S3 Table. Starvation survival analysis of Figure 5.

Genotype	**Half-life**	**SEM**	**p-value (vs. wild type)**	**p-value (vs. *daf-16*)**	R^2
wild type	21.9	1.1	N/A	**0.002**	0.976
dbl-1	18.8	0.2	**0.049**	**0.002**	0.945
sma-9	22.3	0.7	0.720	**0.001**	0.970
daf-16	11.5	1.1	**0.002**	N/A	0.988
daf-16; dbl-1	9.7	1.3	**0.002**	0.355	0.976
daf-16; sma-9	9.9	1.1	**0.001**	0.371	0.951
wild type	21.2	0.8	N/A	**0.002**	0.980
daf-36	20.1	1.0	0.298	**0.004**	0.965
daf-9	24.9	0.5	0.060	**3.2×10^{-4}**	0.985
daf-12(rh273)	17.9	1.0	0.090	**0.002**	0.994
daf-16	11.6	0.6	**0.002**	N/A	0.986
daf-16; daf-36	13.2	0.9	**0.003**	0.263	0.959
daf-16; daf-9	11.9	1.5	**0.005**	0.805	0.981
daf-16; daf-12(rh273)	9.9	1.4	**0.001**	0.345	0.992
wild type	21.4	2.0	N/A	**0.011**	0.974
din-1	22.9	1.1	0.538	**0.002**	0.966
daf-12(m20)	21.4	2.0	0.987	**0.010**	0.977
daf-12(rh61rh411)	19.4	2.3	0.542	**0.032**	0.962
daf-16	11.2	1.1	**0.011**	N/A	0.977
daf-16; din-1	11.4	0.9	**0.010**	0.868	0.956
daf-16; daf-12(m20)	7.9	0.8	**0.003**	0.073	0.985
daf-16; daf-12(rh61rh411)	12.6	1.3	**0.020**	0.451	0.911