

Gene Cluster ID	Atp6v1B
Drosophila melanogaster gene	Vha55 (CG17369)
FlyBase ID	FBgn0005671
Predicted function	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B

Atp6v1B CLEAR element conservation:

	<u>5'/5'UTR</u>	<u>intron</u>	<u>intron</u>	<u>intron</u>
Dmel\	CGGGTCACGTGACGGC	GCCGTCACATGACCGT	ACAGTCAGCTGACATA	ACTTTCATGTGAGCAT
Mdom\	TTAATCACATGACAGC	AATGTCATGTGACTTG	CGAGTCAGCTGACCTT	TCTATCATGTGAGACA
Ccap\	TTGGTCACATGACCGC	GCCGTCATGTGACATT	GCAGTCAGCTGACGTT	
Gmor\	TCAATCACATGACAGC	TCAGTCATGTGATTAA		
Llon\	TGTGTCACATGACATT	TTGGTCATATGACACC		
Ppap\	CCAGTCACATGACATT	TTGGTCATATGACCTT		
	<u>5'/5'UTR</u>	<u>intron</u>	<u>intron</u>	
Agam\	TTCAATCACATGACAGA	GATGTCATGTGACGGG	GGTGTTTTGATGTCACATGACTGT	
Agan\	TTCAATCACATGACAGA	GATGTCATGTGACGAG	GGTGTTTTGATGTCACATGACTGT	
Aara\	TTCAATCACATGACAGA	GATGTCATGTGACGAG	GGTGTTTTGATGTCACATGACTGT	
Achr\	TTCAATCACATGACAGA	GATGTCATGTGACGAG	AGTGTTTTGATGTCACATGACTGT	
Aepi\	TTCAATCACATGACAGA	GGAGTCATGTGACGTG	AGTGTTTTGATGTCACATGACTGT	
Amin\	TTCAATCACATGACAGA	TGTGTCATGTGACGGT	ACTGTTTTGATGTCACATGACTGT	
Afun\	TTCAATCACATGACAGA	TGTGTCATGTGACGGT	ACTGTTTTGATGTCACATGACTGT	
Aste\	TTCAATCACATGACAGA	TGTGTCATGTGATATG	ACTGTTTTGATGTCACATGACTGT	
Anil\	TTCAATCACATGACAGT	GTCGTCATGTGACGAT	CCTGTTTTGATGTCACATGACTGT	
Adir\	-----	TACGTCATGTGACGGT	ACTGTTTTGATGTCACATGACTGT	
Aalb\	-----	-----	TCGTTTTGATGTCACATGACTGT	
Adar\	-----	-----	TCGTTTTGATGTCACATGACTGT	
Aaeg\	TGTTTCACATGACAAC	AGTGTTCATGTGATAAC	TCGTTTTGATGTCACATGACTGT	
Cqui\	GCTGTTCACATGAGAG	TGTGTCATGTGATAAC	TCGTTTTGATGTCACATGACACC	
Mdes\	AAAGTCACATGACAGC	CATGTCATGTGACCTA	ATAATCATATGAAAA	
	<u>5'/5'UTR</u>	<u>intron</u>	<u>intron</u>	<u>intron</u>
Bmor\	TGGGTCACGTGACAGCACGTGAAG	TCAGTCACATGAAATT		
Msex\	TGGGTCACGTGACGGCACGTGAAG	TATATCACATGATGAA		
Dple\	TAGATCACGTGACAGCACGTGAAG	AATATCACATGATCAA		
Hmel\	TAGGTCACGTGACAGCACGTGAAG	AGGATCACATGACTTC		
Pxyl\	CGGGTCACGTGACAGCACGTGAAG	GAAATCATATGACCTA		
Tcas\	GCCGTCACGTGACGACACGTGAAT	CGGGTCATATGACCAA	GTGTTCATGTGACCGA	
Dpon\	AGCAATCACATGAGTCAATGAGA	-----	CATGTTCATGTGACATC	
Amel\	TAAGCCACGTGATCGCACGTGCCA	ATAGTCAGCTGATTCT	TCCAATCATGTGACTGG	
Aflo\	TAAAGCCACGTGATGCGACGTGCCA	GTAGTCAGCTGATTTT	TCTATTCATGTGACTAG	
Bter\	TAAGCCACGTGATCGCACGTGCCA	GTAGTCAGCTGATTCT	TGTAATCATGTGACTAT	
Bimp\	TAAGCCACGTGATCGCACGTGCCA	GTAGTCAGCTGATTCT	TGTAATCATGTGACTAT	
Mrot\	CAAGCCACGTGATCGCACGTGCCA	CTAATCAGCTGATTCA	TCTGTTCATGTGACTGT	
Aech\	CGGGCCACGTGATTGACGTGCCT	GGAGTCAGCTGATCTT	AGCGTCATGTGACCAT	
Acep\	CGAGCCACGTGATTGACGTGCCT	GGAGTCAGCTGATCTC	AGCAATCATGTGATCAT	
Pbar\	CGAGCCACGTGATTGACGTGCCT	GGGGTCAGCTGATTCC	AGCAATCATGTGACTGC	
