Equine Genetics and Thoroughbred Parentage Testing

Organised by a standing committee: YES NO

Meeting information

Date: Thursday July 11th
Time: 2:30-6:00 pm
Number of participants: 83

Chair

Name: Cecilia Penedo
Affiliation: Veterinary Genetics Laboratory, VGL, UC Davis.
Contact email: mctorrespenedo@ucdavis.edu

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Agenda

2:30 PM		**Welcoming Remarks.**
2:40 PM		**Horse Comparison Test.**
3:20 PM		**Donkey Comparison Test.**
3:40 PM		**Horse SNP Comparison Test.**
4:00 PM		**Coffee/Tea Break.**
4:30 PM		**ISBC Requirements Update.**
4:50 PM	79935	**Development of an AgriSeq™ targeted GBS panel for Equine SNP Parentage Verification and Sire/Dam Allocation.** P Flynn*[1,3], R Morrin-O'Donnell[1], J Carlsson[3], P Siddavatam[2], S Chadaram[2], H Suren[2], C Carrasco[2], and R Conrad[2], [1]*Weatherbys Scientific, Unit F1, M7 Business Park, Newhall, Naas, Ireland, W91 VX86*, [2]*Thermo Fisher Scientific, 2130 Woodward Street, Austin, TX, USA, 78744*, [3]*University College Dublin, School of Biology & Environmental Science, UCD, Belfield, Dublin, Ireland.*
5:05 PM	79646	**Development of an equine SNP parentage panel which complements historic and current high density genotyping resources.** R.G. Tait Jr.*[1], D.J.G. Arts[2], R. Ferretti[1], H. Hofeneder-Barclay[3], B. Simpson[1], L. Kock[1], and J. Qiu[1], [1]*Neogen GeneSeek Operations, Lincoln, NE, USA*, [2]*KWPN Royal Dutch Sport Horse Studbook, Ermelo, Netherlands*, [3]*Neogen Europe, Ayr, Scotland.*
5:20 PM	79608	**Potential methods of detecting indiscriminate genetic manipulation in thoroughbred racehorses.** Teruaki Tozaki*[1], Aoi Ohnuma[1], Mio Kikuchi[1], Hironaga Kakoi[1], Kei-ichi Hirota[1], Kanichi Kusano[2], and Shun-ichi Nagata[1], [1]*Genetic Analysis Department, Laboratory of Racing Chemistry, Utsunomiya, Tochigi, Japan*, [2]*Ritto Training Center Racehorse Hospital, Japan Racing Association, Ritto, Shiga, Japan.*
5:35 PM		**Election of Committee Members and Any Other Business.**
6:00 PM		**Meeting ends.**

Summary of the meeting

Including votes, decisions taken and plans for future conferences

1. Horse STR Comparison test 2018-2019

Duty laboratory: Dr. med. vet. Torsten Brendel, Eurofins Medigenomix, Germany.

DNA extraction method: chemagic DNA Blood100 Kit, Chemagen (PerkinElmer)/ Maxwell 16 FFS Nucleic Acid Extraction Kit (Promega)

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Samples provided

Sample ID	ng/µl	Volume (µl)	Breed
HCT_01	43	50	Hanoveranian horse
HCT_02	41	50	German riding pony
HCT_03	43	50	n.a.
HCT_04 - Reference	47	50	Haflinger
HCT_05	64	50	Westphalian horse
HCT_06 - Reference	46	50	Oldenburg horse
HCT_07	51	50	Württemberger
HCT_08	52	50	Haflinger
HCT_09	37	50	Oldenburg horse
HCT_10	29	50	n.a.
HCT_11	146	50	Thoroughbred
HCT_12	93	50	Thoroughbred
HCT_13	186	50	Thoroughbred
HCT_14	111	50	Thoroughbred
HCT_15	164	50	Thoroughbred
HCT_16	130	50	Thoroughbred
HCT_17	178	50	Thoroughbred
HCT_18	194	50	Thoroughbred
HCT_19	134	50	Thoroughbred
HCT_20	157	50	Thoroughbred

