

# **Network Characteristic Analysis of ADR-related Proteins and Identification of ADR-ADR Associations**

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## Tables

**Table S1 .the differences between ADR-Protein network and random network**

Metric	ADR-Protein network	Random Networks average	Random Networks Standard Deviation
Clustering Coefficient	0.078363	0.014072	5.15E-04
Average Degree	8.899915	16.43248	0
Degree Distribution	-1.3709	-0.01581	0.527722
Mean Shortest Path	4.172485	2.805762	8.45E-04

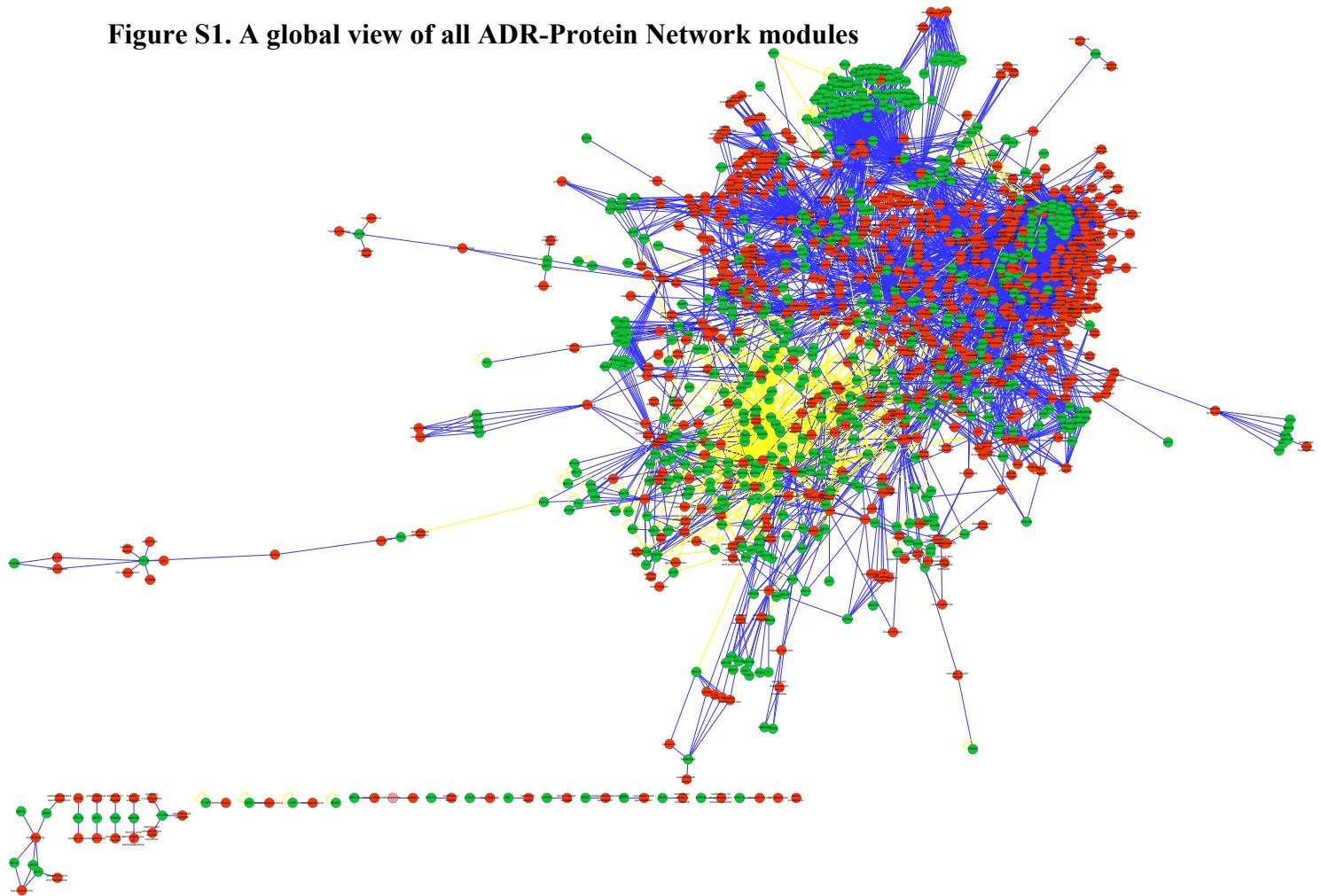
**Table S2. One-to-one relationships between ADRs andADRs**

