

Data Conflict Resolution

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Goals

- Users of the National Cooperators Database will understand:
 - Where to find pedigree and genomic conflicts
 - Impact of incorrect pedigree data on genomic conflicts
 - How to troubleshoot when pedigree fixes for genomic conflicts fail

What is a “useable” genotype?

- A usable genotype (Use=Y) is a genotype that:
 - Passed quality control checks
 - Has no sex conflicts with the pedigree
 - Has no genomic conflicts with close relatives causing the pedigree to appear unreliable

https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/CDCB_Genomic_Dictionary

Pedigree and Genotype Interaction

- Genotype determines animals x, y, and z are all related.
- Pedigrees determine who was born first
- This interaction between pedigree and genotype relies on accurate pedigree birth dates, multiple birth codes (MBCs), and parentage.
 - Genomic conflicts arise when pedigrees are incorrect

Pedigrees

- Pedigree data is provided by many sources
 - Source code indicates who the data provider is
 - If a record needs to be corrected, the organization related to the record source can submit changes.
 - Source code A is generated automatically by CDCB

Code	Description
B	Breed Associations (USA and CAN) and CDDR exchange partners (bulls only)
N/R/I	NAAB, any nominator (except breed associations), Interbull and International pedigree without regular pedigree update
D	Dairy Records Processing Center (DRPC)
H	Pedigree provided in a health record from a National Association of Animal Breeders (NAAB) source
C	CDCB internal use only
A	CDCB

Pedigree Interactions

- Phenotypic data such as breeding, calving, and lactation data provided by DRPCs can interact with pedigrees
 - End of lactation date, fresh dates, progeny
- Goal: Pedigree, phenotypic, and genotypic data all agrees

☐ Select All ☒ Pedigree (fmt-1) ☐ Lactation (fmt-4) ☐ Reproduction (fmt-5) ☐ Health (fmt-6) Apply Clear

▼ Pedigree (fmt-1) | 1 Source File

▼ Errors in File 20260420.1G.

Error Code	Disposition Code	Description	ID	Herd	Source Code	Date
5Fd	Notified	Input is verified (@89) and birth date is within 90 days of master file birth. Source of input and master file pedigree is not breed. Input birth date is within 31 days of dam's calving date. Master file birth date will be updated.		65060092	D	2025-01-15

Sire	Dam	Cross Reference	DOB	Source Code	Processing Date	Record Type	Verification Code	Multi-Birth Code	Registry Status	File Name
JE840003200210433	JE840003210986158		2025-01-11	N	2026-04-20	P	2	2		20260420.1G.

Processing of Pedigrees

- Pedigrees submitted by nominators through Format 1 or Format 1G

0FH0840003282837717H0840003218556317H0840003149596913

20240307B20240321P01399000000

- Format 1/ Format 1G can be submitted in two ways
 - SFTP
 - WebConnect

https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Format_1

General Format 1 structure (first 99 bytes):

0FH0840003282837717H0840003218556317H0840003149596913

20240307B20240321P01399000000

Byte Position(s): 2

Definition: Sex Code

Example: F

Other information: F = Female, M = Male

General Format 1 structure (first 99 bytes):

0FH0840003282837717H0840003218556317H0840003149596913

20240307B20240321P01399000000

Byte Position(s): 3-19

Definition: Animal ID

Example: H0840003282837717

Other information: Breed Code (3-4)

Country Code (5-7)

Unique 12-byte ID (8-19)

General Format 1 structure (first 99 bytes):

0FH0840003282837717H0840003218556317H0840003149596913

20240307B20240321P01399000000

Byte Position(s): 20-36

Definition: Sire ID

Example: H0840003218556317

Other information: Breed Code (20-21)

Country Code (22-24)

Unique 12-byte ID (25-36)

General Format 1 structure (first 99 bytes):

0FH0840003282837717H0840003218556317H0840003149596913

20240307B20240321P01399000000

Byte Position(s): 37-53

Definition: Dam ID

Example: H0840003149596913

Other information: Breed Code (37-38)

