

Table S1									
Species screened for hAT-6_XT									
Turtles	Species name	Assembly	Homology greater than 80% to hAT-6 and presence of TSDs and TIRs (Y/N)						
	<i>Malaclemys terrapin terrapin</i>	terp_v2_2	Y						
	<i>Malaclemys terrapin pileata</i>	rMalTer1.hap1	Y						
	<i>Emys orbicularis</i>	rEmyOrb1.hap1	N						
	<i>Trachemys scripta elegans</i>	CAS_Tse_1.0	Y						
	<i>Gopherus evgoodei</i>	rGopEvg1_v1.p	N						
	<i>Mauremys reevesii</i>	ASM1616193v1	N						
	<i>Gopherus flavomarginatus</i>	rGopFla2.mat.asm	N						
	<i>Dermochelys coriacea</i>	rDerCor1.pri.v4	N						
	<i>Terrapene carolina triunguis</i>	T_m_triunguis-2.0	N						
	<i>Pelodiscus sinensis</i>	PelSin_1.0	N						
	<i>Mauremys mutica</i>	ASM2049712v1	N						
	<i>Chelonoidis abingdonii</i>	ASM359739v1	N						
	<i>Caretta caretta</i>	GSC_CCare_1.0	N						
	<i>Chrysemys picta</i>	Chrysemys_picta_BioNano-3.0.4	N						
	<i>Chelonia mydas</i>	rCheMyd1.pri.v2	N						
	<i>Carettochelys insculpta</i>	ASM3395843v1	N						
	<i>Chelydra serpentina</i>	ASM1885937v1	N						
	<i>Chrysemis picta belli</i>	Chrysemys_picta_BioNano-3.0.4	N						
	<i>Dermatemys mawii</i>	Dermatemys_mawii-1.0	Y						
	<i>Mesoclemmys tuberculata</i>	Mesoclemmys_tuberculata	Y						
	<i>Sternotherus odoratus</i>	rSteOdo2_p1.0	Y						
	<i>Chrysemis picta</i>	Chrysemys_picta_BioNano-3.0.4	N						
Birds	Species name	Assembly	Homology greater than 80% to hAT-6 and presence of TSDs and TIRs (Y/N)						
	<i>Chlamydotis macqueenii</i>	ASM69519v1	N						
	<i>Balearica regulorum gibbericeps</i>	ASM70989v1	N						
	<i>Corvus hawaiiensis</i>	bCorHaw1.pri.cur	N						
	<i>Tympanuchus pallidicinctus</i>	pur_lepc_1.0	N						
	<i>Neopelma chrysocephalum</i>	ASM398488v2	N						
	<i>Corvus moneduloides</i>	bCorMon1.pri	N						
	<i>Nipponia nippon</i>	ASM70822v1	N						
	<i>Melospittacus undulatus</i>	bMelUnd1.mat.Z	N						
	<i>Dryobates pubescens</i>	bDryPub1.pri	N						
	<i>Egretta garzetta</i>	ASM68718v1	N						
	<i>Falco naumanni</i>	bFalNau1.pat	N						
	<i>Aythya fuligula</i>	bAytFul2.pri	N						
	<i>Aquila chrysaetos chrysaetos</i>	bAquChr1.4	N						
	<i>Lagopus leucura</i>	USGS_WTPT01	N						
	<i>Fulmarus glacialis</i>	ASM69083v1	N						
	<i>Apteryx australis mantelli</i>	AptMant0	N						
	<i>Hirundo rustica</i>	bHirRus1.pri.v2	N						
	<i>Chiroxiphia lanceolata</i>	Chiroxiphia lanceolata	N						
Frogs	Species name	Assembly	Homology greater than 80% to hAT-6 and presence of TSDs and TIRs (Y/N)						
	<i>Xenopus tropicalis</i>	UCB_Xtro_10.0	Y						
	<i>Bombina bombina</i>	aBomBom1.pri	N						
	<i>Nanorana parkeri</i>	ASM93562v1	N						
	<i>Bufo bufo</i>	aBufBuf1.1	N						
	<i>Spea bombifrons</i>	aSpeBom1.2.pri	N						
	<i>Rana temporaria</i>	aRanTem1.1	N						
	<i>Bufo gargarizans</i>	ASM1485885v1	N						
	<i>Xenopus laevis</i>	Xenopus_laevis_v10.1	N						
Fishes	Species name	Assembly	Homology greater than 80% to hAT-6 and presence of TSDs and TIRs (Y/N)						
	<i>Etheostoma spectabile</i>	UIUC_Espe_1.0	Y						
	<i>Thalassophryne amazonica</i>	fThaAma1.1	Y						
	<i>Scophthalmus maximus</i>	ASM2237912v1	Y						
	<i>Syngnathus acus</i>	fSynAcu1.2	Y						
	<i>Scleropages formosus</i>	fSclFor1.1	Y						
	<i>Epinephelus lanceolatus</i>	ASM528154v1	N						
	<i>Silurus meridionalis</i>	ASM1480568v1	N						
	<i>Hippocampus zosterae</i>	ASM2543408v3	N						
	<i>Nothobranchius furzeri</i>	UI_Nfuz_MZM_1.0	N						
	<i>Tachysurus fulvidraco</i>	HZAU_PFX_2.0	N						
	<i>Melanotaenia boesemani</i>	fMelBoe1.pri	N						
	<i>Clarias gariepinus</i>	CGAR_prim_01v2	N						
	<i>Carassius gibelio</i>	carGib1.2-hapl.c	N						
	<i>Maylandia zebra</i>	M_zebra_UMD2a	N						

