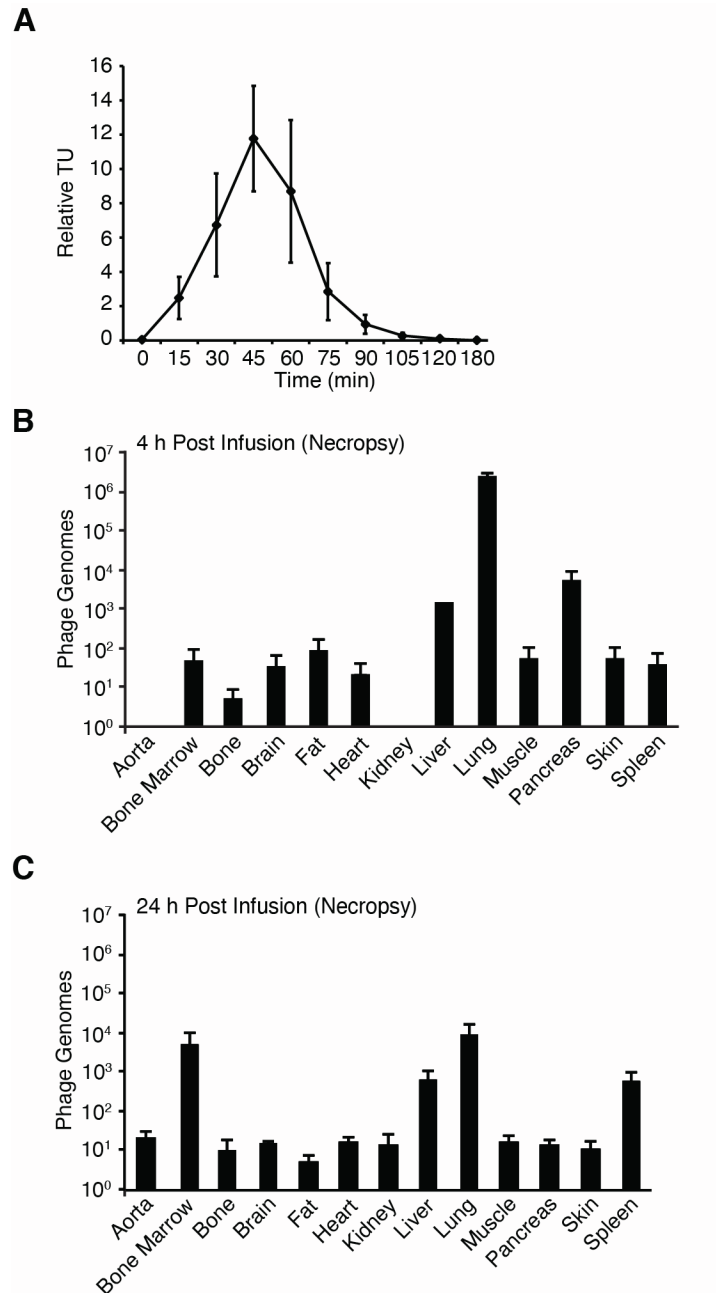


**Supplemental information**

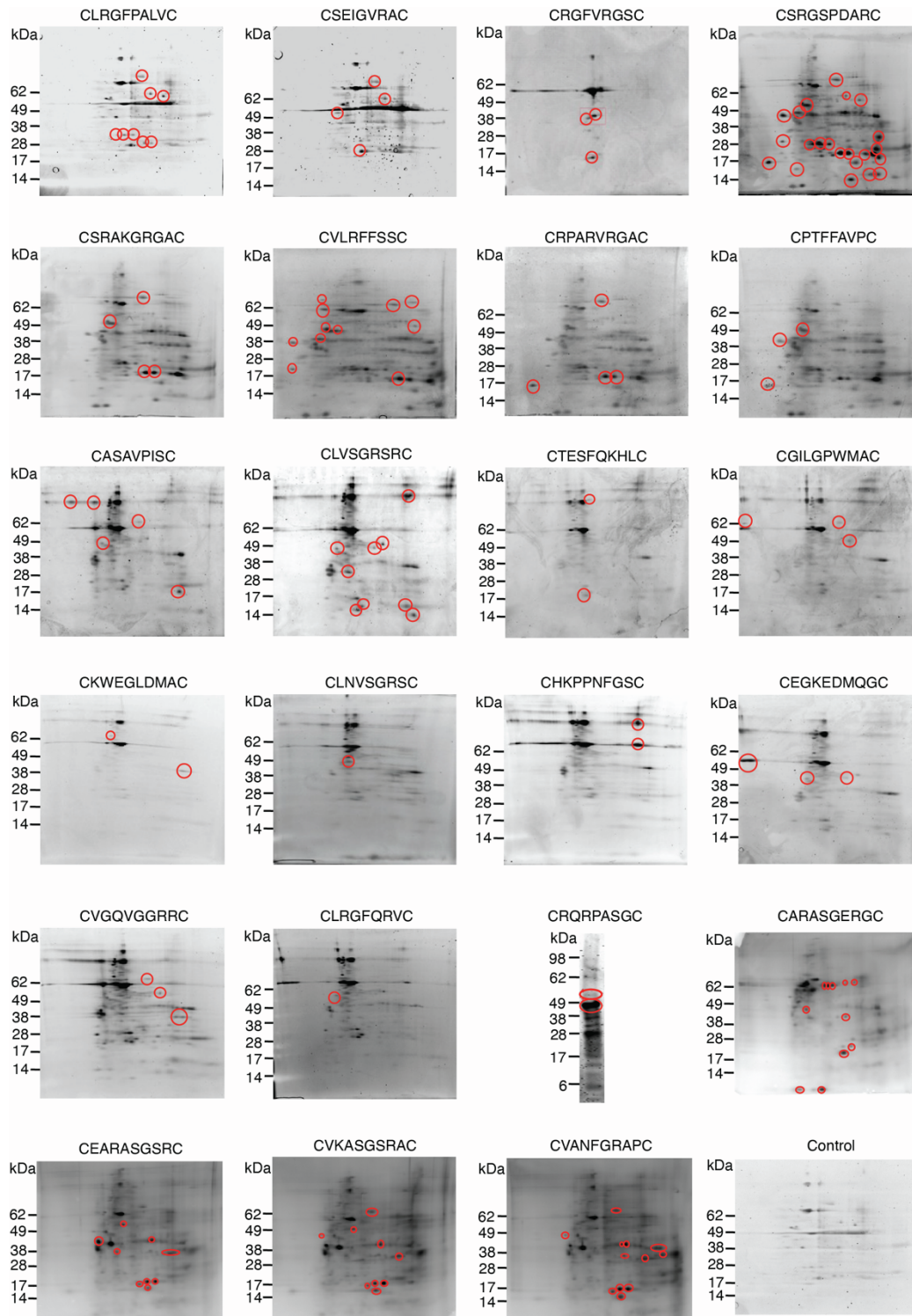
**Conformational ligand-directed targeting  
of calcium-dependent receptors in acute trauma**

**Renata Pasqualini, Christopher Markosian, Daniela I. Staquicini, Andrey S. Dobroff, Esteban Dodero-Rojas, Paul C. Whitford, E. Magda Barbu, Julianna K. Bronk, Marina Cardó-Vila, Dawn R. Christianson, Emmanuel Dias-Neto, Wouter H.P. Driessen, Liliana Guzman-Rojas, Serena Marchiò, Diana N. Nunes, Francislón S. de Oliveira, Michael G. Ozawa, Bettina Proneth, Roberto Rangel, Tracey L. Smith, Glauco R. Souza, Fernanda I. Staquicini, Fenny H.F. Tang, Wallace B. Baze, João C. Setubal, John W. Burns, Michael A. Dubick, Juri G. Gelovani, Andriy I. Batchinsky, Jon E. Mogford, Charles E. Wade, John B. Holcomb, Stephen K. Burley, José N. Onuchic, and Wadih Arap**



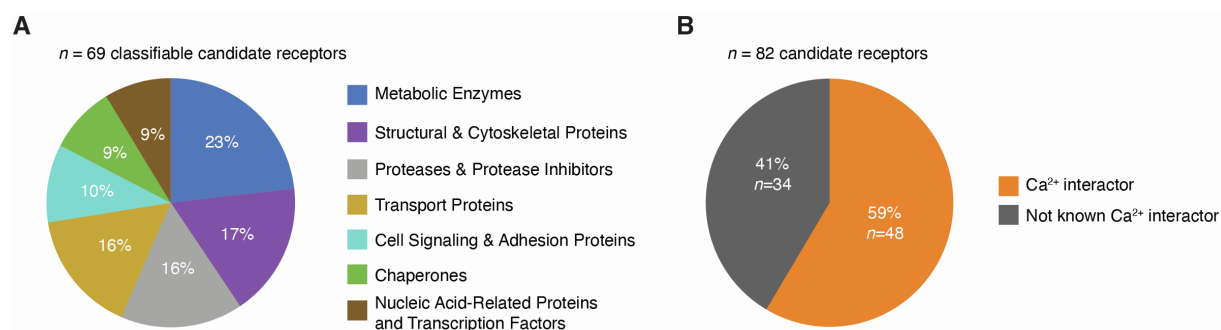
**Figure S1: Systemic administration of *in vivo* phage display peptide library in non-injured pigs with euthanasia at either 4 h or 24 h post infusion, related to STAR Methods. (A)** Profile of phage clearance via arterial blood sample collection at various time points by relative TU. Data presented as mean  $\pm$  standard error of the mean (SEM). **(B, C)** Phage quantification in different tissues by qPCR per 100 ng of

DNA at necropsy performed at (B) 4 h or (C) 24 h post infusion. Data presented as mean + SEM.



