The **Igenity Dairy Heifer Program** family of products contains comprehensive, powerful, and easy-to-use tools for genomic evaluation, at any time in an animal's lifetime. No matter if you use the Igenity Elite, Igenity Prime or Igenity Select, all animals receive a genomic Predicted Transmitting Ability (PTA) based on DNA tests that use 9,000 to nearly 150,000 markers from the bovine genome.

Data from the genomic tests conducted on the samples you provide from your animals are submitted to the Council on Dairy Cattle Breeding (CDCB), where a genomic PTA is derived that gives an accurate measure of that animal's true genetic potential. The genomic PTA contains information on the animal's parents, its relatives, any progeny records that might be available, as well as an estimate of the animal's genomic merit based on the direct examination of the markers in its DNA.

The traits evaluated include a wide variety of measures for productivity, health and type traits, along with composite indexes that include Net Merit, Cheese Merit and Fluid Merit. In addition, you can derive a custom index specific to your herd's need and breeding objectives to give you the ultimate flexibility in selection for genetic improvement.

What is a Genomic PTA?

A genomic Predicted Transmitting Ability (PTA) is a measure of the genetic merit of an animal in a breeding program, and in particular, how the animal and its progeny are likely to perform. It is reported as the deviation from a pre-determined base and is an objective measure that allows you to rank the animal against all others that are in the database of the breed.

A wide range of traits are measured, based on data provided by dairy producers, and are reported on the base in which the trait is measured. For example, a PTA for Milk Yield is reported in pounds, a PTA for Net Merit is reported in dollars, and a PTA for Productive Life is measured in months. Initially, a genomic PTA includes genomic information from the animal's genomic profile and pedigree information, if available. The reliability genomic PTA for milk yield on a young Holstein animal can be over 70%. In contrast, the reliability for traditional parent average is about 30%, assuming the parents have been accurately identified. This improvement in reliability makes obtaining a genomic PTA highly valuable for commercial dairy producers when making selection decisions.

As the animal matures, additional information including the animal's own production records and information about the progeny can be included, further improving the reliability of the genomic PTA.

What is particularly powerful in dairy heifers is that the information from the DNA markers is equivalent to over 20 daughter records when predicting the true merit of an animal. So, a DNA test on a day-old calf is the equivalent of years' worth of records!

Looking at your Igenity report

When you receive your Igenity report, the first thing you will see is information related to **Order Number** (this is a useful reference if you have questions, or if you wish to go online later to view your results), **Order Date** and your contact information. In addition, each animal record includes the animal's **Farm ID** (this is usually the short ID, such as an ear tag), the **Official ID** (this is the unique animal ID as it is in the national database), **Breed** (HO for Holstein, JE for Jersey and BS for Brown Swiss) and **Birth Date**. After that, the results are grouped into various categories, depending on their particular focus.

Farm ID	Official ID	Breed	Birth Date
1501	HOUSA0000xxxxxxxx	HO	6/12/2018
1502	HOUSA0000xxxxxxxx	HO	10/30/2017
1503	HOUSA0000xxxxxxxx	HO	11/6/2017
1504	HOUSA0000xxxxxxxx	HO	5/31/2018
1505	HOUSA0000xxxxxxxx	HO	4/1/2017

Key Traits

The first category of reports contains **Key Traits** that are most often used for the purpose of evaluating animals.

- **Net Merit $.** Net merit is a composite trait, meaning that the results for a number of component traits are combined to provide an estimate of the lifetime profit of the animal, in dollars. The traits included in the calculation, along with their relative weighting, are pounds of Protein (17%), pounds of Fat (27%), Milk Yield (-1%), Productive Life (12%), Somatic Cell Score (-4%), Body Weight Composite (-5%), Udder Composite (7%), Feet and Legs Composite (3%), Daughter Pregnancy Rate (7%), Heifer Conception Rate (1%), Cow Conception Rate (2%); Calving ability dollars (5%), Cow Livability (7%) and Health Trait Dollars (2%).

- **Net Merit Report Rank.** All of the animals included in the report you receive are ranked from top to bottom. If there are 100 animals in the report, the animal with the best Net Merit $ score will be ranked #1 and the animal with the lowest Net Merit $ score will be ranked #100.

- **Genomic Reliability (%).** A PTA reported for any trait, for any animal, always comes with a reliability measure. If only parent average is available, the reliability of the estimate of genetic merit provided by the PTA will be low—around 30%. With the addition of data from genomic markers, the reliability of the prediction will frequently approach 70%, which is a significant improvement and means that you can have confidence that the genomic PTA reported for Net Merit $ will be a reliable measure.

- **Net Merit $ US Percent Rank.** In addition to the Report Rank for Net Merit $, the animals in your report are individually scored against the database of all animals with scores for Net Merit. The result is reported as the US Percent Rank, and gives the percent of the animal in the national herd that are below this individual animal for Net Merit. For example, a score of 99% means this animal is in the top 1% and that 99% of all US animals score lower for Net Merit. A score of 50% means that half of the animals in the US score below this animal, while half score better than this animal for Net Merit.

- **Milk Yield.** The PTA for milk yield is the estimated difference in pounds of milk produced per mature 305-day lactation.

- **Fat Yield.** The PTA for fat yield is the estimated difference in pounds of fat produced per mature 305-day lactation. The estimate of the actual amount of fat produced will be a result of the predicted milk yield, as well as the predicted percent of fat in the milk (fat %). Fat percent is typically reported separately, but most dairymen are interested in total fat yield per lactation.