Country Code (39-41)

Unique 12-byte ID (42-53)

General Format 1 structure (first 99 bytes):

0FH0840003282837717H0840003218556317H0840003149596913 20240307B20240321P01399000000

Byte Position(s): 54-70

Definition: Alternate ID Field

Example: Blank

Other information: Breed Code (54-55)

Country Code (56-58)

Unique 12-byte ID (59-70)

General Format 1 structure (first 99 bytes):

0FH0840003282837717H0840003218556317H0840003149596913

20240307B20240321P01399000000

Byte Position(s): 71-78

Definition: Birth Date

Example: 20240307

Other information: YYYYMMDD format

General Format 1 structure (first 99 bytes):

0FH0840003282837717H0840003218556317H0840003149596913

20240307B20240321P01399000000

Byte Position(s): 79

Definition: Source Code

Example: B

General Format 1 structure (first 99 bytes):

0FH0840003282837717H0840003218556317H0840003149596913

20240307B20240321P01399000000

Byte Position(s): 88
 Definition: Record Type
 Example: P
 Others: P, G, X, R, C, D, Y, N, U are
 all valid values for Format 1
<https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/REFERENCES#Ref121>

Code	Record Type Code Description
P	Pedigree
G	Nomination
X	Cross-Reference
R	ReID
C	Clone
D	Delete Pedigree
Y	Delete Cross-Reference
N	Delete Clone
U	Move Genotype

General Format 1 structure (first 99 bytes):

0FH0840003282837717H0840003218556317H0840003149596913
20240307B20240321P01399000000

Byte Position(s): 89

Definition: Verification Code

Example: 0

Pedigree verification code	
Code	Description
0	No correction or verification (record does not include any corrections or does not require any special override / verification)
1	Identification in record replaces any previously reported information for animal (correction code)
2	Identification correct although somewhat unusual (verification code)
3	Delete CDCB's supplied dam or constructed dam and prevent further fill-in by CDCB
4	Delete CDCB's supplied sire and prevent further fill-in by CDCB
5	Nomination of animal without verification of pedigree (except birth) No correction of existing pedigree. (For use with record type G only) INTERNAL USE ONLY
6	Change dam's service sire to match sire
7	Sire verified unknown (Breed associations only)
8	Dam verified unknown (Breed associations only)
9	Sire and dam verified unknown (Breed associations only)
D	Allow CDCB to resume fill-in of dam again INTERNAL USE ONLY
S	Allow CDCB to resume fill-in of sire again INTERNAL USE ONLY

General Format 1 structure (first 99 bytes):

0FH0840003282837717H0840003218556317H084000314959691320240307B20240321P01399000000

Byte Position(s): 91
Definition: MBC
Example: 3
Other information: Valid values 1-6

Code	Multiple Birth Code Description
1	Single
2	Multiple birth (fraternal or identical twins, not from embryo transfer. Twins share the same genomic and gestational dam).
3	Birth from embryo transfer
4	Split embryo (artificially or naturally after embryo implantation)
5	Clone from nuclear transfer
6	Embryo pedigree (implantation date stored as birth date)

Processing of Pedigrees

- ID is always checked
 - New IDs create new internal keys
 - Existing IDs checked against existing CDCB pedigree
- Pedigree parentage is checked with birth date and MBC
 - This check verifies the pedigree makes sense with the available data
 - Examples of available data
 - Birth date of parents
 - Breeding and lactation date of dam
 - Birth dates and MBC of siblings
 - Existence of other pedigrees with identical parentage and birth dates

Processing of Pedigrees

- Outcomes of pedigree processing
 - Notify (N): an informational notice and the record was accepted
 - Change (C): the information was changed by CDCB but the record continued down the pipeline
 - Rejected (R): part or all parts of the record was rejected
- Notifications regardless of the outcome will be sent to SFTP
 - X.1EX – Pedigree errors Format 1 files
 - notify_VAL.X – Nomination verifications, Y or N
 - notify_ERR.X – Pedigree errors generated from 1G

