

Aging Analysis of Mck-TSC1

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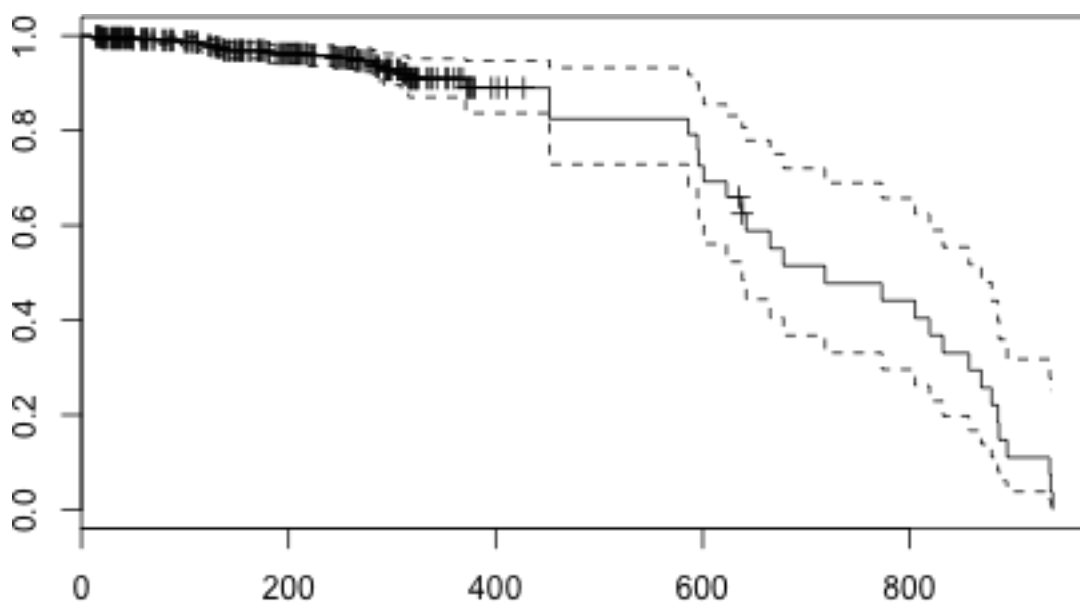
Data Entry

These data are accumulated from the database. The analysis includes all alive animals, animals which were sacrificed and animals which died of natural causes (denoted in the database as “Unknown”). Animals which died with an estimated death date are excluded from the analysis. We are testing the effects of age on death by natural causes. This script is located in /Users/davebridges/Documents/Source/DrosophilaMuscleFunction/Lifespan and was most recently run on Tue Feb 9 17:31:08 2016.

Mck-TSC1 Mice

Analysis

The data is saved in /Users/davebridges/Documents/Source/DrosophilaMuscleFunction/Lifespan with the data saved as ../Data/Mouse Log.csv and analysed using R [?]. The data was analysed using the survival package [?, ?]. Log rank tests were performed using the coin package [?, ?]. This plot analyses all of the natural deaths (marked in the database as unknown)



This analysis contains a total of **625** animals, from which we have detected **49** natural deaths. See Table below for a summary of natural deaths and see the figure below for the combined death curves with errors.

Comparing all Four Genotypes

This analysis looks at all four genotypes for *Ckmm-Tsc1*.

```
##
## Asymptotic K-Sample Logrank Test
##
## data: survobj.mck by
## Genotype (fl/fl; Tg/+, +/+; +/+, +/+; Tg/+, fl/fl; +/+)
## chi-squared = 16, df = 3, p-value = 0.0011
```

The chi-squared test for comparing all four genotypes is significant, with a p-value of 0.00009. The results of these tests are in the table below. The effects of each genotype, relative to the knockout strains are in Table ???. These data are visualised in the figure. This means that the knockout mice are 3.66749 to 5.34657 times more likely to die at any given time, depending on the strain.

Table 1: Muscle TSC1 Knockout Tests

	test	df	pvalue
Likelihood ratio test	19	3	0.000322
Wald test	18	3	0.000348
Score (logrank) test	21	3	0.000088

Table 2: Muscle TSC1 Knockout Coefficients, relative to Knockout

	beta	se	2.5 %	97.5 %	p
Genotype+/+; +/+	-1.676	0.187	-2.648	-0.705	0.000719
Genotype+/+; Tg/+	-1.459	0.232	-2.477	-0.440	0.004996
Genotypefl/fl; +/+	-1.300	0.273	-2.038	-0.561	0.000565

Comparing Floxed to Knockout

This section only compares fl/fl;+/+ to fl/fl;Tg/+.

The chi-squared test for comparing the two genotypes is significant, with a p-value of 0.00152. The results of these tests are in the table below. The effects of each genotype, relative to the knockout strains are in the table below. These results are presented graphically in the figure below. This means that the knockout mice are 3.27717 times more likely to die at any given time.

