

Supporting figures

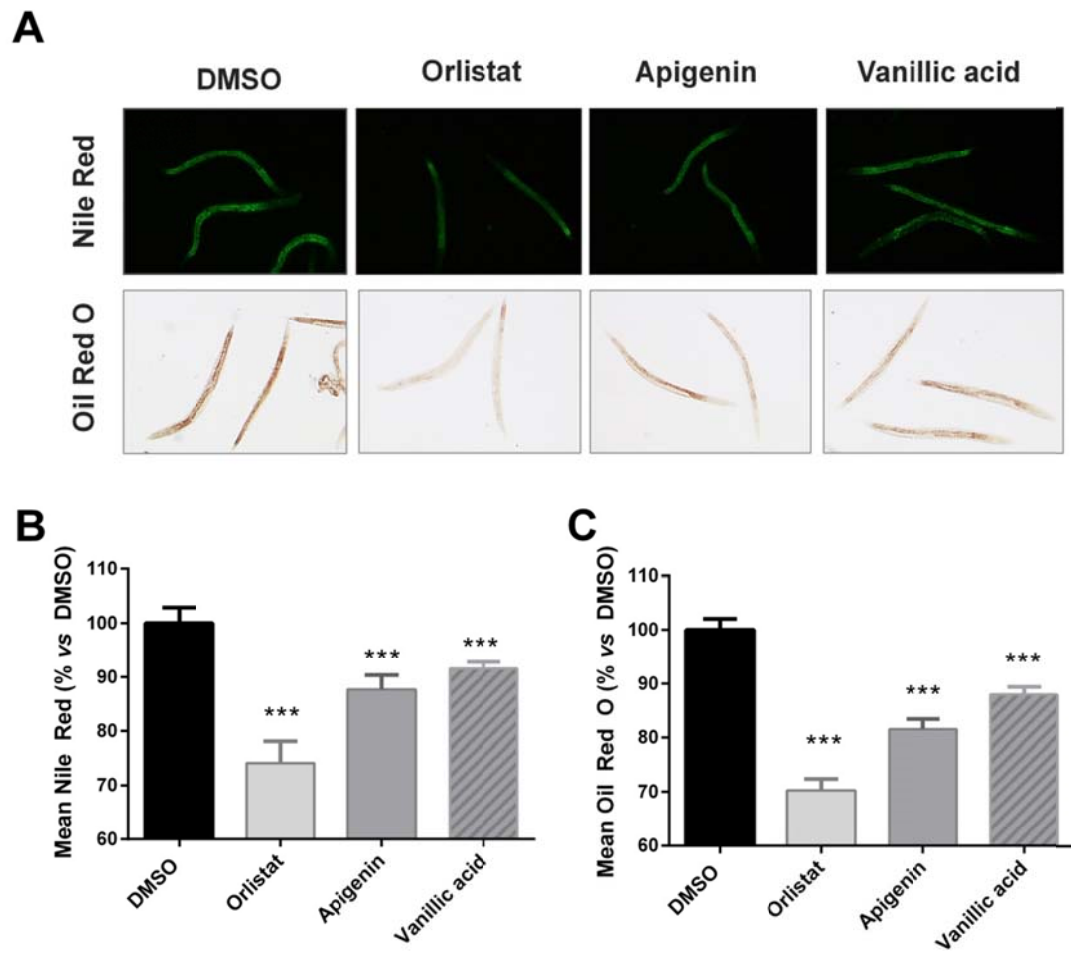


Figure S1. A) Nile Red and Oil Red O staining of DMSO, orlistat (6 μ g/mL, used as positive control), apigenin and vanillic acid (100 μ M)-treated worms. B) Nile Red quantifications of DMSO and treated worms. C) Oil Red O quantifications of DMSO and treated worms. The results are expressed as the mean \pm SD relative to DMSO-treated worms. Significance refers to the effect of the different treatments in comparison with DMSO-control worms (ANOVA followed by LSD test, *** $p < 0.001$).

Supplementary Tables

Table S1. Gene expression probes used for qPCR *.

