Functional characterization of olfactory receptors in three Dacini fruit flies (Diptera: Tephritidae) that respond to 1-nonanol analogs as components in the rectal glands

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ABSTRACT

Dacini fruit flies (Tephritidae: Diptera), including destructive pest species, are strongly affected in their reproductive behaviors by semiochemicals. Notably, male lures have been developed for pest management e.g., aromatic compounds for the Oriental fruit fly *Bactrocera dorsalis* and the melon fruit fly *Zeugodacus cucurbitae*; terpenic α-ionone analogs for the solanaceous fruit fly, *B. latifrons*. Other than those specific male attractants, 1-nonanol analogs have been noticed as major aliphatic components in the male rectal gland, which is considered as a secretory organ of male sex pheromones. Although multiple semiochemicals associated with the life cycle of Dacini fruit flies have been identified, their behavioral role(s) and chemosensory mechanisms by which the perception occurs have not been fully elucidated. In this study, we conducted RNA sequencing analysis of the chemosensory organs of *B. latifrons* and *Z. cucurbitae* to identify the genes coding for chemosensory receptors. Because the skeletons of male attractants are different among Dacini fruit fly species, we analyzed phylogenetic relationships of candidate olfactory receptors (ORs) among the three species. We found that the OR phylogeny reflects the taxonomic relationships of the three species. We further characterized functional properties of OR74a in the three Dacini species to the 1-nonanol analogs related to components in the rectal glands. The three OR74a homologs responded to 1-nonanol, but their sensitivities differed from each other. The OR74a homologs identified from *B. dorsalis* and *Z. cucurbitae* responded significantly to 6-oxo-1-nonanol, but not to 1,3-nonanediol and nonyl acetate, indicating similar binding properties of the homologous ORs.

Keywords: Chemosensory receptor; Tephritidae; 1-nonanol analogs; Functional analysis;

49 *Xenopus* oocyte

50

51 **1. Introduction**

52 The tribe Dacini (Tephritidae: Diptera) contains various fruit fly species in which
53 approximately 770 species have been described (Drew and Hancock, 2000). Among them,
54 the genera *Bactrocera* and *Zeugodacus* include many serious pest species that infest
55 cultivated fruits and vegetables in both tropical and subtropical regions. It is noteworthy
56 that some of the species are closely associated with plant-derived semiochemicals in their
57 life cycles (Tan et al., 2014). Males have a glandular complex in the rectum, known as
58 the rectal gland, which is considered to be a secretory organ of male sex pheromones in
59 many dacine tephritid fly species (Fletcher, 1968). Various compounds, including
60 aromatic and aliphatic volatiles, have been identified as components in the rectal glands
61 (Fletcher and Kitching, 1995). For example, males of the Oriental fruit fly, *B. dorsalis*,
62 and the melon fruit fly, *Z. cucurbitae*, are strongly attracted to specific aromatic
63 compounds, methyl eugenol (ME) and raspberry ketone (RK), respectively, and
64 subsequently ingest the attractants to sequester in their rectal glands as sex pheromone
65 precursor or sex pheromone itself (Nishida et al., 1988; Shelly, 2010). On the other hand,
66 males of the solanaceous fruit fly, *B. latifrons*, are attracted to non-aromatic terpenoid α-
67 ionone derivatives and sequester them in their rectal glands (Ishida et al., 2008; Nishida
68 et al., 2009; Enomoto et al., 2010). Other than those characteristic male attractants, a
69 series of 1-nonanol analogs have also been identified as specific rectal gland components
70 in several Dacini fruit flies. For example, 6-oxo-1-nonanol is produced in the male rectal
71 glands in *B. carambolae*, a species closely related to *B. dorsalis*, together with a minor

component, 1,6-nonanediol (Wee and Tan, 2005; Wee et al., 2007). The production of this compound increases concomitant with sexual maturity and triggers a chemotactic behavior known as zigzag flight in conspecific females. In *Z. cucurbitae*, 1,3-nonanediol is produced as one of the major components in the male rectal glands at a similar level to accumulated RK ingested from floral components (Nishida et al., 1993). Although a defensive role of 1,3-nonanediol against a natural enemy has been demonstrated, its pheromonal role is so far unknown (Tan, 2000). While 1-nonanol analogs are components in the male rectal glands, these compounds have also been identified in host fruits and a vegetable (Light and Jang, 1987; Siderhurst and Jang, 2010). Notably, 1-nonanol elicits electroantennogram detection (EAD) responses in *B. dorsalis* (Light and Jang, 1987). Furthermore, 1-nonanol and its analogs not only elicit EAD responses but also attract females of *Z. cucurbitae* (Siderhurst and Jang, 2010). Therefore, roles of 1-nonanol analogs are interesting from the view of pheromonal communication as well as host recognition.

Although the perception of such glandular semiochemicals seems essential in their life cycles, the constituents required for chemo-recognition have not been well characterized. In insects, three types of chemosensory receptors, olfactory receptors (ORs), gustatory receptors (GRs), and ionotropic receptors (IRs), are necessary to detect various odors and taste substances at the peripheral neurons in chemosensory organs (Fleischer et al., 2017). Recently, draft genome sequences of several Dacini fruit flies including *B. dorsalis*, *B. latifrons*, and *Z. cucurbitae* have been deciphered and reference sequences of them are now available at the NCBI web sites (*B. dorsalis*: https://www.ncbi.nlm.nih.gov/genome/10754; *B. latifrons*: https://www.ncbi.nlm.nih.gov/genome/43857; *Z. cucurbitae* :

https://www.ncbi.nlm.nih.gov/genome/11807). The genetic information enables us to identify sequences coding candidate chemosensory receptors. Most recently, several ORs of *B. dorsalis* that respond to semiochemicals have been characterized, i.e., BdorOR13a and BdorOR82a for plant volatiles (Miyazaki et al., 2018) and BdorOR88a for ME (Liu et al., 2018). However, there is no functional information about chemosensory receptors in tephritid fruit flies except for the abovementioned studies, despite the importance of roles of chemoreception in insect physiology as well as pest management.

In the present study, we identified an entire repertoire of insect chemosensory receptors expressed in chemosensory organs of the fruit fly species in two genera, *B. latifrons* and *Z. cucurbitae* by RNA sequencing (RNA-seq) analyses. Because the skeletons of specific male attractants are different from each other, i.e., α-ionone analogs for *B. latifrons* and aromatic compounds for *B. dorsalis* and *Z. cucurbitae*, we compared phylogenetic relationships of ORs among the three species. Furthermore, we focused on OR74a homologs among the identified chemosensory receptors, because OR74a of *Drosophila melanogaster* responds to 1-nonanol (Kreher et al., 2005). We analyzed functional properties of OR74a homologs in the three Dacini species to see if these ORs respond to analogous components of 1-nonanol found in the rectal glands of Dacini species.

2. Materials and methods

2.1. Insects

For preparation of total RNA, we used strains of *B. latifrons* and *Z. cucurbitae* cultured in Okinawa Prefectural Agricultural Research Center and Okinawa Prefectural Plant Protection Center in Japan, respectively. The strain of *B. latifrons* originally

collected in Yonaguni Island was kept at 26–27 °C under a photoperiod of 14 h light/10 h dark. The strain of *Z. cucurbitae* originating from Taiwan was kept at 25 °C and 60 to 70% relative humidity under a photoperiod of 14 h light/10 h dark, with a dawn and dusk twilight. The adult flies of both species were provided with water and a diet of four parts sucrose and one part dry yeast AY-65 (Asahi Food & HealthCare, Ltd., Tokyo, Japan).

2.2. RNA sequencing and assembly

Adult flies of *B. latifrons* and *Z. cucurbitae* were staged at 0–1, 1–3, 4–6, and 7–9 days and 0–2, 2–4, and 6–8 days, respectively. Approximately two hundred males and females were equally collected from each adult stage. Total RNAs were extracted from male and female antennae and proboscises using TRIzol reagent (GIBCO-BRL, Gaithersburg, MD, USA), and purified by NucleoSpin RNA (Macherey-Nagel, Germany). Sequence libraries were constructed using the TruSeq RNA sample Preparation Kit v2 (Illumina Inc., San Diego, CA, USA). RNA sequencing was performed on an Illumina MiSeq system using the Miseq Reagent Kit v3 600 cycle (Illumina Inc., San Diego, CA, USA). The reads were preprocessed with Trimmomatic v0.33 (Bolger et al., 2014) for quality trimming using the parameters as described previously (Miyazaki et al., 2018). The resulting data from clean reads were deposited in the DNA Data Bank of Japan (DDBJ) Sequence Read Archive under accession numbers PRJDB7958. The pass-through reads were subjected to *de novo* assembly using the Trinity, Bowtie, eXpress, and DEGseq (PE) programs implemented in the maser pipeline of the Cell Innovation Program at the National Institute of Genetics (https://cell-innovation.nig.ac.jp/maser/index_en.html). Fragments per kilobase of exon per million (FPKM) values were calculated to estimate the expression levels of the transcripts. Summary of sequence data was analyzed using

the Seqkit program (https://bioinf.shenwei.me/seqkit).

2.3. Screening and characterization of sequences of candidate chemosensory receptors

We identified candidate chemosensory receptor genes from Trinity contigs using Pfam domains and amino acid sequences of chemosensory receptors in *D. melanogaster*. We obtained the following Pfam domains of *D. melanogaster* from the Pfam database (https://pfam.xfam.org/): 7tm odorant receptor (PF02949), 7tm chemosensory receptor (PF08395), trehalose receptor (PF06151), and ligand gated ion channel (PF00060). We also obtained the following amino acid sequence data of chemosensory receptors in *D. melanogaster* from the InterPro database (https://www.ebi.ac.uk/interpro/): Olfactory receptor (IPR004117), 7TM chemoreceptor (IPR013604), and ionotropic glutamate receptor (IPR001320). We screened the Trinity contigs by similarity to these amino acid sequences using a BLASTX search at an Expect value (E-value) threshold of $1e^{-5}$. We listed the names of contigs hit by the BLASTX search in a text file and built a FASTA file exemplified in File S1 using the Biostrings package within R software. We obtained open reading frames (ORFs) of the extracted contigs using EMBOSS Transeq (https://www.ebi.ac.uk/Tools/st/emboss_transeq/) and used them as queries in a BLASTP search against the NCBI non-redundant protein database. Contigs that ranked highly with ORs, GRs, or IRs were considered candidate genes coding for insect chemosensory receptors. Overlapping variants with identical ORFs were merged at this step by selecting the longest as the representative transcript of a variant group. We also performed RT-PCR to merge the partial sequences of *BlatOR13a*, *BlatOR74a*, *ZcucOR35a*, and *ZcucOR59a* using a pair of primers (Table S1). We named the candidate chemosensory receptors according to gene names of the top blast hits in most cases. In some exceptions, we named

ORs by their homologs in *D. melanogaster* or *B. dorsalis* to match phylogenetic relationships. For homologous chemosensory receptors with amino acid similarities of less than 80%, the names of the homologs were differentiated with a numerical postscript, e.g., BlatOR7a-1 and BlatOR7a-2. In cases where the amino acid similarities were 80% or more, version numbers were assigned to the receptors, e.g., BlatOR49b-v1 and BlatOR49b-v2. In cases where multiple partial sequences of a candidate chemosensory receptor were identified, each sequence was labeled -part1, -part2, etc., e.g., ZcucOR13a-part1 and ZcucOR13a-part2.

