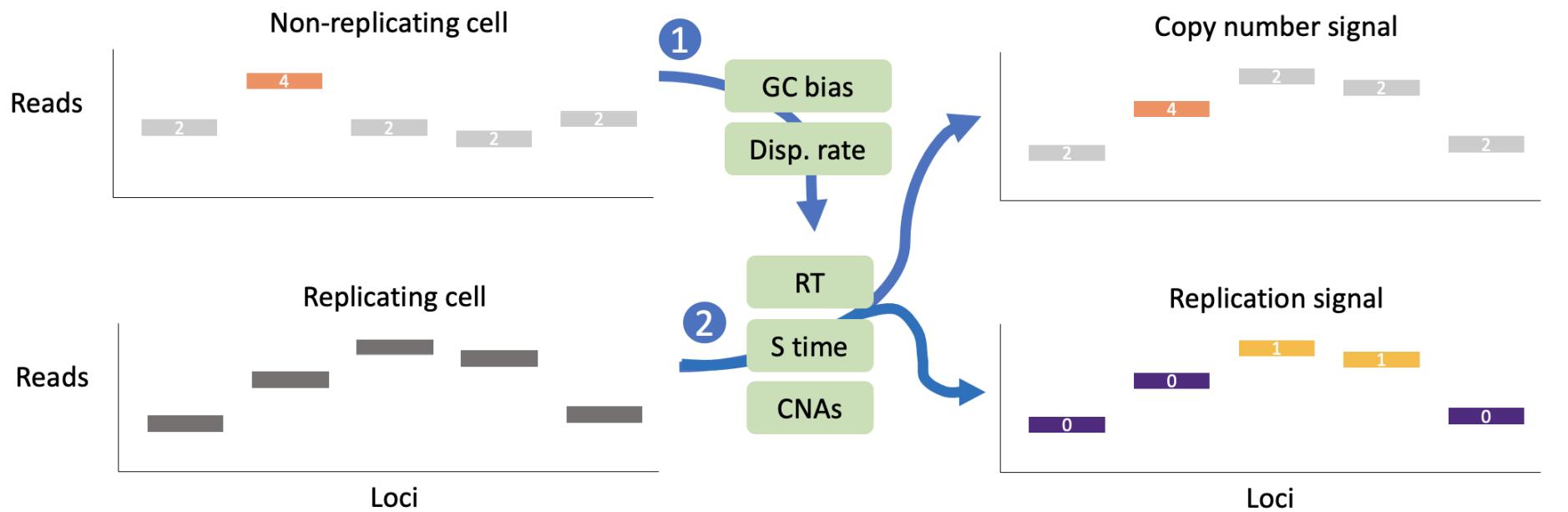
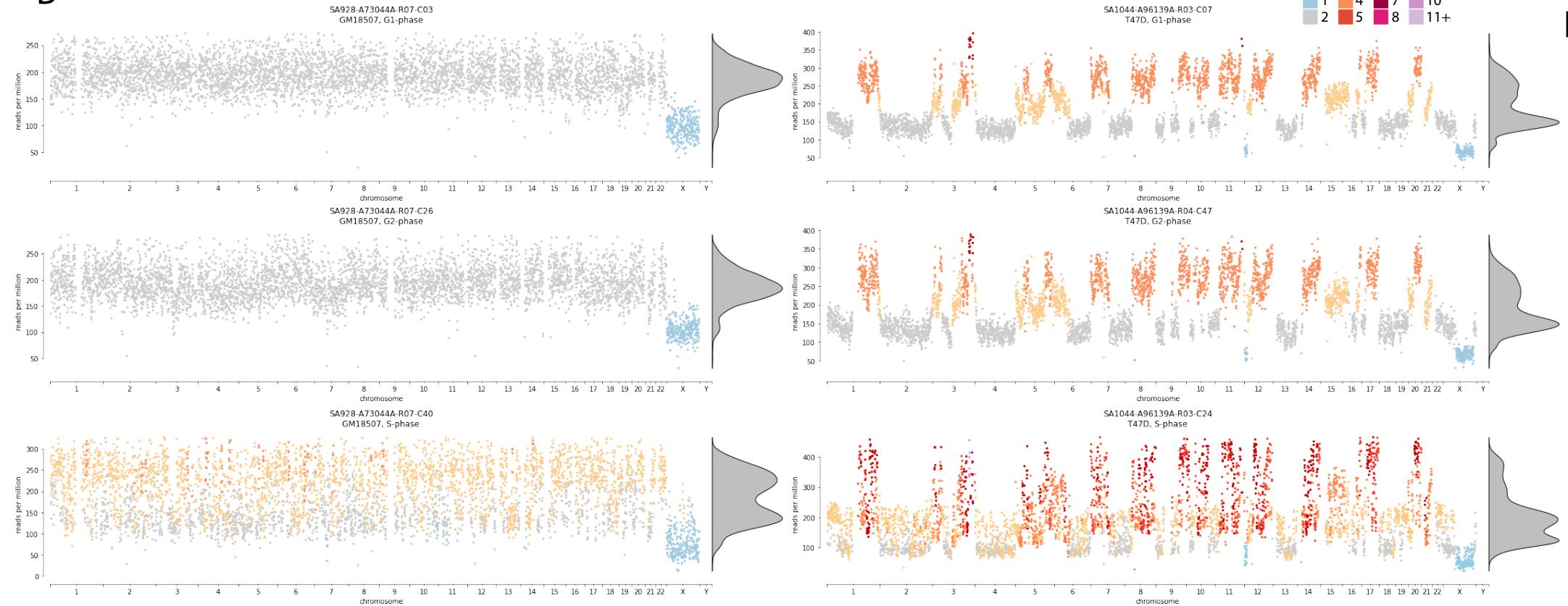


