Improving the inference of population genetic structure in the presence of related individuals

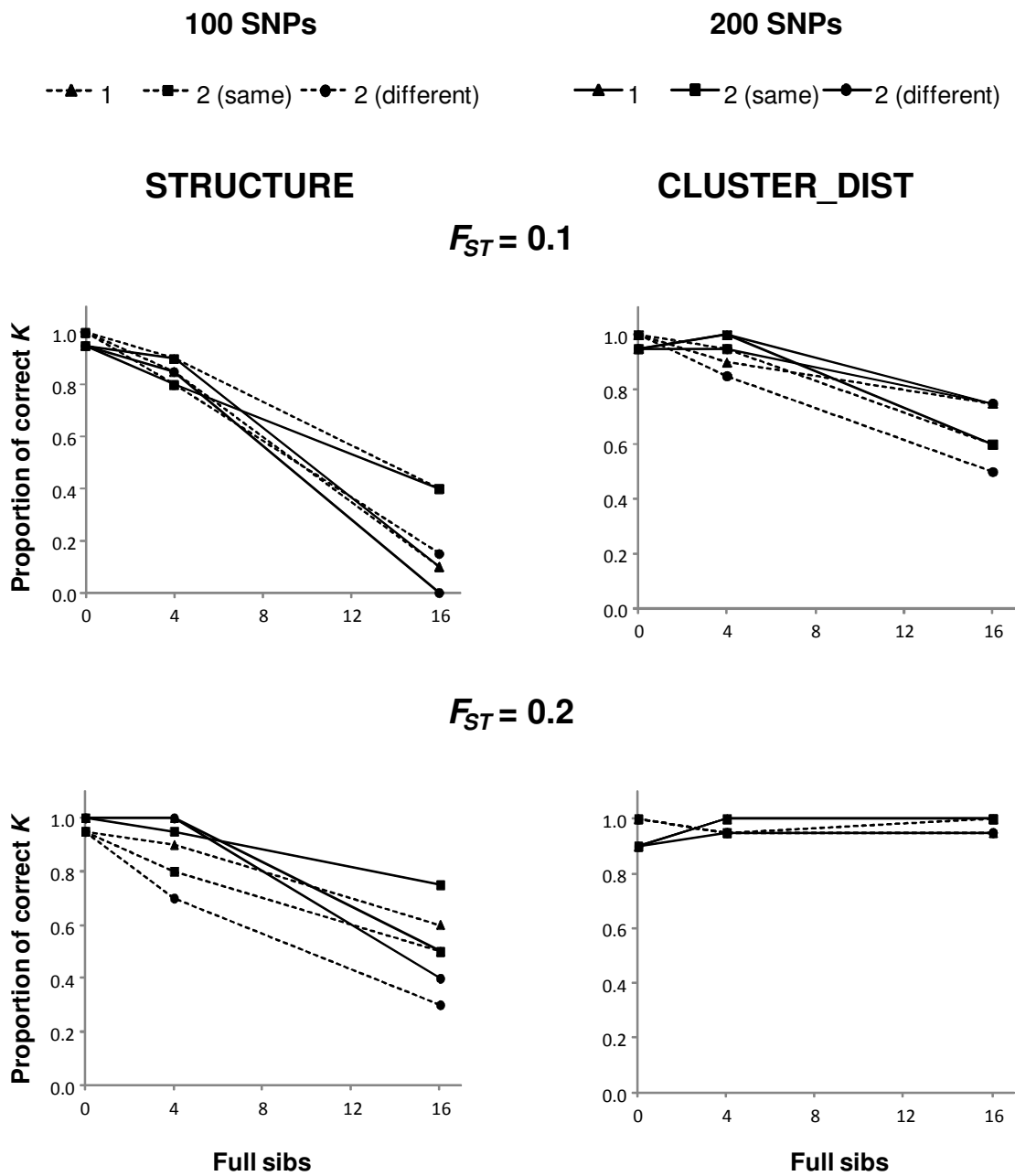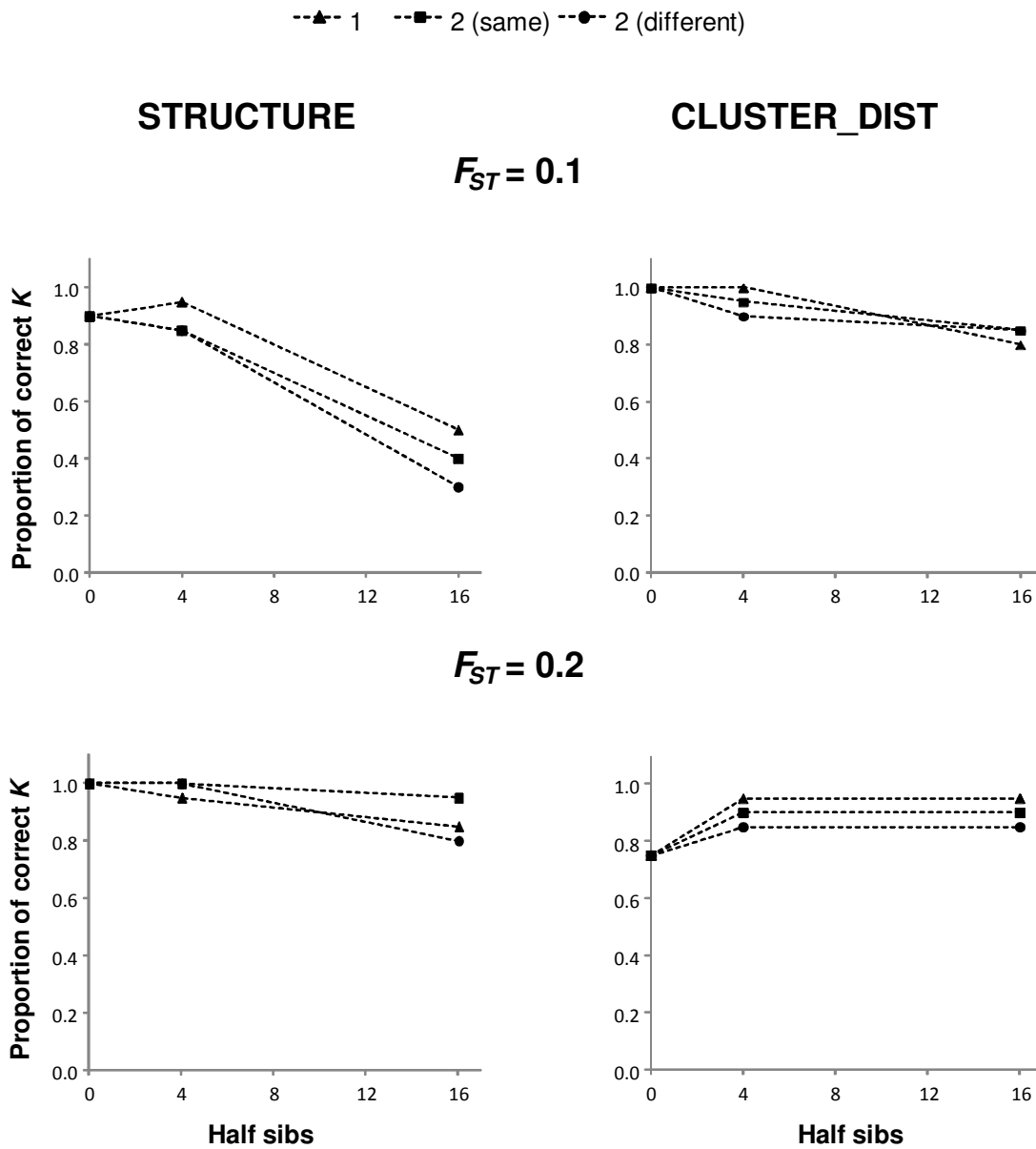Silvia T. Rodríguez-Ramilo, Miguel A. Toro, Jinliang Wang and Jesús Fernández

Supplementary Figure S1. Proportion of replicates where STRUCTURE (left panels) and CLUSTER_DIST (right panels) infer $K = 5$ when $n = 5$ in presence of full-siblings. Dashed and solid lines indicate 10 and 20 microsatellites, respectively. Triangles represent one family, squares indicate two families in the same subpopulation, and circles represent two families in different subpopulations.

100 SNPs **200 SNPs**

STRUCTURE   CLUSTER_DIST

$F_{ST} = 0.1$

$F_{ST} = 0.2$

Full sibs   Full sibs

Supplementary Figure S2. Proportion of replicates where STRUCTURE (left panels) and CLUSTER_DIST (right panels) infer $K = 5$ when $n = 5$ in presence of full-siblings. Dashed and solid lines indicate 100 and 200 SNPs, respectively. Triangles represent one family, squares indicate two families in the same subpopulation, and circles represent two families in different subpopulations.

Supplementary Figure S3. Proportion of replicates where STRUCTURE (left panels) and CLUSTER_DIST (right panels) infer $K = 5$ when $n = 5$ in presence of half-siblings, using 10 microsatellites. Triangles represent one family, squares indicate two families in the same subpopulation, and circles represent two families in different subpopulations.