Pfizer Animal Health

Animal Genetics

GLOSSARY OF TERMS

BOVINE GENOMICS HANDBOOK

Bovine Genomics Handbook

A Reference for Discussing DNA-Marker Technology and its Applications

First Edition

Pfizer Animal Genetics, a business unit of Pfizer Animal Health
New York, NY

Purpose

- Define terms related to bovine genomics
- Promote consistent use of terminology
- Provide a timely resource for stakeholders

Acknowledgements

Our thanks to the experts who developed this handbook:
Sarah Staples, MA, ELS; Ronnie Green, Ph.D; Lewis Frost;
Sharl Liebergreen

Pfizer Animal Genetics
PO Box 5520
Dunedin 9058 New Zealand
Phone: 0880 228 278
Fax: 03 477 5930
E-mail: pahgenetics.nz@pfizer.com
Web site: www.pfizeranimalgenetics.co.nz

A - C

Additive Genetic Effects	When the combined effects of alleles at different loci (or gene markers) are equal to the sum of their individual effects. See *Non-additive Genetic Effects.*
Agricultural Business Research Institute (ABRI)	An Australian-based organisation, the ABRI (abri.une.edu.au) provides a wide range of agribusiness information services including comprehensive breed register software that meets the needs of modern livestock producers. ABRI delivers BREEDPLAN® Estimated Breeding Values to the industry.
Allele	Alternate form of a gene. Genes occur in pairs, and the combination of inherited alleles determines the effect on a trait. Can be thought of as a variation in DNA.
Allele Frequency	The relative occurrence (expressed as a proportion or percentage) of an allele at a genetic locus in a given population.
Animal Genetics and Breeding Unit (AGBU)	The AGBU (www.agbu.une.edu.au) was established in 1976 by the New South Wales State Department of Agriculture and the University of New England to carry out research, development and training in the genetic improvement of livestock for the benefit of Australian agriculture, including research and development for BREEDPLAN.
Bacterial Artificial Chromosome Map	Physical map of a discrete section of DNA made by creating and analysing stable bacterial clones that can be amplified and sequenced.
Base Pair	The complementary bases found within a DNA molecule. There are four different bases: adenine (A), thymine (T), cytosine (C), and guanine (G). A always pairs with T, and C always pairs with G. The base sequence ultimately determines the effect of the gene.
Beef Improvement Federation	A North American organisation founded in 1968 to develop uniform guidelines for measuring and recording performance in beef cattle. Web site at: www.beefimprovement.org.
Best Linear Unbiased Prediction (BLUP)	Statistical technique used in linear mixed models to predict random effects. Used to estimate breeding values.
Biometrics	The application of statistical analyses to biological phenomena.
Breeding Value	1) The value of an animal as a genetic parent, or 2) the part of an individual's genotypic value that is due to additive and therefore transmittable gene effects.
Calpains	The principal enzymes responsible for protein breakdown. Calpains continue to break down protein postmortem, resulting in more tender beef.
Calpastatin	A specific natural inhibitor of calpains. Higher levels of calpastatin result in less tender beef carcases.

C - D

Chromosome	The self-replicating genetic structure of cells that contains genes. Found in pairs—cattle have 30 pairs of chromosomes while sheep and goats have 27 pairs.
cM (centiMorgan)	A unit of measure of genetic recombination frequency which translates to distance along a strand of DNA. One cM is equal to a 1% chance that a marker at one genetic locus will be separated from a marker at another locus due to crossing over in a single generation. In mammals, 1 cM is equivalent, on average, to 1 million base pairs. Cattle have approximately 2.7 billion pairs of DNA.
Codon	A three-base sequence in DNA that ultimately codes for a specific amino acid used in the building of a protein.
Commonwealth Scientific and Industrial Research Organisation (CSIRO)	Australia's national science agency and one of the largest and most diverse research agencies in the world. Web site at: http://www.csiro.au.
Comparative Mapping	The search for large regions of the genome that have been conserved across species and which may function similarly in different species. The myostatin gene that causes double muscling in cattle was discovered through comparative mapping in mice.
Complementary DNA (cDNA)	A DNA copy made from RNA through reverse transcription.
Complex Traits	A genetic trait controlled by a number of genes as opposed to a single gene. Traits such as reproduction characteristics, growth, and carcase quality are controlled by numerous genes. These are also often referred to as Economically Relevant Traits (ERTs).
Composite Map	A linkage map that combines markers developed in a number of maps around the world. The current composite map in cattle contains over 21,000 individual markers localised to bovine chromosomes.
Cooperative Research Centre for Beef Genetic Technologies (Beef CRC)	The Beef CRC (www.beefcrc.com.au) is one of 49 Cooperative Research Centres (CRCs) funded by the Commonwealth Government. It uses the human, mouse and bovine genomes to improve the profitability and productivity of Australian and global beef businesses by maximising the benefits of research through an enhanced process of utilisation, commercialisation and technology transfer.
Diagnostic Tests	Tests used to diagnose, analyse or identify specific areas of weakness and strength to determine the nature of weaknesses or deficiencies.
Dominant Allele	An allele that expresses its phenotypic effect even when heterozygous with a recessive allele; thus if *A* is dominant over *a*, then *AA* and *Aa* have the same phenotype (e.g., a black colour allele is dominant over red).

