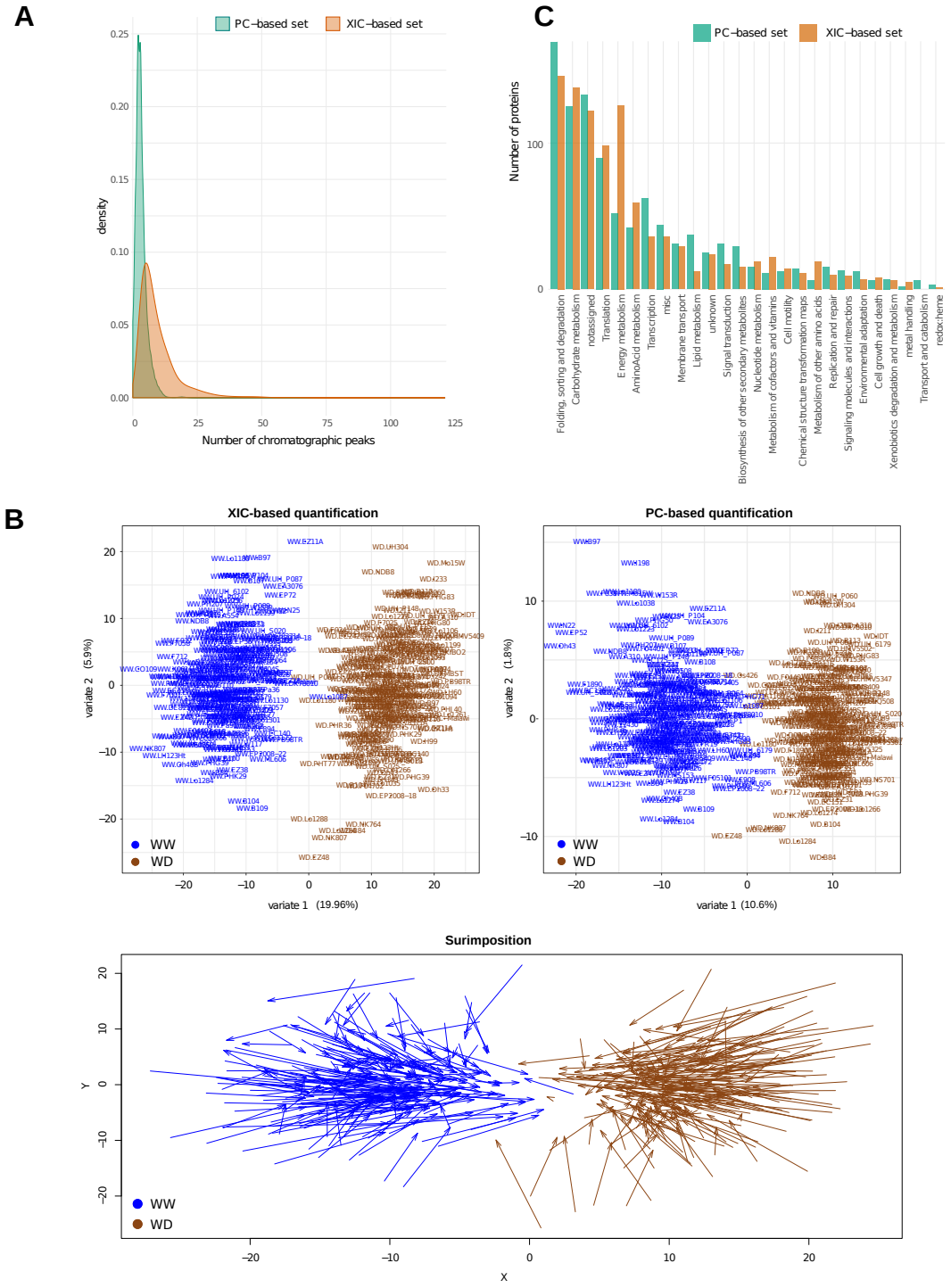
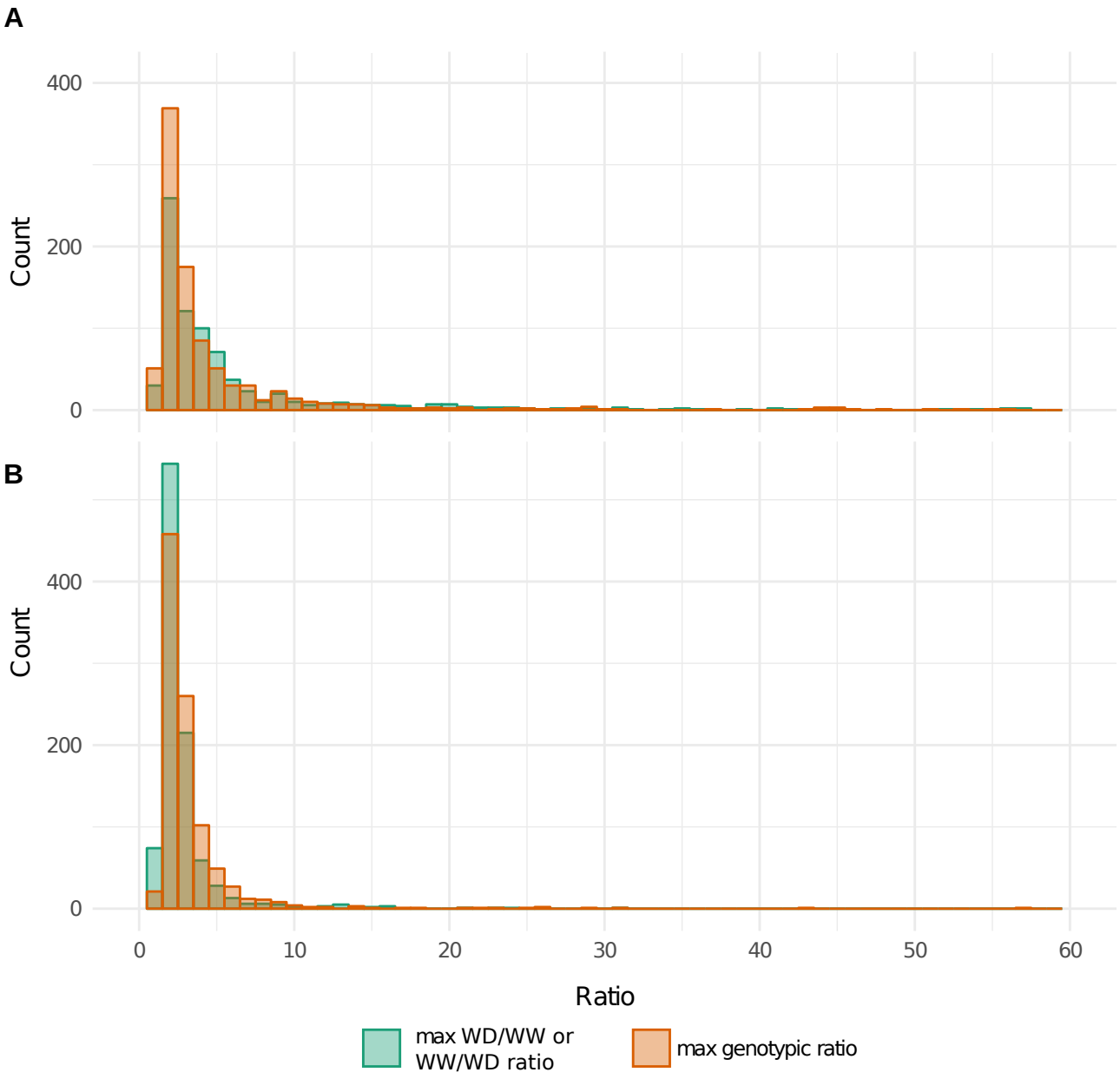
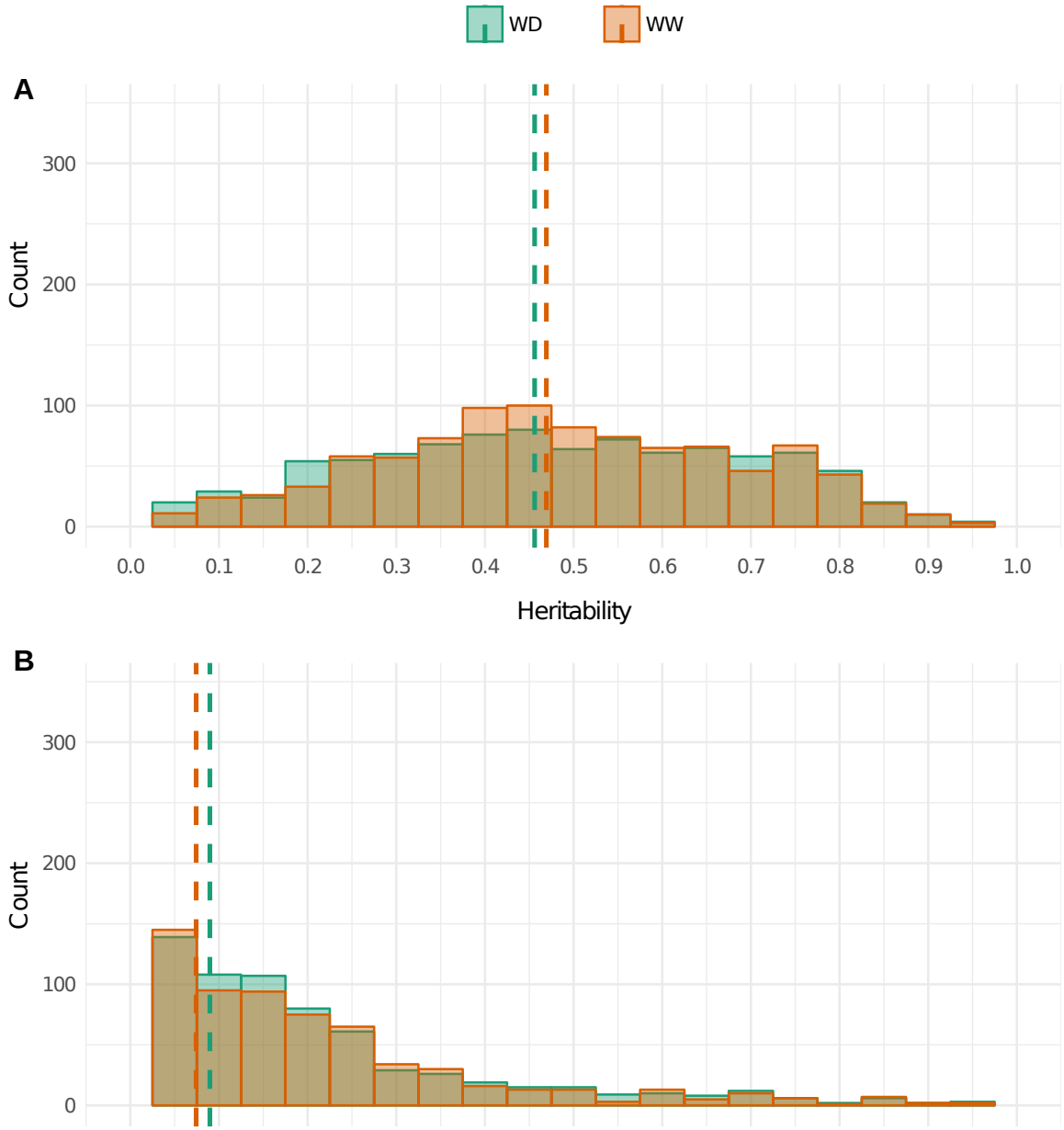


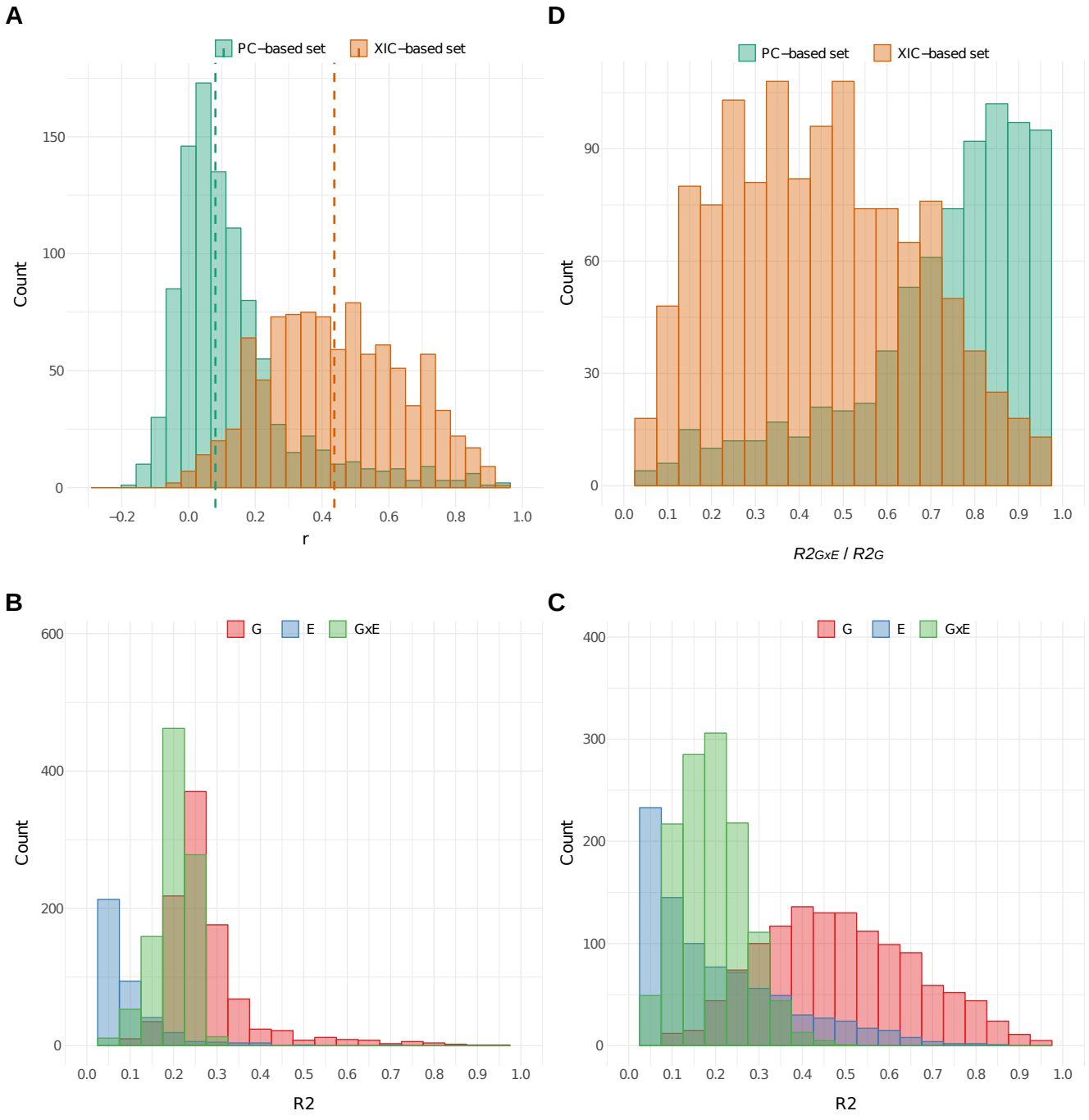
Supplementary Figure 1. The XIC-based and PC-based protein sets exhibit different characteristics. (A) Distribution of the number of chromatographic peaks per protein in the two sets. Here, the proteins of the XIC-based set were quantified based on the number of chromatographic peaks in order to compare the global protein abundance between the two protein sets. (B) Graphical representations of a partial least squares regression relating abundances estimated from peak counts to abundances estimated from peptide intensities. Here, only proteins from the XIC-based