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- (54) Title:** IMPROVING BIOMASS YIELD

[illegible]

- (57) Abstract:** A method for predicting harvestable biomass yield in a crop comprising: genotyping a sample obtained from said crop for one or more markers genetically linked to a portion of the genome, wherein said portion is within the interval corresponding to the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 18, Figure 1, Figure 2 or Figure 17 whereby the markers individually or collectively identify a haplotype associated with harvestable biomass yield in a plurality of crop plants and correlating the haplotype with the harvested biomass yield.

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Improving biomass yield

Field of the Invention

- 5 The present invention relates to methods for improving harvestable biomass yield in plants

Background to the Invention

- 10 The present invention relates generally to the field of molecular biology and concerns a method for increasing total harvestable biomass in field-grown plants in particular a *Salix* (willow) or *Populus* (poplar) plant. More specifically, the present invention concerns a method for increasing total harvestable biomass yield by transfer, through conventional genetics or transgenesis, of a specific genomic region which confers
15 enhanced harvestable yield in field-grown plants.

The total biomass produced above-ground by a plant can be harvested and used as feedstock for food, forage, bioenergy (including heat and power, transport biofuels and biogas), biomaterials and biorefineries.

- 20 Total biomass yield is calculated according to the plants parts that constitute relevant harvestable product, the most precise being the use of only one part (e.g. grain) and the most generic when the total above ground biomass is used.

- 25 In food crops the most important aspect is the yield in terms of harvestable edible portion which ranges from seed, grain and fruits to all types of vegetative parts for vegetable and salad crops (e.g. leaves, roots tubers, modified inflorescences etc). For forage there may be additional parts of the plant that animals can eat or the whole crop may be relevant.

- 30 The production of first generation liquid biofuels requires easily accessible sugars, starches or oils. As these are present in harvestable food portions, the relevant total yield can be calculated according to the relevant edible food portions.

In contrast, for many other end-uses, all the above ground parts may be harvested and utilised – e.g biomass for bioenergy, biomass for advanced generation biofuels and biomass for biorefineries. Whether the total plant is harvested with or without leaves and with or without flowers depends on the crop and precise end-use function.

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Selective breeding has been employed for centuries to improve, or attempt to improve, phenotypic traits of agronomic and economic interest in plants such as yield. Generally speaking, selective breeding involves the selection of individuals to serve as parents of the next generation on the basis of one or more phenotypic traits of interest. However, such phenotypic selection is frequently complicated by non-genetic factors that can impact the phenotype(s) of interest. Non- genetic factors that can have such effects include, but are not limited to environmental influences such as soil type and quality, rainfall, temperature range, and others.

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Variation in agronomic traits falls into two categories: qualitative and quantitative. The term "qualitative trait" is used when variation in the trait falls into discrete categories. Qualitative variation of this kind is normally under the control of one or two genes whose inheritance can be simply monitored in a cross. However, the majority of traits of interest to breeders, including total biomass yield, are quantitative in nature and are under the control of several genes each of which may have an important but small effect on the trait. The effects of each the genes, which may act independently or interact with each other in different ways, are influenced by the environment. Consequently, biomass yield is measured as a quantitative character and genomic regions that influence yield are referred to as quantitative trait loci (QTL).

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It can be very difficult to map the genetic loci that contribute to the expression of quantitative traits. For QTL analysis the progeny of a given cross may be analysed for the trait and each individual assigned a score depending on the phenotype observed. All the individuals in the mapping population are then screened using molecular markers. Association between markers and the trait scores are searched for using software packages. Because of the environmental influence, the mapping population needs to be as big as possible and large numbers of molecular markers need to be used. Moreover, the mapping population should be grown and assessed at

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more than one site to ensure that robust QTL have been identified. Because of the nature of QTL, for a given complex trait such as yield, several QTL may be identified in different locations on the genetic map in a single cross. Attention is focussed on the QTL which contribute most to the heritable variation that is observed in the population. If the same QTL come out strongest when the population is grown at another site, confidence of their importance is gained. By nature, QTL mapping is a long term process and very resource intensive.

Summary

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This disclosure concerns markers that define chromosomal haplotypes that identify a quantitative trait loci (QTL) associated with improved harvestable biomass yield. Methods for predicting harvestable biomass yield in willow, for example, by determining a contribution to harvestable biomass yield by the QTL, using the disclosed markers is disclosed. Kits for performing such methods also form part of the invention.

According to a first aspect of the present invention there is provided a method for predicting harvestable biomass yield in crop comprising: genotyping a sample obtained from said crop for one or more markers genetically linked to a portion of the genome within the interval corresponding to all or part the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 18, whereby the markers individually or collectively identify a haplotype associated with harvestable biomass yield in a plurality of crop plants and correlating the haplotype with the harvested biomass yield.

According to another aspect of the present invention there is provided a method for predicting harvestable biomass yield in crop comprising: genotyping a sample obtained from said crop for one or more markers genetically linked to a portion of the genome within the interval corresponding to all or part the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 1, whereby the markers individually or collectively identify a haplotype associated with harvestable biomass yield in a plurality of crop plants and correlating the haplotype with the harvested biomass yield.

According to another aspect of the present invention there is provided a method for predicting harvestable biomass yield in crop comprising: genotyping a sample obtained from said crop for one or more markers genetically linked to a portion of the genome within the interval corresponding to all or part the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 2, whereby the markers individually or collectively identify a haplotype associated with harvestable biomass yield in a plurality of crop plants and correlating the haplotype with the harvested biomass yield.

10

According to another aspect of the present invention there is provided a method for predicting harvestable biomass yield in crop comprising: genotyping a sample obtained from said crop for one or more markers genetically linked to a portion of the genome within the interval corresponding to all or part the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 17, whereby the markers individually or collectively identify a haplotype associated with harvestable biomass yield in a plurality of crop plants and correlating the haplotype with the harvested biomass yield.

15

According to another aspect of the present invention there is provided a method for predicting harvestable biomass yield in crop comprising: genotyping a sample obtained from said crop for one or more markers genetically linked to a portion of the genome within the interval corresponding to the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 18, whereby the markers individually or collectively identify a haplotype associated with harvestable biomass yield in a plurality of crop plants and correlating the haplotype with the harvested biomass yield.

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According to another aspect of the present invention there is provided a method for predicting harvestable biomass yield in crop comprising: genotyping a sample obtained from said crop for one or more markers genetically linked to a portion of the genome within the interval corresponding to the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 1, whereby the markers individually or collectively identify a haplotype associated with

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harvestable biomass yield in a plurality of crop plants and correlating the haplotype with the harvested biomass yield.

According to another aspect of the present invention there is provided a method for
5 predicting harvestable biomass yield in crop comprising: genotyping a sample
obtained from said crop for one or more markers genetically linked to a portion of the
genome within the interval corresponding to the sequence located between reference
nucleotide position A and reference nucleotide position B as shown in Figure 2,
whereby the markers individually or collectively identify a haplotype associated with
10 harvestable biomass yield in a plurality of crop plants and correlating the haplotype
with the harvested biomass yield.

According to another aspect of the present invention there is provided a method for
predicting harvestable biomass yield in crop comprising: genotyping a sample
15 obtained from said crop for one or more markers genetically linked to a portion of the
genome within the interval corresponding to the sequence located between reference
nucleotide position A and reference nucleotide position B as shown in Figure 17,
whereby the markers individually or collectively identify a haplotype associated with
harvestable biomass yield in a plurality of crop plants and correlating the haplotype
20 with the harvested biomass yield.

According to another aspect of the present invention there is provided a method for
determining the contribution of a Quantitative Trait Loci (QTL) associated with
harvestable biomass yield in a crop, the method comprising: genotyping a sample
25 obtained from a subject a crop plant for one or more markers, which markers
individually or collectively identify a haplotype within the interval corresponding to
all or part of the sequence located between reference nucleotide position A and
reference nucleotide position B as shown in Figure 18; wherein the haplotype is
correlated with a contribution to harvestable biomass yield by a gene comprised in the
30 QTL.

According to another aspect of the present invention there is provided a method for
determining the contribution of a Quantitative Trait Loci (QTL) associated with
harvestable biomass yield in a crop, the method comprising: genotyping a sample

obtained from a subject a crop plant for one or more markers, which markers individually or collectively identify a haplotype within the interval corresponding to all or part of the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 1; wherein the haplotype is
5 correlated with a contribution to harvestable biomass yield by a gene comprised in the QTL.

According to another aspect of the present invention there is provided a method for determining the contribution of a Quantitative Trait Loci (QTL) associated with
10 harvestable biomass yield in a crop, the method comprising: genotyping a sample obtained from a subject a crop plant for one or more markers, which markers individually or collectively identify a haplotype within the interval corresponding to all or part of the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 2; wherein the haplotype is
15 correlated with a contribution to harvestable biomass yield by a gene comprised in the QTL.

According to another aspect of the present invention there is provided a method for determining the contribution of a Quantitative Trait Loci (QTL) associated with
20 harvestable biomass yield in a crop, the method comprising: genotyping a sample obtained from a subject a crop plant for one or more markers, which markers individually or collectively identify a haplotype within the interval corresponding to all or part of the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 17; wherein the haplotype is
25 correlated with a contribution to harvestable biomass yield by a gene comprised in the QTL.

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nucleotide position B as shown in Figure 18; wherein the haplotype is correlated with a contribution to harvestable biomass yield by a gene comprised in the QTL.

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10 nucleotide position B as shown in Figure 1; wherein the haplotype is correlated with a contribution to harvestable biomass yield by a gene comprised in the QTL.

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20 contribution to harvestable biomass yield by a gene comprised in the QTL.

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determining the contribution of a Quantitative Trait Loci (QTL) associated with
25 harvestable biomass yield in a crop, the method comprising: genotyping a sample obtained from a subject a crop plant for one or more markers, which markers individually or collectively identify a haplotype within the interval corresponding to the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 17; wherein the haplotype is correlated with a contribution to harvestable biomass yield by a gene comprised in the QTL.

30 According to another method there is provided a method of identifying an allele that is associated with harvestable biomass yield in a crop comprising: obtaining a sample from a crop plant; amplifying DNA present in said sample comprising all or part of a region of the genome corresponding to the sequence located between reference

nucleotide position A and reference nucleotide position B as shown in Figure 18 and detecting the presence of a polymorphic marker in said region.

5 According to another method there is provided a method of identifying an allele that is associated with harvestable biomass yield in a crop comprising: obtaining a sample from a crop plant; amplifying DNA present in said sample comprising all or part of a region of the genome corresponding to the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 1 and detecting the presence of a polymorphic marker in said region.

10

According to another method there is provided a method of identifying an allele that is associated with harvestable biomass yield in a crop comprising: obtaining a sample from a crop plant; amplifying DNA present in said sample comprising all or part of a region of the genome corresponding to the sequence located between reference
15 nucleotide position A and reference nucleotide position B as shown in Figure 2 and detecting the presence of a polymorphic marker in said region.

According to another method there is provided a method of identifying an allele that is associated with harvestable biomass yield in a crop comprising: obtaining a sample
20 from a crop plant; amplifying DNA present in said sample comprising all or part of a region of the genome corresponding to the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 17 and detecting the presence of a polymorphic marker in said region.

25 According to another method there is provided a method of selecting a crop plant by marker assisted selection of a QTL associated with harvestable biomass yield said method comprising: determining the presence of an allele in the a crop plant where the allele is located in a region corresponding to all or part of the sequence located between reference nucleotide position A and reference nucleotide position B as shown
30 in Figure 18, and is genetically linked to a polymorphic marker and selecting said crop plant comprising the allele.

According to another method there is provided a method of selecting a crop plant by marker assisted selection of a QTL associated with harvestable biomass yield said

method comprising: determining the presence of an allele in the a crop plant where the allele is located in a region corresponding to all or part of the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 1, and is genetically linked to a polymorphic marker and selecting said crop
5 plant comprising the allele.

According to another method there is provided a method of selecting a crop plant by marker assisted selection of a QTL associated with harvestable biomass yield said method comprising: determining the presence of an allele in the a crop plant where
10 the allele is located in a region corresponding to all or part of the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 2, and is genetically linked to a polymorphic marker and selecting said crop plant comprising the allele.

15 According to another method there is provided a method of selecting a crop plant by marker assisted selection of a QTL associated with harvestable biomass yield said method comprising: determining the presence of an allele in the a crop plant where the allele is located in a region corresponding to all or part of the sequence located between reference nucleotide position A and reference nucleotide position B as shown
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According to another method there is provided a method of selecting a crop plant by marker assisted selection of a QTL associated with harvestable biomass yield said
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According to another method there is provided a method of selecting a crop plant by marker assisted selection of a QTL associated with harvestable biomass yield said method comprising: determining the presence of an allele in the a crop plant where the allele is located in a region corresponding to the sequence located between

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- 5 According to another method there is provided a method of selecting a crop plant by marker assisted selection of a QTL associated with harvestable biomass yield said method comprising: determining the presence of an allele in the a crop plant where the allele is located in a region corresponding to the sequence located between reference nucleotide position A and reference nucleotide position B as shown in
10 Figure 2, and is genetically linked to a polymorphic marker and selecting said crop plant comprising the allele.

- According to another method there is provided a method of selecting a crop plant by marker assisted selection of a QTL associated with harvestable biomass yield said
15 method comprising: determining the presence of an allele in the a crop plant where the allele is located in a region corresponding to the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 17, and is genetically linked to a polymorphic marker and selecting said crop plant comprising the allele.

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- According to another aspect of the present invention there is provided an isolated nucleic acid sequence comprising a marker or plurality of markers located within a genome of a crop plant associated with a QTL associated with harvestable biomass yield in a crop wherein the marker or plurality of markers comprise polymorphic
25 nucleotide sequences and said markers are genetically linked to a portion of the genome corresponding to all or part of the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 18, or are within said portion of the genome.

- 30 According to another aspect of the present invention there is provided an isolated nucleic acid sequence comprising a marker or plurality of markers located within a genome of a crop plant associated with a QTL associated with harvestable biomass yield in a crop wherein the marker or plurality of markers comprise polymorphic nucleotide sequences and said markers are genetically linked to a portion of the

genome corresponding to all or part of the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 1, or are within said portion of the genome.

- 5 According to another aspect of the present invention there is provided an isolated nucleic acid sequence comprising a marker or plurality of markers located within a genome of a crop plant associated with a QTL associated with harvestable biomass yield in a crop wherein the marker or plurality of markers comprise polymorphic nucleotide sequences and said markers are genetically linked to a portion of the
- 10 genome corresponding to all or part of the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 2, or are within said portion of the genome.

- According to another aspect of the present invention there is provided an isolated
- 15 nucleic acid sequence comprising a marker or plurality of markers located within a genome of a crop plant associated with a QTL associated with harvestable biomass yield in a crop wherein the marker or plurality of markers comprise polymorphic nucleotide sequences and said markers are genetically linked to a portion of the genome corresponding to all or part of the sequence located between reference
- 20 nucleotide position A and reference nucleotide position B as shown in Figure 17, or are within said portion of the genome.

- According to another aspect of the present invention there is provided an isolated nucleic acid sequence comprising a marker or plurality of markers located within a
- 25 genome of a crop plant associated with a QTL associated with harvestable biomass yield in a crop wherein the marker or plurality of markers comprise polymorphic nucleotide sequences and said markers are genetically linked to a portion of the genome corresponding the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 18, or are within said portion
- 30 of the genome.

According to another aspect of the present invention there is provided an isolated nucleic acid sequence comprising a marker or plurality of markers located within a genome of a crop plant associated with a QTL associated with harvestable biomass

yield in a crop wherein the marker or plurality of markers comprise polymorphic nucleotide sequences and said markers are genetically linked to a portion of the genome corresponding the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 1, or are within said portion of the genome.

According to another aspect of the present invention there is provided an isolated nucleic acid sequence comprising a marker or plurality of markers located within a genome of a crop plant associated with a QTL associated with harvestable biomass yield in a crop wherein the marker or plurality of markers comprise polymorphic nucleotide sequences and said markers are genetically linked to a portion of the genome corresponding the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 2, or are within said portion of the genome.

According to another aspect of the present invention there is provided an isolated nucleic acid sequence comprising a marker or plurality of markers located within a genome of a crop plant associated with a QTL associated with harvestable biomass yield in a crop wherein the marker or plurality of markers comprise polymorphic nucleotide sequences and said markers are genetically linked to a portion of the genome corresponding the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 17, or are within said portion of the genome.

According to another aspect of the present invention there is provided a crop plant comprising a genetic element derived from another crop plant, which genetic element comprises a biomass yield QTL, wherein said QTL is obtained from a portion of the genome corresponding to all or part of the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 18.

According to another aspect of the present invention there is provided a crop plant comprising a genetic element derived from another crop plant, which genetic element comprises a biomass yield QTL, wherein said QTL is obtained from a portion of the

genome corresponding to all or part of the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 1.

5 According to another aspect of the present invention there is provided a crop plant comprising a genetic element derived from another crop plant, which genetic element comprises a biomass yield QTL, wherein said QTL is obtained from a portion of the genome corresponding to all or part of the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 2.

10 According to another aspect of the present invention there is provided a crop plant comprising a genetic element derived from another crop plant, which genetic element comprises a biomass yield QTL, wherein said QTL is obtained from a portion of the genome corresponding to all or part of the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 17.

15 Preferably, the genomic element comprises one or more of Xyld1, Xyld2, Xyld3, Xyld4, Xyld5, Xyld6, Xyld7, Xyld8, Xyld9 and Xyld10.

20 According to another aspect of the present invention there is provided a crop plant comprising a genetic element derived from another crop plant, which genetic element comprises a biomass yield QTL, wherein said QTL is obtained from a portion of the genome corresponding to the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 18.

25 According to another aspect of the present invention there is provided a crop plant comprising a genetic element derived from another crop plant, which genetic element comprises a biomass yield QTL, wherein said QTL is obtained from a portion of the genome corresponding to the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 1.

30 According to another aspect of the present invention there is provided a crop plant comprising a genetic element derived from another crop plant, which genetic element comprises a biomass yield QTL, wherein said QTL is obtained from a portion of the

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5 According to another aspect of the present invention there is provided a crop plant comprising a genetic element derived from another crop plant, which genetic element comprises a biomass yield QTL, wherein said QTL is obtained from a portion of the genome corresponding to the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 17.

10 According to another method there is provided a crop plant comprising a genetic element derived from another a crop plant, which genetic element comprises a harvestable biomass yield QTL linked to at least one marker located between reference nucleotide position A and reference nucleotide position B as shown in Figure 18.

15 According to another method there is provided a crop plant comprising a genetic element derived from another a crop plant, which genetic element comprises a harvestable biomass yield QTL linked to at least one marker located between reference nucleotide position A and reference nucleotide position B as shown in Figure 1.

20 According to another method there is provided a crop plant comprising a genetic element derived from another a crop plant, which genetic element comprises a harvestable biomass yield QTL linked to at least one marker located between reference nucleotide position A and reference nucleotide position B as shown in Figure 2.

25 According to another method there is provided a crop plant comprising a genetic element derived from another a crop plant, which genetic element comprises a harvestable biomass yield QTL linked to at least one marker located between reference nucleotide position A and reference nucleotide position B as shown in Figure 17.

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Preferably, the markers are within an interval of 45, 40, 35, 30, 25, 20, 15, 10, 5, 4, 3, 2, 1 or 0 centimorgans (cM) from reference nucleotide position A or reference nucleotide position B as shown in Figure 18, Figure 1, Figure 2, or Figure 17.

- 5 Preferably the one or more markers are within the interval corresponding to the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 18, Figure 1, Figure 2, or Figure 17.

Plants that are particularly useful in the methods of the invention include in particular
 10 monocotyledonous and dicotyledonous fodder crops, forage crops, ornamental crops, fruit crops, food crops, algae, forestry trees, bioenergy crops and biofuel crops including the following species and species hybrids: *Acacia* spp., *Acer* spp., *Actinidia* spp., *Agave* spp., *Agropyron* spp., *Agrostis* spp., *Allium* spp., *Alnus* spp., *Alopecurus* spp., *Amaranthus* spp., *Ananas* spp., *Apium* spp., *Arachis* spp., *Areca* spp., *Arundo*
 15 spp., *Arrhenatherum* spp., *Asparagus* spp., *Avena* spp., *Atriplex* spp., *Attalea* spp., *Beta* spp., *Betula* spp., *Brassica* spp., *Bromus* spp., *Bouteloua* spp., *Camelina* spp., *Camellia* spp., *Cannabis* spp., *Capsicum* spp., *Carica* spp., *Carex* spp., *Carthamus* spp., *Castanea* spp., *Carum* spp., *Cinnamomum* spp., *Citrus* spp., *Cocos* spp., *Coffea* spp., *Corchorus* spp., *Cotoneaster* spp., *Cucurbita* spp., *Cupressus* spp., *Cynodon*
 20 spp., *Daucus* spp., *Dactylis* spp., *Eucalyptus* spp., *Elaeis* spp., *Eleusine* spp., *Fagus* spp., *Festuca* spp., *Ficus* spp., *Fraxinus* spp., *Geranium* spp., *Ginkgo* spp., *Glycine* spp., *Gossypium* spp., *Helianthus* spp., *Hemerocallis* spp., *Heracleum* spp., *Hedysarum* spp., *Hibiscus* spp., *Hordeum* spp., *Indigo* spp., *Ipomoea* spp., *Lettuca* spp., *Jatropha* spp., *Lotus* spp., *Lactuca* spp., *Lathyrus* spp., *Lens* spp., *Linum* spp.,
 25 *Lolium* spp., *Lupinus* spp., *Lezula* spp., *Lycopersicon* spp., *Malus* spp., *Manihot* spp., *Medicago* spp., *Melilotus* spp., *Mentha* spp., *Miscanthus* spp., *Musa* spp., *Nicotiana* spp., *Olea* spp., *Onobrychis* spp., *Ophiopogon* spp., *Oryza* spp., *Panicum* spp., *Papaver* spp., *Petunia* spp., *Phaseolus* spp., *Pennisetum* spp., *Phalaris* spp., *Phoenix* spp., *Phleum* spp., *Phyllostachys* spp., *Physalis* spp., *Panicum* spp., *Picea* spp., *Pinus*
 30 spp., *Pistacia* spp., *Pisum* spp., *Poa* spp., *Podocarpus* spp., *Pogmania* spp., *Populus* spp., *Prunus* spp., *Quercus* spp., *Ribes* spp., *Robinia* spp., *Rosa* spp., *Raphanus* spp., *Rheum* spp., *Ricinus* spp., *Rubus* spp., *Salix* spp., *Sequoia* spp., *Sesamum* spp., *Setaria* spp., *Saccharum* spp., *Sambucus* spp., *Secale* spp., *Sinapis* spp., *Solanum* spp., *Sorghum* spp., *Trifolium* spp., *Triticum* spp., *Triticosecale* spp., *Trisetum* spp.,

Tagetes spp., *Theobroma* spp., *Triadica* spp., *Vicia* spp., *Vitis* spp., *Vigna* spp., *Viola* spp., *Watsonia* spp., *Zea* spp. amongst others.

Preferably the crop plant is a *Salix* (willow) or *Populus* (poplar) plant.

5

In respect of *Populus*, the portion of the genome referred to above and the markers are located on linkage group (chromosome) 10 of *Populus*. The corresponding chromosome (linkage) group for *Salix* can easily be identified by alignment of the *Populus* and *Salix* genomes. Hanley et al., (Hanley, S., Mallott, M.D. & Karp A. (2006) *Tree Genetics and Genomes*, 3, 35-48) describes the map and the alignment of the willow and poplar genomes.

It should be noted that the nucleotide sequence referred to by the expression “a portion of the genome within the interval *corresponding* to the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 18, Figure 1, Figure 2 or Figure 17” is not to be interpreted as meaning the sequence must include the specific sequence as set out in the figure but must be interpreted as including variants that are found in other plants e.g. *Salix* or *Populus* plants (variants may have, for example, at least 50, 60, 70, 80, 90, 95, 98 or 99 % identity to the specific sequence in Figure 18, Figure 1, Figure 2 or Figure 17). A skilled person will readily appreciate that this region of the chromosome will differ slightly between different strains. Reference to these figures is used merely to enable identification of the locus within any plant, in particular a *Salix* or *Populus* plant. Such sequences can readily be routinely identified.

25

The foregoing and other objects and features of the disclosures will become more apparent from the following detailed description, which proceeds with reference to the accompanying figures.

Figure 1: shows the sequence of a QTL region in *Populus* associated with improved yield. Reference nucleotide position A corresponds to the first nucleotide of this sequence and reference nucleotide position B corresponds to the final nucleotide of this sequence.

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Figure 2 shows the sequence of a QTL region in *Salix* associated with improved yield. The sequence is derived from allele A. Reference nucleotide position A corresponds to the first nucleotide of this sequence and reference nucleotide position B corresponds to the final nucleotide of this sequence.

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Figure 3A: shows the nucleotide sequence of the Xyld1 polynucleotide of *Populus* (SEQ ID NO 4). SEQ ID NO 4 is located within the QTL region shown in Figure 1.

Figure 3B: shows the nucleotide sequence of the Xyld1 allele A polynucleotide of *Salix* (SEQ ID NO 5).

10 Figure 3C: shows the amino acid sequence of the Xyld1 allele A polypeptide of *Salix* (SEQ ID NO 27).

Figure 4A: shows the nucleotide sequence of the Xyld2 polynucleotide of *Populus* (SEQ ID NO 6). SEQ ID NO 6 is located within the QTL region shown in Figure 1.

15 Figure 4B: shows the nucleotide sequence of the Xyld2 allele A polynucleotide of *Salix* (SEQ ID NO 7).

Figure 4C: shows the amino acid sequence of the Xyld2 allele A polypeptide of *Salix* (SEQ ID NO 28).

20 Figure 5A: shows the nucleotide sequence of the Xyld3 polynucleotide of *Populus* (SEQ ID NO 8). SEQ ID NO 8 is located within the QTL region shown in Figure 1.

Figure 5B: shows the nucleotide sequence of the Xyld3 allele A polynucleotide of *Salix* (SEQ ID NO 9).

Figure 5C: shows the amino acid sequence of the Xyld3 allele A polypeptide of *Salix*
25 (SEQ ID NO 29).

Figure 6A: shows the nucleotide sequence of the Xyld4 polynucleotide of *Populus* (SEQ ID NO 10). SEQ ID NO 10 is located within the QTL region shown in Figure 1.

Figure 6B: shows the nucleotide sequence of the Xyld4 allele A polynucleotide of
30 *Salix* (SEQ ID NO 11).

Figure 6C: shows the nucleotide sequence of the Xyld4 allele C polynucleotide of *Salix* (SEQ ID NO 12).

Figure 6D: shows the amino acid sequence of the Xyld4 allele A polypeptide of *Salix* (SEQ ID NO 30).

Figure 6E: shows the amino acid sequence of the Xyld4 allele C polypeptide of *Salix* (SEQ ID NO 31).

Figure 7: shows the nucleotide sequence of the Xyld5 polynucleotide of *Populus*
5 (SEQ ID NO 13). SEQ ID NO 13 is located within the QTL region shown in Figure 1.

Figure 8A: shows the nucleotide sequence of the Xyld6 polynucleotide of *Populus* (SEQ ID NO 14). SEQ ID NO 14 is located within the QTL region shown in Figure 1.

Figure 8B: shows the nucleotide sequence of the Xyld6 allele A polynucleotide of
10 *Salix* (SEQ ID NO 15).

Figure 8C: shows the nucleotide sequence of the Xyld6 allele C polynucleotide of *Salix* (SEQ ID NO 16).

Figure 8D: shows the amino acid sequence of the Xyld6 allele A polypeptide of *Salix* (SEQ ID NO 32).

15 Figure 8E: shows the amino acid sequence of the Xyld6 allele C polypeptide of *Salix* (SEQ ID NO 33).

Figure 9A: shows the nucleotide sequence of the Xyld7 polynucleotide of *Populus* (SEQ ID NO 3). SEQ ID NO 3 is located within the QTL region shown in Figure 1.

20 Figure 9B: shows the nucleotide sequence of the Xyld7 allele A polynucleotide of *Salix* (SEQ ID NO 2).

Figure 9C: shows the nucleotide sequence of the Xyld7 allele C polynucleotide of *Salix* (SEQ ID NO 1).

Figure 9D: shows the nucleotide sequence of the Xyld7 allele A polynucleotide of
25 *Salix* (SEQ ID NO 2) aligned with the Xyld7 allele C polynucleotide of *Salix* (SEQ ID NO 1) to indicate Gene Xyld7 allele A insertion region.

Figure 9E: shows the amino acid sequence of the Xyld7 allele C polypeptide in *Salix* (SEQ ID NO 26).

30 Figure 10A: shows the nucleotide sequence of the Xyld8 polynucleotide of *Populus* (SEQ ID NO 17). SEQ ID NO 17 is located within the QTL region shown in Figure 1.

Figure 10B: shows the nucleotide sequence of the Xyld8 allele A polynucleotide of *Salix* (SEQ ID NO 18).

Figure 10C: shows the nucleotide sequence of the Xyld8 allele C polynucleotide of *Salix* (SEQ ID NO 19).

Figure 10D: shows the amino acid sequence of the Xyld8 allele A polypeptide of *Salix* (SEQ ID NO 34).

- 5 Figure 10E: shows the amino acid sequence of the Xyld8 allele C polypeptide of *Salix* (SEQ ID NO 35).

Figure 11A: shows the nucleotide sequence of the Xyld9 polynucleotide of *Populus* (SEQ ID NO 20). SEQ ID NO 20 is located within the QTL region shown in Figure 1.

- 10 Figure 11B: shows the nucleotide sequence of the Xyld9 allele A polynucleotide of *Salix* (SEQ ID NO 21).

Figure 11C: shows the nucleotide sequence of the Xyld9 allele C polynucleotide of *Salix* (SEQ ID NO 22).

- 15 Figure 11D: shows the amino acid sequence of the Xyld9 allele A polypeptide of *Salix* (SEQ ID NO 36).

Figure 11E: shows the amino acid sequence of the Xyld9 allele C polypeptide of *Salix* (SEQ ID NO 37).

- 20 Figure 12A: shows the nucleotide sequence of the Xyld10 polynucleotide of *Populus* (SEQ ID NO 23). SEQ ID NO 23 is located within the QTL region shown in Figure 1.

Figure 12B: shows the nucleotide sequence of the Xyld10 allele A polynucleotide of *Salix* (SEQ ID NO 24).

Figure 12C: shows the nucleotide sequence of the Xyld10 allele C polynucleotide of *Salix* (SEQ ID NO 25).

- 25 Figure 12D: shows the amino acid sequence of the Xyld10 allele A polypeptide of *Salix* (SEQ ID NO 38).

Figure 12E: shows the amino acid sequence of the Xyld10 allele C polypeptide of *Salix* (SEQ ID NO 39).

- 30 Figure 13: shows QTL analysis of yield related traits in the K8 mapping population for a 5.1 cM region of chromosome X as delimited by markers X_15341094 and X_15945623. QTL confidence intervals are indicated by thick bars (1 LOD below peak) and lines (2 LOD below peak). The percentage of the variance explained by the QTL is shown *in parentheses*.

Figure 14 shows representation of the public annotation of the poplar genomic sequence represented by the QTL region. Ten genes are predicted (not to scale).

- 5 Figure 15 shows the QTL region of Figure 1 wherein markers derived from the sequence that we used in QTL identification are indicated by bold type. Gene sequences are labelled and underlined.

- 10 Figure 16 shows the QTL region of Figure 2 wherein markers derived from the sequence that we used in QTL identification are indicated by bold type. Gene sequences are labelled and underlined.

- Figure 17 shows the QTL region of Figure 2 wherein the sequence of Xyld7 allele A has been replaced with Xyld7 allele C. Reference nucleotide position A corresponds to the first nucleotide of this sequence and reference nucleotide position B corresponds to the final nucleotide of this sequence.
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- Figure 18 shows the sequence of a QTL region in *Populus* associated with improved yield wherein the poplar sequence is derived from the public sequence annotation of the poplar genome (www.phytozome.net). Reference nucleotide position A corresponds to the first nucleotide of this sequence and reference nucleotide position B corresponds to the final nucleotide of this sequence.
- 20

25 Detailed description

- This disclosure concerns markers that define chromosomal haplotypes that identify a quantitative trait locus (QTL) associated with improved harvestable biomass yield. The corresponding QTL region in *Populus* is shown in Figure 1 and Figure 18. The corresponding QTL region in *Salix* is shown in Figure 2. The *Populus* QTL comprises ten genes, Xyld1, Xyld2, Xyld3, Xyld4, Xyld5, Xyld6, Xyld7, Xyld8, Xyld9 and Xyld10.
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The Xyld1 polynucleotide is shown in SEQ ID NO 4 and SEQ ID NO 5. SEQ ID NO 4 (as shown in Figure 3A) shows a sequence of the gene in *Populus* and SEQ ID NO 5 (as shown in Figure 3B) shows a sequence of the gene (allele A) in *Salix*. SEQ ID NO 27 (as shown in Figure 3C) shows the *Salix* Xyld1 allele A polypeptide sequence.

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The Xyld2 polynucleotide is shown in SEQ ID NO 6 and SEQ ID NO 7. SEQ ID NO 6 (as shown in Figure 4A) shows a sequence of the gene in *Populus* and SEQ ID NO 7 (as shown in Figure 4B) shows a sequence of the gene (allele A) in *Salix*. SEQ ID NO 28 (as shown in Figure 4C) shows the *Salix* Xyld2 allele A in *Salix* polypeptide sequence.

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The Xyld3 polynucleotide is shown in SEQ ID NO 8 and SEQ ID NO 9 and homologues thereof. SEQ ID NO 8 (as shown in Figure 5A) shows a sequence of the gene in *Populus* and SEQ ID NO 9 (as shown in Figure 5B) shows a sequence of the gene (allele A) in *Salix*. SEQ ID NO 29 (as shown in Figure 5C) shows the *Salix* Xyld3 allele A polypeptide sequence.

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The Xyld4 polynucleotide is shown in SEQ ID NO 10, SEQ ID NO 11 and SEQ ID NO 12. SEQ ID NO 10 (as shown in Figure 6A) shows a sequence of the gene in *Populus*. SEQ ID NO 11 (as shown in Figure 6B) shows a sequence of the gene (allele A) in *Salix*. SEQ ID NO 12 (as shown in Figure 6C) shows a sequence of the gene (allele C) in *Salix*. SEQ ID NO 30 (as shown in Figure 6D) shows the *Salix* Xyld4 allele A polypeptide sequence. SEQ ID NO 31 (as shown in Figure 6E) shows the *Salix* Xyld4 allele C polypeptide sequence.

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The Xyld5 polynucleotide is shown in SEQ ID NO 13. SEQ ID NO 13 (as shown in Figure 7) shows a sequence of the gene in *Populus*.

The Xyld6 polynucleotide is shown in SEQ ID NO 14, SEQ ID NO 15 and SEQ ID NO 16. SEQ ID NO 14 (as shown in Figure 8A) shows a sequence of the gene in *Populus*. SEQ ID NO 15 (as shown in Figure 8B) shows a sequence of the gene (allele A) in *Salix*. SEQ ID NO 16 (as shown in Figure 8C) shows a sequence of the gene (allele C) in *Salix*. SEQ ID NO 32 (as shown in Figure 8D) shows the *Salix* Xyld6

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allele A polypeptide sequence. SEQ ID NO 33 (as shown in Figure 8E) shows the *Salix* Xyld6 allele C polypeptide sequence.

The Xyld7 polynucleotide is shown in SEQ ID NO 3, SEQ ID NO 2 and SEQ ID NO 1. SEQ ID NO 3 (as shown in Figure 9A) shows a sequence of the gene in *Populus*. SEQ ID NO 2 (as shown in Figure 9B) shows a sequence of the gene (allele A) in *Salix*. SEQ ID NO 1 (as shown in Figure 9C) shows a sequence of the gene (allele C) in *Salix*. An alignment of Xyld7 allele A (SEQ ID NO 2) sequence with the Xyld7 allele C sequence (SEQ ID NO 1) (as shown in the alignment of Figure 9D) indicates Xyld7 allele A has an insertion region with extra nucleotides that are not present in Xyld7 allele C sequence SEQ ID NO 1. SEQ ID NO 26 (as shown in Figure 9E) shows the *Salix* Xyld7 allele C polypeptide sequence.

The Xyld8 polynucleotide is shown in SEQ ID NO 17, SEQ ID NO 18 and SEQ ID NO 19. SEQ ID NO 17 (as shown in Figure 10A) shows a sequence of the gene in *Populus*. SEQ ID NO 18 (as shown in Figure 10B) shows a sequence of the gene (allele A) in *Salix*. SEQ ID NO 19 (as shown in Figure 10C) shows a sequence of the gene (allele C) in *Salix*. SEQ ID NO 34 (as shown in Figure 10D) shows the *Salix* Xyld8 allele A polypeptide sequence. SEQ ID NO 35 (as shown in Figure 10E) shows the *Salix* Xyld8 allele C polypeptide sequence.

The Xyld9 polynucleotide is shown in SEQ ID NO 20, SEQ ID NO 21 and SEQ ID NO 22. SEQ ID NO 20 (as shown in Figure 11A) shows a sequence of the gene in *Populus*. SEQ ID NO 21 (as shown in Figure 11B) shows a sequence of the gene (allele A) in *Salix*. SEQ ID NO 22 (as shown in Figure 11C) shows a sequence of the gene (allele C) in *Salix*. SEQ ID NO 36 (as shown in Figure 11D) shows the *Salix* Xyld9 allele A polypeptide sequence. SEQ ID NO 37 (as shown in Figure 11E) shows the *Salix* Xyld9 allele C polypeptide sequence.

The Xyld10 polynucleotide is shown in SEQ ID NO 23, SEQ ID NO 24 and SEQ ID NO 25. SEQ ID NO 23 (as shown in Figure 12A) shows a sequence of the gene in *Populus*. SEQ ID NO 24 (as shown in Figure 12B) shows a sequence of the gene (allele A) in *Salix*. SEQ ID NO 25 (as shown in Figure 12C) shows a sequence of the gene (allele C) in *Salix*. SEQ ID NO 38 (as shown in Figure 12D) shows the *Salix*

Xyld10 allele A polypeptide sequence. SEQ ID NO 39 (as shown in Figure 12E) shows the *Salix* Xyld10 allele C polypeptide sequence.

5 Xyld1 shows best homology in *Arabidopsis thaliana* with Locus AT3G12740, or *ALIS1* (ALA-Interacting Subunit). *ALIS1* is a member of a family of phospholipid transporters (*ALIS1* -*ALIS5*) which are homologs of the Cdc50p/Lem3p family in yeast that are essential for the trafficking of yeast P4-ATPases. The *Arabidopsis* *ALIS* proteins are 27-30% identical to yeast Cdc50p and similarity ranges from 48-53%. In
10 yeast *ALIS1* shows strong affinity to *ALA3*. In *Arabidopsis*, *ALA3* has been shown to be important for *trans*-Golgi proliferation of slime vesicles containing polysaccharides and enzymes for secretion. In yeast, *ALA3* function requires interaction with the *ALIS1*. In *Arabidopsis* plants, *ALIS1*, like *ALA3*, is localised to membranes of Golgi-like structures and is expressed in root peripheral columella
15 cells. It has been proposed that the *ALIS1* protein is a β - sub-unit of *ALA3* in *Arabidopsis* and that this protein is important part of the Golgi machinery in plants required for secretory processes during development.

Xyld2 shows strongest homology to *Arabidopsis thaliana* gene *ALDH5F1* (Locus
20 AT1G79440 ; previous nomenclature *SSADH*; EC 1.2.1.24) which is a member of the aldehyde dehydrogenases (*ALDHs*) protein superfamily of NAD(P)C-dependent enzymes that oxidize a wide range of endogenous and exogenous aliphatic and aromatic aldehydes. The *Arabidopsis* genome contains 14 unique *ALDH* sequences encoding members of nine *ALDH* families, including eight known families and one
25 novel family (*ALDH22*) that is currently known only in plants. Of these, there is one succinic semialdehyde dehydrogenase gene, *ALDH5F1*, which encodes a protein of 528 amino acids. *ALDH5F1* is the only confirmed identified member of the succinic semialdehyde family in plants. The *Arabidopsis* protein is localized to mitochondria and a kinetic analysis showed that the recombinant enzyme was specific for succinic
30 semialdehyde and regulated by adenine nucleotides. T-DNA knockout mutants of *ALDH5F1* result in dwarfed plants with necrotic lesions and are sensitive to both ultraviolet-B light and heat stress. Plants with *ssadh* mutations accumulate elevated levels of H₂O₂, suggesting a role for this gene in stress regulation detoxification

pathway plant, providing defense against environmental stress by preventing the accumulation of reactive oxygen species.

Xyld3 shows strongest homology with *Arabidopsis thaliana* *ALTERED PHLOEM DEVELOPMENT (APL)* gene (Locus AT1G79430), which encodes a MYB coiled-coil-type transcription factor that is required for phloem identity in *Arabidopsis*. *APL* has been proposed to have a dual role both in promoting phloem differentiation and in repressing xylem differentiation during vascular development.

10 Xyld4 shows strongest homology in *Arabidopsis thaliana* to Locus AT1G79420.

Xyld5 shows strongest homology with AtOCT2 in *Arabidopsis thaliana* (Locus AT1G79360). AtOCT2 is one of six *Arabidopsis* organic cation/carnitine transporter (OCT) -like proteins, named AtOCT1–AtOCT6 (loci At1g73220, At1g79360, At1g16390, At3g20660, At1g79410 and At1g16370, respectively) that have been identified. These proteins cluster in a small subfamily within the ‘organic solute cotransporters’ included in the large sugar transporter family of the major facilitator superfamily (MFS). AtOCT1 shares features of organic cation/carnitine transporters (OCTs). In animals, mammalian plasma membrane OCTs are involved in homeostasis and distribution of various small endogenous amines (e.g. carnitine, choline) and detoxification of xenobiotics such as nicotine. AtOCT1 is able to transport carnitine in yeast and is likely to be involved in the transport of carnitine or related molecules across the plasma membrane in plants.

Xyld6 shows best fit with AtOCT3 *Arabidopsis* ORGANIC CATION/CARNITINE TRANSPORTER2). AtOCT3 is one of six *Arabidopsis* organic cation/carnitine transporter (OCT) -like proteins, named AtOCT1–AtOCT6 (loci At1g73220, At1g79360, At1g16390, At3g20660, At1g79410 and At1g16370, respectively) referred to above. These proteins cluster in a small subfamily within the ‘organic solute cotransporters’ included in the large sugar transporter family of the major facilitator superfamily (MFS).

Xyld7 shows homology with members of the R2R3-type *MYB* gene family in *Arabidopsis*. Although no functional data are available for most of the 125 R2R3-type *AtMYB* genes, a number of functions have been assigned concerning many aspects of

plant secondary metabolism, as well as the identity and fate of plant cells. This includes regulation of phenylpropanoid metabolism, control of development and determination of cell fate and identity, plant responses to environmental factors and mediating hormone actions.

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Xyld8 shows best fit with ANAC028, Arabidopsis NAC domain containing protein (Locus AT1G65910). NAC (NAM, ATAF, and CUC) is a plant-specific gene family. NAC family transcription factors are involved in maintaining organ or tissue boundaries regulating the transition from growth by cell division to growth by cell expansion. Most NAC proteins contain a highly conserved N-terminal DNA-binding domain, a nuclear localization signal sequence, and a variable C-terminal domain. 75 and 105 NAC genes were predicted in the *Oryza sativa* and *Arabidopsis* genomes, respectively. The functions of only some of these have been described. The first reported NAC genes were *NAM* from petunia and *CUC2* from Arabidopsis that participate in shoot apical meristem development. *CUC1*, *CUC2* and *nam* are expressed at the boundaries between cotyledonary primordial and between floral organs and are specifically involved in shoot apical meristem formation and separation of cotyledons and floral organs. Other development-related NAC genes have been suggested with roles in controlling cell expansion of specific flower organs e.g. *NAP* or auxindependent formation of the lateral root system e.g. *NAC1*. Some of NAC genes, such as *ATAF1* and *ATAF2* genes from *Arabidopsis* and the *StNAC* gene from potato, are induced by pathogen attack and wounding. More recently, a few NAC genes, such as *AtNAC072* (*RD26*), *AtNAC019*, *AtNAC055* from *Arabidopsis*, and *BnNAC* from *Brassica* (31), were found to be involved in responses to environmental stress. Seven members of NAC family At2g18060, At4g36160, At5g66300, At1g12260, At1g62700, At5g62380, and At1g71930 have been designated as *VASCULAR-RELATED NAC-DOMAIN PROTEIN 1* (*VND1* to *VND7*). Members of these could induce transdifferentiation of various cells into metaxylem- and protoxylem-like vessel elements, respectively, in Arabidopsis and poplar. Similarly ANAC012 and ANAC073 also appear to have a role in xylem development and secondary wall thickening in Arabidopsis.

Xyld9 show strongest homology in *Arabidopsis thaliana* to Locus AT1G79390.

Xyld10 shows homology to the RGLG2 (RING DOMAIN LIGASE2) locus of *Arabidopsis thaliana* (Locus AT1G79380). In functional terms, the RING domain can basically be considered a protein-interaction domain. RING-finger proteins have been implicated in a range of diverse biological processes and biochemical activities, from transcriptional and translational regulation to targeted protein degradation.

The information provided by the QTL described here could be used in several ways.

1. Direct application in genetic improvement.

10

The QTL region defined here facilitates direct use for selection of high yielding plants in breeding programmes. As a high degree of synteny and colinearity can exist between genomes, molecular markers linked to the QTL region could be used immediately in marker-assisted selection. Several laboratories have collections of polymorphic markers for general use in mapping studies or for assessing genetic diversity. Now that the QTL position has been identified here and the sequence provided, if markers linked to the QTL region described here are available in these laboratories they could be directly employed in selection programmes for improving yield.

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The efficiency of the use of QTL-associated marker in marker-assisted selection strategies will be dependent on the degree of genetic linkage that exists between the marker to be used and the causal polymorphism that underlies the QTL. To maximise the efficiency of marker-assisted selections based on a QTL, such as that described here, markers that are tightly linked to the region would be required to minimise the likelihood that linkage between the marker and the causal polymorphism will breakdown through recombination. The information described here provides a route to efficient achievement of the identification of markers whose linkage to the causal polymorphism will not be broken easily by recombination. Although anonymous markers such as Amplified Fragment Length Polymorphism (AFLP) and Random Amplified Polymorphism (RAPD) classes for example, could be screened in large numbers to identify those that may fall into regions of the genome linked to the QTL by chance, more efficient methods based on the sequence information provided here can be used in more direct approaches.

Using knowledge of the underlying sequence information that is publicly available in *Populus* (http://genome.jgi-psf.org/Poptr1_1/Poptr1_1.home.html) or that which is provided here for willow, specific markers can be developed that are targeted directly at this region or to a region that is closely linked in genetic terms. Markers of this class could include, as examples, microsatellite markers, Restriction Length Fragment Length Polymorphisms (RFLP), Cleaved Amplified Polymorphisms (CAPS), Single Nucleotide Polymorphisms (SNPS) and INSerion/DELetion (INDELs). For microsatellite markers, primer pairs that amplify potentially highly polymorphic simple sequence repeat units could be designed from *Salix* or *Populus* sequence in this region. These could be specific to either genus or could be directly transferable from one genus to the other, if nucleotide sequence is sufficiently conserved at the priming sites. This is often true if priming sites are selected within coding regions (Hanley, S.J., Mallott, M.D. & Karp A. (2006) *Tree Genetics and Genomes*, 3, 35-48). Microsatellite primer sets would then be tested for their ability to detect polymorphisms in the germplasm under study, and those that distinguish between alleles could be used in marker-assisted selections. Similarly, for the development of other markers types (SNP, CAPS, INDEL) sequence information for the QTL region could be used to design primer sets to generate amplicons that could then be examined for polymorphisms in the germplasm under study, either from sequencing or restriction digestion analysis.

2. Application in other plant genera using knowledge of the genes within the QTL

The information provided on the genes contained within the QTL region provides a route to exploitation in crops, other cultivated plants or model plants, not directly related to *Populus* or *Salix* where, it is expected that synteny and colinearity has broken down and genomes have become re-organised. In such cases, homologous genes to those identified as present within the QTL interval defined here, can often be identified through *in silico* sequence similarity searches for crops/cultivated or model plants for which such sequence resources exist. Where such resources are lacking, standard molecular biology methods can be employed to clone homologous genes. As examples, degenerate primers can be designed to amino acid sequences and used in PCR

to amplify and clone target genes, or alternatively, sequences can be used in hybridisation approaches if sufficient similarity is expected.

Once homologous genes are identified by any such approach, and the crop/plant specific sequence is determined, polymorphisms within a given gene can identified through sequencing or restriction analysis, as examples.

3. Application in transgenic genetic improvement strategies.

The sequences supplied provide a route to crop improvement through genetic manipulation via transgenic approaches. The sequences provided could be used directly to generate constructs for testing in transformation experiments. Such experiments may involve overexpression, gene-silencing or introduction of a beneficial allele into any recipient genotype. Such experiments may utilise the *Salix* or *Populus* sequences provided here or be based on homologous genes derived from any plant of interest.

Provided below is an example of the use of a diagnostic molecular marker derived from the QTL region that can be used to select for favourable alleles within a breeding programme:

A microsatellite marker was developed to screen for the three QTL alleles segregating in members of the K8 population. The microsatellite marker is amplified by PCR using the following pair of primers:

Forward primer 5'- CAAAAACGCACCCTATTCTTCC – 3'

Reverse primer 5'- CCAGAGTCCCCTTGAACACAC – 3'

The sequence of the amplified region for allele A (179bp) is:

CAAAAACGCACCCTATTCTTCCCTATTTGCATCGCATTGTTCTTGAATCTC
 TTTGTATTCCCTGAGTCTCAGAGAGAGAGAGAGAGAGAGAGAAGGAA
 AGAGAGAATGTTCCATACCAAGAAACCCTCAACTATGAATTCCCATGATA
 GACCCATGTGTGTTCAAGGGGACTCTGG

These primers generate amplicons of three different lengths in the K8 mapping population and thus are informative for the three alleles that are segregating in the yield QTL region. The female parent of the cross, cultivar 'S3' produces two alleles of different length (A & B). The male parent, cultivar 'R13' contains two alleles (A & C) where A is a common allele that is present in S3.

