

Supplementary Tables and Figures

Table S1: Primers sequences used for RACE-PCR and complete gene isolation.

Gene	Primers sequence (5'→3')	Aim
<i>OeAOX1a</i>	GSP1: CTAAGAATGTGACAGGGCGTGGTG	5' end isolation
	GSP2: ACCAAACTCGACTCTGCGCATGTA	3' end isolation
	OeAOX1a_14Fw: CCGTGTTGCATTATAGATCTTGTTTC OeAOX1a_1420Rv: ACGCAAAGCGATTACTAGTTCA	Complete gene isolation
<i>OeAOX1d</i>	OeAOX1d_5end: 5'-GCATTGCAAATACACCTTGG-3'	5' end isolation*
	GSP2: CGAGGCACACCATCGTGACCTTAAC	3' end isolation
	OeAOX1dFw: TTATTTTGTGTTTATTCTTTCTA OeAOX1dRev: ATCATTTATTGTCATCTATTATCG	Complete gene isolation
	OeAOX1d_24Fw: ATTATTTTGTGTTTATTCTTTCT OeAOX1d_1085Rev: CCTTTTGTCTTCAGTGGT	Complete gene isolation

* primers obtained from a previous work [14].

Table S2. Primers used for RT-qPCR analysis.

Gene	Acc. number	Primers sequence 5'→3'	AS (bp)	[nM]	E (%)
<i>OeAOX1a</i>	-	Fw: CGGCTATTGCCATCGACTAT Rv: GGGATTCCCTCAGTTCATGTC	150	300 300	101
<i>OeAOX1a</i> _transcript variant X1	MG208095	Fw: CGGCTATTGCCATCGACTAT Rv: CATCAGAAATTGTGATCAGTGAAA	311	900 900	110
<i>OeAOX1a</i> _transcript variant X2	MF410314	Fw: CGGCTATTGCCATCGACTAT Rv: AAATACGCAAAGCGATTACTAGT	379	300 300	88
<i>OeAOX1d</i>	-	Fw: CTCAAATCCCCACCTACTTGTTT Rv: AGCTGCCACCGTCTCTAGGA	75	300 300	98
<i>OeAOX1d</i> _transcript variant X1	MF410315	Fw: GGCACACCATCGTGACCTTA Rv: GGATATTCCTTTAGCTCGTGTCTT	72	300 300	98
<i>OeAOX1d</i> _transcript variant X2	JX912721	Fw: GGCACACCATCGTGACCTTA Rv: CGTCGACAAGGAAAATGAAAATCT	65	300 300	91
<i>OeActin</i>	AF545569	Fw: TTGCTCTCGACTATGAACAGG Rv: CTCTCGGCCCAATAGTAATA	106	300 300	95
<i>OeEF1a</i>	AM946404	Fw: TTTTGAGGGTGACAACATGAT Rv: CAGGGTTGGGCCCTTGAT	64	300 300	100

Acc. number: accession number at the NCBI databases (National Center for Biotechnology Information, <http://www.ncbi.nlm.nih.gov/>); AS: amplicon size; [nM]: final concentration of each primer in the RT-qPCR reaction mix; E: PCR efficiency.

Table S3. Eudicot plant species used in the NJ analysis. .

O	F	Species	Accession number
Brassicales	Brassicaceae	<i>Arabidopsis lyrata</i>	AL1G33660 AL3G24680 AL3G24690 AL5G06730 AL0G08000 AL8G30860
		<i>Arabidopsis thaliana</i>	AT1G32350 AT3G22360 AT3G22370 AT3G27620 AT5G64210
		<i>Boechera stricta</i>	Bostr.19424s0421.1 Bostr.19424s0422.1 Bostr.3359s0124.1 Bostr.0568s0383.1
		<i>Brassica rapa</i>	Bra010153 Bra001865 Bra031351 Bra023835 Bra037768
		<i>Capsella grandiflora</i>	Cagra.1189s0011.1 Cagra.1189s0012.1 Cagra.5575s0007.1 Cagra.3957s0019.1 Cagra.0248s0102.1
		<i>Capsella rubella</i>	Carubv10014065m Carubv10019557m Carubv10009739m Carubv10026681m
		<i>Eutrema salsugineum</i>	Thhalv10021013m Thhalv10009342m Thhalv10005697m
		<i>Thellungiella parvula</i>	TP3G20130 TP3G20140 TP2G27270
	C	<i>Carica papaya</i>	evm.model.supercontig_8.29 evm.model.supercontig_42.47
Curcubi	Curc	<i>Citrullus lanatus</i>	CL10G07420
		<i>Cucumis melo</i>	CM00136G00010
		<i>Cucumis sativus</i>	Cucsa.398150.1
Fabales	Fabaceae	<i>Glycine max</i>	GM04G14800 GM08G07690 GM08G07700 GM05G24455
		<i>Lotus japonicus</i>	LJ2G020780 LJ4G005280 LJ4G005290
		<i>Medicago truncatula</i>	MT5G026620 MT5G070680

O	F	Species	Accession number
			MT5G070870 MT5G070880
		<i>Phaseolus vulgaris</i>	Phvul.002G127100.1 Phvul.002G209100.1 Phvul.002G209200.1
Malvales	Malvaceae	<i>Gossypium raimondii</i>	Gorai.008G296600.1 Gorai.012G142200.1 Gorai.005G220400.1 Gorai.005G220500.1
		<i>Theobroma cacao</i>	TC03G031300 TC02G011670
Malpighiales	Linac	<i>Linum usitatissimum</i>	Lus10035670 Lus10005372 Lus10020523
	Salicaceae	<i>Populus trichocarpa</i>	PT03G09340 PT12G01430 PT12G01440 PT15G01960
		<i>Salix purpurea</i>	SapurV1A.1470s0080.1 SapurV1A.0346s0170.1 SapurV1A.0377s0140.1 SapurV1A.0377s0150.1 SapurV1A.3352s0030.1 SapurV1A.0894s0160.1
	Eu	<i>Manihot esculenta</i>	ME10292G00060
		<i>Ricinus communis</i>	RC30063G00030
	H	<i>Hypericum perforatum</i>	EU330415.1 EU330413.1
Ranunc	Ranun	<i>Aquilegia coerulea</i> Goldsmith	Aquca_105_00003.1 Aquca_043_00024.1 Aquca_008_00134.1 Aquca_033_00110.1
Rosales	Rosaceae	<i>Fragaria vesca</i>	FV5G29310 FV5G21950
		<i>Malus domestica</i>	MD00G028680 MD00G081720 MD13G026910 MD16G016620
		<i>Prunus persica</i>	Prupe.5G018700.1 Prupe.1G061800.1 Prupe.1G061900.1 Prupe.1G061400.1
Sapindales	Rutaceae	<i>Citrus clementina</i>	Ciclev10001766m Ciclev10003687m Ciclev10028835m
		<i>Citrus sinensis</i>	orange1.1g037339m orange1.1g019765m orange1.1g020532m
Solan	Solan	<i>Solanum lycopersicum</i>	Solyc08g005550 Solyc08g075540 Solyc08g075550

