# *News - NAV evaluation*
# *5 May 2026*

**Dairy cattle**
The latest NAV official evaluation for yield, fertility, conformation, udder health, general health, calving traits, milkability, temperament, growth, longevity, youngstock survival, claw health, saved feed, methane and NTM took place as scheduled. NAV carried out three evaluations per trait group:

*Holstein evaluation*, including data from: Danish Holstein, Swedish Holstein, Norwegian Holstein, Finnish Holstein, Finnish Ayrshire and Finncattle.

*Red Dairy Cattle evaluation*, including data from: Danish Red, Swedish Red, Finnish Ayrshire, and Finncattle.

*Jersey evaluation*, including data from: Danish Jersey, Swedish Jersey, Finnish Jersey, Norwegian Jersey and French Jersey.

Dates for extraction of data from national databases for the latest official evaluations are given in Table 1.

Table 1. Dates for extraction of data from the national databases

| Trait | Denmark | Finland | Sweden |
|---|---|---|---|
| **Yield** | 16.3.2026 | 12.3.2026 | 5.3.2026 |
| **Type, milkability and temperament** | 16.3.2026 | 12.3.2026 | 5.3.2026 |
| **Fertility** | 16.3.2026 | 12.3.2026 | 7.3.2026 |
| **Udder health and other disease** | 16.3.2026 | 12.3.2026 | 7.3.2026 |
| **Calving**[1)] | 16.3.2026 | 12.3.2026 | 7.3.2026 |
| **Longevity** | 16.3.2026 | 12.3.2026 | 7.3.2026 |
| **Growth**[1)] | 16.3.2026 | 12.3.2026 | 6.3.2026 |
| **Claw health** | 16.3.2026 | 12.3.2026 | 7.3.2026 |
| **Youngstock survival**[1)] | 16.3.2026 | 12.3.2026 | 7.3.2026 |
| **Saved feed** | 16.3.2026 | 12.3.2026 | 5.3.2026 |
| **Methane** | 15.2.2026 | No data | No data |
| **Pure beef cattle** | 27.3.2026 | 31.3.2026 | 26.3.2026 |

[1)]Including data for the evaluation of beef bulls used on dairy

**Data used in genomic prediction.**
Genotypes were extracted from the joint Nordic SNP data base 15 April 2026. INTERBULL information from April 2026 was included in the genomic prediction.

## News in relation to NAV dairy genetic evaluation

**Dairy pure**
- New weight for saved feed in NTM
- Publication of methane index
- Change in publication rules

**DairyxDairy**
- No changes

**BeefxDairy**
- No changes

**Beef pure**

- Latest evaluation took place 14.4.2026

# Genetic evaluation of dairy breeds

## New weight for saved feed in NTM

In the May index run, the weights in NTM were changed according to the wishes of the breed associations. Holstein and Jersey followed the economic value, while RDC requested a weight slightly below the economic optimum, at 0.43. The weights for saved feed included in NTM are: Holstein 0.35, RDC 0.35, and Jersey 0.38.

The index correlation between the current NTM and the new NTM, with a higher weight on Saved feed, is very high: 0.99 for Holstein and Jersey while it is 0.98 for RDC. These very high correlations result in only minor re-ranking among animals born in the same year group. The correlations are calculated based on genomic tested Holstein and Jersey bull calves born in 2022 and 2023, and RDC genomic tested bull calves born in 2023 and 2024.

Table 2 shows how the young genomic tested bulls included in the correlation calculations will change in NTM as a result of the adjusted weight on saved feed. For Holstein, the bulls change by a maximum of 4 index units, and more than 75% of the bulls change only by a maximum of 1 index unit. For Jersey, the bulls change by a maximum of 5 index units, and 75% of the bulls change only by a maximum of 1 index unit. RDC experienced the largest relative increase in weight, and therefore it was also expected that RDC would show the largest changes in NTM. The RDC bulls change by a maximum of 6 index units, and 70% of the bulls only change by a maximum of 1 index unit. For all breeds, there is a slight tendency for more animals to increase rather than decrease in NTM, which was also expected, as there is a positive genetic trend for saved feed.

