DGI: HOMA Insulin Resistance (HOMA-IR) Trait Document

Calculation:
\((\text{Insulin}_0 \times \text{Glucose}_0) / 22.5\)
Units: insulin in \(\mu\text{U}/\text{ml}\) and fasting plasma glucose in mmol/L

Measurement:
Insulin \((\mu\text{U}/\text{ml})\) measured using radioimmunoassay kits:
1) Pharmacia
2) DAKO insulin
3) Delfia
Plasma glucose (mmol/L) measured by a glucose oxidase method
1) Fasting blood glucose from venous blood (B-Gluc) and converted to plasma glucose value (correction factor 1.13)
2) Plasma from venous blood using Beckman or Hemocue Glucose Analyzers
3) Plasma from capillary blood using a Hemocue Glucose Analyzer

Trait Distribution:

<table>
<thead>
<tr>
<th>Sample</th>
<th>n</th>
<th>Mean</th>
<th>SD</th>
<th>Median</th>
<th>IQR</th>
</tr>
</thead>
<tbody>
<tr>
<td>Non-diabetes controls</td>
<td>1515</td>
<td>1.68</td>
<td>1.38</td>
<td>1.38</td>
<td>1.12 (0.95, 2.07)</td>
</tr>
<tr>
<td>Males</td>
<td>726</td>
<td>1.73</td>
<td>1.62</td>
<td>1.40</td>
<td>1.11 (0.95, 2.05)</td>
</tr>
<tr>
<td>Females</td>
<td>789</td>
<td>1.64</td>
<td>1.11</td>
<td>1.36</td>
<td>1.11 (0.96, 2.07)</td>
</tr>
</tbody>
</table>

SD=standard deviation, IQR=interquartile range (25% value, 75% value), units: mU*mmol/L

Plot of log (HOMA-IR) (normal plot overlaid)

Description of Trait Modeling:
1. HOMA-IR was logarithmically transformed to fit a normal distribution.
2. Z scores were prepared separately by gender and recruiting region (Botnia, Skara, Malmo or Helsinki) and regressed against age, log BMI and type of insulin measurement.

**Covariates:**
Gender, recruiting region, age, log BMI, type of insulin measurement

**Correlation among related quantitative traits:**

Pearson correlations:
- HOMA-IR and insulinogenic index: 0.29
- HOMA-IR and Fasting Plasma Glucose: 0.33
- HOMA-IR and TG/HDL ratio*: 0.27

* TG/HDL ratio in controls is used as a measure of insulin resistance

**Counts of individuals used to generate results on Web-site:**

<table>
<thead>
<tr>
<th>Trait</th>
<th>Analysis sample</th>
<th>Unaffected Sibs</th>
<th>Unaffected UNR</th>
<th>Unaffected Total</th>
<th>T2D Affected Sibs</th>
<th>T2D Affected UNR</th>
<th>T2D Affected Total</th>
<th>Total analyzed</th>
</tr>
</thead>
<tbody>
<tr>
<td>HOMA-IR</td>
<td>controls only</td>
<td>136</td>
<td>1257</td>
<td>1393</td>
<td></td>
<td></td>
<td></td>
<td>1393</td>
</tr>
</tbody>
</table>

**Summary of association testing method:**
Linear regression was used to test the association between SNP genotype and HOMA-IR z-score. Unrelated individuals and siblings were included in this analysis. P values are reported after correction by genomic control. Genomic inflation factor (based on the median chi-squared) was 1.03.