



Council on Dairy Cattle Breeding

Navigation guide for Nominators

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1. Data Flow and Exchange

1.1 Report Cards

Report Cards are made available to genomic nominators on a monthly basis. They provide summary statistics from the genotypes submitted by each genomic nominator. Since the data available in the different situations is different, not all metrics are considered strictly (herds with registered cattle usually have more accurate pedigree data than non-registered herds with *commercial* orientation).

1. **Total genotypes.** Determined by monthly release dates.
2. **Number of genotypes for each chip type.**
3. **Genotypes missing nomination when loaded.** Nominators are required to submit a nomination for each animal *before* the genotype is submitted to the CDCB collaborator database, as stated in the *Quality Certification Requirements for Genomic Nominators* (<https://redmine.uscdcb.com/documents/8>).
4. **Genotypes with unknown animal ID (Identification).** This occurs when the animal has not been nominated and the genotype submission: i) does not contain animal ID information, or; ii) the animal ID has not been entered in the CDCB collaborator database.
5. **Sires pedigree missing.** Frequency of missing sire ID information in the CDCB database. Common reasons are: the sire ID provided is invalid, a herd bull is not enrolled with a breed association, or a foreign bull's pedigree has not been provided. It's nominator responsibility to provide this information.
6. **Dam pedigree missing.** Frequency of missing dam ID information in the CDCB database.
7. **Dam blanked due to conflict.** Dam ID was provided but the information was not stored due to a conflict. Common reasons are: the animal's birth date did not agree with the dam's calving date, a maternal sibling has a birth date within 9 months of the animal submitted, etc. These checks are bypassed for animals coded as having resulted from an embryo transfer birth.
8. **IDs with 573/574.** Numeric IDs starting with these digits are assigned by the nominator and typically not attached to the animal. The preferred solution is to identify the animal by a tag attached to the animal.
9. **Group name not found in fee table for codes 1 or 2.** The DHI herd code supplied was not found among the herd codes that have a fee code assigned. This can be expected to occur for those herds that have begun testing recently.
10. **Group name not found as a herd of the animal or dam.** The herd code assigned by the nominator does not agree with the one in the CDCB collaborator database, which came through DHI.
11. **Genotypes not usable due to conflicts.** Genomic conflicts are results of incorrect data, such as incorrect pedigree, identification, breed code, sex etc. Therefore this frequency of the genomic conflict inversely related to accuracy of submission.

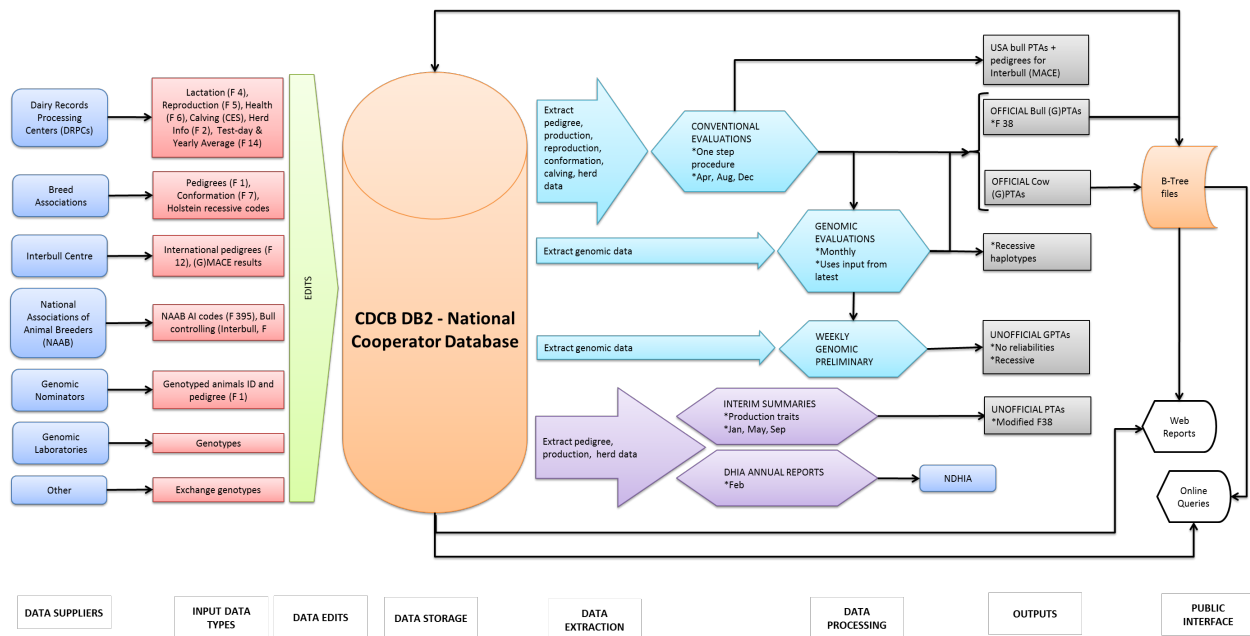
12. **Genotypes with fee code = N** A complete nomination requires assignment of fee code, therefore no nomination should be left with fee code= N.
13. **Genotypes with assignment to animal changed** A genotype reassignment indicates incorrect indication of pedigree/nomination. This report shows number of genotypes that were reassigned during the month.
14. **Animals with a change in sire or dam** Changing a sire/dam indicates incorrect pedigree. It is nominator's responsibility to ensure correct pedigree.