Sinv\	CCGGCCACGTGATTGACGTGCCT	CGGGTCAGCTGATCTC	AGCGTCATGTGACTGC	
Lhum\	CGAGCCACGTGATTGACGTGCCT	TGGGTCAGCTGATCCC	AGCGTCATGTGACTGC	AATATTCACATGATTTTA
Hsal\	CGAGCCACGTGATTGACGTGCCT	TGGGTCAGCTGATCCC	GGCGTCATGTGACTAC	
Cflo\	CAAGCCACGTGATTGACGTGCCT	TGCATCAGCTGATCCC	CTTGTTCATGTGACTGC	
Ngir\	CGAGCCACGTGATCCACGTGCTT	CTGGTCAGCTGATCGG	TGTGTCATGTGACTGC	GGAGTCATGTGACACG
Nlon\	CGAGCCACGTGATCCACGTGCTT	CTGGTCAGCTGATCGG	TGTGTCATGTGACTGC	GGAGTCATGTGACACG
Nvit\	CGAGCCACGTGATCCACGTGCTT	CTGGTCAGCTGATCGG	TGTGTCATGTGACTGC	GGAGTCATGTGACACG
Phum\	CTTGTCATGTGATTTCACGTGATC			
Lful\	ctggTCACGTGATTCACGTGAtt			
Dpul\	tctgacagTCATATGAtcgagaga			
Isca\		tggtagtagcggTCATGTGActcaggatgtca		

Atp6v1B gene structure comparison:

Legend: UTR region. CDS region INTRON

Order	Species	Atp6v1B orthologs	5'exon	intron	exon			intron	exon3'	Extended CLEAR region	Position	bps from TSS				
Diptera (Drosophilidae)	<i>Drosophila_melanogaster</i>	Dmel\Vha55	308	73	1221	1262			61	138	1005	acgcgtgacgggTCATGTGAcggcacgtgacg aaattttcccgTCACATGAcgttcgtcgtc ccagttggacagTCAGCTGAcataattagcc agattccgactTCATGTGAacattgcgcgac	5'UTR intron1 intron1 intron1	45 701 1052 1141		
Diptera (Muscidae)	<i>Musca_domestica</i>	Mdom\Atp6v1B	ND	79	1522	1262 (506+756)			644	138		ggatttcgttaaTCACATGAcagcacgtgaga ttttactgaagTCATGTGAactgtttttgct ttttgtcacagTCAGCTGActttattgcttt tggttttaictaTCATGTGAacattaaacat	5' intron1 intron1 intron1	>-331 >561 >1320 >1553		
Diptera (Tephritidae)	<i>Ceratitis_capitata</i>	Ccap\Atp6v1B	ND	79	926	506	71	756	102	138	ND	ctctgcctttggTCACATGAcggcacgtgaca catttagtcgcgTCATGTGAcattgggtgtgc ttcaatttcgagTCAGCTGAcgttcgttacgt	5' intron1 intron1	>-315 >425 >805		
Diptera (Glossinidae)	<i>Glossina_morsitans</i>	Gmor\Atp6v1B	265	67	599	506 (119+130+132+125)	64	756 (231+103+155+138+129)	58	138	ND	acattttacaaTCACATGAcagcacgtgagt tatcttttcagTCATGTGAttaacttcagag	5' intron1	53 656		
Diptera (Psychodidae)	<i>Lutzomyia_longipalpis</i>	Llon\Atp6v1B	ND	73	85	995		1586	405		ND	caacctgaggggTCACATGAaactcgttttaa acgattttttgTCACATGAacattttgtctca cttccactttggTCATATGAacctccataic	5' 5' 5'	>-556 >-511 >-125		
	<i>Phlebotomus_papatasi</i>	Ppap\Atp6v1B	145+347+27	73	599	995 (119+130+132+125+231+103+155)		ND	405 (138+129+138)		325	atccgtcccagTCACATGAacatttctctag cttccactttggTCATATGAacccataicic	5' intron1	>-22 385		
Diptera (Culicidae)	<i>Anopheles_gambiae</i>	Agam\Atp6v1B AGAP002884	91+96+63	97	1051	326	67	1074			361	ttcgtttctcaTCACATGAcagaattataa gcccgcaagatgTCATGTGAcggcggtgaag ggtgttttgatTCACATGActgtcaaaacac gtgtgcgcgtcTCACATGAtagattttctt	5' intron2 intron2 intron2	-20 467 822 1182		
