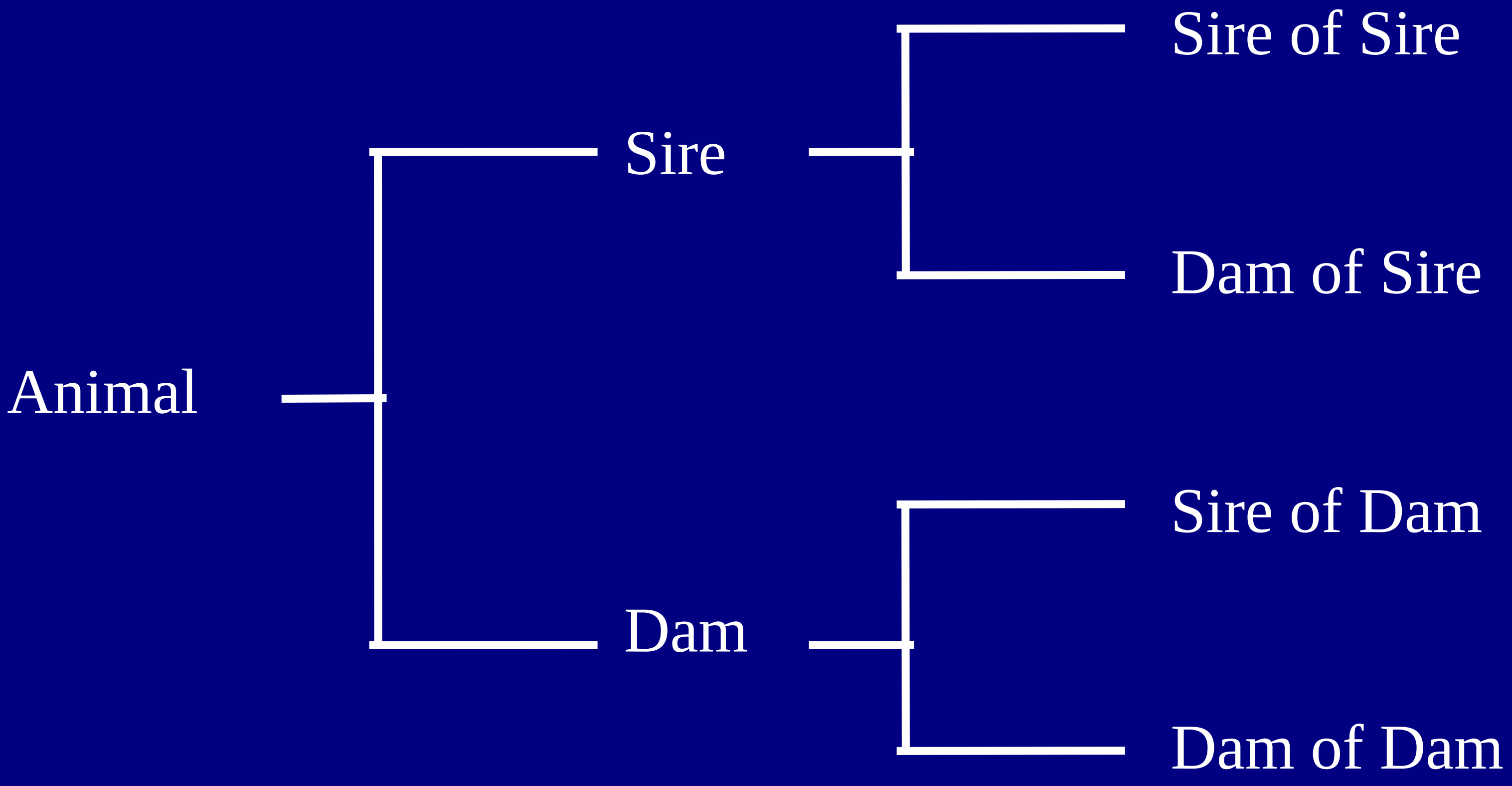
Genotyping Dairy Cattle Samples with Infinium BovSNP50 BeadChips and VeraCode Universal Oligo Beads

Dr. Michael Cowan
General Manager
Genetic Visions, Inc.

Traditional Pedigree Selection



Animal

Sire

Dam

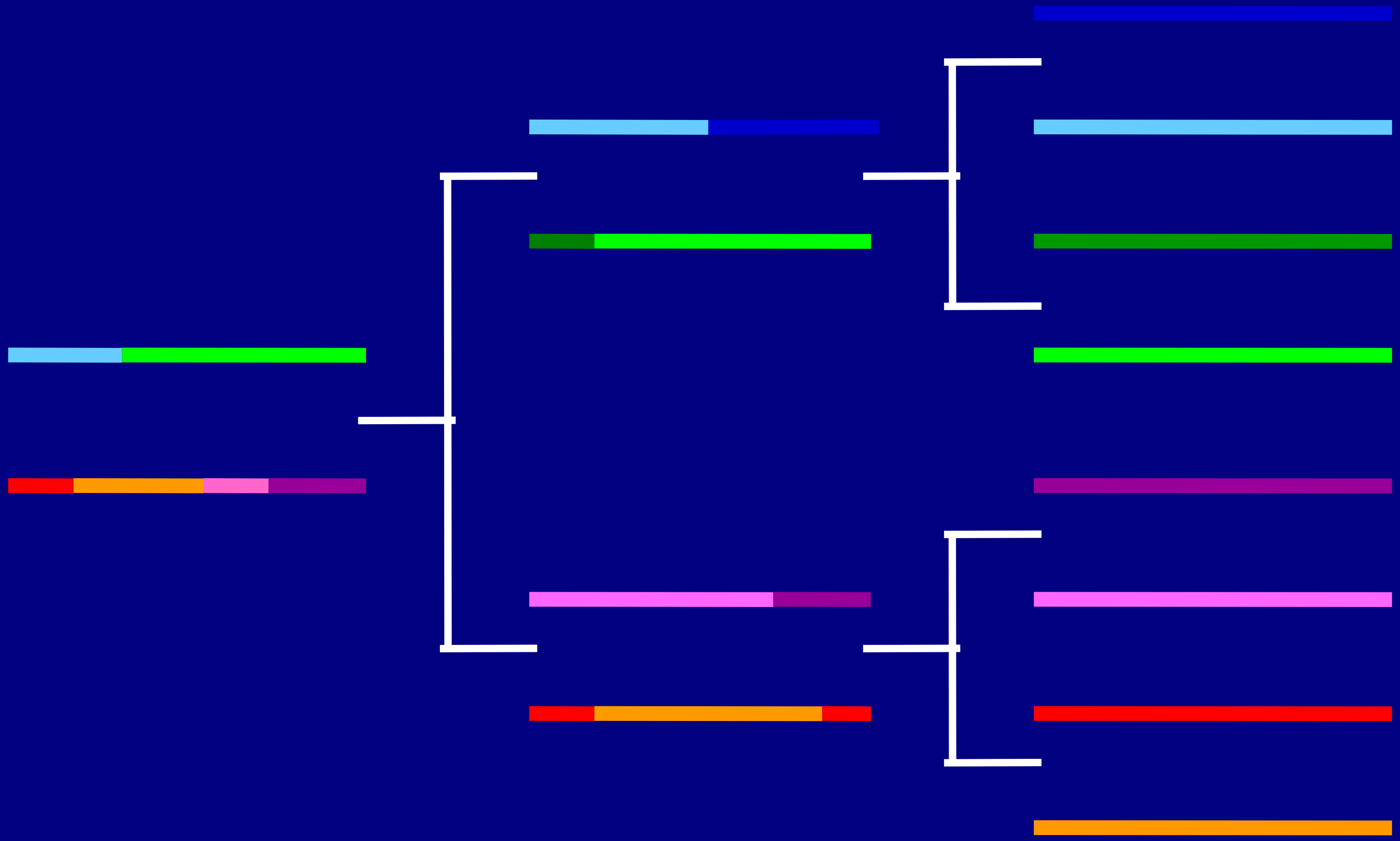
Sire of Sire

Dam of Sire

Sire of Dam

Dam of Dam

Genomic Pedigree



How Related are Relatives?

- Example: Full Sibs
  - Expected to share 50% of their DNA, SD 5%
  - May actually share 40 to 60% of their DNA because each animal inherits a different mixture of chromosome segments from each parent
- Combine genotype and pedigree data to determine exact fractions

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What Was Needed To Advance Selection?

- Expanded sequence data from bovine genome – various breeds
- Technology advances making it possible to find large numbers of genetic markers, means to test animals quickly and at a lower cost.
- Dense marker maps, ideally equally spaced.
- Expanded methodologies to estimate SNP effects in dairy populations.