- **Protein Yield.** The PTA for protein yield—like fat yield—is the estimated difference in pounds of protein produced per mature 305-day lactation.

- **Somatic Cell Score (SCS).** The PTA for Somatic Cell Score is an estimate of the number of somatic cells per milliliter of milk (divided by 100,000) and is an estimate of udder health. Somatic cells are natural defense mechanisms during times of udder infection (mastitis), and animals with a lower SCS suggests improved resistance to udder infections and mastitis. For SCS, a lower score is preferred.

- **Productive Life (PL).** The PTA for Productive Life is a prediction of the longevity of the animal in the herd and is measured in months. Longer is better in this case because herds with greater longevity, on average, require fewer replacement females, which is a very important component of the cost of production.

- **Daughter Pregnancy Rate (DPR).** The trait of Daughter Pregnancy Rate measures the percent of open cows that become pregnant each 21 days. Animals—and herds—with higher DPR are more fertile and better able to conceive following calving.

					KEY TRAITS									
Farm ID	NM$	NM$ Report Rank	Genomic REL %	NM $ US Percent Rank	Milk Yield	Fat (lbs)	Pro (lbs)	SCS	PL	DPR	DCE	IPI	PTA Type	GFI
1501	488	1	67	93	1838	74	56	3.04	1.6	-1	5.3	2051	2.46	2.5
1502	361	2	69	82	201	44	18	2.73	2.2	-0.2	6.5	1798	1.58	5.9
1503	243	3	68	62	759	37	21	2.88	0.7	-1	7.8	1728	1.7	6
1504	217	4	68	57	686	23	22	3.02	1	1.1	6.8	1654	1.04	2.3
1505	62	5	70	25	236	52	13	3.3	-1.9	-0.9	6	1451	0.63	3.4

Key traits sheet shows some of the most important traits to consider when evaluating your dairy herd. When reports are returned, the animals are sorted by Net Merit($). In this case, the top ranking heifer (#1501) has a NM$ of $488 while the bottom heifer (#1505) has a NM$ of $62. Based on this example, we would expect #1501 to produce $852 [($488-$62) x2] more profit than #1505 over her lifetime. The difference in NM$ is multiplied by 2 since the estimate of the animal's own performance is 2 times the PTA, or what they would contribute to their progeny.

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- **Daughter Calving Ease (DCE).** Daughter calving ease is a measure of the ability of an animal to have an unassisted birth. The trait measures the percentage of difficult births among heifers; therefore, a lower score is desirable.

- **Igenity Production Index (IPI).** The Igenity Production Index—like Net Merit—is a composite trait that combines and weights the values for individual traits to come up with an overall estimate of genetic merit based on specific breed standards. For Holstein, the weighting for the major categories include: 46% on production traits, 28% on health and fertility traits and 26% on conformation traits. For Jersey, 53% of the composite is based on production traits, 27% on health and fertility traits and 20% on conformation traits.

- **PTA Type (PTAT).** The PTA for Type is a composite score of up to 19 individual structural and anatomic traits, related to things such as feet and legs, udder, body frame and other measures that are known to be positively associated with longevity and performance in dairy cattle. Daughters of sires are scored by classifiers from breed associations, relative to their overall type, and that information is then used to predict structural soundness of dairy animals and their progeny. A higher score for type is preferred and is included in the category of Key Traits because it is the best measure of overall conformation.

- **Genomic Future Inbreeding (GFI).** GFI is a measure of the level of inbreeding in an individual animal, and is derived in this case directly from the DNA marker information. Animals that are more inbred tend to be homozygous (meaning the same gene is inherited from both parents) and this inbreeding is known to reduce performance. In this case, a lower score is desired as a means of reducing inbreeding in the herd.

Tips for wading through genomic data: Use composite indexes

Igenity reports contain over 50 traits that can be used for decision-making. Looking at composite indexes can be a great way to summarize this information in a way that is useful to your specific breeding goals. The following composite indexes with relative traits and their associated weightings are included:

Trait	Net Merit (NM$)	Cheese Merit (CM$)	Fluid Merit (FM$)	Grazing Merit (GM$)
Milk (lbs)	–1	–8	18	–1
Fat (lbs)	27	23	27	23
Protein (lbs)	17	21	0	14
Productive life (months)	12	10	12	7
Somatic cell score	–4	–4	–2	–4
Body size composite	–5	–5	–5	–6
Udder composite	7	6	8	7
Feet/legs composite	3	2	3	3
Daughter pregnancy rate	7	6	7	18
Calving ability dollars	5	4	5	5
Heifer conception rate	1	1	1	2
Cow conception rate	2	1	2	4
Cow livability	7	6	7	5
Health trait dollars	2	2	2	2

Health Traits

There are several health traits that are particularly important for dairy production, and these traits are grouped together within the Health Trait category. These include **Daughter Pregnancy Rate** (defined as the percent of open cows that become pregnant every 21 days, **Productive Life** (prediction of the longevity of the animal and its progeny in the herd and is measured in months) and **Somatic Cell Score** (a measure of the number of somatic cells per milliliter of milk, reflecting udder health).

HEALTH TRAITS			
Farm ID	DPR	PL	SCS
1501	-1	1.6	3.04
1502	-0.2	2.2	2.73
1503	-1	0.7	2.88
1504	1.1	1	3.02
1505	-0.9	-1.9	3.3

Looking at Productive Life (PL) in the herd above, we would expect #1502 to be in the herd 8.2 months longer than #1505 [(2.2-(-1.9))x2]. The difference in PL is multiplied by 2 since the estimate of the animal's own performance is 2 times the PTA, or what they would contribute to their progeny.

