

Genomics in Action for Angus breeders

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The South African Angus breeders have taken full advantage of the second round of the Beef Genomics Program (BGP2). From the very first year of BGP2, the breed has set the pace by exceeding their allotted genotyping quota by over 300 animals and achieving an impressive 161% compliance rate. The momentum has continued into year two, with the breed on course to reach their allotted quota. This has allowed the breed to grow their genomic reference population to over 1 300 animals. Several herds from breeds registered with SA Stud Book have adopted genomic testing as an essential breeding and management tool. This level of adoption reflects a clear understanding of the long-term value of genomics, allowing the breeders to reap the full benefit of the latest technology.

Polledness

The two POLLED mutations that can be tested for genomically, are the Celtic (Pc) and Friesian (Pf) variants. The more recently discovered Mongolian (P_M) and Guarani (P_G) mutations, which also cause polledness, are being investigated by the SA Stud Book team to be provided via a genomic test soon. Genomic testing for both the Celtic and the Friesian POLLED variants has revealed that the Celtic POLLED variant is the only variant segregating in over 98% of the South African Angus population.

Double Muscling

E226X is the new double-muscling variant that has been found in the South African beef cattle population. Although described as Beef Shorthorn specific, lessons learnt with the “Belgian Blue double-muscling” variant *nt821*, these mutations can sporadically occur in other breeds. Less than 4% of the total SA Angus population tests as a carrier, with the *nt821* variant having been identified as the primary variant segregating within the SA Angus population (Figure 1). In the cases where an animal is a carrier, of either *nt821*, *Q204X* or *F94L*, it has been traced back to cows brought in as Section A for upgrading purposes. This highlights a need to screen these animals to reveal their double-muscling status prior to considering them, with the added benefit of genomically enhanced breeding values assisting the prediction of their breeding potential.

