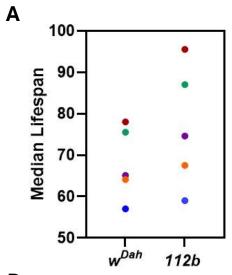
Genotype	Median Lifespan	n Dead	n Censored	% Increase	p-value (log rank)	Control
	(days)	0		0	vs control	-2- MPP200-07
W ^{Dah}	69	129	4	50		*
DmGluRA [112b]	76	137	0	10	2.133E-30	
dFmr1 [392]	71	117	3	3	2.142E-10	
dFmr1 ^[392] ;DmGluRA ^[1126]	71	152	2	3	2,708E-08	
Cox Proportional Hazard	I (CPH) analysis					
Details	Coefficient	Coefficient	exp(coeff)	SE (coeff)	L	p
		(estimate)	- 10.00 M Vs			A ⁵
dead = 544	w Dah vs DmGluRA [112b]	-1.7472	0.1743	0.1408	-12.413	<2E-16
	w Dah vs dFmr1 [302]	-0.5648	0.5685	0.1296	-4.357	3.20E-05
censored = 7		4.0000	5.3699	0.1855	9.057	<2E-16
	w Dah vs dFmr1 [302] : DmGluRA [112b]	1.6802	0.3033	0.1000		
censored = 7 Effect of <i>DmGluRA</i> [^{(172b]} mutation analysed using	w Dah vs dFmr1 [302] : DmGluRA [112b]	1.6802	3.3033	0,1000	0.007	

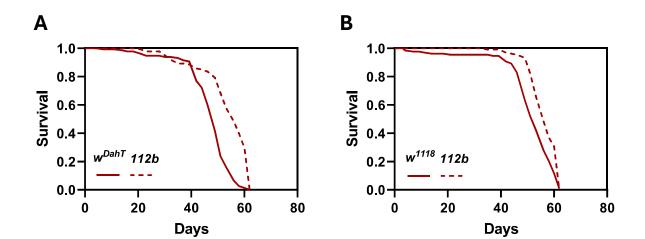


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Experiment/Genotype	Median Lifespan (Days)	n Dead	n censored	% increase	p-value (log rank) vs control	Control
Experiment 1						
wDah	75.5	136	6	15	4.64727E-23	*
112b	87	117	19			
Experiment 2						
wDah	78	133	11	22	4.67583E-33	*
112b	95.5	151	7			
Experiment 3						
wDah	64.1	124	8	12	2.69596E-05	*
112b	71.6	110	12			
Experiment 4						`
wDah	57	111	28	4	0.003455884	*
112b	59	117	27			
Experiment 5						
wDah	65.1	138	8	4	0.001247704	*
112b	67.5	146	6			

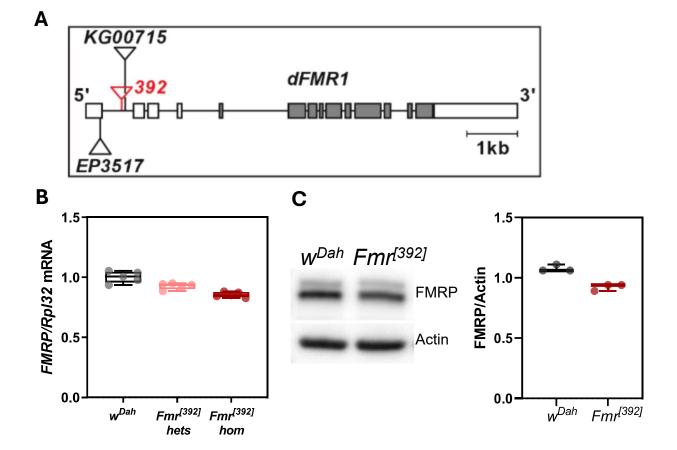
Supplementary Figure S1. Survival data for repeat independent experiments comparing $DmGluRA^{[112b]}$ homozygous females to w^{Dah} controls.

(A) Median survival for w^{Dah} and $DmGluRA^{[112b]}$ females across 5 independently replicated experiments. Colours indicate individual experiments. (B) Numbers of individuals (deaths and censors) and Log-rank p-values for the experimental data displayed in (A).



Supplementary Figure S2. Mutation of *DmGluRA* extends female lifespan irrespective of *Wolbachia* status or genetic background.

(A) Survival of female $DmGluRA^{[112b]}$ homozygous mutant flies after backcrossing into the Wolbachia-deficient w^{DahT} genetic background. (w^{DahT} controls: n = 116 dead/ 22 censored; $DmGluRA^{[112b]}$ homozygous mutants: n =127 dead/ 15 censored; $p = 2.5 \times 10^{-16}$, Log-rank test). (B) Survival of female $DmGluRA^{[112b]}$ homozygous mutant flies after backcrossing into the w^{1118} genetic background. (w^{1118} controls: n = 123 dead/ 12 censored; $DmGluRA^{[112b]}$ homozygous mutants: n = 125 dead/ 15 censored; $p = 1.6 \times 10^{-6}$, Log-rank test).



Supplementary Figure S3. Reduced *dFmr1* transcript and protein expression in *dFmr1*[392] mutants.

(A) Schematic of the *Drosophila dFmr1* locus showing the position of the *dFmr1* $^{[392]}$ pelement insertion. Black boxes represent exons and shaded boxes indicate the *dFmr1* coding sequence. (B) Quantitative RT-PCR analysis of *dFmr1* mRNA relative to *rpl32* in 10-day old female flies of the indicated genotypes (hets represent heterozygous and hom represents homozygous $dFmr1^{[392]}$ mutants). (n = 5 replicates of 15 female flies, p<0.05, ANOVA). (C) Representative Western blot showing FMRP protein expression in head extracts of 10-day old $dFmr1^{[392]}$ homozygote females compared to w^{Dah} controls. Box plots represent the relative expression of FMRP normalised to actin from three replicate Western blots (scaled to batch average). Data were analysed with a mixed effects linear model with sample batch as a random effect. The effect of genotype was significant (n=3, p<0.05).