



**Fig. S1. Western blot analysis of transformed *S. cerevisiae* cells.** Protein extracts of (A) Nvit\_D12a ( $M_w = 46610$  Da) and (B) Nvit\_D12b ( $M_w = 465247$  Da) and empty vector controls were separated on 13% SDS-PAGE gels and blotted on PVDF membranes. (FLAG)<sub>3</sub>-tagged proteins were visualised by chemiluminescence.

Rep. 1

**Protein Report**  
**111 Carbamido Propionamid N vi SDR\_2018-08-31 11:14:31**

**Protein 8: PREDICTED: stearoyl-CoA desaturase 5-like [Nasonia vitripennis]**

Accession:	gi 156542104	Score:	941.6										
Database:	Nasonia_vit_SDR	Seq. Coverage [%]:	42.8										
MW [kDa] / pl:	42.1 / 6.6	No. of Peptides:	15										
Modification(s):	Carbamidomethyl, Oxidation, Deamidated												
10      20      30      40      50      60      70      80      90      100	MPPNEQIYEH ILPEAVEADPL KTLDIPGFDG YDEQYKDSEF NMSAEYYKEK VLSKPFLQRT DIKGWGNLFLM VVMHAVALYG FLTYPYLEKK MTFVWGWLFLA												
110     120     130     140     150     160     170     180     190     200	IVANFGVASG VHRLWSHRAF KAKLPPFKIIS IICYLTSQQY SAIWWSRDRH LHHHKSETDA DPVNAARGFW FSHIGWLCKM RHPEVLIGKAK QLDLSDIAND												
210     220     230     240     250     260     270     280     290     300	PVIKFEIYHF QVLRIMPTFI IPTLVPVYFW NESWYWAILS QCFMRYVYSL NCTWGINSLA HRPGGHPYDK NIEPSENFLM TLATGGEGWH NYHHAPFADY												
310     320     330     340     350     360     370	KASELGFNYI TNVNLTTCCLI DLAAKIOWAY DLKEPSEKLL KAVIKNRGDG SHPISETVK TE												
<b>MS/MS Peptide Matches</b>													
Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range	Type
39	777.7352	3	1.86	0.0014	70.28	57.85	2	0.0	0	M.PPNEQIYEHILPEAVEADPLK.T		2-21	CID
18123	778.0633	3	1.60	0.0012	72.79	29.59	1	0.703	0	M.PPNEQIYEHILPEAVEADPLK.T	Deamidated: 5	2-21	CID
444	880.9054	2	1.22	0.0011	68.18	80.04	7	0.0	0	K.TLDIPGFDGYDEQYK.E		22-36	CID
2142	1069.7927	3	0.39	0.0004	68.25	64.15	3	0.0	1	K.TLDIPGFDGYDEQYK.DSEFNMSAEYYK.E	Oxidation: 21	22-48	CID
245	733.2942	2	1.61	0.0012	39.77	83.71	4	0.0	0	K.DSEFNMSAEYYK.E	Oxidation: 6	37-48	CID
16989	725.2966	2	1.43	0.0010	48.95	26.95	1	0.0	0	K.DSEFNMSAEYYK.E		37-48	CID
4865	574.9116	3	2.28	0.0013	36.60	56.92	3	0.0	1	K.DSEFNMSAEYYK.V	Oxidation: 6	37-50	CID
22351	861.1107	3	0.10	0.0001	111.88	66.61	4	0.0	0	K.MTFVWGWLAVANFGVASGVHL.R	Oxidation: 1	91-113	CID

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Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range	Type
39120	636.6509	3	1.20	0.0008	33.49	32.98	1	0.0	1	R.LHHHKSETDADPVNAAR.G		151-167	CID
3050	697.3167	2	2.23	0.0016	39.82	92.47	7	0.0	0	K.FSETDADPVNAAR.G	Deamidated: 10	155-167	CID
594	696.8246	2	2.10	0.0015	41.48	109.43	8	0.0	0	K.FSETDADPVNAAR.G		155-167	CID
17480	562.2653	3	2.99	0.0017	78.09	27.79	1	0.0	0	R.GFWFSHIGWLCKM.R	Carbamidomethyl: 11; Oxidation: 12	168-180	CID
78	770.9162	2	2.21	0.0017	67.22	107.44	3	0.0	0	K.QLDLSDIANDPVIK.F		191-204	CID
3388	891.409	4	0.59	0.0005	72.16	62.22	1	0.0	0	K.NIEPSENFLMLATGGEGWHNYHAFPADYK.A	Oxidation: 10	271-301	CID
428	483.2608	2	5.41	0.0026	59.41	43.41	6	0.0	0	K.IGWAYDLK.E		326-333	CID