Pedigree Errors

Error Information

☐ Select All ☒ Pedigree (fmt-1) ☐ Lactation (fmt-4) ☐ Reproduction (fmt-5) ☐ Health (fmt-6)

Apply

Clear

▼ Pedigree (fmt-1) | 1 Source File

▼ Errors in File 20260507.10

Error Code	<u>Disposition Code</u>	Description	ID	Herd	<u>Source Code</u>	Date
2Hc	Rejected	Input sire identification differs with master file sire identification. Update of clone's sire's pedigree is not valid.	HOCAN000014260000			

Sire	Dam	Cross Reference	DOB	<u>Source Code</u>	<u>Processing Date</u>	<u>Record Type</u>	<u>Verification Code</u>	<u>Multi-Birth Code</u>	<u>Registry Status</u>	File Name
HOCAN000014260000	HO840003275852638		2025-10-25	N	2026-05-07	P	2	3		20260507.10

Pedigree Errors

Home / Error Documentation

WebConnect has launched and is officially open to all collaborators.
Visit WebConnect at : <https://webconnect.uscdcb.com> .

Master File Pedigree Discrepancy (Rejected)					Error Codes
Code	Description	Action	Returned Data	Updated	Complete Error Lists
2Ha	Input sire identification differs with master file sire identification. Source of input and master file pedigree is not breed. Input is not verified and lactations or progeny exist for animal (not a calf).	Reject	Conflicting sire identification and pedigree source	09/23/2019	CSV/Excel
2Hb	Input sire identification differs with master file sire identification. Update of estimated sire's pedigree is not valid.	Reject	Conflicting sire identification and pedigree source	10/25/2004	Tab Separated
2Hc	Input sire identification differs with master file sire identification. Update of clone's sire's pedigree is not valid.	Reject	Conflicting sire identification and pedigree source	08/30/2011	0 General Record
2Hd	Input sire identification differs with master file sire identification. Input is format 6 from non-DRPC. Update of sire is not valid.	Reject	Conflicting sire identification and pedigree source	01/08/2020	1 Animal Identification

2 Sire Identification
2A Obvious Unknown Sire
2B Obvious Misidentification
2C Unusual Identification
2D Invalid Format
2E Invalid Format
2F Miscellaneous
2G Master File Pedigree Discrepancy
2H Master File Pedigree Discrepancy
2I Master File Pedigree Discrepancy
2J Master File Service

https://queries.uscdcb.com/formats/geterr.cfm?ecode_in=0J#StartBody

Pedigree Corrections: WebConnect

- Limitations with Fix_FMT1:
 - Fix_FMT1 can only submit one change at a time
 - WebConnect is limited for the record types that can be submitted to resolve genomic conflicts

Genotype Confirmations, Conflicts, and Other Close Relatives

Sample ID: Z005066159 - Barcode & Position: 209152800063 R07C03 - Usability Indicator: N

MGS Info PGS Info Show All

Genotype Confirmations			Genotype Conflicts					
Confirmation Type	Confirmed Genotype		Pedigree Change	Conflict Type	Code	Conflicting Genotype		
	Barcode & Position	Confirmed ID				Barcode & Position	Conflicting ID	USE
No records available.				Discovered missing sire	QQ	206448080052 R15C04	BS840003232308577 [M]	Y
				Discovered missing dam	QI	207477850097 R10C01	BS985152020244237 [E]	Y

1 - 2 of 2 items

Fix_FMT1

Other Close Relatives					
Relative ID	Relative Barcode & Position	USE	SNP		
			Compared	Same	Conflicts
No records available.					