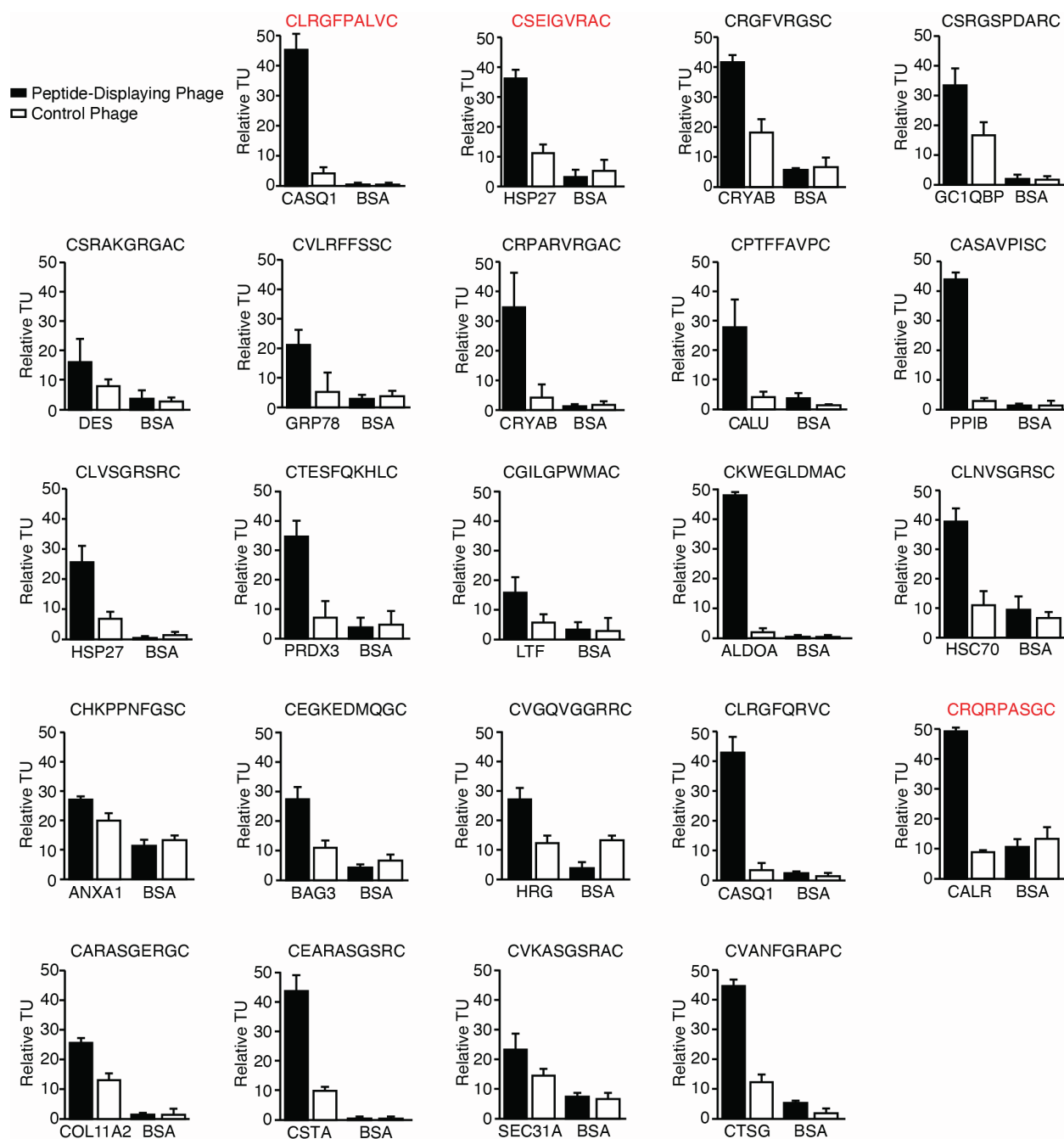
**Figure S2: Two-dimensional SDS-PAGE after peptide-affinity chromatography for identification of candidate receptors from injured pig tissue (muscle for peptides #1–#19 and bone for peptides #20–#23), related to STAR Methods. Circled bands,**

which correspond to exclusive bands that were not observed in a matching receptor isolation from control pig tissue for each peptide, were excised for matrix-assisted laser desorption/ionization coupled to time-of-flight (MALDI-TOF) mass spectrometry. N.B.: One-dimensional SDS PAGE was performed for CRQRPASGC (peptide #19).



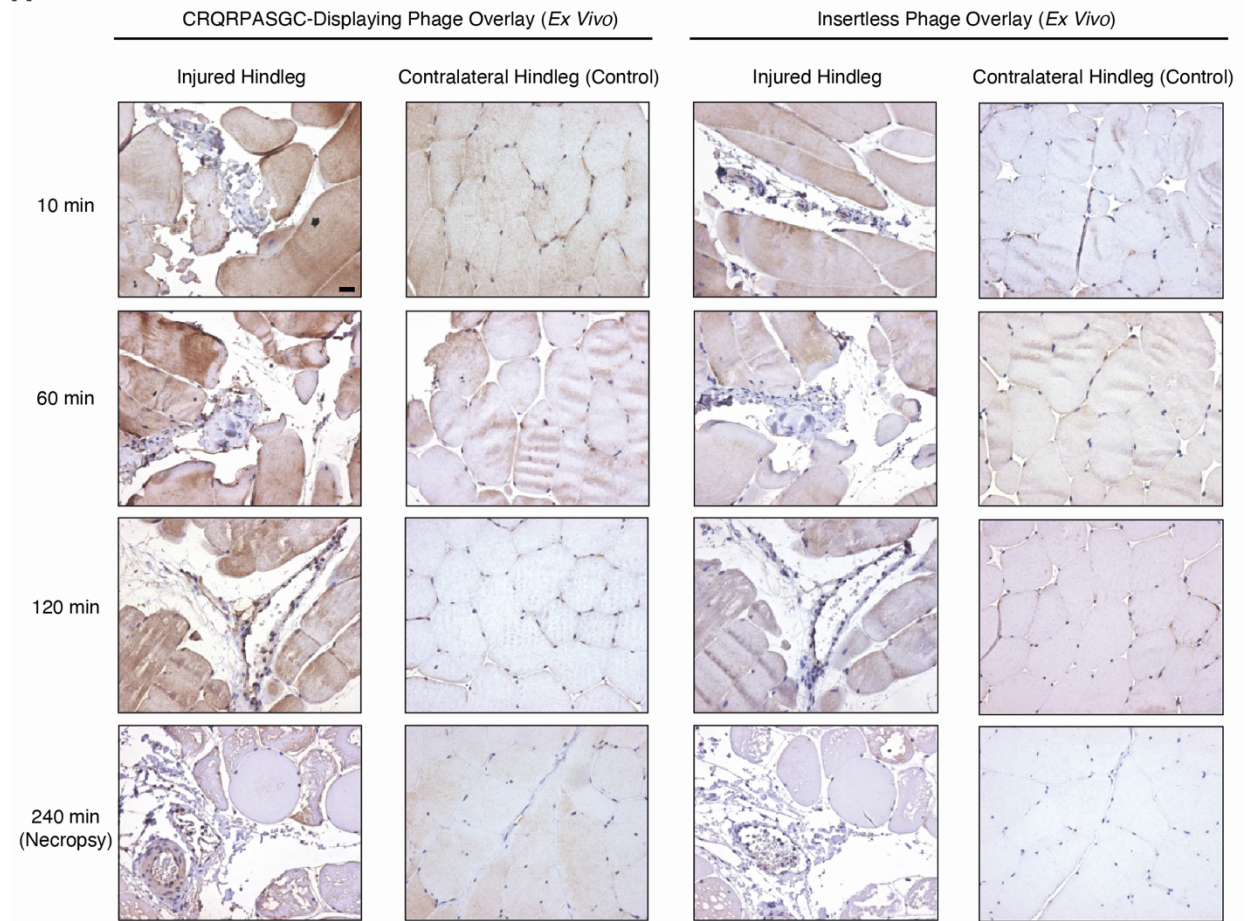
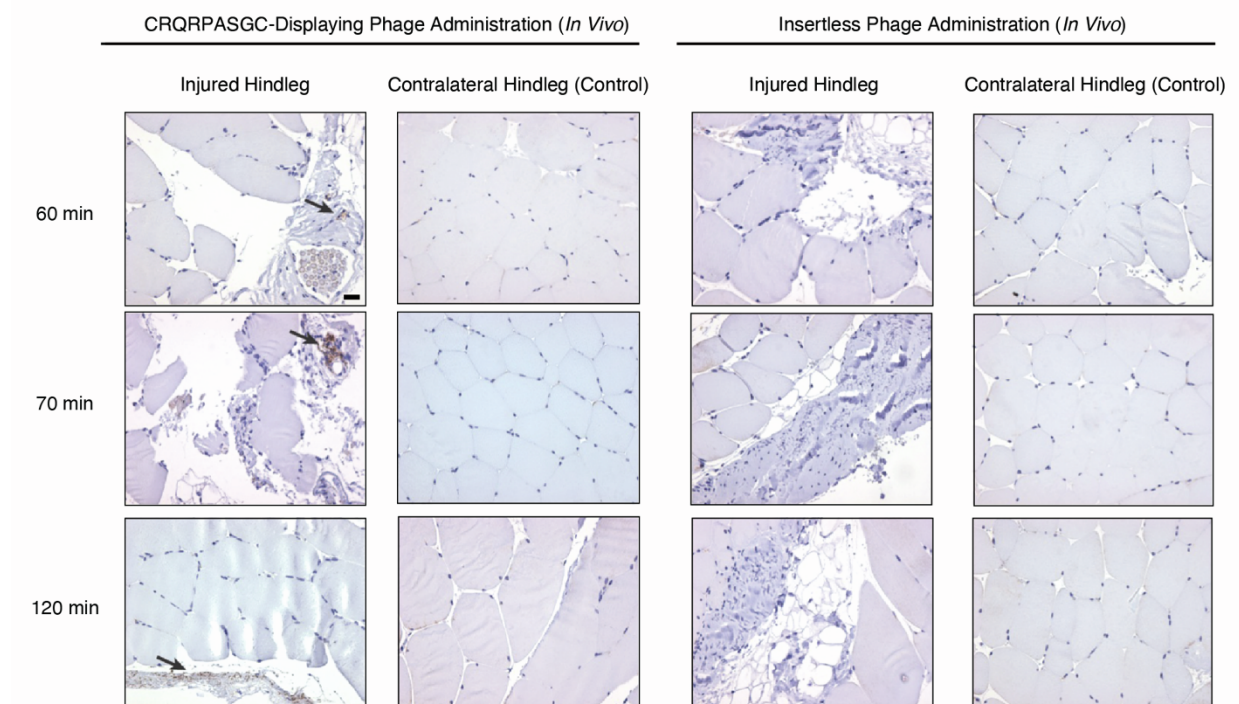
**Figure S3: Distinct candidate receptors (n=82) of the 23 lead peptides identified by MALDI-TOF mass spectrometry, related to STAR Methods. (A)** The PANTHER class of each protein was identified and subsequently assigned to a broader classification group via a customized scheme. Broad classifications groups are comprised of the following PANTHER classes: Metabolic Enzymes (dehydrogenase, hydrolase, oxidoreductase, peroxidase, aldolase, ATP synthase, deacetylase, glycosyltransferase, hydratase, lyase, non-receptor serine/threonine protein kinase, phosphatase), Structural and Cytoskeletal Proteins (intermediate filament binding protein, actin or actin-binding cytoskeletal protein, intermediate filament, actin binding motor protein, extracellular matrix protein, extracellular matrix structural protein, microtubule binding motor protein, non-motor actin binding protein), Proteases and Protease Inhibitors (serine protease, protease, protease inhibitor, metalloprotease), Transport Proteins (calmodulin-related, calcium-binding protein, transfer/carrier protein, transporter, membrane traffic protein, vesicle coat protein), Cell Signaling and Adhesion Proteins (cadherin, cell adhesion molecule, complement component, integrin, scaffold/adaptor protein), Chaperones (chaperone, Hsp70 family chaperone), Nucleic Acid-Related Proteins and Transcription Factors (RNA metabolism protein, basic helix-loop-helix transcription factor, DNA metabolism protein, HMG box transcription factor, translation initiation factor). The remaining 13 proteins did not have a PANTHER

