

Supplementary materials

NMR-based metabolomic study on *Phaseolus vulgaris* flour fermented by lactic acid bacteria and yeasts

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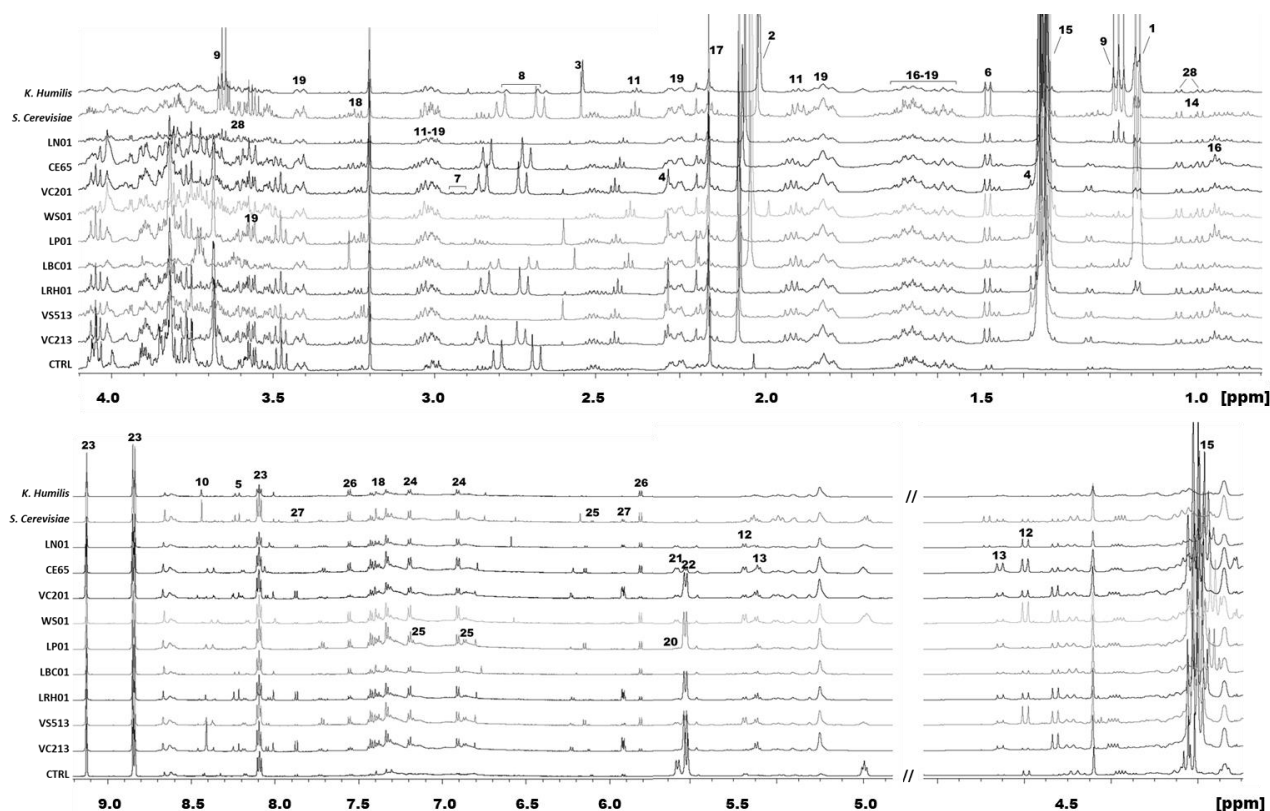


Figure S1. ¹H NMR spectra of aqueous extracts of all small-scale fermented bean flour samples, compared to control (CTRL). The numbers refer to metabolite peak assignments, as reported in Table 2.

