

Genotype	mean LS/RS± std. error	% change	P-value	N=
Life span experiment 1a:				
<i>daf-16(mu86);daf-7(e1372)</i>	13.2 ±0.2	--	--	72
<i>daf-16(mu86)</i>	14.3 ±0.3	+8%	0.0004	95
<i>daf-7(e1372)</i>	21.3 ±0.8	+61%	<0.0001	97
wild type	17.6 ±0.6	--	--	72
Life span experiment 1b:				
<i>daf-16(mu86);sma-2(e502)</i>	15.0 ±0.6	--	--	
<i>daf-16(mu86)</i>	14.3 ±0.3	-5%	0.23	95
<i>sma-2(e502)</i>	18.4 ±0.3	+23%	<0.0001	96
wild type	17.6 ±0.6	--	--	72
Life span experiment 2:				
<i>daf-16(mu86);sma-2(e502)</i>	16.6 ±0.4	--	--	71
<i>daf-16(mu86)</i>	14.7 ±0.5	-11%	0.009	72
<i>sma-2(e502)</i>	18.6 ±0.3	+12%	0.005	72
wild type	17.0 ±0.4	--	--	72
Reproductive span experiment 1:				
<i>daf-16(mu86);sma-2(e502)</i>	12.1 ±0.5	--	--	60
<i>daf-16(mu86)</i>	3.5 ±0.2	-71%	<0.0001	30
<i>sma-2(e502)</i>	10.0 ±0.3	-17%	0.12	60
Reproductive span experiment 2:				
<i>daf-16(RNAi);sma-2(e502)</i>	8.8 ±0.4	--	--	50
wild type; <i>daf-16(RNAi)</i>	3.5 ±0.1	-60%	<0.0001	30
<i>sma-2(e502);control (RNAi)</i>	8.4 ±0.3	-5%	0.47	48
wild type; <i>control(RNAi)</i>	3.8 ±0.2	--	--	30
Reproductive span experiment 3:				
<i>daf-16(RNAi);dbl-1(nk3)</i>	5.6 ±0.2	--	--	60
wild type; <i>daf-16(RNAi)</i>	3.4 ±0.1	-39%	<0.0001	30
<i>dbl-1(nk3);control(RNAi)</i>	5.2 ±0.2	-7%	0.04	60
wild type; <i>control(RNAi)</i>	3.7 ±0.1	--	--	30
Reproductive span experiment 4:				
<i>daf-16(RNAi);sma-2(e502)</i>	6.5 ±0.2	--	--	26
<i>sma-2(e502);control RNAi</i>	7.0 ±0.5	+8%	0.58	20
Reproductive span experiment 5:				
<i>daf-16(mu86);daf-7(e1372)</i>	4.6 ±0.2	--	--	
<i>daf-7(e1372)</i>	5.5 ±0.2	+20%	0.004	
<i>daf-16(mu86)</i>	3.5 ±0.1	-24%		
Reproductive span experiment 6a:				
<i>daf-16(mu86);sma-2(e502)</i> mated	9.7 ±0.4	--	--	30
<i>sma-2(e502)</i> mated	10.0 ±0.6	+3%	0.42	29
<i>daf-16(mu86)</i> mated	6.1 ±0.2	-37%	0.001	34
Reproductive span experiment 6b:				
<i>daf-16(mu86);daf-7(e1372)</i> mated	6.7 ±0.4	--	--	44
<i>daf-7(e1372)</i> mated	7.8 ±0.2	+16%	0.02	39
<i>daf-16(mu86)</i> mated	6.1 ±0.2	-9%	0.13	34