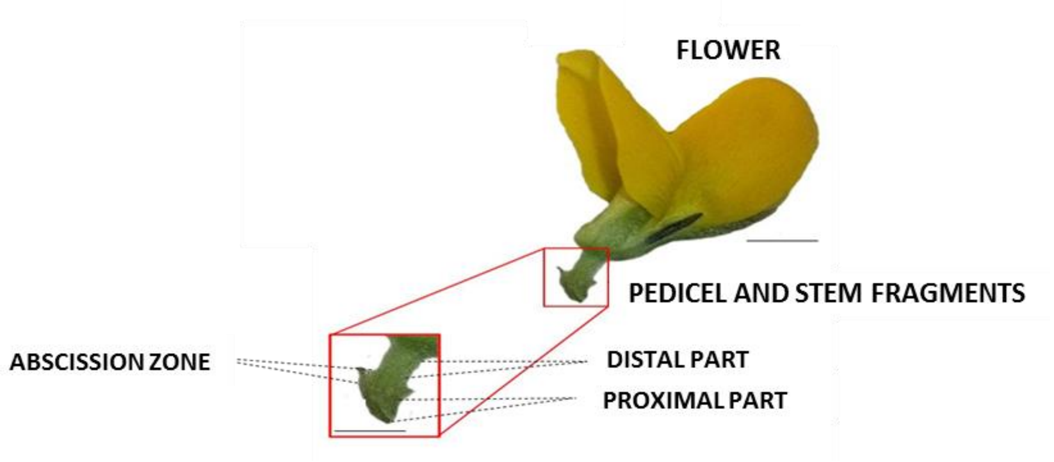
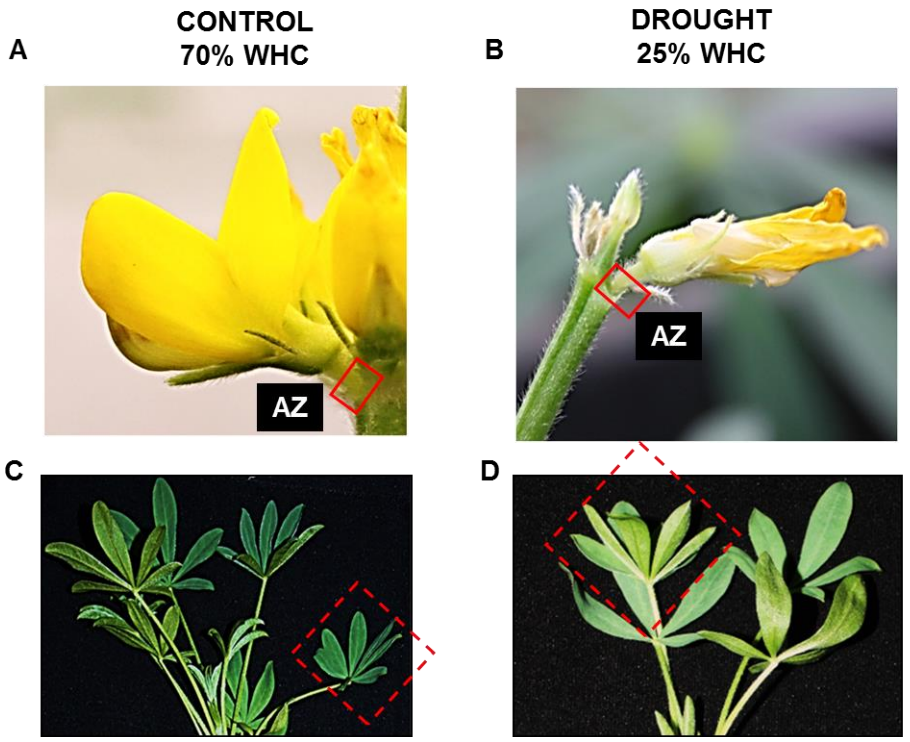
Acronyms used in the text

ABBREVIATIONS in alphabetical order	**DEFINITION**
ABA	abscisic acid
ACC	aminocyclopropane-1-carboxylic acid
AZ	abscission zone
CAT	catalase
DIST	flower pedicel fragments above the az
ET	ethylene
LlACO	*AMINOCYCLOPROPANE-1-CARBOXYLIC ACID OXIDASE from Lupinus luteus*
LlACS	*AMINOCYCLOPROPANE-1-CARBOXYLIC ACID SYNTHASE from Lupinus luteus*
LlHSL	*RECEPTOR-LIKE PROTEIN KINASE HAESA-like from Lupinus luteus*
LlIDL	*INFLORESCENCE DEFICIENT IN ABSCISSION-like from Lupinus luteus*
LlMPK6	*MITOGEN-ACTIVATED PROTEIN KINASE6 from Lupinus luteus*
LlZEP	*ZEAXANTHIN EPOXIDASE from Lupinus luteus*
PROX	stem fragments below the AZ
RWC	relative water content
VB	vascular bundles
WHC	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.



