

Association of Sonic Hedgehog with the extracellular matrix requires its zinc-coordination center

Supplemental Figures

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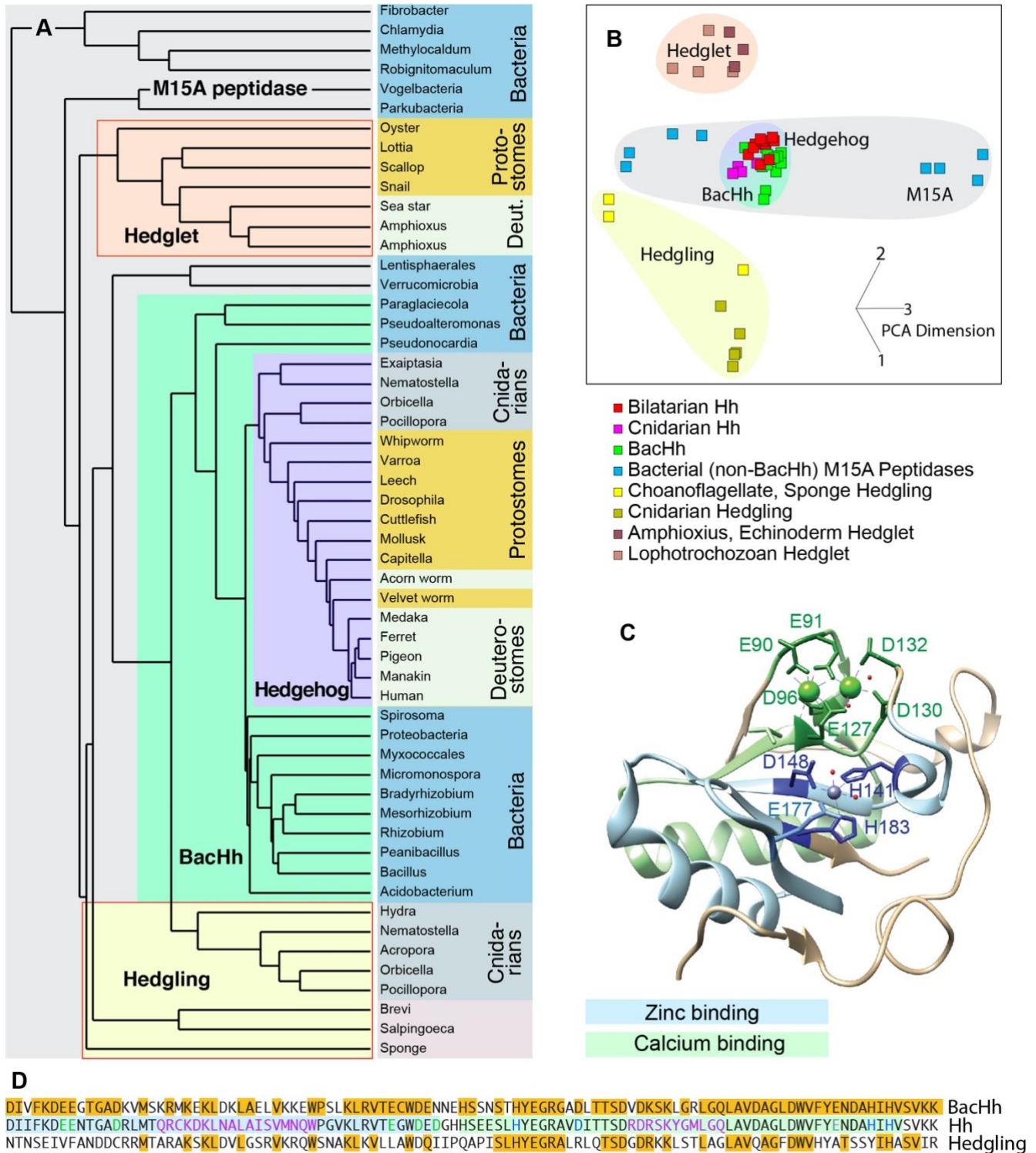
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Short title:

The putative peptidase function of Shh

Supplementary Figure 1



Supplementary Figure 1. Sequence similarities between BacHs, Hhs, Hedglings, and Hedglets.

A: a similarity tree of Hh sequences encompassing the calcium and zinc coordinating motifs. All Hhs are closely related and root from within the BacHhs. Hedglings (present in Choanoflagellates, Sponges, and Cnidarians) and Hedglets (present in Lophotrochozoans, Amphioxus and Echinoderms) form outgroups, but

all are related to bacterial M15 peptidases. Organisms in the same phylum or clade are color coded, and common names of the organisms are used. The sequences used, their accession numbers, and numbering of aligned residues can be found in this supplemental file. Hedglings and Hedglets (red borders) are predicted to be unable to mediate catalysis. **B:** PCA plot of the tree presented in A. **C:** Structure of Shh with salient residues and domains indicated. **D:** Sequence lineup of the conserved domains of Mesorhizobium BacHh (ESZ55121.1), human Dhh (NP_066382.1), and Choanoflagellate Hedgling (XP_001749037.1). Identical residues are indicated in amber. Salient residues are color coded and color coordinated with C.

Supplementary Figure 1 Sequences. Below are the sequences used to generate the tree and PCA plot shown in Supplementary Figure 1. Accession number and stretch of residues used in the lineups are indicated.

