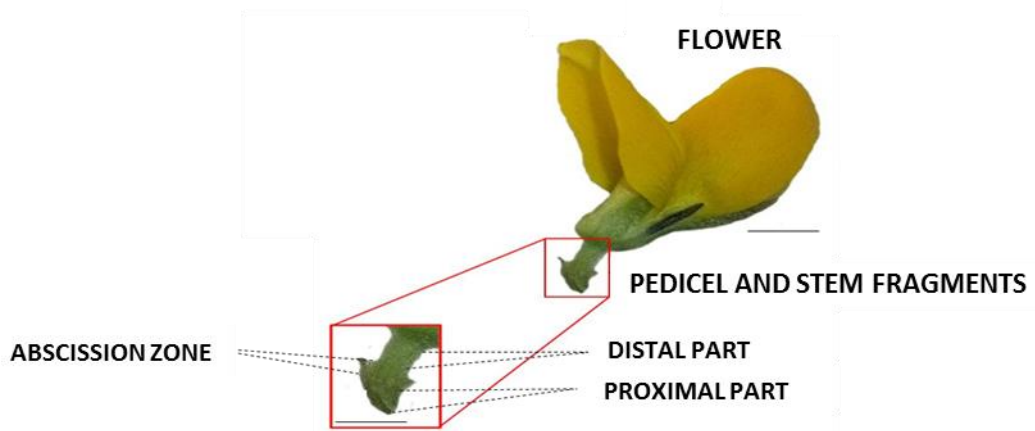
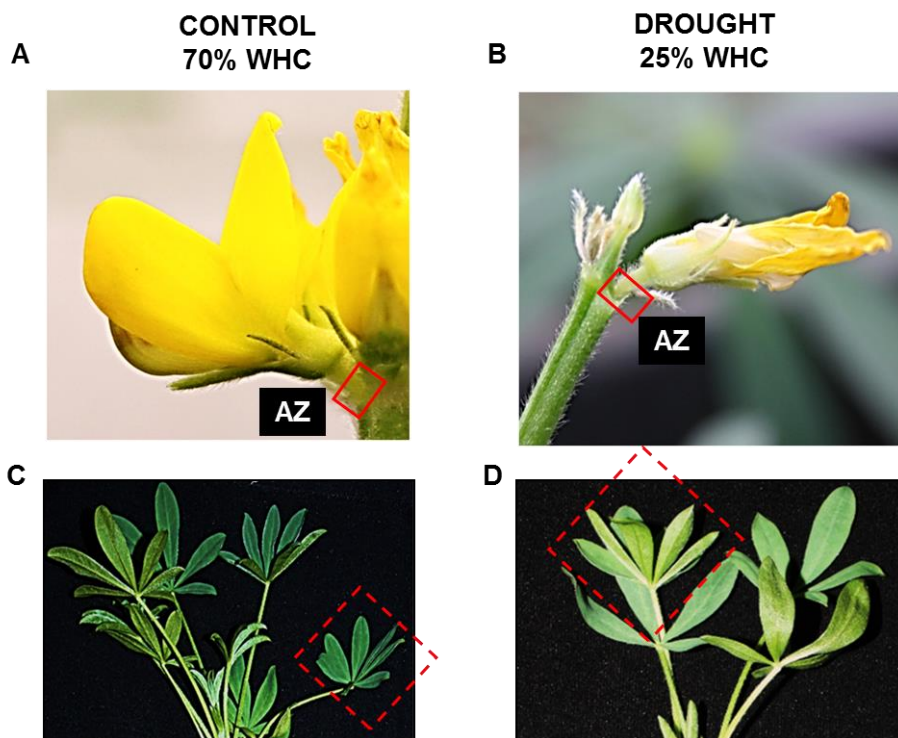


## Acronyms used in the text

| ABBREVIATIONS<br>in alphabetical order | DEFINITION  |
|--|---|
| <b>ABA</b>                             | abscisic acid   |
| <b>ACC</b>                             | aminocyclopropane-1-carboxylic acid                                     |
| <b>AZ</b>                              | abscission zone   |
| <b>CAT</b>                             | catalase  |
| <b>DIST</b>                            | flower pedicel fragments above the az                                   |
| <b>ET</b>                              | ethylene  |
| <b>LIACO</b>                           | <i>AMINOCYCLOPROPANE-1-CARBOXYLIC ACID OXIDASE from Lupinus luteus</i>  |
| <b>LIACS</b>                           | <i>AMINOCYCLOPROPANE-1-CARBOXYLIC ACID SYNTHASE from Lupinus luteus</i> |
| <b>LIHSL</b>                           | <i>RECEPTOR-LIKE PROTEIN KINASE HAESA-like from Lupinus luteus</i>      |
| <b>LIIDL</b>                           | <i>INFLORESCENCE DEFICIENT IN ABSCISSION-like from Lupinus luteus</i>   |
| <b>LIMPK6</b>                          | <i>MITOGEN-ACTIVATED PROTEIN KINASE6 from Lupinus luteus</i>            |
| <b>LIZEP</b>                           | <i>ZEAXANTHIN EPOXIDASE from Lupinus luteus</i>                         |
| <b>PROX</b>                            | stem fragments below the AZ   |
| <b>RWC</b>                             | relative water content  |
| <b>VB</b>                              | vascular bundles  |
| <b>WHC</b>                             | water holding capacity  |



**Supplementary Figure 1.** Flower of *Lupinus luteus* L. Tissue fragments (indicated by red boxes) containing abscission zone (AZ) dissected 1 mm above (distal part) and below AZ (proximal part) were collected for analyses. Scale bars: 5 mm.



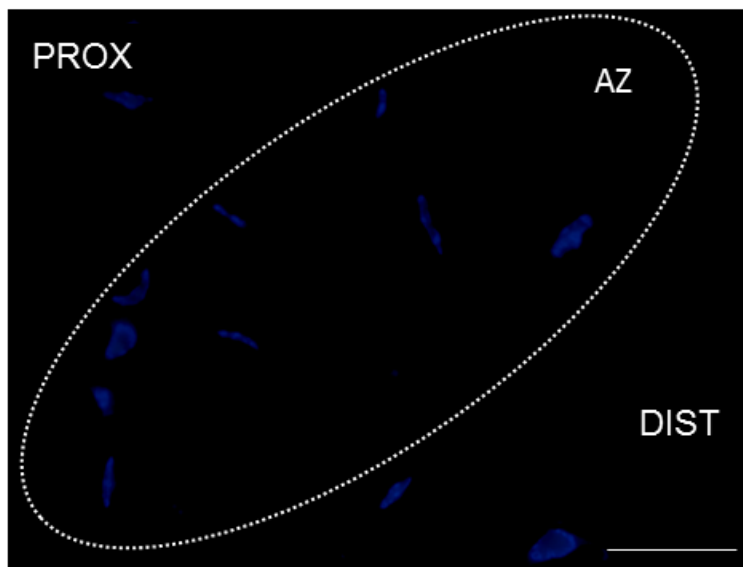
**Supplementary Figure 2.** Non-abscised flower of yellow lupine (*Lupinus luteus* L.) with inactive abscission zone (A) and flower containing active AZ from plants cultivated under drought conditions (B). The AZ regions were marked by red squares. Leaves of control plants (C) and leaves from drought-stressed lupines (D) used for analyses.

