IRISH CATTLE BREEDING FEDERATION

SNP Selection for Nationwide Parentage Verification and Identification in Beef and Dairy Cattle

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ICAR Technical Workshop,
Krakow, Poland, 9th June, 2015

IDB SNP chip
(International Dairy and Beef)

Parentage Verification / Prediction

Microsatellite Imputation

Sex Verification

Genomic Breeding Value

Disease/Major Gene Status

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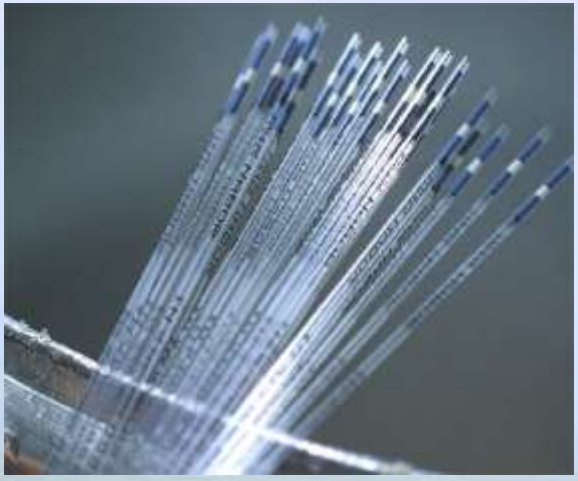
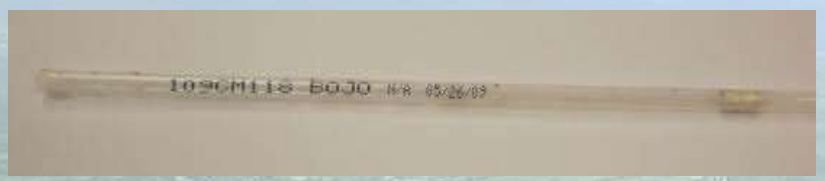
Parentage Validation/Prediction





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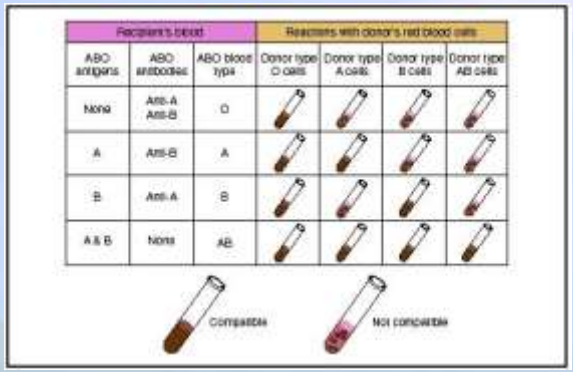
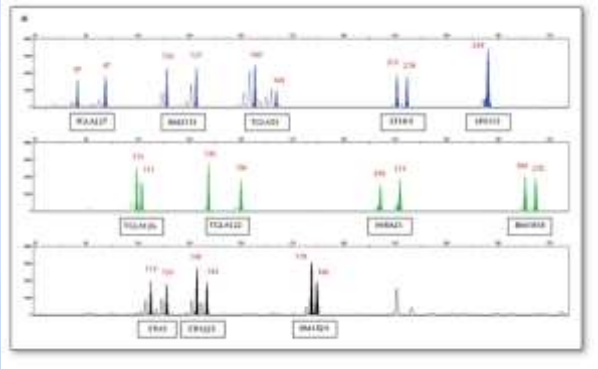
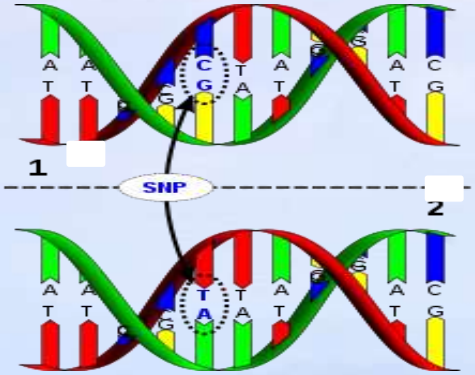
Parentage Validation
How many markers are needed?



Blood Typing



Microsatellite Markers



SNPs

Microsatellites

ISAG Panel: BM1824, BM2113, INRA023, SPS115, TGLA122, TGLA126, TGLA227, ETH10, ETH225, ETH3, SPS115, TGLA53

Additional panel of MGTG4B, CSRM60, SPS113, ILSTS006, RM067, CSSM66

SNP: ISAG100
ISAG200
More???