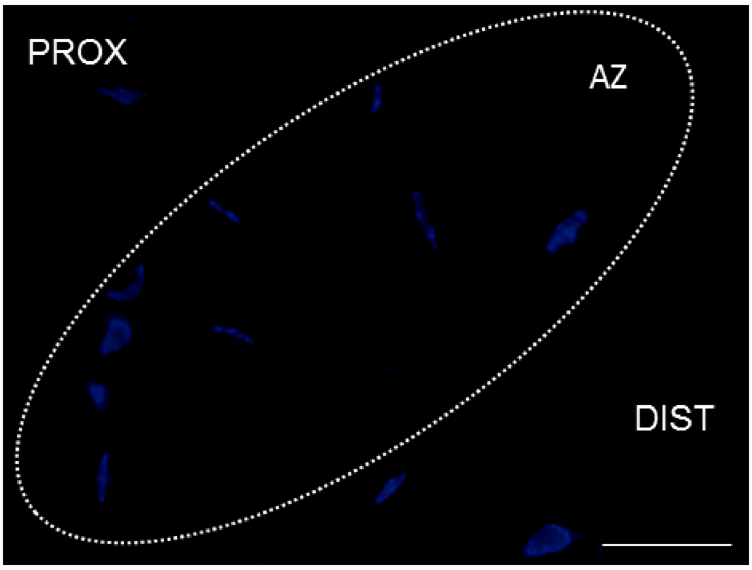
Supplementary Figure 2. Non-abscised flower of yellow lupine (*Lupinus luteus* L.) with inactive abscission zone (**A**) and flower containing active AZ from plants cultivated under drought conditions (**B**). The AZ regions were marked by red squares. Leaves of control plants (**C**) and leaves from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



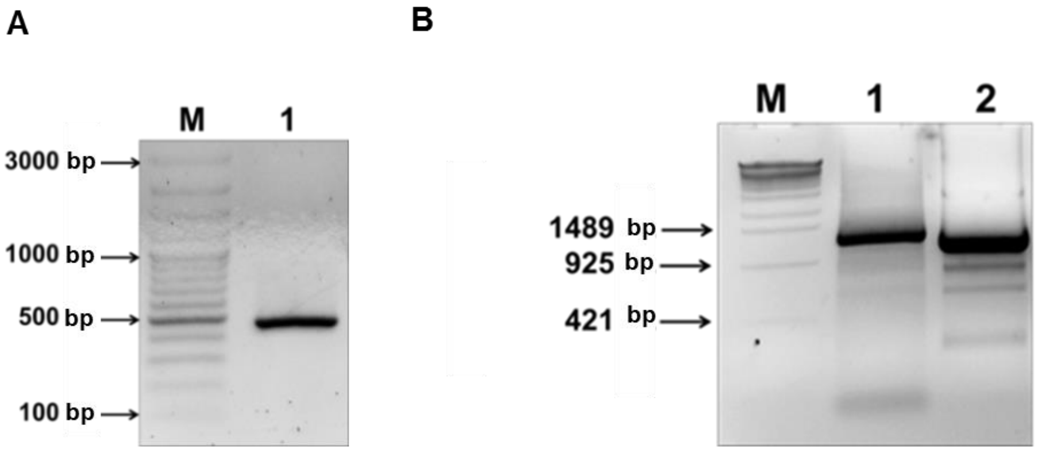
Supplementary Figure 3. The results of a control reaction performed with omitting primary antibodies anti-ACC, anti-ABA, anti-CAT, and anti-MPK6. Control reaction produced negative results compared with those of standard reactions. Nuclei were stained with DAPI. The abscission zone (AZ) region was highlighted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

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

	cDNA of gene	Primer sequence 5’-3’
Degenerate primers	*LlZEP*	FP: GCTAYACTTGTTAYACYGGNA RP: CCVACRCCHARRTAWGCYTT
RACE-PCR primers	*LlZEP*	FP: CATGCAGCCAAATATGGGCCAAGGA RP: AATCACCGAGCAAAGTCACACGACC
Specific primers	*LlHSL*	1FP: TCCCTCTCTCTAACCCAAGACG 1RP: CTCGTCCTGCAATGAGAAGGGTGG 2FP: TTGCAACTGGAAAGTGGCTCT 2RP: ATCACGAACAATTCCACCCGGA 3FP: GCAAGTTTGTGCAATGGGGGA 3RP:CCTAAGTATACGGGAAGCTCTG
	LlMPK6	1FP: GCAACTTGTTCGTGCGTCTCGGA 1RP: GCAACTTGTTCGTGCGTCTCGGA 2FP: AGGGTTCTCACACATGGTGG 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.
