

**Table S1.** All strains used in this study.

<b>Strains</b>	<b>Genotype</b>
N2	Wild-type
TJ356	zIs356 [daf-16p::daf-16a/b::GFP + rol-6(su1006)]
TJ375	gpIs1 [hsp-16.2p::GFP]
PS3551	hsf-1(sy441) I
GR1307	daf-16(mgDf50) I

**Table S2.** List of primers used for the quantitative real-time reverse transcription-polymerase chain reaction

<b>Gene name</b>	<b>Primer sequence (5'to3')</b>
<i>act-1F</i>	CTACGAACTTCCTGACGGACAAG
<i>act-1R</i>	CCGGCGGACTCCATACC
<i>daf-16F</i>	CTAACTTCAAGCCAATGCCACTA
<i>daf-16R</i>	TCCAGCTTGACTCAGCTCATGTC
<i>sod-3F</i>	CTCCAAGCACACTCTCCCAG
<i>sod-3R</i>	TCCCTTTCGAAACAGCCTCG
<i>hsf-1F</i>	TTTGCATTTTCTCGTCTCTGTC
<i>hsf-1R</i>	TCTATTTCCAGCACACCTCGT
<i>hsp-16.2F</i>	GGTGCAGTTGCTTCGAATCTT
<i>hsp-16.2R</i>	TCTTCCTTGAACCGCTTCTTTC
<i>nhr-80 F</i>	AATTCCGATTTCCAGCTTCTTC
<i>nhr-80 R</i>	TCTGCAGATTTGGTGCATACTATAA

<i>fat-6 F</i>	GGCAAACCGTGATTTTCACATT
<i>fat-6 R</i>	TCACGAGCCCATTCGATGAC
<i>daf-12 F</i>	TCCAATGCCAGCTGAAACAACACC
<i>daf-12 R</i>	TGGAATGGCTGACACGGTTGAATG
<i>fard-1 F</i>	CGCATTCGCCAAGAGAAACC
<i>fard-1 R</i>	ACGTTGACATTGTCTCGGATGA

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**Table S3.** The lifespan of N2 and mutant *C. elegans*.

Genotype	Treatment	Mean lifespan (day) $\pm$ SEM	Percentage	<i>p</i> value (log-rank significance)
N2	Control	16.13 $\pm$ 0.43		
	1 $\mu$ g/mL	17.98 $\pm$ 0.53	11.36%	0.0089
	10 $\mu$ g/mL	18.28 $\pm$ 0.46	13.20%	0.0017
	100 $\mu$ g/mL	17.79 $\pm$ 0.53	10.19%	0.0243
	EGCG 500 $\mu$ M	18.53 $\pm$ 0.51	14.76%	0.0017
N2	Control	18.16 $\pm$ 0.41		
	1 $\mu$ g/mL	19.31 $\pm$ 0.43	6.36%	0.0378
	10 $\mu$ g/mL	19.45 $\pm$ 0.39	7.09%	0.0172
	100 $\mu$ g/mL	19.43 $\pm$ 0.47	6.33%	0.021
	EGCG 500 $\mu$ M	19.40 $\pm$ 0.33	9.72%	0.0063
N2	Control	18.58 $\pm$ 0.36		