classification. **(B)** Number of candidate receptors that directly or indirectly (i.e., through one protein mediator) interact with  $\text{Ca}^{2+}$  according to Ingenuity Pathway Analysis (IPA). N.B.: Three candidate receptors (“anion transporter –K2”, “Actin-binding protein,” and “hyaluronic acid binding protein”) were excluded from both analyses due to ambiguity associated with identifying a single protein from the *Sus scrofa* proteome.

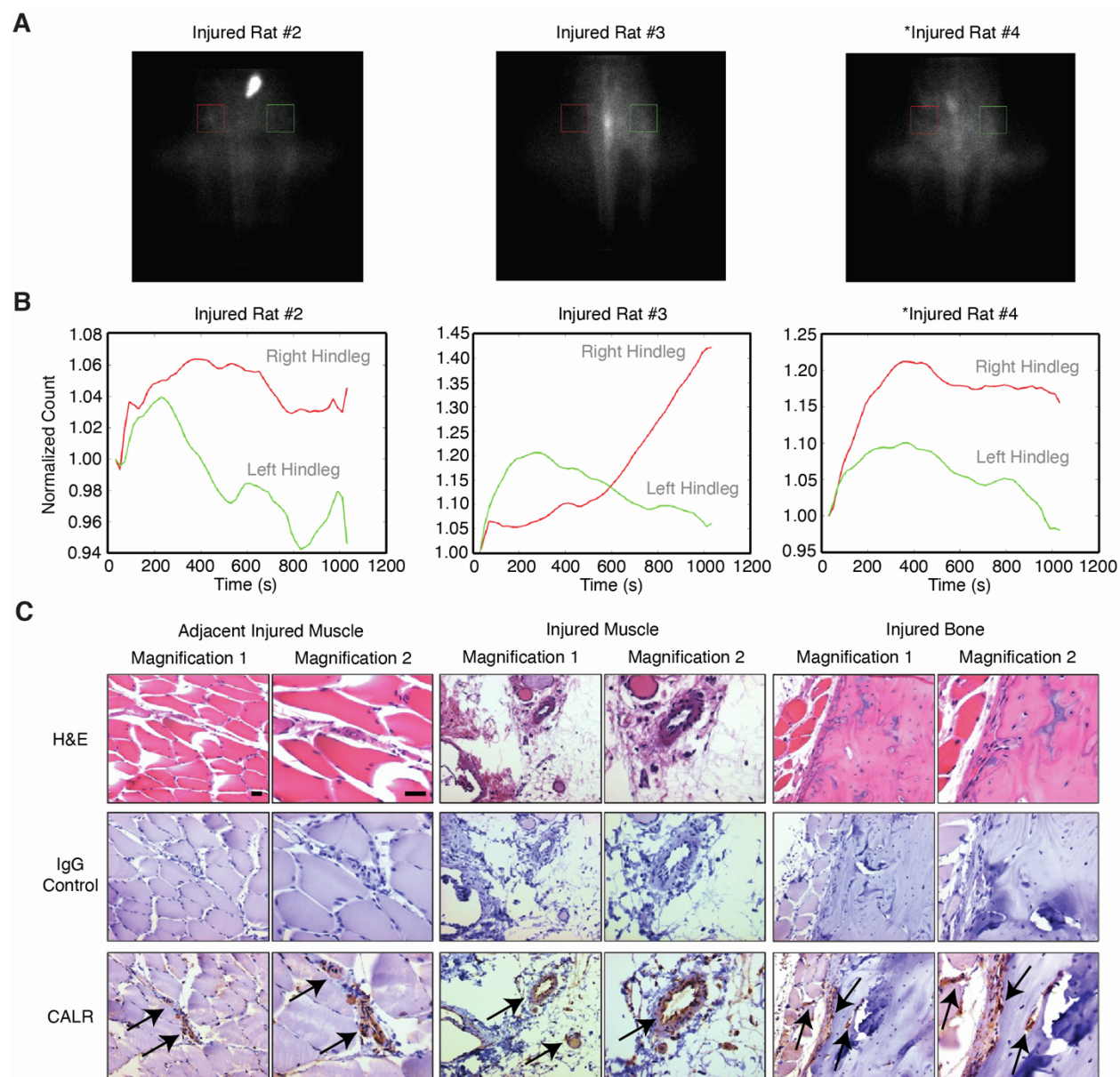


**Figure S4: Validation of candidate receptors for 23 selected targeted phage (each displaying a lead peptide candidate) by *in vitro* phage-binding assays, related to Figure 2 and Table 1.** Phage binding is represented by relative TU. BSA and insertless phage were used as negative controls. Peptides denoted in red were

pursued in subsequent experiments. Data presented as mean + standard deviation (SD).

**A****B**

**Figure S5: Immunohistochemical staining of phage particles in injured and contralateral (control) hindlegs of the porcine model of acute trauma, related to Figures 2 and 3. (A)** Staining of phage particles in biopsy and necropsy samples following *ex vivo* overlay with CRQRPASGC-displaying or insertless phage (negative control) (scale bar, 250  $\mu$ m). **(B)** Staining of phage particles in biopsy samples following *in vivo* administration of CRQRPASGC-displaying or insertless phage (negative control) (scale bar, 250  $\mu$ m).



**Figure S6: Targeting of the CRQRPASGC-CALR ligand-receptor *in vivo* in rats that underwent acute traumatic injury (i.e., femur fracture and soft tissue injury) over time (in addition to the representative example plus non-injured rat), related to Figure 4. (A) Planar SPECT scan of both hindlegs (right, injured; left, non-injured) in two injured rats (n=2; Injured Rat #2 and Injured Rat #3) from 0–18 min following IV administration of  $^{111}\text{In}$ -DOTA-labeled CRQRPASGC. (B) Quantification of planar**

SPECT from the two injured rats (n=2; Injured Rat #2 and Injured Rat #3). Counts are normalized to the first time point. \*N.B.: Injured Rat #4 moved during the SPECT portion of the experiment and consequently the SPECT scan could not be co-registered to the CT scan; hence, this animal was not able to be properly evaluated at all fixed time points throughout the experiment, and was therefore excluded from the study (i.e., unable to be included in Figures 4F and 4G). **(C)** Immunohistochemical staining of adjacent injured muscle, injured muscle, and injured bone (scale bars, 250  $\mu$ m).

