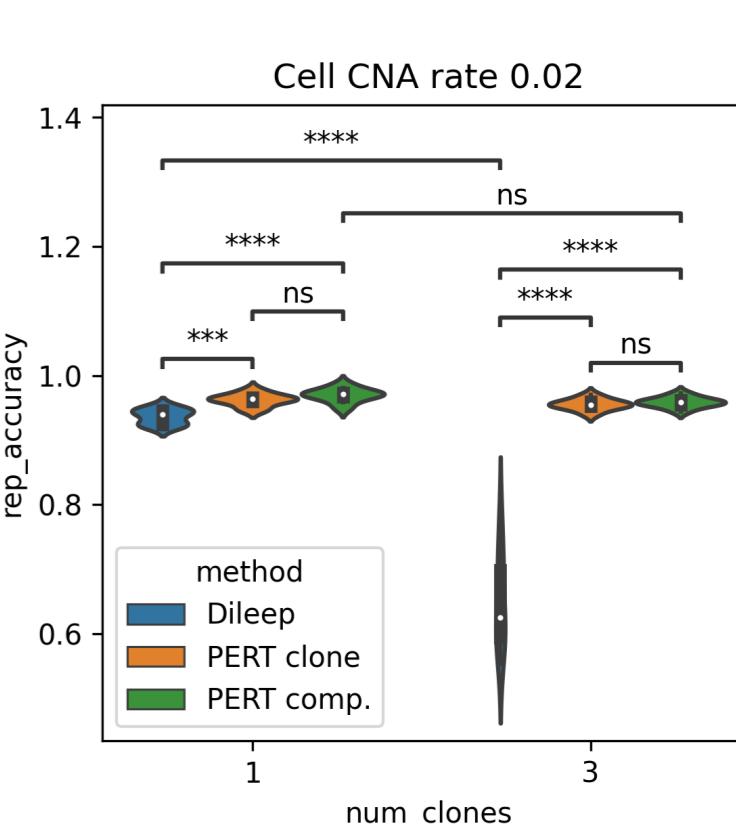
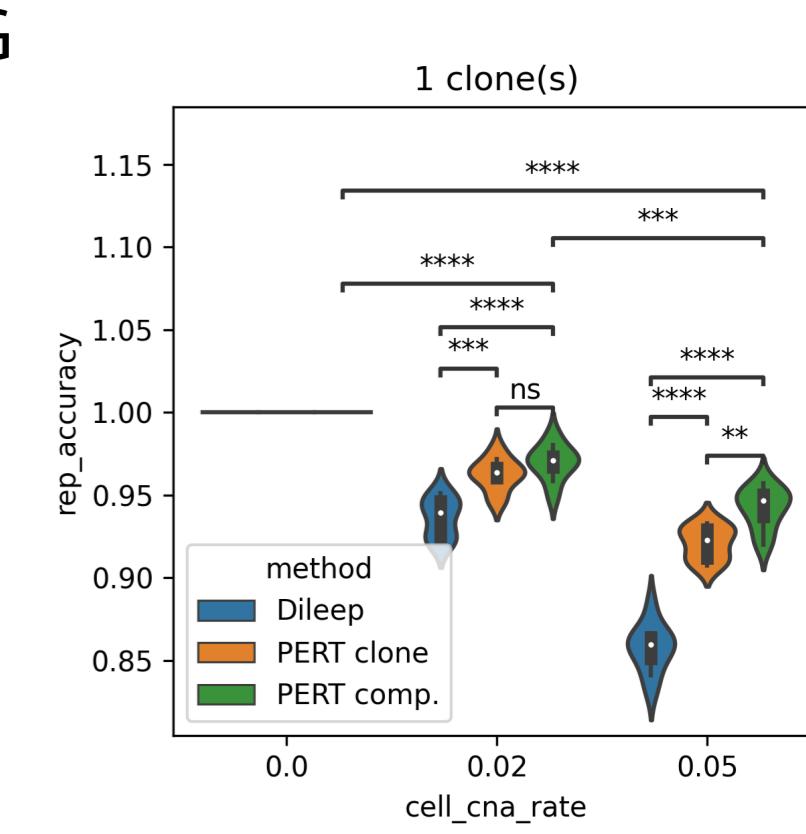
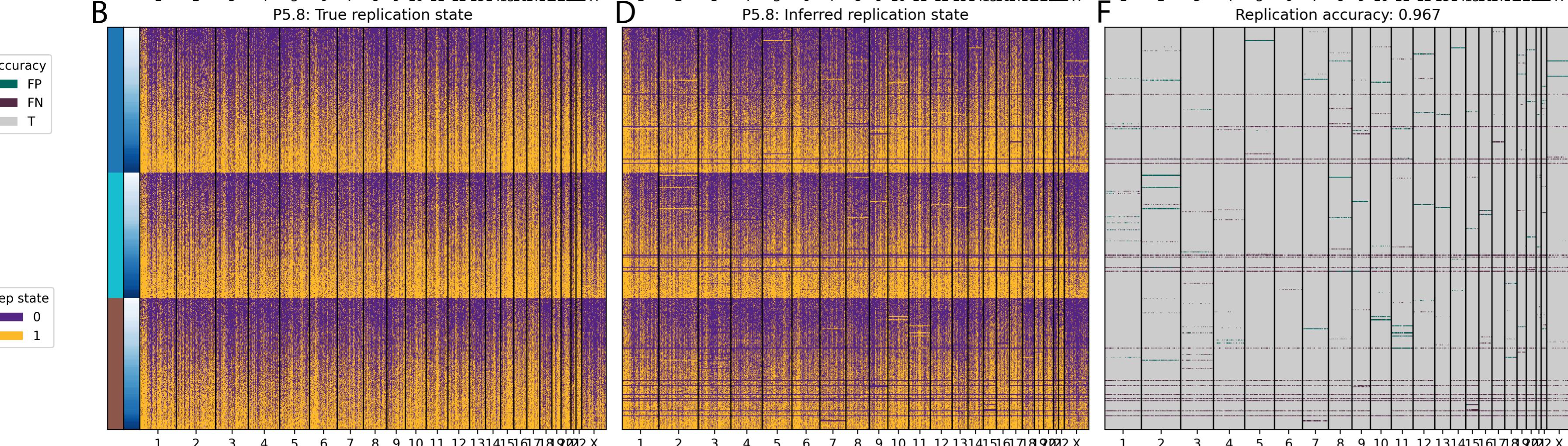
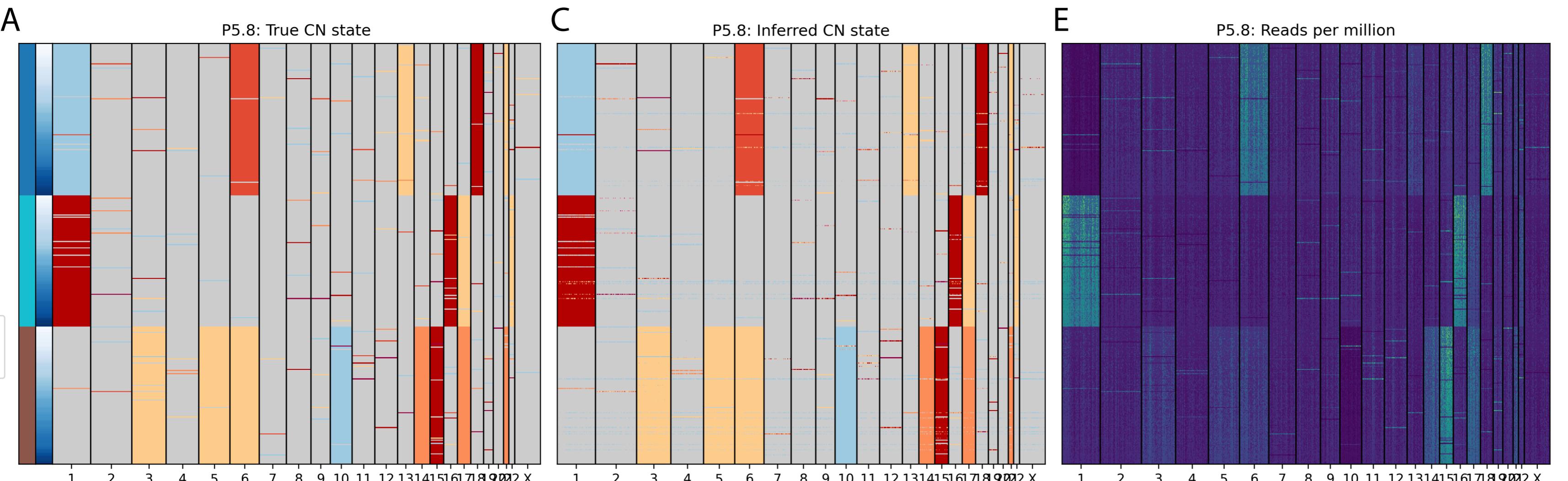
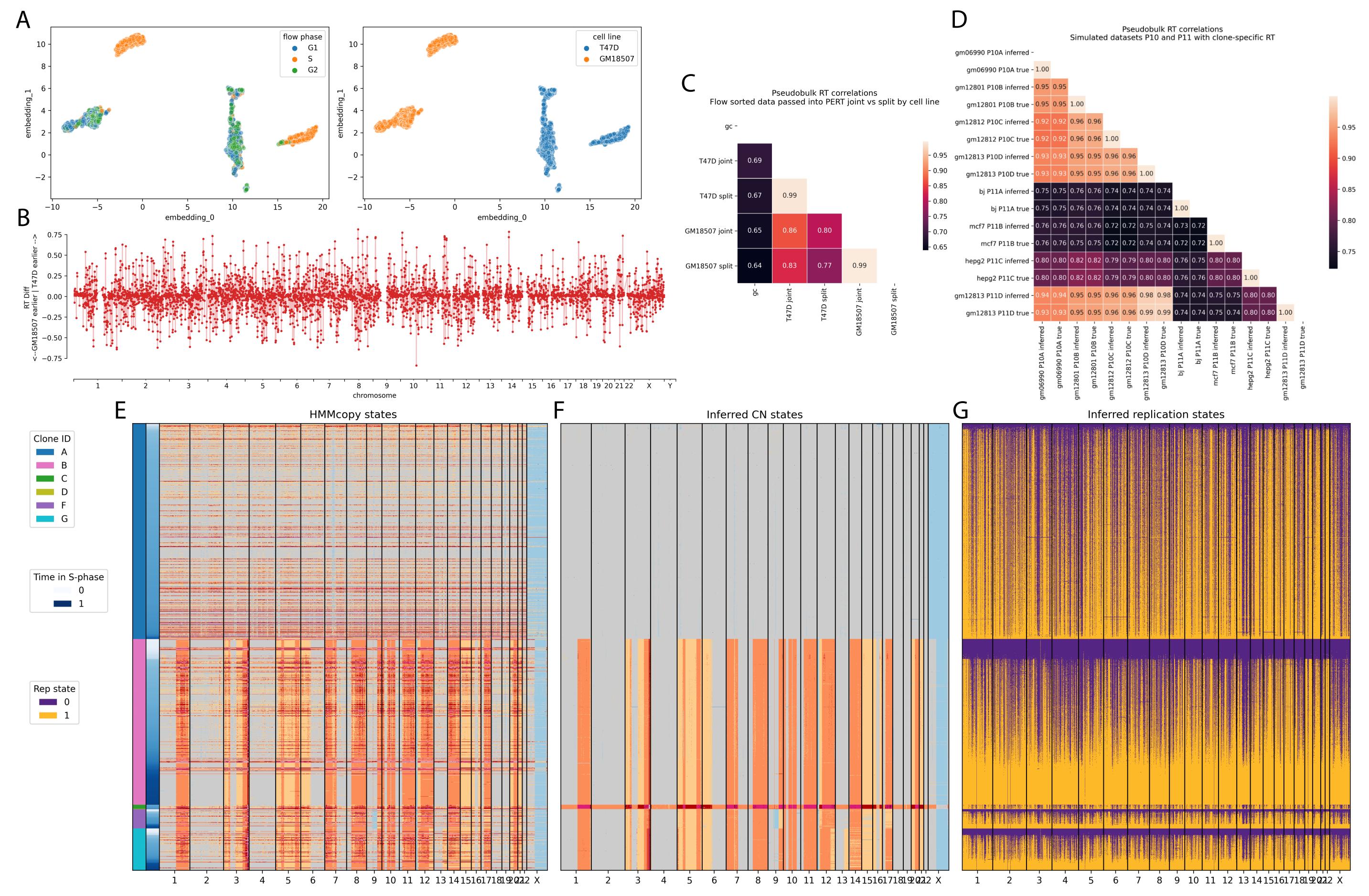
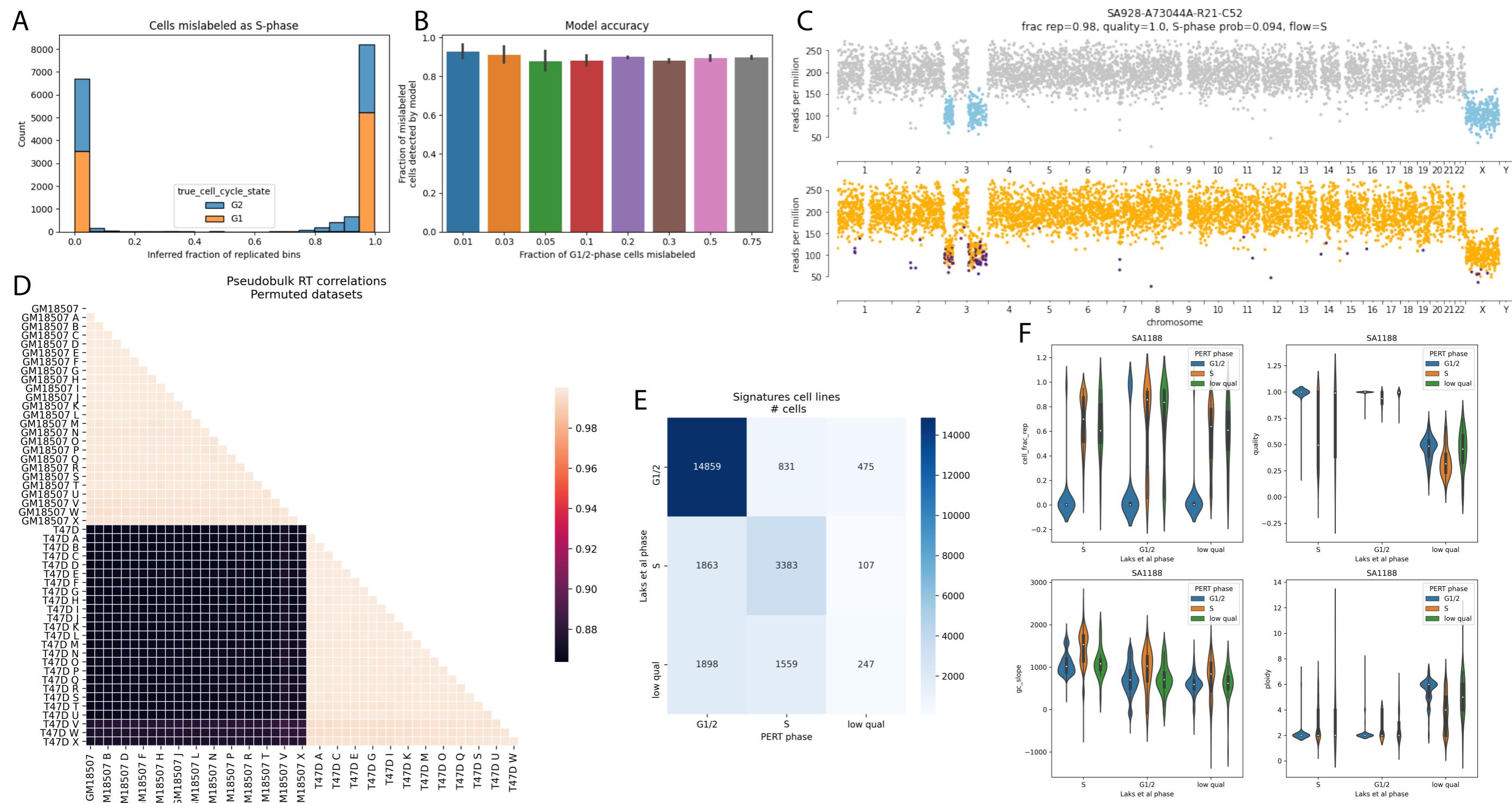
