Sadd et al. The genomes of two key bumblebee species with primitive eusocial organization

Additional data file 1: supporting data

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Supplementary information, statistics and verification of *B. terrestris* genome

Sequence data for the *B. terrestris* genome

	Roche 454 GS FLX Titanium		
Mate-pair Distance	**Fragment**	**8 kb**	**20 kb**
Number of Reads	13.8 M	2.5 M	1.4 M
Pairs	No	Yes	Yes
Sequence Coverage[1]	17.5 x	2.2 x	1.7 x
SRA Accession	SRX016989	SRX016990, SRX016992	SRX016991

[1] Sequence coverage calculated as the total trimmed bases divided by estimated genome size of 274 Mb.

B. terrestris assembly comparison[1] to cDNA data

Minimum Length of cDNA in the alignment	≧80 %	≧90 %	≧95 %
Fraction of cDNAs aligned to Scaffolds	91.1 %	88.4%	84.8 %

[1] Comparison to 42,816 cDNA assembled transcripts aligned to scaffolds of the *B. terrestris* genome assembly. Most (91.1%) of the cDNAs aligned to the genome over at least 80% of their length.

Mapping of contigs and scaffolds onto chromosome linkage groups for *B. terrestris*

Linkage Group	Total Length	Percentage of Genome	Scaffold N50	Number of Scaffolds	Spanned Gaps
B01	17,153,651	7%	1,991,050	10	322
B02	13,603,873	5%	3,020,712	4	248
B03	14,656,165	6%	3,865,109	6	282
B04	14,241,696	6%	10,399,280	5	270
B05	11,918,102	5%	11,411,890	2	214
B06	12,724,418	5%	6,596,734	5	205
B07	18,145,390	7%	13,651,897	4	344
B08	9,733,834	4%	2,773,881	5	157
B09	15,655,298	6%	2,342,655	6	318
B10	13,618,662	5%	10,902,106	4	290
B11	17,228,712	7%	3,403,609	5	359
B12	12,868,931	5%	7,767,148	3	195
B13	9,884,808	4%	5,175,709	6	168
B14	11,649,563	5%	3,128,055	8	223
B15	11,467,329	5%	6,603,705	6	186
B16	5,274,633	2%	2,779,439	3	114
B17	3,558,169	1%	3,506,793	2	129
B18	3,466,108	1%	2,916,968	3	126
Unplaced	31,804,902	13%	626,856	5,591	844
Total	248,654,244				

Core Protein Set Alignments to the *B. terrestris* genome[1]

Species	Total Core proteins	Matched in *B. terrestris*	Percent Mapping
A. thaliana	458	438	96%
C. elegans	458	451	98%
D. melanogaster	457	456	100%
H. sapiens	456	449	98%
S. cerevisiae	458	432	94%
S. pombe	458	437	95%

[1] Alignments to the CEGMA core protein sets from named species.

Detailed overview for the repetitive elements in *B. terrestris* (Bter) and *B. impatiens* (Bimp). For each group, the number of elements (putative families), fragments/copies in the genome, cumulative length, proportion of the genome, and features (number containing chimeric or nested inserts of other elements/ appearing complete [all typical structural and coding parts present, even if containing stop codons or frameshifts]/ with RT or Tase domain/ potentially active containing an intact ORF with the all typical domains even though they could lack other structural feature like terminal repeats/ containing an intact ORF for the RT domain or parts of the Tase domain and could be partly active). Uncategorized or those containing features of *Bombus* coding regions are shown at the bottom, and likely do not belong to the repetitive elements.

Type	**Number (putative families)**		**Fragments (full length copies)**		**Coverage (kb)**		**% genome**		**Features**	
	Bter	**Bimp**	**Bter**	**Bimp**	**Bter**	**Bimp**	**Bter**	**Bimp**	**Bter**	**Bimp**
repetitive DNA	123900	56712	156534 (2005)	210488 (2286)	36228.7	44598.3	14.77	17.90	88/31/106/7/13	190/16/177/6/8
non-interspersed repeats	123174	55517	349 (20)	372 (17)	6157.8	3607.4	2.51	1.45	na/na/na/na/na	na/na/na/na/na
SSR	94915 (na)	28931 (na)	()	()	3886.9	1221.9	1.59	0.49	na/na/na/na/na	na/na/na/na/na
low complexity	28249 (na)	26580 (na)	()	()	2048.4	1983.8	0.84	0.80	na/na/na/na/na	na/na/na/na/na
Satellite	10 (0)	6 (3)	349 (20)	372 (17)	222.5	401.7	0.09	0.16	na/na/na/na/na	na/na/na/na/na
interspersed repeats	726	1195	156185 (1985)	210116 (2269)	30070.9	40990.8	12.26	16.45	88/31/106/7/13	190/16/177/6/8
class I - Retrotransposons	541	948	105281 (1133)	155558 (1365)	20776.1	30391.5	8.47	12.20	40/17/54/2/10	94/4/121/0/5
LTR Retrotransposon	150	252	9917 (386)	22348 (514)	3182.8	6614.3	1.30	2.65	16/13/37/2/6	50/4/67/0/2
Copia	22 (2)	27 (7)	1404 (37)	2587 (45)	377.6	744.6	0.15	0.30	3/4/8/1/1	6/0/13/0/0
Gypsy	114 (15)	198 (76)	7704 (331)	16495 (440)	2444.0	4801.0	1.00	1.93	12/7/26/1/4	37/3/50/0/2
Bel-Pao	12 (1)	20 (4)	713 (13)	1384 (22)	330.8	624.2	0.13	0.25	0/2/2/0/1	4/0/3/0/0
Retrovirus, Gypsy-like Errantiviridae	1 (0)	4 (0)	46 (4)	213 (4)	18.0	154.3	0.01	0.06	0/0/0/0/0	1/1/1/0/0
unclassified LTR retrotransposon	1 (0)	3 (2)	50 (1)	1669 (3)	12.4	290.3	0.01	0.12	1/0/1/0/0	2/0/0/0/0
LINE (non-LTR) Retrotransposon	69	154	12128 (152)	16342 (245)	3557.9	4378.4	1.45	1.76	12/4/17/0/4	26/0/53/0/3
R2 (NeSL, R2, R4, CRE)	1 (1)	11 (2)	99 (6)	664 (14)	74.5	253.0	0.03	0.10	0/0/1/0/0	2/0/6/0/0
RTE	5 (1)	14 (5)	1823 (11)	3522 (16)	406.5	672.5	0.17	0.27	1/0/1/0/0	4/0/4/0/0
Jockey (Rex,Jockey,Cr1,Kiri,L2,crack,Daphne)	48 (26)	81 (57)	9072 (83)	10021 (111)	2596.8	2589.7	1.06	1.04	11/4/10/0/3	18/0/26/0/0
L1 (Tx1. L1)	0 (2)	0 (0)	0 (0)	0 (0)	0.0	0.0	0.00	0.00	0/0/0/0/0	0/0/0/0/0
I (R1, I, Nimb, outcast, Tad, Loa)	14 (7)	43 (19)	1114 (51)	1912 (97)	474.3	804.0	0.19	0.32	0/0/4/0/1	1/0/17/0/3
unclassified LINE	1 (1)	5 (2)	20 (1)	223 (7)	5.7	59.2	0.00	0.02	0/0/1/0/0	1/0/0/0/0
SINE, unclassified, putative	8 (0)	9 (0)	436 (90)	169 (16)	130.6	23.9	0.05	0.01	3/na/0/na/na	0/na/0/na/na
unclassified Retrotransposon	2 (0)	13 (0)	500 (3)	2700 (13)	117.5	578.6	0.05	0.23	0/0/0/0/0	1/0/1/0/0
LARD	210 (0)	357 (0)	75925 (212)	103869 (360)	11886.4	17118.6	4.85	6.87	9/na/0/na/na	15/na/0/na/na
TRIM	102 (0)	163 (0)	6375 (290)	10130 (217)	1901.0	1677.7	0.78	0.67	0/na/0/na/na	2/na/0/na/na

class II - DNA Transposons	130	153	26598 (786)	14374 (804)	5408.4	3625.4	2.21	1.45	20/14/34/5/3	22/12/44/6/3
TIR	86	108	17516 (417)	11789 (397)	3626.5	2856.0	1.48	1.15	15/14/34/5/3	20/12/44/6/3
Tc1/Mariner	28 (33)	38 (32)	4807 (112)	3479 (112)	1044.4	887.7	0.43	0.36	3/8/19/5/3	3/7/26/4/3
hAT	0 (2)	5 (2)	0 (0)	173 (10)	0.0	39.9	0.00	0.02	0/0/0/0/0	0/0/0/0/0
Mutator (MULE, MuDR)/Rehavkus	0 (0)	0 (2)	0 (0)	0 (0)	0.0	0.0	0.00	0.00	0/0/0/0/0	0/0/0/0/0
P	0 (1)	0 (0)	0 (0)	0 (0)	0.0	0.0	0.00	0.00	0/0/0/0/0	0/0/0/0/0
PiggyBac	43 (14)	52 (30)	10188 (262)	7533 (218)	2036.5	1720.0	0.83	0.69	9/6/15/0/0	13/5/18/2/0
CACTA (EnSpm)	0 (0)	0 (1)	0 (0)	0 (0)	0.0	0.0	0.00	0.00	0/0/0/0/0	0/0/0/0/0
Academ	4 (0)	0 (1)	120 (7)	0 (0)	55.5	0.0	0.02	0.00	0/0/0/0/0	0/0/0/0/0
Kolobok	1 (0)	3 (2)	10 (1)	56 (6)	5.0	20.6	0.00	0.01	0/0/0/0/0	0/0/0/0/0
Sola	0 (0)	1 (0)	0 (0)	10 (2)	0.0	2.5	0.00	0.00	0/0/0/0/0	0/0/0/0/0
unclassified TIR DNA Transposon	10 (5)	9 (1)	2391 (35)	538 (49)	485.2	185.3	0.20	0.07	3/0/0/0/0	4/0/0/0/0
Helitron	0 (1)	0 (0)	0 (0)	0 (0)	0.0	0.0	0.00	0.00	0/0/0/0/0	0/0/0/0/0
unclassified DNA-Transposon	6 (1)	2 (18)	7580 (6)	560 (2)	1282.0	77.6	0.52	0.03	5/na/0/0/0	1/na/0/0/0
MITE	38 (0)	43 (0)	1502 (363)	2025 (405)	499.9	691.8	0.20	0.28	0/na/0/na/na	1/na/0/na/na
unclassified, putative element	55 (0)	94 (0)	24306 (66)	40184 (100)	3886.4	6974.0	1.58	2.80	28/na/18/na/na	74/na/12/na/na
other DNA elements	76	103	8142 (280)	12607 (354)	2008.7	2818.6	0.82	1.13	0/0/0/0/0	0/0/0/0/0
not categorized	24 (0)	30 (0)	1711 (202)	2174 (241)	737.6	874.3	0.30	0.35	0/na/0/na/na	0/na/0/na/na
potential host gene	52 (0)	73 (0)	6431 (78)	10433 (113)	1271.1	1944.3	0.52	0.78	0/na/0/na/na	0/na/0/na/na

Table of gene prediction methods, number of gene models and database locations

Method	***B. terrestris***	***B. impatiens***	**Database**
NCBI RefSeq	10,178	10,226	ftp://ftp.ncbi.nih.gov/genomes/Bombus_terrestris/ ftp://ftp.ncbi.nih.gov/genomes/Bombus_impatiens/
NCBI Gnomon	13,390	14,758	ftp://ftp.ncbi.nih.gov/genomes/Bombus_terrestris/ ftp://ftp.ncbi.nih.gov/genomes/Bombus_impatiens/
AUGUSTUS	11262	9635	http://bioinf.uni-greifswald.de/bioinf/katharina/bombus/
Fgenesh++	18,340	18,918	
GeneID	32,231	32,616	
SGP2	28,356	35,368	
GLEAN	10,979	15,896	

Protein domains

Overview of species gene sets used in the analysis of protein domains

Species	Version	#Genes with Pfam domains
Bombus terrestris	au6	7,487
Apis mellifera	4.5	8,216
Atta cephalotes	1.2	12,767
Culex cinquefasciatus	1.2	13,198
Drosophila melanogaster	5.48	10,551
Daphnia pulex	FrozenGene Catalog20110204	14,370
Harpegnathos saltator	3.3	10,164
Pediculus humanus	1.2	7,998
Tribolium castaneum	3	10,834

Expansion and contraction of protein domains in *B. terrestris* (Bter) v *A. mellifera* (Amel). P-values are from Fisher's Exact tests. TE-transposable element related.

Domain	Counts		P-value		Function (PFAM)
	Amel	Bter			
PF03022 (down)	22	6	0.00693		Major royal jelly proteins
PF07993 (up)	0	6	0.0117		Male sterility protein
PF02949 (down)	110	13	1.15E-18		7tm Odorant receptor
PF00001 (down)	60	32	0.0156		7tm receptor (rhodopsin family)
PF08395 (down)	7	0	0.0163		7tm Chemosensory receptor
PF14223 (up)	0	6	0.0117	TE	gag-polypeptide of LTR copia-type
PF03372 (up)	7	19	0.0103	TE	Endonuclease/Exonuclease/ phosphatase
PF07530 (up)	0	26	4.23E-09	TE	Associated with zinc fingers
PF00078 (up)	0	84	7.46E-28	TE	Reverse transcriptase
PF13843 (up)	0	13	0.000065	TE	Transposase IS4
PF00665 (up)	0	12	0.000137	TE	Integrase core domain
PF01359 (up)	3	18	0.000593	TE	Transposase (partial DDE domain)
PF07841 (down)	15	1	0.00062	TE	DM4/DM12 family
PF07727 (up)	0	9	0.00127	TE	Reverse transcriptase
PF03564 (up)	0	5	0.0246	TE	Protein of unknown function
PF00651 (up)	12	23	0.041	TE	BTB/POZ domain

Expansion and contraction of protein domains in *B. terrestris* (Bter) and *A. mellifera* (Amel) to *Atta cephalotes* (Acep) and *Harpegnathos saltator* (Hsal). P-values are from Fisher's Exact tests. TE-transposable element related.

Domain	Counts				P-value					Function (PFAM)
	Amel	Acep	Bter	Hsal	Acep-Amel	Acep-Bter	Hsal-Amel	Hsal-Bter		
PF00089 (down)	60	86	59	111	0.00886	0.00637	0.00204	0.00259		Trypsin
PF01826 (up)	13	5	11	4	0.000345	0.00159	0.0256	0.0397		Trypsin inhibitor
PF13912 (up)	29	0	27	10	1.3E-15	7.89E-15	0.000609	0.00138		Zincfinger, C2H2
PF00075 (down)	1	18	1	12	0.0124	0.021	0.00417	0.00458	(TE)	Rnase H
PF07776 (up)	27	27	24	13	0.00298	0.0134	0.0106	0.0306	TE	Zincfinger, C2H2
PF12017 (down)	0	10	0	18	0.0377	0.0387	0.000012	0.000015	TE	Transposase
PF13465 (up)	121	0	107	29	5.62E-63	1E-56	2.4E-17	1.3E-14	TE	Zincfinger, C2H2

Expansion and contraction of protein domain arrangements in *B. terrestris* (Bter) and *A. mellifera* (Amel) to *A. cephalotes* (Acep) and *H. saltator* (Hsal). P-values are from Fisher's Exact tests. TE-transposable element related.

Arrangement	Counts				P-value					Function (PFAM)
	Amel	Acep	Bter	Hsal	Acep-Amel	Acep-Bter	Hsal-Amel	Hsal-Bter		
PF01826 (up)	12	2	9	3	0.000481	0.00316	0.00794	0.0368		Trypsin inhibitor
PF00096, PF13465, PF13894 (up)	18	0	15	3	4.63E-08	3.26E-07	2.06E-04	5.41E-04	TE	Zincfinger, C2H2
PF00075 (down)	0	9	0	11	0.0147	0.0313	0.00156	0.00354	(TE)	Rnase H
PF00096, PF13465 (up)	18	0	14	4	4.63E-08	8.83E-07	7.87E-04	0.00332	TE	Zincfinger, C2H2
PF05699 (down)	0	9	0	22	0.0147	0.0313	2.59E-06	8.01E-06	TE	hAT family dimerisation domain

Maximal count of a repeated domain in an arrangement in *A. mellifera* and *B. terrestris*. P-values are from Fisher's Exact tests.

Arrangement	Domain	Counts		P-value	Function (PFAM)
		Amel	Bter		
PF06582, PF07679	PF07679	7	35	1.42E-05	Immunoglobulin I-set domain
PF06582, PF07679	PF06582	2	14	0.00413	Repeat of unknown function
PF01607	PF01607	3	16	0.00437	Chitin binding Peritrophin-A domain; protease resistance,peritrophic matrix
PF00057, PF00058, PF07645	PF00057	1	11	0.0063	Low-density lipoprotein Receptor domain class A
PF00041, PF00057, PF00058	PF00057	9	2	0.0372	Low-density lipoprotein Receptor domain class A
PF02363	PF02363	58	17	1.02E-06	Cysteine rich repeat; Function unknown
PF01391, PF01607	PF01391	8	1	0.0206	Collagen triple helix repeat
PF00028, PF01049, PF02210, PF12661	PF00028	12	4	0.0473	Cadherin domain

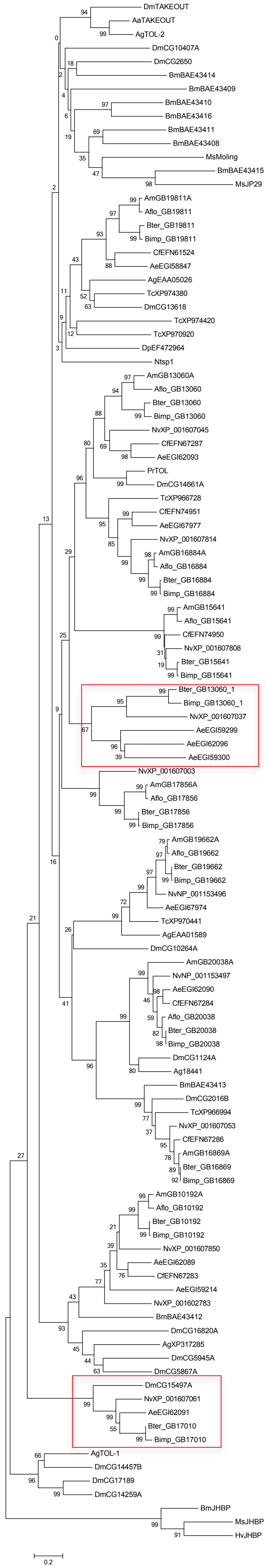
Minimal count of a repeated domain in an arrangement in *A. mellifera* and *B. terrestris*. P-values are from Fisher's Exact tests.

Arrangement	Domain	Counts		P-value	Function (PFAM)
		Amel	Bter		
PF06582, PF07679	PF07679	7	35	1.42E-05	Immunoglobulin I-set domain
PF06582, PF07679	PF06582	2	14	0.00414	Repeat of unknown function
PF00630	PF00630	1	15	0.000511	Filamin/ABP280 repeat
PF00307, PF00630	PF00630	18	3	0.000736	Filamin/ABP280 repeat
PF00053, PF00055	PF00053	1	13	0.00181	Laminin EGF-like
PF00057, PF00058, PF07645, PF12662	PF00057	8	27	0.00183	Low-density lipoprotein Receptor domain class A
PF00057, PF00058, PF07645	PF00057	1	11	0.0063	Low-density lipoprotein Receptor domain class A
PF00041, PF00057, PF00058	PF00057	9	2	0.0363	Low-density lipoprotein Receptor domain class A
PF01391, PF01607	PF01391	8	1	0.02	Collagen triple helix repeat
PF00028, PF01049, PF02210, PF12661	PF00028	12	4	0.0463	Cadherin domain

To/JHBP: Putative genes encoding proteins from the Takeout/ JH binding proteins (To/JHBP) family in bumblebees

List of To/JHBPs in the bumblebees *B. terrestris* and *B. impatiens*.

				JH binding domain			Signal peptide	
Protein ID	Related RefSeq	Length	Genomic location	Start	End	*E*-value	SMART	signalP
Bter_GB19811	XP_003397291	251	LG B08	19	250	2.26E-44	1-18	1-18
Bter_GB17856	XP_003398030	252	LG B09	23	252	2.14E-54	1-17	1-17
Bter_GB13060	XP_003398035	246	LG B09	20	245	7.68E-56	1-19	1-19
Bter_GB10192	XP_003398037	247	LG B09	23	245	1.21E-39	1-21	1-21
Bter_GB20038	XP_003398008	248	LG B09	24	248	4.12E-56	1-20	1-20
Bter_GB16884	XP_003398032	248	LG B09	20	247	4.25E-58	NS	1-20
Bter_GB19662	XP_003398029	265	LG B09	37	264	1.04E-52	1-23	1-23
Bter_GB16869	XP_003398036	251	LG B09	22	251	1.46E-47	1-18	1-18
Bter_GB15461	XP_003398031	247	LG B09	19	247	1.92E-33	NS	1-19
Bter_GB17010	XP_003398007	226	LG B09	4	222	4.04E-32	NS	NS
Bter_GB13060_1	XP_003398034	242	LG B09	18	240	7.61E-28	1-17	1-17
Bimp_GB19811	XP_003488074	251	-	19	250	4.46E-43	1-18	1-18
Bimp_GB17856	XP_003485406	252	-	23	252	9.84E-54	1-19	1-19
Bimp_GB13060	XP_003485403	246	-	20	245	1.03E-56	1-19	1-19
Bimp_GB10192	XP_003485401	247	-	23	245	7.42E-40	1-21	1-21
Bimp_GB20038	XP_003485419	248	-	21	245	4.12E-56	1-17	1-17
Bimp_GB16884	XP_003485404	248	-	20	247	1.61E-58	NS	1-20
Bimp_GB19662	XP_003485423	265	-	37	264	7.34E-53	1-23	1-23
Bimp_GB16869	XP_003485402	251	-	22	251	8.38E-48	1-18	1-18
Bimp_GB15461	XP_003485405	247	-	19	247	8.34E-34	NS	1-19
Bimp_GB17010	XP_003485420	226	-	4	222	7.21E-29	NS	NS
Bimp_GB13060_1	XP_003485421	242	-	18	240	1.67E-24	NS	1-18



Phylogenetic relationships between To/JHBP proteins in insects. The red boxes show the two JHBPs that are proposed to have been lost in the lineage leading to honeybees. The numbers at the branching points are bootstrap values (%). Branch lengths are proportional to the sequence distance indicated by the bar below the tree. Species abbreviations: Aa—*Aedes aegypti* (yellow fever mosquito, Diptera); Ae— *Acromyrmex echinatior* (Panamanian leafcutter ant, Hymenoptera); Aflo—*Apis florea* (dwarf honey bee, Hymenoptera); Ag—*Anopheles gambiae* (African malaria mosquito, Diptera); Am—*Apis mellifera* (honey bee, Hymenoptera); Bimp—*Bombus impatiens* (bumblebee, Hymenoptera); Bm—*Bombyx mori*, (silk moth, Lepidoptera); Bter— *Bombus terrestris* (bumblebee, Hymenoptera); Cf—*Camponotus floridanus* (Florida carpenter ant, Hymenoptera); Dm—*Drosophila melanogaster* (fruit fly, Diptera); Dp—*Diploptera punctata* (Pacific beetle cockroach, Dictyoptera); Hv—*Heliothis virescens* (tobacco budworm, Lepidoptera); Ms—*Manduca sexta* (tobacco hornworm, Lepidoptera); Nt—*Nasutitermes takasagoensis* (nasute termite; Isoptera); Nv—*Nasonia vitripennis* (parasitoid wasp, Hymenoptera); Pr—*Phormia regina* (black blowfly, Diptera); Tc—*Tribolium castaneum* (red flour beetle, Coleoptera). Accession numbers for proteins indicated by abbreviated name: AaTakeout (AF458100), AgTOL-1 (AAO39755), AgTOL-2 (AAO39756), BmJHBP (AAP41112), DmTakeout (AF261748), HvJHBP (AAA68242), MsJHBP (AAB25736), MsJP29 (AAA21588), MsMoling (AAO65575), Ntsp1 (BAD91203), PrTOL (BAD83405).

The genomic arrangement of putative JHBPs encoding genes in *B. terrestris*

Biogenic amines

An overview of the biogenic amine receptors and their gene identification numbers present in *B. impatiens*, *B. terrestris*, *D. melanogaster*, and *A. mellifera*

Ligand	*B. impatiens*	*B. terrestris*	*D. melanogaster*	*A. mellifera*
octopamine	Bimp11589	XP_003403017.1	CG31351	Am1
octopamine	Bimp11590	on GL898805		Am2
octopamine	Bimp21653	XP_003402376.1	CG6989	Am3
octopamine	Bimp11588	XP_003397143.1	CG6919	Am4
octopamine	Bimp18006	XP_003401247.1	CG3856	Am5
Tyr./Octop.	Bimp13424	XP_003392960.1	CG7485	Am7
Tyramine	Bimp25232	XP_003393336.1	CG7461	Am13
Dopamine	Bimp16334	XP_003401133.1	CG18741	Am6
Dopamine	Bimp21538	XP_003397774.1	CG17004	Am8
Dopamine	Bimp14827	XP_003401071.1	CG9652	Am9
Dopmine/Ecd.	Bimp21034	XP_003395933.1	CG18314	Am19
5HT	Bimp17521	XP_003400301.1	CG15113	Am11
5HT			CG16720	
5HT	Bimp18142	XP_003402761.1	CG12703	Am12
5HT	Bimp12301	XP_003397807.1	CG1056	Am16
Adenosine	Bimp13953	XP_003394193.1	CG9753	Am20
Acetylcholine	Bimp16572	XP_003401764.1	CG4356	Am15
Acetylcholine	Bimp13324	XP_003397629.1	CG7918	Am14
orphans	Bimp19381	XP_003401590.1	CG18208	Am10
orphans			CG16766	
orphans	Bimp21141	XP_003398431.1	CG42796	Am17
orphans	Bimp14525	XP_003393279.1	CG13579	Am18
Total	**20**	**20**	**21**	**20**

Neuropeptides

Bumblebee neuropeptide fasta sequences. Immature neuropeptides are marked with yellow. Green indicates putative cleavage sites for prohormone convertase. Glycine residues that are converted into C-terminal amide groups in the mature peptides are highlighted with blue. Signal peptides predicted by SignalP 4.1 are underlined.