The diploid K8 mapping population can therefore inherit the following combinations of alleles : AA, AB, AC, BC. Table 1 shows the mean trait values for each of these classes in the population for total fresh weight harvested, maximum stem diameter and maximum stem height. Analysis is based trait data collected at Long Ashton Research Station in 2003. The non-parametric rank-sum test of Kruskal-Wallis (KW) (Lehmann, 1975) was used to determine associations between marker genotypes and trait scores.

Table 1. Mean trait values associated with inheritance of particular QTL alleles (A, B and C) in the K8 mapping population as determined by the application of a microsatellite marker.

Trait	N ^o	microsatellite genotype				KW	df	Significance
		AA	AB	AC	BC			
Total fresh biomass harvested per stool (kg)	902	1.30	1.90	1.75	2.17	132.76	3	*****
Maximum stem diameter per stool (cm)	849	16.30	20.12	19.22	21.37	186.37	3	*****
Maximum stem height per stool (m)	902	3.16	3.79	3.69	3.96	223.95	3	*****

N^o: Number of plants included in analysis

KW: Kruskal-Wallis test statistic

df: degrees of freedom

Significance: ***** = 0.0001

In this example, plants of genotype AA often give the lowest yield and plants of genotype BC often give rise to the highest yields. Where the goal of a breeding programme is to increase harvestable biomass yield, plants of genotype BC would be preferentially selected using the marker. Similarly, potential parents of genotype AA might be excluded from a crossing programme as this allele can be associated with lower yields.

This disclosure relates to representative markers, and alleles thereof, that correspond to and identify a locus that is associated with harvestable yield.

5 The methods, markers, and alleles of the present invention provide a simple, inexpensive and reliable means of identifying the haplotype associated with the harvestable biomass yield locus. By identifying the chromosome haplotype in this region, it is possible to predict whether the harvestable biomass yield associated QTL contributes to small or large yield of plant.

10

Thus, one aspect of this disclosure concerns markers (and alleles thereof) genetically linked to or localized to a portion of the genome associated with a harvestable biomass yield associated QTL that provides a contribution to harvestable biomass. Typically, the marker (or markers) includes polymorphic nucleotide sequences
15 genetically linked or situated in the interval between a region of linkage group 10 corresponding to the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 18, Figure 1, Figure 2 or Figure 17.

20 Kits including probes that detect the markers described herein are also a feature of this disclosure.

Another aspect of this disclosure concerns a method for predicting harvestable biomass yield in a crop. The method can include genotyping a sample obtained from a
25 subject crop for one or more markers genetically linked to the interval corresponding to the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 18, Figure 1, Figure 2 or Figure 17. e.g., that spans the harvestable biomass yield locus. The markers are chosen to individually or collectively identify a haplotype associated with harvestable biomass yield. The
30 haplotype is correlated with harvestable biomass yield providing a prediction of the harvestable biomass yield of the subject plant. Typically, the selected markers localize to the interval between a region of the genome corresponding to the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 18, Figure 1, Figure 2 or Figure 17.

In certain embodiments, the haplotype is correlated with harvestable biomass yield by comparing the haplotype to an index of average harvestable biomass yield by plant variety.

5

Optionally, *Salix* or *Populus* identified by the disclosed methods as having a desired harvestable biomass yield can be crossed to produce progeny *Salix* or *Populus* with a desired harvestable biomass yield.

10 Definitions

The poplar and willow chromosomes are referred to as 'linkage groups'. This is because there are more sequence contigs than chromosomes in the poplar assembly.

15 An "allele" is understood within the scope of the invention to refer to a given form of a gene, or of any kind of identifiable genetic element such as a marker, that occupies a specific position or locus on a chromosome. Variant forms of genes occurring at the same locus are said to be alleles of one another. In a diploid cell or organism, the two alleles of a given gene (or marker) typically occupy corresponding loci on a pair of
20 homologous chromosomes.

An allele associated with a quantitative trait may comprise a single gene or multiple genes or even a gene encoding a genetic factor contributing to the phenotype represented by said QTL.

25

The term "breeding", and grammatical variants thereof, refer to any process that generates a progeny individual. Breedings can be sexual or asexual, or any combination thereof. Exemplary non-limiting types of breedings include crossings, selfings, doubled haploid derivative generation, and combinations thereof.

30

By "exogenous gene/polynucleotide" it is meant that the gene/polynucleotide is transformed into the unmodified plant from an external source. The exogenous nucleotide may, for example, be derived from a genomic DNA or cDNA sequence. Typically the exogenous gene is derived from a different source and has a sequence

different to the endogenous gene. Alternatively, introduction of an exogenous gene having a sequence identical to the endogenous gene may be used to increase the number of copies of the endogenous gene sequence present in the plant.

- 5 The term "Homozygous" refers to like alleles at one or more corresponding loci on homologous chromosomes.

The term "Heterozygous refers to unlike alleles at one or more corresponding loci on homologous chromosomes.

10

The term "Gene" refers to a unit of DNA which performs one function. Usually, this is equated with the production of one RNA or one protein. A gene may contain coding regions, introns, untranslated regions and control regions.

- 15 As used herein, the phrase "genetic marker" refers to a feature of an individual's genome (e.g., a nucleotide or a polynucleotide sequence that is present in an individual's genome) that is associated with one or more loci of interest. Typically, a genetic marker is polymorphic and the variant forms (or llet. Genetic markers include, for example, single nucleotide polymorphisms (SNPs), indels (i.e.,
20 insertions/deletions), simple sequence repeats (SSRs), restriction fragment length polymorphisms (RFLPs), random amplified polymorphic DNAs (RAPDs), cleaved amplified polymorphic sequence (CAPS) markers, Diversity Arrays Technology (DArT) markers, and amplified fragment length polymorphisms (AFLPs), Microsatellites or Simple sequence repeat (SSRs) among many other examples.
25 Genetic markers can, for example, be used to locate genetic loci containing alleles that contribute to variability in expression of phenotypic traits on a chromosome.

- A genetic marker can be physically located in a position on a chromosome that is within or outside of to the genetic locus with which it is associated (i.e., is intragenic
30 or extragenic, respectively). Stated another way, whereas genetic markers are typically employed when the location on a chromosome of the gene that corresponds to the locus of interest has not been identified and there is a non-zero rate of recombination between the genetic marker and the locus of interest, the presently disclosed subject matter can also employ genetic markers that are physically within

the boundaries of a genetic locus (e.g., inside a genomic sequence that corresponds to a gene such as, but not limited to a polymorphism within an intron or an exon of a gene). In some embodiments of the presently disclosed subject matter, the one or more genetic markers comprise between one and ten markers, and in some
5 embodiments the one or more genetic markers comprise more than ten genetic markers.

The term "genotype" refers to the set of alleles present in a subject at one or more loci under investigation. At any one autosomal locus a genotype will be either
10 homozygous (with two identical alleles) or heterozygous (with two different alleles).

The term "haplotype" refers to the set of alleles an individual inherited from one parent. A diploid individual thus has two haplotypes. The term "haplotype" can be used in a more limited sense to refer to physically linked and/or unlinked genetic
15 markers (e.g., sequence polymorphisms) associated with a phenotypic trait. The phrase "haplotype block" (sometimes also referred to in the literature simply as a haplotype) refers to a group of two or more genetic markers that are physically linked on a single chromosome (or a portion thereof). Typically, each block has a few common haplotypes, and a subset of the genetic markers (i.e., a "haplotype tag") can
20 be chosen that uniquely identifies each of these haplotypes.

As used herein, the terms "hybrid", "hybrid plant," and "hybrid progeny" refers to an individual produced from genetically different parents (e.g., a genetically heterozygous or mostly heterozygous individual).

25 If two individuals possess the same allele at a particular locus, the alleles are termed "identical by descent" if the alleles were inherited from one common ancestor (i.e., the alleles are copies of the same parental allele). The alternative is that the alleles are "identical by state" (i.e., the alleles appear the same but are derived from two different
30 copies of the allele). Identity by descent information is useful for linkage studies; both identity by descent and identity by state information can be used in association studies such as those described herein, although identity by descent information can be particularly useful.

The term "linkage"/ "genetic linkage", and grammatical variants thereof, refers to the association of two or more (and/or traits) at positions on the same chromosome, preferably such that recombination between the two loci is reduced to a proportion significantly less than 50%. The term linkage can also be used in reference to the association between one or more loci and a trait if an allele (or alleles) and the trait, or absence thereof, are observed together in significantly greater than 50% of occurrences. A linkage group is a set of loci, in which all members are linked either directly or indirectly to all other members of the set.

- 10 "linkage disequilibrium" (also called "allelic association") refers to a phenomenon wherein particular alleles at two or more loci tend to remain together in linkage groups when segregating from parents to offspring with a greater frequency than expected from their individual frequencies in a given population. For example, a genetic marker allele and a QTL allele can show linkage disequilibrium when they
- 15 occur together with frequencies greater than those predicted from the individual allele frequencies. Linkage disequilibrium can occur for several reasons including, but not limited to the alleles being in close proximity on a chromosome
- 20 "Locus" refers to a region on a chromosome, which comprises a gene or a genetic marker or the like.

As used herein, the phrase "nucleic acid" refers to any physical string of monomer units that can be corresponded to a string of nucleotides, including a polymer of nucleotides (e.g., a typical DNA, cDNA or RNA polymer), modified oligonucleotides (e.g., oligonucleotides comprising bases that are not typical to biological RNA or DNA, such as 2'-O-methylated oligonucleotides), and the like. In some embodiments, a nucleic acid can be single-stranded, double-stranded, multi-stranded, or combinations thereof. Unless otherwise indicated, a particular nucleic acid sequence

25 of the presently disclosed subject matter optionally comprises or encodes complementary sequences, in addition to any sequence explicitly indicated.

30

The term "protein" includes single-chain polypeptide molecules as well as multiple-polypeptide complexes where individual constituent polypeptides are linked by covalent or non-covalent means.

- 5 The phrase "phenotypic trait" refers to the appearance or other detectable characteristic of an individual, resulting from the interaction of its genome with the environment.

- 10 "The term Microsatellite or SSRs (Simple sequence repeats) (Marker)" refers to a type of genetic marker that consists of numerous repeats of short sequences of DNA bases, which are found at loci throughout the plant's DNA and have a likelihood of being highly polymorphic.

- 15 "Polymorphism" refers to the presence in a population of two or more different forms of a gene, genetic marker, or inherited trait.

- 20 The term "quantitative trait locus" (QTL) refers to an association between a genetic marker and a chromosomal region and/or gene that affects the phenotype of a trait of interest. Typically, this is determined statistically; e.g., based on one or more methods published in the literature. A QTL can be a chromosomal region and/or a genetic locus with at least two alleles that differentially affect the expression of a phenotypic trait (either a quantitative trait or a qualitative trait).

- 25 "Sequence Homology or Sequence identity" is used herein interchangeably. The terms "identical" or percent "identity" in the context of two or more nucleic acid or protein sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same, when compared and aligned for maximum correspondence, as measured using one of the following sequence comparison algorithms or by visual inspection. If two sequences
30 which are to be compared with each other differ in length, sequence identity preferably relates to the percentage of the nucleotide residues of the shorter sequence which are identical with the nucleotide residues of the longer sequence. Sequence identity can be determined conventionally with the use of computer programs such as the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix,

Genetics Computer Group, University Research Park, 575 Science Drive Madison, WI 53711). Bestfit utilizes the local homology algorithm of Smith and Waterman, Advances in Applied Mathematics 2 (1981), 482-489, in order to find the segment having the highest sequence identity between two sequences. When using Bestfit or
5 another sequence alignment program to determine whether a particular sequence has for instance 95% identity with a reference sequence of the present invention, the parameters are preferably so adjusted that the percentage of identity is calculated over the entire length of the reference sequence and that homology gaps of up to 5% of the total number of the nucleotides in the reference sequence are permitted. When using
10 Bestfit, the so-called optional parameters are preferably left at their preset ("default") values. The deviations appearing in the comparison between a given sequence and the above-described sequences of the invention may be caused for instance by addition, deletion, substitution, insertion or recombination. Such a sequence comparison can preferably also be carried out with the program "fasta20u66" (version 2.0u66,
15 September 1998 by William R. Pearson and the University of Virginia; see also W.R. Pearson (1990), Methods in Enzymology 183, 63-98, appended examples and <http://workbench.sdsc.edu/>). For this purpose, the "default" parameter settings may be used.

20 Preferably, reference to a sequence which has a percent identity to any one of SEQ ID NOs: 1-43 as detailed herein refers to a sequence which has the stated percent identity over the entire length of the SEQ ID NO referred to.

Another indication that two nucleic acid sequences are substantially identical is that
25 the two molecules hybridize to each other under stringent conditions.

In general, unless otherwise specified, when referring to a "plant" it is intended to cover a plant at any stage of development, including sing cells and seeds. Thus, in particular embodiments , the present invention provides a plant cell.

30

A "plant cell" is a structural and physiological unit of a plant, comprising a protoplast and a cell wall. The plant cell may be in form of an isolated single cell or a cultured cell, or as a part of higher organized unit such as, for example, plant tissue, a plant organ, or a whole plant.

"Plant cell culture" means cultures of plant units such as, for example, protoplasts, cell culture cells, cells in plant tissues, pollen, pollen tubes, ovules, embryo sacs, zygotes and embryos at various stages of development.

5

"Plant material" refers to leaves, stems, roots, flowers or flower parts, fruits, pollen, egg cells, zygotes, seeds, cuttings, cell or tissue cultures, or any other part or product of a plant.

- 10 A "plant organ" is a distinct and visibly structured and differentiated part of a plant such as a root, stem, leaf, flower bud, or embryo.

- "Plant tissue" as used herein means a group of plant cells organized into a structural and functional unit. Any tissue of a plant in planta or in culture is included. This term
15 includes, but is not limited to, whole plants, plant organs, plant seeds, tissue culture and any groups of plant cells organized into structural and/or functional units. The use of this term in conjunction with, or in the absence of, any specific type of plant tissue as listed above or otherwise embraced by this definition is not intended to be exclusive of any other type of plant tissue.

20

- "Harvestable biomass yield" is calculated according to the plants parts that constitute relevant harvestable product. In one embodiment, a harvestable biomass yield corresponds to the total of the above ground biomass being the harvestable product. Preferred examples, where the harvestable product of the crop may be the above
25 ground biomass are trees such as, for example (but not limited to), *Salix* or *Populus*. In another embodiment, a harvestable biomass yield corresponds to only one part of the plant being the harvestable product. Preferred examples, where the harvestable product of the crop may be a part of the plant are parts of food crops such as, for example (but not limited to), the kernel in maize or the grain in rice.

30

The genomic DNA can be assayed to determine which markers are present using any method known in the art. For example, single-strand conformation polymorphism (SSCP) analysis, base excision sequence scanning (BESS), restriction fragment length polymorphism (RFLP) analysis, heteroduplex analysis, denaturing gradient gel

electrophoresis (DGGE), temperature gradient electrophoresis, allelic polymerase chain reaction (PCR), ligase chain reaction direct sequencing, mini sequencing, nucleic acid hybridization, or micro-array-type detection can be used to identify the polymorphisms present in the sample.

5

The methods described herein include genotyping a sample of genetic material obtained from a subject plant for one or more markers to determine the allele present at the marker locus.

10 Detection of alleles

The nucleic acids obtained from the sample can be genotyped to identify the particular allele present for a marker locus. A sample of sufficient quantity to permit direct detection of marker alleles from the sample can be obtained from the plant.

15

Alternatively, a smaller sample is obtained from the subject and the nucleic acids are amplified prior to detection. Optionally, the nucleic acid sample is purified (or partially purified) prior to detection of the marker alleles. Any target nucleic that is informative for a chromosome haplotype in the interval corresponding to the sequence located between reference nucleotide position A and reference nucleotide position B can be detected. The target nucleic acid may correspond to a marker locus localized in this interval. Any method of detecting a nucleic acid molecule can be used, such as hybridization and/or sequencing assays.

20

25 Hybridization

Hybridization is the binding of complementary strands of DNA, DNA/RNA, or RNA. Hybridization can occur when primers or probes bind to target sequences such as target sequences within genomic DNA. Physical methods of detecting hybridization or binding of complementary strands of nucleic acid molecules, include but are not limited to, such methods as DNase I or chemical footprinting, gel shift and affinity cleavage assays, Southern and Northern blotting, dot blotting and light absorption detection procedures. The binding between a nucleic acid primer or probe and its target nucleic acid is frequently characterized by the temperature (T_m) at which 50%

30

of the nucleic acid probe is melted from its target. A higher (T_m) means a stronger or more stable complex relative to a complex with a lower (T_m).

5 More generally, complementary nucleic acids form a stable duplex or triplex when the strands bind, (hybridize), to each other by forming Watson-Crick, Hoogsteen or reverse Hoogsteen base pairs. Stable binding occurs when an oligonucleotide molecule remains detectably bound to a target nucleic acid sequence under the required conditions.

10 Complementarity is the degree to which bases in one nucleic acid strand base pair with the bases in a second nucleic acid strand. Complementarity is conveniently described by percentage, that is, the proportion of nucleotides that form base pairs between two strands or within a specific region or domain of two strands.

15 For example, if 10 nucleotides of a 15-nucleotide oligonucleotide form base pairs with a targeted region of a DNA molecule, that oligonucleotide is said to have 66.67% complementarity to the region of DNA targeted.

‘Sufficient complementarity’ means that a sufficient number of base pairs exist
20 between an oligonucleotide molecule and a target nucleic acid sequence to achieve detectable binding. When expressed or measured by percentage of base pairs formed, the percentage complementarity that fulfills this goal can range from as little as about 50% complementarity to full (100%) complementary. In general, sufficient complementarity is at least about 50%, for example at least about 75%
25 complementarity, at least about 90% complementarity, at least about 95% complementarity, at least about 98% complementarity, or even at least about 100% complementarity.

A thorough treatment of the qualitative and quantitative considerations involved in
30 establishing binding conditions that allow one skilled in the art to design appropriate oligonucleotides for use under the desired conditions is provided by Beltz et al. *Methods Enzymol* 100:266-285, 1983, and by Sambrook et al. (ed.), *27 Molecular Cloning: A Laboratory Manual*, 2nd ed., vol. 1-3, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

Hybridization conditions resulting in particular degrees of stringency will vary depending upon the nature of the hybridization method and the composition and length of the hybridizing nucleic acid sequences. Generally, the temperature of hybridization and the ionic strength (such as the Na^+ concentration) of the hybridization buffer will determine the stringency of hybridization. Calculations regarding hybridization conditions for attaining particular degrees of stringency are discussed in Sambrook et al., (1989) Molecular Cloning: a laboratory manual, second edition, Cold Spring Harbor Laboratory, Plainview, NY (chapters 9 and I 1).

10

The following is an exemplary set of hybridization conditions and is not limiting.

Very High Stringency (detects sequences that share at least 90% complementarity)

Hybridization: 5x SSC at 65°C for 16 hours

15 Wash twice: 2x SSC at room temperature (RT) for 15 minutes each

Wash twice: 0.5x SSC at 65°C for 20 minutes each

High Stringency (detects sequences that share at least 80% complementarity)

Hybridization: 5x-6x SSC at 65°C-70°C for 16-20 hours

Wash twice: 2x SSC at RT for 5-20 minutes each

20 Wash twice: 1x SSC at 55°C-70°C for 30 minutes each

Low Stringency (detects sequences that share at least 50% complementarity)

Hybridization: 6x SSC at RT to 55°C for 16-20 hours

Wash at least twice: 2x-3x SSC at RT to 55°C for 20-30 minutes each.

25 Methods for labeling nucleic acid molecules so they can be detected are well known. Examples of such labels include non-radiolabels and radiolabels. Non- radiolabels include, but are not limited to an enzyme, chemiluminescent compound, fluorescent compound (such as FITC, Cy3, and Cy5), metal complex, hapten, enzyme, colorimetric agent, a dye, or combinations thereof. Radiolabels include, but are not limited to, ^{125}I and ^{35}S . For example, radioactive and fluorescent labeling methods, as well as other methods known in the art, are suitable for use with the present disclosure. In one example, primers used to amplify the subject's nucleic acids are labeled (such as with biotin, a radiolabel, or a fluorophore). In another example, amplified target nucleic acid samples are end-labeled to form labeled 28 amplified

material. For example, amplified nucleic acid molecules can be labeled by including labeled nucleotides in the amplification reactions.

5 Nucleic acid molecules associated corresponding to one or more marker loci can also be detected by hybridization procedures using a labeled nucleic acid probe, such as a probe that detects only one alternative allele at a marker locus. Most commonly, the target nucleic acid (or amplified target nucleic acid) is separated based on size or charge and transferred to a solid support. The solid support (such as membrane made of nylon or nitrocellulose) is contacted with a labeled nucleic acid probe, which
10 hybridizes to it complementary target under suitable hybridization conditions to form a hybridization complex.

Hybridization conditions for a given combination of array and target material can be optimized routinely in an empirical manner close to the T_m of the expected duplexes,
15 thereby maximizing the discriminating power of the method. For example, the hybridization conditions can be selected to permit discrimination between matched and mismatched oligonucleotides. Hybridization conditions can be chosen to correspond to those known to be suitable in standard procedures for hybridization to filters (and optionally for hybridization to arrays). In particular, temperature is
20 controlled to substantially eliminate formation of duplexes between sequences other than an exactly complementary allele of the selected marker. A variety of known hybridization solvents can be employed, the choice being dependent on considerations known to one of skill in the art (see U.S. Patent 5,981,185).

25 Once the target nucleic acid molecules have been hybridized with the labeled probes, the presence of the hybridization complex can be analyzed, for example by detecting the complexes.

Methods for detecting hybridized nucleic acid complexes are well known in the art. In
30 one example, detection includes detecting one or more labels present on the oligonucleotides, the target (e.g., amplified) sequences, or both. Detection can include treating the hybridized complex with a buffer and/or a conjugating solution to effect conjugation or coupling of the hybridized complex with the detection label, and treating the conjugated, hybridized complex with a detection reagent. In one example,

the conjugating solution includes streptavidin alkaline phosphatase, avidin alkaline phosphatase, or horseradish peroxidase. Specific, non-limiting examples of conjugating solutions include streptavidin alkaline phosphatase, avidin alkaline phosphatase, or horseradish peroxidase. The conjugated, hybridized complex can be treated with a detection reagent. In one example, the detection reagent includes enzyme-labeled fluorescence reagents or calorimetric reagents. In one specific non-limiting example, the detection reagent is enzyme-labeled fluorescence reagent (ELF) from Molecular Probes, Inc. (Eugene, OR). The hybridized complex can then be placed on a detection device, such as an ultraviolet (UV) transilluminator (manufactured by UVP, Inc. of Upland, CA). The signal is developed and the increased signal intensity can be recorded with a recording device, such as a charge coupled device (CCD) camera (manufactured by Photometrics, Inc. of Tucson, AZ).

In particular examples, these steps are not performed when radiolabels are used.

In particular examples, the method further includes quantification, for instance by determining the amount of hybridization.

Allele Specific PCR

Allele-specific PCR differentiates between target regions differing in the presence of absence of a variation or polymorphism. PCR amplification primers are chosen based upon their complementarity to the target sequence, within the genomic DNA. The primers bind only to certain alleles of the target sequence. This method is described by Gibbs, Nucleic Acid Res. 17:12427 2448, 1989.

Allele Specific Oligonucleotide Screening Methods

Further screening methods employ the allele-specific oligonucleotide (ASO) screening methods (e.g. see Saiki et al., Nature 324:163-166, 1986).

Oligonucleotides with one or more base pair mismatches are generated for any particular allele. ASO screening methods detect mismatches between one allele in the target genomic or PCR amplified DNA and the other allele, showing decreased

binding of the oligonucleotide relative to the second allele (i.e. the other allele) oligonucleotide. Oligonucleotide probes can be designed that under low stringency will bind to both polymorphic forms of the allele, but which at high stringency, bind to the allele to which they correspond. Alternatively, stringency conditions can be devised in which an essentially binary response is obtained, i.e., an ASO corresponding to a variant form of the target gene will hybridize to that allele, and not to the wildtype allele.

Ligase Mediated Allele Detection Method

10

Ligase can also be used to detect point mutations, such as the SNPs in Table 3 in a ligation amplification reaction (e.g. as described in Wu et al., Genomics 4:560-569, 1989). The ligation amplification reaction (LAR) utilizes amplification of specific DNA sequence using sequential rounds of template dependent ligation (e.g. as described in Wu, supra, and Barany, Proc. Nat. Acad. Sci. 88:189-193, 1990).

15

Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. DNA molecules melt in segments, termed melting domains, under conditions of increased temperature or denaturation.

20

Each melting domain melts cooperatively at a distinct, base-specific melting temperature (T_m). Melting domains are at least 20 base pairs in length, and can be up to several hundred base pairs in length.

25

Differentiation between alleles based on sequence specific melting domain differences can be assessed using polyacrylamide gel electrophoresis, as described in Chapter 7 of Erlich, ed., PCR Technology, Principles and Applications for DNA Amplification, W. H. Freeman and Co., New York (1992).

30

Generally, a target region to be analyzed by denaturing gradient gel electrophoresis is amplified using PCR primers flanking the target region. The amplified PCR product is applied to a polyacrylamide gel with a linear denaturing gradient as described in Myers et al., Meth. Enzymol. 155:501-527, 1986, and Myers et al., in Genomic
5 Analysis, A Practical Approach, K. Davies Ed. IRL Press Limited, Oxford, pp. 95 139, 1988. The electrophoresis system is maintained at a temperature slightly below the T_m of the melting domains of the target sequences.

10 In an alternative method of denaturing gradient gel electrophoresis, the target sequences can be initially attached to a stretch of GC nucleotides, termed a GC clamp, as described in Chapter 7 of Erlich, supra. In one example, at least 80% of the nucleotides in the GC clamp are either guanine or cytosine. In another example, the GC clamp is at least 30 bases long. This method is particularly suited to target sequences with high T_m 's.

15 Generally, the target region is amplified by the polymerase chain reaction as described above. One of the oligonucleotide PCR primers carries at its 5' end, the GC clamp region, at least 30 bases of the GC rich sequence, which is incorporated into the 5' end of the target region during amplification. The resulting amplified target region is run
20 on an electrophoresis gel under denaturing gradient conditions as described above. DNA fragments differing by a single base change will migrate through the gel to different positions, which can be visualized by ethidium bromide staining.

Temperature Gradient Gel Electrophoresis

25 Temperature gradient gel electrophoresis (TGGE) is based on the same underlying principles as denaturing gradient gel electrophoresis, except the denaturing gradient is produced by differences in temperature instead of differences in the concentration of a chemical denaturant. Standard TGGE utilizes an electrophoresis apparatus with a
30 temperature gradient running along the electrophoresis path. As samples migrate through a gel with a uniform concentration of a chemical denaturant, they encounter increasing temperatures. An alternative method of TGGE, temporal temperature gradient gel electrophoresis (TTGE or tTGGE) uses a steadily increasing temperature of the entire electrophoresis gel to achieve the same result. As the samples migrate

through the gel the temperature of the entire gel increases, leading the samples to encounter increasing temperature as they migrate through the gel. Preparation of samples, including PCR amplification with incorporation of a GC clamp, and visualization of products are the same as for denaturing gradient gel electrophoresis.

5

Single-Strand Conformation Polymorphism Analysis

Target sequences or alleles can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, for example as described in Orita et al., Proc. Nat. Acad. Sci. 85:2766-2770, 1989. Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids can refold or form secondary structures which are partially dependent on the base sequence. Thus, electrophoretic mobility of single-stranded amplification products can detect base-sequence difference between alleles or target sequences.

15

Chemical or Enzymatic Cleavage of Mismatches

Differences between target sequences can also be detected by differential chemical cleavage of mismatched base pairs, for example as described in Grompe et al., Am. J. Hum. Genet. 48:212-222, 1991. In another method, differences between target sequences can be detected by enzymatic cleavage of mismatched base pairs, as described in Nelson et al., Nature Genetics 4:11-18, 1993. Briefly, genetic material from an animal and an affected family member can be used to generate mismatch free heterohybrid DNA duplexes. As used herein, 'heterohybrid' means a DNA duplex strand comprising one strand of DNA from one animal, and a second DNA strand from another animal, usually an animal differing in the phenotype for the trait of interest.

25

30

Non-gel Systems

Other possible techniques include non-gel systems such as TaqManTM (Perkin Elmer). In this system oligonucleotide PCR primers are designed that flank the mutation in

question and allow PCR amplification of the region. A third oligonucleotide probe is then designed to hybridize to the region containing the base subject to change between different alleles of the gene. This probe is labeled with fluorescent dyes at both the 5' and 3' ends. These dyes are chosen such that while in this proximity to each other the fluorescence of one of them is quenched by the other and cannot be detected.

5 Extension by Taq DNA polymerase from the PCR primer positioned 5' on the template relative to the probe leads to the cleavage of the dye attached to the 5' end of the annealed probe through the 5' nuclease activity of the Taq DNA polymerase. This removes the quenching effect allowing detection of the fluorescence from the dye at

10 the 3' end of the probe. The discrimination between different DNA sequences arises through the fact that if the hybridization of the probe to the template molecule is not complete, i.e. there is a mismatch of some form, the cleavage of the dye does not take place. Thus only if the nucleotide sequence of the oligonucleotide probe is completely complimentary to the template molecule to which it is bound will quenching be

15 removed. A reaction mix can contain two different probe sequences each designed against different alleles that might be present thus allowing the detection of both alleles in one reaction.

Primer Design Strategy

20

Increased use of polymerase chain reaction (PCR) methods has stimulated the development of many programs to aid in the design or selection of oligonucleotides used as primers for PCR. Four examples of such programs that are freely available via the Internet are: PRIMER by Mark Daly and Steve Lincoln of the Whitehead Institute

25 (UNIX, VMS, DOS, and Macintosh), Oligonucleotide Selection Program (OSP) by Phil Green and LaDeana Hiller of Washington University in St. Louis (UNIX, VMS, DOS, and Macintosh), PGEN by Yoshi (DOS only), and Amplify by Bill Engels of the University of Wisconsin (Macintosh only).

30 Generally these programs help in the design of PCR primers by searching for bits of known repeated-sequence elements and then optimizing the T_m by analyzing the length and GC content of a putative primer. Commercial software is also available 35 and primer selection procedures are rapidly being included in most general sequence analysis packages.

Designing oligonucleotides for use as either sequencing or PCR primers to detect requires selection of an appropriate sequence that specifically recognizes the target, and then testing the sequence to eliminate the possibility that the oligonucleotide will
5 have a stable secondary structure. Inverted repeats in the sequence can be identified using a repeat-identification or RNA-folding programs.

If a possible stem structure is observed, the sequence of the primer can be shifted a few nucleotides in either direction to minimize the predicted secondary structure.
10

When the amplified sequence is intended for subsequence cloning, the sequence of the oligonucleotide should also be compared with the sequences of both strands of the appropriate vector and insert DNA. Obviously, a sequencing primer should only have a single match to the target DNA. It is also advisable to exclude primers that have
15 only a single mismatch with an undesired target DNA sequence. For PCR primers used to amplify genomic DNA, the primer sequence should be compared to the sequences in the GenBank database to determine if any significant matches occur. If the oligonucleotide sequence is present in any known DNA sequence or, more importantly, in any known repetitive elements, the primer sequence should be
20 changed.

Examples

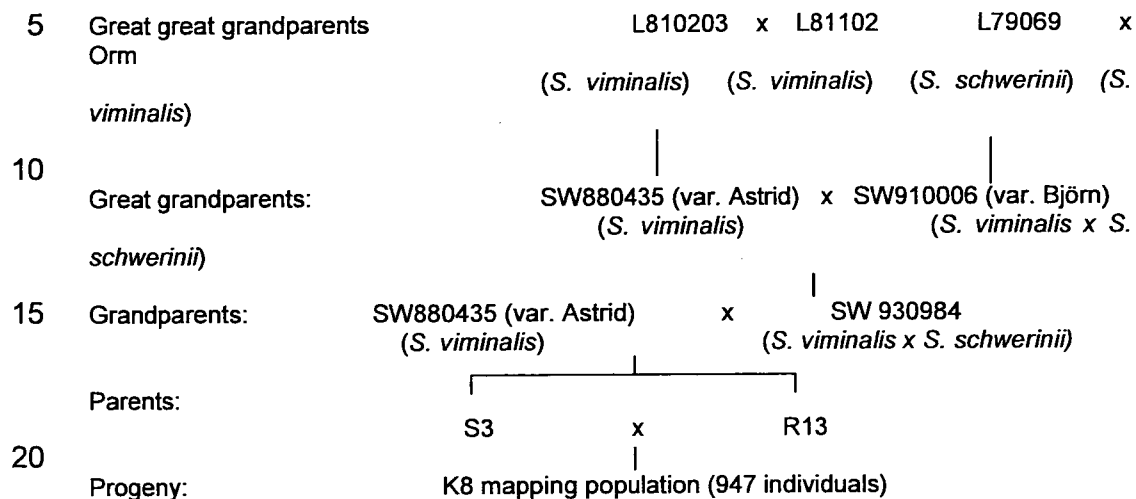
25

Example 1

Plant material

30 This study focuses on the K8 willow mapping population. This population comprises 947 full-sib individuals and was produced at Long Ashton Research Station (LARS), in 1999. The pedigree of the population is shown in Table 1.

35

Table 1**The K8 mapping population pedigree**

The population was established in a field experiment at LARS in 2000 and later at
 25 Rothamsted Research (RRes), Harpenden, Herts, UK in 2003. Six clonal replicates of
 each K8 genotype were planted as single plots, each in a 2×3 arrangement within the
 field experiment. Plots were arranged in a 52×23 plot row by column design. To
 facilitate identification of any environmental inconsistencies across the trial site, and
 to allow subsequent adjustment of trait values prior to QTL analyses, a reference
 30 willow variety was planted at 64 pre-selected plot positions throughout the site. The
 biomass cultivar, *S. viminalis* var. Jorr, was selected for this role at the LARS site and
 the cultivar Bowles Hybrid was used at RRes. These control genotypes were also
 used to surround the entire site to minimise any edge effects and also to form internal
 tramline columns after every fourth (RRes) or fifth (LARS) column of K8 progeny.
 35 Progeny were arranged in random order in the design. For additional details, see
 Hanley SJ (2003) Genetic mapping of important agronomic traits in biomass willow.
 PhD thesis, University of Bristol, UK).

Both plantations were established from 15 cm stem cuttings, allowed to grow for one
 40 year, after which the plants were coppiced during the winter by removing the first
 year's growth from the stool. Plants were then allowed to grow for a further two
 years before a second cutback. Plants were then coppiced after each period of three
 seasons of growth.

Trait measurements

5 Trait measurements were made according to Table 2 below.

Table 2

Trait measured	'single stem'		'multi stem'				
	Nursery	Establishment year	1st year post cutback	2nd year post cutback	1st year post cutback	2nd year post cutback	3rd year post cutback
Biomass yield	-	LARS	-	LARS,RRes	-	-	LARS,RRes†
Maximum stem height	LARS	LARS	LARS	LARS,RRes	-	-	LARS,RRes†
Mean stem height	-	LARS	LARS	LARS,RRes	-	-	LARS,RRes†
Maximum stem diameter‡	-	LARS	LARS,RRes*	LARS,RRes	-	-	LARS,RRes†
Mean stem diameter							
Shoot no.per stool	-	LARS	LARS	LARS,RRes	-	-	LARS,RRes†
% Moisture content	-	LARS	-	LARS,RRes	-	-	LARS,RRes†
Rust resistance	-	LARS	LARS	LARS	-	-	-

10 *: trait measured on 480 progeny only
 †: RRes data available Spring 2008
 ‡: stem diameters measured at 55cm from the stool

1st cutback 2nd cutback 3rd cutback

15

Trait data was first analysed for spatial inconsistencies across the trial site and data adjusted to account for this. The method of Residual Maximum Likelihood (REML) (Patterson and Thompson 1971; Robinson et al. 1982) was used to fit mixed (involving fixed and random effects) models (Searle et al. 1992) to the trait data, employing GenStat software (©Sixth Edition, Lawes Agricultural Trust, Rothamsted Experimental Station, 2002). Using theory developed by Gleeson and Cullis (1987), Cullis and Gleeson (1991) and Cullis et al. (1998), the most appropriate model to correctly describe the effects of spatial trends, defined as autoregressive components for rows and or columns, for data from each assessment was identified. This utilised the trait information provided by a reference genotypes (Jorr or Bowles Hybrid). Changes in model deviance (Genstat Committee 1993) were used to assess the significance ($P < 0.05$) of any extra (spatial) terms in models, these changes being

20

25

asymptotically distributed as chi-squared on degrees of freedom equal to the number of extra parameters.

Adjusted trait scores were then utilised in QTL analysis according to standard
5 methodologies as included in the software package MapQTL (Kyazma).

Identification and high resolution mapping of the yield QTL

The yield QTL was first identified following an initial QTL screen based on K8
10 progeny numbers 1- 480 only. The K8 linkage map comprised amplified fragment length polymorphism (AFLP) and microsatellite markers. In addition, a genome-wide set of Single Nucleotide Polymorphism (SNP) markers was developed and included in analysis for aligning the K8 willow map to the publicly-available poplar genome sequence. Further details of this approach are available in Hanley, S., Mallott, M.D.
15 & Karp A. (2006) *Tree Genetics and Genomes*, 3, 35-48.

Once the approximate position of the QTL was determined (on Linkage Group X; Linkage group nomenclature is as provided for the poplar genome sequence ; http://genome.jgi-psf.org/Poptr1_1/Poptr1_1.home.html) through the initial QTL
20 screen, an additional 11 SNP markers were developed to target this region to increase mapping resolution and further delimit the locus. The SNP markers were derived from sequencing willow orthologues of genes in this region of the poplar genome sequence. Full details of the method developed for identifying SNP markers are described in Hanley, S., Mallott, M.D. & Karp A. (2006) *Tree Genetics and*
25 *Genomes*, 3, 35-48.

Marker	Class	Forward PCR primer(5'→3')	Reverse PCR primer (5'→3')	SnapShot primer	Type
X_15341094	SNP	GGGAAACAGATAGTGGGCAGTC	GCCTCCTTCTCCTGTAAGCAC	ACCTTAACCTGCAGCTCTTACCTTAA	ACxAC
X_15478832	SNP	TGATGCTCCAAAGTTTCTC	TCCTGGCGTGTTCCATAGAGGT	GATGGGAAGTAAAAATTATCCGAGCAAGAT	ACxAC
X_15533399	SNP	GTGGCTCTTCTCCAATTGCTGT	GTGCTTTTGTCTCCACCTTTG	AATAGCAAATATGGGGGCTT	ATxAT
X_15727779	SNP	AGAAGGGATGTGCCAAAGTGA	ACAAGCTGGATTGGTGGAAGA	ACTTTTGATATTTCTAACCTTTTCTCTATTGTA	CTxCT
X_15758822	SSR	CAAAAACGCACCTATTCTTCC	CCAGAGTCCCTTGAACACAC	-	abxac
X_15777280	SNP	AAAACAACCTCCCTCCCTTGA	TCTGCAAGCCCACTTTTCTT	TTTGAGGAAGACGGCAAATG	TGxTG
X_15905315	SNP	CAACATATTGTGGATGCAGga	CAGTGATACAATGTCTGCAAGGA	AGGATTTCACAGATTGGTTTCAC	CGxCG
X_15917077	SNP	TTCTTGTTTGGCTTTGGTG	CCATCGCCTGTATCCACACTT	ATTCAGCTGTCGAATTGATTGATT	TGxTG
X_15951166	SNP	TGGTGAGCGAGAGTACGTGAA	AATCTTCTGCGCCCTCAAAAC	GGGTATGCTCAGCCTGCC	ACxAC
X_15945623	SNP	ATTGGAATCTCTGGGGCTTT	CACCTGCTCCATAATCCCTCT	TCAATTGATACTGCTATTGTCCCCAGA	AGxAG
X_15958515	SNP	CAGAGACCCAAATGGACTGGA	AACGACCTAATCCCTGGAAA	TCAATGCATGACGGTGTCTGTGGTGACAGT	AGxAG

* It should be noted that the marker numbers do not necessarily refer to the most up date position available in the poplar genome and this may change due to ongoing annotation and assembly.

5

All of these SNP markers were heterozygous in both mapping population parents (S3 & R13) and segregated according to the expected 1:2:1 (AA:AB:BB) ratio in the progeny. All 11 markers were used to genotype the 947 individuals of the mapping population. Forty three individuals were not included in subsequent analysis as genotyping failed in some instances and some plants had died in the field and DNA for screening was no longer available. A fine-scale linkage map was then calculated based on the 11 markers. The order of markers on the willow map is co-linear with the poplar genome sequence.

10

15 The resulting linkage map spanned 5.1 cM. This map was used in conjunction with the genotype and trait data in a second round of QTL analysis. Results of interval mapping are shown in Fig. 12 for total fresh weight for two harvest years at the LARS site (2003 & 2006) and for the RRes site in 2005. QTL for maximum stem diameter and maximum stem height are also shown for both sites for equivalent years. These traits are highly correlated with total harvestable yield in this population (Hanley SJ (2003) Genetic mapping of important agronomic traits in biomass willow. PhD thesis, University of Bristol, UK).

20

The sequences for willow markers X_15341094, X_15758822, X_15905315 and X_15958515 also yielded SNPs that were specific to each parent indicating that there are three haplotypes segregating in this region in the K8 population. Due to the nature

25

of the cross that generated the K8 population, there is a maximum of three alleles segregating at any given locus in this population.

Sequence analysis of the QTL region based on the poplar genome.

5

QTL indicates that the most likely position of the QTL is between markers X_15727779 and X_15917077. The position of these markers in the poplar genome was determined by BLASTN homology searches using the willow sequence used to derive the SNP markers.

10

The homologous genomic region in poplar is predicted to contain 10 genes. The physical size of this region is predicted to be 196118 base pairs in length. However, a gap in the public sequence prevents an accurate measure of the length. Eight of the genes have EST sequence to support their expression. Two willow BAC clones have been identified that cover the region delimited by the two markers. Partial sequencing of these clones indicates that homologues to 9 of the 10 genes within the QTL region in poplar can be identified in willow plant 'R13'. 'R13' contains two alleles (A and C) and Figure 2 shows the sequence of the QTL region of allele A. Alleles A and C of the 9 willow genes were identified using routine techniques and are shown in the Figures.

20

The amino acid sequences of the polypeptides encoded by Alleles A and C of the 9 willow genes are shown in the Figures. These were identified using cDNA sequences that allowed exons in the gene sequences to be identified and thus the polypeptide sequence to be predicted. The cDNA sequences were predicted by full sequencing of salix transcripts that allowed intron-exon boundaries to be identified. In some cases the exons were predicted using annotation information on the public poplar genome website. These predictions are based on transcript sequencing in poplar and gene prediction algorithms. Polypeptide sequences were predicted using partially sequenced willow transcripts in conjunction with public poplar genome annotation data which is based on gene finding algorithms and poplar transcript sequence information (Tuskan et al., 2006. The Genome of Black Cottonwood, *Populus trichocarpa* (Torr. & Gray) Science 313 p5793.)

25

30

Details of the genes are detailed below:

1. Xyld1

- 5 Shows best homology in *Arabidopsis thaliana* with Locus AT3G12740, or *ALIS1* (ALA-Interacting Subunit). *ALIS1* is a member of a family of phospholipid transporters (*ALIS1* -*ALIS5*) which are homologs of the Cdc50p/Lem3p family in yeast that are essential for the trafficking of yeast P4-ATPases. The Arabidopsis *ALIS* proteins are 27-30% identical to yeast Cdc50p and similarity ranges from 48-53%. In
- 10 yeast *ALIS1* shows strong affinity to *ALA3*. In Arabidopsis, *ALA3* has been shown to be important for *trans*-Golgi proliferation of slime vesicles containing polysaccharides and enzymes for secretion. In yeast, *ALA3* function requires interaction with the *ALIS1*. In Arabidopsis plants, *ALIS1*, like *ALA3*, is localised to membranes of Golgi-like structures and is expressed in root peripheral columella
- 15 cells. It has been proposed that the *ALIS1* protein is a β - sub-unit of *ALA3* in Arabidopsis and that this protein is important part of the Golgi machinery in plants required for secretory processes during development.

Relevant publications

- 20 Poulsen LR, López-Marqués RL, McDowell SC, Okkeri J, Licht D, Schulz A, Pomorski T, Harper JF, Palmgren MG. 2008 The Arabidopsis P4-ATPase *ALA3* localizes to the golgi and requires a beta-subunit to function in lipid translocation and secretory vesicle formation. *Plant Cell*. 3:658-76.
- 25 Bosco CD, Lezhneva L, Biehl A, Leister D, Strotmann H, Wanner G, Meurer J. 2004 Inactivation of the chloroplast ATP synthase gamma subunit results in high non-photochemical fluorescence quenching and altered nuclear gene expression in *Arabidopsis thaliana*. *J Biol Chem*.279(2):1060-9.

2. Xyld 2

Shows strongest homology to *Arabidopsis thaliana* gene ALDH5F1 (Locus AT1G79440 ; previous nomenclature SSADH; EC 1.2.1.24) which is a member of the
5 aldehyde dehydrogenases (ALDHs) protein superfamily of NAD(P)C-dependent enzymes that oxidize a wide range of endogenous and exogenous aliphatic and aromatic aldehydes. The Arabidopsis genome contains 14 unique ALDH sequences encoding members of nine ALDH families, including eight known families and one novel family (*ALDH22*) that is currently known only in plants. Of these,
10 there is one succinic semialdehyde dehydrogenase gene, *ALDH5F1*, which encodes a protein of 528 amino acids. *ALDH5F1* is the only confirmed identified member of the succinic semialdehyde family in plants. The Arabidopsis protein is localized to mitochondria and a kinetic analysis showed that the recombinant enzyme was specific for succinic semialdehyde and regulated by adenine nucleotides. T-DNA knockout
15 mutants of *ALDH5F1* result in dwarfed plants with necrotic lesions and are sensitive to both ultraviolet-B light and heat stress. Plants with *ssadh* mutations accumulate elevated levels of H₂O₂, suggesting a role for this gene in stress regulation detoxification pathway plant, providing defense against environmental stress by preventing the accumulation of reactive oxygen species.

20

Relevant publications

- Hueser, AF, UI L. 2008 Analysis of GABA-shunt metabolites in *Arabidopsis thaliana*
19th International Conference on Arabidopsis Research
25
- Ludewig F, Hüser A, Fromm H, Beauclair L, Bouché N. 2008 Mutants of GABA transaminase (POP2) suppress the severe phenotype of succinic semialdehyde dehydrogenase (*ssadh*) mutants in Arabidopsis. PLoS ONE 3(10):e3383
- 30 Zybilov B, Rutschow H, Friso G, Rudella A, Emanuelsson O, Sun Q, van Wijk KJ. 2008 Sorting signals, N-terminal modifications and abundance of the chloroplast proteome. PLoS ONE 3(4):e1994

Fait A, Yellin A, Fromm H. 2005 GABA shunt deficiencies and accumulation of reactive oxygen intermediates: insight from Arabidopsis mutants. FEBS Lett. 579(2):415-20

- 5 Kirch HH, Bartels D, Wei Y, Schnable PS, Wood AJ. 2004 The ALDH gene superfamily of Arabidopsis. Trends Plant Sci. 9(8):371-7

- Breitkreuz KE, Allan WL, Van Cauwenberghe OR, Jakobs C, Talibi D, Andre B, Shelp BJ. 2003 A novel gamma-hydroxybutyrate dehydrogenase: identification and
10 expression of an Arabidopsis cDNA and potential role under oxygen deficiency. J Biol Chem. 278(42):41552-6

3. Xyld3

- 15 Shows strongest homology with *Arabidopsis thaliana* *ALTERED PHLOEM DEVELOPMENT (APL)* gene (Locus AT1G79430), which encodes a MYB coiled-coil-type transcription factor that is required for phloem identity in Arabidopsis. *APL* has been proposed to have a dual role both in promoting phloem differentiation and in repressing xylem differentiation during vascular development.

20

Relevant publications

- Truernit E, Bauby H, Dubreucq B, Grandjean O, Runions J, Barthélémy J, Palauqui JC. 2008 High-resolution whole-mount imaging of three-dimensional tissue
25 organization and gene expression enables the study of Phloem development and structure in Arabidopsis. Plant Cell. 20(6):1494-503

- Lehesranta S, Lindgren O, Tähtiharju S, Carlsbecker A, Helariutta Y 2008 The role of APL as a transcriptional regulator in specifying vascular identity 19th International
30 Conference on Arabidopsis Research

Carlsbecker A, Lindgren O, Bonke M, Thitamadee S, Tähtiharju S, Helariutta Y 2004 Genetic analysis of procambial development in the Arabidopsis root 15th International Conference on Arabidopsis Research

Bonke M, Hauser M-T, Helariutta Y 2002 The APL locus is required for phloem development in *Arabidopsis* roots. 13th International Conference on Arabidopsis Research

5

4. Xyld4

Show strongest homology in *Arabidopsis thaliana* to Locus AT1G79420. Function not yet described.

