Supplemental Table 1. Nucleotide frequency at Segregating Sites in the *Aedes triseriatus* Inhibitor of Apoptosis 1 gene.

Nuc.	Freq. of the Most Common Nucleotide	Hexp	Hobs	Probability of Hardy-Weinberg Equilibrium	Substitution	Codon	Amino Acid
-390	0.7692	0.3551		0.7602	a > g		
-389	0.6538	0.4527		0.1772	g > t		
-370	0.963	0.0713		0.1649	g > a		
-363	0.9556	0.0849	0	0.1667	t > g		
-361	0.7167	0.4061	0.0112	0.0001	c > a		
-353	0.978	0.043	0	0.2884	a > g		
-351	0.9451	0.1038	0	0.5386	c > t		
-344	0.989	0.0218	0	0.1505	a > t		
-341	0.9670, 0.0220	0.0643	0	0.391, 0.2884, 0.1505	a > c > t		
-340	0.9615	0.074	0.0112	0.678	c > t		
-335	0.9176, 0.0549	0.1542	0.0112	0.0654, 0.5386, 0.0249	g > a > -		
-334	0.9725	0.0535	0.0112	0.0249	a > -		
-333	0.9615, 0.0275	0.0746	0.0112	0.0076, 0.0249, 0.1596	a > - > g		
-332	0.9451	0.1038	0	0.5386	g > c		
-326	0.9945	0.0109		0.3107	a > g		
-324	0.9945	0.0109	0.0112	0.3213	c > a		
-321	0.9780, 0.0110	0.0433	0.0225	0.3014, 0.2063, 0.1505	c > g = t		
-320	0.967	0.0638	0	0.0138	a > g		
-319	0.989	0.0218	0	0.1596	a > g		
-318	0.9121, 0.0549, 0.0275	0.1643	0.0449	0.3168, 0.5386, 0.1817, 0.3107	c > a > g > t		
-316	0.9615	0.074	0.0562	0.0577	- > g		
-315	0.9615	0.074	0.0562	0.0577	- > a		

-314	0.9451	0.1038	0	0.5386	g > -		
-313	0.9451	0.1038	0	0.5386	a > -		
-310	0.989	0.0218	0	0.1505	g > c		
-298	0.9945	0.0109	0.0112	0.3107	a > g		
-286	0.9835	0.0325	0.0337	0.5734	c > t		
-282	0.9341, 0.0440	0.125	0	0.2479, 0.1572, 0.2884	a > - > t		
-281	0.956	0.0841	0	0.1572	c > -		
-280	0.956	0.0841	0	0.1572	g > -		
-279	0.989	0.0218	0	0.1505	a > -		
-278	0.989	0.0218	0	0.1505	c > -		
-277	0.9780, 0.0110	0.0433	0	0.2884, 0.1596, 0.1505	g > c = -		
-276	0.9945	0.0109	0.0112	0.3213	g > -		
-274	0.9945	0.0109	0.0112	0.3213	g > -		
-272	0.989	0.0218	0	0.1596	t > c		
-271	0.989	0.0218	0	0.1596	g > a		
-270	0.9945	0.0109	0.0112	0.3213	t > -		
-269	0.9945	0.0109	0.0112	0.3213	t > -		
-266	0.989	0.0218	0	0.1596	a > g		
-265	0.989	0.0218	0	0.1596	c > t		
-263	0.989	0.0218	0	0.1596	a > g		
-259	0.9945	0.0109		0.3107	a > g		
-257	0.956	0.0841	0.0225	==0.0042==	c > t		
-254	0.967	0.0638	0	0.422	t > c		
-244	0.978	0.043	0	==0.0409==	c > t		
-235	0.9945	0.0109	0.0112	0.3107	c > t		
-228	0.9286	0.1326	0.0337	0.4109	g > a		