Example of a report card:

1000,Total genotypes for NOMINATORX for YYYY
130,CHIP 1
870,CHIP 2
4,Genotypes missing nomination when loaded
1,Genotypes with unknown animal ID
5,Sire pedigree missing
926,Dam pedigree missing
22,Dam blanked due to conflict
5,IDs with 573/574
12,Group_Name not found in fee table for fee codes 1 or 2
9,Group_Name not found as a herd of animal or dam
16,Genotypes not usable due to conflicts
22,Genotypes with fee code = N
13,Genotypes with assignment to animal changed
84,Animals with a change in sire or dam

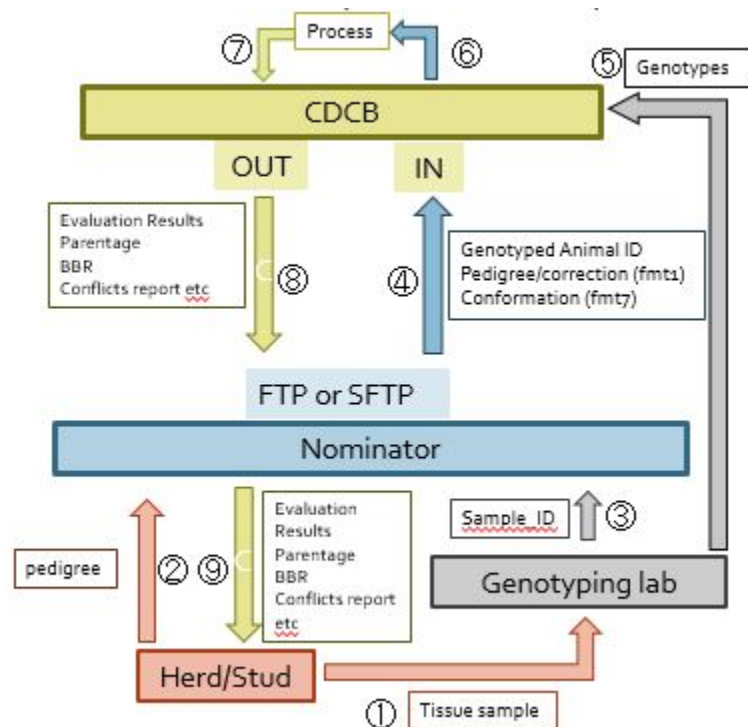
1.2 Dynamics of Data Flow

There are 5 categories of organizations that interact with the CDCB collaborator database: Purebreed Dairy Cattle Associations (PDCA), Dairy Records Processing Centers (DRPC), Dairy Record Providers (DRP), National Association of Animal Breeders (NAAB) and several international partners. Once each organization submits their data, it is first quality checked and good records are loaded into the CDCB collaborator database. The data is then used to obtain and provide a plethora of CDCB services, including genetic and genomic evaluations. The diagram below summarizes the data flow:



1.3 Data Flow between Nominators and CDCB

The following diagram describes specifically the role of Genomic Nominators in data exchanges with the CDCB collaborator database.



The process starts with the decision of a dairy producer or a company (e.g. a stud) to obtain a genomic evaluation from CDCB. The Genomic Nominator has a key role in transforming this decision into an actual service. It manages the collection of biological samples and ensures they are sent to one of the CDCB certified laboratories with the complete and correct information. It nominates the animal before the genotype arrives at CDCB. It is important to stress this: Genomic Nominators are required to complete the nomination process before CDCB receives the genotype, as the pedigree is an essential part of the QC process of the genotype. Nomination can be done through a web application (<https://queries.uscdcb.com/CF-queries/Nom2.cfm> - PASSWORD PROTECTED) or by submitting format1G to the Genomic Nominator “in” directory in the CDCB sftp area.

Once both nomination and genotype submission steps are successfully completed and all conflicts/errors have been eventually corrected, the genomic nominator will receive a first non-official weekly evaluation and monthly official evaluation results. As listed in the “Core requirements for Genomic Nominators” in the Quality Certification Requirements for Genomic Nominators (<https://redmine.uscdcb.com/documents/8>), the nominator is expected to deliver the results to the herd/stud originally requesting CDCB services.

1.4 Steps to Receive Evaluation Results from CDCB

1. The genomic nominator collaborates with a producer and a CDCB approved Genotyping Laboratory to arrange the biological sample collection and submission to the lab. The Genomic Nominator is responsible that all information correlated with the sample is accurate and complete.
2. Before the samples are genotyped and submitted to the CDCB collaborator database, the genomic nominator is expected to complete the nomination process. Nominations can be completed on a web query or in batch (i.e. multiple nominations done contemporarily), through the submission of a format1G (https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Format_1) to the “in” folder of the CDCB SFTP area (<ftp.uscdcb.com>). In this latter case, typically a “notify” file is generated in the “out” directory. The nominator is expected to check this file: it contains the outcome of the nomination and linked information.
3. After the genotype is loaded into the CDCB collaborator database, genotypes with errors are reported back in the “out” folder of the CDCB sftp area. The “genomic error” file contains a large number of information that the genomic nominator should use to correct the errors. Only genotypes flagged as “usable” with complete nomination (and fee code assigned) qualify to receive CDCB evaluations.
4. New individuals will obtain a non-official weekly evaluation (released on the next Tuesday in the “out” directory after the genotype became usable). These animals will receive official monthly evaluations every month as long as their genotype is flagged as “usable”.
5. Nominators are responsible to distribute the results back to the producer.
6. Nominators will receive the initial fee invoice from CDCB, based on the fee code assigned. All service fee for males being marketed using US genomic evaluations should be paid to NAAB.

1.5 Data Exchange through secure FTP

CDCB and genomic nominators can exchange data through the CDCB web query system or through a secure FTP area. The web query is typically used when processing a small number of records or few records need to be displayed. However, when large number of animals/genotypes need to be processed, this typically is done through batch submissions. Files produced by CDCB are placed in the “out” directory. Files submitted by genomic nominators are placed in the “in” folder”.