10

5. Xyld5

Shows strongest homology with AtOCT2 in *Arabidopsis thaliana* (Locus AT1G79360). AtOCT2 is one of six Arabidopsis organic cation/carnitine transporter (OCT) -like proteins, named AtOCT1–AtOCT6 (loci At1g73220, At1g79360, At1g16390, At3g20660, At1g79410 and At1g16370, respectively) that have been identified. These proteins cluster in a small subfamily within the ‘organic solute cotransporters’ included in the large sugar transporter family of the major facilitator superfamily (MFS). AtOCT1 shares features of organic cation/carnitine transporters (OCTs). In animals, mammalian plasma membrane OCTs are involved in homeostasis and distribution of various small endogenous amines (e.g. carnitine, choline) and detoxification of xenobiotics such as nicotine. AtOCT1 is able to transport carnitine in yeast and is likely to be involved in the transport of carnitine or related molecules across the plasma membrane in plants.

25

The orthologous gene sequence has not yet been identified in willow.

Related publication

Tohge T, Nishiyama Y, Hirai MY, Yano M, Nakajima J, Awazuhara M, Inoue E, Takahashi H, Goodenowe DB, Kitayama M, Noji M, Yamazaki M, Saito K. 2005 Functional genomics by integrated analysis of metabolome and transcriptome of *Arabidopsis* plants over-expressing an MYB transcription factor. *Plant J.* 42(2):218-35

6. Xyld6

Shows best fit with ATOCT3 Arabidopsis ORGANIC CATION/CARNITINE
5 TRANSPORTER2). ATOCT3 is one of six Arabidopsis organic cation/carnitine
transporter (OCT) -like proteins, named AtOCT1–AtOCT6 (loci *At1g73220*,
At1g79360, *At1g16390*, *At3g20660*, *At1g79410* and *At1g16370*, respectively)
referred to above. These proteins cluster in a small subfamily within the ‘organic
solute cotransporters’ included in the large sugar transporter family of the major
10 facilitator superfamily (MFS).

Relevant publications

Lelandais-Brière C, Jovanovic M, Torres GA, Perrin Y, Lemoine R, Corre-Menguy F,
15 Hartmann C. 2007 Disruption of AtOCT1, an organic cation transporter gene, affects
root development and carnitine-related responses in Arabidopsis. *Plant J.* 51(2):154-
64

Price J, Laxmi A, St Martin SK, Jang JC. 2004 Global transcription profiling reveals
20 multiple sugar signal transduction mechanisms in Arabidopsis. *Plant Cell.* 16(8):2128-
50

7. Xyld7

25 Shows homology with members of the R2R3-type *MYB* gene family in Arabidopsis.
Although no functional data are available for most of the 125 R2R3-type *AtMYB*
genes, a number of functions have been assigned concerning many aspects of plant
secondary metabolism, as well as the identity and fate of plant cells. This includes
regulation of phenylpropanoid metabolism, control of development and determination
30 of cell fate and identity, plant responses to environmental factors and mediating
hormone actions.

Relevant publications

Stracke R, Werber M, Weisshaar B. 2001 The R2R3-MYB gene family in *Arabidopsis thaliana*. *Curr Opin Plant Biol.* 4(5):447-56

Riechmann JL, Heard J, Martin G, Reuber L, Jiang C, Keddie J, Adam L, Pineda O,
 5 Ratcliffe OJ, Samaha RR, Creelman R, Pilgrim M, Broun P, Zhang JZ, Ghandehari D,
 Sherman BK, Yu G. 2000 *Arabidopsis* transcription factors: genome-wide
 comparative analysis among eukaryotes. *Science.* 290(5499):2105-10

8. Xyl8

10

Shows best fit with ANAC028, *Arabidopsis* NAC domain containing protein (Locus AT1G65910). NAC (NAM, ATAF, and CUC) is a plant-specific gene family. NAC family transcription factors are involved in maintaining organ or tissue boundaries regulating the transition from growth by cell division to growth by cell expansion.

15

Most NAC proteins contain a highly conserved N-terminal DNA-binding domain, a nuclear localization signal sequence, and a variable C-terminal domain. 75 and 105 NAC genes were predicted in the *Oryza sativa* and *Arabidopsis* genomes, respectively. The functions of only some of these have been described. The first reported NAC genes were *NAM* from petunia and *CUC2* from *Arabidopsis* that

20

participate in shoot apical meristem development. *CUC1*, *CUC2* and *nam* are expressed at the boundaries between cotyledonary primordial and between floral organs and are specifically involved in shoot apical meristem formation and separation of cotyledons and floral organs. Other development-related NAC genes have been suggested with roles in controlling cell expansion of specific flower organs

25

e.g. *NAP* or auxindependent formation of the lateral root system e.g. *NAC1*. Some of NAC genes, such as *ATAF1* and *ATAF2* genes from *Arabidopsis* and the *StNAC* gene from potato, are induced by pathogen attack and wounding. More recently, a few NAC genes, such as *AtNAC072* (*RD26*), *AtNAC019*, *AtNAC055* from *Arabidopsis*, and *BnNAC* from *Brassica* (31), were found to be involved in responses to environmental

30

stress. Seven members of NAC family At2g18060, At4g36160, At5g66300, At1g12260, At1g62700, At5g62380, and At1g71930 have been designated as *VASCULAR-RELATED NAC-DOMAIN PROTEIN 1* (*VND1* to *VND7*). Members of these could induce transdifferentiation of various cells into metaxylem- and protoxylem-like vessel elements, respectively, in *Arabidopsis* and poplar. Similarly

ANAC012 and ANAC073 also appear to have a role in xylem development and secondary wall thickening in *Arabidopsis*.

Relevant publications

5

Ooka H, Satoh K, Doi K, Nagata T, Otomo Y, Murakami K, Matsubara K, Osato N, Kawai J, Carninci P, Hayashizaki Y, Suzuki K, Kojima K, Takahara Y, Yamamoto K, Kikuchi S. 2003 Comprehensive analysis of NAC family genes in *Oryza sativa* and *Arabidopsis thaliana*. *DNA Res.* 10(6):239-47

10

Riechmann JL, Heard J, Martin G, Reuber L, Jiang C, Keddie J, Adam L, Pineda O, Ratcliffe OJ, Samaha RR, Creelman R, Pilgrim M, Broun P, Zhang JZ, Ghandehari D, Sherman BK, Yu G. 2000 *Arabidopsis* transcription factors: genome-wide comparative analysis among eukaryotes. *Science* 290(5499):2105-10

15

9. Xyld9

Show strongest homology in *Arabidopsis thaliana* to Locus AT1G79390. The function of this expressed protein has not yet been described

20

10. Xyld10

<http://www.arabidopsis.org/servlets/TairObject?type=locus&name=AT1G79380>

25

Shows homology to the RGLG2 (RING DOMAIN LIGASE2) locus of *Arabidopsis thaliana* (Locus AT1G79380). In functional terms, the RING domain can basically be considered a protein-interaction domain. RING-finger proteins have been implicated in a range of diverse biological processes and biochemical activities, from transcriptional and translational regulation to targeted protein degradation.

30

Relevant publications

Kosarev P, Mayer KF, Hardtke CS. 2002 Evaluation and classification of RING-finger domains encoded by the Arabidopsis genome. Genome Biol. 3(4):RESEARCH 0016.1

5 Example 2

Provided below is an example of the use of a diagnostic molecular marker derived from the QTL region that can be used to select for favourable alleles within a breeding programme:

- 10 A microsatellite marker was developed to screen for the three QTL alleles segregating in members of the K8 population of *Salix*. The microsatellite marker is amplified by PCR using the following pair of primers:

Forward primer 5'- CAAAAACGCACCCTATTCTTCC – 3'

- 15 Reverse primer 5'- CCAGAGTCCCCTTGAACACAC – 3'

The sequence of the amplified region for allele A (179bp) is:

CAAAAACGCACCCTATTCTTCCCTATTTGCATCGCATTGTTCTTGAATCTC
20 TTTGTATTCCCTGAGTCTCAGAGAGAGAGAGAGAGAGAGAGAAGGAA
AGAGAGAATGTTCCATACCAAGAAACCCTCAACTATGAATTCCCATGATA
GACCCATGTGTGTTCAAGGGGACTCTGG

- 25 These primers generate amplicons of three different lengths in the K8 mapping population and thus are informative for the three alleles that are segregating in the yield QTL region. The female parent of the cross, cultivar 'S3' produces two alleles of different length (A & B). The male parent, cultivar 'R13' contains two alleles (A & C) where A is a common allele that is present in S3.

- 30 The diploid K8 mapping population can therefore inherit the following combinations of alleles : AA, AB, AC, BC. Table 3 shows the mean trait values for each of these classes in the population for total fresh weight harvested, maximum stem diameter and maximum stem height. Analysis is based trait data collected at Long Ashton Research Station in 2003. The non-parametric rank-sum test of Kruskal-Wallis (KW)

(Lehmann, 1975) was used to determine associations between marker genotypes and trait scores.

Table 3. Mean trait values associated with inheritance of particular QTL alleles (A, B and C) in the K8 mapping population as determined by the application of a microsatellite marker.

Trait	N ^o	microsatellite genotype				KW	df	Significance
		AA	AB	AC	BC			
Total fresh biomass harvested per stool (kg)	902	1.30	1.90	1.75	2.17	132.76	3	*****
Maximum stem diameter per stool (cm)	849	16.30	20.12	19.22	21.37	186.37	3	*****
Maximum stem height per stool (m)	902	3.16	3.79	3.69	3.96	223.95	3	*****

N^o: Number of plants included in analysis

KW: Kruskal-Wallis test statistic

df : degrees of freedom

Significance: ***** = 0.0001

In this example, plants of genotype AA often give the lowest yield and plants of genotype BC often give rise to the highest yields. Where the goal of a breeding programme is to increase harvestable biomass yield, plants of genotype BC would be preferentially selected using the marker. Similarly, potential parents of genotype AA might be excluded from a crossing programme as this allele can be associated with lower yields.

20 Example 3

Disruption of Xyld7 gene sequence in QTL haplotype A

An alignment of Gene Xyld7 allele A (SEQ ID NO 2) sequence with the Gene Xyld7 allele C sequence (SEQ ID NO 1) (as shown in the alignment of Figure 9D) indicates Gene Xyld7 allele A has an insertion region with extra nucleotides that are not present in Gene Xyld7 allele C sequence SEQ ID NO 1. SEQ ID NO 26 (as shown in Figure 9E) shows the amino acid sequence of the *Salix* Xyld7 allele C polypeptide.

A comparison of Xyld7 gene sequences for both alleles of plant R13 (alleles A and C) identified an insertion in Xyld7_A allele which is not present in the Xyld_C allele

sequence. To determine whether the insertion is in coding sequence, the transcript of allele C of this gene was fully sequenced which confirmed that the insertion in allele A is within exon 3 of the gene. The resulting allele A transcript, if expressed, would not be expected to encode a functional protein. Indeed, while both allele B and C transcripts have been identified, no allele A derived transcript has yet been identified in plants S3 and R13 (the K8 parents which carry either the A and B alleles or the A and C alleles, respectively). It is therefore possible that allele A of this gene is non-functional in the K8 mapping population and this may contribute to the underlying phenotypic variation that is represented by the biomass yield QTL.

Example 4

Several approaches are applicable to the identification of the causal gene and perhaps, the underlying sequence polymorphism.

1. Where null mutants for the corresponding genes are available, the crop genes may be used in transformation experiments. The contrasting alleles which are present in high or low yielding crop may be checked for a corresponding differential effect in Arabidopsis. There is evidence that willow genes can have the capacity to rescue Arabidopsis mutant phenotypes. Where null mutant are not available, overexpression studies may be possible.

2. Quantitative PCR may be used to identify whether there are differences in gene expression levels when high and low yielding types are compared.

3. High yielding and low yielding crop genotypes including bred commercial varieties and selected lines in a breeding programme may be screened using primers for each gene to determine whether the presence of only one allele at one of the genes is associated with the high yielding phenotype.

4. At such time that populations are established for association mapping (also known as Linkage Disequilibrium mapping) in the crop, variation in phenotype may be tested against allelic variation in each of the genes in the region. Depending on the degree

of LD remaining in the region, mapping with higher resolution than that afforded by QTL analysis may be possible.

- 5 5. Classical genetics approaches may be applied in which recombinant individuals with different homozygous stretches of the QTL region may be generated and the progeny tested for the presence of the QTL. Such an approach may further delimit the current interval size.

- 10 All publications mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described methods and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments.
- 15 Indeed, various modifications of the described modes for carrying out the invention which are apparent to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

Claims:

1. A method for predicting harvestable biomass yield in a crop comprising:
5 genotyping a sample obtained from said crop for one or more markers genetically linked to a portion of the genome, wherein said portion is within the interval corresponding to all or part of the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 18, Figure 1, Figure 2 or Figure 17 whereby the markers individually or collectively identify a
10 haplotype associated with harvestable biomass yield in a plurality of crop plants and correlating the haplotype with the harvested biomass yield.
2. A method according to claim 1 wherein the one or more markers are within
the interval corresponding to the sequence located between reference nucleotide
15 position A and reference nucleotide position B as shown in Figure 18, Figure 1, Figure 2 or Figure 17.
3. A method for determining the contribution of a Quantitative Trait Loci (QTL)
associated with harvestable biomass yield in a crop, the method comprising:
20 genotyping a sample obtained from a subject crop plant for one or more markers, which markers individually or collectively identify a haplotype located within a portion of the genome, wherein said portion is within the interval corresponding to all or part of the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 18, Figure 1, Figure 2 or Figure 17; wherein
25 the haplotype is correlated with a contribution to harvestable biomass yield by a gene comprised in the QTL.
4. A method according to claim 3 wherein the one or more markers are within
the interval corresponding to the sequence located between reference nucleotide
30 position A and reference nucleotide position B as shown in Figure 18, Figure 1, Figure 2 or Figure 17
5. A method of identifying an allele that is associated with harvestable biomass yield in a crop comprising: obtaining a sample from a crop plant; amplifying DNA

present in said sample comprising all or part of a region of the genome corresponding to the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 18, Figure 1, Figure 2 or Figure 17 and detecting the presence of a polymorphic marker in said region.

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6. A method according to claim 5 wherein the one or more markers are within the interval corresponding to the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 18, Figure 1, Figure 2 or Figure 17.

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7. A method of selecting a crop plant by marker assisted selection of a QTL associated with harvestable biomass yield said method comprising: determining the presence of an allele in the crop plant where the allele is located in a portion of the genome corresponding to all or part of the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 18, Figure 1, Figure 2 or Figure 17 and is genetically linked to a polymorphic marker and selecting said crop plant comprising the allele.

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8. A method according to claim 7 wherein the one or more markers are within the interval corresponding to the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 18, Figure 1, Figure 2 or Figure 17.

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9. A method according to any preceding claim wherein the crop is a monocotyledonous and dicotyledonous fodder crop, forage crop, ornamental crop, fruit crop, food crop, an algae, a forestry tree, a bioenergy crop or a biofuel crop, *Acacia* spp., *Acer* spp., *Actinidia* spp., *Agave* spp., *Agropyron* spp., *Agrostis* spp., *Allium* spp., *Alnus* spp., *Alopecurus* spp., *Amaranthus* spp., *Ananas* spp., *Apium* spp., *Arachis* spp., *Areca* spp., *Arundo* spp., *Arrhenatherum* spp., *Asparagus* spp; *Avena* spp., *Atriplex* spp., *Attalea* spp., *Beta* spp., *Betula* spp., *Brassica* spp., *Bromus* spp., *Bouteloua* spp., *Camelina* spp., *Camellia* spp., *Cannabis* spp., *Capsicum* spp., *Carica* spp., *Carex* spp., *Carthamus* spp., *Castanea* spp., *Carum* spp., *Cinnamomum* spp., *Citrus* spp., *Cocos* spp., *Coffea* spp., *Corchorus* spp., *Cotoneatser* spp., *Cucurbita* spp., *Cupressus* spp., *Cynodon* spp., *Daucus* spp., *Dactylis* spp., *Eucalyptus* spp.,

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- Elaeis* spp., *Eleusine* spp., *Fagus* spp., *Festuca* spp., *Ficus* spp., *Fraxinus* spp., *Geranium* spp., *Ginkgo* spp., *Glycine* spp., *Gossypium* spp., *Helianthus* spp., *Hemerocallis* spp., *Heracleum* spp., *Hedysarum* spp., *Hibiscus* spp., *Hordeum* spp., *Indigo* spp., *Ipomoea* spp., *Lettuca* spp., *Jatropha* spp., *Lotus* spp., *Lactuca* spp.,
 5 *Lathyrus* spp., *Lens* spp., *Linum* spp., *Lolium* spp., *Lupinus* spp., *Lezula* spp., *Lycopersicon* spp., *Malus* spp., *Manihot* spp., *Medicago* spp., *Melilotus* spp., *Mentha* spp., *Miscanthus* spp., *Musa* spp., *Nicotiana* spp., *Olea* spp., *Onobrychis* spp., *Ophiopogon* spp., *Oryza* spp., *Panicum* spp., *Papaver* spp., *Petunia* spp., *Phaseolus* spp., *Pennisetum* spp., *Phalaris* spp., *Phoenix* spp., *Phleum* spp., *Phyllostachys* spp.,
 10 *Physalis* spp., *Panicum* spp., *Picea* spp., *Pinus* spp., *Pistacia* spp., *Pisum* spp., *Poa* spp., *Podocarpus* spp., *Pogmania* spp., *Populus* spp., *Prunus* spp., *Quercus* spp., *Ribes* spp., *Robinia* spp., *Rosa* spp., *Raphanus* spp., *Rheum* spp., *Ricinus* spp., *Rubus* spp., *Salix* spp., *Sequoia* spp., *Sesamum* spp., *Setaria* spp., *Saccharum* spp., *Sambucus* spp., *Secale* spp., *Sinapis* spp., *Solanum* spp., *Sorghum* spp., *Trifolium* spp., *Triticum* spp.,
 15 *Triticosecale* spp., *Trisetum* spp., *Tagetes* spp., *Theobroma* spp., *Triadica* spp., *Vicia* spp., *Vitis* spp., *Vigna* spp., *Viola* spp., *Watsonia* spp. or *Zea* spp..

10. A method according to any preceding claim wherein the crop plant is a *Salix* (willow) or *Populus* (poplar) plant.

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11. An isolated nucleic acid sequence comprising a marker or plurality of markers located within a genome of a crop plant associated with a QTL associated with harvestable biomass yield in a crop wherein the marker or plurality of markers comprise polymorphic nucleotide sequences and said markers are genetically linked
 25 to a portion of the genome corresponding to all or part of the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 18, Figure 1, Figure 2 or Figure 17 or are within said portion of the genome.

12. An isolated nucleic acid sequence according to claim 11 wherein the crop is a
 30 monocotyledonous and dicotyledonous fodder crop, forage crop, ornamental crop, fruit crop, food crop, an algae, a forestry tree, a bioenergy crop or a biofuel crop, *Acacia* spp., *Acer* spp., *Actinidia* spp., *Agave* spp., *Agropyron* spp., *Agrostis* spp., *Allium* spp., *Alnus* spp., *Alopecurus* spp., *Amaranthus* spp., *Ananas* spp., *Apium* spp., *Arachis* spp., *Areca* spp., *Arundo* spp., *Arrhenatherum* spp., *Asparagus* spp; *Avena*

spp., *Atriplex* spp., *Attalea* spp., *Beta* spp., *Betula* spp., *Brassica* spp., *Bromus* spp., *Bouteloua* spp., *Camelina* spp., *Camellia* spp., *Cannabis* spp., *Capsicum* spp., *Carica* spp., *Carex* spp., *Carthamus* spp., *Castanea* spp., *Carum* spp., *Cinnamomum* spp., *Citrus* spp., *Cocos* spp., *Coffea* spp., *Corchorus* spp., *Cotoneaster* spp., *Cucurbita* spp., *Cupressus* spp., *Cynodon* spp., *Daucus* spp., *Dactylis* spp., *Eucalyptus* spp., *Elaeis* spp., *Eleusine* spp., *Fagus* spp., *Festuca* spp., *Ficus* spp., *Fraxinus* spp., *Geranium* spp., *Ginkgo* spp., *Glycine* spp., *Gossypium* spp., *Helianthus* spp., *Hemerocallis* spp., *Heracleum* spp., *Hedysarum* spp., *Hibiscus* spp., *Hordeum* spp., *Indigo* spp., *Ipomoea* spp., *Lettuca* spp., *Jatropha* spp., *Lotus* spp., *Lactuca* spp., *Lathyrus* spp., *Lens* spp., *Linum* spp., *Lolium* spp., *Lupinus* spp., *Lezula* spp., *Lycopersicon* spp., *Malus* spp., *Manihot* spp., *Medicago* spp., *Melilotus* spp., *Mentha* spp., *Miscanthus* spp., *Musa* spp., *Nicotiana* spp., *Olea* spp., *Onobrychis* spp., *Ophiopogon* spp., *Oryza* spp., *Panicum* spp., *Papaver* spp., *Petunia* spp., *Phaseolus* spp., *Pennisetum* spp., *Phalaris* spp., *Phoenix* spp., *Phleum* spp., *Phyllostachys* spp., *Physalis* spp., *Panicum* spp., *Picea* spp., *Pinus* spp., *Pistacia* spp., *Pisum* spp., *Poa* spp., *Podocarpus* spp., *Pogmania* spp., *Populus* spp., *Prunus* spp., *Quercus* spp., *Ribes* spp., *Robinia* spp., *Rosa* spp., *Raphanus* spp., *Rheum* spp., *Ricinus* spp., *Rubus* spp., *Salix* spp., *Sequoia* spp., *Sesamum* spp., *Setaria* spp., *Saccharum* spp., *Sambucus* spp., *Secale* spp., *Sinapis* spp., *Solanum* spp., *Sorghum* spp., *Trifolium* spp., *Triticum* spp., *Triticosecale* spp., *Trisetum* spp., *Tagetes* spp., *Theobroma* spp., *Triadica* spp., *Vicia* spp., *Vitis* spp., *Vigna* spp., *Viola* spp., *Watsonia* spp. or *Zea* spp..

13. An isolated nucleic acid sequence according to claim 11 wherein the crop plant is a *Salix* (willow) or *Populus* (poplar) plant.

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14. A crop plant comprising a genetic element derived from another crop plant, which genetic element comprises a biomass yield QTL, wherein said QTL is obtained from a portion of the genome corresponding to all or part of the sequence located between reference nucleotide position A and reference nucleotide position B as shown in Figure 18, Figure 1, Figure 2 or Figure 17.

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15. A crop plant according to claim 14 wherein the crop is a monocotyledonous and dicotyledonous fodder crop, forage crop, ornamental crop, fruit crop, food crop, an algae, a forestry tree, a bioenergy crop or a biofuel crop, *Acacia* spp., *Acer* spp.,

Actinidia spp., *Agave* spp., *Agropyron* spp., *Agrostis* spp., *Allium* spp., *Alnus* spp.,
Alopecurus spp., *Amaranthus* spp., *Ananas* spp., *Apium* spp., *Arachis* spp., *Areca*
spp., *Arundo* spp., *Arrhenatherum* spp., *Asparagus* spp.; *Avena* spp., *Atriplex* spp.,
5 spp., *Camelina* spp., *Camellia* spp., *Cannabis* spp., *Capsicum* spp., *Carica* spp.,
Carex spp., *Carthamus* spp., *Castanea* spp., *Carum* spp., *Cinnamomum* spp., *Citrus*
spp., *Cocos* spp., *Coffea* spp., *Corchorus* spp., *Cotoneatser* spp., *Cucurbita* spp.,
Cupressus spp., *Cynodon* spp., *Daucus* spp., *Dactylis* spp., *Eucalyptus* spp., *Elaeis*
spp., *Eleusine* spp., *Fagus* spp., *Festuca* spp., *Ficus* spp., *Fraxinus* spp., *Geranium*
10 spp., *Ginkgo* spp., *Glycine* spp., *Gossypium* spp., *Helianthus* spp., *Hemerocallis* spp.,
Heracleum spp., *Hedysarum* spp., *Hibiscus* spp., *Hordeum* spp., *Indigo* spp., *Ipomoea*
spp., *Lettuca* spp., *Jatropha* spp., *Lotus* spp., *Lactuca* spp., *Lathyrus* spp., *Lens* spp.,
Linum spp., *Lolium* spp., *Lupinus* spp., *Lezula* spp., *Lycopersicon* spp., *Malus* spp.,
Manihot spp., *Medicago* spp., *Melilotus* spp., *Mentha* spp., *Miscanthus* spp., *Musa*
15 spp., *Nicotiana* spp., *Olea* spp., *Onobrychis* spp., *Ophiopogon* spp., *Oryza* spp.,
Panicum spp., *Papaver* spp., *Petunia* spp., *Phaseolus* spp., *Pennisetum* spp., *Phalaris*
spp., *Phoenix* spp., *Phleum* spp., *Phyllostachys* spp., *Physalis* spp., *Panicum* spp.,
Picea spp., *Pinus* spp., *Pistacia* spp., *Pisum* spp., *Poa* spp., *Podocarpus* spp.,
Pogmania spp., *Populus* spp., *Prunus* spp., *Quercus* spp., *Ribes* spp., *Robinia* spp.,
20 *Rosa* spp., *Raphanus* spp., *Rheum* spp., *Ricinus* spp., *Rubus* spp., *Salix* spp., *Sequoia*
spp., *Sesamum* spp., *Setaria* spp., *Saccharum* spp., *Sambucus* spp., *Secale* spp.,
Sinapis spp., *Solanum* spp., *Sorghum* spp., *Trifolium* spp., *Triticum* spp.,
Triticosecale spp., *Trisetum* spp., *Tagetes* spp., *Theobroma* spp., *Triadica* spp., *Vicia*
spp., *Vitis* spp., *Vigna* spp., *Viola* spp., *Watsonia* spp. or *Zea* spp..

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16. A crop plant according to claim 14 wherein the crop plant is a *Salix* (willow) or *Populus* (poplar) plant.

FIGURE 1- SEQ ID NO. 40

Reference nucleotide position A

↓
TTAGTGCATCCAGGACCTCTGTTCCATGATAAGAAGGTAGGATCACCAAGCCGCTGAGATGACACAG
TAAAGAGAAAACAGTAAGAAAATATTAACATATATCTCACAAACAATCGAATACACATAGCATATGAAAA
TTTTATGCTGCCGACTATGGGGCCATGCTCCACAAGTCAGAGCCTCACTCCATATATGATGCTGGGCAC
ACTTCCAAATCCTCACCATAAAATGCAAGCCTTATGAAGGGCAATTCTAACAGCCTCACTCTTTCAAAA
GCCGTGACGCCGCACACTTGTGACAGCGTGCATTTTGACTTTAATAACCAGTTTATTAAAGTCACGAGA
ACTAGGCTCCTAAATTCAAGAATTAATTTGTATCTATGATCAACTTACCTAGGCTTGACAAAATACACA
ATTGTGAAACCCATTGACAAGGCGAAGCATATCATCCAACAGTGAGATAAGCAATGCCAAGAAAGTCA
TTTCTTCCACCAATCCAGCTTGTAAGTTGAAAGCACAAGTTTCTTCTTGCCATTAAACTGTATGTGTTA
TAGTTGTTACCCAGTGTAACATTTATGACTTCTTTTGCATCAAGATCCACCTCTATCTTCCCATACAAC
TTTCTAAAAGTTGGCAGAGCTGCAGTTTCGCATCCAAACCATGAGGTCCTCCTGATCGCTCAGCTGTTAC
ACAAAATCATATAAGACCAGGTCAAGTCACATACCAATTACTTGAAGCAATTTGCATAGAAAAGAAACAG
GAGAAAAATTTATGGTTCCTCTAGTATATTTTTCACGTTTTAGCAATAGAAGAGGGGAAATGACACGCAAC
AATATCTCATCATTTTAAAGCATTTACACCAAGTCTCTCACGTCTCCAAGGTATAAGCCTAATACTCAAC
ACCTTGGGTTTAAAAAATCAACTCCTTCATGAATGAAAGAATAACTGAGGTCACATCTTCAATACTAAT
CCTGAAGTTGAGGTTAAGCAACCTGAAAATACCACTCTAATAACACAACAGCAACGCAGTTTGAATC
TACCAATGTCCAGAGTGTTATTAACATTATTAAGCCTCTAAAGGTATTTTCCAGGATGAAGTTAGAAC
AGTTATTTAATTAGTTATTTAGTTAGTGATAAGATGAGTTGCTTATATATTAATTGAAGTAATAGTAA
AGGGAGGCTTACAGCTGTTAATGGATCGAGCCTTGACCACCTACAAGACCTCCACCCTGAAAGTTTCT
AGGAAAGACATCTTTACCAACCTTTTCTCCTTATCACTCTTCCAAGCAATTCCTTCTTATTCACTGT
CAACGACTGTTTCAGGCGGGAGAAGCTATAGGTATCATTAAACAACTCCAAGCTATCAGACCACAGGG
TACAATTGCCCCCTCCCCGTTGCAGTATCTTCTGGCTCACAAGAAGTGTATCATTCTCTTTACTCGC
ACTTTTCAACTGTTTCATCACTTCGGCTCTTCACATACCTGATTTATTAGAGCAATCATTAAAAATTATGC
CAAATAATCACCACATAAACTCAATTACATGTGCTTCAACTTTCAGTGAGTAAGCATCCAGTTTATGA
TCATGATAATCATGACAGTTTTCACACTGTTCAATAGTTTTTATAAAATGATGGGTTGCTTTCATTATTA
AACACTTGAAAGAATGTAATTTTCTACCATCAACAAATAGTCAAACACACTATTCTGAGATGAGAAACA
TGATATTAACCACCAATTAAGCATGCATAGAGGAGCCCTTTCCTCAACGTGTAACAACATCCTAGGTCC
TAGGCTGTAACGTCTGTAATTTCTGAAAATCACAACATCGCCATCTTGACTTATAAAATGTGGCAGGA
AAATCTAAAAGGTGCACCTCCTGAACCACATGTTATAATTGGTTCTCTGGACCATCACCTATGATCTA
CATAAATTACGCGCCTGGATAGTCTGAATATCAATGCTCCCAATTTATATGAACAATATACCTCTGAC
CATTATGTAAAAATCTACACATGATTACTTGAACCCATCAGAAATTATATGCTGATAGAGTACATGAAG
TTGATGACATACCTACGATGATTCTGGTAGAAGTTGTCAAGCTGATAGTAAACATAAATAGGTTGCTTC
ATACGCTTAGGGATCTGGCAAGAAAAACAAGAGTTGAGAACAGAAGATCGTTATTTACTGCTTAACCTC
AGGTCATGATGGCTAATTTCTATAATTAGCATAAGTCATGTTGCATGCGAGAAAAAGATATTGGCATGG
GTTTTTTGTAAGGAGTAGCATAAAGTAACCTACTGGCTACTAATACTGCTGATATAGCACCCTTAC
AGCTCTGACAAAAAGGGAATGCCACCAAGTGAACAGATAAACAATGAAGGTATATTGTATAACAGA
AAATAATATTGGCATGGGCTTTTCTTGTAGCTTATAAATCCACAACACTGCTAATAAAGAACATAG
AAAAAGACAACAACACATCAACCATAAATTGCAAGAACAGGACTTACCGTCATTGATATTGTGCATG
TTTTATCAGCAGCGCTTTGTATAAATTGGACTTCATTGCCTCTATTTCCAACCGGAATGCATTCTGTTT
CATACCGTTTAAACAACCTCAACAACCTGATAAAGGAGGATAAACCATAAAAAACCATAGGTGGAAATA
TAACTAGAATTGCAAGGATTTAGGTGACACTAGAGCTCACATCTCGGGAACCAAGCAAGCAAGCAATGC
CGATAGGGATGAAGACAATGGCAACAAGCATGAATGCAGACACTACCTGCACAAAGAGATATATTAGGA
GTTAATAACTTTGAGCACTCATTTGCATCAGACGAAACCAGATAAAAAGAATGATAAAAACTTACCCAT
CGTGGTGTGAGAATTGGCTTGCAAGCAGGAAGTTCTTGTTGAGTAACTTTGAATCTGAAAGAAAACGA
AACATTTTGTAGTTCCATAAAAAATCACATGTACACCCATTACCCATATGTGCTCGTGTAGTGAAAAACAA
TTTGTGAGCTGTGATTGAAACATCAGATAAAGAAGCTGCTCAGCTGTGCTCTCTCTATTTTACTTTTC
TTGTTTTTTTTTAACAGCTACACTACAATAAGATTACAAGTGCATTTTAATAAAATGACCAAAAAATCGCA
GATTTTTTGTCTCTGGCAATACAATACATCCCTATAAATTTAAATGTTTTTCATCCATCTATCTTGCTT
TGCAGGATAACAATTACGCAGTCAGGCAACTATTCTGAACACTGGAAAACATTCTGTTTTCAATCTTAC
TGATAGTACATGAGCATACATGCTTAGACTTAGATGCATGTAATGATAATACAGCCAAAATTAATAAA
ATTCTTATTCGTGTAATGGAAAAATGTCCAATTATCTCATGGCATGTTATAGCTGAGTTTCATTAATAT
CTTGTTTATCAAACCCAAATTTAGTTTCATTTTATTGCTAACAAAGTTTAATAGCCGTATTTCTCTTCAA
AAGGGGAATTTCCAAATATATCTTGATGAGGAATTAAAAAAACAGGTAAGGCTATTCAAAAACGGAA
AGACTAAATGATCAATATAAAGAAAATTAGATTCTTAATATGAAACAAAATAATCAAAAAAGAGCTCAC

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CCAATAGAGAGGCCTGCGTTGATTTGCCAGATTGTTTTATTTGCTATCGGGGTTGATTTGTTAGACG
AAGCCTGCGTTGCCGAGTATATTTAGAGTGACTGTGGCTGTTGATGATCATTTCATGAATTAATATAC
AGAAGTTGATAAATTCGTGAGCAATTATAACTTCTTTAATCAGATCCATTATTGAACTCAATATATC
TGATATACGCCATTTACCATGTATGATTATTTTCAGGTTTTGTATGTATATATATTTTTATGAGCTA
ACTATTAATAGTTATTCTATTAGAATATTAGTAGGTTATTTATCTTCGTTAAAAAATATTCAAGCATT
ATCAACGTGATTTTAAAAATAAAAAAAATTATATAGAGATTGATCTAATATAACTTAGTCAACTTGAA
AAAAAACATAAATTTAATTGAAAAAACTTTAAAGTGATATCTTTTAAAAAATATTAAAGATTTGAA
TCGGCTTAAGTCAACCCATGTGAACATGTAAATCTATGATTTCGAATCATGAGATCGTAATAATATCAT
GAAGAGCAAATTAAAAAAAACATATTGAAATACAATTCTTAATCAACTCAATGTTGAATAATGAAAT
TAAAAAAAATTAATTAAAAAATAACAAAAAATCTGAGTCAACTCAAGTTAACCTGTATCATGAGAC
CAAATAACCTAATAAAAAACAAATCAAAACAAATTATAAAATTCAAATCTCAATCAATCTATGTTGAA
AAATGTAGTTGAATAAAAAACAATTAAAAAAACAAAAAACCTAAGTCAATCTAGTTTAACTCACCAA
ATCCTTGACTCGGGTCATAACACCATGATAACCTCATGAAAAACAATCAAAAAATAAGTATGAAGCTTA
ATTTCTATCAATTCAAATAATAAATGATGAGATTGAAAAAAATTATATTACAAAAATAAAAAATAAA
AACTCGAGTCAATTGCTTTAACTCACAAAACCTATAATTATATTAATAAACATTATAAAAAATAAATT
GAAGTAATGAAGATCAATCACTAATATCTATAATATTAAAAAAAATTATAATTCATGAGGAAGAGGAC
TGTAATTTCCCTTCTTCAATCATCTCTAGGTGATTAAAAATAATTTTTCAATTTTATCCATACTTCTTAT
GTGTCAAGATTTCTTCGCGCAAACAGATGATTTGTCTCCAAAATCCCGCAGTTGCAGCATTTGCCAG
ATTGCGGTTGCGGTGAATTTATAATAAAGAATCAAGCACAACTCCATTGACAGCATTTGCCAGATTGCGG
GTGCGAGAAGTTAATAAAGAATCAAGCACAACTCCATTGACAGCATTTGCCAGATTGCGGGTCGGAGAA
GTTAATAAAGAATCAAGCACAACTCCATTGACCGTCTTTCATAGACATGATTGGTATTTTGCTCTGAA
CCAATTACGAGTCTAATAATTATATGCTTGAGATAAAGGAAGGACGAGTGGTTGTATACATGCTGCTC
GTTTTCTCTATCTCAACGGTCCCTTCAGTATGTATGGGAAAAAAGCAGATCATTTTATTTTTCTTTT
TAAAAACAGCTGTTTCTTGATTGACGTGGTCTCTCTCTGAAATTAATATAATTGAGGGTGA
TTAGTAGTTGACTGAGAAAAAACCCTTCTCTAATCTCTACGATGAACACGAAGCTTTCTCTG
CCATGAACCTTGATAGATGTTTTGAGCCAAAGCAAATTATGCTTTATATGAAGTTTTGATCACTTGGA
TTCTATTCTGTGTCTCAGCTGTGCGTGCAATAACTATTTGTTCTGATCTAGAAATCATGCAACTGTT
AATGAGAATTACACTGCCTCCATTCAATTCATTAATTGCAATTTCTGTGATTAACAGAACAGGCTGTTAT
AAGAGGAAAAATATGGCGAACAAAGGATGCAATGTTGGCGAAGATGGTGGTTTTCTCCGAACACATATGA
TGCTTAACCTTGTCTTTGAAAATCCGTGACCTCTCCCATCTGCAATCACCTCCAAAAATAAATCT
CCGAGGATATGAGTGACAGGAGAATGAAATAGATGCACAGCTGATAGACAACCTACTGTATCTTTCTC
CAGGATAGCTATAATCTGTGTGTCCGCCCTTAAAGAGAGCTATGTATATTCAAATTCATGCGAGG
TTCTTGTTTAATCATATCCATTGGCAGTTTCCAAGAAGGCTTGGATCTAGTTAAAGAGGCCATCAACAG
AACAAGGTACAACGAGAGAATAAAGATGACCACCTGATCCATGGTGTGCTCGCCTAGCGGTGATAAAGTT
AGCTGAGCACGTTTTTAAGTTCAGAAATCCATTCTGGGATACTTACTTTTGGACCCCATTTATGATTGCA
TTTGACAGAGCAGTTCTAAATTTATTTATTTTCTTATTTTTCATATCTTTGTTAATAATTTGGATCTCA
AGTTGATTTTATTTTCTGGTATGGCCTTTGATGAAAAAGGACAACTATTTATACTATTTGTACGTAAT
TTTTTTGGCCATTATTATTAAAAAATCAGAAATCTAGTCTCGAGAGTTTTCTTATAGTTCTACTCTGT
TTTCTTTTGAAGATTTTAAAGTACAAACAAATCCCATGTTCTTCATTGTACGCAGACAGTCGTAACA
TTGTTGAAGCTCTTAACATCATCCAGATTACCATAGTTAGGGCATCTCAAGCAAAGATGATATTTTAA
GTGATATTTTAAATAATATAAATATATTTTTATTATTATATATATTTTAAATAGAAAAAAGCTATTTAA
AAAGCTAATTGTATAAAAAATAAAAAAAATACTTTATTTTTTAATGAATTTGATGTTTAATGTCATC
TTTTTTTATATGGCTGCATTTAATTGGGTTTTTTTTTTTTTTTGTGTTGGTCTTTTTTTTTTATTTTTTAAAGA
CATGTAAGAATATATTTTTTGAAGAGAAAAATGCAATTTCTCATTTTTATTTATTTAGCACTCCTTTAGAGC
ACATGTAAGCAATTTATGAAAAACCATAATATATCTTTATTTTTTTATTTTCAATTTATCACAAACC
CATGGAATTGCTCTTACTGGCCACGATAGCAATACCTACCCACTCTCCTTTCTATGCAAAGGATACGTC
ATAATTACTAATTTTACCTCATCCATTGCTGGGGTTCCAAAGCTAAAAGGTGGATTAATTTCTGTGAT
TTGTGTTAAAAAGAAAAAGAAAAATATATTGTCGAATACTTTATCGTGGTAGTATTTTGGGACCCCAA
ATTTAATGTTTCTCTCTCGACTATTTCCAAGAAGTTTGTCTTTATCTTCAACCAATTACCACTTCGTG
CGCGATAATGGCGACTTGTGCACCAACACTTTTTTCTAAAAAGTTTAAATTTATTTTCTGATTATCTTT
TATTCATAAAAAATCAAATTTCTCATCGAGGAATCTTAAGCGTGTGTTTACACTGCTGTGTGTGTGTG
TGTGTGTGTATCATAAATTTCTATTTTTTTTTTGTACAGAGCAATTAGACTTGTACTCTGTGTGTAT
CCAGGGGCGGAACAGGGAAGGCAAGCAGGCCCGATCCCTATAAAATATTTTAAATTTTTTTTTTATTT
AATATTTTATTATTTAAATAAATAAATTTTTTAATAATATATATTTATTTATTTAGCCTTCCCT
GTAAAAATAAACCTAGCTACGCCCTGTGTGTATCGATTGAACTTTTTCTTTCACACTACAATCAGAATA
TTAAACACGCATCAAGTCGTCCAACAGTCATTGATTCTAAAAAAGAAACGAAGAAATTGTCTGTAA
TTTCGATCGAGAATTGGAAAGTTCTTGCTCATGTACCAATGGAGTGCACCCTCCATATTTTGCCGGAG
TGGCCGAACAGCCATCCATTAAATGGCTAAGTGCCCTTGAGAGAGACAGATTTTCACTTTATATAGCAT
CAGTACTCGTGTGGATAATACGCTCTTCAATTTCTTACTGCCCACTCTTGTATGTAATTTCTGCGTTGC
GTGTTATAGTTTCTTTGACCTGAATAACAGTATCTTGTGGATTTCCCTAGACAAAAGCAATAGTGATT
AACAAATAGGGTGTTACAGTCTAATTATATTTTAAAAACATTTAAATTTTTATAGGTTTTGGATCATTTT

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GCTTGACTGGTTCCCTTTGCTTGACTGCTAGTATCACTACCAGTGGCTCTAGCAGTATTACTCAGTGAC
GATGATGGCTCCTTGGACAT



Reference nucleotide position B

FIGURE 2 – SEQ ID NO. 41

SEQUENCE OF THE WILLOW QTL REGION (ALLELE A). GENETIC SEQUENCE OF XYLD7 IS LABELLED AND UNDERLINED. INSERTION IN XYLD7 GENETIC SEQUENCE IS SHOWN IN *ITALICS*.

↓ Reference nucleotide position A

AGAAGGGATGTGCCAAAGCGATGCAGGGCCTCTGTTCCAATAGGAAGAGAGGGATGTGTTTTAAACATCAAAAGA
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Insertion in XYLD7

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[N]* - repetitive portions

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XYLD7

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TTTGAAAGTGAAAGGACAGGCCAACCAATTTTATTTATGCACAGATTTGAACCAAGACGTGCTGACCAGTTTTAGA
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AACAGTTTATCAACCTACCCGATAATACAAAGCTCGTCAGCTGCCTTATACTGGAGGGGAATCTCCATCAGAGC
AGCTAGAGCAAAAGCAGTTTTCTTTCTCAGAGATAGTTGTGTTTTTGGACATTATTGCAGTGAATTAACGAACTG
CACACAATACATGTTGATAAAGTGCTAATATGTATAAAAAATTAATCAGAATGTTGGATGGAATTCGAGCTTAA
CATTCATTTTGTATCCTGTACCTGAAAATTGTCAAATTCACGTGCTGGGATTTTGTATCAAATCTCTGCATG
TCTTCCCATGGTCCATCACCACTCCAACAAGAATTATTGAAAGCGGGTATGAACTGGTTAAGAATATCATAAGG
TTACACATTGTAATAGCTTTTTCATAAAAGAAACGGCAACACATTTTCAGTATAAACACGACACCATTTTCTGGCAT
TGTTAAAAATCTGATGATTGATGTCATCAGATTCAACTTTACACCCCTTACTGCTGATACAGGTTGACTGACATG
TTCCGACACTAAACAGGTAACTCGTTGCAATAAAATAATGTTCTGTGTGGACCGAGTGTTTTTTCACATACAAAT
GCAATATCAGGCTAGCATGACAAACAAATAATTGAATAACAAGCTGGTTATGATGCAATATAAATCTGTATACGT
ACTAGGACCTAAAAGTAGATTGTTAACCCCTTATGATTCATTTGATATTTTACAAGTGTGACATCACTAAATG
GGATCACTTCTCAATAAATAAAGACAGCCATCAGTTAACACCTTCTTTTTATGCAACTGCCCAAGTCATATACA
TCTATCTAGGCAAGTCATGTAACAACAGAAGCTCTAAAAAGTAATAGTTCTAATAAGAACCCTAAGTTTGTCAAT
TAATTAGATGAAAGTTATCATATGACCATAGGATATATTTTCTATGAAAGTTAGTCTAAGCAAGTATAAATGATT
TGCATTTATCTTTAAGGCTCGACCTTGACCTCAACAATTGCCCTGATTGTTTGCTCTTCTTGAGACTCATTCTC
CATCGCTGTATTACACTTCTTGTGACCTTCACAGTAAAGAGACTATTACTTCGATTACATATGCATCCATAC
ATACAGAAACAAACACATGCAAGCATGCAGGAAAGGAGAGAGGATTTTAAATTTCAAACCTGGCCATCTGCAATG
ATGAGCAATACATGATATTGACCTTTACTTTTTGTCCACAATGTCGATTGCAGCCTCAATCACCGGTCCATACGAA
GTTGGTCTTTAAACCAAAACATATATATTTGTGAAGATTTATTTGACTCGAGAAATAAGTAAACACAAGAATC
TTTGTAGAAGTAATGTTTCAGCCATCATTCTAATTAAGTAACTAAGGAGTTGATAAAAGACCGAATTGCAGCATC
AAATAATCAAAGAGCAAACCTGAAAGTCGCAAGTTTGGAAACAATCTTTTTGTAGCATGCCAGGACTTCTTCAAAA
CCATGGCAAGATGAATGATCACTGTGAAAGCTAAACACCTCTTGATCATGAGTGGTGGCTGTATAGATATAATAA
ATCAATCAATTCGACAGCTGAATTATAAGGGGCAAACTAGAAACAACATTGTTAGAATCAACTTCCAGGGACT
GAACCTACCATCGCCAAAGCCAAAACAAGGAATGAGGTGTCTTCATCAAAAGGAGCCATCGTCTTTCCAATAAT
AGAGATGGCTTTTCTCGTATGGATTAGGTGTGTCTCCGATGGCATGAAGGCAACGTTTATTGAATGAGACTTGGCC
TTTAAATGAAACCAGCACATTGACATGCATGAGAGACAAGCCAAAACACAAACCATTTCAAAGGAACAGAAAA
CACGAGGATATAATTTAAATAGCCTTTTTATAACCATTCCAGTCTTAGTATATGATTGAATCATCTCTATATAT
TATTAGATTGCCTCCTTAGGTTTTTAAAGATTGGTTTTTTCAGCTCTGGATACTTATTTCAACTTCACGGAAGTCT
CAAAATCCAAATTCCTGAATAACTGATAAAGTAGAACACAATGCTTAAGGTACAAATCGACGATAGGATGACTTC
ACTTGACATACCTGTCCATTCAATTGCTTTTAGTGAAATCAATTCCAACAATGAGATTGATGATTCCAGTCCAG
CTTCCCTCAAGGCTTTCGTAACCTGTAAAGAGGGGGGAGGGGGGGGACTGTGAGAGTTCAACCAGGTAGCCATTT
TTATTCCTATACTGAAGCAACAAGCTTCTGTTATGAAATTACGTACATTGCTAGCAAATGATTCCATTCTTAA
TAAACAAGCACTTCAAAACAATACCTAACGTTTAAATGCCAGAACACATGGTGAACGTTTGCAGAAAGTTTACAGA
AAGCTCTGCGTGGTTTGAAGTCGCAACTTGCACCTCACCGCTTAACTAGTGAAGTGAAGTGAAGTGAAGTGAAGT
CGAATGTATTTCTTTTTTGCAGGATACCGGTCTAAATGACTATAAAGTTAATAAGAATACAATCTATTATTATT
ATT
TTACCTAACTTTTGCAGTGTATTATATTCAAAATGAATCGTGAATTTTAAACGACTGGCTTCTCTATAAAAAAT
AACTCTGAGAAAAAATCTGAACGAGAAATTTCACTGTAAACACATGCGTAGAAAAGAAAAAATAATTGATGA
AATTTGAGAATAAAAACGGACTATTTTAATTATTTACCTGTTTTTTTTTTTTTTTTTATTTAATAATATAAAAAA
TCAGCCCGTCAATTACTTGAACAGTTTCAGTACTGCCTGGGGTCACCAATAATAATTGATGAATAAAAAAGCTTG
CTTTCTTTTATTATCTTTATCCAACCTCCACGTTTCCGTTGAGTGAAGAAAGAAACCGTGTGACGACGGGATGA
CCTACAACGCGTTCGCTTTATTGCCAGTCGTTGTCAATTATGGCCCTCTTCTCGCAGGGTTTCAAAAAA
TATTTTATATTTTATTTTAAATTAATTTTAAATGAGTTAATATCATAAATAATTTAAAAATATATATTAT
TTAATATATTTTAAATAAAAAATCAATTTTCAAAACAAATTAATCAAACAATTAACATATTCAATTAATCACGT
GAGATAATTATTTATCTAGGTAGCGAGAGGCCTAGAGTACAGTCAAACTTTGAATACGGCCAACCTAAAAA
CAAGACTGGGTCAAATTAAGTGCATACATCAATATTTTTTCTCTTAAATATATATAAATATTTTTTATTTA
TAAATAAACACATTAACTATTAAAAAATAGTAATTTAATATATTTTCAATTAATAATATTTTAAACACG
CATAAACAACTTCCAAACACCAAAATAAATAGTGGCTAAGTAGTTATATCATTTTTTTTTTTTACTTTGGTTTAA
AAAGATTGTACTCTACCGTGATAATTGGGAGTTATTTTAAACAATGAGTGTTATTTTTATTTTAGTAGTGATTT
AAGAGTCGGTTCGATTAAATTTTTTCAAATTTTTGTTTTCTCAGAAAAACCATTAAATTAATATTGTTTTAATG
TTTTTTGGTGTTTTAAGATGTTGATGTAATAAATAAATAATTTTAAATAAAAAACATTCCACCTTAATTT
CAATATACATAATCTCCAGTACAAAGATGCATAAGTAGTGTTTTTGTGTTTTGAAAAAATAAATGTTTATC
AGTGATGGAGTGAATAGAAATGATTGTTTTTAAATTTATTTATTTAATAACAAAAAATAATATGTTACCAG
TTTGGGTAAATATAAATAAAGACCTGGCGATACCTTGATATGTTGAATTATAATTTTTTTTTTGAATAA
CAACATTTGAAAGCAAACGGAACTTTTGGAGTTGAGTGGAGTGGAGTGTGCAAGCTGGAAGAAGATTCCCCCG
AGATGCCGTGAGAGAAAAGTCAATCAGAAAAATTGACTAAGCTTTTTGTATTTTCGGTTTAAATTGACATCAGCG
AGAATTTGAATTTTAAAAAATAAATAAATTTGTAATGTATCCGACAGATGGGGGTGCGATACAATTAATTA

