**Figure S2 – Application of invFBA to two fully coupled reactions in long-term evolved *E. coli* strains**

A projection (onto a two dimensional subspace) of the set of objective functions compatible with experimentally measured fluxes. The graph is obtained through a two-dimensional version of OVA: for each possible value of the growth flux coefficient of the objective function ($c_{\text{Biomass}}$), one can find the minimal and maximal value of the objective function coefficient for the transaldolase (Left, $c_{\text{Transaldolase}}$) or transketolase (Right, $c_{\text{Transketolase}}$) flux, obtaining areas that correspond to objective functions compatible with the measured fluxes. Such regions can be computed for the ancestral and all evolved *E. coli* strains. As shown in Table S5, the fluxes through these reactions are identical for each evolved *E. coli* strain, as one would expect from two fully coupled reactions.