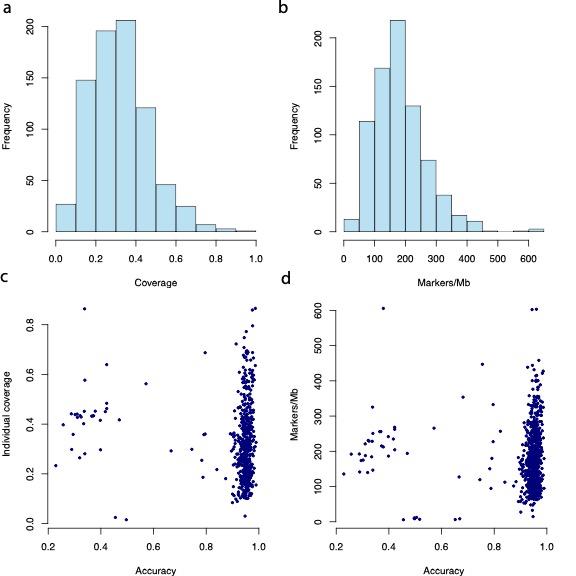
**Additional information for:**  
Genotyping by low-coverage whole-genome sequencing in intercross pedigrees from outbred founders: a cost efficient approach

Yanjun Zan, Thibaut Payen, Mette Lillie, Christa F. Honaker, Paul B. Siegeland Örjan Carlborg



***Figure S4. Ilustration of relationship between sequencing coverage, marker density and imputation accuracy.******A/B)*** *Histograms of the sequencing coverage/marker densities for the 803 genotyped F2 individuals;* ***C/D)*** *Scatter plots of individual coverage/marker density vs imputation accuracy measured as proportion of sites that has same genotype with the averaged genotype probabilities estimated by* (Wahlberg et al., 2009) *using genotypes of 434 SNP and microsatellite markers with the Haley and Knott algorithm* (Haley et al., 1994)*.*