Bombus terrestris neuropeptide FASTA sequences

>**Bter-AKH** (in the C-terminal part of XP_003401166.1; manual curation)
MHSSLYMHRKIRLEFLVFSVILLLCLILNSGAEAQLNFSTGWGKRSQRLEWSAVRPECPSQ
ARPSFEQLLNVYHLIQEARKMLECRKPSE

>Bter-allatotropin (XP_003398476.1)
MRASVIIVLAFATGIVVATSRNHNYSHFVKHHARPRVIRGFKPEYMSTAYGFGKRQSTIDV
PKLNKQERILSTLLRYFPQGIPVDWLLQQLKTNPTFATKLTQALMDGRTDFTSMIDRSNPER
ITWLY

>**Bter-Ast-A** (XP_003397004.1)
MKIRTGLLTSSVAFLYLIGIVERPVLAMEEAPPYSMNLHDYNSMLNSMEFDDSVPEKRAYT
YVSEYKRLPVYNFGIGKRWVDTNDNKRGRDYSFGLGKRRQYSFGLGKRNDNPDYPVRLN
MDYLPVDNLAYHSQENLDDLLEAKRSRPYSFGLGKRAAHPNNGQPIGPKRPNDLMSQRY
HFGLGKRMSEDEEDSSQ

>**Bter-Ast-C** (XP_003399378.1)
MSSLRTVIFLAMVLMVLIDLSIALPAADKERLLNEVDLVDDDGSIETALINYLFTKQIVKRL
RNQLDIGDLQRKRSYWKQCAFNAVSCFGK

>**Bter-Ast-CC** (XP_003399426.1)
MGNGVIPLMLVAMVPIIGGTIGQRALSKRNAPTNLDYPDYSTKYDEYPVVVPKRAALLFD
QLMVALQKVVDNQNRGELGGRTLPGPSGPHLPVGNSQKIPSTDEQTMDLQRRGQAKGRV
YWRCYFNAVTCFKRK

>**Bter-bursa** (annotation XP_003402297.1; split into bursa and bursb)
MLLYHIVGASVLICLLSETAEALIGVDECQATPVIHFLQYPGCVPKPIPSYACRGRCSSYLQV
SGSKIWQMERSCMCCQESGEREASVSLFCPRAKPGEKKFRKVITKAPLECMCRPCTSVEEY
AIIPQEIAGFADEGPFTTSAHFRRSSDLQ

>**Bter-bursb** (annotation XP_003402297.1; split into bursa and bursb)
MFIFALFFVLTAFIYMNDTVAQVTDDENCETLQSEVHITKDQYDEIGRLKRTCSGDITVTKC
EGFCSSQVQPSVASTTGFSKECYCCRESYLKERHITLHHCYDADGIKLMNEEDGVMEIKIRE
PAECKCIKCGDISR

>**Bter-capa** (XP_003397181.1)
MRNHLFVFLVVLIFSTSFSQGVKLKLNDRRASGLMAYPRVGRSDVPIPNLNFNRRHAIEPDT
DFQFYSPEFDSVSDKDYEDVRNTAPGSLGRSMNLKHADKFPKEASWLISDRIRSPKDYQLW
QKIDDGRFVYPGSLLLTRGSRNIQLNGYTPRLGRENDDDRTVCK

>**Bter-CCAP** (XP_003401568.1)
MKAINHVCCIFIFVCLVNLTQSENPQDKIEQQLLNAFSTDESLKMKRPFCNAFTGCGRKRNF
HENSMESQGMEANGSIRLPISVYKALLRAATKNIRNTIQRNTNDYQLSGIPQVYLSGRMPL
HKRFDISSTSLN

>**Bter-CCHa1** (XP_003397060.1)
MAIGSENSVAVLIRNWTFMIIFCFAGYAAGSCLEYGHSCWGAHGKRSGGHSNAYLVPLKT
SNEIQQEIPSLTKEQFILSRLIDRPSISNKYKAKWDRLLKLKTSLPESWDGDAFNAQLISDEPS
RDQNNNEDMNLGKRKQTNNMQDITGNTNGERREIPEILLIPNNEDNQHGSKPQNVELFKFL
TDTNGDFE

>**Bter-CCHa2-like** (XP_003397131.1)
MLVDGLTPCLIKSLLLLAKDFNFTSLCRLYGQSCLGGHGKRFDSHIQGNVLQENQVDAATS
DKHQEMEPLRLRNEFVIPGRKFEGQEEMLLPQTRRQDSTRFDPFTLSFIVRQWLTSQHRLH
QPDVELNNN

>**Bter-corazonin-like** (XP_003393262.1)
MDNARVLILFILSLTVMTVTCQSYHYTPDWASGKRSTSMLEEIVNFANKNAGQLDNALVN
CKLQKLRLLLQGNINNQLLQVPCDLLTSGKRSLSENTIIDHFHRQPTPTVNNNY

>**Bter-DH** (XP_003395619.1, XP_003395620.1, 2 isoforms)
MHQRMVSFYILLVVAVLFVSSNLSTNAAPQQGYWEEDPEALMEIISRLGHTMIRNPELENN
KRGLDLGLSRGFSGSQAAKHLMGLAAANYAGGPGRRRRSEQP

>**Bter-DH/CRF** (XP_003403344.1)
MTLMSLLLSLLFIAMTKCQPISYVYDERELSRDNHPLLLLVDHRIPDLENEMFDSGNDPEST
VVRTKRLESKRIGSLSIVNSLDVLRQRVLLELARRKALQDQQQIDANRRILKTIGKRSLPLY
NKDVPKAMDARIRNGIDYVFEQEEKSHDRDVMPERNPDRMQNWLRNDDSAFRERQDDQ
MRRIQANELRLL

>**Bter-EH** (XP_003395267.1)
MVMNASTRILLVLFVSYAIAFMLVAGSVPFDRAIGVCIRNCAQCKKMFGPYFLGQKCADS
CVKYKGKLIPDCEDEGSIQPFLQALDSDY

>**Bter-elevenin** (XP_003402670.1)
MVTVVAYIQRCMIIFAILLCYFHVRSERSESVNCEAFPYHQMCRGSMSRKRAMFPIMYGLG
CEGSEGNINCIKEFEERHRIPYIPLSKSKLLIALLDDDLQKDITRSARHKLRNDEMNKRKPSII
ENFLSELDSSDSY

>**Bter-ETH** (XP_003400029.1)
MTSLRSLGFSRRFIVGALTVGVLALLACENLSKADEVPAFFLKIAKNIPRVGRSEGYNDFLK
SRRNIPQVSGYNSRAQAESWAPYASDKTFSRPIKRRVDYPSIDDAWAWQHFPLAIEGPREL
WRTLAGYSKDTSDDVDNDVWKRKKRTGNEPVISEDN

>**Bter-FMRFa** (XP_003402122.1)
MKRSLTSLYVLSFICNWALIFSSILTPMKADGSLRIFKDGPNDFEYVLKRHEVDRSSEDLDS
KERRSSMGSSFIRYGRSDVDGNIERVSNSDSDGSSKVNRYPRWKSPDIIIRFGRSSFKSLNDD
THYRHGRNNLNFLRYGRNVQVYPLEIDVTAMCSDLLSNDEGNDLHPYEARLLRLCNILNN
SDIEHRNSLDFLEDRLGSKHN

>**Bter-ILP-B** (XP_003400778.1)
MRMYANRLYALMSLILVIVILIPLAEHASDTYKQRNIHGSDVFQYGQKGQSRDQSRDQSRD
QSMTEMHQYCGRILSSTLQIICGSVYNSRFKKSNQEMEMDDYMAYSYDLHPYKSIKNAKK
MIRFRRNGRGIHEECCLKSCTTEELRSYCGAR

>**Bter-ILP-C** (maker-group8.1-pred_gff_fgeneshpp-gene-10.56)
MFGRSRARTIVLVGLVLLTLLDTVNSTPYKRSLLRLCSKSLSDALYLACKDRGYNEPFSYSS
EDSPMDSVGPGLAEECCYHTCTYTQLQQYCKPEKSSSVDAVNSPVWIEKYPYLSTRSATSS
SLEERSRSDIDYVHGTIKCKIHGSKGARRKGANMDRDDDAGGCDRKNPLRRHRAGHCGC
RHRRQRRRRLGKMLERTSGVKSGAPLKKEVETETKATTREAPF

>**Bter-ITP** (maker-Group10.1-pred_gff_sgp2-gene-93.22)
...MHRQQRLRSSSSSLSSLTLPLSMSRSSIPSTTTSISSVTMPSSTTTSTSPSPSPSTPSSPLSSSSP
LSSSSIFLPLSTTWPTSNLSSYSWSVQQTSCSRLPSLPSESSIVSTVSIPCPKLVSVLAWSVTLL
LVSSCIGLTDAGILNGHPLGKRSFIDIQCKGIYDKSIFARLDRICEDCYNLFREPQLHQLCRK
NCFTSDYFKGCLDVLLLQDEVEKIQTWIKTLHGAEPGV

>**Bter-kinin** (XP_003397027.1)
MWLVFPIVSLLIRAILANSEIDDIVLPDIMDLENESNDVLTDNYTDRPGNDIWKVWKKTSFD
PWSGKRAKEYSRSKVDSQGKRTKLTHDWYDRDTPTNEFSNVKRITESVEWTPFNSWGGK
RAGKVNNRDSILALTRDPHNLHLMAEDELIAGRKLGDEKLSIEMKNWLSSMCNTCTKKHC
CSEIEKKTEQNEQYKKPRAWGPWHGKRSLKTYTFRFGNEYFTVPVDSIKAERNFSPFRKHN

>**Bter-myosuppressin** (XP_003398693.1)
MMSSTIVILFSMTTMAISYNNVLAALPTQCNPGFLDDLPPRIRKVCAALSRIYELGSEMESYI
DDKDNHISGFHESIPLLDSGVKRQDVDHVFLRFGRRR

>**Bter-neuroparsin** (XP_003395782.1)
MLAAQTIRIAVLLAIVLLHDKCSGYPSVRQKQEMALCTGCGDSCHKCEYGVVISNACGVP
QCAKGPDEPCGGRGERLGICAEGMSCICNQCFGCSSEKLKCSKIKDPCWRDFNVPVRRPAI
M

>**Bter-NPF** (XP_003400279.1)
MQSCLNSIYLVVVLFILGTGIVHGEPGPMARPTQPDIFTNQEELKKYLDHVTDFYSLNGKA
RYGKRGNVLSSVPEVNYVWDSMKTILENSQRSQQPKANRQFEKRKQEESGFLDEVEKYGP
KKSTSRIDSPPCHVLDTVEKYYDDVQ

>**Bter-NPLP1** (XP_003400507.1)
MGLTGNHFVSLLLYILVVNEIRLPLVTCQDEDNTQCMPKAAFLALLRHPEVSSNLAAYSRA
ARITQDAKSRNDMAHLRALTEEADDTEICVPGRVYLQLLKDPVMRGDLSIILNGRTQKLPD
LLGRLLDDSDEMDAREFLPESQKRSLATLAKNDDLPISIQDRIAENEDDEEKRAAISSEQPG
QNDAGISRDYLLSGGRSDLQAFARDFQMEKRNVGALARDFALPPGRRNIASLVRDYDQSK
NNNRESTLPYNGKRNVASLARTFTLPQNGKRNVASVARDYGLPYGKRYVGSLARTGDFPT
RNQRSVASLAKNSAWPVSLKRGIFLPGSVILRALSRHGRSMVDETNARNDLLDLQELSNLE
QSQRNDYETAEEKLNDSLTKIDSNIRRPKRQIGFSDEYPLPVMQNTNGFDYEEVVEALSGQ
YPNAEKRFMGRIPQMGPRPTTPPTRRQGR

>**Bter-orcokinin** (maker-Group11.1-pred_gff_fgeneshpp-gene-5.4)
MTRHCFLVLSILALSIAGCVLAVQAETSSLRREFYGPSKPEFLVEYLEGHAARKQRDDQDD
PADDRPRRVRPFARDTQARLSSGSTRYLADDYADESSAASKSIALSPIDRQLLERFVKRNID
EIDRTAFDNFFKRNLDEIDRVGWSGFVKRFADDTITGDGRINVLAQRG

>**Bter-PDF** (XP_003399126.1)
MTPVKYVLILLVMLGITYQTLGATEDSYRNLLGFNLPYGRGMNNDLQFARLLMLPPCLCH
SKRNSELINSLLGLPKNMNNAGK

>**Bter-pyrokinin** (XP_003396136.1)
MIGSVAFLSFNRLMTITVCVLLCVVYLVSCASGEYEGRDSSSSMSNDRTPSNEFGSCSDGK
CIKRTSQDITSGMWFGPRLGRRRRADRKPEIDSDIETLANALDGSRWAVITIPGSDRRQATQ
FTPRLGRESGEEYFSYGFPKDQEELYAEEQIFPPLFAPRLGRKVPWTPTPRLGRQLHNIIDKS
RQNFDDARF

>**Bter-RYa** (XP_003400572.1, corrected)
MVMCLWIACMVLTLVASQQKFYIQGRYGKRQEPRTDSFFVSGGRYGRSENTQKASKSLPK
LVEVEVPRIDRFFWGSRYGKLSPPDYRTVSSVNRFSAILNFMDQVNLDRENDESNRNDLDL
LP

>**Bter-SIFa** (XP_003400028.1, corrected)
MMSSRFVVAIVVALFILAIAVDAAYRKPPFNGSIFGKRSNAITDYELTSRAMSSVCETVSET
CNAWLARQDSN

>**Bter-sNPF** (XP_003394766.1, corrected)
MSIKFYAKSLLLFIIVGLVVAAENYIDYGDEVTEKTPIENIREIYKILMQRSALENARLGETPL
EHLMIRKSQRSPSLRLRFGRSDPRLSQFYQNL

>**Bter-tachykin** (XP_003397025.1)
MIIPSTFLLMVSVTFAIAEESMSENVLSDKRAVMGFQGMRGKKNFDSLDSEDFGILKRAIM
GFQGMRGKKNSIIADVENQLFPEETNKRAPMGFQGMRGKKASLDDEYYKRAPMGFQGMR
GKKSLEEILDEIKKTTTRFQDPRSKDMYVIDYPEDYEKRILSMEGYPNIFDKEGEFLWEKRA
PMGFHGMRGKKLILDPWQDLDKQDVMEFQGLQRRKDTFDDYLDYSMNPSDYEKRAADF
QDIESGSDSFKRARMGFHGMRGKRNVEEIYGSNSNPTQTTIGYQGVNNRGNNLAVYEIEK
RSPFRYLGVRGKKNPRWEFRGKFVGVRGKKASSLQSVY

>**Bter-trissin** (XP_003402499.1)
MNCTYVVLFFIVCALWVFGETLSCEQCGRECAEKCGTRQFRACCFNNMKKRQFDLGLKW
RMRPQLYTNWLYPNIDMY

***Bombus impatiens* neuropeptide FASTA sequences.**

>**Bimp-AKH** (BIMP14855)
...HRKVRLEFLVFSIILLLCLILNSGAEAQLNFSTGWGKRSQRLEWSAVRPECPSQARPSLEQ
LLNVYHLIQMEARKMLECRKPNE

>**Bimp-allatotropin** (BIMP21229)
MRASVIIVLAFATGIVVATSRNHNYSHFVKHHARPRVIRGFKPEYMSTAYGFGKRQSTIDV
PKLNKQERILSTLLRYFPQGIPVDWLLQQLKTNPTFATKLTQALMDERTDFTSMIDRSNPER
ITWLY

>**Bimp-Ast-A** (BIMP11558)
MKIRTGLLTSSIAFLYLIGIVERPVLAMEEAPPYSTNLHDYNAMLNSMEFDDSVPDKRAYT
YVSEYKRLPVYNFGIGKRWIDTSDNKRGRDYSFGLGKRRQYSFGLGKRNDNSDYPVRLN
MDYLPVDNLAYHSQENLDDLLEAKRSRPYSFGLGKRAAHPNNGQPIGPKRPNDLMSQRY
HFGLGKRLPEDEENSSQ

>**Bimp-Ast-C** (BIMP21837)
MPSLRTVIFLAMVLMVLIDLSIALPAADKERLLNEVDLVDDDGSIETALINYLFTKQIVKRL
RNQLDIGDLQRKRSYWKQCAFNAVSCFGK

>**Bimp-Ast-CC** (BIMP21913)
MGNGVIPLMLVAMVPIIGGTIGQRALSKRNAPTNLDYPDYSTKYDEYPVVVPKRAALLFD
QLMVALQKVVDNQNRGELGGRTLPRSSGPHLPVGNSQNIPATDEQTVKMDLQRRGQAKG
RVYWRCYFNAVTCFKRK

>**Bimp-bursa** (BIMP18662)
MLLYHIVGASVLICLLSETAEALIGVDECQATPVIHFLQYPGCVPKPIPSYACRGRCSSYLQV
SGSKIWQMERSCMCCQESGEREASVSLFCPRAKPGEKKFRKVITKAPLECMCRPCTSVEEY
AIIPQEIAGFADEGPFTTSAHFRRSSDLQ

>**Bimp-bursb** (Bimp18661)
MFIFALFFVLTAFIYMNDTVAQVTDDENCETLQSEVHITKDQYDEIGRLKRTCSGDITVTKC
EGFCSSQVQPSVASTTGFSKECYCCRESYLKERHITLHHCYDADGIKLMNEEDGVMEIKIRE
PAECKCIKCGDISR

>**Bimp-capa** (Bimp23791)
MRNHLFVFLVVLIFSTSFNQGEKLKLNDRRASGLMAYPRIGRSDVPIPNLNFNRRHANEPD
TDFQFYSPEFDSVSDKDYEDVRNTAPGSLGRSMNLKHADKFPKEASWLISDRIRSPKDYQL
WQKIDDGRFVYPGSLLLTQDSRNIQPSGYTPRLGRESDVDRTVCK

>**Bimp-CCAP** (Bimp15632)
MKAINHVCCIFIFVCLVNLTQSENPQDKIEQQLLDAFLTDESLKMKRPFCNAFTGCGRKRNF
HENSIESQGMETNGSIRLPISVYKALLRAATQNTRNTIQRNTNDYQLSGIPQVYLSGRMPLH
KRFDISSTSLN

>**Bimp-CCHa1** (Bimp23716)
MAIGSENSVAVLIRTWTFMIIFCFAGYAAGSCLEYGHSCWGGHGKRSGGHSNAYLVPSKTS
NEIQQEIPSLTKEQFILSRLIDRPSIPNKYKARWDRLLKLKTSFPESWDGDAFNAQLISDGPSR
DQNNNEDMNLGKRKQTNNMQDITGNTNGERREIPEILLISNNEDNQHGSKPQNVELFKFLS
DTNGDFE

>**Bimp-CCHa2-like** (Bimp23727)
MKSNATSGLPLSICVSVCTLVILLSVSETVYAKRGCSAFGHSCFGGHGKRFDSHLQGNVLQ
ENQIDAATSDKHQEMEPLRMRNEFVIPGRKFEGQEEMLLPQTRRQDSTRFDPFTLSFIVRQ
WLTSQHRLHQPDVELNNK

>**Bimp-corazonin-like** (Bimp25646)
MGNARVLILFILSLTVMTVTCQSYHFSIPDWTNEKTSIFKEIVNAINKYISQSNNVLANCELQ
KLKLLLQGNINYQLFQVPCDLLVSGKKSFSENTITDYFHRQPTPVNNNY

>**Bimp-DH** (Bimp18864)
MHQRMVSFYILLVVAVLFVSSNLSTNAAPQQGYWEEDPEALMEIISRLGHTMIRNPELENN
KRGLDLGLSRGFSGSQAAKHLMGLAAANYAGGPGRRRRSEQP

>**Bimp-DH/CRF** (Bimp22606)
MTLMSLLLSLLFVAMTKCQPISYVVYDERELSRDNHPLLLLVDHRIPDLENEMFDSGNDPES
TVVRTKRLESKRIGSLSIVNSLDVLRQRVLLELARRKALQDQQQIDANRRILKTIGKRSLPL

YNKDVPKAIDSRIRNGIDYVFEQEEKSHDRDVVPERIPDRMQNWLRNDDSAFRERQDDQM
RRIQANELRLL

>**Bimp-EH** (BIMP17811)
MNASTRILLVLFVSYAIAFMLVAGSVPFDRAIGVCIRNCAQCKKMFGPYFLGQKCADSCV
KYKGKLIPDCEDEGSIQPFLQALDSDY

>**Bimp-elevenin** (Bimp20439)
MVTVVAYIQRCMIIFAILLCYFHVRSERSESVNCEAFPYHQMCRGSMSRKRAMFPIMYGLG
CEGSEGNINCIKEFEERHRIPYIPLSKSKLLIALLDDDLQKDITRSARHKLRNDEMNKRKPSII
ENFLSELDSSDNY

>**Bimp-ETH** (Bimp11504)
MTSLRSLGFSRRFIVGALTVGVLALLACENLSKADEVPAFFLKIAKNIPRVGRSEGYNDFLK
SRRNIPQVSGYNSRAESWAPYASDKTFSRPIKRRVDYPSIDDAWAWQHFPLAIEGPRELWR
TLAGYSKDTSDAVDNDVWKRKKRTGNEPVISEDN

>**Bimp-FMRFa** (Bimp17850)
MKSSLTSLYVLSFICNWALVSSSILTPMKADGSLRIFKDGPNDFEYVLKRHDVDRSSEDPDS
KERRSSMGSSFIRYGRSDLDGNIERVSSSDGDGSSKVNRYPRFKSPDIIIRFGRSGFKNLNDD
THYRHGRNNLNFLRYGRNVQVYPLEIDMTAMCSDLLSNNEINDLHPYEARLLRLCNILNNS
DIEHRNSPDFLEDRLGSKHN

>**Bimp-ILP-B** (Bimp17968)
MRMYANRLYALMSLILVIVILIPVAEHASDTYKQRNIHGSDVFQYGQKGQSRDQSRDQSR
DQSMTEMHQYCGRILSSTLQIICGSVYNSRFKKSNQEMEMDDYMAFSYDLHPYKSIKNAK
KMIRFRRNGRGIHEECCLKSCTTEELRSYCGAR

>**Bimp-ILP-C** (BIMP11552)
MFGRSRARTIVLVGLMLLTLLDTVNSTPYKRSLLRLCSKSLSDALYLACKDRGYNEPFSYS
SEDSPMDSVGPGLAEECCYHTCTYTQLQQYCKPEKSSSVDAV...

>**Bimp-ITP** (BIMP10086)
...WPTSNLSSYSWSVQQTSCSRLPSLPSESSIVSTVSIPCPKLVSVLAWSVTLLLVSSCIGLTD
AGILNGHPLGKRSFIDIQCKGIYDKSIFARLDRICEDCYNLFREPQLHQLCR..

>**Bimp-kinin** (BIMP21628)
MWLMFAIVSLLIRAILANSEIDDIVLPDIMDLENESNDILTDNYTDRPGNDIWKVWKKTSFD
PWSGKRAKEYSRSKVDSQGKRTKLTHDWYDRDTPTNEFSNVKRITESVEWTPFNSWGGK
RAEKLNNRDSVLALTRDPHSLHLMAKGKL

>**Bimp-myosuppressin** (BIMP11018)
...MAISYNNVLAALPTQCNPGFLDDLPPRIRKVCAALSRIYELGSEMESYIDDKDNHISGFHE
SIPLLDSGVKRQDVDHVFLRFGRRR

>**Bimp-neuroparsin** (BIMP12385)
MLAAQTIRIAVLLAIVLLYDKCSGYPSVRQKQEMALCSGCGDFCHKCEYGVVISNACGVP
QCAKGPDEPCGGRGERLGICAEGMSCICNQCFGCSSEKLKCSKIKDPCWRDFNVPVRRPAI
M

>**Bimp-NPF** (BIMP23618)
MQSCSNSIYLFLVLFILGTGIVHGEPGPMARPTRPEIFKNQEELRKYLDHVSDFYSLNGKAR

YGKRGSVLSSVPEVNYVWDSMKTILENSQRSQQPKANRQFEKRKQEESGFLDEVEKYDPK
KSTSRIDSPPCHVLDTVEKYYDDVQ

>**Bimp-NPLP1** (BIMP24350)
...MVTCQDEDNTQCMPKAAFLALLRHPEVSSNLAAYSRTARITQDVKSRNDMAHLRALTE
EADDTEICVPGRVYLQLLKDPVMRGDLSIILNGRTQKLPDLLGRLLDDSDEMDAREFLLES
QKRSLATLAKNDDLPISIQDRIADNEDDEEKRAAISSEQPGQNDAGISRDYLLSGGRSDLQA
FARDFQMEKRNVGALARDFALPPGRRNIASLVRDYDQSKSNNRESTLPYNGKRNVASLAR
TFTLPQNGKRNVASVARDYGLPYGKRYVGSLARTGDFPARNQRSIASLAKNSAWPVSLKR
GIFLPGSVILRALSRHGRSMMDETNARNDLLDLQELSNLEQSQRNDYETAEEKLNDSLTKI
DSNIRRPKRQIDFSDEYPLPVMQNTNGFDYEEMMEALSGQYPNAEKRFM

>**Bimp-orcokinin** (gnl|Bimp_2.0|scf_0361 NT_176780.1)
...IALSPIDRQLLERFVKRNIDEIDRTAFDNFFKRNLDEIDRVGWSGFVKRLADDVVTGDGRT
NVLAQRG

>**Bimp-PDF** (BIMP18458)
...MLGITYQILGTTEDSYRNLLGLNLPYGRGMNNDLQFARLLMLPPCLCHSKRNSELINSLL
GLPKNMNNAGK

>**Bimp-pyrokinin** (BIMP24713)
MIGSVAFLSFNRLMTMAICVLLCVVYLVSCASGEYEGRDSSSSTSNDRAPSNEFGSCSDGK
CIKRTSQDITSGMWFGPRLGRRRRTDRKPELDFDIETLANALDGSRWAIITIPGTDRRQAKQ
FTPRLGRESGEEYFSYGFPNDQEELYAEEQIFPPLFAPRLGRKVPWIPTPRLGRQLHNIIDKP
RQNFDDARF

>**Bimp-RYa** (BIMP19768)
MCLWIACMVLTLVASQQKFYIQGRYGKRQEPRTDSFFVSGGRYGRSENTQKASKSLPKLV
EVEVPRIDRFFWGSRYGKLSPPDYRTVSSVNRFSAILNFMDQVNLDRENDASNRNDLDLVP

>**Bimp-SIFa** (BIMP11503)
MMSFRFVLVIVVVAFILAIAVDAAYRKPPFNGSIFGKRSNAITDYELISRAMSSVCETVSETC
NAWLARQDSN

>**Bimp-sNPF** (BIMP24462)
MSIKFYAKSLFLFIIVGLVVGAENYIDYGDEVAEKTPVENIHELYRILMQRNALENAGLGET
PLEHLMIRKSQRSPSLRLRFGRSDPRSS

>**Bimp-tachykin** (BIMP21639)
MIIPSTFLLMVSVTFAIAEESMSENVLSDKRAVMGFQGMRGKKNFDSLDSEDFGILKRAIM
GFQGMRGKKNSIIADVENQLFPEETNKRAPMGFQGMRGKKASLDDEYYKRAPMGFQGMR
GKKSLEEILDEIKKTTTRFQDPRSKDMYVIDYPEDYEKRILSMEGYPNIFDKEGEFLWEKRA
PMGFHGMRGKKLILDPWQDLDKQDVMSFQGLQRRKDTFDDYLDYSMNPSDYEKRVADF
QDIESGSDSFKRARMGFHGMRGKRNVGEIYGSNSSPTQTTIGYQGVSNPGNNLAVYEIEKR
SPFRYLGVRGKKNPRLEFRGKFVGVRGKKASSLQSVY

>**Bimp-trissin** (BIMP10534)
MNCTYVALFFIVCALWVFGETLSCEQCGRECAEKCGTRQFRACCFNNMKKRQFDLGLKW
RMRPQLYTNWLYPNIDMY

Corazonin

A

>**Bter-corazonin-like** (XP_003393262.1)
MDNARVLILFILSLTVMTVTCQSYHYTPDWASGKRSTSMLEEIVNFANKNAGQLDNAL
VNCKLQKLRLLLQGNINNQLLQVPCDLLTSGKRSLSENTIIDHFHRQPTPTVNNNY

>**Bimp-corazonin-like** (BIMP25646)
MGNARVLILFILSLTVMTVTCQSYHFSIPDWTNEKTSIFKEIVNAINKYISQSNNVLANCE
LQKLKLLLQGNINYQLFQVPCDLLVSGKKSFSENTITDYFHRQPTPVNNNY

B

Bombus impatiens: pQSYHFSIPDWTNEKTSI…
Bombus terrestris: pQSYHYT-PDWASamide
Apis mellifera: pQTFTYS-HGWTNamide
Apis florea: pQTFTYS-HGWTNamide
Magachile rotundata: pQTFQYS-HGWTNamide
Pogonomyrmex barbatus: pQTFQYS-HGWTNamide
Atta cephalotes: pQTFQYS-RGWTNamide
Acromyrmex echinatior pQTFQYS-RGWTNamide
Linepithema humile: pQTFQYS-RGWTNamide
Solenopsis invicta: pQTFQYS-RGWTNamide
Camponotus floridanus: pQTFQYS-RGWTNamide
Harpegnathgos saltator: pQTFQYS-RGWTNamide
Nasonia vitripennis: pQTFQYS-RGWTNamide

Drosophila melanogaster: pQTFQYS-RGWTNamide

A comparison of corazonin and corazonin preprohormones between different insect species. (A) A comparison of the corazonin preprohormones in *B. terrestris* and *B. impatiens*. In the *B. terrestris* (Bter) corazonin preprohormone, first the signal peptide (underlined) is removed by a signal peptidase, after which the corazonin sequence (highlighted in yellow) is excised by a prohormone convertase (PC 1/3), cleaving at the C-terminal side of pairs of basic amino acid residues (highlighted in green). The remaining peptide has a C-terminal glycine residue (highlighted in blue) that is converted into an amide group, and an N-terminal glutamine residue that is converted into a pyroglutamate (pQ) group. The *B. impatiens* (Bimp) corazonin preprohormone cannot be processed in this way, because both the pair of basic and the glycine residues are lacking. The preprohormone will, therefore, only be processed into a prohormone lacking the signal peptide, but having an N-terminal pyroglutamate group. (B) Comparison of mature corazonin sequences within the Hymenoptera. Note that the ant corazonins are always identical to the *D. melanogaster* corazonin (bottom), which represent the standard insect corazonin sequence. The five bee species (at the top) have various deviations from the standard sequence (highlighted in grey). These deviations are strongest in the two *Bombus* species.

