Supplemental Material

Expanded Materials & Methods

Cell culture

H9C2 cells (American Type Culture Collection) were cultured in high-glucose Dulbecco's Modified Eagle Medium (DMEM) supplemented with fetal calf serum (10%), 2 mM of L-glutamine, 100 U/mL of penicillin and 100 g/mL of streptomycin at 37 °C in 5% CO_2. Only cells with a low number of passages (6-10) were used for the experiments.

Animals

All rats were treated according to the Guide for the Care and Use of Laboratory Animals published by the US National Institutes of Health (NIH publication no. 85–23, revised 1996) and approved by the Institutional Laboratory Animal Care and Use Committee of the NIH, Bethesda, MD, USA.

Male Dahl SS rats (Charles River, Wilmington, MA) were either switched from a low salt diet (0.3% NaCl) to a high salt diet (8% NaCl) (diastolic dysfunction) or kept at low salt diet (control) at 7 weeks of age. After 6-7 weeks, rats with induced diastolic dysfunction were randomly assigned to allogeneic CDC treatment (injection of $5x10^5$ cells re-suspended in 100 µl phosphate buffered saline (PBS, pH 7.4) or vehicle (PBS). Animals unable to move, drink and eat (as assessed by an animal technician not involved in the study and not aware of the treatment) before onset of CDC or placebo treatment were euthanized and recorded as dead in order to comply with institutional animal welfare policy and excluded from experiments. Further, only animals that were showing pathophysiological symptoms of HFpEF (no reduction of ejection fraction with clear signs of diastolic dysfunction) in echo readings were included into the study. CDCs were generated from explanted Wistar-Kyoto rat hearts (Charles River, Wilmington, MA) hearts. Endomyocardial biopsies from the right ventricle were obtained from the septal wall. Samples were cut into fragments, washed and partially digested enzymatically. The tissue fragments were cultured on dishes coated with fibronectin and once confluent, the cells surrounding the explants were harvested by gentle enzymatic digestion. These cardiosphere-forming cells were seeded at 2 to 3×10^4 cells/mL on poly-d-lysine–coated dishes in cardiosphere medium containing 35% IMDM and 65% DMEM/F-12 Mix (Invitrogen), 3.5% FBS, 1% penicillin-streptomycin, 1% L-glutamine, 0.1mM 2-mercaptoethanol, thrombin, B-27, bFGF, EGF, and Cardiotrophin-1 at final working concentrations. Several days later, detached cardiospheres were plated on fibronectin-coated flasks and expanded. CDCs were subsequently passaged by trypsinization and splitting at a 1:2 ratio. Isolation of the cardiosphere-forming cells was repeated up to 3 more times from the same specimen.

Echocardiography and/or hemodynamic measurements were performed to characterize heart phenotypes 4 weeks after treatment (24).

Sample handling and preparation for proteomics

Freshly harvested rat left ventricle (LV) tissue was shortly rinsed in ice-cold homogenization buffer (300 mM sucrose, 250 mM HEPES-NaOH, 1 mM EDTA, pH 8.0) supplemented with a broad-spectrum protease inhibitor (Thermo Fisher Scientific, Waltham, MA) for total protein analysis, or phosphatase inhibitor cocktail (Thermo Fisher Scientific) for protein phosphorylation analysis. Samples were snap frozen in liquid nitrogen. Left ventricle tissue was fractionated into cytosolic-, myofilament-, and in-soluble-enriched fractions by the "in sequence" method. The left ventricle was cryohomogenized at an approximate ratio of tissue weight: buffer volume 1:4 in homogenization buffer for 1 min with a frequency of 30/s. Following centrifugation at 14,000 g for 10 min at 4°C supernatant was kept at 4°C (cytosolic fraction) the pellet was resuspended in 1:4 homogenization buffer with 1% trifluoroacetic acid (TFA) and cryohomogenized. Following centrifugation at 14,000 g for 10 min at 4°C supernatant was kept at 4°C (membrane fraction) and pellet was resuspended in 1:4 homogenization buffer with 2% SDS and cryohomogenized for receiving the in-soluble fraction. In order to cheer the DNA, the in-soluble fraction was sonication for 10 min with 10 sec on/off with an amplitude of 70% at 4°C with a Q800R3 Sonicator (QSonica, Newtown, CT) and DNA was pelleted by centrifugation at 14,000 g for 10 min at 4°C. Protein concentration was determined by BCA (Pierce, Waltham, MA). Quantification of total peptides and quantification of phospho-enriched peptides were performed in separate MS runs due to enrichment required for isolation of the phospho-peptides. One hundred µg of each fraction (total protein quantification) or 1 mg of protein of each fraction (phosphorylation quantification) were reduced using 1 mM TCEP. Sample clean-up and alkylation, filter-aided sample preparation (FASP 10 kDA, Promega, Madison, WI) was used. Samples were digested for 15–18h at 37°C using ultra-grade Trypsin (Promega) at a 1:100 enzyme: protein ratio. Samples were desalted using Oasis HLB plates (30 µm and 5 mg sorbent, Waters Milford, MA), vacuum dried and stored at -80°C until analysis. For analyzing phosphorylated peptides, samples were enriched post-digestion using TiO_2 beads. Digestion was stopped by the addition of FA to 0.1% final concentration. Each sample was desalted using an Oasis HLB plate with 5 mg sorbent per Well (Waters, Milford, MA) and peptides were eluted in TiO2 starting buffer containing

80% ACN, 5% TFA, and 1M glycolic acid. TiO2 enrichment solution containing 15 mg of TiO2 beads per 1 mL of TiO2 start buffer was added to the samples and incubated for 2h at room temperature with shaking. Samples were then quickly spun in a centrifuge to pellet the TiO2 beads and the supernatant was removed. Beads were then washed three times with 80% ACN, 5% TFA and once with 80% ACN, 0.1% TFA. Phosphopeptides were eluted with 10% ACN, 3% NH4OH (pH ~10) with shaking for 10 min at room temperature. After centrifugation, the pH of the supernatant containing the phosphopeptides was acidified with 0.5% TFA and desalted using Oasis HLB plates with 30 µm sorbent per well (Waters, Milford, MA). Peptides were eluted in 70% ACN, 0.1% FA), vacuum dried and stored at -80°C until analysis.

Additionally, in-gel digestion of the titin band cut from a 4% SDS Coomassie Blue stained gel was performed. The gels were loaded with 400 ug protein and selectively the titin bands were cut into small pieces and transferred to a tube. Gel pieces were washed 3 times with 25mM NH_4HCO_3/50% ACN and vacuum dried. Dried gel pieces were covered with 10 mM DTT in 25 mM $NH_4HCO_3$and incubated at 56°C for 1h. Supernatant was removed, gel pieces were covered with 55 mM iodoacetamide in 25 mM NH_4HCO_3 and incubated in the dark for 45 min at room temperature. The digested peptides were extracted from the gel by adding 1:2 (vol/vol) 5% formic acid/acetonitrile. Supernatant was removed and gels were washed with 100 µl 25 mM NH_4HCO_3 and mixed for 10 min. Supernatant was removed and gels were washed with 100 µl 25 mM NH_4HCO_3 and mixed for 10 min. Gels were dehydrated by covering pieces with 25 mM NH_4HCO_3 in 50% ACN twice with each 5 min mixing. Gel pieces were vacuum dried rehydrated for 10 min with 25 mM NH_4HCO_3 at 4°C and then digested with either 2.5 ug LysC or Trypsin. Digest solution was transferred into a clean tube. Gel pieces were washed twice with 50% ACN/5% formic acid, mixed for 20 min each and extracted digests vacuum dried to reduce volume to 10 µL. Digests were combined, desalted, vacuum dried, and stored at -80°C until analysis.

Samples obtained from cell culture were lysed in 8 M Urea in 50 mM Ammonium bicarbonate and sonicated with 70% amplitude for 10 min. Prior to reduction, alkylation and digestion, Urea was diluted with 5 times volume of buffer.

Western blot

Quantification of PKC isoforms, phosphorylation, and PKC regulator changes among treatment groups was performed by western blot analysis. A total of 30 µg of LV rat tissue was minced and lysed in 2% SDS using a glass homogenizer. Cell debris was pelleted at 13,000g for 10 min at 4°C. Protein concentration of supernatants was estimated using the BCA assay using BSA as a standard. Samples were separated by electrophoresis on a 4–10% gradient Bis–Tris SDS-Gels (Bio-Rad, Hercules, CA) and transferred to PVDF membranes. Protein transfer was controlled by membrane staining with direct blue. After blocking, membranes were incubated with primary antibodies. The corresponding IgG HRP-conjugate combined with chemiluminescent substrate (Bio-Rad) and was scanned by a luminescent image quantifier (ImageQuant LAS 4000, GE Healthcare, Chicago, IL).

In vitro PKC kinase assay

The phosphorylation sites that were changed in HFpEF rats and with CDC treatment which contain a consensus sequence for PKC were confirmed by *in vitro* experiments. Before adding recombinant kinase, a buffer exchange on LV lysate from control (low salt diet) was performed using FASP 100 kDA filter columns (Promega). Then 10 μmol of recombinant kinase PKC α, βI, and δ was incubated with 500 μg of protein in kinase buffer (20 mM HEPES, 10 mM MgCl2, 100 μM MgCl2, pH 7.4) with 100 μM ATP (Promega) at 30°C for 30 min. Following another buffer exchange, the samples were reduced, alkylated and digested in 50 mM ammonium bicarbonate as described above. Ten percent of the digested sample was taken as loading control and 90% was assigned to enrichment for MS quantification of phosphorylation.

PKC inhibition in hypertrophic H9C2 cells

The phosphorylation sites that were changed in HFpEF rats and with CDC treatment which contain a consensus sequence for PKC were confirmed by *in vitro* experiments. H9C2 cells were starved for 24h before inducing hypertrophy for 48 h by adding 50 μM phenylephrine hydrochloride or PBS. Following, cells were treated with 2 nm 1,2,3,4-Tetrahydro Staurosporine (PKCα inhibitor, Satan Cruz Biotechnology), PKCβ Inhibitor (CAS 257879-35-9, Santa Cruz Biotechnology), 1 μm Rottlerin (PKC δ inhibitor, Santa Cruz Biotechnology), 2.3 μm Bisindolylmaleimide VIII (selective protein kinase C, Santa Cruz Biotechnology), 12 μm C-1 (PKA and PKC inhibitor, Tocris), or DMSO for 30 min, washed 3 times with PBS and cell pellets were snap frozen. Samples were stored at -80°C until sample preparation for MS quantification of phosphorylation and total protein was carried out.

PKC overexpression in H9C2 cells

The phosphorylation sites that were changed in HFpEF rats and with CDC treatment which contain a consensus sequence for PKC were confirmed by *in vitro* experiments. The PKC isoforms (α and β) and/or the two PKC regulators (Pdlim5 and Ldb3) were overexpressed in H9C2 cells to confirm PKC phosphorylated sites. H9C2 cells were transfected using Lipofectamine® 3000 Reagent (Thermo Fisher Scientific) according to the manual instructions with 5 μg of the following constructs: Rattus norvegicus protein kinase C, alpha (Prkca), mRNA (NM_001105713.1, GenScript), Rattus norvegicus protein kinase C, beta (Prkcb), transcript variant 1, mRNA (NM_012713.4, GenScript), Rattus norvegicus protein kinase C, beta (Prkcb), transcript variant 2, mRNA (NM_001172305.1, GenScript), Rattus norvegicus LIM domain binding 3 (Ldb3), transcript variant 1, mRNA (NM_001277165.1, GenScript), and Rattus norvegicus PDZ and LIM domain 5 (Pdlim5), mRNA (NM_053326.1, GenScript) inserted in pcDNA3.1+/C-(K)DYK vector. When a combination of two constructs was co-transfected the amount of plasmid was adjusted to a final concentration of 5 μg. As a negative control, cells were transfected with an empty vector. Efficiency of transfections was analyzed by western blot.

PKC co-immunoprecipitations

PKC co-immunoprecipitations from 200 μg LV rat lysate were carried out for total PKC and each isoform α, β, and δ using the above listed antibodies and dynabeads Protein G (Invitrogen Waltham, MA). The immunoprecipitation was performed according to the user manual.

Antibodies

The following antibodies were used in this study: mouse monoclonal anti-PKC α (H-7) (sc-8393, Santa Cruz Biotechnology, Dallas, TX), mouse monoclonal anti-PKC βI (E-3) (sc-8049, Santa Cruz Biotechnology), mouse monoclonal anti-PKC δ (G-9) (sc-8402, Santa Cruz Biotechnology), rabbit anti-phospho-PKCα/β II (Thr638/641) (9375, Cell Signaling, Danvers, MA), rabbit anti-Phospho-PKCδ (Thr505) (9374, Cell Signaling), rabbit anti-Phospho-PKC (pan) (βII Ser660) (9371, Cell Signaling), mouse monoclonal anti-HSPB2 (6) (sc-136339, Santa Cruz Biotechnology), mouse monoclonal anti-Pdlim5 (G-2) (sc-515621, Santa Cruz Biotechnology), and normal mouse IgG antibody (sc-2025, Santa Cruz Biotechnology used as negative control for immunoprecipitation).

Mass spectrometry, database searching, processing, and statistical analysis

MS data generation and MS raw spectra conversion to peptide and protein identification were blinded. Peptides were analyzed in two replicate runs by liquid chromatography-tandem mass spectrometry (LC-MS/MS) on a Dionex Ultimate 3000 NanoLC connected to an Orbitrap Elite (Thermo Fisher Scientific) equipped with an EasySpray ion source or on a Dionex Ultimate 3000 NanoLC connected to an Orbitrap Fusion™ Lumos™ Tribrid™ Mass Spectrometer (Thermo Fisher Scientific) equipped with an EasySpray ion source as previously reported as previously reported (72). Data acquisition was done blinded to experimental groups.

Raw MS/MS data files were converted to mzXML format using MSconvert version v.3.0.6002 from ProteoWizard (73) for peaklist generation and used for database searching using two engines, X!Tandem (74) algorithm version 2013.06.15.1 and Comet (75) algorithm version 2014.02 rev.2. The dataset was searched against the concatenated target/decoy (76) rat (8,231 proteins), mouse (32,741 proteins) and human (20,218 proteins) in the Uniprot database (77) and additionally included non-reviewed protein IDs of the rat database (163,172 proteins on April 07, 2016). The uniqueness of identified sequences assigned to non-reviewed proteins was validated by manual Bastp search, thus filtering multiple assigned peptides.

Protein isoforms were only reported if a peptide comprising an amino acid sequence that was unique to the isoform was identified. The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE (http://www.proteomexchange.org) partner repository with the dataset identifier PXD025555 (78) Username: reviewer_pxd025555@ebi.ac.uk, Password: sflhF8HM).

MS protein quantification was carried out by averaging the raw peptide intensity among technical replicates and summed among cellular sub-fractions. The peptide signal intensity was normalized to the median of the overall sample signal intensity and protein level abundance inference was calculated using the linear mixed effects model built into the open sources MSSTATs (v3.2.2) software suite (79). MSstats implements the iterative least squares modeling procedure and models the data based on flexible loess fit. Thus, LC-MS peaks with larger variances will have reduced weights in the resulting model-based conclusion. It follows the standard testing procedure and calculates the ratio of the estimated differences and their standard error (in statistical terminology, the test statistic) for each protein, compares the test statistics to the Student distribution with the appropriate degrees of freedom to obtain p-values, and adjusts the p-values for multiple comparisons to control the False Discovery Rate in the list of differentially abundant proteins (79, 80).

For quantification of PTMs, intensities were normalized to the relative signal intensity of sample loading instead. Phosphorylated residues of peptides with missed cleavages or different charge states were summed before comparing MS1 intensity. Assignment of the exact phosphorylation sites is based on transition level data and was quantified by modified (+80) peptide abundance. Statistical significance was determined at a nominal *p-value* ≤0.05. Upstream kinases potentially targeting significantly changed phosphorylated residues were identified using the Group-based prediction system v3.0 software.

Protein quantity of analyzed Western blots was normalized to direct blue staining, site-specific phosphorylation was normalized to the total of the equivalent protein. Normal distribution of data was analyzed using a non-parametric Kolmogorov-Smirnov test and significance was tested using the non-parametric Kruskal-Wallis one-way ANOVA (p<0.05) to compare experimental differences.

Expanded discussion

Titin phosphorylation

Unbiased wholesale phosphorylation analysis revealed that, even at baseline, cardiac titin is highly phosphorylated (83 phosphorylated sites) with four novel phosphorylation sites reported here for the first time: T4417, S13497, T22932 and T28577. Only five of the 83 identified residues (S20869, S33927, S33961, T33962 and T4117) were significantly different in diastolic dysfunction compared to control. This study is the first to suggest, that these sites are related to diastolic dysfunction prompting speculation that these sites could be key regulatory factors mediating titin's role in pathological cardiac stiffness. Paradoxically, several animal studies have demonstrated hypo-phosphorylation of total titin (81-83), whereas others have shown hyper-phosphorylation (84, 85). In humans with end-stage dilated cardiomyopathy, total titin phosphorylation was unchanged and only modest hyper-phosphorylation of total titin was detected in human hypertrophic cardiomyopathy hearts (86). Most studies investigating the relationship between titin phosphorylation and cardiac stiffness have focused on titin's spring elements, especially the two spring elements located within the isoform N2B and N2BA domains. These spring regions are comprised of three different structural motives, the N-terminal Ig – like domains, the N2B element and the PEVK region, which are all highly susceptible to posttranslational modifications (PTMs) (87). Investigations of myocardial samples from various species showed that phosphorylation within the N2Bus element predominantly decreases passive tension and phosphorylation of the PEVK element increases myocyte passive tension (7, 8, 81, 83). In patients with hypertensive HFpEF, hypo-phosphorylation of residue S4185 within the N2Bus element is described (32). Furthermore, in human failing hearts phosphorylation of residues S4010, S4099 and S4185 was reduced (86). In contrast, phosphorylation of PEVK at sites S11878 was increased in a dog model of early HFpEF, and in humans with heart failure (83, 86). In metabolic-risk induced HFpEF, obese rats showed elevated phosphorylation at S12022 (S12884 rat), but residue S11878 (S12742 rat) was not altered (83). Both residues are targets of PKCα and CaMKII kinases (88, 89). Taken together, evidence from previous studies is not definitive, with mixed evidence of increased, decreased or unaltered total titin phosphorylation in various models of HFpEF. Mixed findings in the literature could relate to differences in disease stage analyzed, animal models used or other experimental complexities.

GRK kinase

In this study, the GRK kinase family also showed increased amounts of shared consensus sequences with myofilament protein. We identified dysregulated G-protein-coupled receptor signaling in HFpEF rats via an increase of guanine nucleotide-binding protein G(i) subunit alpha-1 (Gnai1). An increase in Gnai1 is leading to reduced cAMP levels (90), via reduction of guanine nucleotide-binding protein G(i) subunit alpha-2 (Gnai2) and inhibiting adenylate cyclase in response to β-adrenergic stimuli (91). Inhibition of adenylate cyclase is increasing Rho guanine nucleotide exchange factor 12 (Arhgef12), which is acting as guanine nucleotide exchange factor (GEF) for RhoA GTPase. The latter may act as GTPase-activating protein for GNA12 and GNA13 (92). β-Adrenergic signaling plays an important role in regulating cardiac functions controlled by GRK phosphorylation events (93). In HF GRK upregulation causes pathological dysregulation of β-adrenergic receptors (94) whereas GRK2 inhibition restores cardiac function (95). The β-adrenergic-receptor kinase contains a phosphorylation motif attributed to PKC and PKA (96). The proteomic characterization of this HFpEF rat model suggests hyperactivity of β-adrenergic signaling is driving enhanced phosphorylation events via hyperactivity of GRK and PKC. In this scenario β-adrenergic activation would lead also to an upregulation of PKA activity, but the induced PKA hyperactivity is internally blunted via the upregulation of PKIA (14-fold increase in HFpEF compared to control). This is congruent with the relatively low amount of hyperphosphorylated residues within PKA consensus sequences found in this study. Further, it has been demonstrated that PKCα has a modulatory effect on cardiac contractility via β-adrenergic receptor modulation (97). Following CDC treatment, Gnai2 and Arhgef12 reverted to control levels indicating CDC treatment influences the β-adrenergic signaling. In line with these findings, PKC (specifically PKCβ) and PKIA revert towards control levels, thus suggesting a beneficial downregulation of β-adrenergic signaling via CDC therapy in HFpEF.

Online Tables I - V

Supplemental Table I A: MS data of significant and trended changed phosphorylation sites for HFpEF animals compared to control (n=6) of sarcomeric proteins, their location, known function, and information about the changed phosphorylation site are listed. Total protein and phosphorylation changes are presented in log2 foldchanges (log2FC). Listed p-values were calculated using the linear mixed effects model built into MSSTATs.

Protein Name	Gene Name	Location	Role	HFpEF vs control		Phospho-site	HFpEF vs control	
				log2FC	p-value		log2FC	p-value
Actin, aortic smooth muscle	*Acta2*	Actin cytoskeleton	muscle contraction	1.16	0.041	S241	1.23	0.021
Actin, aortic smooth muscle	*Acta2*	Actin cytoskeleton	muscle contraction	1.16	0.041	Y242	0.98	0.026
Actin-binding LIM protein 1	*Ablim1*	Actin cytoskeleton	Cytoskeletal organization, actin binding	0.46	0.003	S496	1.28	0.037
Actin-binding LIM protein 1	*Ablim1*	Actin cytoskeleton	Cytoskeletal organization, actin binding	0.46	0.003	S499	1.28	0.037
A-kinase anchor protein 13	*Akap13*	Actin cytoskeleton	Regulation of sarcomere organization	NA	NA	S1585	1.39	0.012
A-kinase anchor protein 13	*Akap13*	Actin cytoskeleton	Regulation of sarcomere organization	NA	NA	S1520	0.94	0.020
A-kinase anchor protein 13	*Akap13*	Actin cytoskeleton	Regulation of sarcomere organization	NA	NA	S1891	1.11	0.001
A-kinase anchor protein 13	*Akap13*	Actin cytoskeleton	Regulation of sarcomere organization	NA	NA	S1583	1.27	0.006
A-kinase anchor protein 13	*Akap13*	Actin cytoskeleton	Regulation of sarcomere organization	NA	NA	T1590	1.17	0.049
A-kinase anchor protein 2	*Akap2*	Actin cytoskeleton	Regulation of sarcomere organization	0.88	0.023	S730	0.80	0.032
Alpha-actinin-2	*Actn2*	Z disc	Actin filament uncapping, Titin Z domain binding	0.61	6.82E-06	S574	1.71	0.044
Alpha-crystallin B chain	*Cryab*	M band, Z disc	Muscle organ development	0.57	9.58E-09	S59	1.42	3.492E-05
Alpha-crystallin B chain	*Cryab*	M band, Z disc	Muscle organ development	0.57	9.58E-09	S19	1.62	0.042
Band 4.1-like protein 1	*Epb41l1*	Cytoskeleton	Actomyosin structure organization	NC	NS	S782	0.85	0.054
CapZ-interacting protein	*Rcsd1*	Actin cytoskeleton	Actin filament assembly	NA	NA	S53	1.01	0.038
CapZ-interacting protein	*Rcsd1*	Actin cytoskeleton	Actin filament assembly	NA	NA	S68	1.72	0.009
CapZ-interacting protein	*Rcsd1*	Actin cytoskeleton	Actin filament assembly	NA	NA	S90	0.83	0.059
CapZ-interacting protein	*Rcsd1*	Actin cytoskeleton	Actin filament assembly	NA	NA	S186	0.77	0.046
Catenin alpha-1	*Ctnna1*	Actin cytoskeleton	Actin filament assembly, actin binding, integrin signaling	1.13	2.4E-10	T654	2.56	0.017
Catenin alpha-1	*Ctnna1*	Actin cytoskeleton	Actin filament assembly, actin binding, integrin signaling	1.13	2.4E-10	T658	2.56	0.017
Catenin alpha-1	*Ctnna1*	Actin cytoskeleton	Actin filament assembly, actin binding, integrin signaling	1.13	2.4E-10	S657	0.80	0.039
CLIP-associating protein 2	*Clasp2*	Cytoskeleton	Actin filament binding	-0.62	0.016	S581	1.35	0.051
Cordon-bleu protein-like 1	*Cobll1*		Actin filament polymerization	NA	NA	S666	0.87	0.027

Cysteine and glycine-rich protein 3	*Csrp3*	Z disc	Cardiac muscle contraction	1.57	6.9E-12	S111	1.43	0.019
Cytoplasmic linker-associated protein 1	*Clasp1*	Cytoskeleton	Regulation of actin cytoskeleton organization	NC	NS	S1088	1.05	0.043
Desmin	*Des*	Z disc	Muscle-specific type III intermediate filament	NC	NS	S28	1.73	0.056
Desmin	*Des*	Z disc	Muscle-specific type III intermediate filament	NC	NS	S25	1.73	0.056
Desmin	*Des*	Z disc	Muscle-specific type III intermediate filament	NC	NS	S32	1.73	0.056
Desmin	*Des*	Z disc	Muscle-specific type III intermediate filament	NC	NS	S300	1.74	0.018
Desmin	*Des*	Z disc	Muscle-specific type III intermediate filament	NC	NS	S303	1.74	0.018
Drebrin	*Dbn1*	Z disc	Actin filament organization, negative regulation of muscle filament sliding	NC	NS	S142	0.63	0.049
E3 ubiquitin-protein ligase UBR4	*Ubr4*	Membrane	Cytoskeletal organization, regulates integrin-mediated signaling	NC	NS	S2715	1.21	0.040
E3 ubiquitin-protein ligase UBR4	*Ubr4*	Membrane	Cytoskeletal organization, regulates integrin-mediated signaling	NC	NS	S2719	0.51	0.054
E3 ubiquitin-protein ligase UBR4	*Ubr4*	Membrane	Cytoskeletal organization, regulates integrin-mediated signaling	NC	NS	S2897	2.10	0.030
Erythrocyte membrane protein band 4.1-like 2	*Epb41l2*	Cytoskeleton	Actin binding	NA	NA	S57	1.60	0.004
FH1/FH2 domain-containing protein 1	*Fhod1*	Cytoskeleton	Actin binding	NA	NA	S141	1.19	0.034
Filamin-A-interacting protein 1	*Filip1*	Actin cytoskeleton	Actin binding	NC	NS	S979	1.36	0.011
Filamin-C	*Flnc*	Z disc	Actin filament organization	1.21	2.16E-04	S2234	0.78	0.015
Filamin-C	*Flnc*	Z disc	Actin filament organization	1.21	2.16E-04	S2237	2.35	0.004
Formin-like protein 1	*Fmnl1*		Actin filament severing, actin filament binding			S965	0.74	0.039
Heat shock protein beta-1	*Hspb1*		Actin organization	1.41	4.22E-11	S86	1.18	0.002
Heat shock protein beta-1	*Hspb1*		Actin organization	1.41	4.22E-11	S13	1.05	0.034
Heat shock protein beta-1	*Hspb1*		Actin organization	1.41	4.22E-11	S15	1.20	0.006
Heat shock protein beta-3	*Hspb3*		Inhibitor of actin polymerization	0.27	0.022	T64	0.95	0.033
Influenza virus NS1A-binding protein homolog	*Ivns1abp*	Actin cytoskeleton	Stabilizer of actin filaments	NA	NA	S246	2.38	0.006
Influenza virus NS1A-binding protein homolog	*Ivns1abp*	Actin cytoskeleton	Stabilizer of actin filaments	NA	NA	S336	1.56	0.007
Influenza virus NS1A-binding protein homolog	*Ivns1abp*	Actin cytoskeleton	Stabilizer of actin filaments	NA	NA	S338	1.47	0.010
Junction plakoglobin	*Jup*	Z disc	Regulation of ventricular cardiac muscle cell action potential	NC	NS	T78	1.86	0.059
KN motif and ankyrin repeat domain-containing protein 1	*Kank1*		Negative regulation of actin filament polymerization	NA	NA	S323	1.05	0.037

