Supplemental information

Multiple timescales in bacterial growth homeostasis

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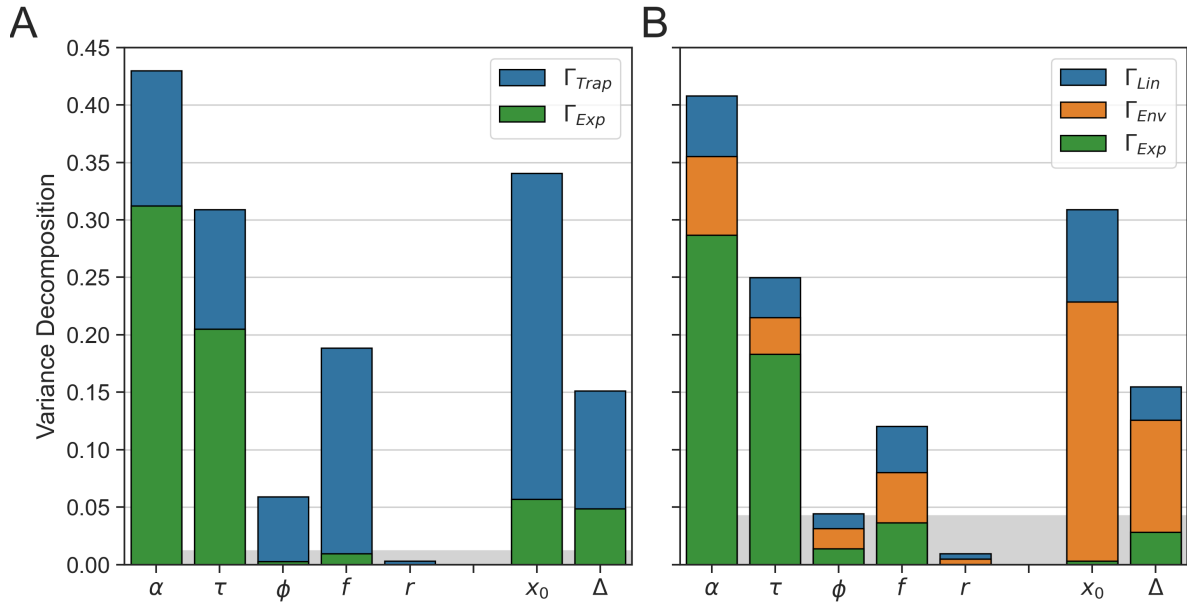
Supplementary Figures

Figure S1: **Effect of experiment on variance decomposition.** Related to Figs. 3,4. The same data as in Figures 3B, 4D in the main text was used to further parse the total variance to include also the contribution from different experiments. This contribution is depicted by the green portions of the bars. **(A)** Data from mother machine; variance is decomposed to its contributions from individual traps and groups of traps belonging to the same experiment. Growth-rate and inter-division time have significant relative contributions from experiment identity to their variance, whereas initial size and added length less so. Dimensionless variables have almost no contribution to variance from experiment. **(B)** Sisters data decomposed to 4 contributions - lineage, environment, experiment and noise (complementary of bar height to 1).
