Protocol S6. Monochromatic analysis

The monochromatic analysis on the high-confidence GIs was performed essentially as described

[1]. Briefly, a monochromatic score was computed for each pairwise process using the ratio of

aggravating to alleviating GIs based on their overall distribution in the high confidence GI

network. The following equation was used to compute the monochromatic score: $\frac{1}{n}\sum xn$,

where n is the total number of interactions observed between processes, and $xn = 1$ for

alleviating and -1 for aggravating. To identify the monochromatic GIs between processes, we

used MultiFun schema to group the recipient genes into 321 distinct categories, including a

functional grouping for 'unknown' genes, whereas the donor query genes were grouped into 11

core bacterial processes as defined in Table S1. In total, we tested 2,693 process pairs that are

associated with epistatic connections between the donor and recipient functional groups. We then

employed Fishers two-sided exact test (p-value ≤ 0.05) to delineate the genuine monochromatic

GIs between processes. Of the 2,693 tested pairs, we found that 125 non-redundant MultiFun

processes based on the recipient genes tended to exhibit significant (p-value ≤ 0.05)

monochromatic relationships with 11 donor core bioprocesses.

References:
1. Michaut M, Baryshnikova A, Costanzo M, Myers CL, Andrews BJ, et al. (2011) Protein complexes are central in the yeast genetic landscape. PLoS Comput Biol 7: e1001092.