

<b>Gene / ORF</b>	<b>q value</b>	<b>Viability / Mutant phenotype</b>
<i>CDC33</i> / YOL139C (eIF4E)	0.04	E. / g. d.
<i>GCD1</i> / YOR260W	0.04	E. / g. d.
<i>GCD2</i> / YGR083C	0.04	E. / g. d.
<i>GCD11</i> / YER025W	0.04	E. / g. d.
<i>SUI3</i> / YPL237W	0.03	E. / g. d.
<i>TIF3</i> / YPR163C	0.04	N. E.
<i>TIF11</i> / YMR260C	0.04	E. / g. d.
<i>TIF34</i> / YMR146C	0.05	E.
<i>TIF35</i> / YDR429C	0.04	E. / g. d.
<i>TIF4631</i> / YGR162W	0.04	N. E. / g. d.
<i>TIF5</i> / YPR041W	0.04	E. / g. d.
<i>NIP1</i> / YMR309C	0.04	E. / g. d.
<i>PRT1</i> / YOR361C	0.04	E. / g. d.
<i>RPG1</i> / YBR079C	0.02	E. / g. d.

**Table S8**

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**Table S8. Growth-rate-regulated significance (q value; obtained by ANCOVA analysis) of transcription of genes involved in translational initiation (formation and regulation of the eIF4E-cap complex), and mutant phenotypes from corresponding systematic deletion mutants.** Nomenclature: *CDC33* (or eIF4E), cytoplasmic mRNA cap binding protein; *TIF* genes, Translation Initiation Factors; *GCD* genes, General Control Derepressed translation initiation factors; *SUI3*, beta subunit of the translation initiation factor eIF2, involved in the identification of the start codon; *NIP1*, translation initiation factor eIF3 subunit; *PRT1* (or *CDC63*), subunit of the core complex of translation initiation factor 3 (eIF3); *RPG1*, subunit of the core complex of translation initiation factor 3 (eIF3). Abbreviations: N. E., non-essential gene; E, essential gene; g. d., gene disruption resulting in either inviable or growth defect phenotype in functional genomics systematic deletion studies under different conditions (Affymetrix annotation, July 12<sup>th</sup>, 2006; SGD [5]).