Rep. 2

**Protein Report**  
**Compi\_Nasvi\_SDR\_301117\_2017-11-30 13:15:54**

**Protein 242: PREDICTED: stearoyl-CoA desaturase 5-like [Nasonia vitripennis]**

Accession:	gi 156542104	Score:	578.1										
Database:	Nasonia_vit_SDR	Seq. Coverage [%]:	23.5										
MW [kDa] / pl:	42.1 / 6.6	No. of Peptides:	9										
Modification(s):	Oxidation, Deamidated												
10      20      30      40      50      60      70      80      90      100	MPPNEQIYEH ILPEAVEADPL KTLDIPGFDG YDEQYKDSEF NMSAEYYKEK VLSKPFLQRT DIKGWGNLFLM VVMHAVALYG FLTYPYLEKK MTFVWGWLFLA												
110     120     130     140     150     160     170     180     190     200	IVANFGVASG VHRLWSHRAF KAKLPPFKIIS IICYLTSQQY SAIWWSRDRH LHHHKSETDA DPVNAARGFW FSHIGWLCKM RHPEVLIGKAK QLDLSDIAND												
210     220     230     240     250     260     270     280     290     300	PVIKFEIYHF QVLRIMPTFI IPTLVPVYFW NESWYWAILS QCFMRYVYSL NCTWGINSLA HRPGGHPYDK NIEPSENFLM TLATGGEGWH NYHHAPFADY												
310     320     330     340     350     360     370	KASELGFNYI TNVNLTTCCLI DLAAKIOWAY DLKEPSEKLL KAVIKNRGDG SHPISETVK TE												
<b>MS/MS Peptide Matches</b>													
Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range	Type
9931	777.7329	3	-1.10	-0.0009	49.53	42.35	3	0.0	0	M.PPNEQIYEHILPEAVEADPLK.T		2-21	CID
9986	880.9031	2	-1.39	-0.0012	49.66	58.99	3	0.0	0	K.TLDIPGFDGYDEQYK.D		22-36	CID
9662	1069.7912	3	-1.01	-0.0011	48.96	78.11	1	0.0	1	K.TLDIPGFDGYDEQYK.DSEFNMSAEYYK.E	Oxidation: 21	22-48	CID
1779	733.292	2	-1.39	-0.0010	32.26	58.12	2	0.0	0	K.DSEFNMSAEYYK.E	Oxidation: 6	37-48	CID
30511	861.8598	2	-2.32	-0.0020	25.17	40.08	3	0.0	1	K.DSEFNMSAEYYK.V	Oxidation: 6	37-50	CID
5391	544.334	2	-1.39	-0.0008	26.31	57.5	2	0.0	0	K.VLSKPFLQR.T		51-59	CID
21799	697.3132	2	-2.79	-0.0019	28.98	34.95	1	0.0	0	K.FSETDADPVNAAR.G	Deamidated: 10	155-167	CID
1489	696.8222	2	-1.35	-0.0009	29.35	96.11	10	0.0	0	K.FSETDADPVNAAR.G		155-167	CID
9728	770.9131	2	-1.81	-0.0014	49.12	111.88	3	0.0	0	K.QLDLSDIANDPVIK.F		191-204	CID

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**Fig. S2. Results the two replicates (Rep. 1 and Rep. 2) of the mass spectrometric analysis of the Δ12-desaturase Nvit\_D12a in the rectal vesicles of male *N. vitripennis*.**

Ten rectal vesicles of 1–2 day old wasps were pooled per replicate and subjected to SDS-PAGE. *In-gel* trypsin digested proteins were analysed by LC/MS/MS. Protein database searching of the resulting mass spectra was performed using the Mascot search engine.