O	F	Species	Accession number
			Solyc01g105220
		<i>Solanum tuberosum</i>	PGSC0003DMT400019708 PGSC0003DMT400019707 PGSC0003DMT400047562 PGSC0003DMG400012558
<i>Amborellales</i>	<i>Amborellaceae</i>	<i>Amborella trichopoda</i>	ATR_00048G01570 evm_27.model.AmTr_v1.0_scaffold00048.158 ATR_00038G01180 evm_27.model.AmTr_v1.0_scaffold00038.119

	<i>Caryophy</i>	<i>Amaranta</i>	<i>Beta vulgaris</i>	BV5G19180 BV9G03180
			<i>Amaranthus hypochondriacus</i>	AHYPO_008129-RA AHYPO_002393-RA AHYPO_002394-RA
	<i>Saxifragales</i>	<i>Crassulaceae</i>	<i>Kalanchoe laxiflora</i>	Kalax.0453s0008.1 Kalax.1476s0004.1 Kalax.0496s0017.1 Kalax.0907s0011.1 Kalax.0414s0014.1
			<i>Kalanchoe fedtschenkoi</i>	Kaladp0418s0013.1 Kaladp0067s0033.1 Kaladp0062s0189.1
		<i>Phry</i>	<i>Mimulus guttatus</i>	Migut.J01127.1 Migut.E01358.1 Migut.N01067.1
	<i>Lamiales</i>	<i>Olea</i>	<i>Olea europaea</i>	Galega vulgar_MF410314* Galega vulgar_MF410315* Galega vulgar_JX912721* Galega vulgar_JX912722 Dolce Agogia_KM514920 Leccino_KM514918 Dolce Agogia_KM514921 Leccino_KM514919 Leccino_GCJV01040584 Picual_GBKW01105538 Farga_FKYM01004812 Farga_FKYM01030627 Farga_FKYM01003481
	<i>Myrt</i>	<i>Myrt</i>	<i>Eucalyptus grandis</i>	Eucgr.E01214.1 Eucgr.E01213.1 Eucgr.I02663.1
	<i>Vita</i>	<i>Vit</i>	<i>Vitis vinifera</i>	VV02G09030 VV02G09050 VV00G00110

O: order; Caryophy: *Caryophyllales*; Curcubi: *Curcubiales*; Lam: *Lamiales*; Mytr: *Myrtales*; Ranunc: *Ranunculales*; Vita: *Vitales*; F: family; Amaranta: *Amarantaceae*; C: *Caricaceae*; Curc: *Curcubitaceae*; E: *Euphorbiaceae*; H: *Hypericaceae*; Lina:

Linaceae; Myr: *Myrtaceae*; Olea: *Oleaceae*; Phry: *Phrymaceae*; Ranun: *Ranunculaceae*; Vit: *Vitaceae*.; In grey the AOX2 sequences. *olive sequences characterized in the present research.

Table S4. Monocot plant species used in the NJ analysis.

In grey the AOX2 sequence.

Species	Accession number
<i>Brachypodium distachyon</i>	BD3G52505 BD5G20540 BD5G20547 BD5G20557
<i>Brachypodium stacei</i>	Brast04G094100.1 Brast09G194700.1 Brast09G194600.1 Brast09G194800.1
<i>Hordeum vulgare</i>	CAJW010038523 CAJW011587016 CAJW010099492
<i>Musa acuminata</i>	GSMUA_Achr5G03810_001 GSMUA_Achr6G01170_001 GSMUA_Achr6G01300_001 GSMUA_Achr1G27800_001
<i>Oropetium thomaeum</i>	Oropetium_20150105_19337A Oropetium Seq1_20150105_01586A Oropetium Seq2_20150105_01586A Oropetium Seq3_20150105_01586A
<i>Oryza brachyantha</i>	OB02G22630 OB02G36280 OB04G30980 OB04G30990
<i>Oryza glaberrima</i>	ORGLA02G0249500 ORGLA04G0206000 ORGLA04G0206100
<i>Oryza sativa</i>	BGIOGA008063 BGIOGA005788 BGIOGA014421 BGIOGA014422
<i>Panicum hallii</i>	Pahal.G02176.1 Pahal.G02177.1 Pahal.G02175.1 Pahal.A03053.1
<i>Panicum virgatum</i>	Pavir.Ab01160.1 Pavir.Aa00784.1 Pavir.Ga00730.1 Pavir.Gb00786.1 Pavir.Ga00729.1 Pavir.Ga00625.1 Pavir.Ab02811.1 Pavir.Gb00785.1

	Pavir.Gb00789.1
<i>Setaria italica</i>	Seita.7G223800.1 Seita.7G223900.1 Seita.7G223700.1 Seita.1G286500.1
<i>Setaria viridis</i>	Sevir.7G235500.1 Sevir.7G235600.1 Sevir.7G235400.1 Sevir.1G291700.1
<i>Spirodela polyrhiza</i>	Spipo20G0025000 Spipo5G0073900 Spipo11G0008300
<i>Sorghum bicolor</i>	SB04G030820 SB06G027410 SB06G027420 SB06G027430
<i>Zea mays</i>	ZM02G05480 ZM02G05490 ZM02G05500 ZM05G37570

Table S5. Information regarding the cis-elements extracted from the 1.5 kbp upstream region of both OeAOX1 genes using the PlantCARE and New Place softwares.

