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Supplementary Information for

Divergence of chemosensing during the early stages of speciation

Bas van Schooten[1, 2,†,*], Jesyka Meléndez-Rosa[1,†,*], Steven M. Van Belleghem[1], Chris Jiggins[3], John Tan[4], W. Owen McMillan[2] and Riccardo Papa[1,2,5,*]

[1]Department of Biology, University of Puerto Rico, Rio Piedras, San Juan, Puerto Rico, United States of America, 00925
[2]Smithsonian Tropical Research Institution, Balboa Ancón, Panama, Republic of Panama
[3]Department of Zoology, University of Cambridge, Cambridge, United Kingdom, CB2 8PQ
[4]Roche NimbleGen Inc., Madison, Wisconsin, United States of America, 53719
[5]Molecular Sciences and Research Center, University of Puerto Rico, San Juan 00907, Puerto Rico

* Corresponding author
†These authors contributed equally to this work

Bas van Schooten – Julio García Díaz (JGD) Building, Room 119, University of Puerto Rico, San Juan, PR 00931; 626-421-5648; basvanschooten@gmail.com
Jesyka Meléndez-Rosa –Julio García Díaz (JGD) Building, Room 119, University of Puerto Rico, San Juan, PR 00931; 787-557-3100; jesykamelendez@gmail.com
Riccardo Papa – Julio García Díaz (JGD) Building, Room 119, University of Puerto Rico, San Juan, PR 00931; 626-421-5648; rpapa.lab@gmail.com

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Supplementary Information Text

Detailed Materials and Methods

Sampling, RNA extraction, and sequencing

We bred 15 *Heliconius melpomene* and 15 *H. cydno* butterflies in semi-natural conditions from November 2013 to March 2014 in Gamboa, Panama (9°7.4′ N, 79°42.2′ W, elevation 60 m). Unmated females were two days old at sampling and both males and mated females were five days old; females were mated within the first two days after eclosing. In order to minimize time of day effects in gene expression, all individuals were sampled during the late morning hours (09:00-12:00 hrs) - the period during which butterflies are the most active in the wild. For each individual we collected tissues of three sensory tissue types: antenna, legs (all six legs), and mouthparts (including the proboscis and labial palps). These were submerged in RNAlater and stored for two weeks in a -20 °C freezer at the Smithsonian Tropical Research Institute before being moved to permanent storage at a -80 °C freezer at the University of Puerto Rico, Rio Piedras.

For each individual butterfly we extracted RNA separately from each of the three sensory tissue types (see above) for a total of 90 individual RNA extractions representing three biological groups (5 males, 5 unmated females, and 5 mated females) of two closely related species (15 *H. melpomene* and 15 *H. cydno*) (S1 Figure in SI Appendix). RNA was extracted using a TRIzol™ RNA isolation protocol followed by additional purification using a RNeasy minikit (Qiagen). RNA quality was assessed using RNA 6000 Pico BioAnalyzer chips (Agilent) (1) and concentrations were determined using a NanoDrop spectrophotometer (ThermoFisher) (2). Two Illumina libraries, each representing 45 individually barcoded RNA extractions for either *H. melpomene* or *H. cydno*, were generated using the Illumina TruSeq™ RNA sample preparation kit according to the manufacturer's low-throughput protocol. Each library was sequenced three times on a HiSeq2500 Illumina system for a total of six Illumina sequencing lanes (50bp SR). Sequencing was performed at the Knapp Center for Biomedical Discoveries at the University of Chicago.

Targeted resequencing and chemosensory gene annotation improvement

We first used CrossMap (3) and manual verification to update the annotation of chemosensory gene models on the *Heliconius melpomene* genome v2 Hmel2 genome version (4, 5). For this, we used previously published gene models for 252 chemosensory genes: a) 33 chemosensory proteins (6), b) 43 olfactory binding proteins (6), c) 70 olfactory receptors (6), d) 73 gustatory receptors (7), and e) 31 ionotropic receptors (8).

We further improved the chemosensory gene models by producing a target RNA resequencing data set for the genes of interest (S1 Figure in SI Appendix). For a subset of the sampled *Heliconius melpomene* butterflies (two males, two unmated females, and two mated females) we pooled equal amounts of RNA extracted from the antenna, legs, and mouthparts for each individual using a NanoDrop spectrophotometer (ThermoFisher). The pooled samples (N = 6) were sent to Roche for targeted enrichment of sequencing libraries using the NimbleGen SeqCap protocol (9) followed by sequencing on the Illumina Hiseq2500 platform (100bp PE), generating a total of 168,344,748 (50 bp) reads. We then used the targeted capture data to improve the annotation of the chemosensory genes, in particular, the beginnings and ends of genes, and to find previously unannotated genes in the Hmel2 genome. We used 'Bowtie' (10) to create a BAM file and verified the alignment visually using the Integrative Genomics Viewer (11) for accuracy.

Using a genome guided assembly approach, we aligned our reads to 252 chemosensory genes with a high coverage (237 X) that allowed for a substantial improvement of the chemosensory gene models (S1 Table in SI Appendix). The combined dataset (NimbleGen SeqCap and RNA-seq data) had more power to identify start and stop codons, missing exons, and exon/intron boundaries. Overall, we improved the gene models for 115 (45 ORs, 41 GRs, 22 OBPs, and 7 CSPs) chemosensory genes (S1 Table in SI Appendix).

The major change that emerged from our analysis was related to the number of genes characterizing specific chemosensory gene families. Compared to previous studies (4, 6–8), we reduced the number of Olfactory Receptors (ORs), Gustatory Receptors (GRs) and Chemosensory Proteins (CSPs), while increasing the gene models for olfactory binding proteins (OBPs) (S1 Table in SI Appendix). We detected the erroneous annotation of 6 chemosensory genes in the earlier *Heliconius* genome version (Hmel1): *HmCSP33*, *HmGR37*, *HmGR41, HmOR73, HmOR48* and *HmOR47*. These 6 genes were identical to *HmCSP34*, *HmGR38*, *HmGR40, HmOR43, HmOR24,* and *HmOR50*. We found no evidence to indicate that these genes represent real duplications, rather, they appear to be the product of erroneous annotation caused by heterozygosity and were discarded from our gene models and

analyses (4, 6). We confirmed, as suggested by Vogt *et al.* (2015), the existence of 8 additional OBPs. Vogt *et al.* (2015) also suggested the existence of a 9th OBP named *HmelOBP41*. Our analyses, however, could not recover a full gene model for *OBP41*, indicating that it represents a partial copy. To this point, we did not identify - in either our NimbleGen SeqCap or RNA-seq datasets - a single sequence corresponding to the *OBP41* gene. While superficially *OBP41* appears to be a real partial gene duplication, the lack of evidence for the existence of an associated functional gene suggests that it is either the result of errors during genome assembly or a pseudogene. For this reason, we chose to remove *OBP41* from downstream analyses, bringing the total number of OBPs from 51 to 50. Our analyses detected the existence of an additional 29 copies of 23 genes, which we believe likely represent genome assembly errors. These include 9 CSPs, 1 OBP, 4 IRs, and 9 GRs (S1 Table in SI Appendix). Additionally, our data indicate that three previously annotated OR genes (*HmOR56*, *HmOR58,* and *HmOR59*) (6) are actually splice variants of a single larger gene. The three splice variants share four smaller exons totaling 411 bp in length and contain one larger exon, from 790-808 bp, that differs between the three genes. These splice variants were treated as individual genes in downstream analyses.

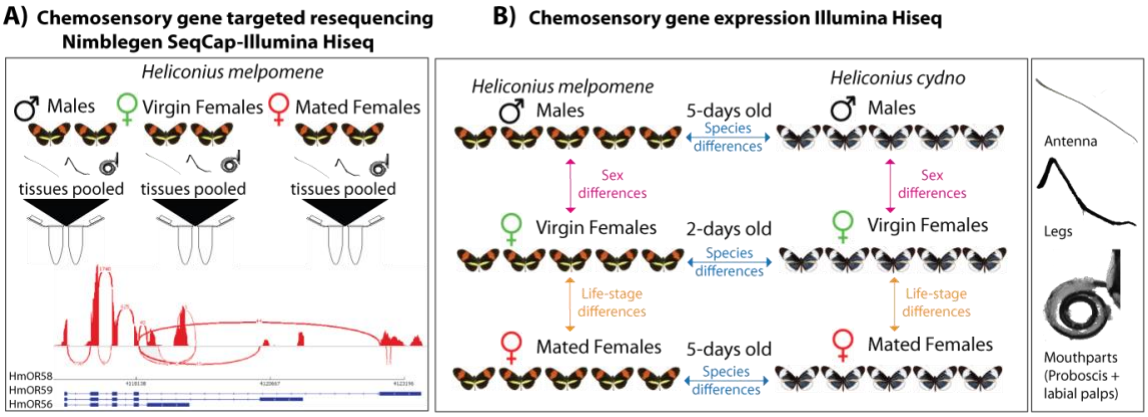
Raw data processing and differential expression analyses

The Illumina RNA-seq data was aligned to the Hmel2 genome using 'Tophat' (*q*-value threshold = 0.05; for per-gene *q*-values see the 'q-values.xlsx' data set) and differential expression analyses were performed with 'Cufflinks' (12). Differential expression analyses were conducted by tissue and biological group as follows. For the tissue-specific expression analyses, we combined data for all 30 butterflies and compared across tissue types. For species-, sex-, and life-stage -specific expression analyses, the data were analyzed for each tissue type independently (antennae, legs, or mouthparts). Species-specific differences were assessed by comparing males, unmated females or mated females of *H. melpomene* to their biological equivalents in *H. cydno*. Here, differences in chemosensory gene expression between closely related species were hypothesized to reflect differences in mate or host-plant choice. Sex-specific differences were assessed by comparing males and unmated females. This comparison was established to identify genes potentially central to both female- and male-choice. Life-stage-specific differences were assessed by comparing unmated and mated females. Here, differences between unmated and mated females were hypothesized to reflect a shift in sensory focus from mate searching (unmated females) to host-plant detection for oviposition (mated female). Expression plots based on FPKM (Fragments Per Kilobase of transcript per Million mapped reads) values were created using the 'heatmap.2' function of the 'gplots' package in R (13).

For *H. melpomene,* we sequenced a total 527,608,789 (50 bp) reads of which 387,543,981 (73.45%) aligned to the Hmel2 genome (4, 5). For *H. cydno* we sequenced a total of 455,172,761 reads of which 358,702,600 (78.81%) aligned to the Hmel2 genome. Despite being a different, albeit closely related, species the *H. cydno* genes mapped better to the Hmel2 genome, alleviating concerns about the use of a *H. melpomene* reference to align and analyze the *H. cydno* data. 7,804,978 (1.05%) of the RNA-seq reads aligned to the 252 chemosensory genes.

Admixture and Linkage Disequilibrium (LD) analyses

In order to further narrow down genes underlying species-level recognition, we compared results from our species-level differential expression analyses to admixture estimates for the sympatric *H. melpomene – H. cydno* pair from Panama (14). The admixture values (f_d) are based on the ABBA-BABA test (15) which measures an excess of derived allele sharing between the sympatric non-sister taxa compared to an allopatric population of *H. melpomene* form French Guiana. We included *H. numata* as an outgroup (Figure 3A). Negative f_d values indicate low admixture or sharing of derived alleles between the sympatric Panama populations of *H. melpomene* and *H. cydno* whereas positive f_d values indicate high admixture. The f_d values were calculated for 100 kb windows with a step size of 20 kb. For chemosensory genes overlapping windows were averaged. With this approach, we were able to identify chemosensory genes that were both significantly differentially expressed (over-expressed) and presented low admixture between the two species. Chemosensory genes at the intercept of these two estimates are likely to be involved in species-specific processes. Finally, because the color pattern locus *optix* has been shown to be associated with mate preference behavior in *H. melpomene* and *H. cydno* (16), and linkage between chemosensory and color pattern genes could facilitate the forming of smell-based prezygotic barriers (17), we tested for the nonrandom association of chemosensory loci (50 kb around transcription start site) at and around the *optix* gene (1,000 kb region) in 50 kb windows. Pairwise comparisons of SNPs within each 50 kb window were averaged to produce a mean r^2.



S1 Figure: Overview of experimental setups. A) Chemosensory gene targeted resequencing: We sampled a total of 6 *H. melpomene* butterflies representing three biological groups (two unmated females, two mated females, and two males). For each individual, we extracted RNA from the antenna, legs, and mouthparts separately. RNA extractions from the three tissues were pooled into one library for each individual (N = 6 libraries). The libraries were sequenced and the targets were enriched as per the Nimblegene SeqCap-Illumina Hiseq protocol. **B)** Chemosensory gene expression: Each biological group contained 5 replicates for both *H. melpomene* and *H. cydno*. For each individual, we extracted RNA from the antenna, legs, and mouthparts separately. We tested for differential expression of chemosensory genes between species, sexes, and life-stages for each tissue type.

S1 Table: Overview of major annotation improvements. For each chemosensory gene category, from left to right: '# of genes' the number of genes remaining after the initial Hmel2 genome annotation; 'Improved annotation' the number of gene models improved at more than 6 base pairs; 'OBPs in Vogt (2015)' (18) the number of OBP genes first published, which also includes one incorrect annotation (*OBP41*) listed in the parenthesis; 'Redundant in Hmel2' the number of redundant genes (the same gene with a different name) mapped to the same location in the Hmel2 genome; 'Identical copies in Hmel2' the number of genes with partial or complete copies (likely generated *in silico*) in the Hmel2 genome, as well as the copy number for each gene provided in parenthesis; 'Splice variants' the number of splice variants identified and the number of genes in parenthesis.

	# of genes	Improved annotation	OBPs in Vogt (2015)	Redundant in Hmel2	Identical copies in Hmel2 (copy number)	# of splice variants (# of genes)
CSP	33	7	-	1	9(13 copies)	0
OBP	50	22	8(1)	0	1	0
GR	71	41	-	2	9(11 copies)	0
IR	31	0	-	0	4	0
OR	67	45	-	3	0	3(1 gene)
Total	**252**	**115**	**9**	**6**	**23(29)**	**3(1 gene)**

S2 Table: Tissue specific expression of chemosensory genes. For each chemosensory gene category, we provide the number of genes presenting tissue specific expression for the various sensory tissue types: antennae, mouthparts, and legs.