A full description of the files generated by CDCB and placed in the “out” folder is available in https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/CDCB_general_files_distributed_to_nominators .

2. Fee Code information

2.1 How CDCB Collects Fees through Genomic Nominators

The CDCB genomic fees are structured to reward producers that are providing the most data or information for the greatest value to the CDCB cooperator database. The current fee schedule encourages contributors to not only maintain, but to increase the amount and kinds of data they are contributing to the system, to improve accurate genetic evaluations.

All required Initial Fees are to be collected by the genomic nominator. The AI Service Fee is collected by NAAB. All fees collected will be then be forwarded to the CDCB. The female and initial male fees will be charged only to the first genotype submitted for the animal.

There will be no refund of fees, except for errors generated by CDCB. Even if the genomic test results do not work to the submitter's satisfaction or a male is not placed into service.

The detailed information is described in <https://www.uscdcb.com/wp-content/uploads/2016/03/CDCB-Fee-Schedule-Update-7-15-2016.pdf>. The CDCB has two online applications (GT_Fee: https://queries.uscdcb.com/CF-queries/GT_Fee.cfm [PASSWORD PROTECTED] and getfee: <https://queries.uscdcb.com/CF-queries/getfee.cfm> [PASSWORD PROTECTED]) to help genomic nominators determining the appropriate fee codes (details in 6. Nomination and Data Correction Using Web Query). The CDCB has also created an application tool "CDCB Fee Schedule": https://www.uscdcb.com/fs_01/ to help genomic nominators determining the appropriate fee codes. Finally, on the day prior to the monthly genomic release, CDCB places file *NOMNAME_Check_Fee_Code_1705.csv* in the "out" directory of each genomic nominator to show the fee assigned to each individual genotyped. This file is reviewed by CDCB staff and forwarded to the CDCB treasurer who then prepares the invoice, which is then sent to the genomic nominator.

3. Nomination

3.1 Nomination information

Nomination is one of the most important data CDCB receives from its clients. Nomination is a process where a series of critical information is included in the CDCB collaborator database:

- *Pedigree of the animal (if the pedigree is not in our database already):* The pedigree of an animal is important not only for the evaluation itself but also to check for parent-progeny conflicts during genotype submission. Without knowing the parentage, we are not able confirm that the genotype is from the intended animal. This is the one of the reasons why nomination should be completed before submission of genotypes.
- *Association between the sample ID and the Animal ID:* Association between sample ID and the animal ID is extremely important. Missing association will not allow linking the genotype to the correct animal (event also known as “genotype with zero key”).
- *Providing the correct fee code:* The correct fee code is required, in order to fairly charge for the evaluation. Failing to indicate the fee code will leave the fee code “N”, which means “no CDCB prediction will be delivered, and no fee imposed”.
- *Providing correct parentage indicator:* The parentage only indicator is necessary to determine the type of service required. If parentage only code is determined, there will be no fees billed to the nominator (and no other service released).
-

3.2. Nomination Through WebQuery

The CDCB web query called **CDCB-Nomination_Q** can be used when the animal’s pedigree is already in the CDCB collaborator database (e.g. the animal is in a DHI herd, or is a registered animal¹).

- 1) Go to the Animal Queries: <https://queries.uscdcb.com/login>
- 2) Log in using your credentials. Accept the “Terms of Use”
- 3) Choose the CDCB-Nomination_Q (<https://queries.uscdcb.com/CF-queries/Nom2.cfm>)
- 4) Input Nominator ID (if needed), Parentage Indicator (PI), Group/Herd ID, Fee Type, Animal ID, and Sample ID in each designated box like above and click submit.
(Parentage Indicator and Fee Type (code) are explained in <https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki#COMMONLY-USED-CODES>)

¹ It is unlikely a pedigree is in the CDCB collaborator database if the animal is registered with a foreign breed association other than Canada

Information about this Query (updated {ts '2017-01-12 16:51:20'})

The defaults in this form have been changed (6/03/2013) please pay attention.

Perform query as affiliate / requester / nominator : <#

Parentage Indicator:

Group/Herd ID: #> Fee_Type:

Animal ID(s) [sample ID(s)] :

- 5) If the animal's pedigree already exists in the CDCB collaborator database, parentage and the animal's nomination status are displayed as below. If the genomic nominator confirms the nomination information is all correct, then by just clicking "Add This NEW Record" button, the nomination is completed.

User Input	Sex/Anim. ID	NAAB ID/Name	Sire ID	Dam ID	Birth Date
HOUSA000071068142M	HOUSA000071068142	VER-NAN MAYFIELD RUDY-ET	HOUSA000069473980	HOUSA000066879821	2013-02-12

Entry Date	Record	PI	Sample ID	Sold	Nominator	Stud Code	Group / Herd ID	Fee Code	Record Action
2013-03-19	S	<input type="text" value="N"/>	HAU0791867A-01	\$=>	HO	0	35370953	<input type="text" value="1"/>	<--- Submit Changes
2013-03-21	N	<input type="text" value="N"/>	HOUSAM00007106814			14		<input type="text" value="1"/>	<--- Submit Changes <--- Delete This Nomination
The NEXT ROW is for ADDING a NEW Nomination it IS NOT an existing record!									
2017-10-24	NEW	<input type="text" value="N"/>	HOUSAM00007106814		AIPL			<input type="text" value="1"/>	<--- Add This NEW Record

: using default Sample_ID of HOUSAM000071068142 : New-Form Fee_Code must be one of (1,2,3,4,5,6,N).

- 6) If the animal's pedigree is not in the CDCB collaborator database, the following message will be displayed. By clicking on "Request pedigree from non-CDCB source", prompts a request to find the animal's pedigree from external sources, such as breed associations or Interbull. The returned outcome (if any) can be accepted – and the nomination process completed - by compiling the information and clicking on "Submit Format 1g".

