

Supplementary Materials

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

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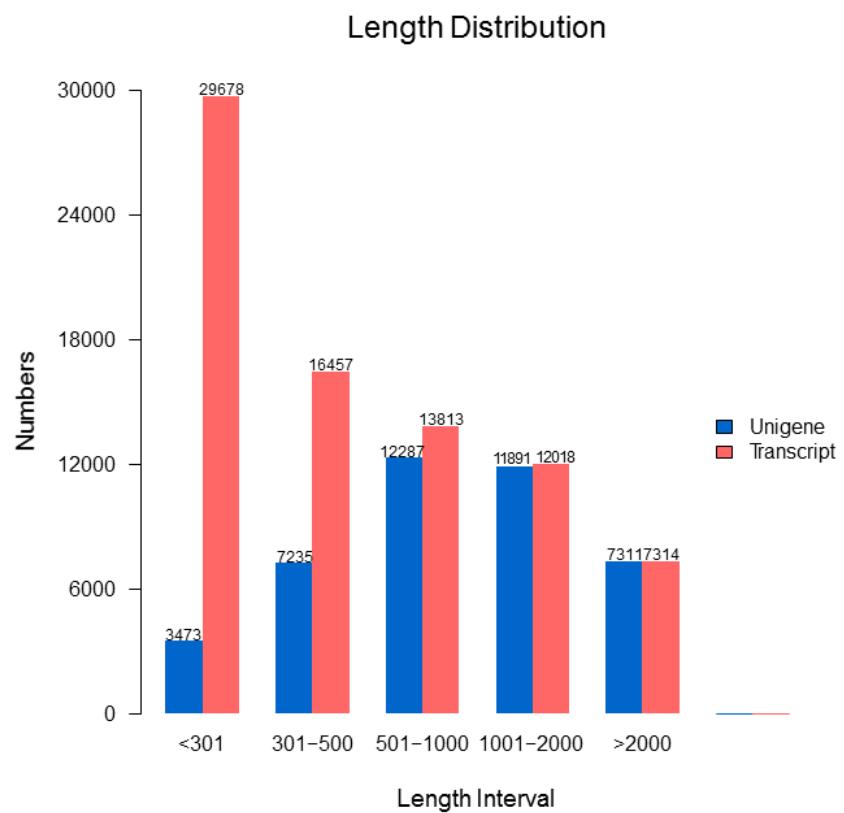


Figure S1. Distribution of Unigenes and Transcripts length interval in the *A. bungii* transcriptome assembly.

The abscissa is the spliced transcript/gene length interval, and the ordinate is the number of spliced transcripts/genes at each length.

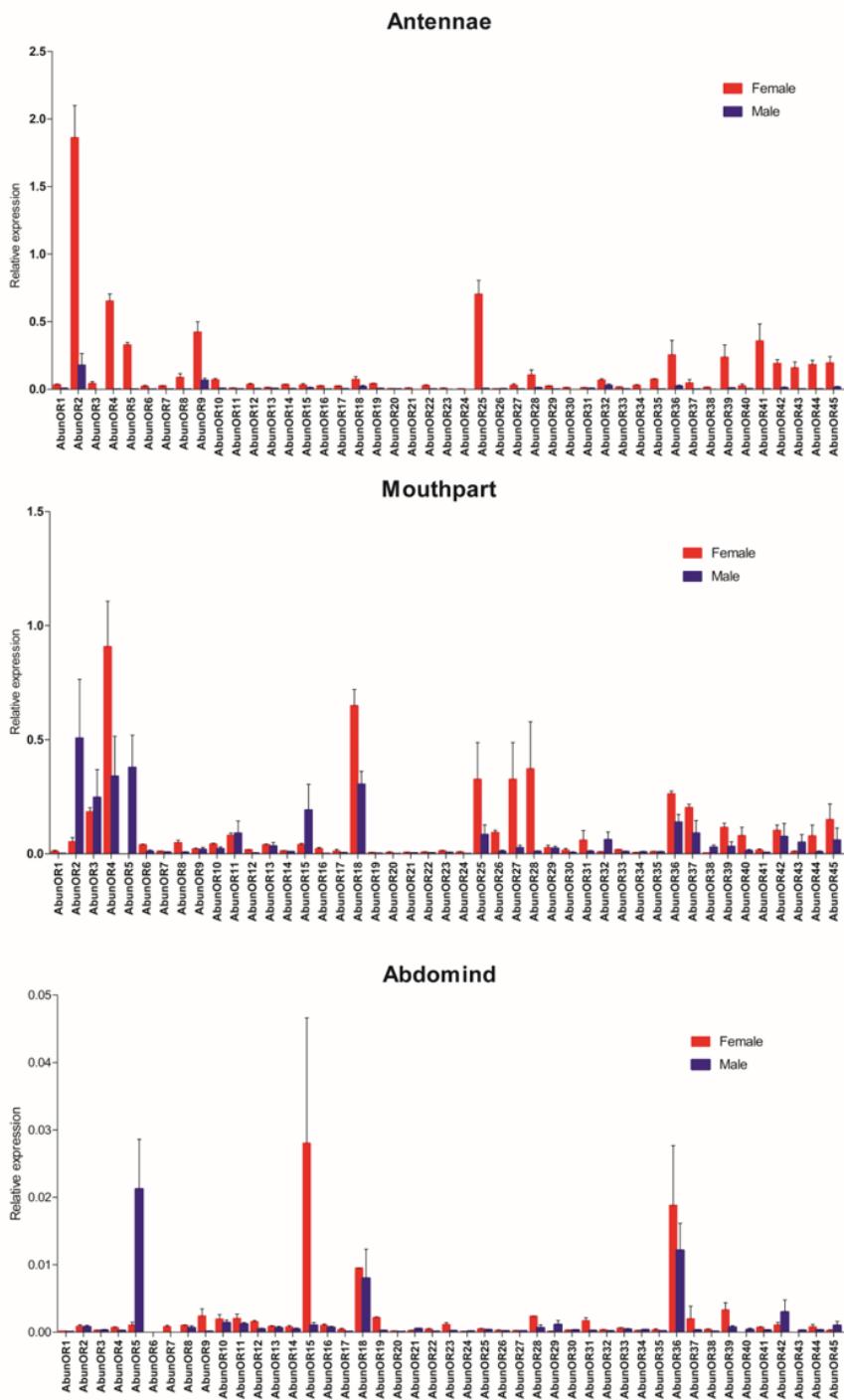


Figure S2. Analysis of the relative expression of 45 AbunORs in female and male tissues. The X-axis represents AbunORs, and the Y-axis represents relative expression. The relative mRNA levels were normalized to those of the actin gene and analyzed using the Q-gene method. All values are shown as mean \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.