set were used. They were quantified by using the two methods (XIC-based and PC-based) in order to compared the discrimination power provided by each method. The analysis was performed using the Mixomics R package. Top: samples representation in the space spanned by the first two components for each quantification method. Bottom: surimposition of the samples representation obtained for the two quantification methods. Each sample is indicated by an arrow whose start indicates the location of the sample when quantification is based on XIC and tip indicates the location of the sample when quantification is based on PC. Orientation of the arrows indicates that the two watering conditions are better separated when proteins are quantified based on XIC. (C) Distribution of the proteins of the two sets in KEGG categories.



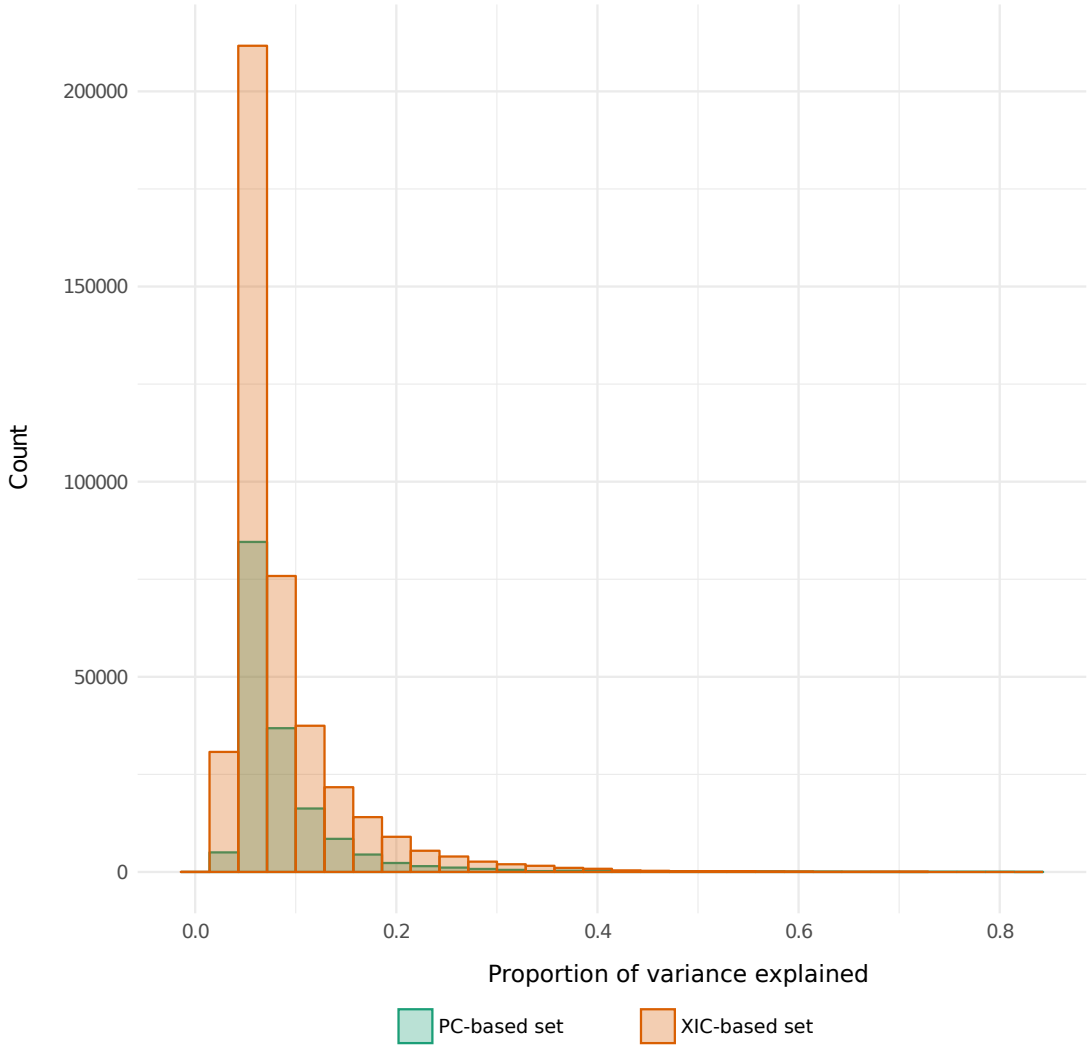
Supplementary Figure 2. Distribution of maximum amplitudes of abundance variations in response to water deficit or to a genotypic change. (A) In the PC-based set. (B) In the XIC-based set. For each protein, the maximum amplitude of abundance variation in response to water deficit was the highest WD/WW or WW/WD ratio found across all genotypes. To compute the maximum amplitude of abundance variation in response to a genotypic change over the two conditions, we first computed the average protein abundance in each genotype and then the ratio between the highest and the lowest average abundances.