	CSP	GR	IR	OBP	OR	Total
expressed in all tissues	11	66	23	16	130	147
antenna specific	1	2	5	12	26	46
mouthparts specific	3	2				5
leg specific	1			2		3
mixed expression	17	1	3	20	11	52
total	33	71	31	50	67	252

S3 Table: Overview of chemosensory gene (transporters) differential expression patterns. For each tissue type we indicate transporters (OBPs and CSPs) differentially expressed as a function of sex, species, and life-stage. For the species category, we highlight genes (in red and blue) showing consistent differential expression patterns between unmated females, mated females, and males. For the sex and life-stage categories, we highlight genes showing consistent differential expression patterns in both species (*H. cydno* and *H. melpomene*). These highlighted genes correspond with the genes shown in Figure 2 of the manuscript. Bolded and underlined genes are differentially expressed, but don't show consistent expression patterns across sex, life-stage or species. An excel version of this table is available on the Open Science Repository (DOI 10.17605/OSF.IO/2MB38).

ANTENNA

Sex differences

Higher expression	Comparison	Transporter
FEMALE	cydno	HmOBP16, HmOBP17, HmOBP19, HmOBP26, **HmOBP31**, **HmOBP42**, HmOBP52, **HmOBP9**, HmCSP19, **HmCSP22**, **HmCSP29**
	melpomene	**HmOBP31**, HmOBP39, **HmOBP42**, HmOBP5, HmCSP15, **HmCSP22**, HmCSP28, HmCSP30, HmCSP6, HmCSP7
MALE	cydno	HmOBP10, HmOBP15, HmOBP38, HmOBP40, **HmOBP47**, HmOBP50, HmOBP51, HmCSP13, HmCSP16, HmCSP3, HmCSP5, HmCSP8
	melpomene	**HmOBP47**, **HmOBP9**, **HmCSP29**

Species differences

Higher expression	Comparison	Transporter
cydno	MALE	HmCSP15, HmCSP16, HmCSP2, HmCSP29, HmCSP5, HmCSP6, HmCSP8, **HmCSP9**, **HmOBP19**, **HmOBP29**, HmOBP39, HmOBP40, HmOBP47
melpomene	MALE	HmCSP12, **HmOBP15**, **HmOBP20**, **HmOBP38**, HmOBP9
cydno	MATED FEMALE	HmCSP10, HmCSP13, HmCSP2, HmCSP5, HmCSP8, **HmCSP9**, HmOBP16, **HmOBP19**, **HmOBP29**, HmOBP39, HmOBP40, HmOBP42, HmOBP47
melpomene	MATED FEMALE	HmCSP1, HmCSP12, HmCSP7, HmOBP1, HmOBP14, **HmOBP15**, HmOBP2, **HmOBP20**, **HmOBP38**, HmOBP45, HmOBP51, HmOBP9
cydno	VIRGIN FEMALE	HmCSP19, HmCSP29, HmCSP31, **HmCSP9**, HmOBP16, **HmOBP19**, HmOBP22, HmOBP26, **HmOBP29**, HmOBP42
melpomene	VIRGIN FEMALE	HmCSP13, HmCSP28, HmCSP30, HmCSP7, **HmOBP15**, HmOBP18, **HmOBP20**, **HmOBP38**, HmOBP5, HmOBP51

Lifestage differences

Higher expression	Comparison	Transporter
VIRGIN FEMALE	cydno	HmOBP19, HmOBP26, **HmOBP31**, **HmOBP42**, **HmOBP5**, HmOBP9, HmCSP19, HmCSP25, **HmCSP29**, HmCSP6, **HmCSP7**
VIRGIN FEMALE	melpomene	**HmOBP31**, **HmOBP42**, **HmOBP5**, **HmCSP13**, HmCSP2, HmCSP28, HmCSP30, **HmCSP7**
MATED FEMALE	cydno	HmOBP38, HmOBP40, **HmOBP47**, HmOBP50, **HmCSP13**, HmCSP16, HmCSP8
MATED FEMALE	melpomene	**HmOBP47**, **HmCSP29**

LEGS

Sex differences

Higher expression	Comparison	Transporter
FEMALE	cydno	HmOBP25, **HmOBP31**, **HmOBP5**, **HmOBP52**, HmCSP2, HmCSP25, HmCSP9
FEMALE	melpomene	HmOBP29, **HmOBP31**, HmOBP39, **HmOBP5**, **HmOBP52**, HmCSP10, HmCSP11, HmCSP22, HmCSP30, HmCSP6, HmCSP7, HmCSP8
MALE	cydno	HmOBP45, HmOBP47, **HmOBP50**, HmCSP1, HmCSP14
MALE	melpomene	**HmOBP50**, HmCSP5

Species differences

Higher expression	Comparison	Transporter
cydno	Male	HmOBP31, HmOBP39, HmOBP47, **HmOBP48**, HmCSP22, HmCSP29, HmCSP30, HmCSP31, HmCSP6, HmCSP8
melpomene	Male	HmCSP25, HmCSP3, **HmCSP7**
cydno	Mated female	HmOBP27, HmOBP29, HmOBP47, **HmOBP48**, HmCSP14, HmCSP15, HmCSP22, HmCSP31, HmCSP6
melpomene	Mated female	HmOBP11, HmOBP14, HmOBP16, HmOBP18, HmOBP21, HmOBP30, HmOBP35, HmOBP8, HmOBP9, HmCSP1, HmCSP13, HmCSP23, HmCSP25, **HmCSP7**
cydno	virgin female	HmOBP31, HmOBP48, HmCSP2, HmCSP29, HmCSP9
melpomene	virgin female	HmOBP14, HmOBP30, HmOBP5, HmOBP8, HmCSP13, HmCSP14, HmCSP30, **HmCSP7**

Lifestage differences

Higher expression	Comparison	Transporter
VIRGIN FEMALE	cydno	HmOBP25, **HmOBP31**, **HmOBP5**, **HmCSP2**, HmCSP25, HmCSP9
VIRGIN FEMALE	melpomene	HmOBP29, **HmOBP31**, **HmOBP5**, HmOBP52, HmCSP10, HmCSP11, HmCSP13, **HmCSP2**, HmCSP22, HmCSP7
MATED FEMALE	cydno	**HmOBP11**, HmOBP12, HmOBP41, HmOBP45, HmOBP47, **HmOBP50**, **HmOBP8**, HmCSP14, HmCSP16
MATED FEMALE	melpomene	**HmOBP11**, HmOBP15, HmOBP16, **HmOBP50**, **HmOBP8**, HmOBP9, HmCSP29

MOUTHPARTS

Sex differences

Higher expression	Comparison	Transporter
FEMALE	cydno	**HmOBP31**, **HmOBP39**, **HmOBP5**, **HmOBP52**, HmOBP8, **HmCSP10**, HmCSP13, **HmCSP15**, **HmCSP16**, **HmCSP19**, HmCSP25, HmCSP5, **HmCSP6**, **HmCSP8**
FEMALE	melpomene	**HmOBP31**, **HmOBP39**, **HmOBP5**, **HmOBP52**, **HmCSP10**, **HmCSP15**, **HmCSP16**, **HmCSP19**, HmCSP22, HmCSP28, HmCSP29, **HmCSP6**, **HmCSP8**
MALE	cydno	HmOBP17, **HmOBP18**, **HmOBP50**, HmCSP23, HmCSP29, HmCSP30, HmCSP7
MALE	melpomene	HmOBP15, **HmOBP18**, HmOBP43, **HmOBP50**, HmCSP13, HmCSP2

Species differences

Higher expression	Comparison	Transporter
cydno	Male	**HmOBP16**, HmOBP17, HmOBP31, HmOBP39, HmOBP40, HmOBP53, **HmCSP1**, **HmCSP28**, HmCSP29, HmCSP9
melpomene	Male	HmOBP14, HmOBP43, HmOBP45, HmOBP8, **HmCSP14**, HmCSP2, HmCSP25, **HmCSP7**
cydno	Mated female	HmOBP12, **HmOBP16**, HmOBP17, HmOBP5, HmCSP13, HmCSP19, HmCSP22, **HmCSP28**, HmCSP30, HmCSP8
melpomene	Mated female	HmOBP19, HmOBP45, HmOBP50, HmOBP52, HmOBP8, **HmCSP1**, **HmCSP14**, **HmCSP7**
cydno	virgin female	**HmOBP16**, HmOBP22, HmOBP26, HmOBP31, HmOBP39, HmOBP43, **HmCSP1**, HmCSP13, HmCSP25, HmCSP9
melpomene	virgin female	HmOBP14, HmOBP18, HmOBP50, HmCSP11, **HmCSP14**, **HmCSP28**, HmCSP30, **HmCSP7**

Lifestage differences

Higher expression	Comparison	Transporter
VIRGIN FEMALE	cydno	**HmOBP31**, HmOBP39, HmOBP43, HmOBP52, HmOBP53, HmCSP1, **HmCSP10**, HmCSP25
VIRGIN FEMALE	melpomene	**HmOBP31**, HmOBP5, **HmCSP10**, HmCSP16, HmCSP19, HmCSP22, **HmCSP25**, **HmCSP28**, **HmCSP30**
MATED FEMALE	cydno	**HmOBP12**, HmOBP16, HmOBP17, **HmOBP18**, **HmOBP50**, **HmOBP8**, HmCSP23, **HmCSP28**, **HmCSP30**, **HmCSP7**
MATED FEMALE	melpomene	**HmOBP12**, HmOBP15, **HmOBP18**, HmOBP19, HmOBP45, **HmOBP50**, **HmOBP8**, **HmCSP7**

S4 Table: Overview of chemosensory gene (receptors) differential expression patterns. For each tissue type we indicate receptors (OR, GRs, and IRs) differentially expressed as a function of sex, species, and life-stage. For the species category, we highlight genes (in red and blue) showing consistent differential expression patterns between unmated females, mated females, and males. For the sex and life-stage categories, we highlight genes showing consistent differential expression patterns in both species (*H. cydno* and *H. melpomene*). These highlighted genes correspond with the genes shown in Figure 2 of the manuscript. Note the increase in the number of differentially expressed genes in the species comparison (particularly for antennae) relative to the sex or life-stage comparisons. An excel version of this table is available on the Open Science Repository (DOI 10.17605/OSF.IO/2MB38).

ANTENNA

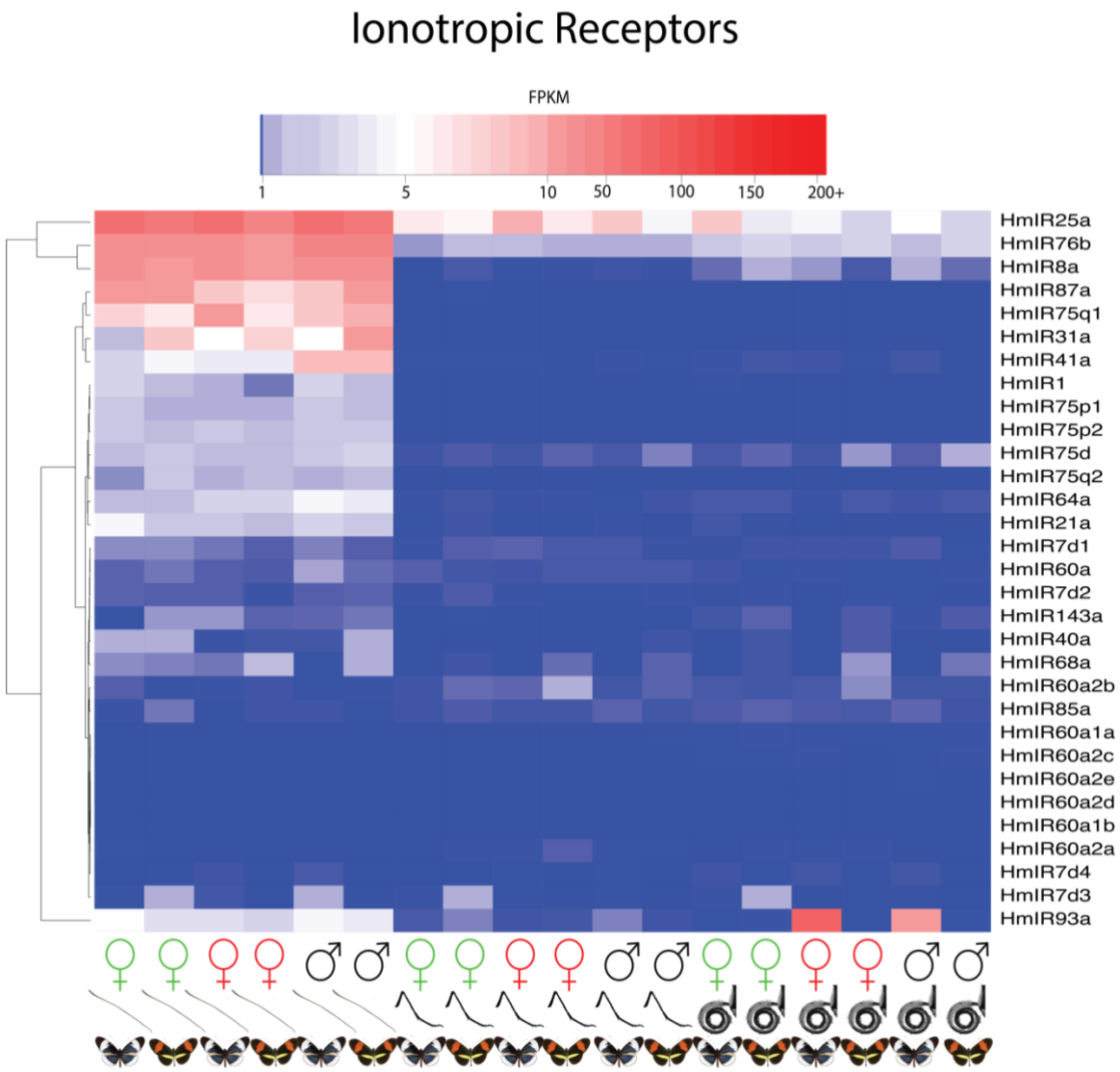
Sex differences			Species differences			Lifestage differences		
Higher expression	**Comparison**	**Receptor**	**Higher expression**	**Comparison**	**Receptor**	**Higher expression**	**Comparison**	**Receptor**
FEMALE	cydno	*HmOR19, HmOR26, HmOR5, HmOR71*	cydno	MALE	*HmOR11, HmOR14,* ***HmOR26,*** *HmOR30, HmOR43, HmOR54, HmOR59*	UNMATED FEMALE	cydno	*HmGR56, HmOR6*
	melpomene	*HmOR53*	melpomene		*HmGR64, HmIR31a, HmOR10, HmOR16, HmOR33, HmOR40,* ***HmOR51, HmOR6,*** *HmOR71*		melpomene	
MALE	cydno	*HmIR41a, HmOR13, HmOR41, HmOR43, HmOR57*	cydno	MATED FEMALE	*HmGR22, HmIR25a, HmIR75q1, HmIR76b, HmIR8a, HmOR12, HmOR14, HmOR19,* ***HmOR26,*** *HmOR3, HmOR30, HmOR32, HmOR58, HmOR69, HmOR9*	MATED FEMALE	cydno	*HmOR12*
	melpomene	*HmOR16*	melpomene		*HmGR1, HmIR68a, HmOR16,* ***HmOR51, HmOR6***		melpomene	*HmOR16*
			cydno	UNMATED FEMALE	*HmOR26, HmOR62*			
			melpomene		*HmIR31a, HmOR13,* ***HmOR51,*** *HmOR57,* ***HmOR6***			

