

Table S1. Details of neuropeptide and neurohormone precursor genes. Columns are: Gene – the gene and protein name we are assigning; VectorBase code – the official gene number in the RproC3 genome assembly, prefix is RPRC; Scaffold – the RproC3.3 genome assembly supercontig ID; AAs – number of encoded amino acids in the protein; Comments – comments on the OGS gene model and repairs performed in the genome assembly based on Blast searches against *de novo* antennal transcriptome assemblies. NTE: Amino terminal region; CTE: Carboxyl terminal region.

Gene	Gene symbol	VectoBase code	Scaffold	Isoforms	AAs.	Hit against the antennal <i>de novo</i> assemblies	Comments
Adipokinetic hormone/corazonin-related peptide	<i>ACP</i>	-	KQ035347	-	126	Yes	New gene model created based on GenBank sequence KM975505 [1] and included in the edited genome GFF
Adipokinetic hormone	<i>AKH</i>	RPRC000416	KQ034546	A	71	No	VectorBase prediction identical to GenBank sequence Acc. N° KM283242 [2]
				B	70	Yes	New isoform identified based on antennal assemblies and included in the edited genome GFF
AstA	<i>AstA</i>	-	KQ034293	-	203	Yes	New gene model created based on GenBank sequences Acc. N° GQ856315 and JN559385 [3] and included in the edited GFF
Allatostatin B	<i>MIP</i>	-	KQ034158	-	254	Yes	New gene model created based on Ons <i>et al.</i> 2011 and included in the edited genome GFF
Allatostatin CC	<i>AstCC</i>	RPRC000300	KQ034374	-	117	Yes	No changes in VectorBase prediction
Allatostatin CCC	<i>AstCCC</i>	-	KQ034609	-	100	No	New gene model was created based on Ons <i>et. Al.</i> 2011 and included in the edited GFF. Previously, it was annotated as <i>AstC</i>
Allatotropin	<i>AT</i>	-	KQ034313	-	119	Yes	New gene model created was created based on GenBank sequence Acc. N° GQ162783 [3] and included in the edited genome GFF
Bursicon alpha	<i>Burs-alfa</i>	RPRC000797	KQ034200	-	169	Partial	No changes in VectorBase prediction
Bursicon beta	<i>Burs-beta</i>	-	KQ034059	-	107	No	Identified in this work using <i>T. castaneum</i> GenBank sequence Acc. N° NM_001114308.1 as query. Gene model included
Diuretic hormone 31	<i>Dh31</i>	RPRC000977	KQ034472 (5'UTR); KQ034594 (rest of the gene model) and KQ037272 (last exon)	A	146	Yes	Identical to GenBank sequences Acc. N° GQ856316 and AEA51300 [3]. Last 42 amino acids are located in the KQ037272 supercontig
				B	109	No	Identical to GenBank sequences Acc. N° GQ856317 and AEA51301 [3]
				C	206	Yes	Identical to GenBank sequence Acc. N° HM030714.1 [4]
Cardioacceleratory peptide (CAPA/CAP2b)	<i>CAPA</i>	RPRC000639	KQ034830	A	158	No	VectorBase prediction identical to GenBank sequence Acc. N° ABS17680 [5]. In VectorBase classified as non-translating CDS
		RPRC000563	KQ034830	B	158	No	VectorBase prediction was identical to GenBank sequence Acc. N° ACH70295. In VectorBase classified as non-translating CDS

