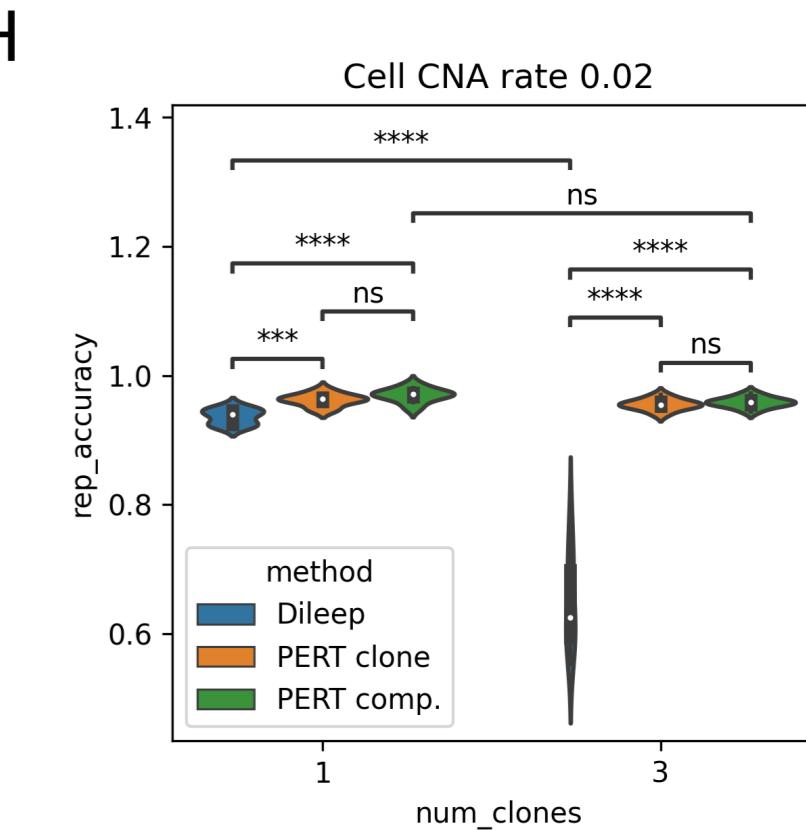
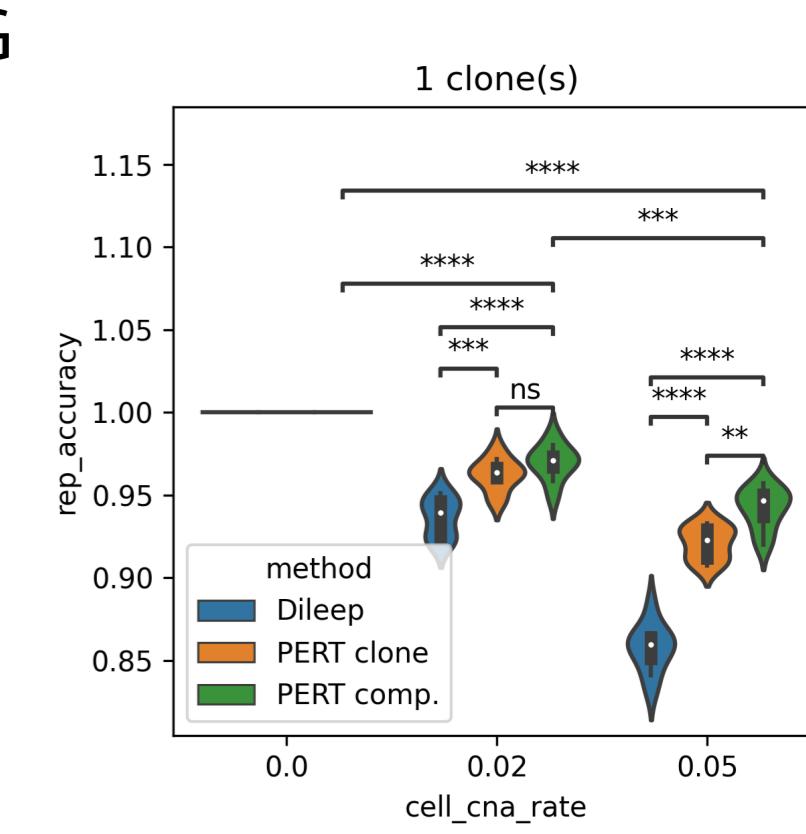
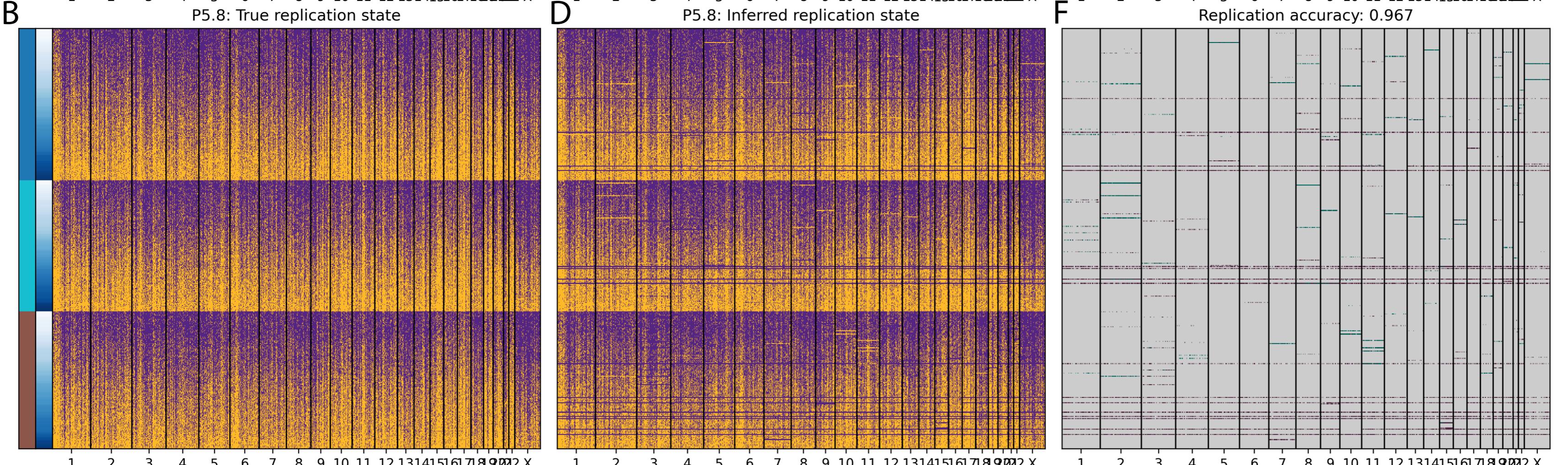
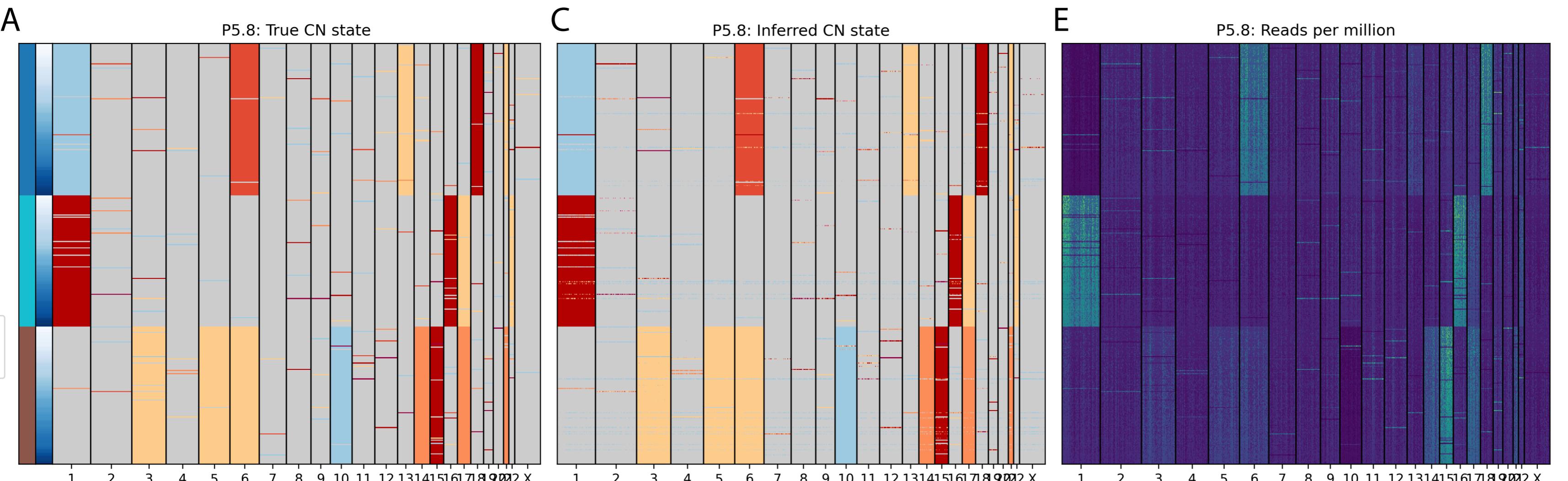
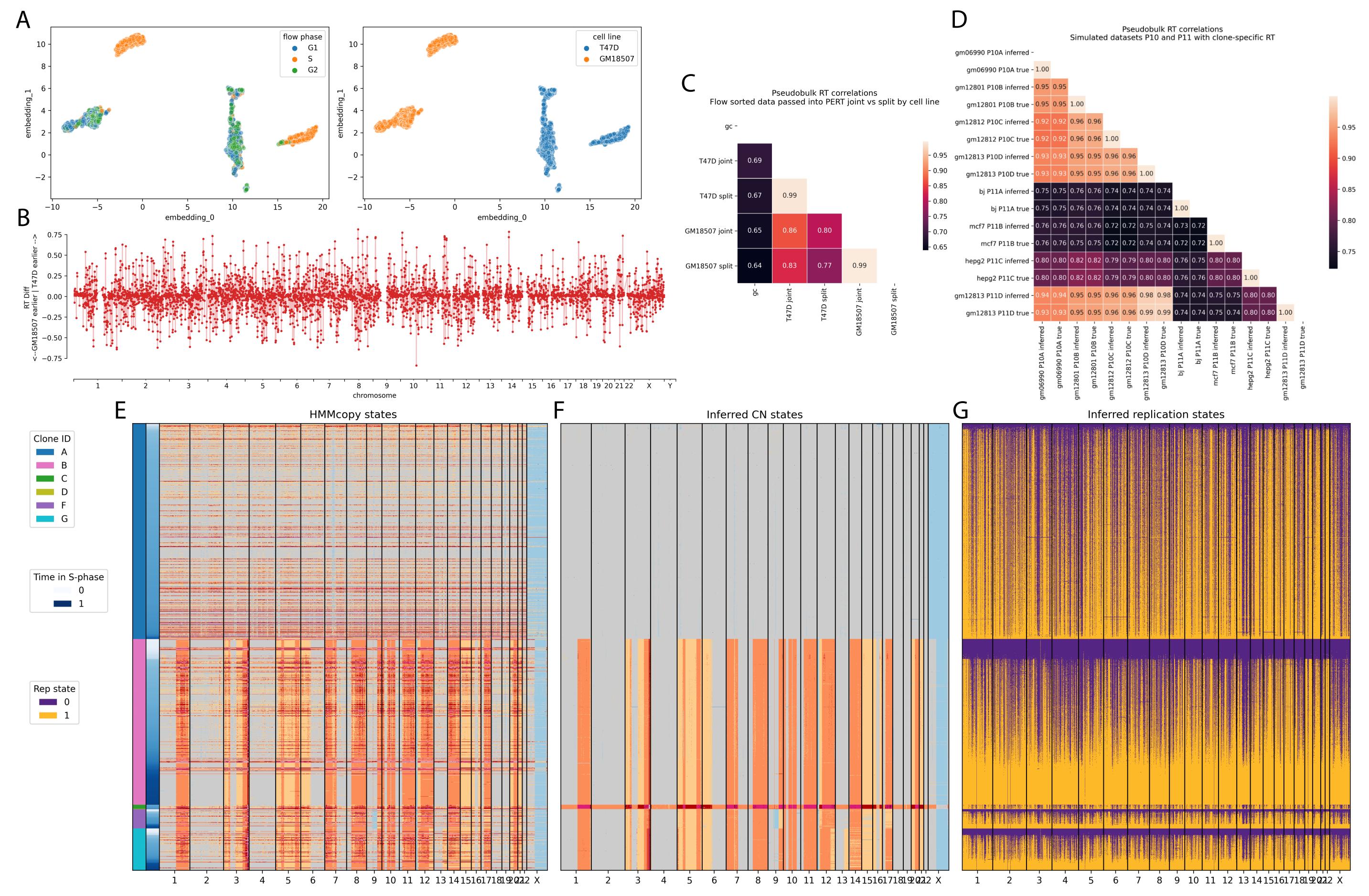
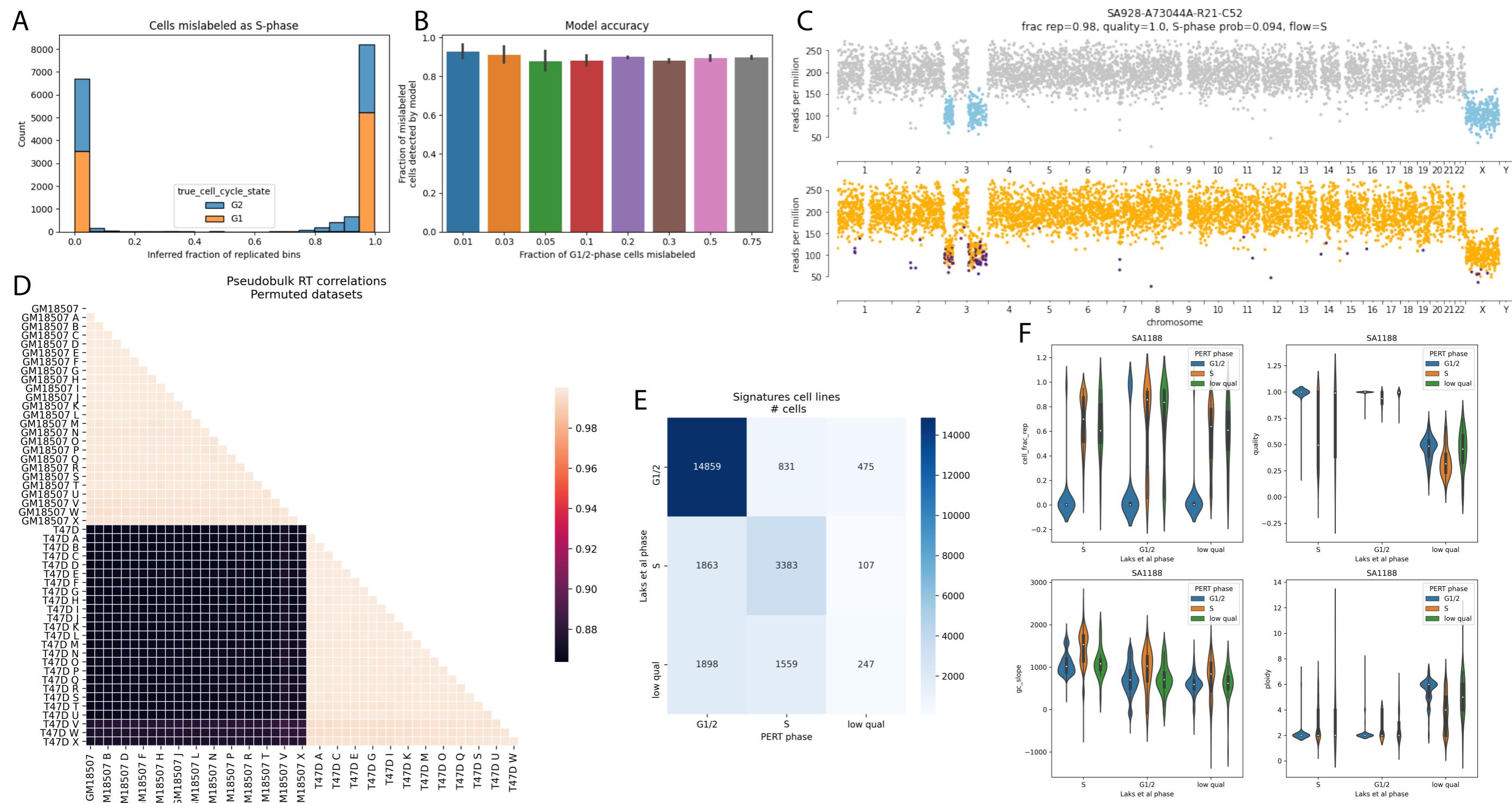
