Figure S1. Nucleotide and deduced amino acid sequence from *M. sexta* **PLIN2.** cDNA nucleotide (1-1350) sequence, **JF809664.1**, is shown above the deduced amino acid sequence (1-304), **AEJ33049**. Amino acid residues are aligned with the second nucleotide of each codon. The amino acid sequences underlined represents the matched peptides obtained from the MS/MS analysis of *M. sexta ovary* lipid droplets. These peptides are 100% identical to *Bombyx mori* Lsd2 (NP_001138804). The stop codon TAA is marked by short dash line.

Figure S2. Protein sequence alignment of vertebrate PLIN2 and MsexPLIN2. Alignments were produced with Clustal Omega. The sequences identifiers and abbreviations used are: HsPLIN2: *Homo sapiens* perilipin-2 (NP_001113.2); MmPLIN2: *Mus musculus* perilipin-2 (NP_031434.3); XIPLIN2: *Xenopus laevis* perilipin 2 (NP_001081960.1); MsexPLIN2: *Manduca sexta* lipid storage droplet protein 2 or Perilipin 2 (AEJ33049.1).

Figure S3. A. Protein sequence alignment of PLIN2 from 13 insect species. Alignments were produced with Clustal Omega. The sequences identifiers and abbreviations used are: Hsal: *Harpegnathos saltator* (EFN86125.1); Mr: *Megachile rotundata* (XP_003703225.1); Bi: *Bombus impatiens* (XP_003485735.1); Bt: *Bombus terrestris* (XP_003397531.1); Am: *Apis mellifera* (XP_003249235.1); Af: *Apis florea* (XP_003697663.1); Bm: *Bombix mori* (NP_001138804.1); Msex: *Manduca sexta* (AEJ33049.1); Cc: *Ceratitis capitata* (XP_004524967.1); Dm: *Drosophila melanogaster* (NP_001036276.1); Md: *Musca domestica* (XP_005188653.1); Aa: Aedes aegypti (XP_001658058.1); Ag: *Anopheles gambiae* (XP_310971.5)

Figure S4. Identity matrix of PLIN2 proteins. The sequences identifiers and abbreviations used are: Hsal: *Harpegnathos saltator* (EFN86125.1); Mr: *Megachile rotundata* (XP_003703225.1); Bi: Bombus impatiens (XP_003485735.1); Bt: *Bombus terrestris* (XP_003397531.1); Am: *Apis mellifera* (XP_003249235.1); Af: *Apis florea* (XP_003697663.1); Bm: *Bombix mori* (NP_001138804.1); Msex: *Manduca sexta* (AEJ33049.1); Cc: *Ceratitis capitata* (XP_004524967.1); Dm: *Drosophila melanogaster* (NP_001036276.1); Md: *Musca domestica* (XP_005188653.1); Aa: *Aedes aegypti* (XP_001658058.1); Ag: *Anopheles gambiae* (XP_310971.5)

Figure S5. Supplement to Figure 7, Protein levels of PLIN2 in 5th-larval fat body. A representative PLIN2 western blot (right panel) image with the corresponding Ponceau S staining (left panel) is shown in the figure. Labels: M, molecular weight marker; 1, 2, 3, 4, and 5 correspond to LDs samples from the fat body of 5th instar larvae on day 1, 2, 3,4 and 5, respectively. Alternatively, when the age of the larvae is expressed as a fraction of the total length of the feeding period (5 days), Day 1,2,3,4, and 5 of the 5th instar corresponds to fraction 0.2, 0.4, 0.6, 0.8 and 1, respectively.

Figure S6. Supplement to Figure 8, Effect of low caloric diet on the lipid accumulation and PLIN2 protein levels in 5th-larval fat body. A representative PLIN2 western blot (right panel) image with the corresponding Ponceau S staining (left panel) is shown in the figure. Labels: M, molecular weight marker; 1, 2, 3, 4, 5, 6 and 7 correspond to LDs samples from the fat body of 5th instar larvae on day 3, 4, 5, 6, 7 and 8, respectively. Alternatively, when the age of the larvae is expressed as a fraction of the total length of the feeding period (9 days), Day 3, 4, 5, 6, 7, 8 and 9 of the 5th instar corresponds to fraction 0.33, 0.44, 0.56, 0.76, 0.89 and 1, respectively.

