Table S2. **Complete data of all experiments displayed in Figs. 1–8 and Figs. S1–4**

Data for Fig. 1 and Figs. S1 and S2

Target gene **RNAi ID**	**Retraction frequency (%)**						***n***
	m1/9 2/10	**P vs. cntr**	**m6/7**	**P vs. cntr**	**m4**	**P vs. cntr**	
Control	1.0 ± 0.7		2.1 ± 1.4		2.1 ± 1.4		12
CK2β VDRC32377	51.4 ± 4.0	1.69×10^{-6}	20.8 ± 6.6	0.021279	18.3 ± 5.6	0.012127	9
PP2A-29B^{1} VDRC49671	48.7 ± 3.9	1.05×10^{-8}	64.3 ± 5.2	7.62×10^{-9}	56.7 ± 3.9	1.21×10^{-9}	14
PP2A-29B^{2} BL29384	40.0 ± 5.6	7.1×10^{-5}	47.1 ± 7.8	7.27×10^{-5}	27.9 ± 5.1	0.000258	10
IPP CG9784 VDCR30098	35.6 ± 7.3	0.001135	25.0 ± 7.9	0.01713	16.3 ± 4.6	0.013086	10
CKIα^{1} VDRC13664	33.3 ± 4.9	4.65×10^{-5}	19.4 ± 4.7	0.006391	27.8 ± 6.2	0.002846	12
CKIα^{2} BL25786	25.0 ± 3.9	0.000191	16.7 ± 4.4	0.007965	28.1 ± 3.8	1.61×10^{-5}	9
Mnb^{1} VDRC35282	22.9 ± 5.5	0.004315	10.8 ± 3.0	0.014565	10.0 ± 2.2	0.005673	9
Mnb^{2} VDRC107066	9.6 ± 1.6	0.000101	13.9 ± 5.3	0.059316	8.3 ± 3.0	0.079648	15
MAST205 VDRC35100	19.8 ± 3.3	0.000137	8.3 ± 3.6	0.124167	11.5 ± 4.5	0.066975	12
PI4KIIIα^{1} VDRC15993	12.5 ± 2.6	0.001906	5.6 ± 2.2	0.204143	11.1 ± 5.3	0.133384	9
PI4KIIIα^{2} VDRC105614	8.3 ± 2.1	0.007792	2.8 ± 1.8	0.767835	6.9 ± 3.0	0.173138	9
PP4-19C VDRC25317	12.5 ± 2.6	0.000817	2.1 ± 2.1	1.0	16.7 ± 3.9	0.003262	12
inR VDRC991	10.4 ± 1.8	0.000679	6.9 ± 3.0	0.173138	9.7 ± 4.6	0.140024	9
Mipp2 VDRC14163	7.6 ± 1.4	0.00115	8.3 ± 2.9	0.079648	11.1 ± 3.3	0.027233	9
Cdc2 VDRC41838	6.9 ± 1.6	0.006733	5.6 ± 3.0	0.32043	5.6 ± 2.2	0.204143	9

Transgenic RNAi lines were crossed to *elav*^{C155}-GAL4; UAS-*dcr2*. P-values were calculated relative to controls. The IDs (VDRC or Bloomington [BL]) of the RNAi-lines are indicated for all genotypes. Retraction frequencies represent synaptic retractions per animal for the indicated muscle groups. *n* equals number of animals analyzed. cntr, control; m, muscle.

Data for Fig. 2

Genotype	**Retraction frequency (%)** **m1/9 2/10**	**P vs. cntr**	***n***
control	1.0 ± 0.7		12
Neu>CK2β RNAi	51.4 ± 4.0	1.69×10^{-6}	9
Muscle>CK2β RNAi	1.4 ± 0.9	0.767835	9
Neu>CK2β RNAi; neu>CK2β	3.8 ± 1.4	0.1025	10
Neu>CK2β RNAi; neu>GFP	33.9 ± 2.8	9.59×10^{-8}	12
CK2β$^{26\text{-}2}$/mbuP1	13.8 ± 3.0	0.002341	10
CK2β$^{26\text{-}2}$; ubi>CK2β	2.9 ± 1.1	0.185102	13

