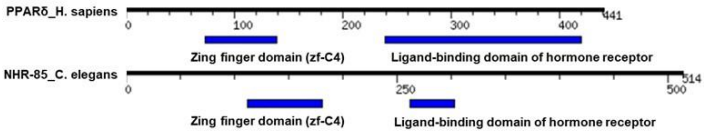
A

```
PPARδ_H.sapiens     --------------------MEQPQE-----EAPEVREEEEKE---EVAEAEGAPELNGG     32
NHR-85_C.elegans    MDLSTSGSLPCHLPLSLLTNLQTPPIDTSFSSPPATSSSSLLSPSPSSAFRPVVPKSLMN     60
                                        :: *       . * . ...  .   . *    .*:   .

PPARδ_H.sapiens     PQHALPS----------------SSYTDLSRSSSPPSLLDQLQMGCDGASCGSLNMECRV     76
NHR-85_C.elegans    PQPAMDTFYMSAIQSLVVSTTNDDQYSEHGALEGSKSL-----AKDENASTSAGTILCQV     115
                    ** *: :                ..*:: .  ..  **        :.** .: .: *:*

PPARδ_H.sapiens     CGDKASGFHYGVHACEGCKGFFRRTIRMKLEYEKCER--SCKIQKKNRNKCQYCRFQKCL     134
NHR-85_C.elegans    CSDKASGFHYGVFACEGCKGFFRRSIQQKITYRACTRAEDCLILRNNRNRCQCCRLKKCL     175
                    *.**********.***********:*: *: *. * *  .* * ::***:** **::***

PPARδ_H.sapiens     ALGMSHNAIRFGRMPEAEKRKLVAGLTANEGSQYNPQVA----DLKAFSKHIYNAYLKNF     190
NHR-85_C.elegans    AVGMSRDAVRFGRVPKREKARMFEEMQKTNVQSQRDQIAIQYENLTEVMHKINQAFGTLQ     235
                    *:***::*:****:*: ** ::.  :  .: .. . *:*    :*. . ::* :*: .

PPARδ_H.sapiens     NMTKKKARSILTGKASHTAPFVIHDIETLWQAEKGLVWKQLVNGLPPYKEISVHVFYRCQ     250
NHR-85_C.elegans    ATLEKCTGPIYTDRCPITSNF-------------------------------------     256
                       :* :  * *.:.  *: *

PPARδ_H.sapiens     CTTVETVRELTEFAKSIPSFSSLFLNDQVTLLKYGVHEAIFAMLASIVNKDGLLVANGSG     310
NHR-85_C.elegans    --IVIPLKAAIDFANSIPAFLSITQTQRVHLLQNSVFDVMLLASASASTSQ-HFPPGGLT     313
                      *  ::   :**:***:* *:  .::* **: .*.:.::   **  ..:  :  .*

PPARδ_H.sapiens     FVTR-------EFLRSLRKPFSDII---EPKFEFAVKFNALELDDSDLALFIAAIILC--     358
NHR-85_C.elegans    YDQSSANPIIPQAIQSISARIRQLPPQTVPILTAIAVCQADLLPESQQPMLLAERLWCVL     373
                    :          : ::*:   : ::     * :   .  :*  * :*:  :::*  : *

PPARδ_H.sapiens     GDRPGLMNVPRVEAIQDTILRALEFHLQANHPDAQYLFPKLLQKMADLRQLVTEHAQMMQ     418
NHR-85_C.elegans    GKLGGIQSLAT-------------------------APSLLADVRTLRQWHSDRLRQMS     407
                    *.  *: .:                            *.** .:  ***  ::: : *.

PPARδ_H.sapiens     RIKKTETETS-------------------------------------LHPLLQEI----     436
NHR-85_C.elegans    QISQHFSQNLLIAPVAAAAPVLLPPAFLSPPASATSTSSSSVKSEFIERHPSIASLLERP     467
                    :*.:  ::.                                        ** : .:

PPARδ_H.sapiens     ----------------------YKDMY------------------   441
NHR-85_C.elegans    RRISSSGAQEPLNLSLPHVRHQVKRDVDSDEQLEEMKVSPVPTTLSE   514
                                         :*:
```