>Monosiga brevicollis, [XP_001749037.1](#), 354-458
GLSFAPSSGNMYPNVVSARMASRLKVLANLVPRVFGESA AVLVLDAYRAAPLVAAEATLHNTGRAALLTVINVTASLDDELAALASVCADA
GFDVYVLYNSSAAIY

>Human, [BAA33523.2](#), 89-193
IIFKDEENTGADRLMTQRCKDRLNLSLAISVMNQWPGVKLRVTEGWDEDEGHHSEESLHYEGRAVDITTSRDRNKYGLLARLAVEAGFDWVY
YESKAHVHCSVKSE

>Mesorhizobium sp. L103C131B0, [ESZ55121.1](#), 173-277
IVFKDEENTGADRMMPRLKSKLDSLAVVASEWPGAKLRVTEAWDEDENEHADASLHYEGRADLTTPVDGAKLGRRLARLAVDAGCDWVF
FEDSSHIHVSVKAG

>Micromonospora sp. HK10, [WP_082159544.1](#), 1063-1166
IVFKDEEKTADRMMPRLRDMVNELAALVVKQWPGKLRVTEGWDEENNEHTAESTHYEGRAVDMTVSDLDAKLGRLARLAVDAGFDWVF
YENALHVHASVKK

>Nematostella1 vectensis [XP_001635678.1](#), 84-187
IVFKDEERTGADRLMSKRCREKLRNLATKVKQKWKGVKLRVTEAWDEDEGQHSLSLSLHYEGRAVDISTSDKDPKLPDLGSLAVDAGFDWVY
YDRRSSIHASVRS

>Nematostella2 vectensis, [ABX84114.1](#), 69-171
EVVFENDDCRRTTARAKSKLDVLA SRVRQEWAGRKLKVIKAWTDQRTAQDPASLHYEGRALRLQLDNDRSMLSRLAGLALASGFDWVSYF
LNSDYIHASVIRA

>Pseudoalteromonas piratica, [WP_040135141.1](#), 60-162
PVFKFEEGNFTDVQASEKLC AAIMDLNKLVMKEWPGKTLRVTEAYDQDGEHAKFSLHNEGRAADMTVSDRDLKKGRLGLFLATKAGFSWVY
YEHNHIHASVKR

>Spirosoma aerolatum, [WP_080055297.1](#), 211-317
VVFKNEEGDGSDRMMPVLKTHVDRLADLVRSEWGAGVSLRVTEAWDDTGEHSSSHSLHYEGRAVDLTTSDDLKSKLGRGLAVDAGFNW
VYYENLLHIHASVTKA

>Varroa destructor, [XP_022667503.1](#), 83-186
IRFLDDEGTGADRIMTQRCKRDLDTLAVSVMTQWPGVKLRVIESWDEYSHHKSGSLHYEGRAVDFTTDDRQAKYGMRLARLAVEAGFDWVY
YETKRHVHASVKP

>Drosophila melanogaster, [NP_001034065.1](#), 144-247
ILFRDEEGTGADRLMSKRCREKLNVLAYSVMNEWPGIRLLVTESWDEDEYHHGQESLHYEGRAVTIATSDRDQSKYGMRLARLAVEAGFDWVS
YVSRRHICYSVKS

>Crocodylus porosus, [XP_019386078.1](#), 87-190
IIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVTEGWDEDEGHHSEESLHYEGRAVDITTSRDRSKYGMRLARLAVEAGFDWVY
YESKAHIHCSVKA

>Amphimedon queenslandica, [ABX90059.1](#), 74-180

SSQATYLHFASSDCRIMSSRLYTRLSSLAEEAYWRYHIKILVLKAWTPYPDYSLDNTSLHYEGRSVRIHVTSRNVTRLLKMAVSAGFDWVM
YDKKGYARMSVIPDAC

>Salpingoeca rosetta, [XP_004997926.1](#), 540-646
TVKPDPTSNGDPVSMKRLRRHITTLASVVRGVFGDDAYVRVLEAYVEPPADISKASLHNVGRAARITIEGVPDDFASDRLGVLGGLAVE
AGFDYVAYTSRDSLYV

>Orbicella1 faveolata, [XP_020616832.1](#), 68-170
IVFANDDCRRMTARAKSKLDVLSRVKRWNSNAKLKVLAWTDQIIPQAPISLHYEGRALRLQTS DGDRKKLSTLAGLAVQAGFDWVHYAT
SSYIHASVIRDV

>Pocilloporal damicornis, [XP_027055961.1](#), 66-167
EIDFANDDCRRMTARAKSKLDVLSRVKRWNSNAKLKVLAWTDQIMPQAPISLHYEGRAVRLQTS DGDTGKLS TLAGLAVQAGFDWVHYA
TNSYIHASVIR

>Hydra vulgaris, [XP_004209904.1](#), 72-174
IDFQTEDSRLMTSRKQKIDTLAGLVTTTRFGKNMKVNVLKAWTDVVEKEDKLSLHYEGRAFLIRASNNDKLLSDMLVLAREAGFDWVYK
NEDSIYLSVIPD

>Orbicella2 faveolata, [XP_020632016.1](#), 84-183
IIFRDEEGTGADRLMSKRCKELTTLAGLVKGEWPSVKLVVTEAWDEQDQHS PNSLHYEGRAVDLRLSDRDKTKIGLLGRLAVEAGFDWVL
YESRSHIHA

>Pocillopora2 damicornis, [XP_027044648.1](#), 88-190
IIFKDEEGTGADRLMSKRCQDKLNTLADLVRQWPTVKLVVTEAWDEQDQHS NSLHYEGRAVDLRLSDKDRTKIGYLGRLAVDAGFDWVY
YQKRTHIHASVR

>Exaiptasia pallida, [XP_020892909.1](#), 87-190
IVFKDEEGTGADRIMSKRLREKLRILAKKVKEKWRGSTRLRVIEAWDEDGTHSAHSLHYEGRAVDITTS DLDKQKYPELGRLAVEAGFDWV
FYESQEHIHASVY

>Acidobacteria bacterium, [PYS76727.1](#), 46-149
IVFKDEEHTGDDRMMSRSLRSARVDDLAARVKREFPGLKLRITEAWDDSTIHAPTSRHLEGRAVDITTS DVHKKLGRLAGLAVEAGFDWV
FENDLHVHASVKK

>Bacillus pseudomycoloides, [WP_098188151.1](#), 989-1092
IQFKDEEGTGADFLMSTRSLSDKLNLTALILVNQEWPNIKLRVTEAWDEDNEHSSGSTHYEGRAADITTS DRDGNKLGRLAQLAVDAGFDWVY
YENKYHIHVS VKK