- **Cow Livability (LIV).** Cow Livability measures the difference in the cow's ability to stay alive. While Productive Life measures any reason an animal leaves the herd, Cow Livability distinguishes animals that leave due to death. That's an important distinction because these animals have no salvage or cull cow value, plus a cost associated with disposing the carcass. Higher score is favorable.

- **Displaced Abomasum (DAB).** Displaced Abomasum represents the expected resistance of an animal's offspring to displaced abomasum in a herd with average management conditions. Larger, positive values are more favorable.

- **Hypocalcemia (MFV).** Hypocalcemia represents the expected resistance of an animal's offspring to hypocalcemia, also known as milk fever. Larger, positive values are more favorable.

- **Ketosis (KET).** Ketosis represents the expected resistance of an animal's offspring to ketosis in a herd with average management conditions. Larger, positive values are more favorable.

- **Mastitis (MAS).** Mastitis represents the expected resistance of an animal's offspring to clinical mastitis in a herd with average management conditions. Larger, positive values are more favorable.

- **Metritis (MET).** Metritis represents the expected resistance of an animal's offspring to metritis in a herd with average management conditions. Larger, positive values are more favorable.

- **Retained Placenta (RPL).** Retained Placenta represents the expected resistance of an animal's offspring to retained placenta in a herd with average management conditions. Larger, positive values are more favorable.

Yield Traits

Various yield traits are combined into a single grouping and, as defined above, this includes traits such as **Milk Yield** (number of pounds of milk in a standard 305-day lactation, above or below the industry baseline), **Fat Yield** (number of pounds of fat in a standard 305-day lactation, above or below the industry baseline) and **Protein Yield** (number of pounds of protein in a standard 305-day lactation, above or below the industry baseline). Additional traits in this category include:

- **Fat Percent.** This is a PTA for the fat content of the milk and, when combined with the yield figures, will result in the estimate of the total lactation yield of fat, in pounds. This is a percentage scale, and generally a higher value is more beneficial.

- **Protein Percent.** This is a PTA for protein content of the milk, and when combined with the yield figures, will result in the estimate of the total lactation yield of protein, in pounds. This is a percentage scale, and generally a higher value is more beneficial.

- **Cheese Merit Dollars (CM$).** Like Net Merit, Cheese Merit is a composite index and, because of the economic value of components such as fat and protein for further processing, it places emphasis on the value of components and penalizes animals for excess milk yield. The traits included in the calculation, along with their relative

YIELD TRAITS							
Farm ID	Milk Yield	Fat (lbs.)	Fat %	Pro (lbs.)	Pro %	Cheese Merit	Fluid Merit
1501	1838	74	0.02	56	0	262	363
1502	201	44	0.14	18	0.05	38	50
1503	759	37	0.03	21	-0.01	107	150
1504	686	23	-0.01	22	0	97	135
1505	236	52	0.17	13	0.03	42	58

For operations looking to improve fluid milk production, milk yield is a very important trait. In the herd above, we would expect #1501 to produce 3,274 pounds [(1838-201)x2] more milk than the industry baseline over a 305-day lactation when compared with #1502. That is approximately 10.7 pounds of milk per each day of the lactation, or $2.30 per day for fluid milk at $22.53 cwt.

weighting, are pounds of Protein (21%), pounds of Fat (23%), Milk Yield (-8%), Productive Life (10%), Somatic Cell Score (-4%), Body Weight Composite (-5%), Udder Composite (6%), Feet and Legs Composite (2%), Daughter Pregnancy Rate (6%), Heifer Conception Rate (1%), Cow Conception Rate (1%), Calving ability dollars (4%), Cow Livability (6%) and Health Trait Dollars (2%).

- **Fluid Merit Dollars (FM$).** As the name implies, Fluid Merit is targeted to producers whose marketing system favors milk yield and who do not receive premiums for protein production. The traits included in the calculation, along with their relative weighting, are pounds of Protein (0%), pounds of Fat (27%), Milk Yield (18%), Productive Life (12%), Somatic Cell Score (-2%), Body Weight Composite (-5%), Udder Composite (8%), Feet and Legs Composite (3%), Daughter Pregnancy Rate (7%), Heifer Conception Rate (1%), Cow Conception Rate (2%), Calving ability dollars (5%), Cow Livability (7%) and Health Trait Dollars (2%).

- **Grazing Merit Dollars (GM$).** Like net merit, grazing merit is a composite index that caters to herds that use seasonal calving based around grass production. The selection is around fertility and those traits that favor efficient milk production off grass. The traits included in the calculation, along with their relative weighting, pounds of Protein (14%), pounds of Fat (23%), Milk Yield (-1%), Productive Life (7%), Somatic Cell Score (-4%), Body Weight Composite (-6%), Udder Composite (7%), Feet and Legs Composite (3%), Daughter Pregnancy Rate (18%), Heifer Conception Rate (2%), Cow Conception Rate (4%), Calving ability dollars (5%), Cow Livability (5%) and Health Trait Dollars (2%).

Fertility Traits

This grouping of traits is intended to bring together several measures of reproductive success and includes **Daughter Calving Ease** (measure of the ability to have an unassisted birth). Other measures in this classification include:

- **Sire Calving Ease (SCE).** The trait measures of the ability of calves of a particular sire to have an unassisted birth, lower scores indicate an easier calving.