121 Validation

©Ir 015

How Many SNP to Validate 1 Sire

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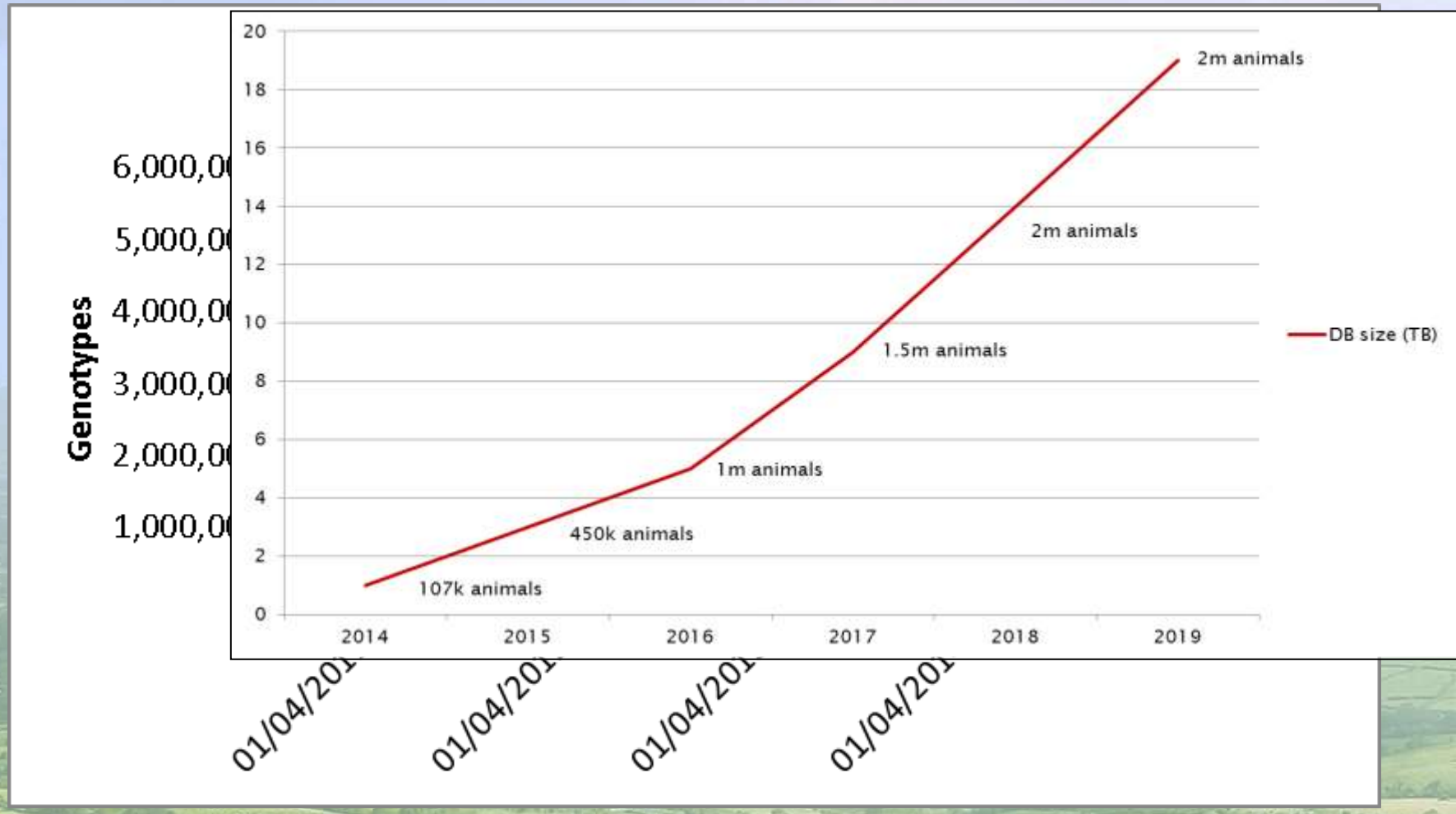
ICBF Actual/Predicted Growth



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Small SNP Sets: Genotype Errors

- Fail Sire A with 121 SNP (ISAG200 subset)

  ≥2 misconcordance = fail

- Predict Sire A with 2,000 SNP

  ≤10 misconcordance = pass

Unsort		C 1	G 3
Map	#t	sire_#t	ARS-USMARC-PARENT-EF093511-RS28[illegible]
1	HERAUSM00000GRKA584	1	B_B
2	HERIRLM141607070601	HERAUSM00010GRKA584	[illegible]
3	HERIRLM151225330379	HERAUSM00010GRKA584	A_A
4	HERIRLM151225340413	HERAUSM00010GRKA584	[illegible]
5	HERIRLM151225360423	HERAUSM00010GRKA584	A_A
6	HERIRLM151225370399	HERAUSM00010GRKA584	A_A
7	HERIRLM151225380425	HERAUSM00010GRKA584	[illegible]
8	HERIRLM151225380441	HERAUSM00010GRKA584	A_A
9	HERIRLM191141760568	HERAUSM00010GRKA584	A_A
10	HERIRLM231305310207	HERAUSM00010GRKA584	A_A
11	HERIRLM241245190385	HERAUSM00010GRKA584	A_A
12	HERIRLM331493150493	HERAUSM00010GRKA584	A_A
13	HERIRLM361055830685	HERAUSM00010GRKA584	A_A
14	HERIRLM361055880665	HERAUSM00010GRKA584	A_A
15	HERIRLM121182590084	HERAUSM00010GRKA584	A_B
16	HERIRLM121201450915	HERAUSM00010GRKA584	A_B
17	HERIRLM121201460899	HERAUSM00010GRKA584	A_B
18	HERIRLM141643520372	HERAUSM00010GRKA584	A_B
19	HERIRLM151225310435	HERAUSM00010GRKA584	A_B
20	HERIRLM151225330412	HERAUSM00010GRKA584	A_B
21	HERIRLM151225390376	HERAUSM00010GRKA584	A_B
22	HERIRLM151313160329	HERAUSM00010GRKA584	A_B
23	HERIRLM151654470902	HERAUSM00010GRKA584	A_B
24	HERIRLM211463520049	HERAUSM00010GRKA584	A_B
25	HERIRLM211463580046	HERAUSM00010GRKA584	A_B
26	HERIRLM231305370204	HERAUSM00010GRKA584	A_B
27	HERIRLM241842660174	HERAUSM00010GRKA584	A_B
28	HERIRLM281110080573	HERAUSM00010GRKA584	A_B
29	HERIRLM291166240641	HERAUSM00010GRKA584	A_B
30	HERIRLM301207290630	HERAUSM00010GRKA584	A_B
31	HERIRLM311122080052	HERAUSM00010GRKA584	A_B
32	HERIRLM311317670240	HERAUSM00010GRKA584	A_B
33	HERIRLM331340371248	HERAUSM00010GRKA584	A_B
34	HERIRLM331358460991	HERAUSM00010GRKA584	A_B
35	HERIRLM121182560081	HERAUSM00010GRKA584	B_B
36	HERIRLM141607090603	HERAUSM00010GRKA584	[illegible]
37	HERIRLM151225340421	HERAUSM00010GRKA584	B_B
38	HERIRLM151225370424	HERAUSM00010GRKA584	B_B
39	HERIRLM151313130326	HERAUSM00010GRKA584	[illegible]

Why validate with small and predict large SNP?

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Small SNP Sets: Validate Wrong Sire

Animal	Listed sire		
LIMIRLF.....554	LIMIRLM.....050		
SNP set	#_mismatches	#SNP_both_genotyped	%_SNP_mismatch
121 SNP	0	118	0.00%
LD_base	267	6848	3.90%
CHAIRLF.....639	CHAIRLM.....163		
SNP set	#_mismatches	#SNP_both_genotyped	%_SNP_mismatch
121 SNP	1	113	0.88%
LD_base	336	6729	4.99%
CHAIRLF.....355	CHAFRAM.....993		
SNP set	#_mismatches	#SNP_both_genotyped	%_SNP_mismatch
121 SNP	1	114	0.88%
LD_base	227	6761	3.36%
LIMIRLF.....500	LIMIRLM.....959		
SNP set	#_mismatches	#SNP_both_genotyped	%_SNP_mismatch
121 SNP	0	112	0.00%
[illegible]	[illegible]	[illegible]	[illegible]
LD_base	0	6711	0.00%

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Sire Validation Errors with Small SNP Sets

- Fail with 121 then predict with 2,000 SNP
- Validate the wrong sire?

