Supporting Information

Liao et al. 10.1073/pnas.1321997111

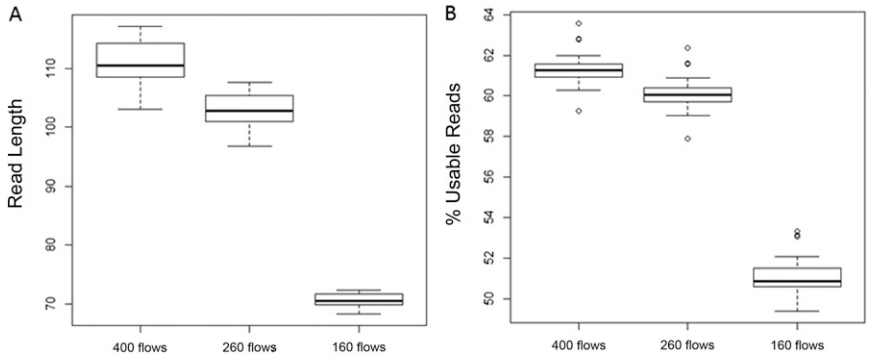

Fig. S1. The data obtained with different sequencing flows (400/260/160 flows). (*A*) Read length. (*B*) Percentage of usable reads.

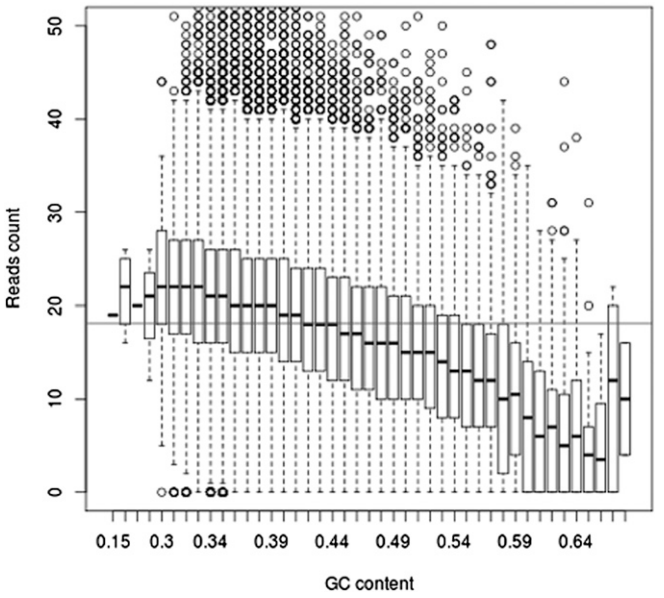

Fig. S2. Illustration of GC bias in semiconductor sequencing platform (SSP) sequencing. A representative sample is shown. The number of unique reads calculated for every 0.1% of GC content was plotted against the GC content of the bin using boxplots. The box represents the interquartile range that contains values between the first and third quartiles. The upper whisker shows the value of the largest observation less than or equal to the upper quartile plus 1.5 times the length of the interquartile range. The lower whisker shows the value of the smallest observation greater than or equal to the lower quartile less 1.5 times the length of the interquartile range. The circles represent the values that lie outside the range between the upper and lower whiskers.

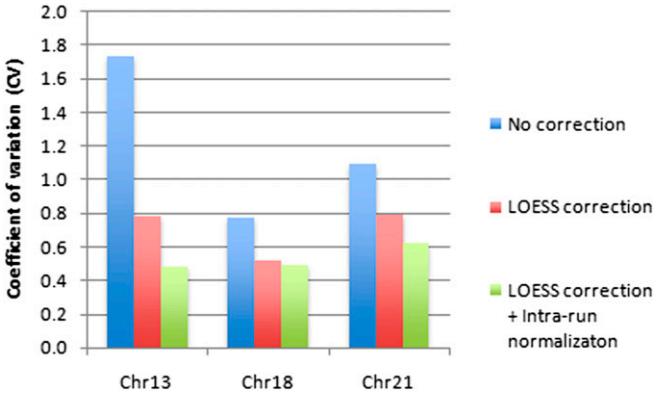

Fig. S3. The coefficients of variation (CVs) for chromosomes 13, 18, and 21 with and without GC correction. The blue bars represent the CVs before correction. The red bars represent the CVs after locally weighted scatterplot smoothing (LOESS) correction. The green bars represent the CVs after LOESS correction and intrarun normalization.