LEGS

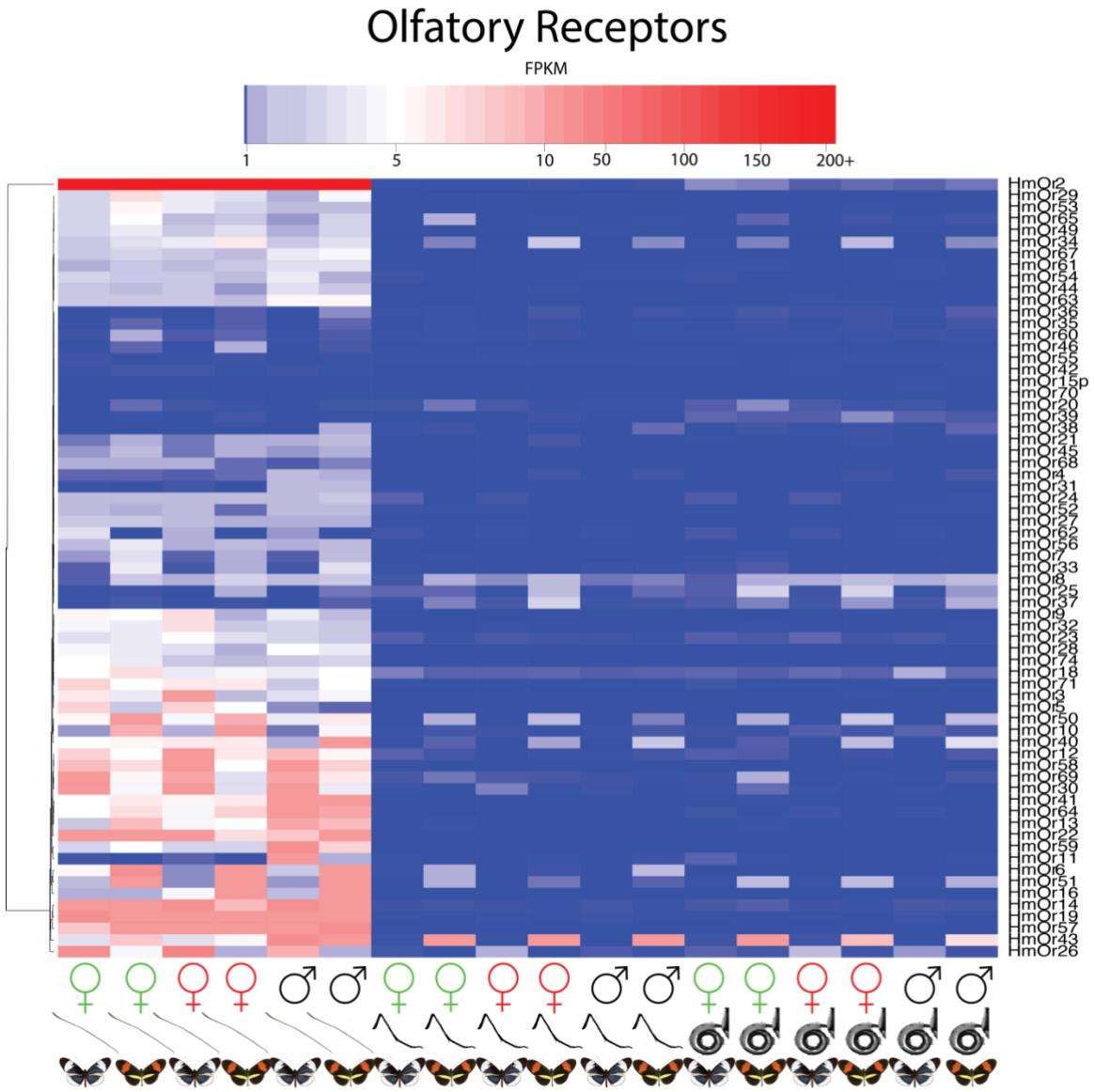
Sex differences			Species differences			Lifestage differences		
Higher expression	**Comparison**	**Receptor**	**Higher expression**	**Comparison**	**Receptor**	**Higher expression**	**Comparison**	**Receptor**
FEMALE	cydno	*HmGR22*	cydno	Male	*HmIR25a*	UNMATED FEMALE	cydno	*HmGR22*
	melpomene		melpomene	Male	*HmGR63*		melpomene	
MALE	cydno		cydno	Mated female	*HmGR56*	MATED FEMALE	cydno	
	melpomene		melpomene	Mated female			melpomene	*HmOR37*
			cydno	Unmated female	*HmGR56*			
			melpomene	Unmated female				

MOUTHPARTS

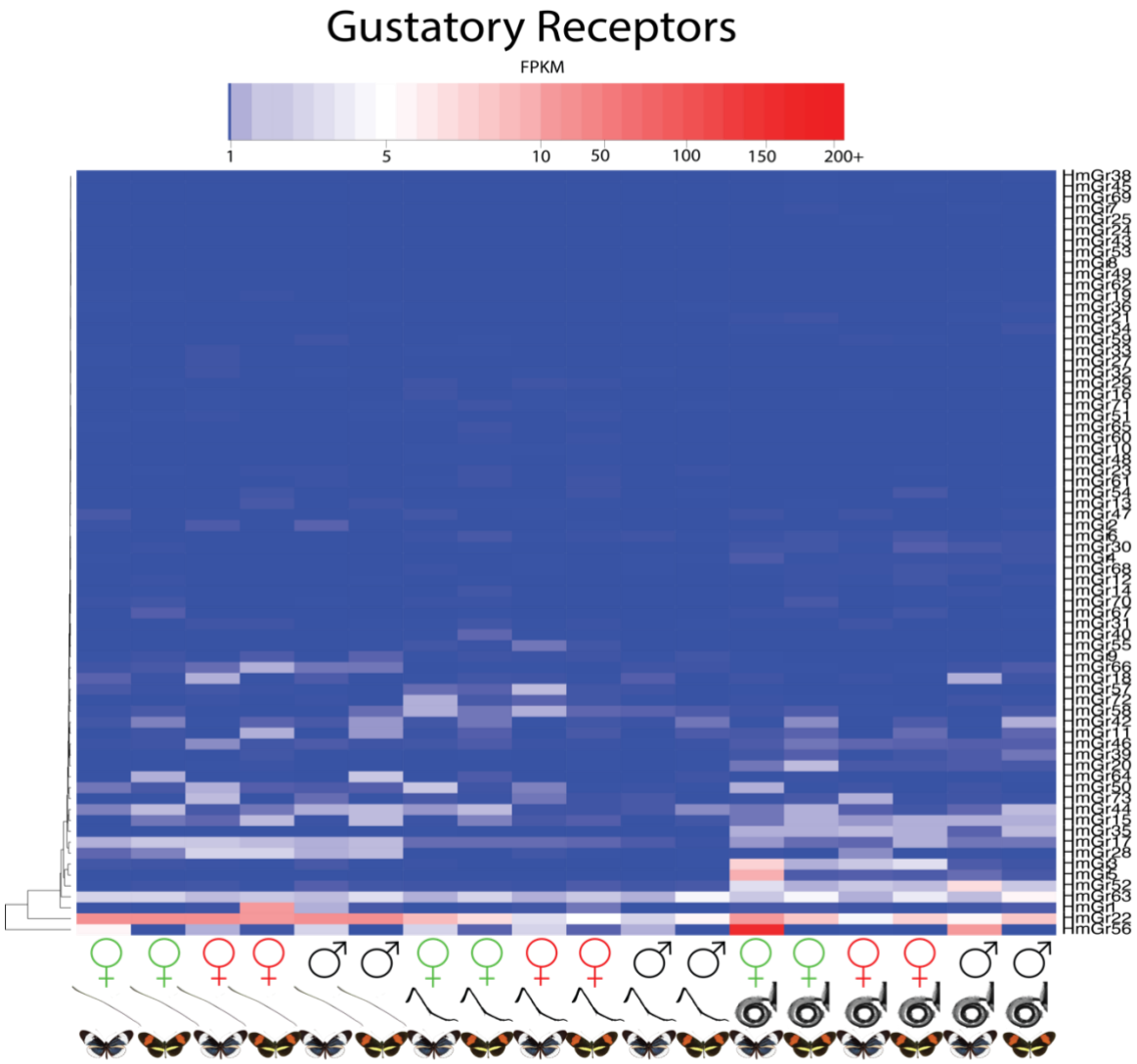
Sex differences			Species differences			Lifestage differences		
Higher expression	**Comparison**	**Receptor**	**Higher expression**	**Comparison**	**Receptor**	**Higher expression**	**Comparison**	**Receptor**
FEMALE	cydno	*HmIR25a, HmGR22, HmGR3, HmGR5, HmGR56,*	cydno	Male	*HmIR25a, HmIR93a, HmGR52, HmGR56*	UNMATED FEMALE	cydno	*HmIR25a, HmGR22, HmGR3, HmGR5*
	melpomene		melpomene	Male	*HmGR63*		melpomene	
MALE	cydno		cydno	Mated female	*HmIR93a*	MATED FEMALE	cydno	
	melpomene	*HmOR40*	melpomene	Mated female	*HmGR63*		melpomene	
			cydno	Unmated female	*HmIR25a, HmGR3, HmGR5, HmGR52*			
			melpomene	Unmated female				



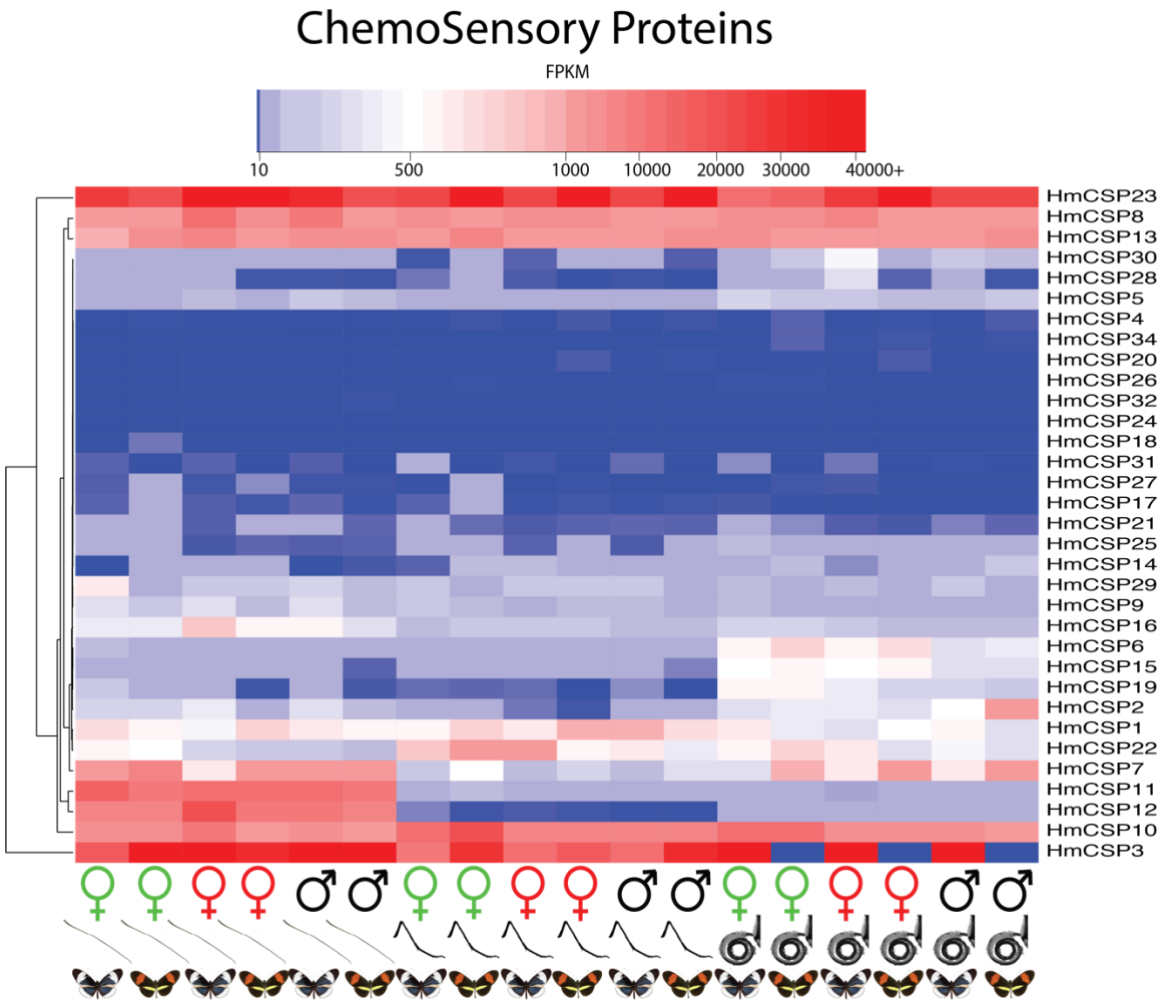
S2 Figure: Expression values (FPKM) for ionotropic receptors. The heatplot illustrates gene expression patterns for ionotropic receptors (IRs). On the y-axis, genes (one per row) are clustered based on expression. On the x-axis, individuals are identified by tissue, species, sex, and life-stage as indicated in the Figure S1 legend. Measures of expression are reported in Fragments Per Kilobase of transcript per Million mapped reads (FPKM); the scale for expression counts is shown under the header of each heatplot. Note how IRs are expressed predominantly in the antenna.



