Analysis Enhancements 2022

A summary for Sheep Genetics members

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From Sheep Genetics

Dear Breeders,

This document includes details about the Analysis Enhancements for 2022.

Sheep Genetics continually strives to provide a world leading genetic evaluation for our clients. Annually we implement enhancements to our analyses to ensure that you are provided with the most accurate breeding values and tools.

This year there are a number of key enhancements being implemented to the analysis. The key themes for this year's enhancements include:

1. More accurate decisions through improved analysis and calculation of breeding values

2. Ensuring the long-term efficiencies of our evaluations.

We will implement the Analysis Enhancements for 2022 on the **1st May 2022 run**. With results anticipated in mid-May when all analyses have been complete.

All breeders will receive links to reports from these runs via email.

Please contact Sheep Genetics if you have any questions. We appreciate your support during this exciting time of development for Sheep Genetics.

Your Sincerely,

Peta Bradley
Manager – Sheep Genetics

On behalf of the Sheep Genetics team.

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Weaning Rate ASBV

Number of Lambs Weaned will be replaced by an improved ASBV called Weaning Rate

Maternal and MERINOSELECT clients have access to component traits that break down reproduction into a series of traits including conception (CON), litter size (LS) and ewe rearing ability (ERA). Previously, the ASBV used to select for improved reproduction was a single trait – Number of Lambs Weaned (NLW).

The breakdown of reproduction into its components has allowed breeders to make more targeted genetic gain in the different drivers of reproduction. It has also allowed for the incorporation of genomic information to inform the traits, and improved the way reproduction data is filtered and utilised.

However, having a single reproduction trait is important to assist commercial producers in making selection decisions, and for inclusion in selection indexes.

Therefore, a combined trait 'Weaning Rate' (WR) has been developed and is available to Maternal and MERINOSELECT evaluations as a replacement for NLW.

What is 'Weaning Rate' (WR)?

Weaning rate is defined as the number of lambs weaned per ewe joined, and is expressed in the units of 'lambs', similar to the component traits. As an example, consider two rams, one with a WR ASBV of 0, and the other with a WR of 0.2. As rams make up half the genetic merit of their progeny, the ram with a WR of 0.2 will have daughters who on average wean 0.1 more lambs per ewe joined, than the daughters of a ram with a WR of 0.

WR is calculated using the improved reproduction traits and is derived by placing an economic value on each component at different average litter sizes. Figure 1 shows the change in the relative economic value (REV) for each component trait at different average litter sizes. We can see that as the flock litter size increases (horizontal axis), that the economic importance (vertical axis) of improving litter size declines, and conception plateaus, while rearing ability continues to increase.

This shows how that at higher litter sizes, the economic importance of ewe rearing ability increases.

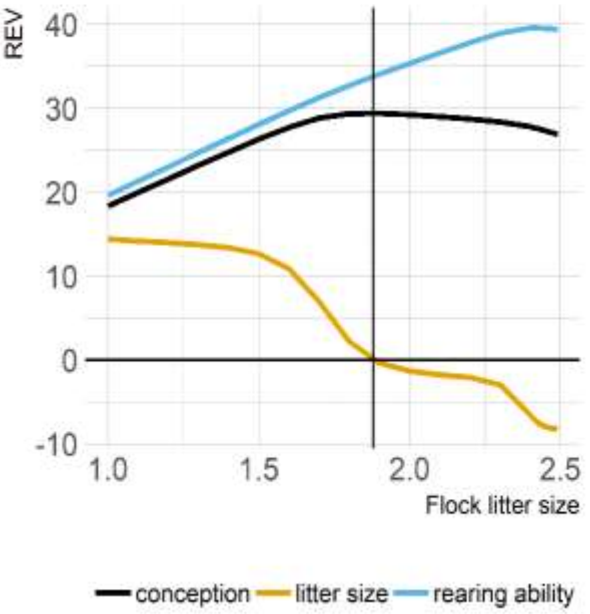


FIGURE 1. THE CHANGE IN RELATIVE ECONOMIC VALUE (REV) FOR EACH COMPONENT TRAIT AT DIFFERENT FLOCK LITTER SIZES

There are differences between WR and NLW, and breeders may notice some re-ranking between the old NLW and the new WR ASBVs.