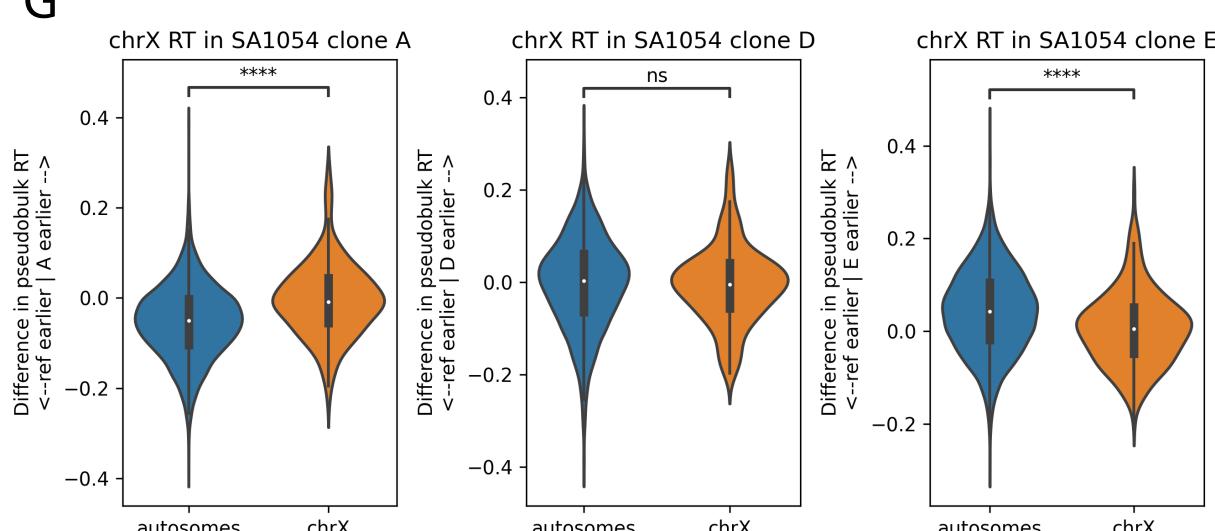
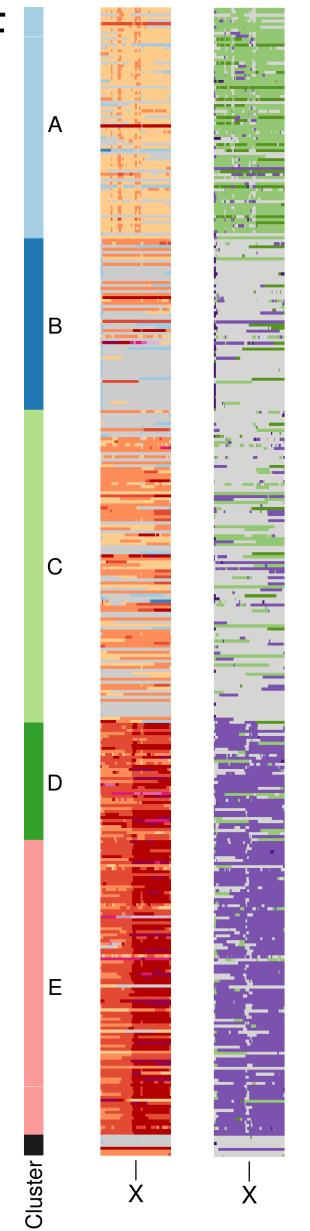
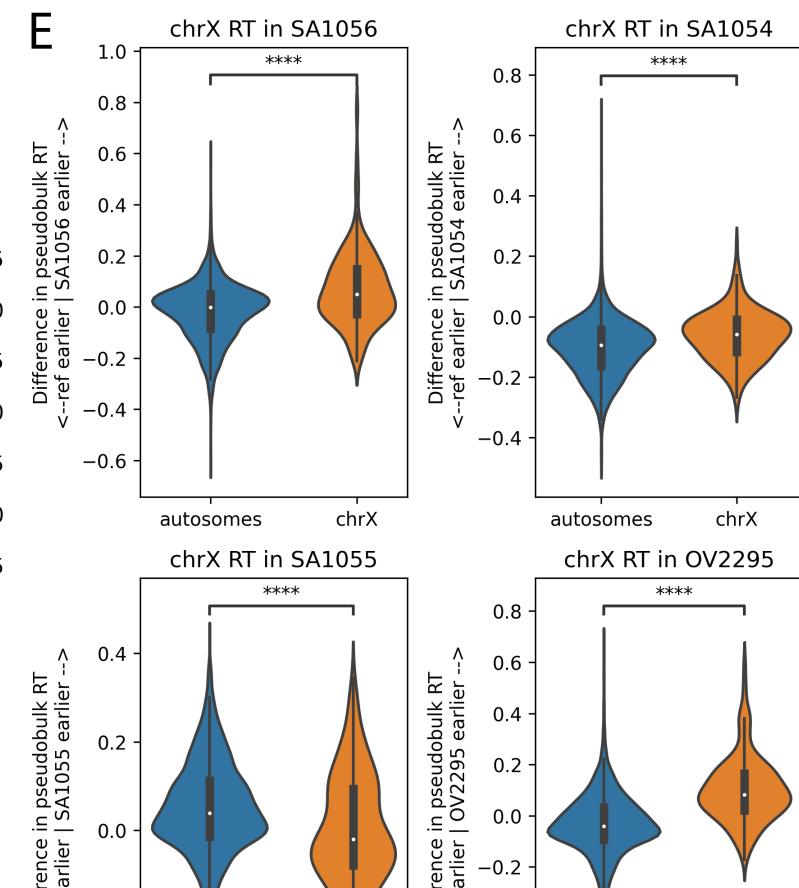
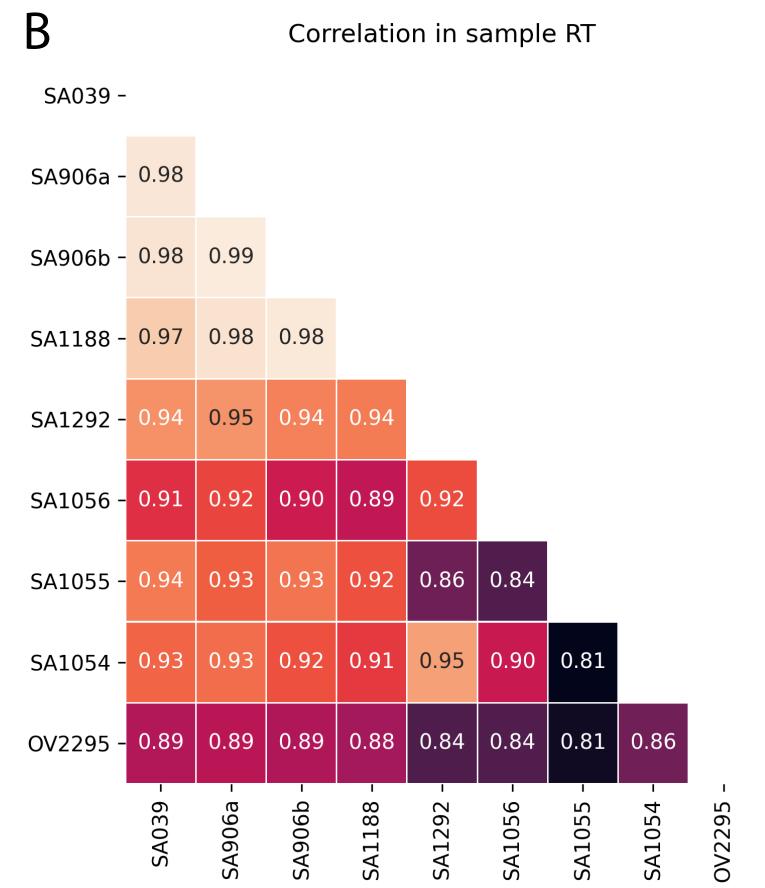
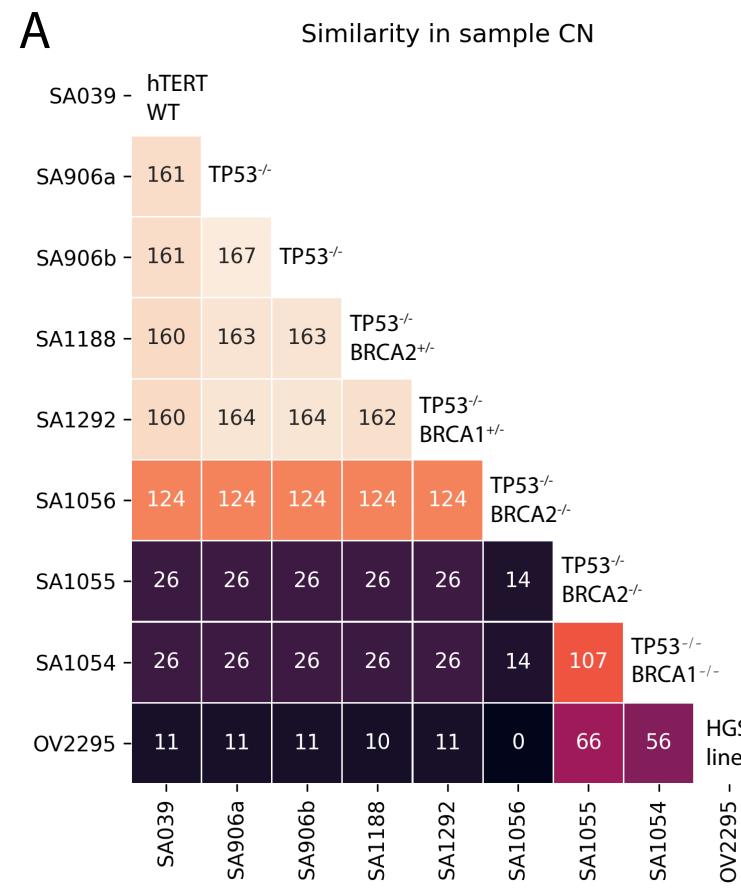