XP\_001599873.1 (unbiased)  
XP\_001599836.1 (male biased)

MPPNEQIHEHVLPEAVEDPLKLDIPGFNDYDEEHKDSEFNMSAEEYNEKVINKPFLQRT  
**MPPNEQIYEHILPEAVEDPLKLDIPGF**DGYDEQYKDSEFNMSAEEYKEKVLSKPFLQRT  
\*\*\*\*\*:\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:  
DIKWGNLYFMVVLHAIALYGFLTPYFEKKMTFVWGWFLAIIVANFGVAGGVHRLWSHRAF  
DIKWGNLLFMVVMHAVALYGFLTPYLEK**KMTFVWGWFLAIIVANFGVASGVHRLWSHRAF**  
\*\*\*\*\*:\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:  
KAKVPLKIIIFILSYLTSGQYSAIWWARDHRIHH**KFSETDADPVNAARGFWF**SHVGWLCKM  
KAKLPFKIISIICYLTSGQYSAIWWSDH**RLHHKFSETDADPVNAARGFWF**SHIGWLCKM  
\*\*\*:\*\*\*:\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:  
RHPEVLKKAKQLDLSDILNDPVIKFEEKHFQVLRLIFAFIIPTLVPVYFWNESWYWAILS  
**RHPEVLKKAKQLDLSDIANDPVIKFEEKHFQVLRLMFTFIIPTLVPVYFWNESWYWAILS**  
\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:  
QCFMRYAYSLNCTWGINSAHMFGNHPYDKHIEPAENFIMTLATGGEWHNYHHVFPADY  
QCFMRYVYSLNCTWGINSLAHRGGHPYDKNIEPSENFLMTLATGGEWHNYHHAFPADY  
\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:  
KASELGFNYITNVNLTTCLIDLA**KIGWAYDLKEPSEKLLKAVIKNRGDGSHPISHEPVK**  
**KASELGFNYITNVNLTTCLIDLA**KIGWAYDLKEPSEKLLKAVIKNRGDGSHPISHETVK  
\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:  
TK  
TE  
\*:\*

**Fig. S3. Sequence alignment of the two Δ12-desaturases Nvit\_D12a (XP\_001599836.1) and Nvit\_D12b (XP\_001599873.1) from *N. vitripennis*.** Sequences detected in the male pheromone gland (rectal vesicle) by LC/MS/MS are indicated in colour (yellow: ranges covered by unique peptides of the male-biased desaturase Nvit\_D12a; green: peptides shared by both Δ12-desaturases).

60

Adom_D12	MDLNEE-----SAPSGVLFEEDVAEQEAKMANGG-PKKGKKLEPYRL
Clug_D12	MAPNAR-----DS-TGVLSEED----AEITPEQ-IEEVHKTSKNRHL
Tcas_D12	MSAQT-----ITTTE-TTQNAQKPQQYHW
Nvit_D12a	MPPNEQIHEHVLPEAVEDPLKTLIPGFNDYDEEHKDSEFNMSAEEYNEKVINKPFLQRT
Nvit_D12b	MPPNEQIYEHILPEAVEDPLKTLIPGFQDGYDEQYKDSEFNMSAEEYKEVKLSKPFLQRT
	*

120

Adom_D12	EIVWFNVLWFVLLHAGALYGVYLIFASAKIYTTLYGFLCELSLLSITAGV
Clug_D12	PLVWRDVVIKFAVLHALGFYGFYLMFTSARIWTSVLVFINYHGLGILGITAGA
Tcas_D12	RMVWRNIILYIIMHHTGFYGLYLAAMFYAQWKTVFYSWFLVIALQGVTAGS
Nvit_D12a	DIKWGNLYFMVVLHAIALYGFLTYPYFEKKMTFWVGWFLAIVANFGVAGGV
Nvit_D12b	DIKWGNLLFMVVMHAVALYGFLTYPYLEKKMTFWVGWFLAIVANFGVASGV
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180

Adom_D12	KAKWPLRLTLMVLNLAYQNSIYEWARD
Clug_D12	KARWPLKLFLAYIQTTLAFQDFIIFWAKY
Tcas_D12	KARLPLRMLLCIFQTLQLQNHIYDWATY
Nvit_D12a	KAKVPLKIIFILSYLTSQYSAIWWARD
Nvit_D12b	KAKLPFKIISIICYLTSQYSAIWWSRD
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	*** * ***
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240

Adom_D12	KHPEVRAKGGRIDLSLERDPIVMFQKRHYKK-LVPFVSFVIPTLIPMYFWGETLSNSWY
Clug_D12	KNPEFETRCNEIDLSDLYSDPIVNQYKYYYQ-ILFVVFLVVPTFIPMYFWNETFVN-A-F
Tcas_D12	PHKDVEDKYKSIDFSDLHADSVVMIQKKYYHTFFAPVIGFYLPAAIPWYFWGENFWTAFF
Nvit_D12a	RHPEVLKKAKQLDLSIDLNDPVVIKFEEKHFQV-LRLIFAFIIPTLVPVYFWNESWYAIL
Nvit_D12b	RHPEVLKKAKQLDLSDIANDPVVIKFEEKHFQV-LRLMFTFIIPTLVPVYFWNESWYAIL
	*
	***
	*

