Figure S9. Genome-wide comparison of using SNP genotype data from all breeds (Total: 46 breeds and N= 847), breeds with minimum 10 samples (Total: 26 breeds and N=753) and breeds with minimum 20 samples (Total: 20 breeds and N=652) for computing CSS (A), XPEHH (B), ΔDAF (C) and F_{ST} (D) for European *Bos taurus* cattle.