Welcome to the Development of SNP-Based Tetraploid Maps for Potato Webinar

Presentation Available at:
http://www.extension.org/pages/63187

Today's Presenters: Dr. Dave Douches & Joe Coombs

Brought to you by: The Plant Breeding and Genomics Community of Practice

Host: Heather Merk

Sign up for PBG News: http://pbgworks.org

extension
more mind re

Please fill out the survey evaluation! (You will be contacted via email)

Watch past webinars and sign up for future webinars!

http://www.extension.org/pages/60426

Development of SNP-Based Tetraploid Maps for Potato

David Douches[1], Kim Felcher[1], Joseph Coombs[1], Dan Zarka[1], Allen Van Deynze[2], John Hamilton[1], Candice Hansey[1] , C. Robin Buell[1]

[1]Michigan State University, East Lansing, MI 48824
[2]University of California-Davis, CA 95616

MICHIGAN STATE UNIVERSITY

Objectives

- Visualizing SNPs in Genome Studio including Five Cluster Calling
- Filtering SNPs for tetraploid mapping populations
- Generating a map using TetraploidMap software
- Initiating QTL analysis
  - Single Marker ANOVAs
  - TetraploidMap

MICHIGAN STATE UNIVERSITY

Genetic maps in potato

- Several linkage maps have been constructed for potato
  - (Bonierbale et al. 1988; Gebhardt et al. 1991; Jacobs et al. 1995; van Os et al. 2006, Felcher et al. 2012 (accepted))
- Diploid potato populations are often used for linkage mapping
- Map size ranges from 606 cM to 1120 cM
- Genetic markers per map range from 85 to 10,000 markers
- Markers used include isozymes, RFLPs, SSRs, AFLPs and more recently SNPs

SolCAP Genome-wide set of SNP markers: potato activities

- Assess concordance between map location of SNPs and the potato genome sequence location (based on pseudomolecules).
  - Felcher et al. 2012 (PLoS ONE, accepted)
- Use the Infinium 8303 potato array to genotype tetraploid mapping populations and generate SNP-based genetic maps
- QTL Analysis of tetraploid populations
- Association analysis of potato diversity panel

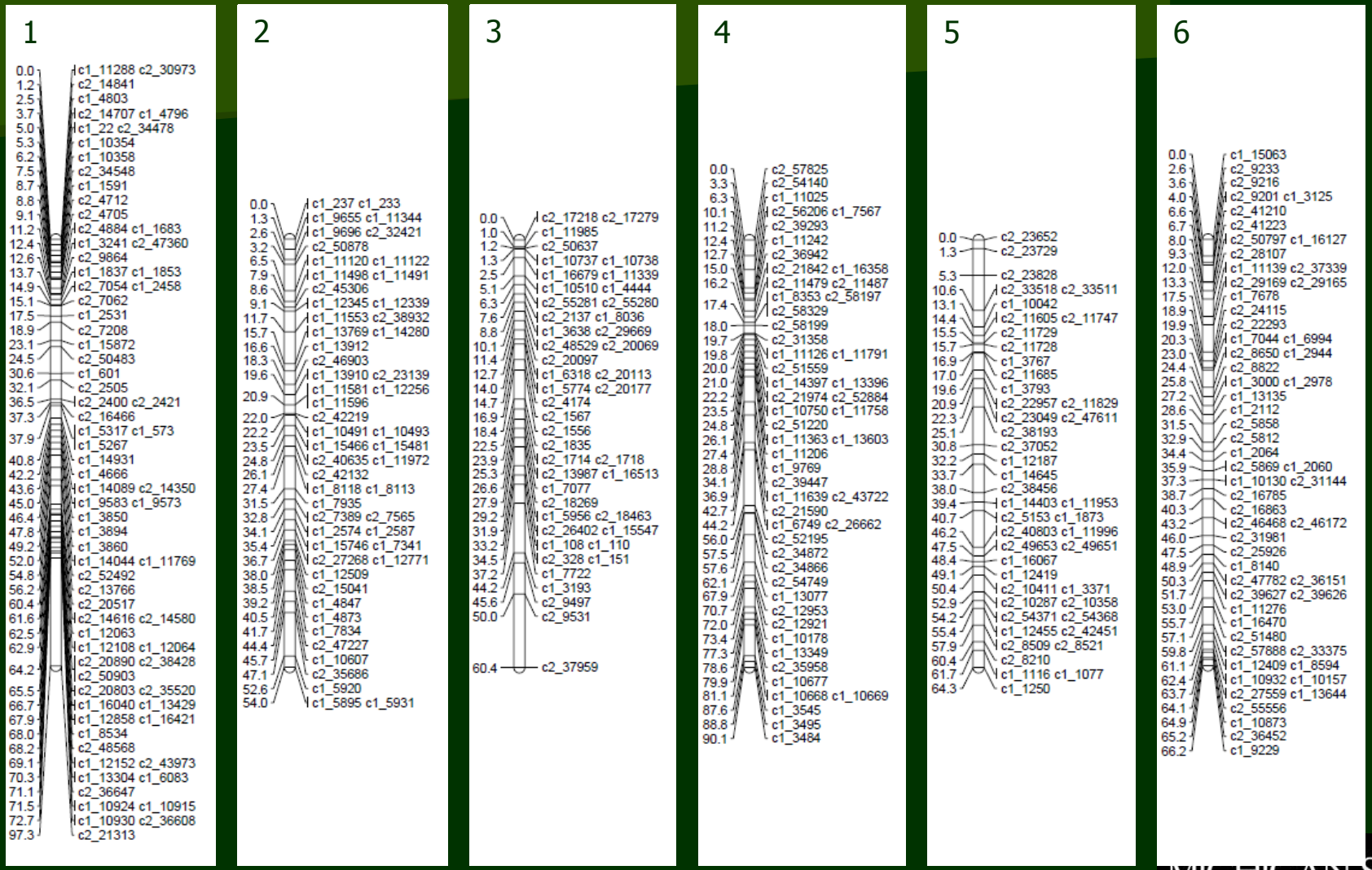
MICHIGAN STATE UNIVERSITY

Integration of Two Diploid Potato Linkage Maps with the Potato Genome Sequence

- DRH (92 progeny)
  - DM x RH (from Virginia Tech) was selected for mapping because the RH parent has been used extensively in potato mapping studies and genome sequencing.
- D84 (92 progeny)
  - DM x 84SD22 (from MSU) was selected for mapping because 84SD22 was shown to have a higher percentage of polymorphic SNPs.

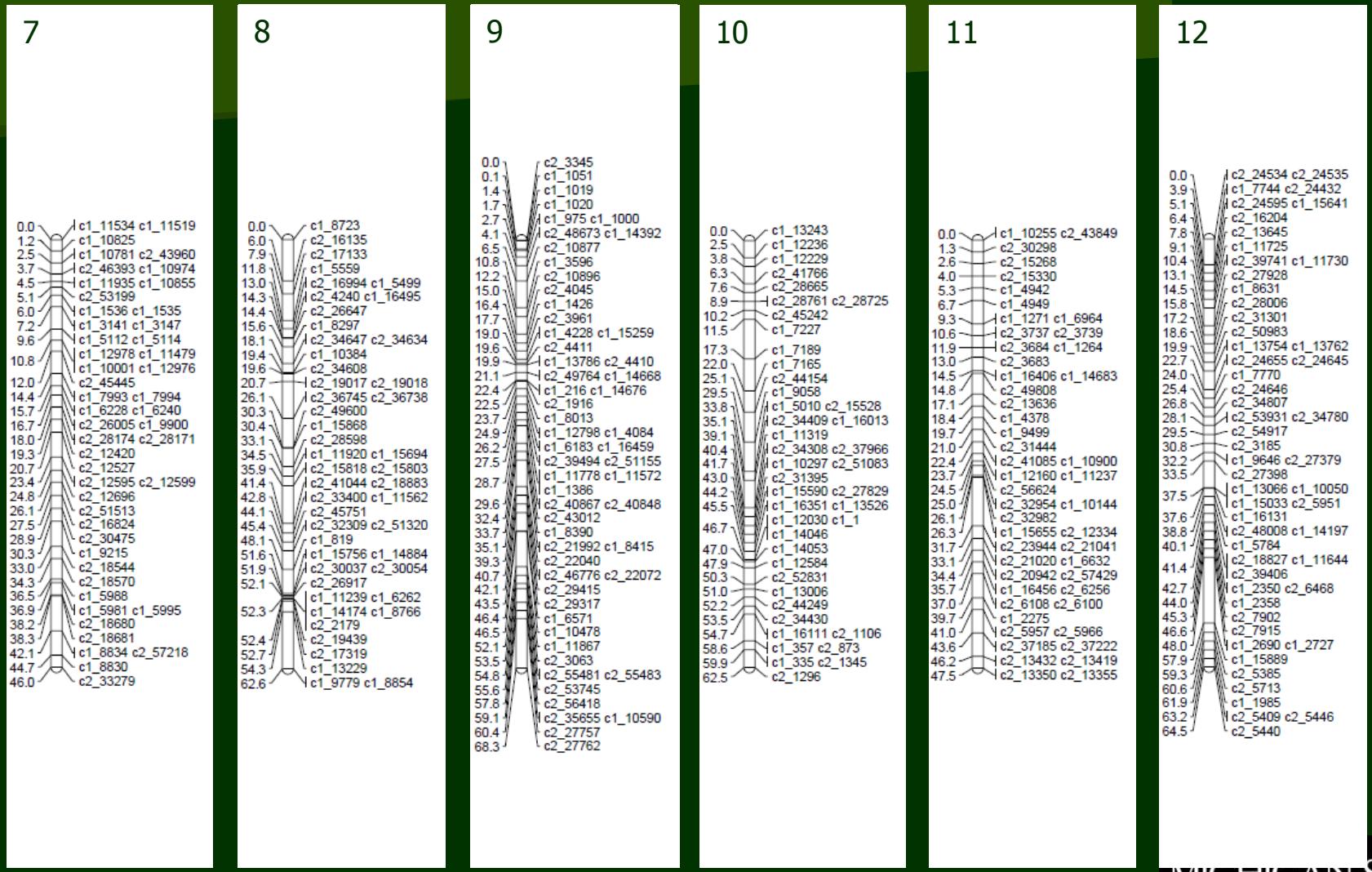
MICHIGAN STATE UNIVERSITY

D84 Chromosomes 1-6



MICHIGAN STATE UNIVERSITY

D84 Chromosomes 7-12



MICHIGAN STATE UNIVERSITY

Comparison of SNPs in the 2x populations DRH and D84

	Number of SNPs						Length			
	Includes Co-segregating SNPs			Mapped Segregating SNPs			(cM)		(Mb)	
Chromosome	DRH	D84	Common	DRH	D84	Common	DRH	D84	DRH	D84
1	268	279	114	121	76	14	125	98	81	81
2	208	270	103	97	55	17	79	53	46	46
3	88	239	26	64	46	6	78	61	48	48
4	230	186	74	105	53	12	89	91	64	64
5	144	158	52	55	46	9	100	65	47	47
6	213	216	110	90	59	19	66	65	52	55
7	146	245	52	66	49	5	70	47	53	53
8	147	183	57	74	48	11	71	67	43	43
9	164	195	62	89	57	8	100	69	53	53
10	115	131	51	66	43	14	82	63	52	52
11	131	171	45	74	50	8	76	48	42	42
12	106	181	41	43	55	4	31	65	54	59
Total	1960	2454	787	944	637	127	965	792	634	642

Total mapped SNPs: 3627

MICHIGAN STATE UNIVERSITY

Tetraploid Map
Materials and Methods

- PRRG – 184 Progeny
  - Premier Russet (PR) X Rio Grande Russet (RG)
  - USDA/ARS –ID (Rich Novy)
- Phenotypic data
  - 21 Traits
  - 3 locations (ID Novy, NC Yencho, MN Thill)
  - 2 years (2010, 2011)

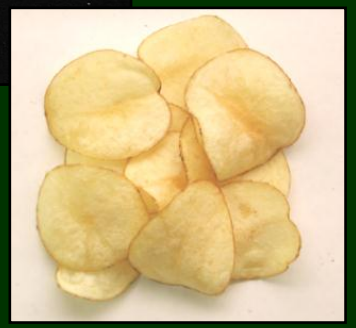
MICHIGAN STATE UNIVERSITY

Traits being evaluated within SolCAP
10 plant plots, two replicates

- specific gravity
- chip color after cold storage
- sucrose/glucose

"The key three"

- skin texture
- tuber shape (l/w/h)
- eye depth
- skin color, flower color
- flesh color
- vine maturity (95, 120 dap)
- growth habit (prostrate, erect, etc.)
- total yield
- heat sprouts
- internal defects



MICHIGAN STATE UNIVERSITY

SolCAP Germplasm & Populations

- Panel (325 clones)
  - Top 50 North American varieties
  - Historical varieties
  - Advanced breeding clones
    - from every US and Canadian program
  - Non-American germplasm
  - Genetic stocks
  - 10 Wild species
- Panel Analyses
  - Association mapping
  - Parental selection
  - Resolve population structure
- Russet Mapping population
  - PR x RG (184 progeny)
  - QTL analysis
- Diploid Mapping populations
  - DM x RH
  - DM x 84SD22

Other US Potato Mapping populations SNP genotyped

- Atlantic x Superior
  - (tuber calcium, reducing sugars, internal defects, specific gravity (starch))
- B1829-5 x Atlantic
  - (chip color, internal heat necrosis, specific gravity, maturity)
- Tundra x Kalkaska
  - (scab R, chip color, reducing sugars, specific gravity, asparagine, acrylamide)
- Jacqueline Lee x MSG227-2
  - (specific gravity, late blight resistance, vine maturity)
- Waneta x Pike
  - (specific gravity, chip color, disease resistance)
- W4 x 524-8 (diploid)
  - (specific gravity, chip color, disease resistance)

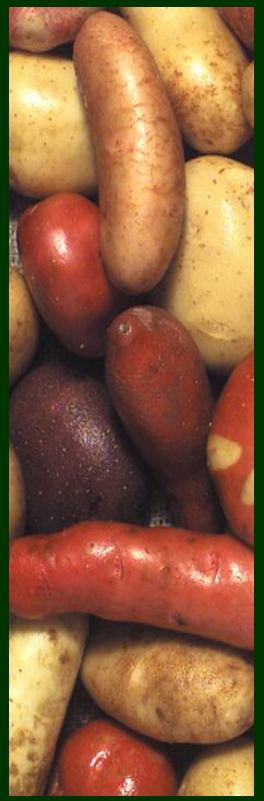
MICHIGAN STATE UNIVERSITY

Potato RNA-Seq for SNP Development

- We sequenced the transcriptomes of three varieties using Illumina RNA-Seq.
  - Snowden (Chipping)
  - Atlantic (Chipping)
  - Premier Russet (Processing-FF)

  } Tuber, Leaf, Flower, Callus

- 2 lanes of 61 bp paired end reads for each variety.
- Total Purity Filtered Sequence:
  - Atlantic: 30,185,186 reads (1.84 Gb)
  - Premier: 31,949,096 reads (1.94 Gb)
  - Snowden: 33,288,120 reads (2.03 Gb)
- ~50-60x coverage of the transcriptome