Neuropeptide barcodes

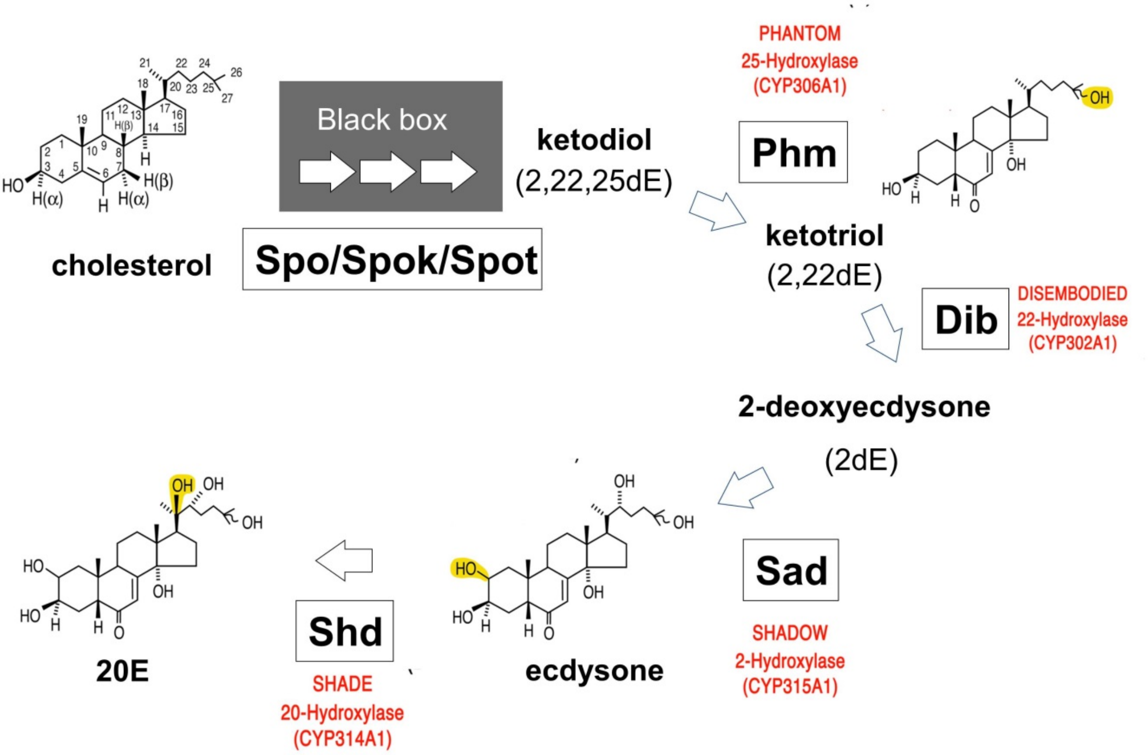
Present (green) and absent (orange) neuropeptide genes in various arthropod species. Hymenopterans are highlighted in yellow. *A. echinatior is* representative of seven ant species and *N. vitripennis* of three *Nasonia* species. *B. terrestris* and *B. impatiens* are identical, and quite similar, but not identical, to *A. mellifera*. We assume these differences may relate to *Bombus*-specific behaviour or physiology. *Dm=D. melanogaster, Bm =Bombyx mori, Tc = T. castaneum, Ae = Acromyrmex echinator, Am = A. mellifera, Bt = B. terrestris, Bi = B. impatiens, Nv = Nasonia vitripennis, Ap = Acyrthosiphon pisum, Dp = Daphnia pulex*

Neuropeptides	**Organism**									
	Dm	***Bm***	***Tc***	***Ae***	***Am***	***Bt***	***Bi***	***Nv***	***Ap***	***Dp***
ACP	absent	present	present	absent	absent	absent	absent	present	present	absent
ADF-b	absent	absent	present	absent	absent	absent	absent	absent	absent	absent
AKH	present	present	present	present	present	present	present	present	present	present
Allatotropin	absent	present	present	present	present	present	present	present	present	present
AST-A	present	present	absent	present	present	present	present	present	present	present
AST-B	present	present	present	absent	absent	absent	absent	absent	present	present
AST-C	present	present	present	present	present	present	present	present	present	present
AST-CC	present	present	present	present	present	present	present	present	present	present
Busricon-a	present	present	present	present	present	present	present	present	present	present
Bursicon-b	present	present	present	present	present	present	present	present	present	present
Capa	present	present	present	present	present	present	present		present	absent
CCAP	present	present	present	present	present	present	present	present	present	present
CCHamide-1	present	present	present	present	present	present	present	present	present	present
CCHamide-2	present	present	present	present	present	present	present	present	present	absent
Corazonin	present	present	absent	present	present	present	present	present	absent	present
DENamide	absent	absent	absent	absent	absent	absent	absent	absent	absent	present
DH (Calc.-like)	present	present	present	present	present	present	present	present	present	present
DH (CRF-like)	present	present	present	present	present	present	present	present	present	present
EFLamide	absent	absent	absent	absent	absent	absent	absent	absent	absent	present
EH	present	present	present	present	present	present	present	present	present	present
Elevenin	absent	absent	absent	present	present	present	present	absent	absent	present
ETH	present	present	present	present	present	present	present	present	present	present
FMRFa	present	present	present	present	present	present	present	present	present	present
GPA2	present	present	present	absent	absent	absent	absent	absent	present	present
GPB5	present	present	present	absent	absent	absent	absent	absent	present	present
ILP-A	present	absent	present	absent	absent	absent	absent	absent	absent	absent
ILP-B	present	present	present	present	present	present	present	present	present	present
ILP-C	present	present	present	present	present	present	present	present	present	absent
Inotocin	absent	absent	present	present	absent	absent	absent	present	absent	present
ITP	present	present	present	present	present	present	present	present	present	present
Kinin	present	present	absent	absent	present	present	present	absent	present	absent
Myosuppressin	present	present	present	present	present	present	present	present	present	present
Neuroparsin	absent	absent	present	present	present	present	present	present	absent	present
NPF	present	present	present	present	present	present	present	present	present	present
NPLP-1	present	present	present	present	present	present	present	absent	present	absent
Orcokinin	absent	present	present	present	present	present	present	present	present	present
PDF	present	present		present	present	present	present	present	absent	present
Proctolin	present	absent	present	absent	absent	absent	absent	absent	present	present
PTTH	present	present	present	present	absent	absent	absent	present	present	absent
Pyrokinin	present	present	present	present	present	present	present	present	present	absent
RYamide	present	present	present	absent	present	present	present	present	present	present
Sex peptide	present	absent	absent	absent	absent	absent	absent	absent	absent	absent
SIFamide	present	present	present	present	present	present	present	present	present	present
sNPF	present	present	present	present	present	present	present	present	present	present
Sulfakinin	present	present	present	present	present	absent	absent	absent	absent	present
Tachykinin	present	present	present	present	present	present	present	present	present	present
Trissin	present	present	present	present	absent	present	present	absent	absent	absent

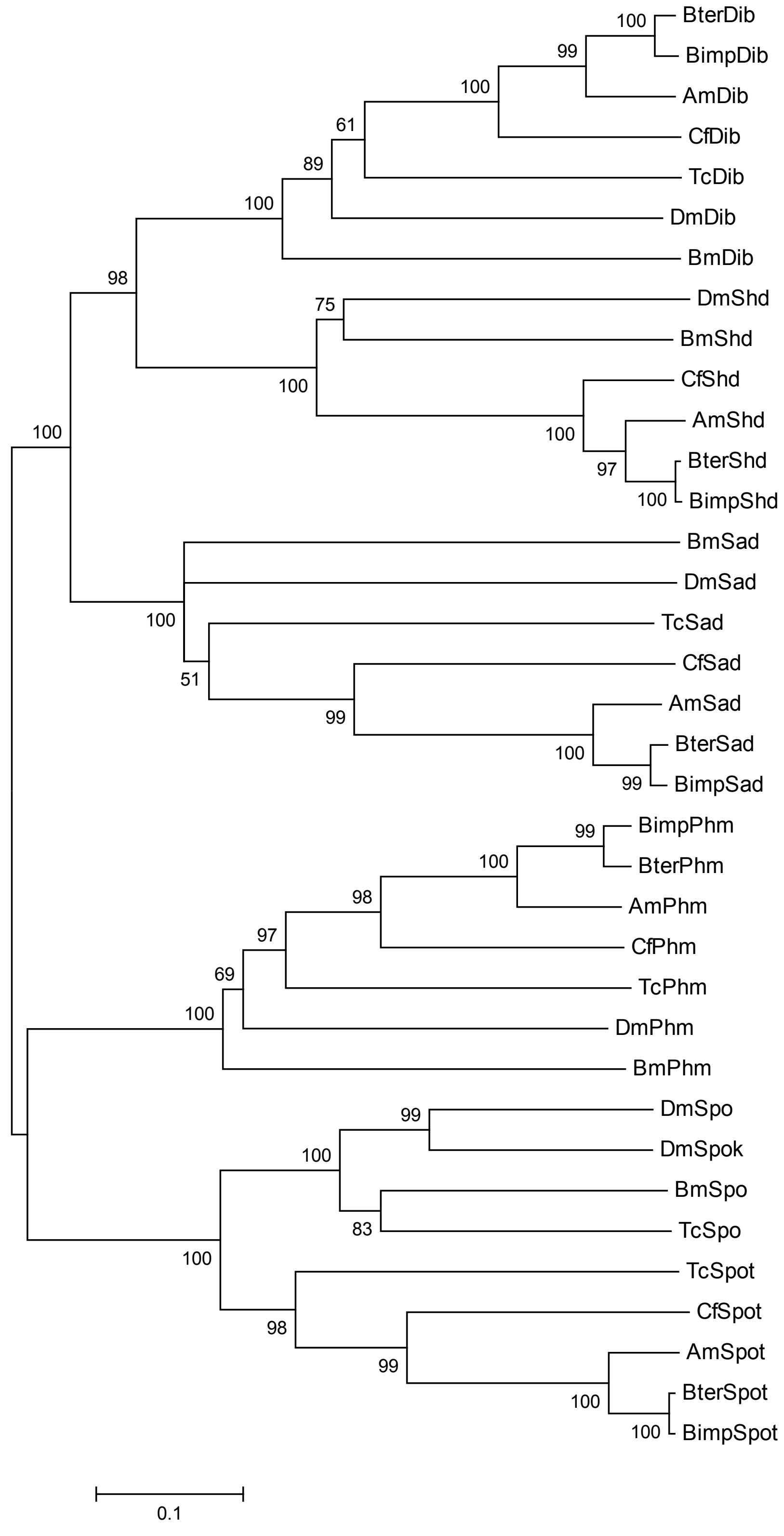
Halloween genes

Halloween genes identified in *B. terrestris and B. impatiens*. Genbank IDs of *D. melanogaster*, *A. mellifera* and *T. castaneum* orthologs are also presented. In the case of *T. castaneum* CYP307A1/2 and CYP307B1, contigs were given on which the gene is found, also for *A. mellifera* CYP307B1. For *B. terrestris*, the NCBI gene ID is provided and for *B. impatiens* the official gene set ID is given.

Name		*D. melanogaster*	*A. mellifera*	*T. castaneum*	*B. terrestris*	*B. impatiens*
CYP307A1	***spook***	AF484415	-	AAJJ01000951	not present	not present
CYP307A2	***spookier***	NM_001110990			not present	not present
CYP307B1	***spookiest***	-	AADG05005080	AAJJ01001163	100642619	BIMP19752
CYP306A1	***phantom***	AF484413	XM_391946	XM_963384	100642897	BIMP23510
CYP302A1	***disembodied***	AF237560	XM_001122832	XM_969159	100649492	BIMP10969
CYP315A1	***shadow***	AY079170	XM_395360	XM_965029	100644009	BIMP17298
CYP314A1	***shade***	AF484414	DQ244074	XM_967606	100649449	BIMP18931



Summary of the biosynthesis of 20-hydroxyecdysone (20E) presenting the different Halloween genes (boxed) and their function in the ecdysteroid biosynthesis pathway. The intermediate products and their structure are also presented. The changes for which the enzyme is responsible are highlighted in yellow.



Phylogenetic tree of the Halloween genes. This tree was constructed with the neighbour-joining method using whole sequence amino acid sequences. Bootstrap values as percentage of a 1000 replicates are indicated on the tree. Halloween genes full amino acid sequences are from *B. terrestris* (Bter), *B. impatiens* (Bimp), *D. melanogaster* (Dm), *T. castaneum* (Tc), *A. mellifera* (Am), *C. floridanus* (Cf) and *B. mori* (Bm).

Odorant Receptors

Details of *B. terrestris* OR family genes and proteins. Columns are: Gene – the gene and protein name we are assigning (suffixes are NTE – N-terminus missing; INT – internal exon unidentified; FIX – assembly or frameshift fixed; JOI – joined across scaffolds; PSE – pseudogene; TRA – trans-spliced model; multiple suffixes are abbreviated Fine as is to single letters); Refseq protein number (prefix is XP_00); Scaffold – the genome assembly scaffold ID (format is GroupX.X, amongst 5678 scaffolds in assembly v1.0); Coordinates – the nucleotide range from the first position of the start codon to the last position of the stop codon in the scaffold; Strand – + is forward and - is reverse; Introns – number of introns in the coding region; ESTs – presence of a spliced EST contig in ILLUMINA RNAseq from male (MH) or queen heads (QH), or queen ovary (QO), or multiple life stages (MLS); AAs – number of encoded amino acids in the protein; Comments – comments on the OGS gene model, repairs to the genome assembly, and pseudogene status (numbers in parentheses are the number of obvious pseudogenizing mutations). Suffixes after the gene/protein names are: PSE – pseudogene; NTE – N-terminus missing; INT – internal sequence missing; FIX – assembly repaired; JOI – gene model joined across scaffolds; TRA – trans-spliced gene model; multiple suffixes are abbreviated to single letters.

Gene	Refseq	Scaffold	Coordinates	Strand	Introns	ESTs	AAs	Comments
OrCo	3402775.1	Un633	553161-561881	-	7		479	Fine as is
Or1	3393987.1	2.3	4649752-4652343	+	4		412	Fine as is
Or2	3393988.1	2.3	4653527-4655914	+	4		403	Fine as is
Or3	3393991.1	2.3	4656694-4658840	+	4		404	Change N-terminus
Or4	3393992.1	2.3	4660888-4663020	+	4		404	Fine as is
Or5	3393901.1	2.3	4667219-4669080	+	4		398	Fine as is
Or6	3393993.1	2.3	4670239-4671916	+	4		399	Fine as is
Or7	3393902.1	2.3	4673961-4675822	+	4		407	Fine as is
Or8	3393903.1	2.3	4676857-4678627	+	4		401	Fine as is
Or9	3393994.1	2.3	4680576-4682671	+	4		409	Fine as is
Or10	3393995.1	2.3	4683642-4685608	+	4		411	Fine as is
Or11	3393996.1	2.3	4686553-4688243	+	4		403	Change N-terminus
Or12	3393904.1	2.3	4689169-4691043	+	4		411	Fine as is
Or13	3393997.1	2.3	4691865-4693744	+	4		405	Fine as is
Or14	3393905.1	2.3	4694422-4696139	+	4		405	Fine as is
Or15	3393998.1	2.3	4696844-4699153	+	4		409	Fine as is
Or16	3393906.1	2.3	4699858-4702380	+	4		405	Deletion in model
Or17	3393907.1	2.3	4702914-4704625	+	4		403	Fine as is
Or18	3393999.1	2.3	4706421-4708168	+	4		403	Fine as is

Or19	3393909.1	2.3	4709060-4712056	+	4		405	Deletion in model
Or20	3393910.1	2.3	4713557-4715341	+	4		406	Fine as is
Or21	3394000.1	2.3	4718202-4719901	+	4		398	Fine as is
Or22	3394001.1	2.3	4720605-4722317	+	4		404	Fine as is
Or23	3393912.1	2.3	4723673-4725381	+	4		404	Fine as is
Or24FIX	3394002.1	2.3	4726944-4728666	+	4		406	Fix frameshift
Or25	3394003.1	2.3	4730494-4733168	+	4		409	Fine as is
Or26	3394004.1	2.3	4733882-4735636	+	4		407	Deletion in model
Or27	3393913.1	2.3	4736765-4738491	+	4		405	Fine as is
Or28	3393914.1	2.3	4739300-4741712	+	4		406	Fine as is
Or29	3393915.1	2.3	4742531-4744305	+	4		405	Fine as is
Or30FIX	-	2.3	4747469-4749277	+	4		411	Fix frameshift
Or31	3393917.1	2.3	4750427-4752262	+	4		411	Fine as is
Or32	3394005.1	2.3	4753075-4754956	+	4		407	Fine as is
Or33	3393918.1	2.3	4756102-4758151	+	4		406	Fine as is
Or34	3393919.1	2.3	4758861-4760750	+	4		410	Fine as is
Or35	3393921.1	2.3	4761664-4763201	+	4		411	Fine as is
Or36	3393920.1	2.3	4764251-4766076	+	4		405	Fine as is
Or37FIX	3403429.1	Un5358, Un3730	<1->941, 1051->1758	-	4		406	Fix assembly
Or38FIX	3394006.1	2.3	<4771050-4772860	+	4		406	Fix assembly
Or39	3394007.1	2.3	4773619-4775362	+	4		405	Fine as is
Or40	3394008.1	2.3	4776241-4778655	+	4		411	Fused gene model
Or41	-	2.3	4779534-4781267	+	4		405	New gene model
Or42	3394008.1	2.3	4782152-4784336	+	4		410	Fused gene model
Or43	3394008.1	2.3	4786038-4788418	+	4		410	Fused gene model
Or44	3394008.1	2.3	4789162-4791442	+	4		410	Fused gene model
Or45	3394008.1	2.3	4792303-4794092	+	4		413	Fused gene model
Or46	3394008.1	2.3	4794814-4796922	+	4		410	Fused gene model
Or47	3403027.1	Un975	2257-4556	-	3		394	Fine as is
Or48	3401114.1	15.5	1989652-1991921	+	3		394	Fine as is
Or49	3401175.1	15.5	1994455-1996889	+	3		394	Different final exon

Or50	3401176.1	15.5	2000732-2003508	+	3		400	Fine as is
Or51	3401113.1	15.5	2004311-2006835	+	3		394	Fine as is
Or52	3401177.1	15.5	2008201-2010824	+	3		394	Fine as is
Or53FIX	3401116.1	15.5, Un4668	2015289->201617, <1-6617	+	3		394	Fix assembly
Or54FIX	3403422.1, 3403233.1	Un4605, Un995	<1-1006, <1-645	-, +	3		394	Fix assembly
Or55FIX	3403234.1	Un995, 15.5	<2020697-2021523	+	3		394	Fix assembly
Or56	3401115.1	15.5	2023109-2025428	+	3		394	Fine as is
Or57	3401178.1	15.5	2028000-2030265	+	3		394	Fine as is
Or58	-	13.5	4730302-4733416	+	4		371	New gene model
Or59	-	13.5	4734462-4736834	+	4		370	New gene model
Or60	-	13.5	4737691-4740007	+	4		372	New gene model
Or61	-	13.5	4741197-4743349	+	4		373	New gene model
Or62	3402693.1	Un586	200-2381	-	4		373	N-terminal extension
Or63FIX	-	Un3418, Un3602, 13.5	<1-327, <1->566, <4747131-4748198	-,-,+	4		371	Fix assembly
Or64	-	13.5	4750858-4753038	+	4		373	New gene model
Or65	-	13.5	4754985-4757201	+	4		373	New gene model
Or66	3400291.1	13.5	4758685-4760704	+	4		371	Fine as is
Or67	3400342.1	13.5	4761733-4763633	+	4		364	Part of another model
Or68	3400342.1	13.5	4764721-4767033	+	4		370	Part of another model
Or69	3398625.1	10.4	212240-214970	+	5		403	Fine as is
Or70	3401565.1	15.6	623438-625960	-	5		403	Fine as is
Or71	3401564.1	15.6	619917-622765	-	5		403	Fine as is
Or72	3401563.1	15.6	616976-618984	-	5		427	Fine as is
Or73	3401562.1	15.6	613310-615833	-	5		410	Fine as is
Or74PSE	-	15.6	606932-609414	-	5		402	Pseudogene (5)
Or75FIX	-	15.6, Un124	<603748-606062, <1-635	-,+	5		406	Fix assembly
Or76FIX	3402395.1	Un124, 15.6	1451->3396, 602134->602306	+,-	5		410	Fix assembly

Or77	3401556.1	15.6	598583-601409	-	5		409	Fine as is
Or78	3401567.1	15.6	593001-595284	-	5		403	Fine as is
Or79FIX	3401561.1, 3403388.1	15.6, Un2327	<590785-591896, <1-1428	-,+	5		409	Fix assembly
Or80	3401561.1	15.6	584441-587522	-	5		400	Fine as is
Or81	3401560.1	15.6	579911-582573	-	5		402	Fine as is
Or82	3401521.1	15.6	576848-579134	-	5		407	Fine as is
Or83	3401559.1	15.6	573872-576107	-	5		408	Fine as is
Or84	3401503.1	15.6	570653-572284	-	5		404	Fine as is
Or85	3403340.1	Un1188	450202-452973	-	5		409	Fine as is
Or86	3397911.1	9.5	1069013-1071323	-	5		389	First half of model
Or87	3397911.1	9.5	1061346-1063764	-	5		389	Second half of model
Or88	-	9.5	1051910-1054157	-	5		389	New gene model
Or89PSE	-	9.5	1049777-1050881	-	4		237	Pseudogene (3)
Or90PSE	-	9.5	1045048-1048089	-	5		390	Pseudogene (1)
Or91FP	-	9.5	1041867-1044343	-	5		388	Fix assembly; pseudogene (1)
Or92NTE	3397949.1	9.5	1036933-1039608	-	5		396	N-terminus unidentified
Or93	-	9.5	1033816-1035955	-	5		394	New gene model
Or94	-	9.5	1026671-1028792	-	5		393	New gene model
Or95	-	9.5	1022653-1025011	-	5		389	New gene model
Or96FIX	-	10.1, Un980	8542326-854268, 2139-3497	+, -	5		412	Fix assembly
Or97	3400864.1	14.7	1090557-1092303	-	4		401	Fine as is
Or98	3400880.1	14.7	2355789-2357517	-	4		401	Fine as is
Or99FIX	3400879.1	14.7	2353569-2354931	-	4		402	Fix assembly
Or100	3400841.1	14.7	2348101-2349850	-	4		402	Fine as is
Or101	3402378.1	Un51	23434-37459	+	5		380	Add N-terminus
Or102	-	Un987	30542-41440	+	5		384	New gene model
Or103	3398618.1	10.4	168327-172295	+	5		387	Multiple changes
Or104FIX	3398619.1	10.4, Un4996, Un2069, 10.4	173353->175348, <1->778, <1->655, <177910-178024	+,-,-,+	5		374	Fix assembly

Or105FIX	3398620.1	10.4	181128-184269	+	5		376	Fix assembly
Or106	3398622.1	10.4	186136-189207	+	5		386	Multiple changes
Or107	3398624.1	10.4	198983-206364	+	5		375	Fine as is
Or108	3397556.1	9.1	340763-343912	-	6		408	Add N-terminus
Or109	-	14.4	188105-189918	+	8		394	New gene model
Or110	3401155.1	15.5	862306-868203	+	4		438	Add N-terminus
Or111	3395372.1	5.1	6136242-6139048	-	6		389	Fine as is
Or112	3393433.1	1.8	565127-568007	-	5		390	Fine as is
Or113PSE	-	1.3	2692343-2693558	+	3		262	Pseudogene (6)
Or114	3396270.1	7.1	1526990-1528796	-	4		400	Part of another model
Or115	-	10.4	93829-98365	-	4		398	New gene model
Or116	-	2.1	1006702-1008643	-	5		377	New gene model
Or117	3397790.1	9.4	1150178-1152426	-	5		373	Remove first exon
Or118	3397835.1	9.4	1147545-1149228	-	5		371	Fine as is
Or119	3397834.1	9.4	1144442-1146409	-	5		371	Fine as is
Or120	3397789.1	9.4	1141593-1143119	-	5		380	Add N-terminus
Or121	-	9.4	1136276-1137784	-	5		374	New gene model
Or122	-	2.2	1155133-1158704	+	5		374	New gene model
Or123	-	2.2	1165659-1167791	+	5		374	New gene model
Or124	3395945.1	6.1	2461465-2463691	-	5		375	First half of model
Or125	3395945.1	6.1	2458431-2460596	-	5		377	Second half of model
Or126	3396148.1	6.3	6319634-6321414	-	5		374	Fine as is
Or127	3402379.1	Un51	48634-58988	+	5		374	Fine as is
Or128JOI	3403225.1	Un706, Un987	40915->18304, <1-7812	+	5		372	Join across scaffolds
Or129NTE	3399230.1	11.4	<3933522-3935970	+	9	QO	397	N-terminus unidentified
Or130NTE	3399231.1	11.4	<3939190-3941259	+	9		397	N-terminus unidentified
Or131	3399232.1	11.4	3943207-3945910	+	9	QH	403	Fine as is
Or132FIX	3403290.1	Un1121	1304-4046	+	9	MH	403	Fine as is; Fix assembly
Or133	3399233.1	11.4	3954125-3956822	+	9	MH, QH	403	Fine as is
Or134NTE	3399234.1	11.4	<3958722-3961754	+	9		401	N-terminus unidentified
Or135NTE	3399235.1	11.4	<3962937-3965186	+	9		400	N-terminus unidentified

Or136NTE	3399237.1	11.4	<3966381-3968592	+	9	MH	401	N-terminus unidentified
Or137NTE	3399238.1	11.4	<3969831-3972027	+	9		401	N-terminus unidentified
Or138	3399239.1	11.4	3972875-3976764	+	9		404	Intron splice changes
Or139	3399240.1	11.4	3977675-3980188	+	9	MH	405	First half of model
Or140NTE	3399240.1	11.4	<3982614-3984703	+	9	MH, QH, QO, MLS	403	Second half of model
Or141	3399599.1	12.1	3536724-3542428	-	8	MH	390	Fused model
Or142FIX	-	12.1, Un872	<3532917-3534948, <1-1310	-, +	8		390	Fix assembly
Or143FIX	-	Un872, 12.1	2790->4726, 3528615->3529889	+, -	8		390	Fix assembly
Or144	3399526.1	12.1	3521012-3526168	-	8	MH	390	Multiple changes
Or145	3399598.1	12.1	3516576-3519938	-	8	MH, QH	391	Fine as is
Or146	3399597.1	12.1	3512014-3515217	-	8	QH	389	Fused model
Or147	3399596.1	12.1	3508203-3511225	-	8		390	Needs N-terminus
Or148	3402807.1	Un706	18016-22266	+	8	QH, QO	390	Needs N-terminus
Or149	3403249.1	Un1054	31073-41514	-	8	MH, QH	390	Needs N-terminus
Or150FIX	-	Un1054	21328-29754	-	8	MH, QH	390	Fix frameshift
Or151	-	4.5	9129684-9132673	-	8		388	New gene model
Or152	-	4.5	9121295-9124201	-	8		388	New gene model
Or153	-	4.5	9115463-9118461	-	8		388	New gene model
Or154	-	4.5	9110023-9113027	-	8		388	New gene model
Or155	-	4.5	9102467-9105462	-	8	MH, QO	388	New gene model
Or156	-	4.5	9097265-9100289	-	8	QH	388	New gene model
Or157	-	4.5	9092287-9095717	-	8		396	New gene model
Or158INT	-	4.5	9084314-9087496	-	8		357	Internal exon missing
Or159INT	-	4.5	9080343-9083575	-	8		379	Gap removes exon
Or160	-	4.5	9075988-9078996	-	8		389	New gene model
Or161FIX	-	4.5	9069120-9072462	-	8		401	Fix frameshift
Or162	3394499.1	3.4	1486491-1493341	+	8		396	Needs N-terminus
Or163FT	3392906.1	1.1, 1.1	5810->5968, <1->4854	+, -	8	MH, QH	409	Trans-spliced model, extended assembly

Or164FT	3403003.1	Un2033, Un687, Un800	1219->1833, <2032->2286, <1-1162	+	8		416	Trans-splice model, Fix assembly
Or165TRA	3398760.1	11.1	168721->168864, 165538->167766	+, -	8	MH, QH	407	Trans-spliced model

Protein sequences of predicted *Bombus terrestris* odorant receptors from the table above

