

Queries: Genotype

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Description

- The Genotype page consists of the following function:
 - Provide information about the selected animal as to below:
 - Information of Animal
 - Pedigree
 - Nomination Status
 - Sample Status
 - Genotype Confirmations
 - Genotype Conflicts
 - MGS Info
 - PGS Info
 - Edit mode:
 - Edit Nomination Status – Submit format 1G
 - Edit Sample Status – Submit format U
 - Fix_FMT1 – Submit Format 1 (Record type = P)
 - Change MGS/PGS Via for Dam/Sire

This guide describes the **ID/Pedigree** and their supported functions

Procedure 1: Access the Genotype page

Step 1: Log in to CDCB page with link <https://40.142.54.172/>

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CATTLE DOCUMENT COLLECTION BOARD

Data Exchange Special Section [Top Animal Listing](#) [Summary Stats](#) Administration [Login](#)

COLLABORATOR LOGIN

Username or Email

Password

[Forgot Password?](#) [Register New Account?](#)

WARNING: This system is for the use of authorized users only. Individuals using this computer system without authority, or in excess of their authority, are subject to having all of their activities on this system monitored and recorded by system personnel. In the course of monitoring individuals improperly using this system, or in the course of system maintenance, the activities of authorized users may also be monitored. Anyone using this system expressly consents to such monitoring and is advised that if such monitoring reveals possible evidence of criminal activity, system personnel may provide the evidence of such monitoring to law enforcement officials.

Dashboard
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The system redirects default to the Queries page after login in successfully and display the **Cattle option** and **Animal ID (17 bytes) Search option** by default

CDCB
COUNCIL ON DAIRY CATTLE BREEDING

Queries Data Exchange Special Section Top Animal Listing Summary Stats Administration Logout

QUERIES

SEARCH FOR Cattle Goat

INPUT: Breed, Country Code, and ID Number.
E.g. JEUSA000067106977
Maximum 50 items/once
Over 50 items: Data Exchange

Animal ID (17 bytes)

Each item must be on a separate line.

Run Query Clear

Dashboard
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Step 2: The user can search with many different **Search Options** depending on the purpose of use. [References Search Option user guide](#)

E.g. To query a Bull with Animal ID (17 bytes) Search option

2.1. Select the **Cattle** option and **Animal ID (17 bytes)** Search option

CDCB
COUNCIL ON DAIRY CATTLE BREEDING

Queries Data Exchange Special Section Top Animal Listing Summary Stats Administration Logout

QUERIES

SEARCH FOR Cattle Goat

INPUT: Breed, Country Code, and ID Number.
E.g. JEUSA000067106977
Maximum 50 items/once
Over 50 items: Data Exchange

Animal ID (17 bytes)

Animal ID (12 bytes)

Animal ID (17 bytes)

Animal ID + Sex Code (18 bytes)

Animal Interbull ID (19 bytes)

Sample ID + Sex Code (20 bytes max)

Run Query Clear

Dashboard
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Step 3: Enter **Animal ID** on the text area and then click on the **Run Query** button

QUERIES

SEARCH FOR Cattle Goat

INPUT: Breed, Country Code, and ID Number.

E.g. JEUSA000067106977

Maximum 50 items/once
Over 50 items: [Data Exchange](#)

Animal ID (17 bytes)

```
HO840003013654627
HOUSA000002294436
HO840003132351592
```

Run Query

Clear



The system will show information on the Result area with the **ID/Pedigree** tab as the default selected.

CDCB COUNCIL COUNTY DISTRICT BREEDERS Queries Data Exchange Special Section Top Animal Listing Summary Stats Administration Logout

QUERIES

SEARCH FOR Cattle Goat Animal ID (17 bytes) Found 3/3 result sets

Requested ID Searches

- HO840003013654627 ✖
- HOUSA000002294436 ✖
- HO840003132351592 ✖

3 results found!

