Genotype	week 1	N1	week 2	N2	week 4	N4	week 5	N5
dFoxo^{21} *x dFoxo*^{25} (1)	0.35	132					0.75	132
dFoxo^{21} (1) *x yw*	0.3	15					0.92	15
S6K$^{1\text{-}1}$*/S6K*^{P1713} (2)	0.37	246					0.23	246
S6K^{P1713} (2) *x yw*	0.17	233					0.68	233
GMH5 (3) *x yw*	0.23	100	0.36	100	0.68	100	0.76	100
UAS-dTOR (4) *x GMH5*	0.69	26	0.72	34	0.94	39	0.99	33
UAS-dTSC1&2 (5) *x GMH5*	0.25	100	0.34	86	0.42	41	0.45	33
UAS-dnS6K (6) *x GMH5*	0.25	130	0.33	167	0.4	147	0.57	107
UAS-dnS6K (6) *x yw*	0.21	159	0.38	134	0.45	127	0.69	103
UAS-dnS6K (6) *x lsp2-Gal4* (7)	0.4	129	0.37	106	0.46	47	0.58	62
UAS-dnS6K (6) *x elav-Gal4* (14)	0.56	100	0.27	100	0.5	100	0.6	100
UAS-dnS6K (6) *x dilp2-Gal4* (12)	0.54	100	0.33	100	0.23	100	0.33	100
UAS-dnTOR (15) *x lsp2-Gal4* (7)	0.32	100	0.44	100	0.53	100	0.68	100
UAS-d4eBP (8) x *GMH5* (3)	0.37	94	0.36	85	0.4	153	0.43	100
UAS-dEif4e (9) x *GMH5* (3)	0.7	201	0.75	112	0.77	93	0.8	64
UAS-dMyc (10) x *GMH5* (3)	0.22	168	0.32	160	0.64	181	0.75	100
UAS-dEif4a (11) x *GMH5* (3)	0.43	42	0.39	48	0.52	118	0.7	103
UAS-dFoxo-RNAi (VDRC) *x GMH5* (3)	0.53	100	0.58	100	0.59	100	0.56	100
UAS-dFoxo-RNAi (VDRC) *x yw*	0.36	100	0.48	100	0.45	100	0.63	100
UAS-d4eBP-RNAi (VDRC) *x GMH5* (3)	0.63	100	0.69	100	0.46	100	0.54	100
UAS-d4eBP-RNAi (VDRC) *x yw*	0.36	100	0.48	100	0.51	100	0.58	100
UAS-d4eBP (8);*UAS-dTOR* (4) *x GMH5*	0.41	100	0.38	100	0.17	100	0.29	100
UAS-d4eBP (8);*UAS-dTOR* (4) *x yw*	0.34	100	0.37	100	0.54	100	0.72	100
UAS-dEif4e (9);*UAS-dTSC1&2* (5) *x GMH5*	0.58	100	0.59	100	0.61	100	0.64	100
UAS-d4eBP (8);*UAS-dFoxo* (3) *x GMH5*	0.24	100	0.3	100	0.38	100	0.36	100
UAS-d4eBP (8);*UAS-dFoxo* (3) *x yw*	0.12	100	0.33	100	0.54	100	0.59	100
UAS-dEif4e (9);*UAS-dFoxo* (3) *x GMH5*	0.64	100	0.6	100	0.73	100	0.69	100
UAS-dEif4e (9);*UAS-dFoxo* (3) x *yw*	0.17	100	0.33	100	0.35	100	0.53	100
UAS-dTOR (4) *x yw*	0.39	118					0.65	92
UAS-dTSC1&2 (5) *x yw*	0.37	173					0.72	100
dilp2-Gal4 (12) *x yw*	0.16	48	0.38	54	0.60	49	0.66	53
UAS-dnTOR (15) *x Canton S*	0.31	85	0.59	132	0.71	41	0.45	38
UAS-d4eBP (8) *x yw*	0.26	172	0.59	132	0.71	41	0.78	14
UAS-dEif4e (9) *x yw*	0.42	45	0.24	160	0.60	111	0.65	100
UAS-dMyc (10) *x yw*	0.22	169	0.32	160	0.64	181	0.75	100
GS-eif4e^{2326} (13) *x yw*	0.18	109					0.76	58
GS-eif4e^{2783} (13) *x GMH5*	0.70	100					0.77	52
GS-eif4e^{2251} (13) *x GMH5*	0.63	85					0.80	46
GS-eif4e^{2326} (13) *x GMH5*	0.75	16					0.80	31
GS-eif4e^{2251} (13) *x yw*	0.37	164					0.72	108
UAS- dFoxo-RNAi (VDRC) *x lsp2-Gal4* (7)	0.34	106	0.40	87	0.12	76	0.54	67
UAS-dFoxo(3x) (3) *x lsp2-Gal4* (7)	0.42	95	0.30	89	0.47	77	0.55	86

