

Supplementary Materials

Identification and Expression Profile of Chemosensory Receptor Genes Based on *Aromia bungii* (Faldermann) Antennal Transcriptome

Zhenchen Wu¹, Jia Ye¹, Jiali Qian¹, Endang Rinawati Purba², Qing-He Zhang³, Longwa, Zhang^{1*}, Dingze Mang^{4*}

¹ Anhui Provincial Key Laboratory of Microbial Control, Engineering Research Center of Fungal Biotechnology, Ministry of Education, School of Forestry & Landscape Architecture, Anhui Agricultural University, Hefei, 230036, China; wuzhenchen8972@163.com (Z.W.); yejia.yj@foxmail.com (J.Y.); qianjiali1995@163.com (J.Q.); zhanglw@ahau.edu.cn (L. Z.)

² Structural Cellular Biology Unit, Okinawa Institute of Science and Technology Graduate University, 1919-1 Tancha, Onna-son, Okinawa, 904-0495, Japan; endang.purba@oist.jp (E.R.P.)

³ Sterling International, Inc., Spokane, WA 99216, USA; qinghezhang2001@yahoo.com (Q.Z.)

⁴ Graduate School of Bio-Applications and Systems Engineering, Tokyo University of Agriculture and Technology, Koganei 2-24-16, Tokyo 184-8588, Japan; mang@go.tuat.ac.jp (D. M.)

*Corresponding authors:

zhanglw@ahau.edu.cn (L. Z.), Tel: 13637082053; mang@go.tuat.ac.jp (D. M.), Tel: +81-080-4375-8788

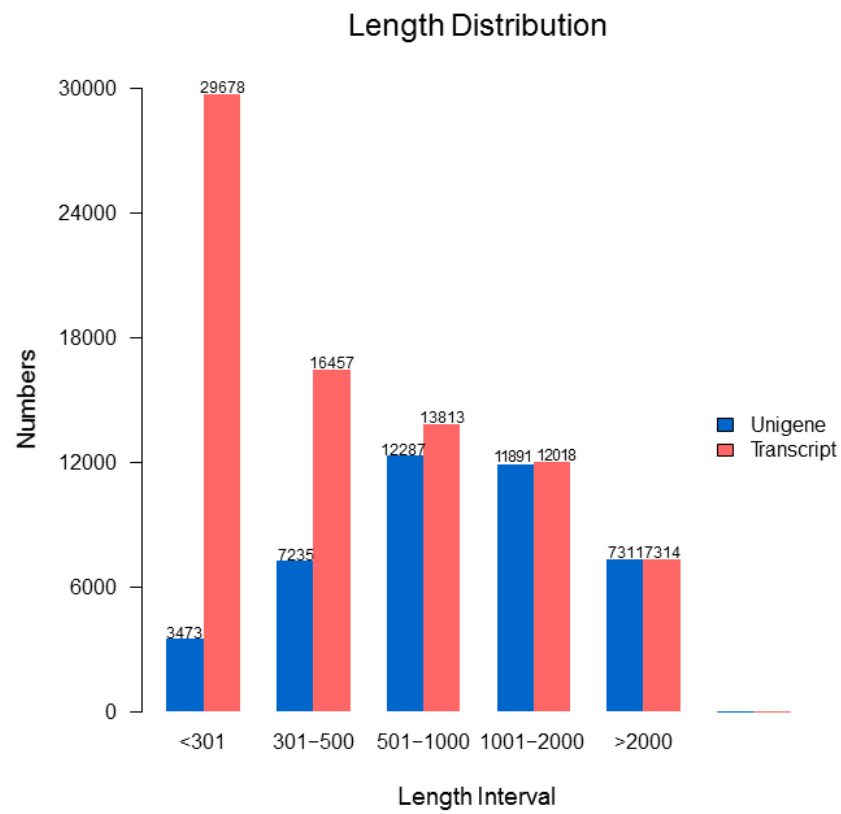


Figure S1. Distribution of Unigenes and Transcripts length interval in the *A. bungii* transcriptome assembly. The abscissa is the spliced transcript/gene length interval, and the ordinate is the number of spliced transcripts/genes at each length.