B



Query	Domain	Position (Independent E-value)
PPARδ_H. sapiens	zf-C4	73…139 (5.1e-28)
PPARδ_H. sapiens	Ligand-binding	239…420 (9.6e-21)
NHR-85_C. elegans	zf-C4	112…181(2e-29)
NHR-85_C. elegans	Ligand-binding	262…303 (0.026)

Fig. S1. Multiple sequence alignment and motif analysis of PPARδ and NHR-85.

A. CLUSTAL 0 (1.2.4) multiple sequence alignment between human PPARδ and nematode NHR-85 showing conserved regions. Amino acids are coloured according to their physicochemical properties (Red-Small + Hydrophobic + Aromatic, Blue-Acidic, Magenta-basic H, Green-Hydroxyl + Sulfhydryl + amine + G). Conserved amino acids are shown by an * (asterisk); conserved substitutions are shown by a : (colon); semi-conserved are shown by a . (dot).

B. CLUSTAL W motif analysis between human PPARδ and nematode NHR-85. The conserved zing finger domain (zf-C4) and the ligand-binding domain are shown with blue. The table shows the e-values (expected values) for each motif indicating the statistical significance of the alignment between the query protein and the motifs in the database.

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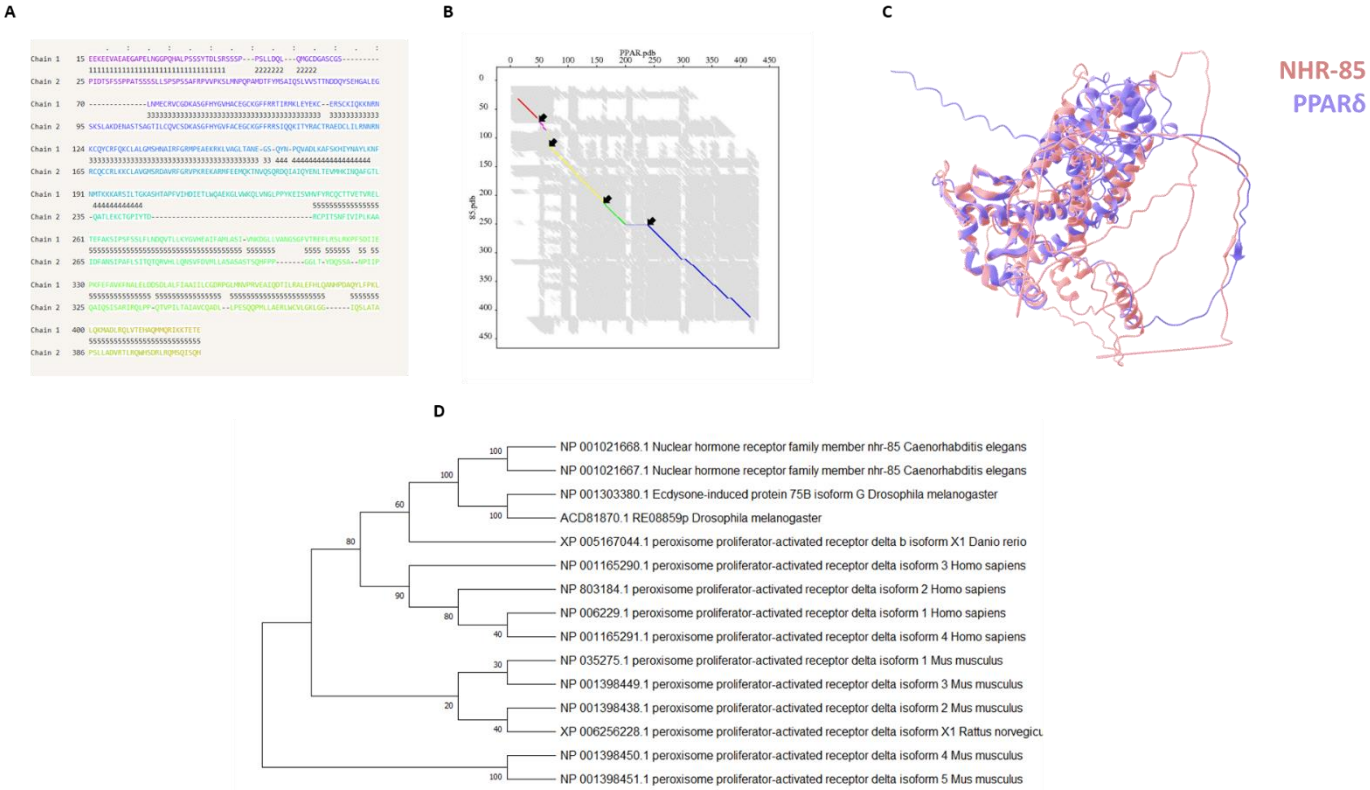