USDA-BFGL, Illumina, AI Industry

- USDA-BFGL Consortium found additional SNPs in dairy populations
- Illumina Infinium BeadChip
- USDA and Illumina collaborated to develop the Bov50K SNP Assay
- USDA and CDDR-AI Studs collaborated to genotype reference populations, estimate additive SNP effects and predict merit of future populations

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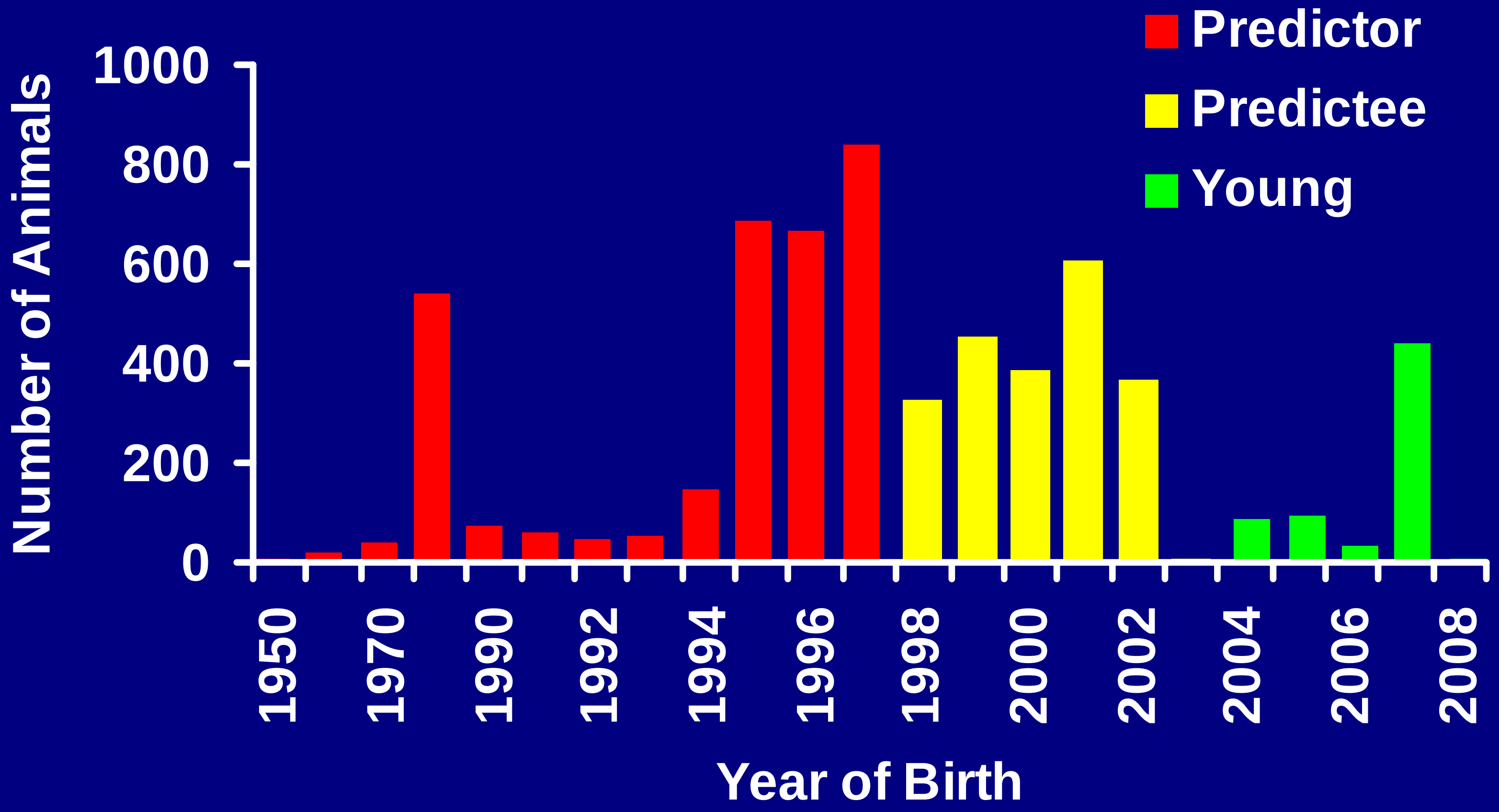
Genotyped Animals (n=6005)

As of April 2008



VanRaden 2008

Genomic PTAs

- Genotypic data submitted to USDA-AIPL
- 38000+ SNPs used in genomic predictions
- Parentage and sex verified
- Calculated by breed, Holstein, Jersey and Brown Swiss
- Genetic evaluations summarized 3X/yr
- Genomic PTAs released monthly

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Flow Chart

CDDR AI Studs, Breed Associations, NAAB-Non CDDR

↓

Genotyping Labs

↓

USDA-AIPL

↓

Publish Official Genomic Evaluations

Increased Accuracy in Predicting Individual's True Genetic Merit

Accuracies Increased For All 27 Traits

- 5 Yield Traits
- 5 Fitness Traits
- 16 Conformation traits
- Net Merit

VanRaden et al. 2009. J. Dairy Sci 92:16-24

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Illumina BovSNP50 BeadChip

- Each chip is unique, requires positioning software
- 12 samples can be genotyped on each beadchip.
- Typical call rate is >99%.
- 116 SNP's are specified for parentage.

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Dairy Cattle DNA Source Materials

- Whole Blood - Chimeras
- Semen – Mature Male
- Hair Roots – Keratin Problems

GENETICVISIONS

Dairy Cattle DNA Source Materials

- Whole Blood - Chimeras
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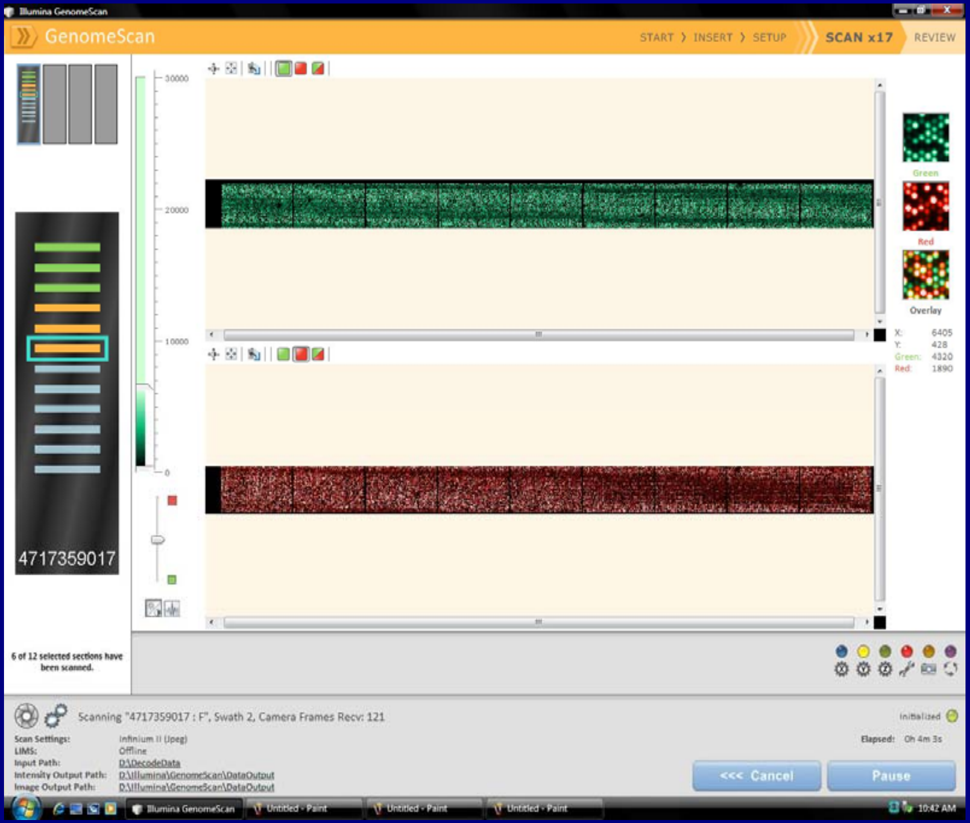
iScan Equipment

- Generates image files
- Later GenomeStudio Software converts images into genotypes and SNP data files

Scanning Samples



X: 6405
Y: 428
Green: 4320
Red: 1890

6 of 12 selected sections have been scanned.