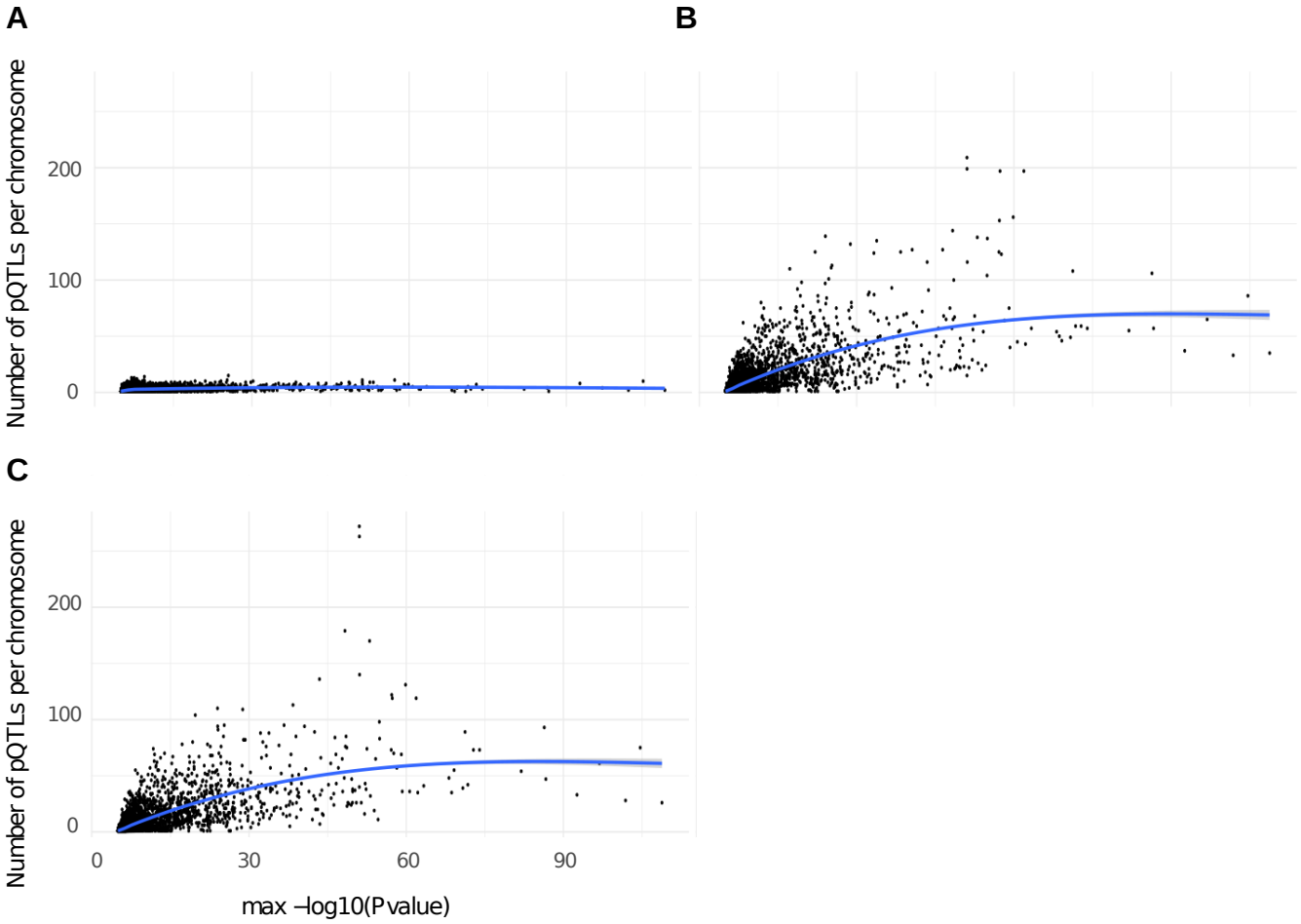
Supplementary Figure 3. Distributions of broad sense heritability for protein abundances in the WW and WD conditions. (A) in the XIC-based set. (B) in the PC-based set. Dashed lines indicate the median values.



