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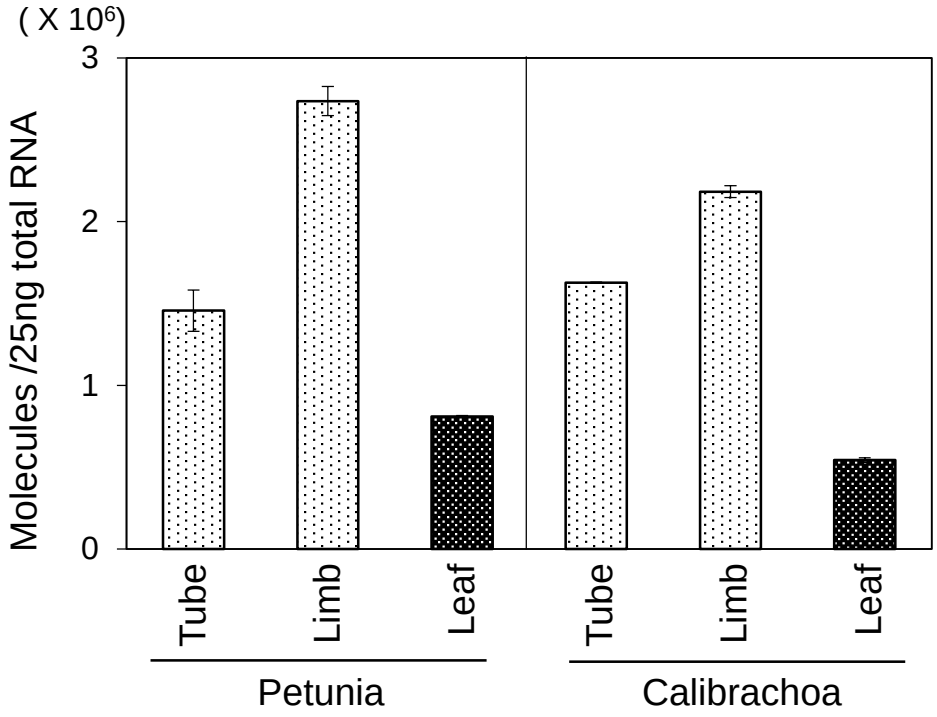


Supplemental Fig. 1. Expression analysis of *Actin* in tubes, limbs, and leaves of petunia and calibrachoa. RT-qPCR analysis were performed in triplicate; means ± SE are shown.

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PhXES      MASLLQNFWASPRLAPNQDYKSQCVGPIRCVASKDSTLLSSDSVSFNGVSSIEEKEKSSP 60
ChXES      MASLLQNFWASPRLALNQDYKFKSITRIRCLASRDSTLLSSDSDRVNDVSSIAEKEKSSP 60
SlPYP1     MASLLHNFWAVPRFGLSPDYKPHCIARFACLANRDSTFLSSDSVIVNGVSSIEEKEKSST 60
           ***** **** **     ***        * *  *** *****   * **** ******

PhXES      IVDVGNGHLTSAINEKRKEDIQDKLEPLWDDGYGTQTVKDFF--AKEILKPDGGPPRWFT 118
ChXES      IVDVENGHLTSAINEKRKEDSQDKLEPLWDDGYGTQTIKDFF--AKKIHSPDGGPPRWFT 118
SlPYP1     IIDVKNSHLAPAIKEKNKEDIQNKLETLWDDGYGTQTVKDYLEIGSEIIKPDGGPPRWFT 120
           * ** * **  ** ** *** * *** ********** **       *  **********

PhXES      PISAGPPLEDSPLLLFLPGMDGTGFGLVLHEKALGKVFQVWCLHIPVYDRTPFEELVKFV 178
ChXES      PISAGPPLKDSPPLLYLPGIDGTGLGLVLHEKALGKVFQIWCLHIPVYDRTPFDELVKLV 178
SlPYP1     PISAGPPLEDSPLLLFLPGMDGTGMGLVLHEKALGKVFQVWCLHIPVYDRTPFDELVKFV 180
           ******** *** ** *** **** ************** ************* **** *

PhXES      ESTVRMKHASSPNKPIYLVGDSFGGCLALAVAARNPKIDLVVILANPATSFGRSPLQPLL 238
ChXES      ERTLRMRHASSPNKPIYVVGDSSGGCLALAVAARNPKIDLVVILANPATSFGRSPLQPLL 238
SlPYP1     GRTVRMKHASSPNKPIYLVGDSFGGCLALAIAAHNPEIDLVLILANPATSFDRTQLQPLL 240
             * ** ********** **** ******* ** ** **** ********* *  *****