Table 3: Muscle TSC1 Knockout Tests (WT vs KO)

	test	df	pvalue
Likelihood ratio test	10	1	0.0015
Wald test	9	1	0.0026
Score (logrank) test	10	1	0.0015

Table 4: Muscle TSC1 Knockout Coefficients, relative to Knockout

	beta	se	2.5 %	97.5 %	p
Genotypefl/fl; +/+	-1.187	0.305	-1.959	-0.415	0.0026

Death Logs

This table shows the age, and at risk individuals for each natural death, along with the % survival and the confidence intervals.

time	n.risk	n.event	n.censor	surv	std.err	upper	lower	strata
10	188	1	0	0.99468	0.00533	1.00000	0.98434	Genotype=fl/fl; Tg/+
17	187	0	3	0.99468	0.00533	1.00000	0.98434	Genotype=fl/fl; Tg/+
18	184	1	7	0.98927	0.00763	1.00000	0.97460	Genotype=fl/fl; Tg/+
19	176	0	1	0.98927	0.00763	1.00000	0.97460	Genotype=fl/fl; Tg/+
21	175	0	3	0.98927	0.00763	1.00000	0.97460	Genotype=fl/fl; Tg/+
22	172	0	1	0.98927	0.00763	1.00000	0.97460	Genotype=fl/fl; Tg/+
28	171	0	2	0.98927	0.00763	1.00000	0.97460	Genotype=fl/fl; Tg/+
30	169	0	1	0.98927	0.00763	1.00000	0.97460	Genotype=fl/fl; Tg/+
31	168	0	2	0.98927	0.00763	1.00000	0.97460	Genotype=fl/fl; Tg/+
33	166	0	1	0.98927	0.00763	1.00000	0.97460	Genotype=fl/fl; Tg/+
34	165	0	1	0.98927	0.00763	1.00000	0.97460	Genotype=fl/fl; Tg/+
41	164	0	3	0.98927	0.00763	1.00000	0.97460	Genotype=fl/fl; Tg/+
42	161	0	3	0.98927	0.00763	1.00000	0.97460	Genotype=fl/fl; Tg/+
43	158	0	1	0.98927	0.00763	1.00000	0.97460	Genotype=fl/fl; Tg/+
48	157	0	2	0.98927	0.00763	1.00000	0.97460	Genotype=fl/fl; Tg/+
50	155	0	1	0.98927	0.00763	1.00000	0.97460	Genotype=fl/fl; Tg/+
58	154	0	1	0.98927	0.00763	1.00000	0.97460	Genotype=fl/fl; Tg/+
60	153	0	1	0.98927	0.00763	1.00000	0.97460	Genotype=fl/fl; Tg/+
62	152	0	2	0.98927	0.00763	1.00000	0.97460	Genotype=fl/fl; Tg/+
63	150	0	3	0.98927	0.00763	1.00000	0.97460	Genotype=fl/fl; Tg/+
64	147	0	1	0.98927	0.00763	1.00000	0.97460	Genotype=fl/fl; Tg/+
69	146	0	1	0.98927	0.00763	1.00000	0.97460	Genotype=fl/fl; Tg/+
71	145	1	0	0.98245	0.01030	1.00000	0.96282	Genotype=fl/fl; Tg/+
78	144	0	2	0.98245	0.01030	1.00000	0.96282	Genotype=fl/fl; Tg/+
85	142	0	2	0.98245	0.01030	1.00000	0.96282	Genotype=fl/fl; Tg/+
89	140	0	2	0.98245	0.01030	1.00000	0.96282	Genotype=fl/fl; Tg/+
102	138	0	2	0.98245	0.01030	1.00000	0.96282	Genotype=fl/fl; Tg/+
103	136	0	3	0.98245	0.01030	1.00000	0.96282	Genotype=fl/fl; Tg/+
108	133	0	4	0.98245	0.01030	1.00000	0.96282	Genotype=fl/fl; Tg/+
110	129	1	0	0.97484	0.01291	0.99981	0.95048	Genotype=fl/fl; Tg/+
111	128	0	1	0.97484	0.01291	0.99981	0.95048	Genotype=fl/fl; Tg/+
112	127	0	1	0.97484	0.01291	0.99981	0.95048	Genotype=fl/fl; Tg/+
114	126	1	0	0.96710	0.01517	0.99628	0.93877	Genotype=fl/fl; Tg/+
123	125	0	1	0.96710	0.01517	0.99628	0.93877	Genotype=fl/fl; Tg/+
124	124	0	3	0.96710	0.01517	0.99628	0.93877	Genotype=fl/fl; Tg/+
125	121	1	0	0.95911	0.01729	0.99217	0.92715	Genotype=fl/fl; Tg/+
130	120	0	1	0.95911	0.01729	0.99217	0.92715	Genotype=fl/fl; Tg/+
132	119	0	6	0.95911	0.01729	0.99217	0.92715	Genotype=fl/fl; Tg/+
137	113	0	1	0.95911	0.01729	0.99217	0.92715	Genotype=fl/fl; Tg/+
138	112	1	0	0.95054	0.01948	0.98753	0.91494	Genotype=fl/fl; Tg/+
147	111	0	1	0.95054	0.01948	0.98753	0.91494	Genotype=fl/fl; Tg/+
148	110	0	3	0.95054	0.01948	0.98753	0.91494	Genotype=fl/fl; Tg/+
150	107	0	3	0.95054	0.01948	0.98753	0.91494	Genotype=fl/fl; Tg/+
153	104	0	2	0.95054	0.01948	0.98753	0.91494	Genotype=fl/fl; Tg/+
160	102	0	3	0.95054	0.01948	0.98753	0.91494	Genotype=fl/fl; Tg/+
164	99	0	2	0.95054	0.01948	0.98753	0.91494	Genotype=fl/fl; Tg/+
172	97	0	4	0.95054	0.01948	0.98753	0.91494	Genotype=fl/fl; Tg/+
174	93	0	1	0.95054	0.01948	0.98753	0.91494	Genotype=fl/fl; Tg/+

