

Appendix

Genetic interaction profiles of regulatory kinases differ between environmental conditions and cellular states

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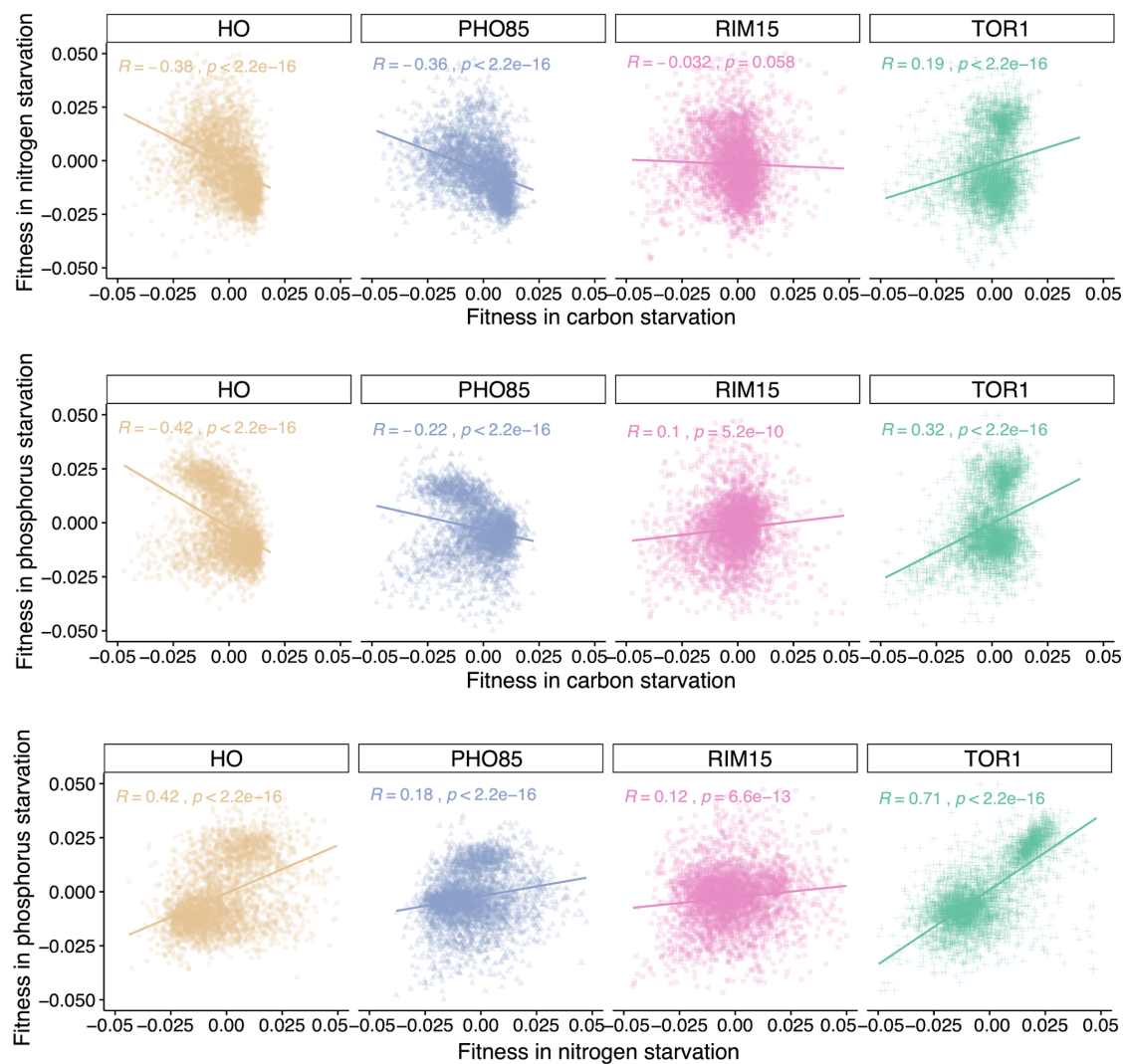
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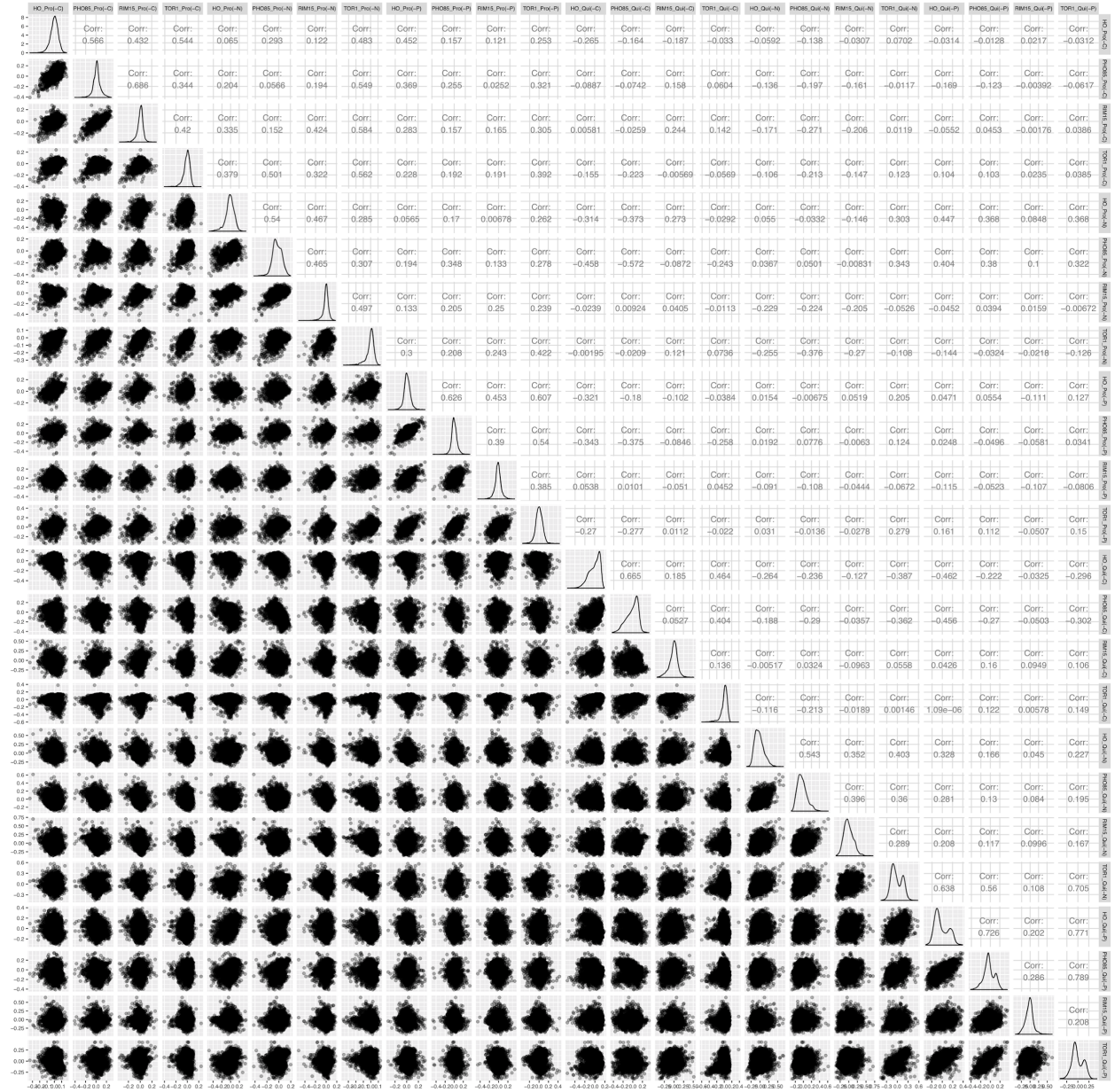
