The genome sequence of *Lactobacillus helveticus* DPC 4571, a Swiss cheese culture, was determined and revealed significant homology to non-dairy gut lactobacilli. Despite adopting notably different environments up to 75% of genes were conserved between the dairy and non-dairy strains. Most significantly there were two hundred and thirteen insertion sequences (IS) in the DPC4571 genome, ten times more than other lactobacilli. IS elements are known for promoting a variety of genetic rearrangements in microbial genomes but genome alignments demonstrated an unprecedented level of genome stability in the IS-saturated *L. helveticus* genome. The sequence diversity between the IS elements of DPC4571 indicates that the integration of the IS elements into the genome is not a recent event. Comparative genome analysis also indicated that the IS elements were not the primary agents of niche adaptation for the *L. helveticus* genome. There was a significant loss of genes involved in sugar metabolism and cell surface proteins, which are important in gut colonization, as well as the acquisition of genes involved in lipid metabolism and restriction enzymes, which are necessary for a dairy lifestyle, in DPC4571.