LABOKLIN
LABOR FÜR KLINISCHE DIAGNOSTIK GMBH & CO. KG

Laboklin GmbH & Co. KG, Steubenstraße 4, 97688 Bad Kissingen

Report No.:	**2304-W-24249**
Date of arrival:	11.04.2023
Date of report:	26.03.2024
Testing started:	11.04.2023
Testing completed:	18.04.2023
Status of the report:	Final report

Species:	Dog
Breed:	Collie Rough
Gender:	Female
Name:	Dennisay's Black velvet
Chip No.:	191035000178816
Date of birth / Age:	21.02.2023
Type of sample:	Swab
Sampler:	Dr. Anne-Marie Dethier
Owner / Animal-ID:	Esser, Dr. Simone
IT No. / Report-ID:	---

supplemental result 15.05.2023
- This result replaces the earlier result with the same number! -

Degenerative Myelopathy - PCR

Result: Genotype N/N (exon 2)

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the high-risk factor for DM in exon 2 of the SOD1-gene.

Trait of inheritance: autosomal-recessive

Please note: In the Bernese Mountain Dog breed the mutation in exon 1 of the SOD1-gene also occurs in correlation with DM.

Inflammatory pulmonary disease (IPD) - PCR

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype allele. It does not carry the causative mutation for IPD in the AKNA gene.

Trait of inheritance: autosomal recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Collie

MDR1 gene variant - PCR

Result: Genotype N/MDR (+/-)

Interpretation: The examined animal is heterozygous for the causative mutation for MDR in the ABCB1-gene.

Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Australian Shepherd, Border Collie, Elo, German Shepherd, Longhaired Whippet, McNab, Old English Sheepdog, Rough/Smooth Collie, Shetland Sheepdog, Silken Windhound, Wõller, White Shepherd

Please note: in individual cases, heterozygous dogs can show clinical signs!

The DNA-test is run according to the publication of Mealey et al. (2001) "Ivermectin sensitivity in collies is associated with a deletion mutation of the mdr1 gene." and detects the mutation MDR1 nt230 (del4).

Dermatomyositis (DMS) - PCR

Locus A	PAN2	**A/A**
Locus B (MAP3K7CL)		**b/b**
Locus C (DLA-DRB1)		**C/c (DRB1*01501/DRB1*00201)**

Assessment of Risk:

The likelihood of an individual dog developing DMS can be classified as low (0%-5%), moderate (33%-50%), or high (90%-100%) based on the genotype combination of Locus A (PAN2), Locus B (MAP3K7CL), and Locus C (DLA-DRB1). Wild type alleles of loci A and B are represented by lower case letters, a and b, while the risk alleles are represented by upper case letters A and B. The risk allele at DLA complex (DLA-DRB1*002:01) is referred to as C, and the lower case letter c represents any alternate allele for DLA-DRB1.

LOW RISK GENOTYPES: aabbCC, aabbCc, AabbCC, AabbCc, aaBbcc, aaBbCC, aaBbCc, AaBbCC, AaBbCc, aaBBCc

MODERATE RISK GENOTYPES: AAbbCC, AAbbCc, aaBBCC, AaBBCc, AABbCc

HIGH RISK GENOTYPES: AABbCC, AaBBCC, AABBCC, AABBCc

Scientific studies found correlation between these markers and signs of the disease in the following breeds: Collie, Shetland Sheepdog

rcd2-PRA - PCR

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for rcd2-PRA in the RD3-gene.

Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Collie

Collie Eye Anomaly (CEA) - PCR *

Result: Genotype N/CEA

Interpretation: The examined animal is heterozygous for the causative mutation for CEA in the NHEJ1-gene.

Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Australian Kelpie and Shepherd, Bearded Collie, Border Collie, Boykin Spaniel, Hokkaido, Lancashire Heeler, Longhaired Wippet, Nova Scotia Duck Tolling Retriever, Rough/Smooth Collie, Shetland Sheepdogs, Silken Windhound

The current result is only valid for the sample submitted to our laboratory. The sender is responsible for the correct information regarding the sample material.The laboratory can not be made liable. Furthermore, any obligation for compensation is limited to the value of the tests performed.

