

Supplementary Figures

Genomic Regions Involved in the Control of 1,000-kernels Weight in Wild Relatives-Derived Populations of Durum Wheat

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Figure S1 Graphical representation of the three steps validation approach. The NAM panel 1 is used for the discovery of QTL, then the GWAS panel 2 is used to investigate haplotype additive effects, and finally the MAS panel 3 is used to validate KASP. The Svevo genome assembly is used as the support for this approach, comparing the same physical regions across different genotyping protocols.



Figure S2 Cluster of Environments





Figure S3 Boxplot of the best linear unbiased Predictors (Blups) for various traits under two different environmental conditions (Drought and irrigated)





Figure S4 Yield stability response to GxE measured as AMMI wide adaptation index (AWAI) vs. grain yield potential (G) measured as BLUP across environments. The overall best entries are in the top right corner.