	ID motif	Sequence	Locus (Strand)	Source	Specific function	References
OeAOX1a	NTBBF1ARROLB	ACTTTA	266 (-)	PLACE_S000273	Required for tissue-specific expression and auxin induction	Baumann et al. 1999
	ARFAT	TGTCTC	305 (+)	PLACE_S000270	ARF (auxin response factor) binding site found in the promoters of primary/early auxin response genes of <i>Arabidopsis thaliana</i>	Inukai et al. 2005, Nemhauser al. 2004, Goda et al. 2004, Hagen and Guilfoyle 2002
	SURECOREATSULTR11	GAGAC	306 (-)	PLACE_S000499	contains auxin response factor (ARF) binding sequence (see above ARFAT)	Maruyama et al. 2005
	BO~TGA-element	AACGAC	890 (-)	PlantCARE	auxin-responsive element	Pastuglia et al. 1997
OeAOX1d	ASF1MOTIFCAMV	TGACG	164 (-)	PLACE_S000024	TGACG motifs are found in many promoters and are involved in transcriptional activation of several genes by auxin and/or salicylic acid	Despres et al. 2003, Klinedinst et al. 2000
	NTBBF1ARROLB	ACTTTA	668 (-) 1109 (+)	PLACE_S000273	Required for tissue-specific expression and auxin induction	Baumann et al. 1999
	D4GMAUX28	TAGTGCTGT	1383 (-)	PLACE_S000331	DNase I protected sequence found in the <i>Glycine max</i> auxin responsive gene, Aux28, promoter	Nagao et al. 1993

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- Inukai Y, Sakamoto T, Ueguchi-Tanaka M, Shibata Y, Gomi K, Umemura I, Hasegawa Y, Ashikari M, Kitano H, Matsuoka M.(2005). Crown rootless1, which is essential for Crown root formation in rice, is a target of an AUXIN RESPONSE FACTOR in auxin signaling. *Plant Cell* 17: 1387-1396
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- M Pastuglia, D Roby, C Dumas, J M Cock (1997). Rapid induction by wounding and bacterial infection of an S gene family receptor-like kinase gene in *Brassica oleracea*. *Plant Cell.* 1997 Jan; 9(1): 49–60.
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- Baumann K, De Paolis A, Costantino P, Gualberti G (1999). The DNA binding site of the Dof protein NtBBF1 is essential for tissue-specific and auxin-regulated expression of the rolB oncogene in plants. *Plant Cell* 11:323-333
- Nagao RT, Goekjian VH, Hong JC, Key JL (1993). Identification of protein-binding DNA sequences in an auxin-regulated gene of soybean. *Plant Mol Biol* 21: 1147-1162

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GAATTTCTCTACCATTTTCATTGATCCTATTTCTTTGATTATAATCTTCTGAAGAACAATGATGATAAAA 140
                                     M M I K

AGCACGACCAGGGTAGCACGGGCGGTGTTATGCCACATGGGCCACGTTATTTTCGACAACCGCCTTGC 210
S T T R V A R A V L C H M G P R Y F S T T A L

ATGGCTGTGTAGCAAGTGATGTGCAAGCAATTAGGGGTGTTTTTGGCGGCACCACCACCTTTCTTCCATGG 280
H G C V A S D V Q A I R G V F G G T T T F F H G

CAATCTTGCCCAGAGTTCTGAAAAGGTGTTGGTAGGGTGTCATGAGGTTGCTGGCGGTTGGTGGTGCGCGT 350
N L A Q S S E K V L V G C M R L L A V G G A R

AAGGCGAGCACTTTGGCCTTGGGTGACAAAAGCAGGAGGAGAGAGAAGGATCAAGGAGGAGAACTG 420
K A S T L A L G D K Q Q E E E K K V Q G G E T

GTGGTGTCCGCGCTGCCGGTGGGGCAATAATAACAAGGGAATAGTGAGTTATTGGGCGTGAGCCTGC 490
G G A A A A G G G N N N K G I V S Y W G V E P A

CAAGATTACTAAAGAGGATGGCTCTGAATGGAGGTGGAAGTCTTAAAGCATGGGAGACCTACAAGGCT 560
K I T K E D G S E W R W N C F K P W E T Y K A

GATCTGTCTATAGATCTGAAGAAACACCATGCCCTGTGCATTCTTAGACAAGGTGGCATATTGGACCG 630
D L S I D L K K H H A P V T F L D K V A Y W T

TCAAGTCTCTCAGATTTCTACAGATATATTCTTTTCAGAGGCGGTATGGATGTCGTCTATGATGCTGGA 700
V K S L R F P T D I F F Q R R Y G C R A M M L E

AACTGTGGCCGCTGTGCCTGGCATGGTTGGAGGGATGCTTCTGCACTGCAAGTCACTGAGGCGATTGAG 770
T V A A V P G M V G G M L L H C K S L R R F E

CACAGTGGTGGTTGGATCAAAGCATTGTTAGAAGAAGCCGAAAATGAAAGAATGCACCTCATGACATTCA 840
H S G G W I K A L L E E A E N E R M H L M T F

TGGAAGTTTCCAGCCCAGATGGTACGAACGCGCTCTTGTATTCACTGTGCAGGGCGTATTTTCAATGC 910
M E V S Q P R W Y E R A L V F T V Q G V F F N A

ATACTTCTTGACCTATCTCGTTTCCCGAAATTGGCGCATCGGGTTGTGGGGTATTGGAAGAGGAGGCG 980
Y F L T Y L V S P K L A H R V V G Y L E E E A

ATCCACTCGTACACCGAGTTCTTGAAAGAGTTGGACAAGGGCACTATTGAGAATGTTCTCTGCTCCGGCTA 1050
I H S Y T E F L K E L D K G T I E N V P A P A

TTGCCATCGACTATTGGCGTATGCCACCAAACCTCGACTCTGCGCGATGTAGTCATGGTAGTTAGAGCTGA 1120
I A I D Y W R M P P N S T L R D V V M V V R A D

CGAAGCTCACCACCGTGATGTTAACCATTTTGCATCGGACATTCATTATCAGGGACATGAACTGAAGGAA 1190
E A H H R D V N H F A S D I H Y Q G H E L K E

TCCCCAGCTCCACTTGGATATCACTGAATGGTCTGAAGAAGTATACTGGAGAAGTATATTTAACCAATAT 1260
S P A P L G Y H *

CTATAATATCGAATAAGATATACTAATTTGTTAAATTTTCCTTTTCTTGAGATTGATTTTCATTGTATGTT 1330
TTTCACTGATCATCATATAATAAGTGTGAATGTCTGTTATTTTACGTTTTTGGTTGAGAAATATCATGA 1400
ACTAGTAATCGCTTTGCGTATTATATTCTTTTAAGGTATTACTAAAAAAAAAAAAAAAAA 1462

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Figure S1. Nucleotide and deduced amino acid sequences of cDNA encoding *AOX1a* of *Olea europaea* L. cv. ‘Galega vulgar’; the sequence corresponds to the first transcript variant (*OeAOX1a_transcript variant X1*, acc. no. MF410314). Since no other ATG codons was found in the beginning of the resultant ORFs it was considered that the selected ones represent the correct initiation of translation. ▼ indicates the position of the three introns, * indicates stop codon.


