CT scanning of carcass traits from the Deer Progeny Test

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CONTENTS

1. Client Summary

- The purpose of this study was to investigate different methodologies for Computed Tomography (CT) scanning of rising yearling deer and compare them with actual meat yields from the slaughter of the Invermay 2013-born DPT cohort.

- CT has been used commercially to predict the amount of fat, lean and bone in deer stud breeding stock in New Zealand for 14 years, allowing accurate selection for carcass characteristics to be made on stud stags without them having to be slaughtered. Generally only stud deer destined to be retained in the breeding herd i.e. not slaughtered for venison are CT-scanned, so there has not been direct comparison between CT-scan prediction yield data and actual post slaughter saleable meat yields.

- New CT scanners and technology means that rising-yearling deer can be scanned differently, at heavier weights and hence at older ages. Previously CT scanning was done around 6-months of age (pre-winter), but it is now possible to do it near time of slaughter at 10-months of age. CT-scanning at 10-months of age also offers selection advantages in that live weight estimated breeding values (EBV) are more accurate and a first round of selections to choose which stags to CT-scan could be done using ultrasonic eye-muscle area information.

- Intuitively there is a lot of growth and development that happens between 6 and 10 months of age in rising yearling deer and it would seem more logical to CT-scan them at age-of–slaughter (10-months), than at younger ages.

- The Deer Progeny Test (DPT) 2011 and 2013 birth cohorts were CT scanned in 2011 at 6 months and in 2013 at 10 months of age. Results suggested that there was a difference in the CT prediction of yields for the 10-month old animal using the methodologies developed for predicting yield at 6-month of age, and that this methodology was likely sub-optimal for predicting yields at 10-months of age.

- In 2014, DPT red deer and wapiti x red deer rising-yearling (n=127) were CT scanned at Invermay using the new spiral CT scanner 2 weeks prior to slaughter. The spiral scanner can take images at any regular interval throughout the carcass to provide a very detailed set of anatomical images very quickly; the previous scanner took individual images at a few set points and quite slowly.

- The animals were all slaughtered on 11 Nov 2014, and the next day the carcasses were boned-off into primal joints (shoulder, loin and rear-leg). A large range of measurements was collected at the deer slaughter plant (DSP), including carcass weights, VIAScan® measurements and boned-out primal joint meat weights. VIAScan® provides automated carcass image (photo) based yield predictions in line, to alleviate the need for complicated and expensive actual weighing of cuts to provide carcass yield detail above carcass weight alone.

- The CT images were virtually dissected (i.e. by people using computer imaging programs) equivalent to the actual carcass dissection (meat bone-out) at the DSP. Each image was assigned an anatomical landmark to identify its location on the carcass. The predicted lean meat yields of the virtual dissection and the actual bone-out meat weights were analysed to provide a set of genetic parameter estimates for each primal joint of meat (shoulder, loin or rear-leg).

- A second analysis was done to determine which anatomical point explained the most variation for each actual primal joint, to find a set of optimal landmarks to collect the minimal number of CT-images to predict carcass yield with the least expense, compared with current fixed-point landmarks.

- CT yield predictions and VIAScan® yield predictions were compared against each other and the boned-off meat weights to investigate the correlations of each measure. Knowing the correlations allows better prediction of carcass traits for stud animals in DEERSelect, using either direct (own CT) or indirect (relatives' VIAScan®) measurements; these correlations could be included in DEERSelect in the future to make carcass trait predictions more accurate.

- DSP hot carcass weight, CT predicted gutted carcass weight, CT total primal meat weight and DSP total primal meat weight were all very highly correlated 0.95-0.98, which means CT predictions for these traits are a very accurate proxy for actual slaughter data.

- Individual primal joints were highly correlated (loin 0.65, shoulder 0.88, rear-leg 0.95). This most likely indicates that the smaller the primal joint and/or the greater amount of cutting/boning (either virtual or actual) the greater the error in the measurement, but that they are still sufficiently well predicted from CT to actual to be included in DEERSelect.

- Genetic parameter estimations were quite different to previous analyses, but were analysed slightly differently. Genetic correlations of DSP boned-off meat with CT traits were all high or very high, which is good for inclusion of CT predictions into DEERSelect.

- Six anatomical landmarks were identified which between them explained >70% of the total variation for each primal region (loin 71%, shoulder 81% and rear-leg 88%). These six landmarks, 7th cervical, 2nd and 12th thoracic, 2nd lumbar and 1st and 7th sacral vertebrae could be used in a new fixed-point CT scan prediction of yield, to minimise labour input and, hence, costs as opposed to analysing many more of the images generated by spiral scanning.

- VIAScan® predictions of meat weight correlated very highly with CT predictions and DSP boned-off meat weight, and so could be included in DEERSelect meat modules, which means that VIAScan® data from relatives of stud animals could be used to increase the accuracy of carcass trait prediction in DEERSelect.

- We recommend that the newly identified six anatomical landmark fixed points be validated in a new set of progeny, after which the genetic parameters are then re-estimated. This should allow inclusion of these new more accurate landmarks and updated genetic parameters in the DEERSelect meat yield modules in preference to the old landmarks to provide more accurate yield predictions from 10-month-of-age CT scans.

- We recommend DEERSelect considers the inclusion of VIAScan® meat weight data along with CT data in a modified meat module if the VIAScan® technology continues to be used by the industry, so that a wider pool of animals (relative to stud deer) can contribute to the meat yield prediction in DEERSelect.

- We recommend two further pieces of analysis in the current DPT datasets. First, that an alternative approach of whole animal non-gutted and non-trimmed prediction of yield from spiral-scans be evaluated; this could provide a totally automated (i.e. no human image dissection required) means of yield prediction which would be quicker and cheaper. CT-scan predicted meat yield EBV, while expensive, are the most accurate way to determine carcass yield of breeding stags (and their future progeny) while retaining them for breeding in the future, at the carcass weights and time their progeny should be slaughtered.

- Second, in order to provide all processors the potential to predict primal joint yields, which could be used to provide value based payments rather than just carcass weight, and also feed in to DEERSelect to improve prediction of carcass traits for retained stud breeding animals, that logistic regression analysis be used to

investigate if other measurements collected at the DSP during the DPT, individually or combined, may provide accurate prediction of carcass primal meat yields. This could provide venison processors (not limited to Alliance Group Limited) with predictor measures that could be collected in-line other than VIAScan® , (which is proprietary to Alliance Group), or collecting full measurements of all primal cuts to accurately measure primal joint yield of slaughtered R1 deer.

- This report should be forwarded to the DEERSelect Manager, DEERSelect Reference Group, Alliance Group, Landcorp Farming Limited and InnerVision™, as stakeholders in this research. Wider publication should wait until the methodology has been validated in another set of animals.

2. EXECUTIVE SUMMARY

In New Zealand, computed tomography (CT) scanning has been used for the past 14 years for farmed deer stud breeding stock to predict relative yields of fat, lean and bone in a live animal. CT scanning technology has changed over time, and the opportunity to use new technology arose in 2014 with the purchase of a new GE LightSpeed 5.X Pro16 CT scanner by InnerVision™ and based at AgResearch Invermay campus. This new CT scanner used spiral scanning as opposed to fixed-axial scanning and could scan larger animals due to a higher weight limit and scanning aperture size. This meant that animals could be scanned at 10 months of age, i.e. at slaughter times and live weights, rather than pre-winter at 6-months of age. This study aimed to investigate if fixed-axial CT scanning, was a good proxy for whole carcass spiral CT scanning and how well each technique at a time close to slaughter predicted in-plant bone-off meat yields.

Analyses of Deer Progeny Test (DPT) data showed differences between two DPT cohorts that had been CT scanned, the Invermay 2011 born and Invermay 2013 born. These cohorts were scanned on different scanners and at different ages, fixed-axial at 6-months of age and spiral at 10-months of age respectively. There was recognition that scanning the 2013 cohort (n=127) represented an opportunity to investigate the suitability of the standard fixed-position CT scanning methodology against spiral techniques, and so the 2013 cohort was spiral scanned at 30 mm intervals. Two weeks after CT scanning on 11 Nov 2014 they were slaughtered at the Alliance Group Makarewa DSP and various carcass and dissected carcass primal weights and measures were collected, including carcass weight, VIAScan® measurements, primal meat weights for striploin, shoulder and rear-legs.

The spiral scan CT images (taken every 30 mm) were virtually dissected to the equivalent to the actual dissection at the DSP. Each image was assigned an anatomical landmark to identify location on the carcass. The predicted lean meat yields of the virtual dissection and the actual boned-off meat weights from the DSP were analysed using an animal model in ASREML, which provided genetic parameter estimations. The analysis for the genetic parameters was slightly different, primarily not accounting for carcass weight, so other DPT analyses are not directly comparable. Other analyses were undertaken, a backwards logistic regression analysis was done to determine which landmarked images explained the most variation for each DSP boned-out primal joint. CT predictions and VIAScan® predictions were compared against each other and DSP boned-off meat weights to investigate the correlations of each of the measures for possible inclusion in DEERSelect in the future.

Whole carcass measures of yield, DSP traits, hot carcass weight and total primal meat weight were all very highly correlated with the equivalent CT predicted traits, CT gutted carcass weight, and CT total primal meat weight 0.95-0.98 respectively. Individual DSP primal joint weights were highly correlated with CT primal joint lean weight estimates (loin 0.65, shoulder 0.88, rear-leg 0.95), but the CT predicted weights were 40-90% higher. Genetic correlations of DSP boned-off meat with CT traits were all high or very high.

Phenotypic correlations were also high but at times were >1.00, possibly due to the small size of the dataset.

The backwards logistic regression analysis identified six anatomical landmarks which between them explained >70% of the total variation for each primal region (loin 71%, shoulder 81% and rear-leg 88%). These six landmarks were mostly different to those currently used by InnerVision[TM] and were as follows, 7th cervical, 2nd and 12th thoracic, 2nd lumbar and 1st and 7th sacral vertebrae. Using these six anatomical landmarks in a new fixed-point CT scan prediction of yield, would provide a solution to minimise labour input and, hence, costs, as the original InnerVision[TM] methodology did with different landmarks.

VIAScan[®] predictions of meat weight correlated very highly with CT predictions of lean meat yield and DSP boned-off meat weight, so while the DPT genetic parameter analysis found that VIAScan[®] measures were lowly correlated with the same traits it used a different methodology. The previous analysis adjusted for carcass weight, this latest analysis shows that carcass weight is critical to the predictive power of VIAScan[®]. These high genetic correlations with meat yields show that VIAScan[®] predictions could be included in DEERSelect meat modules from recorded progeny that are not required for breeding purposes. We recommend that if VIAScan[®] technology continues to be used by processors than DEERSelect should consider the inclusions of VIAScan[®] data in future meat module developments.

We recommend validation of the new six anatomical landmark fixed points be in a different set of progeny, e.g. DEERLink 2015 birth cohort after which the genetic parameters can be then re-estimated, using the same models as the DPT analyses of Ward et al. (2015, 2016). We also recommend two further pieces of analysis in the current DPT datasets, firstly an alternative approach of whole animal non-gutted and non-trimmed prediction of yield from spiral-scans should be evaluated for CT lean yield prediction. Secondly that logistic regression analysis be used to investigate if other measurements collected at the DSP during the DPT, individually or combined these may provide accurate prediction of carcass primal meat yields that processors can adopt to better estimate higher yielding carcasses or better producers.

This report should be forwarded to the DEERSelect Manager, DEERSelect Reference Group, and DPT stakeholders Alliance Group, Landcorp Farming Limited and the CT scanning provider InnerVision[TM]. This report should not be published more widely until the methodology has been validated in another set of animals.

3. BACKGROUND

InnerVision™ has been using Computed Tomography (CT) scanned imaging of livestock at Invermay since 1995, and started including deer in 2004. CT imaging allows breeding livestock to be scanned and fat, lean and bone separated into the three tissue types according to their Hounsfield units (HU). Image pixel density can be converted to physical density by using the relationship between HU value and density, which converts from volume to a weight. This means that the carcass yield (lean, fat and bone weights) of breeding animals can be estimated without them having to be slaughtered.

In 2014 InnerVision™ updated their scanner to a newer technology, spiral scanning (GE LightSpeed 5.X Pro16, GE Healthcare), as opposed to fixed-axial scanning. The new spiral scanner also had a larger scan aperture and stronger bed, allowing larger, heavier animals to be scanned. The old fixed-axial scanner technology dictated that the most cost-effective way to estimate carcass yield was to take images at set points throughout the carcass to predict the entire carcass yield. For deer these images were taken at six positions (or slices), two each in the shoulder, loin and rear leg primal regions (Distal Femur, C1, L6, L3, T6, CV7).

The expense of CT scanning deer at approximately $450 per animal, has meant that breeders have only chosen to CT scan males, due to the potential wide dissemination of genetics for males versus females, and hence higher animal value as opposed to females. The larger aperture and higher weight capacity of the new spiral scanner allowed animals with a live weight >100kg live weight to be CT scanned. This weight limit had previously dictated the time at which male breed stock deer had been CT scanned, being at around 5–months of age (pre-winter). The new CT scanner allows animals to be scanned at slaughter live weights and ages (i.e. around 10 months of age and up to approximately 140kg live weight).

Running cohorts of the Deer Progeny Test (DPT) on The AgResearch Invermay farm provided an opportunity to CT scan animals recorded on DEERSelect that were also going to be slaughtered and have a range of carcass measures collected (Ward et al. 2014). The two years of progeny CT scanned were the 2011 and 2013 birth cohorts. The 2011 birth cohort were scanned in May 2012, on the old scanner and the 2013 birth cohort in October (2-weeks prior to slaughter) using the new spiral scanner. It was noted during the analysis of the DPT dataset that the CT trait phenotypic correlations and heritability estimates for the 2011 cohort were lower than anticipated (Ward et al. 2015, 2016). It was assumed that because the animals grow and change so much between 5 and 10-months of age that the predictions used for 5-month old deer may be of lower accuracy, or at least not optimised for 10-month old deer.

Data from CT scanned deer are uploaded to DEERSelect and used to predict meat yields in the meat module. Deer (rising yearling stags) CT scanned by stud breeders are selected on the basis of their CT meat yield data, using the DEERSelect meat yield estimated breeding values (EBV).

The updated CT scanner and the CT scanning of DPT progeny in 2014 (2013 birth cohort), presented the opportunity to re-evaluate the way deer CT scan data was analysed and processed. The CT scanned DPT 2013-born progeny enabled comparisons to be made between the old 'six slice' image prediction and a detailed (automated) spiral scan (slices every 30mm) whole carcass prediction, and to use the detailed 30mm slices to investigate the best way to CT scan 10-month old deer for future genetic selection applications.

4. METHODS

4.1 Animals, CT scanning, slaughter and dissection

A subset of DPT 2011-born and 2013 -born animals from the Invermay deer farm were CT-scanned at the InnerVision[TM] facility at the Invermay Agricultural Centre. A new spiral CT scanner was used in 2014. This was able to scan larger animals and consequently different aged animals were scanned across the two years. In 2012 the five heaviest male progeny at Invermay (if 5 available) from each sire (total 62 progeny) were CT scanned in May at 5-months of age, 6.5 months prior to slaughter. In 2014 ten progeny per sire, males for maternal sires and males plus additional females if required (to make up to ten) for terminal progeny, were scanned (total 127 progeny) on 28, 29 and 30th October at 10 months of age, two weeks prior to slaughter. Progeny were fasted indoors with access to water overnight, and then weighed (rumen) "empty" the next morning, prior to CT scanning. Animals were lightly sedated during the CT-scanning process, using Fentazin-5 (reversed with Contran-H). In 2014 animals were scanned both at the 6 fixed points historically used (Distal Femur, C1, L6, L3, T6, CV7) and spiral scanned collecting images every 30mm. The standard InnerVision[TM] deer algorithm for computing fat, bone and lean from two cross-sectional images, per primal joint, for each animal was used to provide CT predictions of component yield.

On 10th November all progeny in the Invermay 2013-birth cohort were weighed for a pre-slaughter live weight, prior to transport for slaughter on 11th November. On 5th and 6th November ultrasonic eye-muscle measurements were collected as per the method in Ward et al. (2010). All DPT 2013-born maternal males, terminal males, terminal females were slaughtered at 11 months of age on 12 November, with all transported on the same truck and trailer unit according to deer industry best practice. All slaughtering and processing was at the Alliance Makarewa deer slaughter plant (DSP). All progeny were slaughtered in the same shift at the plant, and then boned-out 24 hours later on 13th November, again in the same shift. A range of carcass and primal joint measurements were collected which are listed in Ward et al. (2015, 2016). Key measurements included bone-in (bone and meat) and boned-out (meat only) weights of the three primal joints. The CT predictions of primal component yields and all other traits measured in the DPT were reported in Ward et al. (2015, 2016), with a sub-matrix of trait correlations in Appendix 1.

The 2014 spiral scan images collected at every 30mm were dissected in 2016. The detail of this process is described in detail in Appendix 2. Briefly the CT image dissection was designed to mimic the DSP processing from whole carcass, to primal joints, to boned-out primal joint meat. This involved a three step process, first creating 'gutted' whole carcass images, secondly dividing the images into their appropriate primal joint regions (shoulder, loin, and rear leg), and finally manually dissecting the images as the primal joints would be boned-off the entire carcass. Primal meat was not dissected off the primal joint bones, as the CT image processing uses InnerVision[TM] in house software which separates the tissue types; fat, lean and bone according to their Hounsfield units (HU). The HU value ranges were 40-130, 131-200, 201 -255 for fat, lean and bone, respectively. These ranges were used to process the 30mm spiral scan images as the 6-slice (fixed position) images for the progeny CT scanned in 2014. This processing step converted pixel density to physical density using the relationship between HU value and density, then by converting from volume of tissue to a weight using the calibration curve derived by Fullerton (1980). Once processed predictions of fat, lean and bone (FLB) image were produced, then combined for each individual slice to produce FLB yield for both the whole 'gutted' carcass and the three 'saleable meat' primal regions. The saleable meat primal regions in this report were:

1. The shoulder: including shoulder, breast, neck and flap removed forward of the 6th thoracic vertebrae, including scapula, radius and ulna, excluding the nuchal ligament.
2. The loin was an 11-rib striploin only, removed forward of the tip of the ilium to the 2nd thoracic vertebrae (tenderloins were excluded, but were included in the wider DPT dataset). The loin extended into the primal shoulder region, but was dissected out of the shoulder for image processing.
3. The rear leg, including both entire leg joints boned off the hip- or H-Bone and severed at the hip joint (rear-leg bone-in trait excluded the H-bone, primal rear leg bone-in trait included H-bone).

Each CT image was later assigned a classification, as to where it was located on the body relative to prominent skeletal structures (anatomical landmarks), which provide fixed points of reference. Reference bones were, cervical vertebrae C1-7 (usually beginning with C3 or C4), thoracic vertebrae T1-13, lumbar vertebrae L1-6, sacral vertebrae S1-8 (tail), ischium ISC (tail length dependent), and finally the tibia TB1-8 (tibia was simply referenced sequentially, as there was no single definitive bone e.g. vertebrae to reference). The way the animals are positioned for CT scanning in a recumbent position, the femur is in the same images as the thoracic or sacral vertebrae (Figure 1). The anatomical landmark classification was used in the analysis as a reference as to which image locations were the most predictive of the boned-out meat yields for each primal region. The CT predicted lean (only) for each individual primal region image was analysed in a raw form representing the number of pixels within the lean HU gates.
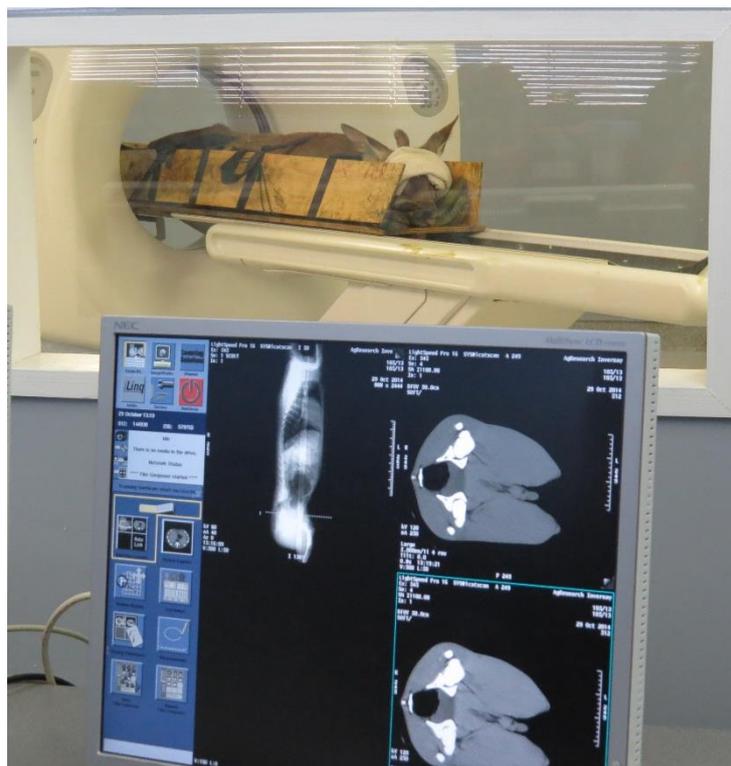
Figure 1. DPT 2013-born male being spiral CT scanned in 2014, imaging the rear leg showing the hip joint at the 4th sacral vertebrae (S5) in the right hand images on screen.

4.2 Analyses

Two separate analyses were carried out, the first using ASREML (Gilmour et al. (2009) to estimate genetic parameters for carcass weight using 30 mm CT primal weight information for the whole carcass using all the 30 mm slices dissected out by primal region. The model used was a full pedigree model with fixed effects of herd year, sex weaning mob, and breed, with animal as a random effect. Other analyses of the DPT datasets have used a similar model, but include a relevant weight term as a fixed effect also (Ward et al. 2014). For example, eye-muscle traits used the live weight at time of eye-muscle ultrasonic scanning (W101112), carcass traits (excluding hot weight (HW)) used hot weight, and CT traits used fasted live weight at time of CT scanning (CTWt). This analysis was used to estimate genetic parameters for the 127 animals CT scanned in 2014, which was a small subset of the entire DPT dataset reported by Ward et al. (2015, 2016).

The second analysis was a backwards logistic regression performed using the R software package (R Core Team, 2016) to determine the relationship between individual CT images and entire primal region lean yields. This analysis was performed using the raw (pixel count for the lean HU) for each 'saleable meat' image classified by skeletal references points for the three primal regions. These raw images were analysed to identify subsets of images that significantly contributed to variation of the total primal region's actual tissue boned-out, off the carcass in the DSP. Then, in a stepwise fashion, models were run starting with the most statistically significant image, then adding the remaining images in order of significance to estimate how much more of the remaining variation could be explained (Appendix 3). Where a second image existed from the same anatomical landmark it was removed from the analysis dataset prior to logistic regression. For the loin primal region the backwards regression model was forced to include T12 as the first trait in the model. This was because this is the location where the ultrasonic eye-muscle is measured (between T12 and T13, Ward et al (2010)), as the CT eye-muscle will need to be included in DEERSelect as a direct measure of the same location as the ultrasonic measure, which is measured far more widely than CT.