Fig. S2. Flexible alignment and phylogenetic tree of PPARδ and NHR-85.

A. The flexible FATCAT alignment between PPARδ and NHR-85 (Chain 1: NHR-85, Chain 2: PPARδ).

B. Chaining result from flexible FATCAT alignment between PPARδ and NHR-85 with the aligned fragment pairs in the optimal alignment shown as coloured lines and all the aligned fragment pairs (AFPs) between the two structures shown as short gray lines in the background.

C. 3D visualization of the superposition between PPARδ and NHR-85 proteins obtained by flexible FATCAT alignment (purple: PPARδ, pink: NHR-85).

D. Phylogenetic tree developed using MEGA 11.0 software, 15 protein sequences were aligned using CLUSTAL W. The alignment was used to construct a tree using the Jones-Taylor-Thornton (JTT) substitution model, p-distance and 10 Bootstrap repetitions. The numbers at the branch points show the bootstrap values.

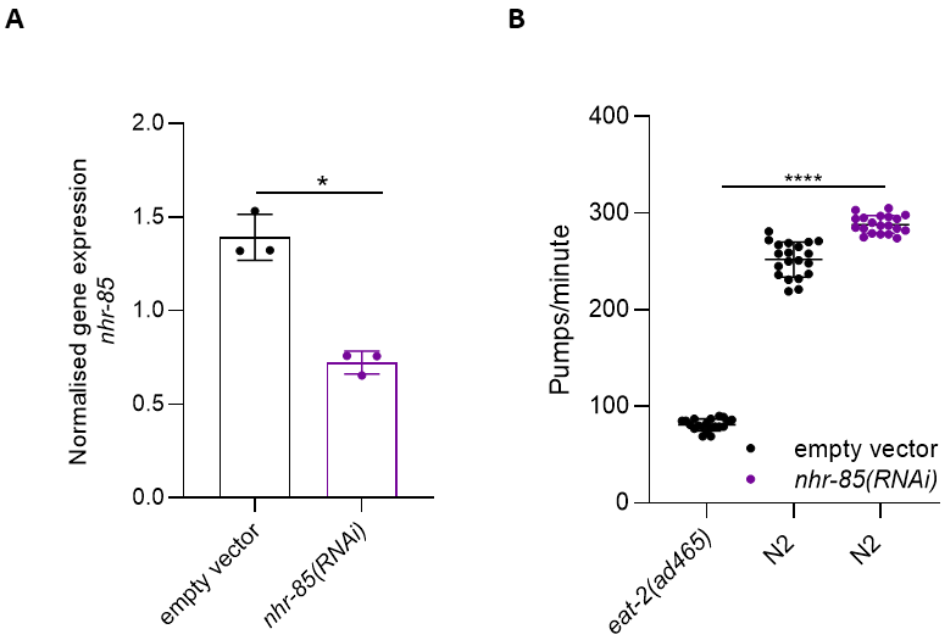

Fig. S3. Downregulation of *nhr-85* by RNAi leads to increased pharyngeal pumping.