>Proteobacteria bacterium, [PZN23661.1](#), 96-197
IVFKDEEATGADLLMTPRLRLRLHELARLVREWPGVRLRVTEAWDEDSEHGENSEIHYEGRAVDVTTSDRRRKLGRLAGLAIQAGFDWVS
HERDHVHASVR

>Vogelbacteria bacterium, [OHA60126.1](#), 199-302
ANGYSGINGPGRTRVHRDVAEATVWVQQLNSDHNLS TQITAAHTEGVGHSAGSEHYEGRAVDIQPTGGNVTS SNLNI IADYCRQAGFTY
VLVENRHVHCDAR

>Methylocaldum marinum, [WP_119628113.1](#), 46-148
KSQPPIAVKKGAILAGLDRRMYFALQKARRVWSRYGKLLVVTSGLDGRHKKGSLHYVGLAVDLRSRYFAPSTRRTVTRELRRNLGDEFQVI
DEKHHIHVEFDP

>Fibrobacter sp., [WP_143394061.1](#), 26-138
NLLIKRVQLKTGVYTGKLDAA MDSAGLVVVAEYHKVMGDSYRPTITSANDYGKHARRSKHYENKALDFRISDVPRNKRSQIVASIRQALGK
RFNVFWEKNTANEHLHIELKE

>Chlamydia trachomatis, [CRH64334.1](#), 1-102
MLQFKNNVRLSGVQEEILFIIDRIQRYFEVRLPKRDFVITSLTDGAHMKGSLHPKGLALDMRSRTLDKKEIEYFVTWFRKNFEKSYDLVVE
IDHIIHIEYDPK

>Parcubacteria group bacterium, [PSO44215.1](#), 232-331
ASGFRGIAGPRTGKVKQPWVEKTKQIQEICENRYGGRPFQVTA ACTYGVGHSNDSTHYRGEAVDLPVDATNQQVISCVKEAGGVPYYLD
EDSHIHSS

>Robiginitomaculum sp., [PHQ68463.1](#), 158-262
DENDIDIKEGADISDLTDDMTDTFDDISEAWADEAPGVTPVITSGGDGTHSTNSLHYDGNVAVDLRTNNTLQAQT TTVASALSTSLGSDYDV
VVESDHIHVEYDPG

>Lentisphaerales bacterium, [TFH13511.1](#), 91-194
WESDHDGENDEDHLMHRGVQPLLNQLEKAVASCGAALKVHDASRPSGGHCATSLHKEGRALDLTADGLTLEDLAKLCWVAGFDWVFNEN
KRGAEHVHCSRA

>Paraglaciecola hydrolytica, [WP_068382217.1](#), 63-166
VVIKFEEGDCSDSKVTKNLKKTIKFLVELIDQEWEGERKLRITEAWDNNAEHTKYSLNHNEGRAADITTTDDRDTKKLSKLACLAMAAGFSWV
KLEKDHVHASVPR

>Rhizobium leguminosarum, [WP_130783679.1](#), 310-413
IVFKDEEGTGADRMM SARLRDGLDRLAAQVGIWPDVKLRVTEAWDENNEHHGASLHYEGRAADLTTSRDPGDKLGRGLKLAVDAGLDWVF
FENSAHIHVSVKR

>Verrucomicrobia bacterium, [HCF95878.1](#), 132-232
ESDHDGDWDTENDHLVHRDILPALIRLNALVLEQEGATLKIQDAYREEGIHAPASLHREGRALDLTADGMSLARLAQLAVQAGFDWVYYESP
KGGGAHIHAS

>Myxococcales bacterium, [RYZ03269.1](#), 109-212
IVFKDEERNRDRFMTPLRRLSLVQLSKLVSQTWPKVLDLRVTEAWDDREHGAGSVHYEGRAADITTSQDPAKLGTLAALAVKAGFDWVF
YENATHVHVSVKR

>Branchiostoma1 floridae, [XP_002599309.1](#), 305-414
RMLGSSLDRCADRVM SKALLDHLRTVQRMVQDEFSGVKLVLEAWDEPHAGATTGDHPAGSLHYEGRAAKLTLSGDAAKLPRLA AFCIC
DGAGYVENKGDHILVAVQK

>Pseudonocardia dioxanivorans, [WP_103381118.1](#), 106-208
VVKDEEGSGADRMMTPRLAELVGVLAHVAVQAFPGRRRLRLTEAWDPDGEHSHSSLHYEGRAADLTVD DRRAKLGRLAALAVQTGF DWVLH
ENDHVHVSVRAG

>Branchiostoma2 belcheri, [XP_019614930.1](#), 311-413
DRCADRVMTKSMLDLLRKVQKMKVDEFTGVKLVLEAWDEPHAGATEGDQPAESLHFEGRAAKLTLDGDTSKLPQLAKNAICAGANFVEH
KGDHIFVAVRKQ

>Acanthaster planci, [XP_022111291.1](#), 310-422
HMKGFALNSRCADRMTSARL MATLKTGKLVSIWEPGVKLLVLEAWDEAHEGSTYTDGQDPAGSLHYEGRAAKLSLSDGDTSKFSRLAGLA
TCAAADYVEHNGDHIFVAAKKQ

>Sepia bandensis, [ALM01450.1](#), 32-143
IVFRDEESNNE DRMM SKRCKDKLNTLAIAMNEWPGVKLRVTEAWDTEGHHAPTSLHYEGRAVDITTS DRERSRYGMLARLAVEAGFDWVY
YESRSIHCSVR

>Lottia gigantea, [XP_009064322.1](#), 299-407
EKPLGNSLNQRCAARLMSQRMYNVLI SLQLKVRANGDKLVKEQAFDEKYAGHVADFDATS LYTEGRLVKVTRSVNPSLAN YKKLTQWAICS
KADFVQNGD HVLIGVKK

>Crassostrea virginica, [XP_022317995.1](#), 275-379
YPGNYLPNRCAVRVMSRPLFNVLVNLKAYASDANLGGPGGKITVEEAWDGGADPSSLRSEGRMIKVKLSAGNTAANLGKLAQLAICAKADH
VSNMGTHLLLSVKK