A	
Peptide #19	CRQRPASGC
TAPBP	370-PVTTEQHGARYACRIHHPSL <b>PASGR</b> SAEVTLEVAGLSGPSLEDS-413
NKX2-1	111-PGWYGANPDPRFPISRFG <b>PASGM</b> NSGMGGLGSLGDVSKNMA-154
VWF	1649-ILIQDFETLPREAPDLVL <b>QRCCSG</b> EGLQIPTLSPAPDCSQPLDV-1692
MPO	68-EAKQLVDKAYKERRESIK <b>QRLRSG</b> SASPMELLSYFKQPVAATRT-111
B	
Peptide #19	CRQRPASGC
TAPBP ( <i>Homo sapiens</i> )	374-EQHGARYACRIHHPSL <b>PASGR</b> SAEVTLEVAGLSGPSLED-412
TAPBP ( <i>Macaca mulatta</i> )	374-EQHGARYACRIHHPSL <b>PASGR</b> SAEVTLEVAGLSGPSLED-412
TAPBP ( <i>Pan troglodytes</i> )	392-EQHGARYACRIHHPSL <b>PASGR</b> SAEVTLEVAGLSGPSLED-430
TAPBP ( <i>Sus scrofa</i> )	375-EQHGARYACRVHHPSL <b>PALGR</b> RSEITLQVAGLSGPSLED-413
TAPBP ( <i>Canis lupus familiaris</i> )	374-KHHGARYACRVHHPTL <b>PLGR</b> SAEVTLEVAGLSGPSLED-412
TAPBP ( <i>Rattus norvegicus</i> )	391-KQHGVRVYACRVHPSL <b>PSGR</b> SAEVTLEVAGFSGPSIED-429
TAPBP ( <i>Equus caballus</i> )	454-EQHGARYACRVHHTSL <b>PALGR</b> SAEVTLEVAGLSRPSLED-492
TAPBP ( <i>Loxodonta africana</i> )	375-EQHGTRYACRIHHPSL <b>PALGR</b> STEVTLKVAGLSRPSLED-413
TAPBP ( <i>Mus musculus</i> )	377-KQHGVRVYCRVYHSSL <b>PASGR</b> SADVTLEVAGFSGPSIED-415
TAPBP ( <i>Xenopus tropicalis</i> )	352-ERHGARYFCKVRHVSA <b>P-EGIT</b> RSNTLQVAGVAGLSLED-389
	::**.* *:: * : * * . **:*:*.* :***

**Figure S7: Similarities between the core peptide motif (RQRPASG) and known**

**endogenous interactors of CALR plus cross-species conservation of the**

**corresponding TAPBP region, related to Figure 6. (A) Amino acid sequence**

alignments of CRQRPASGC with similar endogenous proteins of *Homo sapiens* that also directly interact with CALR: tapasin (TAPBP), homeobox protein Nkx-2.1 (NKX2-1), von Willebrand factor (VWF), and myeloperoxidase (MPO). Results were retrieved from BLASTP suite of the National Center for Biotechnology Information. The alignments were generated by using the core amino acid sequence of peptide #19 (RQRPASG) as the query sequence and the UniProt accession numbers of endogenous proteins that interact with CALR according to Ingenuity Pathway Analysis (IPA) as subject sequences.

**(B)** Amino acid sequence alignments of CRQRPASGC and TAPBP of different species: *Homo sapiens* (human; O15533), *Macaca mulatta* (rhesus macaque; F6TWA1), *Pan troglodytes* (chimpanzee; H2QST3), *Sus scrofa* (pig; K9J6K1), *Canis lupus familiaris* (dog; Q5TJE4), *Rattus norvegicus* (rat; A6JJI5), *Equus caballus* (horse; F6T753), *Loxodonta africana* (elephant; G3U7L8), *Mus musculus* (mouse; Q9R233),

and *Xenopus tropicalis* (Western clawed frog; F7DKG3). Amino acids within the PASG motif are highlighted if identical (green), conserved (orange), or semi-conserved (yellow).

**Table S1: The top 100 distinct CX<sub>7</sub>C and CX<sub>8</sub>C peptides (according to total count followed by alphabetical order) found exclusively in injured tissue, exclusively in non-injured tissue, or in both injured and non-injured tissue for combined samples following *in vivo* phage display peptide library screenings in a porcine model of acute trauma coupled with next-generation sequencing (NGS), related to Figure 1.**

Muscle			Bone		
Injured Only	Non-Injured Only	Both	Injured Only	Non-Injured Only	Both
CCGLGIGSC	CRKFESNMLC	CLRGRGYGSC	CEARASGSR	CTGPFESANC	CLRGRGYGSC
CWAMHISSVC	CRAFWGHSC	CPSAGMDLGC	CSVRRTGSC	CVEFMRIES	CGEGPRRISC
CGRTVDLRVC	CCLNGIWLPC	CRGQDNWLVC	CCDRNSRSC	CAPTVRGYVC	CGRRLGSNVC
CPQVRNRNWC	CALTCGYREC	CLNSGRSGLC	CNLGPRVGGC	CEWDVRYSC	CKWEGLDMAC
CLPQHGCC	CDRLRSRYC	CGEGPRRISC	CRLELEEEPC	CHLDSVKAGC	CPSAGMDLGC
CRSWMVSC	CLMVSNPAYC	CSKLGLSLDC	CSSARFRGC	CSDRRGSLGC	CRGQDNWLVC
CCGGLLAVRC	CWSSMRDASC	CLRSDNWGLC	CLLNICCGC	CEAYGDAGHC	CLNSGRSGLC
CGTFEGMDC	CARLYCSPC	CGRRLGSNVC	CLRESESGC	CLTYVAMVVC	CLRSDNWGLC
CQVWRINVC	CATVGATAC	CMLRLRGVGC	CLVREGLLSC	CWPTGEARC	CMLRLRGVGC
CSRAATRFMC	CGSDEVICYC	CKWEGLDMAC	CPIYQGFDC	CAEASVPLMC	CPAGLEVLLC
CSTRGVPGC	CHGIVGPEGC	CALSIGVWAC	CRPVATRSQC	CCLCASVRC	CDLGHGYSC
CTSMPGDANC	CIAGHHALAC	CPAGLEVLLC	CSKLTAVIC	CDMLILSPC	CALSIGVWAC
CVNLRGIAC	CLASRAGGWC	CAWNSGRSTC	CVNGLVSDWC	CGGFAWTPPC	CRQIGGTERC
CVPHWGVRC	CMGVLLGRC	CRVYSEQAAC	CERCRRVSC	CHSEMRNLC	CRRVEERGLC
CGAWSRRPGC	CNLVIMNWC	CVFTRSWRGC	CGGRIVWRC	CPSMWPYSGC	CRDWVVVAC
CGSISLERC	CRGSYYKRLC	CGYQAGRRCC	CGIRHRSMWC	CRRLLEPGC	CSKLGLSLDC
CLRRHRAGC	CRPWLEFNGC	CRQIGGTERC	CWMEVSGC	CSWRVPWSC	CVFTRSWRGC
CRERRWEWRC	CRSNSRVWMC	CRDWVVVAC	CKWGRTARC	CVEWRTFERC	CTWIWGGVPC
CAVLWRRWC	CAVSRGSR	CHGYIAGFVC	CNAEHDWIEC	CVSVVCRSC	CHGYIAGFVC
CCRIFSWAC	CDSVVQMLGC	CRRVEERGLC	CPSSGLVIYC	CARSPFAVC	CRVYSEQAAC
CDAVAHRYC	CFPGYWDPC	CLNVSGRSC	CSHKHPELGC	CCGEVMRVC	CGLSLSAGWC
CDGWTEAIC	CGRGVFKSMC	CESAVGNPLC	CSYLPMLVC	CDRPAIGVEC	CVANFGDLC
CEERWRGGC	CGTRDEWWT	CRDSSLPC	CVRMDDCC	CDWMERSMGC	CESAVGNPLC
CEEWMLLHWC	CLVQVKFGC	CWNFVGGGC	CWPQFKAEC	CGADLMVSC	CARLRLSLC
CELTGKVLRC	CPARFPVDKC	CTWIWGGVPC	CWQGLIPADC	CGAPIAPP	CVLNSVQRC
CHRLIIRRC	CPGRYGLPVC	CAGVSGRFGC	CAGWPWSC	CGGAEWMD	CDMAEMIVRC
CISLTSGHC	CREKRMVSAC	CGLSLSAGWC	CALSEASKYC	CGGSDFNWC	CWDAFFRRC
CLLGLWSEC	CRQGMPLGHC	CDMAEMIVRC	CAVVSPLRC	CGRQESHARC	CGYQAGRRCC
CLLSPRWGWC	CSSQLGRAIC	CVSVTARHC	CGMVVVVAC	CGSQVGGAYC	CWGMSQLLVC
CPVYRRLPC	CWALVSSGTC	CSGRGWLRC	CIMGQELADC	CGVGVRVGN	CLAYSLG
CRHRLRQTC	CWDSKQQTTC	CLRGFQRC	CKEGLRRNGC	CGSVVVWRC	CAWNSGRSTC
CRQELSGLRC	CWLVSWPAC	CQRDSLASC	CLMRRSRIC	CGVWLRSLKC	CWNFVGGGC
CRQLRLCRLC	CWSVVTPSC	CDLGHGYSC	CNSPTLAVAC	CTGCSAPAC	CLNVSGRSC
CSLGSGRFRC	CARVSYCYWC	CVLNSVQRC	CPPNSGVALC	CITEVGLLHC	CRDSSLPC
CSQRKCTLRC	CAVEGSSRKC	CGQMKDSSGC	CQCSHLCRC	CIWTVHAAYC	CGGLQQTVC
CWYAGSALVC	CCRTLLNLC	CAWVPRRSC	CRALSGTDC	CKEDWWWLWC	CLRGFQRC
CYARLPEHGC	CDGVSREGQC	CLAYSLG	CRQSVLVR	CMIMFNVL	CAWVPRRSC
CYTMGTAEAC	CGRTLNVAC	CVKRGCPGC	CRRAWRLC	CNMWRFGVIC	CSGRGWVLR
CADYAIWDAC	CGVSGCQPC	CNLPYRGVC	CRYSLKIDSC	CPLESKVC	CVSVTARHC
CAEAGWGVGC	CHDGLRSC	CVEPSGGYC	CSRAGNGTTC	CQCRGMKIC	CSLNRYRTC
CAGGHGMS	CKSGQRQSGC	CGGLQQTVC	CSRLVVHWC	CRALEKSTYC	CVGQVGGRR
CARLTSTLC	CMBGRSGC	CVANFGDLC	CSTALCSVC	CRSVEDDSRC	CVEPSGGYC
CARRGVGVKC	CMRRANDVRC	CRARGGSISC	CTHDGRTPC	CSREWARAEC	CMWLARSGC
CCRFCLGQC	CMSTPGTDRC	CWDAFFRRC	CTWDRLERC	CSVTGEALRC	CRARGGSISC
CDFGAIMTGC	CPEWQSRRC	CRLYGGMTHC	CVGPVEVVIC	CTRGGGLGVVC	CLTLGSARC
CDGLLFGTC	CQRAAVSSCC	CLSLGRNVC	CVSTNWGEC	CVSHLGTWYC	CAGVSGRFGC
CGAAPKAWC	CRIRWPGGTC	CMWLARSGC	CYEECGTC	CWGSSRTAC	CQRDSLASC
CGQGEPTYEC	CRKLIGGSC	CPGPSAGPC	CYFEHAARC	CAAQEQAVLC	CSVGDNLVLC
CGRALQSTCC	CRVSNVMRC	CVRGTQSSC	CYMRSSGRMC	CADLERWYC	CIRDLDEGVC
CGVRLNGLRC	CSRSSGRTPC	CLLPRFRFGC	CAAGTDGFC	CAERIYVMD	CLVGGWTC
CHTQVDAVGC	CSVVCSRSC	CARLRLSLC	CAAVRSVSGC	CAIYINDSAC	CGARRAVPC
CITGHNTGGC	CTERCTRAC	CVGQVGGRR	CADRSAAEGC	CAKQTAGLRC	CRWGREWPC