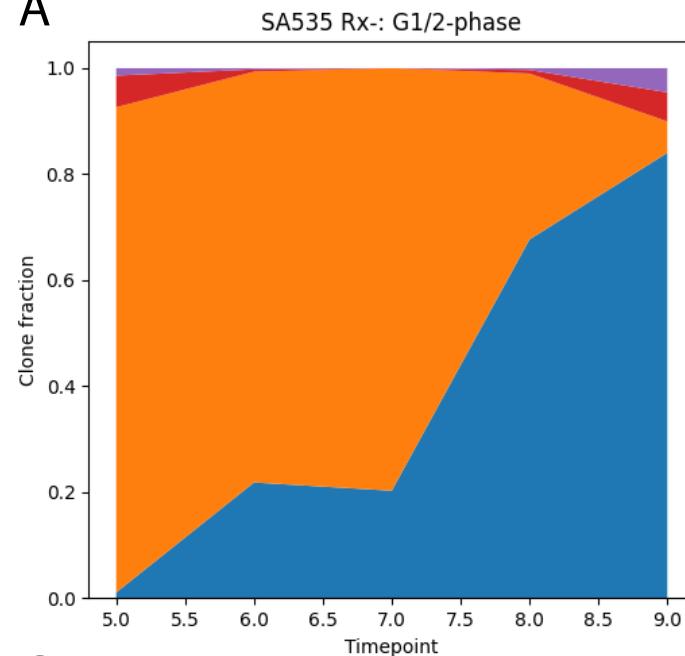
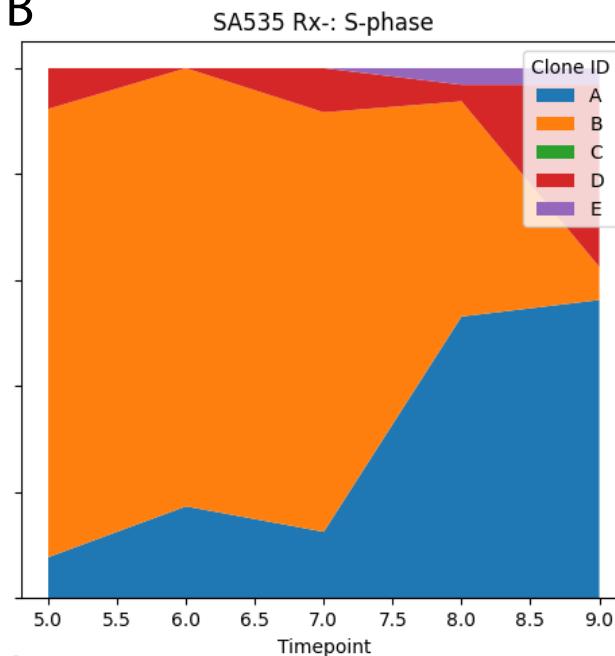
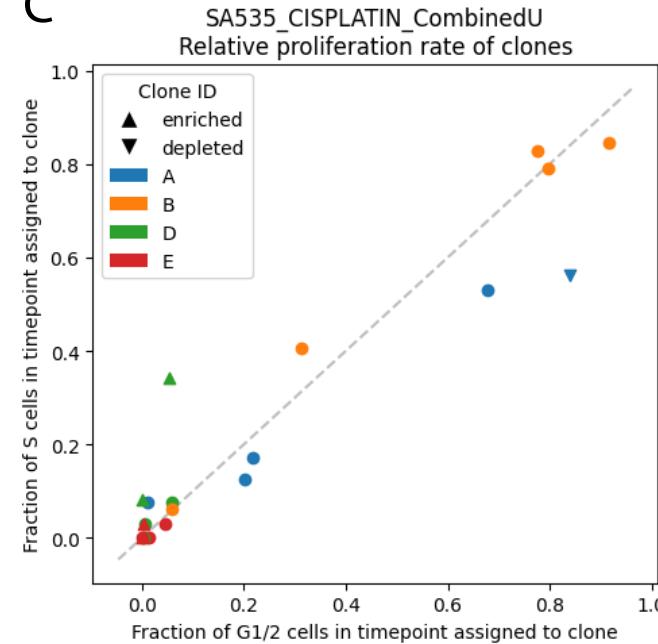
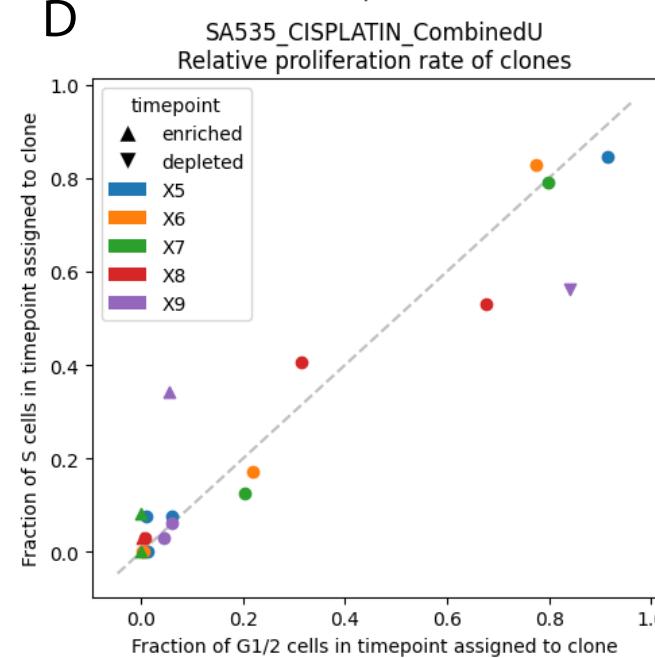
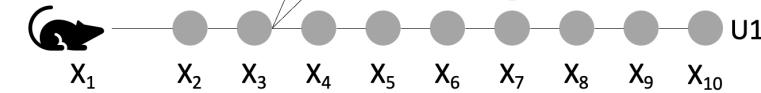
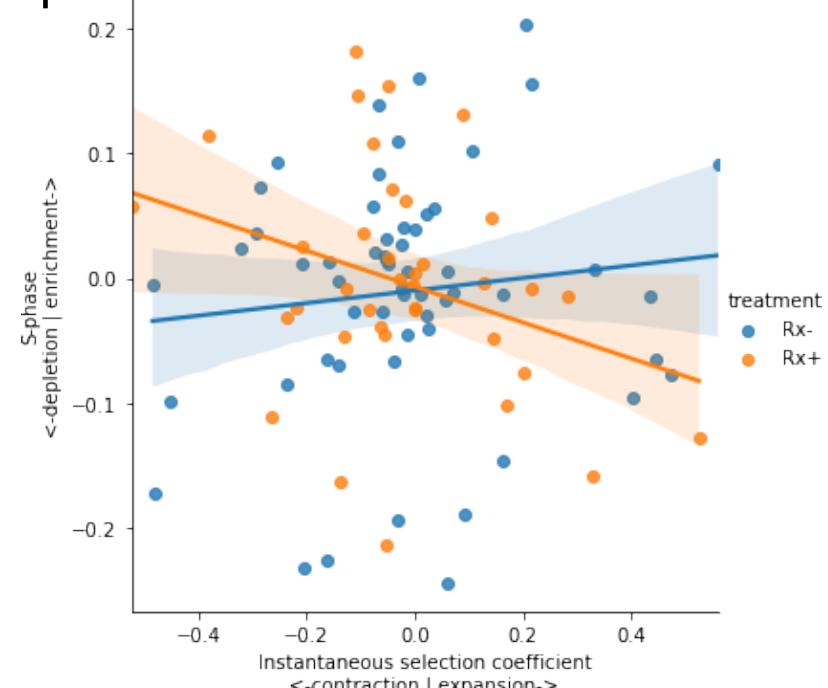
Name	Domain/Distribution	Description
λ	(0, 1)	NB event success probability (overdispersion)
δ	[1, ∞)	# of NB events (Eq 4.4)
γ	[0, 1]	GC content of locus
β_μ	$\sim N(0, 1)$	GC bias polynomial coefficient means
β_σ	(0, ∞)	GC bias polynomial coefficient stdevs
β	$\sim N(\beta_\mu, \beta_\sigma)$	GC bias 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	$\sim \text{Beta}(1, 1)$	replication timing
α	$\sim \Gamma(2, 0.2)$	replication stochasticity term
ϕ	(0, 1)	replication probabilities (Eq 4.5)
Y	$\sim \text{Bernoulli}(\phi)$	replication status
η	[0, 1]	copy number prior concentration
π	$\sim \text{Dir}(\eta)$	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



