

APPENDIX

Mechanism for microbial population collapse in a fluctuating resource environment

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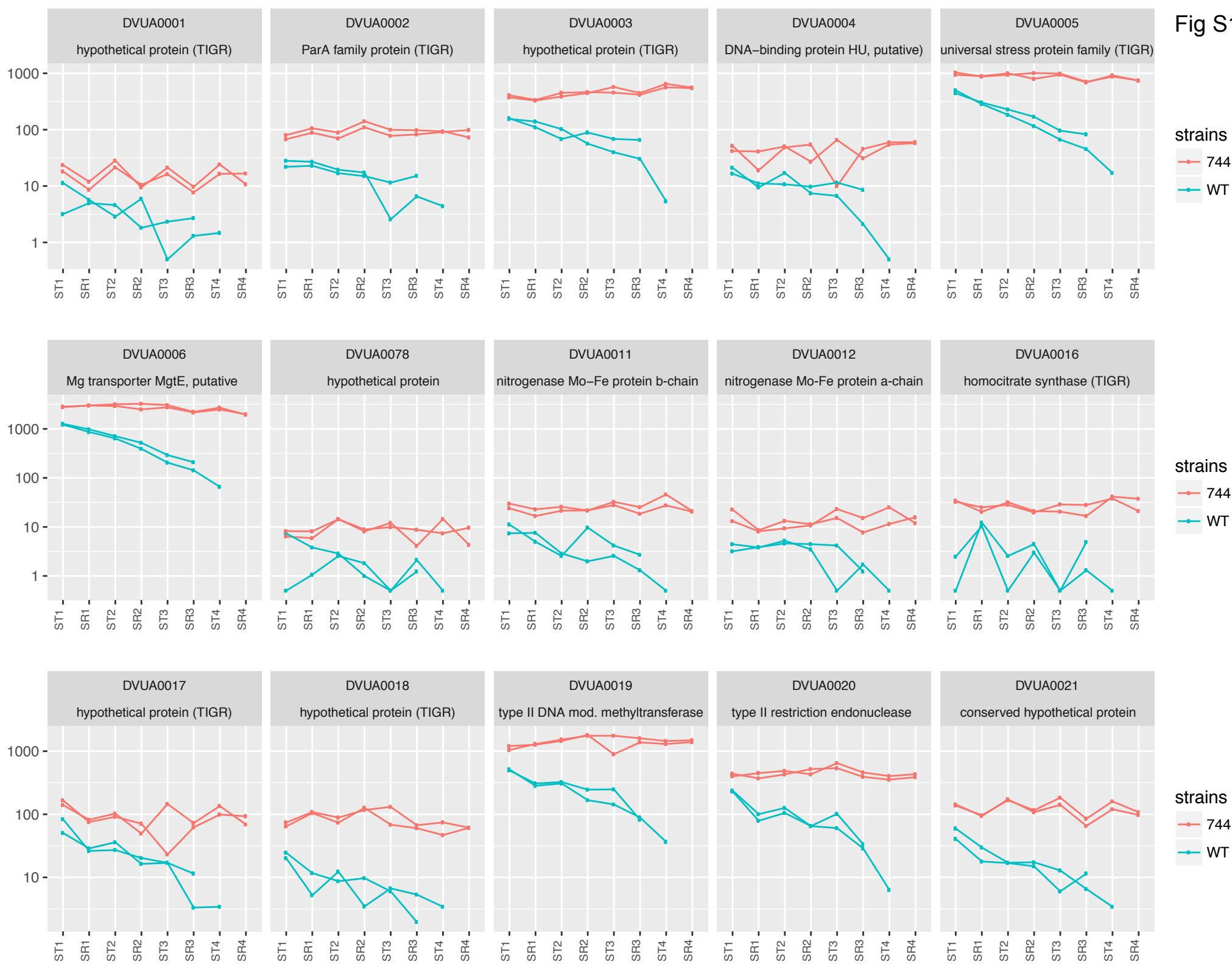
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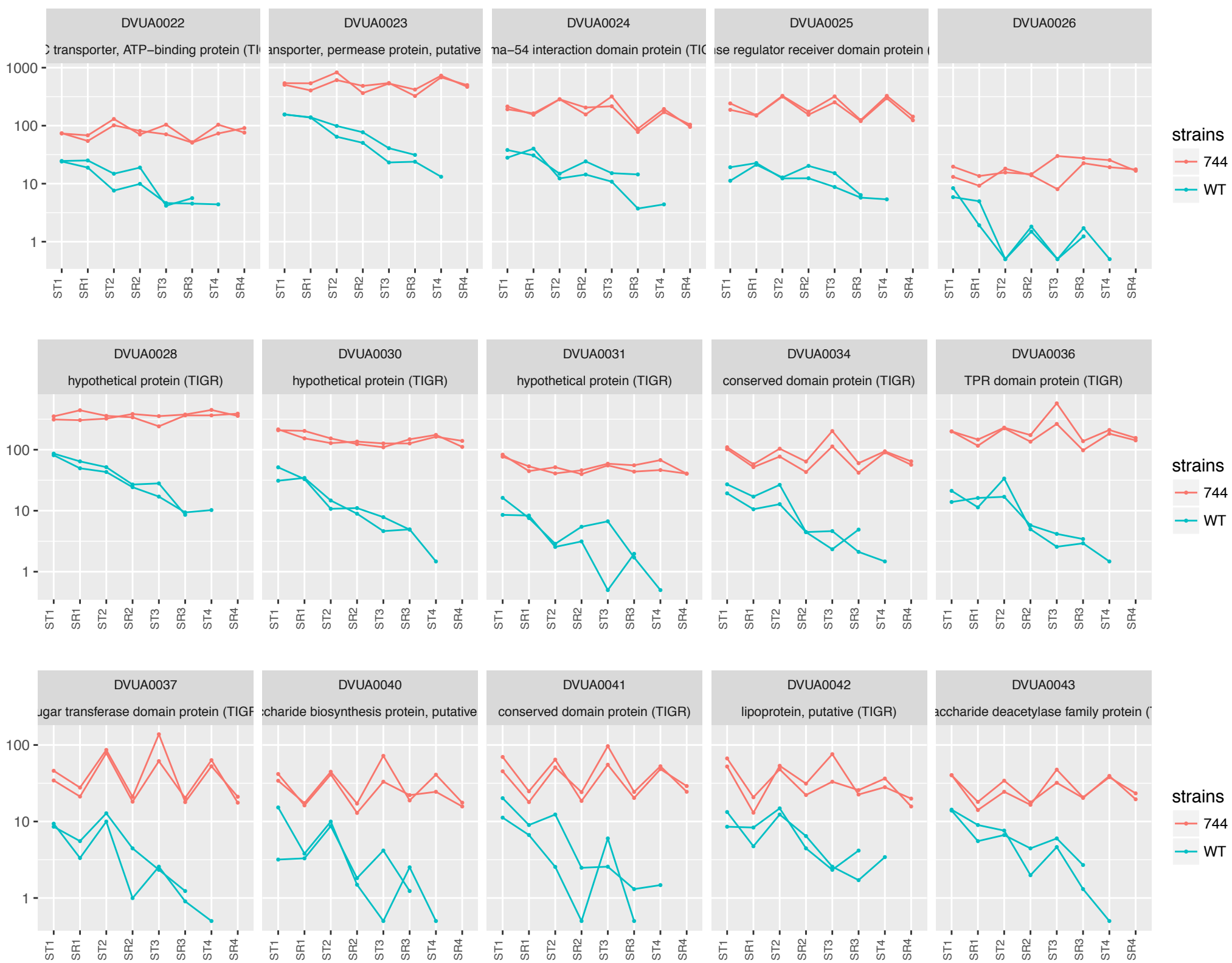
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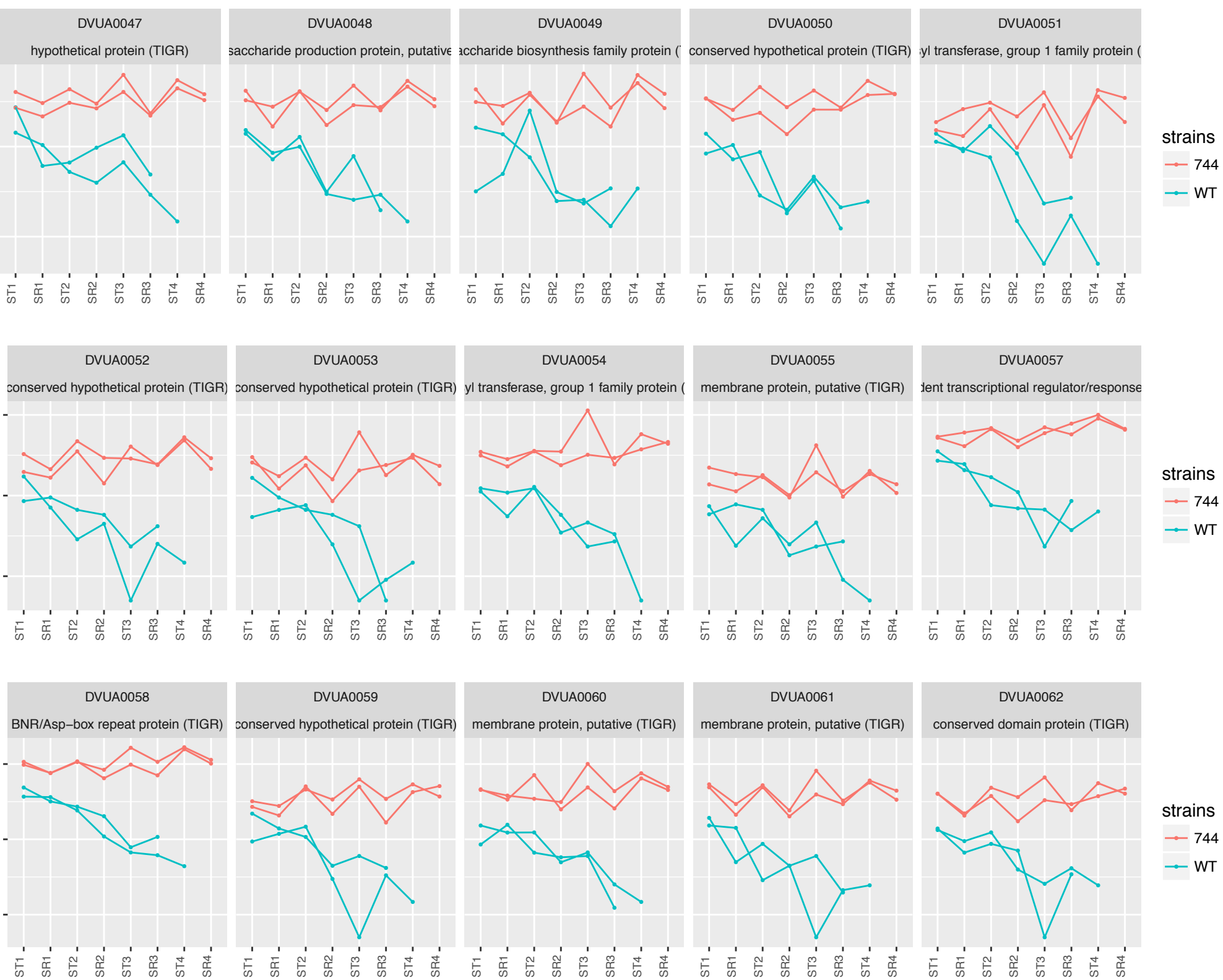
Appendix Figure Legends

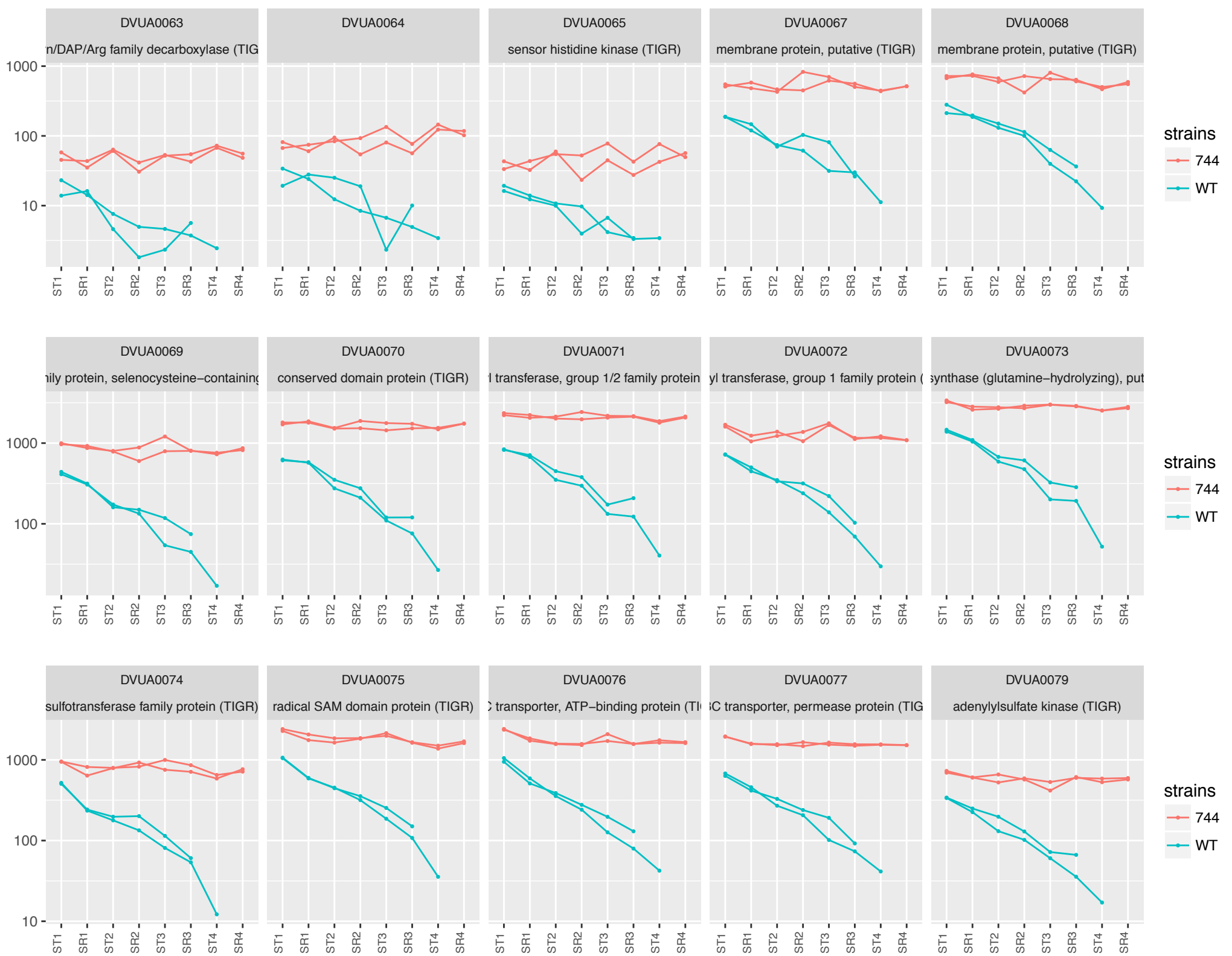
Appendix Figure S1: Change in abundance of selected Dv transcripts during experimental evolution of wild type and mutant co-cultures. Abundance for each transcript is represented as normalized read counts on the y-axis while conditions are listed on the x-axis.

Appendix Figure S2: Change in abundance (\log_2) of selected Dv proteins during experimental evolution of wild type and mutant co-cultures. Protein abundances for each condition are listed as boxplots while trends are represented with a trend line. \log_2 -fold changes between ST1 and SR3 were calculated by Student's t-test or Mann–Whitney U test depending on normality of observed values; normality assessed by Shapiro–Wilk normality test. * indicates p-value < 0.05 or ** indicates p-value < 0.01. Essential gene names are indicated with red font.













