GeneTracker

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GeneTracker Customer Information Pack

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Publication Dates & Deadlines

GeneTracker Publication & Sample Submission Deadline Dates

Official Month of Evaluation	Customer Sample Submission Deadline – Must arrive by post to Harrogate office by: (Thursday)	iReports updated on GeneTracker Website: (Tuesday)
Jan 2018	30th Nov 2017	3rd Jan 2018
Feb 2018	4th Jan 2018	6th Feb 2018
Mar 2018	1st Feb 2018	6th Mar 2018
Apr 2018	26th Feb 2018	(Official Run) 3rd Apr 2018
May 2018	29th Mar 2018	1st May 2018
Jun 2018	3rd May 2018	5th Jun 2018
Jul 2018	31st May 2018	3rd Jul 2018
Aug 2018	28th Jun 2018	(Official Run) 7th Aug 2018
Sep 2018	2nd Aug 2018	4th Sep 2018
Oct 2018	30th Aug 2018	2nd Oct 2018
Nov 2018	4th Oct 2018	6th Nov 2018
Dec 2018	25th Oct 2018	(Official Run) 4th Dec 2018
Jan 2019	6th Dec 2018	8th Jan 2019

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GeneTracker - Frequently Asked Questions

What is geneTracker and what does it do?

GeneTracker is the UK's leading genomic testing service provided by NMR.

The UK's only non-tag, non-hair hassle free system takes a simple tissue punch from an animal's ear – leaving behind no tag whatsoever.

This tissue sample is then inserted into a sealed vial and posted back to the NMR Harrogate office where it is processed and shipped to the laboratory for genotype processing.

The genotype generated as a result of DNA extraction and genotyping process is then submitted to AHDB Dairy and Holstein UK for the creation of all production, health, fertility, PLI and type trait genomic evaluation data for an individual animal, plus the option to run a BVD test (if you are in England & Wales only and you also receive a number of genetic recessives free of charge.

The results are then made available to the customer so they are able to make a more accurate and informed decision on the future of that animal within their herd.

How do I order a test?

The tests are ordered by calling the Customer Services geneTracker number at Harrogate which will be: **03300 241 334** - there is also a dedicated email address which is orders@genetracker.co.uk

Upon calling this number one of the Customer Services geneTracker team will talk the customer through the test options, costs and processes.

Do I have to milk record with NMR to use the service?

No. Any CIS or UDF customer can also use the service, however you DO have to milk record with one of those three organisations. If they are a non-NMR customer, they will be asked to supply their CIS/UDF log-in details which are needed to load the herd up onto the system to search for the animal details. This is vital for the accuracy of the test and ensuring accurate animal IDs. All log-in details will strictly only be used for this purpose and a data protection agreement will be available if required.

How much will it cost?

The price will depend on how many tests ordered. There are several service options based on volume and a discount will apply for greater volumes. We offer a basic 'pay as you go' service where customers just order tests as they need them and pay for them as we receive these and send the test off to the lab.

We also offer a discount for tests on orders over 100 and over 1000.

Please contact Customer Services at Harrogate for further details or your local NMR Area Field Manager/ NMR Customer Account Manager.

What are the criteria for animals? Do they have to be pedigree?

No they do not need to be pedigree. For accurate results however we must insist that both the dam and sire should be identified within the milk recording system.

Can I test bulls as well as females?

To begin with geneTracker will only offer a female testing service. However, the intention is to extend this out to test males later on this year. The testing of males on an either 'official' (where the genomic evaluation can be published and the bull appear on lists) or 'unofficial' (where the genomic evaluation can only be used for private herd management purposes) attracts extra costs, which have been set by the UK Genomic Consortium. These costs will be provided at the point when this becomes available.

What are the testing options?

GeneTracker offers the LD or Low Density 50K SNP chip (LDC). The 50K chip will give farmers a full range of production, type and recessive information.

For those wishing to genotype a high value animal such as a flush cow etc. it may be advised that a higher chip density be used to help increase the accuracy of the progeny evaluation. These higher density chips will become available at a later time.

When we begin offering a bull testing service, rules apply in the UK meaning that these have to be evaluated on either the Medium or HD chip options.

Do I get any other information beside production, health, fertility and type traits?

Indeed. The customer also receives results for a whole suite of known 'genetic recessives' included in the price. Most notably these include such recessives as BLAD, Kappa Casein 1&2, coat colour (red factor etc), polled, Fertility Haplotypes HH1, HH2, HH3.

