

Supplementary Table S1. General features of *Vitis vinifera* fatty acid desaturases superfamily. Proposed grapevine fatty acid desaturases nomenclature, gene locus, protein and nucleotide accessions (from NCBI), chromosome location, exon number, protein length, molecular weight (Mw), isoelectric point (pl) and subcellular prediction are represented.

Group	Sub-group	Proposed nomenclature	Locus	Nucleotide	Protein	Chr. location	Position on chr. (Mb)	Exons	Protein length (aa)	Mw (kDa)	pl	Subcellular location
Membrane-bound fatty acid desaturases	acyl-lipid Δ12/ω6 desaturase	VviFAD2-1	LOC100252129	XM_002279203.4	XP_002279239.1	8	20.2	2	382	44.05	8.94	Endoplasmic reticulum
		VviFAD2-2	LOC100258789	XM_002285604.3	XP_002285640.1	6	1.4	2	376	43.52	8.83	Endoplasmic reticulum
	acyl-lipid Δ15/ω3 desaturase	VviFAD3-1	LOC100243349	XM_002277537.4	XP_002277573.1	6	7.4	9	386	44.54	8.96	Endoplasmic reticulum
		VviFAD3-2	LOC100251798	XM_010652591.2	XP_010650893.1	6	7.4	9	398	45.97	6.89	Endoplasmic reticulum
	acyl-lipid Δ3 desaturase	VviFAD4	LOC100257229	XM_002280947.4	XP_002280983.1	19	6.3	1	307	34.52	8.52	Chloroplast
	acyl-lipid Δ12/ω6 desaturase	VviFAD6	LOC100248377	XM_003634815.2	XP_003634863.1	11	0.1	10	441	51.13	9.05	Chloroplast
	acyl-lipid Δ15/ω3 desaturase	VviFAD7	LOC100260414	XM_002273738.3	XP_002273774.1	13	0.6	8	456	51.55	8.67	Chloroplast
		VviFAD8	LOC100247097	XM_002264314.4	XP_002264350.1	8	7.7	8	452	51.97	8.57	Chloroplast
	sphingolipids Δ8 desaturase	VviSLD-1	LOC100259521	XM_002279153.4	XP_002279189.1	4	0.99	1	447	51.46	8.56	Endoplasmic reticulum
		VviSLD-2	LOC100265385	XM_002279191.3	XP_002279227.1	15	18.6	1	447	51.03	8.16	Endoplasmic reticulum
Soluble desaturases	acyl-lipid Δ9 desaturase	VviADS	LOC100249077	XM_002265374.4	XP_002265410.1	9	6.9	5	382	43.77	9.51	Chloroplast
	sphingolipids Δ4 desaturase	VviDES	LOC100854247	XM_003635372.3	XP_003635420.1	un	un	2	327	37.92	6.39	Endoplasmic reticulum
		VviSAD-1	LOC100242444	XM_002274672.4	XP_002274708.2	5	24.1	3	396	45.37	6.14	Chloroplast
		VviSAD-2	LOC100853715	XM_003635330.3	XP_003635378.1	un	un	3	393	44.99	7.21	Chloroplast
	acyl-ACP Δ9 desaturase	VviSAD-3	LOC100255873	XM_002264759.4	XP_002264795.1	18	13.6	3	389	44.24	6.16	Chloroplast
		VviSAD-4	LOC100252677	XM_002274616.3	XP_002274652.1	5	24.1	3	387	44.63	6.48	Chloroplast
		VviSAD-5	LOC100267952	XM_002274047.3	XP_002274083.1	5	23.9	3	387	44.30	6.48	Chloroplast

Supplementary Table S3. Protein motifs of the *Vitis vinifera* fatty acid desaturases.

Supplementary Table S4. Protein domains of the *Vitis vinifera* fatty acid desaturases.

