Supplementary figure X. Alignment of the SREB receptors from human, *Asterias rubens*, and *Octopus vulgaris* that were cloned and tested in receptor assays in this study. Conserved residues are highlighted, with similar amino acids in gray and 100% conserved residues in black.

SREBHsap85 ---------------------------------------------------------------MANYSHAADNILQNLSP 17

SREBHsap173 ---------------------------------------------------------------MANTTGEPEEVSGALSP 17

SREBHsap27 -------------------------------------------------------------------MANASEPGGSGGG 13

SREBArub MSHIITTRIRPPPARLSFAPTGMSELSTAMSTLLDLGFTNGSTGLNSSAGDSISVTARTVLHAGVRPGEEGGGDADLLAD 80

SREBOvul ----------------------------------------------------------------MHTEVYTHASYSYYSE 16

SREBHsap85 --LTAFLKLTSLGFIIGVSVVGNLLISILLVKDKTLHRAPYYFLLDLCCSDILRSAICFPFVFNSVKNGSTWT---YGTL 92

SREBHsap173 PSASAYVKLVLLGLIMCVSLAGNAILSLLVLKERALHKAPYYFLLDLCLADGIRSAVCFPFVLASVRHGSSWT---FSAL 94

SREBHsap27 EAAALGLKLATLSLLLCVSLAGNVLFALLIVRERSLHRAPYYLLLDLCLADGLRALACLPAVMLAARRAAAAAGAPPGAL 93

SREBArub DHGPRVLWCASLIVVIILSVVGNGILALVVFGNSRLRRPSYFFLFNCALADFVRSLLCFPFVVSAVVSRDWIY----SNS 156

SREBOvul PQYVLALKIISLALIIFTGILGNSMVVYTIIRDKRLHRPPFYYLVSLAMSDLARSVFCLPFVLTTVIQGYVWVY---GEN 93

SREBHsap85 TCKVIAFLGVLSCFHTAFMLFCISVTRYLAIAHHRFYTKRLTFWTCLA-VICMVWTLSVAMAFPPVLDVGTYSFIREEDQ 171

SREBHsap173 SCKIVAFMAVLFCFHAAFMLFCISVTRYMAIAHHRFYAKRMTLWTCAA-VICMAWTLSVAMAFPPVFDVGTYKFIREEDQ 173

SREBHsap27 GCKLLAFLAALFCFHAAFLLLGVGVTRYLAIAHHRFYAERLAGWPCAAMLVCAAWALALAAAFPPVLDGGGD---DEDAP 170

SREBArub LCEILAFFNVYLTYGVLYTLFLISIERYVVLRFHRFHRQKLKGPACLL-LVLASWALAVSMAFPPVFNTRTYSFIEIENQ 235

SREBOvul ACILVGFTNTFFIYSSAVTFLLISGDRYVGVVQTRFYRRKCGGLLSLA-FIVFGWGVAFLVSFPPIFGLGSYTFVPSEAQ 172

SREBHsap85 CTFQHRSFRANDSLGFMLLLALILLATQLVYLKLIFFVHDRRKMKPVQFVAAVSQNWTFHGPGASGQAAANWLAGFGRGP 251

SREBHsap173 CIFEHRYFKANDTLGFMLMLAVLMAATHAVYGKLLLFEYRHRKMKPVQMVPAISQNWTFHGPGATGQAAANWIAGFGRGP 253

SREBHsap CALEQRPDGAPGALGFLLLLAVVVGATHLVYLRLLFFIHDRRKMRPARLVPAVSHDWTFHGPGATGQAAANWTAGFGRGP 250

SREBArub CTFKHQEYKSNETLCFLLFFVAVIAFTHFAYFRVFLFMRAHRKMRPMQFVPAVSNNWTFYGPGSTGQAAANWFLGYRQGP 315

SREBOvul CTYSHTHYRSNDTLVFLLVFTFIMSLSLLLYYRILMFLRNHRKMYPFFHQPARSNNWTFLGPGANGQALVNWLNGFTGFR 252

SREBHsap85 TPPTLLGIRQNANTTGRRRLLVLDEFKME-KRISRMFYIMTFLFLTLWGPYLVACYWRVFARGPVVPGGFLTAAVWMSFA 330

SREBHsap173 MPPTLLGIRQNGHAASRR-LLGMDEVKGE-KQLGRMFYAITLLFLLLWSPYIVACYWRVFVKACAVPHRYLATAVWMSFA 331

SREBHsap27 TPPALVGIRPAGPGRGARRLLVLEEFKTE-KRLCKMFYAVTLLFLLLWGPYVVASYLRVLVRPGAVPQAYLTASVWLTFA 329

SREBArub TPPPLIGLAP--PANGNSTSLSKSDFERE-EKFSKLSLTITISFSVLWLPYTVYCFWQVFQHNNPLPYTYVSIATWLTFF 392

SREBOvul QNPWLNPIAAGFQMPPRQLGRTVNLKVVKGEHLSRLFFTVTLVFDILWVPYLVLSYWQVFEVSHQLSSTFIGVAAWCSYL 332

SREBHsap85 QAGINPFVCIFSNRELRRCFSTTLLYCRK--SRLPREPYCVI---- 370

SREBHsap173 QAAVNPIVCFLLNKDLKKCLRTHAPCWGTGGAPAPREPYCVM---- 373

SREBHsap27 QAGINPVVCFLFNRELRDCFRAQFPCCQSPRTTQATHPCDLKGIGL 375

SREBArub QACINPILCFVVSKEFRQIALQHVFGASAFQQEGHNVQL------- 431

SREBOvul AVAVNPLVYLCCSGTLRRAFRPEIESYSKRGTLRE----------- 367