Additional file 5. Overlapping SNPs between the HapMap Project and three genotyping platforms within the extended MHC region\(^1\).

<table>
<thead>
<tr>
<th>Overlap</th>
<th>HapMap(^2)</th>
<th>Affy 5.0</th>
<th>Affy 6.0</th>
<th>Illumina 550K</th>
</tr>
</thead>
<tbody>
<tr>
<td>HapMap</td>
<td>1(^3)</td>
<td>0.792319</td>
<td>0.822969</td>
<td>0.887571</td>
</tr>
<tr>
<td></td>
<td>(6,749)(^4)</td>
<td>(1,114)</td>
<td>(1,813)</td>
<td>(1,721)</td>
</tr>
<tr>
<td>Affy 5.0</td>
<td>0.165061</td>
<td>1</td>
<td>0.595098</td>
<td>0.139247</td>
</tr>
<tr>
<td></td>
<td>(1,406)</td>
<td>(1,311)</td>
<td>(270)</td>
<td></td>
</tr>
<tr>
<td>Affy 6.0</td>
<td>0.268632</td>
<td>0.932432</td>
<td>1</td>
<td>0.232078</td>
</tr>
<tr>
<td></td>
<td>(2,203)</td>
<td></td>
<td>(450)</td>
<td></td>
</tr>
<tr>
<td>Illumina 550K</td>
<td>0.255001</td>
<td>0.192034</td>
<td>0.204267</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>(1,939)</td>
</tr>
</tbody>
</table>

\(^1\)The range of the extended MHC region is chr6 28,799,220–34,204,868 [31].
\(^2\)HapMap SNPs from the Chinese Han Beijing population.
\(^3\)The proportion of the overlapping SNPs between the two genotyping platforms.
\(^4\)The number of SNPs in each genotyping platform.