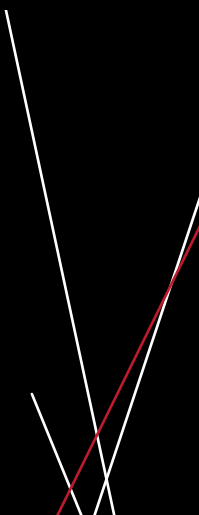




WAGYU BREEDING GUIDE

INTRODUCTION **2021**



This Guide enables
you to apply your own
priorities and select
appropriate sire and dam
breeding for your herd.



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WAGYU in Australia

The Australian Wagyu industry has established itself as the pinnacle of Australian beef production. A unique feature of the Australian Wagyu industry is the prominence of mature Wagyu brands within the majority of export markets.

Approximately 90% of Australian Wagyu production is exported to high-value markets. High marbling has clearly differentiated Wagyu as a unique product compared to other beef delivering an eating experience that is unrivalled. The average of Australian Fullblood Wagyu achieves a marble score greater than 7.5, more than three-fold the average of any other breed.

High value markets in Asia, Middle East, Europe and America recognise Wagyu as their haute cuisine, where only the finest products feature on their menus. Australian Wagyu Fullblood and Crossbred Wagyu boxed beef is demanded by these markets.

Wagyu are extremely tough cattle, operating successfully from the hot, tropical northern environments through to cooler, temperate southern climates. Wagyu cows display exceptional fertility and maternal instincts. Offspring growth is solid and longer maturing in order to lay down the rich marbling for which the breed is renowned.

Many producers have capitalised on the remarkable opportunities with Wagyu, with growth in production of 20% per annum for the past five years. As a result, Wagyu production levels from Australia have reached significant volumes, where a focus on rapid improvement in quality is possible to support market premiums.

The average of Australian Fullblood Wagyu achieves a marble score greater than 7.5, more than three-fold the average of any other breed.



Traditional Japanese origins

In Japan there are four significant breeds described as 'Wagyu'. The largest is the Japanese Black, comprising about 95% of the Japanese national Wagyu herd, and the predominant breed exported to the USA and onward to Australia. The Japanese Brown comprises about 4% of the Japanese herd, comprises two strains, substantially influenced by Simmental and Korean genetics, and is referred to as Red Wagyu (Akaushi) in Australia. The Japanese Polled and Japanese Shorthorn are niche breeds that are not present outside Japan.

There is evidence of the main Wagyu breed, the Japanese Black, from 3,500 years ago. Genetically different, Japanese Black sub-populations were developed in different prefectures. Modern Wagyu cattle are also, to an unmeasured extent, the result of joining native Japanese cattle in Japan with imported breeds.

Crossing began in 1868 under the Meiji restoration, when the Japanese Government imported Brown Swiss, Devon, Shorthorn, Simmental, Ayrshire, and Korean cattle, for use in specific prefectural herds. The policy was revoked in 1910, the subsequent influence of the imported genetics on the native cattle herds in prefectural isolation is not well established and continues to be debated.

By the end of WWII, the enforced segregation of prefectural herds was largely abandoned. Hyogo Prefecture, the home of 'Tajima' cattle, was and remains, the only 'segregated' prefectural herd today. The modern Japanese emphasis on breeding for beef production commenced as recently as the 1950s, as mechanisation swept through Japanese agriculture and cattle ceased to be bred for work applications.

International science has identified patterns of genetic variation in the Japanese Black prefectural herds, forming genetically diverse sub-populations or strains, which are believed to result from centuries of regional isolation and phenotype selection for different types of agricultural work. Of these, three major Japanese Black prefectural sub-breeds have significant influences on current international breeding, these are: Tajiri or Tajima (from Hyogo Pref); Fujiyoshi (Shimane Pref) and Kedaka (Tottori Pref). The fourth important Itozakura (modern) strain formed around the prolific and dominant sire Dai 7 Itozakura from the 1960s.