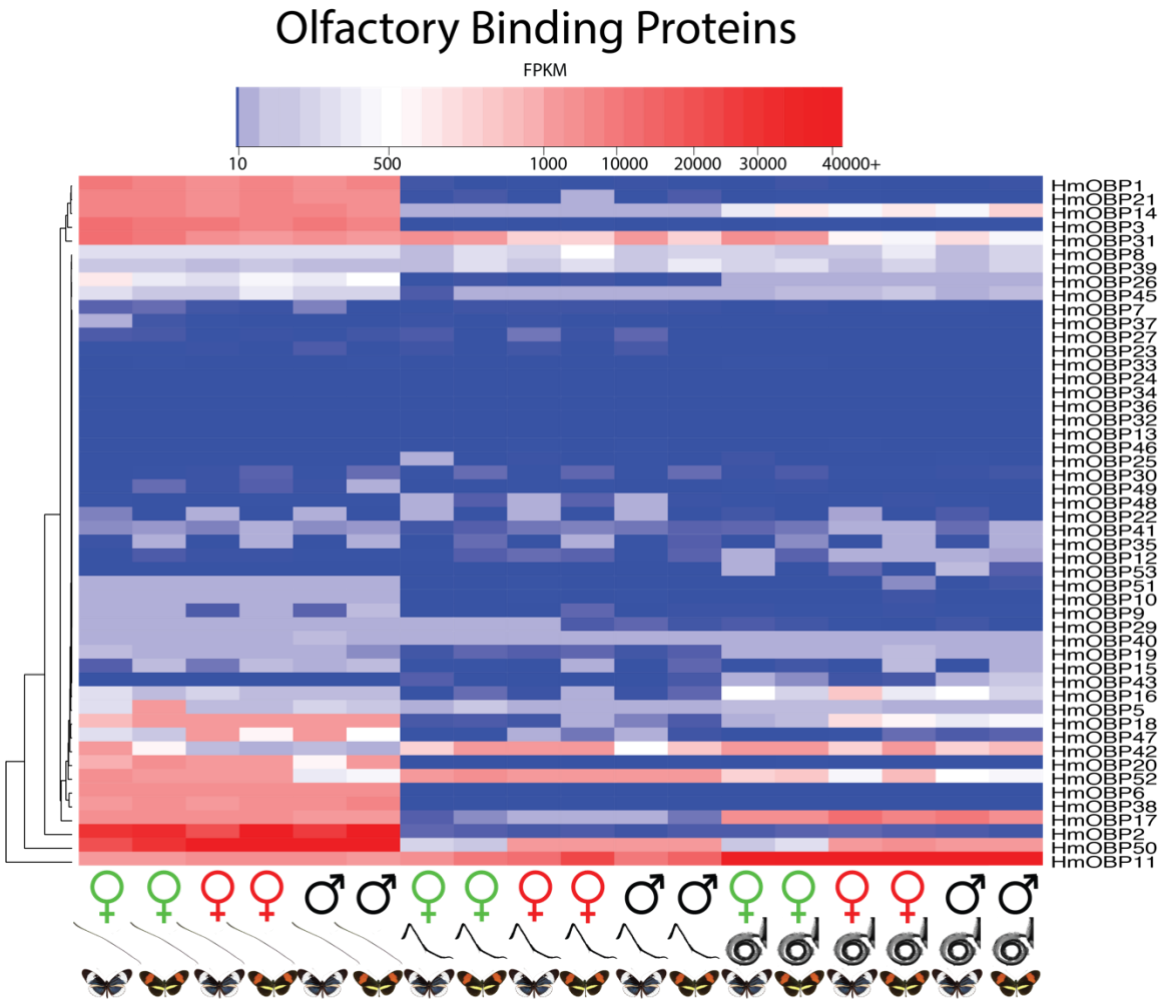
S3 Figure: Expression values (FPKM) for olfactory receptors. The heatplot illustrates gene expression patterns for olfactory receptors (ORs). On the y-axis, genes (one per row) are clustered based on expression. On the x-axis, individuals are identified by tissue, species, sex, and life-stage as indicated in the Figure S1 legend. Measures of expression are reported in Fragments Per Kilobase of transcript per Million mapped reads (FPKM); the scale for expression counts is shown under the header of each heatplot. Note how ORs are expressed predominantly in the antenna.



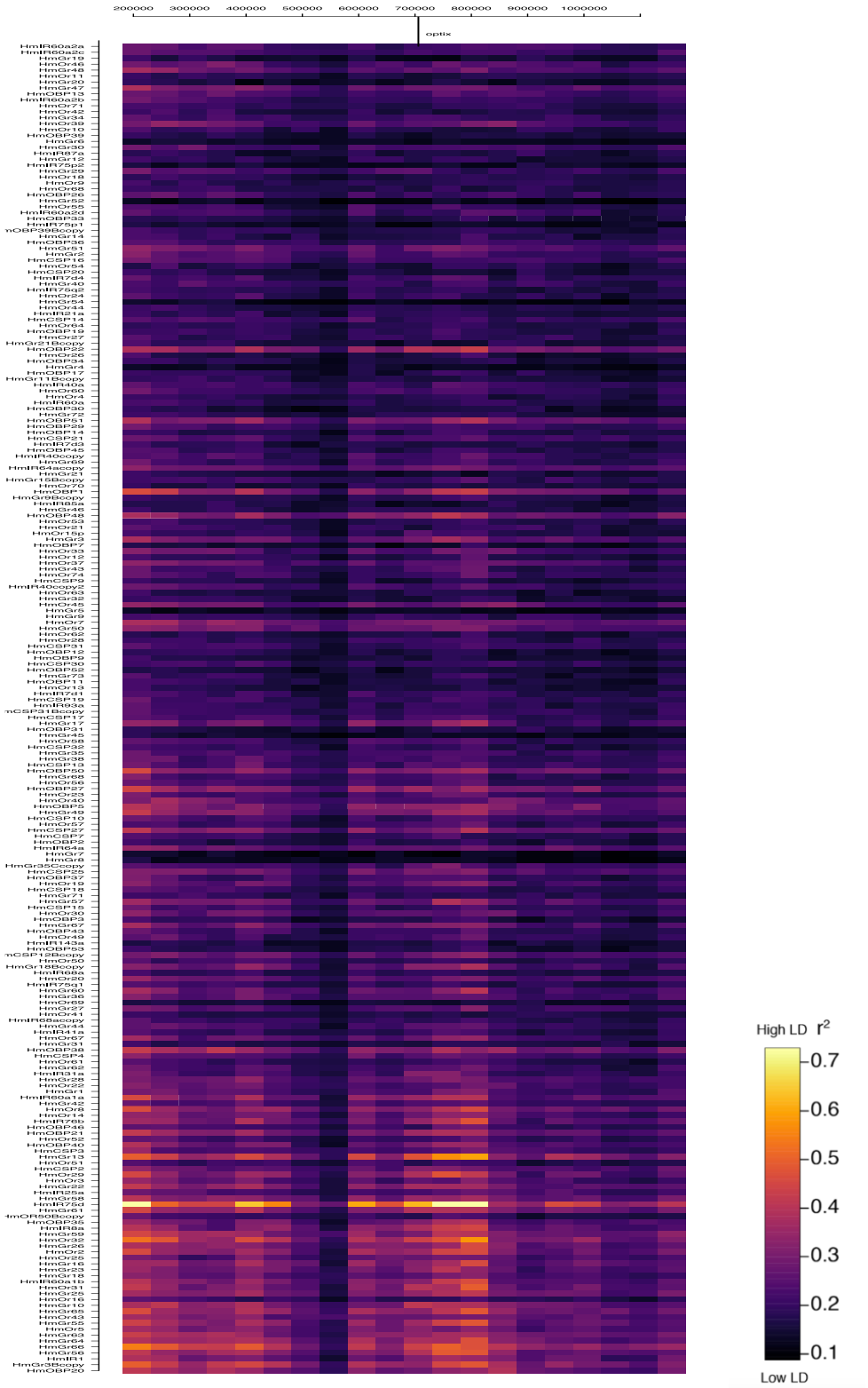
S4 Figure: Expression values (FPKM) for gustatory receptors. The heatplot illustrates gene expression patterns for gustatory receptors (GRs). On the y-axis, genes (one per row) are clustered based on expression. On the x-axis, individuals are identified by tissue, species, sex, and life-stage as indicated in the Figure S1 legend. Measures of expression are reported in Fragments Per Kilobase of transcript per Million mapped reads (FPKM); the scale for expression counts is shown under the header of each heatplot.



S5 Figure: Expression values (FPKM) for chemosensory proteins. The heatplot illustrates gene expression patterns for chemosensory proteins (CSPs). On the y-axis, genes (one per row) are clustered based on expression. On the x-axis, individuals are identified by tissue, species, sex, and life-stage as indicated in the Figure S1 legend. Measures of expression are reported in Fragments Per Kilobase of transcript per Million mapped reads (FPKM); the scale for expression counts is shown under the header of each heatplot. Note that the FPKM scale is different from Figures S6; S7, and S8 - expression counts are higher for transporters relative to receptors. Generally, CSPs show a homogeneous expression pattern throughout tissues, with some individual genes showing comparatively higher expression levels.



S6 Figure: Expression values (FPKM) for olfactory binding proteins. The heatplot illustrates gene expression patterns for olfactory binding proteins (OBPs). On the y-axis, genes (one per row) are clustered based on expression. On the x-axis, individuals are identified by tissue, species, sex, and life-stage as indicated in the Figure S1 legend. Measures of expression are reported in Fragments Per Kilobase of transcript per Million mapped reads (FPKM); the scale for expression counts is shown under the header of each heatplot. Note that the FPKM scale is different from Figures S6; S7, and S8 - expression counts are higher for transporters relative to receptors. Generally, OBPs are characterized by increased expression levels in the antennae, many of these genes are also found to be expressed in the legs and labial palps.



S7 Figure: Linkage disequilibrium (LD) map of chemosensory genes and the color pattern gene *optix*. On the y-axis chemosensory genes are annotated. The x-axis indicates the 1,000kb window around *optix*, the position of which is noted with a line, analyzed in 50kb windows. Please see S5 table for LD values and gene names.

S5 Table: LD analysis statistics (r_2 values) for chemosensory genes and the color pattern gene *optix*. Higher r_2 value cells are colored red and lower r_2 value cells are colored green. Chemosensory gene names are colored by family as per the legend in Figure 3 of the manuscript. Admixture values (f_d) are also provided in the final column. An excel version of this table is available on the Open Science Repository (DOI 10.17605/OSF.IO/2MB38).