**Supplementary Table 1.** Qualitative and quantitative composition of calibration standards used in the ICP-OES analyses.

|    | Concentration [ppm] |     |     |
|----|---------------------|-----|-----|
|    | I                   | II  | III |
| P  | 5                   | 15  | 30  |
| Fe | 0.25                | 1.5 | 4   |
| S  | 2                   | 8   | 15  |
|    | IV                  | V   | VI  |
| Na | 2                   | 15  | 30  |
| K  | 5                   | 20  | 40  |
| Zn | 0.1                 | 0.7 | 1.5 |

**Supplementary Table 2.** List of wavelengths characterized for measurements of emission lines of elements.

| Chemical element | Wavelength [nm] |
|------------------|-----------------|
| Zn               | 206.201         |
|                  | 213.857         |
| Na               | 589.585         |
|                  | 588.998         |
| K                | 766.496         |
| P                | 213.619         |
|                  | 214.919         |
| S                | 180.67          |
|                  | 182.562         |
| Fe               | 238.203         |
|                  | 239.57          |
|                  | 259.938         |



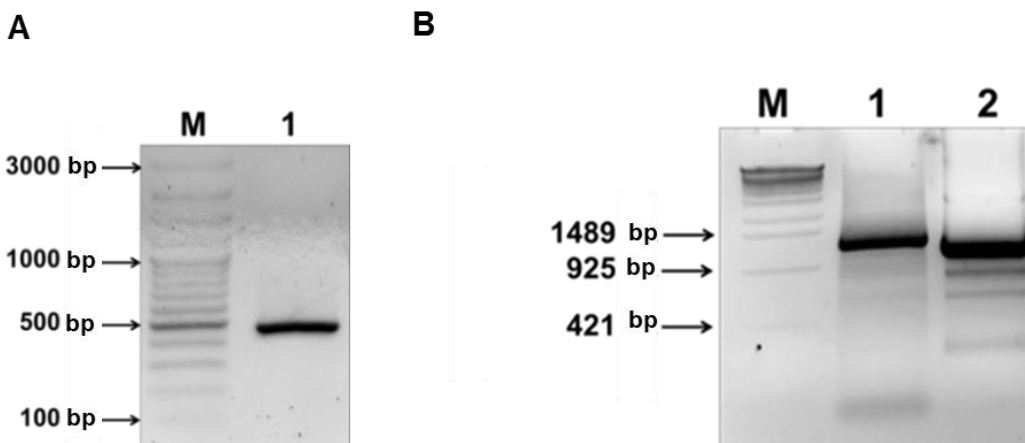
**Supplementary Figure 3.** The results of a control reaction performed with omitting primary antibodies anti-ACC, anti-ABA, anti-CAT, and anti-MPK6. Control reaction produced negative results compared with those of standard reactions. Nuclei were stained with DAPI. The abscission zone (AZ) region was highlighted by white curves. Abbreviations: PROX – stem fragment below the AZ, DIST – flower pedicel fragment above the AZ. Scale bars 100  $\mu$ m.

**Supplementary Table 3.** List of primers used for identification of genes

|                           | cDNA of gene  | Primer sequence 5'-3'  |
|---------------------------|---------------|--|
| <b>Degenerate primers</b> | <i>LIZEP</i>  | FP: GCTAYACTTGTTAYACYGGNA<br>RP: CCVACRCCHARRTAWGCYTT  |
|                           |               | <b>RACE-PCR primers</b>  |
| <b>Specific primers</b>   | <i>LIHSL</i>  | 1FP: TCCCTCTCTCTAACCCAAGACG<br>1RP: CTCGTCCTGCAATGAGAAGGGTGG<br>2FP: TTGCAACTGGAAAGTGGCTCT<br>2RP: ATCACGAACAATTCCACCCGGA<br>3FP: GCAAGTTTGTGCAATGGGGGA<br>3RP: CCTAAGTATACGGGAAGCTCTG |
|                           | <i>LIMPK6</i> | 1FP: GCAACTTGTTCTGTGCGTCTCGGA<br>1RP: GCAACTTGTTCTGTGCGTCTCGGA<br>2FP: AGGGTTCTCACACATGGTGG<br>2RP: AGGGTTCTCACACATGGTGG   |

**Supplementary Table 4.** List of primers and UPL probes used for RT-qPCR reactions

| cDNA of gene  | Primer sequence 5'-3'                                       | UPL no. |
|---------------|---|---------|
| <i>LIIDL</i>  | F: ACAGCACCATGGTCACTTTTC<br>R: TTGTGTTTCCTTGAGGGAGTG        | 137     |
| <i>LIACS</i>  | F: TTCATTCAAGAAGGCAATGGT<br>R: GGTTTGGGTCAAAGTCACC          | 53      |
| <i>LIACO</i>  | F: GTGATGAAGGAATTTGCACAAG<br>R: CCAAGGTTTTTCACACAGCAA       | 53      |
| <i>LIZEP</i>  | F: GGGTTTCCGGTTCTTGAT<br>R: AAAGCCATTCTGACTAATAACTCTTG      | 165     |
| <i>LIACT</i>  | F: TAATGGTTGGGATGGGTCAG<br>R: CAAGGTGAGAATACCCCTCT          | 165     |
| <i>LIHSL</i>  | F: TGATGAAATTGGGTATTTGGGTA<br>R: GAAGCCGGTCAGAAAATTTATTATAG | 147     |
| <i>LIMPK6</i> | F: GCTCCTTCGTCATATGGATCA<br>R: AATGTAGACATCATTAAGCTCTCCTT   | 147     |



**Supplementary Figure 4.** Products of PCR with degenerate primers for *LIZEP* (A) and products of 5'-3'- RACE-PCR reactions (B; 1 and 2 lane, respectively) in agarose gel.