300

Adom_D12	VSTMFRYCLSLNLTLVNSAAHMWGNKPYDKNNINPVENLAVAIGSLGEGHNFHIVFPWD
Clug_D12	CLNLSRYLLSLHCTWLVNSAAHLYGNKPYDKSLYSSENFWVTILVNNGEGWHNYHHAFPWD
Tcas_D12	VATMLRYCACTNITFLVNSWAHIYGSRPYDKNIYPTESATIAVTGGEWHNYHHTFPWD
Nvit_D12a	SQCFMRYAYSLNCTWGINSFAHMFGNHPYDKHIEPAENFIMTLATGGEWHNYHHVFPAD
Nvit_D12b	SQCFMRYVYSLNCTWGINSLAHRFGGHPYDKNIEPSENFLMTLATGGEWHNYHHAFPAD
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	***

360

Adom_D12	YKTSELG---NYSLNFTNAFIDLAVLLGLAYDLKTVPSMIKTRVGRGTDGSHD-----
Clug_D12	YKASELG---IYSTNMTAFFIDAMAKLGLAYDLKSVAPEVVKRRVERTGDGSHP-----
Tcas_D12	YKTGEFG---KYRSNLTGFLDFMAAIGWAYDLKTVSEEMIMKRVLRTGDGTRKFDKIDK
Nvit_D12a	YKASELGFNYITVNLTTCOLIDLAAKIGWAYDLKEPSEKLLKAVIKNRGDGSHP-----
Nvit_D12b	YKASELGFNYITVNLTTCOLIDLAAKIGWAYDLKEPSEKLLKAVIKNRGDGSHP-----
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Adom_D12	-----VWGWDKDLPKELADQTMENR--KTE
Clug_D12	-----IWGWDKDQSEEDKRSALISHK--DT-
Tcas_D12	ILNVDDHHEDMLWGWDSDMAKEEMNYVKIHNR--KED
Nvit_D12a	-----ISHEPVTKT
Nvit_D12b	-----ISHETVKTE
	*

**Fig. S4. Multiple sequence alignment of functionally characterised insect  $\Delta 12$ -desaturases.** The three histidine boxes characteristic for “First” type desaturases (Hashimoto et al., 2008) are shown in yellow frames. Conserved amino acids are indicated by asterisks at the bottom of each column. Sequences identities and similarities are given in Table S3. Adom\_D12 = *Acheta domesticus* (Zhou et al., 2008), Clug\_D12 = *Chauliognathus lugubris* (Haritos et al., 2012), Tcas\_D12 = *Tribolium castaneum* (Zhou et al., 2008), Nvit\_D12a/b = *Nasonia vitripennis* (this study).

**Table S1. Nucleotide and amino acid sequences of Nvit\_D12a (XP\_001599836.1) and Nvit\_D12b (XP\_001599873.1).** The nucleotide sequences were optimised for expression in *S. cerevisiae*. Recognition sites for *Bsal* are underlined and restriction sites are bold.

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### Nucleotide sequences

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***Nvit\_D12a (XP\_001599836.1)***

5'AAAAAAGGTCTCACATGCCACCAACGAACAAATCCATGAACATGTTGCCAGAAGCTGTT  
 GAGGATCCATTGAAAACTTGGATATTCCAGGTTCAACGACTACGATGAAGAACATAAGGAC  
 TCCGAATTCAACATGTCTGCTGAAGAGTACAACGAAAAGGTTATCAACAAGCCATTCTGCAA  
 AGAACCGATATTAAGTGGGTAACTTGACTTCATGGTTCTGCATGCTATTGCCTTGAC  
 GGTTTTTGACTTACCCCATACTTCGAGAAGAAGATGACTTTGTTGGGTTGGTTGGCTA  
 TCGTTGCTAATTTTGGTGGCTGGTGTTCATAGATTGTTGTCACATAGAGCTTTAAGG  
 CTAAGGTTCCACTGAAGATCATTTCATCTTGCTACTTGACCTCCGGTCAATATTCTGCTAT  
 TTGGTGGGCTAGAGATCATAGAATCCATACAAGTTCTGAAACTGATGCTGATCCAGTTAA  
 TGCTGCTAGAGGTTTGGTTCTCATGTTGGTGGTGTGCATGAAGAGACATCCAGAAGT  
 TTTGAAGAAGGCCAAGCAATTGGATTGTCGATATTGAATGACCCGTCATCAAGTTGA  
 AGAAAGCACTTCAAGTCCTGAGATTGATTTCGCCTCATCATTCCAAC  
 TGGTCCAGTTTACTTCTGGAACGAATCTGGTATTGGCCATTGTCTCAATGCTTATGAGATACGCCACT  
 CTTGAACTGTACCTGGGTATTAAC  
 TCCATTCGCTCATATGTTGGTAACCACATACGATAA  
 GCACATTGAACCAGCCAAAAC  
 TCCATTGACTTGGCTACTGGTGGTAAGGTTGGCATAA  
 TTACCATCATGTTTCCAGCTGATTACAAGGCTCTGAATTGGTTCAACTACATCACCAAC  
 GTTAACTTGACCACCTGTTGATTGATTGGCTGCTAAATTGGTTGGCCTACGATTGAA  
 GAACCATCTGAAAAGTTGTTGAAGGCCGTATTAAGAATAGAGGTGATGGTTCTCATCCAATC  
 TCTCATGAACCAGTTAAGACCAAGTAAGAGAGACCAAAAAA3'

