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## Supplementary Material

### Circadian oscillation and development-dependent expression of glycine-rich RNA binding proteins in tomato fruits

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### Table S1. Sequences of the oligonucleotide primers used for quantitative real time RT-PCR

In the first column GenBank Accession N<sup>o</sup> of each sequence is also specified

mRNA	Forward primer	Reverse primer
<i>preLegr1a</i> (AK246918)	5'-ATCGGTTTTGAAGTTTCTGTTTTA-3'	5'-GCCATCAAGTTCCTGACCAT-3'
<i>mLegr1a</i> (JQ613215)	5'-AAGTAGTCGACTCGAAGATCATT-3'	5'-TTGTCTTCCACCACCGAAACCA-3'
<i>asLegr1a</i> (AK323933)	5'-TTATACCATTTCCTTGAAACGATCA-3'	5'-TTGTCTTCCACCACCGAAACCA-3'
<i>preLegr1b</i> (AK320592)	5'-ATGTTTCTCCCCCTCATGC-3'	5'-CCCTTCAATAGCATCCCTCA-3'
<i>mLegr1b</i> (AK224744)	5'-GTGGTCGAATCCAAGATCATC-3'	5'-GTAACCACCCCGCCTCTT-3'
<i>asLegr1b</i> (JQ613216)	5'-ATTCCAATTCCCCGAAACGATCATC-3'	5'-GTAACCACCCCGCCTCTT-3'
<i>preLegr1c</i> (AK324061)	5'-TTTTGTGTTTATTCACCATC-3'	5'-TGATGTTACGACCATCAAGG-3'
<i>mLegr1c</i> (AK323723)	5'-AATGTGGTCGACTCCAAGATT-3'	5'-CAAAACCGCCGCCGCCGCG-3'
<i>asLegr1c</i> (JQ613217)	5'-ATTCCATTTCCTTATACGATT-3'	5'-CAAAACCGCCGCCGCCGCG-3'
<i>LeEF1a</i> (X14449)	5'-GCTGGTATCTCCAAAGATGGTC-3'	5'-CATGTTGTCTCTTCAAAACCA-3'

**Fig. S1.** Alignment of (A) pre-mRNA, (B) mature mRNA and (C) protein sequences of *Legrp1a*, *Legrp1b* and *Legrp1c*. Start and stop codons are highlighted in yellow. Intron regions are highlighted in gray. First part of introns that are retained in the alternative splicing is underlined. RNP1 and RNP2 are highlighted in red.

(A)

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preLeGRP1a      TTAGGGTTTCTCTTT-----TCT-----GGTTTCTC-AGT--TCAGTTT----AATGGC 42
preLeGRP1b      -CACAGCTCTTCCTTACATTCTTTTCAGGGTTTCTCTAGTAGTCTCTGAAAAAAAT 59
preLeGRP1c      -AAATGCACATCCATC-----AGTATTGAAAAAG-----AATGTC 34
                * * * * * * * * * * * * * * * * * * * * * *

preLeGRP1a      CGCCGAAGTTGAGTACAGTTGCTTCGTTGGTGGGCTAGCTTGGGCCACCACCGATAGAAC 102
preLeGRP1b      GGCCGACGTTGAATACAGGTGCTTCGTCGGTGGTCTGGCATGGGCCACCACCGACCAAAC 119
preLeGRP1c      TGCTGAGGTTGAATACAGATGCTTCGTTGGTGGGCTCGCATGGGCTACCAACGATAGAAC 94
                ** ** * * * * * * * * * * * * * * * * * * * * * *

preLeGRP1a      ACTTAGCGATGCTTCTCTACCTACGGCGAAGTAGTCGACTCGAAGTCCGTTTGTGCA 162
preLeGRP1b      ACTTTCGGAAGCTTTTTCTCAGTACGGCGAAGTGGTCGAATCCAAGTTC---TGTTGCA 175
preLeGRP1c      CCTAGTGAAGCTTTTTCTCAGTACGGAAATGTGGTCGACTCCAAGTCCGTTTGTGCA 154
                ** ** * * * * * * * * * * * * * * * * * * * * * *

preLeGRP1a      AAGC---AGAAATCAGATCCGAGCCATTTTTGGTTTCGTTGATGACCTTCTGTTACT 218
preLeGRP1b      GGGC---AGAGATCGGATCCGAGCC-----TTGGGCTTCG--ATGACCCTCTGTTACT 223
preLeGRP1c      CAGCTAGCAGAGATCGGATCG-----TTGATCTCTTAAT--CTCTCTGTTACT 201
                ** ** * * * * * * * * * * * * * * * * * * * * * *

preLeGRP1a      GA-TTACTATCT---CTAT-CTCTGGTTTACTTGATTCAT-CTGTTACT---GTTACT 267
preLeGRP1b      GAATTGTGATCTGTTACTATTCTCTGGTTTACTTGACTGTTACTGTTACTCTATGTTACT 283
preLeGRP1c      CTGTTACTCTCTGTTACTAT-----GTTACTC-----T-CTGTTACTCT--GTTACT 245
                ** ** * * * * * * * * * * * * * * * * * * * * * *

preLeGRP1a      ---CTGTTTAT-ACTGTTATACCA-TTCCTTGAACGGTACGTTCCGCTTCCCTCTCT 321
preLeGRP1b      GTTACTATTTGTTACTATTATTTCCAATTCGCCGAAACGGTACGTTCCGCTTCCCT-CTGT 342
preLeGRP1c      -----ATTTGT-----TTATTCCA-TTCCTTTATACGGTACGTTCAACATTAAT-CGAT 292
                *** * * * * * * * * * * * * * * * * * * * * *

