Table S1. The association between tag SNPs of SLC12A3 and TCHO, TG and HDL-C level by FBAT and HBAT methods

<table>
<thead>
<tr>
<th>Marker</th>
<th>Allele and frequency</th>
<th>Test statistics</th>
<th></th>
<th></th>
<th></th>
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</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>TCHO</td>
<td>TG</td>
<td>HDL-C</td>
<td>Var (S)</td>
<td>z</td>
<td>p</td>
<td>Var (S)</td>
<td>z</td>
<td>p</td>
<td>Var (S)</td>
</tr>
<tr>
<td>rs2304478</td>
<td>G:A 0.14</td>
<td>295.52 -2.26</td>
<td>0.024</td>
<td>-</td>
<td>54.11</td>
<td>-2.03</td>
<td>0.043</td>
<td>0.028</td>
<td>24.02</td>
<td>2.02</td>
<td>0.043</td>
</tr>
<tr>
<td>rs5803</td>
<td>T:C 0.26</td>
<td>291.21 -2.20</td>
<td>0.028</td>
<td>0.019</td>
<td>66.78</td>
<td>-2.34</td>
<td>0.019</td>
<td>0.020</td>
<td>25.01</td>
<td>-2.18</td>
<td>0.029</td>
</tr>
<tr>
<td>rs711746</td>
<td>G:A 0.45</td>
<td>400.36 2.24</td>
<td>0.025</td>
<td>0.041</td>
<td>61.78</td>
<td>2.72</td>
<td>0.006</td>
<td>0.042</td>
<td>32.61</td>
<td>2.26</td>
<td>0.024</td>
</tr>
</tbody>
</table>

Haplotypes rs5803 (T/C)- rs711746 (G/A)

<table>
<thead>
<tr>
<th></th>
<th>Freq.</th>
<th>Var (S)</th>
<th>z</th>
<th>p</th>
<th>Global p</th>
<th>Var (S)</th>
<th>z</th>
<th>p</th>
<th>Global p</th>
<th>Var (S)</th>
<th>z</th>
<th>p</th>
<th>Global p</th>
</tr>
</thead>
<tbody>
<tr>
<td>H1</td>
<td>C-A</td>
<td>0.40</td>
<td>276.98 0.48</td>
<td>-</td>
<td>0.057</td>
<td>36.38</td>
<td>0.57</td>
<td>-</td>
<td>0.117</td>
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<tr>
<td>H2</td>
<td>C-G</td>
<td>0.38</td>
<td>292.95 1.70</td>
<td>-</td>
<td>44.66</td>
<td>2.15</td>
<td>0.047</td>
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<tr>
<td>H3</td>
<td>T-A</td>
<td>0.18</td>
<td>197.79 -2.69</td>
<td>0.042</td>
<td>41.07</td>
<td>-2.49</td>
<td>0.034</td>
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</tr>
</tbody>
</table>

Abbreviations: FBAT, Family Based Association Test with the additive model; Freq., frequency of allele or haplotypes constructed by positive SNPs; Var (S), is a matrix, calculated under the null and used to standardize S.

- Markers, SNPs and haplotypes showing significant association were demonstrated in this table, and frequency < 0.05 was excluded;
- alleles and haplotypes detected in more than 10 informative families; and the lower frequency allele was used in following statistics calculation.
- z-score calculated based on a biallelic marker model for SNPs, positive z values and p < 0.05 indicated a high-risk haplotype;
- p-TBAT, significance test by FBAT with empirical variance estimator option [-e], non-significant markers displayed with hyphen (-);
- p-HBATE, significance test by HBAT with empirical variance estimator option [-e], non-significant haplotypes displayed with hyphen (-);
- Global p e, a global test for all haplotypes with frequency > 0.05.
Table S2. The correlation among blood pressure and lipid parameters