TABLE 1. THE CORRELATION BETWEEN WR AND NLW FOR 2020 DROP SIRES IN THE MATERNAL AND MERINOSELECT EVALUATIONS.

Analysis	Correlation between NLW and WR for 2020 sires
Maternal	0.69
MERINOSELECT	0.59

How is WR different to NLW?

- WR is derived from the component traits, using a different evaluation to NLW with improved data filtering and genomic information.
- Improvements to the way data is filtered means that we have more ewes with component trait records than we did NLW records. This means that we have more sires have a reportable WR ASBV than there was for NLW.
- There is greater variation in performance for WR than NLW
- The updated model has provided the opportunity to review correlations between reproduction and important production traits.

WR has been developed to make selection decisions using the component reproduction traits for ram buyers more straightforward. Although ram breeders can use WR, Sheep Genetics recommends that the component traits themselves are still used in selection decisions for ram breeders.

Breeders interested in Weaning Rate are encouraged to check the Reproduction summaries in their results to ensure their reproduction data is contributing to the evaluation.

Sheep Genetics has resources available to help breeders wanting to record reproduction. For a recording checklist, and how different sources of information contribute to the reproduction traits, go to: https://www.sheepgenetics.org.au/globalassets/sheep-genetics/resources/recording-repro-checklist-breeders-guide.pdf

This information is also available as a video, with more information on how to interpret the reproduction summaries: https://www.youtube.com/watch?v=PO8syoHW_BU&t=30s

Who is impacted?

Maternal and MERINOSELECT breeders.

NLW will no longer be reported, and will be replaced by the improved WR trait. Breeders will see some re-ranking between NLW and WR ASBVs.

Weaning Rate in Indexes

Weaning Rate will replace Number of Lambs Weaned (NLW) in Maternal and MERINOSELECT Indexes.

WR and NLW have the same trait definition – number of lambs weaned per ewe joined, WR is able to be substituted for NLW in indexes as the trait that describes reproductive performance. However, there are differences between WR and NLW ASBVs as described in the previous section. This means that when these traits are included in indexes, there is re-ranking of animals.

Maternal indexes

For Maternal indexes, WR has been swapped as a direct replacement of NLW. Table 2 shows the correlation between 2020 drop sires, using the previous NLW index and new WR indexes. The table also shows the difference in average index between the old and new index.

In general, the correlations are high between the old and new indexes. However, there will be changes to the average index, so it will be important for Maternal breeders to re-benchmark themselves against the new percentile band tables. For example, the average BLX index for Border breeders (02 breed code) moves from around 119 to 112 with the inclusion of WR.

TABLE 2. THE CORRELATION BETWEEN AND AVERAGE INDEX PREVIOUS INDEXES WITH NLW INCLUDED, AND NEW INDEXES WITH WR INCLUDED FOR DIFFERENT COHORTS OF 2020 DROP SIRES.

Index	Correlation between NLW in index, and WR in index	Average of NLW index (previous index)	Average of WR index (new index)
Border Leicester Cross (BLX) in Border Leicesters (02)	0.95	119.3	112.2
Maternal Carcase Production Plus (MCP+) in Composite Maternals (CM)	0.96	141.7	147.3
Maternal Carcase Production (MCP) in Commercial Shedders (CS)	0.96	123.5	114.6

MERINOSELECT indexes

For MERINOSELECT indexes, small adjustments needed to be made to the economic emphasis on reproduction in the Plus indexes, to maintain similar responses across all traits in the index. In this way, the contribution of WR was altered to reflect a similar response to what NLW had previously provided.

Table 2 shows the correlation between 2020 drop sires, using the previous NLW index and new WR indexes. The table also shows the difference in average index between the old and new index.

