Figure S2: Masking classification of the golden mussel *Limnoperna fortunei* genome performed by Repeat Masker.

<table>
<thead>
<tr>
<th>Total bases masked:</th>
<th>544,534,343 bp (32.55%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of elements</td>
<td>Length occupied (bp)</td>
</tr>
<tr>
<td><strong>LINEs:</strong></td>
<td></td>
</tr>
<tr>
<td>LINE2</td>
<td>103,883</td>
</tr>
<tr>
<td>L3/CR1</td>
<td>8,807</td>
</tr>
<tr>
<td></td>
<td>2,598</td>
</tr>
<tr>
<td><strong>LTR elements</strong></td>
<td>4,699</td>
</tr>
<tr>
<td><strong>DNA elements</strong></td>
<td>11,813</td>
</tr>
<tr>
<td><strong>Unclassified</strong></td>
<td>1,602,684</td>
</tr>
<tr>
<td><strong>Total interspersed repeats</strong></td>
<td>52,5479,769</td>
</tr>
<tr>
<td><strong>Simple repeats</strong></td>
<td>263,315</td>
</tr>
<tr>
<td><strong>Low complexity</strong></td>
<td>53,130</td>
</tr>
</tbody>
</table>