Group	Sub-group	Proposed nomenclature	Domain	Start	End
Membrane-bound fatty acid desaturases	acyl-lipid Δ12/ω6 desaturase	VviFAD2-1	Fatty acid desaturase (PF00487)	82	350
		VviFAD2-2	Fatty acid desaturase (PF00487)	71	343
		VviFAD3-1	DUF3474 (PF11960)	4	73
	acyl-lipid Δ15/ω3 desaturase	VviFAD3-1	Fatty acid desaturase (PF00487)	79	339
		VviFAD3-2	DUF3474 (PF11960)	1	85
	acyl-lipid Δ3 desaturase	VviFAD4	TMEM189_B_dmain (PF10520)	119	287
	acyl-lipid Δ12/ω6 desaturase	VviFAD6	Fatty acid desaturase (PF00487)	141	397
		VviFAD7	DUF3474 (PF11960)	1	145
	acyl-lipid Δ15/ω3 desaturase	VviFAD7	Fatty acid desaturase (PF00487)	150	411
		VviFAD8	DUF3474 (PF11960)	1	141
	sphingolipids Δ4 desaturase	VviSLD1	Fatty acid desaturase (PF00487)	146	407
		VviSLD2	Cytochrome b5 (PF00173)	9	101
	acyl-lipid Δ9 desaturase	VviADS	Fatty acid desaturase (PF00487)	135	408
	sphingolipids Δ4 desaturase	VviDES	Sphingolipid Δ-desaturase (PF08557)	69	297
Soluble desaturases	acyl-ACP Δ9 desaturase	VviSAD-1	Fatty acid desaturase 2 (PF03405)	11	47
		VviSAD-2	Fatty acid desaturase 2 (PF03405)	68	390
		VviSAD-3	Fatty acid desaturase 2 (PF03405)	65	387
		VviSAD-4	Fatty acid desaturase 2 (PF03405)	57	383
		VviSAD-5	Fatty acid desaturase 2 (PF03405)	59	381

Supplementary Table S5. Subcellular prediction of the *Vitis vinifera* fatty acid desaturases proteins.

		TargetP 2.0				Lozalizer Version 1.0.4				Predotar Version 1.04						
Group	Sub-group	Proposed nomenclature	Other	Signal peptide	Mitochondrial transfer peptide	Chloroplast transfer peptide	Thylakoid luminal transfer peptide	Chloroplast	Mitochondria	Nucleus	Mitochondrial	Plastid	Endoplasmic Reticulum	Elsewhere	Result	Final Prediction
Membrane-bound fatty acid desaturases	acyl-lipid Δ12/ω6 desaturase	VviFAD2-1	0.9996	0.0001	0	0.0001	0.0002	-	-	-	0,03	0,02	0	0,95	none	Endoplasmic reticulum
		VviFAD2-2	0.9846	0	0.0003	0.0109	0.0041	Y (0.838 1-42)	-	-	0,08	0,52	0	0,44	plastid	Endoplasmic reticulum
	acyl-lipid Δ15/ω3 desaturase	VviFAD3-1	1	0	0	0	0	-	-	-	0,01	0,01	0	0,99	none	Endoplasmic reticulum
		VviFAD3-2	1	0	0	0	0	-	-	-	0,01	0,01	0	0,99	none	Endoplasmic reticulum
	acyl-lipid Δ3 desaturase	VviFAD4	0.149	0	0.0179	0.7856	0.0474	-	-	-	0,28	0,26	0	0,53	plastid	Chloroplast
	acyl-lipid Δ12/ω6 desaturase	VviFAD6	0.0685	0.0002	0.0137	0.9009	0.0167	Y (0.971 1-25)	-	Y (KRVK)	0,04	0,57	0,02	0,41	plastid	Chloroplast
	acyl-lipid Δ15/ω3 desaturase	VviFAD7	0.0527	0.0001	0.0035	0.9316	0.0122	Y (0.994 1-59)	-	-	0,09	0,79	0,01	0,19	plastid	Chloroplast
	sphingolipids Δ8 desaturase	VviSLD-1	0.9999	0	0	0	0	-	-	-	0,01	0	0	0,99	none	Endoplasmic reticulum
		VviSLD-2	1	0	0	0	0	-	-	-	0,01	0	0	0,99	none	Endoplasmic reticulum
	acyl-lipid Δ9 desaturase	VviADS	0.0709	0	0.0005	0.9137	0.0148	Y (1.0 1-41)	-	Y (RRRK,RRRR)	0,05	0,93	0,02	0,07	plastid	Chloroplast
Soluble desaturases	acyl-ACP Δ4 desaturase	VviDES	1	0	0	0	0	-	-	-	0,01	0	0	0,99	none	Endoplasmic reticulum
		VviSAD-1	0.013	0	0.0096	0.9761	0.0013	Y (0.828 1-42)	Y (0.792 1-40)	Y (RKAQDYVCGLAPRFRKL)	0,03	0,33	0,01	0,64	possibly plastid	Chloroplast
	acyl-ACP Δ9 desaturase	VviSAD-2	0.0724	0	0.0339	0.8759	0.0178	Y (0.999 1-26)	-	Y (RKAQDYVCGLAPRIRKL)	0,28	0,88	0	0,09	plastid	Chloroplast
		VviSAD-3	0.0565	0	0.0077	0.932	0.0037	Y (1.0 1-41)	-	Y (RRAQDFVCGLAPRIRKL)	0,18	0,05	0,01	0,77	none	Chloroplast
		VviSAD-4	0.0611	0.0104	0.0093	0.9077	0.0114	Y (0.998 1-51)	-	Y (RKAQDYVCGLAKRLRT)	0,09	0,63	0,16	0,28	plastid	Chloroplast
		VviSAD-5	0.0489	0.0574	0.0223	0.8552	0.0161	Y (0.999 1-51)	-	Y (RKAQDYVCGLAQRLRKL)	0,07	0,62	0,22	0,28	plastid	Chloroplast