5. RESULTS AND DISCUSSION

5.1 CT image dissection, and relationships between virtual (CT) and actual (DSP) carcass primal yields

Most individuals had approximately 45 cross-sectional images spaced approximately 30 mm apart per carcass, and these images were relatively evenly distributed between the three primal regions, with approximately 15 images per region, although the shoulder and loin did overlap approximately 5 images from T2 to T6 (Appendix 2).
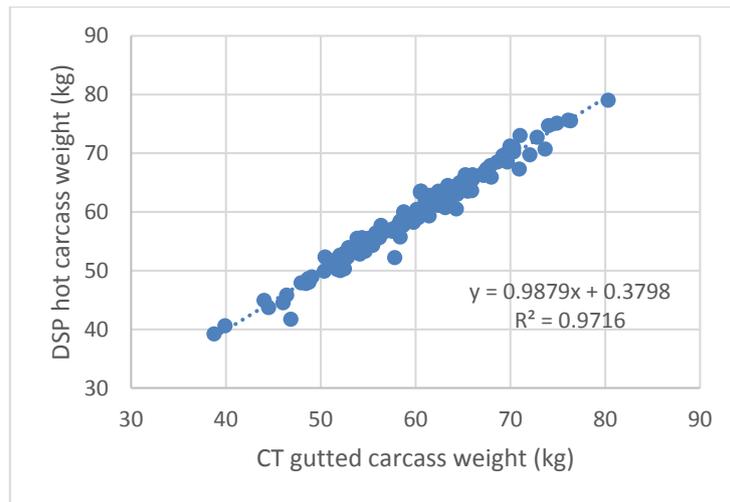
Figure 2. Actual (post-slaughter) hot carcass weight vs. virtual (CT predicted from 30mm slices) gutted carcass weight

The dissection of the carcass, both virtually (CT images) and in the actual at the DSP (boning-out) correlated to quite varying degrees. The actual hot carcass weight and the CT predicted equivalent, gutted whole carcass were very highly correlated $R^2= 0.97$ (Figure 2). The two different virtually dissected CT predicted weights of gutted carcass and total saleable primal yield were also very highly correlated $R^2= 0.98$ (Figure 3). The correlation between CT saleable meat and actual hot carcass weight was also very high at $R^2=0.96$ (Figure 4). The absolute weights predicted for the gutted CT whole carcass were also very similar to those measured post-slaughter as Figure 2 indicates. The mean CT gutted carcass weight was only 0.6% greater than the post-slaughter hot carcass weight, with the range being -4.6 to12.4% (Table 1). Absolute individual primal joint weight CT predictions were much less accurate with mean differences between then and post-slaughter boned-off weights of 39.6-91.9%, with rear-leg being the best and shoulder the worst.
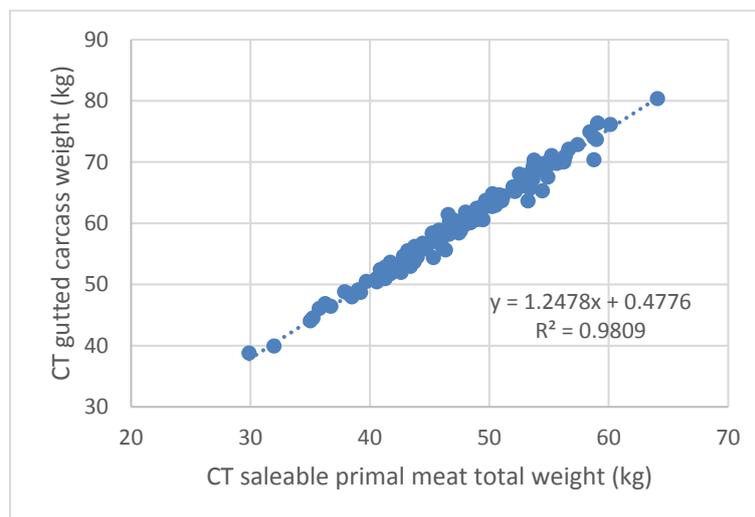
Figure 3. Virtually dissected (CT predicted from 30mm slices) primal saleable meat weight vs. gutted carcass weight
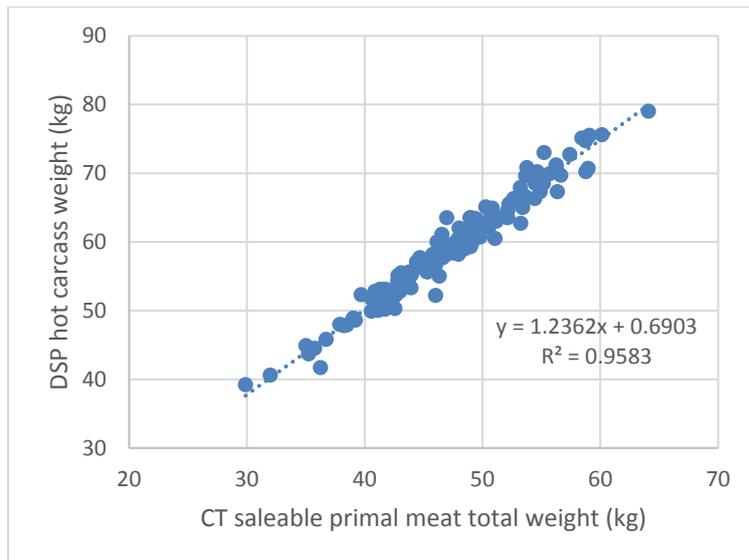
Figure 4. Virtually dissected (CT predicted from 30mm slices) primal saleable meat weight vs. actual (post-slaughter) hot carcass weight

The correlations between CT predicted weights and DSP boned-out weights for individual primal regions were not all as good as to whole carcass correlations, particularly for the loin at R^2=0.65 (Figure 5). Correlations were much better for shoulder at R^2=0.88 (Figure 6) and Rear-Leg (Figure 7). This is most likely attributable to two factors, the accuracy of the cutting and the amount of lean, or tissue, relative to the accuracy of the cutting; it is unlikely increasing imaging density would have improved accuracy. The primal with the worst correlations, the loin, had the lowest amount/weight of tissue (or lean) relative to the potential for cutting/boning errors. The new virtually dissected spiral CT correlations with post-slaughter primal meat weight were higher than the old fixed point CT lean correlations for all primal regions except for the loin. The loin correlations were 10% higher (r^2=0.75) than for the old, and 8, 9 and 24% lower for total (r^2=0.85), shoulder (r^2=0.79) and rear-leg (r^2=0.71) respectively, this suggests that rear-leg is the region that differs the most between the old and new predictions.
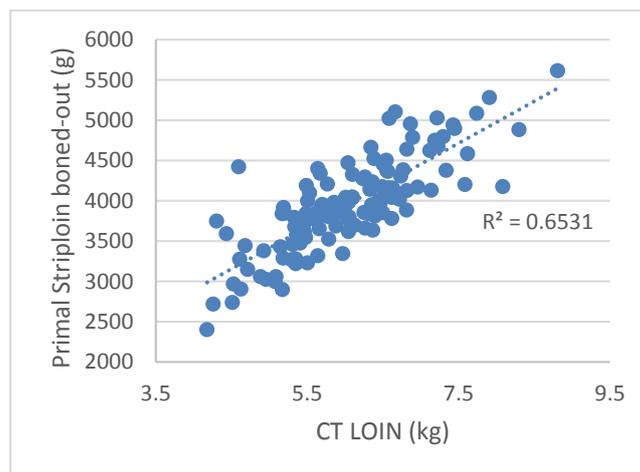
Figure 5. Virtually dissected (CT predicted from 30 mm slices) primal striploin weight vs. actual (post-slaughter) primal striploin weight
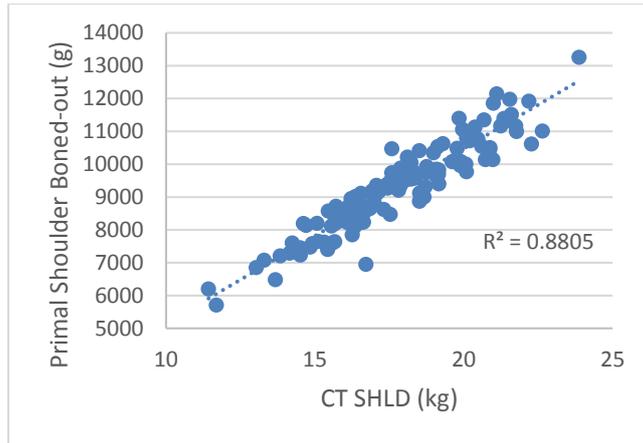
Figure 6. Virtually dissected (CT predicted from 30 mm slices) primal shoulder weight vs. actual (post-slaughter) primal shoulder boned-off meat weight
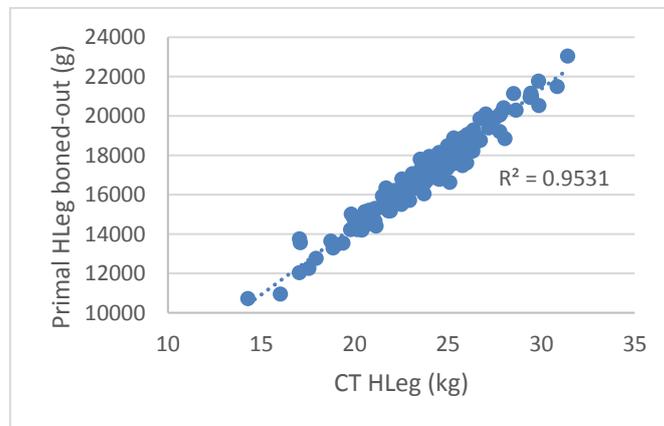
Figure 7. Virtually dissected (CT predicted from 30 mm slices) primal rear-leg weight vs. actual (post-slaughter) primal rear-leg boned-off meat weight
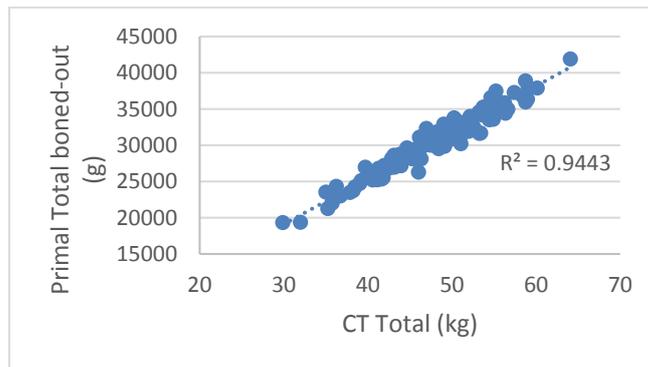
Figure 8. Virtually dissected (CT predicted from 30mm slices) total primal weight vs. actual (post-slaughter) total primal boned-off meat weight

CTLean traits were chosen as the key CTtraits for the analysis, because venison is a lean meat and the CTFat yield predictions (much of which was probably from bone-marrow) produced high CTLean+Fat estimations relative to DSP bone-out tissue weights. CTLean estimations of absolute lean weight were still much higher than DSP bone-out tissue weights as indicated in Figures 5, 6, 7 and 8 and Table 1.

Table 1. Mean CT predicted weights and post-slaughter boned-off meat weights of primal joints and whole carcasses, and differences between mean CT predicted and post-slaughter weights.

Trait	Weight (kg)	Percentage of carcass (%)	CT vs. DSP primal difference (kg)	CT vs. primal difference (%)
CTSHLD	17.77	29.7	8.48	91.9
CTLOIN	6.03	10.1	2.08	53.3
CTHLEG	23.69	39.7	6.71	39.6
CTTotal	47.49	79.5	17.27	57.3
CTGutted	59.74	N/A	0.34	0.6
Primal shoulder	9.28	15.9	-8.48	91.9
Primal striploin	3.95	6.8	-2.08	53.3
Primal rear-leg	16.98	29.9	-6.71	39.6
Primal Total	30.22	51.9	-17.27	57.3
Hot carcass	59.40	N/A	-0.34	0.6

One interesting observation from these correlated data was that the CT rear-leg correlated very well with all other actual primal meat weights, better than striploin with striploin (0.76), slightly worse than shoulder with shoulder (0.84) and the same for total with total (0.94), (Figures 9-11).
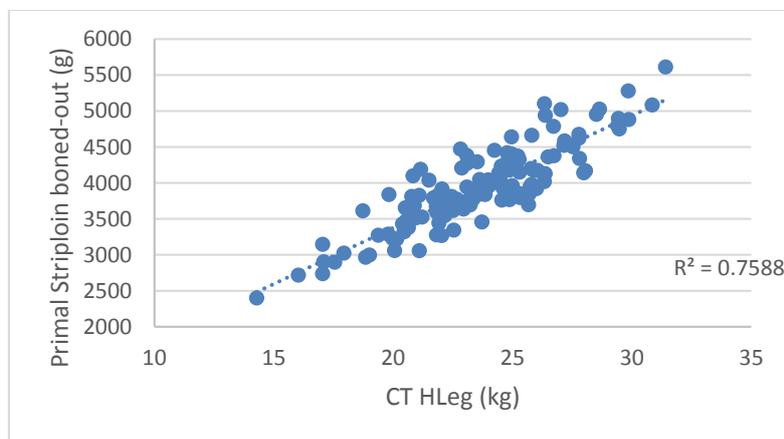
Figure 9. Virtually dissected (CT predicted from 30 mm slices) primal rear-leg weight vs. actual (post-slaughter) boned-out primal striploin.
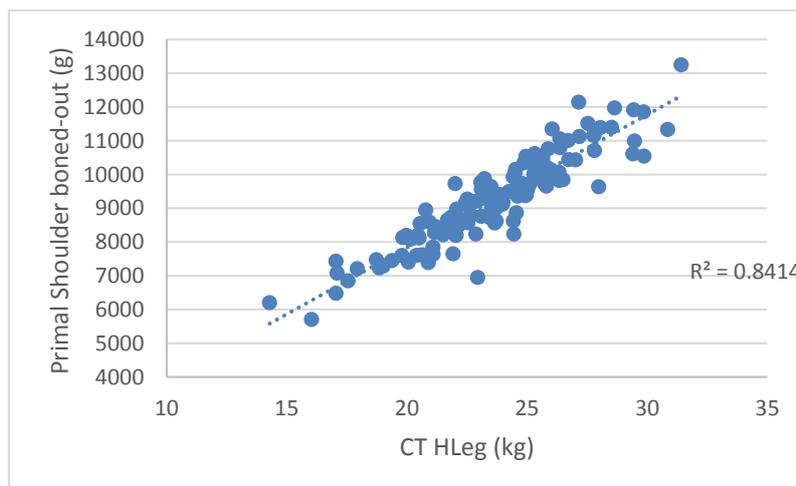
Figure 10 Virtually dissected (CT predicted from 30 mm slices) primal rear-leg weight vs. actual (post-slaughter) boned-out shoulder.
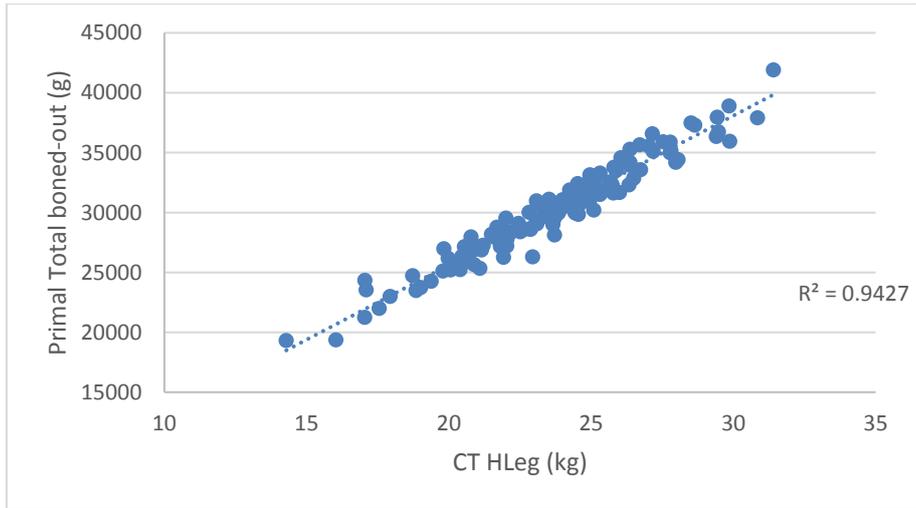
Figure 11. Virtually dissected (CT predicted from 30 mm slices) primal rear-leg weight vs. actual (post-slaughter) boned-out total primal meat.

5.2 Genetic parameters

The ASREML analysis was limited to key traits. These key traits were chosen to be the CTLean predictions for all 30mm slices, CT-T12 area, ultrasonic eye-muscle traits, DSP bone-in and bone-out primal joint weights and bone-out meat yields. Heritability estimates were calculated for all traits, but genetic and phenotypic correlations were only calculated for a sub-set of traits.

The heritability estimates for the CTLean measures were moderate to high (0.35 to 0.58) (Table 2), which was similar to those reported by Ward et al. (2016), of 0.25-0.49 (Appendix 1). The CT –T12 was much higher at 0.51 (Table 2) than CTEMA of 0.07 (Appendix 1), but the old CTEMA was measured at a different place along the loin (6th lumbar vertebrae)). Ultrasonic eye-muscle trait heritability estimates were approaching only half that of those reported by Ward et al. (2016; in parenthesis), with EMA being 0.28 (0.42), EMW 0.11 (0.22) and EMD 0.32 (0.47) in this current analysis. DSP carcass heritability estimates also differed greatly from those previously reported (Appendix 1), with all being lower in this analysis, shoulder estimates being the most different and rear-leg the least different (Table 2). Most heritability estimates (Table 2) differed markedly from those reported for the wider DPT dataset by Ward et al. (2015, 2016), but the reasons for this will be varied. These include a difference in the models used (i.e. live or carcass weight not used as a covariate in this current analysis), less animals (from a single farm and year), a single age of animals (10 months vs. 6 months for 2011-born, and 10 months for 2013-born), and different CT prediction parameters (whole carcass 30mm slices vs. 6-fixed point slices). This makes it difficult to draw conclusions about the reasons for the differences between the heritability estimates from this analysis and previous DPT analyses.

Genetic correlations with the selected traits were generally high or very high, with the exception being primal loin bone-out meat yield and CT Lean (0.04 ± 0.01), and primal shoulder bone-out meat yield and CT Lean (0.22 ± 0.10). Individual primal joint meat weights were highly genetically correlated with CT predicted primal joint lean weights, being 0.92 ± 0.01 for shoulder, 0.85 ± 0.03 for loin and 0.83 ± 0.03 for rear-leg, as was total primal weight, being 0.93 ± 0.01. Hot carcass weight was also highly genetically correlated with all of these CT predicted traits, being 0.91 ± 0.02 for shoulder lean, 0.89 ± 0.02 for loin lean, 0.84 ± 0.03 for rear-leg lean, and 0.93 ± 0.01 for total lean. These genetic correlations (Table 2) differ from the wider DPT ones (Appendix 1), particularly for the rear-leg and total primal weights being -0.59 and -0.34 respectively. Shoulder and loin genetic correlations are quite similar being 0.69 and 0.80 respectively (Appendix 1). Rear-leg makes up a large proportion of total carcass weight and the large difference in correlations may indicate that the original CT predictions for leg were not suitable for animals at 10-months of age.

Phenotypic correlations were mostly high or very high, with eleven being equal to or greater than 1.00 (Table 2). CT and DSP primal region weight phenotypic correlations were as follows; 1.30 ± 0.77 for shoulder, 0.91 ± 0.24 for loin, 0.85 ± 0.23 for rear-leg and 1.00 ± 0.17 for total. Ultrasonic EMA was correlated with CT-T12 ≥ 1.00 at 1.23 ± 0.28. The standard errors for most phenotypic correlations were large or very large. This and the phenotypic correlations of ≥ 1.00 probably reflects the small size of the dataset (Table 2).

Before any DEERSelect meat modules are adapted a new genetic parameter estimation should be undertaken for the recommended CT prediction method moving forward, using the same models as DEERSelect adopts for other meat yield traits.

Table 2. Heritability estimates (diagonal in pink) and selected genetic (below diagonal) and phenotypic (above diagonal) correlations and standard errors, for live animal CT, ultrasonic eye-muscle, and post slaughter carcass traits for 127 DPT progeny born in 2013 at Invermay. Estimates that did not converge represented by a dot (.).

	CTSHLEAN	CTLNLEAN	CTLGLEAN	CTLEAN	CTt12L	EMA	EMW	EMD	HW	PShldrL&Rbone-in	PShldrL&Rboned	PShldrBOMY	PLoinL&R	PLoinBOMY	RearLegL&Rbone-in	PLegL&Rboned	RearLegBOMY	TotalBonedP
CTSHLEAN	0.40 ± 0.35					0.83 ± 0.25	1.09 ± 0.68	0.03 ± 0.67	0.89 ± 0.13		1.30 ± 0.77							1.03 ± 0.21
CTLNLEAN		0.35 ± 0.32				1.12 ± 0.21	.	0.66 ± 0.39	0.92 ± 0.13				0.91 ± 0.24					0.90 ± 0.25
CTLGLEAN			0.58 ± 0.39			0.81 ± 0.29	1.32 ± 0.83	0.37 ± 0.51	0.88 ± 0.16							0.85 ± 0.20		0.84 ± 0.29
CTLEAN				0.43 ± 0.34		0.99 ± 0.16	1.49 ± 1.06	0.41 ± 0.51	0.99 ± 0.05	0.98 ± 0.07	1.17 ± 0.86	-1.43 ± 1.24		-0.75 ± 0.74				1.00 ± 0.17
CTt12L					0.51 ± 0.36	1.23 ± 0.28												
EMA	0.77 ± 0.05	0.72 ± 0.05	0.63 ± 0.06	0.75 ± 0.04	0.67 ± 0.05	0.28 ± 0.30												
EMW	0.61 ± 0.06	.	0.52 ± 0.07	0.61 ± 0.06			0.11 ± 0.24											
EMD	0.57 ± 0.07	0.63 ± 0.06	0.54 ± 0.07	0.63 ± 0.06				0.32 ± 0.31										
HW	0.91 ± 0.02	0.89 ± 0.02	0.84 ± 0.03	0.93 ± 0.01					0.29 ± 0.30									
PShldrL&Rbone-in				0.93 ± 0.01						0.26 ± 0.29								
PShldrL&Rboned	0.92 ± 0.01			0.91 ± 0.02							0.07 ± 0.23							0.98 ± 0.17
PShldrBOMY				0.22 ± 0.10								0.14 ± 0.25						
PLoinL&R		0.85 ± 0.03											0.15 ± 0.26					0.91 ± 0.23
PLoinBOMY				0.04 ± 0.01										0.21 ± 0.27				
RearLegL&Rbone-in															0.25 ± 0.30			0.98 ± 0.04
PLegL&Rboned			0.83 ± 0.03													0.23 ± 0.29		1.00 ± 0.02
RearLegBOMY																	0.21 ± 0.27	-0.82 ± 1.44
TotalBonedP	0.91 ± 0.02	0.89 ± 0.02	0.82 ± 0.03	0.93 ± 0.01							0.97 ± 0.01		0.90 ± 0.02		0.99 ± 0.00	0.99 ± 0.00	0.18 ± 0.09	0.16 ± 0.26

CT Traits
CTSHLEAN: CT predicted weight of primal shoulder lean (kg), CTLNLEAN: CT predicted weight of striploin lean (kg), CTLGLEAN: CT predicted weight of primal rear-leg lean (kg), CTLEAN: CT predicted weight of primal rear-leg lean (kg), CTt12L: CT predicted weight of lean (kg) at the 12th thoracic vertebrae.

