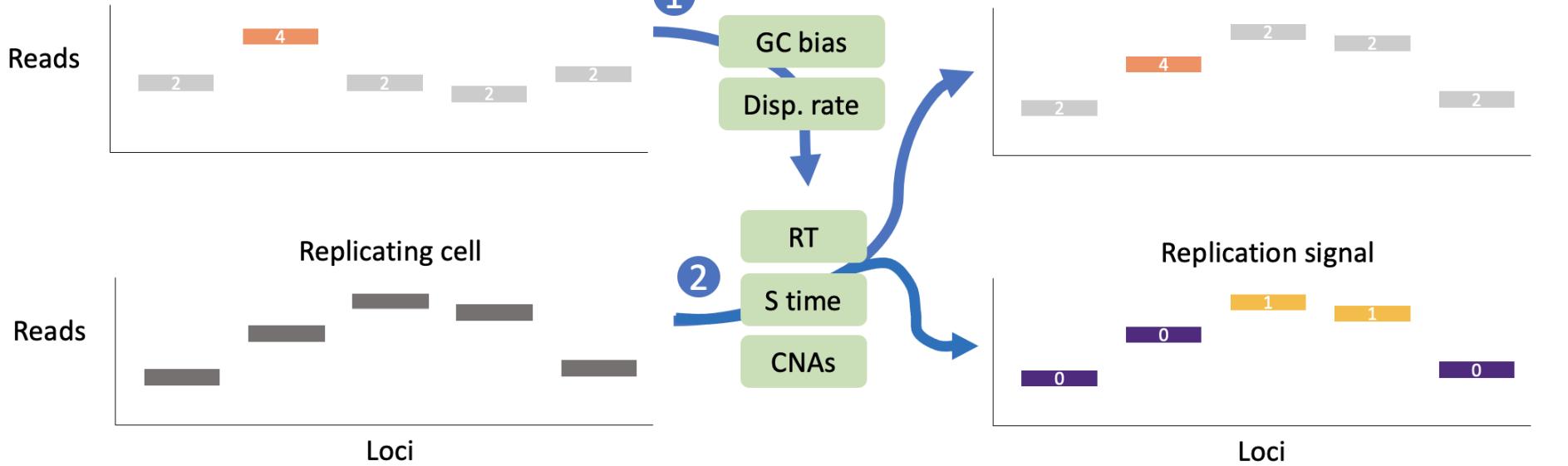
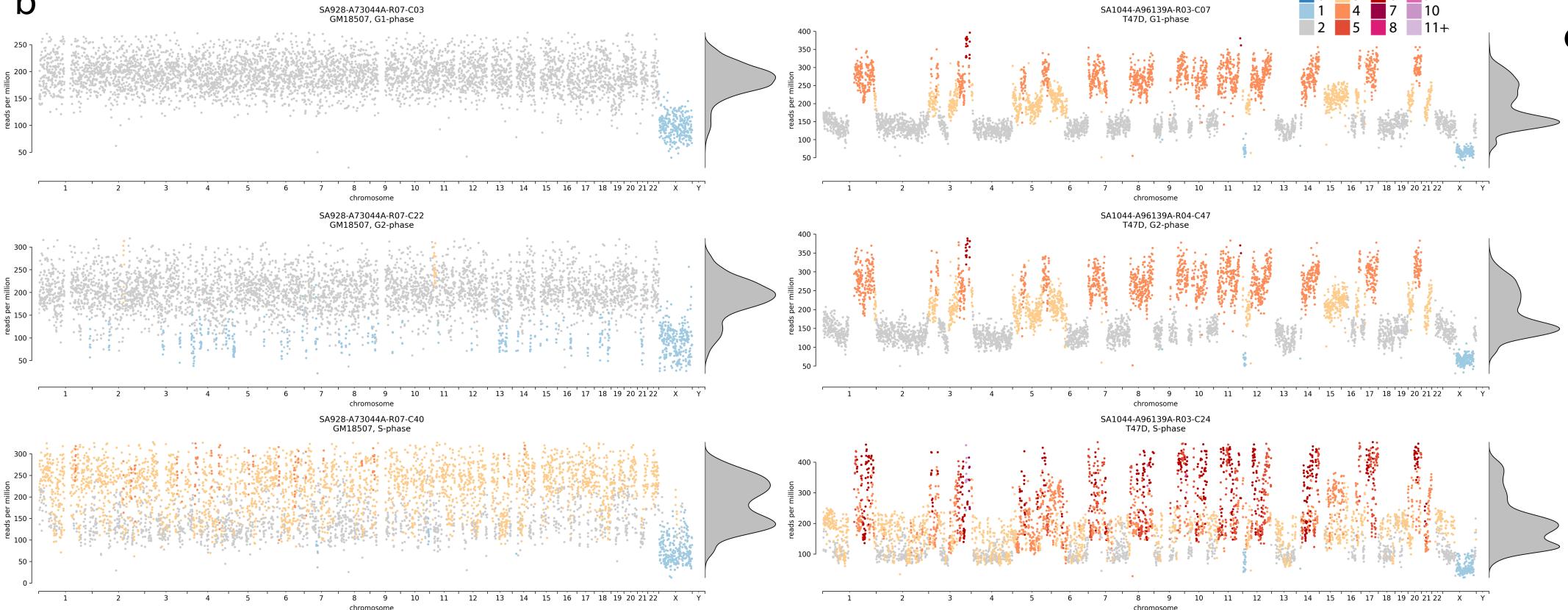


