

A *acvr2a-b* transcript

5' TCGTCGGAGAAGCTGAGGATCGTATCAGGATGTGTTTAAACCCGAGTCCATCATGATTGGGATTTTATGTGTTGATAAACTCGCCAGAGTGA
TCGATACTGATCGATATTAGCTCATAAGTGTATTGGAGACTGTCCAGCACAGTTTGTCTCTGATTCACTGATGACTGTATTAATGTTTGATTTTC
ACCTATGCAGACAGAAACACAGGCACTGAGGATTTGTCAAATCTCTCCAACCTAAACCTCTCTTCAGACTTACACATTGATCCGGACCTGTTTG
CTCACAAATAATGCTTTTGGCAATATTAACCATTAATTTTCGAGGGAGCGGATTATCGGCTTGGGTGTTGCTGGGATTATCGCTGTACAAGAA
TCTGCACTGAAATGAGGACAGACACAACTGGCCTTGCCATATTCCTCGTCTCTGTTTCATCAGGTGCGATTCTGGGCCGCTCGGAGACACAG
M R T D T K L A L I F L V S C S S G A I L G R S E T Q
GAGTGTGTGATTATAATGTGAGCTGGGAGAAGGACGGAACAAACAGGAGCGGCACGGAGTCATGTTATGGAGAAAAGGACAAGCGGCGACACTGT
E C V Y Y N V S W E K D G T N R S G T E S C Y G E K D K R R H C
TTCTCCACCTGGAAGAACCCTCGGGGACCATCGAGATGGTCAAGCAGGGCTGCTGGCTGGACGATGTCAACTGCTACGACAGCAGTGAGTGTGTG
F S T W K N R S G T I E M V K Q G C W L D D V N C Y D S S E C V
GAGCGCAAAGAGAATATTGATGTCTTCTTCTGCTGCTGCGAGGGAACCTGT 3' →
E R K E N I D V F F C C C E G N L

Orange: chrUn_KN150226v1:12087-12345; Green: Start codon; Black: chr6:1724727-1725082; Green: Translation exon 1; Cyan: Translation exon 2; Blue: Translation exon 3; Boxed: Previously predicted start codon (ENSDART00000157415.2, GRCz11)

B *Acvr1b-a*

MLRDGNVAVMPPRRRTAVALLALCGLLAVGDALKCNCTACESTGYVCETDGACMASTSYINGQEEQVVRICIPRVSLVPPGQPIYCL
SAKGLLNTHCCYTDFCNSINLQIPNGIADGKGGSWGVPVELVAVIAGPVFLFCLLLIVGVLLFQHHQRNRYNHRQRLDVEDPSCDHLILA
KDATLQDLNFDLSTSGSGSGLPLFVQRTVARTIVLQEIIGKGRFGEVWRGWRGWDVAVKIFSSREERSWFREAEIYQTIMLRHENIL
GFIAADNKDNGTWTQLWLVS DYHEHGS LFDYLNHYSVTIEGMIKLSAASGLAHLHMEILGTQGKPGIAHRDLKSKNILVKKNGTC
AIADLGLAVRHESITDTIDIAPNQRVGTRKRYMAPEVLDETINMKHFDSEFKADIYALGLVYWEIARRCNAGGIHEDYQLPYDLPVSDP
SIEEMRKVVCDQRLRPNPVNWQSYEALRVMGKIMRECWYANGAARLTALRIKKTLSQLSVQEDIKI

C *Acvr1b-b*

MDPRQILRILIVLSGLNGVCDALCNCTAPH CERDGF KCETNGACVASTSVIEGQEQHVRLCIHKEKLVPPGQPFYCLSAEGLMNTH
CCYTDYCN SIDRLPIVTNGPGAGQDWGPVELTAVVAGPVFVLCVLVLLGLFLFQHHQRAYGHRQRLEVEDPSTEHMFLAKDKTLQ
DLIYDLSTSGSGSGLPLFVQRTVARTIVLQEIIGKGRFGEVWRGWRGWDVAVKIFSSREERSWFREAEIYQTIMLRHENILGFIAAD
NKDNGTWTQLWLVS DYHENGSLFDYLNRYSVTIEGMIKLSAASGLAHLHMEILGTQGKPGIAHRDLKSKNILVKKNGTC
AVRHESITDTIDIAPNQRVGTRKRYMAPEVLDESINMRHFDSEFKADIYALGLVYWEIARRCNAGGIHEDYQLPYDLPVSDP
SIEEMRKVVCDQRLRPNPVNWQSYEALRVMGKIMRECWYANGAARLTALRIKKTLSQLSVQEDIKI

D *Acvr1c*

MSHPRCSDAALFIFTFVQLTAALKCVCHLCVNHTCETEAEAGACWNSVMLINGKEETVKSCVSPSELKGQVFCYSSRNVSKRNCFF
TDFCNNE TLHLNPEQPPEDSGWSQLEVAAVILVPSCLVCGVMLGVCAIQNLRC THIKSLKQDPPEPLDDPTLVSPDKCLKELIYDM
STSGSGSGLPLLVQRTIARTIVLQEIIGKGRFGEVWRGWRGWDVAVKIFSSRDERSWFREAEIYQTIMLRHDNILGFIAADNKDNGS
WTQLWLVS DYHEHGS LFDYLNRYSVTIEGMIKLSAASGLAHLHMEILGTQGKPAIAHRDLKSKNILVKKNGA AVIADLGLAVKHDSNT
NTIDIPINHRVGTRKRYMAPEILDD SINMSSFESFKRADIYSLVFWELARRCSIQGIHEDFQLPYDQVQSDPSLDDMRVVEQKL
RPNIPNQWQSEALRVMGKIMRECWHANPAARLTALRVKKTISQVTWVKDVKE