- **Why validate with small and predict large SNP**

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ICAR-2014: How Many SNP are **used** to Predict Parentage?

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How Many SNP to Predict **1 Correct** Sire

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How Many SNP to Predict 1 **Correct** Sire

- 56,000 genotyped animals
- SNP densities tested
  - ISAG200
  - Plus top 100, 200, …..1800 MAF SNP
- 9,000 sire validated animals
- Predict sire/dams (1% misconcordance)

Animals	56,000
breed	Jun-14
HOL	68.65%
LIM	7.94%
CHA	7.41%
AAN	4.42%
SIM	2.35%
HER	3.06%
BBL	1.01%
MSH	0.06%
SAL	0.04%
JER	0.17%
PAR	0.17%
LMS	1.91%
BAQ	0.04%
AUB	0.00%
CHL	1.68%
PIE	0.55%
HFD	0.17%
MON	0.14%
IRM	0.00%
NWR	0.09%
RED	0.01%

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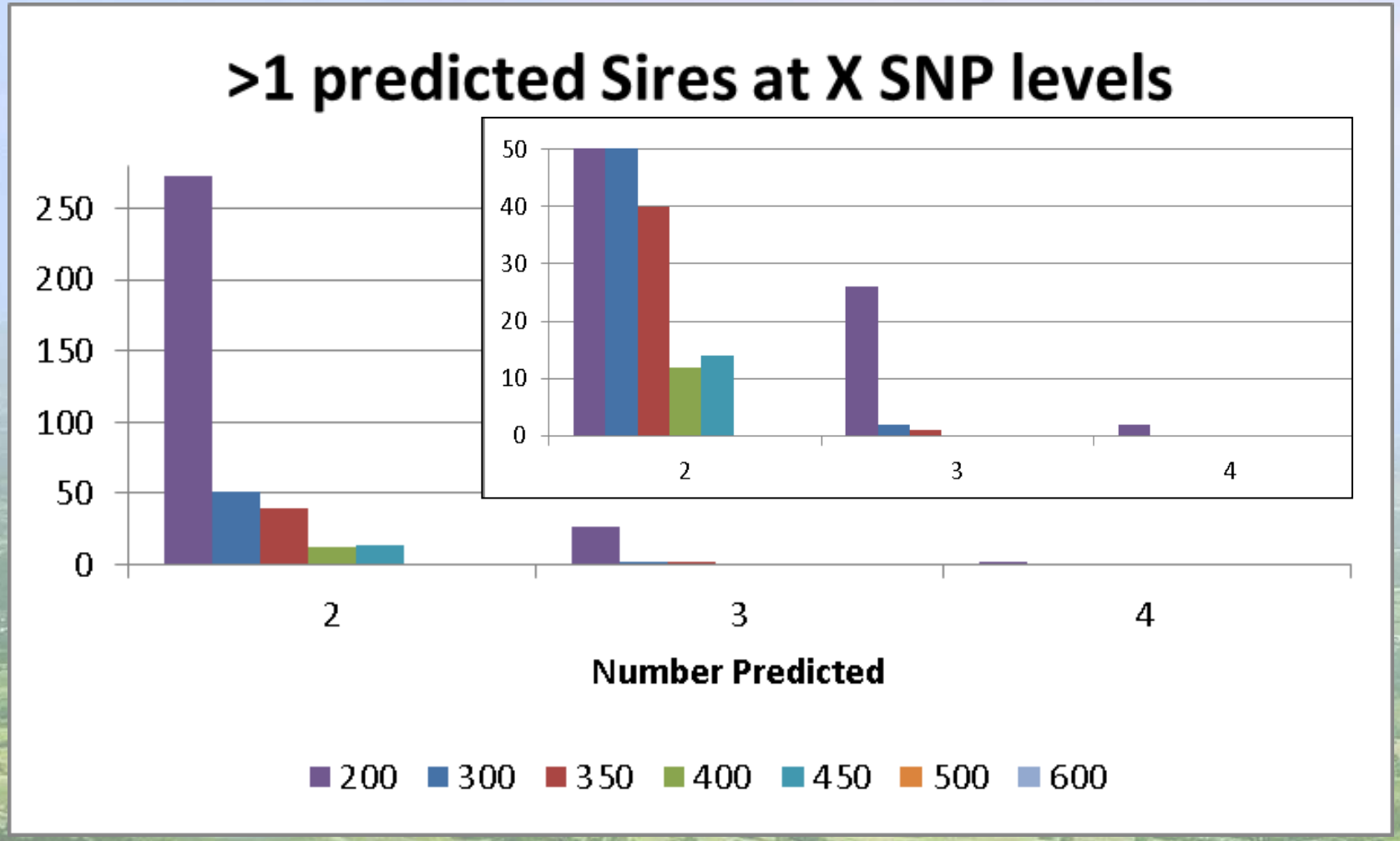
Sire Prediction with 200, 300,… SNP