Marker Consensus

Locus	Percent Consensus	Incidence
HMS6	98.50	11 labs (1 with duplicate sample, 1 with 10)
ASB2	98.09	23 labs (1 with duplicate sample, "B" of sample HCT11 often missing)
VHL20	99.59	7 labs (1 with duplicate sample)
HMS2	99.71	4 labs (1 with duplicate sample)
AHT5	96.92	20 labs (3 with >8, 1 with duplicate sample)
HTG4	99.83	3 labs (1 with duplicate sample)
AHT4	99.65	4 labs (1 with duplicate sample)
ASB17	98.77	8 labs (1 with 15, 1 empty, 1 with duplicate sample)
ASB23	98.55	7 labs (1 with duplicate sample)
HMS7	99.25	9 labs (1 with duplicate sample)
HTG10	98.65	12 labs (1 with duplicate sample, 1 empty)
HMS3	97.45	14 labs (1 with duplicate sample, "M" of samples HCT2 and HCT05)

Parentage questions:

Question 1 - Does HCT_07 qualify as the offspring of HCT_08?

91/94 (97%) labs answered "No"

Question 2 - Are the parents of HCT_01 among samples tested? If your answer is yes, please provide sample IDs.

91/94 (97%) labs answered "No"

Lab Performance:

Rank	Concordance Range	% Labs
1	100 – 98%	86%
2	97.9 – 95%	5%
3	94.9 – 90%	5%
4	89.9 – 80%	3%
5	Below 80%	0%

Average concordance: 98.80% +- 0.03

Horse Extra Panel – TKY markers:

For marker TKY337, in some samples, discrepancies (highlighted in the image below) were seen due to different primer pairs used for amplification.

A 19-bp deletion in some samples explained these results.

TKY337 sequence

GATCCTAAGAAGGAAATAAAGAAGCCAGTAAGACTCAAGAGGTCAATCAGAGGAGAAATTTTTGAGCAGAGC
AGGGTTTAATTACCGAGACTTAGATTGTTTGATGCTAAGTTTGTTACAGAACAACAGGGAAAAGAGGTGAAAG
AAGTAAAGAGTTGGTGTA**CACACACACACACACACACACACACACACA**TGCAGAATTAGAAAGACATGAGGG
GCACAAGCTGTGC***TGCATTAGCATCTATTAGC***AGAATGCAGAGTGGAAGAGTTGGAGAGTAG

: 19 bp deletion makes a difference between P and F depending on primer sequences.

Conclusion: Davis Primers were advised to be used in order to amplify samples with or without the deletion.

It was suggested to use a reference sample during next CT containing this deletion (like HCT06)

2. Donkey STR Comparison test 2018-2019

Deleted:

Deleted:

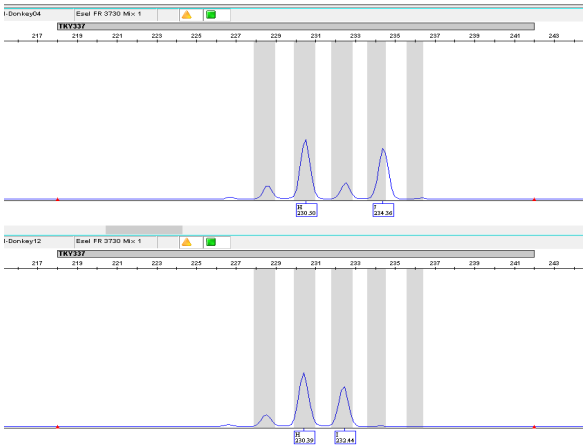
Duty laboratory: Dr. med. vet. Torsten Brendel, Eurofins Medigenomix, Germany.

DNA extraction method: chemagic DNA Blood100 Kit, Chemagen (PerkinElmer)/ Maxwell 16 FFS Nucleic Acid Extraction Kit (Promega)

Breeds tested:

Markers Consensus:

In the Back Up Panel, Marker TKY337 showed discrepancies in samples 04 and 12 due probably to primers used, with labs not detecting allele "H", as shown for the Duty Lab during the workshop presentation (below):



Parentage Questions:

Question 1 - Is Donkey_01 or Donkey_06 the offspring of Donkey_02 and Donkey_03?

20/20 (100%) labs answered "Donkey_01"

Question 2 - Is Donkey_05 or Donkey_08 the mother of Donkey_04?