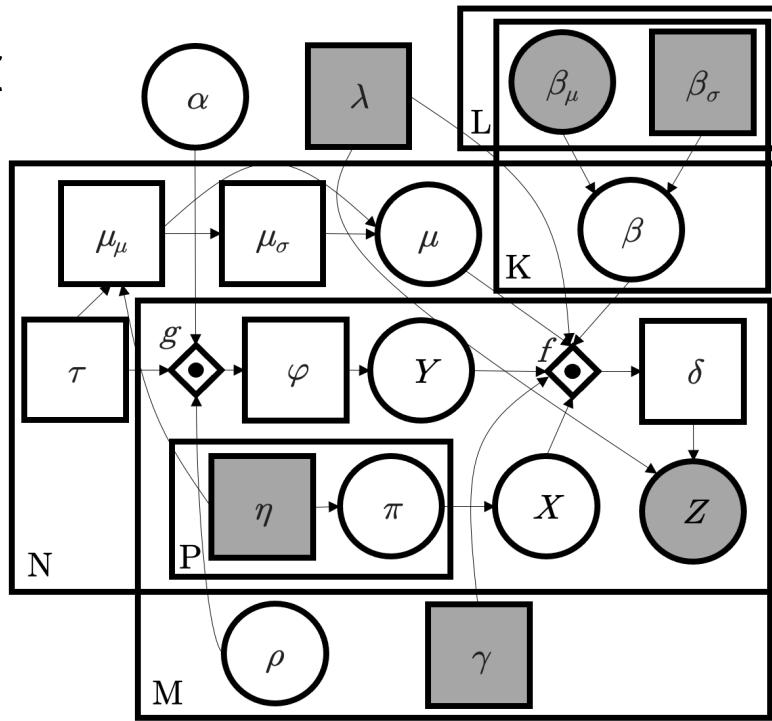
A



B

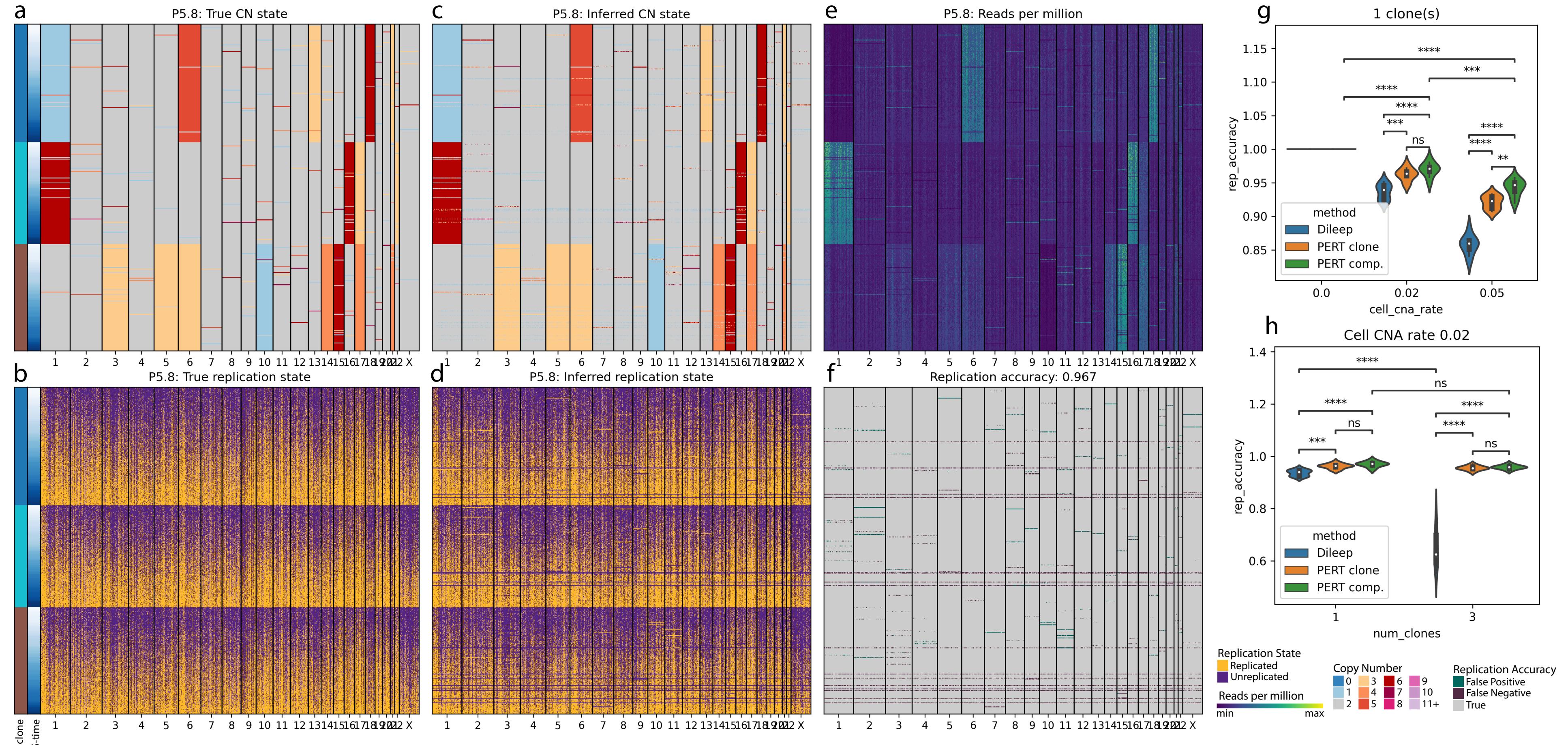


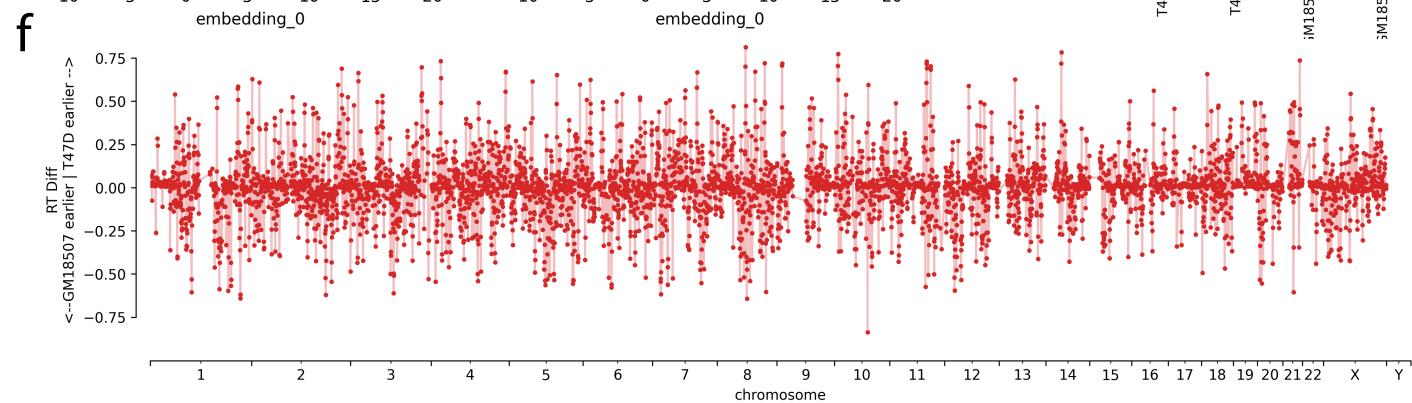
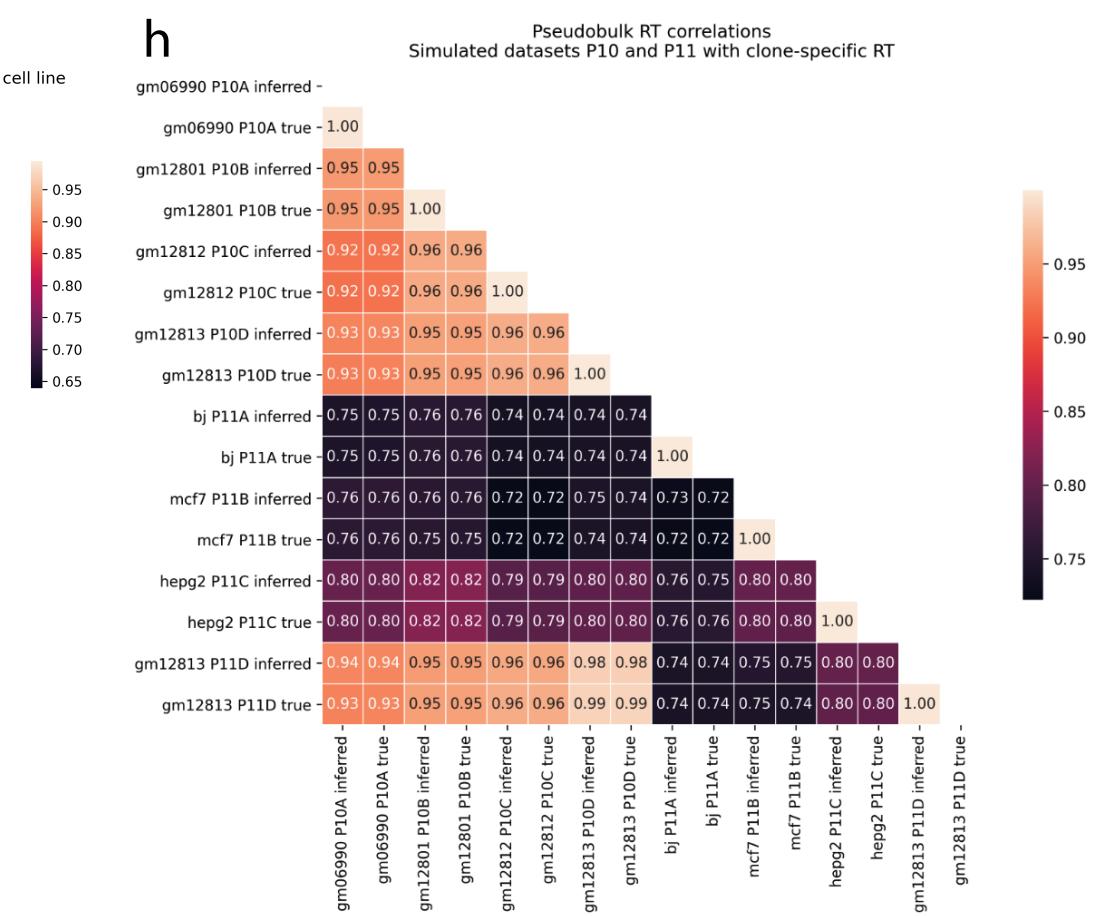
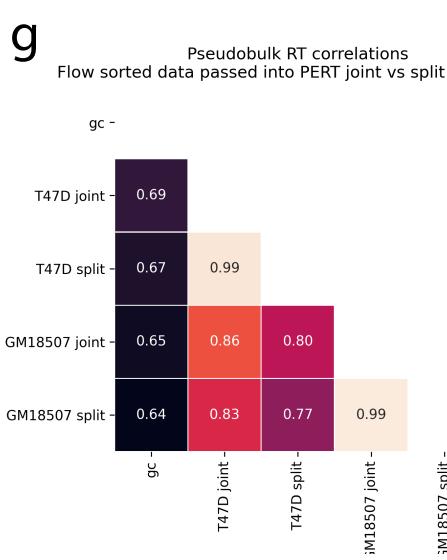
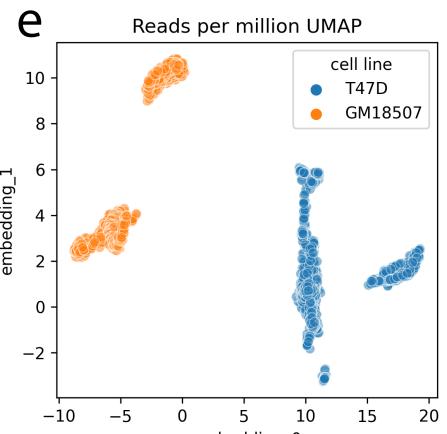