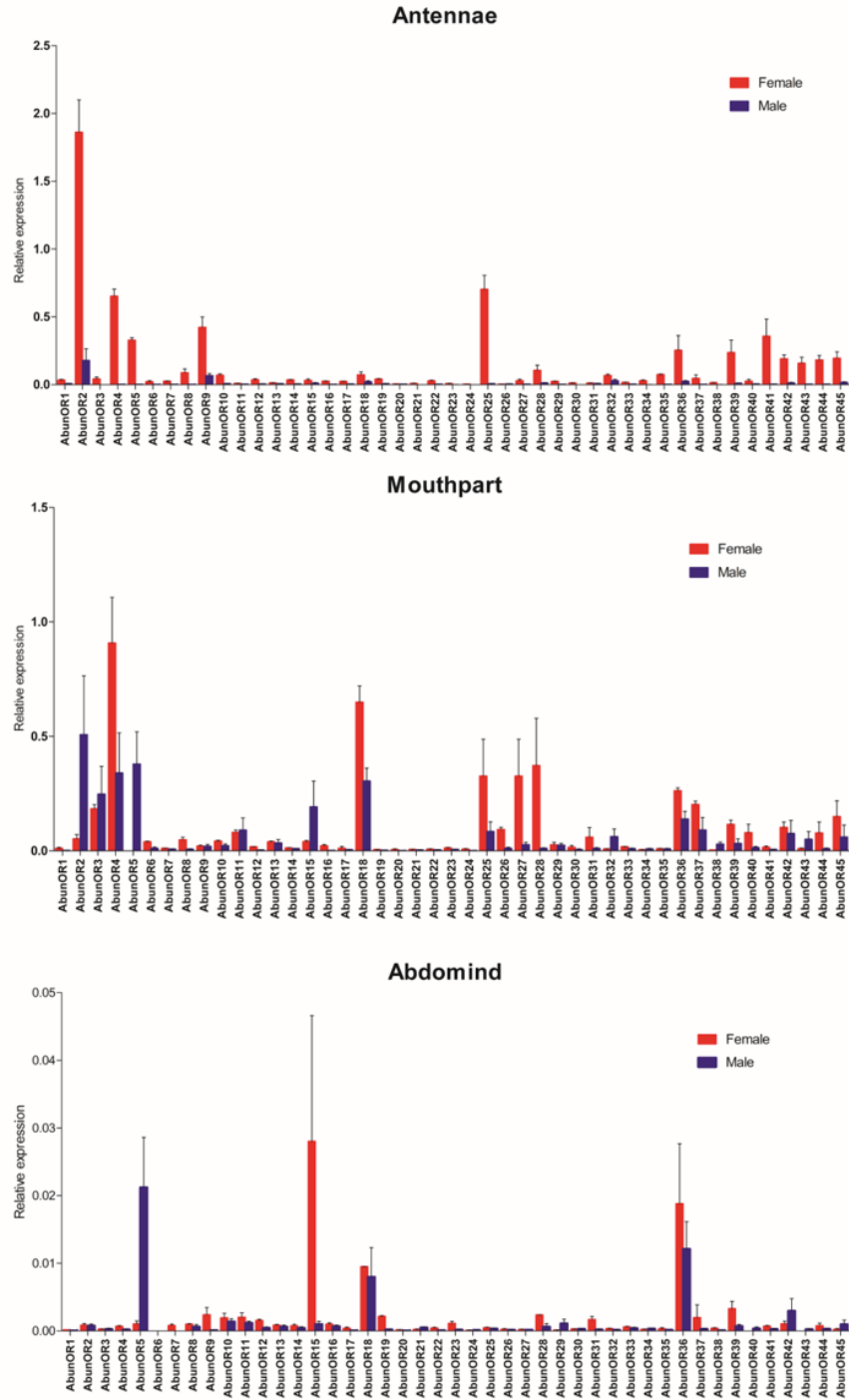


Figure S2. Analysis of the relative expression of 45 AbunORs in female and male tissues. The X-axis represents AbunORs, and the Y-axis represents relative expression. The relative mRNA levels were normalized to those of the actin gene and analyzed using the Q-gene method. All values are shown as mean \pm SEM normalized. The data were analyzed by least significant difference test after one-way analysis of variance. FA: female antennae; MA: male antennae; FM: female mouthpart (maxillary palps and labial palps); MM: male mouthpart (maxillary palps and labial palps); FAb: female abdominal end; MAb: male abdominal end.