Figure S7. Supplement Figure 9, Effect of starvation and refeeding in the expression of PLIN2 in 5th-larval fat body. A representative PLIN2 western blot (right panel) image with the corresponding Ponceau S staining (left panel) of the LDs isolated from the fat body of 5th instar larvae under the following conditions: Fed, day 2 feeding (lane 1); Starved, day 2 subjected to 24h starvation (lane 2); Refeeding, day 2, starved for 24h followed by refeeding for 2h (lane 3); 3h (lane 4); and 6h (lane 5) is shown in the figure.

Figure S8. Supplement Figure 10, Effect of starvation and refeeding in the expression of PLIN2 in the midgut of larvae. A representative PLIN2 western blot (right panel) image with the corresponding Ponceau S staining (left panel) of the LDs isolated from the fat body of 5th instar larvae under the following conditions: Fed, feeding day 2 (lane 1); Starved, day 2, subjected to 24h starvation (lane 2); Refeeding, day 2, starved for 24h followed by refeeding for 2h (lane 3), 6h (lane 4) and 24h (lane 5).

Figure S1

 $^1 \texttt{gacctggagagtgttctgttaacttagcgagcagttgatacgtaaagtgcgttaataaatt}$ M A T E V S ¹²³caagcaccggcagcattgccacaattgcagtcagtccagaaggccatggccttccccact O A P A A L P O L O S V O K A M A F P T $^{183} {\tt qtqqqqqcaqcggtcgaacatgttggagcattctactctaaagtcaaaggagcacactct}$ V G A A V E H V G A F Y S K V K G A H S $^{243} \verb+ctcctqqaatqqqcactgtccaccgctgaagcgggagtagtgctggcggcatccacagcg$ L L E W A L S T A E A G V V L A A S T A ³⁰³gctccctacgtatccgcaccactagcagtcggtgatgcaaaggtcgccgccgccatcgac A P Y V S A P L A V G D A K V A A A I D ³⁶³caqctqqaqcqccqcqtqccqctcgtcaacgagcagccaaaggtcatcgtcgagactacc Q L E R **R V P L V N E Q P K V I V E T T** ⁴²³aaacaaqcaqtqctttctaqaatatcgccgcatgtcaacaaggtttacggagcgcgtgtc K Q A V L S R I <u>S P H V N K V Y G A R</u> V ⁴⁸³qcqqcaqaqqaacqcgtcaagtcgctgaaggaattatcgtgggccaaagcgaacgcgttg A A E E R V K S <u>L K E L S W A K A N A L</u> $^{543} {\tt ctctctactqcatacqqacaqaaqqcqatqcacqqcqtcqactccqqcqccacctacqcc}$ <u>L S T A Y G Q K</u> A M H G V D S G A T Y A ⁶⁰³atgcagctgctagatcattacctgccgcctgtcggtgtcactgaggagcgatcaaccgac M Q L L D H Y L P P V G V T E E R S T D $^{663} {\tt atcaccccgtcgacggcggacccggcgctgcacacggtgcaaactgtgggcaggctcagc}$ I T P S T A D P A L H T V Q T V G R L S ⁷²³gctgtcgccgcgagaagggtgtggggccaacctcgcttacaagatcaacgagcttagacaa A V A A R **R V W A N L A Y** K I N E L R Q ⁷⁸³actqqcataqaactaqacgtgcgtcgttatgtgacagcgttgctagccgccctgcacctc T G I E L D V R R Y V T A L L A A L H L ⁸⁴³gccaaggtgacgagtcagcagcgcgaggagcaggtgcctcctcagcagaacaacgcg A K V T S Q Q Q R E E Q V P P Q Q N N A ⁹⁰³gagccctccccctctggcccggagccctcccacaacacccgcgagtccgcccccaccacc E P S P S G P E P S H N T R E S A P T T ⁹⁶³qctaacaaqqtqaaatccacaccggaggcgaaatccgcggagcattcgcaaaattaatca A N K V K S T P E A K S A E H S Q N ttatatacctattatatacatttaatataagttttgcatttgtataagtgtaattgcatg aacqqcttqtattqqcattttataaaaqqcaataqccqttaqtctaccttqcaaatqatt ${\tt ctcctagttgtaagcaagccacaatgccgatacacaggatgtatccacattgttatggct}$ gttagtttataagtattttatcatatttacactgtcagtgaagactgtctaatgagtctt atatttgtatttatatggcatgaattgtgaagtattttatatggaatgtatttta acaacttatacagcaaaaaaaaaaaaaaa¹³⁵⁰