Leiomodin-2	*Lmod2*	M band	Actin polymerization, sarcomere organization	0.58	2.86E-05	S405	0.76	0.006
Leiomodin-2	*Lmod2*	M band	Actin polymerization, sarcomere organization	0.58	2.86E-05	S394	1.95	0.012
Leiomodin-2	*Lmod2*	M band	Actin polymerization, sarcomere organization	0.58	2.86E-05	S394	1.35	0.006
Leiomodin-2	*Lmod2*	M band	Actin polymerization, sarcomere organization	0.58	2.86E-05	S398	1.95	0.012
Leiomodin-2	*Lmod2*	M band	Actin polymerization, sarcomere organization	0.58	2.86E-05	S422	0.98	0.013
Leiomodin-2	*Lmod2*	M band	Actin polymerization, sarcomere organization	0.58	2.86E-05	S514	2.10	0.004
Leiomodin-2	*Lmod2*	M band	Actin polymerization, sarcomere organization	0.58	2.86E-05	T518	2.10	0.004
Leiomodin-2	*Lmod2*	M band	Actin polymerization, sarcomere organization	0.58	2.86E-05	S398	1.75	0.024
Leiomodin-2	*Lmod2*	M band	Actin polymerization, sarcomere organization	0.58	2.86E-05	S394	2.02	0.014
Leiomodin-2	*Lmod2*	M band	Actin polymerization, sarcomere organization	0.58	2.86E-05	Y396	2.02	0.014
Leiomodin-2	*Lmod2*	M band	Actin polymerization, sarcomere organization	0.58	2.86E-05	S406	0.75	0.006
LIM and calponin homology domains-containing protein 1	*Limch1*	M band	Actomyosin structure organization, actin binding	0.61	0.009	S303	0.81	0.047
LIM and calponin homology domains-containing protein 1	*Limch1*	M band	Actomyosin structure organization, actin binding	0.61	0.009	T302	0.80	0.024
LIM and calponin homology domains-containing protein 1	*Limch1*	M band	Actomyosin structure organization, actin binding	0.61	0.009	S752	2.09	0.044
LIM domain and actin-binding protein 1	*Lima1*	Actin cytoskeleton	Bundles actin filaments	NA	NA	S488	0.80	0.017
LIM domain-binding protein 3	*Ldb3*	Z disc	Sarcomere organization, muscle alpha-actinin binding	0.71	5.59E-05	S44	0.86	0.054
LIM domain-binding protein 3	*Ldb3*	Z disc	Sarcomere organization, muscle alpha-actinin binding	0.71	5.59E-05	S121	1.10	0.017
LIM domain-binding protein 3	*Ldb3*	Z disc	Sarcomere organization, muscle alpha-actinin binding	0.71	5.59E-05	S123	1.11	0.018
LIM domain-binding protein 3	*Ldb3*	Z disc	Sarcomere organization, muscle alpha-actinin binding	0.71	5.59E-05	S98	1.35	0.016
Macrophage-capping protein	*Capg*		Barbed-end actin filament capping	0.75	3.37E-06	S341	0.84	0.019
Misshapen-like kinase 1	*Mink1*		Actin cytoskeleton reorganization	-1.49	7.22E-13	S765	0.81	0.005
Myomesin-2	*Myom2*	M band	Binds myosin, titin, and light meromyosin			S535	1.09	0.035
Myopalladin	*Mypn*	Z disc	Sarcomere organization, muscle alpha-actinin binding	0.80	4.19E-04	S622	0.60	0.031
Myopalladin	*Mypn*	Z disc	Sarcomere organization, muscle alpha-actinin binding	0.80	4.19E-04	S623	0.62	0.022
Myopalladin	*Mypn*	Z disc	Sarcomere organization, muscle alpha-actinin binding	0.80	4.19E-04	S737	0.82	0.025
Myosin XVIIIb	*Myo18b*	Myofilament	Cardiac muscle fiber development	NA	NA	S2298	0.76	0.053
Myosin-1	*Myh1*	Myofilament	Muscle contraction			S1373	1.03	0.022
Myosin-11	*Myh11*	Myofilament	Muscle contraction	0.31	0.006	S1951	1.24	0.008
Myosin-6	*Myh6*	Myofilament	Sarcomere organization, striated muscle contraction	0.89	1.54E-08	S649	0.78	0.054
Myosin-6	*Myh6*	Myofilament	Sarcomere organization, striated muscle contraction	0.89	1.54E-08	S1235	2.49	0.050
Myosin-6	*Myh6*	Myofilament	Sarcomere organization, striated muscle contraction	0.89	1.54E-08	S1089	2.49	0.037
Myosin-7	*Myh7*	Myofilament	Sarcomere organization, striated muscle contraction	NA	NA	S1222	0.84	0.051
Myosin-7	*Myh7*	Myofilament	Sarcomere organization, striated muscle contraction	NA	NA	S643	0.81	0.018
Myosin-7	*Myh7*	Myofilament	Sarcomere organization, striated muscle contraction	NA	NA	S642	0.93	0.008

Myosin-7	*Myh7*	Myofilament	Sarcomere organization, striated muscle contraction	NA	NA	S1491	0.54	0.044
Myosin-7	*Myh7*	Myofilament	Sarcomere organization, striated muscle contraction	NA	NA	S1478	0.69	0.058
Myosin-7	*Myh7*	Myofilament	Sarcomere organization, striated muscle contraction	NA	NA	T210	1.38	0.031
Myosin-7	*Myh7*	Myofilament	Sarcomere organization, striated muscle contraction	NA	NA	T1019	1.63	2.40E-04
Myosin-7	*Myh7*	Myofilament	Sarcomere organization, striated muscle contraction	NA	NA	S1233	2.81	0.027
Myosin-7	*Myh7*	Myofilament	Sarcomere organization, striated muscle contraction	NA	NA	Y1308	2.13	0.032
Myosin-7	*Myh7*	Myofilament	Sarcomere organization, striated muscle contraction	NA	NA	S1102	1.47	0.004
Myosin-7	*Myh7*	Myofilament	Sarcomere organization, striated muscle contraction	NA	NA	S1140	2.23	0.047
Myosin-7	*Myh7*	Myofilament	Sarcomere organization, striated muscle contraction	NA	NA	T1309	2.33	0.046
Myosin-7	*Myh7*	Myofilament	Sarcomere organization, striated muscle contraction	NA	NA	T215	1.48	0.022
Myozenin-2	*Myoz2*	Z disc	Linking Z line proteins localizing calcineurin signaling to the sarcomere	0.37	0.001	T107	0.74	0.055
Myozenin-2	*Myoz2*	Z disc	Linking Z line proteins localizing calcineurin signaling to the sarcomere	0.37	0.001	T111	0.85	0.054
Myristoylated alanine-rich C-kinase substrate	*Marcks*	Actin filament bundle	Actin crosslink formation	-0.29	0.029	T143	1.36	0.048
Nebulin-related-anchoring protein	*Nrap*	Intercalated disk	Muscle alpha-actinin binding	1.53	9.37814E-06	S1693	1.52	0.026
Nebulin-related-anchoring protein	*Nrap*	Intercalated disk	Muscle alpha-actinin binding	1.53	9.37814E-06	S275	1.56	0.025
Nexilin	*Nexn*	Z disc	Maintenance of Z line and sarcomere integrity	0.76	3.45E-05	S345	1.70	0.003
Nexilin	*Nexn*	Z disc	Maintenance of Z line and sarcomere integrity	0.76	3.45E-05	S348	1.55	0.002
Nexilin	*Nexn*	Z disc	Maintenance of Z line and sarcomere integrity	0.76	3.45E-05	T350	1.46	0.003
Nexilin	*Nexn*	Z disc	Maintenance of Z line and sarcomere integrity	0.76	3.45E-05	S330	1.65	0.043
Nexilin	*Nexn*	Z disc	Maintenance of Z line and sarcomere integrity	0.76	3.45E-05	S544	0.92	0.044
Obscurin	*Obscn*	M band, Z disc	Structural constituent of muscle, titin binding, protein localization to M-band	0.57	0.033	S6618	1.50	0.007
Oxysterol-binding protein-related protein 3	*Osbpl3*		Attenuates integrin beta-1 activation at the cell surface.	NA	NA	S272	2.27	0.034
Paxillin	*Pxn*	Z disc	Cytoskeleton organization	NC	NS	S320	0.95	0.031
Paxillin	*Pxn*	Z disc	Cytoskeleton organization	NC	NS	S321	1.14	0.014
Paxillin	*Pxn*	Z disc	Cytoskeleton organization	NC	NS	S328	0.87	0.043
Paxillin	*Pxn*	Z disc	Cytoskeleton organization	NC	NS	S327	0.91	0.031
Paxillin	*Pxn*	Z disc	Cytoskeleton organization	NC	NS	T313	0.69	0.028
Paxillin	*Pxn*	Z disc	Cytoskeleton organization	NC	NS	S317	0.66	0.030
Paxillin	*Pxn*	Z disc	Cytoskeleton organization	NC	NS	S323	0.61	0.043
Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2	*Inppl1*	Cytoskeleton	Actin filament organization	-0.61	0.002	S132	2.41	0.037
Phosphoglucomutase-like protein 5	*Pgm5*	Z disc		NC	NS	T120	1.41	0.013
Phosphoglucomutase-like protein 5	*Pgm5*	Z disc		NC	NS	S122	1.24	0.008
Plectin	*Plec*	Cytoskeleton	Structural constituent of muscle	NA	NA	S4388	1.52	0.040
Plectin	*Plec*	Cytoskeleton	Structural constituent of muscle	NA	NA	S4389	1.52	0.040

Plectin	*Plec*	Cytoskeleton	Structural constituent of muscle	NA	NA	S4411	0.82	0.017
Plectin	*Plec*	Cytoskeleton	Structural constituent of muscle	NA	NA	T4626	1.27	0.042
Plectin	*Plec*	Cytoskeleton	Structural constituent of muscle	NA	NA	S4409	0.66	0.017
Plectin	*Plec*	Cytoskeleton	Structural constituent of muscle	NA	NA	T4414	0.81	0.022
Plectin	*Plec*	Cytoskeleton	Structural constituent of muscle	NA	NA	S4629	1.24	0.046
Protein enabled homolog	*Enah*	Actin cytoskeleton	Actin cytoskeleton organization	NC	NS	S354	1.39	0.007
Protein enabled homolog	*Enah*	Actin cytoskeleton	Actin cytoskeleton organization	NC	NS	S355	1.21	0.010
Paxillin	*Pxn*	Z disc	Cytoskeleton organization	NC	NS	T313	0.69	0.028
Paxillin	*Pxn*	Z disc	Cytoskeleton organization	NC	NS	S317	0.66	0.030
Paxillin	*Pxn*	Z disc	Cytoskeleton organization	NC	NS	S323	0.61	0.043
Protein furry homolog	*Fry*	Cytoskeleton	Actin filament reorganization	NA	NA	S1936	1.56	0.059
Protein phosphatase 1 regulatory subunit 12A	*Ppp1r12a*	Z disc	Regulation of myosin-light-chain-phosphatase activity	0.70	0.017	S873	0.81	0.041
Rho GTPase-activating protein 35	*Arhgap35*	Cytoskeleton	Regulation of actin cytoskeleton organization, Rho signaling	NA	NA	S1179	1.28	0.034
Septin-7	*Sept7*	Cytoskeleton	Actin cytoskeleton organization	-0.26	0.001	T425	1.33	0.022
Serine/threonine-protein kinase D1	*Prkd1*	Cytosol	Regulating integrin alpha-5/beta-3 recycling and promoting its recruitment	1.74	2.10E-04	S161	1.58	0.029
SH3 domain-binding protein 1	*Sh3bp1*		Actin cytoskeleton organization	NC	NS	S539	0.77	0.046
Sorbin and SH3 domain-containing protein 1	*Sorbs1*	Cytoskeleton	Formation of actin stress fibers	1.99	4.8E-05	S401	0.81	0.044
Sorbin and SH3 domain-containing protein 1	*Sorbs1*	Cytoskeleton	Formation of actin stress fibers	1.99	4.8E-05	S345	1.06	0.025
Sorbin and SH3 domain-containing protein 1	*Sorbs1*	Cytoskeleton	Formation of actin stress fibers	1.99	4.8E-05	T404	0.84	0.032
Sorbin and SH3 domain-containing protein 1	*Sorbs1*	Cytoskeleton	Formation of actin stress fibers	1.99	4.8E-05	S92	0.97	0.058
Sorbin and SH3 domain-containing protein 1 Isoform 2	*Sorbs1*	Cytoskeleton	Formation of actin stress fibers	1.99	4.8E-05	S164	1.63	0.004
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	S397	1.58	0.017
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	S396	1.75	0.010
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	Y137	2.31	0.011
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	S138	2.38	0.046
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	S138	1.64	0.039

Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	T136	2.04	0.025
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	Y1112	1.67	0.010
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	S266	1.78	0.023
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	S354	0.84	0.055
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	S324	1.35	0.018
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	S1111	1.60	0.011
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	S1113	1.79	0.016
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	S1114	1.60	0.011
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	S130	1.69	0.003
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	S133	1.89	3.36E-04
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	T136	1.52	0.010
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	S143	1.72	0.006
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	T147	2.06	0.013
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	S334	1.49	0.035
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	S340	1.89	0.022
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	S343	1.89	0.022
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	S341	1.23	0.031
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	S343	1.61	0.052
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	S38	1.19	0.012
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	S399	1.66	0.024
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	0.90	0.001	S340	2.02	0.041
Striatin-interacting protein 1	*Strip1*		Cytoskeletal organization	NA	NA	S335	1.00	0.050
Supervillin	*Svil*	Actin cytoskeleton	Actin filament binding	NA	NA	S240	0.63	0.028
Supervillin	*Svil*	Actin cytoskeleton	Actin filament binding	NA	NA	S242	0.79	0.023
Supervillin	*Svil*	Actin cytoskeleton	Actin filament binding	NA	NA	S866	1.05	0.022
Supervillin	*Svil*	Actin cytoskeleton	Actin filament binding	NA	NA	S728	1.61	0.042
Synaptopodin	*Synpo*	Actin cytoskeleton	Positive regulation of actin filament bundle assembly	0.61	6.05045 E-05	S258	0.79	0.021
Synaptopodin 2-like protein	*Synpo2l*	Z disc	Positive regulation of actin filament bundle assembly	0.64	1.09E-04	T141	1.95	0.020

Synaptopodin 2-like protein	*Synpo2l*	Z disc	Positive regulation of actin filament bundle assembly	0.64	1.09E-04	S143	1.95	0.020
Synaptopodin 2-like protein	*Synpo2l*	Z disc	Positive regulation of actin filament bundle assembly	0.64	1.09E-04	S929	0.80	0.044
Synaptopodin 2-like protein	*Synpo2l*	Z disc	Positive regulation of actin filament bundle assembly	0.64	1.09E-04	S95	0.99	0.029
Synaptopodin 2-like protein	*Synpo2l*	Z disc	Positive regulation of actin filament bundle assembly	0.64	1.09E-04	S97	0.95	0.029
Synaptopodin-2	*Synpo2*	Z disc	Assembly and stabilization of the Z lines	0.43	1.09E-04	S895	0.78	0.054
Syncoilin	*Sync*	Z disc	Coupling of mechanical stress between the myofibril and fiber exterior	NC	NS	S314	0.92	0.025
Synemin	*Synm*	Z disc	Structural constituent of muscle	NA	NA	S780	0.89	0.027
Synemin	*Synm*	Z disc	Structural constituent of muscle	NA	NA	S1041	1.08	0.043
Synemin	*Synm*	Z disc	Structural constituent of muscle	NA	NA	S1042	1.06	0.032
Synemin	*Synm*	Z disc	Structural constituent of muscle	NA	NA	S1047	1.08	0.043
Synemin	*Synm*	Z disc	Structural constituent of muscle	NA	NA	S1047	1.06	0.032
Synemin	*Synm*	Z disc	Structural constituent of muscle	NA	NA	T1104	1.00	0.010
Synemin	*Synm*	Z disc	Structural constituent of muscle	NA	NA	S1105	0.79	0.043
Synemin	*Synm*	Z disc	Structural constituent of muscle	NA	NA	T1107	1.11	0.006
Talin-1	*Tln1*	Cytoskeleton	Structural constituent of cytoskeleton, actin filament binding	0.39	5.11E-05	S981	0.94	0.035
Talin-1	*Tln1*	Cytoskeleton	Structural constituent of cytoskeleton, actin filament binding	0.39	5.11E-05	S979	0.98	0.033
Telethonin	*Tcap*	Z disc	Detection of muscle stretch, titin Z domain binding, sarcomere organization	0.61	0.071	S161	2.17	0.017
Tensin 2	*Tns2*	Actin stress fibers	Response to muscle activity	NA	NA	S455	0.84	0.045
Tensin-1	*Tns1*	Cytoskeleton	Actin binding	NA	NA	S1032	1.39	0.049
Tensin-1	*Tns1*	Cytoskeleton	Actin binding	NA	NA	S1081	0.77	0.042
Tensin-1	*Tns1*	Cytoskeleton	Actin binding	NA	NA	S1222	0.99	0.058
Tensin-1	*Tns1*	Cytoskeleton	Actin binding	NA	NA	S1480	1.28	0.051
Tensin-1	*Tns1*	Cytoskeleton	Actin binding	NA	NA	T1501	1.07	0.027
Tensin-1	*Tns1*	Cytoskeleton	Actin binding	NA	NA	S949	0.87	0.052
Tensin-1	*Tns1*	Cytoskeleton	Actin binding	NA	NA	Y951	0.87	0.052
Tensin-3	*Tns3*		Actin remodeling	NC	NS	S773	0.67	0.057
Titin	*Ttn*	Z disc	Regulation of relaxation of cardiac muscle	NC	NS	T299	3.30	0.078
Titin	*Ttn*	Z disc	Regulation of relaxation of cardiac muscle	NC	NS	S301	3.30	0.078
Titin	*Ttn*	Z disc	Regulation of relaxation of cardiac muscle	NC	NS	T812	1.85	0.060
Titin	*Ttn*	Z disc	Regulation of relaxation of cardiac muscle	NC	NS	S814	1.85	0.060
Titin	*Ttn*	Z disc	Regulation of relaxation of cardiac muscle	NC	NS	S17984	1.04	0.056
Titin	*Ttn*	Z disc	Regulation of relaxation of cardiac muscle	NC	NS	S20869	1.51	0.003
Titin	*Ttn*	Z disc	Regulation of relaxation of cardiac muscle	NC	NS	S22797	1.31	0.070
Titin	*Ttn*	Z disc	Regulation of relaxation of cardiac muscle	NC	NS	S33927	2.48	0.006
Titin	*Ttn*	Z disc	Regulation of relaxation of cardiac muscle	NC	NS	S33961	1.73	0.045
Titin	*Ttn*	Z disc	Regulation of relaxation of cardiac muscle	NC	NS	T33962	1.76	0.011
Titin	*Ttn*	Z disc	Regulation of relaxation of cardiac muscle	NC	NS	T34067	1.84	0.080

Titin	*Ttn*	Z disc	Regulation of relaxation of cardiac muscle	NC	NS	Y34068	1.84	0.080
Titin N2B	*Ttn*		Regulation of relaxation of cardiac muscle	NC	NS	T4117	1.58	0.043
Utrophin	*Utrn*	Cytoskeleton	Muscle contraction, actin filament binding	NA	NA	S933	0.79	0.032
Utrophin	*Utrn*	Cytoskeleton	Muscle contraction, actin filament binding	NA	NA	S935	1.00	0.035
Vasodilator-stimulated phosphoprotein	*Vasp*	Cytoskeleton	Actin cytoskeleton organization, positive regulation of actin filament polymerization	NA	NA	S236	1.65	0.040
Vinculin	*Vcl*	Z disc	Actin binding	0.22	2.18E-07	S290	0.95	0.011
Vinculin	*Vcl*	Z disc	Actin binding	0.22	2.18E-07	T602	1.01	0.013
Vinculin	*Vcl*	Z disc	Actin binding	0.22	2.18E-07	T719	1.41	0.018
Vinculin	*Vcl*	Z disc	Actin binding	0.22	2.18E-07	S721	1.35	0.016
Vinculin	*Vcl*	Z disc	Actin binding	0.22	2.18E-07	S579	1.24	0.031
Vinculin	*Vcl*	Z disc	Actin binding	0.22	2.18E-07	S795	1.63	0.007
Vinculin	*Vcl*	Z disc	Actin binding	0.22	2.18E-07	S97	1.09	0.022
WASH complex subunit 2	*Washc2*		Negative regulation of barbed-end actin filament capping	NA	NA	S387	0.79	0.037
WASH complex subunit 2	*Washc2*		Negative regulation of barbed-end actin filament capping	NA	NA	S611	1.28	0.028
Xin actin-binding repeat-containing protein 1	*Xirp1*	Z disc	Protects actin filaments from depolymerization	NA	NA	S532	1.38	0.017
Xin actin-binding repeat-containing protein 1	*Xirp1*	Z disc	Protects actin filaments from depolymerization	NA	NA	S726	1.45	1.54E-04
Xin actin-binding repeat-containing protein 1	*Xirp1*	Z disc	Protects actin filaments from depolymerization	NA	NA	S295	1.48	0.001
Xin actin-binding repeat-containing protein 1	*Xirp1*	Z disc	Protects actin filaments from depolymerization	NA	NA	S332	2.23	0.002
Xin actin-binding repeat-containing protein 2	*Xirp2*	Z disc	Actin cytoskeleton organization, Protects actin filaments from depolymerization	NA	NA	S2211	1.95	0.009
Xin actin-binding repeat-containing protein 2	*Xirp2*	Z disc	Actin cytoskeleton organization, Protects actin filaments from depolymerization	NA	NA	S3246	1.41	0.057
Xin actin-binding repeat-containing protein 2	*Xirp2*	Z disc	Actin cytoskeleton organization, Protects actin filaments from depolymerization	NA	NA	S1573	1.38	0.037
Xin actin-binding repeat-containing protein 2	*Xirp2*	Z disc	Actin cytoskeleton organization, Protects actin filaments from depolymerization	NA	NA	S2198	2.60	0.003
Xin actin-binding repeat-containing protein 2	*Xirp2*	Z disc	Actin cytoskeleton organization, Protects actin filaments from depolymerization	NA	NA	S2254	1.51	0.033
Xin actin-binding repeat-containing protein 2	*Xirp2*	Z disc	Actin cytoskeleton organization, Protects actin filaments from depolymerization	NA	NA	S2970	0.97	0.029
Xin actin-binding repeat-containing protein 2	*Xirp2*	Z disc	Actin cytoskeleton organization, Protects actin filaments from depolymerization	NA	NA	S3246	1.16	0.027
Xin actin-binding repeat-containing protein 2	*Xirp2*	Z disc	Actin cytoskeleton organization, Protects actin	NA	NA	S565	1.99	0.012

			filaments from depolymerization					
Xin actin-binding repeat-containing protein 2	*Xirp2*	Z disc	Actin cytoskeleton organization, Protects actin filaments from depolymerization	NA	NA	S813	1.95	0.004
Xin actin-binding repeat-containing protein 2	*Xirp2*	Z disc	Actin cytoskeleton organization, Protects actin filaments from depolymerization	NA	NA	S1210	1.69	0.013
Xin actin-binding repeat-containing protein 2	*Xirp2*	Z disc	Actin cytoskeleton organization, Protects actin filaments from depolymerization	NA	NA	S2252	2.53	0.008
Xin actin-binding repeat-containing protein 2	*Xirp2*	Z disc	Actin cytoskeleton organization, Protects actin filaments from depolymerization	NA	NA	S2255	1.80	0.043
Xin actin-binding repeat-containing protein 2	*Xirp2*	Z disc	Actin cytoskeleton organization, Protects actin filaments from depolymerization	NA	NA	S2258	1.90	0.033
Xin actin-binding repeat-containing protein 2	*Xirp2*	Z disc	Actin cytoskeleton organization, Protects actin filaments from depolymerization	NA	NA	S2260	1.80	0.056
Xin actin-binding repeat-containing protein 2	*Xirp2*	Z disc	Actin cytoskeleton organization, Protects actin filaments from depolymerization	NA	NA	S2291	2.03	0.021
Xin actin-binding repeat-containing protein 2	*Xirp2*	Z disc	Actin cytoskeleton organization, Protects actin filaments from depolymerization	NA	NA	S2873	2.03	0.019
Xin actin-binding repeat-containing protein 2	*Xirp2*	Z disc	Actin cytoskeleton organization, Protects actin filaments from depolymerization	NA	NA	T2875	1.63	0.016
Xin actin-binding repeat-containing protein 2	*Xirp2*	Z disc	Actin cytoskeleton organization, Protects actin filaments from depolymerization	NA	NA	S2987	1.28	0.007
Xin actin-binding repeat-containing protein 2	*Xirp2*	Z disc	Actin cytoskeleton organization, Protects actin filaments from depolymerization	NA	NA	S2957	0.94	0.055

Blank spaces represent proteins or phospho-sites, that weren't identified or were unchanged between treatment groups.

Supplemental Table I B: MS data of significant and trended changed phosphorylation sites for CDC treated animals compared to placebo (n=6) of sarcomeric proteins, their location, known function, and information about the changed phosphorylation site are listed. Total protein and phosphorylation changes are presented in log2 foldchanges (log2FC). Listed p-values were calculated using the linear mixed effects model built into MSSTATs.