-227	0.989	0.0218	0	0.1596	a > g		
-225	0.9945	0.0109	0.0112	0.3107	c > t		
-224	0.989	0.0218	0	0.1596	t > c		
-223	0.9451	0.1038	0	0.5386	g > c		
-222	0.9505	0.0941	0.0112	0.3212	a > g		
-220	0.9396	0.1135	0.0112	0.7837	c > t		
-219	0.7363	0.3883	0.2247	0.6707	t > c		
-217	0.9835	0.0325	0.0337	0.0841	c > t		
-212	0.9725, 0.0220	0.0537	0.0562	0.1817, 0.3107, 0.0455	a > g > c		
-208	0.9396	0.1135	0.0562	<mark>0.0057</mark>	a > c		
-202	0.9945	0.0109	0.0112	0.3213	g > t		
-195	0.989	0.0218	0	0.1596	a > c		
-170	0.989	0.0218	0	0.1596	a > g		
-169	0.989	0.0218	0	0.1596	g > a		
-167	0.989	0.0218	0.0225	0.1505	c > t		
-160	0.9945	0.0109	0.0112	0.3213	t > a		
-150	0.9945	0.0109		0.3107	t > c		
-149	0.9945	0.0109	0.0112	0.3107	g > t		
-142	0.9396, 0.0495	0.1146	0.0337	0.3705, 0.7577, 0.1596	c > t > -		
-141	0.967	0.0638	0.0225	<mark>0.0118</mark>	- > c		
-140	0.967	0.0638	0.0225	<mark>0.0118</mark>	- > g		
-139	0.967	0.0638	0.0225	<mark>0.0118</mark>	- > t		
-138	0.9945	0.0109	0.0112	0.3213	c > -		
-137	0.9945	0.0109	0.0112	0.3213	g > -		
-136	0.9780, 0.0165	0.0432	0.0112	0.0455, 0.0841, 0.3213	t > c > -		
-135	0.9835, 0.0110	0.0326	0.0337	0.5476, 0.1505, 0.3213	c > t > -		

-134	0.9945	0.0109	0.0112	0.3213	g > -		
-128	0.9945	0.0109	0.0112	0.3213	g > a		
-126	0.989	0.0218	0	0.1505	c > -		
-125	0.9780, 0.0110	0.0433	0	0.2884, 0.1596, 0.1505	g > c = -		
-124	0.989	0.0218	0	0.1505	- > t		
-123	0.989	0.0218	0	0.1505	- > c		
-122	0.9890, 0.0055	0.0218	0.0112	0.1505, 0.3107, 0.3107	- > g = c		
-121	0.989	0.0218	0	0.1505	t > -		
-120	0.9615	0.074	0.0112	0.7219	- > c		
-119	0.9615	0.074	0.0112	0.7219	- > g		
-118	0.9615	0.074	0.0112	0.7219	- > t		
-114	0.9725	0.0535	0.0112	<mark>0.0219</mark>	g > c		
-101	0.989	0.0218	0	0.1596	t > g		
-94	0.989	0.0218	0	0.1505	a > g		
-77	0.956	0.0841	0	0.1572	t > c		
-76	0.9286	0.1326	0.0112	0.4109	a > t		
-75	0.9286	0.1326	0.0112	0.4109	c > t		
-74	0.989	0.0218	0.0225	0.1505	c > t		
-68	0.989	0.0218	0	0.1505	c > t		
-58	0.9945	0.0109	0.0112	0.3213	g > a		
-57	0.989	0.0218	0	0.1596	a > g		
-50	0.9835	0.0325	0.0112	0.5734	g > a		
-48	0.989	0.0218	0	0.1505	c > t		
-47	0.9231	0.142	0	0.5491	a > g		
-46	0.9505	0.0941	0.0562	0.7071	t > c		
-38	0.989, 0.0055	0.0218	0.0225	0.1596, 0.3212, 0.3213	g > a = t		

-31	0.6154	0.4734	0.0674	0.4674	a > t		
-30	0.9835	0.0325	0.0112	0.5734	a > t		
-29	0.978	0.043	0	0.2884	c > t		
-26	0.989	0.0218	0	0.1596	g > a		
-22	0.989	0.0218	0.0225	0.2063	g > a		
-19	0.989	0.0218	0	0.1505	g > t		
-18	0.9505	0.0941	0.0337	<mark>0.0152</mark>	a > g		
-17	0.989	0.0218	0	0.1505	g > t		
-10	0.989	0.0218	0	0.1596	c > t		
-7	0.967	0.0638	0.0674	0.3491	t > c		
-6	0.989	0.0218	0	0.1505	a > g		
-5	0.989	0.0218	0	0.1505	a > g		
-4	0.9615	0.074	0.0112	0.2356	g > a		
6	0.9945	0.0109		0.3107	G > A	ACG > ACA	T
18	0.989	0.0218	0	0.1596	G > C	CTG > CTC	L
24	0.989	0.0218	0	0.1505	A > T	ATA > ATT	I
36	0.8901	0.1956	0.1124	0.3172	C > T	TTC > TTT	F
61	0.978	0.043	0	<mark>0.0409</mark>	T > C	TCC > CCC	S > P
64	0.989	0.0218	0	0.1596	C > T	CCC > TCC	P > S
71	0.9451	0.1038	0	0.5386	T > -	GTA > G-A = GT- > G--	V > Fr.shift
72	0.9451	0.1038	0	0.5386	A > -		