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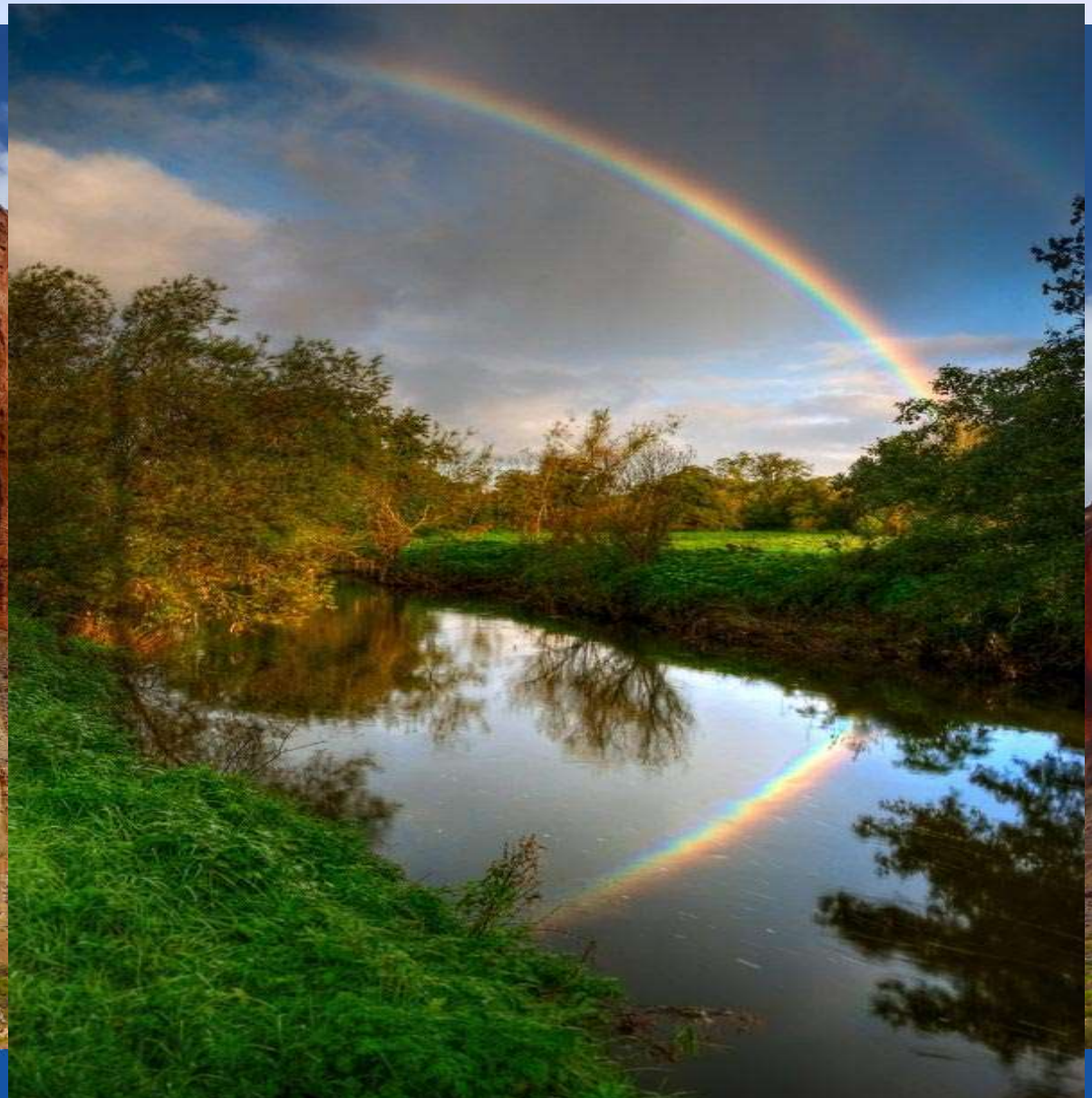
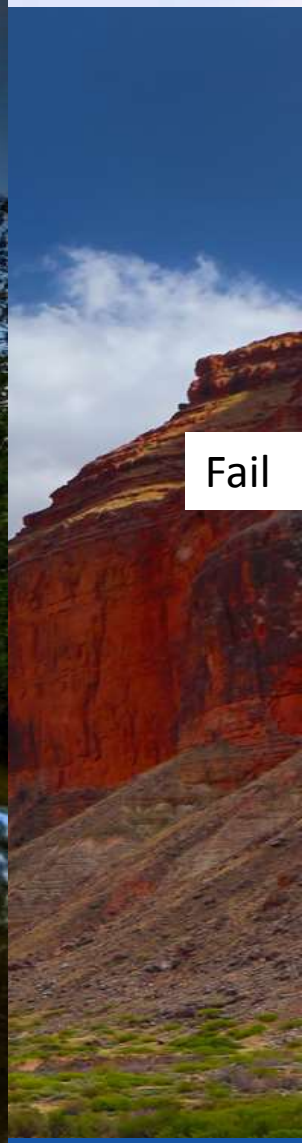
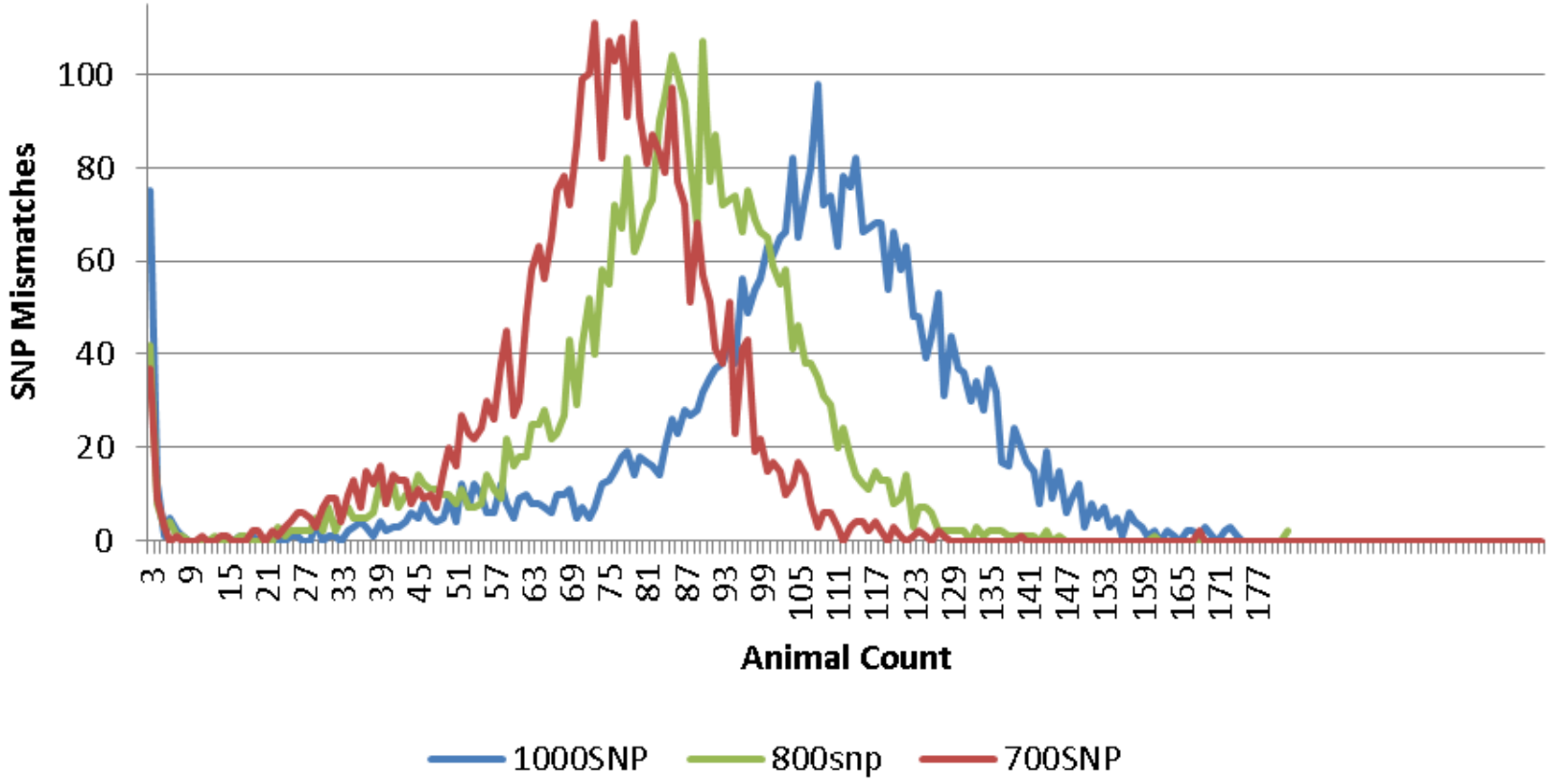
Space between Validation and Fail





