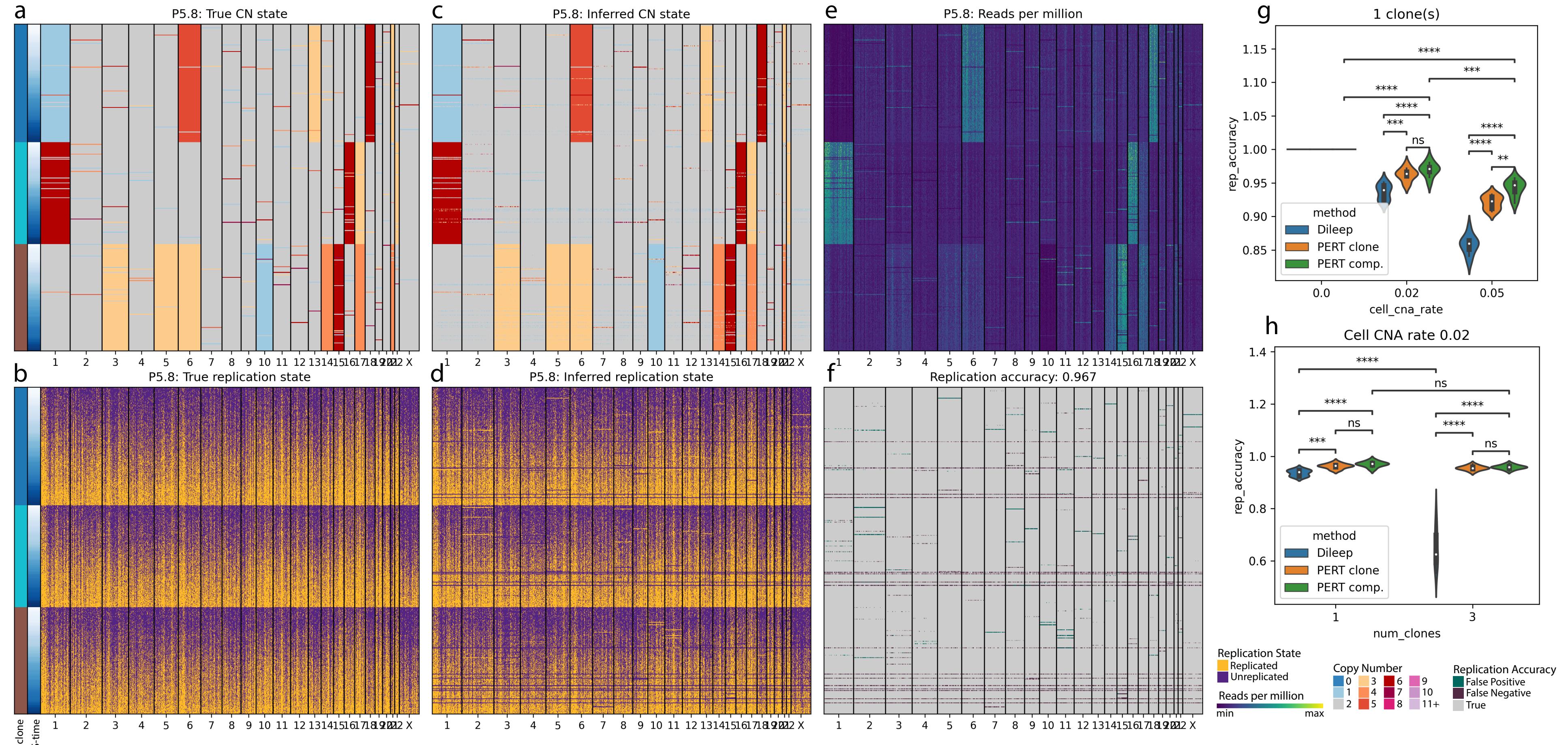
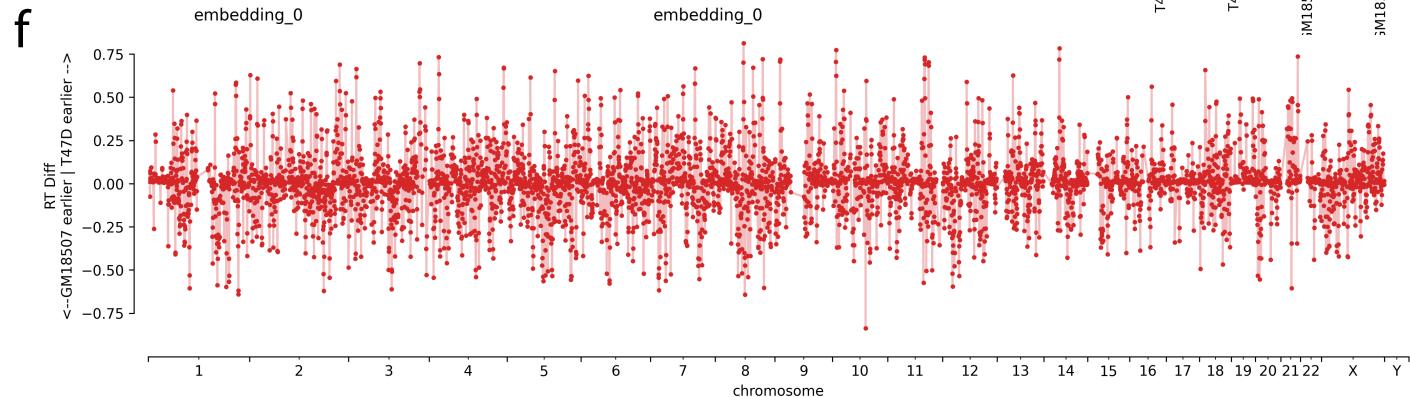