73	0.9725, 0.0165	0.0539	0.0112	0.1659, 0.5476, 0.1505	G > A > C	GGA > GCA > GGG > GGC > AGA > GG- > CGA = GCG > GCC > GC- = ACA = CCA > AGG = AGC*	G > A > G > G > R > Fr.shift > R = A > A > Fr.shift = T = P > R = S*
74	0.8352	0.2753	0.0449	0.206	G > C		
75	0.8956, 0.0495, 0.0440	0.1934	0.0112	==0.0331, 0.0183, 0.1572, 0.1505==	A > G > C > -		
76	0.9451, 0.0440	0.1047	0	0.5386, 0.1572, 0.1505	G > - > C	GTA > -TA > CTA	V > Fr.shift > L
81	0.9451	0.1038	0	0.5386	T > C	ACT > ACC	T
83	0.989	0.0218	0	0.1505	G > A	GGG > GGA > GAG > GAA	G > G > E > E
84	0.9121	0.1603	0.0225	0.633	G > A		
87	0.989	0.0218	0.0225	0.2063	G > A	GCG > GCA	A
96	0.989	0.0218	0	0.1505	G > A	GTG > GTA	V
120	0.9945	0.0109	0.0112	0.3107	C > T	GTC > GTT	V
132	0.989	0.0218		0.1505	C > T	GAC > GAT	D

133	0.989	0.0218	0	0.1596	T > A	TCG > TCA = ACG > ACA	S > S = T > T
135	0.9835	0.0325	0.0112	0.0774	G > A		
138	0.989	0.0218	0	0.1596	C > T	TTC > TTT	F
152	0.9945	0.0109	0.0112	0.3107	T > C	GTT > GCT	V > A
154	0.978	0.043	0.0225	0.3227	T > C	TCG > TTG > CCG > CTG > TCA > TTA > CCA > CTA	S > L > P > L > S > L > P > L
155	0.5659	0.4913	0.2472	0.2578	C > T		
156	0.989	0.0218	0	0.1596	G > A		
162	0.989	0.0218	0	0.1596	C > T	ATC > ATT	I
169	0.9945	0.0109	0.0112	0.3107	G > A	GCT > GAT > ACT > AAT	A > D > T > N
170	0.989	0.0218	0	0.1596	C > A		
174	0.989	0.0218	0	0.1505	G > A	GAG > GAA	E
180	0.9835	0.0325	0	0.0774	C > T	GCC > GCT	A
189	0.8626, 0.0824	0.2461	0.0112	0.4807, 0.1638, 0.5386	C > G > A	GGC > GGG > GGA	G
191	0.9945	0.0109		0.3107	T > A	TTT > TAT	F > Y

194	0.9945	0.0109	0.0112	0.3213	A > C	TAC > TAA = TCC > TCA	Y > stop > S > S
195	0.9945	0.0109	0.0112	0.3107	C > A		
201	0.9945	0.0109	0.0112	0.3107	C > T	GTC > GTT	V
205	0.9231	0.142	0.0225	0.2479	C > G	CCA > GCA > CCC > GCC	P > A > P > A
207	0.989	0.0218	0	0.1596	A > C		
213	0.9945	0.0109	0.0112	0.3107	T > C	GAT > GAC	D
227	0.9945	0.0109	0.0112	0.3107	A > T	TAC > TTC	Y > F
237	0.9835	0.0325	0.0337	0.5476	A > C	CGA > CGC	R
246	0.9945	0.0109	0.0112	0.3107	C > T	ATC > ATT	I
249	0.9945	0.0109	0.0112	0.3107	A > G	GGA > GGG	G
252	0.9396	0.1135	0.0112	0.3705	G > A	CTG > CTA	L
258	0.9945	0.0109	0.0112	0.3107	G > A	GAG > GAA	E
267	0.9945	0.0109	0.0112	0.3213	C > T	GAC > GAT	D
276	0.9835	0.0325	0.0112	0.0841	T > C	CTT > CTC	L
297	0.7198, 0.2747	0.4064	0.2809	0.3587, 0.4499, 0.3107	C > A > G	TCC > TCA > TCG	S
303	0.9945	0.0109	0.0112	0.3213	C > T	TAC > TAT	Y
313	0.9945	0.0109	0.0112	0.3107	C > T	CTG > TTG	L
318	0.9835	0.0325	0.0112	0.0841	T > A	CGT > CGA	R
327	0.967	0.0638	0	0.391	A > G	CAA > CAG	Q
330	0.967	0.0638	0	0.391	C > A	ACC > ACA	T
333	0.9945	0.0109	0.0112	0.3107	C > T	ACC > ACT	T

