

Impact of waste as a substrate on biomass formation, and optimisation of spent microbial biomass re-use by sustainable metabolic engineering.

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Supplementary Information

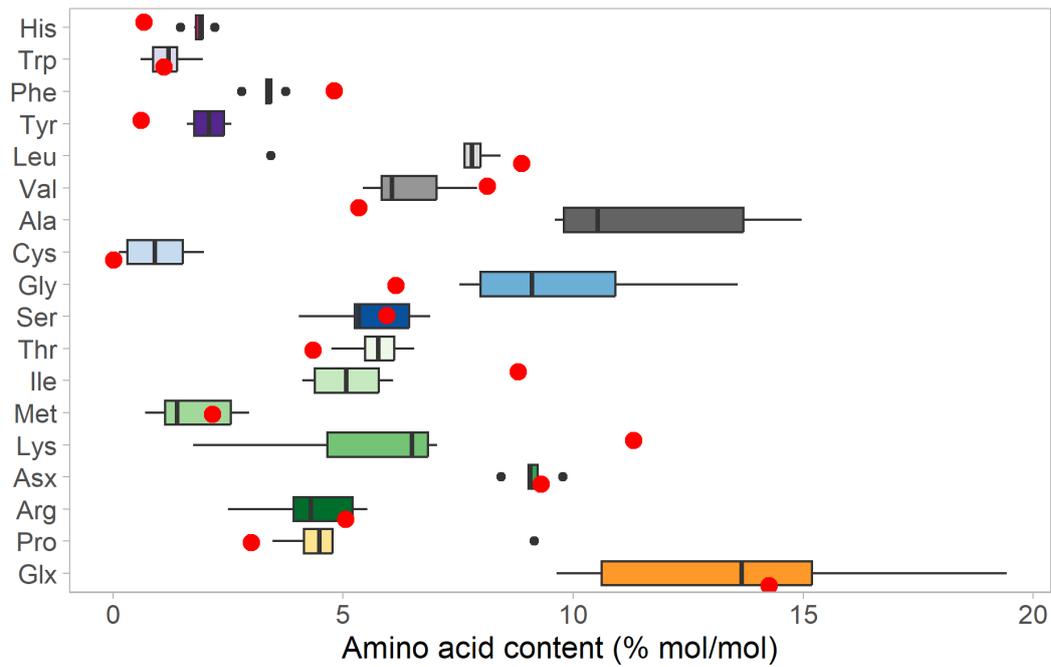


Figure S2. Variability of amino acid composition selected microorganisms and compared to composition of casamino acids (CasAA), shown as red points[18]. The median value is shown as the bold line in the middle of the box. The left and right bounds of box show the 1st and 3rd quartiles, respectively, and whiskers indicate ± 1.5 x the interquartile range (IQR). Outliers in the dataset are indicated as individual black dots. Data based on published literature on *E. coli*, *Corynebacterium glutamicum*, *Streptomyces coelicolor*, *Saccharomyces cerevisiae*, *Pichia pastoris* and *Aspergillus niger* as indicated in main article. Due to the experimental limitations some data sources do not distinguish separately Asp and Asn (pooled fraction is named Asx). Similarly, Glx represents pool of Gln and Glu.