D-E

DNA (Deoxyribonucleic Acid)	The building block of the genetic code. A DNA molecule is composed of two strands of nucleotides wrapped around one another and connected at the bases to form a double helix.
DNA Fingerprint	A technique used to distinguish between two individuals of the same species by comparing genotypes for a panel of highly variable DNA markers. Also called DNA typing or DNA profiling.
DNA Marker	A specific DNA variation, that may vary between animals, that has been associated with a physical characteristic such as marbling or tenderness.
DNA Sequencing	Process of determining the nucleotide order of a given DNA fragment. This is the process used to "sequence" an entire genome, (e.g., the human genome project).
Double Helix	In molecular biology, the spiralling ladder structure of DNA. 
Downregulation	A negative regulatory effect on physiological processes at the molecular, cellular or systemic level. In molecules the major regulatory sites include membrane receptors, genes, messenger RNAs (mRNAs) and proteins.
Economically Relevant Traits (ERTs)	A complex trait that impacts on profitability but most often may be controlled by multiple genes.
Electrophoresis	A process used to separate DNA fragments by length. DNA fragments are placed at the top of a gel matrix and an electric current is run through, causing the fragments to migrate through the pores in the gel at differing rates (the smallest fragments migrate farther).
Epigenetics	Scientific study of how proteins and other molecules that bind to DNA and chromosomes can change gene expression without changing the DNA sequence. The most common example is genomic imprinting.
Epistasis	The suppression of a gene at one locus by the effect of a gene at a separate locus.
Estimated Breeding Values (EBVs)	Prediction of the genetic worth of an animal based on tracking and analysis by BLUP of traits expressed relative to a common baseline for all animals phenotypically measured in contemporary groups. The EBV of an offspring is equal to the average of the EBV of its two parents.
Exclusion Probability	A measure of efficiency in parentage determination testing; the probability that an individual has been correctly identified as the parent of a particular progeny.

E - G

Exon	A nucleic acid sequence that appears in the mature form of an RNA molecule (coding mRNA or a functional form of non-coding RNA, such as rRNA or tRNA).
Expected Progeny Differences (EPDs)	Commonly used term in North America where EPDs are published on animals based upon the expected performance of their progeny.
Expressed Sequence Tag (EST)	A short DNA piece copied from one end of an expressed gene, which is then used as a tag to retrieve that gene from a portion of chromosomal DNA by matching the base pair sequences.
Expression	The cellular product of the protein encoded by a specific gene. Expression involves DNA transcription, processing of the resultant mRNA, and its translation into an active protein which causes phenotype.
Feed Efficiency	Predicted on the basis of net feed intake, which measures how much feed an animal actually consumes per day as compared to what is predicted to be the required feed intake of the animal (also referred to as residual feed intake or net feed efficiency). Animals having a lower net feed intake are more feed efficient.
Feed Intake	Measured as daily dry matter intake of the animal.
Fine Mapping	The identification of markers that are very tightly linked to a targeted gene.
Fingerprint (DNA)	Pattern of DNA fragments unique to an individual. Often found by using restriction enzymes to cut the DNA into fragments. These fragments can be sorted and documented, forming a unique "fingerprint."
FISH (Fluorescent In Situ Hybridisation)	The hybridisation of nucleotides containing fluorescent tags to denatured (single-stranded) DNA. Exposure to ultraviolet light will show where and how many times the tagged primer annealed to the strand or fragment of DNA.
Full-Service Genomic Provision (FSGP)	A customised package of decision support tools, individual consultation, and guidance in applying genomic information to the long-term improvement of an operation's livestock and their management.
Functional Genomics	Study of the biological function of genes and their products.
Gel (Gel Matrix)	A solid, porous substance that allows DNA fragments to migrate through it, thus separating them by size.
Gene	The basic unit of heredity. A specific DNA sequence on a chromosome that codes for a specific functional product (such as a protein or RNA molecule).
Gene Expression	The process by which a gene's encoded information is converted into a functional product, such as a protein or RNA.

