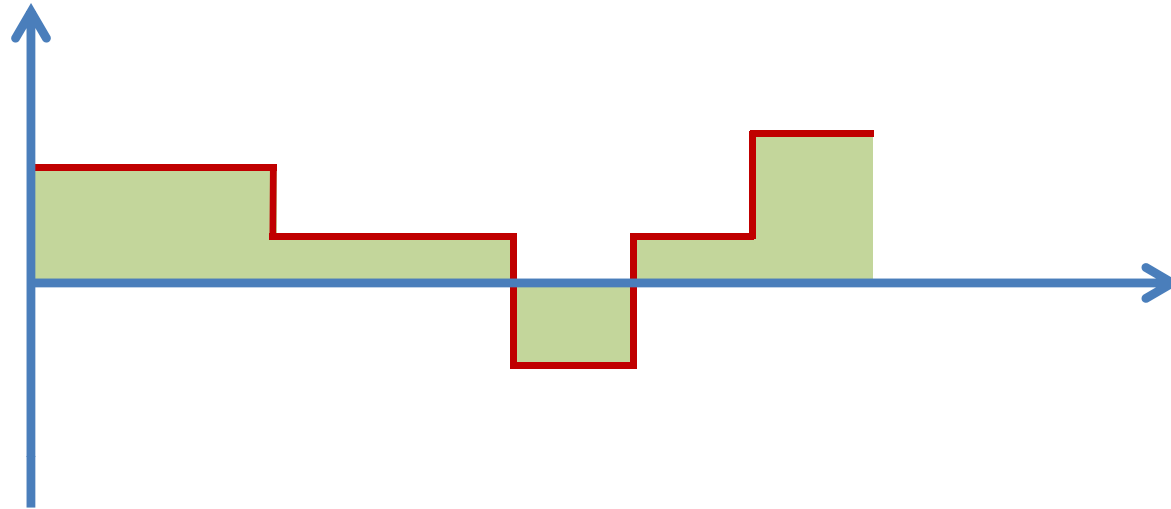# Figure S1. Model of the Total Aberration Index algorithm.

The Total Aberration Index (TAI) reveals the absolute area under the curve defined by the Piecewise Constant Fit (PCF) obtained copy number profile:

$$TAI = \frac{\sum_{i=1}^{R} d_i \cdot \left| \overline{y}_{S_i} \right|}{\sum_{i=1}^{R} d_i}$$

$\overline{y}_S$ = log2-transformed copy number value

$d_1, ..., d_R$ = genomic sizes of the segments

S_i = Indices of the probes belonging to the i'th segment