Comparative genomics of *Picea glauca* and *P.abies*

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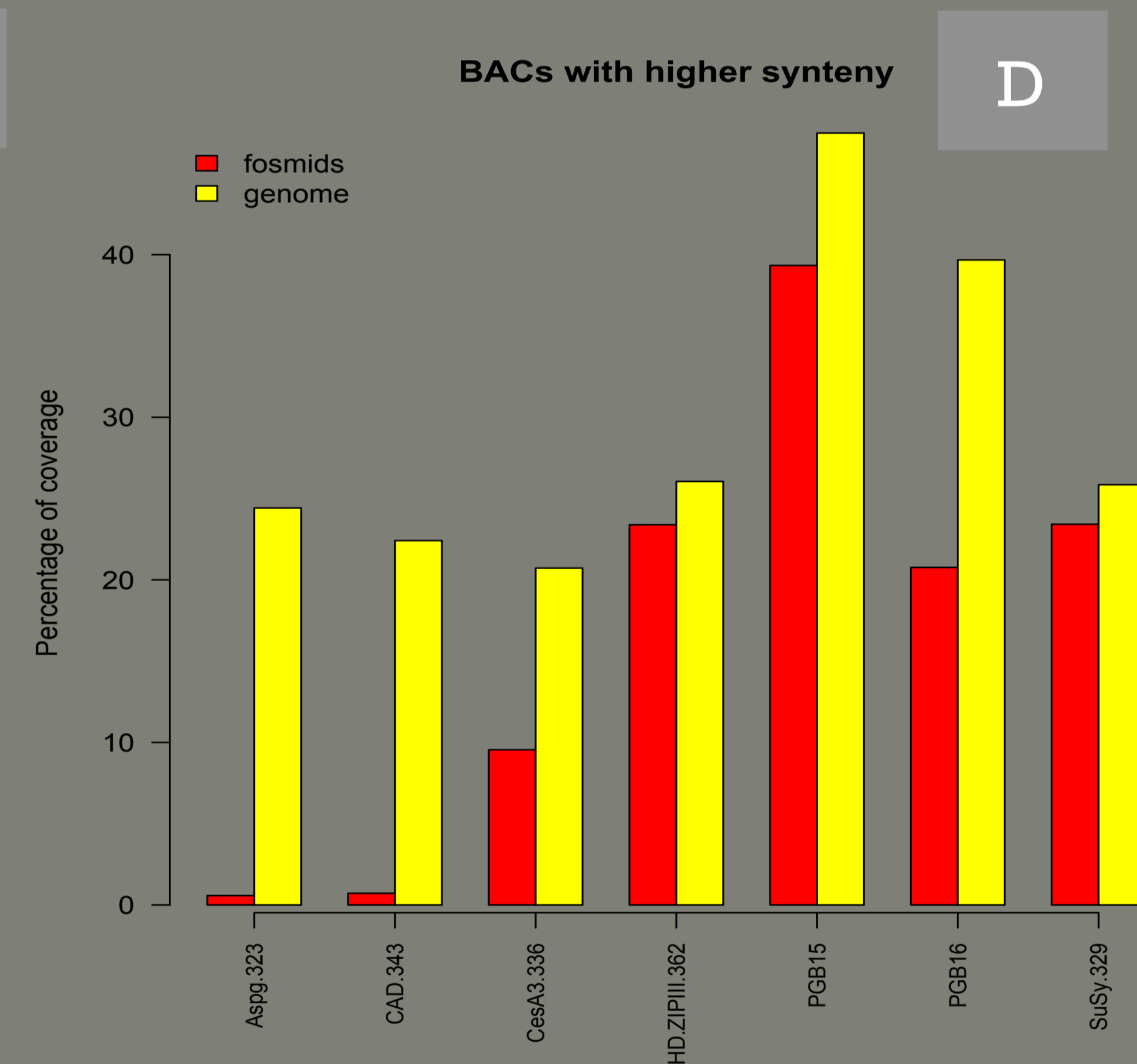