	1 µg/mL	19.91±0.31	6.78%	0.008
	10 µg/mL	19.90±0.42	7.06%	0.0136
	100 µg/mL	19.77±0.32	6.39%	0.0217
N2	Control	17.12±0.47		
	EGCG 500 µM	18.31±0.52	6.97%	0.0303
N2	Control	17.59±0.45		
	Rd 1 µg/mL	19.36±0.30	10.06%	0.0238
N2	Control	17.12±0.47		
	Rd 1 µg/mL	19.20±0.47	12.12%	0.0004
N2	Control	15.18±0.45		
	Rd 1 µg/mL	17.85±0.49	17.60%	<0.0001
N2	Control	16.15±0.43		
	Rg <sub>1</sub> 1 µg/mL	18.10±0.61	10.58%	0.0063
	Rg <sub>2</sub> 1 µg/mL	15.86±0.50	-1.79%	0.8887
	Re 1 µg/mL	16.88±0.46	4.56%	0.2587
N2	Control	18.87±0.47		
	Rg <sub>1</sub> 1 µg/mL	19.79±0.49	2.42%	0.0695
	Rg <sub>2</sub> 1 µg/mL	18.93±0.42	0.31%	0.3385
	Re 1 µg/mL	19.41±0.40	2.88%	0.1775
N2	Control	18.46±0.31		
	Rg <sub>1</sub> 1 µg/mL	18.49±0.35	3.57%	0.1793
	Rg <sub>2</sub> 1 µg/mL	17.53±0.94	0.14%	0.5409

	Re 1 $\mu\text{g/mL}$	18.86 $\pm$ 0.33	2.18%	0.2304
<i>daf-16</i>	Control	16.46 $\pm$ 0.41		
	10 $\mu\text{g/mL}$	17.14 $\pm$ 0.53	4.11%	0.092
<i>daf-16</i>	Control	16.23 $\pm$ 0.36		
	10 $\mu\text{g/mL}$	16.93 $\pm$ 0.43	4.30%	0.1297
<i>daf-16</i>	Control	17.88 $\pm$ 0.45		
	10 $\mu\text{g/mL}$	17.24 $\pm$ 0.51	-3.60%	0.6207
<i>hsf-1</i>	Control	19.56 $\pm$ 0.48		
	10 $\mu\text{g/mL}$	19.00 $\pm$ 0.52	-2.85%	0.6189
<i>hsf-1</i>	Control	19.60 $\pm$ 0.59		
	10 $\mu\text{g/mL}$	19.59 $\pm$ 0.38	-1.85%	0.1432
<i>hsf-1</i>	Control	20.18 $\pm$ 0.35		
	10 $\mu\text{g/mL}$	20.08 $\pm$ 0.43	-0.50%	0.6494
N2 (50 mM PQ)	Control	7.889 $\pm$ 0.12		
	10 $\mu\text{g/mL}$	8.708 $\pm$ 0.11	10.38%	<0.0001
N2 (50 mM PQ)	Control	7.87 $\pm$ 0.12		
	10 $\mu\text{g/mL}$	8.684 $\pm$ 0.11	10.34%	<0.0001
N2 (50 mM PQ)	Control	7.858 $\pm$ 0.11		
	10 $\mu\text{g/mL}$	8.723 $\pm$ 0.11	10.71%	<0.0001

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## **(RNA-seq) Materials and methods**

### 1 Sample collection and preparation

#### 1.1 RNA quantification and qualification

The purity, concentration and integrity of RNA samples are tested using advanced molecular biology equipment to ensure the use of qualified samples for transcriptome sequencing.

#### Library preparation for Transcriptome sequencing

A total amount of 1 µg RNA per sample was used as input material for the RNA sample preparations. Sequencing libraries were generated using NEBNext Ultra™ RNA Library Prep Kit for Illumina (NEB, USA) following manufacturer's recommendations and index codes were added to attribute sequences to each sample. Briefly, mRNA was purified from total RNA using poly-T oligo-attached magnetic beads. Fragmentation was carried out using divalent cations under elevated temperature in NEBNext First Strand Synthesis Reaction Buffer (5X). First strand cDNA was synthesized using random hexamer primer and M-MuLV Reverse Transcriptase (RNase H-). Second strand cDNA synthesis was subsequently performed using DNA Polymerase I and RNase H. Remaining overhangs were converted into blunt ends via exonuclease/polymerase activities. After adenylation of 3' ends of DNA fragments, NEBNext Adaptor with hairpin loop structure were ligated to prepare for hybridization. In order to select cDNA fragments of preferentially 200-250 bp in length, the library fragments were purified with AMPure XP system (Beckman Coulter, Beverly, USA). Then 3 µl USER Enzyme (NEB, USA) was used with size-selected, adaptor-ligated cDNA at 37°C for 15 min followed by 5 min at 95°C before PCR. Then PCR was performed with Phusion High-Fidelity DNA polymerase, Universal PCR primers and Index (X) Primer. At last, PCR products were purified (AMPure XP system) and library quality was assessed on the Agilent Bioanalyzer 2100 system.