MICHIGAN STATE UNIVERSITY

Potato Illumina Infinium Platform Design Summary

- 69,011 SNPs passed all filtering steps
- Further filtering was performed to meet the design criteria for the Infinium platform using the following criteria:
  - Biallelic based on all available sequence
  - Within exons (mapped > 95% to DM1-3 draft genome sequence)
    - 50 bp from exon/intron junction
  - Max 1 SNP within 100 bp window of candidate SNP
  - Passed Illumina Scoring
    - 69,011 SNPs passed all filtering steps
  - *All SNPs are on the potato genome browser*

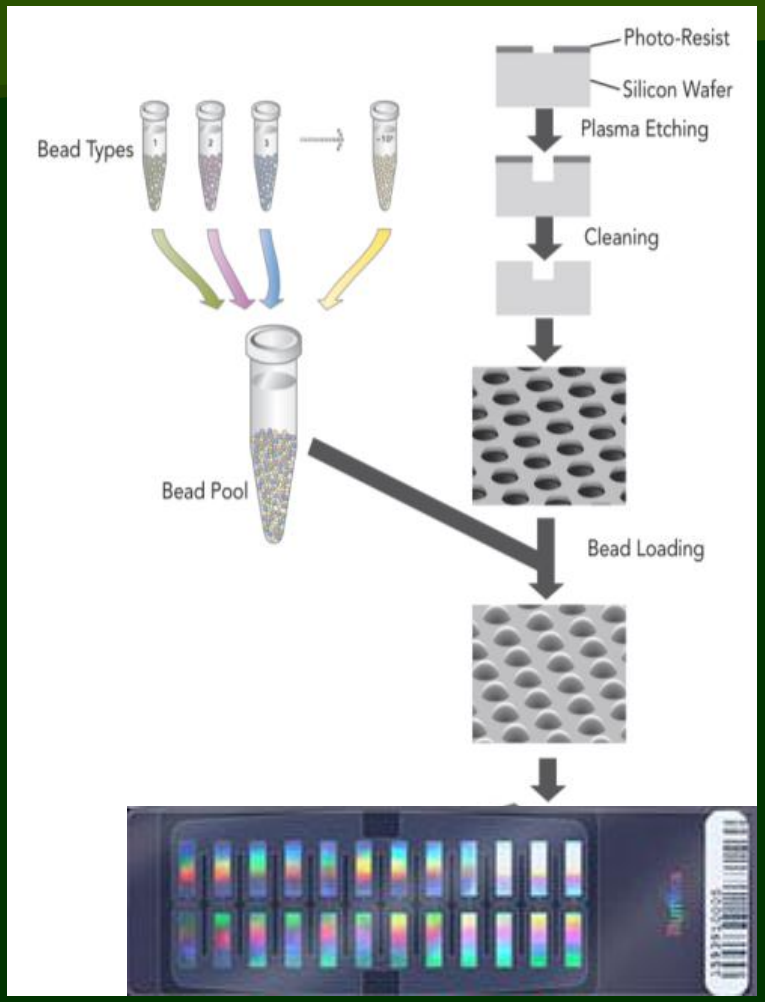
MICHIGAN STATE UNIVERSITY

Infinium 8303 Potato Array Design

- 8303 SNPs in total
  - 3018 SNPs from candidate genes
  - 536 SNPs from previously mapped genetic markers
  - 4749 dispersed SNPs selected to achieve maximum genome coverage

MICHIGAN STATE UNIVERSITY

Infinium 8303 Potato Array
(Single Base Extension)

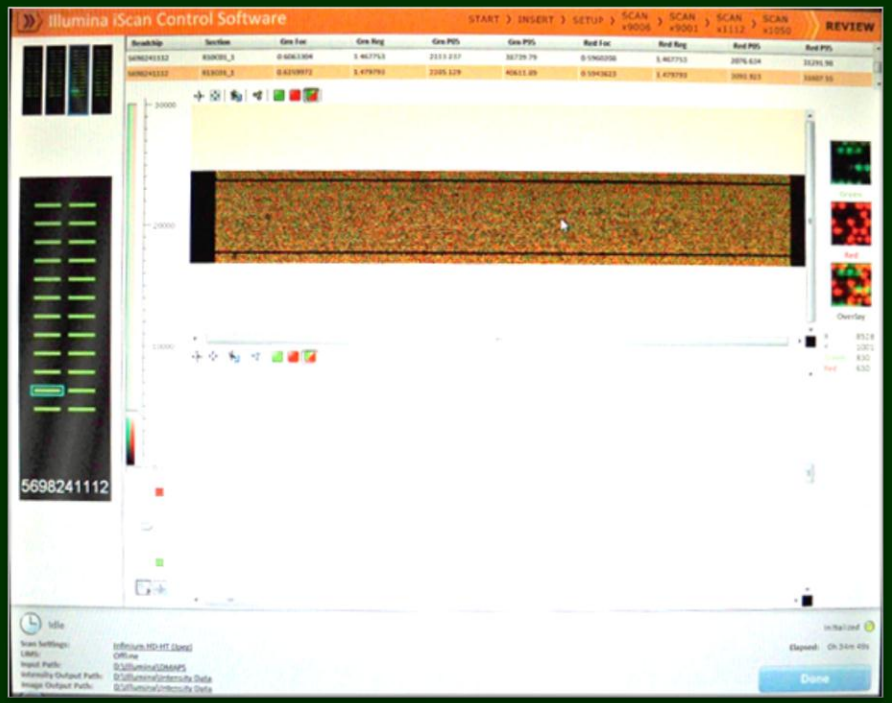


- Unique oligo for each bead type
- Bead Pool is 250,000 per sample
- Random self-assembly of beads onto the chip
- Redundancy averages 15 to 30 beads of each type
- 8,303 SNPs on Illumina Infinium chip
- 24 samples per chip

MICHIGAN STATE UNIVERSITY

Illumina iScan

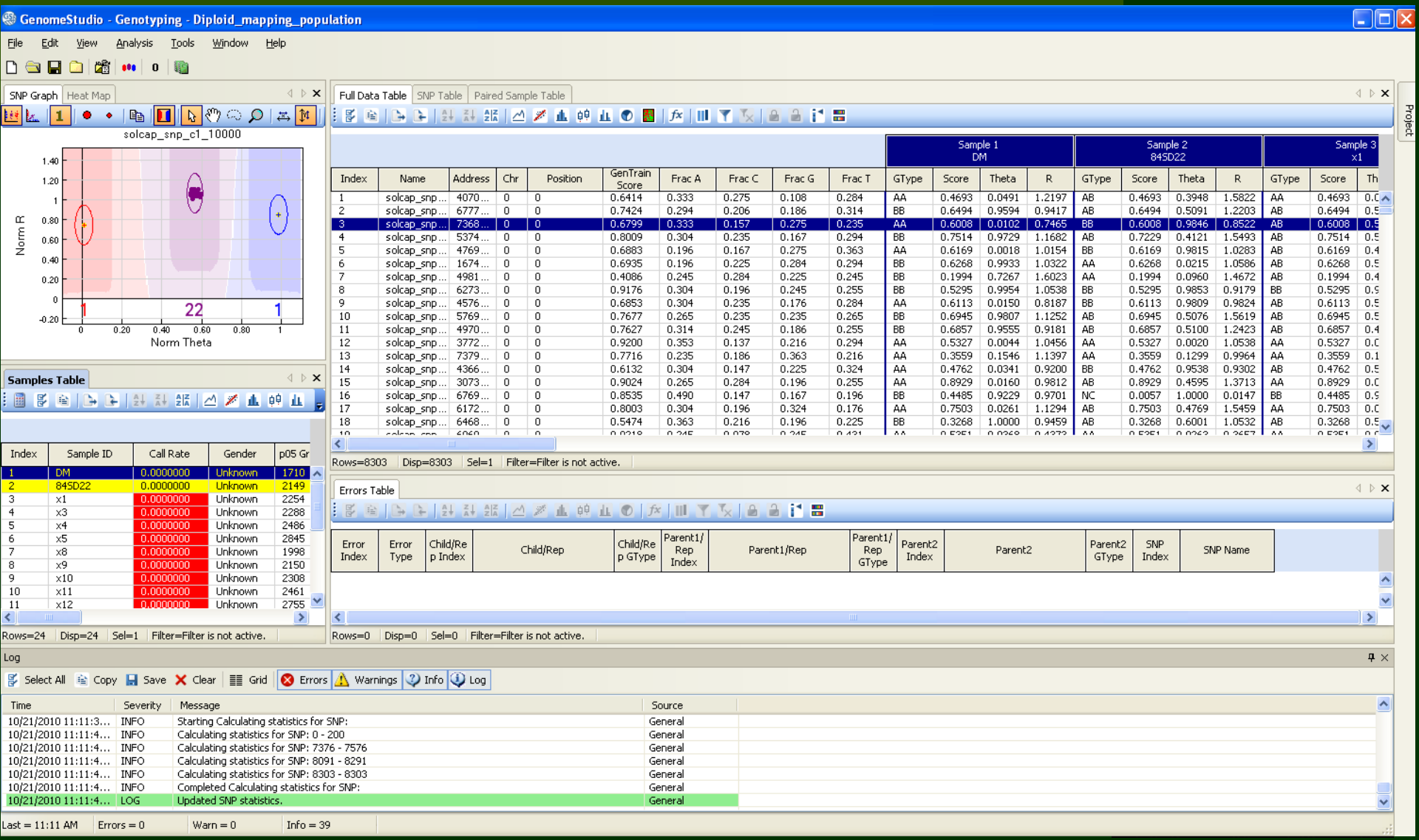
- The bead chips are loaded into the Illumina iScan.



- The iScan uses a laser to excite the red or green fluorophore of the single base extension product on the beads.
- The scanner records high-resolution images of the light emitted from the fluorophores.
- Data analyzed in Genome Studio software

MICHIGAN STATE UNIVERSITY

Illumina Genome Studio Software



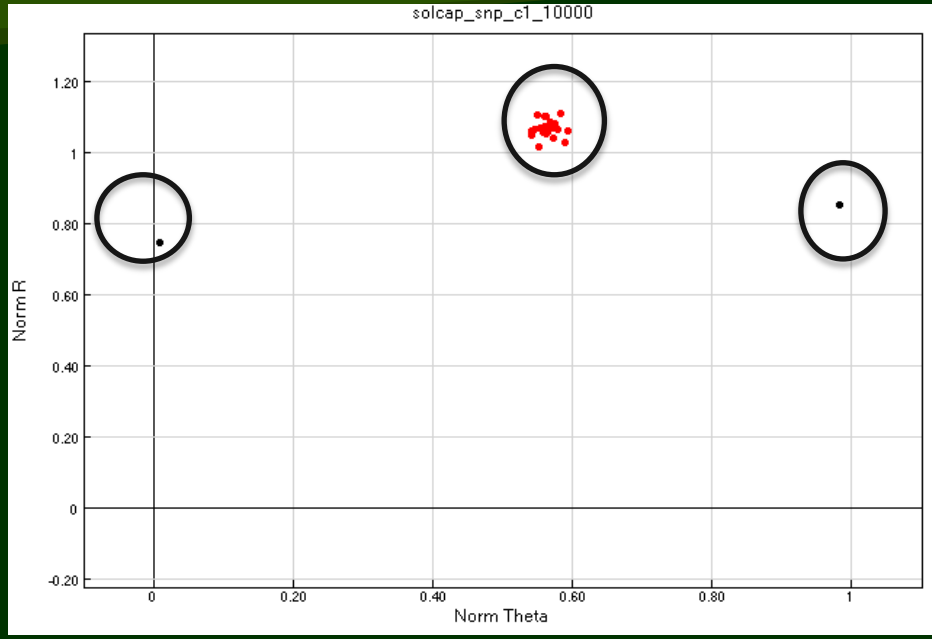
http://www.illumina.com/software/genomestudio_software.ilmn

Calling SNPs with Infinium 8303 Potato Array

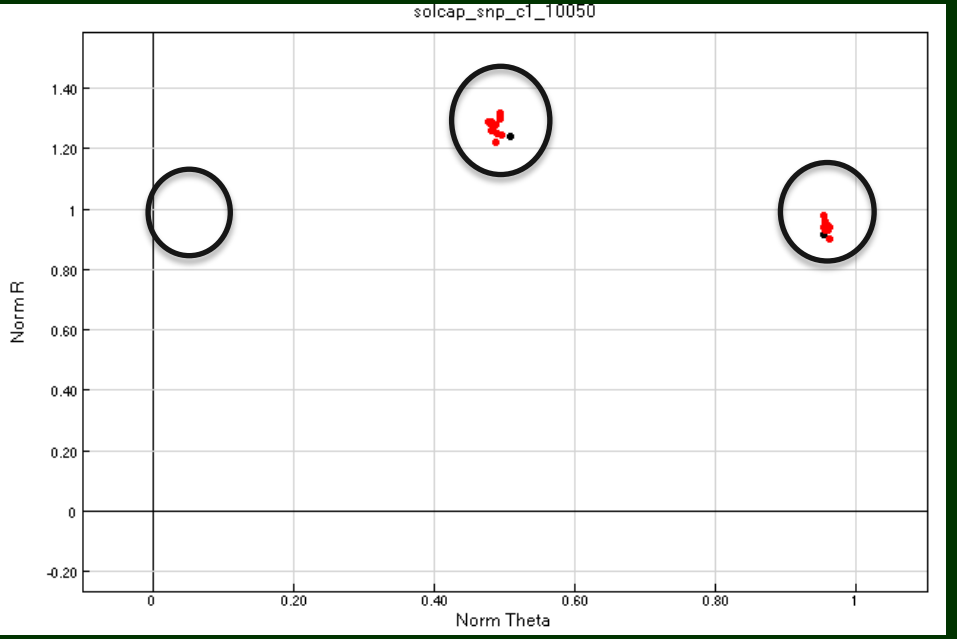
- SolCAP Custom potato calling file
  - Based on potato diversity panel, two 4x populations and one 2x population
  - http://solcap.msu.edu
- 3 Cluster Calling
  - Good - 7412 (89.3%)
  - Questionable - 296 (3.6%)
  - Segregation - 254 (3.1%)
  - Bad - 341 (4.1%)
- Call Rate for only good markers (7412)
  - >90% 7036 (94.9%)
  - >80% 228 (3.1%)
  - >70% 93 (1.3%)
  - <70% 55 (0.7%)

MICHIGAN STATE UNIVERSITY

Scoring Diploid Potato on Infinium Array



Black = Parents (AA x BB)
Red = Population (all AB)



Black = Parents (AB x BB)
Red = Population (1:1 AB:BB)