User Input	Error
HOUSA11112222233 123456789101	NO matching IDs found for HOUSA11112222233. Request pedigree from non-CDCB source.

Records returned from web queries...
 0201604230011 000000

Pedigree information collected for requested animal
 (please fill in missing data)

Sex	ANIM_ID	SIRE_ID	DAM_ID	BIRTH	Multi Birth Status	Pure Breed STATUS	NAME	Sample ID	Group/Herd ID	Fee Type
M	BSUSA000011223456				<input type="checkbox"/> NO					

- 7) If the external research of the animal's pedigree failed, the genomic nominator will have to submit a Format1 through to the CDCB sftp area.
- 8) Most of the information displayed can be updated/corrected. **Please be aware that no changes to fee code are allowed once an evaluation has been released.** For example, the "SOLD function" allows changing the requesterID after nomination is completed. However, please note that only the current nominator can perform that change. An Email will be sent to the new nominator, to notify the change.

Entry Date	Record PI	Sample ID	Sold	Nominator	Stud Code	Group / Herd ID	Fee Code	Record Action
2013-03-19	S	N HAU0791867A-01	\$=>	HO	0	35370953	#-> 1	<--- Submit Changes

3.3. Nomination Through secure FTP (SFTP)

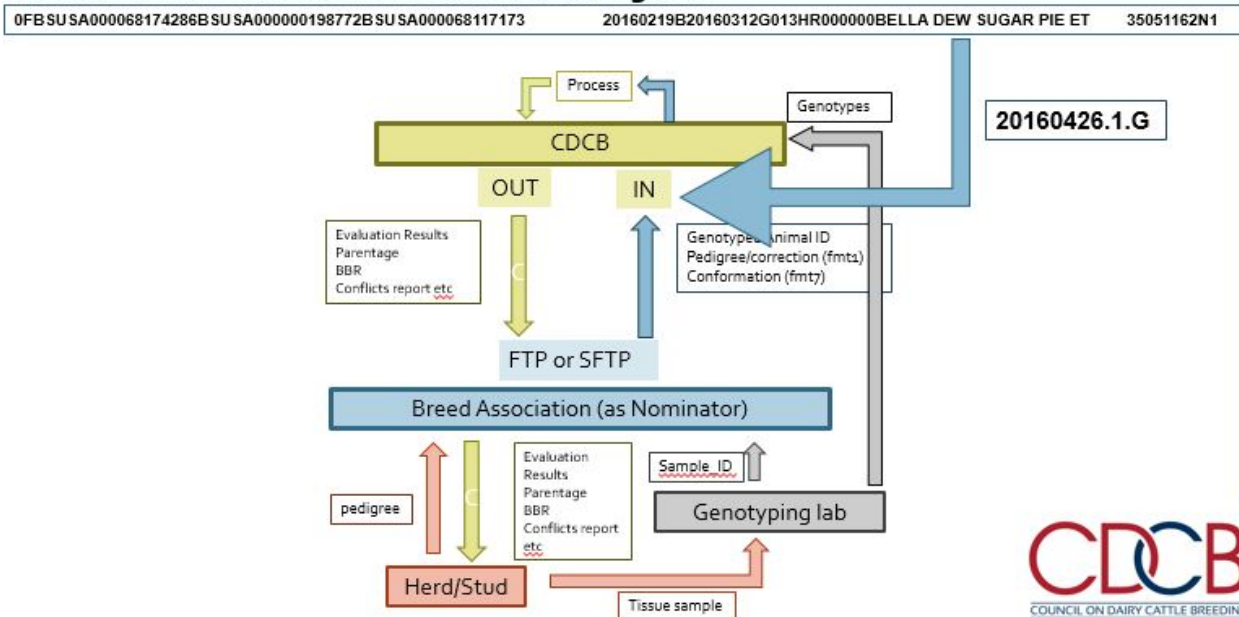
When a large number of animals need to be nominated, submission through SFTP is recommended.

The process is automated in the CDCB system. The genomic nominator should simply place a Format1/Format1G file in the "in" directory of his SFTP area. In order to be recognized, the file should be named according to the following conventions:

- For Format1, files should be named as **YYYYMMDD.1X**, where YYYYMMDD is the year, month and day (e.g. 20170101) and X can be either a letter or number.
- For format1G, files should be named as **YYYYMMDD.1GX**.

Once the submission is processed, a "notify" file (notify.YYYYMMDD.1(G)X) is placed in the "out" directory. This file contains information of errors and the status of the submission. In case of a 1G file, it contains information on the success (or not) of the nomination process.

Nomination (Submission of format1G) through FTP



3.3. Format 1 and Format 1G

Full information on Format1 format is available at: https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Format_1

Format1 is the CDCB standard for a pedigree record. Format1 consists of the animal identification, sire identification, dam identification and cross reference identification, in addition to some other information, such as birthdate, source code, and multiple birth code.

Ex) Format1 for BSUSA000068174286

0FBUSA000068174286BSUSA000000198772BSUSA000068117173 20160219B20160312P013HR000000BELLA DEW SUGAR PIE ET

Format1G is a Format1 that includes nomination data. A Format1 becomes a Format1G by placing a "G" at byte position 88 and by including nomination information:

- sampleID @54-70
- GroupID @130-137
- Parentage Indicator @138
- fee code @139
- Herd code difference reason code @140 (if applicable) .

Ex) 0FBUSA000068174286BSUSA000000198772BSUSA000068117173A1B2C3D4E5F6 20160219B20160312G013HR000000BELLA DEW SUGAR PIE ET 35051162N2

CDCB staff has received multiple requests for clarifications on the following fields for Format1 and Format1G:

Record Source Code (@79) - https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Source_code : Source code is used to prioritize the data submitted. Since CDCB can receive multiple records for one animal from different organizations, the system prioritizes the data depending on the submitter. An organization with lower priority cannot correct records managed by a higher priority source code ("B" has the highest priority among all organizations).

