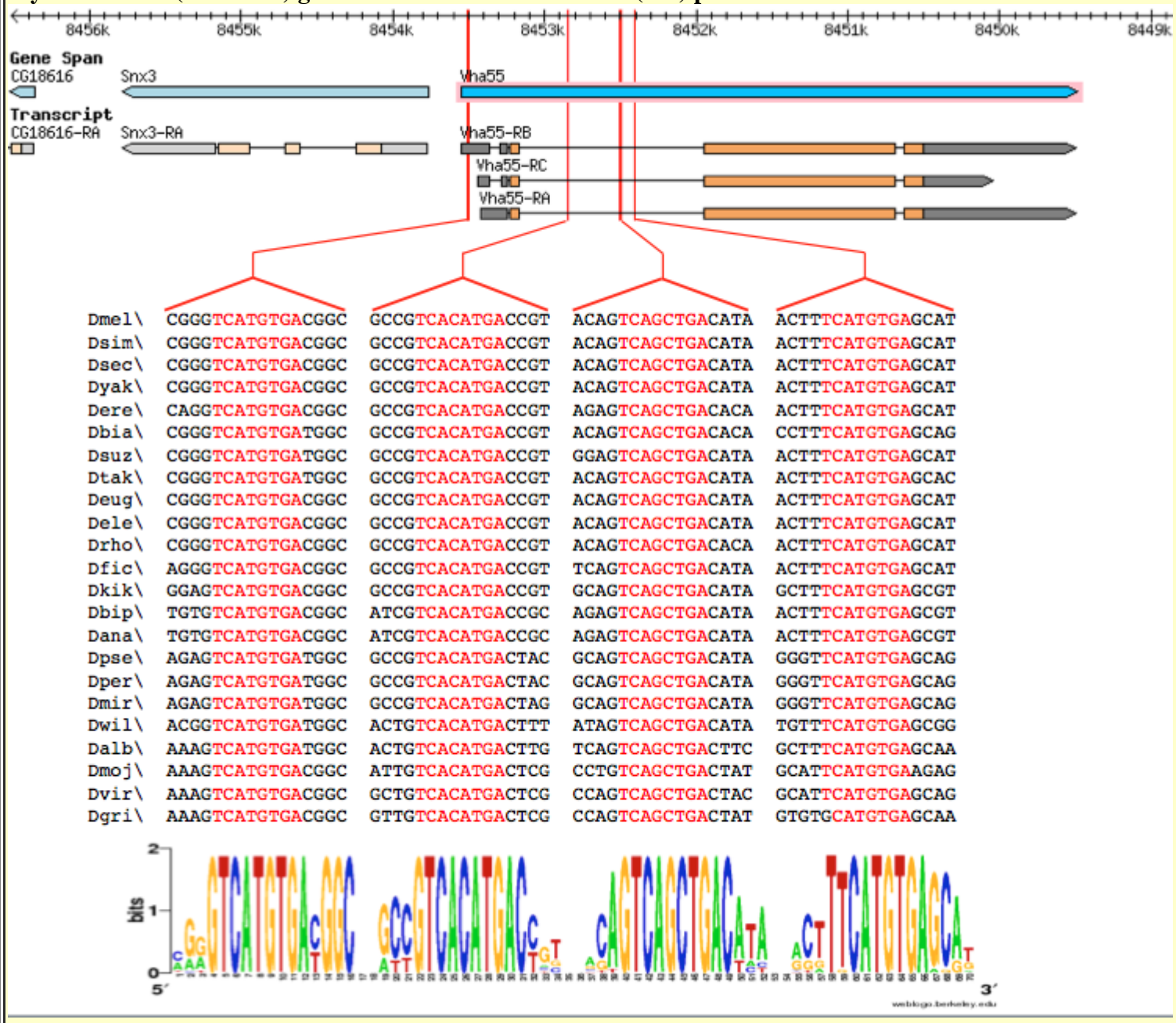
Gene Cluster ID	Atp6v1B
Drosophila melanogaster gene	**Vha55 (CG17369)**
FlyBase ID	FBgn0005671
Predicted function	**ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B**
Protein size	490 amino acids
Cytogenetic map	3R:87C2-87C3
Gene sequence location	3R:8449484..8453551[-]
Dmel CLEAR sequence(s)	**TCATGTGA; TCACATGA; TCAGCTGA; TCATGTGA**
CLEAR sequence location(s)	3R:8453499..8453506; 3R:8452843..8452850; 3R:8452492..8452499; 3R:8452403..8452410