These strains are also recognised as the key reservoir of genetic diversity in the national Japanese Black herd, where effective population size is challenged. To meet this challenge, structured selection of genetics from different prefectural strains is a formal policy component of Japanese national breed conservation and development.

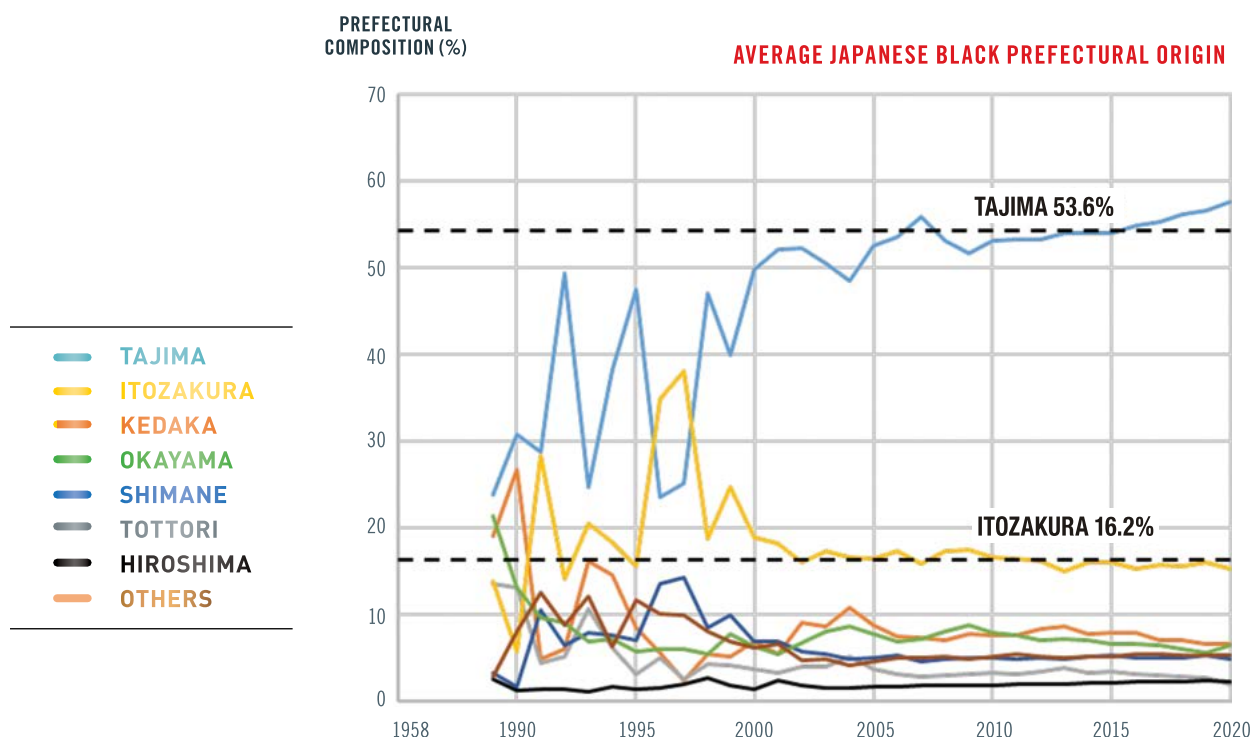


Major Wagyu prefectural bloodlines

There are two Wagyu breeds outside of Japan – Japanese Black and Red Wagyu (or Japanese Brown). In Japan, the Red Wagyu is known as Akaushi.

The three major prefectural sub-populations within the Japanese Black represented in the Australian population are Tajiri or Tajima (Hyogo prefecture), Fujiyoshi (Shimane) and Kedaka (Tottori). These populations were used mainly as agricultural work animals, and the prefecture herds evolved distinctively in regional geographic isolation in Japan.