preLeGRP1a      TTTTGTCAAGAG-----ATGAAGAAAGATCGGTTTGGAA-GTTTCT----- 361
preLeGRP1b      TTTTA-CACGAG-----ATGAAGATAGATCGCTTTT-AT-GTTTCTCCCCCTCATGC 391
preLeGRP1c      TTTTCAAATAAATTTATTTCATCAAATCCATTTGATTGATTATTTTT----- 341
                *** * * * * * * * * * * * * * * * * * * * * *

preLeGRP1a      -----GT-TTTACTAATTA-----TGTAGATCTATTATG-CCT 392
preLeGRP1b      TTTTCTTTCCGATCTGCTTTGT-TTTGGTTGTTAATT--TGTAGATCTGTTGGATCT 448
preLeGRP1c      -----GTGTTTATTCACCATCTACCATTTATCTATTTAGATCT 379
                ** * * * * * * * * * * * * * * * * * * * * *

preLeGRP1a      GA---ATTGTTTCGTTATTGTTTTTGTGTTT-TTTTTCAGATCATTAAATGACAGAGAAACT 447
preLeGRP1b      GACGCAATTGTTATGTTCTTTTTTTAAAAT-TTTTTCAGATCATCAATGACCGGAAACT 507
preLeGRP1c      GT---AATTGT--GGATCTGAATCTGATCATTTTTTCAGATTATCAACGATCGCGAAACA 434
                * * * * * * * * * * * * * * * * * * * * * *

preLeGRP1a      GGTAGATCTAGAGGATTTGGCTTTGTTACCTTCAAGGATGAAAAATCCATGAAGGACGCT 507
preLeGRP1b      GGTAGATCTAGAGGATTTGGATTCGTTACCTTCAAGGATGAGCAAGCCATGAGGGATGCT 567
preLeGRP1c      GGTAGATCGAGAGGATTTGGTTTGTGTTACCTTACTGATGAGAAATCCATGAGGAATGCA 494
                * * * * * * * * * * * * * * * * * * * * * *

preLeGRP1a      ATTTCAGGAATGAATGGTCAGGAACTTGATGGCCGTAACATCACTGTTAACGAAGCTCAA 567
preLeGRP1b      ATTTGAAGGGATGAACGGCCAGGATCTTGATGGTCGCAACATCACCGTGAACGAAGCTCAA 627
preLeGRP1c      ATTTAAGCAATGAATGGCCAGAACCTTGATGGTCGTAACATCACTGTTAACGAAGCTCAA 554
                *** ** * * * * * * * * * * * * * * * * * * * * * *

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preLeGRP1a      GCACGCGGAAG---TGGAGGTGGTGGTGG-----TGGTTTCGGTGGTGGGAAGA 612
preLeGRP1b      TCACGCGGAGGCGGTGGAGGTGGAGGTGGAAGAGCGGGGGTGGTTACGGAGGTGGC--- 684
preLeGRP1c      TCACGCGGAAGC-----GGCGGCGGCGG-----CGGTTTTGGTGGTGGC--- 593
                ***** *          ** * * * *          **** ** *****

preLeGRP1a      CAACGTGAGGGAGGCGGTGGCGGCTACGGAGGAGGCGGCGGAGGCTATGGAGG----- 665
preLeGRP1b      CGACGTGAAGGCGGTGGCGGAGGCTACGGTGGTGGCGGC---GGCTACGGAGGTGGCCGA 741
preLeGRP1c      CGACG-----GGGTGGTGGTGGTTTTGGTGGCGGCGGCGGCGGATAACAATGG----- 640
                * **          ** * * * * * * * * * * * * * * * *

preLeGRP1a      ----AGGCGGCGGTTACGGAGGAGGTGGCGGTGGCTACGGAGGTGGCAGACCGGAAGGA 720
preLeGRP1b      CGTGAAGGCGGCGGCGGCGGCTACGGTGGAGGCGGCTACGGAGGTGGTTCGTCTGAAGGT 801
preLeGRP1c      ----AGGTGGTGGATACGGGCGACGTGAAGGTGGGAACG--GTGCGGTTATGGAGGT 692
                *** * * * * * * * * * * * * * * * * * * * * *

preLeGRP1a      GGTGGTGGTGGAGGCTACGGAGGTGGCCGACGTGAAGGTGGCGGC---GGCGTTAC--- 774
preLeGRP1b      GGTACGGTGGAGGC---GGTGGTGGTTATGGAGGAGGTGACCGCTACAACGATCGCTCT 858
preLeGRP1c      GGTCTGACCGGGGATATGGTGGTGGTGGTATCGTTATGGCGGTGGAGGTGATCGTTAC 752
                *** * * * * * * * * * * * * * * * * * *

preLeGRP1a      -----GGTGGTGGTGGCGGTTACGGTGGTGACCGTT--ATTAGATT---GATAG 818
preLeGRP1b      TCAAGAGGTGGAGGCGGTGGTGGTCCGATGGGAAGTGGAGGAATTAGATTTTCTGTTGG 918
preLeGRP1c      TCA-----AGAGGTGGTGGTGCATCAGAAGGAAGCTGGAGGAATTAGG-----GATAA 800
                * * * * * * * * * * * * * * * * * * * *

preLeGRP1a      CTCTT--AAT--TAGGCCTATGT-----TTTATGGCCTTTATAGATTAGTTTTAATAT 867
preLeGRP1b      CTTTTTAGAT--TGGTCTCGTCTGAAGTACTTATGGT-TTCGAAGTTTGATTGAAGTTA 975
preLeGRP1c      ATTCGAAATATGGGTTTA-----ATAGT-TTTG--GATTAA---AAACTA 841
                *          ** * * *          ** * * *          * * *          *

