Table S1: **Number of differentially expressed genes and accessible chromatin regions detected between liver, lung, and kidney tissues at FDR ≤ 0.1**

<table>
<thead>
<tr>
<th></th>
<th>Tissue comparison</th>
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<tbody>
<tr>
<td></td>
<td>Liver/lung</td>
</tr>
<tr>
<td>Genes</td>
<td></td>
</tr>
<tr>
<td>Up-regulated</td>
<td>2,473 (20.8&lt;sup&gt;a&lt;/sup&gt;)</td>
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<tr>
<td>Down-regulated</td>
<td>3,236 (27.2&lt;sup&gt;a&lt;/sup&gt;)</td>
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<tr>
<td>Total</td>
<td>5,709 (48.0&lt;sup&gt;a&lt;/sup&gt;)</td>
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<tr>
<td>Chromatin regions</td>
<td></td>
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<tr>
<td>Increased accessibility</td>
<td>20,194 (19.6&lt;sup&gt;b&lt;/sup&gt;)</td>
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<tr>
<td>Decreased accessibility</td>
<td>20,603 (19.7&lt;sup&gt;b&lt;/sup&gt;)</td>
</tr>
<tr>
<td>Total</td>
<td>40,797 (39.3&lt;sup&gt;b&lt;/sup&gt;)</td>
</tr>
</tbody>
</table>

<sup>a</sup> Percentage of all tested genes.

<sup>b</sup> Percentage of all tested chromatin regions prior to merging adjacent genomic windows.