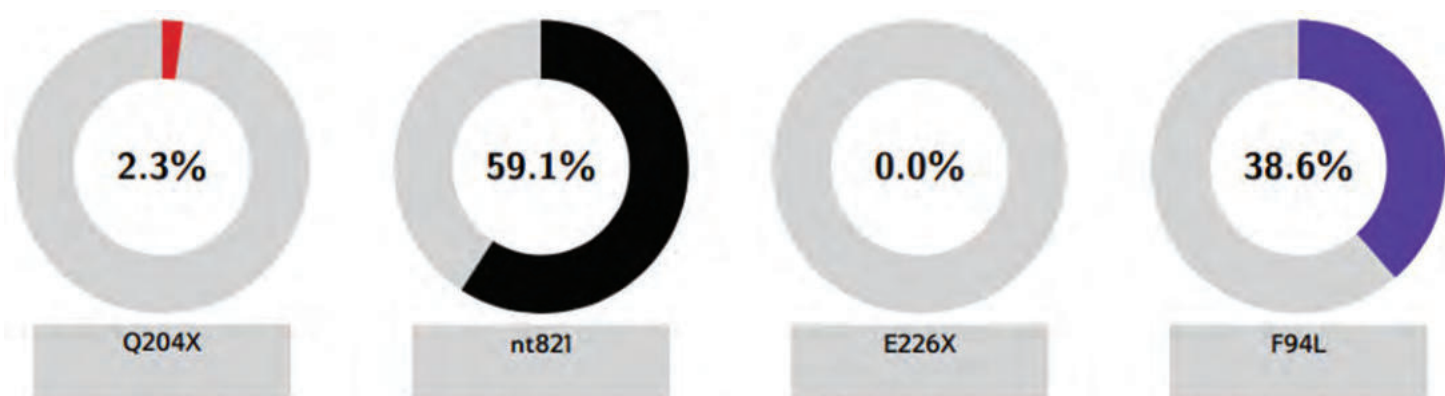


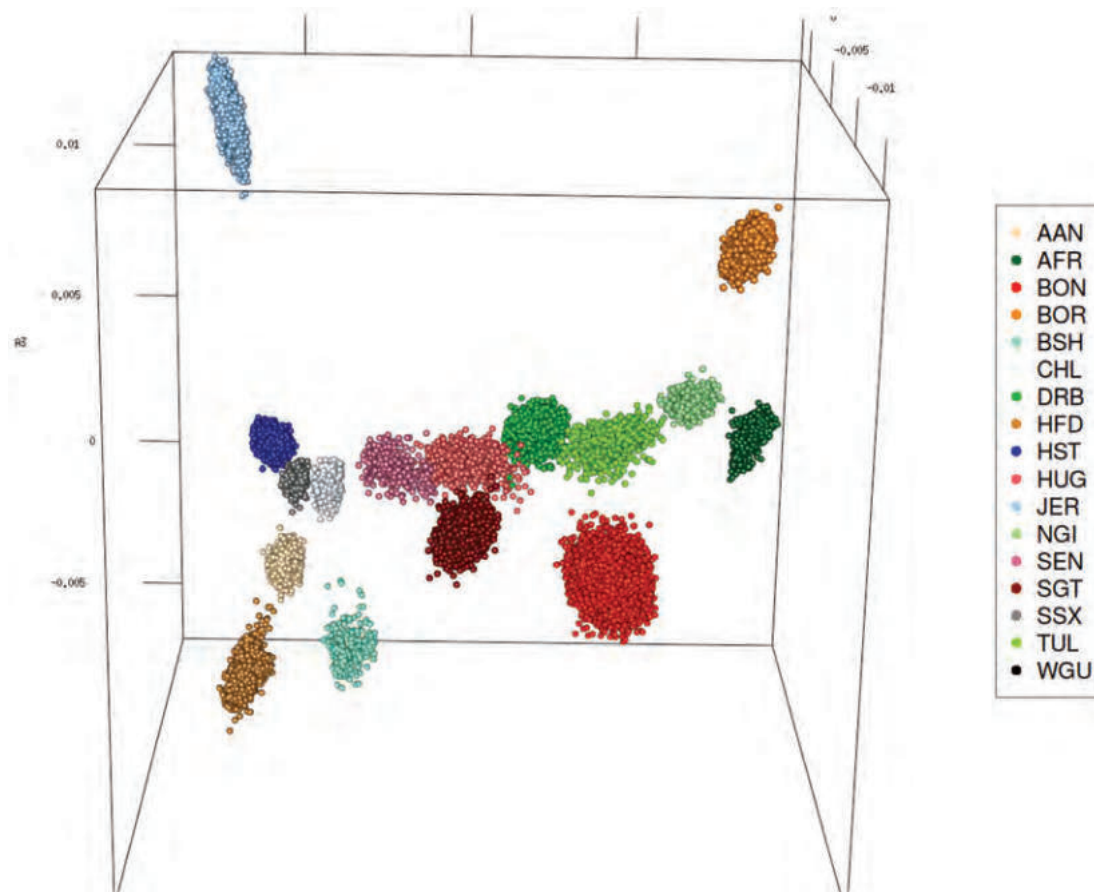
Figure 1. Double muscling gene variants found within the South African Angus population.

Detrimental Recessive Mutations

Genetic disorders such as Crooked Tail, Osteopetrosis, and Mule Foot cause distinctive phenotypic abnormalities, often mistaken for general weakness or poor health in calves. **Glycogen Storage Diseases (GSD)**, including Pompe's disease, resulting from mutations that impair glycogen storage, is a mutation that is currently being monitored to eradicate this recessive mutation from the South African beef cattle population. **Retinitis Pigmentosa (RP1)** is an ocular disorder that causes complete blindness in animals, but is only exhibited in animals over four years of age, meaning it is a progressive degeneration of the photoreceptors. **Maple Syrup Urine Disease (MSUD)** is a lethal genetic abnormality, with two variants observed within the South African beef cattle population. Affected calves are unable to break down complex amino acids due to a defective enzyme. The build-up of these complex amino acids causes lethal brain damage, affected calves are typically born without symptoms, but by 2 to 4 days old become slow, dull and eventually recumbent. The calf will often throw its head back and lie on its side, unable to rise. To reduce the risk of these disorders, genomic testing of sire bulls is essential to exclude carriers and ensure herd health. **Developmental Duplication (DD)** is a recessive mutation found in the *NHLRC2* gene, which plays a critical role in embryonic development. Calves affected by DD are observed to have extra limbs or limb parts on the calf, commonly in the shoulder or neck region, alongside spinal deformities (such as the spine splitting or duplicating) and cranial defects. This disorder is often lethal, resulting in abortions with calves rarely surviving. **Neuropathic Hydrocephalus (NH)**, also known as curly calf syndrome, is a lethal recessive mutation where affected calves display fixated joints, their skulls are dome-shaped, malformed, and have loose bone plates. **Bovine Progressive Ataxia (BPA)** is a neurodegenerative disease caused by a recessive mutation in the *KIF1C* gene, that affects the myelin formation protecting the nerve cells in the brain and spinal cord. Symptoms typically appear between 6 – 18 months. Clinical signs of BPA include a stiff gait, progressive in-coordination of the hind limbs, inability to rise, and muscle tremors. SA Angus breeders are hereby asked that if a calf seemingly exhibits one of the above mentioned recessive disorders, that a hair sample of the calf is taken in order to confirm if it is indeed a recessive genetic disorder.