The Australian Wagyu Association Prefectural analysis deepens knowledge on linkage of Wagyu to the Japanese ancestral breeding regions from which the international herd was developed and can trace its lineage back to Fullblood Sires and Dams registered in the Japanese National Registry. For Japanese Black, there are 369 founder animals (201 sires and 168 dams) from which progeny and frozen genetics were exported from Japan to the US.



Traditional prefectural origin composition of the Australian Wagyu Association registered herd, showing changes in composition reflecting breeding trends over time.



HYOGO PREFECTURE

Descendants of **Hyogo** breeding form the largest segment of the Australian Fullblood herd. Hyogo is the home of Kobe Beef and the sole remaining segregated prefectural herd in Japan. Hyogo cattle are known for superior meat quality but relatively small stature. Carcase weights are significantly lower than the Japanese national average, and average carcase BMS (Japanese Meat Grading Association (JMGA) marble score) is not significantly higher. The most common and well-known Hyogo sire bloodline in Australia is Tajima, but the Kumanami strain is represented in the sire Itoshigenami, also frequently described as Tajima outside Japan.

Hyogo cattle are considered ideal outcross sires in the production of Crossbred Wagyu F1 50% feeder cattle, which explains the numerical dominance of high Hyogo content animals in the Australian herd, a result of original import demand for F1 production sires. This is the most commoditised strain of Black Wagyu both in Australia and Japan. Some infusion of Hyogo genetics is generally regarded as essential in the efficient production of the best quality Wagyu beef. Due to high levels of inbreeding in the Hyogo sub-population, care is needed in joining strategies.



ITOZAKURA LINE

The second most common grouping in Australia, this is a modern bloodline founded on the famous sire Dai 7 Itozakura, combining **Hyogo** and **Okayama** prefectural genetics (in Shimane Prefecture). Many seedstock of Takeda Farm breeding fall within this grouping and the founding sire is prominent in many Australian pedigrees. The line is sometimes mis-described as Fujiyoshi. The founding sire of the line was the premier Japanese Black sire for superior beef production in Japan over a lengthy period, combining consistent high marbling with strong growth.



SHIMANE PREFECTURE

This lightly represented group represents the third highest proportion of the local population and often described as **Fujiyoshi**. The group consists of medium framed cattle with good maternal qualities, growth rates and meat quality.



TOTTORI PREFECTURE

In terms of national calf registrations, **Tottori** prefecture genetics have dominated Japanese Wagyu beef production since the 1960s, but the prefecture is only lightly represented in Australia through the Westholme Fullblood herd. The two main sub-strains are Kedaka and Eikou. Tottori produces larger animals featuring straight, strong back lines, good growth rates, superior maternal ability and high yielding, high quality carcasses. In terms of percentage infusion in national sire production tables Tottori remains the most influential strain in Japanese breeding.

JAPANESE BROWN

Known as 'red' lines (Akaushi), the Kochi and Kumamoto strains present in Australia have been strongly influenced by Korean and European breeds, particularly Simmental.

Advances in WAGYU breeding technology

With the growth in demand for Wagyu beef in Australia and globally, production throughout the value chain is expanding. Well described, high performing Wagyu genetics are called for in both the Fullblood and Crossbred Wagyu supply chains. In response, in the past few years, Wagyu seedstock registrations have increased by about 20% each year – all are DNA parent verified to ensure accurate pedigree.

The Australian Wagyu Association has used the BREEDPLAN genetic analysis technology since 1992, producing Estimated Breeding Values (EBVs) to describe the economically important traits in Wagyu production, including fertility, maternal, growth and carcass.

Further improvement in the Wagyu BREEDPLAN technology has been undertaken since 2013 through the AWA Wagyu Collaborative Genetics Research Project. More than 4,000 Wagyu Fullblood carcasses were analysed using the Japanese digital image camera and Aus-Meat data. Accurate heritabilities and trait correlations were determined for all Wagyu traits including carcass traits for Marble Score, Marbling Fineness, Carcass Weight and Eye Muscle Area.

