



S Figure 1. Regional Integrated Intrinsic Curvature analysis in *L. major*

The Riemann sum for the curvature plot was calculated for a SSR spanning 6176bp in *L. major* Chr22 (from 605990 to 612166) is shown as a vertical dotted line. This score is compared to the density function representing the population of RIIC scores for equal-length regions in the genome (solid line). In this case, the difference is statistically significant ($p < 0.05$).