Supplemental Table 1: Body Weight Development and Food Conversion

<table>
<thead>
<tr>
<th></th>
<th>HFD (Mean ± SD)</th>
<th>SBD (Mean ± SD)</th>
<th>HFD/SBD</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>body weight at 5 wk (g)</td>
<td>15.37 ± 1.32</td>
<td>14.14 ± 1.08</td>
<td>1.08</td>
<td>0.048</td>
</tr>
<tr>
<td>body weight at 6 wk (g)</td>
<td>18.12 ± 1.97</td>
<td>16.66 ± 1.08</td>
<td>1.08</td>
<td>0.073</td>
</tr>
<tr>
<td>body weight at 12 wk (g)</td>
<td>35.59 ± 3.31</td>
<td>24.91 ± 1.43</td>
<td>1.43</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>body weight gain 6-12 wk (g)</td>
<td>17.47 ± 3.08</td>
<td>8.25 ± 2.12</td>
<td>2.12</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>body weight gain/day*(g)</td>
<td>0.55 ± 0.22</td>
<td>0.28 ± 0.12</td>
<td>1.96</td>
<td>0.043</td>
</tr>
<tr>
<td>food consumption/day* (g)</td>
<td>6.15 ± 0.26</td>
<td>7.59 ± 0.17</td>
<td>0.81</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>consumed energy/day* (kcal)</td>
<td>28.9 ± 1.23</td>
<td>30.12 ± 0.69</td>
<td>0.96</td>
<td>0.090</td>
</tr>
<tr>
<td>feed efficiency at 8 wk**</td>
<td>0.028 ± 0.006</td>
<td>0.01 ± 0.004</td>
<td>2.80</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>feed efficiency at 12 wk**</td>
<td>0.016 ± 0.004</td>
<td>0.011 ± 0.004</td>
<td>1.45</td>
<td>0.103</td>
</tr>
</tbody>
</table>

*Data are given for the age between 8 and 12 weeks when food intake was measured.

** body weight gain/consumed energy (g/kcal)

Supplemental Table 1: Body weight development and food conversion for mice fed a high fat diet (HFD) and standard breeding diet (SBD). The energy density for high fat diet (HFD) is 4.70 kcal/g and for standard breeding diet 3.97 kcal/g.
### Supplemental Table 2: Correlation of Fatty Acids with ANOVA Variance Components

<table>
<thead>
<tr>
<th>Fatty Acid</th>
<th>Positive Correlations</th>
<th>Negative Correlations</th>
<th>Total Correlations</th>
</tr>
</thead>
<tbody>
<tr>
<td>C16:0</td>
<td>128</td>
<td>341</td>
<td>469</td>
</tr>
<tr>
<td>C16:1</td>
<td>122</td>
<td>113</td>
<td>235</td>
</tr>
<tr>
<td>C18:0</td>
<td>135</td>
<td>328</td>
<td>463</td>
</tr>
<tr>
<td>C18:1</td>
<td>0</td>
<td>6</td>
<td>6</td>
</tr>
<tr>
<td>C18:2:n-6</td>
<td>37</td>
<td>1</td>
<td>38</td>
</tr>
<tr>
<td>C18:3:n-3</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

**Supplemental Table 2:** The number of significant correlations (positive, negative and total) between fatty acid components and ANOVA variance components for genes that show significant differences in their Diet:Tissue interaction.
Supplemental Table 3: ANOVA Results

Model: \( Y_i = \mu + \text{Diet} + \varepsilon_i \)

<table>
<thead>
<tr>
<th>Tissue</th>
<th>No. of DE probes</th>
<th>No. of DE genes</th>
<th>( \pi_0 )</th>
<th>q-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>BAT</td>
<td>1354</td>
<td>1136</td>
<td>0.57</td>
<td>0.01</td>
</tr>
<tr>
<td>GonF</td>
<td>1160</td>
<td>1000</td>
<td>0.61</td>
<td>0.02</td>
</tr>
<tr>
<td>GlutF</td>
<td>1973</td>
<td>1670</td>
<td>0.53</td>
<td>0.01</td>
</tr>
<tr>
<td>MesF</td>
<td>297</td>
<td>245</td>
<td>0.7</td>
<td>0.07</td>
</tr>
<tr>
<td>RetF</td>
<td>2128</td>
<td>1790</td>
<td>0.56</td>
<td>0.01</td>
</tr>
<tr>
<td>SubF</td>
<td>1710</td>
<td>1426</td>
<td>0.59</td>
<td>0.01</td>
</tr>
<tr>
<td>Liver</td>
<td>330</td>
<td>283</td>
<td>0.94</td>
<td>0.08</td>
</tr>
<tr>
<td>Muscle</td>
<td>113</td>
<td>103</td>
<td>0.92</td>
<td>0.15</td>
</tr>
</tbody>
</table>

Model: \( Y_i = \mu + \text{Diet} + \text{Tissue} + \text{Diet:Tissue} + \varepsilon_i \)

<table>
<thead>
<tr>
<th>No. of DE probes</th>
<th>No. of DE genes</th>
<th>( \pi_0 )</th>
<th>q-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>3165</td>
<td>2842</td>
<td>0.84</td>
<td>0.01</td>
</tr>
</tbody>
</table>

