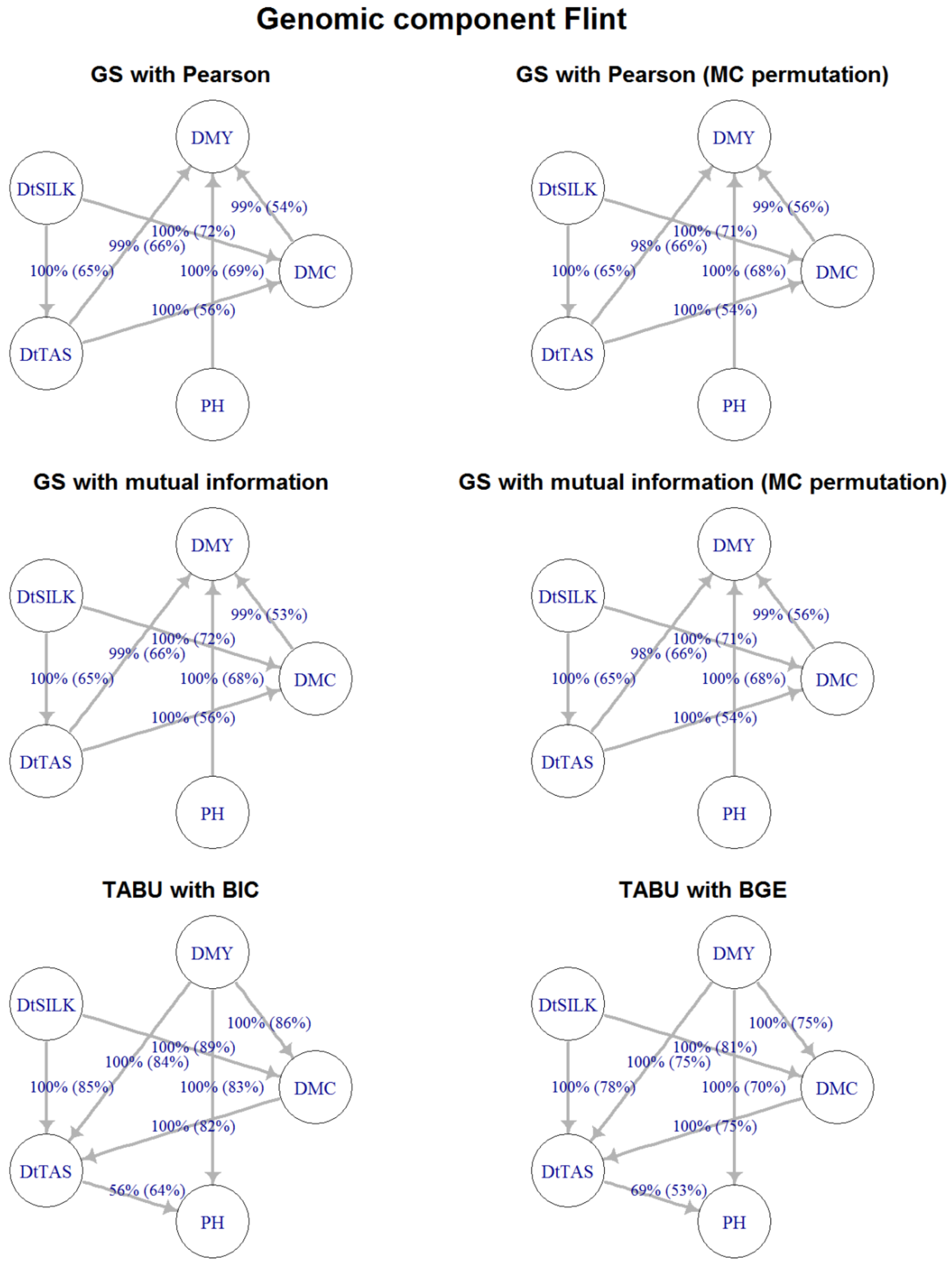

Genomic component Flint

GS with Pearson

GS with Pearson (MC permutation)

GS with mutual information

GS with mutual information (MC permutation)

TABU with BIC

TABU with BGE

Figure S4. Networks of the genomic component in Flint. All algorithms identified the connections from DtSILK to DtTAS, from DtSILK to DMC, between DMY and DMC, between DMY and PH, between DMY and DtTAS, and between DtTAS and DMC. The score-based approaches (TABU 1, 2) oriented the connections with DMY and between DtTAS and DMC in the opposite direction than the constraint-based approaches (GS 1, 2, 3, 4). They also displayed an additional edge from DtTAS to PH. The SEM favored the tabu-search algorithms (TABU 1, 2) over all other settings. Labels of edges indicate the proportion of bootstrap samples supporting the edge and (in parentheses) the proportion having the direction shown. Edges that were not significant in the averaging process due to a network-internal empirical test on the arc’s strength are not shown.