A. Fragment peak height and size data from genotyping software (i.e. PeakScanner or GeneScan)

B. Start bin definition
   All peaks are included in a single bin at the beginning of the analysis.

C. Split the bin
   1. Calculate size intervals between peaks.
   2. Cut the bin at the largest size interval.

D. Is width(sub bin) > Max. bin width?
   Yes → Go to the next bin
   No → E.

E. Is width(sub bin) > Min. bin width?
   No → G. Go to the next bin
   Yes → F. Sub bin includes several peaks that belong to the same sample.
       Yes → H. Produce the binary table
       No → G. Go to the next bin

F. Sub bin includes several peaks that belong to the same sample.

G. Go to the next bin
   Proceed recursively until each sub bin conforms to the constraints.

H. Produce the binary table
   Record presence / absence of a peak for each sample and bin.

I. Go to quality check
   e.g. Remove bins that are out of the scoring range.
   Remove non-reproducible bins.
   Remove singletons.