There is a possibility that other mutations may have caused the disease/phenotype. The analysis was performed according to the latest knowledge and technology.

The laboratory is accredited for the performed tests according to DIN EN ISO/IEC 17025:2018. (except partner lab tests).

Breeding club discounts were granted for discountable services!

Sampling:

The following impartial person (veterinarian, breed warden, or similar) signed the form for the sampling and identity check of the animal:

Dr. Anne-Marie Dethier

These results are based on the sample material submitted to our laboratory.

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*: test performed by partner laboratory

Fr. Dipl.-Ing. Christina Dangel
Abt. Molekularbiologie

***** END of report *****

*** News from the laboratory ***

Spring is just around the corner. After the winter, remember to check the parasite status of your patients. In addition to the classic parasitological examination we also offer many species-specific parasite profiles. Please also take a look at the publication on parasitology in the current edition of "Parasitology Research": https://link.springer.com/article/10.1007/s00436-024-08181-6

LABOKLIN
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Laboklin GmbH & Co. KG, Steubenstraße 4, 97688 Bad Kissingen

Report No.:	**2307-W-93565**
Date of arrival:	12.07.2023
Date of report:	26.03.2024
Testing started:	12.07.2023
Testing completed:	19.07.2023
Status of the report:	Final report

Species:	Dog
Breed:	Collie Rough
Gender:	Female
Name:	Dennisay's Black velvet
Chip No.:	191035000178816
Date of birth / Age:	21.02.2023
Type of sample:	Swab
Sampler:	Dr. Anne-Marie Dethier
Owner / Animal-ID:	Esser, Dr. Simone
IT No. / Report-ID:	---

Additional Order of 12.07.2023 to Report-No. 2304-W-24249 Original Sample received on: 11.04.2023

M-locus* (alleles: Mh, M, Ma+, Ma, Mc+, Mc, m and mosaics) - PCR *

Result: Genotype m/m

Result: Genotype m/m

Interpretation: The examined animal is homozygous for the m-allele for non-merle.

The test detects the alleles Mh (harlequin merle), M (merle), Ma+ and Ma (atypic merle), Mc+ and Mc (cryptic merle) and m (non-merle).

Allelic series: Mh, M, Ma+, Ma, Mc+, Mc > m

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There is a possibility that other mutations may have caused the disease/phenotype. The analysis was performed according to the latest knowledge and technology.

The laboratory is accredited for the performed tests according to DIN EN ISO/IEC 17025:2018. (except partner lab tests).

Sampling:

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Dr. Anne-Marie Dethier

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These results are based on the sample material submitted to our laboratory.

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*: test performed by partner laboratory

Christine Dirauf

Fr. Dr. Christine Dirauf
Abt. Molekularbiologie

***** END of report *****

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Laboklin GmbH & Co. KG , Steubenstraße 4 , 97688 Bad Kissingen

Report No.: 2306-W-93238
Date of arrival: 21.06.2023
Date of report: 18.07.2023
Testing started: 21.06.2023
Testing completed: 18.07.2023
Status of the report: Final report

Species: Dog
Breed: Collie Rough
Gender: Female
Name: Dennisay's Black velvet
Chip No.: 191035000178816
Date of birth / Age: 21.02.2023
Type of sample: Swab
Sampler: Dr. Anne-Marie Dethier
Owner / Animal-ID: Esser, Dr. Simone
IT No. / Report-ID: ---

Additional Order of 15.05.2023 to Report-No. 2304-W-24249 Original Sample received on: 11.04.2023

Premium SNP DNA-profile (ISAG 2020)