Insects	Species name	Assembly	Homology greater than 80% to hAT-6 and presence of TSDs and TIRs (Y/N)				
	<i>Acromyrmex echinator</i>	Aech_3.9	N				
	<i>Drosophila gunungcola</i>	Dgunungcola_SK_2	N				
	<i>Leguminivora glycinivorella</i>	LegGlyc_1.1	N				
	<i>Bombus bifarius</i>	Bblif_JDL3187	N				
	<i>Diaphorina citri</i>	Diaci psyllid	N				
	<i>Cryptotermes secundus</i>	Csec_1.0	N				
	<i>Melitaea cinxia</i>	iMelCinx1.1	N				
	<i>Drosophila santomea</i>	Prin_Dsan_1.1	N				
	<i>Nilaparvata lugens</i>	ASM1435652v1	N				
	<i>Zootermopsis nevadensis</i>	ZooNev1.0	N				
	<i>Myzus persicae</i>	MPER_G0061.0	N				
	<i>Frankliniella occidentalis</i>	Focc_3.1	N				
	<i>Drosophila subpulchrella</i>	RU_Dsub_v1.1	N				
	<i>Solenopsis invicta</i>	Solenopsis invicta	N				
	<i>Bactrocera oleae</i>	MU_Boleae_v2	N				
Snakes & Lizards	Species name	Assembly	Homology greater than 80% to hAT-6 and presence of TSDs and TIRs (Y/N)				
	<i>Podarcis raffonei</i>	rPodRaf1.pri	N				
	<i>Sceloporus undulatus</i>	Sceloporus undulatus	N				
	<i>Pseudonaja textilis</i>	EBS10Xv2-PRI	N				
	<i>Pogona vitticeps</i>	pvi1.1	N				
	<i>Thamnophis sirtalis</i>	Thamnophis_sirtalis-6.0	N				
	<i>Notechis scutatus</i>	TS10Xv2-PRI	N				
	<i>Python bivittatus</i>	Python_molurus_bivittatus-5.0.2	N				
	<i>Gekko japonicus</i>	Gekko_japonicus_V1.1	N				
	<i>Eublepharis macularius</i>	MPM_Emac_v1.0	N				
	<i>Anolis carolinensis</i>	AnoCar2.0	N				
	<i>Pantherophis guttatus</i>	UNIGE_PanGut_3.0	N				
	<i>Thamnophis elegans</i>	rThaEle1.pri	N				
	<i>Varanus komodoensis</i>	ASM479886v1	N				
	<i>Crotalus tigris</i>	ASM1654583v1	N				
	<i>Podarcis muralis</i>	PodMur_1.0	N				
	<i>Zootoca vivipara</i>	UG_Zviv_1	N				
Mammals	Species name	Assembly	Homology greater than 80% to hAT-6 and presence of TSDs and TIRs (Y/N)				
	<i>Pipistrellus kuhlii</i>	mPipKuh1	N				
	<i>Mesocricetus auratus</i>	BCM_Maur_2.0	N				
	<i>Peromyscus leucopus</i>	UCI_PerLeu_2.1	N				
	<i>Cricetulus griseus</i>	CriGri_1.0	N				
	<i>Dipodomys ordii</i>	Dord_2.0	N				
	<i>Suncus etruscus</i>	mSunEtr1.pri.cur	N				
	<i>Microtus fortis</i>	M_Fortis_MF-2015_v1.1	N				
	<i>Mus caroli</i>	CAROLI_EIJ_v1.1	N				
	<i>Dipodomys spectabilis</i>	ASM1905484v1	N				
	<i>Phodopus roborovskii</i>	PHOROB	N				
	<i>Rattus rattus</i>	Rrattus_CSIRO_v1	N				
	<i>Heterocephalus glaber</i>	HetGla_female_1.0	N				
	<i>Nannospalax galili</i>	S.galili_v1.0	N				
	<i>Lipotes vexillifer</i>	Lipotes_vexillifer_v1	N				

Table S2

Representative bucleotide sequences of horizontally transferred hAT-6_XT

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CAGGGGTGTCAAACCTCAATTGCACAGGGGGGCCAAAATCCAAAACACACCTTTAGTGCGGGGCCGAACAGTATAAACATTATTGAACACACTAAAATTCAGTTGCTCTTTGCTCTTATGT
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ACACCCCTTGCTCTAAAC

>hAT-6_XT_Esp (Contains Mariner-4_1Ilyo-like insertion)