- **Heifer Conception Rate (HCR).** The trait measures a maiden heifer's ability to conceive measured by the percentage of inseminated heifers that become pregnant at each service. A score of 1 suggests that the heifer is 1% more likely to become pregnant than heifers with an evaluation of 0.

- **Cow Conception Rate (CCR).** Similar to Heifer Conception Rate, the trait measures the percentage of cows that become pregnant at each service. A score of 1 suggests that the cow is 1% more likely to become pregnant than cows with an evaluation of 0.

- **Daughter Stillbirth.** This trait measures the ability of a cow, or daughters of a bull, to have a live calf that survives past 48 hours. In this case, a lower score is more desirable.

- **Sire Stillbirth.** The trait measures the ability of calves from a particular sire to be born live and survive past 48 hours. In this case, a lower score is more desirable.

- **Gestation Length (GL).** Gestation length measures the difference in length of gestation. Lower score is preferred.

- **Haplotype Status.** Researchers have thoroughly evaluated the database of genotypes and identified that certain combinations of genotypes (referred to as haplotypes) that should be present in the population are simply not present. The absence of the haplotype suggests that the unique combination of those genotypes is somehow lethal to the developing embryo. When the researchers investigate, they are able to identify bulls (or females) that are carriers of the haplotype are less fertile, suggesting embryonic mortality. In several instances, they have identified the causative mutation and confirmed that the change in the DNA does result in a lethal mutation. There are six of these haplotypes known to exist in Holstein (named HH1 through HH6), one in Jersey (named JH1), one in Brown Swiss (named BH2) and two in Ayrshire (named AH1 and AH2). The animal that is normal for the haplotypes is reported as a "T", an animal that is a carrier for the haplotypes is reported as a "C" and an animal that is homozygous affected is reported as an "A".

FERTILITY TRAITS								
Farm ID	DCE	SCE	HCR	CCR	Daughter Stillbirth	Sire Stillbirth	GL	Haplotype Status
1501	5.3	5.2	0.5	1.4	6	7.8	1.2	HH1T HH2T HH3T HH4T HH5T HH6T
1502	6.5	7.9	1.1	0.7	7	7.4	-1.2	HH1T HH2T HH3T HH4T HH5C HH6T
1503	7.8	6.1	0.5	1.4	8.2	7.8	0.2	HH1T HH2T HH3T HH4T HH5T HH6T
1504	6.8	8.7	-1.5	-3.2	7.1	8.1	1.0	HH1T HH2T HH3T HH4T HH5T HH6T
1505	6	8.7	-0.7	-2.3	8.3	7.8	-0.5	HH1T HH2T HH3T HH4T HH5T HH6T

In the example above, #1502 is a carrier for Holstein Haplotype 5. This information can be used to make optimum herd mating decisions.

Type Traits

The CDCB evaluation uses the information on the structural or "type" classification performed by classifiers from the breed associations, and elsewhere, to derive a series of type classifications that describe the conformation and structural makeup of the animal. These type classifications are derived in a way that will relate to longevity and productivity, since dairy animal strength and fitness will definitely influence performance. The Igenity Dairy Heifer Program lists a series of the key type traits as follows:

- **PTA Type (PTAT)** is a compilation of at least 16 different trait evaluations and provides an overall measure of fitness. A larger value is preferred.

- **Feet and Legs Composite (FLC)** consists of Foot Angle, Rear Legs Rear View and Rear Legs Side View. A larger value is generally preferred, indicating strength in the legs and feet, normal claw conformation and health, and appropriate angularity in the leg.

- **Udder Composite (UDC),** like Feet and Legs Composite, rejoins scores for a number of components of quality udders, including udder depth, udder cleft, fore udder attachment, rear udder height, rear udder width, front teat placement, rear teat placement and teat length. A higher value is preferred.

- **Stature (STA)** is essentially a measure of height or vertical depth. In order for there to be sufficient room for a large and functional rumen, lungs and other organs, a dairy cow needs sufficient body size, without being excessively large. Stature is a measure of this. A higher value indicates a taller animal.

- **Strength (STR)** is a measure of traits such as muscle tone, width of chest, strength or linearity of topline and other measures that imply a strong and robust animal, capable of easily moving to and from feeding areas, handling the capacity of a large and functional rumen and other traits that support a long and productive life. A higher value indicates a stronger animal.

- **Body Depth (BDE)**—along with stature—is essentially the amount of capacity in the body for lungs, rumen and other abdominal organs. A highly productive cow needs capacity for large organs required to produce the energy for top quality milk production. A higher value indicates the animal has a greater capacity.

Additional Type Traits

In addition to the key type traits listed above, Igenity includes a number of other type or conformation traits as listed below:

- **Dairy Form (DFM)** is a measure of the amount of angularity in the female. Animals should be moderately angular, suggesting high production, as opposed to being somewhat round (excessive fat cover) or skeletal (insufficient fat cover). A higher value indicates more angular animal.

- **Rump Angle (RPA)** is the slope from the hip bone (ilium) to the pin bone (ischium). A value close to 0 indicates a more desirable slope from hips to pins.

- **Rump-Thurl Width (RTW)** refers to the width of the hips. A higher value indicates a wider animal between the pins.

- **Rear Legs Side View (RLS)** refers the angle of the hock as viewed from the side. Higher values will apear more sickled hocked while lower values will appear post legged. A value nearer to 0 is more desirable.