The customer can also choose to pay for some extra tests, which attracts an additional 'Royalty Fee' because private companies own the rights to these. These include CVM, Brachyspina and Beta Casein A1 & A2. The costs for these extra tests are available within the pricing schedule.

Can I also do a BVD test?

We will be offering in the New Year the opportunity to have the sample submitted for a BVD test. This service is very new and is only offered to farmers in England and Wales at this time. This is because Scotland and Northern Ireland have their own schemes in operation with a 'tag & test' principle that isn't the same as our system.

The cost for this additional option will be £5.50 +VAT

Can I receive a US gTPI evaluation?

A number of breeders will be interested in receiving not only a UK gPLI or gTM evaluation, but also a US index known as the 'gTPI'. This index has become something of an unofficial 'International Benchmark' within the genomic world. Many breeders wishing to sell/buy cattle and embryos on the International market will wish to see the gTPI figures.

The fee for a gTPI evaluation is £20.00 per animal.

Can I do a parentage validation?

At this time we are working on a solution to be able to provide a clear parentage or sire validation service as part of the evaluation. This is not yet ready so this option will appear as an upgrade this year, however, if the genomic evaluation returns a query on a sire we can advise on the correct sire as long as it has been genotyped.

This will slow down the time it takes to receive the result back as corrections have to be made to the ancestry and the evaluation then re-run the following month.

What will I receive in the post after I order?

The customer will receive in the post an individual TSU (Tissue Sampling Unit) for each animal that will be specifically bar-coded and attributed to that animal. These will be provided in individual bags that are labeled and also contain individual paperwork for each animal. This is designed specifically to minimize ID mis-matches and issues.

The customer needs to ensure they ONLY use the TSU unit, paperwork and bag specifically linked to that animal and it is advised that they test the animals one at a time to ensure that they keep the TSU unit together with the paperwork and sample the correct animal each time so they don't waste samples and incur unnecessary costs for re-sampling.

In terms of the ear-notch system – can I use my existing ear-tag applicator?

No, you will not be able to use an existing applicator unless it is an Allflex design, which is specifically suitable for this product. GeneTracker will supply a FREE applicators with all new orders (over 20 units), however all second applicators will attract a charge.

How long does the result take to come back?

Genomic evaluations are run every month with the results being published on the first Tuesday morning of each month. Dependent, upon which stage of the process the customer manages to get their sample back to the office, will depend on whether or not the sample makes it into the next available evaluation.

If all is well – i.e. the tissue sample is of a high enough quality to process at the lab, they manage to extract enough DNA to test accurately and there are no parentage conflicts found during the evaluation process, the fastest you could receive a result back is within a month of testing.

If the submission deadline to the lab is missed, then samples have to wait for the next testing cycle and thus may take 6 weeks to 2 months to come back.

There may also be delays as explained above, if the animal has an incorrect Sire/Dam identified which will need to be corrected and re-submitted the following month for re-evaluation.

A full list of submission dates and deadlines is available from the NMR Customer Services team and the www.genetracker.co.uk website.

How does the customer view their results?

A new website front-end for geneTracker has been developed which is found at www.genetracker.co.uk

The customer will go to this website and put in their log-in details. For NMR customers, this will be their Herd Companion log-in details. For non-NMR customers, they will use specific log-in details that will be given as they first sign up for the service.

The results are then available for viewing through iReports on Herd Companion. These are in the format of both fully interactive and re-rankable lists, as well as a more detailed individual animal report. Examples of these can be found on the genetracker website.

Can any breed use the service or is it just Holsteins?

Initially geneTracker will be available to the Holstein breed only. As the service becomes bedded in and we have access to genomic evaluations for other breeds, these will be introduced.

Where can I find more information?

All the information the customer should need can be found at www.genetracker.co.uk this includes the dates for submission, result release dates, pricing, explanations of the genetic recessives, example reports etc. However if the customer can't find what they are looking for and still has questions – they should call the geneTracker Customer Services number: **03300 241 334** alternatively there is also a dedicated email address which is orders@genetracker.co.uk

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Genetic Recessive Information Sheet

BLAD- Bovine Leukocyte Adhesion Deficiency

What is BLAD?

