

# Supplementary Material

**“Selective sweeps in a nutshell; the genomic footprint of rapid insecticide resistance  
evolution in a major insect pest of tree nuts”**

Bernarda Calla, Mark Demkovich, Joel P. Siegel, João Paulo Gomes Viana, Kim K.O. Walden,  
Hugh M. Robertson, May R. Berenbaum

Corresponding Author: Bernarda Calla

Email: [calla2@illinois.ed](mailto:calla2@illinois.ed)

## **List of Supplementary Materials:**

Tables S1-S8

Figures S1-S4

## Supplementary Tables

**Table S1.** Pooled DNA re-sequencing results.

<b>Strain</b>	<b>Library Name</b>	<b>Number of reads</b>	<b>Read length</b>	<b>Paired</b>	<b>Haploid genome length</b>	<b>Coverage</b>
<b>Almond</b>	Almond_AAGGCCGTCA_L006_R1_001.fastq	120,568,394	150	2	406,468,287	88.987
<b>Fig</b>	Fig_AAGATCTGAG_L006_R1_001.fastq	112,371,554	150	2	406,468,287	82.938
<b>R347</b>	R347_AAGGTGCCTG_L006_R1_001.fastq	119,586,826	150	2	406,468,287	88.263
	<b>Total Reads (paired)</b>	<b>705,053,548</b>				<b>260.1876594</b>

**Table S2.** Nucleotide diversity across scaffold NW\_013535362.1. The number of SNPs, read coverage and the calculated Tajima's  $\pi$  are shown for each of the sequenced populations.

ID	gene_ID	Star	End	gene_name	ALM number of SNPS	ALM coverage	ALM_pi	FIG number of SNPS	FIG coverage	Fig_pi	R347 number of SNPS	R347 coverage	R347_pi
rna4429	XM_013328369.1	3399243	3401314	CYPB56	2	0.966	0.000119055	3	0.932	0.000146796	0	0.999	0
rna4431	XM_013328342.1	3413197	3420607	protein ariadne-1%2C transcript variant X2	11	0.929	0.000169131	19	0.927	0.000340522	1	0.891	0.000012382
rna4443	XM_013328236.1	3549071	3550177	protein kish-A	0	0.536	0	5	0.921	0.00047616	1	1	0.000075361
rna4430	XM_013328341.1	3403909	3420607	protein ariadne-1%2C transcript variant X1	19	0.851	0.000133218	43	0.92	0.000287535	13	0.865	0.000078983
rna4427	XM_013328250.1	3344559	3350148	sodium channel protein para%2C transcript variant X2	1	0.873	0.000016742	7	0.958	0.000106802	6	0.838	0.000121451
rna4426	XM_013328249.1	3344559	3370779	sodium channel protein para%2C transcript variant X1	33	0.829	0.000155447	41	0.898	0.000163303	30	0.826	0.000129155
rna4444	XM_013328238.1	3550487	3554188	protein prenyltransferase alpha subunit repeat- containing protein 1 uncharacterized	21	0.797	0.000809689	33	0.842	0.001342665	5	0.763	0.000158307
rna4432	XM_013328377.1	3421473	3423241	LOC106129721	3	0.939	0.000147596	4	0.993	0.000186148	3	0.949	0.000168929
rna4447	XM_013328187.1	3745239	3796518	protein unc-13 homolog A actin-binding Rho-activating protein-like	623	0.685	0.002149737	728	0.736	0.002379027	75	0.764	0.000174787
rna4448	XM_013328228.1	3800374	3817393	isoleucine--tRNA ligase%2C cytoplasmic	214	0.665	0.002477321	304	0.707	0.003822464	27	0.729	0.000196256
rna4433	XM_013328378.1	3423369	3430390	uncharacterized	11	0.683	0.000210947	32	0.746	0.000671049	15	0.719	0.000265044
rna4445	XM_013328171.1	3584697	3630468	LOC106129575	485	0.659	0.001909073	652	0.653	0.002842798	97	0.675	0.000319536
rna4434	XM_013328269.1	3433176	3489393	dmX-like protein 2 ras GTPase-activating protein 1	408	0.637	0.001241575	449	0.667	0.001385853	121	0.646	0.000323764
rna4442	XM_013328235.1	3529722	3548710	protein 1	173	0.693	0.001636741	241	0.761	0.00197034	52	0.741	0.00035081
rna4428	XM_013328169.1	3387986	3396394	CYPB54-55	31	0.877	0.000374048	67	0.945	0.000832382	30	0.889	0.000397261
rna4449	XM_013328172.1	3826528	3849030	gonadotropin-releasing hormone II receptor-like endophilin-A%2C transcript variant X1	326	0.757	0.002598439	460	0.75	0.004254889	87	0.778	0.00047073
rna4438	XM_013328231.1	3490744	3524106	endophilin-A%2C transcript variant X2	288	0.792	0.001364922	273	0.854	0.001120561	106	0.847	0.000511522
rna4440	XM_013328232.1	3490744	3524106	endophilin-A%2C transcript variant X3	288	0.792	0.001364922	273	0.854	0.001120561	106	0.847	0.000511522
rna4439	XM_013328233.1	3490744	3524106	uncharacterized	288	0.792	0.001364922	273	0.854	0.001120561	106	0.847	0.000511522
rna4446	XM_013328188.1	3631722	3638019	LOC106129590	57	0.629	0.001609691	75	0.677	0.002214825	24	0.611	0.000589032

rna4455	XM_013328217.1	4270710	4272681	tyrosine--tRNA ligase%2C cytoplasmic	15	0.589	0.002191836	22	0.915	0.002546646	8	0.902	0.000683768
rna4390	XM_013328351.1	2580309	2581660	UDP-GlcNAc:betaGal beta-1%2C3-N-acetylglucosaminyltransferase-like protein 1	7	0.949	0.001699828	5	0.919	0.00140442	6	0.865	0.001191301
rna4418	XM_013328423.1	3159383	3164900	uncharacterized LOC106129757	26	0.673	0.001504173	21	0.711	0.001399366	25	0.73	0.001236382
rna4337	XM_013328277.1	1505319	1507681	conserved oligomeric Golgi complex subunit 5	24	0.647	0.003325352	36	0.924	0.004487335	12	0.89	0.001648673
rna4425	XM_013328229.1	3304902	3307354	phosphomevalonate kinase	28	0.914	0.002209508	28	0.967	0.002526449	17	0.712	0.001704432
rna4413	XM_013328280.1	3097871	3099727	GPI mannosyltransferase 2%2C transcript variant X2	10	0.893	0.001245343	7	0.907	0.000848715	6	0.912	0.001815043
rna4414	XM_013328279.1	3097905	3099727	GPI mannosyltransferase 2%2C transcript variant X1	9	0.891	0.001221095	7	0.906	0.000866193	6	0.919	0.001834536
rna4441	XM_013328234.1	3525167	3528547	polyubiquitin-C stress-induced-	51	0.639	0.002994905	40	0.676	0.002750336	26	0.67	0.002126739
rna4391	XM_013328352.1	2581733	2585900	phosphoprotein 1-like protein groucho%2C	50	0.893	0.00302288	54	0.942	0.003067504	31	0.899	0.002209818
rna4422	XM_013328326.1	3204704	3279423	transcript variant X1 uncharacterized	512	0.615	0.00255649	570	0.629	0.002639457	492	0.618	0.00259059
rna4451	XM_013328392.1	4090436	4108229	LOC106129735 protein groucho%2C	333	0.696	0.007056351	396	0.76	0.006815791	213	0.745	0.002636165
rna4423	XM_013328328.1	3204704	3258508	transcript variant X3 protein groucho%2C	410	0.604	0.002993113	461	0.614	0.003024779	386	0.605	0.002909226
rna4424	XM_013328327.1	3204704	3256842	transcript variant X2 putative elongator complex	393	0.593	0.003028286	443	0.603	0.003050611	369	0.593	0.002923422
rna4383	XM_013328409.1	2419495	2425584	protein 1%2C transcript variant X1	90	0.895	0.004315263	94	0.923	0.004142576	66	0.893	0.003205471
rna4384	XM_013328410.1	2419495	2425584	putative elongator complex protein 1%2C transcript variant X2	90	0.895	0.004315263	94	0.923	0.004142576	66	0.893	0.003205471
rna4421	XM_013328247.1	3197609	3199024	Krueppel-like factor 9 small conductance calcium-activated potassium channel	24	0.833	0.005024417	23	0.898	0.004206684	23	0.965	0.003498993
rna4450	XM_013328189.1	3852565	4034421	protein uncharacterized	4722	0.628	0.008780796	5092	0.629	0.00959187	2798	0.693	0.003576904
rna4408	XM_013328167.1	3044389	3048122	LOC106129572 uncharacterized protein	45	0.801	0.002517566	27	0.887	0.001446331	36	0.948	0.003757452
rna4453	XM_013328173.1	4247890	4251407	DDB_G0286591-like DTW domain-containing	71	0.792	0.005590469	75	0.86	0.005145974	42	0.849	0.003790941
rna4530	XM_013328414.1	5881767	5883523	protein 2	25	0.789	0.004663524	25	0.873	0.004628095	20	0.701	0.004146948
rna4508	XM_013328386.1	5483318	5487648	odorant receptor 4-like	138	0.779	0.00653974	120	0.773	0.006490545	83	0.822	0.004175595
rna4331	XM_013328225.1	1473705	1476159	m7GpppN-mRNA hydrolase mitochondrial inner	29	0.927	0.003160619	27	0.933	0.003546826	21	0.901	0.004217887
rna4501	XM_013328240.1	5313693	5315051	membrane protein OXA1L	25	0.993	0.005148463	17	0.722	0.004908737	15	0.712	0.004220994