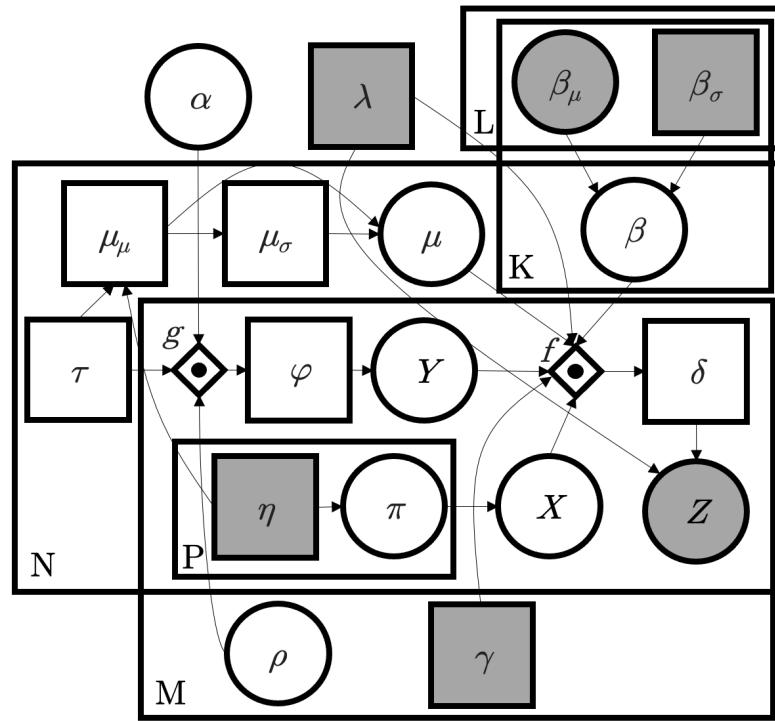
a Non-replicating cell



b

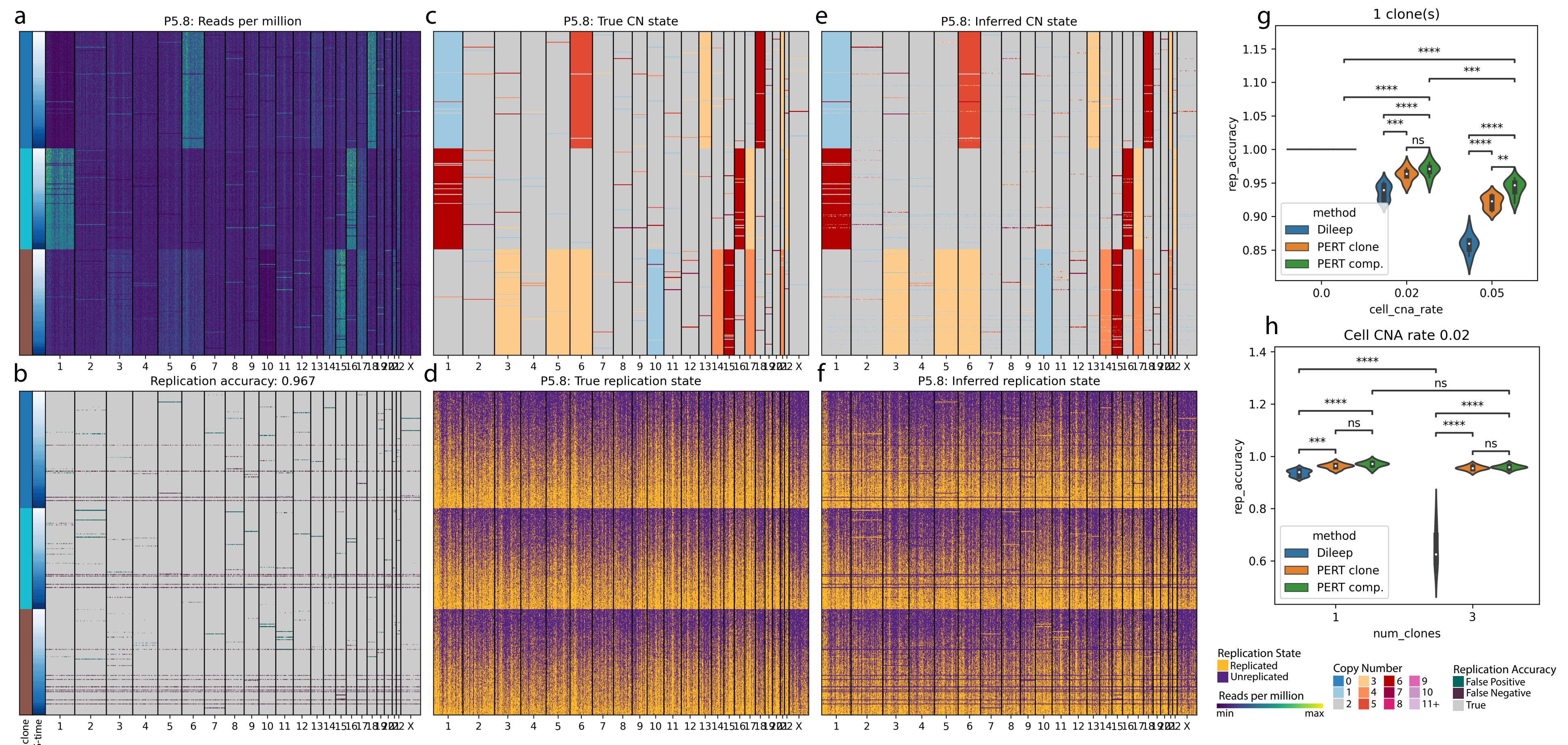


