

Tree Genetics and Genomes:

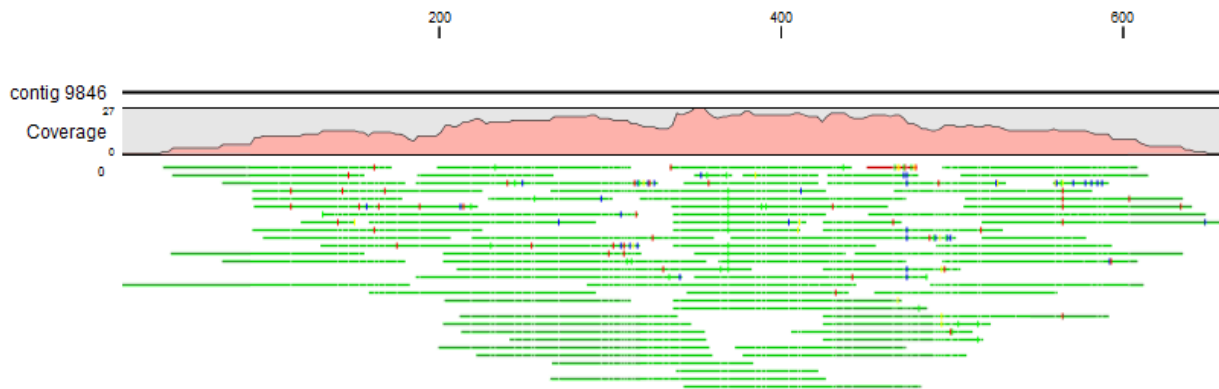
Gene expression analysis of primordial shoot explants collected from mature white spruce trees (*P. glauca*) that differ in their responsiveness to somatic embryogenesis induction"

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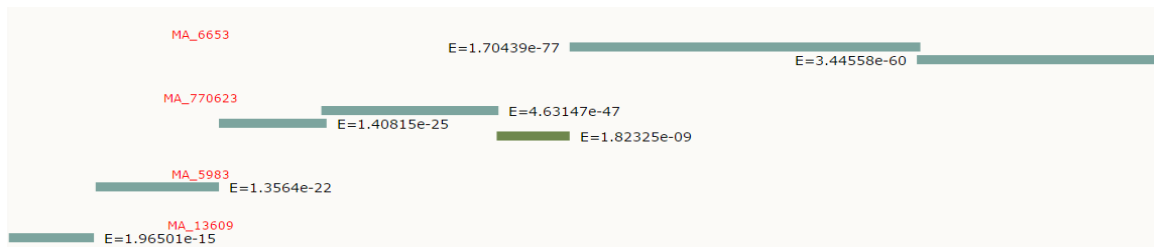
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Contig 9846 de novo assembly summary



Norway spruce genome assembly blast results



>|cl|MA_13609 len=65589

Length = 65,589

Score = 91.6812 bits (46), Expect = 1.96501e-15

Identities = 49/50 (98%), Frame = +1 / +1

```
Query: 1 CTTGTTGTATTTTCTTGCTCGGGAAAGCTCTCTGAATATTCAGTTCCAA 50
          |||
Sbjct: 27776 CTTGTTGTATTTTCTTGCTCGGGAAAGCTCTCTGAATATTCAGTTCCAA 27825
```

Two single base gaps within repeatative motifs

>[lcl|MA_5983](#) len=34196

Length = 34,196

Score = 115.469 bits (58), Expect = 1.3564e-22
Identities = 72/74 (97%), Gaps = 2/74 (2%), Frame = +1 / -1

```
Query: 51 CACGAGCTTCCAATTCAAA-GATGCTCCACTTTCATTTGAAAAATTC-TATATCTCGCCA 108
          |||
Sbjct: 25662 CACGAGCTTCCAATTCAAAAGATGCTCCACTTTCATTTGAAAAATTCATATATCTCGCCA 25603
```

```
Query: 109 CGATCTTCTTCATG 122
          |||
Sbjct: 25602 CGATCTTCTTCATG 25589
```

>[lcl|MA_770623](#) len=7250

Score = 125.381 bits (63), Expect = 1.40815e-25
Identities = 63/63 (100%), Frame = +1 / -1

```
Query: 122 CCTGCACATATGGTCGAGTTCTTCACATTGCTTTTTTCAGCTCTGCGAATTCGCTCTGATC 181
          |||
Sbjct: 735 CCTGCACATATGGTCGAGTTCTTCACATTGCTTTTTTCAGCTCTGCGAATTCGCTCTGATC 676
```

```
Query: 182 CGC 184
          |||
Sbjct: 675 CGC 673
```