The DP+ index sees the biggest change with the inclusion of WR. This is because this index has the most emphasis on reproduction, and therefore most impacted by the change in reproduction trait. The averages of the 2020 drop sires stay relatively similar between old and new.

TABLE 3. THE CORRELATION BETWEEN AND AVERAGE INDEX PREVIOUS INDEXES WITH NLW INCLUDED, AND NEW INDEXES WITH WR INCLUDED FOR 2020 DROP SIRES.

Index	Correlation between NLW in index, and WR in index	Average of NLW index (previous index)	Average of WR index (new index)
Dual Purpose Plus (DP+)	0.86	157.4	159.9
Merino Production Plus (MP+)	0.91	155.6	156.4
Fibre Production Plus (FP+)	0.93	143.0	144.2

Who is impacted?

Maternal and MERINOSELECT breeders.

WR will replace NLW in indexes. This will cause changes to indexes. It will be important for breeders to re-benchmark themselves on the new percentile bands.

Lambing Ease in Terminal Indexes

Updated Terminal indexes to include Lambing Ease (LE)

The index review conducted by Sheep Genetics in 2020 highlighted that breeders and ram buyers were concerned that lambing difficulties were not being considered in any of the terminal indexes. Reducing lamb losses is a key priority to industry therefore all Terminal indexes (TCP, EQ and LEQ) have been updated to include Lambing Ease Direct (LE_DIR) in the indexes.

There are high correlations between the old indexes and the updated indexes that include LE. These correlations range between 97.4% - 98.2% for each of the indexes. This indicates that the ranking of animals is very similar between old and updated indexes. For more information on updated trait contributions to each of the indexes please see Appendix 1. These contributions will also be updated in the index documentation.

If a breeder doesn’t score Lambing Ease, they will still have information informing this trait in the indexes via correlated traits to Lambing Ease such as gestation length and birthweight, however scoring this trait directly will provide the most accurate information for the ASBV and index calculation. More information on scoring Lambing Ease can be found on the Sheep Genetics website.

Who is impacted?

All Terminal sheep will only have indexes reported that include LE.

This will result in some movement in individual indexes with animals that have poor LE_DIR ASBVs being the most impacted.

Improved Accuracy Algorithm

Accuracy calculation for ASBVs has been improved and is now more efficient, precise, and faster

The growing number of genotypes in the database has meant a new way of estimating accuracies has had to be developed.

The new algorithm allows for more efficient estimation of the accuracy figure reported alongside ASBVs. There are several benefits of this new methodology including:

- Efficiencies of accuracy calculation for analyses that have continually expanding genomic populations
- The new program is faster and gives considerable savings in memory usage allowing run times to be maintained with more data than ever before being used in the evaluation
- The new accuracies are more precise in describing the data that is contributing to the estimation of the breeding value

Who is impacted?

Merino, Maternal and Terminal breeders may see a shift in the accuracy of their breeding values for some traits.

Animals most impacted by this enhancement are those with genomic information and limited trait recording and non-genotyped relatives of genomic tested animals.

TBLUP

New analysis logic has been implemented to ensure the evaluations can continue to run with large volumes of genomic data

The MERINOSELECT analysis has experienced significant growth in the amount of genomic information being submitted over the last 5 years (Figure 2) and this is continuing to grow exponentially.