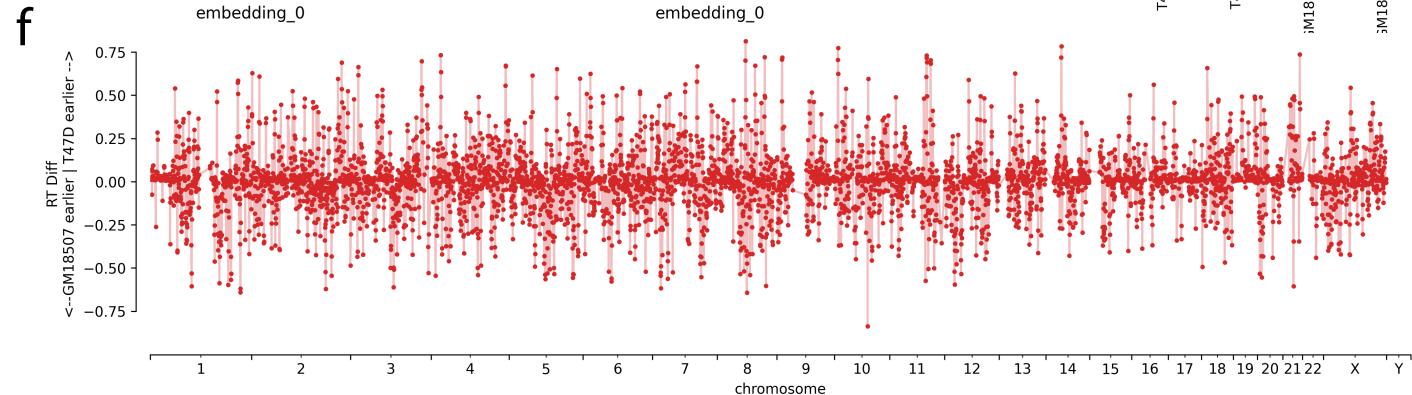
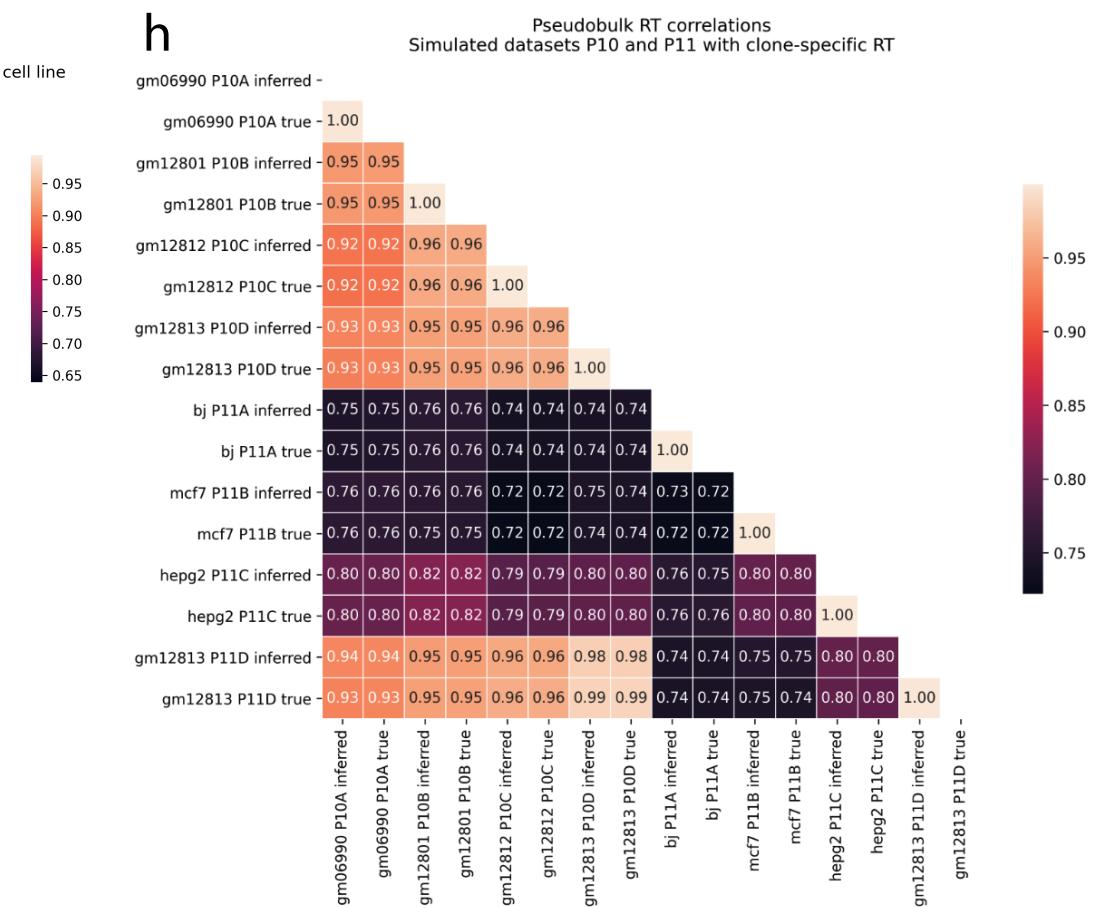
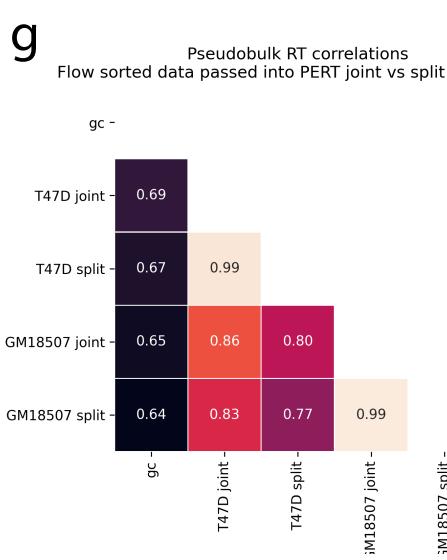