A. Expression analysis of *nhr-85* by RT-qPCR in wild-type (N2) animals treated with empty vector or *nhr-85* RNAi (n = 3 independent experiments, *P < 0.05; two-tailed paired t-test).

B. Quantification of pharyngeal pumping in wild-type (N2) animals treated with empty vector or *nhr-85* RNAi and *eat-2(ad465)* mutants treated with empty vector RNAi (n = 60 animals in total, ****P < 0.0001; one-way analysis of variance (ANOVA)).

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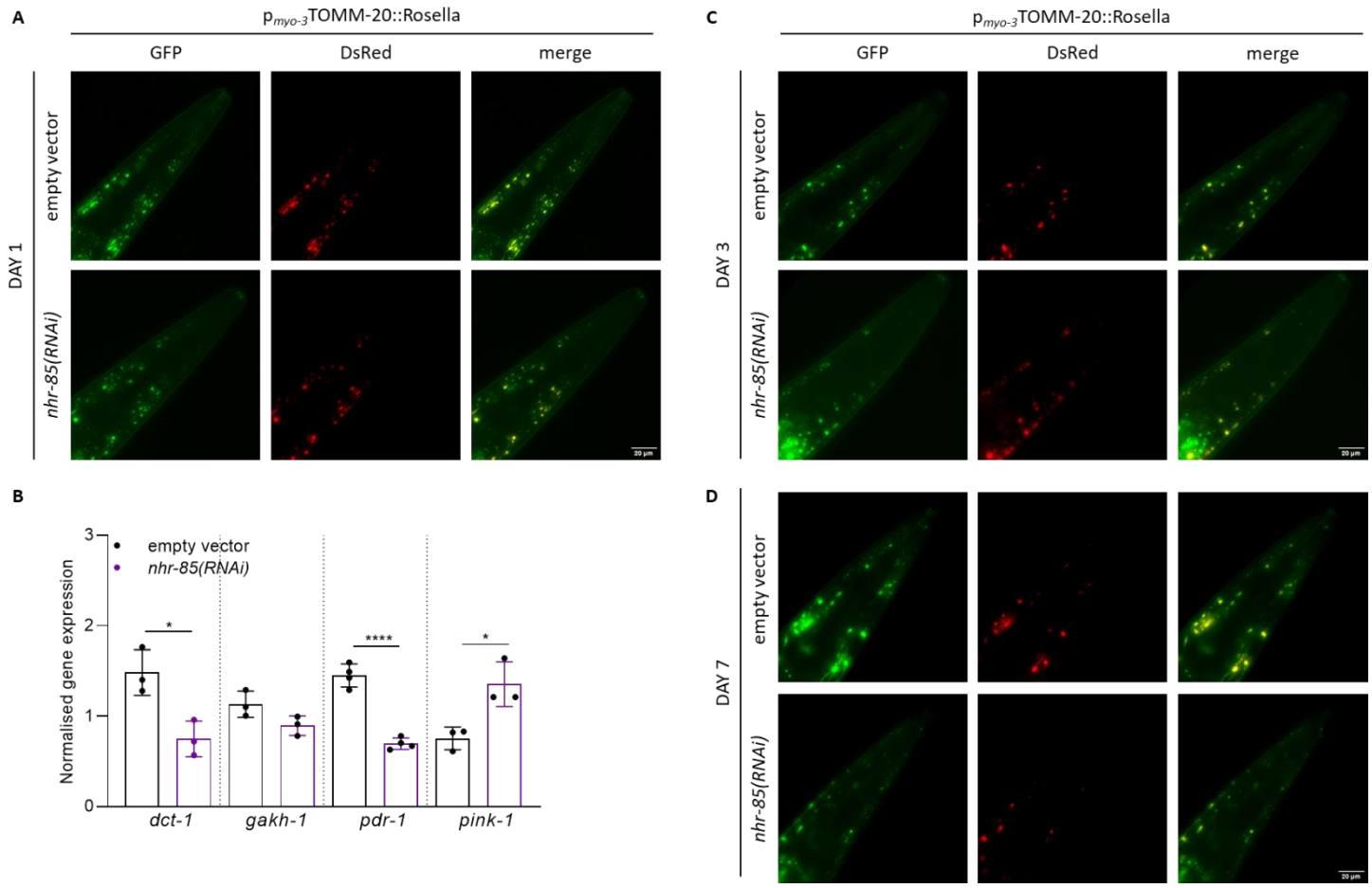

Fig. S4. Downregulation of *nhr-85* exacerbates mitophagy defects during ageing.