Source References: (1) Junger et al. 2003; (2) Montagne et al. 1999; (3) Wessells et al. 2004; (4) Hennig and Neufeld 2002; (5) Potter et al. 2001; (6) Barcelo and Stewart 2002; (7) Cherbas et al. 2003; (8) Mifon et al. 2001; (9) Arquier et al. 2005; (10) de la Cova and Johnston 2006; (11) Li et al. 2005; (12) Ikeya et al. 2002; (13) Krupp et al. 2003; (14) Brand and Perrimon 1993; (15) Hennig and Neufeld 2002. (VDRC) Vienna *Drosophila* Research Center.

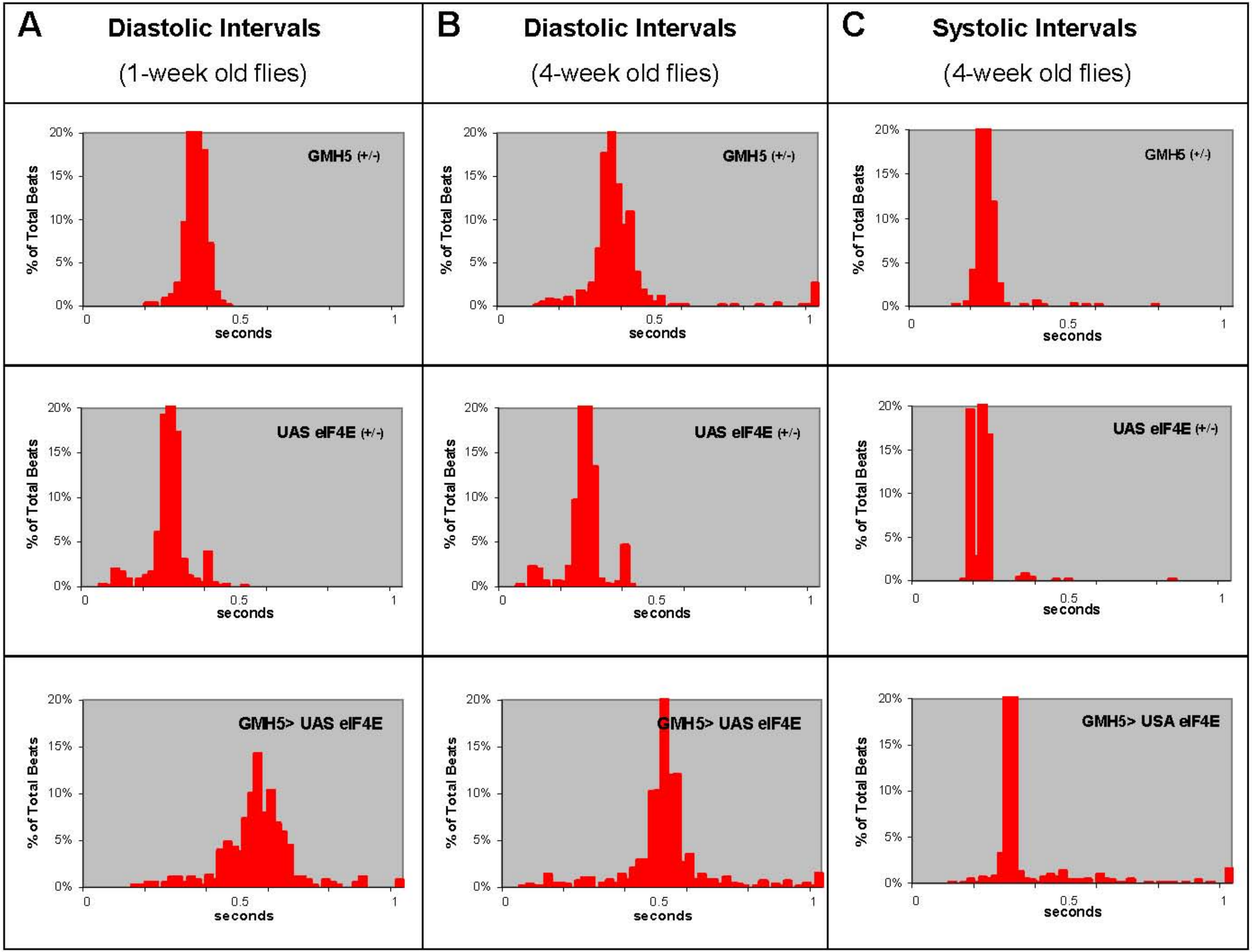
Supplemental Table 1. Summary of failure rate vs. age of various genotypes. Genotype: flies tested are denoted by their genotype or by the cross used to generate them. week 1-5: fraction of flies tested that exhibit heart failure at that age. N1-5 number of flies tested at 1-5 weeks of age.

