

A

Amino acid sequence alignment: Translation of pangolin *IFIH1* pseudogene and human *IFIH1* protein

Pangolin	1	MSNAYSADKSFSPISASHPERTGTSTRRLYWT	100
Human		MSNGYSTDENFRYLISCFFRA-RVKMYIQVEPVL	
Pangolin	101	---SPSFANTHDECPQLMSRLQPTLVDTLEVRDVDRCEEDL	200
Human		TDLPSPSFENAHDEYLQLNLQPTLVDKLVRDVLDCMEELLTI	
Pangolin	201	FKCCAVSSETENLTQ-DGPEVKESHLLAAVQPSPEKEAWDVNNSLESSFMSYIVSESDTSLAEGSVSCLD	300
Human		SDCESNAEIEINLSQVDPQVEQLLSTTVQPNLEKEVWGMENNSSESSFADSVVSESDTSLAEGSVSCLD	
Pangolin	301	SSPENCLSGLTWKRPNCXELPLGPHYQMAAQPAALEKNTIICLLPTGSGKTRASGYVAKDHLDERKQ	400
Human		ASPEP-----ELQLRPHYQMEVAQPALEGNIIICL-PTGSGKTRVAVYIAKDHLDERKQSEPGKVIVLVNK	
Pangolin	401	KKWYQVTGLSVDTQLKISFPEVVKSCDVIISTAQILKNSLLNPENGEDTGVQFSDFSLIIDECHHTK	500
Human		KKWYRVIGLSGDTQLKISFPEVVKSCDIIISTAQILENSLLNLENGEDAGVQLSDFSLIIDECHHTK	
Pangolin	501	PQIPGLTASPGAGGATKQAQAKHEHLKICANLDAFTIKTMKENIEQLKDQIKEPCKKFVISDDTREDQ	600
Human		PQILGLTASPGVGGATKQAQAEHLKICANLDAFTIKTVKENLDQLKNQIQEPCKKFAIADATREDP	
Pangolin	601	GIIQIEKKAKEGNCRDRCACAEHLRKPNGTLQINGTIDMIDAYRHLETFYNDEKES-----GDSGGN	700
Human		AIQMEKKAKEGNRKRERCAEHLRKYNEALQINDTIRMIDAYTHLETFYNEEKDKKFAVIEDDSDEGG	
Pangolin	701	DNKKTLLKLAANPEHENEKLTLERSSILGQSARTESAIGIIFTKTRQSVYALSQRISLSTFAEVGVKA	800
Human		ENNKMLKRLAENPEYENEKLTLEKRNITIMEQYTRTESARGIIFTKTRQSAYALSQWITENEKFAEVGVKA	
Pangolin	801	KIHLIATAVAEEGLDIKECNIVSRDITDETALVQARAGARAEESTVLVGHSGSGAFELATVNDFOEKMTYKAID	900
Human		KINLLIATVAEEGLDIKECNIVIRYGLVTNEIAMVQARGARADESTYVLVAHSGSGVIEHETVNDFREKMYKAI	
Pangolin	901	MEKKIKIKRSRAKRYRDKPSLISHLCKLCSVLACPSEYHVIERMRQGHVTAEFKELCLVRENKALIKKFAHYQANGKI	1000
Human		MEKKMKTKRNIKHYKNNPSLITFLCKNCVSLACSGEDIHVIEKMHVNMTPEFKELYIVRENKALQKKCADYQINGE	
Pangolin	1001	CLKIRNFVVFKNKPKKQYKKVEFPVTFPGLEYSYCLLSDE	1045
Human		CLKIRNFVVFKNKPKKQYKKVEFPVTFPGLEYSYCLLSDE	

B

Amino acid sequence alignment: Translation of pangolin *ZBP1* pseudogene and human *ZBP1* protein

Pangolin	1	MAEVPADPGKEGYPEKKTQVLRDAGSPVKTA	100
Human		MAQAPADPGREAERPQQHAATIPETPGFQFSQQ-----REEDIYRFLKDNQFQALVIAQALGM	
Pangolin	101	KTTKGVVVDLCALNRRLDLDQNSNTLTIQSEDSGGRNQSTTVVYQNPINMICQKGNPSRISTENSGGIQIGHG	200
Human		TRAKVDNRDLRYMKRSHLLDDEQSKAWTIYRPEDSGRRKASASIIYQHNFINMICQNGPNSWISIANSEAIQIGHG	
Pangolin	201	VFW-LDPGGTQTSTWRGVYSDRCSWDATR-----	300
Human		APGDSSTWGLTVDPW-GPDIHMEQSILRVQLGHSNEMRLHGVPSSEGAHIIPGSPPVSAATAAGFEASF	
Pangolin	301	-----	396
Human		IGNSNKMSISPGVAGPGGAGSGEGEPGEDAGRPPADTQSRSHFPDIDGQFITPSHSLTPKLETMTLGNRSHKAAEGSHYVDEASHEGSGWGGGI	

Supplementary Figure S1. Positions of disruptive mutations within the *in silico* translation of *IFIH1* and *ZBP1* pseudogenes of the Malayan pangolin. (A) The pangolin *IFIH1* pseudogene was translated whereby in-frame stop codons and frameshift mutations were marked by “X” on red background (GenBank accession number XP_017517341.1). This theoretical amino acid sequence was aligned to that of human *IFIH1*. Identical amino acid residues are indicated by blue fonts. Numbers indicate amino acid positions. (B) The pangolin *ZBP1* pseudogene was translated whereby in-frame stop codons and frameshift mutations were marked by “X” on red background (GenBank accession number XP_017505753.1). This theoretical amino acid sequence was aligned to that of human *ZBP1*. Identical amino acid residues are indicated by blue fonts. Red dashes indicate the absence of the carboxy-terminal protein segment in this prediction. Numbers indicate amino acid positions. Note that additional deleterious mutations that have not been marked by the automatic gene prediction algorithm, are present in the pseudogenes.