Genotypes for more than 4,000 animals have been generated through the project, including 50K and 80K SNP genomic profiles for sires and the HD 800K SNP for 130 originally imported and highly used AI sires and ET dams. These genotypes and their related performance data were used to develop a combined pedigree and genomic analysis for Wagyu Single-Step Wagyu BREEDPLAN. This analysis produces genomically enhanced EBVs for animals within Wagyu BREEDPLAN improving the accuracy of EBVs through the pedigree.

SINGLE-STEP WAGYU BREEDPLAN

The Australian Wagyu BREEDPLAN has now moved to Single-Step Wagyu BREEDPLAN. Through the use of genomic information, Single-Step Wagyu BREEDPLAN improves the accuracy of Wagyu EBVs, most noticeably for young animals or those with little recorded performance information. The establishment of genomic relationships to ancestors or relatives with recorded performance information can be more accurately ascribed. This allows for improved EBV accuracy to be generated on young animals based on Genomic SNP profiles alone. These changes are a result of more accurate mapping of genetic relationship linkage through genomic relationships of animals with no performance records to animals that have performance records.

Since April 2018, more than 20,000 genomic profiles have been entered into Single-Step Wagyu BREEDPLAN by AWA members, significantly improving EBV accuracy, especially for non-performance recorded animals across the Single-Step Wagyu BREEDPLAN.

WAGYU BREEDPLAN EBVs

AUSTRALIAN WAGYU GENETIC ANALYSIS

Wagyu BREEDPLAN is the genetic evaluation program adopted by the Australian Wagyu Association which uses Best Linear Unbiased Prediction (BLUP) technology to produce Estimated Breeding Values (EBVs) of recorded cattle for a range of economically important production traits (e.g. weight, carcass, fertility). Wagyu BREEDPLAN includes pedigree, performance and genomic information from the Australian Wagyu Association's database to evaluate the genetics of animals. Ongoing BREEDPLAN research and development is supported by Meat and Livestock Australia.

ESTIMATED BREEDING VALUES (EBVs)

An animal's breeding value is its genetic merit, half of which will be passed on to its progeny. While we will never know the exact breeding value, it is possible to make good estimates based on the performance of the animal and its progeny. These are called Estimated Breeding Values (EBVs) and are therefore the best estimate of an animal's genetic merit. EBVs are expressed as the difference between an individual animal's genetics and a historical genetic level (i.e. group of animals) within the Wagyu BREEDPLAN genetic evaluation and are reported in the units in which the measurements are taken.

Estimated Breeding Values for an animal may change as additional performance data or genotype information is provided for that animal or animals within that animal's pedigree. It is not unusual for EBVs to change, particularly where the EBVs are low accuracy (<50%). Submission of performance data can have a large bearing on the estimate of an animal's genetic merit and the merit of progeny. As the accuracy of an EBV improves over time (along with more data and genotype information), EBV values will be more constant. Please refer to the section on Accuracy within this guide for additional information.

USING EBVS TO COMPARE ANIMALS

Wagyu BREEDPLAN EBVs can be used to estimate the expected difference in the genetics of two animals, with the expected difference equating to half the difference in the EBVs of the animals, assuming consistency across other variables (e.g. they are joined to the same animal/s). For example, a bull with a 200 Day Growth EBV of +20 would be expected to produce progeny that are, on average, 5 kg heavier at 200 days of age than a bull with a 200 Day Growth EBV of +10 kg (i.e. 10 kg difference between the sire's EBVs, then halved as the sire only contributes half the genetics).

BENCHMARKING AN ANIMAL WITHIN THE BREED

EBVs can also be used to benchmark an animal's genetics relative to the genetics of other Wagyu animals. To benchmark an animal's genetics relative to other Wagyu animals, the EBV can be compared to the breed average EBV for the trait or the percentile table.

