

Supplementary Data

Supplementary Methods

Supplementary results

SUPPLEMENTARY TABLE S1. DIFFERENTIALLY EXPRESSED AGING-RELATED GENES

<i>Gene symbol</i>	<i>Change</i>	<i>Gene title</i>
<i>dod-21</i>	8.7	C32H11.9/Downstream Of DAF-16
<i>dod-22</i>	4.6	Downstream Of DAF-16
<i>ins-7</i>	2.4	INSulin related
<i>dod-24</i>	1.9	Downstream Of DAF-16
<i>dod-23</i>	1.8	Downstream Of DAF-16
<i>dod-17</i>	1.6	Downstream Of DAF-16
<i>gei-7</i>	1.6	GEX Interacting protein
<i>dod-19</i>	1.5	Downstream Of DAF-16
<i>dod-6</i>	1.4	Downstream Of DAF-16
<i>catalase</i>	1.4	Y54G11A.13/Y54G11A.6/catalase
<i>fkf-3</i>	1.4	FK506-Binding protein family/FKBP-binding protein
<i>ftn-1</i>	1.4	FerriTiN/ferritin heavy chain
<i>akt-1</i>	-1.9	AKT kinase family
<i>let-363</i>	-1.8	LEThal
<i>tag-335</i>	-1.7	C42C1.5/guanylyltransferase
<i>daf-18</i>	-1.7	abnormal DAuer Formation
<i>pat-3</i>	-1.4	Paralysed Arrest at Two-fold//beta integrin
<i>ugt-1</i>	-1.4	AC3.7/UDP-glucuronosyltransferase

Microarray data showing significantly ($p < 0.05$) changed genes in gene ontology (GO) class representing response to aging from GYY4137-exposed (100 μ M) *Caenorhabditis elegans*.