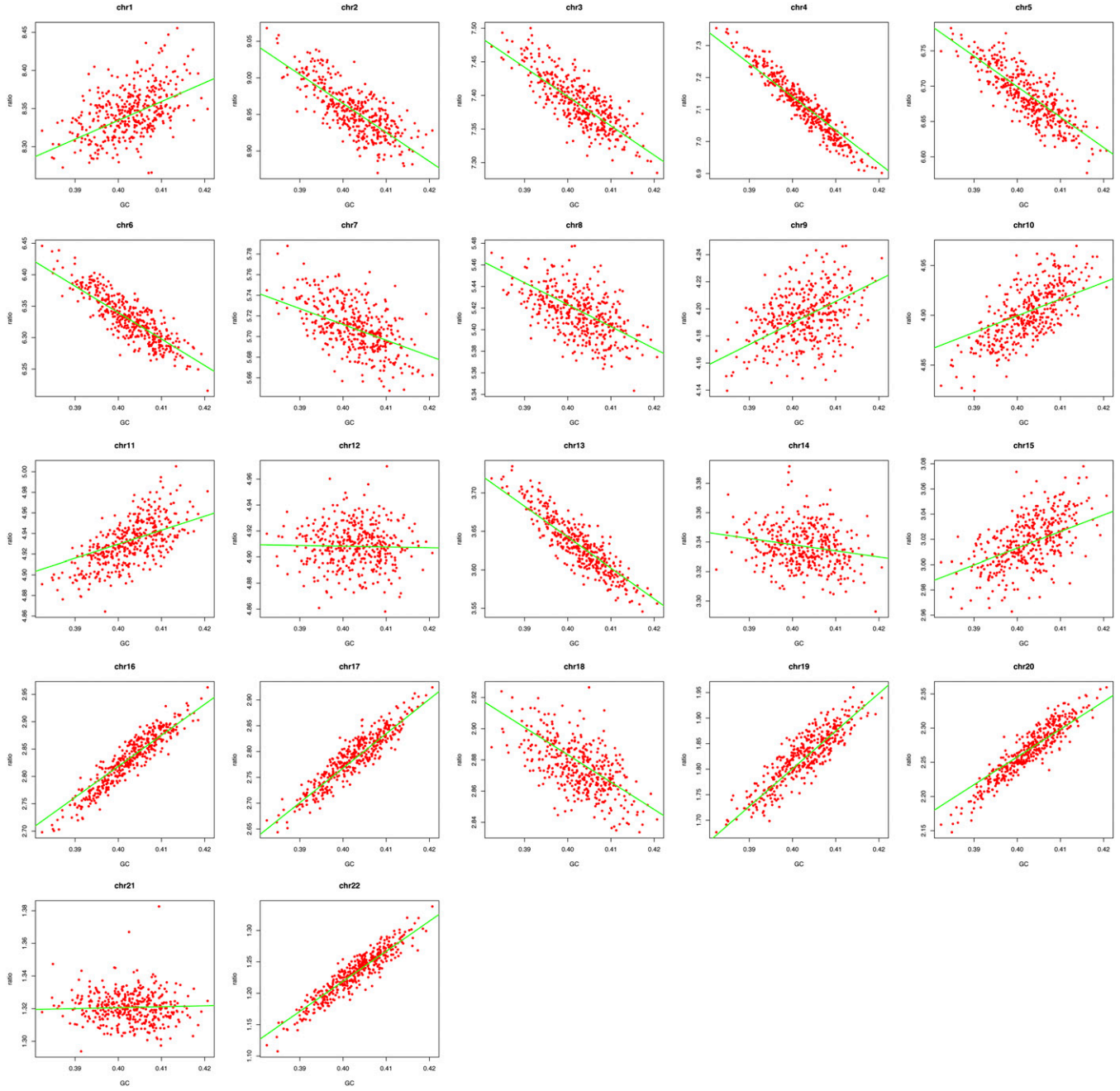

Fig. S4. The relationship of the unique reads ratio and sequencing GC content fitted to a linear model. Each subfigure represents one chromosome. The red dots were plotted as the unique reads ratio of each chromosome versus the sequencing GC content among the euploid controls (n = 426) confirmed by karyotyping.