2.4. Sequence analysis

Deduced amino acid sequences of candidate ORs were aligned using the Clustal W 2.1. program (Thompson et al., 1994). Prior to this process, we merged the partial sequences of ORs in which multiple sequences were partially identified. We selected candidate ORs with sequences of more than 200 amino acid for phylogenetic analysis and constructed a phylogenetic tree from the aligned sequences. We applied the maximum likelihood method with the Jones–Taylor–Thornton (JTT) model, with among-site rate heterogeneity according to gamma distribution with invariant sites (G + I) using MEGA5 software (Tamura et al., 2011). Putative transmembrane domains were predicted using the PHDhtm algorithm (https://npsa-prabi.ibcp.fr/cgi-bin/npsa_automat.pl?page=/NPSA/npsa_htm.html) (Rost et al., 1995).

2.5. Expression analyses of the candidate receptors by quantitative RT-PCR (qPCR)

Total RNAs were prepared from male and female antennae of the staged adults within 2 days after eclosion. Reverse transcription was performed using the ReverTra Ace qPCR

RT Master Mix (TOYOBO, Tsuruga, Japan). The generated cDNAs were used as a template for qPCR using the THUNDERBIRD SYBR qPCR Mix (TOYOBO, Tsuruga, Japan) on a Thermal Cycler Dice Real Time System (Takara, Shiga, Japan). We investigated four or five independent biological samples to quantify the levels of transcription. The transcription levels were normalized with *rpS3* or *rpL23* transcription levels in the same samples of *B. latifrons* or Z. *cucurbitae*, respectively. The primers used for qPCR are listed in Table S1.

2.6. Expression of ORs in Xenopus oocytes and two-electrode voltage-clamp recording

Full-length coding sequences of candidate ORs were cloned into pCS2P+ vectors (https://www.addgene.org/17095/) for heterologous expression. Full- or partial-ORFs of *ORCO* and *OR74a* homologs of the three Dacini fruit flies were PCR amplified from cDNA prepared from male antennae using primers designed from predicted ORFs based on the assembled contigs. The PCR products were cloned into pCS2+ using restriction enzymes—BamHI and XbaI—or an In-Fusion HD cloning Kit (Takara, Otsu, Japan). The primers used for construction are listed in Table S1. Complementary RNAs (cRNAs) were synthesized from linearized pCS2 vectors by mMESSAGE mMACHINE (Thermo Fisher Scientific, Waltham, MA, USA). Preparation of *Xenopus laevis* oocytes, microinjection of receptor gene RNA, and recording of whole-cell currents were performed as described previously (Miyazaki et al., 2018). In brief, Stage V to VII *Xenopus* oocytes treated with collagenase in Ca^{2+}-free saline solution were microinjected with a mixture comprising OR and ORCO cRNAs (25 ng each). Using a two-electrode voltage clamp (OC-725, Warner, Hamden, CT, USA), we recorded whole cell currents from injected oocytes after incubation for 4–5 days at 20 °C in an assay buffer. The inward current was monitored at

a holding potential of −80 mV. Each ligand was diluted with the assay buffer to a specific concentration containing 0.1% dimethyl sulfoxide (DMSO). The assay buffer containing 0.1% DMSO was used as a negative control. Data acquisition and analyses were carried out using Digidata 1322A and pCLAMP software (Axon Instruments, Foster City, CA, USA).

2.7. Chemicals

Chemicals used for functional analyses are listed in Table S2 and their structures are shown in Fig. 4A and S1. Stock solution of chemicals were prepared in DMSO and stored at −20 °C.

3. Results

3.1. RNA sequencing and identification of chemosensory receptors

Using the Illumina MiSeq system, we obtained 279,730 and 89,818 assembled contigs from the transcriptomes of the male and female antennae and proboscises of *B. latifrons* and *Z. cucurbitae*, respectively (File S2 for *B. latifrons*; File S3 for *Z. cucurbitae*). The summary of the assembly is shown in Table 1 and 2. We identified chemosensory receptors—namely, ORs, GRs, and IRs—by a BLASTX search of the contigs against Pfam domains and amino acid sequences of chemosensory receptors in *D. melanogaster* (Table 3 and File S4 for *B. latifrons*; Table 4 and File S5 for *Z. cucurbitae*).

A homology search based on the Pfam domains of the 7tm odorant receptor and the amino acid sequences of the *Drosophila* ORs revealed approximately 50 candidate ORs both in *B. latifrons* and *Z. cucurbitae*. Among them, we merged the partial sequences

of *ZcucOR13a* and *ZcucOR59a* by RT-PCR. In total, full-length coding sequence of 30 and 27 ORs were determined in *B. latifrons* and *Z. cucurbitae*, respectively. To assign names to the ORs, we used these sequences as queries in a BLASTP search against the NCBI non-redundant protein database. Top blast hits were mostly obtained from predicted sequences by automated computational analysis based on reference genome sequences. Others were obtained from databases of several Tephritid fruit flies, *Bactrocera* and *Rhagoletis* species. We named the candidate ORs according to gene names of the top blast hits with some exceptions, i.e., *BlatOR7a-8*, *ZcucOR7a-5*, *ZcucOR7a-7*, *ZcucOR7a-8*, *ZcucOR7a-9*, *ZcucOR35a*, *ZcucOR43a-2*, and *ZcucOR43a-3* were named according to their homologs in *D. melanogaster* or *B. dorsalis*.

We identified several homologs of sugar receptors such as the *GR5a* and *GR64* subfamilies (Freeman and Dahanukar, 2015) by a homology search based on Pfam domains of *Drosophila* trehalose receptors (PF06151). Using Pfam domains of *Drosophila* 7tm chemosensory receptors (PF08395), we also identified 25 and 12 GRs, including homologs of carbon dioxide receptors such as the *GR21a* and *GR63a* subfamilies (Jones et al., 2007; Kwon et al., 2007), from *B. latifrons* and *Z. cucurbitae*, respectively. A single gene of *GR21a* has been identified in *D. melanogaster*, and here, we identified multiple homologs of *GR21a* from *B. latifrons* and *Z. cucurbitae*, as multiple homologs were also found in *B. dorsalis* (Miyazaki et al., 2018). Among GRs, except for *GR21a* and *GR63a* genes coding carbon dioxide receptors, a full-length coding sequence was identified only in *BlatGR64b* from the transcriptomes, likely due to relatively low transcriptional levels of GR genes in the chemosensory organs.

We identified ligand gated ion channels by homology search based on Pfam domains of the *Drosophila* ligand gated ion channel (PF00060) and ligated ion channel

L-glutamate- and glycine-binding site (PF10613). Among them, 19 and 17 candidate IRs were identified by a BLASTP search based on translated protein sequences from *B. latifrons* and *Z. cucurbitae*, respectively. We determined full-length coding sequences of several IRs including *IR8a* and *IR25a* subfamilies which have been characterized as co-receptors (Benton et al., 2009; Rytz et al., 2013). On the other hand, multiple partial fragments were identified in several IRs owing to their large coding region. We found that high FPKM values were sex-specifically shown in several transcripts of both *B. latifrons* and *Z. cucurbitae* (Table S3 and S4). We used qPCR to quantitatively compare the transcription levels of these genes—*BlatIR21a*, *BlatIR40a*, *BlatIR64a-2*, *BlatIR92a-1*, *ZcucIR40a-1*, *ZcucIR40a-2* and *ZcucIR64a*, and *ZcucIR92a*—in male and female antennae. We found that all the IRs tested expressed in both sexes, whereas a significant difference in the transcriptional level of ZcucIR40a was observed between the male and female antennae (Fig. 1).

3.2. Phylogenetic relationship of ORs among three Dacini fruit flies

We have identified ORs expressed in chemosensory organs of three Dacini fruit flies in this and previous studies (Miyazaki et al., 2018). To see a relationship between them, we constructed a phylogenetic tree of ORs with sequences of more than 200 amino acids in the three Dacini fruit flies (Fig. 2). The tree reveals remarkable divergence of several ORs with multiple homologous genes such as OR7a, OR63a, and OR67d subfamilies in the three related species. Although common OR subfamilies of the three species mostly converged on the same lineages, ORs of *Z. cucurbitae* were slightly apart from those of *B. dorsalis* and *B. latifrons* in most cases. Because *B. dorsalis* and *B. latifrons* belong to the same genus but *Z. cucurbitae* is taxonomically apart from them

(Krosch et al., 2012), the phylogenetic relationship of OR families corresponds to the taxonomic relationship.

3.3. Transcriptional profiles of OR74a homologs

Among the identified candidate ORs, we focused on *OR74a* homologs, because *Drosophila* OR74a is a receptor for 1-nonanol (Kreher et al., 2005) which is an analog of rectal gland components in several Dacini fruit flies. Since only male flies possess rectal glands, chemical factors in the tissue likely function as sexual cues. Therefore, we compared transcription levels of the *OR74a* homologs between male and female chemosensory organs by qPCR to see if sexually biased expression could be observed in these receptors. However, there were no significant differences in the transcription levels of *BlatOR74a* and *ZcucOR74a* between male and female antennae (Fig. 1). We also compared the deduced amino acid sequences of the three OR74a receptors. A 96 % similarity was noted between the amino acid identities of BdorOR74a and BlatOR74a. ZcucOR74a revealed an 89 % and 87 % similarity between amino acid identities with BdorOR74a and BlatOR74a, respectively (Fig. 3).