rna4517	XM_013328185.1	5724518	5727850	uncharacterized LOC106129587	34	0.743	0.00451717	54	0.939	0.004745916	41	0.852	0.004393735
rna4405	XM_013328243.1	3002489	3003978	cytochrome c oxidase assembly protein COX16	27	0.712	0.006641446	19	0.83	0.005655548	23	0.85	0.004474807
rna4456	XM_013328325.1	4275218	4323747	homolog%2C mitochondrial RNA polymerase II	966	0.783	0.006161608	978	0.829	0.005349858	571	0.798	0.004598154
rna4396	XM_013328380.1	2593141	2603646	elongation factor ELL myelin expression factor 2- like%2C transcript variant X2	145	0.608	0.007917822	152	0.588	0.008019857	110	0.601	0.004679833
rna4321	XM_013328346.1	1399170	1408734	uncharacterized LOC106129698	161	0.71	0.006730182	160	0.689	0.006518281	85	0.622	0.004759801
rna4330	XM_013328241.1	1471195	1473165	syntaxin-18	30	0.758	0.007262027	33	0.697	0.008038343	18	0.688	0.004929163
rna4420	XM_013328361.1	3164948	3193977	unconventional myosin-IXa- like%2C transcript variant X1	579	0.756	0.005938819	548	0.797	0.005037003	496	0.774	0.005021211
rna4419	XM_013328362.1	3164948	3193977	unconventional myosin-IXa- like%2C transcript variant X2	579	0.756	0.005938819	548	0.797	0.005037003	496	0.774	0.005021211
rna4338	XM_013328278.1	1508705	1518258	GTPase HRas	131	0.659	0.006153678	126	0.693	0.006000635	100	0.672	0.005151254
rna4340	XM_013328422.1	1519937	1520766	dolichol-phosphate mannosyltransferase subunit 3%2C transcript variant X2	17	0.882	0.007364632	18	0.861	0.007774272	12	0.972	0.005275164
rna4454	XM_013328174.1	4268658	4270209	uncharacterized LOC106129578	43	0.922	0.007847321	45	0.918	0.0065733	41	0.852	0.005321223
rna4536	XM_013328244.1	6012409	6013623	uncharacterized protein C19orf52	20	0.737	0.004995216	31	0.891	0.007180479	19	0.792	0.005331318
rna4521	XM_013328393.1	5745189	5751175	gbkey=mRNA	85	0.62	0.005618301	85	0.623	0.005251222	94	0.693	0.005670913
rna4393	XM_013328382.1	2593138	2598806	myelin expression factor 2- like%2C transcript variant X4	79	0.626	0.008517212	81	0.592	0.008954112	65	0.617	0.005697184
rna4298	XM_013328239.1	880578	883070	protein bud22	49	0.868	0.005870367	49	0.893	0.005227974	44	0.878	0.005884998
rna4339	XM_013328421.1	1519661	1520744	dolichol-phosphate mannosyltransferase subunit 3%2C transcript variant X1	24	0.885	0.008233695	25	0.869	0.008556691	16	0.956	0.006077829
rna4378	XM_013328165.1	2399919	2400599	uncharacterized LOC106129569	13	0.921	0.007158843	15	0.938	0.007078859	11	0.927	0.006090894
rna4496	XM_013328333.1	5271861	5273537	neugrin	32	0.769	0.0075507	40	0.908	0.007070333	30	0.882	0.006332797
rna4380	XM_013328417.1	2410837	2412344	beta-ureidopropionase-like	25	0.854	0.005200978	29	0.936	0.005376323	23	0.885	0.006505778
rna4381	XM_013328418.1	2412449	2413979	eukaryotic translation initiation factor 2 subunit 2	19	0.673	0.004709099	25	0.943	0.004881273	23	0.94	0.006689415
rna4406	XM_013328367.1	3012239	3045757	tyrosine-protein kinase CSK%2C transcript variant X1	558	0.648	0.007588042	530	0.702	0.006464824	463	0.68	0.006805918
rna4385	XM_013328242.1	2425702	2429091	leucine-rich repeat protein 1	68	0.792	0.007598856	67	0.804	0.006949772	53	0.814	0.006885488
rna4392	XM_013328399.1	2587577	2592737	integrator complex subunit 3 homolog	84	0.716	0.008476183	90	0.864	0.007165859	88	0.719	0.007058129
rna4511	XM_013328182.1	5504764	5505982	lipase 1-like	17	0.587	0.007667123	31	0.974	0.009696404	27	0.996	0.007102324

rna4359	XM_013328358.1	1827009	1830838	vacuolar protein sorting-associated protein 33B%2C transcript variant X2	73	0.552	0.01019639	60	0.46	0.011606181	48	0.539	0.007282337
rna4360	XM_013328357.1	1827979	1830838	vacuolar protein sorting-associated protein 33B%2C transcript variant X1	73	0.74	0.01019639	60	0.616	0.011606181	48	0.722	0.007282337
rna4300	XM_013328258.1	887424	889772	ribose-phosphate pyrophosphokinase 2	42	0.755	0.007613161	43	0.858	0.006280155	43	0.883	0.007461008
rna4348	XM_013328291.1	1577783	1581428	BTB/POZ domain-containing protein 2-like%2C transcript variant X1	81	0.68	0.011976623	81	0.681	0.011489997	64	0.672	0.00752791
rna4407	XM_013328368.1	3019509	3045757	tyrosine-protein kinase CSK%2C transcript variant X2	492	0.681	0.008041054	472	0.742	0.006853115	415	0.723	0.007566126
rna4452	XM_013328198.1	4240437	4246388	extensin-like	260	0.789	0.015132831	260	0.809	0.013739108	178	0.84	0.007591015
rna4389	XM_013328350.1	2572396	2580080	gbkey=mRNA alpha-(1%2C3)-	148	0.667	0.00859795	151	0.665	0.008366142	130	0.68	0.007648406
rna4354	XM_013328201.1	1651101	1653941	fucosyltransferase C-like	98	0.778	0.012263638	106	0.841	0.013055453	63	0.659	0.007756923
rna4534	XM_013328246.1	6000856	6002196	uncharacterized LOC106129643	27	0.961	0.00609803	26	0.936	0.005062659	27	0.919	0.00785931
rna4493	XM_013328336.1	5236222	5238866	uncharacterized LOC106129692	67	0.783	0.008596993	71	0.952	0.008128525	65	0.846	0.007874551
rna4525	XM_013328271.1	5775698	5788089	uncharacterized LOC106129662%2C transcript variant X2	196	0.592	0.007924001	204	0.625	0.007401777	207	0.574	0.0080822
rna4526	XM_013328270.1	5775698	5786474	uncharacterized LOC106129662%2C transcript variant X1	196	0.681	0.007924001	204	0.719	0.007403688	207	0.659	0.0080822
rna4500	XM_013328224.1	5310573	5313063	U3 small nucleolar RNA-associated protein 15 homolog	52	0.679	0.009316192	75	0.933	0.008723168	45	0.729	0.00821631
rna4522	XM_013328200.1	5753445	5759187	uncharacterized LOC106129599	106	0.669	0.008081293	79	0.596	0.006874992	82	0.542	0.008634491
rna4281	XM_013328149.1	70277	73054	uncharacterized LOC106129551	70	0.949	0.006904584	76	0.979	0.007707778	78	0.967	0.00865995
rna4347	XM_013328292.1	1575910	1581428	BTB/POZ domain-containing protein 2-like%2C transcript variant X2	116	0.576	0.012664871	119	0.583	0.012238872	96	0.565	0.009015599
rna4507	XM_013328387.1	5479669	5483229	pancreatic lipase-related protein 2-like	112	0.858	0.010547971	129	0.906	0.011299822	95	0.929	0.009177413
rna4386	XM_013328214.1	2429317	2434186	G kinase-anchoring protein 1-like	132	0.752	0.012244815	128	0.73	0.011291087	95	0.724	0.009191826
rna4328	XM_013328196.1	1466142	1467679	RNA-binding protein NOB1	35	0.888	0.009440154	36	0.916	0.009234366	30	0.845	0.009248617
rna4343	XM_013328379.1	1553769	1557284	membrane-bound alkaline phosphatase-like	74	0.617	0.008592208	76	0.608	0.009571366	57	0.588	0.009338058
rna4403	XM_013328219.1	2977372	2991119	ADAM 17-like protease	242	0.457	0.011319361	219	0.5	0.008955323	195	0.512	0.009365391
rna4345	XM_013328290.1	1563041	1565652	membrane-bound alkaline phosphatase-like	66	0.873	0.009084757	62	0.892	0.007516861	55	0.755	0.010169592

rna4409	XM_013328206.1	3049409	3053897	DET1 homolog 28S ribosomal protein	92	0.804	0.0053506	79	0.875	0.003573386	82	0.766	0.010415605
rna4382	XM_013328215.1	2415442	2418993	S30%2C mitochondrial	129	0.852	0.013025224	125	0.84	0.012615374	99	0.787	0.010437139
rna4531	XM_013328415.1	5884495	5886643	40S ribosomal protein S15 A disintegrin and metalloproteinase with thrombospondin motifs 7- like	66	0.752	0.011841779	74	0.872	0.010363965	61	0.874	0.010457711
rna4387	XM_013328412.1	2436696	2532139	uncharacterized LOC106129588	2049	0.597	0.011803109	2047	0.617	0.011169004	1781	0.604	0.010484045
rna4529	XM_013328186.1	5830408	5878979	dual specificity mitogen- activated protein kinase kinase dSOR1	1115	0.587	0.010991996	1164	0.586	0.011132651	1045	0.581	0.011062135
rna4467	XM_013328376.1	4842481	4850978	putative nuclease HARBI1 uncharacterized LOC106129648	286	0.812	0.01048265	292	0.873	0.009530437	234	0.817	0.011341106
rna4352	XM_013328364.1	1632464	1635170	putative nuclease HARBI1 uncharacterized LOC106129648	75	0.743	0.01204676	91	0.762	0.012629692	65	0.685	0.011566315
rna4400	XM_013328253.1	2883596	2887227	LOC106129648	135	0.766	0.015635148	137	0.811	0.01543218	102	0.792	0.011600085
rna4329	XM_013328197.1	1467658	1470732	UPF0528 protein CG10038 uncharacterized LOC106129672	93	0.84	0.014087576	109	0.801	0.014739893	57	0.712	0.011617053
rna4461	XM_013328287.1	4473947	4534011	LOC106129672	2056	0.697	0.013389586	2151	0.729	0.012438962	1599	0.701	0.01164602
rna4509	XM_013328180.1	5490242	5493926	odorant receptor 4-like	163	0.842	0.015328105	149	0.796	0.014657463	135	0.875	0.011770148
rna4460	XM_013328288.1	4419275	4437090	protein giant-lens methyl-CpG-binding domain protein 3%2C transcript variant X1	483	0.573	0.013003857	487	0.576	0.012881567	421	0.594	0.012005888
rna4416	XM_013328281.1	3101631	3107700	methyl-CpG-binding domain protein 3%2C transcript variant X2	141	0.739	0.006844267	119	0.823	0.005241431	121	0.717	0.012030669
rna4415	XM_013328282.1	3101631	3107700	probable isocitrate dehydrogenase [NAD] subunit alpha%2C mitochondrial%2C transcript variant X3	141	0.739	0.006844267	119	0.823	0.005241431	121	0.717	0.012030669
rna4361	XM_013328345.1	1831183	1847961	tubulin polyglutamylase TTL13-like	432	0.581	0.01368344	454	0.619	0.013274785	387	0.614	0.012033377
rna4411	XM_013328168.1	3067370	3078948	probable isocitrate dehydrogenase [NAD] subunit alpha%2C mitochondrial%2C transcript variant X1	262	0.693	0.006962775	211	0.671	0.00557638	260	0.689	0.012051446
rna4362	XM_013328343.1	1831299	1847961	pancreatic lipase-related protein 2-like	430	0.579	0.013766682	453	0.617	0.013375931	385	0.611	0.012077437
rna4506	XM_013328203.1	5471655	5477166	membrane-bound alkaline phosphatase-like	123	0.432	0.016173196	137	0.444	0.017888798	111	0.46	0.012177467
rna4342	XM_013328158.1	1549021	1552044	putative odorant receptor 92a	95	0.765	0.011345937	99	0.908	0.009984343	97	0.943	0.012457168
rna4510	XM_013328181.1	5500322	5503424	putative odorant receptor 92a	191	0.872	0.023127907	184	0.869	0.021780068	144	0.864	0.012824788