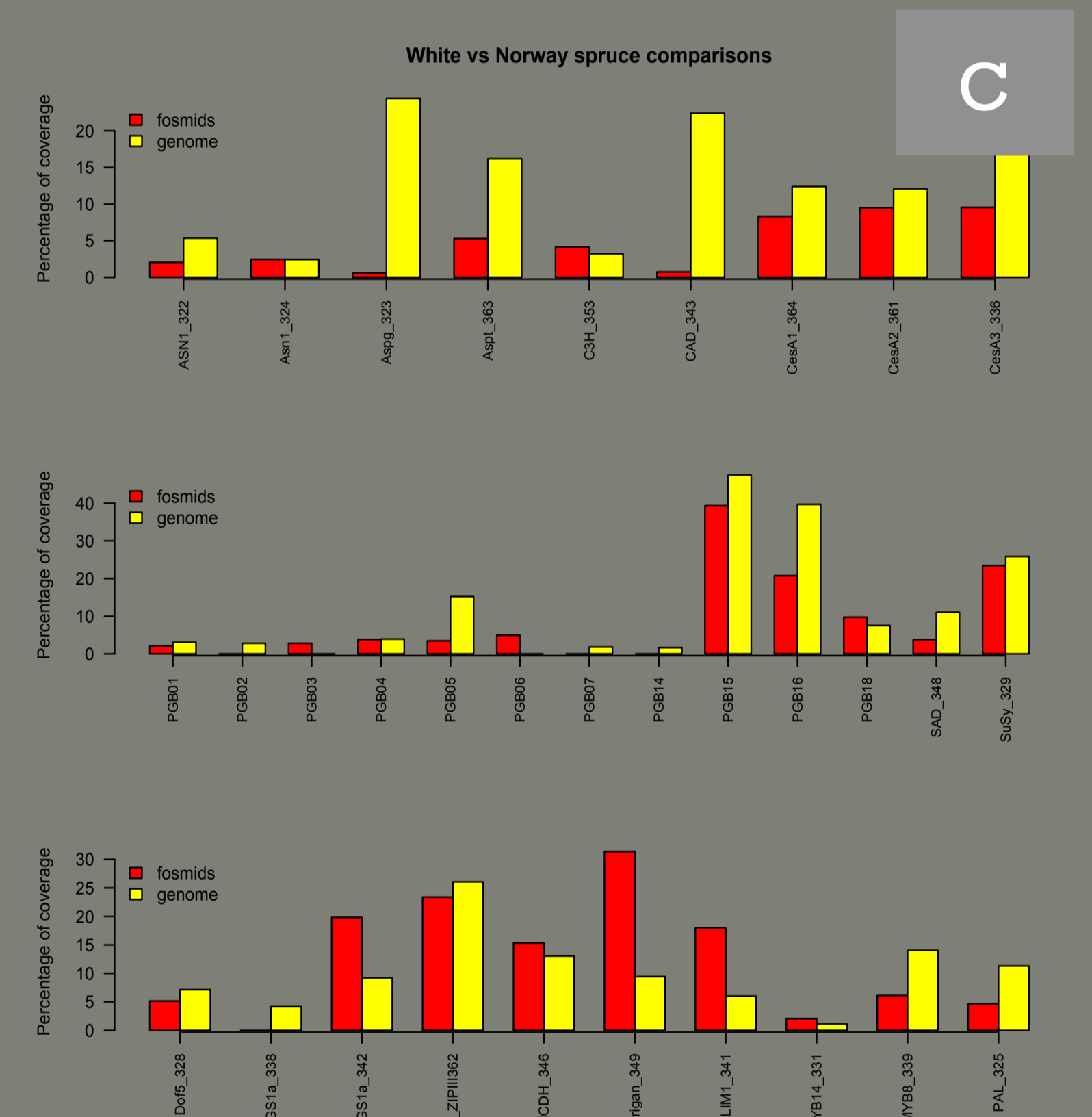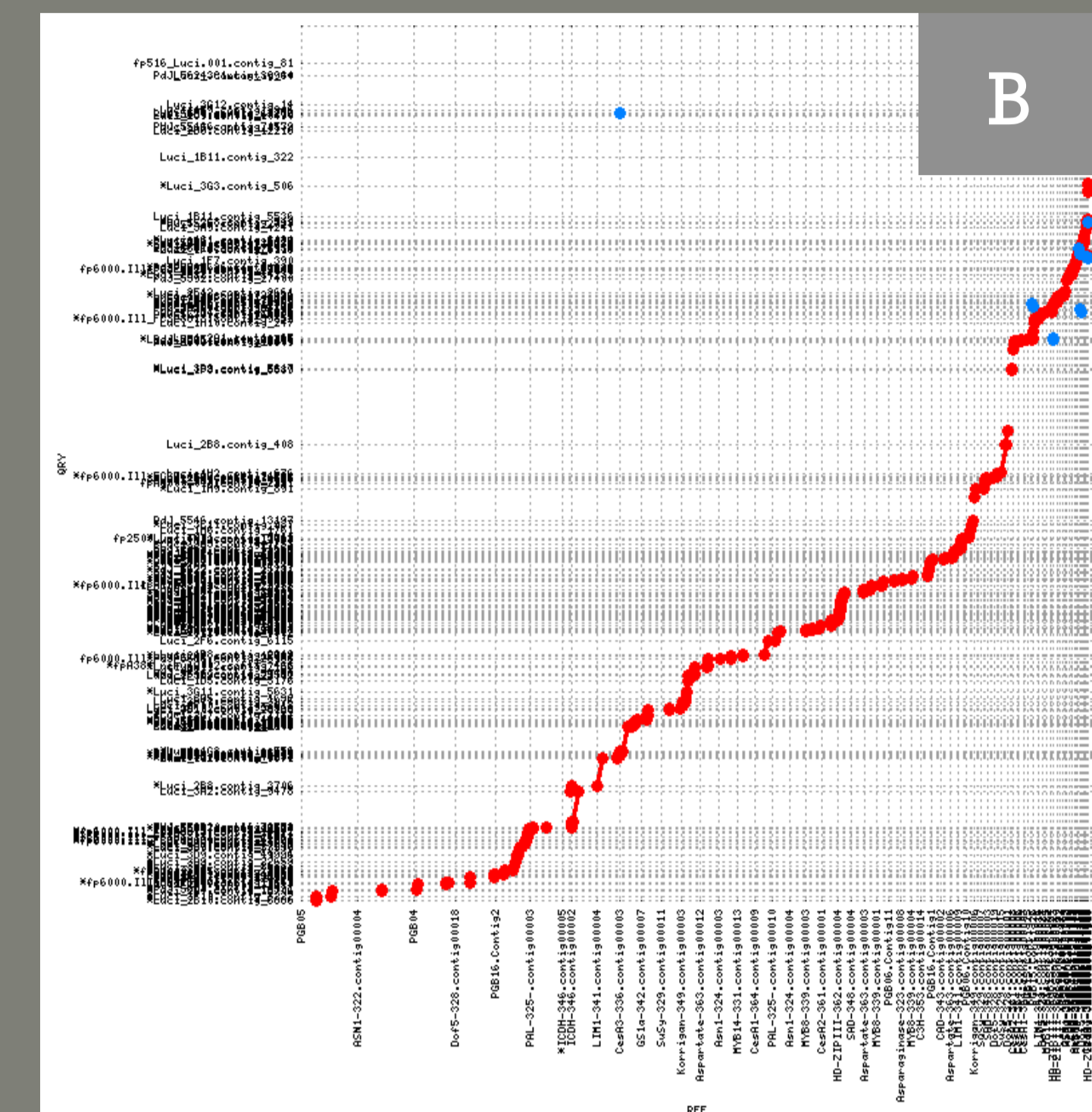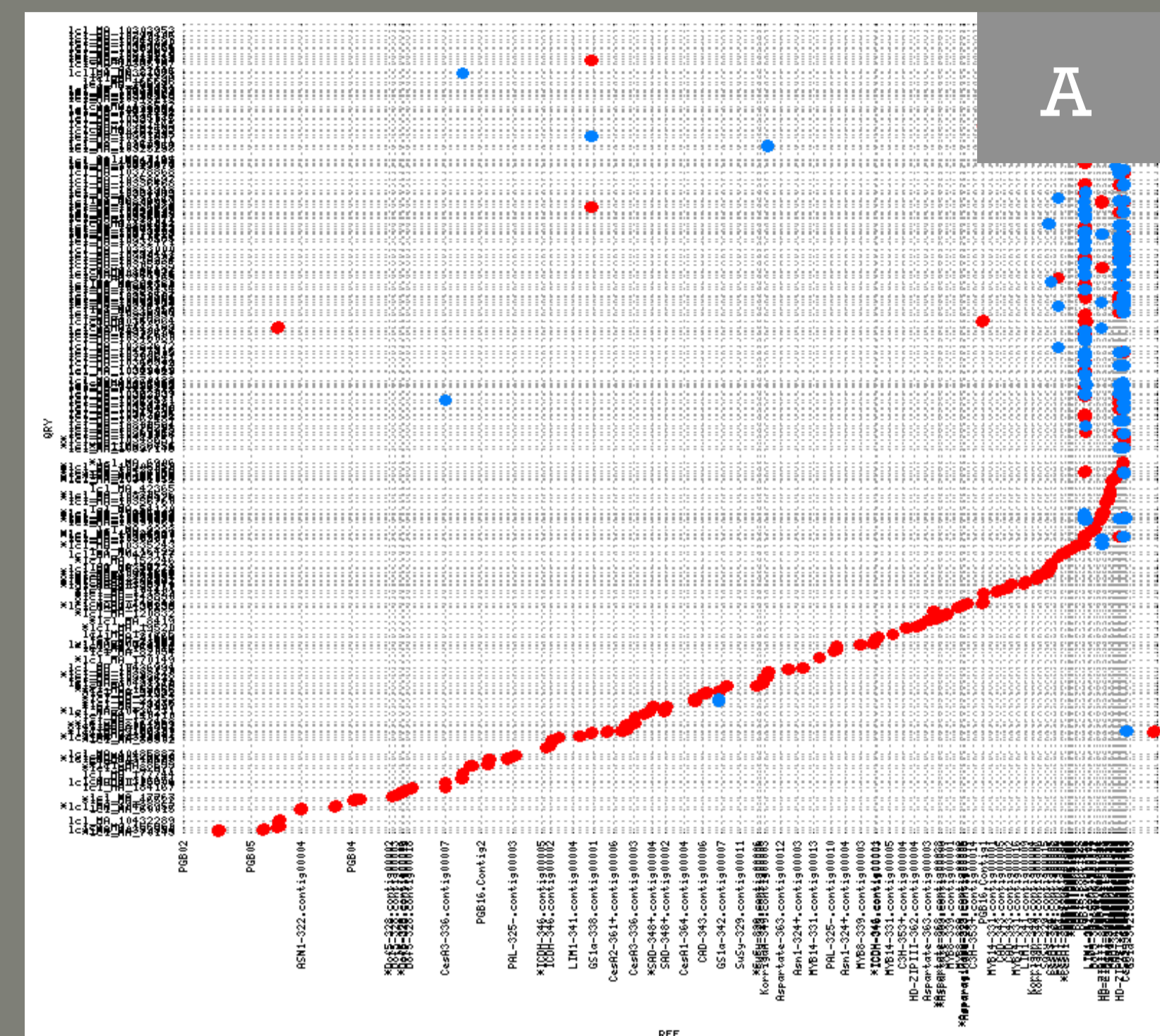Umeå Plant Science Centre, Department of Ecology and Environmental Science
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A

