

This Supplemental materials file contains code used in the analysis and figure construction of “Copy number variation alters local and global mutational tolerance”.

Supplemental code and (where necessary additional data objects required for the analysis) have been provided, separated into thematic folders based on the experiment, analysis, and project:

SCode1_

SCode2_Growth_rate_analysis

Files associated with the calculation of growth rates in YPGal, YPGal + CCCP and Glutamine limited media. Code for the generation of Figures 1B,C; 3D,E; and Supplemental Figures S3, S15B, S26

SCode3_RNAseq_analysis

Files associated with RNAseq analysis, including the replicate correlation, copy-number correction, DESeq2, and the GSEA. Code for the generation of Figure 4; and Supplemental Figures S4, S15A, S16, S17, S18, S25

SCode4_Hermes_analysis

Files associated with the analysis of HERMES data, including the conversion from alignments to unique insertion sites, replicate correlation, copy-number correction, and DESeq2. Code for the generation of Figure 2B; 3A,C; and Supplemental Figures S6, S7, S8, S9, S10, S11, S12, S13

SCode5_Tn_to_GSEA

Files associated with the GSEA of HERMES data, including DESeq2, heatmap plots, GSE and GSEA GO term compression. Code for the generation of Figure 3B and Supplemental Figures S14

SCode6_Compare_to_Prev

Files associated with comparison of gene set expression data between this study and previous studies. Code for the generation of Figure 5 and Supplemental Figures S19, S20, S21, S22, S23, S24

SCode7_Miscellaneous_analysis

Files not associated with any single or substantial aspect of analysis, including downstream TF analysis, ncRNA enrichment, and zscore calculation. No association with any figures.

Figure source data and code used in analysis

Figure 1A

Data from: [10.1128/mra.00729-22](https://doi.org/10.1128/mra.00729-22)

Figure 1B

Data from: [10.1371/journal.pbio.3000069](https://doi.org/10.1371/journal.pbio.3000069)

"Fitness_Final_Lauer2018.csv" from: journal.pbio.3000069.s009

Analyzed by:

SCode2_Growth_rate_anaylsis/Growth_rate_summary.rmd

Section "Figure 1B"

Figure 1C

Raw Data:

SCode2_Growth_rate_anaylsis/growth_curves/

Analyzed by:

SCode2_Growth_rate_anaylsis/Growth_rate_summary.rmd

Section "Figure 1C"

Figure 2B

Normalized insertions per gene from Supplemental_Table_S9

Analyzed by:

SCode4_Hermes_analysis/Make_Fig2B.py

Figure 3A

Normalized strain insertion data from: Supplemental_Table_S9

Analyzed by:

SCode4_Hermes_analysis/Make_Fig3A.rmd

Figure 3B

Normalized strain insertion data from: Supplemental_Table_S9

All data is located in SF5_Tn_to_GSEA/

Analyzed by:

SCode5_Tn_to_GSEA/make_gse.r

SCode5_Tn_to_GSEA/make_compressed.py

SCode5_Tn_to_GSEA/make_insert_GSEA.py

Figure 3C

Normalized strain insertion data from: Supplemental_Table_S9

Analyzed by:

SCode4_Hermes_analysis/Make_Fig3C.rmd

Figure 3D

Raw Data:

SCode2_Growth_rate_anaylsis/growth_curves/

Analyzed by:

SCode2_Growth_rate_anaylsis/functions.r

SCode2_Growth_rate_anaylsis/Growth_rate_summary.rmd

Section "Figure 3D"

Figure 3E

Raw Data:

SCode2_Growth_rate_anaylsis/growth_curves/

Analyzed by:

SCode2_Growth_rate_anaylsis/functions.r

SCode2_Growth_rate_anaylsis/Growth_rate_summary.rmd

Section "Figure 3E"

SCode2_Growth_rate_anaylsis/errorBars/errorBars*_mult.py

Figure 4

Normalized expression data from: Supplemental_Table_S23

Analyzed by:

SCode3_RNAseq_analysis/ Make_Fig4.py

Figure 5

All previously published data is located in SF6_Compare_to_Prev/

Analyzed by:

SCode6_Compare_to_Prev/Compare_to_Previous_Studies.rmd

Supplemental_Fig_S1

Based on previously published data: 10.1128/mra.00729-22

Supplemental_Fig_S2

Based on previously published data: 10.1128/mra.00729-22

Supplemental_Fig_S3

Copy-number sizes from Supplemental_Table_S4

Relative fitness in glutamine limited media from:

“Fitness_Final_Lauer2018.csv” from: journal.pbio.3000069.s009

Relative growth rate (YPGal) from

rel_growth_YPGal.csv from

Analyzed by:

SCode2_Growth_rate_anaylsis/Growth_rate_summary.rmd

Supplemental_Fig_S4

Copy-number sizes from Supplemental_Table_S4

TPM data from Supplemental_Table_S28

DESeq2 data from Supplemental_Table_S23, Supplemental_Table_S24

Analyzed by:

SCode3_RNAseq_analysis/Make_Supplemental_Core_Figure.py

Supplemental_Fig_S6

CDS lengths for each gene derived from SGD peptide sequences.