Scanning "4717359017 : F", Swath 2, Camera Frames Recv: 121

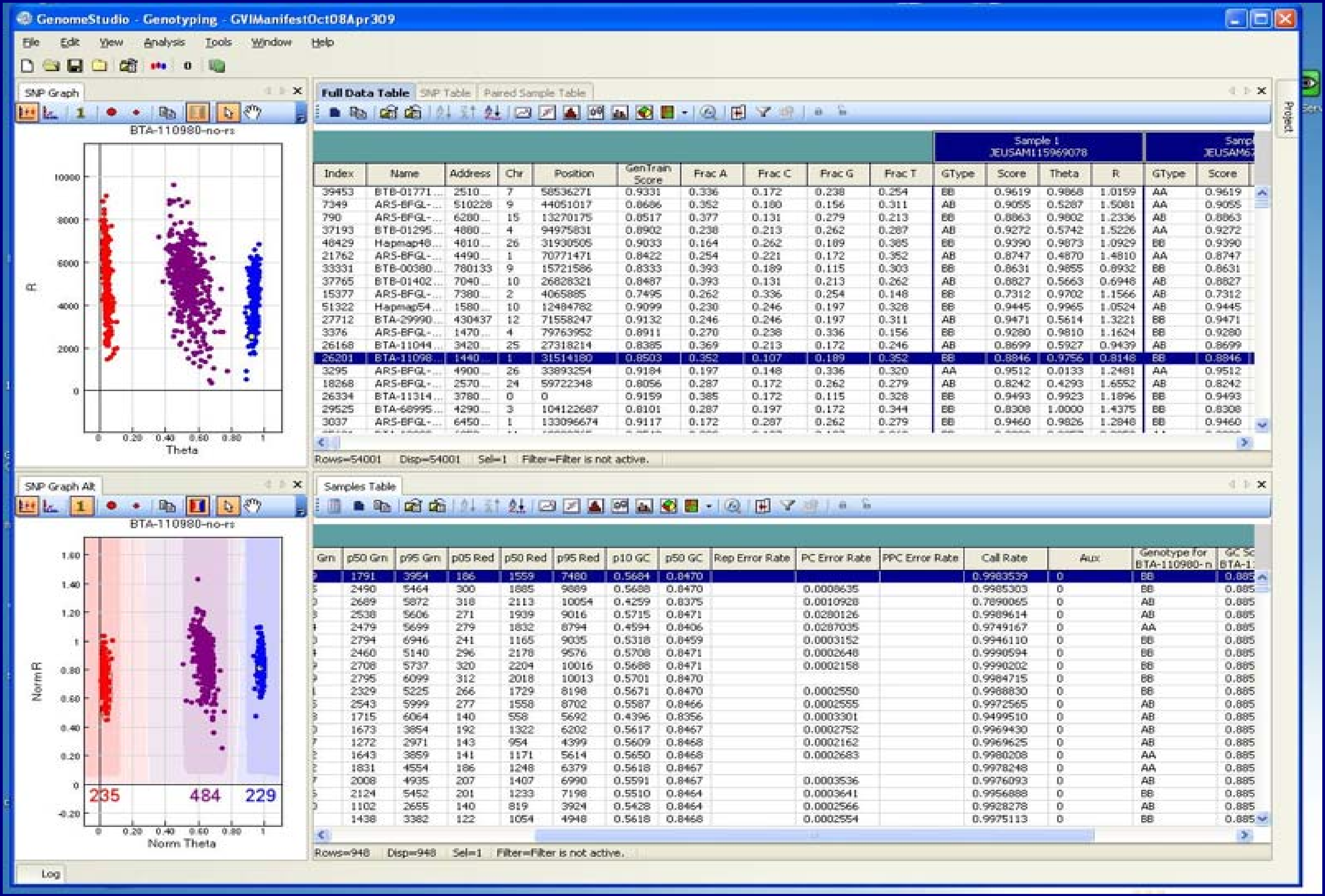
Initialized

Scan Settings: Infinium II (Jpeg)
LIMS: Offline
Input Path: D:\DecodeData
Intensity Output Path: D:\Illumina\GenomeScan\DataOutput
Image Output Path: D:\Illumina\GenomeScan\DataOutput

Elapsed: 0h 4m 3s

- Red and Green Dyes, individual or overlay
- Each bar is a different sample
- Scan Status indicated

GENETICVISIONS



Index	Name	Address	Chr	Position	GenTrain Score	Frac A	Frac C	Frac G	Frac T	Sample 1 JEUSAM115969078 GType	Score	Theta	R	Samp JEUSAM6 GType	Score
39453	BTB-01771...	2510...	7	58536271	0.9331	0.336	0.172	0.238	0.254	BB	0.9619	0.9868	1.0159	AA	0.9619
7349	ARS-BFGL-...	510228	9	44051017	0.8686	0.352	0.180	0.156	0.311	AB	0.9055	0.5287	1.5081	AA	0.9055
790	ARS-BFGL-...	6280...	15	13270175	0.8517	0.377	0.131	0.279	0.213	BB	0.8863	0.9802	1.2336	AB	0.8863
37193	BTB-01295...	4880...	4	94975831	0.8902	0.238	0.213	0.262	0.287	AB	0.9272	0.5742	1.5226	AA	0.9272
48429	Hapmap48...	4810...	26	31930505	0.9033	0.164	0.262	0.189	0.385	BB	0.9390	0.9873	1.0929	BB	0.9390
21762	ARS-BFGL-...	4490...	1	70771471	0.8422	0.254	0.221	0.172	0.352	AB	0.8747	0.4870	1.4810	AA	0.8747
33331	BTB-00380...	780133	9	15721586	0.8333	0.393	0.189	0.115	0.303	BB	0.8631	0.9855	0.8932	BB	0.8631
37765	BTB-01402...	7040...	10	26828321	0.8487	0.393	0.131	0.213	0.262	AB	0.8827	0.5663	0.6948	AB	0.8827
15377	ARS-BFGL-...	7380...	2	4065885	0.7495	0.262	0.336	0.254	0.148	BB	0.7312	0.9702	1.1566	AB	0.7312
51322	Hapmap54...	1580...	10	12484782	0.9099	0.230	0.246	0.197	0.328	BB	0.9445	0.9965	1.0524	AB	0.9445
27712	BTA-29990...	430437	12	71558247	0.9132	0.246	0.246	0.197	0.311	AB	0.9471	0.5614	1.3221	BB	0.9471
3376	ARS-BFGL-...	1470...	4	79763952	0.8911	0.270	0.238	0.336	0.156	BB	0.9280	0.9810	1.1624	BB	0.9280
26168	BTA-11044...	3420...	25	27318214	0.8385	0.369	0.213	0.172	0.246	AB	0.8699	0.5927	0.9439	AB	0.8699
26201	BTA-11098...	1440...	1	31514180	0.8503	0.352	0.107	0.189	0.352	BB	0.8846	0.9756	0.8148	BB	0.8846
3295	ARS-BFGL-...	4900...	26	33893254	0.9184	0.197	0.148	0.336	0.320	AA	0.9512	0.0133	1.2481	AA	0.9512
18268	ARS-BFGL-...	2570...	24	59722348	0.8056	0.287	0.172	0.262	0.279	AB	0.8242	0.4293	1.6552	AB	0.8242
26334	BTA-11314...	3780...	0	0	0.9159	0.385	0.172	0.115	0.328	BB	0.9493	0.9923	1.1896	BB	0.9493
29525	BTA-68995...	4290...	3	104122687	0.8101	0.287	0.197	0.172	0.344	BB	0.8308	1.0000	1.4375	BB	0.8308
3037	ARS-BFGL-...	6450...	1	133096674	0.9117	0.172	0.287	0.262	0.279	BB	0.9460	0.9826	1.2848	BB	0.9460

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p50 Grn	p95 Grn	p05 Red	p50 Red	p95 Red	p10 GC	p50 GC	Rep Error Rate	PC Error Rate	PPC Error Rate	Call Rate	Aux	Genotype for BTA-110980-n	GC Sc BTA-1
1791	3954	186	1559	7480	0.5684	0.8470				0.9983539	0	BB	0.885
2490	5464	300	1885	9889	0.5688	0.8470		0.0008635		0.9985303	0	BB	0.885
2689	5872	318	2113	10054	0.4259	0.8375		0.0010928		0.7890065	0	AB	0.885
2538	5606	271	1939	9016	0.5715	0.8471		0.0280126		0.9989614	0	AB	0.885
2479	5699	279	1832	8794	0.4594	0.8406		0.0287035		0.9749167	0	AA	0.885
2794	6946	241	1165	9035	0.5318	0.8459		0.0003152		0.9946110	0	BB	0.885
2460	5140	296	2178	9576	0.5708	0.8471		0.0002648		0.9990594	0	BB	0.885
2708	5737	320	2204	10016	0.5688	0.8471		0.0002158		0.9990202	0	BB	0.885
2795	6099	312	2018	10013	0.5701	0.8470				0.9984715	0	BB	0.885
2329	5225	266	1729	8198	0.5671	0.8470		0.0002550		0.9988830	0	BB	0.885
2543	5999	277	1558	8702	0.5587	0.8466		0.0002555		0.9972565	0	AB	0.885
1715	6064	140	558	5692	0.4396	0.8356		0.0003301		0.9499510	0	AB	0.885
1673	3854	192	1322	6202	0.5617	0.8467		0.0002752		0.9969430	0	AB	0.885
1272	2971	143	954	4399	0.5609	0.8468		0.0002162		0.9969625	0	AB	0.885
1643	3859	141	1171	5614	0.5650	0.8468		0.0002683		0.9980208	0	AA	0.885
1831	4554	186	1248	6379	0.5618	0.8467				0.9978248	0	AA	0.885
2008	4935	207	1407	6990	0.5591	0.8467		0.0003536		0.9976093	0	AB	0.885
2124	5452	201	1233	7198	0.5510	0.8464		0.0003641		0.9956888	0	BB	0.885
1102	2655	140	819	3924	0.5428	0.8464		0.0002566		0.9928278	0	AB	0.885
1438	3382	122	1054	4948	0.5618	0.8468		0.0002554		0.9975113	0	BB	0.885