preLeGRP1a      CCATACTGGTTTAAAGTGTGGTT---TTAA-----GTTATTTGCTCTTATATTTGGT- 915
preLeGRP1b      CGTTTATGGTTTTGCCGTGGTACTGTTAGTGTCTCGTTTTTGACCGCTATTGTTACCG 1035
preLeGRP1c      CTAATATGTTTCTGTGTTGGGT---TT-----TTGTTTAGTGTATGTTTCTC 887
                *          ** * *          ** *          ** * *          ** * *

preLeGRP1a      -TGATAAGA-TACTGTGAATCTGTATTT-TGCGAAGTTC-CATGGAATCAAGTAAAAGCA 971
preLeGRP1b      -TGATGTTA-CCCTGTGGATCCTTGTTT-ACAAAGTTCTCATGAATGGAAGTGAATGGA 1091
preLeGRP1c      GTCATGTTACTACCGTGAG---GGATTTGTGCAAATTC-----AATC---TAAA---- 931
                * * * * * * * * * *          ** * * * *          *          * * *

preLeGRP1a      TGTTTGCGAAA-----AAAAAAAAA 992
preLeGRP1b      GATTTATTAATTATAGTCCAATCTCCTGTTTTCATCAAAAAAAAAA 1140
preLeGRP1c      -GTTT-TAAATGAT-----CAAAAAAAAAA 954
                *** **          *****

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(B)

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LeGRP1b      ----CACATT-CTCTTCAGGGTTTCTCTAGTAGTCTCTCTGAAAAAAA--AATG---GC 49
LeGRP1c      ---GCACATC-CA--TCAGTATT-----GAAAAAG--AATGTCTGC 33
LeGRP1a      TTAGGGTTTCTCTTTTCTGGTT-----CTCAGTTCAGTTTAATGCGCCG 45
              * *   ** *   **
              * *   *   *   *

LeGRP1b      CGACGTTGAATACAGGTGCTTCGTGGTGGTCTGGCATGGGCCACCACCGACCAAACT 109
LeGRP1c      TGAGGTTGAATACAGATGCTTCGTGGTGGGCTCGCATGGGCTACCAACGATAGAACCT 93
LeGRP1a      CGAAGTTGAGTACAGTTGCTTCGTGGTGGGCTAGCTTGGGCCACCACCGATAGAACT 105
              ** * ** * * ** * * ** * * ** * * ** * * ** * * ** * *

LeGRP1b      TTCGGAAGCTTTTTCTCAGTACGGCGAAGTGGTGAATCCAAGATCATCAATGACCGGGA 169
LeGRP1c      AGGTGAAGCTTTTTCTCAGTACGGAAATGTGGTGCACCTCAAGATTATCAACGATCGCGA 153
LeGRP1a      TAGCGATGCTTTCTCTACCTACGGCGAAGTAGTGCACCTCAAGATCATTAATGACAGAGA 165
              ** * ** * * ** * * ** * * ** * * ** * * ** * *

LeGRP1b      AACTGGTAGATCTAGAGGATTTGGATTCTTACCTTCAAGGATGAGCAAGCCATGAGGGA 229
LeGRP1c      AACAGGTAGATCGAGAGGATTTGGTTTTGTACCTTTACTGATGAGAAATCCATGAGGAA 213
LeGRP1a      AACTGGTAGATCTAGAGGATTTGGCTTTGTACCTTCAAGGATGAAAAATCCATGAAGGA 225
              *** * ** * * ** * * ** * * ** * * ** * * ** * *

LeGRP1b      TGCTATTGAAGGGATGAACGGCCAGGATCTTGATGGTGC AACATCACCGTGAACGAAGC 289
LeGRP1c      TGCAATTGAAGCAATGAATGGCCAGAACCCTTGATGGTGC AACATCACTGTTAACGAAGC 273
LeGRP1a      CGCTATTTCAGGAATGAATGGTCAGGAACCTTGATGGCCGT AACATCACTGTTAACGAAGC 285
              * * ** * * ** * * ** * * ** * * ** * * ** * *

LeGRP1b      TCAATCACGCGGAGGCGGTGGAGGTGGAGGTGGAAGAGGCGGGGTGGTTACGGAGGTGG 349
LeGRP1c      TCAATCACGCGGAAGCGGCGG-----CGGCGCGGTTTTGGTGGTGG 315
LeGRP1a      TCAAGCACGCGGAAGTGGAGGTGG-----TGGTGGTGGTTTCGGTGGTGG 330
              *** * ** * * ** * * ** * * ** * * ** * * ** * *

LeGRP1b      C---CGACGTGAAGGCGGTGGCGGAGGCTACGGTGG---TGGCGGCGGCTACGGAGG--- 400
LeGRP1c      C---CGACGGGGTGGTGGTGGTTTTGGTGGCGGCGG---CGGCGGATACAATGGAGG--- 366
LeGRP1a      AAGACAACGTGAGGGAGGCGGTGGCGGCTACGGAGGAGGCGGCGGAGGCTATGGAGGAGG 390
              * ** * * ** * * ** * * ** * * ** * * ** * *

LeGRP1b      TGGCCGACGTGAAGGCGGCGGCGGCTACGGTGGAGGCGGCTACGGAGGTGGTCTCGT 460
LeGRP1c      TGGTGGATACGGGCGACGTGAAGGTGGGAACGGTGG---CGGTTATGGAGGTGGTCTG-- 421
LeGRP1a      CGGCGGTTACGGAGGAGGTGGCGGTGGCTACGGAGGTGGCAGACGCGGAAGGAGGTGGT-- 448
              ** * * ** * * ** * * ** * * ** * * ** * * ** * *

LeGRP1b      TGAAGGTGGTTACGGTGGAGGCGGTGGTGGTTATGGAGGAGGTGACCGCTACAACGATCG 520
LeGRP1c      -GACCGGGGATATGGTGGTGGTGGTATCGTTATGGCGGTGGAGGT-----GATCG 471
LeGRP1a      -GGTGGAGGCTACGGAGGTGGC-----CGACGTGAAGGTGGCGGC-----GGCGG 492
              * * ** * * ** * * ** * * ** * * ** * * ** * *

