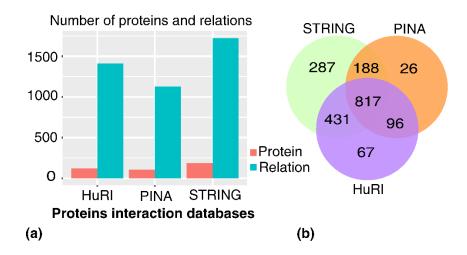
## **Supplementary material**

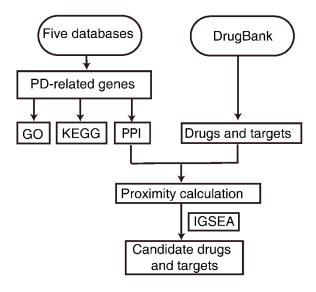
## Integrated network analysis identifying potential novel drug candidates and targets for Parkinson's disease

Pusheng Quan, Kai Wang, Shi Yan, Shirong Wen, Chengqun Wei, Xinyu Zhang, Jingwei Cao, Lifen Yao'

## **Supplementary Figures**



**Supplementary Figure S1: PPI collection**. (a) Bar chart showing the number of proteins and interactions obtained from three databases. (b) Veen diagram show the number of protein-protein interactions collected from three databases. PPI, protein-protein interactions.



Supplementary Figure S2. The workflow of the study.

## **Supplementary Table**

**Supplementary Table S1**. GO and KEGG enrichment analysis of the nine differentially expressed drug-target genes.

Category	Term	FDR	GC*	Gene ID
GO-BP	GO:0006979~response to oxidative stress	0.000314789	5	BCL2/TXNRD1/JUN/AKT1/PML
	GO:0009314~response to radiation	0.000314789	5	BCL2/KIT/JUN/AKT1/PML
KEGG	hsa04722: Neurotrophin signaling pathway	0.003836	3	BCL2/JUN/AKT1
	hsa04210: Apoptosis	0.003836	3	BCL2/JUN/AKT1
	hsa04915: Estrogen signaling pathway	0.003836	3	BCL2/JUN/AKT1
	hsa04010: MAPK signaling pathway	0.01463	3	KIT/JUN/AKT1
	hsa04151: PI3K-Akt signaling pathway	0.017499	3	BCL2/KIT/AKT1

GC\*: Gene count