#### 1.2 Clustering and sequencing

The clustering of the index-coded samples was performed on a cBot Cluster Generation System using TruSeq PE Cluster Kit v4-cBot-HS (Illumina) according to the manufacturer's instructions. After cluster generation, the library preparations were sequenced on an Illumina HiSeq 2500 platform and paired-end reads were generated.

### 2 Data analysis

#### 2.1 Quality control

Raw data (raw reads) of fastq format were firstly processed through in-house perl scripts. In this step, clean data (clean reads) were obtained by removing reads containing adapter, reads containing ploy-N and low-quality reads from raw data. At the same time, Q20, Q30, GC-content and sequence duplication level of the clean data were calculated. All the downstream analyses were based on clean data with high quality.

## 2.2 Comparative analysis

The adaptor sequences and low-quality sequence reads were removed from the data sets. Raw sequences were transformed into clean reads after data processing. These clean reads were then mapped to the reference genome sequence. Only reads with a perfect match or one mismatch were further analyzed and annotated based on the reference genome. Tophat2 tools soft were used to map with reference genome.

## 2.3 Gene functional annotation

Gene function was annotated based on the following databases: Nr (NCBI non-redundant protein sequences); Nt (NCBI non-redundant nucleotide sequences); Pfam (Protein family); KOG/COG (Clusters of Orthologous Groups of proteins); Swiss-Prot (A manually annotated and reviewed protein sequence database); KO (KEGG Ortholog database); GO (Gene Ontology).

## 2.4 SNP calling

Picard - tools v1.41 and samtools v0.1.18 were used to sort, remove duplicated reads and merge the bam alignment results of each sample. GATK2 software was used to perform SNP calling. Raw vcffiles were filtered with GATK standard filter method and other parameters (cluster WindowSize: 10; MQ0 >= 4 and (MQ0/(1.0\*DP)) > 0.1; QUAL < 10; QUAL < 30.0 or QD < 5.0 or HRun > 5), and only SNPs with distance > 5 were retained.

## 2.5 Quantification of gene expression levels

Quantification of gene expression levels Gene expression levels were estimated by fragments per kilobase of transcript per million fragments mapped. The formula is shown as follow:

$$FPKM = \frac{cDNA\text{Fragments}}{Mapped\text{Fragments}(Millions) * TranscriptLength(kb)}$$

## 2.6 Differential expression analysis

Differential expression analysis of two samples was performed using the edgeR. The FDR < 0.01 & Fold Change  $\geq 2$  was set as the threshold for significantly differential expression. 2.7 GO enrichment analysis

Gene Ontology (GO) enrichment analysis of the differentially expressed genes (DEGs) was implemented by the GOseq R packages based Wallenius non-central hyper-geometric distribution (Young et al, 2010), which can adjust for gene length bias in DEGs.

## 2.8 KEGG pathway enrichment analysis

KEGG (Kanehisa et al., 2008) is a database resource for understanding high-level functions and utilities of the biological system, such as the cell, the organism and the ecosystem, from molecular-level information, especially large-scale molecular datasets generated by genome sequencing and other high-throughput experimental technologies (<http://www.genome.jp/kegg/>). We used KOBAS (Mao et al., 2005) software to test the statistical enrichment of differential expression genes in KEGG pathways.

## 2.9 PPI (Protein Protein Interaction)

The sequences of the DEGs was blast (blastx) to the genome of a related species (the protein protein interaction of which exists in the STRING database: <http://string-db.org/>) to get the predicted PPI of these DEGs. Then the PPI of these DEGs were visualized in Cytoscape (Shannon et al, 2003).

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