

Abstract Submitted  
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**Genomic Mapping of Human DNA provides Evidence of Difference in Stretch between AT and GC rich regions**<sup>1</sup> JEFFREY REIFENBERGER, BioNano Genomics, KEVIN DORFMAN, University of Minnesota - Twin Cities, Department of Chemical Engineering and Materials Science, HAN CAO, BioNano Genomics — Human DNA is not a polymer consisting of a uniform distribution of all 4 nucleic acids, but rather contains regions of high AT and high GC content. When confined, these regions could have different stretch due to the extra hydrogen bond present in the GC basepair. To measure this potential difference, human genomic DNA was nicked with NtBspQI, labeled with a cy3 like fluorophore at the nick site, stained with YOYO, loaded into a device containing an array of nanochannels, and imaged. Over 473,000 individual molecules of DNA, corresponding to roughly 30x coverage of a human genome, were collected and aligned to the human reference. Based on the known AT/GC content between aligned pairs of labels, the stretch was measured for regions of similar size but different AT/GC content. We found that regions of high GC content were consistently more stretched than regions of high AT content between pairs of labels varying in size between 2.5 kbp and 500 kbp. We measured that for every 1% increase in GC content there was roughly a 0.06% increase in stretch. While this effect is small, it is important to take into account differences in stretch between AT and GC rich regions to improve the sensitivity of detection of structural variations from genomic variations.

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Jeffrey Reifengerger  
BioNano Genomics

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