Figure S2

Msex Lsd2 vs PLIN2 from vertebrates

CLUSTAL O(1.2.1) multiple sequence alignment

MsexPLIN2 Xenopous MmPLIN2 HsPLIN-2	MATH 	EVSQA-PAA -MSAAVEQQI MAAAVVI MASVAVI *	LPQLQSVQ EQQQSVVD DPQQSVVM DPQPSVVT * · *	KAMAFPT RIINLPF RVANLPL RVVNLPL : :*	GAAVEHV /SSTYDMV /SSTYDLV /SSTYDLM *: : :	GAFYSKV SSAYTNT SSAYVST ISSAYLST .: *	GAHSLLEW ENHPYIKS OQYPYLRS OQYPYLKS : :.	VALSTAEAGV VCDVAEKSV VCEMAEKGV VCEMAENGV · · ** ·*	59 56 54 54	
MsexPLIN2 Xenopous MmPLIN2 HsPLIN-2	VLAA KSII KTVI KTII	ASTAA ISVALTSAM ISAAMTSAL ISVAMTSAL :*.*	PYVSA PIIHRLEP PIIQKLEP PIIQKLEP * :.	PLAVGDAN QIAIANN QIAVANT QIAVANT :*:.:	(VAAAIDQ IACIGLDK ZACKGLDR ZACKGLDR	ULERRVPLV IEEKLPII MEERLPII IEERLPII :*.::*:	/NEQPKVIV LYQPSDKIV LNQPTSEIV LNQPSTQIV : : **	YETTKQAVL- YSNASDAVAG YASARGAVTG YANAKGAVTG .: * <u>*</u>	111 116 114 114	
MsexPLIN2 Xenopous MmPLIN2 HsPLIN-2	AK AKDV AKD2	/VTTTMAGA) AVTTTVTGA)	SRI -ETVLQSI KDSVASTV KDSVASTI . :	SPHVNKVY TGVVDKTH SGVVDKTH TGVMDKTH : ::*.	YGARVAAE (GAVHDSV (GAVTGSV (GAVTGSV ** :	ERVKSLKE EMTKAV ERTKSV EKTKSV * .*::	ELSWAKANA VNGSINI VNGSINI VSGSINI *:	LLSTAYGQK VLGSGVVQM VLGMVQF VLGSRMMQL :*. *	154 162 169 171	
MsexPLIN2 Xenopous MmPLIN2 HsPLIN-2	AMHO MNTO MNSO VSSO	GVDSGATYAI GVNTALTTSI GVDNAITKSI GVENALTKSI	MQLLDHYL ENLLEQYL ELLVDQYF ELLVEQYL *:::*:	PPVGVTEI PPTDEELA PLTQEELI PLTEEELI * .	ERSTDITE AIEAAKTE EMEAKKVE EKEAKKVE	ST-ADPAI GFESGKQI GFDMVQKI GFDLVQKI	LHTVQTVGF PNYYVRLGS PSNYERLES PSYYVRLGS	LSAVAARRV LSTKARKRA LSTKLCSRA LSTKLHSRA **: *.	213 222 229 231	
MsexPLIN2 Xenopous MmPLIN2 HsPLIN-2	WANI YQQ <i>P</i> YHQ <i>P</i> YQQ <i>P</i> : :	LAYKINELR ALGRISDAK ALSRVKEAK ALSRVKEAK ::.::	QTGIELDV SRSQE QKSQE QKSQQ :	RRYVTALI AIAQLI TISQLI TISQLI :: *	LAALHLAK NKTMDLIE NSTVHLIE NSTVHLIE ::.* :	SVTS FAKKNVNS FARKNMHS FARKNVYS	SQQQREEQV SANQ SANQKIQGA SANQKIQDA ' :*	YPPQQNNA KLYNTWV QDKLYVSWV QDKLYLSWV :	266 270 284 286	
MsexPLIN2 Xenopous MmPLIN2 HsPLIN-2	EPSI DWTI EWKI EWKI	PSGPEPSHN' (SSGDP (SIGYD (SIGYD *	TRESAPTT 	ANKVKSTI ANI DTI DTI	PEAKSAEH EGNESAEQ DESHCVEH DESHCAEH	ISQN DIESRILSN DIESRTLAI DIESRTLAI	ITRNLTQQI IARNLTQQI IARNLTQQI	QTTCHSLVM QTTCQTVLV QTTCHTLLS	304 314 328 330	
MsexPLIN2 Xenopous MmPLIN2 HsPLIN-2	SVQ(NAQ(NIQ(GLPQNIQDK' GLPQNIQDQ GVPQNIQDQ	THRVGAMA AKHLGVMA AKHMGVMA	.GEMYHNFI .GDIYSVFI .GDIYSVFI	RSASSLKE RNAASFKE RNAASFKE	VSDNILT VSDGVLTS VSDSLLTS	ISRGQLQKM SSKGQLQKM SSKGQLQKM	IKDSMDDVMD IKESLDEVMD IKESLDDVMD	304 374 388 390	
MsexPLIN2 Xenopous MmPLIN2 HsPLIN-2	YLVI YFVI YLVI	YLVNNTPLNWLVPDFSITDLSSEMDENPDVLEEDEMEMQDFSRLNGRVVNRDIS YFVNNTPLNWLVGPFYPQSTEVNKASLKVQQSEVKAQ YLVNNTPLNWLVGPFYPQLTESQNAQDQGAEMDKSSQETQRSEHKTH								
1: Msex 2: Xenc 3: MmPI 4: HsPI	PLIN2 ppous JIN2 JIN-2	100.00 22.30 24.63 24.09	22.30 100.00 57.49 59.67	24.63 57.49 100.00 82.59	24.09 59.67 82.59 100.00) ,)				

