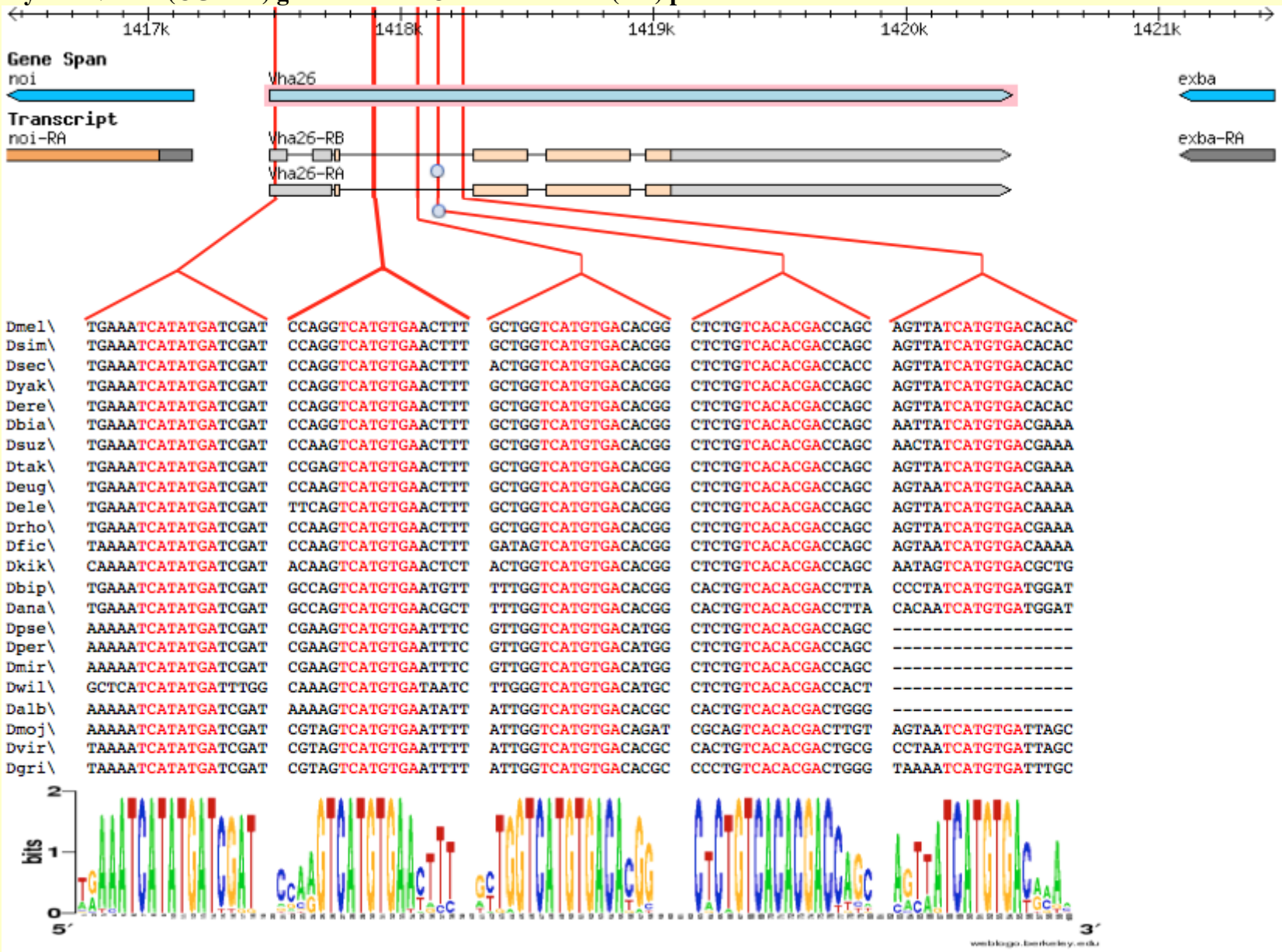
Gene Cluster ID	Atp6v1E
Drosophila melanogaster gene	**Vha26 (CG1088)**
FlyBase ID	FBgn0015324
Predicted function	**ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E**
Protein size	226 amino acids
Cytogenetic map	3R:83B4-83B4
Gene sequence location	3R:1417453..1420429[+]
Dmel CLEAR sequences	**TCATATGA; TCATGTGA; TCATGTGA; TCACACGA; TCATGTGA**
CLEAR sequence locations	3R:1417501..1417508; 3R:1417899..1417906; 3R:1418066..1418073; 3R:1418145..1418152; 3R:1418246..1418253