	<i>Anopheles_arabiensis</i>	Aara\Atp6v1B	ND	97	1054	326	67	1074			ND	ttcgtttctcaTCACATGAcagaattataa gcccgctagatgTCATGTGAcagcggtgaag ggtgttttgatTCACATGActgtcaaaacac gtgtgcgcgtcTCACATGAtagattttctt	5' intron2? intron2? intron2?	>-271 >217 >476 >935		
	<i>Anopheles_quadriannulatus</i>	Aqan\Atp6v1B	ND	97	1061	326	67	1074			ND	ttcgtttctcaTCACATGAcagaattataa gcccgcaagatgTCATGTGAcagcggtgaag ggtgttttgatTCACATGActgtcaaaacac gtgtgcgcgtcTCACATGAtagattttctt	5' intron2? intron2? intron2?	>-264 >218 >572 >944		
	<i>Anopheles_christyi</i>	Achr\Atp6v1B	ND	97	998	326	62	1074			ND	ttcgtttctcaTCACATGAcagaatccataa gtctgtcgatgTCATGTGAcagcggtgaag agtgttttgatTCACATGActgtcaaaacac taagccctcgtTCACATGAatcctcgtcgc	5' intron2? intron2? 3'UTR?	>-270 >216 >569 >2567		
	<i>Anopheles_epiroticus</i>	Aepi\Atp6v1B	ND	97	977	326	70	1074			ND	tacctatctcaTCACATGAcagaatccgtaa cgtgacgggagTCATGTGAcgtgcgtgaag agtgttttgatTCACATGActgtcaaaacac	5' intron2? intron2?	>-244 >221 >582		
	<i>Anopheles_minimus</i>	Amin\Atp6v1B	ND	97	995	326	60	1074			ND	ttcgtttctcaTCACATGAcagaatccattg ttgtgagatgTCATGTGAcgtggaagtgat actgttttgatTCACATGActgtcaaaacac	5' intron2? intron2?	>-245 >218 >572		
	<i>Anopheles_funestus</i>	Afun\Atp6v1B	ND	97	1007	326	69	1074			ND	ttcgtttctcaTCACATGAcagaatccataa gtgtgagatgTCATGTGAcgtggaagtgat actgttttgatTCACATGActgtcaaaacac	5' intron2? intron2?	>-238 >217 >582		
	<i>Anopheles_stephensi</i>	Aste\Atp6v1B	ND	97	972	326	88	1074			ND	ttcgtttctcaTCACATGAcagaattgctaa ccgtgagatgTCATGTGAatggtatagt actgttttgatTCACATGActgtcaaaacac	5' intron2? intron2?	>-250 >219 >567		
	<i>Anopheles_dirus</i>	Adir\Atp6v1B	ND	97	1016	326	67	1074			ND	gcccggtgtacgTCATGTGAcgtgtgttgaa actgttttgatTCACATGActgtcaaaacac	intron1	>213 >556		
	<i>Anopheles_nili</i>	Anil\Atp6v1B	ND	97	940	326	83	1074			ND	cgtttctctcaTCACATGAcagttggcaaaa aagatgtctcgTCATGTGAcgatgtgaagt cctgttttgatTCACATGActgtcaaaacac	5' intron2? intron2?	>-264 >192 >527		
	<i>Anopheles_albimanus</i>	Aalb\Atp6v1B	ND	97	906	326	91	1074			ND	ttcgttttgatTCACATGActgtttgtgtgc	intron2?	>496		
	<i>Anopheles_darlingi</i>	Adar\Atp6v1B	ND	97	863	326	79	1074			ND	ttcgttttgatTCACATGActgtttgtgtgc	intron2?	>473		
	<i>Aedes_aegypti</i>	Aaeg\Atp6v1B AAEL005798	ND	91	4094	326	63	1074			ND	ttcactgtttgtTCACATGAcaactaatgtt agctcagaagtTCATGTGAaacttccaaa aattgtaaaaTCATATGAaggaataagcctt tctgttttgatTCACATGActgtcaaaacac	5' intron1 intron1 intron1	>-619 >198 >292 >572		
	<i>Culex_pipiens_qui.</i>	Cqui\Atp6v1B CPI003418	ND	79	ND	326	65	1074			ND	actagcgagctgTCACATGAagggtgttgaa ttttcgagatgTCATGTGAaactcttattt tctgttttgatTCACATGAacacactgtcaa	5' intron1 intron1	>-322 >179 >531		