HO840003013654627

ID/Pedigree Evaluation Genotype Progeny Errors Lactations

Animal

Requested Information: [HO840003013654627](#)
 Preferred ID: HO840003013654627
 Name: BACON-HILL PETY MODESTY-ET
 DOB: 2014-06-25
 Sex: M
[Multi-Birth Code](#): 3
[Registry Status](#): **
[Source Code](#): B
 Mod Date: 2019-11-06

Cross References

ID	Name	Sex	Mod	Reg
HOUSA000073098342		M	2019-08-28	

Sire

Animal: [HO8400030105660326](#)
 Name: SIEMERS MOGUL PETY
 DOB: 2012-09-08
[Source Code](#): B
 Genotyped: ✓

Paternal Grand sire

Animal: [HO840003006972816](#)
 Name: MOUNTFIELD SSI DCY MOGUL-ET
 DOB: 2010-06-22
[Source Code](#): B
 Genotyped: ✓

Paternal Grandam

Animal: [HOUSA000069379131](#)
 Name: RANSOM-RAIL EXPLODE PETY-ET
 DOB: 2010-06-22
[Source Code](#): B
 Genotyped: ✓

Dam

Animal: [HO840003010945893](#)
 Name: BACON-HILL SUPRS MODESTY-ET
 DOB: 2012-11-22
[Source Code](#): B
 Genotyped: ✓

Maternal Grand sire

Animal: [HOUSA000069981349](#)
 Name: SEAGULL-BAY SUPERSIRE-ET
 DOB: 2010-12-28
[Source Code](#): B
 Genotyped: ✓

Maternal Grandam

Animal: [HOUSA000139121711](#)
 Name: UNIQUE-STYLE BOLTON MONEY
 DOB: 2007-09-25
[Source Code](#): B
 Genotyped: ✓

Clonal Family Members – No Clones Known

Parentage Validation Record [Export CSV](#)

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Step 4: Click on the **Genotype** tab- The system will show the Genotype page with the following information:

- Evaluation Run/Breed
- Animal Box
- Pedigree Tree
- Nomination Status
- Sample Status
- Genotype Confirmations and Genotype Conflicts

Procedure 2: Information of the Animal

- Run: Evaluation Date
- Evaluation Breed: Breed Code - Breed Name

QUERIES

SEARCH FOR Cattle Goat Found 4/4 result sets

JE840003206179418

Run: N/A

Evaluation Breed: N/A

Animal

Preferred ID: JE840003206179418

Name: JX VIERRA ANVIL 30113 (4)

DOB: 2019-04-09

Sex: F

Multi-Birth Code: 1

Source Code: B

Blend Code:

Sire

Animal: JE840003135124283

Name: JX FARIA BROTHERS JACK BAUER (

DOB: 2016-06-23

Source Code: B

Genotyped: ✓

Maternal Grand sire

Animal: JEUSA000115479865

Name: DUTCH HOLLOW LEXICON-P

DOB: 2007-03-20

Source Code: B

Genotyped: ✓

Dam

Animal: JEUSA000067811658

Name: AHLEM LEXICON VALERIE 11658

DOB: 2016-01-23

Source Code: B

Genotyped: ✓

2. Animal Box

This area includes animal: **Preferred ID, Name, DOB, Sex, Multi-Birth, Source Code, Blend Code.**

JE840003206179418

Run: N/A

Evaluation Breed: N/A

Animal

Preferred ID: JE840003206179418

Name: JX VIERRA ANVIL 30113 (4)

DOB: 2019-04-09

Sex: F

Multi-Birth Code: 1

Source Code: B

Blend Code:

Sire

Animal: JE840003135124283

Name: JX FARIA BROTHERS JACK BAUER (

DOB: 2016-06-23

Source Code: B

Genotyped: ✓

Maternal Grand sire

Animal: JEUSA000115479865

Name: DUTCH HOLLOW LEXICON-P

DOB: 2007-03-20

Source Code: B

Genotyped: ✓

Dam

Animal: JEUSA000067811658

Name: AHLEM LEXICON VALERIE 11658

DOB: 2016-01-23

Source Code: B

Genotyped: ✓

3. Pedigree Tree.

This draws a pedigree hierarchy with three objectives as **Sire, Dam, and Maternal Grand sire.**

QUERIES

SEARCH FOR Cattle Goat Found 4/4 result sets

JE840003206179418

Requested ID Searches

- JE840003206179418 ✖
- HO840003136255540 ✖
- HOUSA00058VTK9080 ✖
- HOUSA00042CXY8733 ✖

ID/Pedigree
Evaluation
Genotype
Progeny
Errors
Lactations

Animal:

Preferred ID: JE840003206179418

Name: JX VIERRA ANVIL 30113 (4)