ADR	ADRP(Gene Symbol)
hemolytic anemia	HK1
toxicological effects of l-alanosine	ADSS
kidney diseases	ABCC2
increased lipid peroxidation	CRAT
pulmonary fibrosis	COL1A1
neuronal toxicity	HSD11K
bulla	TYMP
bone marrow damage	CYP2E1
homocystinuria	CBS
methemoglobinemia	NPR1
inefficiency of drug absorption across intestine	CHRM4
lung damage	CYP2F1
hypercholesterolemia-induced retardation	NT5E

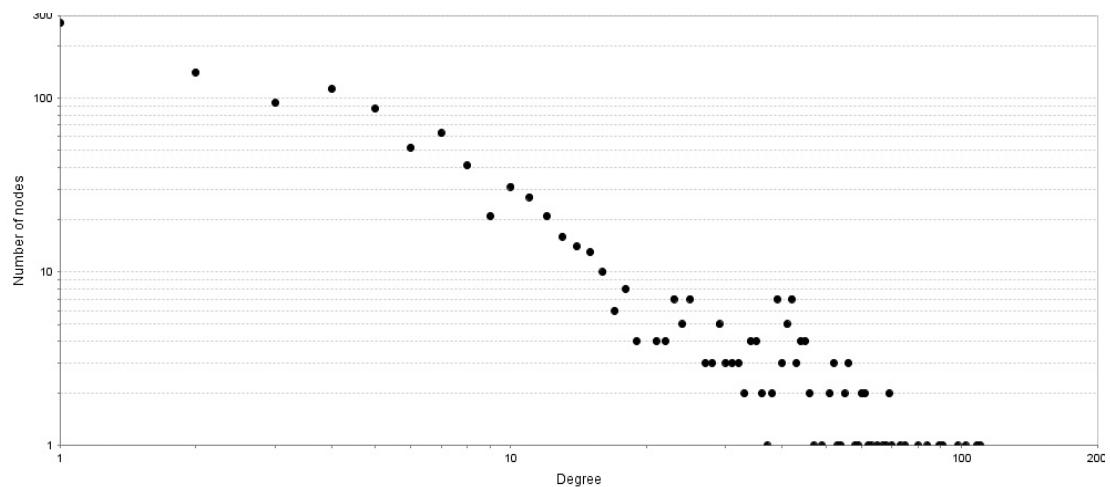
**Table S3, S4 and S5.** Appear in a separate tab -delimited excel file named **Table S3-S5.**

## Figures

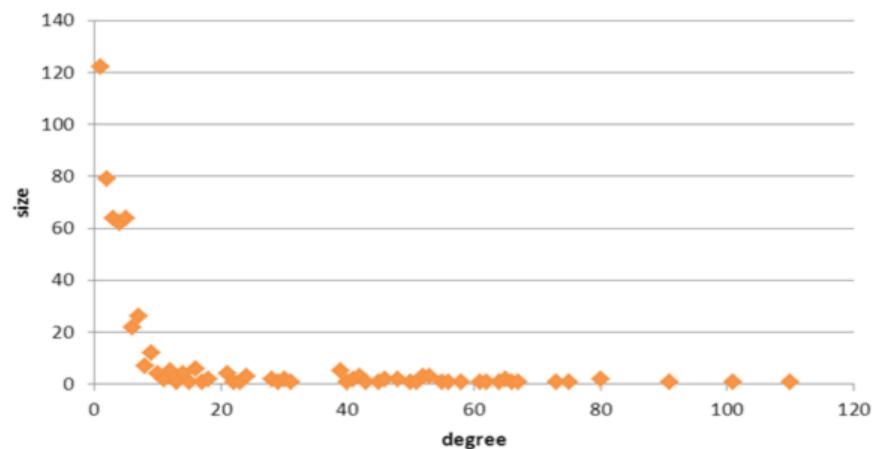
Figure S1. A global view of all ADR-Protein Network modules