LlIDL	F: ACAGCACCATGGTCACTTTTC R: TTGTGTTTCCTTGAGGGAGTG	137
LlACS	F: TTCATTCAAGAAGGCAATGGT R: GGTTTGGGTCAAAAGTCACC	53
LlACO	F: GTGATGAAGGAATTTGCACAAG R: CCAAGGTTTTCACACAGCAA	53
LlZEP	F: GGGTTTCCGGTTCTTGGTAT R: AAAGCCATTCGACTAATAACTCTTG	165
LlACT	F: TAATGGTTGGGATGGGTCAG R: CAAGGTGAGAATACCCCTCT	165
LlHSL	F: TGATGAAATTGGGTATTTGGGTA R: GAAGCCGGTCAGAAAATTTATTATAG	147
LlMPK6	F: GCTCCTTCGTCATATGGATCA R: AATGTAGACATCATTAAAGCTCTCCTT	147



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

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   1 atggggactttgttgccccttgtttttctatatcagatatattattagggacgaaaaaa
  62 ctcaacctctaacaatctttatcttcatttaaattattgcataccagttattggcttatg
 122 agtttggaaagttagagccactgaaagacacgtaacacaacacaacacacacttgagttt
 182 gttcctaagctttcttcttctgcaaccATGGCTTCTACCTTGTGTTACAATTCTCTTAAT
                                M  A  S  T  L  C  Y  N  S  L  N    11