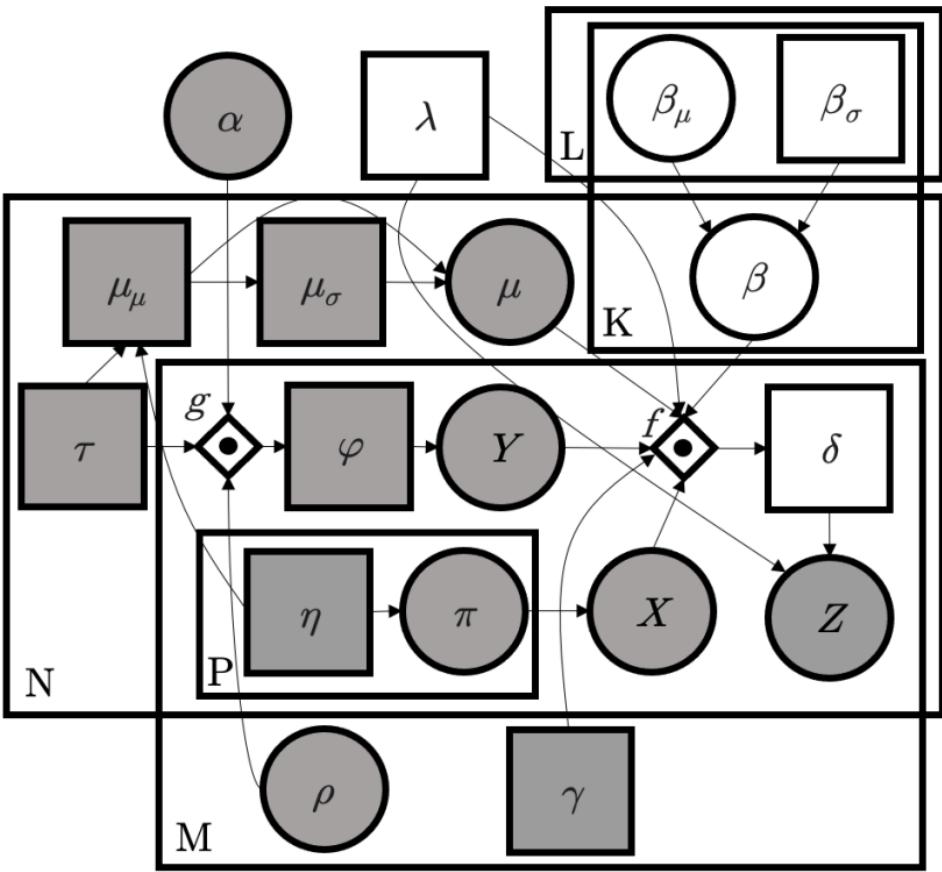




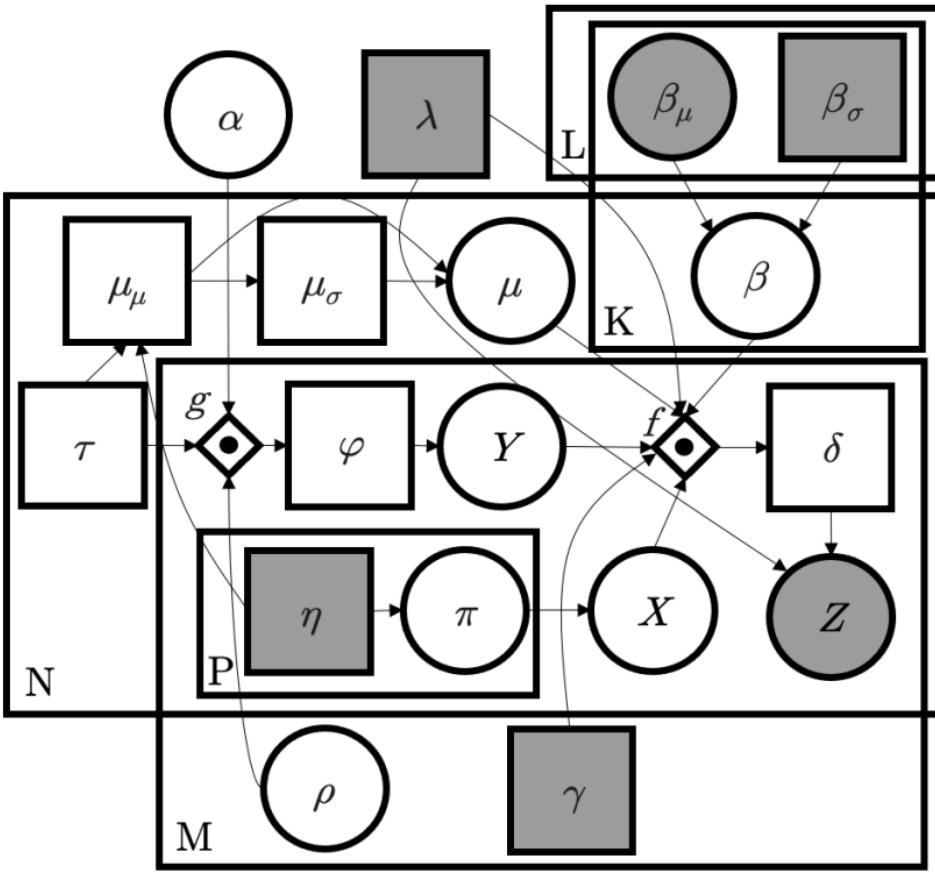


A**B****C****D****E****SA609-TNBC****F**

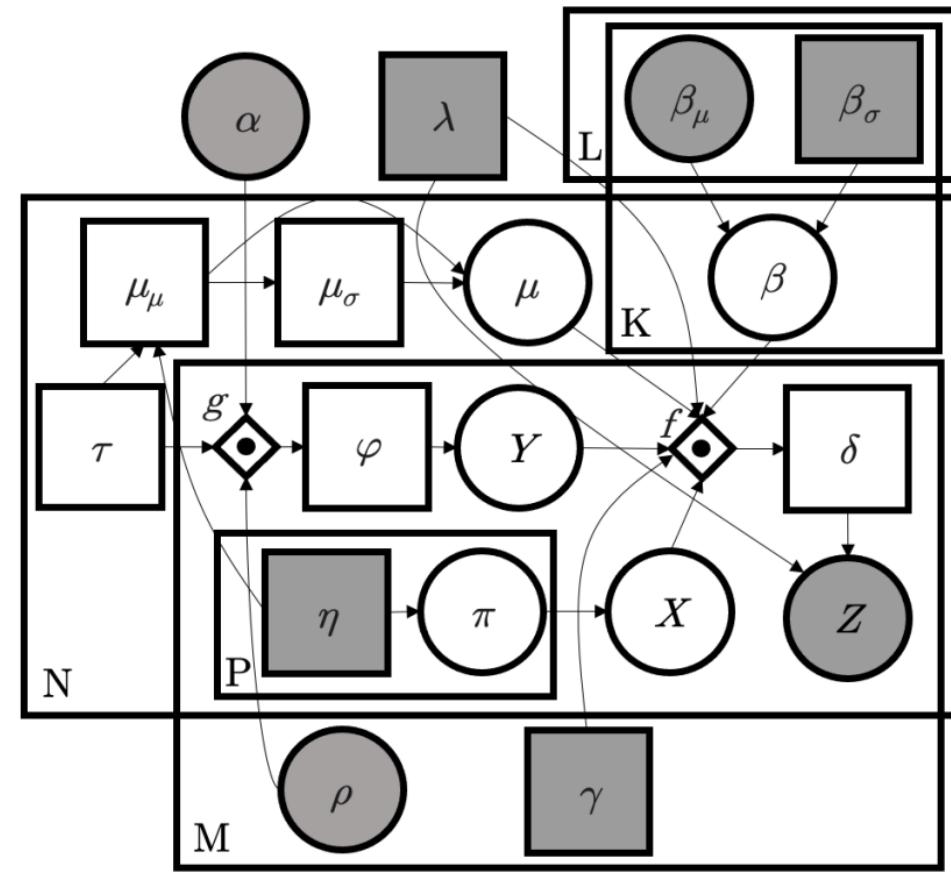
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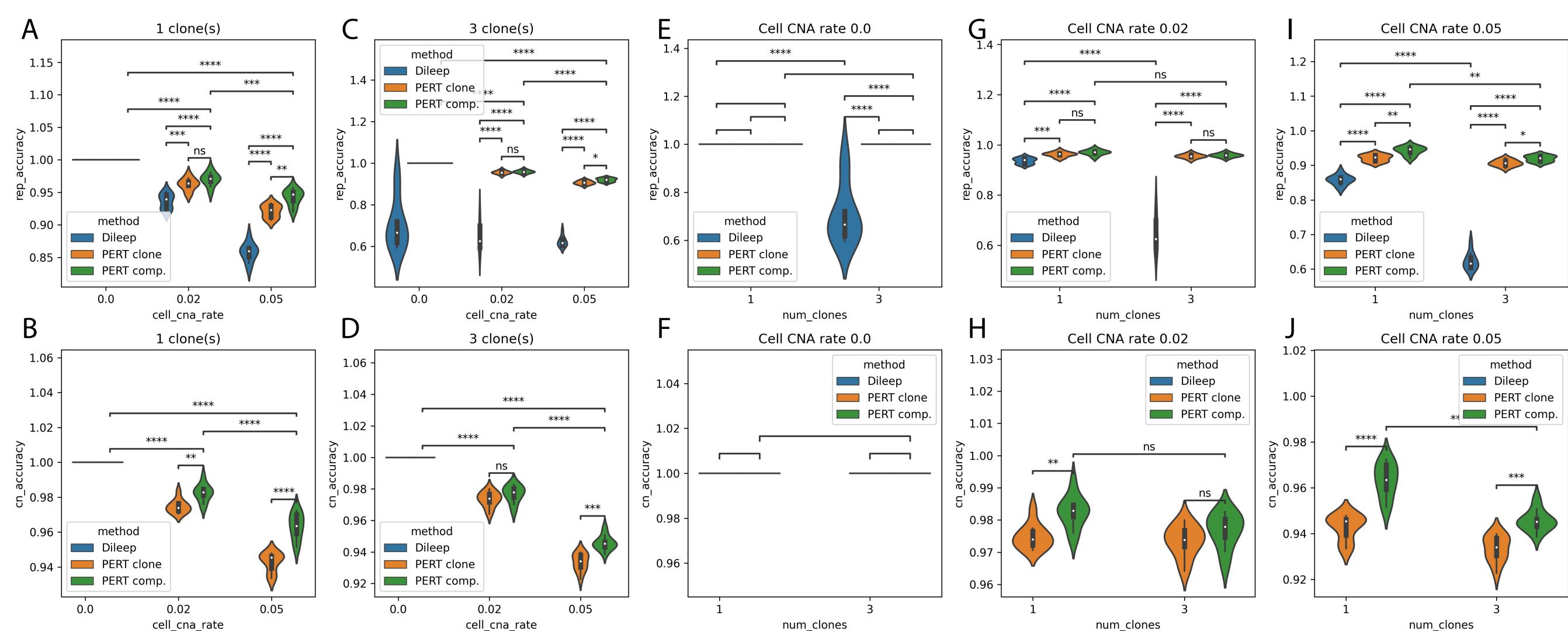


