

Quality reports for genomic service providers

Technote # 23

Quality reports are provided with each genomic evaluation. The quality reports include the most recent issues as well as older issues to follow up. The following explanation will help readers to interpret these reports. In the case of errors, the explanation will assist resolve the issue so that a breeding value can be generated.

Quality reports, also known as genoinconsistency reports are excel files that provide you with information about every animal that has an error or a warning. The report includes background information about the animal as well as details on the issue that has been identified.

You will receive a quality report if you are a Genomic Service Provider that has uploaded some nominations for genomic services into DataGene's genetic evaluation system.

A preview of a section of the report is shown in Figure 1.

There are a range of issues that can be identified for an animal and its genotype. To help readers to interpret the reports and decide how to resolve the issue, the following table provides a description of each field and an explanation of the results.

	B	C	D	E	F	G	H	I	J	K
Name		Breed	Date of Birth	Sire ID	Dam ID	MGS ID	Sample ID	Recipient	Billing Party	Genotype
TEST CASE 1		FFFF	25/02/2018	A000288XX	C14025XX	A00020675	13144XX	XXX	XXX	ZL5
TEST CASE 2		BBBB	13/03/2018	A000388XX	G020311XX	A00031737	840M0031423XX	XXX	XXX	GGPUHDv5

Figure 1: Section of a sample quality report

Field description and result explanations for quality reports

Field	Description	Explanation of results
National ID	Unique animal identifier in the Australian system	
Herd National ID	Unique herd identifier in the Australian system	Blank for bulls
Herd Name	Herd Name, as recorded by the data supplier	Blank for bulls
Within Herd Cow ID	Within herd identification, as recorded by the data supplier	Blank for bulls
Name	Animal name, as recorded by the data supplier	
Sex	Single letter code for animal sex	M Male F Female
Breed	Four letter breed code	F Holstein Friesian J Jersey Refer to DataGene Dif Doc on datagene.com.au for full details for all breeds. For an animal to be included in genomic analyses it's breed of analysis needs to be F or J. For bulls this is the first letter of their 4 letter breed code, for cows it is the breed of analysis of their sire, unless they have no sire and it is the first letter of their own 4 letter breed code.

Field	Description	Explanation of results
Breed of Analysis	Single letter breed code	For bulls, this is based on the first letter of the 4 letter breed code. For females with known sires, this is based on the Breed of Analysis code of the sire. For females with unknown sires, this is based on the first letter of her 4 letter breed code.
Date of Birth	Date of birth of the animal	
Sire ID	National ID of the sire as recorded in the pedigree of this animal	A blank means that the sire recorded in the pedigree was inconsistent and has been removed or the sire was not provided.
Dam ID	National ID of the dam as recorded in the pedigree of this animal	A blank means that the dam recorded in the pedigree was inconsistent and has been removed or the dam was not provided.
MGS ID	National ID of the dam's sire as recorded in the pedigree of this animal	A blank means that the dam recorded in the pedigree was inconsistent and she and her sire were removed, or the MGS was not provided.
Sample ID	Sample ID supplied in the nomination	This is the sample ID loaded in the SNP file and nomination. An X in front of the sample ID may indicate that the sample was originally loaded in our previous genomic database, as X was used for versioning.
Recipient	Recipient code where the result is sent	The recipient code is supplied with the nomination.
Billing Party	Code of the party to be invoiced by DataGene	The billing party code is supplied with the nomination.
Genotype Panel	Description of the panel	Supplied with the SNP file.
Sample Quality	OK or Reject	OK means the sample was able to be evaluated Reject means that there is a problem. For information on the problem see column named Sample Reject Reason.
Sample Reject Reason	This field explains why the sample quality was not OK.	Blank: the sample was OK LOW_CR: low call rate GENOTYPE DISAGREES WITH ANIMAL SEX: the nominated animal is a male, but the genotype is for a female SAMPLE HETEROZYGOSITY TOO HIGH: too many heterozygotes, suspect contamination
Sample Being Used	Sometimes an animal has many genotypes linked to it. This field indicates if this sample is used in the evaluation.	Active sample: this sample is being used in the evaluation. Inactive sample: there is either another sample in use for this animal or this sample is not able to be used.
Sample Size OK?	Are there enough markers observed for the sample to be used for a genomic breeding value?	OK or Too few markers observed for genomic breeding value.
Is ABVg Required	Has a genomic evaluation been requested?	Y: Yes, a genomic evaluation has been requested for this animal. N: No, a genomic evaluation has not been requested for this animal. Another service may have been requested (such as parentage verification).
Sire Genotype OK?	Is the sire's genotype consistent with the animal?	OK or

Field	Description	Explanation of results
		Genotype Inconsistent – the genotype of the sample is inconsistent with the genotype of the sire recorded in the pedigree.
Dam Genotype OK?	Is the dam's genotype consistent with the animal?	OK or Genotype Inconsistent: the genotype of the sample is inconsistent with the genotype of the dam recorded in the pedigree.
MGS Genotype OK?	The animal's genotype is not specifically tested against the maternal grandsire (MGS).	OK or Genotype Inconsistent: the genotype of the sample is inconsistent with the genotype of the dam.
Breed OK?	Is the breed supplied for the animal able to be evaluated? Currently this is Holstein and Jersey breeds.	Breed OK for bulls: breed is ok if the first letter code for a bull is F or J. Breed OK for cows: the breed is OK if the sire breed is OK, or in case the sire is missing or his breed is X, the cow's breed starts with F or J. Otherwise: Breed of Animal or Sire is not valid for genomics.
Birth date OK?	Is the birth date supplied for the animal able to be evaluated?	Birth date OK: Birth date is not in the future or blank. Otherwise: Birth date is not valid for genomics.
Date Sample In Use	This is the date the sample was linked to a nomination.	Use this field to find the most recent issues.
With ABVg result but with a warning	ABVg was generated but a warning is shown because the pedigree is incomplete. Updating pedigree details will improve the reliability of the result.	Blank – OK Warning - No Sire recorded Warning - No Dam recorded Warning - No Sire and Dam recorded The lack of sire or dam does not stop the calculation of genomic breeding values, but it is detrimental to the accuracy.
Sample arrives after run start	The sample was loaded but after the start of the run	1 – means the sample was loaded after the start of the run 0 - OK
Discovered Sire	Results of parentage discovery program that matches the genotype of the sample to the genotype of the sire's sample.	More than one animal may appear, including the sire that was submitted.
Discovered Dam	Results of parentage discovery program that matches the genotype of the sample to the genotype of the sire's sample.	More than one animal may appear, including the sire that was submitted.
Sire of Discovered Dam	Sire assigned to the dam of the discovered dam.	

More information

Contact the genotyping service desk

E: genotypes@datagene.com.au

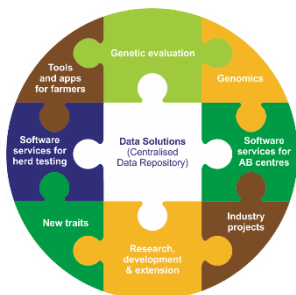
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DataGene is a Dairy Australia and industry collaboration.

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