rna4333	XM_013328427.1	1476505	1484339	glycosylated lysosomal membrane protein B-like%2C transcript variant X2	200	0.704	0.010096267	221	0.727	0.011198945	181	0.648	0.012865083
rna4332	XM_013328426.1	1476505	1484348	glycosylated lysosomal membrane protein B-like%2C transcript variant X1	201	0.704	0.010105206	221	0.727	0.011187163	182	0.648	0.012878185
rna4350	XM_013328300.1	1621486	1629660	monocarboxylate transporter 1-like%2C transcript variant X1	256	0.681	0.015368042	244	0.645	0.015738436	227	0.68	0.013095432
rna4537	XM_013328428.1	6014289	6025097	exception=annotated by transcript or proteomic data	315	0.696	0.011987582	321	0.726	0.011711206	328	0.71	0.013096788
rna4322	XM_013328354.1	1415367	1429459	zinc finger protein 135-like%2C transcript variant X2	453	0.594	0.018622603	476	0.59	0.018443142	267	0.517	0.013110547
rna4357	XM_013328161.1	1795791	1810707	uncharacterized LOC106129566	526	0.66	0.018768043	519	0.7	0.017989018	408	0.622	0.013126036
rna4476	XM_013328309.1	5164520	5213764	casein kinase I isoform gamma-3%2C transcript variant X6	1778	0.689	0.01438096	1813	0.728	0.014184591	1446	0.729	0.01322272
rna4477	XM_013328313.1	5164520	5213764	casein kinase I isoform gamma-3%2C transcript variant X9	1778	0.689	0.01438096	1813	0.728	0.014184591	1446	0.729	0.01322272
rna4482	XM_013328304.1	5164520	5213751	casein kinase I isoform gamma-3%2C transcript variant X2	1778	0.689	0.014386049	1813	0.728	0.014189739	1446	0.729	0.013227508
rna4481	XM_013328305.1	5164520	5213751	casein kinase I isoform gamma-3%2C transcript variant X3	1778	0.689	0.014386049	1813	0.728	0.014189739	1446	0.729	0.013227508
rna4480	XM_013328310.1	5164520	5213751	casein kinase I isoform gamma-3%2C transcript variant X7	1778	0.689	0.014386049	1813	0.728	0.014189739	1446	0.729	0.013227508
rna4479	XM_013328311.1	5164520	5213751	casein kinase I isoform gamma-3%2C transcript variant X8	1778	0.689	0.014386049	1813	0.728	0.014189739	1446	0.729	0.013227508
rna4478	XM_013328314.1	5164520	5213751	casein kinase I isoform gamma-3%2C transcript variant X10	1778	0.689	0.014386049	1813	0.728	0.014189739	1446	0.729	0.013227508
rna4485	XM_013328317.1	5164520	5213751	casein kinase I isoform gamma-3%2C transcript variant X13	1778	0.689	0.014386049	1813	0.728	0.014189739	1446	0.729	0.013227508
rna4486	XM_013328318.1	5164520	5213751	casein kinase I isoform gamma-3%2C transcript variant X14	1778	0.689	0.014386049	1813	0.728	0.014189739	1446	0.729	0.013227508
rna4484	XM_013328319.1	5164520	5213751	casein kinase I isoform gamma-3%2C transcript variant X15	1778	0.689	0.014386049	1813	0.728	0.014189739	1446	0.729	0.013227508
rna4483	XM_013328320.1	5164520	5213751	casein kinase I isoform gamma-3%2C transcript variant X16	1778	0.689	0.014386049	1813	0.728	0.014189739	1446	0.729	0.013227508
rna4487	XM_013328303.1	5164520	5213739	casein kinase I isoform gamma-3%2C transcript variant X1	1778	0.689	0.014391142	1813	0.728	0.014194494	1446	0.729	0.013231931



rna4488	XM_013328308.1	5164520	5213731	casein kinase I isoform gamma-3%2C transcript variant X5	1778	0.689	0.014394538	1813	0.727	0.014197666	1446	0.729	0.013234881
rna4363	XM_013328344.1	1831299	1842059	probable isocitrate dehydrogenase [NAD] subunit alpha%2C mitochondrial%2C transcript variant X2	354	0.66	0.01500007	366	0.705	0.014674234	315	0.7	0.013238679
rna4489	XM_013328315.1	5164520	5213712	casein kinase I isoform gamma-3%2C transcript variant X11	1778	0.689	0.014402613	1813	0.727	0.014205205	1446	0.729	0.013241893
rna4490	XM_013328307.1	5164520	5213697	casein kinase I isoform gamma-3%2C transcript variant X4	1778	0.688	0.014408993	1813	0.727	0.014211163	1446	0.729	0.013247434
rna4491	XM_013328316.1	5164520	5213680	casein kinase I isoform gamma-3%2C transcript variant X12	1778	0.688	0.014416232	1813	0.727	0.014217921	1446	0.729	0.013253719
rna4351	XM_013328301.1	1621486	1629516	monocarboxylate transporter 1-like%2C transcript variant X2	253	0.677	0.015556926	240	0.64	0.015965943	224	0.676	0.013263462
rna4397	XM_013328166.1	2628373	2634398	putative odorant receptor 85d	171	0.636	0.014448566	180	0.667	0.014342764	151	0.625	0.013279379
rna4402	XM_013328221.1	2922570	2976883	dynein heavy chain%2C cytoplasmic	1839	0.608	0.015209379	1734	0.624	0.013681591	1319	0.61	0.013491432
rna4417	XM_013328283.1	3128643	3157699	phospholipid-transporting ATPase ID	550	0.61	0.006533429	479	0.63	0.005536496	591	0.605	0.013728037
rna4367	XM_013328394.1	1871706	1877740	uncharacterized family 31 glucosidase KIAA1161-like%2C transcript variant X1	227	0.771	0.014574838	206	0.719	0.01482246	173	0.669	0.013877593
rna4366	XM_013328395.1	1871706	1878974	uncharacterized family 31 glucosidase KIAA1161-like%2C transcript variant X2	227	0.64	0.014574838	206	0.597	0.01482246	173	0.556	0.013877593
rna4369	XM_013328416.1	1888912	1894807	uncharacterized family 31 glucosidase KIAA1161-like	187	0.646	0.015901968	190	0.675	0.01622541	165	0.618	0.013886772
rna4516	XM_013328385.1	5717817	5721577	40S ribosomal protein S6 arginine-glutamic acid dipeptide repeats protein-like	141	0.808	0.016680076	126	0.747	0.015159258	119	0.771	0.013921093
rna4457	XM_013328363.1	4325443	4337300	chromatin assembly factor 1 subunit A	404	0.648	0.01402339	374	0.668	0.011080246	346	0.711	0.013923976
rna4466	XM_013328178.1	4834313	4841636	zinc finger protein 135-like%2C transcript variant X1	434	0.639	0.020277646	455	0.625	0.020355006	255	0.553	0.014106421
rna4323	XM_013328353.1	1417895	1429459	A-kinase anchor protein 17A%2C transcript variant X1	253	0.593	0.013673796	230	0.567	0.014024146	220	0.588	0.014323947
rna4320	XM_013328400.1	1384695	1394057	A-kinase anchor protein 17A%2C transcript variant X1	253	0.593	0.013673796	230	0.567	0.014024146	220	0.588	0.014323947
rna4319	XM_013328401.1	1384695	1394057	A-kinase anchor protein 17A%2C transcript variant X2	253	0.593	0.013673796	230	0.567	0.014024146	220	0.588	0.014323947

rna4318	XM_013328402.1	1384695	1394057	A-kinase anchor protein 17A%2C transcript variant X3	253	0.593	0.013673796	230	0.567	0.014024146	220	0.588	0.014323947
rna4317	XM_013328403.1	1384695	1394057	A-kinase anchor protein 17A%2C transcript variant X4	253	0.593	0.013673796	230	0.567	0.014024146	220	0.588	0.014323947
rna4316	XM_013328404.1	1384695	1394057	A-kinase anchor protein 17A%2C transcript variant X5	253	0.593	0.013673796	230	0.567	0.014024146	220	0.588	0.014323947
rna4515	XM_013328424.1	5705067	5712195	geranylgeranyl transferase type-1 subunit beta%2C transcript variant X1	319	0.777	0.019859861	354	0.801	0.020228957	302	0.816	0.014330747
rna4514	XM_013328425.1	5705067	5712195	geranylgeranyl transferase type-1 subunit beta%2C transcript variant X2	319	0.777	0.019859861	354	0.801	0.020228957	302	0.816	0.014330747
rna4341	XM_013328157.1	1524364	1540086	integral membrane protein DGCR2/IDD-like uncharacterized	500	0.627	0.016272457	506	0.645	0.015666339	380	0.617	0.014409885
rna4305	XM_013328265.1	917570	930179	LOC106129656	383	0.516	0.017309033	347	0.477	0.017272682	344	0.577	0.014794716
rna4356	XM_013328227.1	1667064	1770730	gonadotropin-releasing hormone II receptor-like probable ATP-dependent	2501	0.502	0.013139661	2641	0.517	0.013387471	2322	0.517	0.014889395
rna4326	XM_013328321.1	1449157	1465233	RNA helicase YTHDC2 ubiquitin-like modifier	395	0.492	0.017093656	402	0.486	0.016996883	324	0.51	0.015137028
rna4518	XM_013328199.1	5731508	5738487	activating enzyme ATG7	341	0.744	0.018723624	391	0.784	0.020415932	323	0.786	0.015780398
rna4399	XM_013328195.1	2740022	2773970	hemacentin-2-like regulator of nonsense transcripts 1 homolog	1411	0.7	0.018305714	1269	0.711	0.01579168	1105	0.681	0.015959163
rna4388	XM_013328405.1	2562109	2571267	transcripts 1 homolog	260	0.623	0.01448283	234	0.63	0.011783985	212	0.593	0.016005798
rna4375	XM_013328207.1	2213901	2250952	cell adhesion molecule 3-like lon protease homolog%2C mitochondrial%2C transcript variant X1	1117	0.553	0.017373042	1189	0.582	0.017199421	1037	0.565	0.016310751
rna4335	XM_013328275.1	1490555	1505353	lon protease homolog%2C mitochondrial%2C transcript variant X2	441	0.495	0.019835248	460	0.506	0.018761867	353	0.514	0.016329611
rna4336	XM_013328276.1	1490555	1505353	synaptic vesicle glycoprotein 2C-like%2C transcript variant X1	1090	0.654	0.016902493	1121	0.652	0.01678627	1069	0.663	0.016341617
rna4364	XM_013328430.1	1849499	1858817	nucleolar protein 6 39S ribosomal protein L2%2C mitochondrial%2C transcript variant X2	387	0.631	0.01841051	373	0.676	0.017427999	315	0.666	0.016504625
rna4519	XM_013328211.1	5739062	5743761	elongation factor Tu GTP- binding domain-containing protein 1	144	0.41	0.023212282	155	0.473	0.023363934	123	0.462	0.01668886
rna4462	XM_013328175.1	4535269	4543692	katanin p60 ATPase- containing subunit A-like 2	296	0.568	0.017343452	274	0.57	0.015638323	301	0.665	0.016740826
rna4346	XM_013328159.1	1568083	1573750	containing subunit A-like 2	253	0.786	0.017294694	244	0.793	0.015920924	229	0.799	0.016830798

