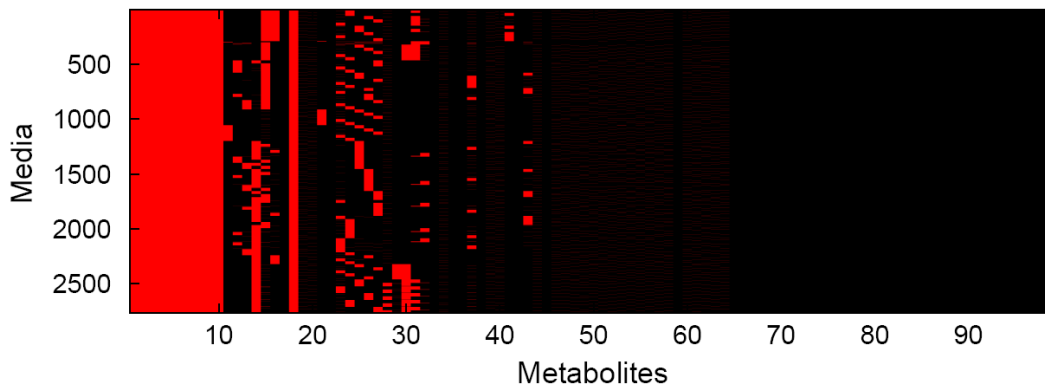
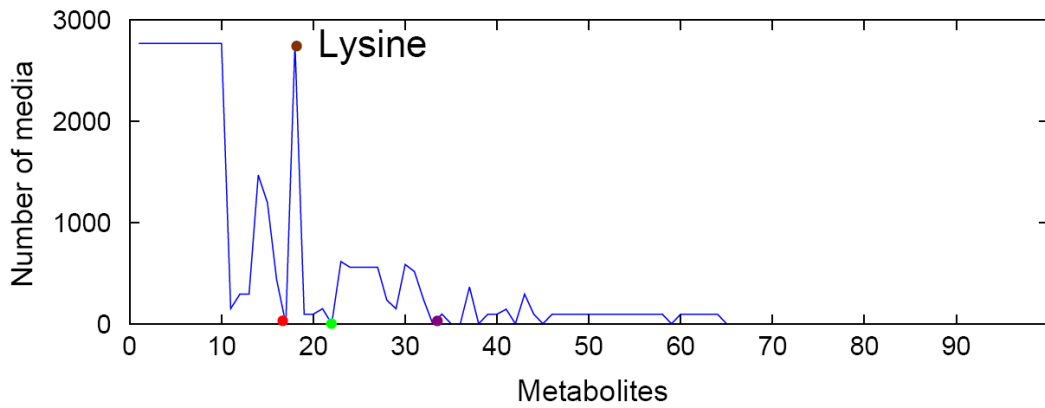


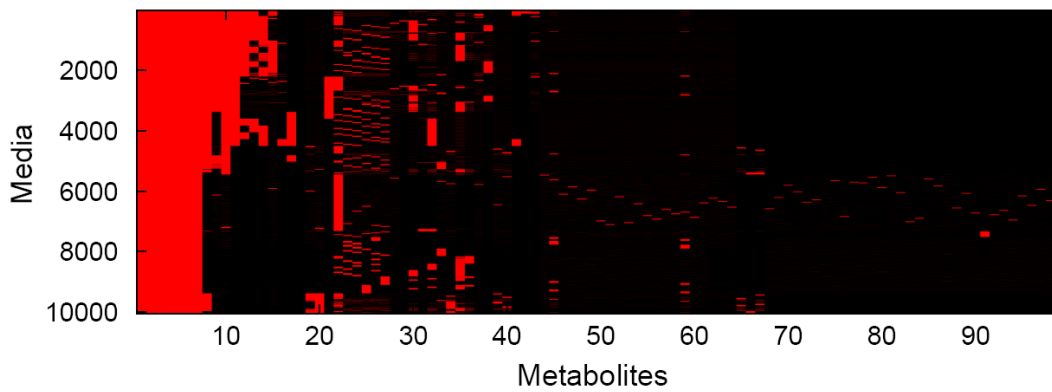
A Commensalism-Inducing Media (Lys- → Ade-)



B



C Commensalism-Inducing Media (Ade- → Lys -)



D

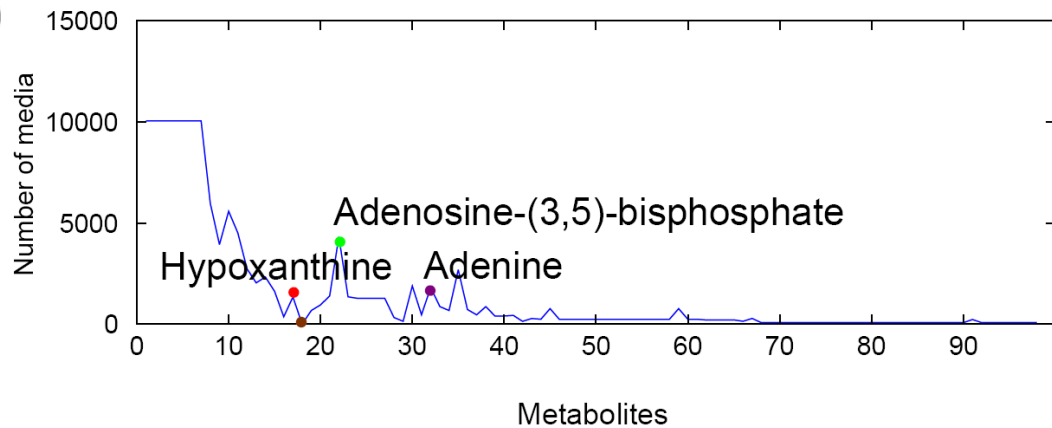


Figure S3

Metabolite usage predicted for the pair of engineered yeast strains in media that induce commensal interactions. Metabolites in all panels of this figure are clustered according to their presence in all media analyzed (see Methods).

A Binary map of metabolite usage (black = not used; red = used) across all (Lys- \Rightarrow Ade-) commensal- inducing media. A large set of metabolites is used in different combinations, forming a complex map of mutual capacities to compensate each other.

B By looking at the overall frequency of metabolite usage across all (Lys- \Rightarrow Ade-) commensalism-inducing media, one can see that lysine is always present, as expected, while adenine derivative metabolites are absent.

C The binary map (as in A) for all (Ade- \Rightarrow Lys-) commensal-inducing media.

D Frequency of metabolites across all (Ade- \Rightarrow Lys-) commensalism-inducing media. These media never contain the lysine, but do contain many adenine derivatives as is expected.