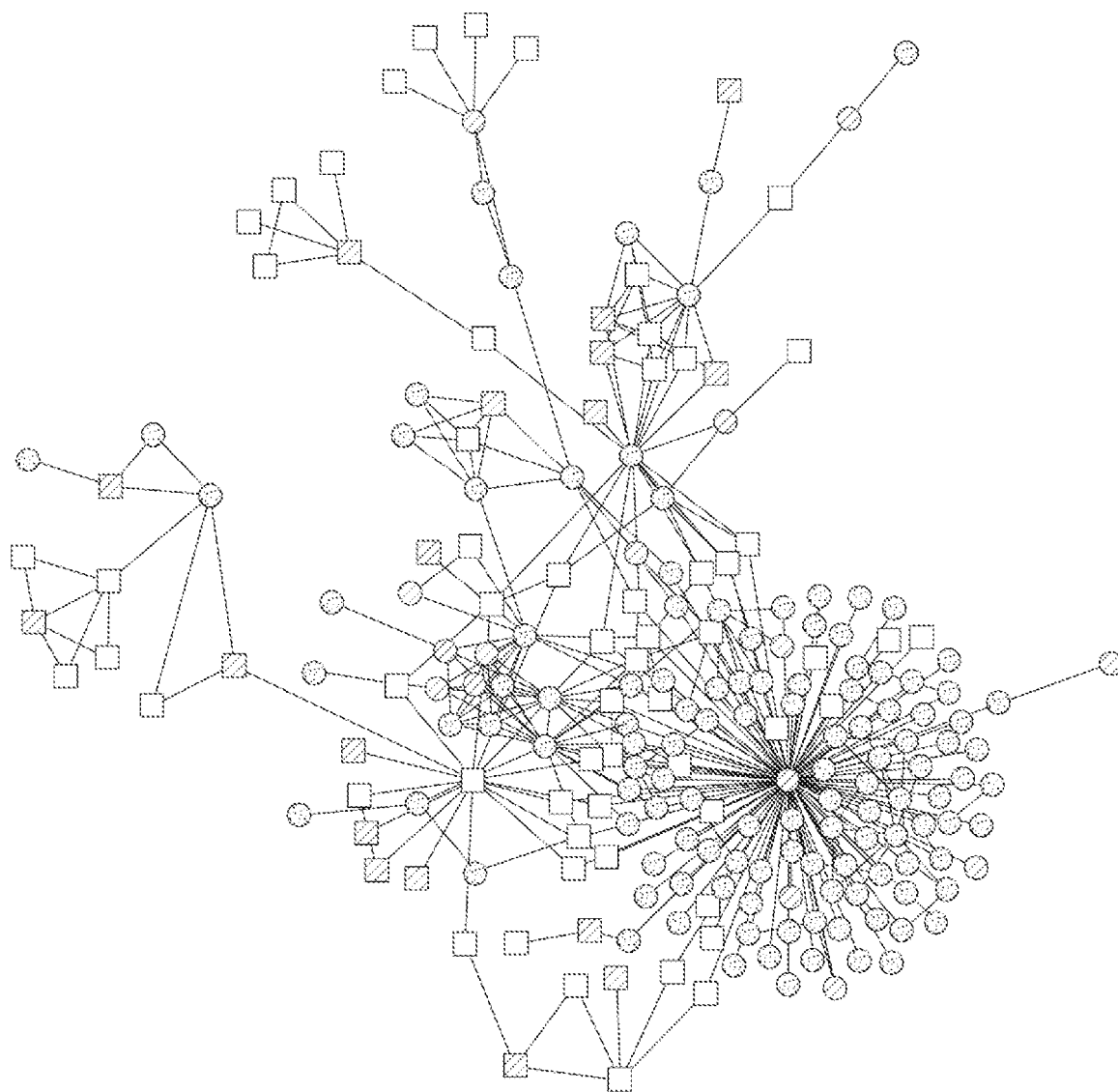


Fig. 47

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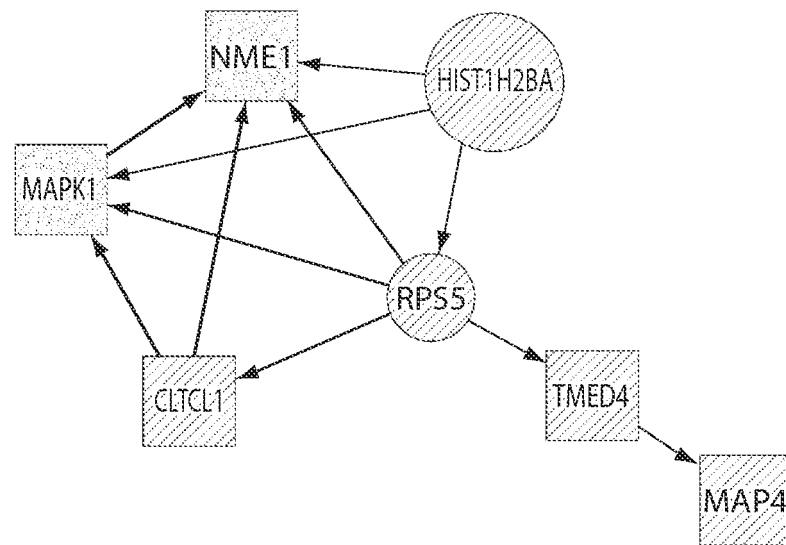