- **Rear Legs Rear View (RLR)** refers to differences in width of stance between the rear legs as viewed from behind. A higher value indicates the animal tracts straighter on its rear legs.

- **Foot Angle (FTA)** is the steepness of the angle of the rear foot from the hairline. A higher value indicates greater hoof angle.

- **Feet and Legs Score (FLS)** measures overall feet and legs by combining mobility and feet and leg structure. A higher value is preferred.

TYPE TRAITS																				
Farm ID	PTAT	FLC	UDC	STA	STR	BDE	DFM	RPA	RTW	RLS	RLR	FTA	FLS	FUA	RUH	RUW	UCL	UDP	FTP	RTP	TLG
1501	1.64	0.99	1.52	0.74	1.11	0.88	0.34	0.77	0.98	-0.16	0.93	1.22	1.03	1.88	2.28	0.98	1.88	1.38	1.37	1.67	0.23
1502	1.78	1.09	1.43	0.55	0.18	0.42	1.3	0.45	1.42	0.83	1.45	0.49	1.54	1.92	2.04	1.3	1.98	1.26	1.34	1.64	0.29
1503	2.35	1.26	1.88	1.71	0.51	1.00	2.31	0.23	2.13	1	1.4	1.27	1.54	2.28	2.95	-0.36	1.89	1.72	0.98	1.42	-0.21
1504	0.64	0.47	0.35	0.01	0.7	0.33	-0.39	0.77	0.43	-1.07	0.72	0.18	0.43	0.81	0.21	2.01	0.91	0.31	1.27	1.28	-0.44
1505	1.4	1.39	1.24	0.86	0.91	0.91	1.14	-0.22	1.33	0.29	1.61	1.48	1.52	1.53	1.93	0.45	1.49	1.04	0.2	0.44	1.45

For the example above, Rear Legs Side View (RLS) is low for #1504 at -1.07 and high for #1503 at 1. We would expect #1504 to physically appear more post legged than #1503 who would likely appear sickle hocked. #1501 has the closest value to 0, so her legs should appear most ideal when viewed from the side.

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- **Fore Udder Attachment (FUA)** is an evaluation of the strength of attachment of the fore udder to the body wall. A higher value indicates a stronger attachment of the fore udder.

- **Rear Udder Height (RUH)** is measured as viewed from the rear at the crease where the udder meets the leg, in relation to the midpoint between the point of hock and pins. A higher value indicates a higher rear udder.

- **Rear Udder Width (RUW)** is measured at the point of udder attachment and is an indicator of udder capacity. A higher value indicates a wider rear udder.

- **Udder Cleft (UCL)** is a measure of the depth of cleft of the udder between the rear teats. A higher value indicates a stronger udder cleft.

- **Udder Depth (UDP)** is a measure of the depth of udder floor relative to the hock. A higher value indicates a more desirable depth between the lowest point of the udder floor and the point of the hock.

- **Front Teat Placement (FTP)** is a measurement of the placement of the front teats on the quarter. A higher value indicates a closer distance between the front teats.

- **Rear Teat Placement (RTP)** is a measurement of the placement of the rear teats on the quarter. A higher value indicates a closer distance between the rear teats.

- **Teat Length (TLG)** is the length of the front teats from the base to the end of the teat. A value close to 0 is preferred.

Genetic Conditions

Coat Color (including Black/Red). The Igenity Dairy Heifer Program uses haplotypes to determine black or red coat color. The four alleles present on MCR1 are dominant black (E^D), Black/Red (E^{BR}), wild type red (E^+), and recessive red (e). The black (E^D) gene is dominant over red (e). Black/Red, also known as Telstar (E^{BR}), results in red coat color at birth that changes to black, usually by 3-6 months. Wild type red (E^+E^+) produces red animals that are darker at the extremities, particularly as the animal ages. The order of dominance is E^D>E^{BR}>E^+>e. Animals will appear as described below only in the absence of dominant red.

E^DE^D	Homozygous Black—will not produce red offspring. Over 90% of Holsteins have this genotype.
E^DE^{BR}	Black, Black/Red carrier
E^DE^+	Black, Wild Type carrier
E^De	Black, Recessive red carrier
$E^{BR}E^{BR}$	Black/Red—this animal cannot produce true red offspring.
$E^{BR}E^+$	Black/Red, wild type carrier
$E^{BR}e$	Black/Red, recessive red carrier
E^+E^+	Wild type red
E^+e	Wild type red, carrier of recessive red
ee	Recessive red. When bred to another ee will only produce red offspring.

Dominant Red Coat Color. As the name implies, dominant red coat color that occurs in Holsteins will lead to a red coat regardless of the alleles expressed for traditional coat color.

N/N.	No copies of Dominant Red present. Color is dependent on the gene for traditional coat color.
N/DR.	One copy of Dominant Red present. The animal will appear red and white, but only produce red and white offspring 50% of the time.
DR/DR.	Two copies of Dominant Red present. The animal will appear red and white and will always produce red and white offspring.

Haplotype Polled. A dominant trait in cattle—only animals with two horned recessive genes will appear horned. Animals appearing polled will not require the labor associated with dehorning. Animals will be reported as "HH" (meaning they carry two horned genes), "HP" (meaning they appear polled, but carry the horned gene) or "PP" (meaning they carry two polled genes). If a HP animal is mated with a HH animal, 50% of offspring will be HP. If an animal is PP, all of its offspring will appear polled (HP or PP). The haplotype for the polled trait is derived from the CDCB evaluation. (For purebred breeding purposes, a conformation test using the causative polled test is suggested.)