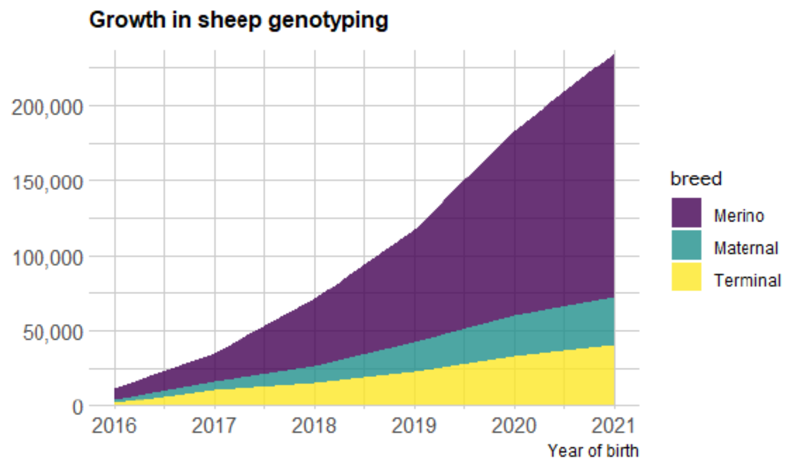


FIGURE 2. THE GROWTH IN THE NUMBER OF GENOTYPES USED IN THE MERINO, MATERNAL AND TERMINAL ANALYSIS OVER TIME

Computationally, to deal with this growing amount of genomic information, a new methodology has been implemented called TBLUP. Whilst this is an exciting technical development that creates efficiencies and improvements in the evaluation this enhancement does not result in changes to breeding values.

Who is impacted?

SS-TBLUP will be implemented for the Merino analysis only

This enhancement will not contribute to any change in breeding values or accuracies

Retirement of the Maternal $ Index

The Maternal $ Index will no longer be reported from the Maternal evaluation

Sheep Genetics have, for a number of years, been working to phase out the Maternal $ Index. As part of the index review process and consultation conducted last year Sheep Genetics notified its clients that the Maternal $ Index would no longer be reported as of Analysis Enhancements 2022.

The Maternal $ Index has been superseded by the MCP, MCP+ and BLX indexes. Whilst there is negative pressure applied to adult weight, Maternal $ still results in long term increases in adult weight. The newer Maternal indexes place a cap on adult weight to maintain mature size.

For more information on the Maternal indexes currently reported, go to: https://www.sheepgenetics.org.au/getting-started/asbvs-and-indexes/

Who is impacted?

Maternal breeders will no longer be able to access the Maternal $ Index

Database Redevelopment

The Sheep Genetics Database Redevelopment is a key enabler to the long-term development and security of our Sheep Genetics systems

The Sheep Genetics database systems have been redeveloped for several key reasons:

- To make the Sheep Genetics systems more serviceable
- To future proof the genetic evaluation systems
- Allow integration of genetic databases with other industry databases
- Equip the systems to deal with growing amounts of genomic information
- To use the best data available for evaluation

The redevelopment process involved consolidating the different LAMBPLAN, MERINOSELECT and Research Databases into a single Data Warehouse. Once the Data Warehouse was developed, ways of importing data from on-farm software had to be developed, along with ways of sending that data off to evaluation. New methodology of reporting flock reports back to breeders had to also be developed.

Changes as a result of the redeveloped database

Breeders will notice changes to their breeding values for 5 key reasons. These reasons most commonly relate to the development of the new pathway to send data to evaluation. These reasons include:

1. Updated business rules about which breed codes and pedigree get sent to analysis.
2. Updated data filtering including threshold ranges for traits
3. Updated age stage ranges. The ranges of age stages are shown in Table 1. Going forward breeders are encouraged to record animals for traits when the average age of the group fits within the age range they are targeting.

TABLE 4. THE UPDATED AGE RANGES FOR EACH OF THE AGE STAGES

	Standard Age	Minimum Age	Maximum Age
B	0	0	
L	21	1	39
W	100	40	149
P	225	150	299
Y	365	300	449
H	540	450	659
A	700	660	6059

4. Updated methods for building files that contain data from research kills. This new method accurately accounts for how animals have been managed on-farm as well as the group they were slaughtered in.
5. Updated lifetime group logic to ensure that the environment an animal has been raised in is accurately accounted for.

These updates have been made to ensure that the best available data is available to underpin the calculation of breeding values.

When receiving results after an analysis run breeders will be sent an email from Sheep Genetics. Results will now be accessed from the Sheep Genetics search site. Here you can find customisable, printable reports. You will also be able to download ASBVs to import into your software.

Who is impacted?