	Position										*optix*									
GeneID	205604	255604	305604	355604	405604	455604	505604	555604	605604	655604	705604	755604	805604	855604	905604	955604	1005604	1055604	1105604	1155604	*fd*
HmIR60a2a	0.2766	0.2291	0.2181	0.2063	0.2606	0.2081	0.1935	0.1683	0.2125	0.2104	0.2432	0.2532	0.2806	0.2041	0.1554	0.1930	0.2024	0.1911	0.1733	0.2059	0.7185
HmIR60a2c	0.2287	0.2049	0.2147	0.1991	0.2431	0.2005	0.2099	0.1655	0.2163	0.1857	0.2050	0.2434	0.2277	0.2053	0.1529	0.2127	0.1895	0.1700	0.1632	0.1866	0.6414
HmGr19	0.1273	0.1349	0.1405	0.1515	0.1412	0.1326	0.1059	0.1099	0.1270	0.1341	0.1358	0.1396	0.1260	0.1210	0.1174	0.1185	0.1497	0.1122	0.1138	0.1253	0.5733
HmGr48	0.3272	0.2611	0.2471	0.2252	0.3029	0.2232	0.2042	0.1510	0.2551	0.2180	0.2538	0.2793	0.3072	0.2587	0.1641	0.2086	0.1995	0.1778	0.1765	0.2175	0.5384
HmOr11	0.1384	0.1383	0.1353	0.1390	0.1300	0.1471	0.1257	0.1166	0.1278	0.1214	0.1387	0.1174	0.1494	0.1236	0.1104	0.1159	0.1176	0.1254	0.1143	0.1145	0.5050
HmGr20	0.1466	0.1340	0.1363	0.1565	0.1252	0.1284	0.1293	0.1121	0.1379	0.1141	0.1137	0.1390	0.1396	0.1338	0.1099	0.1267	0.1103	0.1241	0.1222	0.1314	0.5043
HmGr47	0.2800	0.2925	0.2271	0.2109	0.2532	0.2359	0.2127	0.1528	0.2328	0.2318	0.2627	0.2607	0.3262	0.2197	0.1596	0.1890	0.2343	0.1974	0.2005	0.1833	0.4879
HmIR60a2b	0.2395	0.1894	0.2094	0.2160	0.2720	0.2030	0.1797	0.1647	0.2320	0.1773	0.2244	0.2407	0.2633	0.1845	0.1570	0.1856	0.1741	0.1804	0.1510	0.1600	0.4610
HmOr71	0.1613	0.1474	0.1459	0.1386	0.1522	0.1444	0.1493	0.1139	0.1521	0.1402	0.1459	0.1358	0.1452	0.1484	0.1213	0.1447	0.1282	0.1456	0.1248	0.1326	0.4600
HmOr42	0.1339	0.1511	0.1282	0.1375	0.1360	0.1358	0.1465	0.1155	0.1334	0.1202	0.1405	0.1243	0.1508	0.1381	0.1056	0.1169	0.1243	0.1245	0.1147	0.1368	0.4406
HmGr34	0.2142	0.1815	0.1698	0.1681	0.1801	0.1820	0.1297	0.1447	0.1824	0.1829	0.1477	0.1880	0.1920	0.1933	0.1433	0.1488	0.1555	0.1404	0.1467	0.1573	0.4289
HmOr39	0.2737	0.2473	0.2154	0.2369	0.2682	0.2342	0.1762	0.1568	0.2545	0.2270	0.2345	0.2758	0.2654	0.2418	0.1636	0.2038	0.1802	0.1910	0.1796	0.1990	0.4280
HmOr10	0.1187	0.1296	0.1273	0.1156	0.1060	0.1288	0.1071	0.1116	0.1126	0.1031	0.1220	0.1484	0.1116	0.1215	0.1156	0.1021	0.1055	0.1148	0.1082	0.0982	0.4156
HmOBP39	0.1830	0.1490	0.1493	0.1603	0.1488	0.1488	0.1315	0.1398	0.1555	0.1384	0.1458	0.1603	0.1505	0.1391	0.1228	0.1506	0.1287	0.1566	0.1406	0.1490	0.4129
HmGr6	0.1236	0.1290	0.1475	0.1398	0.1423	0.1575	0.1280	0.1383	0.1508	0.1298	0.1323	0.1340	0.1502	0.1449	0.1145	0.1303	0.1221	0.1368	0.1394	0.1351	0.3990
HmGr30	0.1791	0.1718	0.1635	0.2094	0.1714	0.1679	0.1542	0.1301	0.1894	0.1559	0.1948	0.1749	0.1826	0.1632	0.1323	0.1494	0.1610	0.1604	0.1453	0.1464	0.3884
HmIR87a	0.1634	0.1571	0.1440	0.1605	0.1617	0.1266	0.1272	0.1251	0.1570	0.1491	0.1337	0.1588	0.1485	0.1692	0.1202	0.1255	0.1636	0.1437	0.1312	0.1491	0.3837
HmGr12	0.2384	0.2104	0.1902	0.2031	0.1877	0.1888	0.1548	0.1547	0.2088	0.1910	0.1899	0.1839	0.2116	0.2020	0.1670	0.1786	0.1729	0.1709	0.1612	0.1734	0.3835
HmIR75p2	0.1285	0.1135	0.1171	0.1227	0.1258	0.1190	0.1143	0.1145	0.1180	0.1161	0.1195	0.1211	0.1508	0.1165	0.1136	0.1373	0.1066	0.1172	0.1043	0.1247	0.3821
HmGr29	0.1818	0.1852	0.1786	0.1834	0.1799	0.1641	0.1541	0.1487	0.1680	0.1611	0.1778	0.2060	0.1900	0.1760	0.1424	0.1663	0.1583	0.1347	0.1507	0.1558	0.3815
HmOr18	0.1579	0.1552	0.1814	0.1870	0.1304	0.1330	0.1480	0.1323	0.1682	0.1542	0.1405	0.1687	0.1851	0.1459	0.1201	0.1361	0.1352	0.1364	0.1285	0.1197	0.3740
HmOr9	0.1772	0.1403	0.1614	0.1586	0.1557	0.1557	0.1341	0.1297	0.1724	0.1388	0.1342	0.1845	0.1593	0.1681	0.1256	0.1369	0.1404	0.1345	0.1081	0.1285	0.3693
HmOr68	0.1491	0.1246	0.1483	0.1504	0.1362	0.1192	0.1348	0.1187	0.1445	0.1391	0.1436	0.1421	0.1453	0.1486	0.1105	0.1210	0.1256	0.1192	0.1188	0.1159	0.3665
HmOBP26	0.2478	0.2436	0.2091	0.2098	0.2374	0.1818	0.1710	0.1484	0.2406	0.2043	0.2229	0.2558	0.2183	0.1953	0.1659	0.2037	0.1628	0.1798	0.1757	0.1820	0.3657
HmGr52	0.1570	0.1455	0.1619	0.1417	0.1392	0.1455	0.1298	0.1237	0.1402	0.1457	0.1688	0.1439	0.1583	0.1467	0.1080	0.1487	0.1190	0.1095	0.1239	0.1195	0.3647
HmOr55	0.2324	0.2379	0.1940	0.2272	0.2070	0.1984	0.1875	0.1570	0.2217	0.1810	0.2126	0.2303	0.2172	0.1753	0.1533	0.1869	0.1919	0.1686	0.1551	0.1838	0.3629
HmIR60a2d	0.2244	0.1962	0.1844	0.2181	0.1969	0.1907	0.1550	0.1468	0.2432	0.1884	0.2050	0.1953	0.2120	0.1799	0.1567	0.1618	0.1782	0.1779	0.1486	0.1590	0.3615
HmOBP33	0.1916	0.1680	0.1625	0.1629	0.1659	0.1542	0.1385	0.1665	0.1805	0.1455	0.1635	0.1827	0.2125	0.1486	0.1244	0.1532	0.1647	0.1264	0.1325	0.1650	0.3595
HmIR75p1	0.1276	0.1058	0.1317	0.1279	0.1239	0.1228	0.1206	0.1124	0.1230	0.1072	0.1244	0.1481	0.1277	0.1118	0.1205	0.1215	0.1169	0.1195	0.1223	0.1120	0.3568
HmOBP39Bcopy	0.2203	0.1906	0.1713	0.1863	0.1708	0.1752	0.1639	0.1374	0.1784	0.1421	0.1688	0.1995	0.1842	0.1631	0.1384	0.1383	0.1342	0.1565	0.1380	0.1585	0.3559
HmGr14	0.1972	0.2244	0.1838	0.2042	0.2070	0.1965	0.1764	0.1572	0.1922	0.1935	0.1919	0.2104	0.2232	0.2023	0.1405	0.1891	0.1606	0.1871	0.1676	0.1726	0.3548
HmOBP36	0.2446	0.1861	0.1889	0.1840	0.2198	0.1853	0.1758	0.1537	0.2065	0.1824	0.2195	0.2223	0.1939	0.2021	0.1379	0.1499	0.1662	0.1626	0.1365	0.1498	0.3524
HmGr51	0.2863	0.2627	0.2163	0.2202	0.2748	0.2330	0.2033	0.1646	0.2638	0.2320	0.2453	0.2943	0.3111	0.2376	0.1584	0.2109	0.2223	0.2087	0.1718	0.2032	0.3479
HmGr2	0.3534	0.3085	0.2796	0.2538	0.2798	0.2689	0.2423	0.1975	0.2800	0.2908	0.2841	0.3501	0.3652	0.2951	0.2052	0.2575	0.2798	0.2310	0.2060	0.2454	0.3456
HmCSP16	0.2132	0.1797	0.1819	0.1990	0.2157	0.1828	0.1594	0.1341	0.1965	0.1849	0.1661	0.2204	0.2200	0.1845	0.1453	0.1900	0.1789	0.1572	0.1410	0.1488	0.3447
HmOr54	0.1949	0.1438	0.1541	0.1793	0.1550	0.1740	0.1422	0.1190	0.1558	0.1601	0.1769	0.1651	0.1618	0.1518	0.1364	0.1385	0.1626	0.1439	0.1271	0.1592	0.3445
HmCSP20	0.1303	0.1433	0.1339	0.1379	0.1384	0.1458	0.1184	0.1045	0.1274	0.1442	0.1590	0.1477	0.1297	0.1205	0.1121	0.1182	0.1244	0.1228	0.1269	0.1327	0.3425
HmIR7d4	0.2083	0.2217	0.1736	0.2052	0.2155	0.1718	0.1770	0.1552	0.2166	0.1682	0.1919	0.2343	0.2402	0.1875	0.1345	0.1778	0.1629	0.1714	0.1537	0.1825	0.3417
HmGr40	0.2218	0.1719	0.1932	0.2035	0.2140	0.1610	0.1682	0.1551	0.2052	0.1762	0.2074	0.2014	0.1935	0.1959	0.1302	0.1617	0.1606	0.1612	0.1445	0.1651	0.3394
HmIR75q2	0.2128	0.1919	0.1713	0.1851	0.1903	0.1772	0.1724	0.1302	0.1919	0.1795	0.1810	0.2038	0.1965	0.1687	0.1479	0.1744	0.1582	0.1436	0.1584	0.1666	0.3358
HmOr24	0.1914	0.1879	0.1752	0.1696	0.2030	0.1521	0.1625	0.1489	0.1703	0.1526	0.1681	0.1747	0.1975	0.1753	0.1513	0.1561	0.1413	0.1554	0.1339	0.1562	0.3357
HmGr54	0.1043	0.0999	0.1041	0.1093	0.1143	0.1056	0.0996	0.0962	0.0936	0.0912	0.1062	0.1147	0.0985	0.0994	0.1011	0.1034	0.0949	0.0972	0.0946	0.1144	0.3355
HmOr44	0.2107	0.1839	0.1702	0.1839	0.1848	0.1624	0.1692	0.1378	0.1851	0.1575	0.1581	0.2386	0.1977	0.1617	0.1338	0.1387	0.1712	0.1340	0.1320	0.1567	0.3313
HmIR21a	0.2034	0.1307	0.1663	0.1499	0.1675	0.1604	0.1445	0.1184	0.1396	0.1380	0.1622	0.1642	0.1615	0.1643	0.1287	0.1547	0.1414	0.1229	0.1218	0.1363	0.3303
HmOr64	0.2634	0.2001	0.2179	0.2119	0.2114	0.1989	0.1806	0.1551	0.2098	0.1749	0.2192	0.2164	0.2163	0.1789	0.1460	0.1933	0.1913	0.1701	0.1503	0.1979	0.3240
HmOBP19	0.2410	0.1898	0.1861	0.1868	0.2331	0.2166	0.1525	0.1524	0.1877	0.2014	0.2102	0.2379	0.2171	0.2062	0.1321	0.1649	0.1781	0.1720	0.1625	0.1767	0.3164
HmOr27	0.2388	0.2083	0.1818	0.1967	0.2010	0.1819	0.1575	0.1394	0.1839	0.2002	0.2163	0.2009	0.2620	0.2123	0.1239	0.1598	0.1624	0.1673	0.1451	0.1471	0.3116
HmGr21Bcopy	0.1469	0.1344	0.1368	0.1443	0.1353	0.1303	0.1323	0.1265	0.1328	0.1414	0.1362	0.1461	0.1397	0.1333	0.1223	0.1362	0.1247	0.1291	0.1293	0.1243	0.3093
HmOBP22	0.4184	0.3132	0.2860	0.3131	0.3631	0.3056	0.2679	0.2089	0.3334	0.2886	0.3817	0.3450	0.3504	0.2806	0.2331	0.2836	0.2680	0.2399	0.2374	0.2490	0.3056
HmOr26	0.1670	0.1347	0.1423	0.1489	0.1558	0.1738	0.1307	0.1313	0.1822	0.1514	0.1772	0.1882	0.1578	0.1593	0.1190	0.1379	0.1458	0.1498	0.1156	0.1433	0.3035
HmOBP34	0.2267	0.1719	0.1666	0.1761	0.1850	0.1617	0.1439	0.1317	0.1834	0.1512	0.1736	0.1674	0.1927	0.1509	0.1267	0.1587	0.1580	0.1382	0.1352	0.1670	0.2972
HmGr4	0.1310	0.1156	0.1337	0.1475	0.1092	0.1280	0.1270	0.1250	0.1280	0.1175	0.1243	0.1328	0.1077	0.1120	0.1322	0.1128	0.1078	0.1083	0.1018	0.1175	0.2937
HmOBP17	0.1884	0.2005	0.1754	0.1904	0.1958	0.1899	0.1611	0.1500	0.1913	0.1910	0.2173	0.1978	0.2239	0.1986	0.1367	0.1697	0.1571	0.1632	0.1533	0.1535	0.2845
HmGr11Bcopy	0.1788	0.1440	0.1507	0.1639	0.1853	0.1404	0.1613	0.1233	0.1734	0.1628	0.1768	0.1795	0.1858	0.1559	0.1368	0.1511	0.1249	0.1505	0.1368	0.1404	0.2804
HmIR40a	0.2176	0.1867	0.1881	0.1907	0.1781	0.1433	0.1739	0.1489	0.1908	0.1843	0.2145	0.2074	0.1699	0.1686	0.1478	0.1779	0.1917	0.1624	0.1648	0.1857	0.2766
HmOr60	0.2063	0.2040	0.2145	0.2087	0.2479	0.2218	0.1931	0.1448	0.2317	0.2070	0.2106	0.2483	0.2306	0.1935	0.1589	0.1693	0.2010	0.1713	0.1696	0.1843	0.2762
HmOr4	0.2534	0.1988	0.1744	0.1766	0.2056	0.2148	0.1583	0.1491	0.1895	0.1656	0.2450	0.2184	0.2142	0.1851	0.1492	0.1624	0.1700	0.1585	0.1546	0.1744	0.2700
HmIR60a	0.2760	0.2271	0.2082	0.2041	0.2209	0.1925	0.1890	0.1546	0.2313	0.2001	0.2386	0.2558	0.2445	0.1993	0.1573	0.1780	0.1791	0.1687	0.1630	0.1950	0.2699
HmGr72	0.2321	0.2274	0.1547	0.1911	0.1691	0.1757	0.1633	0.1312	0.1828	0.1706	0.1889	0.1910	0.2057	0.1945	0.1440	0.1712	0.1478	0.1495	0.1629	0.1600	0.2671
HmOBP30	0.1916	0.2065	0.1747	0.1628	0.2047	0.1831	0.1531	0.1385	0.1635	0.1626	0.2156	0.1983	0.1761	0.1865	0.1533	0.1505	0.1724	0.1430	0.1515	0.1457	0.2671
HmOBP51	0.3752	0.2910	0.2743	0.2590	0.3291	0.2891	0.2335	0.1958	0.2614	0.2674	0.3109	0.3591	0.3251	0.2935	0.1945	0.2273	0.2607	0.2184	0.2160	0.2229	0.2651
HmOBP29	0.2210	0.1969	0.1985	0.1957	0.2574	0.1803	0.1631	0.1378	0.2430	0.1717	0.2042	0.2404	0.2612	0.2231	0.1449	0.1623	0.1805	0.1720	0.1493	0.1632	0.2631
HmOBP14	0.2413	0.1849	0.1697	0.1970	0.1942	0.1723	0.1681	0.1510	0.2177	0.1712	0.1971	0.2537	0.2052	0.2118	0.1340	0.1543	0.1655	0.1668	0.1374	0.1685	0.2626
HmCSP21	0.2322	0.1732	0.1736	0.1816	0.1978	0.1742	0.1634	0.1380	0.1826	0.1647	0.2065	0.2139	0.2116	0.1684	0.1284	0.1844	0.1686	0.1421	0.1450	0.1585	0.2597
HmIR7d3	0.2061	0.1633	0.1573	0.1722	0.1596	0.1577	0.1593	0.1462	0.1857	0.1513	0.1615	0.1875	0.1537	0.1497	0.1417	0.1485	0.1541	0.1432	0.1630	0.1538	0.2556
HmOBP45	0.2863	0.2413	0.2092	0.2104	0.2498	0.2149	0.1943	0.1491	0.2424	0.2309	0.2304	0.2675	0.2777	0.2156	0.1597	0.1731	0.2148	0.1829	0.1754	0.2158	0.2546
HmGr69	0.2280	0.1957	0.2052	0.2003	0.2124	0.2232	0.1607	0.1563	0.2361	0.1933	0.2211	0.2245	0.2552	0.1816	0.1639	0.2241	0.1832	0.1851	0.1428	0.1702	0.2511
HmGr21	0.1429	0.1413	0.1496	0.1523	0.1697	0.1221	0.1281	0.1206	0.1193	0.1409	0.1213	0.1413	0.1528	0.1458	0.1213	0.1290	0.1305	0.1206	0.1147	0.1215	0.2475
HmGr15Bcopy	0.2249	0.1884	0.1963	0.1936	0.2088	0.2026	0.1952	0.1614	0.2488	0.1849	0.2205	0.2144	0.2227	0.2405	0.1762	0.1615	0.1892	0.1880	0.1684	0.1889	0.2425
HmOr70	0.1659	0.1408	0.1494	0.1298	0.1985	0.1507	0.1398	0.1228	0.1509	0.1207	0.1378	0.1410	0.1579	0.1364	0.1278	0.1383	0.1312	0.1279	0.1154	0.1392	0.2418
HmOBP1	0.4770	0.3815	0.3321	0.3473	0.4059	0.3335	0.2725	0.2107	0.4033	0.3312	0.3861	0.4297	0.4398	0.3344	0.2053	0.2643	0.3166	0.2367	0.2361	0.2614	0.2397
HmGr9Bcopy	0.1836	0.1868	0.1438	0.1670	0.2007	0.1842	0.1451	0.1274	0.1957	0.1691	0.1999	0.2097	0.1930	0.1449	0.1497	0.1520	0.1932	0.1499	0.1552	0.1600	0.2383
HmIR85a	0.1609	0.1749	0.1582	0.1546	0.1715	0.1558	0.1438	0.1465	0.1689	0.1518	0.1658	0.1595	0.1542	0.1382	0.1353	0.1435	0.1448	0.1396	0.1332	0.1372	0.2366
HmGr46	0.2344	0.2237	0.2001	0.1900	0.2081	0.2092	0.1696	0.1543	0.1574	0.1834	0.1840	0.2243	0.2049	0.1645	0.1429	0.1495	0.1585	0.1541	0.1697	0.1673	0.2350
HmOBP48	0.3894	0.2940	0.2649	0.3098	0.3509	0.2605	0.2507	0.1921	0.2976	0.2787	0.3172	0.3756	0.3430	0.3154	0.2175	0.2885	0.2845	0.2559	0.2006	0.2494	0.2287
HmOr53	0.2427	0.2249	0.1961	0.2086	0.2149	0.2063	0.1607	0.1493	0.2415	0.1971	0.1936	0.2434	0.2404	0.2078	0.1564	0.1819	0.1925	0.1665	0.1621	0.1646	0.2256
HmOr21	0.2111	0.1771	0.1704	0.1584	0.1806	0.1540	0.1722	0.1307	0.1939	0.1740	0.1609	0.1731	0.1846	0.1711	0.1355	0.1518	0.1448	0.1515	0.1357	0.1465	0.2233
HmOr15p	0.2257	0.2080	0.1731	0.1846	0.2320	0.1902	0.1793	0.1469	0.2111	0.1840	0.1958	0.2562	0.2341	0.2094	0.1366	0.1531	0.1798	0.1601	0.1618	0.1673	0.2230
HmGr3	0.3620	0.3259	0.2485	0.2526	0.2781	0.2895	0.2083	0.1913	0.2993	0.2633	0.3072	0.3646	0.3218	0.2822	0.2097	0.2328	0.2664	0.2268	0.2123	0.2279	0.2225
HmOBP7	0.1881	0.1563	0.1531	0.1825	0.1657	0.1573	0.1485	0.1419	0.1626	0.1635	0.1515	0.1719	0.1873	0.1565	0.1371	0.1475	0.1553	0.1345	0.1293	0.1781	0.2220
HmOr33	0.2929	0.2100	0.1942	0.2368	0.2198	0.2015	0.1881	0.1538	0.2270	0.2219	0.2703	0.2828	0.2944	0.2352	0.1494	0.1919	0.1961	0.1711	0.1578	0.1875	0.2217
HmOr12	0.2627	0.2465	0.2029	0.2260	0.2269	0.2072	0.2005	0.1484	0.2122	0.1898	0.2216	0.2546	0.2584	0.1978	0.1418	0.1848	0.1618	0.1844	0.1611	0.1712	0.2205
HmOr37	0.2790	0.2546	0.2124	0.2389	0.2084	0.2570	0.1894	0.1441	0.2577	0.2266	0.2653	0.2623	0.3002	0.2485	0.1612	0.2115	0.2161	0.1807	0.1655	0.2145	0.2203
HmGr43	0.2513	0.2155	0.1902	0.2053	0.2285	0.1800	0.2220	0.1466	0.2016	0.1778	0.2341	0.1995	0.2354	0.2184	0.1626	0.1953	0.1964	0.1717	0.1591	0.1960	0.2193
HmOr74	0.2832	0.2010	0.2258	0.2170	0.2626	0.2214	0.1893	0.1530	0.2498	0.2106	0.2408	0.2699	0.2845	0.2222	0.1808	0.2237	0.2012	0.1881	0.1586	0.1944	0.2129
HmCSP9	0.1892	0.1647	0.1852	0.2011	0.2206	0.1729	0.1453	0.1377	0.1719	0.1413	0.2078	0.1729	0.1738	0.1679	0.1297	0.1795	0.1636	0.1523	0.1385	0.1405	0.2120
HmIR40copy2	0.2164	0.1989	0.2141	0.2056	0.1964	0.2181	0.1716	0.1396	0.1698	0.1796	0.2001	0.2228	0.2044	0.1899	0.1420	0.1547	0.2155	0.1738	0.1555	0.1602	0.2073
HmOr63	0.2464	0.2015	0.1745	0.1718	0.1894	0.1753	0.1567	0.1371	0.1903	0.1516	0.2075	0.2211	0.2374	0.1788	0.1492	0.1676	0.1670	0.1601	0.1656	0.1619	0.2048
HmGr32	0.1889	0.2123	0.1900	0.1763	0.2114	0.1901	0.1814	0.1329	0.1827	0.1661	0.1883	0.2503	0.2191	0.2094	0.1503	0.1616	0.1944	0.1603	0.1602	0.1886	0.2006
HmGr5	0.1823	0.1699	0.1552	0.1539	0.1849	0.1558	0.1358	0.1264	0.1609	0.1293	0.1648	0.1722	0.1745	0.1419	0.1222	0.1325	0.1375	0.1242	0.1121	0.1156	0.1979
HmGr9	0.2169	0.2016	0.2086	0.1807	0.1651	0.1954	0.1792	0.1475	0.1994	0.2009	0.2088	0.2164	0.2148	0.1859	0.1467	0.1703	0.1488	0.1633	0.1475	0.1839	0.1977
HmGr50	0.2585	0.2759	0.2288	0.2701	0.3012	0.2388	0.2145	0.1671	0.2419	0.2030	0.2457	0.2441	0.3067	0.2316	0.1515	0.1995	0.2291	0.2045	0.2017	0.2049	0.1969
HmOr62	0.2298	0.1963	0.1846	0.1785	0.2033	0.1957	0.1598	0.1610	0.2021	0.1812	0.1856	0.1845	0.2024	0.1737	0.1452	0.1690	0.1682	0.1617	0.1519	0.1714	0.1955
HmOr28	0.2464	0.2161	0.2017	0.2220	0.2319	0.2464	0.1853	0.1490	0.2182	0.2111	0.2517	0.2158	0.2632	0.2190	0.1353	0.2043	0.2190	0.1774	0.1717	0.1905	0.1948
HmCSP31	0.2478	0.2237	0.2139	0.2204	0.1922	0.2240	0.1869	0.1750	0.2088	0.1899	0.2086	0.2439	0.2407	0.1882	0.1476	0.1846	0.1995	0.1866	0.1588	0.2007	0.1941