MICHIGAN STATE UNIVERSITY

Tetraploid SNP analysis

1:1

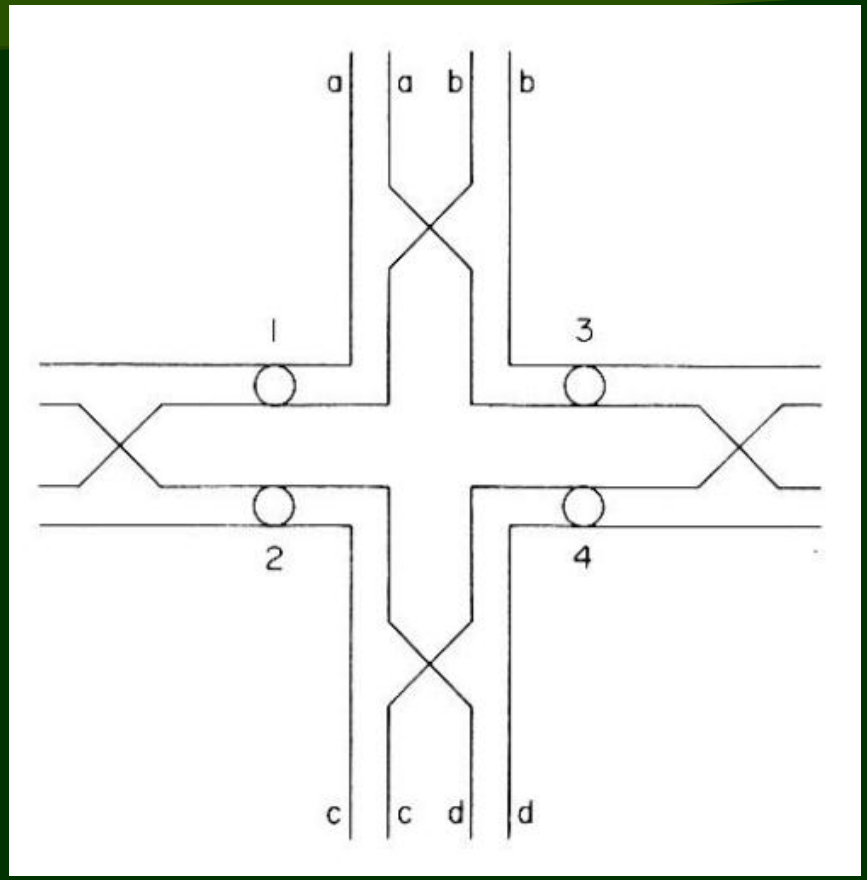
1:1

1:4:1

1:8:18:8:1

1:2:1

1:5:5:1



1:8:18:8:1

1:4:1

1:2:1

1:5:5:1

1:2:1

1:1

1:4:1

1:5:5:1

1:8:18:8:1

MICHIGAN STATE UNIVERSITY

Tetraploid Segregation

		F1 Progeny				
Parent1	Parent2	AAAA	AAAB	AABB	ABBB	BBBB
AAAA	AAAB	1	1			
AAAA	AABB	1	4	1		
AAAA	ABBB		1	1		
AAAB	AAAB	1	2	1		
AAAB	AABB	1	5	5	1	
AAAB	ABBB		1	2	1	
AAAB	BBBB			1	1	
AABB	AABB	1	8	18	8	1
AABB	ABBB		1	5	5	1
ABBB	ABBB			1	2	1
ABBB	BBBB				1	1
BBBB	AAAB			1	1	
BBBB	AABB			1	4	1
BBBB	ABBB				1	1

MICHIGAN STATE UNIVERSITY

Illumina Genome Studio Software

- Designed for use with diploid populations
  - Clusters are called as AA, AB, BB
- Potato is tetraploid with 5 marker classes
  - AAAA, AAAB, AABB, ABBB, BBBB
  - Nulliplex, Simplex, Duplex, Triplex, Quadriplex
- Codominant and dosage sensitive markers are ideal

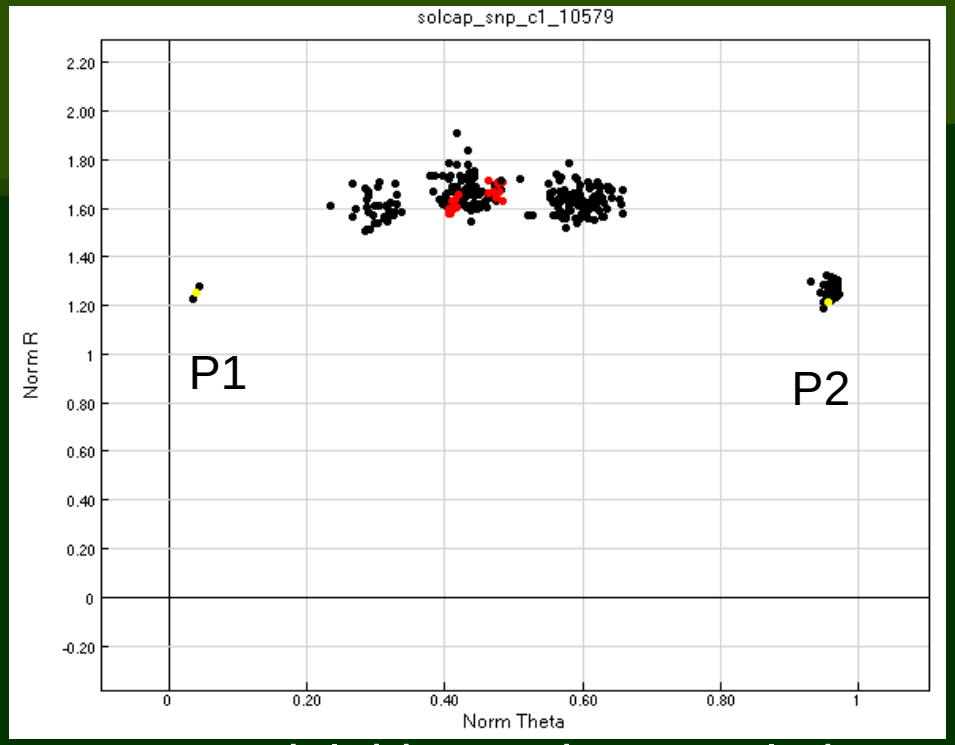
MICHIGAN STATE UNIVERSITY

Calling SNPs with 8303 Infinium Array

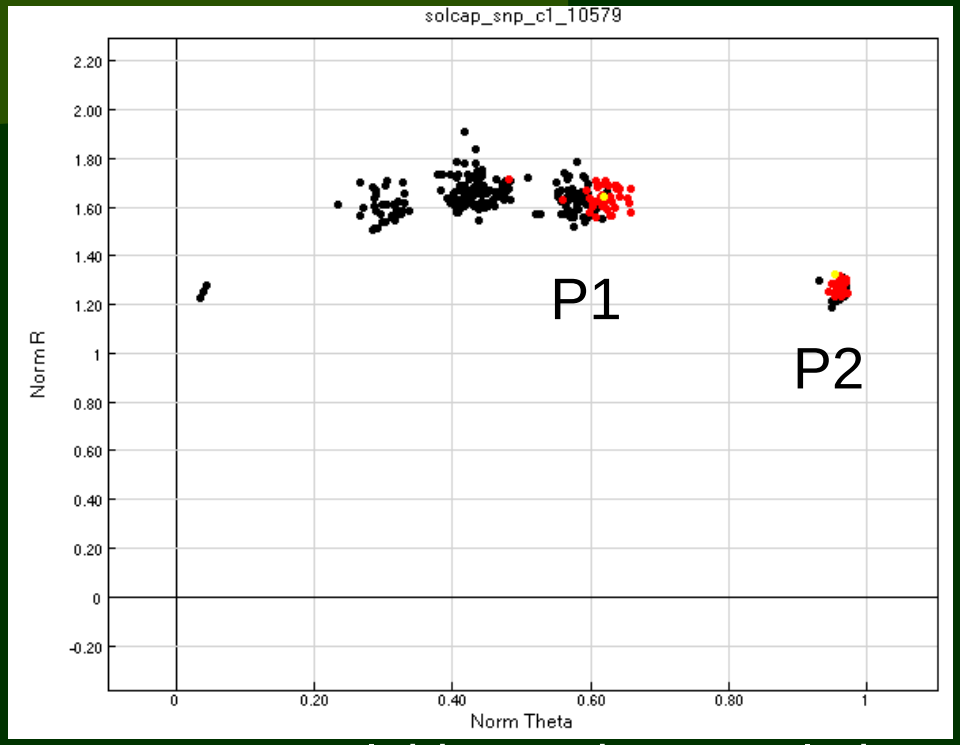
- 5 cluster custom calling using theta values
  - Based on potato diversity panel, two 4x populations and one 2x population (same as 3 cluster calling)
- Summary of SNPs categories:
  - Total: 5031
  - 5 clusters: 2645
  - 4 clusters: 858
  - 3 clusters: 945
  - 2 clusters: 583
  - 1 cluster or bad SNPs: 3272

MICHIGAN STATE UNIVERSITY

Ideal Marker



Diploid mapping population
Yellow Samples = Parents
Red Samples = Population

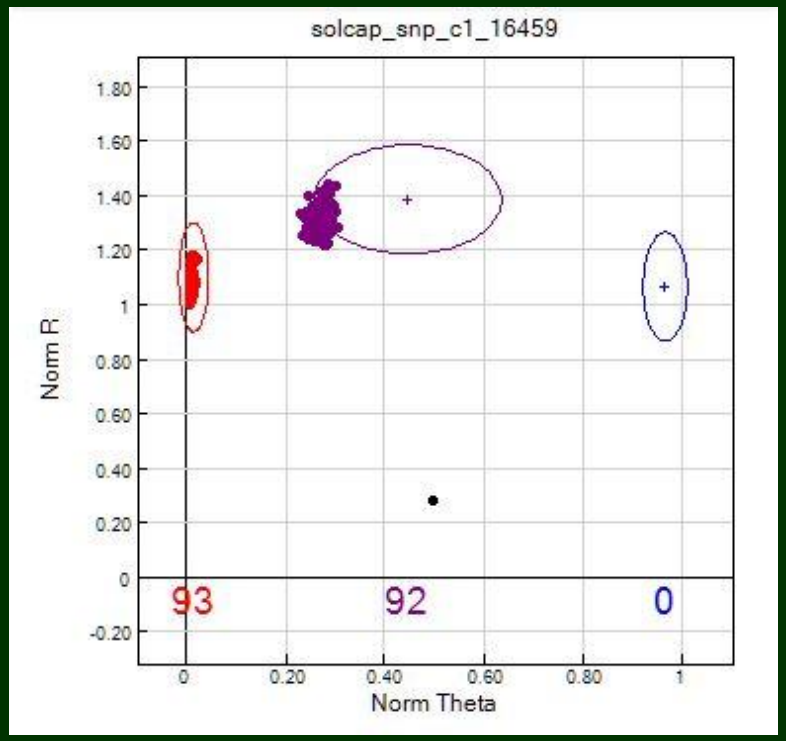


Tetraploid mapping population
Yellow Samples = Parents
Red Samples = Population

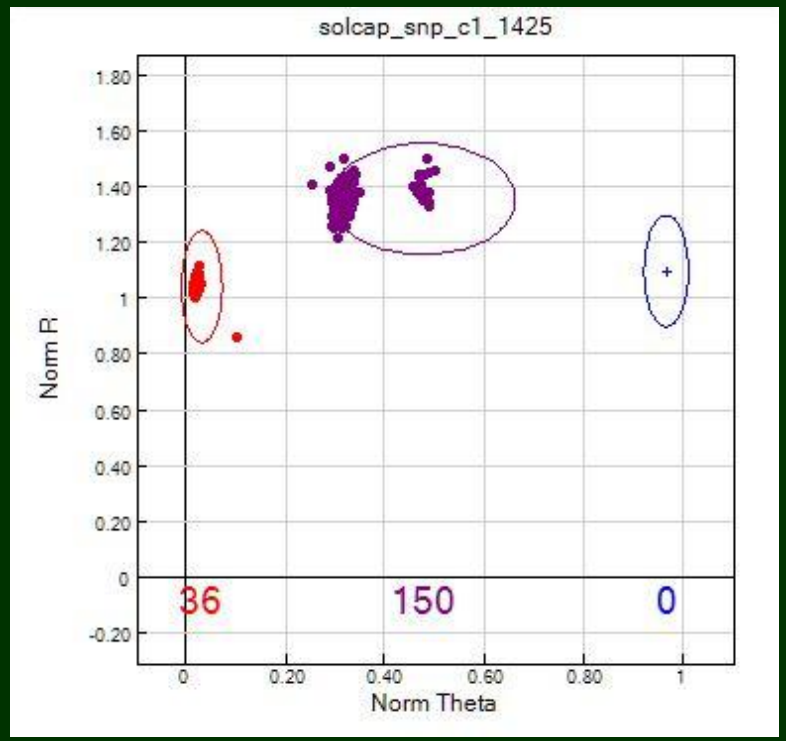
This marker is ideal of both 2x and 4x germplasm. The 2x AA cluster overlaps the 4x AAAA cluster, the 2x AB cluster overlaps the 4x AABB cluster, and the 2x BB cluster overlaps the 4x BBBB cluster.

Scoring Tetraploid Potato
Five cluster calling

		Progeny					
PR	RG	AAAA	AAAB	AABB	ABBB	BBBB	NC
AAAB	AAAA	93	93	0	0	0	0
Expected Ratio		1	1				



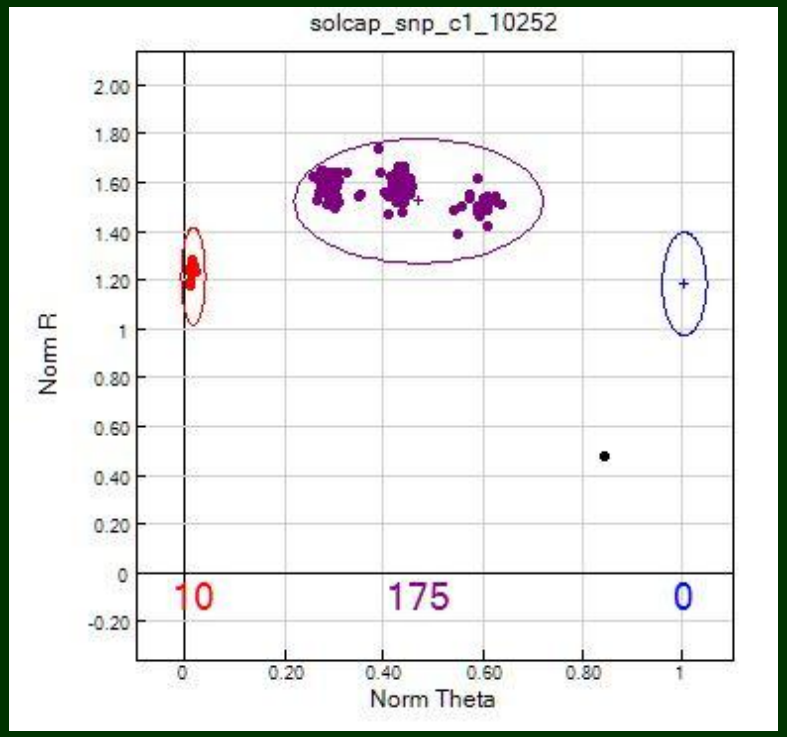
		Progeny					
PR	RG	AAAA	AAAB	AABB	ABBB	BBBB	NC
AAAA	AABB	37	127	23	0	0	0
Expected Ratio		1	4	1			