DOB: 2019-04-09

Sex: F

Multi-Birth Code: 1

Source Code: B

Blend Code:

Sire

Animal: [JE840003135124283](#)

Name: JX FARIA BROTHERS JACK BAUER [

DOB: 2016-06-23

Source Code: B

Genotyped: ✔

Dam

Animal: [JEUSA000067811658](#)

Name: AHLEM LEXICON VALERIE 11658

DOB: 2016-01-23

Source Code: B

Genotyped: ✔

Maternal Grandsire

Animal: [JEUSA000115479865](#)

Name: DUTCH HOLLOW LEXICON-P

DOB: 2007-03-20

Source Code: B

Genotyped: ✔

Procedure 3: Nomination Status

The nomination includes the date that the requester requests the Genotype information of a sample, the fee for that nomination.

Nomination Status ^

✎ Edit

Nomination						
Nom. Date	Requester	Group/Herd	Herd Code Difference Reason Code	Fee	Fee Assigned Date	Mod. Date
2014-08-04	Select			1	2014-08-04	2014-08-12 12:00

✎ Edit

Billing					
Bill. Date	Requester	Fee	Amount (\$)	Use Weekly	Mod. Date
2014-09-01	Select	1	20	2015-06-22	2020-09-15 07:51

Procedure 4: Sample Status

Sample status contains all information of the sample such as Chip, Barcode & Position, Lab...

- The row content non-usable/negative key animals will be highlighted in red.

✎ Edit

Sample ID	Barcode & Position	Chip Name	Fee	Usability Ind.	Pending	Sire Status	Dam Status	Progeny Count	Tissue Source	Lab	Requester	SNP Read	Geno Arrival Date	Breed SNP Conflicts	Conflicts
HOCANM12371170	200180750129 R06C02	GH2	P	Y		1	1	297		GeneSeek	Semex	138619	2016-04-15	0%	YES
HOCANM000012371170	201375300152 R02C02	50K3	M	M		1	1	0		Eurofins Bio Diagnostics Inc.	Semex	52532	2017-09-28	0%	NO
HOCANM000012371170	SMP4_0718936 R11C22	AM2	M	M		1	1	0		Eurofins Bio Diagnostics Inc.	Semex	44748	2018-03-08	0%	NO

Procedure 5: Genotype Confirmations & Genotype Conflicts

Genotype Confirmations and Genotype Conflicts include two table genotype Confirmations and Confirmed Genotype.

- Table genotype show information: Confirmation Type, Confirmed Genotype.
- Genotype Conflicts show information: Show list animal conflicts genotype.

Genotype Confirmations and Genotype Conflicts

MGS Info PGS Info Show All

Sample ID: JEUSA000000665185 - Barcode & Position: 9969486124 R05C01 - Usability Indicator: Y

Genotype Confirmations			Genotype Conflicts			
Confirmation Type	Confirmed Genotype		Conflict Type	Code	Conflicting Genotype	
	Barcode & Position	Confirmed ID			Barcode & Position	Conflicting ID
Sire	5381287024 R06C01	JEUSA000000651068 [M]	No records available.			
Progeny	1992267362 C	JEUSA000113234596 [M]				
Progeny	200205750137 R04C01	JEUSA000119461929 [F]				
Progeny	200500990143 R01C01	JEUSA000117630095 [M]				
Progeny	202481070083 R02C02	JEUSA000067084948 [F]				
Progeny	202756080128 R09C01	JEUSA00000601905 [F]				
Progeny	4019593193 F	JECAN000102058939 [M]				
Progeny	4019593590 J	JEUSA000113526075 [M]				
Progeny	4294034129 F	JEUSA000067085093 [F]				
Progeny	4298094069 E	JEUSA000113299593 [M]				

1 - 10 of 54 items

Sample ID: 665185 - Barcode & Position: 4302188090 J - Usability Indicator: M

Sample ID: JEUSA000000665185 - Barcode & Position: 4302188054 J - Usability Indicator: M

Procedure 6: Access to [MGS/PGS] Info

1. Maternal Grand Sire Information popup

Step 1: On the Genotype page, click on the "MGS Info" button in the "Genotype Confirmations and Genotype Conflicts" section

Q Search

Requested ID Searches

- HO840003013654627 ✖
- JEUSA000000665185 ✖**
- HO124000012112202 ✖
- HOLUX000899724527 ✖
- AY840003123620583 ✖
- AYUSA000100711923 ✖

6 result(s) found!