BLAD is a birth defect that is identified by persistent bacterial infections, delayed wound healing and stunted growth. These characteristics are caused by a deficiency of normally occurring proteins needed for white blood cells (or leukocytes), to travel to sights of infection and help fight them off. The disease has only been reported in Holstein cattle. Calves that are born with BLAD are generally poor doers but the symptoms may not be noticeable until the calf is a couple of weeks old. The calf can suffer several different illnesses such as recurrent bacterial infections, pneumonia, enteritis, diarrhoea or delayed wound healing and often die by four months of age. Animals that survive past this stage often have stunted growth and suffer from recurring skin infections, gastrointestinal problems and/or respiratory issues.

How is BLAD transmitted?

Like Brachyspina and CVM, BLAD is transmitted as an autosomal recessive, meaning that two copies of the abnormal gene (one from the dam and one from the sire) must be present in order for the trait to be expressed: this makes the animal homozygous for the undesirable allele. This means that a carrier animal does not exhibit the symptoms of BLAD but will transmit the gene to 50% of their offspring. Therefore:

- Mating a carrier (BL) animal and a non- carrier (BB) animal would be *expected* to result in 50% of the offspring being carriers and 50% being non carriers. Studies have been carried out to try and prove that carrier cows may have decreased mastitis resistance and lower birth weights, but it was found that carriers have no disadvantage to normal animals.

	B	L
B	BB	BL
B	BB	BL

50% non-carriers (BB)
50% carriers (BL)

- Mating two carrier animals would be *expected* to result in 25% of the offspring being normal, 50% of the offspring being carriers and the final 25% being affected by BLAD. Consequently, breeders are strongly recommended to avoid mating two known carrier animals.

	B	L
B	BB	BL
L	BL	LL

25% non-carriers (BB)
25% affected (LL)

50% carriers (BL)

How is BLAD negative to the breed?

Since the immunity animals suffering BLAD is compromised, there are several financial implications such as reduced milk yield and increased veterinary costs. Luckily, the frequency of BLAD is reducing as all homozygous animals can be traced back to a single male ancestor and breeding from their gene pool is

greatly reduced. Most bulls sold in the UK are tested for BLAD, so it is easy to identify which are carriers of the disease and be cautious of using them.

CIT- Citrullinemia

What is CIT?

Bovine citrullinemia is a rare metabolic genetic disorder found in cattle. It is breed specific and CIT causes increased circulatory ammonia and associated neurological signs. Calves that are affected by CIT can be identified by symptoms such as loss of full body control, aimless wandering, blindness, head pressing, convulsions and death.

How is CIT transmitted?

Similar to BLAD and DUMPS, CIT is an autosomal recessive disease, meaning that two copies of the abnormal gene must be present in order for the trait to be expressed: this makes the animal homozygous for the undesirable allele. This means that a carrier animal does not exhibit the symptoms of CIT but will transmit the gene to 50% of their offspring. Therefore:

- Mating a carrier (NC) animal and a non- carrier (NN) animal would be *expected* to result in 50% of the offspring being carriers and 50% being non carriers.

	N	C
N	NN	NC
N	NN	NC

50% non-carriers (NN)
50% carriers (NC)

- Mating two carrier animals would be *expected* to result in 25% of the offspring being normal, 50% of the offspring being carriers and the final 25% being affected by CIT. Consequently, breeders are strongly recommended to avoid mating two known carrier animals.

	N	C
N	NN	NC
C	NC	CC

25% non-carriers (NN)
25% affected (CC)

50% carriers (NC)

How is CIT negative to the breed?

Although calves can be born alive that suffer CIT, they often have to be euthanased at a young age due to neurological disorders. Most bulls sold in the UK are tested for CIT, so it is easy to identify which are carriers of the disease and be cautious of using them.

DUMPS- Deficiency of Uridine Monophosphate Synthase

What is DUMPS?

DUMPS is a disease of Holstein cattle which is characterised by lowered blood activity of enzyme uridine monophosphate synthase (UMPS). This then leads to embryonic death in the early stages of pregnancy. Luckily, the disease is fairly rare.

How is DUMPS transmitted?

DUMPS is transmitted as an autosomal recessive, meaning that two copies of the abnormal gene must be present in order for the trait to be expressed: this makes the animal homozygous for the undesirable allele. This means that a carrier animal does not exhibit the symptoms of DUMPS but will transmit the gene to 50% of their offspring. Therefore:

- Mating a carrier (Bb) animal and a non- carrier (BB) animal would be *expected* to result in 50% of the offspring being carriers and 50% being non carriers.

	D	P
D	DD	DP
D	DD	DP

50% non-carriers (DD)
50% carriers (DP)

- Mating two carrier animals would be *expected* to result in 25% of the offspring being normal, 50% of the offspring being carriers and the final 25% being affected by DUMPS. Consequently, breeders are strongly recommended to avoid mating two known carrier animals.