001_012: **AG_AG_GG_AA_GG_GG_GG_AA_GG_CC_GG_GG**
013-024: **AA_GG_GG_AA_GG_AA_AA_AA_AG_AA_AG_GG**
025-036: **AG_GG_AG_AA_AG_AA_AG_GG_GG_AA_AA_AA**
037-048: **AA_AG_AC_CC_GG_AA_AA_GG_AA_AA_AA_AA**
049-060: **GG_AA_AG_AA_GG_AG_AG_AA_GG_AG_AA_AA**
061-072: **AC_CC_GG_AG_AG_GG_AG_GG_GG_AA_AC_CC**
073-084: **GG_CC_AA_AG_AC_GG_..._GG_AA_AG_AA_CC**
085-096: **GG_AA_GG_GG_GG_GG_AC_GG_AG_AA_GG_AA**
097-108: **AG_AG_AA_AA_GG_AA_AA_AC_AG_GG_GG_GG**
109-120: **GG_GG_AA_AG_AG_GG_AA_GG_AA_AA_AG_AG**
121-132: **AG_GG_AA_GG_GG_AA_AA_AA_GG_AG_GG_GG**
133-144: **AG_GG_AG_AA_GG_AG_AG_AA_GG_AA_AG_GG**
145-156: **AA_AA_AA_GG_GG_AG_GG_CC_GG_AA_AA_GG**
157-168: **AA_GG_GG_CC_AA_AG_AA_AA_GG_AA_AA_AA**
169-180: **AA_GG_CC_AA_AA_AG_GG_GG_GG_AG_GG_GG**
181-192: **AA_AG_GG_GG_AA_GG_GG_GG_AG_AA_AA_GG**
193-204: **AA_GG_GG_..._AA_GG_GG_AA_AA_GG_AA_AG**
205-216: **AA_AA_AG_AA_AA_CC_AA_AG_AA_AA_AG_AG**
217-228: **GG_GG_AG_CC_AG_AC_GG_GG_AG_AG_AA_AG**
229-230: **AC_AA**
sex: **X/X**

Information on the Premium SNP DNA Profile

The Premium SNP DNA Profile is your animal's genetic fingerprint and uinquely identifies it. It remains the same throughout the animal's life and cannot be manipulated. Every one of the DNA profiles created in our laboratory is saved in our DNA database and is available to you permanently. The DNA profile does not contain any information on traits or diseases of your pet. The Premium SNP DNA Profile evaluates all of the SNPs recommended by the ISAG from (1) the core panel and (2) the auxiliary panel (numbers 001-230). The following table lists the corresponding internationally valid ISAG nomenclature (Cfa_Chromosom:Position) of the examined SNPs.