B

C

White vs Norway spruce comparisons

D

BACs with higher synteny

E

F
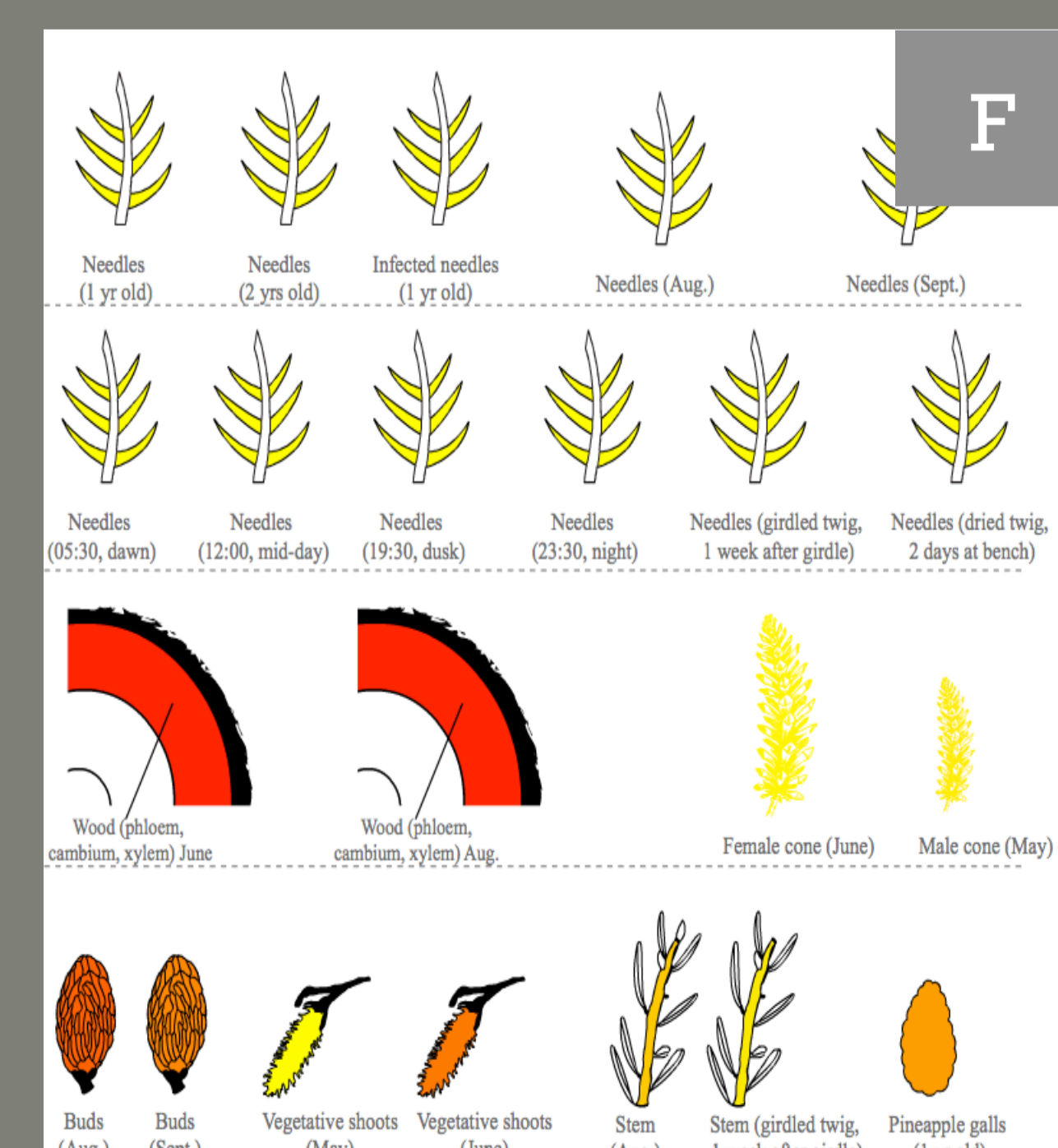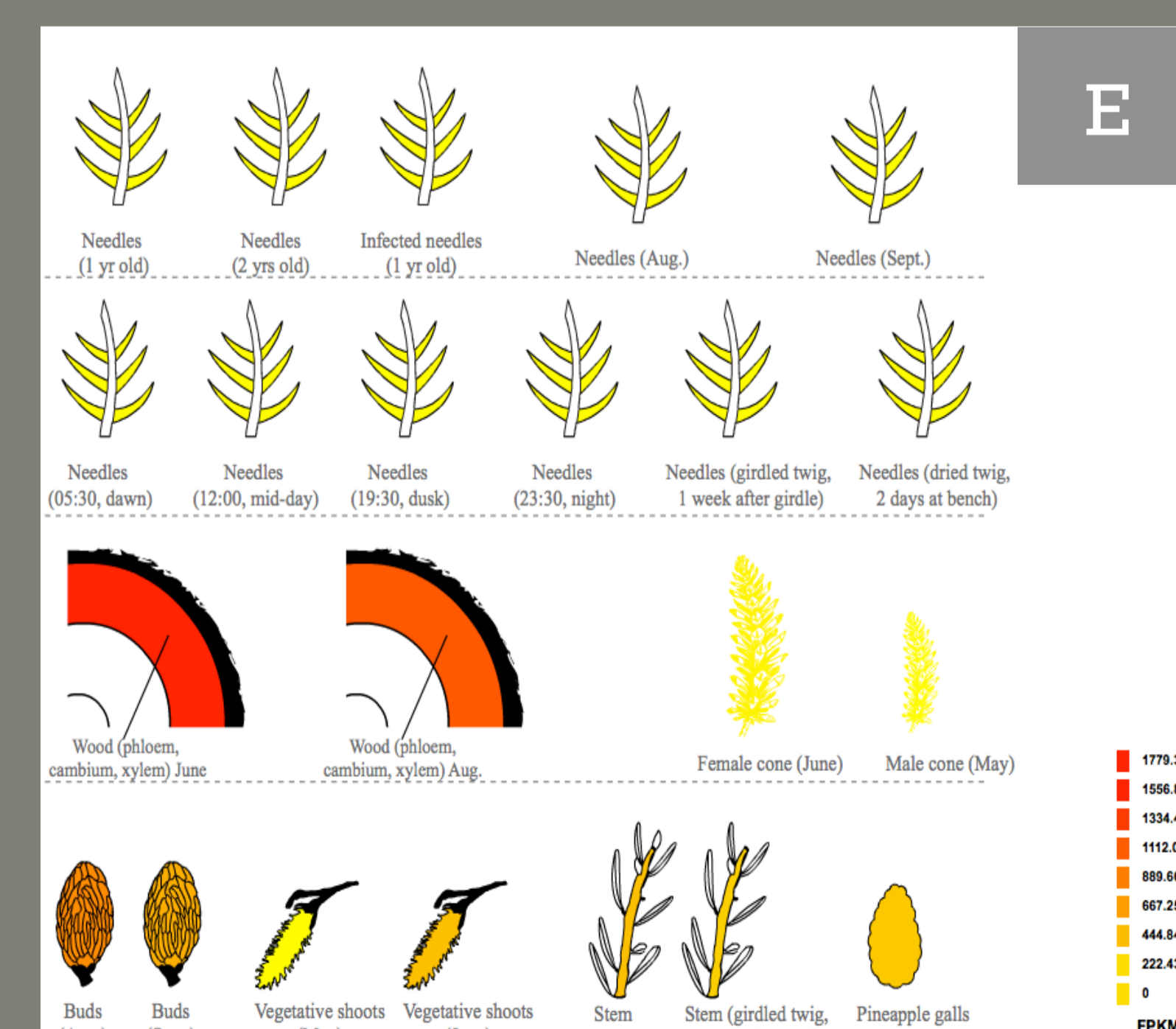
Introduction

