## Description of the Datasets

A brief description of each dataset used in this present study is provided below:

1. Total RNA extracted from multiple male, female, seed, and leaf tissues at different developmental stages were sequenced as the single-end reads (SRP006463) (Davidson et al. 2011).
2. Total RNA isolated from the 23 tissues of B73 at different developmental stages were sequenced as the single-end reads (SRP029238) (Walley et al. 2016).
3. Total RNA isolated from the ear, tassel, and leaf samples of the B73 plants grown in well-watered and drought conditions at four developmental time points (4 time points x 4 replicates x 3 tissues x 2 treatments) were sequenced as the single-end reads (SRP062027) (Thatcher et al. 2016).
4. Total RNA samples from the tunica (L1) and corpus (L2) cell layers of the shoot apical meristem from the 14 days old plants were sequenced as the single-end reads (SRP001844) (Schnable et al. 2009).
5. The mRNA acquired from the starchy endosperm at 6 days after pollination was sequenced as the single-end reads (SRP043224) (Thakare et al. 2014).
6. The B73 maize plants were treated with low or high nitrate and total RNA extracted from the stele of 7-8 cm shoot borne roots at 63 days was sequenced as the paired-end reads (SRP058076) (Yu et al. 2015).
7. The mRNA was extracted from the plant materials obtained from the sperm, egg, zygotes (12 and 24 hours after pollination), apical, and basal cells using manual dissection. Three biological replicates of each cell type were sequenced as the paired-end reads (SRP105764) (Chen et al. 2017).
8. Total RNA obtained from the shoot of the maize seedlings grown under simulated shade and far-red mediated de-etiolation conditions. A total of 27 samples (3 treatments x 3 time points x 3 biological replicated) were sequenced as the paired-end reads (SRP068070) (Wang et al. 2016).
9. Total RNA isolated from the three biological replicates each of severe and minimal C. zeina infected leaf samples was sequencing as paired-end reads (SRP074850) (Christie et al. 2017).
10. Total RNA extracted from the six biological replicates each of inner stem tissue (at V2 stage) from seedlings and husk tissue samples was sequenced as the single-end reads ([SRP098550](https://www.ncbi.nlm.nih.gov/sra?term=SRP098550)) (Oka et al. 2017).
11. Total RNA samples from the leaves at the V7 stage under sufficient and limited nitrogen availability were sequenced as the paired-end reads (SRP059655) (Lv et al. 2016).
12. Total RNA samples from the two replicate each of ovaries and leaf meristem of plants grown in well watered and drought conditions were sequenced as single-end reads (SRP014792) (Kakumanu et al. 2012).
13. Total RNA was isolated from the primary roots of plants grown in well watered, mild water deficit, and severe water deficit conditions at two developmental stages (6 and 24 hours). RNA-Seq libraries were sequenced as the single-end reads (SRP032921) (Opitz et al. 2014).
14. Total RNA isolated from the normal and salt stressed leaf tissues was sequenced as the single-end reads (SRP075906).
15. Total RNA was isolated from the three replicates each of embryo sacs, ovules, mature pollen, and seedlings of the B73 plants and sequenced as the paired-end reads (SRP006965).
16. Total RNA isolated from the embryo tissues at 10 days after pollination was sequenced as the paired-end reads (SRP037558).
17. Total RNA was extracted from the leaf tissues with on infestation, wounded, two-spotted spider mite infestation, and Banks grass mite infestation at different time points and sequenced as the paired-end reads (SRP109545).
18. Total RNA samples with the four biological replicates from the three different roots types (primary, seminal, and crown) were sequenced as the paired-end reads (SRP060587).
19. Two Total RNA samples from the seedling were sequenced as paired- and single-end reads (SRP073222).
20. Long non-coding RNA samples from the embryo and endosperm at three different developmental stages were sequenced as paired-end reads (SRP116297).
21. Total RNA isolated from the seedling roots at 3 days with three replicates was sequenced as the paired-end reads (SRP077762).
22. Total RNA from four biological replicates each of wild type and mutant rtcs B73 embryos across three developmental stages were sequenced as the paired-end reads (SRP079373) (Tai et al. 2017).
23. Total RNA was collected from the two biological replicates each of aleurone cell layer and starchy endosperm at two different developmental stages and sequenced as the single-end reads (SRP101358).
24. Total RNA isolated from the seedling roots at 3 days with three replicates was sequenced as the paired-end reads (SRP118717).

# References

Chen, Junyi, Nicholas Strieder, Nadia G. Krohn, Philipp Cyprys, Stefanie Sprunck, Julia C. Engelmann, and Thomas Dresselhaus. 2017. “Zygotic Genome Activation Occurs Shortly after Fertilization in Maize.” *The Plant Cell* 29 (9): 2106–25. https://doi.org/10.1105/tpc.17.00099.

Christie, Nanette, Alexander A. Myburg, Fourie Joubert, Shane L. Murray, Maryke Carstens, Yao-Cheng Lin, Jacqueline Meyer, et al. 2017. “Systems Genetics Reveals a Transcriptional Network Associated with Susceptibility in the Maize-Grey Leaf Spot Pathosystem.” *The Plant Journal* 89 (4): 746–63. https://doi.org/10.1111/tpj.13419.