LeGRP1b      CTCTTCAAGAGGTGGAGGCGGTGGTGGTCCGATGGGAACTGGAGGAATTAGATTTTCTG 580
LeGRP1c      TTACTCAAGAGGTGG-----TGGTGCATCAGAAGGAAGCTGGAGGAATTAGG-----G 519
LeGRP1a      TTAC---GGTGGTGG-----TGGCGGTTACGGTGGTACCCTTT---ATTAGATT---G 536
              * * ** * * ** * * ** * * ** * * ** * * ** * *

LeGRP1b      TTGGCTTTTTAGATTGGTCTCGTCTGAACTTACTTATGGTTTCGAAGTTTGTATGAAGTT 640
LeGRP1c      ATAAATTCCGAAATA-----TTGGGTTTA---ATAGTTTGGGA--TTAA---AAACT 563
LeGRP1a      ATAGCTCTTAA-----TTAGGCCTA----TGTTTTATGGCCTTTAT--AGATT 578
              * * * * ** * * ** * * ** * * ** * * ** * *

LeGRP1b      ACGTTTATGGTTTTGCGGTGG-TTACTGTT-AGTGTCTCGTTTTTGCACCGCTATTGTTA 698
LeGRP1c      ACTAATATGTTTTCTGTGTTGGGTTTTTGTGTTAGTGTATGGTTTCTCGTCA-TGTTACTA 622
LeGRP1a      AGTTTTA-ATATCCATACTGG-TTTAAGTGTGGTTTTA-AGTTATTTGCTCTTATATTTG 635
              * ** * * ** * * ** * * ** * * ** * * ** * *
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<i>LeGRP1b</i>	CCGTGATGTTACCCTGTGGATCC-TTGTTTACAAAGTTCTCATGAATGGAAGTGAATGGA	757
<i>LeGRP1c</i>	CCGTGAGGGATTGTGCAAATTT-CAATCTA--AAGTTT-----AAATGATCAAC	670
<i>LeGRP1a</i>	GT-TGATAAGATACTGTGAATCTGTATTTTGCGAAGTTCC-ATGGAATCAAGTAAA-AGC	692
	***                   **   **                   * *   *****                   ** * *	
 <i>LeGRP1b</i>	 GATTTATTAATAAAAAAAAAAAAAAAAAAAAAA	 785
<i>LeGRP1c</i>	CCCTTTTCTAAAAAAAAAAAA-----	689
<i>LeGRP1a</i>	ATGTTTGCGAAAAAAAAAAAAAAAA-----	714

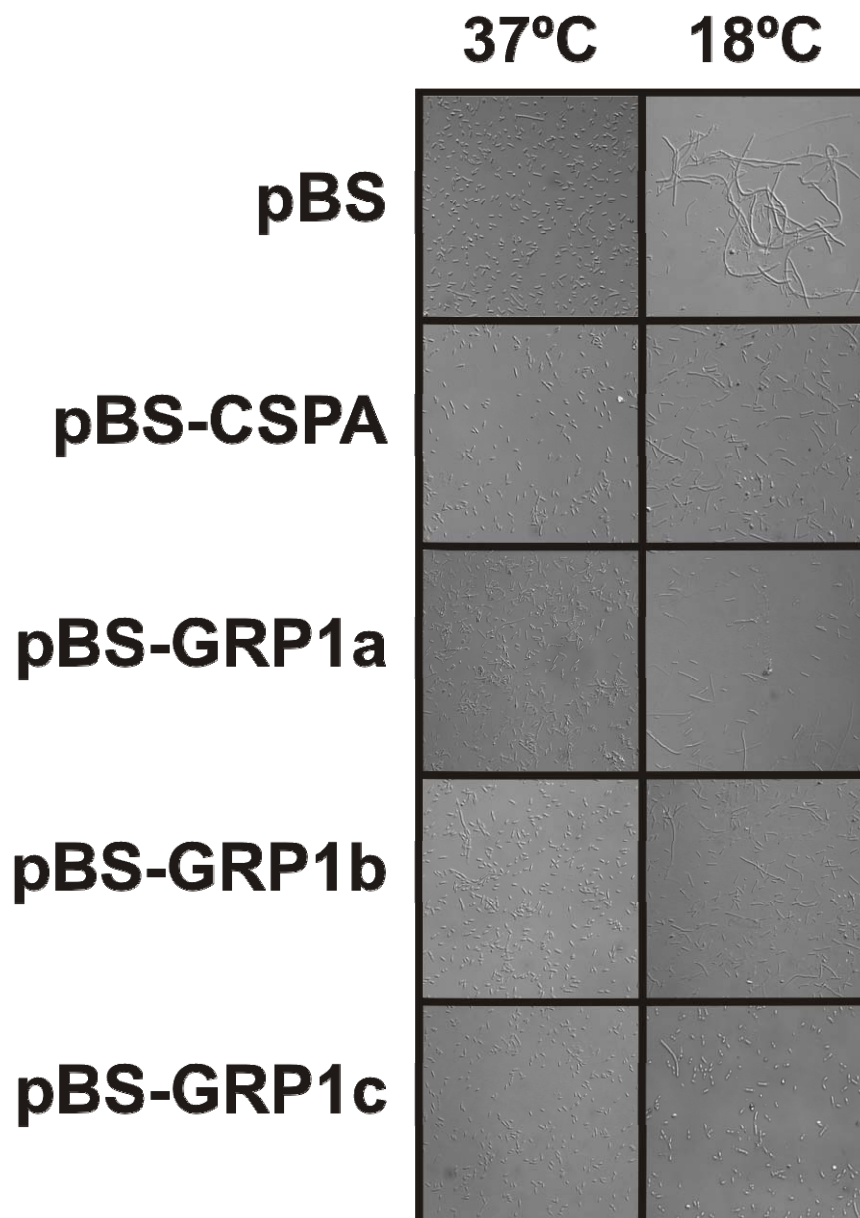
(C)