	D	P
D	DD	DP
P	DP	PP

25% non-carriers (DD)
25% affected (PP)

50% carriers (DP)

How is DUMPS negative to the breed?

Since embryos are often reabsorbed during the first two months of gestation, fertility costs are increased due to more services per calving and longer calving intervals. Most bulls sold in the UK are tested for DUMPS, so it is easy to identify which are carriers of the disease and be cautious of using them.

Haplotypes

What are Haplotypes?

Haplotypes impact fertility and a haplotype is a group of DNA sequences at different locations on a chromosome that are transmitted together as a group. Three of the haplotypes that have been discovered in Holsteins are referred to as HH1, HH2 and HH3 and they operate independently of each other because they are situated on different chromosomes. This means that HH1 has no effect on HH2, or HH2 on HH3, etc.

How are Haplotypes transmitted?

In Holsteins, these three haplotypes each have carrier frequencies of 3-6% and some animals can carry two different haplotypes. If animal inherits the same haplotype from each parent (homozygous) then the animal will not survive birth: the haplotypes have never been discovered in their living animal in a homozygous form. There is a fairly high likelihood of an animal carrying at least one haplotype, but the probability of mating animals carrying the same haplotype is fairly low. Haplotypes follow a similar inheritance pattern as recessive genes. Therefore:

- Mating a carrier (CT) animal and a non- carrier (TT) animal would be *expected* to result in 50% of the offspring being carriers and 50% being non carriers.

	C	T
CT	TT	T
CT	TT	T

50% non-carriers (TT)
50% carriers (CT)

- Mating two carrier animals would be *expected* to result in 25% of the offspring being normal, 50% of the offspring being carriers and the final 25% being affected by that haplotype. Consequently, breeders are strongly recommended to avoid mating two known carrier animals.

	C	T
CC	CT	C
CT	TT	T

25% non-carriers (CC)
25% affected (TT)

50% carriers (CT)

How are Haplotypes negative to the breed?

Since haplotypes have a negative impact on fertility, it is important to be cautious of using bulls carrying certain haplotypes. However, many carrier bulls have a high genetic merit, and eliminating them from breeding policies can be detrimental to genetic progress in other areas. Therefore, it is important to instead be cautious of the carrier status of the females that a carrier bull is being mated too.

MF- Mulefoot (Syndactylism)

What is Mulefoot?

Mulefoot is a birth defect whereby the digits in calves are fused, causing the animal to be born with one or more feet with only one claw. The right front leg is the most commonly affected, followed by the left front leg. Affected calves can display varying levels of lameness, have a high step gait and may walk slowly. Calves can survive but require extra attention and many will succumb to hypothermia. Although the condition has been reported in several breeds, it is most common in the Holstein and Angus.

How is Mulefoot transmitted?

Mulefoot has been identified as a simple autosomal recessive trait with varying degrees of severity. The variation in gene transmission in Holstein cattle is clinically significant in that even if only one copy of the effected gene is inherited, some form of the disease may be present. However, generally classic cases of Mulefoot require two copies of the abnormal gene (one from the dam and one from the sire) must be present in order for the trait to be expressed: this makes the animal homozygous for the undesirable allele. Therefore:

- Mating a carrier (MF) animal and a non- carrier (MM) animal would be *expected* to result in 50% of the offspring being carriers and 50% being non carriers.

	M	F
MM	MF	M
MM	MF	M

50% non-carriers (MM)
50% carriers (MF)

- Mating two carrier animals would be *expected* to result in 25% of the offspring being normal, 50% of the offspring being carriers and the final 25% being affected by Mulefoot. Consequently, breeders are strongly recommended to avoid mating two known carrier animals.

	M	F
M	MM	MF
F	MF	FF

25% non-carriers (MM)
25% affected (FF)

50% carriers (MF)

How is Mulefoot negative to the breed?

Mulefoot is not a lethal condition and although affected animas have locomotive problems, they can live to maturity. Most bulls sold in the UK are tested for Mulefoot, so it is easy to identify which are carriers of the disease and be cautious of using them.

Myoclonus

What is Myoclonus?

Myoclonus is a rare birth defect found in Hereford and Holstein cattle. Although newborn calves are often bright, alert and responsive, they also display several neurological signs. These signs include jerking of the whole body, abnormal sensitivity to touch or pain and rolling eyes.