time	n.risk	n.event	n.censor	surv	std.err	upper	lower	strata
177	92	0	6	0.95054	0.01948	0.98753	0.91494	Genotype=f1/f1; Tg/+
180	86	1	3	0.93949	0.02272	0.98227	0.89857	Genotype=f1/f1; Tg/+
182	82	1	0	0.92803	0.02582	0.97621	0.88224	Genotype=f1/f1; Tg/+
191	81	0	2	0.92803	0.02582	0.97621	0.88224	Genotype=f1/f1; Tg/+
195	79	0	1	0.92803	0.02582	0.97621	0.88224	Genotype=f1/f1; Tg/+
196	78	0	1	0.92803	0.02582	0.97621	0.88224	Genotype=f1/f1; Tg/+
200	77	0	4	0.92803	0.02582	0.97621	0.88224	Genotype=f1/f1; Tg/+
202	73	0	3	0.92803	0.02582	0.97621	0.88224	Genotype=f1/f1; Tg/+
204	70	0	3	0.92803	0.02582	0.97621	0.88224	Genotype=f1/f1; Tg/+
209	67	0	3	0.92803	0.02582	0.97621	0.88224	Genotype=f1/f1; Tg/+
216	64	0	1	0.92803	0.02582	0.97621	0.88224	Genotype=f1/f1; Tg/+
221	63	0	1	0.92803	0.02582	0.97621	0.88224	Genotype=f1/f1; Tg/+
225	62	0	3	0.92803	0.02582	0.97621	0.88224	Genotype=f1/f1; Tg/+
243	59	0	1	0.92803	0.02582	0.97621	0.88224	Genotype=f1/f1; Tg/+
244	58	1	0	0.91203	0.03113	0.96942	0.85805	Genotype=f1/f1; Tg/+
245	57	0	1	0.91203	0.03113	0.96942	0.85805	Genotype=f1/f1; Tg/+
248	56	0	1	0.91203	0.03113	0.96942	0.85805	Genotype=f1/f1; Tg/+
251	55	0	1	0.91203	0.03113	0.96942	0.85805	Genotype=f1/f1; Tg/+
256	54	0	2	0.91203	0.03113	0.96942	0.85805	Genotype=f1/f1; Tg/+
257	52	0	1	0.91203	0.03113	0.96942	0.85805	Genotype=f1/f1; Tg/+
261	51	0	2	0.91203	0.03113	0.96942	0.85805	Genotype=f1/f1; Tg/+
264	49	1	0	0.89342	0.03734	0.96126	0.83037	Genotype=f1/f1; Tg/+
266	48	0	3	0.89342	0.03734	0.96126	0.83037	Genotype=f1/f1; Tg/+
267	45	0	1	0.89342	0.03734	0.96126	0.83037	Genotype=f1/f1; Tg/+
270	44	0	1	0.89342	0.03734	0.96126	0.83037	Genotype=f1/f1; Tg/+
273	43	0	2	0.89342	0.03734	0.96126	0.83037	Genotype=f1/f1; Tg/+
276	41	0	1	0.89342	0.03734	0.96126	0.83037	Genotype=f1/f1; Tg/+
280	40	0	2	0.89342	0.03734	0.96126	0.83037	Genotype=f1/f1; Tg/+
281	38	1	0	0.86991	0.04589	0.95177	0.79509	Genotype=f1/f1; Tg/+
283	37	0	1	0.86991	0.04589	0.95177	0.79509	Genotype=f1/f1; Tg/+
287	36	0	1	0.86991	0.04589	0.95177	0.79509	Genotype=f1/f1; Tg/+
292	35	1	0	0.84505	0.05428	0.93991	0.75977	Genotype=f1/f1; Tg/+
296	34	0	1	0.84505	0.05428	0.93991	0.75977	Genotype=f1/f1; Tg/+
297	33	0	1	0.84505	0.05428	0.93991	0.75977	Genotype=f1/f1; Tg/+
299	32	0	1	0.84505	0.05428	0.93991	0.75977	Genotype=f1/f1; Tg/+
308	31	0	1	0.84505	0.05428	0.93991	0.75977	Genotype=f1/f1; Tg/+
309	30	1	0	0.81689	0.06400	0.92605	0.72059	Genotype=f1/f1; Tg/+
310	29	0	2	0.81689	0.06400	0.92605	0.72059	Genotype=f1/f1; Tg/+
313	27	0	2	0.81689	0.06400	0.92605	0.72059	Genotype=f1/f1; Tg/+
314	25	0	1	0.81689	0.06400	0.92605	0.72059	Genotype=f1/f1; Tg/+
316	24	1	1	0.78285	0.07686	0.91012	0.67338	Genotype=f1/f1; Tg/+
317	22	0	1	0.78285	0.07686	0.91012	0.67338	Genotype=f1/f1; Tg/+
318	21	0	1	0.78285	0.07686	0.91012	0.67338	Genotype=f1/f1; Tg/+
319	20	0	1	0.78285	0.07686	0.91012	0.67338	Genotype=f1/f1; Tg/+
320	19	0	1	0.78285	0.07686	0.91012	0.67338	Genotype=f1/f1; Tg/+
323	18	0	1	0.78285	0.07686	0.91012	0.67338	Genotype=f1/f1; Tg/+
324	17	0	1	0.78285	0.07686	0.91012	0.67338	Genotype=f1/f1; Tg/+
338	16	0	1	0.78285	0.07686	0.91012	0.67338	Genotype=f1/f1; Tg/+
343	15	0	1	0.78285	0.07686	0.91012	0.67338	Genotype=f1/f1; Tg/+
352	14	0	1	0.78285	0.07686	0.91012	0.67338	Genotype=f1/f1; Tg/+
371	13	1	0	0.72263	0.11098	0.89822	0.58136	Genotype=f1/f1; Tg/+
375	12	0	2	0.72263	0.11098	0.89822	0.58136	Genotype=f1/f1; Tg/+