Insertion medians calculated from Supplemental_Table_9

Analyzed by:

SCode4_Hermes_analysis/Make_Supplemental_Fig_S6.r

Supplemental_Fig_S7

Strain insertion data from: Supplemental_Table_S8

Analyzed by:

SCode4_Hermes_analysis/Make_Supplemental_Fig_S7.py

Supplemental_Fig_S8

Essential ORFs from Winzeler 1999

Normalized strain insertion data from: Supplemental_Table_S9

Analyzed by:

SCode4_Hermes_analysis/Make_Supplemental_Fig_S8.py

Supplemental_Fig_S9

Essential ORFs from Winzeler 1999

Quartile essential ORFs from Costanzo et al 2021

Strain insertion data from: Supplemental_Table_S8

Analyzed by:

SCode4_Hermes_analysis/Make_Supplemental_Fig_S9.Rmd

Supplemental_Fig_S10

Normalized strain insertion data from: Supplemental_Table_S9

Analyzed by:

SCode4_Hermes_analysis/Make_Supplemental_Fig_S10.Rmd

Supplemental_Fig_S11

Normalized strain insertion data from: Supplemental_Table_S9

Analyzed by:

SCode4_Hermes_analysis/Supplemental_Fig_S11_Make_Insert_R-squared.r

SCode4_Hermes_analysis/Make_Supplemental_Fig_S11.py

SCode4_Hermes_analysis/Supplemental_Fig_S11_Enrichment_of_outliers.py

Supplemental_Fig_S12

Normalized strain insertion data from: Supplemental_Table_S9

Analyzed by:

SCode4_Hermes_analysis/Make_Supplemental_Fig_S12.py

Supplemental_Fig_S13

Copy number per gene from Supplemental_Table_S6

Normalized strain insertion data from: Supplemental_Table_S9

Analyzed by:

SCode4_Hermes_analysis/Make_Supplemental_Fig_S13.r

Supplemental_Fig_S14

Normalized strain insertion data from: Supplemental_Table_S9

All data is located in SF5_Tn_to_GSEA/

Analyzed by:

SCode5_Tn_to_GSEA/make_gse.r

SCode5_Tn_to_GSEA/make_compressed.py

SCode5_Tn_to_GSEA/make_insert_GSEA.py

Supplemental_Fig_S15A

RNA read abundance from: Supplemental_Table_S21

Analyzed by:

SCode3_RNAseq_analysis/Make_Supplemental_Fig_S15.rmd

Supplemental_Fig_S15B

Raw Data:

SCode2_Growth_rate_anaylsis/growth_curves/

Analyzed by:

SCode2_Growth_rate_anaylsis/functions.r

SCode2_Growth_rate_anaylsis/Growth_rate_summary.rmd

Section "Figure 3E"

SCode2_Growth_rate_anaylsis/errorBars/errorBars*_additive.py

Supplemental_Fig_S16

RNA read abundance from: Supplemental_Table_S21

Analyzed by:

SCode3_RNAseq_analysis/Make_Supplemental_Fig_S16.rmd

Supplemental_Fig_S17

RNA read abundance from: Supplemental_Table_S21

Normalized strain insertion data from: Supplemental_Table_S9

Analyzed by:

SCode3_RNAseq_analysis/Make_Supplemental_Fig_S17.r

Supplemental_Fig_S18

TPM normalized RNA from Supplemental_Table_S22

Copy number per gene from Supplemental_Table_S6

Analyzed by:

SCode3_RNAseq_analysis/Make_Supplemental_Fig_S18.r

Supplemental_Fig_S19, Supplemental_Fig_S20, Supplemental_Fig_S21, Supplemental_Fig_S22, Supplemental_Fig_S23, Supplemental_Fig_S24

All previously published data is located in SF6_Compare_to_Prev /

Analyzed by:

SCode6_Compare_to_Prev/Compare_to_Previous_Studies.rmd

Supplemental_Fig_S25

Using DESeq2 data from SCode3_RNAseq_analysis/Supplemental_File_DESeq_for_GSEA/

Analyzed by:

SCode3_RNAseq_analysis/make_gse_for_rna.r

Supplemental_Fig_S26

Raw Data:

SCode2_Growth_rate_anaylsis/growth_curves/

Analyzed by:

SCode2_Growth_rate_anaylsis/functions.r

SCode2_Growth_rate_anaylsis/Growth_rate_summary.rmd

Section "Effect of CCCP"