

**Table S3 Annotation of Rhagoletis genomic sequence contigs resulting from tblastx analysis**

First four blastx hits ordered from most to least similar	Max identity %	E-value
<b>Rhagoletis contig 1 CG9000 search</b>		
<i>CG9000</i>	79.53	0
<i>CG9001</i>	40.29	2.00E-88
<i>CG9002</i>	37.43	6.00E-78
<i>CG7573</i>	26.2	6.00E-33
<b>Rhagoletis contig 2 CG9000 search</b>		
<i>CG9000</i>	56.72	3.00E-23
<i>CG9001</i>	31.82	3.00E-07
<i>CG9002</i>	31.58	8.00E-07
<i>small wing</i>	29.17	5.00E-04
<b>Rhagoletis contig CG9001 search</b>		
<i>CG9000</i>	83.42	1.00E-124
<i>CG9001</i>	52.38	6.00E-73
<i>CG9002</i>	46.7	3.00E-61
<i>CG7573</i>	31.22	9.00E-29
<b>Rhagoletis contig 1 CG9002 search</b>		
<i>CG9000</i>	78.5	3.00E-60
<i>CG9001</i>	51.89	2.00E-40
<i>CG9002</i>	45.87	2.00E-32
<i>CG7573</i>	34.31	2.00E-15
<b>Rhagoletis contig 2 CG9002 search</b>		
<i>CG9000</i>	88.42	5.00E-59
<i>CG9001</i>	52.33	2.00E-28
<i>CG9002</i>	48.89	3.00E-25
<i>CG7573</i>	29.63	2.00E-11
<b>Rhagoletis contig 2 CG4852 search</b>		
<i>CG4852</i>	79.27	7.00E-46
<i>alpha-spectrin</i>	42.11	0.001
<i>rigor mortis</i>	34.78	0.003

The Rhagoletis contigs that served as queries are in bold with the best blast hits for each query listed below. Each Rhagoletis contig was assembled from genomic reads that had been identified by a blast search as being similar to the listed *D. melanogaster* locus. Some searches of the Rhagoletis genome with a single *Drosophila* locus resulted in 2 separate non-overlapping contigs. Note that no contig in the Rhagoletis genome could be constructed from a search with *Drosophila* CG7573 due to the absence of any homologous sequences. See Materials and Methods for further details.