GTCTAGAACAGGGGTGTCAAACCTAATTGCACAGGGGGCCAAAACCTCAAACACACATTAATGTGAGGGGCCGAACAGTATTAAACATTATTAAACAGACTAAATATTGGTGTTTTTAA CGATTAATATGAATCAAATACAGGATATCATTTCCAAATAAATAAATTCAACTTAAATATTTTGCTCTTCATAAAACAATATCCTGTCAATGCAATACATTCAAAATCTGTACATGCTGG AATATAACAACATCTGAAAATGTAAATGAAAATGTAATTTAAAGTAAAGTTAAATCATACAAAACATAACATTCAAATTTCTTGCTCTATTAGTCAGAGCCTGAGACTTGGAGTCTTTT CTTTGCAACAAGTTGGTTTATGTTTGGGGTCAGGTTCTGTGTTTGGGAGATTCTCAGGATGGATTGCAGATTGTCATCAGTGAGGCGGCTCCTGTGTGACGTTTTGTAAATTTTCATCA CAGAGAACAGCTGCTCGCACACATACAGTGGTGCTCAAAAGTTTACATACACATGCTTAAGTTGACTAAAAAGAGGAATAAAAAATCATGTTTTGGAATTTATTTTAATACCTAAATATA AAAATGAGTAAAACTCAACCTTTAAGGCACCAATTTCTTTGTGAATGAATAACGTATTGTAAATAATAAATGTCTTATTAAAAATACAGGGGTCAAGATACACATCCCCATGT AAATTTCCCATAGAGGCGAGGCAGATTTTTATTATTAAGGCCAGTTATTTCTGGATTACAGGATATTATGCATCCTGATAAAGTCCCTTGGCCCTTTAGAATTAATAAGCCCCACATCCT CACATACTCTTACCATGCTTAGAGATAGGCATGGGATCTTCTATAAAATCATCTCTCAATGCAAATCAAACCCAGGTATTAGTCTAACTGAAATAAAACCATGCCTATCTCTAAGCAT GGTGAAGAGTATTGAGGATGTGGGGCTATTTAAATCTAAAGGCCAAGGGAACTTATCAGGATGCATAATATCCTGAATCCAGGAAATAACTGGCCCTTTAAATAAAAAATCTGGCCT GCCTCTATGGGAATTTAAACATAGGGGTATGTATACTTATGACCCCTGTATTTTAAATAAGAACATTTATTTATTACAATACGTTATTCATTACAAAAGAAAATTTGGTGTCCCTTAAAGGTT GGATTTTACCTCATTTTTTAATTTAGGTATTAATAAATTTCCAAAACATGATTTTTTATTCCTCTTTTAGTCAACTTAAGCATGTGTATGAAACTTTTGAGCACCATGTATGTCTGC CAAACATGGACAGGATTCGAGCGCATGTTGGCGGAGCTGCGGCATCGCTTCAGGAAGGAAGCGGGTGAACCTGTGCTGGCCCTCAGTGTCTACTTTGCCCTTCAGTGTCTCCGTTA CACTGCAGTTCTATCAGCTCCATCTGCATTTCTACTGGTGGGTTTCCACGTGCACTGCAAAATGGGTTGCGAAGCAGCTCGAAATTAATTTCTGTGCCTCAAAGTCACTGAAGCGCC GGCGAACTCAGTGCCGAGCGCGCTGAGTTTTTCCAGCAAAGTGCGCATTTGGGAAAACCTGTGTCATCTTTCTGGTTTCAGTATTACTTGGCAACAGGGAAGTGAGACAAGTTGCATT GGTGCAATTTGGGTCTCCCATAGCGCAGCTTCACTTGAATGCCTTCACTGCATCATGCATACAGTTATATTGTGCTCCCGTCCCTGGAGTTGAAGGTTTAAAGCGCTAAGATGCGCA CTGTGCAGTGCAGCGAAGCGCAACTTCATCTCCAGCGCCAGGAGTATGCAACAAAACCTTTGCTCTTTCAACTGATGCTCCATGAACCTGGCAGATTTTCCCTCCGAGCTCAAAAGTGTCTTT TGAGAACTTTTCCCGACTCAGCCACCGGACCTCCGTATGATACGGCATATCGCCAAAACTCGCAATCTATTTCCCGCAGAAAAGACTGGAATTTGGCGGTGATTTAAACCGTGGGCTCT GATAAAGTTGACGGTTTGTGTACAGGTTCCATCATCATGATCCATTTTAGAGCTTTAGCAGTCAAGCATCTCTGGTGATGATGCAGTGATATACTGTCAACTCACCGGCAGCTGCTCT CTTCCCGCATCTTTGAGCGCATCTTCCACATGCTCAATTTTTTCCACACATCGCAGGTGCGCCATCTGTTGTGAAGTCCCAACAGTTTTCCTATGGCAGCTGCATGTCCGGTTAC ACTTTGAAATACATTTCCAAAAGATGTCTTCTCCTTTTGGTTGTCGCGTGCATCGATTAAATGTCAGTATTTTCTCTGTTACGCAAAATTTGGAATCCATCCACGGATGAATATCGCCAG CTGTGCAGTGCAGTGCAGTGTGTTTTCATCCAGCGCCAGGAGTATGCAACAAAACCTTTGCTCTTTCAAACTGATGCTCCATGAACCTGGCAGATCTCACAACCCGATTAAG CAACAGTGTCTGCTGAGGCTTACATTTGGGAATGCTCGCGTTTTATCTGGACAACAGCAGCTCGCACATTTTCATCATACAATTTCTACGAAATCCCCCTCGGTAACGGCCGCTCT GATTTGCGCATCTTTCGGCCAACTGAACCTGCTTTCACAGCAGCTTCACTTTTGATTTGCTTTGGTGA AAAACGCTGCTGCTGGGATGCTCAAACTCTCTTCAACTCCTCTACCTTT TGTAGCTTCTGCTGCTGAGTCAAGTTTTTAACTTGTCTCATGTTTTGTCTGAGTGGCGCTGTAGGTTATACCTCTTATTACAGCGAGCTTATCCCGCAAGGAGACACATTAAT TTACCTGCAATTTTCAGTAACATATACCTATTCTCCACCGCGCTTTGAAGAGTTCGGTTTTTCAGAAATACATTTTGGCTCTGGCCATTTGTTGTGGTCTAGCTTTGATTTAGCGTTG TAGACCGGAACTTGAAACCGCGCTTCGCGTTGGCGGCAATTCATGTCATCGGATTTGAGTTTGGCGGCTCATATCACAGGGCCATTAACAACAGATATATACAATGATCAC GCGGGCCGGATATAATTGTATGGCGGGCGGATGTGCCCCGAGGCCCTTGAGTTTGACACATGTGGTCTAGAA
>hAT-6_XT_SF0 AATTAATCAGGGGTGTCAAACCTAATTGCACAGGGGGCCAAAACCTCAAAGCACACTTTAGTGTGCGGGGCCGAACAGGATAACCATTTATTGAACACACTAAAACCTTTAAAC TTTAAAACCTTAACCTTTTTGAACATAAAAAATGAATAAAAAACAGACAGGAATATTATCCGGAATAAATCAACTCAAACCTTAAATAACTTATAATATTTGCTCTCCATAAAAAATATATGCTG TCTAAATATACAAATTCAAAACATGAACATGCTGCATAACAAAACCTGGAATATAAAATAAAATTTGTGCTTTTTCAGCAATAACAAATCAAATCATTTCGGTTGTCTTTGCTCTTATGTCTAT TTTTACAGAGCTGGACGCTTGGCATCTTTTTTGGCAACAAGTTTCGTTTATGTTTGGTGTGAGGTTCTGTGTTGTGGAGATTCTCAGGATGGACTGCAGGTGCTCATCAGTGAGACGA CTCCCGTGTGCTGTTTTTGTAGTCTTCATCACTGAGAAGAGCTTCTCACACAGATATGTGCTACCAAAACATGCACAAGGTTTCGAGCCGCATGTAGACGGAAGCTGGGGCATTTCTGCGG GAATGGAGTGAATAAACTGTGCGGGCCCTGCAGTGTCTGACTTTTGCCTTCAGTTGCGCATTAAGTGCAGCTCAATCAGCTCCATCTGAATCTCAGACGTTCCACATCTGCATCGAC GGCAATGGGTGCGAAGAACTCAAATCTTTTTTGTCTTCAAAGTCACCAAGCGCCGTGCGAAGTCAAGTGTGCGCGGTGCGCTCAGTTATCAGCAAAGTGCATTTTGGGAAC ACCGTTGTGCGGACTTTGGTTCAACATTACTTTGGCAACAGGGAAGTGGGGCAAGTTGCACTGGCGCATTTGTGCTCCCATAAAGCAGCTTCACTTGAATGCCTTCACTGCGTCAT