Record Type Code (@88) - https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Record_type_code : Record type code is used to indicate how the record should be processed by the CDCB system. Since Format1 can contain different types of information, indication of record type is necessary. So by assigning Record Type code, genomic nominators can add/delete/change the information currently stored in the CDCB collaborator database.

Multiple Birth Code (@91) - https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Multiple_birth_code : Multiple Birth Code (MBC) should indicate the type of birth of the animal. This information is used to verify the relationship with its sire, dam and siblings.

4. Common Reasons for not receiving an Evaluation (and How to Correct errors)

There are a number of possible reasons that prevent genomic nominators from receiving a genetic evaluation on the animals. The two most common cases are: A) the genotype of the animals is not flagged as “usable”, meaning there are conflicts preventing the CDCB system to use the genotype, and; B) the nomination is not complete (fee code is set to “N”), meaning the nomination was not completed successfully. In this section, the genomic nominators will find a set of useful information to prevent that from happening.

4.1 Where to Find Genomic Conflicts

During the genotype loading process, the CDCB system checks the quality of the data, such as parent-progeny conflicts, Hardy–Weinberg equilibrium, missing information, and (many) more. It also generates report files to inform genomic nominators on what should be corrected for the genotype to be flagged as “usable”. As discussed before, it is one of genomic nominator’s responsibilities to make the genotype usable.

Once a CDCB genotyping laboratory loads a batch of genotype data, genomic nominators receive a .zip file named LAB_YYYYMMDDXX.NOM.zip (ex. GSec_20170426A1.ABS.zip). The file is placed in the genomic nominator “out” directory. The .zip file contains some or all of the following files:

- [NOM_Nominator_Report.csv](#): *Reports on number of errors/conflicts*
- [NOM_Genomic_conflicts.htm](#): *Animals with error codes (web version)*
- [NOM_Genotype_Conflicts.csv](#): *Animals with error code (csv version)*
- [NOM_Parentage.csv](#): *Parentage information*
- [BB_LABCHIPYYYYMMDDX_No_Nomination.csv](#): *animals with missing information*
- [NOM_PGS_unlikely.csv](#): *Unlikely PGS (if any)*

The file called “NOM_Genotype_Conflicts.csv” contains a maximum of 6 error codes for each sample. Animals rarely have more than 6 conflicts, but it is common that multiple errors exists for one sample including errors related to its parents, siblings, and grandparents.

Requester, ID18, Sample_ID, Name, date, code1, ID1, code2, ID2, code3, ID3, code4, ID4, code5, ID5, code6, ID6

Columns named “code[1-6]” indicate the error codes describing the conflict(s) detected for the genotype (documented in: <https://redmine.uscdcb.com/projects/cdcb-customer->

[service/wiki/Genomic_error_codes](https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Genomic_error_codes)). Columns named “ID[1 – 6]” are the ID(s) related to those errors and conflicts.

The NOM_Genomic_conflicts.htm (web browser friendly) contains the same information but on a more human-friendly view.

Genomic Conflicts						
ID	sample_ID	name	error	other_ID	other_name	source
UNKNOWN			Animal is unknown or is not identical to existing gt			
UNKNOWN			Sex conflict for female			
UNKNOWN			Non-pedigree parent-progeny rel			
UNKNOWN			Non-pedigree parent-progeny rel			

4.2 Common reasons for not receiving an evaluation

Genotype was not usable due to a conflict, low call rate, being a crossbred (PI=“B”)

Genomic conflicts are definitely the main reasons that prevent an animal from obtaining an evaluation (even when the nomination was done correctly). Resolving these conflicts is one of the most important roles of genomic nominators. Therefore, it is very important for nominators to understand the meaning of conflicts/errors reported and how to fix them in order to make the genotype usable for CDCB evaluations. Full documentation on these errors can be found at https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Genomic_error_codes

As for the SNP-based test to detect crossbreds, documentation of the current thresholds is referenced in:

https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/CDCB_Genomic_Dictionary#Breed-conflict-determination

The genotype became usable after the genotypes were extracted for the evaluation

CDCB releases 3 types of evaluations: weekly, monthly, and triannual evaluations.

It is important that genomic nominators make the necessary corrections to their data before the cutoff deadline. The link below provides deadlines and release dates for CDCB evaluations.

(<https://queries.uscdcb.com/reference/sched.cfm>)

Weekly evaluations

A weekly evaluation is not an official evaluation. The purpose of a weekly evaluation is to help producers in making quick mating, culling, and marketing decisions.

The data must be loaded by 6:00 pm on Sunday. CDCB Genotyping Laboratories have to submit their data earlier than that, as substantial processing time is required to control large files. In this evaluations, only animals having a usable genotype for the first time before the deadline will be included. No further weekly evaluation is provided after the first one was released. The results are released every Tuesday at ~8:00 am.

Monthly evaluation

The monthly evaluation is official. All qualifying genotyped animals are included. No updates in the phenotypic records are applied. The cutoff for the monthly evaluation is on Sunday at 6:00 pm after the genotype submission + correction week and the release day is the first Tuesday of the month (might be different during the months of triannual evaluations are released) at 8:30 am.

Triannual Evaluation

The triannual evaluations are official and are released... 3 times a year: April, August, and December. Unlike the first two evaluation types, this evaluation includes new phenotypic data. All animals, genotyped or ungenotyped, are distributed. The updated traditional evaluations are an input to the genomic evaluation system.