Num	Panel	Chr:Pos
001	1	Cfam_1:3962719
002	1	Cfam_1:20842130
003	1	Cfam_1:70238933
004	1	Cfam_1:80971770
005	1	Cfam_1:106430955
006	1	Cfam_1:119414584
007	1	Cfam_2:2610859
008	1	Cfam_2:38293797
009	1	Cfam_2:77806065
010	1	Cfam_3:1252765
011	1	Cfam_3:24757939
012	1	Cfam_3:73570828
013	1	Cfam_4:31301072
014	1	Cfam_4:64121754
015	1	Cfam_4:75910211
016	1	Cfam_4:86049027
017	1	Cfam_5:5410890
018	1	Cfam_5:26320165
019	1	Cfam_5:85451804
020	1	Cfam_6:11553458
021	1	Cfam_6:33976751
022	1	Cfam_6:64006720
023	1	Cfam_7:76294
024	1	Cfam_7:15011628
025	1	Cfam_7:36555518
026	1	Cfam_8:5291824
027	1	Cfam_8:18121580
028	1	Cfam_8:45852939
029	1	Cfam_8:63196958
030	1	Cfam_9:22610227
031	1	Cfam_9:40096141
032	1	Cfam_9:52710991
033	1	Cfam_9:60437147
034	1	Cfam_10:10652659
035	1	Cfam_10:22409408
036	1	Cfam_10:30034450
037	1	Cfam_10:66922269
038	1	Cfam_11:5318488
039	1	Cfam_11:23907101
040	1	Cfam_11:65603333
041	1	Cfam_12:5579055
042	1	Cfam_12:35306641
043	1	Cfam_12:55201839
044	1	Cfam_12:68125319
045	1	Cfam_13:8704192
046	1	Cfam_13:59896033
047	1	Cfam_14:50063321
048	1	Cfam_14:58465266
049	1	Cfam_15:19299365
050	1	Cfam_15:22834903
051	1	Cfam_16:29634940
052	1	Cfam_16:46884446
053	1	Cfam_16:57958947
054	1	Cfam_17:10649078
055	1	Cfam_17:34462308
056	1	Cfam_17:39124697
057	1	Cfam_18:6745949
058	1	Cfam_18:54361347
059	1	Cfam_19:841347
060	1	Cfam_19:15926130
061	1	Cfam_19:27288167
062	1	Cfam_19:47470564
063	1	Cfam_20:13740894
064	1	Cfam_20:49900586
065	1	Cfam_20:57167714
066	1	Cfam_21:15558670
067	1	Cfam_21:25537675
068	1	Cfam_21:35719434
069	1	Cfam_22:641125
070	1	Cfam_22:26694580
071	1	Cfam_22:55308193
072	1	Cfam_23:42886681
073	1	Cfam_23:50772488
074	1	Cfam_24:23393510
075	1	Cfam_24:29909901
076	1	Cfam_24:47381908
077	1	Cfam_25:2073511
078	1	Cfam_25:33986348
079	1	Cfam_25:47708600
080	1	Cfam_26:20004896
081	1	Cfam_26:35071515
082	1	Cfam_27:2619058
083	1	Cfam_27:22599860
084	1	Cfam_27:41049333
085	1	Cfam_28:9877730
086	1	Cfam_28:18509221
087	1	Cfam_28:38885325
088	1	Cfam_29:251970
089	1	Cfam_29:9625359
090	1	Cfam_29:17561258
091	1	Cfam_29:36319325
092	1	Cfam_30:3896482
093	1	Cfam_30:15542105
094	1	Cfam_30:32852404
095	1	Cfam_31:21068798
096	1	Cfam_31:39391935
097	1	Cfam_32:679380
098	1	Cfam_32:17792284
099	1	Cfam_32:32382778
100	1	Cfam_33:15018500
101	1	Cfam_33:23742061
102	1	Cfam_34:195313
103	1	Cfam_34:24396298
104	1	Cfam_35:15345329
105	1	Cfam_36:3565500
106	1	Cfam_36:12714421
107	1	Cfam_36:23459390
108	1	Cfam_37:9398945
109	1	Cfam_37:15436615
110	1	Cfam_37:27667297
111	1	Cfam_38:9224942
112	1	Cfam_38:17657161
113	1	Cfam_38:20441216
114	2	Cfam_1:72613047
115	2	Cfam_1:74450772