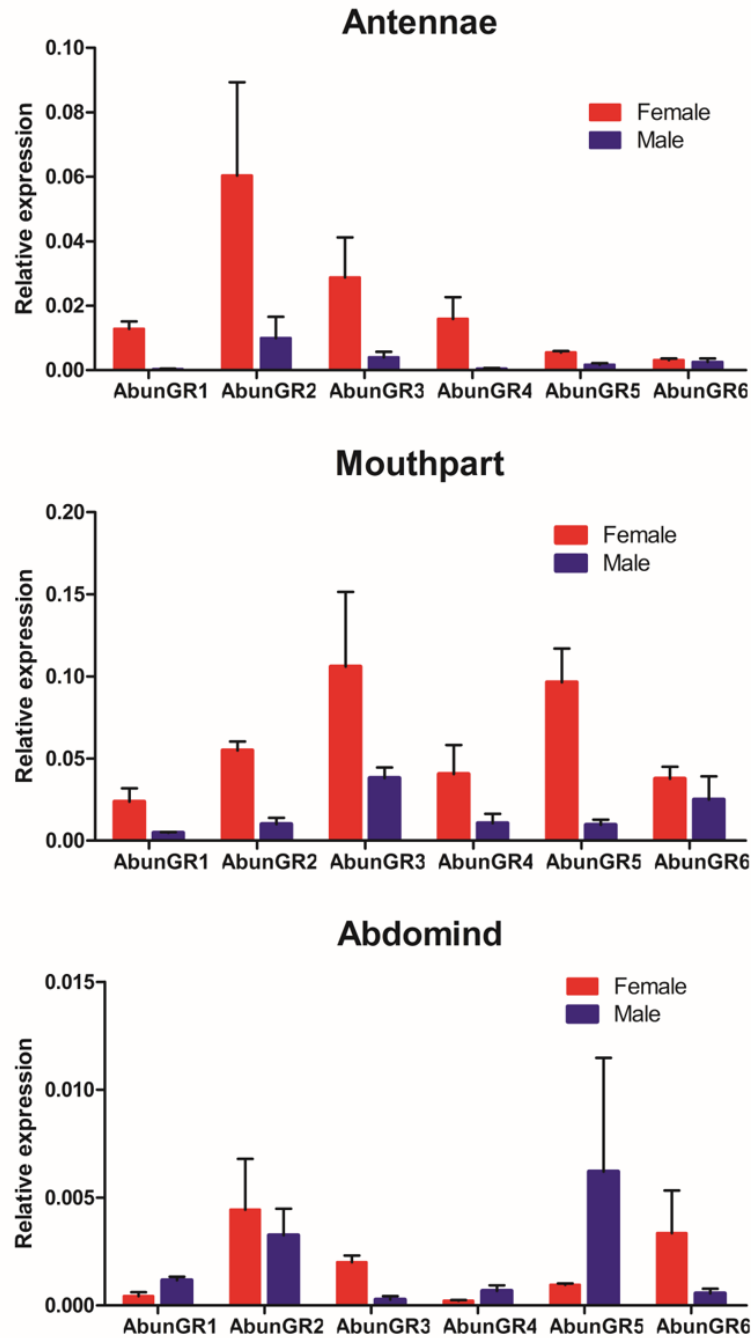


Figure S3. Analysis of the relative expression of 6 AbunGRs in female and male tissues. The X-axis represents AbunGRs, and the Y-axis represents relative expression. The relative mRNA levels were normalized to those of the actin gene and analyzed using the Q-gene method. All values are shown as mean \pm SEM normalized. The data were analyzed by least significant difference test after one-way analysis of variance. FA: female antennae; MA: male antennae; FM: female mouthpart (maxillary palps and labial palps); MM: male mouthpart (maxillary palps and labial palps); FAb: female abdominal end; MAb: male abdominal end.

```

AbunIR2 ----- 1
PstrIR47 -----MRPVLLLLTLFRVITGDQQSVTVDLISDFLLKLNAPTkinahI 43
AcorIR75q FETMISWKYNTLLFTALCITVICSENMEFIEIFKDFLLMQKRPTKVFLYL 50

AbunIR2 ----- 1
PstrIR47 CWPKEEQIALLKRLSSSNFGCRIGNFNINISYSTPAEHQLFLDLSCKGSE 93
AcorIR75q CWPVKEKVLVARYLNKYSFSFQFNTQLKLPIFKKSTEQLFLDLIRCTQYL 100

AbunIR2 ----- 1
PstrIR47 KILNKASELNLFNQPFRLWMGVMDSILDNFIYRLDSRVFIVEKETEDA 143
AcorIR75q NLLYMANLNKLYQQPYRWFLIVNESITLPHFLEILVDSQLYIVQNASPAV 150

AbunIR2 -----MGAPF 5
PstrIR47 YRIESPYKVTEENSLEYSMNVVAEWNRIIGGFSVYRELSYSRNRNLMGLNI 193
AcorIR75q YVSISSLYKISKYSENFVENDVARWSRLRFSYFHPVSAVRNRRTNLLGMPM 200
               : * :

AbunIR2 RVSYPVDFNPDLSNHIYDYRDRHIDTVSKSNYLAVHYMMEAINTEVPPEKI 55
PstrIR47 NISYVVTNKDTMNHLEDYRNKHIDPISKLNWFIMKHLISLLNATST-PLF 242
AcorIR75q NISYVITNNDLSNHLWDYRDKHIDGVSKLNYLSHYIIDAINVSGY-FIV 249
               .:***. * :*:***: ***:***: ** *: : : : : :*: .: 35

AbunIR2 YNTRGYKKRDTD-KYDNMFGDIQRNEIEISGVSSIITAERMKIQEFIHKS 104
PstrIR47 QPSWGYRDNVSTKFTGMTGDLQSGKAFFGGTALFFTIDRIDVIEYIAPS 292
AcorIR75q RSTWGYKNVTTN-LYDGLIGDLQSGLAEEFAGTASFTPDRLIIVDYIAPT 298