1 atgggggactttgttgccttgttttttctatatcagatatattataggggacgaaaaaa  
62 ctcaacctctaacaactctttatcttcaatttaaattatgcataccagttatggcttatg  
122 agtttgggaaagttagaggcactgaaagacacgtaacacaacacaacacacacttgagttt  
182 gttcctaagctttcttctcttctgcaaccATGGCTTCTACCTTGTGTTACAATTCTCTTAAT  
M A S T L C Y N S L N 11  
242 ACCTCAACAACCTTCTTTCTCAAGAACCCTTCTCAGTTCCAATCAATAAAGAGCTTTCA  
T S T T S F S R T H F S V P I N K E L S 31  
302 CTAGATATTTACCTTTTGTAGTACGGCTATCACCTAGGAACCAAGACTAGGAAGCAG  
L D I S P F V S Y G Y H L G T R T R K Q 51  
362 AAGAAGAAAGTGATGCTGCATGTAAGAGCTGGTGCAGTTGCTGAAGCTCCACCTTCAAAG  
K K K V M L H V K A G A V A E A P P S K 71  
422 AAATCTGAGGCTGAAAATGGTGGGAATGGAATTACCCATCAGAAGAAGAAGCTTAGGATA  
K S E A E N G G N G I T H Q K K K L R I 91  
489 CTTGTGGCAGGTGGTGGGATTGGTGGCTTGGTTTTTGGCTTTGGCTGCTAAGAGAAAAGGG  
L V A G G G I G G L V F A L A A K R K G 111  
542 TTTGAGGAGGTGGTGGTTTGGAGGGACTTGGTGTATAAGAGGTGAGGGACAGTATAGG  
F E E V V F E R D L S A I R G E G Q Y R 131  
602 GGTCCAATTGATACAAAGTAATGCATTGGCTGCTTTGGAAGCTATAGATTGATGTT  
G P I Q S I N A L A A L E A I D S D V 151  
662 GCTGATGAAGTTATGAGAATTGGTGCATCACAGGTGATAGAATCAATGGACTTGTGAT  
A D E V M R I G C I T G D R I N G L V D 171  
722 GGGGTTCCGGTCTTGGTATGTCAAGTTGATACATCACTCCTGCAGTTGAACGTGGG  
G V S G S W Y V K F D T F T P A V E R G 191  
782 CTTCCAGTCACAAGGTTATTAGTCGAATGGCTTTACAAGAGATCCTTGTAGTGCAGTT  
L P V T R V I S R M A L Q E I L A S A V 211  
842 GGGGAAGATATCATCATGAATGGCAGTAATGTTGTAATTTTGTAGATGATGGAACAAG  
G E D I I M N G S N V V N F V D D G N K 231  
902 GTAACAGTAGAGCTTGAAGTGGTGAAGAAATGAAGGAGATCTTTTGGTGGAGCTGAT  
V T V E L E N G E K Y E G D L L V G A D 251  
962 GGTATACGCTCCAAGGTGAGGAATCAGTTATTGGTCCAAAAGAAGCTGTTACTCGGG  
G I R S K V R N Q L F G P K E A V Y S G 271  
1022 TATACTGTTTACTGGTATTGCAGATTTTGTGCCTGCTGACATTGATTCTGTTGGGTAC  
Y T C Y T G I A D F V P A D I D S V G Y 291  
1082 CGAGTTTTCTGGGACACAACAATACCTTGTATCTTCAGATGTTGTTCTGGAAAGATG  
R V F L G H K Q Y F V S S D V G S G K M 311  
1142 CAATGGTATGCATTTCAAAAGAAGCTCCTGGTGGTGTGATATCCCAATGGAAAAG  
Q W Y A F H K E A P G G V D I P N G K K 331  
1202 GAAAGGCTGCTTAGGATATTTGAGGGCTGGTGTGACAATGCAATAGATCTGATACTGGCT  
E R L L R I F E G W C D N A I D L I L A 351  
1262 ACAGACGAGACGGAAATCTGCGACGAGACATCTATGACAGGATACCAACTGAACTGG  
T D E T E I L R R D I Y D R I P T L N W 371  
1322 GGAAGGGTCGTTGACTTTTGTCTCGGTGATTCGGTCCATGCCATGCAGCCAAATATGGGC  
G K G R V T L L G D S V H A M Q P N M G 391  
1382 CAAGGAGGTGTCATGGCTATTGAGGACAGTTACCACTAGCATGGAGGTGGACAATGCA  
Q G G C M A I E D S Y Q L A L E V D N A 411  
1442 TGGGAGCAAAGTATAAAATCAGGCCAACTAGCATTGGAGGTGGACAATGCAATGGGAGCAA  
W E Q S I K S Q L A L E V D N A W E Q 431  
1502 AGTATAAAATCAGGGTCTCCGATTGACGTTGACTCTCCCTTAGGAGCTACGAGAGAGAA  
S I K S G S P I D V D S S L R S Y E R E 451  
1562 AGAAGACTACGGGTGTCATAATTCATGGAATGGCTAGAATGGCCGCTCTGATGGCTTCC  
R R L R V A I I H G M A R M A A L M A S 471  
1622 ACCTACAAGGCATCTAGGCGATGGTCTGGCCCTTGGAGTTTTTGACCAAGTTTCGG  
T Y K A Y L G D G L G P L E F L T R 491  
1682 ATACCGCATCCTGGAAGAGTTGGAGGAAGGTTTTTGTGACATGTTTCATGCCTTCTATG  
I P H P G R V G G R F F V D M F M P S M 511  
1742 TTAAGTTGGTCTTAGGTGGCAATAGCTCCAACTTGAAGGCAGACCCTAAGTTGCAGA  
L S W V L G G N S S K L E G R P L S C R 531  
1802 CTCTGCAAAAGCAAATGACCAGTTGCGTAGATGGTTTGAAGATGATGCACTTGAG  
L S D K A N D Q L R R W F E D D D A L E 551  
1862 CGTGCTAATAGTGGAGAGTGGACTTTATTACCACAAGGAGAAGAAAAGGTCATTCAAAA  
R A N S G E W T L L P Q G E E T G H S K 571  
1922 CCTATAAGTTTAAAGTCGAGATGAGATGAAACCGTGCATGATCGGGAGTGCACAGGAAAT  
P I S L S R D E M K P C M I G S A Q E N 591  
1982 GATTTTATGGCAATTCAATAACAATACCTTACCCAGGTTTCTCGAGACTGCTCGA  
D F I G N S I T I P S P Q V S P R H A R 611  
2042 ATTAGCTATAAGGATGGTGCCTTCTTCTGACTGATTTGCGAAGTCAACATGGCACTTCC  
I S Y K D G A F F V T D L R S Q H G T S 631  
2102 ATCATTGACATTGAAGGAAGGAAATATCGGGTACCTCAAATATCCTGCTCAGGTCCAC  
I I D I E G R K Y R V P P N Y P A Q V H 651  
2162 CCAACCGATGTTTATGAGTTTGGCTCTGATAAGGCTTCATTTGGGTTAAGGTTATCAGA  
P T D V I E F G S D K A S F R V K V I R 671  
2222 TCTGCACCAAGAGTATCTGAGAAGGAGGAAATGACAAAAGTTCTGTGAAAGTATAAgtg  
S A P R V S E K E E M T K V P V K V 690  
2282 attatatttagttattaattacagtttgaagtgttacagaaaagtgttacagcaaaat  
2342 ttgaaaaggtagagccactatcttccctttaaattgggtattatacaatagtgtcagtc  
2402 ataaaggtatgaaacatattacaaattttaaattggaatcatagaatgaaggtatag  
2462 ttgttgatataataggaacaaagtttaagtttttccg