G

Gene Frequency	The relative occurrence (expressed as a proportion or percentage) of the alleles of a particular gene in a given population. Synonymous with allele frequency.
Gene Mapping	Identifying the relative physical locations of genes on a chromosome.
Gene Marker	A known DNA sequence, easily identified using a simple assay, which can vary from animal to animal.
GeneSTAR®	The brand for Pfizer Animal Genetics DNA-marker testing for traits.
GeneSTAR Molecular Value Prediction (MVP)	A molecular value prediction (molecular breeding value) based on an animal's DNA-marker profile for a given trait. It is expressed in +/- units of the trait as a deviation from zero. The GeneSTAR platform currently produces Molecular Value Predictions (MVPs) for the traits of feed efficiency, marbling and tenderness.
GeneSTAR MVP™ Reliability	Reliability value is the standard for assessing the accuracy and predictive power of the MVP for a trait. Reliability is based on the correlation between the MVP and the animal's genetic breeding value if all information were known. The reliability value is expressed as a percentage of the maximum accuracy attainable and is a useful indication of how much additional information may be added in the future as greater numbers of markers are added to the panels used to calculate the MVP.
Genetic Evaluation	Systematic programme for identifying, analysing and measuring the important genetic differences within populations to increase the rate of genetic improvement by selective breeding. Programme results provide performance benchmarks that stimulate testing and selection procedures and can further increase the rate of genetic improvement.
Genetic Improvement	Selective breeding for desirable and heritable production traits.
Genetic Linkage Map	A diagram showing where genes and markers are located on a chromosome and their relationship to one another based upon genetic linkage.
Genetic Profiling	Describing the significant genetic characteristics of an individual to establish identity, relationship and genetic predisposition to certain traits or diseases. Utilisation of GeneSTAR MVPs across all traits available.
Genetic Variation	The natural differences in gene frequencies observed between the genomes of individuals or groups of the same species. Can be measured at both the individual level (differences between individual animals) and at the population level (differences between populations living in different regions).
Genetics	The study of patterns of inheritance of specific traits.

G - H

Genome	The entire complement of an individual's DNA; all of its genes.
Genome-enabled EBVs	The combination of genetic marker information with existing phenotypic and pedigree information for traits of importance, which can be applied to achieve genetic improvement. Also known as marker-assisted breeding values. The Trial Tenderness EBV™, which incorporates GeneSTAR® marker results and phenotypic records, has been developed and used in the Brahman breed. Plans are underway to develop more marker-assisted EBVs using GeneSTAR markers.
Genomic Prediction	Examination of a specific portion of the genome in order to assess the likelihood of genetically determined traits or characteristics.
Genomic Selection	Relies on gene marker data as the basis for choosing breeding stock and conducting breeding programmes for genetic improvement.
Genomics	The science of mapping, sequencing and analysing the genes that make up a genome. The term was first used in 1986.
Genotype	Refers to 1) the entire genetic makeup of an animal, or 2) the specific combination of alleles at a single locus (or many loci).
Genotyping (DNA-marker Testing)	The process by which an animal is tested to determine the particular alleles it is carrying for a specific genetic test.
Germline Cells	Cells that are progenitors of egg and sperm cells and are passed along to offspring.
Growth Rate	Measured as postweaning average daily gain.
Haplotype	A combination of alleles at multiple loci that are transmitted together on the same chromosome. May refer to as few as two loci or to an entire chromosome, depending on the number of recombination events that have occurred. "Haplotype" is a contraction of "haploid genotype."
Heritability	Capable of being inherited from a parent. The percentage of the variation observed in a population's phenotypes for a trait that is due to breeding value differences.
Heterosis	The increased strength of different characteristics in hybrids; the superiority of crossbred offspring over the average of the parent purebreds.
Heterozygote	A genotype in which the two alleles for a given gene are different, e.g., *Aa.*
High-throughput Sequencing	An automated process for determining the DNA base codes of a genome.
Homozygote	A genotype in which the two alleles for a given gene are identical, e.g., *AA.*