Studies have shown that Myoclonus in calves is associated with a deficiency of inhibitory glycine receptors in the brain stem and spinal cord.

How is Myoclonus transmitted?

Myoclonus is an autosomal recessively inherited defect meaning that two copies of the abnormal gene (one from the dam and one from the sire) must be present in order for the trait to be expressed: this makes the animal homozygous for the undesirable allele. This means that a carrier animal does not exhibit the symptoms of Myoclonus but will transmit the gene to 50% of their offspring. Therefore:

- Mating a carrier animal and a non- carrier animal would be *expected* to result in 50% of the offspring being carriers and 50% being non carriers.

- Mating two carrier animals would be *expected* to result in 25% of the offspring being normal, 50% of the offspring being carriers and the final 25% being affected by Myoclonus. Consequently, breeders are strongly recommended to avoid mating two known carrier animals.

How is Myoclonus negative to the breed?

Although affected calves can be born alive, very few live past a couple of weeks due to the severity of the problem. Most bulls sold in the UK are tested for Myoclonus, so it is easy to identify which are carriers of the disease and be cautious of using them.

Protoporphyria

What is Protoporphyria?

Protoporphyria was first reported in South African Shorthorn cattle but most cases have since been reported in Holstein cattle, and it probably affects all meat producing animals. Affected animals display a reddish brown discolouration of the teeth, bones and urine at birth and these persist for life. If teeth, bones and urine are exposed to near- ultra violet light, they fluoresce pink. Affected animals can also develop skin lesions when exposed to sunlight. This means that animals that are not protected from sunlight become less thrifty.

How is Protoporphyria transmitted?

Protoporphyria is an autosomal recessively inherited defect meaning that two copies of the abnormal gene (one from the dam and one from the sire) must be present in order for the trait to be expressed: this makes the animal homozygous for the undesirable allele. This means that a carrier animal does not exhibit the symptoms of Protoporphyria but will transmit the gene to 50% of their offspring. Therefore:

- Mating a carrier animal and a non- carrier animal would be *expected* to result in 50% of the offspring being carriers and 50% being non carriers.

- Mating two carrier animals would be *expected* to result in 25% of the offspring being normal, 50% of the offspring being carriers and the final 25% being affected by Protoporphyria. Consequently, breeders are strongly recommended to avoid mating two known carrier animals.

How is Protoporphyria negative to the breed?

Morbidity of affected animals can be controlled by keeping them indoors and out of direct sunlight. However, prevention is recommended and since many bulls sold in the UK are tested for Protoporphyria, it is easy to identify which are carriers of the disease and be cautious of using them.

SMA- Spinal Muscular Atrophy

What is SMA?

SMA is a neurological disorder which promotes locomotion difficulties in young calves. These difficulties can then lead to partial paralysis of the limbs. These problems are a result of the degeneration and loss of motor neurons in the spinal cord as well as increased swelling/ abscesses of remaining motor neurons. Although many affected calves can appear normal and bright with a good suckling reflex at birth and even for a couple of weeks, the course of the disease is progressive and the calves become progressively weaker and all limbs can then become affected. Death is often the consequence, usually due to respiratory failure.

How is SMA transmitted?

SMA is an autosomal recessively inherited defect and is most prolific in the Brown Swiss breed. This means that two copies of the abnormal gene (one from the dam and one from the sire) must be present in order for the trait to be expressed: this makes the animal homozygous for the undesirable allele. This means that a carrier animal does not exhibit the symptoms of SMA but will transmit the gene to 50% of their offspring. Therefore:

- Mating a carrier animal and a non- carrier animal would be *expected* to result in 50% of the offspring being carriers and 50% being non carriers. If a carrier cow is mated with a non-carrier bull (or vice versa) then SMA would not be responsible for locomotive problems.

- Mating two carrier animals would be *expected* to result in 25% of the offspring being normal, 50% of the offspring being carriers and the final 25% being affected by SMA. Consequently, breeders are strongly recommended to avoid mating two known carrier animals.

How is SMA negative to the breed?

Although affected calves can be born alive, very few live past a couple of weeks due to problems linked to locomotion and respiratory issues. Most bulls sold in the UK are tested for SMA, so it is easy to identify which are carriers of the disease and be cautious of using them.

Polled

What is polled?

Polled/ hornless cattle are preferred over horned cattle, and many farmers dehorn animals when they are young. Now, genetic selection is playing an important part to breed for naturally polled animals.