| <i>C. elegans</i> gene | Fw sequence | Rv sequence | Probe sequence |
|------------------------|---------------------------|-------------------------|--|
| <i>fat-7</i> | ACAAGTTAAGGAGCATGGAGG | TCTCCTCCAGAAATAACGGG | /56-FAM/CAGAGAAAG/Zen/CACTATTTCCCACTGGTCA/3IABkFQ/ |
| <i>gpx-3</i> | TATGAACGGGCTTACCTATGTG | CAACAGTTTGTGGGCAAGAC | /56-FAM/CTCGTAAAG/Zen/TGGGTGATGATTGTCTCCG/3IABkFQ/ |
| <i>F49E12.10</i> | TTTGTATGGCTATGGATGAAATTGG | TGCGTGTTCAAGTGGATGAG | /56-FAM/ATGCTGGAA/Zen/ATCGAAACTGGTGCG/3IABkFQ/ |
| <i>acdh-1</i> | ATCCGAGCTTCATCCAATTG | CAGTCCAATCATTGTGCTCC | /56-FAM/AGCCTTTTC/Zen/CATACTCTCCCAGAATTGC/3IABkFQ/ |
| <i>F25E2.3</i> | AGATACTGAGCCAATGTCGATG | CCGTTTCTGATATGAGGTCGTAC | /56-FAM/ATCACCGTC/Zen/TCCATCAGTGCCTC/3IABkFQ/ |
| <i>F56A4.3</i> | AAGAGATTGTGCAGACTGGAG | CAGAGCTTCTATCAGGCATCC | /56-FAM/TGCGTCATT/Zen/TGGGAAGAGTTCATGGA/3IABkFQ/ |
| <i>F09C8.1</i> | TTCTAATGTCTTGTACCTCCG | TCAAGCTGATCATGGCACTAG | /56-FAM/CGAGGATCC/Zen/GGTAGCAGTCTTCT/3IABkFQ/ |
| <i>acdh-2</i> | TGAGCTAACCCGACCATTG | CAGGAACCATTGCTCAAGTG | /56-FAM/ACGCTATTG/Zen/AAGTTCTGAATGCCAGTCG/3IABkFQ/ |
| <i>c17c3.1</i> | AAGAGCATCGAAGAGCAGAAG | TTTTGGATGAGAGCAGGAGG | /56-FAM/TCCACAGAT/Zen/GGCTGATCGCTTACAAC/3IABkFQ/ |
| <i>gpx-5</i> | GCGTACACCCAGCAATACA | TCAGCTGGCTCTTGCAAATA | /56-FAM/CCAAGGAT/Zen/TTACTCTCATTGCCTTCCC/3IABkFQ/ |
| <i>gpdh-1</i> | TTAGGGTGACAACGGATTATGAG | CAGACGGATGATAGCGGATTT | /56-FAM/TGGAGCTTT/Zen/GCGGAGCACTAAAGA/3IABkFQ/ |
| <i>cyp-37b1</i> | GGCTGAAGCCTTTATGGTACT | GGAAGCTTCCCATTTCTCCTT | /56-FAM/CCCGGCCAT/Zen/GAGTATGACAGACAT/3IABkFQ/ |
| <i>f44e5.5</i> | GCAGCTCGTAATCCAGAGAAT | CTCCAAATGGCCAATGCTTAC | /56-FAM/TGGACGACG/Zen/TTTCGATGAATCAACAGT/3IABkFQ/ |
| <i>lip-5</i> | CTCTGCGACAACGTCCTATT | CATGAGTAGCGTAGACTGGAAC | /56-FAM/AGTGACCAA/Zen/TGGAACCAGACACGT/3IABkFQ/ |
| <i>ncx-8</i> | CCTGGGAATCTACGCAGTTTAT | TCACTTCCAGCTGCTTCTT | /56-FAM/CCGTACTCG/Zen/GCGGAAGAACTTGAAA/3IABkFQ/ |
| <i>cyp13a6</i> | GAAGTAGCTGTACAGGCAAGAA | GAAGCTGGGCATCAAGGAATA | /56-FAM/AAAGGAGTT/Zen/GAGCCAGGAGAACCT/3IABkFQ/ |

* The expression level of each gene was normalized comparing to the expression of the *pmp3* (Ce02485188_m1) and *tba1* (Ce02412618_gH) genes from *Life Technologies* (TaqMan Gene Expression Assays), as housekeeping gene controls.

Table S2. Differentially expressed genes after treatment with resveratrol (200 μ M) vs DMSO-control worms (ANOVA $p < 0.05$; $-2 \leq FC \leq 2$). Results obtained in Transcriptomic Array Console (TAC, Affymetrix).

