

**Table S9. Evaluation of the effect of the disrupted ultraconserved region *CG15121-CG16894* in heterozygosis on a variety of traits**

<b>Trait</b>	<b>Contrast</b>	<b><i>n</i></b>	<b>Statistical Test</b>	<b>D.F.</b>	<b><i>P</i></b>
Progeny size <sup>a</sup>					
<i>Females</i>	INV-1, INV-2, REC	10-15	ANOVA	2, 32	0.1053
<i>Males</i>	INV-1, INV-2, REC	10-15	ANOVA	2, 32	0.3556
<i>Total</i>	INV-1, INV-2, REC	10-15	ANOVA <sup>c</sup>	2, 19.52	0.1301
Female to male ratio <sup>a, b</sup>	INV-1, INV-2, REC	10-15	ANOVA	2, 32	0.1111
Mendelian ratios (1:2:1)					
<i>Females</i>	REC/SIM1	5	<i>G</i> -test	2	0.1691
	INV1/SIM1	5	<i>G</i> -test	2	0.8908
	INV2/SIM1	5	<i>G</i> -test	2	0.1026
	REC/REV1	5	<i>G</i> -test	2	0.5663
	INV1/REV1	5	<i>G</i> -test	2	0.3147
	REC/REV2	5	<i>G</i> -test	2	0.5233
<i>Males</i>	INV2/REV2	5	<i>G</i> -test	2	0.8822
	REC/SIM1	5	<i>G</i> -test	2	0.8969
	INV1/SIM1	5	<i>G</i> -test	2	0.8635
	INV2/SIM1	5	<i>G</i> -test	2	0.2068
	REC/REV1	5	<i>G</i> -test	2	0.6153
	INV1/REV1	5	<i>G</i> -test	2	0.6434
<i>Total</i>	REC/REV2	5	<i>G</i> -test	2	0.2708
	INV2/REV2	5	<i>G</i> -test	2	0.1055
	REC/SIM1	5	<i>G</i> -test	2	0.2719
	INV1/SIM1	5	<i>G</i> -test	2	0.8321
	INV2/SIM1	5	<i>G</i> -test	2	0.0908
	REC/REV1	5	<i>G</i> -test	2	0.7035
<i>Total</i>	INV1/REV1	5	<i>G</i> -test	2	0.6829
	REC/REV2	5	<i>G</i> -test	2	0.1723
	INV2/REV2	5	<i>G</i> -test	2	0.2331

<sup>a</sup> Upon pooling the data from the various genetic backgrounds in which the chromosomes tested (REC, INV1, INV2) were in heterozygosis (SIM1, REV1, and REV2). <sup>b</sup> Upon log transformation. <sup>c</sup> Welch's ANOVA.