3.4. Functional characterization of OR74a homologs by two-electrode voltage-clamp recording

We co-expressed each of the OR74a homolog proteins with the co-receptor ORCO in *Xenopus* oocytes to analyze responses to the candidate 1-nonanol analog ligands. We tested four analogs including rectal gland components as shown in Fig. 4A. We found that the three OR74a homologs robustly responded to 1-nonanol at a concentration of 100 μM (Fig. 4B). While BdorOR74a revealed an average current of

more than 0.2 μA at this concentration, BlatOR74a and ZcucOR74a exhibited smaller currents (Table 5). The oocyte expressing BdorOR74a with BdorORCO also responded to 6-oxo-1-nonanol, which is found in the related species *B. carambolae* (Wee and Tan, 2005). The current value induced by 6-oxo-1-nonanol was significantly higher than that by the control (DMSO) (Fig. 4C). We occasionally observed weak responses of the BdorOR74a to nonyl acetate which showed an attractive activity to *B. dorsalis* females as a volatile contained in a host fruit (Siderhurst and Jang, 2006), but there were no significant differences between the current values induced by this compound and those by the control. We also observed a significant response by 6-oxo-1-nonanol, but not by 1,3-nonanediol, known as a rectal component of *Z. cucurbitae* (Nishida et al., 1993), in the oocytes expressing ZcucOR74a with ZcucORCO. The attractants and sex pheromones of the Dacini fruit flies did not elicit any response of BlatOR74a and ZcucOR74a (Fig. S2). While 1-nonanol evoked the responses of BdorOR74a and ZcucOR74a in a dose-dependent matter, the response of BlatOR74a failed to reach a plateau up to 1 mM, probably due to a low responsiveness (Fig. 4D, E).

Discussion

The specific and different attractiveness to plant-derived semiochemicals among Dacini fruit flies have been well characterized (Tan et al., 2014), but it is unclear how the related species have acquired a chemosensory system to respond to specific volatiles to gain sex-pheromone sources. Based on the different affinity to the attractants among the three Dacini fruit flies, i.e., aromatic compounds for *B. dorsalis* and *Z. cucurbitae* and α-ionone analogs for *B. latifrons,* we speculated that *B. dorsalis* and *Z. cucurbitae* share more similar chemosensory receptors in the chemo-recognition system at peripheral neurons

than those in *B. latifrons*, although *B. dorsalis* and *B. latifrons* are closely related species divergent from *Z. cucurbitae* (Krosch et al., 2012). However, the phylogenetic analysis of ORs shows that *B. dorsalis* and *B. latifrons* share more similar homologous genes than *Z. cucurbitae*. With regards to the ME receptor OR88a (Liu et al., 2018), the amino acid sequence of BdorOR88a is more similar to that of BlatOR88a (92% similarity) than that of ZcucOR88a (69% similarity). It is intriguing whether BlatOR88a and ZcucuOR88a respond to their attractants. If so, it is also interesting how the different responsiveness to the attractants occurs among the similar receptors. We should note that a few substitutions of critical amino acids possibly change a ligand-binding property. We also found divergent homologs and variants in several ORs including OR7a and OR67d subfamilies in the three species, suggesting that these repertoires are necessary for detection of semiochemicals which are commonly recognized by Dacini fruit flies.

We identified candidate GRs and IRs of *B. dorsalis* and *Z. cucurbitae*, although their full-length coding sequences could not be determined in most cases due to low transcriptional levels and/or long coding regions. With regards to GRs, we found 25 and 12 uncharacterized candidate GRs, except for sugar and carbon dioxide receptors, in *B. latifrons* and *Z. cucurbitae*, respectively. Because the attractants also show phagostimulant activities, it is intriguing whether GR is involved in the recognition of the attractants in gustatory organs. We also found the 19 and 17 candidate IRs from *B. latifrons* and *Z. cucurbitae*, respectively. Because IRs function as both olfactory and gustatory receptors, IRs are possibly associated with detection of the attractants in olfactory and gustatory organs. We noticed that FPKM values of several transcripts coding IRs were sex-specifically observed. However, all the IRs analyzed by qPCR were expressed in both sexes, although the transcriptional level of *ZcucIR40a-2* was

359 significantly higher in male antennae than that in female antennae. Because we observed
360 indistinguishable transcriptional levels between male and female in ORs of *B. dorsalis* in
361 a previous study (Miyazaki et al., 2018), sexually dimorphic behavior such as the male
362 specific responsiveness to attractants is probably triggered by information processing in
363 the central nervous system, based on inputs from peripheral neurons via chemosensory
364 receptors, regardless of receptor type. Further, because IRs are thought to form
365 heteromeric ion channels in which a co-receptor, namely IR8a or IR25a, partners one or
366 multiple ligand-specific IRs (Abuin et al., 2011; Rytz et al., 2013), knockout of the co-
367 receptor(s) using CRISPR/Cas9 editing will give us a clue to clarify the molecular system
368 underlying chemo-recognition.

369 Because 1-nonanol analogs have been identified as the major components, other
370 than aromatic compounds, in the male rectal glands of several Dacini fruit flies, we
371 characterized OR74a homologs of the three fruit flies. The three OR74a homologs co-
372 expressed with their cognate ORCO robustly responded to 1-nonanol, as reported in
373 DmOR74a, suggesting a conservation of olfactory system between Dacini and
374 *Drosophila* at the molecular level. Among the Dacini OR74a homologs, the sensitivities
375 to 1-nonanol differed from each other. Despite the very high similarities of amino acid
376 sequences between BdorOR74a and BlatOR74a, BdorOR74a exhibited the highest
377 sensitivity to 1-nonanol, but BlatOR74a showed the weakest responsiveness, as the
378 average current value of BlatOR74a was about one-fifth of that of BdorOR74a (Table 5).
379 It is possible that an efficiency of expression in the heterologous expression system using
380 *Xenopus* oocyte is different among the three OR74a homologs owing to their amino acid
381 or nucleotide sequences. Because 1-nonanol is a repellent to larvae of *D. melanogaster*
382 (Cobb, 1992), OR74a homologs are possibly necessary to recognize unfavorable odorants

383 in Dacini fruit flies. We also found that BdorOR74a significantly responded to 6-oxo-1-
384 nonanol which is contained in male rectal glands in the closely related species, *B.*
385 *carambolae*, but this was not the case in *B. dorsalis*. It is interesting to note that
386 reproductive interference, i.e., antagonistic sexual interaction, among these species has
387 been reported (Kitano et al., 2018). Considering this interspecific sexual interaction,
388 BdorOR74a may detect 6-oxo-1-nonanol to avoid the competitive species, thereby
389 reproductive success could be elevated. To examine this possibility, it is necessary to
390 observe a behavior of *B. dorsalis* to 6-oxo-1-nonanol, and to characterize an OR74a
391 homolog of *B. carambolae*. Besides the predicted repellent roles in dipteran species, 1-
392 nonanol analogs may play as cues for seeking host fruits and vegetables. While roles of
393 1-nonanol analogs have not been well elucidated, characterization of OR74a homologs
394 of the Dacini fruit flies gives us clues to find the roles of these compounds.
395 In the present study, we characterized functional properties of ORs that respond
396 to rectal gland components following the previous identification of ORs responding to
397 plant volatiles. Although semiochemicals play critical roles in the life cycles of Tephritid
398 fruit flies, only a few studies have attempted functional characterization of ORs.
399 Furthermore, according to our knowledge, there is no study that identifies a ligand for
400 other chemosensory receptors, namely GRs and IRs. Comprehensive elucidation of
401 properties of chemosensory receptors, including those for attractants and pheromones,
402 will provide insights into the mechanisms underlying the chemosensory abilities that
403 Dacini fruit flies have acquired to favorably utilize semiochemicals in their life cycles. It
404 will also give us clues to develop effective attractants for pest control of these destructive
405 pest fruit flies.
406

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Declarations of interest

none

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Figure captions

Fig. 1. Transcriptional levels of candidate ionotropic receptors (IRs) and olfactory receptors (ORs) identified in *Bactrocera latifrons* and *Zeugodacus cucurbitae*. MA: male antennae; FA: female antennae. Each value is plotted as a dot (n = 4–5). The box plot shows 25–75% (box), median (band inside), and minima to maxima (whiskers). Student's t-test: *p <0.05.

Fig. 2. Phylogenetic tree of candidate olfactory receptors (ORs) identified in the three Dacini fruit flies, *Bactrocera dorsalis*, *B. latifrons* and *Zeugodacus cucurbitae*. Branch length is proportional to genetic distance estimated by the maximum likelihood method.

Fig. 3. Comparison of deduced amino acid sequences of olfactory receptors (ORs). Alignments of BdorOR74a, BlatOR74a and ZcucOR74a are shown. Predicted seven transmembrane domains (TM1–TM7) are indicated by solid lines.

Fig. 4. Responses of *Xenopus* oocytes expressing OR74a with its cognate ORCO in the three Dacini fruit flies, *Bactrocera dorsalis*, *B. latifrons* and *Zeugodacus cucurbitae* to 1-nonanol analogs. (A) Structures of 1-nonanol analogs tested as candidate ligands. (B) Current traces of an oocyte upon successive exposures to 1-nonanol analogs including DMSO (the control). Each chemical at 100 μM was applied at the time, indicated by the arrowhead. (C) Current values measured in oocytes responding to 1-nonanol analogs at 100 μM. Each value is plotted as a dot (n = 9 for BdorOR74a; n = 6 for ZcucOR74a). The box plot shows 25–75% (box), median (band inside), and minima to maxima (whiskers). Significant differences between current values responding to a ligand and those

responding to DMSO (control) were shown by Student's *t*-test: $**p < 0.001$, $***p < 0.0001$. (D) Responses of each oocyte to 1-nonanol at various concentrations. (E) Dose-response curves of oocytes responding to 1-nonanol. Each point represents the mean current value. Error bars indicate SE (n = 6 for BdorOR74a; n = 4 for BlatOR74a; n = 7–8 for ZcucOR74a)

Supplementary materials

Table S1. The primers used for qPCR experiments.

Table S2. Chemicals used for functional analysis of ORs.

Table S3. Transcripts coding for candidate chemosensory receptors.

Table S4. Transcripts coding for candidate chemosensory receptors.

Fig. S1. Chemical structures of tested compounds for the functional analysis of candidate olfactory receptors.

Fig. S2. Responses of *Xenopus* oocytes expressing BlatOR74a or ZcucOR74a with its cognate ORCO to attractants, sex pheromones and/or their related compounds. Only 1-nonanol elicited the responses of BlatOR74a and ZcucOR74a as shown in Fig. 3. The structure of each compound and its corresponding abbreviation are shown in Fig. S1.