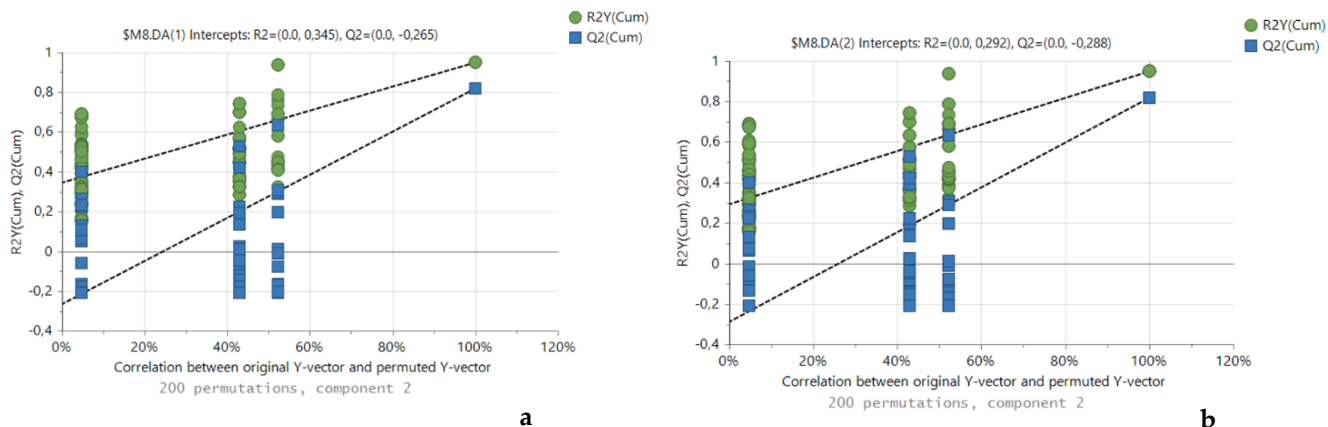


Figure S2. Permutation tests for OPLS-DA performed according to LAB metabolism, considering the complete ^1H NMR spectra, and 200 rounds of random permutations for each class: **a)** hetero- and **b)** homofermentative LAB-fermented samples.