>Mizuhopecten yessoensis, [XP_021349176.1](#), 304-415
GIVGSALSKRCAARTMSYRMKVINTLQK FVRHNMTLTDKLVKAWDEPYADATTGDTSYSRLHTEGRAVVQLVSSNTASNLEELSHFA
ICAGADFISHKGDKLEIAVKK

>Bradyrhizobium sp. WSM4349, [WP_018460114.1](#), 210-314
SIVFKDEEGTGADRMMSTRMQAKLDALASLVSAEWPGVKLRVTEAWDENDEHSPTALHYEGRAADITTPPDGAKLGRRLARLAVNAGCDWV
FYEDTNHVHVSVKK

>Paenibacillus sp. CAA11, [WP_108465644.1](#), 1027-1131
DIVFKDEEGTGADKVM SKRMKEKLDKLAELVKKEWPSLKL RVTECWDENNEHSSNSTHYEGRGADLTTS DVDKSKLGRGLQAVDAGLDWV
FYENDAHIHVSVKK

>Columba livia, [PKK32334.1](#), 86-190
DIIFKDEENTGADRMLTQRCKDKLNALAI SVMNQWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTS DRDRSKYGM LARLAVEAGFDWV
YYESKAHIHCSVKA

>Ptychodera flava, [BAR45718.1](#), 88-192

DIIFKDEEGTGADRLMTQRCKDKLNSLAILVMNQWEGIQLRVTEGWDEDGHHHAENSLHYEGRAVDITTSDRDKKYGMLARLAVQAGFDWV
YFESKSHVHCSVRS

>Antalis entails, [APD15681.1](#), 86-190
DIVFKDEEGTGADRMMSKTCRDKLDTLAI FVMNQWTVGVKLRVTEAWDEEHHHAKDSLHYEGRAVDVTTSDRDRSKYGMLARLAVNAGFDWV
YYESRAHIHCSVNS

>Helobdella robusta, [AAM70491.1](#), 270-374
NII FQNSEGTGADRVMKRCSDKLNLSLMEQWPGVRLRVVEAWDEDETHPEDSLHYEGRAVDVTTSDKDKSKYGMLARLAVEAGFDWV
HYEYRSHIHCSVKS

>Oryzias melastigma, [ACL81248.1](#), 46-150
DIIFKDEENTGADRLMTQRCKDKLNSLAISVMNQWPGVKLRVTEGWDEGDHGFEEESLHYEGRAVDITTSDRDKSKYGTLSRLAVEAGFDWV
YYESKAHIHCSVKA

>Trichuris suis, [KFD51835.1](#), 95-199
NIVFKDEEGTGADRIMTNRCRYKLNLLALVSNFVWPGVRLRVDAWEERNRQVVGSLHYEGRAVDITTSDRDNRKIPRLARLAVQAGFDWV
YFESRQHVHASVKS

>Capitella teleta, [AAZ04357.1](#), 82-186
DVVFKDEEGTGADRIMSQRCKDKINTLAISVMNQWPGVKLKRVTEAWDEEDGFHAKDSLHYEGRAVDITTD RDRSKYGMLARLAVEAGFDWV
YYENRGHIHCSVKS

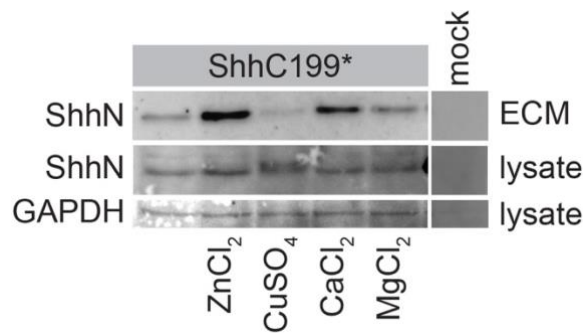
>Pipra filicauda, [XP_027590561.1](#), 84-188
DIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRVTEGWDEGDHGHSEESLHYEGRAVDITTSDRDRNKYGMLARLAVEAGFDWV
YYESKAHIHCSVKS

>Branchiostoma3 floridae, [XP_002607850.1](#), 269-370
HPVGFTPSQRCADRVMKRLYTALLRVDKHVREQLNARLRITEAWDEPHSGAADGDQAENSLHYEGRAAKLELSGSSDLTSLAKYCICADI
DYVEHKGTYLF

>Acropora millepora, [XP_029199742.1](#), 68-170
EIDFANDDCRRMTARAKSKIDVLASRVGRWSNVRLRVILGWTDQIPVDTQKLLHYEGRALRLQTSDRDSSKLRITLAGLAVEAGFDWVYYA
SSSYIHASVIRD