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ATGATGATAAAAAGCACGACCAGGGTAGCACGGGCGGTGTTATGCCACATGGGCCCACGTTATTTTCGA 70
M M I K S T T R V A R A V L C H M G P R Y F S

CAACCGCCTTGCATGGCTGTGTAGCAAGTGATGTGCAAGCAATTAGGGGTGTTTTGGCGGCACCACCAC 140
T T A L H G C V A S D V Q A I R G V F G G T T T

TTTCTTCCATGGCAATCTTGCCAGAGTTCGAAAAGGTGTTGGTAGGGTGCATGAGGTTGCTGGCGGTT 210
F F H G N L A Q S S E K V L V G C M R L L A V

GGTGGTGCGCGTAAGGCGAGCACTTTGGCCTTGGGTGACAAACAGCAGGAGGAAGAGAAGAAGGTACAAG 280
G G A R K A S T L A L G D K Q Q E E E K K V Q

GAGGAGAACTGGTGGTGCCGCGCTGCCGGTGGGGGCAATAATAACAAGGGAATAGTGAGTTATTGGGG 350
G G E T G G A A A G G G N N N K G I V S Y W G

CGTGGAGCCTGCCAAGATTACTAAAGAGGATGGCTCTGAATGGAGGTGGAAGTCTTTAAGCCATGGGAG 420
V E P A K I T K E D G S E W R W N C F K P W E

ACCTACAAGGCTGATCTGTCTATAGATCTGAAGAAACACCATGCCCTGTACATTCTTAGACAAGGTGG 490
T Y K A D L S I D L K K H H A P V T F L D K V

CATATTGGACCGTCAAGTCTCTCAGATTTCTACAGATATATTCTTTTCTCAGAGGCGGTATGGATGTCTGTC 560
A Y W T V K S L R F P T D I F F Q R R Y G C R A

TATGATGCTGAAACTGTGGCCGCTGTACCTGGAATGGTCGAGGGATGCTTCTGCACTGCAAGTCACTG 630
M M L E T V A A V P G M V G G M L L H C K S L

AGGCAATTCGAGCACAGTGGTGGTTGGATCAAAGCATTGTTAGAAGAAGCCGAAAATGAAAGAATGCACC 700
R Q F E H S G G W I K A L L E E A E N E R M H

TCATGACATTATGGAAGTTTCCAGCCCAGATGGTACGAACGCGCTCTGTATTCACTGTGCAGGGCGT 770
L M T F M E V S Q P R W Y E R A L V F T V Q G V

ATTTTTCAATGCCTACTTCTTGACCTATCTCGCTTCCCCGAAATTGGCTCATCGGATCGTGGGGTATTTG 840
F F N A Y F L T Y L A S P K L A H R I V G Y L

GAAGAGGAGGCGATCCACTCGTACACCGAGTTCTTGAAAGAGTTGGACAAGGGCACTATTGAGAATGTTT 910
E E E A I H S Y T E F L K E L D K G T I E N V

CTGCTCCGGCTATTGCCATCGACTATTGGCGTATGCCACCAAACCTCGACTCTGCGCGATGTAGTCACGGT 980
P A P A I A I D Y W R M P P N S T L R D V V T V

GGTTAGAGCTGACGAGGCTCATCACTGTGATGTTAACCATTTTGCATCGGACATTCATTATCAGGGACAT 1050
V R A D E A H H C D V N H F A S D I H Y Q G H

GAACTGAAGGAAGCCCCGGCCCCAATTGGATATCACTGAATGGTCTGAAGAACTATACCTGGAGAAGTAT 1120
E L K E A P A P I G Y H *

ATTTAACCAATATCTATAATATTGAATAAGATATACTAATATGTTAAATTTTCCTTTCTTAAGGTTGAT 1190
TTCATGTACATTTTCACTGATCACAATTTCTGATGGATAATAAAAAAAAAAAAAAAAAA 1249

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Figure S2. Nucleotide and deduced amino acid sequences of cDNA encoding *AOX1a* of *Olea europaea* L. cv. ‘Galega vulgar’; the sequence corresponds to the second transcript variant (*OeAOX1a_transcript variant X2*, acc. no. MG208095). Since no other ATG codons was found in the beginning of the resultant ORFs it was considered that the selected ones represent the correct initiation of translation. ▼ indicates the position of the three introns, * indicates stop codon.