How is polled transmitted?

Unlike many other characteristics (e.g. CVM, Brachyspina, BLAD and DUMPS) that are controlled by a single gene, the polled gene has a dominant mode of expression rather than a recessive mode. This means that all animals that carry either one or two copies of the polled allele will be polled, so all horned animals must not carry the gene at all.

If an animal is DNA tested and found to carry two copies of the polled gene (POS), then 100% of its progeny will be polled, regardless of the status of the animal it is mated with. If an animal is visually polled (but hasn't been tested) then they will be a carrier of at least one copy of the polled gene and will be recorded as POC.

Animals that carry one copy of the polled gene would normally produce 50% of their progeny without horns. When two polled animals are mated together then about 75% of the resulting progeny will be polled if each mate just carried one copy of the gene, but this would reach 100% polled if either parent carried two copies of the polled gene.

Animals that are horned cannot transmit the polled gene and if two such animals are mated, none of the progeny will be polled.

Since the polled gene is dominant over the horned gene, the use of polled sires results in at least 50% of their progeny being polled. This has helped to speed up the increase of polled animals and select for genetically improved polled animals.

Coat Colour

Coat Colour Genetics

Although coat colour is simple to determine visually, the genetics behind it are complex with many possible genotypes determining the animal's appearance.

On the Holstein genome, there are two different locations that influence coat colour. One of these locations affects recessive red coat colour and the black/red colour form, whilst the other affects a dominant red colour. Recessive red is the most common form of red coat colour in Holstein cattle, but it is located at a different part of the genome than dominant red (they are different conditions that both affect the coat colour trait).

Recessive Red and Black/Red

There are four known forms of the gene at the recessive red location. There are two copies of the gene (one from sire and one from dam) that interact with each other depending on the forms present to produce colour patterns.

- Allele E^D (dominant form) codes for black and white coat colour
- Allele E^{BR} (black/ red form) codes for black/red condition
- Allele E+ (wild type form) codes for red and white coat colour
- Allele e (recessive form) codes for red and white coat colour

At the recessive red location, E^D dominates so animals with at least one copy of the E^D form of the gene will be black and white regardless of the other copy (unless altered by the dominant red gene).

Animals which have at least one copy of the E^{BR} form of the gene (and no dominant E^D) have the black/red condition and are usually born red and turn back over time, sometimes retaining some red colouring around the nose, ears and topline.

The wild type form is the most recently identified and is similar in effect to the recessive form of the gene. The most common type of red and white appearance is a result of two copies of the wild type or two copies of recessive, or one wild type and one recessive.

Dominant Red

Dominant red is a more recently reported trait which is completely independent of recessive red and was previously known as variant red. The dominant red trait follows a similar inheritance pattern of other dominant traits such as polled, and the dominant form (D) of the gene will also dominate over recessive red. This means that is an animal is expected to be black and white due to the recessive red part of the genome, will be red and white if it has at least one copy of the D form of the dominant gene. The transmission of dominant red typically resonates as:

Parent Genotype	Progeny Appearance	Progeny Genotype
DD x DD	All red & white	All DD
DD x Dd	All red & white	50% DD & 50% Dd
DD x dd	All red & white	All Dd
Dd x Dd	75% red & white, 25% black & white	50% Dd, 25% DD, 25% dd
Dd x dd	50% red & white, 50% black & white	50% Dd & 50% dd
dd x dd	All black & white	All dd

Milk Components

Milk Components

Milk is made up of energy, water, carbohydrates, fat, protein, vitamins, minerals and enzymes. Milk protein consists of about 82% casein and 18% whey and they offer health benefits and improve cheese yield. Herds that carry dominant traits for favourable milk proteins are increasing in value for breeding and human nutrition.

Kappa Casein

Kappa casein is one of the major milk proteins comprising 14.5% of all caseins and 12% of all milk proteins. Kappa casein is a key protein in the cheese making process because the Kappa casein variant of the milk influences the renneting time and curd firmness. The cheese production properties of milk are better if the renneting time is short and the curd is firm. There are several variants of Kappa casein in the cattle population, and the percentage of Kappa casein not only varies between breed but also between individual animals depending on their genotype.

There are three possible gene combinations in a cow for Kappa casein:

- BB: preferred genotype for milk/ cheese production
- AB: intermediate for cheese production
- AA: least favoured genotype for milk production

Studies have found that cheese yield can be greatly improved with BB milk compared to AA milk and the renneting time is shorter.