The breed of evaluation is not among those we generate evaluations for

We currently calculate (G)PTAs for 5 breeds: Ayrshire, Brown Swiss, Guernsey, Jersey, and Holstein. To ensure as much as possible to provide accurate evaluation results to producers, CDCB performs an approximate breed check for all genotyped animals when their genomic data is processed. The system checks that the breed declared in the sample is the breed with the fewest unlikely breed specific alleles. Animals failing this check, still can be included in the evaluations if their BBR (Breed Base Representation) values are higher than 90% for the declared breed. However, since this value is obtained during the evaluation of other animals, the evaluation for animals failing the approximate SNP test, but passing the BBR threshold will be distributed the week after.

The animal's genotype conflicted its imputed dam

Since 2016, genomic nominators have been notified when an animal's genotype has a conflict with its dam's imputed genotype. Unless the conflict is fixed, this animal with the conflict will be excluded from our evaluations.

The "affiliate specific genotype reports" allow all genomic nominators to obtain a list of these animals at any given time.

affiliate specific genotype reports

Select desired report : ▼
Select affiliate to build report for : ▼

The fee code is "N (No fee paid)" or "H (Historic)"

Fee code "N" means that no payment of a fee has been indicated for the animal. It will not be evaluated until a different fee code is assigned to the animal.

If a fee code is indicated as H, then the animal is designated as historical. These animals with fee code "H" are used in the reference population to increase accuracy of estimates, but those animals do not receive an evaluation.

Reference on available fee codes: https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Genomic_fee_codes

The bull has semen marketed and it's not a triannual evaluation release

For bulls being marketed, the evaluation is updated only for the triannual evaluation: on April, August, and December.

The owner of the bull is not located in the US and AI service fee has not been paid, so the evaluation is not public

CDCB does not publish foreign bulls' evaluations unless AI service fee has been paid, in order to respect the policies of individual countries.

The genotype is designated parentage verification only (PI="P")

Reference on Parentage verification codes: https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Parentage_indicator_codes

The bull is foreign, over 15 months of age and no AI service fee has been paid

Genotyped U.S. males will receive a genomic evaluation monthly. Foreign genotyped males receive a genomic evaluation monthly up through 15 months of age with the genomic evaluation only provided to the genomic nominator. Foreign males must have the AI Service Fee paid to get a genomic evaluation released publicly (or even to the nominator past 15 months of age).

Wrong animal ID

Evaluation results are distributed using a specific ID, which is the one considered "preferred" in the CDCB collaborator database for that animal. The animal ID consists of a 2 character breed code plus 3 character country code and a 12 digit registration ID, therefore a total of 17 digits. If the animal is cross referenced, you may need to search for an alternate ID as there are some queries that do not access the cross references.

5. Web Queries

5.1 What is Web Query and what can we do with it

Web Queries are tools developed by USDA (AGIL) for certified genotyping laboratories and genomic nominators to be able to submit data or query data easily. Because of the simplicity of the usage, most genomic nominators prefer using the web query. The direct link to the Web Queries is:

<https://queries.uscdcb.com/login>

Most frequently used queries are CDCB-Nomination (to add/remove/update nominations and UPDATE genotype information), Genotype Query (to show (and fix) the usability/error status of received genotypes) and genotype Move/Swap APP (to correct bad genotype to animal assignments). For detailed information and instructions of those queries will be described in the next 10 topics.

5.2 CDCB-Nomination_Q

As discussed before, CDCB-Nomination_Q is used to nominate animals or to change a nomination status of a nomination that was done previously. The fields that can be changed (updated) using this query are:

- 1) Parentage Only Indicator (PI) - Only from P to N (not vice-versa)
- 2) Fee Code - Only changes allowed are fee codes from N to a correct fee code. In case of error including the fee code, the nominator should contact CDCB customer service (redmine@redmine.uscdcb.com) .
- 3) Nominator ID - Nomination information, as described previously.
- 4) Group/HerdID - used to validate the fee code. It is most important for domestic data to distinguish among fee codes 1, 2 and 3.

5.3 Affiliate specific genotype reports

Lists genotypes with fee code=N loaded in the past 6 months

As mentioned before, the animal will not get evaluation results when the fee code is "N". This report will display which animals have genotypes loaded into the CDCB collaborator database, but the fee code is N.

Fee codes for genotypes loaded since the last invoice

This report will summarize which fee code was given to which animal/sample ID.

Lists parentage only genotypes since the previous genomic run

This report shows animals indicated as parentage only (PI=P), which do not get an evaluation including haplotype analysis.

Reports missing animal ID for a requester

This report shows the Sample ID, date of genotype loaded and chip type for those genotypes loaded without valid nomination. Those genotypes will not get evaluated.

Conflicts for genotypes loaded in the past 45 days

This report shows the conflicts (including genomic error codes) for animals that were loaded in the past 45 days.

Check for missing pedigree of animals nominated in the past 75 days

This report includes animal IDs that have been nominated with unknown parents or unknown grandparents and their genotypes have not arrived at CDCB yet.

List conflicting genotypes within animal (negative key)

A negative key is given to a genotype that is found to conflict with other genotypes for the same animal, when the animal has multiple genotypes. Since a negative key genotype is not included in the evaluations, re-assigning the negative key genotype to the correct animal is required. If another key is assigned to the genotype, the new animal will get evaluated using the genotype.

Animals with unlikely grandsire

Animals with unlikely grandsire(s) are excluded from our evaluation, in order to avoid inaccurate pedigree information being used in our evaluations. Unlikely MGS/PGS are indicated as “U” (unlikely) and likely MBS/PGS are indicated as “L” (likely) in this report.

Animals with genotypes that conflict with imputed dam genotypes

Genomic conflicts between an animal and its dam make the genotype unusable; therefore this information is reported here.