14/20 (70%) labs answered "Donkey_05"

Lab Performance:

Average concordance: 97.50% +- 0.04

3. Horse SNP Comparison Test

Participants: 10 laboratories.

-1 lab reported results for 2 platforms.

-2 labs reported results for additional 66 & 441 SNPs (not reviewed).

New platforms used (relative to 2017-2018 CT)

-Ion S5 genotyping by Sequencing (3)

- ABI Quant Studio 12 K Flex RT (1)

Parentage questions: answered correctly

Overall outcome: Excellent across labs/platforms but problem markers present in compared SNP set.

Overall SNP Performance

# SNPs (n = 148)	% SNPs	Concordance Rate	Notes
106	71%	100%	
11	7%	99.5%	
10	7%	99.0 - 99.3%	
10	7%	98.2 - 98.6%	
6	4%	95.0-97.6%	
1	1%	93%	
3	2%	84.7 - 89.3%	one with 3 alleles
2	1%	75.2 -78.0%	one with 3 alleles

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Overall Performance

Labs	Platform	# SNPs Reported	# SNPs Compared	% Consensus
84414	Ion S5	154	148	99.0%
84414	MassArray	154	148	99.7%
84422	Ion S5	153	148	97.7%
84451	QS 12K Flex RT	155	148	98.4%
84460	Illumina SNP70 BeadChip	80	77	99.6%
84485	Affymatrix Axiom MNCc670P	101	98	98.9%
84486	Illumina Infinium	101	98	99.7%
84764	Ion S5	151	147	99.2%
90224	Illumina	154	153	99.6%
110956	MassArray	154	149	98.6%
119078	Illumina iScan	101	98	99.7%

For selected set of SNPs concordance ranged from 97.7%-99.7%

Two SNPs with 3 alleles contributed to error counts if not detected by assay.

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Why Fewer SNPs Used For Comparison?

- A set of 5 SNPs appear to have underlying sequence issues (missing results) or the correct genotype in 1-3 samples could not be determined.
  - 3 SNPs already flagged in 2017-2018 CT "watch list"
  - 2 additional SNPs came up as problematic in 2018-2019 CT

SNP ID	Issue
BIEC2-183251 (Etalon Panel)	Correct type not clear, 3 samples. Also in 2017 watch list
BIEC2-444978 (Etalon Panel)	Correct type not clear, 1 sample, null? Also in 2017 watch list
BIEC2-1095371 (Etalon Panel)	Underlying sequence problem? Also in 2017 watch list
BIEC-189021 (Tozaki Panel)	Correct type not clear, 1 sample
BIEC-884767 (Tozaki Panel)	Correct type not clear, 2 samples

- Arbitrary decision of compiler to exclude the 5 SNPs from concordance analysis.
- These Markers will be not considered in the SNPs list for the Core Panel

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BIEC2-1095371 – missing types in 3 designs, another design with discordant results

Ion S5	84414	BIEC2-1095371	AG	AG	*	AA	GG	GG	AG	GG	AA	AA	AG	GG	GG	GG	AG	AA	AG	AG	AG	GG
MassArray	84414	BIEC2-1095371	AG	*	*	AA	GG	GG	*	GG	AA	AA	*	GG	GG	GG	*	AA	*	AG	*	GG
Ion S5	84422	BIEC2-1095371	AG	AG	AG	AA	GG	GG	AG	*	AA	AA	AG	*	*	GG	AG	AA	AG	AG	AG	GG
QS 12K Flex RT	84451	BIEC2-1095371	AG	AG	AG	AA	GG	GG	AG	GG	AA	AA	AG	GG	GG	GG	AG	AA	AG	AG	AG	GG
Illumina SNP70 BeadChip	84460	BIEC2-1095371	AG	AG	AG	AA	GG	GG	AG	GG	AA	AA	AG	GG	GG	GG	AG	AA	AG	AG	AG	GG
Affy Axiom MNCo670P	84485	BIEC2-1095371	AG	AG	AG	AA	GG	GG	AG	GG	AA	AA	AG	GG	GG	GG	AG	AA	AG	AG	AG	GG
Illumina Infinium	84486	BIEC2-1095371	AG	AG	AG	AA	GG	GG	AG	GG	AA	AA	AG	GG	GG	GG	AG	AA	AG	AG	AG	GG
Ion S5	84764	BIEC2-1095371	AG	AG	AG	AA	GG	GG	AG	GG	AA	AA	AG	GG	GG	GG	AG	AA	AG	AG	AG	GG
Illumina	90224	BIEC2-1095371	AG	AG	AG	AA	GG	GG	AG	GG	AA	AA	AG	GG	GG	GG	AG	AA	AG	AG	AG	GG
MassArray	110956	BIEC2-1095371	AG	AA	AA	AA	GG	GG	AA	GG	AA	AA	AA	GG	GG	GG	AA	AA	AA	AG	AA	GG
Illumina iScan	119078	BIEC2-1095371	AG	AG	AG	AA	GG	GG	AG	GG	AA	AA	AG	GG	GG	GG	AG	AA	AG	AG	AG	GG

