

Supplemental material

Table S1. Primer sequences used for quantitative real-time polymerase chain reaction

| Gene symbol | GenBank accession [PrimerBank ID] | Forward primer 5'→3' | Reverse primer 5'→3' | Amplicon size (bp) |
|---------------------------------|------------------------------------|-------------------------|-------------------------|--------------------|
| <i>Abcb1a</i> | NM_011076.1 [6755048a1] | CAGCAGTCAGTGTGCTTACAA | ATGGCTCTTTTATCGGCCTCA | 205 |
| <i>Aldh1a1</i> | NM_013467.2 [7304881a1] | ATACTTGTCGGATTTAGGAGGCT | GGGCCTATCTTCCAAATGAACA | 192 |
| <i>Ces2</i> ⁺ | NM_145603.1 | CACGGAACCAACTACATAAC | AGACATAGGGAAGGAAGACA | 362 |
| <i>Fabp2</i> | NM_007980.2 [6679737a1] | GTGGAAGTAGACCGGAACGA | CCATCCTGTGTGATTGTCTAGTT | 117 |
| <i>Igfbp5</i> | NM_010518.2 [6754312a2, 6754312a3] | TTGCCTCAACGAAAAGAGCTAC | CACAGTTGGGCAGGTACACAG | 362 |
| <i>Ppara</i> ⁺ | NM_011144.2 | GGTGTGTATGAAGCCATCT | AGCCACAAACAGGGAAAT | 206 |
| <i>Sult1a1</i> | NM_133670.1 [5420463a3] | CAGCCCCACGGATCATTAAG | ACGACCCATAGGACACTTTC | 216 |
| Reference genes | | | | |
| <i>Canx</i> * | NM_007597.2 | CTGAAGGCTGGCTAGACGACGAA | GCTGACTCACACTTGGGGTTGG | 130 |
| <i>Cyclophilin</i> ⁺ | NM_008907.1 | CACTGCCAAGACTGAATG | CTACAGAAGGAATGGTTTGA | 200 |

* Primer originally described by Dommels et al. [26].

⁺ Primers designed using Primer3 software.

Abcb1a = ATP-binding cassette, subfamily B, member 1, *Aldh1a1* = aldehyde dehydrogenase 1 family, member A1, *Ces2* = carboxylesterase 2, *Fabp2* = fatty acid binding protein 2, *Igfbp5* = insulin-like growth factor binding protein 5, *Ppara* = peroxisome proliferator-activated receptor α , *Sult1a1* = sulfotransferase family 1A, phenol-preferring, member 1, *Canx* = calnexin, *Cyclophilin* = Cyclophilin A or peptidylprolyl isomerase A.

Table S2. Significant biological functions and pathways in colon tissues of (1) *Il10*^{-/-} vs. C57 mice fed OA diet, (2) EPA- vs. OA-fed *Il10*^{-/-} mice and (3) EPA- vs. OA-fed C57 mice

The global functional analysis identified biological functions (molecular and cellular functions; physiological system development and function) and diseases that were most