Protein Name	Gene Name	Location	Role	CDC vs Placebo		Phospho-site	CDC vs Placebo	
				log2FC	p-value		log2FC	p-value
Actin-binding LIM protein 1	*Ablim1*	Actin cytoskeleton	Cytoskeletal organization, actin binding	-0.40	0.005	S496	-1.16	0.064
Actin-binding LIM protein 1	*Ablim1*	Actin cytoskeleton	Cytoskeletal organization, actin binding	-0.40	0.005	S475	1.31	0.041
Actin-binding LIM protein 1	*Ablim1*	Actin cytoskeleton	Cytoskeletal organization, actin binding	-0.40	0.005	S499	-2.06	0.024
Actin-binding LIM protein 1	*Ablim1*	Actin cytoskeleton	Cytoskeletal organization, actin binding	-0.40	0.005	S499	-1.16	0.064
Actin-binding LIM protein 1	*Ablim1*	Actin cytoskeleton	Cytoskeletal organization, actin binding	-0.40	0.005	T495	-2.06	0.024
Fructose-bisphosphate aldolase A	*Aldoa*	M band, Z disc	Muscle contraction	NC	NS	T37	-2.10	0.035
Fructose-bisphosphate aldolase A	*Aldoa*	M band, Z disc	Muscle contraction	NC	NS	S36	-0.50	0.074

Fructose-bisphosphate aldolase A	*Aldoa*	M band, Z disc	Muscle contraction	NC	NS	T52	-2.32	0.075
Cdc42 effector protein 1	*Cdc42ep1*	Cytoskeleton	Positive regulation of actin filament polymerization	NA	NA	S347	-1.36	0.083
Cdc42 effector protein 1	*Cdc42ep1*	Cytoskeleton	Positive regulation of actin filament polymerization	NA	NA	S350	-1.36	0.083
Catenin alpha-1	*Ctnna1*	Actin cytoskeleton	Actin filament assembly, actin binding	-0.22	0.033	T647	-1.80	0.062
Catenin alpha-1	*Ctnna1*	Actin cytoskeleton	Actin filament assembly, actin binding	-0.22	0.033	S643	-1.80	0.062
Desmin	*Des*	Z disc	Muscle-specific type III intermediate filament	NC	NS	S31	-2.22	0.033
Desmin	*Des*	Z disc	Muscle-specific type III intermediate filament	NC	NS	S32	-2.22	0.033
Desmin	*Des*	Z disc	Muscle-specific type III intermediate filament	NC	NS	S28	-2.65	0.051
Desmin	*Des*	Z disc	Muscle-specific type III intermediate filament	NC	NS	S25	-1.67	0.027
Desmin	*Des*	Z disc	Muscle-specific type III intermediate filament	NC	NS	S31	-1.67	0.027
Desmin	*Des*	Z disc	Muscle-specific type III intermediate filament	NC	NS	S25	-2.65	0.051
Filamin-C	*Flnc*	Z disc	Actin-cross-linking protein	NC	NS	S2633	0.94	0.057
LIM domain and actin-binding protein 1	*Lima1*	Actin cytoskeleton	Bundles actin filaments	NA	NA	S488	0.61	0.058
LIM and calponin homology domains-containing protein 1	*Limch1*		Actomyosin structure organization, actin binding	NC	NS	S217	-1.72	0.089
LIM and calponin homology domains-containing protein 1	*Limch1*		Actomyosin structure organization, actin binding	NC	NS	T215	-1.72	0.089
Leiomodin-2	*Lmod2*	M band	Actin polymerization, sarcomere organization	NC	NS	S394	-0.90	0.048
Leiomodin-2	*Lmod2*	M band	Actin polymerization, sarcomere organization	NC	NS	S394	-3.45	0.013
Leiomodin-2	*Lmod2*	M band	Actin polymerization, sarcomere organization	NC	NS	S514	-2.05	0.015
Leiomodin-2	*Lmod2*	M band	Actin polymerization, sarcomere organization	NC	NS	S514	-1.74	0.057
Leiomodin-2	*Lmod2*	M band	Actin polymerization, sarcomere organization	NC	NS	S517	-1.74	0.057
Leiomodin-2	*Lmod2*	M band	Actin polymerization, sarcomere organization	NC	NS	S517	-0.93	0.067
Leiomodin-2	*Lmod2*	M band	Actin polymerization, sarcomere organization	NC	NS	T518	-2.05	0.015
Leiomodin-2	*Lmod2*	M band	Actin polymerization, sarcomere organization	NC	NS	Y396	-3.45	0.013
Myosin-binding protein C, cardiac-type	*Mybpc3*	M band, Z disc	Actin filament organization, cardiac muscle contraction	-0.26	0.024	S302	-2.27	0.075
Myosin-6	*Myh6*	Z disc	Sarcomere organization, striated muscle contraction	-0.51	2.4E-05	S1270	-0.98	0.089
Myosin-6	*Myh6*	Z disc	Sarcomere organization, striated muscle contraction	-0.51	2.4E-05	S1089	-1.90	0.088
Myosin-7	*Myh7*	Z disc	Sarcomere organization, striated muscle contraction	NA	NA	S560	-1.10	0.100
Myosin-7	*Myh7*	Z disc	Sarcomere organization, striated muscle contraction	NA	NA	T1605	-1.50	0.072
Myosin-7	*Myh7*	Z disc	Sarcomere organization, striated muscle contraction	NA	NA	Y410	-2.29	0.043
Myosin-9	*Myh9*	Actin cytoskeleton	Actomyosin structure organization	NC	NS	S1944	-1.20	0.071
Myomesin-1	*Myom1*	M band, Z disc	Sarcomere organization, striated muscle contraction	-0.22	0.019	Y118	1.86	0.071
Obscurin	*Obscn*	M band, Z disc	Structural constituent of muscle, titin binding, protein localization to M-band	NC	NS	S454	-2.13	0.068

Septin-7	*Sept7*		Organization of the actin cytoskeleton	-0.24	0.001	T425	-1.13	0.046
SH3 and multiple ankyrin repeat domains protein 3	*Shank3*		Negative regulation of actin filament bundle assembly	NC	NS	T1235	-1.88	0.063
Shroom family member 3	*Shroom3*	Cytoskeleton	Actin cytoskeleton organization	NA	NA	S763	1.06	0.099
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	-0.40	0.029	S143	-1.43	0.081
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	-0.40	0.029	S340	-1.46	0.077
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	-0.40	0.029	S343	-1.46	0.077
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	-0.40	0.029	S394	1.91	0.025
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	Cytoskeleton	Actin cytoskeleton organization	-0.40	0.029	T136	-1.43	0.081
Spectrin alpha chain, non-erythrocytic 1	*Sptan1*		Actin cytoskeleton reorganization	NC	NS	S1029	-0.48	0.072
Synaptopodin	*Synpo*	Actin cytoskeleton	Positive regulation of actin filament bundle assembly	-0.46	0.001	S525	-1.67	0.025
Synaptopodin-2	*Synpo2*	Z disc	Assembly and stabilization of the Z lines	-0.28	0.004	S546	-2.61	0.014
Synaptopodin-2	*Synpo2*	Z disc	Assembly and stabilization of the Z lines	-0.28	0.004	S548	-2.61	0.014
Synaptopodin 2-like protein	*Synpo2l*	Z disc	Positive regulation of actin filament bundle assembly	NC	NS	S143	-2.21	0.042
Synaptopodin 2-like protein	*Synpo2l*	Z disc	Positive regulation of actin filament bundle assembly	NC	NS	S143	-1.70	0.046
Synaptopodin 2-like protein	*Synpo2l*	Z disc	Positive regulation of actin filament bundle assembly	NC	NS	T141	-1.70	0.046
Synaptopodin 2-like protein	*Synpo2l*	Z disc	Positive regulation of actin filament bundle assembly	NC	NS	Y138	-2.21	0.042
Tropomyosin alpha-1 chain	*Tpm1*	Actin cytoskeleton	Muscle contraction	-1.42	1.82E-08	S283	-0.92	0.021
Tropomyosin alpha-1 chain	*Tpm1*	Actin cytoskeleton	Muscle contraction	-1.42	1.82E-08	T282	-1.95	0.044
Titin	*Ttn*	M band	Regulation of relaxation of cardiac muscle	NC	NS	S34488	-2.00	0.020
Titin	*Ttn*	Z disc	Regulation of relaxation of cardiac muscle	NC	NS	S1444	-2.52	0.087
Titin	*Ttn*		Regulation of relaxation of cardiac muscle	NC	NS	S16620	1.21	0.026
Titin	*Ttn*		Regulation of relaxation of cardiac muscle	NC	NS	S20869	-0.95	0.017
Titin	*Ttn*	Z disc	Regulation of relaxation of cardiac muscle	NC	NS	S322	-1.72	0.012
Titin	*Ttn*	M band	Regulation of relaxation of cardiac muscle	NC	NS	S33927	-1.34	0.077
Titin	*Ttn*	M band	Regulation of relaxation of cardiac muscle	NC	NS	T34067	-1.23	0.090
Titin	*Ttn*	M band	Regulation of relaxation of cardiac muscle	NC	NS	T34067	-2.18	0.034
Titin	*Ttn*	M band	Regulation of relaxation of cardiac muscle	NC	NS	Y34068	-2.18	0.034
Titin	*Ttn*	M band	Regulation of relaxation of cardiac muscle	NC	NS	Y34068	-1.69	0.014
Vinculin	*Vcl*	Z disc	Actin binding	-0.14	3.54E-05	S346	-0.56	0.069
Whirlin	*Whrn*	Actin filament		NA	NA	S637	-1.26	0.035
Xin actin-binding repeat-containing protein 1	*Xirp1*	Z disc	Protects actin filaments from depolymerization	NA	NA	S745	0.63	0.044

Blank spaces represent proteins or phospho-sites, that weren’t identified or were unchanged between treatment groups.

Supplemental Table II A: MS data of upstream kinases and their regulators. Shown are the fold change values (log2) of HFpEF compared to control for total protein concentration (n=3-4) and phosphorylation of S/T/Y residues (B, n=6). Total protein and phosphorylation changes are presented in log2 foldchanges (log2FC). Listed p-values were calculated using the linear mixed effects model built into MSSTATs.

Protein Name	Gene Name	Regulates Upstream Kinase	Phospho-site	HFpEF vs control (log2FC)	p-value
Cyclin-H	*Ccnh*	CDK2		-3.45	5.09E-05
Casein kinase I isoform delta	*Csnk1d*	CK1		2.22	0.033
5'-AMP-activated protein kinase subunit gamma-2	*Prkag2*	PHK	S196	1.02	0.046
A-kinase anchor protein 12	*Akap12*	PKC		-1.19	0.001
Cysteine and glycine-rich protein 3	*Csrp3*	PKC		1.54	6.9E-12
Cysteine and glycine-rich protein 3	*Csrp3*	PKC	S111	1.43	0.019
Heat shock protein beta-1	*Hspb1*	PKC		1.41	4.22E-11
Heat shock protein beta-1	*Hspb1*	PKC	S13	1.05	0.034
Heat shock protein beta-1	*Hspb1*	PKC	S86	1.18	0.002
Heat shock protein beta-1	*Hspb1*	PKC	S15	1.20	0.006
LIM domain-binding protein 3	*Ldb3*	PKC		0.71	5.59E-05
LIM domain-binding protein 3	*Ldb3*	PKC	S121	1.10	0.017
LIM domain-binding protein 3	*Ldb3*	PKC	S123	1.11	0.018
LIM domain-binding protein 3	*Ldb3*	PKC	S98	1.55	0.013
LIM domain-binding protein 3	*Ldb3*	PKC	S44	0.86	0.054
PDZ and LIM domain protein 5	*Pdlim5*	PKC		1.19	1.55E-05
Protein kinase C delta type	*Prkcd*	PKC	S643	1.44	0.042
Receptor of activated protein C kinase 1	*Rack1*	PKC		0.49	2.98E-04
Sequestosome-1	*Sqstm1*	PKC		0.44	0.048
Neutral alpha-glucosidase AB	*Ganab*	PKD1		0.36	0.043
Serine/threonine-protein kinase D1	*Prkd1*	PKD1		1.74	2.10E-04
A-kinase anchor protein 13	*Akap13*	PKD1	S1891	1.11	0.001
A-kinase anchor protein 13	*Akap13*	PKD1	S1583	1.27	0.006
A-kinase anchor protein 13	*Akap13*	PKD1	T1590	1.17	0.049
A-kinase anchor protein 13	*Akap13*	PKD1	S1520	0.94	0.020
A-kinase anchor protein 13	*Akap13*	PKD1	S1585	1.39	0.012

* Kinase is not regulated in the direction of its potential targets according to MS data and thus were not considered as relevant upstream kinase.

Supplemental Table II B: MS data of upstream kinases and their regulators. Shown are the fold change values (log2) of CDC treatment compared to placebo for total protein concentration (n=4) and phosphorylation of S/T/Y residues (B, n=6). Total protein and phosphorylation changes are presented in log2 foldchanges (log2FC). Listed p-values were calculated using the linear mixed effects model built into MSSTATs.

Protein Name	Gene Name	Regulates Upstream Kinase	Phospho-site	CDC vs Placebo (log2FC)	p-value
Cyclin-H	*Ccnh*	CDK2		2.63	4.89E-04
A-kinase anchor protein 12	*Akap12*	PKC		0.86	0.005
Cysteine and glycine-rich protein 3	*Csrp3*	PKC		-0.63	8.36E-06
PDZ and LIM domain protein 5	*Pdlim5*	PKC	S228	-2.63	0.059
PDZ and LIM domain protein 5	*Pdlim5*	PKC		-0.43	0.042
Protein kinase C delta type	*Prkcd*	PKC		-1.81	1.01E-07
Receptor of activated protein C kinase 1	*Rack1*	PKC		-0.29	0.012

Supplemental table III A: Confirmed PKC phosphorylation sites by recombinant kinase assay. Phosphorylated residues uniquely detected in the group of cell lysate receiving recombinant kinase are labeled with Inf. Phosphorylation changes are presented in log2 foldchanges (log2FC). Listed p-values were calculated using the linear mixed effects model built into MSSTATs.

Protein Name	Gene Name	Phospho-site	PKCα vs Control		PKCβ vs Control		PKCδ vs Control	
			log2FC	p-value	log2FC	p-value	log2FC	p-value
A-kinase anchor protein 13	*Akap13*	S1585	1.28	0.069	NC	NS	NC	NS
Alpha-crystallin B chain	*Cryab*	S59	NC	NS	NC	NS	1.18	0.052
Catenin alpha-1	*Ctnna1*	S643	NC	NS	0.54	0.088	NC	NS
Desmin	*Des*	S28	2.43	0.073	0.94	0.044	1.76	0.016
Drebrin	*Dbn1*	S142	0.73	0.077	NC	NS	NC	NS
E3 ubiquitin-protein ligase UBR4	*Ubr4*	S2715	0.83	0.072	NC	NS	NC	NS
E3 ubiquitin-protein ligase UBR4	*Ubr4*	S2719	0.83	0.072	NC	NS	NC	NS
Filamin-A-interacting protein 1	*Filip1*	S979	0.33	0.048	NC	NS	0.51	0.006
Filamin-C	*Flnc*	S2234	0.63	0.054	NC	NS	0.50	0.056
Filamin-C	*Flnc*	S2237	NC	NS	Inf		NC	NS
Fructose-bisphosphate aldolase A	*Aldoa*	T37	1.25	0.005	NC	NS	0.77	0.022
Heat shock protein beta-1	*Hspb1*	S86	0.83	0.050	NC	NS	0.70	0.092
Leiomodin-2	*Lmod2*	S394	1.24	0.049	NC	NS	NC	NS
Leiomodin-2	*Lmod2*	S405	0.74	0.104	NC	NS	0.75	0.102
LIM domain-binding protein 3	*Ldb3*	S44	NC	NS	NC	NS	1.66	0.014
Misshapen-like kinase 1	*Mink1*	S765	NC	NS	NC	NS	1.41	0.023
Myosin-1	*Myh1*	S1373	1.07	0.072	NC	NS	1.11	0.063
Myosin-6	*Myh6*	S1270	1.02	0.039	NC	NS	0.89	0.042
Myosin-6	*Myh6*	S649	2.39	0.000	1.31	0.007	1.99	0.000
Myosin-7	*Myh7*	S1222	NC	NS	NC	NS	2.29	0.077
Myosin-7	*Myh7*	S1478	NC	NS	NC	NS	0.82	0.045
Myosin-7	*Myh7*	S1491	1.30	0.026	NC	NS	1.07	0.057
Myosin-7	*Myh7*	S560	Inf		Inf		Inf	
Myosin-7	*Myh7*	S642	2.39	0.000	1.31	0.007	1.99	0.000
Myosin-7	*Myh7*	S643	2.30	0.000	1.18	0.008	2.01	0.000
Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2	*Inppl1*	S132	NC	NS	-3.08	0.025	NC	NS
Plectin	*Plec*	S4388	1.41	0.034	0.75	0.055	NC	NS
Plectin	*Plec*	S4389	1.41	0.034	0.75	0.055	NC	NS
Plectin	*Plec*	S4629	Inf		NC	NS	Inf	
Rho GTPase-activating protein 35	*Arhgap 35*	S1179	0.81	0.095	NC	NS	1.15	0.025
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S396	NC	NS	0.99	0.029	0.96	0.033
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S397	0.85	0.006	0.96	0.003	0.97	0.003
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S40	NC	NS	NC	NS	0.95	0.088
Talin-1	*Tln1*	S979	NC	NS	0.65	0.025	NC	NS
Talin-1	*Tln1*	S981	NC	NS	1.18	0.021	NC	NS
Titin	*Ttn*	S301	NC	NS	0.47	0.087	NC	NS
Titin	*Ttn*	S34488	NC	NS	0.75	0.105	NC	NS
Titin	*Ttn*	T299	NC	NS	0.47	0.087	NC	NS
Vinculin	*Vcl*	S346	1.20	0.058	NC	NS	NC	NS

WASH complex subunit 2	*Washc2*	S387	0.89	0.069	NA	NA	NC	NS
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2211	1.02	0.092	NA	NA	NC	NS

Blank spaces represent proteins or phospho-sites, that weren't identified or were not statistical different between treatment groups.

Supplemental table III B: Confirmed PKC phosphorylation sites by kinase inhibition. Phosphorylation changes are presented in log2 foldchanges (log2FC). Listed p-values were calculated using the linear mixed effects model built into MSSTATs.

Protein Name	Gene Name	Phospho-site	PKCα vs Control		PKCβ vs Control		PKCδ vs Control		PKC vs Control	
			log2FC	p-value	log2FC	p-value	log2FC	p-value	log2FC	p-value
Filamin-C	*Flnc*	S2234	NC	NS	NC	NS	-0.99	0.03	NC	NS
Filamin-C	*Flnc*	S2237	NC	NS	NC	NS	-0.99	0.03	NA	NA
Filamin-C	*Flnc*	S2633	NC	NS	-0.89	0.02	NC	NS	NC	NS
Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2	*Inppl1*	S132	NC	NS	NC	NS	NC	NS	-2.67	0.018
Myosin-9	*Myh9*	S1944	NC	NS	-1.03	0.057	NC	NS	-0.97	0.074
Nexilin	*Nexn*	S544	-2.15	0.022	NC	NS	-2.13	0.019	-2.51	0.034
Paxillin	*Pxn*	S317	NC	NS	-0.92	0.095	NC	NS	NC	NS
Plectin	*Plec*	S4388	NC	NS	NC	NS	NC	NS	-0.73	0.054
Plectin	*Plec*	S4389	NC	NS	NC	NS	NC	NS	-0.73	0.054
Plectin	*Plec*	S4409	NC	NS	NC	NS	NC	NS	-1.19	0.094
Plectin	*Plec*	S4411	NC	NS	NC	NS	NC	NS	-1.73	0.019
Septin-7	*Sept7*	T425	NC	NS	NC	NS	NC	NS	-1.11	0.011
SH3 domain-binding protein 1	*Sh3bp1*	S539	NC	NS	NC	NS	NC	NS	-2.08	0.083
Sorbin and SH3 domain-containing	*Sorbs2*	S38	NC	NS	NC	NS	-1.91	0.01	NC	NS
Sorbin and SH3 domain-containing	*Sorbs2*	S397	-1.5	0.01	NC	NS	NC	NS	NC	NS
Spectrin alpha chain	*Sptan1*	S1029	-2.15	0.01	-2.00	0.016	-2.15	0.01	NC	NS
E3 ubiquitin-protein ligase UBR4	*Ubr4*	S2897	NC	NS	NC	NS	NC	NS	-1.08	0.07
Vinculin	*Vcl*	S290	NC	NS	NC	NS	NC	NS	-1.36	0.080
Vinculin	*Vcl*	S346	NC	NS	NC	NS	NC	NS	-1.36	0.0
WASH complex subunit 2	*Washc2*	S387	NC	NS	NC	NS	NC	NS	-0.82	0.018
WASH complex subunit 2	*Washc2*	S611	NC	NS	NC	NS	NC	NS	-0.85	0.072

Blank spaces represent proteins or phospho-sites, that weren't identified or were not statistical different between treatment groups.

Supplemental table 3C: Confirmed PKC phosphorylation sites by kinase and kinase regulator overexpression. Phosphorylation changes are presented in log2 foldchanges (log2FC). Listed p-values were calculated using the linear mixed effects model built into MSSTATs.

Protein Name	Gene Name	Phospho-site	PKCα + Ldb3 vs control		PKCα + Pdlim5 vs control		PKCβ + Ldb3 vs control		PKCβ + Pdlim5 vs control	
			log2FC	p-value	log2FC	p-values	log2FC	p-value	log2FC	p-value
Heat shock protein beta-1	*Hspb1*	S13	NC	NS	2.44	0.034	0.67	0.055	NC	NS
Vinculin	*Vcl*	S290	NC	NS	0.91	0.079	NC	NS	0.99	0.059

Blank spaces represent proteins or phospho-sites, that weren't identified or were not statistical different between treatment groups.

Supplemental Table IV A: MS data of significantly changed phosphatases in HFpEF animals compared to control for total protein (n=3-4) and phosphorylation (n=6). Total protein and phosphorylation changes are presented in log2 foldchanges (log2FC). Listed p-values were calculated using the linear mixed effects model built into MSSTATs.

Protein Name	Gene Name	Phospho-site	HFpEF vs control	
			log2FC	p-value
[Pyruvate dehydrogenase [acetyl-transferring]]-phosphatase 1, mitochondrial	*Pdp1*		-0.36	1.91E-06
[Pyruvate dehydrogenase [acetyl-transferring]]-phosphatase 2, mitochondrial	*Pdp2*		8.10	1.65E-09
3'(2'),5'-bisphosphate nucleotidase 1	*Bpnt1*		0.51	2.30E-06
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2	*Pfkfb2*	S469	0.76	0.060
Diphosphoinositol polyphosphate phosphohydrolase 1	*Nudt3*		0.28	0.044
Diphosphoinositol polyphosphate phosphohydrolase 2	*Nudt4*		1.95	0.001
Dual specificity protein phosphatase 3	*Dusp3*		0.59	2.33E-06
Haloacid dehalogenase-like hydrolase domain-containing protein 2	*Hdhd2*		-1.74	0.005
Inactive dual specificity phosphatase 27	*Dusp27*	S32	0.99	0.037
Inactive dual specificity phosphatase 27	*Dusp27*	S965	1.00	0.050
Inactive phospholipid phosphatase 7	*Plpp7*		-1.89	0.050
Inorganic pyrophosphatase 2, mitochondrial	*Ppa2*		-0.65	0.001
Magnesium-dependent phosphatase 1	*Mdp1*		1.93	0.001
Myotubularin-related protein 3	*Mtmr3*		-1.21	0.036
PH domain leucine-rich repeat protein phosphatase 1	*Phlpp1*	S1598	2.27	0.007
Phosphatidate phosphatase LPIN1	*Lpin1*		0.54	7.67E-07
Phosphatidylinositide phosphatase SAC1	*Sacm1l*		-0.35	0.004
Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2	*Inppl1*	S132	2.41	0.037
Phosphoethanolamine/phosphocholine phosphatase	*Phospho1*		-0.46	0.007
Protein phosphatase 1 regulatory subunit 12A	*Ppp1r12a*		0.53	2.74E-04
Protein phosphatase 1 regulatory subunit 12A	*Ppp1r12a*	S873	0.81	0.041
Protein phosphatase 1 regulatory subunit 12B	*Ppp1r12b*		0.38	0.011
Protein phosphatase 1 regulatory subunit 14A	*Ppp1r14a*		-0.91	5.77E-07
Protein phosphatase 1 regulatory subunit 14B	*Ppp1r14b*		1.08	0.043
Protein phosphatase 1 regulatory subunit 32	*Ppp1r32*	Y335	1.26	0.026
Protein phosphatase 1 regulatory subunit 3A	*Ppp1r3a*		-2.75	0.001
Protein phosphatase 1A	*Ppm1a*		0.37	0.042
Protein phosphatase 1L	*Ppm1l*		2.19	1.49E-09
Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	*Ppp2r2a*		0.36	0.004
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform	*Ppp2r5e*		0.52	0.009
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	*Ppp2r1b*		0.47	0.002
Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	*Ppp3ca*		-0.55	4.54E-04
Serine/threonine-protein phosphatase 5	*Ppp5c*		0.41	0.001
Serine/threonine-protein phosphatase 6 catalytic subunit	*Ppp6c*		-1.45	0.009
Serine/threonine-protein phosphatase 6 regulatory subunit 2	*Ppp6r2*	S628	1.13	0.008
Serine/threonine-protein phosphatase CPPED1	*Cpped1*		1.09	0.001
Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	*Ppp1ca*		-1.19	5.52E-05
Serine/threonine-protein phosphatase PP1-beta catalytic subunit	*Ppp1cb*		0.42	4.88E-04
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	*Ppp1cc*		0.38	0.004
Tyrosine-protein phosphatase non-receptor type 11	*Ptpn11*		0.38	0.010
Tyrosine-protein phosphatase non-receptor type 21	*Ptpn21*		0.94	0.001
Tyrosine-protein phosphatase non-receptor type 23	*Ptpn23*	S985	2.22	0.009
Tyrosine-protein phosphatase non-receptor type 23	*Ptpn23*	S986	1.72	0.013
Tyrosine-protein phosphatase non-receptor type 23	*Ptpn23*	S1179	2.72	3.15E-05
Uridine phosphorylase 2	*Upp2*		0.65	3.97E-04

Supplemental Table IV B: MS data of significantly changed phosphatases in CDC treated animals compared to placebo for total protein (n=3-4) and phosphorylation (n=6). Total protein and phosphorylation changes are presented in log2 foldchanges (log2FC). Listed p-values were calculated using the linear mixed effects model built into MSSTATs.

Protein Name	Gene Name	Phospho-site	CDC vs placebo	
			log2FC	p-value
[Pyruvate dehydrogenase [acetyl-transferring]]-phosphatase 1, mitochondrial	*Pdp1*		0.14	0.001
Diphosphoinositol polyphosphate phosphohydrolase 2	*Nudt4*		-1.37	0.006
Haloacid dehalogenase-like hydrolase domain-containing protein 2	*Hdhd2*		1.58	0.006
Inactive phospholipid phosphatase 7	*Plpp7*		1.97	0.028
Laforin	*Epm2a*		0.59	0.009
PH domain leucine-rich repeat protein phosphatase 1	*Phlpp1*	S1598	-1.57	0.041
Phosphatidate phosphatase LPIN1	*Lpin1*		-0.42	7.67E-07
Phosphatidylinositide phosphatase SAC1	*Sacm1l*		0.34	0.003
Protein phosphatase 1 regulatory subunit 12A	*Ppp1r12a*		-0.41	0.002
Protein phosphatase 1 regulatory subunit 14A	*Ppp1r14a*		0.55	0.000
Protein phosphatase 1 regulatory subunit 14B	*Ppp1r14b*		-1.21	0.018
Protein phosphatase 1 regulatory subunit 3A	*Ppp1r3a*		2.36	0.003
Protein phosphatase 1 regulatory subunit 7	*Ppp1r7*		0.36	0.006
Protein phosphatase 1L	*Ppm1l*		-2.26	0.000
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform	*Ppp2r5c*		-0.74	0.001

Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	*Ppp3ca*		0.52	0.000
Serine/threonine-protein phosphatase 6 catalytic subunit	*Ppp6c*		1.07	0.025
Serine/threonine-protein phosphatase 6 catalytic subunit	*Ppp6c*		1.04	0.020
Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	*Ppp1ca*		0.58	0.002
Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	*Ppp1ca*		1.17	5.52E-05
Serine/threonine-protein phosphatase PP1-beta catalytic subunit	*Ppp1cb*		-0.28	0.008
Tyrosine-protein phosphatase non-receptor type 21	*Ptpn21*		-0.72	0.006
Tyrosine-protein phosphatase non-receptor type 23	*Ptpn23*	S986	-0.95	0.038

Supplemental Table V: Output data of the GPS3.0 consensus sequence analysis of significant changed phosphor-peptides of HFpEF versus control and CDC versus placebo comparisons. Shown are the analyzed sequences and their score and cutoff values for shared consensus sequences with PKC and PKC isoforms.