TAATTATCTATTCTAGAAGAAAAATATAAGCAAACTTCCAGGAAATGAAAGAAAATAGTTATGAGGCTCATAC
CTGTTCTAGGGAAGTGAAATTATCAGGGATGAACTGTATTTCTGCTTGATGGATTGCTTCTTATCCAATTTGGA
ACCAGCCTTTGCTTGACTTTTAGAATCACCGCCGGTGGCACTAGCAGTATTACACAGTGACGACGGTGGTTCGCT
GGACAT



Reference nucleotide position B

FIGURE 3A

Genomic sequence of *Populus Xyld1* – SEQ ID NO. 4

ATGAGTAGCCACACGGGCATCCTCCAGTAATGGAGGCAACGGATCGGGTGATTCTGGTGCTCCAAGAAGG
 AATTCAAAGCGACCCAAATGTGATTCTCTCTTTACTTCTCGTTTTTTTTTTTTTTTTCTATTTTGGGCA
 AATTCATGTCTGCCCTCTTGATCATGGTGTTAGTTGTGTTTTTAAATTGCAAAGTTTTGAACCCGT
 CCTAATTTTCTTGCTTAGTTTGTTCAGAGACTCAGGTATTTGAATGTTTTTGGGATCACTAGTGGGT
 TTATAGGCATCCATGTGGAGGTTTATGCATATTTTGTGAGGTTCTTGTTATTTTGATTTCGCTGTTGGT
 TTTGTTGCATGAGAGTGGTCGTGTGAGCTCTTTTTTGTATTATTTGTTTCATATTAAGAATCTAATTTT
 CTTTATATTGATCATTTAGTCTTTCCGTTTTTGGAAATAGCCTTACCTGGTTTTTTTTAATTCCTCATCAA
 GATATATTTGGAATTTCCCTTTTTGAAAGAGAAATACGGCTATTAACTTTGTAGCAATAAAATGAAC
 TAAATTGGGTTTGATAAACAAGATATTAATGAACTCAGCTATAACATGCCATGAGATAATTGGACATT
 TTTCCATTACACGAATAAGAATTTTAGTAATTTTGGCTGTATTATCATTACATGCATCTAAGTCTAAGC
 ATGTATGCTCATGTGATCTACAGTAAGATTGAAAACAGAATGTTTTCCAGTGTTTCAAGATAGTTGCCTG
 ACTGCGTAATTGTTATCCTGCAAAGCAAGATAGATGGATGAAAACATTTTAAATTTATAGGGATGTATT
 GTATTTGCCAGAGCAAAAAATCTGCGATTTTGGTCAATTTTATTAATGCACCTGTAATCTTATGTGA
 GTGTAGCTGTTAAAAAACAAGAAAGTAAAAATAGAGAGACACAGCTGAGCAGCTTCTTTATCTGA
 TGTTTCAATCACAGCTCACAAATGTTTTTCTACTACAGGACACATATGGGTAATGGGTGTACATGTGA
 TTTTTATGGAATAAAAAATGTTTCTGTTTTTTCAGATTCAAAGTTTACTCAACAAGAATCTCTGCTT
 GCAAGCCAAATCTCACACCAGATGGGTAAGTTTTATCATTTCTTTTTATCTGGTTTTCTGCTGATGCAA
 ATGAGTGCTCAAAGTTATTAACCTCCTAATATATCTCTTGTGAGGTAGTGTCTGCATTCATGCTTGTT
 GCCATTGCTTTCATCCCTATCGGCATTGCTTGCTTGCTTGCTTCCGAGATGTGAGCTCTAGTGTCCACC
 TAAATCCTTGCAATTTCTAGTTATATTTCCACCTATGGTTTTTTATGGGTTATCCTCCTTTATCAGGTT
 GTTGAAGTTGTTAAACGGTATGAAACAGAATGCATTCCGGTTGGAATAGAGGCAATGAAGTCCAATTT
 ATACAAAGCGCTGCTGATAAAACATGCACAATATCAATGACGGTAAGTCTGTTCTTGCAATATTATG
 GTTGATGTGTTGTTGTCATTTTCTATGTTCTTTATTAGCAGTGTGTTGTGGATTTATAAGCTAACAAGGA
 AAGACCCATGCCAATATTATTTTCTGTTATACAATATACCTTCATGTTATTGTTATCTGTTCACTGGTG
 GCATTCCCTTTTTTGTGAGAGCTGTAAGTGGTGCTATATCAGCAGTGTATTAGTAGCCAGTAGGTTACTT
 TATGCTACTCCTTACAAAAAACCCTATGCCAATATCTTTTTCTCGCATGCAACATGACTTATGCTAATTA
 TAGAAATTAGCCATCATGACCTGAGGTTAAGCAGTAAATAACGATCTTCTGTTCTCAACTCTTGTTTTT
 CTTGCCAGATCCCTAAGCGTATGAAGCAACCTATTTATGTTTACTATCAGCTTGACAACCTTACCAGA
 ATCATCGTAGGTATGTCATCAACTTCATGTACTCTATCAGCATATAATTTCTGATGGGTTCAAGTAATC
 ATGTGTAGATTTTTACATAATGGTCAGAGGTATATTGTTTCATATAAATTGGGAGCATTGATATTGAGGA
 CTATCCAGGCGCGTAATTTATGTAGATCATAGGTGATGGTCCAGAGAACCAATTATAACATGTGGTTCA
 GGAAGTGCACCCCTTTTAGATTTTCTGCCACATTTTATAAGTCAAGATGGCGATGTTTGTGATTTTCAA
 GAATTACAGACGTTACAGCCTAGGACCTAGGATGTTGTTACACGTTGAGGAAAGGGCTCCTCTATGCAT
 GCTTAATTGGTGGTTAATATCATGTTTCTCATGATGATAAAGCAACCCATCATTTTATAAAAACTATTGAACAGTGT
 GAAACTGTCTGATTATCATGATGATAAAGCAACCCATCATTTTATAAAAACTATTGAACAGTGT
 GAGTTTATGTGGTGATTATTTGGCATAATTTTAATGATTGCTCTAATAAATCAGGTATGTGAAGAGCCG
 AAGTGATGAACAGTTGAAAAGTGCGAGTAAAGAGAATGATACAAGTTCTTGTGAGCCAGAAGATACTGC
 AACGGGGAGGGGGGCAATTGTACCCTGTGGTCTGATAGCTTGAGGTTTGTGTTAATGATACCTATAGCTT
 CTCCCGCTGAACAGTCTGTTGACAGTGAATAAGAAGGGAATTGCTTGGAAGAGTGATAAGGAGAAAAG
 GTTTGGTAAAGATGTCTTTTCTAATAAAGTTTCAAGGTGAGGTTCTGTAGGTGGTGAAGGCTCGATCC
 ATTAACACGTGTAAGCCTCCCTTTACTATTACTTCAAATTAATATATAAGCAACTCATCTTATCACTAA
 CTAAATAACTAATTAATAAAGTCTTAACCTTCATCCTGGAAAATACCTTTAGAGGCTTTAATAATGTT
 AATAACACTCTGGACATTGGTAGATTTCAAAGTGCCTTGCTGTTGTGTTATTAGAGTGGTATTTTTCAG
 GTTGCTTAACCTCAACTTCAGGATTAGTATTGAAGATGTGACCTCAGTTATTCTTTTATTATGAAGGA
 GTTGATTTTTTAAACCCAAGGTGTTGAGTATTAGGCTTATACCTTGAGAGCTGAGAGACTTGGTGTAA
 ATGCTTAAATGATGAGATATTGTTGCGTGTCATTTCCCTCTTCTATTGCTAAACGTGAAAATATAC
 TAGAGAACCATAAATTTTTCTCCGTGTTTCTTCTATGCAAATTGCTTCAAGTAATTGGTATGTGACTG
 ACCTGGTCTTATATGATTTTTGTGTAACAGCTGAGCGATCAGGAGGACCTCATGGTTTTGGATGCCAAGT
 CAGCTCTGCCAATTTTTAGAAAGTTGTATGGGAAGATAGAGGTGGATCTTGATGCAAAAGAAGTCATAA
 ATGTTACACTGGGTAACAATAACACATACAGTTTAAATGGCAAGAAGAACTTGTGCTTTCAACTA
 CAAGCTGGATTGGTGGGAAGAAATGACTTTCTTGGCATTGCTTATCTCACTGTTGGGATGATAGCTTCG
 CCTTGTCAATGGGTTTCACAATTGTGTATTTGTCAAGCCTAGGTAAGTTGATCATAGATACAAATTAA
 TTCTTGAATTTAGGAGCCTAGTTCTCGTGACTTTAATAAAGTGGTTATTAAAGTCAAAATGCACGCTGT
 CACAAGTGTGCGGCTCACGGCTTTTGAAGAGTGAGGCTGTTAGAATTGCCCTTCATAAGGCTTGCAT
 TTTATGGTGAGGATTTGGAAGTGTGCCAGCATCATATATGGAGTGAGGCTCTGACTTGTGGAGCATGG

CCCCATAGTCGGCAGCATAAAATTTTCATATGCTATGTGTATTTCGATTGTTTGTGAGATATATGTTAAT
 ATTTTCTTACTGTTTCTCTTTACTGTGTCTATCTCAGGCGGCTTGGTGATCCTACCTTCTTATCATGGAA
 CAGAGGTCTGGATCGCACTAA

FIGURE 3B

Genomic sequence of *Salix* Xyld1 allele A – SEQ ID NO. 5

ATGAGTAGCCACACGGCATCGTCCAGTAATGGAGGCAACGGATCGGGTGATTCTGGCGTTCCAAAAAGG
 AATTCAAAGCGACCCAAATGTGATCTCTTCTTCACTTTTTAGTTATTTTTGCTATTTAGGCAAACCTC
 ATGACTGCCACTCGTGATTATGTTGTTAGTTTTGTTTTAAGTTGCTAAGTTTTGAACCTTGTCTTAAA
 TTTCTTGCTAGCCTGTTCCATAGACTCAGGTTTTTATTTCTTTCTGGGATCACTAGTGGGTTTTATAG
 GCATCCACGCGGAGGTTTATGTATATTTTTATGGGTTCTGTGATTTTGATTTGCTGTTGGTTTTGCA
 TGAGATTGGTTGTGTGAGCTCTTTCTGACTATTTTTATTTTCATACCAAGCATCTAATTTGCTCTATATT
 GATCATGAAGTCTTTCCGTTTTTGGAAATATCCGTGCCTTTTTTTTTATTCTCAAAAAATATATTTGG
 AAATCCCCCTTTGAAAGAGAAATATGGCTGGCTATTAACTTTGTTGGCAATAAAATGAATTAAATTG
 GGTTCGATAACAAGATATTAATGAAACTCAGTAATTGGACATTTCCATTACATGAATCGGAATCTTAG
 TAATTTTGGTTGTATTAACATTACACACATCCAAGTCCAAGCATGAATGCTCATGTGATCTACTTTAAG
 ATTGAAAACAGAAATGTTTCTAGTGTTTCAAGATAGTTGCCTGTCAGCGTAATTGTTATCTTCAAGCAA
 CATAGAGGGATAGAAACATTTAAATTTATAGGGATGCATTATATTTTCCAGAGCAAAAAATCTGCAAT
 TTTTTTTCATTTTATTAATAATACACTTGTAATCTTATTGTAATGTAGCTGTTAAAAACAACAAGACAG
 TAAAAATAGAGAGAGACCGCTGAGCAGCTTCTTTATCTGATGTTTCAATTGCAGCTCCCAAAATGTCT
 TTTTCACCACACAAGCACATATGGGGTGACGTGTGATTTTCAAGGAACTAAATTGTTTCGTTTTCTTT
 CAGATTCAAAGTTTACTCAACAAGAACTTCTGCTTGCAAGCCAATTCTCACACCACGATGGGTAAGTT
 TTTATTATTCTTTTTAACTGGTTTTGTCTGATGCAAATGAGCACTTAGAGTTATTAACCTCAAATATAT
 CTCTTTGTGACGGTGGTGTCTACATTCTGCTTATTGCCATTGTCTTCATCCCTATCGGCATTGCTTGC
 TTGATTGGTTCCCGAGATGTGAGCTTGAGTGTACCTAAATCTTTGCAATCCTAGCTATATTTTCACCT
 ATGGTTGTTTATAGGTTATTCTCCCTTTATCAGGTTGTTGAAGTTGTTGAACGGTATGAAACAAAATGC
 ATTCCGGTTCTAAATAGAACCAATAAAGTCCAATTTATACAAAGCGACGCTGATAAAACATGCACAATA
 TCCATGACGGTAAGTCTGTCTTGAATTATTATGGTTGATGTGTTGTCAATTTCTATGTTCTTTATT
 AGCAGTGTTTGTGGATTTATAAGATAACAAGGAAAGACCTATTCCAGTATTATTTTCTGCTATACAATA
 TACCTTCATTTTATTGTTATCTATCGACTAGTGACATTGCCTTTTTTGTGAGAGCTGCAAGTGGTGCTGT
 ATCAGTAGTGATTAGTAGCCAGTAGGTTACTTTATGCTACTTCTGACAAAAATCTACACCAGTATCT
 TTTTCTCTCATACAACGTGGCTTCAATGCTAATCATAGAAATTAACCTACCATGACCCGAGGCTAAACAG
 TGAATAATGATCTTCCATCCTGTATTCTTGTTTTCTTGCCAGATCCCTAAGCGTATGAAGCAACCTAT
 TTATGTTTACTATCAGCTTGACAACCTTCTACCAGAATCATCGTAGGTATGTCATCAACCTCGTGACTC
 TATCAGCTTGTAATTTCTGACGGGTTCAAGTAATCATGTCTAGAATTTACATAATGGTTCTAGGTATAT
 TGTTTCATATAATCATATTGGGGGCATTGATATCCAGGACTATCCAGGTGTGTAATTTACGTAGATATA
 GCGCAGGATAGAGAACCAATTATAAAATGTGGTTTCAGGAAGTGCGCATGCTTAATTTGGTGGTCAACA
 TTATGTTTCTCATCTCAGAAATAGTGTGTTGACTATTTTTTGATGCTAGAAAATTACTCTCTTTTCATGT
 GTTTAATAATGAAAAGCAACCCATCAATTTATAAGATACTAAAATTAGATCAAATCAGAATTGTCAAAA
 CTATTGAACAGGCTGTGAACTGTGATGATTACCATGATCATAAACTGGACGCTTACTCACTGAAAAGTT
 GAAGCACATGTAATTAAGTTTATATGTGGTGATTATTTGGCTTAATATTAATGATTGCTCAAATAAATC
 AGGTATGTGAAGAGCCGAAGTGATGAACAGTTGAAAAGTGCGAGTAAAGAGAATGATACAAGTGCTTGT
 AAGCCAGAAGATATTGCAATGGTAGGGGGGCAATTGTACCCTGTGGTCTGATAGCTTGGAGTTGTTT
 AATGATACTTATAGCTTCTCCCGCCAGAACCAGTCATTGACAGTGAATAAGAAGGGAATTGCTTGAAG
 AGTGATAAGCAGAAAAGGTTCCGTAAAAATGTCTTTCTTAAAACTTTTCAGGGGGGAGGTCTTGTAGGT
 GGTGCAACTCTCAATGAATCGATACCAGTAAGCCGCCCTCGACTATTACTCATCTGGTCAAATTAATAT
 ATAAGCAACTCCTCTGATCACACACTAAAGAAGTGTCAACTTCATCCTGAAAAATACCCTTAGAGGCT
 TTAATAATGTTAATAACACTATGGACATTTGGTATATTTCAATACTATGTTGCTGTTGTGTTTATTAGA
 GTTGTATTTTCAGGTTGCTAACTTCAACTTCAGGATTATTTTAGGTGTGACCTCAGTTATTCTTTTCATT
 CATGAAGGAGTTGATTTTTATTAAACCAAGGTGTTGAGTATTAGGCTTATAAAATGATGGGATATTGT
 TGCGTGTATATCCCTCTTCTAATGCTAAAATGTGAAAATATACTAGAGAACCATCAATTTTTCTCAC
 TGTTTCTTTTCTATTCTATGCAAATTACTTCAAGTAATTGGCACGTGACTGACTTGGTCATATATGATT
 TTGTGTAACAGCTGAACGAGCAGGAGGACCTCATGGTTTGGATGCGAACTGCAGCTCTGCCAACTTTTA
 GAAAGTTGTATGGGAAGATAGAGGTGGATCTCGAGGAAAAAGATCATAAACGTGACACTGATGAACT
 ACTATAACACATACAGTTTAAATGGCAAGAAGAACTCGTGCTTTCAACAACAAGCTGGATTGGCGGAA
 GAAATGACTTTCTTGGCATTGCTTATCTCACTGTTGGGATGATAAGCTTCGCTTTGTCAATGGGTTTCA
 CAATTGTGTATTTCTGCAAGCCTAGGTAAGTTGATCACAGACACAAATTTGAATTTAGGGTTCTTGAAA
 GAGTGAGGCTGTTAGAACTTAGAATTGCCCTTCATAAGGCTTGCAATTTTATAATGAGGATTTCCAAGT

GTGCCCAGCATCAGACTTGTGGAGCATGGTCCCATTAGTCGGCAGCATAAGATTTTCATATGCTGTGTA
TTCGACTATTTGTGAGATGCTATTAAATAGATAACTTTTGATATTTTCTAACCTTTTCTCTTATTGTAC
CATCTCAGGCGACTTGGTGACCCTACCTTCTTATCATGGAACAGAGGTCCTGGATCGCACTAA

FIGURE 3C

Amino acid sequence of *Salix* Xyld1 allele A - SEQ ID NO 27

MSSHTASSSNGGNGSGDSGVPKRNSKRPKYSKFTQQELPACKPILTPRWVSTFMLIAIV
FIPIGIACLIISRDRVVEVERYETKCIPVLNRTNKVQFIQSDADKTCTISMTIPKRMKQP
IYVYYQLDNFYQNHRRYVKSRSDQLKSASKENDTSACKPEDIANGRGAIVPCGLIAWSL
FNDTYSFSRQNSLTVNKKGIAWKSDKQKRFKGNVFPKNFQGGGLVGGATLNESIPLNEQ
EDLMVWMRTAALPTFRKLYGKIEVDLEEKEVINVTLMNYNTYSFNGKKKLVLSTTSWIG
GRNDFLGIAYLTVGMISFALSMGFTIVYFVKPRRLGDPTFLSWNRGPGSH

FIGURE 4A

Genomic sequence of *Populus Xyld2* -SEQ ID NO. 6

ATGACGTTAGGGAGAATAGCTCTGGCACGCATCCCGGCGACTAGGTGCAAAATACACAGTCTCTTCTCT
 GCTCCACACTCGTCTTCTTCCACGAATCGCACCTCTCCTCCACTATCTCGCCACGTAACCGCTACTCAT
 CTTCTTTTACTTGCGCATAAGCATCAATAGCTTTCATCCTTGTGTTGCTAATTGAATACAGCGATCGCG
 ATTTTGAATTATCTAAATTTTGTTTAATTCATGTTTTAATCGCTTAGAAATAAGTAGTATTTTAGTAAT
 TACTGGTTC AATTGATAAAATAATTTGTTTCATTAATGTTCAATGTAAGTATAATCTCTGTTTGAATGTA
 TTTTGTGTTTCTGGTATTGTTAGTTGCGAATTCAGCTAGGTTTAAAATTTGTTAATGTTTTTATGGCAG
 ATGAGCATGAAGAGTGAAAATCTGGTTTCGAAGCTAACTAGTTCTGGTCTATTAAAGACCCAGGGTCTT
 ATCGATGGAAAATGGGTTGATGCAAATGATGGTGACACTATTAAGGTCTGCCATTATTGTGCGTGTGTT
 TGTTTGTAAATTTTGTCTACTGCGGCTACTAGTTTGGGTATTGTTTCTTTCTTTGTACACAAGACAT
 CACATGTATGTGTTCTTTTCATGGAATGACAGGTTCTCAATCCGGCCACGGGTGAAGTTGTAGCTATTG
 TCCCATGCATGGGCCAGAGCGAGACGAATAATGCTATATCATCTGCCTATGATGCATTTAGATGTAAGA
 AACTTCACACTGAACCAACCTAACGTTTCAGTAAATGTATTTATGCTAGTTAACCTTCTCCTACTGGCG
 CTATCATTTTCTAAGTTTGAATTTTGTAGAGGAATATGGTTTATTTTGCATGCGAGGATTATCTTTC
 AGTAGTAATAGGGGAATTGCTAGTAGAGGATTGGTCATGGAAGTGAGTTATTGCTGTGCTGTCTTTG
 TAGGTTAGAATCCATGCTTTCAGAAGGTAATGGCACTTGGATGTCTCTTTTACAGTATGTCAACCTTAT
 TACTGAATTGGAGAGCATATATACGTTTTTTTCTGAACTCATGTGACACCATCTTGGTTATTCTTTTCA
 AAGAGTTTGGATTTTCATGACAATTGGGTGAAGTCTTATTTTACTACATCAATCCACTATTATTCTTTTC
 AATTGACCTGCAACTCGCACCTGCTTTATAGCCCGCACCACGTAACCTAAGTCTACAATACATTAAATA
 CTTCAACTCATACTCAAACGCTTGTGGTATTATGATAATAATCACTGTAAACATGCAGTGGTGCACAC
 TCTTGAAATATTACTTCCAAGCTTCTATGTGTTGCATTTTATTCCTCTTATCCTAGCTTTTCGAGCA
 CAATTTGTTGGTAATTTACTGTCCTACAGATCATTTATTTAGCTGTCTCTTCGAGAGTTATGTGGTACT
 CTAGAAGCAAAGAGTGAATGGAATGGATTAAATCGAGTACCAATCTAGTTTTTATGACTTACAAGTTGA
 TATGCCCTTCAAAGACTTACATAGACCTTTGCATAGATACAATCTTAATAGGATCTACTCATCTGACTT
 AAAATATGGAATCTCTTGTTTTTTACCATAAGCTTGCTAAACTCCTCATTGTTTATATGGATTTTTCT
 TGTTTAGCTGTAATACTAGCATATTTTGTATGGCCCTTTTCTGATATAGCTTGACATTGTTTTTTTTTT
 TTTGATTTATATCTTTTGTCTTACTGGACTTCAAATGATATTGAATTTTTTTTTTAAAAATCTTGCTGA
 TGGTTGCAACATGTTTATTGTCTTTTATTTGGCCAGCATGGAGTAACTCACTGCTTCTGAGAGGAGCC
 AACGTATACGAAAATGGTATTTAACCCTTCCAATACGATCTTATTAAATTATCTGTGTTGTGAATGTAA
 ATACTTCCAAATTAATCAAATAGTTGAAAATAACTGTGTTGTATTGGTAGAGTATTATGGTTCTCTACA
 CTGAATCTCATATGATTCTTTCCACCTGTATTGTAAGGTATGACCTACTAATTGCTCACAAGGAAGAGC
 TGGGACAATTAATAACCTTGGAGCAAGGGAAACCTCTGAAAGAGGCCATGGGTGAGGTATCTCATCTCA
 ACTTTGCTTTTCGGAATTAAGAGATAAGCGTTAACCCTACATTGTGTTACTGGTCAATTGTCAAGCAACA
 TGTGATCCAAGTCTCTAATAACAGGTTAGCTATGGAGCTAGTTTTATTGAGTTCTACGCAGAGGAGGCG
 AAACGTGTATATGGAGATATAATTCCAGCGACTCTTGGTGATCGTTCGGTTATTTGTTCTAAAGCAGGTG
 GCTATAACTGTTTGTGATATATGAAATCCTGTTAATTGCAAAATACGAGTAAATTAGTTCTTCCGACAG
 CCTGGCTACTCCTATAGACCTCGATAATTTGCCCTTGGTTTGGGTCTCTTTACAAGGCCCTTTCAAAT
 GTGTTTTAATTTCTGGCACCAGCATGTATGTTTAAATGCACCAATATTTGTTAAACCACATAAACTCA
 TGATTTTTAGGAATTAATACTCGGGTTCAATATCTATGAGAAGAAGAGGGCCCGAGATCTTGGGACA
 CATTCTTGCATGAAGTGTGTTTTAGTCAACTTTATCCTGGTAGCGGTCCAGAAATCTGTTTCTTAATG
 ATCTATCTTGATGAATAGTTCTTGTGCAACTTTTCTTCTTTGAGCTGTTTGCATGGCTTTGATAATTT
 CCCAGCGTTGCTTGTCTTGTGCAATCCATTTATTCAGCTATTTATCCAGCAATCTTCATGAGTTTTTG
 CAGCTGTAGGTGTTGTTGGGGCAATTACACCTTGAACCTTTCCATTGGCAATGATTACTAGAAAAGGTG
 TGTTCAATTTTGAATGATTCTGTGCAAGAAAGTTAACTTTTCTGGTGATGAGTTTGTGTTGAAGA
 ATAACATACTTTTTTCTCACTTGATAGGTTGGTCTGCTCTTGCTTGTTGTTGTACAGTTGTTTTAA
 AACCTCTGAACTCACACCTCTCACAGCTTTAGCAGCAGCTGAGTTGGCCCTTCAAGCTGGAATACCAC
 CAGTGAGTCTCAAACCTTTTTACGTGCACAGTGGAAGTTTCTTAATTATTTAGGCCGTGTAAGATGCAAG
 TGCTTGGATATAATGTGGCCTTGGTTGTCTTTGTAAATTTGTGTCTGTTAGACATTGATGATAAAGTTG
 ATACTTTATGGTTGTTTCAATGAGAAAGACTTATCCTCTGCGATGCAATGAAGTTTTTGGAGTAAGTTT
 TGGTTGGAACTAGGATACTTGTAAATGTTTTATTATAGTCTCAGCATCCAAAAATATTCTATTATCTGG
 TTGTGCAAGAAGAAGCTGCAGCAAGCTAACATTTAGAATATTTACTAAAGAGTGCTTAAAAAGTAAGGA
 GGGATGGGAATGTAACATAATAAAATCCAAGTATCATCCCATGGGTATTAGATGTTTATCACAAGATTC
 CACTAAGCAAAGTACTGAAGAAAAATGCCCTTGTGACTGTAAATTGAGTGACTTTGTGTTGCAGGA
 ACACCTACTGAAGAACCACAATTGACAAATAGAGTGAAATGCTCTTTGTATTTTATATCTCATCATAC
 CTGTGTTATGATTGCTAACCTATGCTAATAATCAGTTGAGCATCCTTACCGAGCAATGAAACAGAAAAT
 ACCCATCACTGGCAATCTTTTTAGCTCCGTTCTGGTTTAGCATGTCTTGCATCACCAGGACAACAGCAG
 GATCTGGTCTATCGTCTGATCAAACCTGCTTTCTGCTTTGAATGACATAATGATGGAATGAATGAAGCT

TTTTCTGGTCTGCTTTTGTAGATGCATGTCATACACAATTGATGTGTTATATTAGCTAATATGAGTTCA
AATTTGTTGGAATTCTGTTCAATTTGTTTTTAATGGTTTTAATTTCAATATTTAGGGTGTCTGAATGT
GGTTATGGGGAAAAGCTCCTGATATTGGTGATGCTTTACTAGCAAGTCATGAGGTTTTACACCTTCCTC
TATTTCTTAAACCAACCTTCTCTCTCTTTGACAACATGGCATTGTCCTGGCCAGAGTAGTTGGATAT
TCAATGACATAATGTTGATATTCTTGCTTTTATACATCTGATTGAGGTAAGAAAAATCACTTTCACAGG
ATCAACAGCTGTGGGAAAGAAGTTGATGGCTGGTGTCTGGAACAGTTAAAAGGGTATGCATTGGATG
CAAAATGAATCAATGTGATGATGTTTCAGAAATCATCTTATGGCTAATTGTCTTTTCCCTTAATCTTTC
TAGTTATCTCTGGAACCTTGGCGGCAATGCACCTGCATAGTATTTGATGATGCAGACCTAGATGTGGCA
GTTAAAGGATCAGTAAGTTAGAGGGGTTCCCTGTGCATGTTTATTTTGATTGTGGTATTGTGCATGGATA
TTTCTGAGTGCCATTTAATAATGTTTACTTTACATGTTTAGACATATCAGATGGACACACTAAGCTTCC
TATCTGACTGGAATGGATTTTGGTGCCGAGGGTGTAAATTGTTGGTTAGACATGGGGGTCCATGTCTC
CATTTTGGAGTGAACTTTTGTGTGAATTGCATTGGTGAAGCCATTTGATTTACTGATTTTCAGGACA
GCCTATTACTGCAGAGGCTTTGATTCAGGATTTTGAAATGTGCTTTTGTGTTGCATTCAATTATGGGA
GGTATTGTGCATGGTGGTGGTAATCTTATCAAATCATTTCAATATCATTGCAGCTTGCAGCGAAGTTCCTG
AATAGTGGACAAACATGTGTTTGTGCAACAGAATAATTGTGCAAGAGGGTATCCAACACAGAATTAC
AGCCCTGATTTTACCCCTTAATTTCTAATTTTATATGTAATATGCAGCCATTTTGATTTGTGATATATTG
CCTTTTATGTGCAGTATCTACGACAAATTTGCAGATTCTTTTCAAAGCTGTTTCAGAGTATGCAAG
TTGGGGATGGCTTTAGCGAAGGTGTGACGCAGGTAGGGGTGCATTTTTTTTTTAAATATTTTCGTAA
TTGTTCCCTTGTGTAATAATAATTTGTGCAAAGCTAGTCAGGTATTCTATGTTTCCCTAGATTTAGCAGT
TTCTAGGGATGATAGCATTTCATGGTTGGTGACACATGCTAGACTGCTTTATCATCTTTATTGCTCCC
TATCTCGTTGAGTTTGTCCACCTTTTCATTTGAGTTGTCTAAAATTATTGCCGACTATGAAAAGTCA
AAATTATTAACCATTTGGTCTTCTGCTATATCCTTAATTTACTCATTTTATTTTATTTTAAATTC
CTACTTTCTCCCTCGTAAACTAGATTTAAATAAACTCTTTATTTCTTGAGTTTTTCAAACACAATTC
TTATTAATTGAGGGAGTAAATATATCAATGAATTTACAATGAAAAATTGTCTTAATTGTACTATTTATT
TAGATTATAATATGTGATTTAGCAAGAAAAATAATGCCACACATGCTAAAAAGTTGTGATTAATATAC
TTAAAAAATTGTTCTTTCTTTGTAGTTTCAAACCTTGATCAACTACTTTGCACATTAAACCTCTCACC
ACTAGCCCAACCACCTTGATATGATTGGTTCTGGAATATAATAAAAGGGTAATACTAGAAAGTGATGAA
GGAATGGATAAACATGTCATCCCATTAAATGTTCCCTCTTAATCTTTGTGAAAGTCGAAGGGTACTAGA
CTTTGGGTAATAGGGAGTCTGTAATTTGTTTGGATGAAGATATTCTAATCACACATTCATGCAGAGATG
TAGTTTGTGTTGTTTATACATCTAGAACCTTTTATTAGCTACTTTTCATGAGATTTGAAGTGAACAGATC
ATGGTGATAACTATTAGTTTCCCTCACAGGGTCCATTAATTAATGAAGCTGCAGTCCAGAAGGTTAGTTG
CATTTTATACATACAATTGGCCAGCCATCTTGCTTGTGATAATCCTTTTTAATTAATGAGATTTGTTGT
CAATTGGTCCCTTTGTGATTTGGGTTTCAGGTTGAATCATTTGTTCAAGATGCCATCTTTAAGGTTTGC
CTTTTCTGCTTTATCTTATTCAATGTACTAGGTTGAATAAACTTCATGCATTATATTGTCTTTACATC
TTCAAATATTTCTCTTCTCTCCCGCAATACACTCGACCTATGATAGCATTATATTTTATGACCAAGG
GAGAAAACCTTTTGGAGGTTGGAGTAACTTTTGTATGTTTGGTGAAACCTAGAAAGTATTGTAAATATT
TTCAACGCCAAAAAATTCTATAATGCAATTAGGTTACTTCGACATTCTGTTTCTTTGTTCCCTCGCACT
TCATTATATGAAAAGCTGAAGCCAAATAATAGACTTGGTTACAGTAATTAAGTTTCACTGGCATAATTG
TTCTTCAATTATTTGTTCTGTATATATCTCATTTCTAATTAACCAAAATTTGACTTGAAGGGAGCAAAA
GTCCTCCTTGGGGGAAAAAGGCATAGCCTTGAATGAATTTCTATGAACCAACCATAATTAGCAATGTC
ACTGAAGCAATGCTTCTATCGAGGTAAATACATGAAGATAATTTATTCATTCTGCAATTCTCAGCTGTA
TAATTAAGATGTCCATCAGCTTTCTTACAACAGGTAAAAGGATAGTGGCTGTTGTTCTCTGCCACTTG
CTGATGGGTATACATTCTTACCTCAGTGCAGGCTGGTTGAAACATGCAGCCATGCTAAAACTAACAGG
CCAACCTTTAGGTTTTGGCATCTAATCATGGACACTCATGGTGGTTTTGTTTTTAGCTCTTTCTTAAC
CATGGCATGTAAAATTCAATTGCAAACCTTAAGGTTAATGTTCTTAGACAAACCAAAATTGAGGTCTTGT
TTATTGATCGGGGACTAATCCAGGTTTCGAGTAGATGACAAAATTGAAGGCTCCTTAGGAAATGTTGCA
TCCACAAATACTGCCTTTTAATCAAATGAAGTTGAAGGACTGGCCATTGCTTTCAGTTCTTTTATGTGA
TTTTGGAGTTGGTACTTCATAATTAACCTTGCTGCAAAATTCATTTTCAAATTATAGAATTTCTTATTAA
TCAGAGCTTAGCTCGAAGAGTTAATGGATATGTGTAGGTTTATAATGGAGCACGGTGTGGTTTGCATTT
TCATTTTTGCTCTTTGAAGTATTTTGGTTTGCACATTGTTGATATCAGTAGCGTTAGCTTTTGGTTTGT
TAAATGCGGCATCATTGATTTGTTTACATTAACATAATTTAATCCATGTCATTGAAGTTCCTTAACAT
TACCTATAGGTTTATACTCATTGAGGATGTTAATATGCTCTCCTCTGCCTTGTTCAGGGAGGAAGTAT
TTGGCCAGTGGCACCTCTGTTGCGGTTCAAACTGAGGAAGAAGCCATCTTGATGGCTAATAACACAA
AAGCAGGTTCTTTTCGTCTGCCTTTACATGCATACATGTACACGATTTATCTTTTTGTTTCCCTCATTC
TATCATTTTAAATATCAATTATCTGAGAGTATTACAGATGAAAGTTTGTAAATATACTCCTTAACCCAGT
TTCATTTTCCATACTATTGTCTTTATCTATTGTCAATGGTAAACAGACTTATGGTCAACTGTAATACAGG
ATTCTAGCTTATCTTTTCTGGTAAACGATGCAGGTTAGCTGCATATATTTTCAACAAACATGTTCAAC
GTTTCATGGCGTGTCTACTGAAGCTCTTGAGTATGGACTTGTGGTGTCAATGAAGGACTTATTTCAACAG
AGGTGGGACTTATCTGTGTTCCCATTTGGAACCATAGATTGGCTTCTTAAACCTTAAAAAATGTCTG
TTGCTAAACAGGTAGCTCCATTTGGAGGAGTTAAACAATCTGGTCTTGGACGGGAAGGCTCCAAGTATG
GAATGGATGAATATCTGGAGGTAAAGATTACTTTTAATGCATCTTAGGAAAAAGTGAAGCTATCTTCT

CTCCCTCTCGCTCCCATGTTTAAGAACACAAATTGGGTATTCTAATCTTCTAGCTTGCTTTTAGGACTG
 CATTGTTTATCAACTTAATCACACACATACAGATCTACATTTCTTTATTCTTTCTATTTGAGGGTTTTC
 AACCTGTATTTATGTGTGAGGGAGATGATTTACTAATTACCCTGGTTTTCAATTCCTAAGGATCAAGT
 TCTTGGTTTATTTGCACCTCTTTTAGACCTTTACTATCATCATAACGAGGTATTCTTGCATGCCGTGC
 AGATGAAATATGTCTGCTTAGGCGATATGAACAGAAAATGA

FIGURE 4B

Genomic sequence of *Salix* Xyld2 allele A – SEQ ID NO.7

ATGACGTTAGGGAGAATAGCTCTGGCAGCATCCCGGCGACCAGGGGCACAATACACAGACTCTTCTCT
 ACAACACTTTTCGTCTTCTTCCAAGAATCGCACCTCTCCTCCACTCTCTCGCCACGTAACACTACTCGT
 CGTCTTTTACTAACGCATAAGCATCAATAGCTTTTCATCTTTGTCTTGCTAATTGAATACAGCGATCGCG
 CTTTTGAATTTATTTACATCTTGTTTAATTCATGTTTTAATCGCTTTGAAATAAGTAGCATTTTCAGCAA
 ATACTGGTTCAATTGACAAATAATTTGTTTCATTAATGTAAGTATAATTTCTGTTTGATTTTTTTTCTG
 TCATTGTTAGTTGCGAATTTTATTAATGTTTTTCATGGCAGATGAGCATGAAGAGTGACAACCTGGTTTC
 AAAGCTAACTAGCTCTGGTCTATTAAAGACCCAGGGTCTTATCGATGGAAAATGGGTGCGATGCACATGA
 TGGTGACACTATTAAGGTCTGCCATTATTGTGCGTGTATTTGTTTGTGTTTTCTCTACTGCGGCTACT
 AGTTTTGGGCATTGTTTCTTCTGCCACCCATCACATGACATGTATATGTTCTTTTCATGGGACGGCAG
 GTTCTCAATCCGGCCACGGGTGAAGTTGTAGCTAATGTCCCATGCATGGGTGAGAGCGAGACGAATGAT
 GCTATATCATCTGCCATGATGCATTTAGATGTAAGAACTTCATACTGAACCAACCGTTCAGTTCAGT
 AAAATGTATTACTGCATTTATGCTATTCACATCAATAAAGTAATTAATTAACCTTCTCCTACTGGCGCT
 ATCATTCCCTATGTTTTGAATTTTGAAGAGGAATATGGTTTTATTTTGCATGCGTGGACTATCTTTTCAG
 TACTGGCAGGGGGAATTTCTAGTAGAGGATTGGTTATGGAAGTGAGTTATTGATGTGTTGTCTTTGTGTA
 GGTTAGCATCCATGCCTTCAGAAGGTAATGACACTTGGATGTCTCCTTTACAGTATGCCAACCTCATTA
 CTGAATCGTAGAGCATACATATGTTTTCACTGAACTTACGTGCATCATCTTGGTTATTCTTTAAAAG
 AATCTGGGTTTTATGACAATTGGGTGAAGTATTATTACCACACTAATCCACTATTATTGTTCTCAATCA
 ACCTGCAATTTCGTACAGCCTGCACCACATGACTATTTGCTACAATATATTAAATACCACAACCTCACACA
 CAAAAGCTTGTGGTGTGTTGTGATAATAATCACCGTAAACATGGCAGTGATGCACACTCTTGAAATTTCTA
 CTTTCAAGCTTCTATGTGTTGCATCTTTATTCCTCTTATCCTTAGCTTTTCGCAGCACAATTTGTTGGTG
 TTTTACTGCCTTTTCAGCTCCCTATCTTAGTTGTCTCTTTGAGAGTTATGTGATACTCTAGAAGCAAAGA
 GTGAATGAAATGGTTTAAATTGAGTAGTTCTTACGACTTACTAGTTGATATACCTTCAAAGTATTACA
 TAGACCTTTGCGTAGATATAATCTTAATAGGATCTACTCATATGACTTAGATATGGAACCTCTTGTTT
 TTTACCATAAGCTTGCTAAACTCCTCATTGTTTATACGCTTTTTTCTGCTCAGCTATAATACTAGCAT
 ATTTTGATGCACCTTTTCTGATATAGCTTGACATTTTTTTTTTGTCTTTTGTCTTTACTGGACTTCAA
 ATGATATTGAAATTTGAAAAAACTTCTTGCTGATGATCGCAACATGTTCAATTGTTTTTATTTGTCCA
 GCATGGAGTAACTTACTGCTTCTGAGAGGAGCCAACGTTTACGAAAATGGTATTTGATTCTTCCATAA
 TGATTTTATTAAATTACATGTGTTGTAATGTAATACTTCCAAATTAATCAAATAGTTGGAAATAACT
 GTGTTGTATCGGTACAGTATTATGGTTCTTACCCTTTACTGAATCTCATATGATTTCCCCCTATTGTA
 AGGTATGACCTACTAATTTCCACAAGGAAGAGCTAGGACAATTAATAACCTTGGAGCAAGGGAAACCT
 CTGAAAGAGGCCATGGGTGAGGTATCTCATCTGAACTTTGCTTTCAGAAATCAGGAGATAAGCGTTAAC
 CCTACATCTTGTAACCTGGTCATTGTCAAGCAACATGTGATCCAAGACTCCACTAACAGGTTATTTATGG
 AGCTAGTTTTATCGAGTTCTACGCAGAGGAGGCGAAACGTGTATATGGAGATATAATTCATCGACTCT
 TGGTGATCGTCGGTTATTTGTTCTAAAGCAGGTGACTATAACTGTTTGTGATATTTGAAATCTTGTTTA
 ATTGACAGATATGAGTAAATTAGTTCTTCCGACAGCCTGGCTACTCATATAGATGTCGACAATTTCCGCT
 TGGTTTGAGTCTCTTAAACAAGGCCTTTTCAAATTGAGTTTTAATTTCTGGCACCAGCATGCATGTTTA
 ATGCACCGATATTTGTTAAACTACATAAACTCGTGATTGGGACACATTCCTTACATGAATTGTGCTT
 CAGTCTACTTTATCCTGTGAGCAGTCCAGAAATGATTTCTCAATGATCTATCGTGATGAATAGTTCTT
 GCCACAACCTTTCTTCTGTGAGCTGTTTACATGGCTTTGATAATTTTCAAGTGTGTTTCTGTGCA
 ATCCATTTATCCAGCAATCTCATGAGTTTTTCCAGCCTGTAGGTGTTGTTGGGGCAATCACACCTGGA
 ACTTTCTTTGGCAATGATTACTAGAAAGGTGTGTTCAATGTAGGATGATTTTGTGCAAGAGAGTTTA
 CTTTTCTGTGTGAGTTATTGTAAGAACTTCTGATACTTTTCTCACTTGCATAGGTTGGTCCTG
 CTCTTGTCTGTGTTGTACAGTTATTGTAAGAACTTCTGATACTTCAACCTCTCACAGCTTTAGCAGCGG
 CTGAGCTGGCCCTTCAAGCTGGAATACCACCGGTGAGTCTCAAACCTTTTATGTGCACTGTGGAAGTTT
 CTTAATTTCTAGGCTGTGTAAGATGCAAGTGCTTGGATATAATGTGGCCTTGGTCATCTATGTAAATT
 GTGTCTTGCTAGACATTGAAGATAAAGTTGATACTTTATGGTTTCAATGATAAAGACTTATCCTTTGTG
 ACACAATGAAGTTTTTGGAGCAAGTTTTGGTTGGAACTAGGATACTTGTAAATGTAGGATTTTAGTCTT
 AGCATCCAAAATATTCTATTATCTGGTTGTGCAAGAAGAGCTGCAGCAAGTTAACAAATTAGAAATAT
 TTAATAAGAGCTTAAAAAGTAAGGAGGGATGATAATGTAACAAAATGAATCTAAGCATCATCCCATGG
 TTATTAGATGTTTATCACAAGATTCCAACCTAAGCAAAGCACTGAAGAAAATGCTCTTGCTGACTGTTA

AATTGAGTGACTTTGTGTTGCATGCACACCTTCTATTGAAGAACCATAATTGACAAATCAAGTGAAATG
CTCAGTTGTATTTATATCACATCATAATGATTGCTGACCTATGCTAATAGTCAGCTGAGCATCCTTACT
GAGCATTGAAACAGAGAATATCCATCACTGGCAGTCGTTTTTGCTCCATATTCTGGTTTAGCATGTCTCT
TGCATCACAGGACAACAGCAGGATCTGGTCTATCATCCTGATCAAACCTGCATTCTGCTTGAATGAGAT
AATGATGGAATGAATGTAGCCTTTTTCTGGCCTTTTTAGATGCATGTCATACACAATTGATGTGTTATAT
TAGCGAATATGAGTTCAAATTTGTTGAAATCTGTTCAATTTGTTTTAATGGTTTTAATTTTCAATATT
TCAGGGTGTCTGAATGTGGTTATGGGGAAGCTTCTGATATTGGTGATGCTTTACTAGCAAGTCTCTGA
GGTTTCATATCCTTCCTCTATTTCCCTTAACTTTCTTCTCTTTGACAACATGGCATTGTCTTGGACAG
AGTAAATGGATATTCAATGACATAATGTTGATACTCTTGCTTTTATACATCTGATTTCAGGTAAGAAAAAT
CACTTTCACAGGATCAACAGCTGTGGGAAAGAAGTTGATGGCTGGTGCTGCTGGAACAGTTAAAAGGGT
ATGCATAGCATGCAAAATGAATCAATGTGATGATGTTTCAGAACTATCTTATGGCTAACTGTCTTTTC
CCTTAATCTTTGTAGCTGTCTCTGGAACCTTGGTGGCAACGCACCCTGCATAGTATTTGATGATGCAGAC
CTAGATGTGGCAGTTAAAGGATCAGTAAGTTAGAGGGGTTCACAGTGCATGCTTATATTGATAGTGGTA
TCGACGTGGATATTTCTGAGTGCCATTTAATATTGTTTACTTTTCATGTTTAGACATATCAGATGGACA
CACACTAAACCTCTGATCTGACTAGGATGGATATTGGTGCAGTGGGTGTTAATTGTTGGTTAGACATG
GGGGTCCATGCCTCCATATTTGGAAGTGTAACCTTTTGTGTTGATTACATTGGTGAAGCCATTTAATTT
ACTGATTTTTCAGGACAGCCTATAAGAGGCTTTGATTTCAGGATTTTGAGAATGTGTCCTTCCCTTCATGATA
TAGCTCTTTGTTTTCATCCAAATATTGGGTGGTCTTGTGATGGTGGTAATCTTATCAAATCATTTTATA
TCATTCAGCTTTCAGCAGCAAGTTCCGTAATAGTGGACAAACATGTGTTTGTGCAACAGAAATAATTGTG
CAAGAGGGTATCCAACTACAGAATTACAGCCCTGATTTACCCCTTAATTCGAATTTCTATATGTAATATG
CAGCATTATGATTTCTGATGTGTTGCGCCTTTATGTGCAGGTATCTATGACAAATTTGCAGATGCTTTT
TCAAAAGCTGTTTCAGAGTATGCAAGTTGGGGATGGCTTTAGTGAAGGTGTGATGCAGGTATGGGTAGCA
TTTTCTCTTTTAAATATTTTCGTAATTTGTTCCCTTATTGAATAATAATTTGTGCAAAGCTAGTCAGTTA
CTCTATGTTTCTAGATTTAGCAGTCTCTAAGGATGATGACATTCAGTGGTTGGTGACGCAAGCTAGGC
TGCTTTATCATCTTTATCACTTCCTGTTTCAAAGAGTTTGGCCACCTTCCCTTTTTGAGCTGTCTTAA
ACTATTGCTGACTATGAAAAGCCGAAATTATCAACAACCTTGATCTTCTTGCTATATGATGAGGGTCACA
TCACTATATCCTTAATTTAACTCATTTTATTTTATTTTATTTTGTGTTCACTACTTTCTCCCTTGTAATAATTA
GATTTAAACGAAACCCCTTCATTTATTGAGTTTTTCAAACATAATTCATATTAATTGAGGAGTAAATATA
TCAATGAATTTCAATGAAAAATTGTCTTAATTTATCTATTTTATTTTGTGCTAGAAATTTATGCCTACACATG
GTAGAAAAGTTGTGGTTAACATGTCTCATAAAAAAATGTTCTTTCTTTGTAGTTTCAAACCTTGATCA
ACTACTTTGTATATCAAACCTCTCACCATTCCCTTCATAACCACCTTGATATGATTGGTTTTGAAATATA
ATAAAGGCTAATACTGGAAAGTTATGAAGGAATGGATGACATGCCATCCAATTAAATGTTCTTTTCATAA
TCTTTGTGAAAAGTGGAAGGGTACTAACTTTGGGTAAAGAGGAGTATGTAATTTGTTTGGATGAAGAT
ATTCTGCTTACACATTCACGCAGAGATGTAGTGTGTTGTGTTTATACATCTAGAACCCTTTTTATTAGCT
ACTTTTCATGAGATTTGAAGTGAACAGATCATGGTGATACTATTAGTTTCCCTCACAGGGTCCATTAAT
AATGAAGCTGCAGTCCAGAAGTTAGTTGCATTTTATACATACATATTGGCCACCATTGCTTGTGTTA
ATCCTTGTGTTTATGATGAGATTTGATGTCTTGTGTTTGTGCTTTTGTGATTTGGGTTTCAGGTTGAATCATT
TGTTGAAGATGCCATCTTTAAGGTTTGCCTTTTCTGCTTTACCTTGTTCAATGTACTAGGTTGAATAAA
CTCCACGCATTATATTTGTCTTTAAATCTTTCAATATTTCTCTTCCCTCCCCACAATACCCTCGACCTAT
GATAGCATTATATTTTTATGACCAAGGGAGAATTTTTGTAGGCTGTGGTAAACATTTTTTATGTTTTGG
TGAAACCTAGAAGTATTTGAAATATTTTCAACGCTCAAAAACCTCTATAATGCAATTAGGCTACCTTGAC
ATTCTGTTTCTTTTTTATATATTTCTCATTTCTAATTAACCAAATTTGTACTTGAAGGGAGCAAAAGTC
CTCCTTGGGGGAAAAAGGCATAGCCTTGGAAATGACTTTCTATGAACCAACTGTAATTAGCGATGTCACC
GAAGCAATGCTTCTTTCGAGGTAAATACATGAAGTTAATATATTGATCCTGCAAGTCTCAGCTGAATAA
TTAAAGCTGTCTTTCAGCTTTCATACGACAGGTAAAAGGATAGTGGTGGTTGTTCTCTGCCACTTGCTG
ATGGGTATACATTCTTACCTTCAGTGCAGCTGGTTGAAACATGCAGCCATACTAAAACTAATAGTCCA
ACCTTTAGGTTTTGGCATCTAATCATGGACACTCATGGTGGTTTGTTTTTTTTACTCTTCTTAATCAT
GGCATGTAAAGTTCAATTGCAAAATTAAGGTGAATGAGTTTAGACAAACCAAACCTTGAGGTATTGGTTT
CTGATTGGGGACTAATCCAGGTTTGCAGTAGATGACACAATTGAAGGCTCATTAGAAATGTTACATACA
AAAACACTGCTGTTTATCAAATGAAGTTGAGGGGCTGGTCATTCCCTATCAGTTCTTTTTATGGGGTTTT
GGAGCTGGTATTTCAATAATTAACCTTGACGGGTTTCAATGTCAAATTATAGAACCCTTATTAATCAGAGCT
TAGCTCGAAGAGTTAATGAATATGTATAGGTTTATAATGGAGCACGCTGTGGTTTGCATTTTCTTTTTCT
GCTCTCTGAAGTGTTTTGGTTTGCACAGTGTGACATCAGTAGCATTAGCTTTTGTTTTGACAAATGTG
ACATCATTTATTTGCTTACATTAACATAACTCTAATCCATTTCAAGGAAGTTCCCTGAACATTATCTATA
CGGTTTGTACTCATTCAAGATGTTAATATGCTCTCCTCTGCCTTGCTACAGGGAGGAAGTATTTGGCCC
AGTGGCACCTCTGTTGCGGTTCAAAACCTGAGGAAGAAGCTATCTTGATGGCTAATAACACAAAAGCAGG
TTCTTTTCATCTGCCTTTTCATGCATACATTTCCACATATTTATCTTTTTTGTTCCTCATTACTATCATT
TAACCTGCATTTAACAAATATATTGATTATCTGAGAGTATTACAGATGAAGTATGCAATGTAACTCCTTA
ACCCAGTTTCGTTACTATTGTCTGTCTGTTGCTTGGTAAACAGACTGATGGTCAATGTAACTACAGG
ATTTCTAGCTCATCTTTTCCGGTAAACAAATGAGGTTAGCTGCATATATCTTACAAACAATGTTTCAGC
GTTTCATGGCGTGTCACTGAAGCTCTTGAGTATGGACTTGTGGTGTCAATGAAGGACTAATTTCAACAG