CKGRGYVSLC	CVRVLIVTC	CMYEVLTC	CAGRWSCLC	CAPGFRAIC	CPGPSAGPC
CLGVTVGAC	CWLLMSSEFC	CRADTGEP	CALDKSGSVC	CARVIWMVC	CAGLERWYC
CLSGACDDC	CAFGSRGPEC	CGTLGGLVC	CALLIQYSC	CASRSVVYC	CLGFTFKSC
CLSRASYVLC	CAGRQSGLSC	CNRCWPTFC	CAVVIIVMSC	CASYRFMMRC	CARVTGSFSC
CLYPRVWVC	CASGRTGEC	CARVTGSFSC	CEQGSHRGHC	CAVTRDSSGC	CVKRGCPGC
CMAYRSSKQC	CATGQGLRPC	CLGFTFKSC	CEQWVADPC	CCGRSFTC	CGQMKDSSGC
CMFSVVKGLC	CATSRGVVLC	CLNQLSDMVC	CERLCGSNVC	CCFTPRRGVC	CLNQLSDMVC
CPIASTPGFC	CCLSVRLQNC	CWSGRGEWC	CFCRPVGFC	CCRLPGSVC	CVRGTSSEEC
CRGLFQGAFC	CDVVSNSSC	CSVGDNLVLC	CFMLDAWGRC	CEARGANWLC	CGTLGGLVC
CRLGVWEC	CEEGCNGGWC	CWGMSQLLVC	CGSPGWVRC	CEFCGRIGC	CMLRKAVSDC
CRNVRCLSC	CGTGQWCIC	CAGLERWYC	CGTGCRRVC	CEGGRTHTHC	CMYEVLTC
CRRGINAEYC	CGGEGGYSC	CVWRNKGQDC	CGVCMCVVC	CEMMTDLRLC	CVVELAGWC
CRSSRLGMAC	CGHGVWQEC	CVRANPGLC	CHRQGPISGC	CENGWEVFC	CLLPRFRFGC
CRWNDQITC	CGGSPREPEC	CLRAMAKGC	CHSPCLWFC	CERSGLGSC	CLSLGRNVC
CSGLLRRNTC	CGPPRMLHC	CGARRAVPC	CIDDAAGWQC	CFFSFSNEC	CNRCWPTFC
CSHRFGDC	CGQSRVRS	CGILGPWMAC	CIFYIVRLC	CFGIEAGVVC	CGERVMRPC
CSIPLCREC	CGTTSDEVC	CRWGREWDC	CILTIRVC	CGAACDTSC	CAWRLWPHSC
CSLVVQILGC	CGTVGKTAQC	CAWRLWPHSC	CIPTPVQQLC	CGDLGSVQLC	CTESFQKHL
CSRSVALGSC	CGYQLQGCC	CIRDLDEGVC	CKGLQWLPWC	CGERGVCLC	CVRANPGLC
CSVARSTFFC	CHGEHVRASC	CGERGEGRAC	CKRSSGCYRC	CGHWRVSC	CRADTGEP
CTSRSHFAC	CKQGGWRSQC	CSLNRYRTC	CKTSANGGWC	CGILTHKGWC	CWSGRGEWC
CVGDGDSRC	CLAMEFLRC	CLVGGVWGC	CKVGGEDSC	CGLAGGRTLC	CDRQDPLIC
CVVKYQHLVC	CLAPWDGRC	CLTLGSARC	CLGNIWTVGC	CGLRCLGVC	CLMGGSGTC
CWPPRCVFC	CLDKCGYVGC	CEGKEDMGGC	CLWASWFC	CGLVATGIDC	CRLYGGMTHC
CYSVHVGLC	CLGGYGRLC	CGASVMSMVC	CLWRRHLRC	CGPAYPRVAC	CGILGPWMAC
CAAGVVGLLC	CLSGCTLRC	CRQPGPLFC	CMRQLQHGTC	CGPRDCAHC	CNLPYYRGVC
CAGGSRSRVC	CPDGTIWRRC	CWTPRCGWC	CMRQWWVVC	CGPYKFYSPC	CEGKEDMGGC
CARLECITSC	CPDSHAWHLC	CMLRKAVSDC	CNVEWRRKDC	CGRELREAAC	CPPKSLIPHC
CARLEVQHC	CPQNSVTGPC	CVVELAGWC	CPGGSAAARC	CGRLFRIEC	CRSDGGITC
CATMGDYGVC	CPWSTLTAC	CCMAGRGGC	CPGQACCRPC	CGSHHVMRRC	CVWRNKGQDC
CCAGMQSPC	CQSRREHAWC	CTESFQKHL	CPHYLRTAC	CGSSGAAGSC	CVRD LGVGC
CCAPSVQWC	CRFIRYTSNC	CLMGGSGTC	CPLATDSCC	CGTEALASVC	CWTPRCGWC
CCWIAFECC	CRGGAARPC	CPPKSLIPHC	CQTREVRAC	CGVHRCLSC	CLVWGLRC
CDAMGRDLKC	CRGGTAGRWC	CRASEGRGGC	CRAAGCGAC	CGYQAGRRC	CGERGEGRAC
CDDLQYISIC	CRKRLTSPWC	CLGGVYHGC	CRCRGQPWRC	CHGCCTLRSC	CFTGAGDRC
CEVFIATCC	CRLEVQRC	CVRD LGVGC	CRELKSGRMC	CHSWNVRLC	CVAYDGGGSC
CGCSGERSVC	CRLVKSPPRC	CYLPYALLC	CREPQQWTC	CHWLGPVAGC	CCMAGRGGC
CGDQATTPC	CRMTALGPRC	CRLVWGLRC	CRFSDPSPC	CHYASYLRC	CRQPGPLFC
CGGGEYVLKC	CRRFVGLGC	CDRRQDPLIC	CRGPGAGARC	CIGGVLRQGC	CLRAMAKGC
CGGTNRWGRC	CRRGGIHEC	CGERVMRPC	CRLGSHFIC	CIGKRLRTL	CRASEGRGGC
CGQVKGLGMC	CRSRFERQSC	CGHFYFLRC	CRLGVKRAVC	CKCRAHYVC	CGHFYFLRC
CGRSSWSMGC	CRSTASGVC	CRSDGGITC	CRNGSPALC	CKLDSPAVRC	CVVFPVRAC
CGRVKCSGMC	CRWAFQRWYC	CVAYDGGGSC	CRRDVARVGC	CKSAQMCACW	CYLPYALLC
CGTELGFRC	CSDTSTLAVC	CPRFFAVPC	CRWAFKGGC	CKVLAHRAMC	CGASVMSMVC
CGTLGSRFC	CSGITVMEGC	CHKPPNFGSC	CSGDRAFRSC	CLARFSSVVC	CGGPREPEC
CGYLAAVRIC	CSLLASENPC	CVVFPVRAC	CSSISLAC	CLGA AVAGC	CLGGVYHGC
CHGLPGCSC	CSMMLANVSC	CGGPREPEC	CSSSVSARC	CLGRQVYSC	CPRFFAVPC
CHGPWMPSPC	CSRLYYSVC	CGGSKLGGQC	CSVWRGKASC	CLPGRVSYIC	CHKPPNFGSC

**Table S2: Data underlying saturation plot of distinct peptide sequences in the biopsy and necropsy samples (injured tissues) from injured pigs screened *in vivo* with phage display peptide libraries, related to Figure 1.** Data were obtained via random shuffling and sampling of the recovered peptide sequences that were detected more than once; after each shuffle, recovered peptide sequences were divided into groups of 100 [except for one group with a value of  $(n \bmod 100)$ , where  $n$  is the total number of recovered peptide sequences for a sample not divisible by 100]. The first row corresponds to the set with the greatest number of distinct peptide sequences, the second row corresponds to the sum of the prior row and the set with the next greatest number of distinct peptide sequences, the third row corresponds to the sum of the prior rows and the set with the next greatest number of distinct peptide sequences, etc. Data listed as mean and standard deviation (SD) of distinct peptide sequences across 100 rounds of random shuffling/sampling.