Ultrasonic eye-muscle traits (measured between 12th and 13th thoracic vertebrae):
EMA: ultrasonic eye-muscle measured area between (cm^2), EMW: ultrasonic eye-muscle width (cm), EMA: ultrasonic eye-muscle depth (cm)

Post-slaughter in DSP measured traits
HW: hot carcass weight skinned and gutted (kg), PShldrL&Rbone-in: weight of both primal shoulders boned off the carcass (kg), PShldrL&Rboned: weight of both primal shoulder's tissue (meat) boned off the scapula, humerus, radius and ulna (kg), PShldrBOMY: boned-out-meat yield of primal shoulder weight, as a percentage of total carcass weight (PShldrL&Rboned/HW x 100), PLoinL&R: weight of striploins and tenderloins boned off the carcass (kg), PLoinBOMY: boned-out-meat yield of primal loin weight, as a percentage of total carcass weight (PLoin/HW x 100), RearLegL&Rbone-in: weight of both rear-legs boned off the carcass at the hip (kg), RearLegL&Rboned: weight of both rear-leg's tissue (meat) boned off the tibia, fibia, etc (kg), RearLegBOMY: boned-out-meat yield of primal rear-leg weight, as a percentage of total carcass weight (RLegL&Rboned/HW x 100), TotalBonedP: combined weight of all three boned-off primal regions , shoulder, loin and rear-leg (kg).

5.3 Prediction of actual carcass primal yields using anatomically landmarked individual CT images.

Not all sets of CT spiral scan images for an individual contained exactly the same set of anatomical landmarks and some contained the same anatomical landmark twice, especially for thoracic vertebrae. This was due to the animals being of different sizes (lengths) and each image being collected at exactly 30mm, not at precise landmarks throughout the body, which meant in some cases longer anatomical landmarks (e.g. thoracic vertebrae) were captured in two images and shorter ones (e.g. sacral vertebrae) were not captured in some images.

For the anatomical landmarks modelled in the backwards logistic regression for the three primal regions there were differing numbers which attained statistical significance in regard to their contribution to prediction of the post-slaughter boned-off meat weight. The anatomical landmarks with the highest levels of significance for each primal region are shown in table 3 and appendix 3. These landmarks were sequentially added to the logistic regression models in decreasing order of significance.

Table 3. CT image anatomical landmarks modelled by backwards logistic regression for the three primal regions and their statistical significance as variables explaining the post-slaughter meat weigh of the corresponding boned-off primal joints.

CTLoin landmark	Significance	CTSHLD landmark	Significance	CTHLEG landmark	Significance
T2	P>0.001	C4	P>0.05	L5	NS
T6	P>0.01	C7	P>0.01	S1	P>0.05
T7	P>0.05	T1	P>0.01	S2	P>0.05
T10	P>0.1	T2	P>0.01	S3	NS
L2	P>0.01	T6	P>0.05	S4	P>0.05
L3	NS			S5	P>0.1
				S7	P>0.001

Table 4. CT image anatomical landmarks which explained the greatest percentage of total variation in post-slaughter boned-off meat weight for primal striploins, modelled using backward logistic regression.

Model name	Landmark name	Landmark code	Percent of total variation explained
Loin 1	12th thoracic vertebrae	T12	**55.2%**
Loin 2	12th thoracic vertebrae	T12	55.2%
	2nd thoracic vertebrae	T2	10.9%
	Sum		**66.0%**
Loin 3	12th thoracic vertebrae	T12	55.2%
	2nd thoracic vertebrae	T2	10.9%
	2nd lumbar vertebrae	L2	5.4%
	Sum		**71.4%**

Table 5. CT image anatomical landmarks which explained the greatest percentage of total variation in post-slaughter boned-off meat weight for primal shoulders, modelled using backward logistic regression.

Model name	Landmark name	Landmark code	Percent of total variation explained
Shoulder 1	7th cervical vertebrae	C7	**59.8%**
Shoulder 2	7th cervical vertebrae	C7	60.1%
	2nd thoracic vertebrae	T2	21.3%
	Sum		**81.4%**
Shoulder 3	7th cervical vertebrae	C7	60.1%
	2nd thoracic vertebrae	T2	21.3%
	1st thoracic vertebrae	T1	2.2%
	Sum		**83.5%**

Table 6. CT image anatomical landmarks which explained the greatest percentage of total variation in post-slaughter boned-off meat weight for primal rear-legs, modelled using backward logistic regression.

Model name	Landmark name	Landmark code	Percent of total variation explained
Rear-leg 1	7th sacral vertebrae	S7	**86.3%**
Rear-leg 2	7th sacral vertebrae	S7	86.3%
	1st sacral vertebrae	S1	1.5%
	Sum		**87.8%**
Rear-leg 3	7th sacral vertebrae	S7	86.3%
	1st sacral vertebrae	S1	1.5%
	4th sacral vertebrae	S4	2.2%
	Sum		**90.0%**

From the logistic regression, shoulder and rear-leg would only require two images to be captured at fixed points and virtually dissected at selected anatomical landmarks, and the loin region would require three, because of the forced inclusion of T12 (Tables 4, 5 & 6) to maximise the total variation explained, which minimising virtual dissection. As two regions, loin and shoulder, both use T2 images (Tables 4 & 5) there are only six fixed point images that need to be captured for whole joint prediction. Using this approach explains between 74 and 88% of the total variation for the individual primal regions, with the heaviest region (rear-leg) being the most accurate (Tables 4, 5 & 6). Adding a third dimension to these measures, that being length it was possible to increase the percentage of explained variation by approximately 5% with the previous fixed point CT-scanning methodology, so results should be similar for these fixed points also. The selected fixed points have a minimum of 90mm (shoulder, C7-T2), and a maximum of 420 (loin, T2-L2) between them, which should provide reasonable scope for calculating a volume.

All of the six selected anatomical landmarks are relatively simple to manually virtually dissect as shown in Appendix 1 and are shown as the following image numbers; C7 shoulder image 7, T2 shoulder or loin image 10, T12 loin images 20 and 21, L2 image 24, S1 image 32 and S7 image 38. This new fixed point methodology now needs to be validated on a new set of animals where the fixed anatomical landmark images are

collected precisely on the anatomical landmark, rather than near it at each 30mm. Another alternative method to be investigated would involve spiral scanning the whole carcass, but not virtually dissecting it, and analysing all of the images in a raw undissected form (i.e. not gutted or trimmed). If this method was successful it would remove the step which requires people to dissect the images, but may require some adjustment to greyscale gates and determination of appropriate anatomical landmarks to separate primal regions automatically.

5.4 Relationships between different virtual (CT and VIAscan®) predictions of carcass primal yields

There were strong correlations between VIAScan® predicted meat weights and post-slaughter boned-off primal meat weights (Figures 12-15). These correlations were as high as or higher than for the CT predicted meat weights with post-slaughter boned-off primal meat weights (Figures 5-8). These VIAScan® predicted meat weights, were the VIAScan® predicted yield percentage multiplied by the hot carcass weight. These high correlations contrast with correlations reported previously from the DPT, by Everett-Hincks et al. (2013), Mathias-Davis et al. (2014) and Ward et al. (2015, 2016), where it was found that when carcass weight was adjusted for, or when VIAScan® predicted yield alone was used, the correlations with boned-off primal weights were low or zero. This shows that hot carcass weight is a very important factor in explaining post-slaughter primal meat weight.
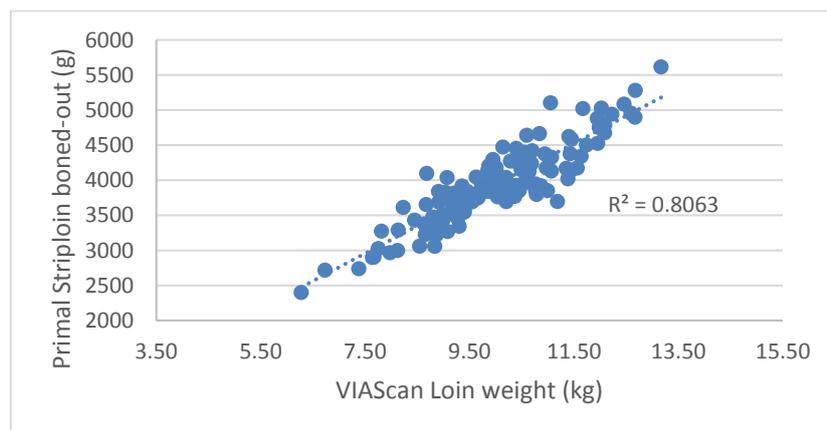
Figure 12. VIAScan® predicted loin (yield multiplied by hot carcass weight) weight (kg) vs. post-slaughter boned-off striploin weight.
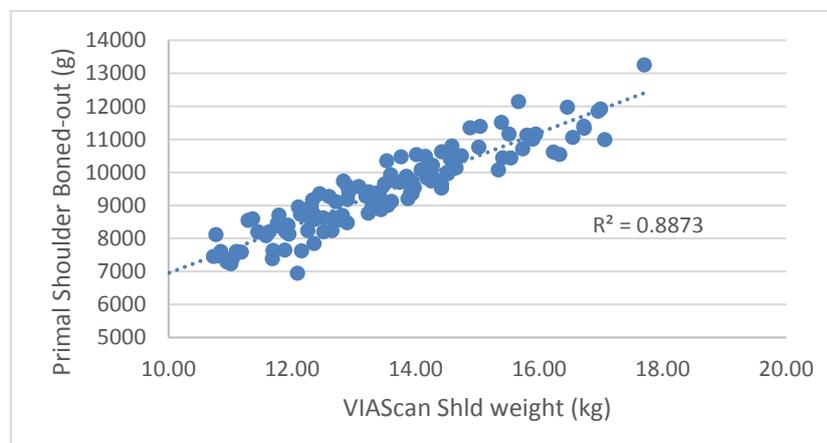
Figure 13. VIAScan® predicted shoulder (yield multiplied by hot carcass weight) weight (kg) vs. post-slaughter boned-off primal shoulder weight.
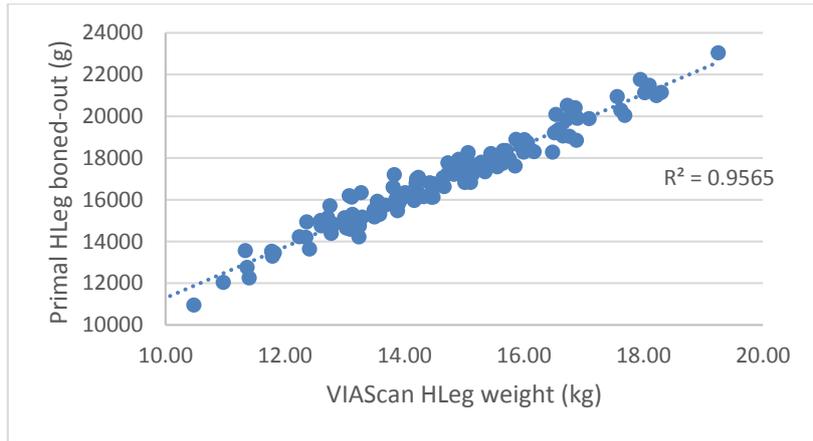
Figure 14. VIAScan® predicted hind-leg (rear-leg) (yield multiplied by hot carcass weight) weight (kg) vs. post-slaughter boned-off primal rear-leg meat weight.
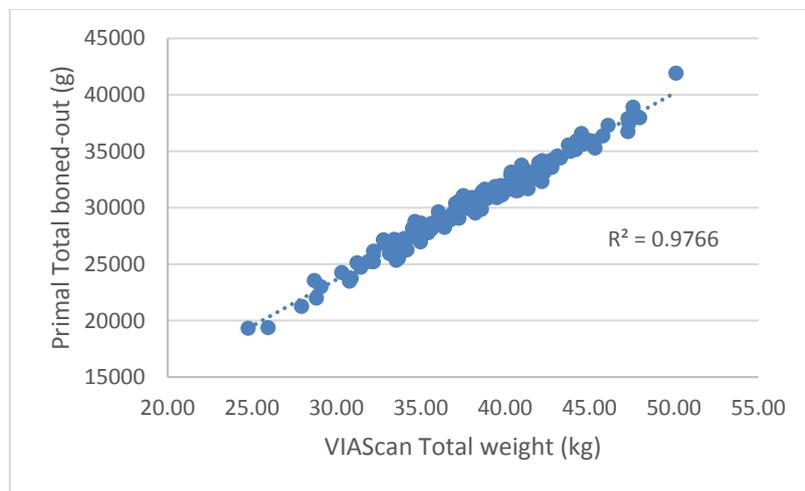
Figure 15. VIAScan® predicted total (yield multiplied by hot carcass weight) weight (kg) vs. post-slaughter boned-off total primal meat weight.

The correlations between VIAScan® predicted meat weights and CT predicted meat weights were also high and very similar to the correlations between CT predicted meat weight and boned-off meat weight (Figures 16-19). The primal of most note being the loin, which had the lowest correlation (0.66 Figure 16), which was the same as CT predicted meat weight with boned-off meat weight (0.65, Figure 5), but 0.15 lower than VIAScan® with boned-off meat (0.81, Figure 12). This VIAScan® prediction is for the entire middle of the carcass, including all of the flap (i.e. much more meat), all of which was trimmed from the CT striploin images. This is a good indication that virtual cutting error for the CT striploin, was the largest contributor to the low correlation for CT predicted meat weight with bone-out meat weight for the primal striploin relative to shoulder or rear-leg. When combined with hot carcass weight VIAScan® predictions of meat weight would be suitable for inclusion in DEERSelect meat modules alongside CT scan data, as they are well correlated with each other and boned-off meat plant. Backwards logistic regression analysis would be a useful approach to use to investigate the yield predictive potential of other measurements collected during the DPT in relation to predicting primal meat yields or weights.
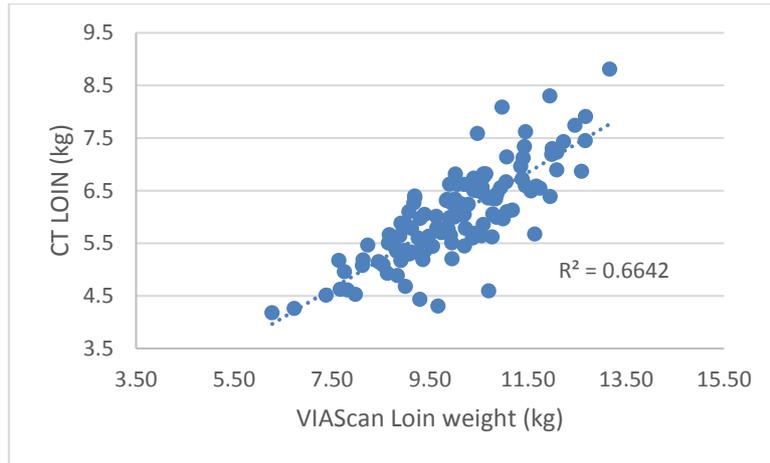
Figure 16. VIAScan® predicted loin (yield multiplied by hot carcass weight) weight (kg) vs. virtually dissected (CT predicted from 30mm slices) striploin weight (kg).
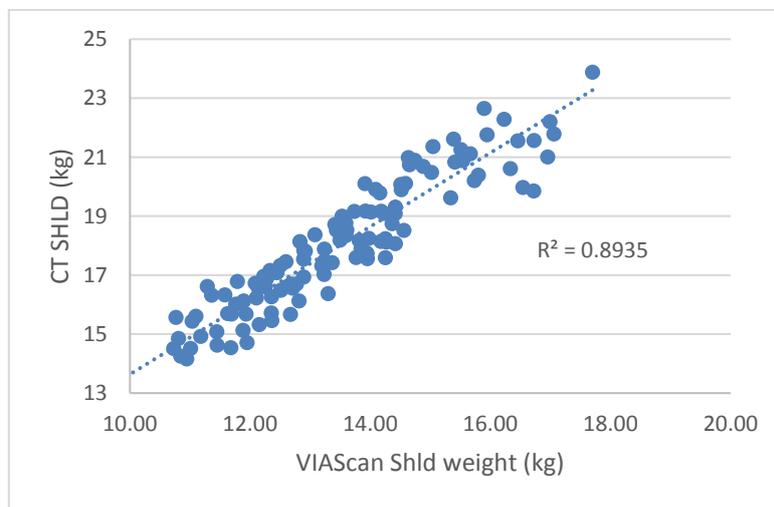
Figure 17. VIAScan® predicted shoulder (yield multiplied by hot carcass weight) weight (kg) vs. virtually dissected (CT predicted from 30mm slices) primal shoulder weight (kg).
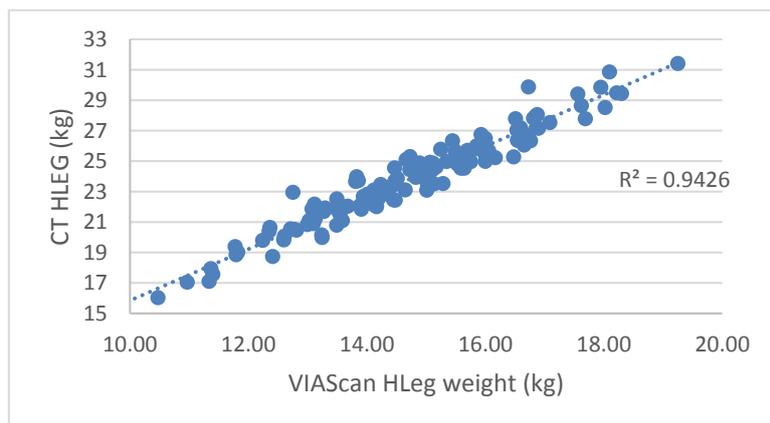
Figure 18. VIAScan® predicted hind-leg (rear-leg) (yield multiplied by hot carcass weight) weight (kg) vs. virtually dissected (CT predicted from 30mm slices) primal rear-leg weight (kg).
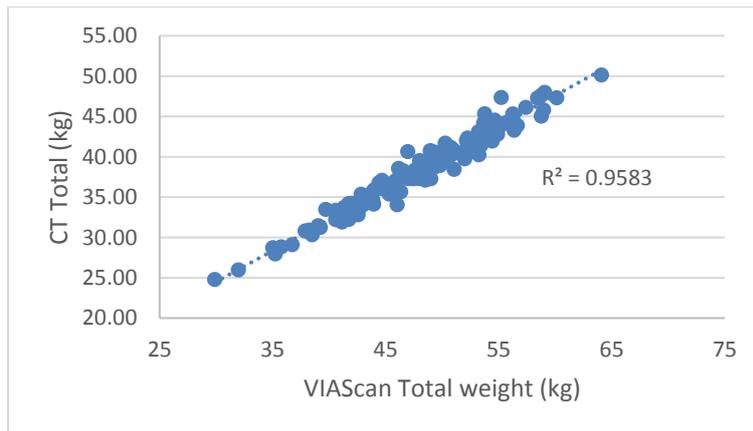
Figure 19. VIAScan® predicted total (yield multiplied by hot carcass weight) weight (kg) vs. virtually dissected (CT predicted from 30mm slices) total primal joint weight (kg).

6. RECOMMENDATIONS

- That the new six anatomical landmark fixed points be validated in a new set of progeny (e.g. DEERLink 2015-born progeny), that are CT-scanned both for 30 mm spiral scan and the six fixed points.

- That the alternative approach of whole animal non-gutted and non-trimmed prediction of yield from 30 mm spiral-scans be evaluated using the current (Invermay DPT 2013-born) dataset.

- That genetic parameters are re-estimated for the new fixed point anatomical landmark based CT predictions after more animals are CT scanned during the validation, using the same models as the DPT analyses of Ward et al. (2015, 2016).

- That DEERSelect considers the inclusion of VIAScan® meat weight data along with CT data in a modified meat module if the VIAScan® technology will continue to be used by the industry.

- That the logistic regression analysis approach be used to determine the predictive power of other measurements collected at the deer slaughter plant during the DPT, to see if any individual or combined measures may provide accurate prediction of carcass primal meat yields.

- That this report should be forwarded to the DEERSelect Manager, DEERSelect Reference Group, Alliance Group, Landcorp Farming Limited and InnerVision™, as stakeholders in this research. Wider publication should wait until the methodology has been validated in another set of animals.

7. ACKNOWLEDGEMENTS

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9. APPENDICES

Appendix 1. Trait genetic correlation sub-matrix of selected ultrasonic eye-muscle, carcass yield and venison quality traits for Deer Progeny Test rising yearling progeny, with traits analysed as bivariates using ASREML.