**Supplementary Figure 5.** cDNA sequence of *LIZEP* and predicted amino acid *LIZEP* sequence. The positions of nucleotides and amino acids are marked on the left and right side, respectively. START and STOP codons are indicated by large, black, italics letters. UTR regions were highlighted before ATG and after TGA codons (small, blue letters). Predicted *LIZEP* sequence contains conserved domains for the zeaxanthin epoxidase protein family: the FAD/NAD(P)-binding domain (blue colored) containing FAD-binding motif (black squares) and FHA - Forkhead-associated domain indicated by yellow.



63 tcttcatccaccttttctcttcttcaaaaagaacagaaaactcagcaccacaacaacat  
123 catcaacaaccttcacaattcaca**ATG**CTCCTCCCTTCTTCTTCTCATTCTC  
M L L S L L F L 12  
183 TCCACTCTTACCTCTCCCTCTCTTAACCCAAGACGGTCTTCTCTTACAAGCCAAA  
S T L H L S L S L T Q D G L F L L Q A K 32  
243 CGCCACCTCTCGACCCCTTCAACTCCCTCTCCTGGAACCTCCGACCCACCCCT  
R H L S D P S N S L S S W N S S D P T P 52  
303 TGCAACTGCTCGCGTTACATGCCGCAACCACTGTCACCGCGTCAACTCCTC  
C N W Y G V T C R N T T V T A V N L T S 72  
363 CTCTCCCTCTCGCGCCCTTCCCACTCCCTGTCAGCATCCCTTCTCACCCTCCCTC  
L S L S G P F P I S L C S I P **S L L T S L** 92  
423 TCCTCTCCAACAACCTTCACTCAACTCCCTCCCTCCCTCACCTCCCAACTGCCG  
**S L S N N F I N S S L F S L T L P N C R** 112  
483 CACCTCCGCCACTCGACCTTCCCAAAATACCCTTGTGGGCCCATCCCACTCTCT  
**H L R H L D L S Q N T L V G F I F H S L** 132  
543 TCTCAAATCTCTTCACTCCAACACATGACCTCTCATTCAACAACCTCTCAGGCCATC  
**S Q I S S L Q H I D L S F N N L S G P I** 152  
603 CCCTTTCCCTCGTACTTACAAAACCTTGAATCATTGATCCTTGTATATACTCCCT  
**F S S L A T L E K L E S L I L Y N F L** 172  
663 ACTGGACCCGTTCTGATTCTCTGGTAACATTCATCACTGAAACTTCTCACCTTGCT  
T C P V P D S L G N I S S L K L L H L A 192  
723 TATAACCCCTTACACCCAGTCACTGCGGAGTCAACTCGTAACTTGACCAAACTCGAG  
Y N P F T P S H L F S Q L A N L T K L E 212  
783 AGCCTTTGGTGCAGGCTGCAGTCTGGTGGGTTCGATTCCCAATTCACCTTGGTGCATC  
S L W C T S L V G S I P H S I G A L 232  
843 GGTAACCTTAAGAACCTTGATCTAGCTGAGAATAACCTCACTGGTACTATTCTGAATCG  
G N L K N L D L A E N N L T G T I P E S 252  
903 TTCTCTGGTTGAAGAGTGTGACTCAGATTGAGCTTATTCTAATTCGCTTCTGGCAAG  
**F S G L K S V T Q I E L Y S N S L S G K** 272  
963 TTACCGCTCGGTTATCGAAGCTTGAAGTGGAAAGTTTGTGATGCTTCGATGAAACGAG  
L P L G L S N L T Q L E S F D A S M N E 292  
1023 TTGACTGGGACATTCGAAGGTTGTGTGGATTGAAACTCGCCTCACTGAATTTGTTT  
L T G T I P E G L C G L **K L A S A N L E** 312  
1083 AGCAACAATCTCGGAGGTTGTCAGAGGTTGATAGCGACTCGCCAACTTACGAG  
**S N N L G G S L P E V I A T S P K L Y E** 332  
1143 CTCAAATGTCAACAATACCTTGTCTGGGAGTTGCCGAGTTATTGGAAGAATTTCT  
**L K L F N N N L A G E L P S Y L G R N S** 352  
1203 CCCTTGAATCATATTGATGTTTCTATAATAACTTTTCCGGCGAGATTCGGGCAAGTTG  
P L N H I D V S Y N N F S G E I P A S L 372  
1263 TGCAATGGGGACAGTTGGAGGAGCTGATTTGATTTACAATTCATTCTCGGGGAAAT  
C N G G L E L I L I Y N S F S G E I 392  
1323 CCGGAGACTTTGGGAACTGCAAGAGCTTAAGGAGGTTAGGCTTAGGAATAAATACTT  
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1383 AATGGAGTAGTCTCTGTTGTTTGGGGTCTGCCCATATGATTTGCTTGCAGTTATC  
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1443 GAAATTTCTTATCTGGGCATGTTTCTAATTCATCTCTGGTCCGAAAACCTTGTCTACC  
E N S L S G H V S N S I S G A K **N L S S** 452  
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**L L I S K N Q F N G S I P D E I G Y L G** 472  
1563 AAACCTTTGGAGTTGATGGCAGCTATAATAAATTTTCTGACCGGCTCCGGATAGTATG  
K L L E F D G S Y N K F S D R L P D S M 492  
1623 GTGAGCTTCAAGCAGTTGAATACTTGTATCTTACTCACAATGAATTTTCTGGAGAAAT  
V R L S **Q L N N L D L S H N E F S G E I** 512  
1683 CCGGATGCAATTTCTGATTCGACTCAGCTCAATGATCTTAATTTAGCAATAAATAGG  
**E G G I V R D W T Q L N D L N L A N N E** 532  
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**F N G K I F I E L G S L F A L N Y L D I** 552  