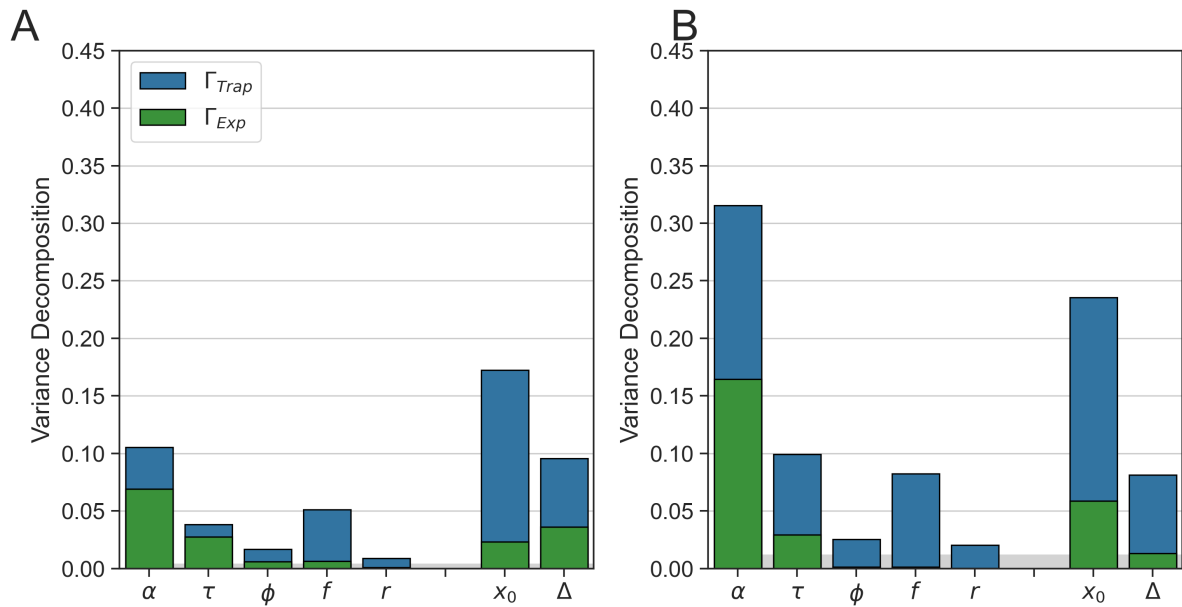
Figure S2: **Variance decomposition for two** *E. coli* **strains.**Related to Fig. 3. Same analysis as in Fig. S1A, applied to publicly available mother machine data (Wang et al., 2010). Measurements on two strains: **(A)** MG1655 (CGSC 6300), **(B)** MG1655 lexA3.
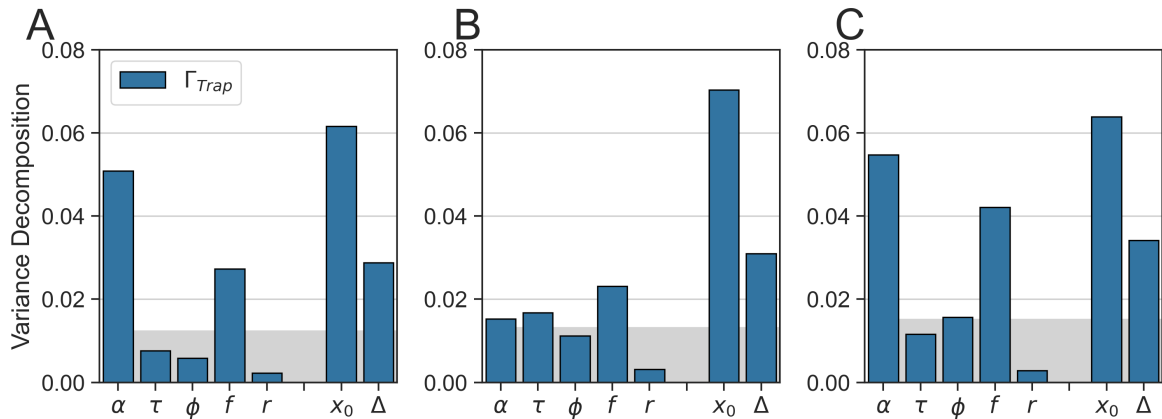

Figure S3: **Variance decomposition at three temperatures.** Related to Fig. 3. This figure shows results of the same analysis as in Fig. S1A, performed on mother machine experiments from Tanouchi et al. (2015). Bacteria were grown in $25, 27$ and $37°C$ in **A,B,C** respectively. All values of Γ_{trap} in this set of experiments are particularly small compared to other experiments examined The relative values share some of the qualitative properties seen in the other data-sets.