Beta Casein (A2 Milk)

Several forms of Beta casein are present in cows milk depending on the cows genetic make up and Beta casein is 30% of the total protein content of cows milk. Two of these Beta caseins are A1 and A2. Neither the A1 or the A2 variant appears to be dominant so transmission is usually equal. Therefore,

- A1/A1 cows will only produce A1 Beta casein
- A2/A2 cows will only produce A2 Beta casein
- A1/A2 cows will likely produce milk with equal amounts of A1 and A2 Beta casein

A2 milk was the original Beta casein found it milk, and it wasn't until natural mutations occurred that A1 was introduced. Milk containing mainly A2 proteins are often said to be better for allergies such as gut, skin, rashes and hayfever compared to mainly A1 milk. Holstein cows generally have more A1 protein in their milk whilst breeds such as Guernsey and Jersey have more A2 proteins in their milk.

Beta Lactoglobulin

Beta lactoglobulin is the major whey protein found in cows milk, making up 59% of all whey proteins and 10% of total milk proteins. Beta lactoglobulin can be found in three forms:

- AA is considered the most favourable for milk and protein yield, but least favourable for fat yield
- AB is intermediate
- BB is least favourable for protein yield, but most favourable for fat content (better for cheese making)

ABCG2 Gene Mutation

The ABCG2 gene is linked to milk production and content.

- AA lower protein yield and concentration
- AC intermediate
- CC highest protein yield and concentration

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Accessing Genetracker Results in iReports

Follow these steps to access your Genetracker results:

1. Go to www.genetracker.co.uk
2. Enter your email and password into the log-in boxes located at the top right of the screen, this will log you into Herd Companion.
3. Once in Herd Companion click on the Breeding and Fertility header.
4. Click on 'Genetracker Results' from the drop down menu.
5. You will find your 'Production' results which can be switched easily between the other criteria's, from Feet & legs to Health & Fitness. You will also find the 'USA' option for viewing your GTPI results (if requested. Fees apply).
6. You can then re-rank by any results column or choose a different set of traits by checking a different criteria box and clicking 'Apply'.
7. You will also see the option of 'Field Chooser' which allows you to add/remove different headings e.g. birth date.
8. On each screen you will see the option 'Export Data'. This allows you to export that particular screen to an Excel spreadsheet.
9. To view the results for an individual animal, click on the line number which will take you to the full animal record – it will automatically open under the 'Genetracker' tab to view the animals 'CV' style report.
10. Here you will find another option to see the USA data if you have requested a GTPI evaluation (fees apply).
11. If you need any further assistance, please call our customer service number on 03300241334. If our team are unable to answer the query directly they will be able to forward you on to the department who will be able to assist you further.

Animal Record

Line Number: 0012 **DoB:** 10/08/16 **Breed:** HOLSTEIN **Eartag:** UK320533704261

Name: 12 **Lactation:** **Long Name:** 12

HBN: **D.I.M.:** **Fertility status:** Not Served **Milking Status:** N/A

Recording data | Event data | Ancestry | Lactations | Offspring | GeneTracker | Disease

More information is available in the USA Genomic Animal Report

Key Indexes	GPTA	Rel %
£PLI	£149	56
Type Merit	1.39	56

Production Traits	GPTA	Rel %
Milk kg	343	68
Fat kg	5.60	68
Protein kg	6.50	68
Fat %	-0.10	68
Protein %	-0.06	68

Health and Fitness	GPTA	Rel %
Mammary Composite	0.62	59
Feet and Legs Composite	0.81	52
Temperament	0.86	53
Ease of Milking	0.62	58
Locomotion	1.17	49
Condition Score	0.68	54
TB advantage	0.80	50
Lifespan	0.20	60
SCC	-7.00	69
Fertility	2.60	62

Date	Disease Test	Interpretation
No data to display		

Test Type	Test Results	Test Results
BetaLact	AA	Lower casein number, less desirable for cheese making
BLAD	Non-Carrier	Bovine Leukocyte Adhesion Deficiency Non-Carrier
Citrullinemia	Non-Carrier	Non-Carrier of Citrullinemia
DUMPS	Non-Carrier	Deficiency of Uridine Monophosphate Synthase Non-Carrier
HH1	Non-Carrier	Holstein haplotype 1 Non-Carrier

There is a GeneTracker FAQ and the Recessive Tests are explained here.