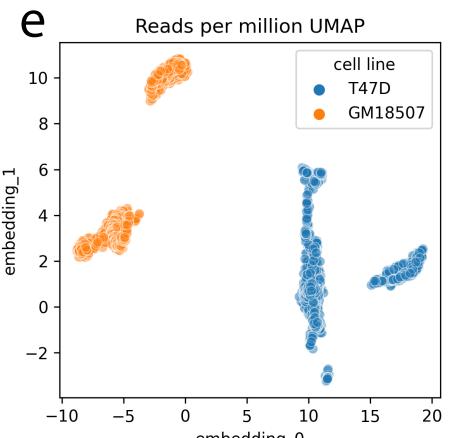
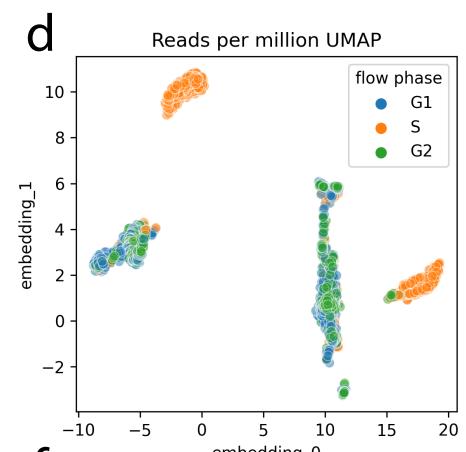