Genomic Positioning of the Breed

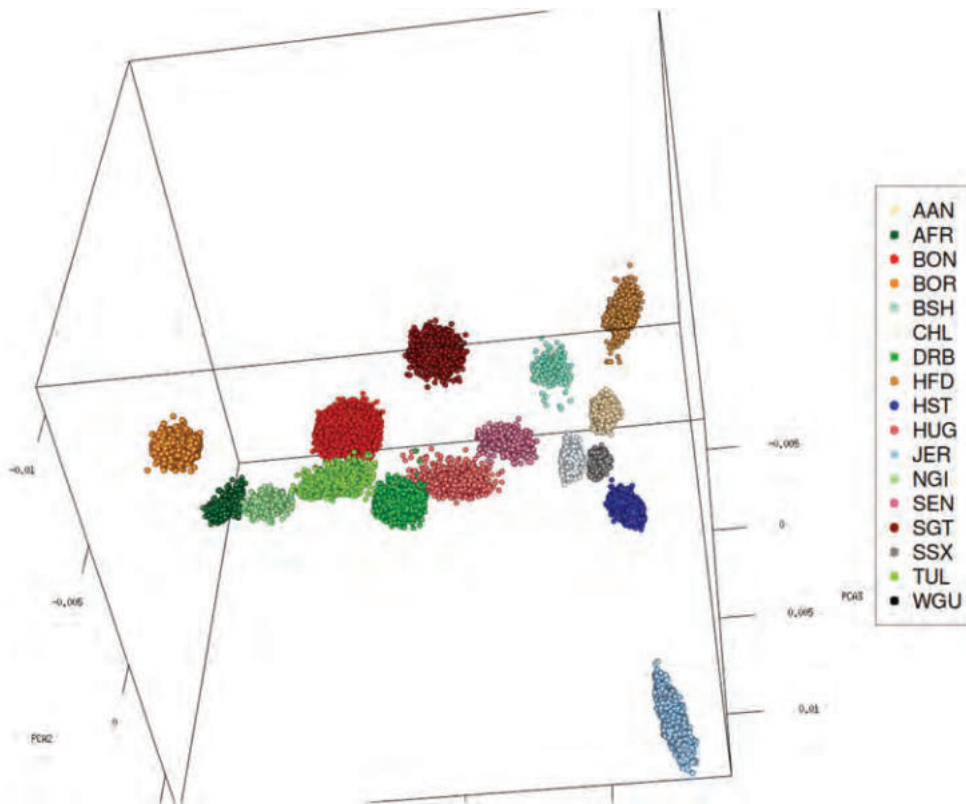
The (3-dimensional) Principal Component Analysis (PCA) plot (Figures 2 and 3), simply referred to as a “GeneBox”, illustrates the genetic relationship of the South African Angus breed relative to other South African breeds. Each dot represents an individual animal, and clustering reflects shared genetic similarity across thousands of genomic markers. Two GeneBoxes have been included from different angles to encapsulate the three-dimensional aspect of the plot. The SA Angus cluster (light pink cluster in the



bottom left of the first picture, and top right in the second picture) forms a distinct, well-defined cluster with clear separation from the other breeds. The SA Angus cluster sits between the other *Taurine* breeds, the Beef Shorthorn cluster (light blue cluster at the bottom of the first image and on the right-hand side on the second image), the Hereford cluster (light brown), the Sussex (grey) and the Charolais (white). These breeds are of British - or European ancestry and therefore cluster in similar areas. As more genotypes for each breed are added and the genetic reference populations per breed are expanded, the genomic relationships between the clusters will become even more apparent.

Figure 2. GeneBox to show the SA Angus genetic relatedness to other breeds, Angle 1.

The integration of genomic testing into the breed provides an increasingly powerful framework for managing the SA Angus breed. The GeneBox highlights the breeds' distinct yet composite genomic architecture. At the same time, the detection and management of detrimental mutations remain critical to safeguard the long-term fitness of the population.



These latest “Geneboxes” are a part of the ongoing development of the Breed Composition Purity Key. SA Stud Book will launch the newest Breed Key in 2026, introducing this as an added feature when genomically testing animals, and will allow for accurate tracing of upgrading, as well as identifying the breed history in contributing to a composite or admixed animal.

The future of the SA Angus breed will not be shaped by chance, but by informed selection. By embracing genomic technology today, Angus breeders secure stronger herds, greater profitability, and a legacy of performance that will stand the test of time.

Figure 3. GeneBox to show the SA Angus position in relation to other breeds, Angle 2.



Photo: Anton Vermaak