ETALON DIAGNOSTICS

REPORT DATE:	HORSE:	OWNER:
MAY 20, 2024	HARMONY COCO FINDIL	XXXXXXXX ICHO Aline Verschuren

Genetic profile test results

DB# 435

HORSE ID:	PACKAGES:
050924_014	ICHO | PROPANEL

Horse and owner information

Horse
Harmony Coco Findil

Date of birth
05-27-2017

Breed
Curly Horse

Age
6 y.o.

Color
Black Smoky Tobiano

Sex
Mare

Discipline
Pleasure

Height
-

Registry

Reg number 2463-D

Sire
Corigan De Findil 1605-D

Dam
Maker A Blondie ABC 2876

Sire Reg & No.

Dam Reg & No.

Owner
XXXXXXXXXX ICHO Aline Verschuren

Address
322 Tulie Gate Rd

Phone
5757404159

City, State
Tularosa, NM

Email
office@curlyhorses.org

Postal code
88352

Results Summary

Variant summaries:

Genetic note: **Curly Coat (CU): One Curly Coat 1 variant detected.**

Color: **a/a, E/e, nd1/nd2, TO/n, PATN1/n, CR/n**

Modifier: **CU1/n** KRT25 +/-

Health: **CIAR/n, EHMR/n**

Speed: **Mid-distance Type**

Temperament: **Curious/Vigilant** DRD4 +/-

Gait: **DMRT3 Carrier** DMRT3 +/-

Performance and Abilities:

Curious & Vigilant
One Curiosity and one Vigilance variant; horse is likely both curious and vigilant (*ongoing study).

DMRT3 "Gait Carrier"
One DMRT3 or "gaited" variant; may display a wide variation in locomotion, partial "gaiting" and possible difficulty with 3 beat canter, lead change, tempi changes, or gait transitions.

Mid-Distance
Mid-distance type; horse may have multidistance capabilities including sprint and endurance.

Health Variants:

Recurrent Laryngeal Neuropathy Risk (RLNR) - n/n
No Recurrent Laryngeal Neuropathy Risk (RLNR) variants detected.

Laminitis Susceptibility Risk - Equine Metabolic Syndrome related (LAM) - n/n
No Laminitis Susceptibility Risk (LAM) variants detected. Horse has average risk for EMS-related Laminitis.

Equine Recurrent Uveitis Susceptibility Risk (ERUR) - n/n
No Equine Recurrent Uveitis Susceptibility Risk (ERUR) variant detected. Horse has normal risk of ERU.

Equine Recurrent Uveitis Symptom Severity (ERUS) - n/n
No Equine Recurrent Uveitis Symptom Severity (ERUS) variants detected. Horse has normal susceptibility for ERU symptom severity if contracted.

Equine Metabolic Syndrome Susceptibility Risk (EMS) - n/n
No Equine Metabolic Syndrome Susceptibility Risk (EMS) variants detected. Horse has average risk for Equine Metabolic Syndrome.

Chronic Idiopathic Anhidrosis Risk (CIAR) - CIAR/n
CIA/n -One Chronic Idiopathic Anhidrosis Risk (CIAR) variant detected. Horse has moderate risk of developing the chronic form of anhidrosis (mostly represented by mild and sporadic cases of anhidrosis), and has 50% chance of passing to any offspring.

Equine Herpes Myeloencephalopathy Risk (EHMR) - Equine Herpes Virus type 1 (EHV1) related - EHMR/n
EHMR/n - One Equine Herpesvirus Myeloencephalopathy Risk (EHMR) variant detected. Horse has 1.43x increased risk of developing the neurological form Equine Herpesvirus Myeloencephalopathy (EHM) if infected by Equine Herpes Virus type 1 (EHV-1).

Coat color:

Smoky Black
Black (E) + Cream (CR/n): When a black horse has one Cream (CR) variant, its color may appear black to a dark brown. Thus, a smoky black may be visibly indistinguishable from a true black, dark Bay or dark Chestnut.

Black (base)
Black (E) is the base coat color for this horse and is a relatively uncommon coat color on its own (usually it is found in combination with other colors or modifiers such as in Bay horses). A visible difference between a true black (Ee or EE), a dark chestnut (ee) or a bay (Aa or AA + E) can sometimes be seen in the fine hairs around the eyes and muzzle. On a true black these hairs typically remain black even if the horse is sun-bleached, while on other colors they will be lighter. Horse with one copy of the black variant (Ee) is "heterozygous black" and has a 50% chance of passing on black or red to any offspring.