Protein Name	Gene Name	Phospho-site	Peptide Modified Sequence	Input Sequence	Position	Code	Kinase	Peptide	Score	Cutoff
Actin, aortic smooth muscle	*Acta2*	S241	S[+80]YELPDGQVITIGNER	TAASSSSLEKSYELPDGQVIT	11	S	PRKCA	SSSSLEKSYELPDGQ	14.657	7.372
Actin, aortic smooth muscle	*Acta2*	S241	S[+80]YELPDGQVITIGNER	TAASSSSLEKSYELPDGQVIT	11	S	PRKCB	SSSSLEKSYELPDGQ	11.172	10.858
Actin-binding LIM protein 1	*Ablim1*	S499	ST[+80]SQGS[+80]INSPVYSR	DVRDRMIHRSTSQGSINSPVY	11	T	PKC	DRMIHRSTSQGSINS	1.855	1.416
Actin-binding LIM protein 1	*Ablim1*	S499	ST[+80]SQGS[+80]INSPVYSR	RMIHRSTSQGSINSPVYSRHS	11	S	PKC	HRSTSQGSINSPVYS	1.512	1.416
Actin-binding LIM protein 1	*Ablim1*	S499	ST[+80]SQGS[+80]INSPVYSR	DVRDRMIHRSTSQGSINSPVY	11	T	PKCa	DRMIHRSTSQGSINS	7.913	4.803
Actin-binding LIM protein 1	*Ablim1*	S499	ST[+80]SQGS[+80]INSPVYSR	RMIHRSTSQGSINSPVYSRHS	11	S	PKCa	HRSTSQGSINSPVYS	9.091	4.803
Actin-binding LIM protein 1	*Ablim1*	S499	ST[+80]SQGS[+80]INSPVYSR	DVRDRMIHRSTSQGSINSPVY	11	T	PRKCA	DRMIHRSTSQGSINS	14.808	7.372
Actin-binding LIM protein 1	*Ablim1*	S499	ST[+80]SQGS[+80]INSPVYSR	RMIHRSTSQGSINSPVYSRHS	11	S	PRKCA	HRSTSQGSINSPVYS	19.116	7.372
Actin-binding LIM protein 1	*Ablim1*	S499	ST[+80]SQGS[+80]INSPVYSR	DVRDRMIHRSTSQGSINSPVY	11	T	PRKCD	DRMIHRSTSQGSINS	3	2.514
Actin-binding LIM protein 1	*Ablim1*	S496	STS[+80]QGS[+80]INSPVYSR	RMIHRSTSQGSINSPVYSRH	11	S	PKC	HRSTSQGSINSPVYS	1.645	1.416
Actin-binding LIM protein 1	*Ablim1*	S496	STS[+80]QGS[+80]INSPVYSR	QDVRDRMIHRSTSQGSINSPV	11	S	PKCa	RDRMIHRSTSQGSIN	6.174	4.803
Actin-binding LIM protein 1	*Ablim1*	S496	STS[+80]QGS[+80]INSPVYSR	RMIHRSTSQGSINSPVYSRH	11	S	PKCa	HRSTSQGSINSPVYS	8.761	4.803
Actin-binding LIM protein 1	*Ablim1*	S496	STS[+80]QGS[+80]INSPVYSR	QDVRDRMIHRSTSQGSINSPV	11	S	PRKCA	RDRMIHRSTSQGSIN	15.465	7.372
Actin-binding LIM protein 1	*Ablim1*	S496	STS[+80]QGS[+80]INSPVYSR	RMIHRSTSQGSINSPVYSRH	11	S	PRKCA	HRSTSQGSINSPVYS	20.268	7.372
Actin-binding LIM protein 1	*Ablim1*	S475	TLS[+80]PTPSAEGFQDGR	QSLGESPRTLSPTPSAEGFQD	11	S	PKC	GESPRTLSPTPSAEG	1.644	1.416
Actin-binding LIM protein 1	*Ablim1*	S475	TLS[+80]PTPSAEGFQDGR	QSLGESPRTLSPTPSAEGFQD	11	S	PKCa	GESPRTLSPTPSAEG	7.287	4.803
Actin-binding LIM protein 1	*Ablim1*	S475	TLS[+80]PTPSAEGFQDGR	QSLGESPRTLSPTPSAEGFQD	11	S	PRKCA	GESPRTLSPTPSAEG	12.066	7.372
A-kinase anchor protein 13	*Akap13*	S1891	FLSHS[+80]TDSLNK	MSNTWKFLSHSTDSLNKICKV	11	S	PKC	TWKFLSHSTDSLNKI	2.214	1.416
A-kinase anchor protein 13	*Akap13*	S1891	FLSHS[+80]TDSLNK	MSNTWKFLSHSTDSLNKICKV	11	S	PRKCA	TWKFLSHSTDSLNKI	10.904	7.372
A-kinase anchor protein 13	*Akap13*	S1585	SFS[+80]LEGLTGGGGVGNKPSSSLEISSANSSELR	LNADFNIRSFSLEGLTGGGGV	11	S	PKCa	DFNIRSFSLEGLTGG	7.122	4.803
A-kinase anchor protein 13	*Akap13*	S1585	SFS[+80]LEGLTGGGGVGNKPSSSLEISSANSSELR	LNADFNIRSFSLEGLTGGGGV	11	S	PRKCA	DFNIRSFSLEGLTGG	15.985	7.372
A-kinase anchor protein 13	*Akap13*	S1520	SLS[+80]PFRR	SFLRNSMRSLSPFRRHSWGPG	11	S	PKC	RNSMRSLSPFRRHSW	1.765	1.416
A-kinase anchor protein 13	*Akap13*	S1520	SLS[+80]PFRR	SFLRNSMRSLSPFRRHSWGPG	11	S	PKCa	RNSMRSLSPFRRHSW	10.491	4.803
A-kinase anchor protein 13	*Akap13*	S1520	SLS[+80]PFRR	SFLRNSMRSLSPFRRHSWGPG	11	S	PRKCA	RNSMRSLSPFRRHSW	15.707	7.372
A-kinase anchor protein 13	*Akap13*	S1583	S[+80]FSLEGLTGGGGVGNKPSSSLEISSANSSELR	AALNADFNIRSFSLEGLTGGG	11	S	PRKCA	NADFNIRSFSLEGLT	14.702	7.372
A-kinase anchor protein 13	*Akap13*	T1590	SFSLEGLT[+80]GGGGVGNKPSSSLEISSANSSELR	NIRSFSLEGLTGGGGVGNKPS	11	T	PRKCA	SFSLEGLTGGGGVGN	9.677	7.372
A-kinase anchor protein 2	*Akap2*	S730	TLS[+80]MIEEEIR	KLRSRKQRTLSMIEEEIRAAQ	11	S	PKC	SRKQRTLSMIEEEIR	5.154	1.416

A-kinase anchor protein 2	*Akap2*	S730	TLS[+80]MIEEEIR	KLRSRKQRTLSMIEEEIRAAQ	11	S	PKCa	SRKQRTLSMIEEEIR	4.961	4.803
A-kinase anchor protein 2	*Akap2*	S730	TLS[+80]MIEEEIR	KLRSRKQRTLSMIEEEIRAAQ	11	S	PRKCA	SRKQRTLSMIEEEIR	14.758	7.372
Alpha-actinin-2	*Actn2*	S574	ATLPEADGERQS[+80]ILAIQNEVEK	TLPEADGERQSILAIQNEVEK	11	S	PKC	EADGERQSILAIQNE	1.97	1.416
Alpha-actinin-2	*Actn2*	S574	ATLPEADGERQS[+80]ILAIQNEVEK	TLPEADGERQSILAIQNEVEK	11	S	PKCa	EADGERQSILAIQNE	5.226	4.803
Alpha-actinin-2	*Actn2*	S574	ATLPEADGERQS[+80]ILAIQNEVEK	TLPEADGERQSILAIQNEVEK	11	S	PRKCA	EADGERQSILAIQNE	15.354	7.372
Alpha-actinin-2	*Actn2*	S574	ATLPEADGERQS[+80]ILAIQNEVEK	TLPEADGERQSILAIQNEVEK	11	S	PRKCB	EADGERQSILAIQNE	12.828	10.858
Alpha-crystallin B chain	*Cryab*	S59	APS[+80]WIDTGLSEMR	LRPPSFLRAPSWIDTGLSEMR	11	S	PKC	PSFLRAPSWIDTGLS	2.581	1.416
Alpha-crystallin B chain	*Cryab*	S59	APS[+80]WIDTGLSEMR	LRPPSFLRAPSWIDTGLSEMR	11	S	PRKCA	PSFLRAPSWIDTGLS	15.944	7.372
Alpha-crystallin B chain	*Cryab*	S19	RPFFPFHS[+80]PSR	WIRRPFFPFHSPSRLFDQFFG	11	S	PRKCA	RPFFPFHSPSRLFDQ	9.556	7.372
Band 4.1-like protein 1	*Epb41l1*	S782	SLS[+80]PIIGK	QTVATEIRSLSPIIGKDVLTS	11	S	PRKCA	ATEIRSLSPIIGKDV	8.015	7.372
CapZ-interacting protein	*Rcsd1*	S90	AMVSPFHS[+80]PPSTPSSPGIR	GLKAMVSPFHSPPSTPSSPGI	11	S	PRKCA	AMVSPFHSPPSTPSS	9.717	7.372
CapZ-interacting protein	*Rcsd1*	S186	SKDPGS[+80]PQPNQEAGADR	VFPSKSKDPGSPQPNQEAGAD	11	S	PKC	SKSKDPGSPQPNQEA	1.687	1.416
CapZ-interacting protein	*Rcsd1*	S186	SKDPGS[+80]PQPNQEAGADR	VFPSKSKDPGSPQPNQEAGAD	11	S	PKCa	SKSKDPGSPQPNQEA	6.265	4.803
CapZ-interacting protein	*Rcsd1*	S186	SKDPGS[+80]PQPNQEAGADR	VFPSKSKDPGSPQPNQEAGAD	11	S	PRKCA	SKSKDPGSPQPNQEA	14.571	7.372
CapZ-interacting protein	*Rcsd1*	S68	VELGQNGEEKS[+80]PSSTSHPPK	VELGQNGEEKSPSSTSHPPKI	11	S	PKCa	GQNGEEKSPSSTSHP	7.761	4.803
CapZ-interacting protein	*Rcsd1*	S68	VELGQNGEEKS[+80]PSSTSHPPK	VELGQNGEEKSPSSTSHPPKI	11	S	PRKCA	GQNGEEKSPSSTSHP	14.46	7.372
CapZ-interacting protein	*Rcsd1*	S68	VELGQNGEEKS[+80]PSSTSHPPK	VELGQNGEEKSPSSTSHPPKI	11	S	PRKCB	GQNGEEKSPSSTSHP	18.914	10.858
CapZ-interacting protein	*Rcsd1*	S53	VKSS[+80]PLIEK	SHPPKIKVKSSPLIEKLQANL	11	S	PRKCA	PKIKVKSSPLIEKLQ	11.404	7.372
Catenin alpha-1	*Ctnna1*	S657	SRTS[+80]VQTEDDQLIAGQSAR	TEDFDVRSRTSVQTEDDQLIA	11	S	PKC	FDVRSRTSVQTEDDQ	2.108	1.416
Catenin alpha-1	*Ctnna1*	S657	SRTS[+80]VQTEDDQLIAGQSAR	TEDFDVRSRTSVQTEDDQLIA	11	S	PKCa	FDVRSRTSVQTEDDQ	10.104	4.803
Catenin alpha-1	*Ctnna1*	S657	SRTS[+80]VQTEDDQLIAGQSAR	TEDFDVRSRTSVQTEDDQLIA	11	S	PRKCA	FDVRSRTSVQTEDDQ	19.409	7.372
Catenin alpha-1	*Ctnna1*	S657	SRTS[+80]VQTEDDQLIAGQSAR	TEDFDVRSRTSVQTEDDQLIA	11	S	PRKCD	FDVRSRTSVQTEDDQ	2.772	2.514
Catenin alpha-1	*Ctnna1*	T654	T[+80]SVQT[+80]EDDQLIAGQSAR	ETEDFDVRSRTSVQTEDDQLI	11	T	PKC	DFDVRSRTSVQTEDD	1.59	1.416
Catenin alpha-1	*Ctnna1*	T654	T[+80]SVQT[+80]EDDQLIAGQSAR	ETEDFDVRSRTSVQTEDDQLI	11	T	PKCa	DFDVRSRTSVQTEDD	9.461	4.803
Catenin alpha-1	*Ctnna1*	T654	T[+80]SVQT[+80]EDDQLIAGQSAR	ETEDFDVRSRTSVQTEDDQLI	11	T	PRKCA	DFDVRSRTSVQTEDD	14.172	7.372
Catenin alpha-1	*Ctnna1*	T654	T[+80]SVQT[+80]EDDQLIAGQSAR	FDVRSRTSVQTEDDQLIAGQS	11	T	PRKCA	RSRTSVQTEDDQLIA	9.354	7.372
Catenin alpha-1	*Ctnna1*	S643	TPEELDDS[+80]DFET[+80]EDFDVR	MIRTPEELDDSDFETEDFDVR	11	S	PRKCA	TPEELDDSDFETEDF	8.081	7.372
Cdc42 effector protein 1	*Cdc42ep1*	S347	ELAGVLPQVHGS[+80]WES[+80]LNEEWSAPPASSR	LAGVLPQVHGSWESLNEEWSA	11	S	PRKCA	VLPQVHGSWESLNEE	8.49	7.372
Cdc42 effector protein 1	*Cdc42ep1*	S347	ELAGVLPQVHGS[+80]WES[+80]LNEEWSAPPASSR	VLPQVHGSWESLNEEWSAPPA	11	S	PRKCA	QVHGSWESLNEEWSA	16.606	7.372
CLIP-associating protein 2	*Clasp2*	S581	VLNTGS[+80]DVEEAVADALK	VSAMRVLNTGSDVEEAVADAL	11	S	PRKCA	MRVLNTGSDVEEAVA	11.364	7.372
Cordon-bleu protein-like 1	*Cobll1*	S666	ENHLTAS[+80]PGPDQK	KSSRENHLTASPGPDQKLNQP	11	S	PRKCA	RENHLTASPGPDQKL	9.263	7.372
Cordon-bleu protein-like 1	*Cobll1*	S666	ENHLTAS[+80]PGPDQK	QSSRENHLTASPGPDQKSNQP	11	S	PRKCA	RENHLTASPGPDQKS	8.742	7.372
Cysteine and glycine-rich protein 3	*Csrp3*	S111	AATTSNPSKFS[+80]AK	AATTSNPSKFSAKFGESEKCP	11	S	PKC	TSNPSKFSAKFGESE	4.432	1.416
Cysteine and glycine-rich protein 3	*Csrp3*	S111	AATTSNPSKFS[+80]AK	AATTSNPSKFSAKFGESEKCP	11	S	PKCa	TSNPSKFSAKFGESE	10.63	4.803

Cysteine and glycine-rich protein 3	*Csrp3*	S111	AATTSNPSKFS[+80]AK	AATTSNPSKFSAKFGESEKCP	11	S	PKCd	TSNPSKFSAKFGESE	3.824	3.771
Cysteine and glycine-rich protein 3	*Csrp3*	S111	AATTSNPSKFS[+80]AK	AATTSNPSKFSAKFGESEKCP	11	S	PRKCA	TSNPSKFSAKFGESE	18.924	7.372
Cysteine and glycine-rich protein 3	*Csrp3*	S111	AATTSNPSKFS[+80]AK	AATTSNPSKFSAKFGESEKCP	11	S	PRKCB	TSNPSKFSAKFGESE	14.362	10.858
Cytoplasmic linker-associated protein 1	*Clasp1*	S1088	NSSNAGVGS[+80]PSNTIGR	LKNSSNAGVGSPSNTIGRTPS	11	S	PRKCA	SSNAGVGSPSNTIGR	15.566	7.372
Desmin	*Des*	S25	RTFGGAPGFS[+80]LGS[+80]PLSSPVFPR	FGGAPGFSLGSPLSSPVFPRA	11	S	PKC	EKSAVRPSPSPERSS	1.813	1.416
Desmin	*Des*	S25	RTFGGAPGFS[+80]LGS[+80]PLSSPVFPR	RRTFGGAPGFSLGSPLSSPVF	11	S	PKCa	APGFSLGSPLSSPVF	5.152	4.803
Desmin	*Des*	S25	RTFGGAPGFS[+80]LGS[+80]PLSSPVFPR	FGGAPGFSLGSPLSSPVFPRA	11	S	PKCa	EKSAVRPSPSPERSS	7.743	4.803
Desmin	*Des*	S25	RTFGGAPGFS[+80]LGS[+80]PLSSPVFPR	RRTFGGAPGFSLGSPLSSPVF	11	S	PRKCA	APGFSLGSPLSSPVF	12.48	7.372
Desmin	*Des*	S25	RTFGGAPGFS[+80]LGS[+80]PLSSPVFPR	FGGAPGFSLGSPLSSPVFPRA	11	S	PRKCA	EKSAVRPSPSPERSS	11.374	7.372
Desmin	*Des*	S25	RTFGGAPGFS[+80]LGS[+80]PLSSPVFPR	FGGAPGFSLGSPLSSPVFPRA	11	S	PRKCB	EKSAVRPSPSPERSS	15.224	10.858
Desmin	*Des*	S300	S[+80]KVS[+80]DLTQAANK	EAEEWYKSKVSDLTQAANKNN	11	S	PKC	EWYKSKVSDLTQAAN	2.097	1.416
Desmin	*Des*	S300	S[+80]KVS[+80]DLTQAANK	EAEEWYKSKVSDLTQAANKNN	11	S	PKCa	EWYKSKVSDLTQAAN	6.287	4.803
Desmin	*Des*	S300	S[+80]KVS[+80]DLTQAANK	NISEAEEWYKSKVSDLTQAAN	11	S	PRKCA	EAEEWYKSKVSDLTQ	13.904	7.372
Desmin	*Des*	S300	S[+80]KVS[+80]DLTQAANK	EAEEWYKSKVSDLTQAANKNN	11	S	PRKCA	EWYKSKVSDLTQAAN	11.46	7.372
Desmin	*Des*	S25	TFGGAPGFS[+80]LGSPLS[+80]SPVFPR	APGFSLGSPLSSPVFPRAGFG	11	S	PRKCA	FSLGSPLSSPVFPRA	8.591	7.372
Drebrin	*Dbn1*	S142	LSS[+80]PVLHR	RLSNGLARLSSPVLHRLRLRE	11	S	PKC	NGLARLSSPVLHRLR	2.057	1.416
Drebrin	*Dbn1*	S142	LSS[+80]PVLHR	RLSNGLARLSSPVLHRLRLRE	11	S	PRKCA	NGLARLSSPVLHRLR	7.707	7.372
Erythrocyte membrane protein band 4.1-like 2	*Epb41l2*	S57	ASQPGPTAESQS[+80]SPHR	SQPGPTAESQSSPHRRKRGKD	11	S	PKC	GPTAESQSSPHRRKR	1.682	1.416
Erythrocyte membrane protein band 4.1-like 2	*Epb41l2*	S57	ASQPGPTAESQS[+80]SPHR	SQPGPTAESQSSPHRRKRGKD	11	S	PKCa	GPTAESQSSPHRRKR	11.196	4.803
Erythrocyte membrane protein band 4.1-like 2	*Epb41l2*	S57	ASQPGPTAESQS[+80]SPHR	SQPGPTAESQSSPHRRKRGKD	11	S	PRKCA	GPTAESQSSPHRRKR	12.732	7.372
Erythrocyte membrane protein band 4.1-like 2	*Epb41l2*	S57	ASQPGPTAESQS[+80]SPHR	SQPGPTAESQSSPHRRKRGKD	11	S	PRKCB	GPTAESQSSPHRRKR	13.672	10.858
FH1/FH2 domain-containing protein 1	*Fhod1*	S141	RSLFS[+80]LK	SGPELRRSLFSLKQIFQEDKD	11	S	PKC	ELRRSLFSLKQIFQE	4.333	1.416
FH1/FH2 domain-containing protein 1	*Fhod1*	S141	RSLFS[+80]LK	SGPELRRSLFSLKQIFQEDKD	11	S	PKCa	ELRRSLFSLKQIFQE	9.661	4.803
FH1/FH2 domain-containing protein 1	*Fhod1*	S141	RSLFS[+80]LK	SGPELRRSLFSLKQIFQEDKD	11	S	PRKCA	ELRRSLFSLKQIFQE	23.859	7.372
Filamin-A-interacting protein 1	*Filip1*	S979	AMS[+80]PVTITTISR	DPTLGPERAMSPVTITTISRE	11	S	PKCa	LGPERAMSPVTITTI	6.104	4.803
Filamin-A-interacting protein 1	*Filip1*	S979	AMS[+80]PVTITTISR	DPTLGPERAMSPVTITTISRE	11	S	PRKCA	LGPERAMSPVTITTI	11.652	7.372
Filamin-C	*Flnc*	S2234	ERLGS[+80]FGSITR	GDFLGRERLGSFGSITRQQEG	11	S	PKC	LGRERLGSFGSITRQ	2.103	1.416
Filamin-C	*Flnc*	S2234	ERLGS[+80]FGSITR	GDFLGRERLGSFGSITRQQEG	11	S	PKCa	LGRERLGSFGSITRQ	7.961	4.803
Filamin-C	*Flnc*	S2234	ERLGS[+80]FGSITR	GDFLGRERLGSFGSITRQQEG	11	S	PRKCA	LGRERLGSFGSITRQ	16.01	7.372
Filamin-C	*Flnc*	S2237	LGSFGS[+80]ITR	LGRERLGSFGSITRQQEGEAS	11	S	PKC	ERLGSFGSITRQQEG	1.968	1.416
Filamin-C	*Flnc*	S2237	LGSFGS[+80]ITR	LGRERLGSFGSITRQQEGEAS	11	S	PKCa	ERLGSFGSITRQQEG	10.7	4.803
Filamin-C	*Flnc*	S2237	LGSFGS[+80]ITR	LGRERLGSFGSITRQQEGEAS	11	S	PRKCA	ERLGSFGSITRQQEG	19.641	7.372

Filamin-C	*Flnc*	S2633	GASYSSIPKFS[+80]SDASK	GASYSSIPKFSSDASKVVTRG	11	S	PKCa	YSSIPKFSSDASKVV	7.074	4.803
Filamin-C	*Flnc*	S2633	GASYSSIPKFS[+80]SDASK	GASYSSIPKFSSDASKVVTRG	11	S	PRKCA	YSSIPKFSSDASKVV	14.773	7.372
Filamin-C	*Flnc*	S2633	GASYSSIPKFS[+80]SDASK	GASYSSIPKFSSDASKVVTRG	11	S	PRKCB	YSSIPKFSSDASKVV	12.897	10.858
Formin-like protein 1	*Fmnl1*	S965	EAAADTSGREEPPAPKS[+80]PPK	SGREEPPAPKSPPKARRQQMD	11	S	PKC	EEPPAPKSPPKARRQ	3.024	1.416
Formin-like protein 1	*Fmnl1*	S965	EAAADTSGREEPPAPKS[+80]PPK	SGREEPPAPKSPPKARRQQMD	11	S	PKCa	EEPPAPKSPPKARRQ	8.652	4.803
Formin-like protein 1	*Fmnl1*	S965	EAAADTSGREEPPAPKS[+80]PPK	SGREEPPAPKSPPKARRQQMD	11	S	PRKCA	EEPPAPKSPPKARRQ	15.874	7.372
Fructose-bisphosphate aldolase A	*Aldoa*	S36	IVAPGKGILAADES[+80]TGSIAK	PGKGILAADESTGSIAKRLQS	11	S	PKC	GILAADESTGSIAKR	2.899	1.416
Fructose-bisphosphate aldolase A	*Aldoa*	S36	IVAPGKGILAADES[+80]TGSIAK	PGKGILAADESTGSIAKRLQS	11	S	PRKCA	GILAADESTGSIAKR	9.828	7.372
Fructose-bisphosphate aldolase A	*Aldoa*	T37	IVAPGKGILAADEST[+80]GSIAKR	GKGILAADESTGSIAKRLQSI	11	T	PKC	ILAADESTGSIAKRL	2.107	1.416
Fructose-bisphosphate aldolase A	*Aldoa*	T37	IVAPGKGILAADEST[+80]GSIAKR	GKGILAADESTGSIAKRLQSI	11	T	PRKCA	ILAADESTGSIAKRL	8.879	7.372
Fructose-bisphosphate aldolase A	*Aldoa*	T52	RLQSIGTENT[+80]EENRR	KRLQSIGTENTEENRRFYRQL	11	T	PKCa	QSIGTENTEENRRFY	4.948	4.803
Fructose-bisphosphate aldolase A	*Aldoa*	T52	RLQSIGTENT[+80]EENRR	KRLQSIGTENTEENRRFYRQL	11	T	PRKCA	QSIGTENTEENRRFY	13.682	7.372
Heat shock protein beta-1	*Hspb1*	S86	QLS[+80]SGVSEIR	AFSRALNRQLSSGVSEIRQTA	11	S	PKC	RALNRQLSSGVSEIR	1.985	1.416
Heat shock protein beta-1	*Hspb1*	S86	QLS[+80]SGVSEIR	AFSRALNRQLSSGVSEIRQTA	11	S	PKCa	RALNRQLSSGVSEIR	5.23	4.803
Heat shock protein beta-1	*Hspb1*	S86	QLS[+80]SGVSEIR	AFSRALNRQLSSGVSEIRQTA	11	S	PRKCA	RALNRQLSSGVSEIR	13.596	7.372
Heat shock protein beta-1	*Hspb1*	S13	S[+80]PSWEPFRDWYPAHSR	ERRVPFSLLRSPSWEPFRDWY	11	S	PRKCA	VPFSLLRSPSWEPFR	8.672	7.372
Heat shock protein beta-1	*Hspb1*	S15	SPS[+80]WEPFR	RVPFSLLRSPSWEPFRDWYPA	11	S	PKC	FSLLRSPSWEPFRDW	2.445	1.416
Heat shock protein beta-1	*Hspb1*	S15	SPS[+80]WEPFR	RVPFSLLRSPSWEPFRDWYPA	11	S	PKCa	FSLLRSPSWEPFRDW	6.591	4.803
Heat shock protein beta-1	*Hspb1*	S15	SPS[+80]WEPFR	RVPFSLLRSPSWEPFRDWYPA	11	S	PRKCA	FSLLRSPSWEPFRDW	15.414	7.372
Heat shock protein beta-3	*Hspb3*	T64	ALAEDSDSAGT[+80]PPGEGK	ALAEDSDSAGTPPGEGKSRFQ	11	T	PRKCA	EDSDSAGTPPGEGKS	9.192	7.372
Influenza virus NS1A-binding protein homolog	*Ivns1abp*	S246	LLDGNPLDGQAEVFGS[+80]DDDHIQFVQK	PLDGQAEVFGSDDDHIQFVQK	11	S	PRKCA	GQAEVFGSDDDHIQF	9.101	7.372
Influenza virus NS1A-binding protein homolog	*Ivns1abp*	S336	S[+80]LSFEMQPDELLEKPMSPMQYAR	SPTSTPKLSKSLSFEMQPDEL	11	S	PKCa	STPKLSKSLSFEMQP	7.448	4.803
Influenza virus NS1A-binding protein homolog	*Ivns1abp*	S336	S[+80]LSFEMQPDELLEKPMSPMQYAR	SPTSTPKLSKSLSFEMQPDEL	11	S	PRKCA	STPKLSKSLSFEMQP	14.99	7.372
Influenza virus NS1A-binding protein homolog	*Ivns1abp*	S338	SLS[+80]FEMQPDELLEKPMSPMQYAR	TSTPKLSKSLSFEMQPDELLE	11	S	PKC	PKLSKSLSFEMQPDE	2.957	1.416
Influenza virus NS1A-binding protein homolog	*Ivns1abp*	S338	SLS[+80]FEMQPDELLEKPMSPMQYAR	TSTPKLSKSLSFEMQPDELLE	11	S	PKCa	PKLSKSLSFEMQPDE	7.9	4.803
Influenza virus NS1A-binding protein homolog	*Ivns1abp*	S338	SLS[+80]FEMQPDELLEKPMSPMQYAR	TSTPKLSKSLSFEMQPDELLE	11	S	PRKCA	PKLSKSLSFEMQPDE	20.081	7.372
Influenza virus NS1A-binding protein homolog	*Ivns1abp*	S338	SLS[+80]FEMQPDELLEKPMSPMQYAR	TSTPKLSKSLSFEMQPDELLE	11	S	PRKCB	PKLSKSLSFEMQPDE	12.655	10.858
Junction plakoglobin	*Jup*	T78	KTTTYTQGVPQSQGDLEYQMST[+80]TAR	SQGDLEYQMSTTARAKRVREA	11	T	PKC	DLEYQMSTTARAKRV	3.206	1.416
Junction plakoglobin	*Jup*	T78	KTTTYTQGVPQSQGDLEYQMST[+80]TAR	SQGDLEYQMSTTARAKRVREA	11	T	PKCa	DLEYQMSTTARAKRV	11.648	4.803
Junction plakoglobin	*Jup*	T78	KTTTYTQGVPQSQGDLEYQMST[+80]TAR	SQGDLEYQMSTTARAKRVREA	11	T	PRKCA	DLEYQMSTTARAKRV	15.884	7.372