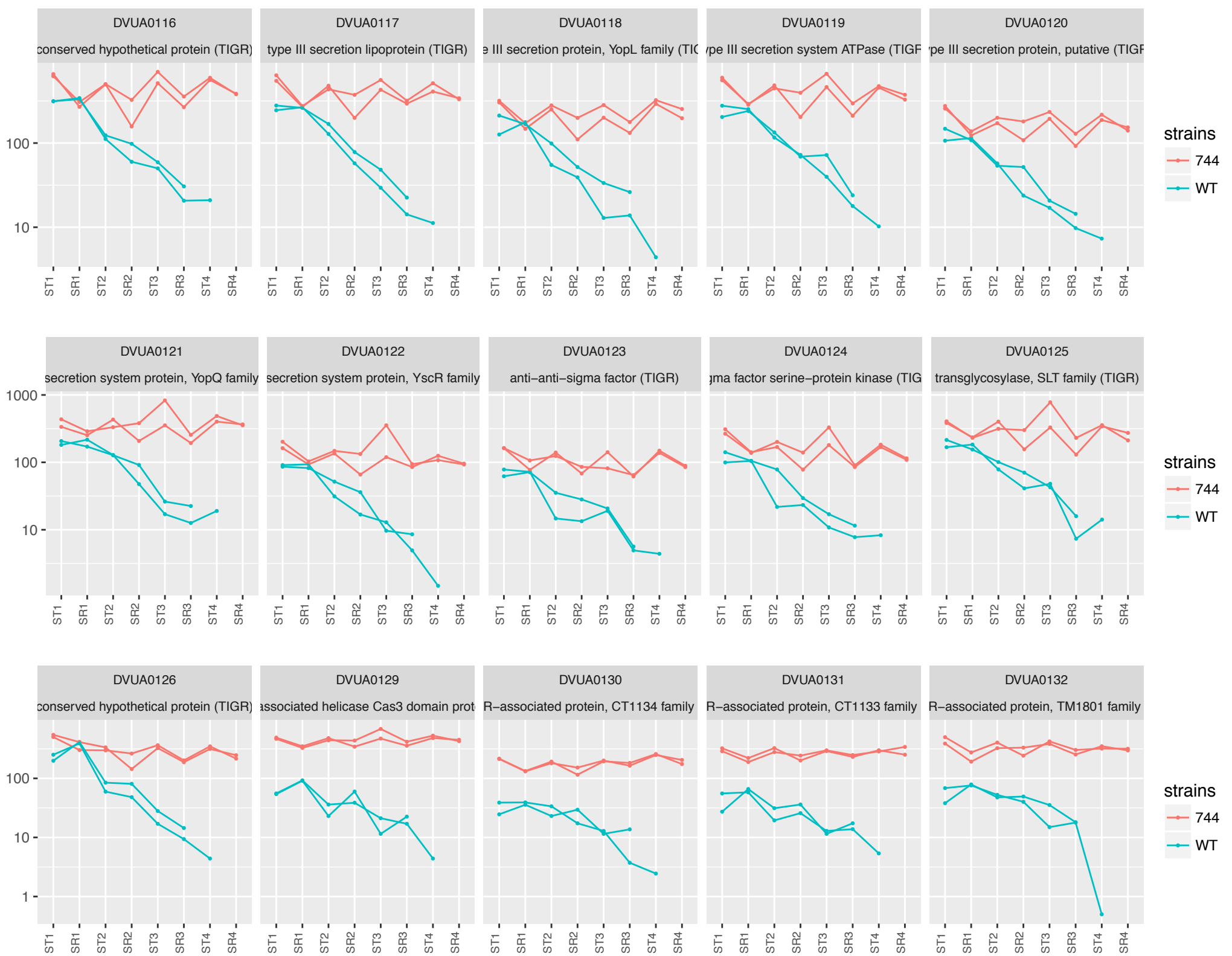


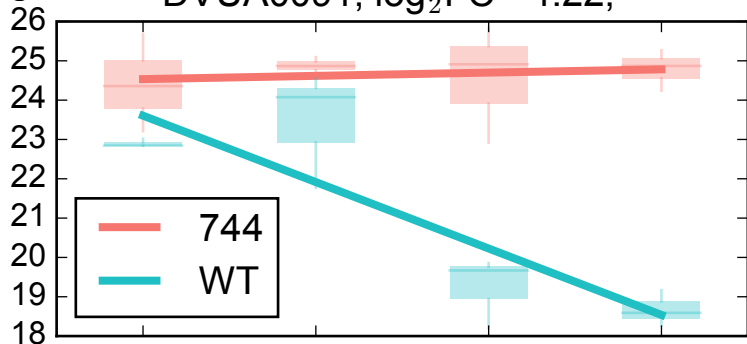




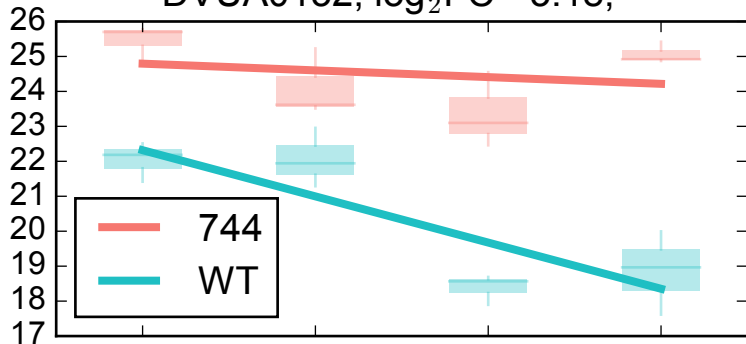


Fig S2

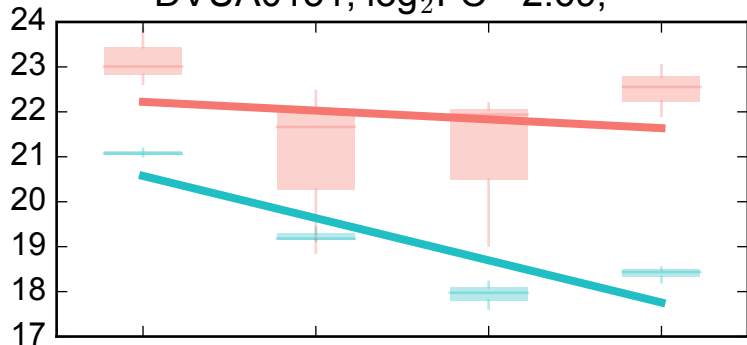
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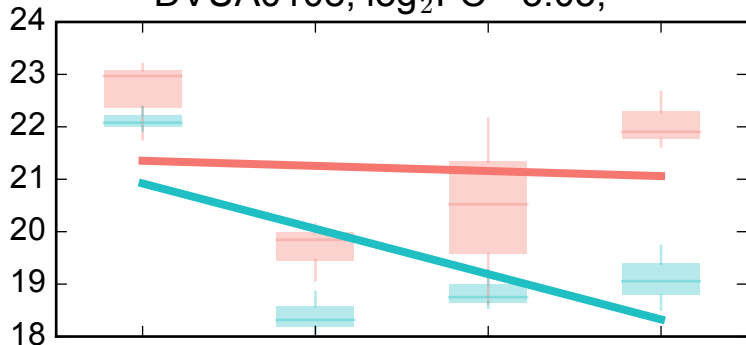
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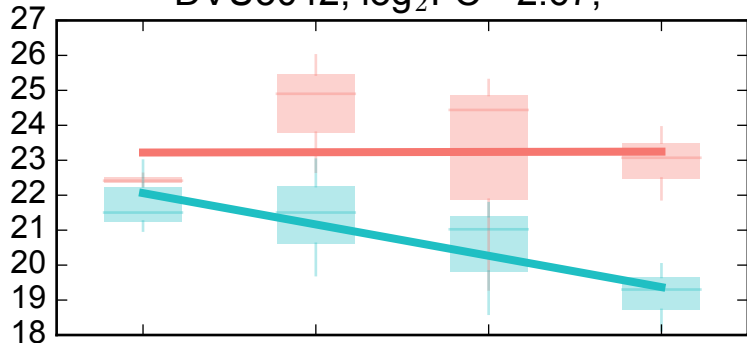
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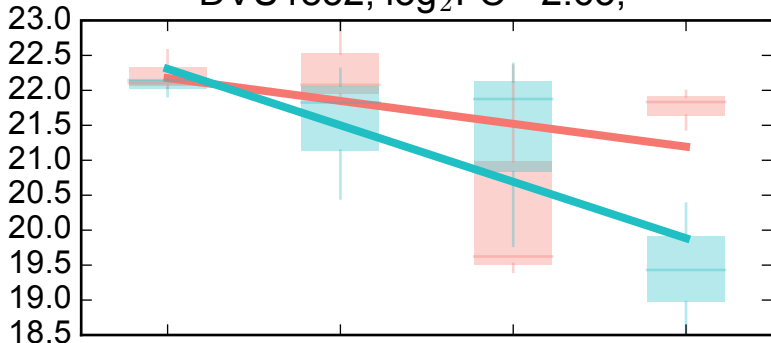
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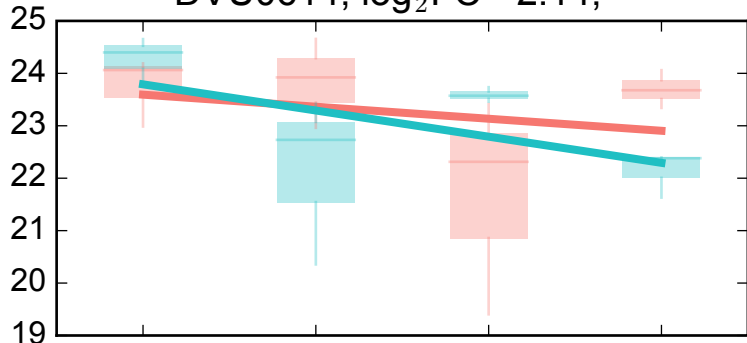
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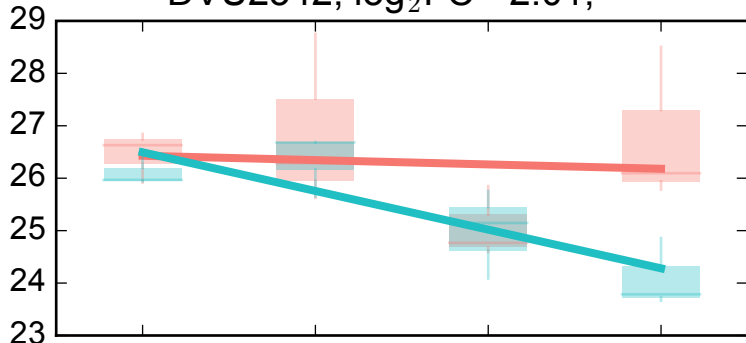