Diptera (Cecidomyiidae)	<i>Mayetiola_destructor</i>	Mdes\Atp6v1B	ND	79	737	1133 (119+130+132+125+231+103+155+138)			92	129	116	138	ND	taataccaaaagTCACATGAcagcacgtgagc aacaatgacatgTCATGTGAacctaataatg tgacttcaataaTCATATGAaaaaataagcaat	5' intron1 intron1	>-177 >608 >644

Lepidoptera	<i>Bombyx_mori</i>	Bmor\Atp6v1B	ND	85	1803	119	569	130	628	132	576	125	490	231	1021	103	361	155	602	138	335	129	684	138	ND	ccttgatgggTCACGTGAacgacgtgaag actgtgatcagTCACATGAatttgtagtc	5'UTR? intron1	>-110 >-338			
	<i>Manduca sexta</i>	Msex\Atp6v1B	ND	85	ND	119	ND	130	108	132	152	125	198	231	325	103	306	155	259	138	922?	129	295	138	ND	ccttgatgggTCACGTGAacgacgtgaag tatgtgttataTCACATGAatgaatttatct	5'UTR? intron1	>-111 >-923			
	<i>Danaus_plexippus</i>	Dple\Atp6v1B	ND	85	1033	119	229	130	788	132	648	125	498	231	161	103	351	155	519	138	303	129	162	138	ND	tcttgatagaTCACGTGAacgacgtgaag atttaacaataTCACATGAatcaattattta	5'UTR? intron1	>-106 >-590			
	<i>Heliconius_melpomene</i>	Hmel\Atp6v1B	ND	85	960	119	1102	130	371	132	319	125	386	231 (86+145)	278	103	597	155	371	138	381	129	379	138	ND	tcttgatagTCACGTGAacgacgtgaag ttctattagaTCACATGAacttctcttctac	5'UTR? intron1	>-107 >-665			
	<i>Plutella_xylostella</i>	Pxy\Atp6v1B	ND	94	1790	119	1433	130	658	132	529	125	287	86	359	145	328	103	3466	155	1259	138	562	129	475	138	ND	ccttgacgggTCACGTGAacgacgtgaag atgctctgaatTCATATGActtagttatgc	5'UTR? intron1	>-102 >-1211	
Strepsiptera	<i>Mengenilla_moldrzyki</i>	Mmol\Atp6v1B	ND	73	69	381 (119+130+132)					1152	752 (125+231+103+155+138)										2681	267 (129+138)			ND	ND				
Coleoptera	<i>Tribolium_castaneum</i>	Tcas\Atp6v1B LOC656208	23	91	300	288				51	506 (304+202)					2342	339 (196+143)					49	267			572	cataattcgccgTCACGTGAacgacgtgaat acacaaacgggTCATATGAacaaaatttctc clgttgggtgTCATGTGAacgaatctcatg			5'UTR? intron1 intron1	>-45 207 351
	<i>Dendroctonus_ponderosae</i>	Dpon\Atp6v1B	138	79	219	288				311	304			61	202		55	196		59	143	355	267			257	attgatttagcaTCACATGAataacgtcattg gtcagttgcgtgTCACATGAacaaaactgga ggcaatccatgTCATGTGAactatccctatga			5' 5'UTR intron1	-13 6 371
Hymenoptera	<i>Apis_mellifera</i>	Amel\Atp6v1B GB19171	61	88	565	467					109	666										81	267			468	acttagtataagCCACGTGAatcgacgtgccga gattfaccatagTCAGCTGAatcgaaattgat tagagacatccaTCATGTGAactgtagcagca			5' intron1 intron1	-267 266 421
	<i>Apis_florea</i>	Aflo\Atp6v1B	ND	82	590	467					125	666										86	267			ND	acttagtataaaCCACGTGAatcgacgtgccga gattfaccatagTCAGCTGAatcgaaattgat tagagacatctaTCATGTGAactgtagcagca			5' intron1 intron1	>-328 >199 >349