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**S S N Y F S G E I P K Q L O N L K L N V** 572  
1863 TTGAATTTGTCAACAATCAGCTTCTGGGGACATTCCTCCCTTTTGGCAATGAGAAT  
**L N L S N N Q L S G D I P P L F A N E N** 592  
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Y R M S F E G N P G L C S D L P G L C P 612  
1983 AGCTCTGGTGAAGTAAGAAACCGAAGTGTCTTGGATTTTCACTTTTGTGCTT  
S S G E S K R K C S W I F S I F V L 632  
2043 GCTGGGTTTGTGTAATTTGGGGTGGCTGGTCTTACTTGAATATAGGAGCATGAAG  
A G V L F V I G V G W F Y L K Y R S M K 652  
2103 AAGTTGAAGAAGGGTTTAACATTTCAAGTGGAGTCTGTTCCACAAGTTGGGTTTAC  
K L K G K F N I S K W R S F H K L G F S 672  
2163 GAGTTTGAGTTGTGAATGCTGAGTGAAGGCAATGTGATAGGGAGTGGGATCCTGGA  
E F E I V K L **L S E G N V I G S G A S G** 692  
2223 AAGTATACAAGTGGTACTTAGCAATGGTGGTGGCAGTGAAGAATTTGGGGG  
**K V Y K V V L S N G E V V A V K K L W G** 712  
2283 ACAACTACGAAATTTAGTGGATTTGTTCTGTAAGAAAGATGAATTTGAGGCTGAAGTT  
**T T T K F S G V S S E K D E F E A E V** 732  
2343 GAAACACTAGGAAGATTAGGCACAAGAATATTGTGAGGTTGGTGTGCTGCAACAGT  
**L T L G K L S H K N I V R L W C C C N S** 752  
2403 GGTGAAGACTACTTGTATGAGTATATGCCAATGGGAGCTGGGATGATATGTTG  
**S E S R A L L V Y E Y M E N G S L S D M** 772  
2463 AAGGGTAGCAAGAAATCTTGGTGGATTGGCCTATTAGGTATAAAATTTGCTATTGATGCC  
**K G S K K T L L D W F I R Y K I A I D A** 792  
2523 GCTGAGGGCTTGTCTTATTGTCATCAGGATTTGTGCTCCTCCATTGTTTCAATGGGACGTA  
**A E G L A Y L H H D C A P P I V H R D V** 812  
2583 AAATCTAACAATATATTGCTGGATGGAGAGTTTGTGCAAAAAGTTGCAGATTTGGAGTT  
**K S N N I L L D G E F C A K V A D F G V** 832  
2643 GCCAAAGTTGTTGGAGGAGTTGGCCCTGGGGCAGAATCCATGCTGTAATTCAGGAGTCC  
**A K V V G G V G E G A E S M S I A G V** 852  
2703 TATGGTTACATGCACCAGAATATGCATFACTCTTCGGGTGAACGAAAGAGTGATATT  
**S S Y I A P E Y A V T L R V N E K S D** 872  
2763 TACAGTTTCGGCATGGTGAATTTAGAAATGGTAACCTGAAAACCCCCATTGATCCAGAG  
**V S F G M V I L E L V T G K P P I D F E** 892  
2823 TATGGGAAAGTATCTTTGAAAATGGGTTCTTCCACATTAGAACAGAAAGGACTGAGC  
**V G E S D L V K W V S S T L E Q K G L S** 912  
2883 TTTGATGATCCATCTTTGGATTCCAATACACTGAGGTAATCAGCAAGGTTGCTTAGT  
**E V I D F S L D S K Y T E V I S K V L S** 932  
2943 GTGGGCTTATTTGTACAAGTTCTCTTATAACTCGTCTGCAATGAGAAGGTTGGTG  
**V G L L I C T S S L P E I T R E A M E R R V** 952  
3003 AAAATGCTCAAGAAGCAACAGTTCCCAATCCACAACCTGTTAAGGATGGAAAATC  
**K M I Q E A** T V P K S T T V K D G K L 972  
3063 TCCCTTATTACTATGAAGAGGGTTATGTTTCATCAAGGAAGTGTGGCTTGAgcattcttc  
S P Y Y E E G Y V H Q G S V A - 988  
3123 ttaaaaaatttacagccacctcaaaatattatggttacaatatttgatgtgataaagggtga  
gattttgtagaccatccagatcattatagtgtaggaaccacatcaatttagttggtagt  
3243 acttgatccttgaatgaaactgcaattgtaagaggtgtagtaaatatcggatataaa  
3303 atattccttaaatfactggtgattatataacttaaaaataaaatcgcctagat  
3363 tagagaatgaglataaaaggaaaagattcttcttcagagcttcccgtataacttaggata  
3423 aaaagttaacaactaaaaatcctcg

**Supplementary Figure 6.** cDNA sequence of *LIHSL* and predicted amino acid *LIHSL* sequence. The positions of nucleotides and amino acids are marked on the left and right side, respectively. START and STOP codons are indicated by large, black, italics letters. UTR regions were highlighted before ATG and after TGA codons (small, blue letters). Leucine-rich repeat (LRR) receptor motif characteristic for serine/threonine protein kinases responsible for protein-protein interactions is indicated by blue. The catalytic domain is marked by green. N-terminal domain is glycine-rich (underlined G) and contains lysine residue (K, grey indicated) determining ATP binding. The second region important for catalytic activity in the central part of the domain is underlined. It contains conserved aspartic acid (bolded and grey) (Knighton et al. 1991).