Hsal Mrot Bi Bt Am Af Bm Msex Cc Dm Md Aa Ag		 ✓ 88 ✓ 88 ✓ 88 ✓ 88 I 88 L 88 L 120 L 113 L 107 L 99 L 111 :
Hsal	EVKLPIIKEEPKQILNRTRSIVSERLRPAVKTFTDLTYETKORVRIMTLLTYYKVHYLRV YSWOOADRVMSTETGINILKTVDNTTDFAEIMLDKYLPPPLEEPH-HD	195
Mrot	EVKLPIIKEEPEQIINRTKSIVSKSLEPAVKTFIELKQETEHKVRIMTLLTYYKVYYLRI YSWQQADRVMSTEIGISILKTVDNTTDFVELLLDKYLPVPYHEFHTST	196
Bi	EVKLPIIKEEPKQIINRTKSLVSERLRPAVKTFTDLKKGTKHRVKVIKLHTYYKVHYLRM YSWQQADRVMSTETGISILKTVDSTTDFVELILDKYLPIPSDDFHNNE	196
Bt	EVKLPIIKEEPKQIINRTKSLVSERLRPAVKTFTDLKKGTKHRVKVIKLHTYYKVHYLRM YSWQQADRVMSTETGISILKTVDSTTDFVELILDKYLPIPSDDIHNKG	196
Am Af	EVKLPIIKEEPEQIINQTKSLVSVHLRPAVKTFTDLKHETKHKVKVMKLHTYCKVHYLRI YSWQQADKVMSTETGINILKTIDSTTDFIELILDKYLPIPY-DFDTNV	195
AI Bm	EIKLPIIKEEPEQIINQTKSLVSVHLKPAVKTFTDLKHETKHKVKIMKLHTYCKVHYLKT YSWQQADRVMSTETGINILKTIDSTTDFIELILDKYLPIPY-DFDTNV	195
Msex	ERRVPLVIEDFRVIVETIKOAVLSRISPHVNKVIGARAVAEOKVKSLKE LSWAKANALLSIAIGOKAMHGVDIGATIAMOLLDHILPPVGAOEEPG ERRVPLVNEOPKVIVETTKOAVLSRISPHVNKVYGARVAAEERVKSLKE LSWAKANALLSIAIGOKAMHGVDIGATIAMOLLDHILPPVGAOEEPG	184
Cc	EVSAPIIKDTPQEIYNQAKNKVVEVVQPHIERVTKFKTAGQQKASSLKD LAWAKANEVLATQYGSLAVSGVDNTTALAERLLEYYFPKGEGDVEEDNDNKQIAVVQN	227
Dm	EVKAPIIKDTPQEIYNQAKSKVIDVVQPHLERVVKFKAAGQQKAASLKD LAWQKANEVLATQYGSLAVNGVDTTTALAERLLEYYFPKCESDVEEDNDDKQNAVVQN	220
Md	EVKAPIIKDTPQEIYNQAKNKVIDVVQPHIDRVVKFKTAGQQKAASLKD LAWQKANEVLATQYGSLAVNGVDTTTALAERLLEYYFPKSDSDVEEDNDVKEIAVTQNGH	216
Aa Aa	EVSAPIIKEQPQEIYNQAKSKVLGTVKPYTEKVCELRQASQQKAASLKE LSWKKANEVLASQYGSIAVNGVDTTAQLAERLLDYYFPKCEGDDEDD	195
Ag	EVNAPIIKEQPADIYQQARTRVIESVKPHIEKVCELRSASQQRAASLKD LSWRKANEVLATQYGSLAVNGVDTTAQLAERLLDYYFPKSDTESEDD	207
Hsal Mrot Bi Am Af Bm Msex Cc Dm Md Aa Ag	TERLCSEHAKLHHTMERLSGFSIRASRRIYFALMDKFWNTYKIETLILI LHGLAVVQAITLLEVIISSIFKLISDCLFSPLS	- 277 - 276 - 261 - 261 - 259 - 260 3 289 A 287 3 331 3 326 J 317 3 291 3 310
Hsal Mrot Bi Bt Am Af Bm Msex Cc Dm Md Aa Ag Hsal	TERLCSEHAKLHHTMERLSGFSIRASRRIYFALMDKFWNTYKIETLILI LHGLAVVQAITLLEVIISSIFKLISDCLFSPLS	- 277 - 276 - 261 - 259 - 260 3 289 4 287 3 331 3 326 4 317 3 291 3 310