Supplemental Table 3: Distribution of permutation P-values from the F_s statistic for the test contrasting diet within each tissue \( (Y_i = \mu + \text{Diet} + \varepsilon_i) \) and the interaction between diet and tissue \( (Y_i = \mu + \text{Diet} + \text{Tissue} + \text{Diet:Tissue} + \varepsilon_i) \) (1). A P-value cutoff of 0.001 was used to generate the genelists. The estimated proportion of null hypothesis is given as \( \pi_0 \) and the q-value is the estimate of the proportion of differentially expressed probes that are false discoveries (2). No. of DE probes is the number of probes differentially expressed, and No. of D.E. genes is the number of probes with unique Entrez Gene Identifiers.
### Supplemental Table 4: Overlaps in Up-regulated and Down-Regulated differentially expressed genes from ANOVA tests for diet within Tissue

<table>
<thead>
<tr>
<th>Tissue</th>
<th>BAT</th>
<th>GonF</th>
<th>GlutF</th>
<th>MesF</th>
<th>RetF</th>
<th>SubF</th>
<th>WAT</th>
<th>Liver</th>
<th>Muscle</th>
</tr>
</thead>
<tbody>
<tr>
<td>BAT</td>
<td>577/597</td>
<td>217</td>
<td>214</td>
<td>44</td>
<td>281</td>
<td>238</td>
<td>428</td>
<td>8</td>
<td>1</td>
</tr>
<tr>
<td>GonF</td>
<td>123</td>
<td>441/559</td>
<td>306</td>
<td>37</td>
<td>422</td>
<td>250</td>
<td>559</td>
<td>6</td>
<td>3</td>
</tr>
<tr>
<td>GlutF</td>
<td>139</td>
<td>214</td>
<td>815/855</td>
<td>37</td>
<td>402</td>
<td>313</td>
<td>855</td>
<td>9</td>
<td>1</td>
</tr>
<tr>
<td>MesF</td>
<td>60</td>
<td>54</td>
<td>62</td>
<td>160/85</td>
<td>25</td>
<td>57</td>
<td>85</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>RetF</td>
<td>173</td>
<td>284</td>
<td>328</td>
<td>76</td>
<td>752/1038</td>
<td>275</td>
<td>1038</td>
<td>8</td>
<td>4</td>
</tr>
<tr>
<td>SubF</td>
<td>204</td>
<td>211</td>
<td>264</td>
<td>101</td>
<td>252</td>
<td>691/735</td>
<td>735</td>
<td>13</td>
<td>5</td>
</tr>
<tr>
<td>WAT*</td>
<td>311</td>
<td>441</td>
<td>815</td>
<td>160</td>
<td>752</td>
<td>691</td>
<td>1686/1686</td>
<td>20</td>
<td>12</td>
</tr>
<tr>
<td>Liver</td>
<td>13</td>
<td>6</td>
<td>17</td>
<td>1</td>
<td>11</td>
<td>13</td>
<td>23</td>
<td>125/158</td>
<td>4</td>
</tr>
<tr>
<td>Muscle</td>
<td>8</td>
<td>8</td>
<td>13</td>
<td>6</td>
<td>8</td>
<td>8</td>
<td>14</td>
<td>4</td>
<td>53/50</td>
</tr>
</tbody>
</table>

### Percentage of overlap of differentially expressed genes from ANOVA tests for diet within Tissue

<table>
<thead>
<tr>
<th>Tissue</th>
<th>BAT</th>
<th>GonF</th>
<th>GlutF</th>
<th>MesF</th>
<th>RetF</th>
<th>SubF</th>
<th>WAT</th>
<th>Liver</th>
<th>Muscle</th>
</tr>
</thead>
<tbody>
<tr>
<td>BAT</td>
<td></td>
<td>30</td>
<td>35</td>
<td>9</td>
<td>41</td>
<td>38</td>
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<tr>
<td>GonF</td>
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<td>9</td>
<td>71</td>
<td>47</td>
<td>4</td>
<td>3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>GlutF</td>
<td>24</td>
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<td>7</td>
<td>45</td>
<td>36</td>
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<td>2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>MesF</td>
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<td>44</td>
<td>42</td>
<td>66</td>
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<td>7</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RetF</td>
<td>26</td>
<td>40</td>
<td>41</td>
<td>6</td>
<td>34</td>
<td>3</td>
<td>2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SubF</td>
<td>32</td>
<td>33</td>
<td>42</td>
<td>11</td>
<td>40</td>
<td>5</td>
<td>3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>WAT*</td>
<td>22</td>
<td>28</td>
<td>48</td>
<td>7</td>
<td>51</td>
<td>42</td>
<td>4</td>
<td>2</td>
<td></td>
</tr>
<tr>
<td>Liver</td>
<td>19</td>
<td>14</td>
<td>24</td>
<td>3</td>
<td>20</td>
<td>43</td>
<td>23</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td>Muscle</td>
<td>25</td>
<td>25</td>
<td>31</td>
<td>18</td>
<td>27</td>
<td>57</td>
<td>33</td>
<td>11</td>
<td></td>
</tr>
</tbody>
</table>

*WAT includes all genes differentially expressed in gonadal, gluteal, mesenteric, retroperitoneal and subcutaneous adipose tissues.

**Supplemental Table 4:** Top: Overlap in the number of up-regulated (red) and down-regulated (green) differentially expressed genes from the ANOVA tests for diet within tissue. The number of differentially expressed genes in WAT is the union of the white adipose tissue gene lists. Bottom: The percent of overlap in differential expression between tissue types. The table is read row-wise, e.g., of the differentially expressed genes in BAT, 30% are also differentially expressed in gonadal, 35% in gluteal, etc.