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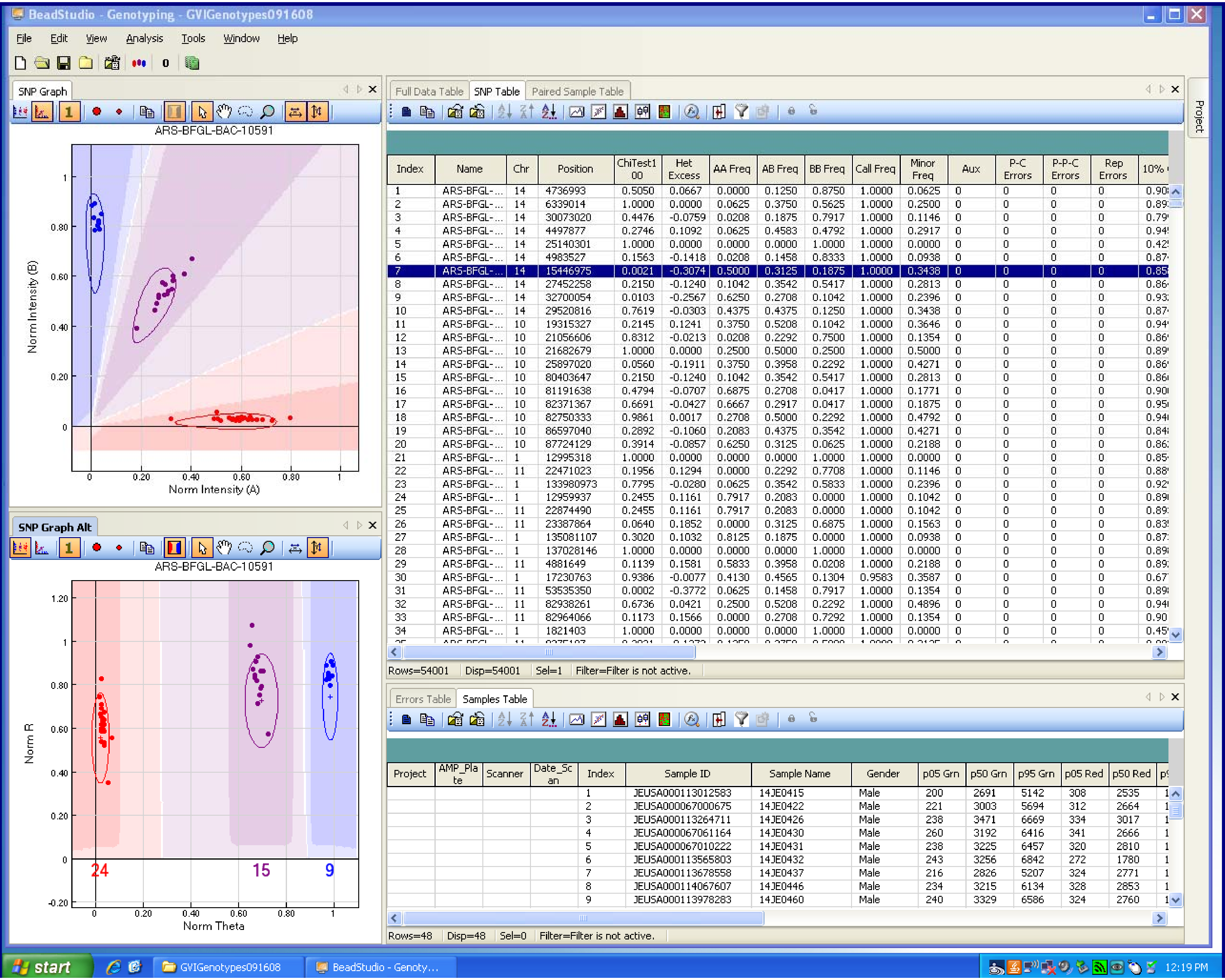

Index	Name	Chr	Position	ChiTest100	Het Excess	AA Freq	AB Freq	BB Freq	Call Freq	Minor Freq	Aux	P-C Errors	P-P-C Errors	Rep Errors	10%
1	ARS-BFGL-...	14	4736993	0.5050	0.0667	0.0000	0.1250	0.8750	1.0000	0.0625	0	0	0	0	0.90
2	ARS-BFGL-...	14	6339014	1.0000	0.0000	0.0625	0.3750	0.5625	1.0000	0.2500	0	0	0	0	0.89
3	ARS-BFGL-...	14	30073020	0.4476	-0.0759	0.0208	0.1875	0.7917	1.0000	0.1146	0	0	0	0	0.79
4	ARS-BFGL-...	14	4497877	0.2746	0.1092	0.0625	0.4583	0.4792	1.0000	0.2917	0	0	0	0	0.94
5	ARS-BFGL-...	14	25140301	1.0000	0.0000	0.0000	0.0000	1.0000	1.0000	0.0000	0	0	0	0	0.42
6	ARS-BFGL-...	14	4983527	0.1563	-0.1418	0.0208	0.1458	0.8333	1.0000	0.0938	0	0	0	0	0.87
7	ARS-BFGL-...	14	15446975	0.0021	-0.3074	0.5000	0.3125	0.1875	1.0000	0.3438	0	0	0	0	0.85
8	ARS-BFGL-...	14	27452258	0.2150	-0.1240	0.1042	0.3542	0.5417	1.0000	0.2813	0	0	0	0	0.86
9	ARS-BFGL-...	14	32700054	0.0103	-0.2567	0.6250	0.2708	0.1042	1.0000	0.2396	0	0	0	0	0.93
10	ARS-BFGL-...	14	29520816	0.7619	-0.0303	0.4375	0.4375	0.1250	1.0000	0.3438	0	0	0	0	0.87
11	ARS-BFGL-...	10	19315327	0.2145	0.1241	0.3750	0.5208	0.1042	1.0000	0.3646	0	0	0	0	0.94
12	ARS-BFGL-...	10	21056606	0.8312	-0.0213	0.0208	0.2292	0.7500	1.0000	0.1354	0	0	0	0	0.86
13	ARS-BFGL-...	10	21682679	1.0000	0.0000	0.2500	0.5000	0.2500	1.0000	0.5000	0	0	0	0	0.89
14	ARS-BFGL-...	10	25897020	0.0560	-0.1911	0.3750	0.3958	0.2292	1.0000	0.4271	0	0	0	0	0.86
15	ARS-BFGL-...	10	80403647	0.2150	-0.1240	0.1042	0.3542	0.5417	1.0000	0.2813	0	0	0	0	0.86
16	ARS-BFGL-...	10	81191638	0.4794	-0.0707	0.6875	0.2708	0.0417	1.0000	0.1771	0	0	0	0	0.90
17	ARS-BFGL-...	10	82371367	0.6691	-0.0427	0.6667	0.2917	0.0417	1.0000	0.1875	0	0	0	0	0.95
18	ARS-BFGL-...	10	82750333	0.9861	0.0017	0.2708	0.5000	0.2292	1.0000	0.4792	0	0	0	0	0.94
19	ARS-BFGL-...	10	86597040	0.2892	-0.1060	0.2083	0.4375	0.3542	1.0000	0.4271	0	0	0	0	0.84
20	ARS-BFGL-...	10	87724129	0.3914	-0.0857	0.6250	0.3125	0.0625	1.0000	0.2188	0	0	0	0	0.86
21	ARS-BFGL-...	1	12995318	1.0000	0.0000	0.0000	0.0000	1.0000	1.0000	0.0000	0	0	0	0	0.85
22	ARS-BFGL-...	11	22471023	0.1956	0.1294	0.0000	0.2292	0.7708	1.0000	0.1146	0	0	0	0	0.88
23	ARS-BFGL-...	1	133980973	0.7795	-0.0280	0.0625	0.3542	0.5833	1.0000	0.2396	0	0	0	0	0.92
24	ARS-BFGL-...	1	12959937	0.2455	0.1161	0.7917	0.2083	0.0000	1.0000	0.1042	0	0	0	0	0.89
25	ARS-BFGL-...	11	22874490	0.2455	0.1161	0.7917	0.2083	0.0000	1.0000	0.1042	0	0	0	0	0.89
26	ARS-BFGL-...	11	23387864	0.0640	0.1852	0.0000	0.3125	0.6875	1.0000	0.1563	0	0	0	0	0.83
27	ARS-BFGL-...	1	135081107	0.3020	0.1032	0.8125	0.1875	0.0000	1.0000	0.0938	0	0	0	0	0.87
28	ARS-BFGL-...	1	137028146	1.0000	0.0000	0.0000	0.0000	1.0000	1.0000	0.0000	0	0	0	0	0.89
29	ARS-BFGL-...	11	4881649	0.1139	0.1581	0.5833	0.3958	0.0208	1.0000	0.2188	0	0	0	0	0.89
30	ARS-BFGL-...	1	17230763	0.9386	-0.0077	0.4130	0.4565	0.1304	0.9583	0.3587	0	0	0	0	0.67
31	ARS-BFGL-...	11	53535350	0.0002	-0.3772	0.0625	0.1458	0.7917	1.0000	0.1354	0	0	0	0	0.89
32	ARS-BFGL-...	11	82938261	0.6736	0.0421	0.2500	0.5208	0.2292	1.0000	0.4896	0	0	0	0	0.94
33	ARS-BFGL-...	11	82964066	0.1173	0.1566	0.0000	0.2708	0.7292	1.0000	0.1354	0	0	0	0	0.90
34	ARS-BFGL-...	1	1821403	1.0000	0.0000	0.0000	0.0000	1.0000	1.0000	0.0000	0	0	0	0	0.45