FlyBase Vha26 (CG1088) gene model & CLEAR element (red) positions:



Atp6v1E gene structure comparison:

Key: UTR region, CDS region

Species	Vha26 Atp6v1E orthologs	5'exon		intron	exon	intron	exon	intron	exon3'		Extended CLEAR region	Position	bps from TSS
Drosophila_melanogaster	Dmel\Vha26	275	33	529	213	78	327	61	108	1353	actttcgtgaaaTCATATGAtcgatttgcagt ggatctcccaggTCATGTGAacttttcaccgc aattcgtgctggTCATGTGAcacggcccccgc catgtccagttaTCATGTGAcacacaggcaac	5'UTR? intron1 intron1 intron1	48 447 614 794
Drosophila_simulans	Dsim\GD19797		33	514	213	76	327	61	108		actttcgtgaaaTCATATGAtcgatttgcagt gtatctcccaggTCATGTGAacttttcaccgc aattcgtgctggTCATGTGAcacggcccccgc catgtccagttaTCATGTGAcacacaggcaac	5'UTR? intron1 intron1 intron1	
Drosophila_sechellia	Dsec\GM10818		33	520	213	76	327	61	108		actttcgtgaaaTCATATGAtcgatttgcagt ggatctcccaggTCATGTGAacttttcattgc aattcgtactggTCATGTGAcacggcccccgc catgtccagttaTCATGTGAcacacaggcaac	5'UTR? intron1 intron1 intron1	
Drosophila_yakuba	Dyak\GE10141		33	499	213	69	327	61	108		actttcgtgaaaTCATATGAtcgatttgcagt ggatctcccaggTCATGTGAacttttcaccgc aattcgtgctggTCATGTGAcacggcccccgc taaatgcagttaTCATGTGAcacacaggcaac	5'UTR? intron1 intron1 intron1	
Drosophila_erecta	Dere\GG12936		33	504	213	67	327	61	108		actttcgtgaaaTCATATGAtcgatttgcagt ggatcttccaggTCATGTGAacttttcaccac aattcgtgctggTCATGTGAcacggcccccgc taagtgcagttaTCATGTGAcacaccggcaac	5'UTR? intron1 intron1 intron1	
Drosophila_biarmipes	Dbia\Vha26		33	531	213	71	327	62	108		cttcccgtgaaaTCATATGAtcgatttgcagt acgtcccccaggTCATGTGAactttctgtgcc aattcgtgctggTCATGTGAcacggcccccgc aaagtgcaattaTCATGTGAcgaaaggcgcaa	5'UTR? intron1 intron1 intron1	
Drosophila_suzukii	Dsuz\Vha26		33	530	213	64	327	63	108		cctcccctgaaaTCATATGAtcgatttgcagt atgttcaccaagTCATGTGAacttttttatgcc agttcgtgctggTCATGTGAcacggcccccgc gaaatgcaactaTCATGTGAcgaaaggggcaa	5'UTR? intron1 intron1 intron1	
Drosophila_takahashii	Dtak\Vha26		33	521	213	65	327	61	108		cttcgcgtgaaaTCATATGAtcgatttgcagt atgttccccgagTCATGTGAactttccatccc aattcgtgctggTCATGTGAcacggcccccgc ccaatgcagttaTCATGTGAcgaaatgggcaa	5'UTR? intron1 intron1 intron1	
Drosophila_eugracilis	Deug\Vha26		33	482	213	56	327	62	108		ctacccgtgaaaTCATATGAtcgatttgcagt atgtcccccaagTCATGTGAacttttttacatc aattggtgctggTCATGTGAcacggcccccgc ccaatgcagtaaTCATGTGAcaaaaggggtta	5'UTR? intron1 intron1 intron1	
Drosophila_elegans	Dele\Vha26		33	517	213	66	327	62	108		cttcccgtgaaaTCATATGAtcgatttgcagt gtccccttcagTCATGTGAacttttcagcac aattcgtgctggTCATGTGAcacggcccccgc ccaatgcagttaTCATGTGAcaaaaaaaggca	5'UTR? intron1 intron1 intron1	
Drosophila_rhopaloa	Drho\Vha26		33	516	213	74	327	62	108		cttttcgtgaaaTCATATGAtcgatttgcagt tgttcccccaagTCATGTGAacttttcatccg aattggtgctggTCATGTGAcacggccccgca cgaatgcagttaTCATGTGAcgaaaaggacaa	5'UTR? intron1 intron1 intron1	