KN motif and ankyrin repeat domain-containing protein 1	*Kank1*	S323	SYS[+80]AGNASQLELLSR	EACGVRKRSYSAGNASQLELL	11	S	PKC	GVRKRSYSAGNASQL	3.912	1.416
KN motif and ankyrin repeat domain-containing protein 1	*Kank1*	S323	SYS[+80]AGNASQLELLSR	EACGVRKRSYSAGNASQLELL	11	S	PKCa	GVRKRSYSAGNASQL	7.757	4.803
KN motif and ankyrin repeat domain-containing protein 1	*Kank1*	S323	SYS[+80]AGNASQLELLSR	EACGVRKRSYSAGNASQLELL	11	S	PRKCA	GVRKRSYSAGNASQL	13.758	7.372
Leiomodin-2	*Lmod2*	S394	GTPGSS[+80]PYASPR	KVWQRGTPGSSPYASPRQSPW	11	S	PKCa	QRGTPGSSPYASPRQ	5.278	4.803
Leiomodin-2	*Lmod2*	S394	GTPGSS[+80]PYASPR	KVWQRGTPGSSPYASPRQSPW	11	S	PRKCA	QRGTPGSSPYASPRQ	10.742	7.372
Leiomodin-2	*Lmod2*	S399	GTPGSSPYAS[+80]PR	RGTPGSSPYASPRQSPWSSPK	11	S	PKCa	PGSSPYASPRQSPWS	5.47	4.803
Leiomodin-2	*Lmod2*	S399	GTPGSSPYAS[+80]PR	RGTPGSSPYASPRQSPWSSPK	11	S	PRKCA	PGSSPYASPRQSPWS	19.338	7.372
Leiomodin-2	*Lmod2*	S514	MEESS[+80]RPS[+80]TPQR	SVQEKKMEESSRPSTPQRSAH	11	S	PKC	EKKMEESSRPSTPQR	2.181	1.416
Leiomodin-2	*Lmod2*	S514	MEESS[+80]RPS[+80]TPQR	EKKMEESSRPSTPQRSAHENL	11	S	PKC	MEESSRPSTPQRSAH	3.361	1.416
Leiomodin-2	*Lmod2*	S514	MEESS[+80]RPS[+80]TPQR	SVQEKKMEESSRPSTPQRSAH	11	S	PKCa	EKKMEESSRPSTPQR	7.087	4.803
Leiomodin-2	*Lmod2*	S514	MEESS[+80]RPS[+80]TPQR	EKKMEESSRPSTPQRSAHENL	11	S	PKCa	MEESSRPSTPQRSAH	13.861	4.803
Leiomodin-2	*Lmod2*	S514	MEESS[+80]RPS[+80]TPQR	SVQEKKMEESSRPSTPQRSAH	11	S	PRKCA	EKKMEESSRPSTPQR	14.247	7.372
Leiomodin-2	*Lmod2*	S514	MEESS[+80]RPS[+80]TPQR	EKKMEESSRPSTPQRSAHENL	11	S	PRKCA	MEESSRPSTPQRSAH	22.434	7.372
Leiomodin-2	*Lmod2*	S514	MEESS[+80]RPS[+80]TPQR	SVQEKKMEESSRPSTPQRSAH	11	S	PRKCB	EKKMEESSRPSTPQR	14.414	10.858
Leiomodin-2	*Lmod2*	S514	MEESS[+80]RPS[+80]TPQR	EKKMEESSRPSTPQRSAHENL	11	S	PRKCB	MEESSRPSTPQRSAH	12.414	10.858
Leiomodin-2	*Lmod2*	S514	MEESS[+80]RPST[+80]PQR	KKMEESSRPSTPQRSAHENLM	11	T	PKC	EESSRPSTPQRSAHE	2.341	1.416
Leiomodin-2	*Lmod2*	S514	MEESS[+80]RPST[+80]PQR	KKMEESSRPSTPQRSAHENLM	11	T	PKCa	EESSRPSTPQRSAHE	9.443	4.803
Leiomodin-2	*Lmod2*	S514	MEESS[+80]RPST[+80]PQR	KKMEESSRPSTPQRSAHENLM	11	T	PRKCA	EESSRPSTPQRSAHE	18.556	7.372
Leiomodin-2	*Lmod2*	S405	QSPWS[+80]SPK	YASPRQSPWSSPKVSKKVHTG	10	S	PKC	SPRQSPWSSPKVSKK	1.438	1.416
Leiomodin-2	*Lmod2*	S405	QSPWS[+80]SPK	YASPRQSPWSSPKVSKKVHTG	10	S	PKCa	SPRQSPWSSPKVSKK	6.757	4.803
Leiomodin-2	*Lmod2*	S405	QSPWS[+80]SPK	YASPRQSPWSSPKVSKKVHTG	10	S	PRKCA	SPRQSPWSSPKVSKK	10.778	7.372
Leiomodin-2	*Lmod2*	S406	QSPWSS[+80]PK	YASPRQSPWSSPKVSKKVHTG	11	S	PKC	PRQSPWSSPKVSKKV	2.884	1.416
Leiomodin-2	*Lmod2*	S406	QSPWSS[+80]PK	YASPRQSPWSSPKVSKKVHTG	11	S	PKCa	PRQSPWSSPKVSKKV	7.826	4.803
Leiomodin-2	*Lmod2*	S406	QSPWSS[+80]PK	YASPRQSPWSSPKVSKKVHTG	11	S	PRKCA	PRQSPWSSPKVSKKV	14.111	7.372
Leiomodin-2	*Lmod2*	S422	SRPPS[+80]PVAPPPPPPPPPLPPHMLPPPPPPPAPPLPEK	KVHTGRSRPPSPVAPPPPPP	11	S	PKCa	TGRSRPPSPVAPPPP	6.739	4.803
Leiomodin-2	*Lmod2*	S422	SRPPS[+80]PVAPPPPPPPPPLPPHMLPPPPPPPAPPLPEK	KVHTGRSRPPSPVAPPPPPP	11	S	PRKCA	TGRSRPPSPVAPPPP	13.51	7.372
LIM and calponin homology domains-containing protein 1	*Limch1*	S752	MPETDQLHLPNLNSQADS[+80]PSSEK	HLPNLNSQADSPSSEKSPAST	11	S	PKCa	NLNSQADSPSSEKSP	6.143	4.803
LIM and calponin homology domains-containing protein 1	*Limch1*	S752	MPETDQLHLPNLNSQADS[+80]PSSEK	HLPNLNSQADSPSSEKSPAST	11	S	PRKCA	NLNSQADSPSSEKSP	14.015	7.372
LIM and calponin homology domains-containing protein 1	*Limch1*	T215	SRQT[+80]PS[+80]PDVVLR	SFGSRSRQTPSPDVVLRGSSD	9	T	PKC	FGSRSRQTPSPDVVL	1.468	1.416
LIM and calponin homology domains-containing protein 1	*Limch1*	T215	SRQT[+80]PS[+80]PDVVLR	LDSFGSRSRQTPSPDVVLRG	13	S	PKCa	SRSRQTPSPDVVLRG	5.491	4.803

LIM and calponin homology domains-containing protein 1	*Limch1*	T215	SRQT[+80]PS[+80]PDVVLR	SFGSRSRQTPSPDVVLRGSSD	9	T	PRKCA	FGSRSRQTPSPDVVL	8.737	7.372
LIM and calponin homology domains-containing protein 1	*Limch1*	T215	SRQT[+80]PS[+80]PDVVLR	LDSFGSRSRQTPSPDVVLRG	13	S	PRKCA	SRSRQTPSPDVVLRG	14.884	7.372
LIM and calponin homology domains-containing protein 1	*Limch1*	S303	SWSTATS[+80]PLGGERPFR	EFRKSWSTATSPLGGERPFRY	11	S	PKCa	KSWSTATSPLGGERP	5.983	4.803
LIM and calponin homology domains-containing protein 1	*Limch1*	S303	SWSTATS[+80]PLGGERPFR	EYRKSWSTATSPLGGERPFRY	11	S	PKCa	KSWSTATSPLGGERP	5.983	4.803
LIM and calponin homology domains-containing protein 1	*Limch1*	S303	SWSTATS[+80]PLGGERPFR	EFRKSWSTATSPLGGERPFRY	11	S	PRKCA	KSWSTATSPLGGERP	10.192	7.372
LIM and calponin homology domains-containing protein 1	*Limch1*	S303	SWSTATS[+80]PLGGERPFR	EYRKSWSTATSPLGGERPFRY	11	S	PRKCA	KSWSTATSPLGGERP	10.192	7.372
LIM domain and actin-binding protein 1	*Lima1*	S488	GENEETLGRPAQPPSAGETPHS[+80]PGVEDAPIAK	QPPSAGETPHSPGVEDAPIAK	11	S	PRKCA	SAGETPHSPGVEDAP	8.379	7.372
LIM domain-binding protein 3	*Ldb3*	S44	AAQSQLS[+80]QGDLVVAIDGVNTDTMTHLEAQNK	PGSKAAQSQLSQGDLVVAIDG	11	S	PRKCA	KAAQSQLSQGDLVVA	11.237	7.372
LIM domain-binding protein 3	*Ldb3*	S121	DPSLDTNSSLATPS[+80]PSPEAR	LDTNSSLATPSPSPEARASPG	11	S	PKC	NSSLATPSPSPEARA	1.783	1.416
LIM domain-binding protein 3	*Ldb3*	S121	DPSLDTNSSLATPS[+80]PSPEAR	LDTNSSLATPSPSPEARASPG	11	S	PKCa	NSSLATPSPSPEARA	7.6	4.803
LIM domain-binding protein 3	*Ldb3*	S121	DPSLDTNSSLATPS[+80]PSPEAR	LDTNSSLATPSPSPEARASPG	11	S	PRKCA	NSSLATPSPSPEARA	13.212	7.372
LIM domain-binding protein 3	*Ldb3*	S123	DPSLDTNSSLATPSPS[+80]PEAR	TNSSLATPSPSPEARASPGTS	11	S	PKCa	SLATPSPSPEARASP	6.591	4.803
LIM domain-binding protein 3	*Ldb3*	S123	DPSLDTNSSLATPSPS[+80]PEAR	TNSSLATPSPSPEARASPGTS	11	S	PRKCA	SLATPSPSPEARASP	14.535	7.372
LIM domain-binding protein 3	*Ldb3*	S123	DPSLDTNSSLATPSPS[+80]PEAR	TNSSLATPSPSPEARASPGTS	11	S	PRKCB	SLATPSPSPEARASP	11.569	10.858
Macrophage-capping protein	*Capg*	S341	YSPNTQVEILPQGRES[+80]PIFK	QVEILPQGRESPIFKQFFKNW	11	S	PKC	ILPQGRESPIFKQFF	1.938	1.416
Macrophage-capping protein	*Capg*	S341	YSPNTQVEILPQGRES[+80]PIFK	QVEILPQGRESPIFKQFFKNW	11	S	PRKCA	ILPQGRESPIFKQFF	10.662	7.372
Misshapen-like kinase 1	*Mink1*	S765	SDSVLPASHGHLPQAGS[+80]LER	ASHGHLPQAGSLERNRNRVGA	11	S	PKC	GHLPQAGSLERNRNR	1.417	1.416
Misshapen-like kinase 1	*Mink1*	S765	SDSVLPASHGHLPQAGS[+80]LER	ASHGHLPQAGSLERNRNRVGA	11	S	PKCa	GHLPQAGSLERNRNR	12.252	4.803
Misshapen-like kinase 1	*Mink1*	S765	SDSVLPASHGHLPQAGS[+80]LER	ASHGHLPQAGSLERNRNRVGA	11	S	PRKCA	GHLPQAGSLERNRNR	22.222	7.372
Misshapen-like kinase 1	*Mink1*	S765	SDSVLPASHGHLPQAGS[+80]LER	ASHGHLPQAGSLERNRNRVGA	11	S	PRKCB	GHLPQAGSLERNRNR	13.586	10.858
Myomesin-2	*Myom2*	S535	NYVVLSWDPPS[+80]PR	NYVVLSWDPPSPRGKEPLMYF	11	S	PKC	VLSWDPPSPRGKEPL	2.173	1.416
Myomesin-2	*Myom2*	S535	NYVVLSWDPPS[+80]PR	NYVVLSWDPPSPRGKEPLMYF	11	S	PKCa	VLSWDPPSPRGKEPL	7.857	4.803
Myomesin-2	*Myom2*	S535	NYVVLSWDPPS[+80]PR	NYVVLSWDPPSPRGKEPLMYF	11	S	PRKCA	VLSWDPPSPRGKEPL	19.232	7.372
Myopalladin	*Mypn*	S622	ISEPS[+80]SPVKEPPPVLAKPK	NGQEARISEPSSPVKEPPPVL	11	S	PKC	EARISEPSSPVKEPP	1.461	1.416
Myopalladin	*Mypn*	S622	ISEPS[+80]SPVKEPPPVLAKPK	NGQEARISEPSSPVKEPPPVL	11	S	PKCa	EARISEPSSPVKEPP	7.422	4.803
Myopalladin	*Mypn*	S622	ISEPS[+80]SPVKEPPPVLAKPK	NGQEARISEPSSPVKEPPPVL	11	S	PRKCA	EARISEPSSPVKEPP	14.253	7.372
Myopalladin	*Mypn*	S622	ISEPS[+80]SPVKEPPPVLAKPK	NGQEARISEPSSPVKEPPPVL	11	S	PRKCB	EARISEPSSPVKEPP	12.603	10.858
Myopalladin	*Mypn*	S623	ISEPSS[+80]PVKEPPPVLAKPK	GQEARISEPSSPVKEPPPVLA	11	S	PKCa	ARISEPSSPVKEPPP	6.083	4.803
Myopalladin	*Mypn*	S623	ISEPSS[+80]PVKEPPPVLAKPK	GQEARISEPSSPVKEPPPVLA	11	S	PRKCA	ARISEPSSPVKEPPP	12.409	7.372
Myopalladin	*Mypn*	S737	TVS[+80]KESLLMTHPSTQGR	NTPQTIQRTVSKESLLMTHPS	11	S	PKC	QTIQRTVSKESLLMT	1.54	1.416
Myopalladin	*Mypn*	S737	TVS[+80]KESLLMTHPSTQGR	NTPQTIQRTVSKESLLMTHPS	11	S	PKCa	QTIQRTVSKESLLMT	5.73	4.803
Myopalladin	*Mypn*	S737	TVS[+80]KESLLMTHPSTQGR	NTPQTIQRTVSKESLLMTHPS	11	S	PRKCA	QTIQRTVSKESLLMT	16.773	7.372

Myosin XVIIIb	*Myo18b*	S2298	VKS[+80]PLGAEGNAGATGGLSR	GDLSLRTRVKSPLGAEGNAGA	11	S	PKC	SLRTRVKSPLGAEGN	1.575	1.416
Myosin XVIIIb	*Myo18b*	S2298	VKS[+80]PLGAEGNAGATGGLSR	GDLSLRTRVKSPLGAEGNAGA	11	S	PKCa	SLRTRVKSPLGAEGN	6.409	4.803
Myosin XVIIIb	*Myo18b*	S2298	VKS[+80]PLGAEGNAGATGGLSR	GDLSLRTRVKSPLGAEGNAGA	11	S	PRKCA	SLRTRVKSPLGAEGN	16.035	7.372
Myosin-1	*Myh1*	S1373	ANS[+80]EVAQWR	ELQRAMSKANSEVAQWRTKYE	11	S	PKC	RAMSKANSEVAQWRT	1.79	1.416
Myosin-1	*Myh1*	S1373	ANS[+80]EVAQWR	ELQRAMSKANSEVAQWRTKYE	11	S	PKCa	RAMSKANSEVAQWRT	6.526	4.803
Myosin-1	*Myh1*	S1373	ANS[+80]EVAQWR	ELQRAMSKANSEVAQWRTKYE	11	S	PRKCA	RAMSKANSEVAQWRT	16.04	7.372
Myosin-11	*Myh11*	S1951	RVIENTDGS[+80]EEEMDAR	GRRVIENTDGSEEEMDARDSD	11	S	PRKCA	VIENTDGSEEEMDAR	13.51	7.372
Myosin-6	*Myh6*	S1089	EFDIS[+80]QQNSK	EKLKKKEFDISQQNSKIEDEQ	11	S	PKC	KKKEFDISQQNSKIE	3.119	1.416
Myosin-6	*Myh6*	S1089	EFDIS[+80]QQNSK	EKLKKKEFDISQQNSKIEDEQ	11	S	PRKCA	KKKEFDISQQNSKIE	18.343	7.372
Myosin-6	*Myh6*	S1235	EKSEFKLELDDVTS[+80]NMEQIIK	EFKLELDDVTSNMEQIIKAKA	11	S	PRKCA	LELDDVTSNMEQIIK	14.778	7.372
Myosin-6	*Myh6*	S1270	VKLEEAQRS[+80]LNDFTTQR	YRVKLEEAQRSLNDFTTQRAK	11	S	PKC	KLEEAQRSLNDFTTQ	2.097	1.416
Myosin-6	*Myh6*	S1270	VKLEEAQRS[+80]LNDFTTQR	YRVKLEEAQRSLNDFTTQRAK	11	S	PKCa	KLEEAQRSLNDFTTQ	7.978	4.803
Myosin-6	*Myh6*	S1270	VKLEEAQRS[+80]LNDFTTQR	YRVKLEEAQRSLNDFTTQRAK	11	S	PRKCA	KLEEAQRSLNDFTTQ	21.475	7.372
Myosin-7	*Myh7*	T1019	ALQEAHQQALDDLQAEEDKVNT[+80]LTK	DLQAEEDKVNTLTKAKVKLEQ	11	T	PKC	AEEDKVNTLTKAKVK	3.141	1.416
Myosin-7	*Myh7*	T1019	ALQEAHQQALDDLQAEEDKVNT[+80]LTK	DLQAEEDKVNTLTKSKVKLEQ	11	T	PKC	AEEDKVNTLTKSKVK	2.714	1.416
Myosin-7	*Myh7*	T1019	ALQEAHQQALDDLQAEEDKVNT[+80]LTK	DLQAEEDKVNTLTKAKVKLEQ	11	T	PKCa	AEEDKVNTLTKAKVK	7.896	4.803
Myosin-7	*Myh7*	T1019	ALQEAHQQALDDLQAEEDKVNT[+80]LTK	DLQAEEDKVNTLTKSKVKLEQ	11	T	PKCa	AEEDKVNTLTKSKVK	9.578	4.803
Myosin-7	*Myh7*	T1019	ALQEAHQQALDDLQAEEDKVNT[+80]LTK	DLQAEEDKVNTLTKAKVKLEQ	11	T	PRKCA	AEEDKVNTLTKAKVK	17.783	7.372
Myosin-7	*Myh7*	T1019	ALQEAHQQALDDLQAEEDKVNT[+80]LTK	DLQAEEDKVNTLTKSKVKLEQ	11	T	PRKCA	AEEDKVNTLTKSKVK	19.207	7.372
Myosin-7	*Myh7*	T210	DQT[+80]PGKGTLEDQIIQANPALEAFGNAK	AIGDRSKKDQTPGKGTLEDQI	11	T	PKC	DRSKKDQTPGKGTLE	2.899	1.416
Myosin-7	*Myh7*	T210	DQT[+80]PGKGTLEDQIIQANPALEAFGNAK	AIGDRSKKDQTPGKGTLEDQI	11	T	PRKCA	DRSKKDQTPGKGTLE	13.268	7.372
Myosin-7	*Myh7*	S1222	EKS[+80]EFKLELDDVTSNMEQIIK	RVKQKLEKEKSEFKLELDDVT	11	S	PKC	QKLEKEKSEFKLELD	2.704	1.416
Myosin-7	*Myh7*	S1222	EKS[+80]EFKLELDDVTSNMEQIIK	RVKQKLEKEKSEFKLELDDVT	11	S	PKCa	QKLEKEKSEFKLELD	6.796	4.803
Myosin-7	*Myh7*	S1222	EKS[+80]EFKLELDDVTSNMEQIIK	RVKQKLEKEKSEFKLELDDVT	11	S	PRKCA	QKLEKEKSEFKLELD	18.051	7.372
Myosin-7	*Myh7*	S1222	EKS[+80]EFKLELDDVTSNMEQIIK	RVKQKLEKEKSEFKLELDDVT	11	S	PRKCB	QKLEKEKSEFKLELD	11.569	10.858
Myosin-7	*Myh7*	T1309	GKLTYT[+80]QQLEDLKR	SQLTRGKLTYTQQLEDLKRQL	11	T	PKC	TRGKLTYTQQLEDLK	2.005	1.416
Myosin-7	*Myh7*	T1309	GKLTYT[+80]QQLEDLKR	SQLTRGKLTYTQQLEDLKRQL	11	T	PRKCA	TRGKLTYTQQLEDLK	10.838	7.372
Myosin-7	*Myh7*	S1102	IEDEQALGS[+80]QLQK	ARIEDEQALGSQLQKKLKELQ	11	S	PKC	EDEQALGSQLQKKLK	2.904	1.416
Myosin-7	*Myh7*	S1102	IEDEQALGS[+80]QLQK	ARIEDEQALGSQLQKKLKELQ	11	S	PKCa	EDEQALGSQLQKKLK	5.313	4.803
Myosin-7	*Myh7*	S1102	IEDEQALGS[+80]QLQK	ARIEDEQALGSQLQKKLKELQ	11	S	PRKCA	EDEQALGSQLQKKLK	13.217	7.372
Myosin-7	*Myh7*	T215	KDQTPGKGT[+80]LEDQIIQANPALEAFGNAK	SKKDQTPGKGTLEDQIIQANP	11	T	PKC	DQTPGKGTLEDQIIQ	2.605	1.416
Myosin-7	*Myh7*	T215	KDQTPGKGT[+80]LEDQIIQANPALEAFGNAK	SKKDQTPGKGTLEDQIIQANP	11	T	PRKCA	DQTPGKGTLEDQIIQ	17.146	7.372
Myosin-7	*Myh7*	S642	KGS[+80]SFQTVSALHR	DKGKGKAKKGSSFQTVSALHR	11	S	PKC	KGKAKKGSSFQTVSA	7.796	1.416
Myosin-7	*Myh7*	S642	KGS[+80]SFQTVSALHR	GKGKGGKKKGSSFQTVSALHR	11	S	PKC	KGGKKKGSSFQTVSA	6.778	1.416
Myosin-7	*Myh7*	S642	KGS[+80]SFQTVSALHR	DKGKGKAKKGSSFQTVSALHR	11	S	PKCa	KGKAKKGSSFQTVSA	10.013	4.803
Myosin-7	*Myh7*	S642	KGS[+80]SFQTVSALHR	GKGKGGKKKGSSFQTVSALHR	11	S	PKCa	KGGKKKGSSFQTVSA	10.013	4.803

Myosin-7	*Myh7*	S642	KGS[+80]SFQTVSALHR	DKGKGKAKKGSSFQTVSALHR	11	S	PRKCA	KGKAKKGSSFQTVSA	19.455	7.372
Myosin-7	*Myh7*	S642	KGS[+80]SFQTVSALHR	GKGKGGKKKGSSFQTVSALHR	11	S	PRKCA	KGGKKKGSSFQTVSA	19.455	7.372
Myosin-7	*Myh7*	S643	KGSS[+80]FQTVSALHR	KGKGKAKKGSSFQTVSALHRE	11	S	PKC	GKAKKGSSFQTVSAL	7.548	1.416
Myosin-7	*Myh7*	S643	KGSS[+80]FQTVSALHR	KGKGGKKKGSSFQTVSALHRE	11	S	PKC	GGKKKGSSFQTVSAL	9.417	1.416
Myosin-7	*Myh7*	S643	KGSS[+80]FQTVSALHR	KGKGKAKKGSSFQTVSALHRE	11	S	PKCa	GKAKKGSSFQTVSAL	10.922	4.803
Myosin-7	*Myh7*	S643	KGSS[+80]FQTVSALHR	KGKGGKKKGSSFQTVSALHRE	11	S	PKCa	GGKKKGSSFQTVSAL	10.922	4.803
Myosin-7	*Myh7*	S643	KGSS[+80]FQTVSALHR	KGKGKAKKGSSFQTVSALHRE	11	S	PKCd	GKAKKGSSFQTVSAL	4.514	3.771
Myosin-7	*Myh7*	S643	KGSS[+80]FQTVSALHR	KGKGGKKKGSSFQTVSALHRE	11	S	PKCd	GGKKKGSSFQTVSAL	4.514	3.771
Myosin-7	*Myh7*	S643	KGSS[+80]FQTVSALHR	KGKGKAKKGSSFQTVSALHRE	11	S	PRKCA	GKAKKGSSFQTVSAL	24.783	7.372
Myosin-7	*Myh7*	S643	KGSS[+80]FQTVSALHR	KGKGGKKKGSSFQTVSALHRE	11	S	PRKCA	GGKKKGSSFQTVSAL	24.783	7.372
Myosin-7	*Myh7*	S643	KGSS[+80]FQTVSALHR	KGKGKAKKGSSFQTVSALHRE	11	S	PRKCB	GKAKKGSSFQTVSAL	11.224	10.858
Myosin-7	*Myh7*	S643	KGSS[+80]FQTVSALHR	KGKGGKKKGSSFQTVSALHRE	11	S	PRKCB	GGKKKGSSFQTVSAL	11.224	10.858
Myosin-7	*Myh7*	S643	KGSS[+80]FQTVSALHR	KGKGKAKKGSSFQTVSALHRE	11	S	PRKCD	GKAKKGSSFQTVSAL	2.895	2.514
Myosin-7	*Myh7*	S643	KGSS[+80]FQTVSALHR	KGKGGKKKGSSFQTVSALHRE	11	S	PRKCD	GGKKKGSSFQTVSAL	2.895	2.514
Myosin-7	*Myh7*	S1491	LKNAYEES[+80]LEHLETFKR	LFKLKNAYEESLEHLETFKRE	11	S	PRKCA	LKNAYEESLEHLETF	12.975	7.372
Myosin-7	*Myh7*	S1491	LKNAYEES[+80]LEHLETFKR	LFKLKNAYEESLEHLETFKRE	11	S	PRKCB	LKNAYEESLEHLETF	15.466	10.858
Myosin-7	*Myh7*	S560	LYDNHLGKS[+80]NNFQKPR	AKLYDNHLGKSNNFQKPRNIK	11	S	PRKCA	YDNHLGKSNNFQKPR	15.838	7.372
Myosin-7	*Myh7*	S1140	SDLS[+80]RELEEISER	AKVEKLRSDLSRELEEISERL	11	S	PKC	EKLRSDLSRELEEIS	1.949	1.416
Myosin-7	*Myh7*	S1140	SDLS[+80]RELEEISER	AKAEKQRSDLSRELEEISERL	11	S	PKC	EKQRSDLSRELEEIS	2.503	1.416
Myosin-7	*Myh7*	S1140	SDLS[+80]RELEEISER	AKVEKLRSDLSRELEEISERL	11	S	PRKCA	EKLRSDLSRELEEIS	13.061	7.372
Myosin-7	*Myh7*	S1140	SDLS[+80]RELEEISER	AKAEKQRSDLSRELEEISERL	11	S	PRKCA	EKQRSDLSRELEEIS	13.061	7.372
Myosin-7	*Myh7*	S1478	SLS[+80]TELFK	ESSQKEARSLSTELFKLKNAY	11	S	PKC	QKEARSLSTELFKLK	1.808	1.416
Myosin-7	*Myh7*	S1478	SLS[+80]TELFK	ESSQKEARSLSTELFKLKNAY	11	S	PKCa	QKEARSLSTELFKLK	5.452	4.803
Myosin-7	*Myh7*	S1478	SLS[+80]TELFK	ESSQKEARSLSTELFKLKNAY	11	S	PRKCA	QKEARSLSTELFKLK	12.101	7.372
Myosin-7	*Myh7*	T1605	VVDSLQTSLDAET[+80]RSRNEALR	DSLQTSLDAETRSRNEALRVK	11	T	PKC	QTSLDAETRSRNEAL	2.076	1.416
Myosin-7	*Myh7*	T1605	VVDSLQTSLDAET[+80]RSRNEALR	DSLQTSLDAETRSRNEALRVK	11	T	PKCa	QTSLDAETRSRNEAL	4.804	4.803
Myosin-7	*Myh7*	T1605	VVDSLQTSLDAET[+80]RSRNEALR	DSLQTSLDAETRSRNEALRVK	11	T	PRKCA	QTSLDAETRSRNEAL	16.545	7.372
Myosin-9	*Myh9*	S1944	KGTGDCS[+80]DEEVDGKADGADAK	RIVRKGTGDCSDEEVDGKADG	11	S	PRKCA	RKGTGDCSDEEVDGK	7.884	7.372
Myosin-binding protein C, cardiac-type	*Mybpc3*	S302	DS[+80]FRRDSKLEAPAEEDVWEILR	DFSSLLKKRDSFRRDSKLEAP	11	S	PKC	SLLKKRDSFRRDSKL	14.263	1.416
Myosin-binding protein C, cardiac-type	*Mybpc3*	S302	DS[+80]FRRDSKLEAPAEEDVWEILR	DFSSLLKKRDSFRRDSKLEAP	11	S	PKCa	SLLKKRDSFRRDSKL	26.913	4.803
Myosin-binding protein C, cardiac-type	*Mybpc3*	S302	DS[+80]FRRDSKLEAPAEEDVWEILR	DFSSLLKKRDSFRRDSKLEAP	11	S	PKCd	SLLKKRDSFRRDSKL	6.027	3.771
Myosin-binding protein C, cardiac-type	*Mybpc3*	S302	DS[+80]FRRDSKLEAPAEEDVWEILR	DFSSLLKKRDSFRRDSKLEAP	11	S	PRKCA	SLLKKRDSFRRDSKL	35.813	7.372
Myosin-binding protein C, cardiac-type	*Mybpc3*	S302	DS[+80]FRRDSKLEAPAEEDVWEILR	DFSSLLKKRDSFRRDSKLEAP	11	S	PRKCB	SLLKKRDSFRRDSKL	23.621	10.858