>BtORCO
MMKFKQQGLVADLMPNIRLMKATGHFMFNYYTDNSTKTIHRIFAVVHLILMLMQFGFCGINLIFEKEDVDDLTANTITMLFFTHSVVKVVYF
AVRSKLFYRTLGIWNNPNSHPLFAESNSRYHQVAVRKMRILLLAVLVTTMLSAISWTSITFIGDSVKKVIDPITNETTYVEIPRLMLRSWYPYN
ASHGMAHILTLIFQFYWLVFCMADANLLDVLFCSWLLFACEQIQHLKNIMKPLMEFSATLDTVVPNSGDLFKAGSAEQPRDHDPLPPTTPTA
PGENMLDMDLRGIYSNRTDFTATFRPTAGMTFNGSVGPNGLTKKQEMLVRSAIKYWVERHKHIVRLVTAIGDAYGVALLLHMLITTITLTLL
AYQATKINAVDTYAASVIGYLLYSLGQVFMLCIFGNRLIEESSSVMEAAYSCHWYDGSEEAKTFVQIVCQQCQKAMSISGAKFFTVSLDLFAS
VLGAMVTYFMVLVQLK
>BtOr1
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SNYIFFTVENSPIYEITFVLQIFISSIILSTNCGIYSLIASITMHCCGLFEVTSRRIETLHKWNKCDLHDRVVDIVQYHLEAIGYSALIGKSLSIVFLS
EMVGCTIIICFLEFGVIMELEDHKTLSTLTYFVLMTSIFVNVFIISFIGDRLKQESERIGETSYFLPWYDFPVDVAKNINTIMLRTSLPSCLSGANIL
ELSLQAFCDVCKTSAAYFNFLRAMTV
>BtOr2
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YEITFVVQMCISCIIMTTNYGIYSLIASITMHSCCLFEVTNRRIEKLRNWDKRDLHDRIADIVQCHLKAIEYSAVIGKSLSFVFLSEMIGCTIVICF
LEFGVIMEWEDHKTFSTITYFVLMTSMFVNVFIISFIGDRLKQESERIGETSYFLPWYDFPLNEAKNVRTIILRTRLPSSLSGAKILDLSLQAFCD
VVKTSAAYFNVLRAMAA
>BtOr3
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FVLQVLSGFCIYTVFSGAIGITMMICLHACSLIRILIDKLVDLTDKSNTSEEIIQEKIVNIVGYHRKIKKFLSNGQQLSEYISFLELFNGAGIICLIGY
AVIVEWENLNTITVIVCFTLLTTFTFTSYTICSIGQLLLDESNNLAQTCVTLNWYRLPMKQARYVVLMMIMSNDPIKLTAVKVMDVSLSTFSDI
MKASMGYLNMLRNVT
>BtOr4
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FVLQVLSGLFIYTVFSGAIGIMMMICLHTCGLIRILTDKLMDLIDKSNTSEEIIQEKIVNIVEYHRKIKKFLSNGQQLSEYISFLELFNGTIIIGLLG
YCVILEWESHNTIGLMVYITLLTTFTFTSYTICSIGQLLLDESNNFARTCVTLEWYRLPVRKTRYMIMIIIMSSDPIKLTAAKMMDVSLLTFSDI
MKGAMGYLNMLRKVN

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>BtOr5
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VLQIMGGFLNYTILCSTMGVCLMLCLHLSSLLRILMNKMIELTSQLDTSETAVQKKISDIVAYQTKVKEFANSVEEITPYLYFFEIFNYAIEACI
VGYCIIVEWEESNAASIIVYLMFQGICIFCNYAMCYIGQLLINESENVRRMSITLNWYRFPMKKARSLILIIIMSNYPIKLTAGKIVDISLATFTDII
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>BtOr6
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LQILGAFVIYTILCGSLGLISLLCVHMSSLLRILANMMIELSDQPDTSENAVYKMIKDIVEYRTKVKKFSDKVEHIMSYISCLEIFNGTCIACLVG
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SIGYLNVLRNSVK
>BtOr7
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QKSPNYEILFLVQILAGFVIYAVISGSCGLSALFVLHACSMLRILVDKMKALVDMRDMSDTMVQRRIMDIVEYQTKIKRFLKNIETITEYICLT
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>BtOr8
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ILLCRASEIQNGLNVIKQDWVTATEENRLIFRSKAKIARRVVLTVAITMYGGGLCYRTVLPLLKGTIVTPGNITIRPLPCPSYFVILDEQKSPNYE
ILFVLQVMAGFVIYAVISGSCGLSALFVLHVCSMLSILVDKMKALVDMRDMSDTMVQRRIMDIVEHQTKIKGFLKNIETITQYVCLSEMICGT
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>BtOr9
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RTIVDARRSPINEIFYTIQLLSGFVAHDITVAACGLAALLAMHACGQLQVLMSWLEKLVDGRENDDESLDQRLANIVEQHVRIINFIALTEDLL
REISLVEVVGCTMNICFLGYHSMMEWDFNHPVTGFTYIILLISVTFNIFIFCYIGEVLAEQTVKVGQKSYMIDWHRMPWKKSLVVPLMISMSR
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>BtOr10
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MAFAKYYSLIVHKADIRECLERIKWDWKNMTNREDREIMTVNASFGRKLVVVCTLFMYSGFVFYYIAIPISVGKIAAENESLTFIPLVFPFSRFI
VDTRYSPTNEIVFSIQLVAGCLMHGITSAACSLAAAFAVHACGQMQVLMNWLKHLVDGRSDMSERVDGRIADIVCQHVRILKFLTLIENTIQ
QISFAEFLGCTLDICLVGYYVIMELKSNDVTSALTYMILLISITFNIFIFCYIGEIVTEECRKIGETSYMIEWYRLQGNKKLCCVLIIAMSNCTIKLT
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>BtOr11
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LGCTLDICLLGYYIIMEWNSNHLTDVMTYSVLLVSLTFNIFIFCYIGELVADKSRKVGEMTYMIEWYRLYGKKKLCCVLIIAMSDSSRKLTAG
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>BtOr12
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DTRYSPINEIVFSLQLVSGCLMHSITSAACSLAAIFAVHACGQMQVLTSWLKHLIDGRSDMYNNVDSRIAIVVSQHVRILNFLALTEKTLQQVS
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>BtOr13
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DVRSSPSNEIIFSIQTLTGVVMHTVTSAACSIAAVFAVHACGQMQVLMNWLEHLVDGRSDMSNIVDERIASIVTQHNRILRFLALTESALQQIS
FVEFLGCMMNMCLLGYYFIVEWSSNDIMHSITHMILMISFSFNIFIFCYIGELVAEQCKKVGEMTYMIDWYRLTGKKKLGCILIIAMSNSSIKFT
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>BtOr14
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PCNEIFYFIQTLTGAVMHTVTSAACSIAAVFAVHACGQMKVMMNWLEYLVDGRPDMSNTVNGRIAKIVIQHNRILKFLALTENALQQISFVE
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>BtOr15
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TNLLDVRFSPANEIVLTLQLLSGFVVTSVTVGACGLAAVLTMHASGQLNVVMARLDNLVNTKEEEKQEEQKAAQRKLGIIVEHHLRTLSLM
ASIEKVMNMICLVELVGCTMNMCMIKYYLLTEKSKDVIIAYAILYASMVFNIFIFCYIGEIITEQGERVGKKVYMTEWYRLPPKTALGLVLVIS
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ANEIVLVMQFLSAFIADSSGIGFYTLASVLAAHACGQLSVLTICISDYVNEAGNRKEDTSFRKIGTIVEHHLRTLDFIARIEEVMSWVCMTELFR
CVLAICMVGYYIVTEWSDHDVRSLTSYFIIFASVTFNTFLLCYIGELLTEQCMKVGEIVYMTNWYILPRKRILELILIIARSSVVIEITAGKLIHMS
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>BtOr17
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VDESPTNEIVLFLQAWSTIIANSSTVGIFSLAAVLAAHACGQLNVVMVWITEFVNEPKKANGPKGIGVIVERHLRTLNFIGYIENLMNRIYFLEI
FRCTMDICILGYYILSEWDDQNVQSLVTYVMIYISIGFNVFLICYIGEILTEQSKKVGEVVYMTNWYYLPDKTILDLILIIARSSVVVQITAGKM
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>BtOr18
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NVDESPTNEIVLFLQAWCTIIANSSTVGMFSLAAVLAAHACGQLNVVMVWITEFVNEPKKADGPKGIGVIVERHLRTLNFIGYIEKLMNRVYF
LEIFRCTMNICILGYYILSEWADQNVQSLITYIMIYISIGFNVFLICYIGEILTEQSKKVGEVVYMTNWYYLPDKAILDLILIIARSGVVVQITAGK
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>BtOr19
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SPANEIVLVVQFLSAFIADSSGIAFYTLASVLAAHACGQLGVLTIWINDYVNEARNRKQDTSFRKIETIVKHHLRILDFIARIEEIMSWVCMTEL
FRCVLAICMVGYYIVMEWSDHDVRSLTSYFVICASLTFNTFVLCYIGEVLIEQCMKVGEIVYMTNWYFLPRKRILELILIIARSSVVIEITAGKLI
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DESPANEIMLFLQIWAALIANSSTVGIFSLAAVLAAHACGQLDVIMMWITKFVKEAKQRKKTSSFREIGVIVERHLRTLNFISCIEDVMNRIYFL
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NEIMLSLQIWSALIANSSTVGIFSLAAVLAAHACGQLDVIMAWITEFVKETSSFQEIGVIVERHLRTLNFISCIEVVMNKIYLLEMLRCTMNICLI
AYYILSEWDEHDIRNLTSYFMMFVSICFNIFVICYIGEILTEQSKKIGDAVYLTNWYYLPNKEIHNLILIIVRSSMVVQLTAGKMIQMTINTFGN
VVKTGFAYLNLLQQMM
>BtOr22
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ALLLHSKDIRQCIEHMETDWRTLIREEDQHVMLKNAKFGRYVAAFCAIFMQGSVLCFCFVTALNTFEIQIGNETRVLHVLPCAVYKKLVNVD
ESSRNQIMLFLQVLSAIIANSSTIGIFSLAAVLAAHACGQLNVVMLWINEFVNEARGEKTSSIQIGAIVERHLRTLNFISYIENVMNKICLLEMLR
CTMDICVTGYYILSEWTEHDIQNLSSYFMMLVTICYNIFVICYIGEILSEQCKKIGEVVYMTNWYYLPGKTILDLIMVIARSNVVVQITAGKLV
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>BtOr23
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PTNEFMIFLQIWSTFIANCSTVGIFSLAAVLAAHACGQLNVVMLWIVEFVNEAKVERRADGFMEIGIIVERHLRTLNFISYIEGVMNKICFLEM
LRCTMDICVIGYFIVSEWAEHDVRNLTSYSMMFVAICYNIFILCYIGELLTEQCKKIGEVVYMTNWYYLPGKTILDLIMVIARSNVVVQITAGK
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>BtOr24FIX
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IPTNELMLFFQIWSTVIANFSTIGIFSLAAVLTAHACGQLNVITLWIVEFVNETRVEKKTGGFIQIGVIVERHLRTLNFISYIEDVMNKICLLEML
RCTMDICVIGYYILSEWDEHDIRNLASYFMMFVTICFNIFIICYIGELLTEQCKKIGEVVYMTNWYYLPSKTILDLIMVIARSNVVIHITAGKLV
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>BtOr25
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NLLDARFSPANEIVFVLQILSGLIVTSVTVGACGLAAVLTMHASGQLNMVVARLDNLVDTKIEEKQEAQTVAQKKLGIIVEHHLRTLSLIASIE
KVMNMICLVELVGCTINMCMIKYYFLTEKSKDMRIVYAIVYASMVFNIFIFCYIGEIVIEQGERVGKKVYMTEWYRLPHKTALGLVLVISRSS
MVVKITAGKFVQISITTFGIVFKTSFAYLNMIRTML
>BtOr26
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ALLTQGKNIRQCIEHIEADWRTVTREEDKNVMLKNAKLGRYIAGFSVIFVQGSVLCFFFVTALNTVEIQIGNETRVLHLLPCAVYKKLVNVDD
SLTNEIMLLLQMWSTIIANSSTSGIFGLSAVLAAHSCGQLNVIMVWITEFVNKARERKKTGSFIEIGMIVERHLRTLNFISCIEDVMFKIYFVEMF
RSTMDICVIGYYILSEWADHDFQNLITYFMMLISICFDIFVICYISEILTEQCQKVGEVVYMTNWYYLPNKVILDLILIIARSSIVVQLTAGKFIQ
MSVYTFGNVLKTGFAYLNMLQQMTR
>BtOr27
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TNEIILFMQFLTGFIVSSSTLGILSITVVLIAHACGQLNVVMTWITEFVNESRKEKIAPFENIGIIVERHLRTLSFVSSIEETVNRIFFLEVLRSTLHM
CMLSYYIVTEWSDSDIQILTTYSMLLASICFNIFVICYIGETLTEQSRKVGDVVYMANWYYLTEKRILELILIIMRSSVVVEITAGKIIHMSIQTFS
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>BtOr28
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SPMNEIVLATQFISGFIVNSSAVAAITIGAVFTAHAYGQFTVLMRWINEFVNRSEDQKKDVEFNEIGEIVEHHLRILSLIAGIENVLTQFCFMELL
KSKLDISMLGYYIITEWAEHDIRNLTTYFMIMASMSFNIFTVCYIGDILTEQSKKFGDVVYMTKWYYLPNKDMFDLILIISRSNSAIKITAGKIT
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>BtOr29
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EIILASQFVSGFIANSSAVGAVGMAAVFAAHAYGQLTILMIWIKEFVNRSKDYSRNVGLNEIGEIVEHHLRVLSFIAGIEDVMNEICFMELFKC
TMNMCMIGYYILMEWRDHDIQYMPAYLIILFSMTFNIFVICYIGETLKEQCEKVGEVAYMTNWYYLPYKDILNLIQIILRSSMMIKITAGKLVH
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>BtOr30FIX
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PRTSPSFEIVQFMQCLAGFVIYSVTVGACSLAAVFVMHVCGQFGILVKKLQRLVGSLEEEKNLNVHEQRLGDIVEHHLHILGFISQIEDLLNEIC
FVELIGCTVNICFLAYHLLTEWEQNDTIGTLTYCTLLISFTFNIFILCYIGEILSEQCRNISISAYMIDWYRLPQKKALGLILIFAVANSSTKLTAGK
IVELSLASFCSVLKSAFAYLSLLRTLTI
>BtOr31
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RTSPSFEIVQLMQCLAGFVIYSVTVGACSLAAVFVMHVCGQFGILVKKLQRLVGSLEEEKNLNVHEQRLGDIVEHHLHILGFISQIEDLLNEIC
FVELIGCTMNICFLGYYLLTEWEQSETIGTLTYCTLLISFTFNIFILCYIGEILSEQCRNISLSAYMIDWYRLPQKKALGLILIFAVANTSTKLTAG
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>BtOr32
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MFKCMLGMCMPSYYILVEWSEHNIQNITAYVLIIISMTCNIFLVCYIGEIIMEKCKKIGDMVYMADWYHLPDQDIINLIMIISRSSMEVKITAGK
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>BtOr33
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VQTNPTHDIILGTQFLSALVVSSGAAGSFSLATVFASHALGQLNIMVTWVDEFTNQTKQQNKQAQINKIGVIVEHHLRVLSLIARIERIMSPICF
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>BtOr34
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LFLIEVMLSTLLICLLEYYCMMEWETSDSAAISTYIILLTSFTFNILIYCYVGELLLGQGSEIATALYDIGWYNLPGRKARDIVLVLAISKYPLKL
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>BtOr35
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ALREICLAEIVESTIIMCLLEYYCMMEWQNSDAIAILTYVTLLISFTFNIFIFCYIGEILTEQCSQIGTTSYEIEWYQLPAKRAYNLILLISISQYPPK
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>BtOr36
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LTEIVECTICMCILEYYCLMEWANSDLIATLTYLTLLTSFTFNIFIFCYIGELLTEQCSQIGTTSYEIEWYQLPAKRAYDLILLISISQYPPKLTAGK
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>BtOr37FIX
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>BtOr39
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EFVGTTLVVCFLEYYCLTDWQSNNKIGVATYSMLLVSLTFNMFLLCYIGNLLLEKSSDIGISCYLIDWYRLPPKTVQDLMLIIAMSNTPVKISA
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>BtOr40
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VLQEVCFFEFVGSTFVICLLEYYCITDWQQNNKIGLATYSMLLVSLTFNMFLLCYIGNLLLEKSTNIGISCYMIDWYRLPVKTVQDLMLIIAMS
NSPVKISGGRMFLLSLPTFGNILKTSFAYLNFIRNTLM
>BtOr41
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FFEFVGSTLVICLLEYYCITEWQDNNKIGVATFSMLLVSLTFNMFLLCYIGNLLIEKSTNIGISCYLIDWYRLPPKTVQDLMLIIAMSNNPVKISA
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VLQEVCFFEFVGSTFVICLLEYYCITDWQQNDRIGLATYSMLLVSLTFNMFLLCYIGNLLIDKSTSVGISCYMIDWYRLPIKTVQDLILIITMSNS
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QEVCFFEFVGSTFVICLLEYYCITDWQQNNKIGLATYSMLLVSLTFNMFLLCYIGNLLIEKSTSVGISCYMIDWYRLPVKTVQDLILIIAMSNSP
AKISAGRIFLLSLPTFGNVLKTSFAYLNFVRNTIMY
>BtOr44
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GLFDTQRSPVYEIVYVFQCVYAFMCLSVTVGCCGLAALFATHACGQIDVVISQLDDLVDGTFSKKSSNPNTRLMEIVKHHIRILKFSAMIETV
LQEVCFFDFIGTTLLICSLQYLCITDLQYNNKIGLATYSMLLIGFTVNMALLCYIGNLLMDKSTSVGISCYMIEWYRLPGKTMQDLILIIAMSNS
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GLYDVQKSPVYELVYILQCMCGYVFDTVTVGACGLAALFATHTCGQIDVIMSRLNDLIDGKFSKENSNTSVRLMEIVEHHIRTLKFSAMVET
VLQEVCFLEFIGTTFVMCLLEYYCITDWQQNNKIGLTTYSLLLISLTFNMFLLCYIGDLLIEKSTNVGISCCMIDWYRLPAKSVQDLVLIIAMSS
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>BtOr46
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DVQSSPIYDLVYVIHCMCGYVMYSITAGACGLAALFATHTCGQIDIVISRLNDLVRGEYMKETLNLNARLIEIVERHLRILRFSAAVEMVLQE
VCFLEFIGSTCMICLLEYYCITDWEQSNTISLTTYTMLLISLTFNIFILCYIGELLIEKSSSVGTSCFMIDWFHLPTKTIQGLILVIAMSNNPAKISA
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LDLSVGNIVMTIKEFIILNAMLVQLFAYSYVGEYLKLQMEGVGDSLYFCSWYDIPTSITKDIIYVIMRSQDPVFLKAGRFFIVNMETYMSIVKT
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>BtOr48
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EYLMLLFTSTGNLGSDTLFFGIIFHLCGQVEILRLEFNRLGNKNERTMERFIVLIKRHIYLLNLAHMLNETISSILVMQLFSSCVLICTTGFQLILA
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>BtOr49
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IIEYLMLLFTSTGNLGSDSLLFGIIFHLCGQVEILKLEFNKLGNENERIMERFIVLIKRHVYLLNLAKMLNETISSVLVVQLFTSCILICTTGFQFIL
DLSVGNIVMAMKTFIVMSCLLVQLFAYSYVGEYLKRQMESVGDSVYFCNWYHIPKNVAKGIVFVIMKSQDPVSLKAGKFFIVNMETYMSIL
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PLLPQICVLILQAMHIFVNAVAHCANDGLFFSLTMHLCGQFEVLKMNFTKFELQEFGCHKKLRFLVKRHCQLLMLANDLEQTFNMIILVQLL
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IIEYLMLLFTSTGNLGSDSLFFGITFHLCGQVEILKLDFQRLKIEGERTREHFNVLTKRHIYLIKLANMLNETISSILVMQLFTSCILICTSGLQLIL
ALNIGNIVMVIKTFIVLSTLMVQLFAYSYVGEYLRRQMEGIADSMYFCNWYDIPKSVAKDIIYVIMRAQEPVFLRAGQFLVVNMETYTSIIKTS
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EYLMLLFTSTGNLGSDTLFFGITFHLCGQVEILKLDFQRLKIEGERTREHFNVLTRRHIYLIKLANMLNETISSILAVQLFTSCILICTSGLQLILA
LSIGNIVMVIKTFMVLSALMVQLFAYSYVGEYLRRQMEGIADSMYFCNWYDIPRSVAKDIIYVIMRAQEPVFLRAGQFLVVNMETYTSIIKTS
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LISNFTSAVKDYNELNDQEKRVIVRRHAYMGRVAGISVVFFAYFGSTLFMTLPMLAAEEVEDIVNVTEDNTPEYPIPSEKVMELIKMPDNLYF
IVFIVEYLMLLLTSNGNLGSDSLFFGIIFHLCGQVEILRLDFRRLSNDNERTIEHFIALSKRHVYLLKLAKMLNETISSILAVQLFTSCIVICTSGLQ
FIIALSVGNIVMTIKSFIVLSTLLVQLFAYSYVGEYLKRQMEGIGDSAYFSIWYDIPKSVAKDIIYVIMRTQDPVFLKAGKFFIVNMETYMSIIKT
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>BtOr54FIX
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YFIVFIVEYLMLLLTSNGNLGSDSLFFGIIFHLCGQVEVLRLEFSRLSNENEKAKEHFNVLSKRHVYLLNLAKMLDDTISSILAVQLFTSCILICT
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FIVEYLMLLLTSNGNLGNDSLFFGITFHLCGQVEILKLDFKRLRNENERTKERFSVLTKRHVYLLNLAKMLDDTISSILAVQLFTSCVLICTSGL
QFIIALSVGNIVMTIKTFLVLSTLLVQLFAYSYVGDYLKRQMEGIGDSIYSCSWYDIPNSVAKDIIYVIMRTQDPVYLKAGRFFIVNMETYMSI
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>BtOr56
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KIGNIVMTIKTFIVSTTLLLQLFAYSYVGEYLKRQMEGVGNSVYFCSWYNIPKCVAKDIIYVIMRGQDPVFLRAGKFFVVNMETYMSIIKTSM
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>BtOr59
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CDSLIWTLLMFICNQIEIFGYRLRKIEQGTNDCKLCIRYHNLIYRFATMINEEFKLMIFVQFAVSTLTICMNLYILTGTNVSLEMIVKIIMFSSCM
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>BtOr61
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FDTFFAGLLLQICCQFEMLMNRLHNIEGNEIQSLKNCVWHHNTIFRFAEIVNKFFNKMMFVQFMVSTVAICFTLYQLTEANDSLQIIGWASFM
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>BtOr62FIX
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>BtOr63
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>BtOr65
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>BtOr66
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>BtOr67
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>BtOr68
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>BtOr69
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>BtOr70
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>BtOr71
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>BtOr72
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>BtOr73
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>BtOr80
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>BtOr81
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>BtOr82
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>BtOr83
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>BtOr84
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>BtOr86
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>BtOr94
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GISYSCFDTFLAVPVIHLCGQLTVLRMALEDLANATKDDNYARFQERLGFIVNRHNLLSRFAVTVEDCFNLTLLVQTVICTTMFCLTGYRMIT
SVDQEQADVRIVGLIFFIIHVIYTMLHLFIYCYIGEMLLGESTGVGQSAYECDWYNLPPKNAISLIIVICRARVSFQITAGKFSPFSLELFNAILKT
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>BtOr95
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FYAATTYTAVDTFVVLLIFHVCGQLSNLRDDLRKIQSYDTKDVEKKLQKIIQKHEYINRFANKIENSFNMMLLLQMLSCTIQICSQSYQVIMSF
GEEETEYMILQLSFLLIYVVYVMLHLFLYCYMGEKLTSESAEIANTAYNAEWYNLPPKNARWLIIIMCRARASPLKITAGKFCSFTLVLFSQVL
KTSMGYVSVLHAMKNK
>BtOr96FIX
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CRRRRIKDLIDITNSEMFNRDNDKYEHITAYYTWQAIFHQITFQTFGFIAVISWGSTPILYQISGTSKQLPMVGWYPYNVTSTPVFEFTSLHQFM
VVCTSCVNNIAIDTLATGFIVTACCQLTILNYNISSIRCIIEKKYTLLNDNVSIENSTLKVYSKMYEDLKHCIEHTIMIFDFSKQIQDVFGTLIFLQ
LLVDCIVICAILFNLSQMKDYVTSEFLGTLLYTCCVIYQIFIYCWHGNELHFHSMRICSSAYANNWWDNSKDFKHALLIIMARAQWPLILIVGN
VMELSLQNFVLILRTSYSIFTVLRTSTAT
>BtOr97
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QLLSAALSITSIAGLDCSFMTTMLHVSAQFKLINTWISNIGTEINCNPNYKQKIKVDLTRCIRHHQRIIHVVNEVNNLLTPIVFLQILTSGIEVCLS
GYAILDTGKAEADLVKFICYFISMAVHLLLWCWPGEILVQESQEIGHAVYFNVPWYDLPPIYQRYLCLMIVRAQQYSSISALTFQTLSIHTLTA
VFNTAASYFTLLQQIQQT
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>BtOr98
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QIMTAMIGLSAITAIDCTFMTMILHVSGQFILIKTWINKIGFEMNHKSIDMDKFEEDLFKCIRHHQRMIHVVNDVNNLLTPIIFMQLLTSGLEICL
SGYAMLDNGTKITDILKFTSYFISVTVQLLLWCWPGEILVQESQEVGQIVYFSVPWYNLPPIYRNHVCLMIIRAQQYCSITALTFKVLSIQTLTA
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>BtOr99FIX
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FICQILSSMVCATTISGLDASFMTTILHVSAQFRLINTWISNMGIEINCNPNYTRKIKIELMRCIRHHQRMIHVVKEVNNLLTPIIFMQILTSGIEIC
LSGYAMLDSGTAKADLVKFISYFISMGIQLLLWCWPGEILVRESQDIGQVVYLNVPWYDLPPIYQQHLCLMIVRAQQYCSISALTFQTLSIHTL
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>BtOr100
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CQILSSMVCATTICGLDTSFMTTILHVSAQFKLINTWISNIGTEINCNPNYTRKIKIELMRCIRHHQRMIHVVNDVNNLFTPIIFMQILTSGIEICLS
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VFNTAASYFTLLRQIQEK
>BtOr101
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ALILHVGSQIDLLCCKLTEISHNCDKEKLQKHIIDDIVGKHQRIIQFSKNIEKIFTYISLCQFVSNMLVICFISFILVVSSHMDQATVIIMKCFPYYI
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FMALIATFVLHLASQIDILCDRLTEILNNHSEEQLRITVIKNLIVKHQRIISLSENVESVFTLISLLQFFFNTVVICFVGFLLVTSLSSGQAPAVITKC
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>BtOr103
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GISIAMLDALIITLILHIGGQIEMLHEALENISIKDEKHGSLRNVIKSLTDHHYRIILNSEYIEKLFSYIALMQLLCNTIVICCIGFLIIVAVNSYGDIK
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>BtOR104FIX
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LLFMTIVHVGCQIDIMCQNLTYAFPKNENKLKFFIGRYQEIIAFAEKIEKLFTYIALSQLISNTVSTCCEGFLIVLAVNDQSGLVVLIKCVLFYIVI
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DCQKYANIDINNLVTKTGVFSFYVTSMIMSSYLVSAVSYLGGAIAFQGTNDSMSRELLLKMDLPFETSESPNYELVVTTQFIIHFSAALAFGTF
TALLFMMIVHVGCQIDIMCQNLTYAFPTNENKLKFFIGRYQEIIAFAEKIEKLFTYIALSQLVSNTVNTCCEGFLIVLAVNDENGLAIAILIKSVV
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VGIVVKIVLFYIAIMLEAFVFSYAGEYLSSKSLSISTSAYGSSWYLLEPRNRRVVILLMIRSQRRLTITAGKFMDLSMFGFASILKASASYVSVL
YARY
>BtOr107
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>BtOr108
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>BtOr109
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ATALLHTCGHFAVLRKNVKQLDSYIYRITSLKTNSKHINANLYEIKIQIIHVIKHHQVVLWFCDNMEKNFHLILFLQAMISSLLICFVGFQVSAT
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MLQSFNSES