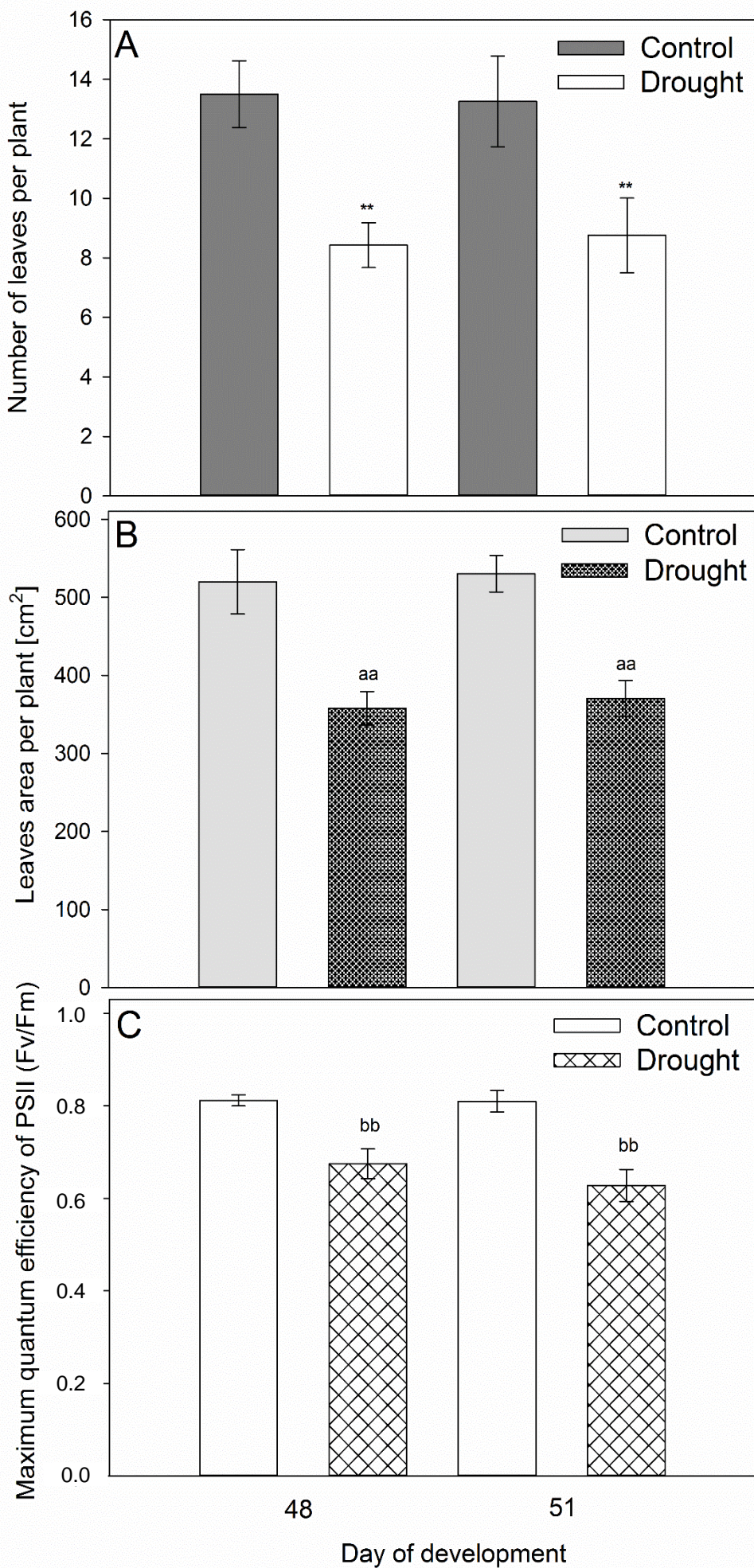
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1   cttttttgtcctttttgatgtgtttctacaaccaactttttttgtgtgtcaaatttgcttaca
63  caaatgtttgttctaaagaacataagtatagaatcagttgaataagttccttatcttaag
123 gtaattagtaatttcattagaacagtgaggtatagcaatatacatggcttagaagaccc
183 tgtgttatagtcttatcatagaacATGGCCACAAAAGAATCAAGCTCAGCTGCTTCTGCT
      M A T K E S S S A A S A 12
243 TCAGGGGAAGCTAAAATCAAAAGGGTCTCACACATGGTGGTAAATATGCACAATACAAT
      S G E A K I K R V L T H G G K Y A Q Y N 32
303 GTGTATGGAACTTGTTTGAAGTGTCTCCTCCAAGTACATGCCGATTCGCCCTATCGGTAGA
      V Y G N L F E V S S K F M P I R P I G R 52
363 GGTGCTTGTGGCACTGTCTGTGCTGCTGTTAATCCGAGACGCACGAACAAGTTGCCATA
      G A C G T V C A A V N S E T H E Q V A I 72
423 AAGAAGATAGCTAATGCATTGACAATATAGTTGATGCTAAAAGGACATTGAGGGAAGTT
      K K I G N A F D N I V D A K R T L R E V 92
483 AAGC'CC'CC'CG'CA'AT'GGAT'CA'GAAAA'AT'CA'AT'GCCA'CAAGGAT'AT'CA'AAAGCCA
      K L L R H M D H E N I I A I K D I I R E 112
543 CCAAAAAGCACAGCTTTAATGATCTCTACATTCTTTATCAATTGATGCACACTGATCTT
      F K K E S F N D V Y I V Y E L M D T D 132
603 CA'CA'AT'AA'T'CA'AT'CCGACCAACCC'CTCAC'GAT'GAT'CACT'GT'CAGT'AC'CT'AT'ATAC
      H H I I H S D Q F L T D D H C Q Y F L Y 152
663 CAGCTGTACGGGGGCTGAAATATGTGCACTCGGCTAATGTTTGCACCGTGATCTTAAG
      D L L R G L K Y V H S A N V L H R D L R 172
723 CCAAGTAATTTACTTATGAATGCAAACTGTGACCTTAAAATCGGGGACTTTGGCTTGGCA
      F S N L L M N A N C D L K I G D F G L A 192
783 AGGACAACATCTGAGACAGACTTCATGACTGAATATGTTTGTG
      R T T S E T D F M T E Y V V 206