| | <i>Il10</i> ^{-/-} vs. C57 (fed OA) | EPA vs. OA (in <i>Il10</i> ^{-/-}) | EPA vs. OA (in C57) |
|--|---|--|--|
| <i>Biological functions</i> | | | |
| Diseases and disorders | Immunological disease (238) Inflammatory disease (239) Connective tissue disorders (159) Skeletal and muscle disorders (181) Metabolic disease (129) | Hepatic system disease (17) Cancer (57) Infectious disease (9) Organismal injury and abnormalities (17) Inflammatory disease (24) | Inflammatory disease (33) Cancer (68) Connective tissue disorders (21) Immunological disease (28) Skeletal and muscle disorders (26) |
| Molecular and cellular functions | Cellular movement (275) Cell-to-cell signalling and interaction (283) Cellular growth and proliferation (393) Cell signalling (513) Cell death (343) | Lipid metabolism (45) Vitamin and mineral metabolism (25) Amino acid metabolism (41) Cell signalling (66) Drug metabolism (25) | Lipid metabolism (45) Molecular transport (15) Small molecule biochemistry (29) Cellular growth and proliferation (65) Amino acid metabolism (20) |
| Physiological system development and functions | Immune response (300) Haematological system development and function (264) Immune and lymphatic system development and function (239) Tissue morphology (182) | Behaviour (6) Nervous system development and function (15) Organismal survival (12) Connective tissue development and function (11) | Tumour morphology (6) Skeletal and muscular system development and function (19) Cardiovascular system development and function (12) Visual system development and function (10) |
| | Tissue development (206) | Tissue morphology (9) | Organismal survival (25) |
| <i>Pathways</i> | LPS/ <i>Il1</i> -mediated inhibition of <i>Rxr</i> function (53/192) Fibrosis/stellate cell activation (41/131) <i>Il10</i> signalling (22/68) Metabolism of xenobiotics by cytochrome P450 (27/213) Fatty acid metabolism (33/187) Tryptophan metabolism (31/237) | Xenobiotic metabolism signalling (19/251) Metabolism of xenobiotics by cytochrome P450 (12/213) LPS/ <i>Il1</i> -mediated inhibition of <i>Rxr</i> function (13/192) Fatty acid metabolism (10/187) Tryptophan metabolism (8/237) Cholestasis (8/162) | Phenylalanine metabolism (5/107) Complement system (5/37) PI3K/AKT signalling (9/147) Metabolism of xenobiotics by cytochrome P450 (6/213) Linoleic acid metabolism (5/123) Cholestasis (6/162) |
| | Leukocyte extravasation signalling (41/188) | <i>Il10</i> signalling (3/68) | Arachidonic acid metabolism (5/211) |

significant to the dataset. The top five functions and the number of genes differentially expressed in each category are summarized.

The number or ratio in parentheses represents the total number of differentially expressed genes associated with each biological function or associated with the total number of genes in that pathway.

Table S3. Differentially expressed genes associated with fatty acid metabolism, xenobiotic metabolism, tryptophan metabolism, immune and inflammatory response pathways in the (1) genotype comparison (*Il10*^{-/-} vs. C57 mice fed OA diet), (2) diet comparison (EPA vs. OA) in *Il10*^{-/-} mice, and (3) diet comparison (EPA vs. OA) in C57 mice