H - M

Hybridisation	Process of taking two single strands of DNA from different sources and joining them together to form a double-stranded structure.
Inheritance	Biological inheritance refers to the manner in which a gene is transmitted. This involves considerations such as the number of loci (mono-, oligo- or poly-genetic), the number of chromosomes (autosomal, gonosomal, X or Y, or mitochondrial chromosomes), and the correlation of genotype to phenotype (dominant, intermediate, or recessive).
Intron	DNA that does not code for a product. An intron is transcribed, but is excised and not translated.
Linkage	The occurrence of two or more loci of interest on the same chromosome within 50 cM linkage distance of one another.
Linkage Mapping	Chromosome map of a species that shows the position of its known genes relative to each other in terms of recombination frequency rather than actual physical distance.
Linked Markers	Genes so closely associated on the chromosome that they are inherited together in ≥80% of cases.
Loci	Plural form of "locus."
Locus	The specific location of a gene on a chromosome.
Marbling	A visual assessment of the degree of intramuscular fatness in the *longissimus dorsi* (ribeye) muscle and a predictor of overall eating quality.
Marker Assisted Management (MAM)	The process by which DNA-marker information is used to sort (group) animals to enhance production efficiency. Example: Using DNA-marker information to sort animals with a higher genetic propensity to marble to be targeted for a specific branded-product programme.
Marker Assisted Selection (MAS)	The process by which DNA-marker information is used along with phenotypic data or on its own to select parents for the next generation. Example (1): The use of DNA markers to add accuracy to a marbling EBV of a young animal. Example (2): The use of DNA-marker information to identify carriers of Arthrogryposis Multiplex to assist breeding decisions for the next generation.
Marker Effect	The relative degree of change in a trait or phenotype that can be predicted by a single genetic marker.
Marker Panels	Combinations of DNA markers that are used to predict genetic value for a trait. Also used to describe panels of markers used for individual animal identity and parentage determination.

M - N

Marker-assisted EBVs	The addition of genetic markers to phenotypically derived EBVs to increase the accuracy of prediction.
MassARRAY/Mass Spectrometry	A high throughput single nucleotide polymorphism (SNP) genotyping technique for rapid SNP genotyping using a MassARRAY platform.
Meat Animal Research Center (MARC)	Scientists at the Roman L. Hruska U.S. Meat Animal Research Center (USMARC) develop new technology in order to increase the efficiency of livestock production and benefit consumers. The USMARC was authorised by Congress on June 16, 1964, and development began in the spring of 1966 on 35,000 acres near Clay Center, Nebraska. Presently, research programmes are using a female breeding population of 6500 cattle of 18 breeds, 3000 sheep of 10 breeds, and 700 swine litters per year. The USMARC is administered by the Agricultural Research Service (ARS) within the United States Department of Agriculture (USDA). Visit the Web site at: http://www.ars.usda.gov/Main/docs.htm?docid=2340.
Microarray	A chip containing a large number of nucleic acids that are known to govern specific traits, which is used to test a biological sample for the presence of those genes.
Microsatellite	Repeating, short sequence of DNA used as a genetic marker to track inheritance. A specific type of short tandem repeat marker.
Molecular Genetics	The study of the structure and function of genes at the molecular level, specifically how genes are transferred from generation to generation.
MVP™	A Molecular Value Prediction (true breeding value) based on its DNA-marker profile for a given trait. It is expressed in +/- units of the trait as a deviation from zero. See *GeneSTAR MVP.*
mRNA (Messenger RNA)	Carries information from DNA to the ribosomes, which form the molecular machinery to read messenger RNA and translate the information it carries into protein production.
Mutation	Any inheritable change in DNA sequence. Mutations can be silent (no phenotypic effect) or causative of phenotypic variation.
National Beef Cattle Evaluation Consortium (NBCEC)	A U.S.-based organisation (www.ansi.cornell.edu/nbcec/nbcec.html) that conducts independent validation to verify associations between genetic tests and traits claimed by commercial genotyping companies using phenotypes and DNA from different cattle populations.
National Center for Biotechnology Information (NCBI)	Part of the National Institutes of Health (NIH). The repository for molecular level information on the genomes of a wide array of species, including whole genome sequence, SNPs, ESTs, etc. Web site at: www.ncbi.nlm.nih.gov/.