AGGTGGGACTCATCCTGTGATCCCCATTGGAACCATAGATTGGCTTCTTAAACTTACAAAATGTCTG
TTGCAAAACAGGTAGCTCCATTTGGAGGACTTAAGCAATCTGGTCTTGGACGGGAAGGCTCCAAGTATG
GAATGGATGAATATTTGGAGGTAAAGTAAGATTACTTTTAAATGCATCTTAGGAACCCCCGTTTTTTAGG
GTTTTCAACCTGTGTTTATGTGCGCGAGAGATGATCTACTTGTTATACCCCTGGTTTCCAATCCCTAA
AGATCACCTCTTTTACTGCCATAACGAGGTACTCTTGCATGCCGTGCAGATGAAATATGTCTGCTTAGG
CGACATGAACAGAAAATGA

FIGURE 4C

Amino acid sequence of *Salix* Xyld2 allele A - SEQ ID NO. 28

MTLGRIALARI PATRGTIHRLFSTTLSSSSKNRTSPPLSRHMSMKSDNLVSKLTSSGLLK
TQGLIDGKWVDAHDGDTIKVLNPATGEVVANVPCMGQSETNDAISSAYDAFRSWSKLTAS
ERSQRLRKWYDLLISHKEELGQLITLEQGKPLKEAMGEVIYGASFIEFYAEEAKRVYGDI
IPSTLGDRRLFVLKQPVGVVGAITPWNFPLAMITRKVGPALACGCTVIVKPSELTPLTAL
AAAELALQAGIPPGVLNVVMGKASDIGDALLASPEVRKITFTGSTAVGKKLMAGAAGTVK
RLSLELGGNAPCIVFDDADLDVAVKGSAAKFRNSGQTCVCANRIIVQEGIYDKFADAFS
KAVQSMQVGDGFSEGVMQGPLINEAAVQKVESFVEDAIFKGAKVLLGGKRHSLGMTFYEP
TVISDVTEAMLLSREEVFGPVAPLLRFKTEEEAILMANNTKAGLAAYIFTNNVQRSWRVT
EALYGLVGVNEGLISTEVAPFGGLKQSGLGREGSKYGMDEYLEMKYVCLGDMNRK

FIGURE 5A

Genomic sequence of *Populus* Xyld3 – SEQ ID NO.8

ATGTTCCATACCAAGAAACCCTCAACTATGAATTCCCATGATAGACCCATGTGTGTTCAAGGGGACTCT
 GGTCTTGCTCCTCACCACAGACCCCAAGCCCCGTCTCCGCTGGACTGTTGAGCTCCATGAACGCTTTGTG
 GATGCCGTTACTCAGCTTGGAGGCCAGATAGTACTTAATCTCTCTTTGACTAGCTAGTCTTTAGTTCT
 ATTTTTATGTACGTTCCCTAATTTGTTTGTGCTGATAACTTCTTCAATCTCTCTAATACGTGTTCTATTG
 CCCCCCTCTCTATGCTTGATCAAAAAATTTGCAGAGGCCACTCCAAAACCATCATGAGAGTCATGGG
 TGTGAAGGGTCTTACCCCTTACCACCTCAAAGCCATCTTCAGGTTTGAATAGAACATTCTTTTCATGCC
 TCTTTTGCTTTTGATTGACACCTTTGCGGCATTTTCGATGTAGGGTTGGCTTGATTTCATTCTTT
 TTCCTTCTATCTTTAATTTTCATTTCTTTAACGTTTCTTTTCTCTTAATTTAGAAATTCAGACTTGAA
 AGCAACCACACAAGGATTTCAATGATCATTCAATTAAGGATGGTAAGAGAGCTAATTAAGCCATCTTTA
 TATACAGGGTTTTTATTTTTATTTTTATTTTTATCCTTTTCGGTTGTTAAAGGTGGCAAGGAAAGACTCG
 GATTCGACTCCCTTTCCCTTTCTTTTGCTTTACACAGAGAGTGCTAAAATTAATCTAAATGCTTACCTGTT
 CTTTTTTAATTTTCCTTGCTTTGATTCTTATACATGCACAATGTGATCAAAATGATCAGATTAATTTTT
 TCATAATTTTCCATGGCAAGCAGCTTCGGCGTTAGATCTTCAACGAAGTGCAGCATCTTCATCTGGCAT
 GATGAGCCGCAGTATGAATGAGTAAGTATTACATTCAAAAATACCTCTCTCTTAAACCAACAATTACG
 AACAAGCAGAGTTCATGCAATTTTCATTTTCTTCTAAGGATAACAATAACGATATAAACAAAATCGCTT
 AAGTTTCTTTCTTTTCATTTCTGTGGAATATATGTGTGAAACTGTACATAGCAGTAACCTCACACATGATT
 GATGCGATTAGGATGCAAATGGAGGTGCAGAGAAGACTGCATGAACAATTAGAGGTAAGCACAGATCGA
 TTGTTTCTCAACATCTACTCCACCCCTTTTTTTTTATATATAAACTATTTTCCTTAATAAAGACAGTCCGT
 GTAGACTTTATTTGATGCATATAAATTAATTCAGGTTCAAAGACACCTTCAATTAAGGACCGAGGCTC
 AAGGGAAATATATACAAAGTTTGTGGAGAAAGCTTGCCAAACCCTAGCAGGTGATCAAACTTTGGCTT
 CTGGAAGCTATAAGGGAATGGGGAATCAAGGAATTCCTGGTATGGGTGCAATGAAAGAATTTGGCACGC
 TGAATTTTCCAGCATTTCAAGACCTTAACATTTATGGGGGTGACCAACTTGACCTTCAACACAATATGG
 ATAGGCCATCACTCGATGGTTTCATGCCGAACAACGACAACATTTGTTTGGGAAAGAAGAGGCCTAGTC
 CTTACGATGGTAGTGGAAAGAGCCCTTGATTTGGCCGGACGATCTGCGTTTGCAGGATTTGGGATCAG
 GACCGGCATGTCTGAACCCCAAGATGATCCTTTCAAAGGTGATCAAATCCAGATGGCACCACCATCAA
 TGGATAGGGGTACTGATCTGGATTCCATATCTGACATGTATGAAATAAAGCCAGCGCTTCAGGGTGATG
 CACTGGATGAGAAGAAATTTGAAGCATCAGCAAAGCTAAAAAGGCCATCCCCAAGAAGATCACCACCTAG
 CAGCCGAAAGGATGAGCCCTATGATCAATACTGGCGCCATGCCACAAGGCAGAACTCACCATTTGGTT
 GA

FIGURE 5B

Genomic sequence of *Salix* Xyld3 allele A – SEQ ID NO.9

ATGTTCCATACCAAGAAACCCTCAACTATGAATTCCCATGATAGACCCATGTGTGTTCAAGGGGACTCT
 GGTCTTGCTCCTCACCACAGACCCTAAGCCCCGTCTCCGCTGGACTGTTGAGCTCCATGAACGCTTCGTT
 GATGCTGTTGCTCAGCTTGGAGGCCAGATAGTACTGAATCTCGATCTCTTTGACTAGCTCGATAGTCT
 TTAGTTATATTTCTATGTACGTTCCCTAATTTGTTTGTGTTGATCACTTGTTCAAATCTCTAATACGTGT
 TCTATTGCACTGCCCCCTCCCCCGCTTGATCAAAAAATTTGCAGAGGCCACTCCAAAACCATCAT
 GAGAGTCATGGGTGTGAAGGGTCTTACGCTTTACCACCTCAAAGCCATCTTCAGGTTTGAATAGAACA
 TTCTTTTCATCCATCTTTTGCTTTTCTGCTGACACCTTTGCGACATTTTCGATGTAGGGCTGGCTTGATT
 TCATTCAATCTTTTCTTCTATATTTAATTTTGCAATTTCTTTAACGTTTCTTTTCTTTTAAATTTAGAAA
 TTCAGACTCGGAAAGCAGCCACACAAAGATTTCAATGATCATTCAATTAAGGATGGTAAGAGAGCTAAG
 CCATCTTTATATCCAGGGTTTTTGTTTTTGTTTTTGTTTTTGTTTTTATCCTTACGGTTGTTAAAGGTG
 GCAAGGAAAGACTCGGATTCGACTCCATTTCTTTTCTGTACACAGAGAGTGCTAAAATTAATCT
 AAATGCCTACCTGTTCTGTTTTCTTTTCTTTGATTTGATTCTTATACATGCACAATGTGATCAAATGA
 TCAGATGATTTTTTTCATAATTTTCCATGGCAAGCAGGTTTCGGCGTTAGATCTTCAACGAAGTTCTGCA
 TCTTCATCTGGCATGATGAGCCGCAGTATGAATGAGTAAGTGTTGCATTCAAAAATATTTCTTTCTTAA
 ACCAAACAATATACGAATTTGAACAAGCAGAAGTCATGCAATTTTCATTTTCTTAATTTTAAGGACAACAA
 TGATGATATATAAAAATCTCTTAAGTTTCTCCTTTTCATTTCTGTGGAATATATGTGTGAAACTGTATA
 TAGCAGTAACCTCACACATGATTGATACGATTAGGATGCAAATGGAGGTGCAGAGAAGACTGCATGAGCA
 ATTGGAGGTAAAACACAGATCGATTGTTTCTCAACATCTACTCCACCCATTTTTTTTTTATAATTTAT
 TTCCTTAATAAAGACAGTCGGTATAGACTCTTTTTTTATGCACATATATAAATTAATTCAGGTTCAAA
 GACACCTTCAATTAAGGACTGAGGCTCAAGGGAAATATATACAAAGTTTGTGGAGAAAGCTTGTCAAA
 CCCTAGCAGGTGATCAAACTTTGGCTTCGGTAAGCTATAAGGGAATGGGGAATCATGGAATTTCTGATA

TGGGTGGAATGAAAGAATTTGGCACACTGAATTTCCCAGCATTTCAGACCTTAACATTTATGGGGGTG
ACCAACTTGACCTTCAACACAATATGGACAGGCCATCACTTGATCATGGTTTCATGCCGAACAACGACA
ACATTTGTTTGGGAAAGAAGAGGCCTAGTCCTTACGGTGGCAGTGGCAAGAGCCCTTTGATTTGGTCGG
ACGATCTGCGTTTGCAAGATCTGGGATCGGCACCGGCGTGTCTCGAACCTCATGATGATCCTTTCAAAG
GTGATCAGATCCAGATGGCACCGCCATCAATGGATAGGGGTACTGATCTGGATTCCATGTCTGACATTT
ATGAAATAAAGCCATCGCATCAAGGTGATGCACTGGATGAGAAGAAATTCGAAGCATCCGCGAAGCTAA
AAAGGCCATCCCCAAGAAGAGCCGAAAGGATGAGCCCTATGATCAATACTGGTGGCATGCCACAAGGCA
GAAACTCACCATTTGGTTGA

FIGURE 5C

Amino acid sequence of *Salix* Xyld3 allele A - SEQ ID NO. 29

MFHTKKPSTMNSHDRPMCQVQDGLVLTTPKPRLRWTVELHERFVDAVAQLGGPDKATP
KTIMRVMGVKGLTLYHLKSHLQKFRLGKQPHKDFNDHSIKDGSALDLQRSSASSSGMMSR
SMNEMQMEVQRRLEQLEVRHLQLRTEAQGKYIQSLLEKACQTLAGDQNLASVSYKGMG
NHGISDMGGMKEFGTLNFPFQDLNIYGGDQLDLQHNMDRPSLDHGFMPNNDNICLGKKR
PSPYGGSGKSPLIWSDDLRLQDLGSAPACLEPHDDPFKGDQIQMAPPSMDRGTDLDSMSD
IYEIKPSHQDALDEKKFEASAKLRPSPRRAERMSPMINTGGMPQGRNSPFG

FIGURE 6A

Genomic sequence of *Populus Xyld4* – SEQ ID NO.10

ATGGGCTCAAGAGCAAGAAGGAAGCAAGATGGAGCACACAAACCTTAACTCCGCTGCTAGAAAGGTCCCT
 GACCCCGACATGCAAGAAGAAGGTAACAAAAAGGAAAGCTCATGGGAAGTAATTCGTGAATGGTTTCGA
 TTGCAAAAGGGTCTTCCAGCAGGTAACAGTTTTTTCAGTATCGTTACATGGGAGTATTCAGTCAAAGGA
 CAAGATTTAAGGCTTTTACTTGGAGTTTTGGGCTGCCCTCTAGCTCCAATCCCTCTAGTTAACGACCCC
 ATTCATCGCATTACATTAAAAACACTCCTATTGTAAGTTCTTCTACACTACTTATCCATATGTTTATT
 TTCTTAATTTCGGCAACTCCATCTTATCAATTTTTCTATAGGAAAATTCTGCCGCGCATTATATCATCC
 AACAATATTTGGCAGCAACAGGGTGTTTAAAGCAACAAAAATGTATGAAAAACATGTATTCAACAGGGA
 GTGTGAAGATGATTCGTTGCGAGACAGAAATTTCTCGGGAAAAAACGTGAAGAGCTTGGGGACTAGAA
 GTGGCGAAAATGGGTGCTTTGTTCTTTGGCAAATGTTGCCGGGGATGTGGTCTCTTGAATTGGTTGTTG
 GGGAAAATAAGGTCATAGCAGGCAGCGATGGGAAGACCGTGTGGCGTCACACTCCTTGGCTTGGCACTC
 ATGCTGCCAAGGGACCCCAACGCCCTCTACGTCGCATAATCCAGGTACAACTATATATATAGTGCATC
 AAATTCAATATTAATCTTGATGAAATTGCCCCCTTAAAAATTGAAGACCATAGTTTTAGTTAATCATAA
 AGAAACATTAGCCAGAAAACCTAGTGATCTAAAACCTGGTAGTGCAATATCGGGCTATGAGGGAGAAGAAA
 CAACAGGGTGAAGTGAAGGAATATTTCTGTTTTTCTCTAGGTTGAAGACGATAAGACAAAATTAGGAACA
 TTGCTTTTTACTCTACAATTTACTTTTAATCTACTTTAATCGAATTTACATACCAGACATAAGGATGGG
 GATGGAAGACCAATACAAGTTTTTTTTCTTTTAAAAAAAATAGAATTTGAAGACCTATCTATATGTATAG
 ATCACAATCCCGAGAAATGGTAGGATCTATGTACAAGTAGCTGACATGATAGGGAAACTGTCTTGAGCT
 TTACCAGACAGACTAGCTTCTTTTTTTGAACTCTCACGTTATTCAGAGTTAGGAATGGCACGTGATTTT
 GTTTTTGACGTCATCTTTGATCATGTTCAAAGTATATTTTTGGGACTGCAGCTTGTAATCATCCTTTGC
 ACTTTACTTTTCCTTTTTTGCACCTTTAGTGAATAACACCTGATTTATTGCATTATCGCCCCCTTGCTTTT
 CTTGCCTTCCCCCCCCCTCTTCTTTGTTTATTTTCTTCTCGTTCCCATGTCAATCGTTTTCTTCTCTCC
 TTTCTCAAATTTCTGTTTTTTTTTTTTCGTTTTTCGAAATTATGGCGAGTTTCAAAGTTAGAAACTATC
 GTGGCATACTTGAAGATTGAATCCAGTACCTCGTCCGGGGTTCCTTCTTTGCCTCTAGCCCCAAGT
 GAGTCAAGTGACGGAGGGATGAACATTCCTTTGGAGTTTTTGGGCCAAGCCCCGTTTCCACAAAAAAC
 CAGGGAATTAGTCAAACTTGTGGAGGAACATTTATGCTTAGGTTTTCTTTTTTTTTTTTTTTCAGGAGTGG
 CATCCCCATTTTGTATATGTTTCTTTGCTTGCCATGACATGAGAGGAATCACTGGCCTGCAGCTGTTG
 AGATTTTGTGCACCTTGAATAAAAAACATATGATTCTACTTCCTTTATTTTCGTGTATTATTGAAATTA
 TTAGGATGTCAAAGCTGAGCTAGAATATGTGTGGAAGTACCAAATATTTGGACCTCCCTCGTCATCAT
 ATCCTTGTTCTTTTACTAATTAATAATTGAGGCTTAGATCAGCTATCCTCCATTCTCAGACGAAAAGA
 TAGGGATCAGTGTCTAACAGTATTTTATTGAATTTCTTTGAAATTTATGAATTTAATTTGTGGTTCTTTC
 ATTTGATTTTCAAGTGTCTTGTGATGCTTCCTTAGTTTTATATATATATATATATATATATATATATA
 TATATATATATATATATATATAAGCTCAAACCTGAAACCTCTTAAATTACAAGTTATTAGTACCCTGTC
 CTGCATCTAATTATGTGCTCGAACACTAATATCACCTAAAACCTTAGACCTTTTCTTCGTGCACCTTAATT
 AATCATGTGGTGGTATTCCAGGGCCTGGATCCAAAGAGTACAGCCAGCTTATTTGCTAAAGCACAAATGC
 TTAGGGGAGAAAAGAATTGGCGAGGATGATTGCTTCGTTTTTAAAGTAGCTGCTGATCGAGAAGCTGTA
 ATGGAAAGAAGTGAAGGGCCAGCTGAGGTGCTTAGGCATGTACTGTATGGCTATTTTTTGCCAAAAAAGT
 GGCCTCTTAATGTATTTGGAGGACTCCCATCTAACAAGGGTACAACTCCAGAAAATGAACTATCTAT
 TGGGAGACTACTATAGGAAGTAGTATTGGCGACTATAGAGATGTGGATGGTGTGTTAATTGCTCATCAA
 GGAAGGTCAATTGCTACAGTTTTTCGATTTCGAGGAAGTGTGAGTGAACACAGTAGGACTAGAATGGAA
 GAAGTATGGAGGATCGATGATGTCGTGTTCAATGTGCCAGGGCTTTCCATGGATTATTTTATCCCTCCT
 GCTGATATCTATGATGCTTCTCCATGA

FIGURE 6B

Genomic sequence of *Salix Xyld4* allele A – SEQ ID NO.11

ATGGGCTCGAGAGCTAGAAGGAAGCAGCGATGGTGCGCACAAACCCTAACTCCACTTCTGGAAGGTCCC
 GACCCCGACATGCAAGAAGAAGGTAACAAAAAGGAAAGTTTCATGGGAGGTGATTTCGTGAATGGTTTCGG
 TTGCAAAAGGGTCTTTCAGCAGGAACAATTTCTCAGTACCGTTATACGGGAGTATTCGGGTCAAAGA
 CAGGATTTAAGGCTTTTACTTGGAGTTCTGGGCTGCCCTCTAGCTCCAATCCCTCTGGTTAACGACCCC
 ATCCATCGCATTACATTAAAAACACCCCTATTGTAAGTTCTTCTACACTCCTTAATTATCATTTTTGTT
 TTTTGTTTTCAATTCGGCAGCTCCATTTTATCAGATTTTTTTACAGGAAAATTCGCCGCGCATTATAT
 CATAACAGCAGTATTTGGCAGCAACAGGGTGTTTAAAGCAACAGAAATGTATGAAAAACATGTACTCAAC
 AGGAAGTGTGAAGATGATTGTTGCGAGACAGAAATCTCCTCGGGAAAAAATGTGAAGAGCTTGGGGAC
 TAGAAGTGGCGAAAACGGGTGCTTTGTTCTTTGGCAAATGTTGCCGGGGATGTGGTCTCTTGAATTGGT

TGTCGGAGAAAAATAAAGTCATAGCAGGCAGCGACGGGAAGACTGTGTGGCGTCACACTCCTTGGCTCGG
 CACTCATGCTGCCAAGGGACCCCAACGCCCTCTACGTCGCATAATCCAGGTACGAAGTACGATAAATATTT
 TGTTTTCTCCTGGTTGAAGATGATAAGACAAGATCAGGAACATTGTTTTTACTCTGCAATATATTTT
 TAATCTACTTTAATCGAATTTACATACCGGATATAAGGATAGAGATGGAAGAACAATAAGTTTTCTT
 TAAAGAAAAATTTAAAAAATTGAAGACCTGTAAATCACAATCCCGAGAAATGGTAGGATCTATGTACAAG
 CAGCTGACATGATAGGGAACTGTCCCGAGCTTTACCAGACAGATTACCTTCTTTTTTTGAACACTCGC
 ATTATTGACAGGGTTAGGAATGGCACGTGATTTTGTTTTTGACGTCATCTTTGATCGTGTTCAAAGCAT
 ATACACGTATATTTTTTGGGACTGCAGCTTGTAAATCATCACTTTGCGCTTTACTTTTCTTTTTTGACA
 CTTTAGTTAATAAAAAACCTGATTTATTGCATTATCGCCCCCTGCTTTTCTTGCCCTCCCCCCCCCTCTT
 CCTCTGTCTTACTTTCTACCGTTCCACGTCAATTTCCGTCTCTCTTTTCTCCTTTTTTTTTTTTTTG
 AATAATGGTGAGCCTCAAAGTTAGAGACTATCGTGGCATTCTTGAAAATTGAAATCCCAATATCTCGTC
 CGGGGCTACTTCTTTGCTCTAGCCCCAAGTGACGGAGGGAGGAACATTCCCTTTGGAGTTTGGGCCA
 AACCTATTTCTGACCAAAAAAACTAGGGATTAGTCATGACTCGTGGGAAGAACAATTATGGTTTTTTTT
 TTTAATTATTATTATTAATACTAGGGAATTTGTATATGTTTCTTTGTTTGCCATGACATGAGAGGAA
 TCACTAGCCTCCAGTTGTTGACATTATTTGTCTCATCGAGAGTTCCATTGAAATTATTTTTAAAAATAT
 TTTTGTCTTAAAAATATATTAATAAATATTTTTATTTTTAAAAAATTATTTTTAACATTAGTACATGA
 AAATGATCTAAAAAATAAAAAAATAAATTTCAAGTAAATAAAAAATAAATAAAAAATCATTTTTTTT
 CAAAAATGTTTTTAAATACAGTGTTAAACACCCCTATGTCCACGAAAGCATATTACTGTGTACCTCCT
 TTATTTTGGTGTATTATATTGAAATTGCAAGGTTATAATGTCAAAGCTGAGGTAGAACATGTATAGAAG
 CACCAAAATATTTGTAGCTCCCTCCTCATCATGCCCTTGTCTTGTACTAATTAGTAATTCGAGACTTA
 AATCATCTATCCTCCAATCTCAAACGAAAAGATAAGGATCGATGTAGCTTACAATATTTTCATTGATTTT
 TTTGAAATTTATGAATTATATTTGTGGTCTTTTCATTTGATTTTCAGGTATCTTGCCATGCTTCCTTAGT
 TTTTTTTTTATCATAGCTCAAACATGAAACCTCTTAAATTATAAGTTATTAGTACCACCCTGTCTTGCA
 TCTAAATATCATATATAGCCTGGACCTTTTCTTCGTGCACTTAATAATCATCTGGTGGTACGTATTCC
 AGGGCCTGGATCCAAAGTGACAGCCAATTTATTTGCCAAGGCACAGTGCTTAGGGGAGAAAACAATTG
 GCGAGGATGACTGCTTCGTTCTAAAAGTAGCTGCTGATCGAGAAGCTGTAATGGAAAGAAGCGAAGGGC
 CAGCTGAGGTGCTGAGGCATGTTCTATACGGCTATTTTTGCCAAAAAAGTGGCCTCTTGATGTATTGG
 AAGACTCCCATCTAACAAGGTACAGACTCCAGAAAATGAACTATTTACTGGGAACCAACCATAGGAA
 GTAGTATCGGCGACTACAGAGACGTGGATGGCGTGTTAATTGCTCATCAGGGGAGGTCATTGTCTACAG
 TCTTTCGATTCGAGGAAGTGTCTGTGCAGCACAGTAGGACTAGAATGGAAGAGGTATGGCGGATAGACG
 ACGTCGTGTTCAACGTGCCAGGGCTTCCATGGATTATTTTATCCCTCCTGCTGATATCTTTGATGCTT
 CTCCATGA

FIGURE 6C

Genomic sequence of *Salix* Xyld4 allele C – SEQ ID NO.12

ATGGGCTCGAGAGCTAGAAGGAAGCAGCGATGGTGCGCACAAACCCTAACTCCACTGCTGGAAGGTCCC
 GACCCCGACATGCAAGAAGAAGGTAACAAAAAGGAAAGTTTCATGGGAGGTGATTTCGTGAATGGTTTCGG
 TTGCAAAAGGGTCTTTCAGCAGGAACAATTTCTCAGTACCGTTATATGGGAGTATTCGGGTGAAAAGA
 CAGGATTTAAGGCTTTTACTTGGAGTCTGGGCTGCCCTCTAGCTCCAATCCCTCTGGTTAACGACCCC
 ATCCATCGCATTACATTAAAAACACCCCTATTGTAAGTTCTTCTACACCTTAATTATCATTGTTTTT
 TTGTTTTCAATTCGGCAGCTCCATTTTATCAGATTTTTTTACAGGAAAATTCGCCGCGCATTATATCA
 TACAGCAGTATTGGCAGCAACAGGGTGTTTTAAAGCAGCAGAAATGTATGAAAAACATGTACTCAACAG
 GAAGTGGCGAAAACGGGTGCTTTGTTCTCTGGCAAATGTTGCCGGGCATGTGGTCTCTGAATTGGTTG
 TCGGAGAAAATAAAGTCATAGCAGGCAGCGACGGGAAGACTGTGTGGCGTCACACTCCTTGGCTCGGCA
 CTCATGCTGCCAAGGGACCCCAACGCCCTCTACGTCGCATAATCCAGGTACGAAGTACGATAAATATTTT
 TTTTCTCCTGGTTGAAGATGATAAGACAAGATCAGGAACATTGTTTTTACTCTGCAATATATTTTTTA
 ATCTACTTTAATCGGATTTACATACCAGATATAAGGATAGAGATGGAAGAACAATAAGTTTTCTTTA
 AAGAAAATTTAAAAAATTGAAGACCTGTAAATCACAATCCCGAGAAATGGTAGGATCTATGTACAAGCA
 GCTGACATGATAGGGAACTGTCCCGAGCTTTACCAGACAGATTACCTTCTTTTTTTGAACACTCGCAT
 TATTGACAGGGTTAGGAATGGCACGTGATTTTGTTTTTGACGTCATCTTTGATCGTGTTCAAAGCATAT
 ACACGTATATTTTTTGGGACTGCAGCTTGTAAATCATCACTTTGCGCTTTACTTTTCTTTTTTTGACACT
 TTAGTTAATAAGAACCTGATTTATTGCATTATCGCCCCCTGCTTTTCTTGCCCTCCCCCCCCCTCTCCTTG
 TTTACTTTCTACCCGTTCCACGTCAATTTCCGTCTCTCTTTTCTCCTTTTTTTTTTTTTTGGAAATAAT
 GGTGAGCTTCAAAGTTAGAGACTATCGTGGCATTCTTGAAAATTGAAATCCCAATATCTCGTCCGGGGC
 TACTTCTTTGCTCTAGCCCCAAGTGACGGAGGGAGGAACATTCCCTTTGGAGTTTGGGCCAAACCAA
 ACCCTATTTCTGACCAAAAAAACTAGGGAATTTGTATATGTTTCTTTGTTTGCCATGACATGAGAGGAATC
 TAATTATTATTATTAATAAATAAGGGAATTTGTATATGTTTCTTTGTTTGCCATGACATGAGAGGAATC

ACTAGCCTCCAGTTGTTGACATTATTTGTCTTATTGATAGTTTGATTAAAAATTGTTTTTAAAAGTATTT
 TTCGTTTAAAAATATATTTAAAAAGATGTTTTTTTATTTTTTTTAAATTATTTTTTAATATTAGTACATGA
 AAATAATCTAAAAATATCAAAAAAATTAATTTCAACTAAAAATAAAAAAATCAATTTTTTTT
 TTAATAATATTTTTTAAATACAGTGTTAAACACCCCTGTGTCCACGAAAGCATATTACTGTGTACCTC
 CTTTATTTTGGTGTATTATATTGAAATTGCAAGGTTATAATGTCAAAGCTGAGGTAGAACATGTATAGA
 AGCACCAAAATATTTGTAGCTCCCTCGTCATCATGCCCTTGTCTTGTACTAATTAGTAATTCGAGACT
 TAAATCATCTATCCTCCAATCTCAAACGAAAAGATAAGGATCGATGTAGCTAACAGTACTTCATTGATT
 TCTTTGAAATTTATGAATTTAATTCGTGGTTCTTTTCATTTGATTTTCAGGTATCTTGCCATGCTTCCTTA
 GTTTTTTTTTTTTTTTAAATCATAGCTCAAACATGAAACCTCTTGAATTATAAGTTACTAGTACCACCTG
 CCCTGCATCTAAATATCACATATAACCTGGACCTTTTCTTCGTGCACTTAACATAATCATCTGGTGGTAC
 GTATTCCAGGGCCTGGATCCAAAGTGTACAGCCAATTTATTTGCCAAGGCACAGTGCTTAGGGGAGAAA
 ACAATTGGCGAGGATGACTGCTTCGTTCTAAAAGTAGCTGCTGATCGAGAAGCTGTAATGGAAAGAAGC
 GAAGGGCCAGCTGAGGTGCTGAGGCATGTTCTATACGGCTATTTTTGCCAAAAAGTGGCCTCTTGATG
 TATTTGGAAGACTCCCATCTAACAAGGGTACAGACTCCAGAAAATGAAACCATTACTGGGAAACCACC
 ATAGGAAGTAGTATCGGCGACTACAGAGATGTGGATGGCGTGTTAATTGCTCATCAGGGAAGGTCGATT
 GCCACAGTTTTTTTCGATTTCGAGGAAGTGTCTGTGCAGCACAGTAGGACTAGAATGGAAGAAGTATGGCGG
 ATAGACGACGTCGTGTTCAACGTGCCAGGGCTTTCCATGGATTATTTTATCCCTCCTGCTGATATCTTT
 GATGCTTCTCCATGA

FIGURE 6D

Amino acid sequence of *Salix* Xyld4 allele A - SEQ ID NO. 30

MGSRARRKQRWCAQTLTPLLEGPDPMQEEGNKKESSWEVIREWFRLQKGLSAGNNFSVP
 LYGSIPVKRQDLRLLGLVLCPLAPIPLVNDPIHRIHIKNTPIENSAHYIIQQYLAATG
 CLKQKCMKNMYSVGSKMIRCETEISSGKNVKSIGTRSGENGCFVLWQMLPGMWSLELV
 VGENKVIAGSDGKTVWRHTPWLGTAAKGPQRPLRRIIQGLDPKCTANLFAKAQCLGEKT
 IGEDDCFVLKVAADREAVMERSEGPAEVLRHVLYGYFCQKSGLLMYLEDShLTRVQTPEN
 ETIYWETTIGSSIGDYRDVDGVLIAHQGRSIATVFRFEEVSVQHSRTRMEEVWRI DDVVF
 NVPGLSMDYFI PPADIFDASP

FIGURE 6E

Amino acid sequence of *Salix* Xyld4 allele C - SEQ ID NO. 31

MGSRARRKQRWCAQTLTPLLEGPDPMQEEGNKKESSWEVIREWFRLQKGLSAGNNFSVP
 LYGSIPVKRQDLRLLGLVLCPLAPIPLVNDPIHRIHIKNTPIENSAHYIIQQYLAATG
 CLKQKCMKNMYSVGSKMIRCETEISSGKNVKSIGTRSGENGCFVLWQMLPGMWSLELV
 VGENKVIAGSDGKTVWRHTPWLGTAAKGPQRPLRRIIQGLDPKCTANLFAKAQCLGEKT
 IGEDDCFVLKVAADREAVMERSEGPAEVLRHVLYGYFCQKSGLLMYLEDShLTRVQTPEN
 ETIYWETTIGSSIGDYRDVDGVLIAHQGRSIATVFRFEEVSVQHSRTRMEEVWRI DDVVF
 NVPGLSMDYFI PPADIFDASP

FIGURE 7

Genomic sequence of *Populus Xyld5* – SEQ ID NO.13

ATGGCAACTTCAGCTCCACTTATCTCAAAATCCCAGTTATCGTCCGGCATAGAAACCTTGGATCATCAG
GAGCAACACTCGCTAGATGACACCATCGAAAAATACATAGAAGGTTTTGGACCGGCACAATATCTGCAA
GTCATCCTTGTGTCAATTGGCATTCTGTTCGATGGACAGCAAACCTTCATTAGTGACTTTTCTGATGCT
GTACCCTCATGGCACTGCACTGATTTTAGTAATCAAACCTTGTTACTCGAGCTCCAATTTTGAATCTC
TCAAACACTGAATGGGCTGGGATGAGCCAGCCAGCTCATCGATAGTTTCCGATTGGGCCCTTGAATGT
GGCAGTTCAGTCATCGTCCGGCTTACCGGCTTCAAGTTACTTTGTGGGCTCCCTGATTGGTGGATTTACT
CTTGCTACGCTTGCTGATTCCCTGGCTTGGTAGAAAGAAGTTGCTCTTCCTAACTTGTATGGGTATGTCC
ACAATGGCACTTATCACTGCCTTCTCCACCAATGTGTGGATCTATTCAGGTTTGAGATTTGTTAGTGGA
CTTTTTCGCGCATCAATTGGAACGTGTGTTGTTGTGATGTCAACAGAAATGGCAGGGAAGAAATCGGGT
GGATTTGTAAGGGTGGTGGGCTTCTTGTTTTTGTCTTAGGAGCACTCTCACTGCCCCTTATAGCTTAC
TTGAATAGAGGTTCTCCATGGAGATATCTTTACATTTATACCTCTATTCCAGCCATCGTTTACTGTATA
ATAGCTTATTTCTTTGTTAGTGAGTCTCCAAGATGGCTTTGCATGCGGGGACGTGAAGCTGAAGCAGTT
GCAATTCTGAATAAAATGGTTCCAACAAAAATATTAGTAGCTCTATTCTAAAATCTGCCTACAAGCCC
CTCGACCATGAGCAGTCGAATCTTGACATATATTCATCGATGAAGAGCTTGCTGGAGAGGAGATGGGCT
TTGAAAAGGTTGTTGGCTGCAATGACTCTTGGTTTTGGTGTGGGAATGGTATACTATGGCATGTTCTTG
GGGGTTGGAAGCTTGGGTTTCAACATCTACCTTAGCGTGACACTTACTGCATCCTTGACCATACCTTCT
ATTCTTTTGCTCCCTTATGTAATAGAAAGATTTAATAGGAGAAGTTCAGTTGTGGCCTTTGGTATAGCA
AGTGGGGTATGTAGCATTGTCTGTGCAATAATTGGTGAAGAACTAAAGACTGTCCAGATTATCATGTCT
TTAGCATCTGCTTCTGCTCGTGTGCTGCACTTAACGTCCTGCAATATACACTACAGAGTTGTTCCCT
ACTTGTGTAAGGATTTAGCCACATCAATGTTTAGGCAAGCTATAAACTTCGGTCCCATATTTGTTCCA
CTGTTAGTTTCAGCTGCCAGGAGAAATAATTCTGTAGTTTATGGAGTCTTTGGATCAGTAGAAATATCC
TGTATCTTCTTTGTAATCTTCTTGCCAGAGACCAGGGGTTTGTCACTTTCCAACGCCATGGATGAACAA
GAGAAGAAGGATAATGCAAACGCGTATGTAAGCTGA

FIGURE 8A

Genomic sequence of *Populus Xyld6* – SEQ ID NO.14

ATGGCAGATTCAACACCACTTCTTCTCTCTCGACCGGACCCTTCCAATGAGTCAAAACAACCTCCTTCC
 CTTGATGAAACCATTGAACGTTGTATTGGAGAGTTTGGGCTCGCCCCAACTCCTCCAAGCCATCCTTGTG
 TCATTTGCATGGGTGTTTGTATGCACAACAAACATTCAATAGTGTCTTCACTGATGCTGAGCCAAAATGG
 CACTGCACAAGTGATTCAATGACTTCACTCTCCGACATTTGCCATCTTCTCCTCAAAATTCATGGGCTTGG
 GATAGCCCTAAGGACACATCAATCATATCAGAATGGGGACTTGAGTGTGCTAGTTCAATAATCAAAGGC
 CTACCCGCATCTTCATTTTTTCATGGGGTGCCTCATTTGGAGGACTGATGCTAGCCACGCTTGCTGATTCC
 TTGCTTGGTTCGAAGAATTTGCTGTTTCTATCATGCCTAATGATGTCTTTCTCTGGATTATTTCACTGTC
 TTCTCCAACAACATATGGATCTACTCGGCCTTGAAATTCGTTAATGGTGTTCGGCCGTGCAACAATTGGA
 ACATGCGCCCTTGTGTTATCAACTGAGCTTGTAGGGAAACGTTGGCGAAGCCAGGTAGGAGTTATTGGT
 TTCTTTTGTGTTTACGCTAGGGTTTTTAACATTACCCGCTTTTGCATATATGAATAGAGGTTCTCTTGG
 AGAAGCTTTTATCTATGACTTCACTACCAACAATTTTCTACTCCATATTAGTTCAATTTCTTAGTTTGA
 GAGTCTCCAAGATGGCTTTTTTGTTCGCGGACGTAAAGAAGAAGCCGTGACTATACTGAAGAGTATTGCT
 ACGGCTGGGAGTAGTGGCATACTCATGAGCTTCTCAAATTTGGAATTCGGGAAAGAGTCATGGAATGTT
 GATACTTATTAGCAATCAAGATTCTCTTAAAGAAAAAGTGGGCTTGCAGAAGACTGTTGACAGTCATG
 GCAGTGGTATTTCGGTATTGGAATGGTGTATTACGGCATGCCATTAGGCCTCGGAAATTTGTCAATCAAT
 CTCTACTTGAGTGTACATTTAATGCCTTGTGAGAGCTACCTGCCTCATTAGTGACATTCTTCTCTCGTA
 GACAACTAAACCGAAAGGATTCGCTGCTTGTTCACCACTCTAAGTGGGGTTTGTAGCATCCTTTCA
 GTTGTGATGGGCGAGACATCTGCAATCTACAAATGGGGCTGGAGCTGGTATCTTTTTTCTGCGCATGT
 ACAGCATTCAACATTTCAATGATCCACACACTAGAGTTATTCCCTACATGTGTGAGGAATTCGGCAATA
 TCAATGGCTAGACAATCTCTTGTATTTCGGGGGTATGTTCACTCCGGTGTGGTGGCGGTTGGAAGTAAG
 AACAGGTTTCTGTACATACGGGATATTTGGGATGGTAATAGGGATTTGTGGGTGTTTGTGATATTCTTG
 CCGGAGACAAGGGGCGAGACAATTTGTGACACCATGGATGAGGAAGAGTACAACAGTACAAACAATGAT
 CTGCCTGTGTTGGGGTGA

FIGURE 8B

Genomic sequence of *Salix Xyld6* allele A – SEQ ID NO.15

ATGGCAGATTCAACACCACTTCTTCTCTCTCGGTTCGGAGTCTTCAAATGAGTCAAAACAGCCTCCTCCC
 TCCCTTGATGAAACCATTGAGCACTGTATTGGAGAGTTTCGGTGTGGCCCAACTCTTCCAAGCCATCCTC
 GTGTCGTTTGCATGGGTGTTTGTATGCACAGCAAACATTCAATAGTGTCTTCACTGATGCCGAGCCAAACA
 TGGCACTGCACCAAGTGATTCAATGCACTTCAAGCTCCGACATTTGCCGTCTTCTCCTCAAAATTCATGGGCT
 TGGGATAACCTTAATGACACGTCAATCATATCAGAATGGGGACTTCAATGTGCTAGTTCAATAATCAGA
 GGCCTGCCCCGATCTTCATTTTTTCATGGGGTGCCTCATTTGGAGGACTCATGCTAGCCACGCTTGCTGAT
 TCCATGCTTGGTTCGAAAGAACTTGCTGTTTCTATCATGCCTGGTGTATGTCGTTCTCTGGATCATTCAAC
 ATCTTCTCCAACAACATATGGACCTACTCGGCCTTGAAATTCGTTAATGGATTTCGGCCGTGCAACAATT
 GGAACGTGCGCCCTTGTGCTATCAACTGAGCTTGTAGGGAAACGTTGGCGGAGTCAGGTAGGAGTTATT
 GGTTCCTTTGTTTACGCTAGGGTTTTTAACATTACAGCTTTCGCATATGTAAATAGAGGTTCTCTCC
 TGGAGAAATCTTTATCTATGGACTTCTGTACCAACAATTTTCTACTCCATATCAGTTCAATTTCTTAGTC
 CGAGAGTCTCCGAGATGGCTGTTTGTTCGCGGACGTAAAGGATGAAGCTGTGTCTATACTGAAGAGTATT
 GCAACGGCTGGGAGCAGCGCATCCTCATGAGCTTCTCGAAGCTTGAATTAAGGAAAGAGTCATGGAAT
 GTCGATACTTATTCAGCAATCAAGATTCTCTTGAAGAAGAAGTGGGCTTGCAGAAGACTTCTGACAGTC
 ATGGCAGTGGTATTGTTGTTATTGGATTGGTGTATTACGGCATGCCACTAGGCCTTGCAAAATTTGTCAATC
 AATCTCTACCTGAGCGTCACATTCAATGCCTTGTCCGAGCTACCAGCCTCATTGGTGCATTTCTCTCTC
 GTAGACAAGCTGAACAGAAAGGATTCTCTCTCGTTTTTCACTACTCTAAGTGGTGTGTTGTAGCATCCTC
 TCCGTCGTGACGGGCGAGAGATCTGCGAACCTGCAAAATGGGGCTGGAGCTGGTGTCTTTCTTCACTGCA
 TGCATGCAATCAACATCTCGTTGATATACACACTCGAGCTATTTCTTACATGCGTGAGGAAGTCCGGCA
 ATATCAATGGCTAGACAATCTCTTGTGTTTCGGCGGCATGTTCACTCCAGTTCTGGTGGCGGCAGGAAGC
 AGAAACAGGTTTCTGTGCTATGGGATATTCGGGATGGTGTATAGGGATTTGCGGGCTGTTTGTGATATGC
 TTGCCGAGACGAGGGGCAAAACAATCTGTGACACCATGGATGAGGAAGAGTACAATAGCACAAAGATT
 GATCTACCTGTGGTGGGGTGA

FIGURE 8C

Genomic sequence of *Salix* Xyld6 allele C – SEQ ID NO.16

ATGGCAGATTCAACACCACTTCTTCTCTCTCGGTGCGAGTCTTCAAATGAGTCAAAACAGCCTCCTCCC
 TCCCTTGATGAAACCATTGAACATTGTATTGGAGAGTTCGGTGTGGCCCACTCTTCCAAGCCATCCTC
 GTGTCGTTTGCATGGGTGTTTGTATGCACAGCAAACATTCAATTAGTGTCTTCACTGATGCCGAGCCAACA
 TGGCACTGCACCAAGTATTGATGCACCTTCAGCCTCCGCCATTTGCCGTCTTCCCTCAAAATTCATGGGCT
 TGGGATAACCCTAATGACACGTCAATCATATCAGAATGGGGACTTCAATGTGCTAGTTCAATAATCAGA
 GGCTGCCCCGCATCTTCATTTTTTCATGGGGTGCCTCATTGGAGGACTCATGCTAGCCACGCTTGCTGAT
 TCCATGCTTGGTCGAAAGAACTTGCTGTTTCTATCATGCCTGGTGATGTCTTTCTCTGGATCATTACCC
 ATCTTCTCCAACAACATATGGACCTACTCGGCCCTTGAAATTCGTTAATGGATTCCGCCGTGCAACAATT
 GGAACGTGCGCCCTTGTGCTATCAACTGAGCTTGAGGGAAACGTTGGCGGAGTCAGGTAGGAGTTATT
 GGTTTCTTTTGTTCACGCTAGGGTTTTTAACATTACCAGCTTTCGCTTATGTAAATAGAGGTTCCCTCT
 TGGAGAAATCTTTATCTATGGACTTCTGTACCAACAATTTTCTACTCCATATCAGTTCATTTCTTAGTT
 CGAGAGTCTCCGAGATGGCTGTTTGTTCGCGGACGTAAGGATGAAGCTGTGTCTATACTGAAGAGTATT
 GCAACGGCTGGGAGCAGCGGCATCCTCATGAGCTTCTCGAACTTAGAATTAAGGAAAGAGTCATGGAAT
 GTCGATACTTATTAGCAATCAAGATTCTCCTGAAGAAAAAGTGGGCTTGCAAGAACTTCTGACAGTC
 ATGGCAGTGGTATTTGGTATTGGATTGGTGTATTACGGCATGCCACTAGGCCCTTGCAAATTTGTCATTC
 AATCTCTACCTGAGCGTCACATTCAATGCCTTGTCGAGCTACCAGCCTCATTTGGTGACATTCCTCCTC
 GTAGACAAGCTGAACAGAAAGGATTCTCTCCTCGTTTTACCACCTCTAAGTGGTGTGTTGTAGCATCCTC
 TCCGTCGTGACGGGCGAGAGATCTGCGAACCTGCAAAATGGGGCTGGAGCTGGTGTCTTTTTCAGTGCA
 TGCCTGCGTTCAACATCTCGTTGATATACACGCTCGAGCTATTTCCCTACATGCGTGAGGAACCTCGGCA
 ATATCAATGGCTAGGCAATCTCTTGTGTTTCGGCGGCATGTTCACTCCAGTTCTGGTGGCGGCAGGAAGC
 AGAAACAGGTTTCTGTGCTATGGGATATTCGGGATGGTGATAGGGATTTGCGGGCTGTTTGTGATATGC
 TTGCCAGAGACGAGGGGCAAAACAATCTGTGACACCATGGACGAAGAAGAGTACAACAGCACAAAGATT
 GATCTACCTGTGGTGGGGTGA