354	0.9945	0.0109	0.0112	0.3213	C > T	AGC > AGT	S
366	0.9231	0.142	0.0899	0.5093	G > A	CAG > CAA	Q
369	0.9615	0.074	0.0112	0.678	G > T	CTG > CTT	L
372	0.9725	0.0535	0.0337	0.6682	G > A	CCG > CCA	P
384	0.9835	0.0325	0.0337	0.5734	C > T	TAC > TAT	Y
390	0.9945	0.0109	0.0112	0.3213	C > A	ACC > ACA	S
402	0.9725	0.0535	0.0562	0.1817	G > A	AGG > AGA	R
417	0.9945	0.0109	0.0112	0.3213	C > T	TCC > TCT	S
420	0.9835	0.0325	0.0225	0.5734	G > A	GTG > GTA	V
423	0.9725	0.0535	0.0562	0.1817	A > T	GCA > GCT	A
429	0.989	0.0218	0	0.1505	T > C	AAT > AAC	N
438	0.989	0.0218	0.0225	0.1505	T > A	TCT > TCA	S
441	0.8956	0.187	0.2135	0.4366	G > A	TCG > TCA	S
444	0.9835	0.0325	0.0337	0.5734	G > C	TCG > TCC	S
448	0.9615	0.074	0.0787	0.678	C > A	CGA > AGA	A
456	0.967	0.0638	0	<mark>0.0138</mark>	T > C	AGT > AGC	S
462	0.7637, 0.1538	0.3863	0.1011	0.6592, 0.6657, 0.4447	T > A > C	GGT > GGA > GGC	G
468	0.9945	0.0109	0.0112	0.3107	A > G	CTA > CTG	L
471	0.989	0.0218	0.0225	0.2063	G > A	TCG > TCA	S
480	0.989	0.0218	0.0225	0.2063	C > T	CCC > CCT	P
483	0.9451	0.1038	0	0.5386	C > T	AGC > AGT	S
490	0.9945	0.0109	0.0112	0.3107	A > C	ACG > CCG	T > P
508	0.9451	0.1038	0	0.5386	T > C	TTA > CTA	L
523	0.989	0.0218	0.0112	0.2063	A > G	ATC > GTC	I > V

526	0.7802	0.343	0.2247	0.087	C > G	CCC > GCC > CCT > GCT	P > A > P > A
528	0.989	0.0218	0	0.1505	C > T		
540	0.9945	0.0109	0.0112	0.3213	T > A	CCT > CCA	P
541	0.9451	0.1038	0	0.5386	G > C	GCG > GTG > GCA > CTG > GTA > CCG > CCA > CTA	A > V > A > L > V > P > P > L
542	0.7637	0.3609	0.3258	0.0288	C > T		
543	0.978	0.043	0	0.2884	G > A		
546	0.9945	0.0109	0.0112	0.3213	C > T	CCC > CCT	P
549	0.9396	0.1135	0.0112	0.7837	G > A	GCG > GCA	A
555	0.6703	0.442	0.0225	0.0023	A > T	CCA > CCT	P
561	0.967	0.0638	0.0449	0.1024	G > A	CAG > CAA	Q
565	0.978	0.043	0.0449	0.3227	C > A	CGG > AGG	R
570	0.9176	0.1512	0.1573	0.0534	G > A	CCG > CCA	P
594	0.9835	0.0325	0.0337	0.5476	G > A	GAG > GAA	E
597	0.9615	0.074	0.0112	0.2598	G > A	GCG > GCA	A
600	0.8516	0.2528	0.2135	0.4917	G > A	AAG > AAA	K
603	0.5549, 0.2473	0.5918	0.4831	0.2264, 0.1439, 0.7222	A > C > G	CGA > CGC > CGG	R