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Project	AMP_Plate	Scanner	Date_Scan	Index	Sample ID	Sample Name	Gender	p05 Grn	p50 Grn	p95 Grn	p05 Red	p50 Red	p
				1	JEUSA000113012583	14JE0415	Male	200	2691	5142	308	2535	1
				2	JEUSA000067000675	14JE0422	Male	221	3003	5694	312	2664	1
				3	JEUSA000113264711	14JE0426	Male	238	3471	6669	334	3017	1
				4	JEUSA000067061164	14JE0430	Male	260	3192	6416	341	2666	1
				5	JEUSA000067010222	14JE0431	Male	238	3225	6457	320	2810	1
				6	JEUSA000113565803	14JE0432	Male	243	3256	6842	272	1780	1
				7	JEUSA000113678558	14JE0437	Male	216	2826	5207	324	2771	1
				8	JEUSA000114067607	14JE0446	Male	234	3215	6134	328	2853	1
				9	JEUSA000113978283	14JE0460	Male	240	3329	6586	324	2760	1

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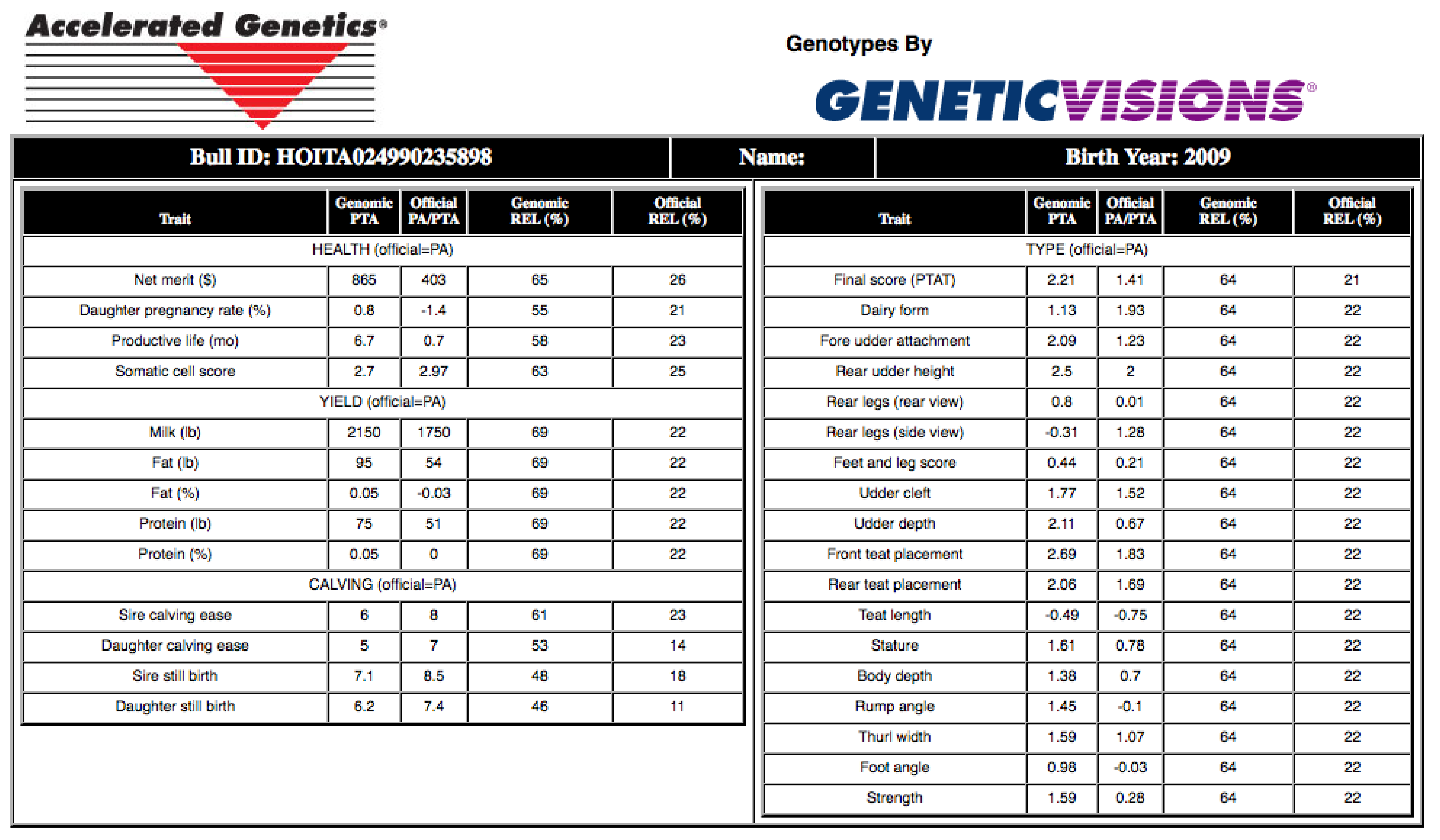

Accelerated Genetics®

Genotypes By

GENETICVISIONS®

Bull ID: HOITA024990235898	Name:	Birth Year: 2009

Trait	Genomic PTA	Official PA/PTA	Genomic REL (%)	Official REL (%)
HEALTH (official=PA)				
Net merit ($)	865	403	65	26
Daughter pregnancy rate (%)	0.8	-1.4	55	21
Productive life (mo)	6.7	0.7	58	23
Somatic cell score	2.7	2.97	63	25
YIELD (official=PA)				
Milk (lb)	2150	1750	69	22
Fat (lb)	95	54	69	22
Fat (%)	0.05	-0.03	69	22
Protein (lb)	75	51	69	22
Protein (%)	0.05	0	69	22
CALVING (official=PA)				
Sire calving ease	6	8	61	23
Daughter calving ease	5	7	53	14
Sire still birth	7.1	8.5	48	18
Daughter still birth	6.2	7.4	46	11

Trait	Genomic PTA	Official PA/PTA	Genomic REL (%)	Official REL (%)
TYPE (official=PA)				
Final score (PTAT)	2.21	1.41	64	21
Dairy form	1.13	1.93	64	22
Fore udder attachment	2.09	1.23	64	22
Rear udder height	2.5	2	64	22
Rear legs (rear view)	0.8	0.01	64	22
Rear legs (side view)	-0.31	1.28	64	22
Feet and leg score	0.44	0.21	64	22
Udder cleft	1.77	1.52	64	22
Udder depth	2.11	0.67	64	22
Front teat placement	2.69	1.83	64	22
Rear teat placement	2.06	1.69	64	22
Teat length	-0.49	-0.75	64	22
Stature	1.61	0.78	64	22
Body depth	1.38	0.7	64	22
Rump angle	1.45	-0.1	64	22
Thurl width	1.59	1.07	64	22
Foot angle	0.98	-0.03	64	22
Strength	1.59	0.28	64	22

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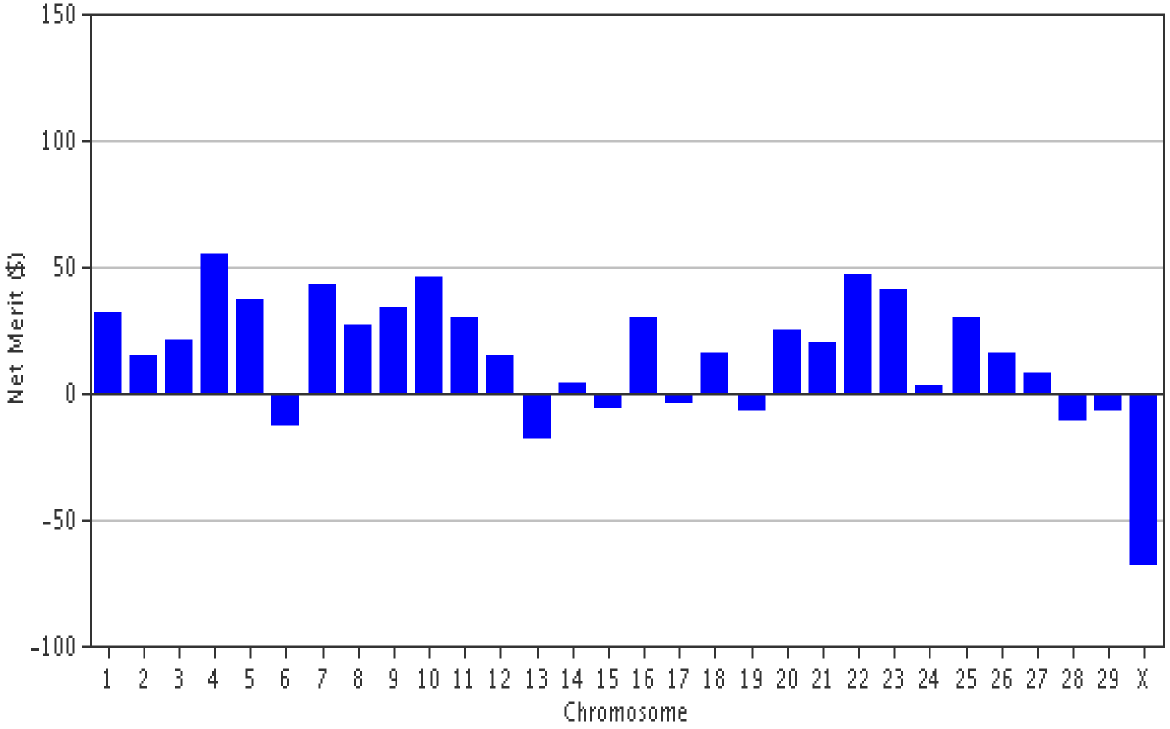
Application genPTAs – Full Sibs