FIGURE 8D

Amino acid sequence of *Salix* Xyld6 allele A - SEQ ID NO. 32

MADSTPLLLSRSESSNESKQPPPSLDETHCIGIEFGVAQLFQAILVSFAWVFDAQQTFI
 SVFTDAEPTWHCTSDSCTSASDICRLPQNSAWDNPNDTSIISEWGLQCASSIIRGLPAS
 SFFMGCLIGGLMLATLADSM LGRKNLLFLSCLVMSFSGSFTIFSNNIWTYSALKFVNGFG
 RATIGTCALVLSTELVGKRWRSQVGVIGFFCFTLGFLTLPFAFAYVNRGSSWRNLYLWTSV
 PTIFYSISVHFLVRESRWLFVVRGRKDEAVSILKSIATAGSSGILMSFSNLELRKESWNV
 DTYSAIKILLKKKWACRRLLTVMVVFVIGLVYGMPLGLANLSFNLYLSVTFNALSELP
 ASLVTFVLVDKLNKRDSSLVFTTSLGVCSILSVVTGERSANLQMGLELVSFFSACTAFNI
 SLIYTLELFPTCVNRSAISMARQSLVFGGMFSPVLVAAGSRNRFLSYGIFGMVIGICGLF
 VICLPETRGTICDTMDEEEYNSTKIDLPVVG

FIGURE 8E

Amino acid sequence of *Salix* Xyld6 allele C - SEQ ID NO. 33

MADSTPLLLSRSESSNESKQPPPSLDETHCIGIEFGVAQLFQAILVSFAWVFDAQQTFI
 SVFTDAEPTWHCTSDSCTSASAIICRLPQNSAWDNPNDTSIISEWGLQCASSIIRGLPAS
 SFFMGCLIGGLMLATLADSM LGRKNLLFLSCLVMSFSGSFTIFSNNIWTYSALKFVNGFG
 RATIGTCALVLSTELVGKRWRSQVGVIGFFCFTLGFLTLPFAFAYVNRGSSWRNLYLWTSV
 PTIFYSISVHFLVRESRWLFVVRGRKDEAVSILKSIATAGSSGILMSFSNLELRKESWNV
 DTYSAIKILLKKKWACRRLLTVMVVFVIGLVYGMPLGLANLSFNLYLSVTFNALSELP
 ASLVTFVLVDKLNKRDSSLVFTTSLGVCSILSVVTGERSANLQMGLELVSFFSACTAFNI
 SLIYTLELFPTCVNRSAISMARQSLVFGGMFSPVLVAAGSRNRFLSYGIFGMVIGICGLF
 VICLPETRGTICDTMDEEEYNSTKIDLPVVG

FIGURE 9A

Genomic sequence of *Populus* Xyld7 – SEQ ID NO.3

ATGGGCCATAGGTGCTGCAGCAAACAGAGAGTTCAAAGAGGGCTGTGGTCTCCTGAAGAAGATGAGAAG
 CTTGTCAAATATATCGCCACTCATGGTCATGGAAGCTGGAGCTCTGTCCCTAAATTTGCAGGTATAAAT
 GTGTGTGTGTGTGTGTTAATACCCCTTTTTTTTTTGCATGCATTAGAACTCAAATCAAGCTATCTGATC
 CATTTTTGACGCATACTTTGCTTTGTACTTGCAGGTTTAAAAAGGTGTGGCAAGAGTTGCCGTTGAGA
 TGGCTGAACACTTAAGACCAGAACTCAAGAGGGGTTGCTTTTCTGCGCTAGAAGAGCAGGTCAATCATA
 GATGCTCATAGAATTTTGGGCAACAGGTAAGGATTAATATTTGAGTCTAAATAAGGAAGTGTATAAAAA
 GGTAGAAATTTAAATAAATAAATAAAAAACACTGTTTCTAACAATGGGGACGGTAGATCACTAGATGACA
 TGAATAGAGTAGAAGAATTACTTAGCCTATATATTCTTTCACTGCATTTTGATTACAAGAACTTTATAC
 TTGTAACAGATGGTCTCAGATATCAAACATCTCCCAGGAAGGACAGATAATGAGGTGAAGAATTTCTG
 GAACTCACGCATAAAGAAAAAGCTCATGGCACAAGGCTTGGACCCAAAAACTCACAACCTTGATTCCTTC
 TCATCAGAGGGCAGCTAATAAGGTTGCATGCAATATATCACCATCTAACCAACAACCCCTTTCAATTAT
 CTCCCAGGATTCAAAGATGAAAGATGTTTCCATGGAGATAAACCCCTCCTATTCTAACACTAGCTTCCCC
 TTATCGTTTCTCATGGCAGCACTCGACTTTTCGTTGCTTCAAACAACAACCGGCTTACCCTTGCCACCTC
 TTGCTATGATAACCCTAGTGTCAATTTGGAATGTAAATACTCAAATTTCTTATGATTCTTCCCTTTTTCC
 TTGCGTGTCTATCCATTGAGAATCAGCGTTTCCCTTCTATCTTCGACTTCGGTGAACCCAACTGGGTT
 TGGTCTCCTAGATGAAGATTGCTTTTGGAGTTGTAGTAACATTGTTGAGCCCTTTGAAGCCACAAAATT
 ATTCGAAGGCATGCGATCACAGGATCAAGAAAACAGCTGAACAAGATTTGTGACACACAAATCGTTGA
 TAAGAATAAAGGAGTTCATGATAATATGGATGCTTCATTTGACACCTCTAGCTATGATCTTGAGTTGGT
 CGACTCCACATTATTTCTGGTTCAATATGTCGTGATCTTGGCTCCATGGATGATCTTTCATGGAACCTT
 TTAG

FIGURE 9B

Genomic sequence of *Salix* Xyld7 allele A – SEQ ID NO.2

ATGGGCCACAGGTGCTGCAACAAACAGAAAGTTAGAAGAGGGCTGTGGTCTCCTGAAGAAGATGAGAAG
 CTTGTGCAATACATCACCCTCGCGATCATGGAAGCTGGAGTTCTGTCCCTAAATCTGCAGGTATGCAC
 GTGCGTGTGTTTTTGTGCTGCATCAGAGATCAAATCAAGCCGTCTGATCTGTGCTTGCAGGTTTGAAA
 AGGTGCGGTAAGAGTTGCCGTTGAGGTGGCTCAACTACCTGAGACCAGAGCTCAAGAGGGGTTCCCTTT
 TCTGCGCTGGAAGAACAGGTCAATCATAGATGTTTATAGAATTCTGGGCAACAGGTAAGGATTATTCGAG
 TCAAATTAATAAGGAAGTACTGTATAAAAAGGTAGAAAAATGAAAAATAAATAAATAAAACACTGTT
 TCTAACAATGGGGAAAGTAGTCTGATTATATATTTTTTCACTGCATTTTGATTTACAAGCTAGAACCTTT
 ATACTGCTTCTAACAGGTGGGCTCAGATATTGTAAGAATTCGAACCTTCGATTAATTTTCACTATATACA
 ATTGATTGTTTGTGCTGTACATTTGGGGAATTATATAGGAAATAATTACAATACATTTTGTAGCTAAA
 ATACAATACATGTTTAACTACCAAAAAATCAATTATCCTATTATAGTAATAAACCGCTATATGGACAT
 AACGGCTATATTTCAACACTCCCCCTCAAGTTGGAGCATAGATATTTATCATGTCCAACCTTGTTAATTG
 CACCATGAAATGCTCTTCCCTGAAACTGCCTTTGTGAGAGTATCGCCATTTCACTGCAATGAGAACACAC
 CAACCCAGTTGCATTTTTTATTTTTCGGTCAACTCGACCAGCCTTTAAATCTCGTCCCCCTCCTTCAAAC
 TGCGCTACCTTATCGAATGTAAATTTTCTGATGGTGATCTCCCCCTGATTAAACAGGGTGAATATCTTC
 GATGGTGATCTCCCTCTGATTAAACAGGGTGTGGAGTCACGGAATATTTTCCGGATGGTGATCTCCCCCT
 GATTAAACAGGGTGTGGAGTCACGTAATATCTTCGGGATTCAGTAATATCTTCGATGGTGATCTCCCCCT
 TGATTAAACAGGGAGTGGAGTCACGGGATATCTTCGATGGTGATCTCCCCCTGATTAAACAGGGTGTGGAG
 TCACGGGATATCTTTGATGGTGATCTCCCCCTGATTAAACAGGGTGTGGAGTCACGGAATATCTTCGGGA
 TGGTGATCTCCTCCTGATTAAACAGGGATGGAGTCACGTAATATCTTCGGGATTCACGGAATATCTTCGG
 ATGGTGATCTCCCCCTGATTAAACAGGGTGTGGAGTCACGGAATATCTTCGATGAGGATCCCCCTGAT
 TAACAGGGTGTGGAGTCTCGGAATATCTTCGTTCTCTTCAATTGTTACTCTCCCCCTGAAGAGAAGGTCC
 GGGAACTCCCCCTGATTAAACAGGGTGTGGAGTCTCGGAATGATTCTCTTCTCATCTCTGATGGTGA
 TCTACTGTTAGTCTGATTTCTCGTTTAACTACCAATAATCTCTCGGGTTAGAATGTCCTGAAAAAA
 CACAAAAGAGAGGCCAAAAAGTGACAGTGCATGCAAGGATAAAAGTAATTTGACTTACTGACAAGAGAT
 TGTATACAAGAGATGGACCAATGAGAACAATATCTATAGTTACATAATCGGTCAAGGTTATAGACCCTT
 CCCTCGTAATAAGAGAGGGTTTCAAGAACCTTAAATTTCCGGAATCCCTGGTCATATTATCAGATGCGC
 CTATATCAATAATTCAAAGGATTATTTTTAATAATGACAGAGTTTGCAGAAGTTTACCAATTGTGTCT
 GGATGAACAACATTCATCGTAGATTGTACCTGTTTCAATTTTCTATAAAATTTACTATACCTTTGCCGATA
 TTTTCCGGGTTTTTCTATAAAATCTCACCAGTCAAGTAGTCAATAATTTCTGATGATCTTTGTTTCGA
 GTGACCCGATTCGCCGCAATAATTAAATAACAACCGTTTCAAGATAACAATTCGAGATAAAAAAATAC
 GTTTCAGATAAAAAATTTGAGATTGCTCGGATCAATATGATTCAAAGAAATACGATTTAAAGGAAAA

AAAATTGAGATTTCGAGATAAAAAATACGTTTCAAGAAAAAAATTCGAGATTTCGAGATACAAAATACGT
 TTCAAGATAAAAAACGTCGAGATTTCGAGATACAAAATACGTTTCAAGATAAAAAAAATTAAGATT
 CGAGATACAAAATACGTTTCAAGATAAAAAAAATTCGAGATTTCGAGATACAAAATAAGTTTCAAGATAA
 AAAATGCAGAGTTGTAGGTGTACCATTATTGTTTCAAGATGACCCGCTTCACCGCAATAAAAAACAAAC
 CAGCCTACCCGGGTTCTTATAACCGGAATTAACCTTTGCCTTTCACTTTCACTTTCTCTCATCTCTGTG
 ACCCATCTGTCTCTACCCGGTCTTATAACCCGAAGTAAACATCTGCATCTCACTTTTATTCTCTC
 ATTTCCAGCCTTGAACCTCTGCCTCATCACTTCTCCACCCGTTCACTTCGACCTTTTCTGTCAAAT
 CGTTGACGAGCTCCGATTCTCAAATACGTTTGCCTGTTGGGCTTTTTTCTTCAGCGGCAGTTTCAGC
 TTCAGCTTTCTTCGAGCCTCGTCAGCAGCCTTAGCTCCTGCCTGCACCCGAGCTTTTCTTCCCTTTTG
 CCTTCTTGCTAATTCCTCAGGATCAGCCTTTTCACTTTTCAATTTCTTTCTCGAGCTTTAAGTAT
 GGTGTGAGCAAAACGGTTCTTCAACAAAGGTGCACGATAGAGCTTATCGGGAGAGACTTGCCTCTCAGG
 TGGAGCACTCTCCCTGTATCAATGCCTGATGTGCAGGTTACCTTTCTGGTGTGTTCTGGTGTGTTG
 GTTGTGATGAGAAATCTGGGTTTGTGGTGTGTTGTTCTGTTTTTTTTCTGTTTTCTTTGTGTGTTGA
 GAAATGAAGGGAGGATGTCTGTGTGTATGAATTGATGGAATTTCTGGGTTTGTGGTTTTTTCCGGGG
 AAAATGTGGCTTTTCCGGGAAATGTGGCTTTTCCGGGAAATCTGGGTTTTCTGGGTTTTACTGTGG
 GGATCGATGGGTATTTTTCTGGGTTGTTGTGTATGAACAGTGTGTTGATGAACAAGCACTGTGCAGAT
 TGAGGTCTGGGTTTCAACCAAGAGAGAGAAAAATGCAGTAATTCGATTTCAAAGAAAAATTCGAG
 ATTTGCTCTGATACCATGTAAGAATTCAACTTCGATTAATTCAGTATATAACAATTGATTGTTGTG
 CTGTTACATTTGGGAATTATATAGGAAATAATTACAATACATTTTCTAGCTAAAAATACAATACA

[N]* - repetitive portions

CATTTTTAGCTAAAATACAATACATGTTTAACTACCAAAAAATCAATTATCCTATTATAGTAATAAAC
 GGCTATATGGACATAACGGCTATATTTCAACAGATATCGAAACATCTCCAGGAAGGACAGATAACGAG
 GTGAAGAATTTCTGGAACCTCGCGCTTGAAGAAAAAGCTCATGGCACAAGGCCTGGACCCGAAAACTCAC
 AACTTGATTCTACTCGCCAGAGGGCAGCTAATAAGGTTGCATGCAGCATGTCACCATCTAACCACGAA
 CCTTTTCAATTACCTCCCATGATTCAAAGATGAAAGATGTTTCTTGGAGATAATTAAACCTCCTAAA
 ATAACACTAGTTTACCTAATTATGCTTCTAATTGCAGCGCCAGCCTCCATTTTTTCAAACAACAACG
 AGCTTGCCCTTGCCCAAATCTTGTTACGATAACCTAGTGTCATTTGGAATGCAAATCTCAAATTTCT
 TATGATTCATCCCTTTTACCTGCGTGTATCCATTGAGAACTCACTCGCTTCTCTCGTCCCTCGTCT
 TCAGCGAACCCAACTGGGTTTGGTCTCGTGGATGAAAAGTCTTTGGAGTTGTAGTGACATTGTTGAG
 CCTTTGAAGCCGCAAAAATATTCGAAAGTGTGCCGCCACAAGATCAAGAAAACAGCTGAACAAGGTT
 TGTGACACCCAAATCGTGGGTGAAGAATAAAGGAGTTCATGACAATATGGAAGCTTCATTCGACACCTCT
 AGCTATGATCTTGGGTTGGTCGACTCCACATTATTTCTGTTTCATTGTGTGATGATCTTAGCTCAATG
 GATGATCTTGCATGGAACTTTTAG

FIGURE 9C

Genomic sequence of *Salix* Xyld7 allele C – SEQ ID NO.1

ATGGGCCACAGGTGCTGCAACAAACAGAAAGTTAGAAGAGGTCTGTGGTCTCCTGAAGAAGACGAGAAG
 CTTGTGCAATACATCACCCTCGCGATCATGGAAGCTGGAGCTCTGTCCCTAAATCTGCAGGTATGCAC
 GTGCGTGTGTTTTTGTCTGCATCAGAGATCAAAATCAAGCCGCTGATCTGTTTTTGACGCATCATTG
 CTCTGTGCTTGCAGGTTTGAAGAGGTGCGGTAAGAGTTGCCGGTTGAGGTGGCTCAACTACCTGAGACC
 AGAGCTCAAGAGGGGTTCTTTTCTGCGCTGGAAGAACAGGTCATCATAGATGTTCATAGAATTCTGGG
 CAACAGGTAAGGATTATTCGAGTCAACTTAAATAAGGAAGTACTGTATAAAAAGGTAGAAAAAATGAAA
 AATAAATAAATAAAACACTGTTTCTAACAATGGGGAAAGTAGTCTGATTATATATTTTGTCACTGCATT
 TTGATTTACAAGCTAGAGCTTTATACTTGTAATTAACAGATGGGCTCAGATATCGAAACATCTCCAGG
 AAGGACAGATAATGAGGTGAAGAATTTCTGGAACCTCGCGCTTGAAGAAAAAGCTCATGGCACAAGGCTT
 GGACCCGAAAACTCACAACCTGATTCTACTCGCCAGAGGGCAGCTAATTATAAGGTTGCATGCAGCAT
 ATCACCATCTAACCACGAACCTTTTCAATTACCTCCCATGATTCAAAGATGAAAGATGTTTCTTGGG
 GATAAACCTCCTGTTCTAACAATAGTTTACCTAATTATCCTTCTAATTGCAGCATCCAGCCTCCATT
 CTTTCAAACAACAACGAGCTTGCCCTTGCCCAAATCTTGTTACGATAACCTAGTGCTGTTTGGAGTTG
 AAATCTCAAATTTCTTATGATTCATCCCTTTTACCTGCGTGTATCCATTGAGAACTCACTCGCTTC
 CTCTTCGTCTCTGTTCTCAGCGAACCCAACTGGGTTTGGTCTCGTGGATGAAAAGTCTTTTGGAGTTG
 TAGTAACATTGTTGAGCCCTTTGAAGCCGCAAAAATATTCGAAAGTGTGCCGCCACAAGATCAGGAAAA
 CCAGCTGAACAAGGTTTGTGACACCCAAATCATGGGTGAAGAATAAAGGAGTTCATGACAATATGGAAGC
 TTCATTGACACCTCTAGCTATGATCTTGGGTTGGTCGACTCCACATTATTTCTGTTTCAATGTGTCA
 TGATCTTAGCTCAATGGATGATCTTGCATGGAACTTTTAG

FIGURE 9D

ALIGNMENT OF *SALIX* XYLD7 ALLELE A (SEQ ID NO. 2) ALIGNED WITH *SALIX* XYLD7 ALLELE C (SEQ ID NO. 1).

Exon sequences are underlined

NNNNNNN = unknown sequence of undetermined length

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Xyld7_C      ATGGGCCACAGGTGCTGCAACAAACAGAAAGTTAGAAGAGGTCTGTGGTCTCCTGAAGAA
Xyld7_A      ATGGGCCACAGGTGCTGCAACAAACAGAAAGTTAGAAGAGGGCTGTGGTCTCCTGAAGAA
              *****
              Exon1

Xyld7_C      GACGAGAAGCTTGTCTGAATACATCACCCTCGCGATCATGGAAGCTGGAGCTCTGTCCCT
Xyld7_A      GATGAGAAGCTTGTCTGAATACATCACCCTCGCGATCATGGAAGCTGGAGTTCTGTCCCT
              ** *****

Xyld7_C      AAATCTGCAGGTATGCACGTGCGTGTTGTTTTTGCTTGCATCAGAGATCAAAATCAAGCC
Xyld7_A      AAATCTGCAGGTATGCACGTGCGTGTTGTTTTTGCTTGCATCAGAGATCAAAATCAAGCC
              *****

Xyld7_C      GTCTGATCTGTTTTTGACGCATCATTGCTCTGTGCTTGCAGGTTTGAAAAGGTGCGGTAA
Xyld7_A      GTCTGATCTGT-----GCTTGCAGGTTTGAAAAGGTGCGGTAA
              *****
                      Exon2

Xyld7_C      GAGTTGCCGGTTGAGGTGGCTCAACTACCTGAGACCAGAGCTCAAGAGGGGTTCCCTTTTC
Xyld7_A      GAGTTGCCGGTTGAGGTGGCTCAACTACCTGAGACCAGAGCTCAAGAGGGGTTCCCTTTTC
              *****

Xyld7_C      TGCGCTGGAAGAACAGGTCATCATAGATGTTTCATAGAATTCTGGGCAACAGGTAAGGATT
Xyld7_A      TGCGCTGGAAGAACAGGTCATCATAGATGTTTCATAGAATTCTGGGCAACAGGTAAGGATT
              *****

Xyld7_C      ATTCGAGTCAACTTAAATAAGGAAGTACTGTATAAAAAGGTAGAAAAATGAAAAATAAA
Xyld7_A      ATTCGAGTCAAATTAAATAAGGAAGTACTGTATAAAAAGGTAGAAAAATGAAAAATAAA
              *****

Xyld7_C      TAAATAAAACACTGTTTCTAACAATGGGGAAAGTAGTCTGATTATATATTTTGTCACTGC
Xyld7_A      TAAATAAAACACTGTTTCTAACAATGGGGAAAGTAGTCTGATTATATATTTTTCCTGC
              *****

Xyld7_C      ATTTTGATTTACAAGCTAGAGCTTTTATACTTGTAATTAACAGATGGGCT
Xyld7_A      ATTTTGATTTACAAGCTAGAACTTTTATACT-GCTTCTAACAGGTGGGCT
              *****
                      Exon3

Xyld7_C      -----
Xyld7_A      CAGATATTGTAAGAATTCGAACTTCGATTAATTTTCAGTATATACAATTGATTGTTTGTG

Xyld7_C      -----
Xyld7_A      CTGTTACATTTGGGGAATTATATAGGAAATAATTACAATACATTTTGTAGCTAAATACAA

Xyld7_C      -----
Xyld7_A      TACATGTTTAAACTACCAAAAAATCAATTATCCTATTATAGTAATAAACGGCTATATGGA

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Xyld7_C
Xyld7_A CATAACGGCTATATTTCAACACTCCCCCTCAAGTTGGAGCATAGATATTTATCATGTCCA

Xyld7_C
Xyld7_A ACTTGTTAATTGCACCATGAAATGCTCTTCCTGAAACTGCCTTTGTGAGAGTATCGCCAT

Xyld7_C
Xyld7_A TTCACTGCAATGAGAACACACCAACCCAGTTGCATTTTTTATTTTCGGTCAACTCGACCA

Xyld7_C
Xyld7_A GCCTTTAAATCTCGTCCCCCTCCTTCAAACGCGCTACCTTATCGAATGTAAAATTTCTT

Xyld7_C
Xyld7_A GATGGTGATCTCCCCCTGATTAACAGGGTGAATATCTTCGATGGTGATCTCCCTCTGATT

Xyld7_C
Xyld7_A AACAGGGTGTGGAGTCACGGAATATTTTCGGGATGGTGATCTCCCCCTGATTAACAGGGT

Xyld7_C
Xyld7_A GTGGAGTCACGTAATATCTTCGGGATTCAGTAATATCTTCGATGGTGATCTCCCCCTGA

Xyld7_C
Xyld7_A TTAACAGGGAGTGGAGTCACGGGATATCTTCGATGGTGATCTCCCCCTGATTAACAGGGT

Xyld7_C
Xyld7_A GTGGAGTCACGGGATATCTTTGATGGTGATCTCCCCCTGATTAACAGGGTGTGGAGTCAC

Xyld7_C
Xyld7_A GGAATATCTTCGGGATGGTGATCTCCTCCTGATTAACAGGGAATGGAGTCACGTAATATC

Xyld7_C
Xyld7_A TTCGGGATTCACGGAATATCTTCGATGGTGATCTCCCCCTGATTAACAGGGTGTGGAGTC

Xyld7_C
Xyld7_A ACAGAATATCTTCGATGAGGATCCCCCCTGATTAACAGGGTGTGGAGTCTCGGAATATC

Xyld7_C
Xyld7_A TTCGTTCTCTTCATTGTTACTCTCCCCCTGAAGAGAAGGTCCGGGAACCTCCCCCTGATTA

Xyld7_C
Xyld7_A ACAGGGTGTGTGGAGTCTCGGAATGATTCTCTCTTCATCCTGATGGTGATCTACTGTT

Xyld7_C
Xyld7_A AGTCTGATTTCTCGTTTAACTACCAATAATCTCTCGGGTTAGAATGTCTTGAAAAA

Xyld7_C
Xyld7_A CACAAAAGAGAGGCCAAAAAGTGACAGTGCATGCAAGGATAAAAAGTAATTTGACTTACTG

Xyld7_C
Xyld7_A ACAAGAGATTGTATACAAGAGATGGACCAATGAGAACAATATCTATAGTTACATAATCGG

Xyld7_C
Xyld7_A TCAAGGTTATAGACCCTTCCCTCGTAATAAGAGAGGGTTCAAGAACCTTAAATTTCCGG

Xyld7_C
Xyld7_A AATCCCTGGTCATATTATCAGATGCGCCTATATCAATAATTCAAAGGATTATTTTTAATA

Xyld7_C
Xyld7_A ATGACAGAGTTTGCAGAAGTTTTACCAATTGTGTCTGGATGAACAACATTCATCGTAGAT

Xyld7_C
Xyld7_A TGTACCTGTTCAAGTTTTTCATAAAATTTACTATACCTTTGCCGATATTTTTCCGGGTTTTT

Xyld7_C
Xyld7_A TCATAAAATCTCACCAGTCAAGTAGTCAATAATTTTCGTAGCATCTTTGTTTCGAGTGACC

Xyld7_C
Xyld7_A CGATTCGCCGCAATAATTAAATAACAACCGTTTCAAGATAACAAATTCGAGATAAAAAAA

Xyld7_C
Xyld7_A TACGTTTCAAGATAAAAAATTTGAGATTCGCTCGGATCAATATGATTCAAAGAAATACGA

Xyld7_C
Xyld7_A TTTAAAGGAAAAAAAAAATTGAGATTCGAGATAAAAAATACGTTTCAAGAAAAAAAAATTCTGA

Xyld7_C
Xyld7_A GATTCGAGATACAAAATACGTTTCAAGATAAAAAACGTCGAGATTCGAGATACAAAATACG

Xyld7_C
Xyld7_A TTTCAAGATAAAAAAAAAAATTAAAGATTCGAGATACAAAATACGTTTCAAGATAAAAA

Xyld7_C
Xyld7_A AAATTCAAGATTCGAGATACAAAATAAGTTTCAAGATAAAAAATGCAGAAGTTGTAGGTG

Xyld7_C
Xyld7_A TACCATTATTGTTTTCGAATGACCCGCTTCACCGCAATAAAAAACAAACCAGCCTACCCGG

Xyld7_C
Xyld7_A GTTCTTATAACCGGAATTAAACCTTTGCCTTTCACTTTCAATTTCTCTCATCTCTGTGACC

Xyld7_C

Xyld7_A	CATCTGTCTCTCACCCGGTTTCTTATAACCCGAAGTAAACATCTGCATCTCACTTTTATT
Xyld7_C	-----
Xyld7_A	TCTCTCATTTCCAGCCTTGAACCTCTGCCTCATCACTTCTCCACCCGTTCAATTCGACCCT
Xyld7_C	-----
Xyld7_A	TTTTCTGTTCAAATTCGTTGACGAGCTCCGATTCTCAAATACGTTTGCCTGTTTCGGCCTT
Xyld7_C	-----
Xyld7_A	TTTTTCTTCAGCGGCAGTTTCAGCTTCAGCTTTCCTTCGAGCCTCGTCAGCAGCCTTAGC
Xyld7_C	-----
Xyld7_A	TCCTGCCTGCACCCGAGCTTTTCCTTCCTTTTGCCTTCTTGCTAATTCCTCAGGATCACG
Xyld7_C	-----
Xyld7_A	CTTTTCACCCTTTTCAATTTCTTTTCTCGAGCTTTAAGTATGGTGTGAGCAAAACGGTT
Xyld7_C	-----
Xyld7_A	CTTCAACAAAGGTGCACGATAGAGCTTATCGGGAGAGACTTGCCTCTCAGGTGGAGCACT
Xyld7_C	-----
Xyld7_A	CTCCCCGTGATCAATGCCTGATGTGCAGGTTACCCTTTCTGGTTGTTTCTGGTTTGTGGT
Xyld7_C	-----
Xyld7_A	GTTTGTGATGAGAAATCTGGGTTTGTGGTGTGTTGTTTCTGTTTTTTTTTCGTTTTCTTTT
Xyld7_C	-----
Xyld7_A	GTGTGTTGAGAAATGAAGGGAGGATGTCTGTGTGTATGAATTGATGGAATTTCTGGGTTT
Xyld7_C	-----
Xyld7_A	GTGGTTTTTTTTCCGGGAAAATGTGGCTTTTCGGGAAAATGTGGCTTTTCCGGGAAAAT
Xyld7_C	-----
Xyld7_A	CTGGGTTTTTCTGGGTTTTTACTGTGGGGATCGATGGGTATTTTTCTGGGTTGTTTGTG
Xyld7_C	-----
Xyld7_A	TATGAACAGTGTTTGATGAACAAGCACTGTGCAGATTGAGGTCTGGGTTTCGAACCAGAA
Xyld7_C	-----
Xyld7_A	GAGAGAGAAAAATGCAGTAATTCGATTTCAAAGAAAAATTCGAGATTTGCTCTGATACC
Xyld7_C	-----
Xyld7_A	ATGTAAGAATTCGAACCTTCGATTAATTTAGTATATACAATTGATTGTTTGTGCTGTTA
Xyld7_C	-----
Xyld7_A	CATTTGGGGAATTATATAGGAAATAATTACAATACATTTTTAGCTAAAATACAATACANN

Xyld7_C
Xyld7_A

NNNNNCATTTTTAGCTAAAATACAATACATGTTTAACTACCAAAAAATCAATTATCCTA

Xyld7_C
Xyld7_A

-----CAGATATCGAAACATC
TTATAGTAATAAACGGCTATATGGACATAACGGCTATATTTCAACAGATATCGAAACATC

Xyld7_C
Xyld7_A

TCCCAGGAAGGACAGATAATGAGGTGAAGAATTTCTGGAACCTCGCGCTTGAAGAAAAAGC
TCCCAGGAAGGACAGATAACGAGGTGAAGAATTTCTGGAACCTCGCGCTTGAAGAAAAAGC

Xyld7_C
Xyld7_A

TCATGGCACAAGGCTTGGACCCGAAAACCTCACAACCTGATTCTACTCGCCAGAGGGCAG
TCATGGCACAAGGCTTGGACCCGAAAACCTCACAACCTGATTCTACTCGCCAGAGGGCAG

Xyld7_C
Xyld7_A

CTAATTATAAGGTTGCATGCAGCATATCACCATCTAACCACGAACCCCTTTTCAATTACCT
CTAAT---AAGGTTGCATGCAGCATGTCACCATCTAACCACGAACCCCTTTTCAATTACCT

Xyld7_C
Xyld7_A

CCCATGATTCAAAGATGAAAGATGTTTCCTTGGAGATAA---ACCCTCCTGTTCTAACAA
CCCATGATTCAAAGATGAAAGATGTTTCCTTGGAGATAATTAAACCTCCTAAAATAACAC

Xyld7_C
Xyld7_A

TAGTTTCACCTAATTATCCTTCTAATTGCAGCATCCAGCCTCCATTCTTTCAAACAACAA
TAGTTTCACCTAATTATGCTTCTAATTGCAGCGCCCAGCCTCCATTTTTCAAACAACAA

Xyld7_C
Xyld7_A

CGAGCTTGCCCTTGCCCAAATCTTGTTACGATAAACCTAGTGTCGTTTGAATGTAAATT
CGAGCTTGCCCTTGCCCAAATCTTGTTACGATAAACCTAGTGTCATTTTGAATGCAAAATT

Xyld7_C
Xyld7_A

CTCAAAATTCTTATGATTTCATCCCTTTTCACCTGCGTGTCATCCATTGAGAACTCACTCG
CTCAAAATTCTTATGATTTCATCCCTTTTCACCTGCGTGTCATCCATTGAGAACTCACTCG

Xyld7_C
Xyld7_A

CTTCCTCTTCGTCTCTCGTCTTCAGCGAACCCAACTGGGTTTGGTCTCGTGGATGAAAACCT
CTTCCTCTTCGTCTCTCGTCTTCAGCGAACCCAACTGGGTTTGGTCTCGTGGATGAAAACCT

Xyld7_C
Xyld7_A

GCTTTTGGAGTTGTAGTAACATTGTTGAGCCCTTTGAAGCCGCAAAAATATTCGAAAGTG
GCTTTTGGAGTTGTAGTGACATTGTTGAGCCCTTTGAAGCCGCAAAAATATTCGAAAGTG

Xyld7_C
Xyld7_A

TGCCGCCACAAGATCAGGAAAACCAGCTGAACAAGGTTTGTGACACCCAAATCATGGGTA
TGCCGCCACAAGATCAAGAAAACCAGCTGAACAAGGTTTGTGACACCCAAATCGTGGGTA

Xyld7_C
Xyld7_A

AGAATAAAGGAGTTCATGACAATATGGAAGCTTCATTTCGACACCTCTAGCTATGATCTTG
AGAATAAAGGAGTTCATGACAATATGGAAGCTTCATTTCGACACCTCTAGCTATGATCTTG

Xyld7_C
Xyld7_A

GGTTGGTCGACTCCACATTATTTCTGGTTCAATGTGTCATGATCTTAGCTCAATGGATG
GGTTGGTCGACTCCACATTATTTCTGGTTCAATGTGTCATGATCTTAGCTCAATGGATG

Xyld7_C
Xyld7_A

ATCTTGCATGGAACCTTTTAG
ATCTTGCATGGAACCTTTTAG

FIGURE 9E

Amino acid sequence of *Salix* Xyld7 allele C - SEQ ID NO. 26

MGHRCCNKQKVRRLWSPEEDEKLVEYITTRDHGSWSSVPKSAGLKRCGKSCRLRWLNYL
RPELKRGSFSALEEQVIIDVHRILGNRWAQISKHLPGRTDNEVKNEFWNSRLKKKLMAQGL
DPKTHNLIPTRQRAANYKVACSISSPSNHEFFSITSHDSKMKDVSLEINPPVLTIVSPNYP
SNCSIQPPFFQTTTSLPLPKSCYDNPSVVWNVNSQNSYDSSLFTCVSSIENSLASSSSSS
SANPTGFGLVDENCFWSCSNIVEPFEEAAKIFESVPPQDQENQLNKVCDTQIMGKNKGVHD
NMEASFDTSSYDLGLVDSTLFPGSMCHDLSSMDDLAWNF

Genomic sequence of *Populus* Xyld8 – SEQ ID NO.17

FIGURE 10B

Genomic sequence of *Salix* Xyld8 allele A – SEQ ID NO.18

ATGGCGCCGGTGAGCCTCCCTCCTGGATTTCAGGTTCCATCCAACCTGATGAAGAGCTCGTTGTTTACTAT
CTCGATAGAAAAATCAACGCCGCCACAGTTGAGCTTGAATTATCCCGGAGGTGGATCTCTATAAATGT
GAGCCATGGGACTTGCCAGGTAATGCTTTACAGATTGAATTAGCTCCGGCCATACCGACATCATCAAT
ATTATTGAGCATCACCCTCATATATGCACCTGACAACCTTTTCTTTTCTTTTCTGTGATGATTCGATC
AACAGAGAAGTCGTTTTTACCAGCAAGGATCTGGAGTGGTATTTTTTAAGCCCCAGGGACAAGAAATA
CCCTAATGGGTCAAGAACGAACAGGGCAACAAAAGCTGGTTACTGGAAAGCCACAGGGAAAGACAGACC
GGTGAGCTCGCAGAAGCGGCCGGTTGGCATGAAGAAGACATTGGTGTACTATAGAGGTAGAGCTCCCCA
TGGCATCAGAACCAACTGGGTAATGCACGAGTATCGCTTGATCGACTCATCATTTGTGCGGCGCCGCATC

ATCAAGTTTAAAGGTATATATTGCACTTAATTACGGCACGATTTCTATTTGATGCATGCACAGAAGTTT
 AATCAAGTAGGGACACAATTTTAAACCATTCGATAATTAATTATGTCCAGAAATGTCATGTAGGTGAAT
 TAATTATGAACAATGAGCCATGCAATATCATGGTGAATTAGCTGGATCTGCCCCATCGATCTGGTGGTT
 TTGGTGGCATTTCATATGTAGACCAGTAGTGAGAGGCTATTAATTAGGGTTTACAAAAAGACAGCCGTAC
 GTGTTTGATTGTGTAGAGATATATATTTCAATAGGATTCACACGCGGCTGCAAGATCAGAGTCTTGG
 TCTCACAGGAAACCTAGTACTAGCAAGGAAGATGAATGTAAAGTGGTCCATGTCTAATTAATTAATTT
 TAATATTAATTTTTACTACTCCAAGTAGATTCTTGATTTTCAGTTCAAATAATCAAATGATTTAGAAAAA
 CATTAAATTTTTTAAGAGCATATTATATACAGGATTATGCTTCTTTATATGACAGATATGCAAAACAT
 ATATAGAGCAGAGATCTTGTCACATTTGCTCTTGTGTTTTGTACACCAACAAATCATTTTTAGATCTTCC
 TTTTCTACTAAATGTTATCTCTCTTTAATAAAGAATACCTTATCATCAACATATATGATGATGAAAGA
 GTCTTTGTTTAGTGACTTTACTTGTACTTGCCTATCTTTGCTTGGTTTCTTGTCTTTTTCTGCTCT
 TTGTGATCTTGCTTTTACAGATCTTTGTCACTGCCTCTTTAACAAGTCTGGCTCTTCTTGCGCGCACC
 ACAGGATTCCTACGCATTATGCCGTGTTTTCAAGAAAACAATACATATTCCAAAACCGAAAGAAGA
 AAATAATGGAAATGATAAGGAGAAGGATGCGGCGGCGGTATCATCAGAAGTGCAATTATTAGGGGACGA
 CACAGTTAGCGGCATTGAAAGTTCTAAAGGGAGAGATAATGCTGATCATCGAGATGAAAAATTTCAACAA
 TGGCTACTGTAAATTTCCATCGGAAACATCTTCTCCGATGTCACTCAAGGGACTCCGATTGAAACTGC
 GATGCCCGATGATTTACAACCTCCGTTTCCCTCCGATGAGGCCATTAGTTCAGCTAGCCTTTATTCCAT
 GGGCGTGGATTTCTCGTCAAATCTAATTCAGGTACTGTTACTTTTTATGACATAATAATCTGGTTCGT
 TAAACAAGGCTCCTTTTACACGTTGGTTTTAGTTTTTGTATGGCTTGATGATCTTTCGATAAATAGTTA
 ATGTGCGTCCAAAAATAGTAATTAATAATAACTAAATATGTAGGTAAGTACTGCATATAGAATATGTC
 TAGATGGGTGTGACATGGAAAGACAGTAGAAAAACATCAGGCCATTGATGGCATGGGCCACGCCTAGAT
 CCACATGCAACAATCATCTTCTCCAACCTCATCCTTTCTGATCATCTCTTTTGCTAGCACCACATTTCC
 ATCGATATTCTGCCCTGTTGCGAGAGCTTCATGTTTACACCAGGGAAAATACCACGTGGCTGTGCTTCA
 CGCAGAGAATGAAAGTACAATCCTGGGGCCAGCATGTGCTGGGAATGGCCACGACACAAGCCCTTTGA
 GTTTCTTTCTTTCTTTTGTATCTTAAGTTGAAAGCCATGAAACTCCCTGTCTTTTCTTAAAGCTTCCCTC
 TAAAAATCTCTCTCACTGACTCCAACCTAGCTTTCTTTTACCACCTCTCAATAACTTCTTTTACTGACT
 CGAACATAATTCAAAGTTCAAACATCTTTCTTCTGATTTTTCTCTCTGGGTCTACTCTATGTGACACC
 ACAATTATCACTACTTCCAATGCACATGTTCCCCACTTGAAACACATTTTGAATCATCTCCAATTCA
 AAACATGTTGCTGGGCTTACATTTTAAATTTAATTACTCAACAATAATCTTCAAAGGAGGTGGAGTTG
 CTTTCTCCACCTCCCGCTGAATCTCTCTCGGTATGAGGCCGATTATTAATCACACAACATATTGTGG
 ATGCAGGATATGCAGATGCCAACTGCTCGAGCTTGCAGTATCAATTTCCGTTCCACCTTTAGAACTT
 AAGGATTTCCACAGATTGGTTTTACGGACGGAATGGAGCCATCAAAGCCTGAAATAATCGACGACTAC
 ATGATGTACAGGGATTGCATGAACGGGATATTTGAAGAAAATTTCTACTTATGA

FIGURE 10C

Genomic sequence of *Salix* Xyld8 allele C – SEQ ID NO.19

ATGGGCGCGGTGAGCCTCCCTCCTGGATTCAAGGTTCCATCCAACCTGATGAAGAGCTCGTTGTTTACTAT
 CTCGATAGAAAAATCAACGGCCGCACAGTTGAGCTTGAAATATCCCGGAGGTGGATCTCTATAAATGT
 GAGCCATGGGACTTGCCAGGTAAATGCTTTACAGATGTAATTAGCTGATCCCATACCGACATCATCAAT
 ATTAGTCAGTATCACCTCATATATGCACCTGACAACCTTTTTTTTCTTTTCTGTGATGATTTCGATCA
 ACAGAGAAGTCGTTTTTACCGAGCAAGGATCTGGAGTGGTATTTTTTAAGCCCCAGGGACAAGAAATAC
 CCTAATGGATCAAGAACGAACAGGGCAACAAAAGCTGGTTACTGGAAAGCCACAGGGAAGACAGACCG
 GTGAGCTCGCAGAAGCGCCGCTTGGCATGAAGAAGACATTTGGTGTACTATAGAGGTAGAGCTCCCCAT
 GGCATCAGAACCAACTGGGTAATGCACGAGTATCGCTTGATCGACTCATCATTTGTGCGGCGGCGCATCA
 TCAAGTTTAAAGGTATATATTAATTGTACTTAATTACGGCACGATTTCTATTTGATGCATGCACAGAAG
 TTTAATCAAATTTAACCCATTGCATAATTAATAATGTCCAGAAATGTCATGGAGGTGAATTAATTATAT
 ATGAACAATGAGCCATGCAATATCATGGTGAAGCTGGATCTGCCCCATCGATCTGGTGGTTTTGGTGGC
 TTTTCATCATATGTAGACCAGGAGTGAGAGGCTATTAATTAGGGTTTACAAAAAGACAGCCGTACGTGTT
 TGATTGTCACTCTGTGTAGAGATATATATTTCAATAGGATTCACACGCGGCTGCAAGATCATCAGAG
 TTCTTGGTCTCACAGGAAACCTAGTAGAAATGACAGATGAATGTAAAGTGGTCCGTGTCTAATTAATT
 CATTTTAATATTAATTTTACTACTCCAAGTAGCTTCTTGATTTTCAGTTCAAATAATCAAATGATTTAGA
 AAAACATTAATATTTTTAAGAGCATATTATATACAGGATTATGCTTCTTTATATGACAGATATGCAAC
 ACATATATAGAGCAGAGATCTTGTCACATTTGCTCTTGTGTTTTGTACACCAACAAATCATTTTTAGATC
 TTCTTTTCTACTAAATGTTTTCTCTCTTTAATAAAGAATACCTTATCATCAACATACATGATGATGA
 AAGAGTCTTTGTTTAGTGACTTTACTTGTACTTGCCTATCTTTGCTTGGTTTCTTGTCTTTTTCTG
 CTCTTTGTGATCTTGCTTTTACAGATCTTTGTCACTGCCTCTTTAACAAGTCTGGCTCTTCTTGCGCG
 CACCACAGGATTCTACGCATTATGCCGTGTTTTCAAGAAAACAATACATATTCCAAAACCGAAACAAG
 AAGAAAATAATGGAAATGATCAGGAGAAGGATGCGGCGGCGGTATCATCAGAAGTGCAATTATTAGGGG

ACGACACAGTTAGCGGCATTGAAAGTTCTAAAGGGAGAGATAATGCTGCTTATCAAGATGAAAATTTCA
 ACAATGGCTGCTGTAAATTTCCATCGGAAACATCTTCCTCCGATGTCACTCAAGGGACTCCGATTGAAA
 CTGCGATGCCCGATGATTTACAACCTCCGTTTCCCTCCGATGAGGCCATTAGTTCAGCTAGCCTTTATT
 CCATGGGCGTGGATTTCCCGTCAAATCTAATTCAGGTACTGTTACTTTTTATGACATAATAATTCTGGT
 TCGTTAAACAAGGCTCCTTTTACACGTTGGTTTTAGTTTTTTGATGGCTTGATGATCTTTTGATAAATA
 GTTAATGTCGGTCCAAAAAATAGTAATTAATAAATACTAAATATGTAGGTAAGTACTGCATATAGAATA
 TGTCTAGATGGGTGTGACATGGAAAGACAGTAGAAAAACATCAGGCCATTGATGGCATGGGCCACGCCT
 AGATCCACATGCAATAATCATCTTCTCCAACATCATCTTTTCTGATCATCTCTTTTGCTAGCACCAT
 TTCCATCGATATTCTGCCCTGTTGCGAGAGCTTCATGTTACACACAGGGAAAATACCACGTGGCTGTGC
 TTCACGCAGAGAATGAAAGTACAATCCTGGGGCCAGCATGTGCTGGGAATGGCCCCACGACACAAGCCCT
 TTGAGTTTCTTTCTGTCTTTTGATCTTAAGTTGAAAGCAGCAAAAGTTGGAAGCCATGAAACTCCCTGT
 CTTTTCTAAAGCTTCCTTCTAAAAATCTCTCTCACTGACTCCAAGTACTGCTTTTCTTTTACCCTCTTCA
 ATAAGTCTTTTCTGACTGACTCGAACATAATTCAAAGTTCAAACATCTTTCTTCTGATTTTCTCTCTG
 GGTCTACTCTGTGTGACACCACAAATATCACTACTTCCAATGCACATGTTCCCCCACTTGAAACACATT
 TTGAAATCATCTCCAATTCAAACATGTTGCTGGGCTTACATTTTTAATTTAATTACTCAACAATAATC
 TTCAAAGGAGGTGGAGTTGCTTTCTCCACCTCCCCGCTGAATTCTCTCTCGGTATGAGGCCGATTATT
 AATCACACAACATATTGTGGATGCAGGATGTGCAGATGCCAACTGGTCGAGCTTGCAGTATCAATTC
 CGTTCCCACCTTTAGAACTTAAGGATTTCCACAGATTGGTTTCACCGACGGCATGGAGCCATCAAAGC
 CTGAAATAATCGACGACTACATGATGTACAGGGATTGCATGAACGGGATATTTGAAGAAAATTTCTACG
 TATGA

FIGURE 10D

Amino acid sequence of *Salix* Xyld8 allele A - SEQ ID NO. 34

MAPVSLPPGFRFHPTDEELVVYYLDRKINGRTVELEIIPEVDLYKCEPVDLPEKSFLPSK
 DLEWYFLSPRDKKYPNGSRTNRATKAGYWKATGKDRPVSSQKRPVGMKKTLVYYRGRAPH
 GIRTNWMHEYRLIDSSLGGAASSSLKDSYALCRVFKKTIHIPKPKKEENNGNDKEKDAA
 AVSSEVQLLGDDTVSGIESSKGRDNADHRDENFNNGYCKFPSETSSSDVTQGTPIETAMP
 DDLQPPFPSDEAIISSASLYSMGVDFSSNLIQDMQMPNCSSLQYQFPFPFPLELKDFPQIGF
 TDGMEPSKPEIIDDYMMYRDCMNGIFEENFYF

FIGURE 10E

Amino acid sequence of *Salix* Xyld8 allele C - SEQ ID NO. 35

MAPVSLPPGFRFHPTDEELVVYYLDRKINGRTVELEIIPEVDLYKCEPVDLPEKSFLPSK
 DLEWYFLSPRDKKYPNGSRTNRATKAGYWKATGKDRPVSSQKRPVGMKKTLVYYRGRAPH
 GIRTNWMHEYRLIDSSLGGAASSSLKDSYALCRVFKKTIHIPKPKQEENNGNDQEKDAA
 AVSSEVQLLGDDTVSGIESSKGRDNAAYQDENFNNGCCKFPSETSSSDVTQGTPIETAMP
 DDLQPPFPSDEAIISSASLYSMGVDFSPNLIQDVQMPNWSSLQYQFPFPFPLELKDFPQIGF
 TDGMEPSKPEIIDDYMMYRDCMNGIFEENFYF

FIGURE 11A

Genomic sequence of *Populus* Xyld9 – SEQ ID NO.20

ATGTCGATACTGTGGAAGAAGAGCGAGGCCTGGAGGTGGATAGTGAGGATGACAAGAGACTCAAAGCCA
 TTCTTCTTCGCATTTCGCTGCATGATGCGGTGTCGTTCCAGGTGTGATTGGGTATTTTCGTGATGCAAACC
 ACCAACTCCCGCAACCCCGAGCTCGAAGCCCGCCTCCGTTAGAACGCGCGTCCCGATTCCCCTGTACGT
 ACGTTATATATATATATATATATATACTTGAATCACCGTTGATTTTCTCCATAAAAACGTTTGATCTGCAG
 ATTTTTGGGCATGGCCCGCTATTTGTGATTATTGACATATCTTAATTCCTGATTATTTTGTAACTTGG
 TTATTTCAAGAATCTGACTCTGACTCTGATGCTATATTTTAAAGTAGTTTAGCATCGAATGCTAGAAAA
 TAATATATGAAAAGTACGTTAATCACTCATAGATATCAAGAGGAAGAATGGAAGGGCGGTAAAGCTTCT
 GAAGGATACCTCAATTAGCATAGAGTTGCAGACTAGTCACTGGATACTTTTCATCTTGGTTAAGCTTCC
 AAATTTCAATATATGGCAGATGGATTTACAGGTAAGGCCACTTCTAACTGAAGTCATCTTTTGGTAAT
 CACAGGAATGAAAGTGCATGGCAGTGACCTCAGAGTAGCTGCTTTAGATACTTAGGTTAGTTCCTCTTT
 AATTTCTGTCTCATATCCTAGAGTTAAGATTGCCCCAAAATCTTGGGTCATGGTTAATAATTATCACCC
 TTTTGATCTTCAAATGGAAGTACATGTTGACAAATTTTGTGTGCTCGAATTTCTCAATCAGATGATGGG
 TAAAGTTAATCGAGAGAGACTGGCAGAATACCTTGCGGAGCTGCAGCGGAAAGAGGATACAAACGATCG
 CTATGTAGCTGCTCTAAGAGGGGAGACATTTACAAGAAACCATATGTAAGGATTCAGTCAATACCCAA
 GCGGAATAACACTGAAGCTGGCAAGGAGCAGAACCTTGATAACGATCAAAGGAAGCAGATTAGTTGA