Parentage verification records for genotypes loaded in the past 45 days

This report shows parentage confirmation and parentage suggestions of genotypes loaded in the past 45 days. For an accurate evaluation, it is important to have complete parentage.

Nominator GRAPH


CDCB reports nominators’ performance every month and conducts nominator performance audit, in order to ensure the quality of data and to understand how

CDCB and nominators should be improved. The graph shows past 10 month performance of the nominator. The details of the criteria are indicated in 1.1 Report Cards.

5.4 Check FMT1 records

This query checks if the Format1 (pedigree) provided matches the information in the CDCB collaborator database.

1. Enter the pedigree in format1 format into the text box and click submit



2. A box including pedigree information is displayed

```
In   F BSUSA000068174286 BSUSA000000198772 BSUSA000068117173 20160219 3
CDCB F BSUSA000068174286 Matched

1 Records read
1 Pedigree matched
```

3. The first row ("In") the record just entered is displayed
4. The second row ("CDCB") shows the record in the CDCB collaborator database.
5. The "matched" at the bottom of the example, means that the information matches.

5.5 Check Dam

This query checks animal pedigree and error information, and dam pedigree/progeny/calving dates. This query is especially useful to find out the reason of dam not being accepted (or blanked), as most common reasons of rejection of dam are:

- a. A sibling who share the same dam has a MBC which conflict with the animals' birthdate/MBC.
 - b. Dam's fresh data does not match with the animal's birthdate/MBC.
1. Enter a 17-digit animal ID of the animal that the genomic nominator wants to know the dam's information for and click submit.

Check Dam
Please provide Anim_ID17 (2-Breed 3-Country 12-ID_Num):

or upload a plain ASCII text file No file chosen

Select affiliate to build report for : AIPL

2. A summary of the pedigree, existing pedigree error(s) and current dam's information (dam's pedigree, calving date(s), and progeny and their birthdate and MBC)is displayed:

```

#####
#                               Pedigree animal: #####                               #
#####

Sex  Animal      Sire      Dam      Alias      Birth  Src Mod date MBC Reg Codes RHA Recessives
Key  #####      #####      #####      - Sire and Dam confirmed with genotype

#####
#                               Errors in pedigree for animal: #####                               #
#####
No error records for #####
* Error code (see https://www.uscdcb.com/formats/geterr.cfm for further information) :

#####
#                               CURRENT Dam Information: #####                               #
#####

* Current dam pedigree
Sex  Animal      Sire      Dam      Alias      Birth  Src Mod date MBC Reg Codes RHA Recessives
F    #####      #####      #####      20040427 B  20100922  3  **  00  e6
Key  #####      #####      - Sire and Dam confirmed with genotype

* Current dam calving dates
Cow  #####      key:- #####
Herd  #####      Barn Name
Lac  Fresh  DIM
1  2006/05/29  373
2  2007/08/03  434
3  2008/12/11  445
4  2010/04/14  588
5  2011/11/22  126
Left herd on 2012/03/27

*Current dam
Progeny for ##### F

Progeny ID  Sex  Birth  Sire ID  Src MB Gt GS
#####
F  20060310  #####  B  3  Y  L
F  20060314  #####  B  3
F  20060316  #####  B  3  Y  L
F  20060317  #####  B  3  Y  L
F  20060318  #####  B  3
M  20060406  #####  B  3  Y  L
M  20060407  #####  B  3
F  20060529  #####  B  1
F  20070803  #####  B  3  Y  L
F  20080727  #####  B  3  Y  L
F  20080807  #####  B  3  Y  L
M  20080809  #####  B  3  Y  L
M  20080821  #####  B  3  Y  L
M  20080909  #####  B  3  Y  L
F  20080917  #####  B  3  Y  L
M  20081021  #####  B  3  Y  L
F  20081201  #####  B  3  Y  L
F  20081211  #####  B  1  Y  L
M  20100104  #####  B  3  Y  L
F  20100106  #####  B  3  Y  L
F  20100221  #####  B  3  Y  L
M  20100223  #####  B  3  Y  L
F  20100227  #####  B  3  Y  L
M  20100407  #####  B  3  Y  L
F  20100410  #####  B  3  Y  L
F  20100414  #####  B  2  Y  L
F  20100414  #####  B  2  Y  L
F  20111122  #####  B  1  Y  L

```

28 Progeny

5.6 Get 116 parentage SNP for a list of animal IDs

This query was designed for genotyping laboratories. Please disregard

5.7 New Genotype Query

This query is used to show usability of the given genotype and also used to fix shown errors if any.

Correcting pedigree information, based on genomic error(s)

1. Submit the animal ID, the genomic nominator will be directed to this screen. This shows sample information, genotype confirmations, and genomic conflicts.

[illegible][Back to Query Form](#)

2. If the genomic nominator want to fix the conflicts, click on `FIX_FMT1`.
3. Step2 will direct you to the next screen showing some suggestions that you can accept, in order to resolve the conflicts:

FMT1 Records:

Sire	ANIM ID17	Sire ID17	Dam ID17	Alias/Clone ID17	Birth (YYYYMMDD)	Proc Date(YYYYMMDD)	Rec Type	Ped_Verl Code	Multi Birth Code	Reg Stat	Future Use	Name(30)	Future Use
current CDCB pedigree data													
0	F				20151009	B 20151211	P	2	1	1	74	000000	
genotype based suggestion													
suggestions are based on genotypes <i>and</i> other data such as current sire/dam/animal pedigree birthdates, sample labeling, etc...													
0	F				20151009	A 20170928	P	2	1	1	74	000000	
User Input													
Please verify ALL input fields !!													
0	F				20151009	A 20170928	P	2	1	1	74	000000	
Submit Changes													

[Return to 'Genotype Status' query](#)

4. The genomic nominator should check before accepting the suggestions and if the genomic nominator thinks that the suggestion is correct then you will click the box "submit changes."
5. Once the change is processed, the genomic nominator should expect to see that the pedigree is updated and the conflicts are gone (after next update program runs at

noon and 5:00 am). But it is recommended that genomic nominators check the updated records to see if the data was updated as intended.