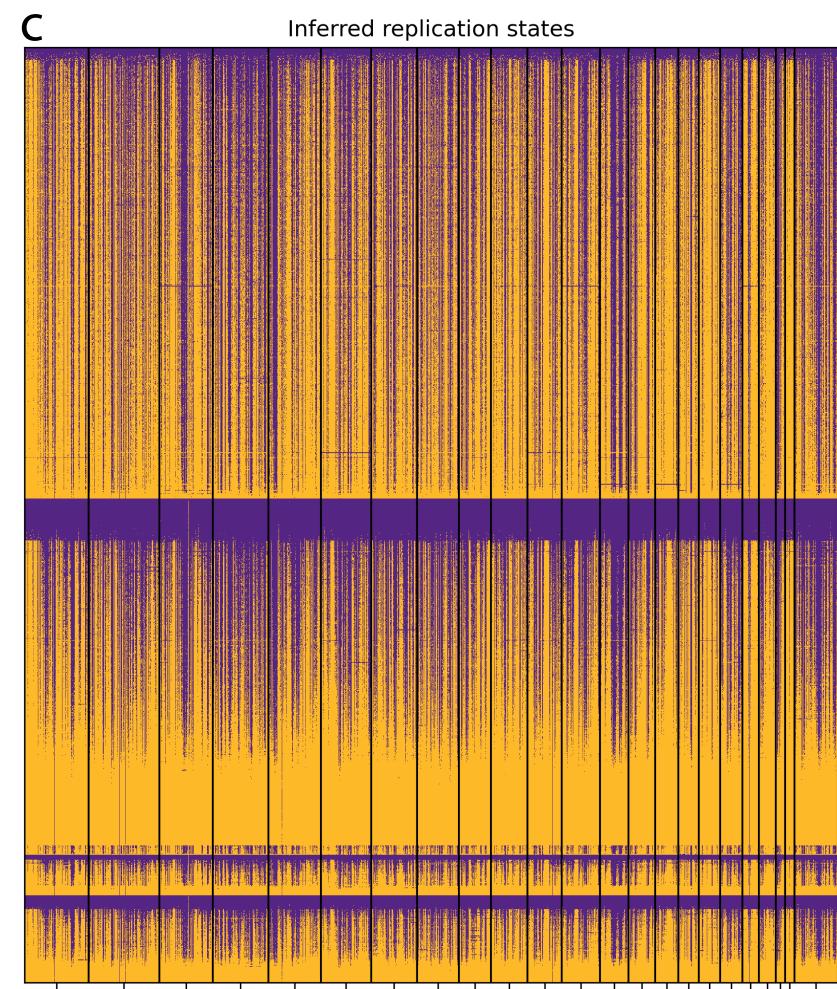
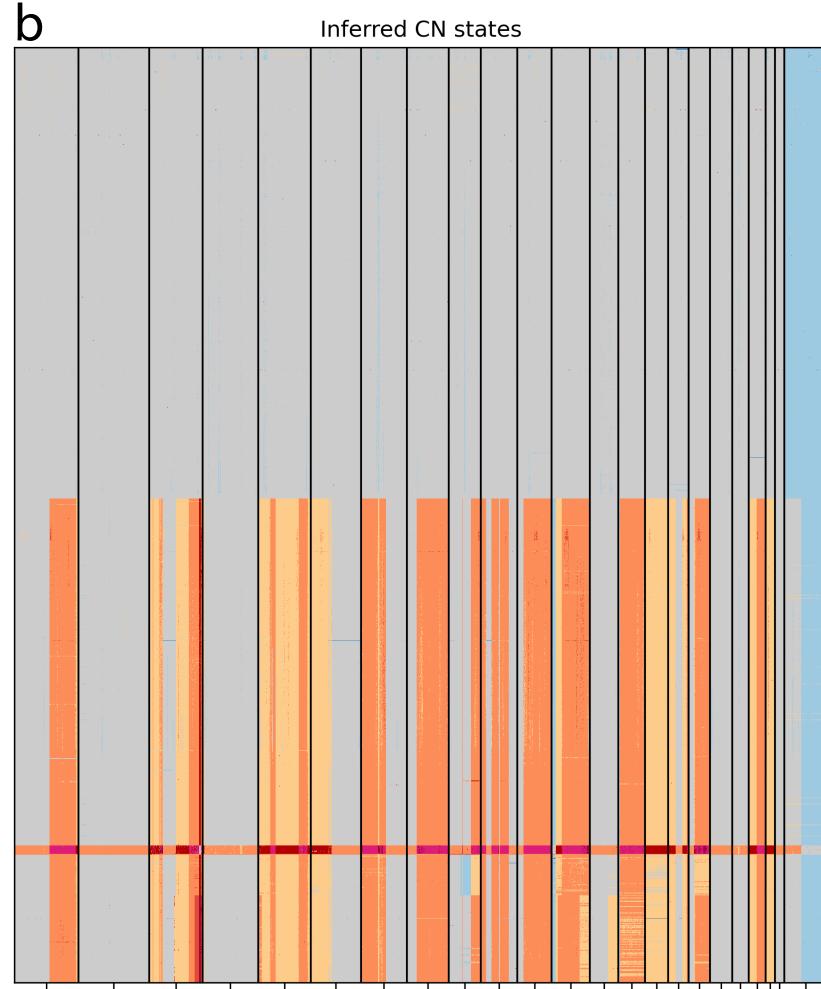
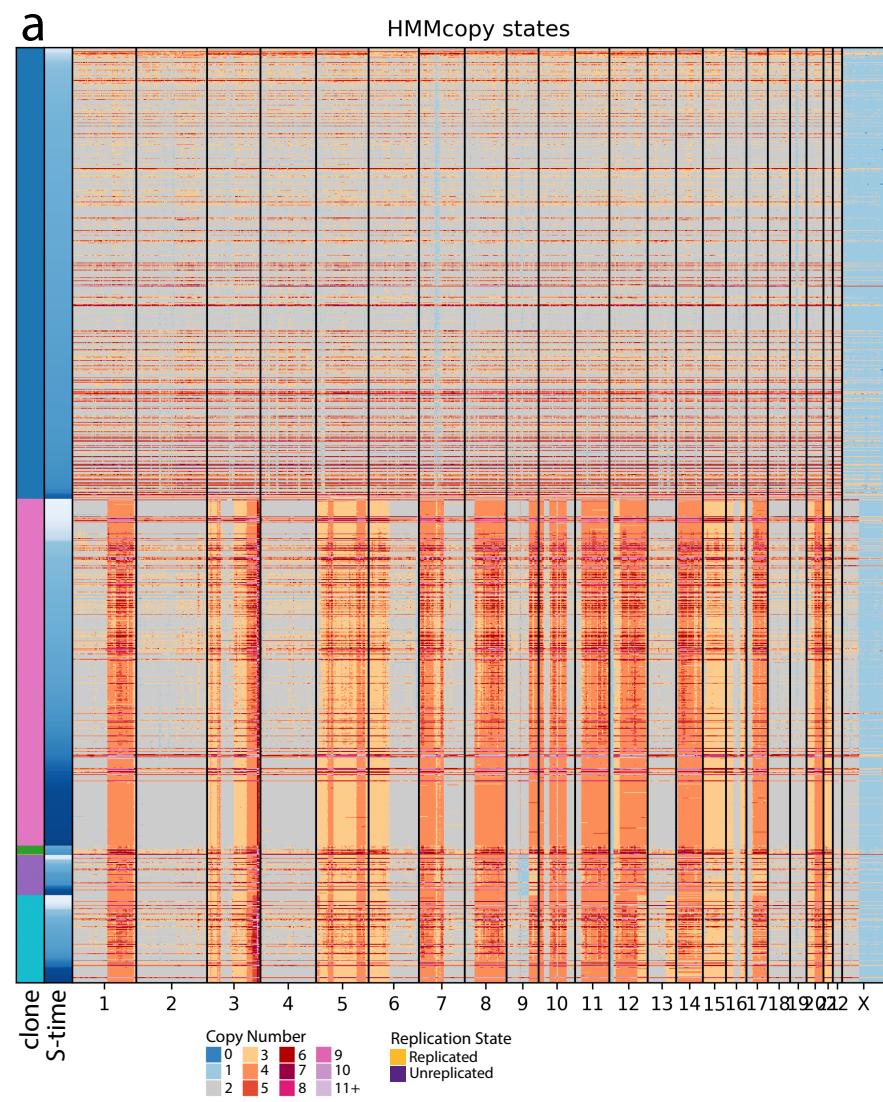
c