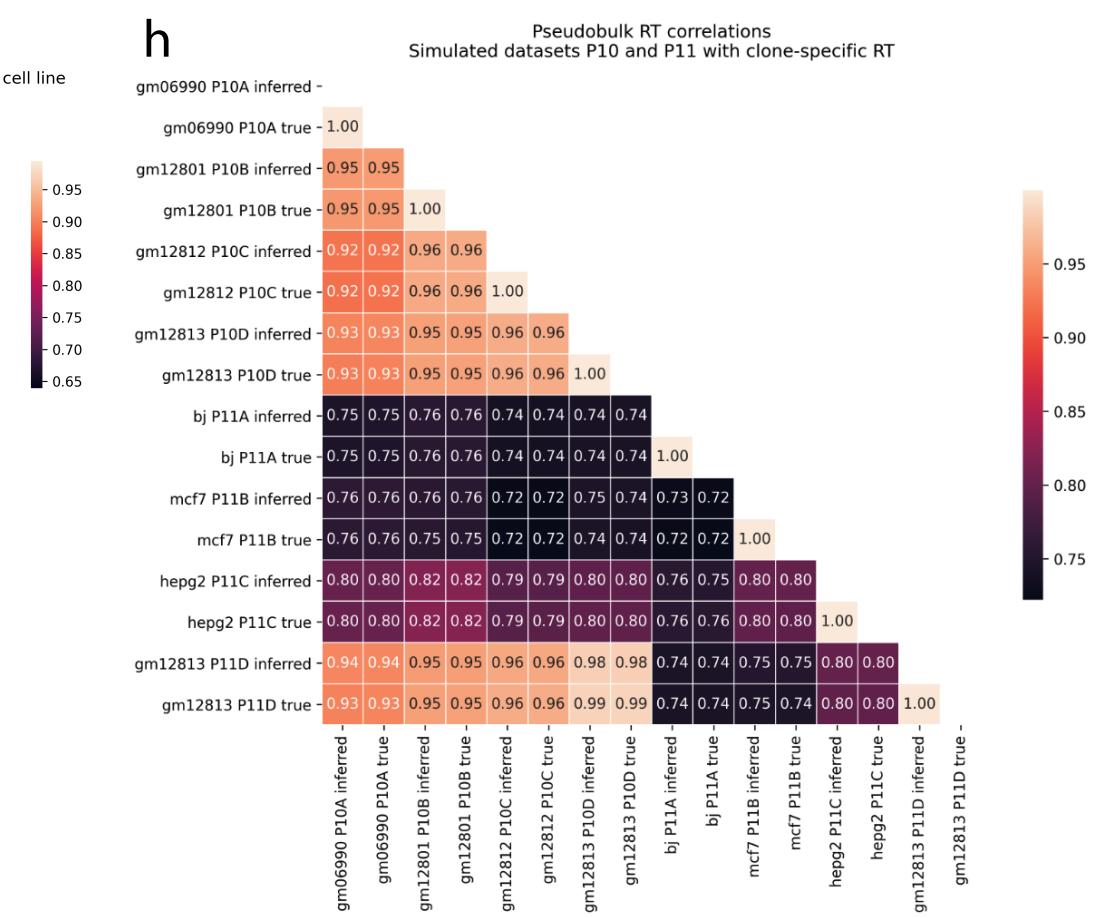
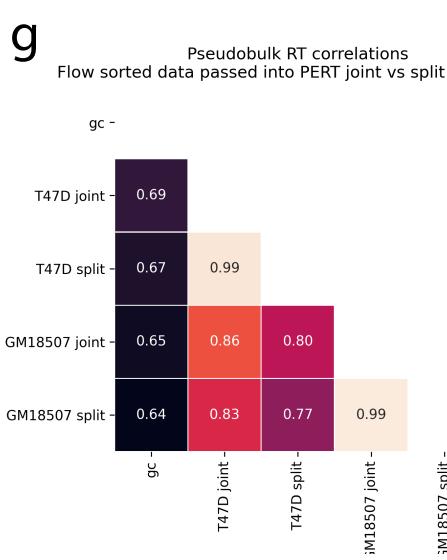