1

Update Information

2

Review Changes and Submit

FMT1 Records

Sex	Animal	Sire	Dam	Cross Reference/Clone	DOB	Source Code	Mod Date	Rec. Type	Ped. Verif	Rec Ver	MBC	HRC
Current CDCB pedigree data												
F	HOITA003990216300		HOITA003990181454		20251114	N	20260417	P	2	1	1	
Genotype based suggestion Suggestion are based on genotypes and other data such as current sire/dam/animal pedigree birthdates, sample labeling, etc..												
F	HOITA003990216300	HO840003250025924			20251114	N	20260512	P	2	1	1	
User Input												
F	HOITA003990216300	HO840003250025924			2025-11-14	N	20260512	P	2	1	1	

Cancel

Next

FMT1

1

Update Information

2

Review Changes and Submit

FMT1 Records

Sex	Animal	Sire	Dam	Cross Reference/Clone	DOB	Source Code	Mod Date	Rec Type	Ped Verif	Rec Ver	MBC	HRC	Reg Stat
Current CDCB pedigree data													
F	HOITA003990216300		HOITA003990181454		20251114	N	20260417	P	2	1	1		
Genotype based suggestion Suggestion are based on genotypes and other data such as current sire/dam/animal pedigree birthdates, sample labeling, etc..													
F	HOITA003990216300	HO840003250025924			20251114	N	20260512	P	2	1	1		
User Input													
F	HOITA003990216300	HO840003250025924			20251106	N	20260512	P	2	1	3		

Back

Submit

Pedigree Corrections: SFTP

- Submitting fixes via Format1
 - Can only make one change to the pedigree per line
 - Can submit multiple records for one animal to make gradual pedigree changes
 - Reminder: some pedigree changes require verification codes
- Corrections to pedigrees:
 - https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Corrections_to_pedigree#Corrections-to-pedigree-PUBLIC
- Birth date rules:
 - https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Birth_Date_Rules

Common ID Updates: Cross Reference

- Cross-Reference
 - Animal has multiple IDs that exist independently
 - All the animal's data will exist under one key
 - Preferred ID
- Cross-Reference creation by CDCB processing
 - IDs have a matching pedigree, country code of ID, and unique 12-digit ID but a different breed code
 - IDs found within the same herd code with the same control number in a 273-day interval
 - IDs have matching pedigrees, MBC of 1 and a birth date within 10 days
 - IDs that have matching pedigrees and identical names

Create Cross Reference WebConnect

ANIMAL: HO124F000007890183

Welcome, htempleton | Administration - National Performance Metrics

1 Update Information **2** Review Changes and Submit

Animal

Requested Information: HO124F000007890183 Preferred ID: HOCAN000007890183

Name: COOPON RAMOS WHYTNEY Sex: ☐ Male ☒ Female

DOB: 2007-12-31 Registry Status: PB

Sire: HODEU000000253642 Dam: HOCAN000009452788

Multi-Birth Code: 3 - Birth from embryo transfer Requester: AY (B)

Source Code: B - Breed Associations (USA and CAN)

Cross References

Animal ID	Name	Sex	Mod Date	SRC	Reg
HO124000007890183		F	2010-12-23	D	

Cancel Next

Animal: HO124F000007890183
Requested Info: HO124F000007890183
Preferred ID: HO124F000007890183
Name: COOPON RAMOS WHYTNEY
DOB: 2007-12-31
Sex: Female
Multi-Birth Code: 3 - Birth from embryo transfer
Registry Status: PB
ID Source Code: B - Breed Associations (USA and CAN)
Pedigree Source: B - Breed Associations (USA and CAN)
Animal Sire Report: HO124F000007890183
Animal Dam Report: HO124F000007890183
Animal Dam Reporter: Generic Breed
Mod Date: 2020-09-15

Sex Mod Date SRC Reg
F 2010-12-23 D

Create Cross Reference FMT1

- Format1

0FH0840003282837717H0840003218556317H0840003149596913 20240307B20240321P01399000000

- Byte Positions: 3-19 (Animal ID)
- Byte Positions: 54-70 (Alternate ID Field)
- Byte Position: 88 record type code : P or X

https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Corrections_to_pedigree#How-to-create-cross-references