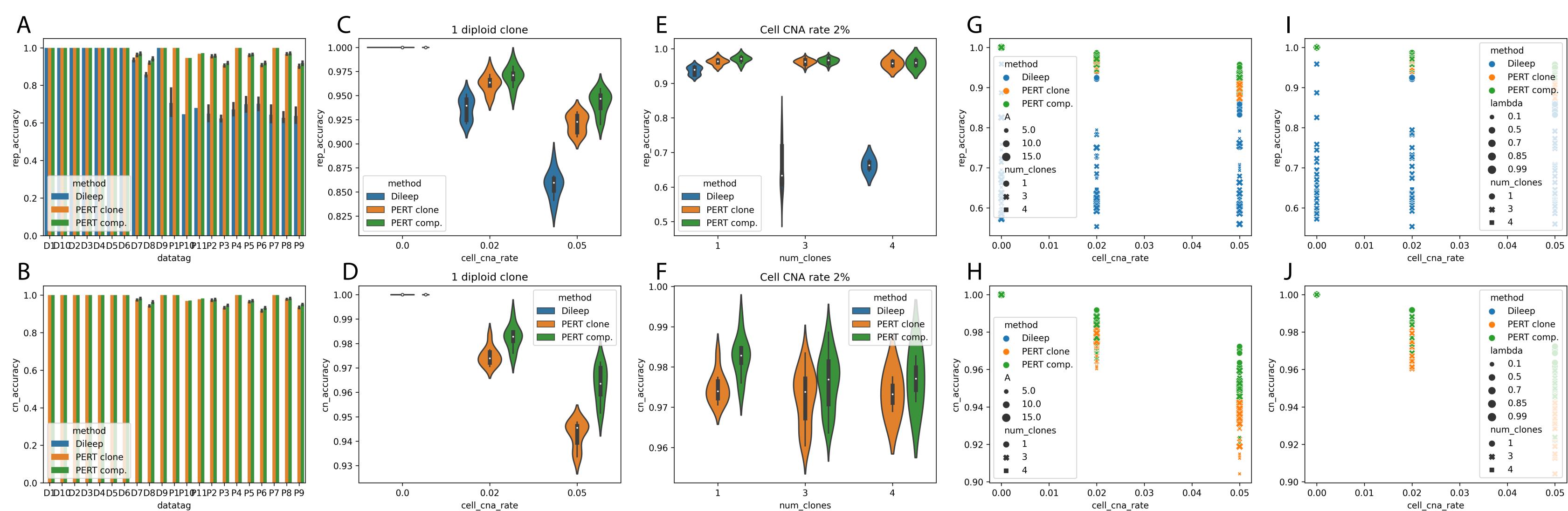
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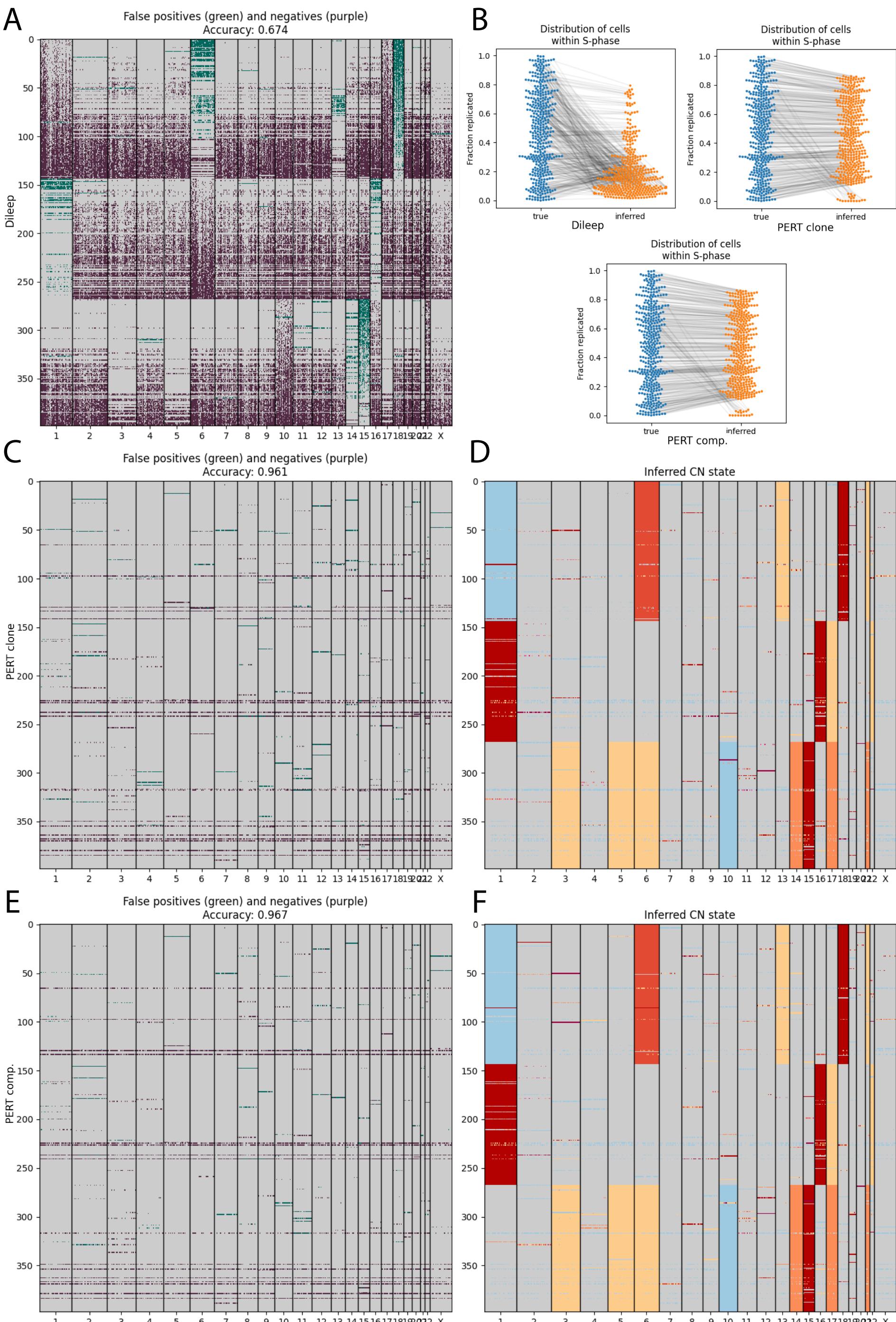