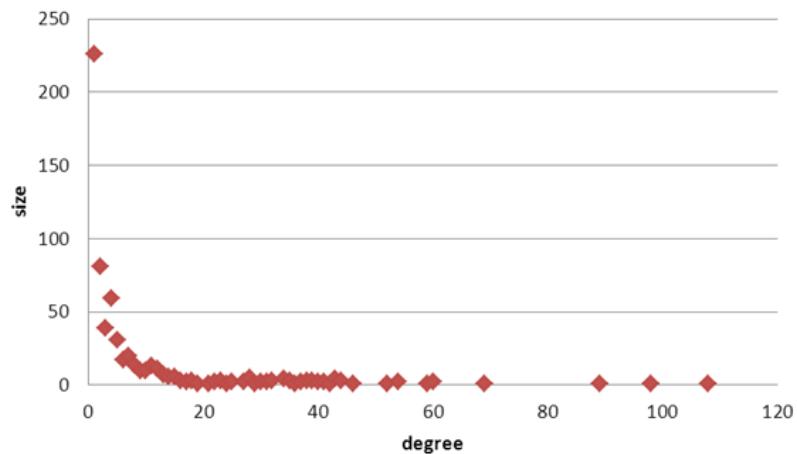
**Figure S2. Degree distribution of all the nodes in ADR- Protein network**



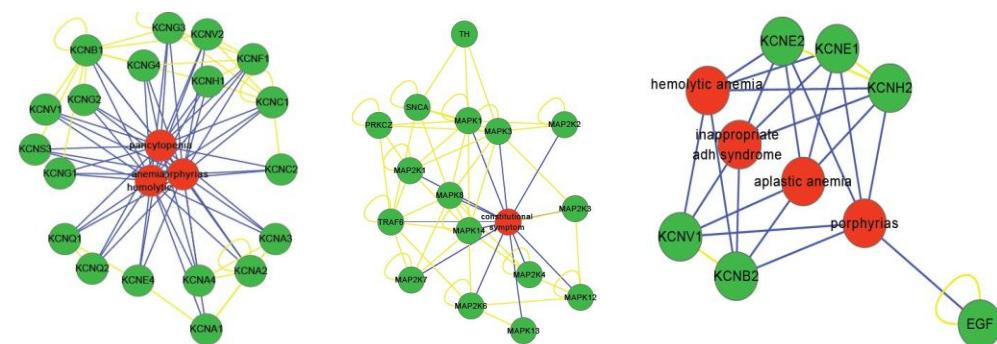
**Figure S3. Degree distribution of all ADRPs in ADR- Protein network**



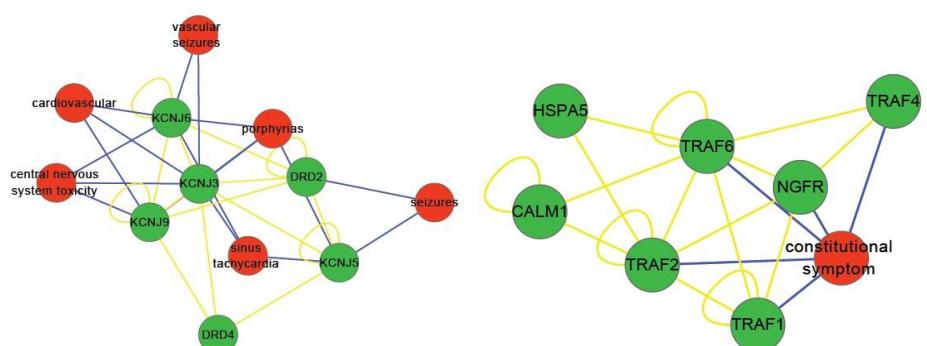
**Figure S4. Degree distribution of all ADRs in ADR- Protein network**