Heritability estimates in pink boxes on the diagonal, significant values (p≤0.05) in green, non-significant in black. Phenotypic correlations are above the diagonal (of the heritability estimates), genetic correlations below the diagonal. For all phenotypic and genetic correlations significant values (p≤0.05) are coloured: green positive correlations, orange negative correlations, black values are non-significant, missing values were not analysed in bivariate analysis or would not converge in the analysis. Correlations >1.00 have been reported to provide an indication of the direction of the correlation and potential relativity of other correlations for the same traits. These correlations >1.00 may be due to a small sample size or the type of measurement used for the traits especially discrete type variables such as those used for sensory measures.
Reproduced from Ward et al. (2016)

		10 WPreSltr	11 EMA	12 EMW	13 EMD	15 HW	16 CW	18 HotDO	19 ColdDO	29 StriploinL&R	32 PLoinL&R	33 PLoinBOMY	38 PShldrL&Rbone-in	39 PShldrL&Rboned	40 PShldrBOMY	42 RearLegL&Rbone-in	44 PLegL&Rboned	45 PLegBOMY	48 TotalBonedP	49 TotalPBOMY	57 CTFAT	58 CTLEAN	59 Ctfat+lean	60 CTEMW	61 CTEMD	62 CTEMA	63 CTSHFAT	64 CTSHLEAN	65 CTSHfat+lean	66 CTLNFAT	67 CTLNLEAN	68 CTLNfat+lean	69 CTLGFAT	70 CTLGLEAN	71 CTLGfat+lean
10	WPreSltr	0.53	-0.05	-0.03	-0.03	0.97	0.96	.	.	-0.45	-0.49	-0.48	-0.18	-0.41	-0.40	-0.33	-0.52	-0.51	-0.70	-0.68	-0.05	-0.44	-0.44	-0.43	-0.31	-0.41	-0.04	-0.31	-0.33	-0.10	-0.47	-0.48	-0.10	-0.14	-0.14
11	EMA	-0.14	0.42	0.65	0.66	0.14	0.15	0.25	0.26	0.40	0.37	0.36	-0.02	0.05	0.05	-0.02	0.06	0.06	0.21	0.20	-0.05	0.29	0.28	0.13	0.34	0.43	-0.10	0.13	0.12	-0.06	0.35	0.34	-0.03	0.07	0.06
12	EMW	-0.38	0.80	0.22	0.40	0.09	0.09	0.15	0.16	0.24	0.22	0.22	-0.03	0.02	0.01	-0.02	0.02	0.03	0.11	0.11	0.04	0.09	0.10	0.15	0.13	0.20	-0.03	0.07	0.06	0.01	0.10	0.10	0.01	-0.01	-0.01
13	EMD	-0.25	0.95	0.66	0.47	0.16	0.16	0.25	0.26	0.33	0.29	0.28	-0.06	0.04	0.04	0.06	0.13	0.14	0.23	0.23	0.02	0.16	0.16	0.12	0.28	0.38	-0.02	0.05	0.05	0.02	0.28	0.28	0.03	0.01	0.01
15	HW	0.97	0.16	-0.10	0.02	0.58	.	0.03	0.03	-0.01	-0.01	0.00	0.01	0.03	0.03	0.02	0.01	0.01	0.00	0.00	-0.09	0.49	0.48	0.08	0.26	.	-0.17	0.54	0.54	-0.18	0.26	0.25	-0.20	0.35	0.33
16	CW	0.97	0.18	-0.07	0.03	.	0.59	.	.	.	.	.	.	.	.	.	.	.	.	.	0.01	0.51	0.51	0.05	0.34	.	-0.07	0.51	0.52	-0.11	0.32	0.31	-0.11	0.37	0.35
18	HotDO	.	0.46	0.49	0.47	0.17	.	0.51	.	0.14	0.16	0.16	0.07	0.16	0.16	0.13	0.19	0.18	0.29	0.28	-0.09	0.46	0.44	0.22	0.27	0.30	-0.10	0.43	0.43	-0.11	0.34	0.33	-0.12	0.21	0.20
19	ColdDO	.	0.52	0.57	0.51	0.18	.	.	0.49	0.17	0.18	0.18	0.15	0.22	0.22	0.19	0.25	0.25	0.38	0.37	-0.05	0.49	0.47	0.22	0.33	0.36	-0.06	0.42	0.42	-0.08	0.39	0.38	-0.08	0.22	0.21
29	StriploinL&R	-0.45	0.82	0.77	0.75	-0.05	.	0.08	0.09	0.63	0.95	0.94	-0.17	-0.08	-0.08	-0.04	0.06	0.06	0.39	0.38	-0.16	0.12	0.09	0.20	0.38	0.43	-0.10	-0.01	-0.02	-0.20	0.43	0.41	-0.20	-0.11	-0.13
32	PLoinL&R	-0.54	0.73	0.68	0.67	-0.05	.	0.17	0.19	0.97	0.52	.	-0.17	-0.08	-0.08	0.00	0.08	0.09	0.42	0.41	-0.19	0.13	0.09	0.20	0.28	0.34	-0.14	0.03	0.01	-0.20	0.38	0.36	-0.22	-0.09	-0.11
33	PLoinBOMY	-0.55	0.71	0.67	0.64	-0.07	.	0.19	0.21	0.96	.	0.52	-0.17	-0.07	-0.07	0.01	0.09	0.10	0.43	0.43	-0.19	0.13	0.09	0.21	0.28	0.33	-0.15	0.03	0.01	-0.20	0.38	0.36	-0.23	-0.09	-0.12
38	PShldrL&Rbone-in	-0.20	-0.13	0.08	-0.16	0.03	.	0.30	0.32	-0.31	-0.30	-0.27	0.59	0.79	0.78	-0.20	-0.17	-0.17	0.24	0.24	0.09	0.11	0.13	-0.05	0.04	.	0.12	0.33	0.36	0.04	-0.01	-0.01	0.10	0.02	0.03
39	PShldrL&Rboned	-0.32	-0.05	0.03	-0.05	0.12	.	0.30	0.36	-0.13	-0.08	-0.07	0.91	0.76	.	-0.02	0.08	0.08	0.54	0.53	0.10	0.12	0.13	0.00	0.09	.	0.12	0.33	0.36	0.04	.	0.01	0.12	0.01	0.02
40	PShldrBOMY	-0.31	-0.04	0.05	-0.04	0.12	.	0.30	0.36	-0.13	-0.08	-0.07	0.90	.	0.75	-0.01	0.08	0.08	0.54	0.54	0.10	0.12	0.14	0.00	0.10	.	0.12	0.33	0.36	0.04	0.02	0.02	0.12	0.02	0.03
41	PShldrMBRatio	-0.66	0.34	0.54	0.47	-0.08	.	0.35	0.47	0.32	0.35	0.34	0.44	0.76	0.78	0.17	0.27	0.27	0.57	0.56	0.06	0.09	0.10	0.06	0.16	0.16	0.03	0.17	0.18	0.02	0.07	0.07	0.08	-0.01	0.00
42	RearLegL&Rbone-in	-0.31	-0.14	-0.16	-0.04	0.18	.	0.35	0.37	-0.16	-0.12	-0.15	-0.33	-0.11	-0.08	0.38	0.91	0.90	0.64	0.65	-0.16	0.10	0.07	0.07	0.06	0.07	-0.17	-0.10	-0.13	-0.10	0.01	0.00	-0.16	0.14	0.13
44	PLegL&Rboned	-0.59	-0.03	-0.07	0.10	0.12	.	0.39	0.43	-0.08	-0.04	-0.06	-0.19	0.15	0.17	0.88	0.35	.	.	.	-0.01	0.18	0.18	0.09	0.20	0.21	-0.08	0.03	0.02	0.02	0.14	0.14	-0.07	0.11	0.10
45	PLegBOMY	-0.62	-0.01	-0.02	0.12	0.08	.	0.41	0.45	-0.06	-0.02	-0.04	-0.21	0.15	0.17	0.87	.	0.32	0.77	.	-0.03	0.20	0.19	0.11	0.21	0.23	-0.11	0.06	0.05	0.01	0.14	0.14	-0.08	0.11	0.10
48	TotalBonedP	-0.78	0.34	0.43	0.46	0.04	.	0.59	0.66	0.34	0.39	0.39	0.37	0.69	0.70	0.45	.	0.71	0.48	.	-0.05	0.25	0.24	0.16	0.33	0.36	-0.05	0.24	0.24	-0.08	0.30	0.29	-0.09	0.00	0.00
49	TotalPBOMY	-0.78	0.33	0.46	0.44	-0.02	.	0.61	0.67	0.35	0.40	0.41	0.36	0.69	0.70	0.43	.	.	.	0.47	-0.07	0.27	0.25	0.18	0.34	0.36	-0.08	0.26	0.25	-0.09	0.31	0.30	-0.11	0.01	0.00
57	CTFAT	-0.11	-0.52	0.08	-0.58	-0.38	-0.28	-0.80	-0.83	-0.45	-0.41	-0.44	0.31	0.28	0.30	-1.06	-0.61	-0.60	-0.40	-0.38	0.24	-0.07	0.13	-0.15	-0.01	0.03	.	-0.11	0.02	0.89	-0.03	0.05	0.85	-0.01	0.07
58	CTLEAN	-0.31	0.37	0.08	0.15	0.68	0.69	0.35	0.29	0.03	0.00	-0.01	0.08	-0.14	-0.11	-0.20	-0.46	-0.47	-0.34	-0.36	-0.15	0.25	0.98	0.23	0.44	.	-0.13	0.58	0.58	-0.03	0.59	0.59	0.08	0.76	0.75
59	Ctfat+lean	-0.31	0.23	0.10	0.02	0.65	0.66	0.06	-0.04	-0.07	-0.10	-0.11	0.14	-0.11	-0.07	-0.40	-0.60	-0.60	-0.45	-0.47	0.04	0.98	0.25	0.20	0.44	.	0.04	0.56	0.58	0.15	0.58	0.59	0.25	.	0.76
60	CTEMW	-0.40	0.81	0.43	1.01	0.43	0.43	0.53	0.62	0.39	0.44	0.45	0.05	0.01	-0.01	0.18	0.27	0.23	0.48	0.46	0.11	0.21	0.24	0.20	0.07	0.44	-0.21	0.15	0.12	-0.11	0.35	0.34	-0.21	0.07	0.05
61	CTEMD	-0.71	0.60	0.09	0.28	-0.29	-0.13	-0.24	-0.20	0.85	0.77	0.74	-1.83	-0.94	-0.94	0.10	-0.07	-0.05	-0.14	-0.15	-0.28	0.29	0.22	-1.29	0.28	0.80	-0.05	0.14	0.14	-0.01	0.72	0.72	0.00	0.10	0.10
62	CTEMA	-0.92	0.73	-0.12	0.82	.	.	-0.13	0.03	1.20	1.27	1.25	.	.	.	-0.21	-0.21	-0.22	-0.08	-0.15	-0.56	.	.	-1.98	0.95	0.07	-0.02	.	.	0.01	0.84	.	0.01	0.10	0.10
63	CTSHFAT	-0.18	-0.58	-0.15	-0.56	-0.53	-0.44	-0.79	-0.79	-0.71	-0.70	-0.70	0.58	0.42	0.42	-0.98	-0.64	-0.65	-0.44	-0.44	.	-0.23	-0.03	-0.01	-0.53	-0.97	0.24	-0.28	-0.13	0.61	-0.06	-0.01	.	0.01	0.08
64	CTSHLEAN	-0.08	-0.16	-0.04	-0.11	0.66	0.64	0.53	0.50	-0.03	0.05	0.05	0.56	0.69	0.71	-0.02	0.01	0.02	0.52	0.53	-0.10	0.20	0.16	-0.59	-0.18	.	-0.18	0.49	.	-0.02	0.21	.	-0.03	0.18	0.17
65	CTSHfat+lean	-0.10	-0.20	-0.07	-0.16	0.63	0.62	0.45	0.42	-0.11	-0.03	-0.03	0.64	0.74	0.76	-0.10	-0.04	-0.04	0.49	0.50	0.01	0.22	0.18	-0.60	-0.24	.	-0.07	.	0.51	0.08	0.20	0.21	0.08	0.19	0.19
66	CTLNFAT	0.21	-0.43	0.38	-0.60	-0.23	-0.13	-0.81	-0.89	-0.31	-0.29	-0.32	0.19	0.06	0.10	-1.07	-0.82	-0.78	-0.61	-0.56	0.97	0.31	0.51	0.26	0.20	-0.18	1.30	0.14	0.25	0.17	-0.01	0.08	0.73	-0.02	0.05
67	CTLNLEAN	-0.54	0.72	-0.01	0.49	-0.01	0.09	-0.04	0.07	0.80	0.81	0.81	-0.73	.	-0.69	-0.05	-0.20	-0.21	-0.07	-0.09	-0.48	0.41	0.26	0.44	0.89	1.09	-0.73	-0.52	-0.60	-0.08	0.46	.	-0.08	0.16	0.14
68	CTLNfat+lean	-0.53	0.70	0.02	0.45	-0.02	0.08	-0.10	-0.01	0.79	0.81	0.80	-0.70	-0.70	-0.67	-0.11	-0.25	-0.25	-0.12	-0.14	-0.42	0.44	0.46	0.90	.	.	-0.67	.	-0.58	-0.02	.	0.45	-0.01	0.15	0.15
69	CTLGFAT	-0.10	-0.47	-0.01	-0.48	-0.40	-0.35	-0.78	-0.83	-0.48	-0.50	-0.55	0.13	0.12	0.14	-0.81	-0.65	-0.67	-0.52	-0.53	0.98	-0.12	0.07	-0.28	-0.31	-0.66	.	-0.07	0.04	0.90	-0.53	-0.49	0.51	0.20	0.29
70	CTLGLEAN	0.36	-0.07	0.26	-0.02	0.64	0.64	-0.06	-0.27	-0.52	-0.63	-0.63	0.11	-0.20	-0.19	-0.29	-0.59	-0.61	-0.74	-0.75	0.35	0.67	.	0.64	-0.15	-4.95	0.50	-0.30	-0.26	0.46	0.05	0.09	0.39	0.42	.
71	CTLGfat+lean	0.36	-0.14	0.25	-0.08	0.61	0.61	-0.22	-0.45	-0.56	-0.66	-0.67	0.12	-0.19	-0.17	-0.37	-0.66	-0.68	-0.78	-0.79	0.44	0.64	0.72	0.60	-3.08	0.57	-0.19	-0.32	-0.26	0.54	-0.03	0.02	0.48	.	0.44

Appendix 2. Standard Operating Procedure for DPT 2013-born CT scan images. Gutting and cutting/selecting primal joints using Alliance Group Ltd Makarewa DSP Primal joint cutting specifications.

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CT images are used to determine the amount of lean tissue (meat), fat and bone in a carcass. This is determined by greyscale, i.e. black is air, dark grey is fat, grey is lean and white is bone. When selecting primal components consider the relevant components that will contribute to the final primal cuts, i.e. bone but not marrow can be left in primal loin images as it will be ignored, but bone needs to be accurately cut in carcass, primal leg and shoulder images as it forms part the total weight we have collected on the same cuts in the deer slaughter plant (DSP).

The CT image selection is intended to provide us with two different sets of data. The first a full gutted carcass breakdown if all lean, fat and bone. This why the images are being gutted as a first step. This will be compared with hot carcass weights and VIAscan® predictions, it will also inform us how much of the total lean is contributed by the primal cuts.

The second is the primal cuts as they were boned off the carcass is the DSP. This provides us a more accurate breakdown of the components, as we do not differentiate lean and bone from our in plant boned-out weights and bones is only estimated by subtraction from bone in weights.

Selected images are to be cut and/or copied into their appropriate sub folders for shoulders (SHLD), loins/middles (MIDDLE) and rear legs (HLEG). After all images are be grouped to the appropriate folder they can then be gutted and saved as primal gutted images, then finally selected or trimmed as the primal cuts as per cutting specifications.

Shoulders and necks
Bone in shoulder primal cut is to be cut as is standard for Alliance: shoulder, breast, neck and flap to be removed forward of the 6th thoracic vertebrae (note this includes nuchal ligament (paddywhack)). Specification: mark centre of sternum bone, identify the 6th and 7th rib counting from neck end, mark on top 6th rib to top of scapula bone. Fleece meat from frame, separate primal shoulder from striploin at the top of the 2nd rib at the shoulder end, fleece neck.

This is also essentially the CT shoulder cut specification for DEERSelect.

<u>Boneless shank on shoulder</u> specification: Complete neck and breast meat to be removed, followed by removal of radius, ulna, humerous and scapula bones. Some minor trim maybe require to remove heavy gristle (e.g. nuchal ligament (paddywhack)), blood or fat etc.

Selecting CT images for the shoulder primal

The key landmark for the shoulder primal is the 6th thoracic vertebrae (TV). Unfortunately this is not easy to discern in transverse CT images. The deer were positioned as such for CT scanning that the posterior tip of the scapula is a suitable landmark for this primal joint. So all images to be selected for primal shoulders will be the first image with any sign of scapula and all those anterior (forward) of that

point. As will all image selection check images anterior and posterior (rear) after your selected image to ensure there is obvious scapula and no-scapula respectively.

Figure 1. Three sequential CT images from animal #1/13 from anterior to posterior showing differentiation points for shoulder primal start at image 16, scapulas arrowed

| Image 15 obvious scapula bottom, faint top 2nd shoulder image | Image 16 faint scapula first shoulder image | Image 17 no scapula first last loin image (at 6-7th TV) extra shoulder images added |

When gutting and primal selecting images think about how a butcher would be cutting the carcass. Components gutted out are mostly loosely attached to the carcass, but meat needs to be cut off, so some is always left attached to the bones or ligaments. Think about the shape of the carcass as you move through images, as some images will not show the likes of ribs when the previous image did. With the likes of the rib cage, it is a oval shape that is very defined for the butchers to cut the primal shoulder off. When removing the primal shoulders, butchers do not get all of the meat with the shoulder the intercostal muscles (between the ribs), are generally bones out after the shoudler is removed. Butchers usually work their knives with smooth sweeping motions, so cuts even off bones do not always perfectly follow the bone contours. Black areas (i.e. air) in the gut cavity do not need to be removed as black is ignored by image interpretation to fat lean and bone components.

These selections and tracings have been made freehand in a single sweep and a not perfect, but should provide a clear indication of the intended path of cuts. In the interests of speed the CT bed and restraint buckles etc have not been removed from these demonstration images.

Remember these animals are very different sizes, the smallest is almost half the weight of the largest, so some animal will have diffent numbers of images and the landmarks for primal grouping are not always going to be at the same image number.

All of the cut and gutted images can be found at DeerCTScan:\CT Images\Jamie demos, and are good visualised moving though using 'Preview' (Windows Photo Viewer).