HmOBP12	0.1946	0.1580	0.1857	0.1711	0.2001	0.1761	0.1459	0.1334	0.1946	0.1528	0.2014	0.2014	0.1939	0.1716	0.1477	0.1854	0.1617	0.1611	0.1551	0.1688	0.1934
HmOBP9	0.2369	0.1867	0.2059	0.1959	0.1942	0.1663	0.1684	0.1390	0.1827	0.1666	0.1871	0.1948	0.1737	0.1709	0.1431	0.1521	0.1803	0.1493	0.1517	0.1490	0.1911
HmCSP30	0.2347	0.2268	0.2031	0.2015	0.1944	0.1983	0.1851	0.1456	0.2091	0.1815	0.2126	0.2551	0.2247	0.2234	0.1673	0.1948	0.1816	0.1664	0.1566	0.1551	0.1884
HmOBP52	0.2252	0.1830	0.2037	0.1934	0.1871	0.1837	0.1632	0.1379	0.2136	0.1742	0.1949	0.2205	0.2012	0.1699	0.1394	0.1648	0.1780	0.1553	0.1556	0.1672	0.1880
HmGr73	0.2168	0.2297	0.2008	0.1686	0.2124	0.1742	0.1617	0.1424	0.2043	0.1845	0.1997	0.2667	0.2375	0.2038	0.1331	0.1754	0.1744	0.1579	0.1559	0.1917	0.1879
HmOBP11	0.1990	0.1720	0.1810	0.2160	0.2197	0.1723	0.1549	0.1350	0.2028	0.1793	0.2065	0.2265	0.1573	0.1501	0.1529	0.1423	0.1426	0.1330	0.1656	0.1523	0.1872
HmOr13	0.2114	0.1836	0.1771	0.1874	0.1751	0.1575	0.1539	0.1326	0.2024	0.1462	0.2009	0.2030	0.1977	0.1839	0.1300	0.1544	0.1395	0.1461	0.1384	0.1555	0.1870
HmIR7d1	0.2609	0.2253	0.1932	0.2509	0.2410	0.2076	0.1732	0.1640	0.2265	0.1974	0.2179	0.2267	0.2741	0.2183	0.1642	0.1775	0.2104	0.1812	0.1686	0.1820	0.1869
HmCSP19	0.2326	0.1889	0.1943	0.2384	0.2121	0.1831	0.1815	0.1495	0.2218	0.2099	0.2069	0.2304	0.2144	0.1764	0.1477	0.1549	0.1836	0.1634	0.1575	0.1586	0.1865
HmIR93a	0.2888	0.2097	0.1958	0.2298	0.2655	0.1940	0.1871	0.1560	0.2262	0.1941	0.2550	0.2303	0.2734	0.2060	0.1414	0.1883	0.1909	0.1676	0.1538	0.1859	0.1865
HmCSP31Bcopy	0.2472	0.1951	0.2428	0.2301	0.2016	0.1879	0.1981	0.1602	0.2164	0.2004	0.2234	0.2464	0.2417	0.1969	0.1563	0.1894	0.1734	0.1666	0.1703	0.1925	0.1842
HmCSP17	0.2954	0.2374	0.2167	0.2220	0.2508	0.2277	0.1892	0.1645	0.2405	0.2081	0.2588	0.3246	0.3079	0.2255	0.1808	0.2214	0.2307	0.2136	0.1657	0.2042	0.1813
HmGr17	0.3297	0.2938	0.2652	0.2887	0.3136	0.2943	0.2446	0.1719	0.3021	0.2755	0.2871	0.3610	0.3414	0.2935	0.1847	0.2360	0.2584	0.2162	0.1942	0.2115	0.1812
HmOBP31	0.2170	0.2105	0.2021	0.1771	0.1978	0.1665	0.1657	0.1436	0.2043	0.1751	0.2031	0.1659	0.2285	0.1817	0.1148	0.1711	0.1474	0.1527	0.1568	0.1649	0.1806
HmGr45	0.1599	0.1589	0.1537	0.1755	0.1668	0.1620	0.1275	0.1266	0.1563	0.1547	0.1659	0.2039	0.1505	0.1574	0.1217	0.1372	0.1304	0.1248	0.1218	0.1258	0.1787
HmOr58	0.2821	0.2204	0.1762	0.2298	0.2871	0.2232	0.1878	0.1542	0.2591	0.2139	0.2179	0.2707	0.2535	0.2006	0.1663	0.2034	0.1890	0.1906	0.1551	0.1713	0.1782
HmCSP32	0.2658	0.2313	0.2060	0.1960	0.2183	0.1955	0.1752	0.1615	0.2088	0.1911	0.2183	0.2102	0.2384	0.2053	0.1562	0.1762	0.1929	0.1797	0.1725	0.1878	0.1777
HmGr35	0.2718	0.2271	0.1932	0.1824	0.2268	0.2444	0.2009	0.1715	0.2240	0.2264	0.2300	0.2020	0.2236	0.2418	0.1628	0.1710	0.2042	0.1857	0.1630	0.1868	0.1775
HmGr38	0.2198	0.2179	0.1892	0.2187	0.2271	0.1857	0.1812	0.1520	0.2350	0.2049	0.2268	0.2016	0.2293	0.2006	0.1500	0.1971	0.1733	0.1542	0.1599	0.1474	0.1770
HmCSP13	0.2857	0.2672	0.2120	0.2286	0.2612	0.2479	0.1932	0.1681	0.2610	0.2352	0.2673	0.2520	0.2747	0.2035	0.1509	0.2144	0.1741	0.2170	0.1973	0.1826	0.1760
HmOBP50	0.3668	0.3519	0.2524	0.2349	0.3191	0.3000	0.2299	0.1946	0.3441	0.2418	0.3239	0.3182	0.3625	0.2499	0.2107	0.2572	0.2492	0.2424	0.2175	0.2495	0.1759
HmGr68	0.2939	0.2315	0.2363	0.2776	0.2537	0.2094	0.2020	0.1698	0.2268	0.2087	0.2603	0.2485	0.3048	0.2218	0.1353	0.2040	0.2079	0.2036	0.1543	0.2098	0.1732
HmOr56	0.2479	0.2093	0.2170	0.2429	0.2232	0.2148	0.1872	0.1437	0.2432	0.2082	0.2415	0.2575	0.2875	0.2114	0.1535	0.1663	0.1689	0.1568	0.1615	0.1619	0.1732
HmOBP27	0.3702	0.2996	0.2567	0.2957	0.3232	0.2660	0.2608	0.2038	0.3171	0.2849	0.3148	0.3589	0.3680	0.2923	0.1782	0.2506	0.2504	0.2359	0.2083	0.2700	0.1727
HmOr23	0.2541	0.2462	0.2146	0.2334	0.2944	0.2435	0.2045	0.1619	0.2785	0.2296	0.2539	0.3154	0.2671	0.2128	0.1643	0.1960	0.2081	0.1820	0.1814	0.1780	0.1727
HmOr40	0.2709	0.2233	0.2125	0.2042	0.2130	0.1672	0.1718	0.1376	0.1771	0.1921	0.1718	0.2367	0.2007	0.1955	0.1266	0.1670	0.1684	0.1464	0.1440	0.1655	0.1707
HmOBP5	0.3515	0.2879	0.2900	0.2655	0.2712	0.2676	0.2278	0.1660	0.2645	0.2639	0.2951	0.3340	0.2929	0.2694	0.2087	0.2170	0.2283	0.2428	0.1822	0.2274	0.1633
HmCSP10	0.2565	0.2471	0.2106	0.2336	0.2202	0.2188	0.1988	0.1601	0.2241	0.2093	0.2474	0.2769	0.2607	0.2209	0.1553	0.1994	0.1860	0.1764	0.1672	0.2143	0.1606
HmOr57	0.2711	0.2374	0.2105	0.2088	0.2146	0.1995	0.1706	0.1424	0.1979	0.2080	0.2466	0.2319	0.2597	0.1957	0.1547	0.1885	0.1655	0.1656	0.1642	0.1853	0.1577
HmCSP7	0.2328	0.2151	0.1975	0.2162	0.2328	0.2251	0.1975	0.1618	0.2199	0.1873	0.2133	0.2366	0.2332	0.2038	0.1523	0.1693	0.1784	0.1698	0.1744	0.1805	0.1543
HmOBP2	0.2138	0.1769	0.1821	0.1834	0.2049	0.1842	0.1609	0.1430	0.1854	0.1645	0.1836	0.1969	0.2035	0.1765	0.1328	0.1689	0.1801	0.1656	0.1481	0.1460	0.1522
HmIR64a	0.2240	0.2199	0.2257	0.2070	0.2828	0.2383	0.2065	0.1509	0.2156	0.2220	0.2132	0.2587	0.2650	0.2179	0.1600	0.1782	0.2031	0.1830	0.1413	0.1927	0.1504
HmGr7	0.1720	0.1325	0.1566	0.1742	0.1519	0.1322	0.1393	0.1319	0.1404	0.1582	0.1533	0.1424	0.1705	0.1256	0.1289	0.1282	0.1264	0.1340	0.1261	0.1085	0.1440
HmGr8	0.1767	0.1440	0.1542	0.1277	0.1380	0.1409	0.1334	0.1477	0.1474	0.1563	0.1681	0.1695	0.1663	0.1392	0.1168	0.1300	0.1415	0.1435	0.1205	0.1411	0.1405
HmGr35Ccopy	0.2434	0.2084	0.1831	0.1951	0.2240	0.1893	0.1865	0.1685	0.2134	0.1838	0.2314	0.2289	0.2336	0.2217	0.1622	0.1866	0.1920	0.1592	0.1705	0.1789	0.1401
HmCSP25	0.3639	0.3058	0.2698	0.2448	0.2958	0.2781	0.2256	0.1860	0.2934	0.2692	0.3169	0.3269	0.3173	0.2583	0.1909	0.2569	0.2809	0.2221	0.2205	0.2313	0.1398
HmOBP37	0.2343	0.2230	0.2041	0.1924	0.2519	0.1987	0.1842	0.1523	0.1949	0.1800	0.2165	0.2473	0.2301	0.2016	0.1427	0.1741	0.1700	0.1817	0.1753	0.1754	0.1384
HmOr19	0.4043	0.3178	0.2895	0.2871	0.3179	0.2893	0.2479	0.1901	0.3127	0.2643	0.3112	0.3310	0.3569	0.2712	0.1827	0.2434	0.2684	0.1978	0.1926	0.2384	0.1380
HmCSP18	0.2725	0.2335	0.2056	0.2289	0.2069	0.2330	0.1923	0.1539	0.2039	0.1951	0.1935	0.2661	0.2405	0.2280	0.1767	0.1706	0.1920	0.1610	0.1718	0.1834	0.1377
HmGr71	0.1987	0.1935	0.1798	0.1576	0.1859	0.1743	0.1705	0.1384	0.1802	0.1710	0.2269	0.1922	0.1996	0.1862	0.1322	0.1660	0.1671	0.1477	0.1527	0.1332	0.1368
HmGr57	0.4062	0.3510	0.2905	0.2974	0.3408	0.3077	0.2635	0.1675	0.2942	0.2586	0.3712	0.3764	0.3297	0.3066	0.2024	0.2359	0.2720	0.2479	0.2334	0.2212	0.1365
HmCSP15	0.2720	0.2184	0.2006	0.2619	0.2028	0.2334	0.1909	0.1552	0.2019	0.2093	0.1865	0.2193	0.2361	0.2001	0.1460	0.1848	0.2076	0.1749	0.1488	0.1556	0.1353
HmOr30	0.3431	0.2904	0.2690	0.2600	0.2624	0.2388	0.2160	0.1786	0.2810	0.2615	0.2754	0.3223	0.2782	0.2605	0.1616	0.2222	0.2326	0.2159	0.1897	0.2342	0.1353
HmOBP3	0.2482	0.1817	0.1805	0.2281	0.2099	0.1896	0.1591	0.1448	0.2178	0.1842	0.2223	0.2297	0.2301	0.1869	0.1352	0.1873	0.1681	0.1826	0.1488	0.1905	0.1346
HmGr67	0.3561	0.2884	0.2381	0.2450	0.2722	0.2669	0.2156	0.1563	0.2874	0.2319	0.2654	0.3367	0.3329	0.2615	0.1696	0.2058	0.2051	0.2091	0.1883	0.2113	0.1336
HmOBP43	0.3729	0.2822	0.2170	0.2510	0.2845	0.2120	0.1994	0.1908	0.2693	0.2505	0.2743	0.2951	0.3236	0.2688	0.1804	0.2057	0.2358	0.2172	0.2150	0.2202	0.1257
HmOr49	0.2583	0.2250	0.1957	0.2142	0.2321	0.1859	0.1932	0.1420	0.2697	0.1969	0.2231	0.2462	0.2387	0.1727	0.1602	0.1838	0.1919	0.1639	0.1539	0.1731	0.1254
HmIR143a	0.1963	0.1843	0.1709	0.1537	0.1786	0.1655	0.1336	0.1268	0.1729	0.1699	0.1750	0.1684	0.2038	0.1493	0.1241	0.1499	0.1690	0.1440	0.1499	0.1417	0.1251
HmOBP53	0.2037	0.1806	0.1794	0.2015	0.1679	0.2107	0.1656	0.1375	0.2179	0.1794	0.1847	0.2111	0.1958	0.1909	0.1258	0.1496	0.1819	0.1611	0.1525	0.1649	0.1191