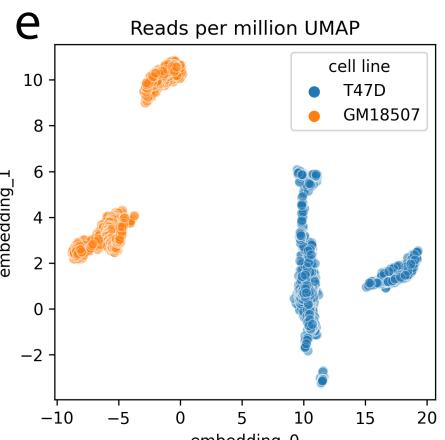
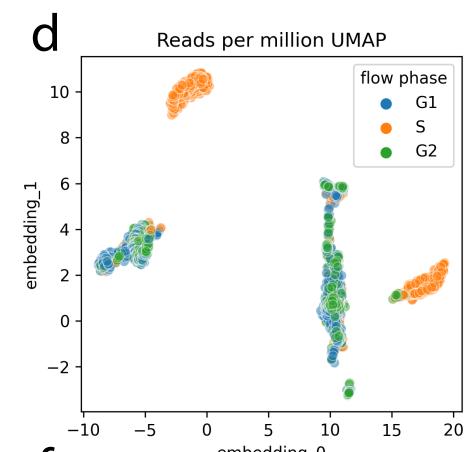
