

Conifer Translational Genomics Network Coordinated Agricultural Project

CATTAGCT **CTGN** **TCA**P CAAGTCATCCATGATTAGCT

Genomics in Tree Breeding and
Forest Ecosystem Management

Module 8 – Genetic Mapping

Nicholas Wheeler & David Harry - Oregon State University

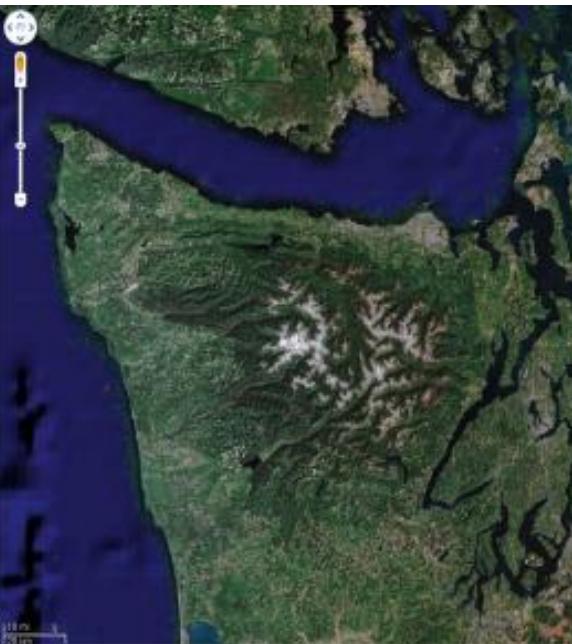


Maps with different information

Terrain



Satellite



Roads and cities



Image Credit: <http://maps.google.com>

Genetic mapping overview

- Linkage maps are based on chromosome recombination during meiosis
- Only genetically variable (heterozygous) regions can be tracked
 - *That is, only polymorphic markers are informative*
- Map distance (measured by Recombination Frequency (RF)) is ~ proportional to physical distance
- Recombination is estimated statistically
 - *With increasing distance (and RF), estimation errors increase*
 - *Mapping functions statistically adjust for sources of error*
- Prediction: Using the allelic state at one locus, we can predict the allelic state at a neighboring locus (if in LD!)

How to build linkage maps

- Identify an appropriate mapping population
- Develop a sufficient number of genetic markers and obtain segregation data, based on those markers, for the mapping population
- Conduct linkage analyses

Overview of meiosis

- Division begins with $2n$ cell
- Chromosome pairing
- Recombination occurs
- Recombined chromosome pairs separate
- Reduction division
- Products with $1n$ (recombined) chromosomes

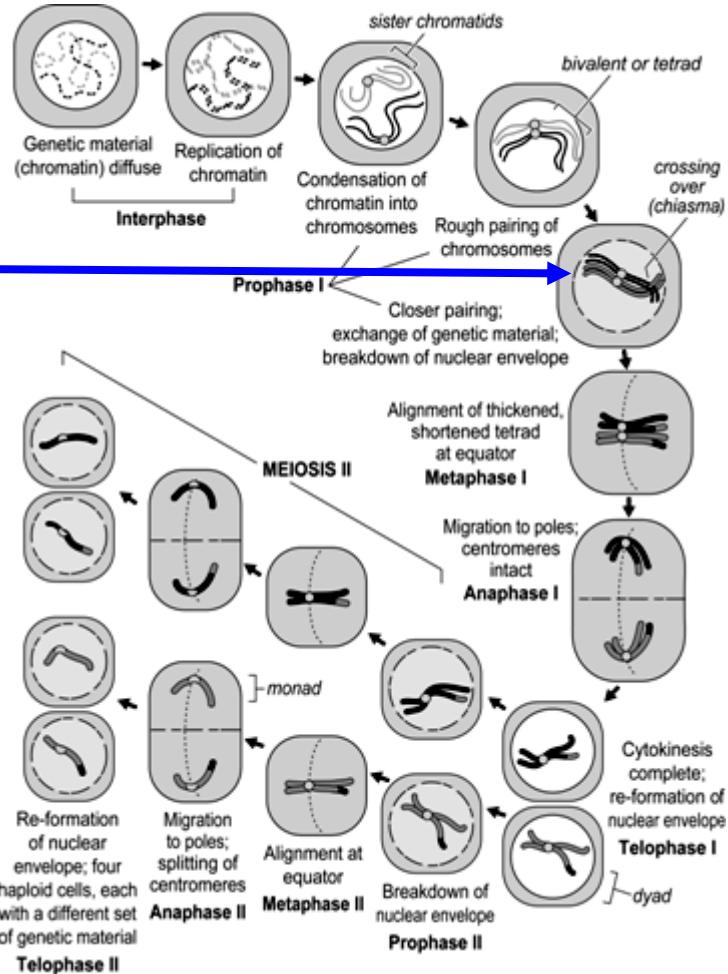
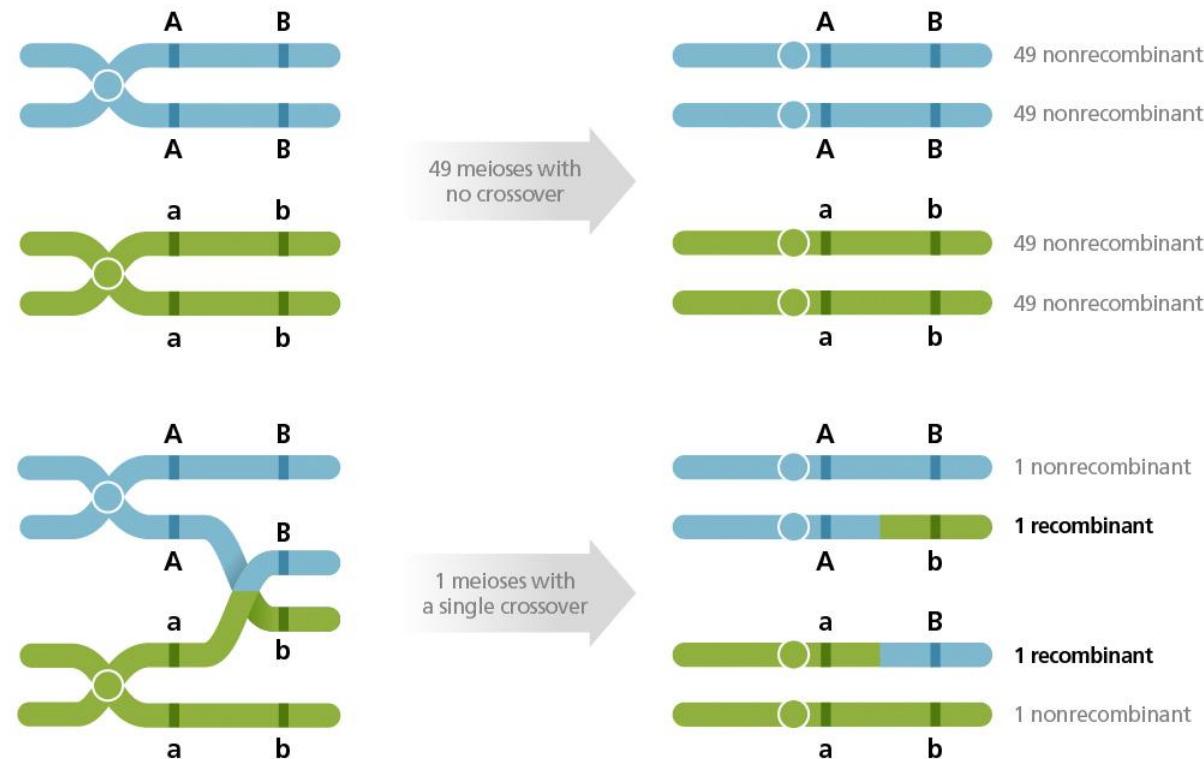


Figure Credit: White, T. L., W. T. Adams, and D. B. Neale. 2007. Forest genetics. CAB International, Wallingford, United Kingdom. Used with permission.

Parental and recombinant chromosomes



$$\text{Frequency of recombination: } r = \frac{1 + 1}{49 + 49 + 49 + 49 + 1 + 1 + 1 + 1} = \frac{2}{200} = 1 \text{ percent} = 1 \text{ map unit} = 1 \text{ cm}$$

Figure Credit: Modified from Hartl and Jones. 2006.