573 **File S1.** An example of a command line to build a fasta file of contigs hit by the BLASTX
574 search using Biostrings package within R software.
575
576 **File S2.** A Trinity file of *Bactrocera latifrons.*
577
578 **File S3.** A Trinity file of *Zeugodacus cucurbitae.*
579
580 **File S4.** A fasta file of chemosensory receptors of *Bactrocera latifrons.*
581
582 **File S5.** A fasta file of chemosensory receptors of *Zeugodacus cucurbitae.*

Table 1. Summary of sequence data analysis in *Bactrocera latifrons*.

	Male		Female	
	Antenna	Proboscis	Antenna	Proboscis
Raw reads	1,991,913	2,972,051	1,934,849	2,692,567
Clean reads	1,390,771	2,004,475	910,187	1,794,188
Assembled contigs	279,730			
Mean length of contigs (bp)	367			

Table 2. Summary of sequence data analysis in *Zeugodacus cucurbitae*.

	Male		Female	
	Antenna	Proboscis	Antenna	Proboscis
Raw reads	869,802	467,912	1,574,403	2,022,842
Clean reads	607,077	322,850	1,101,598	1,393,230
Assembled contigs	89,818			
Mean length of contigs (bp)	474			

Table 3. Candidate chemosensory receptors of *Bactrocera latifrons* identified from transcriptome.

Gene name	Length (AA)	CDS	E-value	BLASTP best hit (Accession number; Name; Species)
ORs				
BlatORCO	473	Full	0	ADK97803.1; Or83b (ORCO) *Zeugodacus cucurbitae*
BlatOR2a-v1	393	Full	0	XP_018802940.1; OR2a-like; *Bactrocera latifrons*
BlatOR2a-v2	379	Full	0	XP_018802940.1; OR2a-like; *Bactrocera latifrons*
BlatOR7a-1	396	Full	0	XP_018783745.1; OR7a-like; *Bactrocera latifrons*
BlatOR7a-2	221	Partial	4e-154	XP_018804184.1; OR42a-like; *Bactrocera latifrons*
BlatOR7a-3	396	Full	0	XP_018798593.1; OR43b-like; *Bactrocera latifrons*
BlatOR7a-4	394	Full	0	XP_018798558.1; OR7a-like; *Bactrocera latifrons*
BlatOR7a-5	400	Full	0	XP_018798592.1; OR43b-like; *Bactrocera latifrons*
BlatOR7a-6	399	Full	2e-171	XP_011178079.1; OR7a-like; *Zeugodacus cucurbitae*
BlatOR7a-7	392	Full	0	XP_019846037.1; OR7a-like; *Bactrocera dorsalis*
BlatOR7a-8-v1	430	Full	0	XP_018798519.1; OR59b-like; *Bactrocera latifrons*
BlatOR7a-8-v2	460	Partial	0	XP_018798519.1; OR59b-like; *Bactrocera latifrons*
BlatOR7a-8-v3	139	Partial	7e-90	XP_018798519.1; OR59b-like; *Bactrocera latifrons*
BlatOR10a	400	Full	0	XP_018791769.1; OR10a; *Bactrocera latifrons*
BlatOR13a	441	Full	0	XP_018784751.1; OR13a; *Bactrocera latifrons*
BlatOR30a	389	Partial	0	XP_019847671.1; OR30a-like; *Bactrocera dorsalis*
BlatOR33b	70	Partial	9e-28	XP_017488833.1; OR33b-like; *Rhagoletis zephyria*
BlatOR35a	320	Partial	0	XP_018789506.1; OR35a-like; *Bactrocera latifrons*
BlatOR42a	139	Partial	3e-93	XP_018804184.1; OR42a-like; *Bactrocera latifrons*

BlatOR42b	394	Full	0	XP_018786776.1; OR42b-like; *Bactrocera latifrons*
BlatOR43a-1-v1	378	Full	0	XP_018793811.1; OR43a; *Bactrocera latifrons*
BlatOR43a-1-v2	304	Full	1e-173	XP_018793811.1; OR43a; *Bactrocera latifrons*
BlatOR43a-2	381	Full	0	XP_018798370.1; Or2-like; *Bactrocera latifrons*
BlatOR43a-3	284	Partial	2e-117	XP_019847596.1; OR30a-like; *Bactrocera dorsalis*
BlatOR43a-4	209	Partial	7e-145	XP_018798369.1; Or43-like; *Bactrocera latifrons*
BlatOR45a	402	Partial	0	XP_018794773.1; OR45a-like; *Bactrocera latifrons*
BlatOR47b	329	Partial	0	XP_018795844.1; OR47b; *Bactrocera latifrons*
BlatOR49a	291	Partial	0	XP_011212431.1; OR49a-like; *Bactrocera dorsalis*
BlatOR49b-v1	386	Partial	0	XP_018796898.1; OR49b; *Bactrocera latifrons*
BlatOR49b-v2	358	Partial	0	XP_018796898.1; OR49b; *Bactrocera latifrons*
BlatOR59a	388	Full	0	XP_018805034.1; OR59a-like; *Bactrocera latifrons*
BlatOR63a-1-v1	415	Full	0	XP_018792788.1; OR63a-like; *Bactrocera latifrons*
BlatOR63a-1-v2	348	Full	0	XP_018783180.1; OR63a; *Bactrocera latifrons*
BlatOR63a-2	417	Full	0	XP_018792788.1; OR63a-like; *Bactrocera latifrons*
BlatOR63a-3	414	Full	0	XP_018783180.1; OR63a; *Bactrocera latifrons*
BlatOR67c-v1	404	Full	0	AKI29044.1; OR67c; *Bactrocera dorsalis*
BlatOR67c-v2	373	Partial	0	XP_018795012.1; OR67c-like; *Bactrocera latifrons*
BlatOR67d-1	388	Full	0	XP_018803798.1; OR67d-like; *Bactrocera latifrons*
BlatOR67d-2	401	Partial	1e-176	XP_017473047.1; OR67d-like; *Rhagoletis zephyria*
BlatOR67d-3-v1	387	Full	0	XP_017473047.1; OR67d-like; *Rhagoletis zephyria*
BlatOR67d-3-v2	71	Partial	2e-31	XP_017483930.1; OR67d-like; *Bactrocera zephyria*
BlatOR67d-4	388	Full	0	XP_018803784.1; OR67d-like; *Bactrocera latifrons*

BlatOR69a-1	414	Full	0	XP_018788172.1; OR69a; *Bactrocera latifrons*
BlatOR69a-2	423	Full	8e-179	XP_019847605.1; OR69a; *Bactrocera dorsalis*
BlatOR74a-1	414	Full	0	XP_011201924.2; OR74a-like; *Bactrocera dorsalis*
BlatOR74a-2	181	Partial	2e-125	XP_018796426.1; OR74a; *Bactrocera latifrons*
BlatOR82a	401	Full	0	XP_018783712.1; OR82a; *Bactrocera latifrons*
BlatOR85d	203	Partial	1e-138	XP_018801739.1; OR85d; *Bactrocera latifrons*
BlatOR88a	411	Full	0	XP_018790415.1; OR88a; *Bactrocera latifrons*
BlatOR92a	384	Full	0	XP_011208819.1; OR92a; *Bactrocera dorsalis*
BlatOR94b	379	Partial	0	XP_018801531.1; OR94b-like; *Bactrocera latifrons*
GRs				
BlatGR5a-1	61; 189	Partial	2e-35; 3e-128	XP_018783851.1; GR5a; *Bactrocera latifrons*
BlatGR5a-2	193	Partial	2e-135	XP_018783883.1; GR5a; *Bactrocera latifrons*
BlatGR5a-3	82	Partial	6e-51	XP_011213356.2; GR5a; *Bactrocera dorsalis*
BlatGR8a-1	83; 126	Partial	1e-48; 7e-79	XP_018792278.1; GR8a; *Bactrocera latifrons*
BlatGR8a-2	76	Partial	1e-42	XP_011185249.1; GR8a-like; *Zeugodacus cucurbitae*
BlatGR21a-1	456	Full	0	XP_018802085.1; GR21a-like; *Bactrocera latifrons*
BlatGR21a-2-v1	428	Partial	0	AOE48126.1; GR6; *Scaeva pyrastri*
BlatGR21a-2-v2	425	Partial	0	AOE48126.1; GR6; *Scaeva pyrastri*
BlatGR21a-2-v3	422	Partial	0	AOE48126.1; GR6; *Scaeva pyrastri*
BlatGR28b-1	452	Partial	0	XP_018796745.1; putative GR28b; *Bactrocera latifrons*
BlatGR28b-2	420	Partial	5e-166	XP_018796745.1; putative GR28b; *Bactrocera latifrons*
BlatGR28b-3	99	Partial	1e-61	XP_011180327.1; putative GR28b; *Zeugodacus cucurbitae*
BlatGR32a-1	267	Partial	3e-96	XP_011183921.1; uncharacterized protein LOC105213073; *Zeugodacus cucurbitae*

BlatGR32a-2	112	Partial	2e-40	XP_018792133.1; uncharacterized protein LOC108970891; *Bactrocera latifrons*
BlatGR32a-3	75	Partial	1e-44	XP_018787660.1; GR32a; *Bactrocera latifrons*
BlatGR33a	84	Partial	4e-52	XP_018794131.1; GR33a; *Bactrocera latifrons*
BlatGR39b	76	Partial	5e-44	XP_018794457.1; putative GR39b; *Bactrocera latifrons*
BlatGR43a-1	101; 80	Partial	2e-62; 6e-48	XP_018786267.1; GR43a-like; *Bactrocera latifrons*
BlatGR43a-2	126	Partial	1e-32	XP_020712594.1; GR43a-like; *Ceratitis capitata*
BlatGR63a	485	Full	0	XP_018793345.1; GR63a; *Bactrocera latifrons*
BlatGR64a	87	Partial	3e-53	XP_018783856.1; GR64a; *Bactrocera latifrons*
BlatGR64b	425	Full	0	XP_011181425.1; GR64b; *Zeugodacus cucurbitae*
BlatGR64c	60	Partial	2e-32	XP_018783854.1; GR64c-like; *Bactrocera latifrons*
BlatGR64e	76; 368; 89	Partial	2e-41; 0; 1e-49	XP_018783853.1; uncharacterized protein LOC108965721; *Bactrocera latifrons*
BlatGR64f	307	Partial	0	XP_018783853.1; uncharacterized protein LOC108965721; *Bactrocera latifrons*
BlatGR66a	105; 119	Partial	3e-68; 1e-77	XP_018803775.1; GR66a; *Bactrocera latifrons*
BlatGR68a	95	Partial	1e-57	AKI28984.1; GR68a; *Bactrocera dorsalis*
BlatGR93a	47	Partial	2e-21	XP_014095798.1; GR93a; *Bactrocera oleae*
BlatGR94a	122	Partial	3e-81	XP_018792091.1; GR94a; *Bactrocera latifrons*
BlatGR98b-1-v1	210; 187	Partial	9e-130; 6e-94	XP_018799113.1; putative GR98b; *Bactrocera latifrons*
BlatGR98b-1-v2	86	Partial	5e-51	XP_014093197.1; putative GR98b; *Bactrocera oleae*
BlatGR98b-2	111	Partial	2e-67	XP_019846334.1; putative GR98b; *Bactrocera dorsalis*
BlatGR98b-3	104	Partial	1e-60	XP_011205406.1; putative GR98b; *Bactrocera dorsalis*
IRs				
BlatIR8a	944	Full	0	XP_011211753.1; glutamate receptor ionotropic, kainate 2; *Bactrocera dorsalis*
BlatIR21a	106; 79; 225	Partial	4e-65; 6e-49; 2e-154	XP_018792132.1; IR21a; *Bactrocera latifrons*

