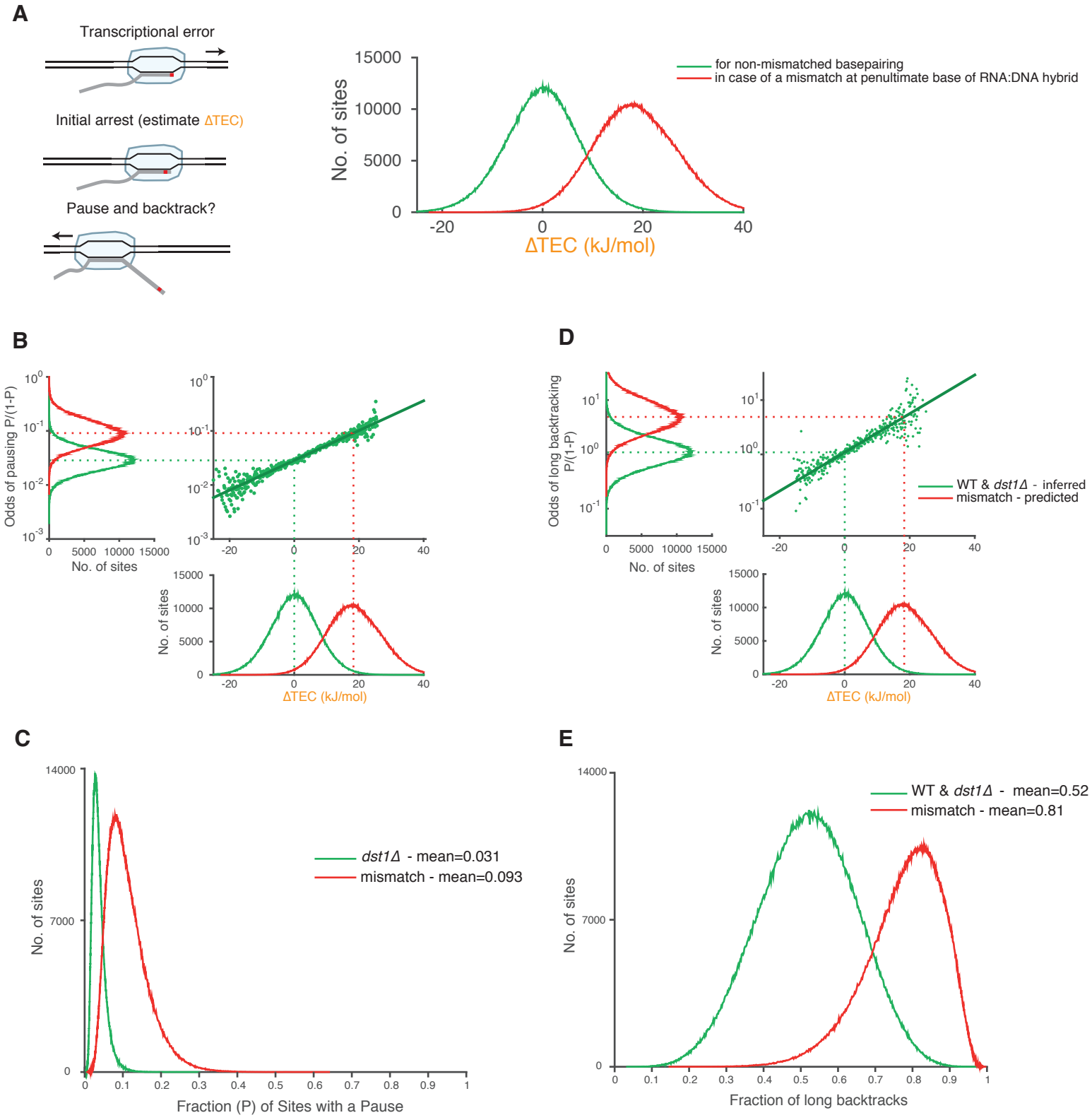
Figure S1


A
Transcriptional error
Initial arrest (estimate ΔTEC)
Pause and backtrack?
No. of sites
ΔTEC (kJ/mol)
for non-mismatched basepairing
in case of a mismatch at penultimate base of RNA:DNA hybrid
B
Odds of pausing P/(1-P)
No. of sites
ΔTEC (kJ/mol)
D
Odds of long backtracking P/(1-P)
WT & dst1Δ - inferred
mismatch - predicted
C
dst1Δ - mean=0.031
mismatch - mean=0.093
Fraction (P) of Sites with a Pause
E
WT & dst1Δ - mean=0.52
mismatch - mean=0.81
Fraction of long backtracks