Table 2. Frequency and percentage difference in NTM between current NTM and New NTM for the genomic tested Holstein and Jerey bull calves born in 2022 & 2023 and RDC bulls calves born 2023 & 2024.

| Breed | Holstein | | RDC | | Jersey | |
|---|---|---|---|---|---|---|
| **Number of animals** | 6,349 | | 4,478 | | 1,120 | |
| **NTM change** | Frequency | Percent | Frequency | Percent | Frequency | Percent |
| **-6** | - | - | - | - | - | - |
| **-5** | - | - | 1 | 0.0 | - | - |
| **-4** | 7 | 0.1 | 21 | 0.5 | 3 | 0.3 |
| **-3** | 78 | 1.2 | 93 | 2.1 | 10 | 0.9 |
| **-2** | 391 | 6.2 | 357 | 8.0 | 90 | 8.0 |
| **-1** | 1247 | 19.6 | 826 | 18.4 | 238 | 21.3 |
| **0** | 2012 | 31.7 | 1,223 | 27.3 | 328 | 29.3 |
| **1** | 1679 | 26.5 | 1,091 | 24.3 | 280 | 25.0 |
| **2** | 740 | 11.7 | 609 | 13.6 | 128 | 11.4 |
| **3** | 167 | 2.6 | 215 | 4.8 | 32 | 2.9 |
| **4** | 28 | 0.4 | 42 | 0.9 | 8 | 0.7 |
| **5** | - | - | 6 | 0.1 | 3 | 0.3 |
| **6** | - | - | 1 | 0.0 | - | - |
| **7** | - | - | - | - | - | - |
| **8** | - | - | - | - | - | - |

More information on the effect of the changed weight of Saved feed can be found at NAV homepage.

## Publication of methane index

NAV released the methane index for Holstein females, as well as for both bulls and females in RDC and Jersey. The methane index describes the genetic potential for lower methane production in the rumen of the cow, thereby reducing methane emissions. The data come from sniffer machines that measure methane and $CO_2$ concentrations in the cow's exhaled air while the cow is eating at the milking robot. The phenotypic trait used in the methane index is methane concentration. The underlying idea is that a lower methane concentration from a cow indicates lower methane production. A higher index value therefore corresponds to lower methane concentration.

For the calculation of the methane index, all available methane data from parities 1 to 5 and from day 1 to day 365 in milk are included in the model. Methane data collected from 2020 until now are used in the calculations, including the following:

- **Holstein:** 18 herds, with a total of 644,410 observations from 5,678 cows. There are 556 sires with a mean of 10 daughters with methane registrations.
- **RDC:** 12 herds, with a total of 195,389 observations from 1,789 cows. There are 256 sires with a mean of 7 daughters with methane registrations.
- **Jersey:** 9 herds, with a total of 431,080 observations from 3,703 cows. There are 227 sires with a mean of 16 daughters with methane registrations.

To receive a methane index, a bull must either have a genomic test in the Nordic system and have paid the Nordic fee or have a minimum of 10 daughters with methane observations. The methane index is calculated for females both with and without a genomic test.

Methane is currently an information trait and is not part of NTM. At present, methane has no defined economic value, and therefore it is not relevant to include methane in NTM. For methane to be included, an economically defined value is required, which could be established in the future if clear economic mechanisms related to methane emissions are introduced.

## Change in publication rules

From the May 2026 evaluation round, the publication rules for genomic tested Holstein bulls have changed. To have genomic breeding values published, the owner of the AI bull must pay fee for index evaluation, and the bull must be 10 months old. With the EuroGenomic fee indices for the Interbull traits are published: Yield, Fertility, Calving, Birth, Type traits, Milking speed, Temperament, Longevity, and NTM. In addition to the EuroGenomic fee, a Nordic fee can be paid, which releases the Nordic traits: Growth, General health, Claw health, Youngstock survival, Persistency, Saved feed, and Methane.

The change affects bulls without payment of the Nordic fee and with a mix of proven and genomic indices. Before May 2026, all indices were published when the bull became proven for yield. For traits with too low reliability to be considered proven, genomic breeding values were published instead. From May 2026, both proven and genomic Interbull indices will be published when the bull becomes proven for yield. The Nordic traits will be published as each individual trait becomes proven. The unpublished genomic values for Nordic traits are still used in the NTM calculation.

Previously published genomic indices for Nordic traits will not be removed from databases, but they will not be recalculated and thereby republished. From May 2026, indices for Nordic traits will be missing if they are not proven. Bulls that were herdbooked, before the fee system was introduced, will still have Nordic genomic indices recalculated and published, except for the traits Saved feed and Methane.

**Publication of NTM for Nordic and foreign bulls**

NTM is published if the bull has official EBVs (NAV (G)EBV or international EBV) for Yield, Mastitis and Type. By official means for NAV EBVs that the NAV thresholds are met, and for international EBVs (IB EBVs) that Interbull EBVs for the single bull exist. For traits without a NAV (G)EBV or an IB (G)EBV a NAV pedigree index is calculated.