Common ID Updates: Re-ID

- If an ID was incorrectly used for an animal and the correct ID has been discovered
- Merge the data under both IDs
- ID designated as incorrect is deleted.
- Information that will be merged and moved includes pedigree, nomination, genotype, lactation data, etc.
- Use if the current ID should not be used

Re-ID via Format1

- Format1

0FH0840003282837717HO840003218556317HO840003149596913HO84000338283771720240307B20240321R21399000000COLDSPRINGS JEWEL 14624-ET

- Byte Position(s): 3-19 (Correct ID)
 - Byte Position(s): 54-70 (Incorrect ID to be deleted)
 - Byte Position(s): 88-89 record type code : R and Verification Code: 2
-
- Re-IDs can not be submitted via WebConnect

Processing Genotypes

- Genotypes are pre-assigned to an animal with a pedigree at CDCB already
 - Remember: Nominations are required before loading genotypes
- After passing quality check, genotype checked against
 - Known pedigree relatives
 - Known clones
 - New relationships are discovered
- If any errors arise, the error files can be found in your SFTP
 - \$NOM_Genomic_Errors.csv
 - \$NOM_Genomic_Errors_YYYYMMDD.csv

Common Genomic Errors

- When pedigrees don't align, genomic conflicts can arise.
- Three most common genomic conflicts:
 - 06: MGS Unlikely
 - P2: Non- Pedigree Relative Close Birth
 - 02: Discovered Duplicate/N9 Discovered Clone
- Corrections can be made via Format1 or WebConnect

https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Genomic_error_codes

O6: MGS Unlikely

- The MGS has been found Unlikely
- Can be resolved by correcting the dam's sire OR blanking the dam
- If the dam has been genomically confirmed, the next step would be to check the dam's genotype
 - If the dam's pedigree requires corrections, they will need to be resolved before the progeny to receive an evaluation
 - Progeny's genotype will be listed as Use=Y even though the conflict is listed

MGS Info PGS Info Show All

Sample ID: AF05523950 – Barcode & Position: 208160590004 R19C03 – Usability Indicator: Y

Genotype Confirmations		
Confirmation Type	Confirmed Genotype	
	Barcode & Position	Confirmed ID
Sire	203253140011 R23C01	JE840003200210433 [M]
Sire	203359330123 R16C03	JE840003200210433 [M]
Sire	203665660007 R11C01	JE840003200210433 [M]
Dam	208025910022 R12C02	JE840003248901399 [F]

<< < 1 > >>

1 – 4 of 4 items

Genotype Conflicts					
Pedigree Change	Conflict Type		Conflicting Genotype		
	Message	Code	Barcode & Position	Conflicting ID	USE
	MGS is unlikely	Q6	203665660037 R04C01	JE840003203116924 [M]	Y

<< < 1 > >>

1 – 1 of 1 items

Other Close Relatives					
Relative ID	Relative Barcode & Position	USE	SNP		
			Compared	Same	Conflicts
No records available.					

Sample ID: AF05523950 – Barcode & Position: 208160590004 R19C03 – Usability Indicator: Y

Maternal Grand Sire Information

Information:

'Unlikely' grandsire indicates that (at time of processing) a genotype associated with the pedigree grandsire, is NOT likely to be the grandsire of genotype associated with the subject animal.
Reasons for this include, but may not be limited to:

1) Any of the genotypes could be associated with the wrong animal.
[GenoMove](#)

2) The Dam indicated in the Animals pedigree could be wrong.
Check genotype errors for suggestions, or

Clear Dam Using Fix_FMT1

3) The grandsire indicated in the Dams pedigree could be wrong.

Change_MGS via FMT1 for the Dam

Detection:

MGS candidates based on [percentage of matching haplotypes](#).
(Higher is better, 50% would be surprisingly high.)