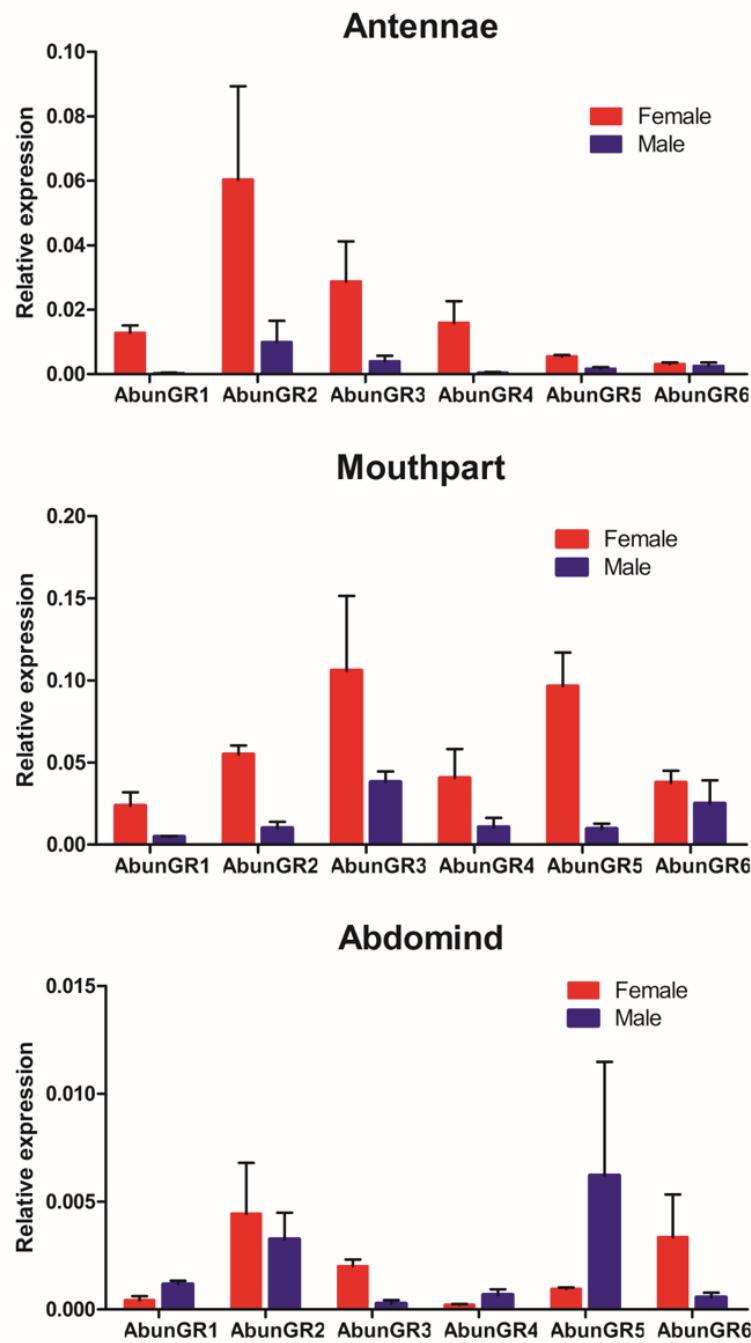


Figure S3. Analysis of the relative expression of 6 AbunGRs in female and male tissues. The X-axis represents AbunGRs, and the Y-axis represents relative expression. The relative mRNA levels were normalized to those of the actin gene and analyzed using the Q-gene method. All values are shown as mean \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	-----	M R P V I L L L T L E R V I T G D Q Q S V T V D L I S D F L L K L N A P T K I N A H I		43
AcorIR75q	F E T M I S W K Y N T L L F T A C I T V I C S E N M E F I E I F K D F L M Q K R P T K V F L Y L			50
AbunIR2	-----	-----	-----	1
PstrIR47	C W P K E E Q I A I L L K R L S S S N F G C R I G N F N N I S Y S T P A E H Q L F L L D L S C K G S E			93
AcorIR75q	C W P V K E K V L V A R Y L N K Y S F S F Q F N T Q L K L P I F K K S T E Q L F L L D I R C T Q Y L			100
AbunIR2	-----	-----	-----	1
PstrIR47	K I L N K A S E L N L E N Q P F R W L M W G V M D R S I L D N F Y I R L D S R V F I V E K T E T D A			143
AcorIR75q	N L L Y M A N L N K L Y Q Q P Y R W F L I V N E S I T L P H F L E I L V D S Q L Y I V Q N A S P A V			150
AbunIR2	-----	-----	M G A P F	5
PstrIR47	Y R I E S P Y K V T E N S L E Y S M N H V A E W N R I G G F S V Y R E L S Y S R N R S N L M G L N I			193
AcorIR75q	Y V I S S L Y K I S K Y S E N F V E N D V A R W S R S L R F S Y F H P V S A V R N R T N L L G M P M			200
 	:	*	:	:
AbunIR2	R V S Y V F D N P D S I L N H I Y D Y R D R H I D T V S K S N Y L A V H Y M M E A I N V T E V P P K I			55
PstrIR47	N I S Y V V T N K D T M N H L E D Y Y R N K H I D P I S K I L N W F I M K H L I S L N A T S T - P L F			242
AcorIR75q	N I S V Y V T N N D S I L N H L W D Y R D K H I D G V S K L N Y I L S H Y I I D A I N V S G Y - F I V			249
 	:	***	:	**
AbunIR2	Y N T R G Y K K R T D - K Y D N M F G D I Q R N E I E I S G V S S I I T A E R M K I Q E F I H K S			104
PstrIR47	Q P S W G Y R D V N D S T K F T G M I G D L Q S G K A E F G G T A L F F T I D R I D V I E Y I A P S			292
AcorIR75q	R S T W G Y K N V T T N - L Y D G L I G D L Q S G L A E F A G T A S F F T P D R L L I V D Y I A P T			298
 	:	**	:	:
AbunIR2	F G S H V R F V F R A P L L A Y V T N I F T V P F D T Y V V W Y A S F V L V A V I L L I L Y V I V R W			154
PstrIR47	V P T F M K F I F R A P P L S Y V S N V F T L P F D T Y V V W Y S C F G L V P L I F V V V V V I V V W			342
AcorIR75q	T P T R A K F I F R A P P L S Y V R N V F T Q P F D K M V W Y A S F L L A V I S I I V V V I V K W			348
 	:	**	:	*
AbunIR2	E W K L F K L D G S A G P V L D ----- E N V F D V F V A E F G A L T Q Q G S E A E P R S V S			197
PstrIR47	E W K D P V F K E K V G E M H A N C I S P L R P S F I D V L V M E L G A I T Q Q G T D E F P K S N A			392
AcorIR75q	E W S S S K F Q N I S T K Q N V ----- M K P K Y V D V L L M E L S A I C Q Q G S E T E P R S G A			393
 	***	:	.	*
AbunIR2	G R T A M L F T F I A F M F L Y N A F C A N I I A V L Q S T S E S I R S P E D L Y N S D I A V G A E			247
PstrIR47	G R I A T V F A F I A C M F L Y T S Y S A N I V A I L Q S T T E S I K T L D D L L N S R I K L G V E			442
AcorIR75q	G O I S V I V V F L T F M F L Y T S Y S A N I V A L L Q S T S D S I Q T V D D L L N S R I K L G V E			443
 	*:	:	**	*
AbunIR2	D I I Y S R V F F K A E T H P V K K K V V D E K L Q ----- F M G V E E G V R R V K N E F F A			290
PstrIR47	D I I V Y A H Y Y F K T A E E P V R K A I Y Q Q K I A P K G Q K P N F M T I E D G M S R V Q K G F F A			492
AcorIR75q	D K P I S Y Y Y F K I Q T E K T R K A I Y T Q K V A P V G Q K P N F M N V E E G I R R M K D E F F A			493
 	*	**	:	*
AbunIR2	F H S E T T N L F K Y I Q E T F A D S D I C R L R Y L N F L E L K F D T H F S V P R N S T Y K E L L			340
PstrIR47	F H V E V S N G Y K V V I A D T F Q E N E K C S I L K E I A F I N L - V E P W V S I K R A S P Y K E I V			541
AcorIR75q	F H V E C A S G Y K I V A D I F Q E S E K C G L R E I E Y W Q I - I D P W M A V K K N S S Y K E L V			542
 	**	*	:	*
AbunIR2	K Y T L T R M R E S C I I D C L R R R L F S E E P K C F S Q G S - F G H V G I V E C Y A A Y K I F A			389
PstrIR47	K V G L R K I L E S C I Q R R E I N Q L Y T K K P V C H S K G S N F D S A S I L D C Y A A F L I G			591
AcorIR75q	K V A Y R K L H E S C I Q R R Y A K K P I C Q S R G S N F I S V G F I D C Y F P F L I G			592
 	*	:	***	**
AbunIR2	V G I A C S V A I L L E E M L W K K I K E K I S S Y T D Y -----			418
PstrIR47	A G L A V S F L C L T F E I L L H R K F K R L M S S N V V L N Y E L P N D D E L A K S S V Y			637
AcorIR75q	V G N L I T I A V L F I E I I L Y K S R - K R F Q Q K I Y I -----			620
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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/>).