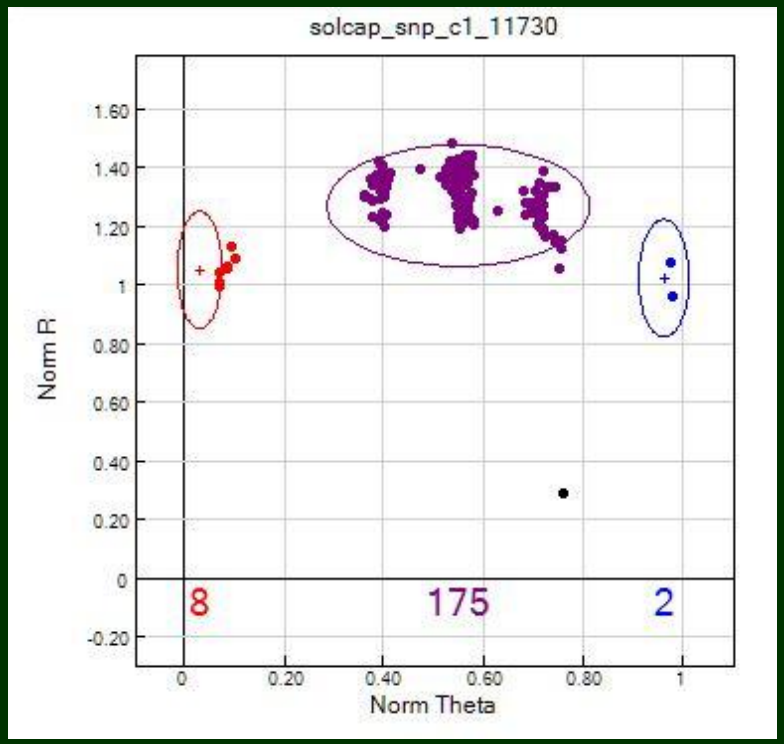
MICHIGAN STATE UNIVERSITY

Scoring Tetraploid Potato on Infinium Array

		Progeny					
PR	RG	AAAA	AAAB	AABB	ABBB	BBBB	NC
AABB	AAAB	10	78	73	20	0	6
Expected Ratio		1	5	5	1		



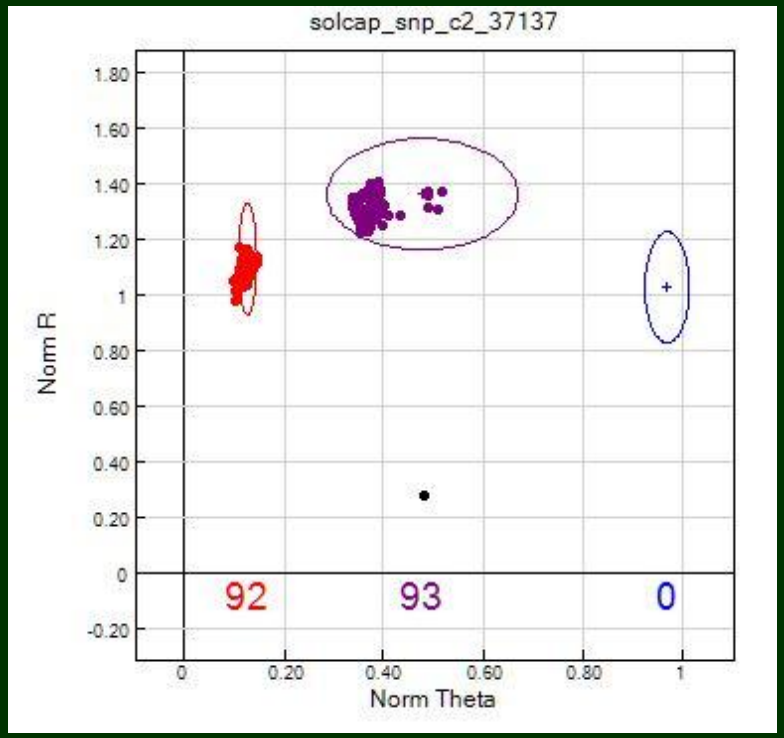
		Progeny					
PR	RG	AAAA	AAAB	AABB	ABBB	BBBB	NC
AABB	AABB	8	40	95	41	3	0
Expected Ratio		1	8	18	8	1	



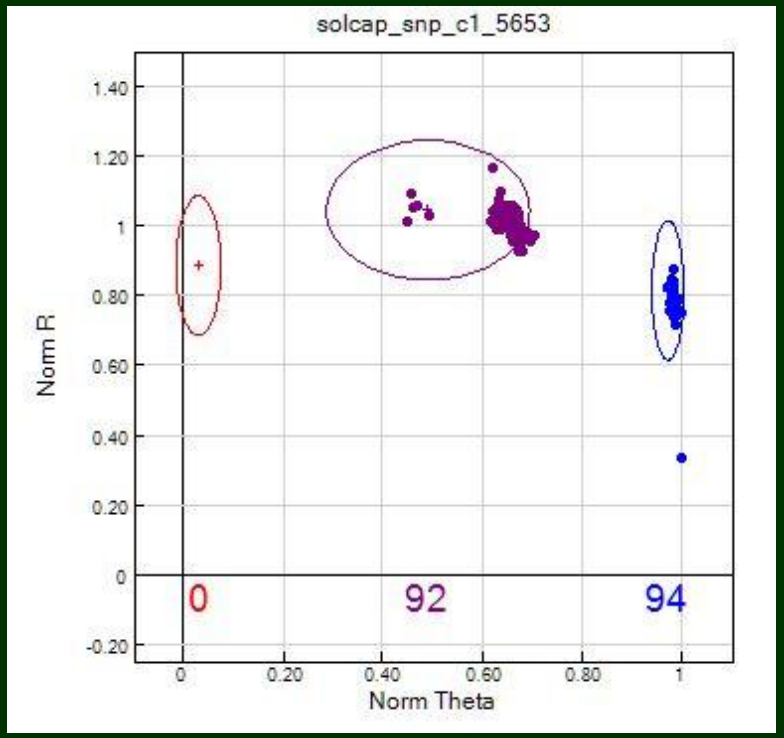
MICHIGAN STATE UNIVERSITY

Double Reduction Example
Tetraploid Potato on Infinium Array

		Progeny					
PR	RG	AAAA	AAAB	AABB	ABBB	BBBB	NC
AAAA	AAAB	92	86	6	0	0	3
Expected Ratio		1	1				



		Progeny					
PR	RG	AAAA	AAAB	AABB	ABBB	BBBB	NC
BBBB	ABBB	0	0	6	87	92	2
Expected Ratio					1	1	



MICHIGAN STATE UNIVERSITY

Double Reduction

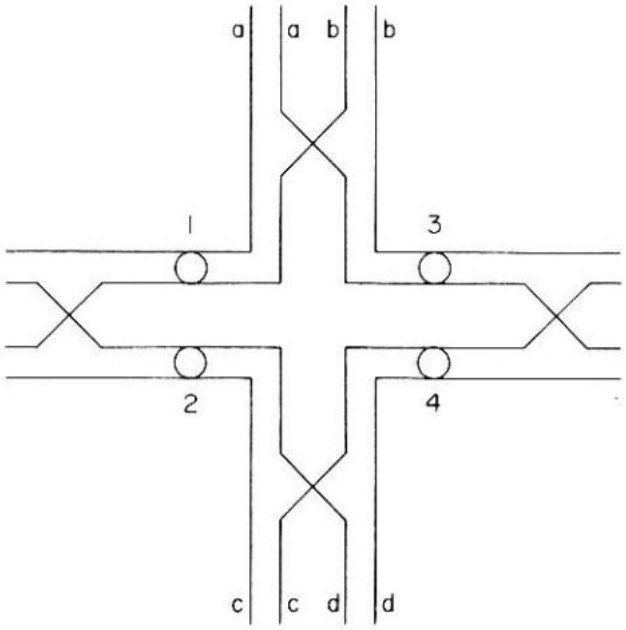


FIG. 52. Scheme for determining the theoretical maximum frequency of double reduction at a single locus in an autotetraploid. One of the three equally probable possible arrangements of the four alleles at one locus, designated a, b, c, and d, is shown together with crossovers between the locus and the centromeres, numbered 1 to 4. By assuming equal frequencies of alternate and two adjacent segregations of the centromeres, (1 + 4)/(2 + 3), (1 + 3)/(2 + 4), (1 + 2)/(3 + 4), respectively, for each of the three arrangements, the kinds of chromatids and their frequencies may be determined, as described in the text.

C.R. Burnham, Discussions in Cytogenetics, 1962

MICHIGAN STATE UNIVERSITY

Double Reduction in Tetraploids

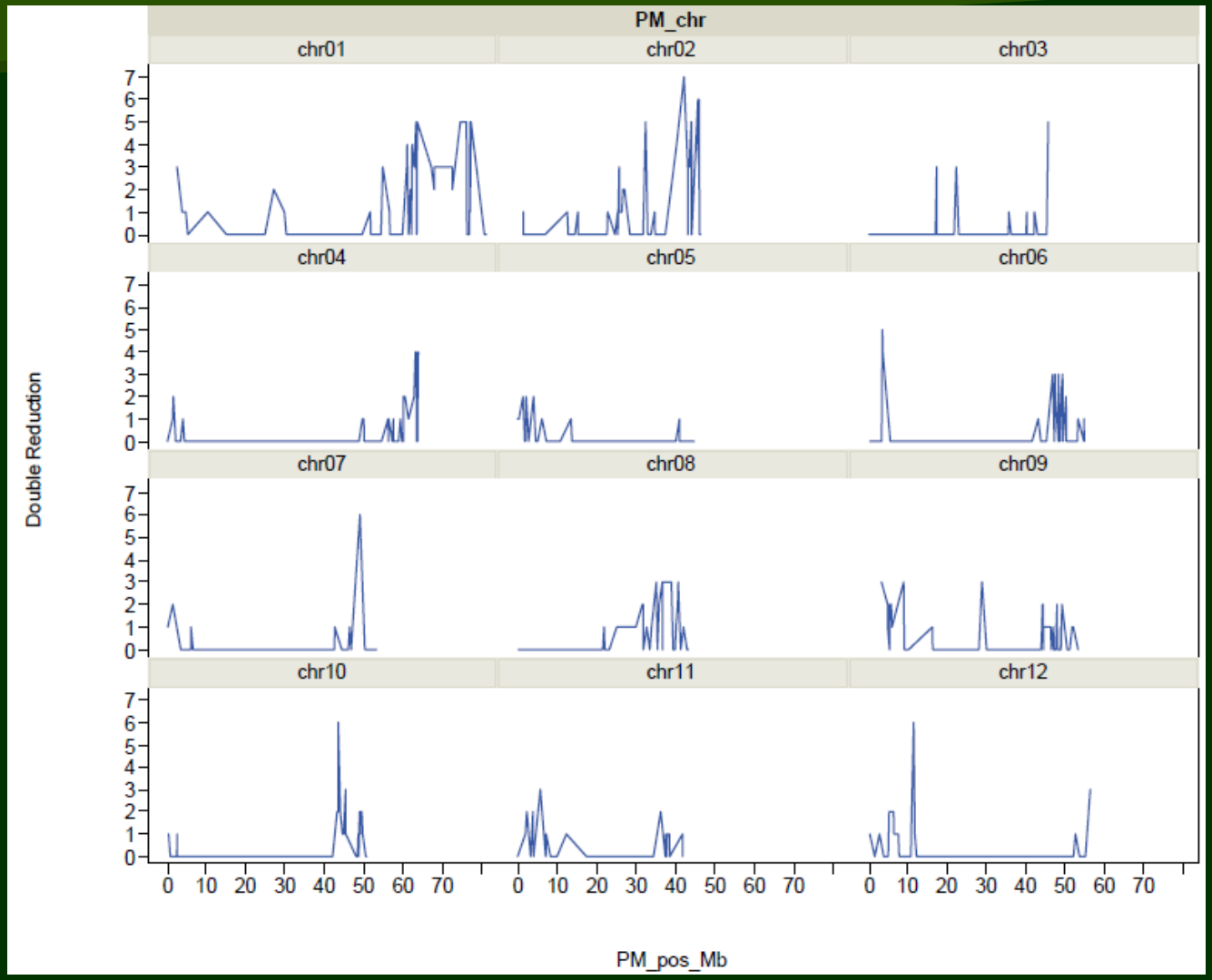
- Autotetraploids can undergo double reduction that results in (the segments of) two sister chromatids being recovered in a single gamete.
- For this to occur, multivalent pairing must take place with a cross-over between a locus and its centromere followed by the two pairs of chromatids passing to the same pole in anaphase I (adjacent segregation).

Distribution of Simplex SNPs with Double Reduction in PRRG

	No. of SNPs		
No. of DR	PR	RG	Total
0	373	168	541
1	47	68	115
2	19	37	56
3	32	14	46
4	7	13	20
5	7	8	15
6	2	4	6
7	0	1	1

MICHIGAN STATE UNIVERSITY

Double Reduction by Pseudomolecule Chromosome Position



MICHIGAN STATE UNIVERSITY

Tetraploid SNP Mapping Summary

PRRG	Remarks
No. of SNPs	
8303	Began with 8303 SNP from the Infinium SNP array
7666	Removed Questionable and Bad SNPs
7017	Removed SNPs unanchored to Pseudomolecule
6931	Removed SNPs mapped to >2 locations on PM
4604	Removed bad SNPs from custom 5 cluster calling
4212	Removed for 10% (19) or more No-calls in progeny
4168	Removed No-calls in Parents
3298	Removed homozygous by homozygous SNPs
3298	Segregating SNPs

MICHIGAN STATE UNIVERSITY

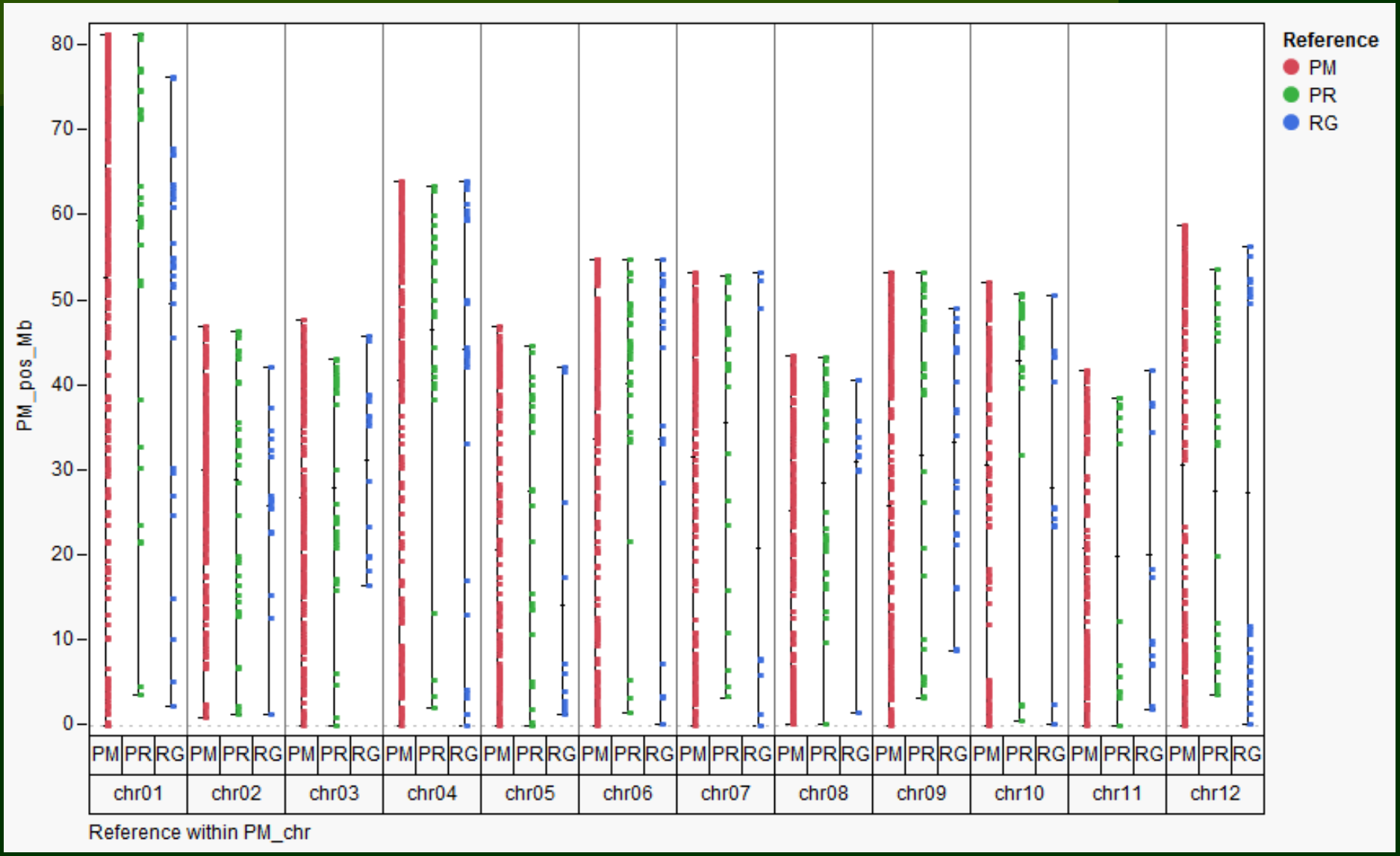
Tetraploid Segregation in PR x RG

		RG					
		AAAA	AAAB	AABB	ABBB	BBBB	NC
PR	AAAA	349	133	75	5	0	1
	AAAB	199	271	206	86	8	5
	AABB	88	295	329	285	126	7
	ABBB	11	79	232	306	288	1
	BBBB	0	14	82	180	521	9
	NC	2	2	7	6	2	2