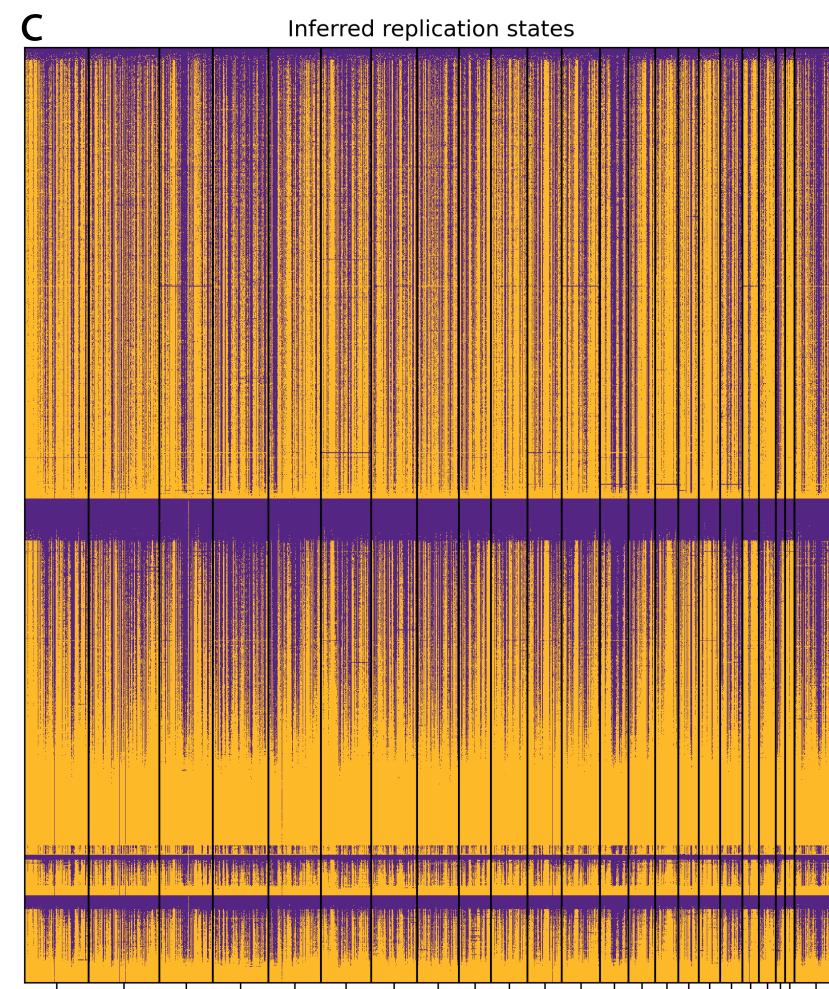
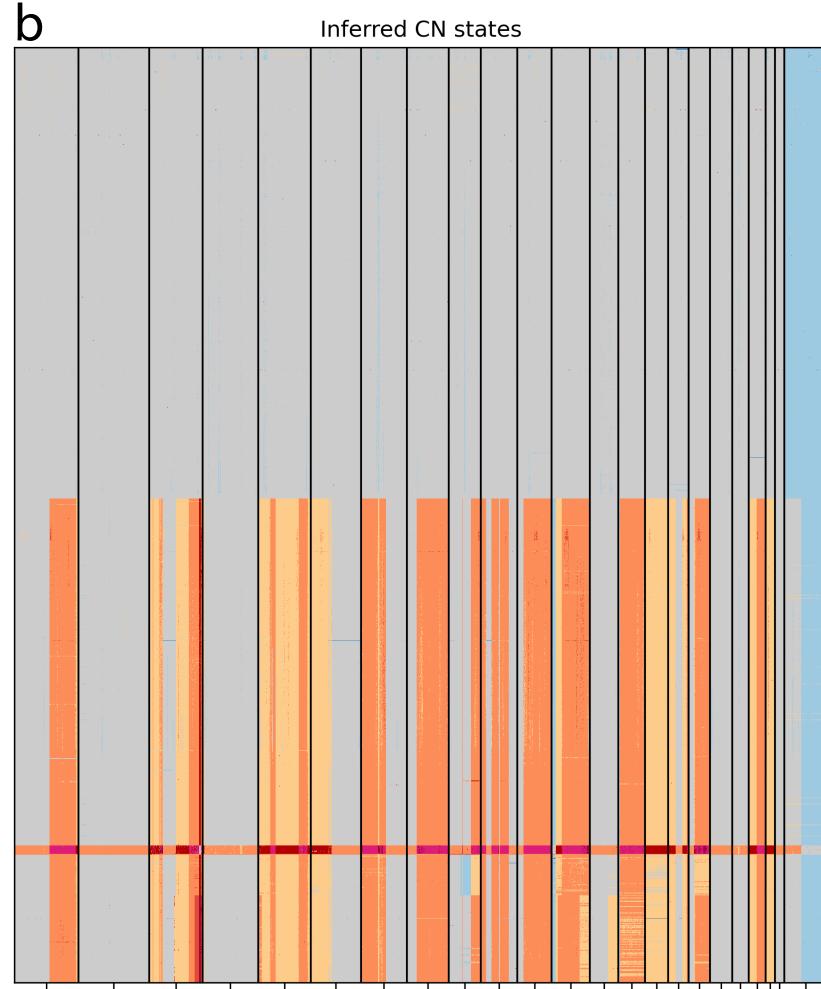