Animal	NM Trad	NM Gen	PL Trad	PL Gen
Bull A	415.5	411	1.3	1.3
Bull B	415.5	207	1.3	-0.2
Bull C	415.5	472	1.3	1.4
Bull 1	546.5	541	4.7	4.7
Bull 2	546.5	813	4.7	7.9
Bull D	378	273	3.6	1.2
Bull E	378	237	3.6	2.3

Chromosomal PTA of Net Merit for KEYSTONE POTTER (014HO03597, housa000128367894)

PTA NM$: +$37, **Rel NM$:** 71%



GENETICVISIONS

Impact On Selection Programs

- Significantly increases the accuracy of predicting an individual's true genetic potential prior to performance or progeny testing.
- Focus is only on additive genetics.
- Has resulted in removal of ~35% of the bulls that would have entered AI young sire progeny test programs.
- In the future, could limit or for go progeny testing.

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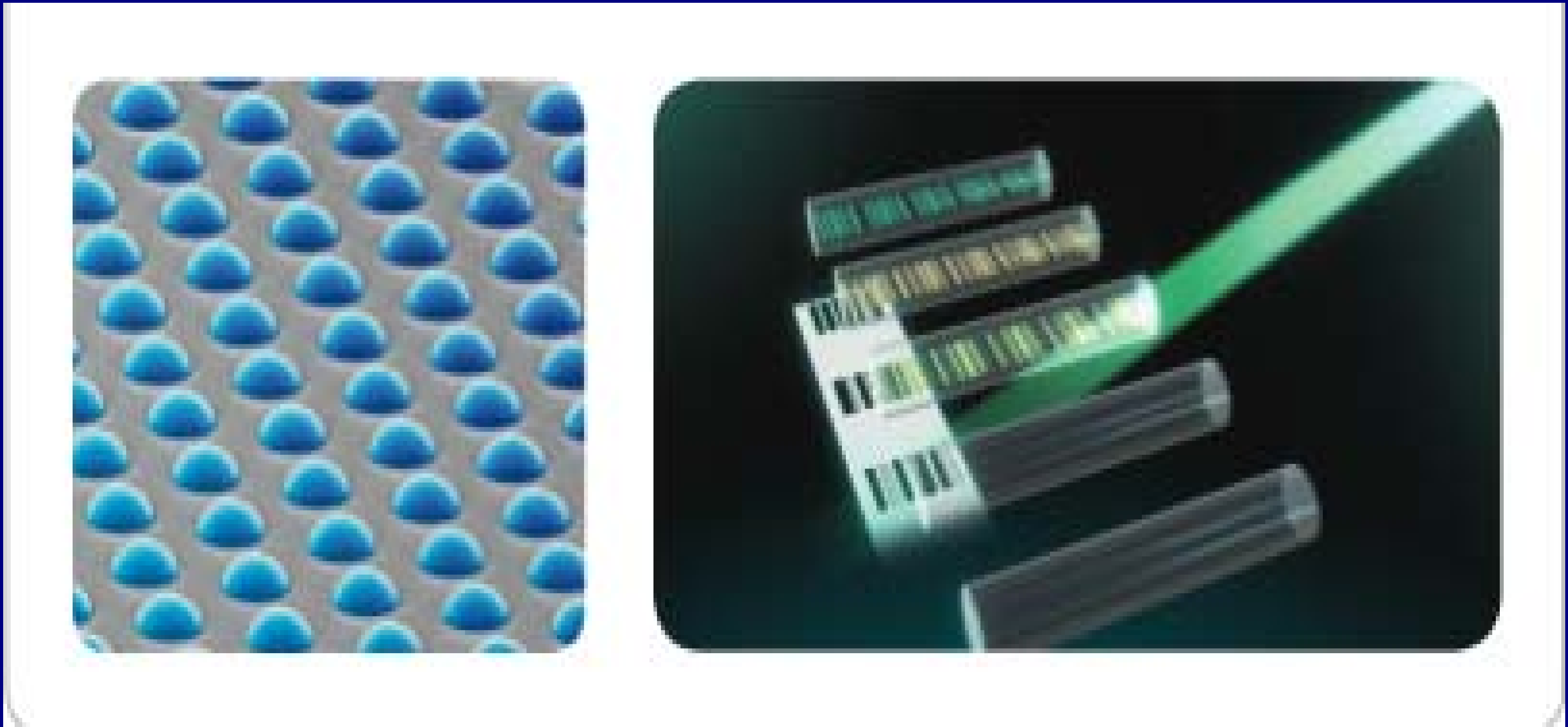
Two Illumina Technologies



VeraCode Universal Oligo Bead Technology

- Low-Plex Assays
- 1 to 384 SNPs
- Custom Design Assays
- Kit beads in 8 well strip plates

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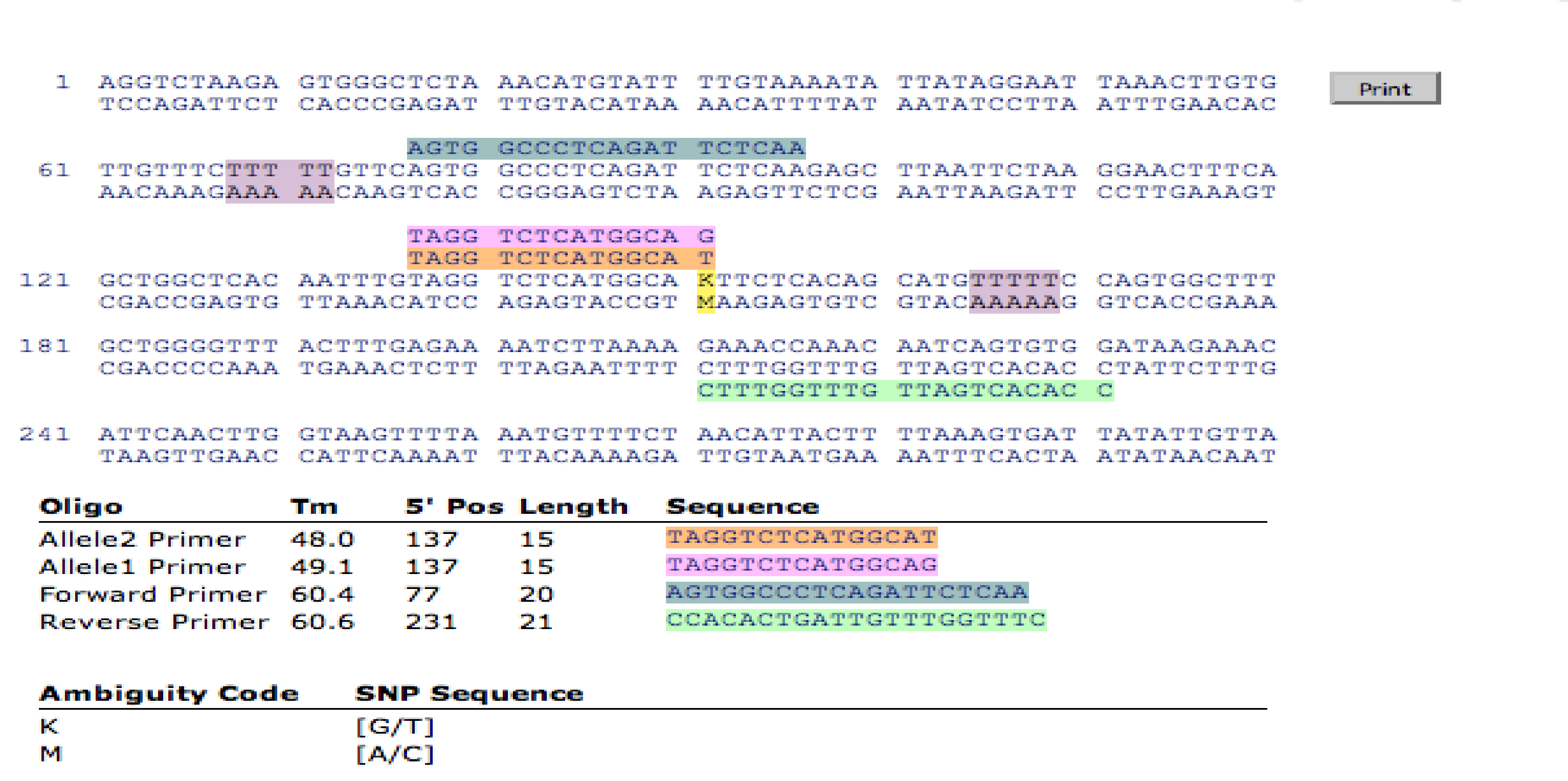
Illumina VeraCode Assay Designer