E *Acvr2a-a*

MGPATKLAFGVFLISCSGAILGRSETQECVFYNNPSLENRGNRS GIEPCVGD KDKRLHCFATWRNVSGTVEIVKQGCWLDDVN
CYDSTECVEKKEDPDVFFCCCEGNMCNEKFYNPNTAPVQTTSNPLTQKPLPFSTLLYSIVPIMGIAAIVLLSFWMYRHHKLAYPPVL
VPTADPGPMPPSPPTLVQKPLQLEIKARGFRGCVWKAQLLNDYVAVKIFPIQDKLSWQNEIYDINIPGMRHENILQFIAEKRGSNL
DIELWLITAYHEKSSLDYLVKANNVSWNELCLIAQTFRGLAYLHEDIPNLKDGHKPAIAHRDFKSKNVLLKNTLACIADFGALALKE
AGKSAGDTHGQVGTTRYMAPEVLEGAINFQRDAFLRIDMYAVGLVLWELAACTASDGPVDEYMLPFEEEEVGQHPTELDQMDEVV
HKKLRPTLRECWQKHPGLAMLCETIEECWDHEAEARLSAGCVEERIVQMQRQTSVSAPEEIVTVMTVNDVYPKESSL

F *Acvr2a-b*

MRTDTKLALAIFLVSCSSGAILGRSETQECVYNNVSWEKDGTNRSGTESCYGEKDKRRHCFSTWKNRSGTIEMVKQGCWLDDVN
CYDSSECKVERKENIDVFFCCCEGNLCNQKFHYNPETVEPTLNPVPPKPDLPFTLLYSLLPIMAVAVILFISFWMYRHLKLTYPPLVPS
QDPGLTPPSPPLGQKPLQLELKARGFRGCVWKAQLLSEAVAVKIFPVQNKQSWQNEIYDINIPGMRHENILQFIAEKRGNGVDI
ELWLITTYHEKSSLDYLVKANNVSWNELCLIAQTFRGLAYLHEDIPNLKDGHKPAIAHRDFKSKNVLLKNTLACIADFGALALKE
STGDTHTGQVGTTRYMAPEVLEGAINFQRDAFLRIDMYAVGLVLWELAACTASDGPVDEYMLPFEEEEVGQHPTELDQMDEVV
RPIFREHWLKHGSLLCETMEECWDHEAEARLSAGCVEERIISMQRSTSIISPDDILSVMTVNDVYPKESSL

G *Acvr2b-a*

MFASLLTLALLLATFAADPSHGEVETRECLYNNVNWVEVEKTNRS GVERCEGEKDKRSHCYASWRNNSGSIQLVKKGWLD DFN
YDRQECVATEENPVFFCCCEGNFCNERFTHLPDISGPVISPPPVSPLLNVLYSLLPLSMLSMAVLLAFWMYRHRKPPYGHVDV
NEDPGPSPSPPLVGLKPLQLELVKARGFRGCVWKAQMINYVAVKIFPIQDKLSWQNEREMFSTPGMKHDNLLRFIAAEKRGSNLE
MEFWLITEFHGSLTDYLVKANNVSWNELCLIAQTFRGLAYLHEDIPNLKDGHKPAIAHRDFKSKNVLLKNTLACIADFGALALKE
FEPGKPPGDTHTGQVGTTRYMAPEVLEGAINFQRDSFLRIDMYAMGLVLWELVSRCKAADGPVDEYMLPFEEEEVGQHPTELDQMDEVV
VWHKKLRPAFKDCWLKHSGLCQMCETMEECWDHDAEARLSAGCVERISQIRRVSSSTSDCLFSMVTSLTNVDLPKESSL

H *Acvr2b-b*

MFVPWLAFALVWCTGVSHA EVATRECVYNNVNDWRTEKTNQSGFERCEGEKDKRLHCYASWLNSTGTIRLVKKGWLD DFN
RQECVATEESPVFFCCCEGNFCNEKFTHLPEAIAPAVKIQQPGPSLFGILVYSLLPLAILSLALVLACWTYHQRKPPYRHVDIGQ
DAGLPPSPPLVGLKPLQLELVKARGFRGCVWKAQLLSEYVAVKIFPIQDKLSWQNERDIYLTGFKHENILHYISAEKRGNTLMEL
WLVTETFERGSLTDYLVKANNVSWPQLCHISASMSRGLAYLHEDIPYRAEGPKPAIAHRDFKSKNVLLKMDLTAVIADFGLA VRFEPG
KPPGDTHTGQVGTTRYMAPEVLEGAINFQRDSFLRIDMYALGLVLWELVSRCTASDGPVGEYQLPFEEEEVGQHPTELDQMDEVV
KMRPVFKDCWVKHQLSGLCETIEECWDHDAEARLSAGCVERISTISKSNNTLNTSTSECLLSMLTSHSDTLPPKDSST

Bold: Signal peptide; Red: Activin receptor domain; Underlined: Transmembrane domain; Blue: GS domain; Italics: Protein kinase domain

Figure 1 – figure supplement 1