BlatIR25a	940	Full	0	XP_018787692.1; IR25a; *Bactrocera latifrons*
BlatIR40a	119; 223	Partial	1e-77; 2e-159	AKI28985.1; IR40a; *Bactrocera dorsalis*
BlatIR41a-v1	677	Full	0	P_018789519.1; uncharacterized protein LOC108969330; *Bactrocera latifrons*
BlatIR41a-v2	505	Full	0	P_018789519.1; uncharacterized protein LOC108969330; *Bactrocera latifrons*
BlatIR48b	318	Partial	0	P_014089212.1; uncharacterized protein LOC106616838; *Bactrocera oleae*
BlatIR64a-1	365	Partial	0	XP_018785740.1; uncharacterized protein LOC108966998; *Bactrocera latifrons*
BlatIR64a-2	112	Partial	9e-53	XP_019845172.1; uncharacterized protein LOC105224490; *Bactrocera dorsalis*
BlatIR75a	85; 549	Partial	4e-43; 0	XP_019845037.1; glutamate receptor; *Bactrocera dorsalis*
BlatIR75b	635	Partial	0	XP_014088428.1; uncharacterized protein LOC106616338; *Bactrocera oleae*
BlatIR75d	558	Partial	0	XP_018803411.1; uncharacterized protein LOC108977898; *Bactrocera latifrons*
BlatIR76a	657	Partial	0	XP_014086277.1; uncharacterized protein LOC106614874; *Bactrocera oleae*
BlatIR76b	660	Full	0	XP_018785025.1; glutamate receptor ionotropic, delta-1; *Bactrocera latifrons*
BlatIR84a	702	Partial	0	XP_011193628.1; glutamate receptor 1; *Zeugodacus cucurbitae*
BlatIR92a-1	173; 156	Partial	9e-117; 3e-105	XP_018789816.1; uncharacterized protein LOC108969515; *Bactrocera latifrons*
BlatIR92a-2	207; 70	Partial	8e-98; 2e-40	XP_019845610.1; uncharacterized protein LOC105225754 *Bactrocera dorsalis*
BlatIR93a-1	98; 79; 389	Partial	1e-56; 1e-44; 0	XP_018791489.1; glutamate receptor ionotropic, kainate 5; *Bactrocera latifrons*
BlatIR93a-2	56	Partial	6e-27	XP_018791489.1; glutamate receptor ionotropic, kainate 5; *Bactrocera latifrons*

Table 4. Candidate chemosensory receptors of *Zeugodacus cucurbitae* identified from transcriptome.

Gene name	Length (AA)	CDS	E-value	BLASTP best hit (Accession number; Name; Species)
ORs				
ZcucORCO	473	Full	0	XP_011183998.1; Or83b (ORCO) *Zeugodacus cucurbitae*
ZcucOR2-1	245	Partial	0	XP_011187627.1; OR2a-like; *Zeugodacus cucurbitae*
ZcucOR2-2	139	Partial	3e-86	XP_011198390.1; OR2a-like; *Bactrocera dorsalis*
ZcucOR7a-1	396	Full	0	XP_019847175.1; OR7a-like; *Zeugodacus cucurbitae*
ZcucOR7a-2	375	Partial	0	XP_019845111.1; OR7a-like; *Bactrocera dorsalis*
ZcucOR7a-3	72	Partial	1e-28	XP_011178079.1; OR7a-like; *Zeugodacus cucurbitae*
ZcucOR7a-4	394	Full	0	XP_011182064.1; OR7a-like; *Zeugodacus cucurbitae*
ZcucOR7a-5	82	Partial	4e-49	XP_018798592.1; OR43b-like; *Bactrocera latifrons*
ZcucOR7a-6	399	Full	0	XP_011178079.1; OR7a-like; *Bactrocera dorsalis*
ZcucOR7a-7	400	Full	0	XP_014086206.1; OR43b-like; *Bactrocera oleae*
ZcucOR7a-8	162	Partial	2e-72	XP_019845105.1; OR43b-like; *Bactrocera dorsalis*
ZcucOR7a-9	129	Partial	4e-67	XP_018798592.1; OR43b-like; *Bactrocera latifrons*
ZcucOR10a-1	402	Full	0	XP_011184667.1; OR10a; *Zeugodacus cucurbitae*
ZcucOR10a-2	138	Partial	4e-36	XP_011184667.1; OR10a; *Zeugodacus cucurbitae*
ZcucOR13a	104; 257	Partial	9e-70; 0	XP_011177369.1; OR13a; *Zeugodacus cucurbitae*
ZcucOR24a	91	Partial	3e-54	XP_011190505.1; OR24a; *Zeugodacus cucurbitae*
ZcucOR30a	178	Partial	4e-126	XP_011187028.1; OR30a-like; *Bactrocera cucurbitae*
ZcucOR33b	104	Partial	7e-27	XP_017488833.1; OR33b-like; *Rhagoletis zephyria*

ZcucOR35a	416	Full	0	XP_011185366.1; OR13a-like; *Zeugodacus cucurbitae*
ZcucOR42a	440	Partial	0	XP_011183261.1; OR42a-like; *Zeugodacus cucurbitae*
ZcucOR42b	394	Full	0	XP_011184786.1; OR42b-like; *Zeugodacus cucurbitae*
ZcucOR43a-1	380	Full	0	XP_011178893.1; OR43a; *Zeugodacus cucurbitae*
ZcucOR43a-2	375	Full	0	XP_011194820.1; OR2a-like; *Bactrocera cucurbitae*
ZcucOR43a-3	375	Full	5e-168	XP_014097484.1; OR2a-like; *Bactrocera oleae*
ZcucOR45a	394	Full	0	XP_011181253.1; OR45a-like; *Zeugodacus cucurbitae*
ZcucOR47b-v1	443	Full	0	XP_011196690.1; OR47b isoform X1; *Zeugodacus cucurbitae*
ZcucOR47b-v2	440	Full	0	XP_011196690.1; OR47b isoform X1; *Zeugodacus cucurbitae*
ZcucOR47b-v3	383	Full	0	XP_011196690.1; OR47b isoform X1; *Zeugodacus cucurbitae*
ZcucOR49a	154; 108	Partial	9e-100; 1e-68	XP_011181266.1; OR49a-like; *Zeugodacus cucurbitae*
ZcucOR49b-v1	371	Full	0	XP_011196302.1; OR49b; *Zeugodacus cucurbitae*
ZcucOR49b-v2	284	Partial	0	XP_011196302.1; OR49b; *Zeugodacus cucurbitae*
ZcucOR59a	136; 141	Partial	5e-86; 3e-95	XP_011188666.1; OR59a-like; *Zeugodacus cucurbitae*
ZcucOR63a-1	415	Full	0	AKI29042.1; OR63a-1; *Bactrocera dorsalis*
ZcucOR63a-2	415	Full	0	XP_011195821.1; OR63a-like; *Zeugodacus cucurbitae*
ZcucOR67c-1	253	Partial	2e-177	XP_011191013.1; uncharacterized protein LOC105217623; *Zeugodacus cucurbitae*
ZcucOR67c-2-v1	236	Partial	1e-171	XP_011191024.1; OR67c-like; *Zeugodacus cucurbitae*
ZcucOR67c-2-v2	167	Partial	4e-112	XP_011191013.1; uncharacterized protein LOC105217623; *Zeugodacus cucurbitae*
ZcucOR67d-1-v1	388	Full	0	XP_011186895.1; OR67d-like; *Zeugodacus cucurbitae*
ZcucOR67d-1-v2	388	Full	0	XP_011186895.1; OR67d-like; *Zeugodacus cucurbitae*
ZcucOR67d-2	386	Full	0	XP_017473047.1; OR67d-like; *Rhagoletis zephyria*

ZcucOR67d-3	388	Full	0	XP_017473047.1; OR67d-like; *Rhagoletis zephyria*
ZcucOR67d-4	243	Partial	6e-175	XP_011186909.1; OR67d-like; *Zeugodacus cucurbitae*
ZcucOR67d-5	144	Partial	2e-83	XP_011186909.1; OR67d-like; *Zeugodacus cucurbitae*
ZcucOR67d-6	86	Partial	9e-38	XP_011186895.1; OR67d-like; *Zeugodacus cucurbitae*
ZcucOR69a-1	413	Full	0	XP_011191101.1; OR69a; *Zeugodacus cucurbitae*
ZcucOR69a-2	98	Partial	7e-65	XP_011191113.1; OR69a isoformA; *Bactrocera cucurbitae*
ZcucOR74a	414	Full	0	XP_011201924.2; OR74a-like; *Bactrocera dorsalis*
ZcucOR82a	241; 79	Partial	2e-173; 7e-48	XP_011181975.1; OR82a; *Zeugodacus cucurbitae*
ZcucOR83a	66	Partial	2e-38	XP_011184140.1; OR83a-like; *Zeugodacus cucurbitae*
ZcucOR85c	98	Partial	2e-62	XP_011192524.1; OR85c; *Zeugodacus cucurbitae*
ZcucOR88a	407	Full	0	XP_011183038.1; OR88a; *Zeugodacus cucurbitae*
ZcucOR92a	384	Full	0	XP_011208819.1; OR92a; *Bactrocera dorsalis*
ZcucOR94a	377	Partial	0	XP_011179733.1; OR94a-like; *Zeugodacus cucurbita*
ZcucOR94b	414	Full	0	XP_014094554.1; OR94a-like; *Bactrocera oleae*
GRs				
ZcucGR5a	68	Partial	1e-33	XP_014092165.1; GR5a; *Bactrocera oleae*
ZcucGR8a	68	Partial	8e-13	XP_012161678.1; GR8a; *Ceratitis capitata*
ZcucGR21a-1-v1	457	Full	0	XP_011194684.1; GR21a-like; *Zeugodacus cucurbitae*
ZcucGR21a-1-v2	79	Partial	1e-48	XP_014101212.1; GR21a-like; *Bactrocera oleae*
ZcucGR21a-2	426	Partial	1e-85	AID61262.1; GR; *Calliphora stygia*
ZcucGR22d	374	Partial	0	XP_018800490.1; GR22d; *Bactrocera latifrons*
ZcucGR23a	41	Partial	7e-11	XP_011194021.1; uncharacterized protein LOC105219521; *Zeugodacus cucurbitae*