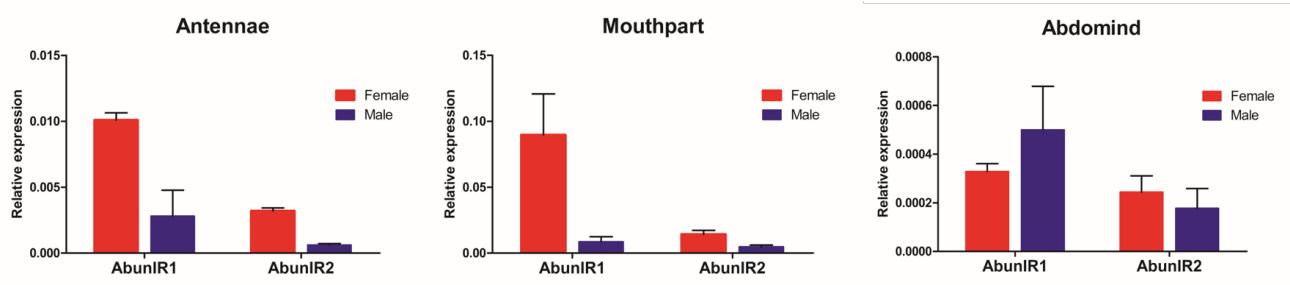


Figure S5. Analysis of the relative expression of 2 AbunIRs in female and male tissues. The X-axis represents AbunIRs, and the Y-axis represents relative expression. The relative mRNA levels were normalized to those of the actin gene and analyzed using the Q-gene method. All values are shown as mean \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	MMKFKVSGLVAIDLMPNIRLIQASGHFMNYADNSGALHTLRLGYCCIHLLVFCLFQYGSIFANLVVEKDD	70
AgerOR25	MMKFKVSGLVAIDLMPNIRLIQTSGHFMNYADNSGALHTLRLAYSCMHLLVFCLFQFGCIFGNLVVEKDD	70
AchiOR1	MMKFKVSGLVAIDLMPNIRLIQASGHFMNYADNSGALHALRLGYSCAHLLFCLFQYGCIFGNLVVEKDD	70
AglaOrco	MMKFKVSGLVAIDLMPNIRLIQASGHFMNYADNSGALHALRLGYSCAHLLFCLFQYGCIFGNLVVEKDD	70
	*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****	65
AbunOR25	VNELAANTITVLFFAHCTKFIYFAVRSKLFYRTLGIWNQANSHPFLFVE SNNRYHALALKMRTLLICVG	140
AgerOR25	VNYLAANTITVLFFTHCTKFIYFAARSKLFYRTLGIWNQSNSHPFLFVE SNNRYHALALKMRTLLICVM	140
AchiOR1	VNYLAANTITVLFFTHCTKFVYFALRSKLFYRTLGIWNQSNSHPFLFVE SNNRYHALALKMRTLLICVT	140
AglaOrco	VNYLAANTITVLFFTHCTKFVYFALRSKLFYRTLGIWNQSNSHPFLFVE SNNRYHALALKMRTLLICVT	140
	:**:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****	132
AbunOR25	TTTVLSAAAWTGITFVGDSVHNICKPDNE NETITEEIPRLLIKSWYPWDAMSGMYYISLVFQIYYVLFS	210
AgerOR25	TTTVFSAVAWTSITFVEESVHNVKDPDNENETITEEIPRLLIKSWYPWNAMSGMAYYSLVFQIYYVLFS	210
AchiOR1	ATTVLSSAAAWTGITFVEESVHNICKPDNE NETITEEIPRLLVKSWYPWDAMSGMAYYGSLIFQIYYVLFS	210
AglaOrco	ATTVLSSAAAWTGITFVEESVHNICKPDNE NETITEEIPRLLIKSWYPWDAMSGMAYYGSLIFQIYYVLFS	210
	:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****	197
AbunOR25	LSHANLMDSLFCSSWLIFACEQLQHLIKEIMKPLMELSASLDTYVPKSADLFRAPSATSQDNLIENDYNACKN	280
AgerOR25	LSHANLMDSLFCSSWLIFACEQLQHLIKEIMKPLMELSASLDTYVPKSADLFRAPSAKSQDNYIEENDYNTKN	280
AchiOR1	LAHANLMDSLFCSSWLIFACEQLQHLIKEIMKPLMELSASLDTYVPKSADLFRAPSAKSQDNYIEENDYNACKN	280
AglaOrco	LAHANLMDSLFCSSWLIFACEQLQHLIKEIMKPLMELSASLDTYVPKSADLFRAPSAKSQDNYIEENDYNACKN	280
	*:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****	265
AbunOR25	EELNLKGVYNARQELGGHFRTGTLQTFGQGGGVGPNGLSKKQELMVRSAIKYWERHKHVVRLVTAIGD	350
AgerOR25	EELNLKGIVNTRQELGGNFRTGALQTEFGQGG--VGPNGLTKKQELMVRSAIKYWERHKHVVRLVTAIGD	350
AchiOR1	EELNLKGIVNTRQELGGNFRTGALQTEFGQGG--VGPNGLTKKQELMVRSAIKYWERHKHVVRLVTAIGD	348
AglaOrco	EELNLKGIVNTRQELGGNFRTGALQTEFGQGG--VGPNGLTKKQELMVRSAIKYWERHKHVVRLVTAIGD	348
	*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****	333
AbunOR25	AYGVALLLHMLTSTVMLTLLAYQATKINGVNTRYAASVIGYLVYSLAQVFHFCIFGNRLIEESSSVMEAA	420
AgerOR25	AYGVALLLHMLTSTVMLTLLAYQATKINGVNTRYAATTIGYLVYSLAQVFHFCIFGNRLIEESSSVMEAA	420
AchiOR1	AYGVALLLHMLTSTVMLTLLAYQATKINGVNTRYAATTIGYLVYSLAQVFHFCIFGNRLIEESSSVMEAA	418
AglaOrco	AYGVALLLHMLTSTVMLTLLAYQATKINGVNTRYAATTIGYLVYSLAQVFHFCIFGNRLIEESSSVMEAA	418
	*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****	402
AbunOR25	SCHWYDGSEEAKTTFVQIVCQQCQKAMSISGAKEFTISLDLFASVLGAVVTVYFMVLVQLK	479
AgerOR25	SCHWYDGSEEAKTTFVQIVCQQCQKAMQISGAKEFTISLDLFASVLGAVVTVYFMVLVQLK	479
AchiOR1	SCHWYDGSEEAKTTFVQIVCQQCQKAMQISGAKEFTISLDLFASVLGAVVTVYFMVLVQLK	477
AglaOrco	SCHWYDGSEEAKTTFVQIVCQQCQKAMQISGAKEFTISLDLFASVLGAVVTVYFMVLVQLK	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/>).