HmCSP12Bcopy	0.4037	0.2677	0.2494	0.2703	0.3125	0.2880	0.2267	0.1917	0.3189	0.2689	0.3126	0.3473	0.3336	0.2635	0.2020	0.2210	0.2512	0.2394	0.2239	0.2555	0.1168
HmGr188copy	0.3707	0.3295	0.2198	0.2999	0.3330	0.2392	0.2358	0.1660	0.2972	0.2336	0.3144	0.3211	0.3510	0.2768	0.1917	0.2696	0.2120	0.2226	0.2139	0.2563	0.1155
HmIR68a	0.2024	0.1955	0.1828	0.1927	0.1627	0.1812	0.1434	0.1526	0.2171	0.1796	0.1714	0.2135	0.2358	0.1739	0.1603	0.1745	0.1614	0.1519	0.1354	0.1926	0.1133
HmOr20	0.3804	0.3270	0.2699	0.2656	0.3062	0.2642	0.2599	0.1956	0.2953	0.2611	0.2945	0.3546	0.3392	0.2997	0.1939	0.2205	0.2376	0.2241	0.2383	0.2403	0.1123
HmIR75q1	0.2465	0.2290	0.2085	0.2134	0.2416	0.1920	0.1825	0.1427	0.2201	0.1999	0.2518	0.2222	0.2379	0.2049	0.1593	0.1830	0.1814	0.1574	0.1566	0.1767	0.1118
HmGr60	0.3624	0.2719	0.2376	0.2887	0.3149	0.2698	0.2181	0.1762	0.3197	0.2554	0.2990	0.3431	0.3438	0.2904	0.1967	0.2284	0.2624	0.2211	0.1763	0.2267	0.1091
HmGr36	0.2848	0.2667	0.2470	0.2281	0.2607	0.2320	0.2427	0.1676	0.2567	0.2262	0.2886	0.2945	0.2912	0.2611	0.1796	0.2125	0.2227	0.2101	0.1823	0.2189	0.1044
HmOr69	0.2008	0.1579	0.1496	0.1584	0.1642	0.1454	0.1389	0.1227	0.1531	0.1538	0.1460	0.1759	0.1819	0.1668	0.1227	0.1467	0.1337	0.1313	0.1166	0.1357	0.1007
HmGr27	0.2943	0.2407	0.2017	0.2361	0.2594	0.2212	0.2141	0.1658	0.2265	0.2167	0.2553	0.2810	0.2656	0.2117	0.1738	0.1785	0.2169	0.1810	0.1723	0.2060	0.0940
HmOr41	0.2041	0.1934	0.1688	0.1900	0.1841	0.1759	0.1763	0.1518	0.1978	0.1652	0.2200	0.1929	0.2103	0.1762	0.1479	0.1624	0.1584	0.1396	0.1472	0.1547	0.0915
HmIR68acopy	0.2556	0.2088	0.1866	0.2113	0.2038	0.1865	0.1708	0.1656	0.2233	0.1862	0.2201	0.2372	0.2229	0.2015	0.1411	0.1528	0.1983	0.1637	0.1751	0.2025	0.0903
HmGr44	0.2456	0.2509	0.1960	0.2257	0.2621	0.2301	0.1825	0.1656	0.2351	0.2141	0.2446	0.2887	0.2647	0.2260	0.1429	0.1935	0.2085	0.1761	0.1718	0.1949	0.0902
HmIR41a	0.2825	0.2240	0.1922	0.2109	0.2128	0.2008	0.1874	0.1455	0.2126	0.1854	0.2274	0.2467	0.2697	0.1863	0.1518	0.1913	0.1983	0.1836	0.1775	0.1696	0.0893
HmOr67	0.2900	0.2813	0.2797	0.2739	0.3098	0.2717	0.2480	0.1642	0.3282	0.2237	0.2628	0.3452	0.3608	0.2772	0.1812	0.2271	0.2256	0.1857	0.1955	0.2410	0.0892
HmGr31	0.1958	0.1670	0.1508	0.1676	0.1903	0.1616	0.1592	0.1246	0.2046	0.1646	0.1920	0.1971	0.2030	0.1645	0.1307	0.1699	0.1500	0.1534	0.1410	0.1376	0.0816
HmOBP38	0.4109	0.3967	0.3081	0.3628	0.3890	0.2997	0.2529	0.2052	0.3461	0.3211	0.3449	0.4120	0.4117	0.3403	0.2365	0.2598	0.2985	0.2601	0.2436	0.2956	0.0784
HmCSP4	0.3164	0.2555	0.2409	0.2694	0.2894	0.2617	0.2217	0.1902	0.2716	0.2281	0.2685	0.2767	0.2994	0.2401	0.1997	0.2396	0.2339	0.2189	0.2015	0.2146	0.0782
HmOr61	0.2409	0.2177	0.2202	0.2147	0.2821	0.2434	0.1930	0.1393	0.2488	0.2081	0.2107	0.2320	0.2725	0.2352	0.1420	0.1862	0.2082	0.1693	0.1626	0.1840	0.0778
HmGr62	0.2940	0.2196	0.2133	0.2766	0.2672	0.2082	0.2262	0.1646	0.2926	0.2211	0.2501	0.2973	0.2948	0.2393	0.1896	0.1899	0.2300	0.2037	0.1777	0.1879	0.0769
HmIR31a	0.3222	0.2678	0.2409	0.2862	0.2717	0.2549	0.2264	0.1763	0.3028	0.2356	0.2844	0.2896	0.2990	0.2169	0.1781	0.2318	0.2178	0.1961	0.2064	0.2371	0.0756
HmGr28	0.3662	0.3098	0.2514	0.2395	0.2993	0.2360	0.2251	0.1826	0.2563	0.2310	0.2961	0.3075	0.3086	0.2419	0.1759	0.2291	0.2469	0.2105	0.1948	0.2183	0.0617
HmOr22	0.4363	0.3397	0.3104	0.3137	0.3977	0.3110	0.2718	0.2068	0.3716	0.3173	0.4054	0.3894	0.4202	0.3005	0.2243	0.2979	0.3021	0.2630	0.2044	0.2643	0.0579
HmGr1	0.3502	0.2645	0.2477	0.2651	0.3340	0.2587	0.2291	0.1631	0.2622	0.2038	0.2852	0.3464	0.3278	0.2464	0.1934	0.2396	0.2422	0.1855	0.1950	0.2514	0.0570
HmIR60a1a	0.4482	0.3543	0.3121	0.3380	0.3707	0.2845	0.2693	0.1910	0.3898	0.3070	0.3758	0.4568	0.4084	0.3283	0.2233	0.2496	0.2839	0.2355	0.2175	0.2665	0.0554
HmGr42	0.2750	0.2420	0.2243	0.2533	0.2384	0.1997	0.1934	0.1713	0.2361	0.2159	0.2135	0.2696	0.3201	0.2292	0.1597	0.1855	0.2204	0.1677	0.1804	0.2216	0.0502
HmOr8	0.4474	0.3510	0.3399	0.3545	0.4291	0.3235	0.2665	0.2242	0.4053	0.3162	0.4105	0.4234	0.4602	0.3470	0.2199	0.3346	0.3156	0.2913	0.2583	0.2871	0.0493
HmOr14	0.3562	0.3086	0.2798	0.3128	0.2952	0.2774	0.2537	0.1782	0.3228	0.3164	0.3324	0.3258	0.3637	0.3087	0.1961	0.2305	0.2568	0.2138	0.1994	0.2341	0.0489
HmIR76b	0.4658	0.3612	0.3252	0.3208	0.3564	0.2811	0.2561	0.2071	0.3702	0.3314	0.3591	0.4122	0.4287	0.3124	0.2006	0.2657	0.2870	0.2251	0.2103	0.2876	0.0465
HmOBP46	0.3748	0.2858	0.2714	0.2843	0.2872	0.2723	0.2156	0.1785	0.2768	0.2428	0.2986	0.3704	0.3832	0.2703	0.1924	0.2296	0.2032	0.2088	0.1899	0.2609	0.0464
HmOBP21	0.3942	0.3522	0.3080	0.3041	0.3466	0.2851	0.2514	0.1789	0.3453	0.2670	0.3445	0.3649	0.3330	0.2891	0.2167	0.2586	0.2817	0.2496	0.1978	0.2386	0.0461
HmOr52	0.3544	0.2759	0.2163	0.2654	0.2764	0.2636	0.2159	0.1707	0.2533	0.2683	0.2956	0.3170	0.2966	0.2764	0.1915	0.2282	0.2399	0.2007	0.1761	0.2328	0.0460
HmOBP40	0.3776	0.3670	0.2872	0.2992	0.3284	0.2866	0.2599	0.1652	0.3325	0.2529	0.3523	0.3387	0.3624	0.3110	0.1849	0.2425	0.2657	0.2435	0.1913	0.2539	0.0423
HmCSP3	0.3276	0.2649	0.2255	0.2557	0.2974	0.2383	0.2006	0.1826	0.2776	0.2287	0.2521	0.3148	0.3005	0.2453	0.1894	0.2522	0.2324	0.1900	0.2118	0.2264	0.0410
HmGr13	0.5638	0.4970	0.3600	0.3771	0.4632	0.4159	0.3538	0.2148	0.4131	0.3399	0.4163	0.5192	0.4781	0.3880	0.2402	0.3354	0.3275	0.3080	0.2494	0.3287	0.0409
HmOr51	0.2608	0.2015	0.2135	0.2441	0.2274	0.2099	0.1882	0.1593	0.2405	0.1792	0.2296	0.2247	0.2751	0.2129	0.1600	0.1795	0.1990	0.1594	0.1742	0.1824	0.0355
HmCSP2	0.3883	0.2989	0.2778	0.2511	0.3350	0.2949	0.2558	0.1861	0.2929	0.2715	0.3221	0.3398	0.3422	0.2985	0.1951	0.2454	0.2656	0.2389	0.2206	0.2479	0.0347
HmOr29	0.5108	0.4419	0.3046	0.3887	0.4610	0.3505	0.3012	0.1882	0.4046	0.3632	0.3677	0.4361	0.4730	0.3692	0.2146	0.3153	0.3027	0.2620	0.2426	0.2720	0.0308
HmOr3	0.3400	0.2443	0.2409	0.2539	0.2620	0.2880	0.2181	0.1762	0.2807	0.2321	0.2637	0.3350	0.3225	0.2671	0.1751	0.2171	0.2104	0.1943	0.1898	0.2168	0.0279
HmGr22	0.4860	0.3805	0.3296	0.3397	0.4262	0.3251	0.2743	0.1724	0.3524	0.2753	0.3903	0.4028	0.4605	0.3190	0.2199	0.2931	0.2927	0.2304	0.2574	0.2897	0.0241
HmIR25a	0.2880	0.2274	0.2507	0.2243	0.2337	0.2144	0.1798	0.1729	0.2519	0.2152	0.2303	0.2675	0.2735	0.1977	0.1719	0.2058	0.1939	0.1682	0.1730	0.1708	0.0201
HmGr58	0.4673	0.3379	0.2830	0.3555	0.3844	0.3545	0.2489	0.1961	0.3281	0.3194	0.3525	0.3670	0.4055	0.3235	0.2188	0.2877	0.2701	0.2615	0.2151	0.2549	0.0166
HmIR75d	0.7255	0.5429	0.4120	0.4817	0.5881	0.4446	0.3495	0.2380	0.5187	0.4254	0.5814	0.6413	0.6429	0.5027	0.3130	0.4165	0.4480	0.3553	0.3770	0.3941	0.0136
HmGr61	0.4412	0.3360	0.2754	0.3771	0.3396	0.3058	0.2724	0.2192	0.3952	0.3191	0.3830	0.4340	0.4328	0.3078	0.2392	0.2985	0.3055	0.2699	0.2594	0.2832	0.0136
HmORS0Bcopy	0.2817	0.2381	0.2265	0.2541	0.2759	0.2071	0.1948	0.1688	0.2338	0.2150	0.2400	0.2629	0.2897	0.2269	0.1722	0.2146	0.2037	0.1831	0.1833	0.1925	0.0086
HmOBP35	0.4372	0.3466	0.3069	0.2935	0.3764	0.3011	0.2726	0.1996	0.3590	0.2959	0.3559	0.4146	0.3748	0.3407	0.2199	0.2579	0.3074	0.2597	0.2395	0.2494	0.0085
HmIR8a	0.3867	0.3478	0.3247	0.3240	0.3758	0.2574	0.2823	0.1986	0.3475	0.2818	0.3551	0.4081	0.3943	0.3244	0.2063	0.2690	0.2603	0.2516	0.2254	0.2752	0.0073
HmGr59	0.4054	0.3618	0.3137	0.3454	0.4043	0.3205	0.2802	0.1807	0.3266	0.3042	0.3967	0.4154	0.4423	0.3514	0.2323	0.2769	0.2946	0.2910	0.2189	0.2645	0.0052
HmOr32	0.5388	0.4443	0.3618	0.3930	0.3961	0.3350	0.2898	0.2273	0.4308	0.3782	0.4521	0.4931	0.4648	0.4177	0.2306	0.3114	0.3398	0.3069	0.2517	0.3199	-0.0071

