**Input:** aCGH dataset with n samples, p clones, and n labels for a two-class problem.

**Step 1** The DNA-probes that discriminate the two classes are identified by SAM analysis.

**Step 2** A window is slid over the genome. Enrichment of relevant probes within each window is determined using a hypergeometric test. Significant windows at different scales (window sizes) are selected.

**Step 3** The genome locations that are judged significant in at least s different scales are identified as relevant regions. (s=9).

**Output:** list of chromosomal regions of aberration.