

Figure S1: Related to Figure 1. Data Quality Controls.

(A) Variation in the lifespan distributions on a trial-by-trial basis. Each trial consists of multiple physical slides run simultaneously.

(B) There is some variation in the lifespan distributions on a slide-by-slide basis, but the results across all slides were comparable. We re-analyzed our data excluding the two slides with fat tails on the left side, and found no substantial changes to our results (data not shown).

(C-G) We also checked for lifespan effects from area of bacterial food source (C), distance from the center of the slide (edge effects) (D), and x (E), y (F), and z-position (G) in the microscope enclosure, finding no substantial biases.

(H–J) Scatterplots of the relationships between total lifespan, adult lifespan, and duration of larval development. (K–L) Gallery of worm segmentations. Randomly selected sample images of manually (K) and automatically (L) detected worm positions.

(M–O) Summary of worm segmentation accuracy. Correlations between summary statistics of manually- and automatically-detected worm positions: cross-sectional size (M), position in the field of view along the x-axis (N), and position in the field of view along the y-axis (O).

Lifespan Cohorts at Day 2.0



Figure S2: Related to Figure 2. Randomly selected sample images of worms in each of our adult lifespan cohorts at day 2 of adulthood.





Normalized

0.05

10 12 14 16

Days of Adult Lifespan

Figure S3: Related to Figure 2. Subpopulation Analysis.

(A–B) Mottled subpopulation sample images. The "mottled" subpopulation is a small subpopulation (13.7% of the total) of small, sickly-looking individuals which appear unhealthy throughout their lives but have very long lifespans. Randomly selected sample images of worms in the "mottled" subpopulation (A), and the non-mottled population (B) at day 2 of adulthood.

(C) Longevity of the "mottled" subpopulation.

(D) A bimodal size distribution in standard conditions. The kernel density estimate shown was generated from 22 surviving individuals at day 12 post-hatch. They were raised at 25°C on a standard NGM plate with minor modifications to match the conditions of our PEG gels: calcium chloride was excluded from the formulation, $4 \times$ the usual concentration of cholesterol was used, a more concentrated OP50 food source (50% by mass) was used, and the pH of the NGM was titrated to 6.3 rather than the usual 6.0.

(E-G) Size distributions of subpopulations over time, at days 2 (E), 6 (F), and 10 (G) of adulthood.

(H–K) Gallery of images illustrating four distinctive morphological "fates" one day before mortality. Randomly selected images for worms exhibiting a clear morphology (H), packing of bacteria within the digestive tract (I), gonadal hypertrophy (J), and a wrinkled-appearing "compressed" or "pressurized" phenotype (K).

(L) Lifespan distributions for subpopulations exhibiting the four distinctive morphological "fates".

(M) p-values from 2-sample Kolmogorov-Smirnov tests among the four "fates" subpopulations.



Figure S4: Related to Figure 3 and Figure 4. Alternate Health Definitions.

(A–H) Key analysis excluding mottled subpopulation. Our key analysis is repeated, excluding the mottled subpopulation.

(I–P) Key analysis using linear regression. Our key analysis is repeated using a linear regression in place of a support vector regression to generate the "prognosis" variable.

(Q–X) Key analysis using youthfulness. We repeat our key analysis by regressing our measured parameters against age to create a "youthfulness" score, instead of regressing against remaining lifespan to create a "prognosis" score. Biomarkers of aging have often been used to estimate an individual's "biological age" in this fashion (Baker and Sprott, 1988). Biological age, or "youthfulness", is closely related to our original measure of prognosis: if a chronologically old individual is nevertheless physiologically youthful appearing (a young "biological age"), it is likely to live for relatively more days (a good "prognosis" score) (Borkan and Norris, 1980). As shown, using this "youthfulness" score (scaled such that young individuals have a high "youthfulness") as an alternative measure of senescence does not alter the results of our analyses.

(Y, inset) Converting from prognosis to 3-day survival. Individual data points were binned into groups of individuals within a 0.5 day range of predicted remaining lifespan, and then the fraction remaining alive after 3 days was calculated to be the survival rate. A polynomial is then fit to convert from prognosis (predicted days of remaining life) to predicted survival rate.

(Y-FF) Key analysis using survival rate. Our key analysis is repeated using "3-day survival" in place of "prognosis".



Figure S5: Related to Figure 5. Thresholding Validation.