| Transcript Cluster ID | FC (RSV) | ANOVA p-value | Gene Symbol | Description |
|-----------------------|----------|---------------|--------------|----------------------------------|
| 18484714 | -13.27 | 0.0007 | F49E12.10 | Protein F49E12.10 |
| 18598738 | -4.55 | 0.0025 | lys-2 | Protein LYS-2 |
| 18632007 | -4.38 | 0.0045 | pgp-6 | Protein PGP-6 |
| 18484756 | -4.16 | 0.0054 | F49E12.9 | Protein F49E12.9 |
| 18453349 | -3.90 | 0.0010 | acdh-1 | Protein ACDH-1 |
| 18570161 | -3.67 | 0.0068 | CELE_F44G3.2 | Protein F44G3.2 |
| 18597749 | -3.64 | 0.0035 | CELE_W03F9.4 | Protein W03F9.4 |
| 18564293 | -3.58 | 0.0051 | C33G8.2 | Protein C33G8.2 |
| 18615561 | -3.56 | 0.0333 | col-169 | Protein COL-169 |
| 18567605 | -3.21 | 0.0162 | CELE_F20G2.5 | Protein F20G2.5 |
| 18520934 | -3.21 | 0.0249 | C06E8.5 | Protein C06E8.5 |
| 18609505 | -3.06 | 0.0017 | abu-10 | Protein ABU-10 |
| 18480145 | -3.05 | 0.0143 | C30G12.2 | Protein C30G12.2 |
| 18528133 | -3.03 | 0.0161 | T24C4.4 | Protein T24C4.4 |
| 18484287 | -3.00 | 0.0367 | F44E5.5 | Protein F44E5.5; Protein F44E5.4 |
| 18589632 | -3.00 | 0.0142 | fol-2 | Protein FOLT-2 |
| 18581627 | -2.99 | 0.0231 | abu-1 | Protein ABU-1 |
| 18615564 | -2.98 | 0.0096 | col-170 | Protein COL-170 |
| 18554228 | -2.97 | 0.0038 | CELE_K08D8.4 | Protein K08D8.4 |
| 18614569 | -2.94 | 0.0121 | abu-9 | Protein PQN-57 |
| 18597331 | -2.92 | 0.0404 | hsp-16.1 | Protein HSP-16.1 |
| 18582396 | -2.91 | 0.0301 | abu-8 | Protein ABU-8 |
| 18574052 | -2.90 | 0.0276 | hacd-1 | Protein HACD-1 |
| 18587679 | -2.90 | 0.0401 | CELE_F19B2.5 | Protein F19B2.5 |
| 18523094 | -2.90 | 0.0205 | col-91 | Protein COL-91 |
| 18568946 | -2.87 | 0.0479 | F32D8.7 | Protein F32D8.7 |
| 18473813 | -2.82 | 0.0043 | CELE_W01A8.6 | Protein W01A8.6 |
| 18575832 | -2.77 | 0.0438 | col-157 | Protein COL-157 |
| 18601944 | -2.74 | 0.0231 | ZK6.11 | Protein ZK6.11 |
| 18615544 | -2.73 | 0.0100 | col-167 | Protein COL-167 |
| 18548494 | -2.68 | 0.0349 | swt-3 | Protein SWT-3 |
| 18550679 | -2.67 | 0.0229 | D2096.6 | Protein D2096.6 |
| 18571247 | -2.66 | 0.0397 | F56A4.3 | Protein F56A4.3 |
| 18520577 | -2.64 | 0.0161 | tsp-2 | Protein TSP-2 |
| 18589884 | -2.58 | 0.0120 | F41E6.11 | Protein F41E6.11 |
| 18526132 | -2.55 | 0.0111 | ugt-62 | Protein UGT-62 |
| 18552629 | -2.54 | 0.0134 | grl-4 | Protein GRL-4 |
| 18498866 | -2.53 | 0.0154 | gst-14 | Protein GST-14 |
| 18574047 | -2.48 | 0.0438 | pqn-54 | Protein PQN-54 |
| 18575197 | -2.47 | 0.0295 | col-146 | Protein COL-146 |
| 18633021 | -2.47 | 0.0230 | Y102A11A.7 | Protein Y102A11A.7 |
| 18617379 | -2.46 | 0.0122 | Y70D2A.1 | Protein Y70D2A.1 |
| 18576993 | -2.45 | 0.0296 | hsp-16.11 | Protein HSP-16.11 |
| 18466529 | -2.45 | 0.0333 | phat-2 | Protein PHAT-2 |
| 18581646 | -2.45 | 0.0211 | col-149 | Protein COL-149 |
| 18502392 | -2.45 | 0.0135 | abu-11 | Protein ABU-11 |
| 18513698 | -2.44 | 0.0280 | tyr-2 | Protein TYR-2 |
| 18556277 | -2.40 | 0.0046 | T14A8.2 | Protein T14A8.2 |
| 18533906 | -2.40 | 0.0285 | C18H7.11 | Protein C18H7.11 |
| 18621038 | -2.39 | 0.0137 | C34E7.4 | Protein C34E7.4 |