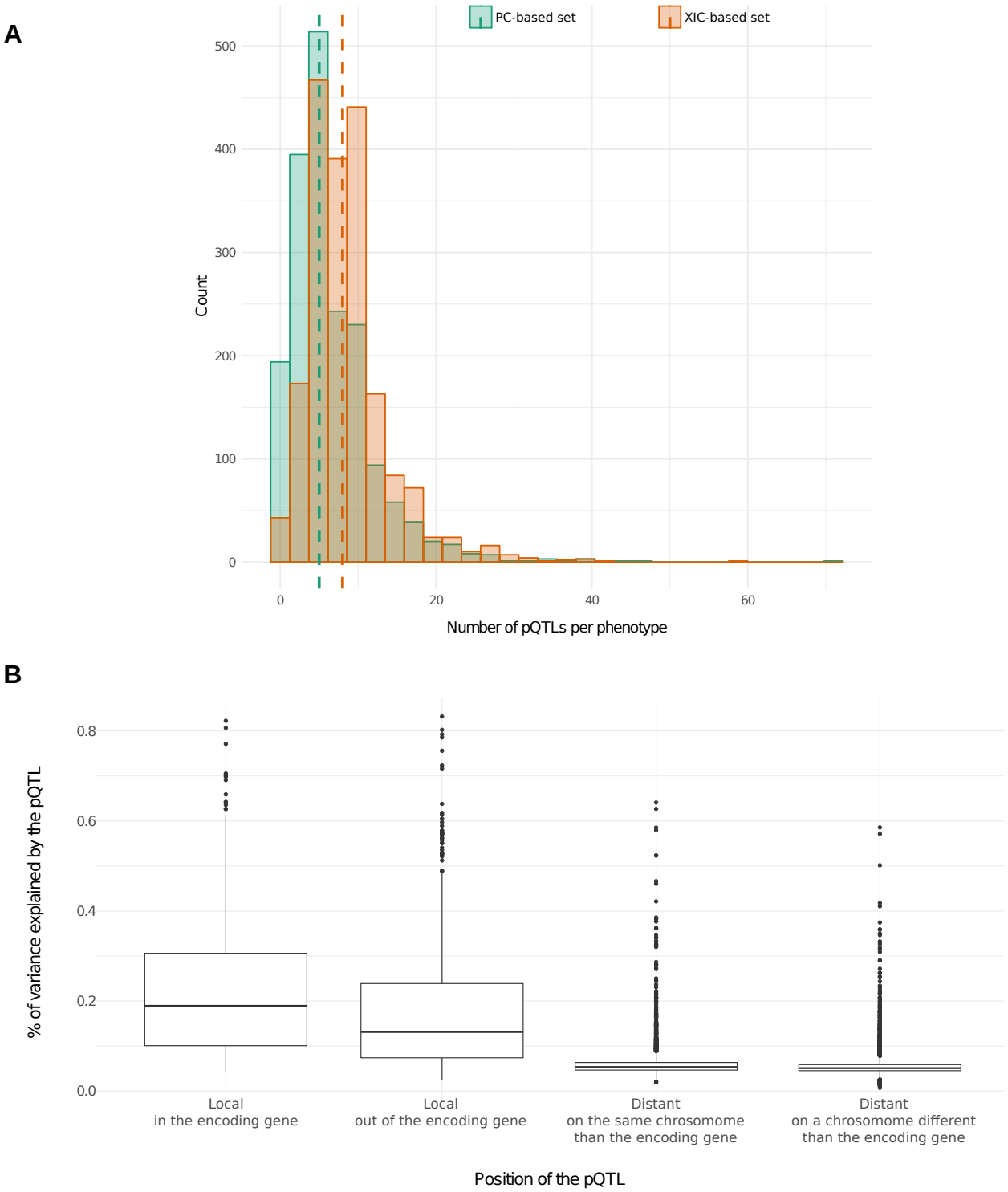
Supplementary Figure 4. Genotype by environment (GxE) interactions at the proteome level. (A) Distributions of the coefficients of correlation of protein abundances between the WW and WD conditions in the PC-based and XIC-based protein sets. Dashed lines indicate median values. (B) Distribution of the proportion of variance explained by the genotype (G), the environment (E) and the GxE interaction in the PC-based set. (C) Same as (B) in the XIC-based set. (D) Distribution of the ratio between the proportion of variance (R2) explained by the genotype GxE interaction and the proportion of variance explained by the genotype (G) in the PC-based and XIC-based sets.



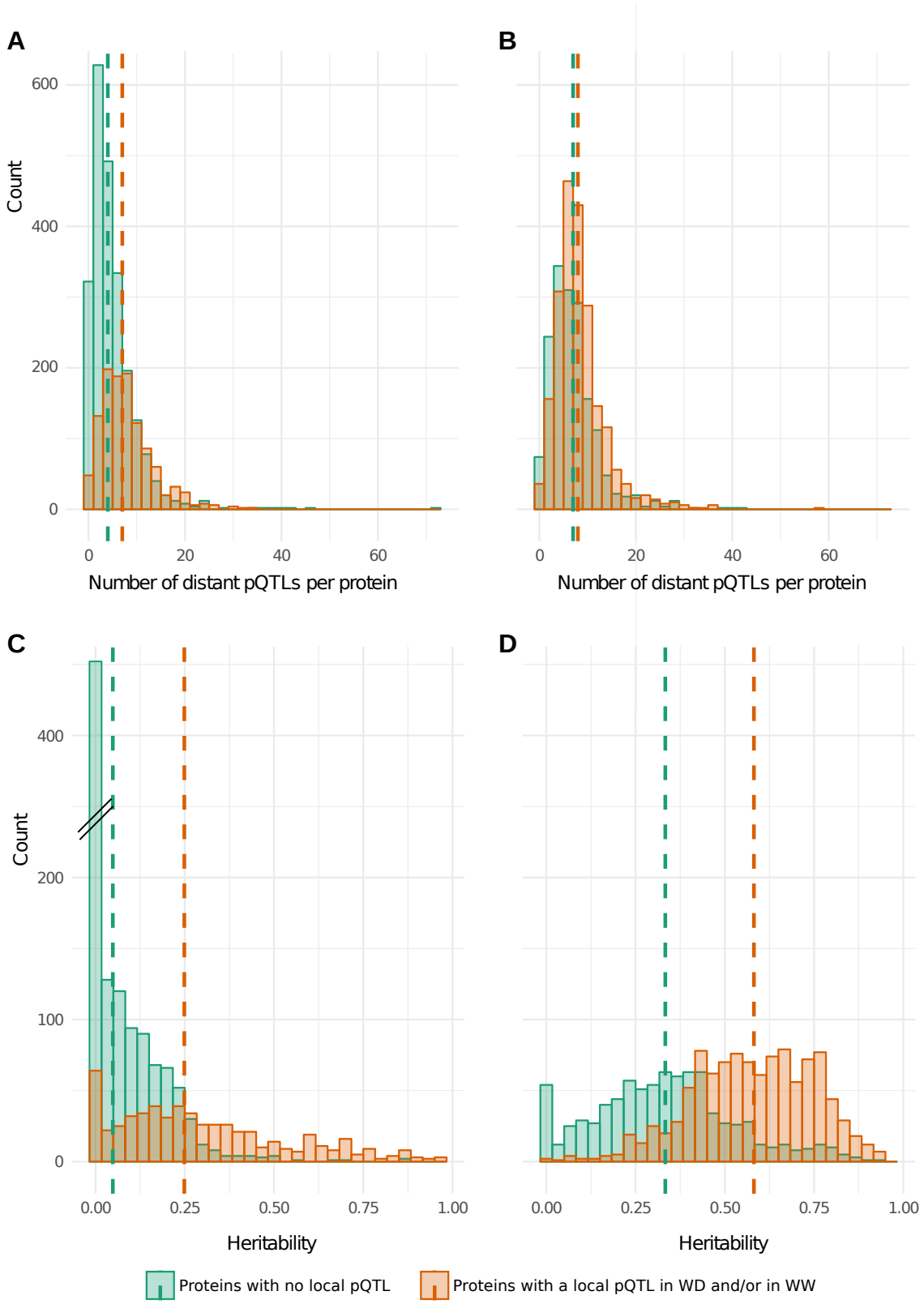
Supplementary Figure 5. Distributions of the proportion of variance explained by the SNPs associated to protein abundance variations in the PC-based and XIC-based sets.



