A

Pass 1

Scan	Sequence	Charge	MH+ theo	MH+ obs	DeltaMH+	N-Gap	C-Gap	PnvScr
1106	LEEELGAAAVYAKK	2	1491.787	1492.553	0.766	0.000	0.000	127.533
1170	VLELGSVTESLEAVK	2	1573.847	1574.133	0.286	0.000	0.000	163.071
1351	LKPSGASTGLYEAL	2	1805.144	1805.173	0.029	0.000	417.434	122.803
1363	FmLLPVQSSFK	2	1899.93	1901.613	1.683	588.250	0.000	105.845
868	YNQLLR	2	806.437	807.353	0.916	0.000	0.000	94.913
972	VYESLLSK	1	938.497	938.5	0.003	0.000	0.000	106.754

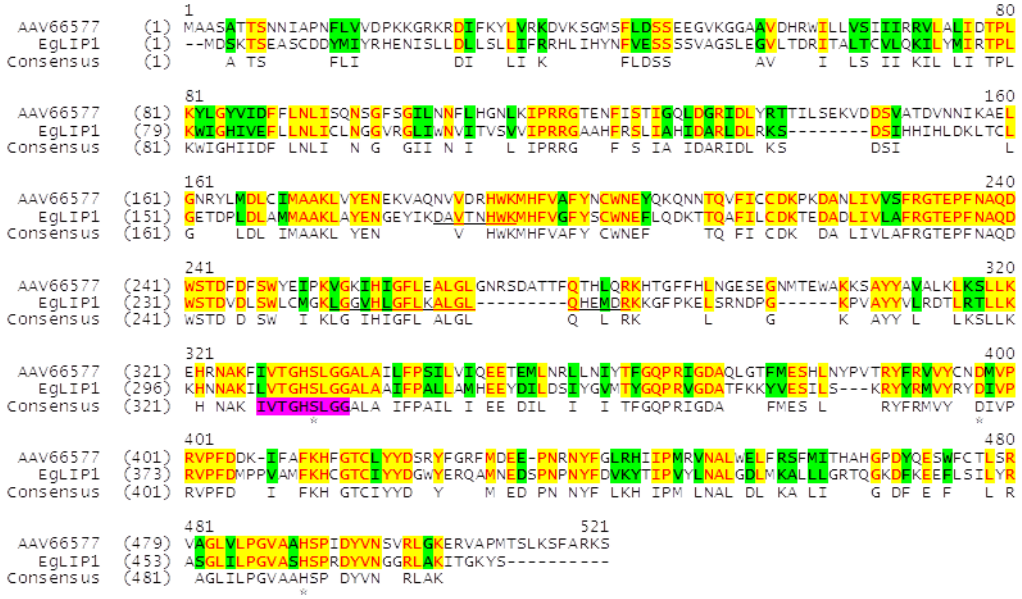
>>gi|365200115|gb|AEW69686.1| enolase1 [Guzmania wittmac (445 aa)
initn: 526 init1: 127 opt: 526 Z-score: 85.7 bits: 104.2 E(): 1e-020
Smith-Waterman score: 526; 72.059% identity (79.412% similar) in 68 aa overlap (1-68:36-436)

