Distribution of Normalized Cut Rate vs. Mismatches for 16hr+gDNA3 2.5 -2.0 -Normalized Cut Rate 0.5 -0.0 -0 2 3 8 9 **Number of Mismatches** 

Cut Rate by Mean Mismatch Position in 16hr+gDNA3 2.5 -2.0 -Normalized Cut Rate Mismatches 2 0.5 -0.0 -0 5 10 15 20 Mean Mismatch Position