rna4520	XM_013328210.1	5739062	5742744	39S ribosomal protein L2%2C mitochondrial%2C transcript variant X1 uncharacterized	138	0.493	0.02372714	148	0.568	0.023889944	119	0.568	0.016839515
rna4465	XM_013328384.1	4817352	4831584	LOC106129727 uncharacterized	595	0.638	0.018827495	612	0.672	0.017066858	481	0.619	0.016952938
rna4311	XM_013328154.1	1063427	1075258	LOC106129557 uncharacterized	549	0.639	0.021962126	500	0.634	0.020626919	461	0.699	0.016967
rna4474	XM_013328347.1	5144998	5163317	LOC106129699%2C transcript variant X1 uncharacterized	851	0.696	0.018764671	789	0.691	0.017536698	694	0.709	0.017073215
rna4475	XM_013328349.1	5145472	5163317	LOC106129699%2C transcript variant X2 uncharacterized	839	0.688	0.019198705	776	0.686	0.017860861	685	0.701	0.017474922
rna4289	XM_013328208.1	507747	509855	LOC106129607	108	0.786	0.019687015	90	0.794	0.017459236	108	0.843	0.017548592
rna4463	XM_013328176.1	4664744	4714572	hemiceitin-2-like uncharacterized protein	2152	0.606	0.020292481	2118	0.62	0.018615133	1829	0.63	0.017549343
rna4458	XM_013328284.1	4354138	4400298	YHR080C-like%2C transcript variant X1	1614	0.56	0.016665457	1534	0.571	0.013892726	1408	0.586	0.017572023
rna4358	XM_013328356.1	1811917	1826990	phosphatidylinositol 3-kinase catalytic subunit type 3	608	0.589	0.022799511	628	0.608	0.022059835	474	0.564	0.017755397
rna4470	XM_013328294.1	4961729	5141211	furin-like protease 1%2C isoform 1-CRR%2C transcript variant X1	6652	0.56	0.018331297	6785	0.572	0.018259894	5726	0.587	0.01777704
rna4471	XM_013328295.1	4961729	5141211	furin-like protease 1%2C isoform 1-CRR%2C transcript variant X2	6652	0.56	0.018331297	6785	0.572	0.018259894	5726	0.587	0.01777704
rna4468	XM_013328297.1	4961729	5141211	furin-like protease 1%2C isoform 1-CRR%2C transcript variant X4	6652	0.56	0.018331297	6785	0.572	0.018259894	5726	0.587	0.01777704
rna4469	XM_013328299.1	4961729	5141211	furin-like protease 1%2C isoform 1-CRR%2C transcript variant X6	6652	0.56	0.018331297	6785	0.572	0.018259894	5726	0.587	0.01777704
rna4353	XM_013328365.1	1635267	1650031	AP-3 complex subunit beta-2	497	0.482	0.019673635	517	0.493	0.019788226	408	0.484	0.01778626
rna4473	XM_013328296.1	4961729	5139591	furin-like protease 1%2C isoform 1-CRR%2C transcript variant X3	6605	0.558	0.018454357	6735	0.57	0.018383854	5691	0.585	0.017901082
rna4472	XM_013328298.1	4961729	5139591	furin-like protease 1%2C isoform 1-CRR%2C transcript variant X5	6605	0.558	0.018454357	6735	0.57	0.018383854	5691	0.585	0.017901082
rna4334	XM_013328156.1	1485721	1490391	probable tRNA (guanine(26)-N(2))-dimethyltransferase uncharacterized protein	215	0.821	0.018499936	223	0.84	0.017830596	172	0.79	0.017903263
rna4459	XM_013328286.1	4367881	4400298	YHR080C-like%2C transcript variant X2	1022	0.514	0.01637634	992	0.521	0.014090233	924	0.538	0.017914521
rna4379	XM_013328205.1	2401400	2408494	microfibrillar-associated protein 1	217	0.598	0.01490628	209	0.613	0.013053112	195	0.579	0.017974082

rna4528	XM_013328274.1	5788149	5807240	synaptic vesicle glycoprotein 2C-like%2C transcript variant X2	781	0.667	0.018624867	796	0.654	0.018646787	777	0.679	0.017990336
rna4494	XM_013328340.1	5239658	5249675	alpha-tocopherol transfer protein-like	543	0.667	0.024193356	535	0.671	0.023512712	475	0.728	0.017992505
rna4377	XM_013328202.1	2397004	2399474	acyl-CoA Delta(11) desaturase-like	95	0.807	0.013121725	91	0.826	0.012078733	105	0.853	0.018038584
rna4370	XM_013328371.1	1915714	1997644	gonadotropin-releasing hormone receptor%2C transcript variant X1	3020	0.565	0.017658915	3207	0.582	0.018459627	2565	0.538	0.018231373
rna4371	XM_013328372.1	1915714	1997644	gonadotropin-releasing hormone receptor%2C transcript variant X2	3020	0.565	0.017658915	3207	0.582	0.018459627	2565	0.538	0.018231373
rna4297	XM_013328212.1	878042	880103	60S ribosomal protein L36 odorant receptor 46a%2C isoform A-like	74	0.586	0.017021303	66	0.605	0.014981928	98	0.756	0.018501056
rna4398	XM_013328251.1	2650908	2658501	zinc metalloproteinase nas-26-like	374	0.816	0.017949239	348	0.817	0.015522419	310	0.798	0.018573135
rna4513	XM_013328183.1	5584108	5587497	uncharacterized LOC106129558	170	0.727	0.020259458	191	0.693	0.022580203	156	0.725	0.018650785
rna4313	XM_013328155.1	1323121	1327462	uncharacterized LOC106129558	271	0.757	0.027620403	255	0.767	0.02655026	160	0.666	0.018674776
rna4283	XM_013328150.1	117071	202199	COUP transcription factor 2 ejaculatory bulb-specific protein 3-like%2C transcript variant X1	3901	0.639	0.020747332	3839	0.644	0.020308331	3463	0.656	0.018676525
rna4524	XM_013328407.1	5764182	5774900	ras-specific guanine nucleotide-releasing factor 2-like	424	0.663	0.017350391	448	0.695	0.016681601	457	0.695	0.018691693
rna4349	XM_013328160.1	1589746	1617720	histone H4 transcription factor%2C transcript variant X1	1042	0.63	0.018533524	1086	0.664	0.016560191	874	0.629	0.018795288
rna4299	XM_013328256.1	886270	900020	membrane-bound alkaline phosphatase-like	577	0.604	0.020228768	579	0.659	0.018517783	538	0.662	0.018815606
rna4344	XM_013328396.1	1559700	1562822	ejaculatory bulb-specific protein 3-like%2C transcript variant X2	138	0.786	0.021208463	136	0.814	0.019345777	129	0.795	0.019003645
rna4523	XM_013328408.1	5763005	5774900	ejaculatory bulb-specific protein 3-like%2C transcript variant X2	482	0.667	0.017765032	494	0.693	0.016863614	521	0.702	0.019232355
rna4324	XM_013328355.1	1429485	1433468	D-amino-acid oxidase	180	0.769	0.022401047	171	0.748	0.021670132	150	0.721	0.019578476
rna4512	XM_013328245.1	5523782	5567906	lachesin-like tyrosine-protein phosphatase non-receptor type 9-like	1999	0.614	0.022743925	2034	0.622	0.022294619	1683	0.619	0.019783072
rna4533	XM_013328302.1	5936832	5986228	uncharacterized family 31 phosphatase non-receptor type 9-like	1915	0.593	0.018338658	1984	0.597	0.019156148	1753	0.582	0.020455713
rna4365	XM_013328213.1	1859120	1867969	glucosidase KIAA1161-like	333	0.553	0.01865628	301	0.504	0.018463486	278	0.574	0.020574957
rna4325	XM_013328323.1	1434200	1447798	TFIIH basal transcription factor complex helicase XPD subunit	470	0.483	0.023278871	455	0.464	0.023244102	403	0.505	0.020644034
rna4312	XM_013328390.1	1276242	1283154	collagenase-like	281	0.542	0.023178141	278	0.537	0.023880987	249	0.578	0.020653982