| | | | | |
|----------|-------|--------|---------------|----------------------------|
| 18581691 | -2.39 | 0.0408 | col-150 | Protein COL-150 |
| 18603456 | -2.38 | 0.0063 | clc-1 | Protein CLC-1 |
| 18516242 | -2.36 | 0.0491 | col-88 | Protein COL-88 |
| 18525560 | -2.35 | 0.0124 | K04C2.5 | Protein K04C2.5 |
| 18557521 | -2.35 | 0.0406 | col-120 | Protein COL-120 |
| 18576356 | -2.33 | 0.0180 | T20D4.4 | Protein T20D4.4 |
| 18492312 | -2.33 | 0.0447 | mlt-7 | Protein MLT-7 |
| 18614621 | -2.30 | 0.0369 | R11.2 | Protein R11.2 |
| 18455073 | -2.29 | 0.0064 | sra-17 | Protein SRA-17 |
| 18595609 | -2.27 | 0.0126 | CELE_T06E4.8 | Protein T06E4.8 |
| 18593334 | -2.27 | 0.0098 | cpt-4 | Protein CPT-4 |
| 18590657 | -2.26 | 0.0361 | F48G7.8 | Protein F48G7.8 |
| 18589217 | -2.25 | 0.0082 | F35B12.4 | Protein F35B12.4 // piit-1 |
| 18611996 | -2.24 | 0.0154 | nas-38 | Protein NAS-38 |
| 18626291 | -2.23 | 0.0247 | mxl-3 | Protein MXL-3 |
| 18596111 | -2.23 | 0.0141 | pmp-5 | Protein PMP-5 |
| 18597632 | -2.22 | 0.0465 | CELE_W02F12.2 | Protein W02F12.2 |
| 18582416 | -2.22 | 0.0192 | abu-6 | Protein ABU-6 |
| 18572639 | -2.20 | 0.0041 | K06H6.1 | Protein K06H6.1 |
| 18567815 | -2.19 | 0.0020 | cth-1 | Protein CTH-1 |
| 18543282 | -2.18 | 0.0204 | abu-5 | Protein ABU-5 |
| 18528112 | -2.17 | 0.0392 | toh-1 | Protein TOH-1 |
| 18482914 | -2.17 | 0.0148 | F23F1.2 | Protein F23F1.2 |
| 18586880 | -2.15 | 0.0210 | fat-7 | Protein FAT-7 |
| 18520595 | -2.15 | 0.0377 | tsp-1 | Protein TSP-1 |
| 18603195 | -2.14 | 0.0147 | C06G1.1 | Protein C06G1.1 |
| 18581856 | -2.14 | 0.0302 | col-145 | Protein COL-145 |
| 18521602 | -2.13 | 0.0023 | CELE_C23G10.6 | Protein C23G10.6 |
| 18622471 | -2.12 | 0.0367 | gcsH-1 | Protein GCSH-1 |
| 18590783 | -2.11 | 0.0261 | oac-32 | Protein OAC-32 |
| 18603588 | -2.10 | 0.0186 | C11E4.1 | Protein C11E4.1 |
| 18465325 | -2.09 | 0.0090 | col-62 | Protein COL-62 |
| 18552963 | -2.09 | 0.0306 | col-133 | Protein COL-133 |
| 18454813 | -2.09 | 0.0187 | col-58 | Protein COL-58 |
| 18547290 | -2.08 | 0.0424 | ZK593.3 | Protein ZK593.3 |
| 18494406 | -2.08 | 0.0304 | acdh-2 | Protein ACDH-2 |
| 18568239 | -2.08 | 0.0451 | asns-1 | Protein ASNS-1 |
| 18505735 | -2.08 | 0.0482 | col-71 | Protein COL-71 |
| 18589579 | -2.08 | 0.0436 | F36H9.5 | Protein F36H9.5 |
| 18574697 | -2.07 | 0.0020 | ugt-53 | Protein UGT-53 |
| 18451679 | -2.07 | 0.0224 | C15C6.1 | Protein C15C6.1 |
| 18601975 | -2.06 | 0.0261 | Iron-2 | Protein LRON-2 |
| 18571942 | -2.06 | 0.0425 | unc-23 | Protein UNC-23 |
| 18536789 | -2.03 | 0.0052 | lys-10 | Protein LYS-10 |
| 18556853 | -2.03 | 0.0282 | pqn-74 | Protein PQN-74 |
| 18525231 | -2.03 | 0.0117 | H10E21.4 | Protein H10E21.4 |
| 18611252 | -2.01 | 0.0493 | aagr-4 | Protein AAGR-4 |
| 18503706 | -2.01 | 0.0289 | T23F4.3 | Protein T23F4.3 |
| 18452642 | 2.03 | 0.0122 | fipr-22 | Protein FIPR-22 |
| 18547230 | 2.04 | 0.0102 | CELE_ZK550.2 | Protein ZK550.2 |
| 18536036 | 2.04 | 0.0080 | tpa-1 | Protein TPRA-1 |
| 18629679 | 2.09 | 0.0058 | M60.7 | Protein M60.7 |
| 18494751 | 2.10 | 0.0131 | tre-5 | Protein TRE-5 |
| 18597214 | 2.11 | 0.0181 | CELE_T26H5.8 | Protein T26H5.8 |
| 18624593 | 2.16 | 0.0111 | F25E2.3 | Protein F25E2.3 |

| | | | | |
|----------|------|--------|---------------|--------------------------|
| 18537273 | 2.16 | 0.0302 | thn-2 | Protein THN-2 |
| 18501194 | 2.22 | 0.0327 | K09F6.5 | Protein K09F6.5 |
| 18568638 | 2.27 | 0.0294 | cyp-37B1 | Protein CYP-37B1 |
| 18561523 | 2.64 | 0.0010 | nlp-29 | Protein NLP-29 |
| 18589254 | 2.91 | 0.0182 | CELE_F35E12.5 | Protein F35E12.5 //irg-5 |
| 18595142 | 2.92 | 0.0000 | CELE_T03E6.8 | Protein T03E6.8 |
| 18558751 | 3.01 | 0.0064 | CELE_Y51H4A.5 | Protein Y51H4A.5 |
| 18623122 | 3.16 | 0.0050 | F09C8.1 | Protein F09C8.1 |
| 18567774 | 3.33 | 0.0010 | CELE_F21F8.4 | Protein F21F8.4 |
| 18555883 | 3.96 | 0.0020 | CELE_T07G12.5 | Protein T07G12.5 |

Table S3. Main GO processes and KEGG signalling pathways affected by resveratrol (200 μ M) treatment. Analysis obtained from EGAN UCSF software.

