Distribution of Normalized Cut Rate vs. Mismatches for 16hr-gDNA2 2.0 -1.5 -Normalized Cut Rate 1.0 -0.5 -0.0 -3 0 2 8 9 **Number of Mismatches** 

Cut Rate by Mean Mismatch Position in 16hr-gDNA2 2.0 -1.5 -Normalized Cut Rate Mismatches 2 1.0 -0.5 -0.0 -0 5 10 15 20 Mean Mismatch Position