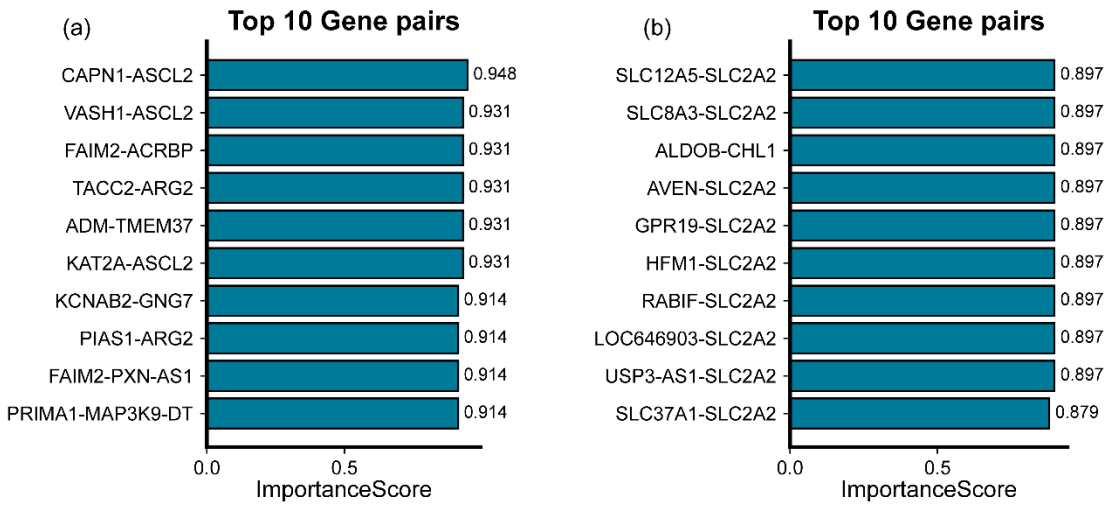
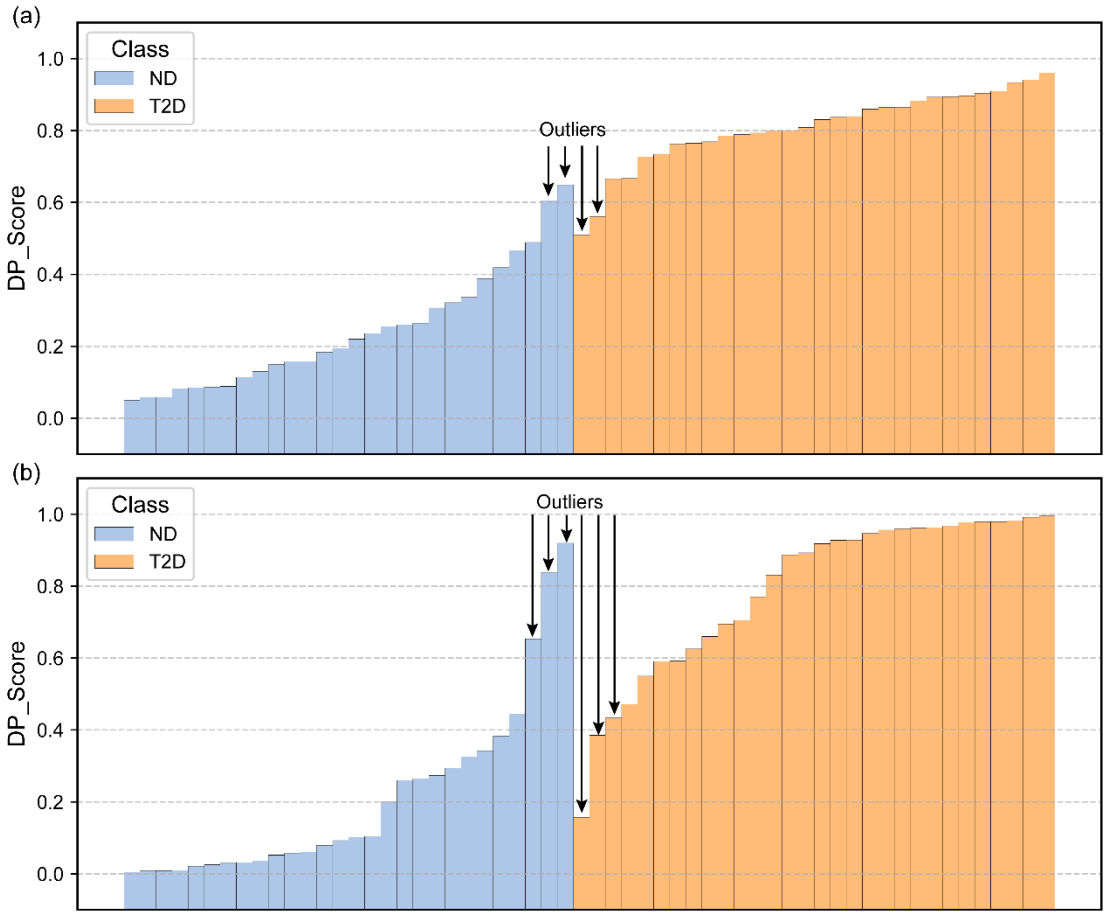
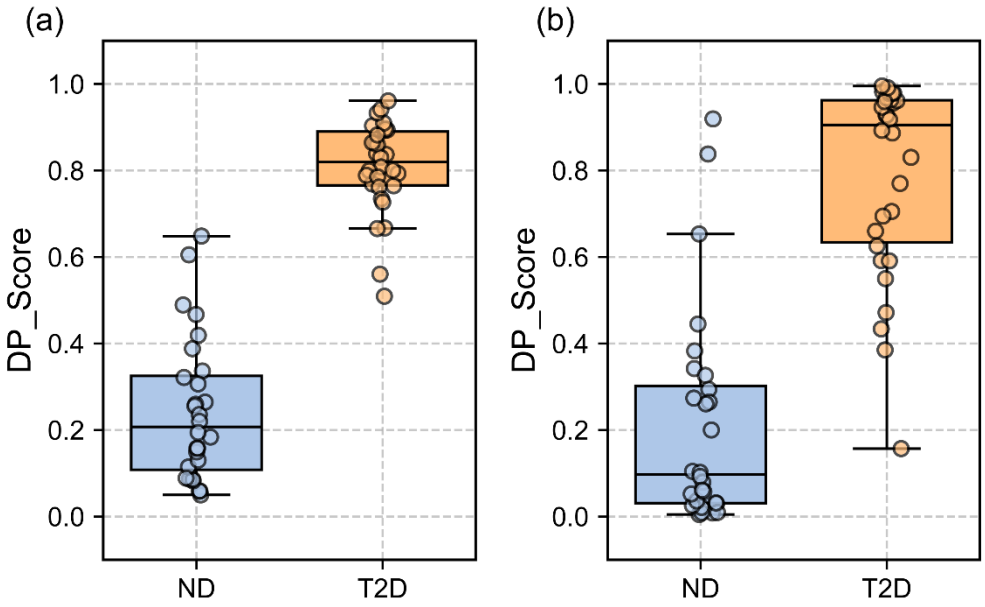