time	n.risk	n.event	n.censor	surv	std.err	upper	lower	strata
396	10	0	1	0.72263	0.11098	0.89822	0.58136	Genotype=f1/f1; Tg/+
411	9	0	1	0.72263	0.11098	0.89822	0.58136	Genotype=f1/f1; Tg/+
452	8	1	0	0.63230	0.17371	0.88876	0.44985	Genotype=f1/f1; Tg/+
586	7	1	0	0.54197	0.23234	0.85457	0.34372	Genotype=f1/f1; Tg/+
595	6	1	0	0.45164	0.29549	0.80598	0.25309	Genotype=f1/f1; Tg/+
601	5	1	0	0.36131	0.37056	0.74698	0.17477	Genotype=f1/f1; Tg/+
635	4	0	1	0.36131	0.37056	0.74698	0.17477	Genotype=f1/f1; Tg/+
638	3	1	1	0.24088	0.55135	0.70975	0.08175	Genotype=f1/f1; Tg/+
832	1	1	0	0.00000	Inf	NA	NA	Genotype=f1/f1; Tg/+
15	125	0	5	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; +/+
16	120	0	5	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; +/+
17	115	0	2	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; +/+
18	113	0	12	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; +/+
19	101	0	3	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; +/+
20	98	1	6	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
21	91	0	3	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
22	88	0	7	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
24	81	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
28	80	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
30	79	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
31	78	0	2	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
32	76	0	2	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
34	74	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
38	73	0	2	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
41	71	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
43	70	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
49	69	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
50	68	0	2	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
70	66	0	2	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
86	64	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
100	63	0	2	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
103	61	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
112	60	0	2	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
138	58	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
143	57	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
156	56	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
170	55	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
193	54	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
195	53	0	3	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
198	50	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
206	49	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
216	48	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
217	47	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
225	46	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
247	45	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
251	44	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
254	43	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
259	42	0	2	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
261	40	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
262	39	0	2	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
263	37	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
266	36	0	2	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+

time	n.risk	n.event	n.censor	surv	std.err	upper	lower	strata
267	34	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
268	33	0	2	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
273	31	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
276	30	0	2	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
280	28	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
283	27	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
284	26	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
286	25	0	2	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
296	23	0	3	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
306	20	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
312	19	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
313	18	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
317	17	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
320	16	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
325	15	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
343	14	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
365	13	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
368	12	0	1	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
372	11	0	2	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
396	9	0	3	0.98980	0.01026	1.00000	0.97010	Genotype=+/+; +/+
642	6	1	0	0.82483	0.18286	1.00000	0.57638	Genotype=+/+; +/+
665	5	1	0	0.65986	0.28886	1.00000	0.37461	Genotype=+/+; +/+
678	4	1	0	0.49490	0.40838	1.00000	0.22228	Genotype=+/+; +/+
857	3	1	0	0.32993	0.57744	1.00000	0.10639	Genotype=+/+; +/+
885	2	1	0	0.16497	0.91293	0.98737	0.02756	Genotype=+/+; +/+
938	1	1	0	0.00000	Inf	NA	NA	Genotype=+/+; +/+
14	104	0	1	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; Tg/+
16	103	0	4	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; Tg/+
17	99	0	3	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; Tg/+
18	96	0	6	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; Tg/+
19	90	0	2	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; Tg/+
20	88	0	5	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; Tg/+
21	83	0	6	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; Tg/+
22	77	0	4	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; Tg/+
24	73	0	2	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; Tg/+
28	71	0	1	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; Tg/+
29	70	0	2	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; Tg/+
30	68	0	1	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; Tg/+
31	67	0	4	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; Tg/+
32	63	0	2	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; Tg/+
33	61	0	1	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; Tg/+
35	60	0	1	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; Tg/+
38	59	0	1	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; Tg/+
46	58	0	4	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; Tg/+
47	54	0	1	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; Tg/+
100	53	0	2	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; Tg/+
112	51	0	1	1.00000	0.00000	1.00000	1.00000	Genotype=+/+; Tg/+
114	50	1	0	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
170	49	0	1	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
188	48	0	2	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
245	46	0	1	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
248	45	0	1	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+