BIEC884767 – 2 samples with missing types or discordant results if present, one design with discordant results

Ion S5	84414	BIEC884767	GG	CC	TT	GT	CC	GG	GT	GG	TT	GT	GT	TT	GT	GG	GT	GT	GT	GT	GG	GT
MassArray	84414	BIEC884767	GG	*	TT	GT	*	GG	GT	GG	TT	GT	GT	TT	GT	GG	GT	GT	GT	GT	GG	GT
Ion S5	84422	BIEC884767	GG	TT	TT	GT	TT	GG	GT	GG	TT	GT	GT	TT	GT	GG	GT	GT	GT	GT	GG	GT
QS 12K Flex RT	84451	BIEC884767	GG	AA	AG	AG	AA	GG	AG	GG	AG	AG	GG	AG	GG	GG	GG	GG	AG	AG	GG	GG
Ion S5	84764	BIEC884767	GG	TT	TT	GT	TT	GG	GT	GG	TT	GT	GT	TT	GT	GG	GT	GT	GT	GT	GG	GT
Illumina	90224	BIEC884767	GG	GG	TT	GT	GG	GG	GT	GG	TT	GT	GT	TT	GT	GG	GT	GT	GT	GT	GG	GT
MassArray	110956	BIEC884767	GG	*	TT	GT	*	GG	GT	GG	TT	GT	GT	TT	GT	GG	GT	GT	GT	GT	GG	GT

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Five Misbehaving SNPs

BIEC2-183251 – 3 samples with missing types, no consensus result if present

Ion S5	84414	BIEC2-183251	CC	AC	CC	CC	CC	AC	CC	AC	CC	AA	AC	AC	CC	CC	*	AA	CC	CC	*	*
MassArray	84414	BIEC2-183251	CC	AC	CC	CC	CC	AC	CC	AC	CC	AA	AC	AC	CC	CC	CC	AA	CC	CC	CC	CC
Ion S5	84422	BIEC2-183251	CC	AC	CC	CC	CC	AC	CC	AC	AC	AA	AC	AC	CC	CC	AC	AA	CC	CC	*	AC
QS 12K Flex RT	84451	BIEC2-183251	CC	AC	CC	CC	CC	AC	CC	AC	CC	AA	AC	AC	CC	CC	*	AA	CC	CC	*	*
Illumina SNP70 BeadChip	84460	BIEC2-183251	CC	AC	CC	CC	CC	AC	CC	AC	CC	AA	AC	AC	CC	CC	*	AA	CC	CC	*	*
Affy Axiom MNCc670P	84485	BIEC2-183251	CC	AC	CC	CC	CC	AC	CC	AC	CC	AA	AC	AC	CC	CC	CC	AA	CC	CC	CC	CC
Illumina Infinium	84486	BIEC2-183251	CC	AC	CC	CC	CC	AC	CC	AC	CC	AA	AC	AC	CC	CC	*	AA	CC	CC	*	*
Ion S5	84764	BIEC2-183251	CC	AC	CC	CC	CC	AC	CC	AC	CC	AA	AC	AC	CC	CC	CC	AA	CC	CC	CC	AC
Illumina	90224	BIEC2-183251	CC	AC	CC	CC	CC	AC	CC	AC	CC	AA	AC	AC	CC	CC	*	AA	CC	CC	*	*
MassArray	110956	BIEC2-183251	CC	AC	CC	CC	CC	AC	CC	AC	CC	AA	AC	AC	CC	CC	AC	AA	CC	CC	AC	*
Illumina iScan	119078	BIEC2-183251	CC	AC	CC	CC	CC	AC	CC	AC	CC	AA	AC	AC	CC	CC	*	AA	CC	CC	*	*

BIEC2-444978 – Null allele?