***Nvit\_D12b (XP\_001599873.1)***

5'AAAAAAGGTCTCACATGCCACCAACGAACAAATCTACGAACATATTTGCCAGAAGCCGTT  
 GAAGATCCATTGAAAACTTGGATATTCCAGGTTCGATGGTACGATGAACAGTACAAAGAC  
 TCCGAATTCAACATGTCTGCTGAAGAGTACAAAAGAGAAGGTTTGCTAAGCCATTCTGCAA  
 AGAACCGATATTAAGTGGGTAACTTGTTCATGGTTATGCATGCTTGCCTTGAC  
 GGTTTTTGACTTATCCACTTGGAGAAGAAGATGACTTTGTTGGGTTGGTTGGCTA  
 TCGTTGCTAATTTTGGTGGCTCTGGTGTTCATAGATTGTTGTCACATAGAGCTTTAAGG  
 CTAAGTTGCCATTCAAGATCATCTCCATTATTGCTACTTGACCTCCGGTCAATATTCTGCTAT  
 TTGGTGGCTAGAGATCACAGATTGCATCACAAATTCTCTGAAACTGATGCCGATCCAGTTAA  
 TGCTGCTAGAGGTTTGGTTCTCTCATATTGGTTGGTGTGCATGAAGAGACATCCAGAAGT  
 TTTGAAGAAGGCCAAGCAATTGGATTGTCGATATTGCTAATGACCCAGTCATCAAGTTGA  
 AGAAAGCACTTCAAGTCCTGAGATTGATGTTCACCTCATTATCCAAC  
 TGGTCCAGTTTACTTCTGGAATGAATCTGGTACTGGCCATTGTCTCAATGTTCATGAGATACGTCTACT  
 CATTGAACTGTACCTGGGTATTAAC  
 TCCATTGGCACATAGATTGGTGGTCATCCACATACGATA  
 AGAACATTGAACCACATCCGAGAATTCTTGATGACATTGGCTACTGGTGGTAAGGTTGGCATA  
 ATTATCATCATGTTTCCAGCTGACTACAAGGCTCTGAATTGGTTAACTACATCACCAA  
 CGTTAACTTGACCACCTGTTGATTGATTGGCTGCTAAATTGGTTGGCCTACGATTGAA  
 AGAACCCCTGAAAAGTTGTTGAAGGCCGTTATTAGAACACAGAGGTGATGGTTCTCATCCAAT  
 TTCTCACGAAACTGTTAAGACCGAGTAAGAGACCAAAAAA 3'

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## Amino acid sequences

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### **Nvit\_D12a (XP\_001599836.1)**

MPPNEQIHEHVLPEAVEDPLKTLDIPGFNDYDEEHKDSEFNMSAEEYNEKVINKPFLQRTDIKWG  
NLYFMVVLHAIALYGFLLTYPYFEKKMTFWGVFLAIVANFGVAGGVHRLWSHRAFKAKVPLKIIIFL  
SYLTSGQYSAIWWARDHRIHHKFSETDADPVNAARGFWFSHVGWLCKRHPVELKKAKQLDLS  
DILNDPVVIKFEEKHFQVLRLIFAFIPTLVFVFWNESWYWAILSQCFMRYAYSLNCTWGINSFAHM  
FGNHPYDKHIEPAENFIMTLATGGEGWHNYHHFPADYKASELGFNYITNVNLTTCLIDLAAKIGW  
AYDLKEPSEKLLKAVIKNRGDGSHPISHEPVKTK\*