116	2	Cfam_1:119306331
117	2	Cfam_3:10255068
118	2	Cfam_3:37849557
119	2	Cfam_3:43055696
120	2	Cfam_3:43063677
121	2	Cfam_3:64084413
122	2	Cfam_3:90291255
123	2	Cfam_3:91626907
124	2	Cfam_4:42104780
125	2	Cfam_4:67040898
126	2	Cfam_4:70217695
127	2	Cfam_5:13080303
128	2	Cfam_5:36642434
129	2	Cfam_5:44650576
130	2	Cfam_5:55349573
131	2	Cfam_5:64611038
132	2	Cfam_7:3318809
133	2	Cfam_7:6423299
134	2	Cfam_7:15017979
135	2	Cfam_7:76487265
136	2	Cfam_8:6188937
137	2	Cfam_8:19076567
138	2	Cfam_8:24614720
139	2	Cfam_8:52381322
140	2	Cfam_8:67183794
141	2	Cfam_9:20867959
142	2	Cfam_9:32506288
143	2	Cfam_9:50114927
144	2	Cfam_9:56021221
145	2	Cfam_10:8085469
146	2	Cfam_10:14685262
147	2	Cfam_10:39548483
148	2	Cfam_10:47923623
149	2	Cfam_10:57954366
150	2	Cfam_11:1161870
151	2	Cfam_11:62157625
152	2	Cfam_11:70698603
153	2	Cfam_12:6337286
154	2	Cfam_12:8532712
155	2	Cfam_12:23059939
156	2	Cfam_12:40681020
157	2	Cfam_12:70657733
158	2	Cfam_13:40616856
159	2	Cfam_14:55735620
160	2	Cfam_16:29675662
161	2	Cfam_16:58093031
162	2	Cfam_17:9407683
163	2	Cfam_17:12787849
164	2	Cfam_17:57371669
165	2	Cfam_18:10189759
166	2	Cfam_18:16385020
167	2	Cfam_18:16388978
168	2	Cfam_18:31579269
169	2	Cfam_18:47325586
170	2	Cfam_19:30246414
171	2	Cfam_19:40189405
172	2	Cfam_19:42756283
173	2	Cfam_20:6046176
174	2	Cfam_20:45777531
175	2	Cfam_20:48602465
176	2	Cfam_21:22581321
177	2	Cfam_21:29796784
178	2	Cfam_21:31751817
179	2	Cfam_22:20498421
180	2	Cfam_22:33934047
181	2	Cfam_22:37522364
182	2	Cfam_22:39647748
183	2	Cfam_22:61153661
184	2	Cfam_23:44497217
185	2	Cfam_23:48055836
186	2	Cfam_24:18599997
187	2	Cfam_24:27925354
188	2	Cfam_24:30954773
189	2	Cfam_24:43589304
190	2	Cfam_24:45191477
191	2	Cfam_25:4614777
192	2	Cfam_27:20948372
193	2	Cfam_27:34444177
194	2	Cfam_27:42526114
195	2	Cfam_28:9703418
196	2	Cfam_28:12804225
197	2	Cfam_28:34478533
198	2	Cfam_28:35104850
199	2	Cfam_29:4020192
200	2	Cfam_29:4022252
201	2	Cfam_29:19681270
202	2	Cfam_29:22992304
203	2	Cfam_30:10012939
204	2	Cfam_30:11735245
205	2	Cfam_30:27619023
206	2	Cfam_31:20912553
207	2	Cfam_32:13183511
208	2	Cfam_33:15233992
209	2	Cfam_33:22070526
210	2	Cfam_33:22472901
211	2	Cfam_33:22648231
212	2	Cfam_34:24351570
213	2	Cfam_34:34993916
214	2	Cfam_34:37323213
215	2	Cfam_34:41703614
216	2	Cfam_35:15283717
217	2	Cfam_36:288045
218	2	Cfam_36:9241262
219	2	Cfam_36:10084888
220	2	Cfam_36:12723744
221	2	Cfam_36:18627936
222	2	Cfam_37:18338930
223	2	Cfam_37:26611359
224	2	Cfam_37:28611801
225	2	Cfam_37:30110473
226	2	Cfam_37:30902202
227	2	Cfam_38:13098194
228	2	Cfam_38:15271384
229	2	Cfam_38:19172567
230	2	Cfam_38:20930997

