



Supplementary Figure S5. Expression of the 55 model genes with the SNP positions  $\pm 120$  kb of the markers linked to common traits listed in Table 3. **(a)**. Expression of the genes in leaf tissue under drought and control condition with T7 maize cultivar used by Forestan et al. (2016). **(b)**. Expression of the genes in leaf tissue under heat and control condition with B73 maize cultivar used by Waters et al. (2017). The genes with dotted red lines are predicted candidate genes based on their annotations retrieved from <https://phytozome-next.jgi.doe.gov/> (accessed on 1 January 2022) (version 13). The color legend is shown on right side of the figure (Green and red mean down- and up-regulated, respectively, while the black indicate zero expression)

- Forestan, C., R. Aiese Cigliano, S. Farinati, A. Lunardon, W. Sanseverino & S. Varotto, 2016. Stress-induced and epigenetic-mediated maize transcriptome regulation study by means of transcriptome reannotation and differential expression analysis. *Scientific reports* 6:30446-30446 <https://doi.org/10.1038/srep30446>.
- Waters, A. J., I. Makarevitch, J. Noshay, L. T. Burghardt, C. N. Hirsch, C. D. Hirsch & N. M. Springer, 2017. Natural variation for gene expression responses to abiotic stress in maize. *The Plant Journal* 89(4):706-717 <https://doi.org/10.1111/tpj.13414>.