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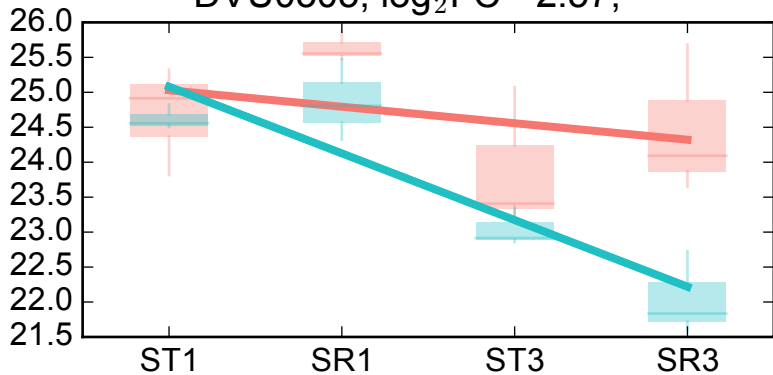
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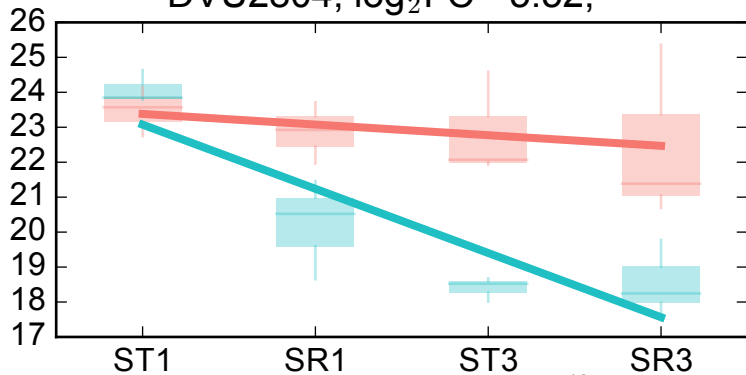
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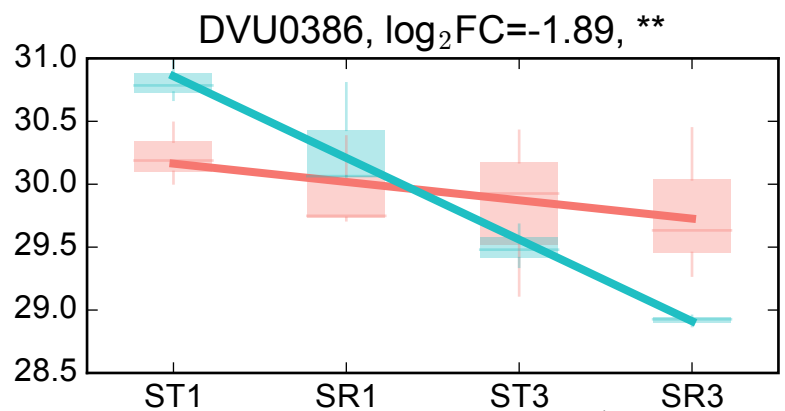
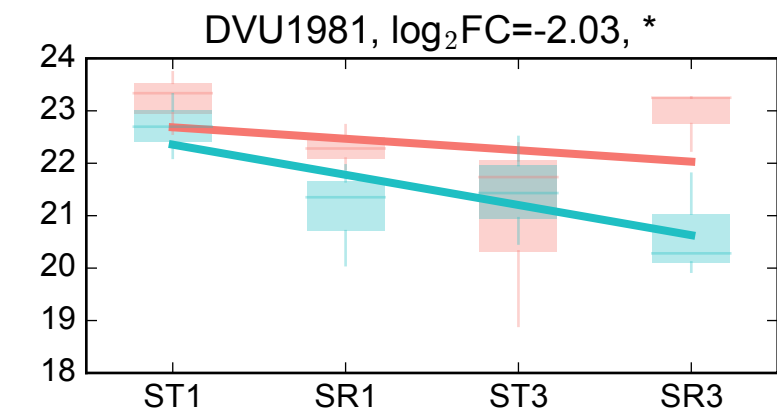
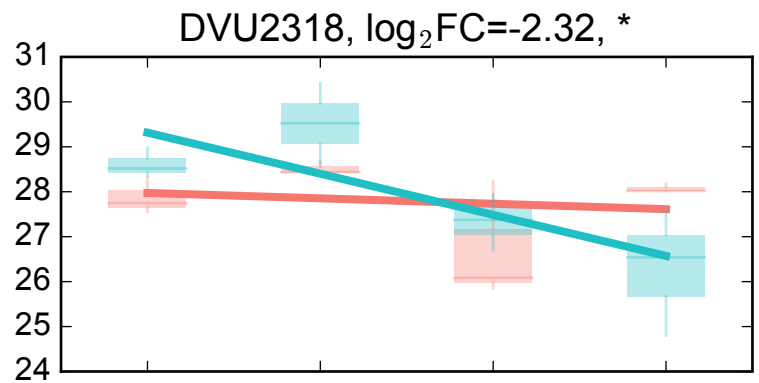
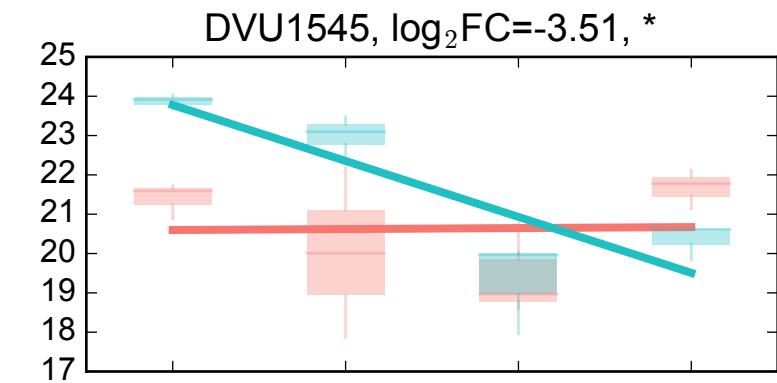
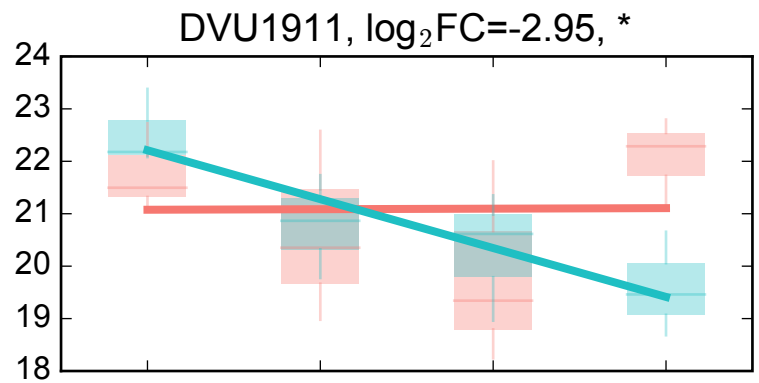
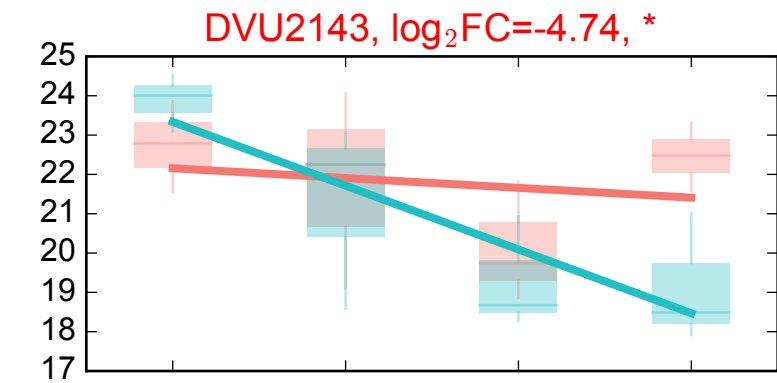
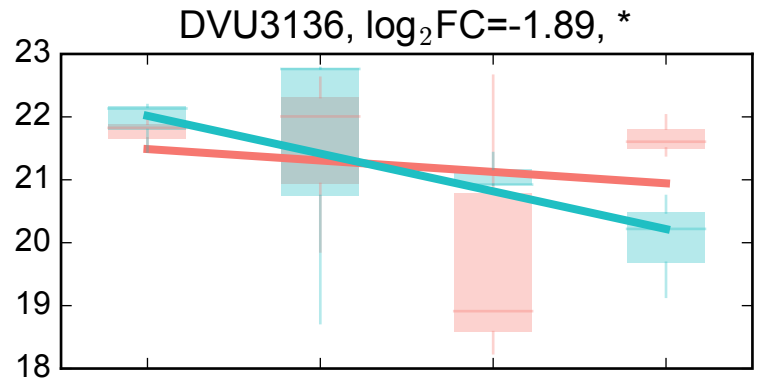
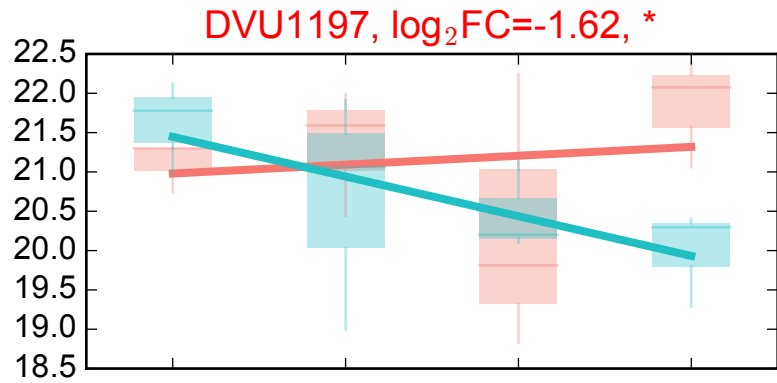
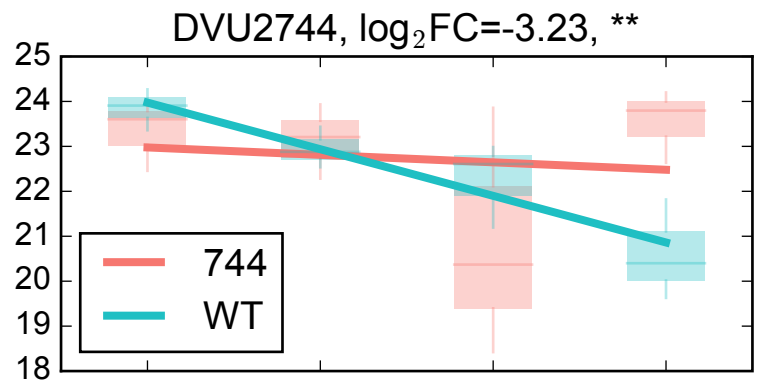
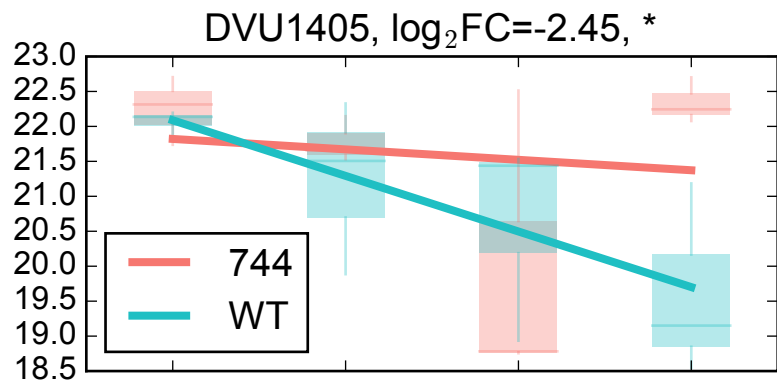


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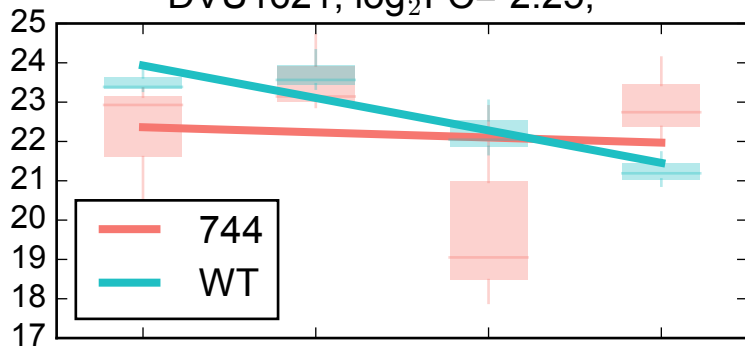