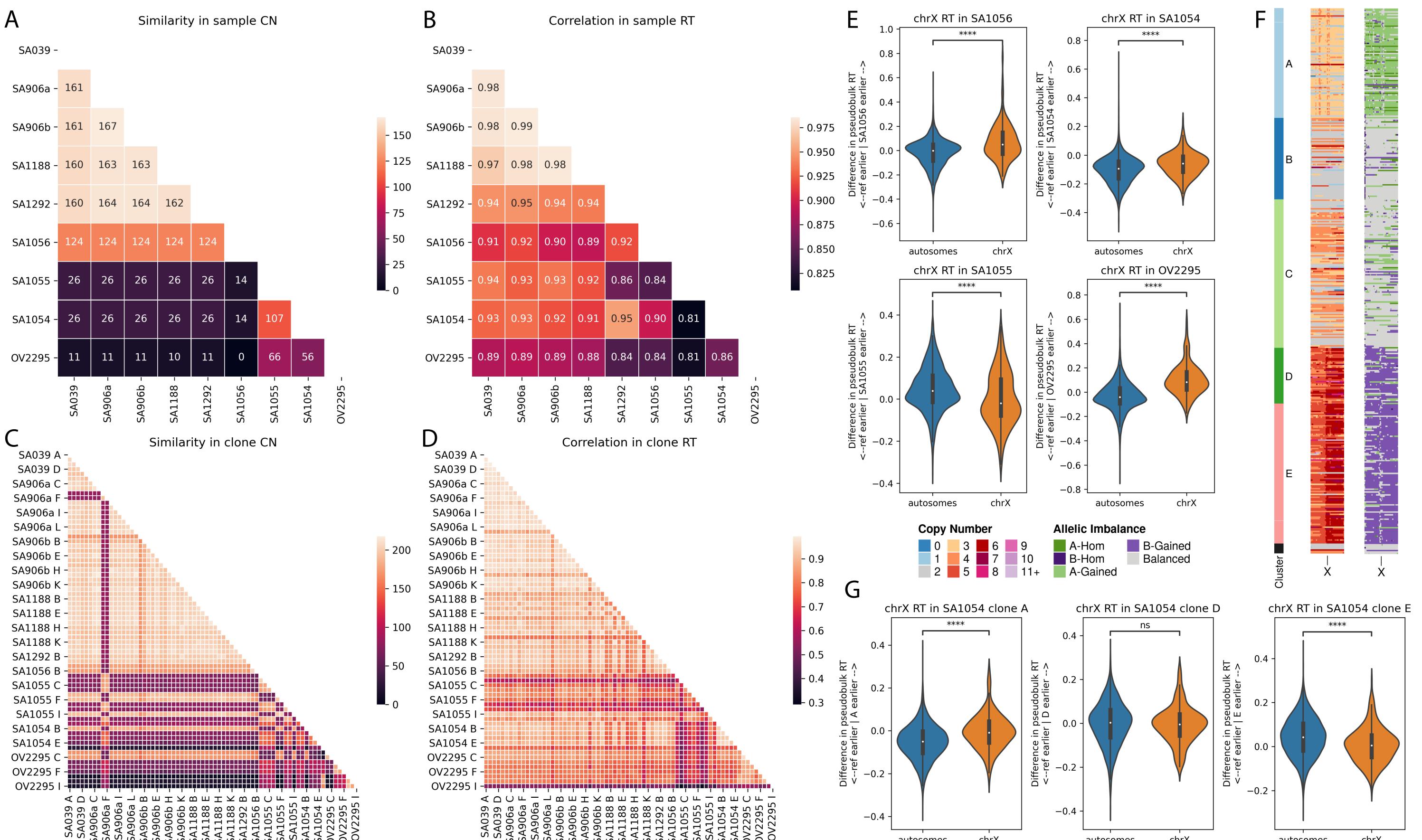


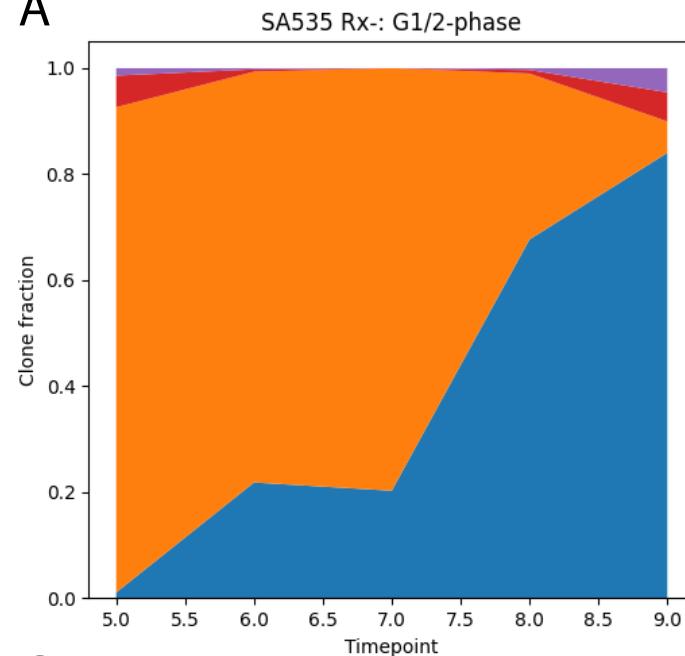
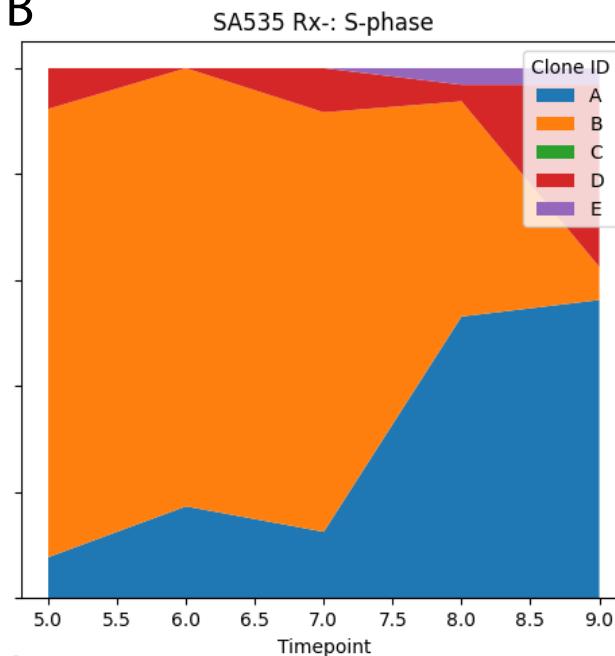
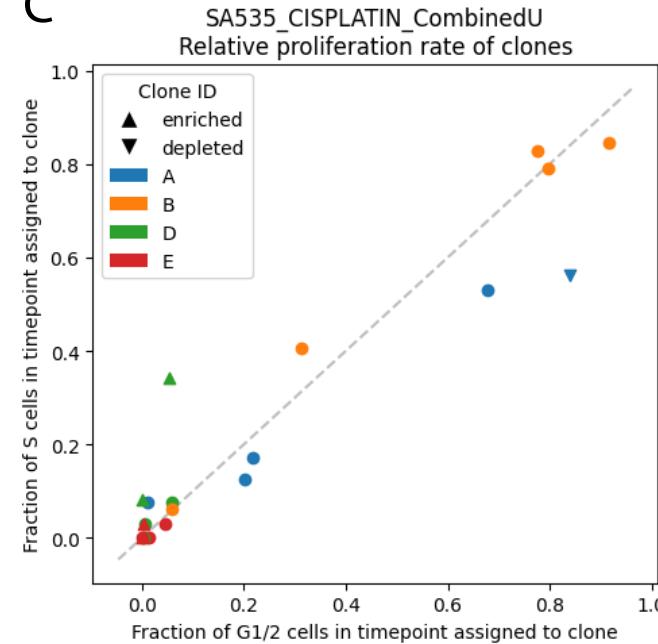
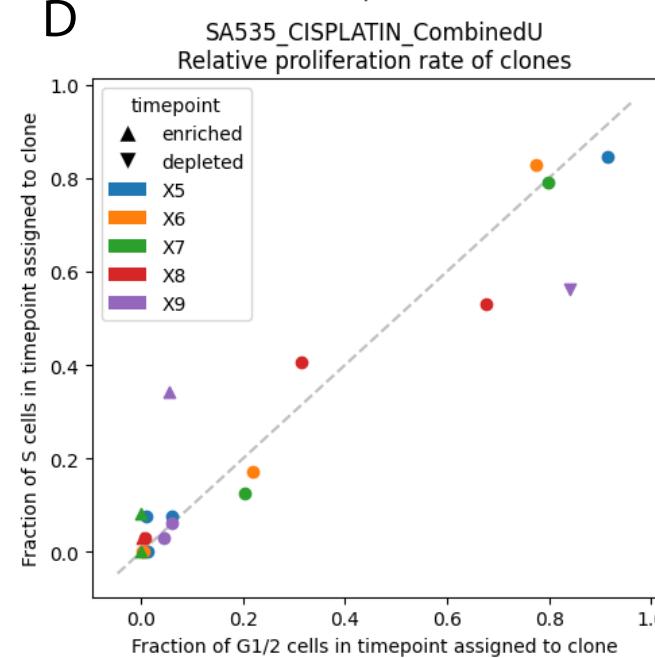
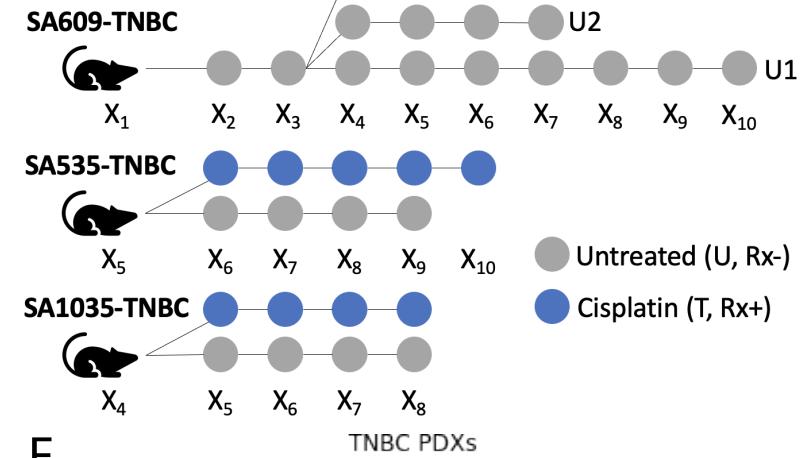