### **Figure S5. Composition map of 41 modules**



Module 1



Module 2

Module 3

Module 4

Module 5

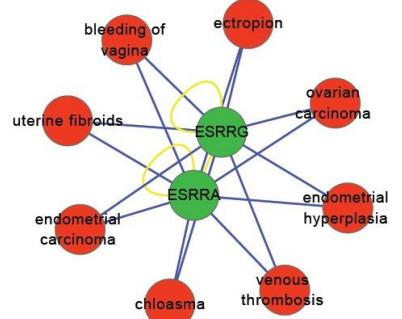
## Module 6

Module 7

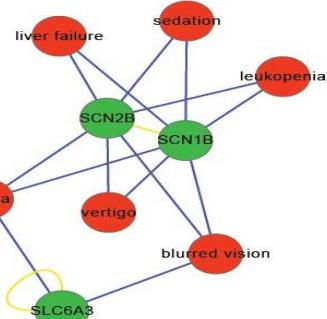
Module 8

The figure consists of two parts. The left part is a complex network graph with numerous nodes (green circles) representing genes and yellow lines representing interactions. Nodes include RARA, EPARA, MED, NPOCT, TSHZ, MAFAT, NHOC, TCPY, CALM, PAR1, AR, TSHZ, TPS3, LCK, TSHZ, TOMM, SNCA, TRAF3, BNP, PRIN2, PYN, TRAF1, CASP8, POMC, PRKDC, ERCC2, CCRBP, TRAF1, APP, CRYAB, PRKDC, and AFM1. The right part is a simplified network diagram with four main nodes: a red circle labeled '[d]respiratory arrest', a green circle labeled 'OPRD1', a green circle labeled 'OPR1', and a red circle labeled 'drug dependence'. 'OPRD1' is at the center, connected to 'respiratory arrest', 'OPR1', and 'drug dependence'. 'OPR1' is also connected to 'respiratory arrest' and 'drug dependence'. 'respiratory arrest' and 'drug dependence' are connected to each other.