               : **: . : : :*: * . *: .: : * *: : :*: :

AbunIR2 FGSHVRFVFRAPLLAYVTNIFTVPFDTYVWYASFVLVAVILLILYVIVRW 154
PstrIR47 VPTFMKFIFRAPPLSYVSNVFTLPFDTYVWYSCFGLVPLIFVVVYVIVWV 342
AcorIR75q TPTRAKFIFRAPPLSYVRNVFTQPFDKMVWYASFLLAVISIIYVIVKW 348
               : :*:***: ***: ***: ***. ***: * *: .: * : :*:***: *

AbunIR2 EWKLFKLDGSGAPVLD-----ENVFDVFVAEFGALTQQGSEAEPRSVS 197
PstrIR47 EWKDPVFKEKVGEMHANCISPLRPSFIDVLVMELGAITQQGTDTEPKSNA 392
AcorIR75q EWSSSKFQNIstkQNV-----MKPKYVDVLLMELSAICQQGSETEPRSGA 393
               ** . : . : . :*: :*: * *: :*:***:***: * 119

AbunIR2 GRTAMLFTFIAFMFLYNACANIIAVLQSTSESIRSPEDLYNSDIAVGAE 247
PstrIR47 GRIATVFAFIACMFLYTSYSANIVAILQSTTESIKTDDLLNSRISLGEV 442
AcorIR75q GQISVIVVFLTFMFLYTSYSANIVALLQSTSDSIQTVDLLNSRIKLGEV 443
               *: : : .:***: ***:***:***:***:***: :* * * * :* * 157

AbunIR2 DIIYSRVFFKAETHPVKKKVDEKLQ-----FMGVEEGVRRVKNEFFA 290
PstrIR47 DIVYAHYYFKTAEPPVRKAIYQOKIAPKGQKPNFMTIEDGMSRVQKGFFA 492
AcorIR75q DKPYSYYYFKIQTEKTRKAIYTQKVAPVGQKPNFMNVEEGIRRMKDEFFA 493
               * *: :** . :*: :*: ** *:***: * :. *** 182

AbunIR2 FHSETTNLFKYIGETFADSDICRLRYLNFLELKFDTFHSVPNRNSTYKELL 340
PstrIR47 FHVEVSNGYKVVDTFQENKCSLKEIAFINL-VEPWVSIKRASPYKEIV 541
AcorIR75q FHVECASGYKIVADIFQSEKCGLEIEYWQI-IDPWWAVKKNSSYKELV 542
               ** * : . : * : : * : : : : : : : : : * .***: 210

AbunIR2 KYTLTRMRRESGIIDCLRRRLFSEEPKCFSGS-FGHVGIVECYAAYKIFA 389
PstrIR47 KVGRLRKILESQIRREINQLYTKKPVCHSKSGNFDASILDCAAFILFG 591
AcorIR75q KVAYRKLHESGIQREYRRLYAKKPIQSRGSGNFISVGFIDCYFPFLIFG 592
               * : : *** . :*:***: ***: * . : : : * : .: 238

AbunIR2 VGIACSVAILLEMLWKKIKEKISSYTDY----- 418
PstrIR47 AGLAVSFLCLTFEILLRKEFKRLMSSNVVLNYPELPNDDELAKSSVY 637
AcorIR75q VGNLITIAVLFIILYKSR-KRFQOKIYI----- 620
               .* : . * :*: * : : : . 249