Significance of rescue between genotypes as listed		**P**
Neu>CK2β RNAi	Neu>CK2β^{RNAi}; > CK2β	5.37×10^{-7}

Genotype	**Retraction frequency (%)** **(all MARCM NMJs)**	**P**	***n***
MARCM control	0.0 ± 0.0		17
MARCM CK2β$^{26\text{-}2}$	29.0 ± 5.0	7.24×10^{-6}	33

Retraction frequencies represent retractions per animals for the indicated muscle groups. For the MARCM analysis, all mCD8-GFP-positive NMJs were evaluated. P values were calculated relative to controls or as indicated. *n* equals number of animals analyzed.

Data for Fig. 3

Genotype	Retraction frequency (%)	P vs. cntr	*n*
	m1/9 2/10		
control	1.1 ± 0.8		12
CK2α$^{P1/P1}$	57.5 ± 3.9	4.22×10^{-10}	15
CK2α$^{P1/P2}$	33.0 ± 3.8	8.84×10^{-7}	14
CK2α$^{P1/Tik}$	40.1 ± 3.4	7.34×10^{-11}	21
CK2α$^{P1/TikR}$	54.0 ± 5.0	7.5×10^{-9}	17
CK2α$^{P1/P1}$ neu>CK2α	1.0 ± 0.7	0.92807	12
CK2α$^{P1/P1}$ neu>CK2α_KD	65.8 ± .9	2.49×10^{-14}	17
CK2α$^{P1/P1}$ muscle>CK2α	52.5 ± 3.3	1.49×10^{-10}	15
CK2α$^{P1/P1}$ ubi>CK2α	0.7 ± 0.5	0.665861	17
CK2α$^{P2/P2}$; ubi>CK2α neu>Gal80	41.7 ± 4.3	6.57×10^{-6}	9

Significance of rescue between genotypes as listed		P
CK2α$^{P1/P1}$	CK2α$^{P1/P1}$ neu>CK2α	4.22×10^{-10}
CK2α$^{P1/P1}$	CK2α$^{P1/P1}$ neu>CK2α_KD	0.099286
CK2α$^{P1/P1}$	CK2α$^{P1/P1}$ muscle>CK2α	0.335885
CK2α$^{P1/P1}$	CK2α$^{P1/P1}$ ubi>CK2α	8.88×10^{-10}

Retraction frequencies represent retractions per animals for the indicated muscle groups. P-values were calculated relative to controls or as indicated. *n* equals number of animals analyzed.

Data for Fig. S3

Genotype	Retraction frequency (%)				*n*
	m1/9 2/10	P vs. cntr	m6/7	P vs. cntr	
control	1.0 ± 0.7		2.1 ± 1.7		12
CK2α^{P1}/CK2α^{P1}	57.5 ± 3.9	4.22×10^{-10}	53.3 ± 7.4	5.66×10^{-6}	15
CK2α^{P1}/CK2α^{P2}	33.0 ± 3.8	8.84×10^{-7}	23.2 ± 4.7	0.000621	14
CK2α^{P1}/CK2α^{Tik}	40.1 ± 3.4	7.34×10^{-11}	33.0 ± 5.0	3.62×10^{-6}	21
CK2α^{P1}/CK2α^{TikR}	54.0 ± 5.0	7.5×10^{-9}	44.9 ± 6.0	1.65×10^{-6}	17
CK2α^{P1}/CK2α^{G703}	36.1 ± 2.9	9.32×10^{-7}	27.8 ± 7.1	0.006451	9
CK2α^{P1}/CK2α^{H3091}	32.8 ± 4.6	1.68×10^{-5}	18.6 ± 4.5	0.003586	12
CK2α^{P2}/CK2α^{P2}	Early lethal				
CK2α^{P2}/CK2α^{Tik}	32.1 ± 2.1	1.5×10^{-17}	16.5 ± 2.5	3.85×10^{-7}	21
CK2α^{P2}/CK2α^{TikR}	Early lethal				
CK2α^{P2}/CK2α^{G703}	38.6 ± 4.1	2.07×10^{-6}	35.2 ± 4.1	5.51×10^{-6}	11
CK2α^{P2}/CK2α^{H3091}	21.9 ± 3.1	2.92×10^{-5}	12.5 ± 4.4	0.040278	12
CK2α^{Tik}/CK2α^{Tik}	Early lethal				
CK2α^{Tik}/CK2α^{TikR}	Early lethal				
CK2α^{Tik}/CK2α^{G703}	30.2 ± 4.9	9.66×10^{-5}	17.7 ± 3.9	0.002108	12
CK2α^{Tik}/CK2α^{H3091}	12.1 ± 2.0	6.2×10^{-5}	10.9 ± 3.0	0.014054	16
CK2α^{TikR}/CK2α^{TikR}	Early lethal				
CK2α^{TikR}/CK2α^{G703}	51.4 ± 5.4	1.5×10^{-5}	47.2 ± 6.2	5.48×10^{-5}	9
CK2α^{TikR}/CK2α^{H3091}	29.9 ± 4.0	0.000103	15.3 ± 4.0	0.01167	9
CK2α^{G703}/CK2α^{G703}	Early lethal				
CK2α^{G703}/CK2α^{H3091}	17.4 ± 3.0	0.000115	15.2 ± 2.7	0.000361	14
CK2α^{H3091}/CK2α^{H3091}	Early lethal				