Shoulder CT images showing gutting (inside green shapes) and primal bone out selection (either inside pink areas retained, or alternatively inside hatched pink areas removed.)
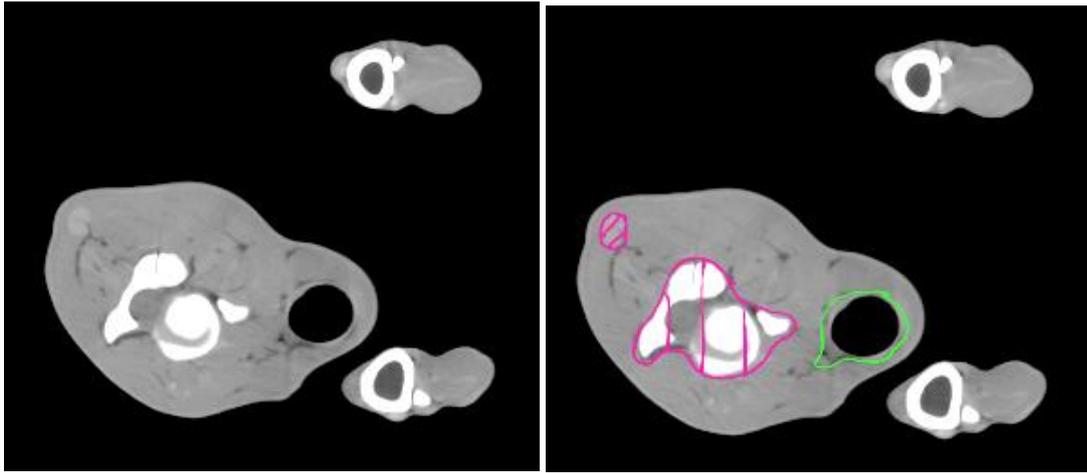
Image 1. Neck and hocks (fore-shanks), gut: remove trachea and oesophagus (if visible). Primal: remove nuchal ligament and cervical vertebrae, retain bone marrow
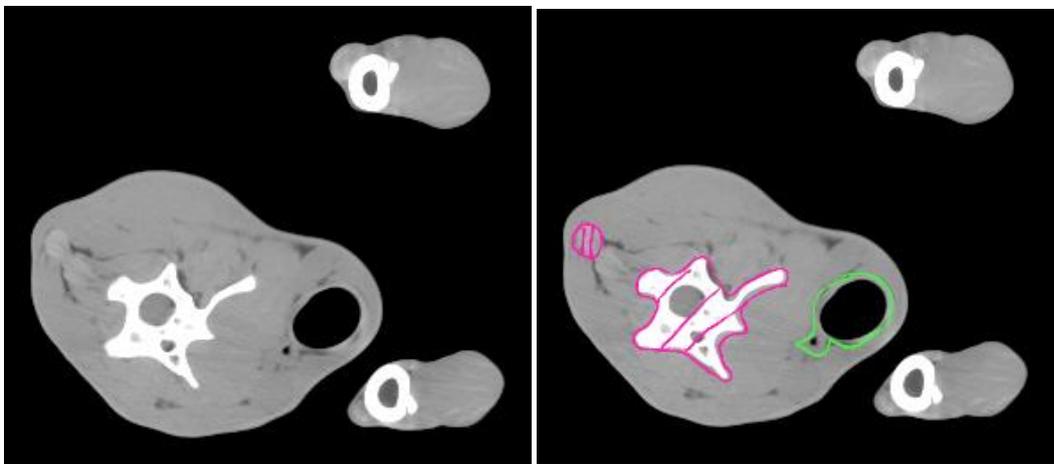
Image 2. Same as for image 1.
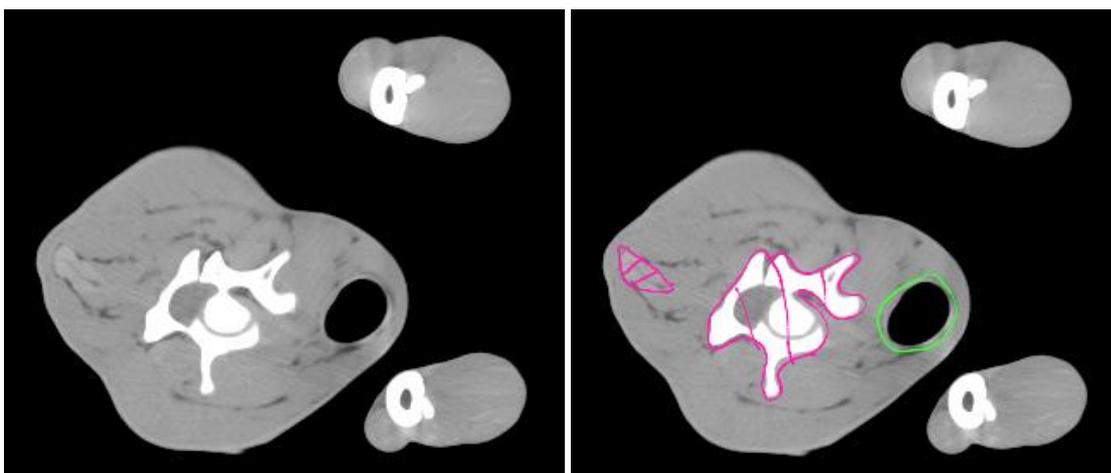
Image 3. Same as images 1 and 2.
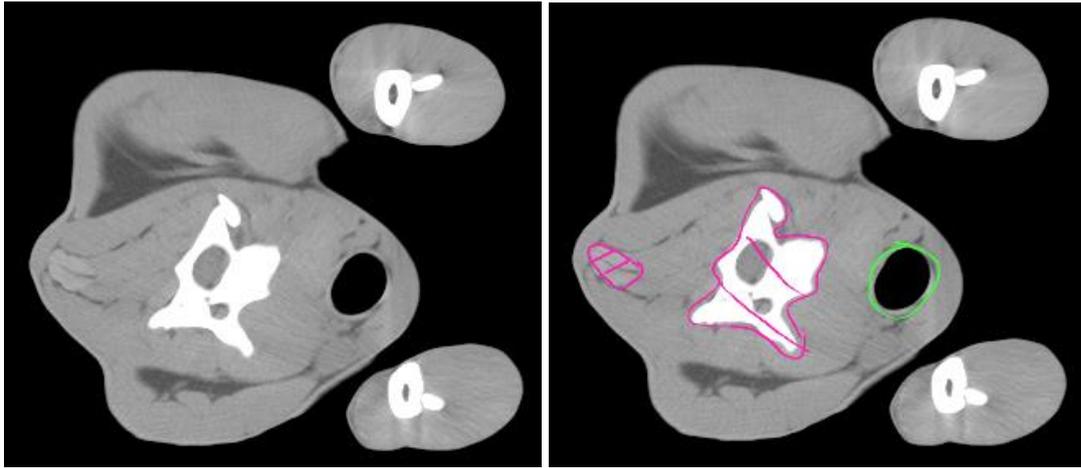
Image 4. Same as previous 3
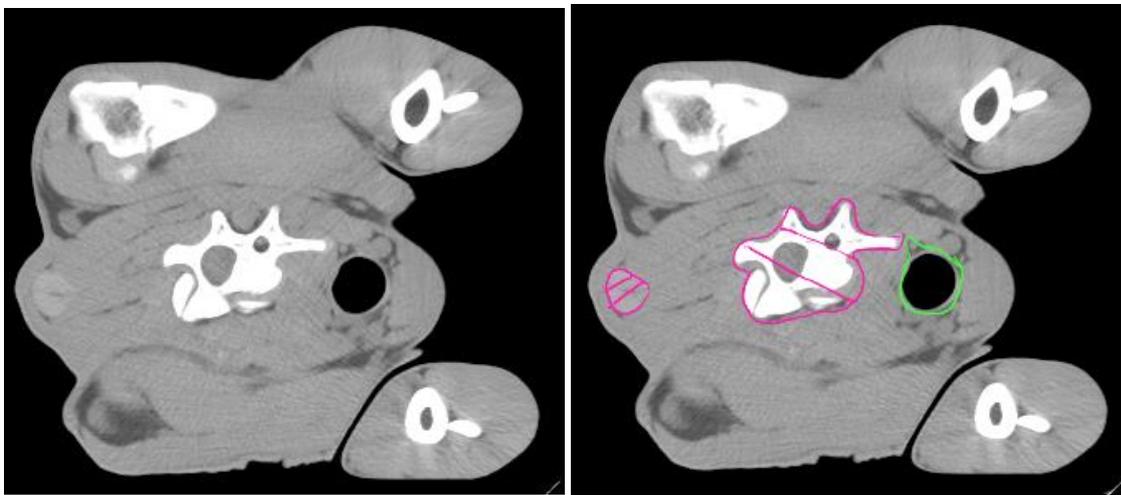
Image 5. Same as previous 4 oesophagus or artery may be visible to gut out
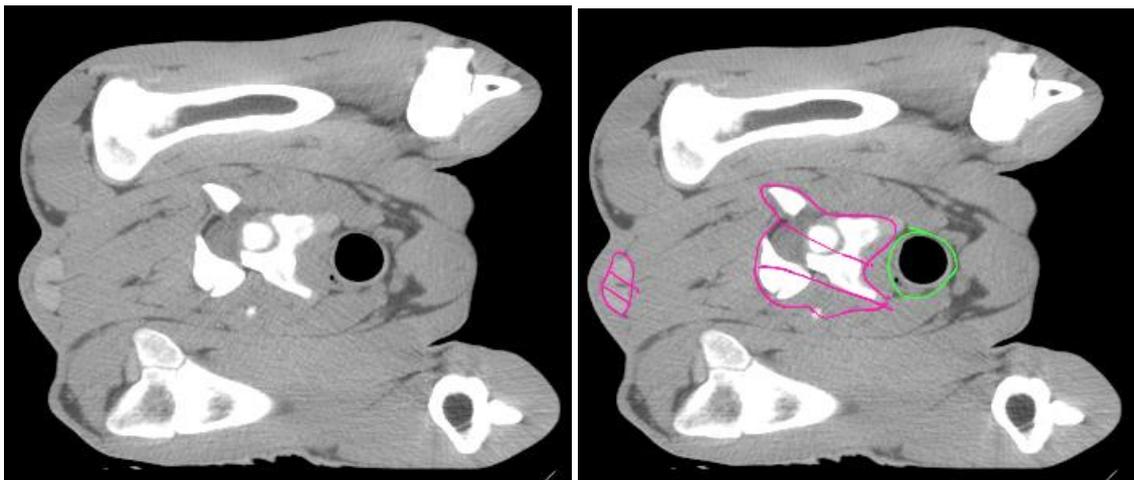
Image 6. Same as previous 5
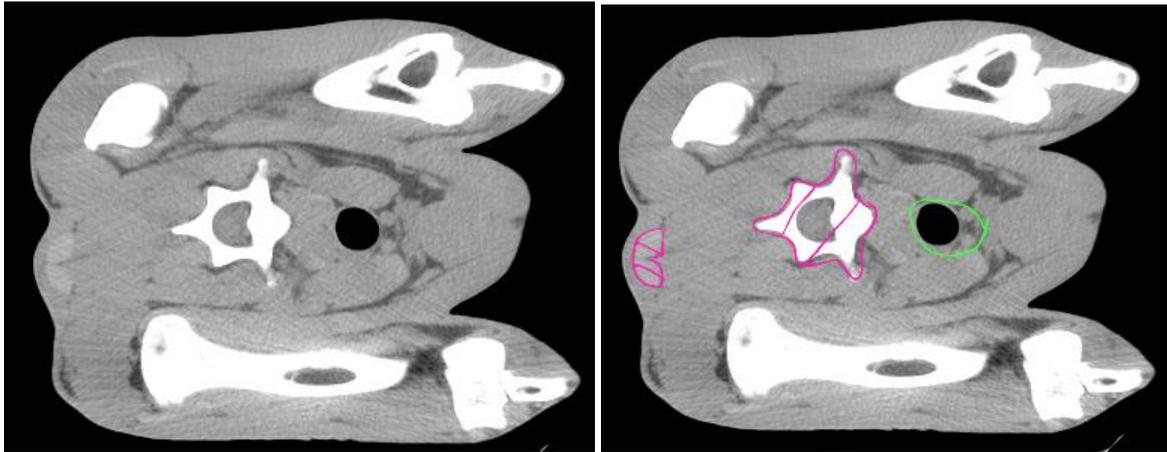
Image 7. Same as previous 6
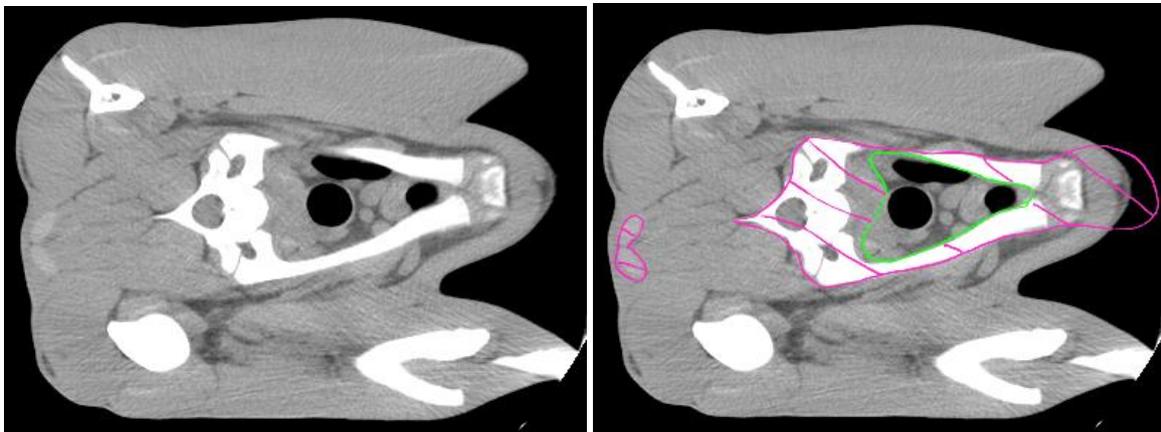
Image 8. Ribs and sternum now visible. Gut: inside ribs, leaving longus colli muscle. Primal: remove nuchal ligament, thoracic vertebrae, ribs sternum and brisket (in line with sternum). Ideally the lower bone would be painted in white where is has been cut off by the CT.
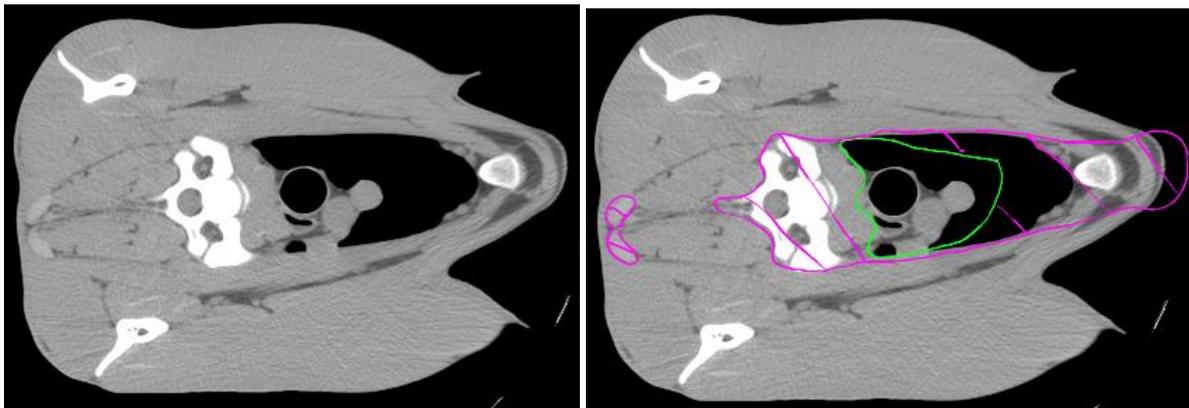
Image 9. Same as for image 8, last image before rib cage and loin removal
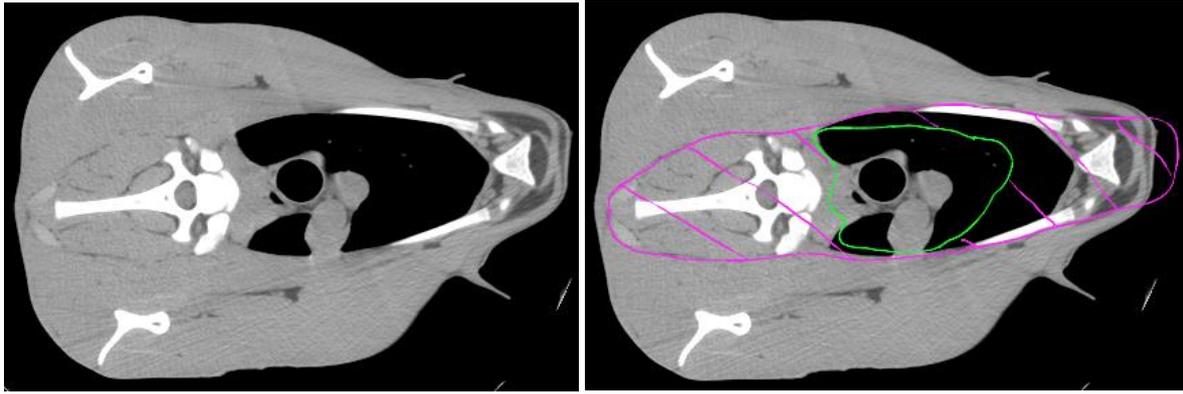
Image 10. First image with thoracic vertebrae. Striploin and nuchal ligament removed and rest as for image 9.
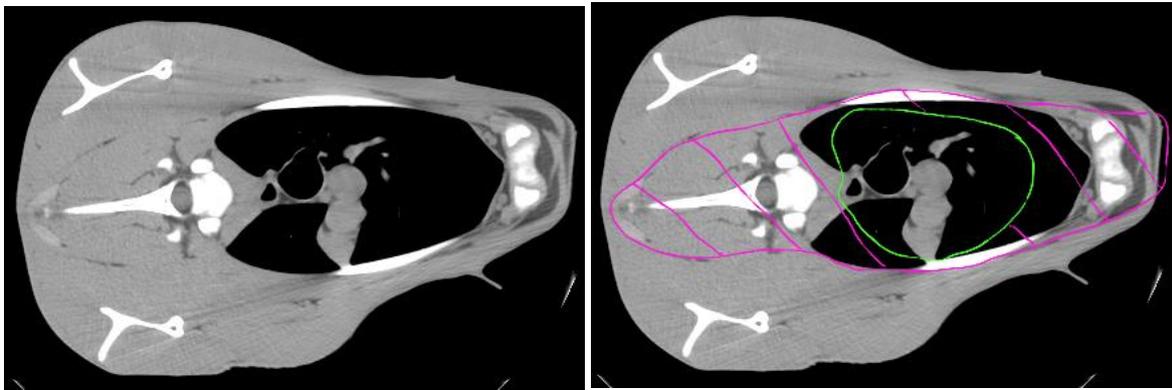
Image 11. Same as image 10, extend the loin cut smoothly to where vertebrae wings would be.
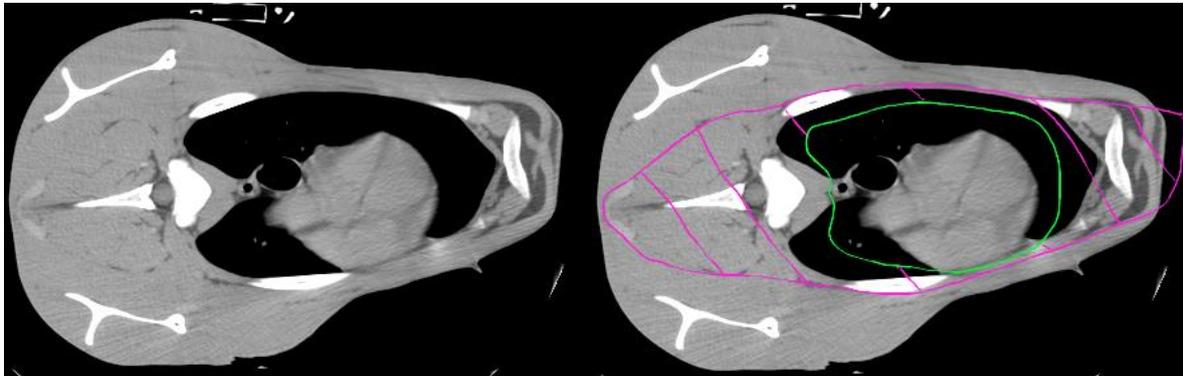
Image 12. Same as previous
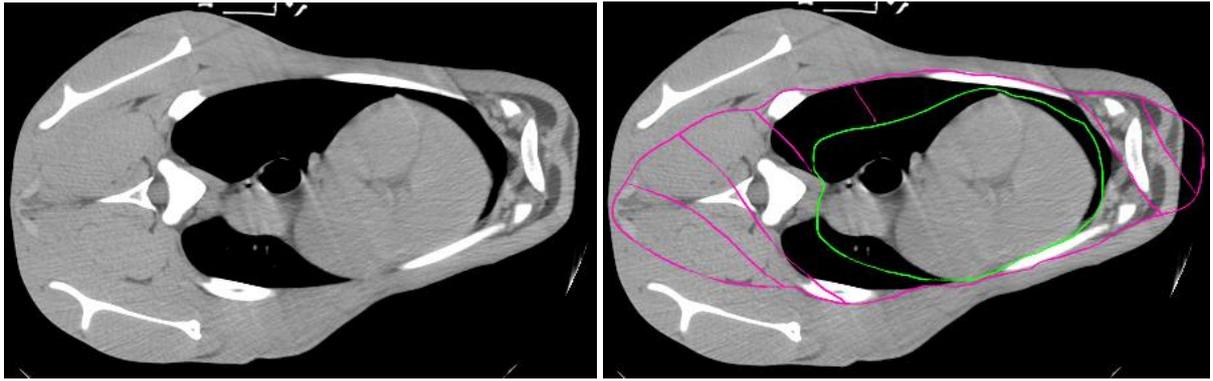
Image 13. Same as previous
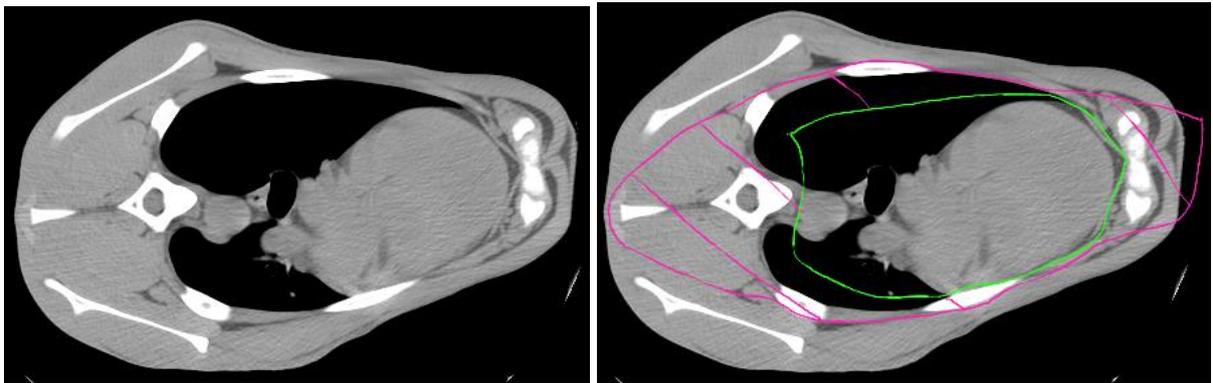
Image 14. Same as previous
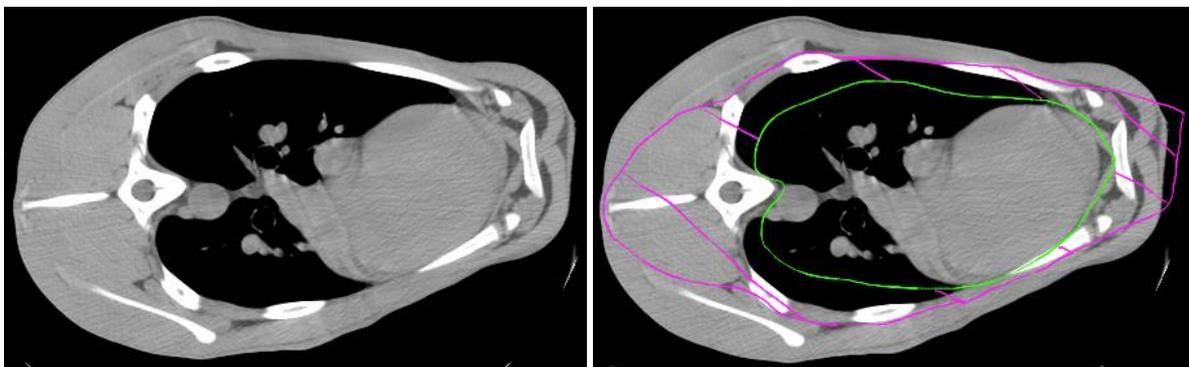
Image 15. Same as previous
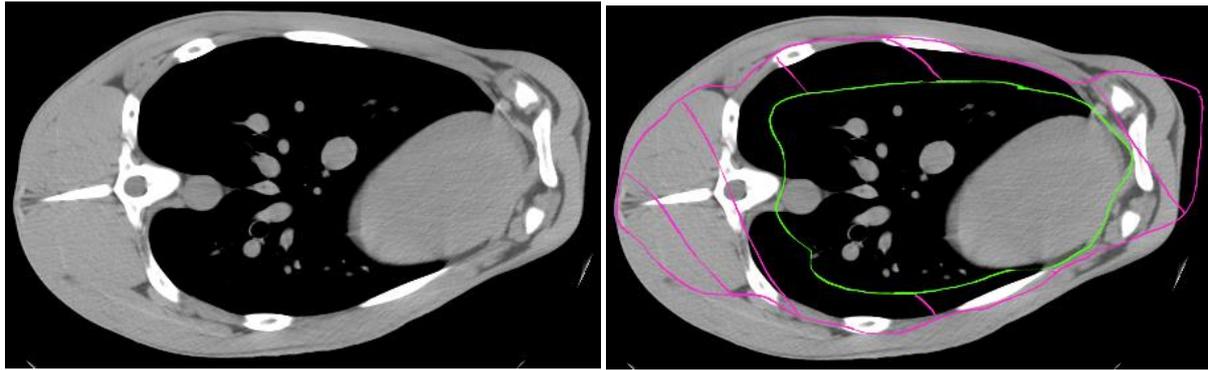
Image 16 final shoulder image, note faint scapula landmark. Gut and primal same as previous

Primal loins – Striploin and tenderloin DPT, (striploin only DEERLink)

All primal striploins should be weighed cap and silverskin on, the nuchal ligament is to be trimmed from the striploin. The striploins are to be removed forward of the tip of the ilium to the 2th thoracic vertebra. Specification: 11 rib striploin: cut directly under point of ilium (H-Bone) - right angles to vertebrae. Mark down either side spinal column remove entire loin.

Tenderloins (DPT only) are to be removed in one piece from the ventral surface of the lumbar vertebrae and the lateral surface of the ilium **Tenderloins are to be trimmed of fat and the M psoas minor (side strap) removed.**

Note we are not including the tenderloins in the primal loin for CT image analysis, as it is has a low heritability and because it is much smaller than the striploin contributes little to a total (strip + tenderloin) primal.

All striploins are to be weighed individually, with the cap and silverskin on, but the nuchal ligament (paddywhack) trimmed off.

All of the rest of the middle e.g. essentially flap are trimmed separately and are not included as part of the high value primal cut.

Selecting CT images for the loin (middles) from shoulder primal images

The key landmark for the loin within shoulder primal is the 2th thoracic vertebrae. Once again this is not easy to determine from transverse images. The defining landmark to locate is the final image with rib showing. The thoracic vertebrae itself should also be distinctive by its shape and the large dorsal ridge of the vertebrae may also be obvious as shown in figure two. Scapula should be decreasing in size and the dorsal tips will almost be quite small. In the images below in figure 2 as we can see prominent dorsal ridges on the TV it is likely these are TV1 and TV2, so the area we want is between, so we err on the side of extra loin.

Figure 2. Three sequential CT images from animal #1/13 from anterior to posterior showing differentiation points of loin primal end at image 10, ribs green arrows, scapula blue arrows, TV ridge orange arrow
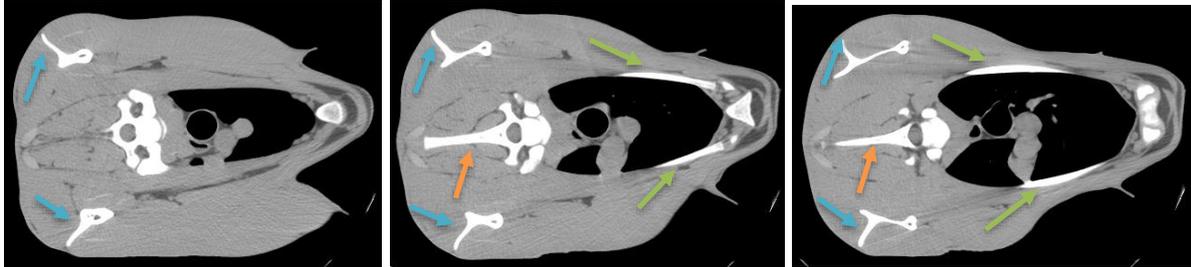
Image 9 no ribs scapula dorsal tips tiny not middles

Image 10 ribs, TV dorsal ridge, scapula small dorsal tips, end /last middles image

Image 11 ribs, TV dorsal ridge scapula obvious dorsal tips, not end/last middles image

Middle (or loin) CT images showing gutting (inside green shapes) and primal bone out retained selection (inside pink areas), pasted as a new image. The primal striploin is boned off the carcass so bone can be left in the primal image as it only fat and lean will be used in further analysis.