Nulliplex X Simplex	800
Nulliplex X Duplex	371
Nulliplex X Triplex	38

MICHIGAN STATE UNIVERSITY

Distribution of 800 Simplex SNPs in PRRG by Chromosome



Distribution of 800 Simplex SNPs in PRRG by Chromosome

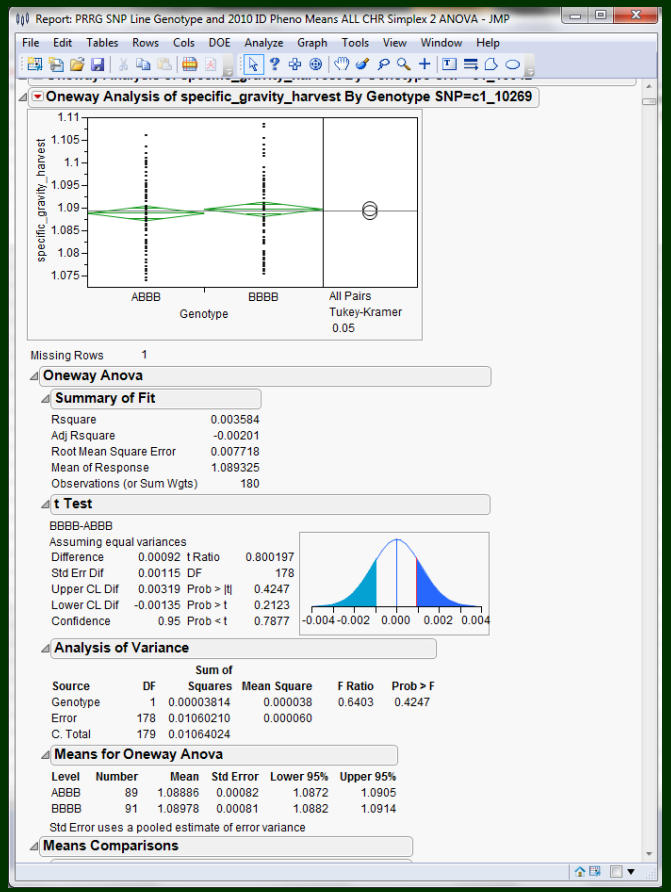
	PR (Mb position)				RG (Mb position)			
PM chr	N	Min	Max	Range	N	Min	Max	Range
chr01	46	3.8	81.3	77.6	33	2.5	76.3	73.9
chr02	56	1.5	46.4	45.0	20	1.5	42.3	40.8
chr03	48	0.0	43.2	43.1	24	16.6	45.8	29.2
chr04	43	2.1	63.5	61.4	50	0.0	64.2	64.1
chr05	33	0.1	44.8	44.7	14	1.4	42.3	40.9
chr06	47	1.6	54.9	53.2	31	0.3	54.9	54.6
chr07	36	3.4	53.0	49.6	15	0.1	53.3	53.2
chr08	46	0.3	43.3	43.1	12	1.7	40.8	39.1
chr09	39	3.2	53.3	50.1	43	8.9	49.2	40.3
chr10	43	0.7	50.9	50.2	19	0.3	50.7	50.4
chr11	17	0.1	38.6	38.6	21	2.0	41.9	39.9
chr12	33	3.8	53.7	49.9	31	0.2	56.4	56.2

MICHIGAN STATE UNIVERSITY

Single Marker ANOVA
Specific Gravity 2010 Idaho

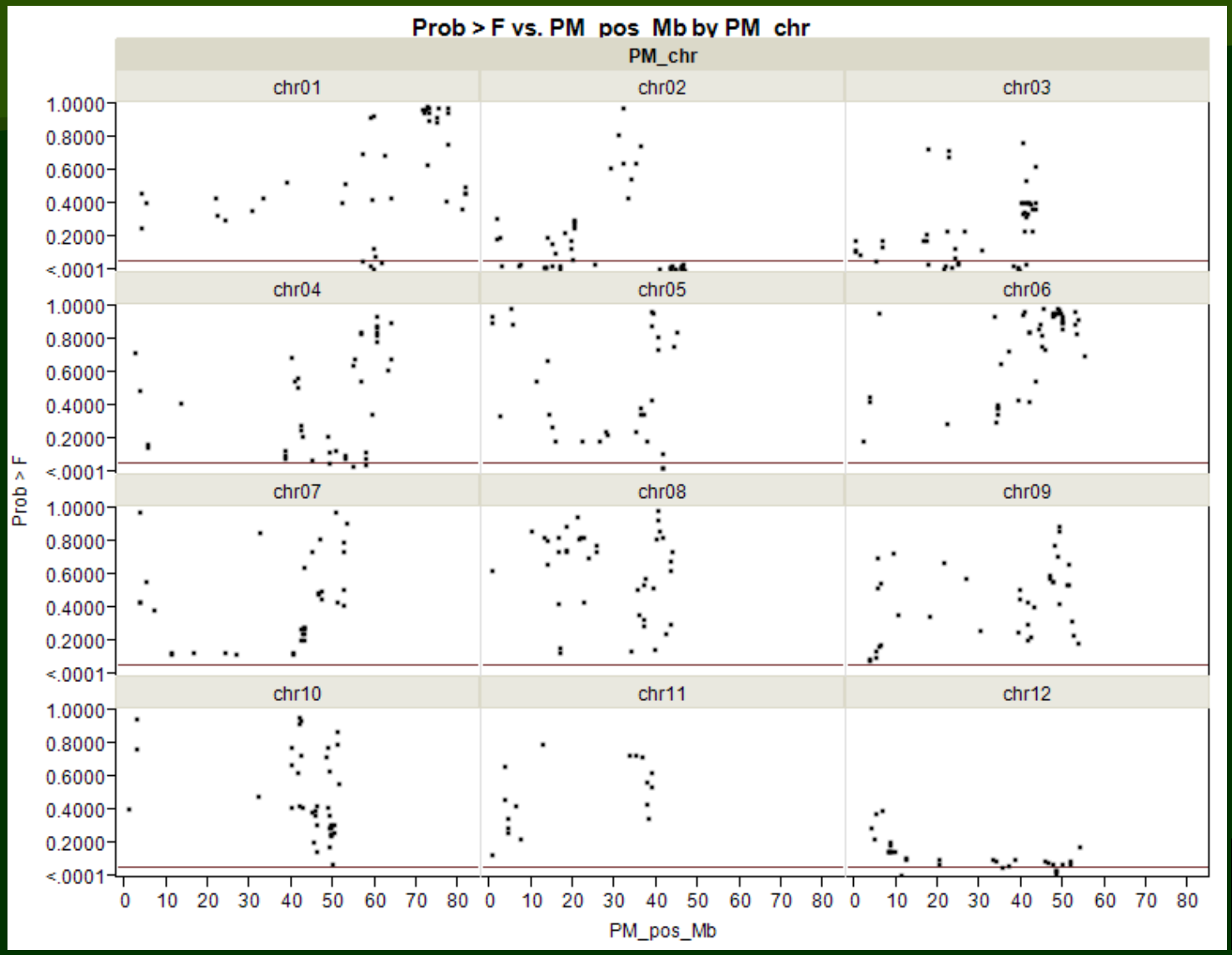
Parent	No. SNPs Total	No. SNPs P<0.05
PR	487	56
RG	313	77
Total:	800	133

- Multiple test corrections were too conservative
  - Bonferroni
  - Sidak-Dunnet