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LeGRP1a  MAAEVEYS CFVGGI AWATTDRTLSDAFSTYGEVVDSKI INDRETGRS RGFQFVTF KDEKS 60
LeGRP1b  -MADVEYR CFVGGI AWATTDQTLSEAFSQYGEVVESKI INDRETGRS RGFQFVTF KDEQA 59
LeGRP1c  MSAEVEYR CFVGGI AWATNDRTLGEAFSQYGNVDSKI INDRETGRS RGFQFVTF IDEKS 60
          *:*** ***** .*:*.*** **:*:*****.***:

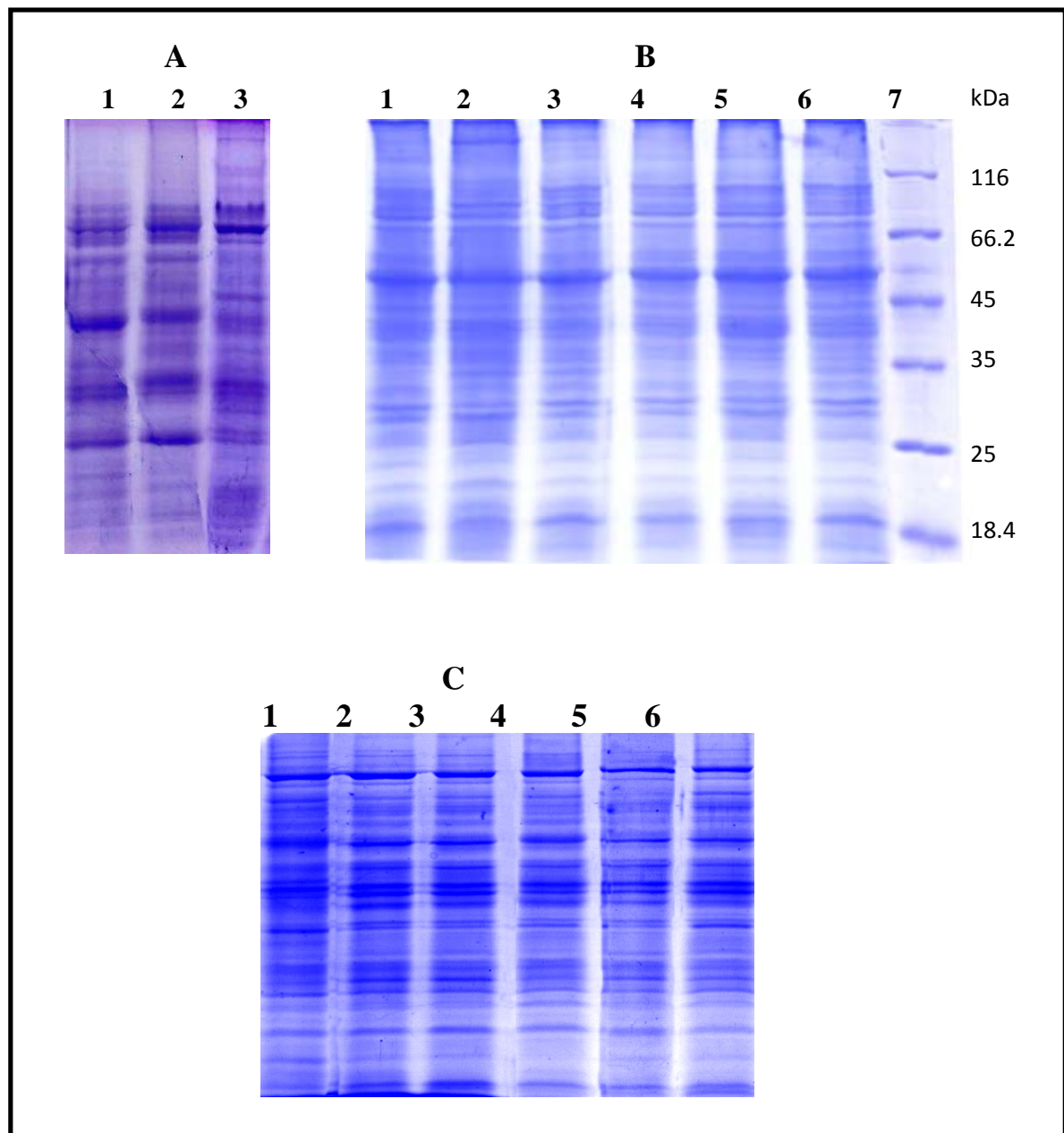
LeGRP1a  MKDAISGMNGQELDGRNITVNEAQARGSGGGGGFGG---RQREGGGGGYGGGGGYG 116
LeGRP1b  MRDAIEGMNGQDL DGRNITVNEAQSRGGGGGGGRGGGGYGGGRREGGGGGYGGGGG-YG 118
LeGRP1c  MRNAIEAMNGQNL DGRNITVNEAQSRGSGGGGG-FGGG-----RRGGGGFGGGGGYN 112
          *:.** .*****:*****:*.***** ** . ***** ** . ***** *

LeGRP1a  GG---GGYGG-GGGGYGGRREG--GGGGYGGRREGGGGGYGGGGYGGDRY-- 164
LeGRP1b  GGRREGGGGGYGGGGYGGRREGGYGGGGYGGDRYNDRSSRGGGGGSDGNWRN 175
LeGRP1c  GGGYGRREGGNGGGYGGGRDRG-YGGGDRYGGG-----GDRYSRGGGASEGSWRN 163
          ** * * .***** .* ** . ***** . . *** . . :
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**Fig. S2.** Images of BX04 cells expressing GRP1a-c, CspA or pBS grown at 18°C. *E. coli* BX04 containing pBS-GRP1a-c, pBS-CSPA (positive control) or pBS (negative control) were grown in LB medium at 18°C for 3 days or at 37°C overnight and observed under a light microscope.