Retraction frequencies represent retractions per animals for the indicated muscle groups. P-values were calculated relative to controls or as indicated. *n* equals number of animals analyzed.

Data for Fig. 4

Genotypes	Retraction frequency (%)		*n*
	m1/9 2/10	P	
Control	1.0 ± 0.7		12
CK2α$^{P1/P1}$	54.4 ± 2.8	1.17×10^{-16}	24
CK2α$^{P1/P1}$ ubi>CK2α	0.7 ± 0.5	0.726453	17
CK2α$^{P1/P1}$ ubi>CK2α_L39A	1.6 ± 0.7	0.684095	16
CK2α$^{P1/P1}$ ubi>CK2α_F52A	2.7 ± 1.1	0.25442	16
CK2α$^{P1/P1}$ ubi>CK2α_L39AF52A	19.9 ± 3.4	3.64×10^{-5}	17

Significance of rescue between genotypes as listed		P
CK2α$^{P1/P1}$	CK2α$^{P1/P1}$ ubi>CK2α_L39AF52A	2.79×10^{-9}

Retraction frequencies represent retractions per animals for the indicated muscle groups. P-values were calculated relative to controls or as indicated. *n* equals number of animals analyzed.

Data Fig. 5

Genotypes	**Retraction frequency (%)**		***n***
	m1/9 2/10	**P**	
Control	1.0 ± 0.7		12
CK2$\alpha^{P1/P1}$	57.5 ± 3.9	4.22×10^{-10}	15
CK2$\alpha^{P1/P1}$ neu > GFP-CK2α	1.4 ± 0.9	0.767835	9

Retraction frequencies represent retractions per animals for the indicated muscle groups. P values were calculated relative to controls or as indicated. *n* equals number of animals analyzed.

Data Fig. S4

Genotype	**Retraction frequency (%)**						***n***
	m1/9 2/10	**P**	**m6/7**	**P**	**m4**	**P**	
Control	1.0 ± 0.7		2.1 ± 1.4		2.1 ± 1.4		12
PP2A-29B[1] VDRC49671	48.7 ± 3.9	1.05×10^{-8}	64.3 ± 5.2	7.62×10^{-9}	56.7 ± 3.9	1.21×10^{-9}	14
PP2A-29B[2] BL29384	40.0 ± 5.6	7.1×10^{-5}	47.1 ± 7.8	7.27×10^{-5}	27.9 ± 5.1	0.000258	10
DN-Mts	23.6 ± 4.1	0.000112	10.6 ± 2.8	0.013737	15.4 ± 4.9	0.021277	13

