



Figure S1. Distribution of S-scores differed between conditions or between query genes, as shown by cumulative probability plots. (A) S-scores for *RTT107*. Kolmogorov-Smirnov test, two-sided, p-values for untreated vs CPT = $6.4\text{e-}09$, untreated vs HU = $1.4\text{e-}07$, untreated vs MMS < $2.2\text{e-}16$. (B) S-scores for *SLX4*. Kolmogorov-Smirnov test, two-sided, p-values for untreated vs CPT = $5.6\text{e-}16$, untreated vs HU = $4.9\text{e-}10$, untreated vs MMS = 0.14. (C) S-scores for *HRQ1*. Kolmogorov-Smirnov test, two-sided, p-values for untreated vs CPT = $2.5\text{e-}03$, untreated vs HU < $2.2\text{e-}16$, untreated vs MMS = $7.0\text{e-}05$. (D) Combined S-scores for all conditions for each query gene. Kolmogorov-Smirnov test, two-sided, p-values for *RTT107* vs *HRQ1* < $2.2\text{e-}16$, *RTT107* vs *SLX4* < $2.2\text{e-}16$, *HRQ1* vs *SLX4* = $7.8\text{e-}16$.