time	n.risk	n.event	n.censor	surv	std.err	upper	lower	strata
259	44	0	2	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
261	42	0	1	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
262	41	0	2	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
266	39	0	3	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
267	36	0	1	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
268	35	0	1	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
273	34	0	1	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
280	33	0	1	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
295	32	0	2	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
296	30	0	1	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
298	29	0	2	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
299	27	0	1	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
306	26	0	2	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
310	24	0	1	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
312	23	0	3	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
313	20	0	2	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
319	18	0	2	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
322	16	0	1	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
325	15	0	1	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
337	14	0	2	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
343	12	0	1	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
354	11	0	2	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
360	9	0	1	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
368	8	0	1	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
372	7	0	1	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
380	6	0	2	0.98000	0.02020	1.00000	0.94195	Genotype=+/+; Tg/+
452	4	1	0	0.73500	0.28938	1.00000	0.41684	Genotype=+/+; Tg/+
773	3	1	0	0.49000	0.50041	1.00000	0.18376	Genotype=+/+; Tg/+
805	2	1	0	0.24500	0.86626	1.00000	0.04485	Genotype=+/+; Tg/+
935	1	1	0	0.00000	Inf	NA	NA	Genotype=+/+; Tg/+
15	208	0	1	1.00000	0.00000	1.00000	1.00000	Genotype=fl/fl; +/+
17	207	0	3	1.00000	0.00000	1.00000	1.00000	Genotype=fl/fl; +/+
18	204	0	9	1.00000	0.00000	1.00000	1.00000	Genotype=fl/fl; +/+
19	195	0	1	1.00000	0.00000	1.00000	1.00000	Genotype=fl/fl; +/+
21	194	0	4	1.00000	0.00000	1.00000	1.00000	Genotype=fl/fl; +/+
22	190	0	3	1.00000	0.00000	1.00000	1.00000	Genotype=fl/fl; +/+
23	187	0	1	1.00000	0.00000	1.00000	1.00000	Genotype=fl/fl; +/+
24	186	0	1	1.00000	0.00000	1.00000	1.00000	Genotype=fl/fl; +/+
28	185	0	2	1.00000	0.00000	1.00000	1.00000	Genotype=fl/fl; +/+
31	183	0	8	1.00000	0.00000	1.00000	1.00000	Genotype=fl/fl; +/+
32	175	0	3	1.00000	0.00000	1.00000	1.00000	Genotype=fl/fl; +/+
36	172	0	1	1.00000	0.00000	1.00000	1.00000	Genotype=fl/fl; +/+
37	171	0	1	1.00000	0.00000	1.00000	1.00000	Genotype=fl/fl; +/+
38	170	0	1	1.00000	0.00000	1.00000	1.00000	Genotype=fl/fl; +/+
39	169	0	3	1.00000	0.00000	1.00000	1.00000	Genotype=fl/fl; +/+
41	166	0	6	1.00000	0.00000	1.00000	1.00000	Genotype=fl/fl; +/+
42	160	0	1	1.00000	0.00000	1.00000	1.00000	Genotype=fl/fl; +/+
43	159	0	1	1.00000	0.00000	1.00000	1.00000	Genotype=fl/fl; +/+
45	158	0	1	1.00000	0.00000	1.00000	1.00000	Genotype=fl/fl; +/+
48	157	0	1	1.00000	0.00000	1.00000	1.00000	Genotype=fl/fl; +/+
49	156	0	1	1.00000	0.00000	1.00000	1.00000	Genotype=fl/fl; +/+
50	155	1	1	0.99355	0.00647	1.00000	0.98102	Genotype=fl/fl; +/+