SNP Mismatches for sire validations
114,000 animals



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Recommend: Use >500 SNP for Validation

- ICBF Switched to 800 SNP July 2014
- Refinement in February 2015
  - More breeds
  - Less Dairy heavy
  - SNP QC

Animals	56,000	180,000
breed	Jun-14	Feb-15
HOL	68.65%	30.08%
LIM	7.94%	22.34%
CHA	7.41%	18.68%
AAN	4.42%	7.22%
SIM	2.35%	6.77%
HER	3.06%	4.66%
BBL	1.01%	2.75%
MSH	0.06%	1.57%
SAL	0.04%	0.92%
JER	0.17%	0.67%
PAR	0.17%	0.64%
LMS	1.91%	0.59%
BAQ	0.04%	0.59%
AUB	0.00%	0.53%
CHL	1.68%	0.52%
PIE	0.55%	0.17%
HFD	0.17%	0.07%
MON	0.14%	0.05%
IRM	0.00%	0.03%
NWR	0.09%	0.03%
RED	0.01%	0.03%

800 SNP list at

http://www.icbf.com/wp/wp-content/uploads/2013/07/ICBF_Parentage_SNP_Selection.csv

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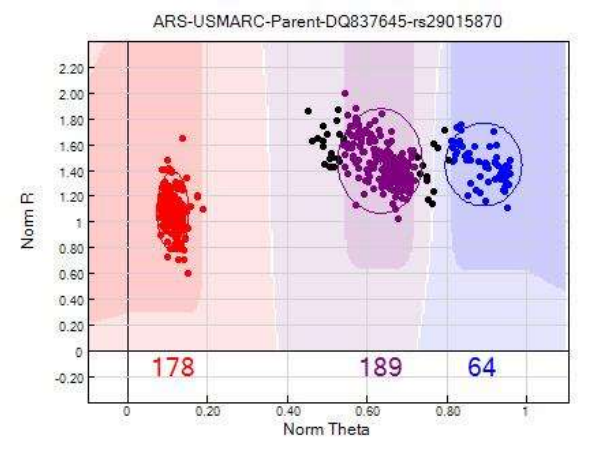
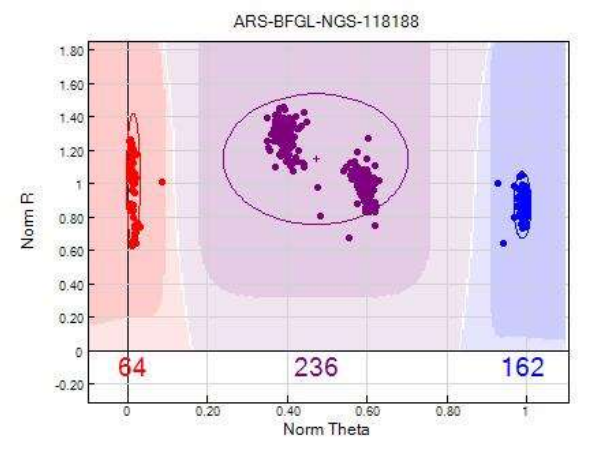
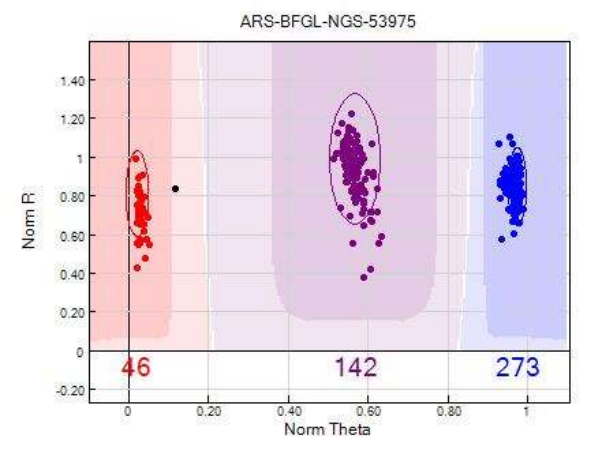
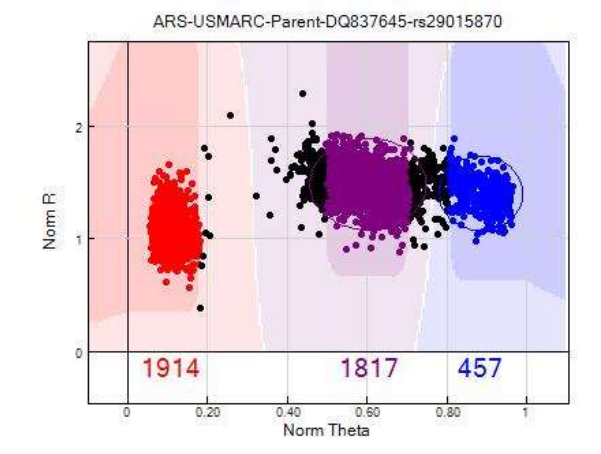
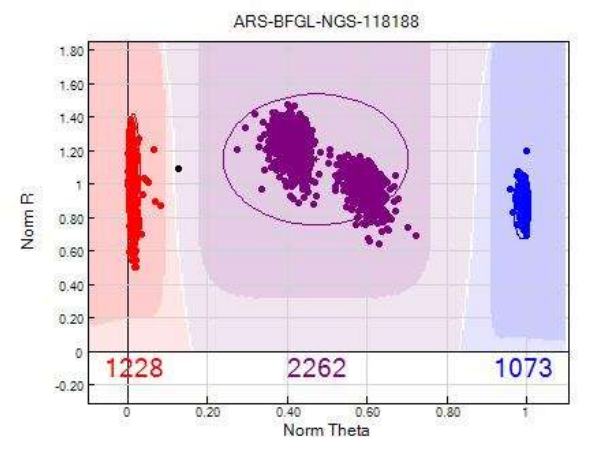
SNP Refinement QC Quality:
Clusters when processing 400 vs 4K / week