HmGr26	0.4483	0.3811	0.2790	0.3423	0.4208	0.3212	0.2944	0.1953	0.3746	0.3091	0.3302	0.3984	0.4237	0.3749	0.2429	0.3035	0.3028	0.2328	0.2117	0.2702	-0.0139
HmOr2	0.5322	0.4242	0.3273	0.3323	0.4141	0.3427	0.2762	0.2091	0.4188	0.3145	0.3966	0.4692	0.5332	0.3280	0.2249	0.3185	0.3076	0.2535	0.2319	0.2917	-0.0139
HmOr25	0.3922	0.3346	0.2903	0.3167	0.3483	0.3075	0.2482	0.2162	0.3218	0.2985	0.3577	0.4224	0.4011	0.3126	0.2132	0.2694	0.2714	0.2562	0.2013	0.2745	-0.0151
HmGr16	0.4706	0.3971	0.3211	0.3478	0.3767	0.3322	0.3022	0.1904	0.3558	0.3057	0.4133	0.4380	0.4448	0.3209	0.1895	0.2911	0.2912	0.2586	0.2263	0.2725	-0.0164
HmGr23	0.4068	0.3529	0.2639	0.2814	0.3456	0.2777	0.2488	0.1781	0.3473	0.2730	0.3119	0.3961	0.3659	0.3050	0.1888	0.2484	0.2713	0.2386	0.2271	0.2345	-0.0167
HmGr18	0.3924	0.3202	0.2689	0.2927	0.3310	0.2548	0.2300	0.1875	0.2940	0.2872	0.3497	0.3733	0.3934	0.2869	0.1888	0.2362	0.2520	0.2649	0.1983	0.2500	-0.0173
HmIR60a1b	0.4574	0.3602	0.3019	0.3125	0.3727	0.3131	0.2776	0.1643	0.3891	0.2686	0.3386	0.3986	0.4650	0.3028	0.2054	0.2697	0.2684	0.2564	0.2587	0.2619	-0.0174
HmOr31	0.3856	0.3528	0.2832	0.3720	0.3678	0.2828	0.2840	0.1971	0.3265	0.2789	0.3782	0.4329	0.3949	0.3375	0.1896	0.2487	0.3004	0.2835	0.2244	0.2894	-0.0193
HmGr25	0.4555	0.3911	0.3062	0.3477	0.3799	0.3578	0.2739	0.1979	0.3704	0.3019	0.3633	0.3958	0.4468	0.3394	0.2187	0.2787	0.3157	0.2969	0.2377	0.2690	-0.0206
HmOr16	0.2297	0.1999	0.1897	0.2014	0.2148	0.2052	0.1737	0.1557	0.2195	0.1729	0.2226	0.2628	0.2324	0.1832	0.1395	0.1835	0.1907	0.1643	0.1519	0.1873	-0.0244
HmGr10	0.4796	0.3950	0.2905	0.3021	0.3817	0.2903	0.2543	0.1854	0.3529	0.2904	0.3791	0.4275	0.4271	0.3207	0.2143	0.2475	0.2894	0.2592	0.2465	0.2862	-0.0357
HmGr65	0.4482	0.3875	0.3072	0.3448	0.4168	0.3622	0.2758	0.1941	0.3587	0.3038	0.3552	0.4549	0.4241	0.2947	0.2296	0.3093	0.2992	0.2689	0.2275	0.2917	-0.0362
HmOr43	0.3742	0.2905	0.2671	0.3021	0.2921	0.2852	0.2670	0.1863	0.3024	0.2826	0.3194	0.3482	0.3623	0.2957	0.1992	0.2740	0.2836	0.2417	0.1956	0.2285	-0.0363
HmGr63	0.4610	0.3775	0.3135	0.2990	0.4064	0.3061	0.2585	0.1831	0.3502	0.2803	0.3320	0.4024	0.4138	0.2999	0.1999	0.2707	0.2901	0.2423	0.2375	0.2713	-0.0808
HmGr64	0.4556	0.3783	0.3130	0.3445	0.3886	0.3162	0.2773	0.1938	0.3358	0.3094	0.3764	0.4026	0.4035	0.3301	0.2000	0.2689	0.3332	0.2803	0.2308	0.2903	-0.0864
HmGr66	0.5122	0.4049	0.3301	0.3925	0.4505	0.3558	0.3398	0.2163	0.4489	0.3589	0.4634	0.5151	0.5209	0.3667	0.2570	0.3747	0.3543	0.2940	0.2940	0.3391	-0.1051
HmGr56	0.4568	0.3926	0.3430	0.3408	0.4309	0.3561	0.2743	0.2138	0.3381	0.2879	0.3192	0.4132	0.4450	0.3554	0.2147	0.2816	0.2901	0.2706	0.2581	0.2536	-0.1093
HmIR1	0.4407	0.3608	0.2792	0.3434	0.4362	0.3355	0.2872	0.1604	0.3847	0.2958	0.4604	0.5064	0.4715	0.3330	0.2177	0.2803	0.3083	0.2833	0.2147	0.2813	-0.1167
HmOBP20	0.3401	0.2767	0.2706	0.2523	0.2970	0.2531	0.2219	0.2028	0.3048	0.2634	0.2817	0.2887	0.3425	0.2585	0.1710	0.2175	0.2374	0.2106	0.1932	0.2552	-0.3562

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