time	n.risk	n.event	n.censor	surv	std.err	upper	lower	strata
58	153	0	1	0.99355	0.00647	1.00000	0.98102	Genotype=fl/fl; +/+
59	152	0	1	0.99355	0.00647	1.00000	0.98102	Genotype=fl/fl; +/+
62	151	0	4	0.99355	0.00647	1.00000	0.98102	Genotype=fl/fl; +/+
69	147	0	1	0.99355	0.00647	1.00000	0.98102	Genotype=fl/fl; +/+
70	146	0	1	0.99355	0.00647	1.00000	0.98102	Genotype=fl/fl; +/+
78	145	0	2	0.99355	0.00647	1.00000	0.98102	Genotype=fl/fl; +/+
81	143	0	1	0.99355	0.00647	1.00000	0.98102	Genotype=fl/fl; +/+
85	142	0	1	0.99355	0.00647	1.00000	0.98102	Genotype=fl/fl; +/+
86	141	0	1	0.99355	0.00647	1.00000	0.98102	Genotype=fl/fl; +/+
89	140	0	1	0.99355	0.00647	1.00000	0.98102	Genotype=fl/fl; +/+
97	139	1	0	0.98640	0.00970	1.00000	0.96783	Genotype=fl/fl; +/+
103	138	0	2	0.98640	0.00970	1.00000	0.96783	Genotype=fl/fl; +/+
106	136	0	1	0.98640	0.00970	1.00000	0.96783	Genotype=fl/fl; +/+
111	135	0	1	0.98640	0.00970	1.00000	0.96783	Genotype=fl/fl; +/+
112	134	0	3	0.98640	0.00970	1.00000	0.96783	Genotype=fl/fl; +/+
124	131	0	1	0.98640	0.00970	1.00000	0.96783	Genotype=fl/fl; +/+
126	130	0	1	0.98640	0.00970	1.00000	0.96783	Genotype=fl/fl; +/+
131	129	0	2	0.98640	0.00970	1.00000	0.96783	Genotype=fl/fl; +/+
132	127	1	1	0.97863	0.01251	1.00000	0.95493	Genotype=fl/fl; +/+
134	125	0	1	0.97863	0.01251	1.00000	0.95493	Genotype=fl/fl; +/+
135	124	1	0	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
141	123	0	1	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
143	122	0	3	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
150	119	0	1	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
153	118	0	2	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
154	116	0	1	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
155	115	0	1	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
160	114	0	2	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
164	112	0	2	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
170	110	0	1	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
171	109	0	2	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
172	107	0	4	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
174	103	0	3	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
177	100	0	2	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
180	98	0	1	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
181	97	0	1	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
188	96	0	2	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
193	94	0	1	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
195	93	0	2	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
196	91	0	2	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
200	89	0	1	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
202	88	0	2	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
204	86	0	2	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
207	84	0	3	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
209	81	0	3	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
210	78	0	1	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
212	77	0	1	0.97074	0.01490	0.99951	0.94280	Genotype=fl/fl; +/+
218	76	1	0	0.95797	0.01994	0.99614	0.92126	Genotype=fl/fl; +/+
221	75	0	1	0.95797	0.01994	0.99614	0.92126	Genotype=fl/fl; +/+
223	74	0	2	0.95797	0.01994	0.99614	0.92126	Genotype=fl/fl; +/+
225	72	0	3	0.95797	0.01994	0.99614	0.92126	Genotype=fl/fl; +/+
240	69	0	1	0.95797	0.01994	0.99614	0.92126	Genotype=fl/fl; +/+

time	n.risk	n.event	n.censor	surv	std.err	upper	lower	strata
243	68	0	1	0.95797	0.01994	0.99614	0.92126	Genotype=f1/f1; +/+
247	67	0	1	0.95797	0.01994	0.99614	0.92126	Genotype=f1/f1; +/+
251	66	0	2	0.95797	0.01994	0.99614	0.92126	Genotype=f1/f1; +/+
256	64	0	2	0.95797	0.01994	0.99614	0.92126	Genotype=f1/f1; +/+
261	62	0	2	0.95797	0.01994	0.99614	0.92126	Genotype=f1/f1; +/+
263	60	0	1	0.95797	0.01994	0.99614	0.92126	Genotype=f1/f1; +/+
266	59	0	3	0.95797	0.01994	0.99614	0.92126	Genotype=f1/f1; +/+
270	56	0	1	0.95797	0.01994	0.99614	0.92126	Genotype=f1/f1; +/+
273	55	0	2	0.95797	0.01994	0.99614	0.92126	Genotype=f1/f1; +/+
276	53	0	1	0.95797	0.01994	0.99614	0.92126	Genotype=f1/f1; +/+
280	52	0	1	0.95797	0.01994	0.99614	0.92126	Genotype=f1/f1; +/+
284	51	1	0	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
286	50	0	1	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
287	49	0	1	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
293	48	0	1	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
294	47	0	1	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
296	46	0	2	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
297	44	0	3	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
298	41	0	1	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
305	40	0	1	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
306	39	0	1	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
310	38	0	1	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
314	37	0	2	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
316	35	0	4	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
317	31	0	6	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
318	25	0	2	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
333	23	0	3	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
343	20	0	1	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
360	19	0	2	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
368	17	0	2	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
375	15	0	1	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
376	14	0	1	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
378	13	0	1	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
402	12	0	1	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
427	11	0	2	0.93918	0.02810	0.99236	0.88886	Genotype=f1/f1; +/+
596	9	1	0	0.83483	0.12116	1.00000	0.65837	Genotype=f1/f1; +/+
623	8	1	0	0.73048	0.18038	1.00000	0.51294	Genotype=f1/f1; +/+
718	7	1	0	0.62612	0.23737	0.99704	0.39320	Genotype=f1/f1; +/+
819	6	1	0	0.52177	0.29946	0.93839	0.29012	Genotype=f1/f1; +/+
869	5	1	0	0.41742	0.37374	0.86835	0.20065	Genotype=f1/f1; +/+
879	4	1	0	0.31306	0.47224	0.78996	0.12407	Genotype=f1/f1; +/+
886	3	1	0	0.20871	0.62424	0.70941	0.06140	Genotype=f1/f1; +/+
894	2	1	0	0.10435	0.94323	0.66280	0.01643	Genotype=f1/f1; +/+
936	1	1	0	0.00000	Inf	NA	NA	Genotype=f1/f1; +/+

