

Figure S7

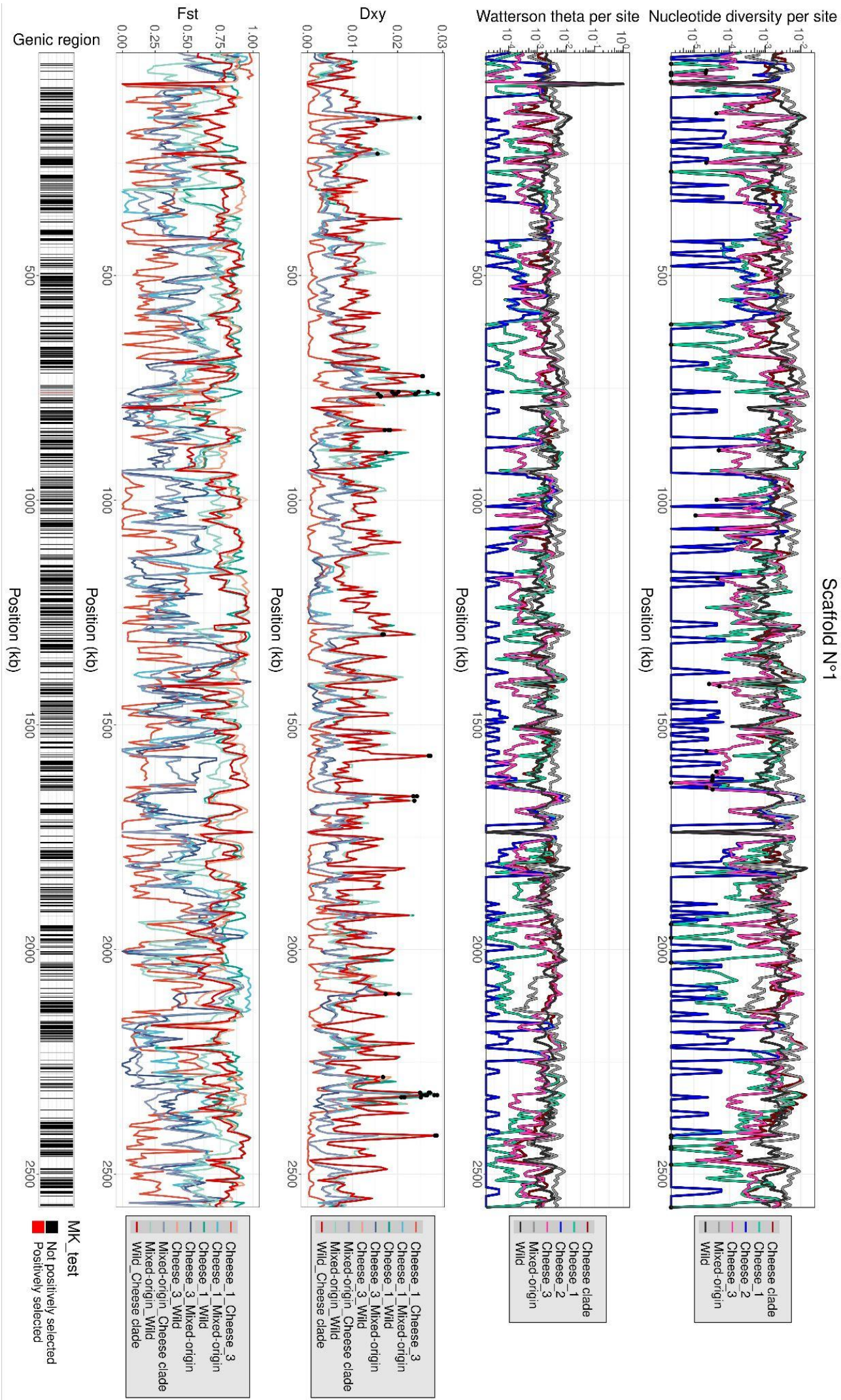


Figure S7: Genomic scan of within-population genetic diversity and between-population differentiation in *geotrichum candidum*.

Genomic of the nucleotide diversity π , watterson's theta θ_w , absolute divergence d_{xy} and fixation index F_{ST} along the scaffold 1 of the CLIB 918 reference genome. At the bottom a guide indicates genic regions in black and non genic regions in white. 7.5kb overlapping windows with a step of 5kb. On the bottom of the figure, genic regions are shown in black (not positively selected) or red (positively selected in the MK test analysis) rectangle. On the first panel (nucleotide diversity π), 5% lowest π values in the three cheese populations were highlighted by black dots. On the third panel (absolute divergence d_{xy}), 1% highest values of d_{xy} of each pairwise comparison were highlighted by back dots. These outliers were checked for gene presence and functions that could be involved in cheese adaptation and subsequently tested for enrichment within this subset of outliers compared to the whole genome