<table>
<thead>
<tr>
<th></th>
<th>gender</th>
<th>age</th>
<th>SBP</th>
<th>DBP</th>
<th>BMI</th>
<th>WHR</th>
<th>TCHO</th>
<th>TG</th>
<th>HDLC</th>
<th>LDLC</th>
</tr>
</thead>
<tbody>
<tr>
<td>gender</td>
<td>0.015</td>
<td>0.009</td>
<td>0.008</td>
<td>0.026</td>
<td>0.033</td>
<td>0.681</td>
<td>0.081</td>
<td>0.005</td>
<td>0.675</td>
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</tr>
<tr>
<td>age</td>
<td>-0.21</td>
<td>&lt;0.001</td>
<td>&lt;0.001</td>
<td>0.210</td>
<td>0.211</td>
<td>0.034</td>
<td>0.166</td>
<td>0.770</td>
<td>0.006</td>
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</tr>
<tr>
<td>SBP</td>
<td>-0.23</td>
<td>0.52</td>
<td>&lt;0.001</td>
<td>&lt;0.001</td>
<td>0.042</td>
<td>0.088</td>
<td>0.027</td>
<td>0.111</td>
<td>0.052</td>
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<tr>
<td>DBP</td>
<td>-0.23</td>
<td>0.48</td>
<td>0.89</td>
<td>0.009</td>
<td>0.014</td>
<td>0.091</td>
<td>0.029</td>
<td>0.189</td>
<td>0.058</td>
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<tr>
<td>BMI</td>
<td>-0.20</td>
<td>0.11</td>
<td>0.34</td>
<td>0.37</td>
<td>0.009</td>
<td>0.340</td>
<td>0.144</td>
<td>0.076</td>
<td>0.050</td>
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</tr>
<tr>
<td>WHR</td>
<td>-0.32</td>
<td>0.19</td>
<td>0.31</td>
<td>0.37</td>
<td>0.393</td>
<td>0.439</td>
<td>0.277</td>
<td>0.701</td>
<td>0.584</td>
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<tr>
<td>TCHO</td>
<td>0.04</td>
<td>0.18</td>
<td>0.15</td>
<td>0.15</td>
<td>0.087</td>
<td>0.120</td>
<td>&lt;0.001</td>
<td>&lt;0.001</td>
<td>&lt;0.001</td>
<td></td>
</tr>
<tr>
<td>TG</td>
<td>-0.15</td>
<td>0.12</td>
<td>0.19</td>
<td>0.19</td>
<td>0.133</td>
<td>0.168</td>
<td>0.44</td>
<td>&lt;0.001</td>
<td></td>
<td></td>
</tr>
<tr>
<td>HDLC</td>
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<td>-0.02</td>
<td>-0.14</td>
<td>-0.12</td>
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<td>-0.060</td>
<td>0.54</td>
<td>-0.24</td>
<td>&lt;0.001</td>
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</tr>
<tr>
<td>LDLC</td>
<td>0.04</td>
<td>0.24</td>
<td>0.17</td>
<td>0.17</td>
<td>0.178</td>
<td>0.085</td>
<td>0.91</td>
<td>0.33</td>
<td>0.43</td>
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</tr>
</tbody>
</table>

Abbreviations: SBP, systolic blood pressure; DBP, diastolic blood pressure; BMI, body mass index; WHR, waist-hip ratio; TCHO, total plasma cholesterol; TG, triglycerides; HDL-C, high-density lipoprotein cholesterol; LDL-C, low-density lipoprotein cholesterol. The Pearson’s correlation coefficient test r score displayed in the bottom left, and P-value associated with the correlation in the upper right.

Table S3. The influence of rs5803 and rs7114746 polymorphism on individuals’ blood pressure.

<table>
<thead>
<tr>
<th></th>
<th>Genotypes groups</th>
<th>t</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>CC (n=72)</td>
<td>T carrier (n=63)</td>
<td></td>
</tr>
<tr>
<td>SBP</td>
<td>143.56±26.55</td>
<td>136.68±29.72</td>
<td>1.41</td>
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<tr>
<td>DBP</td>
<td>92.34±14.63</td>
<td>87.83±17.20</td>
<td>1.63</td>
</tr>
<tr>
<td>rs7114746</td>
<td>AA (n=43)</td>
<td>G carrier (n=86)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>SBP</td>
<td>DBP</td>
<td></td>
</tr>
<tr>
<td>----</td>
<td>---------</td>
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<td>----</td>
</tr>
<tr>
<td></td>
<td>147.23±28.84</td>
<td>137.54±27.26</td>
<td>1.87</td>
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<tr>
<td></td>
<td>94.12±17.28</td>
<td>88.60±15.02</td>
<td>1.87</td>
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</table>