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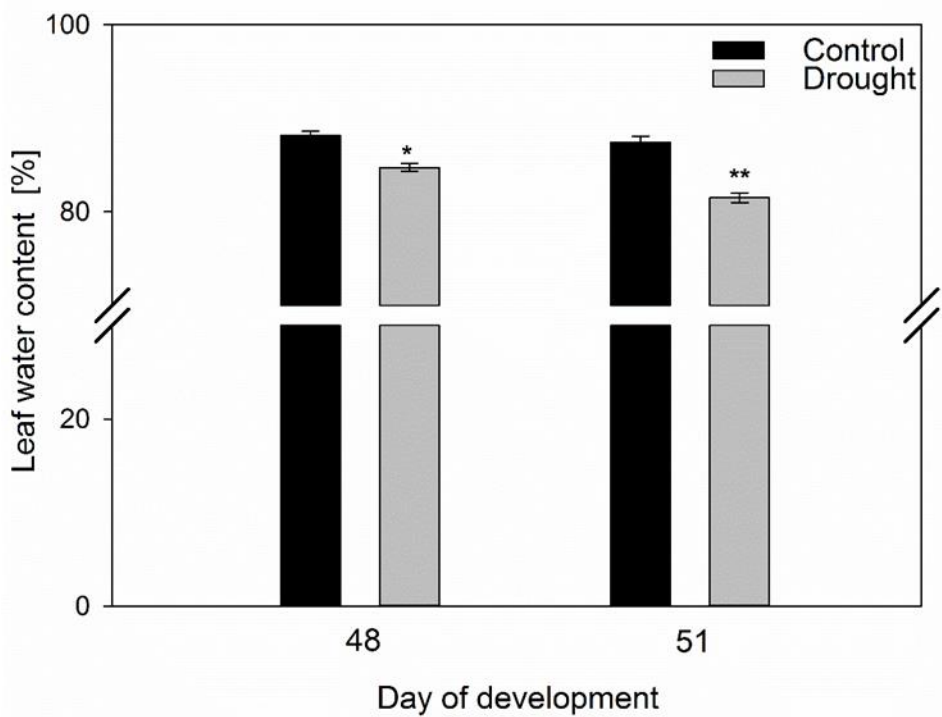
**Supplementary Figure 7.** The fragment of cDNA sequence of *LIMP6* and predicted amino acid LIMP6 sequence. The positions of nucleotides and amino acids are marked on the left and right side, respectively. START and STOP codons are indicated by large, black, italics letters. UTR regions were highlighted before ATG and after TGA codons (small, blue letters). Catalytic domain characteristic for serine/threonine and tyrosine protein kinases is indicated by green. N-terminal, glycine-rich (bolded G) fragment (indicated by grey) is involved in ATP binding. The second active region of the kinase is bolded. It contains conserved aspartic acid (grey D) determining enzymatic activity. The activation loop contains a characteristic TEY motif (bolded black letters) (Knighton et al. 1991).



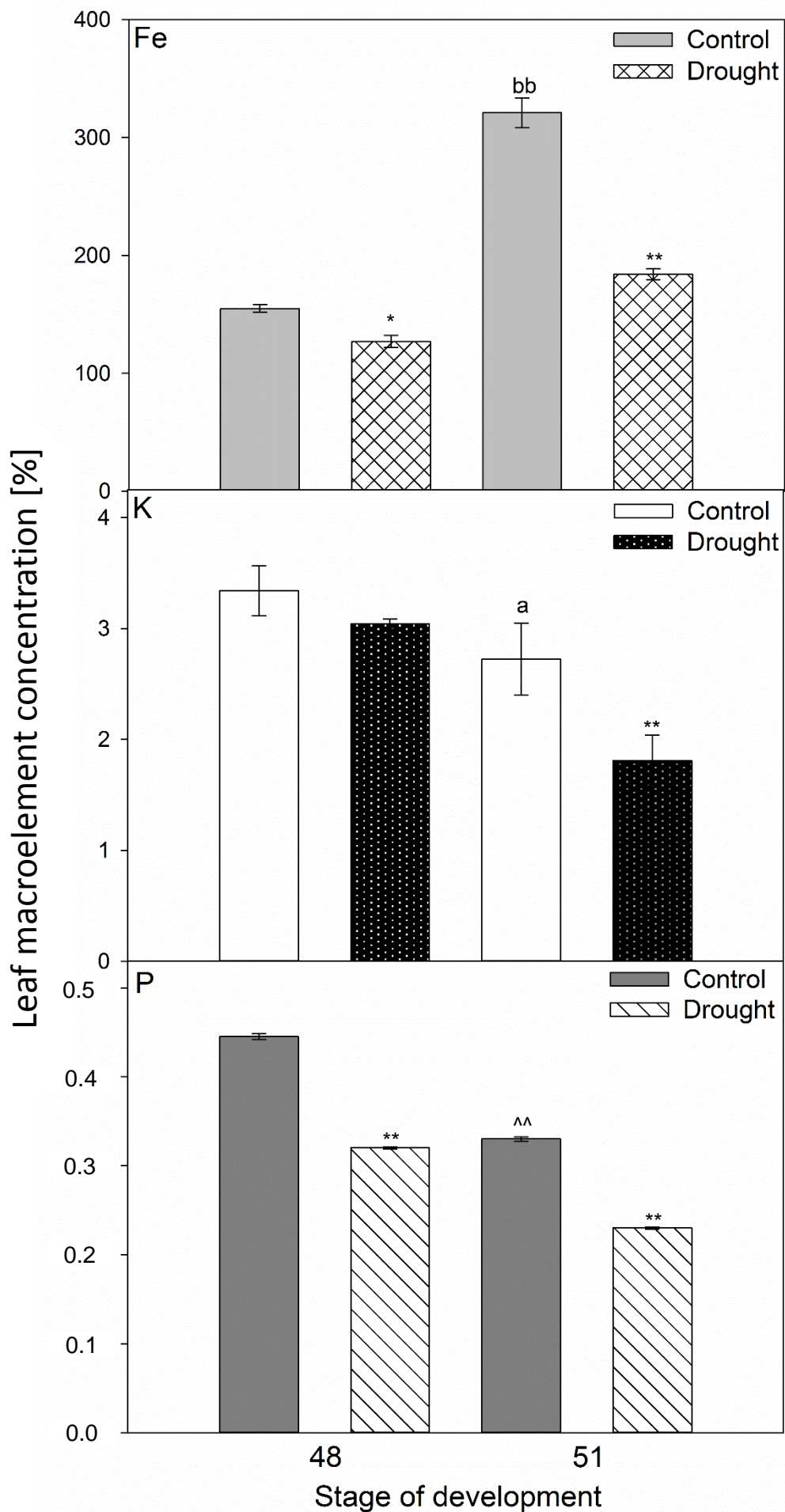


**Supplementary Figure 8.** The influence of soil drought stress on the number of leaves per plant (A), leaves area per plant [%] (B) and maximum quantum efficiency of PS II (C) in *Lupinus luteus* L. Control plants were growing in the soil of optimal moisture (70% WHC). In parallel, part of plants was subjected to drought conditions for 2 weeks (25% WHC). Measurements were performed on the 48th and 51st days of cultivation. The data were presented as averages of 15 technical replicates  $\pm$  SE. Significant differences to stress plants in comparison to control are indicated as  $**P < 0.01$  (A), as  $^{aa}P < 0.01$  (B), as  $^{bb}P < 0.01$  (C), (t-Student test).