FIGURE 11B

Genomic sequence of *Salix* Xyld9 allele A – SEQ ID NO.21

ATGTCGATACTGTGGGAGAAGAGCGAGGCCTGGAGGTGGATAGTGAGGAAGACGAGAGACTCAAAGCCA
 TTCTTCTTCACATTTCGCTACAGTATGCGGTGTCGTTCCAGGTGTGATTGGGTATTTTCGTGATGCAAACC
 ACCAACTCTAGCAACCCCGAGCTCGAAGCCCGCCTCCGTCAGAACGCCCCGTCCCGATTCCCTTGACGT
 ACGTTATATATATCTTGAATCACCGTTGATTCTCTCCATAAAAACGTTTGATATGCAGATTTTTGGGCA
 TGGCCACGTTGTGATTATTAACATTTTAATTCCTTCTTTGTTAACTCGGTTGTTTTAAGAATCT
 GACCCTGACCCTGATGCTATATTTACAAGTAGTTTAGCATCGAATGCTAGAAAATAATATATGAAAAGC
 ATGTTAATCACTCATAGATATCAAGAGGAATAATGGAAGGGGGCAAAGTTTCTGGGGGAGGGGTACA
 ACAATTAGCATAAAGTTGCAACTAATCACTGGAACTTTTCATCTTGGTTAAGCTTCCAAATTTCAAT
 ACATGGCAGATGGATTTCACTAAGGCCACTTCTAACTGAATTCATCGTTTGGTAATCACAGGAATG
 AAAGTGCATTGCAGTGACCTCAGAGTAGCTGCTCTAGATACTTAGGCTAGTTCCTCTCAGTTTCTGTC
 TCATATCCTAGAGGTATATTGCCCCAAAATCTTGATCATGGTTAAACAATCTTAACTGCGTTATCTT
 TACTTGAATTTAAGCAATGTTAGACCTATTATTTTGTGATGAATTCATGCTAGAACTTGATTTTTAA
 GTAGTCTCGACATTGAAACGGCTGTTTTTATTTTAATAAACGAGTTTAATTCTACTGTGATTGTATAAA
 GCCTTTCTCATCTTCAAATGGAATCACTTGTTGACAAATTTGCTTGCTCGACTTCTCAATCAGATGA
 TGGGTAGAGTTAATCGAGAGAGACTAGCAGAATACCTTGCGGAGCTGCAGCGGAAAGAGGATACAAACG
 ATCGATATGTAGCTGCTCTTAGAGGGGAGACATTTACAAGAAACCATATGTAAGAATCCAGCCAATAC
 CCAAGCAGAATAGCACTGAAGCTGACGATCAAAAGAAGCAGATTGTTTGA

FIGURE 11C

Genomic sequence of *Salix* Xyld9 allele C – SEQ ID NO.22

ATGTCGATACTGTGGGAGAAGAGCGAGGCCTGGAGGTGGGTAGTGAGGAAGACAAGAGACTCAAAGCCA
 TTCTTCTTCACATTTCGCTACAGTATGCGGTGTCGTTCCAGGTGTGATTGGGTATTTTCGTGATGCAAACC
 ACCAATTCCAGCAACCCCGAGCTCGAAGCCACCTCCGTCAGAACGCCCCGTCCCGATTCCCTTGACGT
 ACGTTATATATATCTTGAATCACCGTTGATTCCCTCCATAAAAACGTTTGATATGCAGATTTTTGTGCA
 TGGCCCACTGTTTGTGATTATTGACATTTTAATTCCTTCTTTGTTAACTCGGTTGTTTTAAGAAT
 CTGACCCTGACCCTGATGCTATATTTAAAGTAGTTTAGCATCGAATGCTAGAAAATAATATATGAAAA
 GCATGTTAATCACTCATAGATATCAAGAGGAATAATGGAAGGTGGGCAAAGTTTCTGGGGGAGGGGT
 CAACAATTAGCATAAAGTTGCAACTAATCACTGGAACTTTTCATCTTGGTTAAGCTTCCAAATTTCA
 ATACATGGCAGATGGATTTCACTAAGGCCACTTCTAACTGAATTCATCGTTTGGTAATCACAGGAA
 TGAAAGTGCATTGCAGTGACCTCAGAGTAGCTGCTCTAGATACATAGGCTAGTTCCTCTTCAGTTTCTG
 TCTTATCCTAGAGGTATATTGCCCCAAAATCTTGATCATGGTTAAACAATCTTAACTGCGTTATCTT
 TACTTGAATTTAAGCAATGTTAGACCTGTTATTTTGTGATGAATTCATGCTAGAACTTGATTTTTAA
 GTAGTCTCGACATTGAAACGGCTGTTTTTATTTTAATAAACGAGTTTAATTCTACTGTGACTGTATAAA

GCCTTCTCATCTTCAAATGGAATCACTTGTTGACAAATTTTGCTTGCTCGACTTTCTCAATAAGATGAT
AGGTAGAGTTAATCGAGAGAGACTAGCAGAATACCTTGGCGAGCTGCAGCGGAAAGAGGATACAAACGA
TCGATATGTAGCTGCTCTTAGAGGGGAGACATTTACAAGAAACCCATATGTAAGAATCCAGCCAATACC
CAAGCAGAATAGCACTGAAGCTGACGATCAAAGAAGCAGATTGTTTGA

FIGURE 11D

Amino acid sequence of *Salix* Xyld9 allele A - SEQ ID NO. 36

MSILWEKSEAWRWIVRKTRDSKPFFFTFATVCGVVPGVIGYFVMQTTNSSNPELEARLRQ
NARPDSLMMGRVNRERLAEYLGELQRKEDTNDRYVAALRGETFTRNPYVRIQPIPKQNST
EADDQKKQIV

FIGURE 11E

Amino acid sequence of *Salix* Xyld9 allele C - SEQ ID NO. 37

MSILWEKSEAWRWVVRKTRDSKPFFFTFATVCGVVPGVIGYFVMQTTNSSNPELEAHLRQ
NARPDSLMIGRVNRERLAEYLGELQRKEDTNDRYVAALRGETFTRNPYVRIQPIPKQNST
EADDQKKQIV

FIGURE 12A

Genomic sequence of *Populus Xylid10* – SEQ ID NO.23

ATGTCCAAGGAGCCATCATCGTCACTGAGTAATACTGCTAGAGCCACTGGTAGTGATACTAGCAGTCAA
 GCAAAGGGAACCAGTCAAGCAAAGGGTGGTTCCAAATTGGAGAAGAAGCAATCCATCAAGCAGAAATAT
 AGTTTCATCCCTGATAATTTTTCTTCCCTAGAACAGGTACGTGCCAATCATCCTCTTTAATTATTTTCT
 TTCATTTTCTTGGGAAGCCTTGCTGGTAATTTTCATTTCAGGATAGATAATTTTCCACTTATTGAGCAAAC
 TACACACACACACATATTATTCGATAAGAGAATGGATATTAATTTCTTGATGACTTGCGGAAAATTT
 GTCTGGTTAGCCGTTGCGATCTTAGTCAATTTGTCTGATTTGACTTTTCCCTGATGGAATCTCAGGGGA
 ATCTTCTTATCAATTCGCACTCTCCACTCCACTCCATGCCGTTTCGTTTGCTTTTCAAATACTACTTGC
 TTCTTATTCTAAAAAATATTACAATGCTCCATGGAAAAAGATAAAATAATAATGGAAAAGTGATATCC
 GACCAGTCAAAATATCGCAAGGTGCTTTTATTTTATTTTCTGTTAAACAAAGTCACGACAGTACT
 GTTAGTGTGGTCCAGACGCCAATTTCCCTTCTTTTTTTTCCCGCTTGGATTATAAAGGAATAAAGTAGC
 TGTGTTTTTTAAAGTATTTTTTATTAAAAATATATTTAAATATATTTTTTATTTTTTAATAATTATTTT
 TTATATTAATACATTAAAAACAATTTTAAAAAAATTCAAAGTGTTAGAACTTAAGTTGAAATTTGAAA
 TGCTATTCCAATGAAAATTTTCAAATCGAAGAAAATAGGTATTTATTTGACATTTTGTGTGTAATAAC
 TGTCATTTTATTCAAACCGATAACATCCAACAAAGCCACATAAGAGCGAATTTTTTTGAAAGGACTGAA
 AAGAAAAATCATGTTAATTTTTTTTTTTTTTAAAAAAGTGATAGCTATATTGTTATTTTTTAATAAATTG
 AAAAAATACTCGTTATTTATTTTTTCTGATTTTTTTTTCGTTAATCTTAACCTCTTTTTTTTCCGGCGCC
 AAACGGCCAAGGATAAACACTCCTAAGATATACAGGTTTCATGGAACACACGCAGACACTCACGAAACAT
 GTTTTTTTTTTAATCCTTTGATTTCCATGTGTTTTTTTATGGGATATTTAGAAGTGTGATTTTTTAAAGT
 TTTTTTGTGTGAAAAATATATTAATAAATTTATTTTTTAGTTTTTTTAAATATTTTAACACCAACAAA
 TAAAAATAATATGAAAAATATTAAAAAATATTAATTTAAACAAATAAAAAATAAAAAAATTTAATTT
 TTTAAAAAGCAAAATAAACATAACTTTAAAAATATATTAATAATATATATTTTTTATTTTTTAAATA
 AACACATTAAAAATAATAAACATTAAAAAAATAATCTAACACATTTCTAAACAGTCCTAAATCATCA
 AAACAACCTCAAATTTATCACGGTGAGAATACAATTTTTTAAACAAAGAAAAAGAAAGATATAATCATA
 TGTATAGTTTATTTTTACATTTGAAATTATATTTATATGTGATTTAAAAGTGTTTTTTAAATTTATAAAA
 ATATAAAATTAATTTTTTTATAAATCTTATTATTCATAACATCATTAAATCAAATATTAATCAAATTC
 CTAACAAATATTTCACTGAAACATTCGATATGAATTCATAAAAAATCGAAGTTGAAATTTGTCAATTTATGAA
 ACAAGAAAGAAAGTATACACTCCACATGTCATGATTTCCCTGAGAGAAGAGAGGGGCCATTATTGCCAAC
 CACTGGCAATAAAGCTAACCGCTTTTTTGGTCAATCAGTCAACACGGTGTCTTCTCTCAATTTGGAAA
 CGTGAAAGTTAGATAAGATAAATAAAGAAAAAGCAAGTTTTTTCAATCATCAAGTATTATTGGTGACCCCA
 GGCATATTGAAGGTTTTCAAGTAATTTGACTGACTGAATCTCGAGGGATATAATTTAACTAATCAGTTT
 CTAGATTTGTTCTTTAAATATTACTAGTTTAAATTTTTATAAACTCTAGTATTATTAGAAATTTACATGA
 TTATTAACCTTTAGAATCCGTGAGATTAGTCAAGGTACGTGTAAGTTGGCCTAGACACCACATTAATAAT
 AAAAAATAATAATGAATGAGTGATTTTTTTTATAAAAAAACAGGCTACATAATTAATAGTCCGTTT
 TATTCTCAAATTCATCTATTTTTCTTTCTTTCTACTAATGTTTTACAGACAGATTTCTCATTCAAT
 TTTTTTTCTATAAACACACGTGACAGCTATTATTATAGGAGAAGTCAGTCGTTTAAATTCACGAGAC
 TCACACCTTATCATTCACGTTCAATTTGAATATTAATATAGTACAAAACTAAGGTAAATTACAAAAAT
 ATCTTGAAGTATCATAAACTACTAACACCGTAATTTTTTTTTTTAATTTAGACAGTATTTGAAATGCAG
 GCCGATCCACGTTTGTAATAATTTAAAAAAATTTATTTTTTAAATTTGTTTTGATGTACTGATTCAAATA
 TAAATTTTATAAAATTTAAAAATATTATTTTAATGTATTTCAACATGAAAGACACTTTGAAAATCAACC
 GCAACTATAACTTCCAAACAGGCCCTATACAACCCACACCCCTCACGTTCAAATAAATATTATAAAAA
 CCTCATCCTTTTATTTAAAAATGCTTTTAAATATTTTTTGGCATGCATAATTTCTATGTTTCTCATGGTGGTT
 GTTATAATATCTTCATATTTTAGATTATTATTATTATTATTATTATTATTATAAATTTAATGGAAA
 CTATTGTAATTTATCCTAAAAAAAGTCTGCAACTCATTTTCAATTTTCAATGATCGAACTTAAAAATT
 TAATGGAAATCATAAGCTTTATCTCTTGCAATAAATTTATCGATTATCACACGAGTCCACATTCAAGACT
 CGACGAGTTCTACAATATTTTCATGGTAATTATCGCTTAATTTATATGAATAAGCTTATGTTAAGTGAG
 CTTTCGTACAAAGATTTCTCCAAAGCCTGCACCTTGGGAACGGGAGCTGGATTCAATTTCAACGTGAACC
 AAGCTTTAATGTGTGTTCAATAATATAATGTAAAGTGGTTAGTAAAGTGTTTTACAATTTAAAAATATA
 TTAAGATTATATTTCTTAATATTTTATTTATTTTAAAGATTATATATATAACAGTAGAATTTATTGT
 ATTTTTTTTATTAACATGAAAAAATAAATTTAGATTGTATGCTCAAAAAATCATCTTTAGCCTTATTAT
 TTATACTCAATTCCAATCTATTTATAAACTATTCTAGTCAATTTTAGATCGGTATCTGTAAAAAGAAAAAT
 CATTCAAAGAAAAATGTAAACGTGTTACGTGATCCACGTGGACGACTGCTGTTTTGATTAAACAGAAGC
 AAATGACCGAGTCAACTCTACTGGGTTTCGGGACCCTGCTGTGCTTTTGTGCGACTGTTTCAGTTTGACCA
 AAATTAATAAATAAATTTGGGATGGAAATTAATATGGTCCTTGATTTTTATCTTAAATTTATATTTTCAG
 ATTTTATTCTTTAATTTGACCAATATATACCTTAATTTTTAAAAATCCATTAGTCGAGTTAATGGTTCAA
 GGGGTGAGGTGCAAGTTGCAACTTCAAATACGCAGAGCTTTTTGTAAACCTTCTGCAAACGCTCGTCAT
 GTGTTATAGCATTAATTTGTTAACGTTAGGTATTGCTTTGTTGATTATGCATGGAAATCATTTGCTAGC

AACGGGCGTAATTTCAATAACAGAAGTTTGTGCTTCAGTATAGATAAAAAATATGGCTACTCGGTTGAA
 TTCTCGCAGTCTACTACTAACAGGCTCCCCCCTCTTTTACAGGTTACGACAGCCTTGAGGGAAGCTGG
 ACTGGAATCATCGAATCTCGTTGTTGGAATTGATTTCACTAAAAGCAATGAATGGACAGGTATGTGCAA
 GTGAACTAATCACATCGTCGATTTGTACCATAAAATTTGTGTTTTGCTTTATCAGTTATTCAGGAATTT
 GGATTTTGAGACTTCCATGAAGTTGAAATAAGTATTCAGAGTCGAAAAACCAATCTTTAGAAACCTAAG
 GGGGCGGCAATCTAATAATATAGCAGAATGGTTCAATTATATCCTCGTGTCTTTCTGTTCCCTTTGAATTG
 GTTGTCTCTCATGGATGTCAATTGTTGATTTTCATTTTAAAGGCAAAGTCTCGTTCAATAATCGTAGC
 CTTTCATGCCATCGGAGACACACCTAATCCATATGAGAAAGCCATCTCTATTATTGGAAAGACGATGGCT
 CCTTTTGATGAAGACAACCTTAATTCCTTGTGTTTTGGCTTTGGTGATGGTAGGTTTCAGTCCCTGGAAGTTG
 AATTCTAACAATGTTGTTTCTAGTTTTGCACCTTATAACTCAGCTGTTGATTTGATTTTTCTTTTTATC
 TATACAGCCACCCTCATGATCAAGAGGTGTTTAGCTTTCACAGTGATCATTACCTTGCCATGGTTTT
 GAAGAAGTCTTGGCATGCTACAAAAGATTGTTCCAACTTGGGACTTTCAGGTTTGTTCCTTGCTTAT
 TTGACGTTGGAATTTGGTCTTTTATCAGTTCCTTAGTTTTCTTAATTAGACCCATGGTTGAACATTACT
 TCTACAAAGATTCTTGTGTTTTACTTATTTCTCAAGCCACAAAAATCTTCACCGATATATGTTTTGGTT
 TTAAGGGCCGACTTCGTATGGACCGGTGATTGAGGCTGCAATTGACATTGTGGAAAAAGTGGAGGCCA
 ATATCATGTATTGCTCATTCATTGCAGATGGCCAGGTTTGAATTCAAACCCCTCTCTCTTTCTGTCATG
 CTTGCATGTGTTTGTGTTCTGTATGGATGGATGCATAGGGAATCAAAGTAACAGTCTCTTTTTCTGTGAA
 GGTCACAAGAAGTGTGGATACAGGCGATGGAGAAATGAGTCCACAAGAAGAGCAAACAATCAAGGCAAT
 TGTCGATGCAAGGTCGAGCCTTACAGATAAATGCAAATCATTTAACTTGCTCAGACTAACATTCATAG
 AAAATATATCCTAGTGTCACTATAACTTTTCATCTAATTAAAAATGACGAACCTTAGGTTCTTATTAGAA
 CTGTCACTTTCTTGGTGCGCTTCGGGTGCCAGCCCATTTACATTTGGTGTTATGCTGGTTATGGAATAG
 GGTTGCTAATCATTAGCAGCTGCTTGATAAACTTACTTTTCATTGCCACTAGAATGGCCATGACATTCC
 ACTTCACAGACTGCTATACTTGACCTGCTATTGTTACATGACTTGCCCTAGATAGAGATGTACATGACTT
 TGGCAGATGCATAAAAAGAAGGTGGTCAACTGATGACTGTCTTTATTTATTGAGAGGTGATCCCATTTT
 GCGATGTCAATCACTTGTAACCTATCAAATGAATCATAAGGGGTCAACAATCTACTTTTAGATCCTAGT
 AAGTATACAGATTATCTTGCGTCATAACCAGATTGTTATCCAGTTATTTGTTTGTGTCATGCCAGCTCG
 ATATTGCATTTGTATGTGAAAAACACTCAAAGTCCACACAGAACATCGAGGATGCAGAATGATTGCTTC
 ATGTTCTCCTCCACAGTCAGTTATTCATAACTTTATTGCACTGAGTTTACCTGTTTTGTGTTCCCTAAC
 ATGCCAGTCAGCCTGTATCAACAGTAAGTGGATGTAAAGTTGAATCTAATGATTTTCATCATCGGATTC
 TAACAATGCCAGAAAATGGAGTTGTGTTTATTCTGAAATGTGTGCCATTTCTTTTATGAAAAGCAATT
 ACAATGTGTAACCTTATGATATCTTAAACAGTTCATACCCACTTTCGATAATTCTTGTGGAGTTGGT
 GATGGACCTTGGGAAGACATGAAAAGATTGATGACAACTCCAGCACGTGAATTTGACAATTTTCAG
 GTATAGTGATAACAAAATGAATGTTAATTTGCAATGCCATCCAACATTGTGATTTAATTTAATATACGA
 TCTAGCACTTTATCAACTTGTTTCTGAATTGTGTGCACTTCGTTAATTTCACTGCAATTATGTCAAAAA
 ATGCAACCATCTCCGAGAAAAGAAACAGCTTTTGCTCTAGCCGCTCTGATGGAGATTCCTCCAGTATA
 AAGCAGCTGTGTGAGTTTGGTATTATCGGGTAGGTTGATAAACTTGTTTATTCACTGCTCCATTTTTTTA
 ACACAGCTTTGCCAGCATTTGAAAACGTTTGAATAATTTCAAAAATAAAGGCCCTTCAGCAGGGGAGCCAA
 TTCTAAAACCTGGTCAGCACGTCTTAGTTTTGAATCTGGGTATGGAAAAAATTGGTTGGCTTGCCCTTTC
 AATTTCAAAGAGAAAACAGCAATGGAAGGATTTCCATTTTACGTTTCCCAGCATTCCTAATGCACTGG
 CCACTTTGTTCTGCATACCATCCATTTGTTTTTACGTGTTGTCTCATATATTTAAATGGCCTTTGGATA
 AAAGACGTTCCATGGGACAAGCAAAGAAAATCGTACCACGCCCTCCTCCAGTTCCTTATTCTCGTCGTC
 CAGTGCTAGATCGTGAACCAACCCATGTTTCTCTCCGGTCTTGGATGAAAGAACCCAGGTTTGAATAT
 AATCTCGTGTAATGCTGTCTTTTGTCTGGAACATTGTAGCTCGTCTATAATTTATAACTTTGAAATGT
 GTTTTTCAATTTGATTATAGGCCTGCCCTATTTGTCTGACTAATAGAAAGGACTTGGCCTTCGGCTGTG
 GGCACATGGTGAGCTGCCACATAAACATTGCCAGCTTTGTTTTGCTTAACCTTTTTGTTACGATACTA
 ATACCGTTGCTTGGTTGTAGACTTGTAGAGACTGTGGATCTAGAGTATCCAGTTGCCCTATATGCCGCC
 GGCCAATCACCAGCCGTATCAGGCTGTTTGCTTAA

FIGURE 12B

Genomic sequence of *Salix* Xyld10 allele A – SEQ ID NO.24

ATGTCCAGCGAACCACCGTCGTCAGTGTGTAATACTGCTAGTGCCACCGGCGGTGATTCTAAAAGTCAA
 GCAAAGGCTGGTTCCAAATTGGATAAGAAGCAATCCATCAAGCAGAAATACAGTTTCATCCCTGATAAT
 TTCCTTCCCTAGAACAGGTATGAGCCTCATAACTATTTCTTTTCATTTCCCTGGAAGTTTTGCTTATAT
 TTTTTCTTCTAGAATAGATAAATTATAATTATAATTGTATCCGACCCCCCATCTGTCCGATACAATTACA
 ATTTGTTTTTTTTTTTAAAATTCAAATTCCTCGTGATGTCAATTTAAACCGAAATACAAAAGCTTAGT
 CAATTTTTCTGATTTGACTTTTCTCTGACGGCATCTCGGGGGAATCTTCTTACCAGCTTGACACTCCA
 CTCCACTCAACTCCAAAAGTTCCGTTTGCTTTTCAAATGTTGTTATTCAAAAAAAAATTATAATTCAA
 CATATCAAAGTATCGCCAGGTGCTTTTATATTTATAATTTTACCCAACTGGTAACATATTATTTTTTT

GTATTTAATAAATAAATAAATTAAAAAACAATCATTTCTATTCACTCCATCACTGATGAAACATGTTTT
TTTTTTTTCAAACACAAAAACACTACTTATGCATCTTTGTACGTGGAGATTATGTAATTTGAAATTAGGG
TGGAATGTTTTTATTTTAAATATTTATTTTACATCAACATCTTAAACACCAAAAAACAT
TAAACAATATTAAATTAATGGTTTTCTGAAGAAAACAAAAATTTGAAAAAATTAATCCGACCGACT
CTTAAATCACTACTAAATATAAAAATAACACTCATTGTTAAATAACTCCCAATTATCACGGTGAGAGT
ACAATCTTTTTAAACCAAAGTAAAAAATAATGATATACTACTTAGCCACTATTTATTTTGGTGT
GGAAGTTTGTATGCGTGTTTTAAAAATATATTTAATTGAAATATATTAATTTACTATTTTTTAAT
AATGTTAATGTGTTTATTTTATAAATAAAAAATATTTATATATATTTAAGAGAAAAAATATTGAT
GTATGCACTTAATTTGACCCAGTCTTGAAGTTTTTAGTTGGCCGTATTCAAAGTTTGACTGTACTCT
AGGCCTCTCGCTACCTAGATAAATAATTATCTCACGTGATTAATGAATATGTTAATTGTTTGATTAAT
TTTGTTTTGAAATTGATTTTTATTTAAAAATATATTAATAATATATATTTTTTAAATTATTTATGAT
ATTAACCCATTAAATAATTTAATTAATAAATAAATAAATAAATAATTTTTTTTTTGAACCCCTGCGAG
AAGAGGGGCCATAATTGACAACGACTGGCAATAAAGCGAACCGTGTAGGTCATCCCGTCGTCAACAC
GGTTTCTTTCTTCACTCAACGGAAACGTGGAAGTTGGATAAAGATAATAAAGAAAAGCAAGCTTTTTTA
TTCATCAATTATTATTGGTGACCCCAAGGCAGTACTGAACTGTTCAGTAATTGACGGGCTGATTTTTT
TTATATTATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
TCATCAATTATTTTTCTTTCTACGCATGTTGTTTACAGTGAAATTTCTCGTTCAGATTTTTTTCTC
AGAGTTATTTTTATAGGAGAAGCCAGTCGTTTAAATTCACGATTCATTTGAATATAAATAAATAAATA
AAAGTTAGGTAAATTACGAAAATATCATAAATAACTCACACAATAAATAAATAAATAAATAAATAA
ATCCTGCAAAAAGAAATACATTGCAAGAAAAAATTCCTAGTCGAGTCAGTAGTTAAGCGGTGAGGT
GCAAGTTGCGACTTCAAACACGCAGAGCTTTCTGTAAACCTTCTGCAAACGTTACCATGTGTTCTGGC
ATTAACCGTTAGGTATTGTTTTGAAGTGCTTGTATTAAAGAAATGGAATCATTTGCTAGCAATGTACG
TAATTTTCATAACAGAAGCTTGTGCTTCAGTATAGGAATAAAAAATGGCTACCTGGTTGAAGTCTCACA
GTCCCCCCCCCTCCCCCTCTTTTACAGGTTACGAAAGCCTTGAGGGAAGCTGGACTGGAATCATCGAATC
TCATTGTTGGAATTGATTTCACTAAAAGCAATGAATGGACAGGTATGTGCAAGTGAAGTCATCCTATCG
TCGATTTGTACCTTAAGCATTGTGTTCTACTTTATCAGTTATTCAGGAATTTGGATTTTGAGACTTCCG
TGAAGTTGAAATAAGTATCCAGAGCTGAAAACCAATCTTTAAAAACCTAAGGAGGCAATCTAATAATA
TAGAAGAATGATTCAATCATATACTAAGGACTGGAATGGTTATAAAAAGGCTATTTAAATTATATCCTC
GTGTTTTCTGTTCTTTGAAATGGTTTGTGTTTGGCTTGTCTCTCATGCATGTCAATGTGCTGGTTTT
CATTTTAAAGGCCAAGTCTCATTTCAATAAACGTTGCCCTCATGCCATCGGAGACACACCTAATCCATAC
GAGAAAGCCATCTCTATTATTGGAAAGACGATGGCTCCTTTTGATGAAGACAACCTCATTCCTTGTTTT
GGCTTTGGCGATGGTAGGTTCAAGTCCCTGGAAGTTGAGTTCTAACAAATGTTGTTTCTAGTTTTGCCCT
TATAATTCAGCTGTGCAATTGATTGATTTATTATATCTATACAGCCACCACTCATGATCAAGAGGTGTT
TAGCTTTACAGTGATCATTCATCTTGCCATGGTTTTGAAGAAGTCTCGCATGCTACAAAAAGATTGT
TCCAAACTTGCGACTTTCAAGTTTGCTCTTTGATTATTTGATGCTGCAATTCGGTCTTTTATCAACTCC
TTAGTTTACTTAATTAGAATGATGGCTGAACATTACTTCTACAAAGATTCTTGTGTTTTACTTATTTCT
CGAGTCAAAATAATCTTCACAAATATATATGTTTTGTTTTAAGGACCAACTTCGTATGGACCGGTGAT
TGAGGCTGCAATCGACATTGTGGACAAAAGTAAAGGTCAATATCATGTATTGCTCATCATTGCAGATGG
CCAGGTTTGAAATTTAAATCCTCTCTCCTTCTGATGCTTGCATGTGTTGTTTCTGTATGTATGG
ATGCATATGTAATCGAAGTAATAGTCTCTTTTACTGTGAAGGTCAAGAAGTGTGAATACAGGCGATG
GAGAAATGAGTCCACAAGAAGACAAACAATCAGGGCAATTGTTGATGCAAGGTGAGCCTTAAAGATA
AATGCAAAATCATTTTATACTTGCTTAGACTAACTTTTCATAGAAAATATATCCTATGGTCATATGATACT
TTCATCTAATTAAATGACAACTTAGGTTCTTATTAGAATATTACTTTTTAGAGCTTCTGTTGTTAC
ATGACTTGCCCTAGATAGATGTATATGACTTGGGCAGTTGCATAAAAAGAAGGTGGTTAACTGATGGCTG
TCTTTATTTATTGAGAAGTATCCCATTTAGTGATGTCAAGCACTTGTAATAATATCAATGAATCATAA
GGGGTTAACAATCTACTTTTAGGTCCTAGTACGTATACAGATTTATATTGCATCATAACCAGCTTGTTA
TTCAATTATTTGTTTGTGATGCTAGCCTGATATTGCATTTGTATGTGAAAAACACTCGGTCCACACAGA
ACATTATTTTATTGCAACGAGTTTACCTGTTTAGTGTCCGAACATGTCAGTCAACCTGTATCAGCAGTA
AGGGGGTGTAAGTTGAATCTGATGACATCAATCATCAGATTTTAAACAATGCCAGAAAATGGTGTGCTG
TTTATACTGAAATGTGTTGCCGTTTCTTTTATGAAAAGCTATTACAATGTGTAACCTTATGATATTCTT
AACCAGTTCATACCCGCTTTCAATAATTCTTGTGGAGTTGGTGATGGACCATGGGAAGACATGCAGAG
ATTTGATGACAAAATCCCAGCACGTGAATTTGACAATTTTCAGGTACAGTGATGACAAAATGAATGTTA
AGCTCGAATTCATCCAACATTCTGATTTAATTTTTTATACATATTAGCACTTTATCAACATGTATTGT
GTGCACTTCGTTAATTTCACTGCAATAATGTCAAAAAACACAATATCTCTGAGAAAGAACTGCTTTT
GCTCTAGCTGCTCTGATGGAGATTTCCCTCCAGTATAAGGCAGCTGACGAGCTTTGTATTATCGGGTAG
GTTGATAAACTTGTTTTATTTCACTGCTCCACACTAAAGCATTGCCAGCATTGAAAATTTCAAAATAAAA
ACCATCAGCAGTGGAGCCAATTCTAAAACCTGGTCAGCACGTCTTGGTTCAAATCTGTGCATAAATAAAA
TTGGTTGGCCTGTCCTTTCACTTCAAATGAGAAAACAACAATGGAAGGGTTTCCATTTTTACGTTTCCC
GGCATCCTAATGCACTGACCATTTTTTTCTGCATACCATCAACTGTTCTTACGTGTTGTCTCGTACA
TTCAAATGGCTTTCCGAGAAAAGACGTTCTTTGGGACGAGCAAGGACAGTAGTACCACGCCCTCCTCCA

GTTCCTTATTCCCGTCGTCAGTGCTAGATCGCGAACCATCCCATGTTTCTTCTCCGGTCCCTCGATGAA
 AGAACCCAGGTTTGAAAATAATCTCGTGTAATTCTGTCTTTTTGTCTGGAACATTGTAGCTCGTCGATA
 ATTTATACTTTGAAATATTTGTTTTCCAATCTTCCATTTTGATTACAGGCCTGCCCTATTTGCCTGAC
 TAATGGAAAGGACTTGGCCTTTGGCTGTGGGCACATGGTGAGCTGCCACCTAAACATTGCCAAGTTTGT
 TTTTTTAGTGATTGATTAAGAAGCTGTTTACAGTTGCTATTAAAAATATATTTTTTTAGAAATATCAAA
 ATAATATTTTTTTTTATTTTTTAAAAATTATTTCTAATATGAACATGAAAATGACTTAAATAGATTTTTT
 TTTTAAATTTAAATAAACATAAAATTATTTTTTCAAATACAGTGTCAAATACTAATACCTGTTGCTGG
 GTTGTAGACCTGTAGAGACTGTGGACAGAGAGTATCCAATTGCCCAATCTGCCGCCAGCCGATCACCAG
 TCGTATCAGGCTGTATGCTTAA

FIGURE 12C

Genomic sequence of *Salix* Xyld10 allele C – SEQ ID NO. 25

ATGTCCAGCGAACCACCGTCGTCAGTGCTAGTGCCACCGGCGGTGATTCTAAAAGTCAA
 GCAAAGGCTGGTTCCAAATTGGATAAGAAGCAATCCATCAAGCAGAAATACAGTTTCATCCCTGATAAT
 TACTCTTCCCTAGAACAGGTATGAGCCTCATAACTATTTTCTTTTCAATTTCTGGAAGTTTGTCTTATAT
 TTTTTCTTTTAGAATAGATAATTATAATTGTATCCGACCCCCCATCTGTGCGATACAATTACAATTTGT
 TTTTTTTTTTAAATTTCAAATTCTCGCTGATGTCAATTTAAACCGAAATACAAAAGCTTAGTCAATTT
 TTCTGATTTGACTTTTCTCTGACGGCATCTCGGGGGAATCTTCTTACCAGCTTGCACACTCCACTCCAC
 TCAACTCCAAAAGTTCCGTTTGTCTTTCAAATGTTGTTATTCAAAAAAATTTATAATTCAACATATC
 AAAGTATCGCCAGGTGCTTTTATATTTATAATTTTACCCAACTGGTAACATATTATTTTTTGTATTT
 AATAAATAAATAAATAAATAAACAATCATTCTATTCACTCCATCACTGATGAAACATGTTTTTTTTT
 CAAACACAAAAACACTACTTATGCATCTTTGTACGTGGAGATTATGTATTTAAATTTAGGGTGAATGT
 TTTTTATTTTAAATATTTATTTATTTTATTTTACATCAACATCTTAAACACCAAAAAACATTAAAACAA
 TATTAAATTAATGGTTTTTCTGAAGAAAACAAAAATTTGAAAAAATTAACCCGACCGACTCTTAAAT
 ACTACTAAATATAAAAAATAACTCATTGTTAAATAACTCCCAATTATCACGGTGAGAGTACAATCTT
 TTTAAACCAAAGTAAAAAATAATGATATAACTACTTAGCCACTATTTATTTTGGTGTGTTGGAAGTTTG
 TTTATGCGTGTTTTTAAACTATATTTTAAATTGAAAATATATTAAATTACTATTTTTTAAATAATGTTAAT
 GTGTTTATTTTATAAATAAAAAAATATTTATATATATTTTAAAGAAAAAATAATATTGATGTATGCAC
 TTAATTTGACCCAGTCTTGAAGTTTTTTAGTTGGCCGTATTCAAAGTTTTGACTGTACTCTAGGCCTCT
 CGCGACCTAGATAAATAATTATCTCACGTGATTAATGAATATGTTTAAATTGTTTGATTAATTTGTTTT
 GAAAATTGATTTTTTATTTAAATATATTTAAATATTATTATTTTTTAAATTATTTATGATATTAACCCAT
 TAAAATAATTTAATTTAAATAAATAAATAAATAAATTTTTTTTGAACCCCTGCGAGAAGAGGGGCCA
 TAATTGACAACGACTGGCAATAAAGCGAACGCGTTGTAGGTCATCCCGTCGTCACACCGGTTTCTTTCT
 TCACTCAACGGAACGTTGGAAGTTGGATAAAGATAATAAAGAAAATCAAGCTTTTTTATTCATCAATA
 TTATTGGTGACCCAGGCAGTACTGAACTGTTCAAGTAATTGATGGGCTGATTTTTTTTTTATATTATT
 AATAAATAAAAAACAGGGTAAATAATTAAATAGTCCGTTTTTATTCTCAAATTTTACGAATTTATTTT
 TTCTTTTCTACGCATGTTGTTTTACAGTCAAATTTCTCGTTTCAAGTTTTTCTCAGTTATTTTATAG
 GAGAAGCCAATCGTTTAAATTTACGATTTCATTTTGAATATAAATACAGTGCAAAAGTGAGGTAAATTA
 CGAAAATATCATAAATAAATAAATAAATAAATAAATTTGATTTTTTATTAATTTATAGTCAATTTTACGCGGTAT
 CCTGCAAAAAGAAATACATTGCAAGAAAAAATCCACTAGTCGAGTCACTAGTTAAGCGGTGAGGTGC
 AAGTTGCGACTTCAAACACGACAGAGCTTTCTGTAACCTTCTGCAACGTTTACCATTGTGTTCTGGCAT
 TAAACGTTAGGTATTGTTTTGAAGTGCTTGTATTATAAGCATGGAAATCATTTGCTAGCAACGTACGTA
 ATTTTCATAACAGAAGTTTGTGCTTCAGTATAGGAATAAAATGGCTACCTGGTTGAATTCTCACAGT
 CCCCCCTCCCCCTCTTTTACAGGTTACGAAAGCATTGAGGGAAGCTGGACTGGAATCATCGAATCTCA
 TTGTTGGAATTGATTTCACTAAAAGCAATGAATGGACAGGTATGTGCAAGTGAAGTCATCCTATCGTCG
 ATTTGTACCTTAAGCATTGTGTTGACTTTATCGGTTATTCAGGAATTTGGATTTTGAGACTTCCATGA
 AGTTGAAACAAGTATCCAGCTCTGAAAACCAATCTTTAAAAACCTAAGGAGGCAATCTAATAATATAG
 AAGAATGATTCAATCATATACTAAGGACTGGAATGGTTATAACAAGGCTATTTAAATTATATCCTCGTG
 TTTTCTGTTCTTTGAAATGGTTTGTGTTTTGGCTTGTCTCTCATGGATGTCAATGTGTTGGTTTTTCAT
 TTAAAGGCCAAGTCTCATTCAATAAACGTTGCCTTCATGCCATCGGAGACACACCTAATCCATACGAGA
 AAGCCATCTCTATTATTGGAAGACGATGGCTCCTTTTGATGAAGACAACCTCATTCTTGTGTTTGGCT
 TTGGCGATGGTAGGTTTCACTCCCTGGAAGTTGAGTTCTTACAATGTTGTTTCTAGTTTTGCCCCCTATA
 ATTCAGCTGTGCAATTGATTGATTGATTTATTTATTATATCTATACAGCCACCACTCATGATCAAGATG
 TGTTTAGCTTTTACAGTGATCATTATCTTGGCATGGTTTTGAAGAAGTCTGGCATGCTACAAAAAGA
 TTGTTCCAACTTGCGACTTTTCAAGTTTGTCTTTTATTATTTGATGCTGGAATTTGGTCTTTTATCAA
 CTCCTTAGTTTACTTAATTAGAATGATGGCTGAACATTACTTCTACAAAGATTCTTGTGTTTTACTCAT
 TTCTCGAGTCAAATAAATCTTCACAAATATATATGTTTTGGTTTTTAAAGGCCAAGTTCGTATGGACCGG

TGATTGAGGCTGCAATTGACATTGTGGACAAAAGTAAAGGTCAATATCATGTATTGCTCATCATTGCAG
 ATGGCCAGGTTTGAAATTTAAAAATCCTCTCTCCTTTCTGCATGCTTGCATGTGTTTGTCTGTATGT
 ATGGATGCATATGTAATCGAAGTAATAGTCTCTTTTACTGTGAAGGTCAGTAGAAGTGTGAATACAGGC
 GATGGAGAAATGAGTCCACAAGAGAGCAAAACAATCAGGGCAATTGTTGATGCAAGGTCGAGTCTTAAA
 GATAAATGCAAAATCATTTATACTTGCTTAGACTAACTTTCATAGAAAATATATATCCTATGGTCATATG
 ATAACCTTTCATCTAATTAAAAATGACAACTTAGGTTCTTATTAGAACTATTACTTTTTAGAGCTTCTGT
 TGTACATGACTTGCTAGATAGATGTATATGACTTGGGCAGCTGCATAAAAAGAAGGTGGTTAACTGA
 TGGCTGTCTTTATTTATTGAGAAGTGATCCCATTTAGTGATGTCAAGCACTTGTAATAATATCAAATGAA
 TCATAAGGGGTTAACAATCTACTTTTAGGTCCTAGTACGTATACAGATTTATATTGCATCATAACCAGC
 TTGTTATTCAATTATTTGTTTTTCATGCCAGCCTGATATTGCATTTGTATGTGAAAAACACTCGGTCCA
 CACAGAACATAATTTTATTGCAACGAGTTTACCTGTTTAGTGTCGAACATGTGAGTCAACCTGTATCA
 ACAGTAAGGGGTGTAAAGTTGAATCTGATGACATCAATCATCAGATTTTAACAATGCCAGAAAATGGTG
 TCGTGTTTATACTGAAATGTGTGCCATTTCTTTTATGAAAAGCTATTACAATGTGTAACCTTATGATA
 TTCTTAACCAGTTCATACCCGCTTTCAATAATCTTGTGGAGTTGGTGATGGACCATGGGAAGACATG
 CAGAGATTTGATGACAAAATCCCAGCACGTGAATTTGACAATTTTCAGGTATAGTGATAACAAAATGAA
 TGTTAAGCTCGAATTCATCCAACATTCTGATTTAATTTATTATACATATTAGCACTTTATCAACATGT
 TTCTGTATTGTGTGCAGTTCGTTAATTTCACTGCAATAATGTCAAAAAACACAACATCTCTGAGAAAG
 AAACGTCTTTTGCTCTAGCTGCTCTGATGGAGATTCCCTCCAGTATAAGGCAGCTGACGAGCTTTGTA
 TTATCGGGTAGGTTGATAAACTTGTTTATTCTACTGCTCCACACTAAAGCATTGCCAGCATTTGAAAATT
 TCAAAATAAAAAAACCATCAGCGGTGGAGCCAATTCTAAACTGGTCAGCAAGTCTTAGTTCAAATC
 TGTGCATAAATAAAATTTGGTTGGCCTGTCTTTTCACTTCGAATGAGAAAACAACAATCGAAGGGTTTCC
 ATTTTTACGTTTCCCGGCATCCTAATGCACTGACCATTTTTTTTCTGCATACCATCCACTTGTTCTTAC
 GTGTTGTCTCGTACATTCAAATGGCTTTCCGGAGAAAAGACGTTCTTTGGGACGAGCAAGGACAGTAGTA
 CCACGCCCTCCTCCAGTTCCGTATTCCCGTCGTCCAGTGCTAGATCGCGAACCATCCCATGTTTCTTCT
 CCGGTCTCGATGAAAGAACCAGGTTTGAATAATCTCGTGTAATTCTGTCTTTTTGTCTGGAACAT
 TGTAAGCTCGTACATAATTTATAACTTTGAAATATTTGTTTTCCAATCTTCCATTTTGATTACAGGCCTG
 CCCTATTTGCCTGACTAATGGAAGGACTTGGCCTTTGGCTGTGGGCACATGGTGAGCTGCCACCTAAA
 CATTGCCAATTTGTTTTTTTAGTGATTGATTAGAAGCGTTTACAGTTGTTATTAATAATATATTTT
 TTTAGAAATATCAAAATAATATTTTTTTTATTTTTTAAAAATTATTTCTAATATGAACATGAAAATGAT
 TTAAATAGACTATTTTTTTTAAATTTAAATTTATTTTTTCAAATTTATTTTCAAATACAGTGTCAAAT
 ACTAATACCTGTTGCTGGGTGTAGACCTGTAGAACTGTGGACAGAGAGTATCCAATTGCCCAATCTG
 CCGCCAGCCGATCACCAGTCGTATCAGGCTGTATGCTTAA

FIGURE 12D

Amino acid sequence of *Salix* Xyld10 allele A - SEQ ID NO. 38

MSSEPPSSLCNTASATGGDSKSQAKAGSKLDDKQSIKQKYSFIPDNFTSLEQVTKALREA
 GLESSNLIVGIDFTKSNEWTGQVSFNKRCLHAIGDTPNPYEKAISIIGKTMAPFEDNLI
 PCFGFGDATTHDQEVFSFSDHSSCHGFEEVLACYKKIVPNLRLSGPTSYGPVIEAAIDI
 VDKSKGQYHVLLIIADGQVTRSVNTGDGEMSPQEEQTIRAIVDASSYPLSIIILVGVDGP
 WEDMQRFDDKI PAREFDNFQFVNFTAIMSKNTTISEKETAFALAALMEIPLQYKADELCL
 IIGRSLGRARTVVPVPPVPSRRPVLDREPSHVSSPVLDERTQACPICLTNGKDLAGFC
 GHMTCRDCGQVRVSNCPICRQPITSRIRLYA

FIGURE 12E

Amino acid sequence of *Salix* Xyld10 allele C - SEQ ID NO. 39

MSSEPPSSLCNTASATGGDSKSQAKAGSKLDDKQSIKQKYSFIPDNYSSLEQVTKALREA
 GLESSNLIVGIDFTKSNEWTGQVSFNKRCLHAIGDTPNPYEKAISIIGKTMAPFEDNLI
 PCFGFGDATTHDQDVFSFSDHSSCHGFEEVLACYKKIVPNLRLSGLTSYGPVIEAAIDI
 VDKSKGQYHVLLIIADGQVTRSVNTGDGEMSPQEEQTIRAIVDASSYPLSIIILVGVDGP
 WEDMQRFDDKI PAREFDNFQFVNFTAIMSKNTTISEKETAFALAALMEIPLQYKADELCL
 IIGRSLGRARTVVPVPPVPSRRPVLDREPSHVSSPVLDERTQACPICLTNGKDLAGFC
 GHMTCRNCGQVRVSNCPICRQPITSRIRLYA

Figure 13

QTL analysis of yield related traits in the K8 mapping population for a 5.1 cM region of chromosome X as delimited by markers X_15341094 and X_15945623. QTL confidence intervals are indicated by thick bars (1 LOD below peak) and lines (2 LOD below peak). The percentage of the variance explained by the QTL is shown *in parentheses*.

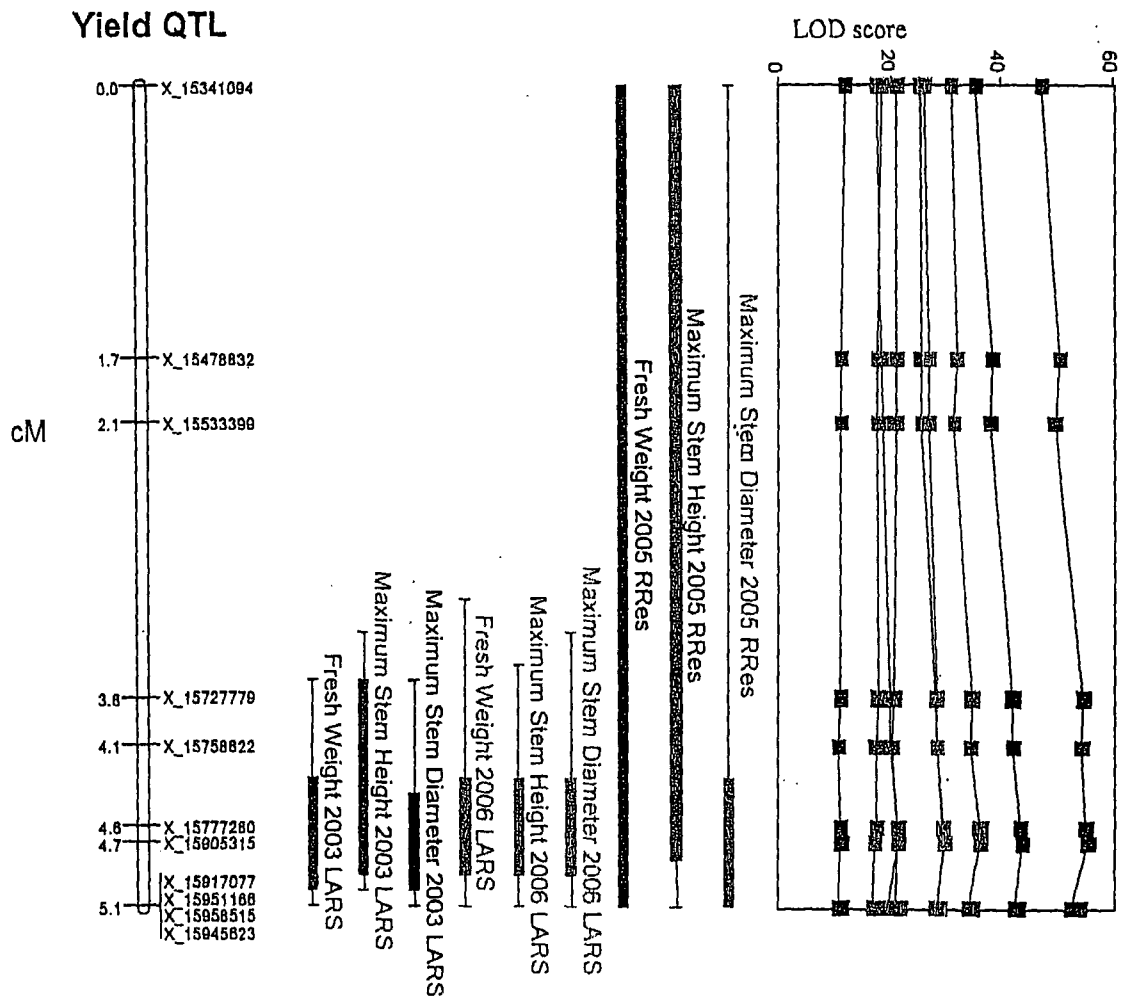


Figure 14

Representation of the public annotation of the poplar genomic sequence represented by the QTL region. Ten genes are predicted (not to scale).