Davidson, Rebecca M., Candice N. Hansey, Malali Gowda, Kevin L. Childs, Haining Lin, Brieanne Vaillancourt, Rajandeep S. Sekhon, et al. 2011. “Utility of RNA Sequencing for Analysis of Maize Reproductive Transcriptomes.” *The Plant Genome Journal* 4 (3): 191. https://doi.org/10.3835/plantgenome2011.05.0015.

Kakumanu, Akshay, Madana M R Ambavaram, Curtis Klumas, Arjun Krishnan, Utlwang Batlang, Elijah Myers, Ruth Grene, and Andy Pereira. 2012. “Effects of Drought on Gene Expression in Maize Reproductive and Leaf Meristem Tissue Revealed by RNA-Seq.” *Plant Physiology* 160 (2): 846–67. https://doi.org/10.1104/pp.112.200444.

Lv, Yuanda, Zhikai Liang, Min Ge, Weicong Qi, Tifu Zhang, Feng Lin, Zhaohua Peng, and Han Zhao. 2016. “Genome-Wide Identification and Functional Prediction of Nitrogen-Responsive Intergenic and Intronic Long Non-Coding RNAs in Maize (Zea Mays L.).” *BMC Genomics* 17 (1): 350. https://doi.org/10.1186/s12864-016-2650-1.

Oka, Rurika, Johan Zicola, Blaise Weber, Sarah N. Anderson, Charlie Hodgman, Jonathan I. Gent, Jan-Jaap Wesselink, et al. 2017. “Genome-Wide Mapping of Transcriptional Enhancer Candidates Using DNA and Chromatin Features in Maize.” *Genome Biology* 18 (1): 137. https://doi.org/10.1186/s13059-017-1273-4.

Opitz, Nina, Anja Paschold, Caroline Marcon, Waqas Malik, Christa Lanz, Hans-Peter Piepho, and Frank Hochholdinger. 2014. “Transcriptomic Complexity in Young Maize Primary Roots in Response to Low Water Potentials.” *BMC Genomics* 15 (1): 741. https://doi.org/10.1186/1471-2164-15-741.

Schnable, P. S., D. Ware, R. S. Fulton, J. C. Stein, F. Wei, S. Pasternak, C. Liang, et al. 2009. “The B73 Maize Genome: Complexity, Diversity, and Dynamics.” *Science* 326 (5956): 1112–15. https://doi.org/10.1126/science.1178534.

Tai, Huanhuan, Nina Opitz, Andrew Lithio, Xin Lu, Dan Nettleton, and Frank Hochholdinger. 2017. “Non-Syntenic Genes Drive RTCS-Dependent Regulation of the Embryo Transcriptome during Formation of Seminal Root Primordia in Maize (Zea Mays L.).” *Journal of Experimental Botany* 68 (3): 403–14. https://doi.org/10.1093/jxb/erw422.

Thakare, Dhiraj, Ruolin Yang, Joshua G. Steffen, Junpeng Zhan, Dongfang Wang, Richard M. Clark, Xiangfeng Wang, and Ramin Yadegari. 2014. “RNA-Seq Analysis of Laser-Capture Microdissected Cells of the Developing Central Starchy Endosperm of Maize.” *Genomics Data* 2 (December): 242–45. https://doi.org/10.1016/j.gdata.2014.07.003.

Thatcher, Shawn R., Olga N. Danilevskaya, Xin Meng, Mary Beatty, Gina Zastrow-Hayes, Charlotte Harris, Brandon Van Allen, Jeffrey Habben, and Bailin Li. 2016. “Genome-Wide Analysis of Alternative Splicing during Development and Drought Stress in Maize.” *Plant Physiology* 170 (1): 586–99. https://doi.org/10.1104/pp.15.01267.

Walley, J. W., R. C. Sartor, Z. Shen, R. J. Schmitz, K. J. Wu, M. A. Urich, J. R. Nery, et al. 2016. “Integration of Omic Networks in a Developmental Atlas of Maize.” *Science* 353 (6301): 814–18. https://doi.org/10.1126/science.aag1125.

Wang, Hai, Guangxia Wu, Binbin Zhao, Baobao Wang, Zhihong Lang, Chunyi Zhang, and Haiyang Wang. 2016. “Regulatory Modules Controlling Early Shade Avoidance Response in Maize Seedlings.” *BMC Genomics* 17 (1): 269. https://doi.org/10.1186/s12864-016-2593-6.

Yu, Peng, Kai Eggert, Nicolaus von Wirén, Chunjian Li, and Frank Hochholdinger. 2015. “Cell Type-Specific Gene Expression Analyses by RNA Sequencing Reveal Local High Nitrate-Triggered Lateral Root Initiation in Shoot-Borne Roots of Maize by Modulating Auxin-Related Cell Cycle Regulation.” *Plant Physiology* 169 (1): 690–704. https://doi.org/10.1104/pp.15.00888.