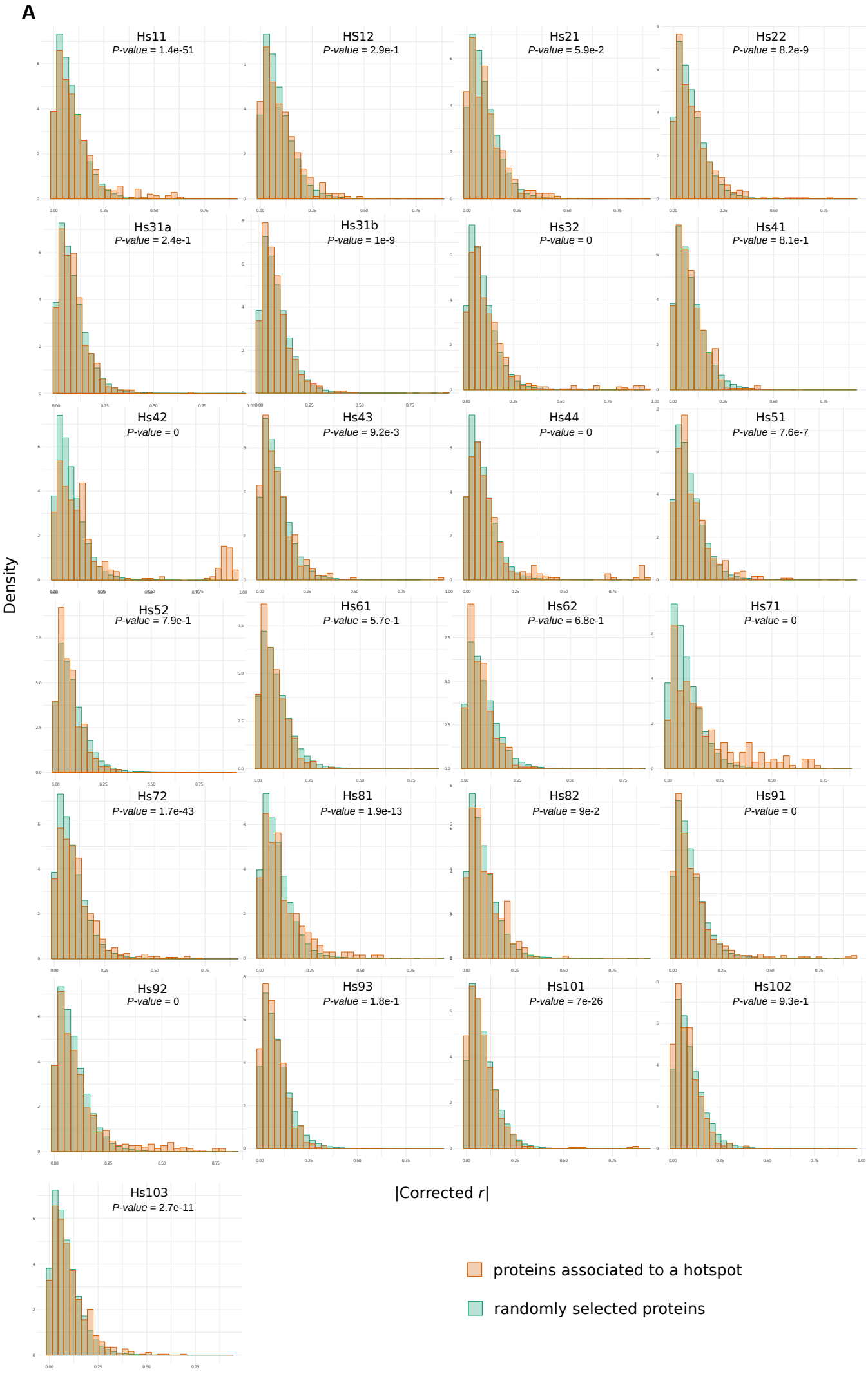
Supplementary Figure 6. Effect of the methods of detection of association peaks on the number of pQTLs detected. Each graph represents the relationships between the number of pQTLs detected per chromosome and the *P-value* of the most strongly associated pQTL of the corresponding chromosome. (A) Geometric method, (B) LD-based method, (C) Genetic method with a 0.1 cM window (see Materials & Methods for details).



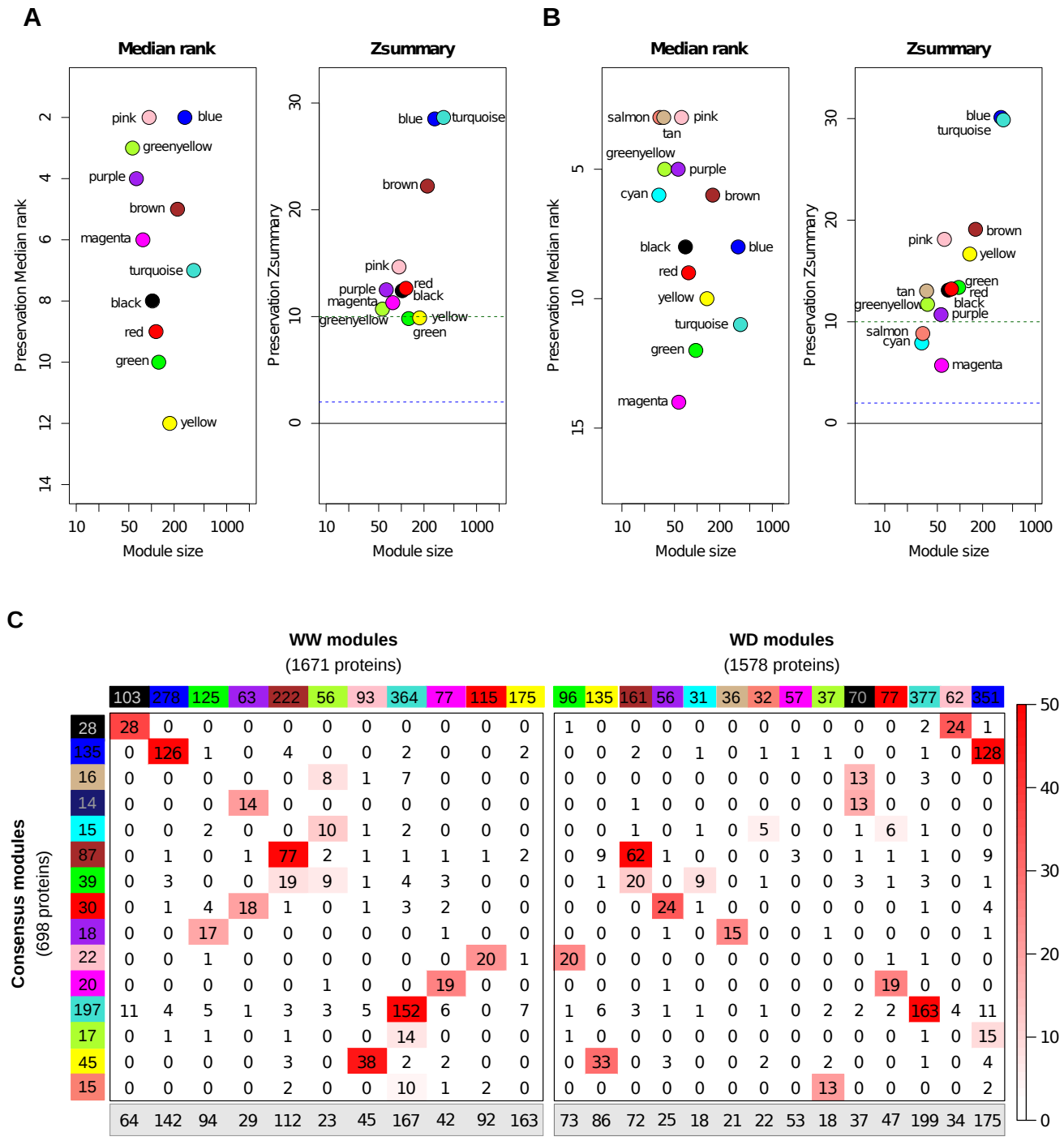
Supplementary Figure 7. Detection of pQTLs. (A) Distributions of the number of pQTLs per molecular phenotype in the PC-based and XIC-based sets. Dashed lines represent the median values. (B) Boxplot of the percentage of variance explained by a pQTL depending on its position relatively to the gene encoding the protein to which it is associated.