Fig. 48

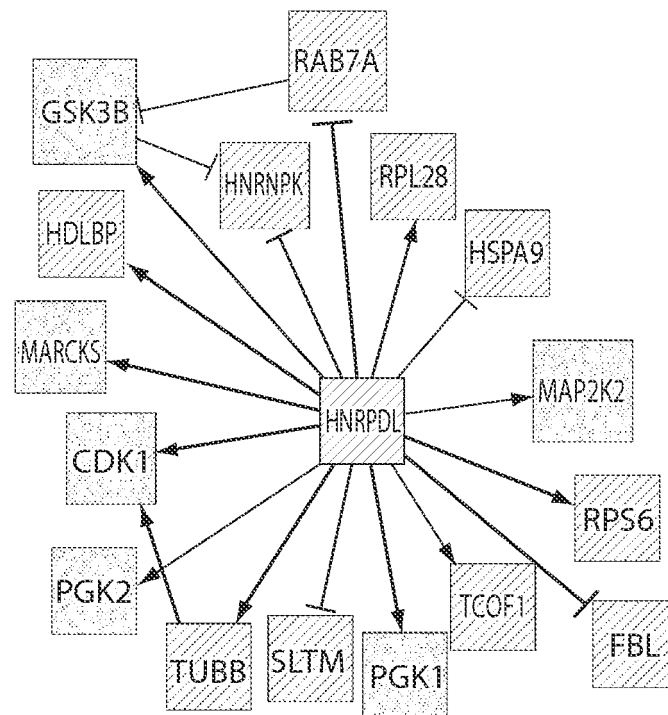


Fig. 49

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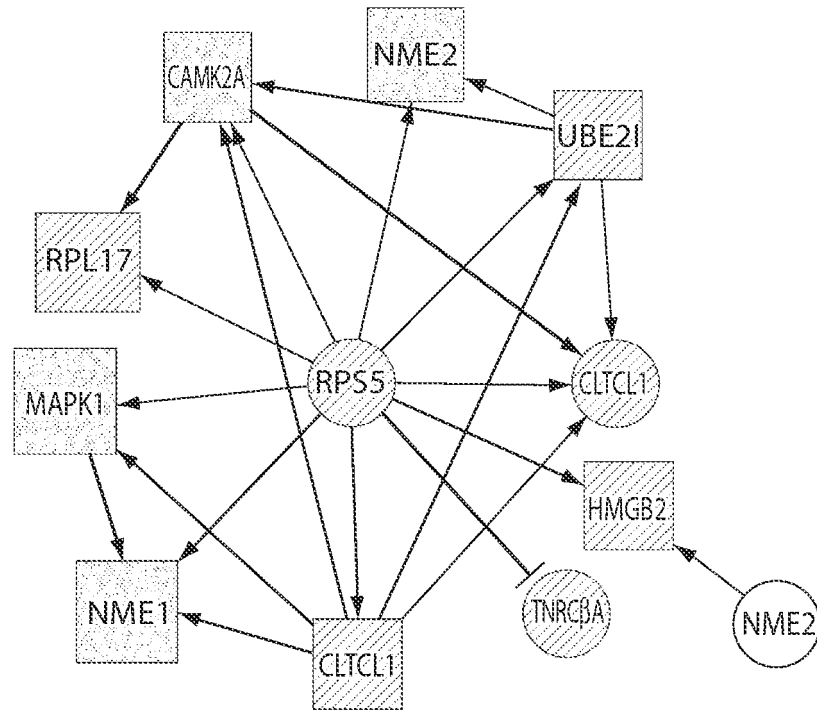


Fig. 50

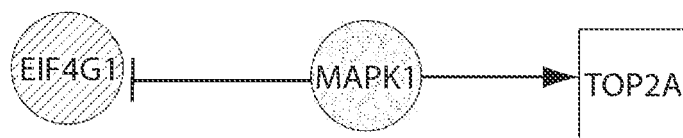


Fig. 51

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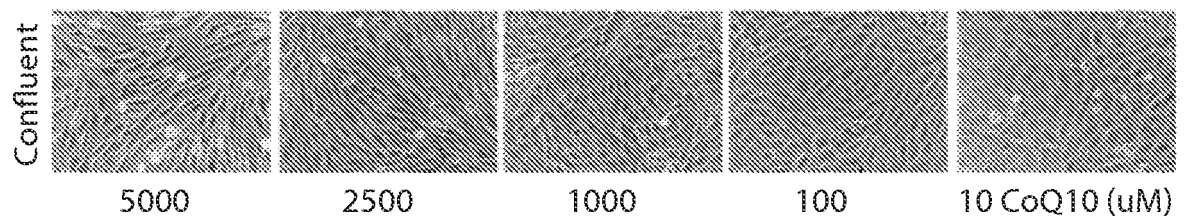


Fig. 52A

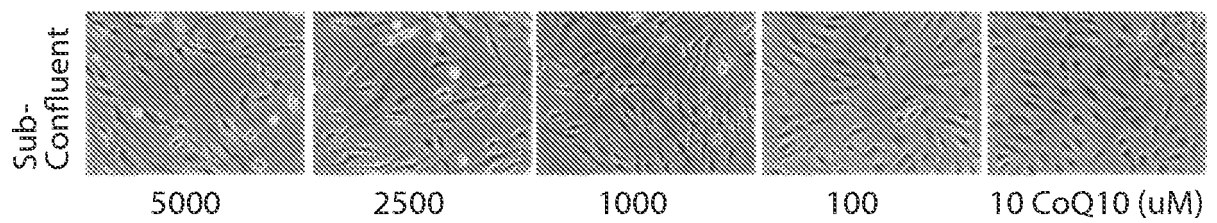


Fig. 52B

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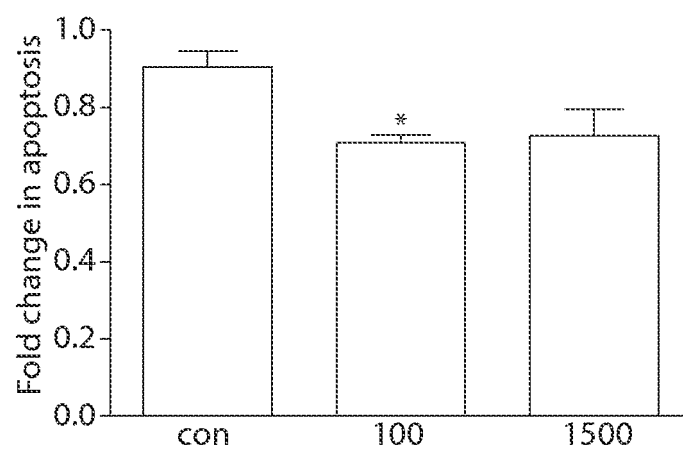


