Residue N° in LiLOX	645	650	688	702;703	836	840	994
Identity							
N. punctiforme LOX2 (13S)	THLA	RTH	AAQ	R L L	QHAA	VN FP	S I N I
P. aeruginosa LOX (15S)	VHLA	QTH	GAA	VMF	QHAA	VN FP	S TN I
F. oxysporum LOX (13S)	THLV	DTH	· AAR	S G F	QHTA	VN YL -	S I L I
C. reinhardtii (13S)	AHFN	RTH	NAR	K T F	HHAA	VN FG	SVS I
L. incisa LOX (13S)	SHFV	RAH	· NAR	GNF	HHAA	IN YG	SVSM
A. thaliana LOX2 (13S)	SHWL	RTH	· RAR	T C F	HHAA	VN FG	S I S I
P. patens LOX7 (13S)	SHWL	RTH	AAR	Q T F	H H A	VN FG	S I S I
G. max LOX1 (13S)	SHWL	NTH	· LAR	T T F	LHAA	VN FG	S I S I
H. sapiens LOX (15S)	SHLL	RGH	RAR	Q I M	QHAS	VH LG	SV A I

Additional file 4 Alignment of five conserved sequence motifs of LOXs. Residue numbers are those from the LiLOX sequence. The five amino acid residues responsible for iron binding are framed and located in the first, fourth and fifth motif. In addition, the second motif shows the arginine residue at position 689 that may interact with carboxylate residue from the fatty acid substrate and the third motif shows two residues that are located at the bottom of the substrate-binding pocket (702 and 703). For every given residue, identity represents its homology between all 13S-LOXs from Figure 7 used in this alignment (Green = $100 \% < Gold < 50 \% \le Red$). Allignment obtained from the software Geneious, Muscle allignment with default parameters. LOXs accession numbers are as indicated in Fig. 2.