ACACCAAAATCAAAGCTCAAAATACAATTCAAATTATTTTGTGTTTATTTCTTTCTATATTCAAAATCCC 70
 GAATTCCAATGAGCCAACGTACAATTTCTAGTATGGTTTTTCGACAGATGCAGTCGAATTTTTCATCTTT 140
 M S Q R T I S S M V F R Q M Q S N F S S F
 TAGTAGTTCGATGAATAATGTCTCCAAGAACTACCGACCCGAATCACTCATATTTTGGAGGCAAGGTAC 210
 S S S M N N V S K N Y R P A I T H I F E A R Y
 TATAGTAGTAACCTAGGTTCAAAGGTAACAAGAAGACGAGCCAGCACAAGCTGTGAAATTCGATTCCA 280
 Y S S N L G S K G N K E D E P A Q A V K F D S
 ACTTTGAAAACGTCGATGGCCAAAATGGTAAGGCCGTCGTAAGCAGCTACTGGGGAGTACCTCCGTGCGAG 350
 N F E N V D G Q N G K A V V S S Y W G V P P S R
 GCGGACCAAGGAGGATGGATCGCCCTGGCGATGGAATTGTTTTCGGCCATGGGAGACTTATAAAGCGGAC 420
 A T K E D G S P W R W N C F R P W E T Y K A D
 ACTTCAATTGATGTGACAAAGCACCACAAGGCAACTACGTTTCATGGACAAAATTTGCCTATTGGACTGTTC 490
 T S I D V T K H H K A T T F M D K F A Y W T V
 AATCTCTCAAATTCACCTTAACCACTTTGCATCGAGACGCCACATGTGCCACGCTATGCTCCTAGAGAC 560
 Q S L K F P T Y L F F Q R R H M C H A M L L E T
 GGTGGCAGCTGTCCCGGGCATGGTGGGGGGGATGCTCCTACACTTAAAGTCGATCCGGCGGTTTGAACAC 630
 V A A V P G M V G G M L L H L K S I R R F E H
 AGCGGTGGTTGGATCAAAGCCCTTCTCGAGGAAGCGGAAAATGAGAGAATGCATCTAATGACATTCTTAG 700
 S G G W I K A L L E E A E N E R M H L M T F L
 AACTATCCCAACCGAAATGGTACCAGAGAGCCCTAGTATTTGCTGTCCAAGGTGTATTTGCAAATGCATA 770
 E L S Q P K W Y Q R A L V F A V Q G V F A N A Y
 CTTTGTGCTCTATGTTGTGTCCCAAACTTGCTCATCGCATAGTAGGCTACCTTGAAGAAGAGGCAGTG 840
 F V S Y V V S P K L A H R I V G Y L E E E A V
 AATTCATACACTGAATTTCTAATTGATTTGGAGAAGGGCCTTGTTGAAAATAGACCGGCGCCGGCAATCG 910
 N S Y T E F L I D L E K G L V E N R P A P A I
 CCATTGATTACTGGCAGTTGCCGTGGAATCAACGTTAAAGATGTTGTACGGTTATCAGGGCAGACGA 980
 A I D Y W Q L P S E S T L K D V V T V I R A D E
 GGCACACCATCGTGACCTTAACCACTTTGCATCGGACATTCAATGTGAAGGACACGAGCTAAAGGAATAT 1050
 A H H R D L N H F A S D I Q C E G H E L K E Y
 CCTGCCCGCTGGGATACCACTGAAGGACAAAAGGTTATTGAATAGAAAAAATTGCATACATATTTATTT 1120
 P A P L G Y H *
 TATTATTTTGAAGAATAATTTCTGTAATTTAGAATAGAATAAATGCATATATATTTATTTATTTATTTG 1190
 AAAAGTAATTTCTGTAATTTCTATTTTGTACTAAAATAATATTATTTCTCCTTTCATAAAAAAAAAAAAA 1260
 AAAAAAAAAAAAAAAAAA 1277

Figure S3. Nucleotide and deduced amino acid sequences of cDNA encoding *AOX1d* of *Olea europaea* L. cv. 'Galega vulgar'; the sequence corresponds to the first transcript variant (*OeAOX1d* transcript variant X1, acc. no. MF410315). Since no other ATG codons was found in the beginning of the resultant ORFs it was considered that the selected ones represent the correct initiation of translation. ▼ indicates the position of the three introns, * indicates stop codon.

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ACACCAAAATCAAAGCTCAAAATACAATTCAAATTATTTTGTGTTTATTTCTTCTATATTCAAATCCC 70
GAATTCCAATGAGCCAACGTACAATTTCTAGTATGGTTTTTCGACAGATGCAGTCGAATTTTTCATCTTT 140
      M S Q R T I S S M V F R Q M Q S N F S S F

TAGTAGTTCGATGAATAATGTCTCCAAGAACTACCGACCCGCAATCACTCATATTTTGGAGCAAGGTAC 210
      S S S M N N V S K N Y R P A I T H I F E A R Y

TATAGTAGTAACCTAGGTTCAAAGGTAACAAGAAGACGAGCCAGCACAAAGCTGTGAAATTCGATTCCA 280
      Y S S N L G S K G N K E D E P A Q A V K F D S

ACTTTGAAAACGTCGATGGCCAAAATGGTAAGGCCGTCGTAAGCAGCTACTGGGGAGTACCTCCGTCGAG 350
      N F E N V D G Q N G K A V V S S Y W G V P P S R
                                ▼
GGCGACCAAGGAGGATGGATCGCCCTGGCGATGGAATTGTTTTCGGCCATGGGAGACTTATAAAGCGGAC 420
      A T K E D G S P W R W N C F R P W E T Y K A D

ACTTCAATTGATGTGACAAAGCACCACAAGGCAACTACGTTTCATGGACAAATTTGCCTATTGGACTGTTC 490
      T S I D V T K H H K A T T F M D K F A Y W T V
                                ▼
AATCTCTCAAATTCGCCACTTCTGTTTTTCAGAGACGCCACATGTGCCACGCTATGCTCCTAGAGAC 560
      Q S L K F P T Y L F F Q R R H M C H A M L L E T

GGTGGCAGCTGTCCCGGCGATGGTGGGGGGATGCTCCTACACTTAAAGTCGATCCGGCGGTTTGAACAC 630
      V A A V P G M V G G M L L H L K S I R R F E H

AGCGGTGGTTGGATCAAAGCCCTTCTCGAGGAAGCGGAAAATGAGAGAATGCATCTAATGACATTCTTAG 700
      S G G W I K A L L E E A E N E R M H L M T F L

AACTATCCCAACCGAAATGGTACCAGAGAGCCCTAGTATTTGCTGTCCAAGGTGTATTTGCAAATGCATA 770
      E L S Q P K W Y Q R A L V F A V Q G V F A N A Y

CTTTGTGTCTTATGTTGTGTCCCAAACTTGCTCATCGCATAGTAGGCTACCTTGAAGAAGAGGCAGTG 840
      F V S Y V V S P K L A H R I V G Y L E E E A V

AATTCATACACTGAATTTCTAATTGATTGGAGAAGGGCCTTGTGAAAAATAGACCGGCGCCGGCAATCG 910
      N S Y T E F L I D L E K G L V E N R P A P A I

CCATTGATTACTGGCAGTTGCGGTGCGGAATCAACGTTAAAGATGTTGTACGGTTATCAGGGCAGACGA 980
      A I D Y W Q L P S E S T L K D V V T V I R A D E

GGCACACCATCGTGACCTTAACCACTTTGCATCGGTAAGAAAAGATTTTCATTTTCTTTTCGACGAAAAT 1050
      A H H R D L N H F A S V R K I F I F L F D E N

ATTCTTAATACTTCAAACCTTGTAGAGAGGTAATTGATCAATATGGTACCAAATCGAGAAAGTCTTTA 1120
      I L N T S N L L E E V I D Q Y G T K I E K V F