(A-D) Spans analysis is repeated using 25% threshold. Our spans analysis is repeated-dividing life into "healthspan" and "gerospan"—using an alternate threshold so that 25% of life in spent in "healthspan". (E-H) Spans analysis is repeated using 37.5% threshold. Our spans analysis is repeated—dividing life into "healthspan" and "gerospan"—using an alternate threshold so that 37.5% of life in spent in "healthspan". (I-L) Spans analysis is repeated using 62.5% threshold. Our spans analysis is repeated-dividing life into "healthspan" and "gerospan"—using an alternate threshold so that 62.5% of life in spent in "healthspan". (M-P) Spans analysis is repeated using 75% threshold. Our spans analysis is repeated-dividing life into "healthspan" and "gerospan"—using an alternate threshold so that 75% of life in spent in "healthspan". (Q) Plasticity analysis is repeated using 40% threshold. The analysis in Figure 51 is repeated for a threshold which partitions 40% of the population's total lifetime into healthspan (black) and the remainder into gerospan (gray). After re-scaling to account for differences in means of the distributions, gerospan remains more variable. (R) Plasticity analysis is repeated using 60% threshold. The analysis in Figure 51 is repeated for a threshold which partitions 60% of the population's total lifetime into healthspan (black) and the remainder into gerospan (gray). After re-scaling to account for differences in means of the distributions, gerospan remains more variable. (S–U) Quality of life analysis. Overall length of life compared to quality of life depends on definition of quality. We defined a parameter analogous to "Quality-Adjusted Life Years" (Weinstein and Stason, 1977). For simplicity, we assumed that the "quality" of a C. elegans life at any point in time is proportional to its prognosis of remaining lifespan as measured by our parameters. We then calculated the total "Quality-Adjusted Life Days" for each animal and analyzed that variable's relationship with lifespan (U). Unsurprisingly, longer-lived worms experience a higher total number of "Quality-Adjusted Life Days". To reflect the fact that it is possible to be in such poor health that an individual may actually experience a negative quality of life, we adjusted our scaling so that having a positive health score of "3 predicted days of life remaining" (T) or "6 predicted days of life remaining" (S) corresponded to zero utility/quality of life. In those cases, the overall "Quality-Adjusted Life Days" were reduced more drastically for long-lived animals, to the point that in the "6 predicted days of life remaining" case, they experienced substantially worse lives overall than their short-lived counterparts.



Figure S6: Related to Figure 1. Measurements Gallery.

(A) Autofluorescence at day 9 of adulthood. Representative randomly selected sample images of worms in the lower (bottom), middle (middle) and upper (top) quintiles of autofluorescence at day 9 of adulthood. For illustration, non-worm regions are masked out in black.

(B) Movement at day 5 of adulthood. Randomly selected sample images of worms in the lower (bottom), middle (middle) and upper (top) quintiles of movement at day 5 of adulthood. For illustration, two consecutive time points (separated by three hours) are superimposed here.

(C) Reproduction (Laid Oocytes) at day 3 of adulthood. Randomly selected sample images of worms in the lower (bottom), middle (middle) and upper (top) quintiles of reproductive output at day 8 of adulthood.

(D) Body size at day 2 of adulthood. Randomly selected sample images of worms in the lower (bottom), middle (middle) and upper (top) quintiles of cross-sectional size at day 2 of adulthood.

(E) Tissue integrity at day 2 of adulthood. Randomly selected sample images of worms in the lower (bottom), middle (middle) and upper (top) quintiles of textural integrity at day 2 of adulthood.

Additional galleries of randomly selected images are available at DOI: 10.17632/9xdthhmm75.1.

	Autofluorescence Prognosis	Body Size Prognosis	Reproductive Prognosis	Texture Prognosis	Movement Prognosis	Overall Prognosis
Autofluorescence Prognosis	1.0	0.198	0.421	0.298	0.566	0.732
Body Size Prognosis	0.198	1.0	0.328	0.179	0.248	0.297
Reproductive Prognosis	0.421	0.328	1.0	0.164	0.297	0.434
Texture Prognosis	0.298	0.179	0.164	1.0	0.587	0.607
Movement Prognosis	0.566	0.248	0.297	0.587	1.0	0.847
Overall Prognosis	0.732	0.297	0.434	0.607	0.847	1.0

Table S1: Related to Figure 2.Correlations between aspects of physiology and longevity.

	Total Lifespan Variance Explained	Unique Lifespan Variance Explained
Movement Prognosis	0.588	0.030
Body Size Prognosis	0.213	0.014
Texture Prognosis	0.418	0.017
Overall Prognosis	0.519	0.024
Autofluorescence Prognosis	0.316	0.005
Reproductive Prognosis	0.695	N/A

Table S2: Related to Figure 2.

Contributions of different aspects of health to our overall prognosis in terms of their ability to predict remaining lifespan. "Total" variance explained is computed as the r^2 value between a prognosis made from only measurements in that physiological category and remaining lifespan, while "unique" variance explained is computed as the difference between the r^2 value between the overall prognosis and lifespan and r^2 value between the overall prognosis excluding that category of physiology and lifespan.