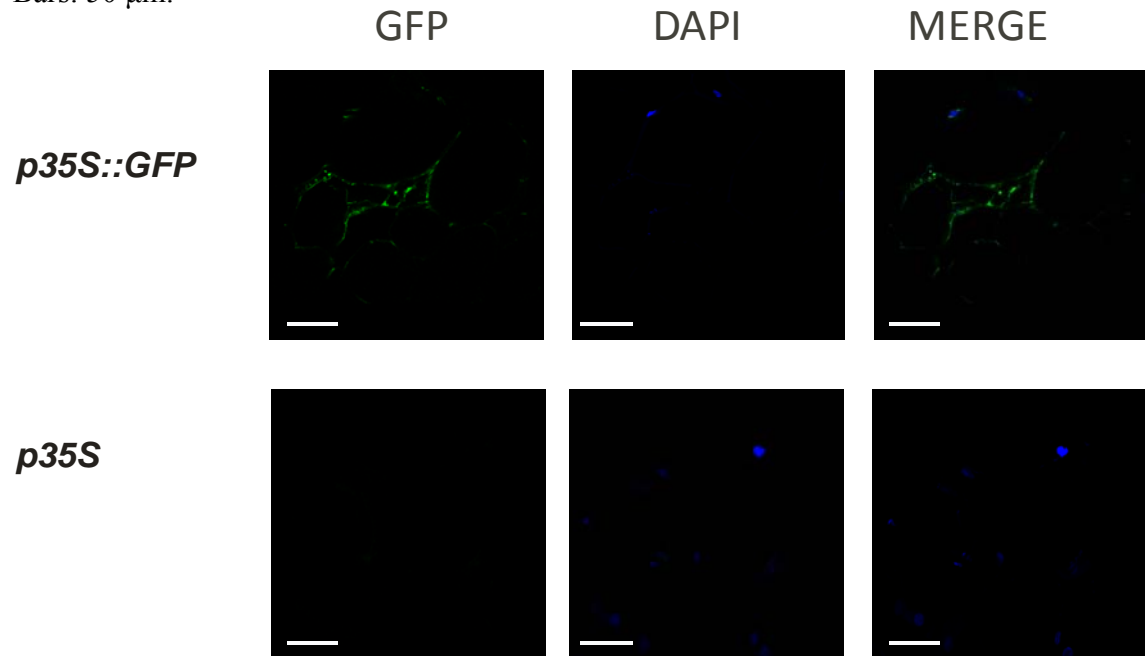


**Fig. S3.** Representatives SDS-PAGEs showing protein bands and loading control. (A) Thirty micrograms of IG (lane 1), MG (lane 2) and RR (lane 1) protein extracts at zt0 were loaded in each lane of the 12% SDS-PAGE. (B) Thirty micrograms of IG protein extracts at zt 0, 4, 8, 12, 16 and 20 (lanes 1 to 6, respectively) were loaded in each lane of the 12% SDS-PAGE. Bands of molecular weight marker (line 7) are shown. (C) Thirty micrograms of MG protein extracts at zt 0, 4, 8, 12, 16 and 20 (lanes 1 to 6, respectively) were loaded in each lane of the 12% SDS-PAGE.