Activation Code: **00862C96030CAEF7**

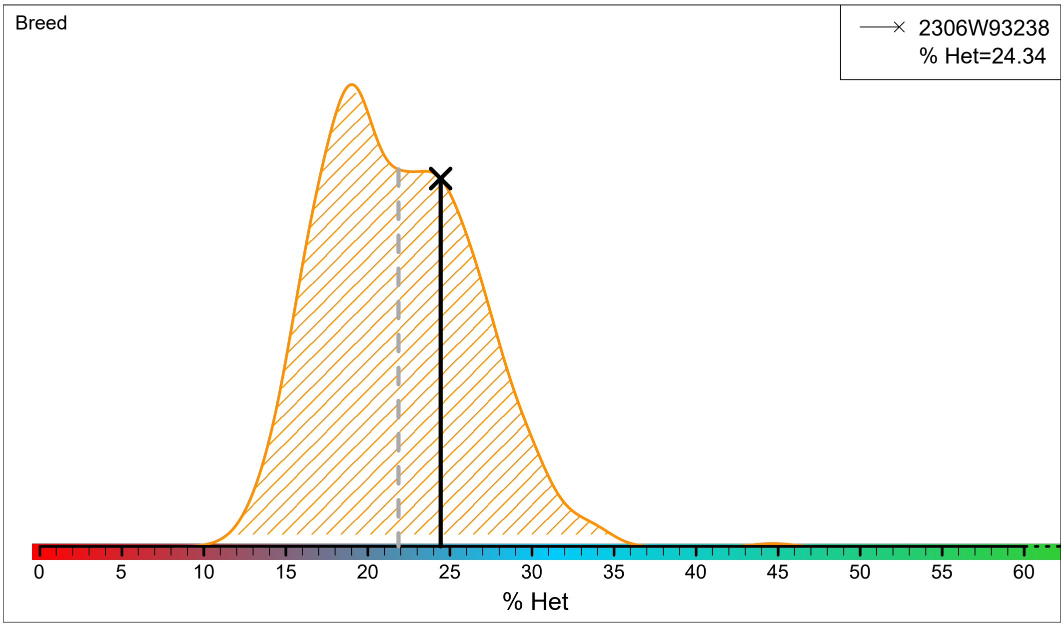
This activation code is used to display the Labogen Diversity Check online at diversity.labogen.com. The Labogen Diversity Check always shows the most up-to-date genetic breed data from the Premium SNP DNA profile (ISAG 2020).

Sampling:

The following impartial person (veterinarian, breed warden, or similar) signed the form for the sampling and identity check of the animal:

Dr. Anne-Marie Dethier

Genetic Variability (Heterozygosity)



This graph shows the genetic variability (heterozygosity) of your animal. Heterozygosity (% Het) describes the percentage of genetic markers (SNPs) for which your dog has inherited different variants from its mother and its father. According to current scientific knowledge, dogs with a high degree of heterozygosity within a breed are less often affected by inbreeding than dogs with a low degree of heterozygosity.

For the calculation of heterozygosity we use the genetic fingerprint (the Premium SNP DNA profile) and hundreds of other genetic markers in your dog's DNA. In the graph, your dog is marked with a cross and a black solid line.

Once LABOKLIN has examined a sufficiently large reference population for your breed, you can see the genetic variability of the entire breed population as an area shaded in orange. The mean value of the breed is marked as a grey dashed line.

Small population sizes and inbreeding can decrease the heterozygosity of a breed. When breeding, animals with a high degree of heterozygosity within their breed might thus contribute to the preservation of the breed's genetic diversity. However, please note that heterozygosity cannot be used to draw any conclusions about individual factors such as genetic diseases or characteristics like coat colour. Maintaining genetic variability can be a building block in responsible dog breeding, but it should not be viewed in isolation. More information can be found on our homepage:
https://shop.labogen.com/en/premium-snp-dna-profile-isag-2020

Breeding club discounts were granted for discountable services!

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Fr. MSc Laura Hübner
Abt. Molekularbiologie

***** END of report *****

Laboklin App

***** FGF23: our new kidney parameter for dogs and cats! *****

FGF23 is a marker for monitoring renal diseases which often indicates disorders of phosphate metabolism earlier than serum total phosphate in dogs and cats with early-stage CKD. With the result, it is possible to assess whether the animal could benefit from phosphate-lowering treatment. (https://www.mdpi.com/2076-2615/13/11/1853)