ACATGTCAAGTGTGAGCGCTGCGGCTCCTGAGCTGGAGGTTTAAAGGCTTGAGATGAGCTGTTATGTGCAGCCAGAAATGCCAACTCGCATTTCCACTTTTCACTCCATAAATTTGGT GGAGTCTTTTCTTTACTGTCTATGAAGTACAGATTTTGGTGTGCTGAGCTCAAACCTCTGTGCGAGAATTTTCCCGGACTTAGCCAAACGCACCTCTGTATGATAAGGAATGTACAGCAA ACTCTGAATCTATCTCCCGCATAAAGGACTGAAATTTGCCGTGATTTAAACCTTTAGCTCGGATAAAGTTACGGTTTTGTGTTAAAGTGTCTATTACATTTGCTCATGTTTGGC CACATAGTGCTTCTGGTGTATGATGCAGTGATATGCCGTTAACTCACCAGTACAGTTTCTCCTCTGCATCTTTACTCGCATCTTCCCACTAGTCCACTTTTTCTACTACACATAGATG GTGCTCCATCAGTTGTAAGTGCAATAAGTTTGTCCAGGGGCAATTTTCATGTGCGTTATACTTTGACATACATTTCAAATAATGTCTTTTCCAGTCTGTTGTCCCGTGCATCGATTAAATGT CCATTATTTCTCTGTGACGCGCAAAATTTGGAAGTCCACTCCACGGATGAAGATGGCCAGCTGTGCAGTATCAGTGTGCTGAGTACTTTTCATCCACAGCAAGAGATATGCAATAAAGTC TTTTGCTCTTTTCACTCAACTGTGTTCTTAAATCAGTGGCCATCTCACAGAACTCGATCAGCAATCGATTTTCTACTCAGGCTTACATTTTCCAGGCATCTGCTTTTGTCTGGACATGATG GTCAAACTGCTTGTATCGCTCTTCAAGAAATCTCCCTCGGTAAATGGCCTGGCTGATTTGCGGCACTCTGCTGCCACGATAAAACTGTCTTCCACAGCAAGCTTCACTTTAGGATT TTGCACGGGTAAAAACATCTGCTGAAGTGTACGATTTCTCTTAACTCTTCTGCTTCTGTATCTTCTGCTGTCAATCAGGTCTTTTCAGGTTATCCTGATGTTTGTCTCATAGTGGCG TCTTAGATCAAAATCTTTAATTACAGCCACATTAGCTCCACAAATGAGACACACAGGGTTTACCGGCAATGTGAGTAACATATACTCAGCCTCCCATCGGTTTTAAAGGCTCTGTGTTTC AGAATCAACTTTTCTCTTCGGCATCGTGAGGGCTAGCTTCGCAATAACTTGCAGATACTTGCAGATGCAAGCTAGACTTTGATTAACCGCGGGAATGTTTCGGCAAGGCTGAAGCGCTGCATTAT GGGATCTGTAGTTTATTGTGTACCAGCGCTTCATATCGCCGGGCCATTAAATAACAATAATATATAAAATGATCTCGCGGGCCGGATATAAATTACAGCGCGGGCCGGATGTGGCCCGC GGGCTTGAGTTTGACACATATGAATTAAT
>hAT-6_XT_Tam TTCTAGGGCAGGGGTGTCAAACCTAATTGCACAGGGGGCCAAAACCTCAAACACACATTTCCGGTACAGGGGCCGAACAGGATAAACATTTATTGAATACATTAACCTTTAAACCTTTTAA ACTTAACTTTTTTGAACATGAATATGAATAAAAAACAGACAGGACTATTATTCTGGAATAAATCAACTTAAACCTTAAATAACTTCTAATATTTTGCTCTCCATAAAAAATATATCCTGTCTAAA TTATACAAGTTAGAAAAAAGTAAACGTTCAAATGTCTTTACTCTTTACATATTTTATATAAAAAATAAACTTAAATTTAAACCTTACTAAAAATATCCCAAAAGATTTTGCTCTCCATAAAAAAT ATCCTGTCAAATTTATACAAATTCAAAATATGAACATGCTGCATAACAAAACCTGGAATATAAAATAAAATTTTCAGCAATAACAAATCAAATCATTTCAGTTTTTTTTTGCTCTTATGTCTGTT TATCAAAGCTGGATGCCGTGGCATCTTTTTTGGCAACAAGTTCCCTTTATGTTTGGTGTGAGTTTCTGTGTTGTGGAGATTCTCAGGATGGACTGCAGGTGCTCATCAGTGAGATGACTC CTGTGTGCTGTTTTGTAGTCTTCATCACTGAGAAGAGCTTCTCACACAGATATGTGCTACCAAAACATGCACAAGTTCGAGCCACATGTAGACGGAGCTGGGGCATTTCTGCAAGGAA TGGCGTGAATAAACTGTGGGGGCCCTGCAGTGTCAATTTTGCCCTCAGTGTGCCATTACACTGCAGCTCAATCAGCTTCATCTGAATCTGCACAGGTGCAGTTTCCACATCGACGGC AAATGGGTTGCGAAGCAACTCAAATTTCTTTTTTGTGTTCTCAAAGTCACCAAGCGCCGTGCAAACTCAGTGCAGTGCAGTCACTGTTTATCAGCAAAAGTGCATATTGGGAACACCG TTGTGCGCGCTTTGGTTCAACATTACTTTGGCAACAGGGAGAGTGGGACATGTTGCACTGGTGCAATTTGTGACTCCCATAAAGCAGCTTCACTTGAATGCCTTTACTGCGTCAATACAT GTCAGTGATCATGCGGTACAGTCCCTTGGAGCTGGAGGTTTAAAGCGTTTGAGATGAGCTGTTATGTGAGCCAGAAATGCCAACTTGCATTTCCACTTTTTCATCCCTAAAAATTTGGTGGAG TCTTTTCTCTTACTGTCCATGAAGTACAGATTTTGTGTGCTGAGCTCAAACCTCTGCTGAGAATTTTCCCAACTTAGCCAAACGCACCTCTGTATGATAAGGAATGTACAGCAAACCTCT GAATCTATCTCTGCAAATTTGCCGCTGATTTAAACCTTTAGCTCGGATAAAGTTTAGGGTTTGTGTTACAGTGCTCATTACATGGTCCATCTTCAGGACTTTGCCACATAGTGCTTCTGTG GCGTATAATGCAGTGATATGCAGTTAACTCAGGAGTATCTCCTGCACTTTTACTGCGACTTCCCACTAGTCCCTCTTTTCTACTACATAGATGGCGCTCATCAGTAGTAAG TGCAATACGTTTGTCCAGGGCGAGTTTCATGTGCGTTATACTTTGACATACATTTTCAAATAATGTCTTTTCCAGTCTGTTGTCCCGTGCATCAATTTAATGTCCATTATTTCTCTGTAAACA CGCAAATTTGGAGTCCACTCCATGGATGAAGATGGCCAGCTGTGCAGTATCAGTGTGCTGAGTACTTTCATCCACAGCAAGAGATGCAATAAAGTCTTTGCTTCTTTCACTCAACTG TGTTCTTAAATCAGTGGCCATCTCACAACCTCGATCAGCAATCATCTTTCTACTCAGGCTTACATTTGCCAGAATCTGCTTTTTGTCTGAGACATAAGACGCTCAAACACCTTGATCATGCA GCTCTTCAGAAATCTCCCTCTGTAAATGGCCTGGCTGATTTGGCGATCTCCTCTGCGCGGATAAACTTGATTTACAGCAGCTTCACTTTGTGATTTTGCACGGGTAAAAATGTCT GCTGAAGTGTCAAATTTCTCTTTAAGTCTTCTGCTCTTCTGATCTTCTGCTCGCATCAGGCTTTTCAGGTTATCCTTGATGTTTTGTCTCAGAGTGGCGCTTAGATTAATTTCTTTAAAT ACAGCCACATTTATCTCCACAAATGAGACACACAGGGTTTACCGGCAATGTGAGTAACATATACTCAGCCTCCCATCGACTTTTAAAGGCTCTGTTTTCAGAATCAACTTTTCTCTTCCG CATCGTAGGGGCTCAATAACTCGGGCGCAATAACTTGCAGCATATAAGTATAGGCTAAATGAACGTGAAGCATTTGGCAAGGCAGCTGAAGCGCTGCATTTAGGATCTGTAGTTTAT TGTCTTTATTGCCAGCGCTTCATATTGCCGGGCCATTAAATAACAATAATATATAAAATGATCTCGCAAGCTGGATAAAATCACACGCCGGGCCGGATATGCCCGCATGCCCTGAGTTT GACACATATGTTCTAGGG
>hAT-6_XT_SA

