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Geschäftsstelle Weimar: Im Boden 1 · 99438 Weimar · Tel.: 0 36 43/ 24 88-0 · Fax: 0 36 43/ 24 88 15



**Pferdezuchtverband
Sachsen-Thüringen e.V.**

SNP data analysis

DE 484840031917

HB 1 Penancing-Brook Bailys (Conne)

Sex: H Year of breeding: 2017 Date of birth: 13.05.2017 Breed: Connemara Color: Dark liver dun

Applicant: 960978, Bonanima CZ 78701 Sumperk, Radnicni 3288/10

Sample: SNP data analysis

Order ID: 868365
Sample ID: H25-16580
Date of receipt: 06.03.2025
Institute: IFN Schönow

Characteristic examined: **Dilution**

Application date: 25.02.2025
Result date: 15.03.2025
Analysis: vit w.V.
Order ID: 868365
Gene locus: Genotype:
Champagne n/n
Cream n/Cr

Result interpretation:

Homozygous normal for Champagne. The genotype n/n at the Champagne locus means that there is no copy of the mutation which is effective as dilution factor. No Ch allele will be passed on to progeny.

Heterozygous for Cream (carrier). The genotype n/Cr at the Cream locus means that there is one copy of the mutation which is diluting red pigment. Dependent on the base color of the horse, its coat color is Palomino (for base color chestnut) or Buckskin (for base color bay). The coat color is called 'Smoky Black' for base color black although the diluting (lightening) effect may not be visible in the black coat. The Cr allele can be passed on to progeny, such that foals with correspondingly diluted coat colors can occur.



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Sachsen-Thüringen e.V.**

SNP data analysis

DE 484840031917

HB 1 Penancing-Brook Bailys (Conne)

Sex: H Year of breeding: 2017 Date of birth: 13.05.2017 Breed: Connemara Color: Dark liver dun

Applicant: 960978, Bonanima CZ 78701 Sumperk, Radnicni 3288/10

Sample: SNP data analysis

Order ID: 868365
Sample ID: H25-16580
Date of receipt: 06.03.2025
Institute: IFN Schönow

Characteristic examined: **Base colors**

Application date: 25.02.2025
Result date: 15.03.2025
Analysis: vit w.V.
Order ID: 868365
Gene locus: Genotype:
Agouti A/A
Extension E/e

Result interpretation:

Homozygous for non-black. The base color of the coat of horses with the genotype A/A at the Agouti locus is dependent on the Extension genotype, so may be bay (E/E, E/e) or chestnut (e/e). Among the progeny, no foals with base color black can occur.

Heterozygous for chestnut (carrier). The base color of the coat of horses with the genotype E/e at the Extension locus is dependent on the Agouti genotype, so may be bay (A/A, A/a) or black (a/a). Among the progeny, foals with base color chestnut can occur.

For breeding use, the overall finding of genotypes E/e A/A implies, that the base color genotype of the chosen mating partner will influence the coat color of the foal. Progeny of the base coat colors chestnut or bay can occur.



SNP data analysis

DE 484840031917

HB 1 Penancing-Brook Bailys (Conne)

Sex: H Year of breeding: 2017 Date of birth: 13.05.2017 Breed: Connemara Color: Dark liver dun

Applicant: 960978, Bonanima CZ 78701 Sumperk, Radnicni 3288/10

Sample: SNP data analysis

Order ID: 868365
Sample ID: H25-16580
Date of receipt: 06.03.2025
Institute: IFN Schönnow

Characteristic examined: **Dominant White**

Application date: 25.02.2025
Result date: 15.03.2025
Analysis: vit w.V.
Order ID: 868365

Gene locus:	Genotype:
Dominantes Weiss / W16	n/n
Dominantes Weiss / W18	-/-
Dominantes Weiss / W20	n/n
Dominantes Weiss / W8	-/-
Dominantes Weiss / W9	-/-

Result interpretation:

Homozygous normal for the W16 mutation of the KIT gene for Dominant White / White Spotting. The genotype n/n at the W16 locus means that there is no copy of the breed- and family-specific mutation which is causing white coat color in the Oldenburg horse. No W16 allele will be passed on to progeny.

No specification of the genotype possible.

Homozygous normal for the W20 mutation of the KIT gene for Dominant White / White Spotting. The genotype n/n at the W20 locus means that there is no copy of the mutation which occurs in different breeds and is causing or intensifying white patterns. No W20 allele will be passed on to progeny.

No specification of the genotype possible.

No specification of the genotype possible.