**Table S2:** lMoMA-predicted epistatic interactions within *S. cerevisiae* genome-scale metabolic model [1].Simulations were performed using three alternative representations of stoichiometry, *S0*, *S1* and *S2* (**Methods**). The yeast genome-scale metabolic model was constrained as in Szappanos *et al.* 2011.

|  |  |  |  |
| --- | --- | --- | --- |
|  | ***S0*** | ***S2*** | ***S1*** |
| Positive interactions | 2219 | 2154 | 2087 |
| Negative interactions | 840 | 781 | 742 |
| Synthetic lethals | 197 | 217 | 97 |
| Total number of interactions | 89676 | | |