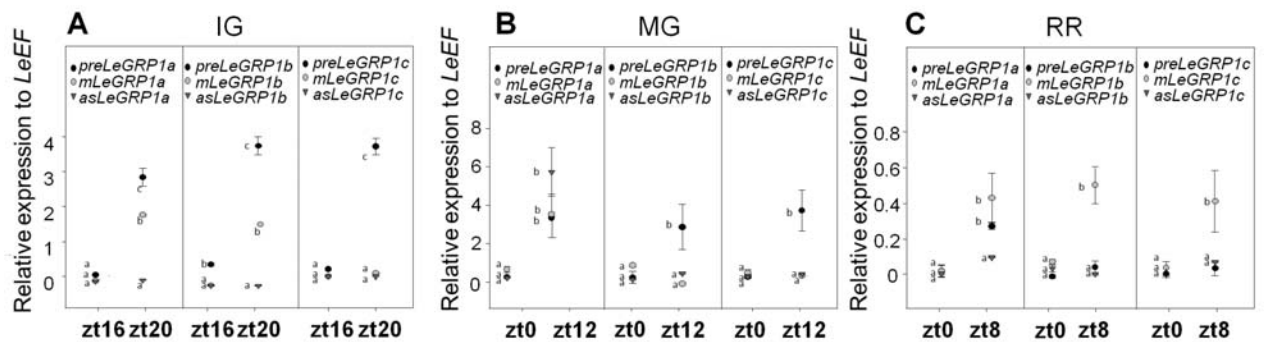




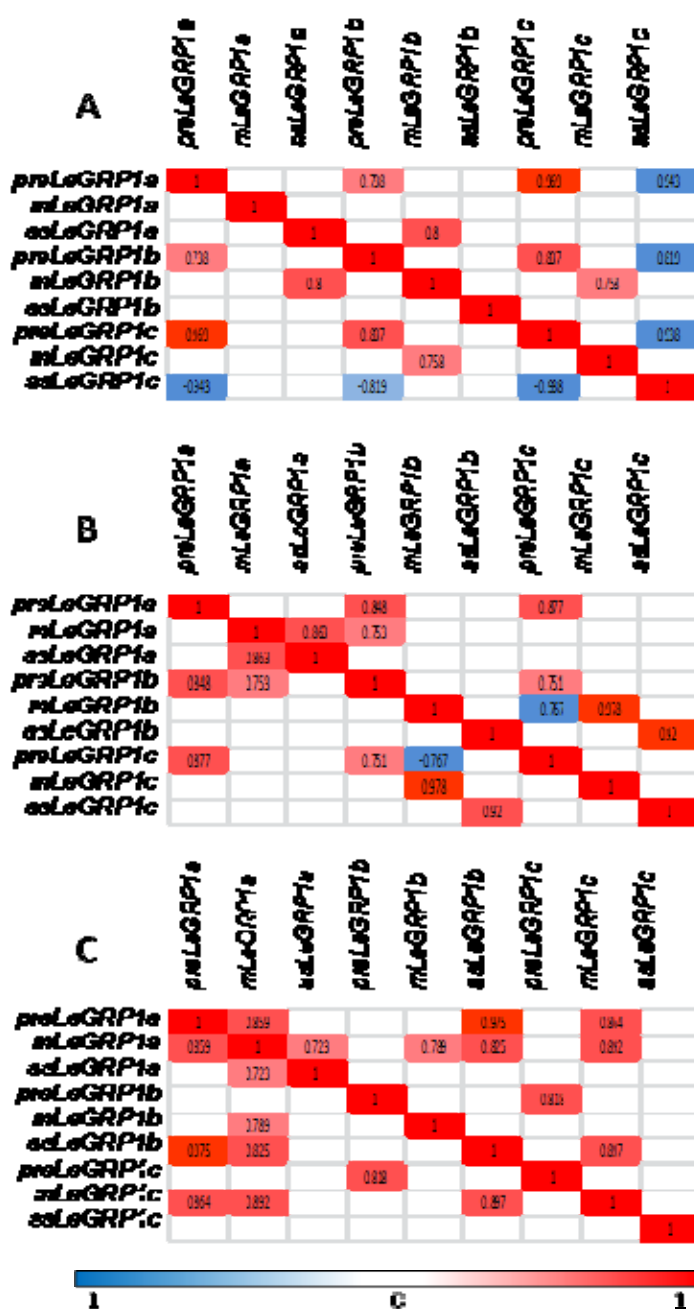
**Fig. S4.** Confocal microscopies showing DAPI and GFP fluorescences in cells of mesocarp tissues infiltrated with *p35S::GFP* or with empty vector (*p35S*). Analysis was conducted 7 days after infiltration. DAPI fluorescence indicates the position of nuclei; GFP fluorescence indicates the localization of GFP. Images were merged to show signal overlap. Bars: 50  $\mu$ m.



**Fig. S5.** Tomato plants with immature green (IG), mature green (MG) or red ripe (RR) fruits grown under a 16-h light/8-h dark photoperiod were transferred to continuous light for a 24 h period and *Legrp1a-c* premature (pre-), mature (m)- and alternative spliced (as)-mRNA were analysed in these fruits. It is shown in this figure, the peak of each *Legrp* form at IG (A, zt20 in relation to zt16), at MG (B, zt12 in relation to zt0) and at RR (zt8 in relation to zt0). The means of the results obtained, using 3 independent mRNAs as template, are shown. Y axis refers to the fold difference in a particular transcript level relative to the Ct values corresponding to *LeEF1 $\alpha$* . Standard deviations are shown. For each form, points with the same letters are not significantly different ( $P < 0.05$ ).



**Fig. S6.** Spearman rank order correlation analysis of the different forms of *Legrpla-c* transcripts levels in tomato fruit at IG (A), MG (B) and RR (C) stages. Cell content shows the correlation coefficient with  $P < 0.05$  for each pair of transcripts analysed. Positive and negative correlation coefficients are shown in red and blue scales, respectively. For positive correlation coefficients both transcripts tend to increase. For negative correlation coefficients one transcript tends to decrease while the other to increase. Pairs with  $P > 0.05$  are shown in white cells and there is no significant relationship between the two variables.



**Fig. S7.** Analysis of (A) LeGRP1a, (B) LeGRP1b and (C) GRP1c promoter sequences. Predicted cis-elements are highlighted in gray. (-) Symbol indicates cis-elements in the minus strand. The ATG start codon is shown in bold and underlined letters.

(A)

AGAGGCAGCAATTTTGCTCTGGTGGGTAAGTCGCTGTTGGTGCAACAATTTACCATTTTGGTTA  
 ATATAAAATTTTATATACTGTTTTAAAATTTTTGTTAATATTTTTTGGGCAACTTTCACATATAG  
 CAAACAAAAAATTCATATTTGTATGCTATAACAACTTTGCATAATTGCGCTCCATAGCAAACAT  
 AAAACTGTATAATTTGCTATACATATATAATTGTATAATTTGCTGACCTAAATTGTATAATTCGC  
 TGGCATAAATTGTATAATTCGCTGACCTATTTGCTGCAATTGTATAAATTGTTTTGCATACAGTT  
 GACTCGAATTAATGTATGTATATTGCATAATTATAAGTGTATAACAAGAAGATATATATTTTT  
 CTCGCTTTATACAAAAACAGAAACACAATATATACTTCTGTTGTATAAAGCTAGAGAAAATT  
 STKST1(-) STKST1(+)  
 GTATTTCACTGCAATTGTATAATTCGTTGGCCTTTTTCTCCGCAATATTTGAAGTAAAATATTTGT  
 AAATTGTATAATTAAGTGTATAAAGCGAGAGAGGCGAGTGAGAATGGAGAGTGACGAGCGAGA  
 STKST1(+)  
 TTTTTGGGAGAGAGACGCTAACAAAGTTTTAGCTAATGTTTTTATGAAGCACAATTAATCAAACC  
 CIACADIANLELHC  
 CTAACTATTTCAATTAATTTATATTATTAGTTTTCTATTATATATAACAATTTCCCTATTTTGTATC  
 CTTTAGGCTTTTGGACTTTTATTTTAAAGCTTATTCAAGTTTTTATTATTATTAATCTCGATCA  
 STKST1(-) STKST1(+)  
 AATTTTTTTGAGTCAAAGAAAAGTGATGAGTTAGGGATGATTTGGACATTTTCTTTGGCAAAAATA  
 EVENINGAT  
 TCTTACACCCTAAGCCCAATTACTTAAAAGCCCATGGACACCTAGCTTCTGCCGCCATAAAAATA  
 GCCCORE  
 TGGGCTTTTCTGTTTAATTTTCATCGCATCTCTCATTTCAGATATTTTATTAGGGTTTCTCTTTTC  
 EVENINGAT (-)  
 TGGTTTCTCAGTTCAGTTTAATG