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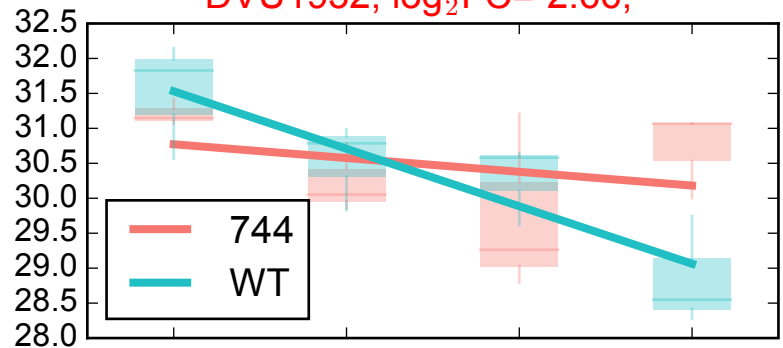




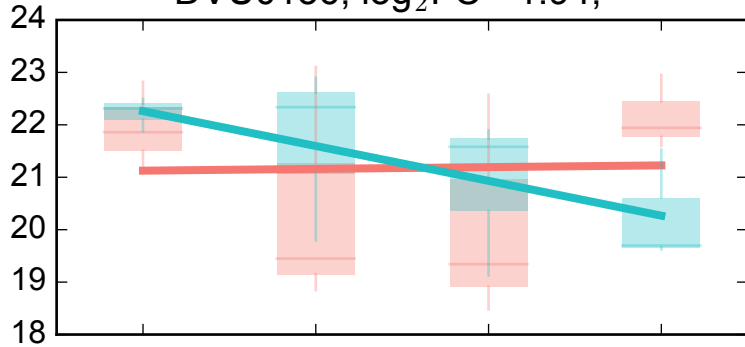
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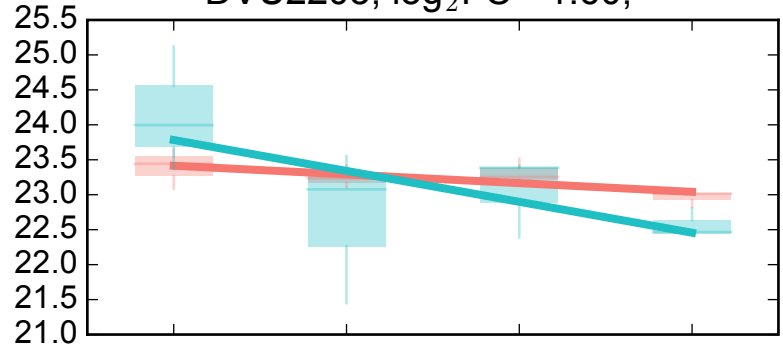
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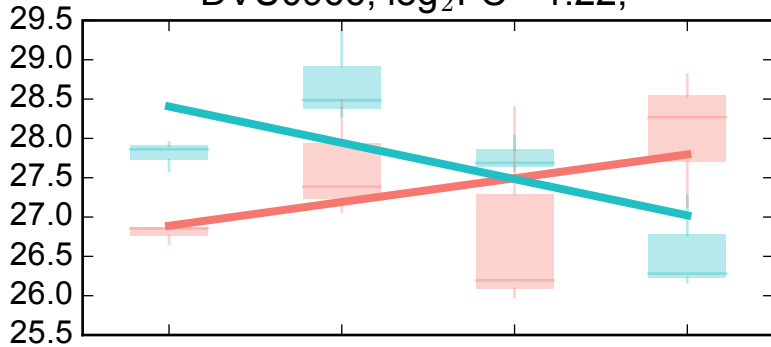
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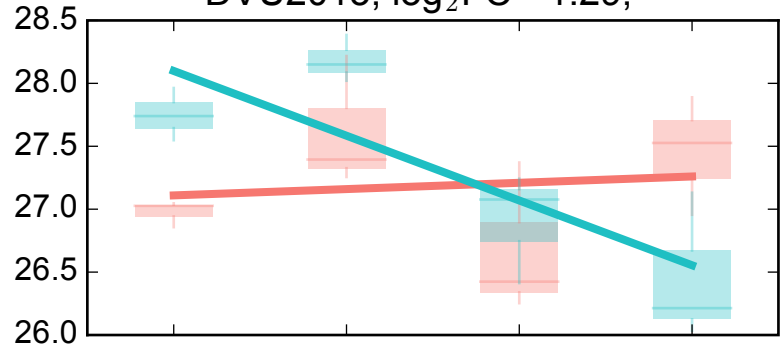
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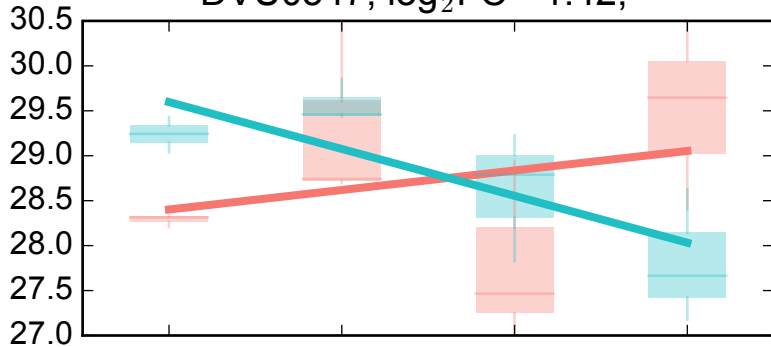
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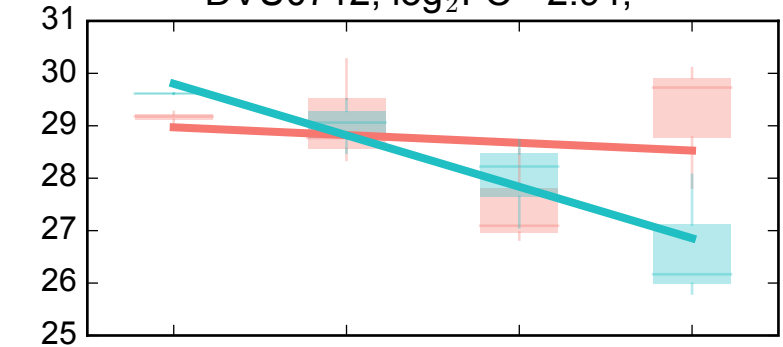
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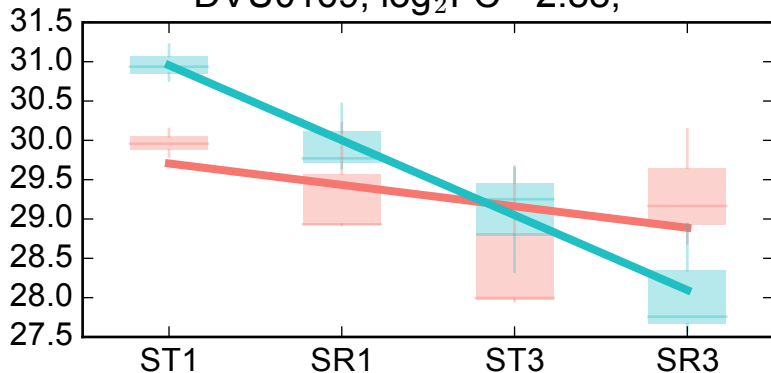