Myosin-binding protein C, cardiac-type	*Mybpc3*	S302	DS[+80]FRRDSKLEAPAEEDVWEILR	DFSSLLKKRDSFRRDSKLEAP	11	S	PRKCD	SLLKKRDSFRRDSKL	4.719	2.514
Myozenin-2	*Myoz2*	T107	IDGSNLEGGSQQAPST[+80]PPNTPDPR	LEGGSQQAPSTPPNTPDPRSP	11	T	PRKCA	GSQQAPSTPPNTPDP	11.641	7.372
Myozenin-2	*Myoz2*	T111	IDGSNLEGGSQQAPSTPPNT[+80]PDPR	SQQAPSTPPNTPDPRSPPNPE	11	T	PRKCA	APSTPPNTPDPRSPP	10.187	7.372
Myristoylated alanine-rich C-kinase substrate	*Marcks*	T143	AEDGAAPSPSSET[+80]PK	DGAAPSPSSETPKKKKKRFSF	11	T	PKC	APSPSSETPKKKKKR	5.719	1.416
Myristoylated alanine-rich C-kinase substrate	*Marcks*	T143	AEDGAAPSPSSET[+80]PK	DGAAPSPSSETPKKKKKRFSF	11	T	PKCa	APSPSSETPKKKKKR	17.696	4.803
Myristoylated alanine-rich C-kinase substrate	*Marcks*	T143	AEDGAAPSPSSET[+80]PK	DGAAPSPSSETPKKKKKRFSF	11	T	PRKCA	APSPSSETPKKKKKR	18.51	7.372
Nebulin-related-anchoring protein	*Nrap*	S275	GVAS[+80]PVGAEGTMTK	QYHREMKGVASPVGAEGTMTK	11	S	PRKCA	REMKGVASPVGAEGT	11.136	7.372
Nebulin-related-anchoring protein	*Nrap*	S1693	RGLGIQGAS[+80]VETEAVELGDHR	NRRGLGIQGASVETEAVELGD	11	S	PKCa	GLGIQGASVETEAVE	5.052	4.803
Nebulin-related-anchoring protein	*Nrap*	S1693	RGLGIQGAS[+80]VETEAVELGDHR	NRRGLGIQGASVETEAVELGD	11	S	PRKCA	GLGIQGASVETEAVE	14.894	7.372
Nexilin	*Nexn*	S345	GVS[+80]QESLTPGK	DDSPEIYKGVSQESLTPGKLE	11	S	PKCa	PEIYKGVSQESLTPG	5.443	4.803
Nexilin	*Nexn*	S345	GVS[+80]QESLTPGK	DDSPEIYKGVSQESLTPGKLE	11	S	PRKCA	PEIYKGVSQESLTPG	14.869	7.372
Nexilin	*Nexn*	S348	GVSQES[+80]LTPGKLEINFEQLLR	PEIYKGVSQESLTPGKLEINF	11	S	PKCa	YKGVSQESLTPGKLE	5.183	4.803
Nexilin	*Nexn*	S348	GVSQES[+80]LTPGKLEINFEQLLR	PEIYKGVSQESLTPGKLEINF	11	S	PRKCA	YKGVSQESLTPGKLE	12.96	7.372
Nexilin	*Nexn*	S544	KREDDEEEEGS[+80]IVNGSTTEDEEQTR	KREDDEEEEGSIVNGSTTEDE	11	S	PKC	DDEEEEGSIVNGSTT	2.038	1.416
Nexilin	*Nexn*	S544	KREDDEEEEGS[+80]IVNGSTTEDEEQTR	KREDDEEEEGSIVNGSTTEDE	11	S	PKCa	DDEEEEGSIVNGSTT	5.104	4.803
Nexilin	*Nexn*	S544	KREDDEEEEGS[+80]IVNGSTTEDEEQTR	KREDDEEEEGSIVNGSTTEDE	11	S	PRKCA	DDEEEEGSIVNGSTT	16.732	7.372
Nexilin	*Nexn*	S544	KREDDEEEEGS[+80]IVNGSTTEDEEQTR	KREDDEEEEGSIVNGSTTEDE	11	S	PRKCB	DDEEEEGSIVNGSTT	13.362	10.858
Nexilin	*Nexn*	S330	SMVLDDDS[+80]PEIYK	ARRSMVLDDDSPEIYKAVSQE	11	S	PRKCA	SMVLDDDSPEIYKAV	9.803	7.372
Obscurin	*Obscn*	S6609	LKLS[+80]PEWGPTEAPEFPGEAVSEDEYR	PAYLDKRLKLSPEWGPTEAPE	11	S	PKC	LDKRLKLSPEWGPTE	2.124	1.416
Obscurin	*Obscn*	S6609	LKLS[+80]PEWGPTEAPEFPGEAVSEDEYR	PAYLDKRLKLSPEWGPTEAPE	11	S	PRKCA	LDKRLKLSPEWGPTE	9.253	7.372
Obscurin	*Obscn*	S454	S[+80]ASPRRPGLLAPEMLYPPGTSPSR	KSPSRSPSRRSASPRRPGLLA	11	S	PKC	SRSPSRRSASPRRPG	3.617	1.416
Obscurin	*Obscn*	S454	S[+80]ASPRRPGLLAPEMLYPPGTSPSR	KSPSRSPSRRSASPRRPGLLA	11	S	PKCa	SRSPSRRSASPRRPG	11.787	4.803
Obscurin	*Obscn*	S454	S[+80]ASPRRPGLLAPEMLYPPGTSPSR	KSPSRSPSRRSASPRRPGLLA	11	S	PKCd	SRSPSRRSASPRRPG	4.365	3.771
Obscurin	*Obscn*	S454	S[+80]ASPRRPGLLAPEMLYPPGTSPSR	KSPSRSPSRRSASPRRPGLLA	11	S	PRKCA	SRSPSRRSASPRRPG	16.621	7.372
Obscurin	*Obscn*	S454	S[+80]ASPRRPGLLAPEMLYPPGTSPSR	KSPSRSPSRRSASPRRPGLLA	11	S	PRKCB	SRSPSRRSASPRRPG	12.603	10.858
Obscurin	*Obscn*	S454	S[+80]ASPRRPGLLAPEMLYPPGTSPSR	KSPSRSPSRRSASPRRPGLLA	11	S	PRKCD	SRSPSRRSASPRRPG	2.772	2.514
Optineurin	*Optn*	S188	LNSGGSSEDS[+80]FVEIR	LNSGGSSEDSFVEIRMTEGE	10	S	PRKCA	SGGSSEDSFVEIRMT	13.172	7.372
Optineurin	*Optn*	S188	LNSGGSSEDS[+80]FVEIR	KLNSGGSSEDSFVEIRMTEGE	11	S	PRKCA	SGGSSEDSFVEIRMT	13.172	7.372
Optineurin	*Optn*	S188	LNSGGSSEDS[+80]FVEIR	LNSGGSSEDSFVEIRMTEGE	10	S	PRKCB	SGGSSEDSFVEIRMT	16.017	10.858
Optineurin	*Optn*	S188	LNSGGSSEDS[+80]FVEIR	KLNSGGSSEDSFVEIRMTEGE	11	S	PRKCB	SGGSSEDSFVEIRMT	16.017	10.858
Paxillin	*Pxn*	T313	T[+80]GSSSPPGGLSKPGSQLDSMLGSLQSDLNK	SDFKFMAQGKTGSSSPPGGLS	11	T	PKCa	KFMAQGKTGSSSPPG	5.704	4.803
Paxillin	*Pxn*	T313	T[+80]GSSSPPGGLSKPGSQLDSMLGSLQSDLNK	SDFKFMAQGKTGSSSPPGGLS	11	T	PRKCA	KFMAQGKTGSSSPPG	14.025	7.372
Paxillin	*Pxn*	S320	TGS[+80]SSPPGGLSKPGSQLDSMLGSLQSDLNK	FKFMAQGKTGSSSPPGGLSKP	11	S	PKCa	MAQGKTGSSSPPGGL	6.196	4.803

Paxillin	*Pxn*	S320	TGS[+80]SSPPGGLSKPGSQLDSMLGSLQSDLNK	GGFMAQGKTGSSSPPGGLSKP	11	S	PKCa	MAQGKTGSSSPPGGL	6.196	4.803
Paxillin	*Pxn*	S320	TGS[+80]SSPPGGLSKPGSQLDSMLGSLQSDLNK	FKFMAQGKTGSSSPPGGLSKP	11	S	PKCd	MAQGKTGSSSPPGGL	3.973	3.771
Paxillin	*Pxn*	S320	TGS[+80]SSPPGGLSKPGSQLDSMLGSLQSDLNK	GGFMAQGKTGSSSPPGGLSKP	11	S	PKCd	MAQGKTGSSSPPGGL	3.973	3.771
Paxillin	*Pxn*	S320	TGS[+80]SSPPGGLSKPGSQLDSMLGSLQSDLNK	FKFMAQGKTGSSSPPGGLSKP	11	S	PRKCA	MAQGKTGSSSPPGGL	18.01	7.372
Paxillin	*Pxn*	S320	TGS[+80]SSPPGGLSKPGSQLDSMLGSLQSDLNK	GGFMAQGKTGSSSPPGGLSKP	11	S	PRKCA	MAQGKTGSSSPPGGL	18.01	7.372
Paxillin	*Pxn*	S321	TGSS[+80]SPPGGLSKPGSQLDSMLGSLQSDLNK	GFMAQGKTGSSSPPGGLSKPG	11	S	PRKCA	AQGKTGSSSPPGGLS	12.46	7.372
Paxillin	*Pxn*	S321	TGSS[+80]SPPGGLSKPGSQLDSMLGSLQSDLNK	KFMAQGKTGSSSPPGGLSKPG	11	S	PRKCA	AQGKTGSSSPPGGLS	12.46	7.372
Paxillin	*Pxn*	S317	TGSSS[+80]PPGGLSKPGSQLDSMLGSLQSDLNK	FMAQGKTGSSSPPGGLSKPGS	11	S	PRKCA	QGKTGSSSPPGGLSK	11.303	7.372
Paxillin	*Pxn*	S328	TGSSSPPGGLS[+80]KPGSQLDSMLGSLQSDLNK	TGSSSPPGGLSKPGSQLDSML	11	S	PRKCA	SSPPGGLSKPGSQLD	15.702	7.372
Paxillin	*Pxn*	S328	TGSSSPPGGLS[+80]KPGSQLDSMLGSLQSDLNK	TGSSSPPGGLSKPGSQLDSM	11	S	PRKCA	SSPPGGLSKPGSQLD	17.045	7.372
Paxillin	*Pxn*	S327	TGSSSPPGGLSKPGS[+80]QLDSMLGSLQSDLNK	SPPGGLSKPGSQLDSMLGSLQ	11	S	PKCa	GGLSKPGSQLDSMLG	5.378	4.803
Paxillin	*Pxn*	S327	TGSSSPPGGLSKPGS[+80]QLDSMLGSLQSDLNK	SPPGGLSKPGSQLDSMLGSLQ	11	S	PRKCA	GGLSKPGSQLDSMLG	17.682	7.372
Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2	*Inppl1*	S132	DAS[+80]DVEDEKPPLPPR	EPDPPDDRDASDVEDEKPPLP	11	S	PKC	PPDDRDASDVEDEKP	3.065	1.416
Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2	*Inppl1*	S132	DAS[+80]DVEDEKPPLPPR	EPDPPDDRDASDVEDEKPPLP	11	S	PKCa	PPDDRDASDVEDEKP	5.013	4.803
Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2	*Inppl1*	S132	DAS[+80]DVEDEKPPLPPR	EPDPPDDRDASDVEDEKPPLP	11	S	PRKCA	PPDDRDASDVEDEKP	10.035	7.372
Plectin	*Plec*	T4626	GYYSPYSVSGSGST[+80]AGSR	SPYSVSGSGSTAGSRTGSRTG	11	T	PRKCA	SVSGSGSTAGSRTGS	11.04	7.372
Plectin	*Plec*	S4388	SS[+80]S[+80]VGSSSSYPISSAVPR	GNAGGFRSRSSSVGSSSSYPI	11	S	PKC	GGFRSRSSSVGSSSS	1.924	1.416
Plectin	*Plec*	S4388	SS[+80]S[+80]VGSSSSYPISSAVPR	NAGGFRSRSSSVGSSSSYPIS	11	S	PKC	GFRSRSSSVGSSSSY	2.988	1.416
Plectin	*Plec*	S4388	SS[+80]S[+80]VGSSSSYPISSAVPR	GNAGGFRSRSSSVGSSSSYPI	11	S	PKCa	GGFRSRSSSVGSSSS	10.304	4.803
Plectin	*Plec*	S4388	SS[+80]S[+80]VGSSSSYPISSAVPR	NAGGFRSRSSSVGSSSSYPIS	11	S	PKCa	GFRSRSSSVGSSSSY	10.443	4.803
Plectin	*Plec*	S4388	SS[+80]S[+80]VGSSSSYPISSAVPR	GNAGGFRSRSSSVGSSSSYPI	11	S	PRKCA	GGFRSRSSSVGSSSS	16.556	7.372
Plectin	*Plec*	S4388	SS[+80]S[+80]VGSSSSYPISSAVPR	NAGGFRSRSSSVGSSSSYPIS	11	S	PRKCA	GFRSRSSSVGSSSSY	20.313	7.372
Plectin	*Plec*	S4388	SS[+80]S[+80]VGSSSSYPISSAVPR	NAGGFRSRSSSVGSSSSYPIS	11	S	PRKCB	GFRSRSSSVGSSSSY	12.224	10.858
Plectin	*Plec*	S4388	SS[+80]S[+80]VGSSSSYPISSAVPR	GNAGGFRSRSSSVGSSSSYPI	11	S	PRKCD	GGFRSRSSSVGSSSS	3.333	2.514
Plectin	*Plec*	S4388	SS[+80]S[+80]VGSSSSYPISSAVPR	NAGGFRSRSSSVGSSSSYPIS	11	S	PRKCD	GFRSRSSSVGSSSSY	3.211	2.514
Plectin	*Plec*	S4409	TQLAS[+80]WSDPTEETGPVAGILDTETLEK	SSAVPRTQLASWSDPTEETGP	11	S	PRKCA	VPRTQLASWSDPTEE	12.187	7.372
Plectin	*Plec*	S4411	TQLASWS[+80]DPTEETGPVAGILDTETLEK	AVPRTQLASWSDPTEETGPVA	11	S	PRKCA	RTQLASWSDPTEETG	7.783	7.372
Plectin	*Plec*	T4414	TQLASWSDPT[+80]EETGPVAGILDTETLEK	RTQLASWSDPTEETGPVAGIL	11	T	PRKCA	LASWSDPTEETGPVA	8	7.372
Plectin	*Plec*	S4629	GYYSPYSVSGSGSTAGS[+80]R	SVSGSGSTAGSRTGSRTGSRA	11	S	PKC	GSGSTAGSRTGSRTG	2.896	1.416
Plectin	*Plec*	S4629	GYYSPYSVSGSGSTAGS[+80]R	YSVSGSGSTAGSRTGSRTGSRAG	12	S	PKC	GSGSTAGSRTGSRTG	2.648	1.416

Plectin	*Plec*	S4629	GYYSPYSVSGSGSTAGS[+80]R	SVSGSGSTAGSRTGSRTGSRA	11	S	PKCa	GSGSTAGSRTGSRTG	9.783	4.803
Plectin	*Plec*	S4629	GYYSPYSVSGSGSTAGS[+80]R	YSVSGSGSTAGSRTGSRTGSRAG	12	S	PKCa	GSGSTAGSRTGSRTG	9.239	4.803
Plectin	*Plec*	S4629	GYYSPYSVSGSGSTAGS[+80]R	SVSGSGSTAGSRTGSRTGSRA	11	S	PRKCA	GSGSTAGSRTGSRTG	18.323	7.372
Plectin	*Plec*	S4629	GYYSPYSVSGSGSTAGS[+80]R	YSVSGSGSTAGSRTGSRTGSRAG	12	S	PRKCA	GSGSTAGSRTGSRTG	16.394	7.372
Plectin	*Plec*	S4629	GYYSPYSVSGSGSTAGS[+80]R	SVSGSGSTAGSRTGSRTGSRA	11	S	PRKCB	GSGSTAGSRTGSRTG	11.966	10.858
Plectin	*Plec*	S4629	GYYSPYSVSGSGSTAGS[+80]R	YSVSGSGSTAGSRTGSRTGSRAG	12	S	PRKCB	GSGSTAGSRTGSRTG	11.793	10.858
Protein enabled homolog	*Enah*	S354	NSRPS[+80]SPVNTPSSQPPAAK	PRPLNKNSRPSSPVNTPSSQP	11	S	PKC	LNKNSRPSSPVNTPS	1.911	1.416
Protein enabled homolog	*Enah*	S354	NSRPS[+80]SPVNTPSSQPPAAK	PRPLNKNSRPSSPVNTPSSQP	11	S	PKCa	LNKNSRPSSPVNTPS	8.739	4.803
Protein enabled homolog	*Enah*	S354	NSRPS[+80]SPVNTPSSQPPAAK	PRPLNKNSRPSSPVNTPSSQP	11	S	PRKCA	LNKNSRPSSPVNTPS	14.894	7.372
Protein enabled homolog	*Enah*	S354	NSRPS[+80]SPVNTPSSQPPAAK	PRPLNKNSRPSSPVNTPSSQP	11	S	PRKCB	LNKNSRPSSPVNTPS	11.931	10.858
Protein enabled homolog	*Enah*	S355	NSRPSS[+80]PVNTPSSQPPAAK	RPLNKNSRPSSPVNTPSSQPP	11	S	PKC	NKNSRPSSPVNTPSS	1.512	1.416
Protein enabled homolog	*Enah*	S355	NSRPSS[+80]PVNTPSSQPPAAK	RPLNKNSRPSSPVNTPSSQPP	11	S	PKCa	NKNSRPSSPVNTPSS	7.674	4.803
Protein enabled homolog	*Enah*	S355	NSRPSS[+80]PVNTPSSQPPAAK	RPLNKNSRPSSPVNTPSSQPP	11	S	PRKCA	NKNSRPSSPVNTPSS	15.096	7.372
Protein furry homolog	*Fry*	S1936	NSDLFTVLS[+80]R	LKNSDLFTVLSRSSSPDLSSS	11	S	PKCa	SDLFTVLSRSSSPDL	6.209	4.803
Protein furry homolog	*Fry*	S1936	NSDLFTVLS[+80]R	LKNSDLFTVLSRSSSPDLSSS	11	S	PRKCA	SDLFTVLSRSSSPDL	13.303	7.372
Protein phosphatase 1 regulatory subunit 12A	*Ppp1r12a*	S873	STGVSFWTQDSDENEQERQS[+80]DTEDGSSKR	DSDENEQERQSDTEDGSSKRD	11	S	PKC	ENEQERQSDTEDGSS	3.119	1.416
Protein phosphatase 1 regulatory subunit 12A	*Ppp1r12a*	S873	STGVSFWTQDSDENEQERQS[+80]DTEDGSSKR	DSDENEQERQSDTEDGSSKRD	11	S	PKCa	ENEQERQSDTEDGSS	7.439	4.803
Protein phosphatase 1 regulatory subunit 12A	*Ppp1r12a*	S873	STGVSFWTQDSDENEQERQS[+80]DTEDGSSKR	DSDENEQERQSDTEDGSSKRD	11	S	PRKCA	ENEQERQSDTEDGSS	13.788	7.372
Protein phosphatase 1 regulatory subunit 12A	*Ppp1r12a*	S873	STGVSFWTQDSDENEQERQS[+80]DTEDGSSKR	DSDENEQERQSDTEDGSSKRD	11	S	PRKCB	ENEQERQSDTEDGSS	11.621	10.858
Rho GTPase-activating protein 35	*Arhgap35*	S1179	TSFSVGS[+80]DDELGPIR	ASYRTSFSVGSDDELGPIRKK	11	S	PRKCA	RTSFSVGSDDELGPI	12.359	7.372
Septin-7	*Sept7*	T425	ILEQQNSSRT[+80]LEK	RILEQQNSSRTLEKNKKKGKI	11	T	PKC	EQQNSSRTLEKNKKK	3.024	1.416
Septin-7	*Sept7*	T425	ILEQQNSSRT[+80]LEK	RILEQQNSSRTLEKNKKKGKI	11	T	PKCa	EQQNSSRTLEKNKKK	12.378	4.803
Septin-7	*Sept7*	T425	ILEQQNSSRT[+80]LEK	RILEQQNSSRTLEKNKKKGKI	11	T	PRKCA	EQQNSSRTLEKNKKK	18.904	7.372
Septin-7	*Sept7*	T425	ILEQQNSSRT[+80]LEK	RILEQQNSSRTLEKNKKKGKI	11	T	PRKCB	EQQNSSRTLEKNKKK	13.672	10.858
SH3 and multiple ankyrin repeat domains protein 3	*Shank3*	T1235	LGAEEERPGT[+80]PELAPTPMQAAAVAEPMPSPR	RLGAEEERPGTPELAPTPMQA	11	T	PRKCA	AEEERPGTPELAPTP	9.288	7.372
SH3 domain-binding protein 1	*Sh3bp1*	S539	ERTESELPKPAS[+80]PK	RTESELPKPASPKVSRSPTDT	11	S	PKC	SELPKPASPKVSRSP	4.591	1.416
SH3 domain-binding protein 1	*Sh3bp1*	S539	ERTESELPKPAS[+80]PK	RTESELPKPASPKVSRSPTDT	11	S	PKCa	SELPKPASPKVSRSP	10.204	4.803
SH3 domain-binding protein 1	*Sh3bp1*	S539	ERTESELPKPAS[+80]PK	RTESELPKPASPKVSRSPTDT	11	S	PKCd	SELPKPASPKVSRSP	4.014	3.771
SH3 domain-binding protein 1	*Sh3bp1*	S539	ERTESELPKPAS[+80]PK	RTESELPKPASPKVSRSPTDT	11	S	PRKCA	SELPKPASPKVSRSP	18.864	7.372
Shroom family member 3	*Shroom3*	S763	RLS[+80]ASSTPALQYK	QTSGMSQRRLSASSTPALQYK	11	S	PKC	GMSQRRLSASSTPAL	3.809	1.416
Shroom family member 3	*Shroom3*	S763	RLS[+80]ASSTPALQYK	QTSGMSQRRLSASSTPALQYK	11	S	PKCa	GMSQRRLSASSTPAL	12.313	4.803

Shroom family member 3	*Shroom3*	S763	RLS[+80]ASSTPALQYK	QTSGMSQRRLSASSTPALQYK	11	S	PKCd	GMSQRRLSASSTPAL	4.216	3.771
Shroom family member 3	*Shroom3*	S763	RLS[+80]ASSTPALQYK	QTSGMSQRRLSASSTPALQYK	11	S	PRKCA	GMSQRRLSASSTPAL	16.727	7.372
Shroom family member 3	*Shroom3*	S763	RLS[+80]ASSTPALQYK	QTSGMSQRRLSASSTPALQYK	11	S	PRKCD	GMSQRRLSASSTPAL	3.526	2.514
Sorbin and SH3 domain-containing protein 1	*Sorbs1*	S345	DIS[+80]PEEIDLK	TNEKMSRDISPEEIDLKNEP	10	S	PRKCA	EKMSRDISPEEIDLK	12.934	7.372
Sorbin and SH3 domain-containing protein 1	*Sorbs1*	S345	DIS[+80]PEEIDLK	LTNEKMSRDISPEEIDLKNEP	11	S	PRKCA	EKMSRDISPEEIDLK	12.934	7.372
Sorbin and SH3 domain-containing protein 1	*Sorbs1*	S401	ES[+80]DGTPGGLASLENER	SSDFHAVKRESDGTPGGLASL	11	S	PKC	FHAVKRESDGTPGGL	2.317	1.416
Sorbin and SH3 domain-containing protein 1	*Sorbs1*	S401	ES[+80]DGTPGGLASLENER	SSDFHAVKRESDGTPGGLASL	11	S	PKCa	FHAVKRESDGTPGGL	5.687	4.803
Sorbin and SH3 domain-containing protein 1	*Sorbs1*	S401	ES[+80]DGTPGGLASLENER	SSDFHAVKRESDGTPGGLASL	11	S	PKCd	FHAVKRESDGTPGGL	4	3.771
Sorbin and SH3 domain-containing protein 1	*Sorbs1*	S401	ES[+80]DGTPGGLASLENER	SSDFHAVKRESDGTPGGLASL	11	S	PRKCA	FHAVKRESDGTPGGL	13.742	7.372
Sorbin and SH3 domain-containing protein 1	*Sorbs1*	T404	ESDGT[+80]PGGLASLENER	FHAVKRESDGTPGGLASLENE	11	T	PRKCA	VKRESDGTPGGLASL	9.116	7.372
Sorbin and SH3 domain-containing protein 1	*Sorbs1*	S92	ETPSSSPVSPQES[+80]PKHENK	PSSSPVSPQESPKHENKSDEW	11	S	PKC	SPVSPQESPKHENKS	2.871	1.416
Sorbin and SH3 domain-containing protein 1	*Sorbs1*	S92	ETPSSSPVSPQES[+80]PKHENK	PSSSPVSPQESPKHENKSDEW	11	S	PKCa	SPVSPQESPKHENKS	10.548	4.803
Sorbin and SH3 domain-containing protein 1	*Sorbs1*	S92	ETPSSSPVSPQES[+80]PKHENK	PSSSPVSPQESPKHENKSDEW	11	S	PRKCA	SPVSPQESPKHENKS	14.636	7.372
Sorbin and SH3 domain-containing protein 1 Isoform 2	*Sorbs1*	S164	LSSLS[+80]DPASER	EQQKRLSSLSDPASERRAGE	10	S	PKC	QKRLSSLSDPASERR	1.965	1.416
Sorbin and SH3 domain-containing protein 1 Isoform 2	*Sorbs1*	S164	LSSLS[+80]DPASER	REQQKRLSSLSDPASERRVGE	11	S	PKC	QKRLSSLSDPASERR	1.881	1.416
Sorbin and SH3 domain-containing protein 1 Isoform 2	*Sorbs1*	S164	LSSLS[+80]DPASER	EQQKRLSSLSDPASERRAGE	10	S	PKCa	QKRLSSLSDPASERR	6.326	4.803
Sorbin and SH3 domain-containing protein 1 Isoform 2	*Sorbs1*	S164	LSSLS[+80]DPASER	REQQKRLSSLSDPASERRVGE	11	S	PKCa	QKRLSSLSDPASERR	6.396	4.803
Sorbin and SH3 domain-containing protein 1 Isoform 2	*Sorbs1*	S164	LSSLS[+80]DPASER	EQQKRLSSLSDPASERRAGE	10	S	PRKCA	QKRLSSLSDPASERR	8.924	7.372
Sorbin and SH3 domain-containing protein 1 Isoform 2	*Sorbs1*	S164	LSSLS[+80]DPASER	REQQKRLSSLSDPASERRVGE	11	S	PRKCA	QKRLSSLSDPASERR	8.611	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S394	ADLPGSSSTFTTSFISSS[+80]PSSPSR	STFTTSFISSSPSSPSRAQG	11	S	PKCa	TTSFISSSPSSPSRA	6.291	4.803
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S394	ADLPGSSSTFTTSFISSS[+80]PSSPSR	STFTTSFISSSPSSPSRAQGG	11	S	PKCa	TTSFISSSPSSPSRA	6.809	4.803
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S394	ADLPGSSSTFTTSFISSS[+80]PSSPSR	STFTTSFISSSPSSPSRAQG	11	S	PRKCA	TTSFISSSPSSPSRA	10.187	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S394	ADLPGSSSTFTTSFISSS[+80]PSSPSR	STFTTSFISSSPSSPSRAQGG	11	S	PRKCA	TTSFISSSPSSPSRA	9.672	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S396	ADLPGSSSTFTTSFISSSPS[+80]SPSR	FTTSFISSSPSSPSRAQGGDD	11	S	PKCa	SFISSSPSSPSRAQG	10.996	4.803
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S396	ADLPGSSSTFTTSFISSSPS[+80]SPSR	FTTSFISSSPSSPSRAQGGDD	11	S	PRKCA	SFISSSPSSPSRAQG	14.758	7.372

Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S396	ADLPGSSSTFTTSFISSSPS[+80]SPSR	FTTSFISSSPSSPSRAQGGDD	11	S	PRKCB	SFISSSPSSPSRAQG	12.31	10.858
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S266	EAPS[+80]PVPPPHVPPRPR	NGTDAFKEAPSPVPPPHVPPR	11	S	PRKCA	DAFKEAPSPVPPPHV	11.965	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S38	ES[+80]HSPDSAWR	SPNLLAAGRESHSPDSAWRSY	11	S	PKCa	LLAAGRESHSPDSAW	6.713	4.803
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S38	ES[+80]HSPDSAWR	SPNLLAAGRESHSPDSAWRSY	11	S	PRKCA	LLAAGRESHSPDSAW	12.621	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S38	ES[+80]HSPDSAWR	SPNLLAAGRESHSPDSAWRSY	11	S	PRKCB	LLAAGRESHSPDSAW	11.724	10.858
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S40	ESHS[+80]PDSAWR	NLLAAGRESHSPDSAWRSYNG	11	S	PRKCA	AAGRESHSPDSAWRS	11.606	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S1111	GSEDYPDPPLPHS[+80]YSSDR	EDYPDPPLPHSYSSDRIYSLS	11	S	PRKCA	PDPPLPHSYSSDRIY	12.273	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S1113	GSEDYPDPPLPHSYS[+80]SDR	YPDPPLPHSYSSDRIYSLSSN	11	S	PKCa	PPLPHSYSSDRIYSL	6.178	4.803
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S1113	GSEDYPDPPLPHSYS[+80]SDR	YPDPPLPHSYSSDRIYSLSSN	11	S	PRKCA	PPLPHSYSSDRIYSL	15.556	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S1113	GSEDYPDPPLPHSYS[+80]SDR	YPDPPLPHSYSSDRIYSLSSN	11	S	PRKCB	PPLPHSYSSDRIYSL	14.5	10.858
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S1114	GSEDYPDPPLPHSYSS[+80]DR	PDPPLPHSYSSDRIYSLSSNK	11	S	PKC	PLPHSYSSDRIYSLS	1.885	1.416
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S1114	GSEDYPDPPLPHSYSS[+80]DR	PDPPLPHSYSSDRIYSLSSNK	11	S	PRKCA	PLPHSYSSDRIYSLS	16.419	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S354	KS[+80]EPAVGPPR	MAGDFRKRRKSEPAVGPPRGL	11	S	PKC	DFRKRRKSEPAVGPP	3.853	1.416
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S354	KS[+80]EPAVGPPR	MAGDFRKRRKSEPAVGPPRGL	11	S	PKCa	DFRKRRKSEPAVGPP	11.078	4.803
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S354	KS[+80]EPAVGPPR	MAGDFRKRRKSEPAVGPPRGL	11	S	PKCd	DFRKRRKSEPAVGPP	5.014	3.771
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S354	KS[+80]EPAVGPPR	MAGDFRKRRKSEPAVGPPRGL	11	S	PRKCA	DFRKRRKSEPAVGPP	17.914	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S354	KS[+80]EPAVGPPR	MAGDFRKRRKSEPAVGPPRGL	11	S	PRKCB	DFRKRRKSEPAVGPP	13.69	10.858
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S354	KS[+80]EPAVGPPR	MAGDFRKRRKSEPAVGPPRGL	11	S	PRKCD	DFRKRRKSEPAVGPP	3.158	2.514
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S130	S[+80]LDSAETYSQHAQSLDGTMGSSIPLYR	NSSIIMPHGRSLDSAETYSQH	11	S	PRKCA	IIMPHGRSLDSAETY	16.086	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S130	S[+80]LDSAETYSQHAQSLDGTMGSSIPLYR	NSSIIMQHGRSLDSAETYSQH	11	S	PRKCA	IIMQHGRSLDSAETY	16.086	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S334	S[+80]LERPSSSASMAGDFR	VSVYQSSIDRSLERPSSSASM	11	S	PKCa	YQSSIDRSLERPSSS	6.883	4.803
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S334	S[+80]LERPSSSASMAGDFR	VSIYQSSIDRSLERPSSSASM	11	S	PKCa	YQSSIDRSLERPSSS	6.883	4.803
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S334	S[+80]LERPSSSASMAGDFR	VSVYQSSIDRSLERPSSSASM	11	S	PRKCA	YQSSIDRSLERPSSS	20.934	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S334	S[+80]LERPSSSASMAGDFR	VSIYQSSIDRSLERPSSSASM	11	S	PRKCA	YQSSIDRSLERPSSS	20.934	7.372

Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S334	S[+80]LERPSSSASMAGDFR	VSVYQSSIDRSLERPSSSASM	11	S	PRKCB	YQSSIDRSLERPSSS	14.621	10.858
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S334	S[+80]LERPSSSASMAGDFR	VSIYQSSIDRSLERPSSSASM	11	S	PRKCB	YQSSIDRSLERPSSS	14.621	10.858
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S133	SLDS[+80]AETYSQHAQSLDGTMGSSIPLYR	IIMPHGRSLDSAETYSQHAQS	11	S	PRKCA	PHGRSLDSAETYSQH	10.833	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S133	SLDS[+80]AETYSQHAQSLDGTMGSSIPLYR	IIMQHGRSLDSAETYSQHAQS	11	S	PRKCA	QHGRSLDSAETYSQH	10.833	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	T136	SLDSAET[+80]YSQHAQSLDGTMGSSIPLYR	PHGRSLDSAETYSQHAQSLDG	11	T	PKCa	RSLDSAETYSQHAQS	5.596	4.803
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	T136	SLDSAET[+80]YSQHAQSLDGTMGSSIPLYR	QHGRSLDSAETYSQHAQSLDG	11	T	PKCa	RSLDSAETYSQHAQS	5.596	4.803
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	T136	SLDSAET[+80]YSQHAQSLDGTMGSSIPLYR	PHGRSLDSAETYSQHAQSLDG	11	T	PRKCA	RSLDSAETYSQHAQS	9.449	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	T136	SLDSAET[+80]YSQHAQSLDGTMGSSIPLYR	QHGRSLDSAETYSQHAQSLDG	11	T	PRKCA	RSLDSAETYSQHAQS	9.449	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S138	SLDSAETYS[+80]QHAQSLDGTMGSSIPLYR	GRSLDSAETYSQHAQSLDGTM	11	S	PRKCA	LDSAETYSQHAQSLD	11.914	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S143	SLDSAETYSQHAQS[+80]LDGTMGSSIPLYR	SAETYSQHAQSLDGTMGSSIP	11	S	PKC	TYSQHAQSLDGTMGS	1.662	1.416
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S143	SLDSAETYSQHAQS[+80]LDGTMGSSIPLYR	SAETYSQHAQSLDGTMGSSIP	11	S	PRKCA	TYSQHAQSLDGTMGS	14.96	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	T147	SLDSAETYSQHAQSLDGT[+80]MGSSIPLYR	YSQHAQSLDGTMGSSIPLYRS	11	T	PRKCA	HAQSLDGTMGSSIPL	13.551	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S324	SLERPS[+80]SSASMAGDFR	SSIDRSLERPSSSASMAGDF	11	S	PKC	DRSLERPSSSASMAG	1.694	1.416
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S324	SLERPS[+80]SSASMAGDFR	SSIDRSLERPSSSASMAGDF	11	S	PKCa	DRSLERPSSSASMAG	9.409	4.803
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S324	SLERPS[+80]SSASMAGDFR	SSIDRSLERPSSSASMAGDF	11	S	PRKCA	DRSLERPSSSASMAG	17.985	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S324	SLERPS[+80]SSASMAGDFR	SSIDRSLERPSSSASMAGDF	11	S	PRKCB	DRSLERPSSSASMAG	11.879	10.858
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S324	SLERPS[+80]SSASMAGDFR	SSIDRSLERPSSSASMAGDF	11	S	PRKCD	DRSLERPSSSASMAG	2.86	2.514
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S340	SLERPSS[+80]SAS[+80]MAGDFR	SIDRSLERPSSSASMAGDFRK	11	S	PKC	RSLERPSSSASMAGD	3.525	1.416
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S340	SLERPSS[+80]SAS[+80]MAGDFR	SIDRSLERPSSSASMAGDFRK	11	S	PKCa	RSLERPSSSASMAGD	7.883	4.803
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S340	SLERPSS[+80]SAS[+80]MAGDFR	SIDRSLERPSSSASMAGDFRK	11	S	PRKCA	RSLERPSSSASMAGD	17.227	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S340	SLERPSS[+80]SAS[+80]MAGDFR	SIDRSLERPSSSASMAGDFRK	11	S	PRKCD	RSLERPSSSASMAGD	2.737	2.514
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S341	SLERPSSS[+80]ASMAGDFR	IDRSLERPSSSASMAGDFRKR	11	S	PKC	SLERPSSSASMAGDF	2.294	1.416
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S341	SLERPSSS[+80]ASMAGDFR	IDRSLERPSSSASMAGDFRKR	11	S	PRKCA	SLERPSSSASMAGDF	16.101	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S341	SLERPSSS[+80]ASMAGDFR	IDRSLERPSSSASMAGDFRKR	11	S	PRKCB	SLERPSSSASMAGDF	16.379	10.858

Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S343	SLERPSSSAS[+80]MAGDFRK	RSLERPSSSASMAGDFRKRRK	11	S	PKC	ERPSSSASMAGDFRK	2.774	1.416
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S343	SLERPSSSAS[+80]MAGDFRK	RSLERPSSSASMAGDFRKRRK	11	S	PKCa	ERPSSSASMAGDFRK	7.648	4.803
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S343	SLERPSSSAS[+80]MAGDFRK	RSLERPSSSASMAGDFRKRRK	11	S	PRKCA	ERPSSSASMAGDFRK	18.773	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S355	SPS[+80]PPPR	SPSTDGLRSPSPPPRSCVPAP	11	S	PKCa	TDGLRSPSPPPRSCV	7.004	4.803
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S355	SPS[+80]PPPR	SPSTDGLRSPSPPPRSCVPAP	11	S	PRKCA	TDGLRSPSPPPRSCV	15.919	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S397	TSPGRADLPGSSSTFTTSFISSSPSS[+80]PSR	TTSFISSSPSSPSRAQGGDDS	11	S	PKC	SSSPSSPSRAQGGDD	1.629	1.416
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S397	TSPGRADLPGSSSTFTTSFISSSPSS[+80]PSR	TTSFISSSPSSPSRAQGGDDS	11	S	PKCa	FISSSPSSPSRAQGG	6.2	4.803
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S397	TSPGRADLPGSSSTFTTSFISSSPSS[+80]PSR	TTSFISSSPSSPSRAQGGDDS	11	S	PKCa	SSSPSSPSRAQGGDD	6.413	4.803
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S397	TSPGRADLPGSSSTFTTSFISSSPSS[+80]PSR	TTSFISSSPSSPSRAQGGDDS	11	S	PRKCA	FISSSPSSPSRAQGG	16.288	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S397	TSPGRADLPGSSSTFTTSFISSSPSS[+80]PSR	TTSFISSSPSSPSRAQGGDDS	11	S	PRKCA	SSSPSSPSRAQGGDD	20.136	7.372
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S399	TSPGRADLPGSSSTFTTSFISSSPSSPS[+80]R	FISSSPSSPSRAQGGDDSKM	10	S	PKC	SSSPSSPSRAQGGDD	1.677	1.416
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S399	TSPGRADLPGSSSTFTTSFISSSPSSPS[+80]R	FISSSPSSPSRAQGGDDSKM	10	S	PKCa	SSSPSSPSRAQGGDD	6.413	4.803
Sorbin and SH3 domain-containing protein 2	*Sorbs2*	S399	TSPGRADLPGSSSTFTTSFISSSPSSPS[+80]R	FISSSPSSPSRAQGGDDSKM	10	S	PRKCA	SSSPSSPSRAQGGDD	20.136	7.372
Spectrin alpha chain, non-erythrocytic 1	*Sptan1*	S1029	KLDPAQS[+80]ASRENLLEEQGSIALR	AYVKKLDPAQSASRENLLEEQ	11	S	PKC	KKLDPAQSASRENLL	1.613	1.416
Spectrin alpha chain, non-erythrocytic 1	*Sptan1*	S1029	KLDPAQS[+80]ASRENLLEEQGSIALR	AYVKKLDPAQSASRENLLEEQ	11	S	PKCa	KKLDPAQSASRENLL	8.113	4.803
Spectrin alpha chain, non-erythrocytic 1	*Sptan1*	S1029	KLDPAQS[+80]ASRENLLEEQGSIALR	AYVKKLDPAQSASRENLLEEQ	11	S	PRKCA	KKLDPAQSASRENLL	18.081	7.372
Striatin-interacting protein 1	*Strip1*	S335	AAS[+80]PPASASDLIEQQQK	IKVIRNMRAASPPASASDLIE	11	S	PKC	IRNMRAASPPASASD	1.904	1.416
Striatin-interacting protein 1	*Strip1*	S335	AAS[+80]PPASASDLIEQQQK	IKVIRNMRAASPPASASDLIE	11	S	PKCa	IRNMRAASPPASASD	5.126	4.803
Striatin-interacting protein 1	*Strip1*	S335	AAS[+80]PPASASDLIEQQQK	IKVIRNMRAASPPASASDLIE	11	S	PRKCA	IRNMRAASPPASASD	12.409	7.372
Supervillin	*Svil*	S240	HIPSSPLQQPAS[+80]PSLPGDSPLSTEAR	IPSSPLQQPASPSLPGDSPLS	11	S	PRKCA	SPLQQPASPSLPGDS	9.207	7.372
Supervillin	*Svil*	S242	HIPSSPLQQPASPS[+80]LPGDSPLSTEAR	SSPLQQPASPSLPGDSPLSTE	11	S	PKC	LQQPASPSLPGDSPL	1.465	1.416
Supervillin	*Svil*	S242	HIPSSPLQQPASPS[+80]LPGDSPLSTEAR	SSPLQQPASPSLPGDSPLSTE	11	S	PRKCA	LQQPASPSLPGDSPL	17.394	7.372
Supervillin	*Svil*	S728	LPS[+80]PTVAR	VTHPVTARLPSPTVARSSVQP	11	S	PKCa	PVTARLPSPTVARSS	5.961	4.803
Supervillin	*Svil*	S728	LPS[+80]PTVAR	VTHPVTARLPSPTVARSSVQP	11	S	PRKCA	PVTARLPSPTVARSS	11.949	7.372
Supervillin	*Svil*	S866	SPS[+80]PVENSDSPVR	SASAPDYKSPSPVENSDSPVR	11	S	PKC	APDYKSPSPVENSDS	2.494	1.416
Supervillin	*Svil*	S866	SPS[+80]PVENSDSPVR	SASAPDYKSPSPVENSDSPVR	11	S	PKCa	APDYKSPSPVENSDS	7.3	4.803
Supervillin	*Svil*	S866	SPS[+80]PVENSDSPVR	SASAPDYKSPSPVENSDSPVR	11	S	PRKCA	APDYKSPSPVENSDS	15.525	7.372

Synaptopodin	*Synpo*	S525	HIMARS[+80]PMVER	PQPQRHIMARSPMVERRLVGQ	11	S	PKCa	QRHIMARSPMVERRL	5.843	4.803
Synaptopodin	*Synpo*	S525	HIMARS[+80]PMVER	PQPQRHIMARSPMVERRLVGQ	11	S	PRKCA	QRHIMARSPMVERRL	12.601	7.372
Synaptopodin	*Synpo*	S258	HLEKVAS[+80]EEEEVPLVVYLK	SLLRHLEKVASEEEEVPLVVY	11	S	PKCa	RHLEKVASEEEEVPL	4.965	4.803
Synaptopodin	*Synpo*	S258	HLEKVAS[+80]EEEEVPLVVYLK	SLLRHLEKVASEEEEVPLVVY	11	S	PKCa	RHLEKVASEEEEVPL	4.965	4.803
Synaptopodin	*Synpo*	S258	HLEKVAS[+80]EEEEVPLVVYLK	SLLRHLEKVASEEEEVPLVVY	11	S	PRKCA	RHLEKVASEEEEVPL	12.308	7.372
Synaptopodin	*Synpo*	S258	HLEKVAS[+80]EEEEVPLVVYLK	SLLRHLEKVASEEEEVPLVVY	11	S	PRKCA	RHLEKVASEEEEVPL	12.308	7.372
Synaptopodin 2-like protein	*Synpo2l*	S929	AELASS[+80]PVPNPDHLESLR	EPIWRAELASSPVPNPDHLES	11	S	PRKCA	WRAELASSPVPNPDH	9.232	7.372
Synaptopodin 2-like protein	*Synpo2l*	S95	S[+80]PSPGELQMLSPLSPLSPEPPGAPVTQAPQPGSLR	RRVAEEGSVRSPSPGELQMLS	11	S	PRKCA	AEEGSVRSPSPGELQ	11.98	7.372
Synaptopodin 2-like protein	*Synpo2l*	T141	SPPDSEAYYGET[+80]DS[+80]DVDGPATHEKPR	DSEAYYGETDSDVDGPATHEK	11	S	PRKCA	AYYGETDSDVDGPAT	8.747	7.372
Synaptopodin 2-like protein	*Synpo2l*	S97	SPS[+80]PGELQMLSPLSPLSPEPPGAPVTQAPQPGSLR	VAEEGSVRSPSPGELQMLSPL	11	S	PKCa	EGSVRSPSPGELQML	7.3	4.803
Synaptopodin 2-like protein	*Synpo2l*	S97	SPS[+80]PGELQMLSPLSPLSPEPPGAPVTQAPQPGSLR	VAEEGSVRSPSPGELQMLSPL	11	S	PRKCA	EGSVRSPSPGELQML	15.838	7.372
Synaptopodin-2	*Synpo2*	S895	AQS[+80]PTPSLPASWK	TVQAHTVRAQSPTPSLPASWK	11	S	PKC	AHTVRAQSPTPSLPA	1.522	1.416
Synaptopodin-2	*Synpo2*	S895	AQS[+80]PTPSLPASWK	TVQAHTVRAQSPTPSLPASWK	11	S	PKCa	AHTVRAQSPTPSLPA	6.87	4.803
Synaptopodin-2	*Synpo2*	S895	AQS[+80]PTPSLPASWK	TVQAHTVRAQSPTPSLPASWK	11	S	PRKCA	AHTVRAQSPTPSLPA	14.364	7.372
Synaptopodin-2	*Synpo2*	S546	MQSSVS[+80]ESS[+80]FQMGR	EESVRMQSSVSESSFQMGRSL	11	S	PKCa	VRMQSSVSESSFQMG	6.443	4.803
Synaptopodin-2	*Synpo2*	S546	MQSSVS[+80]ESS[+80]FQMGR	VRMQSSVSESSFQMGRSLGSV	11	S	PKCa	QSSVSESSFQMGRSL	9.609	4.803
Synaptopodin-2	*Synpo2*	S546	MQSSVS[+80]ESS[+80]FQMGR	EESVRMQSSVSESSFQMGRSL	11	S	PRKCA	VRMQSSVSESSFQMG	11.146	7.372
Synaptopodin-2	*Synpo2*	S546	MQSSVS[+80]ESS[+80]FQMGR	VRMQSSVSESSFQMGRSLGSV	11	S	PRKCA	QSSVSESSFQMGRSL	21.46	7.372
Synaptopodin-2	*Synpo2*	S546	MQSSVS[+80]ESS[+80]FQMGR	VRMQSSVSESSFQMGRSLGSV	11	S	PRKCB	QSSVSESSFQMGRSL	21.569	10.858
Syncoilin	*Sync*	S314	RLS[+80]TQFENLMAESR	GHFLQESRRLSTQFENLMAES	11	S	PKC	LQESRRLSTQFENLM	2.953	1.416
Syncoilin	*Sync*	S314	RLS[+80]TQFENLMAESR	GHFLQESRRLSTQFENLMAES	11	S	PKCa	LQESRRLSTQFENLM	11.204	4.803
Syncoilin	*Sync*	S314	RLS[+80]TQFENLMAESR	GHFLQESRRLSTQFENLMAES	11	S	PRKCA	LQESRRLSTQFENLM	18.303	7.372
Syncoilin	*Sync*	S314	RLS[+80]TQFENLMAESR	GHFLQESRRLSTQFENLMAES	11	S	PRKCD	LQESRRLSTQFENLM	2.544	2.514
Synemin	*Synm*	S780	IDFSTPFQVEEVDDVSPS[+80]PK	QVEEVDDVSPSPKGFVEEEDG	11	S	PKC	EVDDVSPSPKGFVEE	2.253	1.416
Synemin	*Synm*	S780	IDFSTPFQVEEVDDVSPS[+80]PK	QVEEVDDVSPSPKGFVEEEDG	11	S	PKCa	EVDDVSPSPKGFVEE	5.87	4.803
Synemin	*Synm*	S780	IDFSTPFQVEEVDDVSPS[+80]PK	QVEEVDDVSPSPKGFVEEEDG	11	S	PRKCA	EVDDVSPSPKGFVEE	18.01	7.372
Synemin	*Synm*	S1041	RS[+80]SPVPRS[+80]PDREDGEEAPAGGFLFK	SVVRESLTKRSSPVPRSPDRE	11	S	PKC	RESLTKRSSPVPRSP	2.296	1.416
Synemin	*Synm*	S1041	RS[+80]SPVPRS[+80]PDREDGEEAPAGGFLFK	SVVRESLTKRSSPVPRSPDRE	11	S	PKCa	RESLTKRSSPVPRSP	8.196	4.803
Synemin	*Synm*	S1041	RS[+80]SPVPRS[+80]PDREDGEEAPAGGFLFK	SVVRESLTKRSSPVPRSPDRE	11	S	PRKCA	RESLTKRSSPVPRSP	14.96	7.372
Synemin	*Synm*	S1041	RS[+80]SPVPRS[+80]PDREDGEEAPAGGFLFK	LTKRSSPVPRSPDREDGEEAP	11	S	PRKCA	RSSPVPRSPDREDGE	15.879	7.372
Synemin	*Synm*	S1041	RS[+80]SPVPRS[+80]PDREDGEEAPAGGFLFK	SVVRESLTKRSSPVPRSPDRE	11	S	PRKCB	RESLTKRSSPVPRSP	14.948	10.858
Synemin	*Synm*	S1042	RSS[+80]PVPRS[+80]PDREDGEEAPAGGFLFK	VVRESLTKRSSPVPRSPDRED	11	S	PKC	ESLTKRSSPVPRSPD	3.704	1.416
Synemin	*Synm*	S1042	RSS[+80]PVPRS[+80]PDREDGEEAPAGGFLFK	VVRESLTKRSSPVPRSPDRED	11	S	PKCa	ESLTKRSSPVPRSPD	10.183	4.803
Synemin	*Synm*	S1042	RSS[+80]PVPRS[+80]PDREDGEEAPAGGFLFK	VVRESLTKRSSPVPRSPDRED	11	S	PRKCA	ESLTKRSSPVPRSPD	13.616	7.372
Synemin	*Synm*	S1042	RSS[+80]PVPRS[+80]PDREDGEEAPAGGFLFK	VVRESLTKRSSPVPRSPDRED	11	S	PRKCB	ESLTKRSSPVPRSPD	11.586	10.858

Synemin	*Synm*	T1104	VTQGPVSATVEVT[+80]SPTGFVQSHVLEDVSQSVR	QGPVSATVEVTSPTGFVQSHV	11	T	PRKCA	VSATVEVTSPTGFVQ	8.106	7.372
Synemin	*Synm*	S1105	VTQGPVSATVEVTS[+80]PTGFVQSHVLEDVSQSVR	GPVSATVEVTSPTGFVQSHVL	11	S	PRKCA	SATVEVTSPTGFVQS	10.101	7.372
Talin-1	*Tln1*	S979	GSQAQPDS[+80]PSAQLALIAASQSFLQPGGK	GVRGSQAQPDSPSAQLALIAA	11	S	PKC	GSQAQPDSPSAQLAL	2.02	1.416
Talin-1	*Tln1*	S979	GSQAQPDS[+80]PSAQLALIAASQSFLQPGGK	GVRGSQAQPDSPSAQLALIAA	11	S	PRKCA	GSQAQPDSPSAQLAL	14.49	7.372
Talin-1	*Tln1*	S981	GSQAQPDSPS[+80]AQLALIAASQSFLQPGGK	RGSQAQPDSPSAQLALIAASQ	11	S	PKC	QAQPDSPSAQLALIA	1.727	1.416
Talin-1	*Tln1*	S981	GSQAQPDSPS[+80]AQLALIAASQSFLQPGGK	RGSQAQPDSPSAQLALIAASQ	11	S	PRKCA	QAQPDSPSAQLALIA	17.859	7.372
Telethonin	*Tcap*	S161	SMS[+80]QEAQRG	PLRRTLSRSMSQEAQRG	11	S	PKC	RTLSRSMSQEAQRG*	2.633	1.416
Telethonin	*Tcap*	S161	SMS[+80]QEAQRG	PLRRTLSRSMSQEAQRG	11	S	PKCa	RTLSRSMSQEAQRG*	10.717	4.803
Telethonin	*Tcap*	S161	SMS[+80]QEAQRG	PLRRTLSRSMSQEAQRG	11	S	PKCd	RTLSRSMSQEAQRG*	3.838	3.771
Telethonin	*Tcap*	S161	SMS[+80]QEAQRG	PLRRTLSRSMSQEAQRG	11	S	PRKCA	RTLSRSMSQEAQRG*	21.247	7.372
Telethonin	*Tcap*	S161	SMS[+80]QEAQRG	PLRRTLSRSMSQEAQRG	11	S	PRKCB	RTLSRSMSQEAQRG*	15.948	10.858
Tensin 2	*Tns2*	S455	WDS[+80]YENFNQHHEDSVDGSLAHTR	NMTEPAVRWDSYENFNQHHED	11	S	PKC	EPAVRWDSYENFNQH	1.474	1.416
Tensin 2	*Tns2*	S455	WDS[+80]YENFNQHHEDSVDGSLAHTR	NMTEPAVRWDSYENFNQHHED	11	S	PKCa	EPAVRWDSYENFNQH	6.635	4.803
Tensin 2	*Tns2*	S455	WDS[+80]YENFNQHHEDSVDGSLAHTR	NMTEPAVRWDSYENFNQHHED	11	S	PRKCA	EPAVRWDSYENFNQH	16.944	7.372
Tensin-1	*Tln1*	S1081	AASDGQYENQS[+80]PEATSPR	AASDGQYENQSPEATSPRSPG	11	S	PKCa	DGQYENQSPEATSPR	5.096	4.803
Tensin-1	*Tln1*	S1081	AASDGQYENQS[+80]PEATSPR	AASDGQYENQSPEATSPRSPG	11	S	PRKCA	DGQYENQSPEATSPR	12.692	7.372
Tensin-1	*Tln1*	S1032	ETTSDTS[+80]RTPEEEPLNLEGLVAHR	LPLKETTSDTSRTPEEEPLNL	11	S	PKCa	KETTSDTSRTPEEEP	6.361	4.803
Tensin-1	*Tln1*	S1032	ETTSDTS[+80]RTPEEEPLNLEGLVAHR	LPLKETTSDTSRTPEEEPLNL	11	S	PRKCA	KETTSDTSRTPEEEP	13.758	7.372
Tensin-1	*Tln1*	S1480	HLGGS[+80]GSVVPGSPSLDR	SPSLGRHLGGSGSVVPGSPSL	11	S	PRKCA	LGRHLGGSGSVVPGS	12.015	7.372
Tensin-1	*Tln1*	T1501	HVAYGGYST[+80]PEDR	DRHVAYGGYSTPEDRRPTLSR	11	T	PRKCA	VAYGGYSTPEDRRPT	8.298	7.372
Tensin-1	*Tln1*	S949	S[+80]GYIPSGDTLGAPELLSSGR	CQSHPLTQSRSGYIPSGDTLG	11	S	PRKCA	HPLTQSRSGYIPSGD	12.455	7.372
Tensin-1	*Tln1*	S1222	SFS[+80]APATHAYGHETPLR	RAQDVEPKSFSAPATHAYGHE	11	S	PKC	DVEPKSFSAPATHAY	2.302	1.416
Tensin-1	*Tln1*	S1222	SFS[+80]APATHAYGHETPLR	RAQDVEPKSFSAPATHAYGHE	11	S	PKCa	DVEPKSFSAPATHAY	7.67	4.803
Tensin-1	*Tln1*	S1222	SFS[+80]APATHAYGHETPLR	RAQDVEPKSFSAPATHAYGHE	11	S	PRKCA	DVEPKSFSAPATHAY	13.475	7.372
Tensin-3	*Tns3*	S773	KLS[+80]IGQYDNDAGSQVTFSK	DPVGGRLRKLSIGQYDNDAGS	11	S	PKC	GGRLRKLSIGQYDND	4.065	1.416
Tensin-3	*Tns3*	S773	KLS[+80]IGQYDNDAGSQVTFSK	DPVGGRLRKLSIGQYDNDAGS	11	S	PKCa	GGRLRKLSIGQYDND	9.513	4.803
Tensin-3	*Tns3*	S773	KLS[+80]IGQYDNDAGSQVTFSK	DPVGGRLRKLSIGQYDNDAGS	11	S	PRKCA	GGRLRKLSIGQYDND	19.641	7.372
Titin	*Ttn*	S33961	EETS[+80]TSYAELR	TYHVPTKEETSTSYAELRERH	11	S	PRKCA	VPTKEETSTSYAELR	14.449	7.372
Titin	*Ttn*	S33961	EETS[+80]TSYAELR	TYHVPTKEETSTSYAELRERH	11	S	PRKCB	VPTKEETSTSYAELR	12.207	10.858
Titin	*Ttn*	T33962	EETST[+80]SYAELR	YHVPTKEETSTSYAELRERHA	11	T	PKC	PTKEETSTSYAELRE	1.449	1.416
Titin	*Ttn*	T33962	EETST[+80]SYAELR	YHVPTKEETSTSYAELRERHA	11	T	PRKCA	PTKEETSTSYAELRE	8.652	7.372
Titin	*Ttn*	S17984	RSDTGLYS[+80]ITAVNNLGTASK	QSRRSDTGLYSITAVNNLGTA	11	S	PRKCA	RSDTGLYSITAVNNL	10.591	7.372
Titin	*Ttn*	T34067	SLSPT[+80]YIELMRPVSELIR	LLRRRRSLSPTYIELMRPVSE	11	T	PKC	RRRSLSPTYIELMRP	3.365	1.416
Titin	*Ttn*	T34067	SLSPT[+80]YIELMRPVSELIR	LLRRRRSLSPTYIELMRPVSE	11	T	PRKCA	RRRSLSPTYIELMRP	9.909	7.372
Tropomyosin alpha-1 chain	*Tpm1*	T282	YKAISEELDHALNDMT[+80]SI	EELDHALNDMTSI	11	T	PRKCA	DHALNDMTSI*****	13.793	7.372