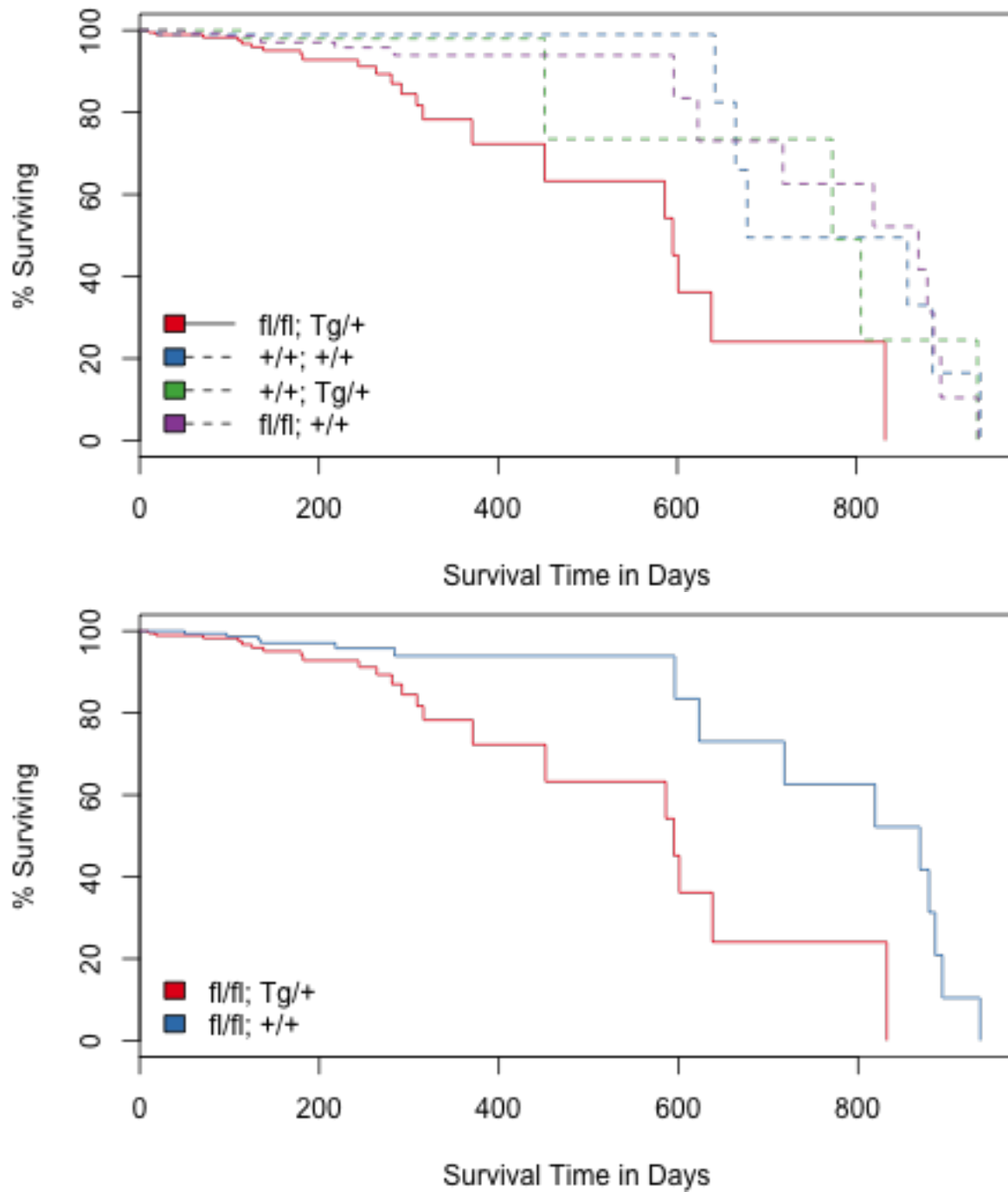
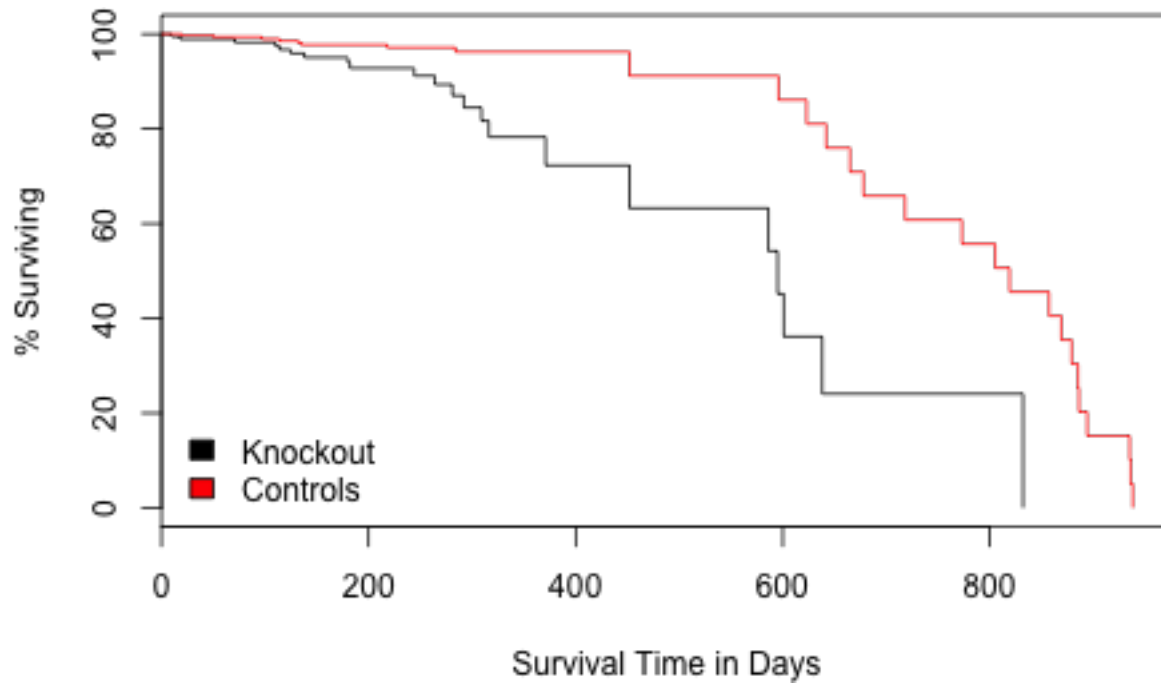


