### The Taste of Vitamin C in Drosophila melanogaster

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**Appendix Table S1.** Median lifespan ( $LT_{50}$ ) and log-rank calculation of (A) male and (B) female related to Figure 1A and 1B. Kaplan-Meier survival analyses were performed to compare the performance of vitamin C unfed and fed conditions at different doses.

(A)

Line				Male			
conc. of vitamin C	0 mM	0.1 mM	1 mM	5 mM	10 mM	30 mM	50 mM
LT <sub>50</sub> (hrs)	46.1 ± 4.27	53.6 ± 5.14	58.3 ± 5.32	71.0 ± 5.97	72.3 ± 9.17	99.3 ± 2.55	120.9 ± 2.31
Log-rank		<10 <sup>-2</sup>	<10 <sup>-3</sup>				

(B)

Line				Female			
conc. of vitamin C	0 mM	0.1 mM	1 mM	5 mM	10 mM	30 mM	50 mM
LT <sub>50</sub> (hrs)	45.6 ± 3.17	56.6 ± 3.78	60.9 ± 5.61	61.5 ± 3.26	62.8 ± 2.97	102.0 ± 3.09	114.6 ± 1.60
Log-rank		<10 <sup>-2</sup>	<10 <sup>-3</sup>				

**Appendix Table S2.** Median lifespan ( $LT_{50}$ ) and log-rank calculation of (A) male and (B) female related to Expanded View Figure 1A and 1B. Kaplan-Meier survival analyses were performed to compare the performance of (a) 0.1% curcumin, 0.5% curcumin, and 50 mM vitamin C fed conditions with unfed condition, (b) 0.1% curcumin and 0.5% curcumin fed conditions with 50 mM vitamin C fed conditions.

(A)

Line			Male	
conditions	Agar only	0.1% curcumin	0.5% curcumin	50 mM vitamin C
LT <sub>50</sub> (hrs)	46.1 ± 4.12	39.3 ± 3.88	34.7 ± 2.63	117.2 ± 2.04
Log-rank (a)		0.9488	<10 <sup>-3</sup>	<10 <sup>-3</sup>
Log-rank (b)		<10 <sup>-3</sup>	<10 <sup>-3</sup>	

(B)

Line			Female	
conditions	Agar only	0.1% curcumin	0.5% curcumin	50 mM vitamin C
LT <sub>50</sub> (hrs)	48.5 ± 2.47	46.0 ± 5.51	29.6 ± 0.95	116.3 ± 2.44
Log-rank (a)		0.0862	<10 <sup>-3</sup>	<10 <sup>-3</sup>
Log-rank (b)		<10 <sup>-3</sup>	<10 <sup>-3</sup>	

**Appendix Table S3.** Median lifespan (LT<sub>50</sub>) and log-rank calculation of (A) male and (B) female related to Expanded View Figure 1C and 1D. Kaplan-Meier survival analyses were performed to compare the performance of (a) 10 mM galactose, 30 mM galactose, 50 mM galactose, and 50 mM vitamin C fed conditions with unfed condition, (b) 10 mM galactose, 30 mM galactose, and 50 mM galactose fed conditions with 50 mM vitamin C fed conditions.

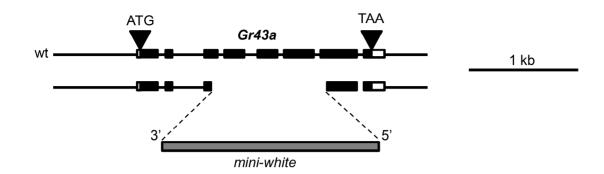
(A)

Line			Male		
conditions	Agar only	10 mM galactose	30 mM galactose	50 mM galactose	50 mM vitamin C
LT <sub>50</sub> (hrs)	46.6 ± 2.71	53.3 ± 7.95	76.7 ± 0.78	58.6 ± 4.91	117.0 ± 5.74
Log-rank (a)		0.0008	<10 <sup>-3</sup>	<10 <sup>-3</sup>	<10-3
Log-rank (b)		<10 <sup>-3</sup>	<10 <sup>-3</sup>	<10 <sup>-3</sup>	