Hsal Mrot Bi Am Af Bm Msex Cc Dm Md Aa Ag Hsal Mrot B;	TERLCSEHAKLHHTMERLSGFSIRASRRIYFALMDKFWNTYKIETLILI LHGLAVVQAITLLEVIISSIFKLISDCLFSPLS	- 277 - 276 - 261 - 259 - 260 3 289 A 287 3 331 3 326 7 317 3 291 3 310
Hsal Mrot Bi Bt Am Af Bm Msex Cc Dm Md Aa Ag Hsal Mrot Bi Bt	TERLCSEHAKLHHTMERLSGFSIRASRRIYFALMDKFWNTYKIETLILI LHGLAVVQAITLLEVIISSIFKLISDCLFSPLS	- 277 - 276 - 261 - 259 - 260 3 289 A 287 3 331 3 326 V 317 3 291 3 310
Hsal Mrot Bi Am Af Bm Msex Cc Dm Md Aa Ag Hsal Mrot Bi Bt Am	TERLCSEHAKLHHTMERLSGFSIRASRRIYFALMDKFWNTYKIETLILI LHGLAVVQAITLLEVIISSIFKLISDCLFSPLS	- 277 - 276 - 261 - 259 - 260 3 289 A 287 3 331 3 326 A 317 3 291 3 310
Hsal Mrot Bi Am Af Bm Msex Cc Dm Md Aa Ag Hsal Mrot Bi Bt Am Af	TERLCSEHAKLHHTMERLSGFSIRASRRIYFALMDKFWNTYKIETLILI LHGLAVVQAITLLEVIISSIFKLISDCLFSPLS	- 277 - 276 - 261 - 259 - 260 3 289 4 287 3 331 3 326 4 317 3 291 3 310
Hsal Mrot Bi Am Af Bm Msex Cc Dm Md Aa Ag Hsal Mrot Bi Bt Am Af Bm	TERLCSEHAKLHHTMERLSGFSIRASRIYFALMDKFWNTYKIETLILI LHGLAVVQAITLLEVIISSIFKLISDCLFSPLS	- 277 - 276 - 261 - 259 - 260 3 289 A 287 3 331 3 326 V 317 3 291 3 310
Hsal Mrot Bi Bt Am Af Bm Msex Cc Dm Md Aa Ag Hsal Mrot Bi Bt Am Af Bm Sex Cc	TERLCSEHAKLHHTMERLSGFSIRASRRIYFALMDKFWNTYKIETLILI LHGLAVVQAITLLEVIISSIFKLISDCLFSPLS	- 277 - 276 - 261 - 259 - 260 3 289 A 287 3 331 3 326 A 317 3 291 3 310
Hsal Mrot Bi Bt Am Af Bm Msex Cc Dm Md Aa Ag Hsal Mrot Bi Bt Am Af Bm Msex Cc Dm	TERLCSEHAKLHHTMERLSGFSIRASRRIYFALMDKFWNTYKIETLILI LHGLAVVQAITLLEVIISSIFKLISDCLFSPLS	- 277 - 276 - 261 - 259 - 260 3 289 A 287 3 331 3 326 N 317 3 291 3 310
Hsal Mrot Bi Am Af Bm Msex Cc Dm Md Aa Ag Hsal Mrot Bi Bt Am Af Bm Msex Cc Dm Mda	TERLCSEHAKLHHTMERLSGFSIRASRRIYFALMDKFWNTYKIETLILI LHGLAVVQAITLLEVIISSIFKLISDCLFSPLS TERLCNEDKFHHTVKRLSEFSSRSKRIYFALME-QHIYRMIRLI SDITCILLFKYTIKSTISKLNNCLVTH	- 277 - 276 - 261 - 259 - 260 3 289 A 287 3 331 3 326 N 317 3 291 3 310
Hsal Mrot Bi Am Af Bm Msex Cc Dm Md Aa Ag Hsal Mrot Bi Bt Am Af Bm Msex Cc Dm Md Aa Af	TERLCSEHAKLHHTMERLSGFSIRASRRIYFALMDKFWNTYKIETLILI LHGLAVVQAITLLEVIISSIFKLISDCLFSPLS	- 277 - 276 - 261 - 259 - 260 3 289 A 287 3 331 3 326 V 317 3 291 3 310