Ion S5	84414	BIEC2-444978	GG	AA	AG	AG	AG	GG	AG	AG	GG	AG	AA	AA	AG	AA	AA	AG	AG	AG	AA	GG
MassArray	84414	BIEC2-444978	GG	AA	AG	AG	AG	GG	AG	AG	GG	AG	AA	AA	AG	AA	AA	AG	AG	AG	AA	GG
Ion S5	84422	BIEC2-444978	GG	AA	AG	AG	AG	GG	AG	AG	GG	AG	AA	AA	AG	AA	AA	AG	AG	AG	AA	GG
QS 12K Flex RT	84451	BIEC2-444978	GG	AA	AG	AG	GG	GG	AG	AG	GG	AG	AA	AA	AG	AA	AA	AG	AG	AG	AA	GG
Illumina SNP70 BeadChip	84460	BIEC2-444978	GG	AA	AG	AG	GG	GG	AG	AG	GG	AG	AA	AA	AG	AA	AA	AG	AG	AG	AA	GG
Affy Axiom MNCc670P	84485	BIEC2-444978	GG	AA	AG	AG	AG	GG	AG	AG	GG	AG	AA	AA	AG	AA	AA	AG	AG	AG	AA	GG
Illumina Infinium	84486	BIEC2-444978	GG	AA	AG	AG	GG	GG	AG	AG	GG	AG	AA	AA	AG	AA	AA	AG	AG	AG	AA	GG
Ion S5	84764	BIEC2-444978	GG	AA	AG	AG	AG	GG	AG	AG	GG	AG	AA	AA	AG	AA	AA	AG	AG	AG	AA	GG
Illumina	90224	BIEC2-444978	GG	AA	AG	AG	GG	GG	AG	AG	GG	AG	AA	AA	AG	AA	AA	AG	AG	AG	AA	GG
MassArray	110956	BIEC2-444978	GG	AA	AG	AG	GG	GG	AG	AG	GG	AG	AA	*	AG	AA	AA	AG	AG	AG	AA	GG
Illumina iScan	119078	BIEC2-444978	GG	AA	AG	AG	GG	GG	AG	AG	GG	AG	AA	AA	AG	AA	AA	AG	AG	AG	AA	GG

BIEC189021 – null allele?

Ion S5	84414	BIEC1890021	GT	GG	TT	GT	TT	TT	GT	TT	GT	TT	TT	GG	GT	TT	GT	GG	GT	GG	TT	GT
MassArray	84414	BIEC1890021	GT	GG	TT	GT	TT	TT	GT	TT	GT	TT	TT	GG	GT	TT	GT	GG	GT	GG	TT	GT
Ion S5	84422	BIEC1890021	GT	GT	TT	GT	TT	TT	GT	TT	GT	TT	TT	GG	GT	TT	GT	GG	GT	GG	TT	GT
QS 12K Flex RT	84451	BIEC1890021	GT	*	TT	GT	TT	TT	GT	TT	GT	TT	TT	GG	GT	TT	GT	GG	GT	GG	TT	GT
Ion S5	84764	BIEC1890021	GT	GT	TT	GT	TT	TT	GT	TT	GT	TT	TT	GG	GT	TT	GT	GG	GT	GG	TT	GT
Illumina	90224	BIEC1890021	GT	GT	TT	GT	TT	TT	GT	TT	GT	TT	TT	GG	GT	TT	GT	GG	GT	GG	TT	GT
MassArray	110956	BIEC1890021	GT	GG	TT	GT	TT	TT	GT	TT	GT	TT	*	GG	GT	TT	GT	GG	GT	GG	TT	GT

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SNPs with Improvement Needed

