ETALON DIAGNOSTICS

REPORT DATE: MARCH 9, 2022

HORSE: GITT A HUNKA BURN N LOVE

OWNER: KATHRYN DOLAN

Genetic profile test results

HORSE ID: 022619_084

PACKAGES: ETALON DNA MINIPANEL, ANCESTRY, COMPOSITION & BREED ANALYSIS

Horse and owner information

Horse
Gitt A Hunka Burn N Love

Breed
Gypsy Vanner

Color
Buckskin

Discipline
Dressage, Trail Class Competition, Ranch Versatility, Cart, Breeding Stallion, All Around, Western Riding, Trail Riding, Recreational, Showmanship, Pleasure Driving, Longe-Line, Horsemanship, Halter, Equitation, English Pleasure, Ranch Horse, Western Dressage

Registry
Gypsy Vanner Horse Society
Gypsy Horse Registry of America

Sire
Roman of HSF

Sire Reg & No.
Gypsy Vanner Horse Society
GV02957P

Owner
Kathryn Dolan

Phone
6127020932

Email
katieskennelsmn@gmail.com

Date of birth
04-17-2014

Age
7 y.o.

Sex
Stallion

Height
14.3 Hands

Reg number
GV03633
B00002434

Dam
Gitt Fancy Schmancy

Dam Reg & No.
Gypsy Vanner Horse Society
GV3108P

Address
10945 200th St SE

City, State
Red Lake Falls, MN

Postal code
56750

Results Summary

Variant summaries:

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

Health: **WNVR/WNVR**

Speed: **Endurance Type**

Temperament: **Curious**

Gait: **Neg for DMRT3**

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). Read more about WNVR by clicking the name of the variant above.

Coat color:

Buckskin
Bay (A, E) + Cream (CR). Buckskin is the combination of at least one Black (E), at least one Agouti/Bay (A) and one Cream (CR) variant. The Bay color will be diluted by the Cream causing Buckskin. The range of Buckskins include a very dark brown to a very light buttermilk golden color. The stark black 'points' are left undiluted. Buckskins are often confused with duns, which can have a similar coat color. However, buckskins lack the 'primitive' markings of the dun unless they also have the non-Dun Primitive Markings variant (nd1). Buckskins will pass Cream to 50% of any offspring. They will also pass Black (E) and/or Agouti/Bay (A) to at least 50% of any offspring (depending if they are Ee, Aa, or EE, Aa, or EE, AA).

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 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.

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 - One Black variant and one Red variant detected.

Modifiers

Grey (G) - n/n	STX17A	Negative

Gene or region: **STX17A**

No Grey (G) 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.

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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.

Dilutes

Sunshine (SUN) - n/n	SLC45ASUN		Negative

Gene or region: **SLC45ASUN**

No Sunshine variants detected.

Cream (CR) - CR/n	SLC45A2		Likely Affected

Gene or region: **SLC45A2**

CR/n - One Cream 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.

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".

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.

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.

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

Gene or region: **EDNRB**

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

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

Gene or region: **TRPM1**

No Leopard Complex Spotting (SP) 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.

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.

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. Read more about LWO by clicking the name of the variant above.

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. Read more about CSNB by clicking the name of the variant above.

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). Read more about MCOA by clicking the name of the variant above.

Immune System

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

Gene or region: **SLC5A3**

No Foal Immunodeficiency Syndrome (FIS) variants detected. Read more about FIS by clicking the name of the variant above.

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

Gene or region: **DNAPK**

No Severe Combined Immunodeficiency (SCID) variants detected. Read more about SCID by clicking the name of the variant above.

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). Read more about WNVR by clicking the name of the variant above.

Immune-mediated Myositis (IMM)	MYH1	Not ordered

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

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Muscle Disorders

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

Gene or region: **GBE1**

No Glycogen Branching Enzyme Deficiency (GBED) variants detected. Read more about GBED by clicking the name of the variant above.

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

Gene or region: **SCN4A**

No Hyperkalemic Partial Paralysis (HYPP) variants detected. Read more about HYPP by clicking the name of the variant above.

Malignant Hyperthermia (MH) - n/n	RYR1		Negative

Gene or region: **RYR1**

No Malignant Hyperthermia (MH) variants detected. Read more about MH by clicking the name of the variant above.

Myotonia (MYT) - n/n	CLCN4		Negative

Gene or region: **CLCN4**

No Myotonia (MYT) variants detected. Read more about MYT by clicking the name of the variant above.

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

Gene or region: **GYS1**

No Polysaccharide Storage Myopathy type 1 (PSSM1) variants detected. Read more about PSSM1 by clicking the name of the variant above.

Neurologic Disorders

Cerebellar Abiotrophy (CA) - n/n	MUTYH	Negative

Gene or region: **MUTYH**

No Cerebellar Abiotrophy (CA) variants detected. Read more about CA by clicking the name of the variant above.

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

Gene or region: **MYO5A**

No Lavender Foal Syndrome (LFS) variants detected. Read more about LFS by clicking the name of the variant above.

Hydrocephalus (HDC)	B3GALNT2	Not ordered

Recurrent Laryngeal Neuropathy (RLN)	ECA3	Not ordered

Reproductive Disorders

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

Gene or region: **AR**

No pattern of Androgen Insensitivity Syndrome (AIS) variants detected. Read more about AIS by clicking the name of the variant above.

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. Read more about IAR by clicking the name of the variant above.

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. Read more about HERDA by clicking the name of the variant above.

Junctional Epidermolysa Bullosis type 1 (JEB1) - n/n	LAMC2	Negative

Gene or region: **LAMC2**

No Junctional Epidermolysa Bullosis type 1 (JEB1) variants detected. Read more about JEB1 by clicking the name of the variant above.

Junctional Epidermolysa Bullosis type 2 (JEB2) - n/n	LAMA3	Negative

Gene or region: **LAMA3**

No Junctional Epidermolysa Bullosis type 2 (JEB2) variants detected. Read more about JEB2 by clicking the name of the variant above.

"Warmblood" Fragile Foal Syndrome (FFS)	PLOD1	Not ordered
Hoof Wall Separation Disease (HWSD)	SERPINB11	Not ordered
Naked Foal Syndrome (NFS)	st14nfs	Not ordered
Chronic Idiopathic Anhidrosis Risk (CIAR)	KCNE4	Not ordered

Occular Disorders

Equine Recurrent Uveitis Susceptibility Risk (ERUR)	BIEC2536712WB	Not ordered
Equine Recurrent Uveitis Symptom Severity (ERUS)	BIEC2421990WB	Not ordered
Squamous Cell Carcinoma Susceptibility Risk (SCC)	DDB2	Not ordered

Skeletal Disorders

Dwarfism (D)	ACAND1...	Not ordered
Friesian Dwarfism (FD)	B4GALT7	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)	BIEC2263524EMS	Not ordered

Laminitis Susceptibility Risk - Equine Metabolic Syndrome related (LAM)	BIEC2263524_LAM	Not ordered

Height

Height (H1)	LCORL	Not ordered
Height (H2)	HMGA2	Not ordered

Performance and Abilities

Gait Type

Non-"Gaited" DMRT3	DMRT3		Detected

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		Detected

Gene or region: **DRD4**

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