| Gene Ontology Process | Process Name | Enrichment | KEGG | Pathway Name | Enrichment |
|-----------------------|--|------------|------|---|------------|
| GO:0006950 | response to stress | 5.45E-11 | 100 | Steroid biosynthesis | 0.0120 |
| GO:0030968 | endoplasmic reticulum unfolded protein response | 1.12E-09 | 590 | Arachidonic acid metabolism | 0.0700 |
| GO:0034620 | cellular response to unfolded protein | 2.66E-09 | 62 | Fatty acid elongation in mitochondria | 0.0756 |
| GO:0006986 | response to unfolded protein | 3.49E-09 | 1040 | Biosynthesis of unsaturated fatty acids | 0.0922 |
| GO:0034976 | response to endoplasmic reticulum stress | 3.49E-09 | 910 | Nitrogen metabolism | 0.1193 |
| GO:0035967 | cellular response to topologically incorrect protein | 3.97E-09 | 500 | Starch and sucrose metabolism | 0.1456 |
| GO:0006952 | defense response | 3.97E-09 | 650 | Butanoate metabolism | 0.1610 |
| GO:0035966 | response to topologically incorrect protein | 1.31E-08 | 4141 | Protein processing in endoplasmic reticulum | 0.1655 |
| GO:0050896 | response to stimulus | 2.60E-07 | 250 | Alanine, aspartate and glutamate | 0.1761 |
| GO:0071310 | cellular response to organic substance | 8.33E-07 | 510 | N-Glycan biosynthesis | 0.1810 |
| GO:0045087 | innate immune response | 1.97E-06 | 330 | Arginine and proline metabolism | 0.1958 |
| GO:0006955 | immune response | 2.15E-06 | 310 | Lysine degradation | 0.1958 |
| GO:0070887 | cellular response to chemical stimulus | 2.20E-06 | 480 | Glutathione metabolism | 0.2055 |
| GO:0002376 | immune system process | 2.24E-06 | 380 | Tryptophan metabolism | 0.2103 |
| GO:0010033 | response to organic substance | 4.25E-06 | 280 | Valine, leucine and isoleucine degradation | 0.2431 |
| GO:0009617 | response to bacterium | 1.73E-05 | 71 | Fatty acid metabolism | 0.2876 |
| GO:0042742 | defense response to bacterium | 1.73E-05 | 4010 | MAPK signaling pathway | 0.3172 |
| GO:0033554 | cellular response to stress | 1.22E-04 | 1100 | Metabolic pathways | 0.5688 |
| GO:0006633 | fatty acid biosynthetic process | 0.0587 | | | |
| GO:0072330 | monocarboxylic acid biosynthetic process | 0.0701 | | | |
| GO:1901136 | carbohydrate derivative catabolic process | 0.0812 | | | |
| GO:0046394 | carboxylic acid biosynthetic process | 0.0977 | | | |

Table S4. Differentially expressed genes after apigenin (100 μ M) treatment vs DMSO-control worms (ANOVA $p < 0.05$; $-1.5 \leq FC \leq 1.5$). Results obtained in Transcriptomic array console (TAC, Affymetrix).

| Transcript Cluster ID | FC (APIG vs. CNT) | ANOVA p-value (APIG vs. CNT) | Gene Symbol | Description |
|-----------------------|-------------------|------------------------------|-----------------|--------------------|
| 18548347 | -3.12 | 0.004376 | lact-6 | Protein LACT-6 |
| 18497698 | -2 | 0.035086 | F16G10.11 | Protein F16G10.11 |
| 18542887 | -1.97 | 0.006494 | CELE_W02A2.9 | Protein W02A2.9 |
| 18464574 | -1.97 | 0.011399 | B0205.13 | Protein B0205.13 |
| 18582764 | -1.94 | 0.019364 | cyp-35C1 | Protein CYP-35C1 |
| 18560391 | -1.91 | 0.025953 | pqn-90 | Protein PQN-90 |
| 18592542 | -1.85 | 0.010530 | CELE_K02H11.9 | Protein K02H11.9 |
| 18599548 | -1.84 | 0.000679 | CELE_Y43F8B.14 | Protein Y43F8B.14 |
| 18487591 | -1.79 | 0.018389 | CELE_T01B7.13 | Protein T01B7.13 |
| 18564936 | -1.77 | 0.003707 | pqp-9 | Protein PGP-9 |
| 18490903 | -1.75 | 0.041863 | Y51H7C.1 | Protein Y51H7C.1 |
| 18573619 | -1.74 | 0.021973 | M03F8.1 | Protein M03F8.1 |
| 18553047 | -1.7 | 0.012934 | CELE_F53B2.8 | Protein F53B2.8 |
| 18582377 | -1.69 | 0.019432 | ugt-51 | Protein UGT-51 |
| 18583320 | -1.67 | 0.009720 | ncx-8 | Protein NCX-8 |
| 18616126 | -1.67 | 0.010287 | T22B7.3 | Protein T22B7.3 |
| 18503466 | -1.66 | 0.013107 | fbxb-37 | Protein FBXB-37 |
| 18498855 | -1.65 | 0.007166 | CELE_F36H5.9 | Protein F36H5.9 |
| 18568638 | -1.65 | 0.012400 | cyp-37B1 | Protein CYP-37B1 |
| 18523225 | -1.64 | 0.014591 | pqn-29 | Protein PQN-29 |
| 18592847 | -1.63 | 0.019143 | K07B1.8 | Protein K07B1.8 |
| 18565064 | -1.62 | 0.022887 | irg-2 | Protein IRG-2 |
| 18625316 | -1.61 | 0.016830 | F38B2.6 | Protein F38B2.6 |
| 18628994 | -1.61 | 0.025156 | cyp-14A2 | Protein CYP-14A2 |
| 18457037 | -1.6 | 0.003582 | F56H6.1 | Protein F56H6.1 |
| 18567575 | -1.59 | 0.020037 | srbc-27 | Protein SRBC-27 |
| 18584695 | -1.58 | 0.029665 | dmd-11 | Protein DMD-11 |
| 18594198 | -1.56 | 0.000312 | cyp-33C8 | Protein CYP-33C8 |
| 18609993 | -1.55 | 0.001214 | F40E10.5 | Protein F40E10.5 |
| 18561846 | -1.55 | 0.013581 | B0554.4 | Protein B0554.4 |
| 18461357 | -1.53 | 0.031891 | CELE_Y18D10A.4 | Protein Y18D10A.4 |
| 18495412 | -1.53 | 0.048672 | gba-2 | Protein GBA-2 |
| 18550503 | -1.51 | 0.040749 | CELE_C53D6.6 | Protein C53D6.6 |
| 18545035 | -1.51 | 0.040928 | Y54G2A.36 | Protein Y54G2A.36 |
| 18607346 | 1.5 | 0.006976 | pcyt-1 | Protein PCYT-1 |
| 18574818 | 1.5 | 0.043886 | T04C12.7 | Protein T04C12.7 |
| 18505097 | 1.53 | 0.001050 | clcc-4 | Protein CLEC-4 |
| 18626238 | 1.53 | 0.004780 | CELE_F46F2.3 | Protein F46F2.3 |
| 18600676 | 1.54 | 0.001062 | CELE_Y69H2.1 | Protein Y69H2.1 |
| 18607658 | 1.54 | 0.031808 | scav-4 | Protein SCAV-4 |
| 18496370 | 1.55 | 0.025311 | D1022.3 | Protein D1022.3 |
| 18558646 | 1.55 | 0.029226 | Y45F10D.2 | Protein Y45F10D.2 |
| 18626595 | 1.55 | 0.036069 | F47B7.7 | Protein F47B7.7 |
| 18569779 | 1.56 | 0.010778 | CELE_F41B5.12 | Protein F41B5.12 |
| 18559956 | 1.56 | 0.035711 | CELE_Y69A2AR.27 | Protein Y69A2AR.27 |
| 18575442 | 1.57 | 0.006905 | CELE_T08G3.7 | Protein T08G3.7 |
| 18574261 | 1.57 | 0.015710 | pqn-60 | Protein PQN-60 |
| 18542406 | 1.57 | 0.038379 | T22B11.4 | Protein T22B11.4 |