All analyses are impacted by the implementation of the redevelopment of the Sheep Genetics Database

Breeders can expect to see changes in breeding values and new ways of accessing results post analysis

Data Quality Score Reports

The Data Quality Score (DQS) report is now available for breeders to access online

Data is the cornerstone of Sheep Genetics' evaluations. Optimising data quality is vital to enhance the reliability of ASBVs, make accurate selection decisions and maximise genetic gains. The Data Quality Score (DQS) will now be routinely reported back to breeders by Sheep Genetics as part of the 2022 Enhancements.

The DQS is made up of measures of data quality, quantity and timeliness as measured by:

- The amount of data, including the number of animals and traits being recorded
- Completeness and accuracy of records, including how well pedigree, birth date and birth types and performance traits are recorded
- Data structure, including progeny numbers and sire representation across groups, and linkage
- Timeliness, which is a measure of how promptly data is submitted to the evaluation from time of collection

Displayed as a single combined score for the flock, the DQS evaluates data from the last 5 years. The score is provided both as a value out of 100, where the higher the value the better the data quality, as well as a star rating to reflect the range that your score fits. For example, a DQS score that sits between 60 and 80 out of 100, will receive a 4-star rating. An example snapshot of the DQS score is shown in Figure 3.

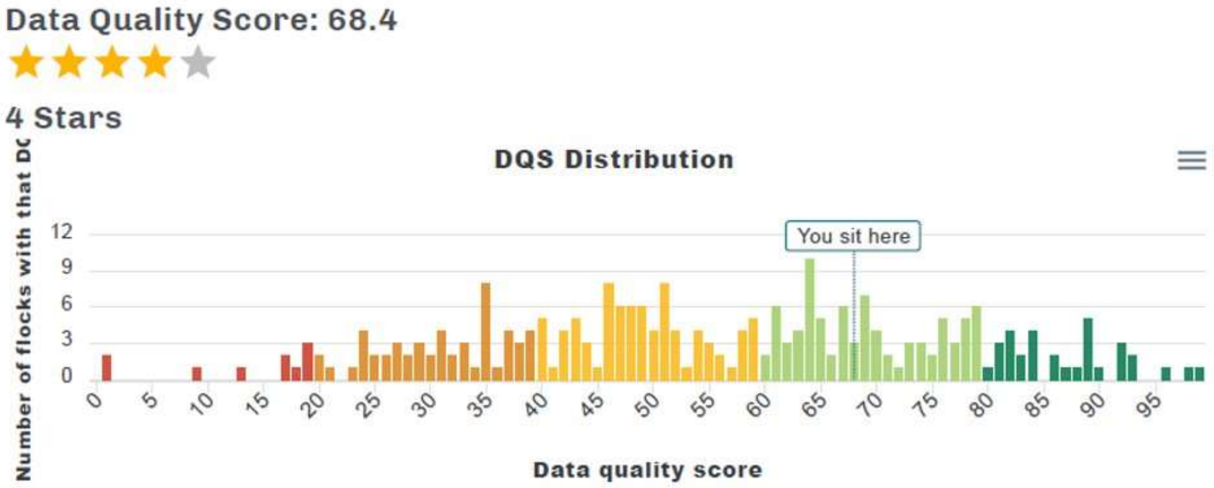


FIGURE 3. AN EXAMPLE SNAPSHOT OF THE DQS REPORT INCLUDING THE DQS SCORE, STAR RATING AND DISTRIBUTION OF FLOCKS IN THE ANALYSIS

It is important to note that the DQS has been developed to explicitly measure the quality of the data being collected and submitted for genetic evaluation. This is different from the accuracy values reported with ASBVs. Accuracy is mainly capturing the quantity of data that contributes to a breeding value, rather than how well that data has been captured. The DQS does include measures on how well pedigree and fixed effects information is captured. For example, the depth of pedigree available or individual birth dates.

Who is impacted?

Any MERINOSELECT, Maternal, Terminal and DOHNE breeder with more than 3 years of data

The DQS is privately reported to breeders via the results portal, in the future the star rating will be displayed publicly. Continue development to make the DQS available to smaller analyses and support for new members of Sheep Genetics.

