



Figure S1. Yeast protein-protein interaction networks of proteins whose absence render cells resistant to MMS. Non-essential proteins are in red, essential proteins in green.

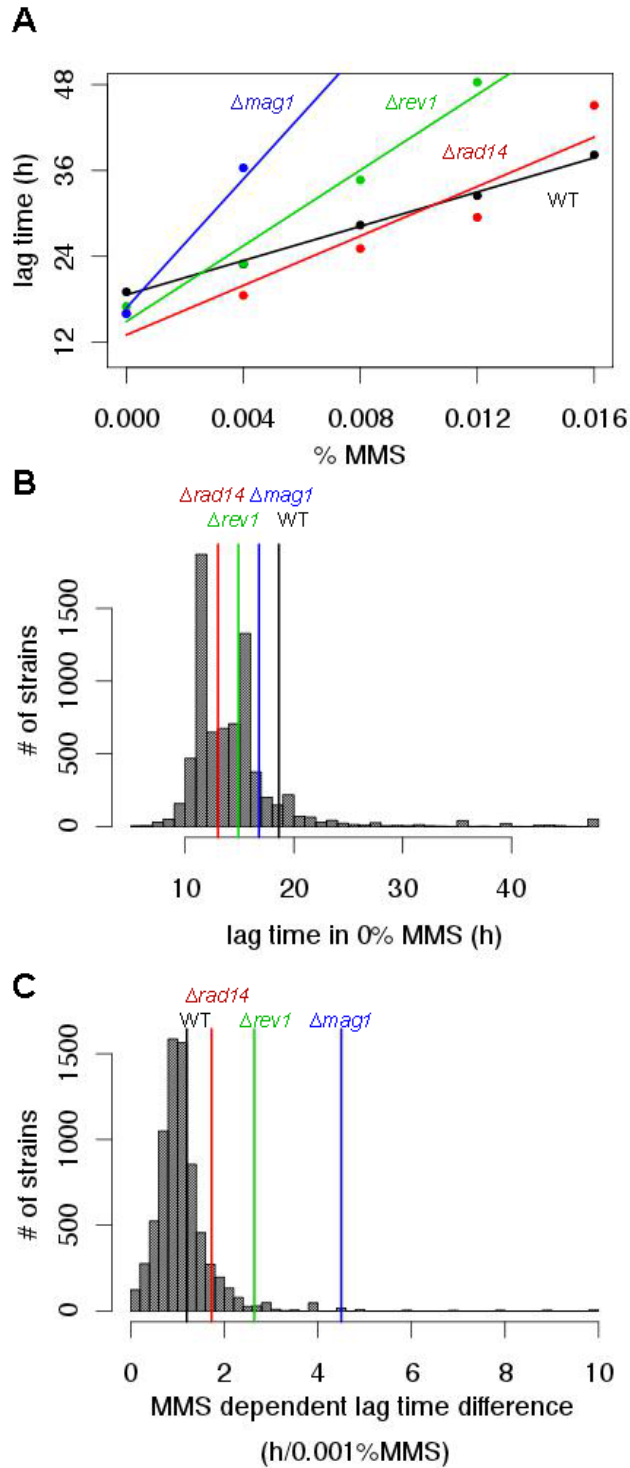


Figure S2. A) Lag time data for the four control strains at the different doses B) Histogram of lag times for the entire strain collection C) Histogram of the MMS dependency of the lag times for the entire strain collection.

A**genomic phenotyping**

You can search for a specific gene name or ORF by typing it in the box below and clicking on the search button.

 MMS

You can also type any word to search for it in a listing of descriptions.

 any sensitivity to

5 strains satisfy criteria.

[YER142C](#) - MAG1 - 3-methyl-adenine DNA glycosylase involved in protecting DNA against alkylating agents; initiates base excision repair by removing damaged bases to create abasic sites that are subsequently repaired
[YAL015C](#) - NTG1 - DNA N-glycosylase and apurinic/apyrimidinic (AP) lyase involved in base excision repair; distribution between nucleus and mitochondrion varies according to which compartment is under oxidative stress and is also sumoylation-dependent
[YOL043C](#) - NTG2 - DNA N-glycosylase and apurinic/apyrimidinic (AP) lyase involved in base excision repair, localizes to the nucleus; sumoylated
[YML060W](#) - OGG1 - Mitochondrial glycosylase/lyase that specifically excises 7,8-dihydro-8-oxoguanine residues located opposite cytosine or thymine residues in DNA, repairs oxidative damage to mitochondrial DNA, contributes to UVA resistance
[YML021C](#) - UNG1 - Uracil-DNA glycosylase, required for repair of uracil in DNA formed by spontaneous cytosine deamination, not required for strand-specific mismatch repair, cell-cycle regulated, expressed in late G1, localizes to mitochondria and nucleus

