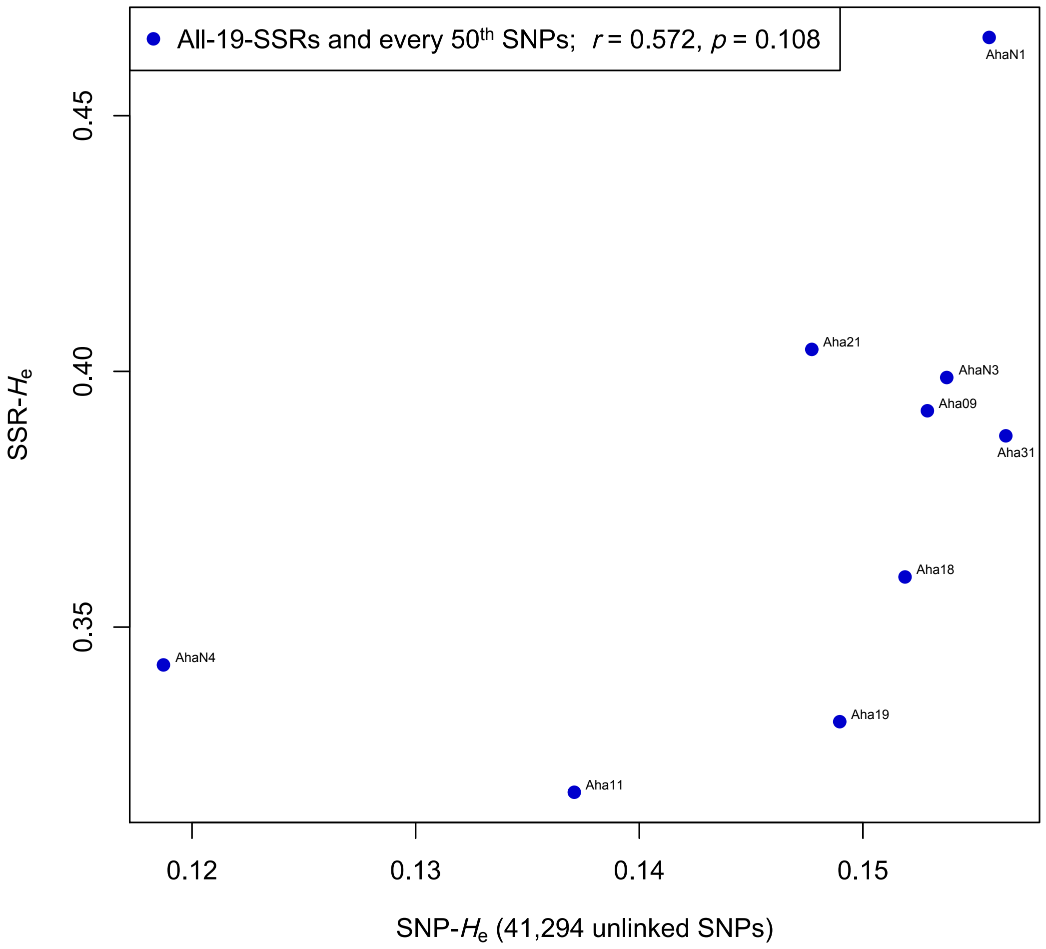

Additional file 8: Figure S4 Relationships between expected SNP heterozygosity (SNP-H_e) and expected microsatellite heterozygosity (SSR-H_e) of *Arabidopsis halleri* estimated on the basis of 19 microsatellites and 41,294 genetically unlinked genome-wide single nucleotide polymorphisms (SNPs). For this analysis only every 50th SNP of the more than 2 million SNPs was used. The median distance among two neighbouring SNPs is 1600 bp on the *A. thaliana* reference genome.