Score = 196.746 bits (99), Expect = 4.63147e-47
Identities = 102/103 (99%), Frame = +1 / -1

```
Query: 181 CTCTCTTACGCGAGCAGATCTTAATCCCATTTCAGTTTCTCCTGCAACGTCTGTAAATT 240
          |||
Sbjct: 560 CTCTCTTACGCGAGCAGATCTTAATCCCATTTCAGTTTCTCCTGCAACGTCTGTAAATT 501
```

```
Query: 241 TTCCAGTGTGATATCTTCAAGATCAGAGCCACCCATTTGCCTG 283
          |||
Sbjct: 500 TTCCAGTGTGATATCTTCAAGATCAGAGCCACCCATTTGCCTG 458
```

A third single base gap within a T repeatative motifs

Score = 71.8576 bits (36), Expect = 1.82325e-09
Identities = 43/44 (97%), Gaps = 1/44 (2%), Frame = +1 / -1

```
Query: 282 CATTTCGTTGCGCCCCATCCATTTG-TTTTGAAGCAATTCGCACT 324
          |||
Sbjct: 356 CATTTCGTTGCGCCCCATCCATTTGTTTTGAAGCAATTCGCACT 313
```

>|cl|MA_6653 len=41165

Length = 41,165

Score = 297.846 bits (150), Expect = 1.70439e-77
Identities = 188/203 (92%), Gaps = 12/203 (5%), Frame = +1 / -1

```
Query: 324  ACCCCAAATGCAAAGAAGTATCATAGTCACCAAATATTGATTCTCCTCGTTATTCTCCT 383
          |||
Sbjct: 31085 ACCCCAAATGCAAAGAAGTATCATAGTCACCGAAATATTGATTC-----TCCT 31038

Query: 384  CGTTGTTATTCAATTGTAGATTAGCATGGATACTTGAAC TTCCAAAGATTGCACTTCAC 443
          |||
Sbjct: 31037 CGTTGTTATTTCGATTGTAGATTAGTATGGATACTTGAAC TTCCAAAGATTGCACTTCAC 30978

Query: 444  AATTTCTTTGTGGCATGGATTCCATCAACAAAGATGCATCTCTTGATGAGCTAACCCCTT 503
          |||
Sbjct: 30977 AATTTCTTTGTGGCATGGATTCCATCAACAAAGATGCATCTCTTGATGAGCTAACCCCTT 30918

Query: 504  CTTGTCCAAATATTGTATTCAAC 526
          |||
Sbjct: 30917 CTTGTCCAAATATTGTATTCAAC 30895
```

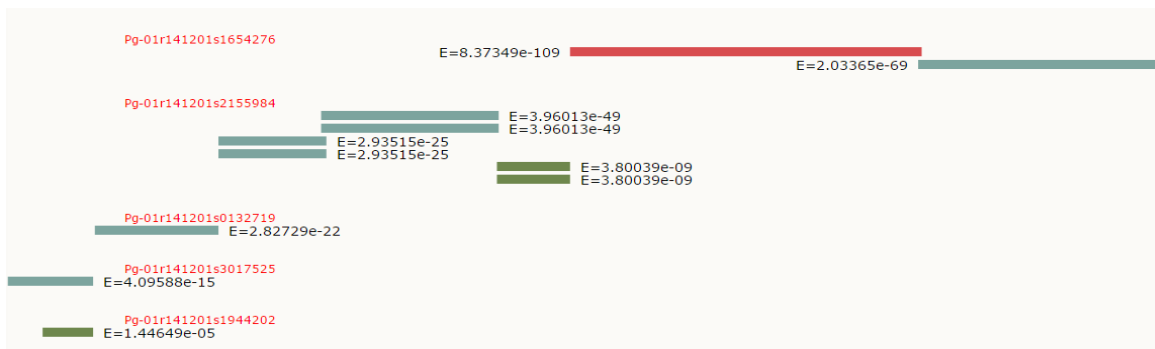
Score = 240.358 bits (121), Expect = 3.44558e-60
Identities = 139/145 (95%), Frame = +1 / -1

```
Query: 524  TTTTTATATTATCACTACTTTACATGGTTAATTAACACTATCAAACATGACCACTATAG 583
          |||
Sbjct: 30795 TTTTTATATTATCACTACTTTACATGGTTAATTAACACTATCAAACATGACCGCTATAT 30736

Query: 584  AGGGTAATGTTGCTGCAACTACTTTTGTACATAAGTGATACCGAAAAGATCAAGCATGAT 643
          |||
Sbjct: 30735 AGGGTAATGTTGCTGCAACTACTTTTGTACATAAGTGATACTGAAAAGACCAAGCATGAT 30676

Query: 644  CATGGATAAGTGGGACTAATTAACC 668
          |||
Sbjct: 30675 CATGGATAAGTGGGATTAATTAACC 30651
```

White spruce genome assembly blast results



>[lcl|Pg-01r141201s3017525](#) No definition line found

Length = 247,946

Score = 91.6812 bits (46), Expect = 4.09588e-15
Identities = 49/50 (98%), Frame = +1 / -1

```
Query: 1      TTGGAACTGGAATATTCAGAGAGCTTTCCCGAGCAAGAAAATACAACAAG 50
             |||
Sbjct: 13563 TTGGAACTGGAATATTCAGAGAGCTTTCCCGAGCCAGAAAATACAACAAG 13514
```