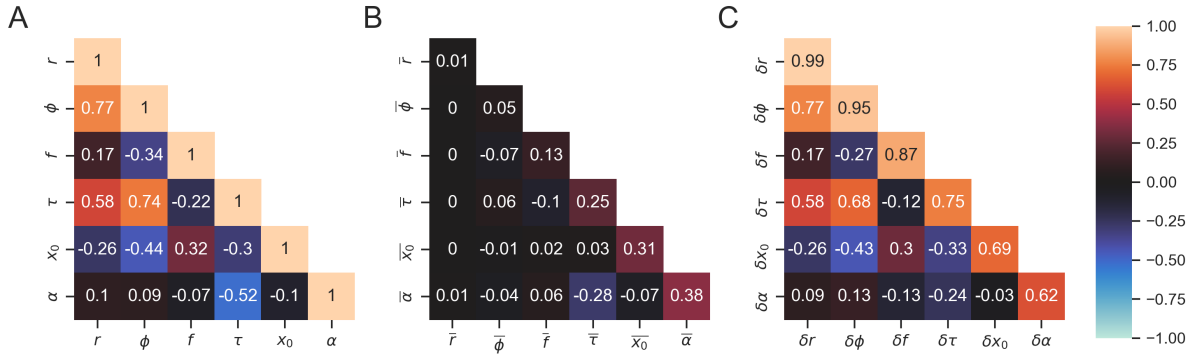
Figure S4: **Covariance decomposition in individual lineages.** Related to Fig. 5. **(A)** Normalized covariance (Pearson correlation coefficient) for all pairs of phenotypic variables over the pooled ensemble. **(B),(C)** are the decomposition of entries in **A** to long-term parts contributed by set-point variation across lineage, and short-term parts contributed by fluctuations around fixed points, respectively (see STAR Methods). Entries on the diagonal are numerical values corresponding to the bar heights depicted in Fig. 3B, showing their hierarchy from the stiffest variable r to the most sloppy one α. All entries in **A** are the sum of corresponding entries in **B**,**C**, as expected. Examining the relative contributions of the two timescales, we find that α and τ have a significant long timescale contribution; other pairs of variables co-vary mostly on the short timescale contributions. In particular, the correlations of cell size with all other variables comes primarily from short-time, relative per-cycle variables.
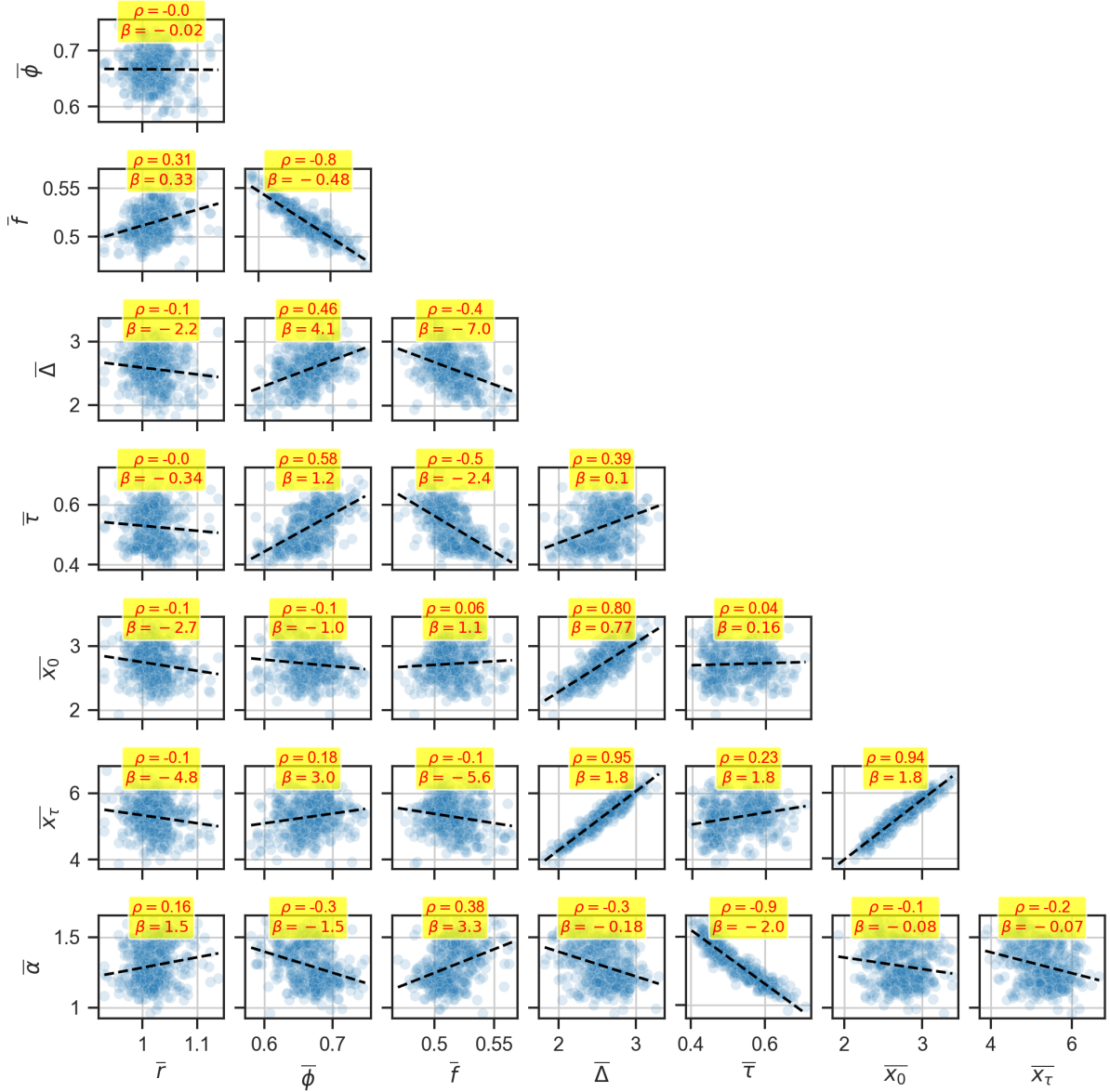
Figure S5: **Set-point correlations can persist over long timescales.** Related to Fig. 5. This matrix of scatter-plots shows the Pearson correlation (ρ) and best-fit slope (β) between a lineage's set-points (time-averages) of two different variables shown in the x- and y-axis labels. Each of the 428 points represents a lineage longer than 15 generations found in the pooled ensemble of the Sisters Machine data (Vashistha et al. 2021). Some variables maintain large dynamic ranges even after averaging, and some exhibit significant correlation with set-points of other variables. Strong correlations seen here are between growth/division variables: $\rho(\overline{\alpha}, \overline{\tau}) = -0.9$, $\rho(\overline{f\phi}) = -0.8$; between different cell-size variables , $\rho(\overline{x_\tau}, \overline{\Delta}) = 0.95$, $\rho(\overline{x_0}, \overline{x_\tau}) = 0.94$, and $\rho(\overline{x_0}, \overline{\Delta}) = 0.8$. In contrast, correlations between growth/division and size variables are very weak or insignificant: $\rho(\overline{x_0}, \overline{\tau}) = 0.04$, $\rho(\overline{x_0}, \overline{f}) = 0.06$, $\rho(\overline{x_0}, \overline{\alpha}) = -0.1$.