rna4355	XM_013328209.1	1658562	1661332	gbkey=mRNA uncharacterized family 31	132	0.851	0.016475081	118	0.766	0.016984606	109	0.725	0.02076845
rna4368	XM_013328190.1	1881341	1887617	glucosidase KIAA1161-like	271	0.578	0.019633061	263	0.578	0.019645999	252	0.593	0.020841519
rna4314	XM_013328230.1	1353928	1366053	cytochrome P450 6B2-like survival motor neuron protein%2C transcript variant X1	506	0.545	0.025493476	436	0.532	0.021572619	386	0.52	0.020849574
rna4307	XM_013328263.1	932579	937549	survival motor neuron protein%2C transcript variant X2	268	0.717	0.023064884	286	0.677	0.024100881	210	0.621	0.021044792
rna4306	XM_013328264.1	932579	937549	uncharacterized LOC106129749	268	0.717	0.023064884	286	0.677	0.024100881	210	0.621	0.021044792
rna4308	XM_013328413.1	938212	946286	alpha-tocopherol transfer protein-like	448	0.713	0.023860812	489	0.762	0.024650573	347	0.713	0.021213124
rna4495	XM_013328337.1	5249756	5270691	bumetanide-sensitive sodium-(potassium)-chloride cotransporter	1070	0.64	0.023430361	1089	0.665	0.021801526	932	0.655	0.021302354
rna4532	XM_013328391.1	5891606	5936552	DENN domain-containing protein 4C%2C transcript variant X1	1427	0.474	0.021341498	1417	0.459	0.021724603	1381	0.472	0.021385654
rna4499	XM_013328329.1	5273552	5310024	DENN domain-containing protein 4C%2C transcript variant X2	1542	0.563	0.022557767	1455	0.543	0.021318098	1466	0.579	0.0219706
rna4497	XM_013328330.1	5273552	5310024	DENN domain-containing protein 4C%2C transcript variant X3	1542	0.563	0.022557767	1455	0.543	0.021318098	1466	0.579	0.0219706
rna4498	XM_013328332.1	5273552	5310024	uncharacterized LOC106129649	1542	0.563	0.022557767	1455	0.543	0.021318098	1466	0.579	0.0219706
rna4401	XM_013328254.1	2892093	2895881	uncharacterized LOC106129650	177	0.741	0.018112111	173	0.774	0.01880833	148	0.73	0.02242318
rna4286	XM_013328255.1	296812	298122	organic cation transporter protein-like	75	0.73	0.024917858	71	0.683	0.026239023	60	0.686	0.023446898
rna4292	XM_013328420.1	782839	797582	organic cation transporter protein-like%2C transcript variant X1	940	0.76	0.024639982	874	0.727	0.024891206	791	0.746	0.023580162
rna4295	XM_013328191.1	851105	875577	organic cation transporter protein-like%2C transcript variant X2	1225	0.591	0.024989271	1111	0.58	0.023653437	1056	0.607	0.023840622
rna4296	XM_013328194.1	852790	875577	histone H4 transcription factor%2C transcript variant X2	1131	0.579	0.024994831	1019	0.567	0.023516426	975	0.595	0.023936719
rna4301	XM_013328257.1	892898	900020	peptidyl-prolyl cis-trans isomerase G	437	0.702	0.026294065	427	0.694	0.026057796	405	0.716	0.024658554
rna4464	XM_013328383.1	4810659	4814482	pancreatic lipase-related protein 2-like	204	0.703	0.022109041	215	0.754	0.021423466	147	0.554	0.024671476
rna4504	XM_013328334.1	5452362	5457029	pancreatic lipase-related protein 2-like	314	0.79	0.023964422	329	0.781	0.024215162	275	0.771	0.025397708
rna4502	XM_013328397.1	5438263	5441330	pancreatic lipase-related protein 2-like	178	0.691	0.028531789	175	0.694	0.02718466	160	0.666	0.025959637

rna4293	XM_013328374.1	808877	830079	organic cation transporter protein-like%2C transcript variant X1	1004	0.551	0.026870029	967	0.537	0.025994914	886	0.537	0.026360269
rna4291	XM_013328431.1	633693	760199	lachesin-like	5027	0.438	0.026772375	4845	0.431	0.026513013	4484	0.433	0.026460228
rna4503	XM_013328179.1	5446800	5451715	pancreatic lipase-related protein 2-like	299	0.699	0.030131834	314	0.727	0.03010721	296	0.736	0.026774886
rna4287	XM_013328252.1	328410	329562	uncharacterized LOC106129647	69	0.635	0.030412102	66	0.547	0.03066087	67	0.714	0.026841506
rna4294	XM_013328375.1	808877	828008	organic cation transporter protein-like%2C transcript variant X2	855	0.518	0.027457545	839	0.508	0.02640907	759	0.5	0.026858788
rna4280	XM_013328223.1	37998	40521	proteasome subunit beta type-3	166	0.697	0.030671404	145	0.657	0.028231876	161	0.736	0.027159099
rna4290	XM_013328153.1	518291	555617	limbic system-associated membrane protein-like	2167	0.628	0.027881285	2052	0.605	0.02781822	2100	0.633	0.027433434
rna4410	XM_013328222.1	3055117	3067241	cyclin-dependent kinase 7	123	0.462	0.004064722	90	0.451	0.003204948	122	0.388	na
rna4278	XM_013328389.1	2546	14627	gbkey=mRNA uncharacterized	119	0.179	na	95	0.153	na	161	0.285	na
rna4284	XM_013328151.1	264305	268869	LOC106129553	48	0.207	na	54	0.212	na	74	0.229	na
rna4285	XM_013328289.1	269265	295932	mediator of DNA damage checkpoint protein 1-like uncharacterized	645	0.347	na	596	0.355	na	635	0.396	na
rna4288	XM_013328152.1	348091	349107	LOC106129555	0	0	na	0	0	na	0	0	na
rna4304	XM_013328259.1	900124	912396	spermine oxidase-like%2C transcript variant X1	208	0.223	na	191	0.207	na	199	0.229	na
rna4302	XM_013328261.1	900124	920223	spermine oxidase-like%2C transcript variant X2	522	0.388	na	487	0.371	na	442	0.396	na
rna4303	XM_013328262.1	900124	913399	spermine oxidase-like%2C transcript variant X3 uncharacterized	208	0.206	na	191	0.191	na	199	0.212	na
rna4309	XM_013328218.1	949659	955857	LOC106129616	25	0.042	na	21	0.058	na	26	0.061	na
rna4315	XM_013328406.1	1367764	1382026	chymotrypsin BII-like uncharacterized	288	0.246	na	237	0.219	na	198	0.219	na
rna4327	XM_013328324.1	1462726	1464554	LOC106129685 uncharacterized	3	0.04	na	5	0.021	na	0	0	na
rna4373	XM_013328373.1	1953448	1954299	LOC106129718 uncharacterized	0	0	na	0	0	na	0	0	na
rna4374	XM_013328162.1	2097656	2098856	LOC106129567 uncharacterized	13	0.06	na	13	0.062	na	14	0.062	na
rna4376	XM_013328164.1	2257330	2262771	LOC106129568	12	0.071	na	13	0.064	na	7	0.044	na
rna4404	XM_013328220.1	2996162	2999913	polyubiquitin-B	58	0.353	na	56	0.37	na	49	0.369	na
rna4412	XM_013328359.1	3079983	3096923	ubiquilin-1-like uncharacterized	132	0.243	na	133	0.259	na	156	0.245	na
rna4435	XM_013328268.1	3476653	3481076	LOC106129658	0	0.009	na	0	0.004	na	0	0.009	na

rna4437	XM_013328266.1	3479317	3481542	uncharacterized LOC106129657%2C transcript variant X1 uncharacterized LOC106129657%2C	0	0	na	0	0	na	0	0	na
rna4436	XM_013328267.1	3479317	3481542	transcript variant X2 uncharacterized LOC106129657%2C	0	0	na	0	0	na	0	0	na
rna4492	XM_013328338.1	5215501	5234703	alpha-tocopherol transfer protein-like	558	0.365	na	593	0.387	na	400	0.356	na
rna4505	XM_013328335.1	5457125	5461303	pancreatic lipase-related protein 2-like	91	0.351	na	93	0.343	na	84	0.369	na

**Table S3.** Scanning of single point mutations relative to reference genome or major allele in the hard sweep region in scaffold NW\_013535362.1 in *A. transitella*

Scaffold	start	end	strand	functional_annotation(NCBI)	Transcript_ID	point mutations or deletions in coding regions
NW_013535362.1	3164948	3193977	-	unconventional myosin-I $\alpha$ -like	XM_013328361.1	polymorphisms end here, R is identical to SPIRL at both ends.
NW_013535362.1	3197609	3199024	-	Krüppel-like factor 9	XM_013328247.1	3 non-silent point mutations
NW_013535362.1	3204704	3279423	-	protein groucho	XM_013328326.1	-----
NW_013535362.1	3304902	3307354	+	phosphomevalonate kinase	XM_013328229.1	E127N (conservative mutation)
NW_013535362.1	3344559	3370779	+	sodium channel protein para	XM_013328249.1	L934F (kdr mutation)
NW_013535362.1	3387986	3396394	-	CYP6B54 and CYP6B55	XM_013328169.1	none
NW_013535362.1	3399243	3401314	-	CYP6B56	XM_013328369.1	none
NW_013535362.1	3403909	3420607	-	protein ariadne-1	XM_013328341.1	none
NW_013535362.1	3421473	3423241	-	uncharacterized LOC106129721	XM_013328377.1	none
NW_013535362.1	3423369	3430390	+	isoleucine--tRNA ligase	XM_013328378.1	none
NW_013535362.1	3433176	3489393	-	dmX-like protein 2	XM_013328269.1	none
NW_013535362.1	3476653	3481076	+	uncharacterized LOC106129658	XM_013328268.1	none
NW_013535362.1	3479317	3481542	-	uncharacterized LOC106129657	XM_013328266.1	none
NW_013535362.1	3490744	3524106	+	endophilin-A	XM_013328231.1	none
NW_013535362.1	3525167	3528547	-	polyubiquitin-C	XM_013328234.1	Q13H (conservative mutation)
NW_013535362.1	3529722	3548710	+	ras GTPase-activating protein 1	XM_013328235.1	none
NW_013535362.1	3549071	3550177	-	protein kish-A	XM_013328236.1	none
NW_013535362.1	3550487	3554188	+	prenyltransferase alpha subunit	XM_013328238.1	none
NW_013535362.1	3584697	3630468	+	uncharacterized LOC106129575	XM_013328171.1	1 alternative start codon (ATG->GTC segregating in 20% of ALM and 20% FIG)
NW_013535362.1	3631722	3638019	-	uncharacterized LOC106129590	XM_013328188.1	none
NW_013535362.1	3745239	3796518	+	protein unc-13 homolog A	XM_013328187.1	none
NW_013535362.1	3800374	3817393	+	actin-binding Rho-activating protein	XM_013328228.1	none
NW_013535362.1	3826528	3849030	-	gonadotropin-releasing hormone II	XM_013328172.1	none
NW_013535362.1	3852565	4034421	-	small conductance calcium-activated	XM_013328189.1	all silent mutations



**Table S4.** Twenty most differentiated SNPs between the reference genome (SPIRL-1966), ALM, FIG and R using Mahalanobis distances (PCAdapt, 1.1, Luu et al., 2017). **pos**: position along scaffold, **rc**: reference character, **allele count**: number of alleles found in all populations; **allele states**: allele characters in all populations (sorted by counts in all populations); **del sum**: sum of deletions in all populations (should be zero, if not the position may not be reliable); **snp type**: SNP type: “pop” a SNP within or between the populations; “rc” a SNP between the reference sequence character and the consensus of at least one population; “rc|pop” both; **major alleles**: most frequent allele in all populations [ALM FIG R]; **minor alleles**: second most frequent allele in all populations [ALM FIG R]