Pass 2

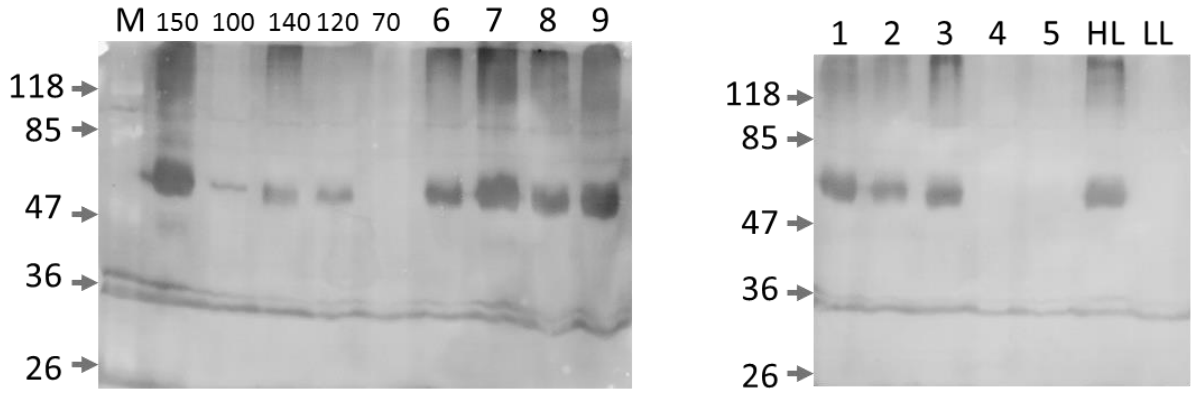
Scan	Sequence	Charge	MH+ theo	MH+ obs	DeltaMH+	N-Gap	C-Gap	PnvScr
1054	GLLPGVASHSPR	2	1461.175	1462.473	1.298	271.535	0.000	91.885
1062	DSPNPNYFDVK	2	1883.867	1885.593	1.726	589.297	0.000	134.044
1104	DSPNPNYFDVK	2	1868.669	1870.633	1.964	574.099	0.000	93.823
1194	LTALTDYLQK	2	1165.637	1166.053	0.416	0.000	0.000	139.721
1510	LPVYLNALGDLFK	2	1725.943	1727.913	1.970	264.143	0.000	96.958
1562	KEEmLSLLYR	2	1558.901	1560.673	1.772	262.251	0.000	122.010
1592	KEEmLSLLYR	2	1558.911	1560.693	1.782	262.261	0.000	124.632
768	LLVTGH	1	639.377	639.41	0.033	0.000	0.000	81.090
808	ALGLQHPD	2	1185.717	1185.353	-0.364	0.000	354.297	70.103

>>gi|357134603|ref|XP_003568906.1| PREDICTED: uncharacte (523 aa)
initn: 442 init1: 85 opt: 442 Z-score: 70.2 bits: 88.8 E(): 4.8e-016
Smith-Waterman score: 442; 67.143% identity (71.429% similar) in 70 aa overlap (1-70:60-507)
220783947 residues in 639158 library sequences