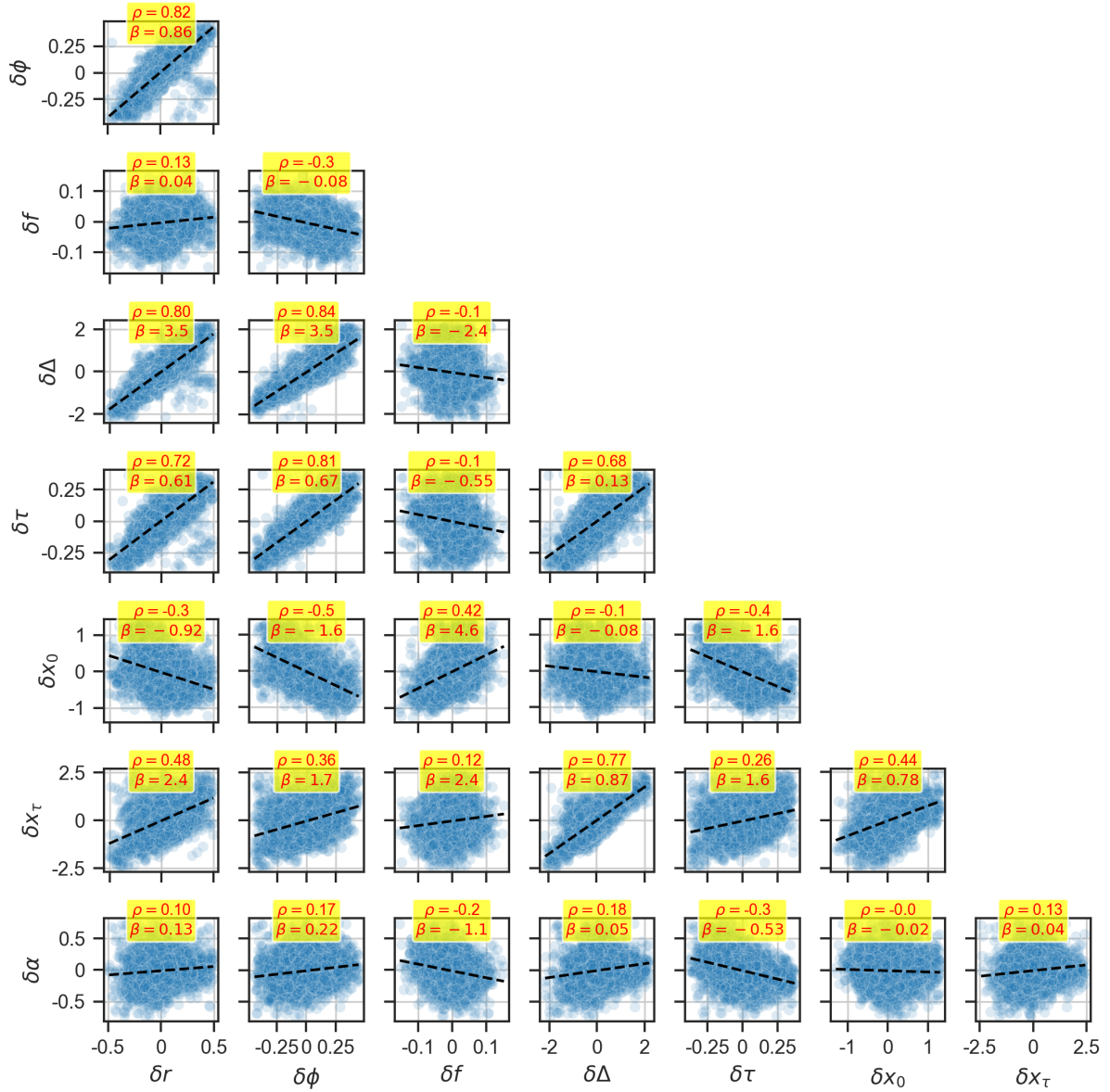
Figure S6: **Short timescale correlations.** Related to Fig. 5. This matrix of scatter-plots shows the Pearson correlation (ρ) and best-fit slope (β) between lineage-centered values of different pairs of phenotypic variables shown in the x- and y-axis labels. Each of 10,900 points represents a single cell-cycle in the pooled ensemble of the Sisters Machine data (Vashistha et al. 2021).
