



1      **Fig. 1**

2      Dimensional measurements, lengths, widths and areas of back and side views of the  
3      carcasses obtained by VIA.

4      <sup>a</sup> straight line through the centre of gravity

5      <sup>b</sup> orthogonal to the centre of gravity

6      <sup>c</sup> vertical in a 90 degree angle to the dividing line

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1    **Table 1**

2    Means, phenotypic standard deviations (SD) and heritabilities ( $h^2$ ) for cold carcass  
3    weight, EUROP scores and primals joint weights.

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Trait	Abbreviation	Mean	SD	$h^2$	s.e.
Cold carcass weight	CCW	18.80	2.42	0.19	0.10
MLC scores					
Conformation (1-5)	CONF	2.92	0.47	0.10	0.07
Fat class (4-20)	FAT	10.4	1.92	0.10	0.07
Predicted primal joint weights (kg)					
Leg primal joint	LEG	4.29	0.52	0.17	0.08
Chump primal joint	CHUMP	0.71	0.09	0.06	0.06
Loin primal joint	LOIN	2.83	0.37	0.05	0.05
Breast primal joint	BREAST	1.43	0.21	0.06	0.06
Shoulder primal joint	SHOULDER	4.77	0.64	0.09	0.07

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1   **Table 2**

2   Means, phenotypic standard deviations (SD) and heritabilities ( $h^2$ ) for the VIA  
 3   dimensional measurements.

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Trait	Abbreviation	Mean	SD	$h^2$	s.e.
VIA lengths (cm)					
Length legs to shoulders	L1	77.32	3.67	0.25	0.10
Length hock to legs	L2	21.73	1.47	0.44	0.13
Total length hock to shoulder <sup>a</sup>	L3	93.40	3.73	0.46	0.11
Half length of tibia to shoulder	L4	79.57	3.23	0.36	0.12
VIA widths (cm)					
Maximum shoulder width	W1	19.05	1.35	0.23	0.10
Minimum breast width	W2	15.92	1.00	0.36	0.11
Maximum breast width	W3	22.08	1.35	0.38	0.12
Minimum waist width	W4	19.26	0.94	0.34	0.11
Maximum legs widths	W5	23.38	0.75	0.39	0.10
Maximum breast width <sup>b</sup>	W6	25.53	1.86	0.23	0.08
Minimum waist width <sup>b</sup>	W7	12.87	0.77	0.27	0.10
Maximum legs widths <sup>b</sup>	W8	15.76	1.15	0.20	0.10
VIA areas (cm <sup>2</sup> )					
Back area of the carcass minus legs	A1	153.62	11.67	0.34	0.10
Back area of the legs	A2	19.36	1.79	0.53	0.15
Side area of the hind legs <sup>b</sup>	A3	48.36	4.11	0.25	0.09
Side area of the saddle <sup>c</sup>	A4	65.06	5.95	0.23	0.09

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6   <sup>a</sup> straight line through the centre of gravity

7   <sup>b</sup> orthogonal to the centre of gravity

8   <sup>c</sup> vertical in a 90 degree angle to the dividing line

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1 **Table 3**

2 Estimates of phenotypic (above) and genetic (below) correlations (standard errors) for  
 3 primal joint weights estimated using MLC-CF on crossbred lambs<sup>a</sup>

Trait <sup>b</sup>	LEG	CHUMP	LOIN	BREAST	SHOULDER	CCW <sup>c</sup>
LEG		0.91	0.84	0.86	0.93	0.91
CHUMP	0.98 (0.11)		0.98	0.99	0.98	0.98
LOIN	0.92 (0.18)	0.97 (0.04)		0.99	0.96	0.97
BREAST	0.84 (0.16)	0.97 (0.03)	0.99 (0.01)		0.97	0.98
SHOULDER	0.93 (0.06)	*	0.99 (0.07)	0.98 (0.04)		0.99
CCW	0.95 (0.05)	0.98 (0.01)	0.98 (0.06)	0.99 (0.03)	0.99 (0.01)	