For bulls with a Nordic herdbook number the pedigree index follows the principles described in the October 2008 routine information. For foreign bulls without a Nordic herd book number the pedigree index is calculated in as ½(EBVsire-100) +1/4(EBVmgs-100) +100. If EBVsire or EBVmgs is not official NAV EBVs then 100 is used.

**Publication of EBVs/GEBVs**
Official EBVs/GEBVs for bulls used for AI in Denmark, Finland or Sweden are published at the NAV Bull Search.

Official NAV GEBVs for foreign AI bulls not used for AI in Denmark, Finland and Sweden are published at NAV homepage. The excel sheets also include GEBVs for bulls used for AI in Denmark, Finland and Sweden. The excel sheets include AI bulls that are 10 months to 5 years old at the date of publication and is mainly useful for foreign AI-companies.

Interbull EBVs/GEBVs are published at the NAV Interbull Search.

## Genetic evaluation of beef bulls used in dairy herds

The latest NAV official evaluation for AI beef bulls based on their crossbred offspring from dairy cows for gestation length, birth, youngstock survival and carcass traits took place as scheduled. Extraction date for the data can be found in table 1. Breeding values for AI beef bulls are estimated four times per year, in connection to the NAV routine genetic evaluation for dairy breeds, and EBVs are published at NAV Beef Search.

**Genetic base**
The genetic base for beef bulls evaluated based on dairy crosses is defined as relative breeding values with a mean of 100 and standard deviation of 10. The genetic base animals for beef bulls evaluated based on dairy crosses constitutes of 2-5 year old crossbreds born after beef breeds which can be used in all 3 countries.

**Fee for EBV of beef bulls based on beef × dairy crossbred offspring**
Nordic Cattle Genetic Evaluation (NAV) conducts a genetic evaluation of AI beef bulls based on beef × dairy crossbred offspring for young stock survival, gestation length, calving and carcass traits. A fee system was introduced 1.1.2020 for the service. It means a fee must be paid for all bulls getting publishable EBVs for the first time after 1.1.2020. No fee needs to be paid for bulls already having official EBVs before 1.1.2020. To get published EBVs the following criteria should be fulfilled for each bull:

- The EBV should meet the criteria for publication.
- A one-time fee of currently 1,300 euro per bull should be paid.

More information about the genetic evaluation and the publication criteria can be found at NAV homepage.

## Genetic evaluation for Purebred Beef animals

The latest genetic evaluation of purebred beef animals took place on 14 April 2026. NAV published EBVs for calving, growth and carcass traits based on phenotypes from purebred beef Angus, Charolais, Simmental, Hereford, Limousine, Highland Cattle, Blonde d 'Aquitaine, Belgian Blue, Dexter, Galloway, Grauvieh, Piemontese, Salers, Shorthorn cattle. Breeding values for growth, slaughter quality, and milk for the five breeds AAN, CHA, HER, LIM, and SIM are estimated in a genomic SS model. Breeding values for pure beef cattle are estimated four times per year (table 3), and all breeding values are published at NAV Beef Search.

## NAV – frequency and timing of official runs

NAV has 4 large dairy evaluations per year, which include updated phenotypic and genomic data, and additional eight small runs including updated genotypes. In table 3 the NAV and INTERBULL release dates for 2026/2027 are shown. The beef evaluation based on beef × dairy crossbreeds take place along with the large NAV dairy runs 4 times a year. The NAV pure beef evaluation has its own time schedule.

Table 3. NAV and INTERBULL release dates in 2026/2027. EBVs released at NAV dates in bold will be delivered to international genetic evaluation.

| | Dairy Cattle | | | Beef Cattle |
|---|---|---|---|---|
| **Month** | **NAV Small run[1)]** | **NAV Large runs[2)3)]** | **INTERBULL** | **NAV Pure Beef** |
| **January 2026** | 6 | | | |
| **February 2026** | | **3** | | |
| **March 2026** | 3 | | | 5 |
| **April 2026** | 7 | | 7 | 14 |
| **May 2026** | | **5** | | |
| **June 2026** | 2 | | | 2 |
| **July 2026** | 7 | | | |
| **August 2026** | | 11 | 11 | |
| **September 2026** | 1 | | | |
| **October 2026** | 6 | | | |
| **November 2026** | | **3** | | 3 |
| **December 2026** | 1 | | 1 | |
| **January 2027** | 5 | | | |

[1)] Genotypes updated; [2)] Genotypes and phenotypes updated; 3) Beef × dairy evaluation

You can get more information about the joint Nordic evaluation:

General about Nordic Cattle Genetic Evaluation: www.nordicebv.info
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