If you prefer the loin selection can be cut from the shoulder images and pasted to middles as a new image at that point.
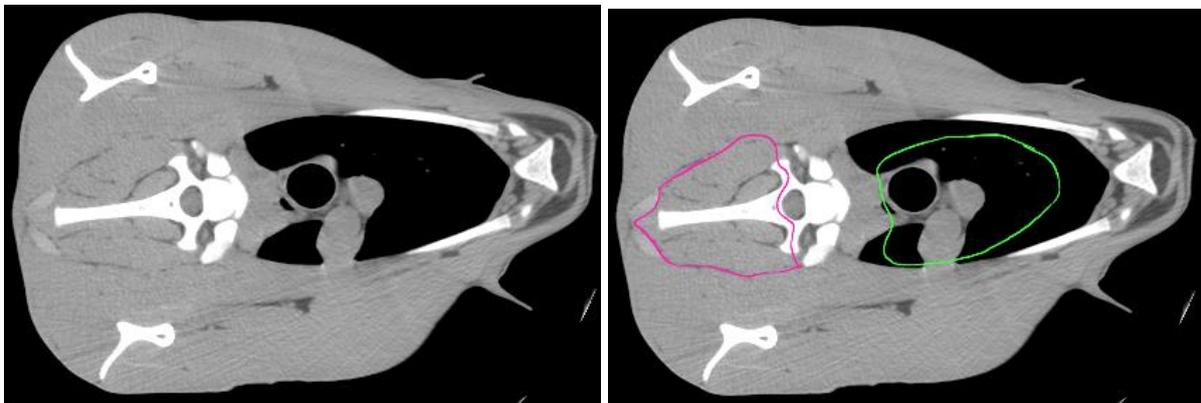
Image 10. Exclude the bone marrow, as loins are cut off the carcass.
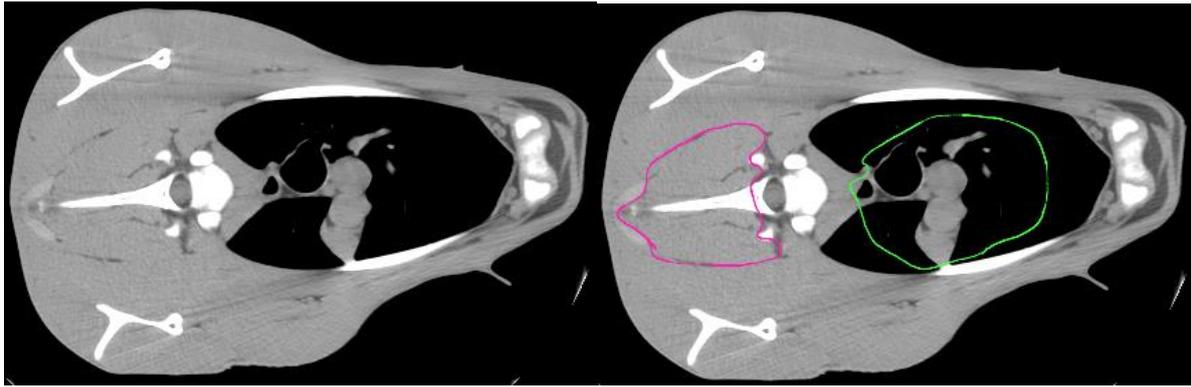
Image 11.
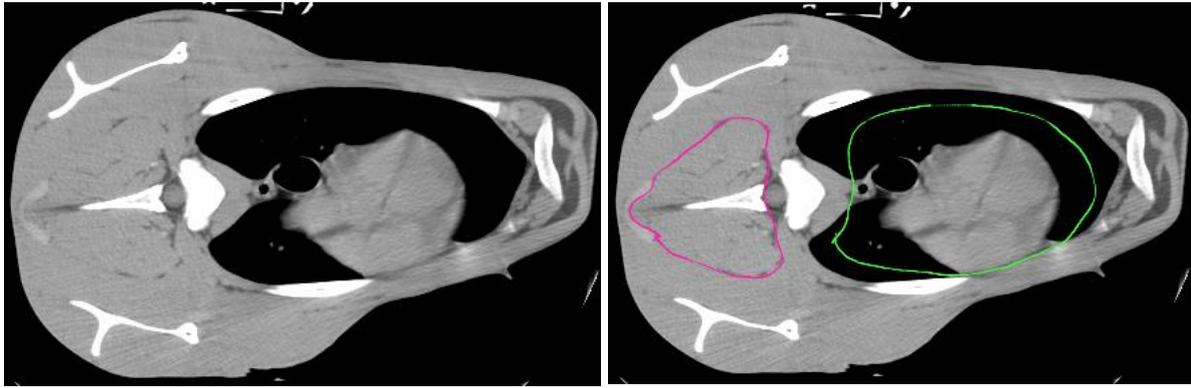
Image 12.
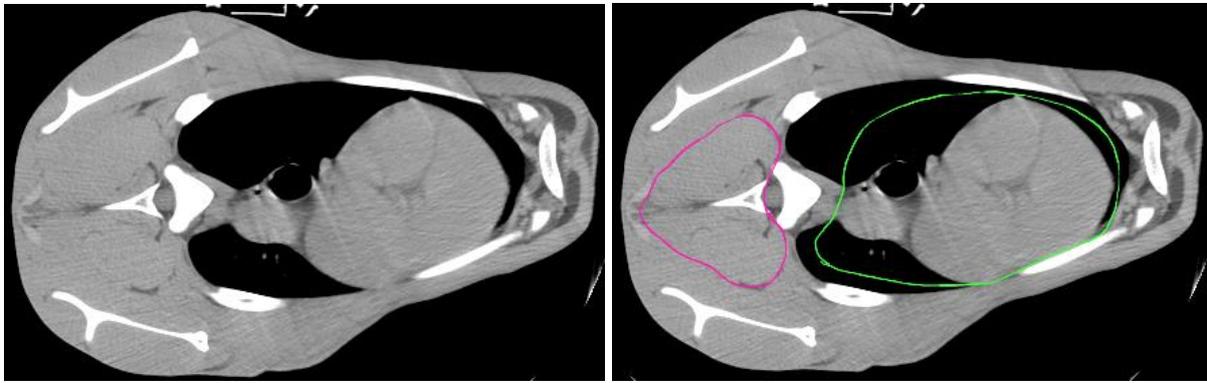
Image 13.
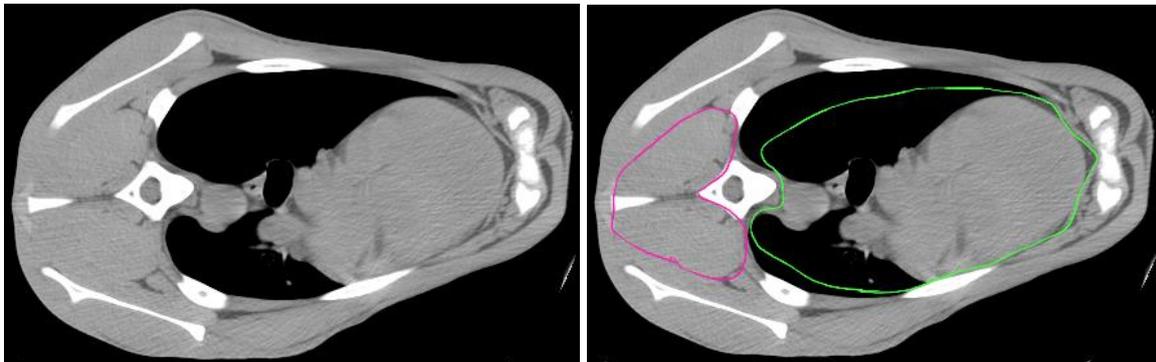
Image 14.
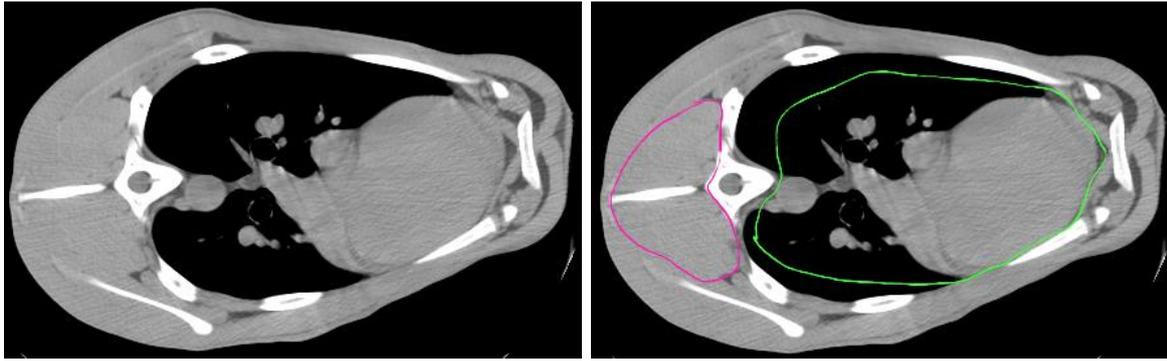
Image 15.
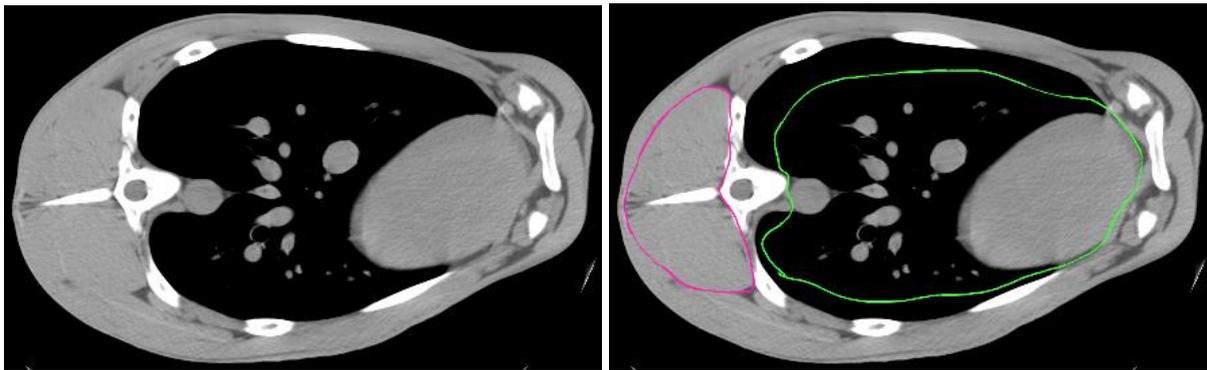
Image 16.
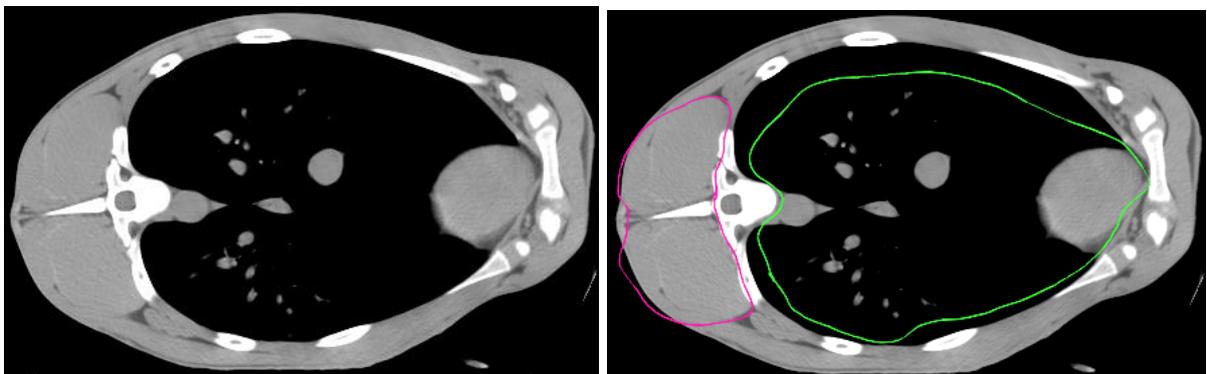
Image 17. First of the loin images beyond the shoulder. Don't worry about removing nuchal ligament beyond this point. Otherwise same as previous.
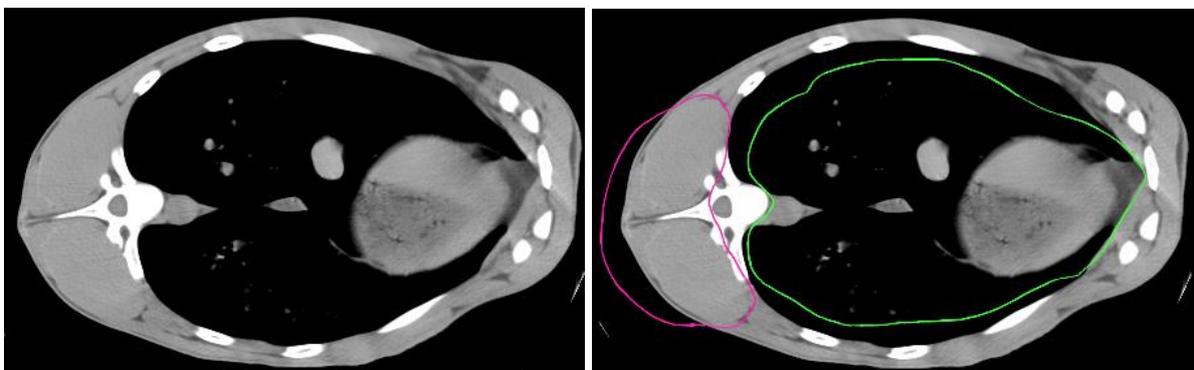
Image 18.
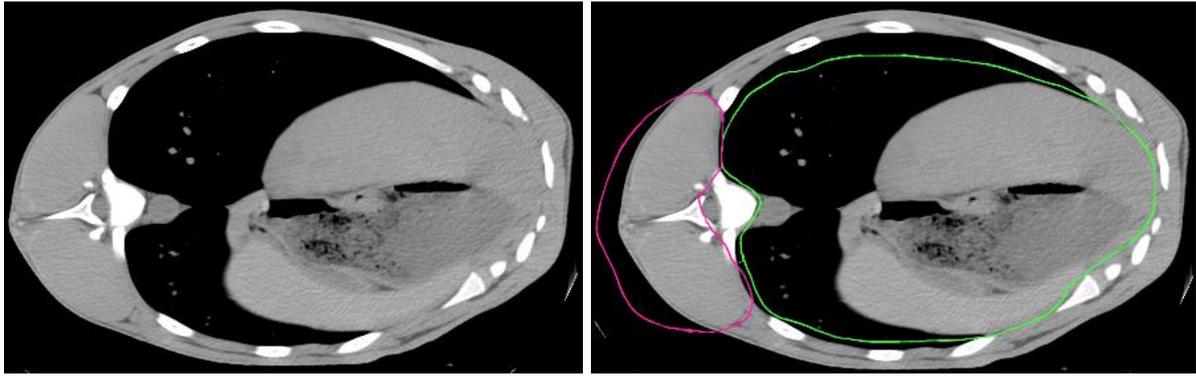
Image 19
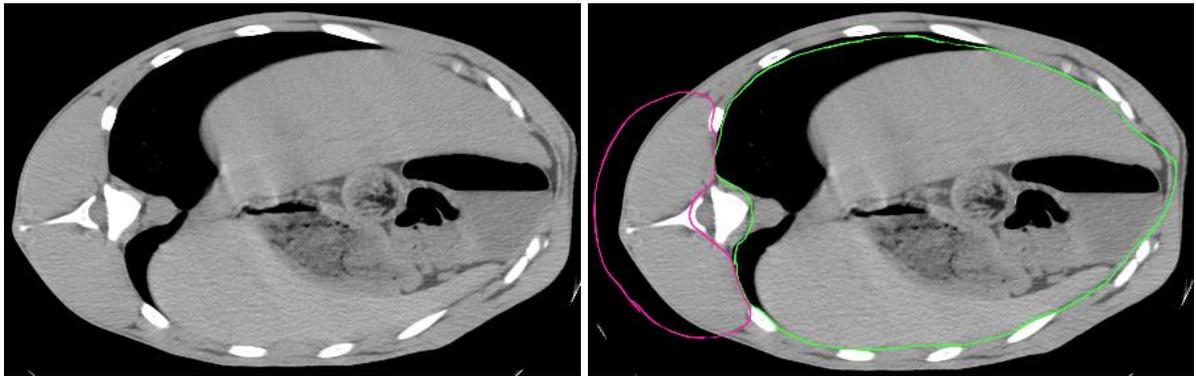
Image 20.
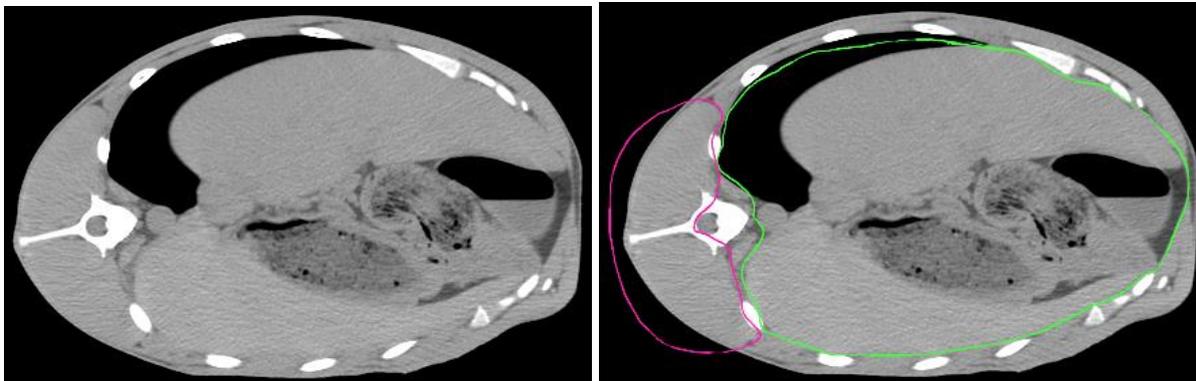
Image 21. Tenderloins becoming obvious.
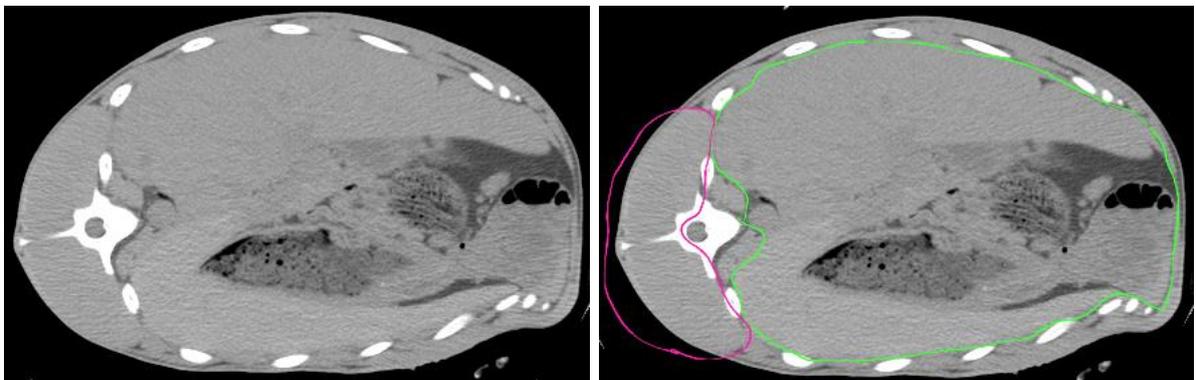
Image 22
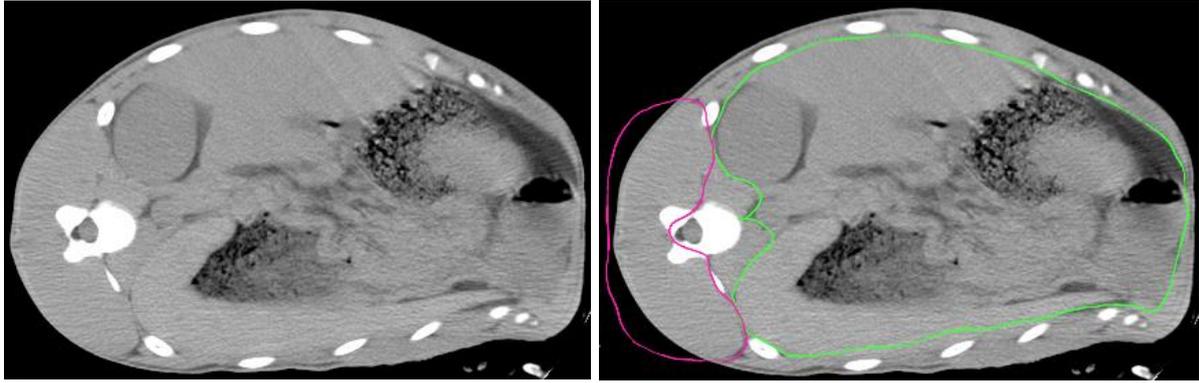
Image 23
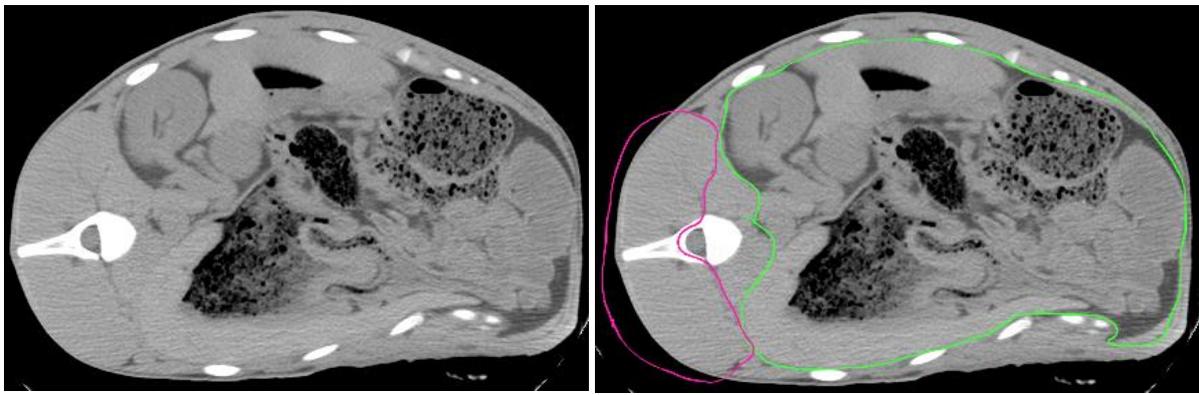
Image 24. Note the compression and warping of the rib cage where animal is lying
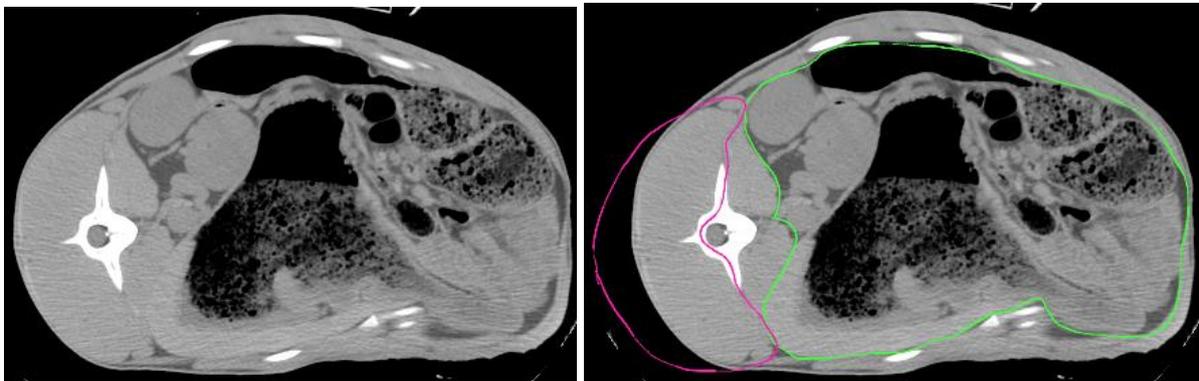
Image 25.
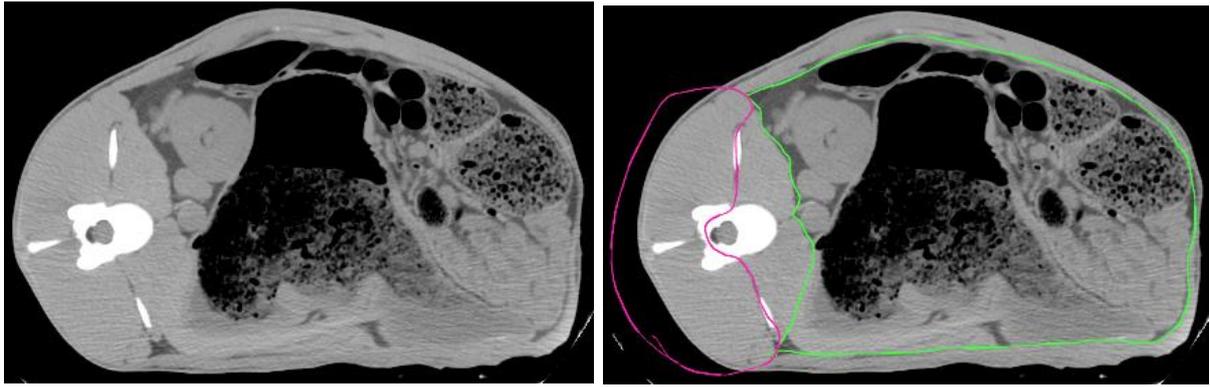
Image 26.
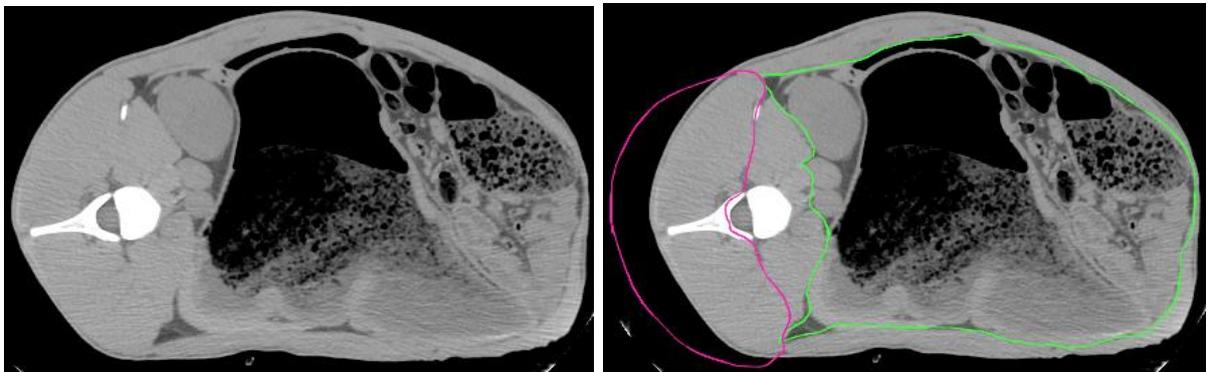
Image 27.
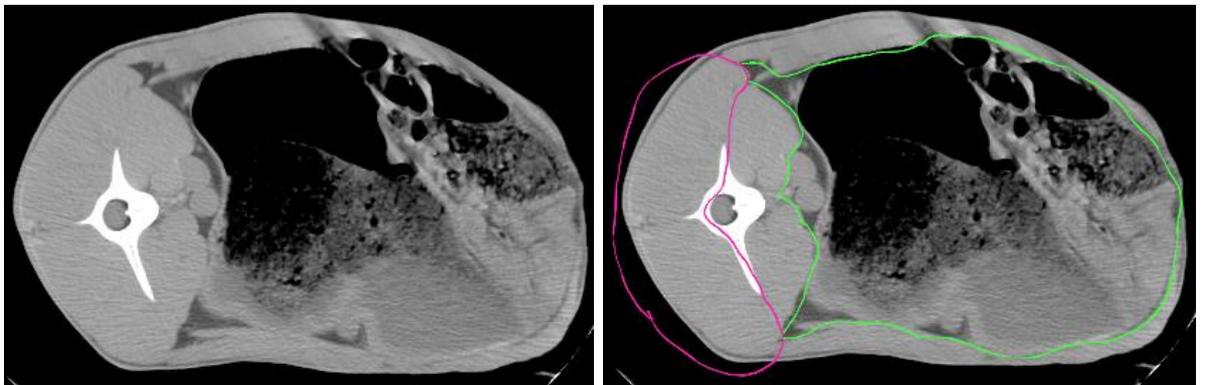
Image 28.
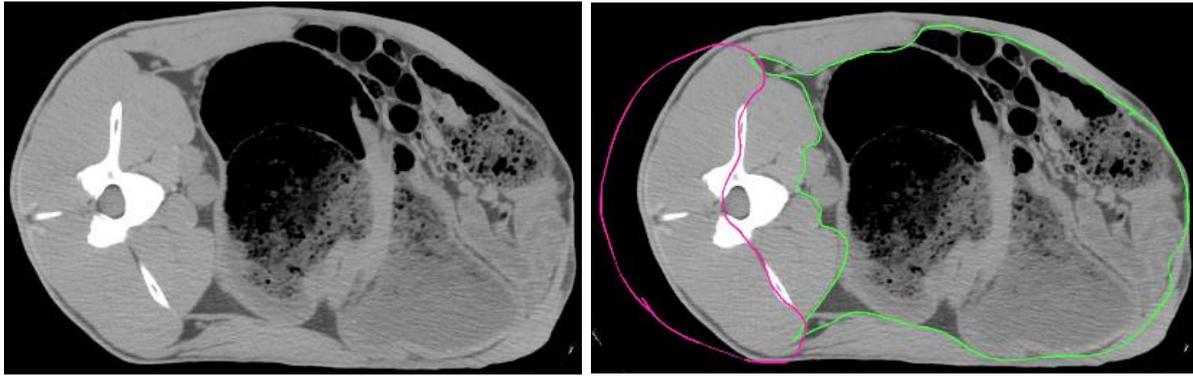
Image 29. Final loin image before hip bone becomes visible

