Supplemental Table 7. The comparison of the original and the newly refined genetic risk score.

<table>
<thead>
<tr>
<th>Cohort</th>
<th>N*</th>
<th>Original Risk Score</th>
<th>Newly Refined Risk Score</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>R²</td>
<td>C (95%CI) **</td>
</tr>
<tr>
<td>Italian Cohort</td>
<td>1,005</td>
<td>2.0% 0.57 (0.53-0.60) 1.30 (1.14-1.49)</td>
<td>1.5 x 10⁻⁴ 3.4% 0.59 (0.56-0.63) 1.43 (1.24-1.64)</td>
</tr>
<tr>
<td>French Cohort</td>
<td>859</td>
<td>1.8% 0.57 (0.53-0.61) 1.27 (1.10-1.45)</td>
<td>7.6 x 10⁻⁴ 2.8% 0.58 (0.55-0.62) 1.36 (1.18-1.57)</td>
</tr>
<tr>
<td>German Cohort</td>
<td>571</td>
<td>2.3% 0.58 (0.53-0.63) 1.35 (1.12-1.62)</td>
<td>1.9 x 10⁻³ 4.4% 0.60 (0.56-0.65) 1.54 (1.26-1.88)</td>
</tr>
<tr>
<td>Czech Cohort</td>
<td>402</td>
<td>1.7% 0.57 (0.51-0.63) 1.23 (1.03-1.46)</td>
<td>2.4 x 10⁻² 2.0% 0.57 (0.52-0.63) 1.23 (1.04-1.45)</td>
</tr>
<tr>
<td>Hungarian Cohort</td>
<td>393</td>
<td>2.8% 0.59 (0.53-0.65) 1.40 (1.10-1.79)</td>
<td>5.7 x 10⁻³ 4.4% 0.61 (0.55-0.67) 1.54 (1.21-1.96)</td>
</tr>
<tr>
<td>Chinese Cohort</td>
<td>595</td>
<td>1.6% 0.57 (0.52-0.62) 1.29 (1.07-1.57)</td>
<td>8.0 x 10⁻³ 2.7% 0.59 (0.54-0.63) 1.36 (1.14-1.62)</td>
</tr>
<tr>
<td>Japanese Cohort</td>
<td>512</td>
<td>2.7% 0.59 (0.54-0.64) 1.34 (1.12-1.60)</td>
<td>1.5 x 10⁻³ 4.0% 0.61 (0.56-0.65) 1.38 (1.17-1.62)</td>
</tr>
<tr>
<td>African-American Cohort</td>
<td>85</td>
<td>4.6% 0.63 (0.50-0.76) 1.50 (0.93-2.41)</td>
<td>9.6 x 10⁻² 5.1% 0.64 (0.51-0.77) 1.63 (0.94-2.82)</td>
</tr>
<tr>
<td>All Replication Cohorts</td>
<td>4,422</td>
<td>2.2% 0.58 (0.56-0.59) 1.29 (1.22-1.37)</td>
<td>5.4 x 10⁻¹⁷ 3.2% 0.59 (0.57-0.61) 1.36 (1.28-1.45)</td>
</tr>
<tr>
<td>GWAS Discovery</td>
<td>2,091</td>
<td>7.0% 0.63 (0.60-0.65) 1.70 (1.54-1.88)</td>
<td>1.9 x 10⁻²⁴ 7.6% 0.64 (0.61-0.66) 1.69 (1.54-1.86)</td>
</tr>
<tr>
<td>GWAS Asian Follow-up</td>
<td>1,384</td>
<td>5.3% 0.61 (0.58-0.64) 1.65 (1.44-1.89)</td>
<td>5.8 x 10⁻¹³ 5.0% 0.61 (0.58-0.64) 1.57 (1.39-1.78)</td>
</tr>
<tr>
<td>GWAS European Follow-up</td>
<td>2,156</td>
<td>4.3% 0.60 (0.58-0.63) 1.46 (1.34-1.60)</td>
<td>1.6 x 10⁻¹⁶ 5.3% 0.61 (0.59-0.64) 1.56 (1.42-1.71)</td>
</tr>
<tr>
<td>All GWAS Cohorts</td>
<td>5,631</td>
<td>5.0% 0.61 (0.60-0.62) 1.51 (1.43-1.60)</td>
<td>3.1 x 10⁻²⁶ 5.7% 0.62 (0.60-0.63) 1.56 (1.47-1.65)</td>
</tr>
<tr>
<td>All Asian Cohorts Combined</td>
<td>4,582</td>
<td>4.5% 0.60 (0.59-0.62) 1.53 (1.43-1.64)</td>
<td>3.0 x 10⁻³⁴ 5.0% 0.61 (0.59-0.63) 1.52 (1.43-1.62)</td>
</tr>
<tr>
<td>All European Cohorts Combined</td>
<td>5,386</td>
<td>2.6% 0.58 (0.57-0.60) 1.34 (1.26-1.41)</td>
<td>3.7 x 10⁻²⁴ 3.6% 0.59 (0.58-0.61) 1.42 (1.34-1.51)</td>
</tr>
<tr>
<td>All Cohorts Combined</td>
<td>10,053</td>
<td>3.8% 0.60 (0.59-0.61) 1.42 (1.36-1.50)</td>
<td>6.2 x 10⁻⁶³ 4.7% 0.61 (0.60-0.62) 1.47 (1.42-1.54)</td>
</tr>
</tbody>
</table>

* Number of analyzed individuals with 100% non-missing genotypes across all 7 scored loci.
* R²: Nagelkerke R square expressed as percent
** C-statistic: area under the ROC curve and its 95% confidence interval.
*** odds ratio per one standard deviation of the standardized risk score and its 95% confidence interval.
**** Wald’s test for risk score as a quantitative predictor of disease status.