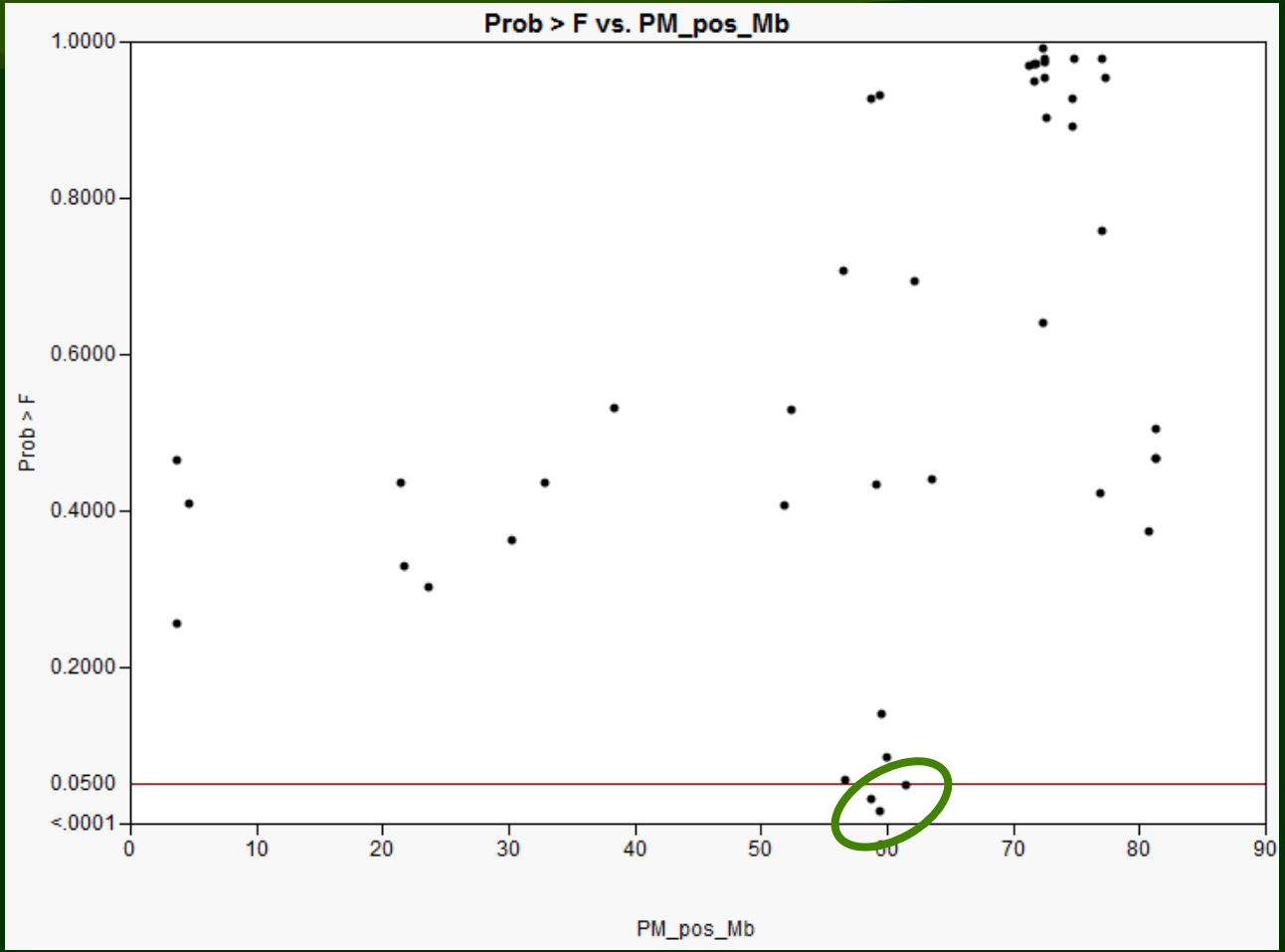
MICHIGAN STATE UNIVERSITY

P-values for single marker ANOVA for 2010 SG in PR



MICHIGAN STATE UNIVERSITY

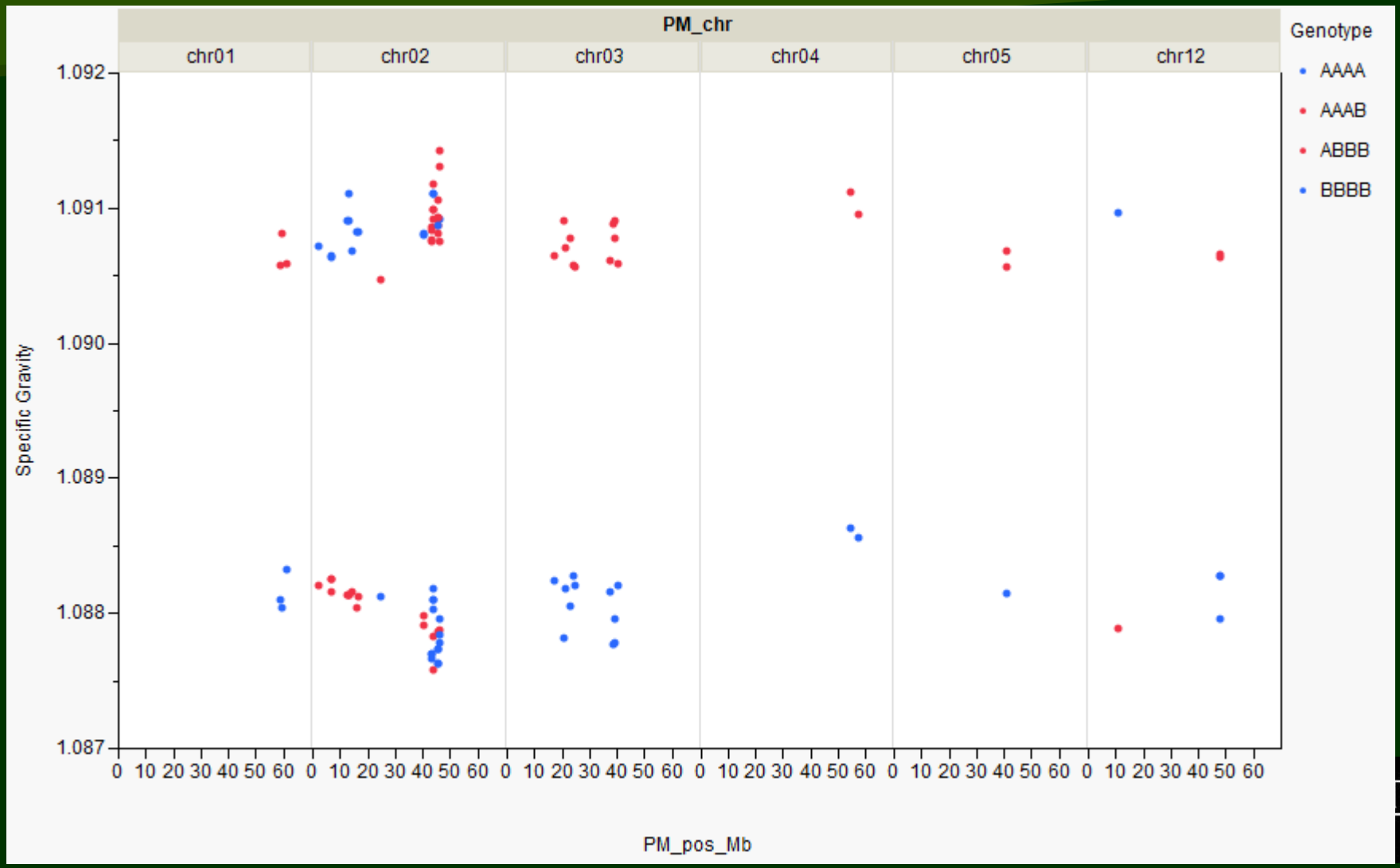
PR chr01 single marker ANOVA example



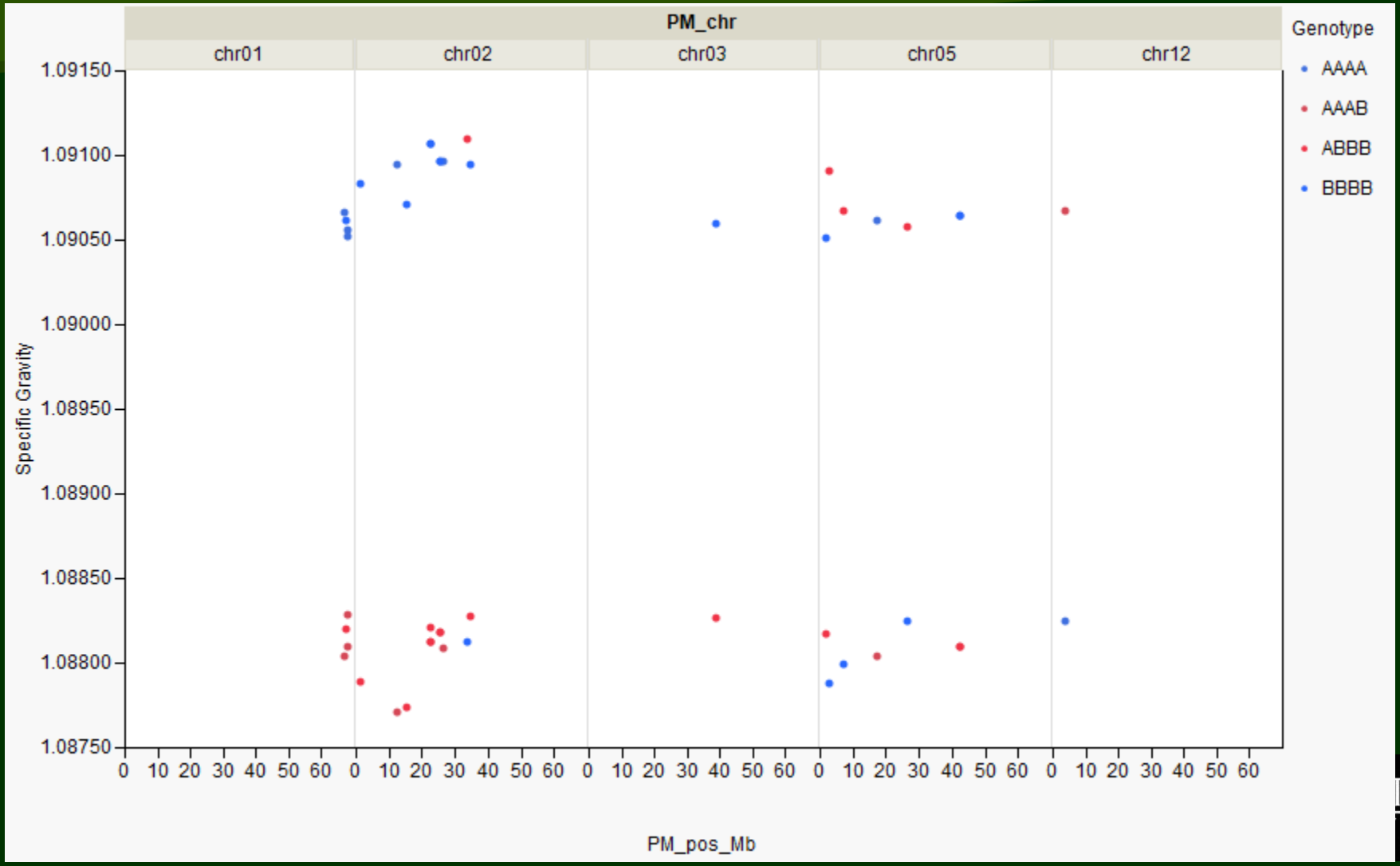
- 3 of 46 SNPs in chr01 were significant at α=0.05

MICHIGAN STATE UNIVERSITY

Simplex SNP genotype specific gravity means vs. PM chromosome position for Premier (P-value < 0.05)

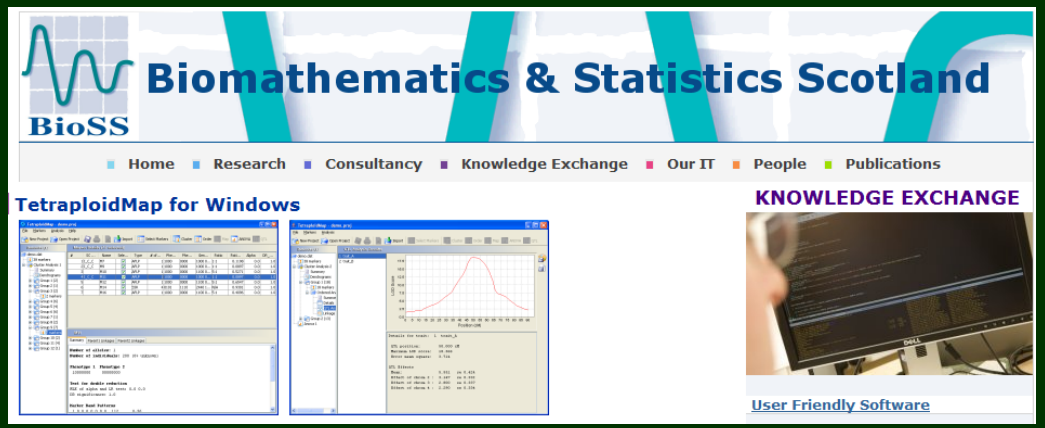


Simplex SNP genotype specific gravity means vs. PM chromosome position for Rio Grande (P-value < 0.05)



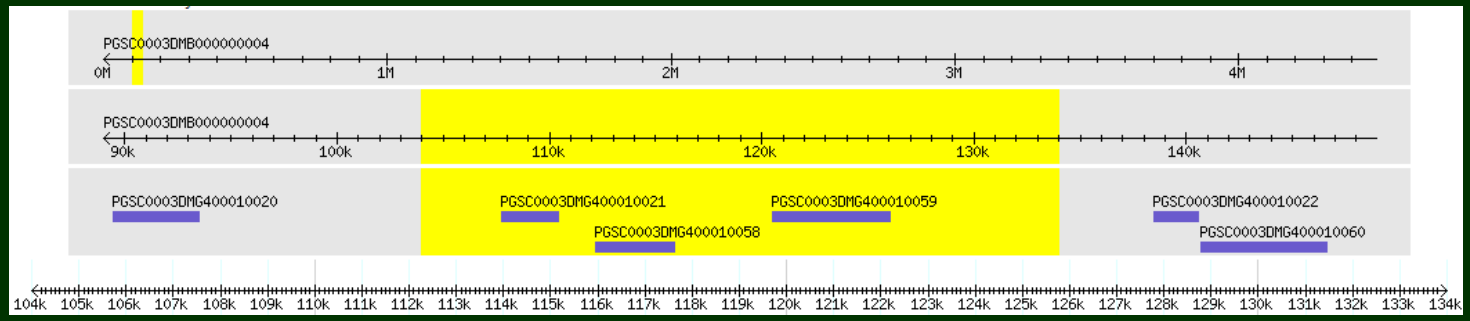
Tetraploid Map

- http://www.bioss.ac.uk/download/tpmap
- Windows XP
- Designed for AFLP and SSR markers
- Maximum of 800 markers per project
- Maximum of 50 markers per linkage group
- Not effective for markers with double reduction



Advantage of Sequenced Potato Genome

- Using only SNPs with known Pseudomolecule chromosome position
- Condordance evaluated in diploid population
- Physical map becomes a reference for comparison with the genetic map



MICHIGAN STATE UNIVERSITY

Recoding SNPs for TetraploidMap

	A	B	C	D	E	F	G	H	I	J	K
1	SNP	PM_chr	PM_pos	Premier R	Rio Grand	PRRG-001	PRRG-002	PRRG-003	PRRG-004	PRRG-005	PRRG-006
2	c2_51812	chr01	3761637	AAAB	AAAA	AAAB	AAAB	AAAA	AAAB	AAAB	AAAB
3	c2_45058	chr01	4714970	AAAB	AAAA	AAAB	AAAB	AAAA	AAAB	AAAB	AAAB
4	c2_56842	chr01	30337216	AAAB	AAAA	AAAA	AAAB	AAAB	AAAB	AAAB	AAAA
5	c1_3234	chr01	74837511	AAAB	AAAA	AAAB	AAAA	AAAA	AAAA	AAAB	AAAA
6	c2_4715	chr01	77129418	AAAB	AAAA	AAAA	AAAA	AAAB	AAAA	AAAA	AAAB
7	c2_22105	chr01	80786464	AAAB	AAAA	AAAB	AAAA	AAAB	.	AAAA	AAAB
8	c2_51810	chr01	3761845	ABBB	BBBB	ABBB	ABBB	BBBB	ABBB	ABBB	ABBB
9	c2_55618	chr01	21514658	ABBB	BBBB	BBBB	ABBB	ABBB	ABBB	ABBB	BBBB
10	c1_5477	chr01	23644208	ABBB	BBBB	BBBB	ABBB	ABBB	ABBB	ABBB	BBBB
11	c2_4665	chr01	76973071	ABBB	BBBB	BBBB	BBBB	ABBB	BBBB	BBBB	ABBB
12	c2_36495	chr01	77367370	ABBB	BBBB	ABBB	ABBB	BBBB	BBBB	ABBB	BBBB
13	c2_30955	chr01	81285208	ABBB	BBBB	ABBB	BBBB	ABBB	.	BBBB	ABBB
14											
15	SNP	PM_chr	PM_pos	PR	RG	PRRG-001	PRRG-002	PRRG-003	RRG-004	PRRG-005	PRRG-006
16	c2_51812	chr01	3761637	1	0	1	1	0	1	1	1
17	c2_45058	chr01	4714970	1	0	1	1	0	1	1	1
18	c2_56842	chr01	30337216	1	0	0	1	1	1	1	0
19	c1_3234	chr01	74837511	1	0	1	0	0	0	1	0
20	c2_4715	chr01	77129418	1	0	0	0	1	0	0	1
21	c2_22105	chr01	80786464	1	0	1	0	1	9	0	1
22	c2_51810	chr01	3761845	1	0	1	1	0	1	1	1
23	c2_55618	chr01	21514658	1	0	0	1	1	1	1	0
24	c1_5477	chr01	23644208	1	0	0	1	1	1	1	0
25	c2_4665	chr01	76973071	1	0	0	0	1	0	0	1
26	c2_36495	chr01	77367370	1	0	1	1	0	0	1	0
27	c2_30955	chr01	81285208	1	0	1	0	1	9	0	1

Recode simplex SNPs as dominant markers ‘1’ or ‘0’ for presence or absence

No-calls or missing data recoded as ‘9’

MICHIGAN STATE UNIVERSITY

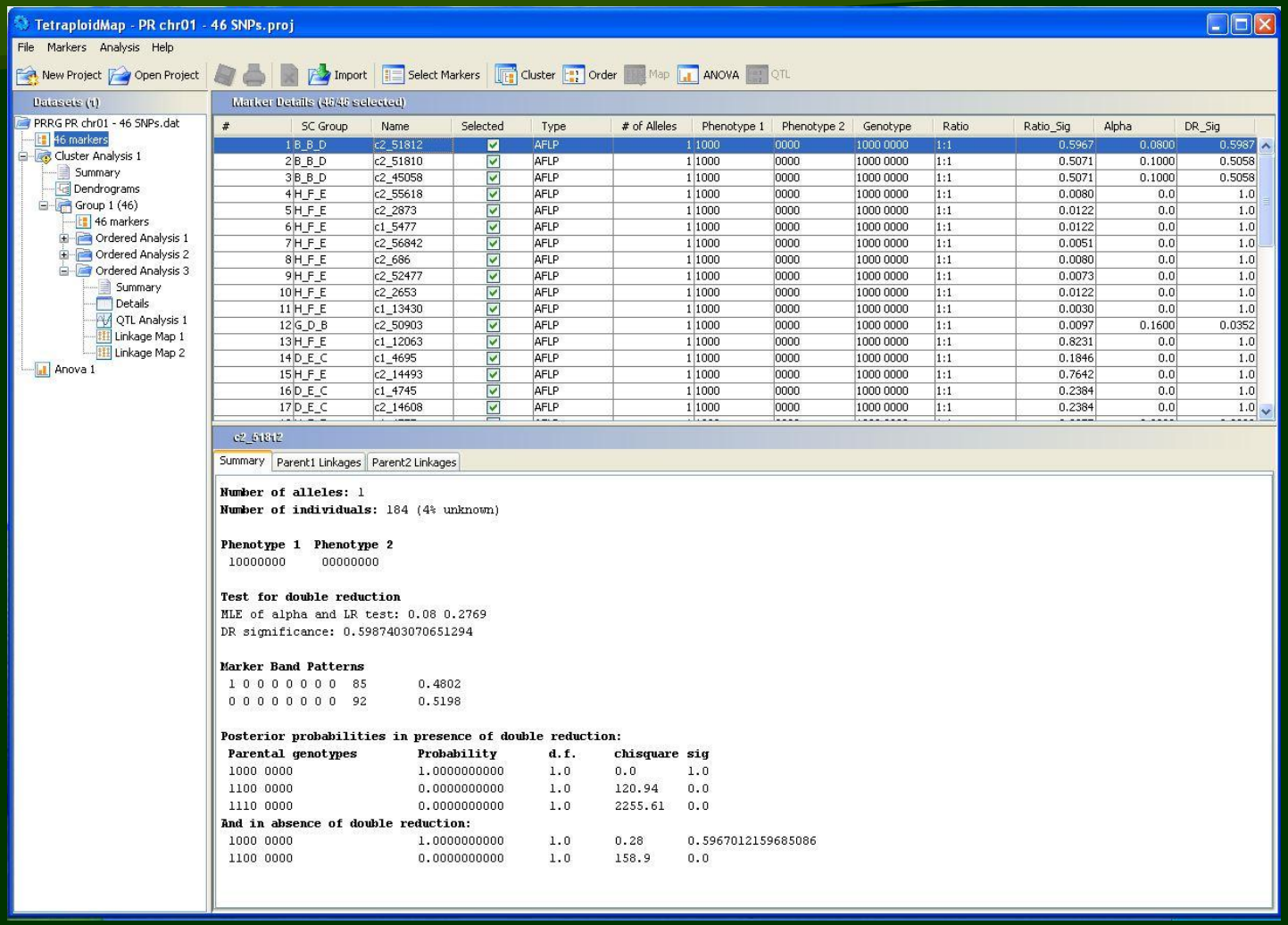
Recoding SNPs for TetraploidMap
Marker data (.dat)