Figure S4

Identity Matrix of Insect PLIN2 Proteins

	Hsal	Mrot	Bi	Bt	Am	Af	Bm	Msex	Cc	Dm	Md	Aa	Ag
Hsal	100.0	67.6	67.7	67.3	64.0	63.3	23.7	24.1	27.0	27.8	27.0	26.7	27.5
Mrot	67.6	100.0	70.1	70.1	67.6	68.1	21.8	22.2	24.4	26.0	24.1	25.3	24.5
Bi	67.7	70.1	100.0	98.1	81.1	80.4	24.0	24.4	28.0	29.2	27.6	28.1	27.7
Bt	67.3	70.1	98.1	100.0	80.3	79.6	24.0	24.4	28.4	29.6	28.0	28.1	27.7
Am	64.0	67.6	81.1	80.3	100.0	95.4	20.9	20.1	27.8	28.6	27.8	26.7	25.1
Af	63.3	68.1	80.4	79.6	95.4	100.0	21.6	20.8	27.7	28.5	27.7	27.0	25.4
Bm	23.7	21.8	24.0	24.0	20.9	21.6	100.0	80.2	32.0	34.7	33.5	37.1	38.3
Msex	24.1	22.2	24.4	24.4	20.1	20.8	80.2	100.0	33.3	33.8	33.6	37.0	37.9
Cc	27.0	24.4	28.0	28.4	27.8	27.7	32.0	33.3	100.0	72.6	79.2	55.3	54.0
Dm	27.8	26.0	29.2	29.6	28.6	28.5	34.7	33.8	72.6	100.0	81.1	55.9	55.4
Md	27.0	24.1	27.6	28.0	27.8	27.7	33.5	33.6	79.2	81.1	100.0	55.5	56.7
Aa	26.7	25.3	28.1	28.1	26.7	27.0	37.1	37.0	55.3	55.9	55.5	100.0	74.8
Ag	27.5	24.5	27.7	27.7	25.1	25.4	38.3	37.9	54.0	55.4	56.7	74.8	100.0

FIGURE S5



FIGURE S6





FIGURE S8