Supplementary Table S6. Reference and target genes transcripts primer sequences, amplicon length, amplification efficiency, annealing and melting temperature are represented.

Gene name	Abbreviation	NCBI Accession Number	Primer Sequence	Amplicon length (bp)	T _a (°C)	T _m (°C)	Amplification efficiency (E)	Reference
Elongation Factor 1-alpha	<i>EF1α</i>	XM_002284888.3	Fw: AACCAAAATATCCGGAGTAAAAGA Rev: GAACTGGGTGCTTGATAGGC	150	60	80.20	1,95	Reid et al. (2006)
Ubiquitin-conjugating enzyme	<i>UBQ</i>	XM_002273532.2	Fw: GTGGTATTATTGAGCCATCCTT Rev: AACCTCCAATCCAGTCATCTAC	182	60	81.28	1,90	Reid et al. (2006)
	<i>VviFAD2-1</i>	XM_002279203.4	Fw: CCCAAACCAAATCCAAACTC Rev: TACTGTAGCGCCTGCCTGAA	139	60	79.51	1,91	
	<i>VviFAD2-2</i>	XM_002285604.3	Fw: GTGCCAAAGCCCCAAATCCAG Rev: ATTATAGGGGCCAGACACATT	138	60	80.79	2,04	
	<i>VviFAD3-1</i>	XM_002277537.4	Fw: ATAGAACGCCAGGGAAAGAAG Rev: CAAAGGATAACGCAAACAAGCA	135	60	80.00	1,96	
	<i>VviFAD3-2</i>	XM_010652591.2	Fw: TGGTACCGTGGCAAGGAAT Rev: ATGCGTGCCAGTGTTATGTT	Not detected				
Membrane-bound fatty acid desaturases	<i>VviFAD4</i>	XM_002280947.4	Fw: TGTCAGCCAGCAGTCCAT Rev: CTCGACACTAGCAGTCCAG	97	60	83.06	1,97	
	<i>VviFADS</i>	XM_002265374.4	Fw: TCGGGTGACTGGTCTATTG Rev: AACCCCACAGTAGGCGAAA	109	58	78.32	2,02	
	<i>VviFAD6</i>	XM_003634815.2	Fw: CATGGTTGGGTTATCACTTCT Rev: CTATCCAACGAGGGTAATCAC	147	60	78.86	1,96	
	<i>VviFAD7</i>	XM_002273738.3	Fw: TACCGCTACTAGAACATTG Rev: TCCTACCCCCACAGATAAAG	72	54	76.35	1,89	
	<i>VviFAD8</i>	XM_002264314.4	Fw: GGCACTTTCCCTCCTCCTT Rev: GGGCCTTATGCCACATTCT	151	58	79.16	2,04	
Soluble desaturases	<i>VviSAD-1</i>	XM_002274672.4	Fw: AGGTCAAGGCATAACTCTC Rev: ACGAAAATGCAACTGGGAAAC	89	58	77.83	1,94	
	<i>VviSAD-2</i>	XM_003635330.3	Fw: TATGTCTGTGGACTGGCTC Rev: AGTTGCTTGCTTCACCCCTC	72	58	77.63	1,96	