Fig. 53A

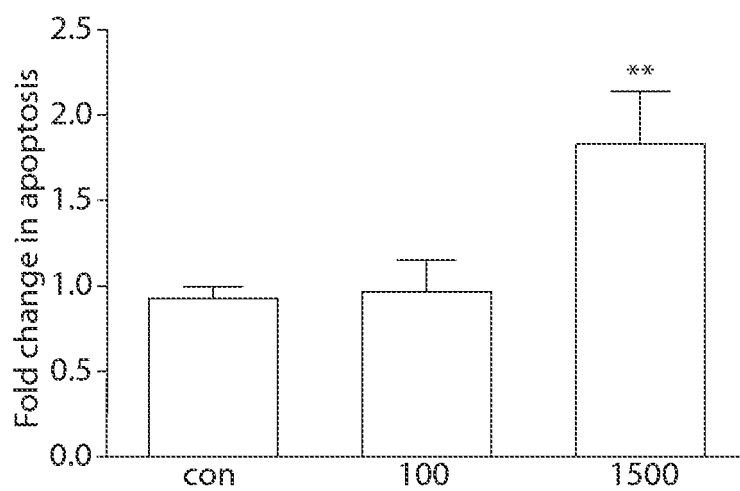


Fig. 53B

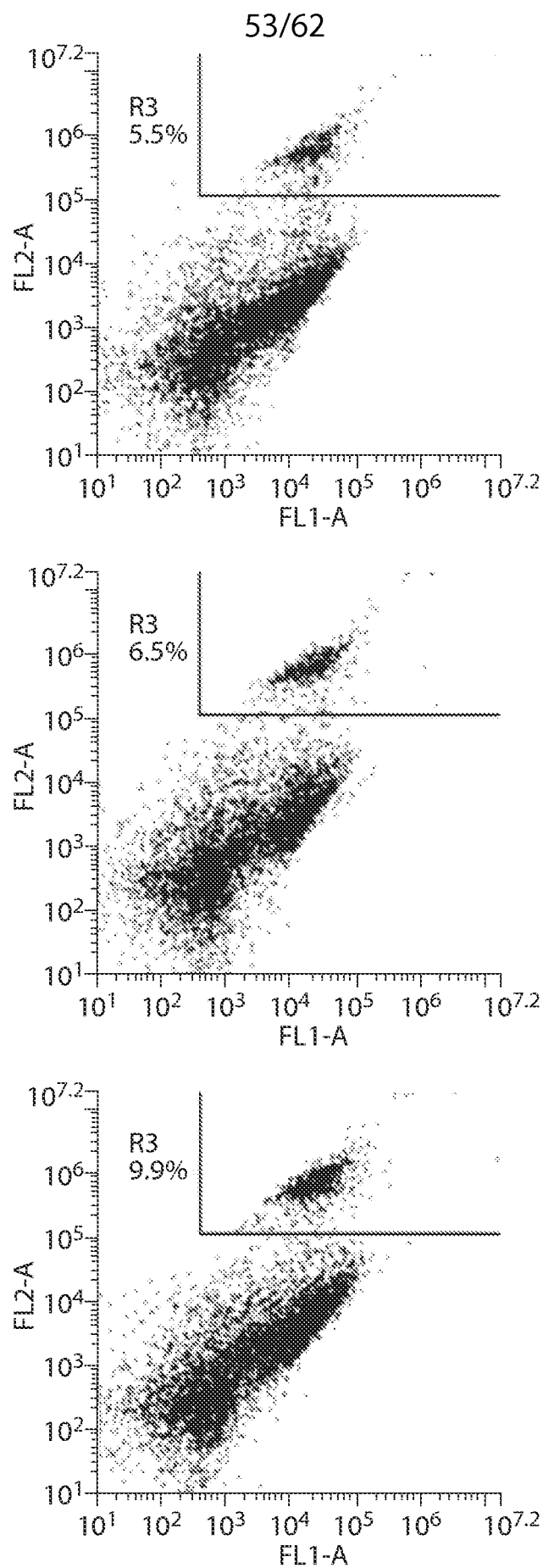


Fig. 53C

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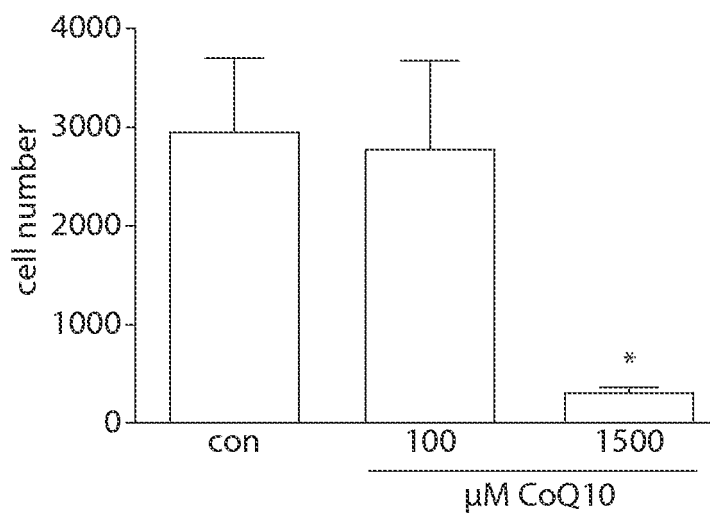


