Supplemental Table S5

Table S5. Genetic Interactions Between *mys* & *rhea*

A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
mys TWOW Shading	mys rhea int. Shading	Test#1 Viability male vs female Column M/N	P=	Test#2 males mys/wt (I/J)/(mys+I/J)	P=	Test#2 females mys het./wt (K/L)/(mys+K/L)	P=	Progeny males mys; rhea/+ rhea/+	Progeny males mys; +/+	Progeny females mys/+; rhea/+	Progeny females mys/+; +/+	rhea/+ % viability males/females (Column I/K)	+/+ % viability males/females (Column J/L)	Temp. °C
b47	b47	0.3	0.00	0.2	0.00	0.9	0.56	7	26	129	141	5%	18%	22
b69	b69	0.1	0.00	0.1	0.00	0.7	0.06	2	24	60	75	3%	32%	25
b13	b13	0.1	0.00	0.1	0.00	1.1	0.71	1	12	44	39	2%	31%	22
b26	b26	leth 18				1.1	0.56	0	0	164	134	0%	0%	18
b33	b33	2.3	0.01	2.2	0.01	0.9	0.59	40	16	170	153	24%	10%	31*
b66	b66	9.0	0.01	8.9	0.01	1.0	0.91	10	1	366	328	3%	0%	18
b65	b65	1.7	0.01	1.4	0.10	0.8	0.12	87	54	106	114	82%	47%	31*
b20	b20	0.8	0.48	0.6	0.02	0.7	0.02	51	75	81	101	63%	74%	31*
b70	b70	0.1	0.00	0.1	0.00	0.8	0.34	4	62	226	261	2%	24%	22
b48	b48	0.6	0.02	0.5	0.00	0.8	1.6	37	69	103	107	36%	64%	31*
b53	b53	0.7	0.22	0.3	0.00	0.4	0.00	16	46	55	105	29%	44%	31*
b42	b42	0.9	0.54	0.8	0.13	0.8	0.14	113	129	164	169	69%	76%	31*
ts2	ts2	0.8	0.36	1.2	0.36	1.8	0.00	71	47	281	153	25%	31%	28
b4	b4	0.5	0.01	0.3	0.00	0.6	0.00	20	57	95	131	21%	44%	31*
b34	b34	1.6	0.05	1.6	0.05	0.9	0.62	78	44	88	80	89%	55%	31*
b32	b32	1.8	0.03	1.7	0.05	1.1	0.75	63	31	65	59	97%	53%	22
b24	b24	2.2	0.00	2.2	0.00	1.0	0.90	87	34	106	90	82%	38%	31*
b39	b39	1.2	0.37	1.3	0.32	1.0	0.78	63	44	94	82	67%	54%	31*
b7	b7	1.06	0.69	1.0	0.91	0.9	0.33	149	133	232	220	64%	60%	31*
b57	b57	24.9	0.00	23.2	0.00	0.9	0.42	53	2	161	151	33%	1%	31*
b46	b46	0.9	0.67	1.0	0.90	1.0	1.00	115	103	159	132	72%	78%	31*
b1	b1	1.2	0.43	1.3	0.22	1.1	0.59	61	40	386	300	16%	13%	31*
b44	b44	2.8	0.00	2.4	0.00	0.9	0.59	132	49	224	235	59%	21%	28
b49	b49	1.1	0.83	1.0	0.97	0.9	0.58	43	38	51	48	84%	79%	31*
b40	b40	0.6	0.17	0.1	0.00	0.2	0.00	12	77	18	66	67%	117%	31*
b63	b63	0.9	0.67	0.8	0.22	0.8	0.20	119	129	148	149	80%	87%	31*
b30	b30	13.3	0.00	15.8	0.00	1.2	0.27	124	7	282	212	44%	3%	18
b45	b45	8.2	0.00	5.7	0.00	0.7	0.00	39	6	149	187	26%	3%	31*
b55	b55	0.4	0.00	0.1	0.00	0.3	0.00	18	144	44	134	41%	107%	31*
b50	b50	0.8	0.22	0.8	0.20	1.0	0.78	57	66	102	89	56%	74%	31*
b22	b22	leth18				1.0	0.98	0	0	130	118	0%	0%	18
b3	b3	4.7	0.01	5.9	0.01	1.4	1.00	20	3	128	91	16%	3%	28
b38	b38	0.8	0.35	0.6	0.01	0.7	0.04	55	82	84	101	65%	81%	31*
b31	b31	1.1	0.56	1.1	0.72	0.9	0.54	149	123	174	158	86%	78%	31*
b56	b56	3.7	0.00	3.2	0.00	0.8	0.14	83	23	166	171	50%	13%	31*
b37	b37	0.7	0.12	0.8	0.28	1.1	0.64	52	58	111	85	47%	68%	31*
b68	b68	13.9	0.00	11.3	0.00	1.0	0.86	55	4	211	213	26%	2%	22
b21	b21	0.7	0.66	0.6	0.56	0.8	0.20	2	3	169	169	1%	2%	31*
b41	b41	2.3	0.04	2.3	0.03	1.0	0.90	26	10	62	55	42%	18%	18
b25	b25	0.9	0.61	0.9	0.43	0.9	0.46	143	143	193	178	74%	80%	31*
b52	b52	3.6	0.04	2.8	0.11	0.8	0.12	10	3	156	169	6%	2%	25*
b29	b29	2.2	0.00	2.0	0.01	0.9	0.29	59	26	213	205	28%	13%	31*
b58	b58	0.5	0.02	0.5	0.02	0.9	0.68	30	49	110	98	27%	50%	31*
b67	b67	0.1	0.00	0.1	0.01	1.2	0.44	1	9	181	143	1%	6%	18
b27	b27	3.5	0.00	3.8	0.00	1.0	0.88	73	17	284	231	26%	7%	31*
b64	b64	9.5	0.00	8.9	0.00	1.0	0.80	20	2	344	328	6%	1%	18
b51	b51	2.1	0.02	2.2	0.03	1.1	0.68	32	13	449	383	7%	3%	18
b23	b23	leth18				0.9	0.49	0	0	88	93	0%	0%	18
Wild type controls														
	mys+	1.03	0.90					109	97	92	84	118%	115%	18
	mys+	1.19	0.43					91	75	88	86	103%	87%	22
	mys+	1.00	1.00					131	109	131	109	100%	100%	25
	mys+	1.27	0.15					157	120	165	160	95%	75%	28
	mys+	0.95	0.72					154	135	230	191	67%	71%	31*