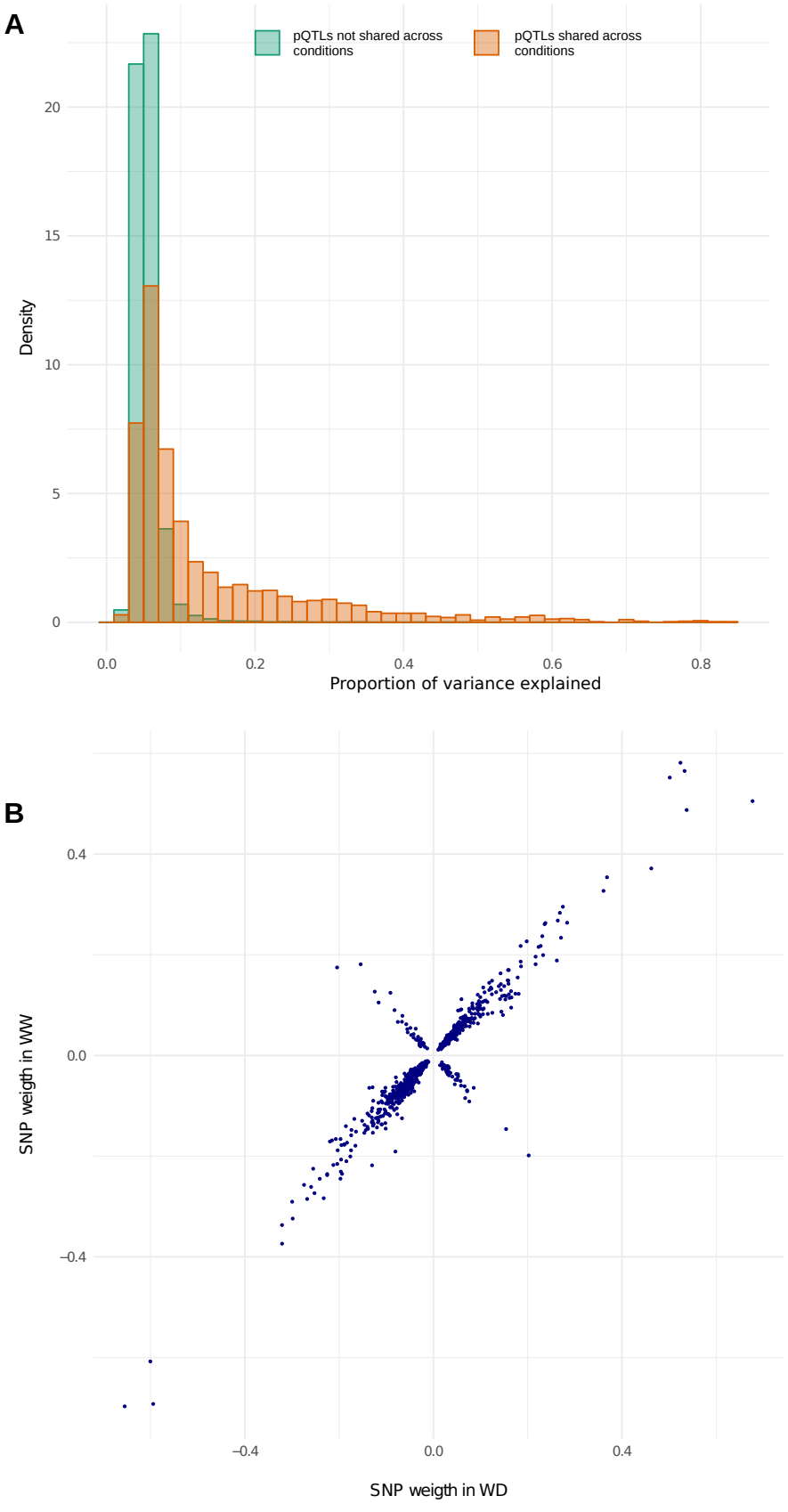
Supplementary Figure 8. Caracterization of the proteins for which no local pQTL was detected. (A, B) Distributions of the number of distant pQTLs per protein in the set of proteins for which no local pQTL was detected *versus* the set of proteins for which a local pQTL was detected in at least one condition in the PC-based set (A) and in the XIC-based set (B). (C, D) Distributions of heritability in the set of proteins for which no local pQTL was detected *versus* the set of proteins for which a local pQTL was detected in at least one condition in the PC-based set (C) and in the XIC-based set (D). Dashed lines represent median values.