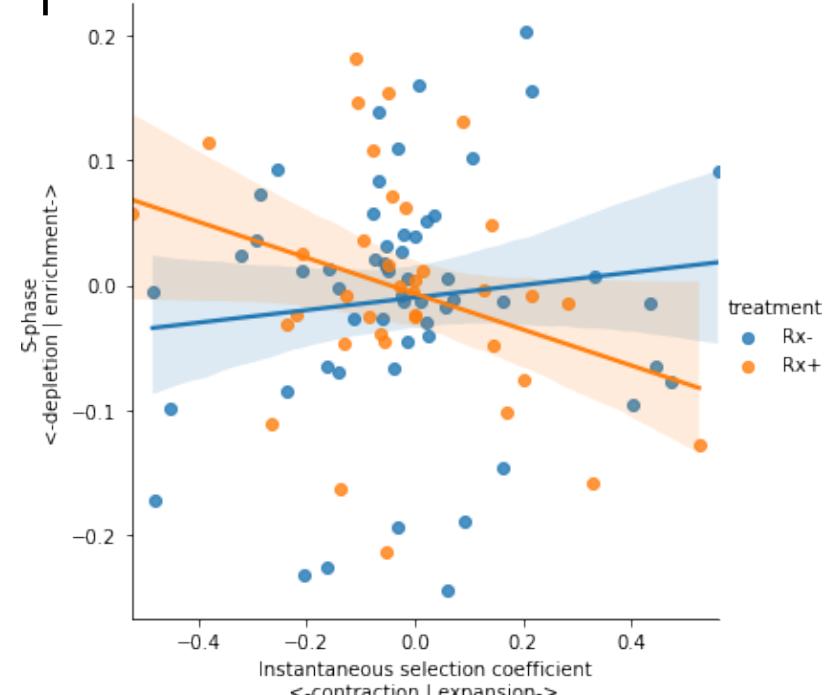
| Name | Domain/Distribution | Description |
|----------------|-----------------------------------|-----------------------------------------------|
| λ | (0, 1) | NB event success probability (overdispersion) |