Mapping functions: Recombination frequency and map distance

- When RF is small ($\leq 15\%$), $RF \sim cM$
- When RF is larger ($>15\%$), then $cM \geq RF$
- Most mapping software includes map function adjustments

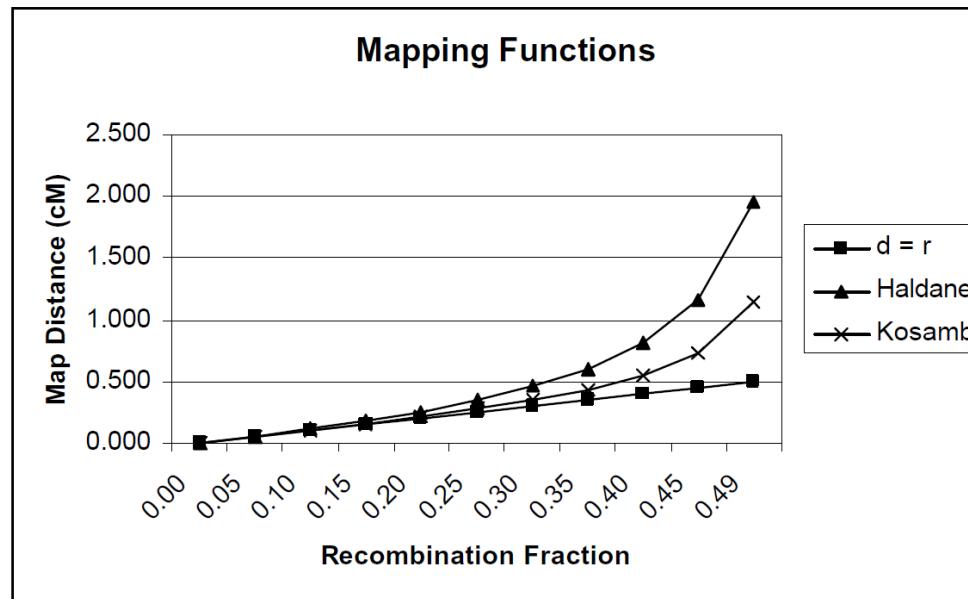
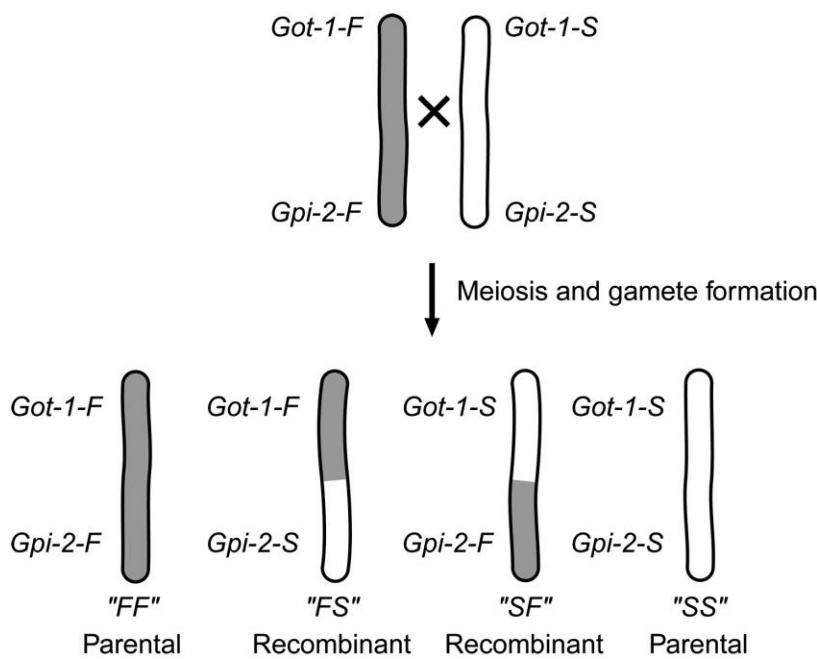


Figure Credit: David Harry, Oregon State University

Types of mapping populations

- Haploid conifer megagametophyte maps
- Full-sib pedigree maps (from controlled crosses)
 - *Back-cross maps (particularly useful with inbred lines)*
 - F_1 test cross
 - F_2 cross
 - *Intercross*

Building a map with linkage analysis



Genotype(s)	Observed	Expected	$(o-e)^2/e$
	(o)	(e)	
FF	90	40	62.5
FS	3	40	34.2
SF	4	40	32.4
SS	63	40	13.2
Total	160	160	142.3

$$r = \# \text{ recombinants} / N$$

$$r = 7/160 = 0.043 \text{ (tightly linked)}$$

Figure Credit: Modified from Guries et al., 1978

Early maps derived from megagametophytes

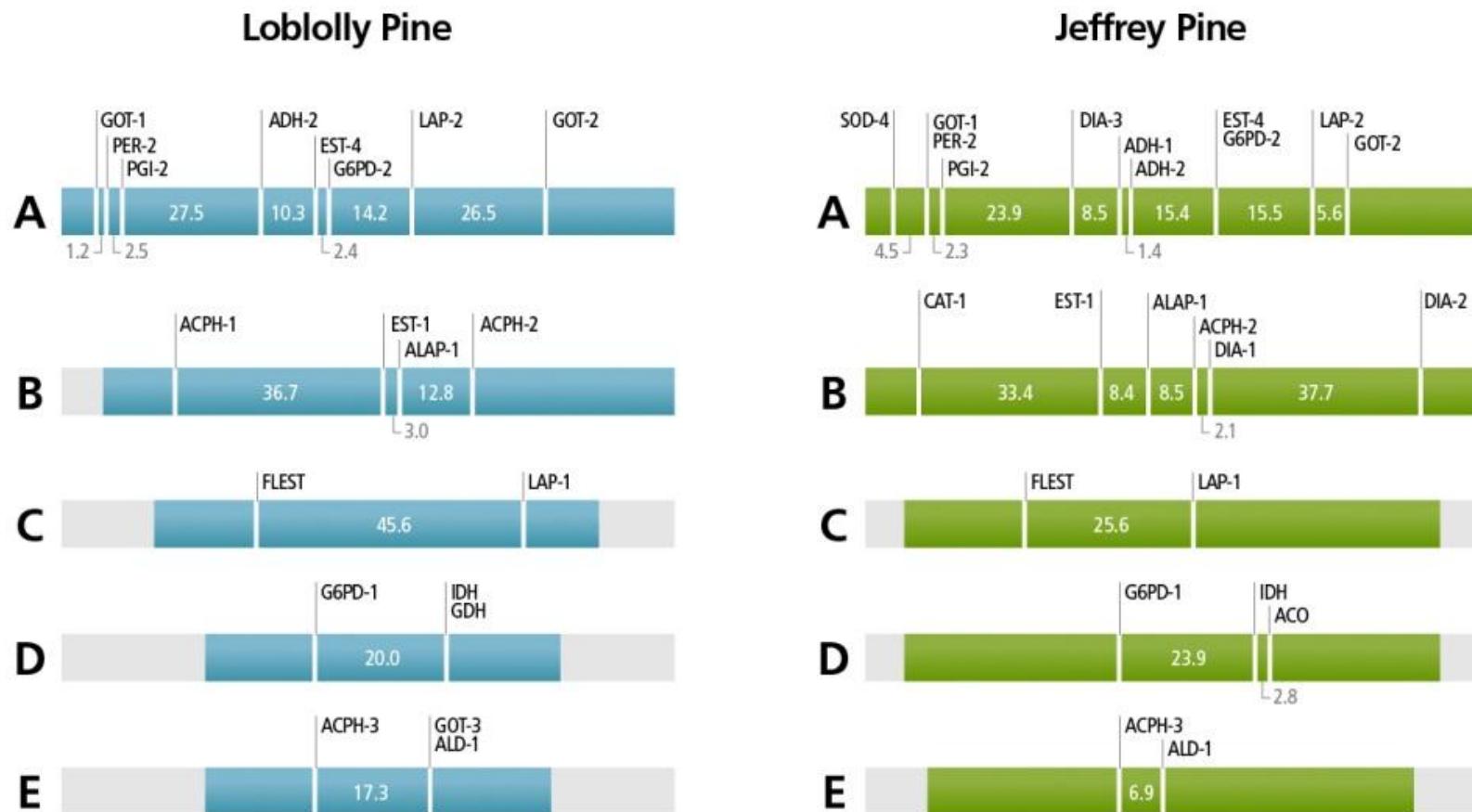
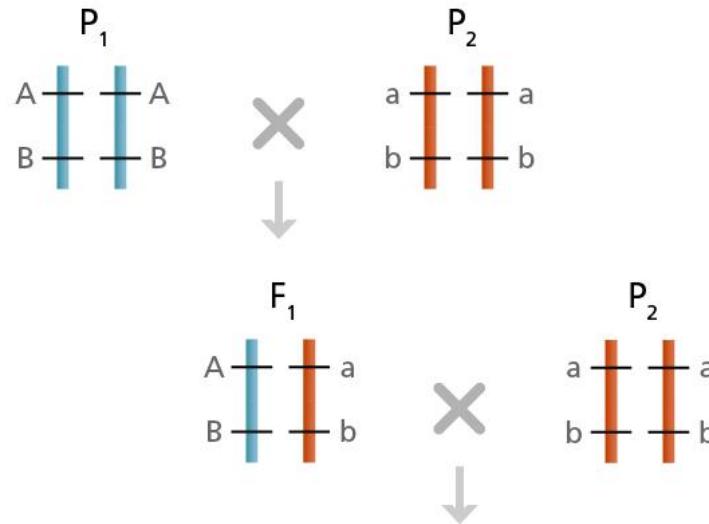