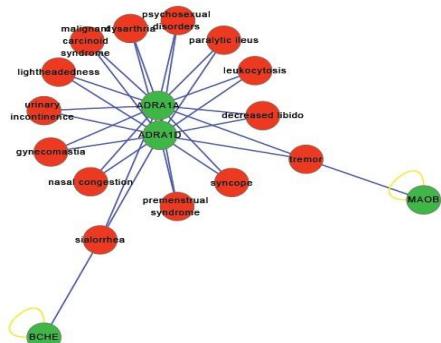
Module 9



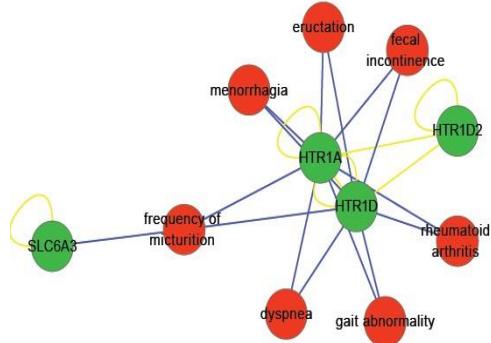
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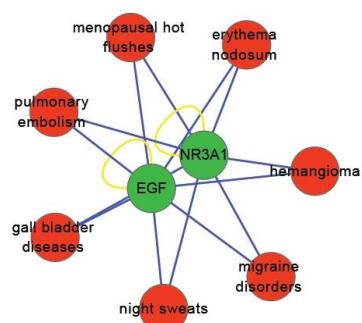
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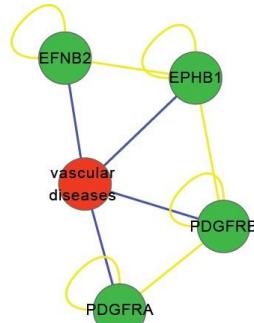
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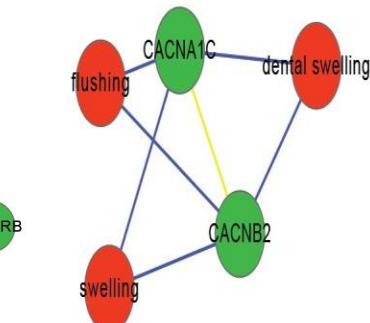
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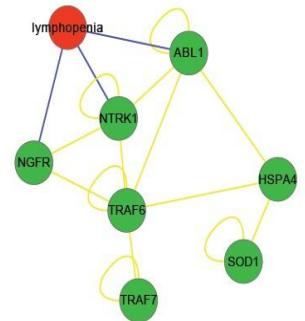