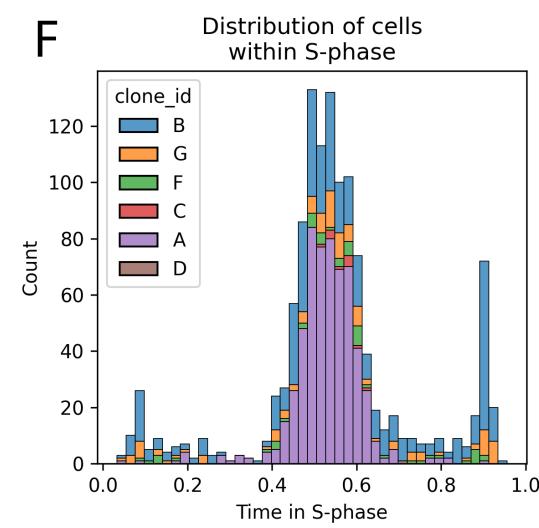
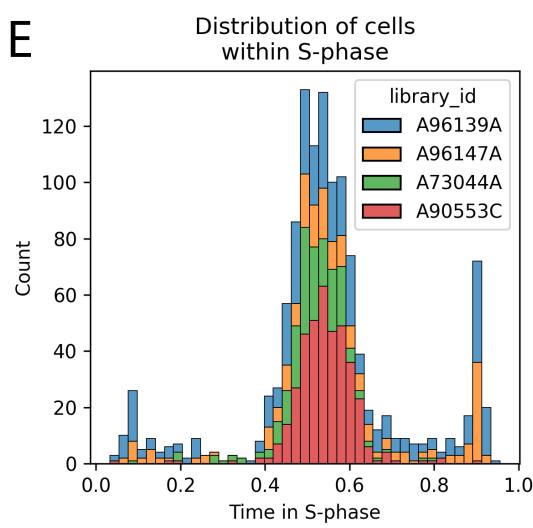
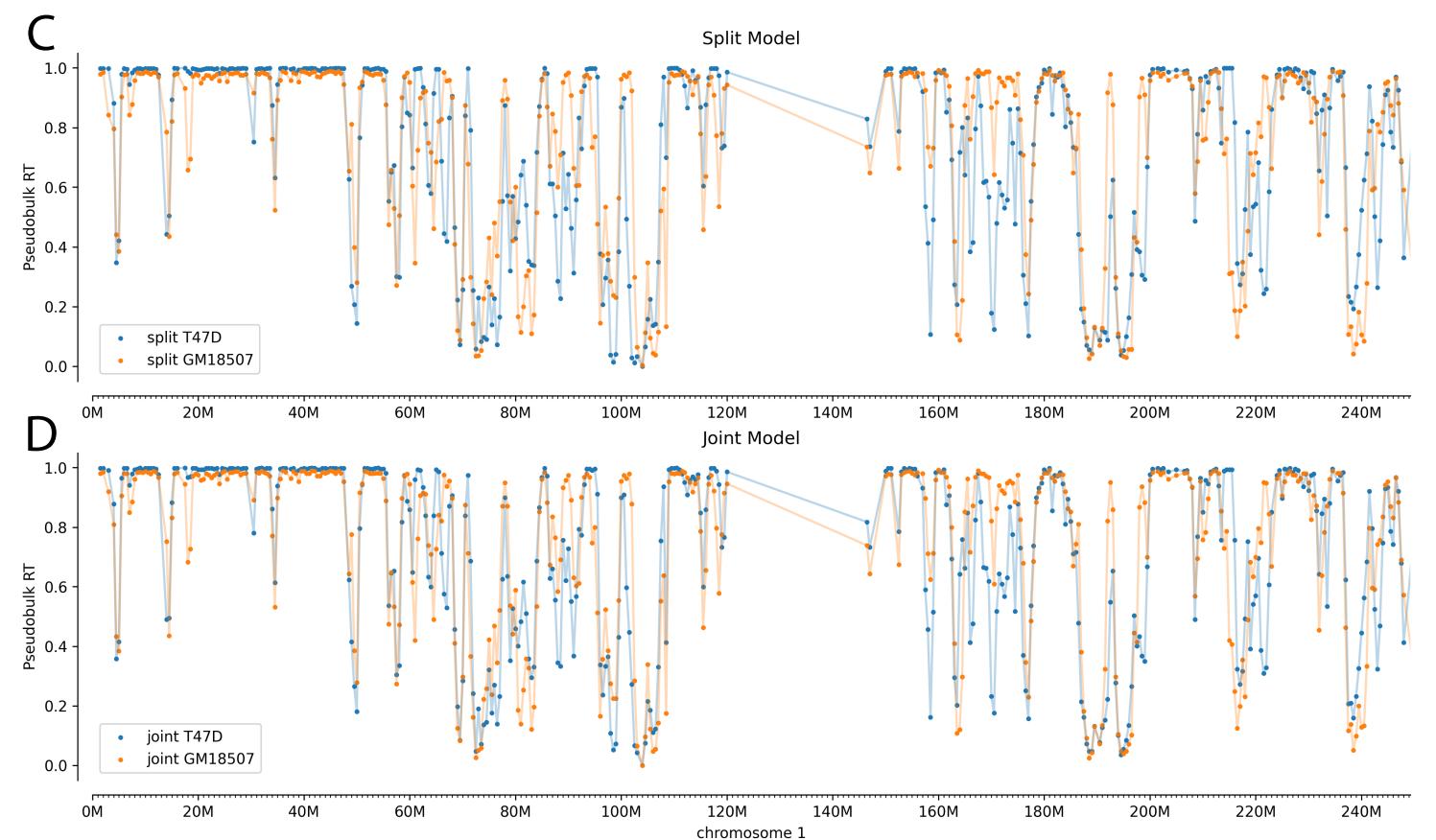
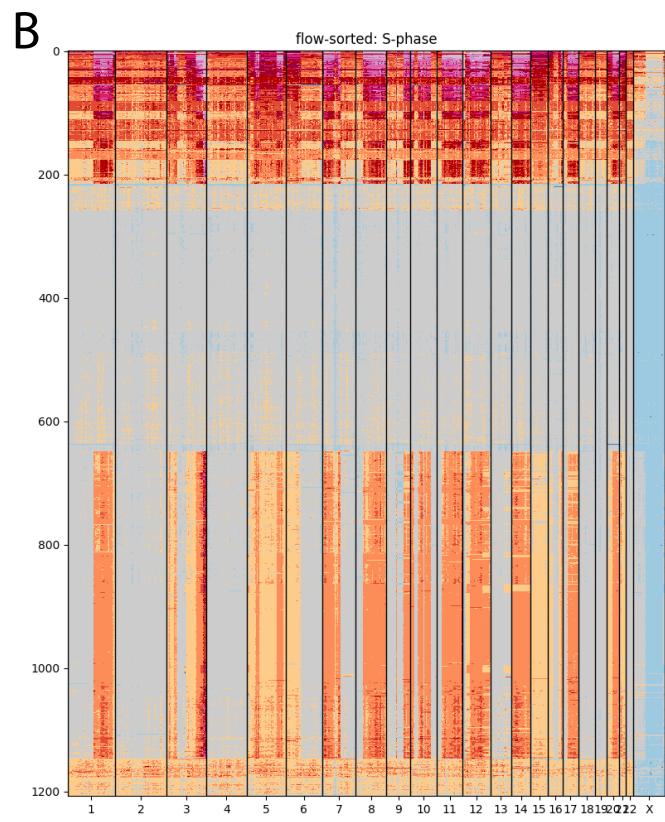
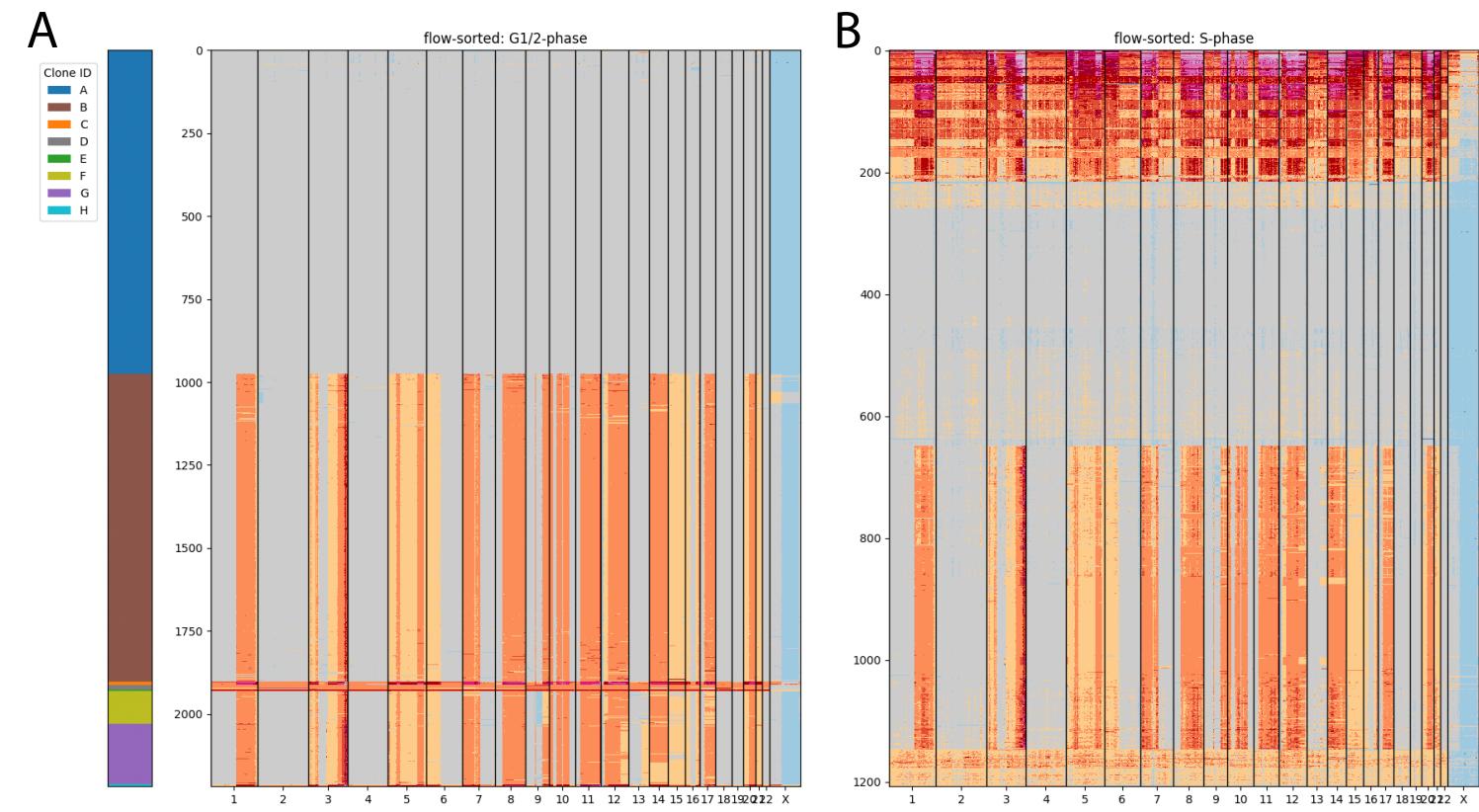
Step 3