Tobiano (TO) - TO/n
TO/n - One Tobiano (TO) variant detected; may result in large white markings on body, face and legs (occasionally produces 'minimal' or 'slipped' Tobiano horse with very little white only on face and lower legs (ongoing heritability study for minimal Tobiano). Horse has 50% chance of passing to any offspring.

Cream (CR) - CR/n
CR/n - One Cream (CR) variant detected. Cream is a partial dominant and may dilute base coat color (Buckskin, Palomino, Smoky Black, etc). Horse has a 50% chance of passing to any offspring.

Pattern 1 (PATN1) - PATN1/n
PATN1/n - One Pattern 1 (PATN1) variant detected. Pattern 1 (PATN1) is a modifier visible when combined with Leopard Spotting Complex (LP) to create a leopard spotted coat. On its own, Pattern 1 has no confirmed effect on the coat color. Studies ongoing. Horse has a 50% chance of passing on to any offspring.

Curly Coat (CU) - CU1/n, n/n
CU1/n, n/n - One Curly Coat (KRT25) variant and no Curly Coat 1 (SP6) variants detected. Horse may exhibit curly hair in varying degrees. Horse has a 50% chance of passing CU1 to any offspring.

Coat color

Base

Agouti (A) - a/a — ASIP — Negative

Gene or region: **ASIP**

a/a - No Agouti (A) variants detected. Agouti (A) restricts black pigment to the outer regions of the body, the legs, mane & tail, nose, ear tips causing the otherwise black horse to appear Bay. Agouti is invisible on the red based coat.

Black (E) - E/e — MC1R — Black Based

Gene or region: **MC1R**

E/e - One Black variant (E) and one Red (e) variant detected.

Modifiers

non-Dun Primitive Markings (nd) - nd1/nd2 — TBX3 — Possibly Affected

Gene or region: **TBX3**

nd1/nd2 - One non-Dun Primitive Markings (ND) variant detected. Non-Dun Primitive Markings can appear as a dorsal stripe, leg barring, shadows on the face and shoulders even in the absence of the Dun variant.

Tiger Eye (TE1) - n/n — SLC24A5TE1 — Negative

Gene or region: **SLC24A5TE1**

No Tiger Eye (TE1) variants detected.

Tiger Eye (TE2) - n/n

SLC24A5TE2MUT — Negative

Gene or region: **SLC24A5TE2MUT**

No Tiger Eye (TE2) variants detected.

Brindle (BR1) - n/n

MBTPS2BR1 — Negative

Gene or region: **MBTPS2BR1**

No Brindle (BR1) variants detected.

Grey (G) - n/n

STX17A — Negative

Gene or region: **STX17A**

No Grey (G) variants detected.

Dilutes

Dun (D) - n/n

TBX3 — Negative

Gene or region: **TBX3**

No Dun (D) variants detected.

Cream (CR) - CR/n

SLC45A2 — Likely Affected

Gene or region: **SLC45A2**

CR/n - One Cream (CR) variant may dilute the base coat color to appear lighter resulting in a Palomino, Buckskin or other lightened coat color.

Champagne (CH) - n/n

SLC36A1

Negative

Gene or region: **SLC36A1**

No Champagne (CH) variants detected.

Pearl (PRL) - n/n

SLC45A2

Negative

Gene or region: **SLC45A2**

No Pearl (prl) variants detected.

Silver (Z) - n/n

PMEL17

Negative

Gene or region: **PMEL17**

No Silver (Z) variants detected. Silver affects only black base (E) coat colors and is invisible on a red-based coat. On black or bay, It has a disproportionate diluting effect on the mane and tail, and is sometimes called, "Chocolate Flaxen".

Snowdrop (SNO) - n/n

SLC45A

Negative

Gene or region: **SLC45A**

No Snowdrop (SNO) variants detected. One Snowdrop variant detected; invisible in the absence of Cream, Pearl, Sunshine, or another Snowdrop variant. One Snowdrop variant when combined with one Cream variant, one Pearl, one Sunshine, or another Snowdrop variant may appear as a double dilute.

Sunshine (SUN) - n/n

SLC45A

Negative

Gene or region: **SLC45A**

No Sunshine (SUN) variants detected.

Mushroom (MU) - n/n | MFSD12 | Negative

Gene or region: **MFSD12**

No Mushroom (MU) variants detected.

Whites

Pattern 1 (PATN1) - PATN1/n | RFWD3 | Possibly Affected

Gene or region: **RFWD3**

PATN1/n - One Pattern 1 variant detected. PATN1 is known to modify Leopard Spotting Complex (LP) resulting in the appearance of Leopard spotting throughout the coat. The effects of PATN1 in the absence of Leopard Spotting Complex are unknown. May be invisible, although some claim to observe white "ticking" of hairs on hips, belly and shoulder.