# Set(s) of Recovered Peptides	Biopsy Muscle 10 min		Biopsy Muscle 60 min		Biopsy Muscle 70 min		Biopsy Muscle 120 min		Necropsy Muscle 240 min		Necropsy Bone 240 min	
	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
1	71.08	3.64	72.68	3.30	73.89	3.46	71.46	3.70	71.56	3.93	71.84	3.65
2	109.73	5.12	113.39	5.29	118.26	5.67	109.72	5.05	110.97	5.78	111.89	4.76
3	135.52	6.13	140.18	5.76	149.23	6.66	134.36	6.26	136.87	6.00	137.94	6.35
4	154.66	6.12	161.19	5.90	173.98	6.66	154.03	7.34	156.99	6.78	157.81	6.83
5	171.02	7.11	179.37	6.66	194.96	7.49	171.39	7.51	172.76	8.33	175.34	7.22
6	185.96	6.68	195.31	7.58	214.54	7.61	186.48	7.60	187.41	8.98	190.47	7.31
7	199.57	7.01	210.29	8.29	232.68	8.38	200.85	8.97	200.38	9.21	205.50	7.72
8	212.25	7.28	224.70	8.89	250.01	9.23	215.05	9.70	212.86	8.44	218.92	7.94
9	224.14	8.42	238.65	9.57	266.82	9.71	228.05	9.95	224.55	8.80	232.06	8.16
10	235.47	8.76	251.09	9.59	282.44	10.16	241.36	9.85	235.94	8.89	245.12	8.06
11	246.31	8.91	263.37	9.55	298.01	10.56	254.33	10.62	246.97	9.23	257.49	8.05
12	257.23	9.52	275.50	9.66	312.93	11.01	266.77	10.75	257.78	8.60	269.14	8.80
13	268.18	9.58	286.83	9.55	327.43	11.03	278.69	11.20	268.00	9.15	280.79	9.31
14	278.46	9.87	298.19	9.99	341.33	10.86	290.59	11.72	277.89	9.77	291.85	9.59
15	288.40	9.45	309.41	9.88	355.32	10.04	302.66	11.96	288.02	9.80	302.37	9.63
16	298.01	9.79	319.67	9.80	368.59	10.46	314.13	12.26	297.41	9.69	313.18	9.65
17	307.14	10.09	329.86	9.76	381.52	11.00	325.86	12.28	306.10	9.11	323.61	9.33
18	315.71	9.83	339.80	10.12	394.73	11.13	337.52	12.82	315.04	8.76	332.95	9.19
19	324.60	9.56	349.39	9.92	406.42	11.03	349.26	13.11	323.62	9.19	343.07	9.41
20	332.86	9.64	358.59	9.66	417.99	11.30	360.59	12.63	331.78	8.51	352.52	9.27
21	340.79	9.35	367.64	9.02	429.92	11.38	371.96	12.68	339.52	8.63	362.04	9.11
22	348.35	9.12	375.81	8.80	441.57	11.43	383.31	13.36	346.92	8.44	370.95	9.05
23	355.93	8.68	384.57	8.63	452.42	11.54	394.35	13.54	354.07	8.36	379.68	9.13
24	363.68	8.90	392.62	8.46	462.81	11.25	405.02	13.97	361.76	8.15	388.06	9.43
25	371.32	9.35	400.23	8.66	473.66	10.85	416.28	14.13	368.30	7.96	396.43	9.34
26	378.22	9.13	408.20	8.72	483.70	10.72	426.65	13.75	375.16	7.87	403.99	9.46
27	385.11	9.26	416.13	8.21	493.67	10.64	437.05	14.04	381.83	7.77	411.80	9.57
28	391.76	9.26	423.64	8.53	503.38	10.54	447.09	14.27	387.83	7.74	419.65	8.79
29	398.17	9.46	430.68	8.65	513.14	10.49	457.05	15.04	393.89	7.42	426.97	8.72
30	404.51	8.98	437.58	8.05	522.32	10.41	467.20	15.56	399.33	7.28	433.90	9.39
31	410.96	8.58	443.89	7.99	531.74	10.49	477.09	15.25	404.93	7.30	440.73	8.88
32	416.93	8.49	450.14	7.81	540.38	10.43	486.74	15.23	410.14	6.97	447.53	8.71
33	422.63	8.30	456.36	7.84	548.46	10.28	496.35	14.41	415.57	7.05	454.08	8.58

34	427.97	8.04	462.00	7.83	556.29	10.44	505.93	14.61	420.53	7.01	460.59	8.43
35	433.29	8.33	467.23	7.73	563.87	10.58	515.15	14.50	425.28	6.69	466.71	8.72
36	438.38	8.03	472.47	7.20	571.29	10.77	524.02	14.11	430.16	6.86	472.78	8.85
37	443.32	7.61	477.72	6.95	578.96	11.00	532.74	13.68	434.67	6.74	478.62	8.76
38	447.74	7.28	482.61	6.99	586.73	10.85	541.69	13.82	438.73	6.59	484.03	8.43
39	452.31	7.20	487.07	6.95	593.95	10.78	550.38	13.26	442.44	6.35	489.51	8.34
40	457.09	7.23	491.69	6.65	600.91	10.68	559.22	13.36	446.50	5.86	494.69	8.20
41	461.21	7.04	495.92	6.00	607.30	10.36	567.71	13.13	450.13	5.67	499.84	8.23
42	465.11	6.76	500.06	5.60	613.77	10.10	576.12	13.24	453.39	5.61	504.65	7.80
43	468.87	6.33	504.12	5.24	620.48	9.90	584.50	13.40	456.69	5.15	509.35	7.28
44	472.44	5.97	507.82	4.81	626.64	9.61	592.92	13.93	460.07	4.95	513.46	7.07
45	476.21	5.84	511.23	4.55	632.65	9.29	601.44	13.66	463.31	4.72	517.65	6.37
46	479.91	5.53	514.58	4.42	638.76	8.52	610.17	14.22	466.12	4.70	521.83	6.26
47	483.51	5.44	517.74	4.50	644.42	8.46	618.07	14.13	468.57	4.29	525.81	5.78
48	486.90	4.95	520.49	4.35	649.73	8.24	626.06	13.99	470.92	4.17	529.85	5.80
49	490.00	4.75	523.10	4.07	654.82	8.06	633.83	13.88	473.22	3.80	533.49	5.47
50	492.82	4.79	525.85	3.98	659.43	7.65	640.88	14.15	475.37	3.56	536.89	5.21
51	495.58	4.55	528.57	3.87	663.97	7.43	648.34	14.42	477.48	3.37	540.41	5.22
52	498.07	4.48	530.74	3.71	668.73	7.37	655.75	14.68	479.45	3.36	543.61	5.10
53	500.60	4.11	532.91	3.43	672.75	7.12	663.24	14.72	481.22	3.18	546.53	4.91
54	502.58	3.82	534.80	3.10	676.88	6.98	670.37	14.28	482.76	2.64	549.76	4.79
55	504.62	3.73	536.45	3.10	681.16	6.61	677.68	14.05	484.18	2.34	552.30	4.52
56	506.53	3.59	537.85	2.68	684.91	6.32	684.74	13.85	485.25	2.02	555.09	4.49
57	508.47	3.21	539.24	2.51	688.30	5.82	691.50	13.68	486.37	1.81	557.47	4.58
58	510.01	2.90	540.54	2.07	692.09	5.89	698.92	13.31	487.35	1.62	559.81	4.51
59	511.80	2.68	541.58	1.80	695.39	5.78	705.76	13.15	488.38	1.25	562.20	4.27
60	513.18	2.42	542.47	1.52	698.82	5.57	712.15	13.03	488.87	1.05	564.24	3.90
61	514.44	2.20	543.23	1.19	702.09	5.34	718.39	13.07	489.39	0.80	566.12	3.65
62	515.54	1.91	543.86	0.96	704.97	5.16	724.72	13.28	489.75	0.50	567.94	3.47
63	516.48	1.65	544.26	0.80	707.58	4.92	730.99	13.63	489.93	0.29	569.72	2.95
64	517.19	1.54	544.74	0.48	710.22	4.89	737.29	13.27	490.00	0.00	571.20	2.90
65	517.91	1.38	544.97	0.17	712.62	4.40	743.39	13.33	490.00	0.00	572.45	2.66
66	518.53	1.20	545.00	0.00	714.80	4.31	749.73	13.73			573.57	2.35
67	518.99	1.02	545.00	0.00	716.96	3.88	755.94	13.39			574.79	2.12
68	519.46	0.78			718.75	3.34	761.64	13.06			575.72	1.86
69	519.78	0.46			720.51	3.06	767.42	12.97			576.59	1.66
70	519.94	0.24			722.07	2.90	772.98	12.89			577.46	1.36
71	520.00	0.00			723.60	2.77	779.00	12.71			578.01	1.09
72					724.75	2.50	784.83	12.70			578.46	0.83
73					725.96	2.11	790.19	12.62			578.75	0.50
74					727.01	1.79	795.69	11.90			578.90	0.30
75					727.91	1.44	801.16	11.90			579.00	0.00
76					728.61	1.14	806.50	11.48				
77					729.13	0.97	811.72	11.34				
78					729.50	0.64	816.97	11.34				
79					729.73	0.51	822.11	10.98				
80					729.96	0.20	826.95	10.82				
81					730.00	0.00	831.73	10.63				
82							836.03	10.17				
83							840.93	9.83				
84							845.50	9.80				
85							849.97	9.95				
86							854.49	10.19				
87							859.05	10.01				
88							863.56	9.99				
89							867.80	10.26				
90							872.00	9.89				
91							876.38	9.97				
92							880.19	9.82				
93							884.24	9.24				
94							888.27	9.15				
95							892.09	8.84				
96							895.74	8.55				
97							899.58	8.61				
98							903.18	8.63				

