**S2 Table** Genes and SNPs identified within the distinct LD block on chromosome 6 and chromosome 8.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **SNPs in distinct LD block** | **Chr.** | **Position** | **Genes in the LD block** | **Annotation** | **Putative functions** |
| PZE-106078719 | 6 | 134460941 | GRMZM2G424783GRMZM2G329033GRMZM2G357198GRMZM2G055678GRMZM2G100067GRMZM2G061469GRMZM2G162702GRMZM2G170646GRMZM2G462625GRMZM2G531738 | Emp24 family proteinTranscription factor IIATransposable element geneProline extensin-like receptor kinase 1RAD3-like DNA-binding helicase proteinSLAC1 homologue 3Serine/threonine-protein kinaseGDSL-like lipase/acylhydrolase Tetratricopeptide repeat (TPR)-like proteinMYB family transcription factor | Response to heat-shock and cell death[[1](#_ENREF_1)]Activated transcription[[2](#_ENREF_2)]Defense responses[[3](#_ENREF_3)]DNA Repair[[4](#_ENREF_4)]Stomatal signalling[[5](#_ENREF_5)]Strss response[[6](#_ENREF_6)]Responses to biotic and abiotic stresses[[7](#_ENREF_7)]Modulates development[[8](#_ENREF_8)]Strss response and development control[[9](#_ENREF_9)] |
| PZE-106078723 | 6 | 134461413 |
| PZE-106078726 | 6 | 134461547 |
| PZE-106078845 | 6 | 134651274 |
| PZE-106078910 | 6 | 134657125 |
| PZE-106078990 | 6 | 134846181 |
| PZE-106079085 | 6 | 134863316 |
| SYN35781 | 6 | 134904332 |
| PZE-106079198 | 6 | 135128415 |
| SYN36674 | 6 | 135143457 |
| PZE-108035543 | 8 | 52204797 | GRMZM2G477457AC205274.3\_FG001GRMZM2G047966GRMZM2G047998GRMZM5G814722GRMZM2G107718AC235535.1\_FG001GRMZM2G017666GRMZM2G439589GRMZM2G302405GRMZM5G850758GRMZM2G180488GRMZM2G173119GRMZM2G015959GRMZM2G384871GRMZM2G131074GRMZM2G094808GRMZM6G514393AC194355.3\_FG002GRMZM2G001755 | K+ uptake transporter 3Pathogenesis-related gene 1Transposable element geneTransposable element geneTransposable element geneRibosomal protein L5Chromatin-remodeling proteinHypothetical proteinNAD(P)-binding proteinTPR-like superfamily proteinHypothetical proteinHypothetical proteinAssociated molecule with SH3 of STAM 3DegP protease 9Phosphoenolpyruvate carboxykinaseHypothetical proteinHypothetical proteinPeroxidase superfamily proteinmTERF family proteinHypothetical protein | Compete for nutrients[[10](#_ENREF_10)]Systemic resistance[[11](#_ENREF_11)] Ribosomal biogenesis stress[[12](#_ENREF_12)]Responses to stresses and plant development[[13](#_ENREF_13)]Disease resistance[[14](#_ENREF_14)] Modulate development[[8](#_ENREF_8)]Intracellular trafficking and vacuole biogenesis[[15](#_ENREF_15)]Thermal and oxidative tolerance[[16](#_ENREF_16)]Photosynthesis[[17](#_ENREF_17)]Plant defense and cell wall metabolism[[18](#_ENREF_18)]Mitochondrion, chloroplast and leaf development[[19](#_ENREF_19)] |
| PZE-108035545 | 8 | 52205440 |
| PZA00498.5 | 8 | 52299429 |
| SYN25157 | 8 | 52299429 |
| PZE-108035582 | 8 | 52299792 |
| PZE-108035583 | 8 | 52299869 |
| PZE-108035671 | 8 | 52902989 |
| PZE-108035778 | 8 | 53329919 |
| SYN34307 | 8 | 53872820 |
| PZE-108035902 | 8 | 53874805 |
| PZE-108035926 | 8 | 53955319 |
| PZE-108035929 | 8 | 53957102 |
| PZE-108035931 | 8 | 53957272 |
| PZE-108036026 | 8 | 54324318 |
| PZE-108036054 | 8 | 54428423 |
| PZE-108036058 | 8 | 54444675 |
| PZE-108036077 | 8 | 54477661 |
| PZE-108036152 | 8 | 54888683 |
| PZE-108036175 | 8 | 55020791 |
| PZE-108036208 | 8 | 55169464 |
| PZE-108036220 | 8 | 55251243 |
| PZE-108036232 | 8 | 55259181 |
| PZE-108036270 | 8 | 55516140 |
| PZE-108036386 | 8 | 55966495 |
| PZE-108036444 | 8 | 56167353 |
| PZA01209.1 | 8 | 56203327 |

**References:**

1. Hwang SO, Boswell SA, Seo J-S, Lee SW (2008) Novel oxidative stress-responsive gene ERS25 functions as a regulator of the heat-shock and cell death response. Journal of Biological Chemistry 283: 13063-13069.