Tobiano (TO) - TO/n | ECA3 | Likely Affected

Gene or region: **ECA3**

TO/n - One Tobiano variant detected; likely white markings. This horse may pass Tobiano to 50% of any offspring.

Leopard Complex Spotting (LP) - n/n | TRPM1 | Negative

Gene or region: **TRPM1**

No Leopard Complex Spotting variants detected.

Sabino1 (SB1) - n/n | KIT | Negative

Gene or region: **KIT**

No Sabino (SB1) variants detected.

Splashed White (SW1) - n/n

MITF

Negative

Gene or region: **MITF**

No Splashed White 1 (SW1) variants detected.

Splashed White (SW2) - n/n

PAX3

Negative

Gene or region: **PAX3**

No Splashed White 2 (SW2/n) variants detected.

Splashed White (SW3) - n/n

MITF

Negative

Gene or region: **MITF**

No Splashed White 3 (SW3) variants detected.

Splashed White (SW4) - n/n

PAX3

Negative

Gene or region: **PAX3**

No Splashed White 4 (SW4) variants detected.

Splashed White 5 (SW5) - n/n

MITF

Negative

Gene or region: **MITF**

No Splashed White 5 variants detected.

Dominant White (W) - n/n	KIT		Negative

Gene or region: **KIT**

No Dominant White (1-21) variants detected.

Splashed White 6 (SW6) - n/n	MITF		Negative

Gene or region: **MITF**

No Splashed White 6 variants detected.

Splashed White 7 (SW7) - n/n	MITF		Negative

Gene or region: **MITF**

No Splashed White 7 variants detected.

Dominant White 22 (W22) - Not Ordered	KIT	Not ordered

Dominant White 30/Aghilasse (W30) - Not Ordered	KIT	Not ordered

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Dominant White 31/Merada (W31) - Not Ordered	KIT	Not ordered

Dominant White 32/Scandalous (W32) - Not Ordered	KIT	Not ordered

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Dominant White 34/Flamboyant (W34) - Not Ordered	KIT		Not ordered
Dominant White 35/Holiday (W35) - Not Ordered	KIT		Not ordered
Splashed White 9/Giltor (SW9) - n/n	MITF		Negative

Gene or region: **MITF**

No Splashed White 9/Giltor variants detected.

Splashed White 10/Giltor (SW10) - n/n	PAX3		Negative

Gene or region: **PAX3**

No Splashed White 10/Giltor variants detected.

Splashed White 8 (SW8) - n/n	MITF		Negative

Gene or region: **MITF**

No Splashed White 8 variants detected.

Dominant White 33 (W33) - Not Ordered	KIT	Not ordered
Eden White 3 (EDXW3) "Irish" - Not Ordered	HSP5	Not ordered

Eden White 2 (EDXW2) "Dream" - Not Ordered	HSP5	Not ordered
Eden White 1 (EDXW1) "Cruz" - Not Ordered	HSP5	Not ordered
Frame/Lethal White Overo (LWO) - n/n	EDNRB	Negative

Gene or region: **EDNRB**

No Frame/Lethal White Overo (LWO) variants detected.

Coat Type

Curly Coat 1 (CU1) - CU1/n	KRT25	Possibly Affected

Gene or region: **KRT25**

CU/n - One Curly Coat (CU-KRT25) variant detected. Horse may have curly coat, mane and tail, possibly affected by incomplete sparse, coarse hair, and may pass this trait to any offspring 50% of the time.

Curly Coat 2 (CU2) - n/n	SP6	Negative

Gene or region: **SP6**

No known Curly Coat (CU-SP6) variants detected.

Health Variants

Color Related Risk

Lethal White Overo (LWO) - n/n	EDNRB	Negative

Gene or region: **EDNRB**

n/n - No Lethal White Overo (LWO) variants detected.

Congenital Stationary Night Blindness (CSNB) - n/n	TRPM1	Negative

Gene or region: **TRPM1**

n/n - No Leopard Complex Spotting (LP) variants detected, which is related to the presence of Congenital Stationary Night Blindness (CSNB) if horse is LP/LP. Horses with one copy of the Leopard Complex Spotting (LP) variant are not currently known to suffer any ill effects as a result. Horses with Congenital Stationary Night Blindness (CSNB) which may experience the inability to see in low to no-light conditions.

Multiple Congenital Ocular Anomalies (MCOA) - n/n	PMEL17	Negative

Gene or region: **PMEL17**

n/n - No Silver variants detected which is related to the presence of Multiple Congenital Ocular Anomalies (MCOA).