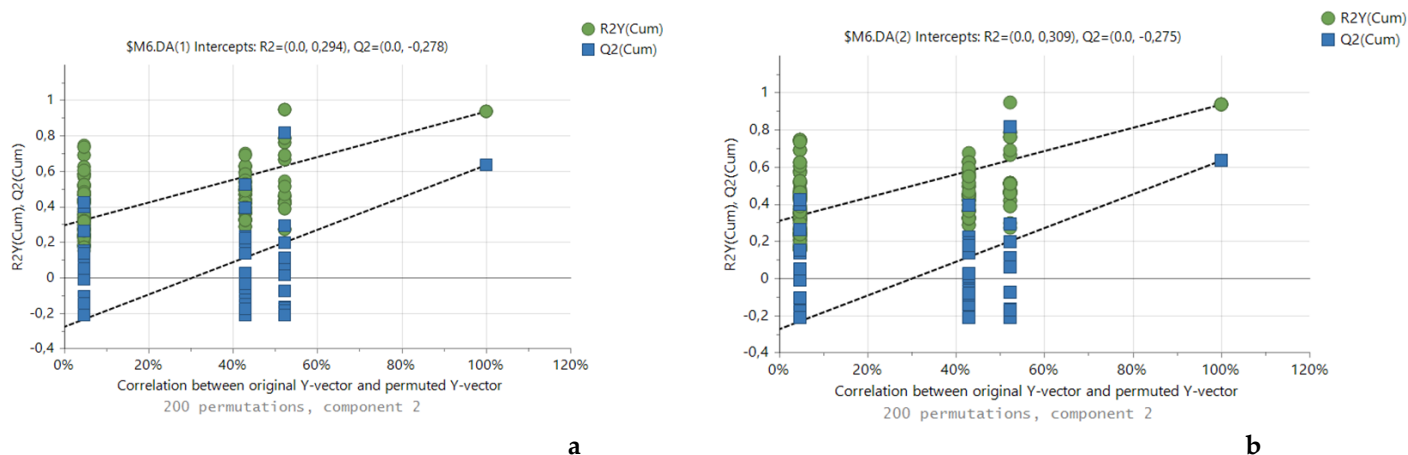
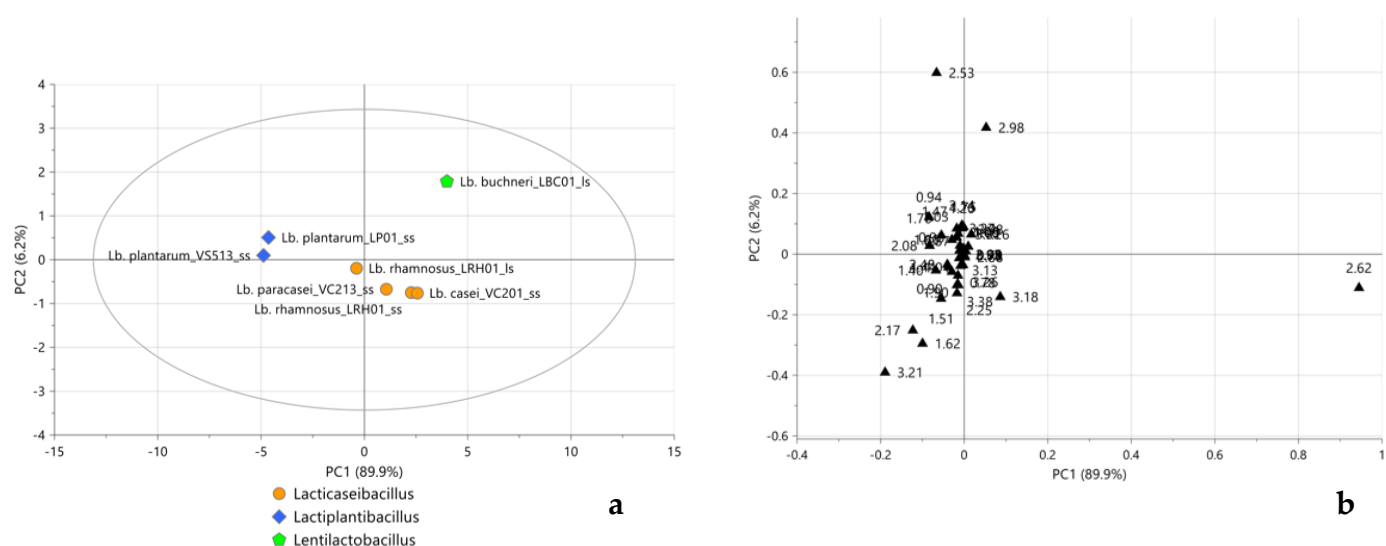
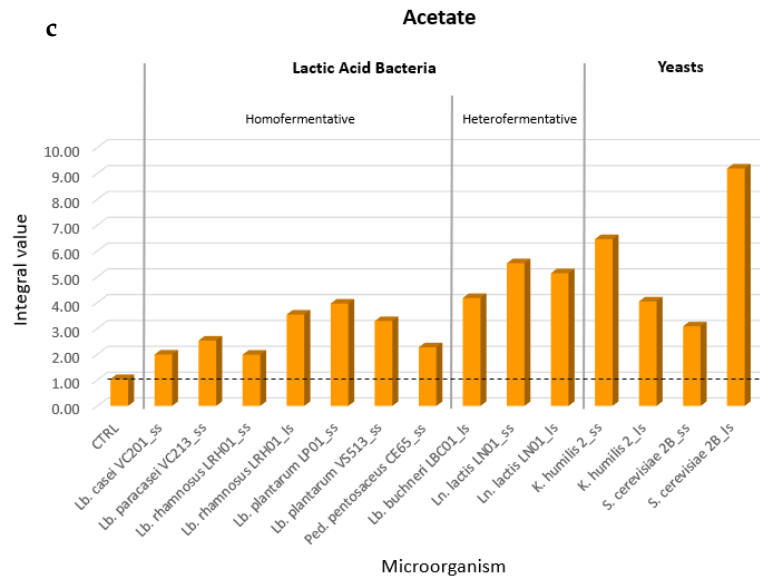