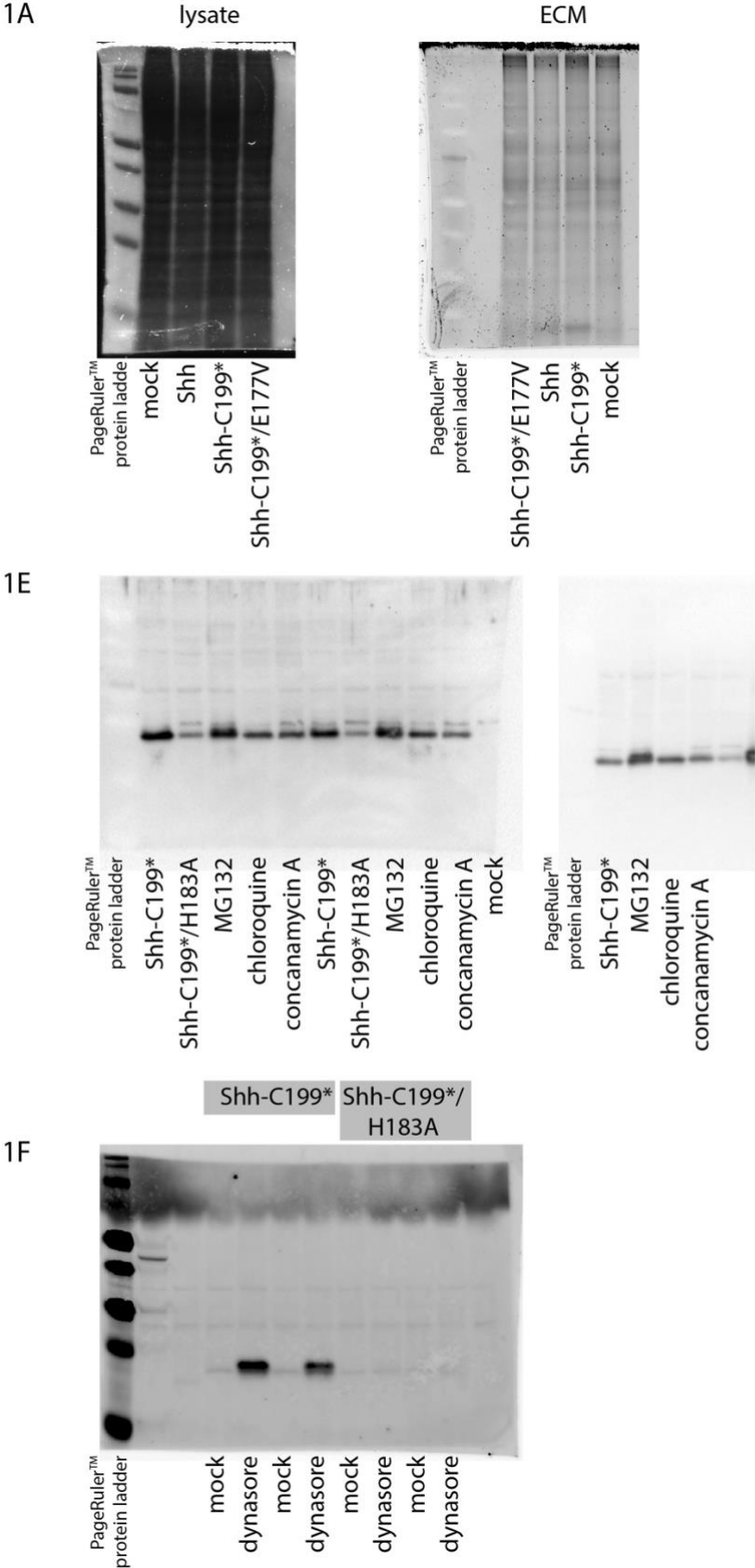
>Euperipatoides kanangrensis, [VDH80594.1](#), 88-190
IIFKDEEGTGADRLMTQRCKEKLNTLAISVMNQWPGIKLRVTEAWDEEDNHHSAESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWV
YESRAHIHCSVK

Supplementary Figure 2



Supplementary Figure 2: Association of Shh with the ECM is enhanced specifically in response to zinc. Western blot analysis of the lysate and ECM of Hek293t cells transfected with *Shh-C199** and cultured in medium containing 0.18 mM calcium and 5 μ M zinc, 5 μ M copper, 1.8 mM magnesium or 1.8 mM calcium as indicated.

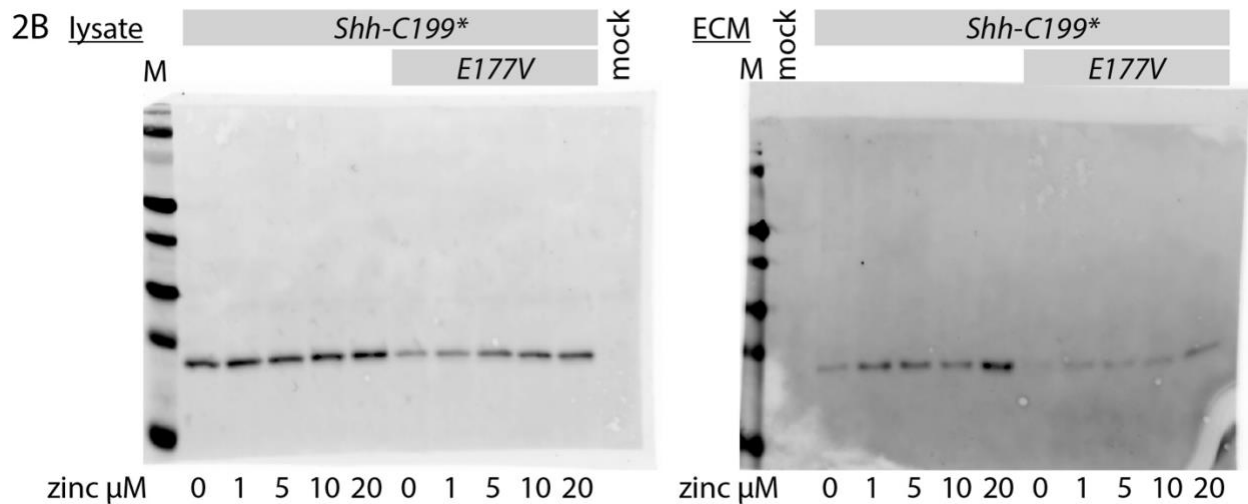
Supplementary Figure 3: Uncropped and unedited gel and Western blots for Figure 1:



Supplementary Figure 3: Active ShhN associates with the extracellular matrix.