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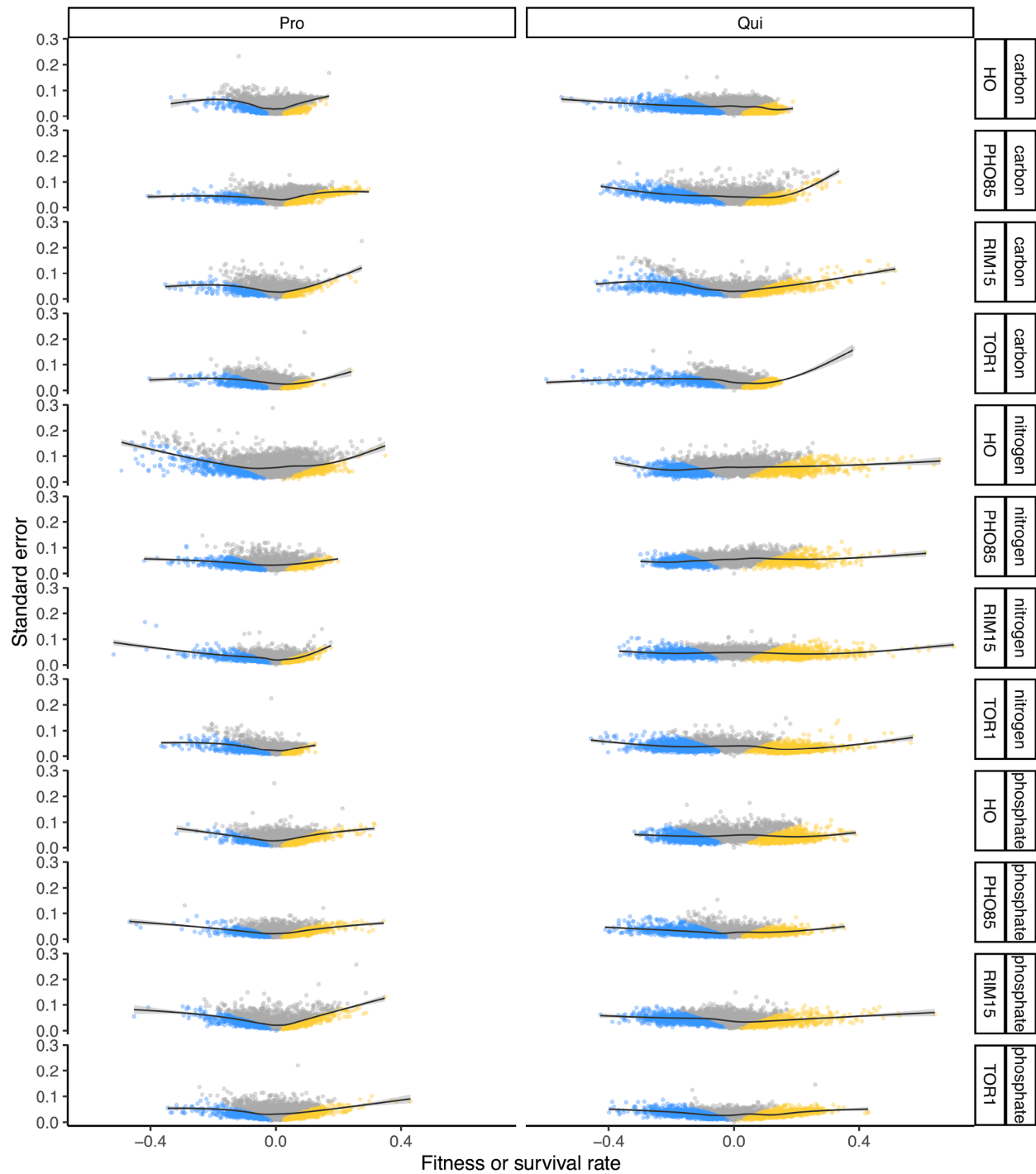
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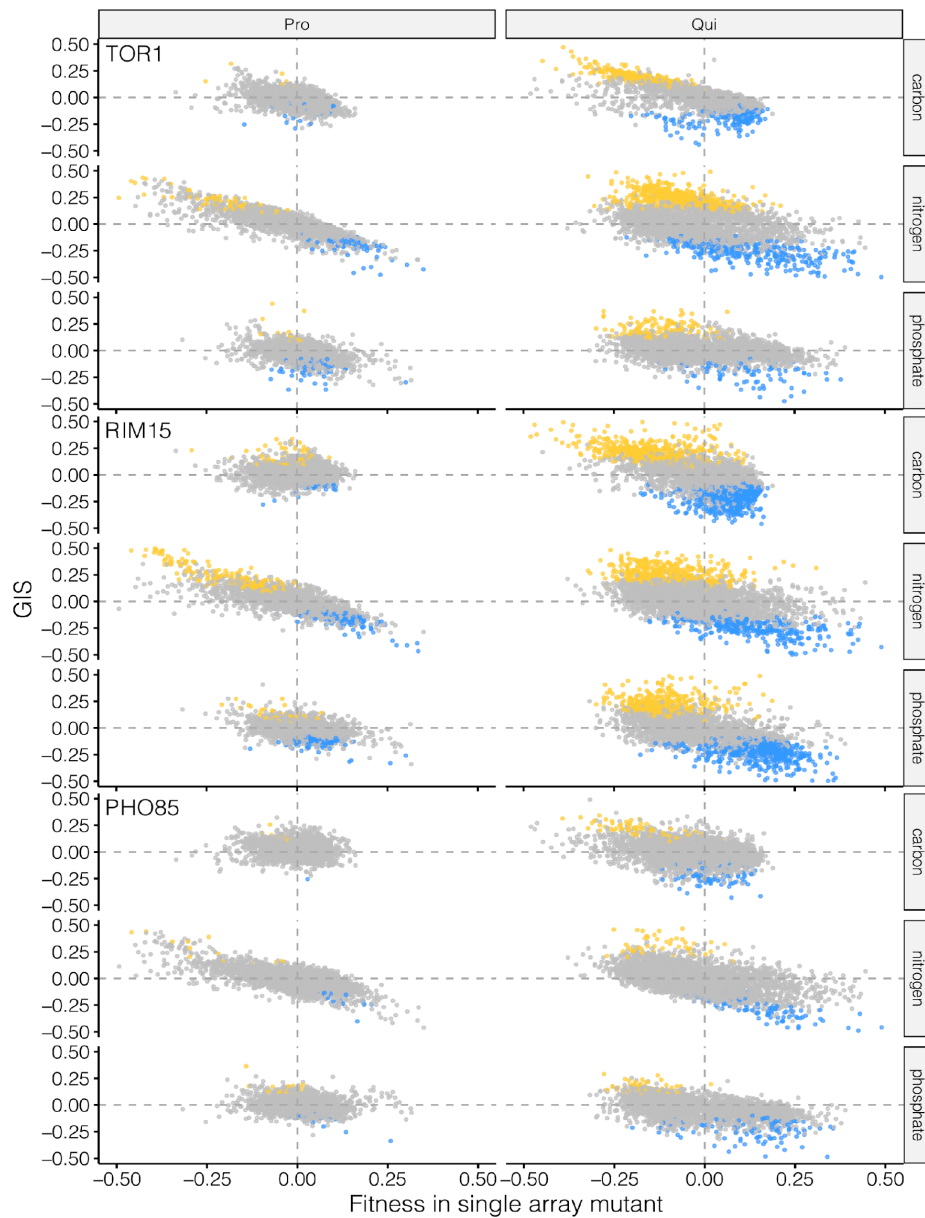


Appendix FigureS1. Correlation of fitness profiles for four mutant libraries across different conditions. Supplementary correlation plot for Figure 1B.

