



Figure S4 Effect of GC adjustment on sequencing coverage.

(A) Mean coverage value per 10 kb bin (y-axis) as a function of the mean GC % per 10 kb bin, before any adjustment was applied. The black line represents a robust local regression fitted on the data.

(B) Adjusted mean coverage value per 10 kb bin (y-axis) as a function of the mean GC % per 10 kb bin.

(C) Distribution of adjusted mean coverage value per 10 kb bins along the genome. The green line corresponds to the adjusted coverage median value for chromosome 4, which was used for normalization as representative of regions with CN 2.