## Supplementary Material

## A comprehensive analysis of the association between $\operatorname{SNCA}$ polymorphisms with the risk of Parkinson's disease

Yuan Zhang ${ }^{1 \dagger}$, Li Shu ${ }^{1 \dagger}$, Qiying Sun ${ }^{2,3,4}$, Hongxu Pan ${ }^{1}$, Jifeng Guo ${ }^{1,3,4,6,7,8}$, Beisha Tang ${ }^{1,2,3,4,5,6,7, \mathbf{8}^{*}}$
${ }^{\dagger}$ These authors have contributed equally to this work and are co-first authors.

* Correspondence: Beisha Tang bstang7398@163.com


(A)

(B)

(C) $\qquad$



(G)



(I)

(J)



Supplementary Figure 4: Funnel plots of the association between each $S N C A$ variant (allele) included and PD risks in total and by ethnicity. (A)-(P) were individually responsive to the variants rs181489(T), rs356165(G), rs356186(A), rs356219(G), rs356220(T), rs356221(A), rs894278(G), rs2301134(A), rs2301135(G), rs2583988(T), rs2619363(T), rs2619364(G), rs2736990(G), rs2737029(G), rs7684318(C), rs11931074(T).