AbunOR25	-MMKFKVSGLVADLMPNIRLIQASGHFMNLHYADNSGALHTLRGYCC1HVFCLFQYGSIFANLVVEKD	69
AgerOR25	-MMKFKVSGLVADLMPNIRLIQTSGHFMNYADNSGALHTLRAYSCMBLVCFLQFGCIFGNLIVVEKD	69
AchiOR1	-MMKFKVSGLVADLMPNIRLIQASGHFMNYADNSGALHALRLGYSCAHLLFCLFQYGCIFGNLIVVEKD	69
AglaOrco	-MMKFKVSGLVADLMPNIRLIQASGHFMNYADNSGALHALRLGYSCAHLLFCLFQYGCIFGNLIVVEKD	69
MaltOR1	-MMKFKVSGLVADLMPNIRLIQASGHFMNYADNSGALHTLRLLYSCMBLVCFLQFGCIFGNLIVVEKD	43
CbowOrco	-MMKFKVSGLVADLMPNIRLIQASGHFMNYADNSGALHTLRLLYSCMBLVCFLQFGCIFGNLIVVEKD	69
McarOR1	-MLKFKVVGLVADLMPNIRLIQASGHFMNYADNSGALHTLRLLYSCMBLVCFLQFGCIFGNLIVVEKD	69
TmolOrco	-MMKFKVSGLVADLMPNIRLIQASGHFMNLHYADNSGAVHTLRLGYCIMBLIFMILLQYGCNFMVLIFERG	69
DponOrco	MINKFVQVGLVADLMPNIRLIQASGHFMNYADNSGLHILRLGYCCMHLFFVLVQYGCIFGNLIVKEKD	70
AcorOrco	-MMQFKPQGLVADLIPNIKLMQPSGHFMNLYYAETTGAVTIQLRGFCFHGLFLQQGFTFGNVLWQQSD	69
*:***:.*:;*; *** . : *:. *.;* * * **: .		
AbunOR25	DVNELAANTITVLFFAHCTIKFIYFAVRSKLFYRTLGIWNQANSHPFLVESENRRYHALALKKMRILLICV	139
AgerOR25	DVNylaantitvlffthc1tkf1yfafvrsklyrtlg1wnqnsnshlpfveesenrryhalalkkmrillicv	139
AchiOR1	DVNylaantitvlffthc1tkfvxfalrsklyrtlg1wnqnsnshlpfveesenrryhalalkkmrillicv	139
AglaOrco	DVNylaantitvlffthc1tkfvxfalrsklyrtlg1wnqnsnshlpfveesenrryhalalkkmrillicv	139
MaltOR1	DVNylaantitvlffthc1tkfvxfalrsklyrtlg1wnqnsnshlpfveesenrryhalalkkmrillicv	113
CbowOrco	NVNDLAANTITVLFFTHC1TKFVYFAVRSKLYRTLG1WNQANSHPFLVESENRRYHALALKKMRILLICV	139
McarOR1	DVNDLAANTITVLFFTHC1TKFVYFAVRSKLYRTLG1WNQANSHPFLVESENRRYHALALKKMRILLICV	139
TmolOrco	DVNDLAANTITVLFFTHC1TKFVYFAAERSKLFRYRTLG1WNQNSHLPFLVESENRRYHALALKKMRILLIVI	139
DponOrco	NVSHLAANTITVLFFTHCLSKFYFAARSKLFRYRTLG1WNQANSHPFLFESNNRHYHALALKKMRSLYII	140
AcorOrco	DVNDLAANTITVLFFTHC1TKFVYFAVRQKLFRYRTLG1WNQNSHLPFLFESNNRHYHALALKKMRILLIVI	139
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AbunOR25	GTTTVLSAAANTGIFTVGDSVHNIKDKOPENETITEEIPRLLIKSWYWPWDAMSQMPYYISLSVFQIYYYVLF	209
AgerOR25	MTTTFVSACVENTITVEEVSVHVKDPPNNEETTEEEIPRLLIKSWYWPWDAMSQMAYYVSVLFQIYYYVLF	209
AchiOR1	TATTVLSAAANTGIFTVEEVSVHNIKDPDNNEETTEEEIPRLLIKSWYWPWDAMSQMAYYGSILFQIYYYVLF	209
AglaOrco	SATTVLSSAAATGIFTVEEVSVHNIKDPDNNEETTEEEIPRLLIKSWYWPWDAMSQMAYYGSILFQIYYYVLF	183
CbowOrco	MATTVLSSASAWIGITFVGDSIHNIKDPDNNEETTEEEIPRLLIKSWYWPWDAMSQSTAYASLIFQIYYYVF	209
McarOR1	GMTTFSASAWIGITFVGDSIHNIKDPDNNEETTEEEIPRLLIKSWYWPWDAMSQMAYYASLVFQIYYYVF	209
TmolOrco	IITWTSFAIATWIGITFVGDSVHNIKDPDNNEETTEEEIPRLLIKSWYWPWDAMSQMPYYITIVFQVYYYYVF	209
DponOrco	LFGTFSASAWTAITFVGDSVHNIKDPDNNEETTEEEIPRLLIKSWYWPWDAMSQMTYVVALVFQIYYYVF	210
AcorOrco	MIGTGSIAWTTITFVGDSDVHTRKDPNNNEETTEEEIPRLLVRWSVYWPWDAMSGAAVYVSVLVQIYYYGF	209
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AbunOR25	SLSHANLMDSSLFCSSWLIFACEQLQHLIKEIMKPLIMELSASDLTYVPKSADLFRAP-SATSQDNLIENDYNA	278
AgerOR25	SLSHANLMDSSLFCSSWLIFACEQLQHLIKEIMKPLIMELSASDLTYVPKSADLFRAP-SAKSQQDNYIEENDYNT	278
AchiOR1	SLABANLMDSSLFCSSWLIFACEQLQHLIKEIMKPLIMELSASDLTYVPKSADLFRAP-SAKSQQDNYIEENDYNA	278
AglaOrco	SLABANLMDSSLFCSSWLIFACEQLQHLIKEIMKPLIMELSASDLTYVPKSADLFRAP-SAKSQQDNYIEENDYNA	278
MaltOR1	SITHANLMDSSLFCSSWLIFACEQLQHLIKEIMKPLIMELSASDLTYVPKSADLFRAP-SAKSQQDNYIEENDYNA	252