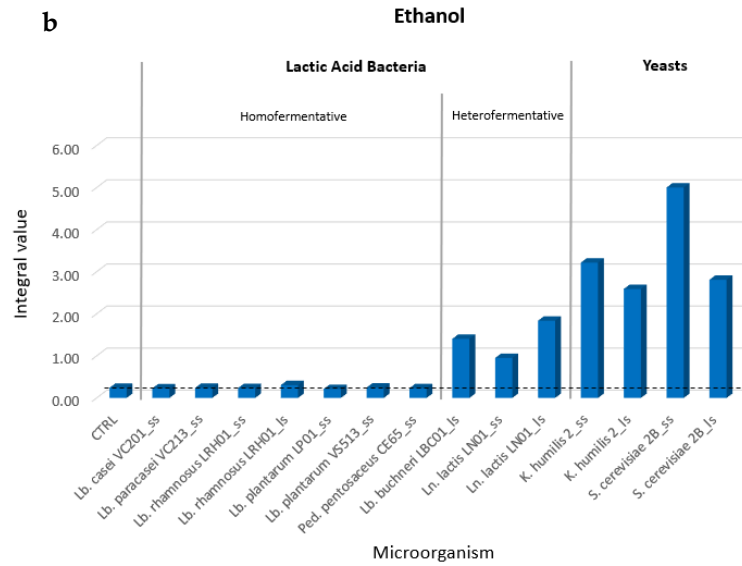
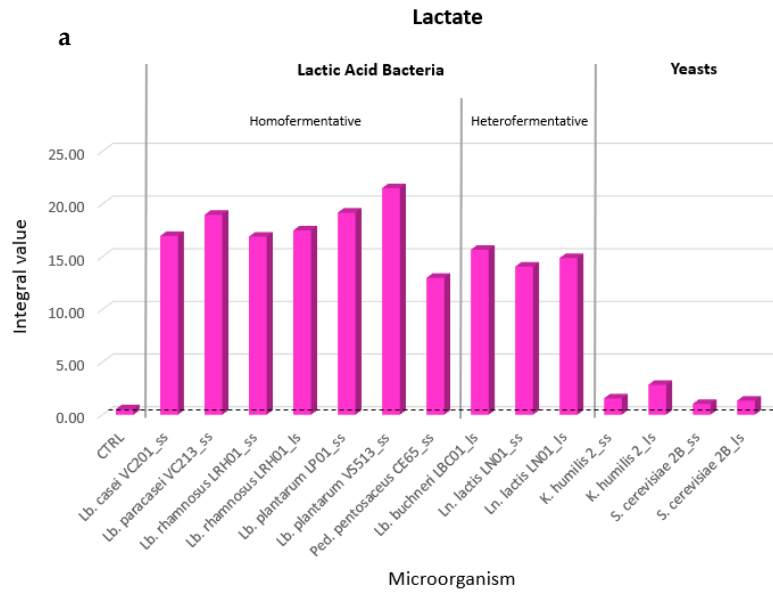