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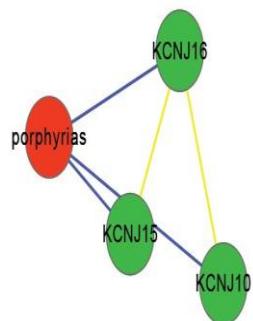
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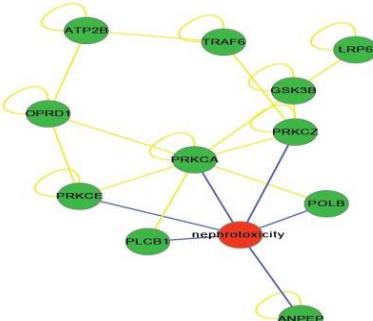
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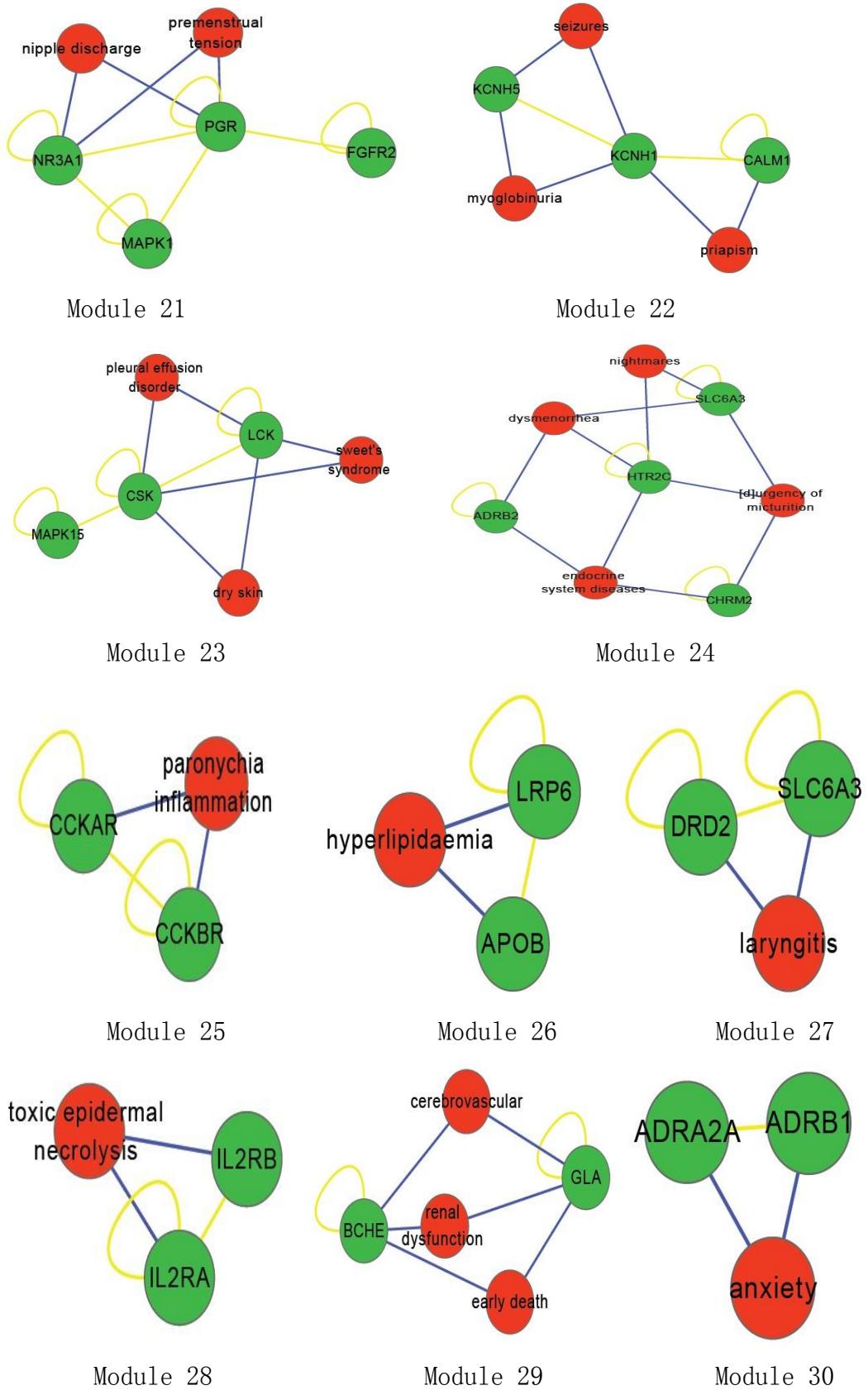
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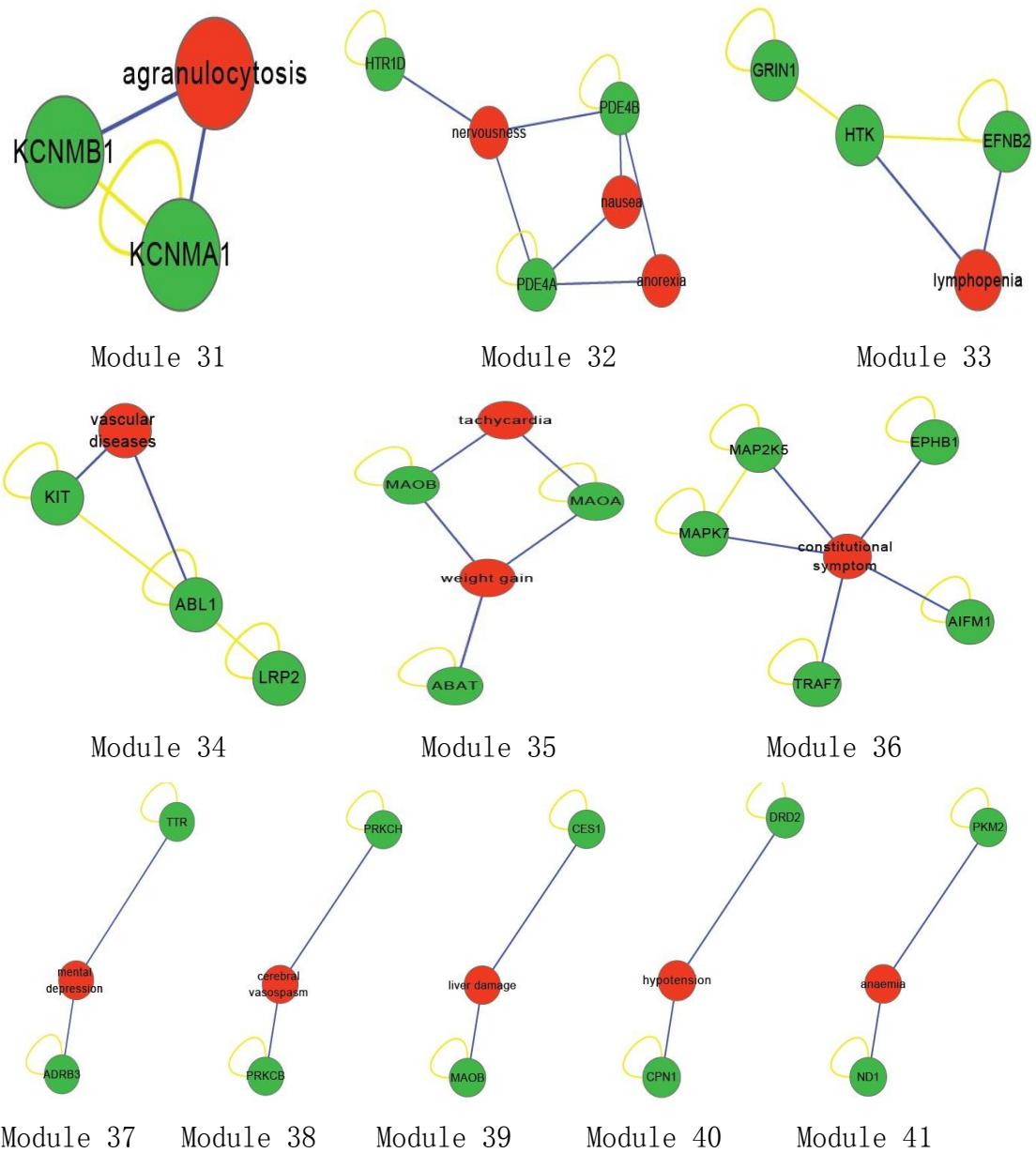