>BtOr110
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>BtOr111
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YSLHQKDMFYVVKTMKEDWILSSHEDRKILAKKTMFAFRLAKYFISTVAMTIVLFMCIPFLEIYVFGNNERVLPFRGYFFINHTISPVFECLYF
FNVTAGGFGGSMIAGATSFNLVVIMHGSGKFAVLRKRLEALSGEDPNSTAIMNNYVIRHQKAIEYADALERIINVLALGQFVTSTGLICFAGF
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SFSYFTVLTATEGD
>BtOr112
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VYLIPASMLLTIGATGADSLLVALTFHLCSQLSILAHRIRNISIEPQIYSPEMRALVERHIELLQLASILAKAFSSLMFIQTLGLIFSLCIVVYQLLM
TTDSGEDINTIHFIIYSCAVILLAFCYCFLGECLINESSEMQVACYFINWYDLPEQYTRSLIFCIARSQKPSYLTAGKFYVFSLETFGVIVKASMA
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>BtOr113PSE
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RFHLANMKDSRYGYETSNHVLGATIEDHIRLIXAINVIENISTLLFLVLLINFNICACIYRLLLITASELIYRIMKDNCETNRKVNDSDIILIFLKYS
EGVHNTAYECEWVSLKFTKAKSLIIIMTRSKRPLHLTTGKFPLTMLKXILKISFSYISFLLIMLH
>BtOr114
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VWNIISVSTGVDGFFSFCLFRISVMLRLLGFEFEMRFSTDEKDKANKEYEENRKRIFQECVNKHALLLKCRDIVQEAYGPVILLTTITSATSLCT
LIFQVLQVRGQIIDKIIICIVFIFMKLLQTFLYAWPADVILTESDRFRRKVYFSDWYKHKDISFAKGFTLILAQRSIVLKACDLMQVSLDLFVKVL
NTAVSYYFLLETIDKDK
>BtOr115
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LDIYTMYIILLTTAQYKYLRMKFATIFEQKPETLNGSYNDSTRQNVSFRKKRMIQEMRVLTRHYETVVEIAVMLKTLLFLNVGVHYINNVFRF
CFLSFMFSTNMFSEKCLIILYTIGALIQFYILCYCIQELLDASNAVADDVIYEKWYLHDVPLQRALLMIISANKLECKLSNSRHIDLTLSSFMSIL
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>BtOr116
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QRRFQMLYFDMENFCKHATKTERMVLERYVHKYKYFHCIYILWSFITTAFVICGPLYSSQTFPTHAIYPFSVKHQPYNSLIFFHQSLVGFQASS
GMGIDTQVALLLRYATARFELLGIQLRNAKTNSEFNVCIQKHIDLLRYTKEIRLSIKYLVLATIATTTAVIFGSLNLIANQPLILKTLYATVVFS
ASVELFMYAWPADGMMRMSERTATSVYGTAWYNRDISVQRKVLRIILRSQKLETIGISGIVPQLSLSHYAKYLYTSLSYFNALRIMVGDPSPL
>BtOr117
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HLQVLTGKVKAFLEVASEHETKAIERYMDRYKQFLSVTAMGYITTAISFSLAPFFSAQELPADGWLPFSTESLGIYCMVYVNQVYCIFQTAFCI
GVDFTIAVLFSFSAARLDILRMKLRHVNSSDILVSCIKEHQEIIGFVEDTKATVETLLFKTNATMGSAVICGAFPLIYNQSLAVMSQYLSFVVSG
CTRLYVISWPADDLKESSVQFAKSITDVQWLGKPKDMKSSMLIMMQRSQKPLLIRMSGLLPPLTLEYFANFITTVSSYFMAMRSMIES
>BtOr118
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>BtOr119
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RIVEEMIVCIKEAEQYEREIFYKYIKKCYVFCGCSIVCTYVTAVGFSLRPAILPVPFPFDVEYPFPVNYTSVYIIIYMQHVCVCFQSAAQICISSFG
GLLLWFTAARFECLAVNLERSTDTDTLIDCVKKQLHLRRYGEEVLNNFRFMVLYAVGVATFALTLCCIMMIVDVPLFVKIQYIGACVTVLTEI
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>BtOr120
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NILCALLLLFAAARFEILMTEIRAVNSVKSLIKCVKKYYTLKRYAEEVANTARYTTLITLCICGIESVFAGIIFIGRQPFTVKLQFVTVSITVLLAV
FMCAWPADNLMDVSESTMRSVYQSKWYEQPLRIQKFILFMMIPQSPVILRIRCIIPAFSLNYYCSFITNVLSMFTALRVVMLQDEDGILEDI
>BtOr121
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LLCTNIFCALLLLFAAARFEILMTEIRAANSVKSLITCVKKYYTRKRYAEEVANTARYTTLITLCICGIESVFAGIIFIGRQPFTLKLQFVTVSVTV
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>BtOr122
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>BtOr123
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SLLLWFTAARFQCLAMELKKTSDVSTLIVCVEKQLHLRRYAKEVVDNLRFIVLYAIAVSTSALTLCGIILLVDVPPMVKIQFVTLCLTVLTEIY
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>BtOr124
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IGVFGALLMWFAAVRFECLVVEIQKTTNIRMLVVCIKKQLHLRRYAEEVVGCFRFIILYVLGMTTFTITLCGILLIMDSSVTTKVELIDASAFCL
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>BtOr125
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CIGVVGALLMWFAAARFECLVVEIGKITNIRMLIICIKKELFLRRYAEEVVGCFRFIVLYVLGMTTFTIALCGILMIMDSPITTKMELVNSSVFC
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>BtOr126
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>BtOr128NTE
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>BtOr129NTE
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EIYKENFEKMFDVIKKDWKLLNDKSQIHILEEITKQGNKIGEIYRTFVLSCMSGFIVIPLYPAFLDIIIPLNETRQRHQMFRLTYFLDENRYFYPIY
FHSLWCSFVTVMIAVTIDSLYIQIVHHDCAIFAICGQNIITATGSTGVRINETYTERFRQCLTMHKNALQLFEMLDDSSRRSFFFQILLTMVGMT
ITAVQAVINLHRPEEALRIGLFLVGQQFHLLIITLPGQVITDHSFELTNDIYRSMWYDMPINVQRILHMMQMRSSKPCKLTAGGIYEMNIENFGI
TFKTCVSYFMVLLSLKD
>BtOr130
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YVYLQLSWTSIVVSIIIVTVDSLLMLIVHHNSGLFIVCGHQIQKSTRHLNSFTNEVMSERYTYKQIRNCVIMHNKAIDFYDILDENNRISYMIQIG
LNMIGITTTAVQTVINLDRPGESIRSAVLCGANQFHLFMLSLPGQILIDHCTELTKQLYNSTWYGVPVKVQRMLYMMQIRTRRPCTLTACGLY
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>BtOr131FIX
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FYVYLQLSWASVVVSISIVTVDSLLMLLVHHNSGLFIVCGHQIQKSTRHLNSFTNEVMSERYTYKQIRNCVIMHNKAIDFYDILDENNRISYMI
QIGLNMIGITTTAVQTVINLDRPGESIKSAVLCGANQFHLFMLSLPGQILIDHCTELTKQLYNSTWYGVPVKTQKMLYMMQIRTRSPCTLTAC
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>BtOr132
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CVYLQLSWAAIVVSISIVTVDSLLMLIVHHNSGLFIVCGHQIQKKTRHLSSFTNEVMSEHYTYKQIRNCVIMHNKAIDFYDILDENNRISYMIQI
GLTMIGITTTAVQTVINLDRPGISIKSAVLCGANQFHLFMLSLPGQILVDHCTELTKQLYGSTWYGVPVKTQKMLYMMQIRTRSPCTLTACGL
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>BtOr133NTE
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QLFWSSVVIVFTIISADWLYMLIIHHSSGLFAVCGYRVHKATVNPNNFTGESMSENYTYEKIRSCAIIHNEAIRFSDILKQSSQGSYLIQVGLNM
LGISATAVQTVINLDRPEEAIRSAVFCGACQFHLLLLSLPGQVLLDHCSDLADNIYSSKWYKAPMQIQKVLYVMQIRCKRFCSLTAGGLYEM
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>BtOr134NTE
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>BtOr136NTE
VLQINEGSEIFHVPYYNKLERYIQLLGQDPRHKSSTRNIIVMIVVISIASITIPATIELLASLHNKDTDGVIECLPHFLASSISAVKVLNMHFNRRN
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QLFYAAAVVVFTIISADWLYMLIIHHVSGLFAVCGHRIQKATLNSNNSTGTAVSEKYTYEKIRNCAIMHSEAILFYNILNGSSQGSYLIQVGLN
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>BtOr137NTE
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YVYMQLAWGSIMVVVTIISVDSLYILIIHHNSGLFAVCGNQVQRATTNLDTNQIISESYMYKQIRDCVITHNEAIQFYNILNESSRTSYLIQVGL
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>BtOr138NTE
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NRENFRKLFEFVRKQWEELKLTNDLRVLEEVTIQGSKMAQLYRNTLLIFMVLFLLVPLLFPILDVVLPLNETRPRQQLFRVNYIFFDHEEYFFY
IYLQLAWGSVIVVMIIVTVDSLYILIIHHSSGLFAVCGHQVHKATSSSIIFSTEAMTETYTYEQIKNCVITHDKAIEFYNILNENSRSSYLLQVGL
NMMGISMTAVQTVANLERPAEAVRTGIFLGAEQFHLFVISLPGQVLLDHCSDLANNIYGSTWYKIPVKIQKMLLMMQIRSKKLCTLTAGGLY
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>BtOr139NTE
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>BtOr140
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VSYFTVLKST
>BtOr141FIX
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VISTFFVFVGCDASYIYMVQHACGQLAVAGHRFKNALSDLSIDNEKGGMQDKSYERVLHSIREHQYATNYLKSIQTSHSVYLCICIGMSMAS
FTVSLVKVASQSEISGVLIKDCVFLLSQLIHILLLTVQGQFVLNSNDEIIESIYDASWYNANKKTQLLFVLSIRSCLSPPILSAGGLLDLNLKTFAE
IIKASVSYFTVLKST
>BtOr142FIX
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VISTFFVYVGCDASYIYMVQHACGQLAVAGHRFKNALSDLSIDNEKGGMQDKSYERVLHSIREHQYATNYLKTIQTSHSVYLCICIGMSMAS
FSVSLVKVASQSEISGVLIKDSVFLLSQLIHILLLTVQGQFVLNSNDEIIESIYDASWYNANKKTQLLFVLSIRSCLSPPILSAGGLLDLNLKNFAE
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ACDINLVHVVHHGCALLAISGYICSKCLVTSIYIFRFVSNTYCYYHDNFVALHYSILHICIKIYVDKVDACHVHYFFIILGLIIVTFTSTFVRLSTM
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RSS
>BtOr144
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VLIVFVGCDTCYMVLVQHACALLTVAGYRFKNAINDLSYNGRNPEKGAKEIYKKLRFSIQGHQRAIMFLRNIESTHVTYLFMCMGIIVLCVSI
TMVEIATMDPCWDFYKFIGFLIIQLLHLFCLTMQGQFIINSSDDIYDAIYEAQWYNANPEMQAFYVLALRRSLTPPRLTAGGLIQLNMQSFSEV
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>BtOr145
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GFVYCACDANYVYAVQHACGLLAITRYRFRNVTEGVLDHYKNDAKLSKFNYRNVCKSIQAHQHALRYLKLIETNHHTYLFISVGMLIMCIC
VSLLQVANEKNDSWLVQCIFLFAQLFHTLILTGQGQFVINGLDSVFNSIYESPWYTFPAKIRALYILALRSCLSPPLLTAGGLIVLNLRSFAEIIK
AAVSYYTVMKTK
>BtOr146
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LSIYIVVIVFVGCDTCYMVLVQHACGLLTVAGYRFKNAINDLPFNARNPEKEAKEIYKKLCFSIQGHQRAIMFLTKIESAHVIYLLLCMGIIVLC
LSITMVQITTMEICLDFYKFVSFLILQFLHLFCLTMQGQFIINSSDMIYNAIYEASWYNANPKTQALYILALRRSLTPRYLTAGGLIELNMRSFSE
VIKLCVSYYTVLRST
>BtOr147
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IYVVLIVFIGCDTCYIVLVQHACGLLTVTGYRYKNAINDLSFNTKDSEEMAKETYERVRFSIQGHQRAIMFLEKIESAHVIYLFMCMGIIVLCV
SITMAQIATMEICVDFYKFISFLMIQFLHLFCLTMQGQFIINSSDEIYDAIYEASWYNTNPKTQALYLLALRRSLTPCYLTAGGLIRLNMESFSEV
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>BtOr148
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TMVQIATMEICMDFYKFTSFLIIQFLHLFYLTMQGQFVINSSDEIYDAIYEASWYKMSTKTQALYILALRRSLTPCYLTAGGLIQLNMQSFSEVI
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>BtOr149FIX
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WKDWSTDRLSDELDIMIEYAKKGAFFSWLYFGVCICCAISFLQLSLTPIVLDIISPMNETRDLMYIFPAYYYVNDQIYRTSISFHMMCTIISTCL
VYIGCDTSYMYIVQHACGQLAVARHRFENAILDFSIVSETSVVQDKIYERVVHSIRGHQYATNYLRTIQSSHSAFLFITVALGMTTLSVTLVKV
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SYFTVLKTT
>BtOr150
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GTELMLVLFAHYMCGLFDITSYRMRKTIAGLSSSRQIDPNFRDFRHVVDSHTNTLQLIDYALSNYMVHYLPPCSVFLVSFSVCLHRLTNAITN
ANDQTEIFICSMFVIIHMVILYLCHYSGQILIDRSLDVFKETYNSTWYCMPVEAQKLLLFIMLRSSTESVIDLFGFFAASHVGFSKMLSTSFSYFT
MIYSLQ
>BtOr151
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ELMLAAFAHWMCGMFEITSYRLRKTIADLSLSRQIDSNFWNFRHVVDCHRNTLQLIDYALSNYMVHYLPPCSVFLVSFSVCLHRLSNAVTNV
NDQTEIFISSMFVISHIVLLYLCHYSGQILIDHSLDVFKETYNSTWYCMPVEAQKLLLFIMLRSSTESVIDLFGFFAASHVGFSKMLSTSFSYFTM
IYSLQ
>BtOr152
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GTDLTFVVFAHYICGMFEITSYRMRKTIAGLSSSRQIDPNFRDFRYVVDHHRNTLHFINYLLSNYTIHYLLPSAVAVVSVSVSLHRLSKMITDA
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SSQ

>BtOr153
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YSSQ
>BtOr154
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LAGTELMLAVFAHWMCGMFEITSYRLRKTIADLSLSRQIGSNFWNFRHVVDCHRNTLQFIDYVLSNYMLHYIPPCSVIVVSFSVSLHRLSNAV
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YFTMIHSLQ
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>BtOr156
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FIAFNIKKALIISVVIILHFGILYFGNFTSQNIRDHHAAIFFYAYSAKWYEAPVWIQKLYLFLMIETTIDIKIILGFYSPSVEGFFRLVNLSVSYLMA
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TVMFLANATSIAAESISTMTFQHLRSLFEIASNRIKEAFIYNSLHDSTSSKTFKMTESLKSSIHLHVKCMINYVLLYIIISMIEIVCLFRVNYTTQT
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ESLVIMWLQHAVSLCKITRYYVKRATLRNAKNHFDRRTKEDIAKVVFAQSRSVQFFQELQGNNVLTYGVILVSVIISLGINLFCLSQSLLSLSEI
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>BtOr159
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GIETLMVTWFQHASSLFAVVRYHIKKAVFEDCVQSHVSRRYLNRNSKRNIEIVINAHRRAMEYAYNLRDRYMFSYGTFLLFVTICLSINLFLL
TQSAFLYRNMEETIIHLVVLSCMLTCMVFFHYMVQFTSDAADNIVTIIYNTNWYEASVPLQKLLLIIMIRSINSFTCTFFGFYSASMEGVSMILR
KSISYFMVMMSMK
>BtOr160FIX
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LFQFAKAMSIRNDIEEFVASLCTVITSVLYAFTVIHFAQKLTDHSSDIFQQLYNIEWYNLPVVEQKVVLFLMRNSLKDLTFIIGGVIVASHDMFT
MYVRTAFSYFMVVYSFD
>BtOr161
MDSAQYEYLRLNKYLLFTIGIWPYQTTLQRSLVAIVFIPIIVAQVILQGGGMVTAITANDIDSLLEGFAPFMISLMCLAKYINFFYNFKQMKRLL
DIMREDWEIYKKLRIEYDLLSEQYAIGKKITISFVAFLFGLITPFAAMPLLLNAADALGLCNISDDRPLAFRVEHFVDVDKYYFPLLVHSYIGTL
AYTTIVLAINSIIAVYVLHESGLCEILRFKLENFVESDVMDVKLHANKRDDKWYQNARDCVLLHEHIIEFANILEDANTTSYLLQIGFNMICVS
FTQFQAVINVQENAALAFRYVSVTISLLCDLLFVSWPGQQLSDSTERIFEFTTNGKWYLSSINCRKLLMMMLSKSITPLKLTAYKFYTLNLESF
SAVARTSFSYTMVLCSVQ
>BtOr162FT
MIIGMDFFEQPAFRLNKRLLSFVGVWPFQSTLPKLSRQSVVLIPIFVLLTAEIRGLSNAWSVNYSLAIECMPPIIALFLSMSMYLNAIFNTKKMR
DVLLFIKNNHHYYANRPEKLILRYYDVQGRKITLYYALYVYTTVVAYITIPAISLLIDFIIPSNHSEEKSFPIELDYGVDTQQYFYYLFIHSYMTI
AMIANLIASCDTTYMLYAQHGCALFAIVSYELRTVHILDASSLINLKDHRLFENYKNTELLPEEEKKISTKLFLCIKEYQNAIRYCNLVESLFAK
SIFVQLFFNVVCLSIAGTVMKLGNAADTIRFGSFTFAQAAHIFVLCLPGQRLLNHSEEVYNAACEAMWYIFPKKCHNLYKFLLARTLVFSKIT
AFKVATMSMETFLAIIQTAMSYFTVLLSTT
>BtOr163FT
MSRNSERNAITNMDFFEQPAFRLNKRLLSTIGVWPFQRTLTKLSRQGIVLFLNITLFIAEVRGLVNVWSISVDSIIECIPPMVTIFLQVASYFNLIF
NTEKFKDILLFIKNDHNYYMNRPENMILQYYARQGSKIILYYVSYIYITITAFVLIPTVSLINELINHSEERSLPIEIDYGIDIQEYFYYLFIPLYISM
FIVPHVIASCDSTYLLYVHHASALFAIVSYELKTIHIFDTSSLINLKDYNLLEKYKNVELSPDEQKKIFKKLLFCIRRHQNAIRYSNLVESFFTKSI
LAQMFCNVVSLSIGGVETVLNLGNTRNVMRFGALALAQAIHIFILCFPGQTLLNHSEEVYAAACEVVWYIFPKRCHNLYMFLLTRTMVFNKI
TAFKLSVMSMETFLSIIQTAMSYFTVLMSTT
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>BtOr164TRA
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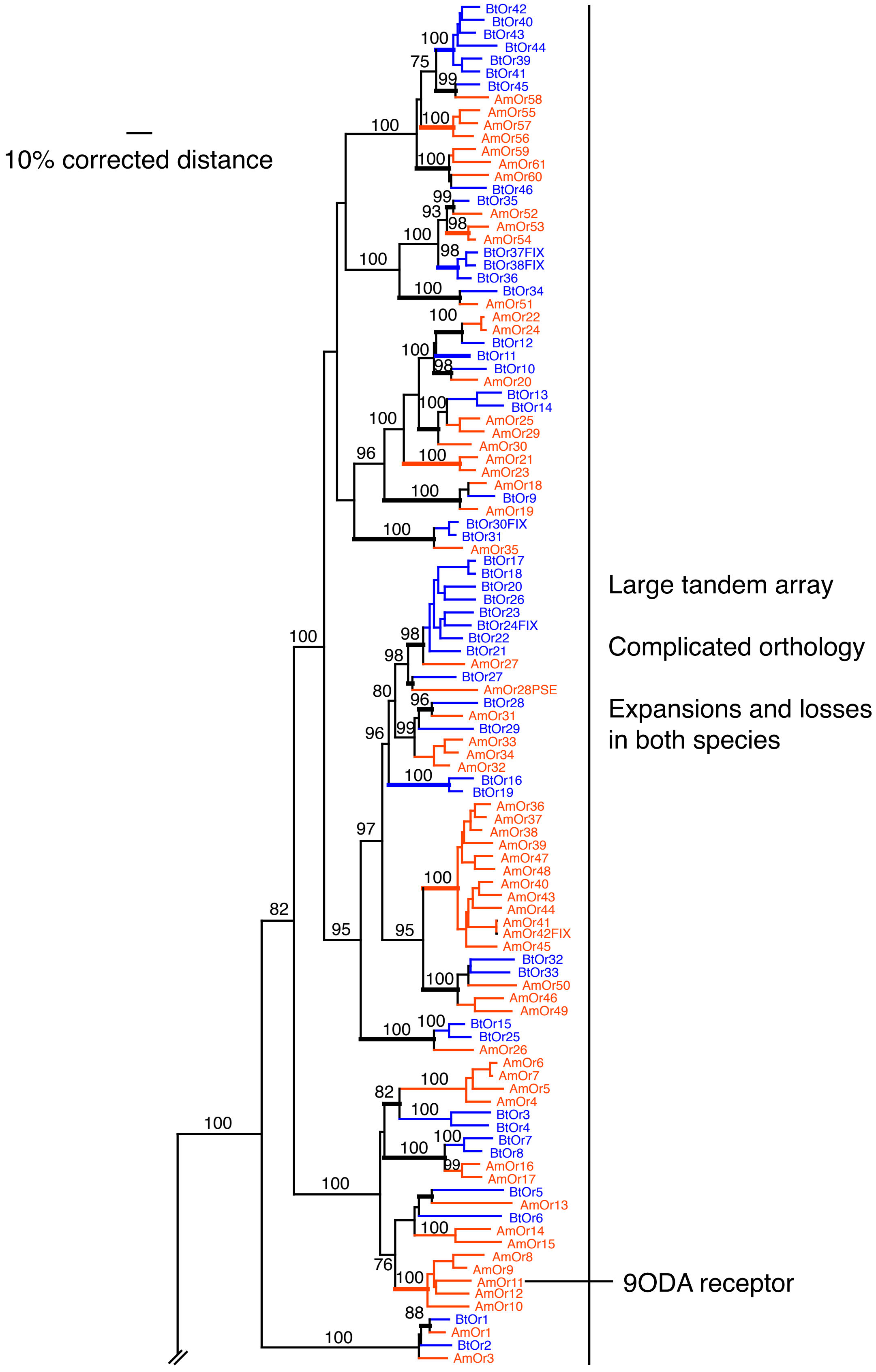
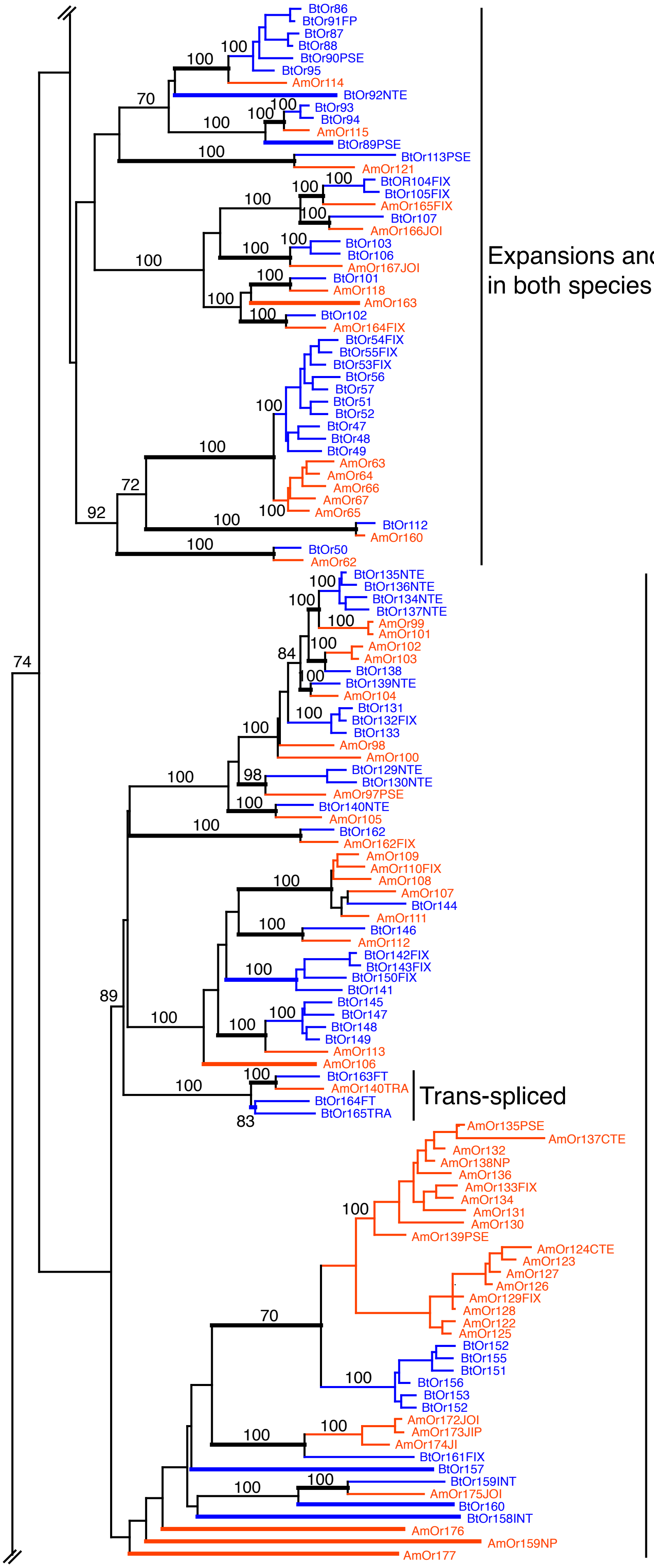
IFTTYSAYMLYVQHACALFAIVSYQLRTMHILDTSSLINLKDRHLLEKYKNVELSQEEKEKIFRKLLLCIKEHKNAIRYSNLLESLFTKFILTQIF
FHIICLSIGGVGIVLNLGNTDEITRFGSLALVQVIHIFILCLPGQRLLNHSEEVYVATCEIVWYMLPKKFHNLYMFLIARTMIFSKITAFKIAVMS
METFLAIIQTTMSYFTMLLSTI

B. terrestris **and** ***A. mellifera*** **Odorant Receptor (OR) phylogenetic tree**





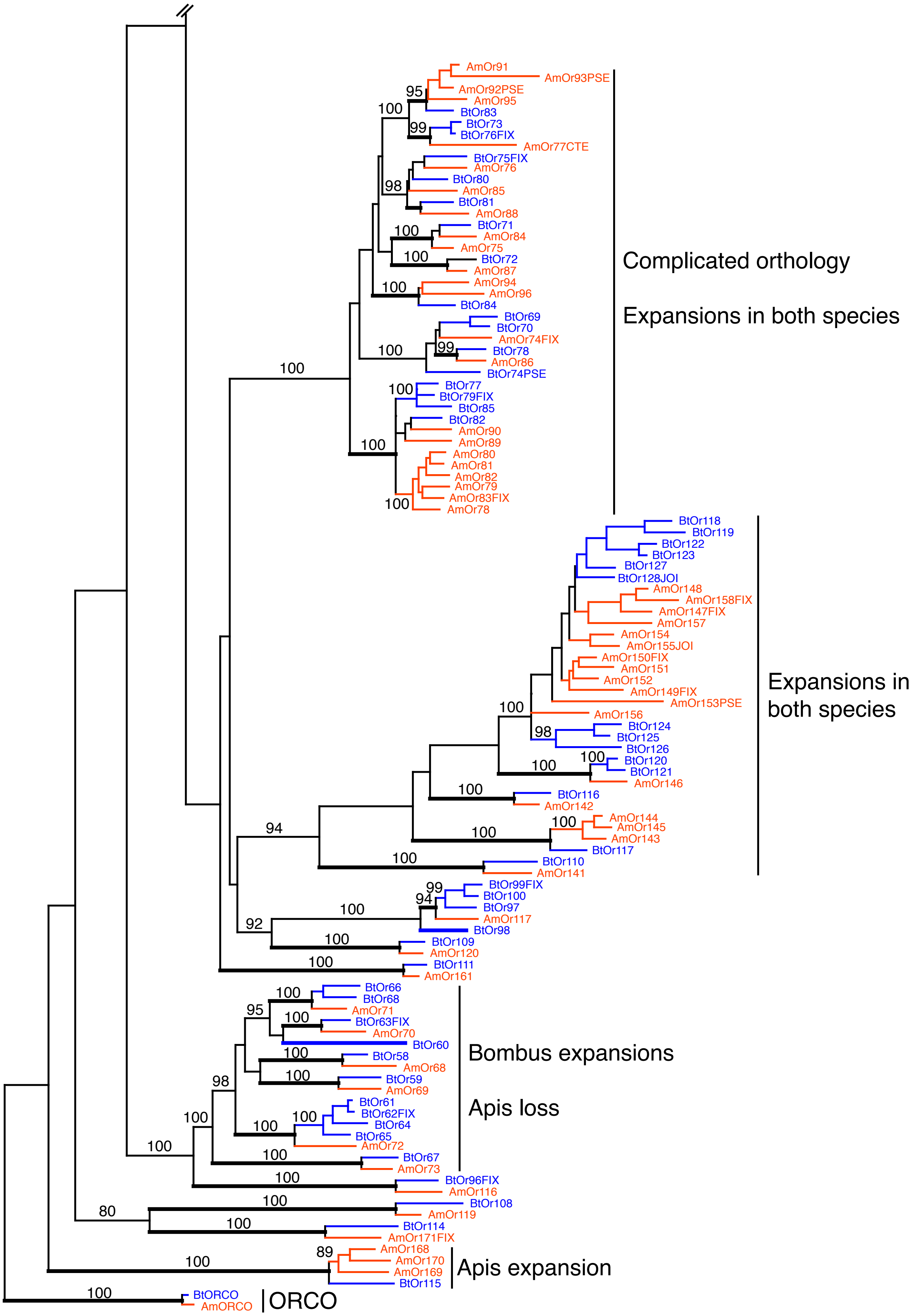
Expansions and losses
in both species

9-exon genes

Candidate cuticular
hydrocarbon receptor

Complicated ortholog

Expansions and losse
in both species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AmOr92PSE
95
AmOr95
100
BtOr83
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BtOr75FIX
AmOr76
98
BtOr80
AmOr85
BtOr81
AmOr88
100
BtOr71
AmOr84
AmOr75
100
BtOr72
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100
AmOr94
AmOr96
BtOr84
BtOr69
BtOr70
AmOr74FIX
100
99
BtOr78
100
AmOr86
BtOr74PSE
100
BtOr77
BtOr79FIX
BtOr85
BtOr82
AmOr90
AmOr89
100
AmOr80
AmOr81
AmOr82
AmOr79
AmOr83FIX
100
AmOr78
Complicated orthology
Expansions in both species
BtOr118
BtOr119
BtOr122
BtOr123
BtOr127
BtOr128JOI
AmOr148
AmOr158FIX
AmOr147FIX
AmOr157
AmOr154
AmOr155JOI
AmOr150FIX
AmOr151
AmOr152
AmOr149FIX
AmOr153PSE
100
AmOr156
BtOr124
98
BtOr125
BtOr126
100
BtOr120
100
BtOr121
AmOr146
100
BtOr116
AmOr142
100
AmOr144
AmOr145
100
AmOr143
94
BtOr117
100
BtOr110
AmOr141
Expansions in both species
99
BtOr99FIX
94
BtOr100
100
BtOr97
92
AmOr117
BtOr98
100
BtOr109
AmOr120
100
BtOr111
AmOr161
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BtOr66
BtOr68
95
AmOr71
100
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AmOr70
BtOr60
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AmOr68
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BtOr59
98
AmOr69
BtOr61
100
100
BtOr62FIX
100
BtOr64
BtOr65
100
AmOr72
100
BtOr67
AmOr73
100
BtOr96FIX
AmOr116
80
100
BtOr108
AmOr119
100
BtOr114
AmOr171FIX
89
AmOr168
AmOr170
100
AmOr169
BtOr115
100
BtORCO
AmORCO
Bombus expansions
Apis loss
Apis expansion
ORCO

Phylogenetic tree of the *A. mellifera* and *B. terrestris* odorant receptors (ORs). This is a corrected distance tree. The ORCO orthologs were declared as the outgroup to root the tree, based on the basal position of this gene in the OR family in analysis of the entire chemoreceptor superfamily in *Drosophila melanogaster* (Robertson et al. 2003). The *A. mellifera* and *B. terrestris* gene/protein names are highlighted in orange and blue, respectively, as are the branches leading to them to emphasize gene lineages. Branches inferred to represent orthology are in double thickness, as are those to genes whose orthologs have been lost. Support for major branches, and all potentially orthologous relationships, is shown above each branch as a percentage of 10,000 bootstrap replications of uncorrected distance analysis. Comments on major gene subfamilies are on the right. Suffixes after the gene/protein names are: PSE – pseudogene; NTE – N-terminus missing; CTE – C-terminus missing; INT – internal sequence missing; FIX – sequence fixed with raw reads; JOI – gene model joined across scaffolds; TRA – trans-spliced gene model; multiple suffixes are abbreviated to single letters.