Supplemental Table 2: Cardiac Failure Rate Analysis

Genotype 1	Genotype 2	Genotype-by-Age p-value
Foxo 21/25	*Foxo21 x yw*	0.221
S6K1-1/S6KP1713	*S6KP1713 x yw*	<0.001
UAS-dTOR x GMH5	*UAS-dTOR x yw*	0.8476*
GS-Eif4e^{2326} x GMH5	*GS-Eif4e^{2326} x yw*	<0.01
UAS-dnS6K x GMH5	*UAS-dnS6K x yw*	0.084
UAS-dnS6K x lsp2-gal4	*UAS-dnS6K x yw*	<0.01
UAS-dnS6K x elav-gal4	*UAS-dnS6K x yw*	<0.001
UAS-dnS6K x dilp2-gal4	*UAS-dnS6K x yw*	<0.0001
UAS-dMyc x GMH5	*UAS-dMyc x yw*	0.986
UAS-dTSC x GMH5	*UAS-dTSC x yw*	0.2621*
UAS-dnTOR x lsp2-gal4	*UAS-dnTOR x Canton S*	0.214
UAS-d4eBP;UASdFoxo x GMH5	*UAS-d4eBP;UAS-dFoxo x yw*	<0.001
UAS-Foxo(3x) x lsp2-gal4	*UAS-Foxo-RNAi x lsp2-gal4*	0.387
UAS-dEif4e x GMH5	*UAS-dEif4e x yw*	<0.001
UAS-dEif4e;UAS-dFoxo x GMH5	*UAS-dEif4e;UAS-dFoxo x yw*	<0.05
UAS-d4eBP x GMH5	*UAS-d4eBP x yw*	<0.001
UAS-d4eBPRNAi x GMH5	*UAS-d4eBP-RNAi x yw*	<0.0001
UAS-d4eBP;UAS-dTOR x GMH5	*UAS-d4eBP;UAS-dTOR x yw*	<0.0001
UAS-dFoxoRNAi x GMH5	*UAS-dFoxoRNAi x yw*	<0.05

Supplemental Table 2: Statistical comparison of cardiac failure rate employing two-way ANOVA followed by a Bonferroni comparison to evaluate the effect of genotype on the effect of age on cardiac failure rate compared to out-crossed controls.

* *dTOR* and *dTSC* cardiac overexpression versus control do not show a significant difference in the slope of age-dependent changes (genotype x age). However, both *dTOR* and *dTSC* overexpression causes significantly higher failure at young ages (student's t-test at 1 week, *dTOR*: $p<0.001$, *dTSC*: $p<0.05$) and at older ages (student's t-test at 5 week, *dTOR*: $p<0.0001$), *dTSC*: $p<0.01$).


A
Diastolic Intervals
(1-week old flies)
B
Diastolic Intervals
(4-week old flies)
C
Systolic Intervals
(4-week old flies)
GMH5 (+/-)
UAS eIF4E (+/-)
GMH5> UAS eIF4E
GMH5> USA eIF4E
% of Total Beats
seconds
0%
5%
10%
15%
20%
0
0.5
1

Supplemental Figure 1 legend:

Distribution of diastolic and systolic Intervals in young and old flies. A) The distributions of diastolic intervals for all 1-week old flies (normalized to the median diastolic interval) are shown. The majority of diastoles from both heterozygous control groups show a relatively tight clustering between 0.3 and 0.4 seconds. The diastolic intervals for flies, where *dEif4e* has been over-expressed specifically in the heart, show a broader distribution compared to controls. B) The diastolic intervals for older (4-week old) flies where *dEif4e* has been over-expressed specifically in the heart also show a broader distribution compared to controls (especially due to ‘outliers’ at some distance from the main peak). C) The distribution of systolic intervals for older (4-week old) flies where *dEif4e* has been over-expressed specifically in the heart show a peak at a time point that is slightly longer that seen for controls ($p<0.05$). Systolic intervals in *dEif4e* overexpression hearts also exhibit a broader distribution compared to controls with a significant number of very long systolic intervals corresponding to the episodes of fibrillation seen in the M-modes in panel (B), (compare GMH5 (+/-) and UAS eIF4E (+/-) with GMH5> *dEif4e*).