>hAT-6 XT SOd

CAGGGGTGTCAAACCTCAATTGCACAGGGGGGCCAAAACCTCAAACCTCGCGGGGTGAACAGTATAACCATTATTATTAACAGACTAAATATTATGTTTTTAACCATTAATATGAACCAAAATACAGGATATCATTTCCAAAATAAATACATTTCAACTTTAAATATTTTGCTCTTTCATAAAAAAATATCCTGTCAATACAATACATTTCAAATCTGTACATGCTGGAATATTAATAATATCTGAAATATAATAAAAAAATGAATTTAAAGCAAAAGTATAATCATAAACAAATCATAAACATTCCATTTTCTTGCTCTATTAGTCAGAGCCTGATACCTGGAGTCTTTTCTTTGCAACAAGTTCGTTATGTTTTGGGGTTAGGTTTCTGTGTTGTGAAGATTCTCAGGATCGATTGCGAGGTGTCATCAGTAGCGCGACTCCTGTGTGACGTTTTGTAAATTTTCATCACAGAGAAGCAGCTGCTCGCACAGATATGTGCTGCCAAACATGACAGAGATTGAGCGCCGATGTTGGCGGAGCTGCGGCATCGCTTCAGGAATGAAGCGAGTGAACCTGTGCTGGCCCCGCGAGTGTGCTACTTTGCCTTCAAGTGTCCGCTGATACATTGCAGTTTCTATCAGCTCCATCTGCATTTCTACAGGTGCGGTTTCCACATCGACTGCAAAATGGGTTGCGAAGCAGCTCGAAGTTACTTTTTCTGTGCCTCAAGTCACTGAAGCGCCGTGCGAACTCAGTGCGCGAGCGCGTGAGTTTTTCAGCAAAAGGTGGCATTGGGAAAACTGTGGCAGCTTTCTGGTTCCGTATTACTTGGCAACAGGGAAAGTGAGACAAGTGCATTGGTGCTGTCTCCCATAGCGCAGCTTCACTTGAATGCCTTCACTGCATCATGCATATCGGTTATTATGTGCTCCCGTCCCTGGAGTTGAAGGTTTAAAGCGCTAAGAGTGCAGCTTATGTTCAGCGGAGAACGCGCAACTCACATTTCCACTTTTCATCCCGCAGAACTGTGCAGTCTTTCCCTTACTGTCCATGAACGTGGCAGATTTTCTCTCGCAGCTCAAAGTGTCTTTGAGAAGCTTTCCCGGACTTAGCCACCGGACCTCCGATGATGATGGCATATGCCAAACTCGCTATCTATTTCCCGCAGAAAAAGACTGGAATTTGGCGGTGATTTAAACCGTGGGCTGTGATAAAGTTGACGGTTTTGTGTTACAGTGTTCATCACATGATCCATTTTAGGACTTTAGTACTCAGCGATTCTGGTGATGATGACGAGTATACATGTCACACTCACCGGCACAGTTTCTCTCCCGCATCTTTGAGCGCATCCTTCCCAACAGTCCATTTTTTCACCACACATAGCAGGTGCGCCATCTGTTGTAAGTCCAACAGAGTTTTTCCCAACGGCAGTTTCTGTCGTTACACTTTGAAATACATTTCCAAGATGTCTTCTCCTTTCTGTTGCCGTGCATCGATTAAATGTCCAGTATTCTCTGTTCACGCAAAATGGAATCCACACCACCGGATAAATATCGCCAGCTGTGCAGTGTGCAGTGCAGTCAGTAGTTTCATCCACGGCAAGGGAGTATGCAACAAAATCTTTGCTCTTTCATCAACTGTGTTTTCAAATCAGTCGCCATCTCACAAACCCGATTGACCAACAGTGTTTCTGCTGAGGCTTACATTTGCAAAACGCTCGCGCTTTATCTGGACAAGGAGCTGCGCACATTTTCATCATACAATCTTTACGAATTCCTCCCTCGGTAACCGCGCTCGTATTGGCGATCTCTTCGGCCACAATGAAACTTGCCTTACAGCAGCTTCACTTTGTGATTTTGCTTTGGTGAAAAACGCTCGCTGGATGTCAAATCTTCTTCAACTCCTCTACCTTTTGAGCTTCTGTCTCGGCTCAGGTTTTGAAATTTGTTCTCATGTTTCGTCTCGTAGTGCCGCTTAGAGTTATCTCCTTCATTACAGCGATATCTCCCGCAAGGAGACACACTGGGTACCTGCAATTTAGTAAGCATATACTCATTCCCAACCGGCTTTGAAAGCCTCGGTTTTGAAATCAATTTTTCTCTGGCCATTGTGGGCTAGCTTTGATTGATATTAGCGTTGTATACATCAACAGACCGCGAACTTGAACCGCGGCTGCGGCTGGTGCGCAATTGCACATGCATCATGGATTGTAGTGTGTGTTATGGGGCGTCATATCACAGGCCATTAATAACAGATATATAAACGATTTTCGCGGGCCGGATATAATTGTATGCGGGGCGCGGATGTGGCCCGCGGGCCTTGAGTTTGACACATGTGCTCTAG

