Oak map database (3PxA4 Full-sib pedigree)
304 individuals x 953 markers

Selection of the Bin set
- Missing data <10%
- Map coverage maximization
- Double Crossing over minimization

Selection of individuals
- Missing data <50%
- Trees still alive

Selective mapping (Mappop)
66 ind. x 128 markers

Map location of SSRs to the closest framework marker

SSR motif search (Mreps) and polymorphism screening
283 EST-SSRs x 14 ind.

Comparison between map and Bin position

Bin position of SSRs
- Graphical genotyping

Genetic map
- Female genetic map: 59 intervals, 12 LG
- Male genetic map: 58 intervals, 12 LG

Bin map
- Female bin map: 44 Bins, 12 LG
- Male bin map: 37 Bins, 12 LG

Oak EST database

- 14 ind.

128 framework markers
839 accessory markers including 50 gSSR

65 EST-SSRs x 92 individuals
146 EST-SSRs x 46 individuals

Selection of evenly spaced EST-SSRs

26 ind. x 128 markers
26 ind.

A priori Bin validation

A posteriori Bin validation