Table 6: Muscle TSC1 Knockout Summary

	Total Animals	Natural Deaths
Genotype=fl/fl; Tg/+	188	22
Genotype=+/+; +/+	125	7
Genotype=+/+; Tg/+	104	5
Genotype=fl/fl; +/+	208	15

Combining the Control Mice



The chi-squared test for comparing the two genotypes is significant, with a p-value of 0. The results of these tests are in the table below. The effects of each genotype, relative to the knockout strains are in the table below. These results are presented graphically in the figure below. This means that the knockout mice are 4.17138 times more likely to die at any given time.

Table 7: Muscle TSC1 Knockout Tests controls combined

	test	df	pvalue
Likelihood ratio test	18	1	0.0000219
Wald test	18	1	0.0000202
Score (logrank) test	21	1	0.0000047

Table 8: Muscle TSC1 Knockout Coefficients, relative to Knockout, controls combined

	beta	se	2.5 %	97.5 %	p
KnockoutTRUE	-1.428	0.24	-2.085	-0.771	0.00002023

Session Information

```
## R version 3.2.2 (2015-08-14)
## Platform: x86_64-apple-darwin13.4.0 (64-bit)
## Running under: OS X 10.11.3 (El Capitan)
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
```

```
##
## attached base packages:
## [1] stats      graphics  grDevices utils      datasets  methods   base
##
## other attached packages:
## [1] bibtex_0.4.0      RColorBrewer_1.1-2 ggfortify_0.1.0
## [4] ggplot2_2.0.0     proto_0.3-10       xtable_1.8-0
## [7] coin_1.1-2        survival_2.38-3    knitr_1.11
##
## loaded via a namespace (and not attached):
## [1] Rcpp_0.12.2      formatR_1.2.1     highr_0.5.1
## [4] plyr_1.8.3       tools_3.2.2       digest_0.6.8
## [7] evaluate_0.8     gtable_0.1.2      lattice_0.20-33
## [10] DBI_0.3.1        yaml_2.1.13       parallel_3.2.2
## [13] mvtnorm_1.0-3    gridExtra_2.0.0   stringr_1.0.0
## [16] dplyr_0.4.3      stats4_3.2.2      grid_3.2.2
## [19] R6_2.1.1         rmarkdown_0.8.1   multcomp_1.4-1
## [22] TH.data_1.0-6    tidyr_0.3.1       magrittr_1.5
## [25] scales_0.3.0     codetools_0.2-14  htmltools_0.2.6
## [28] modeltools_0.2-21 splines_3.2.2     assertthat_0.1
## [31] colorspace_1.2-6 sandwich_2.3-4    stringi_1.0-1
## [34] munsell_0.4.2    zoo_1.7-12
```