(a) Candidate gene selection
- Tool (i): Gene2Mesh and hand search
  Inclusion criteria: \( \geq 2 \) studies reporting association with TUD in a population of European ancestry
- Tool (ii): IPA
- Development of genetic networks: IPA and STRING 9.0

(b) Candidate disorder selection
- Tool: IPA
  Methods 1: Top 20 of disorders with the strongest p-value
  Methods 2: Based on the top 5 disorders by disease category, we selected the Top 20 disorders with the strongest p-value

(c) Genetic similarities between TUD and selected disorders
- Tool: SAS
  Methods: Jaccard Index calculation