Total Lifespan Variance Explained	Unique Lifespan Variance Explained
0.570	0.018
0.416	-0.00
0.425	-0.00
0.290	-0.00
0.046	0.012
0.147	0.002
0.418	0.017
0.519	0.024
0.041	0.006
0.284	0.000
	Total Lifespan Variance Explained 0.570 0.416 0.425 0.290 0.046 0.147 0.418 0.519 0.041 0.284

Table S3: Related to Figure 2.

Contributions of different raw physiological measures to our overall prognosis in terms of their ability to predict remaining lifespan. "Movement (Stimulated A)" is the movement rate of an individual 0.5–2.0 seconds after stimulation with cyan light, and "Movement (Stimulated B)" is the movement rate of an individual 2.0–3.5 seconds after stimulation.

Correlations (Pearson r, r^2) with Adult Lifespan

	Start	Rate	End	Average Deviation	Relative Deviation
Autofluorescence Prognosis	0.031, 0.001	0.685, 0.470	0.487, 0.237	-0.445, 0.198	-0.362, 0.131
Reproductive Prognosis	-0.129, 0.017	0.810, 0.656	0.266, 0.071	-0.144, 0.021	-0.526, 0.277
Movement Prognosis	0.038, 0.001	0.825, 0.681	0.183, 0.034	-0.389, 0.152	-0.452, 0.204
Body Size Prognosis	0.055, 0.003	0.704, 0.496	0.248, 0.062	-0.271, 0.073	-0.105, 0.011
Texture Prognosis	-0.017, 0.000	0.347, 0.120	0.216, 0.047	-0.209, 0.044	-0.166, 0.027
Overall Prognosis	0.105, 0.011	0.822, 0.676	0.408, 0.167	-0.455, 0.207	-0.351, 0.123
Youthfulness Index	-0.043, 0.002	0.747, 0.559	0.500, 0.250	-0.634, 0.402	-0.441, 0.194
Predicted Survival	0.065, 0.004	0.479, 0.230	0.412, 0.170	-0.437, 0.191	-0.300, 0.090
Linear Prognosis	0.041, 0.002	0.706, 0.499	0.330, 0.109	-0.448, 0.201	-0.356, 0.127
Non-Mottled Prognosis	0.041, 0.002	0.706, 0.499	0.330, 0.109	-0.448, 0.201	-0.356, 0.127

Table S4: Related to Figure 3 and Figure 4.

Correlations between geometric characteristics of trajectories and lifespan for individual aspects of physiology and for alternate definitions of health.

Linear Regression Weights

	Weight	Units	Category
Autofluorescence 80th Percentile Intensity	-0.75	Days per Standard Deviation	Autofluorescence
Cross-Sectional Size	-0.21	Days per Standard Deviation	Body Size
Size Rate of Change	0.25	Days per Standard Deviation	Body Size
Textural Degradation	-0.86	Days per Standard Deviation	Texture
Cumulative Oocytes Laid	-0.31	Days per Standard Deviation	Reproductive
Oocyte Laying Rate	0.18	Days per Standard Deviation	Reproductive
Movement	0.99	Days per Standard Deviation	Movement
Movement (Stimulated A)	0.05	Days per Standard Deviation	Movement
Movement (Stimulated B)	0.27	Days per Standard Deviation	Movement
Movement Rate (Unstimulated)	-0.03	Days per Standard Deviation	Movement

 Table S5: Related to Figure 2.

 Contributions of each raw measurement to the linear regression prognosis.

Data S1: Related to Figures 1-6.

Each .tsv contains data from a single animal in either **raw** or **processed** form. The rows are the time points at which measurements were made, and the columns are the individual measures, which are fully described in the metadata files and in the manuscript text. For additional clarification, the "age", "egg_age", and "ghost_age" columns indicate hours since hatching (marking start of life), first oocyte laid (marking adulthood), and death (marking end of life)¹ as determined by manual annotation.

Raw: The files in this folder contain the raw image measurements made at each time point.

Processed: The files in this folder contain the processed measurements, which have been converted to standard units (or to z-scores (standard deviations)). This data also includes some derived variables, such as the rates of change² of body size and laid oocytes, as well as prognostic predictions based on individual aspects of physiology and our overall prognosis measurement. This data has also been temporally re-sampled (each time point represents an age, which is consistent across all individuals, rather than a point in absolute time) to facilitate comparisons between all animals. Finally, this data has also been smoothed (as described in the Methods and Resources section of the manuscript) to reduce the noise from measurement error.

¹Note that our convention is to set "ghost_age" to be negative while the animal is alive.

 $^{^{2}}$ Note that based on the way that the rates of change were computed, these variables, and the overall prognosis measurement, are not available for the very last time point of a worm's life, and the final time point with a computed overall prognosis is 3-6 hours before the worm was observed to be dead (though actual death occurs somewhat earlier than observed).