1. Get genomic mapping and intensities for probes.

2. Sort probes according to genomic position. Calculate M & A for each probe.

3. For each probe, calculate SD of M using sliding windows along the genome. Select probes with SD smaller than a cut off.

4. Segment selected probes.

5. Cluster segmented data for the selected probes using k-means with k=3 to get populations of probes. Merge clusters too close.

6. Calculate lowess correction line for the largest population of probes.

7. Adjust M for all probes according to the population-based lowess correction line.

8. Return normalized intensities for all probes.