Website Enhancements

The Sheep Genetics search site now has a new range of features and updates

As mentioned in the Database Redevelopment enhancement on page 14 breeders and nominated service providers can now access results via the search site when an analysis has finished. These results include reports on genetic trends, exclusions, reproduction summaries and more. Breeders and service providers will receive an email that will contain a link to the search site to access the results.

Other updates and enhancements to the search site include;

- The reinstatement of the trait tick box, showing whether an animal itself has been recorded for a trait, and whether it has progeny recorded for the trait
- The ability to search up to 20 traits at a time
- User login session extended to 24hrs before the session times out
- An animal can appear in more than one catalogue at the same time, which allows maternal and shedding breeds to have a catalogue available under both the main search (e.g., Maternal) and the cohort search (e.g., First cross sire breeds)
- Users can nominate and grant access to service providers for areas such as data importing, catalogue creation, MateSel and access to results
- Pen card optimisation including the improvement of speed to build large catalogues and non-blurry display
- Admin can create a catalogue on a user’s behalf, so that user can still access the catalogue on their account

Who is impacted?

All breeders and service providers

Results are accessed via the search site and additional improvements to the search site based have been implemented

Corriedale Analysis Reporting

Reporting Corriedales from the Maternal analysis only

Corriedales animals will now be reported only from the Maternal analysis. The method that Corriedales are now reported matches what is currently done for the first cross sire breeds and shedding breeds in the Terminal Analysis. Figure 4 shows how breeders will be able to access Corriedale animals from the Maternal analysis but on a Corriedale only percentile bands.

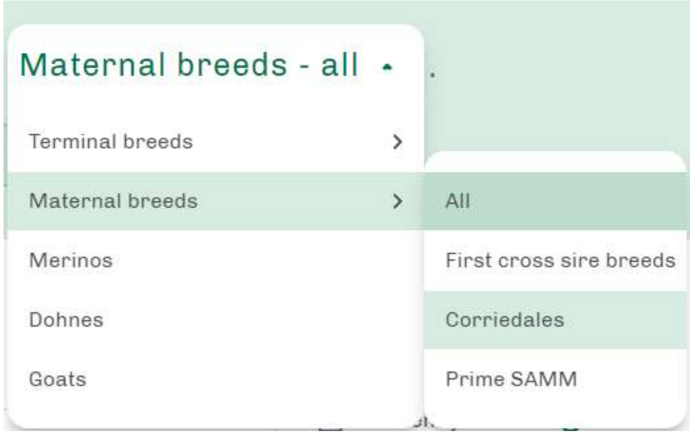


FIGURE 4. A SCREENSHOT SHOWING HOW CORRIEDALE BREEDERS CAN ACCESS RESULTS ON THEIR OWN SUB-SET OF PERCENTILES FROM THE MATERNAL ANAYLSIS

In recent years, many Corriedale breeders have made efforts to capture various information that was not available in the Corriedales only analysis. This information included carcase and eating quality traits through progeny testing and carrying out extensive genomic testing. These kinds of information are used directly in the Maternal analysis, providing Corriedale breeders with carcase and eating quality ASBVs and improving accuracy for hard to measure traits through the use of genomic information in the analysis.

Additionally, in the Maternal analysis Corriedale breeders have access to the component reproduction traits, Conception (CON) Litter Size (LS), Ewe Rearing Ability (ERA) and Weaning Rate (WR). Having these improved reproduction traits enables Corriedale breeders to make more targeted genetic gain for reproduction. The correlation between the old Corriedale only ASBVs and the ASBVs for Corriedales sourced from the Maternal analysis ranges between 96% - 98%. This means the ranking of Corriedale animals has generally remained the same.

Corriedale breeders will need to use the percentile band table from the maternal analysis that is filtered to view just Corriedales to re-rank benchmark.

Who is impacted?

Corriedale breeders.

Corriedales were also reported from the Maternal analysis previously, so other Maternal breeders will see no change resulting from this Corriedale reporting change.