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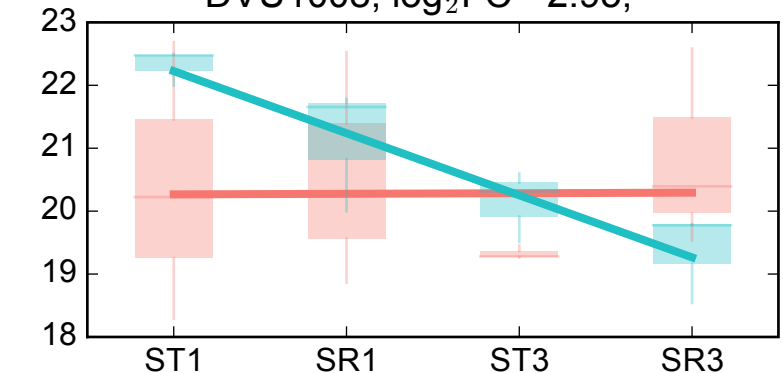
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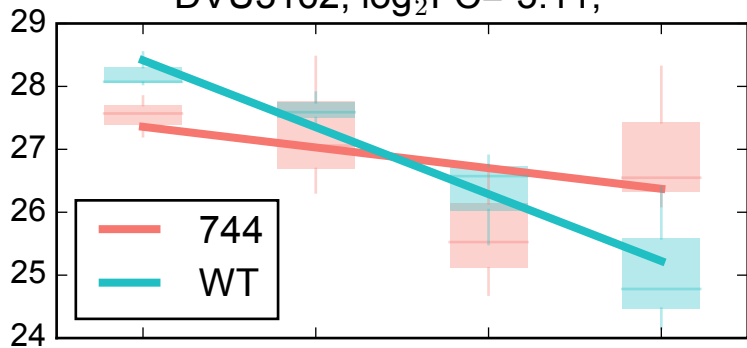
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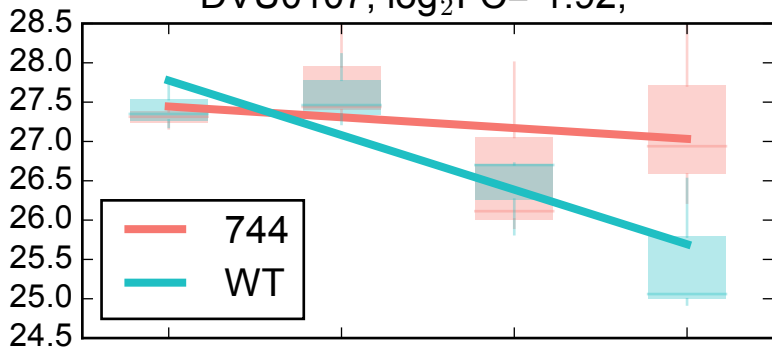
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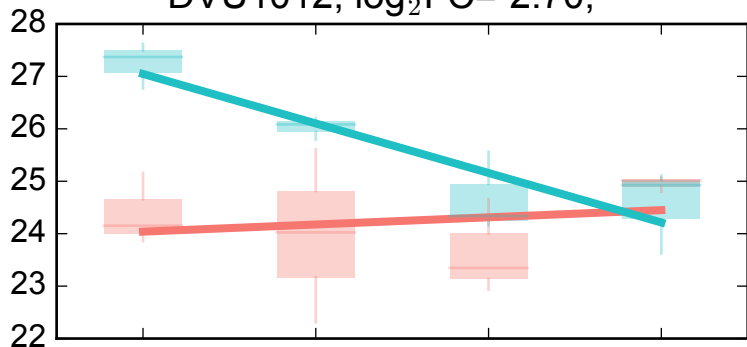
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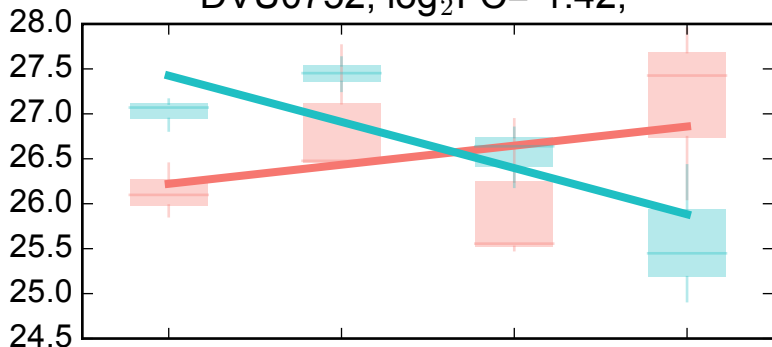
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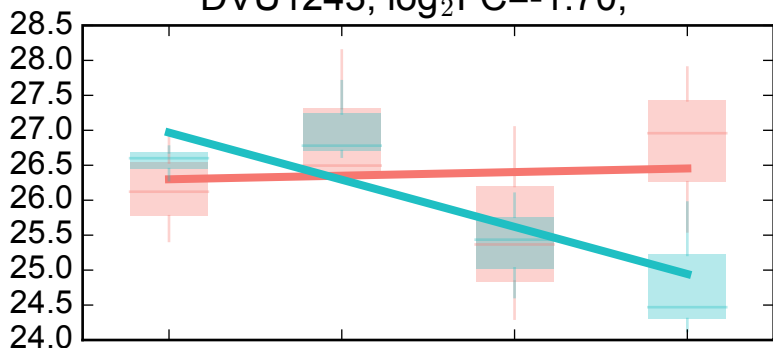
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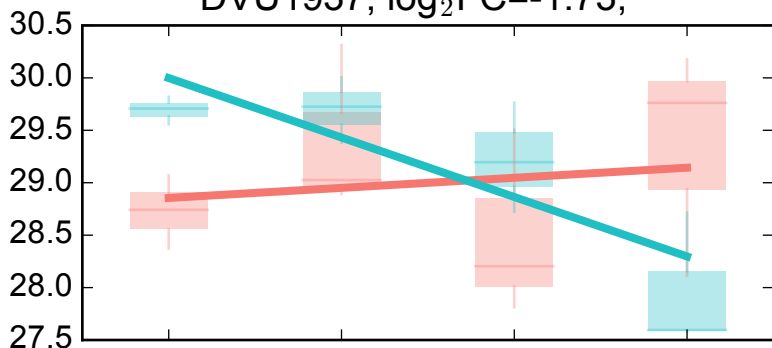
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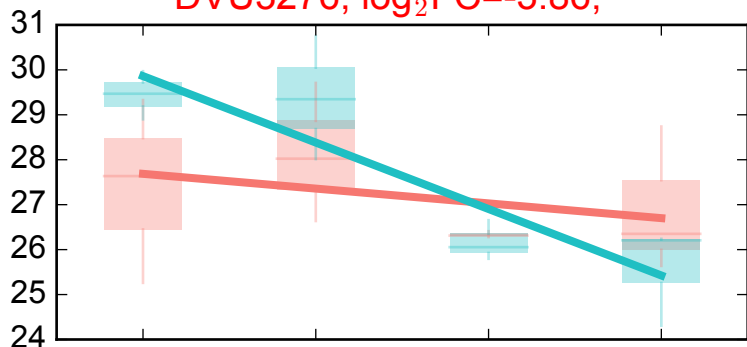