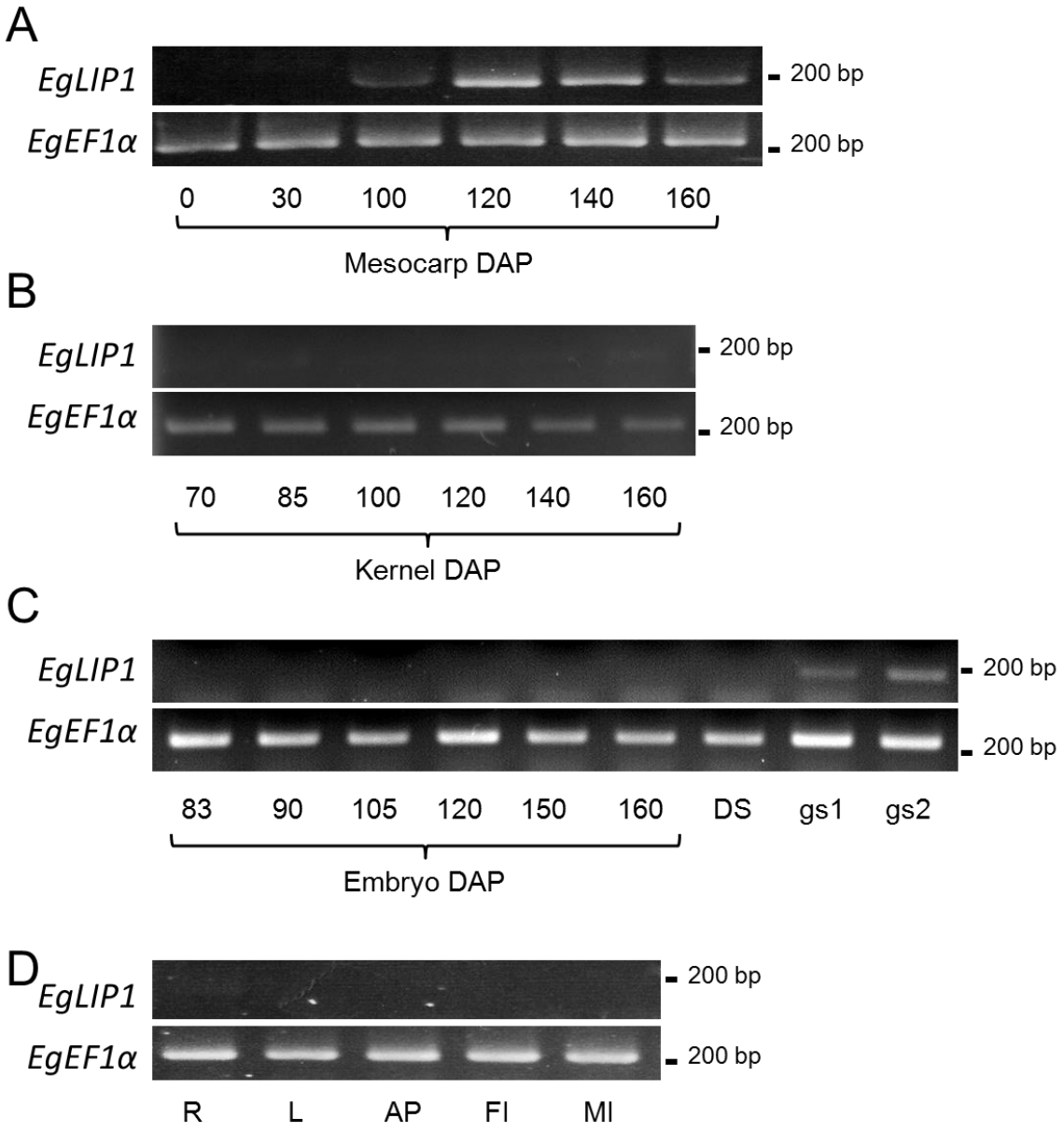
B



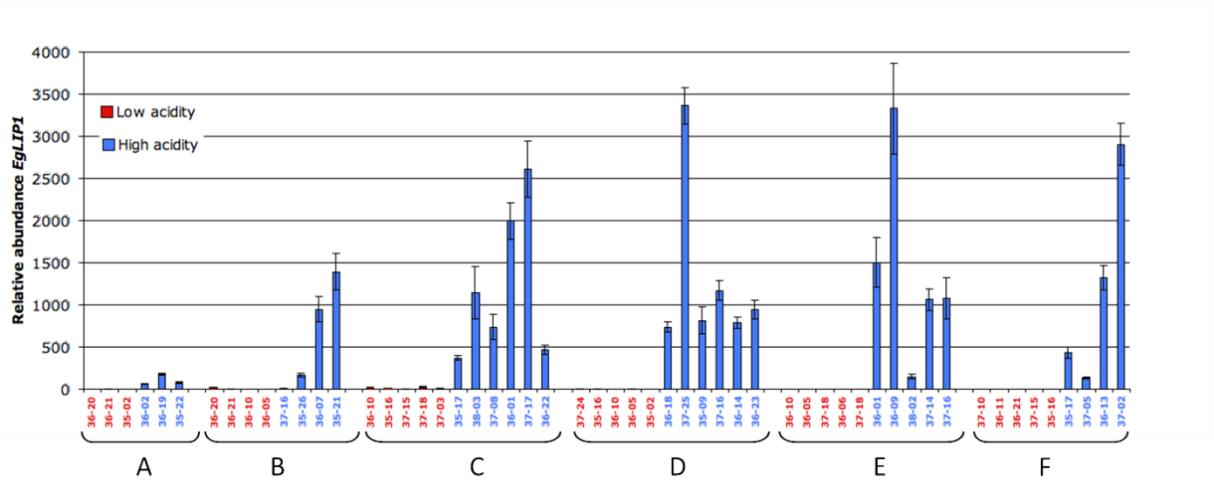
Supplementary Figure S1: Sequence analysis of EgLIP1. (*A*) *De novo* sequencing of putative mesocarp lipase. *De novo* sequencing was carried out essentially as described in Dhouib et al (30). Screening GenBank non redundant protein database restricted to monocots with FASTS [version 34.26 January 12, 2007] yielded two proteins. One is an enolase and the other an uncharacterized protein with 55% similarity to Castor bean acid lipase. (*B*) Sequence alignment of EgLIP1 with castor bean acid lipase (gb AAV66577) using ALIGNX. Conserved residues (34.6%) are in yellow and similar residues (17.2%) in green. Putative residues of the catalytic triad are indicated by a star. Consensus lipase motif (prosite PS00120) is in rose. Peptides identified by MS/MS analysis of tryptic peptides are underlined (22% coverage).