Genotype Confirmations and Genotype Conflicts

MGS Info PGS Info Show All

Sample ID: JEUSA000000665185 - Barcode & Position: 9969486124 R05C01 - Usability Indicator: Y

Genotype Confirmations			Genotype Conflicts			
Confirmation Type	Confirmed Genotype		Conflict Type	Code	Conflicting Genotype	
	Barcode & Position	Confirmed ID			Barcode & Position	Conflicting ID
Sire	5381287024 R06C01	JEUSA000000	No records available.			
Progeny	1992267362 C	JEUSA0001132				
Progeny	200205750137 R04C01	JEUSA000119				
Progeny	200500990143 R01C01	JEUSA0001176				
Progeny	202481070083 R02C02	JEUSA000067				
Progeny	202756080128 R09C01	JEUSA000000				
Progeny	4019593193 F	JECAN000102				
Progeny	4019593590 J	JEUSA0001135				
Progeny	4294034129 F	JEUSA000067				
Progeny	4298094069 E	JEUSA0001132				

1 - 10 of 54 items

Sample ID: 665185 - Barcode & Position: 4302188090 J - Usability Indicator: M

Maternal Grand Sire Information popup will be shown with the following cases:

- If MGS is Likely/Unknown and found no candidate MGS, the **Maternal Grand Sire Information popup** will show as a picture below:

Maternal Grand Sire Information ✕

Information:	Detection:
---------------------	-------------------

MGS: Likely/Unknown

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

No MGS Hap-candidate is available

	MGS candidates based on percentage of SNP conflicts . (Lower is better.)
--	---

No MGS SNP-candidate is available

- If MGS is Unlikely and found candidate MGSs based on the Haplotype method and SNP method, the **Maternal Grand Sire Information popup** will show as the pictures below:
 - In the case of **MGS is Unlikely**, the **Information area** and **Detection area** will show data differently depending on the conditions differently

Eg. Data input is “HO840003136255540” the **Maternal Grand Sire Information popup** will show as a picture below:

Maternal Grand Sire Information ✕

Information:	Detection:
---------------------	-------------------

'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.

MGS unlikely, BUT Dam - MGS relationship was confirmed: 2015-06-03 10:06:56
2015-06-03 10:06:56

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

HOUSA000061488588 (46.3 %)

	MGS candidates based on percentage of SNP conflicts . (Lower is better.)
--	---

HOUSA000070309562 (22.7 %)
HOUSA000061376268 (22.2 %)
HOUSA000069170040 (22.1 %)
HOUSA000140905913 (20.4 %)
HOUSA000061488588 (14.7 %)

Eg. Data input is “HOUSA00042CXY8733” the **Maternal Grand Sire Information popup** will show as a picture below:

Maternal Grand Sire Information ✕

Information:	Detection:
---------------------	-------------------

'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

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

HOITA000908017670 (35.6 %)

	MGS candidates based on percentage of SNP conflicts . (Lower is better.)
--	---

HOITA000908017670 (23.4 %)

2. Paternal Grand Sire Information popup

Step 1: On the Genotype page, click on the “**PGS Info**” button in the “Genotype Confirmations and Genotype Conflicts” section

Genotype Confirmations and Genotype Conflicts

Sample ID: JEUSA000000665185 – Barcode & Position: 9969486124 R05C01 – Usability Indicator: Y

Genotype Confirmations			Genotype Conflicts			
Confirmation Type	Confirmed Genotype		Conflict Type	Code	Conflicting Genotype	
	Barcode & Position	Confirmed			Barcode & Position	Conflicting ID
Sire	5381287024 R06C01	JEUSA000000	No records available.			
Progeny	1992267362 C	JEUSA000113				
Progeny	200205750137 R04C01	JEUSA000119				
Progeny	200500990143 R01C01	JEUSA000117				
Progeny	202481070083 R02C02	JEUSA000067				
Progeny	202756080128 R09C01	JEUSA000000				
Progeny	4019593193 F	JECAN000102				
Progeny	4019593590 J	JEUSA000113				
Progeny	4294034129 F	JEUSA000067				
Progeny	4298094069 F	JEUSA000113				

6 result(s) found!