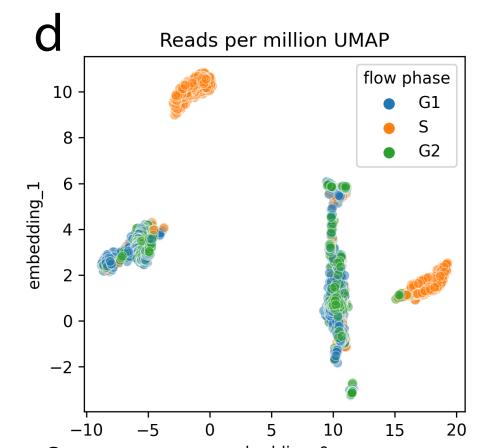
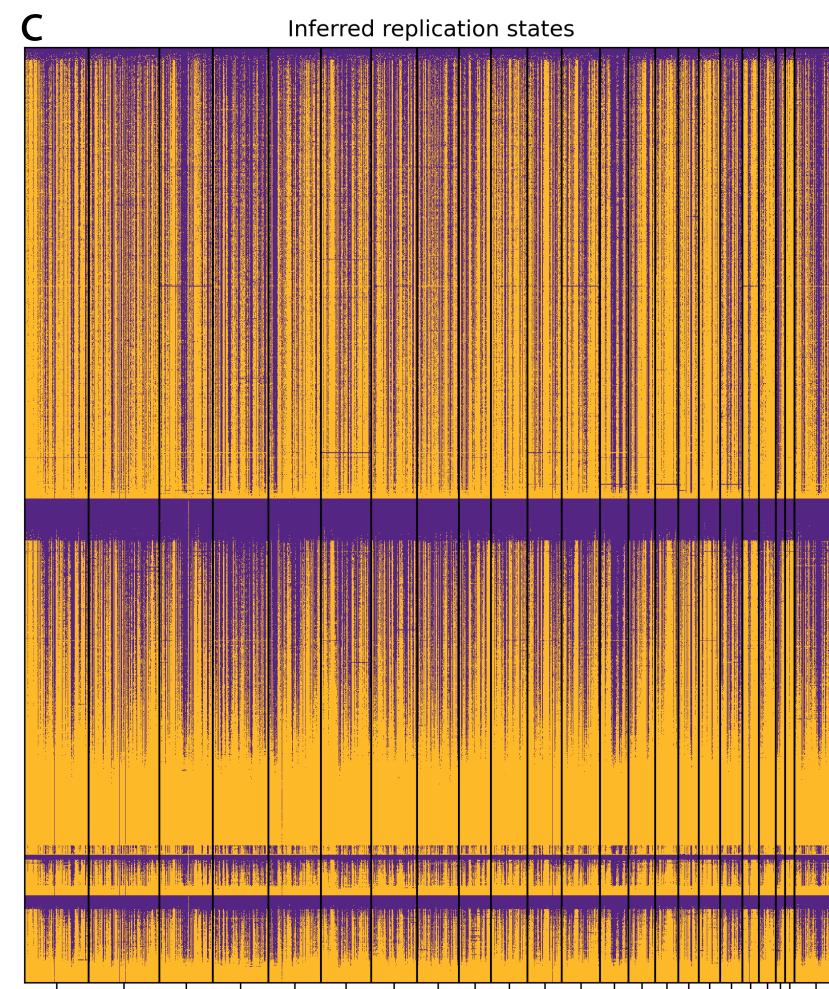
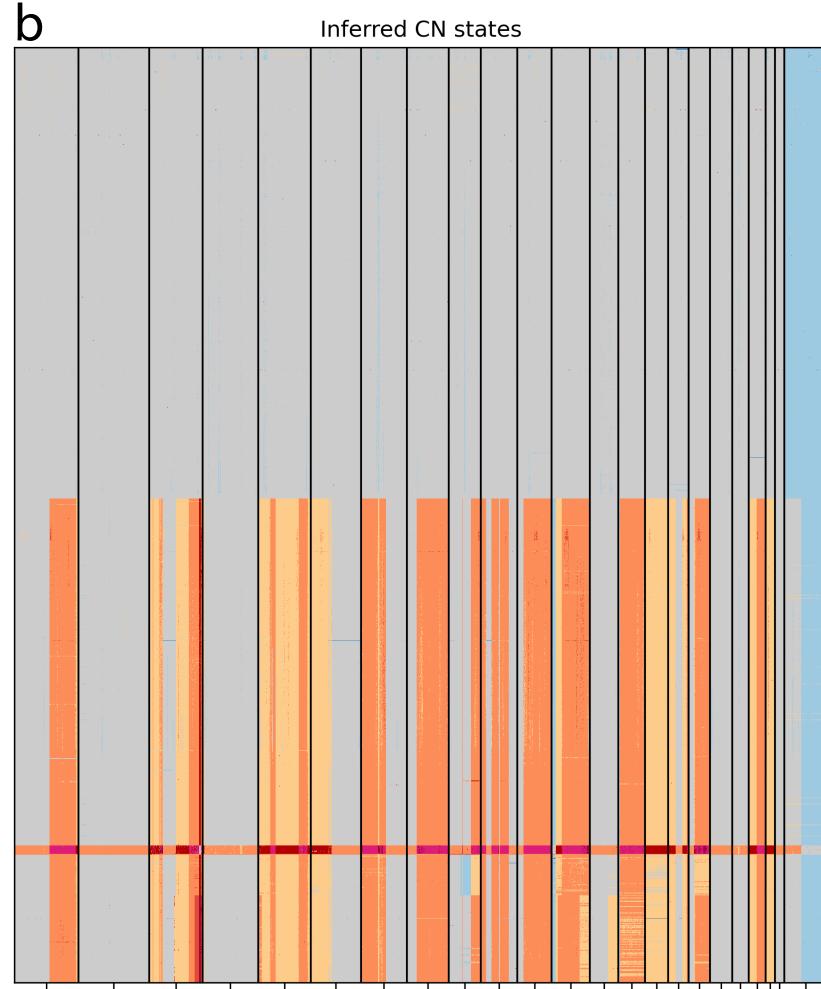
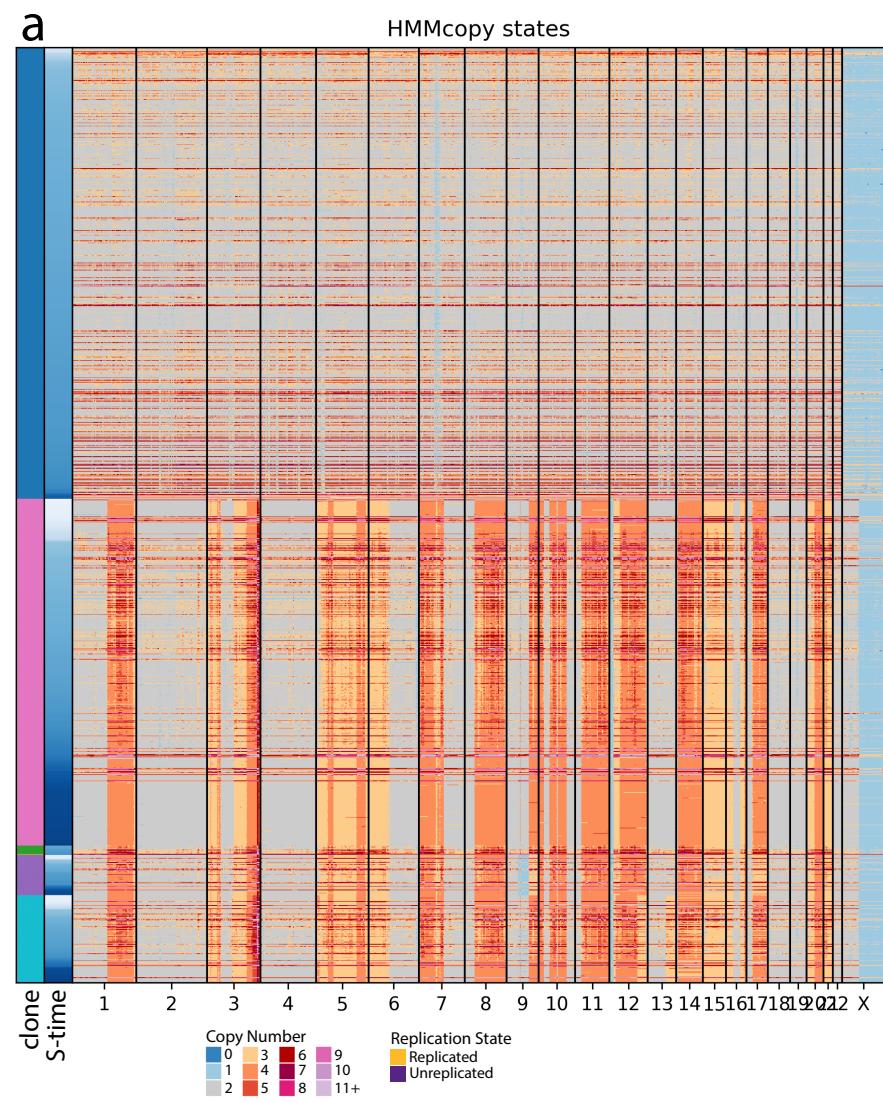
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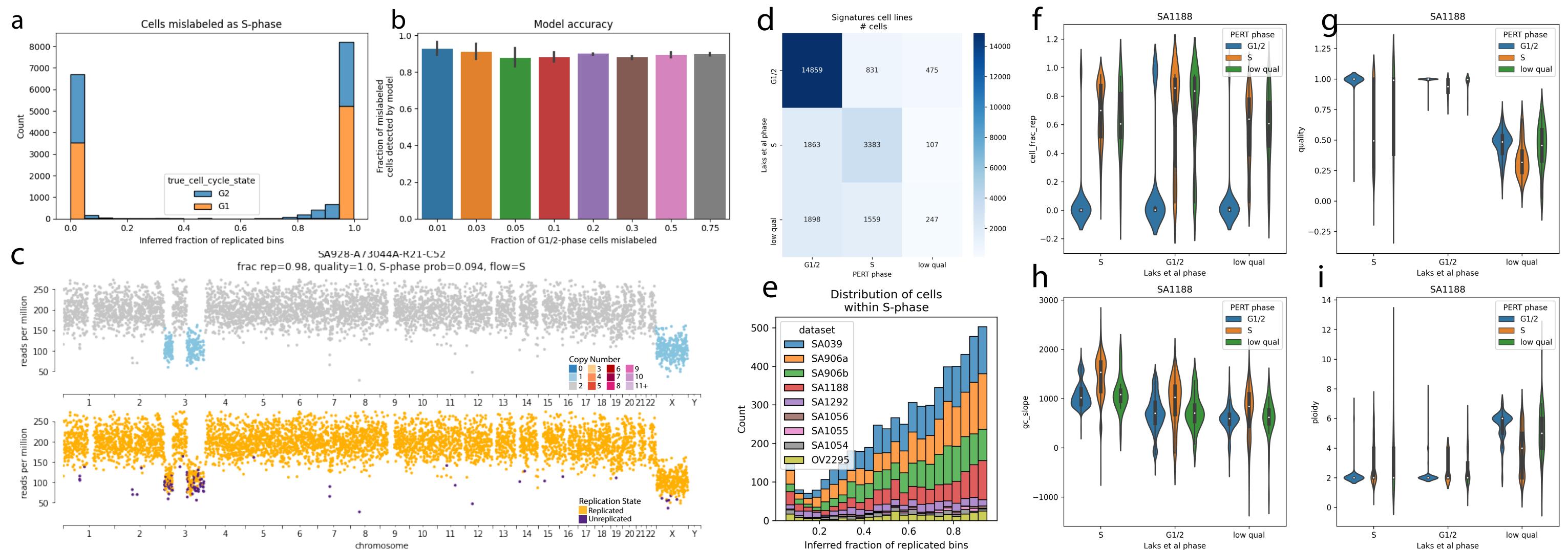