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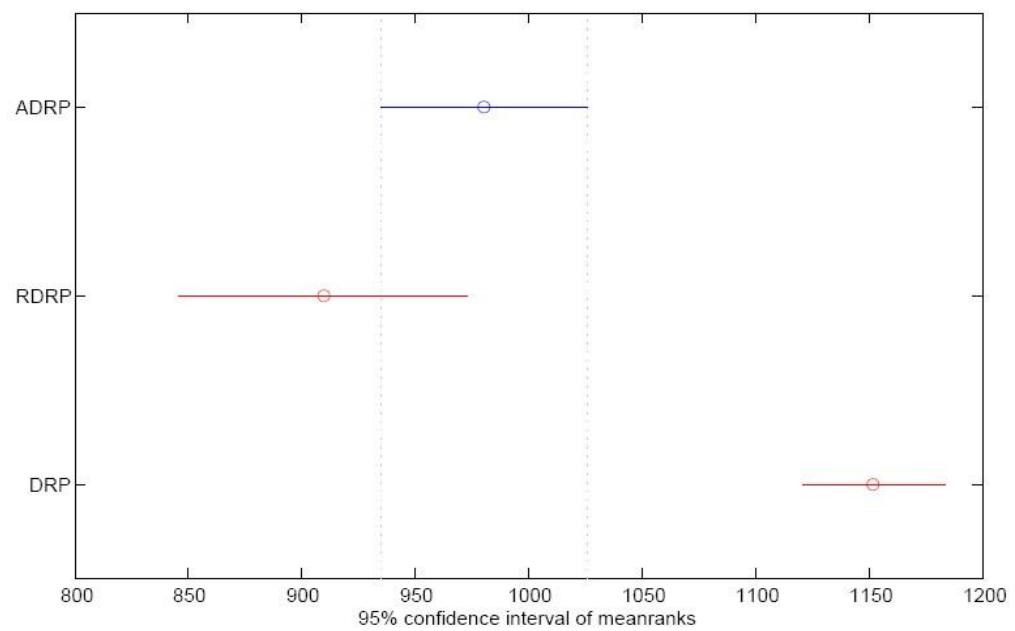


