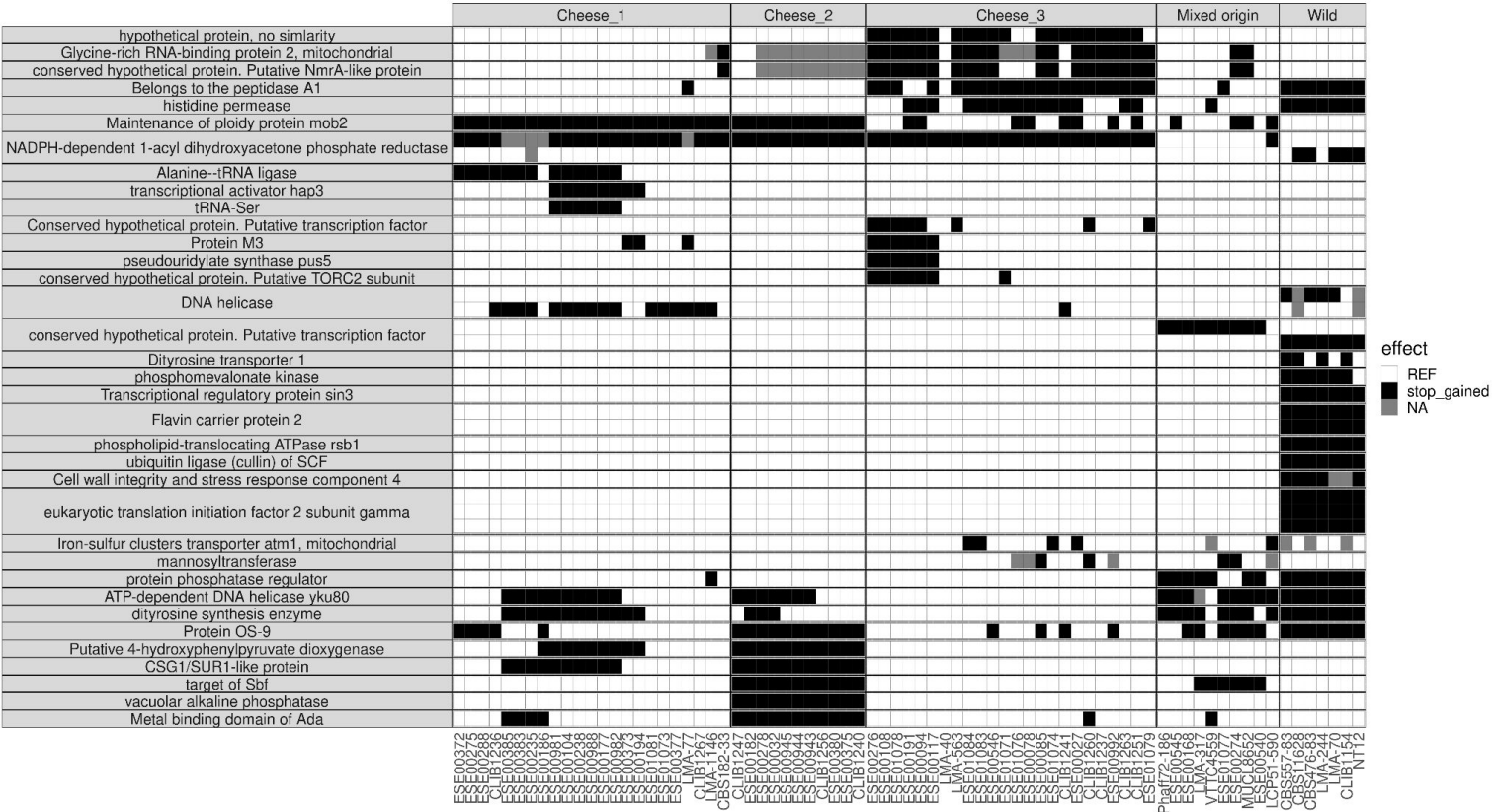


A.



B.

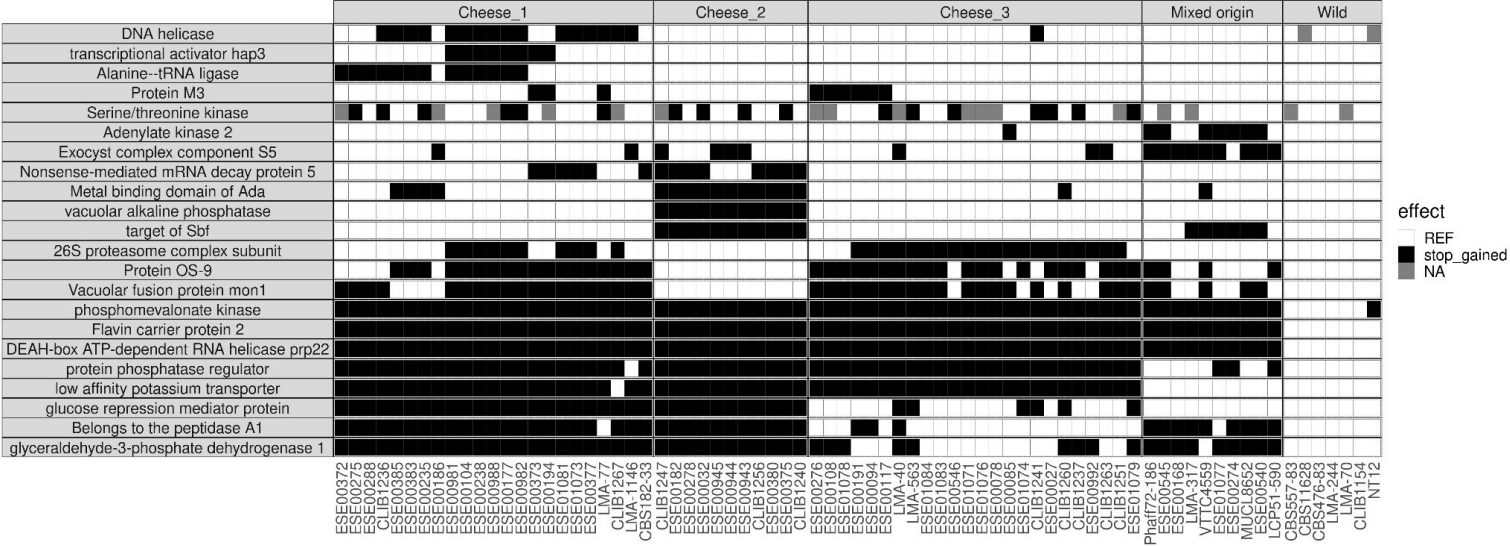


Figure S4: SNPs inducing a premature stop codon for each *Geotrichum candidum* strain.

In order to keep genes that carried a single nucleotide polymorphism (SNP) inducing a premature STOP codon in most of a population, we only showed STOP-inducing SNP that were at least in more than three strains. Columns represent strains and strains are ordered following the ML tree. Cells are colored in black when the corresponding SNP induces a premature stop codon, white when there is no substitution for this site compared to the reference genome and grey when the SNP status could not be attributed during SNP calling, substitution that induces other effects on the protein sequence were not present in this subset of STOP-inducing sites. Each row is a site, when multiple SNPs induced stop codons in the same gene, the corresponding rows were grouped and separated from other genes by black lines. The analysis was done using either the CLIB 918 (Cheese_3) genome (A) or the LMA-244 (Wild) genome (B) as a reference.