CbowOrco	SLABANLMDSSLFCSSWLIFACEQLQHLIKEIMKPLIMELSASDLTYVPKSADLFRAP-SANSQDNLIENDYNA	278
McarOR1	SLSQSNLDDSSLFCSSWLIFACEQLQHLIKEIMKPLIMELSASDLTYVPKSADLFRAP-SATSQDNLIENEYNA	278
TmolOrco	ALSCHANLDDSSLFCSSWLIFACEQLQHLIKEIMKPLIMELSASDLTYVPKSADLFRAP-SATSQDNLIENDYNT	278
DponOrco	SLFQANLDDNLFCSSWLIFACEQLQHLIKEIMKPLIMELSASDLTYVPKSADLFKSPGSATSDHЛИENDFNA	280
AcorOrco	SMLBSNLNDDSSLFCSSWLIFACEQLQHLIKEIMKPLIMELSASDLTYVPKSADLFRAP-SASSQDNLVDSDYNQ	278
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AbunOR25	KNEELNLKGIVNARQELG-GHFRTGTLQTFGGGGGVPNGLSSKQELMVRSAIKYVVERHKHVVRLVTA	347
AgerOR25	KNEELNLKGIVNTRQELG-GNFRTGALQTFQCGQG--GVPGPNGLTKQELMVRSAIKYVVERHKHVVRLVTA	347
AchiOR1	KNEELNLKGIVNTRQELG-GNFRTGALQTFQCGQG--GVPGPNGLTKQELMVRSAIKYVVERHKHVVRLVTA	345
AglaOrco	KNEELNLKGIVNTRQELG-GNFRTGALQTFQCGQG--GVPGPNGLTKQELMVRSAIKYVVERHKHVVRLVTA	345
MaltOR1	KNEELNLKGIVNTRQELG-INFRTGALQTFQCGGGGVPNGLSSKQELMVRSAIKYVVERHKHVVRLVTA	319
CbowOrco	KNEEINLKGIVNTRQELG-INFRTGALQTFQCGGGGVPNGLSSKQELMVRSAIKYVVERHKHVVRLVTA	347
McarOR1	KNEEINLKGIVNTRQELG-INFRTGALQTFQCGGGGVPNGLSSKQELMVRSAIKYVVERHKHVVRLVTA	347
TmolOrco	KNEE--DLKGIVYSTROELGNLNFRSgalQTFQGGGGVGPNGLTKQELMVRSAIKYVVERHKHVVRLVTA	345
DponOrco	KND--DLKGIVYSTROELGNLNFRSgalQTFQGGGGVGPNGLTKQELMVRSAIKYVVERHKHVVRLVTA	348
AcorOrco	SNEDANLRLNLYTTHQEM-VTYRSGNQLQFSSG--GIGPGLSSKQELMVRSAIKYVVERHKHVVRLVTA	345
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AbunOR25	IGDAYGVALLHMLTSTVMTLLLAYQATKINGVNITYAASVIGLVYSLAQVPHCIFGNRLIEESSSVME	417
AgerOR25	IGDAYGVALLHMLTSTVMTLLLAYQATKINGVNITYAATTCIGLVYSLAQVPHCIFGNRLIEESSSVME	417
AchiOR1	IGDAYGVALLHMLTSTVMTLLLAYQATKINGVNITYAATTIGLVYSLAQVPHCIFGNRLIEESSSVME	415
AglaOrco	IGDAYGVALLHMLTSTVMTLLLAYQATKINGVNITYAATTIGLVYSLAQVPHCIFGNRLIEESSSVME	415
MaltOR1	IGDAYGVALLHMLTSTVMTLLLAYQATKINGVNITYAATTIGLVYSLAQVPHCIFGNRLIEESSSVME	389
CbowOrco	IGDAYGVALLHMLTSTVMTLLLAYQATKINGVNITYAATTIGLVYSLAQVPHCIFGNRLIEESSSVME	417
McarOR1	IGDAYGVALLHMLTATVMTLLLAYQATKINGVNITYAASVIGLVYSLAQVPHCIFGNRLIEESSSVME	417
TmolOrco	IGDAYGVALLHMLTSTIMTLLLAYQATKITGVDKYAATSVIGYLFLALAQVPHCIFGNRLIEESSSVME	415
*:***:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:		
AbunOR25	AAYSCHWYDGSEEAKTFVQIVCQQCOKAMSISGAKFFTISLDLFASVLAQVPHCIFGNRLIEESSSVME	479
AgerOR25	AAYSCHWYDGSEEAKTFVQIVCQQCOKAMSISGAKFFTISLDLFASVLAQVPHCIFGNRLIEESSSVME	479
AchiOR1	AAYSCHWYDGSEEAKTFVQIVCQQCOKAMSISGAKFFTISLDLFASVLAQVPHCIFGNRLIEESSSVME	477
AglaOrco	AAYSCHWYDGSEEAKTFVQIVCQQCOKAMSISGAKFFTISLDLFASVLAQVPHCIFGNRLIEESSSVME	477
MaltOR1	AAYSCHWYDGSEEAKTFVQIVCQQCOKAMSISGAKFFTISLDLFASVLAQVPHCIFGNRLIEESSSVME	451
CbowOrco	AAYSCHWYDGSEEAKTFVQIVCQQCOKAMSISGAKFFTISLDLFASVLAQVPHCIFGNRLIEESSSVME	479
McarOR1	AAYSCHWYDGSEEAKTFVQIVCQQCOKAMSISGAKFFTISLDLFASVLAQVPHCIFGNRLIEESSSVME	479
TmolOrco	AAYSCHWYDGSEEAKTFVQIVCQQCOKAMSISGAKFFTISLDLFASVLAQVPHCIFGNRLIEESSSVME	477
DponOrco	AAYSCHWYDGSEEAKTFVQIVCQQCOKSLFISGAKFFTISLDLFASVLAQVPHCIFGNRLIEESSSVME	480
AcorOrco	AAYSCHWYDGSEEAKTFVQIVCQQCOKAMSISGAKFFTISLDLFASVLAQVPHCIFGNRLIEESSSVME	477
*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:*****:		