ZcucGR28a	68	Partial	5e-32	XP_011180394.1; GR28a; *Zeugodacus cucurbitae*
ZcucGR28b	149	Partial	4e-98	XP_018796745.1; GR28b; *Bactrocera latifrons*
ZcucGR32a	85; 158	Partial	3e-53; 1e-108	XP_011178366.1; GR32a; *Zeugodacus cucurbitae*
ZcucGR63a	485	Full	0	XP_011187146.1; GR63a; *Zeugodacus cucurbitae*
ZcucGR64b	104; 67	Partial	2e-66; 6e-39	XP_011181425.1; GR64b; *Zeugodacus cucurbitae*
ZcucGR64e	22	Partial	9e-15	XP_011181429.1; uncharacterized protein LOC105211608; *Zeugodacus cucurbitae*
ZcucGR64f	72	Partial	1e-40	XP_011181429.1; uncharacterized protein LOC105211608; *Zeugodacus cucurbitae*
ZcucGR66a	195	Partial	8e-137	XP_011196225.1; GR66a; *Zeugodacus cucurbitae*
ZcucGR94a	91	Partial	2e-56	XP_011178240.1; GR94a; *Zeugodacus cucurbitae*
IRs				
ZcucIR8a	950	Full	0	XP_011186380.1; uncharacterized protein LOC105214572; *Zeugodacus cucurbitae*
ZcucIR21a	932	Full	0	XP_011183925.1; uncharacterized protein LOC105213077; *Zeugodacus cucurbitae*
ZcucIR25a	940	Full	0	XP_011178452.1; glutamate receptor 3; *Zeugodacus cucurbitae*
ZcucIR31a	97	Partial	2e-54	XP_011194781.1, uncharacterized protein LOC105220077; *Zeugodacus cucurbitae*
ZcucIR40a-1	141; 166	Partial	2e-30; 6e-108	XP_011182177.1; uncharacterized protein LOC105212100; *Zeugodacus cucurbitae*
ZcucIR40a-2	282	Partial	0	XP_011212457.2; uncharacterized protein LOC105232474; *Bactrocera dorsalis*
ZcucIR41a	336; 302	Partial	0; 0	AKI28986.1; IR41a; *Bactrocera dorsalis*
ZcucIR64a	131; 641	Partial	2e-79; 0	XP_011180795.1; uncharacterized protein LOC105211160; *Zeugodacus cucurbitae*
ZcucIR75a-1	166; 481	Partial	4e-87; 0	XP_011180343.1; uncharacterized protein LOC105210861; *Zeugodacus cucurbitae*
ZcucIR75a-2	73; 205; 206	Partial	5e-32; 4e-143; 5e-143	XP_011180358.1; uncharacterized protein LOC105210866; *Zeugodacus cucurbitae*
ZcucIR75d	751	Partial	0	XP_011186430.1; uncharacterized protein LOC105214604; *Zeugodacus cucurbitae*
ZcucIR76a	660	Full	0	XP_011180078.1; uncharacterized protein LOC105210679; *Zeugodacus cucurbitae*

ZcucIR76b	661	Full	0	XP_011180180.1;glutamate receptor ionotropic, delta-1; *Zeugodacus cucurbitae*
ZcucIR84a	703	Partial	0	XP_011193628.1; glutamate receptor 1; *Zeugodacus cucurbitae*
ZcucIR85a	77	Partial	6e-37	XP_017489388.1; uncharacterized protein LOC108377629; *Rhagoletis zephyria*
ZcucIR92a	111; 101; 57; 244	Partial	1e-41; 2e-61; 8e-31; 2e-175	XP_011184367.1; uncharacterized protein LOC105213333; *Zeugodacus cucurbitae*
ZcucIR93a	49; 100; 177; 68; 129	Partial	8e-25; 1e-60; 1e-113; 2e-37; 1e-83	XP_011177762.1; uncharacterized protein LOC105209182; *Zeugodacus cucurbitae*

Table 5. Response properties of OR74a homologs to 1-nonanol.

OR	Response at 100 μM (Mean ± SD)
BdorOR74a	0.202 ± 0.0277 μA
BlatOR74a	0.0424 ± 0.0145 μA
ZcucOR74a	0.0704 ± 0.0051 μA

Fig. 1

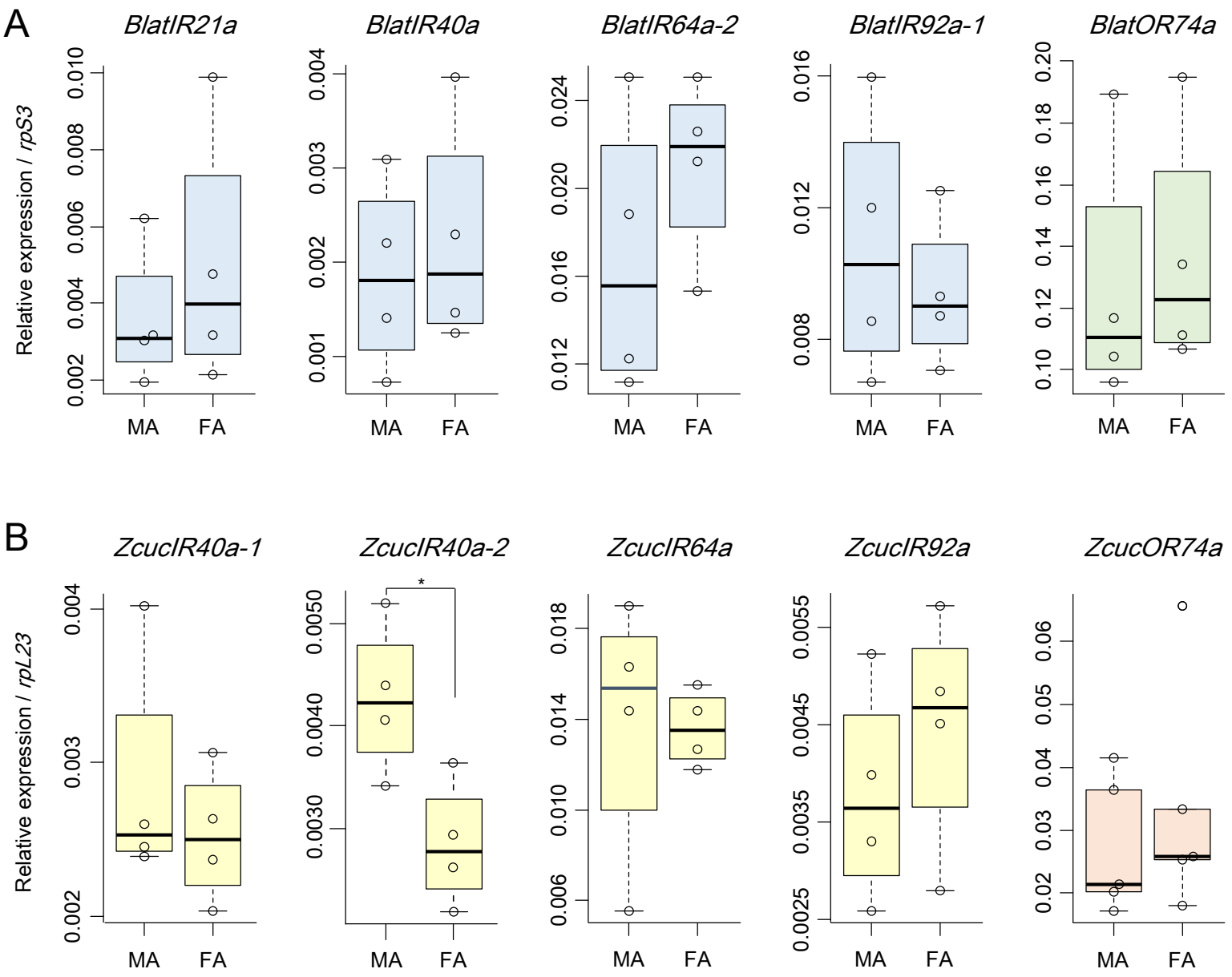

A
BlatIR21a
BlatIR40a
BlatIR64a-2
BlatIR92a-1
BlatOR74a
Relative expression / rpS3
MA
FA
B
ZcucIR40a-1
ZcucIR40a-2
ZcucIR64a
ZcucIR92a
ZcucOR74a
Relative expression / rpL23
*