Gustatory Receptors

Details of *B. terrestris* GR family genes and proteins. Columns are: Gene – the gene and protein name we are assigning (suffixes are PSE – pseudogene, FIX – assembly was repaired; JOI – gene model spans scaffolds; NTE – N-terminus unidentified); Refseq protein number (prefix is XP_00); Scaffold – the genome assembly scaffold ID (format is GroupX.X, amongst 5678 scaffolds in assembly v1.0); Coordinates – the nucleotide range from the first position of the start codon to the last position of the stop codon in the scaffold; Strand – + is forward and - is reverse; Introns – number of introns in the coding region; ESTs – presence of a spliced EST contig in ILLUMINA RNAseq from male (MH) or queen heads (QH), or queen ovary (QO), or 454 RNAseq from multiple life stages (ML); AAs – number of encoded amino acids in the protein; Comments – comments on the OGS gene model, repairs to the genome assembly, and pseudogene status (numbers in parentheses are the number of obvious pseudogenizing mutations). Suffixes after the gene/protein names are: PSE – pseudogene; NTE – N-terminus missing; FIX – sequence fixed with raw reads; JOI – gene model joined across scaffolds.

Gene	Refseq	Scaffold	Coordinates	Strand	Introns	ESTs	AAs	Comments
Gr1	3401991.1	17.2	793766-800484	+	10	-	455	Change first exon
Gr2	3402054.1	17.2	804565-809758	-	8	-	458	Fine as is
Gr3FIX	3401879.1	16.3	2691534-2693608	-	6	-	437	Fix 454 frameshift
Gr4PSE	-	1.4	1673377-1674647	+	3	-	366	Pseudogene (6)
Gr5JOI	-	Un1992, Un16	<1-970, <38365-48937	-	6	-	427	Join across scaffolds
Gr6	3394407.1	3.1	6224665-6226760	+	5	-	419	Multiple changes
Gr7	3397918.1	9.5	1302132-1304956	-	6	MH/ML	422	Needs N-terminus
Gr8	-	13.3	2818921-2820242	-	2	-	391	New gene model
Gr9FIX	-	13.3	2816689-2818550	-	2	-	403	Fix 2 454 frameshifts
Gr10PSE	-	4.5	1496273-1498668	-	5	-	342	Pseudogene (5)
Gr11	-	15.6	909933-911488	-	2	-	426	New gene model
Gr12	3397919.1	9.5	1319950-1322519	-	6	-	451	Part of large model
Gr13	3399602.1	12.1	4239925-4241137	+	3	QH	310	Multiple changes
Gr14FIX	-	Un1870	>1547-492	-	2	-	392	Extend contig
Gr15NTE	3400069.1	13.3	2813014-2814688	-	2	-	362	N-term misassembled
Gr16	3400068.1	13.3	2810767-2812107	-	2	-	392	Part of large model
Gr17PSE	3400068.1	13.3	2808643-2810439	-	2	-	401	Pseudogene (8)
Gr18	3400068.1	13.3	2806510-2807834	-	2	-	392	Part of large model
Gr19	3400067.1	13.3	2804362-2806228	-	2	-	402	Change last exon
Gr20	3400066.1	13.3	2802207-2803528	-	2	-	391	First half of model
Gr21	3400066.1	13.3	2800060-2801895	-	2	-	402	Second half of model
Gr22	3397919.1	9.5	1316550-1318999	-	5	-	451	Part of large model
Gr23	3397919.1	9.5	1313191-1315672	-	5	-	452	Part of large model
Gr24	3397919.1	9.5	1309273-1312305	-	5	-	451	Part of large model
Gr25	3397858.1	9.5	1305830-1308244	-	5	-	447	Multiple changes

Protein sequences of predicted *B. terrestris* (Bt) Gustatory receptors from the table above

>BtGr1
MRSFGVHIVDRDASRRRSPKSSSQFGKLDNLKTEIDTIGMSEPVAASVSAFNPKTDSLHASMRPIIMLAQCFSLFPVSGINNSDASYLRFTWRSP
KFAYCVMSIFGSSMMTIFNILRIVATGVNSTKMTTFVFNGTNLIASLLFLKLSIQWPCLMVTWEKLEKELSYRHRKISRITLATKFSIVTIVVMM
IALVEHGLSIVYGYIQAKECAVHKAEEDILGVYFQMQFPQIFSRIQYSLWKGVLVDICNILSTFSWNFVDLFLILISIALTDQFRQLNSRLNSIRG
KAMPEWWWAEARSEYNHLATLTRQLDSHISVMVLLSFATDLYFICIQLLFSFTPMRGIIEKIYFGFSFGFLLARTTVVSLCAAMIHDESLLPAPI
LYSVSGSSFSTEVMRFLVQVTTDNICLTGMKFFSVTRGLVLTVAGTIVTYELVLVQFNTTQQSEVSNSTVCEVK
>BtGr2
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PSKLQFKTFSFVTFYSAFIASTIFFMTIVSVLHMVKTLNANTIQTRGGIASATVGAVFYGNSLLGSILFFWLSSRWVPLQSEWRAMERCIDSNCI
EPTRLRWKFFFLSSVILMLALIEHILSMFNNVDGYDWNASNSTFRSFLETYTLRSHSFIFDTLNYNFAFGLYIFVVSKLATFTWNFTDLFIMLVA
TALAERYKSLNKKLAVTVTKYRPIFYWRELREHYAILSCVVKKVDEHISPIILLSFANNLYFICLQLLNGLSIAEKSSPLSAVYFFGSFGFLIIRTC
AVTLLTARIHDQSKEALPYLYNCSTSSYGIERLQYQLATDEVALTGLRFFSITRNFMLAVAGAIITYEVVLLQFVDGK
>BtGr3FIX
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SKTYVSSISELIMVHSLLCDTVSLINAAFGVVLLAVTISCLLHLVITPYFLIVQANEKHEWIFLVVQVGWCIFHISRMLIIVQPSYSTVAEGKKTA
ALVSQLLSCCFEADARRELEIFSLQLLHRPLEFSACGLFSLDRNLITSIAGVITTYLVILVQY
>BtGr4PSE
IEFLLFFKFGGLATISLKNQRTLKKNCSEILVFFTGFKLGVFYNLFXCLVIALIFHIPTNHIYNAEYAFMTIVTQIIEISQAVLGSFVFFSILLYYCIN
ESTFVKIGNYLIYLEGALCRLKQSLNWKHISYVLFFMYSFNFSLFVSVFVTDIISFNXSCFIFESILPAIFVSFCFIQYFSALSLTNAISIXCAIQDFC
RSKFGDIIPNTLFETRHVFVSYTKIYLVVRIRDVHGQFCDITNEISRFYYLPILITLTLISYILLYNVCYLFEPIMVRNVGVDYVIIVNTLLRIISML
YPLGLLTSKATKVTNEIEKAENLVHALLNCTIDRZTKVEILSTVTTYMVILIQFQVGTSVPDAYPCNCTQ
>BtGr5JOI
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VAGNCVLFGFIYTGCSKNITARCEQIDNILESFGVEKNYTKIVVYTVRVTSVWGILMISLFVLAWLWWSNGADIMKALCLSLLVSLPVTIICLM
SLTFNIFIRILRDKLHKMNIAMSEVRQLPNENDINIRYKMQPQRAHKLVFVRDYSNQKHYLQHFLQITRQVHFEIVKISRELNHIYGYQLLLEL
AMQFTIIISTLYNVYFEIISSQNVIEIFHSKMAVSAMWWALISSAKVITTNHHCTCFHREAAVTAETLQELATSCSYNSIKDEVQQFSLQLILHPL
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QIVIWTVVNQSGMFAYNETWLFNMSYMCLYVTNATSVYKFFGMTSFLGQRFHRLNQIARDNLPSRVGYKSTSVSKKTIQELHDELMIFGESL
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VLSTLHFLNRRLHFSAGGLFDVKLSLLSSIVGMMSTYLIILLEFPSS
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FLYILYRIIWLDLTMDELVKELVSVICWFLVYASQILYVNHVCAKTNLEVTIMGDVICDLYEPSTSNEFRAEIRNFTLQLIQNPVVFTAHGYFN
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ACFKHINDSLMKVKVILVNDEPHLLRRVYHMQKNPILLTKLRALKKQHLETSEVVQLLNNTCSMQIEAMVTLMFIDITFNMYKYLILFNEIGK
MRSFSFALMFTILYIVHIIITVSIVETTRSQMAKIGSSLHRILVHTFDEQVTTELELFSLQVLQKGNAFVMKGLVIDATLLAKMACGITTFLLILIQ
FLFVESC
>BtGr9FIX
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HGNMYAFLDGLVIVVMYLLTDARLSVIQNLSRTSCILSTKDFKDLSKLIHTKDILGSLFLAIHIPNCFKHNIFVTVRNLTNIYIMMANFSMDIFYI
NCVCILKDCFKKMEESIRQLKKFRINDHMSTQTFMHHEQISPLVVMKLKNLEEKHLEISDGVELLNHTFMIRITIAAITTFIVITFDIYFYIIYSHS
EFPVNSKFWYKPYVMPAAFYFIKFWMMIWACETATNRAREMKTTLWDVFSATNDPFVKREVEIFSLQIMHTTNIFTAKTFDMNSSFLTKIVG
GIIMYILILFQFLLNYVVCTLHM
>BtGr10PSE
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STKFDDSSRRIKLRIICRITMVTSFSHWAIIVYLTYRIGLRLPVFRGMIYFVMDASVNTQILIFVCILFLIEERFRHLCNMMPFSKXPTDRSIEQFD
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VYMICHKFRAINEMIKQLDEKLTSYWIALKIRRIRRLHNEICSIIMTVNEIYGIDLLLCSTNAFIMVVAKLFRIYMSAAEQKSGFIFLNNVIWIIYV
FQFILMCWLCTLTHREIDKIGLYISKFILNTQHSTKFNKLSCFGNKEPEQLGIFDNECRDNVALNLNGFGMESLLRSAFEQDCVRNEINDFSLQL
KQYRITFTACDFFEMNNSLLTRFISVITTYLIILVQFYKPEGF
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LIERIDKVDEIFKELGIHIEYRSLFRHTMIVGSLWLLNAVIIFALFIKMLIQHPALYTTTFLIFIYCYFTNAQSIVLYDYNTAVYWLGSRFKNINQL
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TQLERTKSVDYILNYGFVRYCLNFVVSNLVIMVQWSQHLIKNDPMIITNKTTTFQTLQENTSIVVQ
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RFIQINTILNIITKGKHFISISEMSDMNNVSRYRLLKWLRFELHKTMSLLNEAYSFRFKLMTIIYIGYICLHVCIIYNHTFNTFYAPDVILSFTWSTI
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FLFVESC
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VKSLTLILGYAIYYIVHVIITVAIVEITRDQMQKTGRDVHRILAHTFDEQVTTELELFSLQVLQKGNAFVMNGLVIDATLLTKMACGITTFLLIL
VQFLLVESC
>BtGr19
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HSKFPANIKYWYKPYITPAAFYFIKFGMMIWACEAATNRARKMKTTLWDVFSATNDPFVKREVEIFSLQIMHTTNIFTTKTFDMNSSFLTKIV
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>BtGr20
MFSRSRKLEPRTNKKLKSSSLYFGSYTSLISPGASINRLMGFLPYKLESSKLVYSKSYFVFSTISMIIYSICVIFSLFQVNFSSVQLPTLANKLHITL
LFLCGPVIFISAYANNHSMVRVIDGISNVSRILSSETWHKVATRIVIKDILILILPMCYIPVTIYTNLIFAYISWYTFLGVTALISLYTNNVYVLNV
CFKHINDSLVQVKEILVNDEPHLLRRVYHMQKNPILLTKLRSLKKQHLEMSEIVQLLNNTCSMQIEAMLTILFIDITFNMYNYLSADKKVGEA
KSLTLILGLVIYYAVHIIITVSIVEITRDQMQKTGRDVHRILVHTFDEQVTTELELFSLQVLQKGKAFVMNGLVIDATLLTKMACGITTFLLILV
QFLLVESC
>BtGr21
MILKSTGITEELKKRRTWKLLSATGFESLMYPCFFICWVLGYFPYKYEHQVYSLSKGRFAFSTSMMFIFVCSLMITIYETNIGMKINDSIPKMIH
ENMYAFLDGLVIVVMYLLTDARLSVIQNLSKTSCILSTKDFKDLSKMIHTKDILGSLFLAIHIPNCFKHNIFVTVWNLTNIYIMMANFSMDIFYI
NCVCILKDCFKKMEESIRQLKKFRINDNMSTQTFMHHEQISPLVVMKLKSLEEKHLEISDGVELLNHTFMIRVIVAAITTFSVVTFDIYFYIISIH
SKFPANIKYWYKPYVVPAAFYFIKFWMMIWACETATNRAREMKTTLWDVFSATNDPFVKREVELFSLQIMHTTNIFTVKTFDMNSSFLAKIV
GGIIMYILILFQFLLNYVVCTLHM
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>BtGr22
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ELLETFLLEKYKVEAEESNTETIFEPSHNFRNRFELNNWLSEGSLNVSEVSTTGSVSNVKQKILQEKVHILRQIRFLHLQVCKVSKMVNDIFNA
QILIHTITTLLHCTICVYSLYMNFHRQSNFVIDQLDLTLIYMLDSVVGTLKIALMSYDCEYTMGQANKTIGNIHAYPVHEGNAELTDEILHFSW
QISYTQLEETKSVHYILNYGFIRYCLNFVISYLVIMIQWSQHLIKNDPMIITNKTTTSQTLQENTSTVVQ
>BtGr23
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NVPALIKQIDKVDERLKKLGIEIEYHSLLRHITIVGSFWLLNAVILSAIFIKILIQNLLPPVTIFTIFNYYYITNAQSVVLYDYNTAIYWLGSRFKMI
NELLETFLLEKYKVKAEESNTETIFEPSHNFRNRFELNNWQSEGSLNVSEVSTTSGLSNVKEKILQEKVHILRQIRFVHLQVCKVSRMVNDIFN
AQILIYTITTLLYCTICVYALYMMLHRDPNFIIDRLDLTLIYMLDSVVGTLKIALMSYDCEYTMGQANKTIGNIHAYPVHEGNAELTDEILHFS
WQISYTQLEETKSVHYILNYGFIRYCLNFVISYLVIMIQWSQHLIKKDPMIIANKTTTFQTLQENTSIVVQ
>BtGr24
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NASTLIKQIDKVDERLKKLGIEIEYRTLHRHITIVGSFWLLNAIVESAIFIKILIRNSVAPLEIFIAFVYYYITNAQSVVLYDYNTAIYWLGSRFKMI
NELLETFLLEKYKVKAEESHTETIFDPSHNFRNRFESNNWQSEGSLNVSEVSTTSGISNVKEKILQEKVHILRQIRFLHLQVCKVSKMVNDIFN
VQILIYAITTLLYCTISVYSLYMIFQRGRSCVVDRLDFILIYMLDSVVGTLKIALMSYDCEYTMGQANKTIGNIHAYPVHEGNAELTDEILHFS
WQISYTQLEKTKSVHYILNYGSVRYCLNFVISYLVIMIQWSQHLIKNDLMIVTNKTTTFQTLQENTSIVA
>BtGr25
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STLIKQIDKVDELLKKLGIEIEYRTLHRHITIVGSFWLLNVVVESAIFIMMLTQYSVTPLEVFITFVYYYITNAQSVVLYDYNTAIYWLGSRFKM
INELLETFLLEKYKVKAEESNTETIFEPSHNFRNRFKLNNWQSEGSLNVSEVSTTSGVSNVKQKILQEKVHILRQIRFLHLQVCKVSKMVNDIF
NAQILIYAITTLLYCTICVYNLYMNLHRGSNSAVDLANLILISILDGVVGILKIALMSYDCEYTMGQANKTIGNIHAYPVHEGNAELTDEILHFS
WQISYTQLEKTKSVHYILNYGFIRYCLNFVISYVVIMVQWSQHLIDNDPMIITNETTTLYENTSIVV
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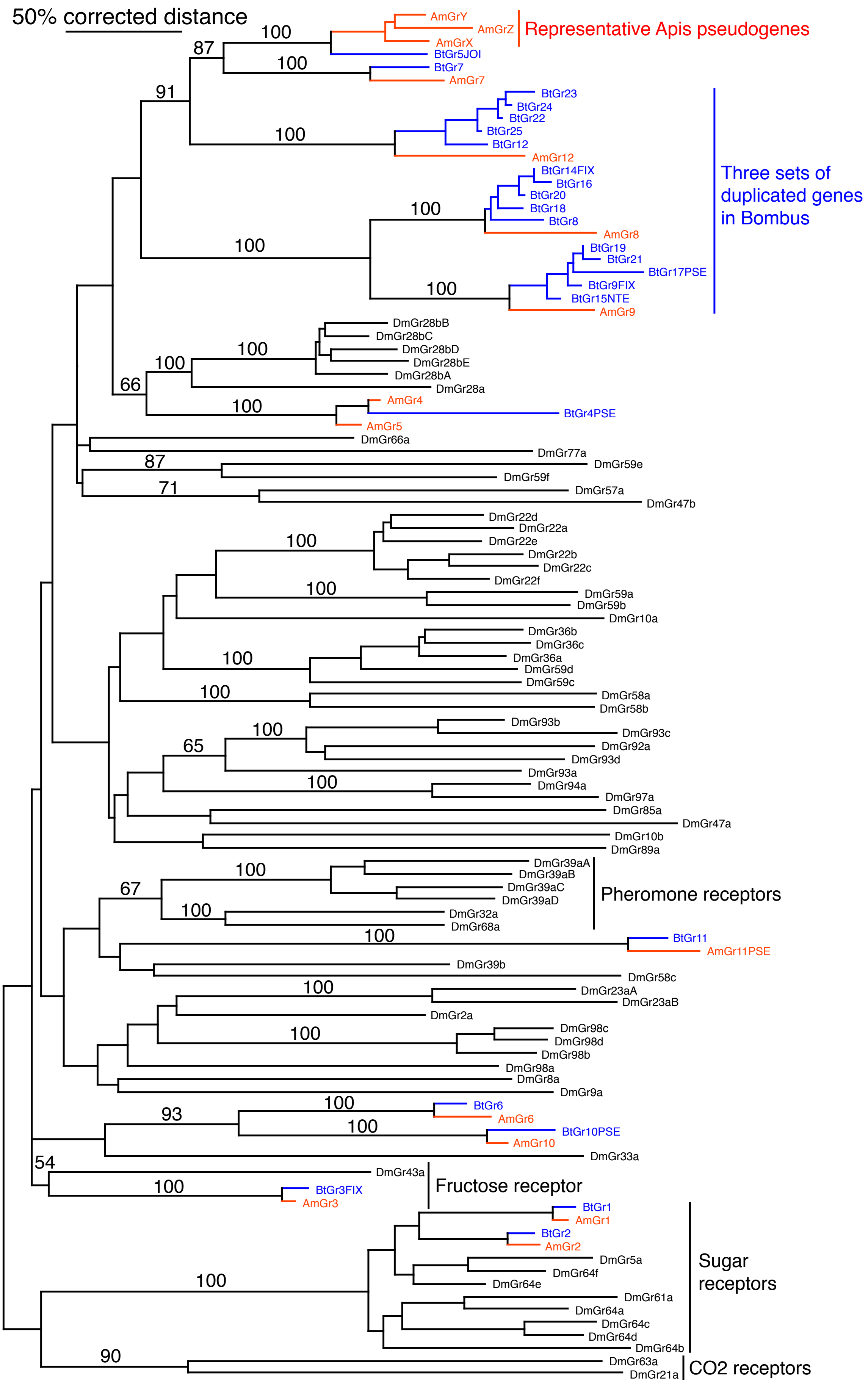
B.s terrestris, A. mellifera **and** ***D. melanogaster*** **Gustatory receptor (GR) phylogenetic tree**



Phylogenetic tree of the *B. terrestris*, *A. mellifera* and *D. melanogaster* GRs. This is a corrected distance tree and was rooted at the midpoint in the absence of a clear outgroup, an approach that clearly indicates the distinctiveness of the sugar and carbon dioxide receptors, as well as their putative distant relatedness. The *B. terrestris* and *A. mellifera* proteins are highlighted in orange and blue, respectively, as are the branches leading to them to emphasize gene lineages. Branches inferred to represent orthology are in double thickness. Bootstrap support levels in percentage of 10,000 replications of uncorrected distance analysis is shown above major branches. Comments on major gene lineages are on the right. Suffixes after the gene/protein names are: PSE – pseudogene; NTE – N-terminus missing; FIX – sequence fixed with raw reads; JOI – gene model joined across scaffolds.

Ionotrophic Receptors

Details of *B. terrestris* IR family genes and proteins. Columns are: Gene – the gene and protein name we are assigning (suffixes are INT – internal exon unidentified); Refseq protein number (prefix is XP_00); Scaffold – the genome assembly scaffold ID (format is GroupX.X, amongst 5678 scaffolds in assembly v1.0); Coordinates – the nucleotide range from the first position of the start codon to the last position of the stop codon in the scaffold; Strand – + is forward and - is reverse; Introns – number of introns in the coding region; AAs – number of encoded amino acids in the protein; Comments – comments on the OGS gene model, repairs to the genome assembly, and pseudogene status (numbers in parentheses are the number of obvious pseudogenizing mutations). INT – internal sequence missing

Gene	Refseq	Scaffold	Coordinates	Strand	Introns	AAs	Comments
IR8a	3402208.1	18.1	1896769-1905248	+	15	894	Fine as is
IR25a.1	3392973.1	1.2	169823-173788	-	4	943	Fine as is
IR25a.2	3392975.1	1.2	190156-192742	+	3	476	Fine as is
IR93a	3401385.1	15.6	3559364-3564574	-	15	862	Change an intron
IR68a	3397511.1	9.1	61620-65919	-	8	693	Fine as is
IR75f.1	3396144.1	6.3	6184986-6188033	+	7	552	Multiple changes
IR75f.2	3396145.1	6.3	6189137-6192524	+	8	597	First half of model
IR75f.3	3396145.1	6.3	6193102-6196198	+	8	655	Second half of model
IR75u	3398764.1	11.1	420735-424186	-	8	705	Multiple changes
IR218	3393505.1	1.9	1558190-1564301	+	11	602	Fine as is
IR328	3395261.1	4.5	7984098-7994889	-	8	807	Fine as is
IR329	3401158.1	15.5	927156-934618	+	9	621	Fine as is
IR330	3393979.1	2.3	2587368-2589967	-	7	610	First half of model
IR331	3393979.1	2.3	2583969-2586708	-	7	659	Second half of model
IR332	3397340.1	8.3	1908987-1913669	-	6	455	Change final exon
IR333INT	3397302.1	8.3	1915646-1919868	-	5	406	Multiple changes
IR334	3395389.1	5.1	7290378-7293889	+	3	697	Fine as is
IR335	-	5.1	7297781-7299913	-	0	710	New gene model
IR336	-	14.8	1307351-1309099	+	0	582	New gene model
IR337	-	2.3	1080706-1084316	+	3	582	New gene model
IR339	-	15.5	2781105-2782973	+	0	623	New gene model

Protein sequences of predicted *B. terrestris* (Bt) ionotropic receptors from the table above, and also corrected *A. mellifera* predictions (Am).

