ETALON
DIAGNOSTICS

REPORT DATE:	HORSE:	OWNER:
SEPTEMBER 16, 2023	VENUS OF RIVER'S EDGE	KATHRYN DOLAN
	HORSE ID:	**PACKAGES:**
	090823_001	ETALON DNA MINIPANEL, MINIPANEL PLUS UPGRADE

Genetic profile test results

Horse and owner information

Horse Venus of River's Edge	Date of birth 07-20-2022
Breed Gypsy Cob/Vanner	Age 1 y.o.
Color Bay, Buckskin	Sex Mare
Discipline All Around	Height 14.2 Hands
Registry Gypsy Vanner Horse Society	Reg number pending
Sire RNG Kate's Back In Black Jett	Dam Preley's Vitrovia of River's Edge
Sire Reg & No. Gypsy Vanner Horse Society GV 06600	Dam Reg & No. Gypsy Vanner Horse Society
Owner Kathryn Dolan	Address 10945 200th St SE
Phone 6127020932	City, State Red Lake Falls, MN
Email katieskennelsmn@gmail.com	Postal code 56750

Results Summary

Variant summaries:

Color: **A/a, E/E, nd2/nd2, W20/W20**

Health: **PSSM1/n, WNVR/WNVR**

Speed: **Endurance Type**

Temperament: **Curious**

Gait: **Neg for DMRT3**

Gypsy: **FIS n/n, PSSM1 PSSM1/n**

Performance and Abilities:

Curious
Two Curiosity variants; horse may be more curious than vigilant.

Non-"Gaited" DMRT3
No DMRT3 variants; likely non-gaited (*variants for novel "gait" abilities are currently in research).

Endurance
Endurance type myostatin; horse may accel at longer distance travel versus short distance sprint type activity.

Health Variants:

West Nile Virus Symptom Susceptibility Risk (WNVR) - WNVR/WNVR
WNVR/WNVR - Two West Nile Virus Symptom Susceptibility Risk (WNVR) variants detected. Horse may have higher severity of West Nile Virus symptoms if contracted. Horse has a 100% chance of passing on to any offspring. (*NOT a test for the presence of WNV).

Polysaccharide Storage Myopathy type 1 (PSSM1) - PSSM1/n
PSSM1/n - One Polysaccharide Storage Myopathy type 1 (PSSM1) variant detected, resulting in "Carrier" and “Possibly Affected” status. Caution is recommended when breeding to avoid another carrier and thus a 25% chance of "Likely Affected" offspring.

Coat color:

Bay
Black (E) + Agouti (A): Bay (A, E) is a very common coat color in horses. Bay requires at least one black variant (E) and at least one Agouti/Bay variant (A). The Agouti restricts the black pigment to the outer points including the mane, tail, lower legs, and sometimes the tips of the ears. Bay horses have black skin under their coat, except beneath white markings. Horse with two Black (EE) and two Agouti (AA) have a 100% chance of passing Black and Agouti to any offspring. Horse with one Black (Ee) and one Agouti (Aa) have a 50% chance of passing Black or Red and a 50% chance of passing Agouti to any offspring.

Dominant White 20 (W20) - W20/W20
W20/W20 - Two Dominant White 20 (W20) variants detected; may result in White markings. Horse has 100% chance of passing to any offspring.

Coat color

Base

Agouti (A) - A/a	ASIP	Likely Affected

Gene or region: **ASIP**

A/a - One Dominant Agouti variant detected. Agouti (which causes "Bay" on black) 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 - Two Black variants detected and no Red.

Modifiers

non-Dun Primitive Markings (nd) - nd2/nd2	TBX3	Negative

Gene or region: **TBX3**

nd2/nd2 - No non-Dun Primitive Markings variants 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.

Grey (G) - n/n	STX17A	Negative

Gene or region: **STX17A**

No Grey (G) variants detected.

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**

n/n - No Brindle (BR1) variants detected. Horse with Brindle (BR1) may display overall haircoat showing streaks of darker and lighter hair, similar to the brindle coat color in other species.

Dilutes

Sunshine (SUN) - n/n	SLC45ASUN	Negative

Gene or region: **SLC45ASUN**

No Sunshine variants detected.

Champagne (CH) - n/n	SLC36A1	Negative

Gene or region: **SLC36A1**

No Champagne (CH) 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".

Cream (CR) - n/n
SLC45A2
Negative

Gene or region: **SLC45A2**

No Cream (CR) variants detected.

Pearl (PRL) - n/n
SLC45A2
Negative

Gene or region: **SLC45A2**

No Pearl (prl) variants detected.