Figure S7. Amino acid sequence alignment of nine known Orcos and a new Orco (AbunOR25) of *A. bungii* identified in this study. Ager, *A. germari*; Achi, *A. chinensis*, Agla, *A. glabripennis*; Malt, *M. alternates*; Cbow, *C. bowringi*; Mcar, *M. caryae*; Tmol, *Tenebrio molitor*; Dpon, *D. ponderosae*; Acor, *A. corpulenta*. The multiple alignment and homology of each Orco were calculated using ClustalW2 (<http://www.ebi.ac.uk/Tools/msa/clustalw2/>).

AbunOR5	MSSNVKLQYFKKHILKWLIKLGIDIEPVEKVWYAQIYRAYAVTLLSYLYSFILELIDIQ	60
McarOR3	MSQKVDPQYFKKHILKWLTWLGIDIPIEKVWYAIPYKLYAFVLLVYVLYSLIEIIDIVK	60
	.:*. *.*****. ***** *;***** *; *.*.** *;****;**;****;:	48
AbunOR5	SPDFNSMTFGLSYFVTHIIGGAKITILALKPRFRQMFILKLESGSFAPNMRGGDEEFRL	120
McarOR3	SSDFNSMTFGLSYSVTIILGAAKITILILKKILRDMILIRLEQGYFVPNKARGGEKEQQI	120
	*.*****.*****;*.***** *** ;*:***;:***.* *.* ***;*: * :*	96
AbunOR5	VKAADVRRRTNIHADVFNTFWLIIIGIRSLYAVFDKGAVATYYDKGLNITVSQRVTLPYKA	180
McarOR3	VNASVIRANLHADIFNTLVLIIGIRCLYAIIFDKGVYVEVLDEKLNVTTLKHIRTLPYKA	180
	;: * *;*:***;*:***;*:*****.***;***. . *; **:*. :;***** 145	
AbunOR5	WSPVLDLNEPAYEIMFAIQTSCLLLYGFYIGFLDSIVYGMMIHMMNTQYLLLHRHLLSRVYVP	240
McarOR3	WLPVLDLNKSPAYEFMFIQASCLVLYGYYIGFLDSLIYGMMIHMMNNQYLILRNILEHYVE	240
	* *****;*****;** **;***;***;*****;*****;*****;***;*: *.;**	200
AbunOR5	IAKKIALN-NRENVQDELS-ESIKLPEGIEKTIILGDPLQKIIKRIVHYSAEHIEILKY	298
McarOR3	LAKNIVLNRPNSVTDDTSTDYIKLHNNGIERQKTLAGPVLDVIEINIAYHCAKYHLAIIDY	300
	:***;*.** * :.* *; * : *** ;***; *..*; .;*:.*.:.***; *;.* 239	
AbunOR5	CDQIESEFSYLMILQFLCSLYIICFQLYQLSLVTNYLSFDSISMCLYLFLMSYQLICYCW	358
McarOR3	CDDIEKEFSNLMLIQLFSSLYIICFQLFQLSLVTNYFSFDCISMCLYLILMMYQLFCYCW	360
	;.*** *****;*****;*****;***.*****;*** ***;*****;*** ***;****	294
AbunOR5	YGNEVVVQSSEFSSYLYNTEWLLFNDSTRKSILLMMMRQRPTIFTAGKFAILSMETYIA	418
McarOR3	YGNAMVIQSLDISSVIYNTDWLVTNESTKKCILLMMMRQRPIIFTAGKFAFLSLPTYMA	420
	*** *;:*** ;:*** ;***;*: *;***;*.*****;*** *****;***; ***;* 347	
AbunOR5	IVRGSAFYFMVLKQMAR	435
McarOR3	IVRGSAFYFMVLQQMQ-	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/>).