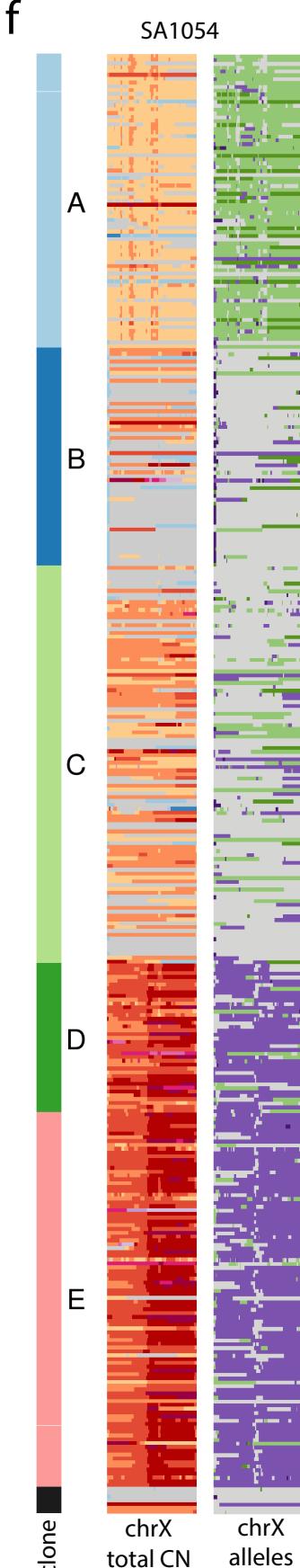
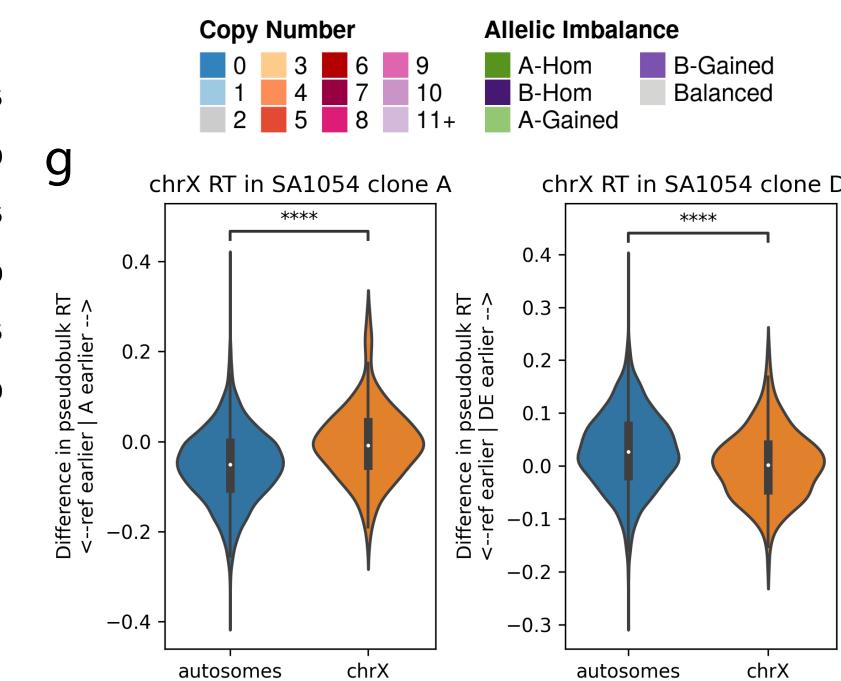
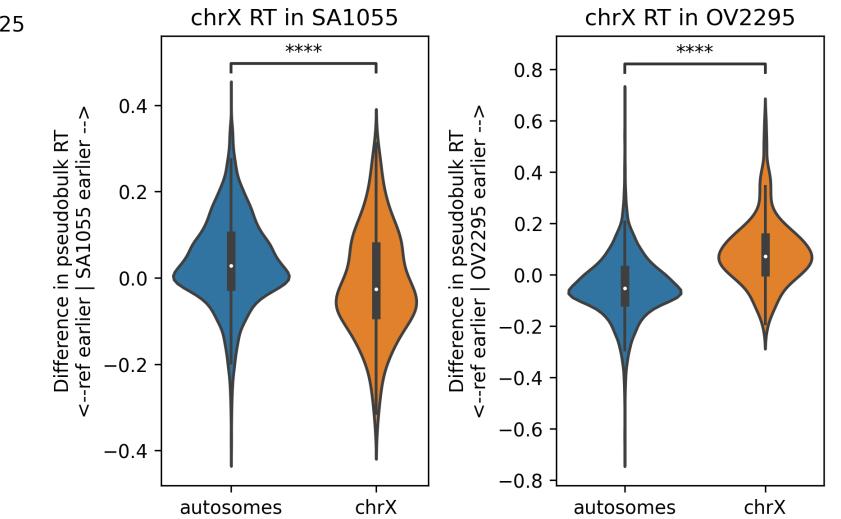
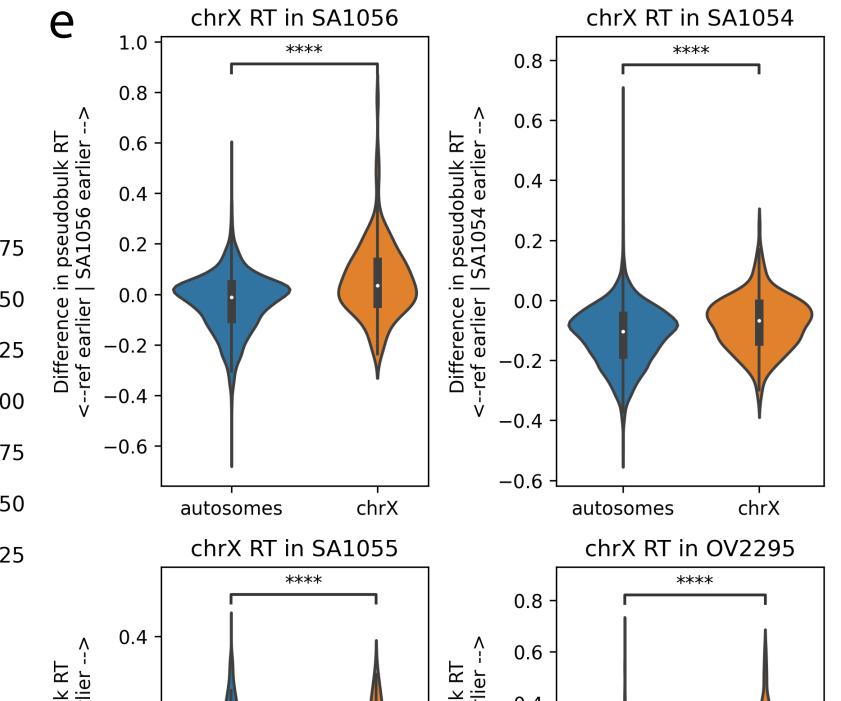
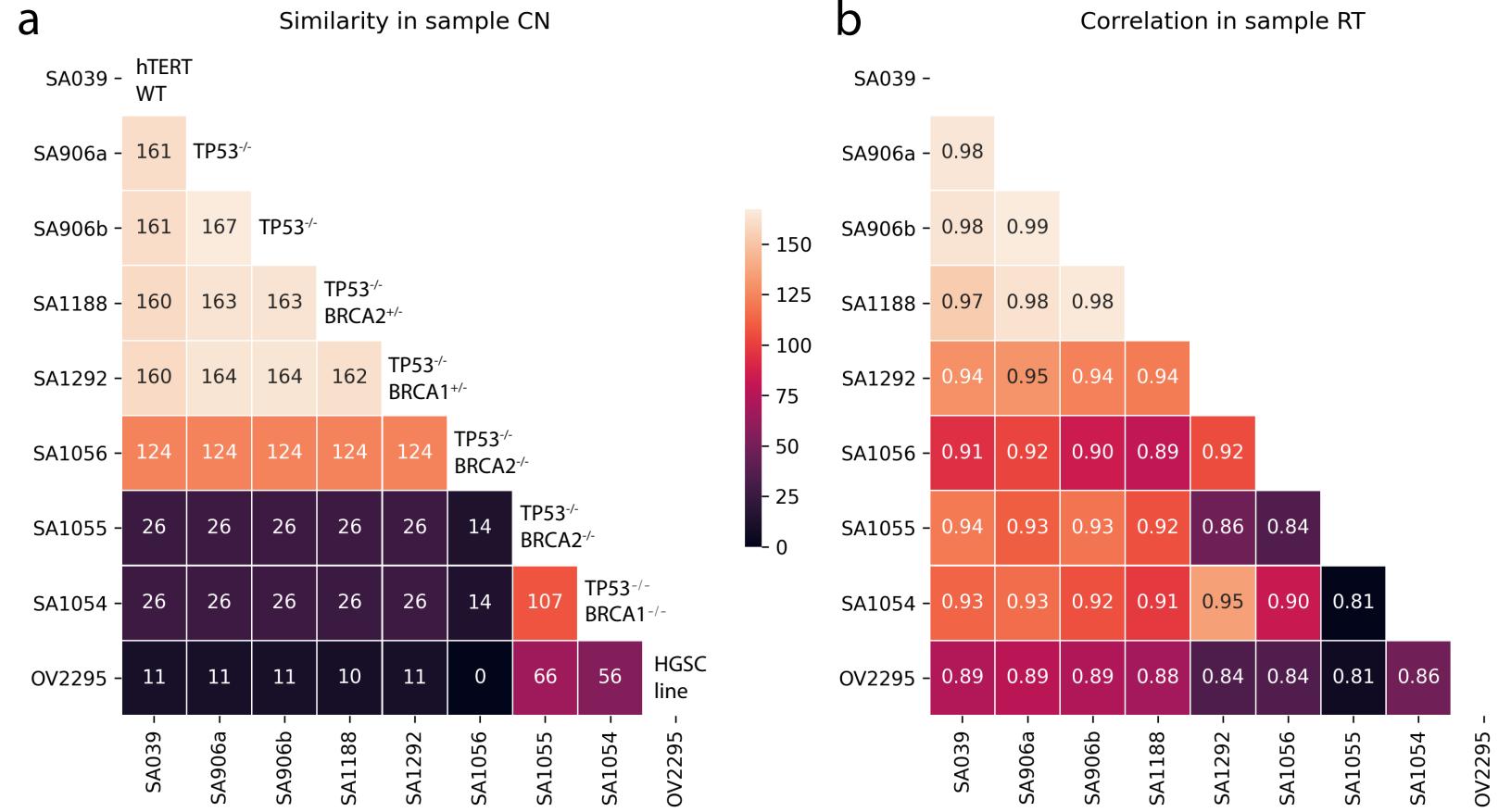
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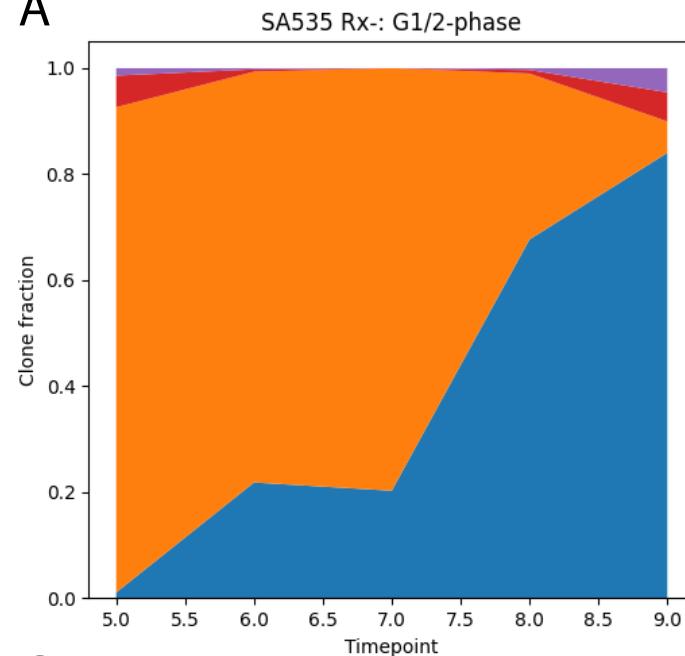
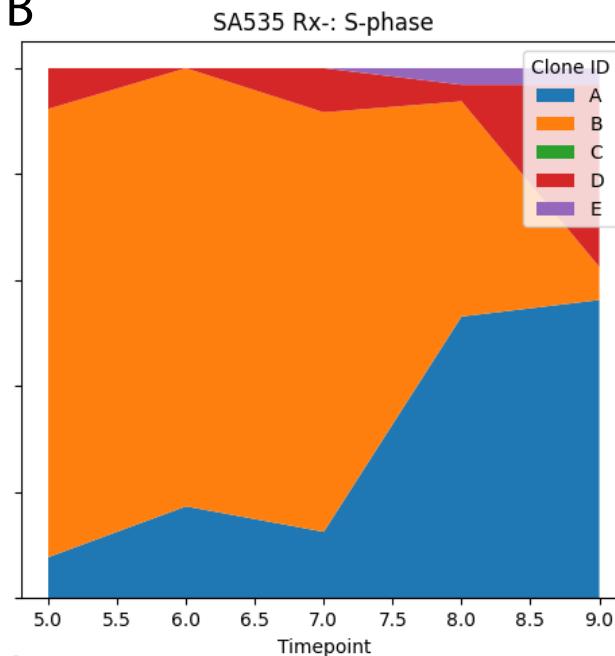
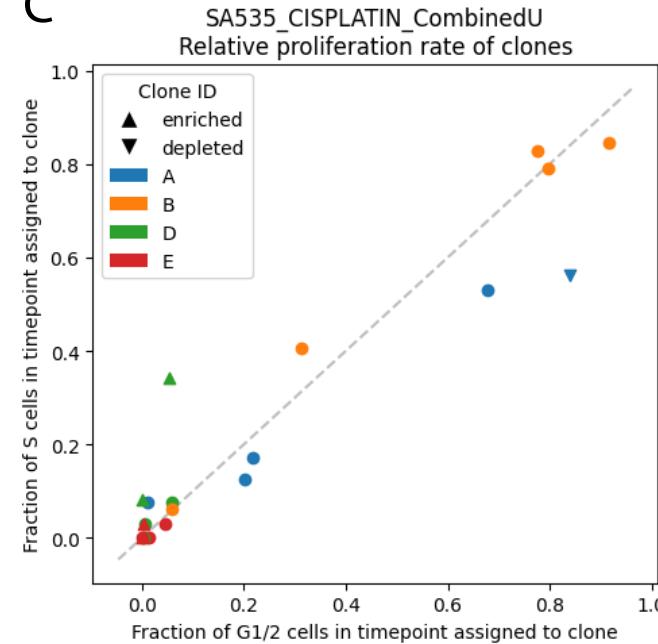
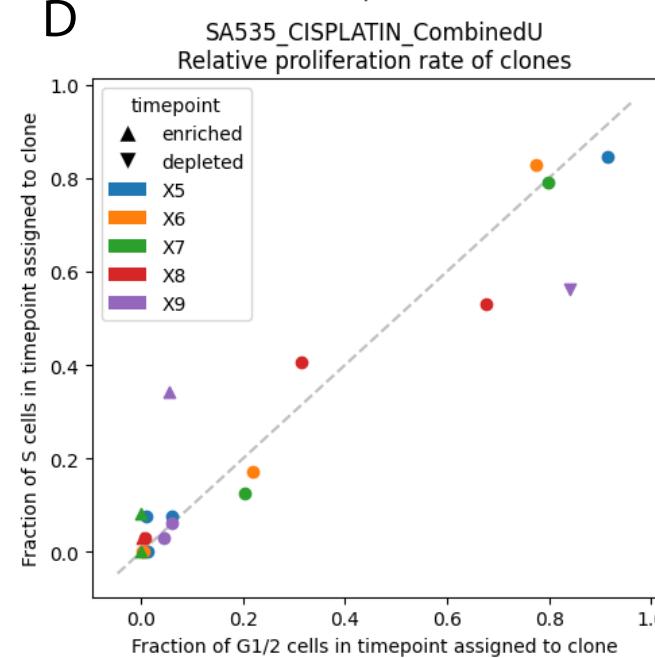
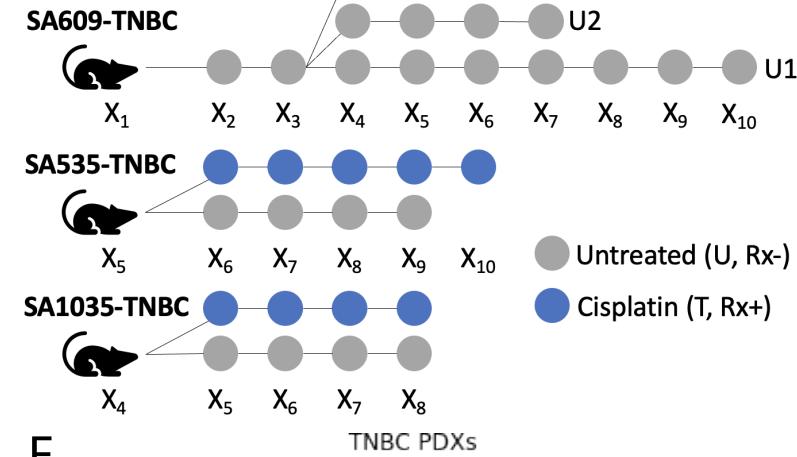
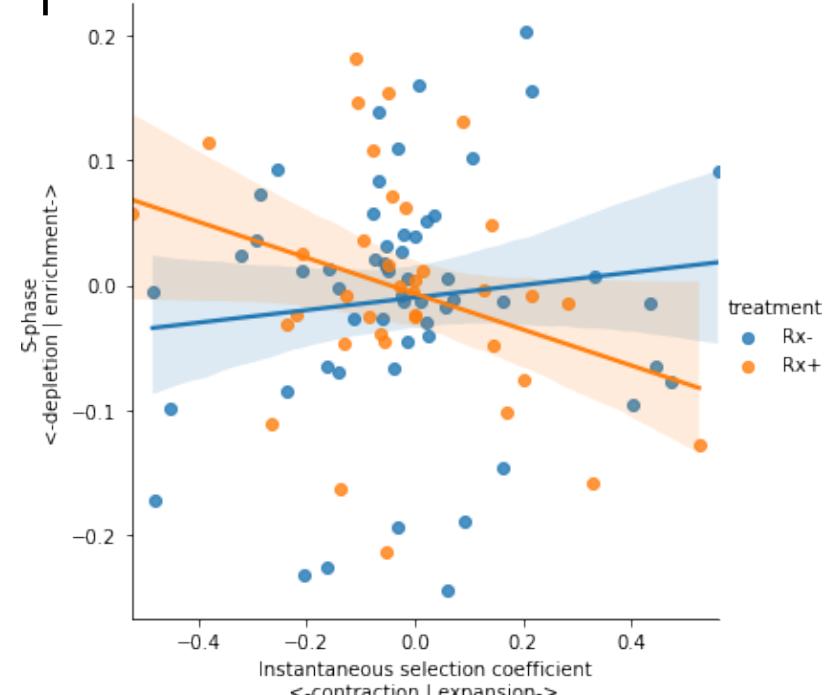
Name	Domain/Distribution	Description
$\lambda$	$(0, 1)$	NB event success probability (overdispersion)
$\delta$	$[1, \infty)$	# of NB events (Eq 4.4)
$\gamma$	$[0, 1]$	GC content of locus
$\beta_\mu$	$\sim N(0, 1)$	GC bias polynomial coefficient means
$\beta_\sigma$	$(0, \infty)$	GC bias polynomial coefficient 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
$\rho$	$\sim Beta(1, 1)$	replication timing
$\alpha$	$\sim \Gamma(2, 0.2)$	replication stochasticity term
$\phi$	$(0, 1)$	replication probabilities (Eq 4.5)
$Y$	$\sim Bernoulli(\phi)$	replication status
$\eta$	$[0, 1]$	copy number prior concentration
$\pi$	$\sim Dir(\eta)$	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



