### Supplemental Table S1. Primers used in qPCR studies

<table>
<thead>
<tr>
<th>Gene name</th>
<th>GenBank accession number</th>
<th>Primer sequence 5′ to 3′</th>
<th>( R^2 )</th>
<th>Amplification efficiency (%)</th>
<th>Amplicon size (bp)</th>
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<tbody>
<tr>
<td><strong>Diet-responsive transcripts</strong></td>
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<tr>
<td><em>Fc receptor-like protein 2</em> (fcr2)</td>
<td>DY734226</td>
<td>Forward</td>
<td>0.993</td>
<td>91.2</td>
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<tr>
<td><em>fatty acid-binding protein, adipocyte</em> (fabp4)</td>
<td>NM_00114203</td>
<td>Forward</td>
<td>0.992</td>
<td>97.9</td>
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<td><em>FAD-linked sulfhydryl oxidase ALR-like</em> (fadox)</td>
<td>GE791133</td>
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<td>0.998</td>
<td>102.3</td>
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<td><em>legumain-like</em> (lgma)</td>
<td>EG917238</td>
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<td><em>lathosterol oxidase</em> (sc5d)</td>
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<td><em>MHC-I</em></td>
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<td><em>Receptors</em></td>
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<td>RNA helicase lgp2 (lgp2)†</td>
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<td><em>CD209 antigen-like protein e</em> (cd209e)</td>
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<td><em>mitogen-activated protein kinase kinase 8</em> (mapk8)</td>
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### Transcription factors

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<th>Gene Name</th>
<th>Accession</th>
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<th>Reverse Primer</th>
<th>Expression</th>
<th>log2 Fold Change</th>
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<td><strong>dual specificity phosphatase 6 (dusp6)</strong></td>
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<td><strong>dual specificity phosphatase 22-a (dusp22a)</strong></td>
<td>NM_001140429</td>
<td>Forward</td>
<td>Reverse</td>
<td>AGCCTTTCGTGTAAGTA</td>
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<tr>
<td><strong>cAMP-responsive element modulator-like (crem)</strong></td>
<td>CB508904</td>
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<td><strong>interferon regulatory factor 7 (irf7)</strong></td>
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<td>Forward</td>
<td>Reverse</td>
<td>AGCCTTTCGTGTAAGTA</td>
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<tr>
<td><strong>cyclic AMP-dependent transcription factor ATF-3 (atf3)</strong></td>
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<td><strong>basic leucine zipper transcription factor, ATF-like 3 (batf3)</strong></td>
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### Immune effectors

<table>
<thead>
<tr>
<th>Gene Name</th>
<th>Accession</th>
<th>Forward Primer</th>
<th>Reverse Primer</th>
<th>Expression</th>
<th>log2 Fold Change</th>
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<tbody>
<tr>
<td><strong>ring finger protein 8, E3 ubiquitin protein ligase (rnf8)</strong></td>
<td>NM_001173788</td>
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<td>Reverse</td>
<td>CAGACAGGATGTTGGTGATG</td>
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<tr>
<td><strong>CASP8 and FADD-like apoptosis regulator (cflar)</strong></td>
<td>EG868960</td>
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<td>Reverse</td>
<td>GCTCTCTATGCAAGCCCTAGTC</td>
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<td><strong>interferon-induced GTP-binding protein Mx (mx)</strong></td>
<td>NM_001139918</td>
<td>Forward</td>
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<tr>
<td><strong>optineurin (optn)</strong></td>
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<td><strong>E3 ubiquitin-protein ligase hrc3 (herc3)</strong></td>
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<td><strong>interferon, gamma (ifng)</strong></td>
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<td><strong>viperin</strong></td>
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<td><strong>beta-1 syntrophin (sntb1)</strong></td>
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<td><strong>cathepsin-L1-like (ctsl1)</strong></td>
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<td><strong>cathepsin-f (ctsf)</strong></td>
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### Normalizers

<table>
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<tr>
<th>Gene Name</th>
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<th>Reverse Primer</th>
<th>Expression</th>
<th>log2 Fold Change</th>
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<td><strong>60S ribosomal protein 32 (rpl32)</strong></td>
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<td>Reverse</td>
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<td>AGGCGGGTTTAAAGGTTCAGAT</td>
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<tr>
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<td>CTCCTTTCTCTCTCTCTCTCTCT</td>
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* These transcripts were not present in the microarray significant gene list.

* The amplification efficiencies of these primers were determined using 4-point serial dilutions of cDNA. The diet-responsive transcripts were selected from RP-identified gene lists. The plC-responsive transcripts were selected from microarray-identified transcripts overlapping between SAM and RP in both dietary groups (783 DEP; see Fig. 2), except for cd209d (RP-identified in the FO5 group), and stat1 and irf7 (SAM-identified in both groups).