Figure Credit: Modified from Conkle, 1979

BC mapping population

Gamete Frequencies

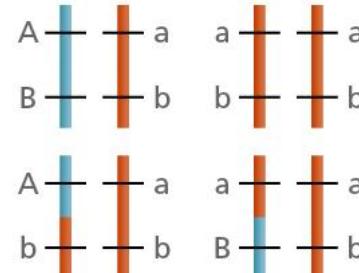
A-B	$(1-r)/2$	
a-b	$(1-r)/2$	
A-b	$r/2$	
a-B	$r/2$	



Genotype Frequencies

AaBb	$(1-r)/2$	
aabb	$(1-r)/2$	
Aabb	$r/2$	
aaBb	$r/2$	

BC₂ Progeny



Parental types

Recombinant types

Figure Credit: Modified from David Neale, University of California, Davis

F_2 mapping population

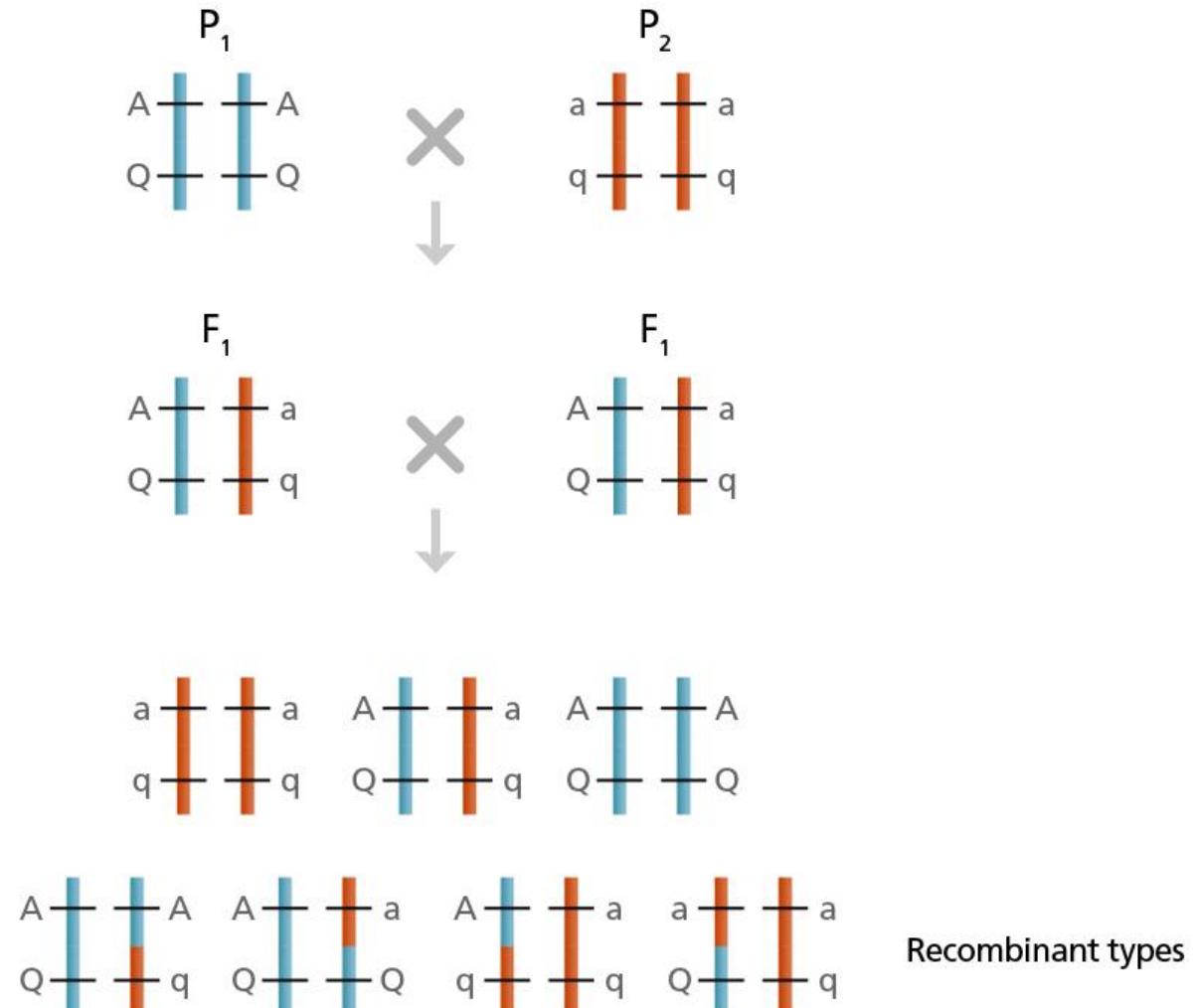


Figure Credit: Modified from David Neale, University of California at Davis

Intercross mapping population

- The number of haplotypes (markers) in the population varies across the genome
- Some loci will have 4 haplotypes (shown here by 4 colors)
- Other loci will have 3, 2, or 1 haplotype(s), depending on the genotypes of the grandparents. These other possibilities are not shown on this slide

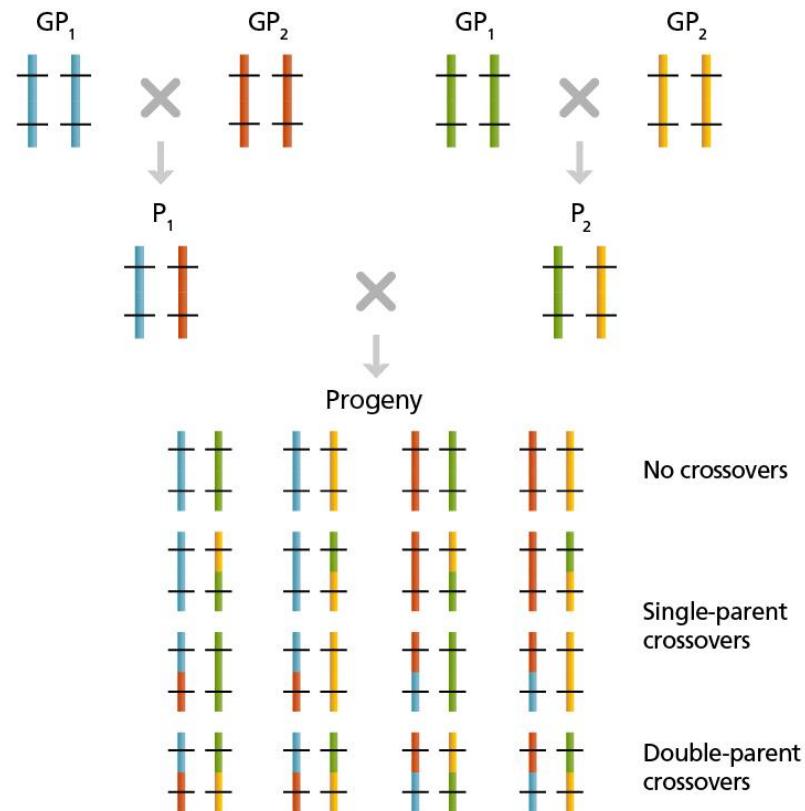


Figure Credit: Modified from David Neale, University of California at Davis

How large should a mapping population be?

The answer depends on your objectives

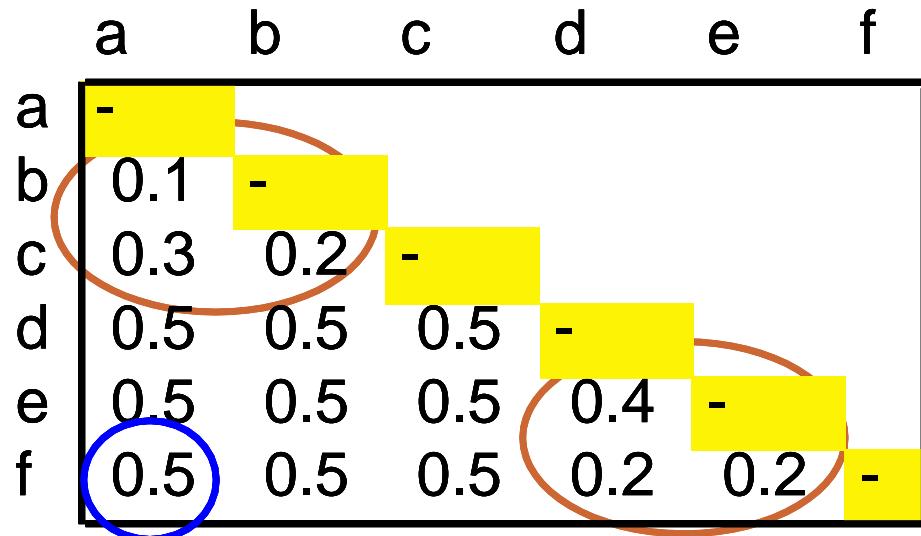
- Gene order / synteny
- Genetic architecture / QTL
- Map-based cloning of candidate genes
- Cost / resources

Summarizing mapping populations

- Genetic mapping infers recombination in the parents (during gametogenesis) by observing parental and recombinant chromosomes in offspring
- BC, F₂, and intercross mapping populations differ in amount of genetic variation in founder parents and grandparents
 - *BC and F₂ populations are common in inbred crops and model organisms*
 - *Intercross populations tend to be more common in outbred organisms, such as most forest trees*
- Mapping populations also differ in how genetic variation is tracked
 - *Variation and phase in genetic markers (and other genes, QTL)*
 - *Linkage disequilibrium within and among families (to be discussed later)*