Genotypes	**Retraction frequency (%)**		***n***
	m1/9 2/10	**p**	
Control	1.0 ± 0.7		12
CK2$\alpha^{P1/P1}$	54.4 ± 2.8	1.17×10^{-16}	24
CK2$\alpha^{P1/Tik}$	40.1 ± 3.4	7.34×10^{-11}	22
CK2$\alpha^{P1/P1}$ neu > CK2α_E165D	2.1 ± 2.1	0.684368	6
CK2$\alpha^{P1/P1}$ neu > CK2α_E165A	2.1 ± 1.3	0.551196	6
CK2$\alpha^{P1/P1}$ neu > CK2α_ENRK165ANAA	1.7 ± 1.2	0.697549	11
CK2$\alpha^{P1/P1}$ neu > CK2α_M161K	32.8 ± 7.1	0.002938	8

Significance of rescue between genotypes as listed		**P**
CK2$\alpha^{P1/Tik}$	CK2$\alpha^{P1/P1}$ neu > CK2α_M161K	0.376674

Retraction frequencies represent retractions per animals for the indicated muscle groups. P-values were calculated relative to controls or as indicated. *n* equals number of animals analyzed.

Data for Fig. 6

Genotype	**Nrg-level (% control)**						***n***
	Distal	**P**	**Center**	**P**	**Proximal**	**P**	
Control	100.0 ± 14.0		100.0 ± 5.1		100.0 ± 4.6		6
CK2$\alpha^{P1/TikR}$	47.5 ± 2.0	0.013809	60.7 ± 5.3	0.000484	70.0 ± 9.0	0.024828	6
CK2$\alpha^{P1/TikR}$; neu > CK2α	86.4 ± 5.2	0.398193	101.7 ± 15.1	0.919937	122.7 ± 10.9	0.127887	6
CK2$\alpha^{P1/TikR}$; neu > CK2α^{KD}	46.7 ± 3.4	0.010084	56.8 ± 5.7	0.000308	66.2 ± 5.7	0.001693	6
CK2$\alpha^{P1/TikR}$; neu > Nrg	64.5 ± 11.4	0.080597	109.1 ± 19.6	0.671471	140.0 ± 16.6	0.068241	6
			Ank2-L-level (% control)				
Control	100.0 ± 5.3		100.0 ± 7.6		100.0 ± 8.4		6
CK2$\alpha^{P1/TikR}$	19.4 ± 3.0	9.99×10^{-7}	59.1 ± 8.3	0.00476	40.5 ± 1.7	0.000945	6
CK2$\alpha^{P1/TikR}$; neu > CK2α	126.8 ± 16.8	0.178839	134.7 ± 12.6	0.046746	98.7 ± 9.8	0.922847	6
CK2$\alpha^{P1/TikR}$; neu > CK2α^{KD}	22.6 ± 5.1	9.65×10^{-7}	52.3 ± 6.9	1.47×10^{-5}	57.7 ± 7.1	0.003219	6
CK2$\alpha^{P1/TikR}$; neu > Nrg	15.9 ± 2.1	5.76×10^{-6}	58.3 ± 5.9	0.001979	45.8 ± 4.3	0.000693	6
			Futsch-level (% control)				
Control	100.0 ± 28.9		100.0 ± 13.2		100.0 ± 15.4		6
CK2$\alpha^{P1/P1}$	47.6 ± 7.8	0.130945	19.8 ± 2.6	0.001876	22.2 ± 4.4	0.002798	7
CK2$\alpha^{P1/P1}$; neu > CK2α	71.3 ± 8.4	0.377404	140.7 ± 15.2	0.070729	105.3 ± 14.2	0.804896	6
CK2$\alpha^{P1/P1}$;	61.7 ± 8.2	0.250647	33.7 ± 6.3	0.002651	35.9 ± 7.7	0.007312	6

neu > CK2α^{KD}							
			DvGlut-level (% control)				
Control	100.0 ± 4.8		100.0 ± 2.8		100.0 ± 2.9		12
CK2α$^{P1/TikR}$	106.4 ± 5.1	0.368138	111.4 ± 3.3	0.015368	110.4 ± 4.2	0.056714	12
			FasII-level (% control)				
Control	100.0 ± 18.0		100.0 ± 12.4		100.0 ± 10.8		6
CK2α$^{P1/TikR}$	80.1 ± 7.1	0.351407	95.6 ± 3.8	0.747492	104.9 ± 11.5	0.76361	6

Analysis of protein levels at distal, central, and proximal boutons of NMJs on m4 segment A4. All genotypes were imaged with settings equivalent to the controls. Quantification was performed using Imaris (Bitplane). P-values were calculated relative to control. *n* equals number of NMJs analyzed.