A. Representative images of 1-day-old transgenic animals expressing mitochondria-targeted Rosella (mtRosella) biosensor in body wall muscle cells after treatment with empty vector or *nhr-85* RNAi (Images were acquired using a x20 objective lens).

B. Expression analysis of the mitophagy genes *dct-1, gakh-1, pdr-1* and *pink-1* by RT-qPCR in wild-type (N2) animals treated with empty vector or *nhr-85* RNAi (n = 3 independent experiments, *P < 0.05; ****P < 0.0001; two-tailed unpaired t-test).

C. Representative images of 3-day-old transgenic animals expressing mitochondria-targeted Rosella (mtRosella) biosensor in body wall muscle cells treated with empty vector or *nhr-85* RNAi (Images were acquired using a x20 objective lens).

D. Representative images of 7-day-old transgenic animals expressing mitochondria-targeted Rosella (mtRosella) biosensor in body wall muscle cells after treatment with empty vector or *nhr-85* RNAi (Images were acquired using a x20 objective lens).

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Table S1. Oligonucleotide sequences used in this study.

Name	Oligonucleotide Sequence
atgl-1 forward RT	TGCAAATGCTTTGAACAGCTTC
atgl-1 reverse RT	CTGGAATACTGAACGTTCTGCAG
lid-1 forward RT	ACCTTATGCTTGGATGTCCTTC
lid-1 reverse RT	GACAATTGCCGGCGCATA
dgat-2 forward RT	GCAATGTGAAGCAAGTGTTC
dgat-2 reverse RT	CATACCGATGCTGAGGAGGA
actin-1 forward RT	AGGCCCAATCCAAGAGAGGTATC
actin-1 reverse RT	TGGCTGGGGTGTTGAAGGTC
fat-5 forward RT	GGCTACAGTTGGATGGGTATTC
fat-5 reverse RT	CTATGCGGGTCAGCATCAG
fat-7 forward RT	AGTTCTTGTATTCCAGAGAAAGCAC
fat-7 reverse RT	CACCAACGGCTACAACTGTG
dgtr-1 forward RT	GAAGGCCAATTCGAGTCACC
dgtr-1 reverse RT	AGATGAGTGTCGGGAGGAAT
acs-2 forward RT	TATGTTCACACAATGCTTGAGGC
acs-2 reverse RT	TCGAAGTTTGCGATCCATGTC
acdh-11 forward RT	TGCTGTACAAATCGATAAGGATACTTAC
acdh-11 reverse RT	GTTCCCAGCTTATTCTTCAATCG
cpt-5 forward RT	AGTACATGGCAGTTGGGGA
cpt-5 reverse RT	AAGTACATGCTTGCTCGGTG
dct-1 forward RT	GGCTCCAACCTTACCACTCC
dct-1 reverse RT	GCAAATCCTACTGCTGCTCC
gakh-1 forward RT	AAGGCGGTTTTGGAACGGTG
gakh-1 reverse RT	AATATCCTTCGTCGCGGCTG
pdr-1 forward RT	CAAGAAGATGCCCAAAATGC
pdr-1 reverse RT	ACACCAATCCATTCCACACG
pink-1 forward RT	AGCATATCGAATCGCAAATGAGTTAG
pink-1 reverse RT	TCGACCGTGGCGAGTTACAAG
nhr-85 forward RT	TTGGAATGTCTAGGGATGCCG
nhr-85 reverse RT	GCTTGCAAAGTTCCAAAAGC

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