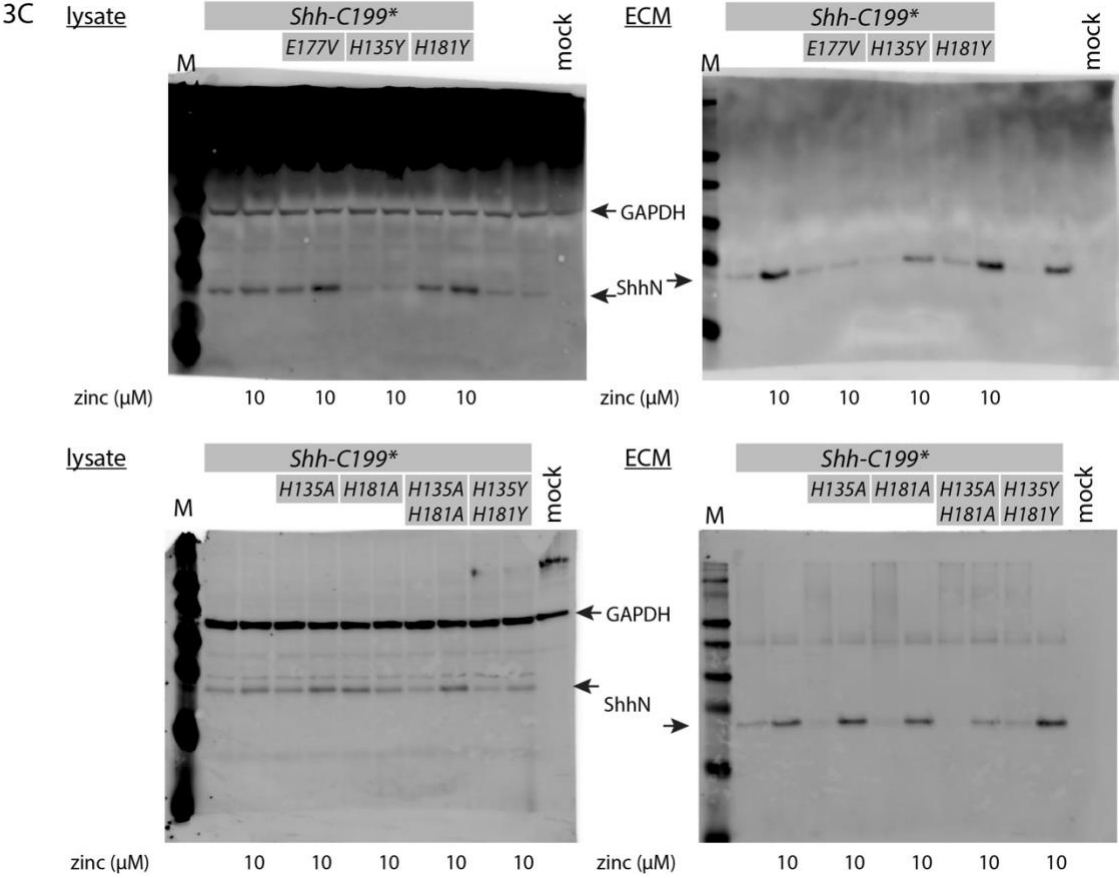
A: Lysate and ECM deposited by mock and *Shh-C199**-transfected Hek293t cells analyzed by SDS-PAGE and SYPRO-Ruby staining. ShhN is indicated. **E:** Western blot analysis of HEK293t cells transfected with the indicated Shh mutants. 100 nM MG-132 (proteasome inhibitor), 100 nM Chloroquine and 100 nM Concanamycin A (inhibitors of endosome acidification) were assessed for their ability to affect Shh accumulation. **F:** Western blot analysis of HEK293t cells transfected with the indicated Shh mutants, and the effects of the dynamin inhibitor Dynasore (50 μ M) was assessed for its effect on Shh accumulation. M = (PageRuler pre-stained protein ladder)

