Additional file 7. Total concordance in top \( X \) fold change lists between Affymetrix (normalised by GC-RMA), Illumina (normalised by loess for liver data and quantile for kidney data) and Operon (vsn and scale) for both tissues and all comparisons, using unfiltered (1,804 genes) and top 25% intensity-based filtering (approximately 280 genes).

<table>
<thead>
<tr>
<th></th>
<th>Liver 100%</th>
<th>Liver 25%</th>
<th>Kidney 100%</th>
<th>Kidney 25%</th>
</tr>
</thead>
<tbody>
<tr>
<td>BNvWKY</td>
<td>5  9  26  44  84  217</td>
<td>4  12  23  53  125  -</td>
<td>4  7  18  30  59  177</td>
<td>4  11  20  43  116  -</td>
</tr>
<tr>
<td>GKvBN</td>
<td>7  11  23  36  73  222</td>
<td>7  12  19  47  128  -</td>
<td>3  10  21  44  89  223</td>
<td>7  12  31  59  132  -</td>
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<td>7  11  28  56  130  -</td>
<td>4  6  15  32  54  163</td>
<td>4  11  22  45  118  -</td>
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<tr>
<td>STZvGK</td>
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<td>8  13  29  59  132  -</td>
<td>4  7  18  30  59  177</td>
<td>4  11  20  43  116  -</td>
</tr>
<tr>
<td>STZvWKY</td>
<td>9  12  29  48  82  218</td>
<td>8  13  31  60  125  -</td>
<td>4  6  15  32  54  163</td>
<td>4  11  22  45  118  -</td>
</tr>
</tbody>
</table>