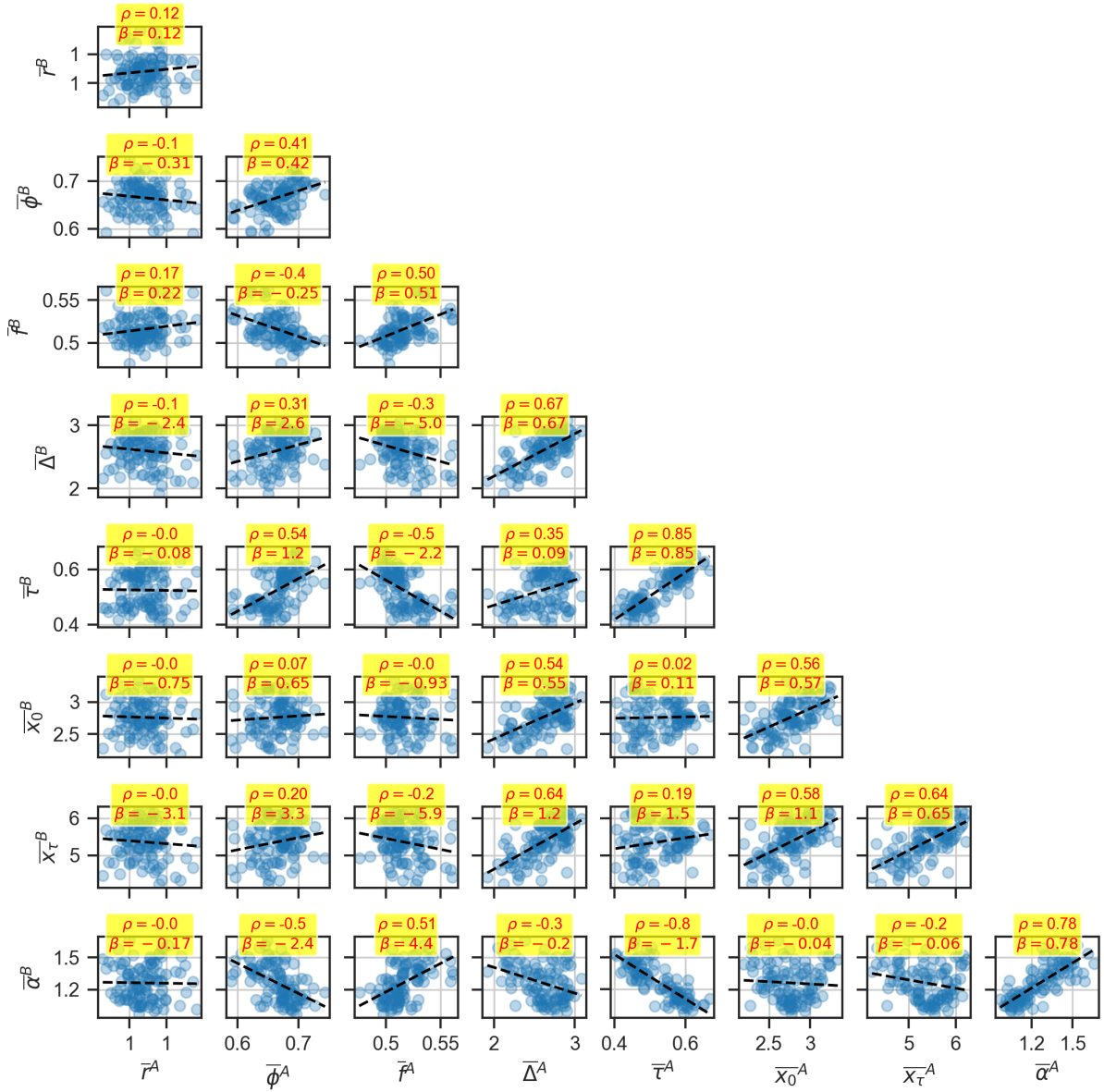
Figure S7: **Long timescale set-point correlations between neighbor lineages.** Related to Fig. 5. This matrix of scatter-plots shows the Pearson correlation (ρ) and best-fit slope (β) between a neighbor lineage set-points of phenotypic variables denoted in the x- and y-axis labels. Each of $106-108$ points represents a lineage longer than 15 generations from the Sisters Machine data (Vashistha et al. 2021). All variables except for r show significant correlations between neighboring cell set-points, that can reach 0.85 for sloppy variables such as τ. experience some micro-environmental influence because of the strong correlations found in the diagonal entries.