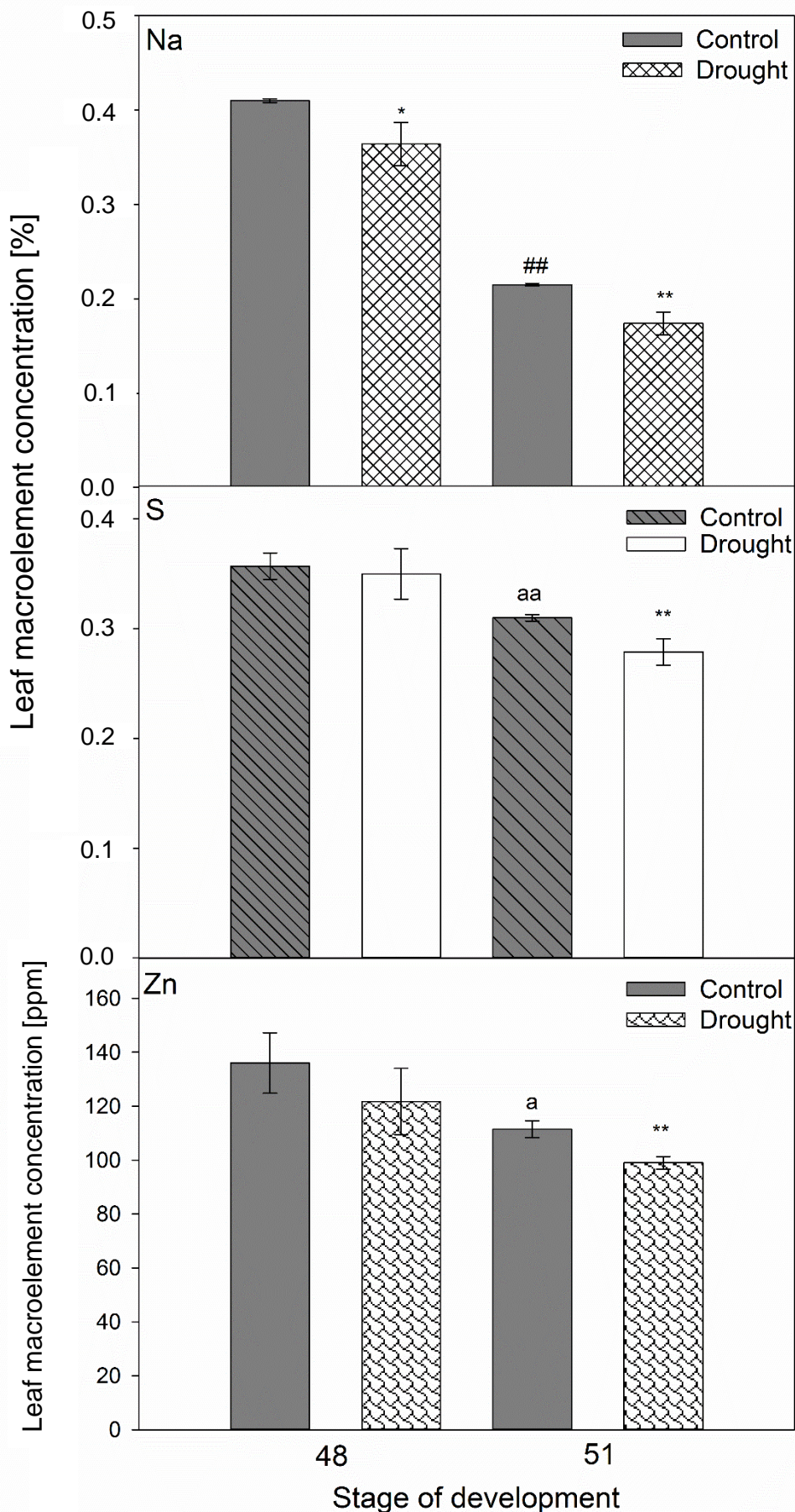




**Supplementary Figure 9.** The influence of soil drought stress on the water content in leaves [%] of *Lupinus luteus* L. Control plants were growing in the soil of optimal moisture (70% WHC). In parallel, part of plants was subjected to drought conditions for 2 weeks (25% WHC). Plant material for water content measurements was collected on the 48th and 51st days of cultivation. The data were presented as averages of 3 technical replicates  $\pm$  SE. Significant differences to stress plants in comparison to control are indicated as \* $P < 0.05$ , \*\* $P < 0.01$  (t-Student test).



**Supplementary Figure 10.** The impact of soil drought on the elements content in leaves [%] of *Lupinus luteus* L. Control plants were growing in the soil of optimal moisture (70% WHC). In parallel, part of plants was subjected to drought conditions for 2 weeks (25% WHC). Material for measurements was collected on the 48th and 51st days of cultivation. The data were presented as averages of 3 technical replicates  $\pm$  SE. Significant differences to stress plants in comparison to control are indicated as \* $P < 0.05$ , \*\* $P < 0.01$  (for Fe); significant differences to stress plants in comparison to control are indicated as \*\* $P < 0.01$ , significant differences to 51-days control plants in comparison to 48-day-old plants are indicated as <sup>a</sup> $P < 0.01$  (for K); significant differences to stress plants in comparison to control are indicated as \*\* $P < 0.01$ , significant differences to 51-days control plants in comparison to 48-day-old plants are indicated as ^^ $P < 0.01$  (for P), (t-Student test).



**Supplementary Figure 11.** Elements content in leaves [%] of yellow lupines cultivated under drought stress conditions. Control plants were growing in the soil of optimal moisture (70% WHC). Part of plants was subjected to drought conditions for 2 weeks (25% WHC). Material for water content measurements was collected on the 48th and 51st days of cultivation. The data were presented as averages of 3 technical replicates  $\pm$  SE. Significant differences to stress plants in comparison to control are indicated as \* $P < 0.05$ , \*\* $P < 0.01$ , significant differences to stress plants in comparison to control are indicated as ## $P < 0.01$  (for Na); significant differences to stress plants in comparison to control are indicated as \*\* $P < 0.01$ , significant differences to 51-days control plants in comparison to 48-day-old plants are indicated as aa $P < 0.01$  (for S); significant differences to stress plants in comparison to control are indicated as \*\* $P < 0.01$ , significant differences to 51-days control plants in comparison to 48-day-old plants are indicated as a $P < 0.05$  (for Zn) (t-Student test).