Preparing for the Analysis Enhancements

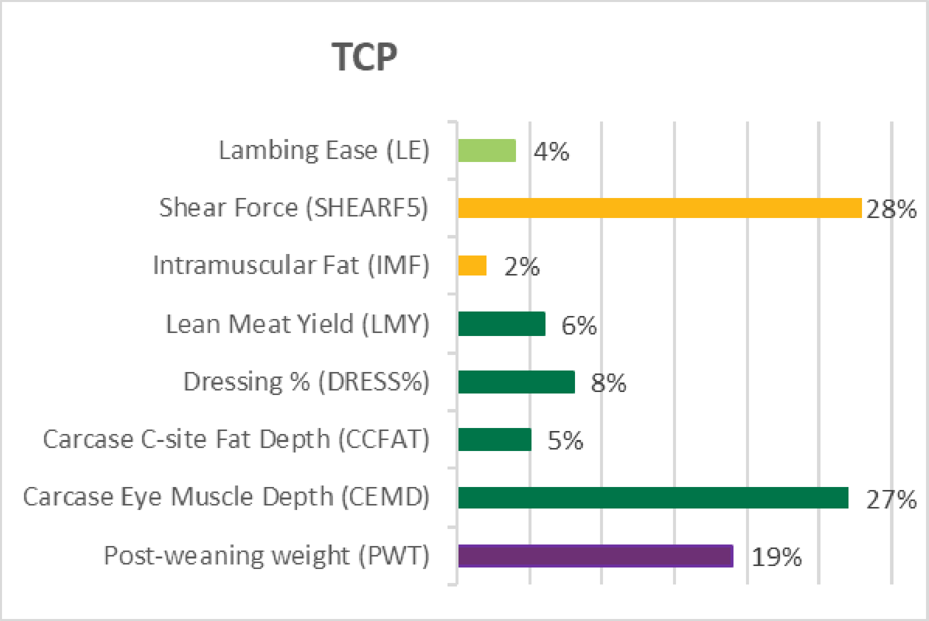
Below is a check list to provide breeders with tips on getting the most out of the 2022 Analysis Enhancements

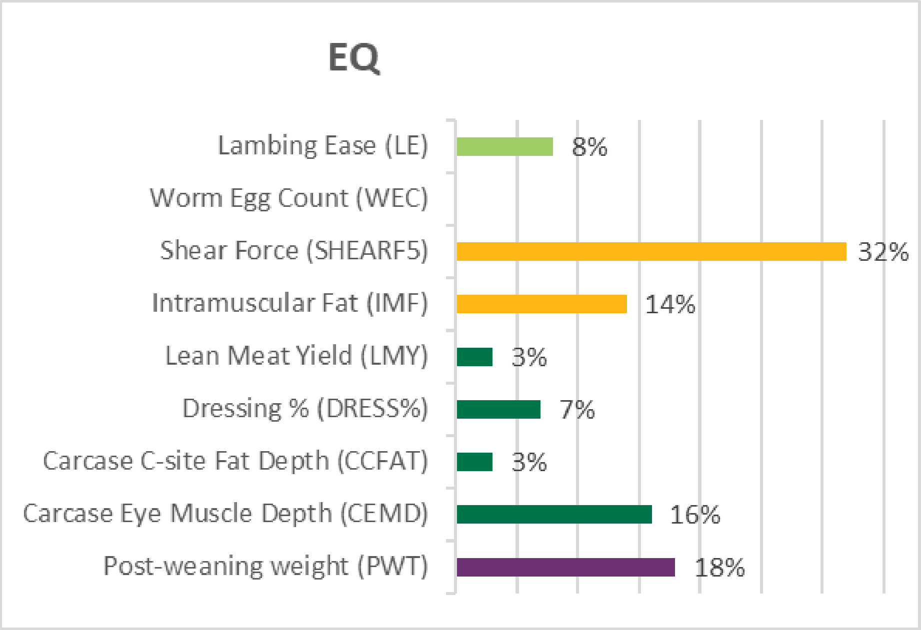
- ✓ Ensure that you are using the latest version of your on-farm software (this includes Pedigree Master) and download and install the latest updates as they become available
- ✓ Sign-up to a Sheep Genetics webinar once results have been released. You can also watch videos on the changes on our website.
- ✓ Come along to a Regional Forum in your local area. Please see the Sheep Genetics website on the dates and locations for this years forum
- ✓ Ensure that if you are using a service provider that they are assigned to your Sheep Genetics website account. If you don’t already have an account, please contact Sheep Genetics to get started
- ✓ Take time to check the percentile bands for indexes, new traits and existing ASBVS to “re-benchmark” yourself
- ✓ Take time to explore the new results section of the website including viewing your Data Quality Score Report
- ✓ For Merino and Maternal breeders check your reproduction summaries to ensure that you are submitting the correct information