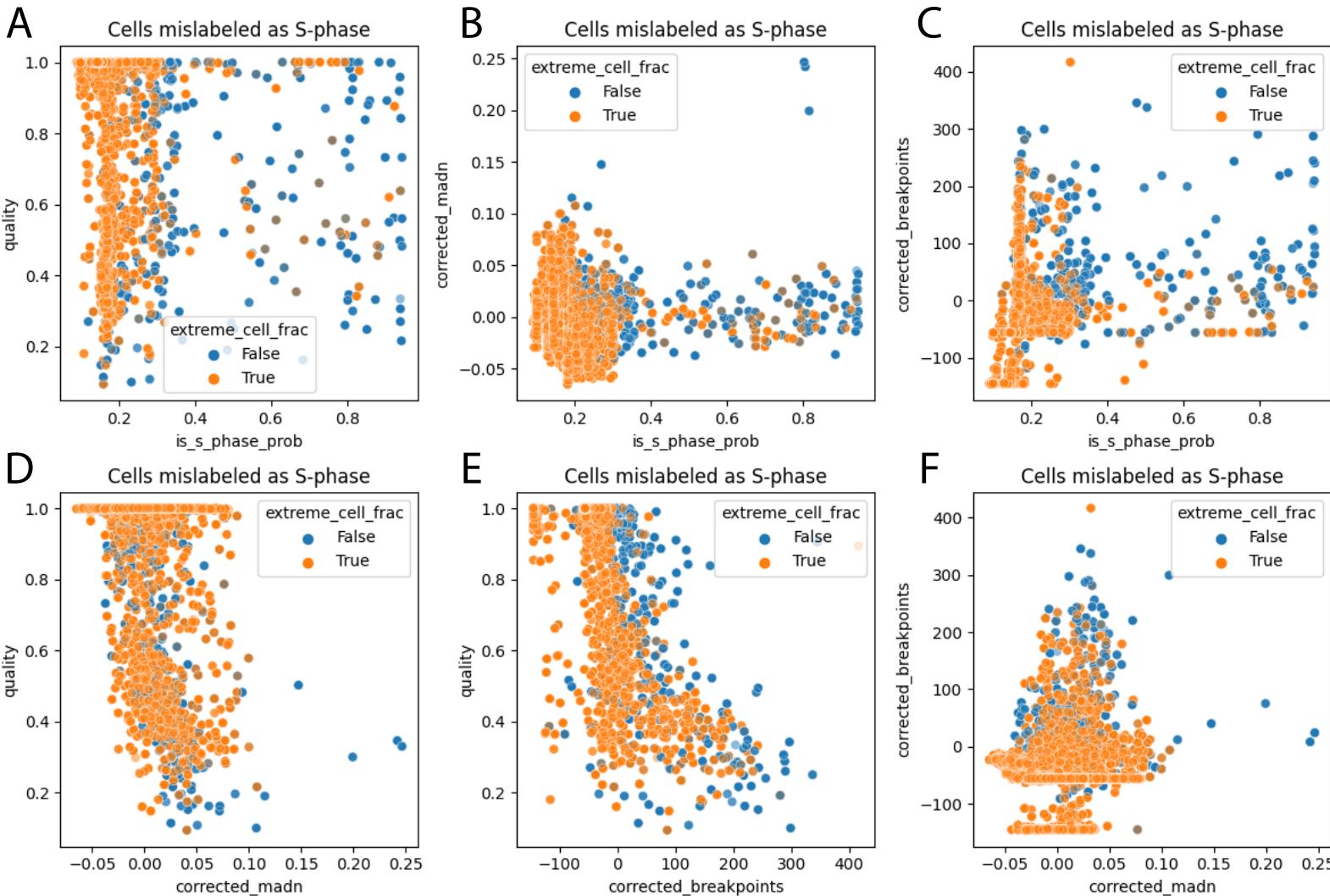


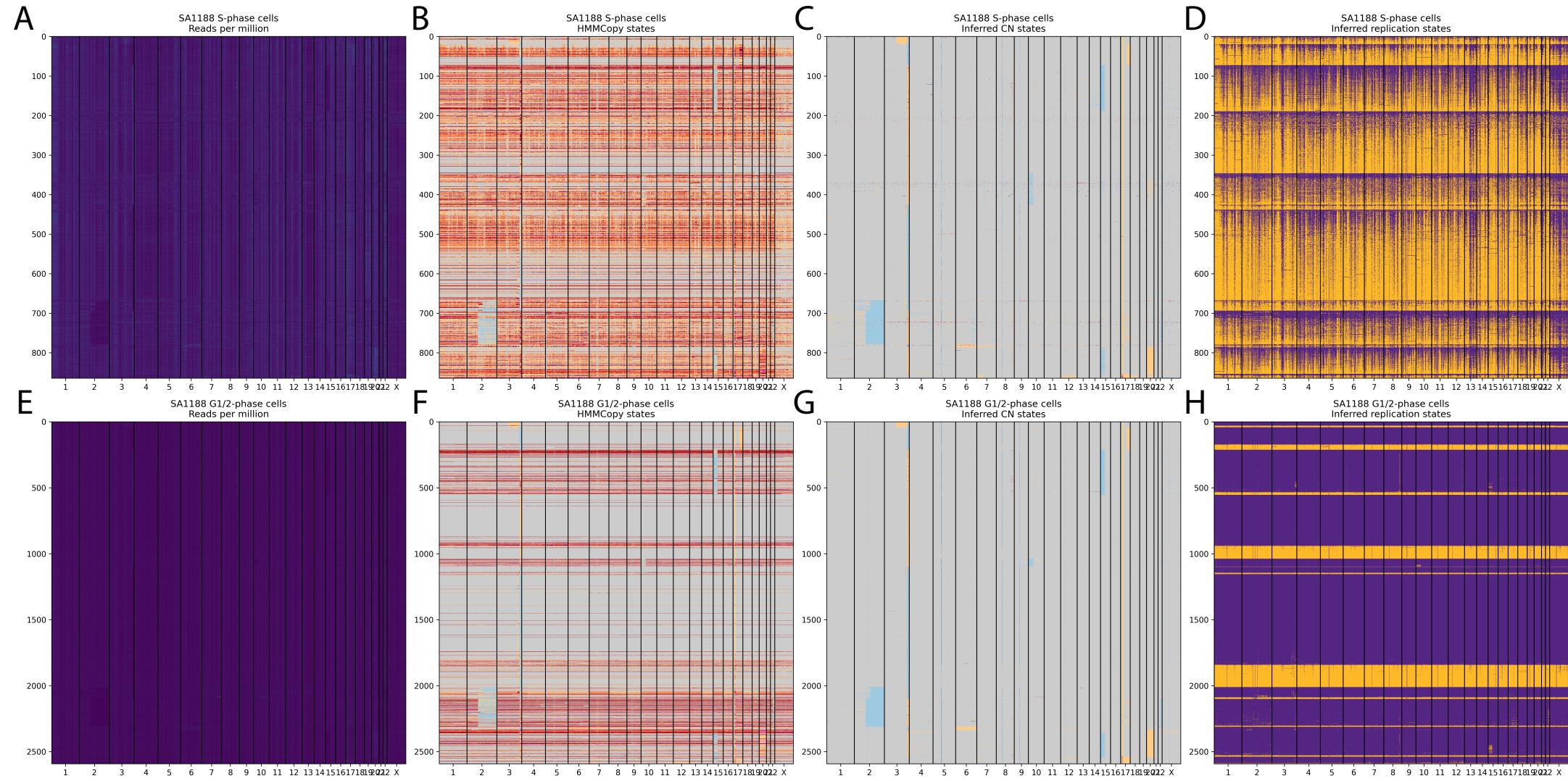


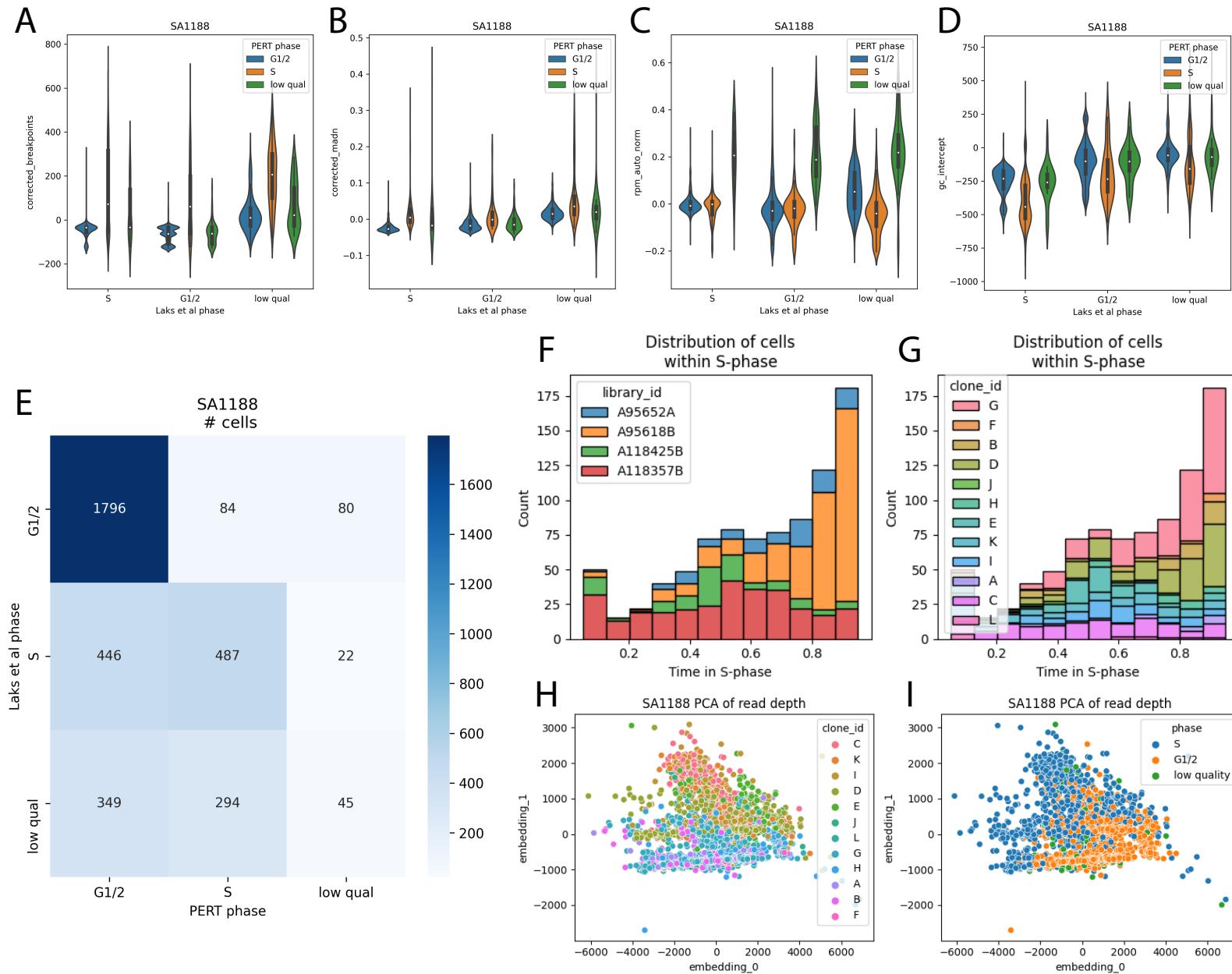


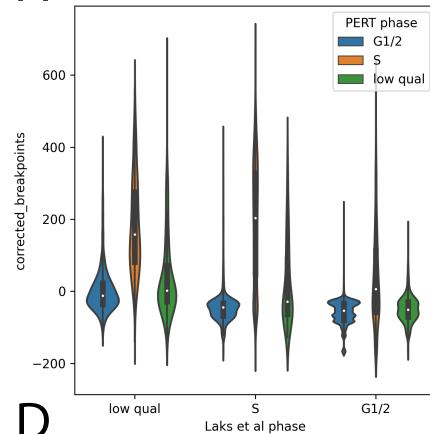
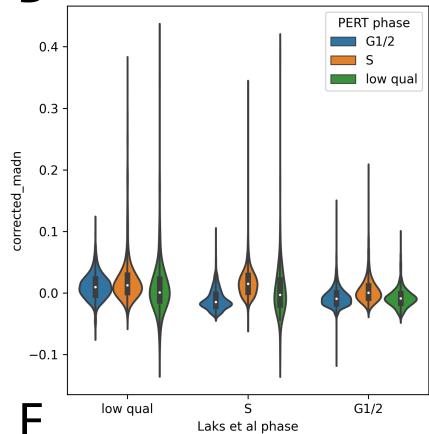
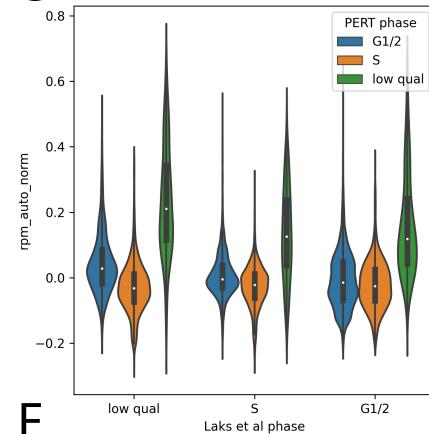
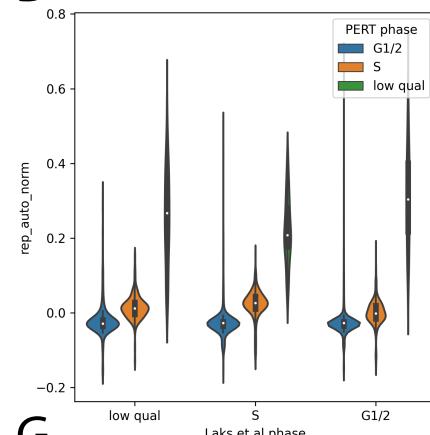
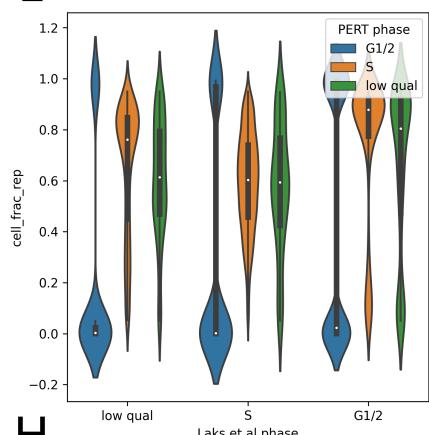
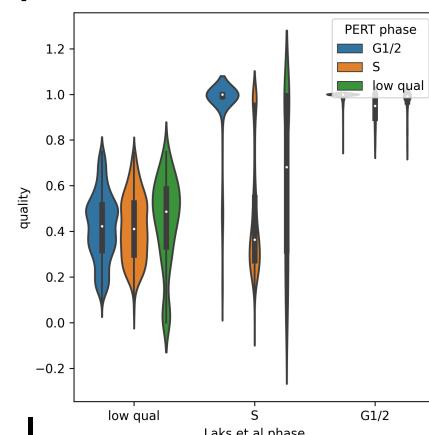
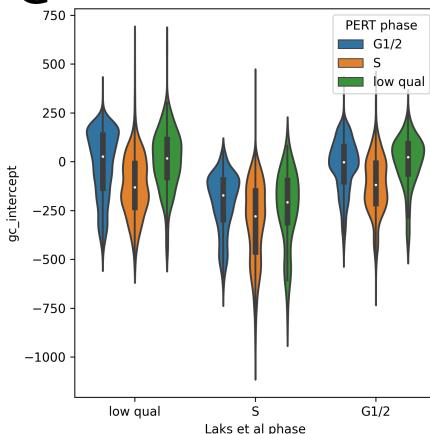
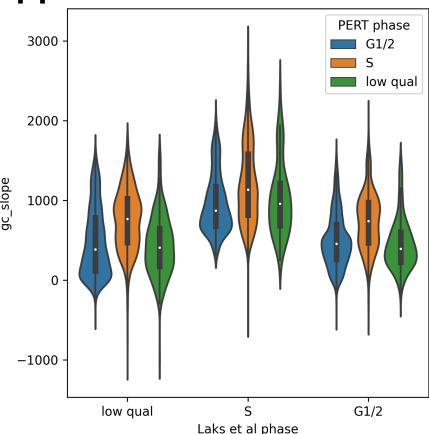
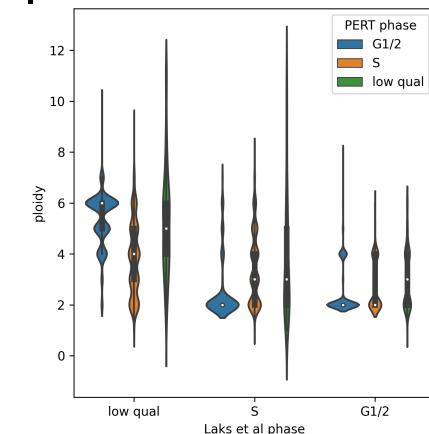