SNP ID	Platform
BIEC-119158 (Tozaki Panel)	Ion S5
BIEC2-158202	Ion S5
BIEC-344848 (Tozaki Panel)	Ion S5
BIEC-811791	MassArray, QS 12K Flex RT

BIEC-811791, some platforms are "missing" the G genotype

Treatment	SampleID	HCT1	HCT2	HCT3	HCT4	HCT5	HCT6	HCT7	HCT8	HCT9	HCT10
Ion S5	BIEC811791	GG	TT	GG	GT	TT	GT	GG	GG	GT	GT
MassArray	BIEC811791	GG	TT	GG	TT	TT	TT	GG	GG	TT	TT
Ion S5	BIEC811791	GG	TT	*	GT	TT	GT	GG	*	GT	GT
QS 12K Flex RT	BIEC811791	GG	TT	GG	TT	TT	TT	GG	GG	TT	TT
Ion S5	BIEC811791	GG	TT	GG	GT	TT	GT	GG	GG	GT	GT
Illumina	BIEC811791	GG	TT	GG	GT	TT	GT	GG	GG	GT	GT
MassArray	BIEC811791	*	TT	GG	TT	TT	TT	GG	GG	TT	TT

3 Allele-Problematic SNPs

- Both in the 2017 and 2019 CT

SNP ID	Issue
BIEC2-1061845	3 alleles
BIEC-349712	3 alleles

These Markers will be not considered in the SNPs list for the Core Panel

Proposals:

1 It was proposed that for the next SNPs equine CT, the report format will be forward and top Calls.

2. Seven problematic SNPs (low performance and 3-allele genotypes) should be eliminated from the SNPs list of markers to be used: BIEC2-1061845, BIEC-349712, BIEC2-183251, BIEC2-444978, BIEC2-1095371, BIEC-189021 and BIEC-884767.

3. The SNPs list for the next SNP CT must be in the ISAG website.

4. FASS should compile results of the next CT, which results won't be officially ranked.

Other business and election committee members.

1 Status of decisions from the ISBC. Link to the file?

2-2020-2021 Comparison Tests.

Next Duty Lab for Horse STR and SNP Comparison Tests: VGL, UC Davis, Rebecca Bellone.

Deleted: Renee

Next Duty Lab for Donkey Comparison Test: Biotechnical Faculty, Animal Science Department, Slovenia, Prof. Peter Dovč.

3-**Election of SC Members:**

Guillermo Giovambattista, Universidad de la Plata Argentina and Rebecca Bellone, University of California -Davis, were elected as new members of SC to replace Lucie Genestout and Marcela Martinez. Marcela Martinez, Sociedad Rural Argentina, was elected as new Chair of the SC to replace Cecilia Penedo who stepped down.

Deleted: Renee

Committee chair (the new chair)

Chair: Marcela Martínez
Term of service: 2019-2023
Affiliation: Sociedad Rural Argentina
E-mail address: mmartinez@sra.org.ar

Committee members (the new committee)

Other members	Term of service	E mail address
Romy Morrin-O´Donnell	2017-2021 (2nd)	rmorrin@weatherbys.ie
Rosina Fossati	2017-2021 (2nd)	fossati@genia.com.uy
Hironaga Kakoi	2017-2021 (2nd)	h-kakoi@lrc.or.jp
Leslie Bickel	2017-2021 (2nd)	labickel@ucdavis.edu
Guillermo Giovambattista	2019-2023 (1st)	guillermogiovambattista@gmail.com
Rebecca Bellone	2019-2023 (1st)	rbellone@ucdavis.edu

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COMPARISON TEST (2018-2019) YES NO (If no delete the rest of this page)

Duty laboratory

Contact person: Dr. Torsten Brendel
Affiliation: Eurofins Medigenomix GmbH, Ebersberg, Germany
E-mail address: TorstenBrendel@eurofins.com

Comments (issues rising)

TKY337 change of Primers

List of recommended markers with primer information

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Horse:

Locus	ECA	Primer sequences		Amplicon length
AHT4	24	F: AACCGCCTGAGCAAGGAAGT	R: CCCAGAGAGTTTACCCT	144-164
AHT5	8	F: ACGGACACATCCCTGCCTGC	R: GCAGGCTAAGGAGGCTCAGC	126-144
ASB2	15	F: CCACTAAGTGTCGTTTCAGAAGG	R: CACAACTGAGTTCTCTGATAGG	216-250
ASB17	2	F: ACCATTCAGGATCTCCACCG	R: GAGGGCGGTACCTTTGTACC	87-129
ASB23	3	F: GAGGGCAGCAGGTTGGGAAGG	R: ACATCCTGGTCAAATCACAGTCC	175-211
CA425/UCDEQ425	28	F: AGCTGCCTCGTTAATTCA	R: CTCATGTCCGCTTGTCTC	226-246
HMS1	15	F: CATCACTCTTCATGTCTGCTTGG	R: TTGACATAAATGCTTATCCTATGGC	170-186
HMS2	10	F: CTTGCAGTCGAATGTGTATTAAATG	R: ACGGTGGCAACTGCCAAGGAAG	222-248
HMS3*	9	F: CCATCCTCACTTTTTCACTTTGTT	R: CCAACTCTTTGTCACATAACAAGA	148-170
HMS6	4	F: GAAGCTGCCAGTATTCAACCATTG	R: CTCCATCTTGTGAAGTGTAACTCA	151-169
HMS7	1	F: TGTTGTTGAAACATACCTTGACTGT **	R: CAGGAAACTCATGTTGATACCATC	165-185
HTG4	9	F: CTATCTCAGTCTTGATTGCAGGAC	R: CTCCCTCCCTCCCTCTGTTCTC	127-139
HTG6	15	F: GTTCACTGAATGTCAAATTCTGCT	R: CCTGCTTGGAGGCTGTGATAAGAT	84-102
HTG7	4	F: CCTGAAGCAGAACATCCCTCCTTG	R: ATAAAGTGTCTGGGCAGAGCTGCT	118-128
HTG10*	21	F: TTTTTATTCTGATCTGTCACATTT	R: CAATTCCCGCCCCACCCCCGGCA	95-115
LEX3	X	F: ACATCTAACCAGTGCTGAGACT	R: GAAGGAAAAAAAGGAGGAAGAC	142-164
VHL20	30	F: CAAGTCCTCTTACTTGAAGACTAG	R: AACTCAGGGAGAATCTTCCTCAG	87-105

*original sequence; can produce null allele. Alternative primers suggested elsewhere in report.

** original sequence; can produce null allele. Alternate sequence for consideration: TGTTSTTGAAACATACATTGACTGT.

Duty laboratory for the next comparison test with contact details

Horse

Contact person: Rebecca Bellone
Affiliation: VGL UC-Davis, California.
E-mail address: rbellone@ucdavis.edu

Duty laboratory for the next comparison test with contact details

Donkey

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Contact person: Prof. Peter Dovč.
Affiliation: Biotechnical Faculty, Animal Science Department, Slovenia
E-mail address: peter.dovc@bf.uni-lj.si

SIGNATURES

Chair	**Duty laboratory**

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For information - please delete this page from the report

IMPORTANT INFORMATION FROM THE WORKSHOP AND STANDING COMMITTEE GUIDELINES:

All members of a standing committee need to have individual membership of ISAG throughout the time of service. If new committee members are not ISAG members when elected it is necessary to become so as soon as possible.

The workshop Chair has to compile the report of the workshop and then circulate it to the members of the Standing Committee for any comment and revision. The report then has to be emailed to the ISAG secretary within the noted deadline.

PLEASE EMAIL A WORD VERSION AND A SIGNED PDF VERSION OF THIS REPORT TO THE ISAG SECRETARY: ISAGsecretary@assochq.org

DEADLINE AUGUST 31st 2019

A draft of this report will be available to all ISAG members on the ISAG web. Workshop participants are allowed to comment and may ask for revision. Such a request for revision has to be given including relevant reasons and arguments. The Secretary will send these requests to the Chair for dispute in the Standing Committee. Within two weeks the Standing Committee has to answer the Secretary. If no comments from participants have been received within two weeks, the report is considered to be approved and published on the ISAG web.

For more information please see the committee guidelines and comparison test rules.