	<i>Bombus_terrestris</i>	Bter\Atp6v1B	ND	88	449	467					97	666										74	267			ND	acttagtataagCCACGTGAatcgacgtgccga attggccagtagTCAGCTGAatcgaaattgat tcgagatattgaTCATGTGAactatacatcaa			5' intron1 intron1	>-320 >193 >343
	<i>Bombus_impatiens</i>	Bimp\Atp6v1B	ND	88	449	467					103	666										74	267			ND	acttagtataagCCACGTGAatcgacgtgccga attggccagtagTCAGCTGAatcgaaattgat tcgagatattgaTCATGTGAactatacatgcaa			5' intron1 intron1	>-320 >193 >343
	<i>Megachile_rotundata</i>	Mrot\Atp6v1B	ND	88	553	467					64	666										75	267			ND	tcttagtacaagCCACGTGAatcgacgtgccga attgcaactaaTCAGCTGAatcaaaaggtag atgataaatctgTCATGTGAactgtagacagag			5' intron1 intron1	>-320 >191 >253
	<i>Acromyrmex_echinaior</i>	Aech\Atp6v1B	ND	88	865	467					180	666										152	267			ND	acttagtccgggCCACGTGAatcgacgtgacct cccaactggagTCAGCTGAatctacttgaaa gagctgccagcgTCATGTGAaccatgagtgaca			5' intron1 intron1	>-518 >187 >376
	<i>Atta_cephalotes</i>	Acep\Atp6v1B	ND	88	831	467					202	666										154	267			ND	acttagtccgagCCACGTGAatcgacgtgacct ccgaactggagTCAGCTGAatcacttgaaaa ctcgagccagcaTCATGTGAatcagtagcaact			5' intron1 intron1	>-390 >184 >365
	<i>Solenopsis_invicta</i>	Sinv\Atp6v1B	ND	88	1438	467					133	666										149	267			ND	cacgtgttccggCCACGTGAatcgacgtgacct gattccctcgggTCAGCTGAatcactcagtaga ctgctcgagcgTCATGTGAactggagcagaca			5' intron1 intron1	>-353 >192 >371
	<i>Camponotus_floridanus</i>	Cflo\Atp6v1B	ND	88	978	467					130	666										135	267			ND	acgtagtccaagCCACGTGAatcgacgtgacct ccccgaactgaTCAGCTGAatccccgaatttc agaccgagcttgTCATGTGAactcgagcagaca			5' intron1 intron1	>-363 >82 >338
	<i>Harpegnathos_saltator</i>	Hsal\Atp6v1B	ND	88	925	467					314	666										244	267			ND	acctagtccgagCCACGTGAatcgacgtgacct tctcaattgggTCAGCTGAatccccgaatttc gagctcgccgggTCATGTGAactaggaacgatt			5' intron1 intron1	>-401 >182 >343
	<i>Pogonomyrmex_barbatus</i>	Pbar\Atp6v1B	ND	88	946	467					108	666										146	267			ND	acctagtccgagCCACGTGAatcgacgtgacct cgacgcagggggTCAGCTGAatccaattgaaa gagccgcagcaTCATGTGAactcggaacgact			5' intron1 intron1	>-398 >191 >359
	<i>Linepithema_humile</i>	Lhum\Atp6v1B	ND	88	ND	467					115	666 (327+339)										130	267			ND	acttagtccgagCCACGTGAatcgacgtgacct ccaccaaatgggTCAGCTGAatccccgaatttc gagctgccagcgTCATGTGAactcgagcagacg gaaatgaataTCACATGAattagttagtag			5' intron1 intron1	>-369 >170 >332 >579
	<i>Nasonia_vitripennis</i>	Nvit\Atp6v1B	ND	88	1138	467					75	327			79	339					110	267			ND	catcagcccgagCCACGTGAatcccaactgctt cccccaactggTCAGCTGAatcgccgttgcgc gtaggtctgtgTCATGTGAactcgagcagacg cactctggggagTCATGTGAacacgtgcgctt			5' intron1 intron1 intron1	>-417 >-379 >-543 >722	