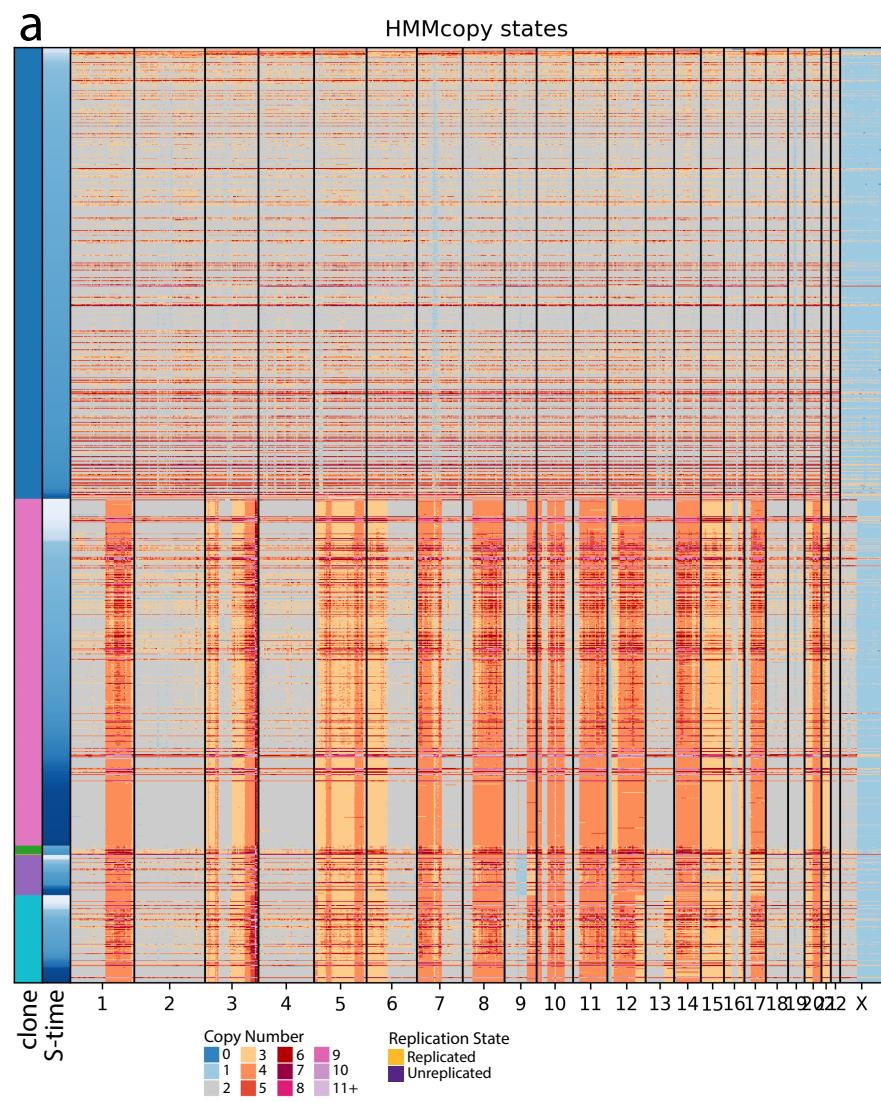
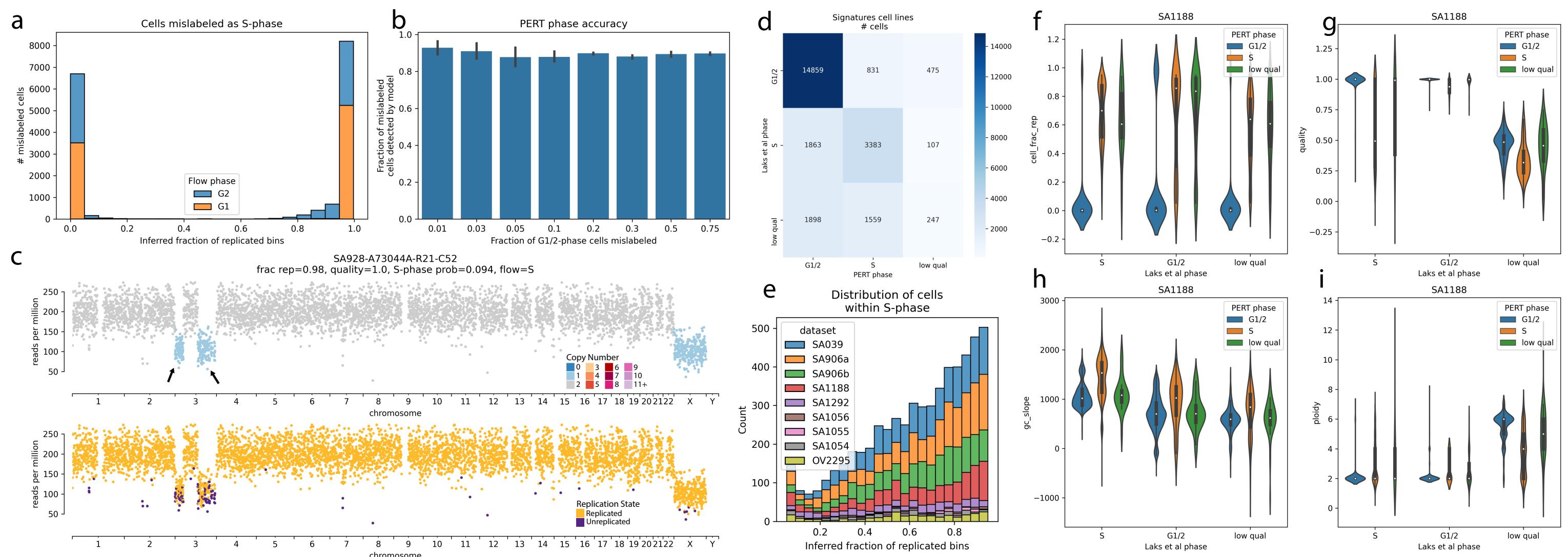


