**Supplementary Table S2.** Marker-trait association analysis and clinical parameters of the Baltic male cohort sample stratified based on the FSHB -211G/T (rs10835638) genotypes of the participants.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>FSHB -211 G/T</th>
<th>Baltic male cohort&lt;sup&gt;b&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>mean ± SD</td>
<td>median (5-95)</td>
</tr>
<tr>
<td>FSH (IU/L)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>G/G</td>
<td>3.2 ± 1.7</td>
<td>2.9 (1.3 – 6.5)</td>
</tr>
<tr>
<td>G/T</td>
<td>2.7 ± 1.5</td>
<td>2.3 (1.1 – 5.6)</td>
</tr>
<tr>
<td>T/T</td>
<td>2.4 ± 1.3</td>
<td>2.4 (0.9 – 6.1)</td>
</tr>
<tr>
<td>LH (IU/L)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>G/G</td>
<td>4.0 ± 1.6</td>
<td>3.8 (1.8 – 6.9)</td>
</tr>
<tr>
<td>G/T</td>
<td>4.1 ± 1.6</td>
<td>3.8 (1.7 – 7.1)</td>
</tr>
<tr>
<td>T/T</td>
<td>5.2 ± 2.4</td>
<td>4.3 (2.5 – 11.9)</td>
</tr>
<tr>
<td>Inhibin B</td>
<td>(pg/mL)</td>
<td></td>
</tr>
<tr>
<td>G/G</td>
<td>234.4 ± 78.5</td>
<td>226.5 (118.2 – 380.7)</td>
</tr>
<tr>
<td>G/T</td>
<td>217.0 ± 76.5</td>
<td>208.0 (106.3 – 361.7)</td>
</tr>
<tr>
<td>T/T</td>
<td>184.9 ± 84.3</td>
<td>160.5 (77.0 – 361.0)</td>
</tr>
<tr>
<td>Total testosterone</td>
<td>(nmol/L)</td>
<td></td>
</tr>
<tr>
<td>G/G</td>
<td>27.8 ± 9.1</td>
<td>26.9 (15.0 – 44.1)</td>
</tr>
<tr>
<td>G/T</td>
<td>26.4 ± 9.3</td>
<td>25.0 (13.7 – 45.6)</td>
</tr>
<tr>
<td>T/T</td>
<td>24.9 ± 7.7</td>
<td>27.3 (11.7 – 34.6)</td>
</tr>
<tr>
<td>Estradiol</td>
<td>(pmol/L)</td>
<td></td>
</tr>
<tr>
<td>G/G</td>
<td>93.9 ± 25.1</td>
<td>90.0 (59.0 – 141.0)</td>
</tr>
<tr>
<td>G/T</td>
<td>92.8 ± 24.9</td>
<td>90.0 (57.3 – 138.7)</td>
</tr>
<tr>
<td>T/T</td>
<td>102.0 ± 32.8</td>
<td>105.0 (59.0 – 161.0)</td>
</tr>
<tr>
<td>Total testes volume (mL)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>G/G</td>
<td>49.4 ± 10.2</td>
<td>50.0 (33.0 – 70.0)</td>
</tr>
<tr>
<td>G/T</td>
<td>48.8 ± 10.5</td>
<td>50.0 (30.1 – 70.0)</td>
</tr>
<tr>
<td>T/T</td>
<td>40.2 ± 12.9</td>
<td>40.5 (20.0 – 70.0)</td>
</tr>
<tr>
<td>Semen volume (mL)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>G/G</td>
<td>3.5 ± 1.6</td>
<td>3.3 (1.3 – 6.5)</td>
</tr>
<tr>
<td>G/T</td>
<td>3.5 ± 1.6</td>
<td>3.5 ± 1.6</td>
</tr>
<tr>
<td></td>
<td>G/G</td>
<td>G/T</td>
</tr>
<tr>
<td>----------</td>
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</tr>
<tr>
<td>Sperm concentration $(10^6$/mL)</td>
<td>83.2 ± 73.0</td>
<td>78.1 ± 80.3</td>
</tr>
<tr>
<td></td>
<td>65.3 (8.2 – 215.0)</td>
<td>60.2 (10.2 – 200.4)</td>
</tr>
<tr>
<td></td>
<td>83.2 ± 73.0</td>
<td>78.1 ± 80.3</td>
</tr>
<tr>
<td></td>
<td>65.3 (8.2 – 215.0)</td>
<td>60.2 (10.2 – 200.4)</td>
</tr>
<tr>
<td>Total sperm count $(10^6)$</td>
<td>282.4 ± 287.5</td>
<td>255.2 ± 235.3</td>
</tr>
<tr>
<td></td>
<td>216.1 (18.2 – 748.1)</td>
<td>181.8 (25.7 – 765.3)</td>
</tr>
</tbody>
</table>

a Baltic young men cohort, n=982; T-allele frequency 12.9%, HWE test $P=0.67$

b Data presented as mean ± SD and median (5-95th percentile)

c FSHB -211 T-allele effect is shown as the estimated linear regression (additive model) statistic $\beta$, standard error of the regression (SE) is shown in brackets. Significant associations ($P<0.05$) are given in bold; asterisk (*) marks $P$-values resistant to Bonferroni correction for multiple testing.