	<i>Nasonia_giraulti</i>	Ngir\Atp6v1B	ND	88	ND	467					74	327			78	339					110	267			ND	catcagcccgagCCACGTGAatcccaactgctt tccctcagctggTCAGCTGAatcgccgttgcgc gtaggtctgtgTCATGTGAactcgagcagacg cactctggggagTCATGTGAacacgtgcgctt			5' intron1 intron1 intron1	>-426 >-381 >-546 >723	
	<i>Nasonia_longicornis</i>	Nlon\Atp6v1B	ND	88	1172	467 (155+312)					ND	327 (102+98+124)			78	339 (151+83+105)					110	267			ND	catcagcccgagCCACGTGAatcccaactgctt tccctcagctggTCAGCTGAatcgccgttgcgc gtaggtctgtgTCATGTGAactcgagcagacg cactctggggagTCATGTGAacacgtgcgctt			5' intron1 intron1 intron1	>-420 >-378 >-542 >719	

Hemiptera	<i>Acyrtosiphon_pisum</i>	LOC100572714		88	603	155	70	312 (172+140)				72	147	521	331		69	188	74	130	71	140		ND														
	<i>Rhodnius_prolixus</i>	Rpro\Atp6v1B		79	205	155	73	172	1383	140	118	147	846	331		861	188	3191	130	87	149		ND															
Phthiraptera	<i>Pediculus_humanus</i>	PHUM253140		79	415	155	135	172	103	287 (140+147)				81	414 (331+83)				83	235 (105+130)		91	149		tacgttgcttgTCATGTGAatTCACGTGAtc				5'UTR?	>.32								
Odonata	<i>Ladona_fulva</i>	Lful\Atp6v1B		88	323	155	101	172	1065	140	82	147	156	180+191+151		89	188	264	130	127	149		tcgagtacgtgTCACGTGAaTCACGTGAatgacatcgaaaattttatticaTCATGTGAatccaccacca tgaatttaggTCACATGAagttagatcca				5' intron	>.23/-13 >1569 >3413										
Crustacea	<i>Daphnia_pulex</i>	Dpu\Atp6v1B		94	86	155(56+99)	57	172	64	140	67	478(105+98+124+151)				78	188 (83+105)	63	273			gtgactgcacgTCATATGAatcgagagaaccc				5'	>-138											
Ixodida	<i>Ixodes_scapularis</i>	ISCW022132	99	85	1630	56	944	99	80	94	57	78	67	140	74	105	820	98	903	358 (124+151+83)		2083	105	93	130	ND	155		tgggtgtagcggTCATGTGAatcaggatgtca		intron1	547						
	<i>Homo_sapiens</i>	ATP6V1B1	87	118	7585	56	14332	99	188	94	591	78	843	140	842	102	573	98	1083	124	261	151		259	83	783	105	193	130	92	164	310	atctccagctcTCAGGTGAacggggcccctc		5'	>-149		
		ATP6V1B2	214	135	6941	56	4893	99	814	94	129	78	530	140(82+58)	335	102	348	98	582	124	1912	151		1444	83	724	105	828	130	1980	140	1294	tcgaatggataTCAGCTGAacgttgccctga		5'	>-121		
Cnidaria	<i>Nematostella_vectensis</i>	Nvec\Atp6v1B	ND	79	152	56	394	99	295	94	174	78	405	82	87	58	96	102	152	98	115	124	199	81	447	70	180	83	334	105	577	130	329	137	ccgttcagggtTCACGTGAatctcttgtag		intron1	>171
Placozoa	<i>Trichoplax_adhaerens</i>	Tadh\Atp6v1B	ND	73	213	56	740	99	344	94	101	160 (78+82)		73	58	85	102	158	98	99	124	72	81	70	70	110	83	79	105	118	130	92	149	cttgaatgactTCACATGAacatcgctatac		5'	>-290	