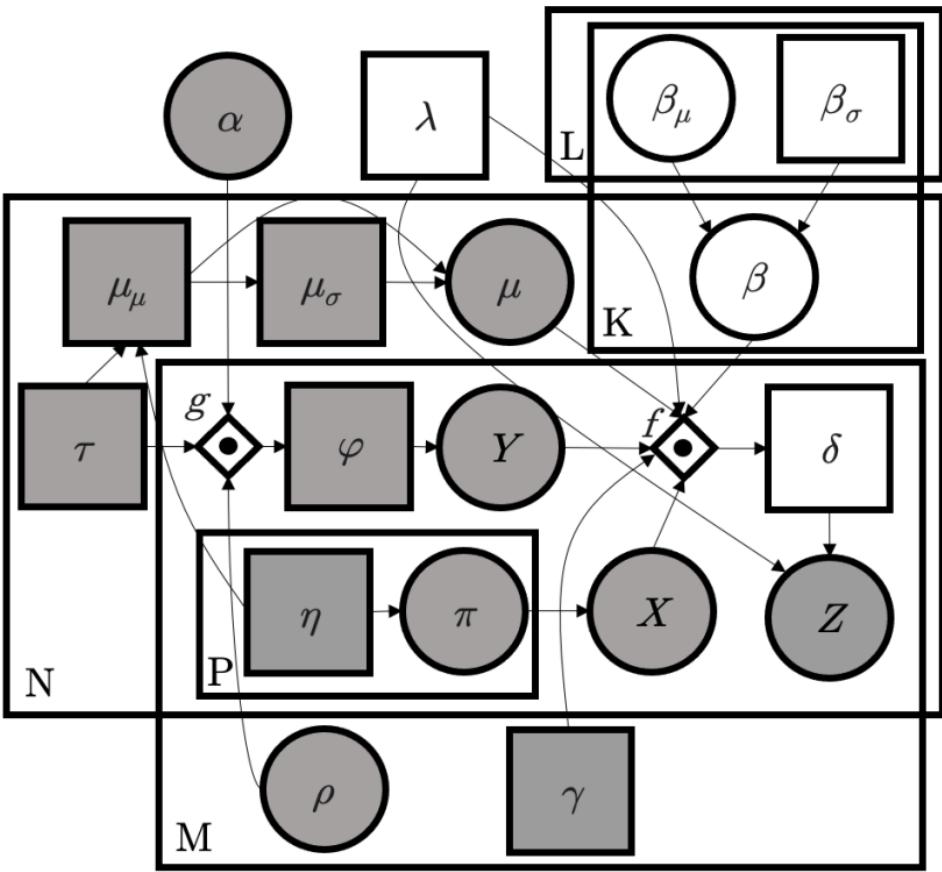




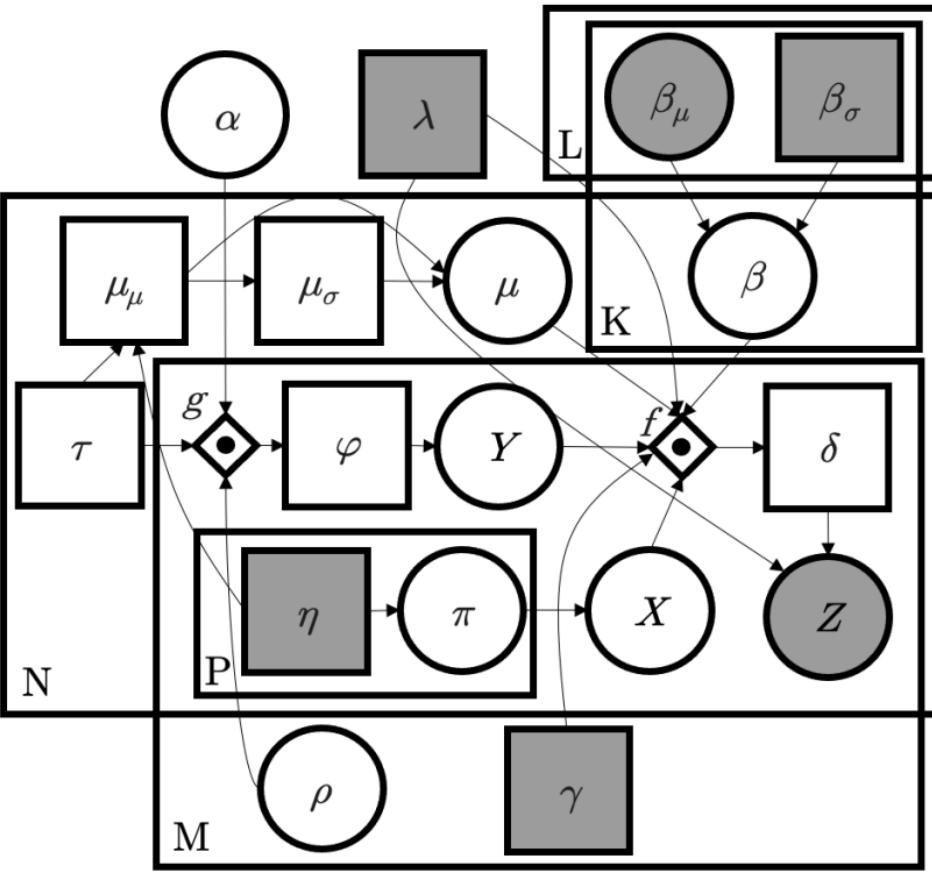


**A****B****C****D****E****F**

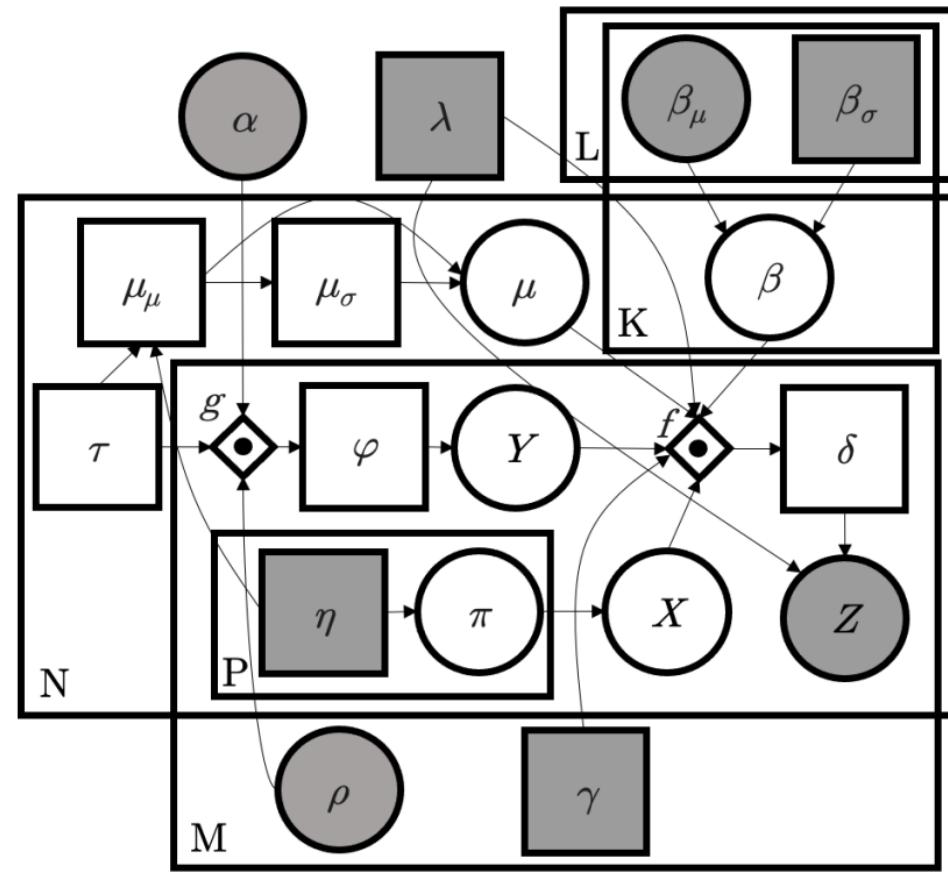
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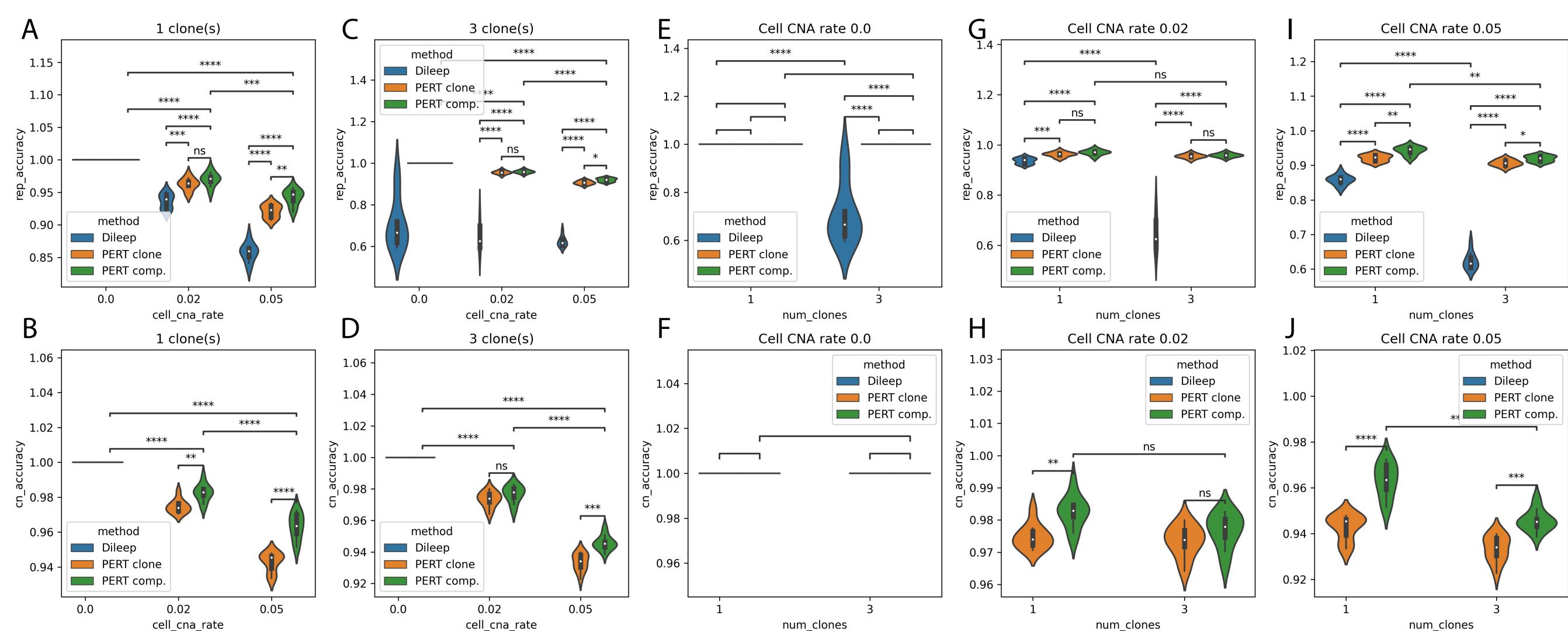


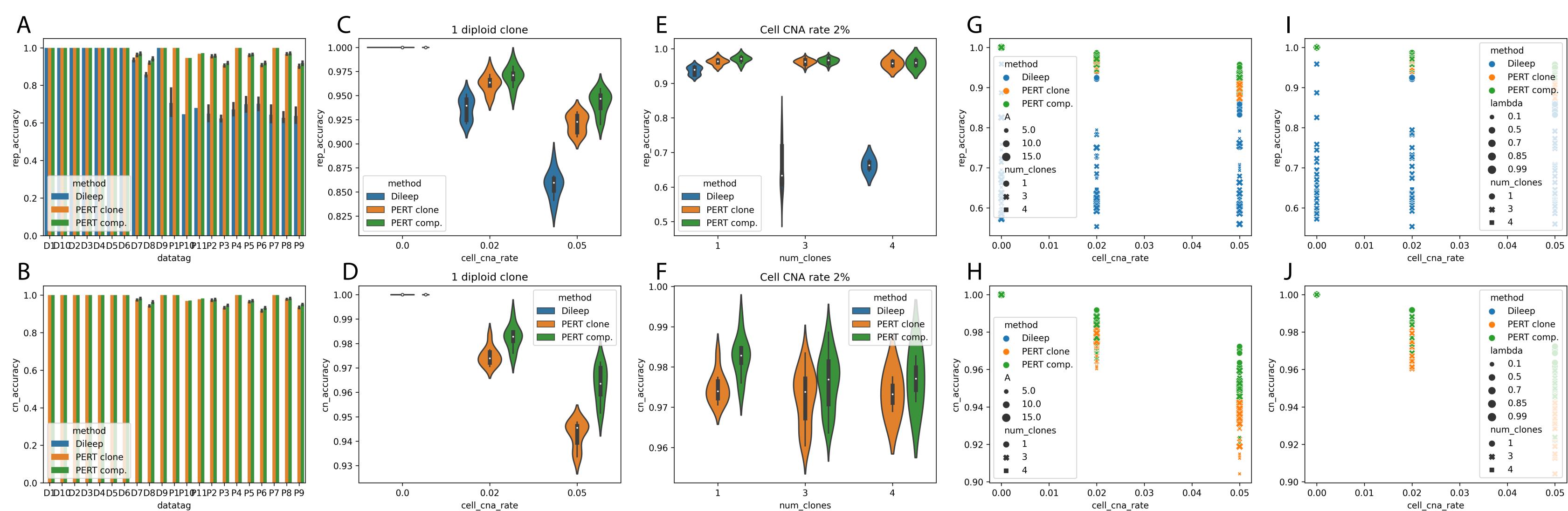
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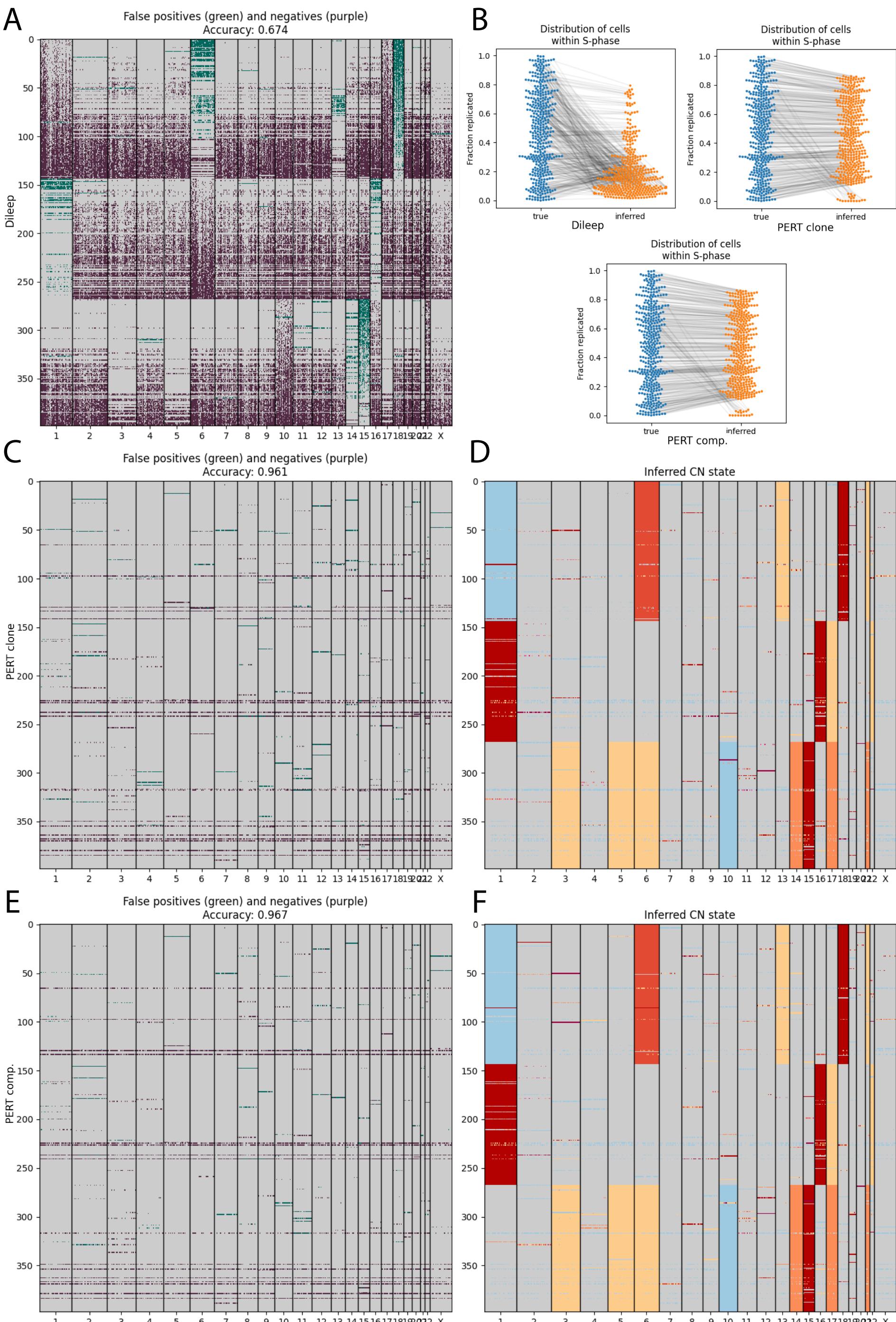


