

Table S2. Protein-coding genes present in the ultraconserved region *CG15121-CG16894*

Code ^a	Gene ^b	Cross-Mapped ^c	FlyAtlas ^d		SEBIDA	Male-Biased	Sperm	Seminal Fluid	Chemosensory
			Expression	Enrichment	Classification ^e	Gene Expression ^f	Proteome ^g	Proteome ^h	Perception ⁱ
20	<i>CG11218</i>	✓	bhcztwgg		Male	mel, sim, yak			<i>Obp56d</i>
21	<i>CG8462</i>	✓	hczaw		Female			mel, sim, yak	<i>Obp56e</i>
22	<i>CG30450</i>		a	a	Male			mel, sim, yak	<i>Obp56f</i>
23	<i>CG8517</i>	✓	tay	t	Male	mel, sim, yak, ana, pse, moj			
24	<i>CG12501</i>	✓			Unclassified				<i>Or56a</i>
25	<i>CG13873</i>	✓	haw		Male	mel, sim, yak, ana, pse		mel, sim, yak	<i>Obp56g</i>
26	<i>CG13874</i>	✓	h	h	Unbiased (male)	sim, yak, vir, moj			<i>Obp56h</i>
27	<i>CG8595</i>	✓			Male				
28	<i>CG30448</i>		ta	a	Male			mel, sim, yak	<i>Obp56i</i>
29	<i>CG13872</i>	✓	t	t	Male	yak, ana, pse, vir, moj			
30	<i>CG30447</i>		ty	t	Male				
31	<i>CG10822</i>		ty	t	Male				
32	<i>CG8654</i>	✓	hcztxywgs		Male	ana, pse, moj			
33	<i>CG16898</i>		hmztxw	m	Male				
34	<i>CG8896</i>	✓	bhcmzotaxywgs		Unbiased (female)				
35	<i>CG11041</i>	✓			Unbiased (female)				
36	<i>CG16894</i>	✓	ty	t	Male	mel, sim, yak, ana, pse, vir, moj			

^a As in Figure 1.

^b FlyBase [1].

^c Inferred to be present within this ultraconserved region prior to the divergence of the lineages that lead to the *Sophophora* and *Drosophila* subgenera [2].

^d Tissues with evidence of expression [3] (brain, b; carcass, w; crop, c; head, h; hindgut, z; larval fat body, y; larval Malpighian tubule, x; male accessory gland, a; midgut, m; ovary, o; salivary gland, s; testis, t; and thoracic abdominal ganglion, g) and preferential expression (five-fold increase in relation to the whole body) as estimated previously [2].

^e Consensus categorization of the sex bias in mRNA abundance based on a reanalysis of several expression datasets [4]. The trend is indicated in parentheses for those cases in which no statistically significant bias was found.

^f As categorized based on species-specific microarray experiments in *D. melanogaster -mel-*, *D. simulans -sim-*, *D. yakuba -yak-*, *D. ananassae -ana-*, *D. pseudoobscura -pse-*, *D. virilis -vir-*, and *D. mojavensis -moj-* [5].

^g As assessed by whole-sperm mass spectroscopy in *D. melanogaster* [6].

^h Species in which evidence of expression was found by mass spectroscopy in recently mated females [7].

ⁱ Common name as a member of a multigene family. Those encoding odorant-binding proteins are organized into two clusters: *Obp56a-Obp56f* and *Obp56g-Obp56i* [8].

Supporting References

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