TAATAAAAATTAATAAATAATATCTTCTACGTAGTAGTTGAATTTGAGAAATGCTACACTTACAAAAT 1190
      I I K I N K *

AGACCCTTGCCAGATCTTTCACATGTGCGGACCCCTACGTGGGACCGACCCCTACAATGAGGGGTCGATA 1260
AAACATCTGTAGGAAATTGTTACGTACACAGAGCAATTTCTTTGAATTTTGTATGAAAGATCGCACAAAT 1330
TCCTAGATATTTGTCAAATAAGAAATTTTCGATAATAGATGACAATAAATGATATCTAGTAGTGGATAA 1400
ATAAAATAACTTATTTTCTAATAATTAGGTCGTACAAAAATTTCTTTATTATTCAAGTGAATGTCCTGGT 1470
CTAAGTACTAAAAGGGATTTTGTACACTATAATATATAAAAGTTCAATTTTATTATAAATCTATAATTC 1540
GTTTAATGTCCTAATAAGGAGTAATAATTTGTGAAATGAAACAAAAAAAAAAAAAAAAA 1597

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Figure S4. Nucleotide and deduced amino acid sequences of cDNA encoding *AOX1d* of *Olea europaea* L. cv. ‘Galega vulgar’; the sequence corresponds to the second transcript variant (*OeAOX1d_transcript variant X2*, acc. no. JX912721). Since no other ATG codons was found in the beginning of the resultant ORFs it was considered that the selected ones represent the correct initiation of translation. ▼ indicates the position of the three introns, * indicates stop codon.

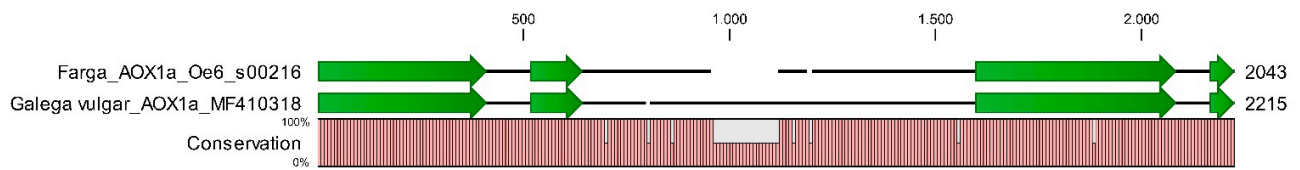
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 CCCAGAGTTCTGAAAAGGTGTTGGTAGGGTGCATGAGGTGCTGGCGGTGGTGGTGCGCGTAAGGCGAGCACTTTGGCC
 TTGGGTGACAAAACAGCAGGAGGAAGAGAAGAAGGTACAAGGAGGAGAACTGGTGGTGCCGCCGCTGCCGGTGGGGGCAA
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 ACTGCTTTAA>GTATGTAGGAAAAAATTAAGAAGCTTCTATATTATTATTTGGTTCATATTCAAATTTTATGAATTAAT
 TTGATTTGGCCTTTTGAATTTAATGATTTATGAAGCCATGGGAGACCTACAAGGCTGATCTGCTATAGATCTGAAGAAA
 CACCATGCCCTGTACATTTCTTAGACAAGGTGGCATATTGGACCGTCAAGTCTCTCAGATTTCTACAGATATATTCTT
 TCA>GTATGTTATTATATTCTCTAGCTTGGTTAATAAAGAAGAGTTTTTTTTTTTTTTTTCAGATTATGATAATTTGTT
 GAAATGAACAGTTGAAAAGTTGATAATAATTATGAGTTTCATGCGTGTGAAAATGAATTCGACGAAAAAAGAGAA
 TTTTCAATAAATAGTAGGGTTAATGTTCTTGATTCAAGTCTTTTAGTGAATAAATGAATTTCTATATTCTTTAGGCT
 TTCCTTCCATCCTGTTTGGTTTAGCTAATTTTAGTCAAAACCTGGTAAAAATGGAAGTTAAGAGTCCATTTGGTACACAT
 TAATGTAATAATGAGAAATGTAATAATAGTCGTTATGGACCTCACACAAGAGATAGAAATTCAAATTTGGTGGCTCGATG
 TGATGGATAAATCATATTTTTCATTTTAAATGAAGAAAAATGGGAAACAAAAGGAGCTAAAATTTAATAATTAATTT
 TAACCATGAAATATGTATCCATGACTCTTATCACTTTTCAATGATATATTTTCATCAACTTTTATAAAATTTATTGAAA
 ATCTAATTTTAAATGCGAAAACTGAAACCAATCTCTATTTTGAACGTATGTAGTTACAAAAAGTTAAAAAGAAAGTAGAA
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 AGCCAACAATTATCAGAAAAATGCTTAGCTGTTGTTCTTTCTATTAGATGGAAAGATACAGGGGGTTAGATGTTGTATT
 GCATTTATGGTTTCTTTGGTGGATTAAACTTTATATTAGTCAAACCTATTAATCAAGCAAAAGTGGATACTTGTGTTGTTG
 GATTATTGTGCTCGTGCAATAGTGCATACCAACAACGCATTTAATTACTTTATCCTGTTACAGAGGCGGTATGGATGT
 CGTGCTATGATGCTGGAACTGTGGCCGCTGTGCTTGGCATGGTTGGAGGGATGCTTCTGCACTGCAAGTCACTGAGGCG
 ATTCGAGCACAGTGGTGGTTGGATCAAAGCATTGTTAGAAGAAGCCGAAAAATGAAAGAATGCACCTCATGACATTCATGG
 AAGTTTCCAGCCAGATGGTACGAACGCGCTCTTGTATTCACTGTGCAGGGCGTATTTTCAATGCATACCTTCTTGACC
 TATCTCGTTTCCCGAAATTTGGCGCATCGGGTTGTGGGGTATTTGGAAGAGGAGGCGATCCACTCGTACACCGAGTTCTT
 GAAAGAGTTGGACAAGGGCACTATTGAGAATGTTCTGCTCCGGCTATTGCCATCGACTATTGGCGTATGCCACCAAACT
 CGACTCTGCGCGATGTAGTCATGGTAGTTAGAGCTGACGAAGCTCACCACCGTGATGTTAACCATTTTGATC>GTACGT
 GCATAAACTTCATATGTTTGTATTTCAAAGCAATTTGATTTAGATGCTTAGGGTTTATTTGTAATGATTGCAGGACAT
 TCATTATCAGGGACATGAAGTGAAGGAATCCCAGCTCCACTTGGATATCACTG>

Figure S5. Genomic sequence of *AOX1a* from *Olea euroaea* L. cv. 'Galega vulgar' (acc. no. MF410318) including the indication of the three exons with conserved sequence size (129, 489 and 57 bp, respectively) interrupted by three size variable introns.