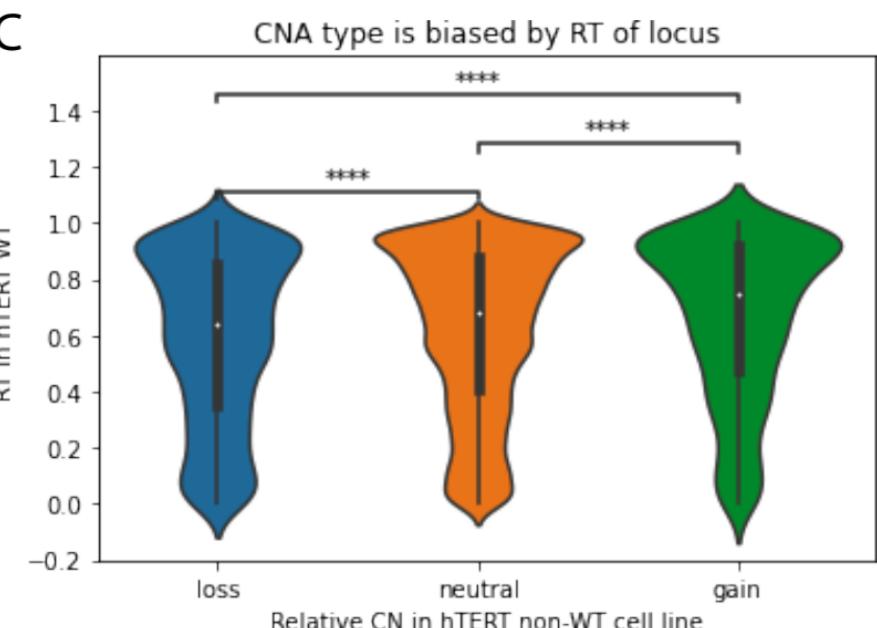
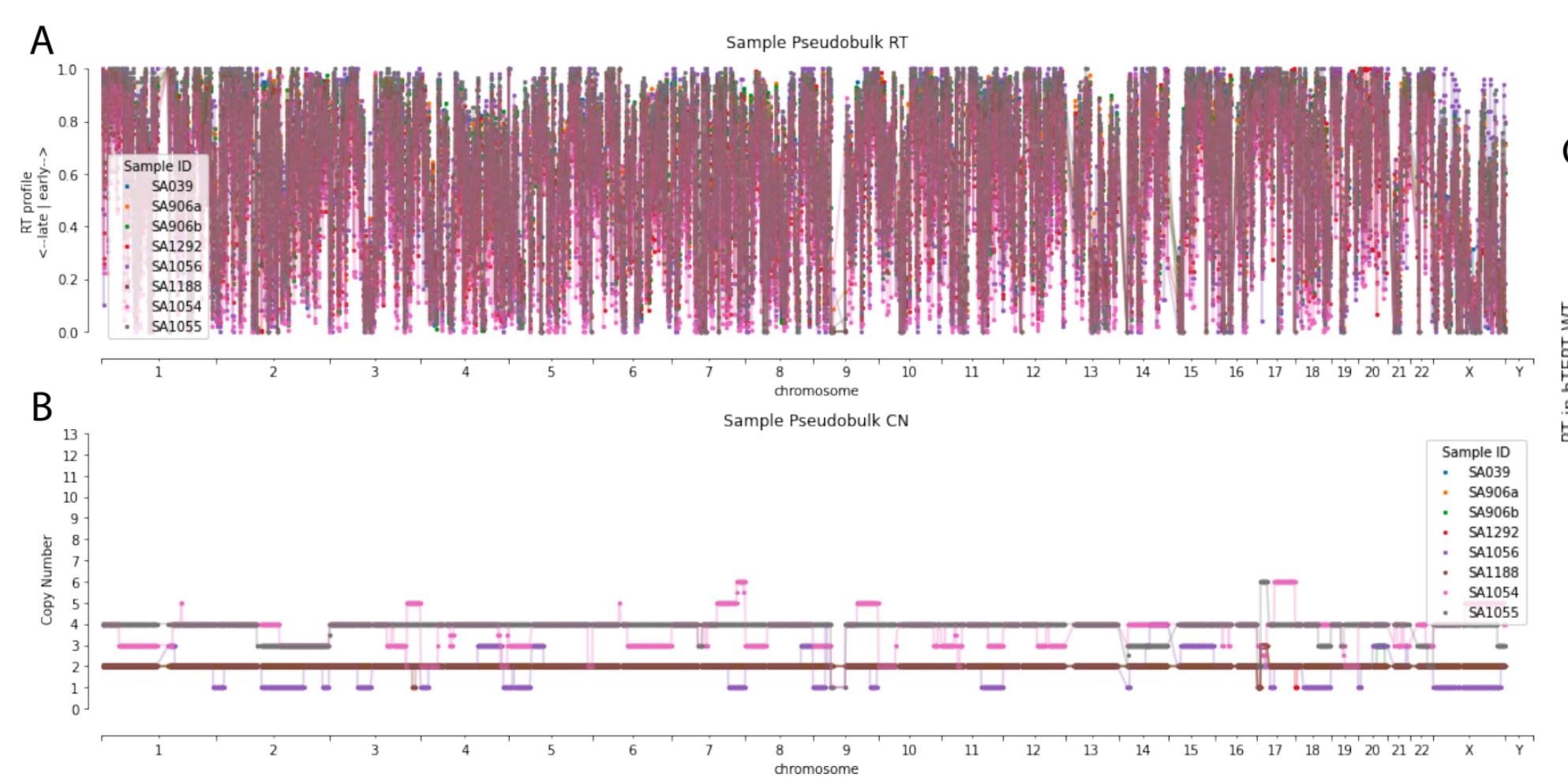






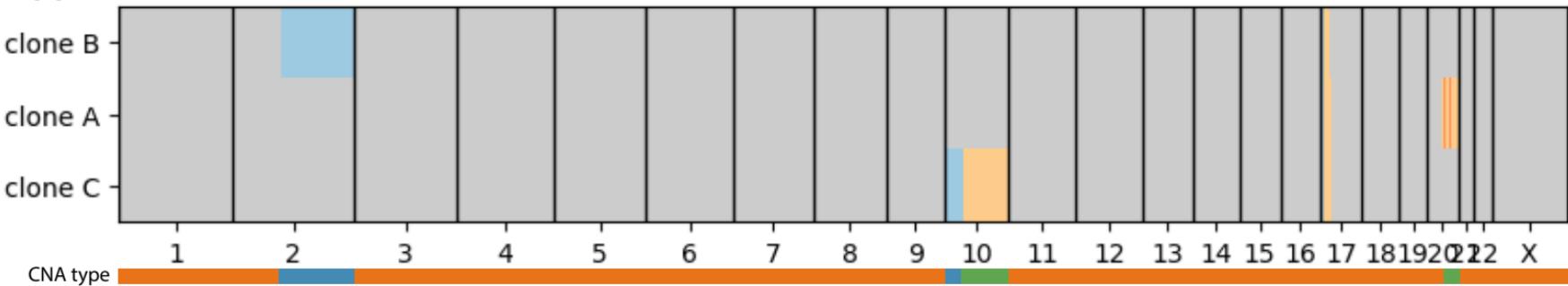


A**B****C****D****E****F****G****H****I**

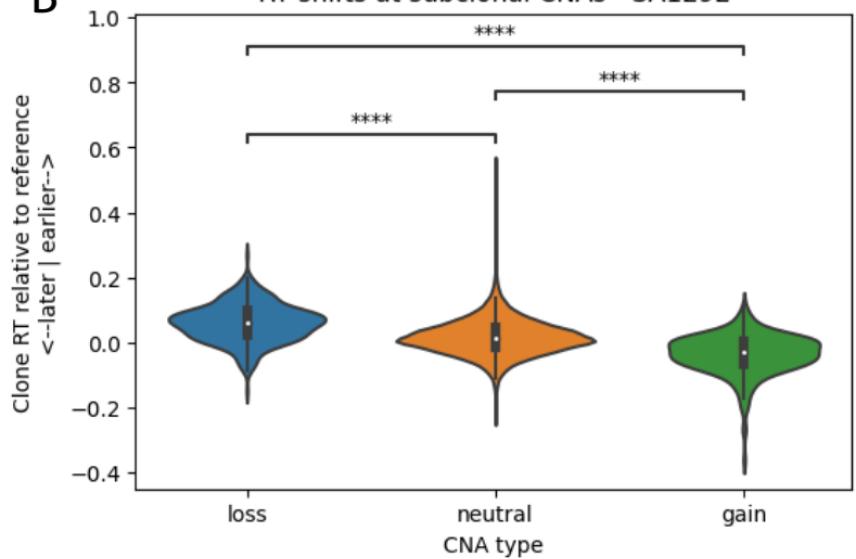


A

SA1292: Pseudobulk CN Profiles

**B**

RT shifts at subclonal CNAs - SA1292

**C**

RT shifts at subclonal CNAs - all hTERTs