Immune System

Foal Immunodeficiency Syndrome (FIS) - n/n	SLC5A3	Negative

Gene or region: **SLC5A3**

No Foal Immunodeficiency Syndrome variants detected.

Severe Combined Immunodeficiency (SCID) - n/n	DNAPK		Negative

Gene or region: **DNAPK**

No Severe Combined Immunodeficiency (SCID) variants detected.

Myosin-Heavy Chain Myopathy (MYHM) - n/n	MYH1		Negative

Gene or region: **MYH1**

No Myosin-Heavy Chain Myopathy variants detected. Normal susceptibility for IMM or nonexertional rhabdomyolysis.

West Nile Virus Symptom Susceptibility Risk (WNVR) - n/n	OAS1		Negative

Gene or region: **OAS1**

No West Nile Virus Symptom Susceptibility Risk (WNVR) variants detected. Normal susceptibility to West Nile Virus symptoms. (*NOT a test for West Nile Virus).

Equine Herpes Myeloencephalopathy Risk (EHMR) - Equine Herpes Virus type 1 (EHV1) related - EHMR/n	TSPAN9		Increased Risk

Gene or region: **TSPAN9**

EHMR/n - One Equine Herpesvirus Myeloencephalopathy Risk (EHMR) variant detected. Horse has 1.43x increased risk of developing the neurological form Equine Herpesvirus Myeloencephalopathy (EHM) if infected by Equine Herpes Virus type 1 (EHV-1).

Muscle Disorders

Glycogen Branching Enzyme Deficiency (GBED) - n/n	GBE1		Negative

Gene or region: **GBE1**

No Glycogen Branching Enzyme Deficiency (GBED) variants detected.

Hyperkalemic Partial Paralysis (HYPP) - n/n	SCN4A		Negative

Gene or region: **SCN4A**

No Hyperkalemic Partial Paralysis (HYPP) variants detected.

Malignant Hyperthermia (MH) - n/n	RYR1		Negative

Gene or region: **RYR1**

No Malignant Hyperthermia (MH) variants detected.

Myotonia (MYT) - n/n	CLCN4		Negative

Gene or region: **CLCN4**

No Myotonia (MYT) variants detected.

Polysaccharide Storage Myopathy type 1 (PSSM1) - n/n	GYS1		Negative

Gene or region: **GYS1**

No Polysaccharide Storage Myopathy type 1 (PSSM1) variants detected.

Neurologic Disorders

Cerebellar Abiotrophy (CA) - n/n	MUTYH		Negative

Gene or region: **MUTYH**

No Cerebellar Abiotrophy (CA) variants detected.

Lavender Foal Syndrome (LFS) - n/n	MYO5A		Negative

Gene or region: **MYO5A**

No Lavender Foal Syndrome (LFS) variants detected.

Hydrocephalus (HDC) - n/n	B3GALNT2		Negative

Gene or region: **B3GALNT2**

No Hydrocephalus (HDC) variants detected.

Recurrent Laryngeal Neuropathy Risk (RLNR) - n/n	ECA3		Average Risk

Gene or region: **ECA3**

No Recurrent Laryngeal Neuropathy Risk (RLNR) variants detected.

Occipitoatlantoaxial Malformation Type 1 (OAAM1) - n/n	HOX		Negative

Gene or region: **HOX**

No Occipitoatlantoaxial Malformation Type 1 variants detected.

Reproductive Disorders

Androgen Insensitivity Syndrome (AIS) - n/n	AR		Negative

Gene or region: **AR**

No pattern of Androgen Insensitivity Syndrome (AIS) variants detected.

Impaired Acrosomal Reaction - Subfertility Risk (IAR) - iar/n,iar/n	FKBP6...		Not Affected

Gene or region: **FKBP6, FKBP6**

No pattern for Impaired Acrosomal Reaction (IAR) - Subfertility Risk variants detected.

Skin, Hoof and Connective Tissue Disorders

Hereditary Equine Regional Dermal Asthenia (HERDA) - n/n	PPIB		Negative

Gene or region: **PPIB**

No Hereditary Equine Regional Dermal Asthenia (HERDA) variants detected.

Junctional Epidermolysis Bullosa type 1 (JEB1) - n/n	LAMC2		Negative

Gene or region: **LAMC2**

No Junctional Epidermolysis Bullosa type 1 (JEB1) variants detected.

Junctional Epidermolysis Bullosa type 2 (JEB2) - n/n	LAMA3		Negative

Gene or region: **LAMA3**

No Junctional Epidermolysis Bullosa type 2 (JEB2) variants detected.