| Gene symbol | Gene description | GeneBank accession No. | <i>Il10</i> ^{-/-} vs. C57 on OA | | EPA vs. OA in <i>Il10</i> ^{-/-} | | EPA vs. OA in C57 | |
|----------------|--|------------------------|--|---------|--|---------|-------------------|---------|
| | | | fold change | p value | fold change | p value | fold change | p value |
| <i>Aldh1a1</i> | aldehyde dehydrogenase 1 family, member A1 | NM_013467 | -2.1 | <.00001 | +2.1 | <.00001 | | |
| <i>Aldh1a3</i> | aldehyde dehydrogenase 1 family, member A3 | NM_053080 | | | | | +1.9 | 0.003 |
| <i>Aldh1a7</i> | aldehyde dehydrogenase family 1, subfamily A7 | NM_011921 | -2.7 | <.00001 | +1.6 | 0.006 | | |
| <i>Aldh1l1</i> | aldehyde dehydrogenase 1 family, member L1 | NM_027406 | +2.3 | <.00001 | | | | |
| <i>Aldh2</i> | aldehyde dehydrogenase 2 family (mitochondrial) | NM_009656 | -1.8 | 0.001 | | | | |
| <i>Aldh3b1</i> | aldehyde dehydrogenase 3 family, member B1 | NM_026316 | +1.4 | 0.006 | | | | |
| <i>Cyp1b1</i> | cytochrome P450, family 1, subfamily B, polypeptide 1 | NM_009994 | +1.5 | 0.001 | | | | |
| <i>Cyp2c9</i> | cytochrome P450, family 2, subfamily C, polypeptide 9 | NM_007815 | -7.7 | <.00001 | | | | |
| <i>Cyp2c18</i> | cytochrome P450, family 2, subfamily C, polypeptide 18 | NM_028089 | | | +3.1 | 0.006 | | |
| <i>Cyp2c37</i> | cytochrome P450, family 2. subfamily c, polypeptide 37 | NM_010001 | -2.6 | <.00001 | | | -1.8 | 0.004 |
| <i>Cyp2c40</i> | cytochrome P450, family 2, subfamily c, polypeptide 40 | NM_010004 | -14.3 | <.00001 | +3.0 | 0.001 | | |
| <i>Cyp2c44</i> | cytochrome P450, family 2, subfamily c, polypeptide 44 | NM_01001446 | | | +1.7 | 0.008 | | |
| <i>Cyp2c54</i> | cytochrome P450, family 2, subfamily c, polypeptide 54 | NM_206537 | -1.6 | 0.002 | | | | |
| <i>Cyp2d6</i> | cytochrome P450, family 2, subfamily D, polypeptide 6 | NM_019823 | -1.7 | 0.005 | | | | |
| <i>Cyp2d26</i> | cytochrome P450, family 2, subfamily d, polypeptide 26 | NM_029562 | -2.5 | <.00001 | +1.8 | 0.003 | | |
| <i>Cyp2j2</i> | cytochrome P450, family 2, subfamily J, polypeptide 2 | NM_010008 | -1.3 | 0.007 | | | -1.5 | <.00001 |
| <i>Cyp2s1</i> | cytochrome P450, family 2, subfamily S, polypeptide 1 | NM_028775 | -1.8 | <.00001 | | | | |
| <i>Cyp3a4</i> | cytochrome P450, family 3, subfamily A, polypeptide 4 | NM_177380 | -1.7 | 0.006 | | | | |
| <i>Cyp3a5</i> | cytochrome P450, family 3, subfamily A, polypeptide 5 | NM_007819 | -2.2 | <.00001 | +1.9 | 0.001 | | |
| <i>Cyp4b1</i> | cytochrome P450, family 4, subfamily B, polypeptide 1 | NM_007823 | -8.3 | <.00001 | | | | |
| <i>Cyp51a1</i> | cytochrome P450, family 51, subfamily A, polypeptide 1 | NM_020010 | | | -1.6 | 0.001 | -1.4 | 0.006 |

Table S4. Gene ontology (GO) terms over-represented in colon inflammation comparing *Il10*^{-/-} vs. C57 mice on OA diet