99							907.01	8.69				
100							910.68	8.59				
101							914.06	8.50				
102							917.29	8.43				
103							920.86	8.08				
104							923.74	8.04				
105							927.03	7.68				
106							929.69	7.63				
107							932.71	7.28				
108							935.67	6.94				
109							938.38	6.66				
110							940.89	6.67				
111							943.70	6.38				
112							946.40	6.49				
113							948.92	6.48				
114							951.59	6.69				
115							954.08	6.50				
116							956.18	6.64				
117							958.42	6.46				
118							960.53	6.16				
119							962.63	6.00				
120							964.81	5.89				
121							966.90	5.66				
122							968.62	5.67				
123							970.86	5.37				
124							972.62	5.20				
125							974.36	4.73				
126							976.01	4.50				
127							977.76	4.38				
128							979.52	4.17				
129							981.06	3.87				
130							982.70	3.94				
131							984.16	3.88				
132							985.36	3.82				
133							986.70	3.57				
134							988.02	3.52				
135							989.15	3.62				
136							990.22	3.50				
137							991.13	3.47				
138							992.24	3.18				
139							993.22	2.90				
140							994.00	2.61				
141							994.87	2.33				
142							995.62	2.02				
143							996.16	2.01				
144							996.82	1.74				
145							997.38	1.61				
146							997.91	1.50				
147							998.27	1.29				
148							998.61	1.13				
149							998.91	1.00				
150							999.25	0.85				
151							999.46	0.72				
152							999.70	0.48				
153							999.86	0.35				
154							999.96	0.20				
155							1000.00	0.00				

**Table S3: Data underlying saturation plot of distinct peptide sequences in the biopsy and necropsy samples (non-injured tissues) from injured pigs screened *in vivo* with phage display peptide libraries, related to Figure 1.** Data were obtained via random shuffling and sampling of the recovered peptide sequences that were detected more than once; after each shuffle, recovered peptide sequences were divided into groups of 100 [except for one group with a value of  $(n \bmod 100)$ , where  $n$  is the total number of recovered peptide sequences for a sample not divisible by 100]. The first row corresponds to the set with the greatest number of distinct peptide sequences, the second row corresponds to the sum of the prior row and the set with the next greatest number of distinct peptide sequences, the third row corresponds to the sum of the prior rows and the set with the next greatest number of distinct peptide sequences, etc. Data listed as mean and standard deviation (SD) of distinct peptide sequences across 100 rounds of random shuffling/sampling.

# Set(s) of Recovered Peptides	Biopsy Muscle 10 min		Biopsy Muscle 60 min		Biopsy Muscle 70 min		Biopsy Muscle 120 min		Necropsy Muscle 240 min		Necropsy Bone 240 min	
	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
1	70.96	4.07	71.28	3.79	70.93	3.64	72.06	3.62	70.92	3.52	70.93	3.41
2	110.19	5.48	109.11	4.83	109.97	5.28	112.52	4.57	107.71	4.55	109.10	5.14
3	134.84	6.08	132.92	5.24	135.56	6.24	139.39	5.37	131.76	5.88	133.66	5.44
4	153.90	6.35	151.12	5.37	155.65	7.12	159.35	6.20	149.62	6.55	150.70	5.75
5	169.23	6.94	165.89	5.26	172.17	7.44	175.93	6.62	164.44	7.25	164.14	6.02
6	184.05	7.17	179.20	5.43	186.78	8.05	190.08	6.57	177.71	7.96	175.36	5.67
7	197.18	7.60	191.21	5.68	200.82	9.17	202.65	6.92	190.36	8.45	185.25	5.49
8	209.79	8.08	202.19	5.93	214.53	9.90	214.16	7.07	202.44	8.90	193.71	5.26
9	221.47	8.83	212.62	6.18	228.08	10.11	224.76	7.26	213.98	8.90	201.25	5.34
10	233.30	9.61	222.70	6.62	241.16	10.31	233.94	7.34	224.91	9.26	208.49	5.06
11	244.24	9.65	232.36	7.06	254.15	10.91	242.56	7.30	235.47	9.35	215.10	4.96
12	255.88	9.93	241.03	6.98	266.89	10.69	250.78	6.53	246.06	9.56	220.86	4.81
13	266.79	10.61	249.61	7.05	279.24	11.00	258.08	6.11	255.90	9.24	225.65	4.35
14	277.68	10.57	257.99	7.26	291.01	11.30	265.09	5.87	265.17	9.27	230.28	4.02
15	288.64	10.95	265.71	7.07	302.95	11.55	271.33	5.94	274.61	9.38	234.56	3.96
16	298.84	10.94	273.47	7.11	314.48	12.10	277.14	5.76	284.18	9.63	238.21	3.71
17	308.68	11.29	280.07	6.73	326.31	11.69	282.86	5.60	294.38	9.71	241.58	3.26
18	318.51	11.75	286.70	6.28	337.77	11.60	287.55	4.75	303.07	10.36	244.42	2.89
19	327.65	11.87	292.98	6.45	348.81	12.01	291.67	3.97	311.56	10.59	247.08	2.39
20	337.17	11.55	298.69	6.57	360.50	12.00	295.52	3.62	320.37	10.44	249.02	2.10
21	346.40	11.50	304.82	6.65	370.80	11.98	298.97	3.10	329.14	10.24	250.89	1.75
22	355.57	11.53	310.62	6.49	381.80	11.82	302.28	2.84	337.55	10.22	252.04	1.31
23	363.99	11.44	316.15	6.33	392.93	11.69	304.75	2.46	345.42	10.41	253.20	0.91
24	372.47	11.56	321.19	6.09	403.02	12.04	307.12	2.19	353.17	10.27	253.68	0.58
25	381.03	11.52	325.97	5.88	413.06	11.84	308.89	1.91	360.82	9.92	253.95	0.22
26	389.39	11.69	330.10	5.91	423.32	12.09	310.31	1.44	367.73	9.82	254.00	0.00
27	397.30	11.86	334.05	5.46	433.67	12.52	311.46	1.23	375.37	9.98		
28	405.03	12.07	337.85	5.27	443.19	12.81	312.32	0.78	382.58	9.79		
29	412.82	11.52	341.51	4.87	452.92	12.71	312.87	0.34	389.26	9.64		
30	419.76	11.07	345.00	4.56	462.80	12.52	313.00	0.00	395.94	9.93		
31	427.28	10.52	347.83	4.40	472.43	12.39			402.52	10.00		
32	434.66	10.61	350.52	4.00	481.92	12.11			408.99	9.65		
33	441.96	10.72	353.32	3.77	490.65	11.99			415.01	9.48		

34	448.91	10.46	355.51	3.35	499.68	12.30			421.30	9.27		
35	455.45	10.11	357.81	3.17	508.79	12.71			427.00	9.51		
36	462.06	9.76	359.83	2.99	517.22	12.63			432.34	9.40		
37	468.43	10.12	361.48	2.87	526.19	12.45			437.85	9.15		
38	474.52	9.98	363.11	2.55	535.20	12.98			443.74	9.29		
39	480.70	9.74	364.35	2.24	543.95	13.17			448.86	9.02		
40	486.76	9.99	365.58	1.90	552.06	13.42			454.07	8.61		
41	492.60	9.38	366.65	1.53	560.29	13.18			459.07	8.34		
42	497.90	9.22	367.50	1.32	568.16	12.82			463.48	7.96		
43	503.04	8.89	368.18	0.88	576.97	12.45			467.71	7.63		
44	508.70	8.76	368.65	0.58	584.99	12.09			472.22	7.36		
45	513.43	8.81	368.96	0.20	592.98	12.24			476.47	7.40		
46	518.38	8.64	369.00	0.00	600.77	12.32			480.84	7.37		
47	523.26	8.39			608.69	12.10			485.00	6.96		
48	528.12	8.29			615.97	12.08			489.01	6.97		
49	533.02	8.08			623.49	11.54			492.81	6.95		
50	537.83	8.05			631.23	10.96			496.48	6.99		
51	542.66	8.25			638.04	10.80			499.94	6.90		
52	546.69	7.87			644.87	10.84			503.38	6.77		
53	550.86	7.77			652.36	10.85			506.57	6.91		
54	554.86	7.38			658.97	11.46			509.72	6.98		
55	558.89	6.81			665.94	11.37			512.82	6.71		
56	563.20	6.81			672.62	11.14			515.74	6.40		
57	567.16	6.65			679.22	10.60			518.45	6.13		
58	570.43	6.47			685.85	10.54			521.10	5.78		
59	574.06	6.39			692.25	10.52			523.35	5.72		
60	577.73	6.23			698.62	10.67			525.66	5.03		
61	581.49	6.17			704.74	10.83			527.81	4.99		
62	584.97	5.90			711.03	11.04			530.12	4.88		
63	588.18	5.66			717.33	11.30			532.34	4.45		
64	591.45	5.80			723.57	11.38			534.26	4.20		
65	594.73	5.93			729.71	11.18			536.17	3.86		
66	597.83	5.84			735.35	10.98			537.94	3.47		
67	600.36	5.48			741.21	10.66			539.31	3.31		
68	602.79	5.38			746.60	10.62			540.79	3.11		
69	605.25	5.32			752.42	10.82			542.13	2.99		
70	607.60	5.29			757.68	10.68			543.21	2.91		
71	609.83	5.01			763.22	10.68			544.23	2.62		
72	611.91	5.02			768.56	10.41			545.22	2.48		
73	614.31	4.65			773.89	10.50			546.04	2.15		
74	616.12	4.30			778.63	10.65			546.88	1.83		
75	618.02	4.13			783.55	10.78			547.59	1.56		
76	619.72	3.84			788.67	10.38			548.33	1.33		
77	621.49	3.61			793.97	9.84			548.85	1.05		
78	623.20	3.33			798.57	9.35			549.26	0.84		
79	624.70	3.10			803.27	9.33			549.54	0.64		
80	626.01	2.97			807.32	9.36			549.90	0.30		
81	627.48	2.65			811.31	9.11			549.98	0.14		
82	628.73	2.46			815.69	9.07			550.00	0.00		
83	629.97	2.24			820.10	9.01						
84	631.16	2.00			824.12	8.67						
85	632.13	1.77			828.38	8.45						
86	632.86	1.72			832.49	8.18						
87	633.64	1.68			836.09	8.15						
88	634.38	1.48			840.02	7.85						
89	634.96	1.34			843.55	8.03						
90	635.51	1.06			847.11	8.19						
91	636.15	0.90			850.76	8.33						
92	636.50	0.61			854.40	8.52						
93	636.71	0.52			857.61	8.34						
94	636.89	0.31			861.02	8.48						
95	636.97	0.17			864.31	8.34						
96	637.00	0.00			867.51	8.18						
97					870.77	8.09						
98					874.04	7.87						