 242 ACCTCAACAACTTCTTTCTCAAGAACCCACTTCTCAGTTCCAATCAATAAAGAGCTTTCA
      T  S  T  T  S  F  S  R  T  H  F  S  V  P  I  N  K  E  L  S   31
 302 CTAGATATTTCACCTTTTGTTAGCTACGGCTATCACCTAGGAACCAGAACTAGGAAGCAG
      L  D  I  S  P  F  V  S  Y  G  Y  H  L  G  T  R  T  R  K  Q   51
 362 AAGAAGAAAGTGATGCTGCATGTAAAAGCTGGTGCAGTTGCTGAAGCTCCACCTTCAAAG
      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 CTTGTGGCAGGTGGTGGGATTGGTGGCTTGGTTTTTGCTTTGGCTGCTAAGAGAAAAGGG
      L  V  A  G  G  G  I  G  G  L  V  F  A  L  A  A  K  R  K  G  111
 542 TTTGAGGAGGTGGTGTTTGAGAGGGACTTGAGTGCTATAAGAGGTGAGGGACAGTATAGG
      F  E  E  V  V  F  E  R  D  L  S  A  I  R  G  E  G  Q  Y  R  131
 602 GGTCCAATTCAGATACAAAGTAATGCATTGGCTGCTTTGGAAGCTATAGATTCAGATGTT
      G  P  I  Q  I  Q  S  N  A  L  A  A  L  E  A  I  D  S  D  V  151
 662 GCTGATGAAGTTATGAGAATTGGTTGCATCACAGGTGATAGAATCAATGGACTTGTTGAT
      A  D  E  V  M  R  I  G  C  I  T  G  D  R  I  N  G  L  V  D  171