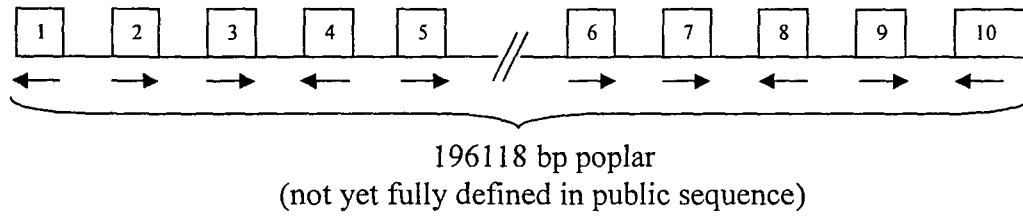


FIGURE 15

SEQUENCE OF THE QTL REGION FROM THE PUBLIC POPLAR GENOME SEQUENCE. POSITIONS OF MARKERS DERIVED FROM THIS SEQUENCE THAT WERE USED IN QTL IDENTIFICATION ARE INDICATED BY **BOLD TYPE**. GENETIC SEQUENCES ARE LABELLED AND UNDERLINED.

AAAAATGCAAATTCCTATAATGTTGAAGTGAGTGAAGTTTTTCGGGAAACAAATAATAAAAAATTGTATTC
AATACTGATGTTGTAATTATACATAAAGATCACTGGTGTATTGCCTAGAAATCAAAAATTCAAACCAAC
AGAATCCTTCCCGAGCCAATGTTATGTTTTAAACATTCCATAGACATTAAAGTTACAATA**AGAAGGGAT**

GTGCCAAAGTGACGCCATCAAAGAAATCCACAGGCATTTTTAGTGCGATCCAGGACCTCTGTTCCATG
X_15727779F- XYLD1

ATAAGAAGGTAGGATCACCAGCCGCTGAGATGACACAGTAAAGAGAAACAGTAAGAAAAATATTAACA
TATATCTCACAACAATCGAATACACATAGCATATGAAAATTTTATGCTGCCGACTATGGGGCCATGCT
CCACAAGTCAGAGCCTCACTCCATATATGATGCTGGGCACACTTCCAAATCCTCACCATAAAATGCAAG
CCTTATGAAGGGCAATTCTAACAGCCTCACTCTTTCAAAGCCGTGACGCCGCACACTTGTGACAGCGT
GCATTTTGACTTTAATAACCAAGTTTATTAAAGTCACGAGAAGTCTAGGCTCCTAAATTCAAGAATTAATTT
GTATCTATGATCAACTTACCTAGGCTTGACAAAATACACAATTGTGAAACCCATTGACAAGGCGAAGCA
TATCATCCCAACAGTGAGATAAGCAATGCCAAGAAAGTCATTTCTTCCACCAATCCAGCTTGTAGTTGA

- X_15727779R

AAGCACAAGTTTCTTCTTGCCATTAAAAGTGTATGTGTTATAGTTGTTACCCAGTGTAACATTTATGAC
TTCTTTTGCATCAAGATCCACCTCTATCTTCCCATACAACCTTTCTAAAAGTTGGCAGAGCTGCAGTTCG
CATCCAAACCATGAGGTCTCCTGATCGCTCAGCTGTTACACAAAATCATATAAGACCAGGTCAGTCAC
ATACCAATTACTTGAAGCAATTTGCATAGAAAGAAACACGGAGAAAAATTTATGGTTCTCTAGTATATT
TTCACGTTTTAGCAATAGAAGAGGGGAAATGACACGCAACAATATCTCATCATTTTAAAGCATTTACACC
AAGTCTCTCACGTCTCCAAGGTATAAGCCTAATACTCAACACCTTGGGTTTTAAAAATCAACTCCTTCA
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GTCTCATATCCTAGAGTTAAGATTGCCCCAAATCTTGGGTCATGGTTAATAATTATCACCTTTTGTAT
CTTCAAATGGAAGTACATGTTGACAAATTTTGTGTCGAAATTTCTCAATCAGATGATGGGTAAAGTT
AATCGAGAGAGACTGGCAGAATACCTTGGCGAGCTGCAGCGGAAAGAGGATACAAACGATCGCTATGTA
GCTGCTCTAAGAGGGGAGACATTTACAAGAAACCCATATGTAAGGATTCAGTCAATACCCAAGCGGAAT
AACACTGAAGCTGGCAAGGAGCAGAACCTTGATAACGATCAAAGGAAGCAGATTAGTTGATGGTTCTTG

XYLD9

CTGATGTGACCCTTTCTATATTTGGTATATTAATGTCATGGCAGCACAAGAAATGCAAAGTGGTCCCTT
TCCTTCTTGTACGCAACAGCTTGTAGCCTGTGTTTTATTTGGAATATTTCTGCTTTGGTATGGTTTTT
TCATACCCGCTGGGAATGACAGCAATTATCTCATATTATAATGTTTCTAATTTGCTTTTGGTTTTGCAT
CTTGAACCCAAATGCTTCTCAGCTATTTGCAGTTTCTTGGTAGTTCATGAAGATGATGTCAGTGCCTA
GGCTTGATTCCAGGCCTGGCATAACGAGCTTGGGAAGAAGTGACATGTTTTATGCACAAGTGCATCATT
TATAAGTTTTTATCGGTGGATACTATAGTTAAGCATACAGGATACGATAATAGGACTCATCGTAATCGC
ATCAGAACGAAAGGTAAGTCATTGATGAATTTCTCACATTGCTTACTTCTATTCTGTTAATTTTAAAG
TTCAATGATGGCAGGGAAGTTGATTGAGACAGAAATTCATACAACCTTAGGCTAAAAGCATTTTGGGCA
CCTTCTTAACCTTCGGGTCAATTTTGCTAATGAGCAGCTGTTTCCCTTTTCGAAAAGCCCTTGCAACCCCT
TGAATTTGCAGATGATCAGTGTAAACCTGGGGCTAACTCCAGTATTGGAGTTGAGAAGGAGGTTAAAGA
CGTGCAGGGGTGGCTTTTGAATTTGGCGAATCGCTTCCCAAAGCCGTAAATTATATTCTAAATTTACTTAC
AGATGAAGTGATTCCACAAGCTAAATTTTGAGCATAGCAAAATATACATCATTCTCAACCGTTAAATA
AGTTCTGCATCAACTTTAGAAACAGAACAGATACAGAGCGAAGAAATCTGACTCTGCCTTCACATCA
AACACACGCTCATGCGCATACACACAAACAGCCTAAAGAAAGCAAGAGAACCACATGTACAGTTCA
AGATACAATTCCTTGATCCAGTCGTTAAGCAAACAGCCTGATACGGCTGGTGATTGGCCGGCGGCATA

XYLD10

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CCTGGGTTCTTTCATCCAAGACCGGAGAAGAAACATGGGTTGGTTACGATCTAGCACTGGACGACGAG
AATAAGGAAGTGGAGGAGGGCGTGGTACGATTTTCTTTGCTTGTCCCATGGAACGTCTTTTATCCAAAG
GCCATTTAAATATATGAGACAACACGTAAAAACAAATGGATGGTATGCAGAACAAAGTGGCCAGTGCAT
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CTGCTGAAGGCCTTTATTTTGAATTTTCAAAACGTTTTCAAATGCTGGCAAAGCTGTGTTAAAAAAT
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GGGGAATCTCCATCAGAGCGGCTAGAGCAAAAGCTGTTTCTTCTCGGAGATGGTTGCATTTTTTGACA
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GTCAAATTCAGTGCTGGGAGTTTGTATCAATCTTTTCATGTCTTCCAAGGTCCATCACCACATCC
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TAAAGTAGATTGTTGACCCCTTATGATTCAATTTGATAGTTTACAAGTGATTGACATCGCAAAATGGGA
TCACCTCTCAATAAATAAAGACAGTCATCAGTTGACCACCTTCTTTTTATGCATCTGCCAAAGTCATGT
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TGGCCATTCTAGTGGCAATGAAAAGTAAGTTTATCAAGCAGCTGCTAATGATTAGCAACCCCTATTCCAT
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GAACCTAAGTTCGTCAATTTAATTAGATGAAAGTTATAGTATGACACTAGGATATATTTTCTATGAATG
TTAGTCTGAGCAAGTTTAAATGATTGCTTTATCTGTAAGGCTCGACCTTGATCGACAATTGCTTG
ATTGTTTGTCTTCTGTGGACTCATTCTCCATCGCCTGTATCCACACTTCTTGTGACCTTCACAGAA

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AAAGAGACTGTTACTTTGATTCCCTATGCATCCATCCATACAGAAACAAACACATGCAAGCATGCAGAA
 AAGGAGAGAGGGTTTTGAATTCAAACCTGGCCATCTGCAATGATGAGCAATACATGATATTGGCCTCCA
 CTTTTTTCCACAATGTCAATTGCAGCCTCAATCACCAGGTCCATACGAAGTCGGCCCTTAAACCAAAC
 ATATATCGGTGAAGATTTTTGTGGCTTGAGAAATAAGTAAACACAAGAATCTTTGTAGAAGTAATGTT
 CAACCATGGGTCTAATTAAGAAAACCTAAGGAAGTATAAGAACACAAATTCACAGTCAAATAAGCAAG
 GAACAAACCTGAAAGTCGCAAGTTTGGAAACAATCTTTTGTAGCATGCCAAGACTTCTTCAAACCATG
 GCAAGGTGAATGATCACTGTGAAAGCTAAACACCTCTTGATCATGAGTGGTGGCTGTATAGATAAAAG
 AAAAATCAAATCAACAGCTGAGTTATAAGGTGCAAAACCTAGAAACAACATTGTTAGAATTCAACTTCCA
 GGGACTGAACCTACCATCACC~~AAAGCCAAACAAGG~~AATTAAGTTGTCTTCATCAAAGGAGCCATCGT

← X_15917077F

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 GGAACAGAAAACACGAGGATATAATTGAACCATTTCTGCTATATTATTAGATTGCCGCCCTTAGGTTT
 CTAAAGATTGGTTTTTCGACTCTGAATACTTATTTCAACTTCATGGAAGTCTCAAATCCAAATTCCTG
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 CCTGTCCATTCAATTGCTTTTAGTGAAATCAATTCCAACAACGAGATTGATGATTCCAGTCCAGCTTCC
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 GTAGCCATATTTTATCTATACTGAAGCAACAACTTCTGTTATTGAAATTACGCCCGTTGCTAGCAAA
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 GTTTCGAGAAGGTTTACAAAAGCTCTGCGTATTTGAAGTTGCAACTTGCACCTCACCCCTTGAACCAT
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 TCAAAGTGTCTTTCATGTTGAAATACATTAAAATAATATTTTTTAAATTTTATAAAATTTATATTTGAAT
 CAGTACATCAAACAATTTAAAATATAATTTTTTTTTAAATTTTACAAACGTGGATCGGCCTGCATTTT
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TCAACTTAAGTTTCTAACACTTTTGAATTTTTTTAAATTTGTTTAAATGTATTAATATAAAAAATAATT
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TTAAAGAGGATGATTGGCACGTACCTGTTCTAGGGAAGAAAAATTATCAGGGATGAACTATATTTCTG
CTTGATGGATTGCTTCTTCTCCAATTTGGAACCACCTTTGCTTGACTGGTTCCTTTGCTTGACTGCT
AGTATCACTACCAGTGGCTCTAGCAGTATTACTCAGTGACGATGATGGCTCCTTGGACAT

XYLD10

FIGURE 16

SEQUENCE OF THE WILLOW QTL REGION (ALLELE A). POSITIONS OF MARKERS USED IN QTL IDENTIFICATION ARE INDICATED BY **BOLD TYPE**. GENETIC SEQUENCES ARE LABELLED AND UNDERLINED. INSERTION IN XYLD7 GENETIC SEQUENCE IS SHOWN IN *ITALICS*.

AGAAGGGATGTGCCAAAGCGATGCAGGGCCTCTGTTCCAATAGGAAGAGAGGGATGTGTTTTAAACATCAAAGA
X_15727779F-

ATTCCACAAACATTTTTAGTGCGATCCAGGACCTCTGTTCCATGATAAGAAGGTAGGGTCACCAAGTCGCCTGAG
XYLD1

ATGGTACAATAAGAGAAAAGGTTAGAAAATATCAAAGTTATCTATTTAATAGCATCTCACAAATAGTCGAATAC
ACAGCATATGAAAATCTTATGCTGCCGACTAATGGGACCATGCTCCACAAGTCTGATGCTGGGCACACTTGGAAA
TCCTCATTATAAAATGCAAGCCTTATGAAGGGCAATTCTAAGTTTCTAACAGCCTCACTCTTTCAAGAACCCTAA
ATTCAAATTTGTGCTGTGATCAACTTACCTAGGCTTGACGAAATACACAATTGTGAAACCCATTGACAAAGCGA
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- X_15727779R

GCACGAGTTTCTTCTTGCCATTAAAACTGTATGTGTTATAGTAGTTCATCAGTGTACGTTTATGACTTCTTTTT
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GAGGGGATATGACACGCAACAATATCCCATCATTTTATAAGCCTAATACTCAACACCTTGGGTTTAAATAAAAATC
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GCTGTGCGCTATGATCTACGTAAATTACACACCTGGATAGTCTGGATATCAATGCCCCCAATATGATTATATGA
ACAATATACCTAGAACCATTAATGTAATTTCTAGACATGATTACTTGAACCCGTCAGAAATTACAAGCTGATAGAG
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XYLD1

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 TTTTTTTTATTATAATTATTAATAATTTAAAAACAATATATATATATATATATATATATATATATATATATA
 TTGCACGCGCGTGTTCTGTAATTCTTGCAACCTATATTGCTCGGAAATTAATGCACCTGTGACGTGCGCGTATTTA
 ATTTCCCTCTACCTTAGCTTGTTATTCCCTCAGGATCGGGTAGATGTAAGAACAGGTGCTGCTAGCTAACTAAA
 AAATAATCCTGTGCGCGGGGCTGCATACTAGTAGCAGCCAAACACATCGGATATAAATTGAGGACTTTCAGGGGA
 GAGGAGTGATGAGATTAGTCCCTCGACATTTTATATATGTTGAGGTAGCTAGCTAGTTGAAGGATGCAGGAGTAG
 CCAGCCAGCTGAATCAGCTGAAGAAGGGAGTAGTGGAGAATATATAGAGATGGGCCACAGGTGCTGCAACAAACA

XYLD7

GAAAGTTAGAAGAGGGCTGTGGTCTCCTGAAGAAGATGAGAAGCTTGTGCAATACATCACCCTCGCGATCATGG
 AAGCTGGAGTTCTGTCCCTAAATCTGCAGGTATGCAGTGCGTGTGTTTTGCTTGCATCAGAGATCAAAATCA
 AGCCGTCTGATCTGTGCTTGCAGGTTTGAAAAGGTGCGGTAAAGAGTTGCCGGTTGAGGTGGCTCAACTACCTGAG
 ACCAGAGCTCAAGAGGGGTTCCCTTTTCTGCGCTGGAAGAACAGGTCATCATAGATGTTTCATAGAATTCTGGGCAA
 CAGGTAAGGATTATTCGAGTCAAAATTAATAAGGAAGTACTGTATAAAAAAGGTAGAAAAATGAAAAATAAATAA
 ATAAAAACTGTTTCTAACAAATGGGGAAAGTAGTCTGATTATATATTTTTTCACTGCATTTTGATTTACAAGCTA
 GAACTTTATACTGCTTCTAACAGGTGGGCTCAGATATTGTAAGAATTGAACTTCGATTAATTTTCACTATATACA

Insertion in XYLD7

ATTGATTGTTTGTGCTGTTACATTTGGGGAATTATATAGGAAATAATTACAATACATTTTTTAGCTAAAATACAA
 TACATGTTTAACTACCAAAAAATCAATTATCCTATTATAGTAATAAACGGCTATATGGACATAACGGCTATATT
 TCAACACTCCCCCTCAAGTTGGAGCATAGATATTTATCATGTCCAACCTGTTAATTGCACCATGAAATGCTCTTC
 CTGAAACTGCCTTTGTGAGAGTATCGCCATTTCACTGCAATGAGAACACACCAACCCAGTTGCATTTTTTATTTT
 CGGTCAACTCGACCAGCCTTAAATCTCGTCCCCCTCCTTCAAACCTGCGCTACCTTATCGAATGTAAATTTTCTT
 GATGGTGATCTCCCCCTGATTAACAGGGTGAATATCTTCGATGGTGATCTCCCTCTGATTAACAGGGTGTGGAGT
 CACGGAATATTTTTCGGGATGGTGATCTCCCCCTGATTAACAGGGTGTGGAGTCACGTAATATCTTCGGGATTCAC
 TGAATATCTTCGATGGTGATCTCCCCCTGATTAACAGGGAGTGGAGTCACGGGATATCTTCGATGGTGATCTCCC
 CCTGATTAACAGGGTGTGGAGTCACGGGATATCTTTGATGGTGATCTCCCCCTGATTAACAGGGTGTGGAGTCAC
 GGAATATCTTCGGGATGGTGATCTCCTCCTGATTAACAGGGAATGGAGTCACGTAATATCTTCGGGATTCACGGA
 ATATCTTCGATGGTGATCTCCCCCTGATTAACAGGGTGTGGAGTCACAGAATATCTTCGATGAGGATCCCCCTT
 GATTAACAGGGTGTGGAGTCTCGGAATATCTTCGTTCTCTTCAATTGTTACTCTCCCCCTGAAGAGAAGGTCCGGG
 AACTCCCCCTGATTAACAGGGTGTGTGGAGTCTCGGAATGATTCATTCTCTTCATCCTGATGGTGATCTACTGTT
 AGTCTGATTTCTCGTTTAACTACCAATAATCTCTCGGGTTAGAATGTCTTGAAAAACACAAAAGAGAGGCC
 AAAAAGTGACAGTGTCAAGGATAAAAGTAATTTGACTTACTGACAAGAGATTGTATACAGAGATGGACCAA
 TGAGAACAATATCTATAGTTACATAATCGGTCAAGGTTATAGACCCTTCCCTCGTAATAAGAGAGGGTTTCAAGA
 ACCTTAAATTTCCGGAATCCCTGGTCATATTATCAGATGCGCTATATCAATAATTCAAAGGATTATTTTTAATA
 ATGACAGAGTTTGCAGAAGTTTTACCAATTGTGTCTGGATGAACAACATTCATCGTAGATTGTACCTGTTCAAGTT
 TTCATAAAATTTACTATACCTTTGCCGATATTTTTCCGGGTTTTTTCATAAAATCTCACCAGTCAAGTAGTCAAT
 AATTTTCGTAGCATCTTTGTTTTCGAGTGACCCGATTTCGCCGCAATAATTAAATAACAACCGTTTCAAGATAACAA

TTCGAGATAAAAAAATACGTTTCAAGATAAAAAAATTTGAGATTGCTCGGATCAATATGATTCAAAGAAATACGA
TTTAAAGGAAAAAATTTGAGATTGAGATAAAAAAATACGTTTCAAGAAAAAATTCGAGATTGAGATACAAA
ATACGTTTCAAGATAAAAAACGTCGAGATTGAGATACAAAATACGTTTCAAGATAAAAAAATTAAGATT
CGAGATACAAAATACGTTTCAAGATAAAAAAATTTCAAGATTGAGATACAAAATAAGTTTCAAGATAAAAAATG
CAGAAGTTGTAGGTGTACCATTATTGTTTTCGAATGACCCGCTTCACCGCAATAAAAAACAAACCAGCCTACCCGG
GTTCTTATAACCGAATTAAACCTTTGCCTTTCACCTTTCATTTCTCTCATCTCTGTGACCCATCTGTCTCTCACC
CGGTTTCTTATAACCGAATTAAACCTTTGCCTTTCACCTTTCATTTCTCTCATCTCTGTGACCCATCTGTCTCTCACC
ATCACTTCTCCACCCGTTTCATTTTCGACCTTTTCTGTTCAAATTCGTTGACGAGCTCCGATTCTCAAATACGTT
TGCCTGTTTCGGCCTTTTTTCTTCAGCGGCAGTTTTCAGCTTCAGCTTTCCTTCGAGCCTCGTCAGCAGCCTTAGC
TCCTGCTGCACCCGAGCTTTTCTTCTTCTTTCCTTCTTTCCTTCTTTCCTTCTTTCCTTCTTTCCTTCTTTC
AATTTCTTCTTCTTCGAGCTTTAAGTATGGTGTGAGCAAAACGGTCTTCAACAAAGGTGCACGATAGAGCTTATC
GGGAGAGACTTGCCTCTCAGGTGGAGCACTCTCCCTGTATCAATGCCTGATGTGCAGGTTACCCTTTCTGGTTG
TTTCTGGTTTGTGGTGTGTGTGATGAGAAATCTGGGTTTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
GTGTGTGTGAGAAATGAAGGGAGGATGTCTGTGTGTATGAATTGATGGAATTTCTGGGTTTGTGGTGTGTGTGTGT
GGGAAATGTGGCTTTTTCGGGAAATGTGGCTTTTTCGGGAAATCTGGGTTTCTGGGTTTCTGTGGGGA
TCGATGGGTTATTTTTCTGGGTTGTGTGTATGAACAGTGTGTGATGAACAAGCACTGTGCAGATTGAGGTCTG
GGTTTTCGAACCAGAAGAGAGAGAAAAAATGCAGTAATTCGATTTCAAAGAAAAATTCGAGATTGCTCTGATACC
ATGTAAGAATTCGAACCTTCGATTAATTTTCAGTATATACAATTGATTGTTGTTGCTGTTACATTTGGGGAATTAT
ATAGGAAATAATTACAATACATTTTTAGCTAAAAATACAATACA

[N]* - repetitive portions

CATTTTTAGCTAAATACAATACATGTTTAACTACCAAAAAATCAATTATCCTATTATAGTAATAAACGGCTAT
ATGGACATAACGGCTATATTTCAACAGATATCGAACATCTCCAGGAAGGACAGATAACGAGGTGAAGAATTTC
TGGAACCTCGCGCTGAAGAAAAAGCTCATGGCACAAGGCCTGGACCCGAAAACCTCACAACCTTGATTCCCTACTCGC
CAGAGGGCAGCTAATAAGGTTGCATGCAGCATGTACCATCTAACACGAACCCCTTTCAATTACCTCCCATGAT
TCAAAGATGAAAGATGTTTCTTGGAGATAATTAAACCTCCTAAAAATAACACTAGTTTACCTAATTATGCTTCT
AATTGCAGCGCCAGCCTCCATTTTTTCAAACAACAACGAGCTTGCCCTTGCCCAATCTGTACGATAACCCCT
AGTGTCAATTTGGAATGCAATTCTCAAATTCTTATGATTATCCCTTTTACCTGCGTGTATCCATTGAGAAC
TCACTCGCTTCTCTCTCGTCTCTCAGCGAACCCAACTGGGTTTGGTCTCGTGGATGAAAACCTGCTTTTGG
AGTTGTAGTGACATTGTTGAGCCCTTTGAAGCCGCAAAAATATTGAAAGTGTGCCGCCACAAGATCAAGAAAAC
CAGCTGAACAAGGTTTGTGACACCCAAATCGTGGGTAAAGATAAAGGAGTTCATGACAATATGGAAGCTTCATTC
GACACCTCTAGCTATGATCTTGGGTTGGTTCGACTCCACATTATTTCTGGTTTCATTGTGTGATGATCTTAGCTCA
ATGGATGATCTTGCATGGAACTTTTAGGCCTCCATATATATGCGTGTATGTACCTCGTGCTACTGTAATAGATAG

XYLD7

CTGGTTTTGCTGAGGTTGTGCATCCCAAATATTTGAAAGGAAAAAATGCTCTTAAAAATAATACAATAAGAACACG
 AACAAAAAATAAACCTGTGAGTGTGAGCAAAAAAATGTTTTTATTGTTTCGATTCAATTTTACATGTACTAGTA
 TATATACCATCCTTTCTTTATTGATCATTATTACATTATAAAGTTTGTATATAAACACCTGATGATTTTTTATT
 TTATTTTCATATGATGAGATAAAGATATTTATAGATATCTTTTGTATAGAAAATAAGTTATGTTTTATAAATA
 AAAAAAACTTCTAAAATAGTTTTATTATTTAAAAAAGAAAGCTTCCATTTCTTTCTAGAATTCGGGAGTGAA
 GTTATTTCGTGATATGAATTAATTTCCCATTTTCATCTAAATTTGGGAAGCTGCTCTCGGATGTTGAGTCATTGATAG
 CCATCGCCTGAATCAATTTCTCCCCCGCATGTTTACCACCATCCCTTGAGTTTGTATGATGATGAGAACATTTTG
 ATTAAGCCTAATTTCTATAGTTGCCTCTTTATCCGTGTTTCATCCATCAGTTGTGTTTTTATATTTCATTTCAATC
 AATTTATCCTTATAAAACCACATAAAAAATATATAGATATGAGTTGATGCTGAGAGAGTGATACTAGACGGTGAT
 AATGATGGTTGATATTTTATATTAATAAAAAATTTTTATTATATTTAATTGAAGTGAAATTTAATCTTGATTGCC
 AAAGATCGTCAGATAGTGTTAATGAAAAAAATTAATAATCATTTTTCTTATTTACATTTAGCATCCGTAATA
 CAAATATTTGAGGTCTAGTAGGTAGATGGCAACTTAAGTGGGCTTCAGCTTACTCCCCAGGCCACTACCTGATA
 GATCGGTTCTAATCACCTAACCCGTGATGATTGTGGTGCCAAAGTTACCACCAGGGCCCAATAACACAGCCAT
 CATAAGGCCCATTATTTCTGTTAATTTGATCTGGGCCATATAACTTTCTTTCTTTCTGGTTCCAAAGGGCCCATT
 ATTTCTGTTGATTTGATCTGGGCCATATCACTTTCTTTCTTTCTGGTTCCATAGGCTTGAGGCGGAAGCAGTCC
 GCATGGCCATGGCTTCTTTCTGGCATTAAAGAGATATAACTAAATGATACGAGTCTCCGACCTCCACGTCCAGT
 ATATCCCCCTTTTCGCCATTTTAGCCAAAGCTTCGACCTTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTTTTGGC
 CGTTACATATCCAGTAGCTTTATTGAAAAACAGTTGGTGGCGATTAGCTCGGCATCAAGACTATTATTTTTTAT
 TTTGGTTGAATAAGCACTTAATTATCAGCTCTCAACGGTGAAAATTATGGAGTCCCCAAAGTTACTGTGTGAG
 CATTGTGGGCTCACATCATGATTCTTTATAACAGAGAATTCTTTTGTGCTTTTACTTTGGCAGAAACAATTGGTT
 ATGTAATTCACAGAGAAATGGAGACAATCTTTTCCAAATATTGGCCCAGAGTTTCAACAAATTCATGAAAAA
 AGAAAATAACAGAAAAGGAAATGATCTTGTAGCCAAGCCTGATCATCATGTGGTTGGCAAAACAATCCCCGTTTT
 TTTTTTTATATATATATATAACCCATCACAATATATCCTACCTTCGTGTCAAATGAATTTTAGCAGTGATACA
 ATGTCTGCAAGGAACATTTTCTTAAGAAAAAATCTTTGTTACTTTGTGGTCATCCTAACTGGCCGGTGGCTCTT
 AGTATTGCATGGGGAGTGCAGTATTGGAGTCATAAGTAGAAATTTCTTCAAATATCCCGTTCATGCAATCCCTG

XYLD8

XYLD8

162/199

CTCTCTTTTTCTTTTTGTTATTTTTCTGCTTTCTTTTCTGCCATCCAAACGACTTGTCTTTTACTGTTTTATTCT
 GTTTCATCTTCCCTTCCCTTTGATTCTTTTCTTTTCTTAAATATCATTTCATATGAGTAAAGACACACTTCC
 TCCTTTAATGATTACAGACCCAAATCTTTGACTGCGGTCTGGTCTCTCTCTCTCAGCGCCACCGCAAT
 ATTATCGATCGATGCAATCTTATACATATACCAGCTATTCCTCCATCAAATATATAGCGCGAGGGTACGTTCTG
 CATGCATATACACTCTTAATACTCCACAGCTAACCATTAAAAATTTAAAGCGCATAAAAACAGCATATTATCT
 AAGCTATTTCTTCCGGTTCGACGGTAAAAATCGTACTTGATCGGTAATTTATAGATGGGCAGACCCGAATGACCCCTC
 TAGTTTCGAGGCCCACCGGAGAAAACAAGTAGTATATATTTATCAAACGGGAAGTTACTAATTTGTTAATTTAG
 GGTTCTTTTCTTTTGGTGGATGAGTCTTTATGGTAGTTACGCTCAAAGGTGGATGTAAATATTTGAATCAATCT
 CTGTGCAAGACAATTACATCGAGAAAGAGAGAGGTGTGGGGTTTCAAGGGGTTTGCCGAAAGATCCTTTTACATT
 CTTTACTGGCTAGCCGCACTCCACGATATTATTACCACGTAATATTGTAGCATAGATACAGTACTAGCTAGCTT
 CACCCTGTGTATGAATCAACATGCATGAAGAAGAAGCTTTGGATTAGCGTAAAAGAGATTCCGAGTTCTTCTTTT
 TCACCAATGGGATTGCAAAAACATGGTGGCTAGGCGCTCTACTTGTAAAAGAAAAGGAAAAGCAACTTGATCC
 GTCAAGCTCGAACTAGAAGTAGTGCCACATTTTGATTCTCCTATGCAGTTGCATAACTTGCATTCTTTATTAAT
 TAATAATTTAATCTAGCTGTGTTTCTTTATTTTAGTTGATTTTCCCTTCTCAAGAATGATAGACACTAGCCAGT
 GGTGTTCTTATGTTAAATGGGCTCTAAAGCCATGCAACCTTTTACACGATCTGAGTGAAGTAAAGCAATGGAAAA
 CACAAGAGATCATGCATGGATCGATGCCTGGGTACTGTGATCCATTAAATGTAGCTGTAGATCGATGACACGTGGT
 CAGCTCTCCATAAAGAAGAGAAAGAGATTCTAAAATGTCGGCTCGATATTATATATCTCTAGATGCCATTTTCACT
 CTGTGCATGCAAAAGACAAATGTTTCAGATCTTCTTCCATTACACGTAACATATACGAGGTGTAGCTTTTATGGT
 ATAGCTGTCTGGGTTGCCCTCCAGTTCCTGAGGGCACGAATGTCATTTGGACATTAGTTTCTGACTTGGCATGCAGT
 AGCTTTGAAAGCATCGTCATGACCTCCTCGTCCATCTTTTCTCCCGTGCCAGGAGCAGCCCTTTGCTGAACTA
 GGACCACGCTGTGACACTGGTGGGATTGAAAGGGACCATTTTCAATTAATCTTCCATAAGAAGCAGCAGCTG
 CTTCTAGTCAAGAAAAGATATGTATGGCGAGTGGACAAGCAATCTAGTCAGTGAATGATCTCTTGCAACTATAA
 CGAGAACCTAGCTAGCTACTCGAAAAATCTGGTCATTCTCGGACTGTAGCTAAGTACTGTTCTGGAGTAGAAGA
 ATTAACCCCGACAAACAAAAATACATTATCTCAGCAATAAATAAATGCAGTGTGCACAAGCAGGATAAG
 ATTTTTCATTCCAGGGAAATCAAATTGATATAAAACAAATAGTGAAGGTGAAAAAGATAGCTTCCACAGTCTAT
 TTTCTTATTCTGAAATGTTTTTTTTGATGGGTGAAATAAATCAGTGAAGTGCTTTTCTATCTAACTGACTAGAAG
 TGACGCTGCAGTGCATTTCAATCGTGGCACTTTTATTTATTAATGAGGTAGTGTCTTCTCGTTCTATTGGA
 TAACTTCAAGTTAACGAGGATCGATTTCTATCCTGCCATATTTTCTCTTTCATTTGTAGCTAGGTTCAAAATCTC
 AATGAGTCATTATGAATCTATAACATTTTCTCTTTATATAGTCCATCCATTTTAAAAATATTTAAAAAAATGA
 ATTTTTTATTTTTATTTTTTAATGTTTTTAAATATTTTGATATGGTAATGTTAAATATTTTAAAAAAATAA
 AAGATATATTTTTGATGTATTTATAAAAAAAACACTTTAAAAACAGTATCAACTACACTCATGAACATACCTT
 AAGTGTTATATTAGAATTGTGTTTTGAATTATTAGTTTTTATTTTAACTATTTATTTTTTTTATTTTTTATCT
 CTTTGATGTGTTAATTTTGAATAAATAAATAAATACTATTCTAATGTATTTAAAAAAATATTTAAAAAGCAA
 TTTTGACTCTCGAATTTTATACCTCTTGCAGTCTTCTAATCCATTTTATCAACCATTGGATTTCAACTATTTA
 TCACGATATGTTAATTCACAGAAAAAATACTAGATCTAGTAATTTTATAGTTGGTTATTTTTTAAGTTGATT
 TTATTTTATTTTAAATAAATAAAGAGATACAATCATGTGATGTTTTTATTATTATTGATAGATCGTATATTTTATA
 TTTTTTCTCTATATATATATATGTGAAATAAATAAGGTTGTAGAAAGTAATTAACAGATAAATAAGTATTTAC
 GAGTATAGTGTAGTTGTTTTTAAATATTTTTTGTGTTGAAATAACAATCAAATAAATACTTTTATTAATGA
 AAATAATACCAGCACATCAGAGTAATATAAATAAATAATTTTTGAAAAAAAATAAGTTTTTTTTTTTAAATG
 CTATTCAAACCTTTGTCAATTAAGTGATTTTATCATCCAATAATCCTGGCCCAAGTTAGTTGACATGTTTGCTG
 TCCGTTATACCGTGCCCAAAATAACCAAGAAAAAATACTGGCCCAACTAAATTACGCTTCATTCACTTTCTG
 GGCCTCCCTATCTTCGCTTCAAACGCAATGGCGAGCCAGATAGAATTGCTCGTTAGTGAGTAAAGCTTCAC
 CCAGTCGAACCTCGGATTGAGAGAGGGGGGTGGAAGATGTGCGATACTGTGGGAGAAGAGCGAGGCTGGAGGTGGA

XYLD9

TAGTGAGGAAGACGAGAGACTCAAAGCCATTCTTCTTACATTTCGCTACAGTATGCGGTGTCGTTCCAGGTGTGA
 TTGGGTATTTTCGTGATGCAAAACCACCAACTCTAGCAACCCCGAGCTCGAAGCCCGCCTCCGTCAGAACGCCCGTC
 CCGATTCCCTTGTACGTACGTTATATATATCTTGAATCACCGTTGATTCTCTCCATAAAAACGTTTGATATGCAG
 ATTTTTGGGCATGGCCACGTTGTGATTATTAACATTTAATTTCCCAATTCTTTGTTAACTCGGTTGTTTTAAG
 AATCTGACCCTGACCCTGATGCTATATTTACAAGTAGTTTAGCATCGAATGCTAGAAAATAATATATGAAAAGCA
 TGTTAATCACTCATAGATATCAAGAGGAATAATGGAAGGGGGGCAAAGTTTCTGGGGGAGGGGTACAACAATTA
 GCATAAAGTTGCAAACTAATCACTGGAACCTTTTCATCTTGGTTAAGCTTCCAAATTTCAATACATGGCAGATGG
 ATTTTCACTAAGGCCACTTCTAAGTGAATTCATCGTTGGTAAATCACAGGAATGAAAGTGCATTGCAGTGACC
 TCAGAGTAGCTGCTCTAGATACTTAGGCTAGTTCTCTTTCAGTTTCTGTCTCATATCCCTAGAGGTATATTGCCCC
 AAAATCTTGGATCATGGTTAAACAATCTTAACTGCGTTATCTTTACTTGAATTTAAGCAATGTTAGACCTATTA
 TTTTGTGATGAATTCAGTTGGTAGAAGCTTGAATTTTAAAGTAGTCTCGACATTGAAACGGCTGTTTTTATTTTAAAT
 AAACGAGTTTAAATCTACTGTGATTGTATAAAGCCTTTCTCATCTTCAAATGGAATCACTTGTGACAAATTTTG
 CTTGCTCGACTTTCTCAATCAGATGATGGGTAGAGTTAATCGAGAGAGACTAGCAGAATACCTTGGCGAGCTGCA
 GCGGAAAGAGGATACAAACGATCGATATGTAGCTGCTCTAGAGGGGAGACATTTACAAGAAACCCATATGTAAG
 AATCCAGCCAATACCAAGCAGAATAGCACTGAAGCTGACGATCAAAGAAGCAGATTGTTTGTAGTGGTTCTCGCT

XYLD9

XYLD10

X 15917077R →

← X 15917077F

AGAGATGGCTTTCTCGTATGGATTAGGTGTGTCTCCGATGGCATGAAGGCAACGTTTATTGAATGAGACTTGGCC
TTTAAATGAAACCAGCACATTGACATGCATGAGAGACAAAGCCAAAAACAAACATTTCAAAGGAACAGAAAA
CACGAGGATATAATTTAAATAGCCTTTTATAACCATTCAGTCCCTTAGTATATGATTGAATCATTCTTCTATAT
TATTAGATTGCCTCCTTAGGTTTTTAAAGATTGGTTTTTCAGCTCTGGTACTTATTTCACTTCACGGAAGTCT
CAAATCCAAATTCCTGAATAACTGATAAAGTAGAACACAATGCCTTAAGGTACAAATCGACGATAGGATGACTTC
ACTTGACATACCTGTCCATTCAATTGCTTTTAGTGAAATCAATCCAACAATGAGATTTCGATGATTCCAGTCCAG
CTTCCCTCAAGGCTTTTCGTAACCTGTAAAAGAGGGGGAGGGGGGAGCTGTGAGAGTTCAACCAGGTAGCCATTT
TTATTCCTATACTGAAGCAACAAGCTTCTGTTATGAAAATTACGTACATTGCTAGCAAATGATTTCCATTCTTAA

XYLD10

FIGURE 17 – SEQ ID NO. 42

SEQUENCE OF THE WILLOW QTL REGION (ALLELE A) WHERE THE GENETIC SEQUENCE OF XYLD7 ALLELE A HAS BEEN REPLACED WITH THAT OF XYLD7 ALLELE C. GENETIC SEQUENCE OF XYLD7 ALLELE C IS LABELLED AND UNDERLINED.

Reference nucleotide position A

AGAAGGGATGTGCCAAAGCGATGCAGGGCCTCTGTTCCAATAGGAAGAGAGGGATGTGTTTTAAACATCAAAAGA
 ATTCCACAAACATTTTTAGTGCGATCCAGGACCTCTGTTCCATGATAAGAAGGTAGGGTCACCAAGTCGCTGAG
 ATGGTACAATAAGAGAAAAGGTTAGAAAATATCAAAAGTTATCTATTTAATAGCATCTCACAAATAGTCGAATAC
 ACAGCATATGAAAATCTTATGCTGCCGACTAATGGGACCATGCTCCACAAGTCTGATGCTGGGCACACTTGGAAA
 TCCTCATTATAAAATGCAAGCCTTATGAAGGGCAATTCTAAGTTTCTAACAGCCTCACTCTTTCAAGAACCCTAA
 ATTCAAATTTGTGTCTGTGATCAACTTACCTAGGCTTGACGAAATACACAATTGTGAAACCCATTGACAAAGCGA
 AGCTTATCATCCCAACAGTGAGATAAGCAATGCCAAGAAAGTCATTTCTTCCGCCAATCCAGCTTGTTGTTGAAA
 GCACGAGTTTCTTCTTGCCATTAAAACTGTATGTGTTATAGTAGTTTCATCAGTGTACGTTTATGACTTCTTTTT
 CCTCGAGATCCACCTCTATCTTCCCATACAACCTTCTAAAAGTTGGCAGAGCTGCAGTTCGCATCCAAACCATGA
 GGTCTCTGCTCGTTGAGTGTACACAAAATCATATATGACCAAGTCAGTCACGTGCCAATTACTTGAAGTAA
 TTTGTCATAGAATAGAAAAGAAACAGTGAGAAAATGATGGTTCTCTAGTATATTTTTCACATTTTAGCATTAGAA
 GAGGGGATATGACACGCAACAATATCCCATCATTTTATAAGCCTAATACTCAACACCTTGGGTTTAAATAAAAATC
 AACTCCTTCATGAATGAAAGAATAAAGTGGGTACACCTAAAATAATCCTGAAGTTGAAGTTAGCAACCTGAAAA
 TACAACCTCTAATAAACACAACAGCAACATAGTATTGAAATATACCAAATGTCCATAGTGTATTAAACATTATTAA
 AGCCTCTAAGGGTATTTTTTCAGGATGAAGTTGAACAGTTCTTTAGTGTGTGATCAGAGGAGTTGCTTATATATTA
 ATTTGACCAGATGAGTAATAGTCGAGGGCGGCTTACTGGTATCGATTTCATTGAGAGTTGCACCACCTACAAGACC
 TCCCCCTGAAAGTTTTTAGGAAAGACATTTTTACCGAACCTTTTCTGCTTATCACTCTTCCAAGCAATTCCCTT
 CTTATTCACTGTCAATGACTGGTTCTGGCGGGAGAAGCTATAAGTATCATTAAACAACTCCAAGCTATCAGACC
 ACAGGGTACAATTGCCCCCTACCATTGCAATATCTTCTGGCTTACAAGCACTTGTATCATTCTCTTTACTCGC
 ACTTTTCACTGTTCATCACTTCGGCTCTTACATACCTGATTTATTTGAGCAATCATTAAATATTAAGCCAAATA
 ATCACCACATATAAATTAATTACATGTGCTTCAACTTTTCAGTGAGTAAGCGTCCAGTTTATGATCATGGTAATC
 ATGACAGTTTCACAGCCTGTTCAATAGTTTGACAATTCTGATTTGATCTAATTTTAGTATCTTATAAATTGATG
 GGTGCTTTTTCAATTATTAAACACATGAAAGAGAGTAATTTTCTAGCATCAAAAAATAGTCAACACACTATTCTG
 AGATGAGAAACATAATGTTGACCACCAATTAAGCATGCGCACTTCCTGAACCACATTTTATAATTGGTTCTCTGG
 GCTGTGCGCTATGATCTACGTAAATTACACACCTGGATAGTCTGGATATCAATGCCCCCAATATGATTATATGA
 ACAATATACCTAGAACCATTATGTAAATCTAGACATGATTACTTGAACCCGTGAGAAATTACAAGCTGATAGAG
 TACACGAGGTTGATGACATACCTACGATGATTCTGGTAGAAGTTGTCAAGCTGATAGTAAACATAAATAGGTTGC
 TTCATACGCTTAGGGATCTGGCAAGAAAAACAAGAATACAGGATGGAAGATCATTATTCACTGTTTAGCCTCGGG
 TCATGGTAGTTAATTTCTATGATTAGCATTGAAGCCAGTTGTATGAGAGAAAAAGATCTGTTGTAGATTTTTT
 GTCAGAAGTAGCATAAAGTAACCTACTGGCTACTAATACACTACTGATACAGCACCCTTGAGCTGTGACAAAA
 AGGCAATGTCACTAGTCGATAGATAACAATAAATGAAGGTATATTGTATAGCAGAAAATAACTGGAATAGGT
 CTTTCTTGTATTCTTATAAATCCACAAACACTGCTAATAAAGAACATAGAAAATGACAACACATCAACCATAAT
 AATTGCAAGGACAGGACTTACCGTCATGGATATTGTGCATGTTTTATCAGCGTCGCTTTGTATAAATTGGACTTT
 ATTGGTTCTATTTAGAACCGGAATGCATTTTGTTCATACCGTTCAACAACCTGATAAAGGGAGAA
 TAACCTATAAACAACCATAGGTGAAAATATAGCTAGGATTGCAAGATTTAGGTGACACTCAAGCTCACATCTCG
 GGAACCAATCAAGCAAGCAATGCCGATAGGGATGAAGACAATGGCAATAAGCATGAATGTAGACACCACCTGCAC
 AAAGAGATATATTTGGAGTTAATACTCTAAGTGCTCATTGTCATCAGACAAAACAGTTAAAAAGAATAATAAA
 AACTTACCCATCGTGGTGTGAGAATTGGCTTGCAAGCAGGAAGTTCTTGTGAGTAACTTTGAATCTGAAAGAA
 AACGAAACAATTTAGTTTCTTGAAAATCACACGTACACCCCATATGTGCTTGTGTGGTGAAAAAGACAATTTGGG
 AGCTGCAATTGAAACATCAGATAAAGAAGCTGCTCAGCGGTGCTCTCTCTATTTTTACTGTTCTTGTGTTTTTA
 ACAGCTACATTACAATAAGATTACAAGTGATTTTAAATAAATGAAAAAAATGACAGATTTTTTGTCTGCGAAA
 ATATAATGCATCCCTATAAATTTAAAAATGTTTCTATCCCTCTATGTTGCTTTGCAGGATAACAATTACGCTGACA
 GGCAACTATTCTGAACACTAGAAAATCTGTTTTCAATCTTAAAGTAGATCACATGAGCATTCTGCTTGGACT
 TGGATGTGTGAATGTTAATACAACCAAAATTAATAAGATTCGGATTCATGTAATGGGAAATGTCCAATTACTGA
 GTTTCATTAATATCTTGTATCGAACCCAATTTAATTCATTTTATTGCCAACAAAGTTTAAATAGCCAGCCATATT
 TCTCTTTCAAAGGGGAATTTCCAAATATATTTTTTTGAGGAATAAAAAAAGGCACGGATATTTCAAAAACGG
 AAAGACTTCATGATCAATATAGAGCAAAATAGATGCTTGGTATGAAATAAAATAGTCAGAAAAGAGCTCACACAA
 CCAATCTCATGCAAAACCAACAGCAAAATCAAAATCACAGGAACCCATAAAAAATATACATAAACCTCCGCGTGGA
 TGCCTATAAAACCCACTAGTGATCCCAGAAAAGAAATAAAAAACCTGAGTCTATGGAACAGGCTAGCAGAAATTT
 AGGACAAGGTTCAAAACTTAGCAACTTAAACAAAACTAACACATAATCACGAGTGGGAGTCAAGATTGTTGCC
 TAAAAATAGCAAAAAATAACTAAAAAGTGAAGAAGAGATCACATTTGGGTGCTTTGAATTCCTTTTTGGAACGCC
 AGAATCACCCGATCCGTTGCCTCCATTACTGGACGATGCCGTGTGGCTACTCATGATTGTGTTGAAAGATGCAAA
 CAAAAACAAACACTTGTAGTTTCTGTCTCTCTTTCTTTCTCTAAAAAACAACAAAAACAGCCGAAGAAAGAA
 AAACCTTAAAGAGAAAGAGAGACTTCAAAAGGAAGGAAATGGTGGAGATGGCTGTGTGATCAAGAGATAAAGG
 CACCTTTTAAAGACTAAGAAAACAGAGAGGGAAAATATAAATAAATAAATTTTCTAAAGAAAGAGTGGCAGTATT

AAAGAAGGTGAGTTTTTAGAGAGAGGGAAGCAAATAAAAAAATCATAAACAATATTCTTAGCCCCTATAGATTCA
AAAATGTTTCATGTTGGTCTCGTGATTTAAATTTCTAACACCAACGTAAGTTTCAAAGGTTTCGATATCATT
GTAAGTATCTATTAGCTAGCAATGAACATTGCCGAGGCCATGTTGAGTTGAGGGGTGTCGGTTGACCCCTCAAC
TTCTCAAAAAGTACTGTGATTACGTGTAAAAAATATAAAAACTTTGTAGTTTGTAAAAATATTGAAAAATCCAT
AGAAGAGGGCTGGATTTATTTTTTTTGCAGAAAAAATAAATGTTCAACTGTTAAATTGCTAAAAAAGTATATT
ATTTTATATTTTATTATTATCTTATCTTCGTCTATATACTATTCTCTTATATCTAATTTAATTTTATTCAAA
ACCTCTCCTCATGTGCTCTTTTAACTTTTATTTTCTCTCTTGTGTGTTTTCGTTTTTTCAAGGATTTTGAT
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XYLD7 allele C

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↑

Reference nucleotide position B

Figure 18 - SEQ ID NO. 43

Reference nucleotide position A

↓
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Reference nucleotide position B

INTERNATIONAL SEARCH REPORT

International application No
PCT/GB2010/000021

A. CLASSIFICATION OF SUBJECT MATTER

INV. C12N15/82 C12Q1/68 A01H5/00
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

C12N C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, Sequence Search, BIOSIS, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	KIKUCHI S ET AL: "Characterization of eight polymorphic microsatellites in endangered willow <i>Salix hukaoana</i> " MOLECULAR ECOLOGY NOTES, vol. 5, no. 4, December 2005 (2005-12), pages 869-870, XP002578208 ISSN: 1471-8278 the whole document marker Shuk123	1-16
A	HANLEY S ET AL: "A genetic linkage map of willow (<i>Salix viminalis</i>) based on AFLP and microsatellite markers." THEORETICAL AND APPLIED GENETICS, vol. 105, no. 6-7, November 2002 (2002-11) , pages 1087-1096, XP002578209 ISSN: 0040-5752 the whole document	1-16

☒ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

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Date of the actual completion of the international search

23 April 2010

Date of mailing of the international search report

07/05/2010

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INTERNATIONAL SEARCH REPORT

International application No
PCT/GB2010/000021

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	TSAROUHAS V ET AL: "An AFLP and RFLP linkage map and quantitative trait locus (QTL) analysis of growth traits in Salix" THEORETICAL AND APPLIED GENETICS, vol. 105, no. 2-3, August 2002 (2002-08), pages 277-288, XP002578210 ISSN: 0040-5752 the whole document	1-16
A	HANLEY S J ET AL: "Alignment of a Salix linkage map to the Populus genomic sequence reveals macrosynteny between willow and poplar genomes" TREE GENETICS & GENOMES, vol. 3, no. 1, January 2007 (2007-01), pages 35-48, XP002578211 cited in the application the whole document	1-16