Unraveling the Molecular Heterogeneity in type 2 Diabetes: A Potential Subtype Discovery Study Followed by Metabolic Modeling

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Figure S1. Accuracy, sensitivity and specificity of SVM classifier for 100 repetition of classification with 10-fold cross-validation



Figure S2. Box plot of fasting glucose values in each diabetic cluster and normoglycemic group.



Figure S3. Box plot of fasting insulin values in each diabetic cluster and normoglycemic group.


Figure S4. Schematic representation of abnormalities in cluster 1



Figure S5. Schematic representation of abnormalities in cluster 2



Figure S6. Schematic representation of abnormalities in cluster 3


Figure S7. Cluster-based study versus cohort study. In a cohort study, a sample consists of several subjects is gathered and examined. In a cluster-based study, a sample that has been collected in a cohort study is broken down into the sub-groups so that the members within each subgroup have the most similarity and differ from the members of the outer sub-groups.

|  |  |
| --- | --- |
| **Name**  | **p-value** |
| Starch and sucrose metabolism | 0.00015 |
| Phenylalanine metabolism | 0.024 |
| Mannose type O-glycan biosynthesis | 0.042 |
| Butanoate metabolism | 0.06 |
| Adipocytokine signaling pathway | 0.076 |
| Tyrosine metabolism | 0.094 |

Table S1. KEGG pathway enrichment of differentially expressed genes in cluster 1

|  |  |
| --- | --- |
| **Name**  | **p-value** |
| ECM-receptor interaction | 0.015 |
| Phenylalanine metabolism | 0.037 |
| Mannose type O-glycan biosynthesis | 0.05 |
| Focal adhesion | 0.07 |
| Tyrosine metabolism | 0.07 |

Table S2. KEGG pathway enrichment of differentially expressed genes in cluster 2

|  |  |
| --- | --- |
| **Name**  | **p-value** |
| Fructose and mannose metabolism | 0.009 |
| Calcium signaling pathway | 0.01 |
| Type II diabetes mellitus | 0.018 |
| MAPK signaling pathway | 0.04 |
| cAMP signaling pathway | 0.07 |
| HIF-1 signaling pathway | 0.07 |
| PI3K-Akt signaling pathway | 0.075 |

Table S3. KEGG pathway enrichment of differentially expressed genes in cluster 3