Picea glauca and P.abies are economically and ecologically important tree species that dominate temperate and boreal forests in North America and Northern Europe. The recent sequencing of their complex and big genomes provides a unique opportunity to study the genome structure evolution in conifer species.

Methods

We assessed the levels of synteny and colinearity between *Picea glauca* and *P.abies*. Sequences from 38 fully sequenced bacterial artificial chromosomes (BACs) from *P. glauca* were compared to 450 *P. abies* fosmid-pools (representing aprox. 50% of the complete genome sequences) and diploid whole genome shotgun data (*P.abies* 1.0 assembly, 19.6 Gb). Selected *P. abies* contigs were correctly oriented and ordered using nucmer and displayed with mummerplot.

Results

We found that the number of BACs with at least one match to *P.abies* varied from 28 (fosmid-pools) to 30 (whole-genome) from a total of 38. The percentage of coverage in the BAC scaffolds by one or several fosmid-pools varied from 0.57 to 47.48%.

Significant synteny was found in twelve BACs, in which >12% of the BAC sequence was contained in one or several *P.abies* contigs. Ten of these BACs contain important genes in wood formation or nitrogen metabolism in both *P.glauca and P.abies*, such as Asparaginase, Cellulose synthase, LIM transcription factor, sucrose synthase, between others.

Future directions

We will broaden our study by including more *P.glauca* BACs, and compare it with other conifer species such as *Pinus pinaster*, and *Pinus sylvestris*.

Acknowledgements

We would like to thank the ProCoGen project (promoting conifer genomic resources) for funding this work, and also the Spruce Genome project and SmartForests Canada for providing the *P.abies* and *P.glauca* genome data.

Figure legends: A) Synteny plot of *P.abies* genome vs *P.glauca* BACs; B) Synteny plot of *P.abies* fosmid-pools vs P.glauca BACs; C) %Coverage of *P.glauca* BACs; D) BACs with higher synteny; E) Expression levels of MA_123269 gene (Sucrose synthase) and F) MA_10429177 in *Picea abies (congenie.org)*.