ACCURACY

An accuracy value is presented with every EBV and gives an indication of the amount of information that has been used in the calculation of that EBV. The higher the accuracy, the lower the likelihood of change in the animal's EBV as more information is analysed for that animal or its relatives.

ACCURACY RANGE INTERPRETATION

LESS THAN 50% = Low accuracy and should be considered a preliminary estimate. The EBV could change substantially as more performance information becomes available.

50 – 74% = Medium accuracy, usually based on the animal's own records and pedigree.

75 – 90% = Medium-high accuracy and usually includes some progeny information. Becoming a more reliable indicator of the animal's value as a parent.

90% AND ABOVE = High accuracy.

FERTILITY AND BIRTH EBVS

Scrotal Size EBV (cm) is an indicator of male fertility in regard to semen quality and quantity in Western breeds of cattle. Higher (positive) EBVs indicate higher fertility. There is also a small negative correlation (desirable) with age of puberty and fertility in female progeny. The relationship between scrotal size and fertility in Wagyu is assumed, but not proven.

Gestation Length EBV (days) is based on AI records. Lower (negative) GL EBVs indicate shorter gestation lengths which generally relate to lighter birth weights and easier calving.

Birth Weight EBV (kg) is based on the measured birth weight of animals, adjusted for dam age. The lower the value the lighter the calf at birth and the lower the likelihood of a difficult birth. This is particularly important when selecting sires for use over heifers.

GROWTH EBVs

200-Day Milk EBV (kg) is an estimate of an animal's milking ability. For sires, this EBV is indicative of their daughter's milking ability as it affects the 200-day weight of their calves.

200-Day Growth EBV (kg) is calculated from the weight of animals taken between 80 and 300 days of age. Values are adjusted to 200 days and for dam age. This EBV is the best single estimate of an animal's genetic merit for growth to early ages.

400-Day Weight EBV (kg) is calculated from the weight of animals taken between 301 and 500 days of age, adjusted to 400 days and for dam age. This EBV is the best single estimate of an animal's genetic merit for yearling weight.

600-Day Weight EBV (kg) is calculated from the weight of animals taken between 501 and 900 days of age, adjusted to 600 days and for dam age. This EBV is the best single estimate of an animal's genetic merit for growth beyond yearling age.

CARCASE EBVs

Carcase Weight EBV (kg) is based on abattoir carcass records and live weight measurements (particularly 600 Day weight) and is an indicator of the genetic differences in carcass weight at the industry average slaughter age of 990 days. Larger positive values are more favourable.

Eye Muscle Area EBV (cm²) estimates genetic differences in eye muscle area at the 12/13th rib site of a 420kg dressed carcass. A higher positive EBV indicates larger eye muscle area and therefore higher retail beef yields. Ultrasound, Aus-Meat and Japanese Digital Image Camera measured Eye Muscle Areas from slaughter animals contribute to this EBV.

Rump Fat EBV (mm) estimates the genetic differences in fat depth at the P8 site of a 420kg dressed carcass. A higher positive EBV indicates more subcutaneous fat and earlier maturity.

Retail Beef Yield Percent EBV (%) estimates the genetic differences in total (boned out) meat yield as a percentage of a 420kg dressed carcass. A higher positive EBV indicates higher percentage yield for the 420kg carcass weight.

Marble Score EBV (Aus-Meat Marble Score) is an estimate of the genetic difference in the Aus-Meat Marble Score in a 420kg carcass. Marble Score EBV utilises Aus-Meat Marble score on a scale of 1 to 10 where 10 is equivalent to an Aus-Meat Marble Score grading of 9+. Where results from the Meat Image Japan digital carcass camera are available, Camera Marbling Percentage and Marble Fineness are also used to calculate Marble Score EBV as the genetic correlations between these measures and Aus-Meat Marble Score are very high. Larger positive values are more favourable.