604	0.5989	0.4804	0.191	0.123	C > T	CTG > TTG > CTA > TTA	L
606	0.7418	0.3831	0.2809	0.0758	G > A		
615	0.9945	0.0109	0.0112	0.3107	C > T	TAC > TAT	Y
639	0.5879	0.4845	0.3483	0.139	G > A	AAG > AAA	K
645	0.9945	0.0109	0.0112	0.3107	G > A	AAG > AAA	K
657	0.9945	0.0109	0.0112	0.3107	A > T	CTA > CTT	L
666	0.8956	0.187	0.0787	0.2454	C > T	GCC > GCT	A
675	0.9945	0.0109	0.0112	0.3107	C > T	TTC > TTT	F
681	0.9396, 0.0440	0.1149	0.1011	0.0324, 0.1572, 0.0841	T > C > A	ACT > ACC > ACA	T
693	0.9780, 0.0165	0.0432	0.0225	0.3227, 0.0841, 0.3107	T > G > C	GAT > GAG > GAC	D > E > D
694	0.989	0.0218	0	0.1596	C > G	CGA > CGT > GGA > GGT	R > R > G > G
696	0.8242	0.2898	0.0225	0.0162	A > T		
699	0.9725, 0.0220	0.0537	0.0337	0.1659, 0.3014, 0.3107	C > G > A	GTC > GTG > GTA	V
710	0.989	0.0218	0	0.1596	G > T	AGC > ATC	S > I
723	0.9890, 0.0055	0.0218	0.0225	0.1505, 0.3107, 0.3107	C > G = A	GGC > GGG = GGA	G
727	0.989	0.0218	0	0.1596	A > C	AAG > AAA > CAG > CAA	K > K > Q > Q

729	0.9835	0.0325	0.0112	0.5734	G > A		
744	0.9111	0.162	0.0225	0.6004	G > A	GAG > GAA	E
775	0.9945	0.0109	0.0112	0.3107	T > C	TAT > CAT	Y > H
783	0.9451	0.1038	0	0.5386	T > C	AAT > AAC	N
806	0.9945	0.0109	0.0112	0.3107	A > C	AAA > ACA	K > T
816	0.9341	0.1231	0	0.477	A > G	GAA > GAG	E
822	0.9945	0.0109	0.0112	0.3213	C > T	ATC > ATT	I
825	0.967	0.0638	0	0.422	C > T	GCC > GCT	A
861	0.9945	0.0109	0.0112	0.3213	G > C	CAG > CAC	Q > H
879	0.9451, 0.0495	0.1043	0.0112	0.5386, 0.7577, 0.3213	G > T > C	GGG > GGT > GGC	G
918	0.978	0.043	0	0.2884	A > T	ACA > ACT	T
921	0.989	0.0218	0	0.1596	C > T	TCC > TCT	S
954	0.9725	0.0535	0.0225	0.1659	G > A	TCG > TCA	S
966	0.956	0.0841	0	0.1572	T > C	AGT > AGC	S
969	0.956	0.0841	0	0.1572	A > T	GCA > GCT	A
972	0.9505	0.0941	0.0225	0.3212	G > A	TCG > TCA	S
984	0.9945	0.0109	0.0112	0.3213	C > T	GTC > GTT	V
994	0.6758	0.4382	0.0112	==0.023==	C > A	CTC > ATC	L > I
998	0.9945	0.0109	0.0112	0.3107	G > C	GGC > GCC	G > A
1010	0.9945	0.0109	0.0112	0.3107	G > T	AGT > ATT	S > I
1041	0.989	0.0218	0	0.1505	T > C	AAT > AAC	N
1059	0.9945	0.0109	0.0112	0.3213	T > C	AGT > AGC	S
1064	0.9451	0.1038	0	0.5386	T > C	ATC > ACC > ATT > ACT	I > T > I > T

1065	0.956	0.0841	0	0.1572	C > T		
1089	0.6044	0.4782	0.0225	0.8408	A > G	GAA > GAG	E
1104	0.989	0.0218	0	0.1505	C > T	TTC > TTT	F
1107	0.8791	0.2126	0.0674	0.1904	G > A	TCG > TCA	S
1110	0.9670, 0.0110	0.0645	0	0.0118, 0.1505, 0.1505, 0.1505	C > A = G = T	CCC > CCA = CCG = CCT	P
1116	0.7033	0.4173	0.0674	0.0856	G > A	GGG > GGA	G
1122	0.9945	0.0109	0.0112	0.3213	A > G	GTA > GTG	V
1137	0.9505	0.0941	0.0112	0.7577	A > G	AAA > AAG	K
1155	0.989	0.0218	0	0.1596	C > T	ACC > ACT	T
1164	0.7527	0.3723	0.0787	0.4388	A > G	CCA > CCG	P
1167	0.967	0.0638	0	0.391	C > T	CTC > CTT	L
1221	0.9888	0.0221	0	0.1596	a > t	A	

* All remaining codon possibilities have a frequency of less than 0.0005
Polymorphic sites that are boxed occur within the same amino acid codon
Sites are the ones shown to be significant using PGtheta analysis of *AtIAP1* sequences.
Sites are ones in which nucleotide frequencies are out of Hardy-Weinberg equilibrium.