Fig. 54A

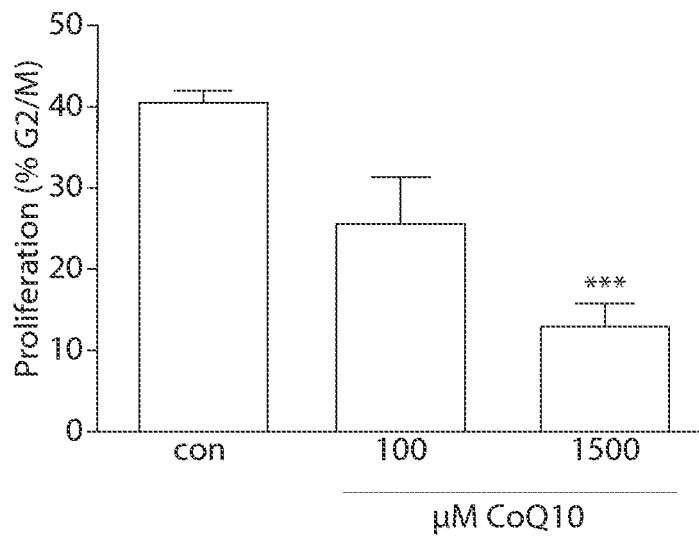


Fig. 54B

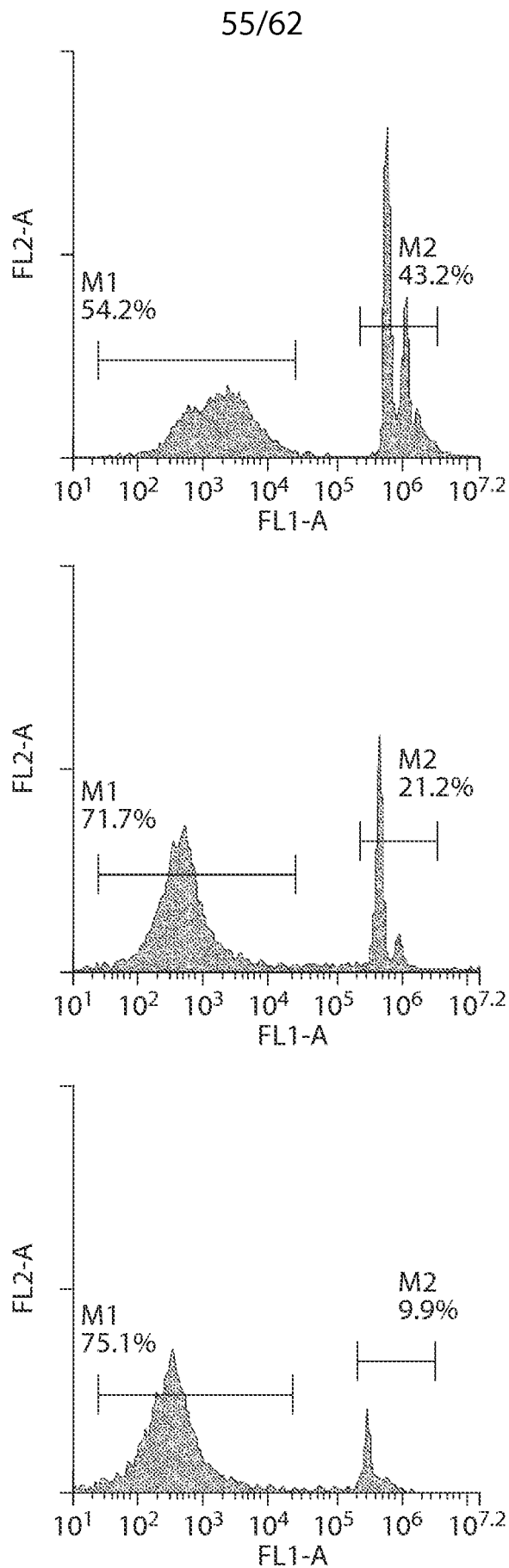


Fig. 54C

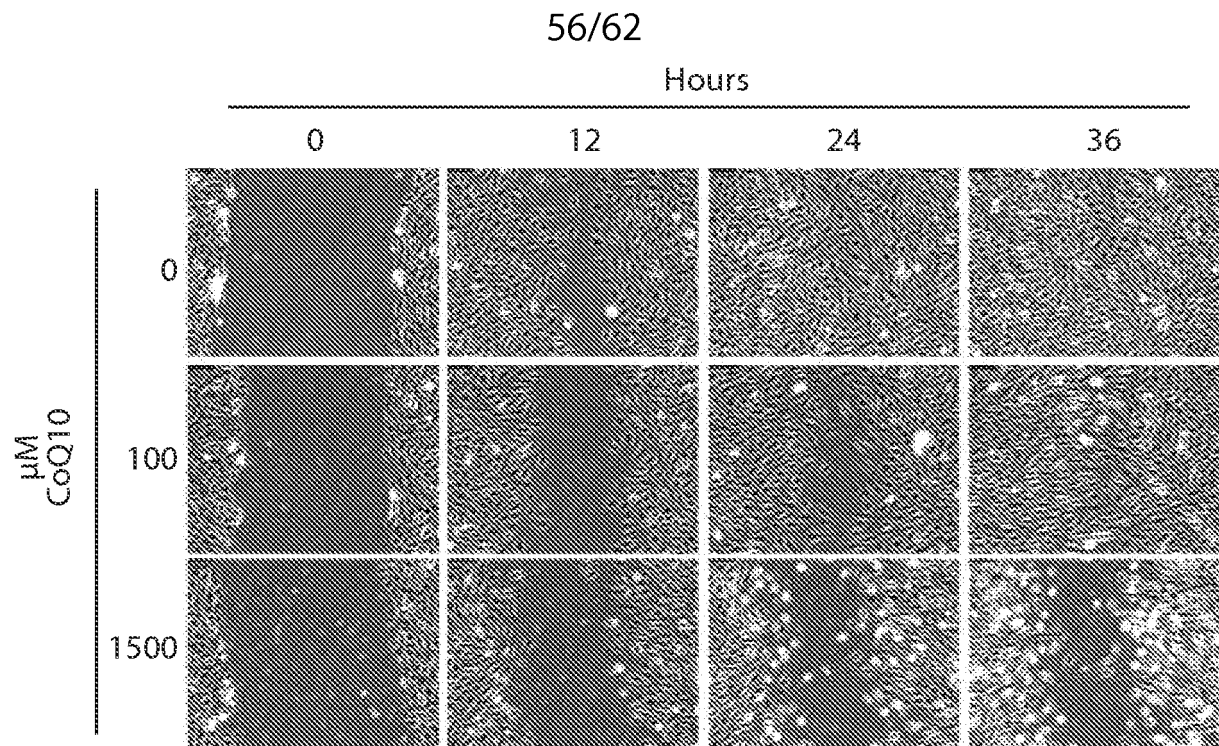


Fig. 55

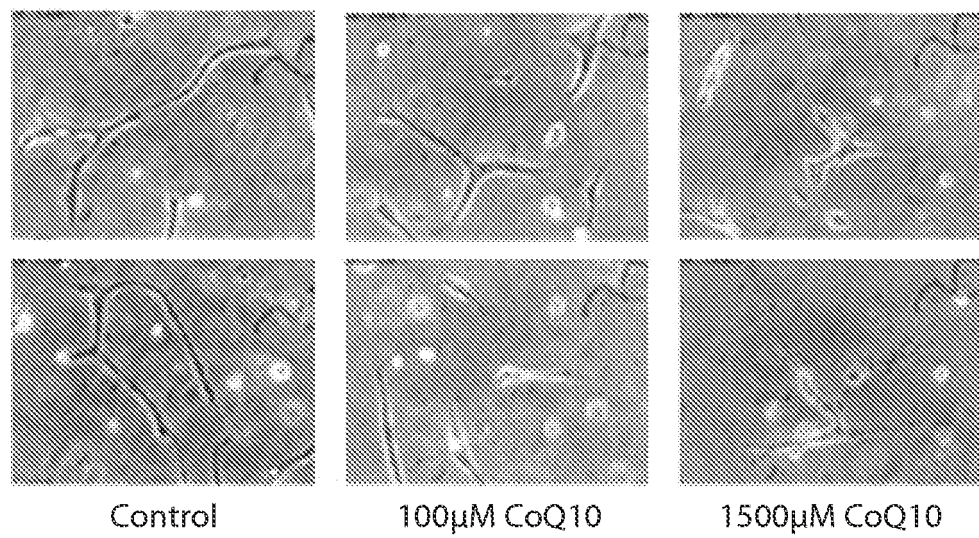


Fig. 56