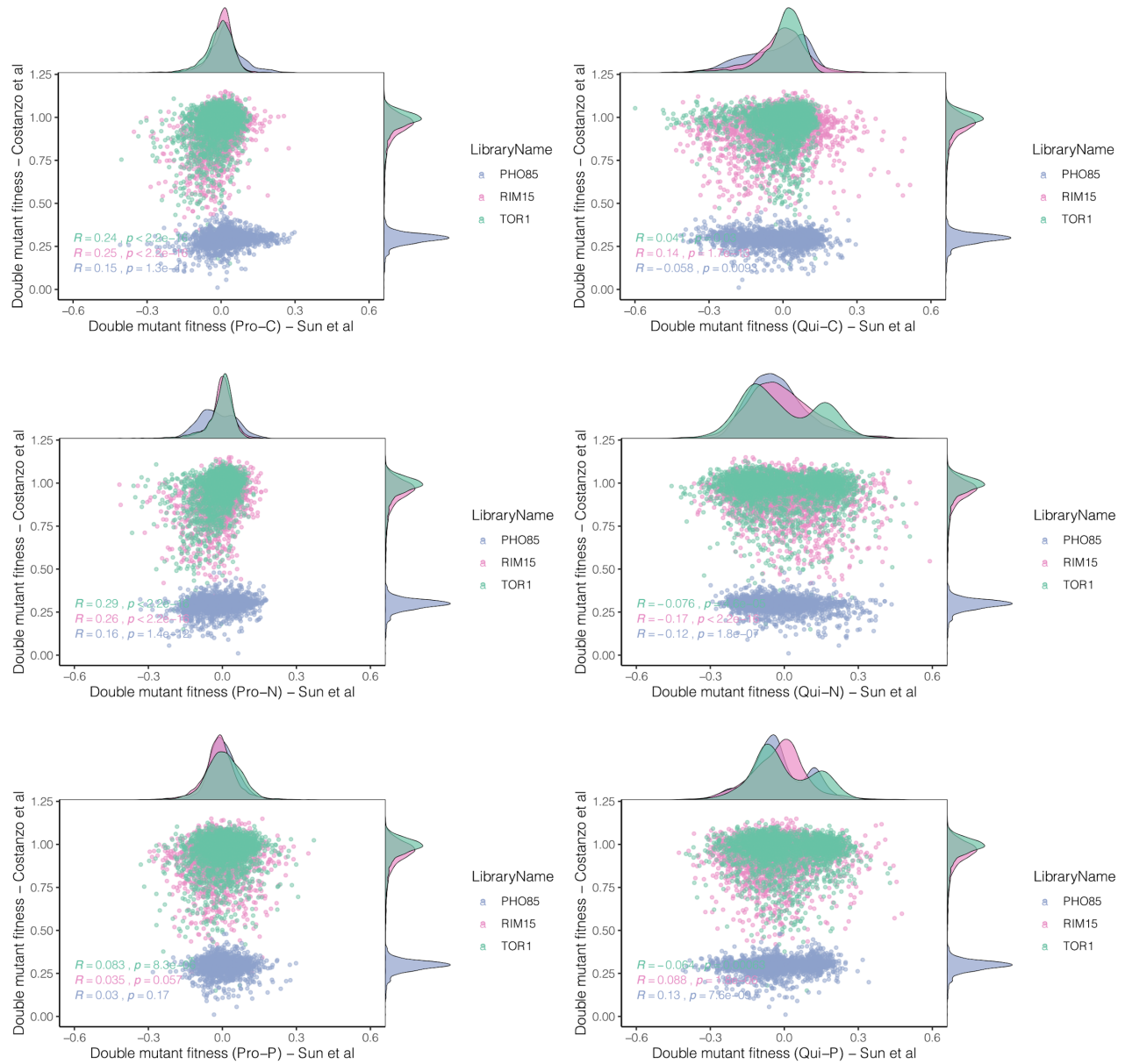




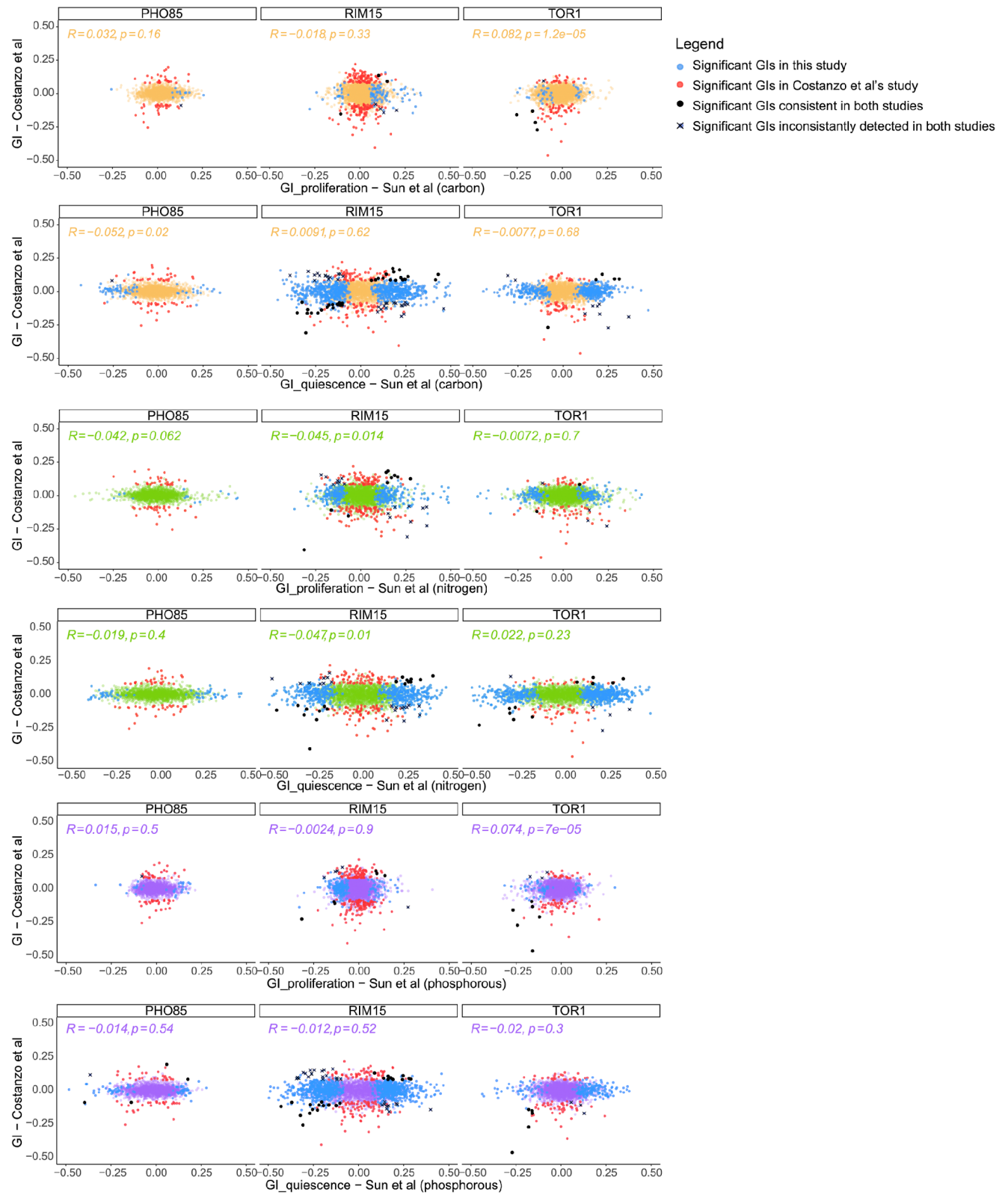
Appendix FigureS3. Diagnostic plots of data quality and model fitting. Scatter plots of the standard error and coefficient for each fitted model (fitness in proliferation and survival in quiescence). The blue and yellow dots are models that are statistically significant with FDR (5%) corrected p-value smaller than 0.05, representing fitness or survival rates that are significantly worse (blue) or better (yellow) in comparison to wild type. Label code: Pro- proliferation, Qui- quiescence.



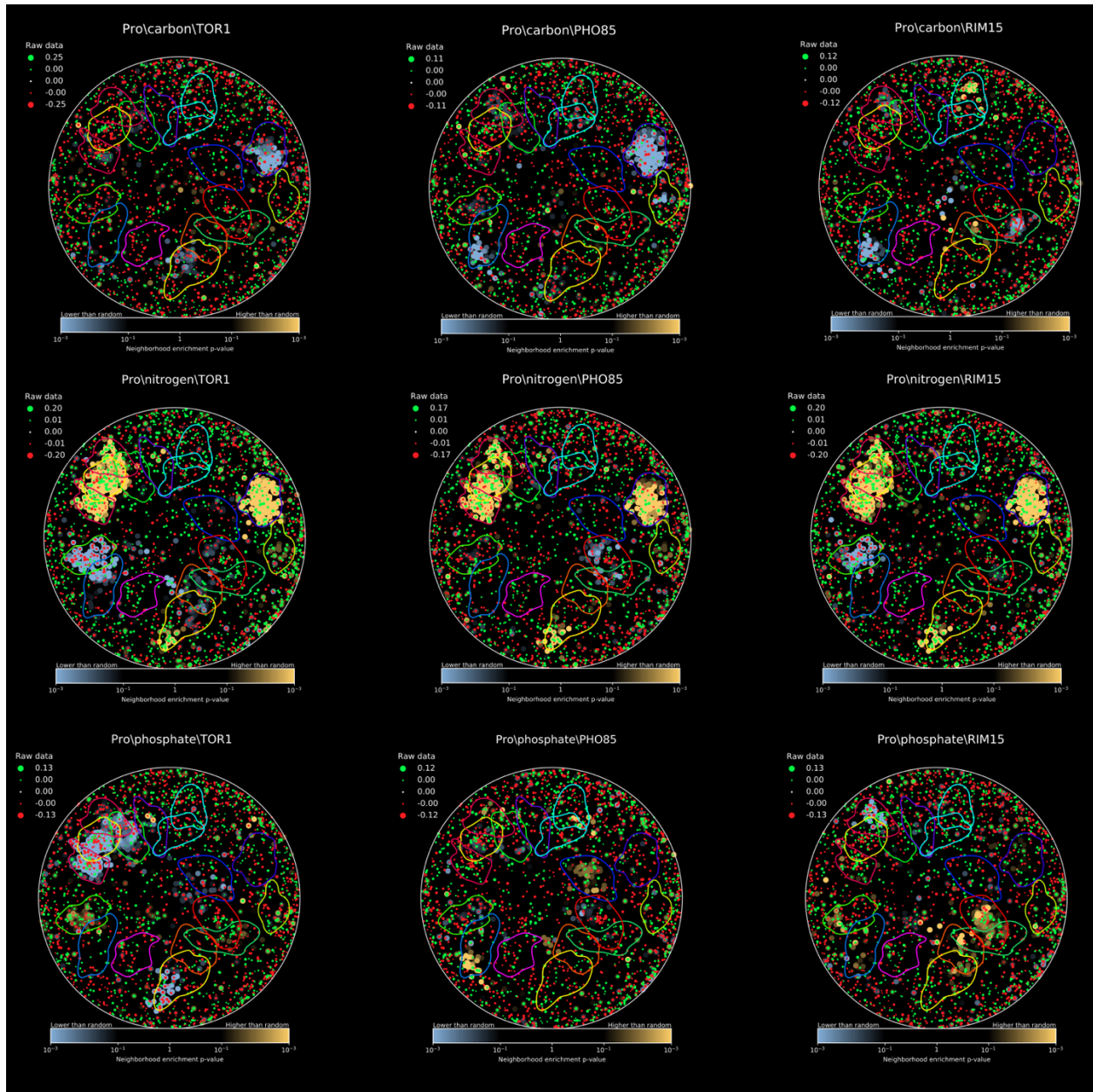
Appendix FigureS4. Comparison of GIS estimated by ANCOVA and single mutant fitness in response to different nutrient restrictions and cellular states. The blue and yellow dots are genetic interactions that are statistically