Scaffold#	pos	Ref	allele count	allele states	SNP type	major alleles (maa)	minor alleles (mia)	FDR pval.	gene model functional annotation
NW_013535379.1	775604	A	3	A/C/G	pop	AAA	CCC	0.01859	inter-genic, nearby CYP341 cluster of P450s
NW_013535334.1	84304	G	3	G/T/A	pop	GGG	TTT	0.01970	zinc finger 224-like
NW_013535359.1	304369	A	2	A/T	pop	AAA	TTT	0.01970	inter-genic
NW_013535509.1	95606	C	2	C/A	rc pop	ACC	CAA	0.01970	inter-genic just upstream of Ecdisteroid Kinase cluster
NW_013535530.1	170651	T	2	T/C	pop	TTT	CCC	0.01970	inter-genic
NW_013535492.1	2659949	T	3	A/G/T	rc pop	AAA	TGG	0.03339	intronic mannose-1-phosphate guanyltransferase alpha
NW_013535509.1	185180	T	2	T/A	rc pop	TTA	AAT	0.03339	intergenic in Ecdysteroid kinase gene cluster
NW_013535854.1	148606	C	2	C/T	pop	CCC	TTT	0.03339	intergenic, just downstream of sorting nexin-2
NW_013535700.1	310754	A	2	A/G	pop	AAA	GGG	0.04845	intergenic, just downstream of protein king tubby
NW_013535323.1	5604262	T	2	T/G	pop	TTT	GGG	0.05023	intergenic
NW_013535492.1	2832430	G	2	G/C	rc pop	GCG	CGC	0.05023	intronic protein CIP2A homolog
NW_013535386.1	3083373	G	2	G/A	pop	GGG	AAA	0.05948	intronic teneurin-3 (downstream of CYP4G cluster)
NW_013535423.1	1590364	A	2	A/C	pop	AAA	CCC	0.05948	intronic neuropeptide F-like
NW_013535319.1	2357306	G	2	G/A	pop	GGG	AAA	0.06952	intronic nuclear migration protein nudC
NW_013535323.1	7237902	T	2	T/A	pop	TTT	AAA	0.06952	intergenic
NW_013535332.1	4322388	A	2	A/T	pop	AAA	TTT	0.06952	intronic protein yellow-like
NW_013535362.1	4099150	T	2	T/C	rc pop	CCT	TTC	0.06952	at intron-exon boundary uncharacterized LOC10612973
NW_013535378.1	1393893	T	2	T/C	pop	TTT	CCC	0.06952	intergenic
NW_013535378.1	874667	T	2	T/C	pop	TTT	CCC	0.06952	intergenic

**Table S5.** Gene expression data in transcripts per million mapped reads (TMM) from *A. transitella* midgut tissue of the susceptible (ALM) and resistant (R347) strains. Caterpillars used in this study were fed on standard diets (C) or diets containing bifenthrin (B). (Demkovich et al., 2019). The data is part of a full transcriptome dataset (NCBI SRA PRJNA548705)

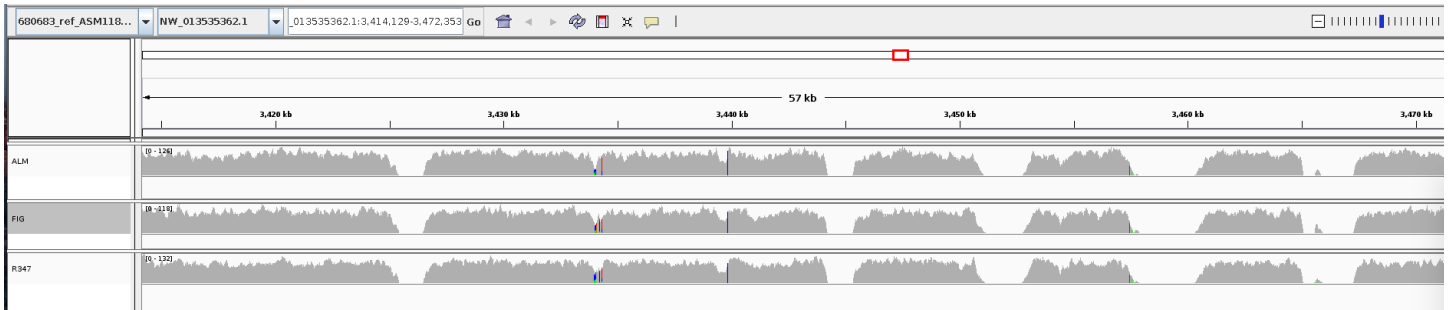
SCAFFOLD	START	END	STRAND	GENE_ID	RNA_id	ALM_B1	ALM_B2	ALM_B3	ALM_C1	ALM_C2	ALM_C3	R_B1	R_B2	R_B3	R_C1	R_C2	R_C3	functional annotation
NW_013535362.1	2922570	2976883	+	gene3366	rna4402	21.198	19.644	19.95	26.068	22.939	20.169	24.703	25.524	24.073	22.457	23.891	19.972	dynein heavy chain, cytoplasmic (LOC106129619), mRNA
NW_013535362.1	2977372	2991119	-	gene3367	rna4403	13.341	11.162	12.851	13.071	11.069	11.717	14.156	12.192	15.585	15.498	11.538	11.719	ADAM 17-like protease (LOC106129617), mRNA
NW_013535362.1	2996162	2999913	-	gene3368	rna4404	1157.374	1170.911	1380.37	845.41	947.265	963.473	773.743	928.322	926.916	941.836	800.146	925.398	polyubiquitin-B (LOC106129618), mRNA
NW_013535362.1	3002489	3003978	-	gene3369	rna4405	61.76	62.52	65.665	67.124	56.987	60.824	59.531	42.463	44.688	52.877	59.556	46.742	cytochrome c oxidase assembly protein COX16 homolog, mitochondrial (LOC106129616), mRNA
NW_013535362.1	3012239	3045757	+	gene3370	rna4407	13.136	12.626	13.481	13.886	11.999	10.649	11.114	11.578	14.678	10.127	9.376	11.568	tyrosine-protein kinase CSK (LOC106129714), transcript variant X2, mRNA
NW_013535362.1	3044389	3048122	-	gene3371	rna4408	0	0	0	0	0	0.37	0	0	0	0	0	0	uncharacterized LOC106129572 (LOC106129572), mRNA
NW_013535362.1	3049409	3053897	-	gene3372	rna4409	5.537	4.442	5.773	4.339	4.65	4.19	4.506	5.388	5.05	4.346	5.297	4.265	DET1 homolog (LOC106129605), mRNA
NW_013535362.1	3055117	3067241	+	gene3373	rna4410	3.627	3.144	4.009	3.556	4.74	4.036	2.949	2.752	3.337	2.489	2.447	2.781	cyclin-dependent kinase 7 (LOC106129620), mRNA
NW_013535362.1	3067370	3078948	-	gene3374	rna4411	0.076	0.031	0.064	0	0	0.062	0.33	0.472	1.23	0.536	1.523	0.942	tubulin polyglutamylase TTL13-like (LOC106129573), mRNA
NW_013535362.1	3079983	3096923	+	gene3375	rna4412	60.637	59.129	64.392	68.098	61.366	54.961	52.067	50.746	54.98	51.307	57.925	60.033	ubiquitin-1-like (LOC106129708), mRNA
NW_013535362.1	3097871	3099727	+	gene3376	rna4413	2.569	2.7	1.828	2.572	3.09	2.66	4.516	3.304	5.292	2.91	2.938	2.63	GPI mannosyltransferase 2 (LOC106129667), transcript variant X2, mRNA
NW_013535362.1	3101631	3107700	-	gene3377	rna4415	18.759	19.129	29.187	18.384	21.319	21.093	19.074	25.043	23.569	24.917	21.395	22.984	methyl-CpG-binding domain protein 3 (LOC106129668), transcript variant X1, mRNA
NW_013535362.1	3128643	3157699	+	gene3378	rna4417	12.671	14.697	11.653	11.261	13.809	14.777	13.414	13.786	14.214	9.055	10.408	9.515	phospholipid-transporting ATPase ID (LOC106129670), mRNA
NW_013535362.1	3159383	3164900	+	gene3379	rna4418	4.879	5.679	4.116	4.668	4.8	5.833	5.805	4.791	5.171	4.987	4.59	4.14	uncharacterized LOC106129757 (LOC106129757), mRNA
NW_013535362.1	3164948	3193977	-	gene3380	rna4420	7.599	6.988	7.633	8.594	8.2	7.425	8.558	9.316	10.232	9.046	7.558	9.471	unconventional myosin-IXa-like (LOC106129709), transcript variant X1, mRNA
NW_013535362.1	3197609	3199024	-	gene3381	rna4421	0.086	0.165	0.086	0.286	0	0	0	0	0	0.392	0	0	Krueppel-like factor 9 (LOC106129644), mRNA
NW_013535362.1	3204704	3279423	-	gene3382	rna4423	35.661	41.639	41.396	36.092	43.048	39.023	30.405	30.164	32.279	38.222	37.454	41.366	protein groucho (LOC106129687), transcript variant X3, mRNA
NW_013535362.1	3304902	3307354	+	gene3383	rna4425	14.118	14.038	15.107	15.887	10.959	14.161	7.568	8.265	7.651	9.544	10.732	14.482	phosphomevalonate kinase (LOC106129627), mRNA
NW_013535362.1	3344559	3370779	+	gene3384	rna4427	0.054	0.072	0.16	0.042	0.13	0.072	0.237	0.196	0.151	0.278	0.128	0.4	sodium channel protein para (LOC106129645), transcript variant X2, mRNA
NW_013535362.1	3387986	3396394	-	gene3385	rna4428	635.126	942.27	790.564	741.602	963.904	1225.47	987.206	819.697	606.378	1120.149	1189.944	1363.85	cytochrome P450 CYP6B54-55
NW_013535362.1	3399243	3401314	-	gene3386	rna4429	1485.169	1056.611	1154.414	1002.488	692.72	1343.165	1244.519	1269.88	1720.282	931.067	635.679	984.551	cytochrome P450 CYP6B56
NW_013535362.1	3403909	3420607	-	gene3387	rna4430	32.272	29.92	32.554	35.404	32.358	33.015	36.478	32.925	35.948	40.979	39.842	43.135	protein ariadne-1 (LOC106129696), transcript variant X1, mRNA
NW_013535362.1	3421473	3423241	-	gene3388	rna4432	34.409	35.661	40.295	30.778	31.048	36.548	29.446	30.565	33.74	33.809	29.503	32.846	uncharacterized LOC106129721 (LOC106129721), mRNA
NW_013535362.1	3423369	3430390	+	gene3389	rna4433	39.007	40.381	36.692	47.057	44.187	52.414	42.324	35.294	41.553	33.915	38.456	27.667	isoleucine--tRNA ligase, cytoplasmic (LOC106129722), mRNA
NW_013535362.1	3433176	3489393	-	gene3390	rna4434	16.255	14.924	16.593	17.178	17.539	14.202	16.527	20.43	20.736	22.658	19.41	23.437	dmX-like protein 2 (LOC106129661), mRNA
NW_013535362.1	3476653	3481076	+	gene3391	rna4435	9.962	0	7.11	0	0	2.773	0	0	0.628	0	0	0	uncharacterized LOC106129658 (LOC106129658), mRNA
NW_013535362.1	3479317	3481542	-	gene3392	rna4437	0	0	0	0	0.49	0	0	0	0	0	0	0	uncharacterized LOC106129657 (LOC106129657), transcript variant X1, mRNA
NW_013535362.1	3490744	3524106	+	gene3393	rna4438	20.756	20.469	28.192	19.475	20.209	19.296	21.487	24.981	30.474	21.538	22.525	34.055	endophilin-A (LOC106129629), transcript variant X1, mRNA
NW_013535362.1	3525167	3528547	-	gene3394	rna4441	766.298	1001.831	1068.671	755.594	739.317	803.993	906.168	974.517	878.216	1018.051	918.148	1123.07	polyubiquitin-C (LOC106129631), mRNA
NW_013535362.1	3529722	3548710	+	gene3395	rna4442	23.195	26.457	27.562	17.961	17.259	17.037	22.373	28.365	22.712	27.626	22.093	36.356	ras GTPase-activating protein 1 (LOC106129632), mRNA
NW_013535362.1	3549071	3550177	-	gene3396	rna4443	52.758	53.481	48.313	56.857	55.657	56.501	41.87	43.461	24.647	50.034	55.438	42.593	protein kish-A (LOC106129633), mRNA
NW_013535362.1	3550487	3554188	+	gene3397	rna4444	9.66	7.792	8.852	7.864	7.36	7.876	7.815	8.71	7.742	9.4	6.565	9.373	protein prenyltransferase alpha subunit repeat-containing protein 1 (LOC106129634), mRNA
NW_013535362.1	3584697	3630468	+	gene3398	rna4445	0.151	0.278	0.15	0.191	0.31	0.175	0.32	0.338	0.343	0.211	0.128	0.24	uncharacterized LOC106129575 (LOC106129575), mRNA
NW_013535362.1	3631722	3638019	-	gene3399	rna4446	1.23	0.258	0.631	0	0.23	0	0	0.338	2.046	0.364	0	0.586	uncharacterized LOC106129590 (LOC106129590), mRNA
NW_013535362.1	3745239	3796518	+	gene3400	rna4447	0.173	0.227	0.192	0.191	0.34	0.246	0.33	0.249	0.393	0.163	0.216	0.373	protein unc-13 homolog A (LOC106129589), mRNA
NW_013535362.1	3800374	3817393	+	gene3401	rna4448	0.572	1.68	1.967	2.413	1.69	1.89	2.175	1.648	0.938	1.254	2.29	2.754	actin-binding Rho-activating protein-like (LOC106129626), mRNA
NW_013535362.1	3826528	3849030	-	gene3402	rna4449	0.259	0.32	0.075	0.064	0	0.082	0.093	0.071	0.171	0.077	0.167	0.444	gonadotropin-releasing hormone II receptor-like (LOC106129576), mRNA
NW_013535362.1	3852565	4034221	-	gene3403	rna4450	0.27	0.216	0.46	0.402	0.35	0.349	0.536	0.579	0.706	0.316	0.383	0.453	small conductance calcium-activated potassium channel protein (LOC106129577), mRNA
NW_013535362.1	4090436	4108229	-	gene3404	rna4451	7.966	5.741	10.05	8.541	7.38	8.113	7.434	8.38	11.724	7.878	8.865	7.463	uncharacterized LOC106129735 (LOC106129735), mRNA
NW_013535362.1	4240437	4246388	+	gene3405	rna4452	0.065	0.134	0.064	0.106	0.18	0.062	0.144	0.169	0	0.373	0.138	0.178	extensin-like (LOC106129597), mRNA
NW_013535362.1	4247890	4251407	+	gene3406	rna4453	0	0	0	0	0	0.031	0	0	0	0	0.027	0	uncharacterized protein DDB_G0286591-like (LOC106129577), mRNA