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 782 CTTCCAGTCACAAGAGTTATTAGTCGAATGGCTTTACAAGAGATCCTTGCTAGTGCGGTT
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 902 GTAACAGTAGAGCTTGAGAATGGTGAGAAATATGAAGGAGATCTTTTGGTTGGAGCTGAT
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1082 CGAGTTTTCTTGGGACACAAACAATACTTTGTATCTTCAGATGTTGGTTCTGGAAAGATG
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1442 TGGGAGCAAAGTATAAAATCAGGCCAACTAGCATTGGAGGTGGACAATGCATGGGAGCAA
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2042 ATTAGCTATAAGGATGGTGCCTTCTTCGTGACTGATTTGCGAAGTCAACATGGCACTTCG
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2102 ATCATTGACATTGAAGGAAGGAAATATCGGGTACCTCCAAATTATCCTGCTCAGGTCCAC
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2462 ttgttgatataataggaaacaaagttaagtttttccg
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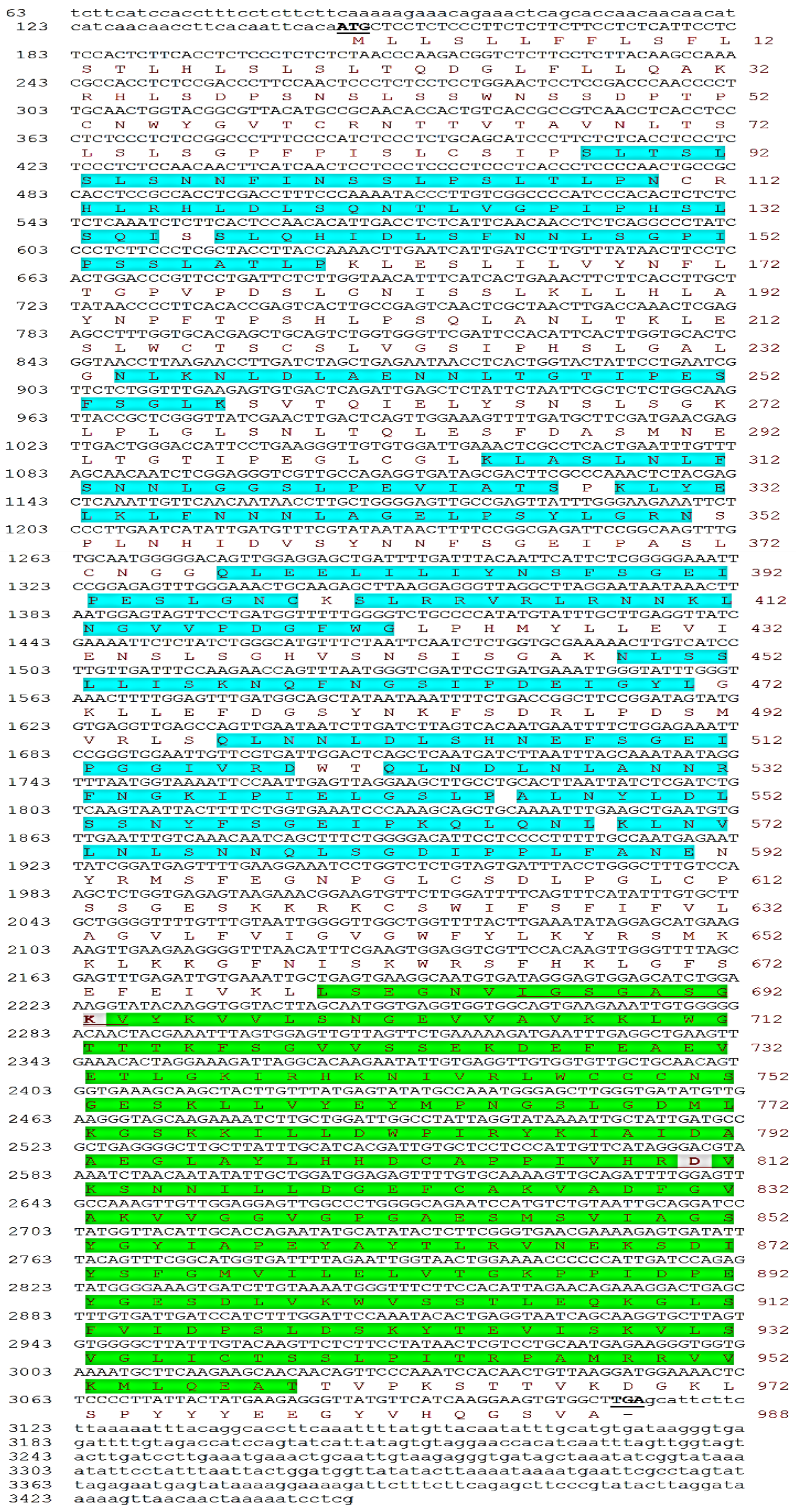