Withdrawing unusable genotype

Withdrawal should be reserved for unusual situations such as the genotype actually came from a beef breed, therefore the genotype cannot be assigned to any animal in the CDCB database, there is no possibility of determining which animal the genotype came from and there is no possibility that the genomic nominator would like to use the genotype. In such situations, you can use New Genotype Query to do so by clicking on withdraw in Use Ind column. Please note that there are 5 possible usability indicators that this column can have, which are Y (Usable), N (Not usable), L (Low call rate), M (Multiple/usable), U (Unreliable) and genomic nominators have the option to withdraw genotypes only when the Use Ind column is N,L, or U.

Animal: ██████████ Sex Code: F Eval Breed: ██████
MGS STATUS : Likely PGS STATUS : Likely

Sample ID	Bar Code	Pos	Chip Name	Use Ind	Confirmations and Errors	Parentage Only	Sire Status	Dam Status	No. Prog	Tissue Source	Lab Source	Requester	Scan Date	Eval Use Date	No. SNP read	30 SNP Genotypes	Breed SNP Conflicts
██████████	██████████	██████████	██████████	withdraw	5	N	2	4	0	T	██████████	██████████	2016-03-27	██████████	██████████	██████████	0

Genotype Confirmations

confirmation type	confirmed genotype Barcode	Position	Currently Associated ID

Genotype Conflicts

conflict type	conflicting genotype Barcode	Position	Currently Associated ID
Sire conflicts	██████████	██████████	██████████ [M]
Unident relative close birth	██████████	██████████	██████████ [F]
Unreported parent conflict	██████████	██████████	██████████ [M]

ERR_SEGMENT_RECORD processing date : 20170927 11:15:34

Error Code	Message	Animal ID	Barcode	Position
P2	Unreported relative (██████████)	██████████	██████████	██████████
D3	Unreported parent-progeny relationship (suggesting sire = ██████████, current pedigree sire = ██████████)	██████████	██████████	██████████
U2	Sire conflict (bad sire = H0B4000300897845, current pedigree sire = ██████████)	██████████	██████████	██████████

[Fix_FMT1: Based on errors from this genotype !](#)

[Back to Query Form](#)

5.8 GT Fee

GT Fee is used to search for a fee code based on a given **herd ID**.

The query will show fee code and kind of participation on the program. This query is useful during nomination, to determine the right fee code for each animal.

5.9 parentage.cfm

This query outputs parentage information in a comma delimited file (csv) for the required animal(s).

5.10 Genotype Move/Swap APP

Genotype Move/Swap APP is used when a genotype has to be re-assigned to another animal. Animal ID or sample ID can be used. Note that an “S+” in front of ID means that the ID that is following S+ is a sample ID, not an animal ID.

How to move a genotype assigned from animal to another

1. Once queried, both animals that are involved in the “move” are displayed.
2. All fields must be provided, including the group name.
3. Once satisfied, click “Reassigning Genotypes”

input:BSUSAF68174286

Gen	ID#	NAAB ID	Name	Sex	Date	DOB	New values to use on moved genotype : (auto fill?)							
S	BSUSAM00068174286		HELLA DEW SIOUX RE IT	M	BSUSAM00068174277	BSUSAM00068174271								
Animal ID	Status	Useability	Barcode	Position	CHIP	SAMPLE ID	REQUESTER ID	ENTRY DATE	GROUP NAME	FEE CODE	TO Animal ID :	Sample ID : (Notes?)	Group/Herd Name :	Fee Code :
BSUSAM00068174286	S	Y	200354490018	R04C01	GP4	BSUSAF68174286	BS	2015-03-12	35051162	2	Don't Move	<-- pick destination animal first *	<-- pick a Sample ID first *	Pick ONE ! *

input:BSUSAM000068162042

Sex	ID17	NAAB_ID	Name	Site	Dam	Birth	New values to use on moved genotype : (auto fill)							
M	BSUSAM000068162042		TORONTO SUPPLEMENT ET	BSUSAM000068162042	BSUSAM000068162042	2014-10-14								
Animal ID	Status	Useability	Barcode	Position	CHIP	SAMPLE ID	REQUESTER ID	ENTRY DATE	GROUP NAME	FEE CODE	TO Animal ID :	Sample ID : (Notes?)	Group/Herd Name :	Fee Code :
BSUSAM000068162042	S	Y	9994034166	R12C02	GP3	BSUSAM000068162042	BS	2014-10-14	93501186	2	Don't Move	<-- pick destination animal first *	<-- pick a Sample ID first *	Pick ONE ! *

Reassign Genotypes

5.11 getfee

This application shows the fee code that is assigned to an animal ID. This is similar to GTfee, but based on animal ID.

6. Genomic Nominator Checklist

1. Communicate with your customer to arrange sample collection
2. Communicate with the lab to coordinate the fee schedule
3. Nominate animals before the genotypes are sent to CDCB
4. Check if pedigree and nomination were successfully loaded to CDCB database by checking format1E/notify file
5. Correct errors from pedigree and nomination submission
6. Once genotypes are loaded by the lab, check existence of genomic conflicts
7. Resolve the genomic conflicts, in order to make the genotype usable
8. You should expect weekly evaluation results (if the genotype was new) and monthly evaluations if everything is correct. So check the evaluation schedule
9. Distribute the evaluation results to your customers once you receive evaluation results from us