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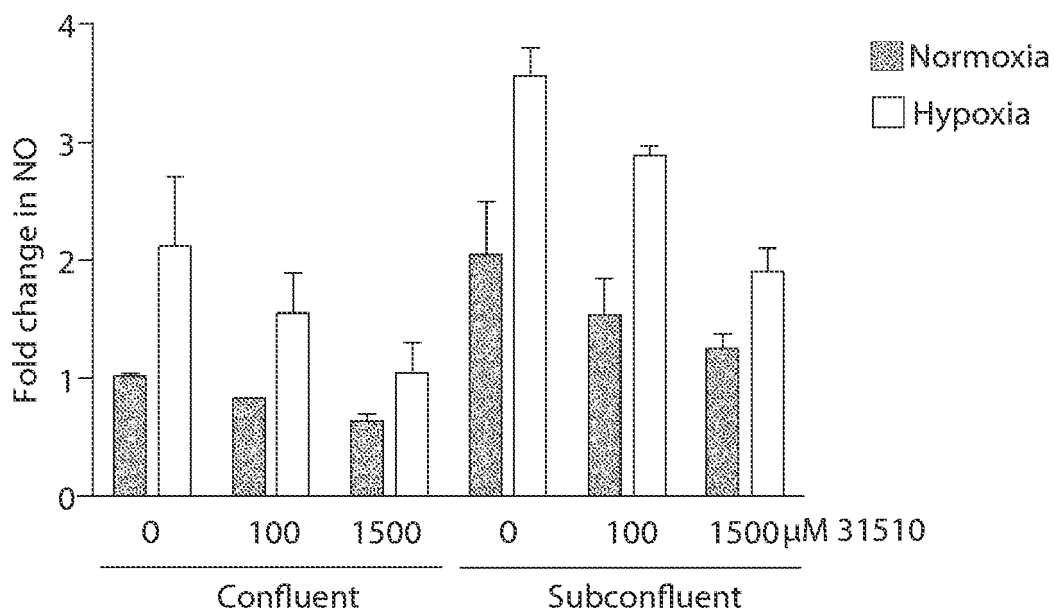


Fig. 57A

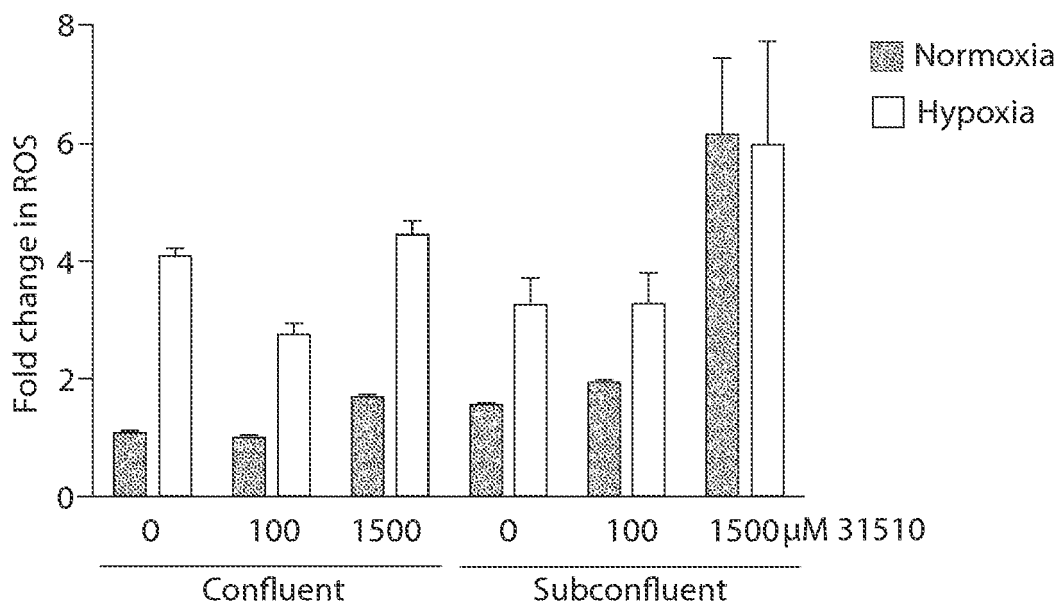


Fig. 57B

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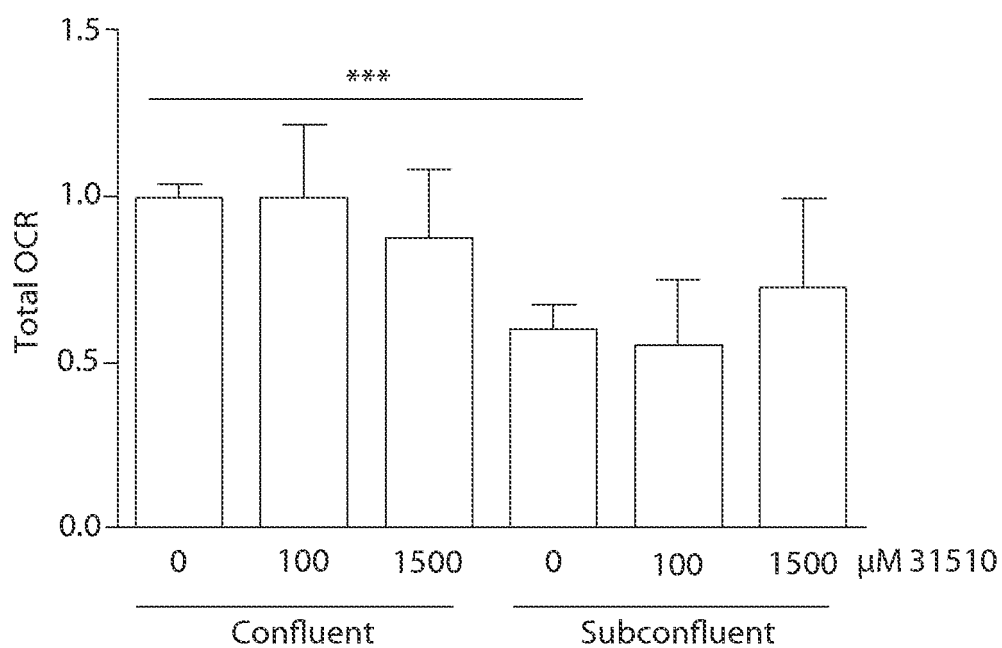


