

Table S6. Details of *to* 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.

Gene	VectorBase code	Scaffold	AAs.	Hit against the antennal <i>de novo</i> assemblies	Comments
<i>to1</i>	RPRC010098	KQ034137	244	Yes	Fine as is
<i>to2</i>	RPRC010096	KQ034137	242	Yes	Annotated as <i>to3</i>
<i>to3</i>	RPRC008440	KQ034102	248	Yes	The initial methionine must be fixed
<i>to4</i>	RPRC008432	KQ034102	191	Yes	Some internal problems detected
<i>to5</i>	RPRC008451	KQ034102	222	Yes	The initial methionine must be fixed
<i>to6</i>	RPRC002313	KQ034398	147	Yes	N-terminal region must be extended until initial methionine. Annotated as <i>to2</i>
<i>to7</i>	RPRC008276	KQ034251	250	Yes	Fine as is
<i>to8</i>	RPRC009613	KQ034205	250	Yes	Fine as is
<i>to9</i>	RPRC010085	KQ034137	247	Yes	Internal problems were fixed*
<i>to10</i>	RPRC011983 and RPRC011984	KQ034059	144	Yes	Two VectorBase predictions must be fused
<i>to11</i>	RPRC005773	KQ034137	248	Yes	Fine as is
<i>to12</i>	RPRC010201	KQ034137	226	Yes	Fine as is
<i>to13</i>	RPRC010202	KQ034137	227	Yes	Fine as is
<i>to14</i>	RPRC005774	KQ034137	259	Yes	Fine as is
<i>to15</i>	RPRC005775	KQ034137	255	Yes	Fine as is

* This model was fixed and 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 *to3*, *to4*, *to5*, *to6*, *to9* and *to10* genes are those obtained after the comparison to our antennal transcriptome assemblies and the adequate correction.