Drosophila_ficusphila	Dfic\Vha26		33	496	213	63	327	64	108		cttcccgtaaaaTCATATGAtcgatttgcagt ggtgcccccaagTCATGTGAacttttcaccac aattcgtgatagTCATGTGAcacgggcccccg ccaatgcagtaaTCATGTGAcaaaatgaggca	5'UTR? intron1 intron1 intron1	
Drosophila_kikkawai	Dkik\Vha26		33	559	213	67	327	69	108		ctccccccaaaaTCATATGAtcgattgtgaaa attgcccacaagTCATGTGAactctttgctac aatacgtactggTCATGTGAcacggcccccgc caaaggaaatagTCATGTGAcgctgtactaac	5'UTR? intron1 intron1 intron1	
Drosophila_bipectinata	Dbip\Vha26		33	657	213	66	327	64	108		cttcacctgaaaTCATATGAtcgatttgcagt cacaatagccagTCATGTGAatgttccccctc atttcaatttggTCATGTGAcacggcccccgc ctgaatgccctaTCATGTGAtggataaaggta	5'UTR? intron1 intron1 intron1	
Drosophila_ananassae	Dana\GF20699		33	638	213	58	327	70	108		cttcacctgaaaTCATATGAtcgatttgcagt cacaatagccagTCATGTGAacgcttcccct atttcattttggTCATGTGAcacggcccccgc ctgaatacacaaTCATGTGAtggataatacga	5'UTR? intron1 intron1 intron1	
Drosophila_pseudoobscura	Dpse\GA10614		33	590	213	67	327	64	108		cacactgaaaaaTCATATGAtcgatttgcagt aatgattcgaagTCATGTGAatttctcatggc aattcgtgttggTCATGTGAcatggactccac	5'UTR? intron1 intron1	
Drosophila_persimilis	Dper\GL21540		33	591	213	67	327	64	108		cacactgaaaaaTCATATGAtcgatttgcagt aatgattcgaagTCATGTGAatttctcatggc aattcgtgttggTCATGTGAcatgggctccac	5'UTR? intron1 intron1	
Drosophila_miranda	Dmir\Vha26		33	589	213	67	327	64	108		cacactaaaaaaTCATATGAtcgatttgctgt aatgattcgaagTCATGTGAatttctcatggc aattcgtgttggTCATGTGAcatgggctccac	5'UTR? intron1 intron1	
Drosophila_willistoni	Dwil\GK22511		33	652	213	76	435 (327+108)				attgtgggctcaTCATATGAtttggccagtga aaattgtcaaagTCATGTGAtaatcattagcg attcgtattgggTCATGTGAcatgctcccca	5'UTR? intron1 intron1	
Drosophila_albomicans	Dalb\Vha26		33	>725	213	351	327	70	108		acgaggtaaaaaTCATATGAtcgatttgtggt gcgagtgaaaagTCATGTGAatattactcgca aatacttattggTCATGTGAcacgcactacac	5'UTR? intron1 intron1	
Drosophila_mojavensis	Dmoj\GI23674		33	704	213	57	327	63	108		acgaagtaaaaaTCATATGAtcgattagtcgt ttctcgccgtagTCATGTGAattttgcgtaca aaagcttattggTCATGTGAcagatattacat agatataagtaaTCATGTGAttagctttgagg	5'UTR? intron1 intron1 intron1	
Drosophila_virilis	Dvir\GJ23234		33	730	213	94	327	62	108		cacgaagtaaaaTCATATGAtcgattggaggt ttctcatcgtagTCATGTGAattttgcgtgca aatgcttattggTCATGTGAcacgcactacac ataggtgcctaaTCATGTGAttagctttaggt	5'UTR? intron1 intron1 intron1	
Drosophila_grimshawi	Dgri\GH14669		33	765	213	71	327	72	108		cacgaagtaaaaTCATATGAtcgatttgtggt ttctctccgtagTCATGTGAattttagcatgc attgcttattggTCATGTGAcacgcactagac gagcaactaaaaTCATGTGAtttgcttaagag	5'UTR? intron1 intron1 intron1	