Fig. 2

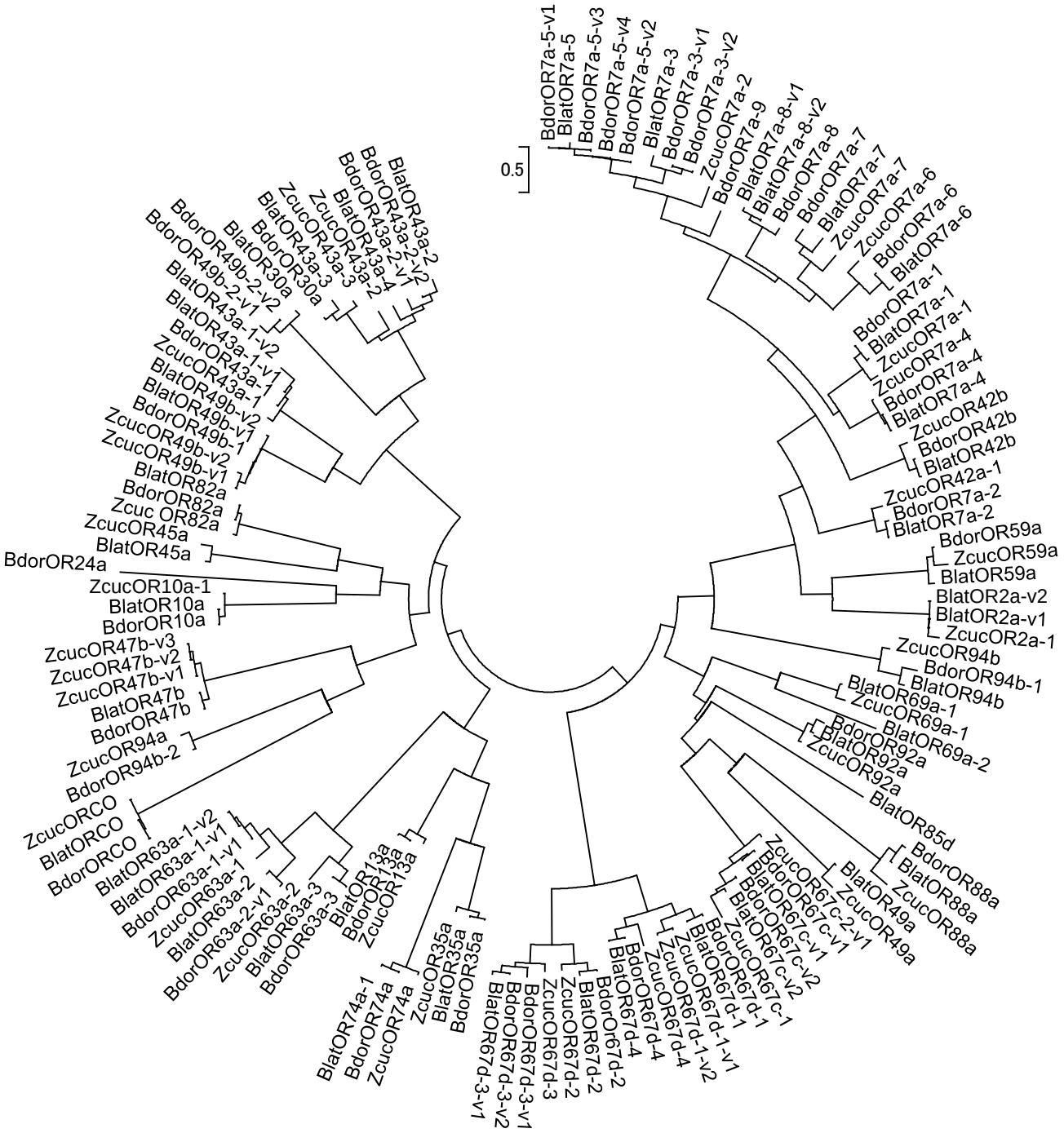
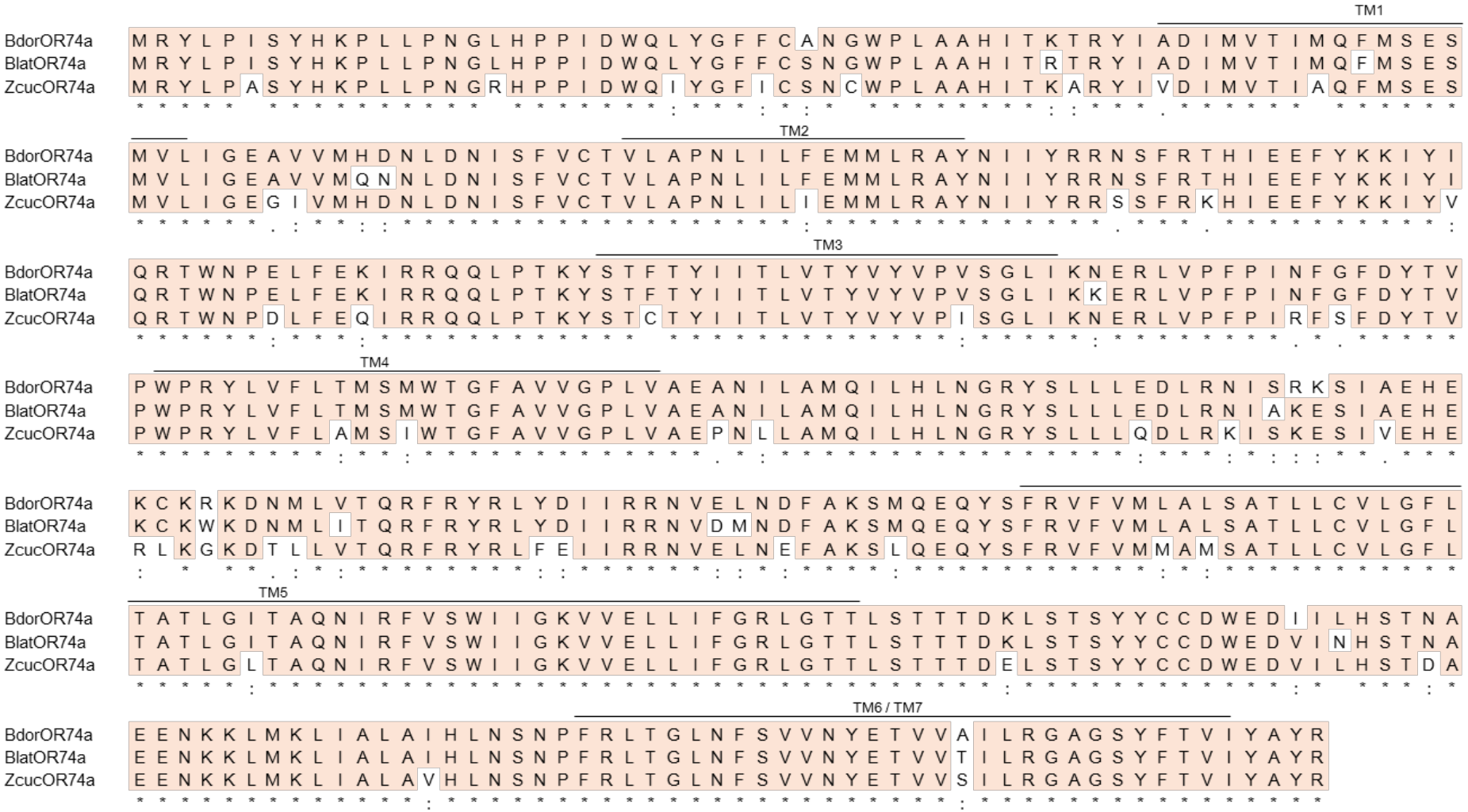

0.5
BdorOR7a-5-v1
BlatOR7a-5
BdorOR7a-5-v3
BdorOR7a-5-v4
BdorOR7a-5-v2
BlatOR7a-3
BdorOR7a-3-v1
BdorOR7a-3-v2
ZcucOR7a-2
BdorOR7a-9
BlatOR7a-8-v1
BdorOR7a-8-v2
BdorOR7a-8
BdorOR7a-7
BlatOR7a-7
ZcucOR7a-7
ZcucOR7a-6
BdorOR7a-6
BlatOR7a-6
BlatOR7a-1
BdorOR7a-1
BlatOR7a-1
ZcucOR7a-1
ZcucOR7a-4
ZcucOR7a-4
BdorOR7a-4
BlatOR7a-4
ZcucOR42b
BdorOR42b
BlatOR42b
ZcucOR42a-1
ZcucOR7a-2
BdorOR7a-2
BlatOR7a-2
BdorOR59a
ZcucOR59a
BlatOR59a
BlatOR2a-v2
BlatOR2a-v1
ZcucOR2a-1
ZcucOR94b
BdorOR94b-1
BlatOR94b
BlatOR69a-1
ZcucOR69a-1
BlatOR69a-2
BdorOR92a
BlatOR92a
ZcucOR92a
BlatOR85d
BdorOR88a
BlatOR88a
ZcucOR88a
BlatOR49a
ZcucOR49a
ZcucOR67c-2-v1
BdorOR67c-v1
BlatOR67c-v1
BdorOR67c-v2
BlatOR67c-v2
ZcucOR67c-1
BdorOR67d-1
ZcucOR67d-1
BlatOR67d-1-v1
ZcucOR67d-1-v2
BdorOR67d-4
ZcucOR67d-4
BlatOR67d-4
BdorOR67d-2
BlatOR67d-2
ZcucOR67d-2
BdorOR67d-3
ZcucOR67d-3
BdorOR67d-3-v1
BlatOR67d-3-v2
BdorOR35a
BlatOR35a
ZcucOR35a
ZcucOR74a
BdorOR74a
BlatOR74a-1
BlatOR13a
BdorOR13a
ZcucOR13a
BlatOR63a-3
ZcucOR63a-3
BdorOR63a-3
BlatOR63a-2
ZcucOR63a-2
BdorOR63a-2
ZcucOR63a-2-v1
ZcucOR63a-1
BdorOR63a-1
BlatOR63a-1-v1
BlatOR63a-1-v2
BdorORCO
BlatORCO
ZcucORCO
BdorOR94b-2
ZcucOR94a
BdorOR47b
BlatOR47b
ZcucOR47b-v1
ZcucOR47b-v2
ZcucOR47b-v3
BdorOR10a
BlatOR10a
ZcucOR10a-1
BdorOR24a
BlatOR45a
ZcucOR45a
ZcucOR82a
BdorOR82a
BlatOR82a
ZcucOR49b-v2
ZcucOR49b-v1
BdorOR49b-1
BlatOR49b-v1
BlatOR49b-v2
ZcucOR43a-1
BdorOR43a-1-v1
BlatOR43a-1-v2
BdorOR49b-2-v1
BlatOR49b-2-v2
BdorOR30a
BlatOR30a
BdorOR43a-3
ZcucOR43a-3
BlatOR43a-3
BdorOR43a-2
BlatOR43a-4
ZcucOR43a-2
BdorOR43a-2-v1
BlatOR43a-2-v2
BlatOR43a-2