Fig. 58A

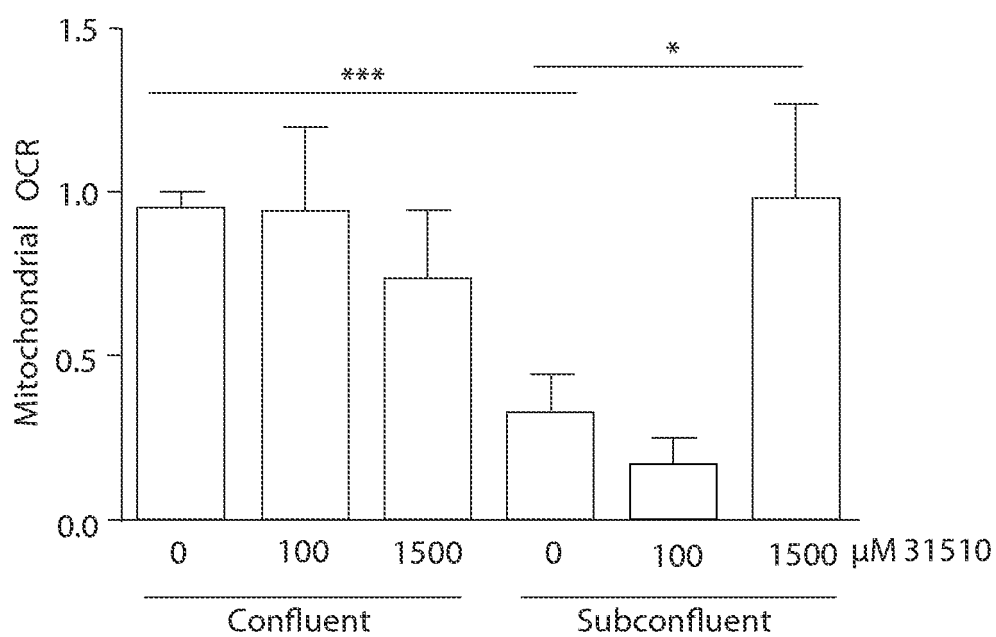


Fig. 58B

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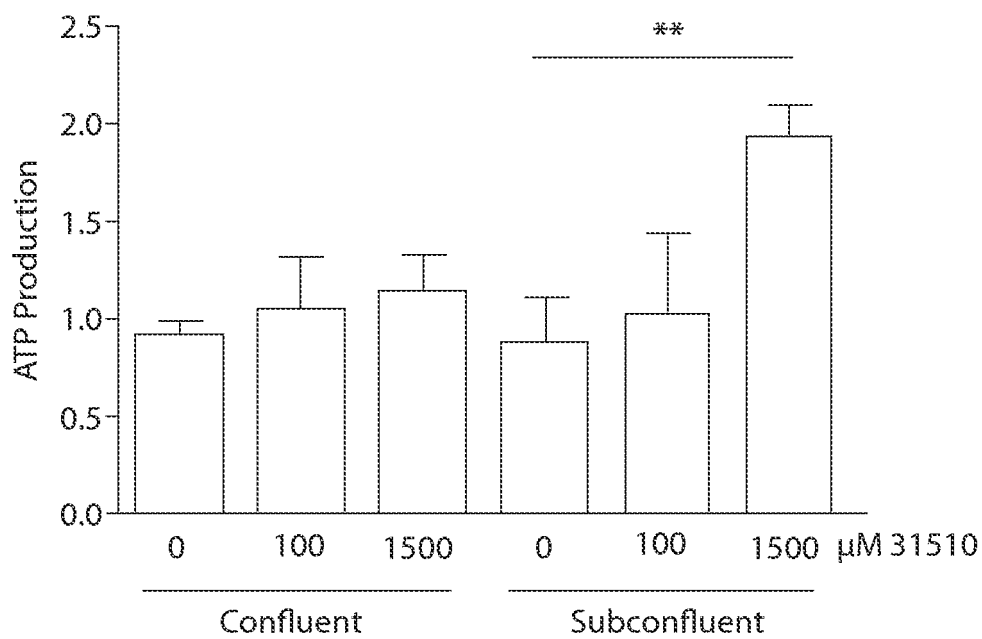