4 <sup>a</sup> Standard errors for phenotypic correlations are less than 0.07

5 <sup>b</sup> At constant age

6 <sup>c</sup> Cold carcass weight

7 \* Out of parameter space

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1 **Table 4**

2 Genetic ( $r_g$ , with standard errors, s.e.) and phenotypic<sup>a</sup> ( $r_p$ ) correlations between VIA  
 3 dimensional measurements and EUROP scores<sup>b</sup>

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	CONF		FAT	
	$r_g$ (s.e.)	$r_p$	$r_g$ (s.e.)	$r_p$
L1	-0.27 (0.51)	-0.10	-0.04 (0.45)	0.18
L2	<b>-0.78 (0.24)</b>	-0.41	-0.55 (0.32)	-0.23
L3	<b>-0.65 (0.30)</b>	-0.04	-0.46 (0.38)	0.09
L4	<b>-0.76 (0.23)</b>	-0.12	-0.62 (0.33)	0.01
W1	0.12 (0.58)	0.20	0.09 (0.48)	0.23
W2	-0.44 (0.58)	0.26	-0.18 (0.66)	0.40
W3	0.63 (0.38)	0.24	-0.37 (0.43)	0.23
W4	0.81 (0.42)	0.28	0.26 (0.41)	0.27
W5	0.40 (0.47)	0.32	-0.39 (0.41)	0.22
W6	-0.17 (0.58)	0.09	0.24 (0.48)	0.17
W7	0.70 (0.51)	0.51	0.29 (0.43)	0.34
W8	-0.15 (0.59)	0.18	0.33 (0.43)	0.38
A1	0.07 (0.53)	0.27	-0.16 (0.47)	0.34
A2	<b>-0.80 (0.18)</b>	-0.28	<b>-0.73 (0.25)</b>	-0.16
A3	-0.43 (0.48)	0.20	-0.10 (0.52)	0.33
A4	-0.33 (0.46)	0.09	0.11 (0.43)	0.22
CCW	-0.22 (0.58)	0.35	-0.06 (0.51)	0.48

5 <sup>a</sup> Standard errors for phenotypic correlations are less than 0.05

6 <sup>b</sup> Significant genetic correlations in bold

1 **Table 5**2 Phenotypic<sup>a</sup> (above the diagonal) and genetic correlations<sup>b</sup> with standard errors (below diagonal) between VIA dimensional measurements

