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Populus Genome Portal

Isabelle Bourgait, Farid Ghazali, Vivianne Judith Koyao-Darinst, Véronique V. Jorge, Franck F. Samson, Sebastien S. Aubourg, Gilles G. Pilate, Philippe Label, Jean-Charles Leplé

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Populus Genome Portal

<http://bioinfo.orleans.inra.fr/Populus>

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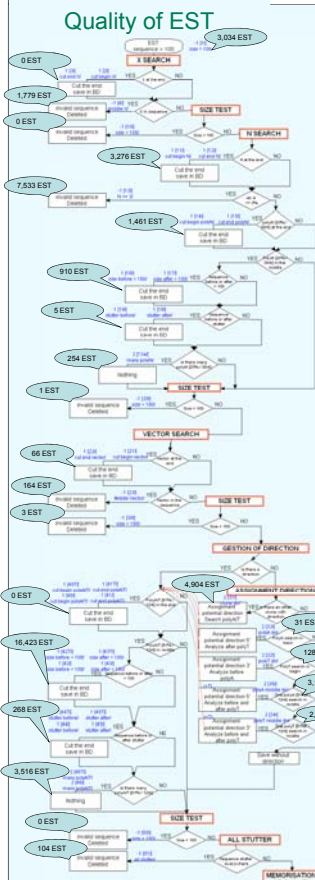
The Poplar Genome Portal project will provide a virtual meeting place for the research community interested in poplar genomics through web access to curated and interoperable gene expression data (EST, SAGE, microarrays), functional annotation, genetic maps, QTLs, SNP and phenotypic data.

¹Bourgait I, ¹Ghazali F, ¹Koyao V, ¹Jorge V, ²Samson F, ²Aubourg S, ¹Pilate G, ¹Label P, ¹Leplé JC

¹INRA, UR588 Unité Amélioration Génétique et Physiologie Forestières, Centre de recherche d'Orléans, 2163 Avenue de la Pomme de Pin, CS 40001 ARDON, 45075 Orléans Cedex 2, France.

²INRA, UMR1165 Unité de Recherche en Génétique Végétale, Centre de Versailles-Grignon, 2 rue Gaston Crémieux CP 5708, 91057 Evry, France.

Data management



In brief for 371,226 Populus public EST:

- 342,513 Good EST
- 10,380 EST with low quality Flag
- 20,589 EST with sequence filtered
 - 66 Vector sequence-end filtered
 - 5,409 N/polyN-sequence-end with or not remaining non-N/polyN < 100 bp or stutter filtered
 - 16,595 PolyA/T-sequence-end with remaining sequence < 100bp or stutter filtered
- 13,814 Bad EST removed
 - 3,038 Sequences <100 bp
 - 1,779 Sequences containing X
 - 7,533 Sequences with more than 3 N
 - 164 Vector sequences
 - 104 Stuttered sequences
- 10,556 EST direction is determined

Textual search

Graphical visualization

Links

- http://genome.jgi-psf.org/Poptr1_1/Poptr1_1.home.html
- <http://www.gramene.org/>
- <http://www.phytozome.net/>
- <http://www.evoltree.eu/>
- <http://www.noveltree.eu/>