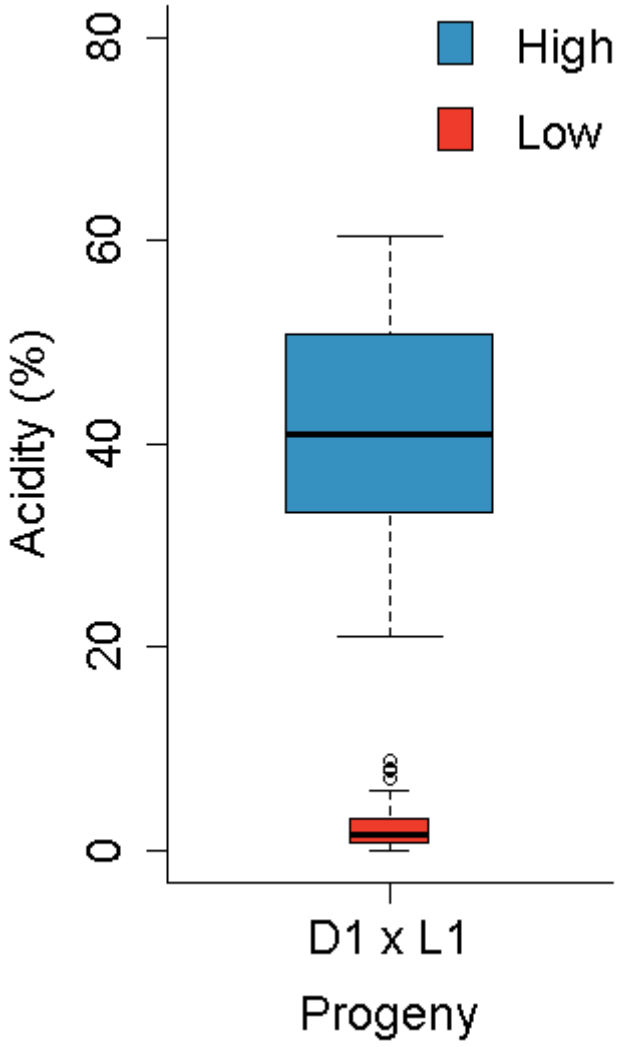
Supplementary Figure S2: Western Blot analyses. Lanes labeled 70 to 150 (weeks after pollination). Lipase levels in the mesocarp during fruit ripening. Lanes labeled 1 to 9: Lipase levels in mesocarp from lines segregating for the lipase trait. Lanes labeled HL (high lipase and LL (low lipase): lipase levels in progenies of D1 x L1 cross. M: molecular weight markers (118, 85, 47, 36, 26 kDa).