Marble Fineness EBV (Marbling Fineness Index) estimates the genetic differences in the Marbling Fineness Index (degree of fineness of marbling fat) as measured by the Japanese Digital Image Camera. A higher more positive EBV indicates higher levels of marbling fineness.

WAGYU BreedObject \$Indexes

BreedObject \$Indexes, which utilise Wagyu BREEDPLAN EBVs, allowing selection of Wagyu seestock based on profitability for different commercial production systems. The suite of Wagyu BreedObject \$Indexes are:

- Self-replacing Breeding \$Index (SRI)
- Wagyu Breeder \$Index (WBI)
- Wagyu Fullblood Terminal \$Index (FTI)
- Wagyu F1 Terminal \$Index (F1I)

Each of the new \$Indexes are targeted specifically to a defined Wagyu production and market scenario and producers should identify and use the index that best suits their purpose. It is not appropriate to compare index values of different \$Indexes as they are based on different production model assumptions. It is not the index with the highest \$ value that you should use, it is the index that best reflects your production system.

BreedObject \$Indexes target economic breeding objectives based on average herd and market conditions and have generally targeted the main markets within the main production systems, combining genetic information within BREEDPLAN into one EBV for each \$Index that considers production costs and realised value.

SELF-REPLACING BREEDING INDEX (SRI)

The Self-Replacing Index can be used to select Fullblood bulls that will produce more profitable females when these are retained in Fullblood or Purebred herds, in addition to profitable slaughter progeny.

The SRI estimates the genetic differences between animals in terms of net profitability per cow joined for production of replacement females and slaughter steers to a carcass weight of 435kg at 32 months of age and a 385kg carcass from surplus heifers at 29 months of age. In terms of relative economic importance, the SRI places the following emphasis on these main traits: 38.5% on marbling score (MS); 13% on Residual Feed Intake (RFI) feedlot; 11% on sale liveweight (which will reflect the growth potential and therefore carcass weight of an animal); 8% on meat yield; 6% on dressing percentage and 23.5% placed on other cow and calf traits.

FULLBLOOD TERMINAL INDEX (FTI)

The Fullblood Terminal Index has an increased weighting on the Marble Score EBV and can be used to select bulls to produce profitable slaughter progeny where none are retained for breeding.

The FTI estimates the genetic differences between animals in terms of net profitability per cow joined based on production of slaughter stock only, with a 435kg carcass from steers at 32 months of age and a 385kg carcass from heifers at 29 months of age. In terms of relative economic importance, the FTI places the following emphasis on these main traits: 64% on MS; 11% on Residual Feed Intake (RFI) feedlot; 9% on sale liveweight; 7% on meat yield; 5% on dressing percentage and 3% placed on other young animal traits and 0% on maternal traits.

F1 TERMINAL INDEX (F1I)

The F1 Terminal Index has an increased weighting on the Marble Score EBV and can be used to select bulls to produce profitable F1 slaughter progeny where none are retained for breeding.

The F1 Index estimates the genetic differences between animals in terms of net profitability cow joined based on production of a 420kg carcass from steers and a 385kg carcass from heifers at 28 months of age. In terms of relative economic importance, the F1 Index places the following emphasis on these main traits: 68% on MS; 9% on Residual Feed Intake (RFI) feedlot; 4% on sale liveweight; 6% on meat yield; 4% on dressing percentage and 9% placed on other young animal traits and 0% on maternal traits.

WAGYU BREEDER \$INDEX (WBI)

The Wagyu Breeder \$Index can be used to select Fullblood bulls that will produce more profitable females with high genetic merit for growth and breed average slaughter progeny for marbling. The WBI is suited to the production of steer progeny for high feedlot-entry weight and higher growth replacement females with larger calves in a low-input, grass-based pastoral environment.

Steers are assumed to be slaughtered at 32 months after 550 days of feedlot finishing targeting 460kg carcasses.