Fig. 58C

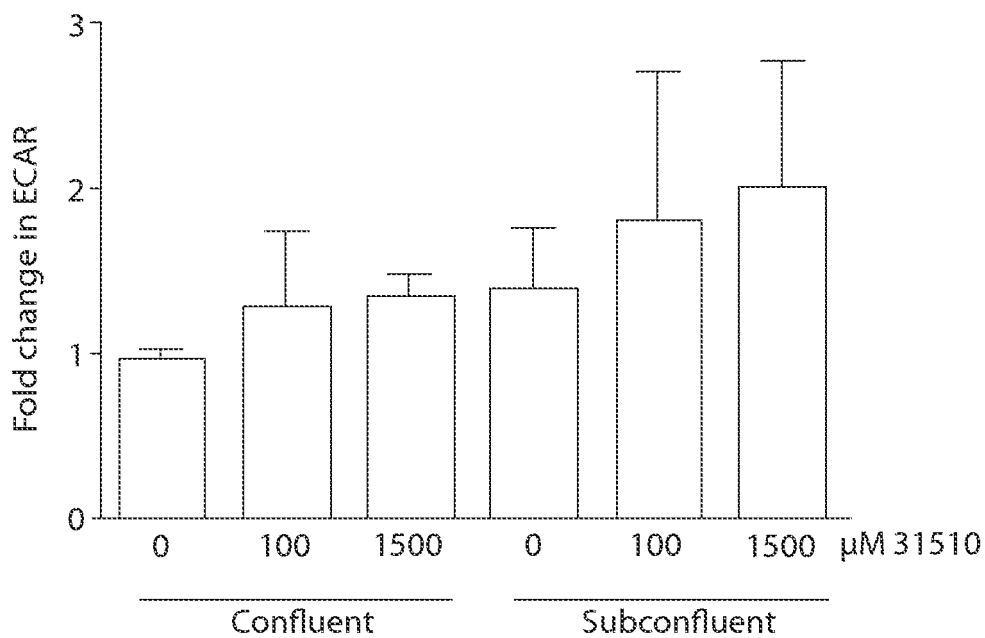


Fig. 58D

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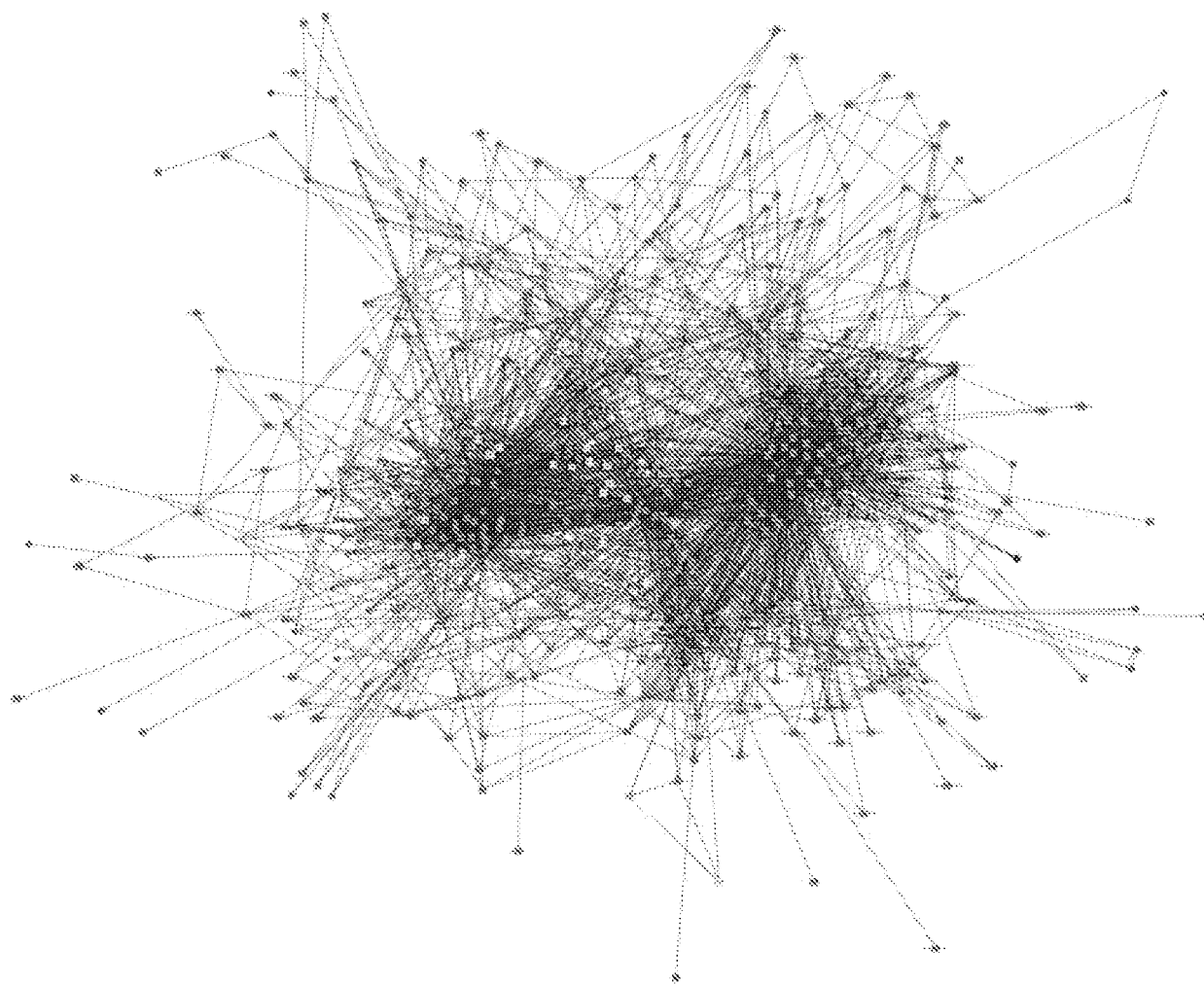