Fig. 3



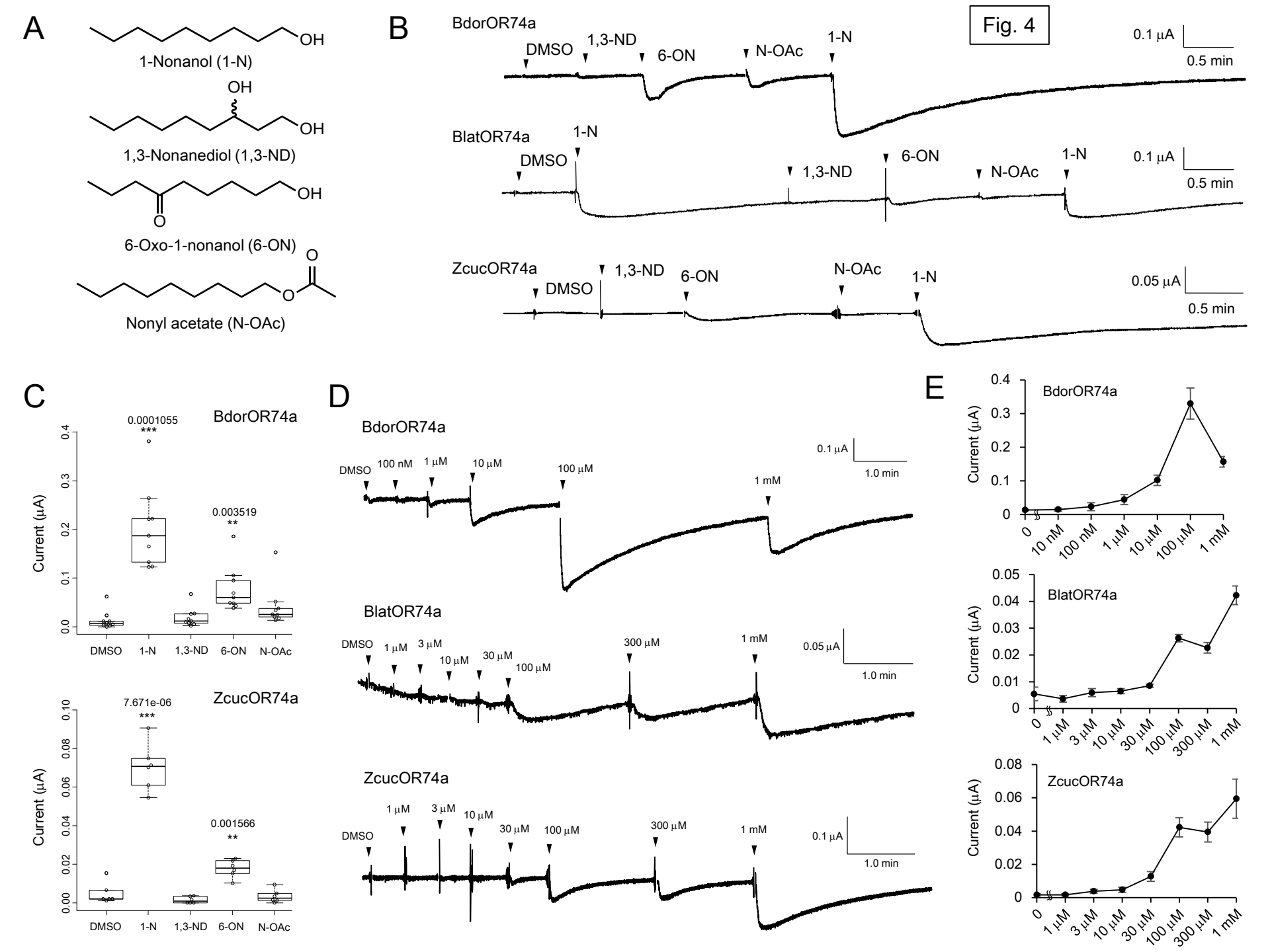
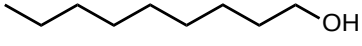
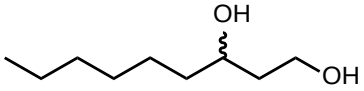


Fig. 4
A
1-Nonanol (1-N)
1,3-Nonanediol (1,3-ND)
6-Oxo-1-nonanol (6-ON)
Nonyl acetate (N-OAc)
B
BdorOR74a
DMSO
1,3-ND
6-ON
N-OAc
1-N
0.1 µA
0.5 min
BlatOR74a
0.1 µA
0.5 min
ZcucOR74a
0.05 µA
0.5 min
C
BdorOR74a
0.0001055
***
0.003519
**
Current (µA)
DMSO
1-N
1,3-ND
6-ON
N-OAc
ZcucOR74a
7.671e-06
***
0.001566
**
D
BdorOR74a
100 nM
1 µM
10 µM
100 µM
1 mM
0.1 µA
1.0 min
BlatOR74a
3 µM
30 µM
300 µM
0.05 µA
ZcucOR74a
E
BdorOR74a
Current (µA)
0
10 nM
100 nM
1 µM
10 µM
100 µM
1 mM
BlatOR74a
3 µM
30 µM
300 µM
ZcucOR74a

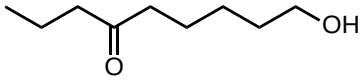
Fig. S1



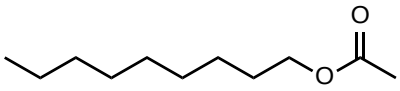
1-Nonanol (1-N)



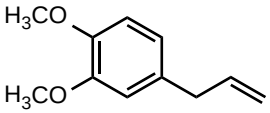
1,3-Nonanediol (1,3-ND)



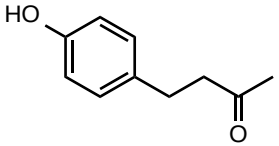
6-Oxo-1-nonanol (6-ON)



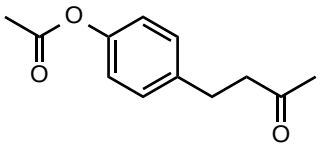
Nonyl acetate (N-OAc)



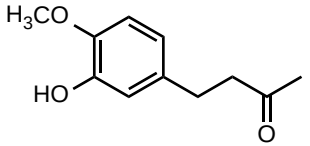
Methyl eugenol (ME)



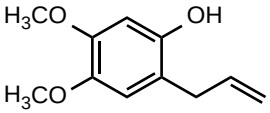
Raspberry ketone (RK)



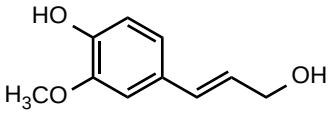
Cue-lure (CL)



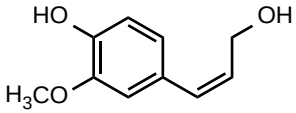
Zingerone (ZN)



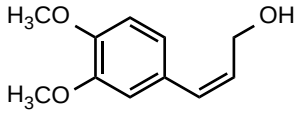
2-Allyl-4,5-dimethoxyphenol (DMP)



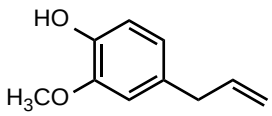
(*E*)-Coniferyl alcohol (CF)



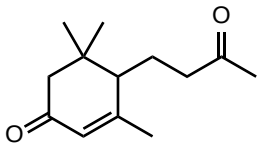
(*Z*)-Coniferyl alcohol (Z-CF)



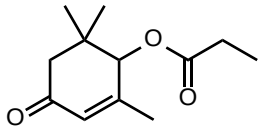
(*Z*)-3,4-Dimethoxycinnamyl alcohol (Z-DMC)



Eugenol (EU)

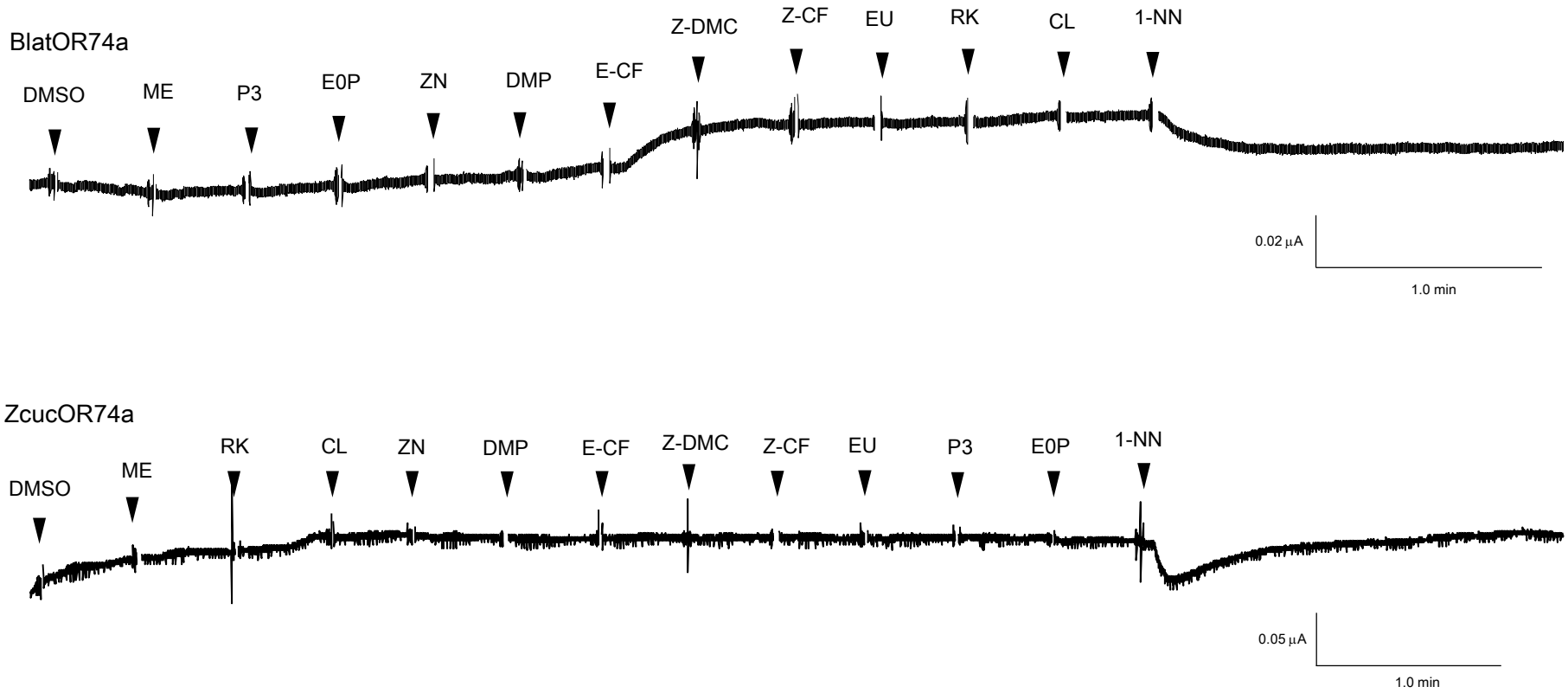


(±)-3-Oxo-7,8-dihydro-α-ionone (P3)



(±)-4-Propionyloxyisophorone (E0P)

Fig. S2


BlatOR74a
DMSO
ME
P3
E0P
ZN
DMP
E-CF
Z-DMC
Z-CF
EU
RK
CL
1-NN
0.02 μA
1.0 min
ZcucOR74a
DMSO
ME
RK
CL
ZN
DMP
E-CF
Z-DMC
Z-CF
EU
P3
E0P
1-NN
0.05 μA
1.0 min