Paternal Grand Sire Information popup will be shown with the following cases:

- If PGS is Likely/Unknown and found no candidate MGS, the **Paternal Grand Sire Information popup** will show as the pictures below:

Paternal Grand Sire Information

Information: PGS: Likely/Unknown

Detection: PGS candidates based on [percentage of SNP conflicts](#). (Lower is better.)
No PGS SNP-candidate is available

- If PGS is Unlikely and found candidates based on a percentage of SNP conflicts, the **Paternal Grand Sire Information popup** will show as a picture below:
 - In the case of **PGS is Unlikely**, the **Information area** and **Detection area** will show data differently depending on the conditions differently

Eg. Data input is “H0GBR961002441056” the **Paternal Grand Sire Information popup** will show as a picture below:

Paternal 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:

- Any of the genotypes could be associated with the wrong animal. [GenoMove](#)
- The Sire indicated in the Animals pedigree could be wrong. Check genotype errors for suggestions, or Contact Breed Association to fix pedigree
- The grandsire indicated in the Sires pedigree could be wrong.

PGS unlikely, BUT Sire - PGS relationship was confirmed: 2018-08-30 01:08:30
2018-08-30 01:08:30

Detection: PGS candidates based on [percentage of SNP conflicts](#). (Lower is better.)

- HOUSA000066626255 (25.8 %)
- HOITA017991056509 (25.2 %)
- HOUSA000071813252 (24.7 %)
- HOUSA000071813253 (23.1 %)
- HOUSA000071813276 (16.0 %)

Eg. Data input is “HO982000026076411” the **Maternal Grand Sire Information popup** will show as a picture below:

Paternal 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 Sire indicated in the Animals pedigree could be wrong.
Check genotype errors for suggestions, or

[Clear Sire Using Fix FMT1](#)
- 3) The grandsire indicated in the Sires pedigree could be wrong.
Current Sire pedigree source code is (B)
Contact breed source to modify Sire's pedigree...

Detection:

PGS candidates based on [percentage of SNP conflicts](#).
(Lower is better.)

- HOUSA000002191824 (12.0 %)
- HOUSA000002206612 (11.9 %)
- HOUSA000002246936 (11.3 %)
- HOUSA000002300892 (11.2 %)
- HOUSA000002171433 (11.1 %)

Procedure 7: Edit functions

1. Edit Nomination Status – Submit format 1G

Step 1: Click on the “Edit” button, there is a popup opened that could be gone through two steps: Update Information, Review Changes and Submit.

ANIMAL: JEUSA000000665185

1

Update Information

2

Review Changes and Submit

Nomination Status

Nom. Date	Requester	Group/Herd	Herd Code Difference Reason Code	Fee	Fee Assigned Date	Mod Date	
2009-06-04	JE			0	2009-06-04	2009-06-04 12:00	

[+](#)

Cancel

Next

Step 2: Click the icon “Edit”. The system will allow the user to edit the following information: Requester, Group/Herd, FEE...

ANIMAL: JEUSA000000665185

1

Update Information

2

Review Changes and Submit

Nomination Status

Nom. Date	Requester	Group/Herd	Herd Code Difference Reason Code	Fee	Fee Assigned Date	Mod Date	
2009-06-04	JE <input type="text"/>	<input type="text"/>	<input type="text"/>	0 <input type="text"/>	2009-06-04	2009-06-04 12:00	

[+](#)

Cancel

Next

In case there is information changed, the row of that information will be highlighted in red.

ANIMAL: JEUSA000000665185

1 Update Information 2 Review Changes and Submit

Nomination Status

Requester	Group/Herd	Herd Code Difference Reason Code	Fee	Fee Assigned Date	Mod Date	
JE			2	2009-06-04	2009-06-04 12:00	✓ ✕

+ Cancel Next

Step 2.1: Click the "Save" icon to save

ANIMAL: JEUSA000000665185

1 Update Information 2 Review Changes and Submit

Nomination Status

Requester	Group/Herd	Herd Code Difference Reason Code	Fee	Fee Assigned Date	Mod Date	
JE			0	2009-06-04	2009-06-04 12:00	🗑️ ✎️

+ Cancel Next

Step 2.2: Click the button "Cancel" to cancel the action

Step 3: Click the button "Trash icon" a pop-up will be shown with a message "Are you sure you want to delete a nomination?" along with a "Yes" and "No" button.