HH: Horned   **HP:** Horned carrier   **PP:** Polled

Haplotype Brachyspina. A lethal recessive that usually causes abortion within the first 40 days of gestation. Carrier animals have no symptoms, but will have a 25% chance of producing an affected offspring if bred to another carrier. The haplotype for Brachyspina is derived from the CDCB evaluation.

T: Tested Free   **C:** Carrier   **A:** Affected

Haplotype Complex Vertebral Malformation (CVM) A lethal hereditary syndrome found in Holstein that is responsible for malformed calves that usually are aborted or die shortly after birth. Carrier animals have no symptoms, but will have a 25% chance of producing an affected offspring if bred to another carrier. The haplotype for CVM is derived from the CDCB evaluation.

T: Tested Free **C:** Carrier **A:** Affected

Bovine Leukocyte Adhesion Deficiency (BLAD). BLAD is a disease that results in impaired function of the white blood cells of the immune system. In order for an animal to demonstrate clinical signs of the disease, it must have two copies of the gene. Carriers (animals with one copy of the gene) are normal, but will have a 25% chance of producing an affected offspring if bred to another carrier.

T: Tested Free **C:** Carrier **A:** Affected

Deficiency of Uridine Monophosphate Synthase (DUMPS). DUMPS is characterized by early embryonic death in animals that have two copies of the gene. Animals with one copy of the gene (carriers) are normal, but will have a 25% chance of producing an affected offspring if bred to another carrier.

T: Tested Free **C:** Carrier **A:** Affected

Haplotype Mulefoot. Mulefoot is a recessive congenital disease in Holstein cattle that causes fusion of the hoof. It is not lethal, but leads to locomotive difficulties in affected animals.

T: Tested Free **C:** Carrier **A:** Affected

Spinal Muscular Atrophy (SMA). A neurological condition affecting the nervous system that is characterized by skeletal muscle atrophy, decreased spinal reflexes and motor weakness. This haplotype is derived from the CDCB evaluation and only known to be present in Brown Swiss cattle. Animals with one copy of the gene (carriers) are normal, but will have a 25% chance of producing an affected offspring if bred to another carrier.

T: Tested Free **C:** Carrier **A:** Affected

Spinal Dysmyelination (SDM). A neurodegenerative disease in cattle that leads to inability to stand immediately upon birth. This haplotype is derived from the CDCB evaluation and only known to be present in Brown Swiss cattle. Animals with one copy of the gene (carriers) are normal, but will have a 25% chance of producing an affected offspring if bred to another carrier.

T: Tested Free **C:** Carrier **A:** Affected

Weaver. Also known as Bovine Progressive Degenerative Myelo-encephalopathy, it is characterized by a noticeable weaving gait of the affected animal. This haplotype is derived from the CDCB evaluation and only known to be present in Brown Swiss cattle. Animals with one copy of the gene (carriers) are normal, but will have a 25% chance of producing an affected offspring if bred to another carrier.

T: Tested Free **C:** Carrier **A:** Affected

Additional content included with Igenity Prime and Igenity Elite

Kappa casein. There are several forms of kappa casein – A, B and E – that are associated with milk protein and quality. These variants are related to renneting process for cheese production. Studies have also shown that cheddar cheese yield can be up to 8% higher and mozzarella up to 12% higher with BB milk versus AA milk. The E variant has an adverse effect on cheese production.

BB: preferred result for cheese production
AB and BE: intermediate for cheese production.
AA and AE: least favorable result for cheese production.

Beta casein. Like kappa casein, there are several different forms of beta casein (A and B). Higher milk yield is associated with the A variant while higher protein and casein yields are associated with the B variant. Beta casein B is similar in effect to Kappa casein B.

Beta lactoglobulin. A major whey protein that has a significant effect on casein number and cheese yield. The B variant has higher casein and cheese yields.

Beta lactoglobulin and Beta casein

BB: most favorable result for casein and cheese yield.
AB: intermediate result for casein and cheese yield.
AA: least favorable result for casein and cheese yield.

Additional information available

In addition to the included traits, Igenity Select, Igenity Prime and Igenity Elite the option to purchase add-on content for an additional fee. Both A2 beta casein and BVD diagnostic testing are available for purchase.

A2 beta casein. A beta casein protein that is less common than the A1 beta casein protein typically found in Holstein milk. Some studies have demonstrated health benefits associated with A2 milk, although this is debated. The milk does sell for a premium which is why some producers are choosing to select for it.

> **A2/A2:** A2 Milk   **A2/A1:** A2 carrier   **A1/A1:** A1 Milk

BVDV Status. Bovine Viral Diarrhea Virus or BVDV is one of the most economically significant diseases in dairy cattle, causing reproductive disorders and increased mortality. If the animal is suspected to be positive for BVDV persistent infection (PI), genomic testing will not proceed unless advised otherwise. It is advisable to cull persistently infected animals as they are sub-optimal performers and a source of infection for other animals.

Negative:	No BVDV detected; sample negative for BVDV Persistent Infection (PI).
Positive:	BVDV detected; sample positive for BVDV Persistent Infection (PI).
Inconclusive:	Sample tested weakly positive for BVDV, but a final diagnosis regarding the BVDV status cannot be made at this time. Presence of BVDV may be from recent vaccination with modified live vaccine, from recent BVDV infection, or from being truly PI.