Gene	Gene symbol	VectoBase code	Scaffold	Isoforms	Aas.	Hit against the antennal <i>de novo</i> assemblies	Comments
Crustacean cardiactive peptide	<i>CCAP</i>	RPRC000466	KQ034330	-	129	Yes	VectorBase prediction was identical to GenBank sequence Acc. N° GQ888668 [3]
CCHamide peptide	<i>CCHa</i>	-	KQ034137	-	104	Partial	New gene model created based Ons <i>et al.</i> 2011 and included in the edited genome GFF
CNMamide peptide	<i>CNMa</i>	RPRC010893	KQ034609	-	150	No	No changes in VectorBase prediction
Corazonin	<i>CZ</i>	-	KQ034239	-		No	New gene model created based on Ons <i>et al.</i> 2011 and included in the edited genome GFF
Diuretic hormone 44	<i>Dh44</i>	RPRC000596	KQ034102	-	151	Yes	No changes in VectorBase prediction, which is identical to GenBank sequence Acc. N° HM153808 [6], annotated as corticotropin releasing factor-like protein
Eclosion hormone	<i>EH</i>	RPRC014242	KQ034677	-	241	No	Partial sequence. Initial methionine is still missed
Elevenin-1	<i>Elevin-1</i>	RPRC003083	KQ034317	-	66	No	No changes in VectorBase prediction
Elevenin-2	<i>Elevin-2</i>	RPRC003084	KQ034317	-	87	Yes	No changes in VectorBase prediction
Ecdysis triggering hormone	<i>ETH</i>	RPRC014486	KQ034462	-	146	Yes	No changes in VectorBase prediction
FLP	<i>FMRFamida</i>	RPRC014988	KQ035274	-	273	Partial	No changes in VectorBase prediction
Glycoprotein hormone alpha 2	<i>GPA2</i>	RPRC007092	KQ034094	-	122	Partial	No changes in VectorBase prediction
Glycoprotein hormone beta 5	<i>GPB5</i>	-	KQ034094	-	156	No	New gene model was created based on <i>C. lectularius</i> sequence XP_014244389.1. Methionine is missed.
Kinin		RPRC000022	KQ034106	-	398	Yes	VectorBase prediction was identical to GenBank sequence Acc. N° BK007870 [7]
IDLSRF-like peptide	-	RPRC000351	KQ034112	-	168	Yes	No changes in VectorBase prediction
Insulin-like peptide	<i>Ilp</i>	RPRC007020	KQ034142	-	126	Yes	VectorBase prediction was identical to GenBank sequence Acc. N° AMS34841.1 [8]
ITG-like	-	-	KQ034255	-	214	Yes	New gene model created based on Ons <i>et. al</i> 2011 and included in the edited genome GFF
Ion transport peptide	<i>ITP</i>	RPRC000519	KQ034208	A	111	No	Annotated as sulfakinin (GenBank sequence Acc. N° GQ2539210). Last 33 amino acids are not in the genome
				B	117	Yes	VectorBase prediction was identical to GenBank sequence Acc. N° GU207866 [3]

Gene	Gene symbol	VectoBase code	Scaffold	Isoforms	Aas.	Hit against the antennal <i>de novo</i> assemblies	Comments
Long Neuropeptide F	<i>NPF</i>	RPRC008107	KQ034255	No	105	Yes	VectorBase prediction extended in NTE region and initial methionine fixed according to GenBank sequence Acc. N° KT898124.1 [9]
Myosuppressin	<i>Ms</i>	RPRC000203	KQ034384	No	88	Yes	VectorBase prediction was identical to GenBank sequence Acc. N° GQ344501 [3]
Natalisin	<i>NTL</i>	RPRC003680	KQ034106	-	196	Partial	No changes in VectorBase prediction
Neuroparsin	<i>NP</i>	RPRC002095	Q034340		113	Yes	VectorBase prediction was identical to GenBank sequence Acc. N° GU207864 [3]
Neuropeptide like precursor 1	<i>NPLP1</i>	RPRC011668	KQ034238	-	454	Yes	VectorBase prediction was identical to GenBank sequence Acc. N° GU207865 [3]
NVP-like	<i>PH2</i>	RPRC003052	ACPB03040762	-	299	Yes	VectorBase prediction was shorter in NTE and CTE regions. Impossible to fix the genome model due to problem in the genome assembly.
Orcokinin	<i>OK</i>	RPRC014678	KQ034149	A	165	Yes	One exon added in NTE region of VectorBase prediction based on GenBank sequence Acc. N° FJ167860
				B	392	Yes	Only first 52 amino acids present in the genome. Sequence identical to GenBank sequence Acc. N° FJ761320 [10]
				C	422	No	Same problem as mentioned for isoform B. Sequence identical to GenBank sequence Acc. N° KF179047
Pigment dispersing factor	<i>PDF</i>	-	KQ034061	-	48	Yes	New gene model created based on <i>Ons et al.</i> 2011 and included in the edited genome GFF
Proctolin	<i>Proc</i>	RPRC000390	KQ034188	-	97	No	VectorBase prediction was identical to GenBank sequence Acc. N° JN543225 [11]
Pyrokinin	<i>PK-PBAN</i>	-	KQ034521	-	122	Yes	New gene model created based on GenBank sequence GU230851 and included in the edited genome GFF
RYamide	<i>RYa</i>	RPRC000461	KQ035177	-	107	Yes	Initial methionine of VectorBase model was fixed according to antennal assemblies
Short Neuropeptide F	<i>sNPF</i>	-	KQ034092	-	92	Yes	New gene model created based on GenBank sequence Acc. N° GQ452380 [3] and included in the edited genome GFF
SIFamide	<i>SIFa</i>	-	KQ035590	-	74	Yes	New gene model created based on GenBank sequence Acc. N° GQ253922 [3] and included in the edited genome GFF
Sulphakinin	<i>SK</i>	-	KQ034228	-	92	Yes	New gene model created based on GenBank sequence Acc. N° GQ162784 [3] and included in the edited genome GFF
Tachykinin	<i>TK</i>	RPRC000843	ACPB03026326	-	215	Yes	VectorBase prediction was identical to GenBank sequence Acc. N° GQ162785 [3]

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