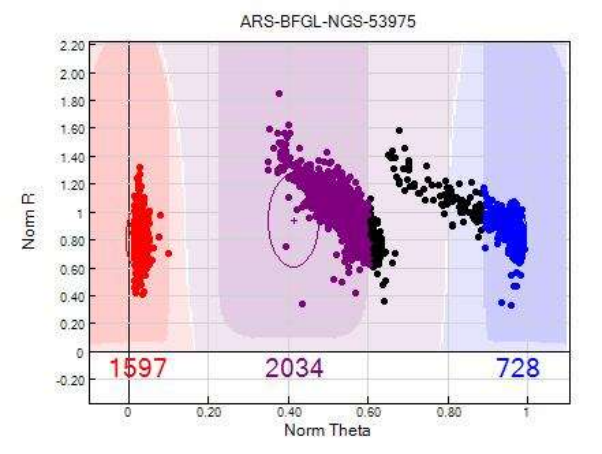












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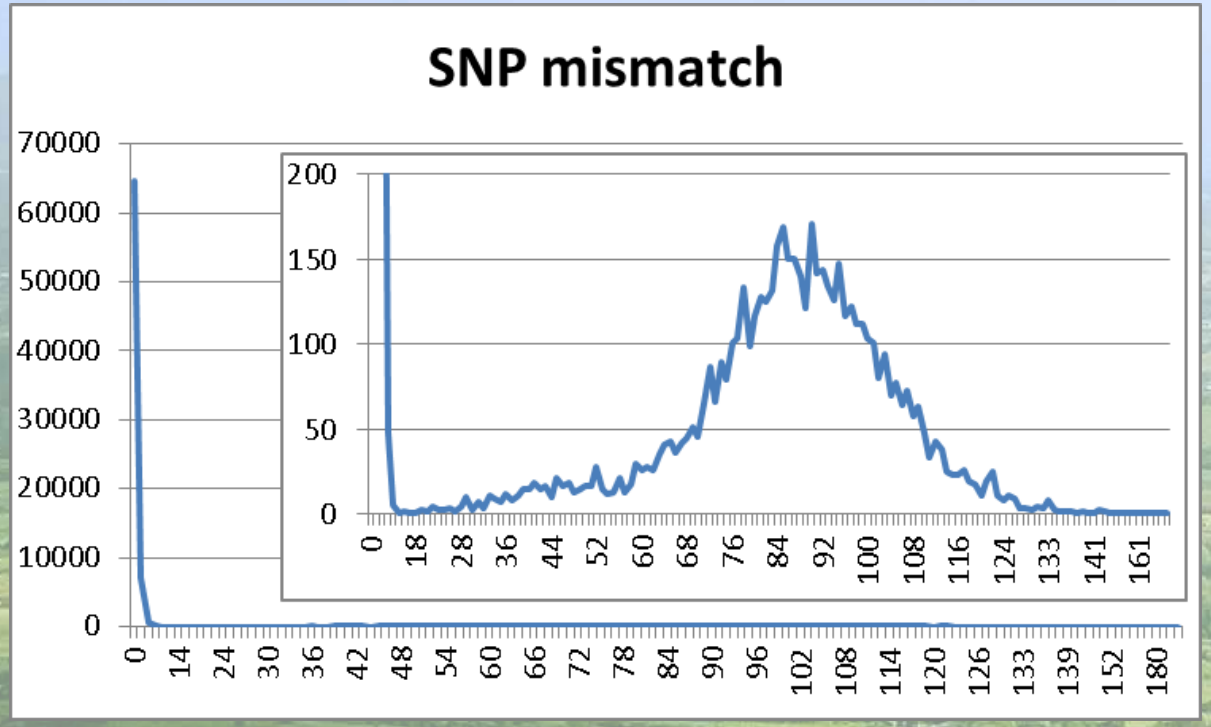
SNP Excluded from ICBF Parentage Analysis Due to

1) Call Rate (CR<0.3)
2) Minor Allele Frequency (MAF<0.01)
3) Probe Clustering issues

SNPID	RS#	ISAG100	ISAG200	CR	MAF	Cluster
ARS-BFGL-NGS-103099	rs110896475	0	0	0.952	0.496	1
ARS-BFGL-NGS-112652	rs109504357	0	0	0.994	0.499	1
ARS-BFGL-NGS-11469	rs111032185	0	0	0.955	0.496	1
ARS-BFGL-NGS-118188	rs42156449	0	0	0.993	0.485	1
ARS-BFGL-NGS-3547	rs110206613	0	0	1	0.493	1
ARS-BFGL-NGS-43361	rs109934313	0	0	0.998	0.494	1
ARS-BFGL-NGS-53975	rs109456438	0	0	0.988	0.484	1
ARS-BFGL-NGS-62906	rs110146023	0	0	0.998	0.484	1
ARS-BFGL-NGS-66558	rs109817790	0	0	0.991	0.495	1
ARS-BFGL-NGS-76191	rs110846944	0	1	0.998	0.385	1
ARS-USMARC-PARENT-DQ786764-NO-RS	rs109943112	1	1	0.952	**<0.001**	-
ARS-USMARC-PARENT-DQ837645-RS29015870	rs29015870	1	1	**0.276**	0.389	1
ARS-USMARC-PARENT-EF034087-NO-RS	rs110665639	1	1	0.984	**0.005**	-
BTA-100621-NO-RS	rs41611675	0	1	0.928	0.452	1
BTB-00147175	rs43356919	0	0	0.99	0.491	1
BTB-01834338	rs42942345	0	0	0.999	0.498	1
HAPMAP47324-BTA-55159	rs41586638	0	0	0.984	0.496	1
UA-IFASA-9571	rs41659357	0	0	0.985	0.485	1

Recommend: Use >500 SNP for Validation

- ICBF Switched to 800 SNP July 2014
- Refinement in February 2015



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Can <800 SNP be Used

- 13,748 animals with ≥1 misconcordance (800 SNP)
- Reran validation process at:

  700, 600, 500, 400, 300, 200, 100 SNP

- Count number of misconcordances <1% rate>
- 1% misconcordances = 0
- Accuracy
- "Gap" between pass/fail

	Fail on 800	Pass on 800
SNP#	Pass on X	Fail on X
700	-	-
600	-	-
500	-	-
400	1	-
300	-	-
200	2	-
100	17	14

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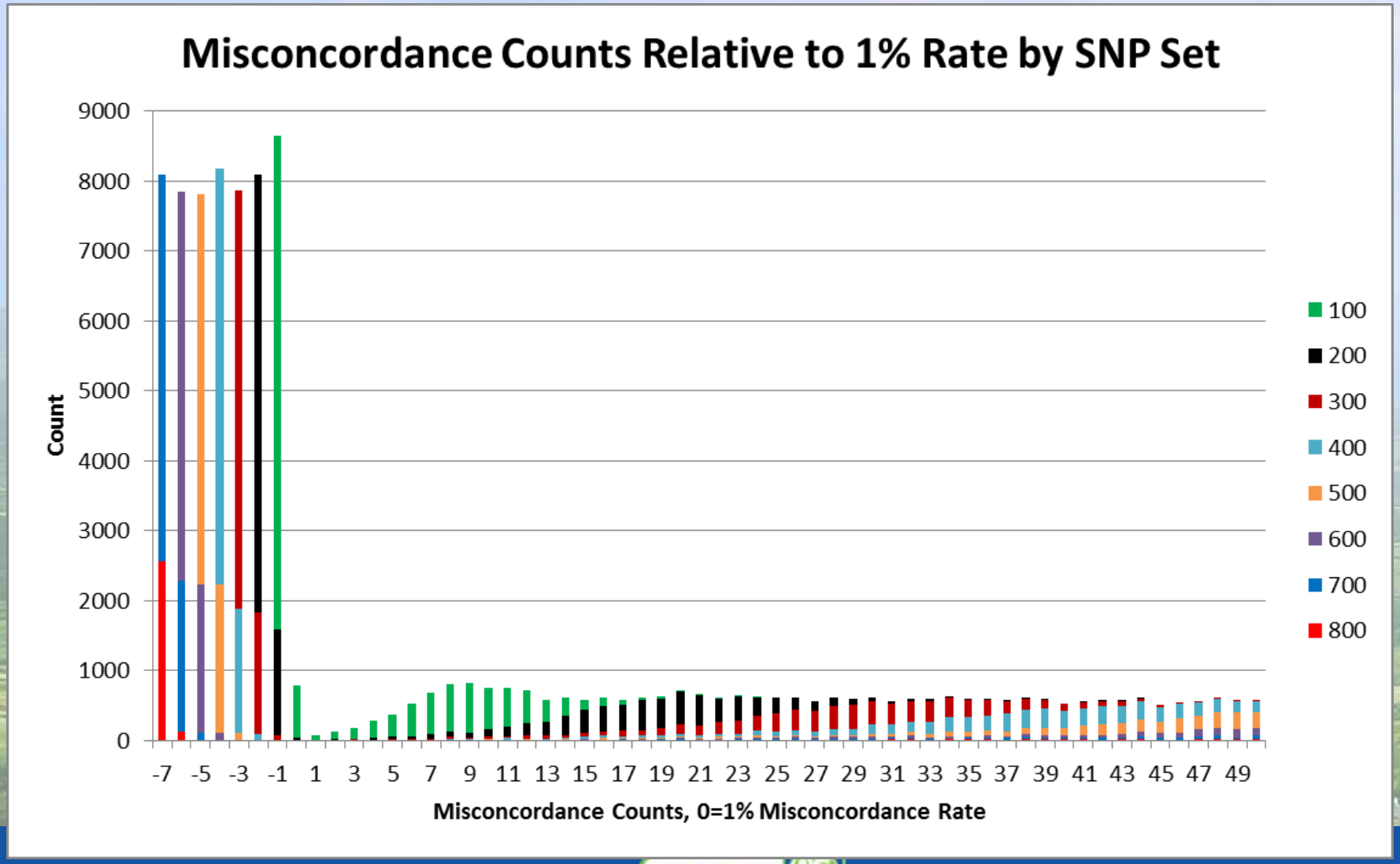
Can <800 SNP be Used



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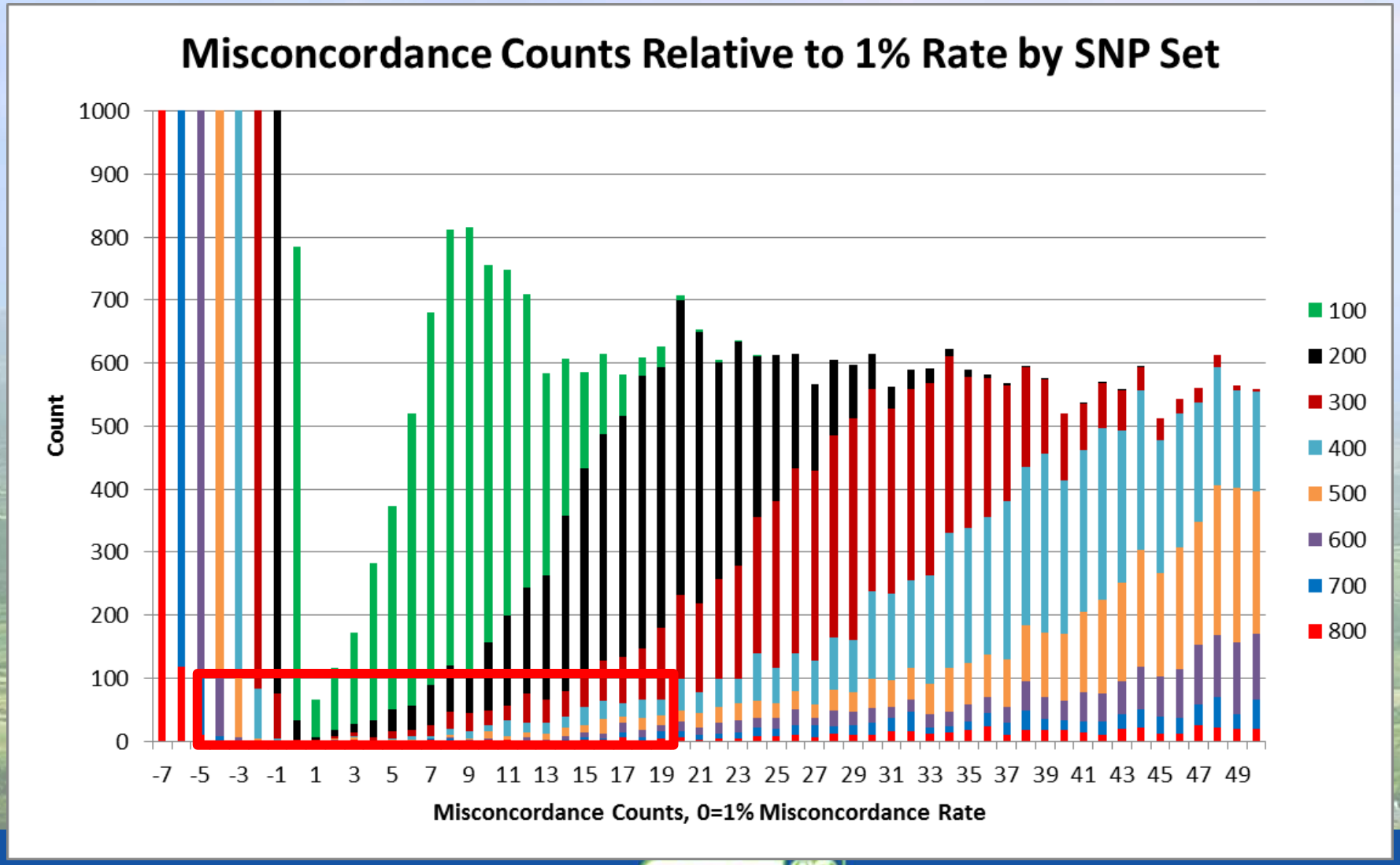
Can <800 SNP be Used