Figure S3. Permutation tests relative to PLS-DA performed according to LAB genera in the early taxonomy, considering the complete ^1H NMR spectra, and 200 rounds of random permutations for each class: **a)** *Leuconostoc* and *Pediococcus* genera, and **b)** *Lactobacillus* genus.





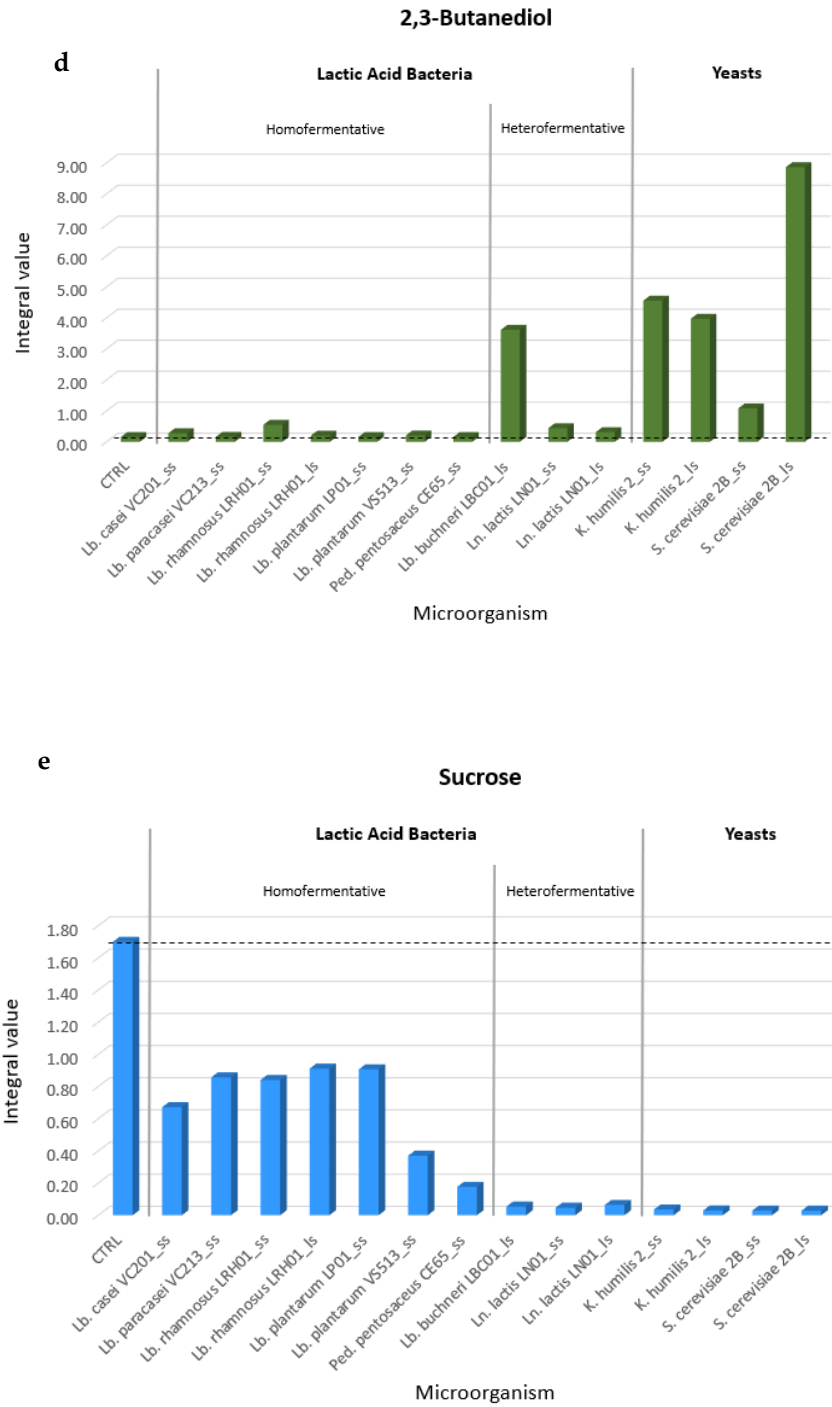


Figure S6. Quantification of the relative content (integral values normalized to the total spectral area) of fermentative metabolites: **(a)** lactate, **(b)** ethanol, **(c)** acetate, **(d)** 2,3-butanediol, and **(e)** sucrose in small- (ss) and large-scale (ls) fermented bean flours (with the exclusion of LBC01_{ss}, and WS01_{ss} samples) compared to control (CTRL). The dotted line indicates the integral value, for each metabolite, in CTRL sample.