FlyBase Vha55 (CG17369) gene model & CLEAR element (red) positions:



Atp6v1B gene structure comparison:

Key: UTR region, CDS region

Species	Atp6v1B orthologs	5'exon		intron	exon	intron	exon3'		Extended CLEAR region	Position	bps from TSS
Drosophila_melanogaster	Dmel\Vha55	308	73	1221	1262	61	138	1005	acgcgtgacgggTCATGTGAcggcacgtgacg aaattttcgccgTCACATGAccgttcgctgct ccagttggacagTCAGCTGAcataatttagcc agattccgacttTCATGTGAgcattgcgcgac	5'UTR intron1 intron1 intron1	45 701 1052 1141
Drosophila_simulans	Dsim\GD20555		73	1224	1262	67	138		acgcgtggcgggTCATGTGAcggcacgtgacg aaattttcgccgTCACATGAccgttcgctgct ccagttggacagTCAGCTGAcataatttaccc agattccgacttTCATGTGAgcattgcgcgac	5'UTR? intron1 intron1 intron1	
Drosophila_sechellia	Dsec\GM25995		73	1243	1262	64	138		acgcgtggcgggTCATGTGAcggcacgtgacg aaattttcgccgTCACATGAccgttcgctgct ccagttggacagTCAGCTGAcataatttaccc agattccgacttTCATGTGAgcattgcgcgac	5'UTR? intron1 intron1 intron1	
Drosophila_yakuba	Dyak\GE24501		73	1346	1262	60	138		acgcgtggcgggTCATGTGAcggcacgtgacg aaattttcgccgTCACATGAccgttcgctgct ccagttagacagTCAGCTGAcataatttaccc agattccgacttTCATGTGAgcattgcgcgac	5'UTR? intron1 intron1 intron1	
Drosophila_erecta	Dere\GG17111		73	1320	1262	60	138		acgcgtgtcaggTCATGTGAcggcacgtgacg aaattttcgccgTCACATGAccgttcgctgct ccagttggagagTCAGCTGAcacaatttaccc agattccgacttTCATGTGAgcattgcgcgac	5'UTR? intron1 intron1 intron1	
Drosophila_biarmipes	Dbia\Vha55		73	1561	1262	60	138		acgcctggcgggTCATGTGAtggcacgtgacg aaattttcgccgTCACATGAccgttcgctgct ccagttggacagTCAGCTGAcacaattaccct agattccccttTCATGTGAgcagtgcgcgac	5'UTR? intron1 intron1 intron1	
Drosophila_suzukii	Dsuz\Vha55		73	1525	1262	59	138		acgcctggcgggTCATGTGAtggcacgtgacg aaattttcgccgTCACATGAccgttggctgct aaccagttggagTCAGCTGAcataatttaccc agattcctacttTCATGTGAgcattgcgcgac	5'UTR? intron1 intron1 intron1	
Drosophila_takahashii	Dtak\Vha55		73	1613	1262	63	138		aacgcctggcgggTCATGTGAtggcacgtgac aaattttcgccgTCACATGAccgttcgctgct ccagttagacagTCAGCTGAcataatttaccc agattcctacttTCATGTGAgcactgcgcgac	5'UTR? intron1 intron1 intron1	
Drosophila_eugracilis	Deug\Vha55		73	1515	1262	59	138		acgcctgacgggTCATGTGAcggcacgtgacg aaattttcgccgTCACATGAccgttcgctgct ccagttggacagTCAGCTGAcataatttagcc agattcccacttTCATGTGAgcattgcgcgac	5'UTR? intron1 intron1 intron1	
Drosophila_elegans	Dele\Vha55		73	1645	1262	67	138		gcgcctggcgggTCATGTGAcggcacgtgacg aaattttcgccgTCACATGAccgttcgctgct ccagttagacagTCAGCTGAcataatttttcc agattcttacttTCATGTGAgcattgcgcgac	5'UTR? intron1 intron1 intron1	