>hAT-6_XT_MTU

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>hAT-6_XT_DMa

CAGGGGTGTCAAACCTCAATTGCACAGGGGGGCCAAAACCTCAAACCTCGCGGGGCCGAACAGTATAACCATTATTATTAACAGACTAAATATTATGTTTTTAACCATTAATATGAACCAAAATACAGGATATCATTTCCAAAATAAATACATTTCAACTTTAAATATTTTGCTCTTTCATAAAAAAATATCCTGTCAATACAATACATTTCAAATCTGTACATGCTGGAATATTAATAAATCTGAAATATAATAAAAAAATGAATTTAAAGCAAAAGTATAATCATAAACAAATCAAACTTCTTGCTCTATTAGTCAGAGCCTGATACTTGGAGTCTTTTCTTTGCAACAAGTTCGTTATGTTTTGGGGTTAGGTTTCTGTGTTGTGAAGATTCTCAGGATCGATTGCGAGGTGTTTCATCAGTGAGGCGACTCCTGTGTGACGTTTTGTAAATTTTCATCACAGAGAAGCTGCTCGCACAGATATGTGCTGCCAAACATGACAGAGATTGAGCGCCGATGTTGGCGGAGCTGCGGCATCGCTTCAGGAATGAAGCGAGTGAACCTGTGCTGGCCCCGCGAGTGTGCTACTTTGCCTTCAAGTGTCCGCTGATACATTGCAGTTTCTATCAGCTCCATCTGCATTTCTACAGGTGCGGTTTCCACATCGACTGCAAAATGGGTTGCGAAGCAGCTCGAAGTTACTTTTTCTGTGCCTCAAAAGTCACTGAAGCGCCGTGCGCAACTCAGTGCGCGAGCGCGTGAGTTTTTCAGCAAAAGGTGGCATTTGGGAAAACTGTGGCAGCTTTCTGGTTCCGTTACTTGGCAACAGGGAAAGTGAGACAAGTGTCAATGGTGCAITTTGTGTCCTCATAGCGCAGCTTCACTTGAATGCCTTCACTGCATCATGCATATCGGTTATTATGTGCTCCCGTCCCTGGAAGTTTAAAGCGCTAAGATGCGACGTTATGTTCAGCGCAGGAACGCCAACTCACATTTCCACTTTTCATCCCGCAGAACTGTGCAGTCTTTCCCTTACTGTCCATGAACGTGGCAGATTTCTCTCGCAGCTCAAAGTGTCTTTGAGAAGCTTTTCCCGGACTTAGCCACCGGACCTCCGATGATGATATGGCATATGCCAAACTCGCTATCTATTTCCCGCAGAAAAAGACTGGAATTTGGCGGTGATTTAAACCGTGGGCTGTGATAAAGTTGACGGTTTTGTGTTACAGTGTTCATCACATGATGATTTTAGGACTTTAGCACTCAGCGATTCTGGTGATGATGACGAGTATACATGTCGTAACCTCACCGGCACAGTTTCTCTCCCGCATCTTTGAGCGCATCCTTCCCAACGATCCATTTTTTCACCACACATAGCAGGTGCGGCCATCTGTTGTAAGTCCAACGAGTTTTTCCCAACGGCAGTTTCTGTCGTTACACTTTGAAATACATTTCCAAGATGTCTTCTCCTTTGCTTGCCTGTCAGTCGATTAATGTCCAGTATTTCTCTGTTCAGCAACAAATGGAATTCACACCACCGGATAAATATCGCCAGCTGTGCAGTGTGCAGTGCAGTCAGTAGTTTCATCCACGGCAAGGGAGTATGCAACAAAATCTTTGCTCTTTCAAGCAACTGTGTTTTCAAATCAGTCGCCATCTCACAAACCCGATTGACCAACAGTGTTTCTGCTGAGGCTTACATTTGCAAAACGCTCGCGCTTTATCTGGACAAGGAGCTGCGCACATTTTCATCATACAATCTTTACGAATTCCTCCCTCGGTAACCGCGCTCGTATTGGCGATCTCTTCGGCCACAATGAAACTTGCCTTACAGCAGCTTCACTTTGTGATTTTGCTTTGGTGAAAAACGCTCGCTGGATGTCAAATCTTCTTCAACTCCTCTACCTTTTGAGCTTTCAGTCTCGGCTCAGGTTTTGAAATTTGTTCTCATGTTTCGTCTCGTAGTGCCGCTTAGAGTTATCTCCTTCATTACAGCGATATCTCCCGCAAGGAGACACACTGGTTTACCTGCAATTTCACTAAGCATATACTCATTCCCAACCGGCTTTGAAAGCCTCGGTTTTGAAATCAATTTTTCTCTGGCCATTGTGGGCTAGCTTTGATTGATATTAGCGTTGTATACATCAACAGACCGCGAACTTGAACCGCGGCTGCGGTTGGCGGCAATTGCACATGCATCATGGATTGTAGTGTGTGTTATGGGGCGTCATATCACAGGCCATTAATAACAGATATATAAACGATTTTCGCGGGCCGGATATAATTGTATGCGGGGCGCGGATGTGGCCCGCGGGCCTTGAGTTTGACACATGTG

>hAT-6_XT_MTT

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>hAT-6_XT_MTP

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>hAT-6_XT_CPB

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>hAT-6_XT_SOD

MAKRKIDSENRFQSRWENEYMFTEIAGNPVCLLCSNVAVMKEYNLRRHYETKHENKFKNLSAGQKLQKVEELKKNLTSQQTFFTKAKSQSEAAVKASFIVAEIIAKSGRPFTEGEFVKNCMKVCDVLCPDKTRAFANVLSRNTVANRVCEMATDLKTQLIERAKDFVAYSLAVDETTDATDTAQLAIFIRGVDSNLCVTQEILDIKSMHGTTKGEDIFGNVFQSVTDMKLPWEKLVGLTTDGA PAMCGEKNGLVGRMRSKMREENCAAGELTVYHCIIHQESLSAKVLKMDHVMNTVTQTVNFIHAGHLNHRQFQSFRLREIDSEFGDMPYHTEVRWLSRGKVLKRHFELREEICQFMDSGKGDCTVLRDEKWKCELFLADITSHLSALNLQLQGREHIITDMHDAVKAFQVKLRLWETHMHQCNLSHFPCQVIRNQESATVPFNATFAEKLALRTEFARRFSDFEAQKSNFELLRNPFAVDVETAPVEMQMELIELQCNGTLKAKYDTAGPAQFTRFIPEAMPQLRQHAARILSMFGSTYLCEQLFSVMKINKTSHRSRLTDEHLQSLRIFTTQNLTPNINELVAKKRLQVSGSD