| δ | [1, ∞) | # of NB events (Eq 4.4) |
| γ | [0, 1] | GC content of locus |
| β_μ | $\sim N(0, 1)$ | GC bias polynomial coefficient means |
| β_σ | (0, ∞) | GC bias polynomial coefficient stdevs |
| β | $\sim N(\beta_\mu, \beta_\sigma)$ | GC bias polynomial coefficients |
| μ_μ | (0, ∞) | coverage/ploidy mean (Eq 4.8) |
| μ_σ | (0, ∞) | coverage/ploidy stdev (Eq 4.9) |
| μ | $\sim N(\mu_\mu, \mu_\sigma)$ | coverage/ploidy scaling term |
| τ | [0, 1] | time in S-phase |
| ρ | $\sim Beta(1, 1)$ | replication timing |
| α | $\sim \Gamma(2, 0.2)$ | replication stochasticity term |
| ϕ | (0, 1) | replication probabilities (Eq 4.5) |
| Y | $\sim Bernoulli(\phi)$ | replication status |
| η | [0, 1] | copy number prior concentration |
| π | $\sim Dir(\eta)$ | copy number probabilities |
| X | $\sim Cat(\pi)$ | copy number state |
| Z | $\sim NB(\delta, \lambda)$ | read depth |
| K | | GC bias polynomial degree |