	A	B	C	D	E	F	G	H	I	J	K	L
1	184[1]	46[2]										
2	c2_51812[3]	1[4]										
3	1[5]	0	1	1	0	1	1	1	0	1	1	1
4	c2_51810	1										
5	1	0	1	1	0	1	1	1	0	1	1	1
6	c2_45058	1										
7	1	0	1	1	0	1	1	1	0	1	1	1
8	c2_55618	1										
9	1	0	0	1	1	1	1	0	0	1	0	0
10	c2_2873	1										
11	1	0	0	1	1	1	1	0	0	0	0	0
12	c1_5477	1										
13	1	0	0	1	1	1	1	0	0	0	0	0
14	c2_56842	1										
15	1	0	0	1	1	1	1	0	0	0	0	0

1. Number of progeny (not including parents)
2. Number of markers
3. Marker name
4. Number of alleles (1)
5. Genotypes: Parent 1, Parent 2, then progeny

MICHIGAN STATE UNIVERSITY

TetraploidMap



- Cluster analysis
- Marker ordering
- QTL Analysis

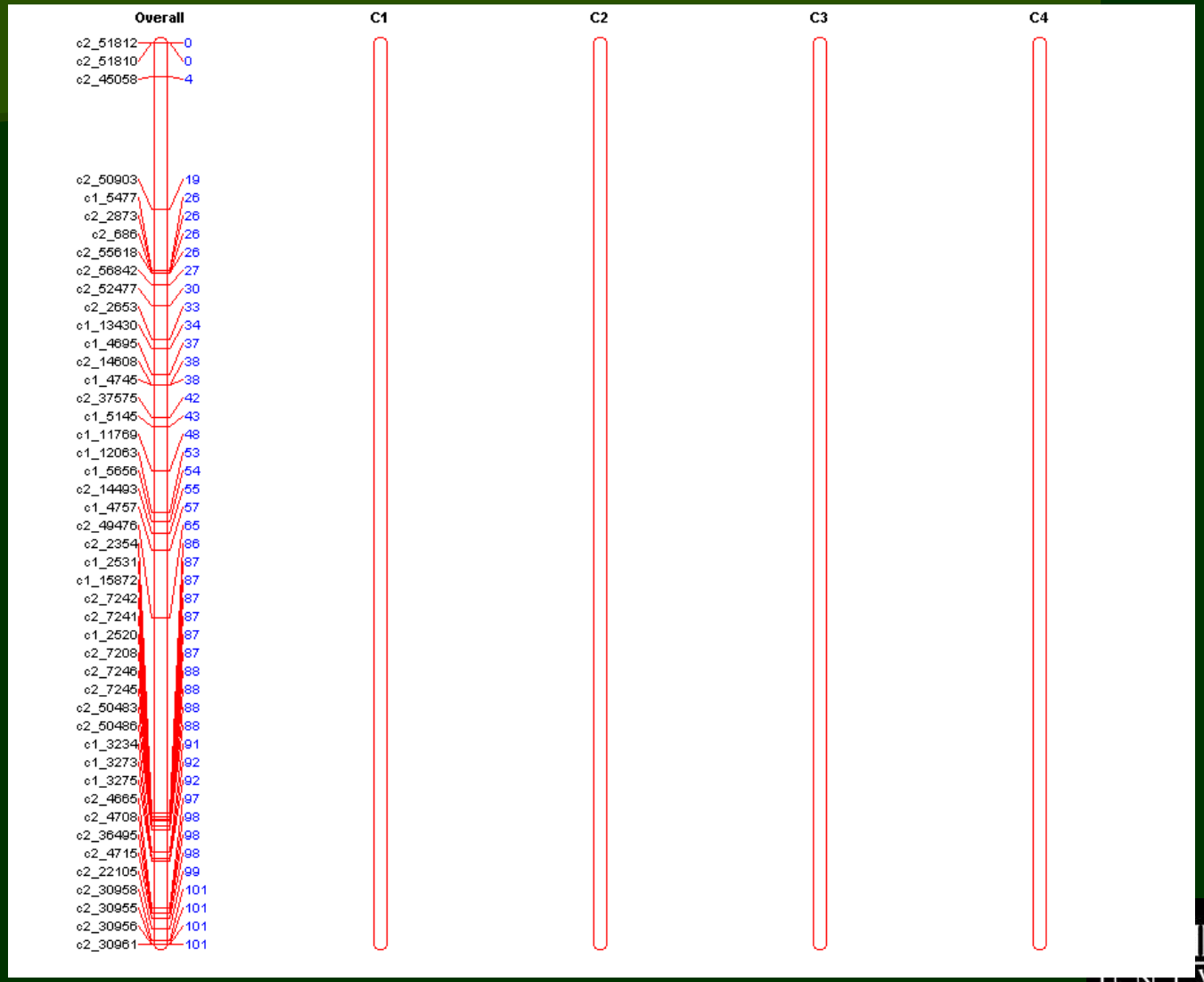
MICHIGAN STATE UNIVERSITY

Linkage Analysis and QTL Mapping in Tetraploids Webinar

- Dr. Christine Hackett
  - Biomathematics and Statistics Scotland
- SolCAP workshop at the Potato Association of America meeting in August 2010
- This workshop is in two parts: linkage analysis, and QTL mapping.
- http://www.extension.org/pages/32471/linkage-analysis-and-qtl-mapping-in-tetraploids-webinar

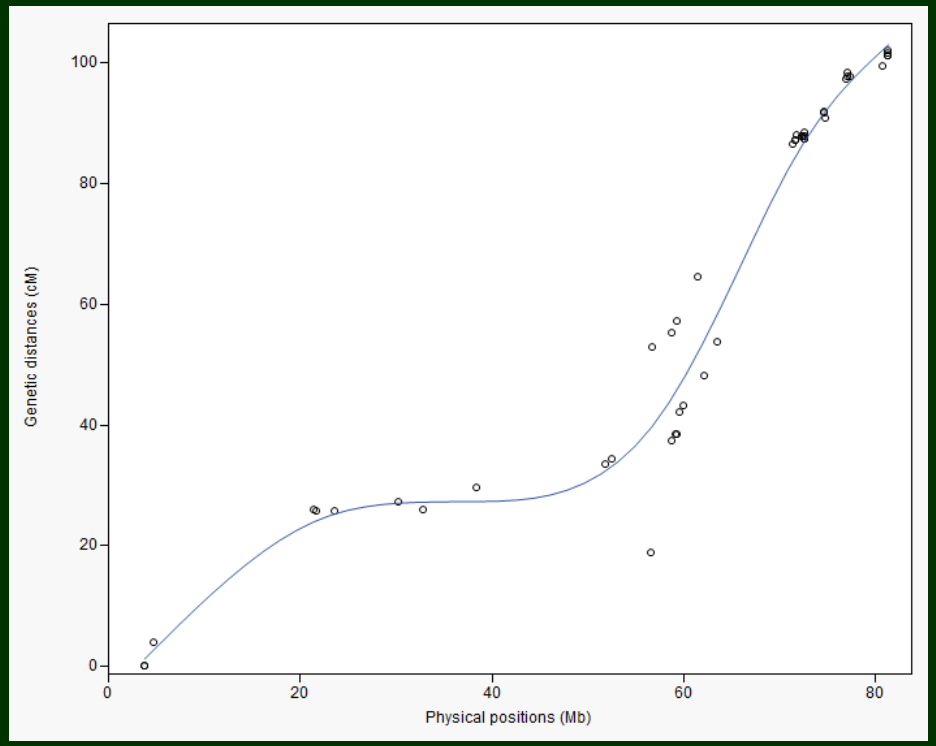
MICHIGAN STATE UNIVERSITY

PR chr01 46 SNPs

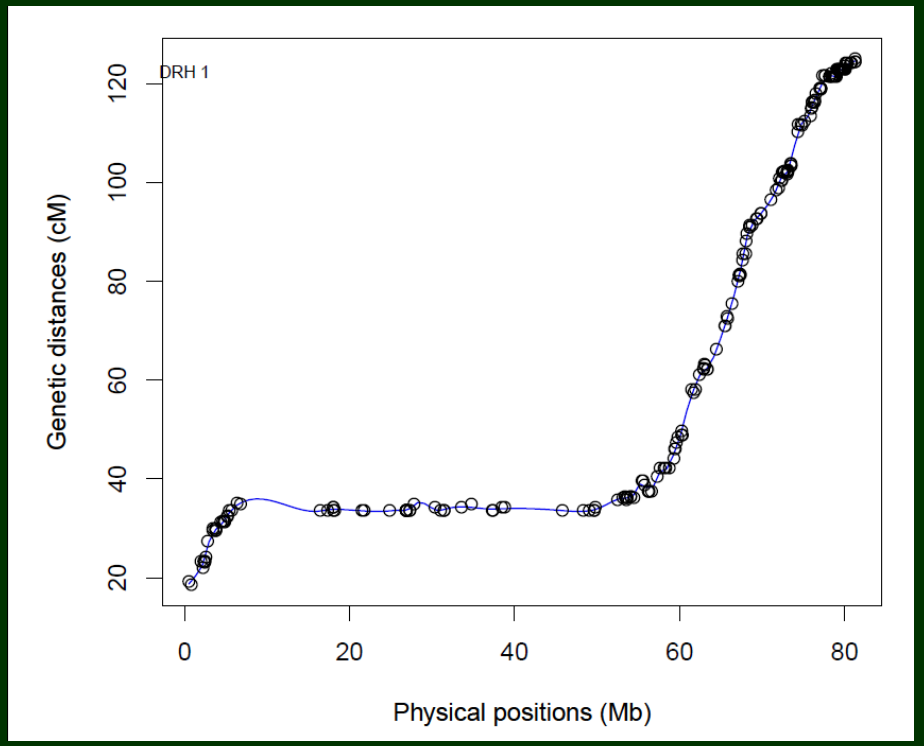


Comparison of 4x and 2x Populations to the Pseudomolecule

PRRG (4x) vs. PM chr01



DRH (2x) vs. PM chr01



MICHIGAN STATE UNIVERSITY

Coding Trait Data for QTL Analysis

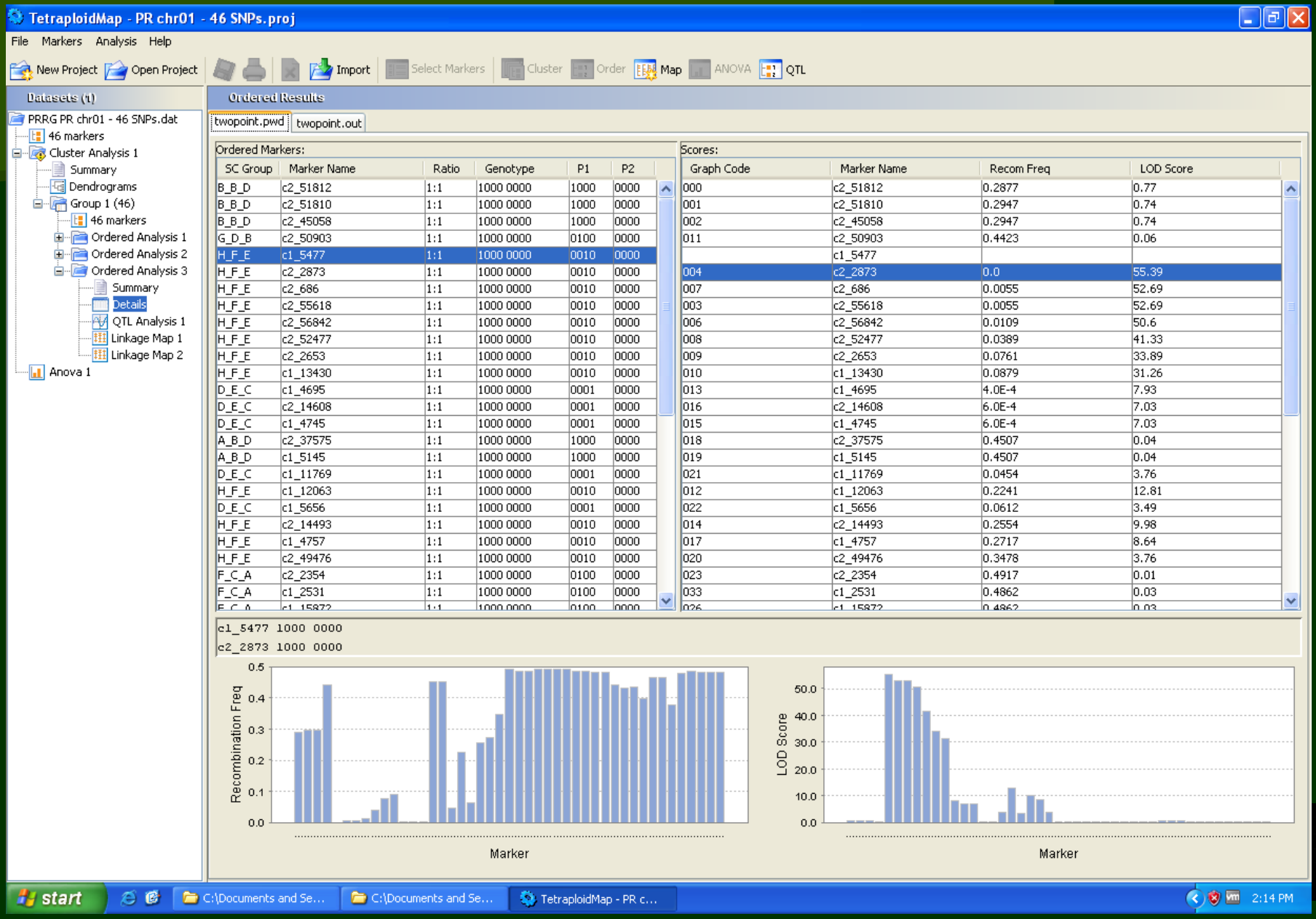
Phenotypic data (.qua)