Name	Domain/Distribution	Description
$\lambda$	(0, 1)	NB event success probability (overdispersion)
$\delta$	[1, $\infty$ )	# of NB events (Eq 4.4)
$\gamma$	[0, 1]	GC content of locus
$\beta_\mu$	$\sim N(0, 1)$	GC bias polynomial coefficient means
$\beta_\sigma$	(0, $\infty$ )	GC bias polynomial coefficient stdevs
$\beta$	$\sim N(\beta_\mu, \beta_\sigma)$	GC bias polynomial coefficients
$\mu_\mu$	(0, $\infty$ )	coverage/ploidy mean (Eq 4.8)
$\mu_\sigma$	(0, $\infty$ )	coverage/ploidy stdev (Eq 4.9)
$\mu$	$\sim N(\mu_\mu, \mu_\sigma)$	coverage/ploidy scaling term
$\tau$	[0, 1]	time in S-phase
$\rho$	$\sim \text{Beta}(1, 1)$	replication timing
$\alpha$	$\sim \Gamma(2, 0.2)$	replication stochasticity term
$\phi$	(0, 1)	replication probabilities (Eq 4.5)
$Y$	$\sim \text{Bernoulli}(\phi)$	replication status
$\eta$	[0, 1]	copy number prior concentration
$\pi$	$\sim \text{Dir}(\eta)$	copy number probabilities
$X$	$\sim \text{Cat}(\pi)$	copy number state
$Z$	$\sim \text{NB}(\delta, \lambda)$	read depth
K		GC bias polynomial degree
L		# libraries
M		# genomic loci
N		# cells
P		# copy number states

