

News genomic prediction - NAV routine evaluation 6 January 2015

The latest NAV routine genomic prediction took place as scheduled. NAV carried out genomic prediction for Holstein, RDC and Jersey:

Data used in genomic prediction

Genotypes were extracted from the joint Nordic SNP data base 15th December 2015. The annual exchanges of genotypes within Eurogenomics for Holstein have taken place and about 1,300 genotypes from the last birth year of bulls with milking daughters are included in the reference population. Nordic phenotypic information for the reference population used in the genomic prediction was the same as in the 2nd November 2014 routine evaluation.

News in relation to NAV genomic prediction

No changes.

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

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