PhXES      PLLESLPDEFHVTVPYLLSYIMGDPMKMATVNIDSSLPPGQIIQRLAHNLTAMLPDLSGL 298
ChXES      PLLESLPDELHVTVPYLLSLIMGDPMKMAMVNIDSSLPPGQIIRHLARNLIAMLPDLSGL 298
SlPYP1     PLLESLPDEFHVTVPYLLSFIMGDPLKMAMVNIDSMLPPGQIIQRLAGNLTDLLAHLYGL 300
           ********* ********* ***** *** ***** *******  ** **   *  * **

PhXES      ADIIPKETLLWKLKLLRSASSYSNSRLHAVNAEVLVLASGKDNMLPSRDEAQRLAKSLRN 358
ChXES      ADIIPKETLLWKLKLLRSASSYSNSRLHAVNAEVLVLASGKDNMLPSGNEAQRLAKSLRN 358
SlPYP1     ADIIPKETLLWKLKLLRSASSYSNSRLHAVNAEVLVIASGKDNMLPSENEAQRLGNSLRN 360
           ************************************ **********  *****  ****

PhXES      CEVRYFKDNGHTILMEDGINLLSVIKYTNKYRRSRRHDYVMDFLPPSMSEFKKAVNDNRL 418
ChXES      CEVRYFRHNGHTILMEDGINLLSIIKYTNKYRRSRRHDCIMDFLPPSKSEFKIIVNFYRW 418
SlPYP1     CTVRYFKDNGHTILLEDGINLLSIIKATSKYRRSKRRDYVKDFLPPSKSEFKNAIKNNSW 420
           * ****  ****** ******** ** * ***** * *   ****** ****

PhXES      YLNLTGSVMLSTMEDGKIVRGLAGVPSEGPVLLVGYHMLMGLEIVPLVEEYLRQTNVLLR 478
ChXES      YLNLTGSVMLSTMEDGKIVRGLAGVPCEGPVLFVGNHMLMGLEIVPLVEEYLRQRKVLLR 478
SlPYP1     YLNITGPVMLSTMENGKIVRGLAGVPREGPVLLVGYHMLMGLEIVPLVQEYMMQTKILLR 480
           *** ** ******* *********** ***** ** ************ **  *   ***

PhXES      GIAHPALFTQ-LIDRQANDGSFVDMLRLYGATPVTAINFFKLLATKSHVLLYPGGAREAL 537
ChXES      GIAHPALFNP-VIDTQTDEGSFIDLLRLYGATPVAANNFFKLLANKSHVLLYPGGAREAL 537
SlPYP1     GIAHPSLFTQLVESRPDA-SSFIDMLKLYGATPVTASNFFKLLATKSHVLLYPGGAREAL 539
           ***** **           ** * * ******* * ******* ***************

PhXES      HRKGEEYKVIWPEQPEFIRMAARFGATIVPFGVVGEDDMVQLVLDYDDLQKIPILSDQIR 597
ChXES      HRKGEEYKVIWPERPEFIRMAARFGATIVPFGVVGEDDIAQLVLDCDDLQKIPILSDQIR 597
SlPYP1     HRKGEEYKVIWPDQPEFIRMAAKFGATIVPFGVVGEDDIAQLVLDYDDLKSIPILGDRIR 599
           ************  ******** ***************  ***** ***  **** * **

PhXES      RENERAARQGVTVRADTTGEVANQVLYIPGLLPKIPGRFYYLFGKPVHTKGRQDLLKDRE 657
ChXES      RDNERAARMGVTVRGGMTGEVANQTLYMPGLLPKIPGRFYYLFGKPVHTQGRQDLLKDRA 657
SlPYP1     SENEEAARRGLAVRADMDGEIANQMLYIPGLLPKIPGRFYFFFGKPIHTKGRQDLVKDRE 659
             ** *** *  **    ** *** ** ************  **** ** ***** ***

PhXES      KARELYLQIKSEVQGNMNFLLKKREEDPYRSVIDRTTYRAFSTSFDDIPTFDF 710
ChXES      KARELYFQIRSEVQNSLNYLLNKREEDPYRSIIDRTTYRAFSATFDDVPTFDY 710
SlPYP1     KARELYLQVKSEVQNNMNYLLKKREEDPYRNFIDRTMYRAFSATSGDVPTFDF 712
           ****** *  ****   * ** ********  **** *****    * ****
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α/β hydrolase fold

LPAT

Supplemental Fig.2. Alignment of deduced amino acid sequences of PhXES (BBB44443), ChXES (BBB44444) and SlPYP1 (XP_004230141). Conserved amino acids are indicated with asterisks. Green boxes show chloroplast transit peptides. Pink bar shows α/β hydrolase fold domain (amino acids 132-383 in PhXES), and blue bar shows a lysophospholipid acyltransferase (LPAT)-like domain (amino acids 407-679 in PhXES). Squares show divergent amino acid in PhXES.