Table S5. Genetic interactions between *mys* mutants and *rhea*. Mutant *mys* alleles were tested for genetic interactions with *rhea* (encoding talin) that alter lethality. mys^{+}; $rhea^{2}/rhea^{+}$ males were mated to *mys*/*mys*; $rhea^{+}/rhea^{+}$ females. Numbers of male and female progeny of each class is given in Columns I-L. The temperature of the crosses that result in significant lethality varied for different *mys* alleles and is indicated in Column O. In this Column 31* indicates that the cross and egg laying were done at either 28°C or 25°C and then shifted up to 31°C. 25* indicates that egg laying was done at 18°C and then shifted to 25°C.

The genetic interaction results are presented based on the previously determined TWOW-1 binding ability of the *mys* alleles (from low to high) and color coding of the alleles in Column A is the same as in Table S2. Color coding of the results of genetic interactions between *mys* alleles and *rhea* is shown in Column B. Where reduction in talin levels rescues lethality of the *mys* allele shading is light green. Where reduction in talin levels increases lethality of the *mys* allele shading is magenta. Where reduction in talin levels had no effect no shading is applied. mys^{b26}, mys^{b22}, and mys^{b23} males were lethal at the lowest temperature tested (18°C) and so could not be examined for *rhea* interactions (brown in Columns B, C, M, and N). Twelve other alleles also could not be examined for interactions with *rhea* in this test because they did not show enough lethality even at the highest temperature (31°C) tested (tan in Columns B, C, M and N).

The relative viability of males hemizygous for the indicated *mys* allele (as *mys* is on the X chromosome) with one versus two wild type copies of *rhea* (located on chromosome 3) was determined in two ways and is displayed in Columns C and E together with P values from two-proportion Z-tests (Columns D and F). Effects of talin reduction on females heterozygous for the *mys* allele is given in Column G (P values in Column H).

For the first two-proportion Z-test, relative lethality was determined by comparing two proportions and the results are given in Column C (with P value in Column D). The first proportion (Column M) is the number of *mys* males with only one wild type copy *rhea* (Column I) as compared to the number of females heterozygous for both *mys* and *rhea* (Column K). The second, control, proportion (Column N) is the number of *mys* males with two wild type copies of the *rhea* (Column J) compared to the number of females heterozygous for *mys* with two wild type copies of rhea (Column L). Dividing the values when only one copy of *rhea* is present (Column M) by that when two copies are present (Column N) results in one test of relative viability (Column C and D). This test has the advantage of having all progeny, experimental and controls, raised in the same vials under identical conditions. It has the caveat, however, that mutant *mys* allele may not always be completely rescued by mys^{+} in heterozygotes.

The second test of *mys* and *rhea* interaction uses two different proportions. The first is the number of *mys* males with only one wild type copy of *rhea* (Column I) compared to the number of *mys* males with two wild type copies of *rhea* (Column J). The second, control, proportion is from a separate cross. mys^{+}; $rhea^{2}/rhea^{+}$ males were mated to wild type females at all temperatures. Results of this cross are at the end of the table and labeled mys+. In these control crosses, wild type males heterozygous for *rhea* (Column I) were compared with wild type males (Column J). Comparing these two proportions gives a relative viability for males (Columns E and F). The same type of analysis was used to compare females heterozygous for *mys* alleles and those bearing two wild type copies of *mys* (Columns G and H).

For male lethality the results of both analyses are very consistent. 17 of 19 of cases where *rhea*/+ shows rescue of *mys* lethality in males are detected by both tests and the exceptions, mys^{b65} and mys^{b52}, trend in that direction in the second test but do not reach significance (P=0.1 & 0.11). Where *rhea*/+ enhances *mys* lethality in males, 9 of 13 are detected by both tests and the exceptions, mys^{b20}, mys^{b40}, mys^{b53}, and mys^{b38} do not show the interaction in the first test due to *rhea*/+ enhanced lethality in both *mys* males and heterozygous females. Interactions between *rhea*/+ and *mys*/+ in females (magenta and light green in Columns G and H) suggest that these mutant βPS proteins can result in dominant effects in the presence of wild type βPS proteins. This is most prominent in mys^{b40} and mys^{b55}.

That heterozygosity for the $rhea^{2}$ allele has no effect on lethality in the absence of a *mys* mutant allele is shown in the wild type, mys+, crosses (end of table, Columns C and D).