<table>
<thead>
<tr>
<th>Exp. Group</th>
<th>2CE DE genes [n]</th>
<th>DE ratio&gt;1 [n (%)]</th>
<th>DE ratio&lt;1 [n (%)]</th>
</tr>
</thead>
<tbody>
<tr>
<td>Parg(110)^+/+ (arrays)</td>
<td>1241</td>
<td>972 (78.3)</td>
<td>269 (21.7)</td>
</tr>
<tr>
<td>Parg(110)^+/+ (NGS)</td>
<td>370</td>
<td>337 (91.1)</td>
<td>33 (8.9)</td>
</tr>
<tr>
<td>PJ34 inj. (arrays)</td>
<td>1095</td>
<td>869 (79.4)</td>
<td>225 (20.6)</td>
</tr>
</tbody>
</table>

Separating differentially expressed genes in 2-cell embryos (2CEDE) into up-regulated (ratio>1) and down-regulated genes (ratio<1) reveals a strong bias of differentially-expressed genes towards up-regulation or illegitimate activation of genes across all experimental groups/platforms used. The numbers in brackets indicate percentage of genes in a category, e.g., 75.4% of all genes detected in the microarrays of *Parg(110)^+/+* 2CE DE were up-regulated and 24.6% were down-regulated. doi:10.1371/journal.pgen.1004317.t002