Hind quarters – DPT included H-Bone weight, DEERLink did not

Specification: Entire leg joints are to be boned off the hip- or H-Bone and severed at the hip joint for primal weights (bone in and bone out).

There will also be further bone out of the primal leg into cap on boneless leg, then into four separate muscle groups: rump, topside, silverside and knuckle (which are standard cuts) these will be weighed **cap on**

Selecting CT images for the rear leg primal images

This is actually quite simple as there is a good obvious landmark where the leg ends and the loin (or middle) begins. This point is the anterior end of the ilium (or hip-bone/H-bone). The when the iliac crest is no longer visible is the first image of middles, and the last image where it appears is the last image of rear legs

Figure 3. Three sequential CT images from animal #1/13 from anterior to posterior showing differentiation points of loin primal start at image 29 and rear leg image end at image 30, iliac crest orange arrow, ilium green arrows

Image 29 first middle, no ilium

Image 30 iliac crest, last rear leg image

Image 31 ilium not iliac crest not last rear leg image

The rear leg primal cuts are boned-off the hip bone, but as we can define and trace the entire hip-bone through the cut we will include it in the primal. In the DSP we weighed the hip-bone as we did with the boned-off legs (bone in and then boned-out). There is still some middle (flap) present in leg images, again this is accounted for in the gutted (whole carcass) and does not contribute to the primal leg. Tails are cut off at the base of the rump before hot carcass weight and VIAscan imaging, which is why we remove them to that point as part of the gutting process for CT images. As the primal rear legs are such leg distinct components, many of the later images require no gutting or selection.

Areas to gut and remove are inside the green outlines, and areas to select for the primal are inside the pink outlines. Leave the bone marrow for rear leg primal cuts as it was weighed with the bones as for shoulders, but not loins.
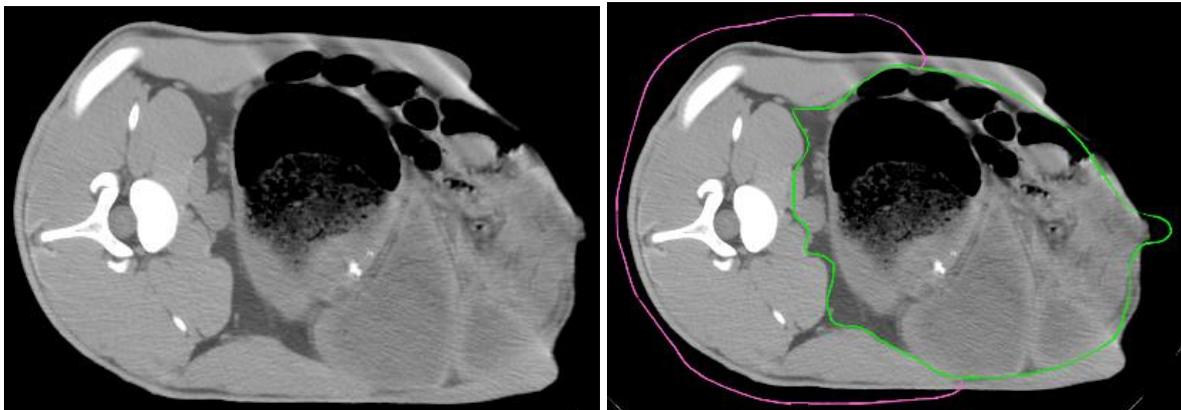
Image 30. First primal leg as ilium tip is visible. Gut essentially as for a middle, but leave the fat between the tenderloins and leg muscles, as this would not be trimmed off a whole leg.
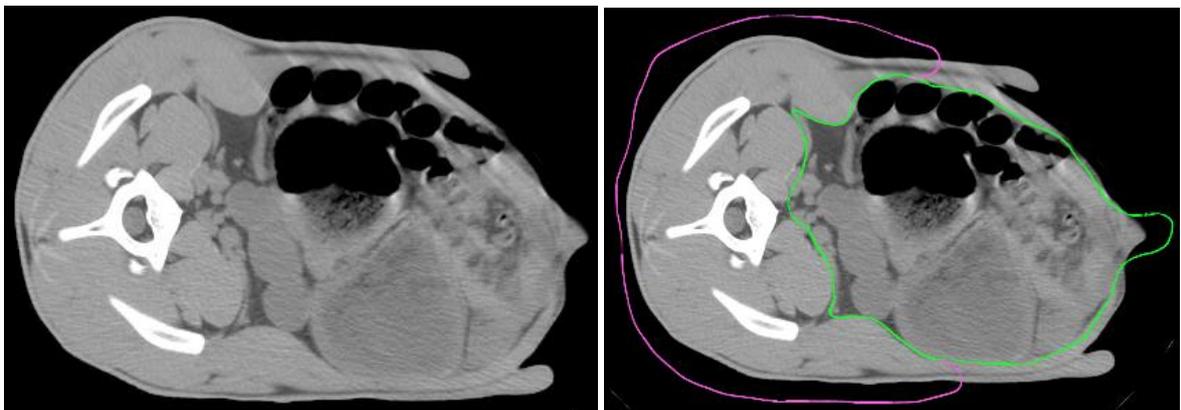
Image 31. Gut as previous image, remove blood vessels below tenderloins and remove pizzle. Retain flaps for whole carcass. Leg/flap area not well defined, be consistent between this and the previous image follow the general shape apparent in the next image.
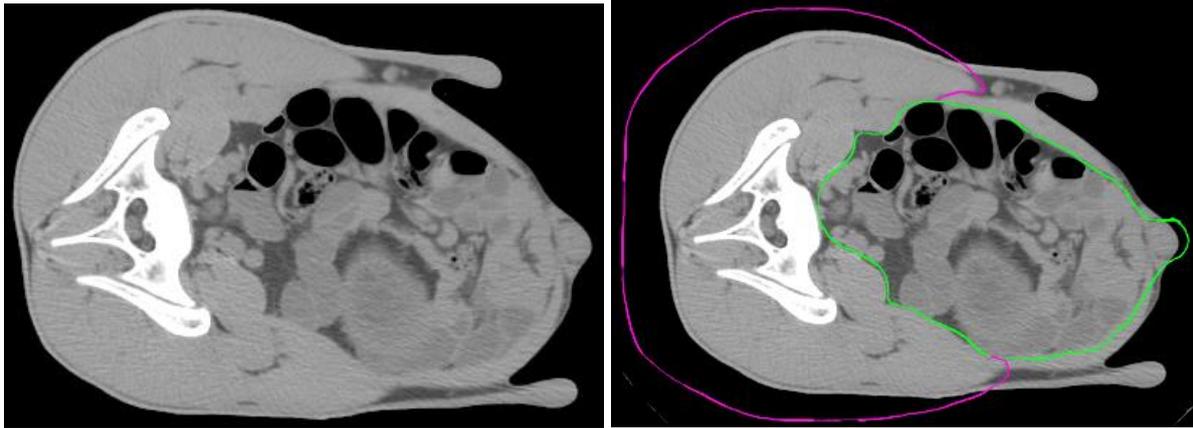
Image 32. Leg proper, leg/flap boundary now obvious.
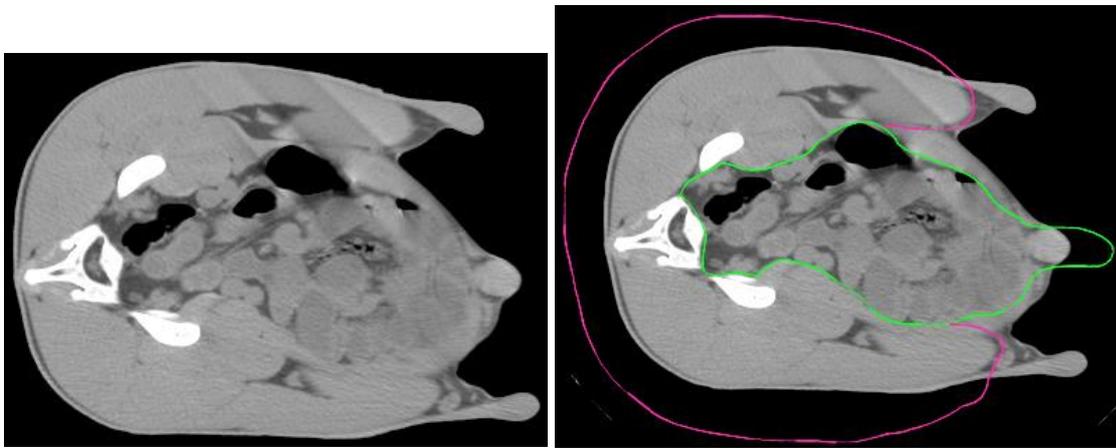
Image 33. As for previous, leave fat/lymph node cavity in leg, do not remove with gut
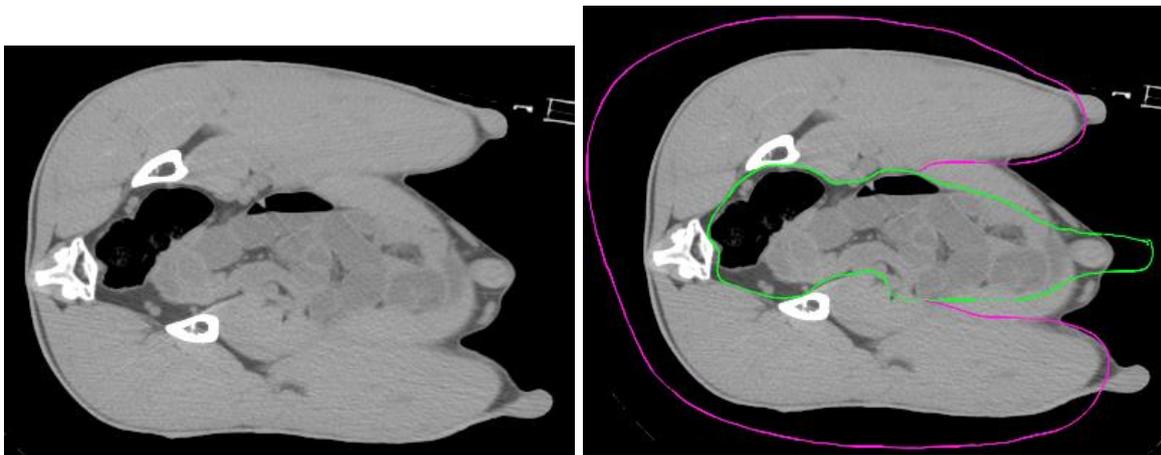
Image 34. Leave thick area of flap low down at gutting, but remove pizzle.
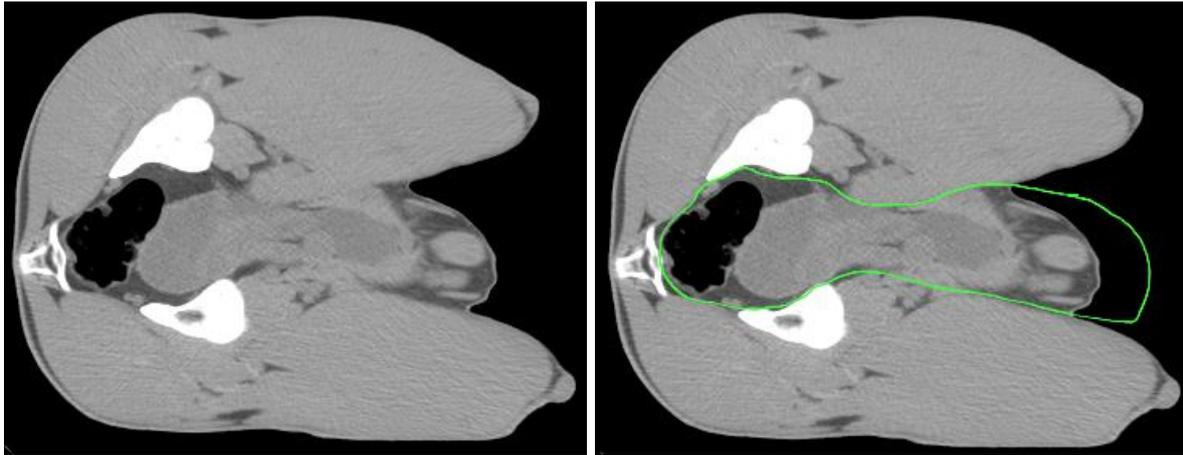
Image 35. Remove rectum, bladder, gut pizzle and testes.
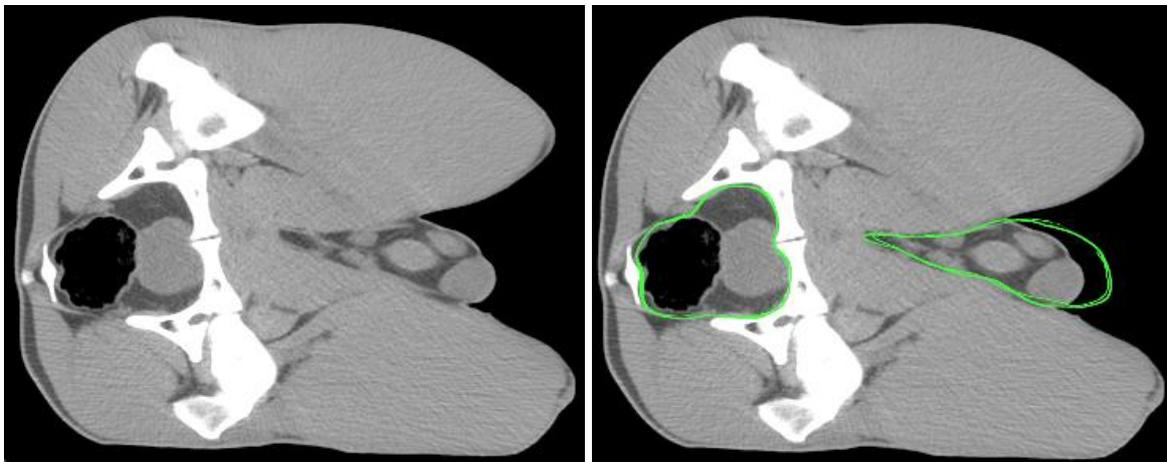
Image 36. Remove rectum, bladder, testes and pizzle. Leave first visible tail vertebrae (1st CV)
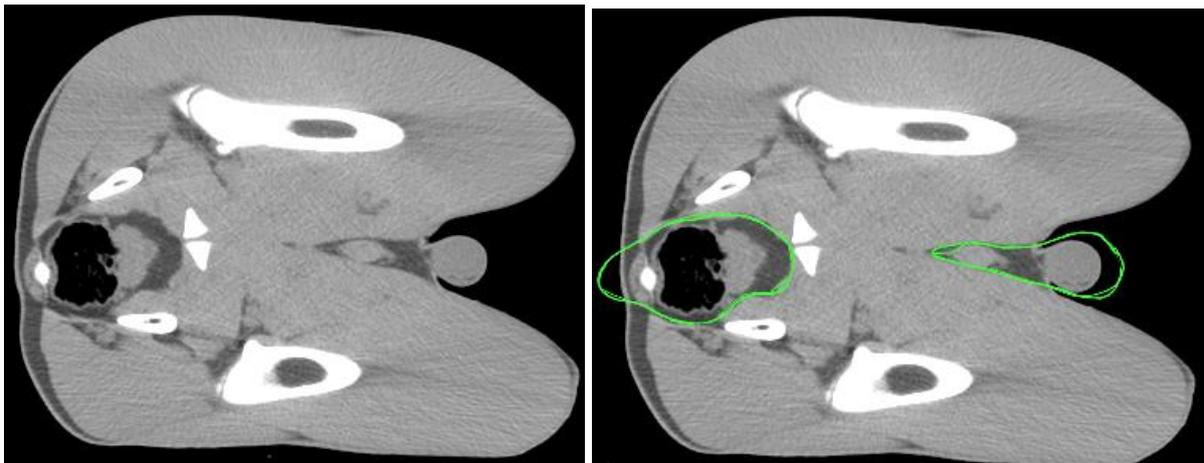
Image 37. Remove tail at, and, after this point.
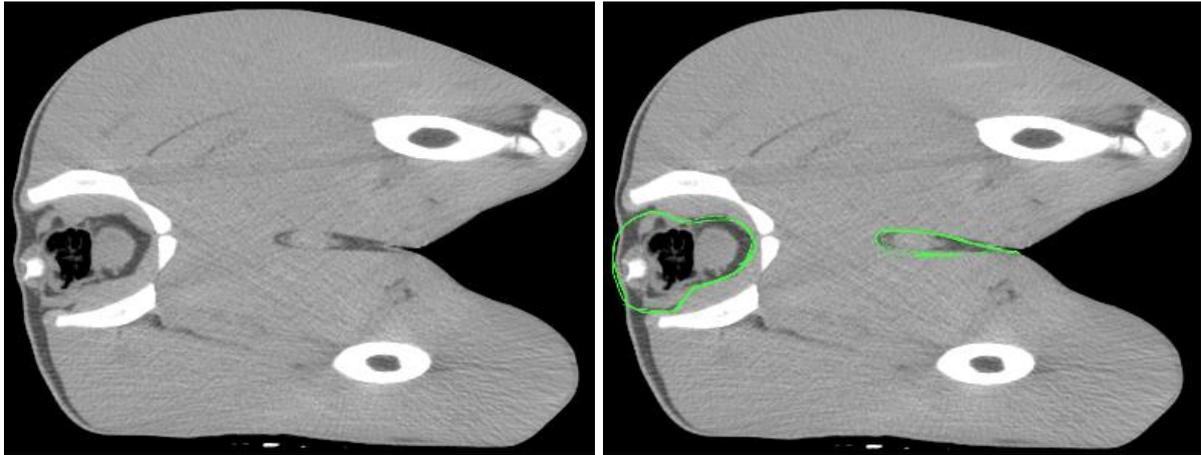
Image 38 As for previous, retain more fat to the sides of the tail than I have.
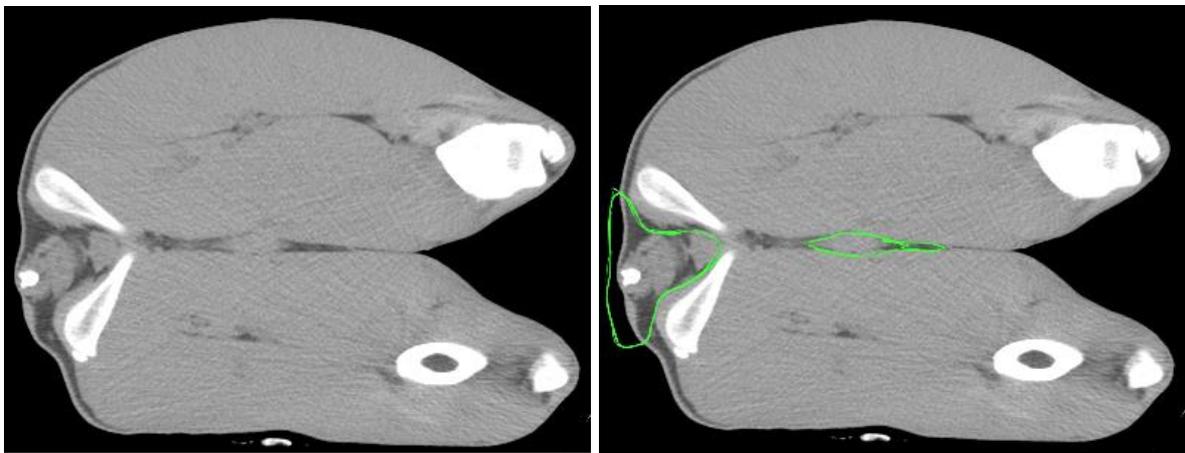
Image 39. Retain a little more fat around the tail than I have here. Remove pizzle.
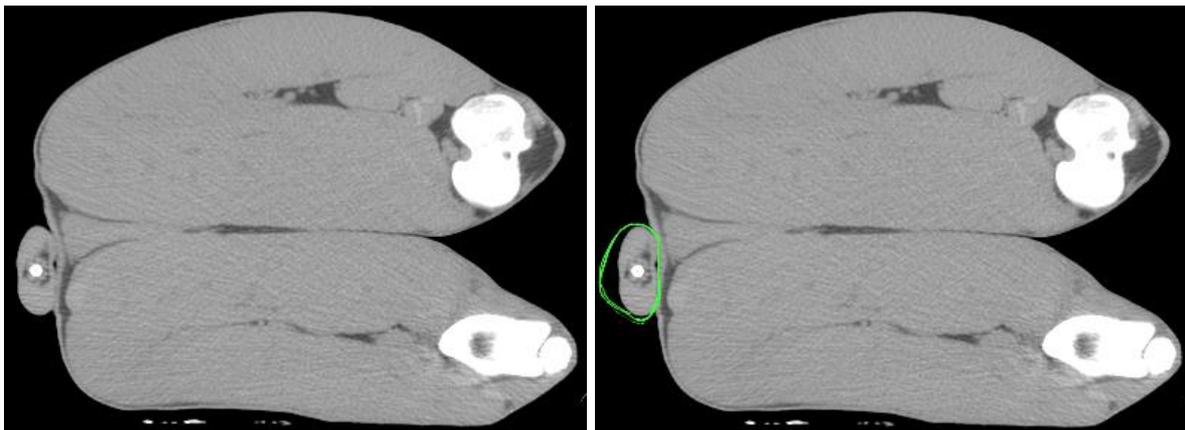
Image 40. Remove tail only
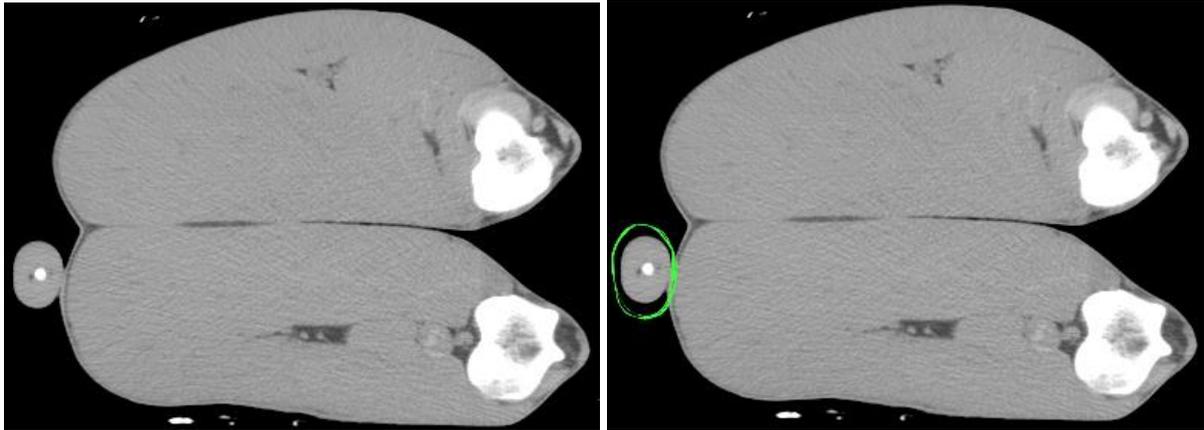
Image 41. Remove tail only
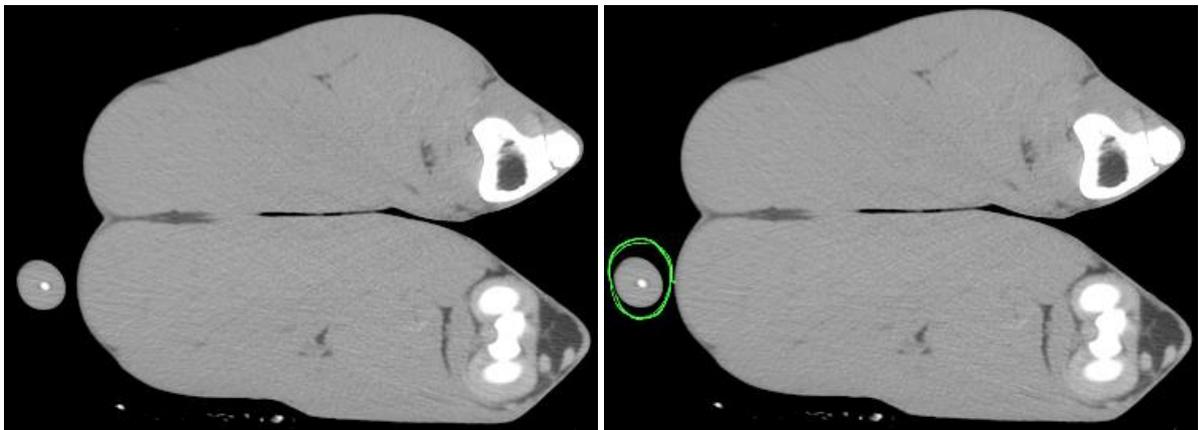
Image 42. As previous, last image in this set which requires gutting or selection.
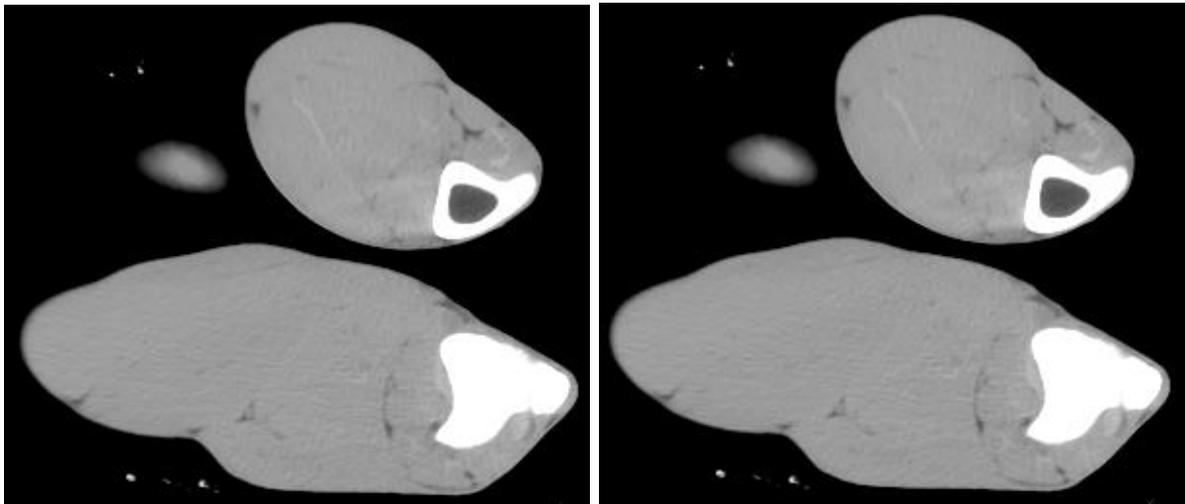
Image 43. Nothing required other than background tidy up – retain 3rd (small grey) blob
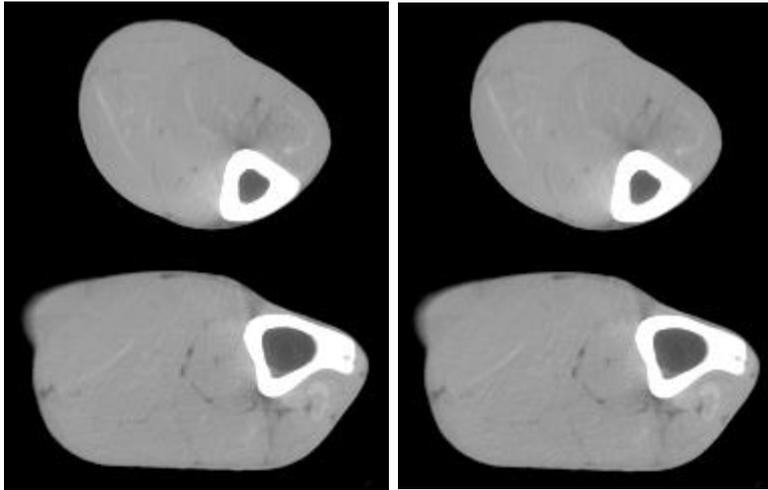
Image 44. Rear shanks - nothing required
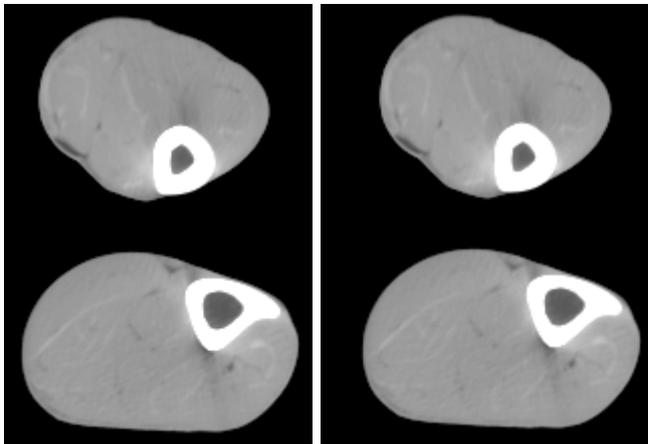
Image 45. Final image, rear shanks – nothing required