Mammary Traits	GPTA	Rel %
Mammary Composite	0.62	59
Fore Udder Attachment	0.75	62
Rear Udder Height	0.82	59
Udder Support	-0.48	60
Udder Depth	0.71	65
Teat Length	1.58	67
Front Teat Placement	-0.13	63
Rear Teat Placement	-0.79	60
Teat Pos Side	0.38	62

Feet and Legs	GPTA	Rel %
Feet and Legs Composite	0.81	52
Rear Leg Side View	-0.70	61
Foot Angle	0.37	58
Locomotion	1.17	49

Body and Dairy Strength	GPTA	Rel %
Stature	-0.06	71
Chest Width	0.43	61
Body Depth	-0.87	63
Angularity	-0.54	61
Rump Angle	0.33	66
Rump Width	-0.20	63

Test Type	Test Results	Test Results
Polled	Horned	Homozygous Horned (animal is horned)
Kappa Casein	BB	Preferred genotype for cheese production
Mulefoot	Non-Carrier	Mulefoot Non-Carrier
HH3	Non-Carrier	Holstein Haplotype 3 Non-Carrier
HH4	Non-Carrier	Holstein Haplotype 4 Non-Carrier

Overview	Production	Health and fitness	Mammary	Feet and legs	USA	Update			Show extra	Export
☐	☐	☑	☐	☐	☐	Apply		Kite Report	Columns	Export

Drag a column header here to group by that column

Line No.	Name	GPLI	Type Merit	L and F	Loco	Mam	Life	Fert idx	TB Adv	TB Adv R%	Cond Sc	Tempe	Ease Mk	Milk kg	Fat %	Prot %	SCC
0012	12	149	1.39	0.81	1.17	0.62	0.2	2.6	0.8	50	0.68	0.86	0.62	343	-0.10	-0.06	-7
0015	15	289	0.42	0.4	0.42	0.27	0.3	1.9	0.4	43	0.27	1.19	-0.06	341	0.03	0.03	-6
0023	23	281	0.15	-0.32	-0.17	0.58	0.3	6.3	1.2	51	0.53	0.4	-0.28	206	0.08	-0.02	-12
0026	26	360	1	-0.09	-0.11	1.11	0.3	3.8	0.7	51	1.7	0.4	-0.57	292	0.09	0.02	-24
0028	28	240	0.78	0.79	0.74	0.4	0.3	6.7	-2.2	44	0.63	-0.05	-0.63	-180	0.15	0.06	-17
0032	32	234	2.23	1.6	1.87	1.25	0.3	5.3	0.4	45	0.98	0.62	-0.32	586	-0.15	-0.11	-15
0036	36	387	1.63	0.39	0.33	1.44	0.3	6.3	0.8	52	0.72	0.41	0.71	543	-0.10	0.00	-9
0041	41	279	1.31	0.31	0.62	0.96	0.3	3.6	0.2	51	0.3	0.24	-0.69	415	-0.03	-0.04	-16
0043	43	287	0.53	0.08	0.08	0.68	0.3	4	0.9	50	1.16	-0.09	-0.36	498	-0.13	-0.04	-16
0046	46	376	1.49	0.79	0.81	1.07	0.4	-0.2	1.3	51	1.14	0.32	-0.37	483	0.01	-0.01	-17
0055	55	270	1.19	1.22	1.27	0.75	0.3	10.2	0.1	52	0.63	-0.09	1.27	369	-0.01	-0.10	-5
0057	57	103	1.03	0.6	0.65	0.31	0	-2	1	48	-0.51	0.16	-0.78	292	0.07	-0.03	6
0062	62	142	-0.09	0.41	0.33	-0.23	0	4	0.4	44	-0.04	-0.43	-0.34	264	-0.04	-0.02	-6
0063	63	315	0.95	1.04	0.98	0.11	0.2	2.8	2	45	0.57	0.76	-0.19	750	-0.09	-0.06	-5
0064	64	408	1.42	0.5	0.61	0.93	0.5	5.5	1.1	51	0.25	0.17	0.94	463	-0.05	0.01	-13
0065	65	409	0.79	0.28	0.37	0.33	0.4	7.3	0.8	51	0.01	0.11	0.71	612	-0.04	-0.01	-4
0066	66	297	-0.4	-0.49	-0.31	-0.43	0.2	3.9	2.1	51	0.36	-0.37	-0.05	520	0.06	-0.02	-8
0071	71	109	0.51	0.52	0.66	0.29	-0.1	4.4	0.8	45	0.99	-0.59	-0.36	405	-0.11	-0.06	-3