| | | | | |
|----------|------|----------|---------------|------------------|
| 18476129 | 1.58 | 0.003490 | Y51F10.7 | Protein Y51F10.7 |
| 18561999 | 1.59 | 0.006068 | CELE_C01G10.4 | Protein C01G10.4 |
| 18623200 | 1.62 | 0.014630 | F09F9.2 | Protein F09F9.2 |
| 18614294 | 1.64 | 0.007574 | scav-5 | Protein SCAV-5 |
| 18459624 | 1.65 | 0.003595 | T21G5.6 | Protein T21G5.6 |
| 18477914 | 1.66 | 0.035780 | B0228.1 | Protein B0228.1 |
| 18538726 | 1.66 | 0.044014 | noah-2 | Protein NOAH-2 |
| 18627064 | 1.67 | 0.010550 | wrt-2 | Protein WRT-2 |
| 18580352 | 1.69 | 0.001353 | glb-33 | Protein GLB-33 |
| 18583384 | 1.69 | 0.011406 | C13G3.1 | Protein C13G3.1 |
| 18544174 | 1.7 | 0.035356 | col-108 | Protein COL-108 |
| 18490177 | 1.71 | 0.034250 | nspe-7 | Protein NSPE-7 |
| 18561500 | 1.72 | 0.002612 | B0024.4 | Protein B0024.4 |
| 18603602 | 1.73 | 0.001004 | C11E4.2 | Protein C11E4.2 |
| 18588166 | 1.73 | 0.006119 | F22F7.8 | Protein F22F7.8 |
| 18581342 | 1.73 | 0.043085 | lipl-5 | Protein LIPL-5 |
| 18472317 | 1.74 | 0.012859 | R11A5.3 | Protein R11A5.3 |
| 18623467 | 1.86 | 0.031159 | F13C5.5 | Protein F13C5.5 |
| 18628595 | 1.97 | 0.008982 | aqp-8 | Protein AQP-8 |
| 18558503 | 2.13 | 0.029505 | CELE_Y43D4A.2 | Protein Y43D4A.2 |
| 18494494 | 2.25 | 0.023256 | CELE_C17F4.7 | Protein C17F4.7 |
| 18505045 | 2.4 | 0.019494 | nspe-1 | Protein NSPE-1 |
| 18503106 | 2.81 | 0.000542 | cyp-13A6 | Protein CYP-13A6 |

Table S5. Main GO processes and KEGG signalling pathways affected by apigenin (100 μ M) treatment. Analysis obtained from EGAN UCSF software.