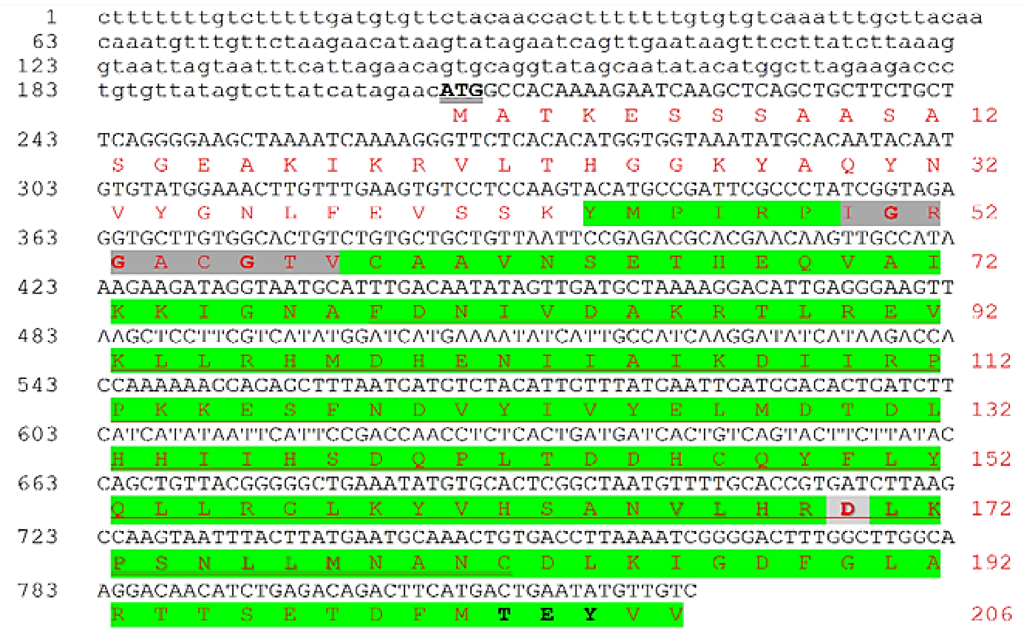
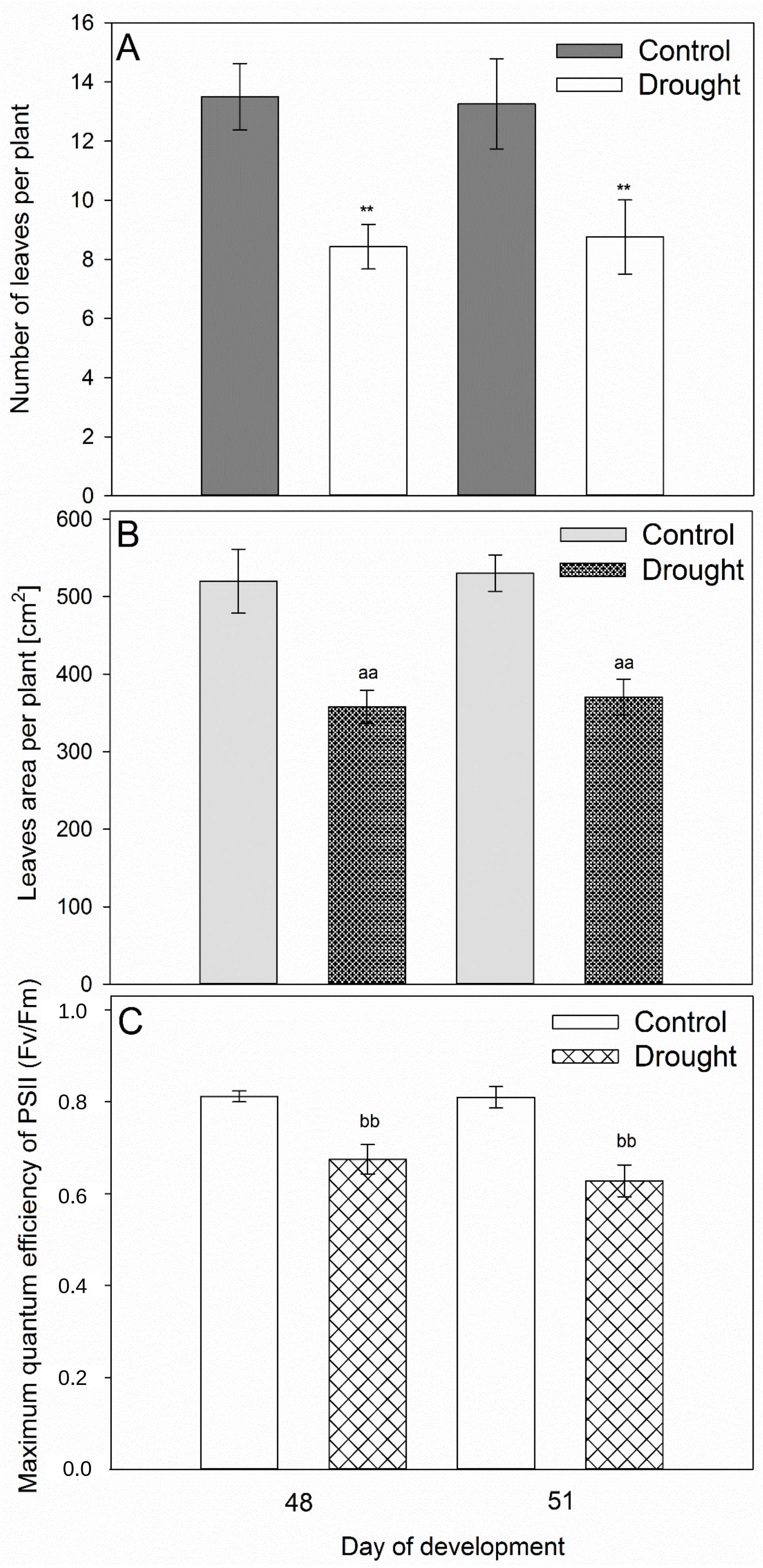
Supplementary Figure 5. cDNA sequence of *LlZEP* and predicted amino acid LlZEP sequence. The positions of nucleotides and amino acids are marked on the left and right side, respectively. START and STOP codons are indicated by large, black, italics letters. UTR regions were highlighted before ATG and after TGA codons (small, blue letters). Predicted LlZEP 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.



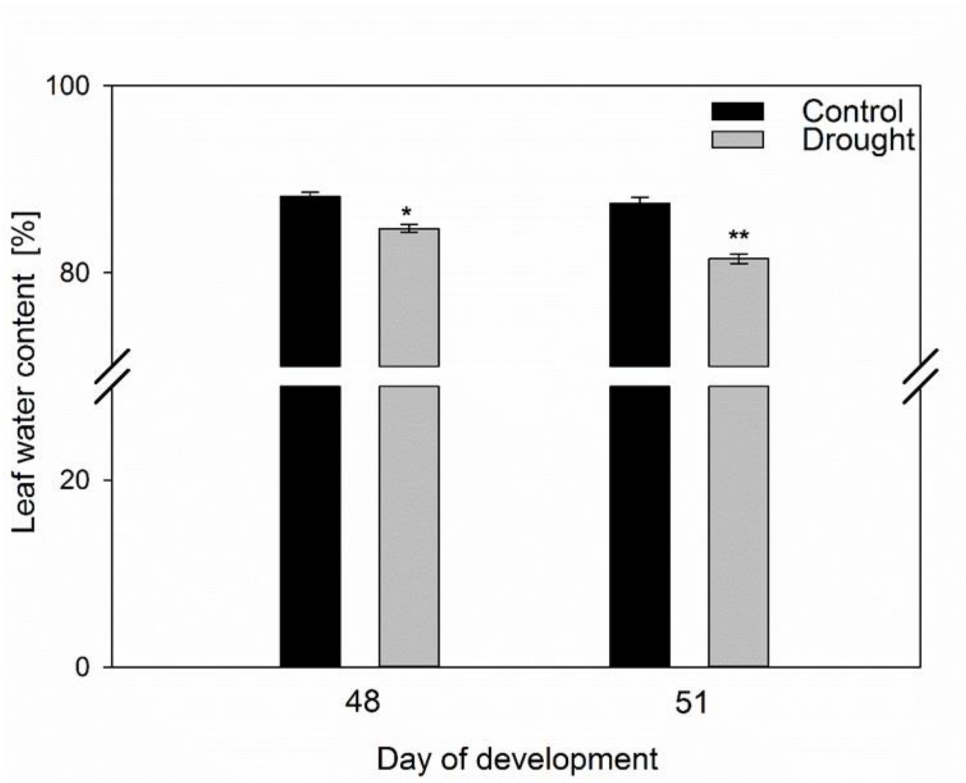
Supplementary Figure 6. cDNA sequence of *LlHSL* and predicted amino acid LlHSL sequence. The positions of nucleotides and amino acids are marked on the left and right side, respectively. START and STOP codons are indicated by large, black, italics letters. UTR regions were highlighted before ATG and 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).