Fig. 59A

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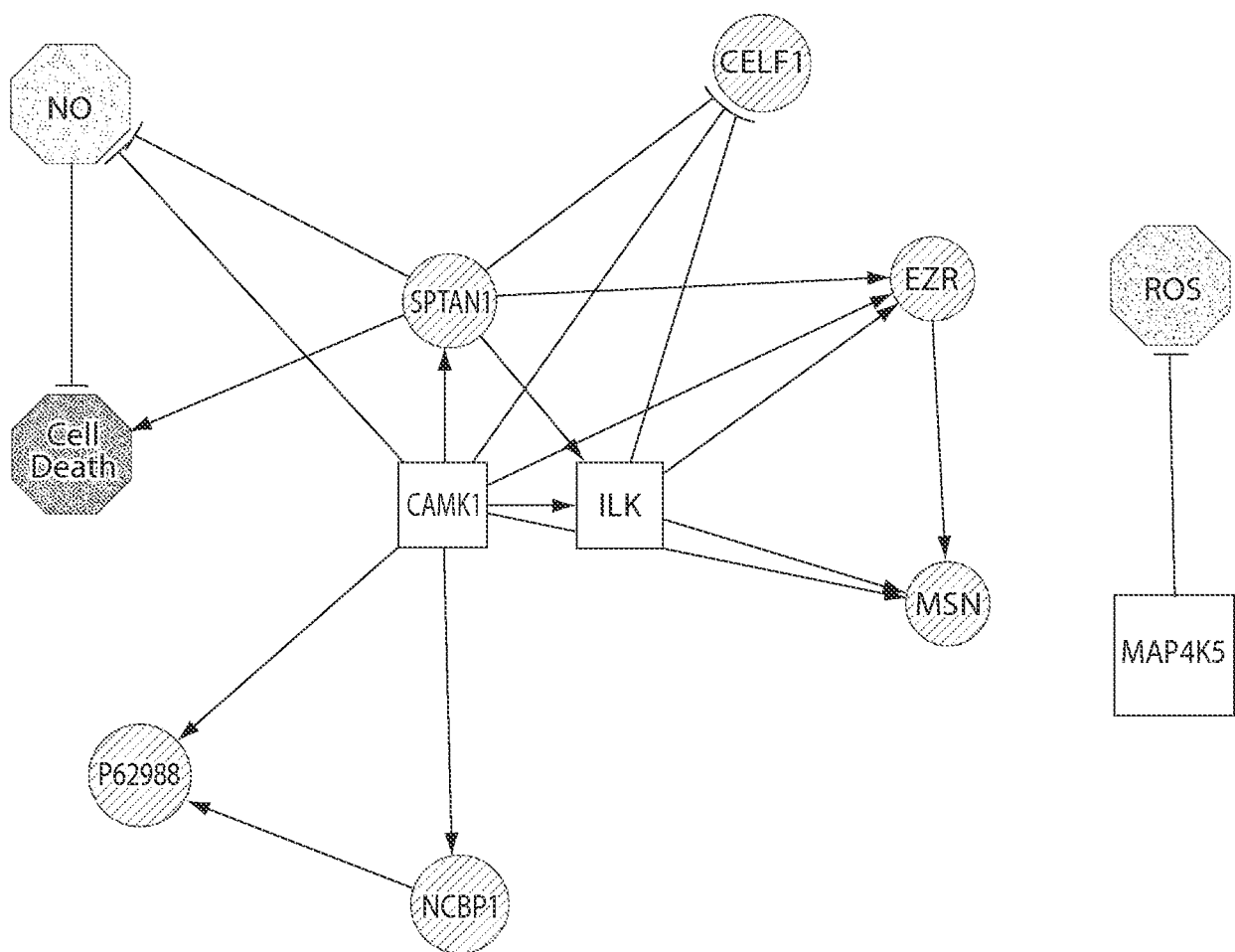


Fig. 59B

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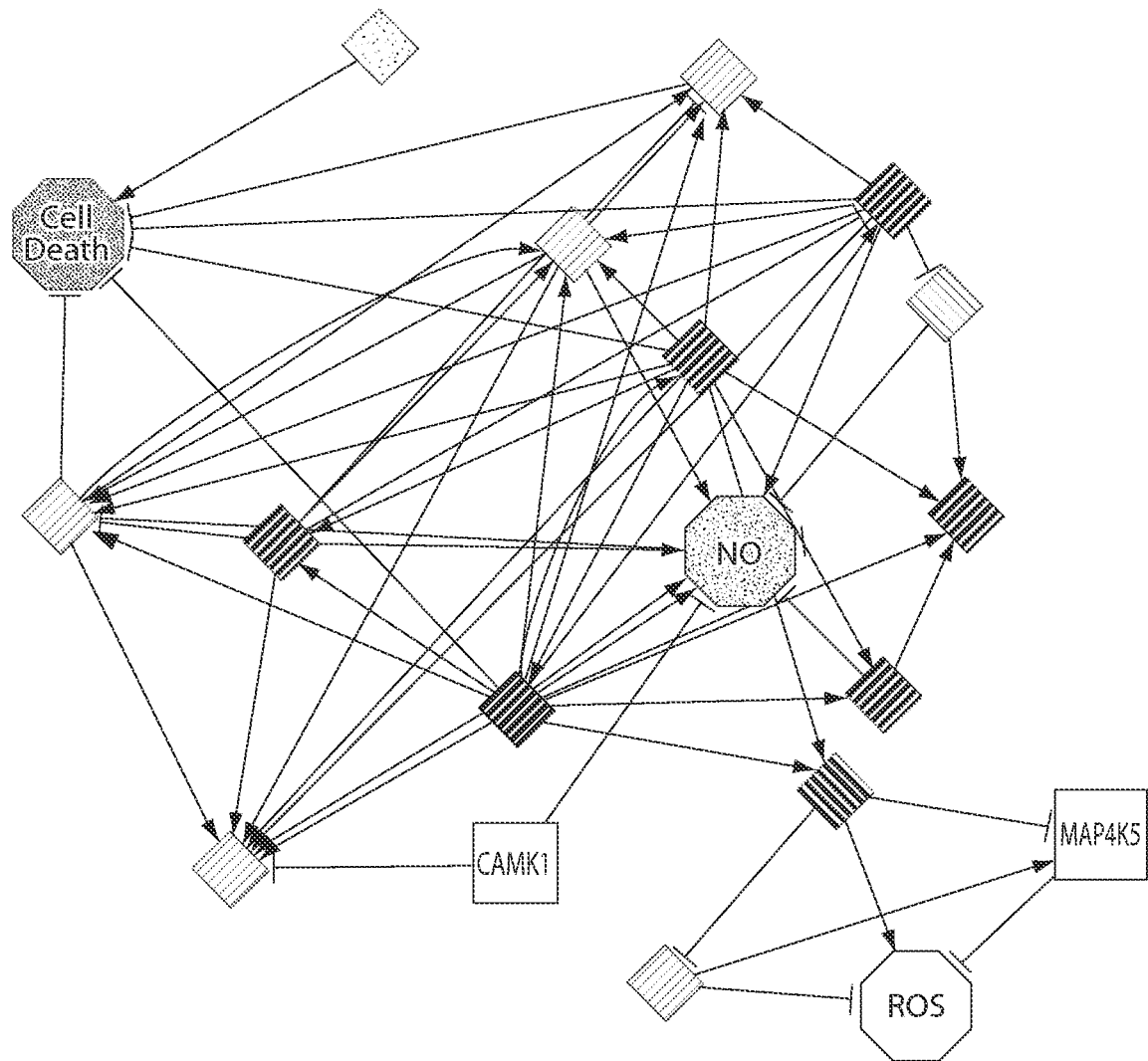


Fig. 59C