| Gene Ontology Process | Process Name | Enrichment | KEGG | Pathway Name | Enrichment |
|-----------------------|---|------------|------|--|------------|
| GO:0009617 | Response to bacterium | 0.00066 | 4020 | Calcium signaling pathway | 0.00797 |
| GO:0042742 | Defense response to bacterium | 0.00066 | 564 | Glycerophospholipid metabolism | 0.01025 |
| GO:0098542 | Defense response to other organism | 0.00115 | 600 | Sphingolipid metabolism | 0.01931 |
| GO:0051707 | Response to other organism | 0.00118 | 100 | Steroid biosynthesis | 0.01946 |
| GO:0009607 | Response to biotic stimulus | 0.00118 | 980 | Metabolism of xenobiotics by cytochrome | 0.03246 |
| GO:0043207 | Response to external biotic stimulus | 0.00118 | 4142 | Lysosome | 0.03717 |
| GO:0006952 | Defense response | 0.00252 | 982 | Drug metabolism - cytochrome P450 | 0.03891 |
| GO:0050829 | Defense response to Gram-negative bacterium | 0.00657 | 310 | Lysine degradation | 0.04819 |
| GO:0009605 | Response to external stimulus | 0.02484 | 480 | Glutathione metabolism | 0.05311 |
| GO:0006950 | Response to stress | 0.03573 | 4320 | Dorso-ventral axis formation | 0.10245 |
| GO:0051704 | Multi-organism process | 0.05546 | 71 | Fatty acid metabolism | 0.10398 |
| GO:0050830 | Defense response to Gram-positive bacterium | 0.06091 | 590 | Arachidonic acid metabolism | 0.11123 |
| GO:0018996 | Molting cycle, collagen and cuticulin-based cuticle | 0.07878 | 514 | Other types of O-glycan biosynthesis | 0.12854 |
| GO:0042303 | Molting cycle | 0.07878 | 511 | Other glycan degradation | 0.12854 |
| GO:0050896 | Response to stimulus | 0.16943 | 830 | Retinol metabolism | 0.13706 |
| GO:0045132 | Meiotic chromosome segregation | 0.24482 | 53 | Ascorbate and aldarate metabolism | 0.14551 |
| GO:0019915 | Lipid storage | 0.30035 | 860 | Porphyrin and chlorophyll metabolism | 0.15387 |
| GO:0098813 | Nuclear chromosome segregation | 0.30199 | 40 | Pentose and glucuronate interconversions | 0.17846 |
| GO:0051235 | Maintenance of location | 0.30460 | 1100 | Metabolic pathways | 0.20077 |
| GO:0010876 | Lipid localization | 0.30601 | 4080 | Neuroactive ligand-receptor interaction | 0.21016 |
| GO:0007059 | Chromosome segregation | 0.31791 | 500 | Starch and sucrose metabolism | 0.22554 |
| GO:0048477 | Oogenesis | 0.34619 | 4070 | Phosphatidylinositol signaling system | 0.24063 |
| | | | 4012 | ErbB signaling pathway | 0.24807 |
| | | | 983 | Drug metabolism - other enzymes | 0.26994 |

Table S6. Differentially expressed genes after vanillic acid (100 μ M) treatment vs DMSO-control worms (ANOVA $p < 0.05$; $-1.5 \leq FC \leq 1.5$). Results obtained in Transcriptomic array console (TAC, Affymetrix).

| Transcript Cluster ID | FC (VAN vs. CNT) | ANOVA p-value (VAN vs. CNT) | Gene Symbol | Description |
|-----------------------|------------------|-----------------------------|----------------------|--------------------------------------|
| 18478405 | 2.31 | 0.020037 | nspb-9 | Protein NSPB-9 |
| 18565542 | 2.29 | 0.016357 | C54D10.9 | Protein C54D10.9 |
| 18484287 | 2.04 | 0.034070 | F44E5.5; F44E5.4 | Protein F44E5.5; Protein F44E5.4 |
| 18599811 | 1.98 | 0.011147 | hsp-16.2 | Protein HSP-16.2 |
| 18478418 | 1.94 | 0.046852 | nspb-7 | Protein NSPB-7 |
| 18516585 | 1.85 | 0.012236 | fbxa-61 | Protein FBXA-61 |
| 18603602 | 1.84 | 0.002737 | C11E4.2 | Protein C11E4.2 |
| 18601841 | 1.8 | 0.039633 | CELE_ZK262.19 | Protein ZK262.19 |
| 18602807 | 1.73 | 0.048613 | nspc-7 | Protein NSPC-7 |
| 18516830 | 1.71 | 0.009942 | fmo-3 | Protein FMO-3 |
| 18456088 | 1.7 | 0.012980 | gpdh-1 | Protein GPDH-1 |
| 18483501 | 1.7 | 0.025977 | nspb-11 | Protein NSPB-11 |
| 18583050 | 1.7 | 0.022649 | str-130 | Protein STR-130 |
| 18563830 | 1.69 | 0.027037 | C25F9.9 | Protein C25F9.9 |
| 18493317 | 1.67 | 0.021547 | nspb-10 | Protein NSPB-10 |
| 18539599 | 1.65 | 0.029163 | nspb-6 | Protein NSPB-6 |
| 18589217 | 1.63 | 0.041958 | F35B12.4 | Protein F35B12.4 |
| 18629289 | 1.62 | 0.044716 | K10C2.14 | Protein K10C2.14 |
| 18573963 | 1.61 | 0.043645 | CELE_R08A2.7 | Protein R08A2.7 |
| 18614327 | 1.59 | 0.032859 | R07B1.9 | Protein R07B1.9 |
| 18622500 | 1.59 | 0.047424 | D1053.3 | Protein D1053.3 |
| 18532772 | 1.56 | 0.046983 | CELE_C01B10.44 | Protein C01B10.44 |
| 18550546 | 1.55 | 0.001434 | C54E4.4 | Protein C54E4.4 |
| 18535549 | 1.54 | 0.021219 | C49A9.9 | Protein C49A9.9 |
| 18580352 | 1.54 | 0.022197 | glb-33 | Protein GLB-33 |
| 18610156 | 1.54 | 0.027160 | cnc-8 | Protein CNC-8 |
| 18544174 | 1.53 | 0.017068 | col-108 | Protein COL-108 |
| 18564629 | 1.53 | 0.039761 | sru-27 | Protein SRU-27 |
| 18589254 | 1.53 | 0.039303 | CELE_F35E12.5 | Protein F35E12.5 |
| 18485054 | 1.52 | 0.002675 | aat-7 | Protein AAT-7 |
| 18582648 | 1.52 | 0.007568 | ugt-63 | Protein UGT-63 |
| 18513858 | 1.51 | 0.017342 | K10D2.7 | Protein K10D2.7 |
| 18576999 | 1.51 | 0.010980 | hsp-16.48; hsp-16.49 | Protein HSP-16.48; Protein HSP-16.49 |
| 18597334 | 1.51 | 0.010980 | hsp-16.48; hsp-16.49 | Protein HSP-16.48; Protein HSP-16.49 |
| 18550503 | -1.5 | 0.018547 | CELE_C53D6.6 | Protein C53D6.6 |
| 18592291 | -1.5 | 0.048792 | srbc-40 | Protein SRBC-40 |
| 18578524 | -1.52 | 0.026553 | CELE_Y37H2C.4 | Protein Y37H2C.4 |
| 18606692 | -1.52 | 0.005479 | C54G7.1 | Protein C54G7.1 |
| 18602419 | -1.53 | 0.003016 | B0416.2 | Protein B0416.2 |

