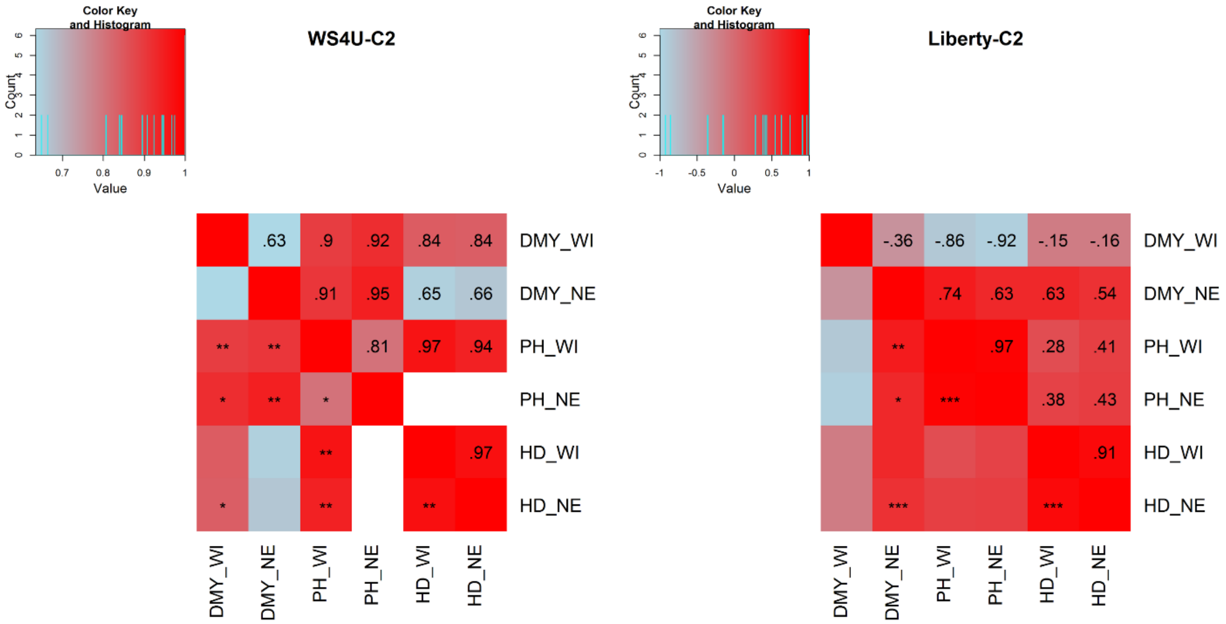

Figure S3. Heatmaps of genomic correlations between trait BLUPs for traits measured (a) in WS4U-C2; (b) in Liberty-C2. White cells show unavailable estimates (due to non-convergence of the fitting algorithm). Significance of inferred genotypic correlations was assessed by likelihood-ratio tests; *: $p < 0.05$, **: $p < 0.01$, ***: $p < 0.001$. Genomic correlations were estimated in a multivariate GBLUP model, with $\mathbf{X}_{\mathrm{Base}}$ as input, using ASREML-R (Butler et al. 2007).