significant with FDR (5%) corrected p-value smaller than 0.05, representing the significant positive (yellow) or negative (blue) with each kinase in labeled condition. Label code: Pro- proliferation, Qui- quiescence.



Appendix FigureS5. Double mutant fitness and survival profiles comparison with the data from Costanzo et al's study. Comparison of double mutant fitness/survival profiles between our study and Costanzo et al's study for all three kinases. Pearson correlation score is labeled in the plot with p-value. Label code: Pro - proliferation, Qui - quiescence, -C - carbon restriction, -N - nitrogen restriction, and -P - phosphorus restriction.



Appendix FigureS6. Comparison of genetic interactions between data from our study and Costanzo et al's study. Comparison of genetic interaction profiles between our study and Costanzo et al's study for all three kinases. Pearson correlation score is labeled in the plot with p-value (color code: yellow - carbon limitation, green - nitrogen limitation, purple - phosphorus limitation, blue - significant GIs in our study ($p_{adj} < 0.05$), red - significant GIs in Costanzo et al's study ($p_{adj} < 0.05$), black dot - Significant GIs consistent in both studies, black cross - significant GIs inconsistently detected in both studies).



Appendix FigureS7. SAFE analysis of genetic interaction profiles in proliferating cells with raw data. Only the genes with a value are plotted as green or red. Green dots represent positive interactions and red dots indicate negative interactions. The size of each green or red dot is associated with the absolute value of interaction strength. Note that the scale of each plot is different.