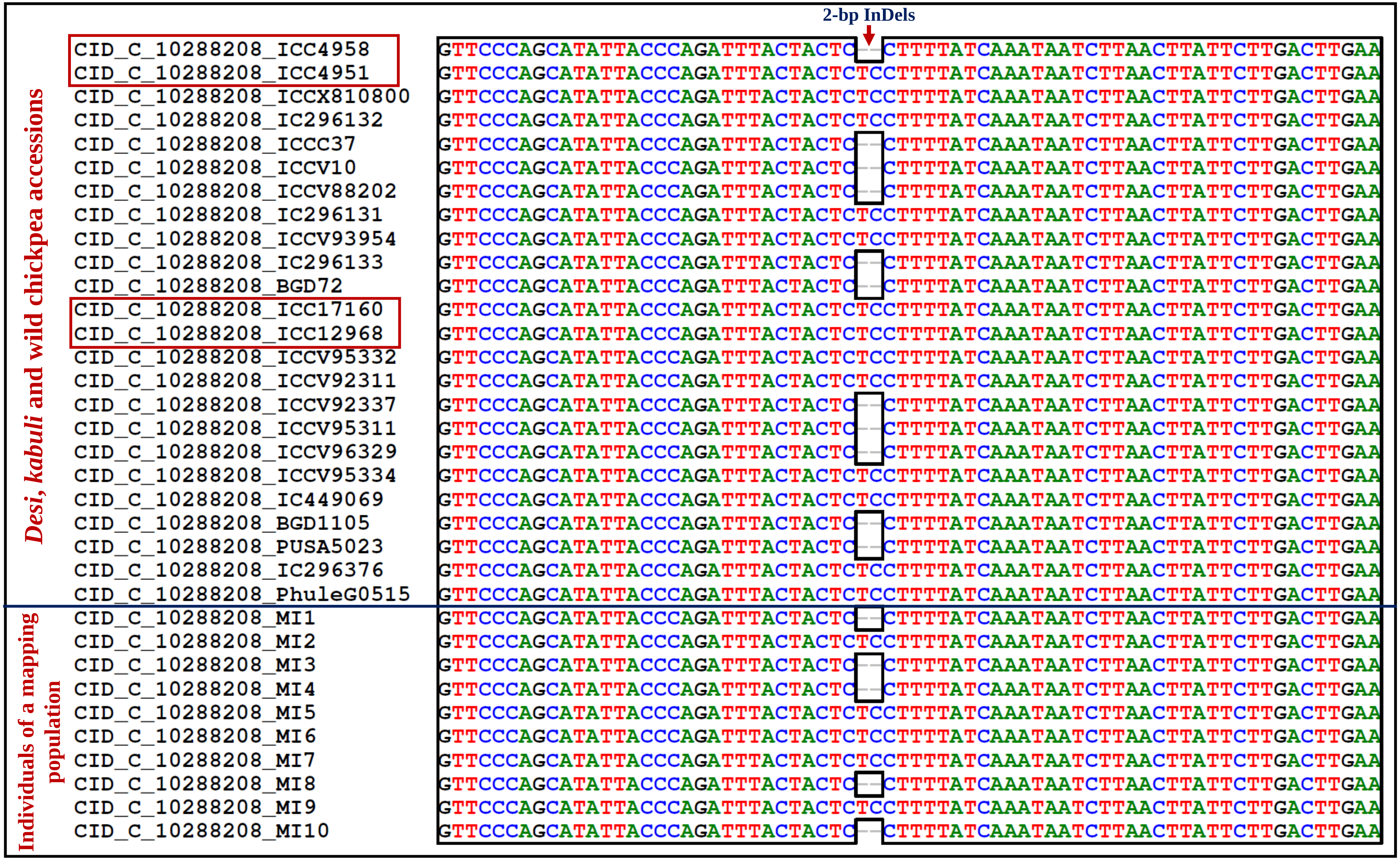

Figure S3: Multiple sequence alignment of resequeneced PCR amplicons generated from a representative set of 24 chickpea accessions and 10 individuals of a mapping population (ICC 4958 x ICC 17160) using a selected InDel marker (CID_C_10288208)-carrying *histone deacetylase* gene. This validated the presence of expected InDels, which corresponded well with our *in silico* prediction of 2-bp fragment length polymorphism commonly detected among four chickpea accessions (ICC 4958, ICC 4951, ICC 12968 and ICC 17160). The efficiency of InDel marker for large-scale validation and genotyping in a diverse set of *desi*, *kabuli* and wild chickpea accessions and individuals of a mapping population based on amplicons resequencing was apparent. The detailed information regarding InDel marker is mentioned in the Table S3.