	A	B	C	D	E	F
1	21					
2		vine_maturity	vine_mat	growth_h	total_yiel	SG_harves
3	1	4	2	7	9.57212	1.0895
4	2	3	1.5	6	6.59428	1.0805
5	3	8	7	5	13.5	1.099
6	4	5	4.5	7	19.9	1.0965
7	5	4	3.5	5	8.78552	1.099
8	6	7.5	7.5	4	4.8216	1.0865
9	7	5	4	5	19.40556	1.0845
10	8	4.5	4.5	4	9.91852	1.085
11	9	6.5	5.5	5	9.96232	1.0805
12	10	4	4	5	7.52976	1.096
13	11	7	6	3	9.02664	1.097
14	12	5	2	5	3.12984	1.092
15	13	4.5	2.5	7	13.7226	1.089
16	14	8	6	3	7.57512	1.091
17	15	6.5	5	4	8.90456	1.091
18	16	3	2	6	12.14684	1.079
19	17	6	4.5	5	12.31436	1.097
20	18	4	2.5	5	15.56384	1.096
21	19	5.5	4	5	6.68396	1.0815
22	20	-99	-99	-99	-99	-99
23	21	6	4	6	12.98756	1.0865

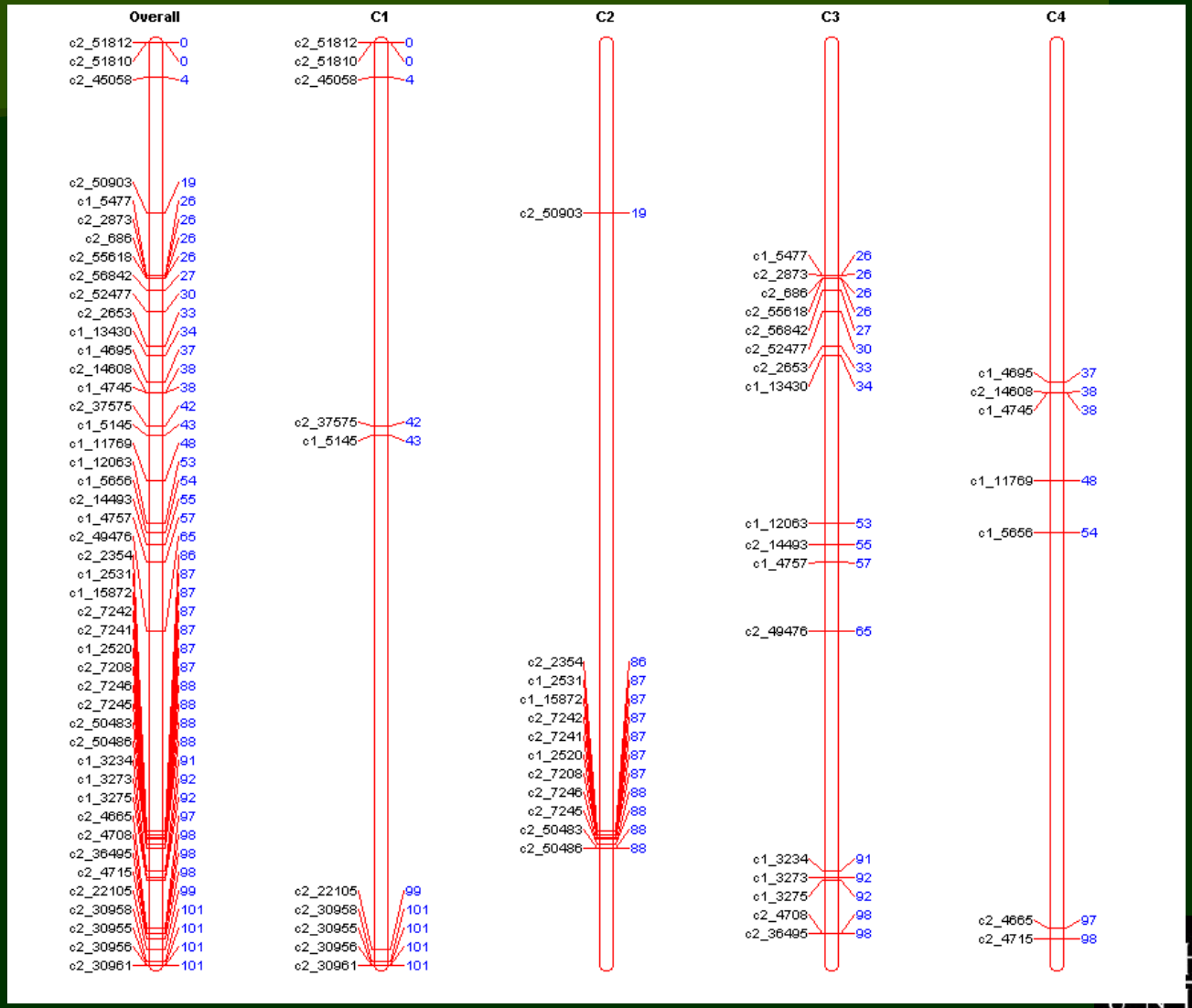
1. Number of traits
2. Progeny number
3. Trait name
4. Missing data coded as -99.0

MICHIGAN STATE UNIVERSITY

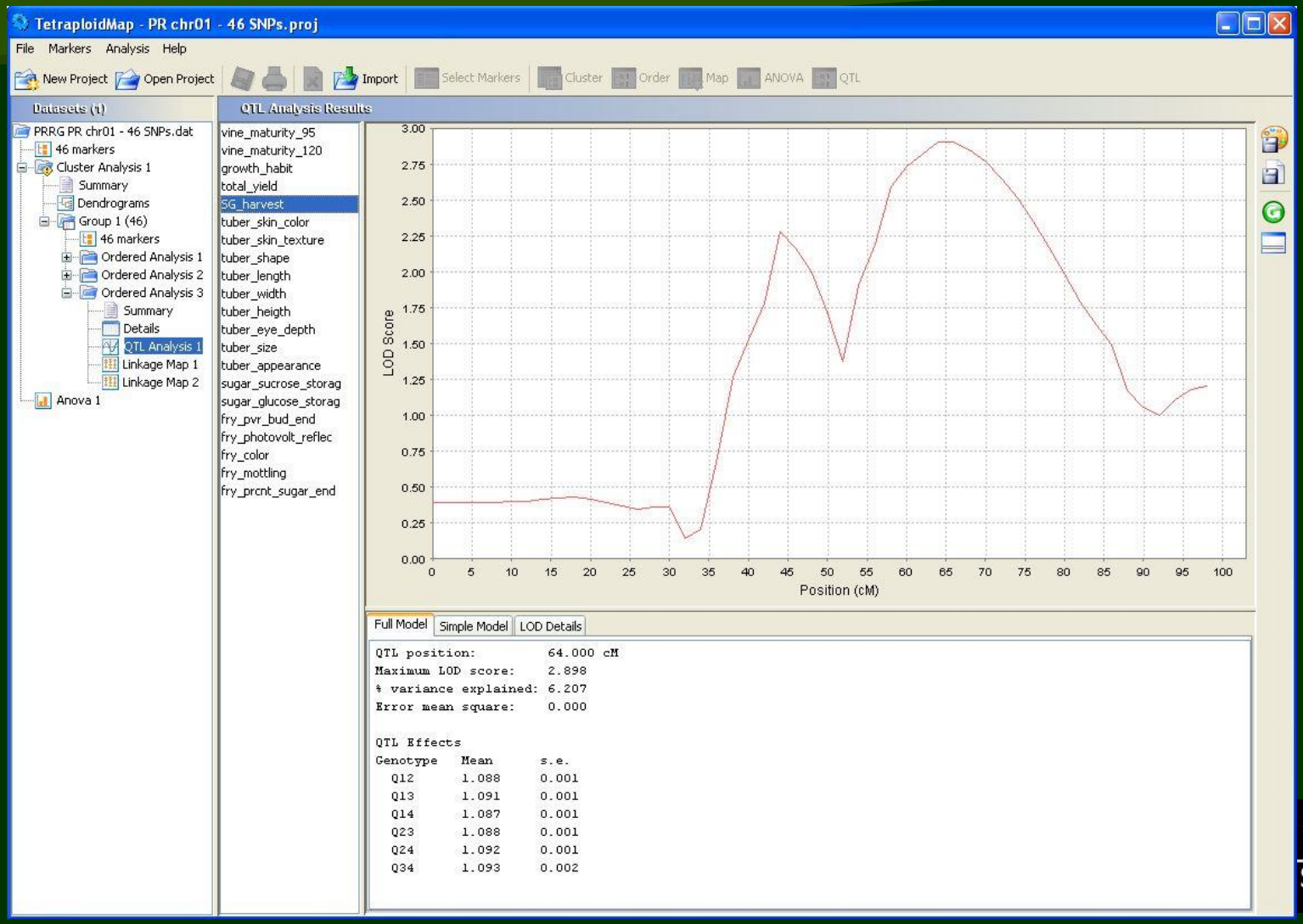
Coupling and Repulsion Analysis



PR chr01 46 SNPs



QTL Analysis in TetraploidMap PR chr01 46 SNPs



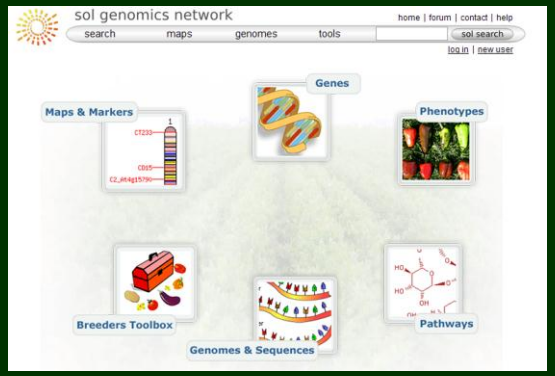
Summary

- Showed five cluster calling of SNPs in Genome Studio
- Showed steps towards filtering SNPs for tetraploid populations
- Demonstrated generating a map of chr01 in PR using TetraploidMap software with simplex markers
- Initiated QTL analysis with simplex markers
  - Single marker ANOVA
  - TetraploidMap

MICHIGAN STATE UNIVERSITY

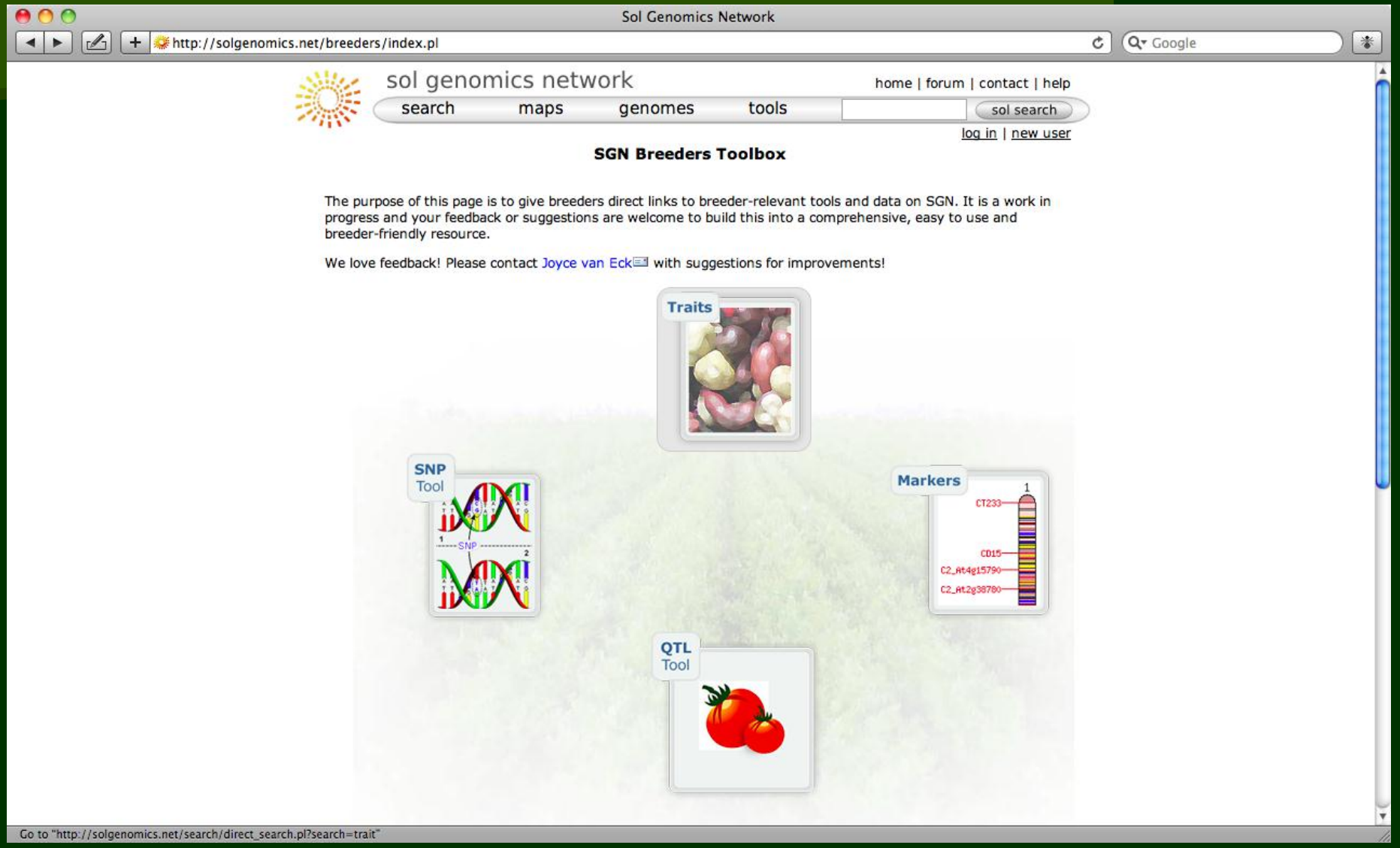
Databases and Resources

- Integrated, breeder-focused resources for genotypic and phenotypic analysis at SGN and MSU
  - http://solcap.msu.edu
  - http://solanaceae.plantbiology.msu.edu
  - http://solgenomics.net



MICHIGAN STATE UNIVERSITY

Breeder's Toolbox



2012 Activities

- SNP genotyping on panels and populations is completed
  - Databases for genotypic and phenotypic data
  - Mining SNP genotype and phenotype data
  - QTL analyses
- Hands on workshops for breeders
- eXtension.org

MICHIGAN STATE UNIVERSITY

Acknowledgments

Collaborators, OSU

David Francis
Sung-Chur Sim
Heather Merk

Collaborators, MSU

David Douches
C. Robin Buell
Candice Hansey
John Hamilton
Kim Felcher
Alicia Massa

Collaborators, Cornell

Walter De Jong
Lukas Mueller
Joyce van Eck
Naama Menda

Collaborators, UCD

Allen Van Deynze
Kevin Stoffel
Alex Kozik
Jeannette Martins

Collaborators, Oregon State

Alex Stone
John McQueen
Roger Leigh

Funding

USDA/AFRI

This project is supported by the Agriculture and Food Research Initiative Applied Plant Genomics CAP Program of USDA's National Institute of Food and Agriculture.

MICHIGAN STATE UNIVERSITY

Please fill out the survey evaluation! (You will be contacted via email)

Today's presentation available at:
http://www.extension.org/pages/63187

Sign up for PBG News
http://pbgworks.org

Watch past webinars and sign up for future webinars!
http://www.extension.org/pages/60426