JE840003211412088 (50.4 %)

Genotype Confirmations		
Confirmation Type	Confirmed Genotype	
	Barcode & Position	Confirmed ID
Progeny	208160590004 R19C03	JE840003283626313 [F]
1 – 1 of 1 items		

Genotype Conflicts					
Pedigree Change	Conflict Type		Conflicting Genotype		
	Message	Code	Barcode & Position	Conflicting ID	USE
	Sire conflict	N3	203665660037 R04C01	JE840003203116924 [M]	Y
	Dam conflict	N4	203718610082 R13C03	JEUSA000067846430 [F]	Y
	Discovered sire	T2	204304290011 R08C02	JE840003211412088 [M]	Y
	PGS is unlikely	O7	201094570009 R05C02	JEUSA000119755026 [M]	Y
1 – 4 of 4 items					

Fix_FMT1

Other Close Relatives					
Relative ID	Relative Barcode & Position	USE	SNP		
			Compared	Same	Conflicts
No records available.					

P2: Non-Pedigree Relative Close Birth

- A parent-progeny relationship has been identified, but the birth dates are too close
 - Birth Date of Parent Incorrect
 - Birth Date of Progeny Incorrect
 - MBC of Progeny Incorrect

Genotype Confirmations, Conflicts, and Other Close Relatives

MGS Info

PGS Info

Show All

Sample ID: 840003314217410 – Barcode & Position: 209998260135 R12C02 – Usability Indicator: N

Genotype Confirmations		
Confirmation Type	Confirmed Genotype	
	Barcode & Position	Confirmed ID
Sire	208158730010 R06C02	HO840003283239642 [M]
<div> <div><<</div> <div><</div> <div>1</div> <div>></div> <div>>></div> </div> <div>1 - 1 of 1 items</div>		

Genotype Conflicts					
Pedigree Change	Conflict Type		Conflicting Genotype		
	Message	Code	Barcode & Position	Conflicting ID	USE
	Non-pedigree relative close birth	P2	208250280125 R23C01	HO840003286848379 [F]	Y
<div> <div><<</div> <div><</div> <div>1</div> <div>></div> <div>>></div> </div> <div>1 - 1 of 1 items</div>					

Other Close Relatives					
Relative ID	Relative Barcode & Position	USE	SNP		
			Compared	Same	Conflicts
HO840003314217409 [F]	209998260135 R12C01	N	3529	3529	0
<div> <div><<</div> <div><</div> <div>1</div> <div>></div> <div>>></div> </div> <div>1 - 1 of 1 items</div>					

Evaluation Breed: **HO – Holstein**

Animal

Preferred ID:

HO840003314217410

Name:

DOB:

2025-12-12

Sex:

F

[Multi-Birth Code:](#)

4

[ID Source Code:](#)

N

[Pedigree Source Code:](#)

N

Animal Sire Reporter:

Zoetis

Animal Dam Reporter:

Zoetis

[Blend Code:](#)

S

Sire

ID:

[HO840003283239642](#)

Name:

PEAK MAPMAKER-ET

DOB:

2024-05-13

[Source Code:](#)

B

Genotyped:

Yes

Dam

ID:

Name:

DOB:

[Source Code:](#)

Genotyped:

Maternal Grandsire

ID:

Name:

DOB:

[Source Code:](#)

Genotyped:

[Does the animal qualify for a genomic evaluation?](#)

Nomination Status

ID/Pedigree

Evaluation

Genotype

Errors

Evaluation Breed: HO – Holstein

Animal

Preferred ID: HO840003286848379
Name: COOKIECUTTER HINDALOOP-ET
DOB: 2024-09-13
Sex: F
[Multi-Birth Code:](#) 3
[ID Source Code:](#) B
[Pedigree Source Code:](#) B
Animal Sire Reporter: Zoetis
Animal Dam Reporter: Zoetis
[Blend Code:](#) S

Sire

ID: [HO840003252557979](#)
Name: BERRYRIDGE SSI KARL-ET
DOB: 2022-10-03
[Source Code:](#) B
Genotyped: Yes

Dam

ID: [HO840003258835951](#)
Name: COOKIECUTTER LET HALATED-ET
DOB: 2023-01-24
[Source Code:](#) B
Genotyped: Yes

