

# High-density genetic linkage map for Scots pine (*Pinus sylvestris*) based on SNP array genotyping

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## CONCLUSIONS & PERSPECTIVES

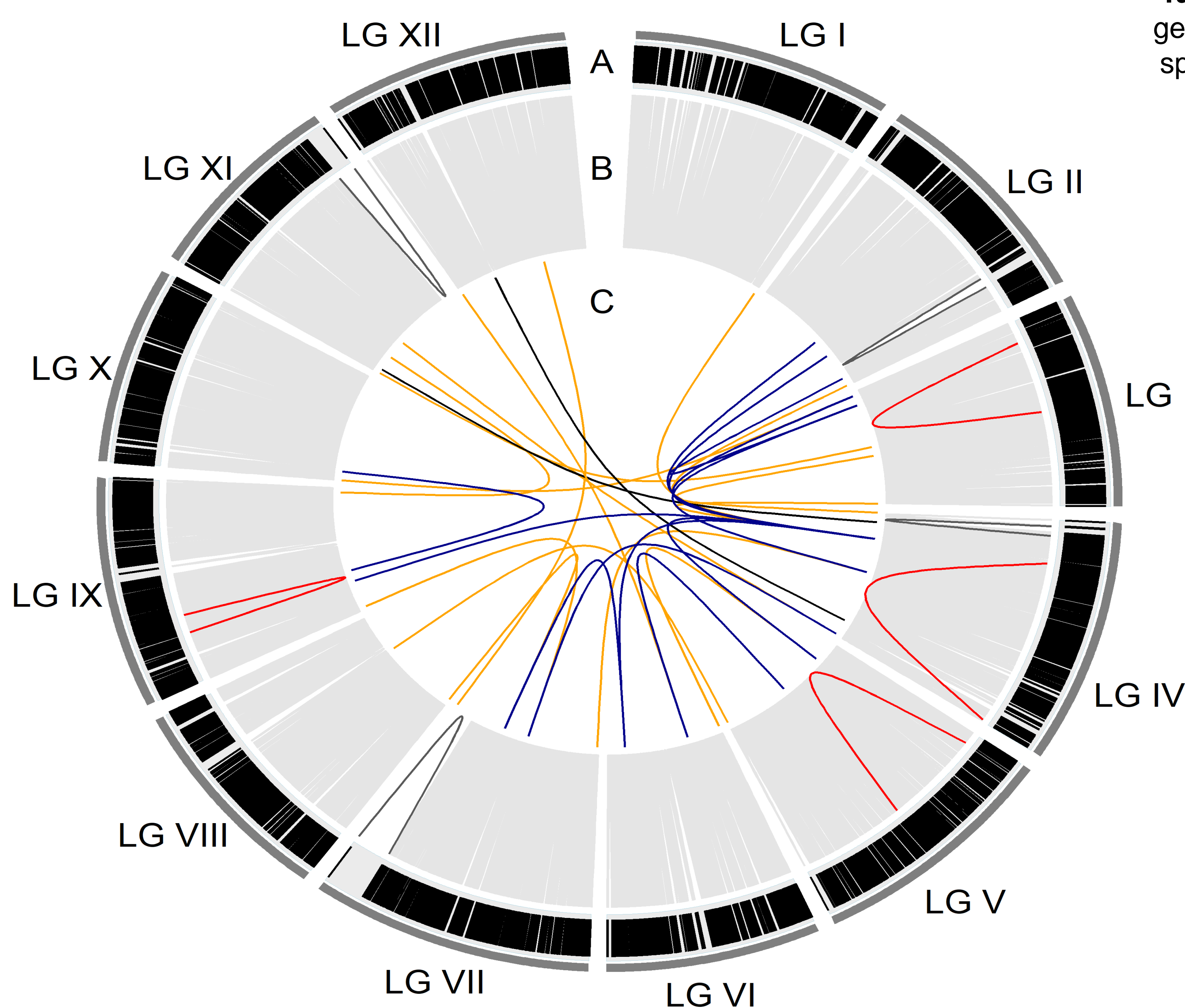
- We present the first **high-density genetic linkage map** for Scots pine, with a consensus length of **1269 cM** and **18536 markers** across **12 linkage groups**.
- This genetic map will be useful for **improving the genome assembly** by assigning unlocalized scaffolds to chromosomes.
- Comparative recombination rates** studies will be carried out between Scots pine and other pine and spruce species using genetic distances.