Module 20

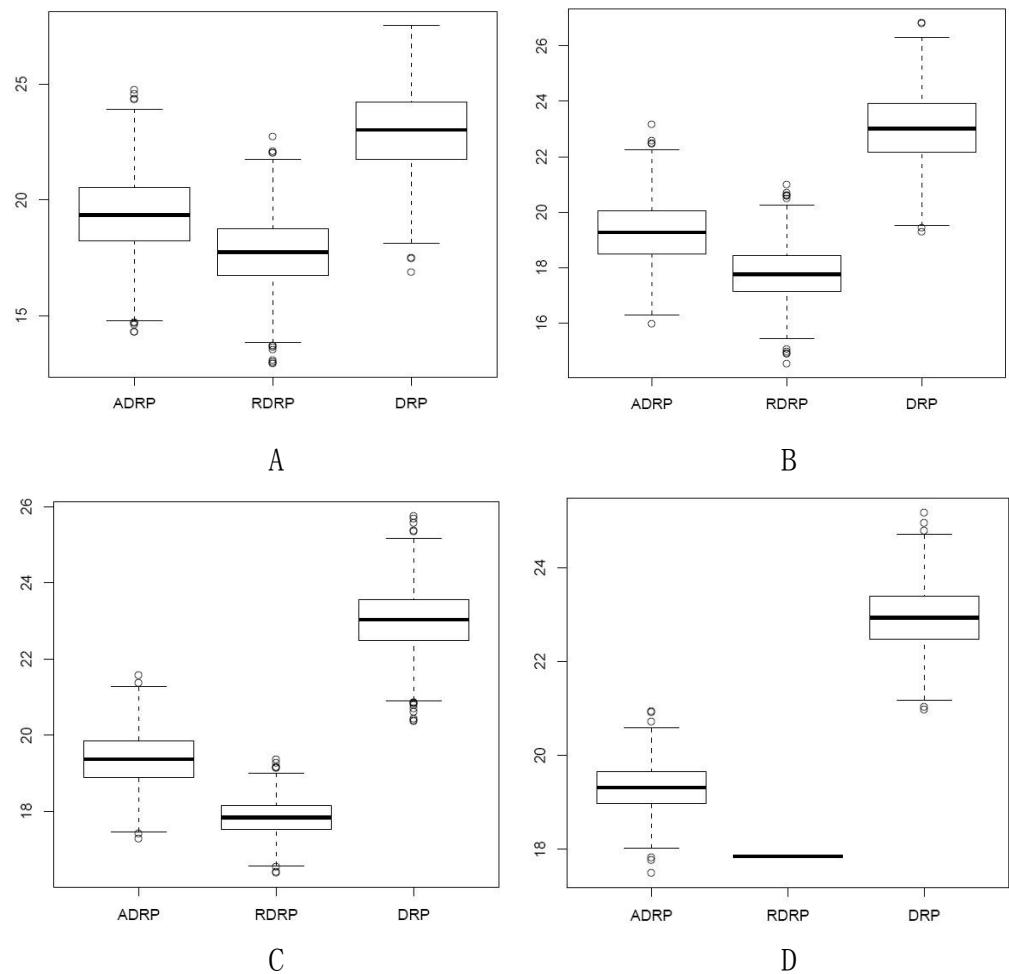




**Figure S6. The result of nonparametric multiple comparison test for tissue distributions**

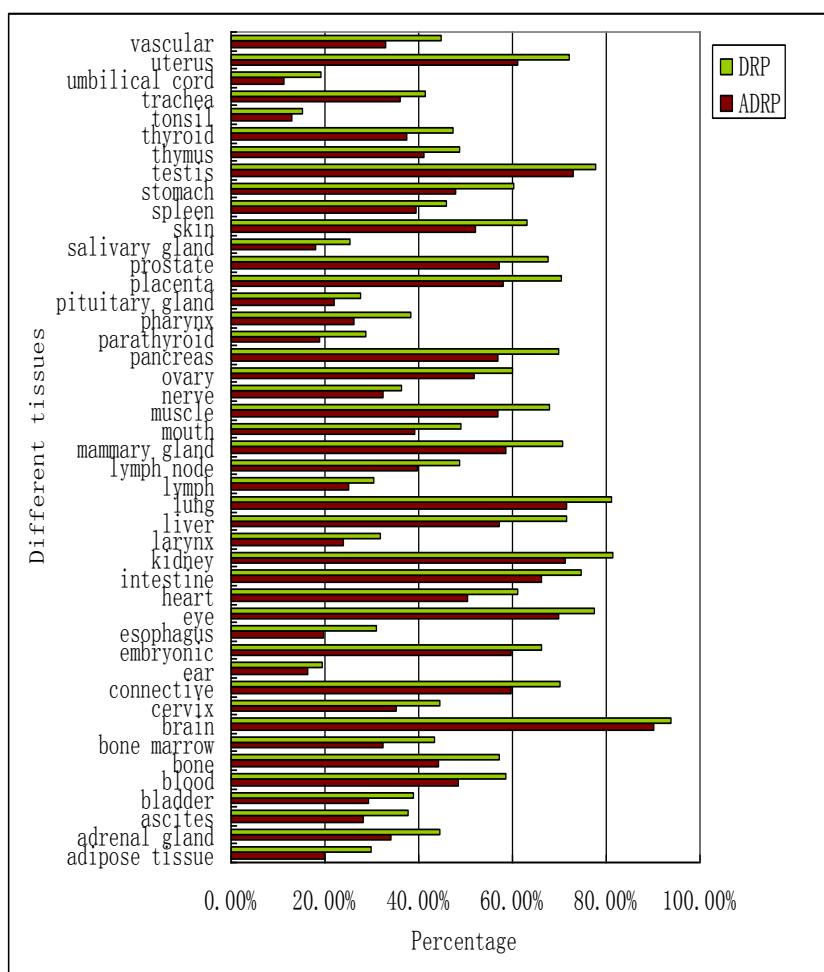


**Figure S7. Tissue distributions of ADRPs, RDRPs and DRPs by randomly select equal numbers (A: 50, B: 100, C: 200, D: 285)**



To address whether Figure 4 is biased due to inequality of sample size, we randomly selected equal numbers (A: 50, B: 100, C: 200, D: 285) of ADRPs, RDRPs and DRPs to calculate the mean of tissue distribution number. The procedure is repeated 1000 times to compare tissue specificity.

**Figure S8. The distribution of ADRPs and DRPs in each tissue**



**Figure S9. The distribution of ADRPs and DRPs in different interval of tissue number**