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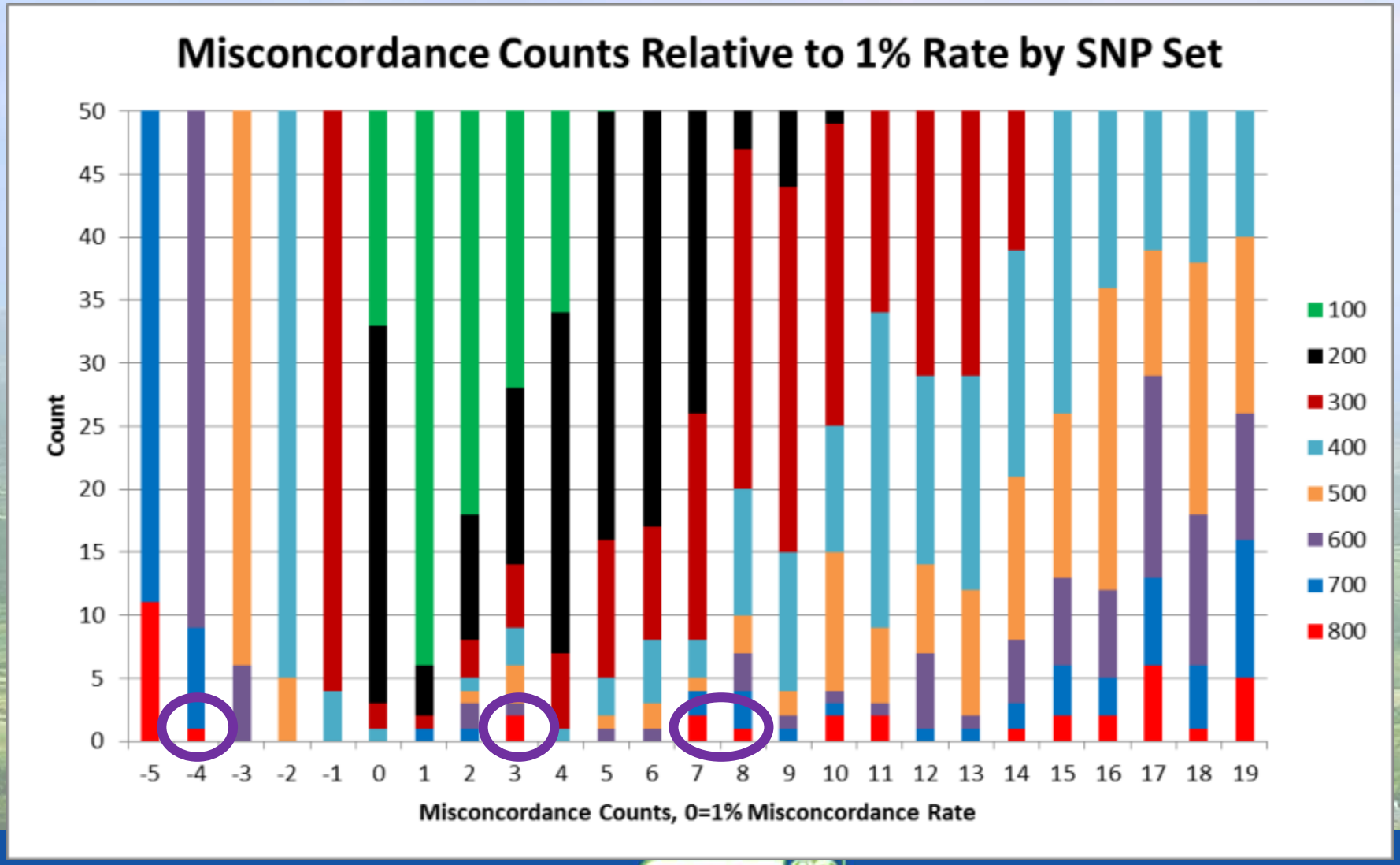
Can <800 SNP be Used



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Final Thoughts

- Some ISAG parentage SNP should be dropped
- Advise using >500 SNP for parentage
- Exact number of SNP to use depends on each groups:
  - Parentage situation (farm level vs national level)
  - Acceptable risk level
  - SNP error rate for your genotyping platform(s)
  - Pass/Fail misconcordance gap they are comfortable with
- "The exact SNP don't matter as long as you have enough quality SNP"—George Wiggans

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Acknowledgements/Funding

- ICBF
- Teagsac
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- Weatherbys
- Irish farmers and herdbooks

- DAFM RSF
  - Molecular Biomarkers of Fertility 11/S/104,
  - GenoTrace 13/F/403

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Thank You

800 SNP list at

http://www.icbf.com/wp/wp-content/uploads/2013/07/ICBF_Parentage_SNP_Selection.csv

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