Distribution of Normalized Cut Rate vs. Mismatches for 16hr+gDNA2 2 -Normalized Cut Rate 0 -0 2 3 6 7 8 1 **Number of Mismatches**

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