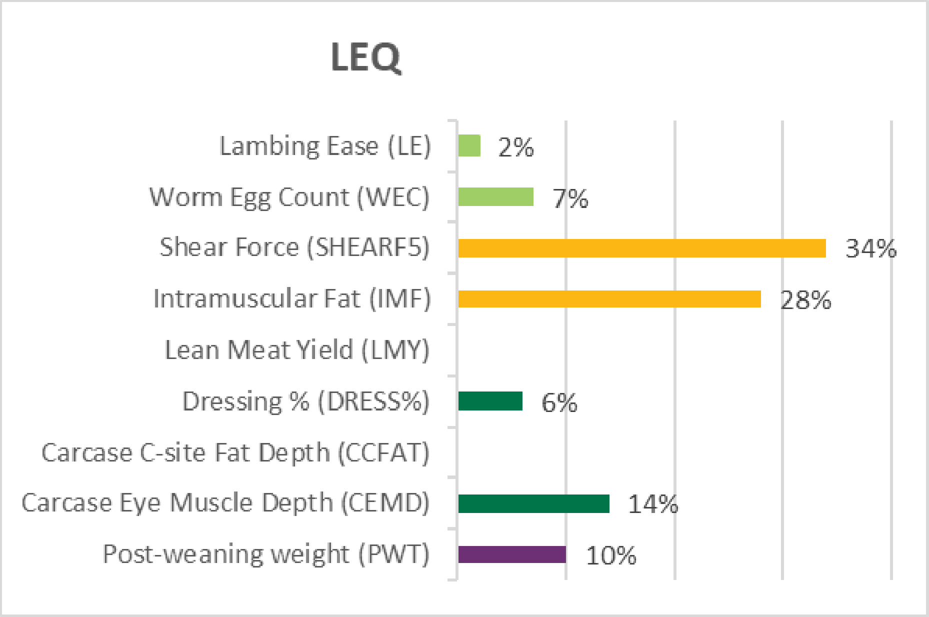
Appendix 1

Terminal index ASBV Contribution to the Index

All the terminal indexes have been updated to include Lambing Ease (LE). Due to correlations between LE and other traits in the index, there are differences in the relative emphasis on each trait. The following graphs show the traits in each of the terminal indexes and how they contribute to the overall balance of the index in the top 10% of current terminal sires.




EQ
Lambing Ease (LE)
Worm Egg Count (WEC)
Shear Force (SHEARF5)
Intramuscular Fat (IMF)
Lean Meat Yield (LMY)
Dressing % (DRESS%)
Carcase C-site Fat Depth (CCFAT)
Carcase Eye Muscle Depth (CEMD)
Post-weaning weight (PWT)
8%
32%
14%
3%
7%
3%
16%
18%


LEQ
Lambing Ease (LE)
Worm Egg Count (WEC)
Shear Force (SHEARF5)
Intramuscular Fat (IMF)
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Dressing % (DRESS%)
Carcase C-site Fat Depth (CCFAT)
Carcase Eye Muscle Depth (CEMD)
Post-weaning weight (PWT)
2%
7%
34%
28%
6%
14%
10%