Maternal Grandsire

ID: [HO840003218470965](#)
Name: AURORA LETCHWORTH-ET
DOB: 2021-03-12
[Source Code:](#) B
Genotyped: Yes

[Does the animal qualify for a genomic evaluation?](#)

Nomination Status

Genotype Confirmations, Conflicts, and Other Close Relatives

MGS Info

PGS Info

Show All

Sample ID: 840003286848379 – Barcode & Position: 208250280125 R23C01 – Usability Indicator: Y

Genotype Confirmations

Confirmation Type	Confirmed Genotype	
	Barcode & Position	Confirmed ID
Sire	206842140020 R24C03	HO840003252557979 [M]
Sire	207036370022 R01C02	HO840003252557979 [M]
Sire	209046180097 R18C04	HO840003252557979 [M]
Sire	209354200147 R14C01	HO840003252557979 [M]
Dam	206002630022 R23C02	HO840003258835951 [E]
Progeny	209998260135 R06C04	HO840003272937671 [M]
Progeny	209998270065 R04C03	HO840003317942218 [E]
Progeny	210066560040 R20C04	HO840003317942371 [E]

<< < 1 > >>

1 - 8 of 8 items

Genotype Conflicts

Pedigree Change	Conflict Type		Conflicting Genotype		
	Message	Code	Barcode & Position	Conflicting ID	USE
	Non-pedigree relative close birth	P2	209998260135 R12C02	HO840003314217410 [E]	N
	Non-pedigree relative close birth	P2	209998260135 R12C01	HO840003314217409 [E]	N

<< < 1 > >>

1 - 2 of 2 items

Other Close Relatives

SNP

HO840003272937671

ID/Pedigree Evaluation **Genotype** Errors

Evaluation Breed: HO – Holstein

Animal

Preferred ID: HO840003272937671
Name: COOKIECUTTER 92984-ET
DOB: 2025-12-22
Sex: M
[Multi-Birth Code:](#) 3
[ID Source Code:](#) B
[Pedigree Source Code:](#) B
Animal Sire Reporter: PEAK
Animal Dam Reporter: PEAK
[Blend Code:](#) S

Sire

ID: [HO840003283239642](#)
Name: PEAK MAPMAKER-ET
DOB: 2024-05-13
[Source Code:](#) B
Genotyped: Yes

Dam

ID: [HO840003286848379](#)
Name: COOKIECUTTER HINDALOO-ET
DOB: 2024-09-13
[Source Code:](#) B
Genotyped: Yes

Maternal Grandsire

ID: [HO840003252557979](#)
Name: BERRYRIDGE SSI KARL-ET
DOB: 2022-10-03
[Source Code:](#) B
Genotyped: Yes

[Does the animal qualify for a genomic evaluation?](#)

P2: Non-Pedigree Relative Close Birth

- MBC does impact the threshold for the number of days between parent and progeny birth dates
 - MBC=1, birth >548 days from parents, 457-548 days with verification
 - MBC=3, birth >304 days from dam birth date with verification
 - MBC=6, implant date within 60 days of dam birth date

https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Birth_Date_Rules

Making Corrections for P2 Errors

- Updating birth dates
 - Birth date can only be changed by 90 days at a time
 - May require multiple records
 - If an animal has progeny or lactation data, the new birth date must agree
- If the birthdate is rejected, check the error file
 - Most commonly, there is lactation data or another animal in conflict

What is a Clone in CDCB Terms?