"Warmblood" Fragile Foal Syndrome (FFS) - n/n	PLOD1		Negative

Gene or region: **PLOD1**

No Fragile Foal Syndrome (FFS) variants detected.

Hoof Wall Separation Disease (HWSD) - n/n	SERPINB11		Negative

Gene or region: **SERPINB11**

No Hoof Wall Separation Disease (HWSD) variants detected.

Naked Foal Syndrome (NFS) - n/n	st14		Negative

Gene or region: **st14**

No Naked Foal Syndrome (NFS) variants detected.

Incontinentia Pigmenti (IP)/Brindle IP - n/n	IKBKG		Negative

Gene or region: **IKBKG**

No Incontinentia Pigmenti (IP)/Brindle IP variants detected.

Chronic Idiopathic Anhidrosis Risk (CIAR) - CIAR/n	KCNE4	Moderate Risk

Gene or region: **KCNE4**

CIA/n -One Chronic Idiopathic Anhidrosis Risk (CIAR) variant detected. Horse has moderate risk of developing the chronic form of anhidrosis (mostly represented by mild and sporadic cases of anhidrosis), and has 50% chance of passing to any offspring.

Occular Disorders

Equine Recurrent Uveitis Susceptibility Risk (ERUR) - n/n	BIEC2536712WB	Average Risk

Gene or region: **BIEC2536712WB**

No Equine Recurrent Uveitis Susceptibility Risk (ERUR) variant detected. Horse has normal risk of ERU.

Equine Recurrent Uveitis Symptom Severity (ERUS) - n/n	BIEC2421990WB	Average Risk

Gene or region: **BIEC2421990WB**

No Equine Recurrent Uveitis Symptom Severity (ERUS) variants detected. Horse has normal susceptibility for ERU symptom severity if contracted.

Squamous Cell Carcinoma Susceptibility Risk (SCC) - n/n	DDB2	Increased Risk*

Gene or region: **DDB2**

No Squamous Cell Carcinoma Susceptibility Risk (SCC) variants detected.

Skeletal Disorders

Dwarfism (D) - n/n

ACAND1... Negative

Gene or region: **ACAND1, ACAND2, ACAND3, ACAND4, ACAND5**

No Dwarfism (D) variants detected.

Friesian Dwarfism (FD) - n/n

B4GALT7 Negative

Gene or region: **B4GALT7**

No Friesian Dwarfism (FD) variants detected.

Kissing Spines Susceptibility (KSS)

ECA25 Not ordered

Lordosis

ECA20...  Not detected

Gene or region: **ECA20, ECA20, ECA20, ECA20**

Horses with one copy in each of the four Lordosis regions are not currently known to suffer any ill effects as a result. Horses with two copies in each of the four Lordosis regions exhibit signs of swayback. Currently studies are only proven in the N. Am. Saddlebred breed.

Endocrine Disorders

Equine Metabolic Syndrome Susceptibility Risk (EMS) - n/n

BIEC2263524EMS Average Risk

Gene or region: **BIEC2263524EMS**

No Equine Metabolic Syndrome Susceptibility Risk (EMS) variants detected. Horse has average risk for Equine Metabolic Syndrome.

Laminitis Susceptibility Risk - Equine Metabolic Syndrome related (LAM) - n/n	BIEC2263524_LAM	Average Risk

Gene or region: **BIEC2263524_LAM**

No Laminitis Susceptibility Risk (LAM) variants detected. Horse has average risk for EMS-related Laminitis.

Blood and Vascular Disorders

Glanzmann Thrombasthenia (GT) - n/n	ITGA2BG...	Negative

Gene or region: **ITGA2BG, ITGA2BG**

No Glanzmann Thrombasthenia (GT) variants detected.

Height

Height (H1) - n/n	LCORL	Negative

Gene or region: **LCORL**

No Height (LCORL) variants detected. Likely no added height affect.

Height (H2) - n/n	HMGA2	Negative

Gene or region: **HMGA2**

No Height (LCORL) variants detected. Likely no added height affect.

Performance and Abilities

Gait Type

DMRT3 "Gait Carrier" — DMRT3 — Possibly Affected

Gene or region: **DMRT3**

One DMRT3 or "gaited" variant; may display a wide variation in locomotion, partial "gaiting" and possible difficulty with 3 beat canter, lead change, tempi changes, or gait transitions.

Performance

Mid-Distance — MSTN — Likely Affected

Gene or region: **MSTN**

Mid-distance type; horse may have multidistance capabilities including sprint and endurance.

Temperament

Curious & Vigilant — DRD4 — Likely Affected

Gene or region: **DRD4**

One Curiosity and one Vigilance variant; horse is likely both curious and vigilant (*ongoing study).