>hAT-6_XT_MTU

MAKRKIDSENRGFQSRWENEYMFTEIAGKPVCLLCGSNIAVMKEYNLRRHYETKHENKFKNLSAGLKLQKVEELKKNLTSQQTFFTKAKSQSEAAVKASFIVAEIEAKSGRPFTEGEFVKNCM
MKVCDVLCPDKTRAFANVSLSRNTVANRVCEMATDLKTQLLERAKDFVAYSLAVDETTDATDTAQLAIFIRGVDNSL CVTEEILDIKSMHGTTKGEDIFGNVFQSVTDMKLPWEKLVGLTTDGA
PAMCGEKNGLVGRMRSKMREENCAGELTVYHCIIHQESLSAKVLKMDHVMNTVTQTVNFIRAHGLNHRQFQSFLEIDSEFGDMPYHTEVRWLSRGKVLKRHFELREEICQFMDSKGKDCT
VLRDEKWKCELAFADITSHLSALNLQLQGREHIITDMHDAVKAFQVKLRLWETQMHQCNSL SHFPCCQVIRNQESATVFPNATFAEKL SALRTEFARRFSDFEAQKSNFELLRNPF AVDVETA
PVEMQMELIELQCNGTLKAKYDTAGPAQFTRFIPEAMPQLRQHAARILSMFGSTYLCEQLFSVMKINKTSHRSRLTDEHLQSILRIFFTQNLTPNINELVAKKRLQVSGSD

>hAT-6_XT_DMa

MAKRKIDSENRGFQSRWENEYMFTEIAGKPVCLLCGSNIAVMKEYNLRRHYETKHENKFKNLSAGLKLQKVEELKKNLTSQQTFFTKAKSQSEAAVKASFIVAEIEAKSGRPFTEGEFVKNCM
MKVCDVLCPDKTRAFANVSLSRNTVANRVCEMATDLKTQLLERAKDFVAYSLAVDETTDATDTAQLAIFIRGVDNSL CVTEEILDIKSMHGTTKGEDIFGNVFQSVTDMKLPWEKLVGLTTDGA
PAMCGEKNGLVGRMRSKMREENCAGELTVYHCIIHQESLSAKVLKMDHVMNTVTQTVNFIRAHGLNHRQFQSFLEIDSEFGDMPYHTEVRWLSRGKVLKRHFELREEICQFMDSKGKDCT
VLRDEKWKCELAFADITSHLSALNLQLQGREHIITDMHDAVKAFQVKLRLWETQMHQCNSL SHFPCCQVIRNQESATVFPNATFAEKL SALRTEFARRFSDFEAQKSNFELLRNPF AVDVETA
PVEMQMELIELQCNGTLKAKYDTAGPAQFTRFIPEAMPQLRQHAARILSMFGSTYLCEQLFSVMKINKTSHRSRLTDEHLQSILRIFFTQNLTPNINELVAKKRLQVSGSD

>hAT-6_XT_TSE

MAKRKIDSENRGFQSRWENEYMFTEIAGKPVCLLCGSNIAVMKEYNLRRHYETKHENKFKNLSAGQKLQKVEELKKNLTSQQTFFTKAKSQSEAAVKASFIVAEIEAKSGRPFTEGEFVKNCM
MKVCDVLCPDKTRAFANVSLSRNTVANRVCEMATDLKTQLIERAKDFVAYSLAVDETTDATDTAQLAIFIRGVDNSL CVTEEILDIKSMHGTTKGEDIFGNVFQSVTDMKLPWEKLVGLTTDGA
PAMCGEKNGLVGRMRSKMREENCAGELTVYHCIIHQESLSAKVLKMDHVMNTVTQTVNFIRAHGLNHRQFQSFLEIDSEFGDMPYHTEVRWLSRGKVLKRHFELREEICQFMDSKGKDCT
VLRDEKWKCELAFADITSHLSALNLQLQGREHIITDMHDAVKAFQVKLRLWETQMHQCNSL SHFPCCQVIRNQESATVFPNATFAEKL SALRTEFARRFSDFEAQKSNFELLRNPF AVDVETA
PVEMQMELIELQCNGTLKAKYDTAGPAQFTRFIPEAMPQLRQHAARILSMFGSTYLCEQLFSVMKINKTSHRSRLTDEHLQSILRIFFTQNLTPNINELVAKKRLQVSGSD

>hAT-6_XT

MPKRKVDSENRAFKNRWEAEYMFDTIAGKPLCLICGANVAVIKEFNLRRHYETKHQDNLKDLNAEQKIQKVEELKKNLTLQQTIFTRAKSESEAAVKASFIVAEIEAKSARPTKGEFLKSCMIK
VFDVLCPDKKQMLANIQMELIELQCNGTLKAKYDTAGPAQFIHSIPAEMPQLRLHAARTLCMFGSTYLCEKLLSVMKTNKTAHRRHLTDEHLQSILRISTQNLTPNINLVCQASSDKMT

>hAT-6_XT_ESp

MAKRKMYSENRIQSRWENEYMFTEIAGKLVCLLCGSNVAVMKEYNLRRHYETKHEDKLNLSAGQKLQKVEELKKNLTSQQTFFTKAKSQSEAAVKASFIVAEIEAKSGRPFTEGEFVKNC
MMKVCDDVCPDKTRAFANVSLSRNTVANRVCEMATDLKTQLIERAKDFVAYSLAVDETTDSTDTAQLAIFIRGVDNSL CVTEEILDIKSMHGTTKGEDIFGNVFQSVTDMRLPWEKLVGLTTDG
APAMCGEKNLWGGKDALKDAGGELCRAHGLNHRQFQSFLEIDCEFGDMPYHTEVRWLSRGKVLKRHFELREEICQFMDSKGKDCTVLRDEKWKCELAFADITSHLSALNLQLQGREHIIT
DMHDAVKAFQVKLRLWETQMHQCNSL SHFPCCQVILNQESD TVFPNATFAEKL SALRTEFARRFSDFEAQKSNFELLRNPF AVDVETA PVEMQMELIELQCNGTLKAKYDTAGPAQFTRFLPE
AMPQLRQHAARILSMFGSTYSGAQKFTYTCLS