Mapping software: Basic tasks

1. Group markers. Use all pairwise estimates of RF.
RF ~ 0.5 means unlinked



Each cell reports the frequency of recombinant gametes

2. Determine order. Begin with smallest RF, and add in other markers so as to minimize total size

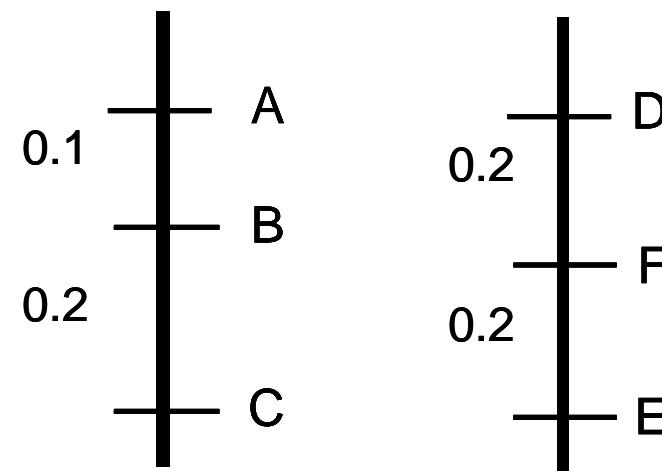


Figure Credits: David Neale, University of California, Davis

Markers: What type and how many

- That depends! (Are you surprised?)
 - *Map purpose*
 - *Resources available*
 - *Genotyping platform*
- Considerations
 - *Dominant vs. co-dominant*
 - *Bi-allelic vs. multi-allelic*

From markers to maps

- An example from Douglas-fir

Fig. 5 Southern blots hybridized with RFLP probe PmIFG_1490.
a Parent/grandparent blot. Lane 1 1-kb ladder, lane 2 maternal grandmother, lane 3 maternal grandfather, lane 4 mother, lane 5 father, lane 6 paternal grandmother, lane 7 paternal grandfather. **b** Progeny blot. Lane 1 1-kb ladder, lanes 2–24 progeny. The transmission of parental genotypes (23×14) resulted in segregation of four genotypes in the progeny (12, 34, 13, 24)

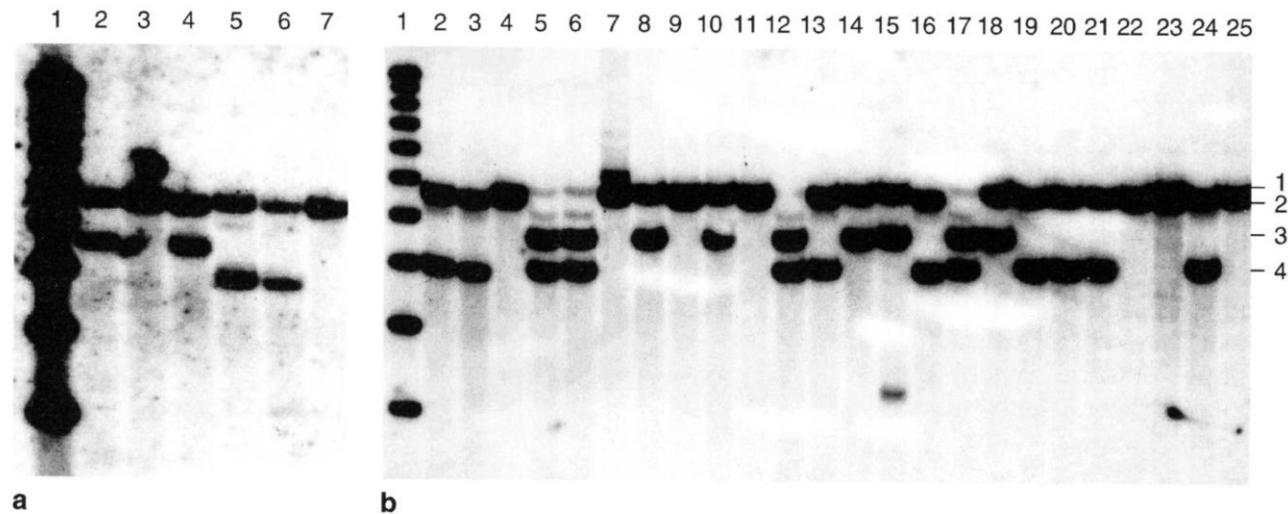


Figure Credit: Modified from Jermstad et al., 1998

A sex-averaged linkage map of Douglas-fir

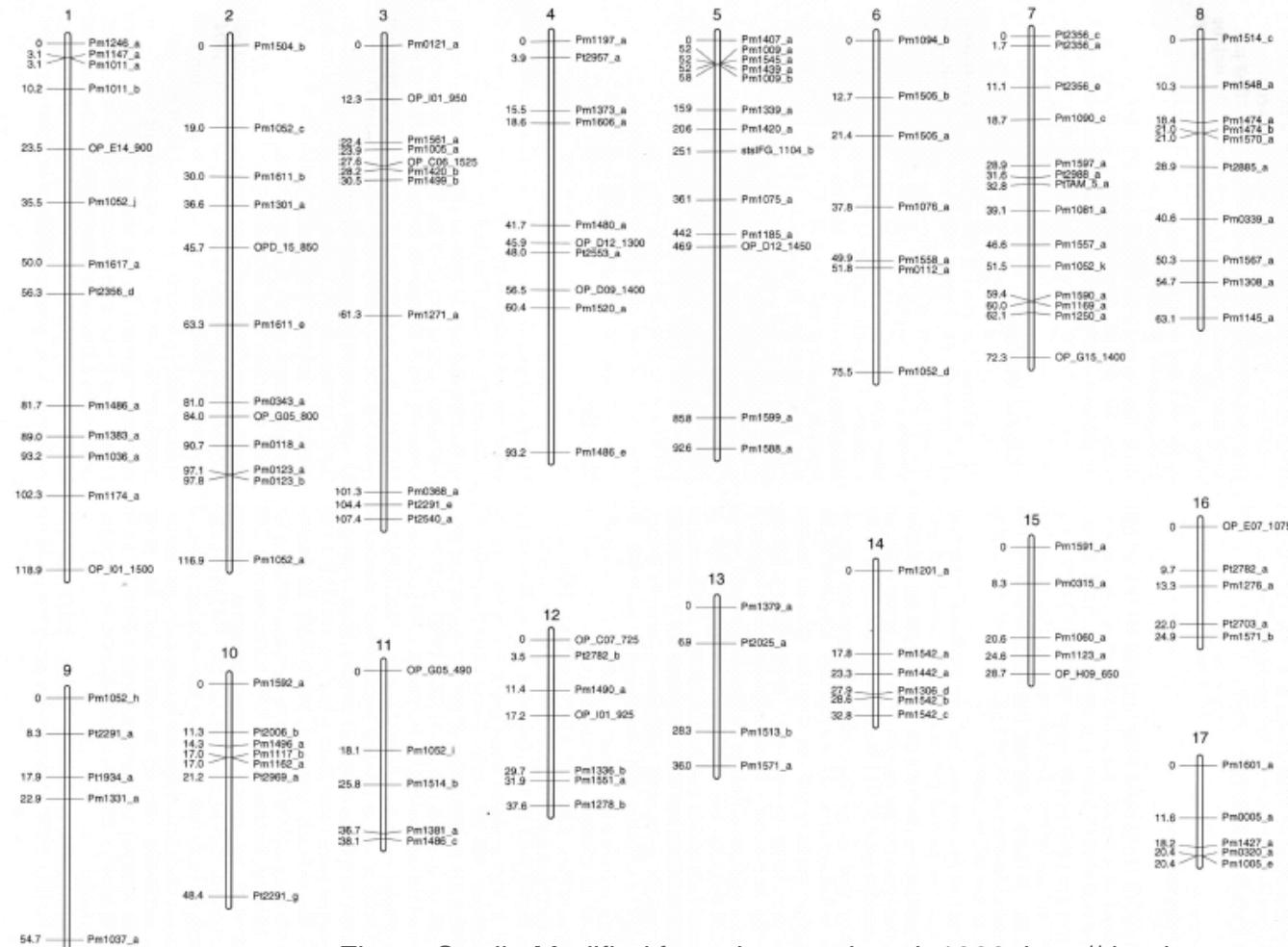
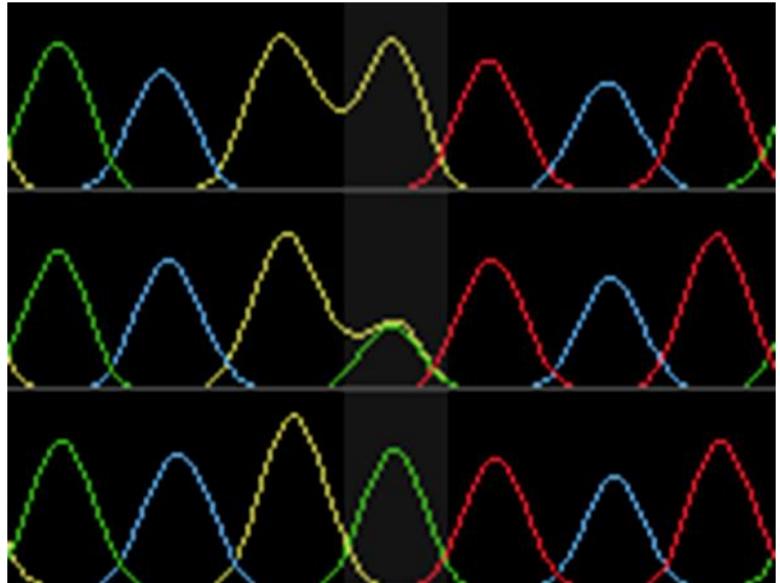