(B)

TCCCCATACAATATTCTAAAAAATTTCTCAACTAGTCCCTTCAATTACACTATATAAACTTATG  
 GTATGACGCAGATGTAATCTTATAACTTAATTACATCATAACGAAATATGTAATTTGTAACAA  
 AAATAATAAGACATGTTTATACTTTAATTACATGATATTAATTTGTACAGGTGAGATGGAGTGG  
 STKST1(-)  
 GTGGTCAGAAGTCCTCTCTCGTGATTGTATTTGAACTATTCATCTTTTTTCTTTTCTTCCACCATA  
 GTATGTGTTTTACAACGGATTTTAAAGCGAGAGAAGTAAATGTAATCACAAATTATGAAGAAAC  
 STKST1(+)  
 ATAACCTTGTTAATTAAGATCGCGGGTAAAATTTGTTCATTTATTAATTATTTTCTCAATTTTTC  
 CATGATTTAAGGGCTGTTAATTGTATATTTCTATGATGATTTAAATTTGACATCTATATTAATATT

CCTCTTTTGG AATATATTGAGATGCCTTTTAAATGAATTTAGTATCATTTATATAGACGTCAACTA  
GAGTTTAAGATTGAGTAATCTTTAAAAATTCTAATTGAAACTGAATACACATTATAGAGTCTCAA  
STKST1(-)  
TTCGAATTGAACATGTATTATAGAGTCTCACAAAATTGCAATCGAAACTAGACCCACTTTCTAGA  
ATTTCAATTTAAATTGAACATATCTTATAAAGTCCTAAAAAATTTCAATCTTTACCGTGGAGAC  
STKST1(+)  
TCAAATTTAATTTAGAACCTCAACTAATTATTTTTCTAATGGGCATGTTTATGTAATTTCAAACAC  
TTCAGGGCCTTCTTCAGTAACATTATGTTGTATAATAGAGTATTGGCAAGTTGAGAAACACGACA  
AACACTAAACGGACAAATTTTTAACTGCACTCTTAACCCGGGTTGCATAGGAGTTAGGAATAG  
ACCGCCGTGCACGATTAGTTTAACTGGCCCAAGGGTAAAACCTAGGCTCCTAATCCAGCCTATA  
AATGAAGGCAAATTTCCCAATTTCTCCACAGCTCTCCTTCACATTCTCTTCAGGGTTTCTCTA  
GTAGTCTCTCTGAAAAAAAAATG

(C)

TGTACTTAAAAGCTGAAATAACTTTTACTAAATGGCCAAAAGTTATAACTCTAAGGGTCATTGG  
ACAAATGCATGGATTATCTATAAATTATAAATTAATAATATTAGAGTTAGTTTATTATAAGTGTT  
MYBLEPR  
TAATTCGTTGTTTTATTTTTATTTTATGTTTGATTTAATATTTTAGAAATAGTCTTTTTCTTTATTTAT  
POLLENILELAT52 STKST1(-)  
TAAGTGTTTAATTCGTTGTTTTTCATTTTATTTTATGTTTGATTTAATATTTTAGAAACAGTCTTTT  
POLLENILELAT52  
TTTATTATACTCTTGAATTATTATGAGATTTTATATTTTACTTTGTCAAGTTAGATATTTAAA  
TATAAATTTAATTTTTTTTTTAGGTTTGATATTCCACCATAGTGATCCTTGATAGTACGATATATT  
TCTAATTTTTTTTTCTGTTGGTCAAGTATACCTTAACTTAACATGAATTTAAGGTTAATTAATTTGT  
TTAAGTATACAAATCTTACTTTTTAAAAAAAATAGTTCAAGCGATCAATTGACGAACTACATTT  
TAAAAATAATGAAAAGATCACCCGATATAACAAATCAAACATAGAGATTTTTTTTTTAATTAAT  
TTATGAAATTATCAAATTACATGGATTGAATTTGAAGAATTTAAAAGATTGTATATAAATATTCT  
CATATAAATTAAGAAAGAAATTAATTAACAAAAAGAAATTAGGAAAAACATTAGGGGAT  
POLLENILELAT52 POLLENILELAT52 IBOX  
AATTAAGTTATTTAAGGATCTTATTGGAAGATCATTAACGTTGAATTAGTTATCCATCCTTTTCT  
CIACADIANLELHC (-)  
AGGAATTAGATAAGATCTAACTAATTTTTATTTTATTAGAATAAAAATAAATATGAGGCGTATG  
IBOX  
TGATTGTTAATGAGGAGTAGTTATCCATTAGCGTCGCAATCGGTAAGTAAGTAGTGTTCTAGTG  
GGCATGAAAAGTAGTGTGGTTGTGCTATAAAAGGGGCATGGAATTTGTAGAGAGAAATGCAC  
POLLENILELAT52  
ATCCATCAGTATTGAAAAAGAATG