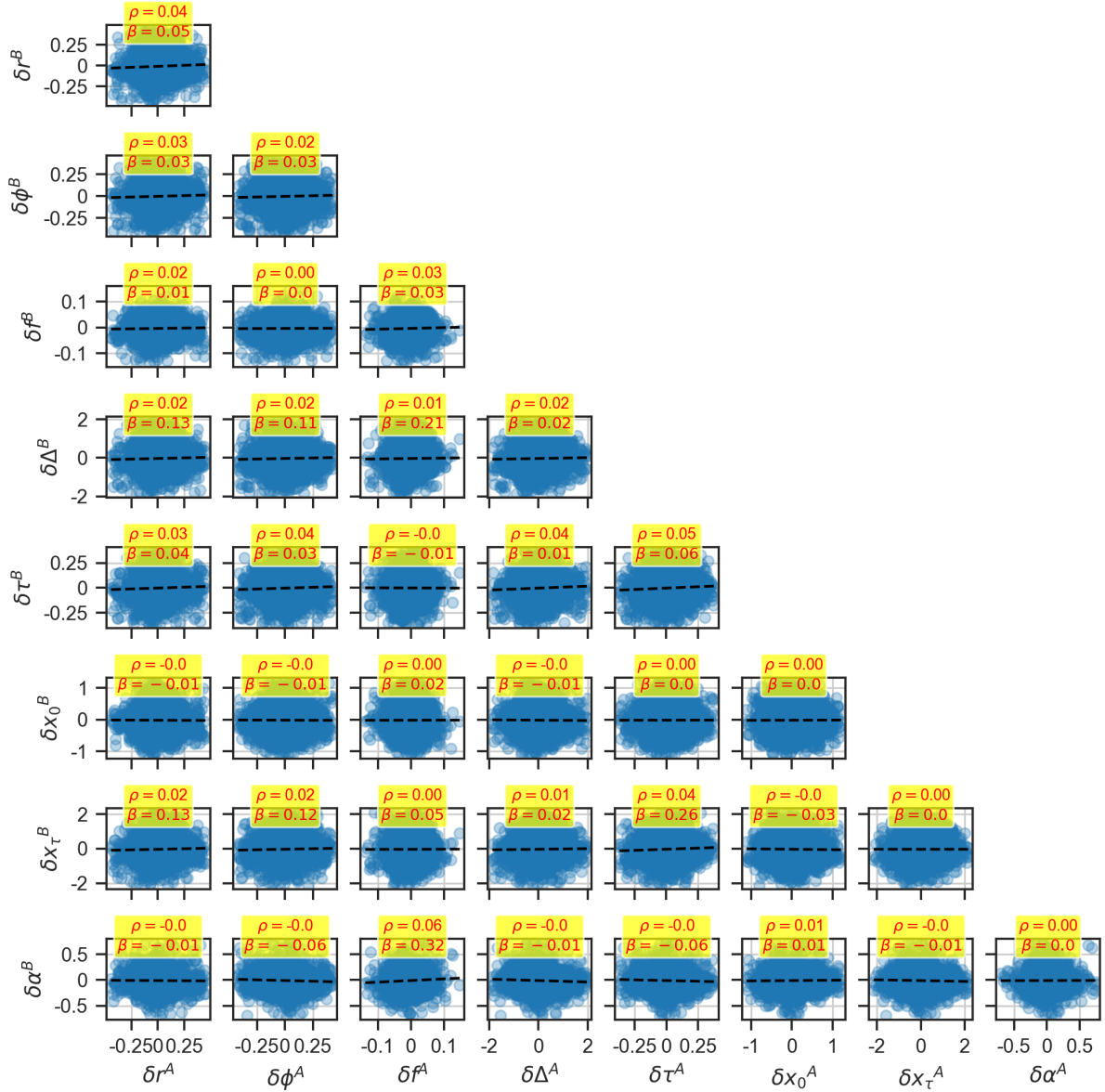
Figure S8: **Short timescale correlations between neighbor lineages.** Related to Fig. 5. This matrix of scatter-plots shows the Pearson correlation (ρ) and best-fit slope (β) between lineage-centered values of neighbor lineages for phenotypic variable pairs corresponding to the x- and y-axis labels. Every point represents a single bacteria in the pooled ensemble of experiments 0-4, ie. Sisters Machine experiments. Every point represents neighbor bacteria of the same generation in the pooled ensemble of the Sisters Machine experiments (Vashistha et al. 2021). There are between $3430 - 3667$ points in each panel. It is clear to see that there are no short timescale correlations between neighbor pair bacteria. This implies that the micro-environment only influences the set-points of a lineage and not the fluctuations around it.
