

Table S1 RT-qPCR quantitative primers of partial ORs.

Gene	Forward primer	Reverse primer
<i>DtarORco</i>	GCACGCAAATCTATTGGACAG	AGCACTCTTCGGAACGTAAG
<i>DtarOR1</i>	GAGCAATTGATTCCACCGGC	TCGCACAATGAGTAACTGCT
<i>DtarOR4</i>	TGTTTCGTCAACTTCCCCGCT	TTCGCTGCGGGATCTCATAC
<i>DtarOR5</i>	ATCACGCCGATATTGTAGCAA	ATCCAATTCGAACCAATCACTTTC
<i>DtarOR7</i>	TGTGTACAGGATGGTTTTGGG	TCCTCACTAAAATCATACCACGG
<i>DtarOR9</i>	ACGTGGCTTCCCTTTGACAT	TTTCGAACACATGCCAAGCC
<i>DtarOR10</i>	TTACCGATGGCAACTTGGCT	TCATTTTCAGCAACACTGGACT
<i>DtarOR12</i>	AATTCGCCCCACTCCAAG	CCATGTGCCTTGAAACTGTG
<i>DtarOR14</i>	AACCCCTTTGATTGGCTACA	ACATGACACCGACGCTTAATG
<i>DtarOR18</i>	GCTCACGCAACAATAACG	ATTCCAACGATGCTGTAAGA
<i>DtarOR20</i>	TGTGATTGGATGAGTGGCAG	AACAGCTACGATGGTACTCAAC
<i>DtarOR22</i>	ACGACATTTTCAGAGTGGTTGGT	TCACCAAACCAGGTGTAGCA
<i>DtarOR23</i>	GACGAAGAAGAAGAGAAGATAC	CAGTGCGAACCAGAGATAA
<i>DtarOR26</i>	TGTTGGATGGCTTTCGGG	CATGGTAAGTCGTAAACTGCG
<i>DtarOR27</i>	AACATTTTCGGTATTTGGACGG	ACATTGTCTCTTGCTTTGTACATG
<i>DtarOR28</i>	TGGTCGTTTACTCGACGCTC	ATAAGATCGCATTGTGCGCC
<i>Tubulin</i>	TCTGCCACTTTCATCGGTAAC	CCATTTTCATCCATACCTTCTCCG

Table S2 PacBio libraries and sequencing results.

cDNA size	Reads of insert	Read bases of insert	Mean read length of inserts	Mean read quality of inserts	Mean number of passes
1-6K	632,484	1,517,111,365	2,398	0.95	14
All	632,484	1,517,111,365	2,398	0.95	14

Tables S3 Summary of sequencing reads after filtering.

cDNA Size	Reads of Insert	Number of filtered short reads	Number of nFL reads	Number of FL reads	Number of FL chimeric reads	Number of FL non-chimeric reads	Average FL non-chimeric read length
1-6K	632,484	14,575	160,159	457,750	9,667	448,083	2,203
All	632,484	14,575	160,159	457,750	9,667	448,083	2,203

Table S4 Summary of functional annotation results.

Annotated databases	number of isoforms
COG	13,877
GO	13,372
KEGG	19,189
KOG	27,408
Pfam	29,758
Swiss-Prot	24,907
eggnoG	45,669
Nr	51,424
All	52,436