```

Figure S4. Multiple amino acid sequence alignment of AbunIR2, PstrIR47 and AcorIR75q. The multiple alignment and homology of each IRs were calculated using ClustalW2 (<http://www.ebi.ac.uk/Tools/msa/clustalw2/>).

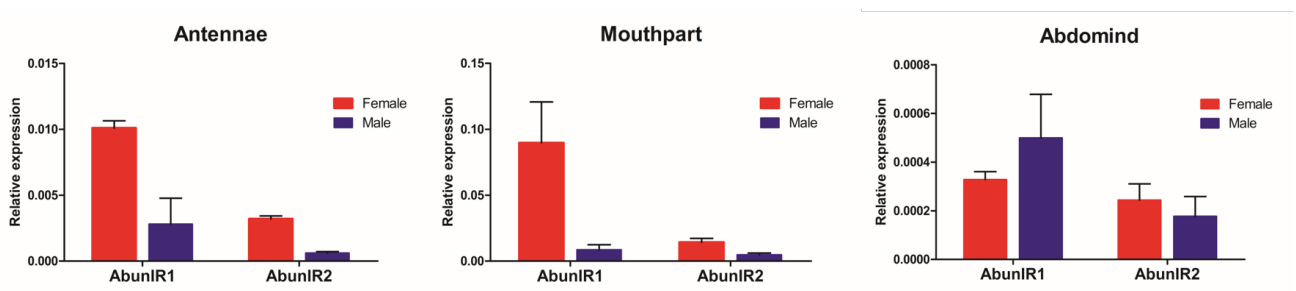


Figure S5. Analysis of the relative expression of 2 AbunIRs in female and male tissues. The X-axis represents AbunIRs, and the Y-axis represents relative expression. The relative mRNA levels were normalized to those of the actin gene and analyzed using the Q-gene method. All values are shown as mean \pm SEM normalized. The data were analyzed by least significant difference test after one-way analysis of variance. FA: female antennae; MA: male antennae; FM: female mouthpart (maxillary palps and labial palps); MM: male mouthpart (maxillary palps and labial palps); FAb: female abdominal end; MAb: male abdominal end.

```

AbunOR25 MMKFKVSGLVADLMPNIRLIQASGHFMLNYHADNSGALHTLRLGYCCIHVLFCLFQYGSIFANLVVEKDD 70
AgerOR25 MMKFKVSGLVADLMPNIRLIQTSGHFMFNYHADNSGALHTLRLAYS CMHLVLFCLFQFGCIFGNLVVEKDD 70
AchiOR1 MMKFKVSGLVADLMPNIRLIQASGHFMFNYHADNSGALHALRLGYSCAHLFLCLFQYGCIFGNLVVEKDD 70
AglaOrco MMKFKVSGLVADLMPNIRLIQASGHFMFNYHADNSGALHALRLGYSCAHLFLCLFQYGCIFGNLVVEKDD 70
*****:*****:*****:***.*.* **:******:*.**.****** 65

AbunOR25 VNELAANTITVLFFAHCITKFIYFAVRSKLFYRTLGIWNQANSHP LFVESNNRYHALALKKMRTLLICVG 140
AgerOR25 VNYLAANTITVLFFTHCITKFIYFAARSKLFYRTLGIWNQNSHP LFVESNNRYHALALKKMRTLLICVM 140
AchiOR1 VNYLAANTITVLFFTHCITKFIYFALRSKLFYRTLGIWNQNSHP LFVESNNRYHALALKKMRTLLICVT 140
AglaOrco VNYLAANTITVLFFTHCITKFIYFALRSKLFYRTLGIWNQNSHP LFVESNNRYHALALKKMRTLLICVT 140
** *****:*****:*** *****:*****:***** 132

AbunOR25 TTTVLSAAAWTGITFVGDSVHNKIDPENENETITEEIPRLLIKSWYPWDAMS GMPYYISLVFIYYVLF 210
AgerOR25 TTTVLSAAAWTSITFVEESVHNKIDPNENETITEEIPRLLIKSWYPWNAMS GMAYYVSLVFQIYYVLF 210
AchiOR1 ATTVLSAAAWTGITFVEESVHNKIDPDNENETITEEIPRLLVKSWYPWDAMS GMAYYGS LFIQIYYVLF 210
AglaOrco ATTVLSAAAWTGITFVEESVHNKIDPDNENETITEEIPRLLIKSWYPWDAMS GMAYYGS LFIQIYYVLF 210
:***:*.***.*** :***:***:*****:*****:*****:*** **.****** 197

AbunOR25 LSHANLMDSLFCSWLIFACEQLQHLKEIMKPLMELSASLD TYVPKSADLFRAPSATSQDNLIENDYNAKN 280
AgerOR25 LSHANLMDSLFCSWLIFACEQLQHLKEIMKPLMELSASLD TYVPKSADLFRAPSAKSQDNYIENDYNTKN 280
AchiOR1 LAHANLMDSLFCSWLIFACEQLQHLKEIMKPLMELSASLD TYVPKSADLFRAPSAKSQDNYIENDYNAKN 280
AglaOrco LAHANLMDSLFCSWLIFACEQLQHLKEIMKPLMELSASLD TYVPKSADLFRAPSAKSQDNYIENDYNAKN 280
*:*****:*****:*****.*** *****:*** 265

AbunOR25 EELNLKGVYNARQELGGHFRTGTLQTFGQGGGVGPNGLSKKQELMVRSAIKYWVERHKKHVRLVTAIGD 350
AgerOR25 EELNLKGIYNTRQELGGNFRSGALQTFGQGGGVGPNGLTKKQELMVRSAIKYWVERHKKHVRLVTAIGD 350
AchiOR1 EELNLKGIYNTRQELGGNFRSGALQTFGQGG--VGPNGLTKKQELMVRSAIKYWVERHKKHVRLVTAIGD 348
AglaOrco EELNLKGIYNTRQELGGNFRSGALQTFGQGG--VGPNGLTKKQELMVRSAIKYWVERHKKHVRLVTAIGD 348
*****:*.***:*****:*.*.***** *****:*****:*****:***** 333

AbunOR25 AYGVALLLHMLTSTVMLTLLAYQATKINGVNTYAASVIGYLVYSLAQVFHFCIFGNRLIESSSVMEAAAY 420
AgerOR25 AYGVALLLHMLTSTVMLTLLAYQATKINGVNTYAATTIGYLVYSLAQVFHFCIFGNRLIESSSVMEAAAY 420
AchiOR1 AYGVALLLHMLTSTVMLTLLAYQATKINGVNTYAATTIGYLVYSLAQVFHFCIFGNRLIESSSVMEAAAY 418
AglaOrco AYGVALLLHMLTSTVMLTLLAYQATKINGVNTYAATTIGYLVYSLAQVFHFCIFGNRLIESSSVMEAAAY 418
*****:*****:*****:*****:*****:*****:***** 402

AbunOR25 SCHWYDGS EEA KTFVQIVCQQCQKAMQISGAKFFTISLDLFASVLGAVVTYFMVLVQLK 479
AgerOR25 SCHWYDGS EEA KTFVQIVCQQCQKAMQISGAKFFTISLDLFASVLGAVVTYFMVLVQLK 479
AchiOR1 SCHWYDGS EEA KTFVQIVCQQCQKAMQISGAKFFTISLDLFASVLGAVVTYFMVLVQLK 477
AglaOrco SCHWYDGS EEA KTFVQIVCQQCQKAMQISGAKFFTISLDLFASVLGAVVTYFMVLVQLK 477
*****:*****:***** ***** ***** 459