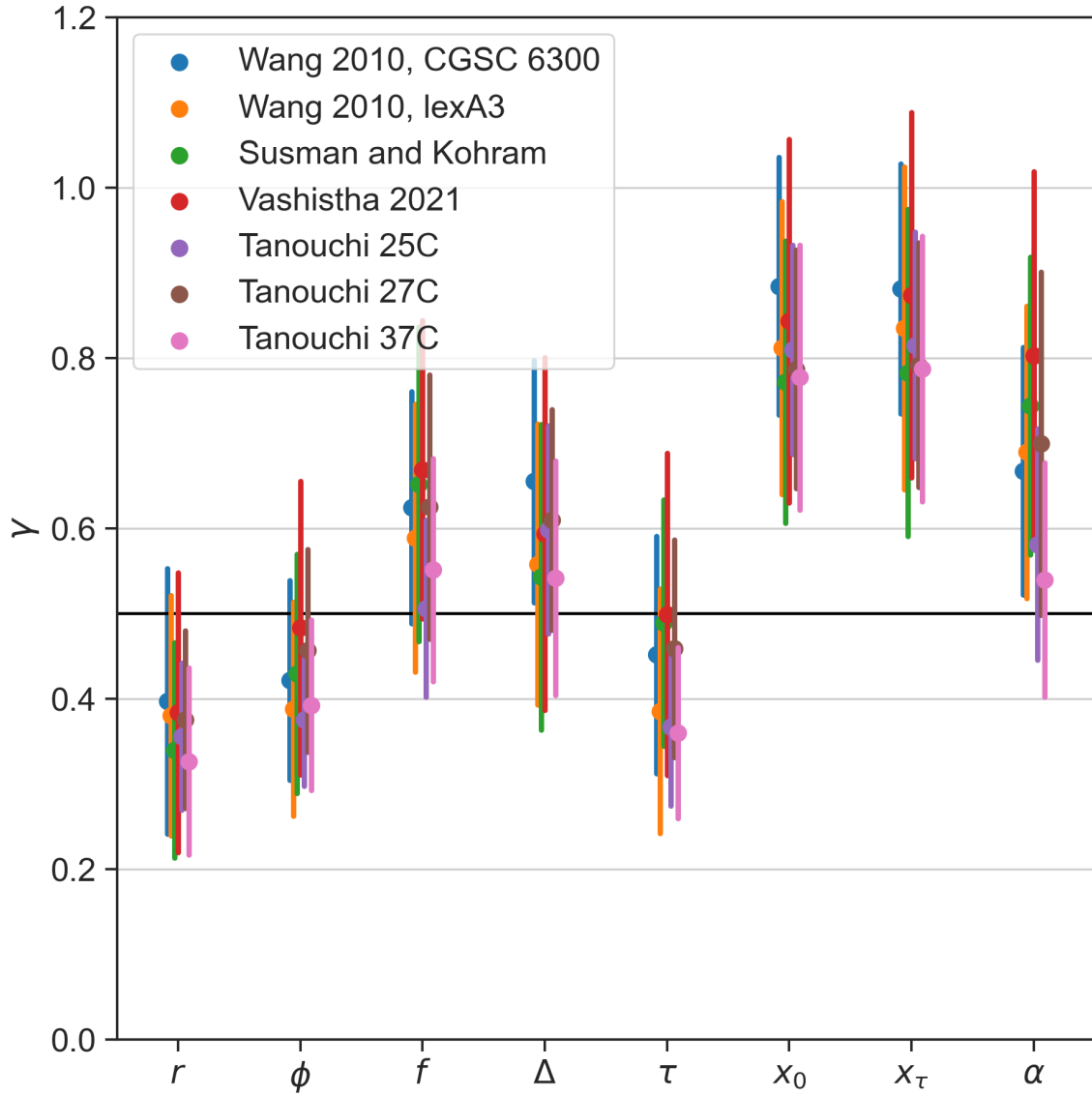
Figure S9: **Persistence of phenotypic variables.** This figure is related to 9C in the main text. It shows the trace lineage scaling exponents for different experiment groups independently (color code in legend). While there is still some variance between data-sets, the relative behavior and trends are consistent with Fig. 9C. The value expected for a random walk, $\gamma = 0.5$, is depicted by a black horizontal line.