ATGAGCCAACGTACAATTTCTAGTATGGTTTTTCGACAGATGCAGTCGAATTTTTCATCTTTTAGTAGTTCGATGAATAA
 TGTCTCCAAGAACTACCGACCCGCAATCACTCATATTTTGGAGCAAGGTACTATAGTAGTAACCTAGGTTCAAAGGTA
 ACAAAGAAGACGAGCCAGCACAAGCTGTGAAATTCGATTCCAACTTTGAAAACGTCGATGGCCAAAATGGTAAGGCCGTC
 GTAAGCAGCTACTGGGGAGTACCTCCGTCGAGGGCGACCAAGGAGGATGGATCGCCCTGGCGATGGAATTGTTTTCGGGT
 ACGTACCCTAAAATTGTAAGAATTTTGCCATTTGGTGTATGAAATAGAAACACAATTTATGGTCAATGTTTAT
 GATCAGTTTTTGAATTTGCATTTTTCAGCCATGGGAGACTTATAAAGCGGACACTTCAATTGATGTGACAAAGCACCAC
 AAGGCAACTACGTTTCATGGACAAATTTGCCTATTGGACTGTTCAATCTCTCAAATTCGCCACCTACTTGTITTTTCAAGT
 TACACAATCATTTTCTGTTACCCATCTTAAACTTGTCAATCATGTCCATTTTGTATAATAAGTTTCGAGTATCGTTTAT
 ATTTAGTACGCAGTTTGGGCACTATACTATCGTCCAAACAAATTCGGTAATCTATAGAAGCTCTTGATATCGTCAACTA
 TTTTAAATTCAGTTATATTTCTAAATTCCTGACTGATAATTTCTTGTAGAGACGCCACATGTGCCACGCTATGCTCCTAG
 AGACGGTGGCAGCTGTCCCGGGCATGGTGGGGGGGATGCTCTACACTTAAAGTCGATCCGGCGGTTTGAACACAGCGGT
 GGTTGGATCAAAGCCCTTCTCGAGGAAGCGGAAAATGAGAGAATGCATCTAATGACATTCTTAGAACTATCCCAACCGAA
 ATGGTACGAGAGAGCCCTAGTATTTGCTGTCCAAGGTGTATTTGCAAATGCCTATTTTGTGTCCTATGTTGTGTCCCAA
 AACTTGCTCATCGCATAGTAGGCTACCTTGAAGAAGAGGCAGTGAATTCATACACTGAATTTCTAATTGATTTGGAAAAG
 GGCTTGTGTGAAAATAGACCGGCGCCGGCAATCGCCATTGATTACTGGCAGTTGCCGTCGGAATCGACATTAAAAGATGT
 TGTACGGTTATCAGGGCAGACGAGGCACACCATCGTGACCTTAACCACTTTGCATCGTAAGAAAGATTTTCATTTTCC
 TTGTGACGAGAAAATATTTTAATACTTCAAACCTGTTAGAAGAGATAATTGATCAATATGGTACCAAATTCGAGAAAGTC
 TTTATAATAAAAAATTAATAATAATAAATTTCTTCTGTGTAGTAGTTTGAATTTTAGATGAAAGATCGTACAATTCCTAGAC
 ATTTTGTAAAATAAGAAATTTTCGATAATAGATGACGATAAATGATATCTAGTAGCGGATAAATAAAATAACTTATTTT
 CTAATAATTAGGTTGTACAAAAATTTCTTTATTAAAGGTTGAACCCCAACCTTAAGGGTCCCCCACCCTCCTTGTCTGA
 AGTATCGTGAGGGAGGTAAATCGCAGGTTATGCCTCCAAGAGTACAGGGTGAAGGCTGCTTGTACACTTGCCTTACCC
 AAGAGCCAAATCCATATTTCAAGATTGCAACCCCTTGATGCGACAGCCTCAAGTAAAACCTGGATTTCTTTATTATTCAAGT
 GAACATCTGGTCTAAGAACTAAAAGGGATTTTGGACAATACAATATACAAATTTCACTTTTTTATTAATAATCTATAATT
 CGTTTAATGTCGTAATAAGGAGTAATAAATTGTGAAATGAAAAAGAAAAAAGAAAAAACACAATCACTTAATTTTTTTA
 TAATGACTTAATTTCTTTAATATGCAGGACATTCAATGTGAAGGACACGAGCTAAAGGAATATCCTGCCCCGCTGGGAT
 ACCACTGA

Figure S6. Genomic sequence of *AOX1d* from *Olea europaea* L. cv. 'Galega vulgar' (acc. no. MF410319) including the indication of the exons/introns structure (exons coloured in green). The indication of the four exons structure with size conservation observed at the three last exons (129, 489 and 57 bp, respectively) known as the most typical *AOX* gene structure described in higher plants corresponds to transcript variant X1; the intron 3 region that is transcribed at transcript variant X2 instead of exon 4 is here indicated in red. Primers used in RT-qPCR analysis for *OeAOX1d* gene (designed to a common region) are indicated in yellow and for transcript variants X1 and X2 are indicated in blue.

I.



II.

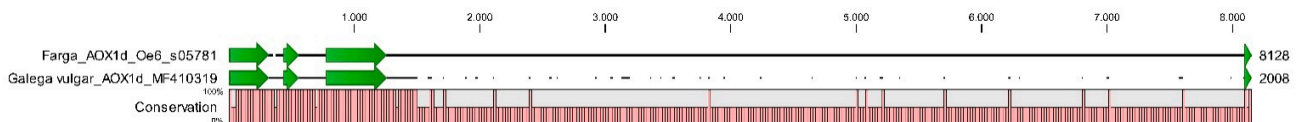


Figure S7. Comparison of *OeAOX* gene sequences isolated in cv. “Galega vulgar” with the sequences available from the olive whole genome sequencing databases in the cv. ‘Farga’. I: *OeAOX1a* gene, II: *OeAOX1d* gene structure.