Dun (D) - n/n
TBX3
Negative

Gene or region: **TBX3**

No Dun (D) variants detected. Dun is a modifier that dilutes the base coat color often revealing Primitive Markings such as a dorsal stripe, leg barring, shadows on the face and shoulders.

Mushroom (MU) - Not Ordered
MFSD12
Not ordered

Snowdrop (SNO) - Not Ordered
SLC45ASNO
Not ordered

Whites

Dominant White 20 (W20) - W20/W20
KIT
Likely Affected

Gene or region: **KIT**

W20/W20 - Two Dominant White 20 variants detected. Likely white markings. Found in many breeds.

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

Gene or region: **EDNRB**

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

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

Gene or region: **TRPM1**

No Leopard Complex Spotting variants detected.

Pattern 1 (PATN1) - n/n
RFWD3
Negative

Gene or region: **RFWD3**

No Pattern (PATN1/n) 1 variants detected.

Sabino1 (SB1) - n/n
KIT
Negative

Gene or region: **KIT**

No Sabino (SB1) variants detected.

Tobiano (TO) - n/n
ECA3
Negative

Gene or region: **ECA3**

No Tobiano 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.

Dominant White 22 (W22) - Not Ordered	KIT	Not ordered
Dominant White 30/Aghilasse (W30) - Not Ordered	KIT	Not ordered
Dominant White 31/Merada (W31) - Not Ordered	KIT	Not ordered

Dominant White 32/Scandalous (W32) - Not Ordered	KIT	Not ordered
Dominant White 34/Flamboyant (W34) - Not Ordered	KIT	Not ordered
Dominant White 35/Holiday (W35) - Not Ordered	KIT	Not ordered
Splashed White 5 (SW5) - Not Ordered	MITF	Not ordered
Splashed White 7 (SW7) - Not Ordered	MITF	Not ordered

Coat Type

Curly Coat 1 (CU1) - n/n	KRT25	Negative

Gene or region: **KRT25**

No known Curly Coat (CU-KRT25) variants detected.

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 (FIS) variants detected.

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

Gene or region: **DNAPK**

No Severe Combined Immunodeficiency (SCID) variants detected.

Immune-Mediated Myositis (MY) - n/n	MYH1	Negative

Gene or region: **MYH1**

No Immune-Mediated Myositis variants detected. Normal susceptibility for IMM or nonexertional rhabdomyolysis.

West Nile Virus Symptom Susceptibility Risk (WNVR) - WNVR/WNVR	OAS1	Possibly Affected

Gene or region: **OAS1**

WNVR/WNVR - Two West Nile Virus Symptom Susceptibility Risk (WNVR) variants detected. Horse may have higher severity of West Nile Virus symptoms if contracted. Horse has a 100% chance of passing on to any offspring. (*NOT a test for the presence of WNV).

Equine Herpes Myeloencephalopathy Risk (EHMR) - after contracting Equine Herpes Virus type 1 (EHV1)	TSPAN9	Not ordered

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) - PSSM1/n	GYS1	Possibly Affected

Gene or region: **GYS1**

PSSM1/n - One Polysaccharide Storage Myopathy type 1 (PSSM1) variant detected, resulting in "Carrier" and “Possibly Affected” status. Caution is recommended when breeding to avoid another carrier and thus a 25% chance of "Likely Affected" offspring.

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 (RLN) - n/n	ECA3	Average Risk

Gene or region: **ECA3**

No Recurrent Laryngeal Neuropathy Risk (RLN) 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/iar, n/n	FKBP6IAR1...	Not Affected

Gene or region: **FKBP6IAR1, FKBP6IAR2**

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)	st14nfs	Not ordered

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) KCNE4 Not ordered

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 Average 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	B4GALT7Dfriesian	Negative

Gene or region: **B4GALT7Dfriesian**

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)

ITGA2BG...

Not ordered

Height

Height (H1) - n/n

LCORL

Negative

Gene or region: **LCORL**

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

Height (H2)

HMGA2

Not ordered

Performance and Abilities

Gait Type

Non-"Gaited" DMRT3	DMRT3	Negative

Gene or region: **DMRT3**

No DMRT3 variants; likely non-gaited (*variants for novel "gait" abilities are currently in research).

Performance

Endurance	MSTN	Likely Affected

Gene or region: **MSTN**

Endurance type myostatin; horse may accel at longer distance travel versus short distance sprint type activity.

Temperament

Curious	DRD4	Likely Affected

Gene or region: **DRD4**

Two Curiosity variants; horse may be more curious than vigilant.