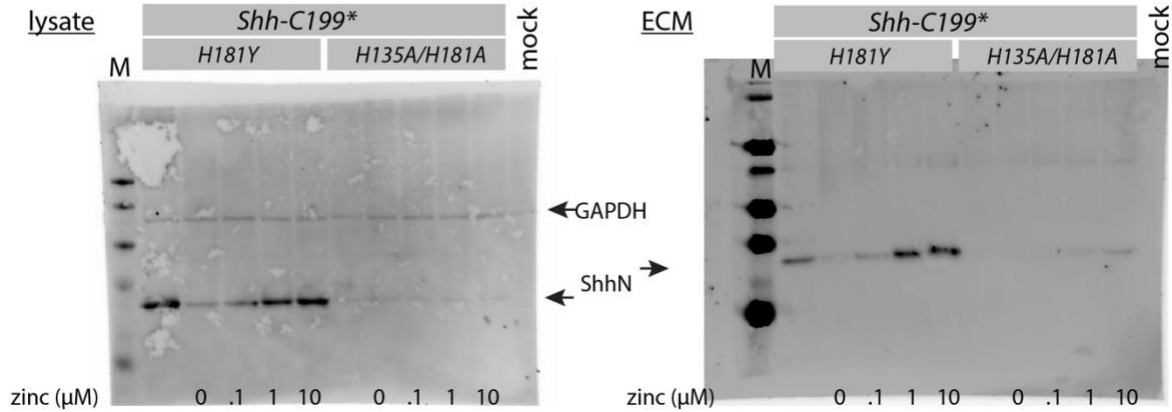
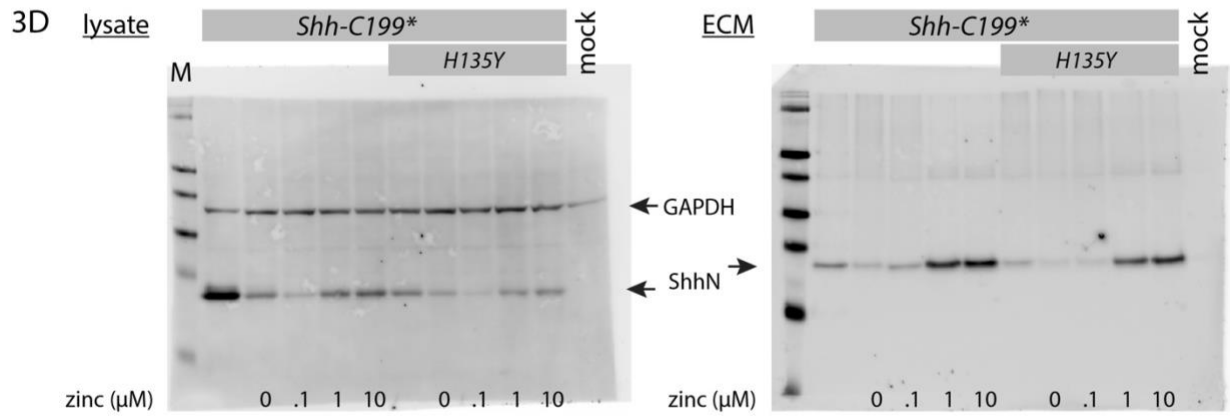
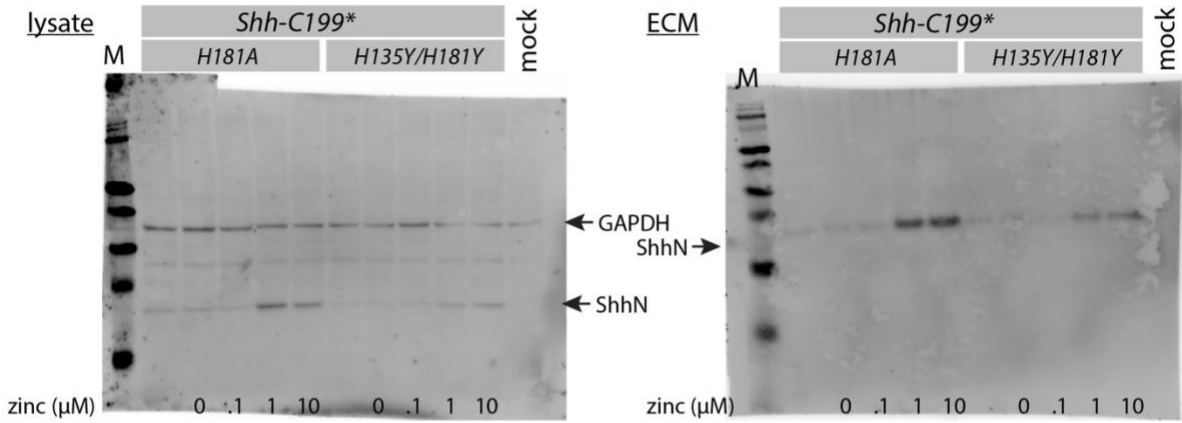
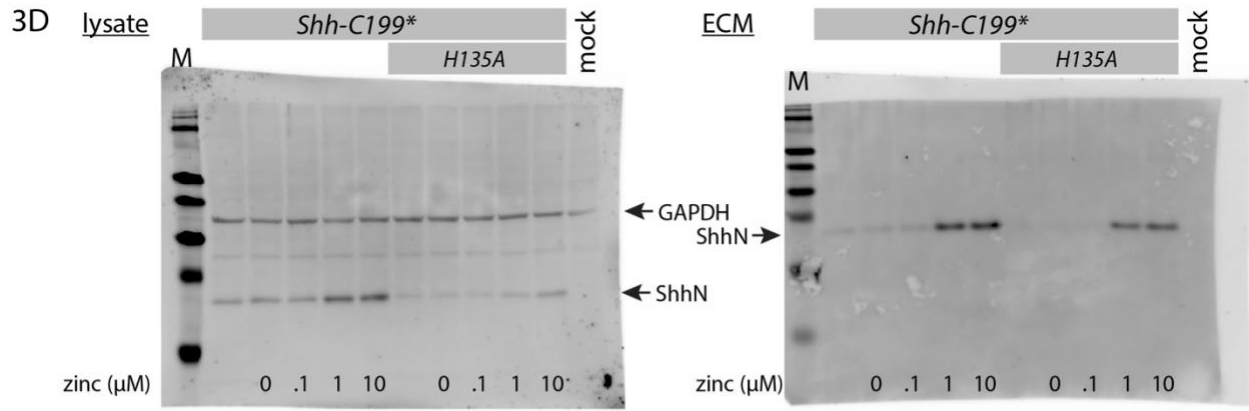
Supplementary Figure 4: uncropped and unedited Western blots for Figure 2



Supplementary Figure 4: ECM-association of ShhN requires zinc and the catalytic E177V residue. B: Western blot analysis of the lysate and ECM of HEK293t cells transfected with *Shh-C199** and *Shh-C199*/E177V* and cultured in DMEM containing 0.18 mM calcium and the indicated concentrations of zinc. M = (PageRuler pre-stained protein ladder)

Supplementary Figure 5: uncropped and unedited Western blots for Figure 3





Supplementary Figure 5: Stacking histidines of the zinc coordination center affect ECM

association. C: The effect of mutations of the transition state-stabilizing residues H135 and H181 to alanine (A) or tyrosine (Y) on the zinc-dependent accumulation in the ECM was analyzed on a Western Blot of the extracted ECM from transfected HEK293t cells cultured in 0.18 mM calcium with or without 10 μM zinc. **D:** zinc dose-response analysis of H135 and H181 mutations assessed by Western blot of the lysate and ECM of HEK293t cells transfected with the indicated mutants and cultured in 0.18 mM calcium and increasing concentrations of zinc (0.1, 1, 10 μM). M = (PageRuler pre-stained protein ladder)

Supplementary Figure 6: uncropped and unedited Western blot for Figure 4

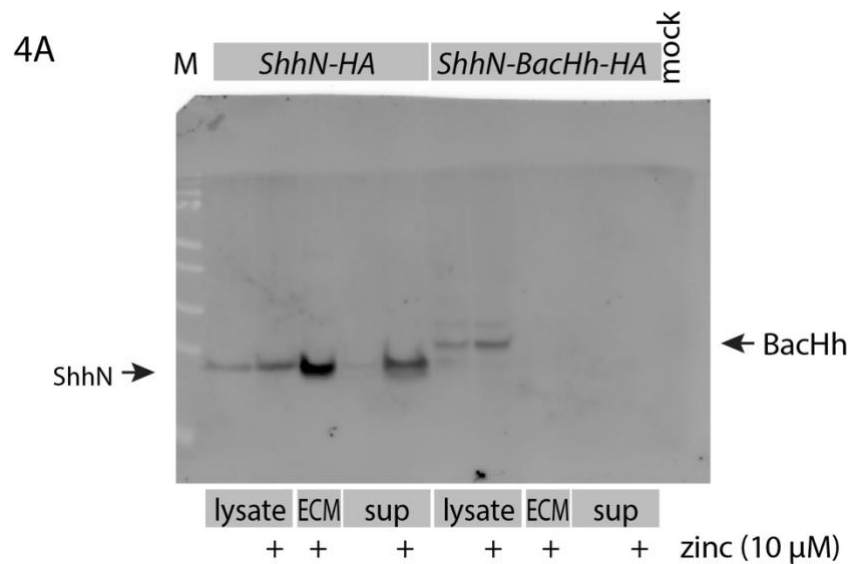


Figure S4: The zinc-coordination domain of BacHh is not sufficient for association with the ECM. A:

Western Blot analysis of the lysate, ECM, and supernatant of *ShhN-HA* or *Shh-BacHh-HA* (diagrams) transfected HEK293t cultured in the indicated zinc concentrations.