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	L1	L2	L3	L4	W1	W2	W3	W4	W5	W6	W7	W8	A1	A2	A3	A4	CCW
L1		0.20	0.68	0.66	0.08	0.20	0.35	0.30	0.53	0.47	0.37	0.24	0.82	0.29	0.42	0.58	0.64
L2	<b>0.68 (0.21)</b>		0.52	0.58	0.03	-0.05	-0.05	-0.08	-0.05	0.28	0.05	-0.05	0.27	0.87	0.22	0.49	0.08
L3	<b>0.95 (0.05)</b>	<b>0.69 (0.14)</b>		0.97	0.30	0.31	0.41	0.30	0.58	0.66	0.62	0.25	0.78	0.68	0.86	0.90	0.07
L4	<b>0.90 (0.07)</b>	<b>0.83 (0.09)</b>	<b>0.98 (0.01)</b>		0.25	0.23	0.35	0.21	0.35	0.58	0.25	0.20	0.68	0.65	0.70	0.81	0.65
W1	0.40 (0.30)	0.48 (0.30)	0.27 (0.28)	0.13 (0.27)		0.76	0.34	0.42	0.48	0.16	0.34	0.35	0.49	0.19	0.42	0.33	0.47
W2	-0.12 (0.40)	0.22 (0.35)	<b>0.51 (0.17)</b>	-0.57 (0.29)	<b>0.65 (0.19)</b>		0.52	0.52	0.61	0.20	0.47	0.43	0.75	0.09	0.50	0.33	0.56
W3	0.21 (0.31)	0.11 (0.30)	0.28 (0.23)	0.16 (0.22)	0.00 (0.23)	-0.22 (0.32)		0.72	0.41	0.26	0.14	0.17	0.76	0.03	0.25	0.37	0.43
W4	0.47 (0.34)	-0.05 (0.28)	0.31 (0.25)	0.23 (0.23)	0.19 (0.27)	-0.13 (0.34)	<b>0.80 (0.09)</b>		0.52	0.20	0.28	0.25	0.67	-0.01	0.30	0.31	0.49
W5	<b>0.55 (0.25)</b>	<b>0.52 (0.24)</b>	<b>0.42 (0.16)</b>	0.16 (0.21)	<b>0.78 (0.12)</b>	<b>0.47 (0.17)</b>	-0.04 (0.22)	0.30 (0.23)		0.20	0.59	0.43	0.80	0.23	0.68	0.52	0.76
W6	<b>0.72 (0.17)</b>	0.14 (0.25)	<b>0.81 (0.11)</b>	<b>0.71 (0.14)</b>	0.02 (0.36)	-0.51 (0.45)	0.11 (0.35)	0.25 (0.27)	-0.50 (0.24)		0.34	0.16	0.57	0.33	0.47	0.75	0.45
W7	<b>0.81 (0.23)</b>	-0.21 (0.32)	<b>0.90 (0.08)</b>	0.56 (0.31)	0.65 (0.27)	<b>0.82 (0.11)</b>	-0.04 (0.35)	0.55 (0.28)	<b>0.50 (0.18)</b>	<b>0.85 (0.24)</b>		0.48	0.65	0.14	0.81	0.70	0.65
W8	-0.10 (0.38)	-0.07 (0.29)	-0.06 (0.31)	-0.06 (0.35)	<b>0.74 (0.18)</b>	<b>0.76 (0.21)</b>	-0.51 (0.27)	0.04 (0.30)	0.33 (0.28)	0.04 (0.38)	0.20 (0.24)		0.42	0.05	0.72	0.62	0.60
A1	<b>0.82 (0.12)</b>	0.52 (0.25)	<b>0.91 (0.05)</b>	0.59 (0.21)	0.41 (0.31)	<b>0.82 (0.08)</b>	<b>0.59 (0.18)</b>	<b>0.75 (0.14)</b>	<b>0.61 (0.13)</b>	<b>0.68 (0.23)</b>	<b>0.98 (0.05)</b>	-0.24 (0.45)		0.30	0.80	0.62	0.49
A2	<b>0.59 (0.22)</b>	<b>0.95 (0.03)</b>	<b>0.89 (0.07)</b>	<b>0.91 (0.07)</b>	0.47 (0.29)	-0.14 (0.37)	-0.33 (0.23)	-0.42 (0.24)	0.11 (0.29)	-0.06 (0.33)	-0.19 (0.28)	-0.23 (0.33)	<b>0.54 (0.22)</b>		0.30	0.48	0.24
A3	<b>0.84 (0.15)</b>	0.49 (0.25)	<b>0.95 (0.04)</b>	<b>0.80 (0.15)</b>	0.31 (0.32)	<b>0.61 (0.17)</b>	-0.42 (0.25)	-0.08 (0.30)	<b>0.67 (0.21)</b>	0.34 (0.35)	<b>0.96 (0.04)</b>	0.50 (0.26)	<b>0.90 (0.06)</b>	0.49 (0.28)		0.78	0.70
A4	<b>0.96 (0.07)</b>	0.51 (0.21)	<b>0.90 (0.06)</b>	<b>0.82 (0.10)</b>	0.23 (0.33)	-0.64 (0.43)	0.22 (0.26)	0.47 (0.24)	<b>0.39 (0.19)</b>	<b>0.93 (0.11)</b>	<b>0.83 (0.15)</b>	<b>0.79 (0.13)</b>	<b>0.72 (0.16)</b>	0.41 (0.25)	<b>0.71 (0.17)</b>		0.81
CCW	0.98 (0.12)	<b>0.66 (0.28)</b>	0.65 (0.61)	<b>0.87 (0.15)</b>	<b>0.71 (0.22)</b>	0.01 (0.57)	0.28 (0.33)	<b>0.73 (0.19)</b>	<b>0.86 (0.10)</b>	<b>0.75 (0.23)</b>	<b>0.98 (0.01)</b>	0.15 (0.48)	<b>0.68 (0.20)</b>	<b>0.62 (0.28)</b>	<b>0.89 (0.12)</b>	<b>0.89 (0.13)</b>	

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5 <sup>a</sup> Standard errors for phenotypic correlations are less than 0.05.  
6 <sup>b</sup> Significant genetic correlations in bold