```

Figure S6. Amino acid sequence alignment of four known Orcos AgerOR25, AchiOR1, AglaOrco from Cerambycidae and AbunOR25 from *A. bungii*. The multiple alignment and homology of each ORs were calculated using ClustalW2 (<http://www.ebi.ac.uk/Tools/msa/clustalw2/>).


```

AbunOR5  MSSNVKLQYFKKHLKWLKILGIDIEPVKQVWYAQIYRAYAVTLLSYLYLYSFLELIDIIQ 60
McarOR3   MSQKVDLPQYFKKHLKWLTLGLGIDIPIEKVWYAIPYKLYAFVLLVYVLYSLLEIIDIVK 60
          *:.*. *****. ***** *:***** *: *.** *:*****:*.***:.* 48

AbunOR5  SPDFNSMTFGLSYFVTHIIGGAKITILALKKPRFRQMFLESGSFAPNMERGGDEEFRL 120
McarOR3   SSDFNSMTFGLSYSVTHILGAAKITILILKKKILRDMILIRLEQGYFVPNKARGGEKEQQL 120
          *.***** *****:*.***** *** :*:.*:.*.* *.* ** *:.*:.* :* 96

AbunOR5  VKAAVRRTNIHADVFNTFVWLIIGIRSLYAVFDKGAVATYYDKGLNITVSRQVRTLPYKA 180
McarOR3   VNASVIRANLHADIFNTLVYLIIGIRCLYAFDKGVYVEVLDEKLNVTTLKHIRTLPYKA 180
          *:.*.* *:.*:***:***:*.*****.***:*****. . *: **.* :.:***** 145

AbunOR5  WSPVDLNEPAYEIMFAIQTSCLLLYGFIYGFGLDSIVYGMMIHMNTQYLLLRHLLSRYP 240
McarOR3   WLPVDLNKSPAYEFMFIIQASCLVLYGYYIGFLDSLIIYGMMIHMNNQYLIILRNILEHYVE 240
          * *****:*****:.* **:*.*:***:*****:.* *****:.*.*:.*:.* 200

AbunOR5  IAKKIALN-NRENVQDELS-ESIKLPEGIEKTIILGDPLQKIIKRIVHYSAEYHIEILKY 298
McarOR3   LAKNIVLNRPNSVTDDTSTDYIKLHNGIERQKTLAGPVLVDVIENIAYHCAKYHLAIDY 300
          :*:.*.* * :.* *: * : *** :***: *.** :.*.*:.*:.*:.*:.*:.*:.* 239

AbunOR5  CDQIESEFSYLMLLQFLCSLYILCFQLYQLSLVTNYLSFDSISMCLYLFMSYQLICYCW 358
McarOR3   CDDIEKEFSNLMLLQFLSSLYILCFQLFQLSLVTNYFSFDCISMCLYLILMMYQLFCYCW 360
          **:.*.*** *****.*****:*****:***.*****:.* ***:***** 294

AbunOR5  YGNEVVVQSSEFSSYLYNTEWLLFNDSTRKSLLMMMRQRPTIFTAGKFAILSMETYIA 418
McarOR3   YGNAVMIQSLDISSVIYNTDWLVNTESTKKCLLLMMMRQRPIIFTAGKFAFLSLPTYMA 420
          *** *:.*:.* :.* *:***:***: *:***:*.*****:*** *****:.*: **.* 347

AbunOR5  IVRGSASYFMVLKQMAR 435
McarOR3  IVRGSASYFMVLQQMQ- 436
          *****:.*

```

Figure S8. Amino acid sequence alignment of AbunOR3 and McarOR3 (Mcar, *M. caryae*). The multiple alignment and homology of each ORs were calculated using ClustalW2 (<http://www.ebi.ac.uk/Tools/msa/clustalw2/>).