The button "Trash icon" is only be displayed when there is no genotype associated with the nomination and it has to be a nomination from the user.

ANIMAL: JEUSA000000665185

1 Update Information 2 Review Changes and Submit

Nomination Status

Nom. Date	Requester	Group/Herd	Herd Code Difference Reason Code	Fee	Fee Assigned	
2009-06-04	JE			0	2009-06-04	🗑️ ✎️

Confirm Deletion

Are you sure you want to delete this nomination?

Cancel Yes

+ Cancel Next

Step 3.1: Click the button "Yes" it will proceed to delete the information.

Step 3.2: Click the button "No" it will close the pop-up

Step 4.1: Click the button “Next”– Clicking on this button, it will navigate to step 2 “Review Changes and Submit” when inputting valid information

Step 4.2: Click the button “Cancel” – It allows the user to cancel the action and close the popup

ANIMAL: JEUSA00000665185

1

Update Information

2

Review Changes and Submit

Nomination Status

Nom. Date	Requester	Group/Herd	Herd Code Difference Reason Code	Fee	Fee Assigned Date	Mod Date	Note
2009-06-04	JE			4	2009-06-04	2009-06-04 12:00	Update Fee

Back
Submit

Step 5.1: Click the button “Back”– It allows the user to go back to step 1 “Update Information”

Step 5.2: Click the button “Submit”– System will be shown a message in the Nomination Status area “Your request has been submitted, your organization will be notified once your request has been processed”.

Nomination Status

✔ Your request has been submitted, your organization will be notified once your request has been processed. ✕

Nomination [Edit](#)

Nom. Date	Requester	Group/Herd	Herd Code Difference Reason Code	Fee	Fee Assigned Date	Mod. Date
2009-06-04	JE			0	2009-06-04	2009-06-04 12:00

Billing

Bill. Date	Requester	Fee	Amount (\$)	Use Weekly	Mod. Date
	JE	0	0	2015-06-22	2020-09-15 07:51

2. Edit Sample Status – Submit format U

The button “Edit Sample Status” only displays when their own nomination.

The row content non-usable/negative key animals will be highlighted in red.

Sample Status [Edit](#)

Sample ID	Barcode & Position	Chip Name	Fee	Usability Ind.	Pending	Sire Status	Dam Status	Progeny Count	Tissue Source	Lab	Requester	SNP Read	Geno Arrival Date	Breed SNP Conflicts	Conflicts
NE00790433	204126250117 R18C04	G9K	N	N		0	0	0	T	GeneSeek	Semex	8750	2020-02-01	1%	NO
NE01231000	204126320029 R12C01	G9K	N	Y		1	4	0	T	GeneSeek	Semex	8872	2020-01-31	4%	NO

Step 1: Click the button “Edit” function for the Sample Status. The system shows a popup with two-step: Update Information, “Review Changes and Submit”

The system will allow the user to edit the following information: **Sample ID, Requester.**

ANIMAL: HOCAN000013672851

1

Update Information

2

Review Changes and Submit

Sample Status

Sample ID	Barcode & Position	Chip Name	Fee	Usability Ind.	Pending	Sire Status	Dam Status	Progeny Count	Tissue Source	Lab	Requester	SNP Read	Geno Arrival Date	Breed SNP Conflicts	Conflicts
NE00790433	204126250117 R18C04	G9K	N	N		0	0	0	T	GeneSeek	Semex	8750	2020-02-01	1%	NO
NE01231000	204126320029 R12C01	G9K	N	Y		1	4	0	T	GeneSeek	Semex	8872	2020-01-31	4%	NO

Cancel
Next

Step 2: Click "Edit" on row information want to edit. Enter information ID Sample and Requester.