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                           AGTG GCCCTCAGAT TCTCAA
 61  TTGTTTCTTT TTGTTCAGTG GCCCTCAGAT TCTCAAGAGC TTAATTCTAA GGAACTTTCA
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                           TAGG TCTCATGGCA G
                           TAGG TCTCATGGCA T
121  GCTGGCTCAC AATTTGTAGG TCTCATGGCA KTTCTCACAG CATGTTTTTC CAGTGGCTTT
     CGACCGAGTG TTAAACATCC AGAGTACCGT MAAGAGTGTC GTACAAAAAG GTCACCGAAA

181  GCTGGGGTTT ACTTTGAGAA AATCTTAAAA GAAACCAAAC AATCAGTGTG GATAAGAAAC
     CGACCCCAAA TGAAACTCTT TTAGAATTTT CTTTGGTTTG TTAGTCACAC CTATTCTTTG
                                      CTTTGGTTTG TTAGTCACAC C

241  ATTCAACTTG GTAAGTTTTA AATGTTTTCT AACATTACTT TTAAAGTGAT TATATTGTTA
     TAAGTTGAAC CATTCAAAAT TTACAAAAGA TTGTAATGAA AATTTCACTA ATATAACAAT
```

Oligo	Tm	5' Pos	Length	Sequence
Allele2 Primer	48.0	137	15	TAGGTCTCATGGCAT
Allele1 Primer	49.1	137	15	TAGGTCTCATGGCAG
Forward Primer	60.4	77	20	AGTGGCCCTCAGATTCTCAA
Reverse Primer	60.6	231	21	CCACACTGATTGTTTGGTTTC

Ambiguity Code	SNP Sequence
K	[G/T]
M	[A/C]

GENETICVISIONS

Overview

Multiplex PCR

↓

EXO/SAP

↓

ASPE PCR – biotin label

↓

Kit beads strip well plates

↓

Hybridize to capture specific sequence - VeraCode Beads

↓

Streptavidin

↓

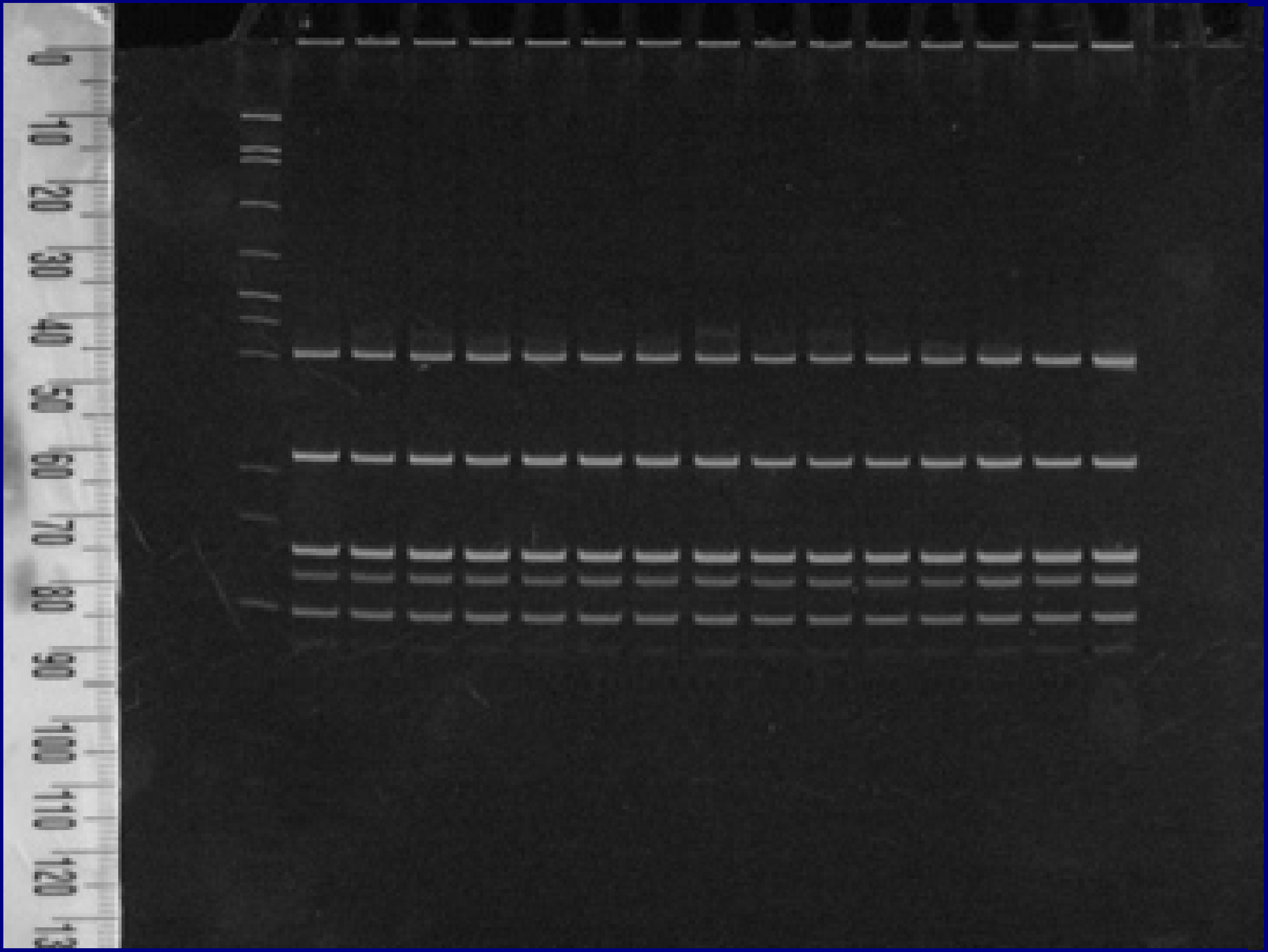
BeadXpress Reader

↓

GenomeStudio Software - Genotypes

GENETICVISIONS

Multiplex PCR



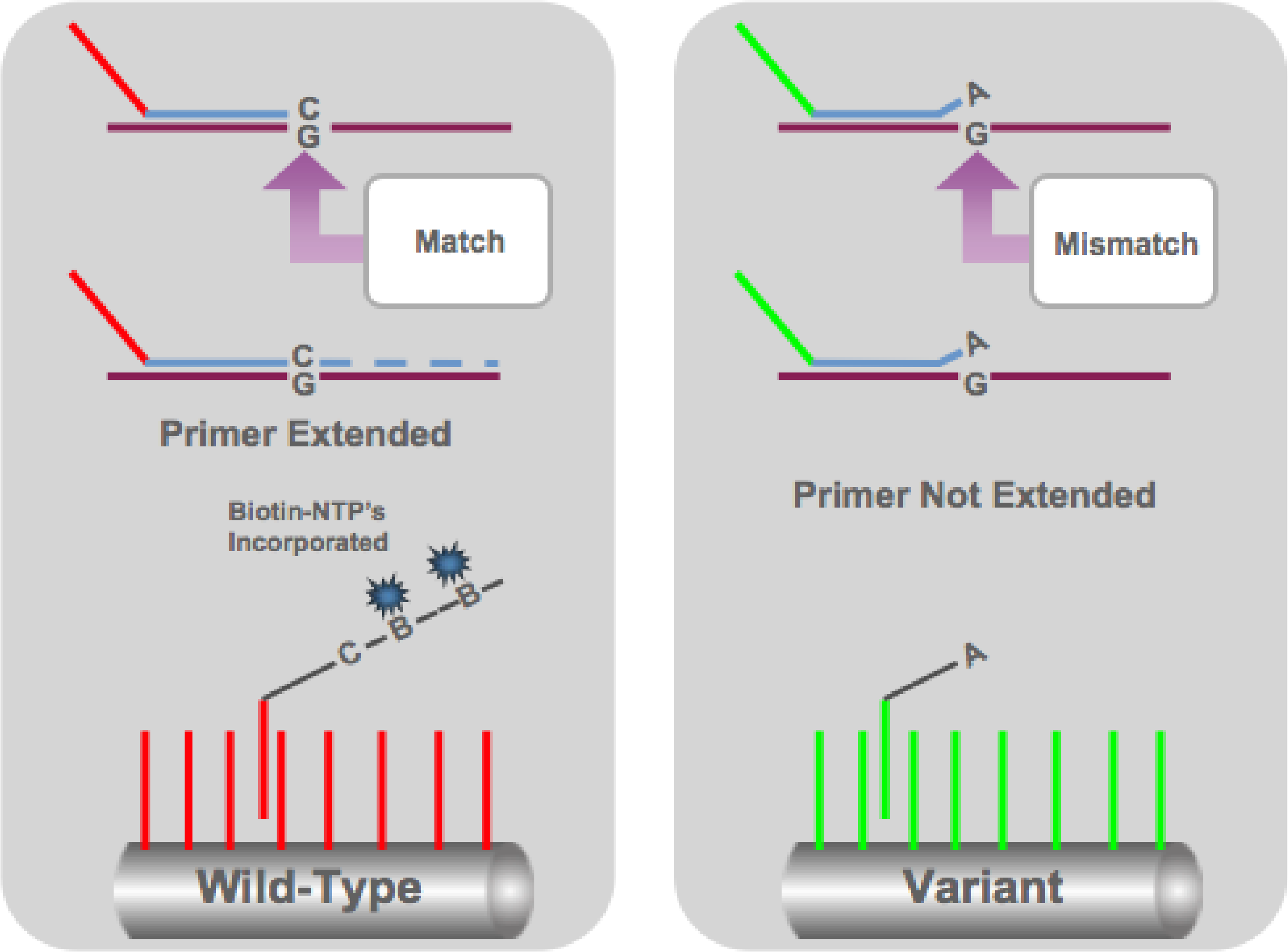
GENETICVISIONS

Each SNP - Capture Sequence ASPE Oligo

GGCACTTCGCACGGGTTACGAA5'-----------ALLELE1-------G3'
(IllumiCode or VeraCode BeadCode) (ASPE Oligo)

TACACAGCGACCGTACCATCGT5'-----------ALLELE2--------T3'
(IllumiCode or VeraCode BeadCode) (ASPE Oligo)

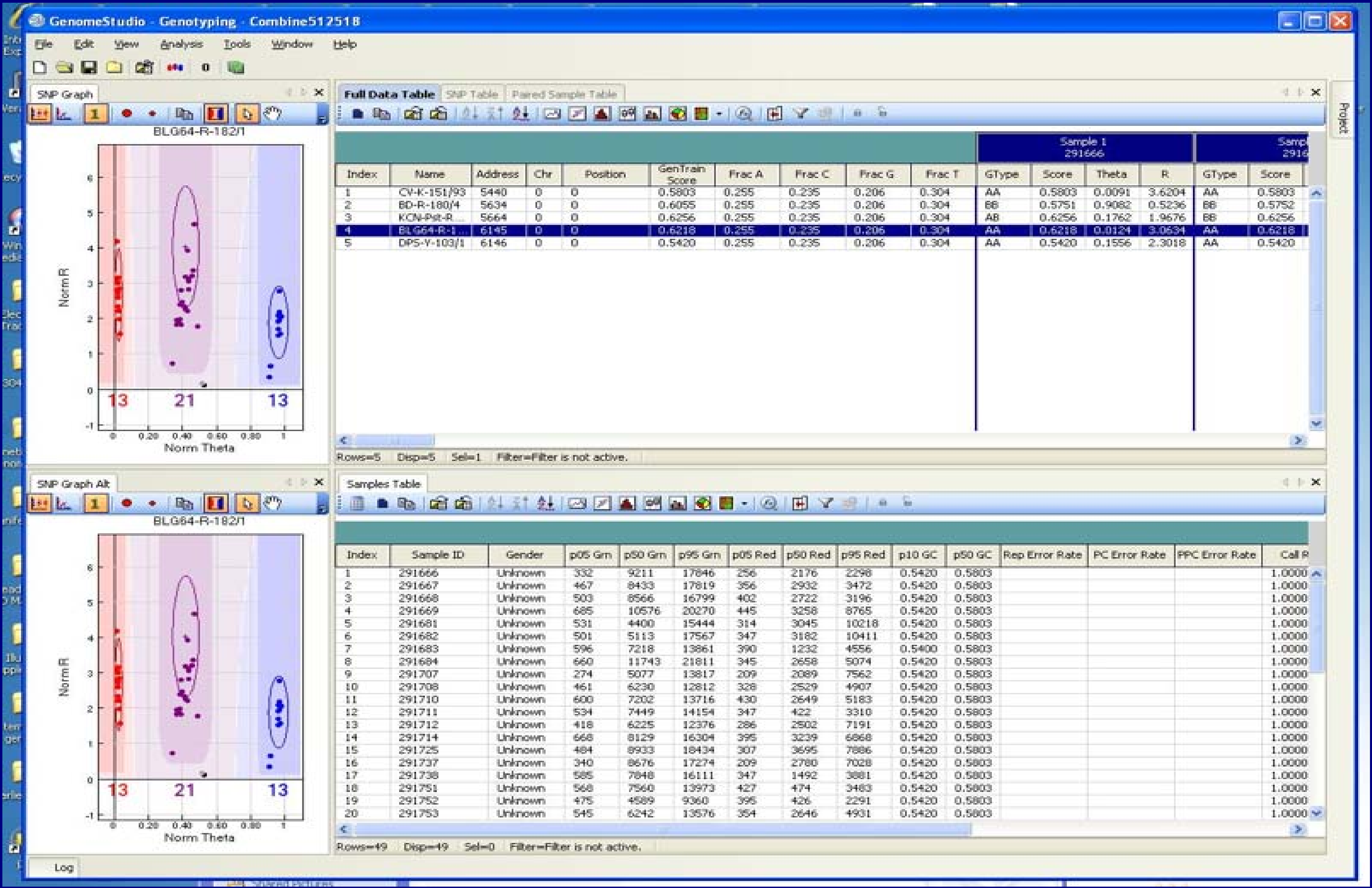
Universal Oligo Capture Beads



Allele Specific Primer Extension Assays

illumina

GENETICVISIONS



										Sample 1 291666				Samp 2916	
Index	Name	Address	Chr	Position	GenTrain Score	Frac A	Frac C	Frac G	Frac T	GType	Score	Theta	R	GType	Score
1	CV-K-151/93	5440	0	0	0.5803	0.255	0.235	0.206	0.304	AA	0.5803	0.0091	3.6204	AA	0.5803
2	BD-R-180/4	5634	0	0	0.6055	0.255	0.235	0.206	0.304	BB	0.5751	0.9082	0.5236	BB	0.5752
