Figure 1: Heatmaps for the performances (Best Linear Unbiased Predictors, BLUPs) of the 686 genotypes in each ESWYT cycle/year from the five prediction models (Table 1) presented by cross-tabulating the genetic relationship matrices among genotypes ($\mathbf{K}_{G \times G}$ matrix) with the correlation matrices among years ($\mathbf{W}_{Y \times Y}$ matrix) calculated from the covariance matrix from the factor analytic (FA) model. (a) BLUPs from the ID model; (b) Lower-triangular $\mathbf{K}_{G \times G}$ matrix calculated using the pedigree (COP-based $\mathbf{K}_{G \times G}$ matrix); (c) BLUPs for COP-based K model; (d) BLUPs from COP-based KFA model; (e) Upper-triangular $\mathbf{W}_{Y \times Y}$ matrix from the COP-based KFA model; (f) Lower-triangular $\mathbf{K}_{G \times G}$ matrix calculated using the marker data (GRM-based $\mathbf{K}_{G \times G}$ matrix); (g) BLUPs from GRM-based K model; (h) BLUPs from GRM-based KFA model; and (i) Upper-triangular $\mathbf{W}_{Y \times Y}$ matrix from the GRM-based KFA model. The white in the heatmaps indicates either a missing BLUP for untested genotypes, zeros in the $\mathbf{K}_{G \times G}$ matrices, or diagonal values in the $\mathbf{W}_{Y \times Y}$ matrix. The ordering of the genotypes is consistent with the respectively optimised dendrograms and is explained in the text