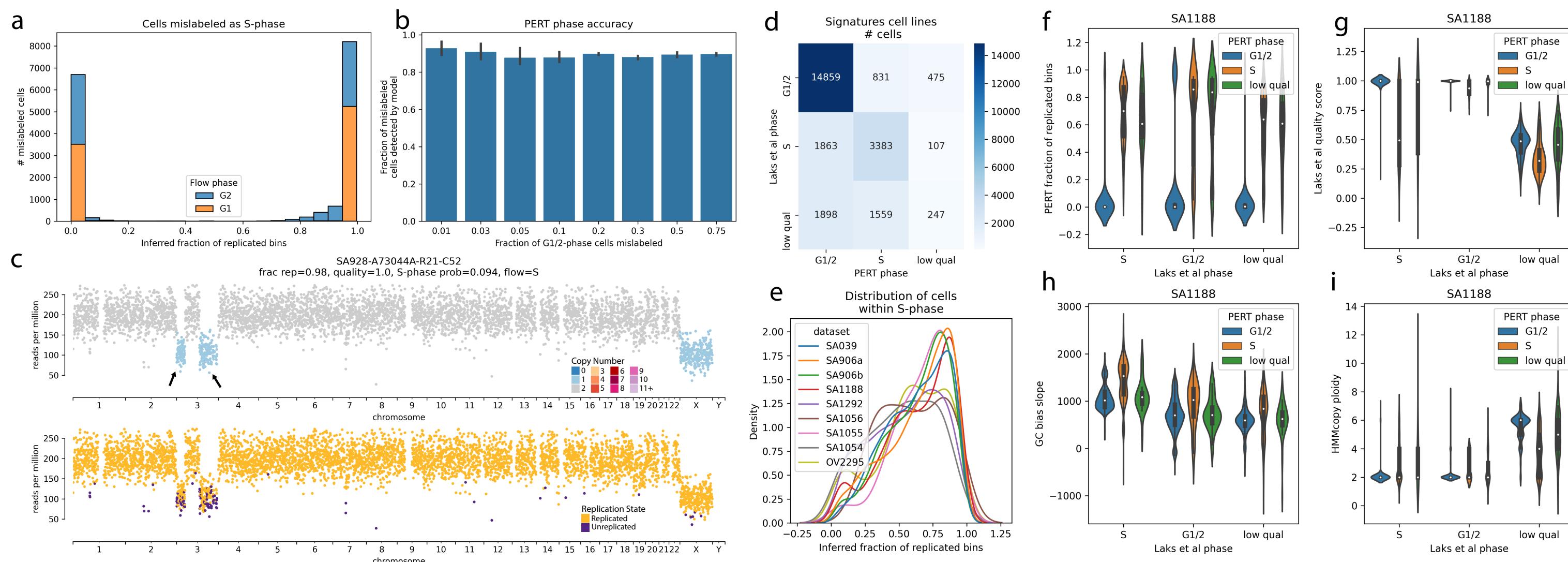


d

Name	Domain/Distribution	Description
λ	$(0, 1)$	NB event success probability (overdispersion)
δ	$[1, \infty)$	# 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	$(0, \infty)$	GC bias polynomial coefficient stdevs
β	$\sim N(\beta_\mu, \beta_\sigma)$	GC bias polynomial coefficients
μ_μ	$(0, \infty)$	coverage/ploidy mean (Eq 4.8)
μ_σ	$(0, \infty)$	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