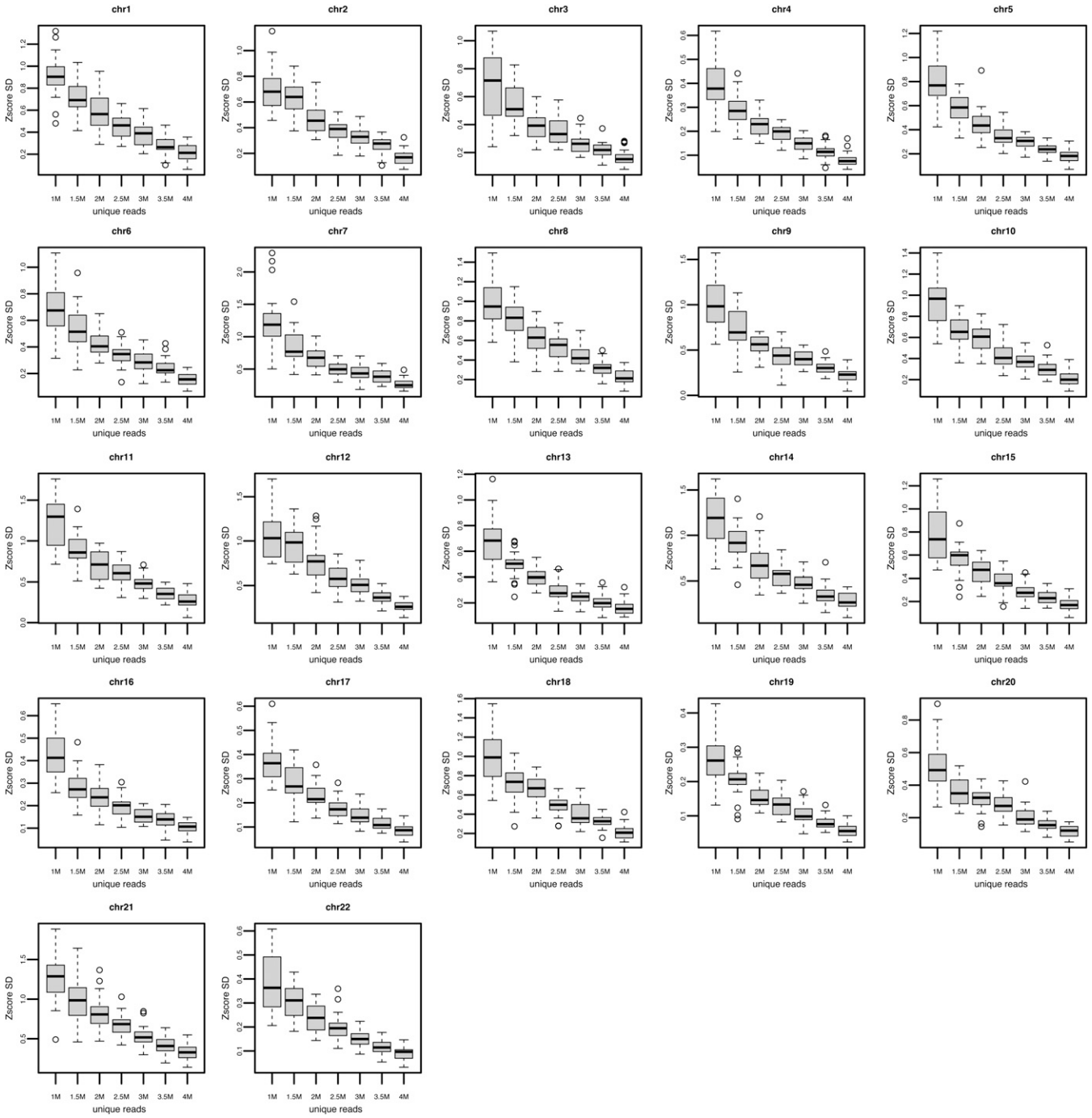

Fig. S5. The relationship between the number of usable reads and the SD of the relative *z* score for each chromosome.