Additional information available with Igenity Prime and Elite

In addition to the included traits for Igenity Prime and Igenity Elite, the option to purchase add-on content is available for the purposes of confirmation on elite breeding animals. The profiles will all include the haplotype information for polled, CVM and Brachyspina; however, by looking at the causative mutation for these genetic conditions, we can be sure of the true status of the animal prior to marketing.

Causative Polled. An independent test for the causative mutation associated with the polled condition in dairy cattle. It is the definitive test for horned/polled that can be performed in any breed of cattle.

Causative CVM. An independent test for the causative mutation associated with complex vertebral malformation. It is the definitive test for the disease in Holstein cattle.

Causative Brachyspina. An independent test for the causative mutation associated with brachyspina. It is the definitive test for the disease in Holstein cattle.

Parentage

Igenity Select, Igenity Prime and Igenity Elite include parentage discovery. Parentage discovery allows the true sire or dam to be discovered out of all animals with a genotype on file at the Council on Dairy Cattle Breeding (CDCB).

A potential sire can be submitted by its registration number or NAAB code and a potential dam can be submitted by registration number, animal identification number (AIN), radio frequency identification (RFID) or a state metal ear tag. If you know the potential dam has been genotyped previously, please submit using that same ID originally submitted.

If a sire is listed on your Igenity report as the **Genomic Sire** and the **Sire Status** is **Confirmed**, this animal is determined to be the sire of the given offspring using DNA markers. Igenity reports provide the Genomic Sire NAAB code and the Genomic Sire Registration Number of confirmed sires. If the Genomic Sire is different than the Submitted Sire, the Submitted Sire will be in red text to alert you to the sire conflict.

In addition, a **Submitted Dam** may be confirmed using genomics. A dam will only be listed as confirmed if they have been previously genomic tested. Your Igenity report will also list the **Maternal Grandsire (MGS)** if available. If the sire and dam are both confirmed, the maternal grandsire will likely be confirmed as well, giving you the complete pedigree of the animal.

PARENTAGE					
Farm ID	Submitted Sire	Genomic Sire	Sire Status	Maternal Grandsire (MGS)	Status of Maternal Grandsire (MGS)
1501	HO840003011611135	HO840003011611135	Confirmed		Unconfirmed
1502	HO840003011611135	HO840003011611135	Confirmed	HOUSA000062658255	Confirmed
1503	HOUSA000073163134		Unconfirmed		Unconfirmed
1504	HOUSA000070694639	HOUSA000070694639	Confirmed		Unconfirmed
1505	HOCAN000103974928	HO840003004886505	Confirmed		Unconfirmed

The parentage analysis has revealed that the sire submitted for #1501 is, in fact, the true sire of the animal. In contrast, the sire submitted for #1505 is not the sire of the animal; however, another sire has been determined as the sire. This is highlighted in red to make it stand out and easy to correct pedigree records.

Animals not reported

On your Igenity report, you may find that some of your animals appear as **Animals Not Reported**. There are many reasons why an animal may not receive genomic results from the CDCB. It is important to include the most accurate information available, including sire and dam information, to minimize the chance of receiving a conflict that will delay your results.

Information on your **Animals Not Reported** report will include **Sample Status** which provides the reason an animal is not reported. Some animals may have multiple reasons that they were not reported. In addition, your report will include **Customer Action** letting you know how to respond to the conflict. For commercial animals or animals outside the U.S., Neogen will correct pedigree conflicts on your behalf. For registered animals in the U.S., corrections will need to be made with your breed association.

Here are just a few of the common conflicts that may occur:

Sire Conflict. Sire conflicts are common, with 15–20% of dairy animals having their sire incorrectly identified. These occur when the animal submitted as the sire has been excluded as the genomic sire.

Discovered Parent(s). Often accompanied by a sire conflict or dam conflict, the Associated ID listed with Discovered Parent(s) indicates that the sire or dam of this animal has been discovered. If automatic parentage corrections have been selected on your submission form, the discovered parent will be accepted and reported back to you on your Excel report and via Igenity Dashboard.

Maternal Grandsire Conflict. These conflicts occur when it is determined unlikely that the Maternal Grandsire (MGS) is related to the animal. This often means that the submitted dam is incorrect or has not been genotyped. The recommended solution is to remove the submitted dam from the pedigree or correct the dam's sire by having her genotyped.

Breed Conflict. Breed conflicts occur when an animal's breed composition is not at least 87% of the submitted breed (e.g., HO, JE, BS, etc.). For example, if an animal is submitted as a Holstein, but has a Jersey sire, it will likely receive a breed conflict and will not receive results, as crossbred animals unfortunately cannot receive a CDCB evaluation at this time.

Duplicate Genotype Identified. These conflicts often occur when an animal has been previously tested under an alternate ID. If it can be confirmed that the Associated ID provided in your report is a valid alternate ID for the submitted animal, the IDs can be cross-referenced at CDCB in order to get results. If the Associated ID is not the same animal, it may indicate a sampling error.

Sex Conflict for Female/Male. This conflict occurs when an animal is submitted as female, but is identified as a male upon genotyping (or vice versa). If the animal can be confirmed as the suggested gender, the results will be released, and the appropriate CDCB fees for males will be applied. Sex conflicts will not be corrected automatically as they often indicate that there was a sampling error.