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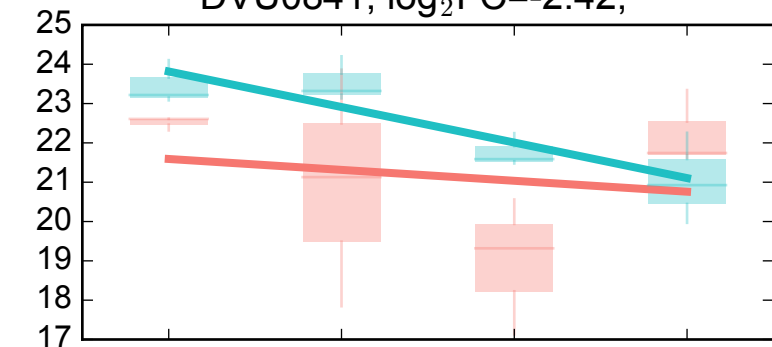
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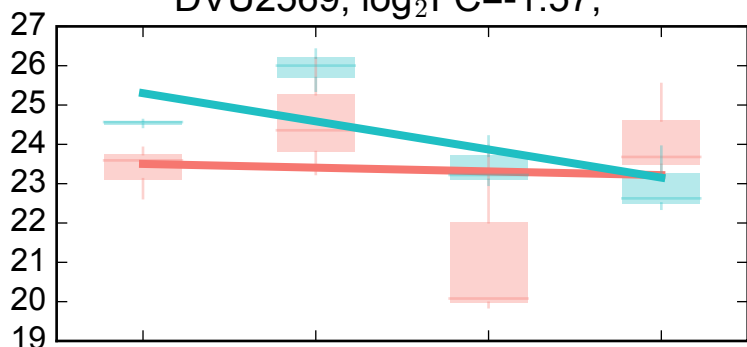
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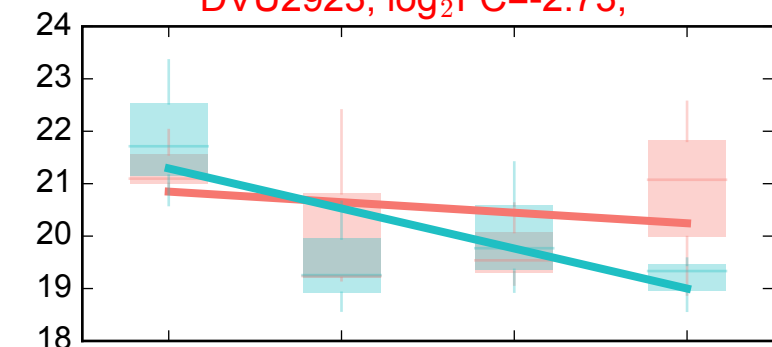
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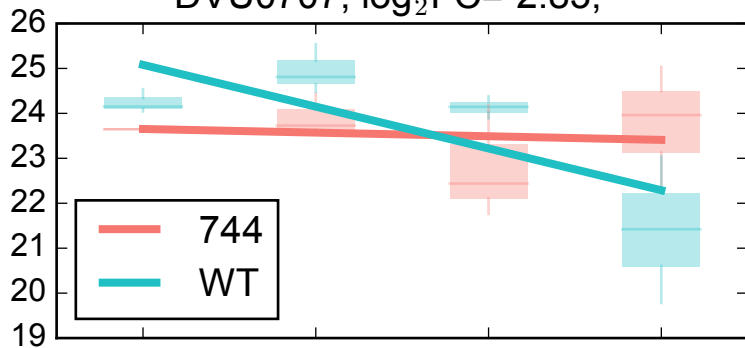
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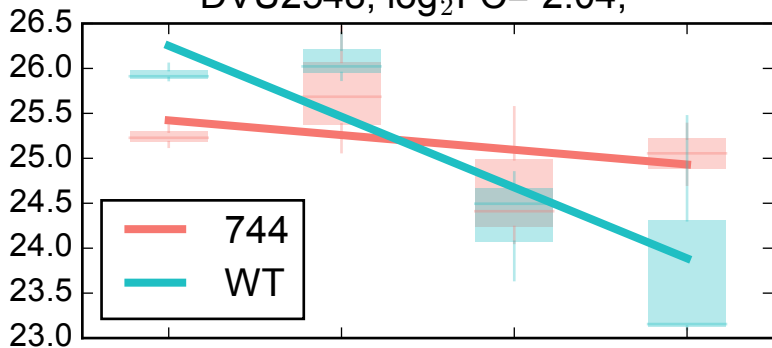
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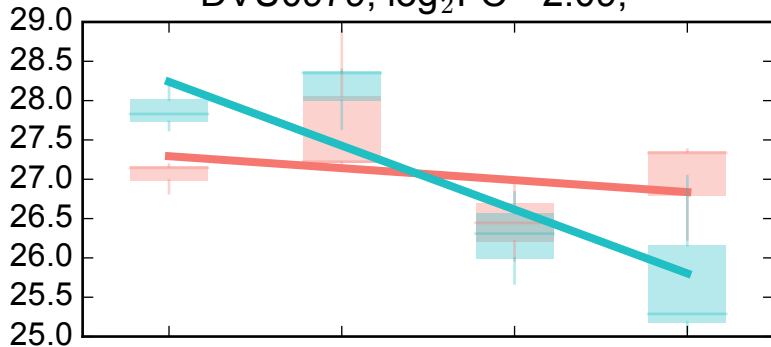
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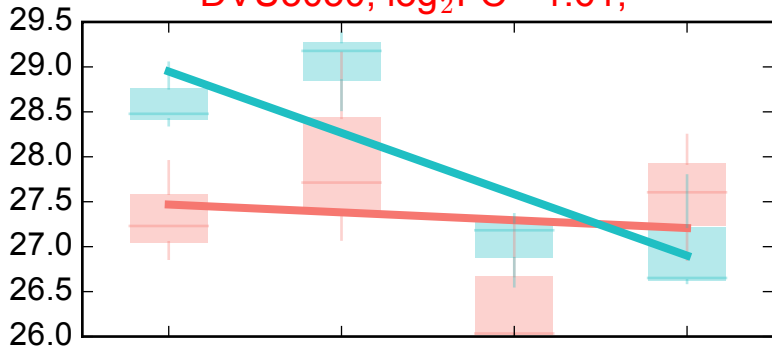