### **Nvit\_D12b (XP\_001599873.1)**

MPPNEQIYEHILPEAVEDPLKTLDIPGFDTGYDEQYKDSEFNMSAEEYKEKVLSKPFLQRTDIKWGN  
LLFMVVVMHAVALYGFLLTYPYLEKKMTFWGVFLAIVANFGVASGVHRLWSHRAFKAKLPFIISIC  
YLTSGQYSAIWWSRDHRLHHKFSETDADPVNAARGFWFSHIGWLCKRHPVELKKAKQLDLSDI  
ANDPVVIKFEEKHFQVLRLMFTFIPTLVFVFWNESWYWAILSQCFMRYVYSLNCTWGINSLAHRF  
GGHPYDKNIEPSENFLMTLATGGEGWHNYHHFPADYKASELGFNYITNVNLTTCLIDLAAKIGW  
AYDLKEPSEKLLKAVIKNRGDGSHPISHETVKTE\*

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**Table S2. Conversion of externally supplied fully labelled  $^{13}\text{C}18:1^{\Delta 9}$  into  $^{13}\text{C}18:2^{\Delta 9,12}$  by *Urolepis rufipes*.** Single 2-d-old wasps ( $n = 12$  for each sex) were treated with an acetone solution of  $^{13}\text{C}18:1^{\Delta 9}$ . After 20 h, lipids of 3 homogenised wasps each (resulting in 4 replicates for males and females, respectively) were extracted, transesterified into fatty acid methyl esters, and analysed by GC/MS. The conversion of  $^{13}\text{C}18:1^{\Delta 9}$  to  $^{13}\text{C}18:2^{\Delta 9,12}$  by the wasps was concluded from the occurrence of the diagnostic molecular ion m/z 312 at the retention time of  $\text{C}18:2^{\Delta 9,12}$  methyl ester. The conversion rate was calculated by relating the peak area of the  $^{13}\text{C}$ -labelled molecular ion of  $\text{C}18:2^{\Delta 9,12}$  methyl ester (m/z 312) to the added peak areas of the  $^{13}\text{C}$ -labelled molecular ions of  $\text{C}18:2^{\Delta 9,12}$  methyl ester plus  $\text{C}18:1^{\Delta 9}$  methyl ester (m/z 314).

	Female 01	Female 02	Female 03	Female 04	Male 01	Male 02	Male 03	Male 04
Area m/z 312	4059	14031	17465	8985	0	0	0	0
Area m/z 314	34633	115906	273316	43249	33488	46539	23350	28169
Conversion rate (%)	10.49	10.80	6.01	17.20	0	0	0	0

**Table S3. Sequence identities and similarities between insect-derived  $\Delta$ 12-desaturases.** Number and percentage of identical amino acid positions (sequence identities) are given in the upper right triangle, number and percentage of identical plus similar amino acid positions (sequence similarity) are given in the lower left triangle.

	Adom_D12	Clug_D12	Tcas_D12	Nvit_D12a	Nvit_D12b
Adom_D12		186/357 (52%)	163/377 (43%)	159/388 (41%)	159/383 (42%)
Clug_D12	244/357 (68%)		157/371 (42%)	149/381 (39%)	141/381 (37%)
Tcas_D12	221/377 (59%)	225/371 (60%)		131/408 (32%)	129/398 (32%)
Nvit_D12a	223/388 (58%)	212/381 (55%)	189/408 (46%)		327/362 (90%)
Nvit_D12b	220/383 (57%)	210/381 (55%)	191/398 (47%)	346/362 (96%)	

## References

- Haritos, V. S., Horne, I., Damcevski, K., Glover, K., Gibb, N., Okada, S. and Hamberg, M.** (2012). The convergent evolution of defensive polyacetylenic fatty acid biosynthesis genes in soldier beetles. *Nat. Commun.* **3**.
- Hashimoto, K., Yoshizawa, A. C., Okuda, S., Kuma, K., Goto, S. and Kanehisa, M.** (2008). The repertoire of desaturases and elongases reveals fatty acid variations in 56 eukaryotic genomes. *J. Lipid. Res.* **49**, 183-191.
- Zhou, X. R., Horne, I., Damcevski, K., Haritos, V., Green, A. and Singh, S.** (2008). Isolation and functional characterization of two independently-evolved fatty acid delta 12-desaturase genes from insects. *Ins. Mol. Biol.* **17**, 667-676.