[Download](#) spreadsheet with data for all strains

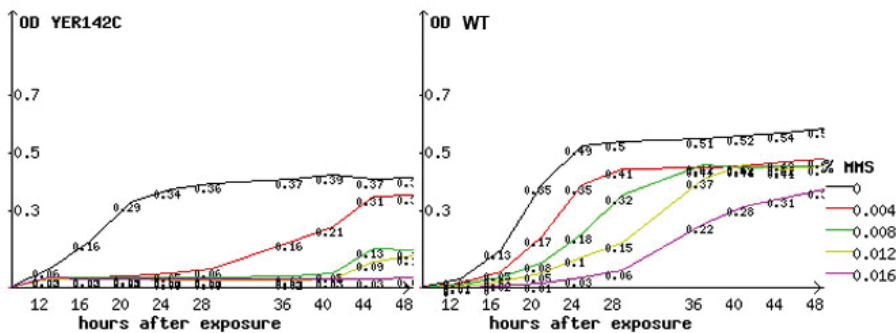
B**genomic phenotyping**

Standard Name: **MAG1**

Alias: **MMS5**

Systematic Name: **YER142C**

GI50: **0.0048% MMS**



YER142C shows **high** sensitivity to MMS

Description: 3-methyl-adenine DNA glycosylase involved in protecting DNA against alkylating agents; initiates base excision repair by removing damaged bases to create abasic sites that are subsequently repaired
 Click [here](#) for more information from SGD

Figure S3. Screenshot of genomic phenotyping website. A) A searchable interface to find any queried strain by systematic name, common name or word used in SGD description (www.yeastgenome.org). B) The search results include both data from individual experiments and averaged data of queried strain and a comparison to the growth of the wildtype strain. Links to SGD and previous data on solid agar (Begley et al. 2004) are provided for additional information.

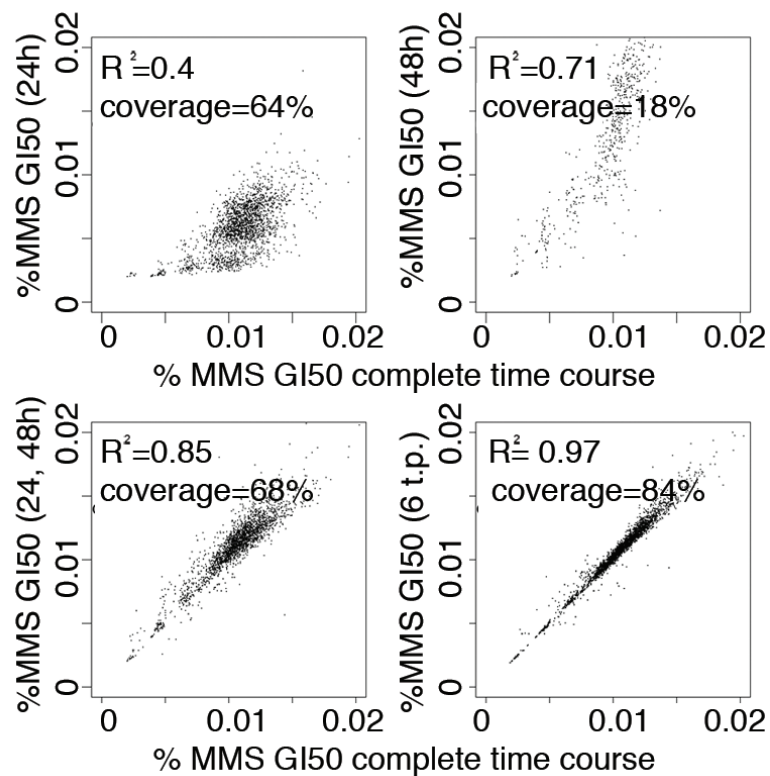


Figure S4. Scatterplots showing the influence of the sensitivity measurements when data composed of a selection of time-points are compared to the full time-course experiment. The tested series are 24h only, 48h only, 24 and 48h and 6 time points (t.p.) i.e. 16, 20, 24, 40, 44, 48h. The goodness-of-fit (R^2) between the two data sets and the coverage as calculated by the percentage of strains passing the linearity criterion ($R^2 > 0.7$ in at least two replicates) for the dose-response.