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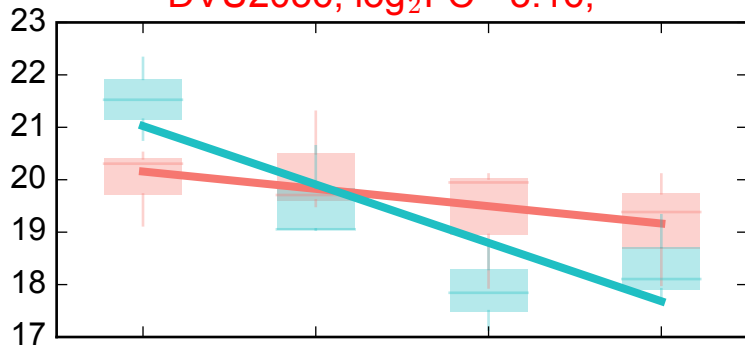
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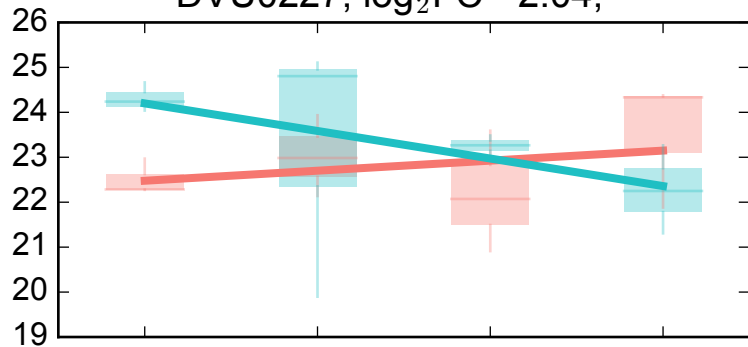
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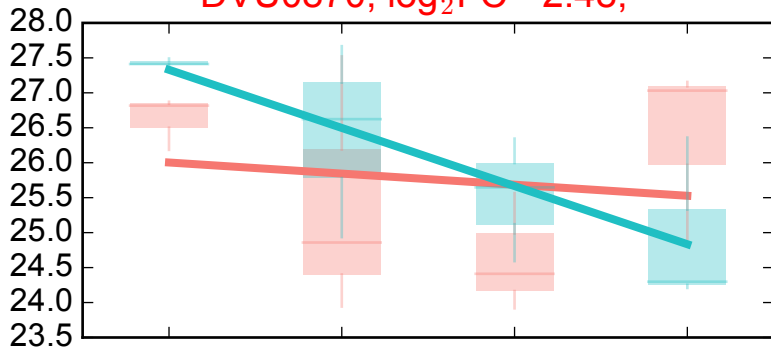
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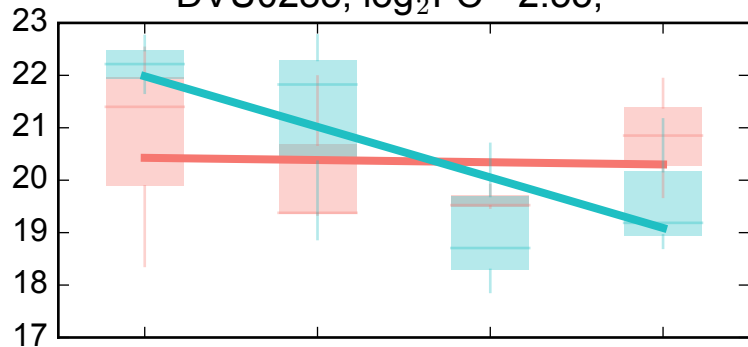
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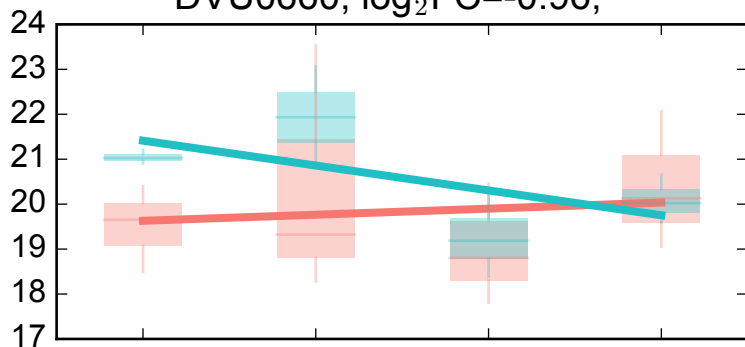
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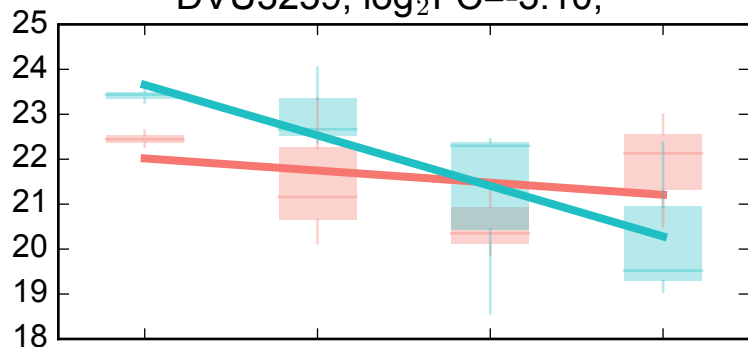
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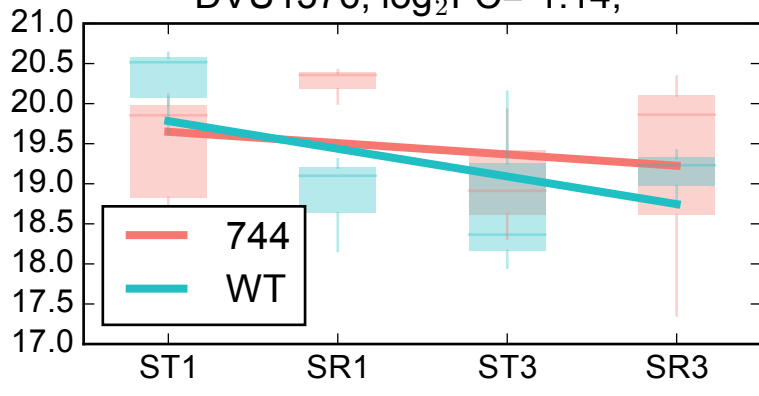
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