**Table S6.** Bifenthrin use as the active ingredient(s) under registered trade names from 2006 – 2017 in almond orchards. Usage intensity (*UI*) is equal to the pounds of bifenthrin applied for each product divided by the treated acres. Trade names which comprise “Other” include Bifenture® EC-CA, Capture® EC-Cal, Swagger®, Helena Bifenthrin® 2EC-Cal, Sniper® Helios, Bifen 2 Ag Gold-Cal, Brigade® 2EC, Fanfare® EC, SPECKoZ® Bifenthrin, Bifenture® LFC, and Bifen 25% EC.

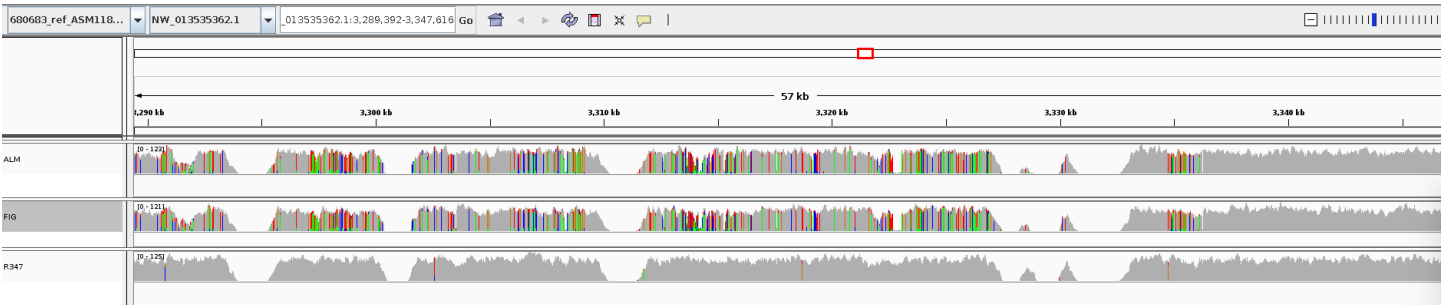
Statewide Almond Use	Brigade® WSB				Fanfare™ 2EC				Bifenture® 10DF				Bifenture® EC			
	Applications	Pounds Bifenthrin	Treated Acres	<i>UI</i>	Applications	Pounds Bifenthrin	Treated Acres	<i>UI</i>	Applications	Pounds Bifenthrin	Treated Acres	<i>UI</i>	Applications	Pounds Bifenthrin	Treated Acres	<i>UI</i>
2006	434	3,904	32,456	0.12	---	---	---	---	---	---	---	---	---	---	---	---
2007	1,398	9,979	96,946	0.10	---	---	---	---	---	---	---	---	---	---	---	---
2008	1,310	10,403	103,107	0.10	---	---	---	---	---	---	---	---	---	---	---	---
2009	1,433	13,819	123,986	0.11	---	---	---	---	---	---	---	---	---	---	---	---
2010	1,101	10,364	91,170	0.11	836	16,112	93,979	0.17	300	2,035	20,287	0.10	---	---	---	---
2011	683	5,574	51,574	0.11	743	12,904	74,310	0.17	139	737	9,530	0.08	1,326	29,504	112,093	0.26
2012	709	5,852	52,406	0.11	925	15,900	90,989	0.17	113	1,061	9,865	0.11	2,023	34,263	170,186	0.20
2013	772	6,144	52,306	0.12	516	6,207	33,981	0.18	127	1,104	10,995	0.10	3,167	41,515	242,981	0.17
2014	673	4,728	42,858	0.11	80	1,016	4,146	0.25	67	449	4,216	0.11	2,795	38,500	230,815	0.17
2015	799	5,794	51,726	0.11	99	518	3,322	0.16	90	499	4,729	0.11	3,437	50,974	281,786	0.18
2016	618	4,633	41,363	0.11	165	1,660	8,651	0.19	38	256	1,721	0.15	2,771	39,664	221,537	0.18
2017	622	4,364	48,724	0.09	183	1,763	10,428	0.17	8	60	547	0.11	2,950	34,773	202,369	0.172
	Sniper®				Athena®				Brigadier®				Hero® EW			
	Applications	Pounds Bifenthrin	Treated Acres	<i>UI</i>	Applications	Pounds Bifenthrin	Treated Acres	<i>UI</i>	Applications	Pounds Bifenthrin	Treated Acres	<i>UI</i>	Applications	Pounds Bifenthrin	Treated Acres	<i>UI</i>
2011	140	5,044	12,840	0.39	158	901	9,603	0.09	1	7	65	0.10	3	13	243	0.053
2012	291	3,834	21,232	0.18	229	1,389	14,499	0.10	1	29	285	0.10	---	---	---	---
2013	604	9,226	49,684	0.19	188	1,490	12,872	0.12	9	56	702	0.08	1	3	40	0.075
2014	565	9,959	52,676	0.19	239	1,606	14,275	0.11	25	144	2,275	0.06	73	176	3,641	0.05
2015	1,026	17,569	92,445	0.19	311	2,074	18,394	0.11	109	424	5,554	0.08	96	397	6,898	0.06
2016	986	15,204	80,879	0.19	130	519	4,882	0.11	109	446	6,060	0.07	20	68	1,166	0.06
2017	1,293	25,618	132,966	0.193	121	586	5,300	0.11	28	32	611	0.05	92	264	4,441	0.06
	Bifen 2 Ag Gold				Fanfare® ES				Aceto Bifenthrin 2EC				Other			
	Applications	Pounds Bifenthrin	Treated Acres	<i>UI</i>	Applications	Pounds Bifenthrin	Treated Acres	<i>UI</i>	Applications	Pounds Bifenthrin	Treated Acres	<i>UI</i>	Applications	Pounds Bifenthrin	Treated Acres	<i>UI</i>
2007	---	---	---	---	---	---	---	---	---	---	---	---	3	0.89	9.5	0.09
2008	---	---	---	---	---	---	---	---	---	---	---	---	2	0.55	5.5	0.10
2009	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
2010	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
2011	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
2012	---	---	---	---	---	---	---	---	---	---	---	---	3	42	305	---
2013	---	---	---	---	325	4,978	25,036	0.20	---	---	---	---	38	1,132	5,805	0.20
2014	878	6,716	48,885	0.14	105	1,251	6,618	0.19	303	4,138	22,062	0.19	13	33	276	0.12
2015	919	6,430	49,713	0.13	246	3,260	17,368	0.19	432	5,139	32,214	0.16	47	628	4,820	0.13
2016	969	6,648	50,174	0.133	410	4,156	28,788	0.14	666	8,282	47,522	0.17	62	370	2,785	0.133
2017	963	7,251	49,020	0.148	616	7,110	40,214	0.18	772	11,092	64,190	0.17	302	3,227	18,939	0.17

**Figure S1.** Snapshot of IGV genome browser showing a portion of the region in scaffold NW\_013535362.1. **A.** Reads of the three sequenced populations are identical to the reference genome; **B.** Portion of the region upstream of the total sweep, where only the resistant genotype (R347) maintains identity with the genome while the susceptible lines ALM and FIG have accumulated polymorphisms. The same pattern is seen downstream of the total sweep (not shown). Read coverage tracks display gray for same nucleotide and color for nucleotide changes.

