

## How to Read the AJCA Genomic Evaluation Report

1. **Release Date:** Date Genomic Evaluation was released
2. **Genotype:** 50K VERSION 2 GENOTYPE (43,000 SNPs) or 3K GENOTYPE (2,900 SNPs).
3. **Identification:** AJCA registration number and registration name. The date of birth and Permanent identification of the animal, labeled by form (either tattoo *or* AJCA-approved tag) and sex. The sire of the animal, his registration number and NAAB number. The dam and her registration number.
4. **Owner:** The current owner, as indicated on the records of the AJCA.
5. **Inbreeding Percents:** Includes three distinctly different inbreeding measures.
6. **Genomic Inbreeding:** A direct measure of homozygosity, genes in common, based on the DNA observed in the genotyping. Values may be positive indicating inbreeding and negative indicating heterosis. The zero point is the average genomic relationship between all the animals for a particular genotyped population.
7. **Pedigree Inbreeding:** An estimate of the percent genes in common based on pedigree information. This remains static unless the pedigree is modified.
8. **Genomic Future Inbreeding:** Estimate of inbreeding of future offspring, based on the percentage of SNPs in common with the genotyped Jersey population. This may change over time as the basis for comparison, the genotyped population, changes.
9. **Note about reports:** The December 2010 Traditional Evaluations for yield traits and the AJCA JPI (Jersey Performance Index™) are shown in the third column from the right (D). Adjustments are applied by AIPL to Traditional Evaluations (E) for yield traits to correct for bias in female genetic evaluations. The resulting Adjusted Evaluations for December 2010 are provided for index and yield traits. The Genomic Impact (C) can be assessed by comparing Genomic Evaluation (A) with the Adjusted Evaluation (B).
10. **Index:** Indexes offer an economic-based combination of traits to achieve a variety of goals. The Jersey Performance Index™ (JPI™) and AIPL's three merit indexes are in the Index block.
11. **Yield:** Includes genetic evaluations for Milk, Fat, Fat %, Protein and Protein %.
12. **Note about reports:** Genomic (A) and Traditional Evaluations (D) for Health, Fitness and Type traits are expressed on similar scales. No adjustments have been applied. A comparison of the Genomic Evaluation with the December 2010 Traditional Eval indicates the Genomic Impact(C).
13. **Health and Fitness:** Includes genetic evaluations for Pregnancy Rate, Productive Life and Somatic Cell Score.
14. **Type:** Includes genetic evaluations for Final Score and fourteen (14) linear type traits. The trait Rear Udder Width is not genomically evaluated. Displayed is a calculated value based on the genetic relationship of Rear Udder Width with the genomic evaluation of Rear Udder Height.

### Columns

- A. **Genomic Evaluation:** Genomic Genetic Evaluation is a **prediction** of what will be transmitted to the next generation based on pedigree, performance and genomic information from the genotype (SNPs observed in the DNA). For Index (10) and Yield (11) traits, the genomic information is combined with the Adjusted Evaluation (B) to produce the Genomic Evaluation (A). For Health and Fitness (13) and Type (14) traits, the genomic information is combined with the Traditional (D) evaluation to produce the Genomic Evaluation.
- B. **Adjusted Evaluation:** Adjustments are applied by AIPL to Traditional Evaluations (E) for yield traits to correct for bias in female genetic evaluations. The result is the Adjusted Evaluation.
- C. **Genomic Impact:** For Index (10) and Yield (11) traits, the Genomic Impact is a comparison of Genomic (A) and Adjusted (B) evaluations. For Health and Fitness (13) and Type (14) traits, the Genomic Impact is a comparison of Genomic (A) and Traditional (E) evaluations.
- D. **Traditional Eval 12/2010:** Traditional Genetic Evaluation based on pedigree and performance only.
- E. **Genomic REL %:** Genomic Reliability, a measure of accuracy, associated with the Genomic (A) genetic evaluation. A comparison with the Traditional (F) REL % with Genomic (E) demonstrates the increase in accuracy of the prediction by adding genomic information to the evaluations.
- F. **Traditional REL %:** Traditional Reliability, a measure of accuracy, associated with the Traditional (D) genetic evaluation.