ANIMALS NOT REPORTED					
Farm ID	Official ID	Sample Status	Associated ID	Customer Action required if animal is	Customer Action required if animal is registered with a U.S.
2418	HOUSA000012345677	Sire Conflict	HOUSAM000055555555	Review and Verify CDCB Suggested Sire	Contact Breed Registry to correct pedigree
		Discovered Parent(s)	HOUSAM000077777777	Review and Verify CDCB Suggested Parent(s)	Contact Breed Registry to correct pedigree
		Maternal Grandsire Conflict	HOUSAM000044444444	Correct Maternal Grandsire or Remove Submitted Dam	Contact Breed Registry to correct pedigree
2419	HOUSA000012345676	Breed Conflict	-	No Action Required; PTAs not possible	No Action Required; PTAs not possible
2420	HOUSA000012345675	Sire Conflict	HOUSAM000139682643	Review and Verify CDCB Suggested Sire	Contact Breed Registry to correct pedigree
		Duplicate Genotype Identified	HOUSAF000068870348	Verify Duplicate Animal's ID or Submit New Sample	Verify Duplicate Animal's ID or Submit New Sample
2421	HOUSA000012345678	Sex Conflict for Female	-	Verify Animal's Sex or Submit New Sample	Verify Animal's Sex or Submit New Sample

The Animals not Reported report reveals that #2418 has a sire conflict and that the sire submitted (HOUSAM000055555555) is not the sire. However, the true sire has been discovered to be HOUSAM000077777777. Assuming this is a commercial herd, the discovered sire will be accepted on your behalf and results will be available the following week.

Sample Received "low call rate" (failure). Samples can fail for a variety of reasons including biological or chemical contamination, improper storage or an insufficient sample. Usually, there are very few samples that will fail within an order. If you are receiving greater than 2% sample failures, please get in touch with your representative to review the sampling process.

Other possible reasons an animal is not reported:

Pedigree Conflicts

Sire Conflict, Discovered Sire, Dam Conflict, Discovered Dam, Discovered Parent(s), Discovered Clone, Progeny Conflict, Discovered Progeny, Maternal Grandsire Conflict, Paternal Grandsire Conflict, Discovered Grandsire, Excessive Parent-Progeny Conflicts, Genotype Unreliable

Genotyping Conflicts

Sample Received "low call rate" (failure), Sample Processing, Sample Reprocessing

Identification Conflicts

Duplicate Genotype Identified, Possible Identical Twin or Split Embryo, Genotype Does Not Match Previously Tested Animal, Possible Parent-Progeny Relationship, Close Birth, Breed Conflict

Sex-Related Conflicts

Probable XXY abnormality, Bull genotype has more heterozygous X-specific SNP than explainable as genotyping error, Sex Conflict (animal likely male), Sex Conflict (animal likely female), Possible Mutation or Chromosome Abnormality; Results Pending, Female with Y SNP Presence.

Implementing genomic results on farm

There are a few strategies that can be utilized to get maximum benefit from your genomic results.

1. **Define your protocol.**

    Start by outlining a plan for how you will utilize your genomic results based on your operation goals. Many producers will opt to use deferential breeding decisions, such as utilizing sexed semen or beef semen. Sexed semen can, on the top-end animals, be used to obtain females out of your best females. Another popular choice is to breed lower end animals with beef semen. This allows you to keep the animals in your milking herd and obtain a premium on the resulting crossbred calves without continuing the poorer performing genetics.

2. **Sort and rank animals.**

    Next, sort and rank your animals by your defined criteria, whether that be an existing index (such as Net Merit) or by a custom index created on Igenity Dashboard.

3. **Implement genomic results.**

    Now it is time to implement your genomic results. Igenity Dashboard makes it easy to do this using the custom categories feature. If your plan is to breed animals greater than your herd's 50th percentile with sexed semen, Igenity Dashboard can help you assign a category to those animals, making it easy to implement on-farm decisions based on genomic results.
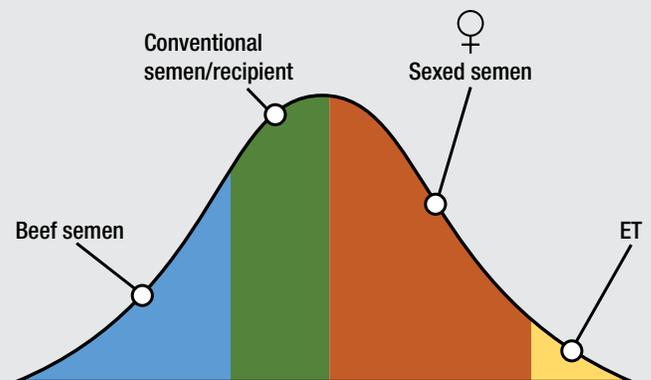
After sorting and ranking animals, a bell curve forms where a few animals are in the extreme ends and most animals fall somewhere in the middle with average scores. These animals can then be classified into groups. This producer is using embryo transfer (ET) on the top 5% and beef semen on the bottom 25%.

Your results are on Igenity Dashboard

Igenity Dashboard is an interactive tool for interpreting genomic results and guiding management decisions. Available from your phone, tablet or computer, Igenity Dashboard is available complimentary to every producer purchasing Igenity, including the ability to share your information with stakeholders on the dairy. With Igenity Dashboard, you can:

- View various reports about the herd.
- Customize reports to show only the desired traits.
- Categorize animals based on breeding decision.
- Create custom indices to meet specific breeding goals.
- Compare the herd to all herds in the breed database.
- See progress in the herd over time.

Questions about your results?

Contact us at 1-877-IGENITY or dairygenomics@neogen.com

We are happy to help!

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