**Table S3:** MiMBL-predicted epistatic interactions within *S. cerevisiae* genome-scale metabolic model [1].Simulations were performed using two alternative representations of stoichiometry, *S0* and *S1* (**Methods**). The yeast genome-scale metabolic model was constrained as in Szappanos *et al.* 2011.

|  |  |  |
| --- | --- | --- |
|  | ***S0*** | ***S1*** |
| Positive interactions | 2019 | 2019 |
| Negative interactions | 811 | 811 |
| Synthetic lethals | 198 | 198 |
| Total number of interactions | 89676 | |