Genotype	**Retraction frequency (%) m1/9 2/10**	**P**	***n***
Wild type	1.1 ± 0.7		12
CK2α$^{P1/P1}$	57.5 ± 3.9	4.49×10^{-10}	15
CK2α$^{P1/P1}$; neu > Nrg	50 ± 4.7	6.55×10^{-6}	9

Statistical comparison between genotypes as listed		**P**
CK2α$^{P1/P1}$	CK2α$^{P1/P1}$; neu > Nrg	0.233614

Retraction frequencies represent retractions per animals for the indicated muscle groups. P-values were calculated relative to controls or as indicated. *n* equals number of animals analyzed.

Data for Fig. 7

Genotype	**Retraction frequency (%)**				***n***
	m6/7	**P**	**m1/9, 2/10**	**P**	
control	2.1 ± 1.4		1.0 ± 0.7		12
neu > CK2α	2.1 ± 1.4	1.0	1.0 ± 0.7	1.0	12
neu > CK2α^{KD}	2.1 ± 1.4	1.0	1.6 ± 0.8	0.633323	12
ank2$^{P2/P2}$	60.8 ± 4.5	6.43×10^{-10}	65.1 ± 4.2	4.24×10^{-9}	15
ank2$^{P2/P2}$ neu > CK2α	31.7 ± 5.4	0.000111	45.8 ± 6.2	1.85×10^{-5}	13
ank2$^{P2/P2}$ neu > CK2α^{KD}	91.7 ± 3.6	1.23×10^{-12}	86.4 ± 4.0	3.37×10^{-10}	12

Statistical comparison between genotypes		**p (m 1/9 2/10)**	**p (m 6/7)**
ank2$^{P2/P2}$	ank2$^{P2/P2}$ neu > CK2α	0.00039	0.019175
ank2$^{P2/P2}$	ank2$^{P2/P2}$ neu > CK2α^{KD}	1.53×10^{-5}	0.001555
ank2$^{P2/P2}$ neu > CK2α	ank2$^{P2/P2}$ neu > CK2α^{KD}	1.14×10^{-8}	2.8×10^{-5}

Retraction frequencies represent retractions per animals for the indicated muscle groups. P-values were calculated relative to controls or as indicated. *n* equals number of animals analyzed.

Genotype	**Retraction frequency (%)**		***n***
	m6/7	**P**	
Control (second instar)	1.8 ± 1.2		11
ank2^{null}	36.4 ± 2.9	5.01×10^{-9}	10
ank2^{null} neu > CK2α	34.1 ± 4.0	1.92×10^{-7}	11
ank2^{null} neu > CK2α^{KD}	41.1 ± 4.3	3.31×10^{-8}	12

Statistical comparison between genotypes		**p (m 6/7)**
ank2^{null}	ank2^{null} neu > CK2α	0.648
ank2^{null}	ank2^{null} neu > CK2α^{KD}	0.393
ank2^{null} neu > CK2α	ank2^{null} neu > CK2α^{KD}	0.248

Retraction frequencies represent retractions per animals for the indicated muscle groups. P-values were calculated relative to controls or as indicated. *n* equals number of animals analyzed.

Genotype	**Retraction frequency (%)**				***n***
	m6/7	**P**	**m1/9, 2/10**	**P**	
control	2.1 ± 1.4		1.0 ± 0.7		12
CK2α$^{P1/+}$	2.1 ± 1.4	1.0	1.0 ± 0.7	1.0	12
Ank2$^{P2/+}$	3.1 ± 1.7	0.633323	1.6 ± 0.8	0.633323	12
CK2α$^{P1/+}$; ank2$^{P2/+}$	3.1 ± 1.7	0.633323	1.6 ± 0.8	0.633323	12
CK2α$^{P1/P1}$	52.4 ± 5.7	1.84×10^{-8}	58.2 ± 3.2	1.82×10^{-13}	21