Figure 4. DPT primal joint areas on deer carcass hanging on a hook at DSP, this is approximately how the carcass is positioned for CT scanning also.
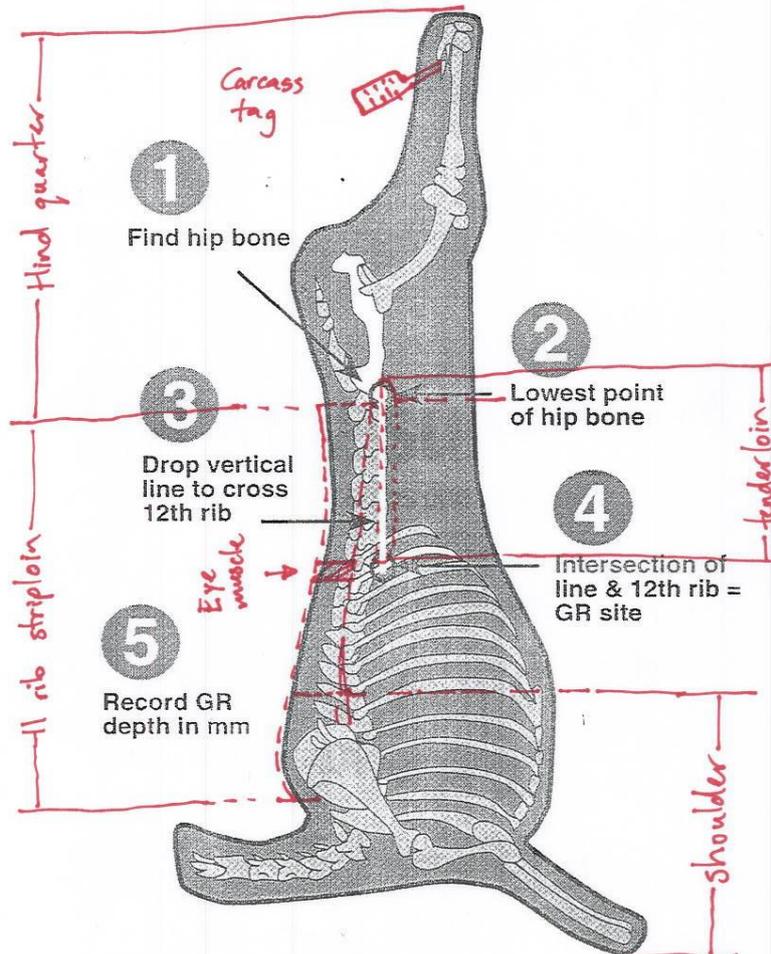
Appendix 3. Backward logistic regression models and outputs for the slaughter plant weights of boned-off tissue for the three deer carcass primal regions using individual images (slices) through the deer carcass every 30mm.

Primal Shoulder L&R Boned (T53):

1. fullmod=glm(t1 ~ c4L + c5L + c6L + c7L + T1L + T2L + T3L + T4L + T5L + T6L, data = d2)

    backwards=step(fullmod,trace=0) ##this suppresses step by step output
    summary(backwards)

    Call:
    glm(formula = t1 ~ c4L + c7L + T1L + T2L + T6L, data = d2)

    Deviance Residuals:
    ```
        Min      1Q    Median      3Q      Max
    -1.04864  -0.40538  -0.05532  0.34164  1.09676
    ```

    Coefficients:
    ```
             Estimate Std. Error t value Pr(>|t|)
    (Intercept) -3.586e+00  5.017e-01  -7.147  1.14e-10 ***
    c4L          3.988e-05  1.541e-05   2.589   0.01098 *
    c7L          4.460e-05  1.327e-05   3.360   0.00108 **
    T1L          6.866e-05  2.305e-05   2.979   0.00358 **
    T2L          7.450e-05  2.405e-05   3.098   0.00249 **
    T6L          7.047e-05  2.983e-05   2.362   0.01997 *
    ---
    Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
    ```

    (Dispersion parameter for gaussian family taken to be 0.2568277)

    ```
        Null deviance: 207.080  on 112  degrees of freedom
    Residual deviance:  27.481  on 107  degrees of freedom
      (8 observations deleted due to missingness)
    AIC: 174.91
    ```

    Number of Fisher Scoring iterations: 2

2. Order of significant slice: c7L T2L T1L c4L T6L
3. Fitting c7L first, then adding 1 slice at a time:
    Proportion of trait variation explained by fitting c7L T2L T1L c4L T6L in that order

	Df	SS	MS	F	Pr(>F)	%ofTotalVariation
c7L	1	129.2225	129.2225	176.9402	2.70E-25	59.78918
c7L	1	128.9602	128.9602	377.1137	2.11E-38	60.08725
T2L	1	45.6513	45.6513	133.4965	4.56E-21	21.27061
Total						81.35786
c7L	1	128.9602	128.9602	422.8736	1.71E-40	60.08725
T2L	1	45.6513	45.6513	149.6953	1.30E-22	21.27061
T1L	1	4.634527	4.634527	15.19709	1.63E-04	2.159395
Total						83.51725
c7L	1	129.1681	129.1681	482.4744	1.22E-41	62.37579
T2L	1	41.10025	41.10025	153.5195	1.81E-22	19.84748
T1L	1	4.083773	4.083773	15.25389	1.64E-04	1.972071
c4L	1	3.814583	3.814583	14.2484	2.62E-04	1.842078
Total						86.03742
c7L	1	129.1681	129.1681	502.9366	3.07E-42	62.37579
T2L	1	41.10025	41.10025	160.0304	5.57E-23	19.84748
T1L	1	4.083773	4.083773	15.90083	1.22E-04	1.972071
c4L	1	3.814583	3.814583	14.85269	1.99E-04	1.842078
T6L	1	1.4332	1.4332	5.580395	2.00E-02	0.692098
Total						86.72952

TotalLoinL&R (T57):

1. fullmod=glm(t2 ~ T2L + T3L + T4L + T5L + T6L + T7L + T8L + T9L + T10L + T11L + T12L + T13L + L1L + L2L + L3L + L4L , data = d1)

backwards=step(fullmod,trace=0) ##this suppresses step by step output
summary(backwards)

Call:
glm(formula = t2 ~ T2L + T6L + T7L + T10L + L2L + L3L, data = d1)

Deviance Residuals:
    Min   1Q   Median   3Q   Max
-0.78982 -0.24982 -0.00932 0.25833 0.83416

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.095e+00 3.449e-01 -3.175 0.001942 **
T2L   4.742e-05 1.391e-05   3.410 0.000908 ***
T6L   8.119e-05 2.807e-05   2.892 0.004600 **
T7L   -7.935e-05 3.232e-05 -2.455 0.015625 *
T10L   5.512e-05 2.968e-05   1.857 0.065921 .
L2L   7.791e-05 2.550e-05   3.055 0.002821 **
L3L   1.880e-05 1.360e-05   1.383 0.169565

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 0.1305006)

Null deviance: 57.084 on 117 degrees of freedom
Residual deviance: 14.486 on 111 degrees of freedom
AIC: 103.36

Number of Fisher Scoring iterations: 2
2. Order of significant slice: T2L L2L T6L T7L T10L L3L
3. Forcing the model to take T12L first, then adding 1 slice at a time:
    Proportion of trait variation explained by fitting T12L T2L L2L T6L T7L T10L L3L in that
    order

	Df	SS	MS	F	Pr(>F)	%ofTotalVariation
T12L	1	31.48311	31.48311	142.6506	6.26E-22	55.15186
T12L	1	31.48311	31.48311	186.6915	7.72E-26	55.15186
T2L	1	6.208024	6.208024	36.81291	1.71E-08	10.87517
Total						66.02703
T12L	1	31.48311	31.48311	220.1868	2.17E-28	55.15186
T2L	1	6.208024	6.208024	43.41772	1.43E-09	10.87517
L2L	1	3.093135	3.093135	21.63279	8.95E-06	5.418529
Total						71.44556
T12L	1	31.48311	31.48311	224.1511	1.37E-28	55.15186
T2L	1	6.208024	6.208024	44.19942	1.10E-09	10.87517
L2L	1	3.093135	3.093135	22.02227	7.61E-06	5.418529
T6L	1	0.428736	0.428736	3.052481	8.33E-02	0.751056
Total						72.19661
T12L	1	31.48311	31.48311	232.538	4.27E-29	55.15186
T2L	1	6.208024	6.208024	45.85321	6.17E-10	10.87517
L2L	1	3.093135	3.093135	22.84627	5.37E-06	5.418529
T6L	1	0.428736	0.428736	3.166695	7.79E-02	0.751056
T7L	1	0.707823	0.707823	5.228065	2.41E-02	1.239958
Total						73.43657
T12L	1	31.48311	31.48311	237.22	2.53E-29	55.15186
T2L	1	6.208024	6.208024	46.77643	4.55E-10	10.87517
L2L	1	3.093135	3.093135	23.30626	4.45E-06	5.418529
T6L	1	0.428736	0.428736	3.230453	7.50E-02	0.751056
T7L	1	0.707823	0.707823	5.333328	2.28E-02	1.239958
T10L	1	0.431998	0.431998	3.255032	7.39E-02	0.75677
Total						74.19334
T12L	1	31.48311	31.48311	239.119	2.36E-29	55.15186
T2L	1	6.208024	6.208024	47.15087	4.09E-10	10.87517
L2L	1	3.093135	3.093135	23.49283	4.14E-06	5.418529
T6L	1	0.428736	0.428736	3.256313	7.39E-02	0.751056
T7L	1	0.707823	0.707823	5.376021	2.23E-02	1.239958
T10L	1	0.431998	0.431998	3.281088	7.28E-02	0.75677
L3L	1	0.248653	0.248653	1.888553	1.72E-01	0.435587
Total						74.62893

HindLeg_L&R_Boned (T94):

1. fullmod=glm(t3 ~ L5L +L6L + S1L + S2L +   S3L + S4L + S5L + S6L +S7L, data = d2)

backwards=step(fullmod,trace=0) ##this suppresses step by step output
summary(backwards)

Call:
glm(formula = t3 ~ L5L + S1L + S2L + S3L + S4L + S5L + S7L, data = d2)

Deviance Residuals:
    Min   1Q   Median   3Q   Max
-1653.4   -324.5   -116.0   456.5   1231.8

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -3.837e+03 1.157e+03 -3.316 0.00179 **
L5L   9.301e-02 6.753e-02   1.377 0.17510
S1L   2.544e-01 9.746e-02   2.610 0.01217 *
S2L   -1.770e-01 7.782e-02 -2.275 0.02762 *
S3L   9.996e-02 7.534e-02   1.327 0.19109
S4L   -1.695e-01 6.546e-02 -2.589 0.01284 *
S5L   9.121e-02 4.671e-02   1.953 0.05694 .
S7L   2.595e-01 4.059e-02   6.393 7.43e-08 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 429251.4)

    Null deviance: 234673147 on 53 degrees of freedom
Residual deviance: 19745563 on 46 degrees of freedom
AIC: 862.96

Number of Fisher Scoring iterations: 2
2. Order of significant slice: S7L S1L S4L S2L S5L L5L S3L
3. Fitting S7L first, then adding 1 slice at a time:
   Proportion of trait variation explained by fitting S7L S1L S4L S2L S5L L5L S3L in that order

	Df	SS	MS	F	Pr(>F)	%ofTotalVariation
S7L	1	2.02E+08	2.02E+08	326.4002	4.59E-24	86.25793
S7L	1	2.02E+08	2.02E+08	359.4602	9.51E-25	86.25793
S1L	1	3529111	3529111	6.266913	1.55E-02	1.503841
Total						87.76178
S7L	1	2.02E+08	2.02E+08	431.6446	3.01E-26	86.25793
S1L	1	3529111	3529111	7.525393	8.42E-03	1.503841
S4L	1	5271810	5271810	11.24148	1.53E-03	2.246448
Total						90.00822
S7L	1	2.02E+08	2.02E+08	454.2506	1.96E-26	86.25793
S1L	1	3529111	3529111	7.91951	7.02E-03	1.503841
S4L	1	5271810	5271810	11.83022	1.20E-03	2.246448
S2L	1	1612522	1612522	3.618583	6.30E-02	0.687135
Total						90.69536
S7L	1	2.02E+08	2.02E+08	462.8437	2.69E-26	86.25793
S1L	1	3529111	3529111	8.069325	6.59E-03	1.503841
S4L	1	5271810	5271810	12.05401	1.10E-03	2.246448
S2L	1	1612522	1612522	3.687036	6.08E-02	0.687135
S5L	1	842745.7	842745.7	1.926941	1.72E-01	0.359115
Total						91.05447
S7L	1	2.02E+08	2.02E+08	464.0641	5.36E-26	86.25793
S1L	1	3529111	3529111	8.090601	6.57E-03	1.503841
S4L	1	5271810	5271810	12.0858	1.10E-03	2.246448
S2L	1	1612522	1612522	3.696758	6.06E-02	0.687135
S5L	1	842745.7	842745.7	1.932022	1.71E-01	0.359115
L5L	1	491403.9	491403.9	1.126559	2.94E-01	0.209399
Total						91.26387
S7L	1	2.02E+08	2.02E+08	471.575	8.12E-26	86.25793
S1L	1	3529111	3529111	8.221548	6.23E-03	1.503841
S4L	1	5271810	5271810	12.28141	1.03E-03	2.246448
S2L	1	1612522	1612522	3.75659	5.88E-02	0.687135
S5L	1	842745.7	842745.7	1.963292	1.68E-01	0.359115
L5L	1	491403.9	491403.9	1.144793	2.90E-01	0.209399
S3L	1	755782.3	755782.3	1.760699	1.91E-01	0.322057
Total						91.58593