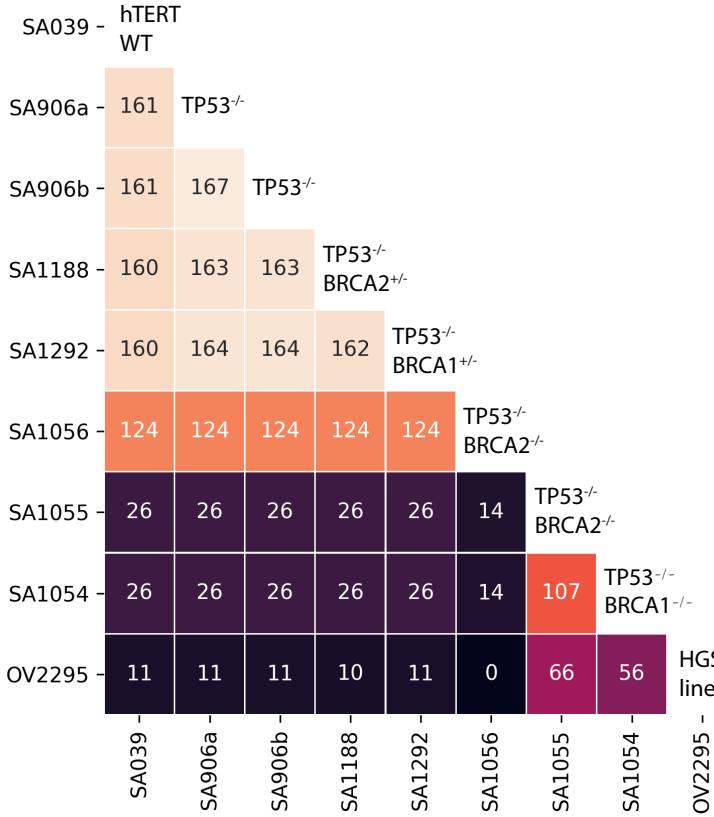




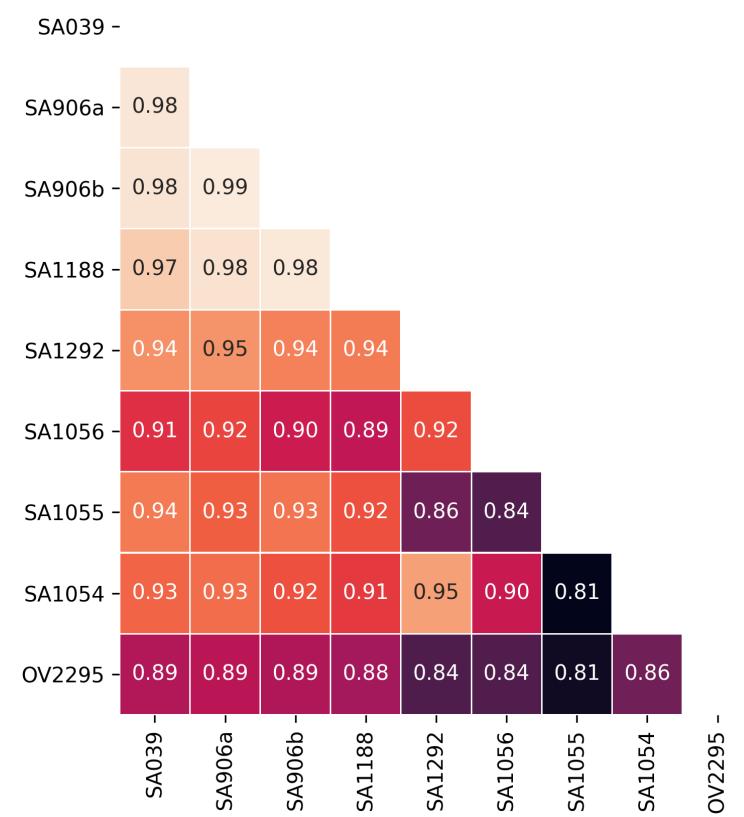


**a**

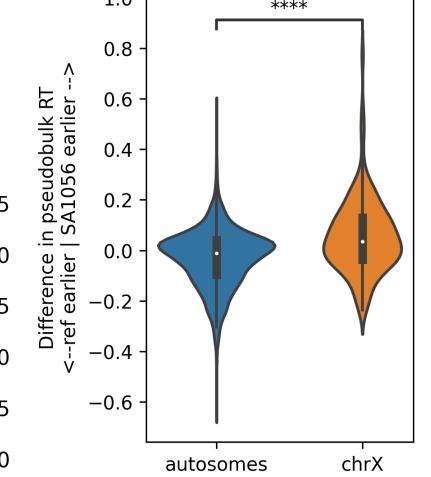
Similarity in sample CN

**b**

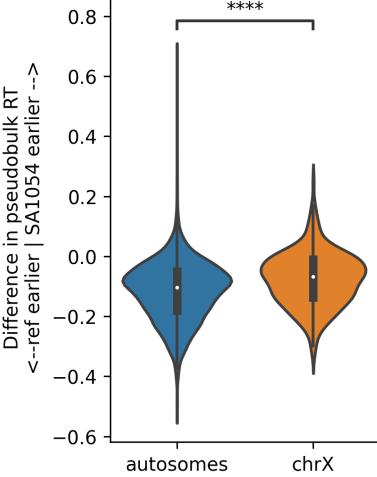
Correlation in sample RT

**e**

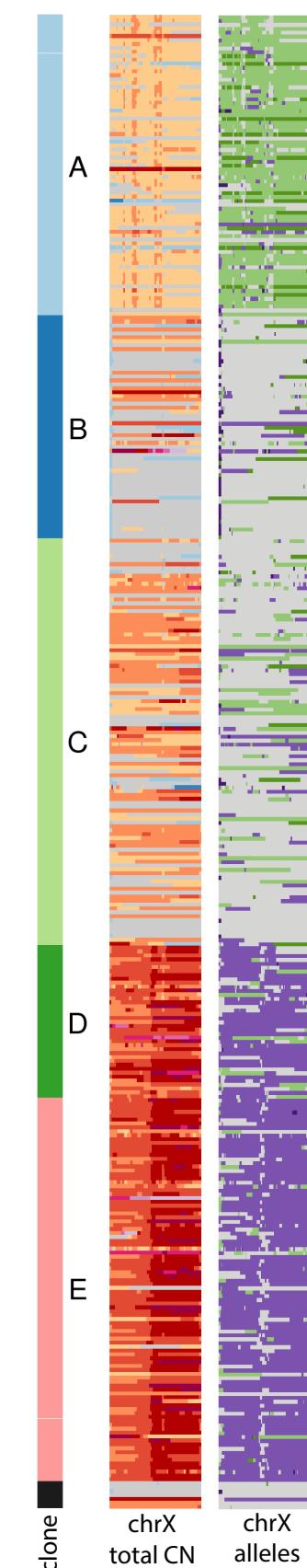
chrX RT in SA1056



