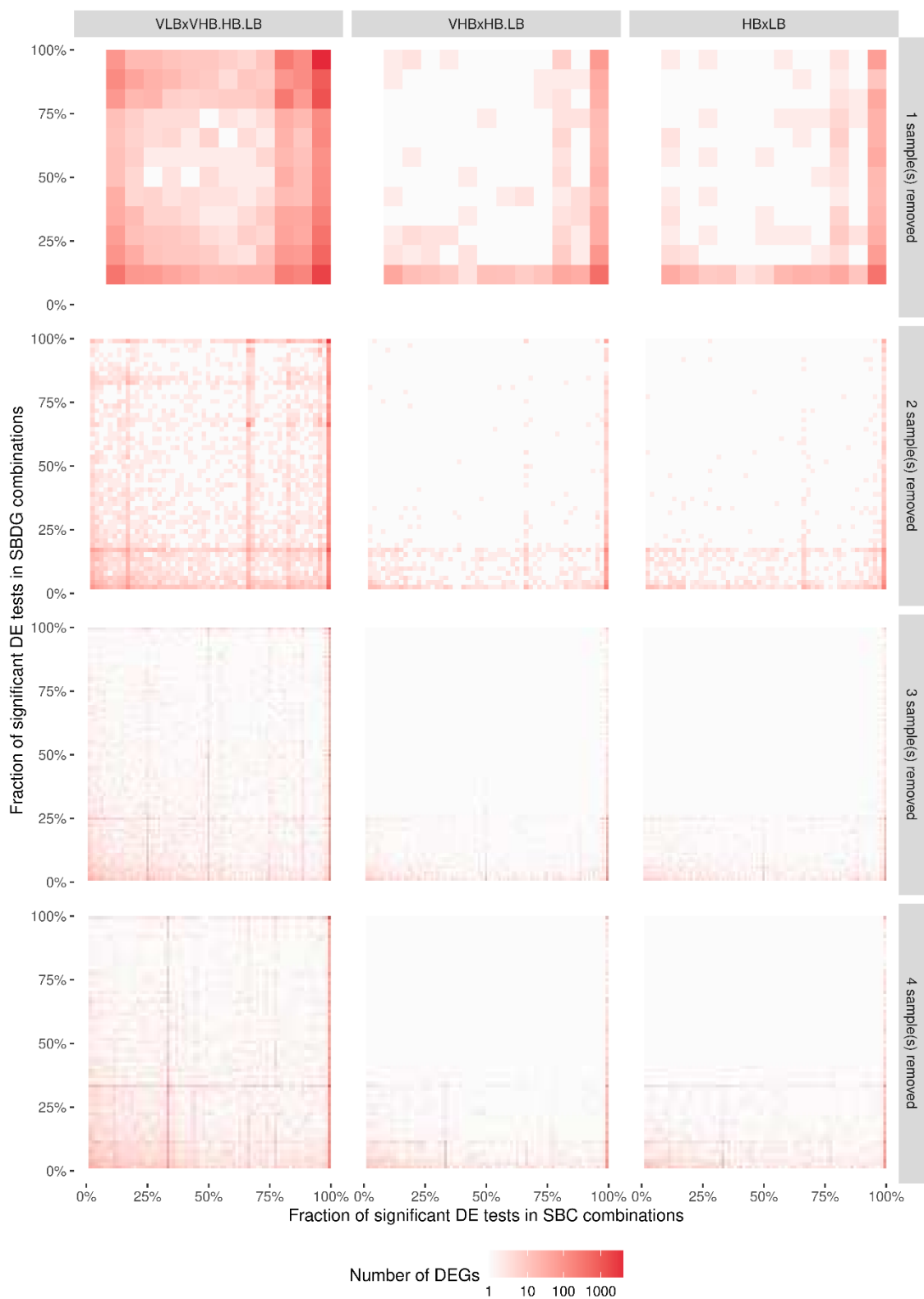


## Supplementary Material to “Sampling strategies for sugarcane using either clonal replicates or diverse genotypes can bias the conclusions of RNA-seq studies”



**Figure S3** - Correspondence between differentially expressed genes found by SBC and SBDG per contrast and number of removed samples. The number of combinations for  $i$  removed sample(s) is  $n_i$ , such that each gene ranges from 0 to  $n_i$  chances to be called as differentially expressed. The heatmap shows the number of DEGs identified by both strategies, for at least one combination of samples, normalized by  $n_i$ .