$CK2\alpha^{P1/P1}$; $ank2^{P2/+}$	77.3 ± 5.0	5.89×10^{-9}	82.4 ± 3.1	4.17×10^{-11}	11
$ank2^{P2/P2}$	60.8 ± 4.5	6.43×10^{-10}	65.1 ± 4.2	4.24×10^{-9}	15
$ank2^{P2/P2}$; $CK2\alpha^{P1/+}$	87.5 ± 4.5	1.47×10^{-11}	91.1 ± 3.0	5.54×10^{-14}	14

Statistical comparison between genotypes		**p (m 1/9 2/10)**	**p (m 6/7)**
$CK2\alpha^{P1/P1}$	$CK2\alpha^{P1/P1}$; $ank2^{P2/+}$	0.002686	1.31×10^{-5}
$ank2^{P2/P2}$	$CK2\alpha^{P1/+}$; $ank2^{P2/P2}$	0.000295	6.8×10^{-5}

Retraction frequencies represent retractions per animals for the indicated muscle groups. P-values were calculated relative to controls or as indicated. *n* equals number of animals analyzed.

Data for Fig. 8

Genotype	**Bouton number m4 (absolute)**	**Bouton number m4 (% control)**	**P**	***n***
Control	17.2 ± 0.5	100 ± 3.2		64
$CK2\alpha^{P1/P1}$	11.8 ± 0.4	68.9 ± 2.5	7.1×10^{-11}	64
$CK2\alpha^{P1/P1}$ neu > $CK2\alpha$	19.7 ± 0.7	114.4 ± 4.0	0.002495	64
$CK2\alpha^{P1/P1}$ neu > $CK2\alpha$_KD	11.2 ± 0.5	65.4 ± 2.9	1.08×10^{-12}	64
$neu^{elav;dcr2}$ > $CK2\beta^{RNAi}$	14.3 ± 0.4	83.1 ± 2.6	3.2×10^{-5}	64

Significance of rescue between genotypes as listed		**P**
$CK2\alpha^{P1/P1}$	$CK2\alpha^{P1/P1}$ neu>$CK2\alpha$	2.57×10^{-15}
$CK2\alpha^{P1/P1}$	$CK2\alpha^{P1/P1}$ neu>$CK2\alpha$_KD	0.424474

The number of type Ib boutons on muscle 4 was quantified. P-values were calculated relative to controls or as indicated. *n* equals number of NMJs analyzed.

Genotype	**DvGlut cluster m4 (absolute)**	**DvGlut cluster m4 (% control)**	**P**	***n***
control	100 ± 4.0	58.3 ± 2.3		48
$CK2\alpha^{P1/P1}$	40.8 ± 2.8	23.8 ± 1.5	1.11×10^{-20}	48
$CK2\alpha^{P1/P1}$ neu > $CK2\alpha$	99.9 ± 4.2	58.2 ± 2.5	0.985266	48
$CK2\alpha^{P1/P1}$ neu > $CK2\alpha$_KD	38.0 ± 2.5	22.1 ± 1.4	6.93×10^{-22}	48
neu^{2x} > $CK2\alpha/CK2\alpha$	170.9 ± 5.5	99.5 ± 3.2	7.89×10^{-17}	48
$neu^{elav;\ dcr2}$ > $CK2\beta^{RNAi}$	60.9 ± 3.2	35.5 ± 1.9	2.01×10^{-11}	48

Statistical comparison between genotypes as listed		**P**
$CK2\alpha^{P1/P1}$	$CK2\alpha^{P1/P1}$ neu>$CK2\alpha$	3.76×10^{-19}
$CK2\alpha^{P1/P1}$	$CK2\alpha^{P1/P1}$ neu>$CK2\alpha$_KD	0.429068

The number of DvGlut clusters per muscle 4 NMJ was quantified. P-values were calculated relative to controls or as indicated. *n* equals number of NMJs analyzed.

Genotype	**Satellite bouton number (m4)**	**P**	***n***
control	0.6 ± 0.2		20
neu>$CK2\alpha/CK2\alpha$	20.5 ± 2.4	1.38×10^{-7}	20

The number of satellite boutons per muscle 4 NMJ was quantified. P-values were calculated relative to controls or as indicated. *n* equals number of NMJs analyzed.