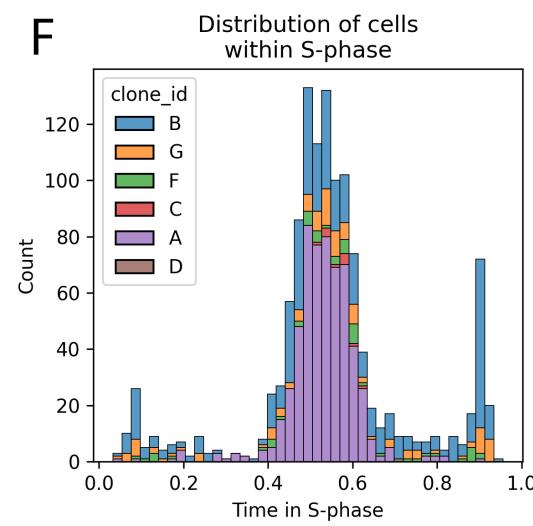
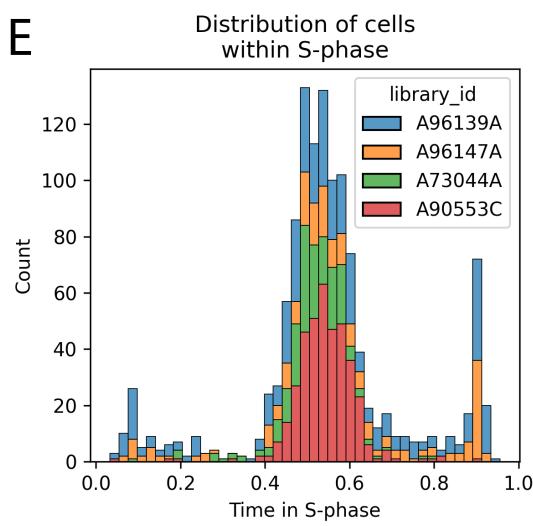
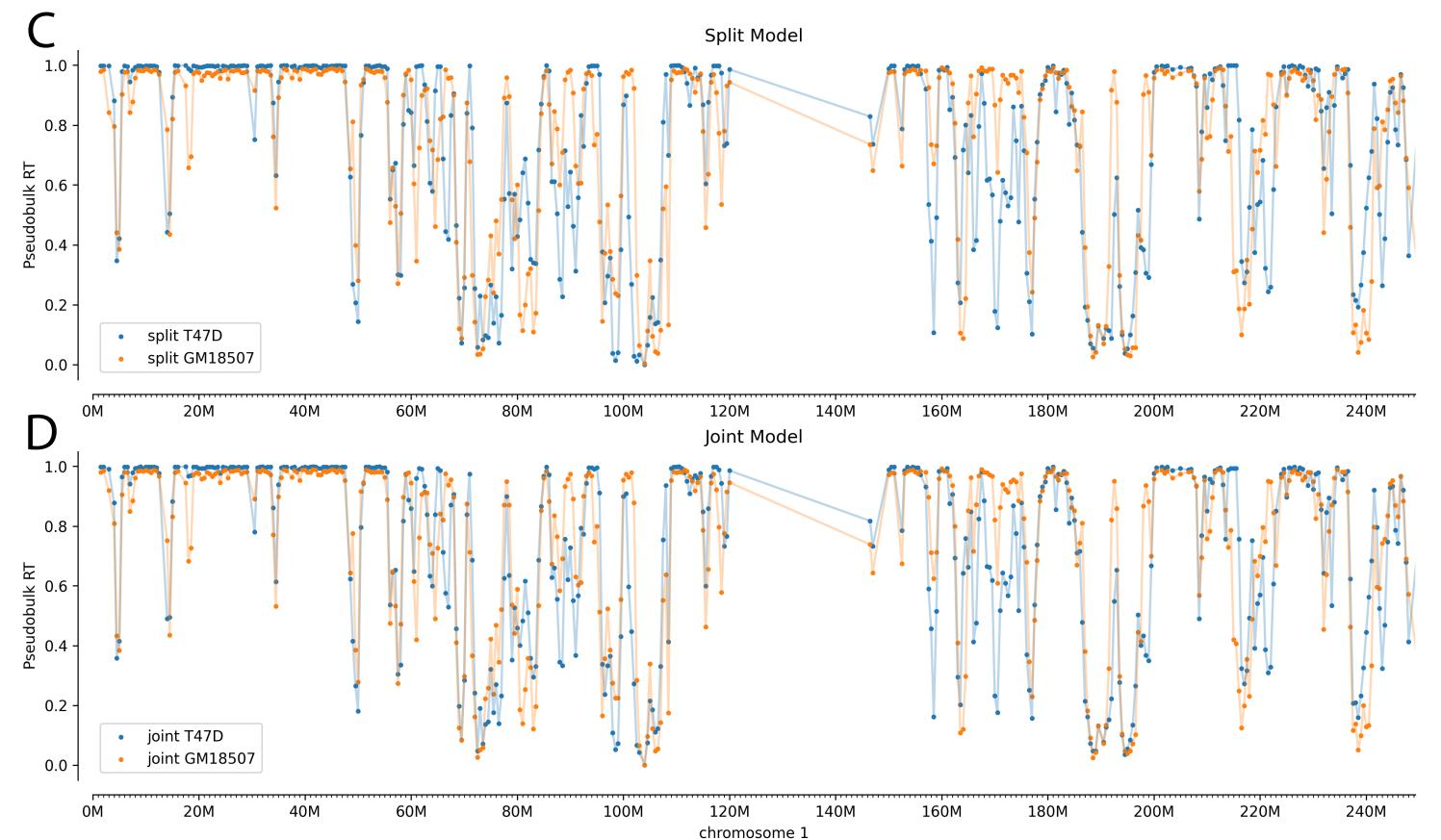
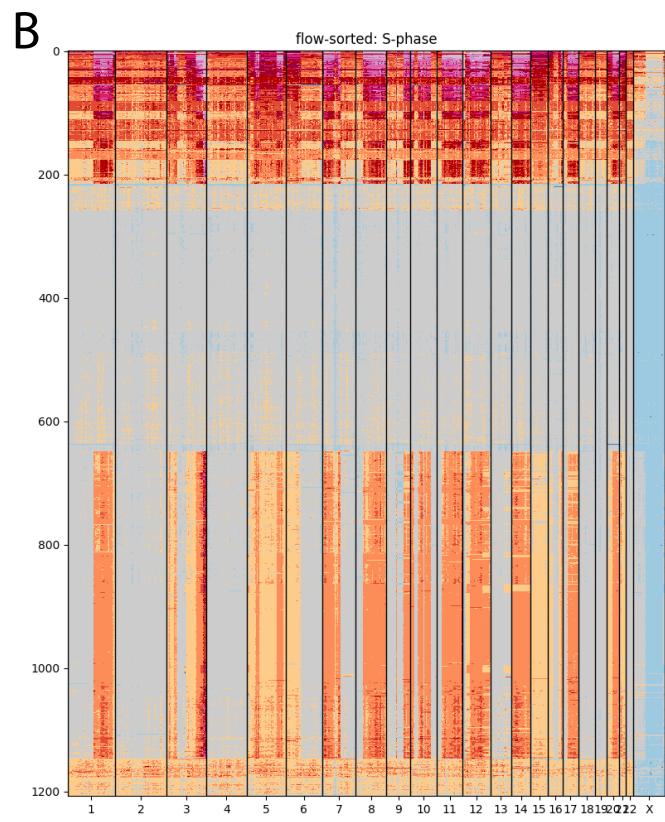
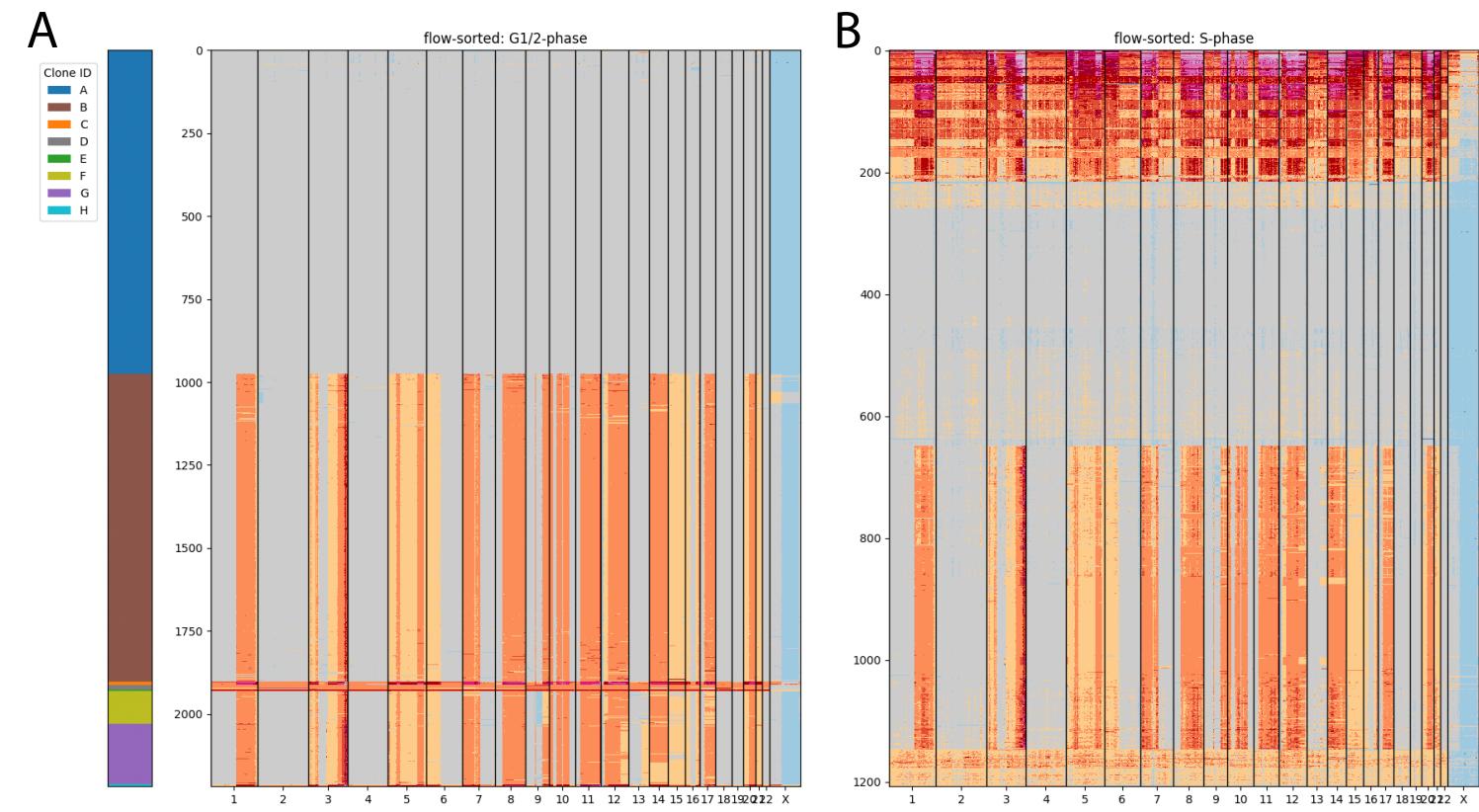
Step 3