2. Ma D, Watanabe H, Mermelstein F, Admon A, Oguri K, et al. (1993) Isolation of a cDNA encoding the largest subunit of TFIIA reveals functions important for activated transcription. Genes & Development 7: 2246-2257.

3. Silva N, Goring D (2002) The proline-rich, extensin-like receptor kinase-1 (PERK1) gene is rapidly induced by wounding. Plant Molecular Biology 50: 667-685.

4. Jones NJ, Strike P (1996) Recent research in DNA repair, mutation and recombination: A report of the DNA Repair Network meeting, held at City University, London on 18 December 1995. Mutation Research/DNA Repair 364: 13-23.

5. Vahisalu T, Kollist H, Wang Y-F, Nishimura N, Chan W-Y, et al. (2008) SLAC1 is required for plant guard cell S-type anion channel function in stomatal signalling. Nature 452: 487-491.

6. Sun X-L, Yu Q-Y, Tang L-L, Ji W, Bai X, et al. (2013) GsSRK, a G-type lectin S-receptor-like serine/threonine protein kinase, is a positive regulator of plant tolerance to salt stress. Journal of plant physiology 170: 505-515.

7. Wang W, Zhao X, Pan Y, Zhu L, Fu B, et al. (2011) DNA methylation changes detected by methylation-sensitive amplified polymorphism in two contrasting rice genotypes under salt stress. Journal of Genetics and Genomics 38: 419-424.

8. Lin Z, Ho C-W, Grierson D (2009) AtTRP1 encodes a novel TPR protein that interacts with the ethylene receptor ERS1 and modulates development in Arabidopsis. Journal of experimental botany: erp209.

9. Du H, Feng B-R, Yang S-S, Huang Y-B, Tang Y-X (2012) The R2R3-MYB transcription factor gene family in maize. PloS one 7: e37463.

10. Ashley M, Grant M, Grabov A (2006) Plant responses to potassium deficiencies: a role for potassium transport proteins. Journal of experimental botany 57: 425-436.

11. Han B, Chen L, Wang J, Wu Z, Yan L, et al. (2015) Constitutive Expresser of Pathogenesis Related Genes 1 Is Required for Pavement Cell Morphogenesis in Arabidopsis. PloS one 10: e0133249.

12. Bursać S, Brdovčak MC, Pfannkuchen M, Orsolić I, Golomb L, et al. (2012) Mutual protection of ribosomal proteins L5 and L11 from degradation is essential for p53 activation upon ribosomal biogenesis stress. Proceedings of the National Academy of Sciences 109: 20467-20472.

13. Reyes JC, Hennig L, Gruissem W (2002) Chromatin-remodeling and memory factors. New regulators of plant development. Plant physiology 130: 1090-1101.

14. Dehury B, Patra MC, Maharana J, Sahu J, Sen P, et al. (2014) Structure-based computational study of two disease resistance gene homologues (Hm1 and Hm2) in maize (Zea mays L.) with implications in plant-pathogen interactions.

15. Isono E, Katsiarimpa A, Müller IK, Anzenberger F, Stierhof Y-D, et al. (2010) The deubiquitinating enzyme AMSH3 is required for intracellular trafficking and vacuole biogenesis in Arabidopsis thaliana. The Plant Cell 22: 1826-1837.

16. Jones CH, Tove'C B, Jones KF, Zeller GO, Hruby DE (2001) Conserved DegP Protease in Gram-Positive Bacteria Is Essential for Thermal and Oxidative Tolerance and Full Virulence inStreptococcus pyogenes. Infection and Immunity 69: 5538-5545.

17. Leegood RC, Walker RP (2003) Regulation and roles of phosphoenolpyruvate carboxykinase in plants. Archives Of Biochemistry And Biophysics 414: 204-210.

18. O’Brien JA, Daudi A, Butt VS, Bolwell GP (2012) Reactive oxygen species and their role in plant defence and cell wall metabolism. Planta 236: 765-779.

19. Quesada V, Sarmiento‐Mañús R, González‐Bayón R, Hricová A, Pérez‐Marcos R, et al. (2011) Arabidopsis RUGOSA2 encodes an mTERF family member required for mitochondrion, chloroplast and leaf development. The Plant Journal 68: 738-753.