(B)

Line	Female						
conditions	Agar only	10 mM galactose	30 mM galactose	50 mM galactose	50 mM vitamin C		
LT <sub>50</sub> (hrs)	47.3 ± 2.52	73.0 ± 7.56	95.1 ± 2.34	75.6 ± 6.89	112.0 ± 5.93		
Log-rank (a)		<10 <sup>-3</sup>	<10 <sup>-3</sup>	<10 <sup>-3</sup>	<10-3		
Log-rank (b)		<10 <sup>-3</sup>	<10 <sup>-3</sup>	<10 <sup>-3</sup>			

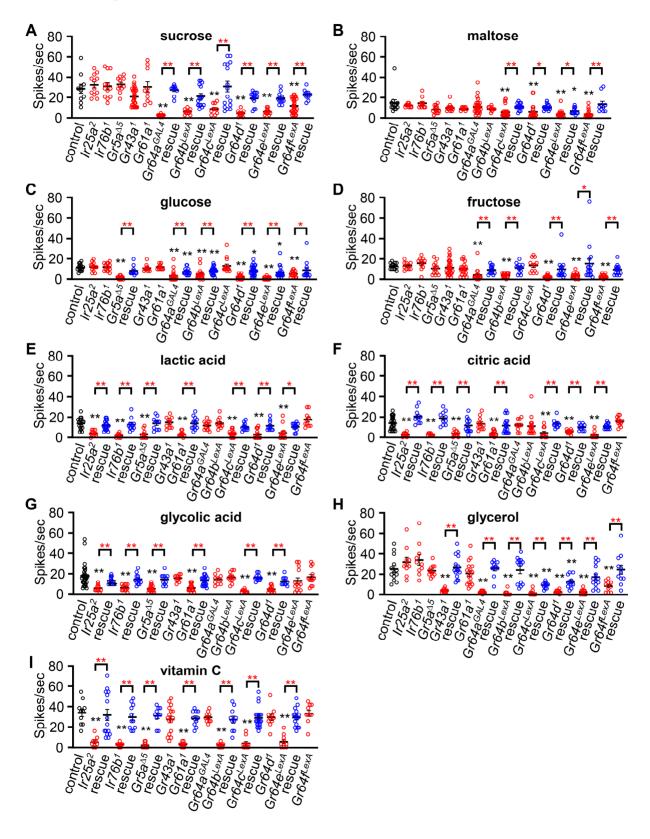
#### **Appendix Figure S1**



## Appendix Figure S1. Gene structure of *Gr43a* and Generation of *Gr43a*1.

*Gr43a* is composed of 8 exons. The mutant was generated by ends-out homologous recombination deleting 955 base pair. The deleted region ranged from +711 to +1666 using the "A" of the "ATG" start codon as a +1.

#### **Appendix Figure S2**



# Appendix Figure S2. Tip recording analysis of sugars, carboxylic acids, glycerol, and vitamin C with 11 potential candidate mutants (related to Figure 4).

**A-I** Electrophysiology with the indicated mutants and control ( $w^{1118}$ ) in the presence of 50 mM sugars ((**A**) sucrose, (**B**) maltose, (**C**) glucose, and (**D**) fructose), 1% carboxylic acids ((**E**) lactic acid, (**F**) citric acid, and (**G**) glycolic acid), (**H**) 10% glycerol and (**I**) 50 mM vitamin C. All the recordings were performed from L4 sensilla except for the glycerol where L7 sensilla was used. The defects of Ir25a, Ir76b, Gr5a, Gr61a, Gr64a, and Gr64f mutants were rescued by their own cDNA expression driven with their own GAL4s, while the rescue of Gr64b, Gr64c, Gr64d, and Gr64e were driven by Gr64f-GAL4, n = 10-29. All error bars represent the SEM. Multiple sets of data were compared using single-factor ANOVA coupled with Scheffe's post hoc test. Black asterisks indicate statistical significance compared with the control and the red asterisks indicate statistical significance compared between the respective mutant and rescue lines. \*p < 0.05, \*\*p < 0.01.