

Table S5. Details of nuclear receptor 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 genome assembly supercontig ID; AAs – number of encoded amino acids in the protein; Comments – comments on the OGS gene model and repairs to be performed on the genome assembly (available on VectorBase) based on Blast searches against *de novo* antennal transcriptome assemblies. NTE: Amino terminal region; CTE: Carboxyl terminal region.

Gene	VectorBase code	Scaffold	AAs.	Hit against antennal <i>de novo</i> assemblies	Comments
<i>Knirps-related 1 (knrl1)</i>	RPRC003216	KQ035852	325	No	Fine as is
<i>Knirps-related 2 (knrl2)</i>	-	ACPB3007969	302	Si	New gene model was created*
Ecdysone-induced protein 75B (<i>Eip75B</i>) isoform A	RPRC000853	KQ034727	717	No	Methionine is missed. Exon 4 th was incorrect and 5 th exon is located in the opposite strand.
Ecdysone-induced protein 75B isoform B	RPRC000853	KQ034727	653	Si	Only exons 2 nd and 3 rd were predicted in VectorBase. Exon 4 th was incorrect and 5 th exon is located in the opposite strand *
Ecdysone-induced protein 78C (<i>Eip78C</i>)	RPRC009045	KQ034642	344	No	Initial methionine is missed
Hormone receptor-like in 3 (<i>HR3</i>)	RPRC003681 and RPRC0000824	KQ034284 and KQ036430	579	Si	Two VectorBase predictions must be fused and edited. NTE region must be extended until initial methionine*
Ecdysone receptor (<i>EcR</i>)	RPRC014174	KQ034515	475	Si	NTE region must be extended until initial methionine*
Hormone receptor-like in 96 (<i>HR96</i>)	RPRC001794	KQ034099	377	No	Fine as is
Hepatocyte nuclear factor 4A (<i>HNF4</i>)	RPRC008212	KQ034483	396	Si	CTE terminal region is incomplete. Initial methionine is missed
Hepatocyte nuclear factor 4B (<i>HNF4</i>)	RPRC001064	KQ034403	325	Partial	Fine as is
<i>Ultraspiracle (usp)</i>	RPRC013330	KQ034117	430	Si	NTE and CTE regions are incomplete*
Hormone receptor-like in 78 (<i>HR78</i>)	RPRC006737	KQ034201	495	Si	NTE and CTE regions are incomplete*
<i>Tailless(tll)</i>	RPRC007025	KQ034142	370	No	Initial methionine is missed
Hormone receptor-like in 51 (<i>HR51</i> or <i>unfulfilled</i>)	RPRC002557	KQ034474	478	No	Initial methionine is missed
<i>Dissatisfaction (dsf)</i>	RPRC010625	KQ034604	195	No	Initial methionine is missed
<i>NR2E6 (PNR- like)</i>	RPRC009755	KQ034409	394	Si	Multiple changes in VectorBase prediction are necessary*
<i>Seven-up (svp)</i>	RPRC000767	KQ034946	227	No	Fine as is
Estrogen-related receptor (<i>ERR</i>)	-	ACPB03009538	426	Si	New gene model was created*
Hormone receptor-like in 38 (<i>HR38</i>)	RPRC001680	KQ034154	287	Si	NTE is missed*
<i>Fushi tarazu transcription factor 1 (Ftz-TF1)</i>	RPRC001915	KQ034834 and KQ034274	618	Si	VectorBase predictions RPRC014120 and RPRC001915 must be fused and edited*
Hormone receptor-like in 39 (<i>HR39</i>)	RPRC002968	KQ034115	695	Si	NTE region must be extended until initial methionine*
Hormone receptor-like in 4 (<i>HR4</i>)	RPRC012796	KQ034081	542	Si	NTE region must be extended until initial methionine and CTE is missed

kni-like and, *PNR-like*, HR39, Estrogen-related receptor gene models were included in the modified GFF file that was used for mapping of our RNASeq reads.

(*) The sequences included in the Additional file 13: Data file S2 for these genes are those obtained after the comparison to our antennal transcriptome assemblies and the appropriate correction.