Drosophila_rhopaloa	Drho\Vha55		73	1596	1262	58	138		gcgcctgacgggTCATGTGAcggcacgtgacg aaattttcgccgTCACATGAccgttcgctgct ccagttggacagTCAGCTGAcacaatttaccc agattctaacttTCATGTGAgcattgcgcgac	5'UTR? intron1 intron1 intron1	
Drosophila_ficusphila	Dfic\Vha55		73	1385	1262	59	138		gcgcctcaagggTCATGTGAcggcacgtgacg aaattttcgccgTCACATGAccgttcgcagct ccagttggtcagTCAGCTGAcataatttacca agattcctacttTCATGTGAgcattgcgagac	5'UTR? intron1 intron1 intron1	
Drosophila_kikkawai	Dkik\Vha55		73	1272	1400 (1262+138)				acgcctggggagTCATGTGAcggcacgtgacg aaattttcgccgTCACATGAccgttcgctcag ccagttgggcagTCAGCTGAcataatttaccg aaattctcgcttTCATGTGAgcgttgcgcgac	5'UTR? intron1 intron1 intron1	
Drosophila_bipectinata	Dbip\Vha55		73	1028	1262	68	138		ctgtcgcctgtgTCATGTGAcggcacgtgacg aaattttcatcgTCACATGAccgctagtctct cgagtcggagagTCAGCTGAcatacttctccc agcttcttacttTCATGTGAgcgttgcgcgac	5'UTR? intron1 intron1 intron1	
Drosophila_ananassae	Dana\GF23001		73	1070	1262	70	138		ctgtcgcctgtgTCATGTGAcggcacgtgacg aaattttcatcgTCACATGAccgctactctct caagtcggagagTCAGCTGAcataatttgccc aacttcttacttTCATGTGAgcgttgcgcgac	5'UTR? intron1 intron1 intron1	
Drosophila_pseudoobscura	Dpse\GA14484	133+68+86	73	835	1262	67	138	1176	acaaccctagagTCATGTGAtggcacgtgacg aaattttcgccgTCACATGActaccatagatc ccagttgggcagTCAGCTGAcataagttcccc tctccaaggggtTCATGTGAgcaggcggccta	5'UTR intron1 intron1 intron1	0 649 960 1043
Drosophila_persimilis	Dper\GL13570		73	835	1262	67	138		acaaccctagagTCATGTGAtggcacgtgacg aaattttcgccgTCACATGActaccatagatc ccagttgggcagTCAGCTGAcataagttcccc tctccaaggggtTCATGTGAgcaggcggccta	5'UTR? intron1 intron1 intron1	
Drosophila_miranda	Dmir\Vha55		73	828	1262	67	138		acaaccctagagTCATGTGAtggcacgtgacg aaattttcgccgTCACATGActagcatagatc ccagttgggcagTCAGCTGAcataagttcccc tctccaaggggtTCATGTGAgcaggcggccta	5'UTR? intron1 intron1 intron1	
Drosophila_willistoni	Dwil\GK13566		73	789	1262	57	138		gcaaccctacggTCATGTGAtggcacgtgacg aaattttcactgTCACATGActttgtgttgt gctcgtggatagTCAGCTGAcataatttaccc actggttgtgttTCATGTGAgcggtagaatcc	5'UTR? intron1 intron1 intron1	
Drosophila_albomicans	Dalb\Vha55		73	959	1262	62	138		tcacacgcaaagTCATGTGAtggcacgtgacg aaattttcactgTCACATGActtgatcgctga ttcgttcgtcagTCAGCTGActtcgttgagtt tggtgtttgcttTCATGTGAgcaacgcttgta	5'UTR? intron1 intron1 intron1	
Drosophila_mojavensis	Dmoj\GI24752		73	847	1262	68	138		tcacacgtaaagTCATGTGAcggcacgtgacg aaattttcattgTCACATGActcgatcatcaa ccagtttgcctgTCAGCTGActatttaacccc ccacttgtgcatTCATGTGAagagcgctattt	5'UTR? intron1 intron1 intron1	
Drosophila_virilis	Dvir\GJ14577		73	847	1262	68	138		tcacacgcaaagTCATGTGAcggcacgtgacg aatttttcgctgTCACATGActcgatcgccga gcagtttgccagTCAGCTGActacttaacccc gccgctttgcatTCATGTGAgcagcgttattg	5'UTR? intron1 intron1 intron1	

Drosophila_grimshawi	Dgri\GH18893		73	862	1262	86	138		tcacacgcaaagTCATGTGAcggcacgtgacg aaattttcgttgTCACATGActcgatcgctga ctggtttgccagTCAGCTGActatttaaccct	5'UTR? intron1 intron1 intron1	