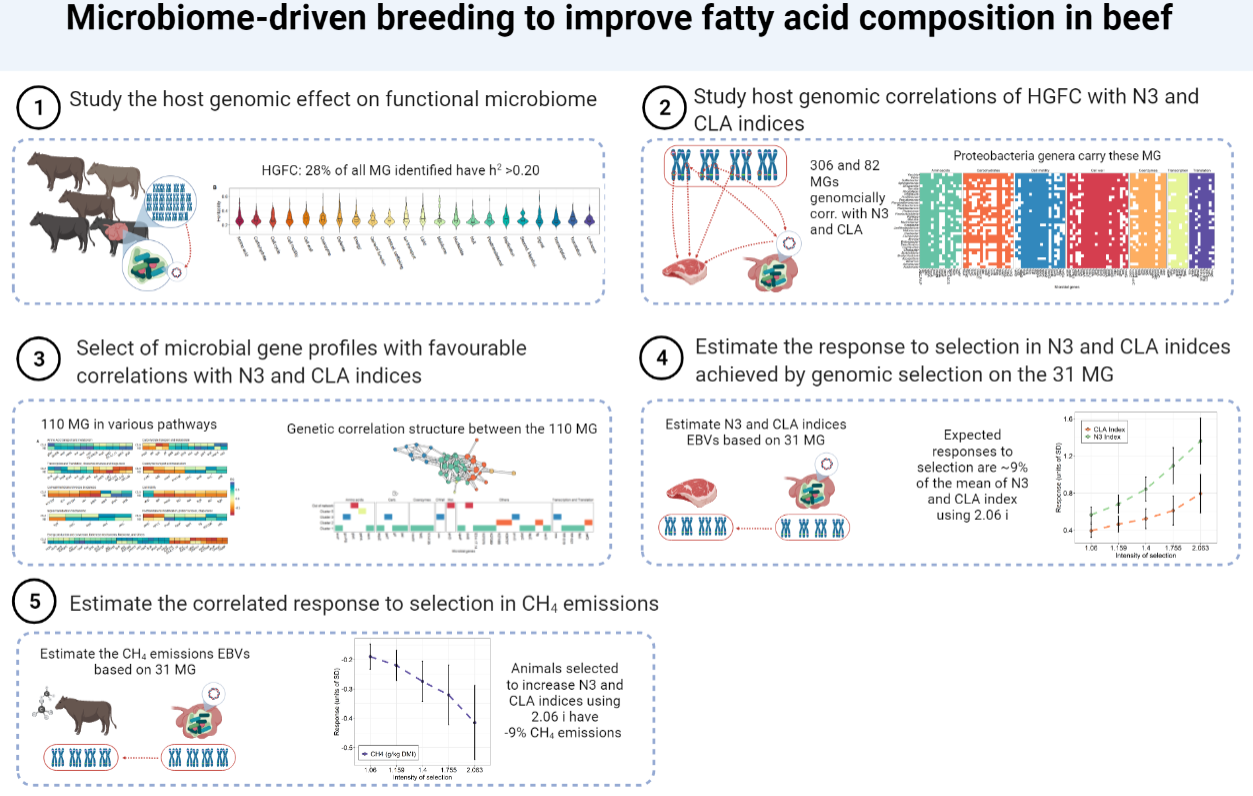
C:\Users\Marina\Documents\Dropbox\SRUC data\Work Fatty Acids\Writting\Making_Graphs\lnCLASFA and lnO3SFA-phenos_and_EBVs\CorrectedFA_coherentpalette_NEW.tiff

**Figure S1.** Distribution of N3 and CLA fatty acid indices in beef in our population. N3 index estimated as the natural logarithm of the ratio between C18:3n-3 +C20:5n-3 + C22:5n-3 + C22:6n-3 and C12:0 + C14:0 + C16:0. CLA index estimated as the natural logarithm of the ratio between *cis-9, trans-11* C18:2 + *trans-11* C18:1 and C12:0 + C14:0 + C16:0. Values are corrected by breed, diet and experiment combined effect.

C:\Users\Marina\Documents\Dropbox\SRUC data\Work Fatty Acids\Writting\Making_Graphs\ALR\359\XYGENE_K01783.tiff

**Figure S2.** Selection of the microbial gene ribulose-phosphate 3-epimerase [EC:5.1.3.1] (*rpe,* KEGG code K01783) - highlighted in red - as a denominator for additive log-ratio transformation based on a balance between maximal Procrustes correlation with the complete pairwise log-ratio geometry and minimal log-ratio variance.



**Figure S3.** Pipeline of the statistical analysis followed in the study. HGFC: host-genomically influenced functional core microbiome; MG: additive log-ratio transformed microbial gene abundances, h2: heritability estimate; CH4: methane: EBVs: host-genomic breeding values; i: selection intensity.