McarOR20	SIK ^{NH} Y ^Y Y ^H I ^L D ^L M ^A I ^M I ^S M ^F T ^T Y ^S F ^S I ^V F ^F F ^N I ^K S ^A V ^R L ^Y M ^T L ^S D ^F E ^D H ^G K ^P R ^N F ^D K ^R T	120
AbunOR37	-----	1
McarOR20	KLIDK ^V V ^T Y ^Y Y ^I Y ^I E ^F L ^I I ^F M ^L S ^T S ^N V ^S S ^G K ^C K ^K K ^N K ^K Y ^C L ^N E ^V C ^G L ^F S ^Y T ^W M ^P F ^E I ^D Y	180
AbunOR37	-----M ^N V ^L K ^N E ^R Q ^C E ^R E ^N L ^E Y ^N F ^H E ^V C ^G L ^A M ^Y T ^W L ^P F ^D I ^D Y	37
	. : . . . : * : : * : * : : * * * * * * * * * * : * * : * * *	
McarOR20	Y ^P V ^K Q ^I Y ^T T ^I C ^Q L ^V G ^T H ^Y L ^I I ^L A ^G V ^V S ^C L ^M A ^E T ^M E ^Q I ^I T ^R I ^H H ^A R ^Y L ^F L ^E A ^I K ^E K ^D Y ^A K ^Q R	240
AbunOR37	F ^P A ^K Q ^I Y ^L S ^F Q ^F F ^G I ^H L ^F A ^V M ^G I ^A A ^W S ^A M ^E T ^V Y ^H V ^I I ^R H ^A K ^H L ^F L ^E A ^I N ^E E ^N Y ^Q R ^Q R	97
	: * . * * * * * * : * . * * * : : * : : . * * : : * * * : * * : * * * * * : * : * : * *	70
McarOR20	Q ^M F ^N T ^A V ^R Y ^H I ^G V ^L D ^L E ^D P ^L N ^E T ^Y G ^F F ^M L ^T H ^L A ^M T ^A P ^I I ^G T ^A L ^Y S ^I L ^Y G ^G S ^G S ^S T ^F I ^C L ^G	300
AbunOR37	E ^K F ^N L ^A V ^R Y ^H E ^S V ^L R ^L E ^D L ^L N ^E T ^F G ^V F ^M F ^T H ^L A ^I T ^A P ^I L ^G T ^G L ^F G ^L L ^H A ^G S ^I S ^S L ^L L ^A I ^G	157
	: * * * * * * * . * * * * * * * : * . * * : * * * : * * * : * * : * * . * : : . * * * * : : : *	117
McarOR20	W ^F I ^G V ^M K ^D C ^C C ^G Q ^R L ^S Q ^S N ^T V ^P I ^A I ^Y D ^S E ^W Y ^T C ^N E ^E I ^K K ^D I ^L F ^V L ^M R ^C R ^R E ^P M ^Y P ^K A ^I S ^F	360
AbunOR37	W ^F F ^G V ^T V ^G C ^L S ^G Q ^R L ^E N ^E S ^L S ^V A ^T T ^I Y ^N S ^P W ^Y N ^C S ^K D ^L R ^R D ^I V ^I V ^L M ^R C ^R R ^E P ^M Y ^L K ^A A ^S F	217
	* * : * * . * . * * * : : * : * . : * * : * * * : * * : * * : * * * * * * * * * * * * * * * * * *	163
McarOR20	G ^V L ^D H ^V M ^F L ^G V ^V K ^A A ^Y S ^Y I ^A L ^L S ^Q T ^T	386
AbunOR37	G ^I M ^N H ^V M ^L L ^G I ^L K ^G S ^Y S ^Y I ^T L ^L A ^Q --	241
	* : : . * * * : * * * : * : * * * : * * * * * *	186

Figure S10. Amino acid sequence alignment of McarOR3 (Mcar, *M. caryae*) and AbunOR37. The multiple alignment and homology of each ORs were calculated using ClustalW2 (<http://www.ebi.ac.uk/Tools/msa/clustalw2/>).

Table S1 Primers of *A. bungii* chemosensory receptor genes used for RT-qPCR

Gene name	Forward primer (5'-3')	Reverse primer (5'-3')
Odorant receptors (ORs)		
<i>AbunOR1</i>	CAAGAGTAAGAAGATACCATAT	AGCATTGTGTAGTAGGAA
<i>AbunOR2</i>	TATGATACTGATGGAGAG	ACTGCTAACAATGAATAC
<i>AbunOR3</i>	CTAGTCTTGACATAGGT	AATAGGTAGTTGAGAATAGC
<i>AbunOR4</i>	ATTACCAGCACAACTTCT	ACTCCTTATCATCATTAGCA
<i>AbunOR5</i>	CAGATATGTTCCGATTGCTAAG	CCAGTATAATTGTCTTCTCTATGC
<i>AbunOR6</i>	GACGAGACCTCTACAATA	GAGTAACACCAGTAACAC
<i>AbunOR7</i>	CTTCGTGTCAGAACTTATAC	CATTATCTCGTTGGCATACT
<i>AbunOR8</i>	CAGAGGAGAATGGATGAGAA	CGTGAACAAGAAGGTTAGC
<i>AbunOR9</i>	CCGAGAAGGACATCCAAGT	AACAAGGTAATAGGCATCAACAG
<i>AbunOR10</i>	GGTATGCTCATTCTCCCAAAC	CGCCAAACACGATTCCAA
<i>AbunOR11</i>	CCGTCTGGAAGTATCAACTAT	TCTGGTGAAGCAAGGTAAG
<i>AbunOR12</i>	AATCCTTCGGCGTTAGTG	TGAACAGTTAGATAATCAGCATTG
<i>AbunOR13</i>	GGAAGTATAATAATGATGA	TAGAATAGCAACTCTTGA
<i>AbunOR14</i>	ATGTCTTTGGAAATGGCCTTAA	GAAGTGAAGCCTGCTGAAG
<i>AbunOR15</i>	TTAGTATTGCTGGAATGAC	TATGAAGTGGTCGTTATTAC
<i>AbunOR16</i>	CGTCTACCGTTAGTGGATTG	CACCGCAGCAGTAGTTAC
<i>AbunOR17</i>	CTGTTACTATTATCTGTATGACT	AATATGTGGTGAAGTATGC
<i>AbunOR18</i>	GTTTATGACATTCCTTGGTTGCGTA	CGAGTTCTGGGTCGTCGTCAT
<i>AbunOR19</i>	TCAATAATGCTGCTTGTATA	ATAACCTGTGCTGGAATA
<i>AbunOR20</i>	TCTGTGGCTATTGTATCT	GGTTCTGCTGTAGTTAAG
<i>AbunOR21</i>	CGTGAGCCAGTTCAGAGTA	ATGTCTCGTTCGCCCTCA
<i>AbunOR22</i>	AAGAGACTACGGCAATAG	AGTGAGATACGAGTAAGAC
<i>AbunOR23</i>	GGCAATTCCATATACTGTCAT	GACTCCTTATCAACATTATCAGA
<i>AbunOR24</i>	ATCCTGATGGTATTCTTC	GATGTCCTTAGTCTTGTCT
<i>AbunOR25</i>	GAAGAAGCAGGAAGTCAAT	TCACCAATAGCAGTAACAA
<i>AbunOR26</i>	CCAGAAGGAGGTTATGAA	TACAAGCAAGAAGAAGGT
<i>AbunOR27</i>	TTAGACGAGACAAGTTCAA	CATCATTATCAGTAAGCAAGT
<i>AbunOR28</i>	CTGATATAACCATACCAATAGA	CTGCTTCATCGTAAGTAAT
<i>AbunOR29</i>	ATATGAAGGTGAATGGTA	CTAATGTGACTAATGAGAG
<i>AbunOR30</i>	TATTCGTCACCACTATCC	TTCTCATACCACTTACTC
<i>AbunOR31</i>	TAATAACGACGACTTCAA	AACAATACATCATAACATCC
<i>AbunOR32</i>	AGAAGGACCGATAAGTATGAGTA	TGTAGATGAAGAGGCTTGTG
<i>AbunOR33</i>	TGAAGATATGTGCGAGTC	AGATTGTAACCGTTGATGA
<i>AbunOR34</i>	ACTTACCTCTGTGTTATACTCTTG	GCTCTTGCCTATATCCATACTC
<i>AbunOR35</i>	CGGTAAGGAGGATAGACA	AATTCAGAGCGGATTCAAT
<i>AbunOR36</i>	ATAGGTTACGGTTATTATAGG	AACATTCACTGGTAACATAT
<i>AbunOR37</i>	CTGTTGGCTGTCTTAGTG	AAGGGCTGTTGTAAATTGT