N - P

National Human Genome Research Institute (NHGRI)	Led the Human Genome Project for the National Institutes of Health, which culminated in the completion of the full human genome sequence in April 2003. Supports research aimed at improving human health and fighting disease. Web site at: http://www.genome.gov/.
Non-additive Genetic Effects	When the combined effects of alleles at different loci (or gene markers) are not equal to the sum of their individual effects. Effects such as dominance and epistasis are non-additive genetic effects. Dominance is the interaction of alleles at the same locus, and epistasis is the interaction of alleles at different loci.
Nucleotide	The structural subunit of DNA or RNA composed of a five-carbon sugar (deoxyribose in DNA and ribose in RNA), a nitrogenous base (adenine, guanine, thymine, or cytosine in DNA; adenine, guanine, uracil, or cytosine in RNA), and a phosphate molecule.
Oligonucleotide/Primer	A short piece of DNA, usually 18 to 20 nucleotides in length, used as a starting point for PCR amplification.
Parentage Verification	Accomplished through analysis of inherited variants of selected DNA regions (microsatellites or other variable markers) taken from blood or other biological samples.
PCR (Polymerase Chain Reaction)	A process used to rapidly amplify DNA. The original DNA is heated, causing the strands to separate. Specific primers are then added and bond to the single strands. DNA polymerase adds nucleotides to the primer, extending the new DNA strand. The PCR process can be repeated to produce many copies.
Pedigree	The recorded ancestry of an animal.
Percentile Rank (% Rank)	An individual's MVP results are ranked against other animals of the same breed. A 10% rank indicates the individual lies within the top 10 percent of animals within the breed. A 20% rank indicates the individual lies within the top 20 percent. Note that a 90% rank indicates the individual lies within the bottom 10 percent of animals within the breed.
Phenotype	The visible or measurable characteristics of an organism; its outward appearance as opposed to its genetic characteristics. The observable properties of an organism, resulting from the interaction of the genotype and the environment.
Phenotypic Selection	Relies on phenotypic data as the basis for conducting breeding programmes.
Plasmid	A circular piece of bacterial DNA often used as a cloning vector to produce recombinant DNA in large quantities.
Polygene	A group of genes that jointly influence a phenotypic trait.

P - R

Polymerase	The enzyme system that facilitates the replication of DNA or RNA.
Polymorphism	The existence of two or more alleles for a gene within a population.
Probe	A substance (such as radioactively labelled DNA) used to obtain specific information for diagnostic or experimental purposes.
Protein	A large molecule composed of one or more chains of amino acids arranged in a specific order. Proteins are required for the structure, function and regulation of the body's cells.
Proteome	Entire complement of proteins produced by an organism.
Proteomics	Scientific study of proteins, particularly their structures and functions.
QTL (Quantitative Trait Locus)	A gene locus on a chromosome that has an effect on a quantitative trait. Often the actual sequence is unknown and is selected for using a known, linked gene marker.
Qualitative Trait	A trait expressed categorically because of a sharp distinction between phenotypes, e.g., black and red coat colour. Usually only one or a few pairs of genes are involved in the expression of a qualitative trait.
Quantitative Genetics	The study of complex traits (such as growth rate) and their underlying mechanisms.
Quantitative Trait	A trait expressed on a continuous/numerical scale because of a gradual variation from one phenotype to another, e.g., weaning weight. Usually many gene pairs and environmental influences are involved in the expression of such traits. Also referred to as complex traits and ERTs.
Radiation Hybrid Chromosome Map	A physical map of genetic markers positioned on the basis of the frequency with which they are separated by radiation-induced breaks.
RAPDs (Randomly Amplified Polymorphic DNAs)	Genetic markers that are randomly amplified using PCR with random primers to find polymorphic regions.
Recessive	An allele or trait that is only expressed when homozygous in the absence of its counter-dominant allele, e.g., *aa*.
Recombinant DNA (rDNA)	The creation of a new combination of DNA originating from two different species.
Restriction Enzyme (Endonuclease)	One of over 150 enzymes derived from bacteria that recognises specific DNA sequences and cuts at those sites.
Restriction Site	A specific site in the DNA sequence where a restriction enzyme cuts.