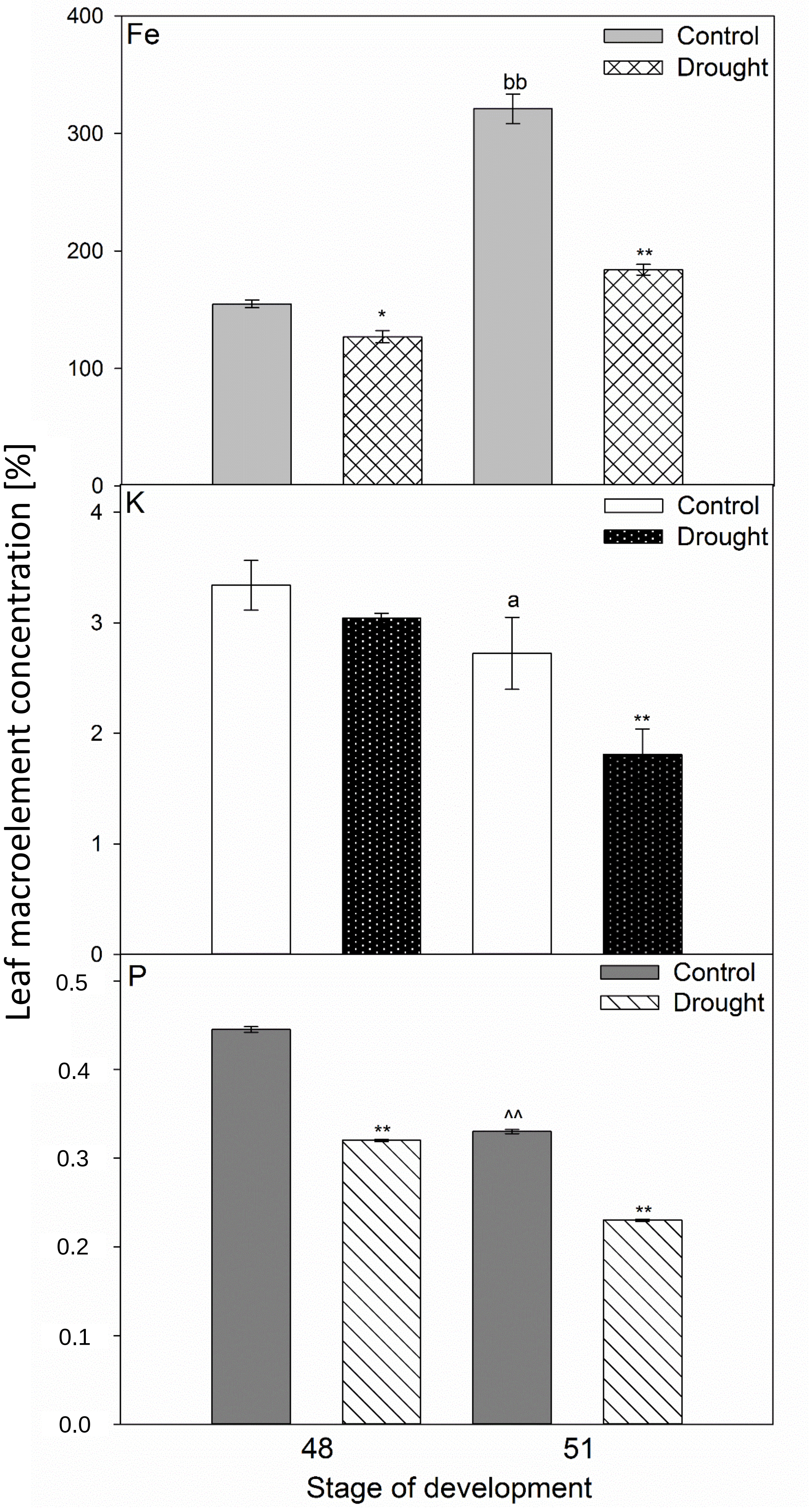
Supplementary Figure 7. The fragment of cDNA sequence of *LlMPK6* and predicted amino acid LlMPK6 sequence. The positions of nucleotides and amino acids are marked on the left and right side, respectively. START and STOP codons are indicated by large, black, italics letters. UTR regions were highlighted 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).