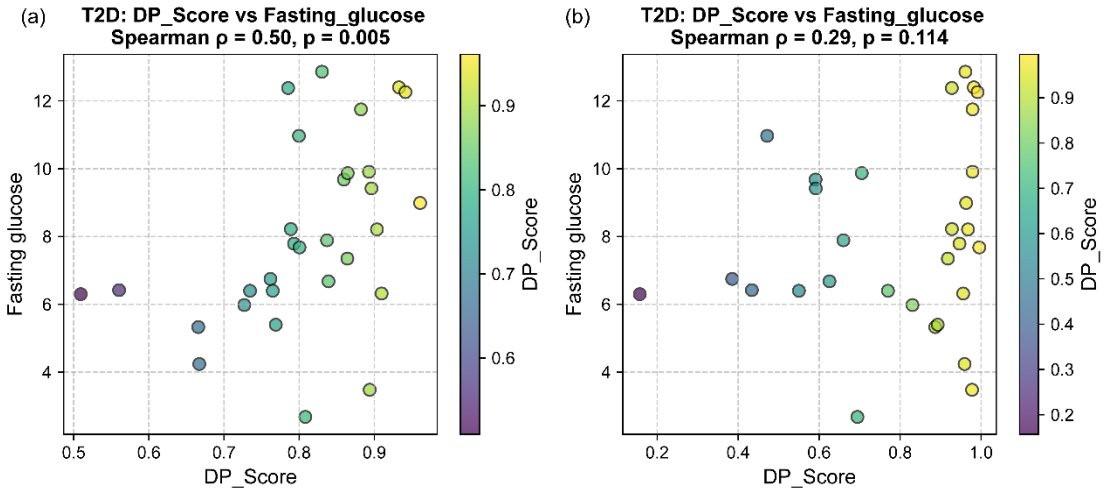
Supplementary Fig. S1: Top 10 gene pairs extracted by DPS-Tool using human islet gene expression profiles, comparing normoglycemic and type 2 diabetes samples. (a) Top 10 characteristic gene pairs identified under the default setting with the complete gene set. (b) Top 10 high-scoring gene pairs identified using the islets β cell identity and function-related gene set.



Supplementary Fig. S2: Bar plot showing ranked perturbation scores of individual samples as analyzed by DSP-Tool. (a) Perturbation scores were calculated using gene pairs derived from the default whole gene set, identifying 4 outlier samples (highlighted); (b) Perturbation scores were calculated using gene pairs extracted from a gene set associated with human islet β cell identity and function, identifying 6 outlier samples.



Supplementary Fig. S3: Boxplot comparison of perturbation scores calculated from human islet gene expression profiles. (a) Perturbation scores based on the default whole gene set; (b) Perturbation scores based on a gene set associated with β cell identity and function. Diabetic samples show significantly higher perturbation scores compared to normoglycemic individuals.



Supplementary Fig. S4: Correlation analysis between perturbation scores and clinical information. (a) Pearson correlation between perturbation scores (based on the whole gene set) and fasting glucose levels, showing a significant positive association; (b) Correlation analysis using perturbation scores derived from a β cell identity and function-related gene set, also demonstrating a positive correlation trend with fasting glucose.