Step 2.1: Click the icon "Save" to save. Information will save to the database when information pass data validation

Step 2.2: Click the icon "Cancel" to cancel the action

ANIMAL: HOCAN000013672851

1 Update Information
2 Review Changes and Submit

Sample ID	Barcode & Position	Chip Name	Fee	Usability Ind.	Pending	Sire Status	Dam Status	Progeny Count	Tissue Source	Lab	Requester	SNP Read	Geno Arrival Date	Breed SNP Conflicts	Conflicts	
NE00790433	204126250117 R18C04	G9K	N	N		0	0	0	T	GeneSeek	Semex	8750	2020-02-01	1%	NO	
NE01231000	204126320029 R12C01	G9K	N	Y		1	4	0	T	GeneSeek	Semex	8872	2020-01-31	4%	NO	

Step 3: Click the button to withdraw the Genotype. The system will be shown a message "Are you sure you want to withdraw this genotype?" along with a "Yes" and "Cancel" button

Step 3.1: "Yes" it will proceed to withdraw that record.

Step 3.2: "Cancel" will close the pop-up.

ANIMAL: HOCAN000013672851

1 Update Information
2 Review Changes and Submit

Sample ID	Barcode & Position	Chip Name	Fee	Usability Ind.	Pending	Sire Status	Dam Status	Progeny Count	Tissue Source	Lab	Requester	SNP Read	Geno Arrival	Breed SNP	Conflicts	
NE00790433	204126250117 R18C04	G9K	N	N		0	0	0	T	GeneSeek	Semex	8750	2020-02-01	1%	NO	
NE01231000	204126320029 R12C01	G9K	N	Y		1	4	0	T	GeneSeek	Semex	8872	2020-01-31	4%	NO	

Confirm withdraw

Are you sure you want to withdraw this genotype?

3. Fix_FMT1 – Submit Format 1 (Record type = P)

The button "Fix_FMT1" will be shown underneath of "Genotype Conflict" table in case there is any following conflict type existing in the "Genotype Conflict" table.

- Sire Conflict
- Dam Conflict
- Discovered Sire
- Discovered Dam

Step 1: Click on this button "Fix_FMT1", a popup will be shown to allow user input changes.

Popup includes three table

- Current CDCB pedigree data – This group presents the current pedigree information of a selected animal
- Genotype based suggestion – This group presents the suggested pedigree information for that animal
- User Input – This group will be pre-filled with values from the Genotype based suggestion

FMT1

FMT1 Records

Sex	Animal	Sire	Dam	Cross Reference/Clone	DOB	Source Code	Mod Date	Rec Type	Ped Verif	Rec Ver	MBC	Reg Stat	Name
Current CDCB pedigree data													
F	JE840003206179418	JE840003135124283	JEUSA000067811658		20190409	B	20191130	P	0	1	1	04	JX VIERRA ANVIL 30113 (4)
Genotype based suggestion Suggestion are based on genotypes and other data such as current sire/dam/animal pedigree birthdates, sample labeling, etc..													
F	JE840003206179418	JE840003135124283	JEUSA000067811658		20190409	B	20191130	P	0	1	1	04	JX VIERRA ANVIL 30113 (4)
User Input													

F	JE840003206179418	JE840003135124283	JEUSA00067811658		2019-04-09	B	20191130	P	0	1	1	04	JX VIERRA ANVIL 3C
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[Submit Changes](#)

Step 2: Click "Submit Changes"

After clicking "Submit Changes" the system displays a message "Your request has been submitted, your organization will be notified once your request has been processed" and the "Fix Fmt1" button will be disabled.

4. Change MGS/PGS via for the Dam/Sire

4.1. Change MGS via for the Dam

If dam's source_code is not 'B', or D_USR_ltr(*) = 'B', or user's affiliation = AIPL then when the user click on the "MGS Info" button, the "Change_MGS via FMT1 for the Dam" button will appear in "MGS Info" popup

Maternal Grand Sire Information ✖

<p>Information:</p> <p>'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:</p> <ol style="list-style-type: none"> 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 <p style="text-align: center;">Clear Dam Using Fix FMT1</p> <ol style="list-style-type: none"> 3) The grandsire indicated in the Dams pedigree could be wrong. <p style="text-align: center;">Change_MGS via FMT1 for the Dam</p>	<p>Detection:</p> <p>MGS candidates based on percentage of matching haplotypes. (Higher is better, 50% would be surprisingly high.)</p> <p style="text-align: center;">HOITA000908017670 (35.6 %)</p> <hr/> <p>MGS candidates based on percentage of SNP conflicts. (Lower is better.)</p> <p style="text-align: center;">HOITA000908017670 (23.4 %)</p>
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Step 1: Click on the "Change_MGS via FMT1 for the Dam" button, the Change MGS via for the Dam popup will be displayed as below:

Change MGS via FMT1 for the Dam ✖

CHANGING A PEDIGREE WILL HAVE AN AFFECT ON EVERY ANIMAL IN THE PEDIGREE TREE(s) !!!
 This will affect both genotypic and traditional evaluations !!!
 You should have proper evidence of what the mistake is BEFORE requesting any change !!