>AmIR8a
MSTTLVAVCALLLTFLGVSICQISMNMLIVIEEPDKSILNILNEALPQAEKNYGNDIISVHISTIEVERSNTDASFKKVCAALFKGISIVLDMTW
TGWDTLRNKANENGIIYKRGDSNINPYIQAIDDLLMLKNATDVALIFEDERELNQSLYYLIGNSILRLIVIDEFTEKTVSKIKSMRPSPSYYAIY
ASTAKMEDYFRTAVQGGLVKRNGIWKLIFTDNNYKDFKYINGDLQLNVSITVLWMKMDVCCRLIGESLCNCPSNVKIFSNYFKRLVGLIVS
LMSELQASGVSVEPKSVKCSSNANQSSNVTIEAFNKNIVAKLGGNDTFEYWPEKGMITYKAEIELKILENGLLEPLATWTRNGKIKEAENKK
ILPAKRFFRIGITPVIKFLPWIIPKIDPATGKVMKNENGNDMWDGYCIDFVKKLSEEMQFDYDLIIPEDRQFGKKLPNGQWNGLIGDLAKGET
DIIVAALTMTSEREEVIDFVAPYFEQSGLLIVMRKPVRKPSLFKFMTVLKVEVWLSIVGALTLTGIMIWILDKYSPYSARNNKQLYPYPCREF
TLKESFWFALTSFTPQGGGEAPKALSSRILVAAYWLFVVLMLATFTANLAAFLTVERMQSPVQSLEQLARQSRINYTVVANSSQHQYFINM
KNAEDKLYTVWKEITLNNTSDEVEYRVWDYPIKEQYGHILQAITQVGPVANSVEGFRKVIESENAEFAFIHDSSEIRYEVTKNCNLTEVGEV
FAEQPYAIAVQQGSHLQEEISRKILDLQKDRYFEMLASKYWNQTQKAQCLNSDDNEGITLESLGGVFIATLFGLALAMITLAGEVFYYRKR
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>BtIR8a
MSTTVVAASVFLLASFLGPTISLTPMNMLIVIEEPDKAILSILNDAVPQAEKNFGQNIIAVHISTVQVDRSNVDSSYERVCAALFKGISIILDMT
WTGWDRLRNLADENGIIYKRGDSNINPYIQAIDDLLMLKNATDVSLIFEDERELNQSLYYLIGNSIIRLVVIDEFTEKTVSKIKTMRPSPSYYA
IYASTAKMEDFFRTAIQGGLVTRNGVWNLVFTDNNYETFKYINGEHKLDVSITILSMKKDICCRLIGESDCSCPSDIQVFSHYFKRLVGLIVSL
MSDLQASGISVEPKIGRCPSPNTSPASNLTSEAFNNNILAKLGSNDTFEYWSEKGMITYKAEIQLEEFNGILEPLAIWTRHGKIKEAKKNKIKP
ARRFFRIGTAPSVPWTVPRLDPVTGKIMKDENGNDMWDGYCVDFIKKLSEEMEFDYDLVVPQDHQFGKKLSNGQWDGLIGDLAKGETDM
VVAALTMTSEREEVIDFVAPYFEQSGILIVMRKPVRKPSLFKFMTVLKVEVWLSIVGALTLTGIMIWILDKYSPYSARNNKQLYPYPCREFTL
KESFWFALTSFTPQGGGEAPKALSSRTLVAAYWLFVVLMLATFTANLAAFLTVERMQSPVQSLEQLARQSRINYTVVANSGVHQYFMNM
KNAEDKLYMVWKEITLNSTSDQVEYRVWDYPIKEQYGHILQAITQVGPVVTSREGFQKVIESENAEFAFIHDSSEIKYEVTRNCNLTEVGEV
FAEQPYAIAVQQGSHLQEEISRKILDLQKDRYFEMLASKYWNQSLKAQCQNSDDNEGITLESLGGVFIATLFGLALAMITLAGEVFYYRKR
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>AmIR25a
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SDSVEFSLPKPILLSAFYYDMIRLAVLAMKSALDDGEWPMEPRHITCDEYNNTNTPERKLNFFGKLKDAYKNITPTYAGIKWGSRNGEHQA
KFVMSVHLVTIKDGVVSNTVDSGSWNASISSPLQLTNNDVMNTTAVKSYRVVTVIHPPFVMYNEEKNEYYGFCIDLLNEIKKTVGFQYEIR
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FTSVLLWIFDRWSPYSYQNNREKYKNDDEKREFNLRECFWFCMTSLTPQGGGEAPKNLSGRLVAATWWLFGFIIIASYTANLAAFLTVSRL
EIPIETLEDLSKQYKIQYAPVINSSAYIYFKRMANIEWKFYEIWKEMSLNDSLSDVERANLAVWDYPVSDKYTKMLQAMEEAGFPASTEEA
LRRVRRLDSNNEFAYIEDSTTIKYLTMTNCDLIQVGEDFSRKPYAIAVQRGSPLKDQFNNAILILLNKRKLEKLKDKWWKKNPNKKDCDAE
NSQSDGISIHNIGGVFVVIFLGIIFACFTLAFEYWYYRHRNAQDTASIWAAPTLSIPSGPLWPTDTTETIFTLSTSLYGYATDTPYQESIVDDSPL
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EVWSVQVNESDVNDTLDRICKPWDSAVKEGGTRVPDLVIDTTTAGLGAKISNSFTAALGIPTLSAQYGQEGDLLYWRNLNTDQESYLIQV
MPPTDLIPEAIRQLCIQLNITNAAILYDHNFVMDHKYKSLLLNVPTRHVINEASQQVMEMRTQLPRLRDLDIVNYFILGDENTINIALEAAEA
LNFTGKKYGWFLLTPQLNVWPRCECRNMNILFMKPEFNKKSPIESSLSKPVISSAFYYDLIQLGVRAMKSALDDGEWPIEPRHITCDKYDKT
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IHPPFVMYNEENGTYYGFCIDLLDEIKDTVGFQYEIRETEDRRYGSLNPNGSWNGMMRELIDKRADIALGSVWVTAERERVVDFTVPYYDL
VGLSIMMLKTKTTSSLFKFLTVLENEVWFCILAAYLFTSVLLWIFDRWSPYSYQNNREKYKDDDEKREFNLRECFWFCMTSLTPQGGGEAP
KNLSGRLVAATWWLFGFIIIASYTANLAAFLTVSRLEIPIETLEDLSKQYKIQYAPVINSSAYIYFKRMAAIEWKFYDIWKEMSLNDSLSDVE
RANLAVWDYPVSDKYTKMLQAMEEAGFPASTEEALRRVRRLDSNNEFAYIEDSTTIKYLTMTNCDLIQVGEDFSRKPYAIAVQQGSPLKD
QFNNAILILLNKRKLEKLKDTWWKKNPDRKDCDAENSQSDGISIQNIGGVFVVIFLGIIFACFTLAFEYWYYRHRTKITKINLNSTTKGKVTQ
VKPLRFNLQPAPTHGFQNSQLRPRF
>BtIR25a.2
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AQVVDFAVPYQRPSGFTIMMLKKRRQVPFLRFLMILEIDVWIGFAFAFLFTIFLLYSLERYSPFSYRNNRAKYRNEADDRFSSLKECFWFAFT
SITPHGGGEMPKNLSGKIVAGTWWLFGFVMVAAYSANLAAYETLERLERNIESMDDLRKQYRVQYSTVANSSAFRYFLAMRRTEEWFYA
NWRRMALDENTPEAKRSDYAVWDYPLEDKFTKMYLAMEDTGFVRSVEEAVKMVREANRTYEFAFIAEAITVKYLMLTNCDFRQIGEEFG
KKPFAFAVQRDSPLRTKLNDAITKLAIERRLNALEKKWWDENPSRANCPADKDFNAGFDVDNLAVTFLLILLGILLAVLILCLQYCWYCYW
LNRRIKKVGLYATTRYISRGK
>AmIR93a
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SRSIFSLRHGNTGSGRKSSVKKMLNDFHVEQLGHCFLVIATVDMVADVMSVANSLNMVHPGSQWLYVITNSVSGNLINTSFINLLAEGGNV
AFMYNATNLDGFYKIKLKCYMKDLIEALAKALEYSLKNEIELFKRMNEDEFEMIRLTKSKKRAELLKNVRIHLSRNTSASNSVCEQCLLWR
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IMLETSQISRSWNTSQFAKLGEKIKEMTMSTTKKVPLEIIDLVRQKKVLLAACALTVNECGNTTFNYTVPIFVQTYSFLTAKPSQLSRVLLFA
SPFTKETWACLAVSIIIMGPILYLIHKYSPYSTKASGLNSSWQCVWYVYGALLQQGGMYLPQNDSARILIGMWWLVVMVLVATYSGSLVA
FLTFPRMDTSILSVEDLIAHKDSISWGFPNGSFLEMYLQNAEEPKYHVLFSRAERHNDTEEERLVERVKEGKHALIDWRSSLRFLMRKDFLL
TGSCHFSLSMDEFLDEPIAMIIPYGSPYLSVINAELHRMLESGLMNKWITEKMPMKDKCWEAPGSNQMVNKRKVNVTDMQGIFFVLFIGIT
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>BtIR93a
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QVNLISRSIFTLKHETTRSERKSSVKKTLNDFHVEQLGHCFLVIATVDMIADVMGVARSLKMVHPGSQWLYVITDSASKNMTNMTAFVDLL
AEGGNVAFMYNATNLSNYCEIKLICYVEELIQALAKALEYSLTSEIDLFKSMEEEKFEMIRLTKRERRAELLKNIRIHLSQNAFASEGFCGRC
LLWRFSSSITWGNFFSRGRNMAHLLDIGTWSPGFGVNLTDVIFPHIAHGFRGTNLPIATYHNPPWQIISVSKTGQKLYEGLVFDAINYLGSKL
NFSYTAITPEVTRNSNSWNTSRYAKLGEKIKEMTMSATRKVPKEVIDLVREREVLLGACAITVNENKKDAINFTVPIFVQTYSFLTSRPKQLS
RALLFASPFTKETWACLAVSIIVMGPILYLVHKYSPYSIKTSGLKSSFQCVWYVYGALLQQGGMYLPHCDSARILIGVWWLIVMVVVATYS
GSLVAFLTFPRMDASILTVDDLLARKDGITWSFPNGSFLEMYMQETDEPKYHTLLSRAESHNDTEEEKLVERVKDGKHALIDWRSSLRFLM
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NIIALTDSTRMLFATWWIFILILTSFYTANLTAFLTRPQFTLSISSLEDIVHKEYNWITYKGRIVDFLLSQNQQNDLSLLNISKQQGKGIFKYYE
PSRPILELVSTKRLFLEETHYLESLIFKDYVNKTRDHLEHNLRCTYVIMPGNILVTSRAFGFSHGSTIEKHINKMLLRLRETGITQFKKKEDLPL
AEICPVDLRSTERQLRNTDLLLTYKVVIGGYTIATIIFLFELIYACISYRLQNRKRQFINGRSYYVITNPVGDRKLIPIRTPSAFLFQYTT
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SQNQENDLSLLNVSKLQGKGVFKYYEHSRAILESVTTKRLFLAETHYLQTLIFKDYMNKTRHHLQHNSRCTYVIMPGSILITSRAFGFPHGST
FEKRINRLLLRLIETGIIHRTKKEDLPLAEICPVDLRSSERQLRNTDLLLTYKVVVGGYTIAAIIFLFEFIYAFILYRVQNGKRKACCYLPYCGR
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>AmIR68a
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LVDGRTVDCNAYIMLISNGYLTAEFLQYTERERLINTRGLFLLLYDLRLFQLNLYYLWKKIINVVFIRQYNAYKHRSGEISFKERIDLNTVYF
PPRKRRLTATKYIDTWYQGKLRYGTNHFTEKTNNLQKKHLQIAVFEHIPAVTEKSKLYYNKQPNNIIQGLGIEFELIQIISKAMNFKPKYYIQ
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FYFLSLSYKKHISSYKSQNTSIKNETKGLYLFTEIGNSILYTYSMLFQVSLPHLPSPWAVRILIGWWWIYSILVAVAYRASMTATLANPVARV
TIDTLAQLAKSSMEVGGLNEESKNFFLKSSDLSSQEIGNKFIIIKHEDEAIEKVANGSFCYYENSYFLQYARVKRQIFEKEKKRNETANNRSSK
HNLHIMEECIINMPIALGMEKNSPLKPKVDILIRRMIEIGLVKKWLNDVMEWPKIMEIRQEAESEKALVNLHKLKGAFFAIIFGYLLAFMILIG
EILYWKYIVLKDPKFDKYHLDIFYNSNNNSKI

>BtIR68a
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FPFRKRKSIVTKYIDTWYKGKLLYGTNHFTEKITNLQEKHLQIAVFEHIPAVTTKSRTYYNKQPNNNTEGLGIEFELMQIISKAMNFKPKYY
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GGVVFYFLSISYKKHISLYKNQMHFQNTSMKKEIKGLYLFTEIENSILYTYGMLFQISLPSLPSSWAVRVLIGWWWIYSILVAVAYRASMTA
TLANPVARVTIDTLEQLAKSSIEVGGWNKENKNFFSMSSDLSSQEIGNKFKLIQEEDKAIEKVANGSFAYYENSYLLQHVRVKRQILEKEQK
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>AmIR75f.1
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FDYAARHTGYSVNTSCDWNCVKSNKDGFLLINGPNTTDISDFFIKDRRDFKLSPLKISIFETSTISFQNGQFSGLDFKYLEEVCKMMNVTFVLI
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LKNERFEAIRQSGTVLFCCEYLTGFYFLEKRNGGVVKIAPKFTKKRAYDEAHGIYLVEKTPNVRSTIKTKKGRSKRFNEICLSFVTWLGRYL
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ALVLNGSTMHRKITIRHLFIPFGILCIGLAMSIIVFIYECLQNNVR
>AmIR335
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DRPLKSFLRRKNDVEGITWLFTIDRFDVIFVYWEWHVWNSNNQYLIVFTERSQVGGIVVWRDVFRTLWKRYHAYRVIVIRADDDFRCMLR
YKPFERYGEDEYGVVYETCLGEGSKVEGDGRRLFENFQNLNHYPVNVSVFESLLMRISYDRGNRLKLDKIDAKALFVLEKAMRASFNIKA
VRKRNIKRDPYSFLINDIERGITDMCITGFFVKTYGRFQKFQFTPSLYEDKICFVMTNYGFIPNMYVFFFPFRARLWLVLITYNVVITLLWRLV
RHLSSLFRRRPTSSNDHRVNGNRAKGVNRGESVKPPEIPRIVEKFFTFFEYLCYPIRDSKYAAERALLTGILFFNLIISGLYQSFLVSSLNKPFH
YYQYHTVDEVVRSGKTMITKYENLKQAFVGSDLWEKIQVIEFQRSTKNIVLTEDKISMTRLYNMQLLPHRHDRGKSSLYMVDECAMTYRI
SYILKLHSPYAERVNFVLLRMAEAGLPEHWIDEMRYFVTLYNRGEMEDFVNIHKLSLGYYVLAFLLLFVGLLLSTLIFFCELQAAKRNRKR
R

>BtIR335
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EKRSNNGFGRVYKSCLEKNHFTKRSSEYDLLQNSPKDYNSGYPGEILRLNRDTRLFENFQNLNHYPLNVLVFESLLMNVSYDTRNRLKLSK
PDANVAFALEKAMGAKFRIKAMRKADFMDDPFTTSLTDIETRNVDMIITGFFVKVYSKFRKFQFTCAMYEDKLCFVSPDSGLVPKAYMPFL
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IEYLTYPFQTSEIPAQRALLLGTLFFALILNGLYQSVLVSSLSKPFHYPQLHNLEDVVDSGKIVITKYANLKNVFLDDTELDATLAQRIRLINT
QRSTKDIVAYEDKIAITRYYSLELDDSDYFDKEGNPLLNLVDECPMNYRVSYVSRLHSPYAEKVDFVLLRLREAGLLNFWFDDMLYRIKIV
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>AmIR336
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DHTLPFEYEKWCPVVPITYQVNAIETRAFAAIIANIVILLAFWAVSALLRFERRLWQPLKIFGILIAASVSMRPGRTLERIVFFLVVLASTVYSA
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NKMDNLHGYPIRIGMVKRAGYLWYMKNSQGYPVMYRGPDVKVIKTLARIMNFTIAVYPSQEVFVDIINEKIDMIIPTLSIFADANAVKCDFT
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>AmIR337
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MFDKTRDLNGYEIRLNAISFEPHLQIDQSKPGLQKFTGDNSEIVKLVLVKLNASLNVRVYTGSVYDLGGVGKHGSMVGMMADVANGEVD
MGMNARSLNNMWKIEHTYPHGDDGLCVITQRAGEIAEFVKLWSFTAPIIHIGNFAIFTIALVILAKYQGFCPAFMNIIRMMTFVSIRKLPRTSS
CRIFFCSVFVLYLIVNALVQSHWASLLTIPVPLPNIRTAKDLKNSGYQIYGSMFHKLELQDPILRSRFHEDTYYACKEHVLRSRYAACLGDCQ
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>BtIR337
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MNARSLYNTWKVEHTYPHGDDGLCVFTQRAGEISEFVKIMSFLSPVIHAANAIVFVIALLVLTKYQGFVKASMNIIRLMTFGSVHRLPGTNS
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HYVRIQNEVRLYRSKKIQQNALVFKTREDWPLLASVTQMIQRTVESGIIGKWQKASIRKTRWAWKKRQLNKNKSFKTLEMHHVLFSFYIL
GSGYLLGIVAFVVEIFMGRKRIDKSSRNRKH
>AmIR338
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REGTNETNKNRDHSWTLFTRTFHPGRTTCGNLDFAKTGTLGGYRMKGMGLHNPPSLTIDPSKGSGGKLGGFNGIITEILLSKLNGSMTVTGI
TNDTRSYKFLHLVASGKYDVFLNTQYVFNKPNITTTYPHVNSGISILTRYPDNEAVYVKVLKFMNPVFILCCAVVGVITVIILEVFVGRGMIH
ASLEMIRVALNNSMTRFPEQGALRVYLITVFLLFMLTSSTFQSNLSSLLTSSIPRLTIDSDEELKTSGFEIYAYHGYRNAVFDDVLFTRVKMV
DHWDCSEYVRKDRNVACAADRTTLLKIAFEKGLHLSKHRINTLFSAYVVRPNWPLKDRFTSMLLHLSETGLIDHWWEKVMAKYVHKWL
KRTEKRTEDEKRNFTVMTLNDLDFAFYILAFGLFASALSFLIEISTRRLRVTLERREKNDFPIFPFTL
>AmIR339
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RRIFTVVVLARVGESVLAAGATSFRPGQPCAPSPPIILDKCGTRSWNLTRSAIRPPKWNKCVLKVAYFVEPPYVVVATNGTTEESLLGFEGM
LTEEILKGESIEREEVAWTENATYVEQIRTILYQADADLVVGRVLLQPQEDIDYSSSYDVLKVVWLIPKVANVSLKGLIQPFHPYVWAALGC
TLVLAVLVKIFLIPDLAYLDIFALIIGASIANRPGKLSTKIQYISWSVFGLFLMEVYVDALADQLINTSDTKIATTEELVSSSFGIGGTSAFKSLF
EEDTSGVVSRIREKFVTFDQNEYVGLFNDVMEGRNSSIALMVLLNSSRSEDIDTLHAYTMSTDVIYSFPLALAVWKGFPKLKRINAKIHDYI
DMGIFDHMIKLAIQKGRLAMMFEFAEEQEYKNNLHLQHFAPAFLVMIIGFSVGFLSIIVEIALYPSDLFFPRKRREEGN
>BtIR339
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IFLFRDLSFLDIFALIIGVSTARQPTRLSTKIHFLAWCIFGLFLTQLYVDSLADQLINMSDLKFETMKELISSSFQIGGTAAFARLFEIFDQDEIVK
SVRKKFVVFDQDEYVRQYYDLLDGTNSSFALVIVLNSSRSGAIETTQAYTITTDVICSFPLALATWKGSPHLEHLNGEINKYIDFGILDFLIQI
ALEKNLRAMSSQTAQDEEYKTELHLQQFVPAFLLVAIGFSSGFLFIILEVVLYPSKLLQ
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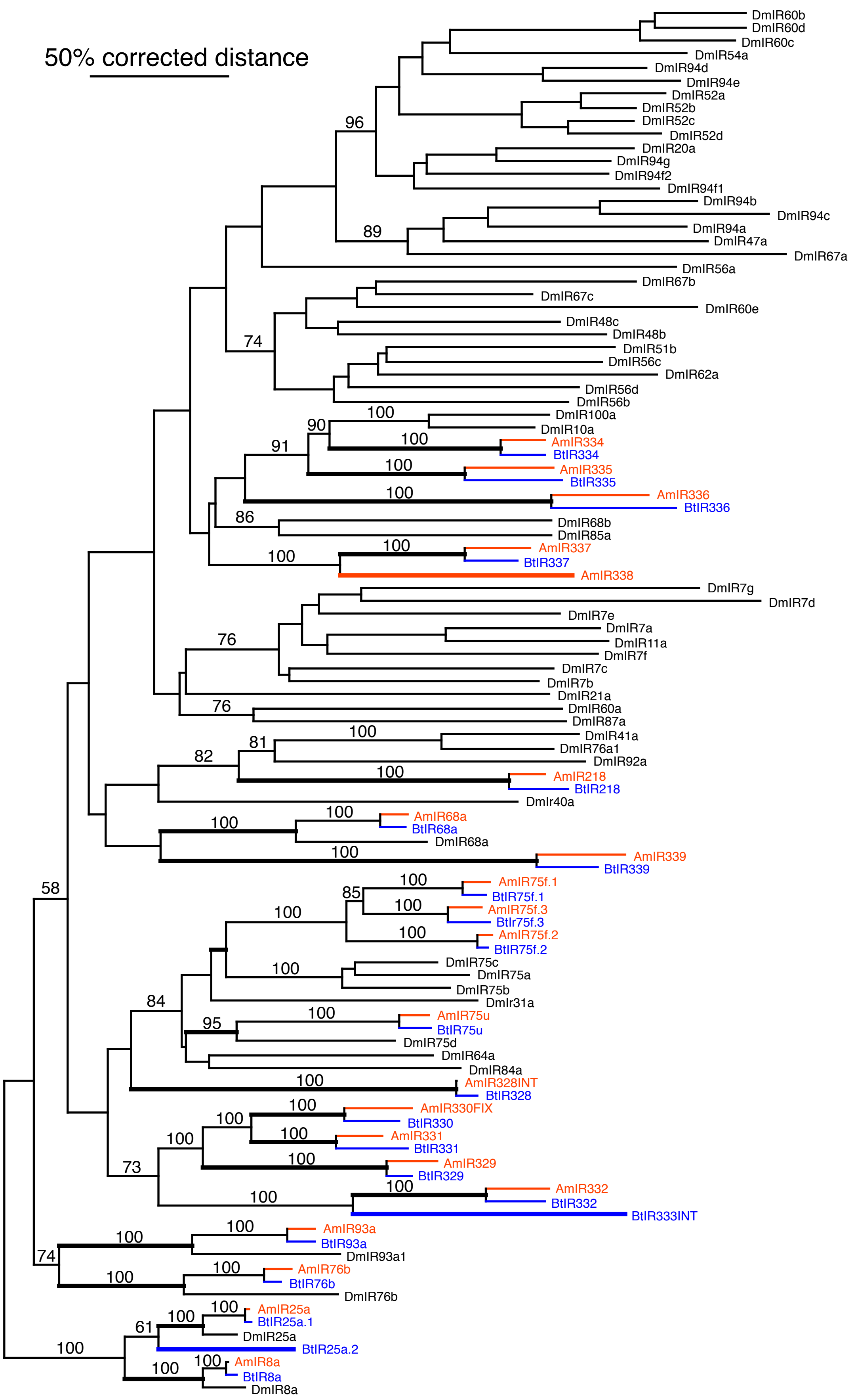
B. terrestris, A. mellifera **and** ***D. melanogaster*** **Ionotropic receptor (IR) phylogenetic tree**



Phylogenetic tree of the *B. terrestris*, *A. mellifera* and *D. melanogaster* IRs. This is a corrected distance tree and was rooted with IR8a/25a as the outgroup, based on their highly conserved sequences and ancestral position in the family. *B. terrestris*, *A. mellifera* and *D. melanogaster* gene/protein names are highlighted in blue, orange, and black, respectively, as are the branches leading to them to emphasize gene lineages. Bootstrap support level in percentage of 10,000 replications of uncorrected distance analysis is shown above major branches. Inferred ancestral and orthologous lineages are highlighted in double thickness. Suffixes after the gene/protein names are: INT – internal sequence missing; FIX – sequence fixed with raw reads.

Odorant Binding Proteins

Details of *B. terrestris* OBP family genes and proteins. Columns are: Gene – the gene and protein name we are assigning (JOI indicates a joined gene model across two scaffolds); Refseq protein number (prefix XP_00); Scaffold – the v1.0 genome assembly scaffold name (prefix GROUP); Coordinates – the nucleotide range from the first position of the start codon to the last position of the stop codon in the scaffold; Strand – + is forward and - is reverse; Introns – number of introns; AAs – number of encoded amino acids in the protein; Comments – comments on the OGS gene model and repairs to the genome assembly. JOI – gene model joined across scaffolds.

Gene	Refseq	Scaffold	Coordinates	Strand	Introns	AAs	Comments
OBP1JOI	3393962.1	UN544, 2.3	<1-7047, <1-2506	-, +	5	141	First exon in separate scaffold
OBP2	3397921.1	9.5	476155-477709	-	4	142	Fine as is
OBP3	3397912.1	9.5	472699-474392	-	5	146	Fine as is
OBP4	3397906.1	9.5	468253-470320	-	4	136	Fine as is
OBP5	3397877.1	9.5	465406-466652	-	4	136	Fine as is
OBP6JOI	3397894.1	9.5, UN3981	462424-464218, <1-965>	-	4	142	Second exon in separate scaffol
OBP7	-	9.5	457824-460037	-	4	146	New gene model
OBP8	3397865.1	9.5	455718-457043	-	4	137	Fine as is
OBP9	3397885.1	9.5	451528-452709	-	4	135	Fine as is
OBP10	3401479.1	15.6	5517044-5519625	+	4	147	Fine as is
OBP11	3401480.1	15.6	5521216-5522898	+	4	133	Fine as is
OBP12	3402792.1	UN637	1234-3000	-	4	136	Fine as is
OBP13	3401135.1	15.5	2870640-2871523	-	4	132	Fine as is
OBP14	3398556.1	10.1	9186283-9187517	-	5	152	Fine as is
OBP15	3398555.1	10.1	9184397-9185245	-	5	143	Fine as is
OBP16	3399482.1	12.1	2267493-2268250	-	4	152	Fine as is

Protein sequences of predicted *B. terrestris* odorant binding proteins from the table above

>BtOBP1JOI
MGGKQALLYLGLVCLQTIFVNAVPDWLPPEIFDMVAEDKARCMSEHGTTQAQIDEVDKGVLKDDTSITCYMFCLLEAFSLVDDEGDIDAD
MLLGLLPDQLQARAESVMSKCTPAPGSDKCDKIYNLAKCAMAEAPDVWFIV
>BtOBP2
MHVKLLLVAMLFAFVAWKPAESATAEQMDKMARSLRRSCLQKIDISEDKVEGMRRGEFPDDPNLKCYTNCIMKLIRTFKNGNIDFAMVIK
QVELSMAPEEAAVMKEAILKCSHMEYTGDECQKSYTFVKCTYDTNPERFFFP

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>BtOBP3
MKGVGVCLLVSLMLVLLAIKDTESKKMNLDELKKSIKNLRKPCSKKNDTPKELLDGQHNGEFPKDERLMCYMKCVLTQTKAMKGDEIM
WDFFVKNARVMILDEYFPRITHLVETCKNSVTATEGCEAAWQFSTCTYATDSELYIIP
>BtOBP4
MRVSLAICCLFFVAGAICDDKAEEFIKAFKEDIIPCLQEVEIPEDQIAKFVDNDLEGEERIKWGCVKACVMKRINIMSDGQMQMDNIKEIMD
KRFDKDSESTTEDMDQIKKCVEEVAGKTDECEIAFEFSRCMTPA
>BtOBP5
MKSLLVGICLLLTITVIQADFIDTYIELSKVPTLKCMKTVGYTETDPKVIFEQEVKLGVDKATCLRSCILKSMNMLKDSKINLDMINEFIKIVH
NEEPEKIEPMKKNAVECLDKVKDMSDDCKMAYAFIQCYVDKY
>BtOBP6JOI
MKTLVTFTCLLAAVTIVRGMDQDAVIGKYMEYLMPDIKPCADELNIAEDTATNIQQPKADADIRKMGCLKVCVMKRMNVLKGTDFNMEP
VYKMIEIVHAGNDEDIKLVKNIANECSAGTKGETDECNIGNKYVDCYIEKLFN
>BtOBP7
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IRFEYLLETAERNNFPIATNQTLNECCKKAQEQDDICKSGFVFATCSLRQSGL
>BtOBP8
MKTVAALFCVLYFVCCGVTANEMSDTCLKQMGLTIADLPSLAHDNSPEVARKRGCLEACVMQKMGLMNGNVINTQKIDELLDNILPDGE
NKEIVRNNVHQCAKDAANDDQCLVAQNFAQCGLEHLKLTARQLLSTIA
>BtOBP9
MKTAVALFCVLYFVCCGVTASEMSETCLKQMGLSVFDLGNLIRDNTPEGIRTRGCFEGCLMQKIGLMDGNVINLRKIDEQIDRAYPDSEKK
DIIRDTVHQCAYSAANDDQCVVAQNFGRCGLDQLRFAELAHRFT
>BtOBP10
MKILAIVFAFCFVGALALSDHKKAQLARFRTSCAIETSINLQLIEDVKRQTIPMNDGRLGCFTYCILRKMGIVEENGNLWIKNNVAKHQLIM
WGSPWHTANKLVKECQNINGANECKKASNLVGCFMKNKSSYKRLLHITKLLSSNE
>BtOBP11
MKILAIVFAFCFVGTLAFSNIVKAKVERFRASCITETSIDPNLIQGAKKGIISKADERLGCYTYCMLRKKGIVEENGHLWVNIAKRQLITYGA
DALMADEMVNKCKNVAGGNECKQASNLIQCFLEIRSSYIF
>BtOBP12
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>BtOBP13
MLRNCHFFLVLSTIIILLHFSKADIRKDCRRESKVSWAALRRMKAGDLEQEDQNLKCYLKCFMMRHGILDKNAEVDVQRALRHLPRSMQD
SSKKLFNKCKSVQSDDPCDKAYKMIKCYVEYHPEILQSVPFL
>BtOBP14
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>BtOBP15
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NILKQVIPNVYKEIGHEMIDSCKDVDAEDKCEKTFMFMKCMYNVNPIAFIAP
>BtOBP16
MKNSAFLASFILYWGLFSQNVIVLHAERPPFPPEIIHDCMDRENITTKELMILDSLPIETIKLLGSNREDFRNIGCFLACAFQQHGDMLGYTMN
LQTMMGRMHGMHHGHMDANPSFANVLQTCSDSVGGTDDECEAALTFHVCLMEAFHNRS
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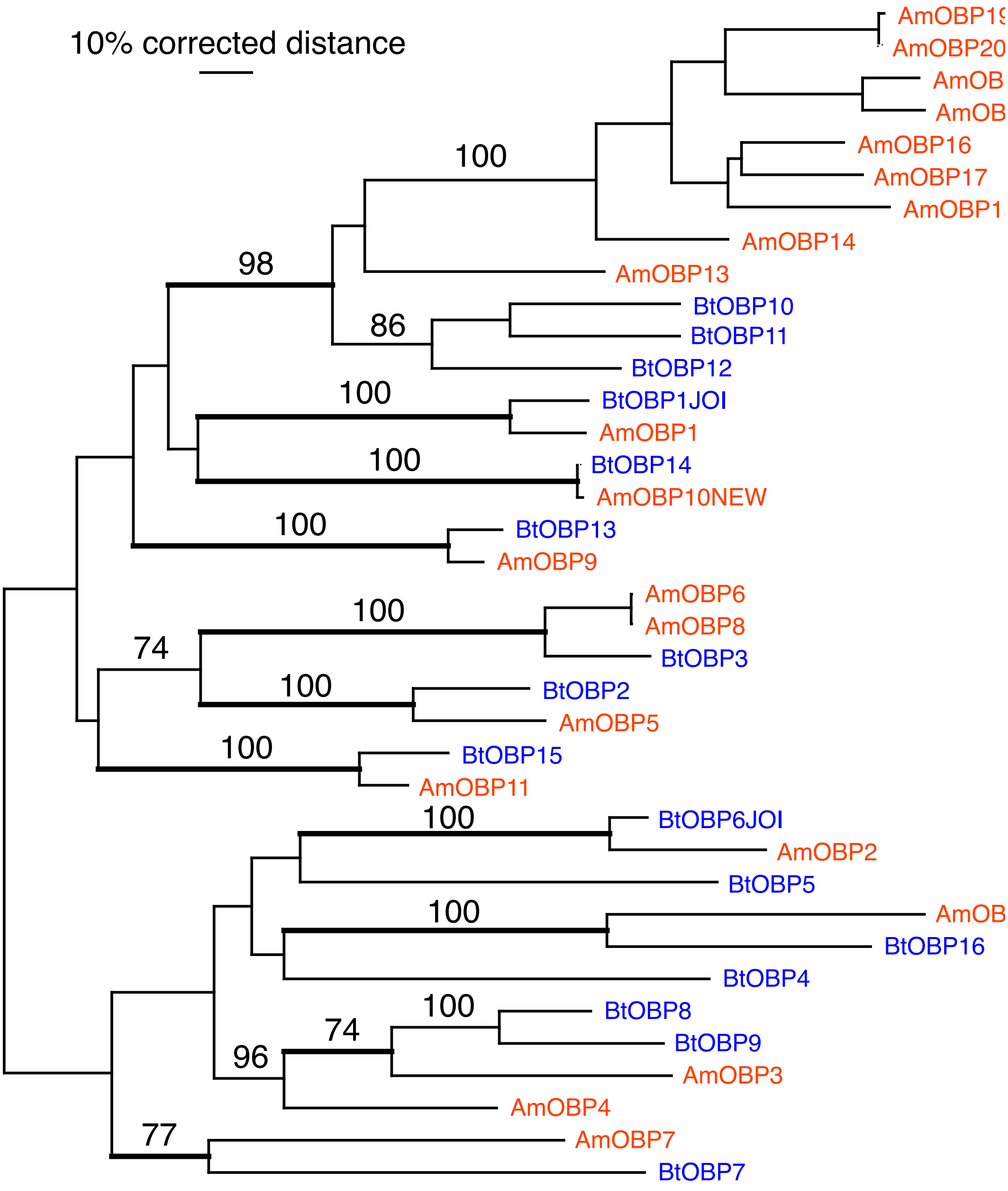
B. terrestris **and** ***A. mellifera*** **Odorant Binding Protein (OBP) phylogenetic tree**