McarOR5	MTDKGYTPHFFRTNEIIIEVYTGAWMYNENLVAPGKKWLLYIWSVLIYIGA	50
AbunOR31	----- MTWDISLIVSA	11
AbunOR29	-----	1
McarOR5	VFFLFLEFLKLRTDMKVSNDFIRQCGLISCHSLCVVKFVILVLRHRKIKR	100
AbunOR31	CIFFVCEILVIKEISDLRQMFHHLG-MLCSHVLDIAKFFVIIQNQERINK	60
AbunOR29	-----	1
McarOR5	LMDTLQDKKYQYEPLG-DFSPGQRFDEARKLTHWCTIGVFCLYSAAVSA	149
AbunOR31	VKGTLQNKLYHYESYGSWFRPGTTFKKSRAFVKFVLICIFSLYYMVGVSA	110
AbunOR29	-----	1
McarOR5	HISAEVLINKDAKRERFDGNITCYEYMTFYFAIPFPSDTKAQCEMSFIFM	199
AbunOR31	MVVVMINFNND---DFKHGSVRCIDLMPYRYKIPFSTTRSSCMYAIIVFM	157
AbunOR29	----- MQYYFYIPFTTETKEQCGYAFLFM	24
	* : : ***.: *: .* :::**	
McarOR5	HFCIDIIYAWFAAGHDSFYAALLNCLRVQVDIILCAFRTIRPRVLRKLELP	249
AbunOR31	VVNIFSHAAHYGCYDVLFSTLLICVKTKLQILNEALRTMKERVLYKMRLP	207
AbunOR29	DISLAIYAWFIACHDGVFVALLNCLRTQLLILGGAFRTIRKRCFKKHNIH	74
	. : :* : . :* . : ** *;::: * * *;*: * : : . :	
McarOR5	QDLSIFHDDDFPKLEEALYRELTHLTELHMILLRVADDLEEVFNLLTQA	299
AbunOR31	KSLDIFRDEEHPAFEAELYNEMRRCAMHLESЛИCNEIESMFTFTTLGQ	257
AbunOR29	EDKLMCYQEHNPELENEIYGELNRCIKHLHILLQTRDDIENTFVYVMLTQ	124
	.. : : ::.* :* : * *: : ** *: : ;::*. * * * 66	
McarOR5	TVSSLIVFASCLFITSTIPLSSPEFFAQVEYFTCMLIELSLFCWFGSAAT	349
AbunOR31	IVTSFIVVASNYMSFAKIPITDPEIFSVVHYTAGVTAQLSMICYFGNEIT	307
AbunOR29	TLVSLFVLASCLYKSSTFPVGSPDFFSQLEYFWCALVQLYVFCWFGNEIT	174
	: *;: *.* : : ..::: .*;: *: :.* : * : ;::*;**. *	
McarOR5	RASEAISPQIYESDWYGTSKRFKQSVLIIMCRMQNPQIYLSIGKFCPLKLD	399
AbunOR31	QVYSSLRSSVYMCNWYASASKRFKQSMIIIMMSRLQKEVYIISIGKFTPLTLA	357
AbunOR29	SASDLIRVSLYEGEWYGASSRFKRSMLITMCRMQRPVYVSIGKFSPSLV	224
	. . : : *: : **. : *.*;: *: * . *: : ;:***** *.*	
McarOR5	TIVMVFKCSFSYYTVFKAVGE	420
AbunOR31	TLVLVFRVGYTYFALFRTE	377
AbunOR29	TLVAVCRGSFSYYTVLKSMK	-244
	; * : . : :* : : :	

Figure S9. Amino acid sequence alignment of McarOR3 (Mcar, *M. caryae*), AbunOR29 and AbunOR31. The multiple alignment and homology of each ORs were calculated using ClustalW2 (<http://www.ebi.ac.uk/Tools/msa/clustalw2/>).