Figure Credit: Modified from Jermstad et al, 1998; <http://dendrome.ucdavis.edu/treegenes/>

Adding sequenced-based markers



LG1	LG2	LG3
PtIG_1918_3	C1462Contig_0446	{UMN-798-01-022 0-006-02-220
0-14961-01-327 0-15448-02-46	C1120Contig_01-109 CL474Contig_01-02-186	{0-9323-0-589 0-407-03-128
0-14972-01-250 2-5711-02-26	C1585Contig_03-307	{0-10722-0-123 0-000-01-000
PtIG_2745_1_0-3995-02-365	C1470Contig_01-02-037	{0-9323-0-137 0-11784-03-109
0-18837-01-303 0-18837-01-294	C1711Contig_01-02-037	{2-6470-01-26
0-17694-02-82 0-1640-01-227	C1472Contig_01-04-154 CL478Contig_01-03-270	{0-9323-0-137 0-11784-03-109
0-7615-02-58 0-5174-02-191	C1473Contig_01-04-154 CL478Contig_01-03-270	{0-9323-0-137 0-11784-03-109
UMN-6124-03-85 0-17694-02-345	PtIG_971_1-0-3467-01-116	{0-10719-0-57 0-993-02-406
UMN-6124-03-373 CL3036Contig1-01-234	C1474Contig_01-04-154 CL478Contig_01-04-155	{0-10723-0-203 2-2824-01-183
UMN-3901-01-56 0-9448-02-217	C1475Contig_01-04-154 CL478Contig_01-04-155	{0-14966-02-399 CL1732Contig1-04-115
-2-6039-01-596	C1476Contig_01-04-154 CL478Contig_01-04-155	{0-14468-01-594 0-6554-02-065
CL760Contig1-02-580 2-9476-01-382	C1477Contig_01-04-154 CL478Contig_01-04-155	{UMN-798-01-022 0-006-02-220
CL3946Contig1-03-173	C1478Contig_01-04-154 CL478Contig_01-04-155	{0-9323-0-137 0-11784-03-109
0-14590-02-108 0-14677-01-255	PtIG_971_1-0-3467-01-116	{0-9323-0-137 0-11784-03-109
0-17776-01-94	C1479Contig_01-04-154 CL478Contig_01-04-155	{0-10719-0-57 0-993-02-406
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UMN-6664-01-168	C1481Contig_01-04-154 CL478Contig_01-04-155	{0-14966-02-399 CL1732Contig1-04-115
0-1824-01-19 UMN-1609-01-323	C1482Contig_01-04-154 CL478Contig_01-04-155	{0-14468-01-594 0-6554-02-065
UMN-327-01-395	C1483Contig_01-04-154 CL478Contig_01-04-155	{0-10719-0-57 0-993-02-406
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CL2216Contig1-03-117	C1495Contig_01-04-154 CL478Contig_01-04-155	{0-10723-0-203 2-2824-01-183
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CL4376Contig1-04-94 UMN-3444-01-231	C1504Contig_01-04-154 CL478Contig_01-04-155	{0-10723-0-203 2-2824-01-183
2-8585-02-472 PtIG_138_B	C1505Contig_01-04-154 CL478Contig_01-04-155	{0-10723-0-203 2-2824-01-183
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0-17577-01-620 PtIG_2068_A	C1514Contig_01-04-154 CL478Contig_01-04-155	{0-10723-0-203 2-2824-01-183
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0-14415-01-190	C1533Contig_01-04-154 CL478Contig_01-04-155	{0-10723-0-203 2-2824-01-183
		{0-10723-0-203 2-2824-01-183}

Figure Credits: Andrew Eckert, University of California, Davis

Linkage relationships: A new perspective

	LG1	LG2	LG3
0.0	PtIFG_1918_3	0.0	C1469Contig1-09_0446
4.1	#0-14961-01-327 0-15448-02-46	2.4	0-1129-01-169 C1469Contig1-02-186
8.0	U-14972-01-250 2-5711-02-26	3.5	0-2810-01-71 0-1748-01-07
11.8	PtIFG_2745_1 0-3959-02-365	4.9	0-1447-01-148 CL447Contig1-01-458
12.5	0-18837-03-003 0-18837-02-194	7.2	0-3120-01-430 PtIFG_149
	0-17694-02-82 0-16400-01-227	8.5	0-1470Contig1-04-154 CL470Contig1-03-270
	0-7615-02-53 0-174-02-191	8.8	0-1687-02-281
12.5	UNN-6124-03-085 0-17694-02-345	12.4	0-1469-01-169 CL1299Contig1-03-442
	UNN-6124-03-372 CL3036Contig1-01-234	15.1	PtIFG_978_1 2-94-752-150
	UNN-3901-01-56 0-9448-02-217	16.5	0-1436-02-181 0-9470-01-116
14.0	2-6039-01-596	26.9	CL288Contig1-01-133
	CL760Contig1-02-580 2-9476-01-382	30.9	0-1448-01-153 CL314Contig1-03-425
14.7	CL3046Contig1-03-75	32.1	0-1368-01-153 CL314Contig1-03-130
15.8	0-14590-02-108 0-14677-01-255	35.0	0-1126-01-409 CL308Contig1-05-177
19.0	0-17694-02-54 0-17694-02-54	35.8	CL314Contig1-05-177
	2-2129-01-265 0-9713-02-44	38.1	0-1469-01-151 PtIFG_149
	UNN-664-01-168	40.5	0-1469-01-169 0-1470-02-430
21.5	0-124-01-207	41.4	0-1469-01-170 0-1470-02-430
28.1	0-1126-02-419 UNN-1609-01-323	52.7	CL15Contig1-06-141
34.6	UNN-CL91Contig1-01-395	53.5	0-1368-01-147 CL308Contig1-04-52
36.9	UNN-CL91Contig1-02-246	54.1	0-1368-01-147 CL308Contig1-04-52
	2-2756-02-152 0-1213-01-379	55.3	0-1368-01-147 CL308Contig1-04-52
38.0	PtIFG_2718_3	57.6	0-1520-02-241
39.0	CL2493Contig1-04-150	58.4	0-1272-02-049
40.9	0-13670-01-69	59.5	UNN-3841-01-481
42.4	0-13310-01-495	61.0	UNN-3841-01-114 PtIFG_291_2
42.7	0-12437-01-222 0-7001-01-143	64.2	CL194Contig1-02-149 CL372Contig1-04-59
43.8	0-738-01-777	64.9	0-1469-01-169
	CL378Contig1-01-122 CL4262Contig1-02-92	71.3	0-2-070-02-152
	0-17492-01-34	73.6	0-1469-01-169 0-1470-02-399
47.6	CL4646Contig1-03-99	74.4	0-189-01-189 CL308Contig1-04-52
47.7	CL2216Contig1-03-117	78.7	0-1069-01-53 CL112Contig1-06-148
51.1	UNN-2660-01-81	80.7	0-1488-01-102 CL288Contig1-02-71
53.3	0-11786-02-99	83.7	0-1798-01-120 2-2450-01-03
55.6	PtIFG_2588_2 PtIFG_2588_1	84.6	UNN-CL17Contig1-03-404
56.7	0-18368-01-502	85.3	PtIFG_728_1
58.0	2-3463-01-608	85.7	0-1469-01-169 PtIFG_1916_2
58.9	UNN-2718-01-98	87.8	0-1469-01-169 0-1469-01-133
63.2	0-18920-01-354	88.5	UNN-354-01-437 0-163-01-136
64.5	0-4352-01-52 2-1243-01-218	90.7	0-1469-01-169 0-1469-01-211
	CL4376Contig1-04-94 UNN-3444-01-231	94.4	0-1469-01-169 0-1469-01-396 UNN-915-01-50
65.8	2-8585-02-472 PtIFG_136_B	97.2	0-1368-01-523 CL308Contig1-03-140
68.7	CL1611Contig1-04-134 2-7532-01-105	98.5	0-1469-01-169 0-1470-02-371
73.2	0-7471-01-229	101.5	0-1368-01-796 0-1368-01-068
74.3	0-14099-02-60	103.9	CL450Contig1-04-98
76.7	2-3256-03-334	105.9	0-1469-01-169 0-1983-01-433
76.9	2-6386-01-165	107.5	0-6005-01-264
77.9	0-1695-01-303	111.4	CL449Contig1-01-82
79.1	0-1695-03-173 UNN-1598-02-647	111.7	0-1469-01-169 0-1469-01-444
81.2	PtIFG_975_3	112.1	0-1469-01-169 0-1469-01-444
83.9	CL755Contig1-01-104-44 PtIFG_2145_1	112.5	0-1469-01-169 0-1469-01-444
86.3	2-8851-01-394	113.4	CL404Contig1-01-184 UNM-5942-02-78
86.9	0-323-02-03 0-1631-02-236	119.2	0-1469-01-169 0-1469-01-452
87.8	CL1691Contig1-01-138	120.8	0-1889-02-053 0-1892-02-6
88.2	UNN-CL54Contig1-07-88	123.4	0-1651-01-72 UNN-2020-01-96
88.6	0-18587-01-200	124.9	0-1469-01-169 0-1469-01-452
	2-3177-03-168 0-17140-01-381	141.8	0-1688-02-061
89.8	2-8017-01-104 0-17140-01-74	142.6	0-1383-01-152 0-1688-02-266
91.2	CL599Contig1-07-109	142.7	0-1469-01-169 0-1469-01-399
91.7	0-1849-01-280 0-6952-01-178	150.5	0-1469-01-87 0-1640-01-391
92.7	2-8851-01-201	161.3	0-1655-01-77
93.8	0-14573-01-380	150.6	D0-1445-01-405 CL117Contig1-09-194
94.9	0-13101-02-166	150.7	D0-1902-01-116
96.1	0-18261-01-455	154.8	D-13837-02-383 2-280-01-530
97.8	PtIFG_2006_C	155.1	D-18483-01-147 0-9538-01-252
99.4	UNN-1842-01-306 0-4435-01-161	159.2	D-18483-01-147 0-9538-01-332
	0-1620-01-114	161.5	D-1662-01-43 0-718-01-144
	0-14415-01-190	164.8	D-337Contig1-01-115