>hAT-6_XT_SFo

MLQVIAKLALTMPKRKVDSENRAFKNRWEAEYMFDTIAGKPVCLICGANVAVIKEFDLRRHYETKHQDNLKDLNAEQKIQAEEILKKNLTLQQMFFTRAKSQSEAAVKASFIVAEIEAKSARPF
TEGEFLKSCMIKVFDVLCPDKKQMLANVSLSRNTIADRVREMATDLRTQLSERSKDFIAYSLAVDESTDMTDTAQLAIFIRGVDNSL RVTEEIMDIKSMHGTTTGKDIFENVCQSITDMKLPWDK
LIALTTDGAPSMCSEKSGLVGRMRVKMQEENCTGELTAYHCIIHQEALCGKVLKMDNVMSTLTQTVNFIRAKGLNHRQFQSFMRIDSEFADIPYHTEVRWLSRGKVLDRVFELSNEICQFIDS
KGKDS TNFRDEKWKCELAFADITAHNLNALNLQLQGRDRMITDMYDAVKAFQVKLLWETQMRQC NLPHFPCCQVMLNQVGT TVFPNTHFADKLSAPRTEFARRFGDFEEQKNFEFLRNP
FAVDVETAPVQIQMELIELQCNGTLKAKYDTAGPAQFIHSIPAEMPQLRLHAARTLCMFGSTYLCEKLSVMKTNKTAHGSRLTDEHLQSILRISTTQNLTPNINELVAKKRCQASSDKMT

>hAT-6_XT_TAm

MPKRKVDSENRAFKSRWEAEYMFDTIAGKPVCLICGDNVAVIKEFNLRRHCETKHQDNLKDLNAEQKIQAEDLKKNLTLQQTFFTRAKSQSEAAVKSSFIAAEEIAKSARPFTEGEFLKSCMI
KVFDVLCPDKKQILANVSLSRKMIADRVCEMATDLRTQLSERSKDFIAYSLAVDESTDMTDTAQLAIFIRGVDNSL RVTEEIMDIKLMHGTTTGKDIFENVCQSITDMKLPWDKRIALT TDGAPSM
CSEKRGVLGRMRVKMQENCTEVRWLSWGVLSRVFELSNKICQFMDSKGKDSTNFRDEKWKCKLAFADITAHNLNALNLQLQGRDRMITDMYDAVKAFQVKLLWESQMHQCNM SHSPC
CQVMLNQAGT TVFPNMH FADKLSALRTEFARRFGDFEEQKNLELLRNPF AVDVETA PVQIQMKLIELQCNGTLKAKYDTAGPPQFIHAIPAEMPQLRLHVARTLCMFGSTYLCEKLSVMKNT
NKT AHRSHLTDEHLQSILRISTTQKLT PNIKELVAKKRCQASSFDKTT

>hAT-6_XT_SAc

MPKRKVDSENRAFKNRWEVEYMFDTIAGKPVCLICGANVAVLKEFNLRHYETKHLNLDNLKDLNAEQKIQKVEELKKLTFQQTFFTRAKSQSEAAVKASFIVAEIEAKAGRPFTEGEFLKSCMV
KVCDIICPDKKQMLANVSLSRNTVADRVCEMATDLRTQLSKRSKDFIAYSLAMDESTDMTDTAELAIFIRGVDSDLRVTEEILDIKPMHGTTTGKDIFENVCQSVTDMKLPWDKLI GLTTDGAPA
MCGEKSGLVGRMRMREKMQEENCTGELTTYHCIIHQEALCGKVLKMDHVMSTVTQTVNFIRSRGLNHRQFQSFMRITIDSEFADIPYHTEVRWLSRGKVLNRVFELSNEICQFMDSKGKDSTVLR
DEKWKCELAFADITAHNLNALNLQLQGRDRMITDMYDAVKAFQVKLILWETQMLQCNSL SHFPCCQVMLNQVGT TVFPNTHFAVKLSALRTEFARRFGDFEEQKNFELFRNPFAVDVESAPV
QIQMELIELQCNGTLKSKYDTAGPTEFIHSIPAAMSQRLRLHVARTLCMFGSTYLCEKLSVMKTNKTAHRSRLTDEHLQSILRVSTTRDLTPNINQLVAKKRCQSSGSDKMA

>hAT-6_XT_SMa

MAKRKVDSENRAFQNRWEAEYMFDTIAGKPVCLVCGANVAVIKEFNIRRH YETKHQELQNLNAEEKIQRVKELKKNLRFQQTFFTRAKSQSEAAVKASFIVAEIEAKSARPFTEGEFLKSCMM
KVCDVLCPENKQMFANVSLSRNTVADRICEMATDLKTQLSERSKDFIAYSLAVDESTDMTDTAQLAIFIREVDSSLCVTEEILDIKSMHGTTTGKDIFENVCQSITDMKLPWDKLI GLTTDGAPA
MCSEKVLVGRMRRAKMQEENCTGELTAYHCIIHQEMLCCKVLKMEHVMNTVTQTVNFIRAKGLNHWQFQSFMRIDSEFADIPYHTEVRWLSRGKVLNRVFELSKEICQFMDSKGKD TTVL
RDEKWKCELAFADVTAHLNVNLNLQLQGRDRITDMYD TVKAFVKLLWETQMRQSNLPHFPCCQVMFNQVGATVFPNTHFADKLSALRTEFARRFGDFFRNPFAVDVETAPVQIQMELIELQ
CNGTLKAKYDTAGPAQFIRSIPETMPQLRLHAAQTLCMFGSTYLCEKLSVMKMKNKTAHRSRLTDGHLQSILRISTAQELTPNLNDLTAKKRCQTCSDKMA

Table S3	
Geographical ranges of species with horizontally transferred hAT-6_XT	
Species	Geographic range
<i>T. s. elegans</i>	North America
<i>M. t. terrapin</i>	North America
<i>E. spectabile</i>	North America
<i>T. amazonica</i>	Amazon
<i>S. maximus</i>	Northeast Atlantic, Mediterranean Sea
<i>S. acus</i>	British Isles, Mediterranean Sea
<i>S. foramsus</i>	Southeast Asia
<i>X. tropicalis</i>	West Africa
<i>M. t. pilenta</i>	North America
<i>C. p. bellii</i>	North America
<i>D. mawii</i>	Central America
<i>S. odoratus</i>	North America
<i>M. tuberculta</i>	South America