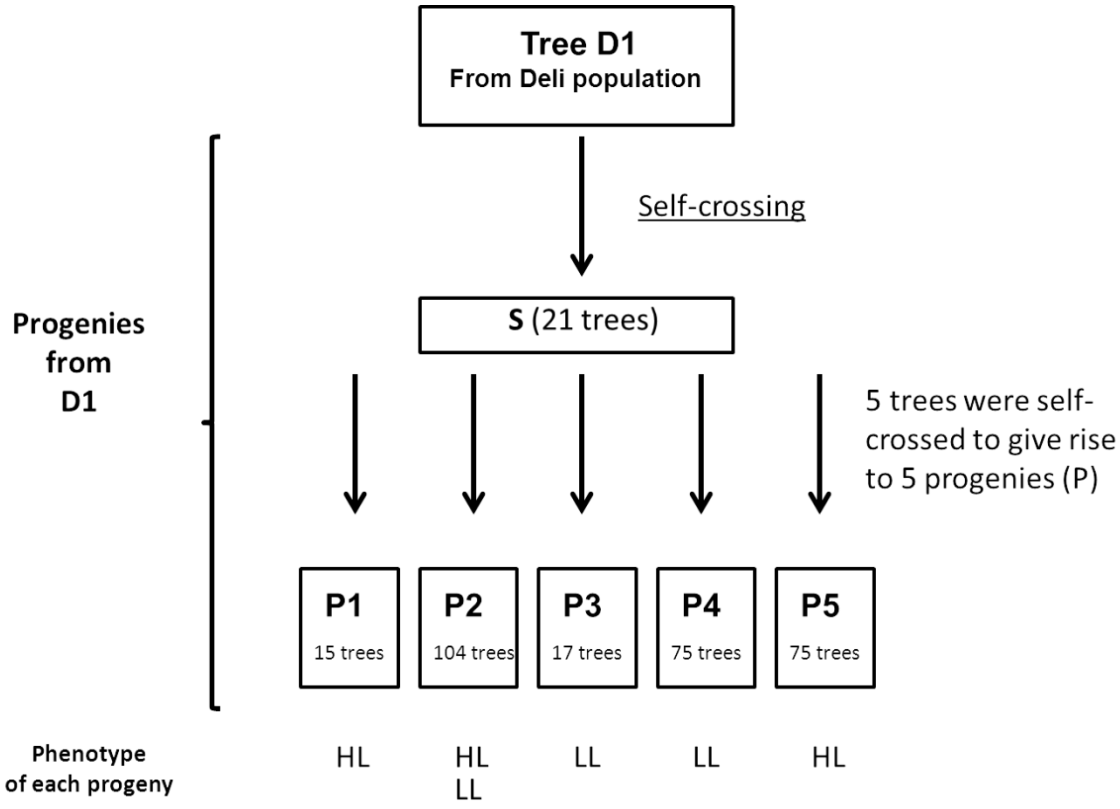
Supplementary Figure S3: RT-PCR analysis of *EgLIP1* transcripts during fruit development and in oil palm tissues. (*A*) *EgLIP1* transcript profile in mesocarp (0 to 160 DAP). (*B*) *EgLIP1* transcript profile in kernel (70 to 160 DAP). (*C*) EgLIP1 transcript profile in embryos (83 to 160 DAP ; DS, dry seed) and gs1, embryo from germinated seed; gs2, embryo from early post-germinated seed. (*D*) *EgLIP1* transcript profile in other tissues (R, root; L, young leaves; AP, vegetative shoot apex; FI, female inflorescence; MI, male inflorescence). Oligonucleotides used to amplify *EgLIP1* transcript were as in Material and Methods section while oligonucleotides EgEF1S2 (GGTGTGAAGCAGATGATTTGC) and EgEF1AS2 (CCTGGATCATGTCAAGAGCC) were used to amplify *EgEF1α.*



Supplementary Figure S4: *EgLIP1* transcript levels in segregating fruits during ripening. Total RNA was extracted from the mesocarp of fruits at different stages of development from high or low lipase lines (P2 progeny) and Q-PCR was carried out as described in the Material and Methods section. Gene abundance is expressed as mean and standard error bars are calculated from three technical replicates. Stage of fruit development (minimum-maximum DAP) A: 76-101, B: 118-125, C: 146-156, D: 160-167; E: 175-179 and F: 183-184. The numbers on the x-axis are the plantation localization coordinates of the individual trees tested.



Supplementary Figure S5: Segregation of the acidity trait in a D1xL1 progeny.
Free fatty acids released during one hour after grinding mesocarp were titrated and two acidity classes were evidenced, with about 5% and 40% FFA, respectively. Width of Boxplots is proportional to the number of trees. The observed 3:1 ratio is consistent with Mendelian inheritance of a monogenic recessive trait (χ^2= 0.303, P=0.58, d.f.=1, N=110).



Supplementary Figure S6: D1 progenies. D1 belongs to Deli germplasm. It is a Dura tree, that is a homozygous Sh+/+; Sh locus controls shell thickness.