Phylogenetic relationships of the *A. mellifera* and *B. terrestris* odorant binding prot corrected distance tree rooted at the midpoint. Percent bootstrap support from 10,000 ite uncorrected distance analysis are shown above branches. *A. mellifera* proteins are in orar

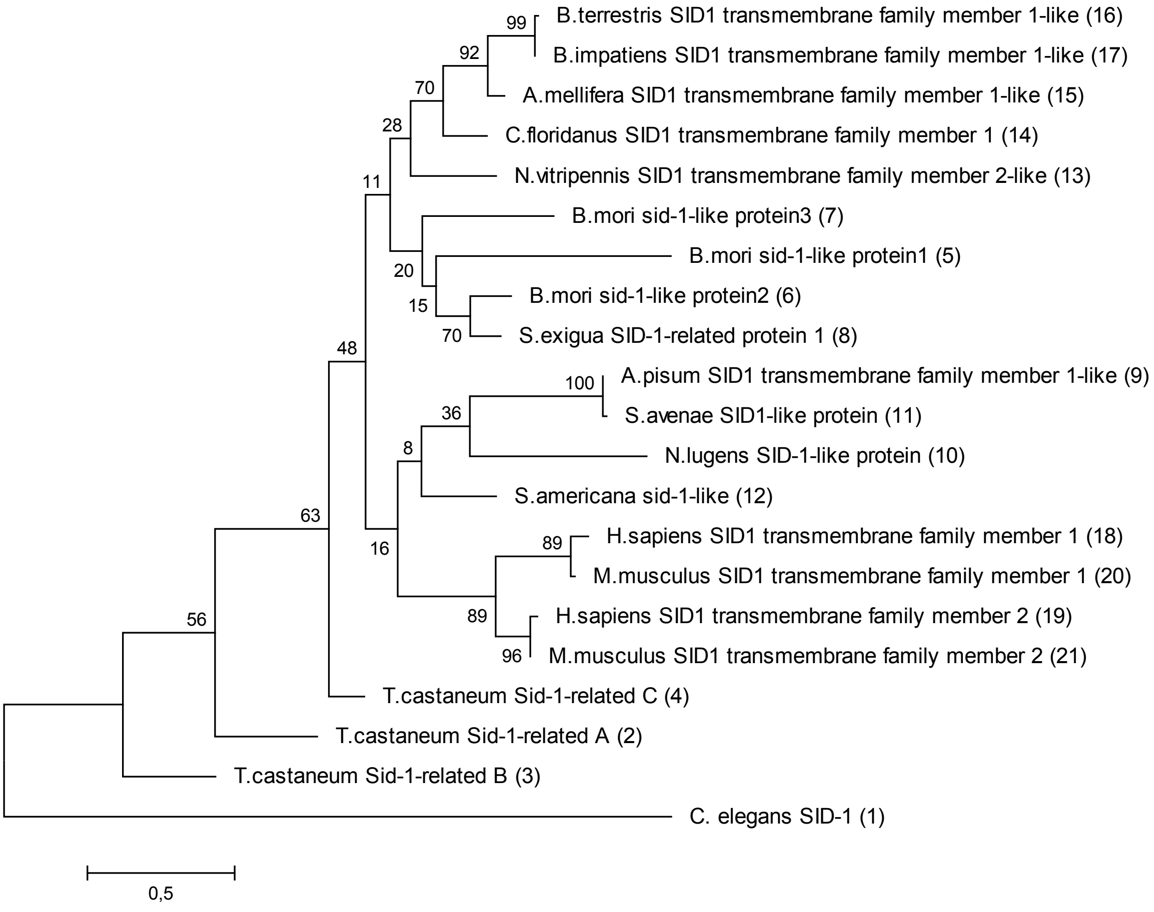
Hypothetical proteins identified within *B. terrestris* queen hemolymph. Functionally annotated *B. terrestris* hemolymph dataset was parsed for the presence of proteins annotated as hypothetical. Identified proteins were searched against the NCBI nr database using Blast2Go to identify level of conservation across phylogenies. For each protein, assigned BterHAP term, NCBI RefSeq protein_ID, functional description, sequence length (amino acids), presence of functional domains, predicted signal peptide domain and previously identified homologue within the hemolymph of the honey bee, *A. mellifera* (Chan et al., 2006), are shown.

BterHAP	**Protein_ID**	**Functional description**	**Sequence length (aa)**	**Functional domain analysis**	**Predicted signal peptide domain**	***Apis* hemolymph homologue**
***Bombus*-specific**						
BterHAP6	NA (au6.g3851.t1)	NA	102	Transmembrane domain (TMHMM)	1-23	-
BterHAP4	XP_003396531.1	PREDICTED: hypothetical protein LOC100650927	188	-	1-16	
Apidae						
BterHAP13	XP_003400053.1					
BterHAP14	XP_003402621.1 (au6.g8405.t1)	PREDICTED: hypothetical protein LOC100647918	93	Transmembrane domain (TMHMM)	1-21	
Apoidea						
BterHAP7	XP_003397710.1	PREDICTED: hypothetical protein LOC100646348	796	-	1-21	
Hymenoptera						
BterHAP9	XP_003398056.1	PREDICTED: hypothetical protein LOC100649338	676	-	1-19	XP_397488.1
BterHAP2	XP_003394564.1	PREDICTED: hypothetical protein LOC100647892	476	-	1-20	
BterHAP13	XP_003401022.1	PREDICTED: hypothetical protein LOC100646603	166	Transmembrane domain (TMHMM)	1-27	
BterHAP5	XP_003396646.1	PREDICTED:	100	Transmembrane domain	1-25	

		hypothetical protein LOC100644966		(TMHMM)		
BterHAP1	XP_003393509.1	PREDICTED: hypothetical protein LOC100644671	281	-	-	XP_001121746.1
BterHAP3	XP_003395760.1	PREDICTED: hypothetical protein LOC100644638	81	-	1-19	
BterHAP11	XP_003399422.1 (au6.g5771.t1)	PREDICTED: hypothetical protein LOC100648951	1111	-	1-15	
Hexapoda						
BterHAP8	XP_003398320.1	PREDICTED: hypothetical protein LOC100652008	177	Prokaryotic lipoprotein (PS51257) Transmembrane domain (TMHMM)	1-20	
BterHAP10	XP_003398591.1	PREDICTED: hypothetical protein LOC100644182	153	Transmembrane domain (TMHMM)	1-23	
BterHAPA1	XP_003393257.1	PREDICTED: hypothetical protein LOC100652150 isoform 2	318	Fn-I-like domain (SSF57603)	1-27	XP_001120895.2
BterHAPA2	XP_003393266.1	PREDICTED: hypothetical protein LOC100643149	327	Fn-I-like domain (SSF57603)	1-42	XP_001120895.2
BterHAPA3	XP_003393186.1	PREDICTED: hypothetical protein LOC100643108	316	Transmembrane domain (TMHMM)	1-28	XP_001120895.2

Overview of the genes coding for RNAi core machinery proteins in various insect species.

Gene family	*D. melanogaster*	*T. castaneum*	*B. mori*	*A. mellifera*	*B. terrestris*	*B. impatiens*
RNAse III	dicer-1 dicer-2 drosha	dicer-1 dicer-2 drosha	dicer-1 dicer-2 drosha	dicer-1 dicer-2 drosha	dicer-1 dicer-2 drosha	dicer-1 dicer-2 drosha
Argonaute	argonaute-1 argonaute-2 argonaute-3 aubergine piwi	argonaute-1 argonaute-2 argonaute-3 aubergine piwi	argonaute-1 argonaute-2 argonaute-3 aubergine	argonaute-1 argonaute-2 argonaute-3 aubergine	argonaute-1 argonaute-2 argonaute-3 aubergine	argonaute-1 argonaute-2 argonaute-3 aubergine
Genes coding dsRNA binding proteins	pasha R2D2 loquacious	pasha R2D2 loquacious	pasha R2D2 loquacious	pasha R2D2 loquacious	pasha R2D2 loquacious	pasha R2D2 loquacious



Phylogenetic tree for 21 SID proteins sequences using a Maximum Likelihood method. The numerical values are the bootstrap values after 250 replications. The scale bar represents the number of nucleotide substitutions per site. Accession numbers: (1) NP_504372.2, (2) ABU63672, (3) ABU63673.1, (4) ABU63674.1, (5) BAF95805.1, (7) BAF95806.1, (8) ACM47363, (9) XP_001951907, (10) ADI88514, (11) ABP98805, (13) XP_001605484, (14) EFN66381, (15) XP_395167.4, (16) annotated XP_003399893, (17) annotated sequence that matches XP_003493581, (18) NP_060169, (19) NP_001035545, (20) NP_001152891, (21) NP_758461.

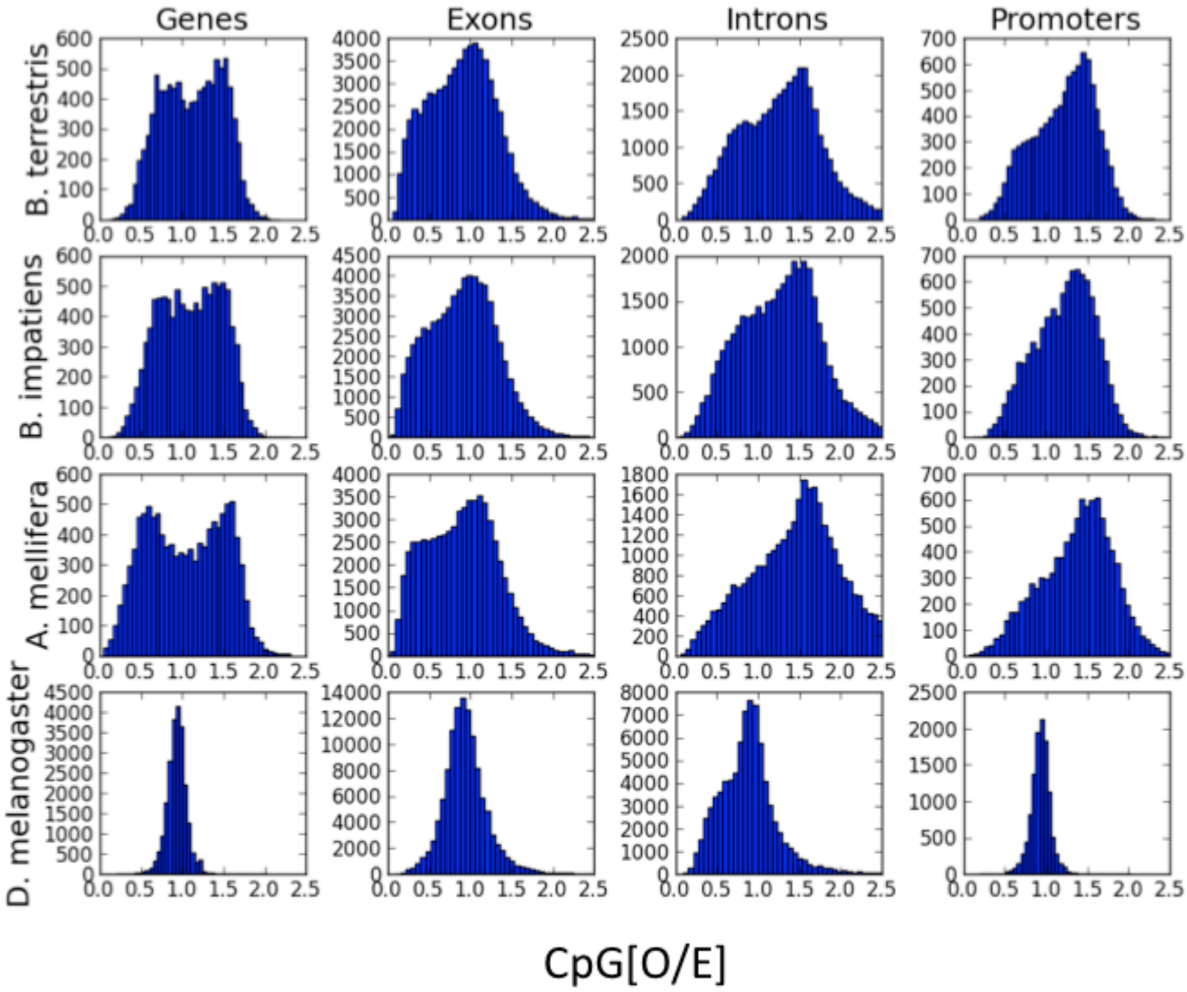
DNA methylation

The *B. terrestris* and *B. impatiens* genomes contain DNA methylation genes. Both the *B. terrestris* and *B. impatiens* genomes contain genes needed for the placement and removal of DNA methylation. This table includes the annotated gene names for the corresponding enzymes needed for de novo DNA methylation (DNMT3), the maintenance of DNA methylation during cell replication (DNMT1), targeting of DNA methylation (PIWI), and DNA de-methylation (TET).

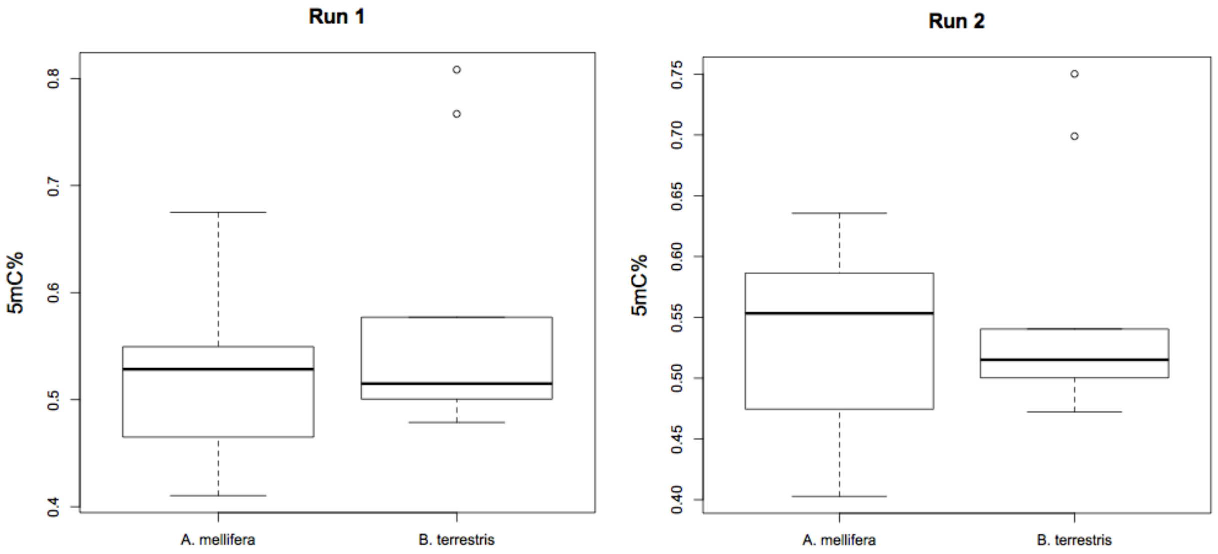
	DNA methyltransferase		tRNA methyltransferase	DNA methylation targeting	DNA de-methylation
	DNMT1	DNMT3	DNMT2	PIWI	TET
B. terrestris	bter_dnmt1a, bter_dnmt2a	bter_dnmt3	bter_dnmt2	bter_aubergine	bter_tet1, bter_tet2
B. impatiens	bimp_dnmt1a, bimp_dnmt2a	bimp_dnmt3	bimp_dnmt2	bimp_ago3	bimp_tet1, bimp_tet2

Methylated genes in *B. terrestris* and *B. impatiens* have the same distinct functional enrichment. Similar to *A. mellifera*, the most significant gene ontology terms (top 5 shown) for methylated bumblebee genes were related to metabolism and ubiquitous housekeeping functions.

GO biological process term	Accession	Fold enrichment (*B. terrestris*)	P-value (*B. terrestris*)	Fold enrichment (*B. impatiens*)	P-value (*B. impatiens*)
Cellular process	GO:0009987	1.29	7.79E-91	1.30	6.12E-105
Cellular metabolic process	GO:0044237	1.50	1.34E-85	1.52	3.60E-100
Primary metabolic process	GO:0044238	1.32	1.89E-43	1.34	1.85E-53
Metabolic process	GO:0008152	1.25	2.09E-38	1.27	1.10E-47
Macromolecule metabolic process	GO:0043170	1.33	6.75E-36	1.36	3.90E-45



DNA methylation is used on a genome-wide scale in *B. terrestris* and *B. impatiens*. DNA methylation in the germline results in CpG depletion through nucleotide deamination. The CpG[O/E] value (=#CpGs observed/#CpGs expected) was used to predict the presence of DNA methylation in a genomic region. The CpG[O/E] distributions are shown for genes, exons, introns, and promoters. The similarity of the CpG[O/E] distributions between the bumblebee and *A. mellifera* genomes indicates that bumblebee DNA methylation is likely targeted to approximately half of all genes and is primarily confined to exons. The lack of bimodality in the promoter regions indicates that the bumblebee genomes lack the promoter DNA methylation that is functional in mammals. The CpG[O/E] distributions for the *D. melanogaster* genome, which contains no measurable DNA methylation, is shown for comparison.



Genomic DNA methylation levels are approximately the same in bumblebees and honeybees. Global DNA methylation patterns in *B. terrestris* and *B. impatiens* using the MethylFlash DNA quantification kit (Fluorometric) from Epigentek. Thoraxes of newly emerged *B. terrestris* and *B. impatiens* workers and collected similar *A. mellifera* samples as controls were used. The two ELISA runs from the MethylFlash kit show that the global 5mc% levels (=% of all cytosines that are methylated) in *B. terrestris* (Run 1 avg. = .573%, Run 2 avg. = .555%, N=9) are similar to *A. mellifera* (Run 1 avg. = .523%, Run 2 avg. = .530%, N=9). Similar results were found for *B. impatiens*.

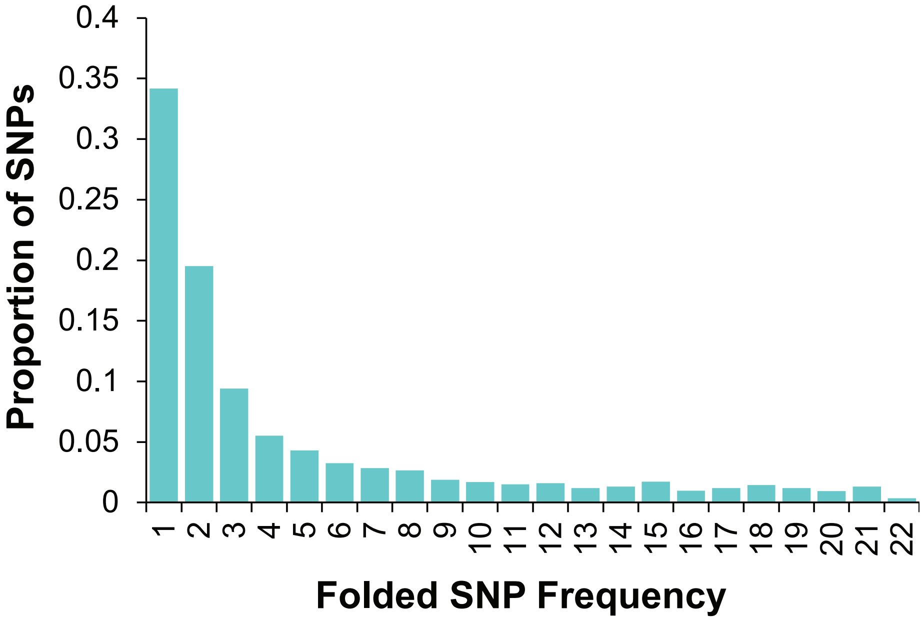
B. impatiens SNPs

Table of samples used in SNP identification

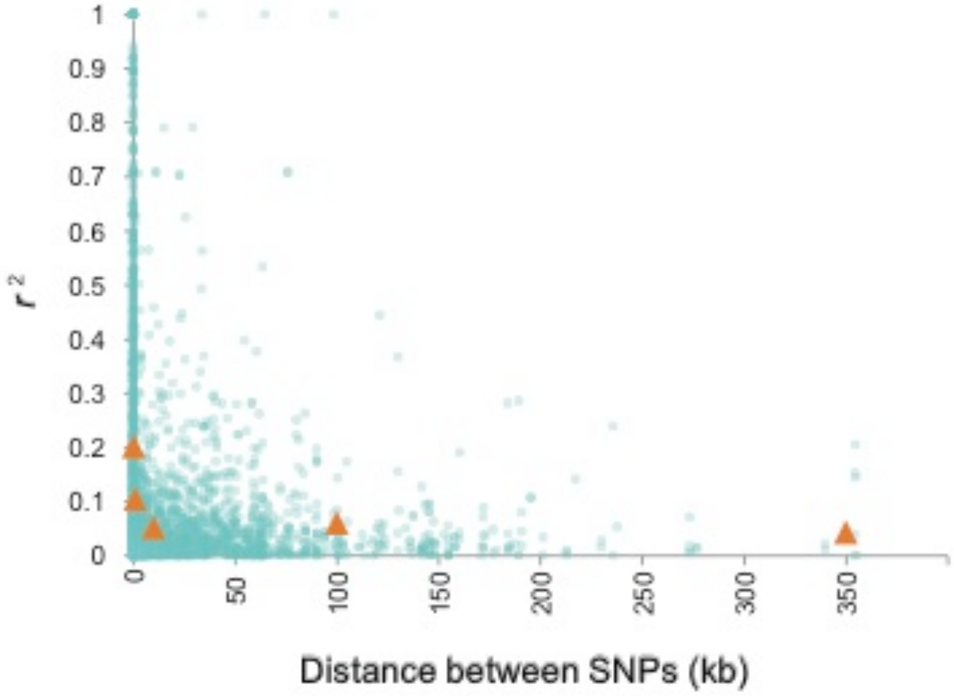
B. impatiens RADseq sample information. Samples from Cameron et al. (2011).

BAM/fastq File Prefix	State	County	Long.	Lat.	No. Sequence Reads	SRA Acc. No. for BAM alignments
UAlabama_JLozier_Bombus_AL09.0090_sequence_1	Alabama	Bibb	33.05	-87.01	2,570,235	SRR1702551
UAlabama_JLozier_Bombus_AR08.0468_sequence_1	Arkansas	Washington	35.82	-94.16	5,114,961	SRR1710771
UAlabama_JLozier_Bombus_CT09.0749_sequence_1	Connecticut	Hartford	41.77	-72.90	1,738,534	SRR1710772
UAlabama_JLozier_Bombus_IA09.0278_sequence_1	Iowa	Crawford	41.99	-95.39	3,997,417	SRR1710773
UAlabama_JLozier_Bombus_IL09.0331_sequence_1	Illinois	Ogle	41.98	-89.36	4,102,329	SRR1710774
UAlabama_JLozier_Bombus_IL09.1316_sequence_1	Illinois	Peoria	40.83	-89.80	7,417,713	SRR1710775
UAlabama_JLozier_Bombus_IN08.0789_sequence_1	Indiana	Montgomery	39.96	-87.07	2,998,470	SRR1713809
UAlabama_JLozier_Bombus_IN09.0200_sequence_1	Indiana	Ripley	39.07	-85.44	6,634,261	SRR1713946
UAlabama_JLozier_Bombus_KS09.0737_sequence_1	Kansas	Osage	38.64	-95.60	3,311,551	SRR1713811
UAlabama_JLozier_Bombus_KY09.0177_sequence_1	Kentucky	McCracken	37.03	-88.76	3,079,121	SRR1713813
UAlabama_JLozier_Bombus_KY09.0915_sequence_1	Kentucky	Franklin	38.16	-84.94	3,237,837	SRR1713814
UAlabama_JLozier_Bombus_MN08.0990_sequence_1	Minnesota	Winona	43.98	-91.43	6,125,072	SRR1713815
UAlabama_JLozier_Bombus_MO09.0593_sequence_1	Missouri	Franklin	38.48	-90.82	16,591,141	SRR1713816
UAlabama_JLozier_Bombus_NC09.0842_sequence_1	North Carolina	Stokes	36.47	-80.39	1,584,066	SRR1713865
UAlabama_JLozier_Bombus_NY09.0009_sequence_1	New York	Seneca	42.68	-76.85	4,305,873	SRR1713866
UAlabama_JLozier_Bombus_OH09.0001_sequence_1	Ohio	Belmont	40.00	-81.14	4,725,157	SRR1713879
UAlabama_JLozier_Bombus_PA09.0299_sequence_1	Pennsylvania	Cameron	41.40	-78.03	3,798,097	SRR1713880
UAlabama_JLozier_Bombus_SC09.0723_sequence_1	South Carolina	Kershaw	34.16	-80.57	1,334,241	SRR1713881
UAlabama_JLozier_Bombus_TN09.0034_sequence_1	Tennessee	Cocke	35.92	-82.98	5,086,922	SRR1713882
UAlabama_JLozier_Bombus_VA09.0646_sequence_1	Virginia	Appomattox	37.26	-78.68	1,133,079	SRR1713883
UAlabama_JLozier_Bombus_VT09.0166_sequence_1	Vermont	Windsor	43.41	-72.71	3,618,134	SRR1713884
UAlabama_JLozier_Bombus_WI08.0504_sequence_1	Wisconsin	Dane	43.04	-89.43	3,168,180	SRR1713885

RAD sequence data in the form of BAM alignments to AEQM02.fasta have been uploaded to Genbank Sequence Read Archive under Project Accession No. SRP051027, and SNP data in vcf format is available from the DRYAD digital repository: http://dx.doi.org/10.5061/dryad.52hj2



Likelihood-based site frequency spectrum estimate for *B. impatiens* RAD tags. For the 1.113×10^6 sites examined $\theta_{pi} = 0.0014$.



Linkage disequilibrium decays rapidly with intra-scaffold distance among RAD-tag SNPs (minor allele frequency >0.05) in *B. impatiens*. Average r^2 for logarithmic distance bins shown as triangles.