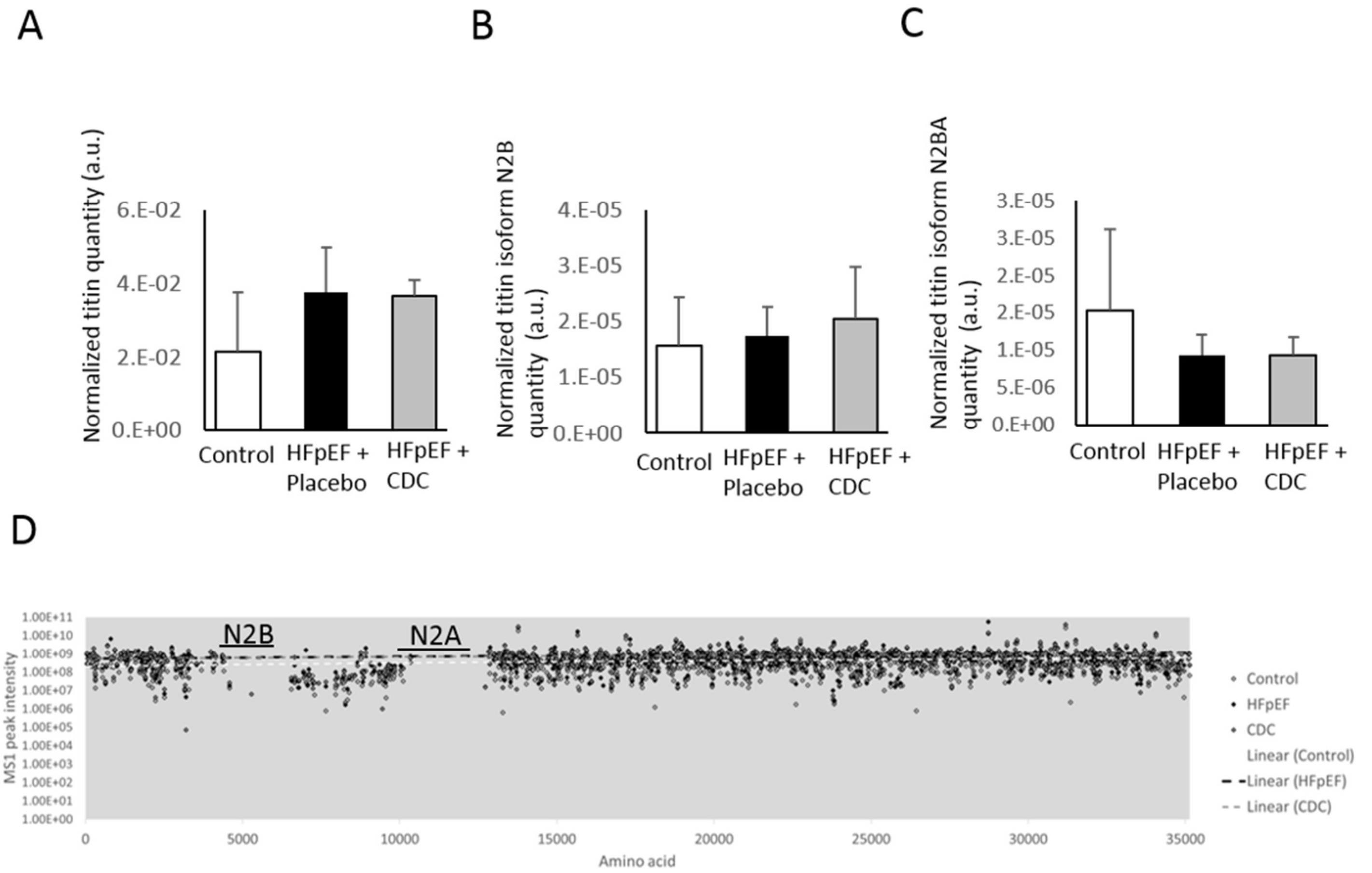
Tropomyosin alpha-1 chain	*Tpm1*	S283	YKAISEELDHALNDMTS[+80]I	KELDHALNDMTSI	12	S	PKCa	HALNDMTSI******	5.209	4.803
Tropomyosin alpha-1 chain	*Tpm1*	S283	YKAISEELDHALNDMTS[+80]I	KELDHALNDMTSI	12	S	PRKCA	HALNDMTSI******	22.707	7.372
Tropomyosin alpha-1 chain	*Tpm1*	S283	YKAISEELDHALNDMTS[+80]I	KELDHALNDMTSI	12	S	PRKCB	HALNDMTSI******	18.207	10.858
Utrophin	*Utrn*	S933	AAQAS[+80]LSALNDPSAVEQALQEK	LSESEKAAQASLSALNDPSAV	11	S	PKC	SEKAAQASLSALNDP	2.767	1.416
Utrophin	*Utrn*	S933	AAQAS[+80]LSALNDPSAVEQALQEK	LSESEKAAQASLSALNDPSAV	11	S	PKCa	SEKAAQASLSALNDP	4.935	4.803
Utrophin	*Utrn*	S933	AAQAS[+80]LSALNDPSAVEQALQEK	LSESEKAAQASLSALNDPSAV	11	S	PRKCA	SEKAAQASLSALNDP	13.556	7.372
Utrophin	*Utrn*	S935	AAQASLS[+80]ALNDPSAVEQALQEK	ESEKAAQASLSALNDPSAVEQ	11	S	PKC	KAAQASLSALNDPSA	1.777	1.416
Utrophin	*Utrn*	S935	AAQASLS[+80]ALNDPSAVEQALQEK	ESEKAAQASLSALNDPSAVEQ	11	S	PRKCA	KAAQASLSALNDPSA	11.586	7.372
Vasodilator-stimulated phosphoprotein	*Vasp*	S236	KVS[+80]KEEASGGPLAPK	AIAGAKLRKVSKEEASGGPLA	11	S	PKC	GAKLRKVSKEEASGG	6.976	1.416
Vasodilator-stimulated phosphoprotein	*Vasp*	S236	KVS[+80]KEEASGGPLAPK	AIAGAKLRKVSKEEASGGPLA	11	S	PKCa	GAKLRKVSKEEASGG	9.561	4.803
Vasodilator-stimulated phosphoprotein	*Vasp*	S236	KVS[+80]KEEASGGPLAPK	AIAGAKLRKVSKEEASGGPLA	11	S	PKCd	GAKLRKVSKEEASGG	3.784	3.771
Vasodilator-stimulated phosphoprotein	*Vasp*	S236	KVS[+80]KEEASGGPLAPK	AIAGAKLRKVSKEEASGGPLA	11	S	PRKCA	GAKLRKVSKEEASGG	20.768	7.372
Vasodilator-stimulated phosphoprotein	*Vasp*	S236	KVS[+80]KEEASGGPLAPK	AIAGAKLRKVSKEEASGGPLA	11	S	PRKCB	GAKLRKVSKEEASGG	14.034	10.858
Vinculin	*Vcl*	S579	ALASQLQDS[+80]LKDLK	ARALASQLQDSLKDLKTQMQE	11	S	PKC	LASQLQDSLKDLKTQ	5.424	1.416
Vinculin	*Vcl*	S579	ALASQLQDS[+80]LKDLK	ARALASQLQDSLKDLKAQMQE	11	S	PKC	LASQLQDSLKDLKAQ	5.639	1.416
Vinculin	*Vcl*	S579	ALASQLQDS[+80]LKDLK	ARALASQLQDSLKDLKTQMQE	11	S	PKCa	LASQLQDSLKDLKTQ	5.443	4.803
Vinculin	*Vcl*	S579	ALASQLQDS[+80]LKDLK	ARALASQLQDSLKDLKAQMQE	11	S	PKCa	LASQLQDSLKDLKAQ	5.752	4.803
Vinculin	*Vcl*	S579	ALASQLQDS[+80]LKDLK	ARALASQLQDSLKDLKTQMQE	11	S	PRKCA	LASQLQDSLKDLKTQ	22.015	7.372
Vinculin	*Vcl*	S579	ALASQLQDS[+80]LKDLK	ARALASQLQDSLKDLKAQMQE	11	S	PRKCA	LASQLQDSLKDLKAQ	21.803	7.372
Vinculin	*Vcl*	S579	ALASQLQDS[+80]LKDLK	ARALASQLQDSLKDLKTQMQE	11	S	PRKCB	LASQLQDSLKDLKTQ	12.586	10.858
Vinculin	*Vcl*	S579	ALASQLQDS[+80]LKDLK	ARALASQLQDSLKDLKAQMQE	11	S	PRKCB	LASQLQDSLKDLKAQ	12.31	10.858
Vinculin	*Vcl*	S346	ARGQGAS[+80]PVAMQK	ADLRARGQGASPVAMQKAQQV	11	S	PKC	RARGQGASPVAMQKA	1.801	1.416
Vinculin	*Vcl*	S346	ARGQGAS[+80]PVAMQK	ADLRARGQGASPVAMQKAQQV	11	S	PRKCA	RARGQGASPVAMQKA	8.091	7.372
Vinculin	*Vcl*	S290	GWLRDPNAS[+80]PGDAGEQAIR	AKGWLRDPNASPGDAGEQAIR	11	S	PRKCA	WLRDPNASPGDAGEQ	12.535	7.372
Vinculin	*Vcl*	S97	LVQAAQMLQS[+80]DPYSVPAR	KLVQAAQMLQSDPYSVPARDY	11	S	PRKCA	QAAQMLQSDPYSVPA	9.838	7.372
Vinculin	*Vcl*	T719	MTGLVDEAIDT[+80]KSLLDASEEAIKK	MTGLVDEAIDTKSLLDASEEA	11	T	PRKCA	LVDEAIDTKSLLDAS	7.813	7.372
Vinculin	*Vcl*	S721	MTGLVDEAIDTKS[+80]LLDASEEAIKK	GLVDEAIDTKSLLDASEEAIK	11	S	PKC	DEAIDTKSLLDASEE	2.078	1.416
Vinculin	*Vcl*	S721	MTGLVDEAIDTKS[+80]LLDASEEAIKK	GLVDEAIDTKSLLDASEEAIK	11	S	PRKCA	DEAIDTKSLLDASEE	15.97	7.372
Vinculin	*Vcl*	S795	TIS[+80]PMVMDAK	AASDELSKTISPMVMDAKAVA	11	S	PKC	DELSKTISPMVMDAK	1.568	1.416
Vinculin	*Vcl*	S795	TIS[+80]PMVMDAK	AASDELSKTISPMVMDAKAVA	11	S	PRKCA	DELSKTISPMVMDAK	11.823	7.372
Vinculin	*Vcl*	T602	TQMQEAMTQEVSDVFSDT[+80]TTPIK	TQEVSDVFSDTTTPIKLLAVA	11	T	PRKCA	VSDVFSDTTTPIKLL	8.439	7.372
WASH complex subunit 2	*Washc2*	S611	ASALFSS[+80]DEEDQWSVADSQTK	PPKKASALFSSDEEDQWSVAD	11	S	PRKCA	KASALFSSDEEDQWS	8.535	7.372
WASH complex subunit 2	*Washc2*	S387	GQPAQGPVSEESPPS[+80]PKPGK	QGPVSEESPPSPKPGKKIPAG	11	S	PKC	VSEESPPSPKPGKKI	2.382	1.416
WASH complex subunit 2	*Washc2*	S387	GQPAQGPVSEESPPS[+80]PKPGK	QGPVSEESPPSPKPGKKIPAG	11	S	PKCa	VSEESPPSPKPGKKI	9.196	4.803

WASH complex subunit 2	*Washc2*	S387	GQPAQGPVSEESPPS[+80]PKPGK	QGPVSEESPPSPKPGKKIPAG	11	S	PRKCA	VSEESPPSPKPGKKI	16.596	7.372
WASH complex subunit 2	*Washc2*	S387	GQPAQGPVSEESPPS[+80]PKPGK	QGPVSEESPPSPKPGKKIPAG	11	S	PRKCB	VSEESPPSPKPGKKI	12.707	10.858
Whirlin	*Whrn*	S637	NRS[+80]PPPPPGIAPTPTPGPSSAR	GIVFSAPRNRSPPPPPGIAPT	11	S	PKCa	FSAPRNRSPPPPPGI	5.265	4.803
Whirlin	*Whrn*	S637	NRS[+80]PPPPPGIAPTPTPGPSSAR	GIVFSAPRNRSPPPPPGIAPT	11	S	PRKCA	FSAPRNRSPPPPPGI	16.854	7.372
Xin actin-binding repeat-containing protein 1	*Xirp1*	S332	DFQPS[+80]PDLIPPGPDVQHQR	IEVDEKDFQPSPDLIPPGPDV	11	S	PRKCA	DEKDFQPSPDLIPPG	10.46	7.372
Xin actin-binding repeat-containing protein 1	*Xirp1*	S332	DFQPS[+80]PDLIPPGPDVQHQR	ILVDEKDFQPSPDLIPPGPDV	11	S	PRKCA	DEKDFQPSPDLIPPG	10.46	7.372
Xin actin-binding repeat-containing protein 1	*Xirp1*	S295	GIS[+80]LEEGALPDVSATR	PSQVRVIRGISLEEGALPDVS	11	S	PRKCA	VRVIRGISLEEGALP	17.455	7.372
Xin actin-binding repeat-containing protein 1	*Xirp1*	S726	GVQETVLS[+80]PGSIPTGSVHK	GKRGVQETVLSPGSIPTGSVH	11	S	PRKCA	GVQETVLSPGSIPTG	7.525	7.372
Xin actin-binding repeat-containing protein 1	*Xirp1*	S532	SPS[+80]TVDVVR	QPLDRLGRSPSTVDVVRGITR	11	S	PKC	DRLGRSPSTVDVVRG	2.512	1.416
Xin actin-binding repeat-containing protein 1	*Xirp1*	S532	SPS[+80]TVDVVR	QPLDRLGRSPSTVDVVRGITR	11	S	PKCa	DRLGRSPSTVDVVRG	8.478	4.803
Xin actin-binding repeat-containing protein 1	*Xirp1*	S532	SPS[+80]TVDVVR	QPLDRLGRSPSTVDVVRGITR	11	S	PRKCA	DRLGRSPSTVDVVRG	17.566	7.372
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2198	AKMS[+80]QDSPSGELER	KLPERIKAKMSQDSPSGELER	11	S	PKC	ERIKAKMSQDSPSGE	4.122	1.416
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2198	AKMS[+80]QDSPSGELER	KLPERIKAKMSQDSPSGELER	11	S	PRKCA	ERIKAKMSQDSPSGE	13.444	7.372
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2198	AKMS[+80]QDSPSGELER	KLPERIKAKMSQDSPSGELER	11	S	PRKCB	ERIKAKMSQDSPSGE	15.897	10.858
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2987	GGDS[+80]PPTITIPVSVNHHVVSGSFR	QIKIESRGGDSPPTITIPVSV	11	S	PRKCA	IESRGGDSPPTITIP	10.328	7.372
Xin actin-binding repeat-containing protein 2	*Xirp2*	S813	GIS[+80]AQEIQAGNVK	LHKFQIIRGISAQEIQAGNVK	11	S	PKC	FQIIRGISAQEIQAG	2.138	1.416
Xin actin-binding repeat-containing protein 2	*Xirp2*	S813	GIS[+80]AQEIQAGNVK	LHKFQIIRGISAQEIQAGNVK	11	S	PKCa	FQIIRGISAQEIQAG	4.93	4.803
Xin actin-binding repeat-containing protein 2	*Xirp2*	S813	GIS[+80]AQEIQAGNVK	LHKFQIIRGISAQEIQAGNVK	11	S	PRKCA	FQIIRGISAQEIQAG	18.354	7.372
Xin actin-binding repeat-containing protein 2	*Xirp2*	S565	GIS[+80]MEENVK	ITEIKVVRGISMEENVKGEVG	11	S	PKC	IKVVRGISMEENVKG	2.165	1.416
Xin actin-binding repeat-containing protein 2	*Xirp2*	S565	GIS[+80]MEENVK	ITEIKVVRGISMEENVKGEVG	11	S	PKCa	IKVVRGISMEENVKG	8.035	4.803
Xin actin-binding repeat-containing protein 2	*Xirp2*	S565	GIS[+80]MEENVK	ITEIKVVRGISMEENVKGEVG	11	S	PRKCA	IKVVRGISMEENVKG	19.47	7.372
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2252	KQLS[+80]ISSANSLSQTVPEIPAPK	FRKSLGRKQLSISSANSLSQT	11	S	PKC	SLGRKQLSISSANSL	4.935	1.416
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2252	KQLS[+80]ISSANSLSQTVPEIPAPK	FRKSLGRKQLSISSANSLSQT	11	S	PKCa	SLGRKQLSISSANSL	11.935	4.803
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2252	KQLS[+80]ISSANSLSQTVPEIPAPK	FRKSLGRKQLSISSANSLSQT	11	S	PRKCA	SLGRKQLSISSANSL	19.348	7.372
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2252	KQLS[+80]ISSANSLSQTVPEIPAPK	FRKSLGRKQLSISSANSLSQT	11	S	PRKCB	SLGRKQLSISSANSL	11.155	10.858

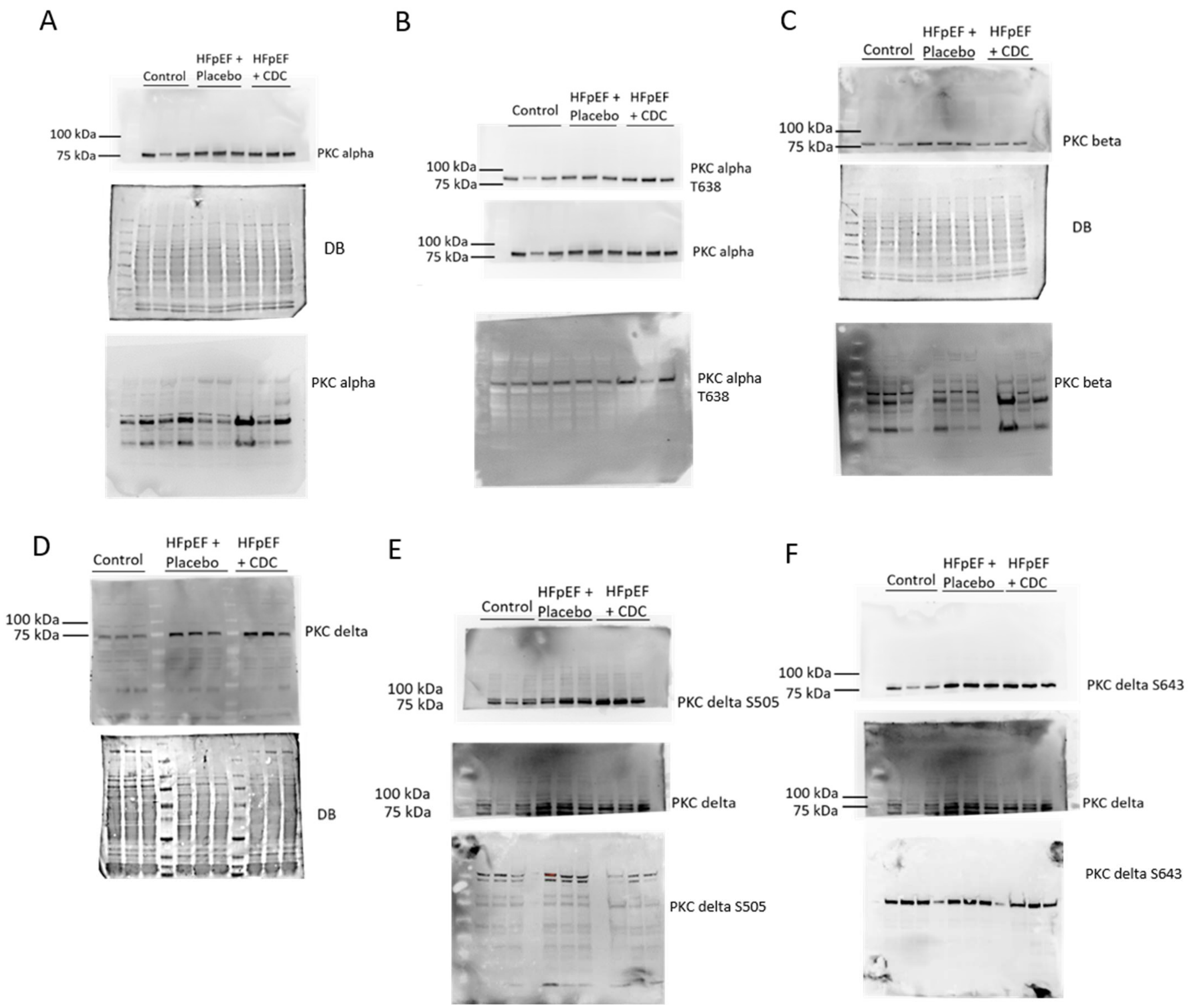
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2254	KQLSIS[+80]SANSLSQTVPEIPAPK	KSLGRKQLSISSANSLSQTVP	11	S	PKC	GRKQLSISSANSLSQ	2.863	1.416
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2254	KQLSIS[+80]SANSLSQTVPEIPAPK	KSLGRKQLSISSANSLSQTVP	11	S	PRKCA	GRKQLSISSANSLSQ	14.808	7.372
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2255	KQLSISS[+80]ANSLSQTVPEIPAPK	SLGRKQLSISSANSLSQTVPE	11	S	PKCa	RKQLSISSANSLSQT	6.513	4.803
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2255	KQLSISS[+80]ANSLSQTVPEIPAPK	SLGRKQLSISSANSLSQTVPE	11	S	PRKCA	RKQLSISSANSLSQT	12.505	7.372
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2258	KQLSISSANS[+80]LSQTVPEIPAPK	RKQLSISSANSLSQTVPEIPA	11	S	PKCa	LSISSANSLSQTVPE	7.065	4.803
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2258	KQLSISSANS[+80]LSQTVPEIPAPK	RKQLSISSANSLSQTVPEIPA	11	S	PRKCA	LSISSANSLSQTVPE	20.232	7.372
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2260	KQLSISSANSLS[+80]QTVPEIPAPK	QLSISSANSLSQTVPEIPAPK	11	S	PKCa	ISSANSLSQTVPEIP	4.93	4.803
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2260	KQLSISSANSLS[+80]QTVPEIPAPK	QLSISSANSLSQTVPEIPAPK	11	S	PRKCA	ISSANSLSQTVPEIP	11.955	7.372
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2970	SEVVMS[+80]PATLR	IVEKRSEVVMSPATLRRQIKI	11	S	PKC	KRSEVVMSPATLRRQ	1.793	1.416
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2970	SEVVMS[+80]PATLR	VVEKRSEVVMSPATLRRQIKI	11	S	PKC	KRSEVVMSPATLRRQ	1.771	1.416
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2970	SEVVMS[+80]PATLR	IVEKRSEVVMSPATLRRQIKI	11	S	PRKCB	KRSEVVMSPATLRRQ	10.897	10.858
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2970	SEVVMS[+80]PATLR	VVEKRSEVVMSPATLRRQIKI	11	S	PRKCB	KRSEVVMSPATLRRQ	10.897	10.858
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2291	SHSFPSGSEQQS[+80]PKPYMR	HSFPSGSEQQSPKPYMRKFKT	11	S	PKC	PSGSEQQSPKPYMRK	3.142	1.416
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2291	SHSFPSGSEQQS[+80]PKPYMR	HSFPSGSEQQSPKPYMRKFKT	11	S	PKCa	PSGSEQQSPKPYMRK	9.752	4.803
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2291	SHSFPSGSEQQS[+80]PKPYMR	HSFPSGSEQQSPKPYMRKFKT	11	S	PRKCA	PSGSEQQSPKPYMRK	18.298	7.372
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2211	SLS[+80]DVEIK	SPSGELERSLSDVEIKTTLSK	11	S	PRKCA	GELERSLSDVEIKTT	9.985	7.372
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2211	SLS[+80]DVEIK	SSSGELERSLSDVEIKATLSK	11	S	PRKCA	GELERSLSDVEIKAT	9.98	7.372
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2211	SLS[+80]DVEIK	SPSGELERSLSDVEIKTTLSK	11	S	PRKCB	GELERSLSDVEIKTT	11.517	10.858
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2211	SLS[+80]DVEIK	SSSGELERSLSDVEIKATLSK	11	S	PRKCB	GELERSLSDVEIKAT	11.19	10.858
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2873	TRPPS[+80]PTFITIESTAR	APPSLKTRPPSPTFITIESTA	11	S	PKC	SLKTRPPSPTFITIE	2.034	1.416
Xin actin-binding repeat-containing protein 2	*Xirp2*	S2873	TRPPS[+80]PTFITIESTAR	APPSLKTRPPSPTFITIESTA	11	S	PRKCA	SLKTRPPSPTFITIE	12.586	7.372
Xin actin-binding repeat-containing protein 2	*Xirp2*	T2875	TRPPSPT[+80]FITIESTAR	PSLKTRPPSPTFITIESTARR	11	T	PKC	KTRPPSPTFITIEST	1.502	1.416
Xin actin-binding repeat-containing protein 2	*Xirp2*	T2875	TRPPSPT[+80]FITIESTAR	PSLKTRPPSPTFITIESTARR	11	T	PRKCA	KTRPPSPTFITIEST	9.934	7.372
Xin actin-binding repeat-containing protein 2	*Xirp2*	S1573	TVS[+80]ETDIIPGDVR	KRQSSIERTVSETDIIPGDVR	11	S	PKC	SSIERTVSETDIIPG	1.633	1.416

Xin actin-binding repeat-containing protein 2	*Xirp2*	S1573	TVS[+80]ETDIIPGDVR	KRQSSIERTVSETDIIPGDVR	11	S	PRKCA	SSIERTVSETDIIPG	12.551	7.372
Xin actin-binding repeat-containing protein 2	*Xirp2*	S1210	TVS[+80]INEIQK	GDKKNYVRTVSINEIQKGNVK	11	S	PKC	KNYVRTVSINEIQKG	3.548	1.416
Xin actin-binding repeat-containing protein 2	*Xirp2*	S1210	TVS[+80]INEIQK	GDKKNYVRTVSINEIQKGNVK	11	S	PKCa	KNYVRTVSINEIQKG	10.022	4.803
Xin actin-binding repeat-containing protein 2	*Xirp2*	S1210	TVS[+80]INEIQK	GDKKNYVRTVSINEIQKGNVK	11	S	PRKCA	KNYVRTVSINEIQKG	18.328	7.372
Xin actin-binding repeat-containing protein 2	*Xirp2*	S3246	VFKS[+80]VGYETSDAHATEMSR	TWQESERVFKSVGYETSDAHA	11	S	PRKCA	ESERVFKSVGYETSD	11.965	7.372

Online Figures I - II



Supplemental Figure I: Shown are titin and titin isoforms N2B and N2BA concentration in the hypertrophic induced HFpEF rat model and following its treatment with CDCs. Listed is the averaged MS1 intensity of titin peptides A peptides of titin isoform N2B B, and peptides of titin isoform element N2BA C normalized to total protein signal intensity for control low salt, n=3, HFpEF induced high salt, n=4, and HFpEF treated with CDCs n=4 animal treatment groups. Significant changes weren't detected among treatment groups with three or four biological repeats. In addition, the distribution of individual titin peptide intensity is shown for the three treatment groups and an equal distribution of peptide signal intensity in titin sequence suggests that the protein was not susceptible to degradation.



Supplemental Figure II: Western blots performed for PKC α (A), β (C), and δ (D) the phosphorylation sites T638 of PKCα (B), S505 (E), and S643 (F) of PKCδ from the identical LV rat samples used for MS analysis. PKC isoforms were normalized to total protein staining (DB) and PKC isoform modifications were normalized to the equivalent total PKC.