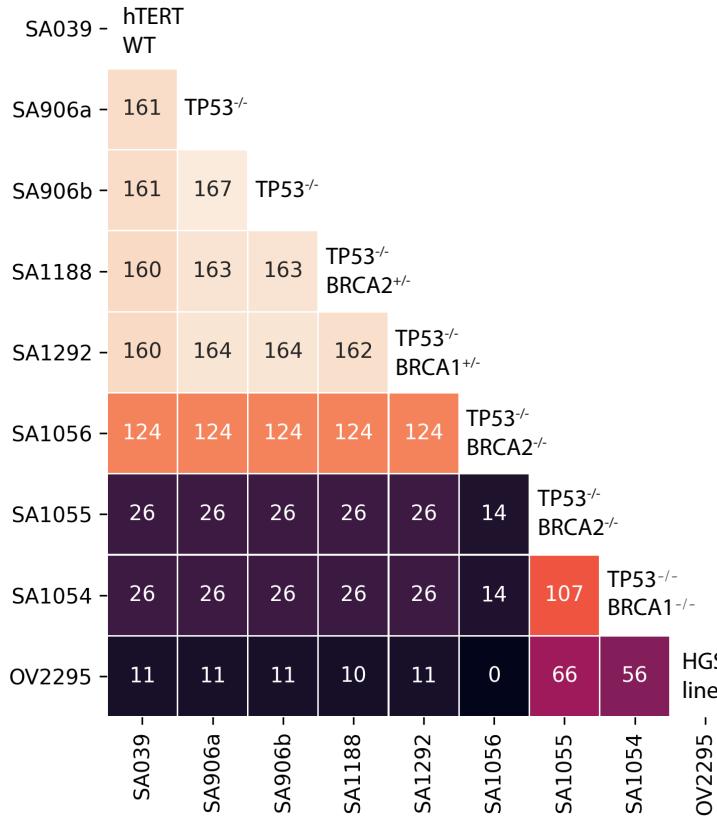




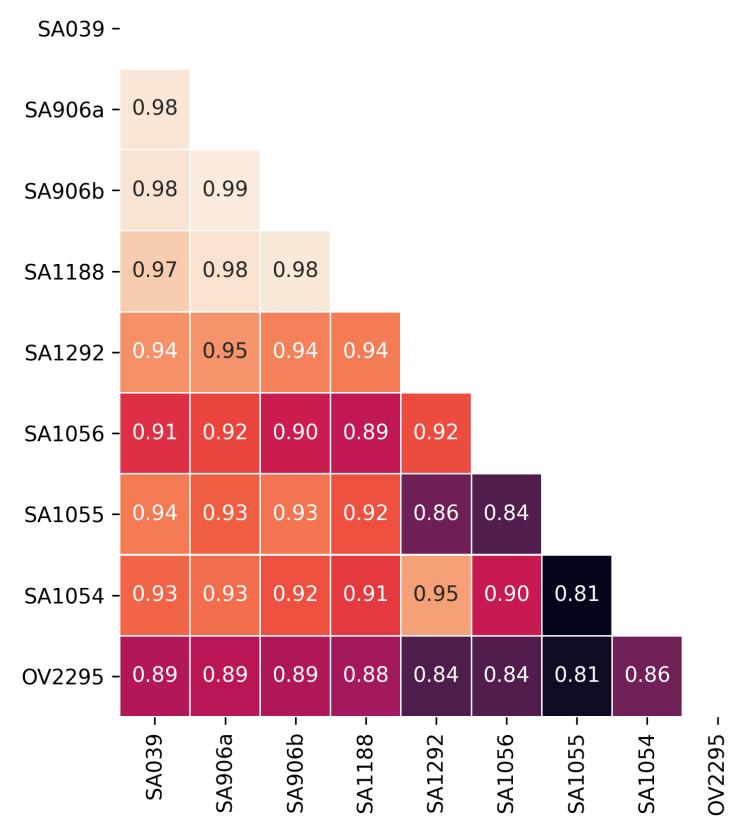


a

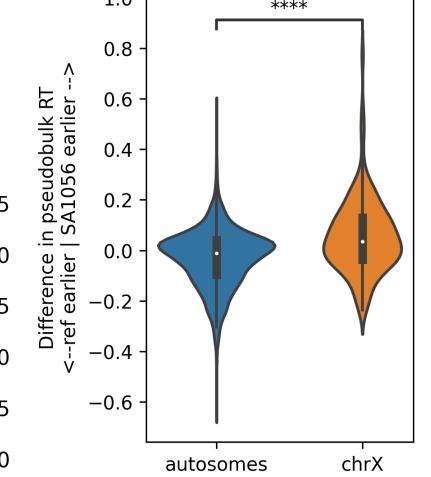
Similarity in sample CN

**b**

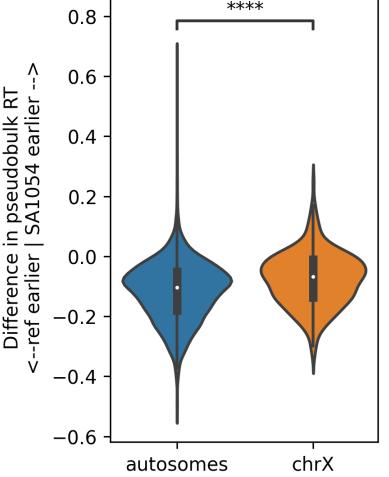
Correlation in sample RT

**e**

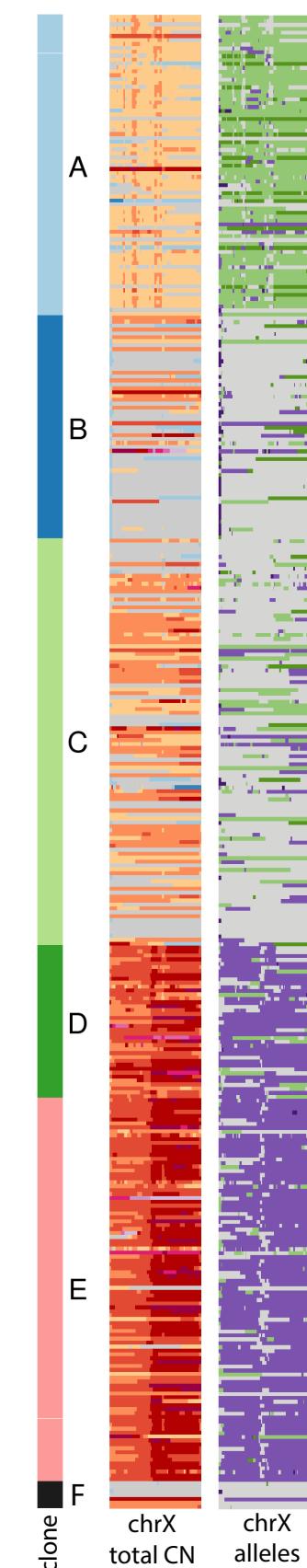
chrX RT in SA1056