- Two animals who share identical DNA
- Examples of animals that would have a clonal relationship at CDCB:
 - Identical twins
 - Animals resulting from embryo transfer split in vitro or in utero
 - An origin animal and its clone

O2: Duplicate/N9: Discovered Clones

- O2: Duplicate; two identical genotypes are assigned to animals with different pedigree parentage
- N9: Discovered Clones; two identical genotypes are assigned to animals with similar pedigrees, and no clone record has been established
- Pedigree expectation of clones
 - Have the same parentage
 - Have MBCs that would spawn animals with identical DNA
 - Have birth dates that logically make sense with the assigned MBCs

Genotype Confirmations, Conflicts, and Other Close Relatives

MGS Info

PGS Info

Show All

Sample ID: IT003990216300 – Barcode & Position: SMP4_1227349 R09C11 – Usability Indicator: N

Genotype Confirmations

Confirmation Type	Confirmed Genotype	
	Barcode & Position	Confirmed ID
No records available.		

Genotype Conflicts

Pedigree Change	Conflict Type	Conflicting Genotype			
	Message	Code	Barcode & Position	Conflicting ID	USE
	Duplicate genotype identified	Q2	SMP4_1827407 R03C11	HOITA003990216288 [E]	Y
	Discovered missing sire	Q0	206862420041 R06C04	HO840003250025924 [M]	Y
	Dam conflict	N4	GV4477096491 R06C12	HOITA003990181454 [E]	Y
	MGS is unlikely	Q6	206602870091 R08C02	HOITA001991334345 [M]	Y

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1 – 4 of 4 items

Fix_FMT1

Other Close Relatives

Relative ID	Relative Barcode & Position	USE	SNP		
			Compared	Same	Conflicts
No records available.					

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HOITA003990216300

ID/Pedigree

Evaluation

Genotype

Progeny

Errors

Lactations

Evaluation Breed: HO – Holstein

Animal

Preferred ID: HOITA003990216300
Name: 216300
DOB: 2025-11-14
Sex: F
[Multi-Birth Code:](#) 1
[ID Source Code:](#) N
[Pedigree Source Code:](#) N
Animal Sire Reporter: Bio-Genesys Ltd
Animal Dam Reporter: Bio-Genesys Ltd
[Blend Code:](#) S

Sire

ID:
Name:
DOB:
[Source Code:](#)
Genotyped:

Dam

ID: [HOITA003990181454](#)
Name:
DOB: 2022-08-01
[Source Code:](#) N
Genotyped: Yes

Maternal Grandsire

ID: [HOITA001991334345](#)
Name: CERETTIESE INSEME DIAMANTE ET
DOB: 2020-05-10
[Source Code:](#) N
Genotyped: Yes

[Does the animal qualify for a genomic evaluation?](#)

Nomination Status

Evaluation Breed: **HO – Holstein**

Animal

Preferred ID: HOITA003990216288
Name: 216288
DOB: 2025-10-21
Sex: F
[Multi-Birth Code:](#) 1
[ID Source Code:](#) N
[Pedigree Source Code:](#) N
Animal Sire Reporter: Bio-Genesys Ltd
Animal Dam Reporter: Bio-Genesys Ltd
[Blend Code:](#) S

Sire

ID: [HO840003250025924](#)
Name: PEAK CASIMIRO-ET
DOB: 2022-09-22
[Source Code:](#) B
Genotyped: Yes

Dam

ID: [HOITA003990151073](#)
Name:
DOB: 2019-09-17
[Source Code:](#) N
Genotyped: No

Maternal Grandsire

ID: [HO840003138277108](#)
Name: CAL-ROY-AL YODA-ET
DOB: 2016-09-09
[Source Code:](#) B
Genotyped: Yes

[Does the animal qualify for a genomic evaluation?](#)

Nomination Status

O2: Duplicate/N9: Discovered Clones

- Troubleshooting
 - Before creating a clone record, consider...
 - Is one animal tested under two different ID?
 - Is one of the genotypes incorrectly assigned to a different ID?
 - Why wasn't the clone record created automatically?
 - For more details about automatic clone records, visit https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Dealing_with_clone_records

Conclusion

- Pedigree conflicts are very closely related to genomic conflicts
- If you are having problems fixing a genomic conflict, check the errors returning on the pedigree
- If you need help investigating an in-depth conflict, please open a ticket on Redmine for CDCB help!

Thank you!