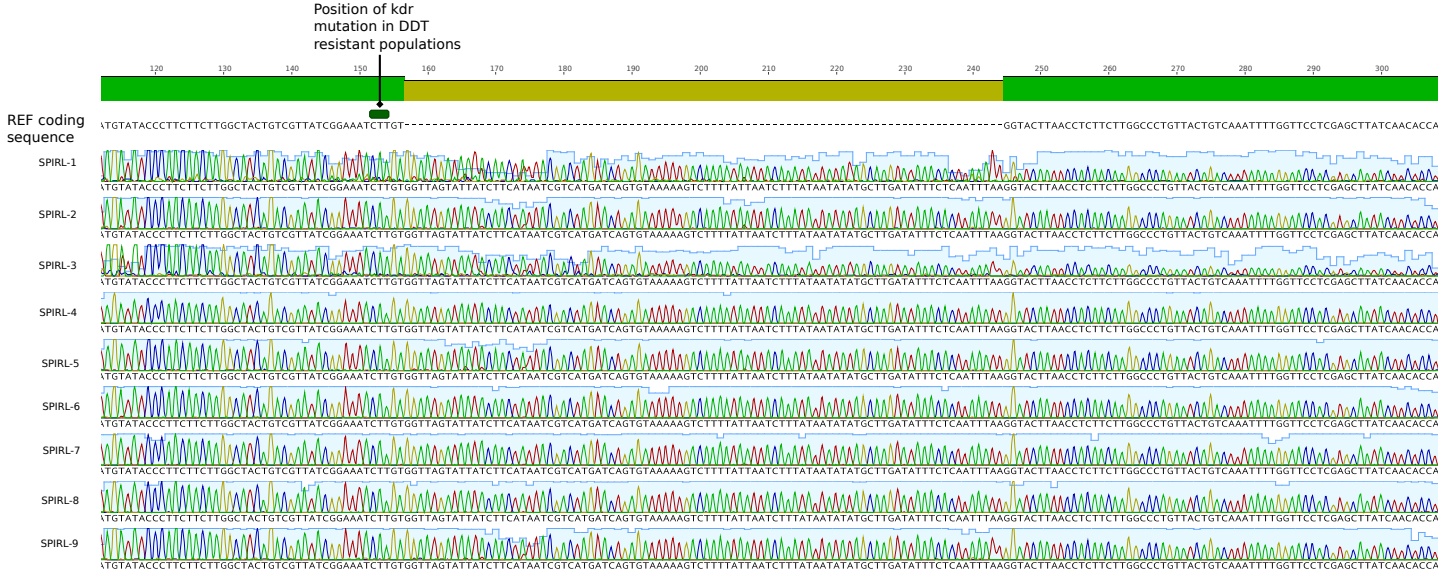
A.



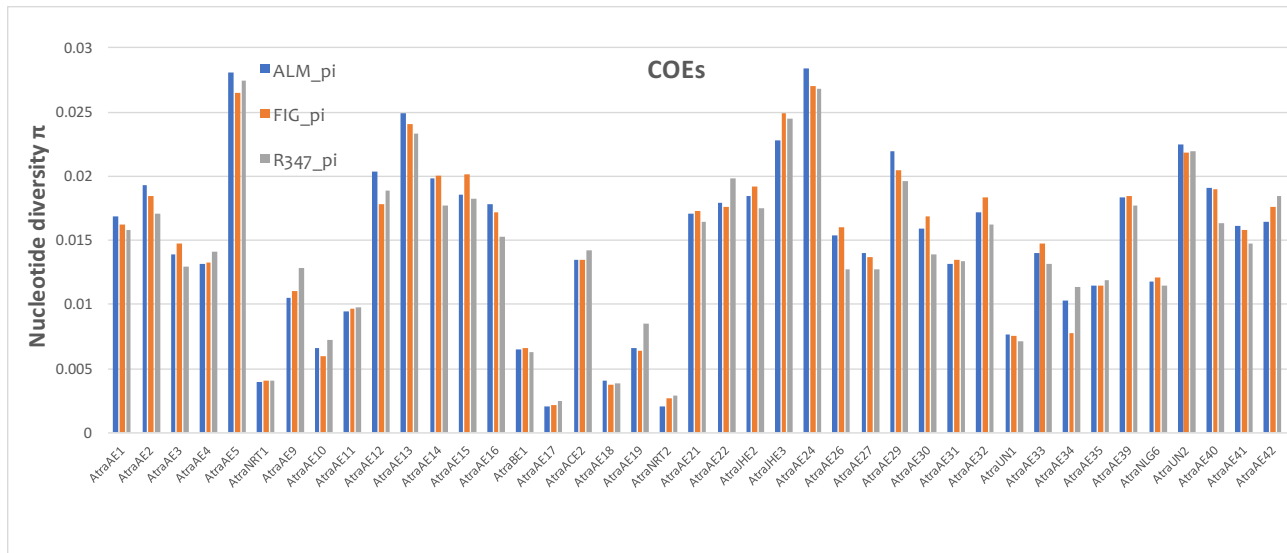
B.



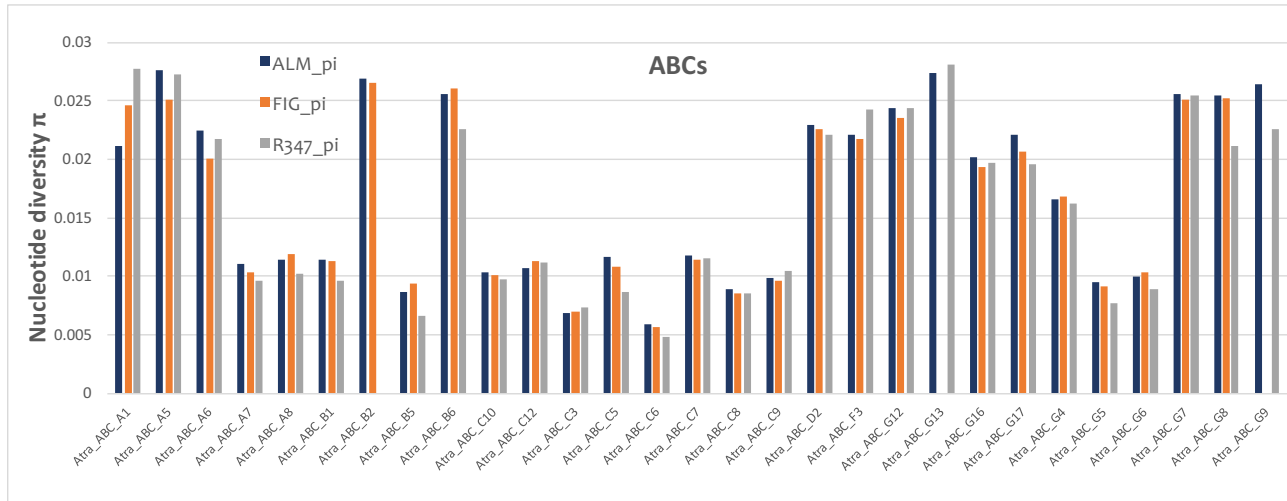
**Figure S2.** Sequence of the region flanking the position of the *kdr* mutation in the para gene in ten museum individuals of the SPIRL-1966 strain.



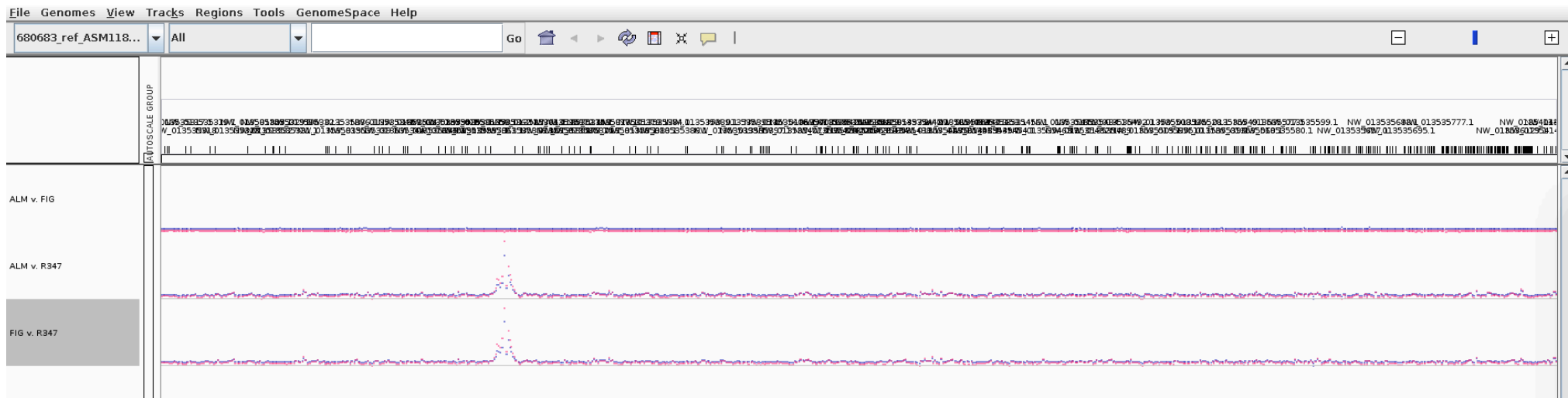




**D.**



**Figure S4.** Comparison of FST values obtained with Popoolation2 vs. Poolfstat. The screenshot shows the full reference genome coordinates (top). Tracks are pairwise FST values. Blue dots are values obtained with Popoolation2, and red dots are values obtained with Poolfstat.





**Figure S5.** Bifenthrin use since its registration in 2006 versus all other pyrethroids reported in the DPR pesticide use records (cyfluthrin, beta-cyfluthrin, (S)-cypermethrin, deltamethrin, esfenvalerate, fenpropathrin, lambda-cyhalothrin, gamma-cyhalothrin, permethrin) in almond orchards from 2006 – 2017.

