## SUPPLEMENTARY TABLES

**Supplementary Table 1. Relative expression of transgenes in control or *ahr-1* RNAi-treated reporter strains.**

| Strain name | Gene | Rel. expression (mean ± SD) | N | n | p-value |
|---|---|---|---|---|---|
| BC14926 | **cyp-14A3** | anterior: 0.97<br>posterior: 1.05 | 38 (con)<br>35 (ahr-1) | 3 | 0.544<br>0.333 |
| SD1444 | **cyp-25A2** | 1.07 ± 0.16 | 38 | 2 | 0.067 |
| BC20334 | **cyp-29A2** | 0.85 ± 0.60 | 42 | 2 | 0.377 |
| cyp-35A2 | **cyp-35A2** | anterior: 8.43 ± 11.96<br>posterior: 1.99 ± 2.14 | 43 (con)<br>42 (ahr-1) | 3 | < 0.001<br>0.005 |
| cyp-35A3 | **cyp-35A3** | 1.08 ± 0.09 | 28 (con)<br>26 (ahr-1) | 2 | 0.02 |
| CY573 | **cyp-35B1** | anterior: 2.60 ± 1.97 | 36 (con)<br>27 (ahr-1) | 2 | < 0.001 |
| | | posterior: 2.90 ± 2.40 | 55 (con)<br>44 (ahr-1) | 3 | < 0.001 |
| BC15044 | **cyp-37A1** | 0.66 ± 0.14 | 46 (con)<br>26 (ahr-1) | 2 | < 0.001 |
| CL2166 | **gst-4** | 1.58 ± 0.37 | 27 (con)<br>29 (ahr-1) | 2 | < 0.001 |
| ugt-29 | **ugt-29** | 0.96 ± 0.05 | 44 (con)<br>36 (ahr-1) | 3 | 0.004 |

The relative expression was measured in worms on their first day of adulthood and normalized to control RNAi treated worms in each replicate. N shows the number of worms and n the number of experiments, Statistical test: 2-tailed unpaired t-test.

**Supplementary Table 2. *C. elegans* strains used in this study.**

| Strain name | *Genotype* |
|---|---|
| **BC14926** | *dpy-5(e907); sEx14926[rCes K09A11.4::GFP + pCeh361]* |
| **BC15044** | *dpy-5(e907); sEx15044[rCes F01D5.9::GFP + pCeh361]* |
| **BC20306** | *cyp-34A9p::GFP* |
| **BC20334** | *cyp-29A2p::GFP* |
| **CL2166** | *pAF15)gst-4p::GFP::NLS* |
| **CY573** | *cyp-35B1p::GFP + gcy-7p::GFP* |
| **cyp35A2** | *cyp-35A2p::GFP* |
| **cyp35A3** | *cyp-35A3p::GFP* |
| **cyp35A5** | *cyp-35A5p::GFP* |
| **cyp33E2** | *cyp-33E2p::GFP* |
| **CZ2485** | *ahr-1(ju145)* |
| **N2** | *wild-type* |
| **NL2098** | *rrf-1(pk1417)* |
| **NL2550** | *ppw-1(pk2505)* |
| **NR222** | *rde-1(ne219); kzIs9[lin-26p::nls::GFP + lin-26p::rde-1 + rol-6(su1006)]* |
| **NV33a** | *cyp-35B1p::GFP + gcy-7p::GFP; ahr-1(ju145)* |
| **NV33wt** | *cyp-35B1p::GFP + gcy-7p::GFP* |
| **NV35a *** | *ahr-1(ju145); (pAF15)gst-4p::GFP::NLS* |
| **NV35wt *** | *pAF15)gst-4p::GFP::NLS* |
| **NV38b *** | *ahr-1(ju145); unc-54p::Q40::YFP* |
| **NV38wt *** | *unc-54p::Q40::YFP* |
| **NV41a *** | *unc-119p::Aβ 1–42; Pmyo-2::YFP; ahr-1(ju145)* |
| **NV41wt *** | *unc-119p::Aβ 1–42; Pmyo-2::YFP* |
| **NV42a *** | *unc-54p::alphasynuclein::YFP, ahr-1(ju145)* |
| **NV42wt *** | *unc-54p::alphasynuclein::YFP* |
| **NV47a *** | *ugt-29p::GFP; ahr-1(ju145)* |
| **NV47wt *** | *ugt-29p::GFP* |
| **SD1444** | *unc-119(ed3); gaIs237 [cyp-25A2p::his-24::mCherry + unc-119(+)]* |
| **TU3311** | *uIs60[unc119p::YFP; unc119p::sid-1]* |
| **TU3401** | *sid-1(pk3321); uls69[myo-2p::mCherry + unc-119p::sid-1]* |
| **ugt-29** | *ugt-29p::GFP* |
| **VP303** | *rde-1(ne300); neIs9 [myo-3::HA::RDE-1+ rol-6(su1006)]* |
| **WM118** | *rde-1(ne219); kbIs7 [nhx-2p::rde-1 + rol-6(su1006)]* |
| **ZG24** | *ahr-1(ia03)* |

Strains are sorted alphabetically.

* these strains where constructed using classical breeding techniques.

**Supplementary Table 3. Primer pairs used in this study to validate genes differentially expressed between *ahr-1(ju145)* and wild-type (Supplementary Figure 3).**

| Gene | | Sequence (5‘ – 3‘) | Annealing temp. (°C) | Efficiency (%) |
|---|---|---|---|---|
| clec-209 | F | TGCTCGGGGAACAACCAAAA | 60 | 88.4 |
| | R | TTGGCTACGAACGATTGATGC | | |
| C01B4.6 | F | TGGCGATGCGAAAATTGATGTAA | 61 | 83.9 |
| | R | ATCTCCAGAAAGTGCTCGGC | | |
| F56A4.3 | F | ACGAGGGGAATGAATGGCAA | 67 | 101.4 |
| | R | CCATAGGGACCAATATCCATGAACT | | |
| C01B4.7 | F | GTTTTGGAATCAGACGCGGG | 67 | 106.6 |
| | R | CAGTGGGGTTCCGTCAAGTT | | |
| atf-2 | F | CGAAGGAACAATGAAGCCGC | 67 | 98.1 |
| | R | CCAAGAGCTGAACTCGTCGT | | |
| K04H4.2 | F | ACGCCGGAATCTGTTGTTCT | 67 | 95.3 |
| | R | CGTTCATTTGGAAAGGAGGCAT | | |
| egl-46 | F | CACCTCAACCGCTTTTCCAAG | 67 | 85.1 |
| | R | ATTTCACATCCGCCTCCTCC | | |
| T20F5.4 | F | TCATCTACCGAGCAGCCAAC | 61 | 94.5 |
| | R | GAGATGCTCGGTCTCACTGC | | |
| ptr-4 | F | TCCTACCAGACGCGCAATC | 66 | 79.5 |
| | R | GCAACCCATACTGACGGAGT | | |
| dyf-7 | F | GTCTGCGTTTCCGTCACAAG | 66 | 124.8 |
| | R | CGGGGAAGCAACAAGTTCTG | | |
| cdc-42 | F | ATTACGCCGTCACAGTAATG | 62 | 100.8 |
| | R | ATCCCTGAGATCGACTTGAG | 58 | 107.2 |
| act-1 | F | GCTCTTGCCCCATCAACCAT | 60 | 99.7 |
| | R | CACTTGCGGTGAACGATGGA | 58 | 98.1 |