Heifers are retained for breeding and therefore maternal traits are of importance. Marbling is targeted at breed average to optimise growth and maternal traits.

Genetic conditions in WAGYU cattle

All breeds of cattle, have undesirable genetic conditions. Fortunately, advances in molecular genetics have facilitated the development of DNA tests for the conditions which enable them to be managed. Breed societies are at the forefront of developing strategies to manage undesirable genetic conditions and seedstock members are leading the industry with their uptake of this technology.

The known genetic conditions of Wagyu are as follows:

SPHEROCYSTOSIS (B3)

Cattle that are homozygous (two copies of the recessive allele) have pernicious anaemia (bleeding caused by the abnormal red blood cells). Death normally occurs within the first seven days after birth. Some cases live to adulthood but there is a severe retardation in growth.

CHEDIAK HIGASHI SYNDROME (CHS)

Cattle that are homozygous (two copies of the recessive allele) have a reduced immune response to disease which reduces their ability to resist bacterial infection. Blood is slow to coagulate so often the first indicator is unusual umbilical cord bleeding at calving. Cattle with this syndrome often have an unusually pale coat colour.

CLAUDIN 16 DEFICIENCY (CL16)

Cattle that are homozygous (two copies of the recessive allele) have terminal kidney failure and the onset can occur any time from late adolescence. Cattle are unlikely to live more than six years.

FACTOR XI DEFICIENCY (F11)

Cattle that are homozygous (two copies of the recessive allele) show prolonged bleeding time after castration or dehorning. It is also possible that Carrier x Carrier matings have increased difficulty producing viable fertilised embryos or full-term pregnancies and may be repeat (return to cycle) breeders.

NOTE – This is generally a non-lethal recessive condition with affected animals being able to live as normal. This Australian Wagyu population has a high frequency of F11 carriers, which makes it an important genetic condition to manage.

Carriers of genetic conditions may be useful in Terminal breeding programs where all the progeny are slaughtered and not used for breeding purposes.

IARS DISORDER

IARS Disorder results in death of affected calves within the last few weeks of gestation, or shortly after birth. Research has identified a mutation in the IARS gene as the cause, resulting in a reduction in activity of a key enzyme, important for protein synthesis for the developing foetus and newborn. Calves affected by this exhibit anaemia, depression, weakness, variable body temperature, difficulty nursing, growth retardation and susceptible to infection.

For more information about the inheritance and management of genetic conditions go to

website  www.wagyu.org.au

CODE EXPLANATION

The first two, three or four characters vary with the genetic condition ie. B3, CHS, CL16, F11 or F13

- __F** Indicates that the sample submitted for this animal **has been tested** and found to be **FREE** of the causative mutation responsible for the indicated genetic condition. This animal is homozygous free, meaning that it has two copies of the normal variant (or allele) of the gene.
Shown in green in the lot listing within the catalogue.
- __C** Indicates that the sample submitted for this animal **has been tested** and found to be a **CARRIER** of the causative mutation responsible for the indicated genetic condition. This animal is heterozygous for the mutation, meaning that it has one mutant allele and one normal allele. This animal could pass the mutation to approximately half of its progeny.
- ___%** Indicates that, based on pedigree information supplied by the breeder of the animal, the animal **has a chance to be a carrier** of the mutation responsible for the indicated genetic condition but **HAS NOT BEEN TESTED**. The higher the indicated percentage, the larger the chance the animal may be a carrier.
- __FU** Indicates that, based on pedigree information supplied by the breeder of the animal, the animal is **expected to be free** of the mutation responsible for the indicated genetic condition. However, this animal **HAS NOT BEEN TESTED** for the causative mutation and the AWA gives no guarantee as to the animal's "free" status.
- __A** Indicates that the sample submitted for this animal **has been tested** and found to be **affected** by the genetic condition. This animal is homozygous for the mutation responsible for the genetic condition and has two copies of the mutant variant of the gene.



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