3	KCN-Pst-R...	5664	0	0	0.6256	0.255	0.235	0.206	0.304	AB	0.6256	0.1762	1.9676	BB	0.6256
4	BLG64-R-1...	6145	0	0	0.6218	0.255	0.235	0.206	0.304	AA	0.6218	0.0124	3.0634	AA	0.6218
5	DPS-Y-103/1	6146	0	0	0.5420	0.255	0.235	0.206	0.304	AA	0.5420	0.1556	2.3018	AA	0.5420

Rows=5 Disp=5 Sel=1 Filter=Filter is not active.

Index	Sample ID	Gender	p05 Grn	p50 Grn	p95 Grn	p05 Red	p50 Red	p95 Red	p10 GC	p50 GC	Rep Error Rate	PC Error Rate	PPC Error Rate	Call R
1	291666	Unknown	332	9211	17846	256	2176	2298	0.5420	0.5803				1.0000
2	291667	Unknown	467	8433	17819	356	2932	3472	0.5420	0.5803				1.0000
3	291668	Unknown	503	8566	16799	402	2722	3196	0.5420	0.5803				1.0000
4	291669	Unknown	685	10576	20270	445	3258	8765	0.5420	0.5803				1.0000
5	291681	Unknown	531	4400	15444	314	3045	10218	0.5420	0.5803				1.0000
6	291682	Unknown	501	5113	17567	347	3182	10411	0.5420	0.5803				1.0000
7	291683	Unknown	596	7218	13861	390	1232	4556	0.5400	0.5803				1.0000
8	291684	Unknown	660	11743	21811	345	2658	5074	0.5420	0.5803				1.0000
9	291707	Unknown	274	5077	13817	209	2089	7562	0.5420	0.5803				1.0000
10	291708	Unknown	461	6230	12812	328	2529	4907	0.5420	0.5803				1.0000
11	291710	Unknown	600	7202	13716	430	2649	5183	0.5420	0.5803				1.0000
12	291711	Unknown	534	7449	14154	347	422	3310	0.5420	0.5803				1.0000
13	291712	Unknown	418	6225	12376	286	2502	7191	0.5420	0.5803				1.0000
14	291714	Unknown	668	8129	16304	395	3239	6868	0.5420	0.5803				1.0000
15	291725	Unknown	484	8933	18434	307	3695	7886	0.5420	0.5803				1.0000
16	291737	Unknown	340	8676	17274	209	2780	7028	0.5420	0.5803				1.0000
17	291738	Unknown	585	7848	16111	347	1492	3881	0.5420	0.5803				1.0000
18	291751	Unknown	568	7560	13973	427	474	3483	0.5420	0.5803				1.0000
19	291752	Unknown	475	4589	9360	395	426	2291	0.5420	0.5803				1.0000
20	291753	Unknown	545	6242	13576	354	2646	4931	0.5420	0.5803				1.0000

Rows=49 Disp=49 Sel=0 Filter=Filter is not active.

GENETICVISIONS

Summary

- Bov50SNP BeadChip is a tool that is enhancing selection of dairy cattle.
- Standard platform used across three dairy breeds with data used to generate an official genetic evaluation.
- VeraCode Universial Olgo Beads provides custom design low-plex assays for routine screening.

GENETICVISIONS