**Table S1:** Number of lMoMA-predicted lethal gene/reaction knockouts in *S. cerevisiae* that differ between alternative representation of stoichiometry (*S1* and *S2*), relative to *S0* (**Methods**). The yeast genome scale model [1] was constrained as per Szappanos *et al*, 2011, and FBA was used to generate the reference flux distributions. Single, double and triple gene/reaction deletions were simulated.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Number of Deletions | ***S2*** | | ***S1*** | | Total number of combinations | |
| Reactions | Genes | Reactions | Genes | Reactions | Genes |
| 1 | 0 | 0 | 4 | 3 | 387 | 424 |
| 2 | 0 | 13 | 1526 | 1166 | 74691 | 89676 |
| 3 | 189 | 4565 | 289664 | 225548 | 9585345 | 12614424 |