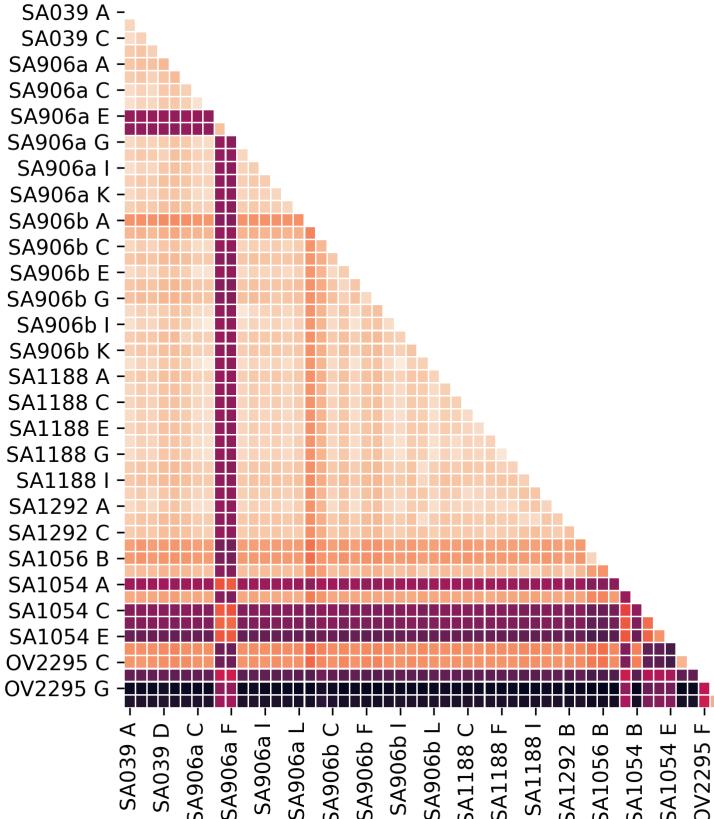
chrX RT in SA1054

**f**

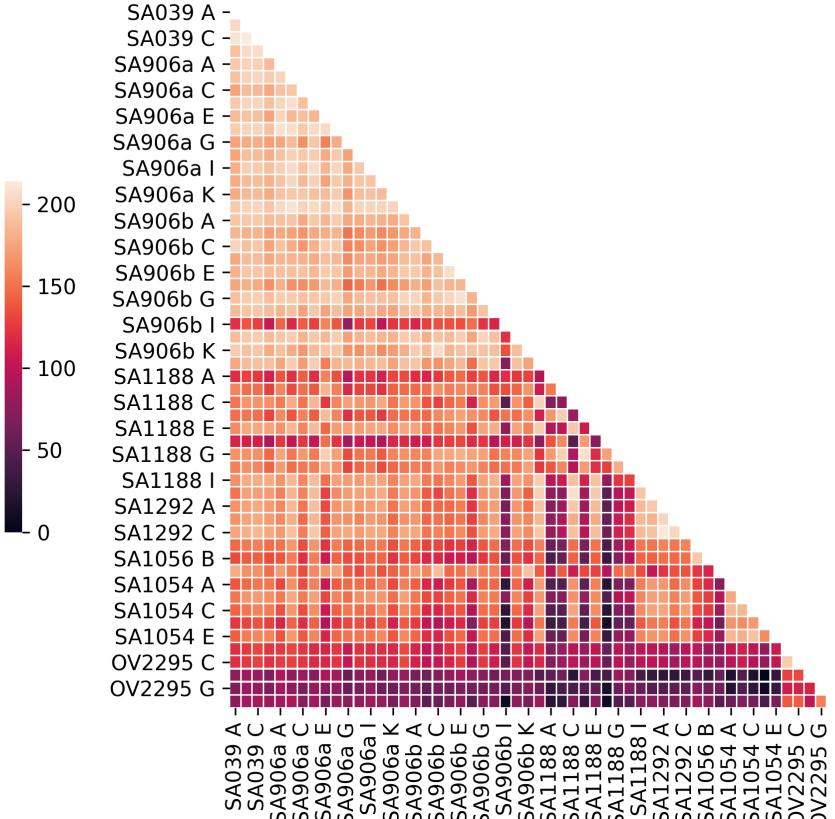
SA1054 SIGNALS

**c**

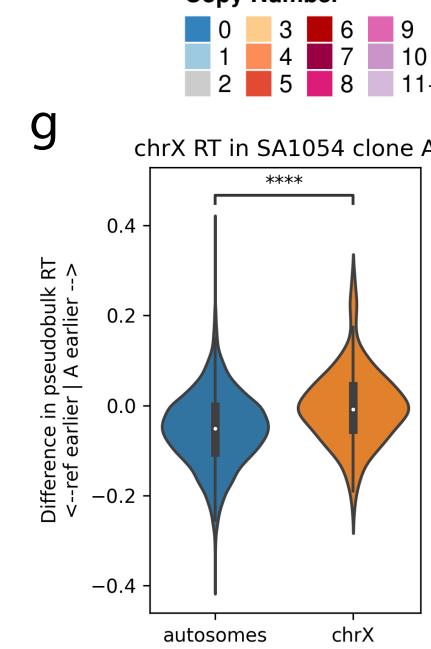
Similarity in clone CN

**d**

Correlation in clone RT

**g**

chrX RT in SA1054 clone A



chrX RT in SA1054 clone DE

