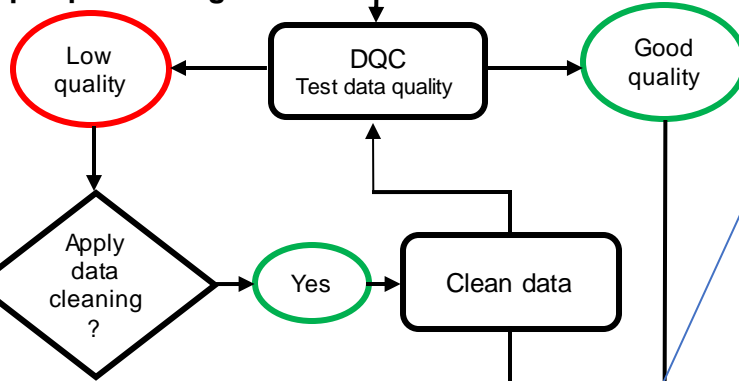


Inputs: genetic and physical maps
from internal or exported sources



Step 0 - Data pre-processing



Outputs: to visualize or download

Recombination
rate estimates

Chromatin
boundaries

Statistics



Interactive
plots



Chromosome
Ideograms



Step 1 - Marey Map-based recombination rate estimation

Correlate
genetic and
physical
distances along
a chromosome

Interpolation: fit
data points with
a third
polynomial
degree

Estimate local
recombination
rate represented
by the prime
derivative of the
polynomial

Step 2 - Chromatin boundaries detection

Measure how
good the
polynomial fits
the data points
using two
cumulative
R-squared curves

Using a sliding
window, apply a
statistical test on
each cumulative
R-squared to
detect
centromeric
boundaries

Detect telomeric
boundaries
identified by the
most significant
depletion on
both R-squared
curves

Step 3 - Extrapolation

Adjust recombination rate estimates on centromeric and telomeric regions according to the detected chromatin boundaries