<i>AbunOR38</i>	ATGCTCGTCCACATAACC	ATTGAAGTAGTTCGTCTCCAT
<i>AbunOR39</i>	AGGTAGCCATCTTGTCGG	CCTCGCCCTGGTAACTCT
<i>AbunOR40</i>	TGCCATGTCAACAGTAAG	TGTCAAGTGCCTCTAACG
<i>AbunOR41</i>	CAATGGACCTCTTGCTCG	TATCGTCTTCGTCTGTTGG
<i>AbunOR42</i>	ATCTCCTGTCCCGTGTG	ACCCATTCCCTTGACCCTC
<i>AbunOR43</i>	TTACAGACGCTTGCTAT	AGTCATCAATGTGGGAAC
<i>AbunOR44</i>	CCTGCGTGGTTTCCTTTC	GCCATCAATAGCGGGTTT
<i>AbunOR45</i>	AGTCTGCCAACTCTACATCTTA	CCATCACTGACGGTCTTC
Ionotropic receptors (IRs)		
<i>AbunIR1</i>	TACCAGCCAATGTCAGAT	TGTCTCCTATTTCCGTATGA
<i>AbunIR2</i>	GATGAAGATACAGGAGTT	GTGAATATGTTGGTTACG
Gustatory receptors (GRs)		
<i>AbunGR1</i>	ATTCTGACGATGACTCTTAA	AGGCATCCATTCTTGAAG
<i>AbunGR2</i>	TCCGACGGTTGAGACTAT	CTATCTTGTAGCGATTCTGATAAC
<i>AbunGR3</i>	TTATTCATCACACAACAGA	CATTAGTAGAGGAGCATAT
<i>AbunGR4</i>	TGATACACAAGATAAGCAACCT	GCCATCCGAATAATACATCCA
<i>AbunGR5</i>	CCATATTCGTTAGCATCAT	GTACCAGGATACTCAGAA
<i>AbunGR6</i>	GGTAGATAACAGAACGAA	CATCAGCATAACGAGATA
Endogenous reference genes		
<i>β-actin</i>	CGACTTGACTGACTATCTC	GGTAGTTCGTAGCTCTTC

Table S2 Summary of the gene annotation success ratio

	Number of Unigenes	Percentage (%)
Annotated in NR	25,407	60.21
Annotated in NT	7,292	17.28
Annotated in GO	19,959	47.29
Annotated in KO	12,154	28.8
Annotated in PFAM	19,426	46.03
Annotated in KOG	11,787	27.93
Annotated in Swiss prot	19,226	45.56

Annotated in all Databases	3,337	7.9
Annotated in at least one	28,221	66.87
Total Unigenes	42,197	100

Table S3 Summary of FPKM value

FPKM value	Number of Unigenes
FPKM=0	2,696
FPKM>1	34,667
FPKM>10	8,761