<p>'Unlikely' grandsire indicates that genotype data and current pedigree do not agree. Reasons for this include, but may not be limited to:</p> <ol style="list-style-type: none"> 1) Any of the genotypes could be associated with the wrong animal. 2) The parents indicated in the Animals pedigree could be wrong. 3) The grandsire indicated in the parents pedigree could be wrong. <p>Any combination of these and maybe other factors could be the actual problem.</p>	<p>Candidates based on percentage of matching HAPlotypes. (Higher is better, 50% would be surprisingly high.)</p> <p style="text-align: center;">HOITA000908017670 (35.6 %)</p> <hr/> <p>Candidates based on percentage of SNP conflicts (Lower is better.)</p> <p style="text-align: center;">HOITA000908017670 (23.4 %)</p>
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FMT1 Records

Sex	Animal	Sire	Dam	Cross Reference/Clone	DOB	Source Code	Mod Date	Rec Type	Ped Verif	Rec Ver	MBC	Reg Stat	Name
Current CDCB pedigree data													
F	HOUA00041VSV4118	HOUA000122358313			20070101	N	20191106	P	0	1	1		DYKSTRA 5619

User Input

Please fill in the correct SIRE !!

Use this pull down to auto-fill the 'sire' field: HAP - HOITA000908017670 (35.6 %)

4.2. Change PGS via for the Sire

If dam's source_code is not 'B', or D_USR_ltr(*) = 'B', or user's affiliation = AIPL then when the user click on the "PGS Info" button, the "Change_PGS via FMT1 for the Sire" button will appear in "PGS Info" popup

Paternal 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 Sire indicated in the Animals pedigree could be wrong.
Check genotype errors for suggestions, or
- 3) The grandsire indicated in the Sires pedigree could be wrong.

Detection:

PGS candidates based on [percentage of SNP conflicts](#).
(Lower is better.)

- HOUSA000002162874 (24.9 %)
- HOCAN000005307144 (24.0 %)
- HOUSA000001491007 (23.5 %)
- HOCAN000000404439 (22.8 %)
- HOUSA000002167741 (21.9 %)

Step 1: Click on the "Change_PGS via FMT1 for the Sire" button, the **Change PGS via for the Sire popup** will be displayed as below:

Change PGS via FMT1 for the Sire
✕

CHANGING A PEDIGREE WILL HAVE AN AFFECT ON EVERY ANIMAL IN THE PEDIGREE TREE(s) !!!

This will affect both genotypic and traditional evaluations !!!

You should have proper evidence of what the mistake is BEFORE requesting any change !!

'Unlikely' grandsire indicates that genotype data and current pedigree do not agree.
Reasons for this include, but may not be limited to:

- 1) Any of the genotypes could be associated with the wrong animal.
- 2) The parents indicated in the Animals pedigree could be wrong.
- 3) The grandsire indicated in the parents pedigree could be wrong.

Any combination of these and maybe other factors could be the actual problem.

Candidates based on percentage of matching HAPlotypes.
(Higher is better, 50% would be surprisingly high.)

Candidates based on percentage of SNP conflicts
(Lower is better.)

- HOUSA000002162874 (24.9 %)
- HOCAN000005307144 (24.0 %)
- HOUSA000001491007 (23.5 %)
- HOCAN000000404439 (22.8 %)
- HOUSA000002167741 (21.9 %)

FMT1 Records

Sex	Animal	Sire	Dam	Cross Reference/Clone	DOB	Source Code	Mod Date	Rec Type	Ped Verif	Rec Ver	MBC	Reg Stat	Name
M	HOUSA000002035456	HOUSA000001697572	HOUSA000011439490		19860731	B	20191106	P	0	1	3	**	PETICOTE DESPERADO-ET

User Input

Please fill in the correct SIRE !!

Use this pull down to auto-fill the 'sire' field

SNP - HOUSA000002162874 (24.9 %)