Two single base gaps within repetitive motifs

>[lcl|Pg-01r141201s0132719](#) No definition line found

Length = 821

Score = 115.469 bits (58), Expect = 2.82729e-22
Identities = 72/74 (97%), Gaps = 2/74 (2%), Frame = +1 / -1

```
Query: 51      CACGAGCTTCCAATTCAAAA-GATGCTCCACTTTTCATTTGAAAAATTC-TATATCTCGCCA 108
             |||
Sbjct: 426      CACGAGCTTCCAATTCAAAAAGATGCTCCACTTTTCATTTGAAAAATTCATATATCTCGCCA 367
```

```
Query: 109     CGATCTTCTTCATG 122
             |||
Sbjct: 366     CGATCTTCTTCATG 353
```

>[lcl|Pg-01r141201s2155984](#) No definition line found

Length = 7,038

Score = 125.381 bits (63), Expect = 2.93515e-25
Identities = 63/63 (100%), Frame = +1 / -1

```
Query: 122     CCTGCACATATGGTCGAGTCTTTCACATTGCTTTTTTCAGCTCTGCGAATTCGCTCTGATC 181
             |||
Sbjct: 4016    CCTGCACATATGGTCGAGTCTTTCACATTGCTTTTTTCAGCTCTGCGAATTCGCTCTGATC 395
```

```
Query: 182     CGC 184
             |||
Sbjct: 3956    CGC 3954
```

Score = 204.675 bits (103), Expect = 3.96013e-49
Identities = 103/103 (100%), Frame = +1 / -1

```
Query: 181     CTCTCTTACGCGAGCAGATCTTAATCCCATTTCAGTTTCTCCTGCAACGTCTGTAAATT 240
             |||
Sbjct: 3841    CTCTCTTACGCGAGCAGATCTTAATCCCATTTCAGTTTCTCCTGCAACGTCTGTAAATT 3782
```

```
Query: 241     TTCCAGTGTGATATCTTCAAGATCAGAGCCACCCATTTGCCTG 283
             |||
Sbjct: 3781    TTCCAGTGTGATATCTTCAAGATCAGAGCCACCCATTTGCCTG 3739
```

A third single base gap within a T repetitive motifs

Score = 71.8576 bits (36), Expect = 3.80039e-09
Identities = 43/44 (97%), Gaps = 1/44 (2%), Frame = +1 / -1

```
Query: 282     CATTTCGTTGCGCCCCATCCATTTG-TTTTGAAGCAATTCGCACT 324
             |||
Sbjct: 3637    CATTTCGTTGCGCCCCATCCATTTGTTTTTGAAGCAATTCGCACT 3594
```

>[lcl|Pg-01r141201s1654276](#) No definition line found

Length = 964

Score = 402.911 bits (203), Expect = 8.37349e-109

Identities = 203/203 (100%), Frame = +1 / +1

Query: 324 GTTGAATACAATATTTGGACAAGAAGGGGTTAGCTCATCAAGAGATGCATCTTTGTTGAT 383
|||||
Sbjct: 265 GTTGAATACAATATTTGGACAAGAAGGGGTTAGCTCATCAAGAGATGCATCTTTGTTGAT 324

Query: 384 GGAATCCATGCCACAAAGAAATTGTGAAGTGCAATCTTTGGAAAGTTCAAGTATCCATGC 443
|||||
Sbjct: 325 GGAATCCATGCCACAAAGAAATTGTGAAGTGCAATCTTTGGAAAGTTCAAGTATCCATGC 384

Query: 444 TAATCTACAATTGAATAACAACGAGGAGAATAACGAGGAGAATCAATATTTTGGTGACTA 503
|||||
Sbjct: 385 TAATCTACAATTGAATAACAACGAGGAGAATAACGAGGAGAATCAATATTTTGGTGACTA 444

Query: 504 TGATACTTCTTTGCATTTGGGGT 526
|||||
Sbjct: 445 TGATACTTCTTTGCATTTGGGGT 467

Score = 272.075 bits (137), Expect = 2.03365e-69

Identities = 143/145 (98%), Frame = +1 / +1

Query: 524 GGTAAATTAGTCCCCTTATCCATGATCATGCTTGATCTTTTCGGTATCACTTATGTACA 583
|||||
Sbjct: 568 GGTAAATTAATCCCCTTATCCATGATCATGCTTGGTCTTTTCGGTATCACTTATGTACA 627

Query: 584 AAAGTAGTTGCAGCAACATTACCCTCTATAGTGGTCATGTTTGATAGTGTTAATTAACCA 643
|||||
Sbjct: 628 AAAGTAGTTGCAGCAACATTACCCTCTATAGTGGTCATGTTTGATAGTGTTAATTAACCA 687

Query: 644 TGTAAGTAGTGATAATATAAAAAA 668
|||||
Sbjct: 688 TGTAAGTAGTGATAATATAAAAAA 712