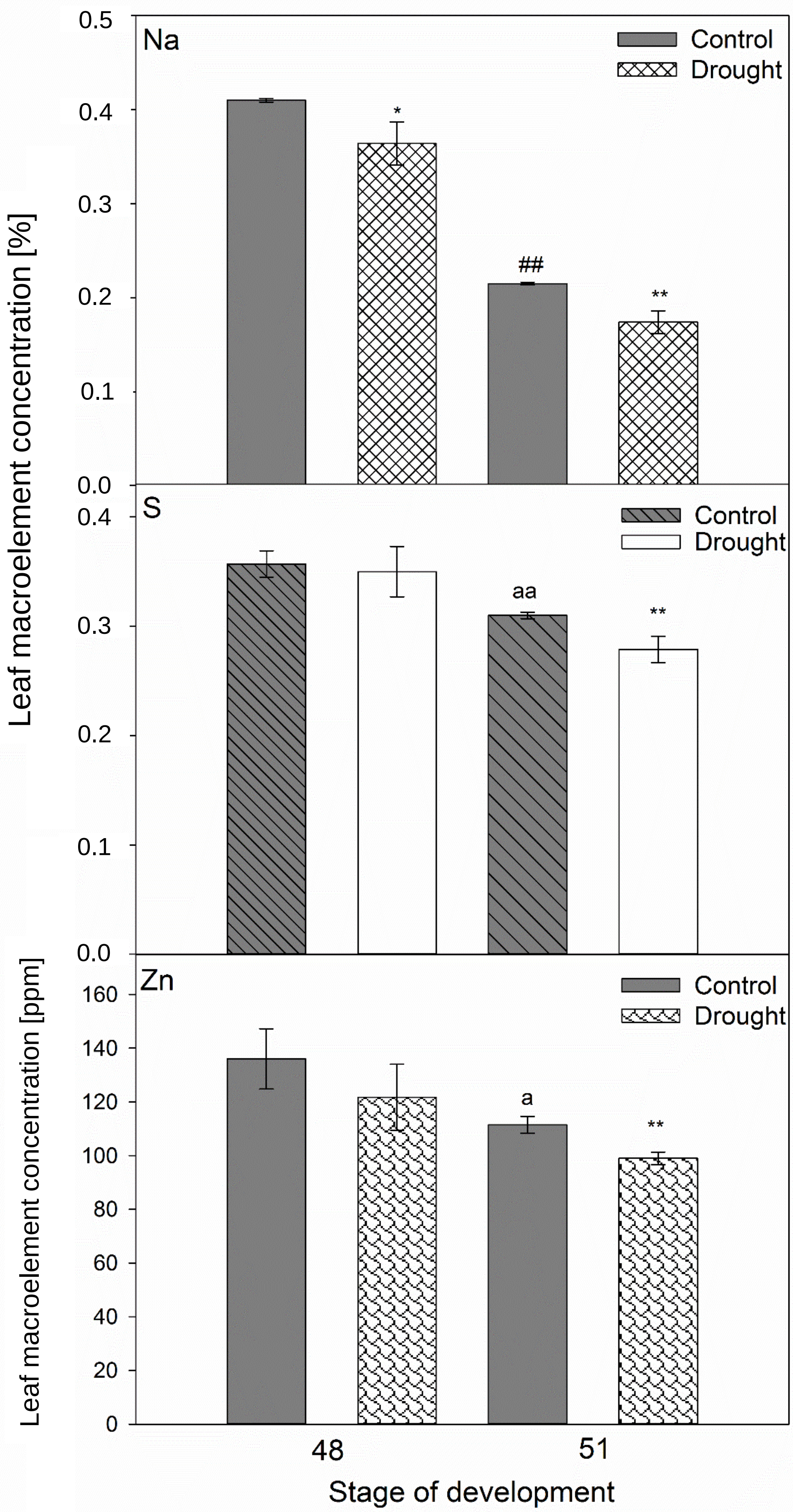
Supplementary Figure 8. The influence of soil drought stress on the number of leaves per plant (**A**), leaves area per plant [%] (**B**) and maximum quantum efficiency of PS II (**C**) in *Lupinus luteus* L. Control plants were growing in the soil of optimal moisture (70% WHC). In parallel, part of 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 ± 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 ± 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 ± 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 ^{a}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 ± 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).