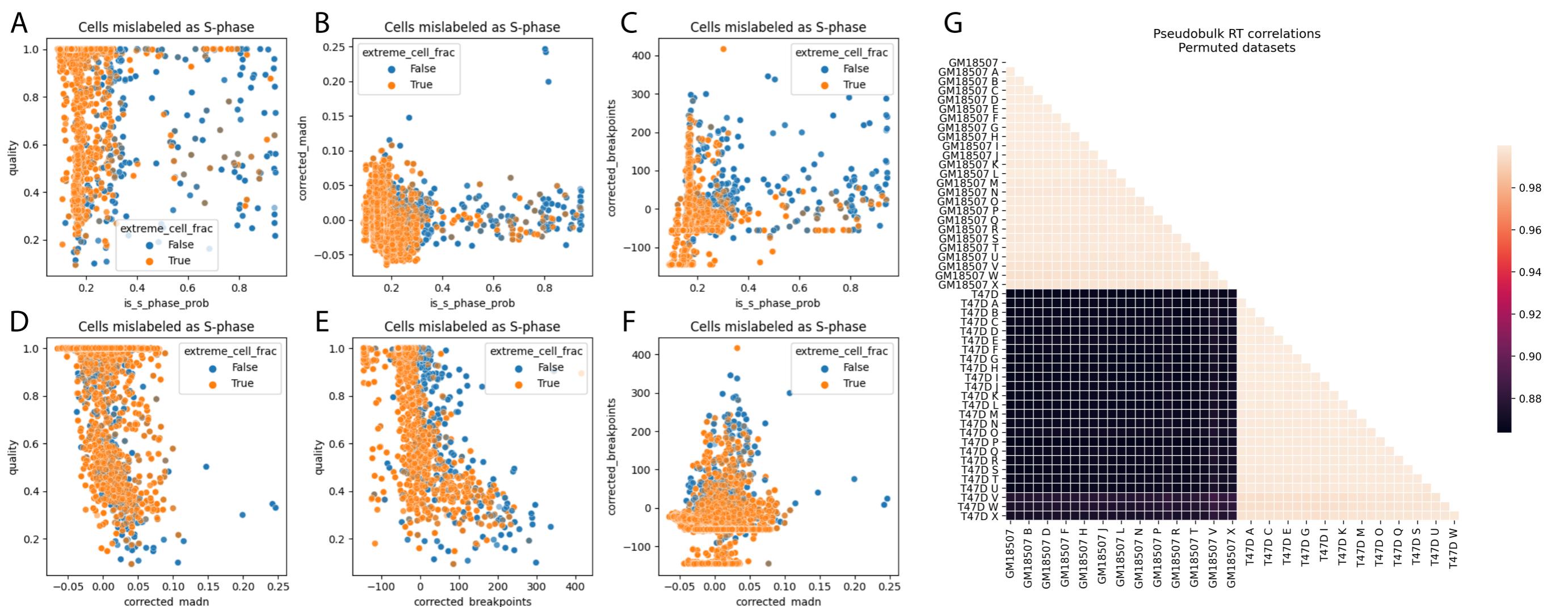


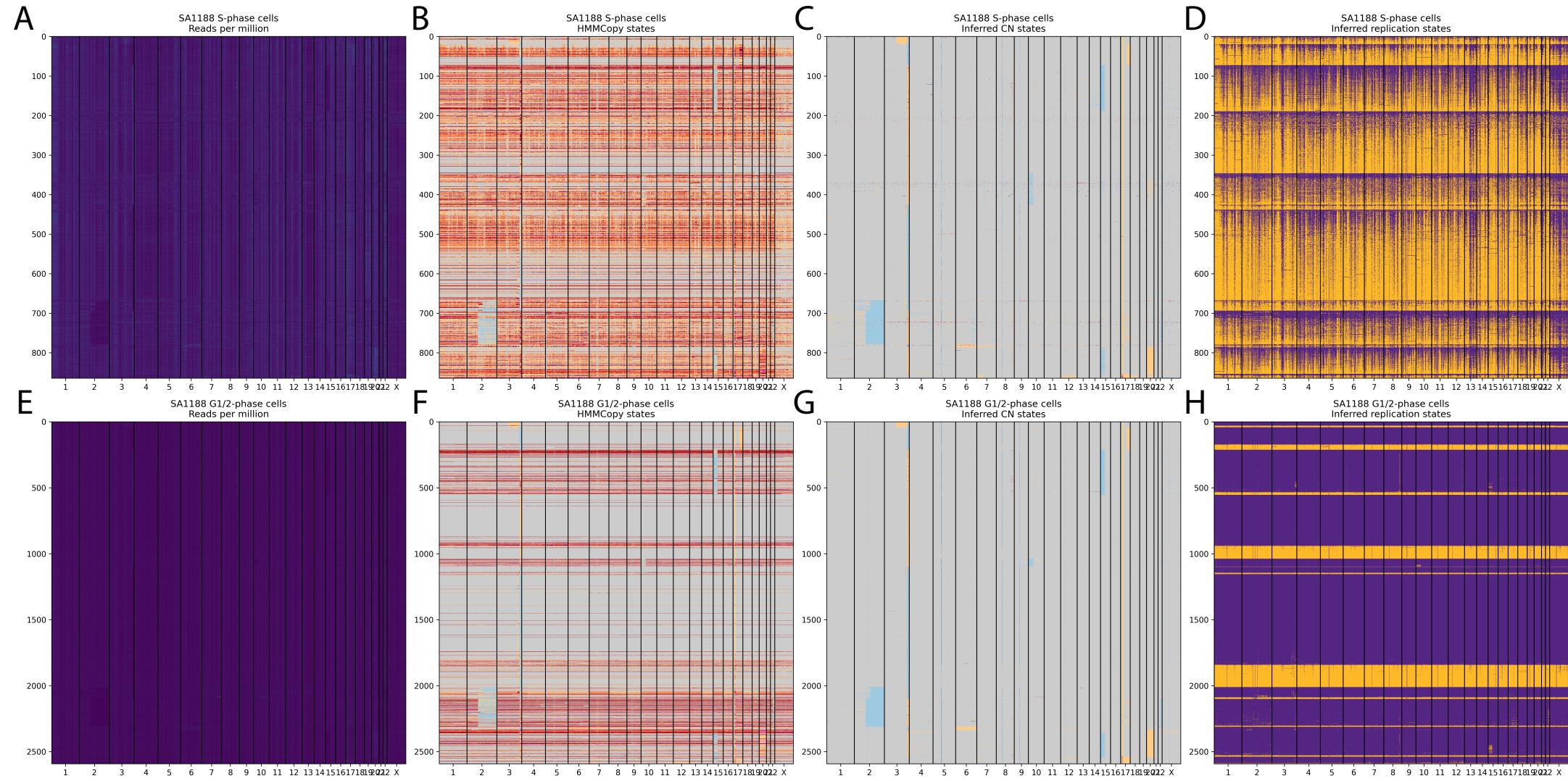


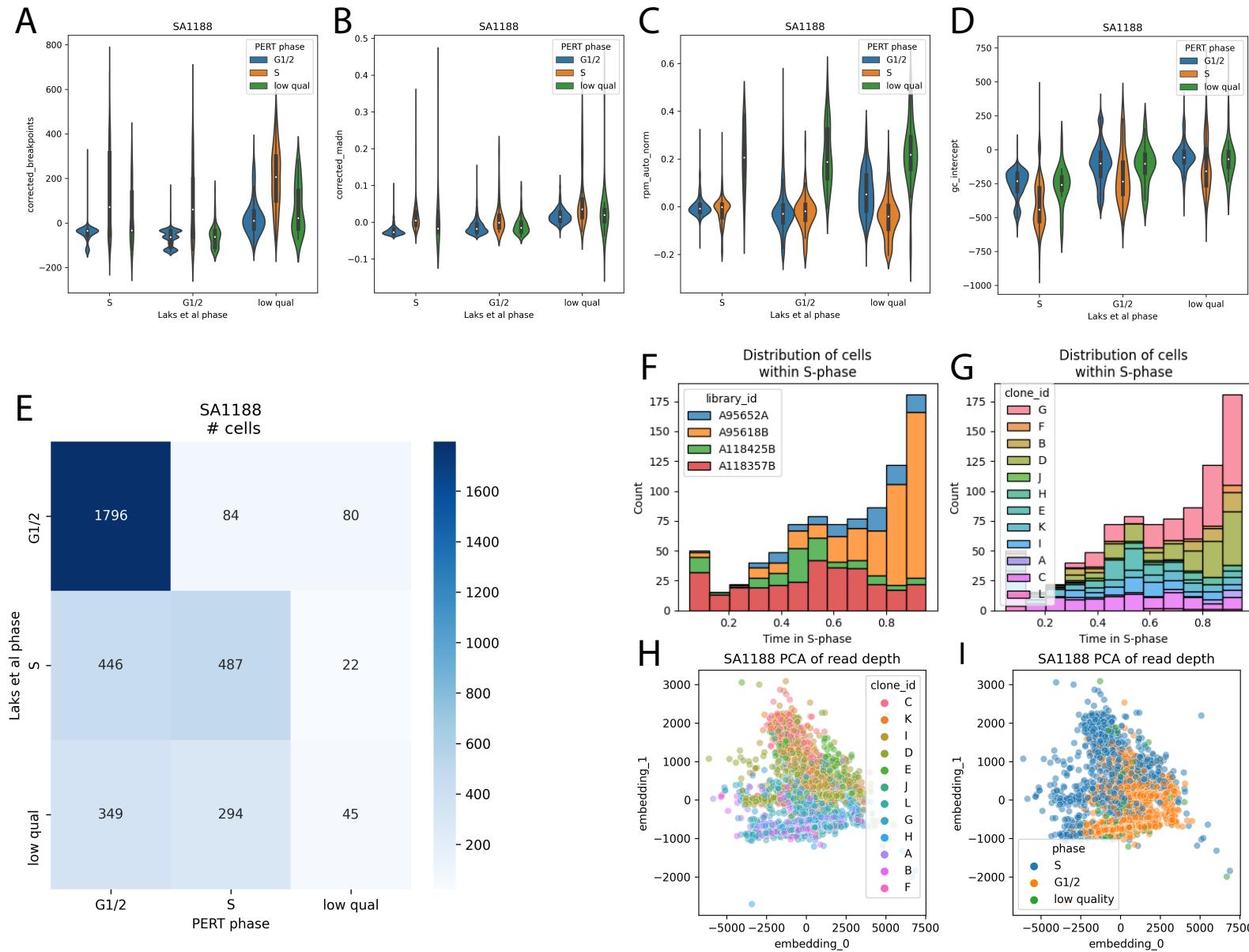


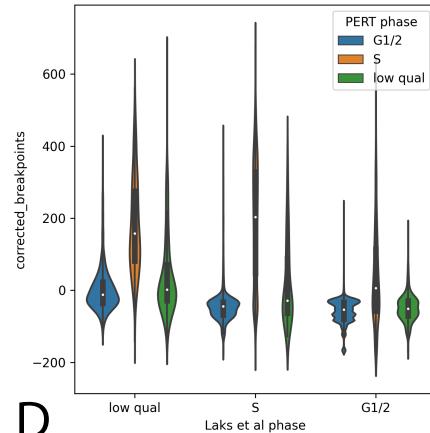
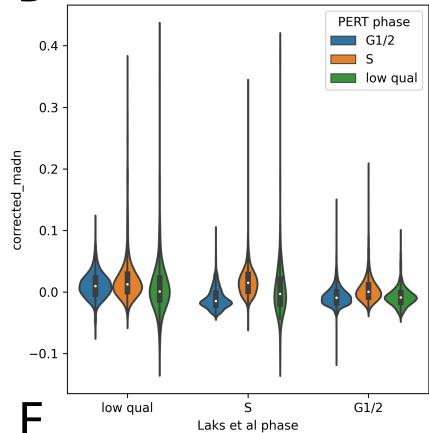
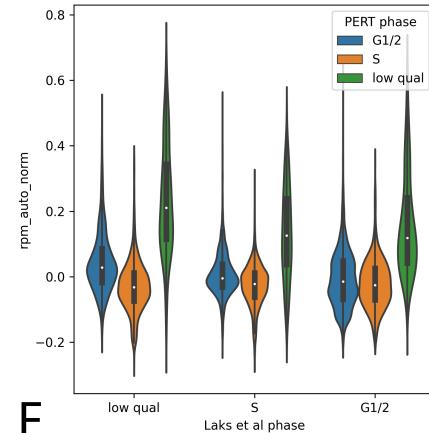
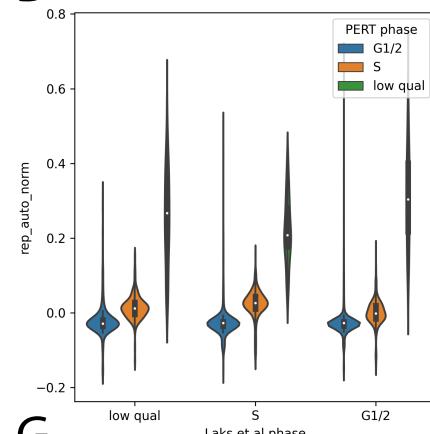
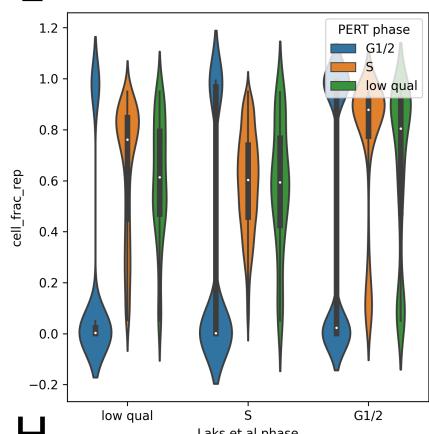
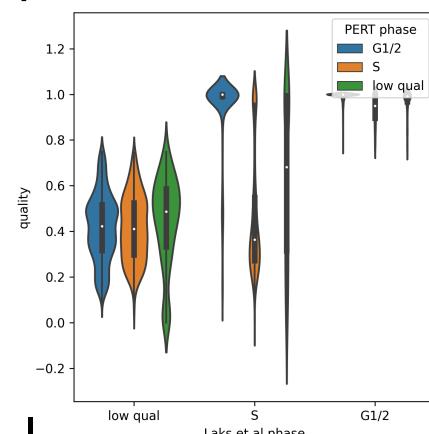
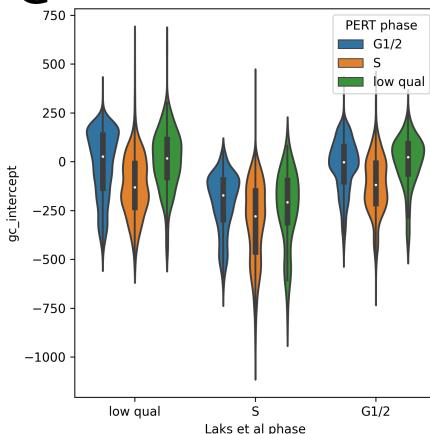
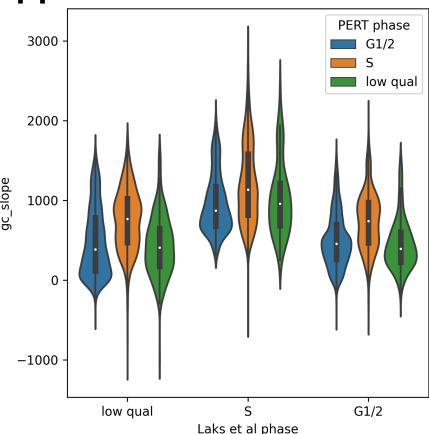
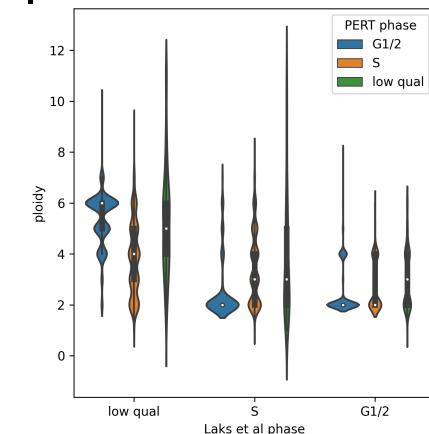