LG	Length (cM)	Markers
1	100.4	99
2	164.8	159
3	161.7	158
4	131.3	147
5	172.8	169
6	177.7	178
7	167.7	161
8	170.9	191
9	168.2	150
10	140.4	166
11	174.7	146
12	168.0	176
Total	1898.6	1900

Figure Credits: Andrew Eckert, University of California, Davis

Syntenic linkage group #6 in five pine species

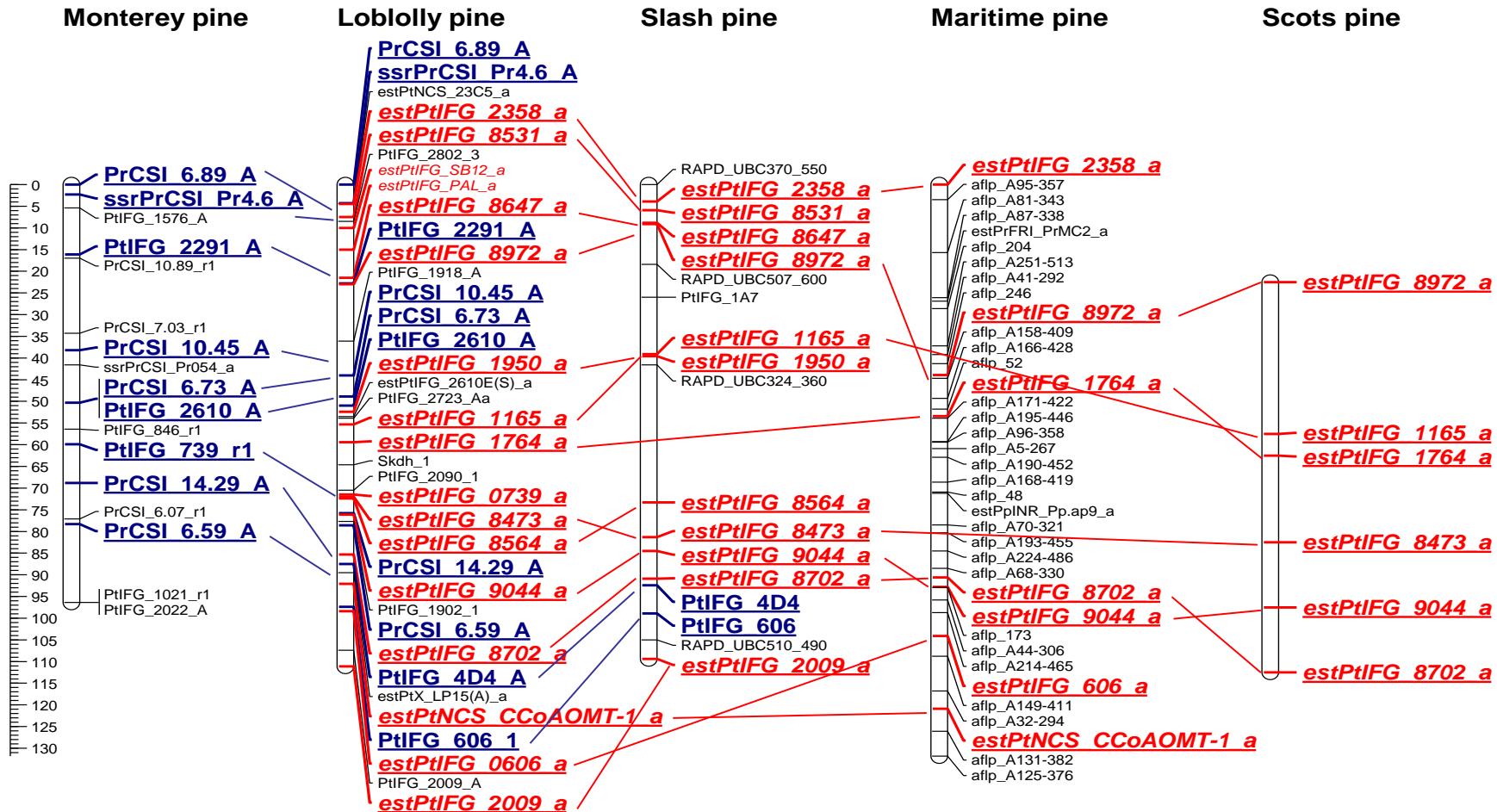


Figure Credit: Kostya Krutovsky, Texas A&M University

Syntenic linkage group #6 in three species from different genera

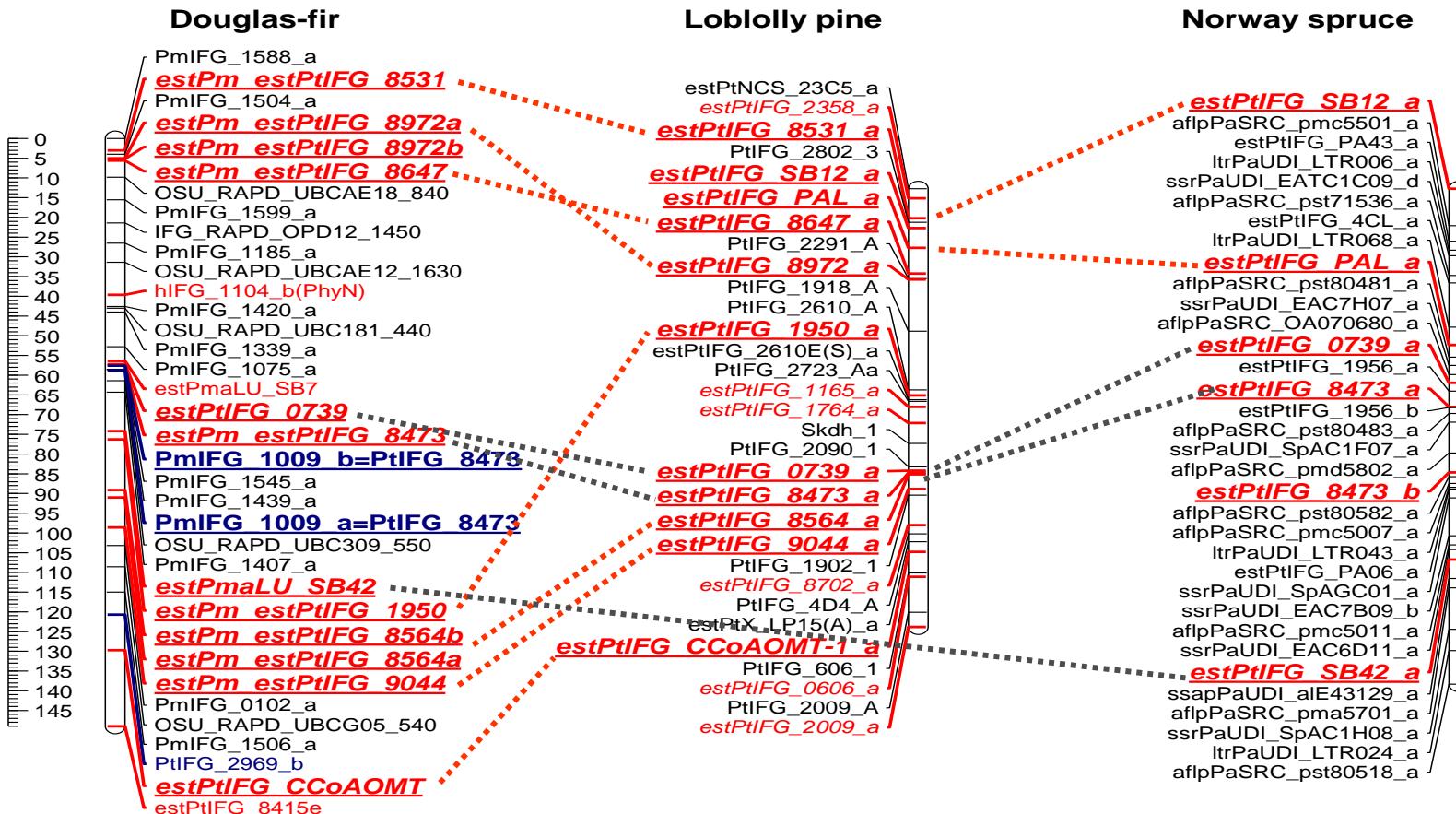


Figure Credit: Kostya Krutovsky, Texas A&M University

An annotated map for *Castanea mollissima*

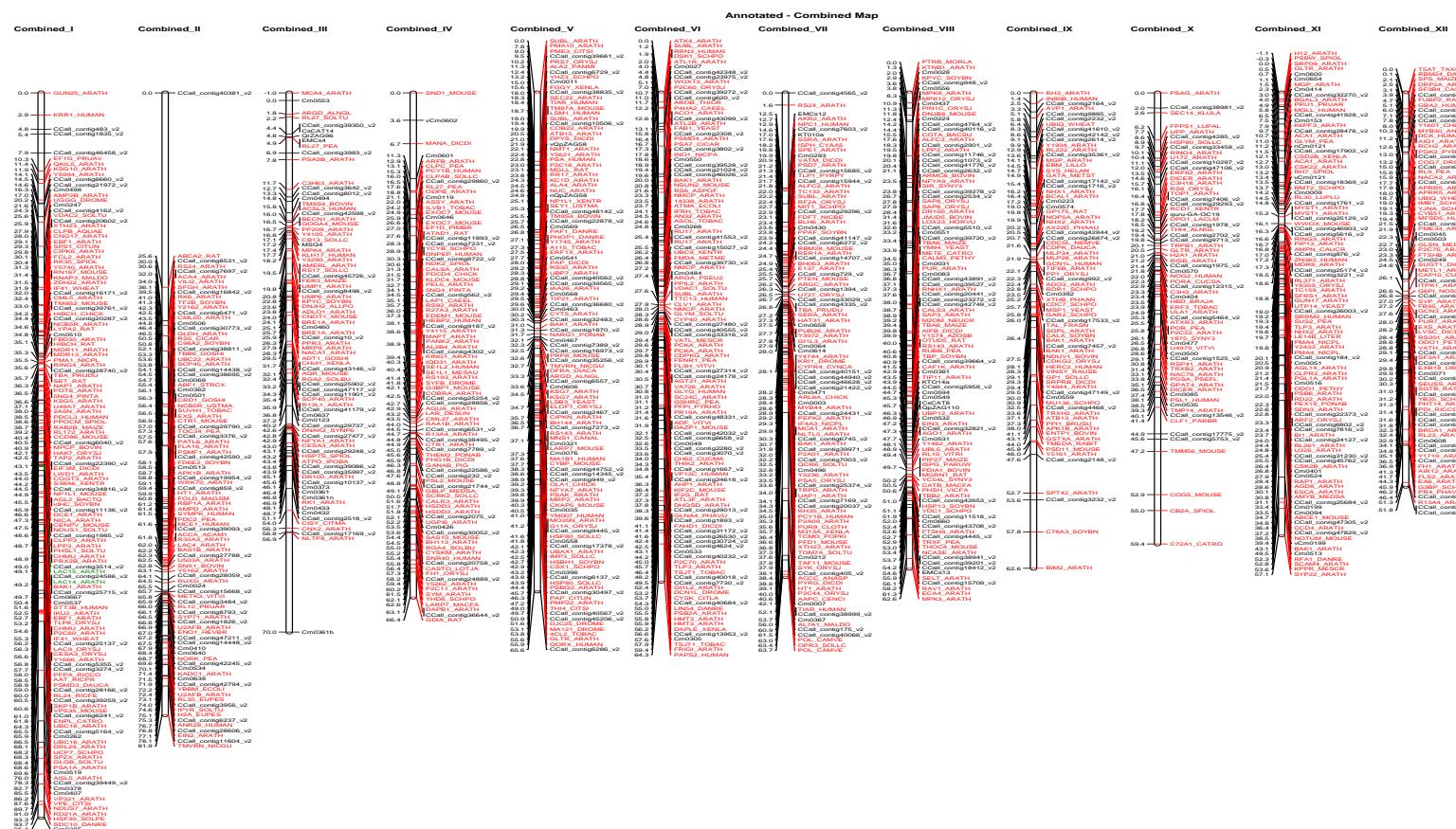


Figure Credit: Tom Kubisiak, United States Forest Service

Candidate defense: Response genes in chestnut

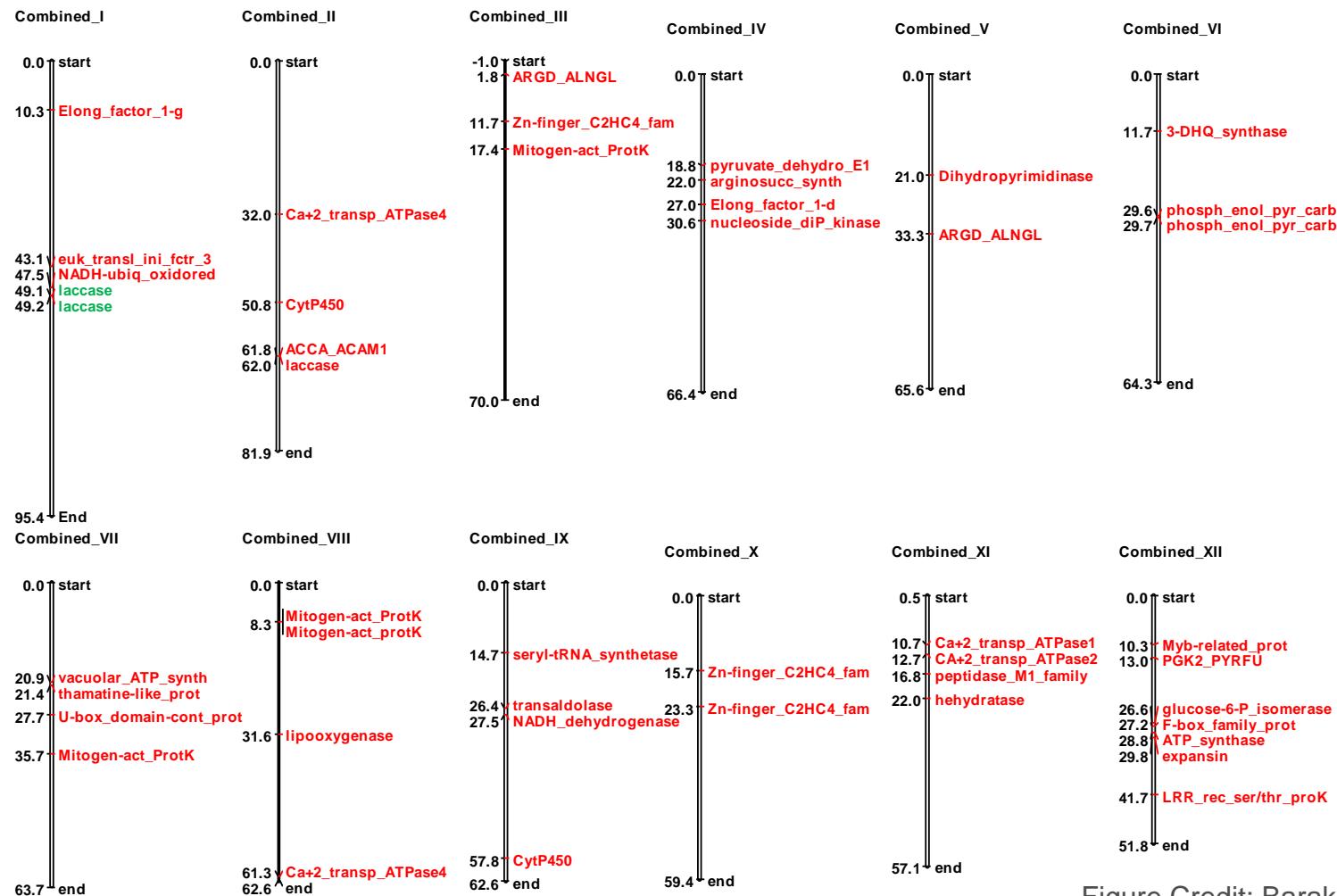


Figure Credit: Barakat et al. 2009

Sequenced “scaffolds” aligned with *Populus* linkage groups