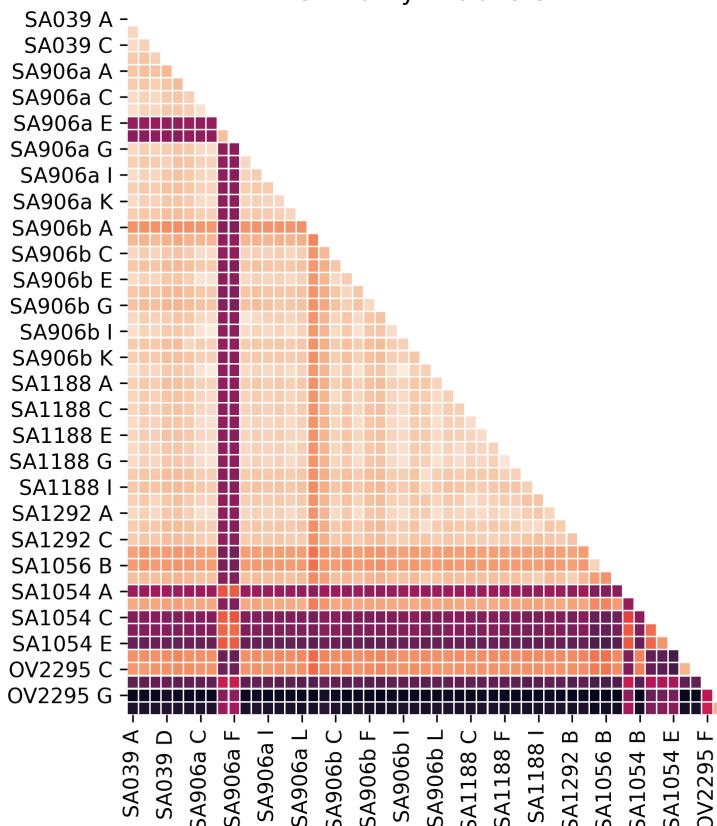
chrX RT in SA1054

**f**

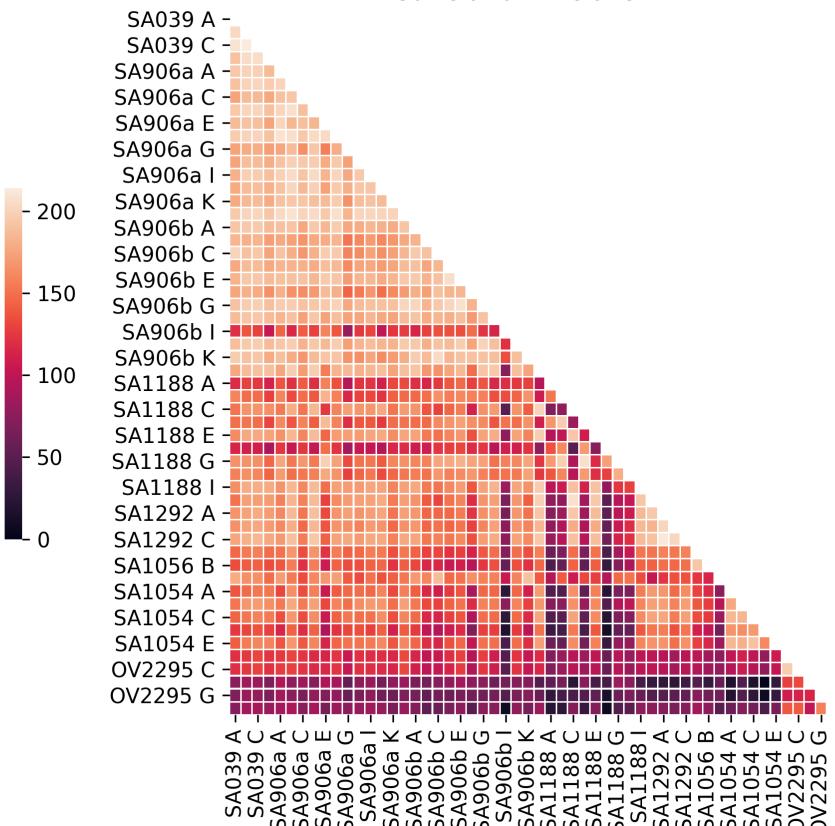
SA1054 SIGNALS

**c**

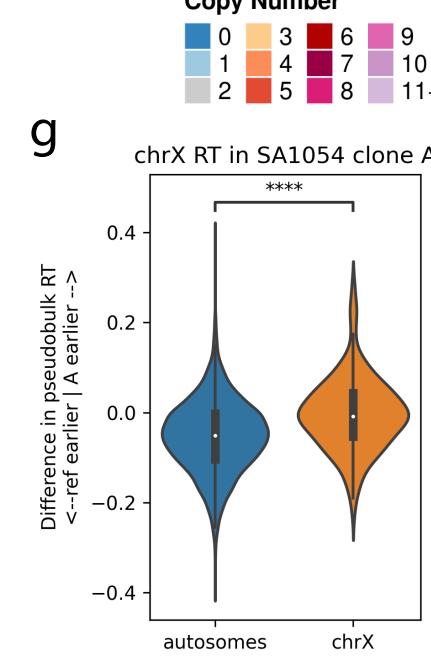
Similarity in clone CN

**d**

Correlation in clone RT

**g**

chrX RT in SA1054 clone A



chrX RT in SA1054 clone DE