McarOR20	SIKNHVYYHIIDLMAIMISMFTTYSFISIVFFFNIKS	AVRLYMTLSDFDEHGKPRNF	DKRT	120		
AbunOR37	-----	-----	-----	1		
McarOR20	KLIDKVVTYYIYIEFLIIFMLSTS	NVSSSGKCKKKNKKYGLNEVCG	GLFSYTWM	PFEIDY	180	
AbunOR37	-----	MNVILKNERQ	CERENLEYNFHEVC	GLAMYTWLPF	DIDY	37
. . . . :*:::* :*.::***** ***:***:***						
McarOR20	YPVKQIYTICQLVGTHYLIIILAGVV	SCLMAETMEQIITRHHARYLF	LEAIKEKD	YAKQR	240	
AbunOR37	FPAKQIYLSFQFFGIHHLFAVMGIA	AWSAMETVYHVIIIRHAKH	LFILEAINEENY	QRQR	97	
:*,**** *:.** *; : *.: . **: ;: * **:****:*****:*: * : **					70	
McarOR20	QMFTA	VRYHIGVLDLEDPLNETYGF	 FMLTHLAMTAPII	GTA	LYGGSGSSTFICLG	300
AbunOR37	EKFNL	AVRYHESVLRLEDLLNETFGV	FMFTHLAITAPILGTG	LFGLLHAGSISS	LLLAI	157
: * * **** . * * * *; *.*:****:****:****:*. * : * .** * : : .*					117	
McarOR20	WFIGVMKDCCCGQRLQSQSNTVPIAIYDSEWYT	CNEEIKKDILFVL	MRCRRPMY	PKAISF	360	
AbunOR37	WFFGVTVGCLSGQRLENE	SLVATTIYNSPWYNCSKDILRR	DIVIVL	MRCRRPMY	LKAASF	217
:* .* .****:.* :*. :**;* **.*.:::::****:*****:*****:***					163	
McarOR20	GVLDHVMFLGVVKAAAYSYIALLSQTT	386				
AbunOR37	GIMNHVMILLGILKG	SYSYSITILLAQ	--	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>	CAAGAGTAAGAAGATAACCATAT	AGCATTGTGAGTAGGAA
<i>AbunOR2</i>	TATGATACTGATGGAGAG	ACTGCTAACAAATGAATAC
<i>AbunOR3</i>	CTAGTCTGGACATAGGT	AATAGGTAGTTGAGAATAGC
<i>AbunOR4</i>	ATTACCAGCACAACTTCT	ACTCCTTATCATCATTAGCA
<i>AbunOR5</i>	CAGATATGTTCCGATTGCTAAG	CCAGTATAATTGTCCTCTATGC
<i>AbunOR6</i>	GACGAGACCTCTACAATA	GAGTAACACCAAGTAACAC
<i>AbunOR7</i>	CTTCGTGTCAGAACTTATAC	CATTATCTCGTTGGCATAAC
<i>AbunOR8</i>	CAGAGGAGAAATGGATGAGAA	CGTGAACAAGAAGGTTAGC
<i>AbunOR9</i>	CCGAGAAGGACATCCAAGT	AACAAGGTAAATAGGCATCAACAG
<i>AbunOR10</i>	GGTATGCTCATTCTCCAAAC	CGCCAAACACGATTCAA
<i>AbunOR11</i>	CCGTCTGGAACATCAACTAT	TCTGGTGAAGCAAGGTAAG
<i>AbunOR12</i>	AATCCTCGGCGTTAGTG	TGAACAGTTAGATAATCAGCATTG
<i>AbunOR13</i>	GGAACGTATAATAATGATGA	TAGAATAGCAACTCTTGA
<i>AbunOR14</i>	ATGTCTTGAAATGCCCTAA	GAACGTAAAGCCTGCTGAAG
<i>AbunOR15</i>	TTAGTATTGCTGGAATGAC	TATGAAGTGGTCGTTATTAC
<i>AbunOR16</i>	CGTCTACCGTTAGTGGATTG	CACCGCAGCAGTAGTTAC
<i>AbunOR17</i>	CTGTTACTATTATCTGTATGACT	AATATGTGGTGAACATATGC
<i>AbunOR18</i>	GTTTATGACATTCTGGTTGCGTA	CGAGTTCTGGGCGTCGTCAT
<i>AbunOR19</i>	TCAATAATGCTGCTGTATA	ATAACCTGTGCTGGAATA
<i>AbunOR20</i>	TCTGTGGCTATTGTATCT	GGTTCTGCTGTAGTTAAG
<i>AbunOR21</i>	CGTGAGCCAGTTCAGAGTA	ATGTCTCGTTGCCTTCA
<i>AbunOR22</i>	AAGAGACTACGGCAATAG	AGTGAGATACGAGTAAGAC
<i>AbunOR23</i>	GGCAATTCCATATACTGTCAT	GACTCCTTATCAACATTATCAGA
<i>AbunOR24</i>	ATCCTGATGGTATTCTTC	GATGTCCTTAGTCTTGT
<i>AbunOR25</i>	GAAGAAGCAGGAACCTCAT	TCACCAATAGCAGTAACAA
<i>AbunOR26</i>	CCAGAAGGAGGTTATGAA	TACAAGCAAGAAGAAGGT
<i>AbunOR27</i>	TTAGACGAGACAAGTCAA	CATCATTATCAGTAAGCAAGT
<i>AbunOR28</i>	CTGATATAACCATAACCAATAGA	CTGCTTCATCGTAACTAAT
<i>AbunOR29</i>	ATATGAAGGTGAATGGTA	CTAATGTGACTAATGAGAG
<i>AbunOR30</i>	TATTGTCACCACTATCC	TTCCCTCATACCACTTACTC
<i>AbunOR31</i>	TAATAACGACGACTTCAA	AACAATACATCATAACATCC
<i>AbunOR32</i>	AGAAGGACCGATAAGTATGAGTA	TGTAGATGAAGAGGCTTGTG
<i>AbunOR33</i>	TGAAGATATGTGCGAGTC	AGATTGTAACCGTTGATGA
<i>AbunOR34</i>	ACTTACCTCTGTGTTACTCTTG	GCTCTGCCTATATCCATACTC
<i>AbunOR35</i>	CGGTAAAGGAGGATAGACA	AATTCAAGCGGGATTCAAT
<i>AbunOR36</i>	ATAGGTTACGGTTATTATAGG	AACATTCACTGGTAACATAT
<i>AbunOR37</i>	CTGTTGGCTGTCTTAGTG	AAGGGCTGTTGTAAATTGT

<i>AbunOR38</i>	ATGCTCGTCCACATAACC	ATTGAAGTAGTCGTCTCCAT
<i>AbunOR39</i>	AGGTAGCCATCTTGTCCG	CCTCGCCCTGGTAACTCT
<i>AbunOR40</i>	TGCCATGTCAACAGTAAG	TGTCAAGTGCCTCTAACG
<i>AbunOR41</i>	CAATGGACCTCTGCTCG	TATCGTCTTCGTCGTGGG
<i>AbunOR42</i>	ATCTCCTGTCCCCTGTTG	ACCCATTCCCTGACCCTC
<i>AbunOR43</i>	TTACAGACGCTTGCTAT	AGTCATCAATGTGGAAC
<i>AbunOR44</i>	CCTCGTGGTTTCCTTTC	GCCATCAATAGCGGGTTT
<i>AbunOR45</i>	AGTCTGCCAACTCTACATCTTA	CCATCACTGACGGTCTTC
Ionotropic receptors (IRs)		
<i>AbunIR1</i>	TACCAGCCAATGTCAGAT	TGTCTCCTATTCCGTATGA
<i>AbunIR2</i>	GATGAAGATACAGGAGTT	GTGAATATGTTGGTTACG
Gustatory receptors (GRs)		
<i>AbunGR1</i>	ATTCTGACGATGACTCTTAA	AGGCATCCATTCTTGAAG
<i>AbunGR2</i>	TCCGACGGTTGAGACTAT	CTATCTTGTAGCGATTGTATAAC
<i>AbunGR3</i>	TTATTCATCACACAACAGA	CATTTAGTAGAGGAGCATAT
<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
