Supplemental Fig. S1. (A) Initial principal components analysis (PCA) using 363 lines (in red are the 270 selected genotypes). (B) PCA on remaining 270 lines after removing outliers and reduction population for genotypes of interest.
Supplemental Fig. S2. Selection coincidence (SC) scheme. SC is represented by the percentage of common individuals in two sets, in this case A and B. At a given selection intensity (e.g., 10% of the best genotypes), A is the group of genotypes selected by GV and B is the group of genotypes selected by GEBV. At a given intensity, mean percentage of coincidence is estimated considering all bootstrap samples. SC is then performed in a range of selection intensities (IS%).