| GO ID | GO term | Number of genes | P over-representation after data refinement |
|---------------------------|---|-----------------|---|
| <i>Molecular function</i> | | | |
| GO:0008009 | chemokine activity | 18 | 4.81E-10 |
| GO:0003823 | antigen binding | 12 | 1.67E-06 |
| GO:0004759 | serine esterase activity | 13 | 1.80E-06 |
| GO:0032395 | MHC class II receptor activity | 7 | 2.88E-06 |
| GO:0004364 | glutathione transferase activity | 10 | 4.48E-06 |
| GO:0048503 | GPI anchor binding | 16 | 5.90E-06 |
| GO:0016787 | hydrolase activity | 275 | 1.29E-05 |
| GO:0004896 | hematopoietin/interferon-class cytokine receptor activity | 18 | 0.00018 |
| GO:0003779 | actin binding | 47 | 0.00019 |
| GO:0016641 | oxidoreductase activity, oxygen as acceptor | 6 | 0.00037 |
| GO:0016493 | C-C chemokine receptor activity | 7 | 0.00042 |
| GO:0004888 | transmembrane receptor activity | 119 | 0.00062 |
| GO:0019865 | immunoglobulin binding | 5 | 0.00075 |
| GO:0016868 | intramolecular transferase activity, phosphotransferases | 5 | 0.00075 |
| GO:0016229 | steroid dehydrogenase activity | 7 | 0.00087 |
| GO:0008375 | acetylglucosaminyltransferase activity | 6 | 0.00092 |
| GO:0004497 | monooxygenase activity | 21 | 0.00216 |
| GO:0016491 | oxidoreductase activity | 136 | 0.00216 |
| GO:0016627 | oxidoreductase activity | 10 | 0.00258 |
| GO:0005044 | scavenger receptor activity | 8 | 0.00343 |
| GO:0004295 | trypsin activity | 18 | 0.00395 |
| GO:0005096 | GTPase activator activity | 31 | 0.00462 |
| GO:0016860 | intramolecular oxidoreductase activity | 8 | 0.00519 |
| GO:0000287 | magnesium ion binding | 40 | 0.00581 |
| GO:0008378 | galactosyltransferase activity | 7 | 0.00593 |
| GO:0004263 | chymotrypsin activity | 17 | 0.00612 |
| GO:0004907 | interleukin receptor activity | 9 | 0.00626 |
| GO:0019965 | interleukin binding | 11 | 0.00712 |
| GO:0016616 | oxidoreductase activity, NAD or NADP as acceptor | 21 | 0.01387 |
| GO:0003824 | catalytic activity | 679 | 0.02905 |
| GO:0008289 | lipid binding | 48 | 0.03051 |
| <i>Biological process</i> | | | |
| GO:0006955 | immune response | 126 | 0.00031 |
| GO:0042127 | regulation of cell proliferation | 36 | 0.00621 |

FUNC analysis was used to identify significantly over-represented GO terms in the colon of *Il10*^{-/-} vs. C57 mice (both fed the OA diet). GO terms annotated to at least 10 genes and with FDR < 0.05 according to the hypergeometric test were passed to data refinement, and those with p < 0.05 after refinement were considered over-represented in the list of differentially expressed genes, compared with other genes on the array. Only GO terms for molecular function and biological process are shown.

Table S5. Gene ontology (GO) terms over-represented in EPA-fed *Il10*^{-/-} mice compared to OA-fed *Il10*^{-/-} mice

| GO ID | GO term | Number of genes | P over-representation after refinement |
|---------------------------|--|-----------------|--|
| <i>Molecular function</i> | | | |
| GO:0004759 | serine esterase activity | 5 | 3.26E-05 |
| GO:0016705 | oxidoreductase activity, with incorporation or reduction of molecular oxygen | 7 | 0.00025 |
| GO:0015020 | glucuronosyltransferase activity | 3 | 0.00027 |
| GO:0004497 | monooxygenase activity | 7 | 0.00051 |
| GO:0016229 | steroid dehydrogenase activity | 3 | 0.00129 |
| GO:0016491 | oxidoreductase activity | 26 | 0.04575 |
| <i>Biological process</i> | | | |
| GO:0044255 | cellular lipid metabolic process | 16 | 0.00024 |
| GO:0008610 | lipid biosynthetic process | 8 | 0.00043 |

FUNC analysis was used to identify significantly over-represented GO terms in the colon of EPA- vs. OA-fed *Il10*^{-/-} mice. GO terms annotated to at least 10 genes and with FDR < 0.05 according to the hypergeometric test were passed to data refinement, and those with p < 0.05 after refinement were considered over-represented in the list of differentially expressed genes, compared with other genes on the array. Only GO terms for molecular function and biological process are shown.

Fig. S1. Histological injury score (HIS) of colon tissue for individual *Il10*^{-/-} mice on OA diet (n = 5) and EPA diet (n = 4), and C57 mice on OA diet (n = 6) and EPA diet (n = 6). The horizontal line indicates the average colon HIS within each group.