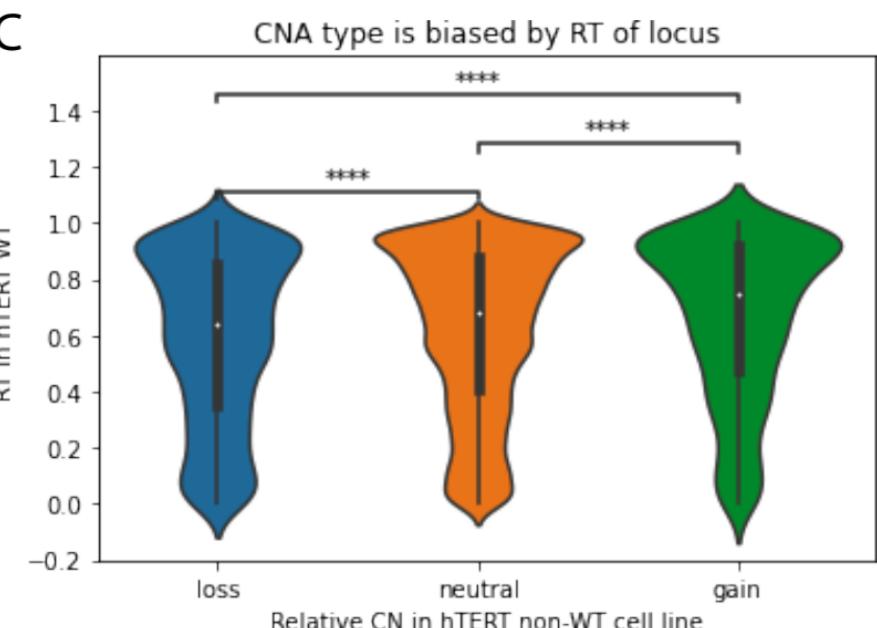
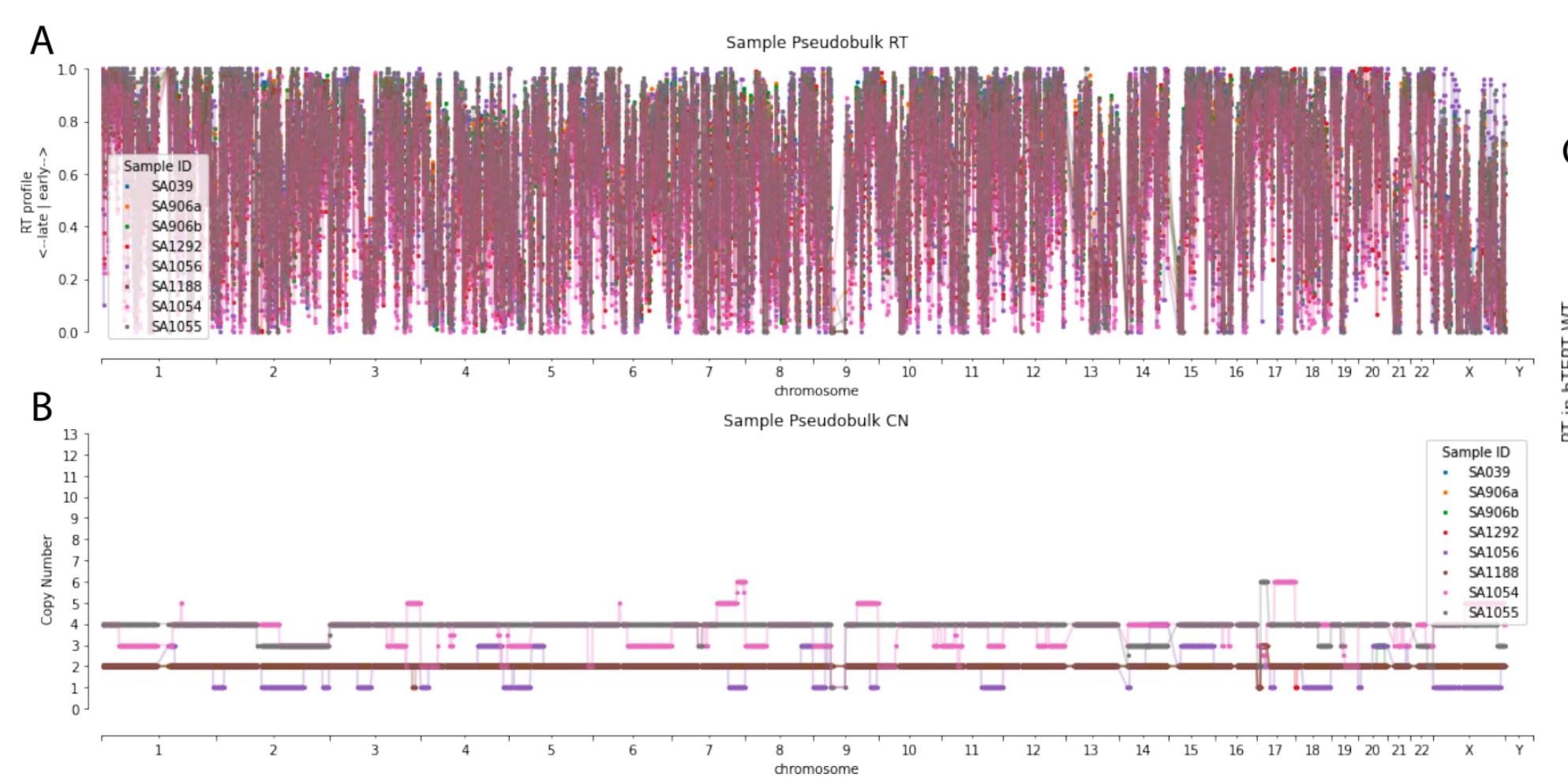






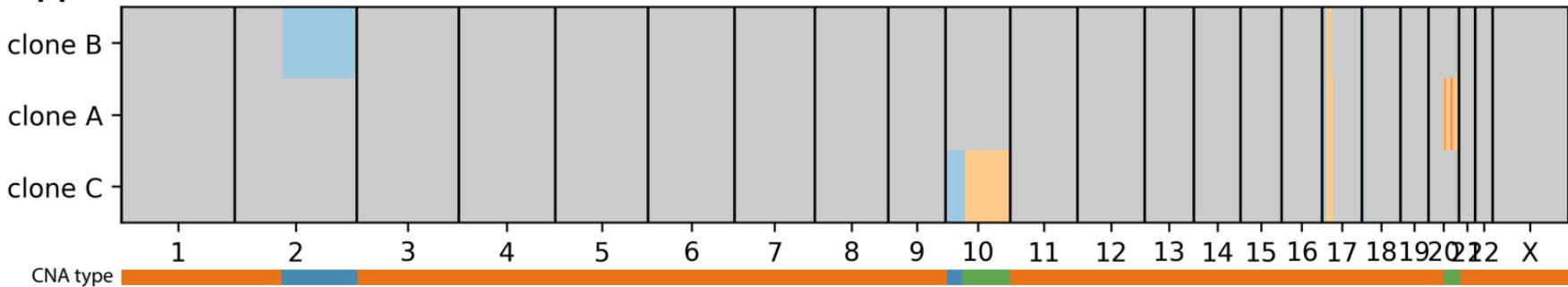


**A****B****C****D****E****F****G****H****I**

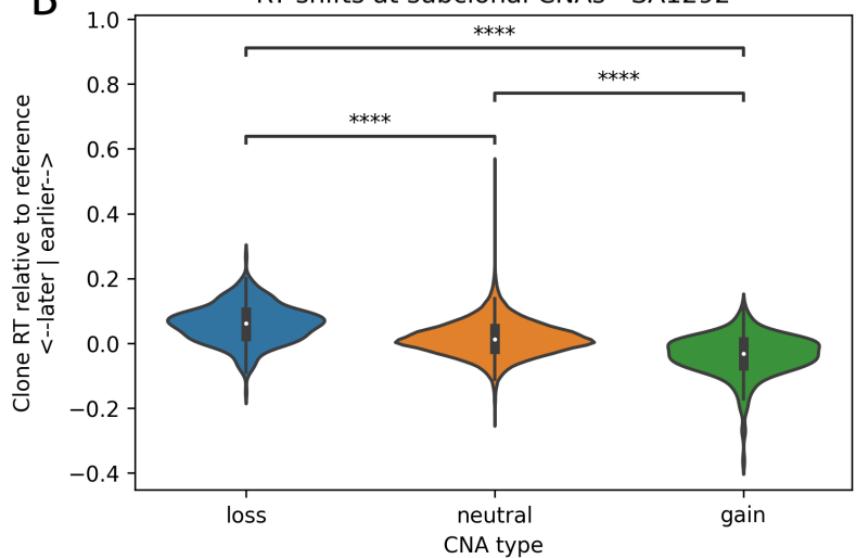


**A**

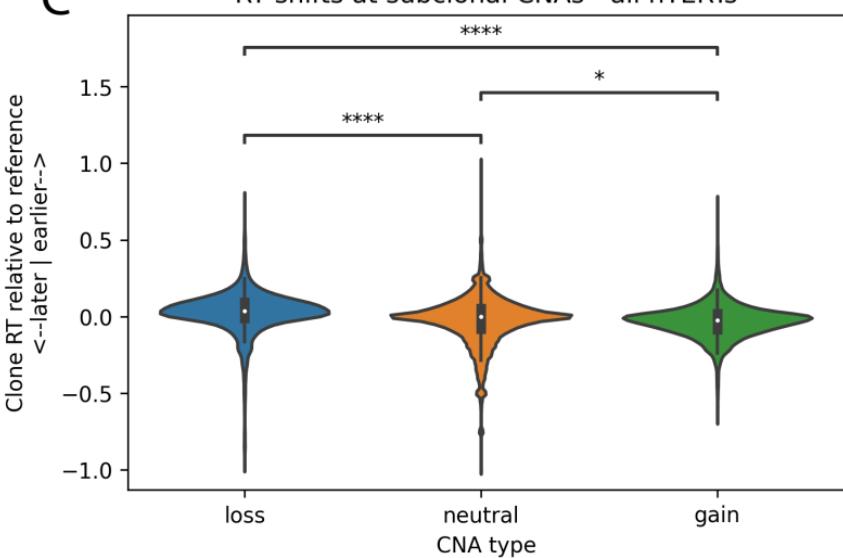
## SA1292: Pseudobulk CN Profiles

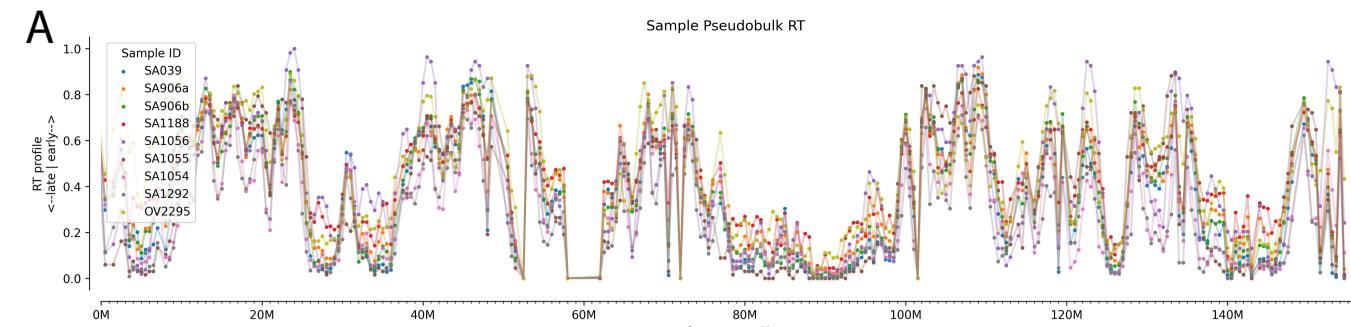
**B**

## RT shifts at subclonal CNAs - SA1292

**C**

## RT shifts at subclonal CNAs - all hTERTs





**B**