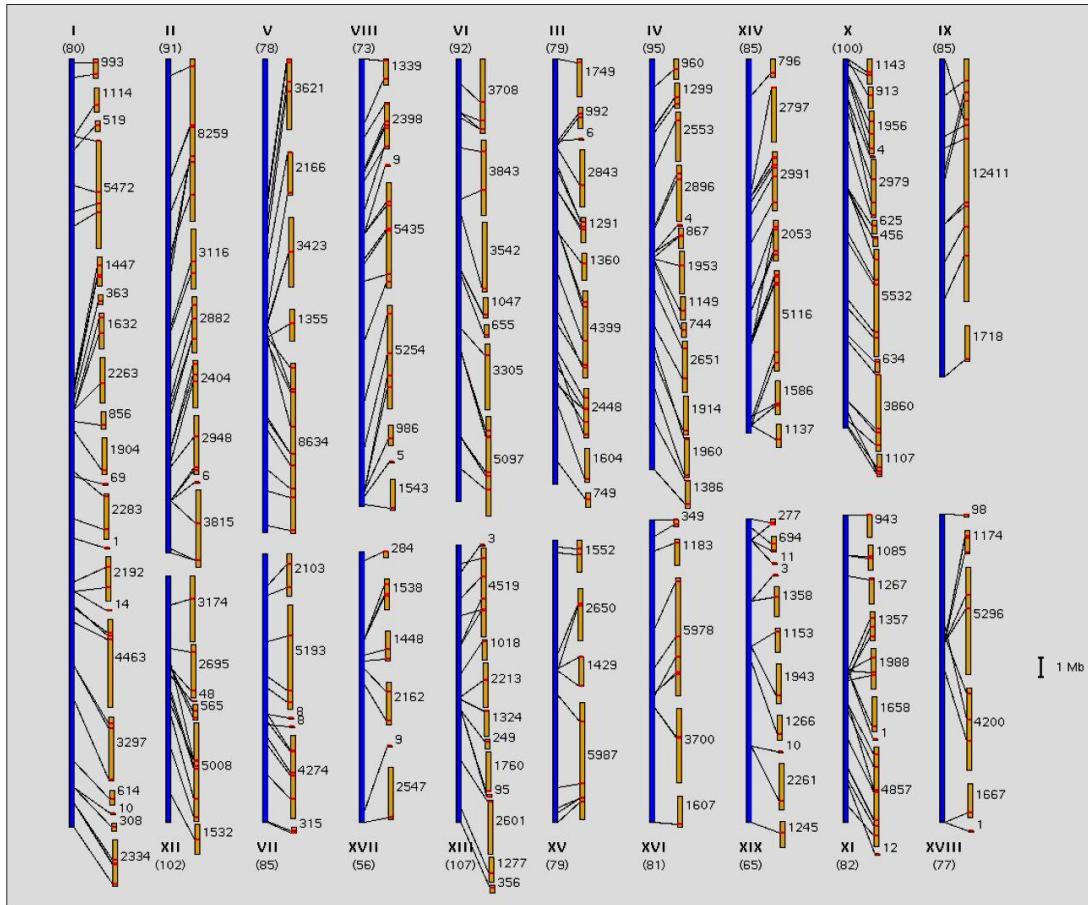


Figure Credit: From Tuskan et al., 2006. Science 313:1596-1604 Figure S3. Reprinted with permission from AAAS.

Duplicated segments in *Populus*

- This diagram reveals that *Populus* is an ancient polyploid whose genome has been extensively rearranged
- Colored bands show duplicated segments across chromosomes

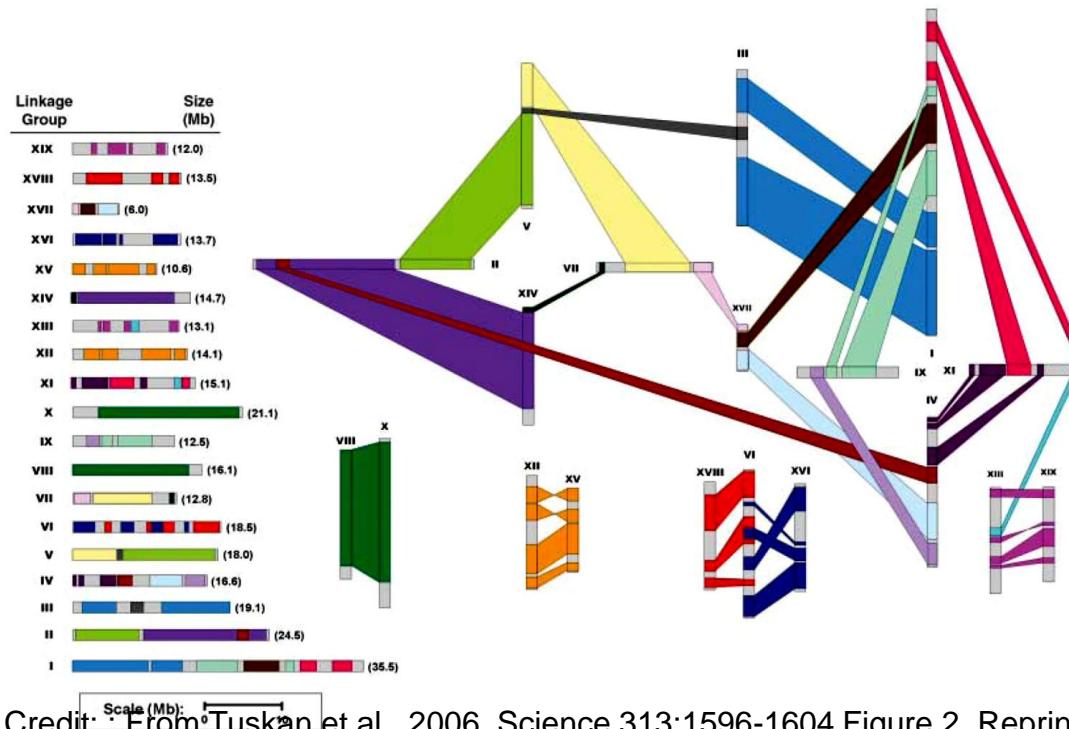
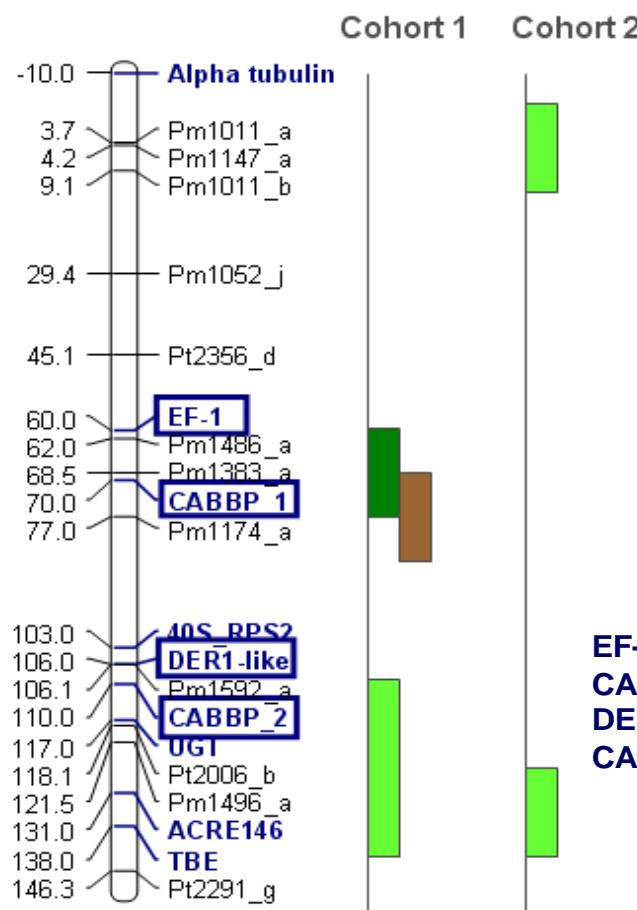


Figure Credit: From Tuskan et al., 2006. Science 313:1596-1604 Figure 2. Reprinted with permission from AAAS.

QTL for spring cold hardiness in Douglas-fir



Genetic markers mapped onto linkage group 1 reveal QTL (colored boxes) associated with cold hardiness traits

Genes mapped to these areas (positional candidate genes) are shown in blue boxes

- Spring cold hardiness (buds)
- Spring cold hardiness (stem)
- Spring cold hardiness (needles)

EF-1 (translation elongation factor-1); Cold induced
CABBP-1 (chlorophyll a/b-binding protein type 1); Regulated by water deficit
DER1-like (degradation of misfolded proteins); Possibly cold induced
CABBP-2 (chlorophyll a/b-binding protein type 2); Regulated by water deficit

Figure Credit: Modified from Wheeler et al., 2005

Summary: Large-scale mapping

- Basic mapping steps are straightforward
- Specifics of mapping process can be much more involved
- Markers vary in information content
- Variation among parental chromosomes
- Combining information from different chromosomes
- Total map distance grows as marker density increases
- Map resolution depends on sample size

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Thank You.

Conifer Translational Genomics Network
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Agriculture

National Institute
of Food and
Agriculture