Supplementary Table S7. Biological process and function of the *Vitis vinifera* fatty acid desaturases proteins.

Group	Sub-group	Proposed nomenclature	Biological process	Putative Function
Membrane-bound fatty acid desaturases	acyl-lipid Δ12/ω6 desaturase	VviFAD2-1	GO:0006629 - lipid metabolic process	None predicted
		VviFAD2-2	GO:0006629 - lipid metabolic process	None predicted
		VviFAD3-1	GO:0006629 - lipid metabolic process	GO:0016717 - oxidoreductase activity
	acyl-lipid Δ15/ω3 desaturase	VviFAD3-2	GO:0055114 - oxidation-reduction process	GO:0016717 - oxidoreductase activity
	acyl-lipid Δ3 desaturase	VviFAD4	None predicted	None predicted
	acyl-lipid Δ12/ω6 desaturase	VviFAD6	GO:0006629 - lipid metabolic process	None predicted
		VviFAD7	GO:0006629 - lipid metabolic process	GO:0016717 - oxidoreductase activity
	acyl-lipid Δ15/ω3 desaturase	VviFAD8	GO:0006629 - lipid metabolic process	GO:0016717 - oxidoreductase activity
	sphingolipids Δ8 desaturase	VviSLD-1	GO:0006629 - lipid metabolic process	GO:0016491 - oxidoreductase activity
		VviSLD-2	GO:0006629 - lipid metabolic process	GO:0016491 - oxidoreductase activity
Soluble desaturases	acyl-lipid Δ9 desaturase	VviADS	GO:0006629 - lipid metabolic process	GO:0016717 - oxidoreductase activity
	sphingolipids Δ4 desaturase	VviDES	GO:0006629 - lipid metabolic process	GO:0042284 sphingolipid delta-4 desaturase activity
			GO:0030148 - sphingolipid biosynthetic process	
			GO:0006631 fatty acid metabolic process	GO:0016491 oxidoreductase activity
		VviSAD-1	GO:0006633 fatty acid biosynthetic process	GO:0045300 acyl-[acyl-carrier-protein] desaturase activity
			GO:0055114 oxidation-reduction process	
			GO:0006631 fatty acid metabolic process	GO:0016491 oxidoreductase activity
		VviSAD-2	GO:0006633 fatty acid biosynthetic process	GO:0045300 acyl-[acyl-carrier-protein] desaturase activity
			GO:0055114 oxidation-reduction process	
	acyl-ACP Δ9 desaturase	VviSAD-3	GO:0006633 fatty acid biosynthetic process	GO:0045300 acyl-[acyl-carrier-protein] desaturase activity
			GO:0055114 oxidation-reduction process	
		VviSAD-4	GO:0006631 fatty acid metabolic process	GO:0016491 oxidoreductase activity
			GO:0006633 fatty acid biosynthetic process	GO:0045300 acyl-[acyl-carrier-protein] desaturase activity
			GO:0055114 oxidation-reduction process	
		VviSAD-5	GO:0006631 fatty acid metabolic process	GO:0016491 oxidoreductase activity
			GO:0006633 fatty acid biosynthetic process	GO:0045300 acyl-[acyl-carrier-protein] desaturase activity
			GO:0055114 oxidation-reduction process	