**Table 1:** Genetic map metrics for each mother tree (AC1017 and Y3088, megagametophytes number in parenthesis) and the consensus map. **LG:** Linkage group. **Bins:** non-redundant markers. **Length** and **maximum gap** in cM.

LG	AC1017 (n = 433)				Y3088 (n = 1091)				Consensus	
	Bins	Markers	Length	Max gap	Bins	Markers	Length	Max gap	Markers	Length
I	239	796	107.96	4.98	332	665	113.95	3.85	1282	114.07
II	160	487	90.86	10.04	376	909	105	6.27	1400	105.59
III	223	737	98.26	4.87	426	1086	100.19	2.65	1755	101.86
IV	213	744	103.83	3.47	409	904	114.89	4.78	1415	115.53
V	278	959	104.62	2.54	389	992	79.64	3.3	1566	111.78
VI	213	717	93.53	3.01	409	988	111.78	2.11	1530	93.67
VII	228	812	105.65	4.17	441	1185	99.35	7.29	1857	123.58
VIII	265	855	108.64	2.54	367	912	91.07	7.25	1835	99.35
IX	231	869	93.67	2.37	428	1152	104.82	2.09	1634	110.24
X	261	1021	123.58	4.77	458	1063	108.74	4.37	1345	94.44
XI	235	852	103.8	4.48	346	850	94.07	2.75	1337	90.86
XII	254	940	97.63	3.14	373	990	105.54	4.6	1580	108.08
Total	2800	9789	1232.03	10.04	4754	11696	1229.04	7.29	18536	1269.05

**Table 2:** Comparative metrics of genetic maps in *Picea* and *Pinus* species. **Length** in cM. Modified from Ritland *et al.*, *Genetic mapping in conifers* (2011).

Species	Marker type	Marker number	Length
<i>Picea abies</i>	SNP	21056	3556
<i>Picea glauca</i>	AFLP, ESTP, SNP, SSR	821	2304
<i>Picea mariana</i>	AFLP, ESTP, SNP, RAPD, SSR	835	1850
<i>Pinus brutia</i>	AFLP, SAMPL, ESTP, SSR	1111	1770
<i>Pinus pinaster</i>	Isozymes, RAPD	463	1860
<i>Pinus radiata</i>	RFLP, SSR	173	1223
<i>Pinus taeda</i>	AFLP	508	1528



**Figure 1:** Circos plot of the consensus map. **A)** Marker distribution across linkage groups (LG). Black vertical lines represent markers (18536 in total) arranged according to their positions in cM. **B)** Links between markers in the same LG. *Light gray* lines link markers at <5cM from each other. *Dark gray* lines link markers separated more than 5cM. *Red* lines link markers annotated in a chromosome different than the rest of the LG's markers. **C)** Links between markers in different LGs annotated in the same chromosome. *Orange* lines link markers where one of them is assigned to the correct LG. *Dark blue* lines (24 markers, 0.13% of the total number) link markers annotated in a chromosome different to both markers' LG.

## INTRODUCTION & METHODS SUMMARY

- Scots pine (*Pinus sylvestris*) is the most **widely distributed** Pinaceae species in the world.
- Important species for **wood production** in Sweden.
- Large** (>20Gbp) and **highly repetitive** genome.
  - Linkage maps are important for **genome-wide association** and **evolution** studies. Also, for improving fragmented genome assemblies.
- Haploid megagametophytes were manually separated from seeds and grounded in liquid nitrogen.
- DNA extraction and genotyping with Psl50K SNP array.
  - Map creation with OneMap and LPmerge.



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