| L | | # libraries |
| M | | # genomic loci |
| N | | # cells |
| P | | # copy number states |



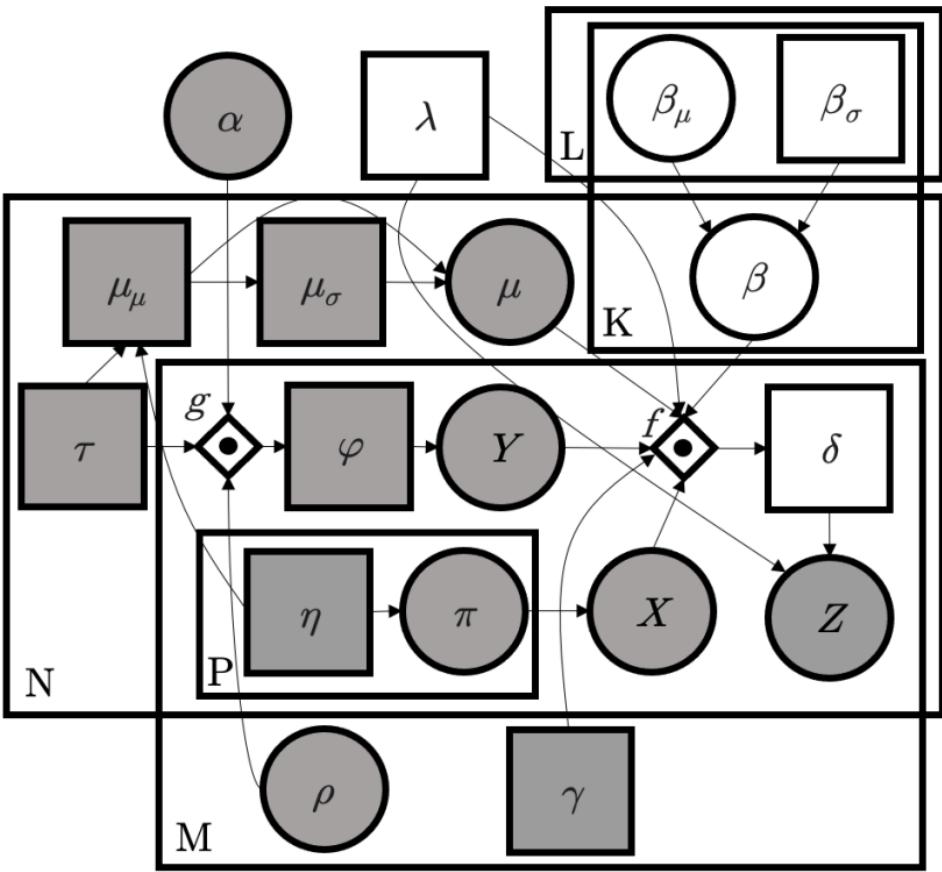




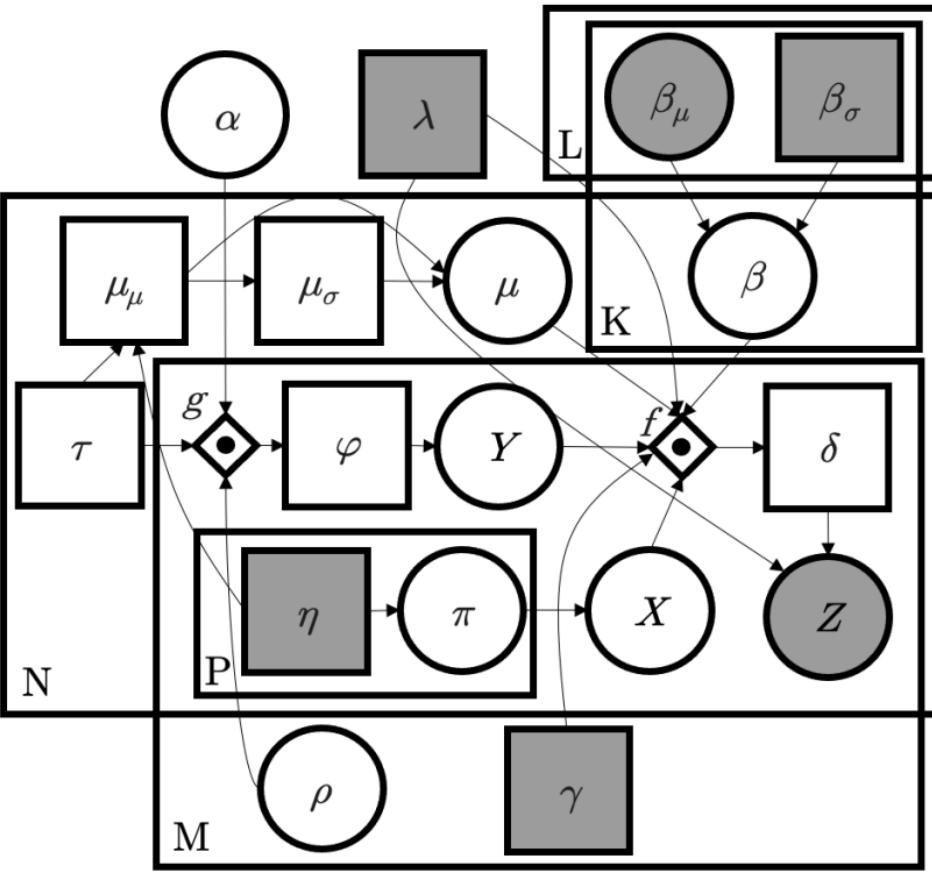


A**B****C****D****E****F**

Step 1



Step 2



Step 3