| | | | | |
|----------|-------|----------|---------------|-------------------------------|
| 18631683 | -1.53 | 0.020527 | dop-3 | Protein DOP-3 |
| 18570288 | -1.54 | 0.023570 | sru-39 | Protein SRU-39 |
| 18564416 | -1.55 | 0.043030 | C35A11.3 | Protein C35A11.3 |
| 18592611 | -1.55 | 0.023098 | srh-118 | Protein SRH-118 |
| 18494801 | -1.57 | 0.020272 | CELE_C24H12.6 | Protein C24H12.6 |
| 18576386 | -1.58 | 0.038045 | T20D4.8 | Protein T20D4.8 |
| 18578207 | -1.6 | 0.030162 | CELE_Y17D7C.1 | Protein Y17D7C.1 |
| 18568638 | -1.63 | 0.017153 | cyp-37B1 | Protein CYP-37B1 |
| 18590701 | -1.63 | 0.014059 | CELE_F49H6.12 | Protein F49H6.12 |
| 18563387 | -1.67 | 0.035391 | C17B7.3 | Protein C17B7.3 |
| 18541006 | -1.72 | 0.047797 | M70.2 | Protein M70.2 |
| 18522338 | -1.75 | 0.026676 | arl-6 | Protein ARL-6 |
| 18630450 | -1.78 | 0.031722 | pqn-57; abu-9 | Protein PQN-57; Protein ABU-9 |
| 18458379 | -1.98 | 0.049408 | CELE_M01G12.5 | Protein M01G12.5 |
| 18562596 | -1.98 | 0.025431 | fbxa-157 | Protein FBXA-157 |

Table S7. Main GO processes and KEGG signalling pathways affected by vanillic acid (100 μ M) treatment. Analysis obtained from EGAN UCSF software.

| Gene Ontology Process | Process Name | Enrichment | KEGG | Pathway Name | Enrichment |
|-----------------------|--|------------|------|-----------------------------------|------------|
| GO:0050830 | defense response to Gram-positive bacterium | 0.03699 | 4122 | Sulfur relay system | 0.01248 |
| GO:0030968 | endoplasmic reticulum unfolded protein response | 0.05985 | 590 | Arachidonic acid metabolism | 0.01360 |
| GO:0034620 | cellular response to unfolded protein | 0.06628 | 982 | Drug metabolism - cytochrome P450 | 0.03589 |
| GO:0006986 | response to unfolded protein | 0.06842 | 480 | Glutathione metabolism | 0.04248 |
| GO:0034976 | response to endoplasmic reticulum stress | 0.06842 | 564 | Glycerophospholipid metabolism | 0.05120 |
| GO:0035967 | cellular response to topologically incorrect protein | 0.06948 | | | |
| GO:0035966 | response to topologically incorrect protein | 0.08008 | | | |
| GO:0009617 | response to bacterium | 0.09783 | | | |
| GO:0042742 | defense response to bacterium | 0.09783 | | | |
| GO:0098542 | defense response to other organism | 0.11728 | | | |
| GO:0051707 | response to other organism | 0.11830 | | | |
| GO:0009607 | response to biotic stimulus | 0.11830 | | | |
| GO:0043207 | response to external biotic stimulus | 0.11830 | | | |
| GO:0071310 | cellular response to organic substance | 0.13236 | | | |
| GO:0070887 | cellular response to chemical stimulus | 0.14915 | | | |
| GO:0010033 | response to organic substance | 0.16178 | | | |
| GO:0006950 | response to stress | 0.17301 | | | |
| GO:0033554 | cellular response to stress | 0.24618 | | | |
| GO:0006952 | defense response | 0.29435 | | | |
| GO:0009605 | response to external stimulus | 0.31772 | | | |
| GO:0007165 | signal transduction | 0.34949 | | | |
| GO:0042221 | response to chemical | 0.37623 | | | |
| GO:0050896 | response to stimulus | 0.37748 | | | |