A
Hs11
P-value = 1.4e-51
HS12
P-value = 2.9e-1
Hs21
P-value = 5.9e-2
Hs22
P-value = 8.2e-9
Hs31a
P-value = 2.4e-1
Hs31b
P-value = 1e-9
Hs32
P-value = 0
Hs41
P-value = 8.1e-1
Hs42
P-value = 0
Hs43
P-value = 9.2e-3
Hs44
P-value = 0
Hs51
P-value = 7.6e-7
Hs52
P-value = 7.9e-1
Hs61
P-value = 5.7e-1
Hs62
P-value = 6.8e-1
Hs71
P-value = 0
Hs72
P-value = 1.7e-43
Hs81
P-value = 1.9e-13
Hs82
P-value = 9e-2
Hs91
P-value = 0
Hs92
P-value = 0
Hs93
P-value = 1.8e-1
Hs101
P-value = 7e-26
Hs102
P-value = 9.3e-1
Hs103
P-value = 2.7e-11
Density
|Corrected r|
proteins associated to a hotspot
randomly selected proteins

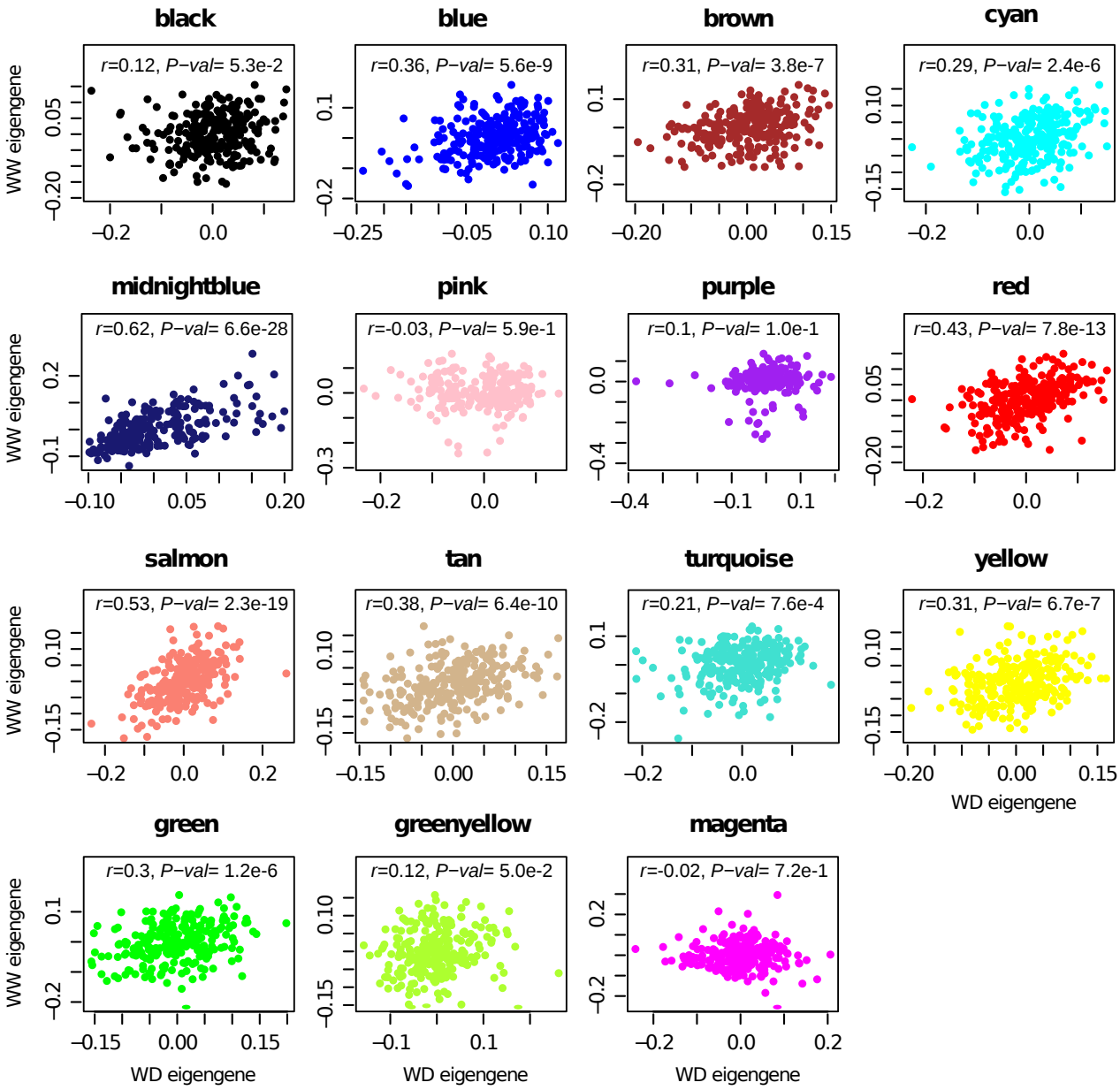
Supplementary Figure 9. Distributions of the absolute values of the coefficient of correlation (r) between abundances of randomly selected proteins or proteins associated to a hotspot. (A) In the well-watered condition. (B) In the water-deficit condition. *r* was corrected to take into account the kinship and structure among maize genotypes. *P-values* for enrichment in co-expressed proteins are indicated.



Supplementary Figure 10. Similarities among the WW and WD networks. (A) Preservation of WW modules in WD data. Zsummary is a composite measure summaring the Z scores computed on several preservation statistics. Zsummary < 2 (blue dashed line) indicates no preservation; 2 < Zsummary < 10 indicates weak to moderate preservation; Zsummary > 10 indicates good preservation. Median rank is based on the ranks of the observed preservation statistics. It does not show dependence on the module size. (B) Preservation of WD modules in WW data. (C) Correspondence of the WW and WD modules (in column) with the consensus modules (in row). Numbers above and on the left of the tables indicate the total number of proteins in each module. Numbers in the tables indicate the number of proteins in the intersection of a WW or WD module with a consensus module. The numbers of proteins of the WW and WD modules that were not mapped to a consensus module are shaded in grey at the bottom of the tables. Significance of the Fisher's exact test for the overlap of two modules is color-coded with the scale of log10(1/*P-value*) shown on the right. No correspondence with a consensus module was found for the yellow module in the WW condition nor for the magenta module in the WD condition, indicating that these two modules were condition specific.



Supplementary Figure 11. pQTLs shared across conditions. (A) Distributions of the proportion of variance explained by the pQTLs shared and not shared across the two watering conditions. (B) Effects of the pQTLs shared across conditions on the abundances of the proteins they were associated to**.**



Supplementary Figure 12. Correlations of consensus module eigengenes between the WW and WD conditions.