M = (PageRuler pre-stained protein ladder)

Supplementary Figure 7, uncropped and unedited Western blots for Figure 5

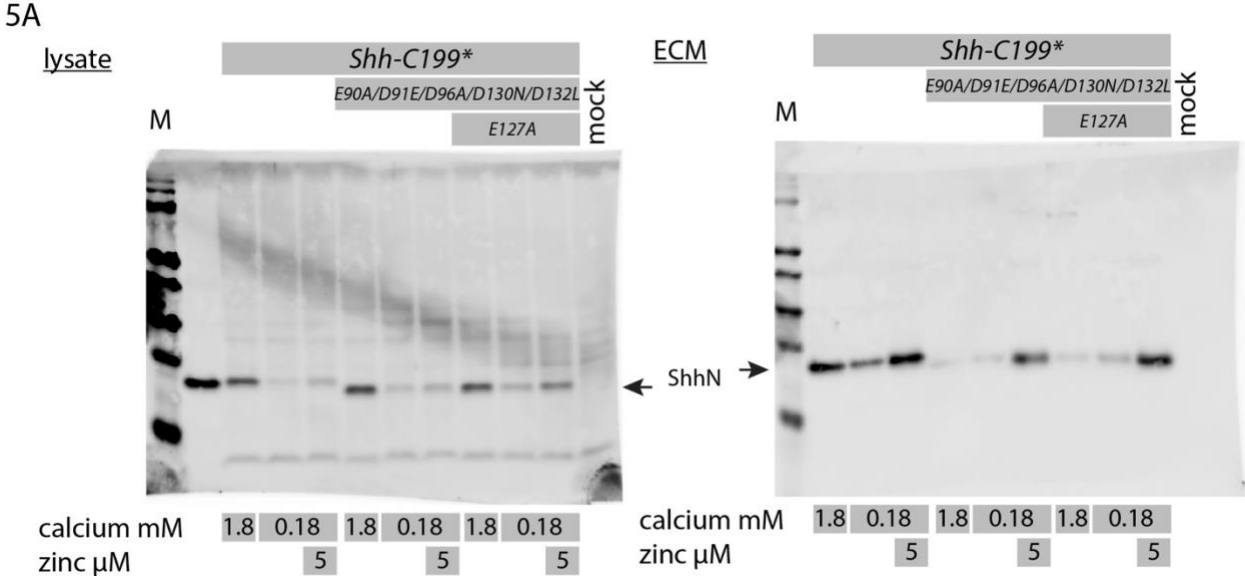


Figure 5: Calcium alters the sensitivity of Shh to zinc. **A:** Western blot analysis of lysates and ECM of HEK293t cells transfected with *Shh-C199** and *Shh-C199*/E90A/E91D/D96AD130N/D132L*, or *Shh-C199** and *Shh-C199*/E90A/E91D/D96A/E127A/D130N/D132L* (Ca^{Free}), cultured in the presence of 0.18 or 1.8 mM calcium, and in the absence or presence of 5 μM added zinc. M = (PageRuler pre-stained protein ladder)

Supplementary Figure 8: uncropped and unedited Western blots for Supplementary Figure 2

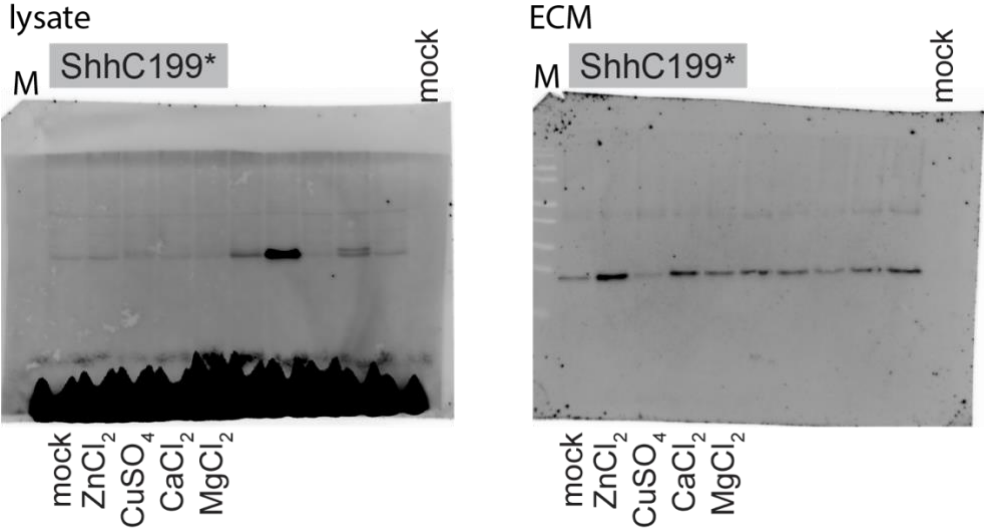


Figure S8: Association of Shh with the ECM is enhanced specifically in response to zinc. Western blot analysis of the lysate and ECM of Hek293t cells transfected with *Shh-C199** and cultured in medium containing 0.18 mM calcium and 5 μM zinc, 5 μM copper, 1.8 mM magnesium or 1.8 mM calcium as indicated.