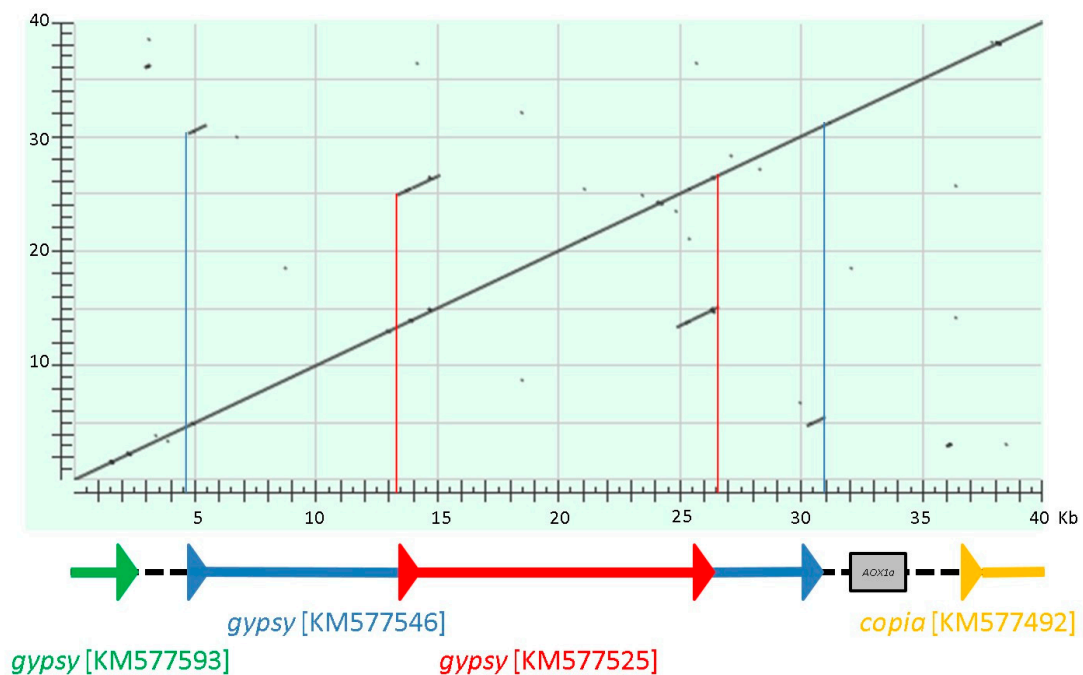


Figure S8. Location of the regulatory elements identified upstream and downstream the *OeAOX1a* gene in cv. ‘Farga’.

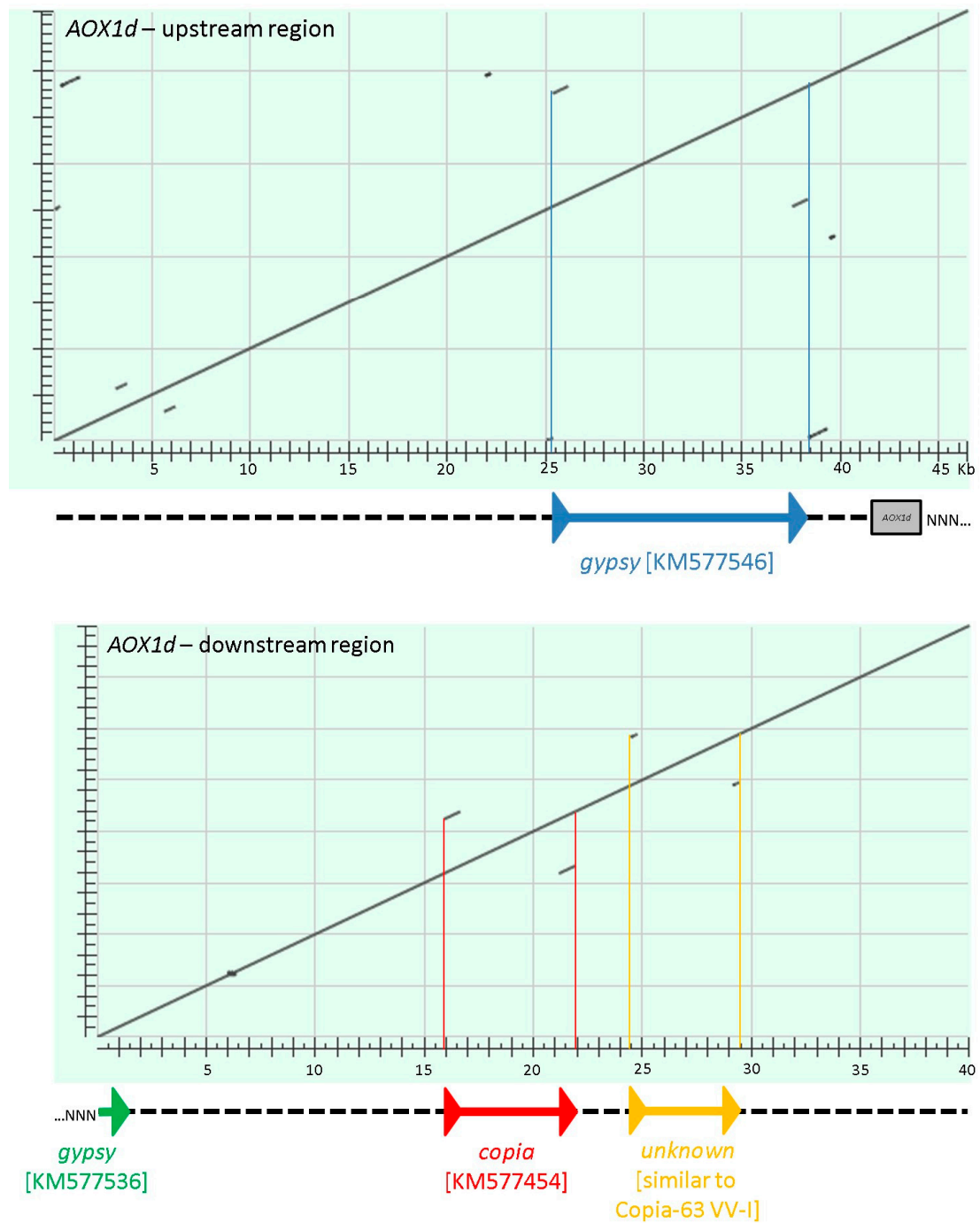


Figure S9. Location of the regulatory elements identified upstream and downstream the *OeAOX1d* gene in cv. 'Farga'.