R-S

RFLP (Restriction Fragment Length Polymorphism)	Polymorphism identified by digesting DNA with a restriction enzyme. Individuals differ in their resulting fragment patterns, which are visualised radioactively after separation through gel electrophoresis or other method.
Ribonucleic Acid (RNA)	A single-stranded molecule composed of ribonucleotides. RNA differs from DNA in that it contains the base uracil (U) instead of thymine (T). RNA is formed from DNA through transcription. RNA facilitates transfer of the genetic message from a gene into its protein product, which is used physiologically by the body.
SABRE	A pan-European coalition of 33 animal breeding research groups and businesses that is using genetic sciences to develop more economically and environmentally sustainable production systems for cattle, pigs and chickens. Web site at: www.sabre-eu.eu.
SAGE (Serial Analysis of Gene Expression)	A sequence-based technology for gene identification and quantitation in which short sequences, called tags, are extracted from specific positions within a transcript. Highly sensitive, scalable and able to detect all genes, including unknown ones.
Saturation	Refers to locating a marker within every X cM in a linkage gene map, e.g., 5 cM saturated.
Seedstock	Breeding stock or animals whose role is to be a parent and contribute genes to the next generation. Often used in the context of genetic improvement.
Selection Index	A method of combining Estimated Breeding Values (EBVs) for different traits into a single $Index Value. Different $Index Values between sires indicate differences in the expected net profitability per cow mated.
Selective Breeding	Deliberate mating intended to pass desirable characteristics from parents to their offspring.
Simple Traits	Traits such as coat colour, horned status or disease status, which are controlled by a single gene.
SmartGene for Beef Project (Australia)	A project to integrate DNA-marker information with BREEDPLAN® phenotypic data and pedigree information to calculate marker-assisted Estimated Breeding Values. EBVs utilising marker data provide a higher accuracy estimate of breeding value than either marker data or phenotypic records alone. Tenderness was the key trait targeted because no EBV had previously been available and the trait cannot be measured on live animals.
SNP (Single Nucleotide Polymorphism)	A single difference in just one of the DNA base pairs (A, T, C, or G) in the genetic sequence, which can affect the functioning of a gene. For example: AAGGTTA is a change from ATGGTTA. Not every SNP causes a phenotypic change in an animal. Pronounced "snip."

S - U

SNP50 Chip	Assay with approximately 50,000 validated SNPs.
Somatic Cells	Body cells and tissues other than the germline.
Southern Blot	A procedure in which DNA fragments that have been separated using gel electrophoresis are transferred to a stable membrane in preparation for hybridisation with a labelled probe.
SSCP (Single-Stranded Conformational Polymorphism)	The use of differing three-dimensional configurations (conformational polymorphisms) formed by single-stranded DNA due to using differing base sequences as markers.
Taq	A thermostable DNA polymerase often used in polymerase chain reaction techniques for amplifying short segments of DNA. Named after the thermophilic bacterium *Thermus aquaticus* from which it was originally isolated.
Template Strand	A polynucleotide (RNA or DNA) that serves as the guide for making a complementary polynucleotide.
Tenderness	Predicted on the basis of the peak force required to shear cooked steak after 14 days of postmortem aging.
Traceability	A general term referring to a process to trace an animal through the production system from birth to product. This process is enabled by an individual's uniqueness, which can be captured through a DNA profile.
Trait	A physical characteristic brought about by the expression of a gene or many genes in concert with environmental influences. Examples of commercially important traits are tenderness, feed efficiency, carcase yield, etc.
Trait Index	A breed index that lists numerous economically important traits for which EBVs are available. Effective sire selection involves identification of bulls that possess a number of these traits.
Transcription	Synthesis of RNA under the direction of DNA.
Transcription Factors	Endogenous substances, usually proteins, that are effective in starting, stimulating or terminating genetic transcription.
Translation	The process by which ribosomes use the information in RNA to synthesise proteins.
Ultrasound % Intramuscular Fat (IMF)	Intramuscular fat assessed by ultrasound scanning.

U - W

Upregulation	A positive regulatory effect on physiological processes at the molecular, cellular or systemic level. In molecules, the major regulatory sites include membrane receptors, genes, mRNAs and proteins.
Validation (DNA Marker)	A study conducted to confirm a reported association between DNA-marker panel predictions and the trait of interest. Validation studies play an important role in ensuring that GeneSTAR® MVPs™ have a real association with the trait of interest in commercial cattle or sheep populations. Validation is performed independently.
Vector	A DNA element—such as a plasmid, the genome of a bacteriophage or a virus—that is self-replicating and can be used to transfer DNA segments into target cells.
VNTR (Variable Number of Tandem Repeats)	Highly variable repeat sequences of DNA that are unlikely to match in unrelated members of the same species. A type of minisatellite that is locus-specific but cannot be generated by PCR.
Whole Genome Scan	Analysis of numerous SNPs in a genome to locate quantitative trait loci (QTL) for desirable production characteristics.
Whole Genome Selection (WGS)	Process of selection based on analysis of SNPs from high-density platforms (e.g., SNP50) in relation to traits of interest.