

Table S1 - Summary of low temperature performance of parental and CRISPR mutant *Drosophila melanogaster* lines. Values indicate the 2 h temperature exposure (LT_{80-2h}) or time at 0°C (Lt_{80}) at which 80% of flies did not survive, or the time ($CCRT_{80}$) at which 80% of flies had recovered from chill coma. Values are mean \pm s.e.m., with N in parentheses, indicating the number of groups of 7-15 flies used to calculate the metric. Each metric is associated with the data and models presented in Fig. 5: LT_{80-2h} , acute cold assay, Fig. 5A, B; Lt_{80} , chronic cold assay, Fig. 5C, D; $CCRT_{80}$, chill coma recovery time assay, Fig. 5E, F. Statistical details in Tables 1 and 2).

Strain	LT_{80-2h} ($^\circ\text{C}$)		Lt_{80} (h) at 0°C		$CCRT_{80}$ (min)	
	Control	RCH-treated	Control	Control	RCH-treated	
Females						
parental (+)	-3.1 \pm 0.14 (10)	-3.2 \pm 0.35 (15)	29.3 \pm 2.2 (15)	36.9 \pm 2.1 (3)	35.4 \pm 1.4 (3)	
Fst^{ins-1}	-4.0 \pm 0.02 (10)	-3.9 \pm 0.17 (15)	30.3 \pm 4.0 (15)	40.1 \pm 1.2 (3)	33.6 \pm 1.8 (3)	
Fst^{ins-2}	-3.4 \pm 0.87 (10)	-4.3 \pm 0.06 (15)	28.7 \pm 3.0 (15)	39.9 \pm 0.8 (3)	37.5 \pm 1.8 (3)	
Fst^{del-1}	-4.1 \pm 0.01 (10)	-4.2 \pm 0.30 (15)	25.7 \pm 1.5 (15)	41.7 \pm 1.1 (3)	40.0 \pm 0.3 (3)	
Fst^{del-2}	-3.1 \pm 0.10 (10)	-4.1 \pm 0.11 (15)	28.0 \pm 1.4 (15)	42.6 \pm 0.3 (3)	40.6 \pm 2.0 (3)	
Males						
parental (+)	-2.9 \pm 0.01 (10)	-3.0 \pm 0.34 (15)	24.1 \pm 0.3 (15)	40.4 \pm 2.4 (3)	37.0 \pm 2.2 (3)	
Fst^{ins-1}	-3.4 \pm 0.20 (10)	-3.4 \pm 0.23 (15)	24.0 \pm 0.4 (15)	38.7 \pm 3.2 (3)	38.5 \pm 2.6 (3)	
Fst^{ins-2}	-3.5 \pm 0.20 (10)	-3.0 \pm 0.14 (15)	28.4 \pm 1.5 (15)	41.4 \pm 1.7 (3)	37.9 \pm 1.2 (3)	
Fst^{del-1}	-3.7 \pm 0.03 (10)	-3.0 \pm 0.03 (15)	22.1 \pm 1.8 (15)	40.9 \pm 1.3 (3)	41.6 \pm 1.7 (3)	
Fst^{del-2}	-2.9 \pm 0.02 (10)	-3.1 \pm 0.34 (15)	24.5 \pm 4.2 (15)	44.3 \pm 0.4 (3)	45.0 \pm 0.9 (3)	

Table S2 – Hazard ratios of chill coma recovery time (CCRT). The hazard ratios (and standard error) are calculated from the survival analysis CCRT model in Table 2. Bold *P*-value indicates a significant difference in CCRT for that group relative to the reference group of control (not RCH-treated), parental strain, female flies.

Group	Hazard ratio	SE	P
<i>Fst</i> ^{ins-1}	0.730	0.249	0.21
<i>Fst</i> ^{ins-2}	0.643	0.226	0.051
<i>Fst</i> ^{del-1}	0.527	0.225	0.004
<i>Fst</i> ^{del-2}	0.453	0.228	0.001
RCH-treated	1.094	0.226	0.69
Males	0.583	0.233	0.021
<i>Fst</i> ^{ins-1} , RCH-treated	1.908	0.334	0.053
<i>Fst</i> ^{ins-2} , RCH-treated	1.225	0.314	0.52
<i>Fst</i> ^{del-1} , RCH-treated	1.078	0.316	0.81
<i>Fst</i> ^{del-2} , RCH-treated	1.169	0.319	0.63
<i>Fst</i> ^{ins-1} , Males	1.795	0.344	0.089
<i>Fst</i> ^{ins-2} , Males	1.416	0.325	0.28
<i>Fst</i> ^{del-1} , Males	1.928	0.320	0.041
<i>Fst</i> ^{del-2} , Males	1.618	0.330	0.14
RCH-treated, Males	0.878	0.347	0.71
<i>Fst</i> ^{ins-1} , RCH-treated, Males	0.479	0.489	0.13
<i>Fst</i> ^{ins-2} , RCH-treated, Males	1.015	0.465	0.98
<i>Fst</i> ^{del-1} , RCH-treated, Males	0.775	0.466	0.58
<i>Fst</i> ^{del-2} , RCH-treated, Males	0.836	0.479	0.71

Table S3: Data for Newman et al., 2017

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