99					877.15	7.56						
100					880.33	7.52						
101					883.19	7.38						
102					886.04	7.42						
103					888.88	7.21						
104					892.10	7.06						
105					894.54	7.03						
106					896.95	6.76						
107					899.37	6.59						
108					901.91	6.24						
109					904.57	6.21						
110					906.74	6.02						
111					908.96	5.92						
112					911.17	5.89						
113					913.50	5.65						
114					915.52	5.55						
115					917.56	5.27						
116					919.63	5.05						
117					921.53	4.81						
118					923.26	4.71						
119					925.04	4.60						
120					926.57	4.30						
121					928.27	4.17						
122					929.78	4.10						
123					931.29	3.98						
124					932.76	3.67						
125					934.00	3.56						
126					935.28	3.28						
127					936.42	3.21						
128					937.56	2.96						
129					938.77	2.76						
130					939.85	2.72						
131					940.77	2.60						
132					941.57	2.50						
133					942.24	2.36						
134					943.09	2.11						
135					943.86	1.79						
136					944.52	1.68						
137					945.08	1.57						
138					945.58	1.36						
139					946.02	1.29						
140					946.42	1.22						
141					946.91	1.01						
142					947.31	0.88						
143					947.63	0.60						
144					947.82	0.39						
145					947.97	0.17						
146					947.98	0.14						
147					948.00	0.00						

**Table S4: Candidate receptors identified by MALDI-TOF mass spectrometry per lead peptide, related to STAR Methods.** Candidate receptors in bold were validated *in vitro*.

Peptide	Candidate Receptor(s) Identified via Mass Spectrometry
Peptide #1 (CLRGFPALVC)	<b>Calsequestrin</b>
Peptide #2 (CSEIGVRAC)	Hsp22 <b>Hsp27</b>
Peptide #3 (CRGFVRGSC)	<b>Alpha beta-crystallin</b>
Peptide #4 (CSRGSPDARC)	<p>Acyloxyacyl hydrolase precursor  ATP synthase subunit alpha, mitochondrial precursor  Coiled-coil-helix-coiled-coil-helix domain-containing protein 3  Desmin  <b>Glycoprotein gC1qBP</b>  Heat shock protein beta-1  Histidine-rich glycoprotein  Hsp22  Hsp27  Hyaluronic acid binding protein  LDLR chaperone MESD  NACA  NADH dehydrog. (Ubiquinone) 1  Nascent polypeptide-associated complex subunit alpha isoform b  Peroxiredoxin 4  Similar to Actin-binding protein  Succinate dehydrogenase complex subunit B  Troponin C  Troponin T  Vimentin</p>
Peptide #5 (CSRAKGRGAC)	<b>Desmin</b>
Peptide #6 (CVLRFFSSC)	<p>Alpha beta-crystallin  ATP synthase beta subunit  Desmin  F1-ATPase  <b>Heat shock 70kDa/BiP</b>  Histidine-rich glycoprotein  Mitochondrial aconitase</p>
Peptide #7 (CRPARVRGAC)	<b>Alpha beta-crystallin</b> Troponin C
Peptide #8 (CPTFFAVPC)	<p>Anion transporter -K2  Cytochrome b-c1 complex subunit 1  Hsc70-interacting protein-like  <b>Similar to calumenin</b>  Similar to Filamin C (Gamma-filamin) (Filamin 2) (FLN-C) (ABP-L) (ABP-280-like protein) isoform 6</p>
Peptide #9 (CASA VPISC)	<p>ATP synthase beta subunit  <b>Cyclophilin Cyp-S1</b>  Glutamate dehydrogenase 1  NADH dehydrogenase 1 alpha  Plectin  Plectin 1</p>

Peptide #10 (CLVSGRSRC)	ATP synthase beta subunit C-alpha subunit Dihydrolipoyl dehydrogenase Glutamate dehydrogenase <b>Hsp27</b> Kinesin family member 22 NADH dehydrogenase NADH-ubiquinone reductase Plectin 4 Proteasome subunit beta 3 Proteasome subunit beta type-3 Thioredoxin-dependent peroxide reductase, mitochondrial Troponin I
Peptide #11 (CTESFQKHLC)	Plectin 1 <b>Thioredoxin-dependent peroxide reductase, mitochondrial</b>
Peptide #12 (CGILGPWMAC)	<b>Lactoferrin</b>
Peptide #13 (CKWEGLDMAC)	<b>Aldolase</b>
Peptide #14 (CLNVSGRSC)	<b>Hsc70</b>
Peptide #15 (CHKPPNFGSC)	<b>Annexin A1</b>
Peptide #16 (CEGKEDMQGC)	<b>BAG family molecular chaperone regulator 3</b> GDH isoform 1 Heat shock cognate 71kDa protein
Peptide #17 (CVGQVGGRRRC)	<b>Histidine-rich glycoprotein</b>
Peptide #18 (CLRGFQRVC)	<b>Calsequestrin</b>
Peptide #19 (CRQRPASGC)	<b>Calreticulin</b>
Peptide #20 (CARASGERGC)	Bifunctional apoptosis regulator <b>Collagen alpha-2(XI) chain</b> Junctophilin-2 Nuclear pore membrane glycoprotein 210 Peripheral-type benzodiazepine receptor-associated protein 1 Plasminogen Polyadenylate-binding protein 4 Target of Nesh-SH3 Telomerase reverse transcriptase
Peptide #21 (CEARASGSRC)	Arginase-1 Arylacetamide deacetylase-like 4 Caspase-14 Caspase-2 <b>Cystatin-A</b> Desmocollin-1 Desmocollin-3 Desmoglein-1 Desmoplakin Epiplakin Fatty acid-binding protein, epidermal Fructose-bisphosphate aldolase A Galectin-7 Integrin alpha-X Kazrin Myotilin Peptidyl-prolyl cis-trans isomerase B Protein POF1B Protein S100-A14

Peptide #22 (CVKASGSRAC)	Ankyrin repeat and SOCS box protein 2 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 H/ACA ribonucleoprotein complex subunit 1 Pigment epithelium-derived factor Procollagen C-endopeptidase enhancer 1 <b>Protein transport protein Sec31A</b>
Peptide #23 (CVANFGRAPC)	Alpha-enolase Azurocidin <b>Cathepsin G</b> EH domain-containing protein 2 Piwi-like protein 2 Protein QN1 homolog Protein S100-A9 Protein transport protein Sec31A Putative 60S ribosomal protein L13a-like MGC87657 Putative high mobility group protein B1-like 1 Transforming growth factor-beta-induced protein ig-h3 Type II inositol-3,4-bisphosphate 4-phosphatase

**Table S5: Amino acid sequence conservation (i.e., percent identity according to BLASTP) for full-length validated candidate receptors in acute trauma across three mammalian proteomes (*Homo sapiens*, *Sus scrofa*, and *Rattus norvegicus*), related to Table 1.**

Candidate Receptor*	Human UniProt	Pig UniProt	Rat UniProt	Human vs. Pig	Human vs. Rat	Pig vs. Rat
CASQ1	P31415	F1RJW7	P19633	94.83%	95.62%	94.06%
HSP27 (HSPB1)	P04792	Q5S1U1	P42930	87.92%	82.76%	84.69%
CRYAB	P02511	Q7M2W6	P23928	97.14%	97.14%	96.57%
GC1QBP	Q07021	A0A0D5BWD2	O35796	85.11%	85.82%	82.56%
DES	P17661	P02540	P48675	98.30%	97.87%	97.24%
GRP78 (BIP; HSPA5)	P11021	P34935	P06761	99.62%	98.47%	99.24%
CALU	O43852	F1SMN1	O35783	98.41%	88.57%	87.62%
PPIB	P23284	A0A286ZW70	P24368	93.52%	93.52%	90.28%
PRDX3	P30048	F1S418	Q9Z0V6	90.48%	85.21%	87.50%
LTF	P02788	P14632	D3ZAB1	70.70%	62.12%	59.22%
ALDOA	P04075	A0A287B8F3	P05065	98.08%	96.98%	97.25%
HSC70 (HSPA8)	P11142	A0A286ZWK2	P63018	97.57%	99.85%	97.42%
ANXA1	P04083	P19619	P07150	88.73%	89.02%	82.95%
BAG3	O95817	F1S415	A6IA08	81.54%	85.47%	81.50%
HRG	P04196	A0A481B9A6	Q99PS8	62.86%	57.88%	64.75%
CALR	P27797	P28491	P18418	95.75%	95.58%	95.86%
COL11A2	P13942	A0A8D1GUD9	Q6MGB2	94.82%	88.54%	87.61%
CSTA	P01040	A0A5S8LC35	P01039	72.45%	58.76%	52.58%
SEC31A	O94979	F1RVD4	Q9Z2Q1	91.05%	87.14%	85.02%
CTSG	P08311	A0A287BDI2	P17977	66.39%	70.08%	63.86%

\* The order of candidate receptors corresponds to the main text (Table 1).